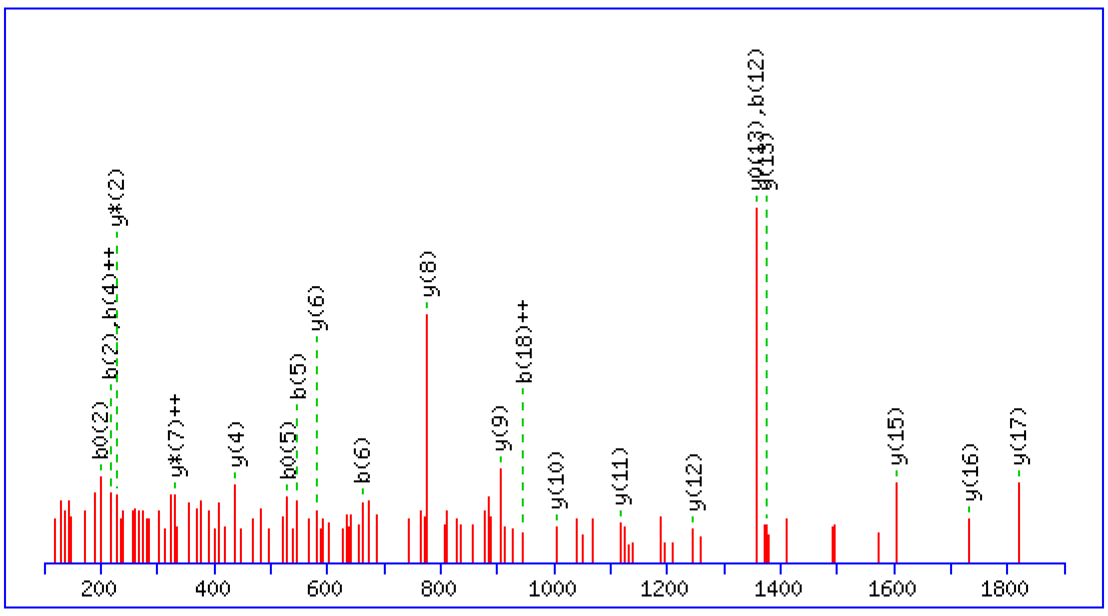
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTSEDIEELVEPVAAHGPK**
Found in **PSMD1_HUMAN**, 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2

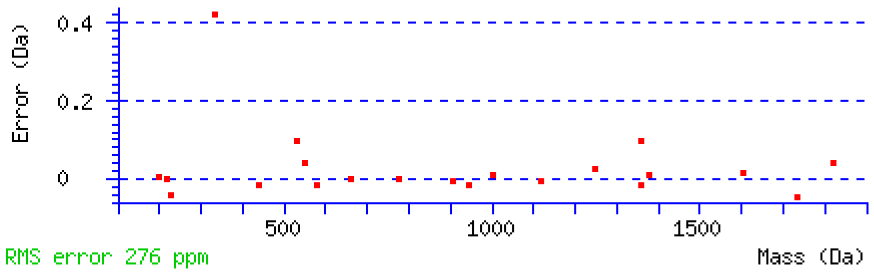
Match to Query 54930: 2034.985992 from(679.335940,3+) rtinseconds(3182) index(43174)
Title: Locus:1.1.1.2811.14
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

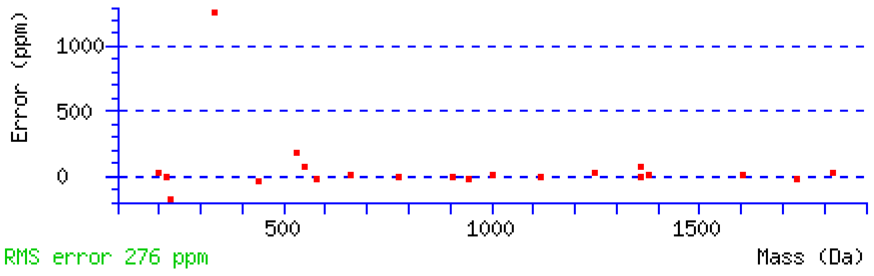
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2034.974564
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4.7e-005
Matches : 22/164 fragment ions using 44 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**							**19**
2	**217.081898**	109.044587	199.071333	100.039304	**T**	1920.954914	960.981095	1903.928365	952.467821	1902.944349	951.975813	**18**
3	304.113926	152.560601	286.103361	143.555319	**S**	***1819.907235***	910.457256	1802.880686	901.943981	1801.896670	901.451973	**17**
4	433.156519	217.081898	415.145954	208.076615	**E**	***1732.875207***	866.941242	1715.848658	858.427967	1714.864642	857.935959	**16**
5	**548.183462**	274.595369	530.172897	265.590087	**D**	***1603.832614***	802.419945	1586.806065	793.906671	1585.822049	793.414663	**15**
6	**661.267526**	331.137401	643.256961	322.132119	**I**	1488.805671	744.906474	1471.779122	736.393199	1470.795106	735.901191	**14**
7	790.310119	395.658698	772.299554	386.653415	**E**	***1375.721607***	688.364442	1358.695058	679.851167	1357.711042	679.359159	**13**
8	919.352712	460.179994	901.342147	451.174712	**E**	***1246.679014***	623.843145	1229.652465	615.329871	1228.668449	614.837863	**12**
9	1032.436776	516.722026	1014.426211	507.716744	**L**	***1117.636421***	559.321849	1100.609872	550.808574	1099.625856	550.316566	**11**
10	1131.505190	566.256233	1113.494625	557.250951	**V**	***1004.552357***	502.779817	987.525808	494.266542	986.541792	493.774534	**10**
11	1260.547783	630.777530	1242.537218	621.772247	**E**	***905.483943***	453.245610	888.457394	444.732335	887.473378	444.240327	**9**
12	**1357.600547**	679.303912	1339.589982	670.298629	**P**	***776.441350***	388.724313	759.414801	380.211039			**8**
13	1456.668961	728.838119	1438.658396	719.832836	**V**	679.388586	340.197931	662.362037	331.684657			**7**
14	1527.706075	764.356676	1509.695510	755.351393	**A**	***580.320172***	290.663724	563.293623	282.150449			**6**
15	1598.743189	799.875233	1580.732624	790.869950	**A**	509.283058	255.145167	492.256509	246.631892			**5**
16	1735.802101	868.404689	1717.791536	859.399406	**H**	***438.245944***	219.626610	421.219395	211.113335			**4**
17	1792.823565	896.915421	1774.813000	887.910138	**G**	301.187032	151.097154	284.160483	142.583879			**3**
18	1889.876329	945.441803	1871.865764	936.436520	**P**	244.165568	122.586422	227.139019	114.073148			**2**
19					**K**	147.112804	74.060040	130.086255	65.546765			**1**





NCBI **BLAST** search of DTSEDIEELVEPVAAHGPK
(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	2034.974564	0.011428	DTSEDIEELVEPVAAHGPK

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

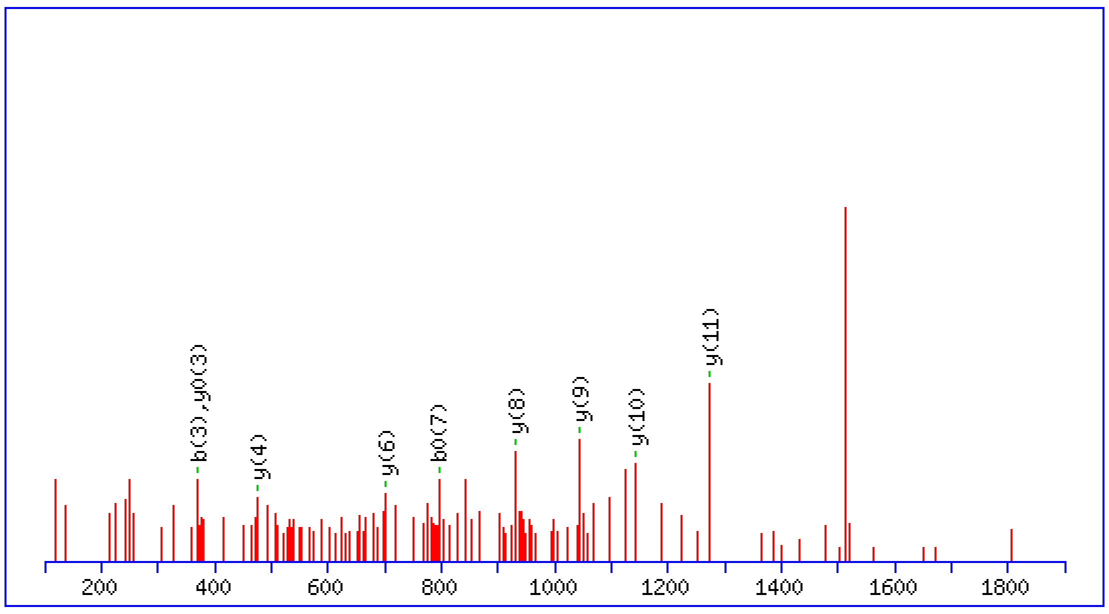
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEVIETLLSLEK**
Found in **PSD12_HUMAN**, 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3

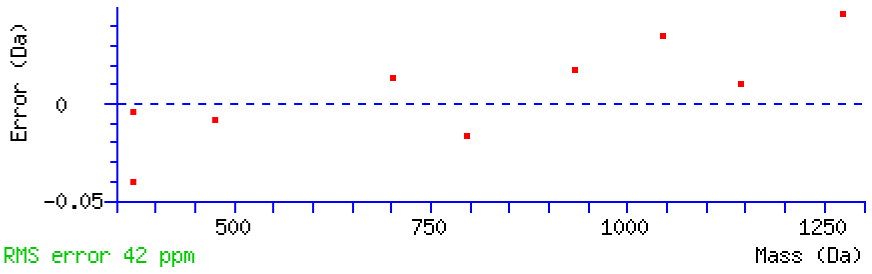
Match to Query 33424: 1513.863648 from(757.939100,2+) rtinseconds(4088) index(62740)
Title: Locus:1.1.1.3037.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

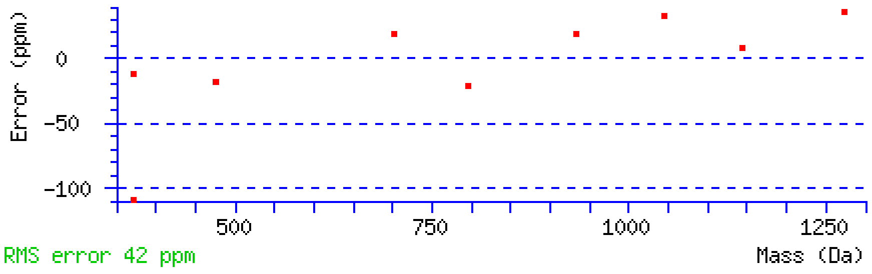
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1513.860291`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 30 Expect: 0.0038`
`Matches : 9/136 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	114.091340	57.549308					L							13
2	242.149918	121.578597	225.123369	113.065323			Q	1401.783538	701.395407	1384.756989	692.882133	1383.772973	692.390125	12
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***1273.724960***	637.366118	1256.698411	628.852844	1255.714395	628.360836	11
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	V	***1144.682367***	572.844822	1127.655818	564.331547	1126.671802	563.839539	10
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	I	***1045.613953***	523.310615	1028.587404	514.797340	1027.603388	514.305332	9
6	712.387582	356.697429	695.361033	348.184155	694.377017	347.692147	E	***932.529889***	466.768583	915.503340	458.255308	914.519324	457.763300	8
7	813.435261	407.221269	796.408712	398.707994	795.424696	398.215986	T	803.487296	402.247286	786.460747	393.734012	785.476731	393.242004	7
8	926.519325	463.763301	909.492776	455.250026	908.508760	454.758018	L	***702.439617***	351.723447	685.413068	343.210172	684.429052	342.718164	6
9	1039.603389	520.305333	1022.576840	511.792058	1021.592824	511.300050	L	589.355553	295.181415	572.329004	286.668140	571.344988	286.176132	5
10	1126.635417	563.821347	1109.608868	555.308072	1108.624852	554.816064	S	***476.271489***	238.639382	459.244940	230.126108	458.260924	229.634100	4
11	1239.719481	620.363379	1222.692932	611.850104	1221.708916	611.358096	L	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
12	1368.762074	684.884675	1351.735525	676.371401	1350.751509	675.879392	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 LQEVIETLLSLEK
(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	1513.860291	0.003357	LQEVIETLLSLEK

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

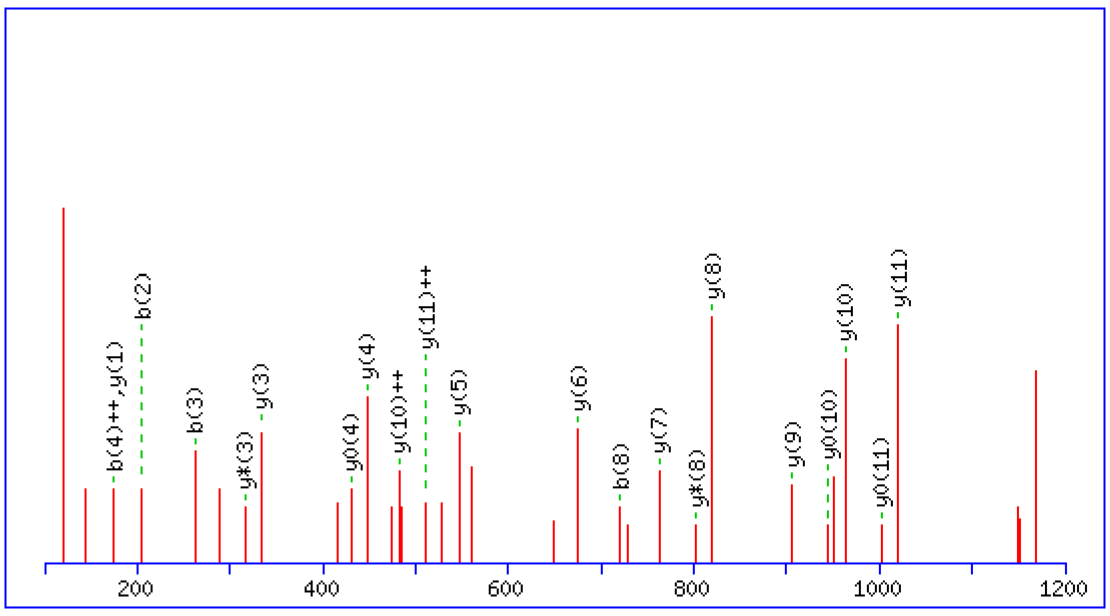
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGGSGSQVDSAR**
Found in **PSMD2_HUMAN**, 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3

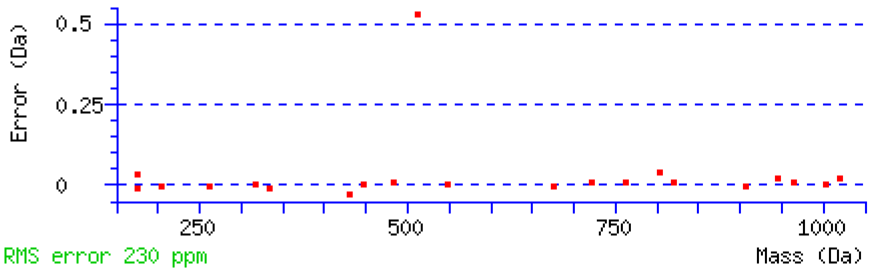
Match to Query 21548: 1166.532208 from(584.273380,2+) rtinseconds(1097) index(7310)
Title: Locus:1.1.1.1056.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

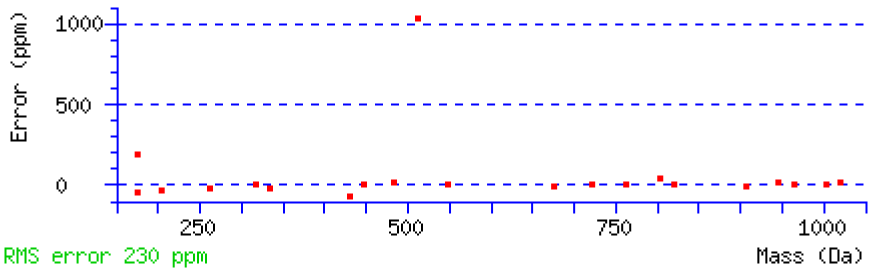
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1166.531631
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 87 **Expect:** 4.6e-008
Matches : 21/110 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							12
2	**205.097154**	103.052215					G	***1020.470477***	510.738877	1003.443928	502.225602	1002.459912	501.733594	11
3	**262.118618**	131.562947					G	***963.449013***	482.228144	946.422464	473.714870	945.438448	473.222862	10
4	349.150646	175.078961			331.140081	166.073679	S	***906.427549***	453.717413	889.401000	445.204138	888.416984	444.712130	9
5	406.172110	203.589693			388.161545	194.584410	G	***819.395521***	410.201398	802.368972	401.688124	801.384956	401.196116	8
6	493.204138	247.105707			475.193573	238.100425	S	***762.374057***	381.690667	745.347508	373.177392	744.363492	372.685384	7
7	621.262716	311.134996	604.236167	302.621722	603.252151	302.129714	Q	***675.342029***	338.174652	658.315480	329.661378	657.331464	329.169370	6
8	**720.331130**	360.669203	703.304581	352.155929	702.320565	351.663921	V	***547.283451***	274.145363	530.256902	265.632089	529.272886	265.140081	5
9	835.358073	418.182675	818.331524	409.669400	817.347508	409.177392	D	***448.215037***	224.611156	431.188488	216.097882	430.204472	215.605874	4
10	922.390101	461.698689	905.363552	453.185414	904.379536	452.693406	S	***333.188094***	167.097685	316.161545	158.584410	315.177529	158.092402	3
11	993.427215	497.217245	976.400666	488.703971	975.416650	488.211963	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 FGGSGSQVDSAR
(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	1166.531631	0.000577	FGGSGSQVDSAR
12.6	1166.529114	0.003094	FGHVYMGNSR
6.4	1166.538986	-0.006778	SCSPSAEFLR
5.7	1166.528442	0.003766	CLGMGRNSSR
4.3	1166.527588	0.004620	DRSGSSQSTSR
3.7	1166.535828	-0.003620	CLQMGMNRK
2.5	1166.521240	0.010968	SCWTVACQK
1.6	1166.535812	-0.003604	MAEMARCIR

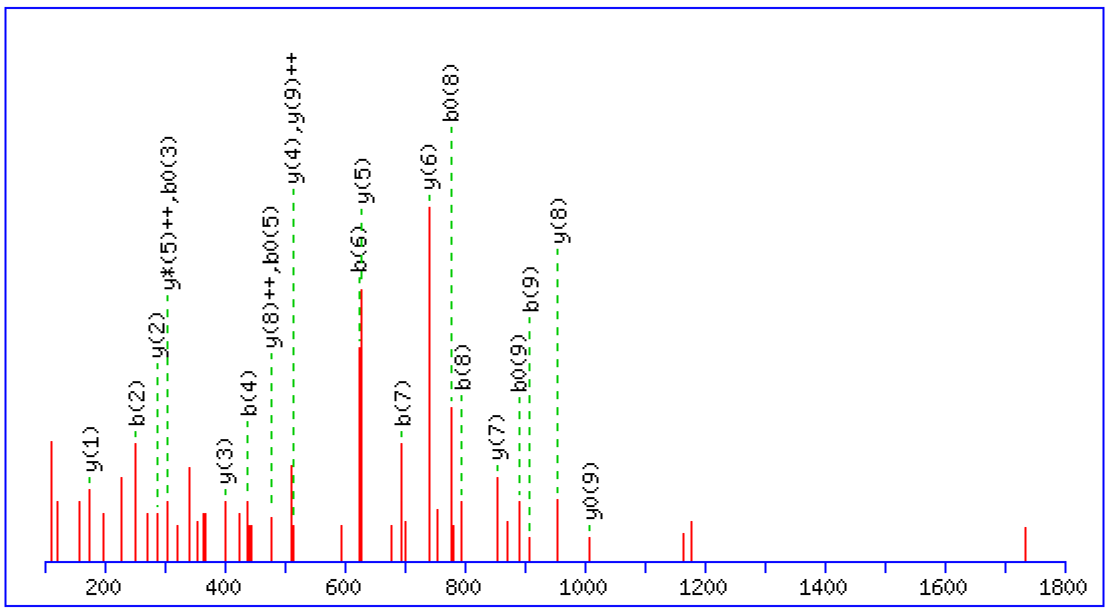
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HDADGQATLLNLLLR**
Found in **PSMD3_HUMAN**, 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2

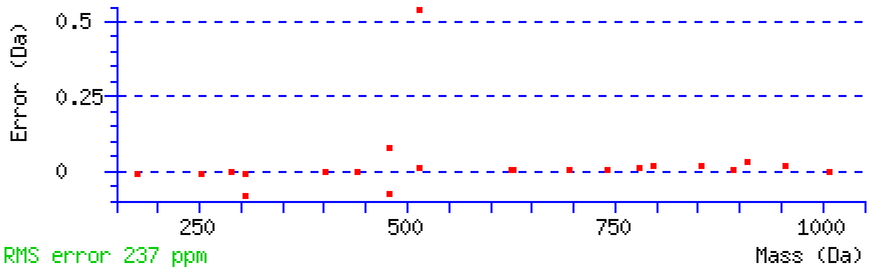
Match to Query 14222: 1648.896072 from(550.639300,3+) rtinseconds(3822) index(54250)
Title: Locus:1.1.1.2996.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

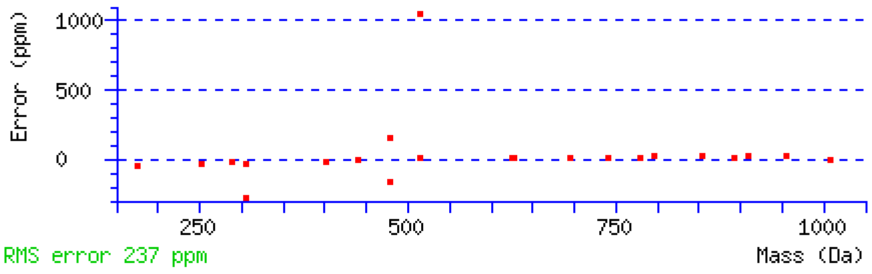
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1648.889648
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 5e-005
Matches : 22/142 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	138.066188	69.536732					H							15
2	***253.093131***	127.050203			235.082566	118.044921	D	1512.838034	756.922655	1495.811485	748.409381	1494.827469	747.917372	14
3	324.130245	162.568761			306.119680	153.563478	A	1397.811091	699.409183	1380.784542	690.895909	1379.800526	690.403901	13
4	***439.157188***	220.082232			421.146623	211.076950	D	1326.773977	663.890626	1309.747428	655.377352	1308.763412	654.885344	12
5	496.178652	248.592964			478.168087	239.587682	G	1211.747034	606.377155	1194.720485	597.863880	1193.736469	597.371872	11
6	***624.237230***	312.622253	607.210681	304.108979	606.226665	303.616971	Q	1154.725570	577.866423	1137.699021	569.353148	1136.715005	568.861140	10
7	***695.274344***	348.140810	678.247795	339.627536	677.263779	339.135528	A	1026.666992	513.837134	1009.640443	505.323859	1008.656427	504.831851	9
8	***796.322023***	398.664650	779.295474	390.151375	778.311458	389.659367	T	***955.629878***	478.318577	938.603329	469.805302	937.619313	469.313294	8
9	***909.406087***	455.206682	892.379538	446.693407	891.395522	446.201399	L	***854.582199***	427.794737	837.555650	419.281463			7
10	1022.490151	511.748714	1005.463602	503.235439	1004.479586	502.743431	L	***741.498135***	371.252705	724.471586	362.739431			6
11	1136.533078	568.770177	1119.506529	560.256903	1118.522513	559.764895	N	***628.414071***	314.710673	611.387522	306.197399			5
12	1249.617142	625.312209	1232.590593	616.798935	1231.606577	616.306927	L	***514.371144***	257.689210	497.344595	249.175935			4
13	1362.701206	681.854241	1345.674657	673.340967	1344.690641	672.848958	L	***401.287080***	201.147178	384.260531	192.633903			3
14	1475.785270	738.396273	1458.758721	729.882998	1457.774705	729.390990	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 HDADGQATLLNLLLR
(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	1648.889648	0.006424	HDADGQATLLNLLLR
2.0	1648.889648	0.006424	DGSASLLLPSRPAPPR
0.6	1648.885834	0.010238	MSSILPFTPPIVKR
0.5	1648.903580	-0.007508	KPPTGPLPPSKEPLK

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

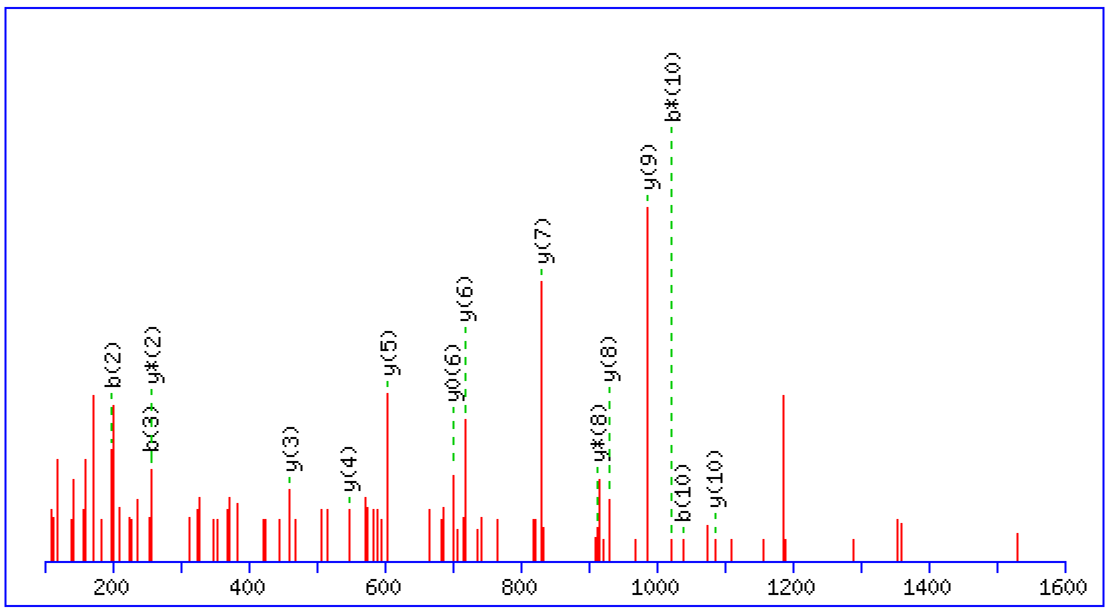
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGVLLGSWQK**
Found in **PSD7_HUMAN**, 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2

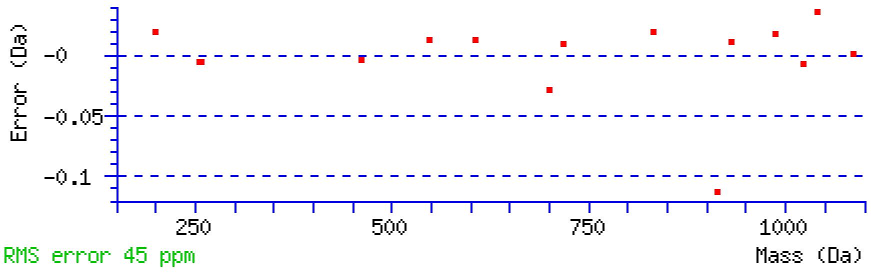
Match to Query 24818: 1184.700048 from(593.357300,2+) rtinseconds(3004) index(39377)
Title: Locus:1.1.1.2634.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

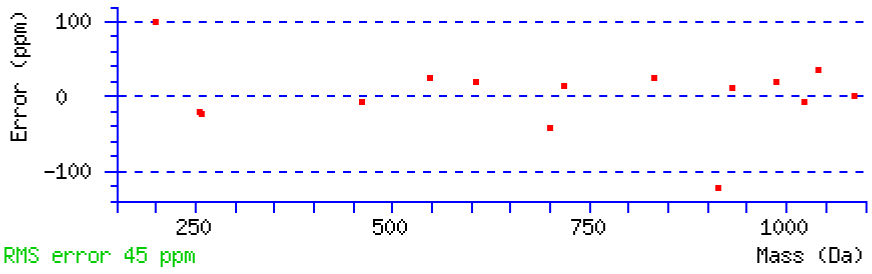
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1184.691757
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0004
Matches : 15/82 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	100.075690	50.541483					V							11
2	**199.144104**	100.075690					V	***1086.630607***	543.818942	1069.604058	535.305667	1068.620042	534.813659	10
3	**256.165568**	128.586422					G	***987.562193***	494.284735	970.535644	485.771460	969.551628	485.279452	9
4	355.233982	178.120629					V	***930.540729***	465.774003	913.514180	457.260728	912.530164	456.768720	8
5	468.318046	234.662661					L	***831.472315***	416.239796	814.445766	407.726521	813.461750	407.234513	7
6	581.402110	291.204693					L	***718.388251***	359.697764	701.361702	351.184489	700.377686	350.692481	6
7	638.423574	319.715425					G	***605.304187***	303.155732	588.277638	294.642457	587.293622	294.150449	5
8	725.455602	363.231439			707.445037	354.226157	S	***548.282723***	274.645000	531.256174	266.131725	530.272158	265.639717	4
9	911.534915	456.271096			893.524350	447.265813	W	***461.250695***	231.128985	444.224146	222.615711			3
10	**1039.593493**	520.300385	1022.566944	511.787110	1021.582928	511.295102	Q	275.171382	138.089329	258.144833	129.576054			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.6	1184.691757	0.008291	VVGVLLGSWQK
6.1	1184.701614	-0.001566	KLLPDTILEK
1.3	1184.701599	-0.001551	IPKLEELLSK
0.6	1184.701614	-0.001566	ALALLEDLVTK
0.5	1184.695084	0.004964	QLILLAQQMK
0.3	1184.691727	0.008321	AAPKAVVLWSK

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

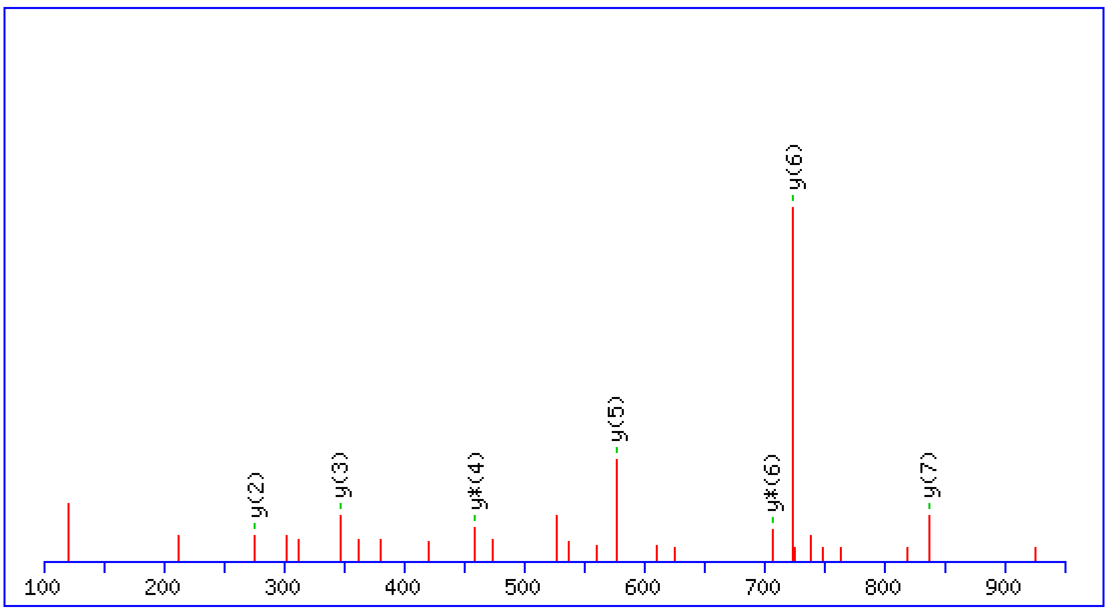
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILFTEATR**
Found in **PSMD8_HUMAN**, 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2

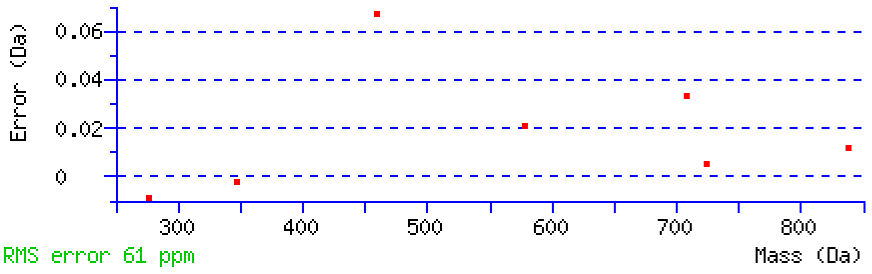
Match to Query 8909: 949.528628 from(475.771590,2+) rtinseconds(2107) index(24555)
Title: Locus:1.1.1.2187.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

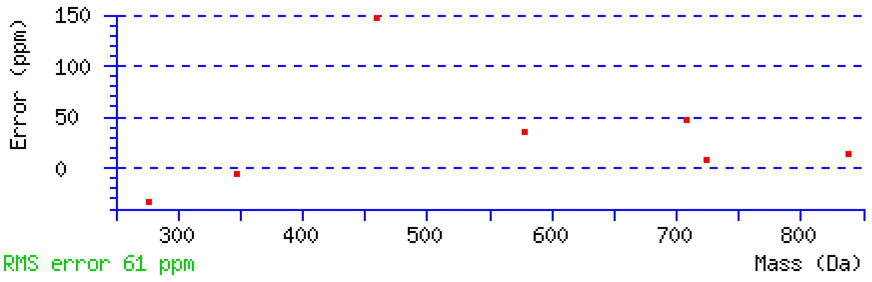
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 949.523270
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00036
Matches : 7/62 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							8
2	227.175404	114.091340			L	*837.446495*	419.226886	820.419946	410.713611	819.435930	410.221603	7
3	374.243818	187.625547			F	*724.362431*	362.684854	707.335882	354.171579	706.351866	353.679571	6
4	475.291497	238.149386	457.280932	229.144104	T	*577.294017*	289.150647	560.267468	280.637372	559.283452	280.145364	5
5	604.334090	302.670683	586.323525	293.665401	E	476.246338	238.626807	459.219789	230.113532	458.235773	229.621524	4
6	675.371204	338.189240	657.360639	329.183958	A	*347.203745*	174.105510	330.177196	165.592236	329.193180	165.100228	3
7	776.418883	388.713080	758.408318	379.707797	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
8					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILFTEATR
(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	949.523270	0.005358	ILFTEATR
13.7	949.523239	0.005389	LLRYEEK
5.9	949.523270	0.005358	ILSSFQGAK
5.9	949.523270	0.005358	LLSSFDLR
3.3	949.534500	-0.005872	IPRNPPPK
3.3	949.534500	-0.005872	IPRNPPPK
3.3	949.534500	-0.005872	IPRNPPPK
2.5	949.523239	0.005389	IIKEYER

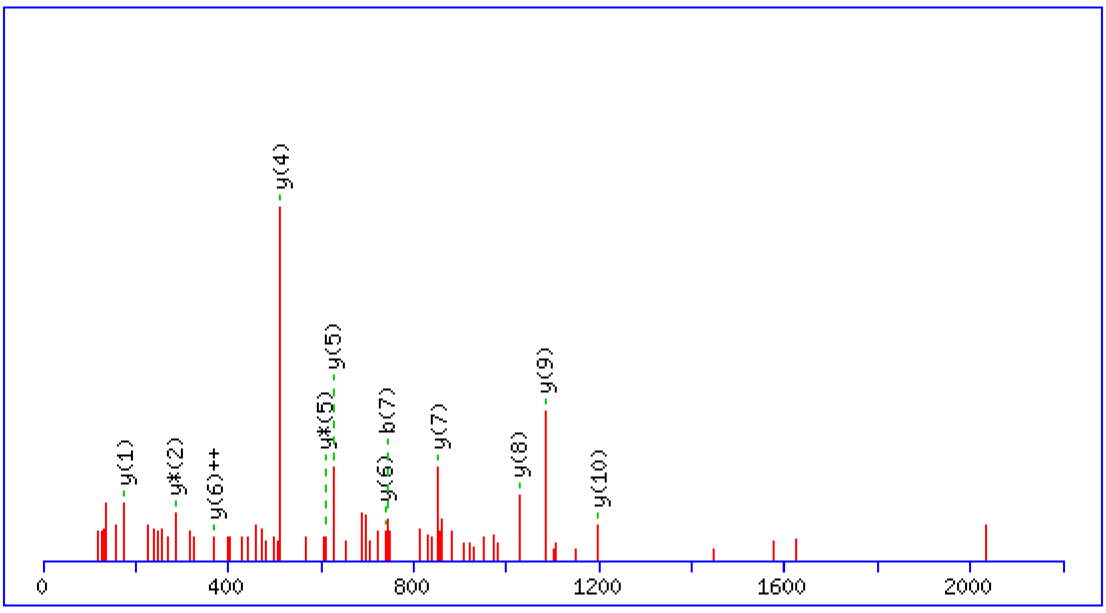
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLLGCNIIPLQR**
Found in **PSMD9_HUMAN**, 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3

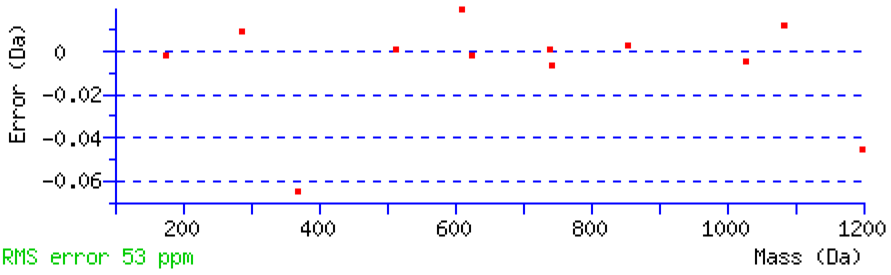
Match to Query 27447: 1366.783048 from(684.398800,2+) rtinseconds(3206) index(38827)
Title: Locus:1.1.1.3028.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

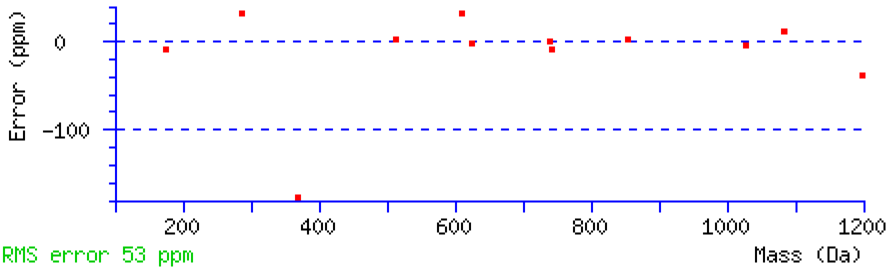
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1366.775467
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0016
Matches : 12/78 fragment ions using 33 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	58.028740	29.518008			G					12
2	171.112804	86.060040			L	1310.761304	655.884290	1293.734755	647.371016	11
3	284.196868	142.602072			L	***1197.677240***	599.342258	1180.650691	590.828983	10
4	341.218332	171.112804			G	***1084.593176***	542.800226	1067.566627	534.286951	9
5	515.264631	258.135954			C	***1027.571712***	514.289494	1010.545163	505.776219	8
6	629.307558	315.157417	612.281009	306.644142	N	***853.525413***	427.266344	836.498864	418.753070	7
7	742.391622	371.699449	725.365073	363.186174	I	***739.482486***	370.244881	722.455937	361.731606	6
8	855.475686	428.241481	838.449137	419.728207	I	***626.398422***	313.702849	609.371873	305.189574	5
9	952.528450	476.767863	935.501901	468.254589	P	***513.314358***	257.160817	496.287809	248.647542	4
10	1065.612514	533.309895	1048.585965	524.796621	L	416.261594	208.634435	399.235045	200.121160	3
11	1193.671092	597.339184	1176.644543	588.825909	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 GLLGCNIIPLQR
(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	1366.775467	0.007581	GLLGCNIIPLQR

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

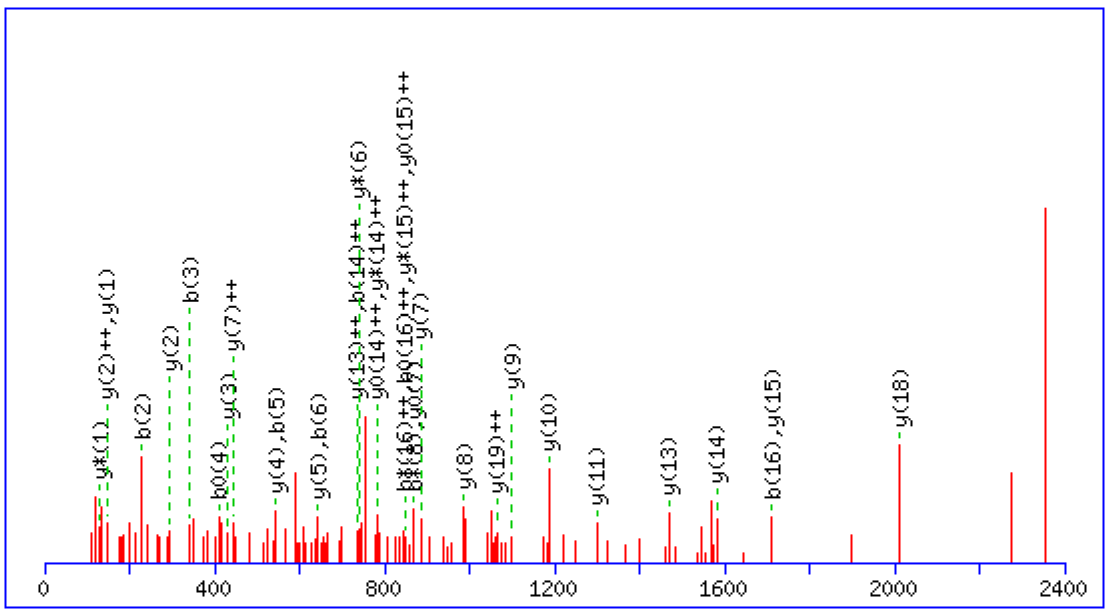
{MATRIX} *{SCIENCE}* Mascot Search Results

Peptide View

MS/MS Fragmentation of **VELSDVQNPAISITENVLHFK**
Found in **HACD3_HUMAN**, 3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2

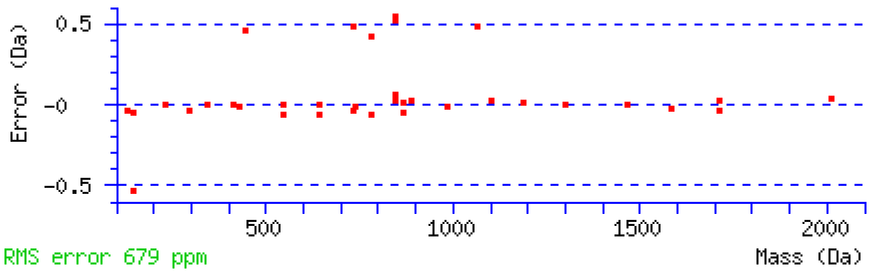
Match to Query 62738: 2352.248052 from(785.089960,3+) rtinseconds(4037) index(60376)
Title: Locus:1.1.1.2987.16
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

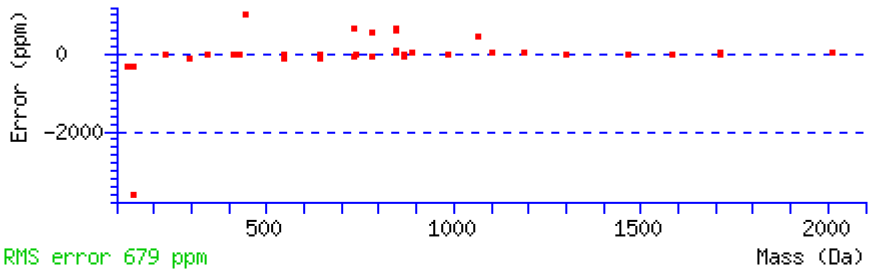
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2352.232513
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 6.8e-006
Matches : 35/214 fragment ions using 73 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							21
2	**229.118283**	115.062780			211.107718	106.057497	E	2254.171388	1127.589332	2237.144839	1119.076057	2236.160823	1118.584049	20
3	**342.202347**	171.604812			324.191782	162.599529	L	2125.128795	1063.068035	2108.102246	1054.554761	2107.118230	1054.062753	19
4	429.234375	215.120826			411.223810	206.115543	S	***2012.044731***	1006.526003	1995.018182	998.012729	1994.034166	997.520721	18
5	**544.261318**	272.634297			526.250753	263.629015	D	1925.012703	963.009989	1907.986154	954.496715	1907.002138	954.004707	17
6	**643.329732**	322.168504			625.319167	313.163222	V	1809.985760	905.496518	1792.959211	896.983243	1791.975195	896.491235	16
7	771.388310	386.197793	754.361761	377.684519	753.377745	377.192511	Q	***1710.917346***	855.962311	1693.890797	847.449037	1692.906781	846.957028	15
8	885.431237	443.219257	868.404688	434.705982	867.420672	434.213974	N	***1582.858768***	791.933022	1565.832219	783.419747	1564.848203	782.927739	14
9	982.484001	491.745639	965.457452	483.232364	964.473436	482.740356	P	***1468.815841***	734.911558	1451.789292	726.398284	1450.805276	725.906276	13
10	1053.521115	527.264196	1036.494566	518.750921	1035.510550	518.258913	A	1371.763077	686.385176	1354.736528	677.871902	1353.752512	677.379894	12
11	1166.605179	583.806227	1149.578630	575.292953	1148.594614	574.800945	I	***1300.725963***	650.866619	1283.699414	642.353345	1282.715398	641.861337	11
12	1253.637207	627.322242	1236.610658	618.808967	1235.626642	618.316959	S	***1187.641899***	594.324588	1170.615350	585.811313	1169.631334	585.319305	10
13	1366.721271	683.864273	1349.694722	675.350999	1348.710706	674.858991	I	***1100.609871***	550.808573	1083.583322	542.295299	1082.599306	541.803291	9
14	1467.768950	734.388113	1450.742401	725.874839	1449.758385	725.382830	T	***987.525807***	494.266542	970.499258	485.753267	969.515242	485.261259	8
15	1596.811543	798.909410	1579.784994	790.396135	1578.800978	789.904127	E	***886.478128***	443.742702	869.451579	435.229427	868.467563	434.737419	7
16	**1710.854470**	855.930873	1693.827921	847.417599	1692.843905	846.925591	N	757.435535	379.221405	740.408986	370.708131			6
17	1809.922884	905.465080	1792.896335	896.951806	1791.912319	896.459798	V	***643.392608***	322.199942	626.366059	313.686667			5
18	1923.006948	962.007112	1905.980399	953.493838	1904.996383	953.001829	L	***544.324194***	272.665735	527.297645	264.152460			4
19	2060.065860	1030.536568	2043.039311	1022.023293	2042.055295	1021.531285	H	***431.240130***	216.123703	414.213581	207.610428			3
20	2207.134274	1104.070775	2190.107725	1095.557500	2189.123709	1095.065492	F	***294.181218***	147.594247	277.154669	139.080972			2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.3	2352.232513	0.015539	VELSDVQNPAISITENVLHFK
3.1	2352.242386	0.005666	EVEEISLLQPQVEESVLNLGK
1.0	2352.232529	0.015523	APPPSLPSPSRLPGPSDTPILPQ

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

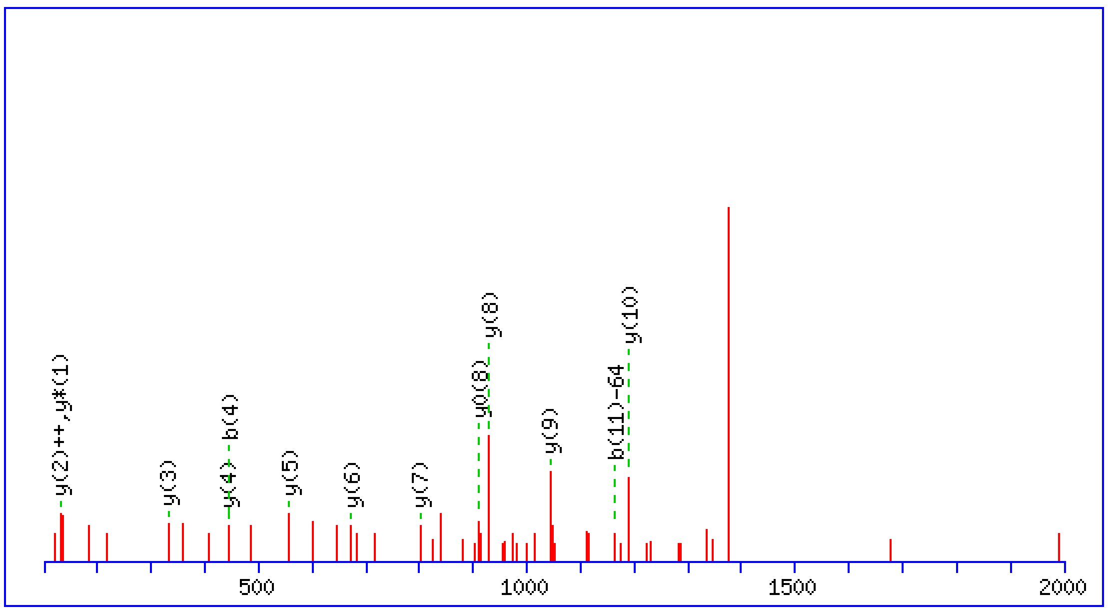
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAMLEEDLLALK**
Found in **HIBCH_HUMAN**, 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2

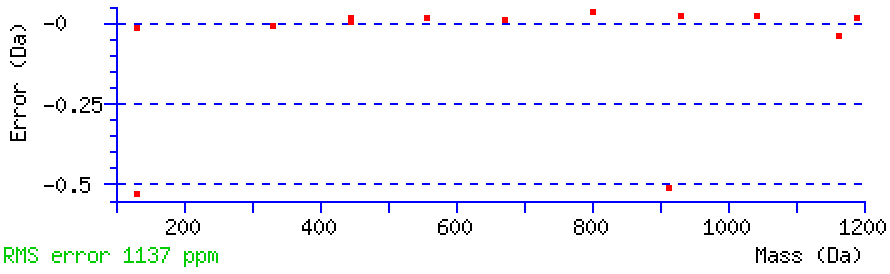
Match to Query 33798: 1373.761228 from(687.887890,2+) rtinseconds(3614) index(49388)
Title: Locus:1.1.1.2957.24
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

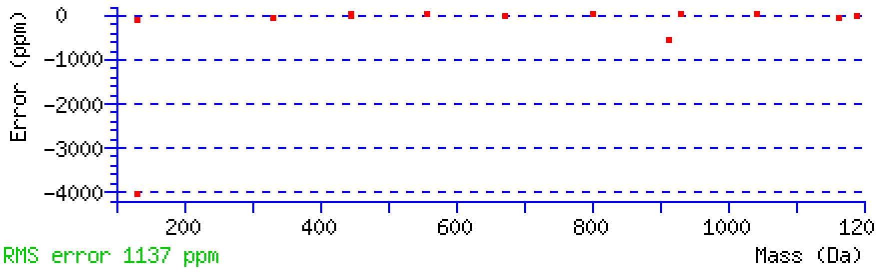
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1373.747559
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: 46 **Expect:** 0.00013
Matches : 13/136 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	1261.670817	631.339046	1244.644268	622.825772	1243.660252	622.333764	11
3	332.163854	166.585565			M	***1190.633703***	595.820489	1173.607154	587.307215	1172.623138	586.815207	10
4	445.247918	223.127597			L	***1043.598303***	522.302790	1026.571754	513.789515	1025.587738	513.297507	9
5	574.290511	287.648894	556.279946	278.643611	E	***930.514239***	465.760757	913.487690	457.247483	912.503674	456.755475	8
6	703.333104	352.170190	685.322539	343.164908	E	***801.471646***	401.239461	784.445097	392.726186	783.461081	392.234178	7
7	818.360047	409.683662	800.349482	400.678379	D	***672.429053***	336.718164	655.402504	328.204890	654.418488	327.712882	6
8	931.444111	466.225694	913.433546	457.220411	L	***557.402110***	279.204693	540.375561	270.691418			5
9	1044.528175	522.767725	1026.517610	513.762443	L	***444.318046***	222.662661	427.291497	214.149386			4
10	1115.565289	558.286282	1097.554724	549.281000	A	***331.233982***	166.120629	314.207433	157.607354			3
11	1228.649353	614.828314	1210.638788	605.823032	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 LAMLEEDLLALK
(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	1373.747559	0.013669	LAMLEEDLLALK
4.2	1373.758804	0.002424	SISLLCLEGLQK
2.7	1373.752289	0.008939	MAKLLSCVLGPR

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

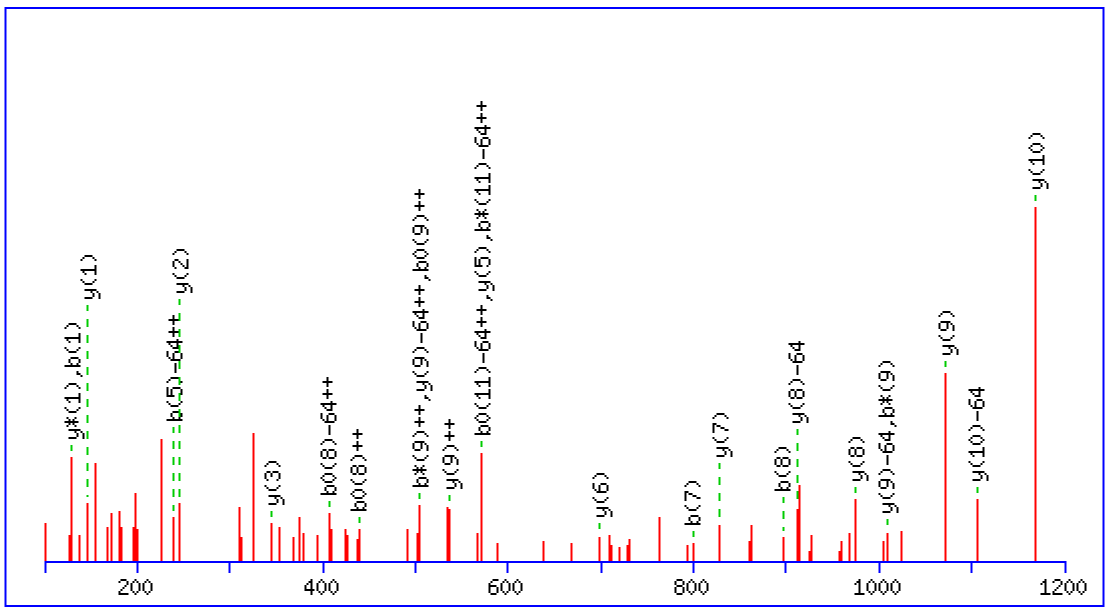
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAPPMEKPEVVK**
Found in **RS15_HUMAN**, 40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2

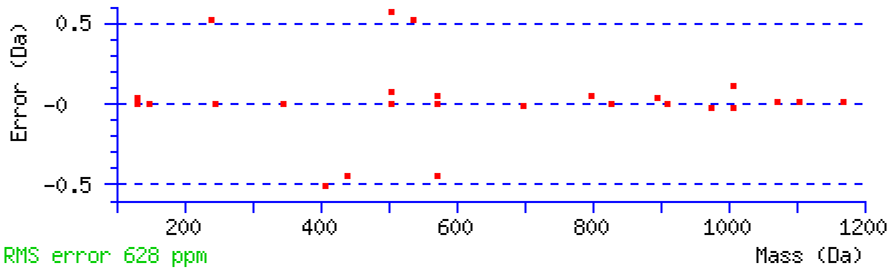
Match to Query 23980: 1368.691902 from(457.237910,3+) rtinseconds(1177) index(1237)
Title: Locus:1.1.1.1974.4
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

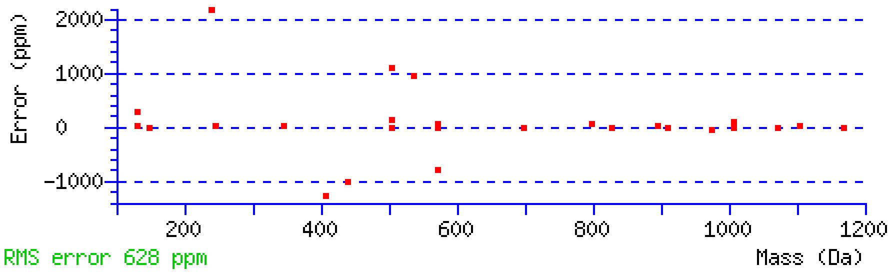
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1368.695877
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: 44 **Expect:** 0.00056
Matches : 26/176 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	**130.049869**	65.528572			112.039304	56.523290	E							12
2	201.086983	101.047130			183.076418	92.041847	A	1240.660587	620.833932	1223.634038	612.320657	1222.650022	611.828649	11
3	298.139747	149.573512			280.129182	140.568229	P	***1169.623473***	585.315375	1152.596924	576.802100	1151.612908	576.310092	10
4	395.192511	198.099894			377.181946	189.094611	P	***1072.570709***	536.788993	1055.544160	528.275718	1054.560144	527.783710	9
5	542.227911	271.617594			524.217346	262.612311	M	***975.517945***	488.262611	958.491396	479.749336	957.507380	479.257328	8
6	671.270504	336.138890			653.259939	327.133608	E	***828.482545***	414.744911	811.455996	406.231636	810.471980	405.739628	7
7	**799.365467**	400.186372	782.338918	391.673097	781.354902	391.181089	K	***699.439952***	350.223614	682.413403	341.710340	681.429387	341.218332	6
8	**896.418231**	448.712754	879.391682	440.199479	878.407666	439.707471	P	***571.344989***	286.176133	554.318440	277.662858	553.334424	277.170850	5
9	1025.460824	513.234050	1008.434275	504.720776	1007.450259	504.228768	E	474.292225	237.649751	457.265676	229.136476	456.281660	228.644468	4
10	1124.529238	562.768257	1107.502689	554.254983	1106.518673	553.762975	V	***345.249632***	173.128454	328.223083	164.615180			3
11	1223.597652	612.302464	1206.571103	603.789190	1205.587087	603.297182	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 EAPPMEKPEVVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	1368.695877	-0.003975	EAPPMEKPEVVK
34.1	1368.695877	-0.003975	EAPPMEKPEVVK
24.3	1368.695877	-0.003975	EAPPMEKPEVVK
10.3	1368.695877	-0.003975	EAPPMEKPEVVK

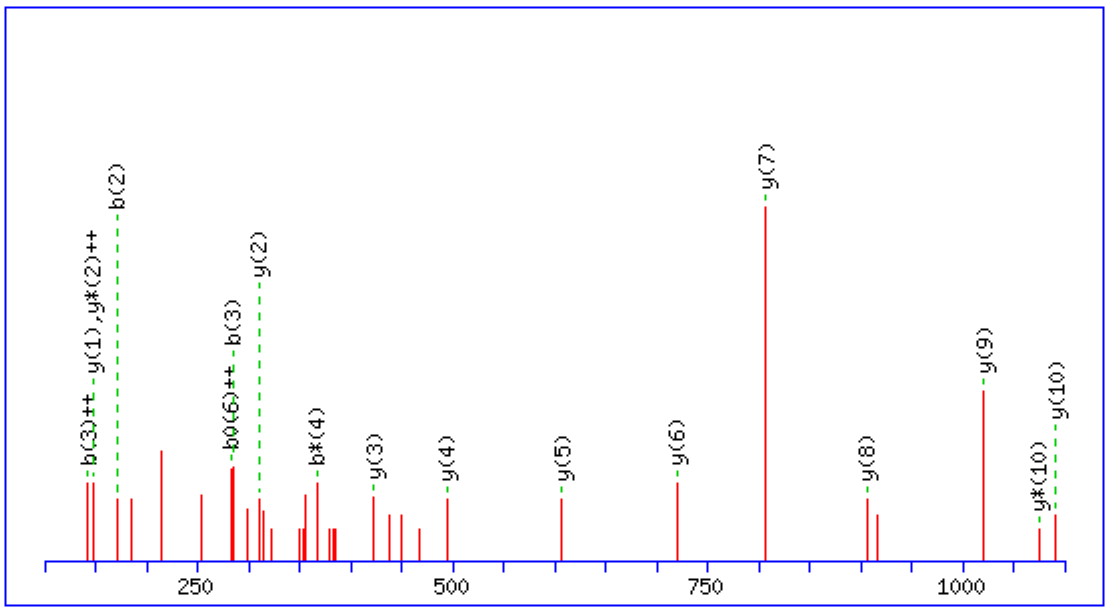
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VANVSLLALYK**
Found in **RS23_HUMAN**, 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3

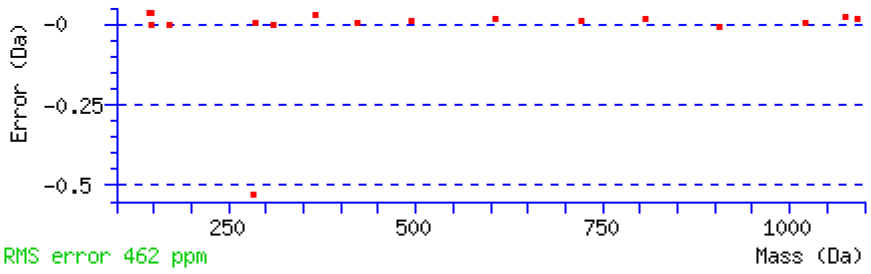
Match to Query 28545: 1189.712108 from(595.863330,2+) rtinseconds(3104) index(33100)
Title: Locus:1.1.1.2691.13
Data file 2011-11-14 - TFD - S 2-6.mgf

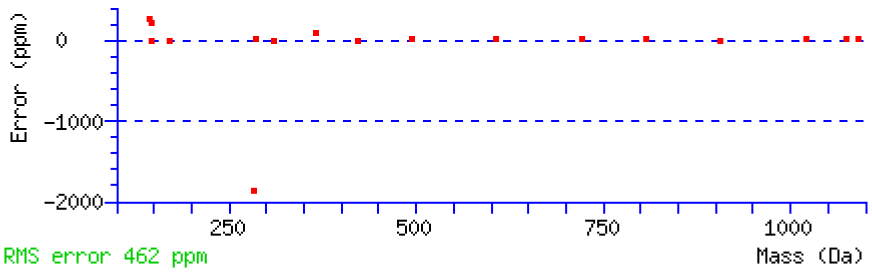
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1100] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1189.707031
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 91 **Expect:** 1.5e-009
Matches : 17/96 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							11
2	**171.112804**	86.060040					A	***1091.645922***	546.326599	1074.619373	537.813325	1073.635357	537.321317	10
3	**285.155731**	143.081504	268.129182	134.568229			N	***1020.608808***	510.808042	1003.582259	502.294768	1002.598243	501.802760	9
4	384.224145	192.615711	367.197596	184.102436			V	***906.565881***	453.786579	889.539332	445.273304	888.555316	444.781296	8
5	471.256173	236.131725	454.229624	227.618450	453.245608	227.126442	S	***807.497467***	404.252372	790.470918	395.739097	789.486902	395.247089	7
6	584.340237	292.673757	567.313688	284.160482	566.329672	283.668474	L	***720.465439***	360.736358	703.438890	352.223083			6
7	697.424301	349.215789	680.397752	340.702514	679.413736	340.210506	L	***607.381375***	304.194326	590.354826	295.681051			5
8	768.461415	384.734346	751.434866	376.221071	750.450850	375.729063	A	***494.297311***	247.652294	477.270762	239.139019			4
9	881.545479	441.276378	864.518930	432.763103	863.534914	432.271095	L	***423.260197***	212.133737	406.233648	203.620462			3
10	1044.608808	522.808042	1027.582259	514.294768	1026.598243	513.802760	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 VANVSLLALYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.6	1189.707031	0.005077	VANVSLLALYK
1.5	1189.707047	0.005061	GPGVYILLSKK

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

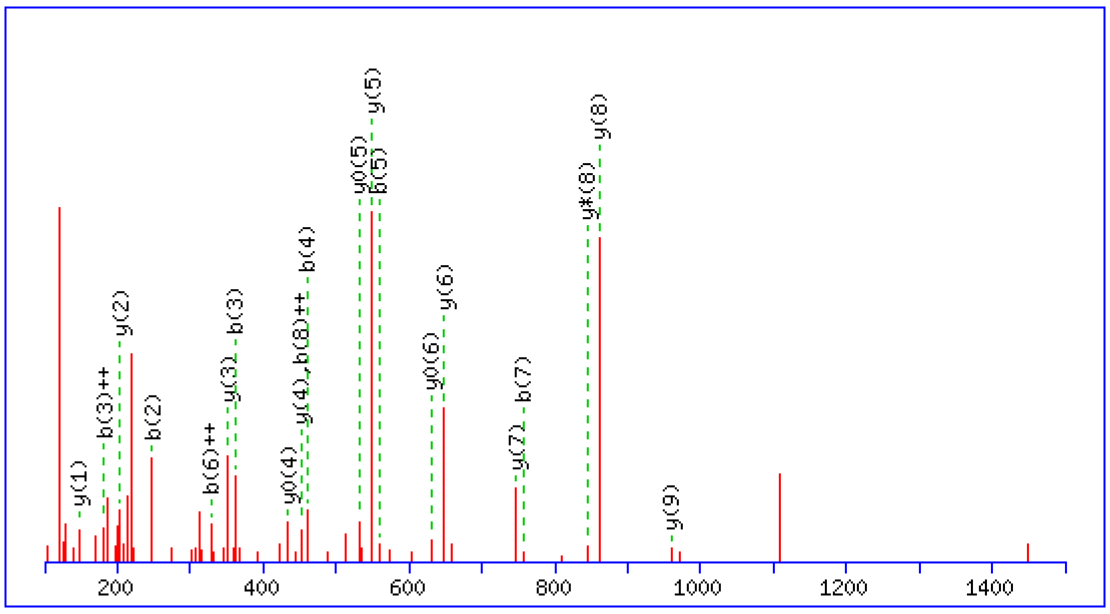
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVNVVPTFGK**
Found in **RS30_HUMAN**, 40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1

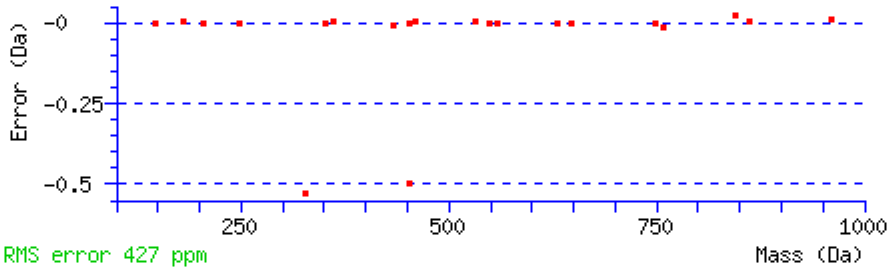
Match to Query 9300: 1106.610008 from(554.312280,2+) rtinseconds(2845) index(10135)
Title: Locus:1.1.1.3099.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

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 ●

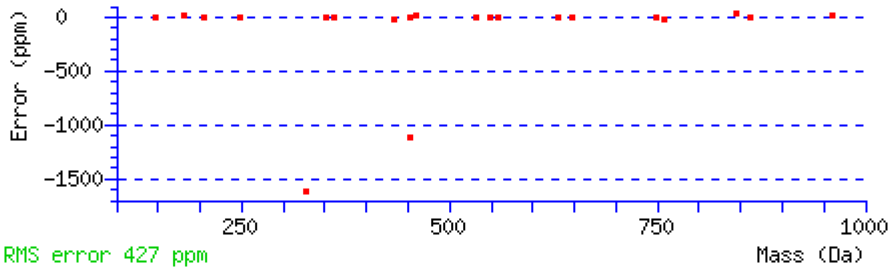


```
Monoisotopic mass of neutral peptide Mr(calc): 1106.612457
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 5.2e-006
Matches : 21/86 fragment ions using 41 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							10
2	**247.144104**	124.075690					V	***960.551294***	480.779285	943.524745	472.266011	942.540729	471.774003	9
3	**361.187031**	**181.097153**	344.160482	172.583879			N	***861.482880***	431.245078	844.456331	422.731804	843.472315	422.239796	8
4	**460.255445**	230.631361	443.228896	222.118086			V	***747.439953***	374.223615	730.413404	365.710340	729.429388	365.218332	7
5	**559.323859**	280.165568	542.297310	271.652293			V	***648.371539***	324.689408	631.344990	316.176133	630.360974	315.684125	6
6	656.376623	**328.691950**	639.350074	320.178675			P	***549.303125***	275.155201	532.276576	266.641926	531.292560	266.149918	5
7	**757.424302**	379.215789	740.397753	370.702515	739.413737	370.210507	T	***452.250361***	226.628818	435.223812	218.115544	434.239796	217.623536	4
8	904.492716	**452.749996**	887.466167	444.236722	886.482151	443.744714	F	***351.202682***	176.104979	334.176133	167.591704			3
9	961.514180	481.260728	944.487631	472.747454	943.503615	472.255446	G	***204.134268***	102.570772	187.107719	94.057498			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 427 ppm



RMS error 427 ppm

NCBI **BLAST** search of FVNVVPTFGK
(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	1106.612457	-0.002449	FVNVVPTFGK

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

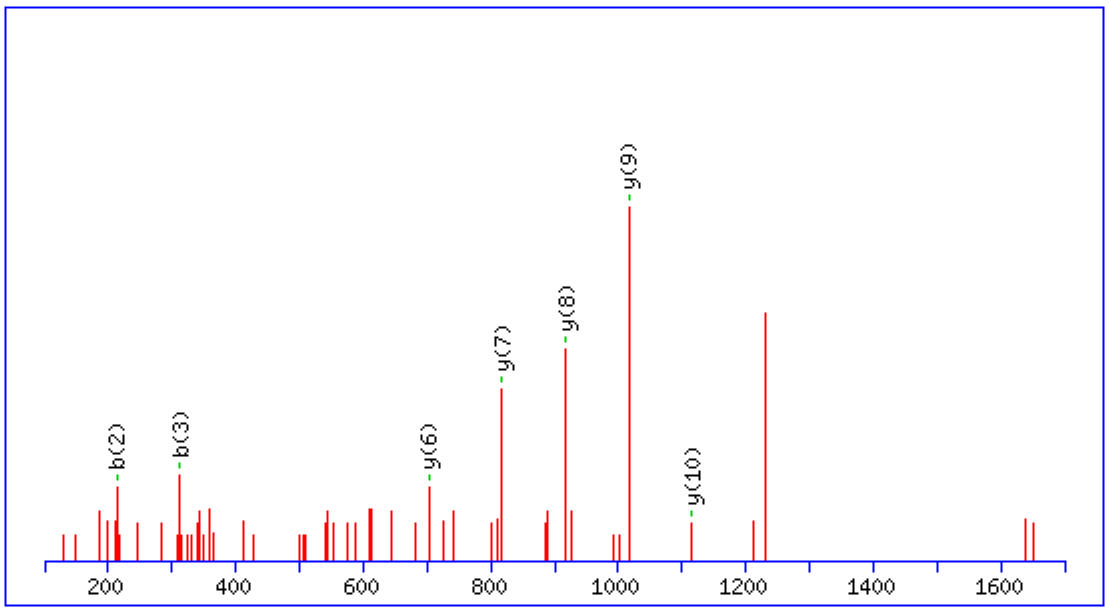
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVVVDENDVVK**
Found in **AAKG1_HUMAN**, 5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1

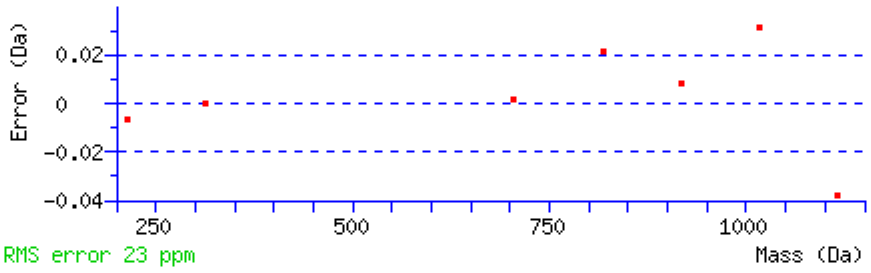
Match to Query 26883: 1227.678228 from(614.846390,2+) rtinseconds(2212) index(24484)
Title: Locus:1.1.1.2334.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

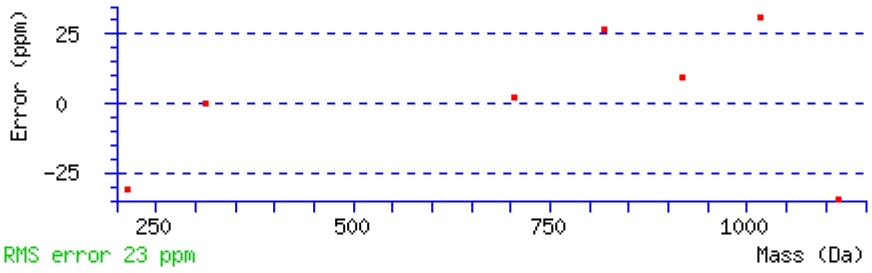
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1227.671082
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.002
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	114.091340	57.549308					L							11
2	**213.159754**	107.083515					V	***1115.594280***	558.300778	1098.567731	549.787504	1097.583715	549.295496	10
3	**312.228168**	156.617722					V	***1016.525866***	508.766571	999.499317	500.253296	998.515301	499.761288	9
4	411.296582	206.151929					V	***917.457452***	459.232364	900.430903	450.719089	899.446887	450.227081	8
5	526.323525	263.665401			508.312960	254.660118	D	***818.389038***	409.698157	801.362489	401.184882	800.378473	400.692874	7
6	655.366118	328.186697			637.355553	319.181415	E	***703.362095***	352.184686	686.335546	343.671411	685.351530	343.179403	6
7	769.409045	385.208161	752.382496	376.694886	751.398480	376.202878	N	574.319502	287.663389	557.292953	279.150114	556.308937	278.658106	5
8	884.435988	442.721632	867.409439	434.208357	866.425423	433.716349	D	460.276575	230.641925	443.250026	222.128651	442.266010	221.636643	4
9	983.504402	492.255839	966.477853	483.742564	965.493837	483.250556	V	345.249632	173.128454	328.223083	164.615179			3
10	1082.572816	541.790046	1065.546267	533.276772	1064.562251	532.784763	V	246.181218	123.594247	229.154669	115.080972			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LVVVDENDVVK
(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	1227.671082	0.007146	LVVVDENDVVK
3.4	1227.671082	0.007146	VLTPPTTAATPK

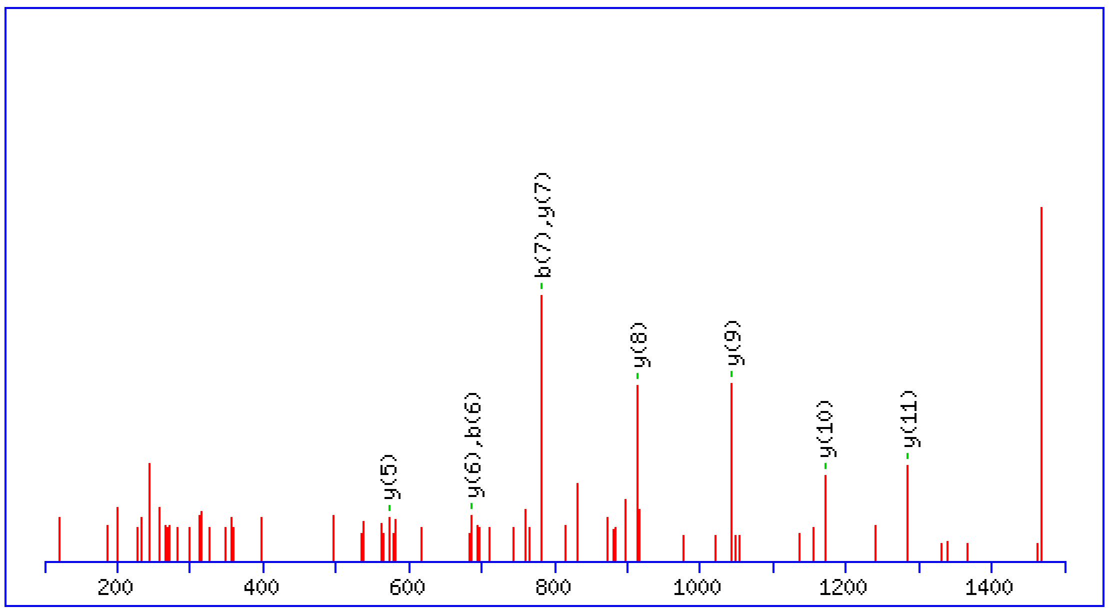
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

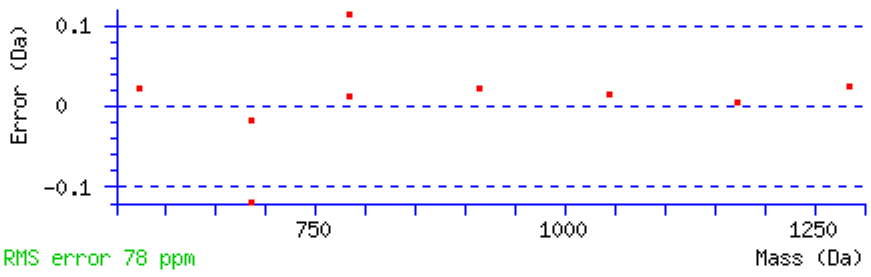
Match to Query 34189: 1467.862888 from(734.938720,2+) rtinseconds(4167) index(59991)
Title: Locus:1.1.1.3127.24
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

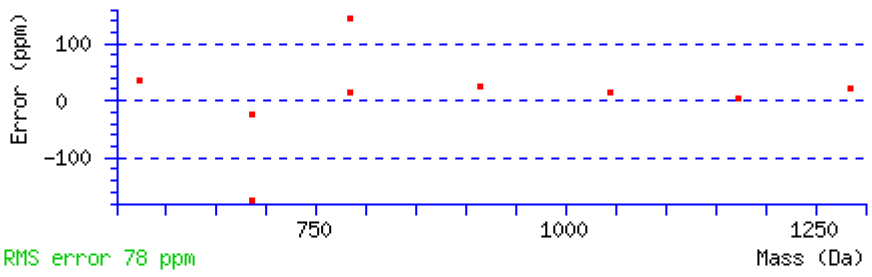
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1467.848282
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00021
Matches : 9/122 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							13
2	185.128454	93.067865					L	1397.818485	699.412881	1380.791936	690.899606	1379.807920	690.407598	12
3	298.212518	149.609897					L	***1284.734421***	642.870848	1267.707872	634.357574	1266.723856	633.865566	11
4	426.271096	213.639186	409.244547	205.125912			Q	***1171.650357***	586.328817	1154.623808	577.815542	1153.639792	577.323534	10
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	E	***1043.591779***	522.299528	1026.565230	513.786253	1025.581214	513.294245	9
6	**686.354174**	343.680725	669.327625	335.167451	668.343609	334.675443	M	***914.549186***	457.778231	897.522637	449.264956	896.538621	448.772948	8
7	**783.406938**	392.207107	766.380389	383.693833	765.396373	383.201825	P	***783.508701***	392.257989	766.482152	383.744714	765.498136	383.252706	7
8	896.491002	448.749139	879.464453	440.235865	878.480437	439.743857	L	***686.455937***	343.731607	669.429388	335.218332	668.445372	334.726324	6
9	997.538681	499.272979	980.512132	490.759704	979.528116	490.267696	T	***573.371873***	287.189574	556.345324	278.676300	555.361308	278.184292	5
10	1068.575795	534.791536	1051.549246	526.278261	1050.565230	525.786253	A	472.324194	236.665735	455.297645	228.152460			4
11	1181.659859	591.333568	1164.633310	582.820293	1163.649294	582.328285	L	401.287080	201.147178	384.260531	192.633903			3
12	1294.743923	647.875600	1277.717374	639.362325	1276.733358	638.870317	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 ALLQEMPLTALLR
(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	1467.848282	0.014606	ALLQEMPLTALLR
8.1	1467.870056	-0.007168	KLNYTYLISILK
4.6	1467.866058	-0.003170	QAPLKVSLLQDLK

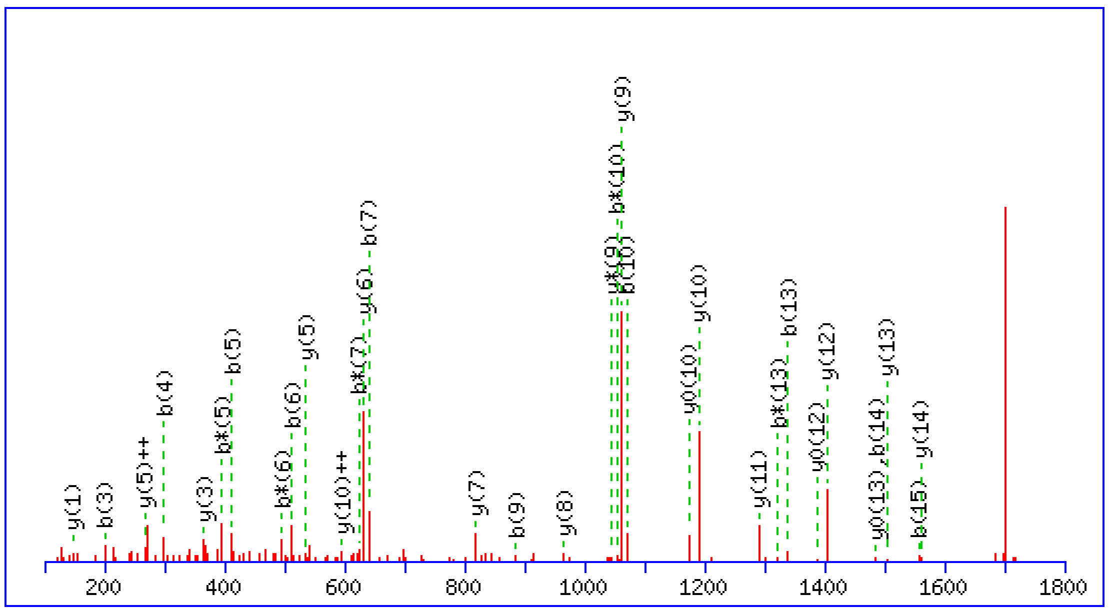
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAGVNVEPFWPGLFAK**
Found in **RLA1_HUMAN**, 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1

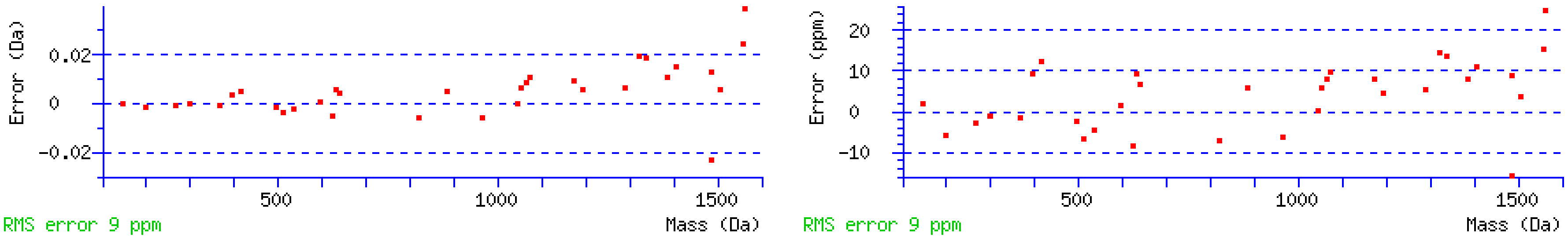
Match to Query 45221: 1701.899688 from(851.957120,2+) rtinseconds(4008) index(40487)
Title: Locus:1.1.1.3027.8
Data file 2011-11-14 - TFD - S 2-6.mgf

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): 1701.887878
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82  Expect: 4.1e-008
Matches : 33/142 fragment ions using 55 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	143.081504	72.044390					A	1631.858041	816.432659	1614.831492	807.919384	1613.847476	807.427376	15
3	**200.102968**	100.555122					G	***1560.820927***	780.914102	1543.794378	772.400827	1542.810362	771.908819	14
4	**299.171382**	150.089329					V	***1503.799463***	752.403370	1486.772914	743.890095	1485.788898	743.398087	13
5	**413.214309**	207.110793	396.187760	198.597518			N	***1404.731049***	702.869163	1387.704500	694.355888	1386.720484	693.863880	12
6	**512.282723**	256.645000	495.256174	248.131725			V	***1290.688122***	645.847699	1273.661573	637.334425	1272.677557	636.842417	11
7	**641.325316**	321.166296	624.298767	312.653022	623.314751	312.161014	E	***1191.619708***	596.313492	1174.593159	587.800218	1173.609143	587.308210	10
8	738.378080	369.692678	721.351531	361.179404	720.367515	360.687396	P	***1062.577115***	531.792196	1045.550566	523.278921			9
9	**885.446494**	443.226885	868.419945	434.713611	867.435929	434.221603	F	***965.524351***	483.265814	948.497802	474.752539			8
10	**1071.525807**	536.266542	1054.499258	527.753267	1053.515242	527.261259	W	***818.455937***	409.731607	801.429388	401.218332			7
11	1168.578571	584.792924	1151.552022	576.279649	1150.568006	575.787641	P	***632.376624***	316.691950	615.350075	308.178676			6
12	1225.600035	613.303656	1208.573486	604.790381	1207.589470	604.298373	G	***535.323860***	268.165568	518.297311	259.652293			5
13	**1338.684099**	669.845688	1321.657550	661.332413	1320.673534	660.840405	L	478.302396	239.654836	461.275847	231.141561			4
14	**1485.752513**	743.379895	1468.725964	734.866620	1467.741948	734.374612	F	***365.218332***	183.112804	348.191783	174.599530			3
15	**1556.789627**	778.898452	1539.763078	770.385177	1538.779062	769.893169	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 AAGVNVEPFWPGLFAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.9	1701.887878	0.011810	AAGVNVEPFWPGLFAK
3.0	1701.912354	-0.012666	KNPYLICPATIGDVK
0.9	1701.893738	0.005950	ADIPVKSSPQAAVPYK

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

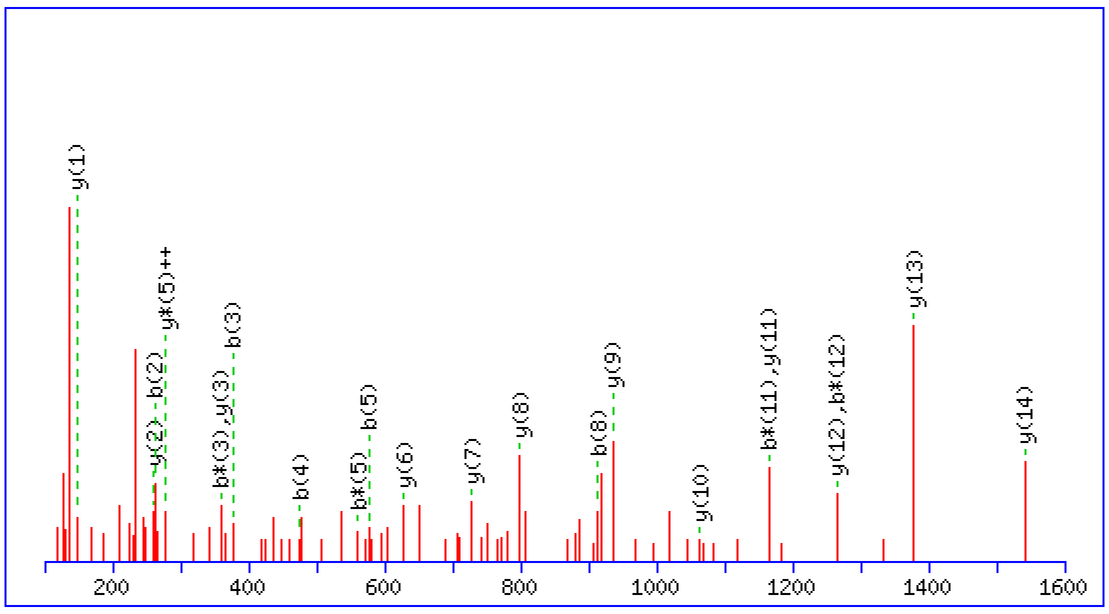
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYNVTQHAVGIVVNK**
Found in **RL21_HUMAN**, 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2

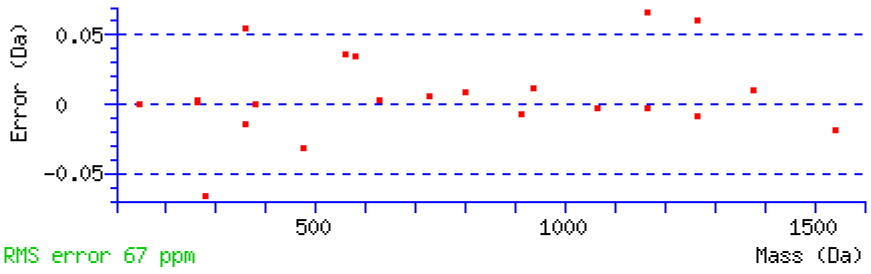
Match to Query 36136: 1639.902642 from(547.641490,3+) rtinseconds(2214) index(20219)
Title: Locus:1.1.1.2655.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

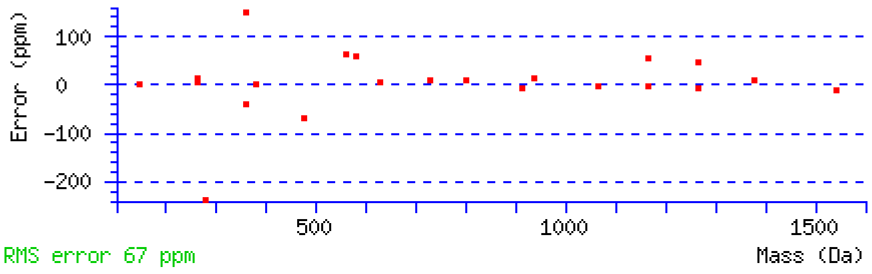
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1639.904602
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 70  Expect: 6.3e-007
Matches : 22/136 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	100.075690	50.541483					V							15
2	**263.139019**	132.073148					Y	***1541.843454***	771.425365	1524.816905	762.912091	1523.832889	762.420083	14
3	**377.181946**	189.094611	360.155397	180.581337			N	***1378.780125***	689.893701	1361.753576	681.380426	1360.769560	680.888418	13
4	**476.250360**	238.628818	459.223811	230.115544			V	***1264.737198***	632.872237	1247.710649	624.358963	1246.726633	623.866955	12
5	**577.298039**	289.152658	560.271490	280.639383	559.287474	280.147375	T	***1165.668784***	583.338030	1148.642235	574.824756	1147.658219	574.332748	11
6	705.356617	353.181947	688.330068	344.668672	687.346052	344.176664	Q	***1064.621105***	532.814191	1047.594556	524.300916			10
7	842.415529	421.711403	825.388980	413.198128	824.404964	412.706120	H	***936.562527***	468.784902	919.535978	460.271627			9
8	**913.452643**	457.229960	896.426094	448.716685	895.442078	448.224677	A	***799.503615***	400.255446	782.477066	391.742171			8
9	1012.521057	506.764167	995.494508	498.250892	994.510492	497.758884	V	***728.466501***	364.736889	711.439952	356.223614			7
10	1069.542521	535.274899	1052.515972	526.761624	1051.531956	526.269616	G	***629.398087***	315.202682	612.371538	306.689407			6
11	1182.626585	591.816931	1165.600036	583.303656	1164.616020	582.811648	I	572.376623	286.691950	555.350074	278.178675			5
12	1281.694999	641.351138	1264.668450	632.837863	1263.684434	632.345855	V	459.292559	230.149918	442.266010	221.636643			4
13	1380.763413	690.885345	1363.736864	682.372070	1362.752848	681.880062	V	***360.224145***	180.615711	343.197596	172.102436			3
14	1494.806340	747.906808	1477.779791	739.393534	1476.795775	738.901526	N	***261.155731***	131.081503	244.129182	122.568229			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.3	1639.904602	-0.001960	VYNVTQHAVGIVVNK

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

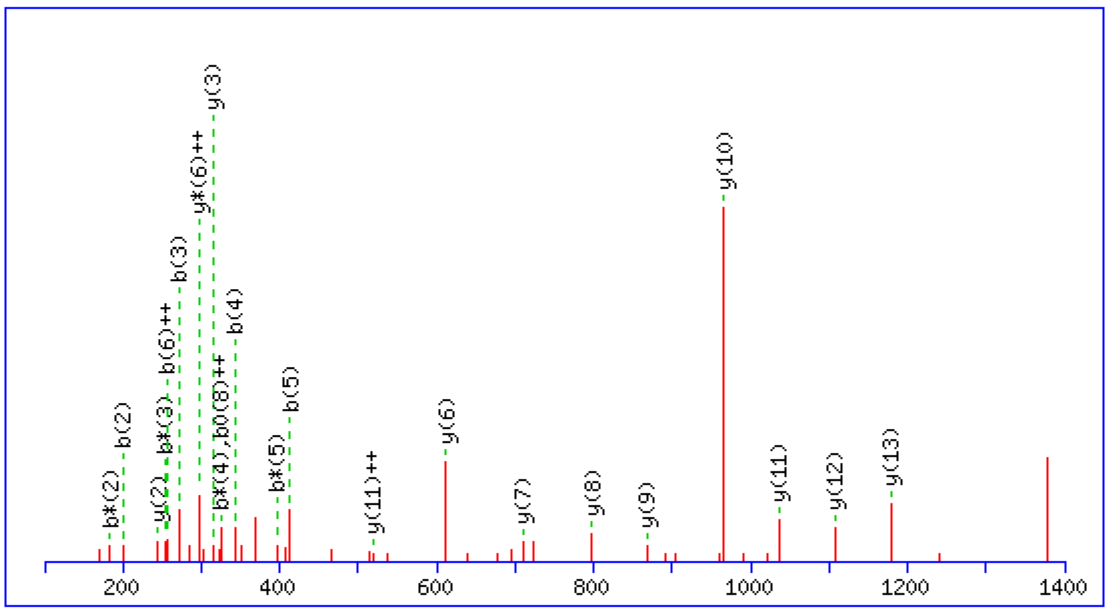
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of AQAAAPASVPAQAPK
Found in **RL29_HUMAN**, 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

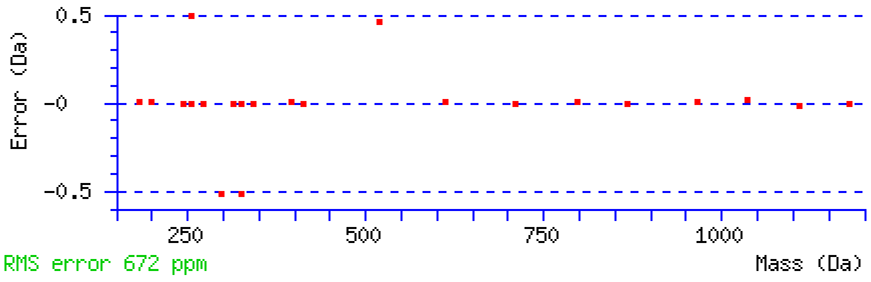
Match to Query 30847: 1376.745188 from(689.379870,2+) rtinseconds(1416) index(10092)
Title: Locus:1.1.1.1981.43
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

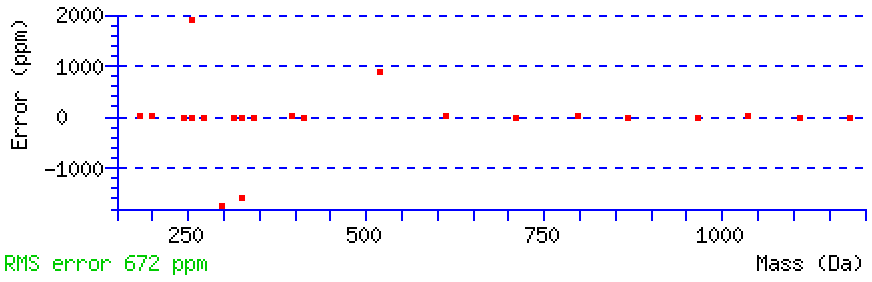
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1376.741180
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 1.4e-005
Matches : 22/138 fragment ions using 42 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							15
2	**200.102968**	100.555122	183.076419	92.041848			Q	1306.711378	653.859327	1289.684829	645.346053	1288.700813	644.854045	14
3	**271.140082**	136.073679	254.113533	127.560405			A	***1178.652800***	589.830038	1161.626251	581.316764	1160.642235	580.824756	13
4	**342.177196**	171.592236	325.150647	163.078962			A	***1107.615686***	554.311481	1090.589137	545.798207	1089.605121	545.306199	12
5	**413.214310**	207.110793	396.187761	198.597519			A	***1036.578572***	518.792924	1019.552023	510.279650	1018.568007	509.787642	11
6	510.267074	255.637175	493.240525	247.123901			P	***965.541458***	483.274367	948.514909	474.761093	947.530893	474.269085	10
7	581.304188	291.155732	564.277639	282.642458			A	***868.488694***	434.747985	851.462145	426.234711	850.478129	425.742703	9
8	668.336216	334.671746	651.309667	326.158472	650.325651	325.666464	S	***797.451580***	399.229428	780.425031	390.716154	779.441015	390.224146	8
9	767.404630	384.205953	750.378081	375.692679	749.394065	375.200671	V	***710.419552***	355.713414	693.393003	347.200140			7
10	864.457394	432.732335	847.430845	424.219061	846.446829	423.727053	P	***611.351138***	306.179207	594.324589	297.665933			6
11	935.494508	468.250892	918.467959	459.737618	917.483943	459.245610	A	514.298374	257.652825	497.271825	249.139551			5
12	1063.553086	532.280181	1046.526537	523.766907	1045.542521	523.274899	Q	443.261260	222.134268	426.234711	213.620994			4
13	1134.590200	567.798738	1117.563651	559.285464	1116.579635	558.793456	A	***315.202682***	158.104979	298.176133	149.591704			3
14	1231.642964	616.325120	1214.616415	607.811846	1213.632399	607.319838	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 AQAAAPASVPAQAPK
(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	1376.741180	0.004008	AQAAAPASVPAQAPK
5.5	1376.741180	0.004008	AAKAGLSQSLFER
0.3	1376.734650	0.010538	CSLLLHAREHK

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

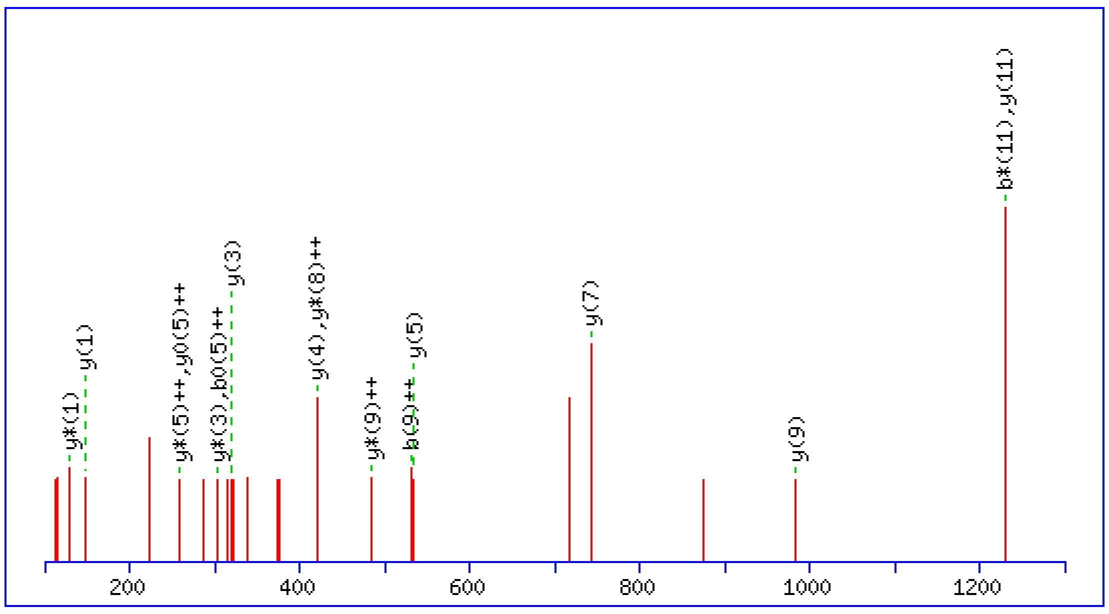
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYCAEIAHNVSSK**
Found in **RL32_HUMAN**, 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2

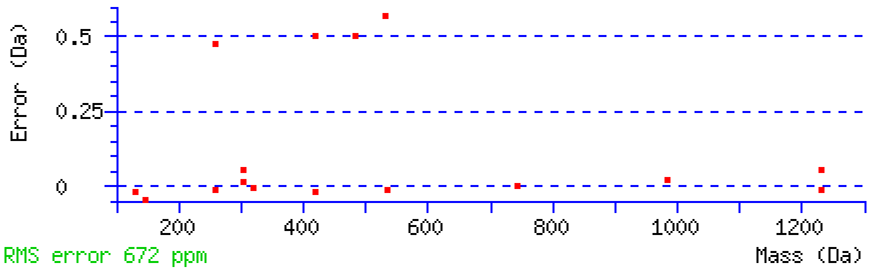
Match to Query 29593: 1478.679402 from(493.900410,3+) rtinseconds(1718) index(8625)
Title: Locus:1.1.1.2118.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

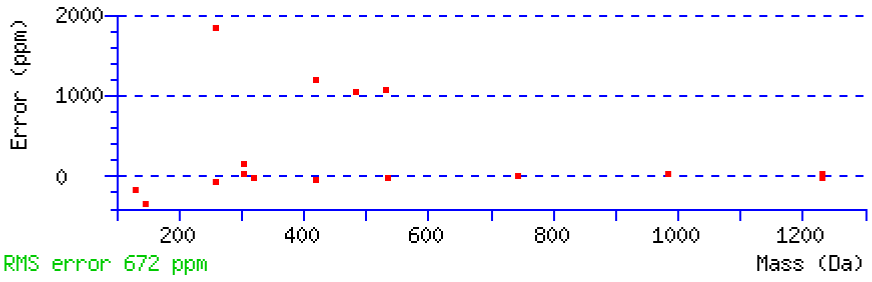
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1478.682343`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 42 Expect: 0.00038`
`Matches : 16/126 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	88.039304	44.523290			70.028739	35.518008	S							13
2	251.102633	126.054954			233.092068	117.049672	Y	1392.657626	696.832451	1375.631077	688.319177	1374.647061	687.827169	12
3	425.148932	213.078104			407.138367	204.072822	C	***1229.594297***	615.300787	1212.567748	606.787512	1211.583732	606.295504	11
4	496.186046	248.596661			478.175481	239.591378	A	1055.547998	528.277637	1038.521449	519.764363	1037.537433	519.272355	10
5	625.228639	313.117958			607.218074	304.112675	E	***984.510884***	492.759080	967.484335	484.245806	966.500319	483.753798	9
6	738.312703	369.659990			720.302138	360.654707	I	855.468291	428.237784	838.441742	419.724509	837.457726	419.232501	8
7	809.349817	405.178547			791.339252	396.173264	A	***742.384227***	371.695752	725.357678	363.182477	724.373662	362.690469	7
8	946.408729	473.708003			928.398164	464.702720	H	671.347113	336.177195	654.320564	327.663920	653.336548	327.171912	6
9	1060.451656	530.729466	1043.425107	522.216192	1042.441091	521.724183	N	***534.288201***	267.647739	517.261652	259.134464	516.277636	258.642456	5
10	1159.520070	580.263673	1142.493521	571.750399	1141.509505	571.258391	V	***420.245274***	210.626275	403.218725	202.113001	402.234709	201.620993	4
11	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774405	S	***321.176860***	161.092068	304.150311	152.578794	303.166295	152.086786	3
12	1333.584126	667.295701	1316.557577	658.782427	1315.573561	658.290419	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 SYCAEIAHNVSSK
(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	1478.682343	-0.002941	SYCAEIAHNVSSK
5.0	1478.688873	-0.009471	EEQEEPYVSLTR
3.4	1478.686401	-0.006999	DLFIQWCQDPK
2.8	1478.685730	-0.006328	SIMDPNQNVKCK
2.0	1478.667084	0.012318	LQRNESEPSEMK

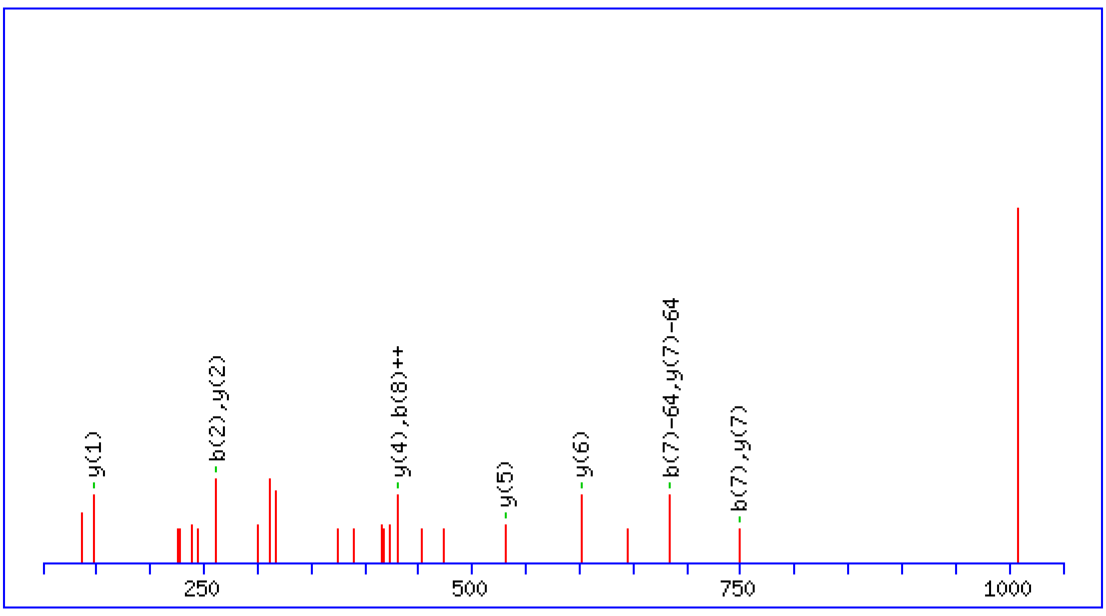
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YPMAVGLNK**
Found in **RL36_HUMAN**, 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3

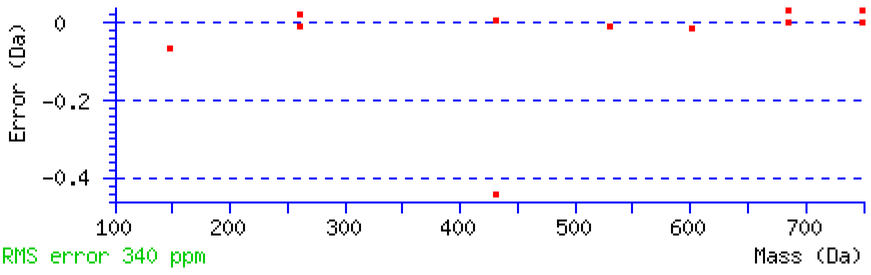
Match to Query 5680: 1007.511728 from(504.763140,2+) rtinseconds(1754) index(2197)
Title: Locus:1.1.1.2518.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

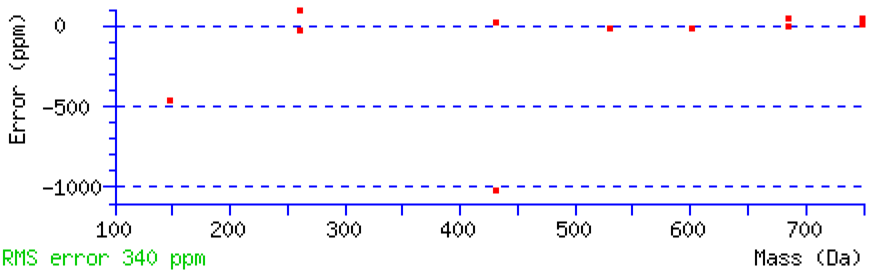
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1007.510986
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: 62  Expect: 6.8e-006
Matches : 11/72 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	164.070605	82.538940			Y					9
2	**261.123369**	131.065322			P	845.454951	423.231113	828.428402	414.717839	8
3	408.158769	204.583022			M	***748.402187***	374.704732	731.375638	366.191457	7
4	479.195883	240.101579			A	***601.366787***	301.187032	584.340238	292.673757	6
5	578.264297	289.635786			V	***530.329673***	265.668475	513.303124	257.155200	5
6	635.285761	318.146519			G	***431.261259***	216.134267	414.234710	207.620993	4
7	**748.369825**	374.688551			L	374.239795	187.623535	357.213246	179.110261	3
8	862.412752	431.710014	845.386203	423.196739	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 YPMAVGLNK
(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	1007.510986	0.000742	YPMAVGLNK
38.4	1007.510986	0.000742	YPMAVGLNK
13.0	1007.506958	0.004770	TLKSNGMNK
12.8	1007.518860	-0.007132	YFPAGPGRK
12.5	1007.510986	0.000742	YPQKVMDK
10.1	1007.503601	0.008127	RTVEDFNK
8.5	1007.503616	0.008112	GDPGIPGNPGK
7.6	1007.517502	-0.005774	EDYIIEVK
7.2	1007.503601	0.008127	ETFRSPQK
3.6	1007.506958	0.004770	MGSNKSKPK

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

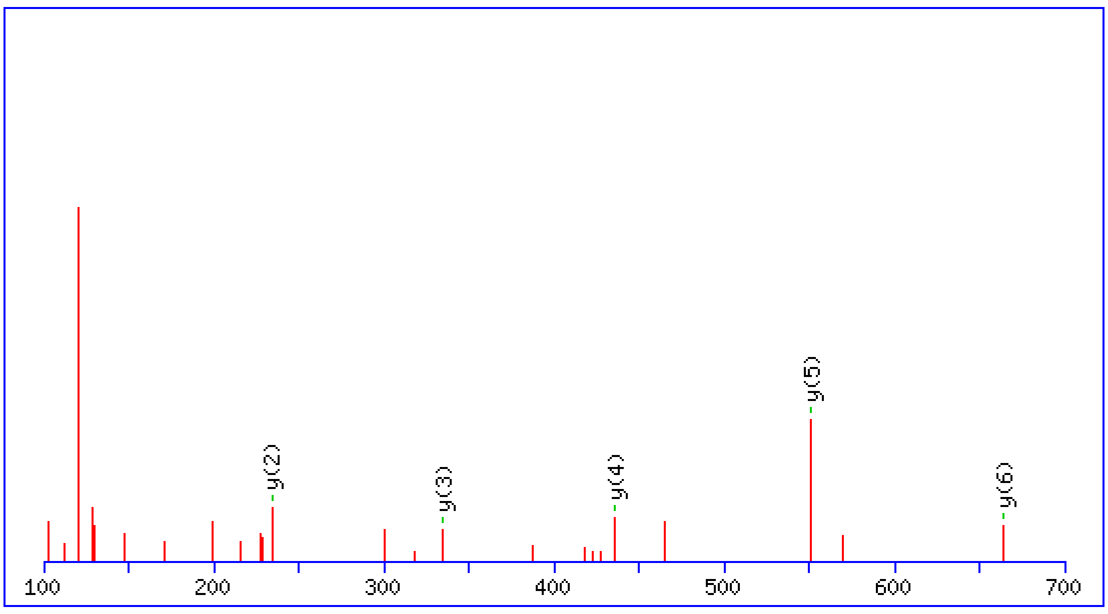
Mascot Search Results

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

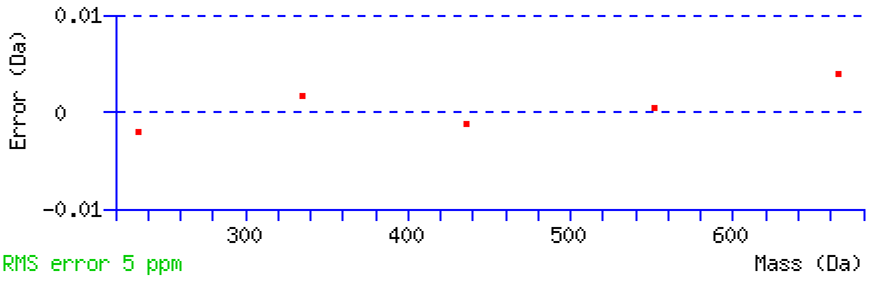
Match to Query 827: 810.405528 from(406.210040,2+) rtinseconds(1067) index(4865)
Title: Locus:1.1.1.1789.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

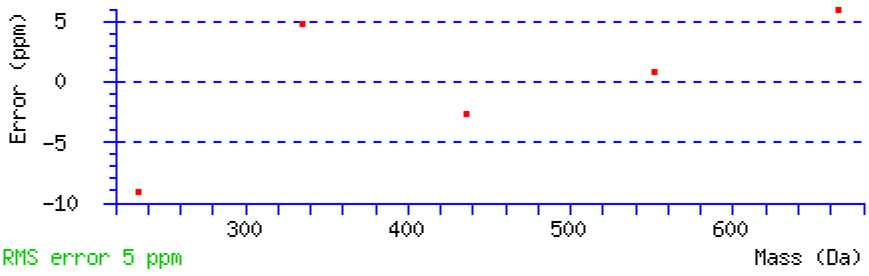
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 810.412338
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00022
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	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
44.8	810.412338	-0.006810	FIDTTSK
5.4	810.405807	-0.000279	FLQTMR
4.8	810.397919	0.007609	LMKMEK
3.9	810.398407	0.007121	QSQPHSK
3.8	810.412323	-0.006795	EVVSYSK
3.4	810.397934	0.007594	MLMSSVK
3.1	810.398407	0.007121	APAPNPGR
2.5	810.412323	-0.006795	LYSPTSK
2.0	810.412323	-0.006795	FSELSTK
1.3	810.398392	0.007136	QEEIHR

{MATRIX SCIENCE}

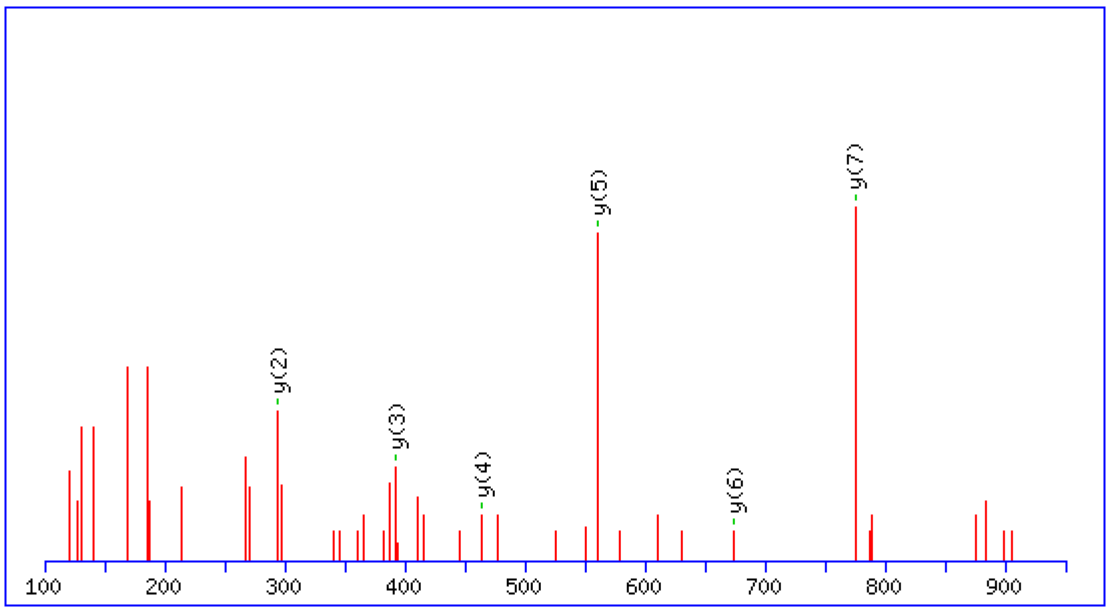
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVTLPAVFK**
Found in **RL4_HUMAN**, 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5

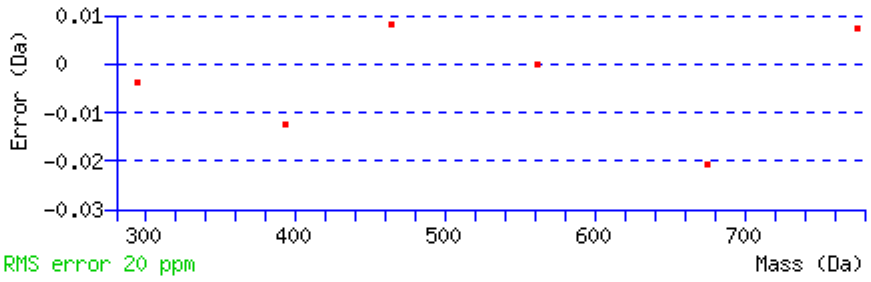
Match to Query 7528: 987.576268 from(494.795410,2+) rtinseconds(2744) index(37385)
Title: Locus:1.1.1.2527.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

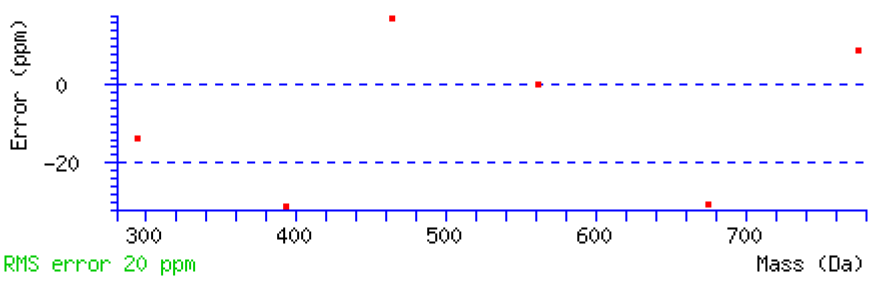
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 987.575317
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 2.9e-005
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	115.050203	58.028740	98.023654	49.515465			N							9
2	214.118617	107.562947	197.092068	99.049672			V	874.539667	437.773472	857.513118	429.260197	856.529102	428.768189	8
3	315.166296	158.086786	298.139747	149.573512	297.155731	149.081504	T	*775.471253*	388.239264	758.444704	379.725990	757.460688	379.233982	7
4	428.250360	214.628818	411.223811	206.115544	410.239795	205.623536	L	*674.423574*	337.715425	657.397025	329.202150			6
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	P	*561.339510*	281.173393	544.312961	272.660119			5
6	596.340238	298.673757	579.313689	290.160483	578.329673	289.668475	A	*464.286746*	232.647011	447.260197	224.133736			4
7	695.408652	348.207964	678.382103	339.694689	677.398087	339.202681	V	*393.249632*	197.128454	376.223083	188.615179			3
8	842.477066	421.742171	825.450517	413.228896	824.466501	412.736888	F	*294.181218*	147.594247	277.154669	139.080972			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NVTLPAVFK
(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	987.575317	0.000951	NVTLPAVFK

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

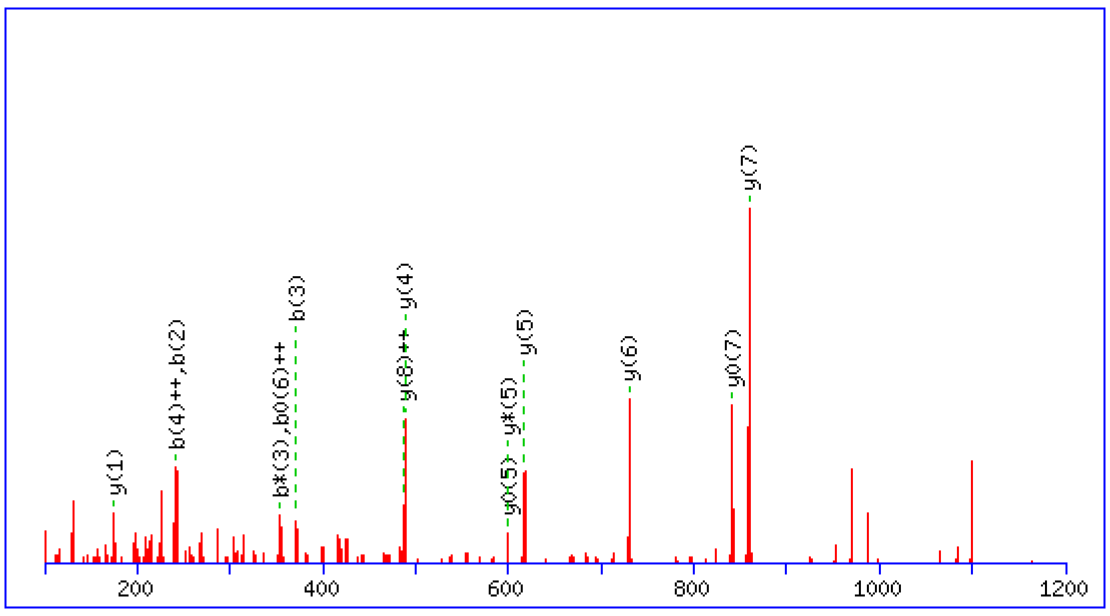
{MATRIX SCIENCE} Mascot Search Results

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

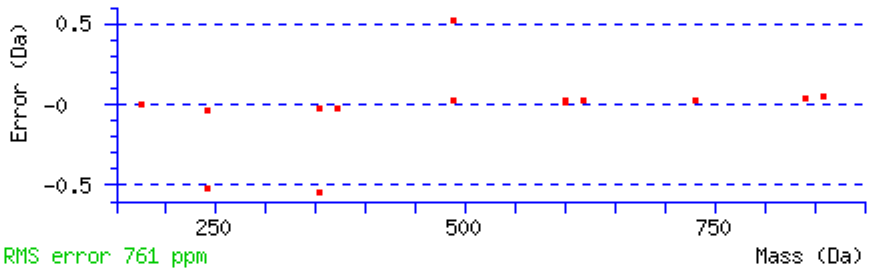
Match to Query 14227: 1099.626488 from(550.820520,2+) rtinseconds(1881) index(18272)
Title: Locus:1.1.1.2251.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

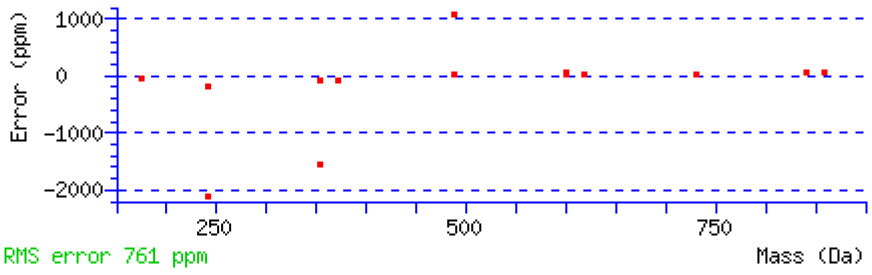
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1099.623672
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0076
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
31.0	1099.623672	0.002816	KLEIEIEAR
15.4	1099.634918	-0.008430	LKQENLSLR
14.0	1099.634918	-0.008430	LGKALENLSR
13.7	1099.623703	0.002785	KPQLLEQTK
13.5	1099.631073	-0.004585	LEELMKPLK
12.5	1099.634933	-0.008445	IQERVSKPK
12.2	1099.617172	0.009316	LMSSLHLKR
9.6	1099.634933	-0.008445	IQPLAKATSR
9.6	1099.623703	0.002785	LETIVQLER
9.1	1099.623672	0.002816	LQKELAEAAK

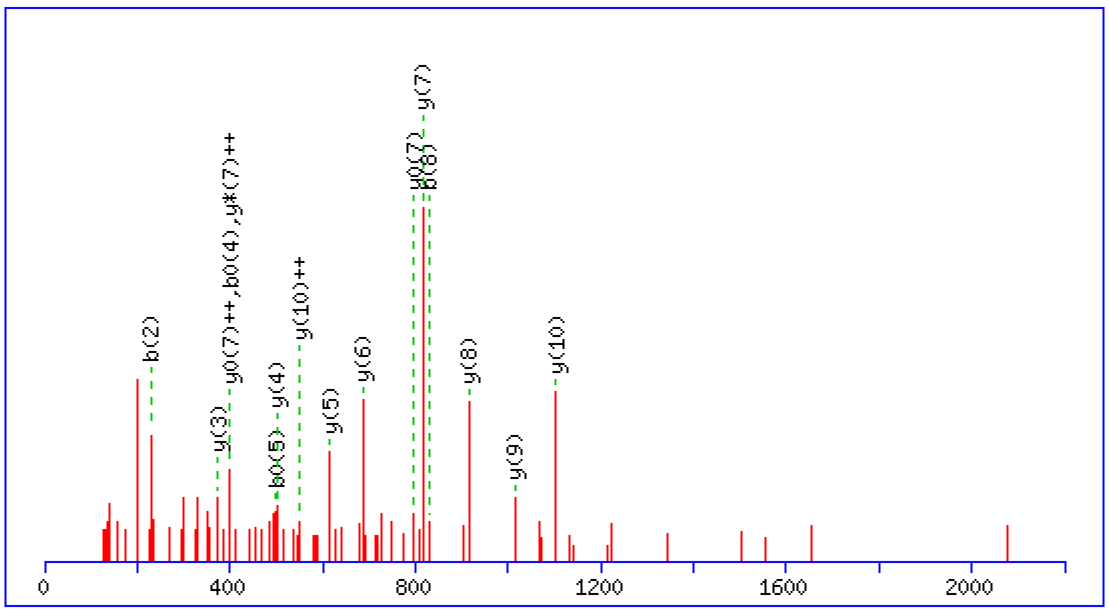
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLSTVEALQNLK**
Found in **AN32E_HUMAN**, Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1

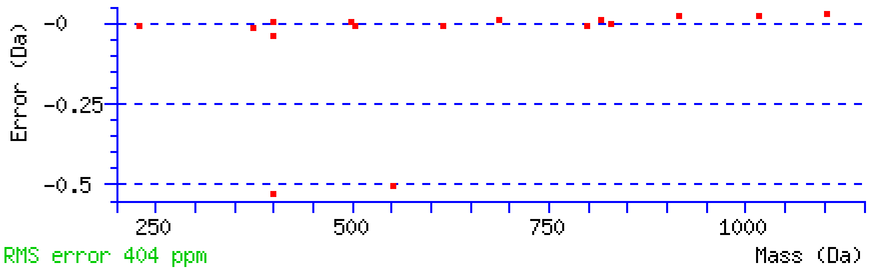
Match to Query 31568: 1329.718048 from(665.866300,2+) rtinseconds(2998) index(41296)
Title: Locus:1.1.1.2525.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

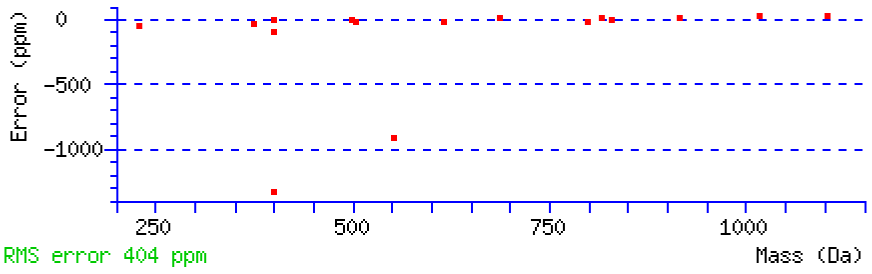
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1329.713974
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 6.4e-006
Matches : 16/104 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							12
2	**229.118283**	115.062779			211.107718	106.057497	L	1215.694329	608.350802	1198.667780	599.837528	1197.683764	599.345520	11
3	316.150311	158.578793			298.139746	149.573511	S	***1102.610265***	551.808771	1085.583716	543.295496	1084.599700	542.803488	10
4	417.197990	209.102633			399.187425	200.097351	T	***1015.578237***	508.292757	998.551688	499.779482	997.567672	499.287474	9
5	516.266404	258.636840			498.255839	249.631558	V	***914.530558***	457.768917	897.504009	449.255642	896.519993	448.763634	8
6	645.308997	323.158137			627.298432	314.152854	E	***815.462144***	408.234710	798.435595	399.721435	797.451579	399.229427	7
7	716.346111	358.676694			698.335546	349.671411	A	***686.419551***	343.713414	669.393002	335.200139			6
8	**829.430175**	415.218726			811.419610	406.213443	L	***615.382437***	308.194857	598.355888	299.681582			5
9	957.488753	479.248015	940.462204	470.734740	939.478188	470.242732	Q	***502.298373***	251.652824	485.271824	243.139550			4
10	1071.531680	536.269478	1054.505131	527.756204	1053.521115	527.264196	N	***374.239795***	187.623535	357.213246	179.110261			3
11	1184.615744	592.811510	1167.589195	584.298236	1166.605179	583.806227	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 DLSTVEALQNLK
(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	1329.713974	0.004074	DLSTVEALQNLK
3.8	1329.707458	0.010590	DLVMGSSPQLKR

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

{MATRIX}
{SCIENCE}

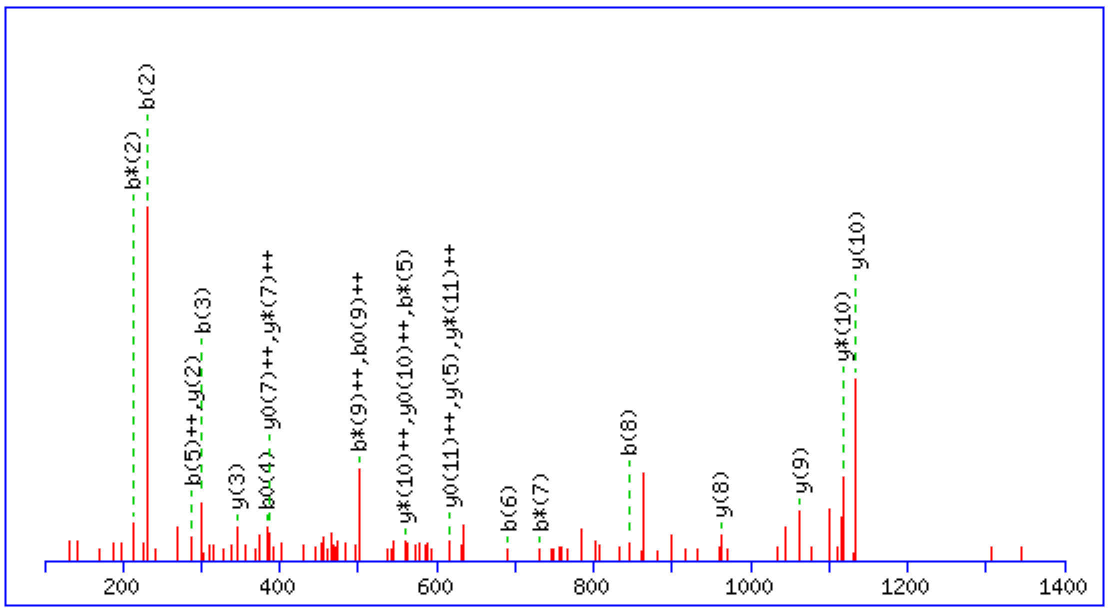
Mascot Search Results

Peptide View

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

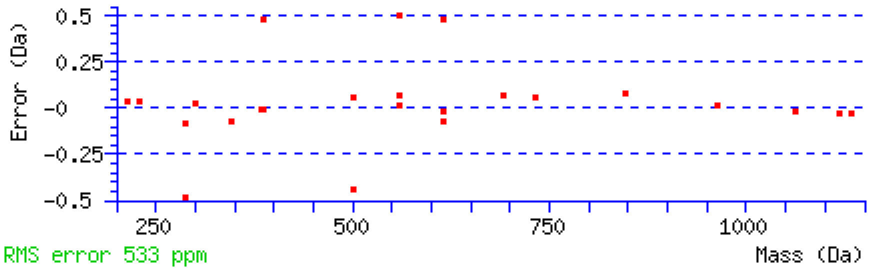
Match to Query 29631: 1362.576828 from(682.295690,2+) rtinseconds(2038) index(21193)
Title: Locus:1.1.1.2312.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

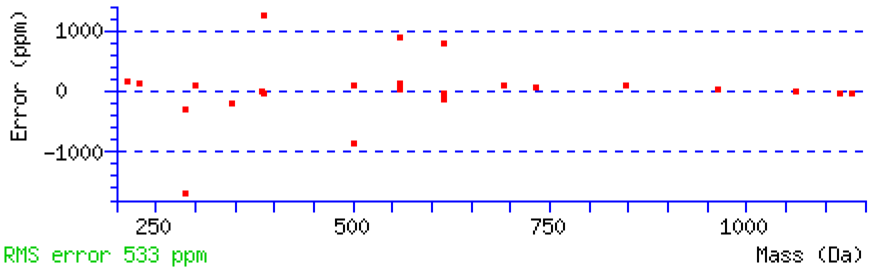
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1362.565628
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0017
Matches : 24/118 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	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
32.1	1362.565628	0.011200	DNATCDGPCGLR
0.7	1362.579544	-0.002716	TAGMMTSAEAFSK

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

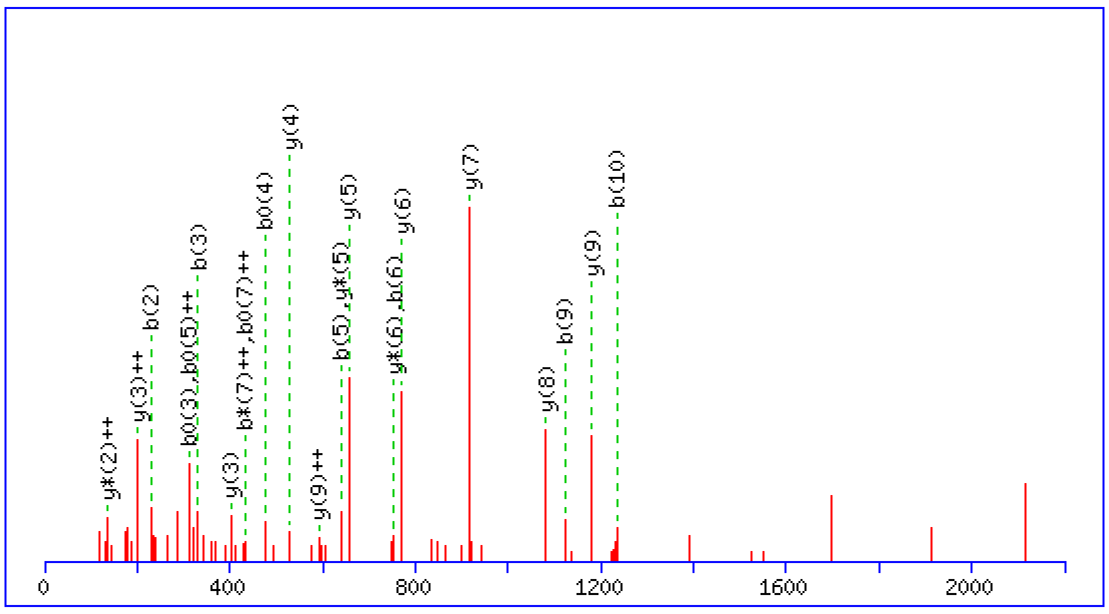
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DITYFIQQLLR**
Found in **ARP3B_HUMAN**, Actin-related protein 3B OS=Homo sapiens GN=ACTR3B PE=1 SV=1

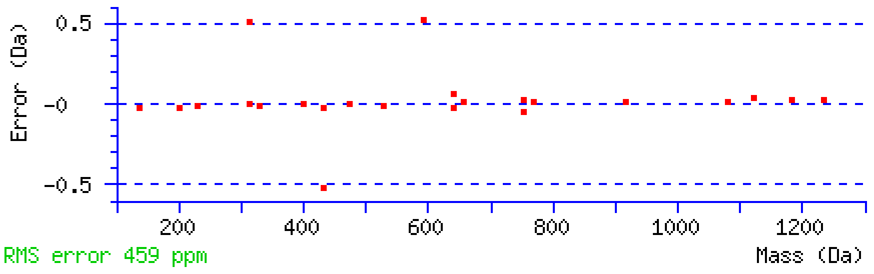
Match to Query 31665: 1408.783508 from(705.399030,2+) rtinseconds(4996) index(72720)
Title: Locus:1.1.1.3442.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

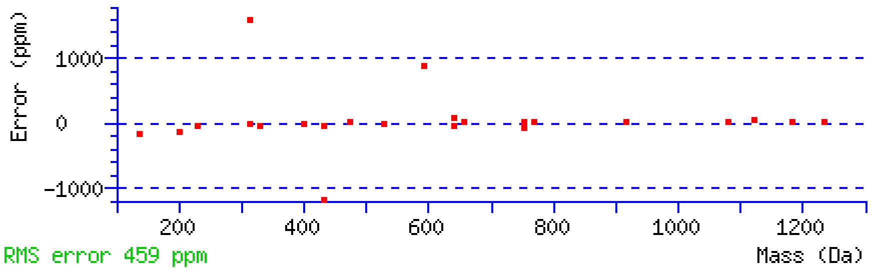
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1408.771439
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 2.5e-006
Matches : 23/92 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	116.034219	58.520748			98.023654	49.515465	D							11
2	***229.118283***	115.062779			211.107718	106.057497	I	1294.751786	647.879531	1277.725237	639.366256	1276.741221	638.874248	10
3	***330.165962***	165.586619			312.155397	156.581336	T	***1181.667722***	591.337499	1164.641173	582.824225	1163.657157	582.332216	9
4	493.229291	247.118283			475.218726	238.113001	Y	***1080.620043***	540.813659	1063.593494	532.300385			8
5	***640.297705***	320.652491			622.287140	311.647208	F	***917.556714***	459.281995	900.530165	450.768720			7
6	***753.381769***	377.194523			735.371204	368.189240	I	***770.488300***	385.747788	753.461751	377.234513			6
7	881.440347	441.223812	864.413798	432.710537	863.429782	432.218529	Q	***657.404236***	329.205756	640.377687	320.692481			5
8	1009.498925	505.253101	992.472376	496.739826	991.488360	496.247818	Q	***529.345658***	265.176467	512.319109	256.663192			4
9	***1122.582989***	561.795133	1105.556440	553.281858	1104.572424	552.789850	L	***401.287080***	201.147178	384.260531	192.633903			3
10	***1235.667053***	618.337164	1218.640504	609.823890	1217.656488	609.331882	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 DITYFIQQLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.3	1408.771439	0.012069	DITYFIQQLLR
10.1	1408.778625	0.004883	AEAEVRPKIPGSR
7.7	1408.792557	-0.009049	LDVLESLIKDHK
6.0	1408.792557	-0.009049	SPEAKPLPGKLPK
6.0	1408.792557	-0.009049	SPEAKPLPGKLPK
6.0	1408.792557	-0.009049	SPEAKPLPGKLPK
5.9	1408.778625	0.004883	EALEQGPRGLALR
2.3	1408.778671	0.004837	LDLPVTTRSVHR

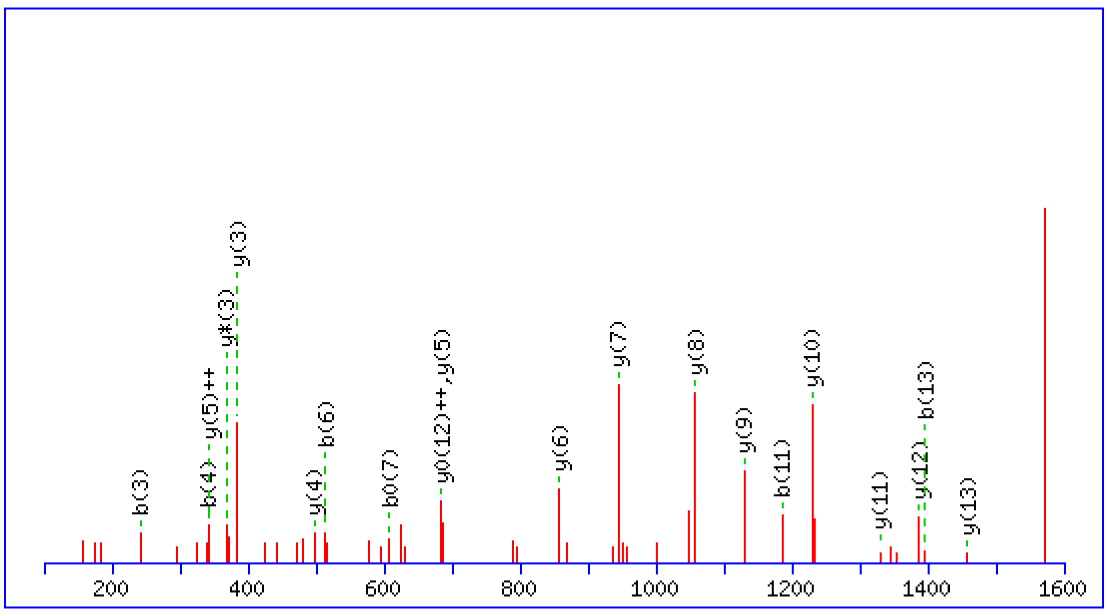
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGVTALSCWLPLR**
Found in **LYPA1_HUMAN**, Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1 PE=1 SV=1

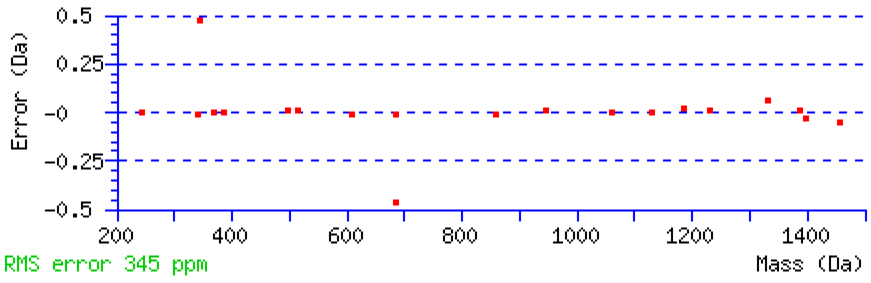
Match to Query 33960: 1569.876728 from(785.945640,2+) rtinseconds(4091) index(52926)
Title: Locus:1.1.1.3361.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

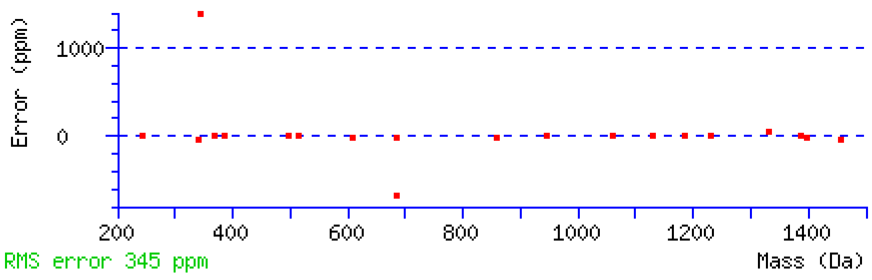
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1569.870102
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 90  Expect: 6.7e-009
Matches : 20/110 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	185.128454	93.067865			A	***1457.793333***	729.400304	1440.766784	720.887030	1439.782768	720.395022	13
3	**242.149918**	121.578597			G	***1386.756219***	693.881747	1369.729670	685.368473	1368.745654	684.876465	12
4	**341.218332**	171.112804			V	***1329.734755***	665.371015	1312.708206	656.857741	1311.724190	656.365733	11
5	442.266011	221.636643	424.255446	212.631361	T	***1230.666341***	615.836808	1213.639792	607.323534	1212.655776	606.831526	10
6	**513.303125**	257.155201	495.292560	248.149918	A	***1129.618662***	565.312969	1112.592113	556.799694	1111.608097	556.307686	9
7	626.387189	313.697233	608.376624	304.691950	L	***1058.581548***	529.794412	1041.554999	521.281138	1040.570983	520.789129	8
8	713.419217	357.213247	695.408652	348.207964	S	***945.497484***	473.252380	928.470935	464.739105	927.486919	464.247097	7
9	887.465516	444.236396	869.454951	435.231113	C	***858.465456***	429.736366	841.438907	421.223091			6
10	1073.544829	537.276052	1055.534264	528.270770	W	***684.419157***	342.713216	667.392608	334.199942			5
11	**1186.628893**	593.818084	1168.618328	584.812802	L	***498.339844***	249.673560	481.313295	241.160285			4
12	1283.681657	642.344466	1265.671092	633.339184	P	***385.255780***	193.131528	368.229231	184.618253			3
13	**1396.765721**	698.886498	1378.755156	689.881216	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 LAGVTALSCWLPLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.3	1569.870102	0.006626	LAGVTALSCWLPLR
12.6	1569.883850	-0.007122	AIRVTISSGPEVSVR
7.1	1569.861359	0.015369	DAKEELTASLVGLPK
6.5	1569.870071	0.006657	KLLASLEWLMPNR
6.2	1569.876617	0.000111	LSEEPLIPPPLPPR
6.2	1569.876617	0.000111	LSEEPLIPPPLPPR
5.4	1569.876617	0.000111	LSEEPLIPPPLPPR
5.3	1569.887863	-0.011135	LALPVNSSPAVIFAR
2.6	1569.872635	0.004093	LTVPTGLSVTSPDKR
2.2	1569.873932	0.002796	LQPHPQLSPEIRR

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

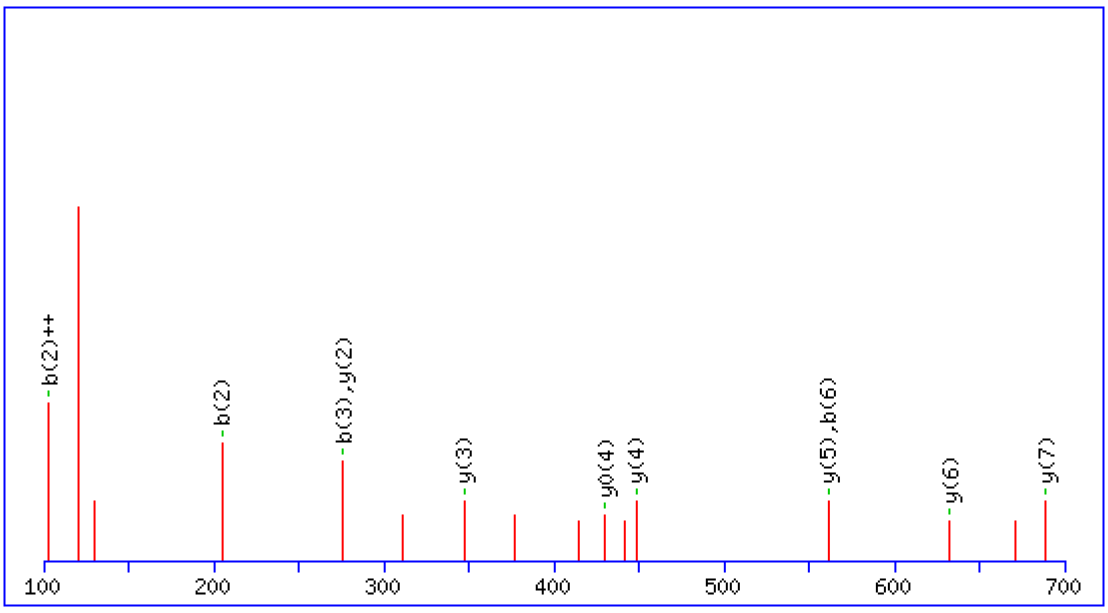
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGALTAEK**
Found in **LYPA2_HUMAN**, Acyl-protein thioesterase 2 OS=Homo sapiens GN=LYPLA2 PE=1 SV=1

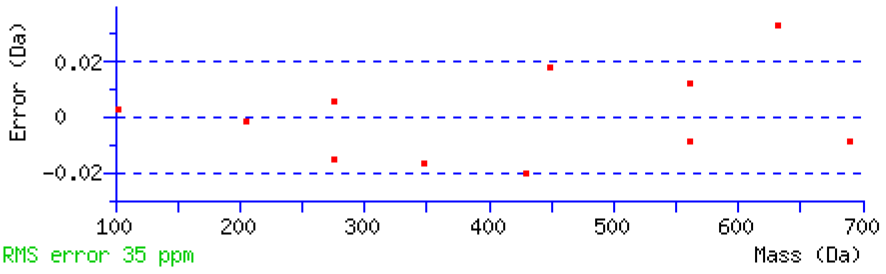
Match to Query 1751: 835.439868 from(418.727210,2+) rtinseconds(1577) index(8478)
Title: Locus:1.1.1.2411.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

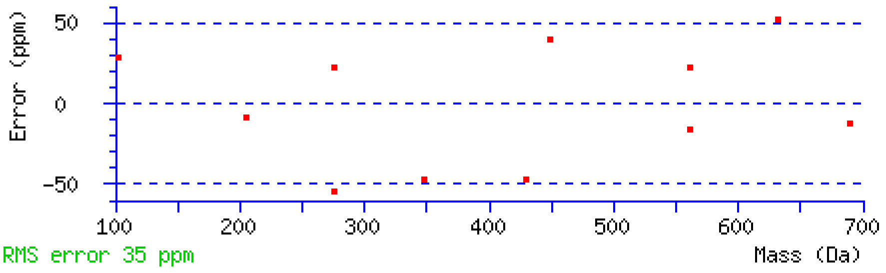
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 835.443954
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 7.5e-005
Matches : 11/60 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							8
2	**205.097154**	103.052215			G	***689.382832***	345.195054	672.356283	336.681780	671.372267	336.189772	7
3	**276.134268**	138.570772			A	***632.361368***	316.684322	615.334819	308.171048	614.350803	307.679040	6
4	389.218332	195.112804			L	***561.324254***	281.165765	544.297705	272.652491	543.313689	272.160483	5
5	490.266011	245.636643	472.255446	236.631361	T	***448.240190***	224.623733	431.213641	216.110458	430.229625	215.618450	4
6	**561.303125**	281.155201	543.292560	272.149918	A	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
7	690.345718	345.676497	672.335153	336.671215	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 FGALTAEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.4	835.443954	-0.004086	FGALTAEK
11.8	835.443970	-0.004102	FLQTSPK
11.8	835.443970	-0.004102	FPKTPSK
1.7	835.433411	0.006457	ASVRMTR

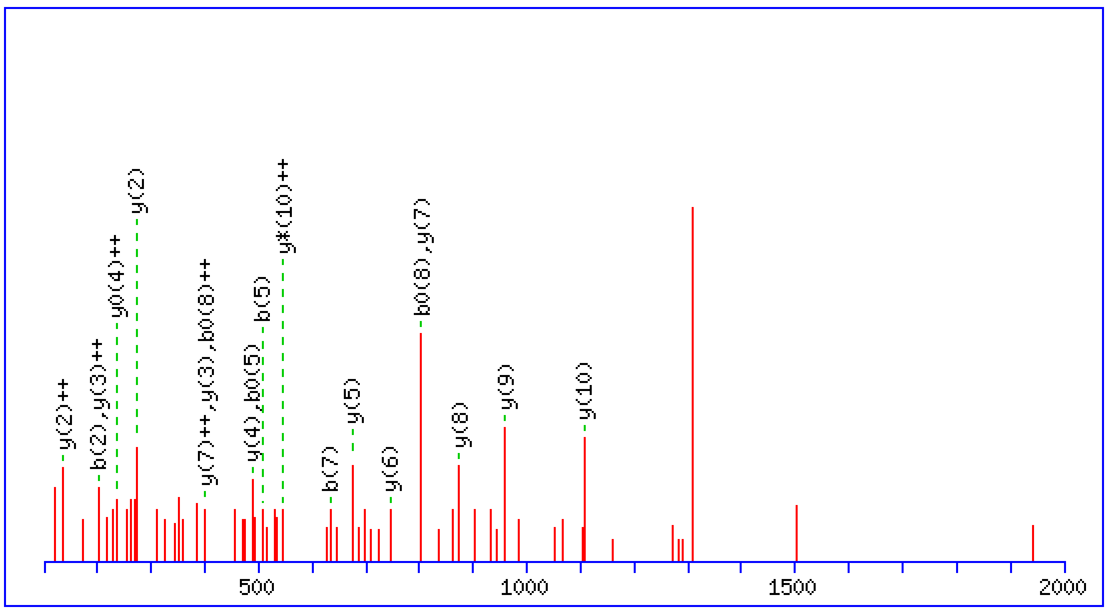
{MATRIX SCIENCE} Mascot Search Results

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

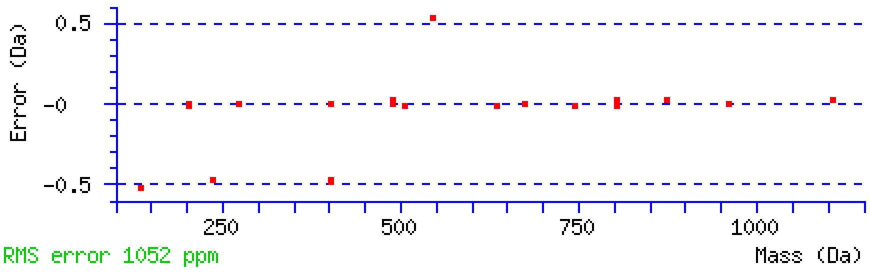
Match to Query 27820: 1306.599928 from(654.307240,2+) rtinseconds(2395) index(28276)
Title: Locus:1.1.1.2356.31
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

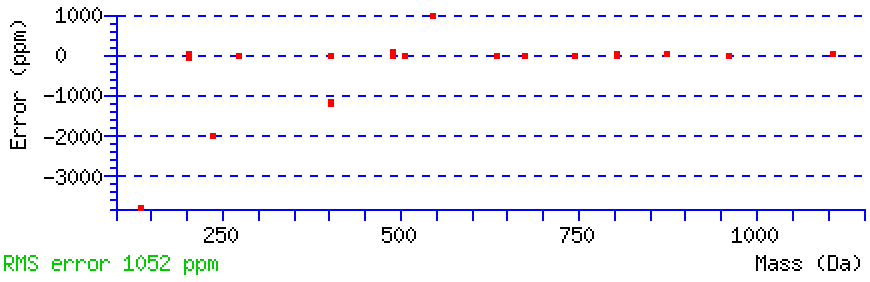
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1306.594193
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58  Expect: 9.1e-006
Matches : 20/104 fragment ions using 34 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
57.6	1306.594193	0.005735	AEFSAGAWSEPR
2.7	1306.604111	-0.004183	EVPVYTDSEPR
2.5	1306.596207	0.003721	EELMQELSSLE

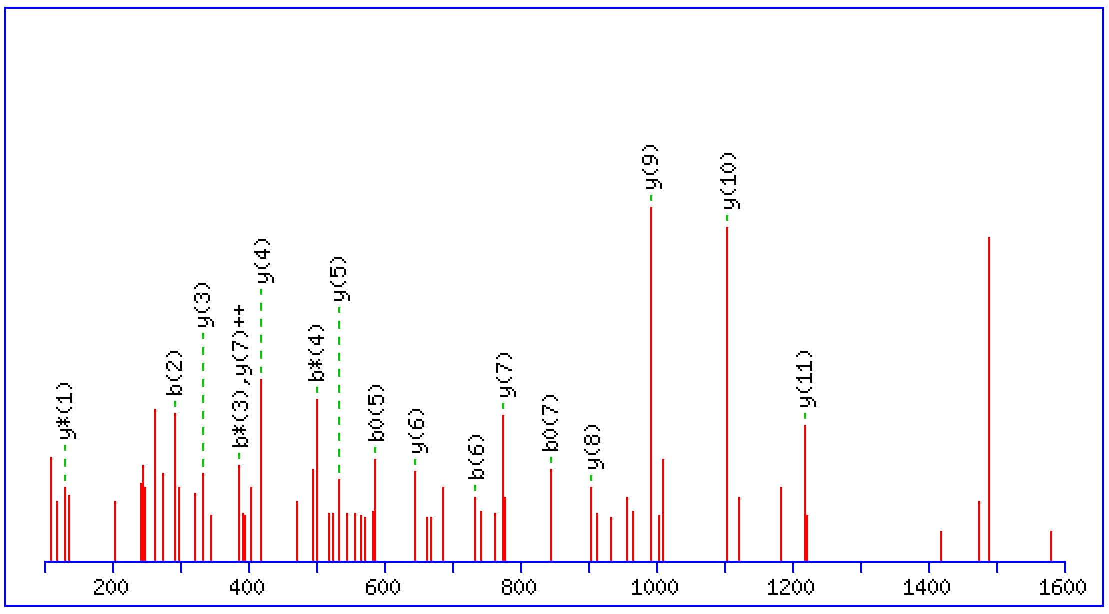
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYIISEELISEGK**
Found in **NUDT5_HUMAN**, ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1

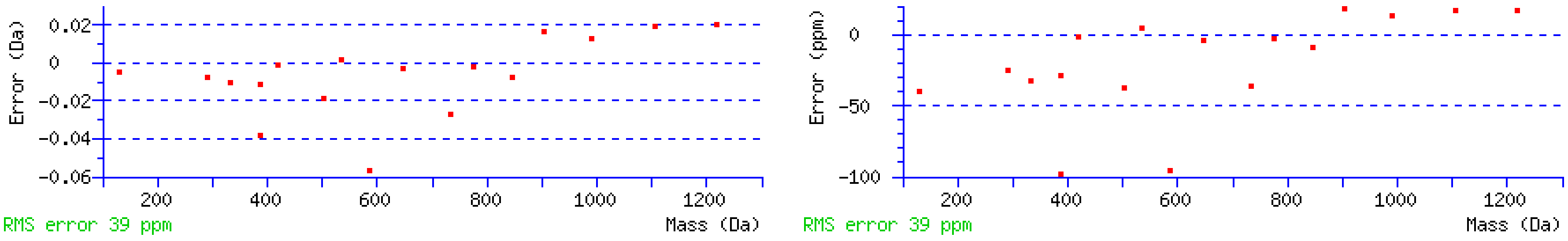
Match to Query 41100: 1507.789308 from(754.901930,2+) rtinseconds(2919) index(37810)
Title: Locus:1.1.1.2602.48
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

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): 1507.776947
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 3.8e-007
Matches : 17/132 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	129.065854	65.036565	112.039305	56.523291			Q							13
2	**292.129183**	146.568230	275.102634	138.054955			Y	1380.725688	690.866482	1363.699139	682.353207	1362.715123	681.861199	12
3	405.213247	203.110262	388.186698	194.596987			I	***1217.662359***	609.334817	1200.635810	600.821543	1199.651794	600.329535	11
4	518.297311	259.652294	501.270762	251.139019			I	***1104.578295***	552.792785	1087.551746	544.279511	1086.567730	543.787503	10
5	605.329339	303.168308	588.302790	294.655033	587.318774	294.163025	S	***991.494231***	496.250753	974.467682	487.737479	973.483666	487.245471	9
6	**734.371932**	367.689604	717.345383	359.176330	716.361367	358.684322	E	***904.462203***	452.734739	887.435654	444.221465	886.451638	443.729457	8
7	863.414525	432.210901	846.387976	423.697626	845.403960	423.205618	E	***775.419610***	388.213443	758.393061	379.700168	757.409045	379.208160	7
8	976.498589	488.752933	959.472040	480.239658	958.488024	479.747650	L	***646.377017***	323.692146	629.350468	315.178872	628.366452	314.686864	6
9	1089.582653	545.294964	1072.556104	536.781690	1071.572088	536.289682	I	***533.292953***	267.150114	516.266404	258.636840	515.282388	258.144832	5
10	1176.614681	588.810979	1159.588132	580.297704	1158.604116	579.805696	S	***420.208889***	210.608082	403.182340	202.094808	402.198324	201.602800	4
11	1305.657274	653.332275	1288.630725	644.819001	1287.646709	644.326992	E	***333.176861***	167.092068	316.150312	158.578794	315.166296	158.086786	3
12	1362.678738	681.843007	1345.652189	673.329732	1344.668173	672.837724	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 QYIISEELISEGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.6	1507.776947	0.012361	QYIISEELISEGK
3.0	1507.799438	-0.010130	EQPPPQLLVAAAAR

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

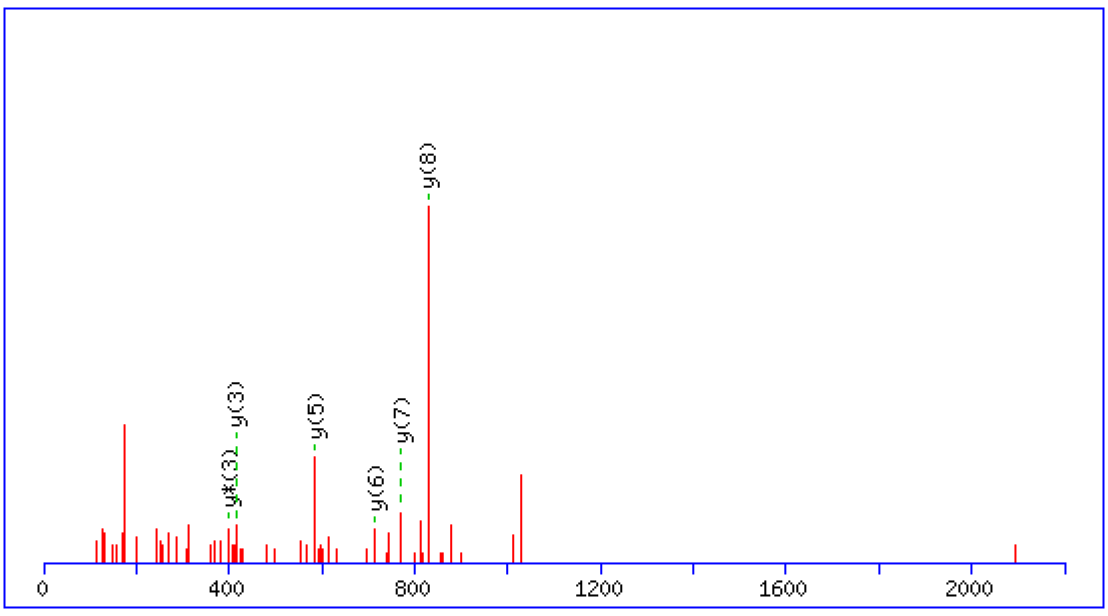
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLGGQAVQIR**
Found in **ADSV_HUMAN**, Adseverin OS=Homo sapiens GN=SCIN PE=1 SV=4

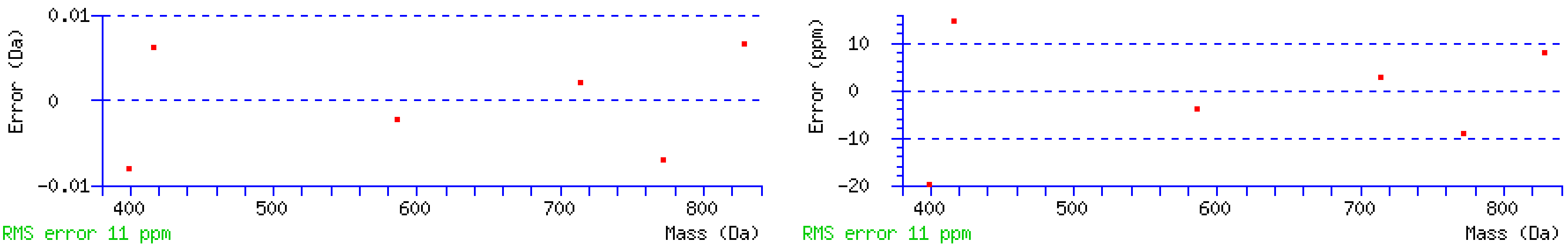
Match to Query 13859: 1027.580268 from(514.797410,2+) rtinseconds(1692) index(18748)
Title: Locus:1.1.1.1286.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

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): 1027.577438
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00094
Matches : 6/82 fragment ions using 9 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	L	941.552692	471.279984	924.526143	462.766710	9
3	258.144832	129.576054			240.134267	120.570771	G	***828.468628***	414.737952	811.442079	406.224678	8
4	315.166296	158.086786			297.155731	149.081503	G	***771.447164***	386.227220	754.420615	377.713946	7
5	443.224874	222.116075	426.198325	213.602800	425.214309	213.110792	Q	***714.425700***	357.716488	697.399151	349.203214	6
6	514.261988	257.634632	497.235439	249.121357	496.251423	248.629349	A	***586.367122***	293.687199	569.340573	285.173925	5
7	613.330402	307.168839	596.303853	298.655564	595.319837	298.163556	V	515.330008	258.168642	498.303459	249.655368	4
8	741.388980	371.198128	724.362431	362.684853	723.378415	362.192845	Q	***416.261594***	208.634435	399.235045	200.121161	3
9	854.473044	427.740160	837.446495	419.226885	836.462479	418.734877	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 SLGGQAVQIR
(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	1027.577438	0.002830	SLGGQAVQIR
14.2	1027.577393	0.002875	EALERALAR
11.6	1027.588669	-0.008401	GTRAGGLALGR
4.7	1027.577423	0.002845	KQQLDGALR
3.2	1027.577438	0.002830	SLPSVTRPR
2.3	1027.577423	0.002845	EPLGATIRR
2.0	1027.588638	-0.008370	RTAQAAAALR
1.4	1027.588669	-0.008401	RGQTLGLQR
1.4	1027.588669	-0.008401	TALLGGGQRR
0.7	1027.581436	-0.001168	AWLIEPRK

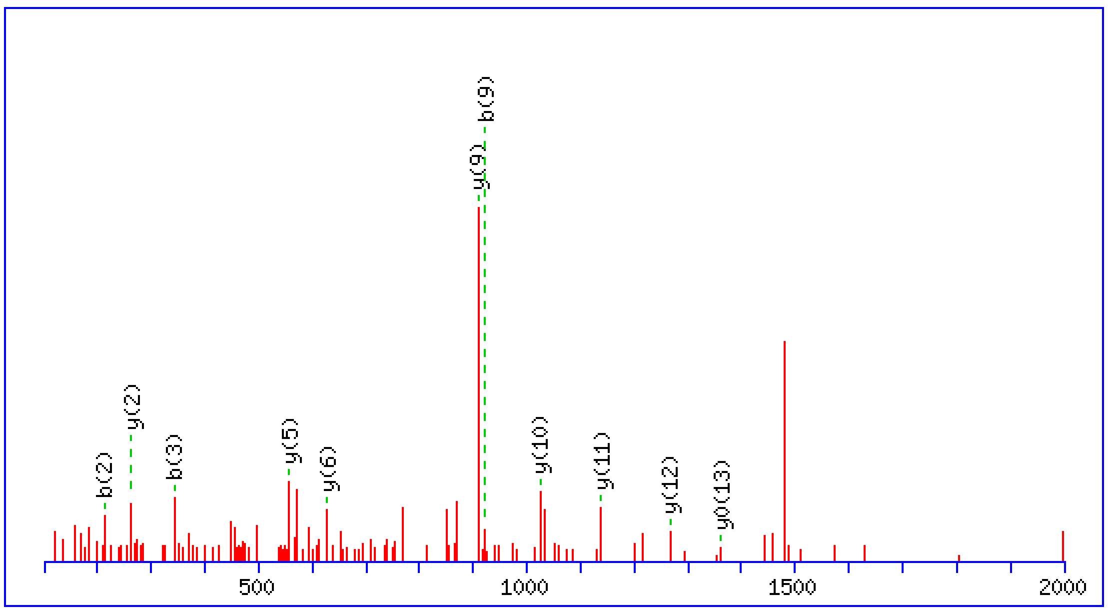
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLELDPALAPVVSR**
Found in **AIP_HUMAN**, AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2

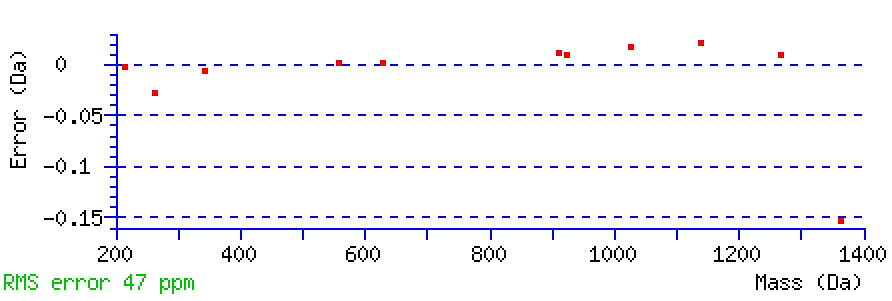
Match to Query 39216: 1477.856768 from(739.935660,2+) rtinseconds(3212) index(43027)
Title: Locus:1.1.1.2619.27
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

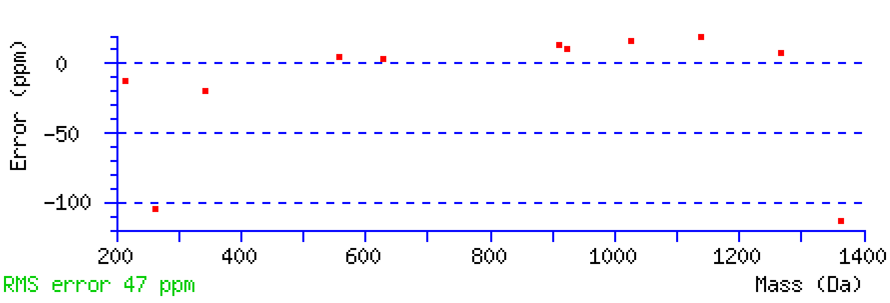
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1477.850418
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 5.7e-006
Matches : 11/124 fragment ions using 14 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.075690	50.541483			V							14
2	**213.159754**	107.083515			L	1379.789292	690.398284	1362.762743	681.885010	1361.778727	681.393002	13
3	**342.202347**	171.604811	324.191782	162.599529	E	***1266.705228***	633.856252	1249.678679	625.342978	1248.694663	624.850970	12
4	455.286411	228.146843	437.275846	219.141561	L	***1137.662635***	569.334956	1120.636086	560.821681	1119.652070	560.329673	11
5	570.313354	285.660315	552.302789	276.655033	D	***1024.578571***	512.792924	1007.552022	504.279649	1006.568006	503.787641	10
6	667.366118	334.186697	649.355553	325.181415	P	***909.551628***	455.279452	892.525079	446.766178	891.541063	446.274170	9
7	738.403232	369.705254	720.392667	360.699972	A	812.498864	406.753070	795.472315	398.239796	794.488299	397.747788	8
8	851.487296	426.247286	833.476731	417.242004	L	741.461750	371.234513	724.435201	362.721239	723.451185	362.229231	7
9	**922.524410**	461.765843	904.513845	452.760561	A	***628.377686***	314.692481	611.351137	306.179207	610.367121	305.687199	6
10	1019.577174	510.292225	1001.566609	501.286943	P	***557.340572***	279.173924	540.314023	270.660650	539.330007	270.168642	5
11	1118.645588	559.826432	1100.635023	550.821150	V	460.287808	230.647542	443.261259	222.134268	442.277243	221.642260	4
12	1217.714002	609.360639	1199.703437	600.355357	V	361.219394	181.113335	344.192845	172.600061	343.208829	172.108053	3
13	1304.746030	652.876653	1286.735465	643.871371	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 VLELDPALAPVVSR
(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	1477.850418	0.006350	VLELDPALAPVVSR

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

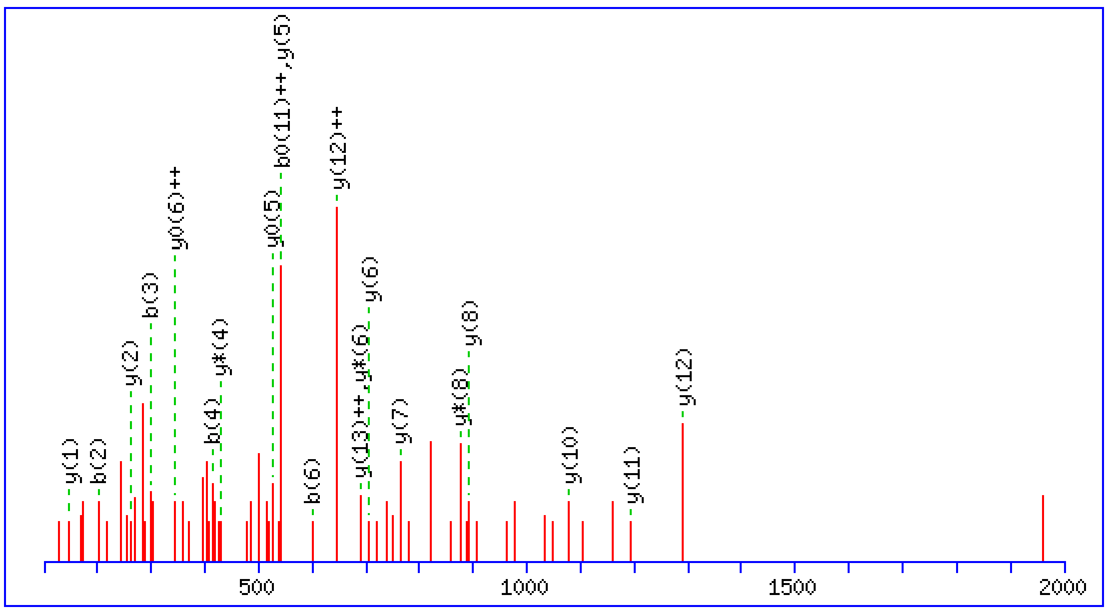
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISPDGEEGYPGELK**
Found in **GALM_HUMAN**, Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1

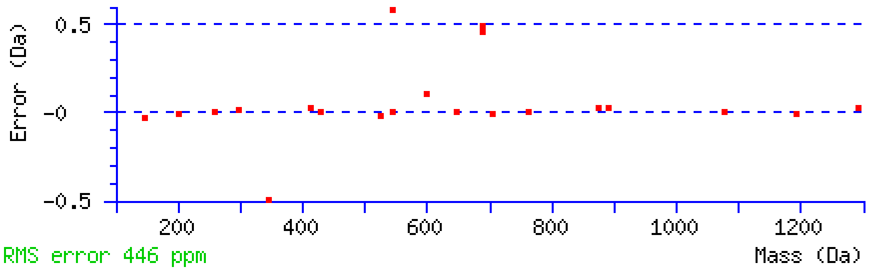
Match to Query 32338: 1489.702128 from(745.858340,2+) rtinseconds(2016) index(16194)
Title: Locus:1.1.1.2338.47
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

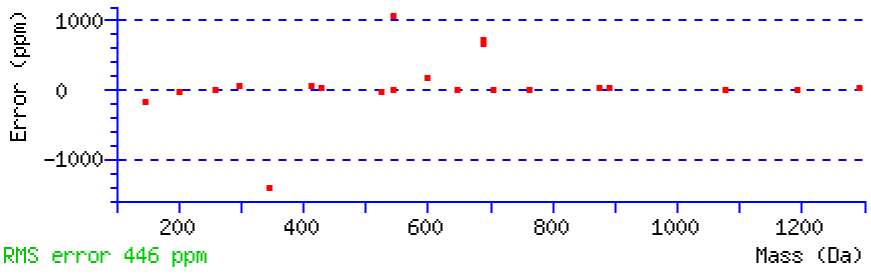
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1489.693634
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0024
Matches : 21/124 fragment ions using 57 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			I							14
2	**201.123368**	101.065322	183.112803	92.060039	S	1377.616867	689.312072	1360.590318	680.798797	1359.606302	680.306789	13
3	**298.176132**	149.591704	280.165567	140.586422	P	***1290.584839***	645.796057	1273.558290	637.282783	1272.574274	636.790775	12
4	**413.203075**	207.105176	395.192510	198.099893	D	***1193.532075***	597.269675	1176.505526	588.756401	1175.521510	588.264393	11
5	470.224539	235.615907	452.213974	226.610625	G	***1078.505132***	539.756204	1061.478583	531.242929	1060.494567	530.750921	10
6	**599.267132**	300.137204	581.256567	291.131922	E	1021.483668	511.245472	1004.457119	502.732197	1003.473103	502.240189	9
7	728.309725	364.658501	710.299160	355.653218	E	***892.441075***	446.724175	875.414526	438.210901	874.430510	437.718893	8
8	785.331189	393.169233	767.320624	384.163950	G	***763.398482***	382.202879	746.371933	373.689604	745.387917	373.197596	7
9	948.394518	474.700897	930.383953	465.695615	Y	***706.377018***	353.692147	689.350469	345.178872	688.366453	344.686864	6
10	1045.447282	523.227279	1027.436717	514.221997	P	***543.313689***	272.160482	526.287140	263.647208	525.303124	263.155200	5
11	1102.468746	551.738011	1084.458181	542.732729	G	446.260925	223.634100	429.234376	215.120826	428.250360	214.628818	4
12	1231.511339	616.259307	1213.500774	607.254025	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
13	1344.595403	672.801339	1326.584838	663.796057	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 ISPDGEEGYPGELK
(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	1489.693634	0.008494	ISPDGEEGYPGELK
6.7	1489.689590	0.012538	ISSENSNPEQELK
4.3	1489.716141	-0.014013	KPPPPPPQDGPGSR
3.0	1489.712280	-0.010152	KDPYTATMIGFSK

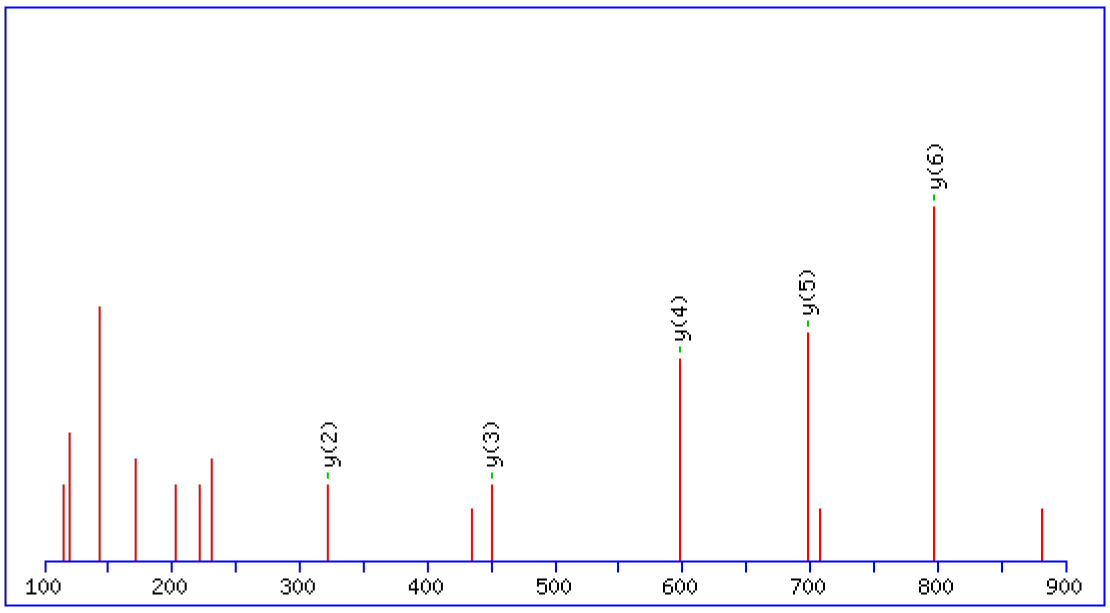
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIVTFQFR**
Found in **MGAT1_HUMAN**, Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT1 PE=2 SV=2

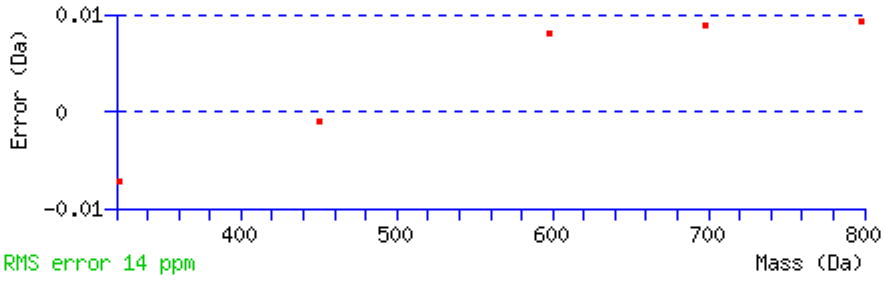
Match to Query 7021: 966.525388 from(484.269970,2+) rtinseconds(2821) index(34019)
Title: Locus:1.1.1.2602.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

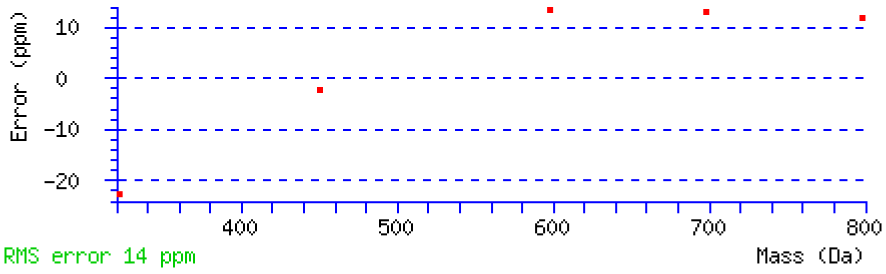
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 966.528717
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.001
Matches : 5/60 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	58.028740	29.518008					G							8
2	171.112804	86.060040					I	910.514515	455.760896	893.487966	447.247621	892.503950	446.755613	7
3	270.181218	135.594247					V	*797.430451*	399.218864	780.403902	390.705589	779.419886	390.213581	6
4	371.228897	186.118087			353.218332	177.112804	T	*698.362037*	349.684657	681.335488	341.171382	680.351472	340.679374	5
5	518.297311	259.652294			500.286746	250.647011	F	*597.314358*	299.160817	580.287809	290.647542			4
6	646.355889	323.681583	629.329340	315.168308	628.345324	314.676300	Q	*450.245944*	225.626610	433.219395	217.113335			3
7	793.424303	397.215790	776.397754	388.702515	775.413738	388.210507	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 GIVTFQFR
(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	966.528717	-0.003329	GIVTFQFR

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

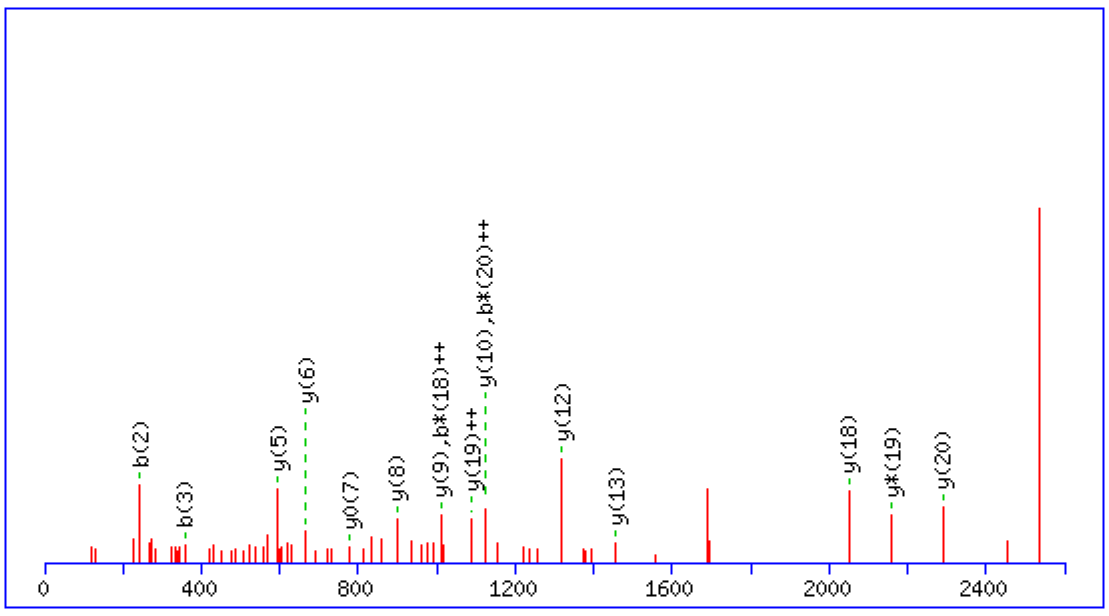
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQLQTFSEEHPVLLTEAPLNPR**
Found in **ACTZ_HUMAN**, Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1

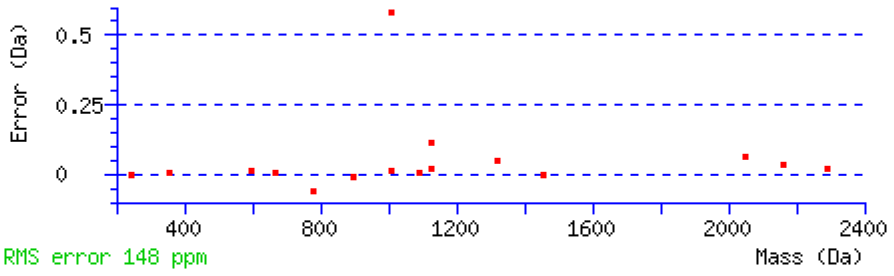
Match to Query 69131: 2533.297062 from(845.439630,3+) rtinseconds(3269) index(44083)
Title: Locus:1.1.1.2640.33
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

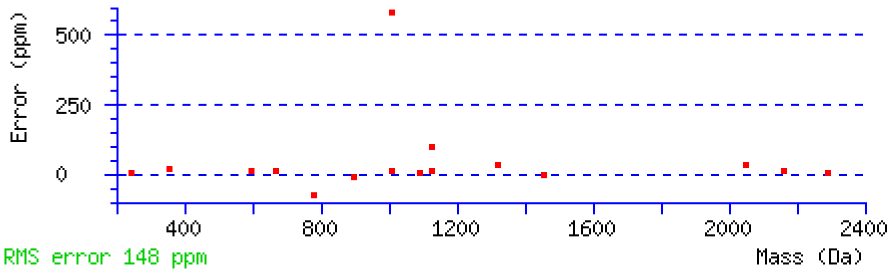
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2533.281250
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 5.7e-006
Matches : 16/238 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	116.034219	58.520748			98.023654	49.515465	D							22
2	**244.092797**	122.550037	227.066248	114.036762	226.082232	113.544754	Q	2419.261602	1210.134439	2402.235053	1201.621164	2401.251037	1201.129156	21
3	**357.176861**	179.092069	340.150312	170.578794	339.166296	170.086786	L	***2291.203024***	1146.105150	2274.176475	1137.591875	2273.192459	1137.099867	20
4	485.235439	243.121358	468.208890	234.608083	467.224874	234.116075	Q	2178.118960	1089.563118	2161.092411	1081.049843	2160.108395	1080.557835	19
5	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	T	***2050.060382***	1025.533829	2033.033833	1017.020554	2032.049817	1016.528546	18
6	733.351532	367.179404	716.324983	358.666130	715.340967	358.174122	F	1949.012703	975.009989	1931.986154	966.496715	1931.002138	966.004707	17
7	820.383560	410.695418	803.357011	402.182144	802.372995	401.690136	S	1801.944289	901.475782	1784.917740	892.962508	1783.933724	892.470500	16
8	949.426153	475.216715	932.399604	466.703440	931.415588	466.211432	E	1714.912261	857.959768	1697.885712	849.446494	1696.901696	848.954486	15
9	1078.468746	539.738011	1061.442197	531.224737	1060.458181	530.732729	E	1585.869668	793.438472	1568.843119	784.925197	1567.859103	784.433189	14
10	1215.527658	608.267467	1198.501109	599.754193	1197.517093	599.262184	H	***1456.827075***	728.917175	1439.800526	720.403901	1438.816510	719.911893	13
11	1312.580422	656.793849	1295.553873	648.280575	1294.569857	647.788567	P	***1319.768163***	660.387719	1302.741614	651.874445	1301.757598	651.382437	12
12	1411.648836	706.328056	1394.622287	697.814782	1393.638271	697.322774	V	1222.715399	611.861337	1205.688850	603.348063	1204.704834	602.856055	11
13	1524.732900	762.870088	1507.706351	754.356814	1506.722335	753.864805	L	***1123.646985***	562.327130	1106.620436	553.813856	1105.636420	553.321848	10
14	1637.816964	819.412120	1620.790415	810.898845	1619.806399	810.406837	L	***1010.562921***	505.785098	993.536372	497.271824	992.552356	496.779816	9
15	1738.864643	869.935959	1721.838094	861.422685	1720.854078	860.930677	T	***897.478857***	449.243066	880.452308	440.729792	879.468292	440.237784	8
16	1867.907236	934.457256	1850.880687	925.943981	1849.896671	925.451973	E	796.431178	398.719227	779.404629	390.205952	778.420613	389.713944	7
17	1938.944350	969.975813	1921.917801	961.462538	1920.933785	960.970530	A	***667.388585***	334.197930	650.362036	325.684656			6
18	2035.997114	1018.502195	2018.970565	1009.988920	2017.986549	1009.496912	P	***596.351471***	298.679374	579.324922	290.166099			5
19	2149.081178	1075.044227	2132.054629	1066.530952	2131.070613	1066.038944	L	499.298707	250.152991	482.272158	241.639717			4
20	2263.124105	1132.065690	2246.097556	1123.552416	2245.113540	1123.060408	N	386.214643	193.610959	369.188094	185.097685			3
21	2360.176869	1180.592072	2343.150320	1172.078798	2342.166304	1171.586790	P	272.171716	136.589496	255.145167	128.076221			2
22							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DQLQTFSEEHPVLLTEAPLNPR
(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	2533.281250	0.015812	DQLQTFSEEHPVLLTEAPLNPR
1.6	2533.314484	-0.017422	AGNNMLLVGVHGPRTPCEEILVK

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

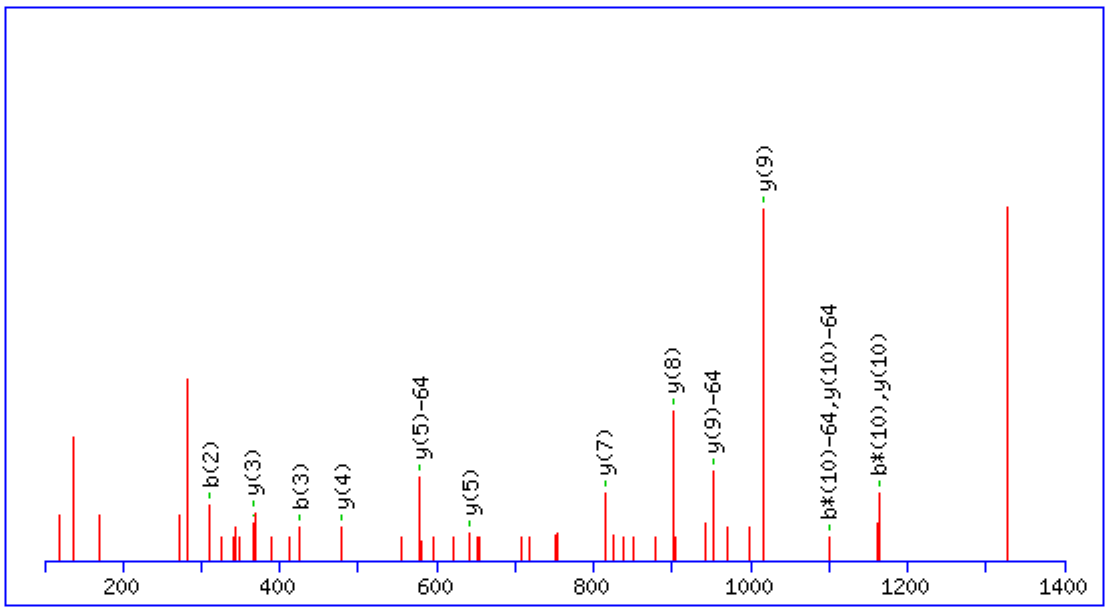
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFDSGDYNMAK**
Found in **ARP19_HUMAN**, cAMP-regulated phosphoprotein 19 OS=Homo sapiens GN=ARPP19 PE=1 SV=2

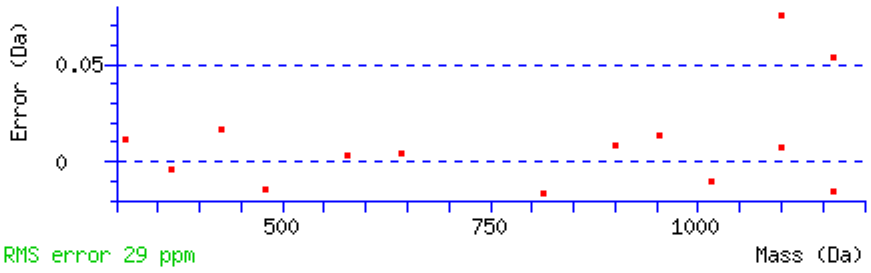
Match to Query 20085: 1325.529848 from(663.772200,2+) rtinseconds(1724) index(6434)
Title: Locus:1.1.1.2167.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

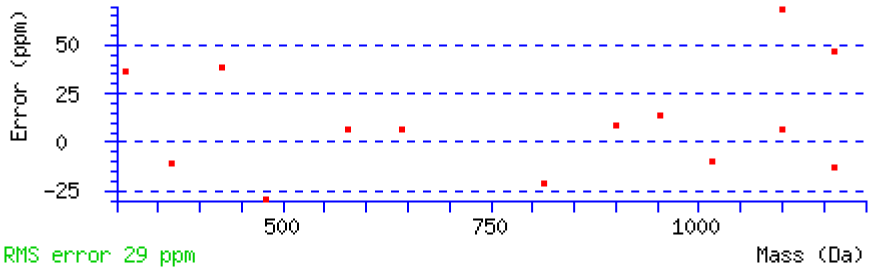
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1325.523407
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: 48  Expect: 2e-005
Matches : 14/146 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	164.070605	82.538940					Y							11
2	**311.139019**	156.073148					F	***1163.467366***	582.237321	1146.440817	573.724047	1145.456801	573.232039	10
3	**426.165962**	213.586619			408.155397	204.581337	D	***1016.398952***	508.703114	999.372403	500.189840	998.388387	499.697832	9
4	513.197990	257.102633			495.187425	248.097351	S	***901.372009***	451.189643	884.345460	442.676368	883.361444	442.184360	8
5	570.219454	285.613365			552.208889	276.608083	G	***814.339981***	407.673629	797.313432	399.160354	796.329416	398.668346	7
6	685.246397	343.126837			667.235832	334.121554	D	757.318517	379.162897	740.291968	370.649622	739.307952	370.157614	6
7	848.309726	424.658501			830.299161	415.653219	Y	***642.291574***	321.649425	625.265025	313.136151			5
8	962.352653	481.679965	945.326104	473.166690	944.342088	472.674682	N	***479.228245***	240.117760	462.201696	231.604486			4
9	1109.388053	555.197665	1092.361504	546.684390	1091.377488	546.192382	M	***365.185318***	183.096297	348.158769	174.583022			3
10	1180.425167	590.716222	1163.398618	582.202947	1162.414602	581.710939	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 YFDSGDYNMAK
(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	1325.523407	0.006441	YFDSGDYNMAK

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

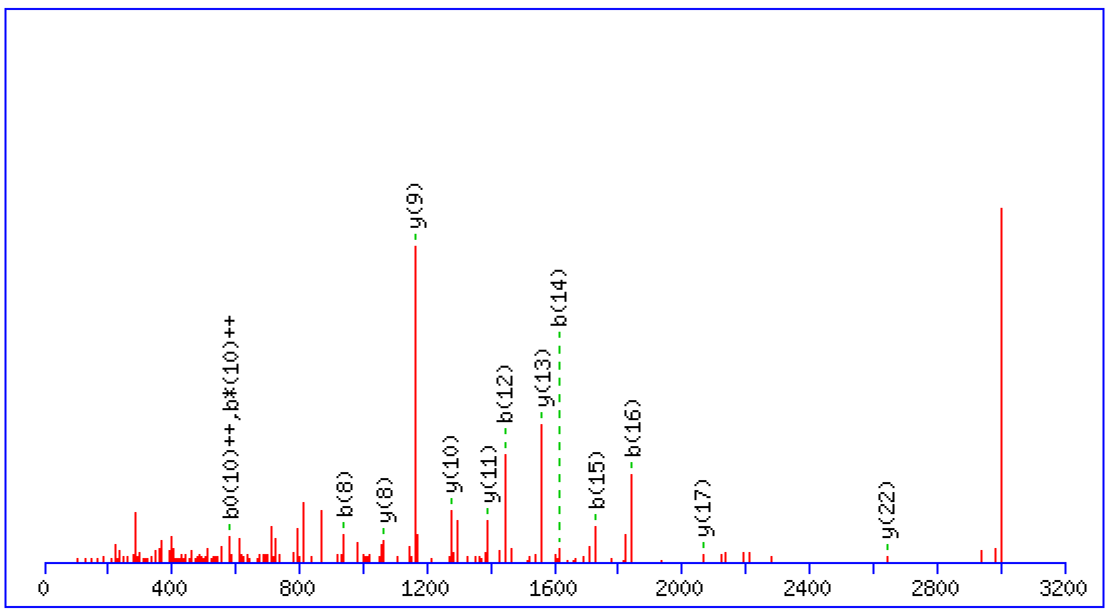
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HHSPSPQHQDYVAPDLPSCIFLEQR**
Found in **ALMS1_HUMAN**, Alstrom syndrome protein 1 OS=Homo sapiens GN=ALMS1 PE=1 SV=3

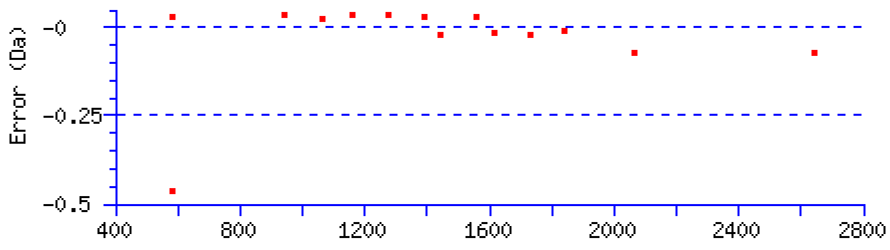
Match to Query 76548: 3003.398382 from(1002.140070,3+) rtinseconds(3316) index(47728)
Title: Locus:1.1.1.2775.46
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-2.mgf

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 ●

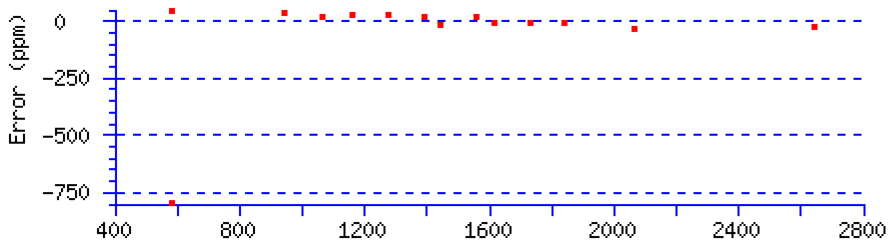


```
Monoisotopic mass of neutral peptide Mr(calc): 3003.393356
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 32  Expect: 0.0052
Matches : 14/268 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							25
2	275.125100	138.066188					H	2867.341721	1434.174498	2850.315172	1425.661224	2849.331156	1425.169216	24
3	362.157128	181.582202			344.146563	172.576920	S	2730.282809	1365.645042	2713.256260	1357.131768	2712.272244	1356.639760	23
4	475.204807	238.106042			457.194242	229.100759	P	*2643.250781*	1322.129028	2626.224232	1313.615754	2625.240216	1313.123746	22
5	562.236835	281.622056			544.226270	272.616773	S	2530.203102	1265.605189	2513.176553	1257.091914	2512.192537	1256.599906	21
6	675.284514	338.145895			657.273949	329.140613	P	2443.171074	1222.089175	2426.144525	1213.575900	2425.160509	1213.083892	20
7	803.343092	402.175184	786.316543	393.661910	785.332527	393.169902	Q	2330.123395	1165.565335	2313.096846	1157.052061	2312.112830	1156.560053	19
8	**940.402004**	470.704640	923.375455	462.191366	922.391439	461.699358	H	2202.064817	1101.536046	2185.038268	1093.022772	2184.054252	1092.530764	18
9	1068.460582	534.733929	1051.434033	526.220655	1050.450017	525.728646	Q	*2065.005905*	1033.006590	2047.979356	1024.493316	2046.995340	1024.001308	17
10	1183.487525	592.247401	1166.460976	583.734126	1165.476960	583.242118	D	1936.947327	968.977302	1919.920778	960.464027	1918.936762	959.972019	16
11	1346.550854	673.779065	1329.524305	665.265791	1328.540289	664.773783	Y	1821.920384	911.463830	1804.893835	902.950556	1803.909819	902.458548	15
12	**1445.619268**	723.313272	1428.592719	714.799998	1427.608703	714.307990	V	1658.857055	829.932166	1641.830506	821.418891	1640.846490	820.926883	14
13	1516.656382	758.831829	1499.629833	750.318555	1498.645817	749.826547	A	*1559.788641*	780.397959	1542.762092	771.884684	1541.778076	771.392676	13
14	**1613.709146**	807.358211	1596.682597	798.844937	1595.698581	798.352929	P	1488.751527	744.879402	1471.724978	736.366127	1470.740962	735.874119	12
15	**1728.736089**	864.871683	1711.709540	856.358408	1710.725524	855.866400	D	*1391.698763*	696.353020	1374.672214	687.839745	1373.688198	687.347737	11
16	**1841.820153**	921.413715	1824.793604	912.900440	1823.809588	912.408432	L	*1276.671820*	638.839548	1259.645271	630.326274	1258.661255	629.834266	10
17	1938.872917	969.940097	1921.846368	961.426822	1920.862352	960.934814	P	*1163.587756*	582.297516	1146.561207	573.784242	1145.577191	573.292234	9
18	2025.904945	1013.456111	2008.878396	1004.942836	2007.894380	1004.450828	S	*1066.534992*	533.771134	1049.508443	525.257860	1048.524427	524.765852	8
19	2199.951244	1100.479260	2182.924695	1091.965985	2181.940679	1091.473977	C	979.502964	490.255120	962.476415	481.741846	961.492399	481.249838	7
20	2313.035308	1157.021292	2296.008759	1148.508017	2295.024743	1148.016009	I	805.456665	403.231971	788.430116	394.718696	787.446100	394.226688	6
21	2460.103722	1230.555499	2443.077173	1222.042224	2442.093157	1221.550216	F	692.372601	346.689939	675.346052	338.176664	674.362036	337.684656	5
22	2573.187786	1287.097531	2556.161237	1278.584256	2555.177221	1278.092248	L	545.304187	273.155732	528.277638	264.642457	527.293622	264.150449	4
23	2702.230379	1351.618828	2685.203830	1343.105553	2684.219814	1342.613545	E	432.220123	216.613700	415.193574	208.100425	414.209558	207.608417	3
24	2830.288957	1415.648117	2813.262408	1407.134842	2812.278392	1406.642834	Q	303.177530	152.092403	286.150981	143.579129			2
25							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 214 ppm



RMS error 214 ppm

NCBI **BLAST** search of HHSPSPQHQDYVAPDLPSCIFLEQR
(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	3003.393356	0.005026	HHSPSPQHQDYVAPDLPSCIFLEQR
11.6	3003.393356	0.005026	HHSPSPQHQDYVAPDLPSCIFLEQR
11.6	3003.393356	0.005026	HHSPSPQHQDYVAPDLPSCIFLEQR

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

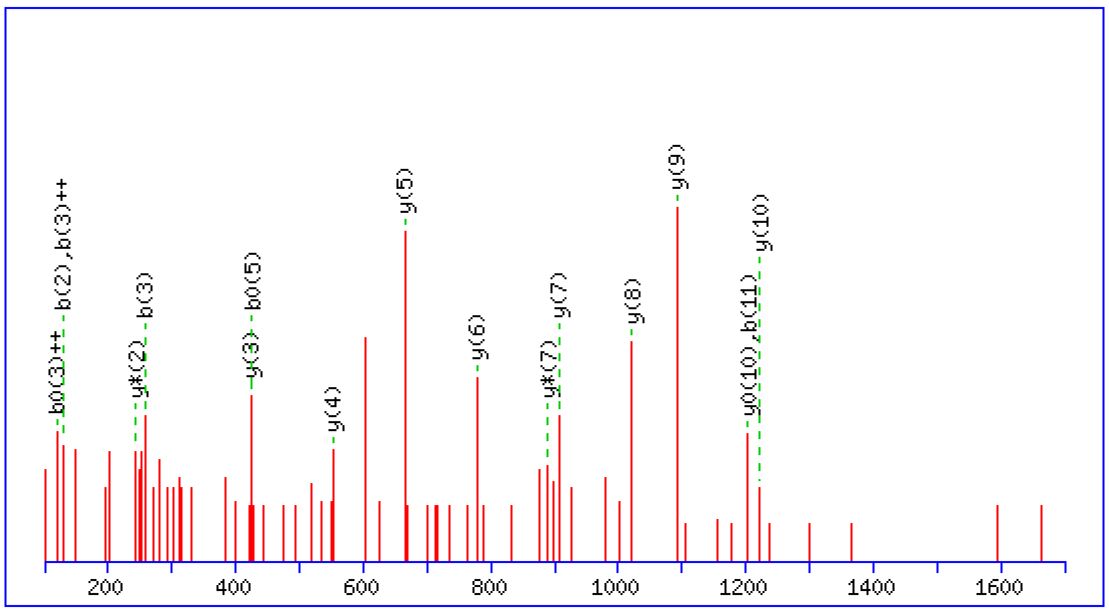
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAEADQIIEYLK**
Found in **AIMP1_HUMAN**, Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2

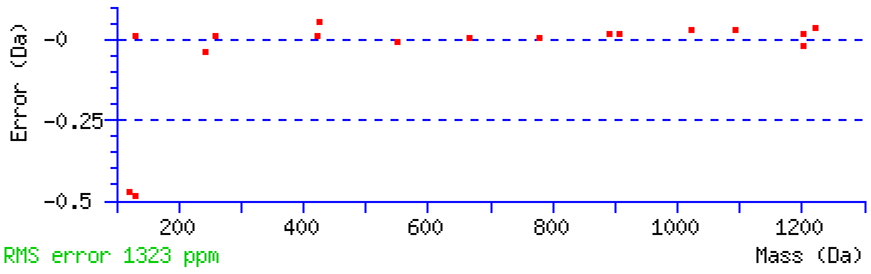
Match to Query 34555: 1348.694328 from(675.354440,2+) rtinseconds(3192) index(42834)
Title: Locus:1.1.1.2705.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

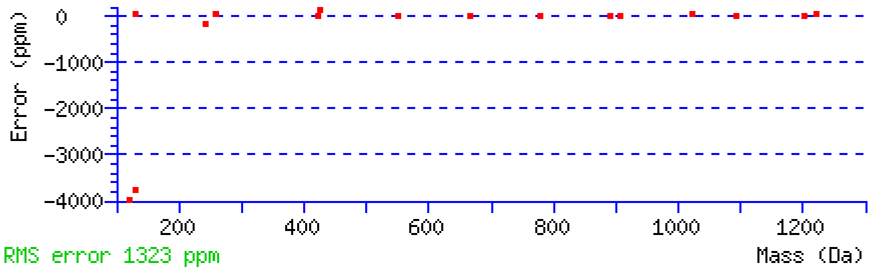
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1348.687408
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 2.4e-005
Matches : 17/112 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	**129.065854**	65.036565					A	1292.673260	646.840268	1275.646711	638.326994	1274.662695	637.834986	11
3	**258.108447**	129.557862			240.097882	120.552579	E	***1221.636146***	611.321711	1204.609597	602.808437	1203.625581	602.316429	10
4	329.145561	165.076418			311.134996	156.071136	A	***1092.593553***	546.800414	1075.567004	538.287140	1074.582988	537.795132	9
5	444.172504	222.589890			426.161939	213.584608	D	***1021.556439***	511.281858	1004.529890	502.768583	1003.545874	502.276575	8
6	572.231082	286.619179	555.204533	278.105905	554.220517	277.613897	Q	***906.529496***	453.768386	889.502947	445.255111	888.518931	444.763103	7
7	685.315146	343.161211	668.288597	334.647937	667.304581	334.155929	I	***778.470918***	389.739097	761.444369	381.225822	760.460353	380.733814	6
8	798.399210	399.703243	781.372661	391.189969	780.388645	390.697961	I	***665.386854***	333.197065	648.360305	324.683790	647.376289	324.191782	5
9	927.441803	464.224540	910.415254	455.711265	909.431238	455.219257	E	***552.302790***	276.655033	535.276241	268.141758	534.292225	267.649750	4
10	1090.505132	545.756204	1073.478583	537.242930	1072.494567	536.750922	Y	***423.260197***	212.133736	406.233648	203.620462			3
11	**1203.589196**	602.298236	1186.562647	593.784962	1185.578631	593.292953	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 GAEADQIIEYLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	1348.687408	0.006920	GAEADQIIEYLK
6.1	1348.698654	-0.004326	KEALSISDPSFR
2.5	1348.684753	0.009575	GEAAPTPAPGPGRR
2.1	1348.690781	0.003547	QMVEEIESLKK
1.9	1348.684753	0.009575	GEAAPTPAPGPGRR
0.3	1348.702698	-0.008370	LSQFPDSLLWK

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

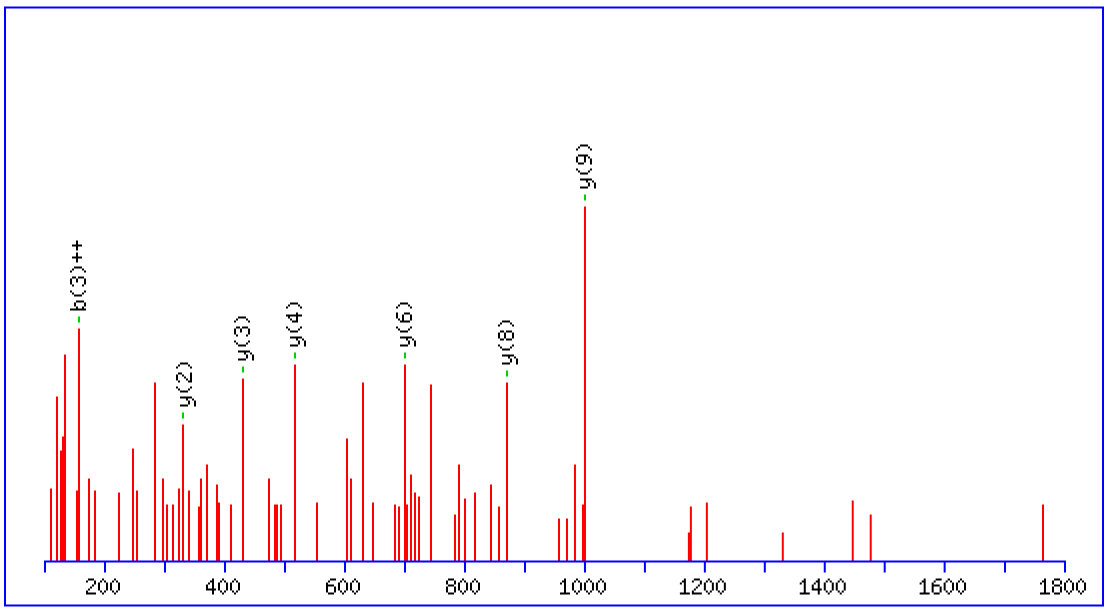
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIEAVAISPWK**
Found in **AMPB_HUMAN**, Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2

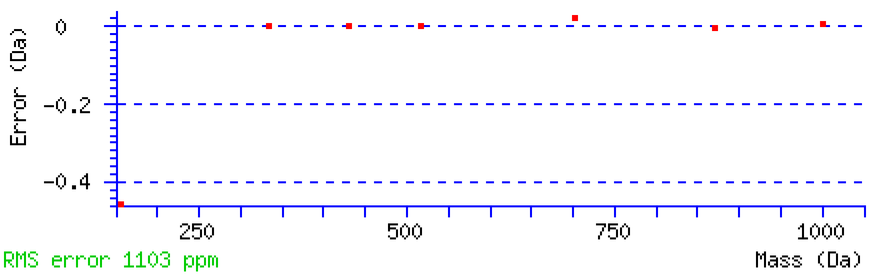
Match to Query 17707: 1183.660208 from(592.837380,2+) rtinseconds(2798) index(33581)
Title: Locus:1.1.1.2593.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

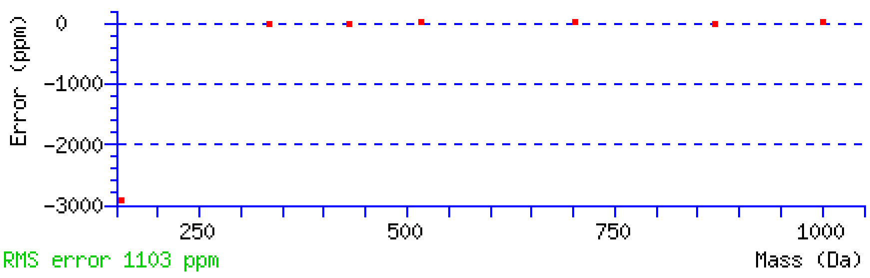
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1183.660080
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00041
Matches : 7/90 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			I	1113.630272	557.318774	1096.603723	548.805500	1095.619707	548.313492	10
3	314.171047	157.589161	296.160482	148.583879	E	***1000.546208***	500.776742	983.519659	492.263468	982.535643	491.771460	9
4	385.208161	193.107718	367.197596	184.102436	A	***871.503615***	436.255446	854.477066	427.742171	853.493050	427.250163	8
5	484.276575	242.641925	466.266010	233.636643	V	800.466501	400.736889	783.439952	392.223614	782.455936	391.731606	7
6	555.313689	278.160483	537.303124	269.155200	A	***701.398087***	351.202682	684.371538	342.689407	683.387522	342.197399	6
7	668.397753	334.702515	650.387188	325.697232	I	630.360973	315.684125	613.334424	307.170850	612.350408	306.678842	5
8	755.429781	378.218529	737.419216	369.213246	S	***517.276909***	259.142093	500.250360	250.628818	499.266344	250.136810	4
9	852.482545	426.744911	834.471980	417.739628	P	***430.244881***	215.626078	413.218332	207.112804			3
10	1038.561858	519.784567	1020.551293	510.779285	W	***333.192117***	167.099696	316.165568	158.586422			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AIEAVAISPWK
(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	1183.660080	0.000128	AIEAVAISPWK
5.0	1183.656067	0.004141	EALQPLLTQR
3.2	1183.656067	0.004141	AELLQGGDLLR

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

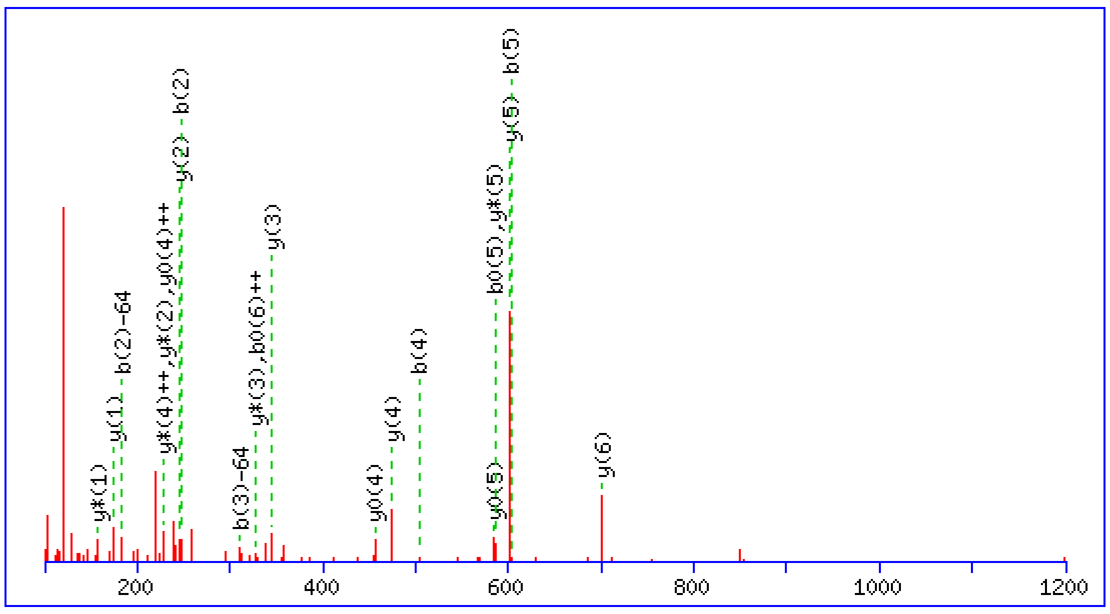
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVKEVAR**
Found in **AMPD3_HUMAN**, AMP deaminase 3 OS=Homo sapiens GN=AMPD3 PE=1 SV=1

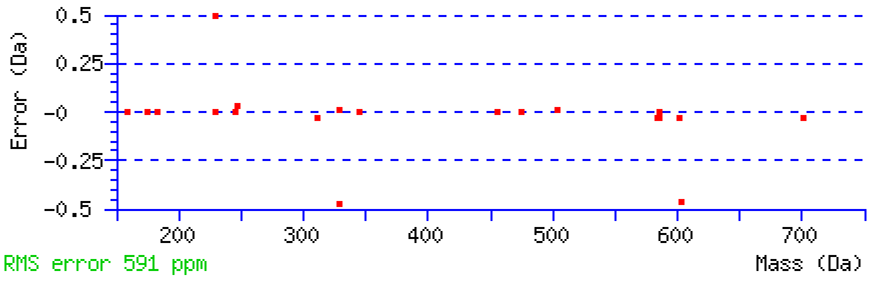
Match to Query 4684: 847.456208 from(424.735380,2+) rtinseconds(1233) index(6813)
Title: Locus:1.1.1.1833.8
Data file 2011-11-14 - TFD - S 2-4.mgf

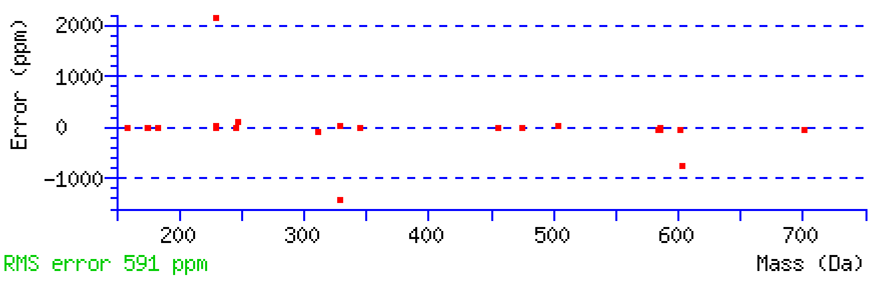
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 847.458557
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: 33  Expect: 0.0052
Matches : 21/82 fragment ions using 38 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.042676	74.524976					M							7
2	**247.111090**	124.059183					V	***701.430450***	351.218863	684.403901	342.705589	683.419885	342.213581	6
3	375.206053	188.106664	358.179504	179.593390			K	***602.362036***	301.684656	585.335487	293.171382	584.351471	292.679374	5
4	**504.248646**	252.627961	487.222097	244.114687	486.238081	243.622679	E	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
5	**603.317060**	302.162168	586.290511	293.648894	585.306495	293.156886	V	***345.224480***	173.115878	328.197931	164.602603			3
6	674.354174	337.680725	657.327625	329.167451	656.343609	328.675443	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 MVKEVAR
(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	847.458557	-0.002349	MVKEVAR
30.5	847.455200	0.001008	FVEQVAR
9.7	847.451157	0.005051	TRSESIR
7.0	847.458557	-0.002349	LSRVINM
6.8	847.455185	0.001023	FVNIAER
6.2	847.458572	-0.002364	MAVVSAVR
6.1	847.458557	-0.002349	KEMVGLR
6.0	847.458572	-0.002364	MVVLGASR

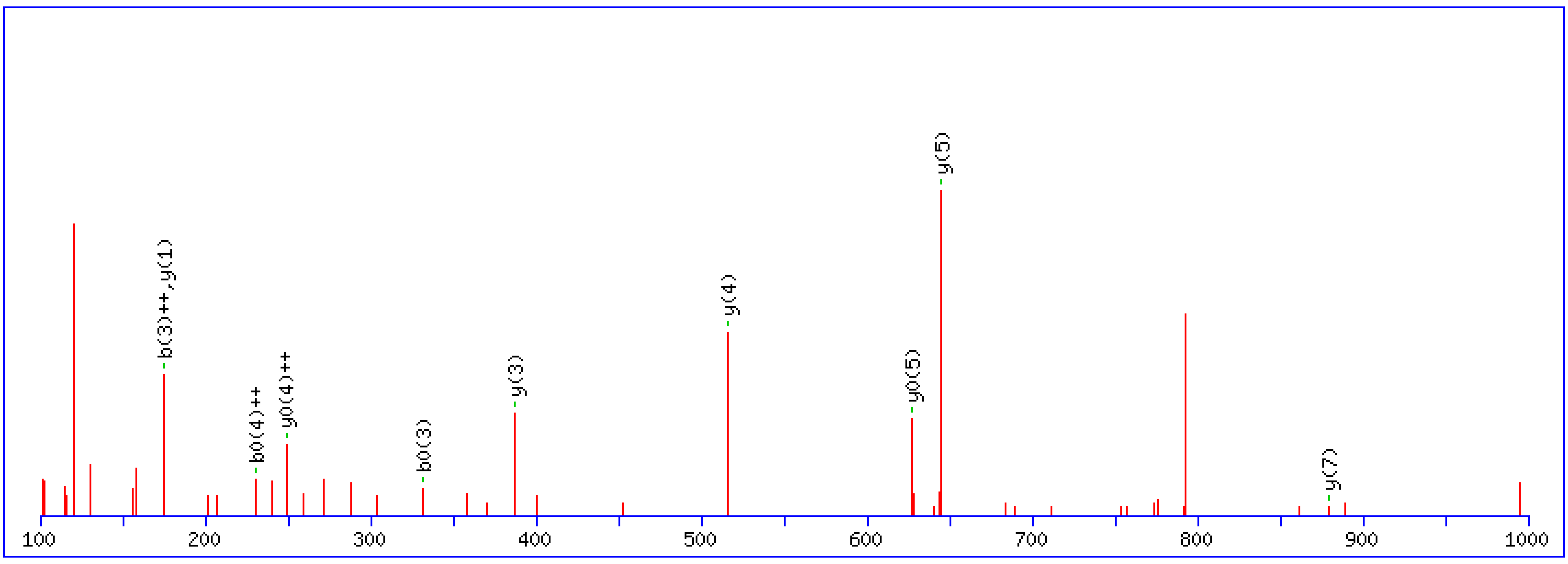
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAYEEIVR**
Found in **ANR24_HUMAN**, Ankyrin repeat domain-containing protein 24 OS=Homo sapiens GN=ANKRD24 PE=2 SV=2

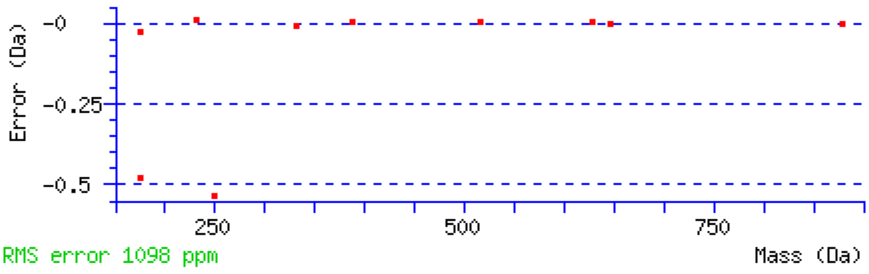
Match to Query 2860: 993.478768 from(497.746660,2+) rtinseconds(2196) index(22687)
Title: Locus:1.1.1.1277.5
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 2.mgf

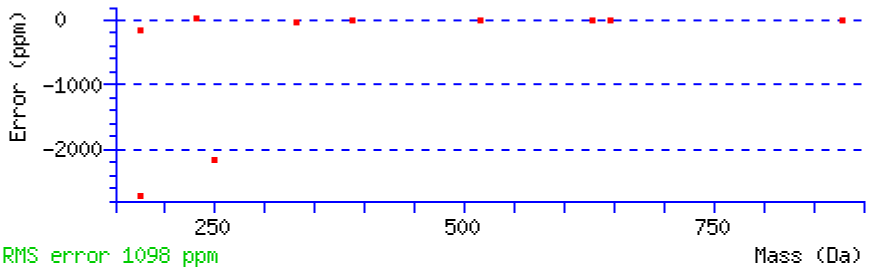
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 993.476700
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0085
Matches : 10/64 fragment ions using 14 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							8
2	187.071333	94.039304	169.060768	85.034022	A	***879.457059***	440.232168	862.430510	431.718893	861.446494	431.226885	7
3	350.134662	175.570969	332.124097	166.565687	Y	808.419945	404.713611	791.393396	396.200336	790.409380	395.708328	6
4	479.177255	240.092266	461.166690	231.086983	E	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
5	608.219848	304.613562	590.209283	295.608280	E	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
6	721.303912	361.155594	703.293347	352.150312	I	***387.271430***	194.139353	370.244881	185.626079			3
7	820.372326	410.689801	802.361761	401.684519	V	274.187366	137.597321	257.160817	129.084047			2
8					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DAYEEIVR
(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	993.476700	0.002068	DAYEEIVR
7.6	993.474045	0.004723	SDGPHPGRR
7.6	993.474045	0.004723	SDGPHPGRR
7.0	993.487946	-0.009178	DFSPSSAKR
6.7	993.487946	-0.009178	DFSDKINR
3.7	993.480103	-0.001335	TGKPTGSALM
2.6	993.476730	0.002038	TEPQSTFGK
1.8	993.476715	0.002053	TGEEINFGK
0.6	993.480087	-0.001319	DTTIMELR

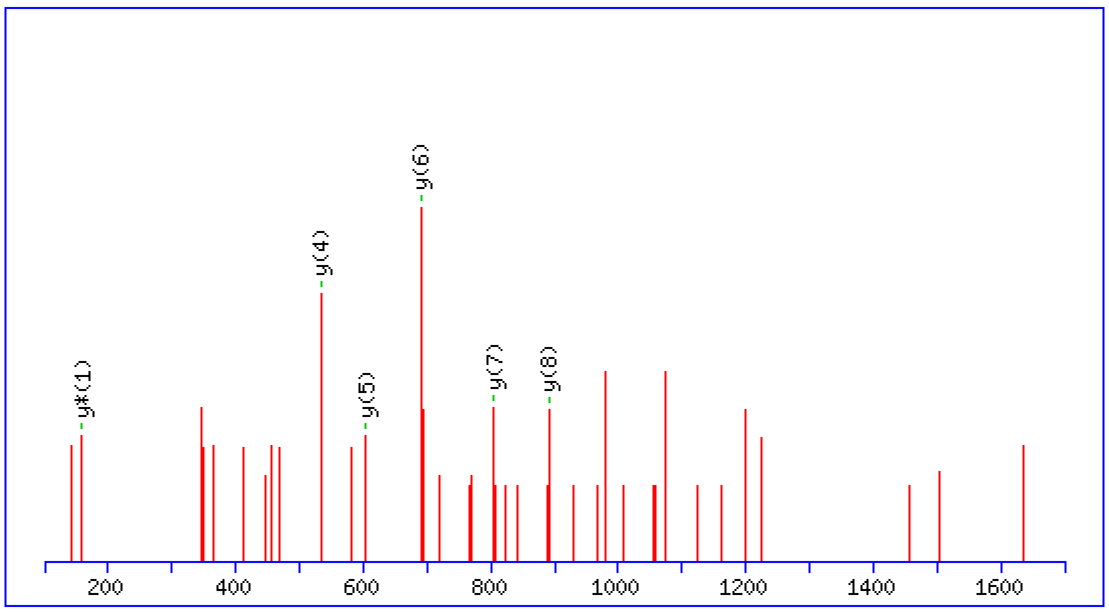
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

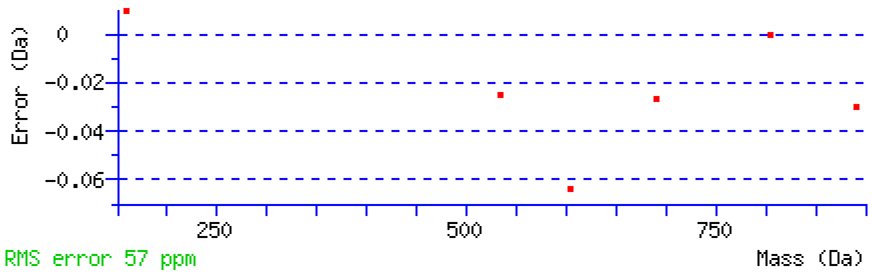
Match to Query 21515: 1310.648668 from(656.331610,2+) rtinseconds(2091) index(16109)
Title: Locus:1.1.1.2446.44
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

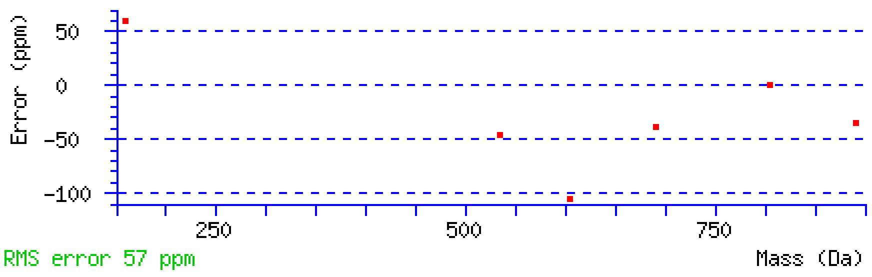
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1310.657867
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6 : Oxidation (P)
Ions Score: 30 **Expect:** 0.0021
Matches : 6/112 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	138.066188	69.536732					H							12
2	225.098216	113.052746			207.087651	104.047463	S	1174.606242	587.806759	1157.579693	579.293485	1156.595677	578.801477	11
3	322.150980	161.579128			304.140415	152.573845	P	1087.574214	544.290745	1070.547665	535.777471	1069.563649	535.285462	10
4	421.219394	211.113335			403.208829	202.108052	V	990.521450	495.764363	973.494901	487.251089	972.510885	486.759081	9
5	508.251422	254.629349			490.240857	245.624067	S	***891.453036***	446.230156	874.426487	437.716882	873.442471	437.224874	8
6	621.299101	311.153189			603.288536	302.147906	P	***804.421008***	402.714142	787.394459	394.200868	786.410443	393.708860	7
7	708.331129	354.669203			690.320564	345.663920	S	***691.373329***	346.190303	674.346780	337.677028	673.362764	337.185020	6
8	779.368243	390.187760			761.357678	381.182477	A	***604.341301***	302.674289	587.314752	294.161014	586.330736	293.669006	5
9	907.463206	454.235241	890.436657	445.721967	889.452641	445.229959	K	***533.304187***	267.155732	516.277638	258.642457	515.293622	258.150449	4
10	1008.510885	504.759081	991.484336	496.245806	990.500320	495.753798	T	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
11	1137.553478	569.280377	1120.526929	560.767103	1119.542913	560.275095	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 HSPVSPSAKTER
(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	1310.657867	-0.009199	HSPVSPSAKTER
8.0	1310.657867	-0.009199	HSPVSPSAKTER
1.8	1310.646637	0.002031	SEHPGLSIGDTAK

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

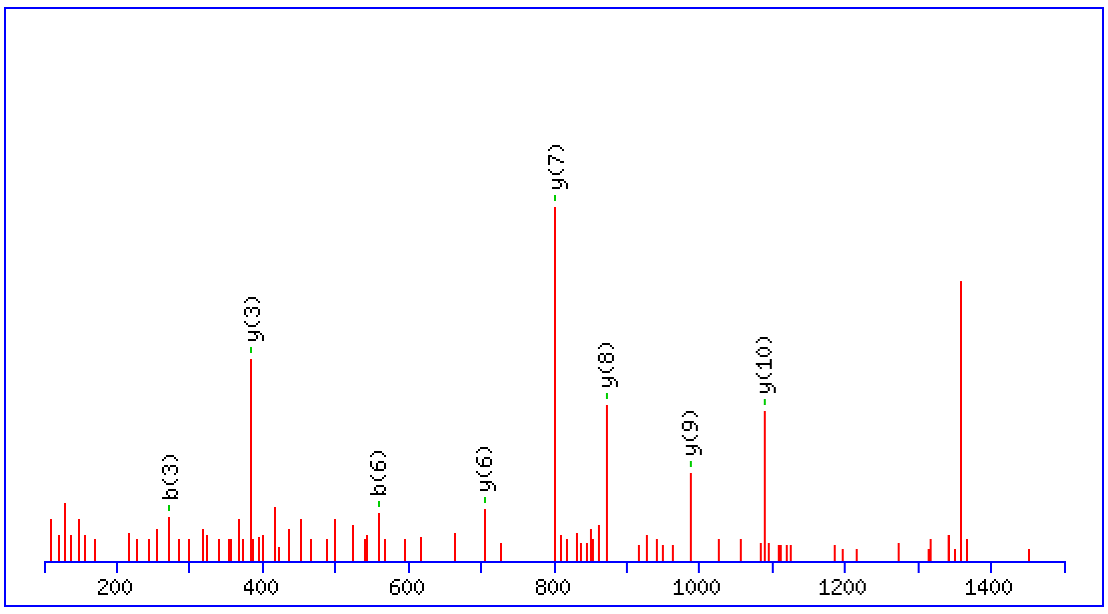
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTITDAPGFDPLR**
Found in **ANX11_HUMAN**, Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1

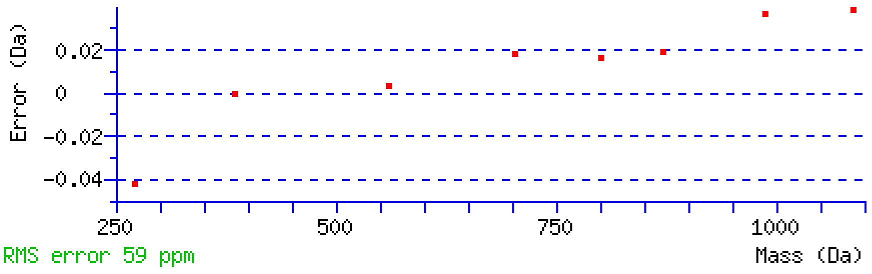
Match to Query 26825: 1358.692388 from(680.353470,2+) rtinseconds(2669) index(35958)
Title: Locus:1.1.1.2498.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

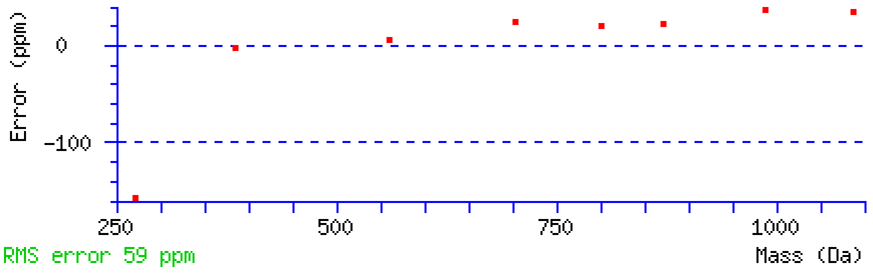
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1358.683044
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00022
Matches : 8/112 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							13
2	159.076419	80.041847	141.065854	71.036565	T	1302.668844	651.838060	1285.642295	643.324786	1284.658279	642.832778	12
3	**272.160483**	136.583879	254.149918	127.578597	I	1201.621165	601.314221	1184.594616	592.800946	1183.610600	592.308938	11
4	373.208162	187.107719	355.197597	178.102437	T	***1088.537101***	544.772188	1071.510552	536.258914	1070.526536	535.766906	10
5	488.235105	244.621191	470.224540	235.615908	D	***987.489422***	494.248349	970.462873	485.735074	969.478857	485.243066	9
6	**559.272219**	280.139748	541.261654	271.134465	A	***872.462479***	436.734877	855.435930	428.221603	854.451914	427.729595	8
7	656.324983	328.666130	638.314418	319.660847	P	***801.425365***	401.216320	784.398816	392.703046	783.414800	392.211038	7
8	713.346447	357.176862	695.335882	348.171579	G	***704.372601***	352.689938	687.346052	344.176664	686.362036	343.684656	6
9	860.414861	430.711069	842.404296	421.705786	F	647.351137	324.179206	630.324588	315.665932	629.340572	315.173924	5
10	975.441804	488.224540	957.431239	479.219258	D	500.282723	250.644999	483.256174	242.131725	482.272158	241.639717	4
11	1072.494568	536.750922	1054.484003	527.745640	P	***385.255780***	193.131528	368.229231	184.618253			3
12	1185.578632	593.292954	1167.568067	584.287671	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 GTITDAPGFDPLR
(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	1358.683044	0.009344	GTITDAPGFDPLR
3.4	1358.704132	-0.011744	SLLADREDSLPK
3.0	1358.704147	-0.011759	RDLDAITDISPK
1.9	1358.682999	0.009389	ELEQSHINYVK
1.0	1358.704117	-0.011729	SLAELSEASLAPR
0.4	1358.690414	0.001974	ASPCLVSLSWLP

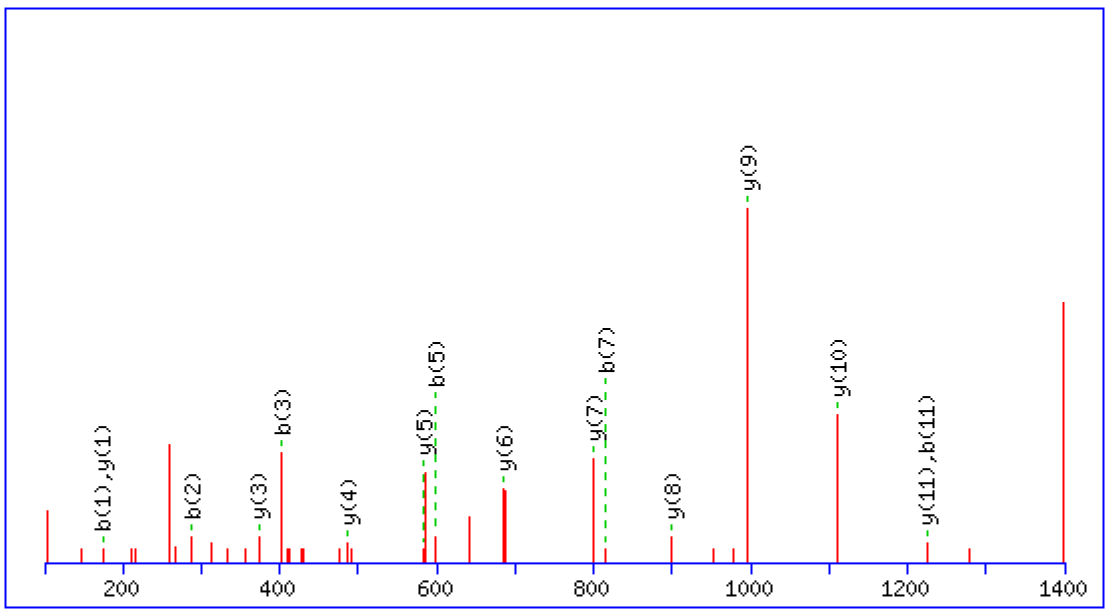
Mascot Search Results

Peptide View

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

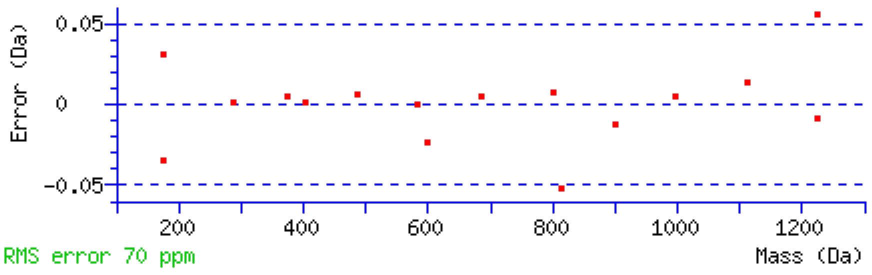
Match to Query 37504: 1397.667948 from(699.841250,2+) rtinseconds(1861) index(10959)
Title: Locus:1.1.1.2220.46
Data file 2011-11-14 - TFD - S 2-6.mgf

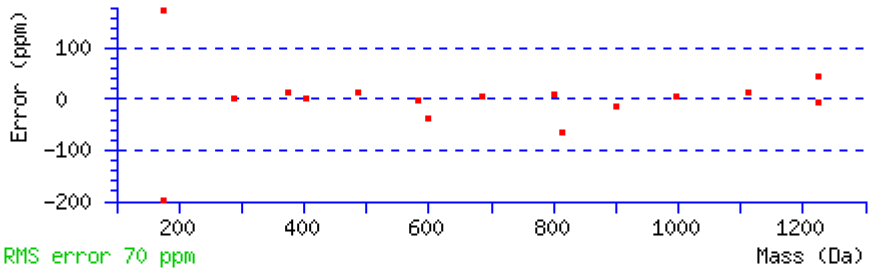
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1397.660919
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 89  Expect: 1.5e-008
Matches : 16/110 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	**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





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
89.0	1397.660919	0.007029	CLDPVDTPNPTR
7.6	1397.664764	0.003184	SPATGRTHSSPPR
4.5	1397.672150	-0.004202	VMSQEHLLGDGGR
4.0	1397.672134	-0.004186	NHVGELCGETLR
1.6	1397.664917	0.003031	CLKEQGYDPFK
1.4	1397.657547	0.010401	TGPQDAELWPPR
1.1	1397.679520	-0.011572	RMIEGVVYEMR
0.8	1397.664917	0.003031	NPFYSLEMPIR

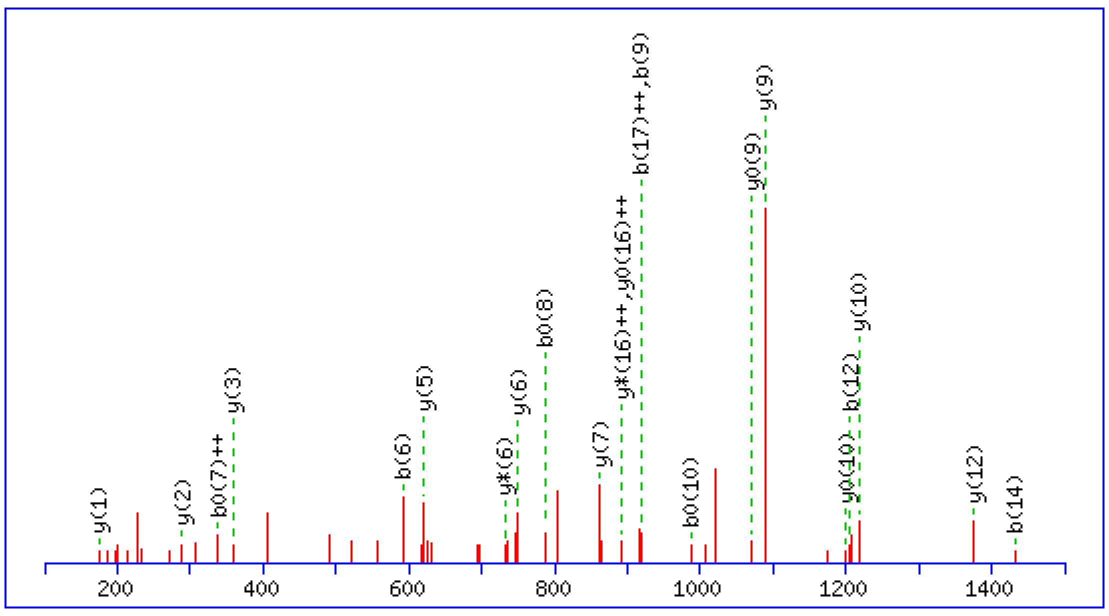
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAPPLVTLLSAEPELQYVALR**
Found in **AP1B1_HUMAN**, AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2

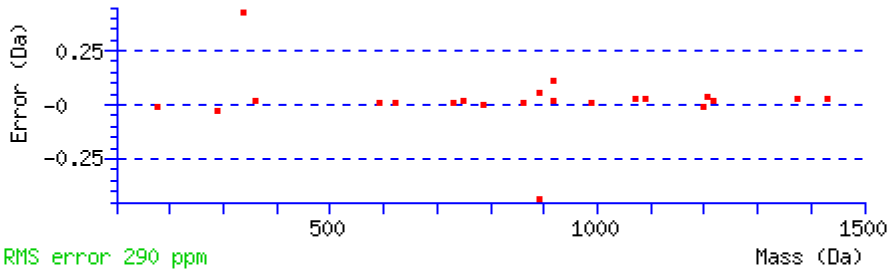
Match to Query 73203: 2292.329772 from(765.117200,3+) rtinseconds(4835) index(74866)
Title: Locus:1.1.1.3124.15
Data file 2011-11-14 - TFD - S 2-2.mgf

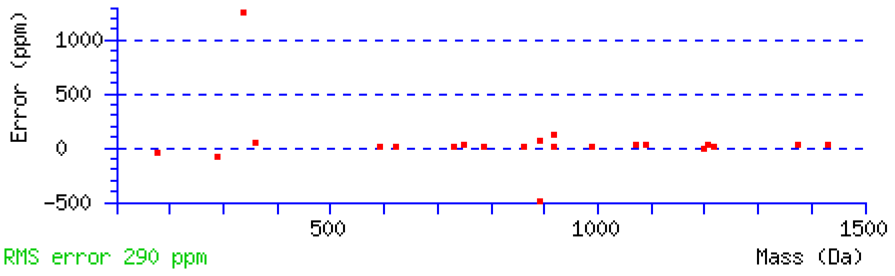
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2292.309280
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0001
Matches : 22/184 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							21
2	185.128454	93.067865					A	2180.232534	1090.619905	2163.205985	1082.106630	2162.221969	1081.614622	20
3	282.181218	141.594247					P	2109.195420	1055.101348	2092.168871	1046.588073	2091.184855	1046.096065	19
4	379.233982	190.120629					P	2012.142656	1006.574966	1995.116107	998.061692	1994.132091	997.569684	18
5	492.318046	246.662661					L	1915.089892	958.048584	1898.063343	949.535310	1897.079327	949.043302	17
6	**591.386460**	296.196868					V	1802.005828	901.506552	1784.979279	892.993278	1783.995263	892.501270	16
7	692.434139	346.720708			674.423574	337.715425	T	1702.937414	851.972345	1685.910865	843.459071	1684.926849	842.967063	15
8	805.518203	403.262740			787.507638	394.257457	L	1601.889735	801.448506	1584.863186	792.935231	1583.879170	792.443223	14
9	**918.602267**	459.804772			900.591702	450.799489	L	1488.805671	744.906474	1471.779122	736.393199	1470.795106	735.901191	13
10	1005.634295	503.320786			987.623730	494.315503	S	***1375.721607***	688.364442	1358.695058	679.851167	1357.711042	679.359159	12
11	1076.671409	538.839343			1058.660844	529.834060	A	1288.689579	644.848428	1271.663030	636.335153	1270.679014	635.843145	11
12	**1205.714002**	603.360639			1187.703437	594.355356	E	***1217.652465***	609.329871	1200.625916	600.816596	1199.641900	600.324588	10
13	1302.766766	651.887021			1284.756201	642.881738	P	***1088.609872***	544.808574	1071.583323	536.295300	1070.599307	535.803292	9
14	**1431.809359**	716.408318			1413.798794	707.403035	E	991.557108	496.282192	974.530559	487.768918	973.546543	487.276910	8
15	1544.893423	772.950350			1526.882858	763.945067	L	***862.514515***	431.760896	845.487966	423.247621			7
16	1672.952001	836.979638	1655.925452	828.466364	1654.941436	827.974356	Q	***749.430451***	375.218864	732.403902	366.705589			6
17	1836.015330	918.511303	1818.988781	909.998029	1818.004765	909.506020	Y	***621.371873***	311.189575	604.345324	302.676300			5
18	1935.083744	968.045510	1918.057195	959.532236	1917.073179	959.040228	V	458.308544	229.657910	441.281995	221.144636			4
19	2006.120858	1003.564067	1989.094309	995.050793	1988.110293	994.558785	A	***359.240130***	180.123703	342.213581	171.610429			3
20	2119.204922	1060.106099	2102.178373	1051.592824	2101.194357	1051.100816	L	***288.203016***	144.605146	271.176467	136.091872			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LAPPLVTLLSAEPELQYVALR
(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	2292.309280	0.020492	LAPPLVTLLSAEPELQYVALR
0.7	2292.316528	0.013244	VVIIGAGKPAAVVLQTKGSPESR

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

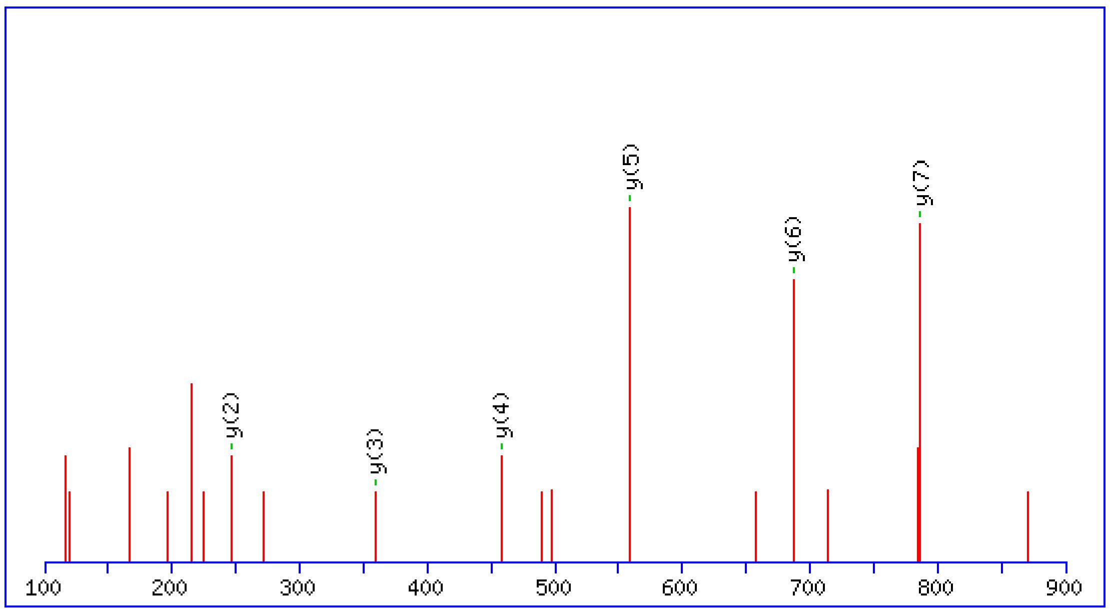
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELVQTVLAR**
Found in **AP1S2_HUMAN**, AP-1 complex subunit sigma-2 OS=Homo sapiens GN=AP1S2 PE=1 SV=1

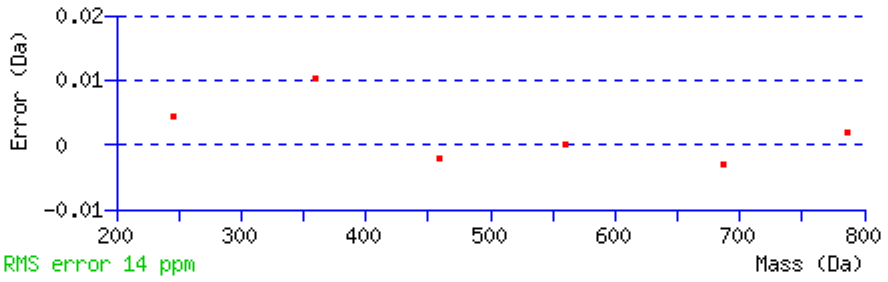
Match to Query 11802: 1027.604228 from(514.809390,2+) rtinseconds(2317) index(18555)
Title: Locus:1.1.1.2380.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

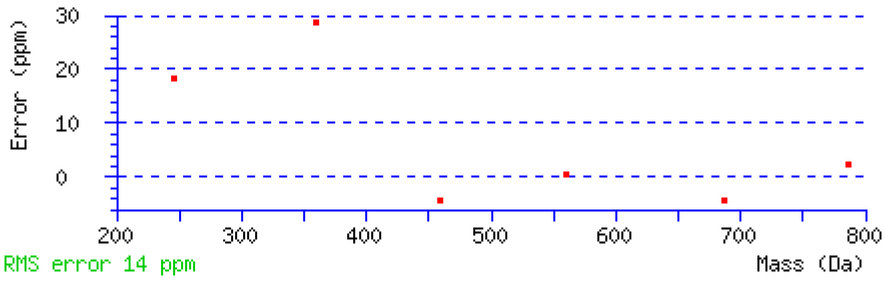
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1027.602585
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.9e-005
Matches : 6/82 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	130.049869	65.528572			112.039304	56.523290	**E**							9
2	243.133933	122.070605			225.123368	113.065322	**L**	899.567279	450.287278	882.540730	441.774003	881.556714	441.281995	8
3	342.202347	171.604812			324.191782	162.599529	**V**	***786.483215***	393.745246	769.456666	385.231971	768.472650	384.739963	7
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**Q**	***687.414801***	344.211038	670.388252	335.697764	669.404236	335.205756	6
5	571.308604	286.157940	554.282055	277.644666	553.298039	277.152658	**T**	***559.356223***	280.181750	542.329674	271.668475	541.345658	271.176467	5
6	670.377018	335.692147	653.350469	327.178873	652.366453	326.686865	**V**	***458.308544***	229.657910	441.281995	221.144635			4
7	783.461082	392.234179	766.434533	383.720905	765.450517	383.228897	**L**	***359.240130***	180.123703	342.213581	171.610428			3
8	854.498196	427.752736	837.471647	419.239462	836.487631	418.747454	**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 ELVQTVLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.9	1027.602585	0.001643	ELVQTVLAR
9.3	1027.602554	0.001674	EISILNIAR

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

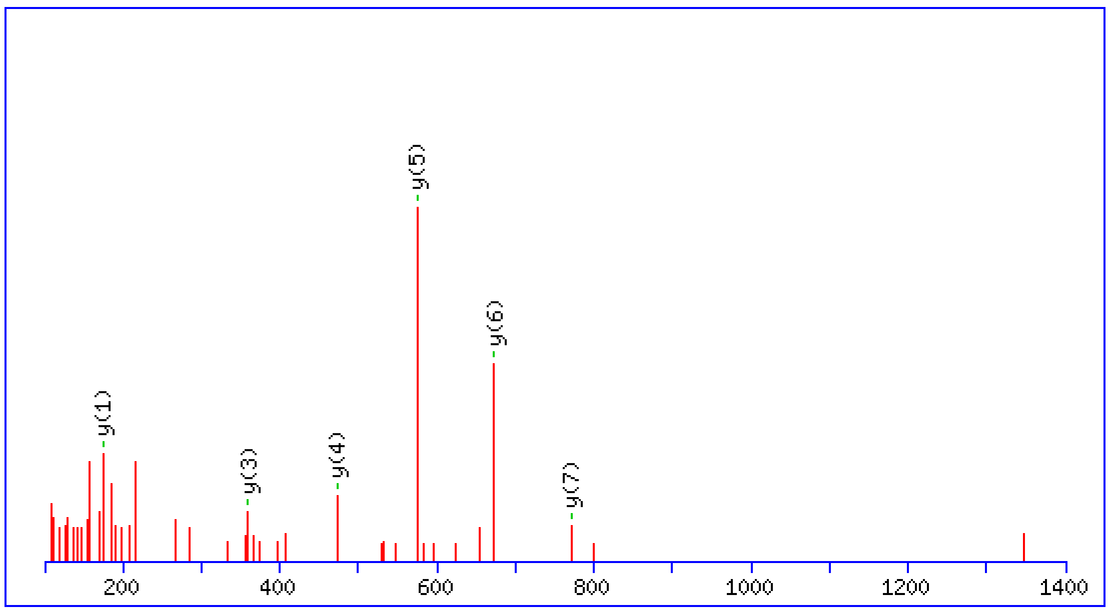
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPVTNIAR**
Found in **AP2M1_HUMAN**, AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2

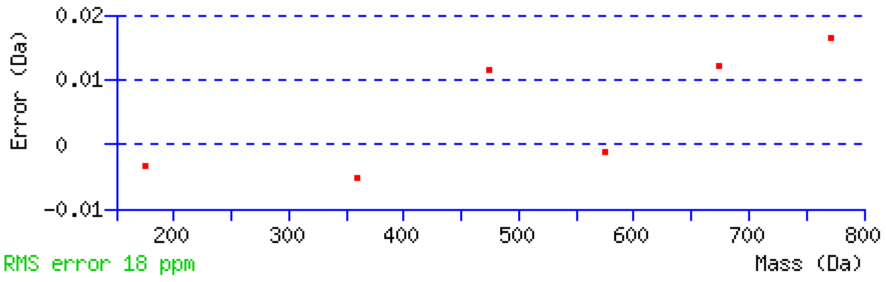
Match to Query 2199: 856.472488 from(429.243520,2+) rtinseconds(1220) index(7860)
Title: Locus:1.1.1.1963.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

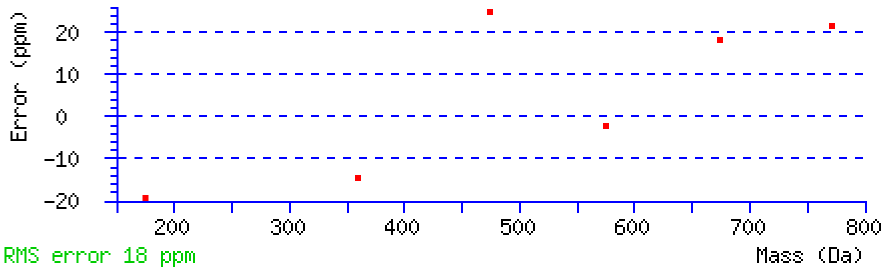
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 856.476654
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61  Expect: 2.5e-005
Matches : 6/68 fragment ions using 7 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**							8
2	185.092068	93.049672			167.081503	84.044389	**P**	***770.451914***	385.729595	753.425365	377.216321	752.441349	376.724313	7
3	284.160482	142.583879			266.149917	133.578597	**V**	***673.399150***	337.203213	656.372601	328.689939	655.388585	328.197931	6
4	385.208161	193.107719			367.197596	184.102436	**T**	***574.330736***	287.669006	557.304187	279.155732	556.320171	278.663724	5
5	499.251088	250.129182	482.224539	241.615908	481.240523	241.123900	**N**	***473.283057***	237.145166	456.256508	228.631892			4
6	612.335152	306.671214	595.308603	298.157940	594.324587	297.665932	**I**	***359.240130***	180.123703	342.213581	171.610428			3
7	683.372266	342.189771	666.345717	333.676497	665.361701	333.184489	**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 SPVTNIAR
(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	856.476654	-0.004166	SPVTNIAR
12.8	856.476639	-0.004151	EPGAKISR
12.8	856.476669	-0.004181	AVPTVAGAR
10.9	856.465424	0.007064	SPSPKPTK
9.0	856.476654	-0.004166	SGPLKPAR
4.9	856.465408	0.007080	LAKEGDPK
4.8	856.476669	-0.004181	AIPQGVTR
4.3	856.476639	-0.004151	LASPNLSR
3.1	856.465424	0.007064	SPSPKPTK
1.6	856.465424	0.007064	ELPVEVR

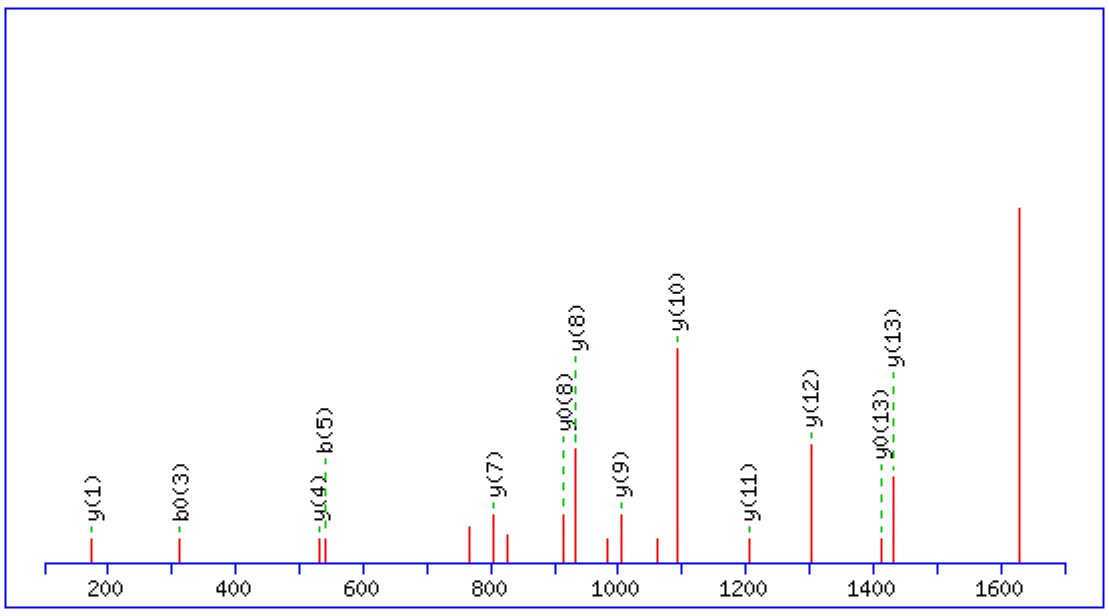
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTEPISAESGEQVER**
Found in **APOL1_HUMAN**, Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5

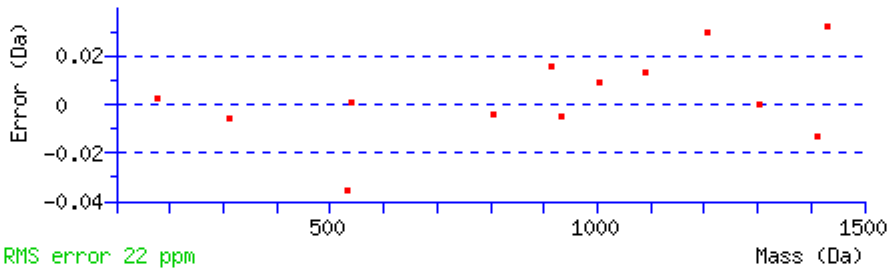
Match to Query 36996: 1629.795448 from(815.905000,2+) rtinseconds(1719) index(10550)
Title: Locus:1.1.1.2225.50
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

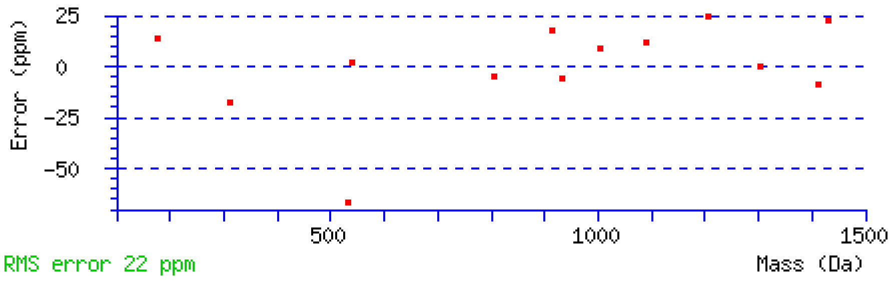
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1629.784576
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 6.7e-007
Matches : 13/142 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	100.075690	50.541483					V							15
2	201.123369	101.065322			183.112804	92.060040	T	1531.723457	766.365367	1514.696908	757.852092	1513.712892	757.360084	14
3	330.165962	165.586619			312.155397	156.581336	E	***1430.675778***	715.841527	1413.649229	707.328253	1412.665213	706.836245	13
4	427.218726	214.113001			409.208161	205.107719	P	***1301.633185***	651.320231	1284.606636	642.806956	1283.622620	642.314948	12
5	540.302790	270.655033			522.292225	261.649751	I	***1204.580421***	602.793849	1187.553872	594.280574	1186.569856	593.788566	11
6	627.334818	314.171047			609.324253	305.165765	S	***1091.496357***	546.251817	1074.469808	537.738542	1073.485792	537.246534	10
7	698.371932	349.689604			680.361367	340.684322	A	***1004.464329***	502.735803	987.437780	494.222528	986.453764	493.730520	9
8	827.414525	414.210901			809.403960	405.205618	E	***933.427215***	467.217246	916.400666	458.703971	915.416650	458.211963	8
9	914.446553	457.726915			896.435988	448.721632	S	***804.384622***	402.695949	787.358073	394.182675	786.374057	393.690667	7
10	971.468017	486.237647			953.457452	477.232364	G	717.352594	359.179935	700.326045	350.666661	699.342029	350.174653	6
11	1100.510610	550.758943			1082.500045	541.753661	E	660.331130	330.669203	643.304581	322.155929	642.320565	321.663921	5
12	1228.569188	614.788232	1211.542639	606.274958	1210.558623	605.782950	Q	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	4
13	1327.637602	664.322439	1310.611053	655.809165	1309.627037	655.317157	V	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
14	1456.680195	728.843736	1439.653646	720.330461	1438.669630	719.838453	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.4	1629.784576	0.010872	VTEPISAESGEQVER
2.5	1629.809738	-0.014290	ISPADTPVSESSSPLK
2.5	1629.809738	-0.014290	ISPADTPVSESSSPLK
1.6	1629.781921	0.013527	AALAATGAASGGGGGGGGAGSR
1.6	1629.784576	0.010872	ESEPAPASVTALTDAR
1.6	1629.784576	0.010872	ESEPAPASVTALTDAR
1.1	1629.803177	-0.007729	LLELACPGATEAEAR
0.5	1629.793304	0.002144	SLCFRLEQGYTSR
0.2	1629.789474	0.005974	SILPFEAVVCMYR

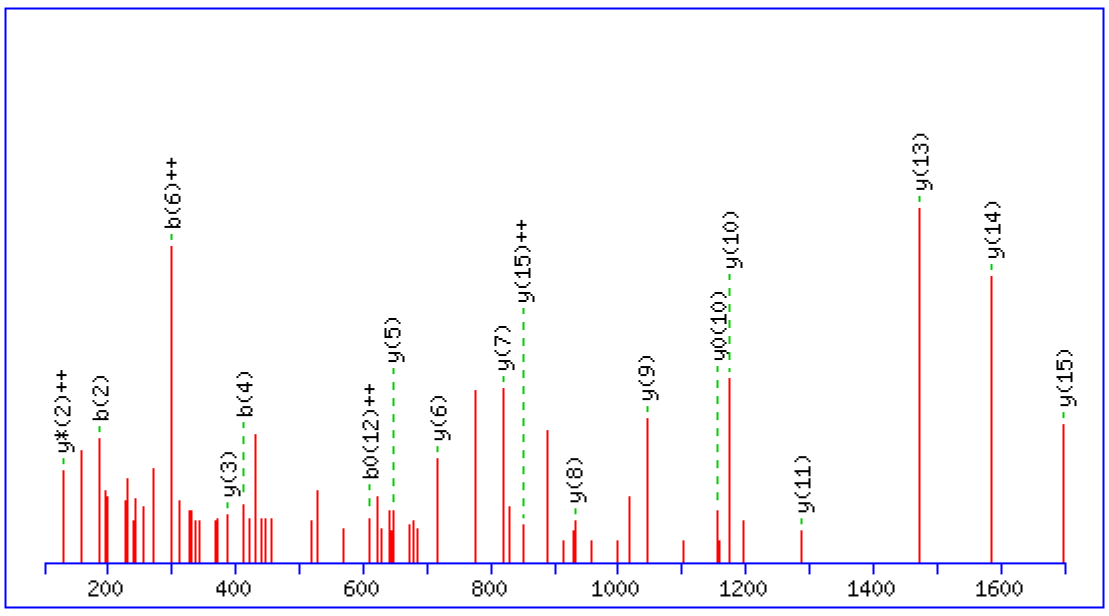
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAILDALENLTAEELKK**
Found in **ASC_HUMAN**, Apoptosis-associated speck-like protein containing a CARD OS=Homo sapiens GN=PYCARD PE=1 SV=2

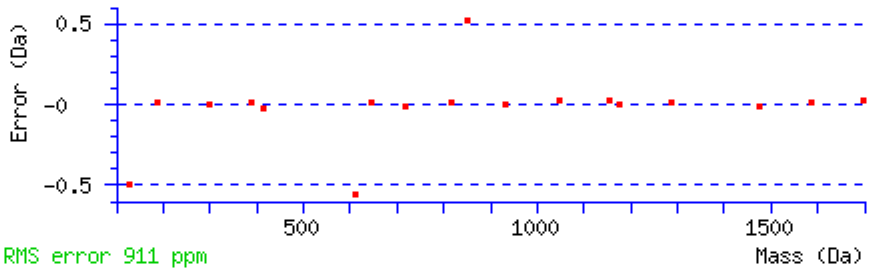
Match to Query 46874: 1885.003032 from(629.341620,3+) rtinseconds(4386) index(55777)
Title: Locus:1.1.1.3470.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

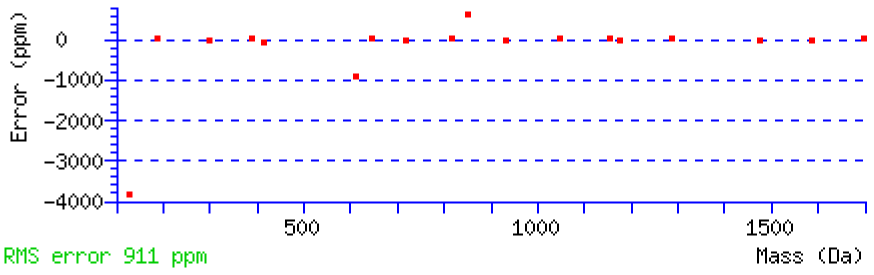
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1885.004364
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 4.8e-006
Matches : 19/170 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	116.034219	58.520748			98.023654	49.515465	D							17
2	**187.071333**	94.039304			169.060768	85.034022	A	1770.984757	885.996017	1753.958208	877.482742	1752.974192	876.990734	16
3	**300.155397**	150.581336			282.144832	141.576054	I	***1699.947643***	850.477460	1682.921094	841.964185	1681.937078	841.472177	15
4	**413.239461**	207.123369			395.228896	198.118086	L	***1586.863579***	793.935428	1569.837030	785.422153	1568.853014	784.930145	14
5	528.266404	264.636840			510.255839	255.631558	D	***1473.779515***	737.393396	1456.752966	728.880121	1455.768950	728.388113	13
6	599.303518	300.155397			581.292953	291.150115	A	1358.752572	679.879924	1341.726023	671.366650	1340.742007	670.874642	12
7	712.387582	356.697429			694.377017	347.692147	L	***1287.715458***	644.361367	1270.688909	635.848093	1269.704893	635.356084	11
8	841.430175	421.218726			823.419610	412.213443	E	***1174.631394***	587.819335	1157.604845	579.306061	1156.620829	578.814053	10
9	955.473102	478.240189	938.446553	469.726915	937.462537	469.234907	N	***1045.588801***	523.298039	1028.562252	514.784764	1027.578236	514.292756	9
10	1068.557166	534.782221	1051.530617	526.268947	1050.546601	525.776939	L	***931.545874***	466.276575	914.519325	457.763301	913.535309	457.271293	8
11	1169.604845	585.306061	1152.578296	576.792786	1151.594280	576.300778	T	***818.461810***	409.734543	801.435261	401.221269	800.451245	400.729261	7
12	1240.641959	620.824618	1223.615410	612.311343	1222.631394	611.819335	A	***717.414131***	359.210704	700.387582	350.697429	699.403566	350.205421	6
13	1369.684552	685.345914	1352.658003	676.832640	1351.673987	676.340631	E	***646.377017***	323.692147	629.350468	315.178872	628.366452	314.686864	5
14	1498.727145	749.867211	1481.700596	741.353936	1480.716580	740.861928	E	517.334424	259.170850	500.307875	250.657576	499.323859	250.165568	4
15	1611.811209	806.409243	1594.784660	797.895968	1593.800644	797.403960	L	***388.291831***	194.649553	371.265282	186.136279			3
16	1739.906172	870.456724	1722.879623	861.943450	1721.895607	861.451441	K	275.207767	138.107521	258.181218	129.594247			2
17							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DAILDALENLTAEELKK
(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	1885.004364	-0.001332	DAILDALENLTAEELKK
9.7	1884.991348	0.011684	RSQAVGILMSSLHLDMK
3.4	1884.991333	0.011699	MARTAICNLILGNPPSK
0.5	1885.005722	-0.002690	VSIAELAQASNSLIAWGR

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

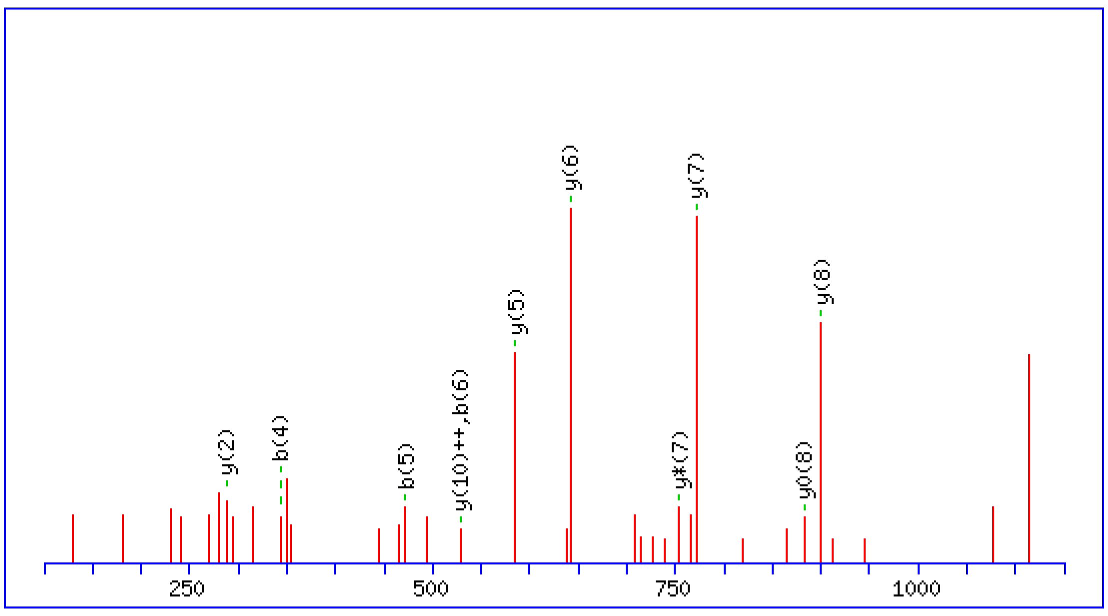
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGVEEGPTVLR**
Found in **ARGI1_HUMAN**, Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2

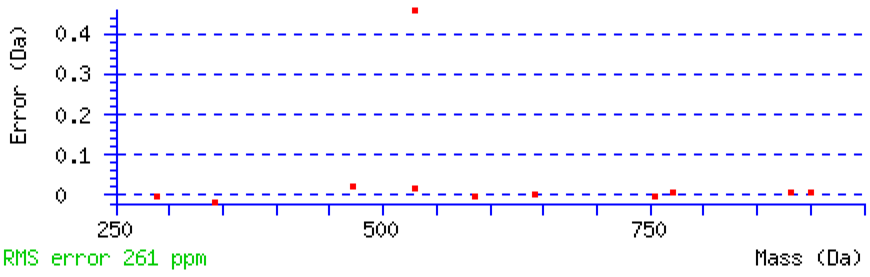
Match to Query 5340: 1112.578788 from(557.296670,2+) rtinseconds(1843) index(1840)
Title: Locus:1.1.1.3010.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

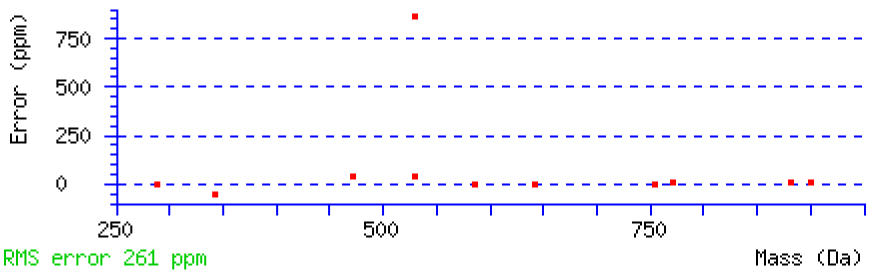
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1112.582596
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.008
Matches : 11/88 fragment ions using 18 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	115.050204	58.028740			**G**	1056.568401	528.787839	1039.541852	520.274564	1038.557836	519.782556	10
3	214.118618	107.562947			**V**	999.546937	500.277107	982.520388	491.763832	981.536372	491.271824	9
4	**343.161211**	172.084244	325.150646	163.078961	**E**	***900.478523***	450.742900	883.451974	442.229625	882.467958	441.737617	8
5	**472.203804**	236.605540	454.193239	227.600258	**E**	***771.435930***	386.221603	754.409381	377.708329	753.425365	377.216321	7
6	**529.225268**	265.116272	511.214703	256.110990	**G**	***642.393337***	321.700307	625.366788	313.187032	624.382772	312.695024	6
7	626.278032	313.642654	608.267467	304.637372	**P**	***585.371873***	293.189575	568.345324	284.676300	567.361308	284.184292	5
8	727.325711	364.166494	709.315146	355.161211	**T**	488.319109	244.663192	471.292560	236.149918	470.308544	235.657910	4
9	826.394125	413.700701	808.383560	404.695418	**V**	387.271430	194.139353	370.244881	185.626078			3
10	939.478189	470.242733	921.467624	461.237450	**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 GGVEEGPTVLR
(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	1112.582596	-0.003808	GGVEEGPTVLR
11.1	1112.582581	-0.003793	TPQPDSALIR
1.4	1112.582550	-0.003762	ASPSLERPEK
1.2	1112.582596	-0.003808	TSPSVTPTPAR
0.8	1112.571365	0.007423	APSSPLPGVPK
0.6	1112.582581	-0.003793	DKLDPVPAAR
0.6	1112.582581	-0.003793	SQPVTLPEAR
0.3	1112.586609	-0.007821	ATLWPATPPK
0.3	1112.586609	-0.007821	ATLWPATPPK
0.3	1112.582581	-0.003793	ELQTGTHKLS

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

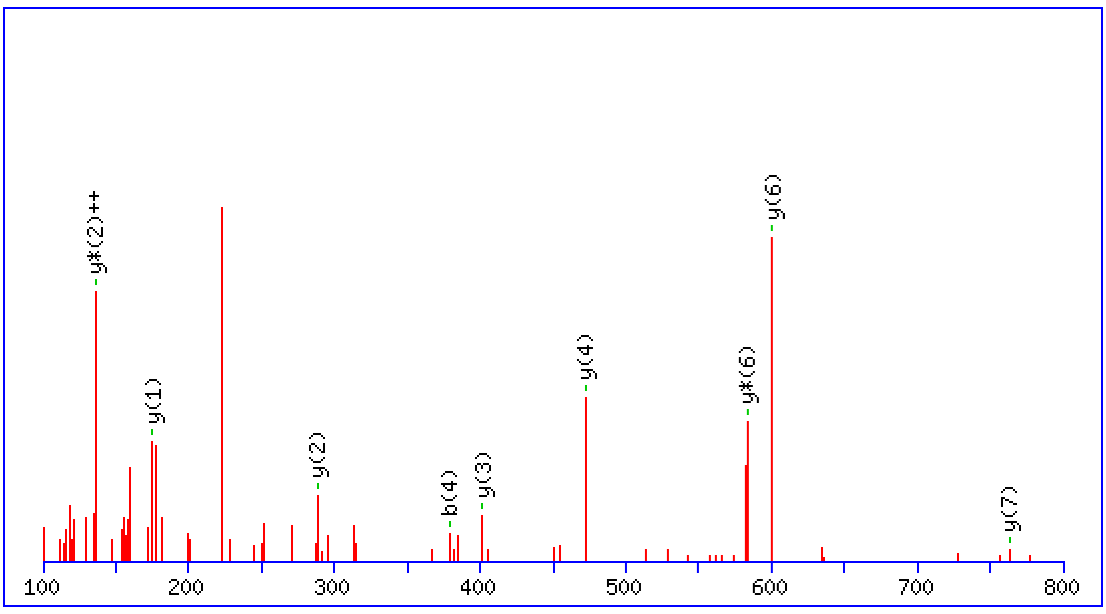
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYGAALLR**
Found in **ARMC5_HUMAN**, Armadillo repeat-containing protein 5 OS=Homo sapiens GN=ARMC5 PE=2 SV=2

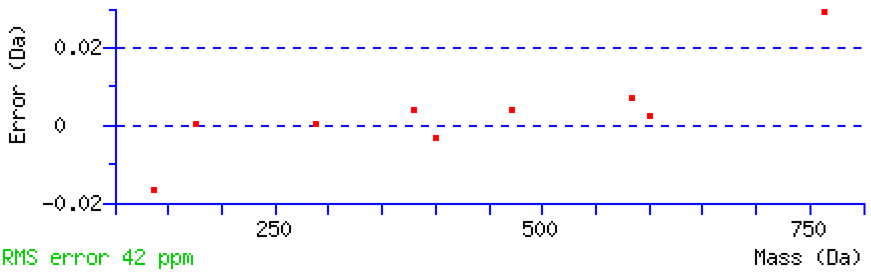
Match to Query 1279: 849.472728 from(425.743640,2+) rtinseconds(1724) index(16384)
Title: Locus:1.1.1.2107.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

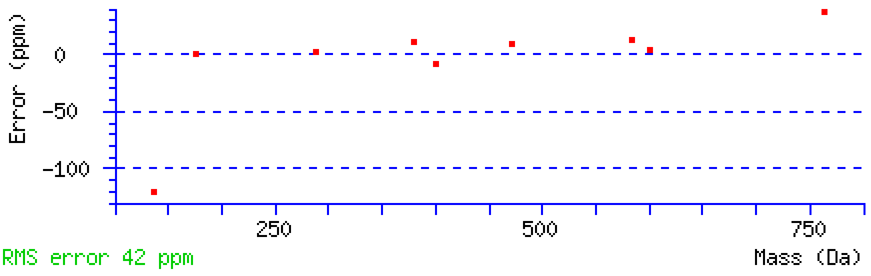
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 849.470825
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00018
Matches : 9/56 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	88.039304	44.523290	70.028739	35.518008	S					8
2	251.102633	126.054954	233.092068	117.049672	Y	***763.446101***	382.226689	746.419552	373.713414	7
3	308.124097	154.565687	290.113532	145.560404	G	***600.382772***	300.695024	583.356223	292.181750	6
4	379.161211	190.084244	361.150646	181.078961	A	543.361308	272.184292	526.334759	263.671018	5
5	450.198325	225.602801	432.187760	216.597518	A	***472.324194***	236.665735	455.297645	228.152460	4
6	563.282389	282.144833	545.271824	273.139550	L	***401.287080***	201.147178	384.260531	192.633903	3
7	676.366453	338.686865	658.355888	329.681582	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 SYGAALLR
(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	849.470825	0.001903	SYGAALLR
14.6	849.470840	0.001888	KSSFIPR
10.8	849.470840	0.001888	SLSALFGR
7.3	849.470856	0.001872	TPPGPPLR
6.5	849.470840	0.001888	SYPTKVR
5.5	849.470840	0.001888	SPFSKIR
5.5	849.470840	0.001888	SPLPAPPR
5.4	849.470840	0.001888	KSFLSPR
4.7	849.470825	0.001903	EFKSALR
4.7	849.470825	0.001903	IYKPSSR

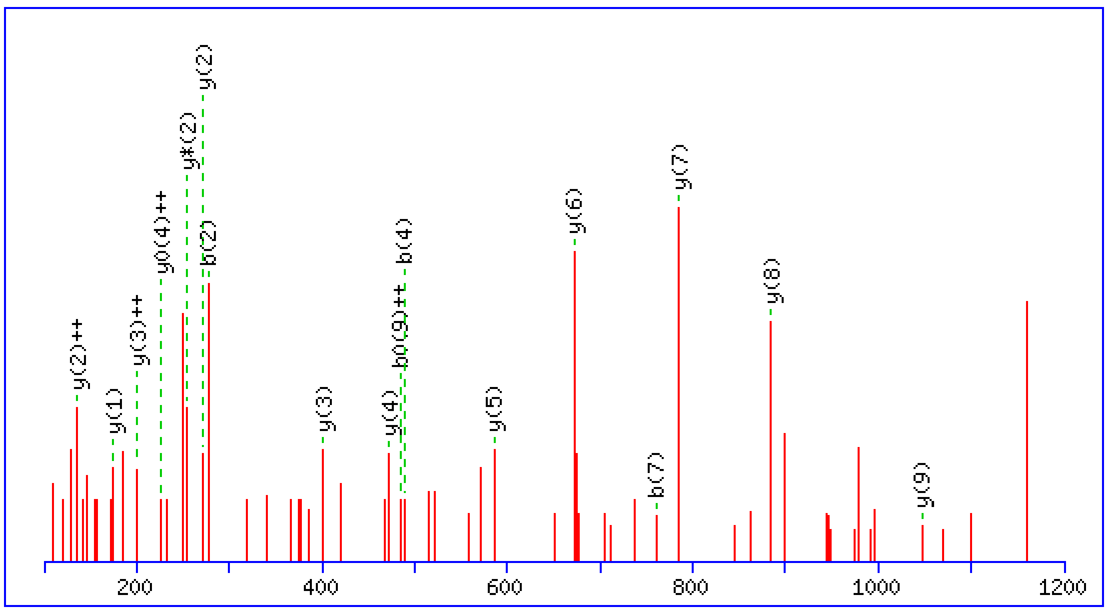
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYVISLAEPR**
Found in **SYDC_HUMAN**, Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2

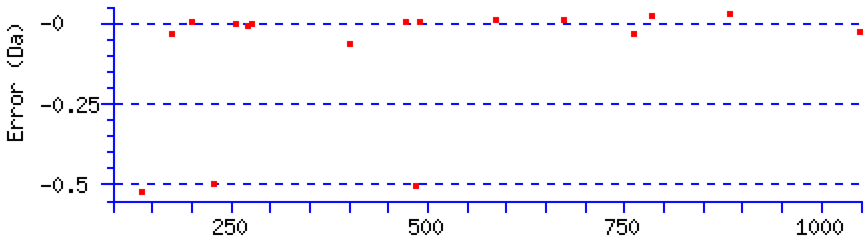
Match to Query 15004: 1159.662948 from(580.838750,2+) rtinseconds(2784) index(38149)
Title: Locus:1.1.1.2542.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

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 ●

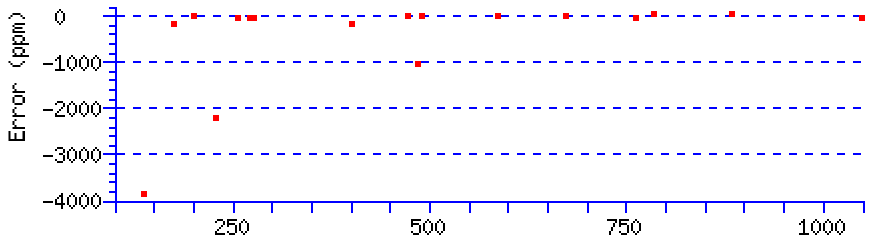


Monoisotopic mass of neutral peptide Mr(calc): 1159.660080
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00018
Matches : 17/78 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							10
2	**277.154669**	139.080973			Y	***1047.583322***	524.295299	1030.556773	515.782025	1029.572757	515.290017	9
3	376.223083	188.615180			V	***884.519993***	442.763635	867.493444	434.250360	866.509428	433.758352	8
4	**489.307147**	245.157212			I	***785.451579***	393.229428	768.425030	384.716153	767.441014	384.224145	7
5	576.339175	288.673226	558.328610	279.667943	S	***672.367515***	336.687396	655.340966	328.174121	654.356950	327.682113	6
6	689.423239	345.215258	671.412674	336.209975	L	***585.335487***	293.171382	568.308938	284.658107	567.324922	284.166099	5
7	**760.460353**	380.733815	742.449788	371.728532	A	***472.251423***	236.629349	455.224874	228.116075	454.240858	227.624067	4
8	889.502946	445.255111	871.492381	436.249829	E	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	3
9	986.555710	493.781493	968.545145	484.776211	P	***272.171716***	136.589496	255.145167	128.076221			2
10					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 1102 ppm



RMS error 1102 ppm

NCBI **BLAST** search of IYVISLAEPR
(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	1159.660080	0.002868	IYVISLAEPR
14.1	1159.671341	-0.008393	AIQVFLLGGSR
9.2	1159.652252	0.010696	IVMETVPVLK
5.8	1159.671326	-0.008378	LGKPFLNISR
4.9	1159.671341	-0.008393	LISPPVHLPR
3.4	1159.671341	-0.008393	LISPPVHLPR
2.0	1159.671341	-0.008393	LISPPVHLPR

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

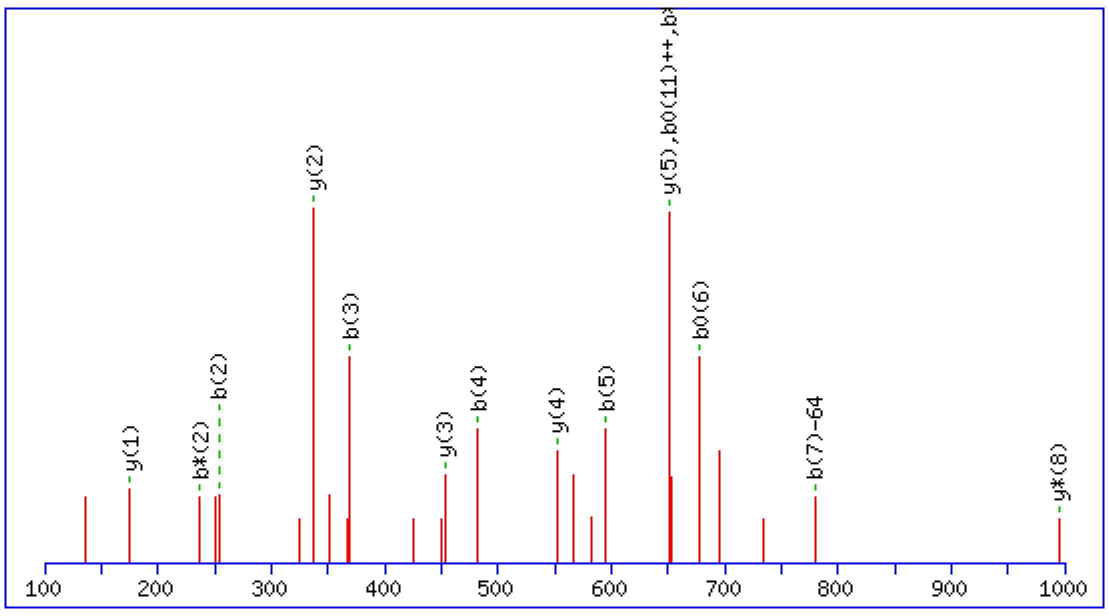
Mascot Search Results

Peptide View

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

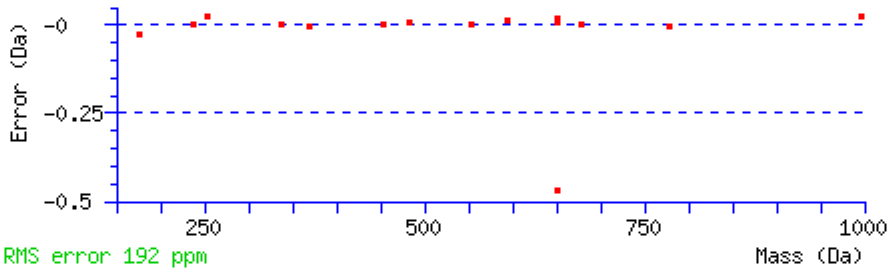
Match to Query 29190: 1492.771932 from(498.597920,3+) rtinseconds(2873) index(28609)
Title: Locus:1.1.1.2591.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

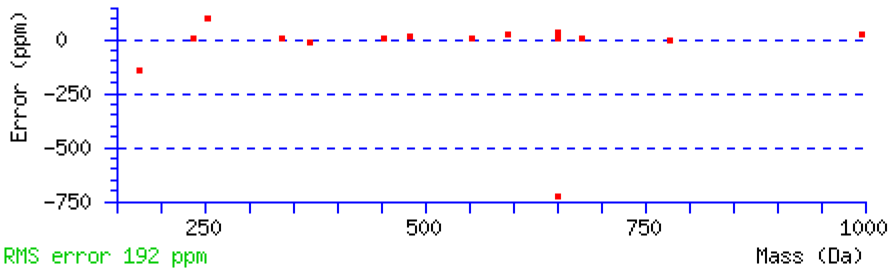
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 60  Expect: 1.2e-005
Matches : 15/190 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	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
59.6	1492.770798	0.001134	RPDLLTMVVDYR
20.3	1492.770798	0.001134	RPDLLTMVVDYR
12.2	1492.777313	-0.005381	TNLTTFNPSILEK
8.0	1492.778656	-0.006724	RTTQPIWGSLYR
4.9	1492.782043	-0.010111	GTFPVLVRTSACR
3.8	1492.770782	0.001150	ECGKAFISLPSVR
2.9	1492.786041	-0.014109	YVKVLMHDVAYR
1.5	1492.772141	-0.000209	HLVPGPWGRLCR
1.1	1492.778656	-0.006724	GPPSPGPAAQPPAPPR
0.9	1492.760895	0.011037	QFRGPMAAISFPR

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

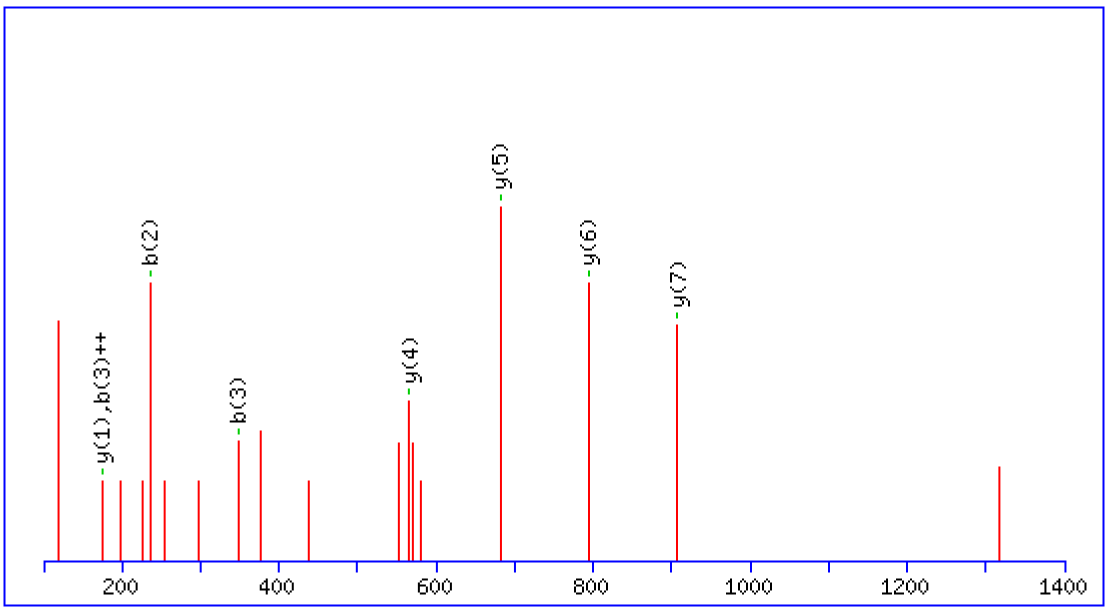
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFILDFMLR**
Found in **ATLA3_HUMAN**, Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1

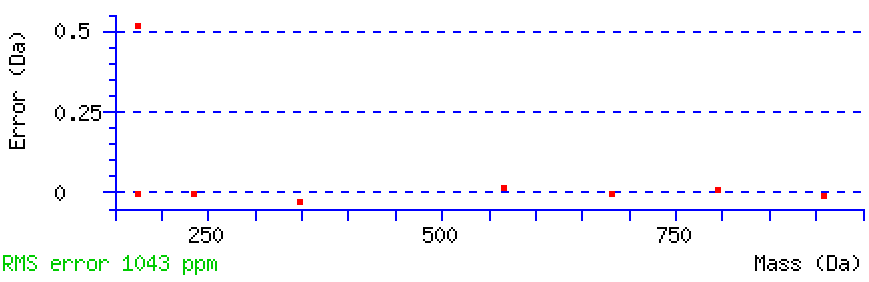
Match to Query 24376: 1140.611428 from(571.312990,2+) rtinseconds(4231) index(65179)
Title: Locus:1.1.1.2945.12
Data file 2011-11-14 - TFD - S 2-3.mgf

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 ●

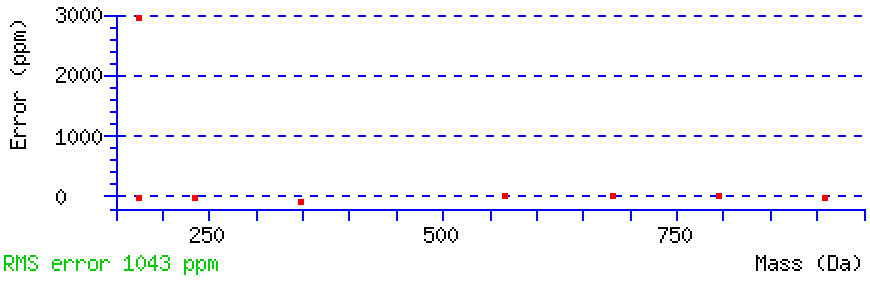


Monoisotopic mass of neutral peptide Mr(calc): 1140.600143
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0023
Matches : 8/72 fragment ions using 12 most intense peaks (help)

#	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	**235.107718**	118.057497	217.097153	109.052214	F	1054.575400	527.791338	1037.548851	519.278064	1036.564835	518.786055	8
3	**348.191782**	174.599529	330.181217	165.594247	I	***907.506986***	454.257131	890.480437	445.743857	889.496421	445.251849	7
4	461.275846	231.141561	443.265281	222.136279	L	***794.422922***	397.715099	777.396373	389.201824	776.412357	388.709816	6
5	576.302789	288.655033	558.292224	279.649750	D	***681.338858***	341.173067	664.312309	332.659793	663.328293	332.167785	5
6	723.371203	362.189240	705.360638	353.183957	F	***566.311915***	283.659596	549.285366	275.146321			4
7	854.411688	427.709482	836.401123	418.704200	M	419.243501	210.125388	402.216952	201.612114			3
8	967.495752	484.251514	949.485187	475.246232	L	288.203016	144.605146	271.176467	136.091871			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 1043 ppm



RMS error 1043 ppm

NCBI **BLAST** search of SFILDFMLR
(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	1140.600143	0.011285	SFILDFMLR
35.8	1140.600143	0.011285	SFLLDFMLR

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

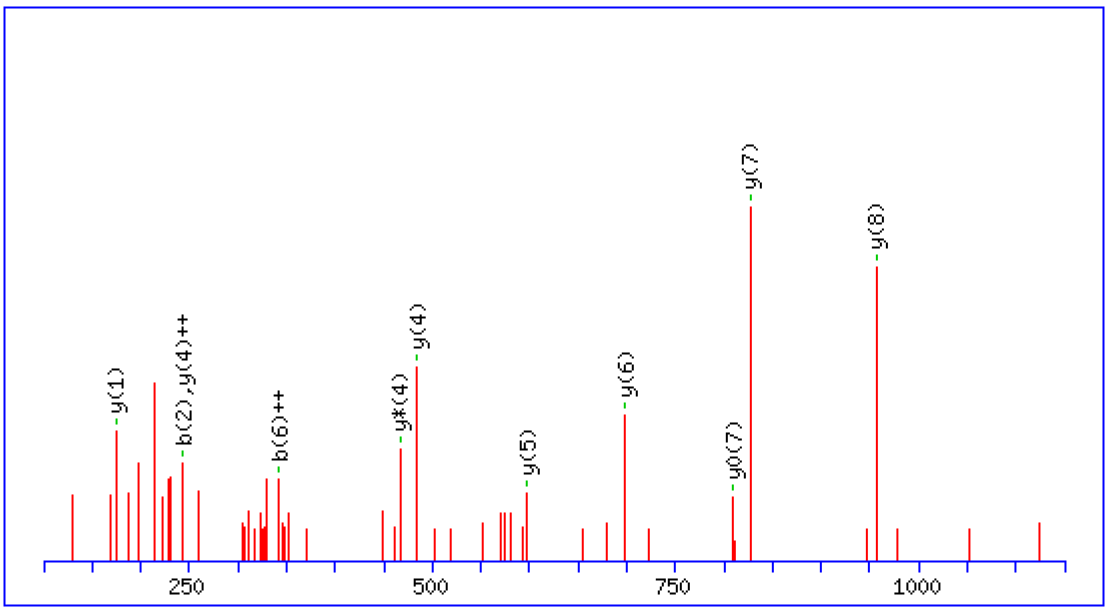
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEETLPVIR**
Found in **ASNA_HUMAN**, ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2

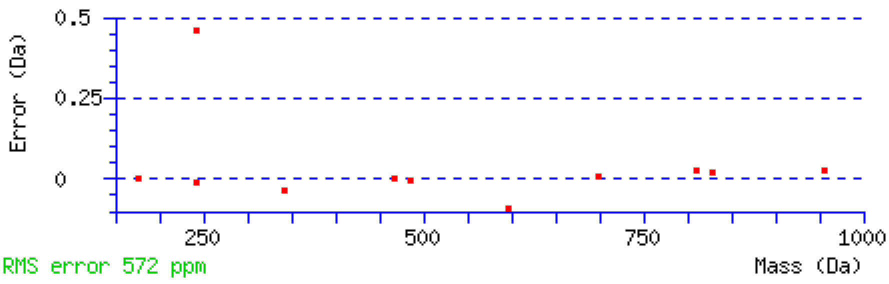
Match to Query 15801: 1068.619068 from(535.316810,2+) rtinseconds(2495) index(31841)
Title: Locus:1.1.1.2334.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

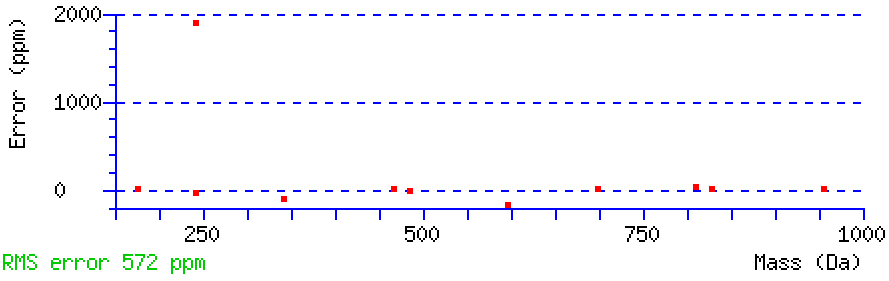
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1068.617889
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0012
Matches : 11/68 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			L							9
2	243.133933	122.070605	225.123368	113.065322	E	***956.541123***	478.774200	939.514574	470.260925	938.530558	469.768917	8
3	372.176526	186.591901	354.165961	177.586619	E	***827.498530***	414.252903	810.471981	405.739629	809.487965	405.247621	7
4	473.224205	237.115741	455.213640	228.110458	T	***698.455937***	349.731607	681.429388	341.218332	680.445372	340.726324	6
5	586.308269	293.657773	568.297704	284.652490	L	***597.408258***	299.207767	580.381709	290.694493			5
6	683.361033	342.184155	665.350468	333.178872	P	***484.324194***	242.665735	467.297645	234.152460			4
7	782.429447	391.718362	764.418882	382.713079	V	387.271430	194.139353	370.244881	185.626078			3
8	895.513511	448.260394	877.502946	439.255111	I	288.203016	144.605146	271.176467	136.091871			2
9					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LEETLPVIR
(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	1068.617889	0.001179	LEETLPVIR
10.7	1068.629135	-0.010067	ITRPPINVK
9.6	1068.617889	0.001179	TLIEAGLPQK

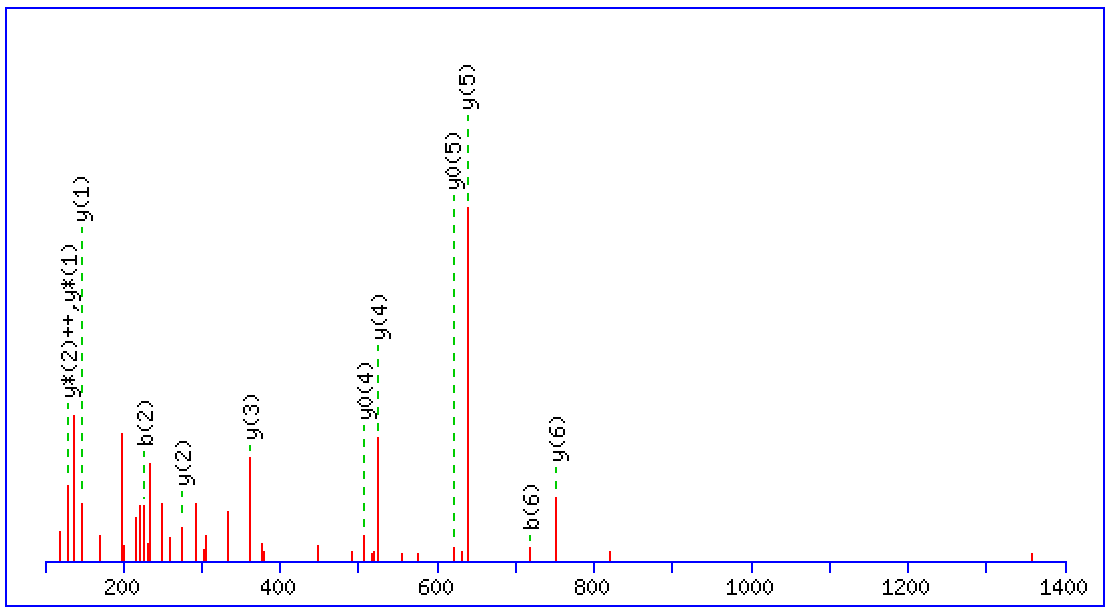
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLYSQK**
Found in **ABCA1_HUMAN**, ATP-binding cassette sub-family A member 1 OS=Homo sapiens GN=ABCA1 PE=1 SV=3

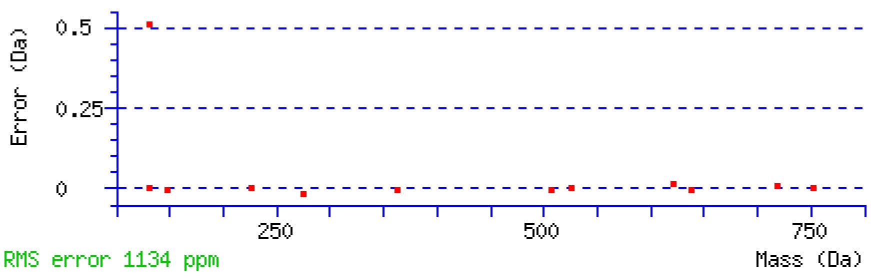
Match to Query 3230: 863.511928 from(432.763240,2+) rtinseconds(2021) index(16548)
Title: Locus:1.1.1.2582.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

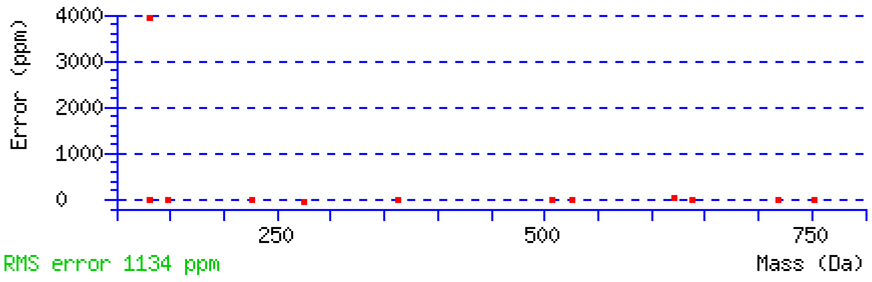
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 863.511627
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0023
Matches : 12/50 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	114.091340	57.549308					L							7
2	**227.175404**	114.091340					L	***751.434867***	376.221072	734.408318	367.707797	733.424302	367.215789	6
3	340.259468	170.633372					L	***638.350803***	319.679040	621.324254	311.165765	620.340238	310.673757	5
4	503.322797	252.165036					Y	***525.266739***	263.137008	508.240190	254.623733	507.256174	254.131725	4
5	590.354825	295.681051			572.344260	286.675768	S	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	3
6	**718.413403**	359.710340	701.386854	351.197065	700.402838	350.705057	Q	***275.171382***	138.089329	258.144833	129.576055			2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLLYSQK
(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	863.511627	0.000301	LLLYSQK
20.9	863.511627	0.000301	LLLSYGAK
14.7	863.511627	0.000301	IIKPYSK
10.9	863.511627	0.000301	LISPYKK
8.1	863.511627	0.000301	KPIYLSK
6.4	863.511627	0.000301	LIKSFEK
6.1	863.511612	0.000316	LIKAYEK
4.2	863.511642	0.000286	IIGVYATK
4.2	863.511612	0.000316	LIYEKAK
3.2	863.511642	0.000286	FISAVLSK

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

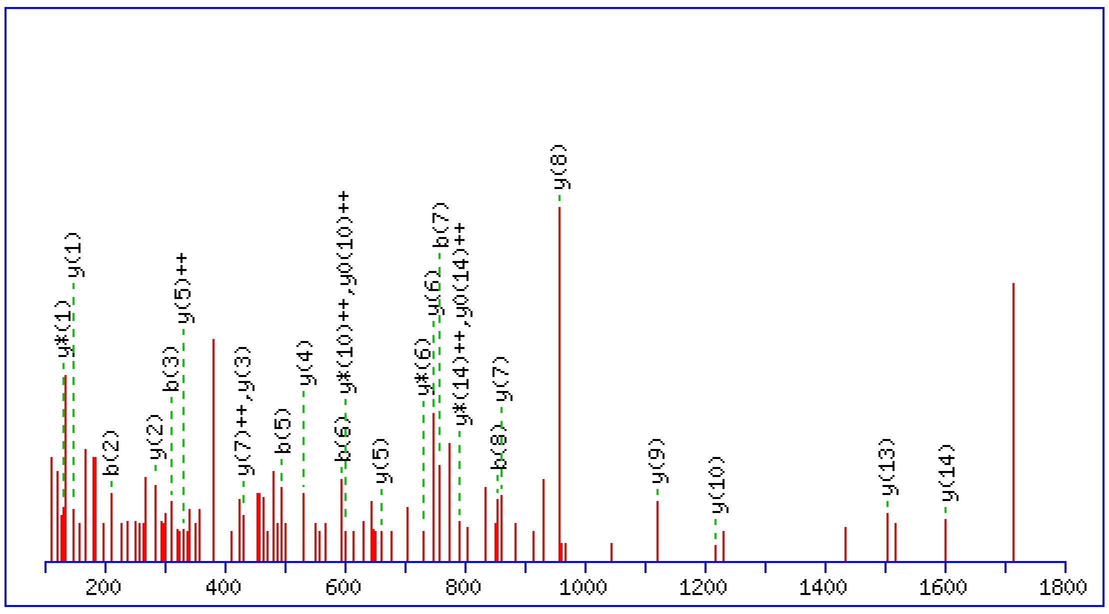
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVADVYPLSQTFHK**
Found in **ABCA6_HUMAN**, ATP-binding cassette sub-family A member 6 OS=Homo sapiens GN=ABCA6 PE=1 SV=2

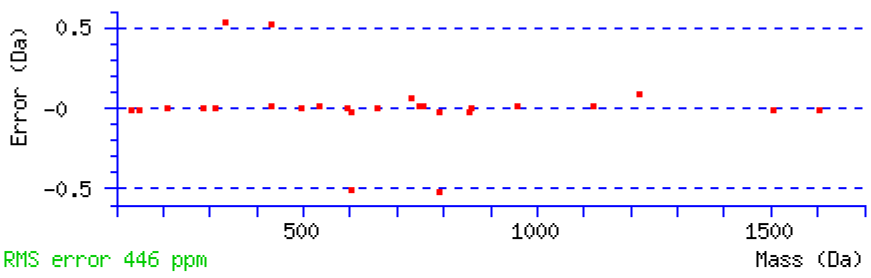
Match to Query 37214: 1713.907512 from(572.309780,3+) rtinseconds(2829) index(34566)
Title: Locus:1.1.1.2861.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

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 ●

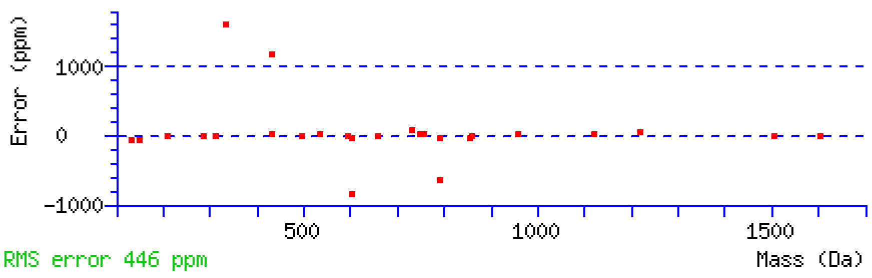


Monoisotopic mass of neutral peptide Mr(calc): 1713.909012
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 8.5e-005
Matches : 26/134 fragment ions using 76 most intense peaks (help)

#	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	**211.144104**	106.075690					P	***1601.832221***	801.419749	1584.805672	792.906474	1583.821656	792.414466	14
3	**310.212518**	155.609897					V	***1504.779457***	752.893367	1487.752908	744.380092	1486.768892	743.888084	13
4	381.249632	191.128454					A	1405.711043	703.359160	1388.684494	694.845885	1387.700478	694.353877	12
5	**496.276575**	248.641925			478.266010	239.636643	D	1334.673929	667.840603	1317.647380	659.327328	1316.663364	658.835320	11
6	**595.344989**	298.176133			577.334424	289.170850	V	***1219.646986***	610.327131	1202.620437	601.813857	1201.636421	601.321848	10
7	**758.408318**	379.707797			740.397753	370.702515	Y	***1120.578572***	560.792924	1103.552023	552.279650	1102.568007	551.787642	9
8	**855.461082**	428.234179			837.450517	419.228897	P	***957.515243***	479.261260	940.488694	470.747985	939.504678	470.255977	8
9	968.545146	484.776211			950.534581	475.770929	L	***860.462479***	430.734878	843.435930	422.221603	842.451914	421.729595	7
10	1055.577174	528.292225			1037.566609	519.286943	S	***747.378415***	374.192846	730.351866	365.679571	729.367850	365.187563	6
11	1183.635752	592.321514	1166.609203	583.808240	1165.625187	583.316231	Q	***660.346387***	330.676832	643.319838	322.163557	642.335822	321.671549	5
12	1284.683431	642.845353	1267.656882	634.332079	1266.672866	633.840071	T	***532.287809***	266.647543	515.261260	258.134268	514.277244	257.642260	4
13	1431.751845	716.379561	1414.725296	707.866286	1413.741280	707.374278	F	***431.240130***	216.123703	414.213581	207.610429			3
14	1568.810757	784.909017	1551.784208	776.395742	1550.800192	775.903734	H	***284.171716***	142.589496	267.145167	134.076221			2
15							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 446 ppm



RMS error 446 ppm

NCBI **BLAST** search of LPVADVYPLSQTFHK
(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	1713.909012	-0.001500	LPVADVYPLSQTFHK
2.5	1713.897095	0.010417	SPLTQEQLIPNLAMK

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

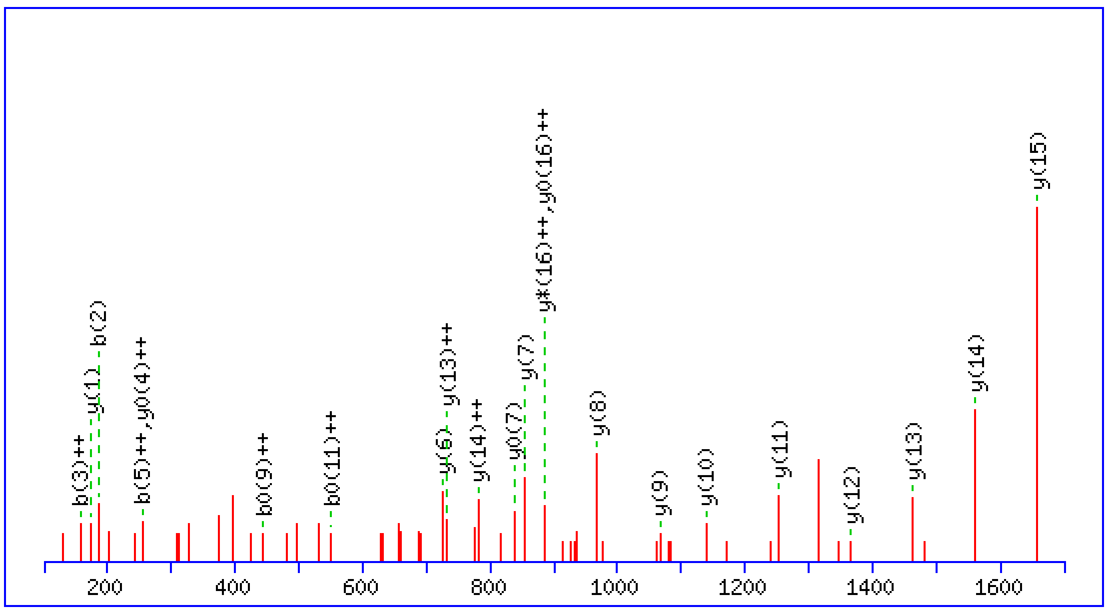
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIEPPPLDAVIEAEHTLR**
Found in **DHX9_HUMAN**, ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4

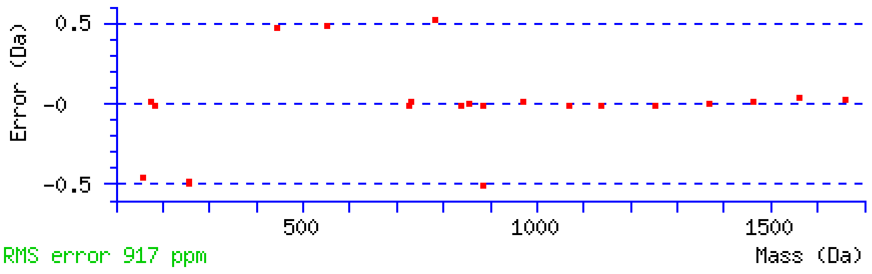
Match to Query 47383: 1970.044032 from(657.688620,3+) rtinseconds(3551) index(42968)
Title: Locus:1.1.1.3285.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

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 ●

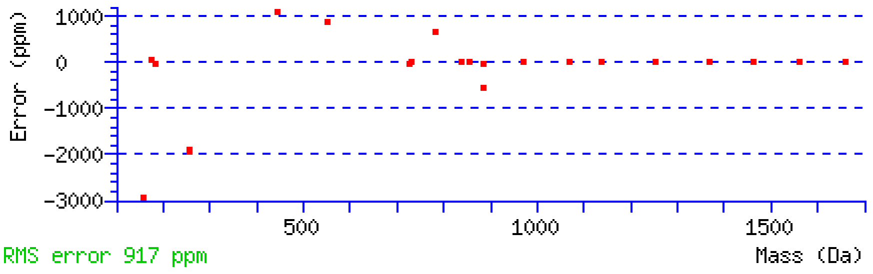


```
Monoisotopic mass of neutral peptide Mr(calc): 1970.047256
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 0.00012
Matches : 22/162 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			**A**							**18**
2	185.128454	93.067865			**I**	1900.017455	950.512365	1882.990906	941.999091	1882.006890	941.507083	**17**
3	314.171047	157.589161	296.160482	148.583879	**E**	1786.933391	893.970333	1769.906842	885.457059	1768.922826	884.965051	**16**
4	411.223811	206.115544	393.213246	197.110261	**P**	***1657.890798***	829.449037	1640.864249	820.935762	1639.880233	820.443754	**15**
5	508.276575	254.641926	490.266010	245.636643	**P**	***1560.838034***	780.922655	1543.811485	772.409380	1542.827469	771.917372	**14**
6	605.329339	303.168308	587.318774	294.163025	**P**	***1463.785270***	732.396273	1446.758721	723.882998	1445.774705	723.390990	**13**
7	718.413403	359.710340	700.402838	350.705057	**L**	***1366.732506***	683.869891	1349.705957	675.356616	1348.721941	674.864608	**12**
8	833.440346	417.223811	815.429781	408.218529	**D**	***1253.648442***	627.327859	1236.621893	618.814584	1235.637877	618.322576	**11**
9	904.477460	452.742368	886.466895	443.737086	**A**	***1138.621499***	569.814387	1121.594950	561.301113	1120.610934	560.809105	**10**
10	1003.545874	502.276575	985.535309	493.271293	**V**	***1067.584385***	534.295830	1050.557836	525.782556	1049.573820	525.290548	**9**
11	1116.629938	558.818607	1098.619373	549.813325	**I**	***968.515971***	484.761623	951.489422	476.248349	950.505406	475.756341	**8**
12	1245.672531	623.339903	1227.661966	614.334621	**E**	***855.431907***	428.219591	838.405358	419.706317	837.421342	419.214309	**7**
13	1316.709645	658.858460	1298.699080	649.853178	**A**	***726.389314***	363.698295	709.362765	355.185020	708.378749	354.693012	**6**
14	1445.752238	723.379757	1427.741673	714.374474	**E**	655.352200	328.179738	638.325651	319.666463	637.341635	319.174455	**5**
15	1582.811150	791.909213	1564.800585	782.903930	**H**	526.309607	263.658441	509.283058	255.145167	508.299042	254.653159	**4**
16	1683.858829	842.433052	1665.848264	833.427770	**T**	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	**3**
17	1796.942893	898.975084	1778.932328	889.969802	**L**	288.203016	144.605146	271.176467	136.091871			**2**
18					**R**	***175.118952***	88.063114	158.092403	79.549839			**1**



RMS error 917 ppm



RMS error 917 ppm

NCBI **BLAST** search of AIEPPPLDAVIEAEHTLR
(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	1970.047256	-0.003224	AIEPPPLDAVIEAEHTLR

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

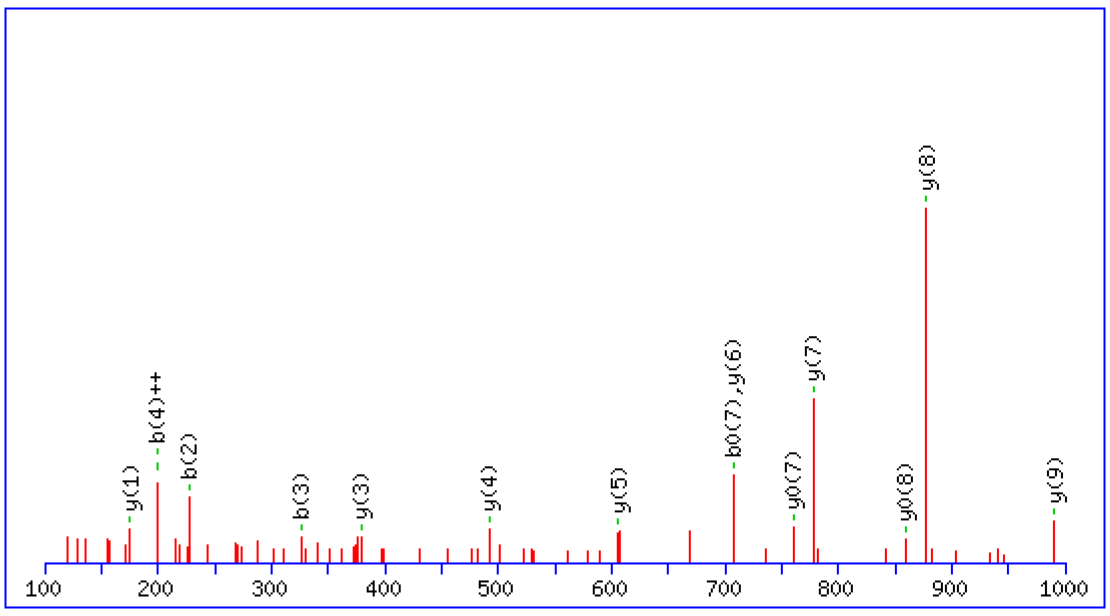
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILVATNLFGR**
Found in **DX39A_HUMAN**, ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2

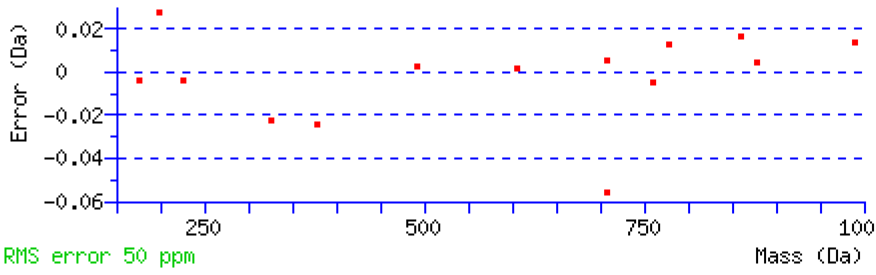
Match to Query 14424: 1102.651468 from(552.333010,2+) rtinseconds(3028) index(39885)
Title: Locus:1.1.1.2691.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

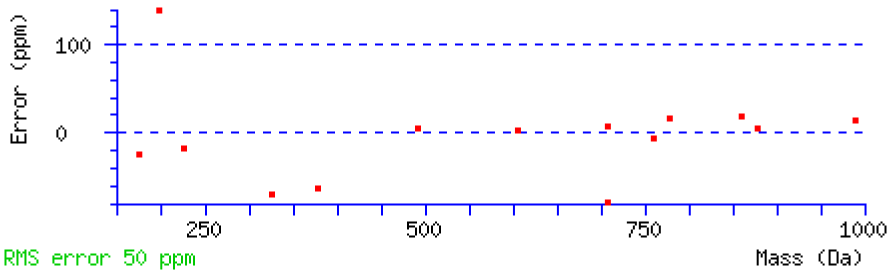
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1102.649872
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 4e-007
Matches : 14/80 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							10
2	**227.175404**	114.091340					L	***990.573092***	495.790184	973.546543	487.276909	972.562527	486.784901	9
3	**326.243818**	163.625547					V	***877.489028***	439.248152	860.462479	430.734877	859.478463	430.242869	8
4	397.280932	199.144104					A	***778.420614***	389.713945	761.394065	381.200671	760.410049	380.708663	7
5	498.328611	249.667943			480.318046	240.662661	T	***707.383500***	354.195388	690.356951	345.682114	689.372935	345.190106	6
6	612.371538	306.689407	595.344989	298.176132	594.360973	297.684125	N	***606.335821***	303.671549	589.309272	295.158274			5
7	725.455602	363.231439	708.429053	354.718165	707.445037	354.226157	L	***492.292894***	246.650085	475.266345	238.136810			4
8	872.524016	436.765646	855.497467	428.252371	854.513451	427.760363	F	***379.208830***	190.108053	362.182281	181.594778			3
9	929.545480	465.276378	912.518931	456.763104	911.534915	456.271096	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 ILVATNLFGR
(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	1102.649872	0.001596	ILVATNLFGR
11.2	1102.649857	0.001611	ILVPSYRQK
8.8	1102.653229	-0.001761	LICKVSTLR
7.4	1102.649872	0.001596	LLFQQLVSR
5.8	1102.649857	0.001611	ILIPKGSYGR
4.5	1102.641998	0.009470	IPTCKITLK
4.3	1102.649872	0.001596	LLSQGVIAFR
1.3	1102.661087	-0.009619	ILPKPNLHR
1.3	1102.649872	0.001596	LPPLPLHIR
1.2	1102.649841	0.001627	LLAYPKLNR

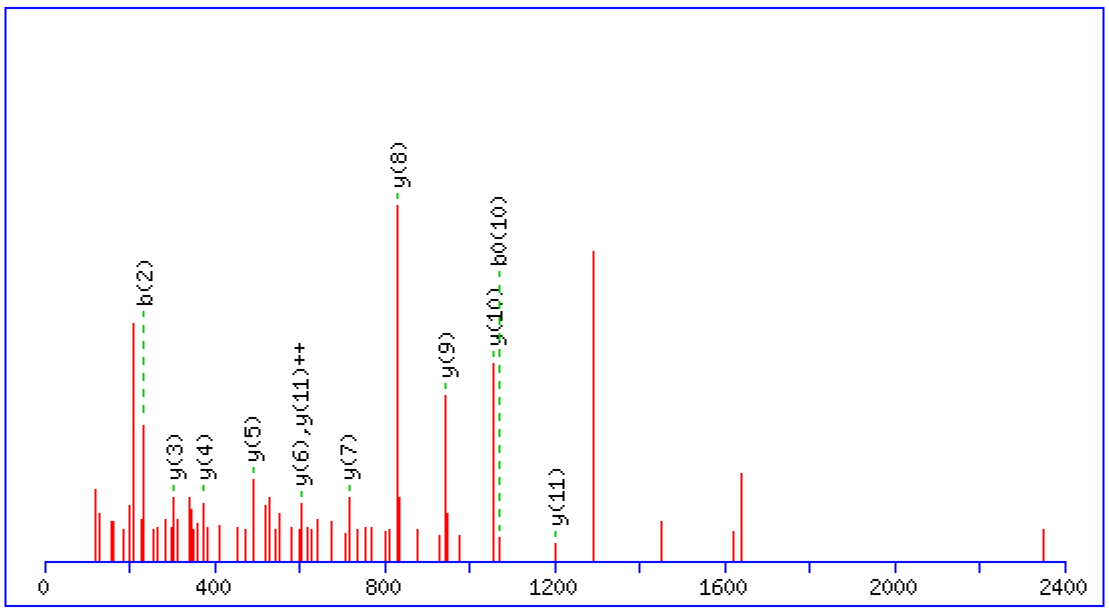
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFLLDLLNATGK**
Found in **DDX3X_HUMAN**, ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3

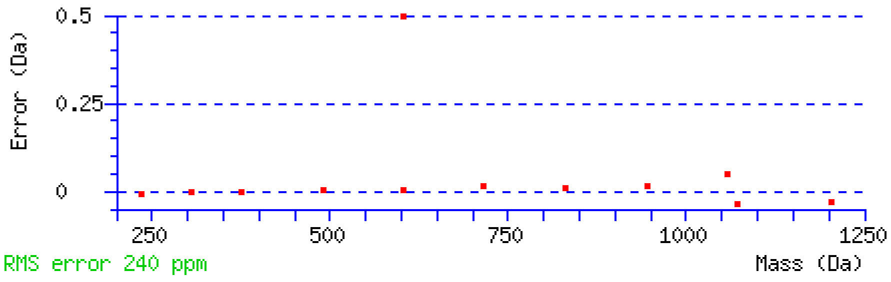
Match to Query 28936: 1290.723268 from(646.368910,2+) rtinseconds(4166) index(65732)
Title: Locus:1.1.1.2233.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

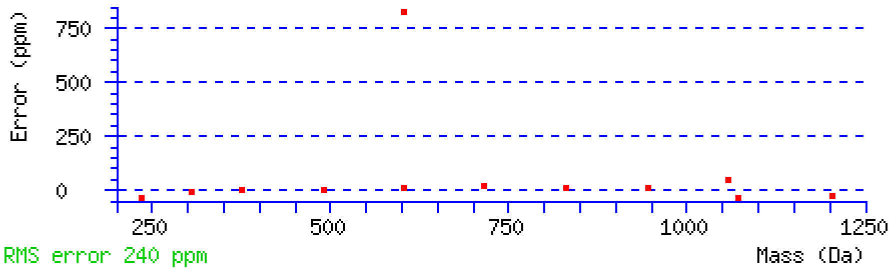
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1290.718338
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 4.9e-006
Matches : 12/114 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	88.039304	44.523290			70.028739	35.518008	S							12
2	235.107718	118.057497			217.097153	109.052214	F	***1204.693601***	602.850439	1187.667052	594.337164	1186.683036	593.845156	11
3	348.191782	174.599529			330.181217	165.594247	L	***1057.625187***	529.316232	1040.598638	520.802957	1039.614622	520.310949	10
4	461.275846	231.141561			443.265281	222.136279	L	***944.541123***	472.774200	927.514574	464.260925	926.530558	463.768917	9
5	576.302789	288.655033			558.292224	279.649750	D	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	8
6	689.386853	345.197065			671.376288	336.191782	L	***716.430116***	358.718696	699.403567	350.205422	698.419551	349.713414	7
7	802.470917	401.739097			784.460352	392.733814	L	***603.346052***	302.176664	586.319503	293.663389	585.335487	293.171382	6
8	916.513844	458.760560	899.487295	450.247286	898.503279	449.755278	N	***490.261988***	245.634632	473.235439	237.121357	472.251423	236.629349	5
9	987.550958	494.279117	970.524409	485.765843	969.540393	485.273835	A	***376.219061***	188.613168	359.192512	180.099894	358.208496	179.607886	4
10	1088.598637	544.802957	1071.572088	536.289682	1070.588072	535.797674	T	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
11	1145.620101	573.313689	1128.593552	564.800414	1127.609536	564.308406	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 SFLLDLLNATGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	1290.718338	0.004930	SFLLDLLNATGK
1.8	1290.733627	-0.010359	SILFVPTFVPR
1.8	1290.729568	-0.006300	SFRVSINIDLK

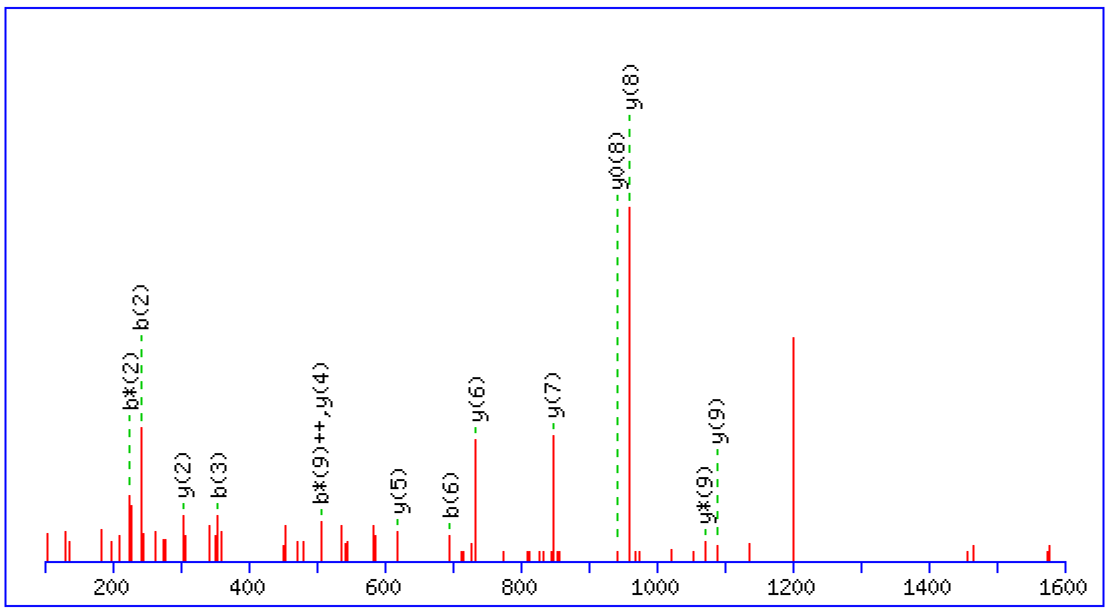
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IKLLNNSDER**
Found in **ARI4B_HUMAN**, AT-rich interactive domain-containing protein 4B OS=Homo sapiens GN=ARID4B PE=1 SV=2

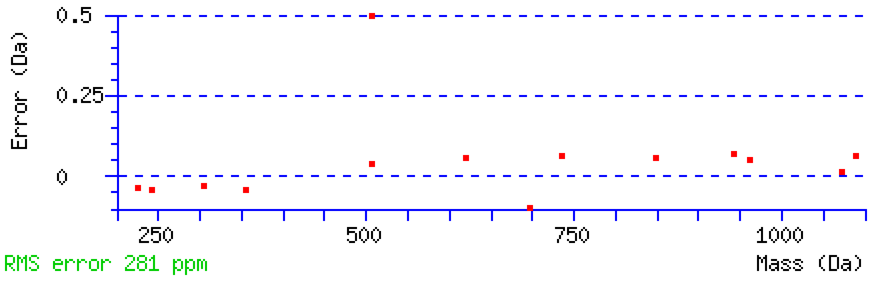
Match to Query 25476: 1200.656208 from(601.335380,2+) rtinseconds(2846) index(36432)
Title: Locus:1.1.1.2575.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

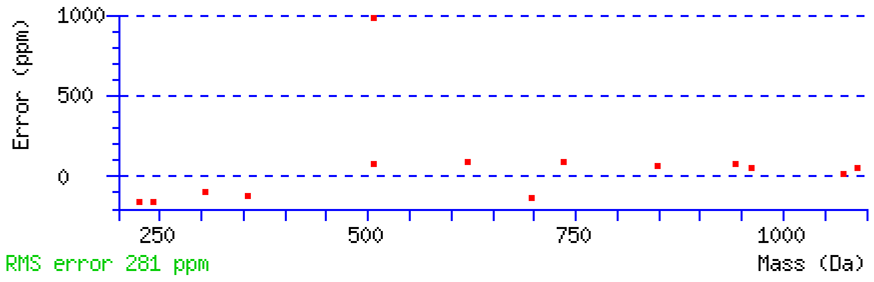
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.646210
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 8.3e-005
Matches : 14/92 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							10
2	**242.186303**	121.596790	225.159754	113.083515			K	***1088.569461***	544.788369	1071.542912	536.275094	1070.558896	535.783086	9
3	**355.270367**	178.138822	338.243818	169.625547			L	***960.474498***	480.740887	943.447949	472.227612	942.463933	471.735604	8
4	468.354431	234.680854	451.327882	226.167579			L	***847.390434***	424.198855	830.363885	415.685580	829.379869	415.193572	7
5	582.397358	291.702317	565.370809	283.189043			N	***734.306370***	367.656823	717.279821	359.143548	716.295805	358.651540	6
6	**696.440285**	348.723781	679.413736	340.210506			N	***620.263443***	310.635359	603.236894	302.122085	602.252878	301.630077	5
7	783.472313	392.239795	766.445764	383.726520	765.461748	383.234512	S	***506.220516***	253.613896	489.193967	245.100621	488.209951	244.608613	4
8	898.499256	449.753266	881.472707	441.239991	880.488691	440.747983	D	419.188488	210.097882	402.161939	201.584607	401.177923	201.092599	3
9	1027.541849	514.274563	1010.515300	505.761288	1009.531284	505.269280	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 IKLLNNSDER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.9	1200.646210	0.009998	IKLLNNSDER
41.7	1200.653610	0.002598	IQLINNMLDK
10.7	1200.653610	0.002598	LKLMDEPALR
10.6	1200.653610	0.002598	LKLMDEPALR
4.6	1200.664856	-0.008648	LQEMVLKGQR
4.1	1200.657486	-0.001278	APGITRTVSQR
3.3	1200.653610	0.002598	AGLLGLLEEMR
0.0	1200.661499	-0.005291	IIQFKPGQDR

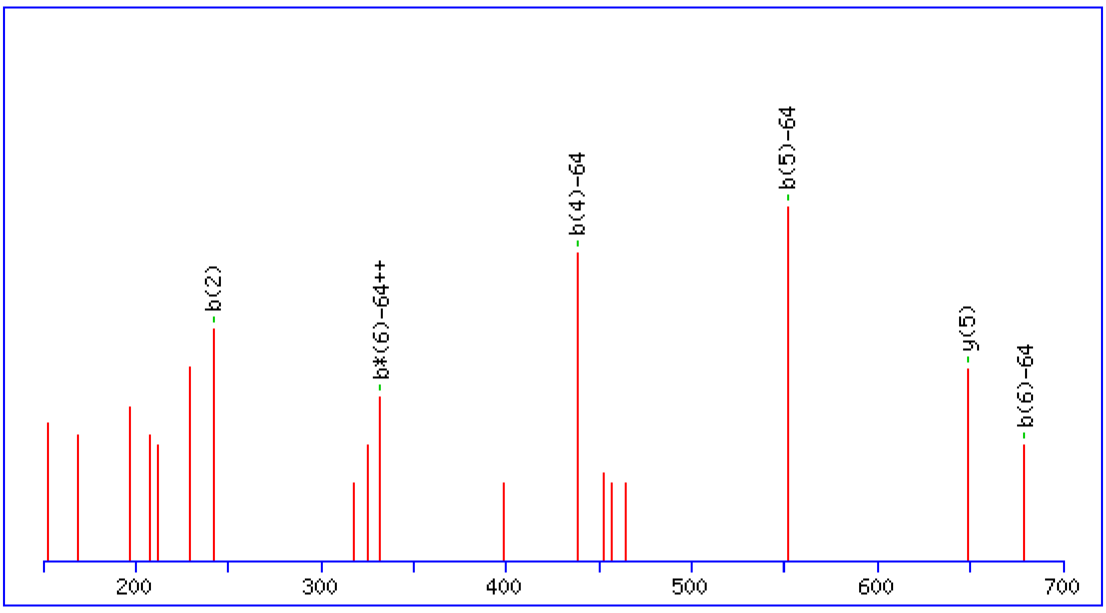
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKLMLQK**
Found in **AUGN_HUMAN**, Augurin OS=Homo sapiens GN=C2orf40 PE=1 SV=1

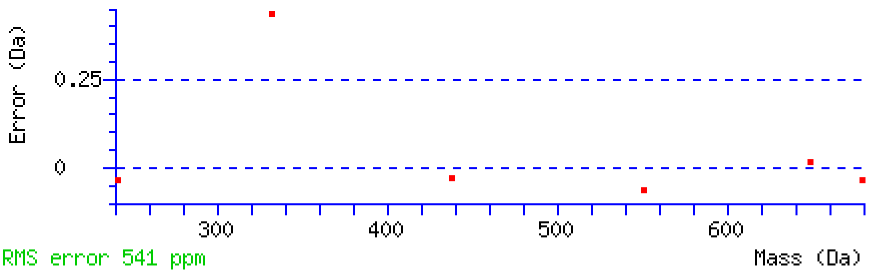
Match to Query 4565: 888.543348 from(445.278950,2+) rtinseconds(2580) index(29393)
Title: Locus:1.1.1.2494.4
Data file 2011-11-10 - TFD - S 8-1.mgf

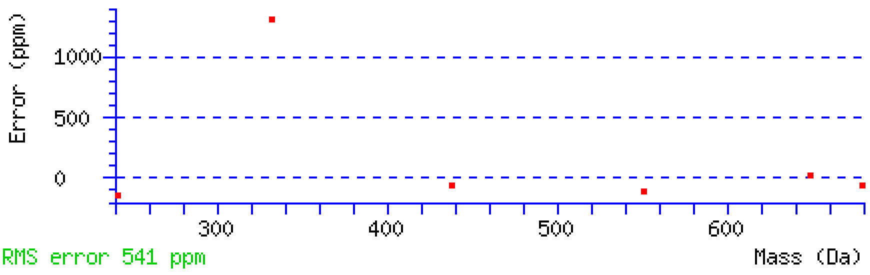
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 888.546631
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: 33  Expect: 0.0012
Matches : 6/70 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			L					7
2	*242.186303*	121.596790	225.159754	113.083515	K	712.471588	356.739432	695.445039	348.226158	6
3	355.270367	178.138822	338.243818	169.625547	L	584.376625	292.691951	567.350076	284.178676	5
4	*438.307482*	219.657379	421.280933	211.144105	M	471.292561	236.149919	454.266012	227.636644	4
5	*551.391546*	276.199411	534.364997	267.686137	L	388.255446	194.631361	371.228897	186.118087	3
6	*679.450124*	340.228700	662.423575	331.715426	Q	275.171382	138.089329	258.144833	129.576055	2
7					K	147.112804	74.060040	130.086255	65.546765	1





NCBI **BLAST** search of LKLMLQK
(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	888.546631	-0.003283	LKLMLQK
9.6	888.546631	-0.003283	KLMVALAK
5.7	888.546631	-0.003283	LLLMKQK
2.0	888.543259	0.000089	KIPQLYK

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

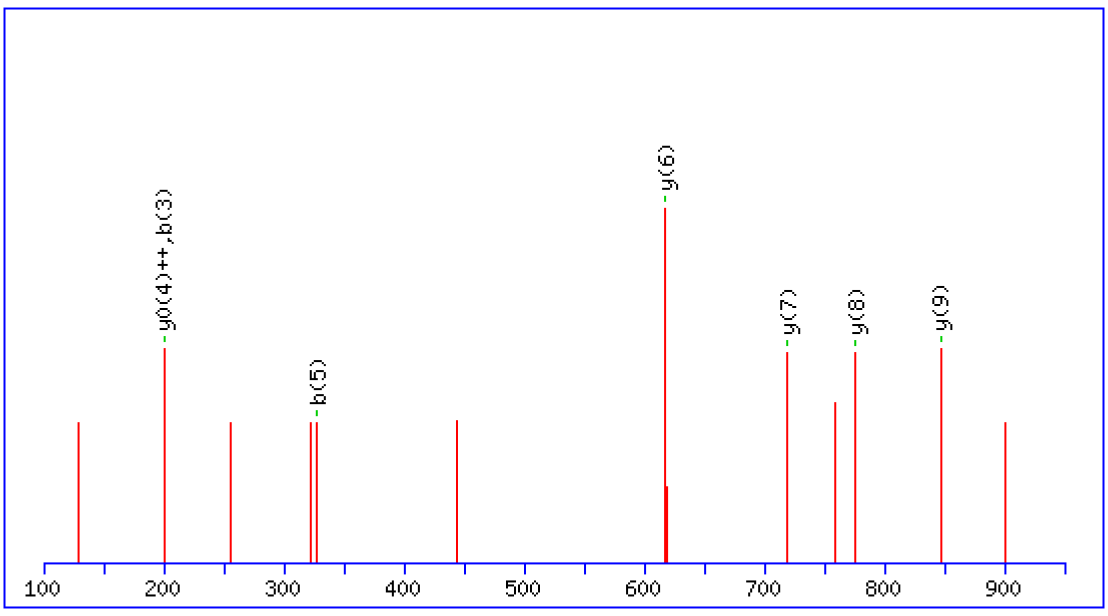
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGAAGTAEATAR**
Found in **BCAM_HUMAN**, Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2

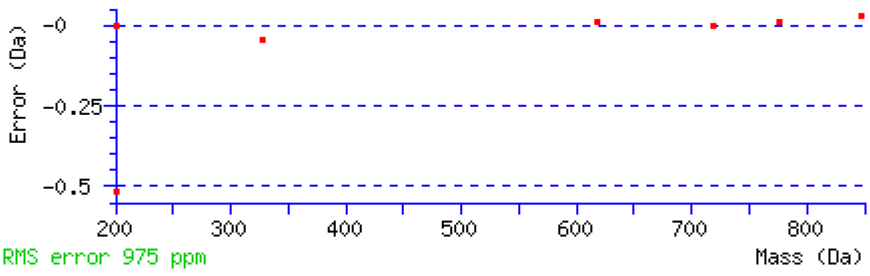
Match to Query 15095: 1045.519748 from(523.767150,2+) rtinseconds(792) index(1787)
Title: Locus:1.1.1.939.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

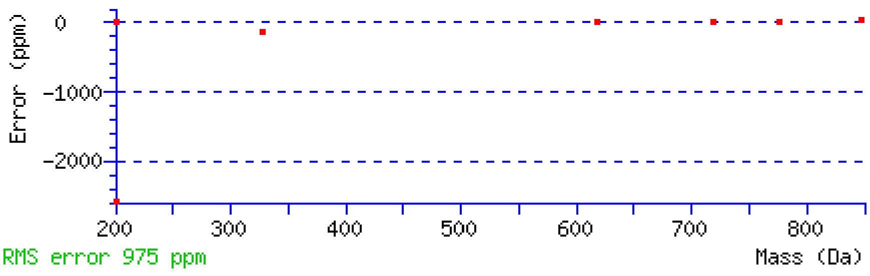
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1045.515213
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0083
Matches : 7/96 fragment ions using 7 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	975.485401	488.246339	958.458852	479.733064	957.474836	479.241056	11
3	**200.102968**	100.555122			A	918.463937	459.735607	901.437388	451.222332	900.453372	450.730324	10
4	271.140082	136.073679			A	***847.426823***	424.217050	830.400274	415.703775	829.416258	415.211767	9
5	**328.161546**	164.584411			G	***776.389709***	388.698493	759.363160	380.185218	758.379144	379.693210	8
6	429.209225	215.108251	411.198660	206.102968	T	***719.368245***	360.187761	702.341696	351.674486	701.357680	351.182478	7
7	500.246339	250.626807	482.235774	241.621525	A	***618.320566***	309.663921	601.294017	301.150647	600.310001	300.658639	6
8	629.288932	315.148104	611.278367	306.142822	E	547.283452	274.145364	530.256903	265.632090	529.272887	265.140082	5
9	700.326046	350.666661	682.315481	341.661379	A	418.240859	209.624068	401.214310	201.110793	400.230294	200.618785	4
10	801.373725	401.190501	783.363160	392.185218	T	347.203745	174.105511	330.177196	165.592236	329.193180	165.100228	3
11	872.410839	436.709058	854.400274	427.703775	A	246.156066	123.581671	229.129517	115.068397			2
12					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AGAAGTAEATAR
(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	1045.515213	0.004535	AGAAGTAEATAR
24.6	1045.522583	-0.002835	KAAMAEPNAK
21.2	1045.515213	0.004535	QAQRGTEEK
15.3	1045.515213	0.004535	KAQQETGER
14.3	1045.522583	-0.002835	KAAMAEPNAK
9.3	1045.519241	0.000507	AQAQVSEWK
7.6	1045.522598	-0.002850	QQQEMLAAK
6.4	1045.522598	-0.002850	QPRIMEEK
3.6	1045.522598	-0.002850	QAMQEQLAK
1.9	1045.515198	0.004550	KQAASEEQR

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

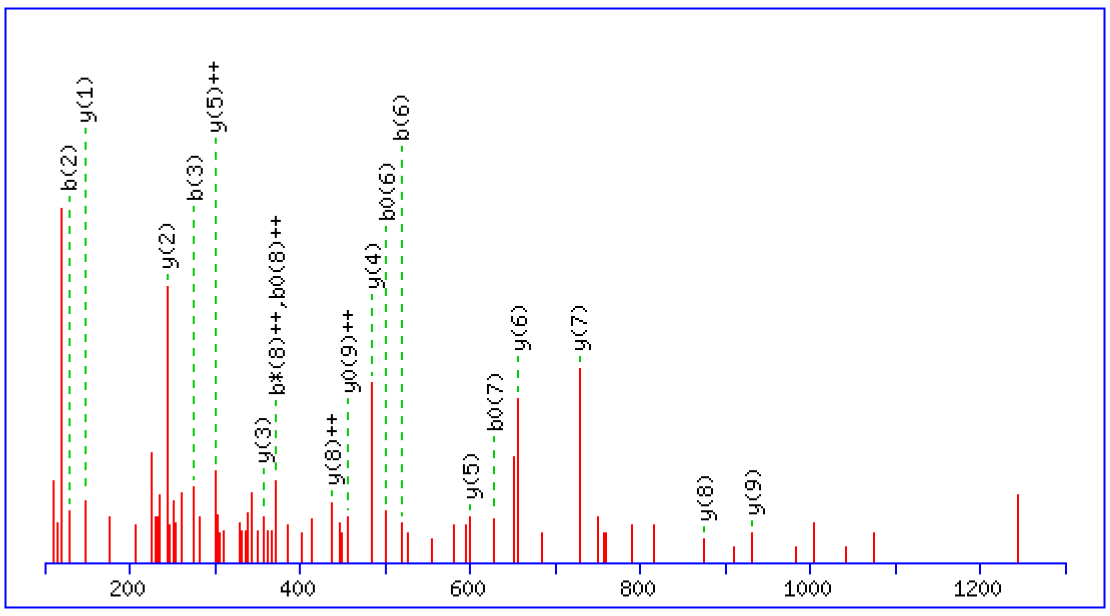
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGFAGDQIPK**
Found in **ACTY_HUMAN**, Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1

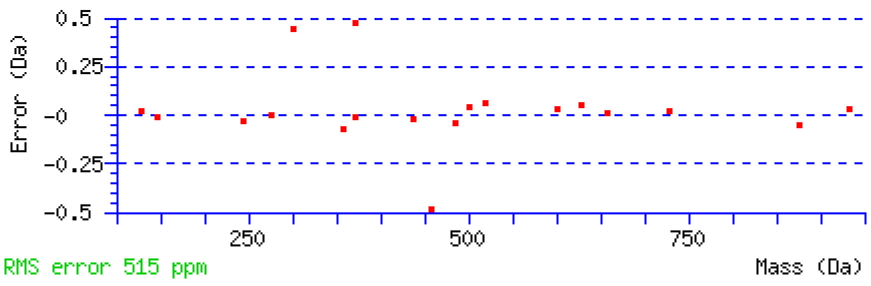
Match to Query 8327: 1002.513688 from(502.264120,2+) rtinseconds(1757) index(18077)
Title: Locus:1.1.1.2170.19
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

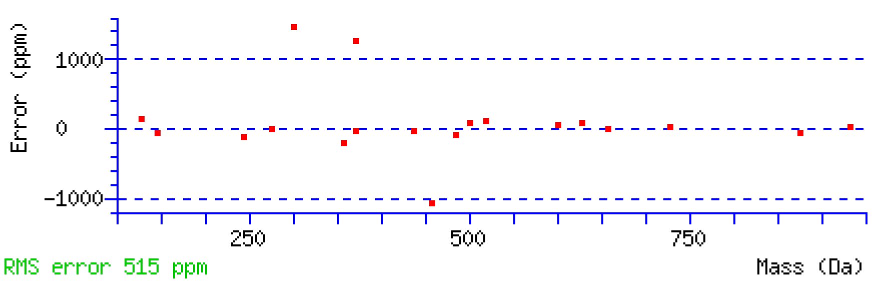
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1002.513443
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 2.8e-006
Matches : 19/78 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	72.044390	36.525833					A							10
2	**129.065854**	65.036565					G	***932.483609***	466.745443	915.457060	458.232168	914.473044	457.740160	9
3	**276.134268**	138.570772					F	***875.462145***	438.234711	858.435596	429.721436	857.451580	429.229428	8
4	347.171382	174.089329					A	***728.393731***	364.700504	711.367182	356.187229	710.383166	355.695221	7
5	404.192846	202.600061					G	***657.356617***	329.181947	640.330068	320.668672	639.346052	320.176664	6
6	**519.219789**	260.113533			501.209224	251.108250	D	***600.335153***	300.671215	583.308604	292.157940	582.324588	291.665932	5
7	647.278367	324.142822	630.251818	315.629547	629.267802	315.137539	Q	***485.308210***	243.157743	468.281661	234.644469			4
8	760.362431	380.684854	743.335882	372.171579	742.351866	371.679571	I	***357.249632***	179.128454	340.223083	170.615180			3
9	857.415195	429.211236	840.388646	420.697961	839.404630	420.205953	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 AGFAGDQIPK
(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	1002.513443	0.000245	AGFAGDQIPK
13.8	1002.513412	0.000276	ENGWIKEK
10.8	1002.509399	0.004289	AGKAEQTGNK
10.1	1002.509384	0.004304	NERSIQEK
8.6	1002.509384	0.004304	QREAEATAK
7.5	1002.516815	-0.003127	KQMPPVGSK
7.4	1002.516815	-0.003127	KQMPPVGSK
5.2	1002.523315	-0.009627	ADLSELVEK
5.0	1002.516815	-0.003127	TCALGVQPK
4.0	1002.516815	-0.003127	QMPPVGSKK

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

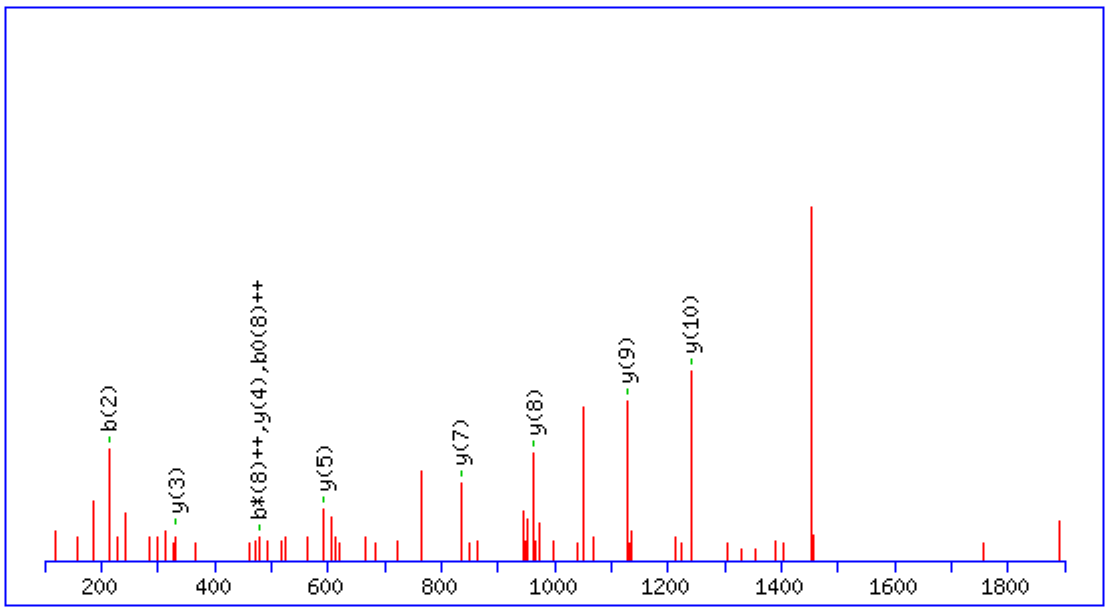
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILYELENFQGK**
Found in **CRBB3_HUMAN**, Beta-crystallin B3 OS=Homo sapiens GN=CRYBB3 PE=1 SV=4

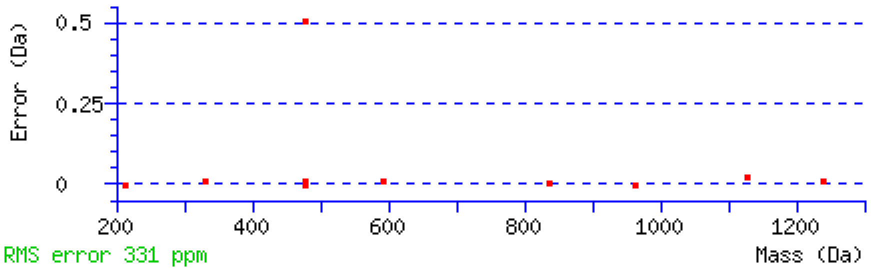
Match to Query 33450: 1451.762608 from(726.888580,2+) rtinseconds(3207) index(43523)
Title: Locus:1.1.1.2661.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

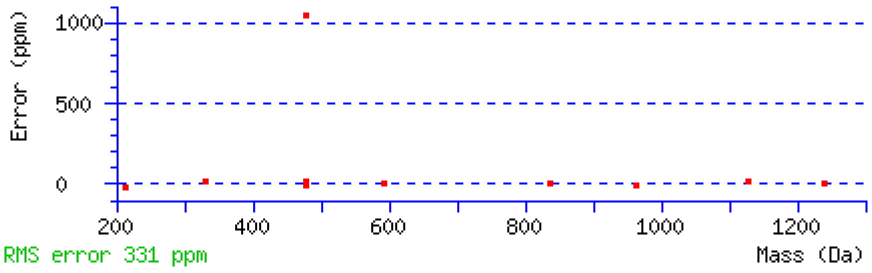
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1451.766006
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00018
Matches : 10/100 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	100.075690	50.541483					V							12
2	213.159754	107.083515					I	1353.704894	677.356085	1336.678345	668.842811	1335.694329	668.350802	11
3	326.243818	163.625547					L	***1240.620830***	620.814053	1223.594281	612.300779	1222.610265	611.808771	10
4	489.307147	245.157211					Y	***1127.536766***	564.272021	1110.510217	555.758747	1109.526201	555.266738	9
5	618.349740	309.678508			600.339175	300.673226	E	***964.473437***	482.740357	947.446888	474.227082	946.462872	473.735074	8
6	731.433804	366.220540			713.423239	357.215258	L	***835.430844***	418.219060	818.404295	409.705785	817.420279	409.213777	7
7	860.476397	430.741837			842.465832	421.736554	E	722.346780	361.677028	705.320231	353.163753	704.336215	352.671745	6
8	974.519324	487.763300	957.492775	479.250026	956.508759	478.758018	N	***593.304187***	297.155732	576.277638	288.642457			5
9	1121.587738	561.297507	1104.561189	552.784233	1103.577173	552.292225	F	***479.261260***	240.134268	462.234711	231.620993			4
10	1249.646316	625.326796	1232.619767	616.813522	1231.635751	616.321514	Q	***332.192846***	166.600061	315.166297	158.086786			3
11	1306.667780	653.837528	1289.641231	645.324254	1288.657215	644.832246	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 VILYELENFQGK
(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	1451.766006	-0.003398	VILYELENFQGK
4.8	1451.765366	-0.002758	TETMTVSSLAIRK

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

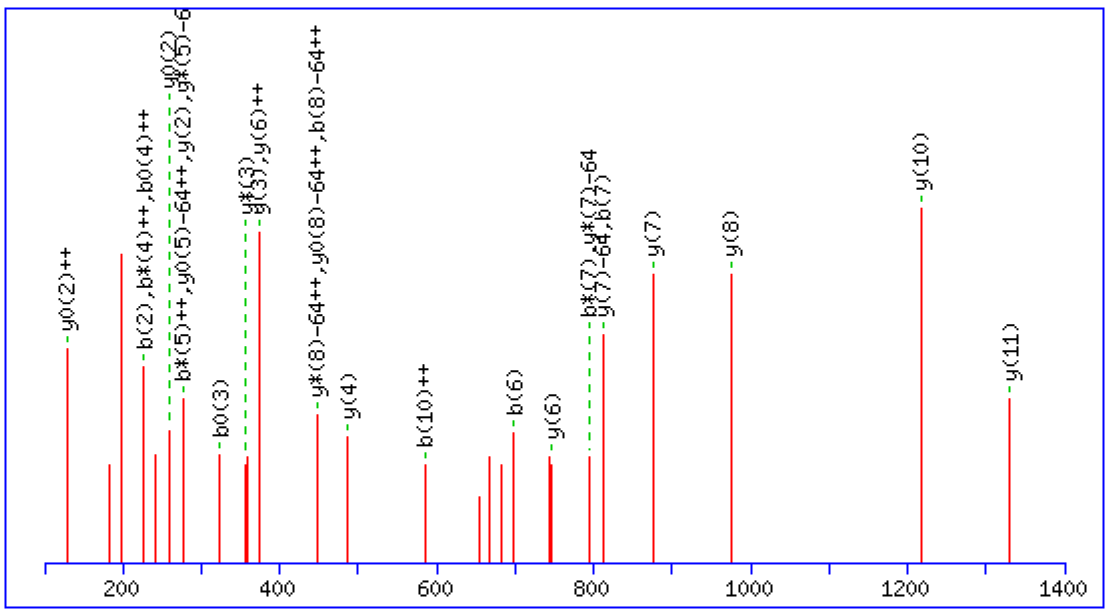
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDKVELMLPEK**
Found in **BR44_HUMAN**, Brain protein 44 OS=Homo sapiens GN=BRP44 PE=1 SV=1

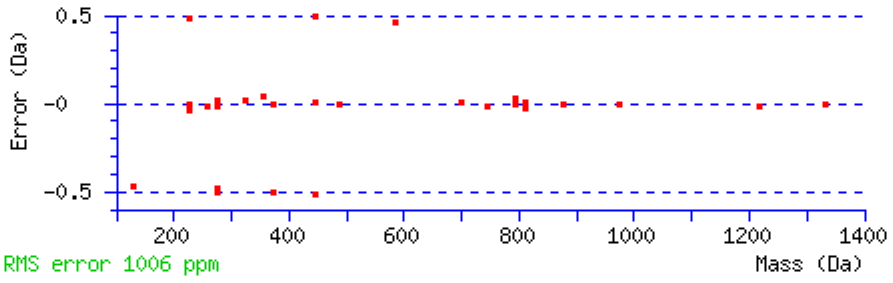
Match to Query 15952: 1442.800992 from(481.940940,3+) rtinseconds(2663) index(8799)
Title: Locus:1.1.1.3031.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

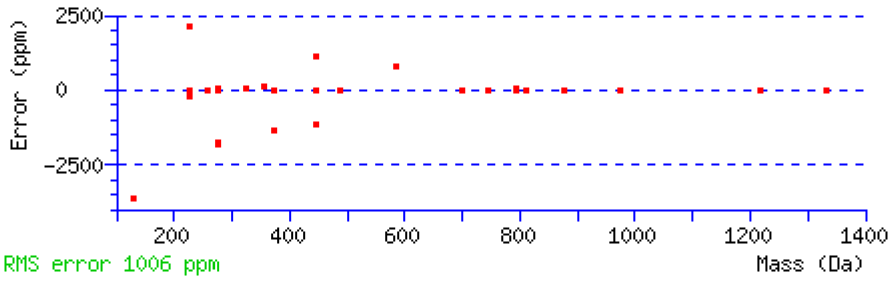
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1442.805420
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: 59  Expect: 9e-006
Matches : 29/186 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							12
2	**227.175404**	114.091340					L	***1330.728666***	665.867971	1313.702117	657.354697	1312.718101	656.862688	11
3	342.202347	171.604811			324.191782	162.599529	D	***1217.644602***	609.325939	1200.618053	600.812664	1199.634037	600.320656	10
4	470.297310	235.652293	453.270761	227.139018	452.286745	226.647010	K	1102.617659	551.812467	1085.591110	543.299193	1084.607094	542.807185	9
5	569.365724	285.186500	552.339175	276.673226	551.355159	276.181218	V	***974.522696***	487.764986	957.496147	479.251711	956.512131	478.759703	8
6	**698.408317**	349.707797	681.381768	341.194522	680.397752	340.702514	E	***875.454282***	438.230779	858.427733	429.717504	857.443717	429.225496	7
7	**811.492381**	406.249829	794.465832	397.736554	793.481816	397.244546	L	***746.411689***	373.709482	729.385140	365.196208	728.401124	364.704200	6
8	958.527781	479.767529	941.501232	471.254254	940.517216	470.762246	M	633.327625	317.167450	616.301076	308.654176	615.317060	308.162168	5
9	1071.611845	536.309560	1054.585296	527.796286	1053.601280	527.304278	L	***486.292225***	243.649750	469.265676	235.136476	468.281660	234.644468	4
10	1168.664609	584.835942	1151.638060	576.322668	1150.654044	575.830660	P	***373.208161***	187.107718	356.181612	178.594444	355.197596	178.102436	3
11	1297.707202	649.357239	1280.680653	640.843964	1279.696637	640.351956	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 LLDKVELMLPEK
(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	1442.805420	-0.004428	LLDKVELMLPEK
33.6	1442.805420	-0.004428	LLDKVELMLPEK
8.5	1442.786789	0.014203	LLASTTPEEILEK
4.3	1442.791519	0.009473	LLSCPGTVAKDLR
4.3	1442.798035	0.002957	VSAIVDEKENVIK
1.1	1442.798004	0.002988	LATALQKLEEAEK
0.5	1442.810623	-0.009631	QLRHLPNHSVVK
0.1	1442.809265	-0.008273	LTSLAALRAGDVEK

{MATRIX SCIENCE}

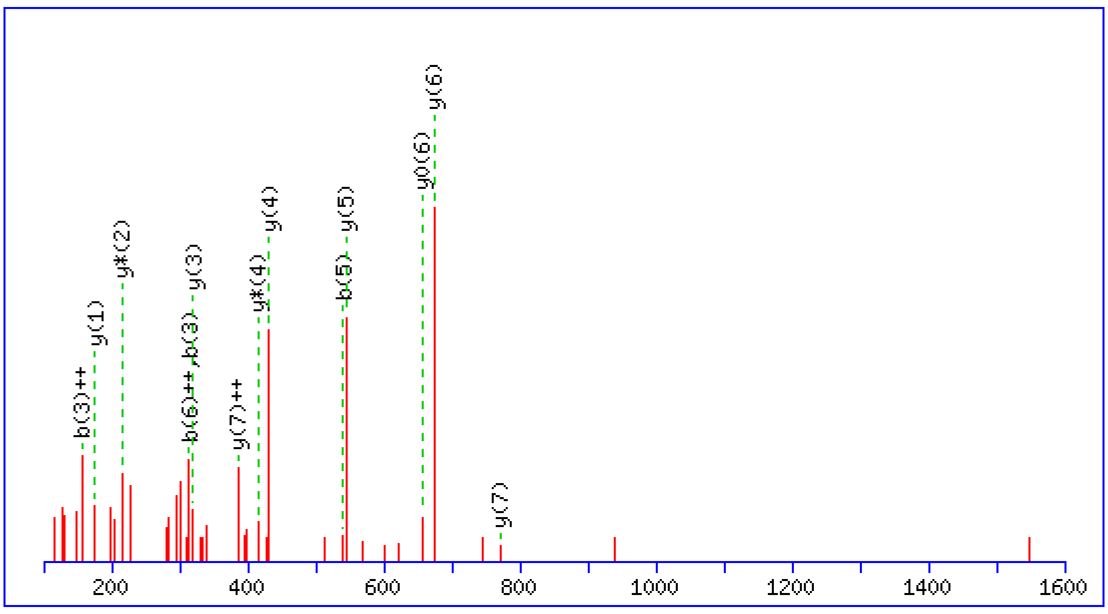
Mascot Search Results

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

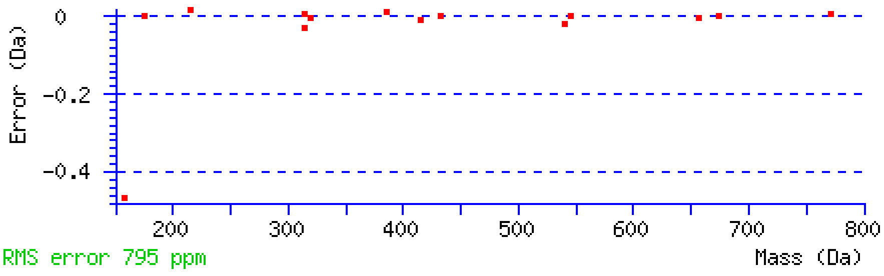
Match to Query 1295: 857.459728 from(429.737140,2+) rtinseconds(1455) index(1624)
Title: Locus:1.1.1.2455.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

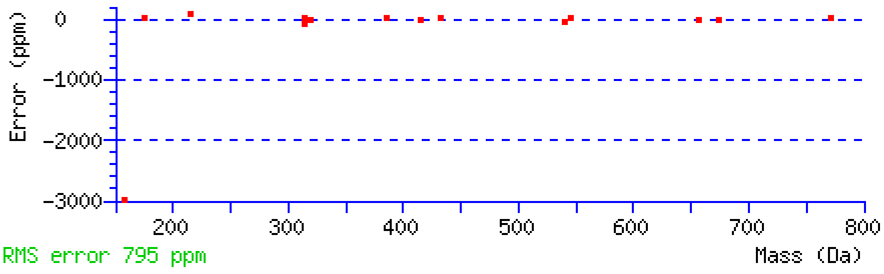
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 857.460663
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.6e-005
Matches : 14/66 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**							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
59.3	857.460663	-0.000935	SPEIISGR
18.6	857.460648	-0.000920	LALEQER
17.8	857.460648	-0.000920	SPEELKR
17.8	857.460663	-0.000935	SPEGLISR
17.5	857.460648	-0.000920	LAEEQLR
9.9	857.460648	-0.000920	AEIIQER
9.9	857.460663	-0.000935	AELISGPR
9.9	857.460648	-0.000920	AELLQER
8.1	857.460663	-0.000935	TDPLEKR
7.9	857.460663	-0.000935	LLEPSSGR

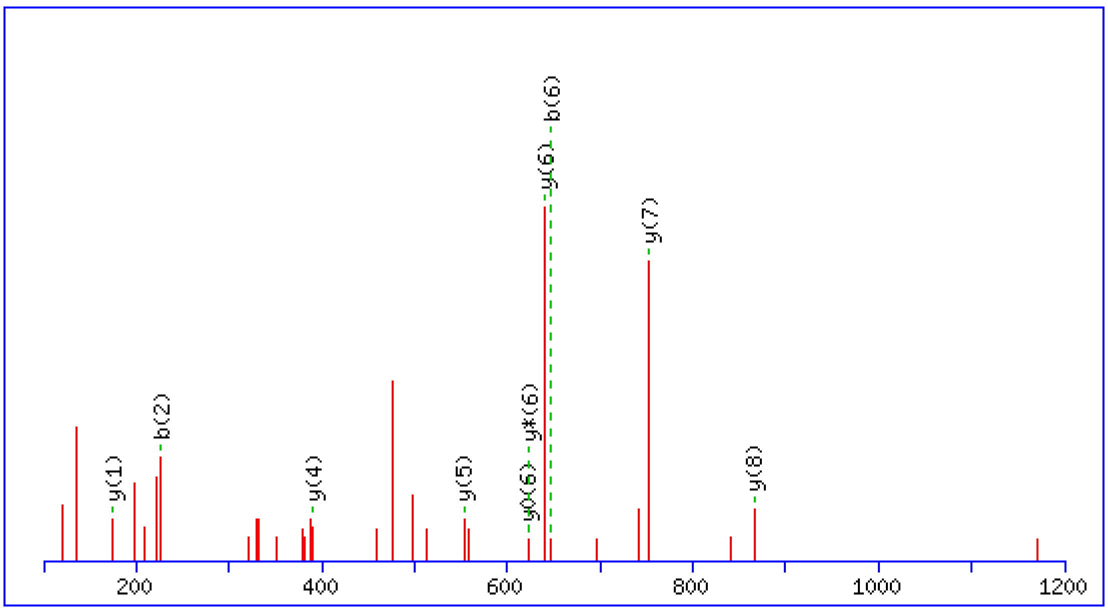
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLSYGASR**
Found in **BARD1_HUMAN**, BRCA1-associated RING domain protein 1 OS=Homo sapiens GN=BARD1 PE=1 SV=2

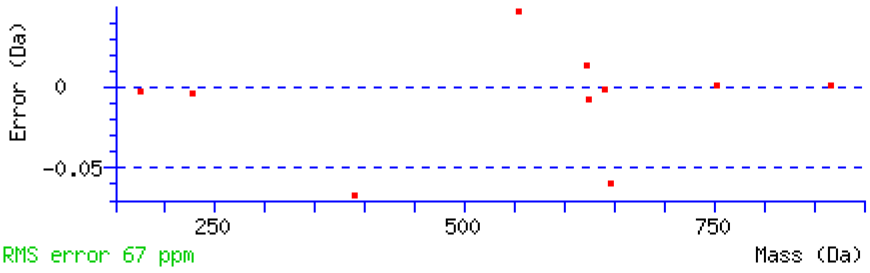
Match to Query 9608: 978.551488 from(490.283020,2+) rtinseconds(2122) index(14941)
Title: Locus:1.1.1.2306.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

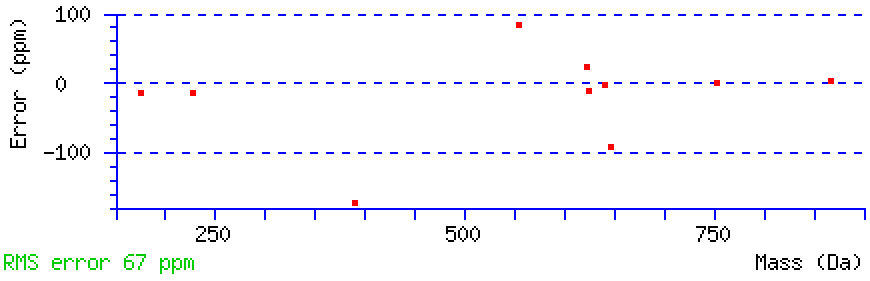
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1200 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 978.549805
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0039
Matches : 10/72 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			L							9
2	**227.175404**	114.091340			L	***866.473043***	433.740160	849.446494	425.226885	848.462478	424.734877	8
3	340.259468	170.633372			L	***753.388979***	377.198128	736.362430	368.684853	735.378414	368.192845	7
4	427.291496	214.149386	409.280931	205.144104	S	***640.304915***	320.656096	623.278366	312.142821	622.294350	311.650813	6
5	590.354825	295.681051	572.344260	286.675768	Y	***553.272887***	277.140082	536.246338	268.626807	535.262322	268.134799	5
6	**647.376289**	324.191783	629.365724	315.186500	G	***390.209558***	195.608417	373.183009	187.095142	372.198993	186.603134	4
7	718.413403	359.710340	700.402838	350.705057	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
8	805.445431	403.226354	787.434866	394.221071	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 LLLSYGASR
(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	978.549805	0.001683	LLLSYGASR
24.4	978.549805	0.001683	LLIYGASSR
0.4	978.553848	-0.002360	ILFFNTPK
0.3	978.561050	-0.009562	LLPSSHVAR

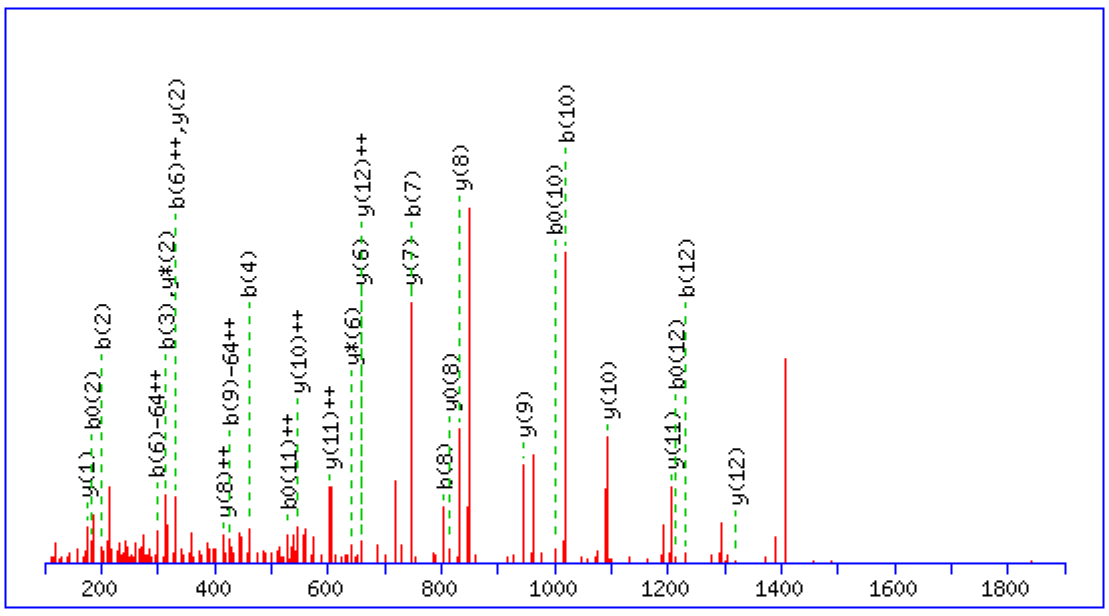
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLPMLSSGLTGRR**
Found in **BAHD1_HUMAN**, Bromo adjacent homology domain-containing 1 protein OS=Homo sapiens GN=BAHD1 PE=1 SV=2

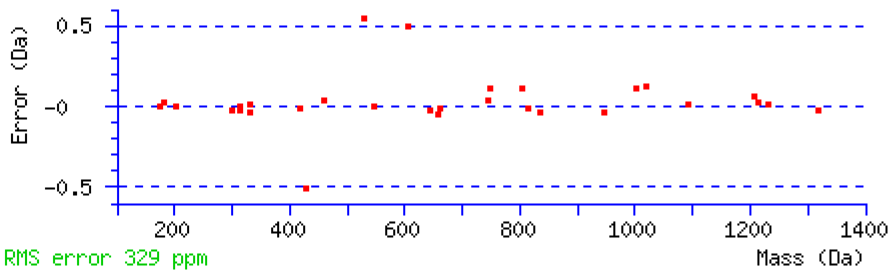
Match to Query 36980: 1405.739628 from(703.877090,2+) rtinseconds(3315) index(49919)
Title: Locus:1.1.1.2547.26
Data file 2011-11-14 - TFD - S 2-1.mgf

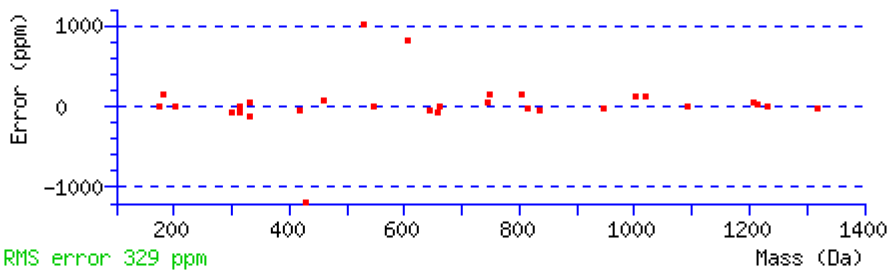
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1405.734741
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
M4      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 37  Expect: 0.0021
Matches : 30/172 fragment ions using 75 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	**201.123368**	101.065322			183.112803	92.060039	L	***1319.709997***	660.358636	1302.683448	651.845362	1301.699432	651.353354	12
3	**314.171047**	157.589161			296.160482	148.583879	P	***1206.625933***	603.816605	1189.599384	595.303330	1188.615368	594.811322	11
4	**461.206447**	231.106861			443.195882	222.101579	M	***1093.578254***	547.292765	1076.551705	538.779491	1075.567689	538.287483	10
5	574.290511	287.648894			556.279946	278.643611	L	***946.542854***	473.775065	929.516305	465.261791	928.532289	464.769783	9
6	661.322539	331.164908			643.311974	322.159625	S	***833.458790***	417.233033	816.432241	408.719759	815.448225	408.227751	8
7	**748.354567**	374.680922			730.344002	365.675639	S	***746.426762***	373.717019	729.400213	365.203745	728.416197	364.711737	7
8	**805.376031**	403.191654			787.365466	394.186371	G	***659.394734***	330.201005	642.368185	321.687731	641.384169	321.195723	6
9	918.460095	459.733686			900.449530	450.728403	L	602.373270	301.690273	585.346721	293.176999	584.362705	292.684991	5
10	**1019.507774**	510.257525			1001.497209	501.252243	T	489.289206	245.148241	472.262657	236.634966	471.278641	236.142958	4
11	1076.529238	538.768257			1058.518673	529.762975	G	388.241527	194.624401	371.214978	186.111127			3
12	**1232.630349**	616.818813	1215.603800	608.305538	1214.619784	607.813530	R	***331.220063***	166.113669	314.193514	157.600395			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SLPMLSSGLTGRR
(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	1405.734741	0.004887	SLPMLSSGLTGRR
9.5	1405.731369	0.008259	ISFIARDVTDNR
6.3	1405.734039	0.005589	ISLFTLPAESSEI
5.5	1405.734726	0.004902	STSTSPAAMLLRR
3.1	1405.728378	0.011250	SLLMCFLHIMK

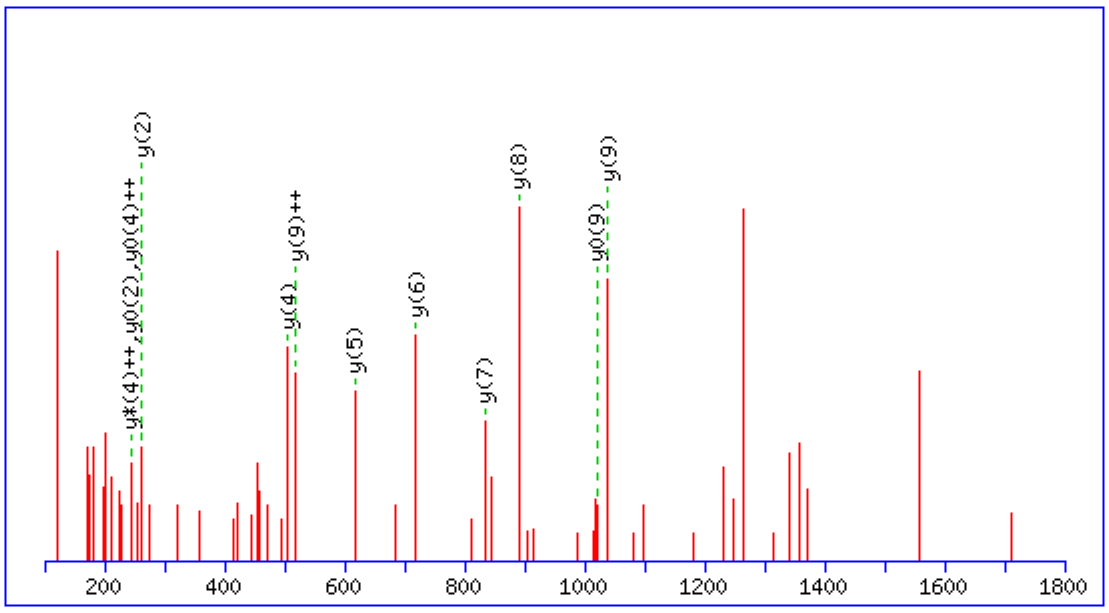
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVFGDTLNESR**
Found in **KCD12_HUMAN**, BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1

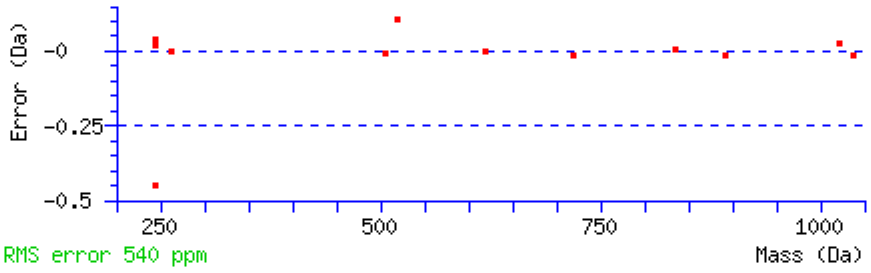
Match to Query 462975: 1265.594708 from(633.804630,2+) rtinseconds(1981) index(650820)
Title: Locus:1.1.1.944.27
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

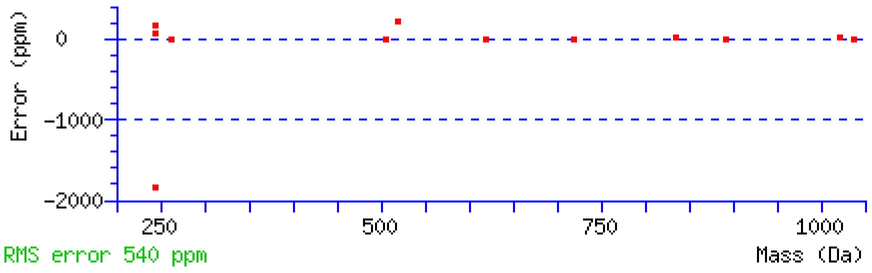
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1265.588791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.0002
Matches : 12/104 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	1137.553478	569.280377	1120.526929	560.767103	1119.542913	560.275095	10
3	376.186697	188.596987			358.176132	179.591704	F	***1038.485064***	519.746170	1021.458515	511.232896	1020.474499	510.740888	9
4	433.208161	217.107719			415.197596	208.102436	G	***891.416650***	446.211963	874.390101	437.698689	873.406085	437.206681	8
5	548.235104	274.621190			530.224539	265.615908	D	***834.395186***	417.701231	817.368637	409.187957	816.384621	408.695949	7
6	649.282783	325.145030			631.272218	316.139747	T	***719.368243***	360.187760	702.341694	351.674485	701.357678	351.182477	6
7	762.366847	381.687062			744.356282	372.681779	L	***618.320564***	309.663920	601.294015	301.150646	600.309999	300.658638	5
8	876.409774	438.708525	859.383225	430.195251	858.399209	429.703243	N	***505.236500***	253.121888	488.209951	244.608613	487.225935	244.116605	4
9	1005.452367	503.229822	988.425818	494.716547	987.441802	494.224539	E	391.193573	196.100425	374.167024	187.587150	373.183008	187.095142	3
10	1092.484395	546.745836	1075.457846	538.232561	1074.473830	537.740553	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 EVFGDTLNESR
(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	1265.588791	0.005917	EVFGDTLNESR
1.8	1265.596176	-0.001468	NNFLGSEPILM

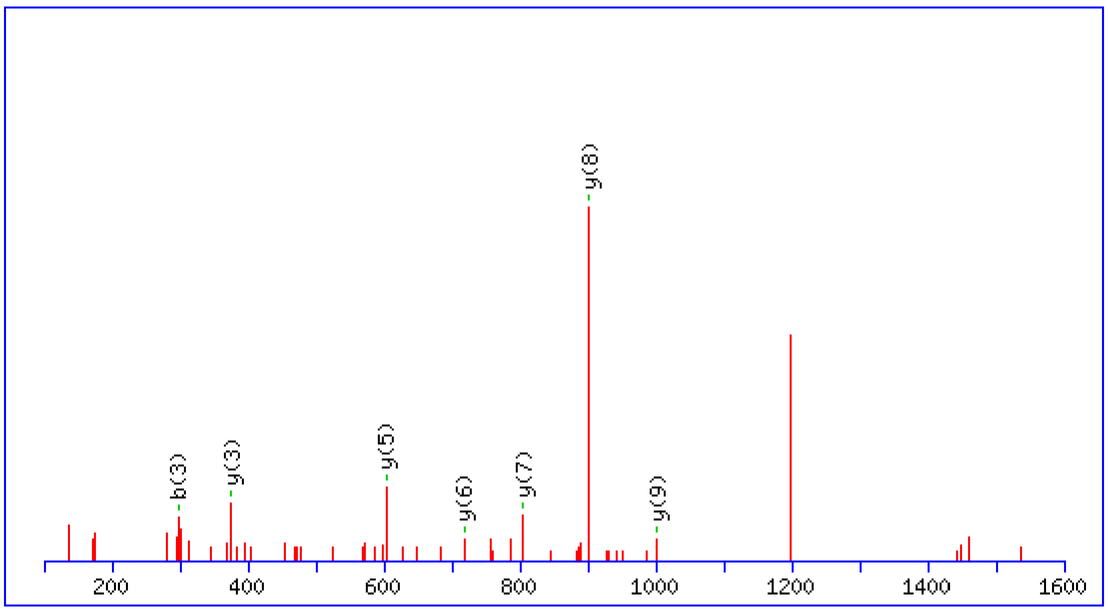
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPVPSDIDISR**
Found in **C1TC_HUMAN**, C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3

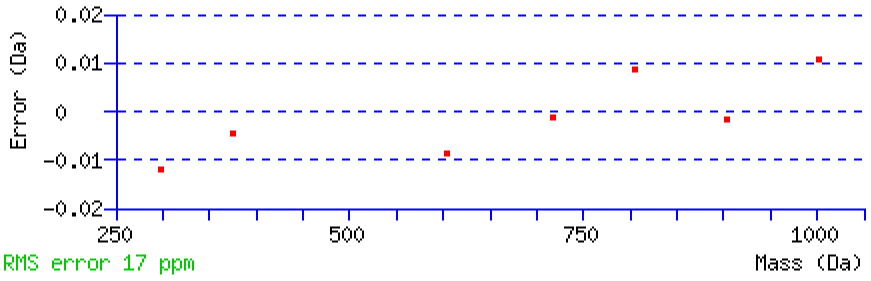
Match to Query 21842: 1198.627808 from(600.321180,2+) rtinseconds(2039) index(23042)
Title: Locus:1.1.1.2257.27
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

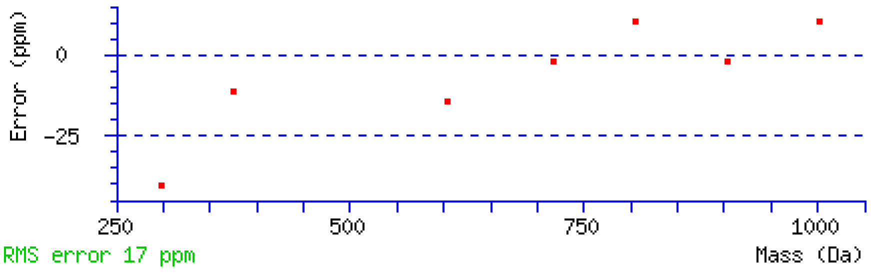
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1198.619370
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00017
Matches : 7/98 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							11
2	199.107719	100.057497	181.097154	91.052215	P	1098.578964	549.793120	1081.552415	541.279846	1080.568399	540.787838	10
3	298.176133	149.591704	280.165568	140.586422	V	***1001.526200***	501.266738	984.499651	492.753464	983.515635	492.261456	9
4	395.228897	198.118087	377.218332	189.112804	P	***902.457786***	451.732531	885.431237	443.219257	884.447221	442.727249	8
5	482.260925	241.634100	464.250360	232.628818	S	***805.405022***	403.206149	788.378473	394.692875	787.394457	394.200867	7
6	597.287868	299.147572	579.277303	290.142290	D	***718.372994***	359.690135	701.346445	351.176861	700.362429	350.684853	6
7	710.371932	355.689604	692.361367	346.684322	I	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
8	825.398875	413.203076	807.388310	404.197793	D	490.261987	245.634631	473.235438	237.121357	472.251422	236.629349	4
9	938.482939	469.745108	920.472374	460.739825	I	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
10	1025.514967	513.261122	1007.504402	504.255839	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 TPVPSDIDISR
(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	1198.619370	0.008438	TPVPSDIDISR
7.4	1198.630585	-0.002777	TPLGTKENPAR

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

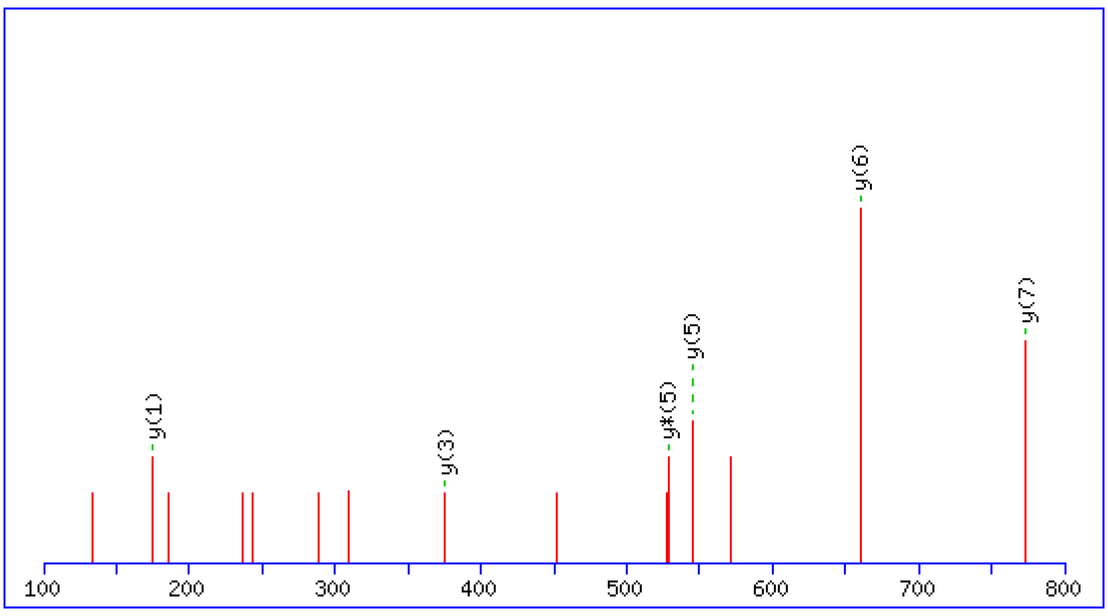
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPDGLLSR**
Found in **C2C4A_HUMAN**, C2 calcium-dependent domain-containing protein 4A OS=Homo sapiens GN=C2CD4A PE=2 SV=2

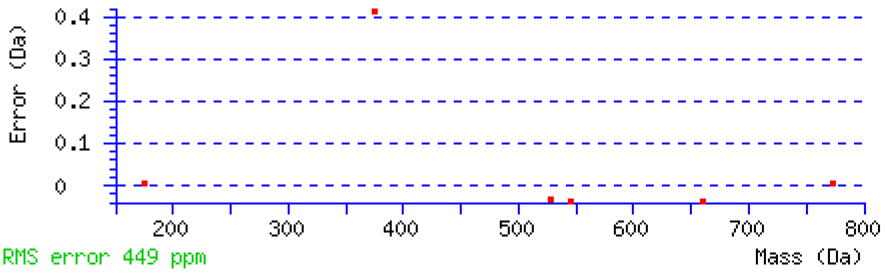
Match to Query 71556: 871.476848 from(436.745700,2+) rtinseconds(1460) index(571192)
Title: Locus:1.1.1.639.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

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 ●

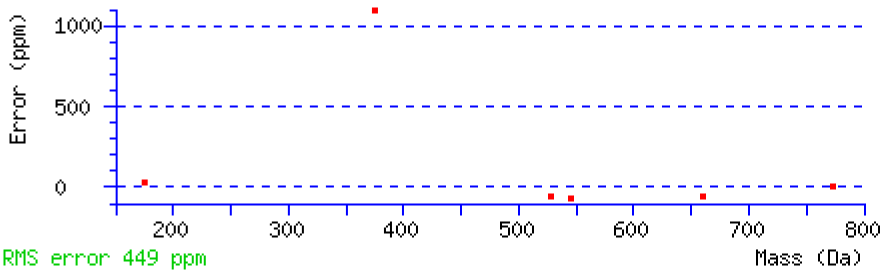


Monoisotopic mass of neutral peptide Mr(calc): 871.476334
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2 : Oxidation (P)
Ions Score: 49 **Expect:** 0.00019
Matches : 6/64 fragment ions using 7 most intense peaks (help)

#	b	b⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	100.075690	50.541483			V							8
2	213.123369	107.065322			P	*773.415194*	387.211235	756.388645	378.697961	755.404629	378.205953	7
3	328.150312	164.578794	310.139747	155.573512	D	*660.367515*	330.687396	643.340966	322.174121	642.356950	321.682113	6
4	385.171776	193.089526	367.161211	184.084243	G	*545.340572*	273.173924	528.314023	264.660650	527.330007	264.168642	5
5	498.255840	249.631558	480.245275	240.626275	L	488.319108	244.663192	471.292559	236.149917	470.308543	235.657909	4
6	611.339904	306.173590	593.329339	297.168308	L	*375.235044*	188.121160	358.208495	179.607885	357.224479	179.115877	3
7	698.371932	349.689604	680.361367	340.684322	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



RMS error 449 ppm



RMS error 449 ppm

NCBI **BLAST** search of VPDGLLSR
(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	871.476334	0.000514	VPDGLLSR
18.1	871.480362	-0.003514	VLDWVPK
14.7	871.476318	0.000530	VLVEQER
8.2	871.476318	0.000530	DIVAEGLR
7.7	871.477661	-0.000813	GHFRSIR
5.8	871.476318	0.000530	LALSPSPR
4.9	871.476318	0.000530	LSPSPSLR
4.4	871.476303	0.000545	TEPIKER
2.3	871.473816	0.003032	VIAPWRM
2.3	871.476318	0.000530	VPKNPSAK

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

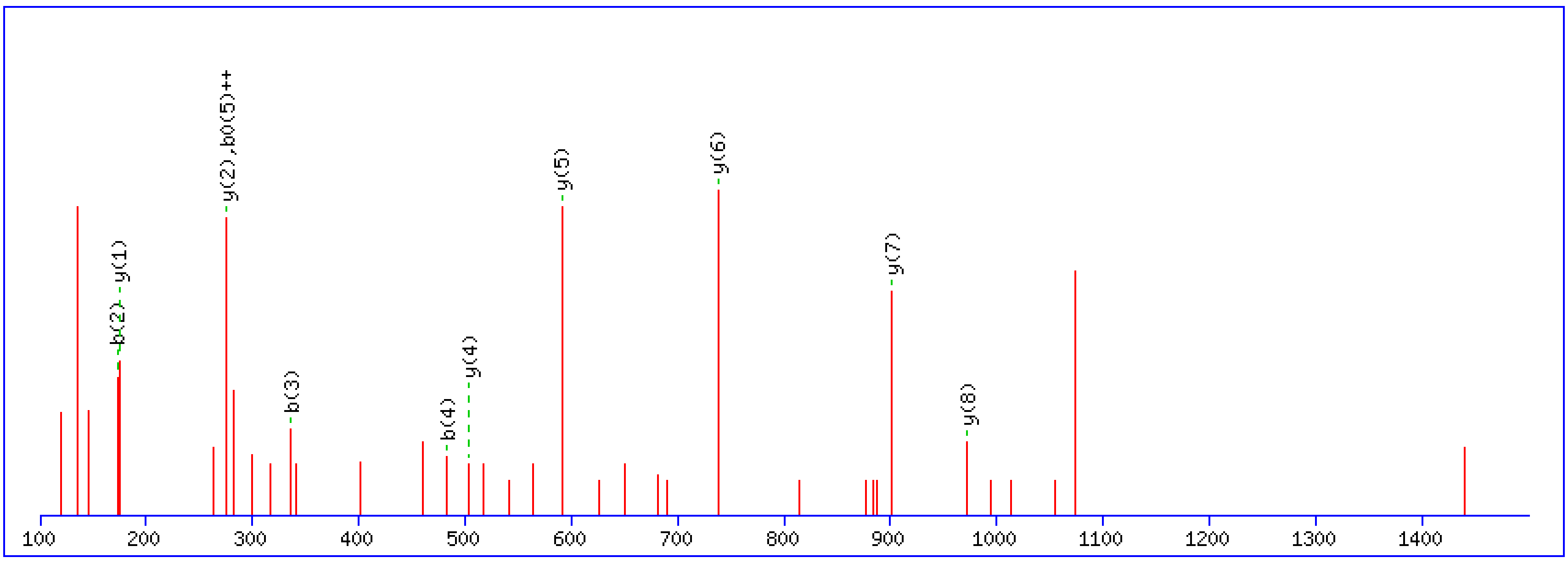
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAYFSLDTR**
Found in **CADH1_HUMAN**, Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3

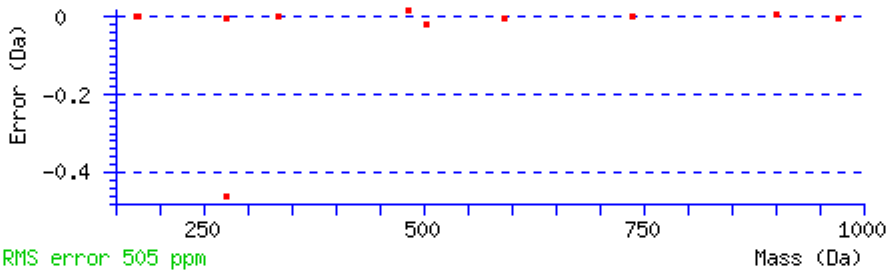
Match to Query 7046: 1072.521208 from(537.267880,2+) rtinseconds(2112) index(22061)
Title: Locus:1.1.1.1510.9
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

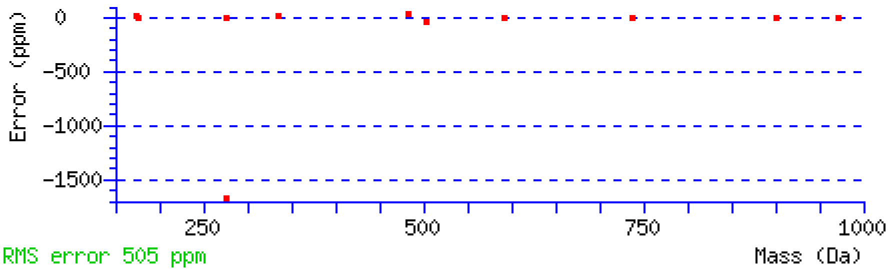
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1072.518921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0016
Matches : 11/78 fragment ions using 27 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	**173.092069**	87.049672	155.081504	78.044390	A	***972.478523***	486.742900	955.451974	478.229625	954.467958	477.737617	8
3	**336.155398**	168.581337	318.144833	159.576055	Y	***901.441409***	451.224343	884.414860	442.711068	883.430844	442.219060	7
4	**483.223812**	242.115544	465.213247	233.110262	F	***738.378080***	369.692678	721.351531	361.179403	720.367515	360.687395	6
5	570.255840	285.631558	552.245275	276.626276	S	***591.309666***	296.158471	574.283117	287.645197	573.299101	287.153189	5
6	683.339904	342.173590	665.329339	333.168308	L	***504.277638***	252.642457	487.251089	244.129182	486.267073	243.637174	4
7	798.366847	399.687062	780.356282	390.681779	D	391.193574	196.100425	374.167025	187.587150	373.183009	187.095142	3
8	899.414526	450.210901	881.403961	441.205619	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 TAYFSLDTR
(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	1072.518921	0.002287	TAYFSLDTR
12.3	1072.522308	-0.001100	TANVPQTVPM
12.3	1072.522308	-0.001100	TANVPQTVPM

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

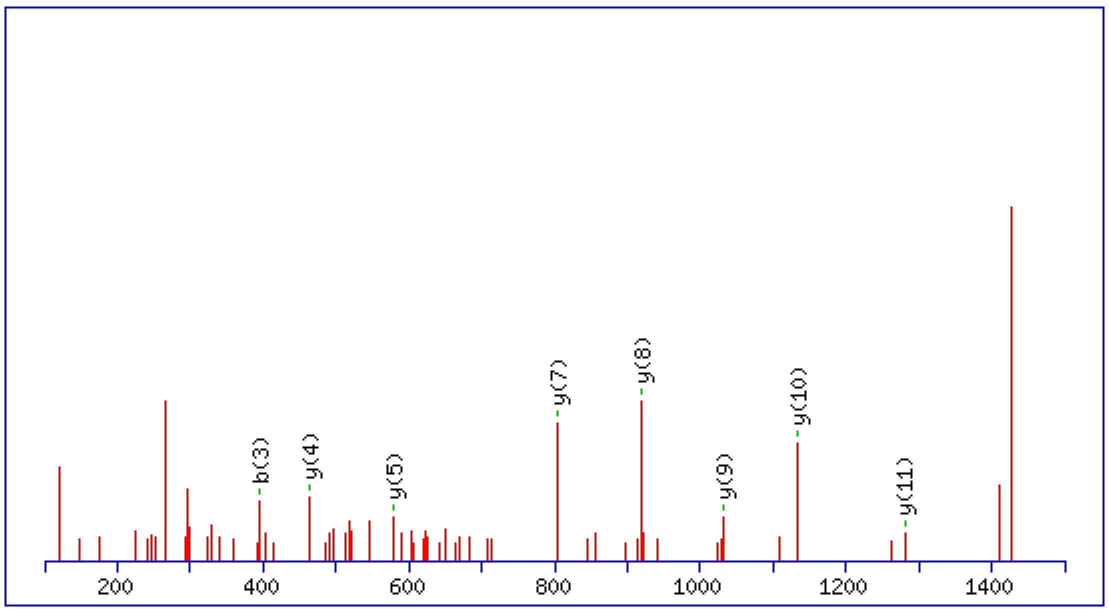
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFTINPEDGFIK**
Found in **CAD11_HUMAN**, Cadherin-11 OS=Homo sapiens GN=CDH11 PE=1 SV=2

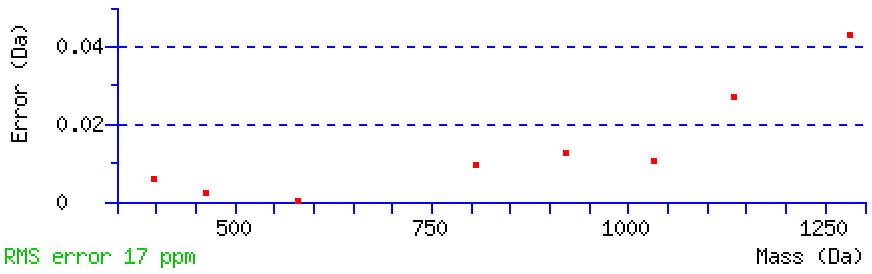
Match to Query 36078: 1426.723968 from(714.369260,2+) rtinseconds(3449) index(52398)
Title: Locus:1.1.1.1959.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

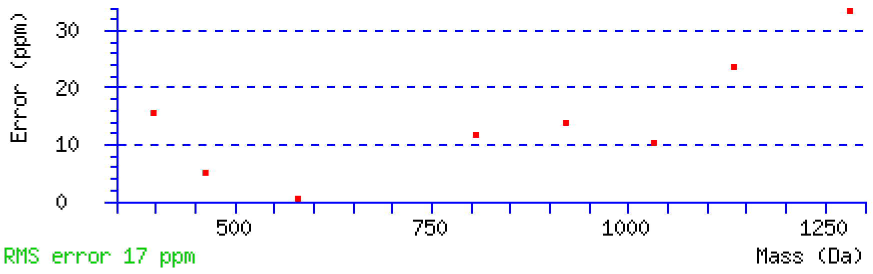
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1426.713272
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 5.2e-005
Matches : 8/112 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	148.075690	74.541483					F							12
2	295.144104	148.075690					F	***1280.652130***	640.829703	1263.625581	632.316429	1262.641565	631.824420	11
3	396.191783	198.599529			378.181218	189.594247	T	***1133.583716***	567.295496	1116.557167	558.782222	1115.573151	558.290214	10
4	509.275847	255.141561			491.265282	246.136279	I	***1032.536037***	516.771657	1015.509488	508.258382	1014.525472	507.766374	9
5	623.318774	312.163025	606.292225	303.649751	605.308209	303.157743	N	***919.451973***	460.229625	902.425424	451.716350	901.441408	451.224342	8
6	720.371538	360.689407	703.344989	352.176133	702.360973	351.684125	P	***805.409046***	403.208161	788.382497	394.694887	787.398481	394.202879	7
7	849.414131	425.210704	832.387582	416.697429	831.403566	416.205421	E	708.356282	354.681779	691.329733	346.168504	690.345717	345.676496	6
8	964.441074	482.724175	947.414525	474.210901	946.430509	473.718893	D	***579.313689***	290.160483	562.287140	281.647208	561.303124	281.155200	5
9	1021.462538	511.234907	1004.435989	502.721633	1003.451973	502.229625	G	***464.286746***	232.647011	447.260197	224.133736			4
10	1168.530952	584.769114	1151.504403	576.255840	1150.520387	575.763832	F	407.265282	204.136279	390.238733	195.623004			3
11	1281.615016	641.311146	1264.588467	632.797872	1263.604451	632.305863	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 FFTINPEDGFIK
(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	1426.713272	0.010696	FFTINPEDGFIK
3.5	1426.710571	0.013397	FFPRQHPGANEK

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

{MATRIX SCIENCE}

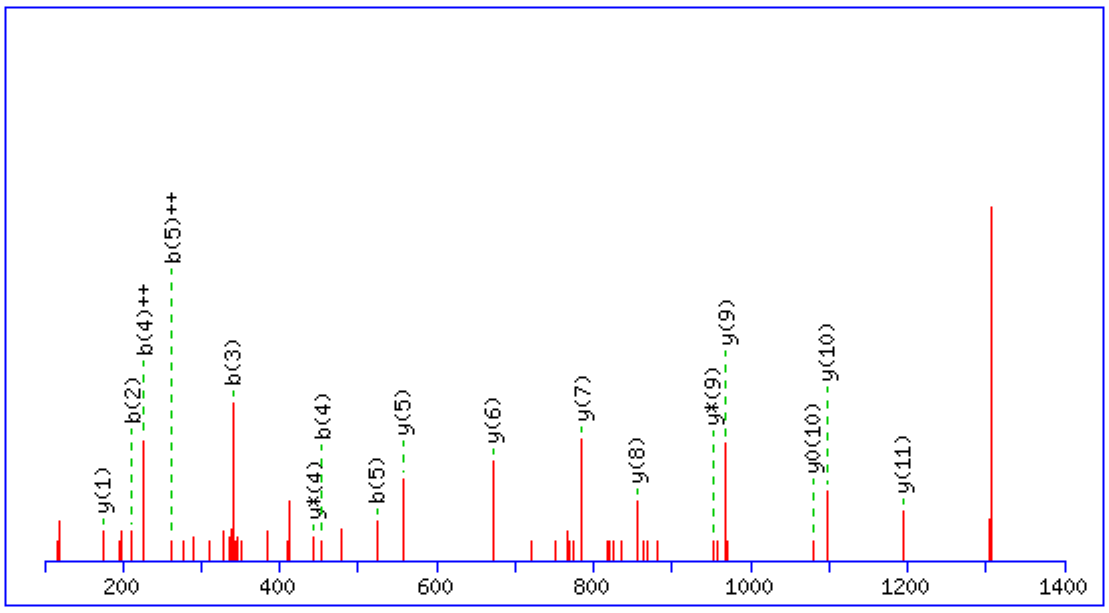
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPELAINPLGDR**
Found in **CHP1_HUMAN**, Calcium-binding protein p22 OS=Homo sapiens GN=CHP PE=1 SV=3

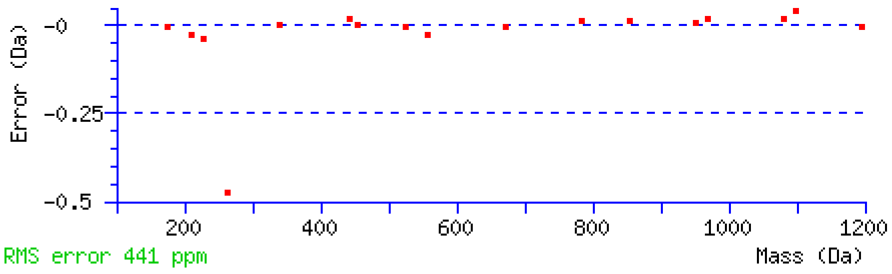
Match to Query 23388: 1306.731488 from(654.373020,2+) rtinseconds(3108) index(32450)
Title: Locus:1.1.1.2679.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

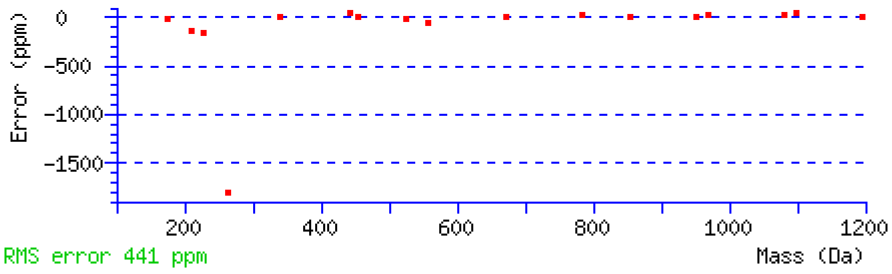
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1306.724472
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 1.2e-005
Matches : 17/114 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	**211.144104**	106.075690					P	***1194.647713***	597.827495	1177.621164	589.314220	1176.637148	588.822212	11
3	**340.186697**	170.596986			322.176132	161.591704	E	***1097.594949***	549.301113	1080.568400	540.787838	1079.584384	540.295830	10
4	**453.270761**	**227.139018**			435.260196	218.133736	L	***968.552356***	484.779816	951.525807	476.266542	950.541791	475.774534	9
5	**524.307875**	**262.657576**			506.297310	253.652293	A	***855.468292***	428.237784	838.441743	419.724510	837.457727	419.232502	8
6	637.391939	319.199608			619.381374	310.194325	I	***784.431178***	392.719227	767.404629	384.205953	766.420613	383.713945	7
7	751.434866	376.221071	734.408317	367.707797	733.424301	367.215789	N	***671.347114***	336.177195	654.320565	327.663921	653.336549	327.171913	6
8	848.487630	424.747453	831.461081	416.234179	830.477065	415.742171	P	***557.304187***	279.155732	540.277638	270.642457	539.293622	270.150449	5
9	961.571694	481.289485	944.545145	472.776211	943.561129	472.284203	L	460.251423	230.629350	443.224874	222.116075	442.240858	221.624067	4
10	1018.593158	509.800217	1001.566609	501.286943	1000.582593	500.794935	G	347.167359	174.087318	330.140810	165.574043	329.156794	165.082035	3
11	1133.620101	567.313689	1116.593552	558.800414	1115.609536	558.308406	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 IPELAINPLGDR
(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	1306.724472	0.007016	IPELAINPLGDR
10.9	1306.735718	-0.004230	LLLDSGINAHVR

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

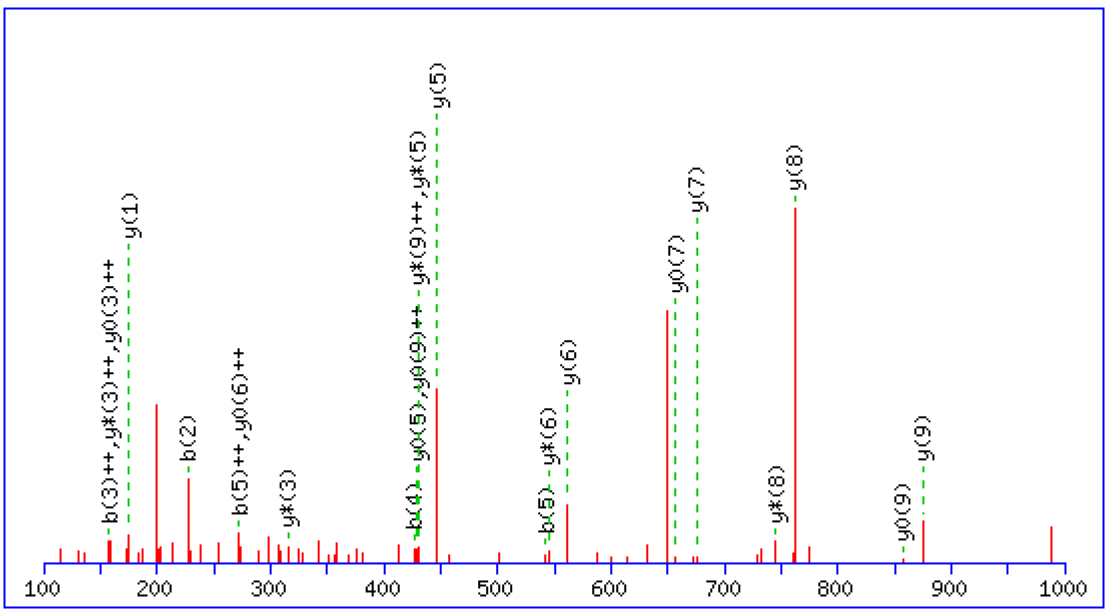
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILSIDGGGTR**
Found in **PLPL8_HUMAN**, Calcium-independent phospholipase A2-gamma OS=Homo sapiens GN=PNPLA8 PE=1 SV=1

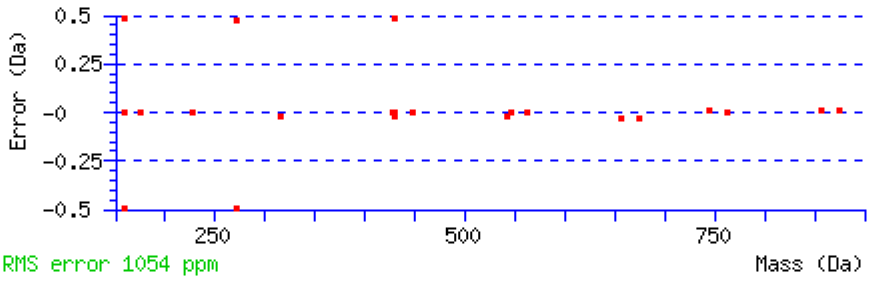
Match to Query 10563: 987.535588 from(494.775070,2+) rtinseconds(1721) index(11239)
Title: Locus:1.1.1.2466.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

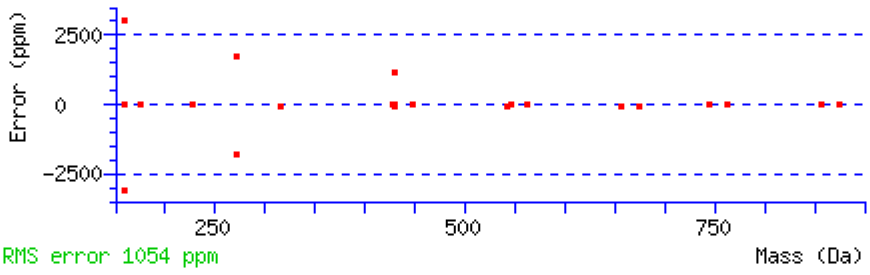
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 987.534912
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0021
Matches : 24/84 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308			I							10
2	**227.175404**	114.091340			L	***875.458122***	438.232699	858.431573	429.719425	857.447557	429.227417	9
3	314.207432	**157.607354**	296.196867	148.602071	S	***762.374058***	381.690667	745.347509	373.177393	744.363493	372.685385	8
4	**427.291496**	214.149386	409.280931	205.144104	I	***675.342030***	338.174653	658.315481	329.661379	657.331465	329.169371	7
5	**542.318439**	**271.662858**	524.307874	262.657575	D	***562.257966***	281.632621	545.231417	273.119347	544.247401	272.627339	6
6	599.339903	300.173590	581.329338	291.168307	G	***447.231023***	224.119150	430.204474	215.605875	429.220458	215.113867	5
7	656.361367	328.684322	638.350802	319.679039	G	390.209559	195.608418	373.183010	187.095143	372.198994	186.603135	4
8	713.382831	357.195054	695.372266	348.189771	G	333.188095	167.097685	316.161546	158.584411	315.177530	158.092403	3
9	814.430510	407.718893	796.419945	398.713611	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
10					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILSIDGGGTR
(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	987.534912	0.000676	ILSIDGGGTR
20.3	987.542297	-0.006709	LLIDMVPR
20.3	987.538940	-0.003352	LLPPTFPR
18.2	987.538925	-0.003337	LLDTVWNK
12.6	987.542297	-0.006709	LLLPGQMGK
12.6	987.542282	-0.006694	LPLPNKMK
11.8	987.534897	0.000691	LLDTQDKR
10.1	987.538910	-0.003322	LLDYSLHK
8.3	987.534882	0.000706	LLESDKQR
8.3	987.528351	0.007237	LLQRCER

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

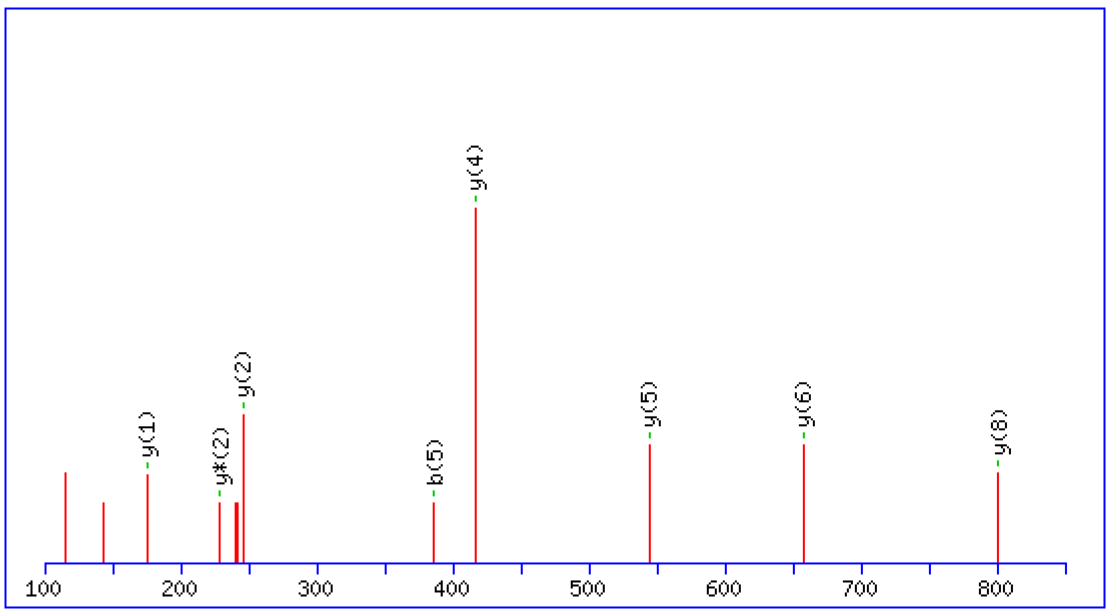
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASGIQGLAR**
Found in **CAYP1_HUMAN**, Calcyphosin OS=Homo sapiens GN=CAPS PE=1 SV=1

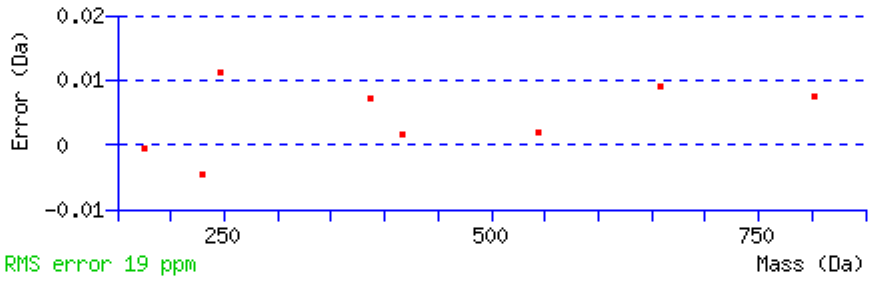
Match to Query 7492: 928.512208 from(465.263380,2+) rtinseconds(1656) index(7709)
Title: Locus:1.1.1.2095.12
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

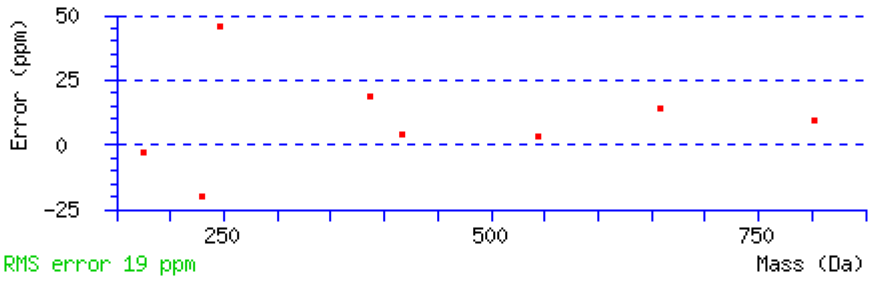
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 928.509018
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 4.2e-005
Matches : 8/80 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	58.028740	29.518008					G							10
2	129.065854	65.036565					A	872.494842	436.751059	855.468293	428.237785	854.484277	427.745777	9
3	216.097882	108.552579			198.087317	99.547296	S	*801.457728*	401.232502	784.431179	392.719228	783.447163	392.227220	8
4	273.119346	137.063311			255.108781	128.058029	G	714.425700	357.716488	697.399151	349.203214			7
5	386.203410	193.605343			368.192845	184.600061	I	*657.404236*	329.205756	640.377687	320.692482			6
6	514.261988	257.634632	497.235439	249.121358	496.251423	248.629350	Q	*544.320172*	272.663724	527.293623	264.150450			5
7	571.283452	286.145364	554.256903	277.632090	553.272887	277.140082	G	*416.261594*	208.634435	399.235045	200.121161			4
8	684.367516	342.687396	667.340967	334.174122	666.356951	333.682114	L	359.240130	180.123703	342.213581	171.610429			3
9	755.404630	378.205953	738.378081	369.692679	737.394065	369.200671	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 GASGIQGLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.2	928.509018	0.003190	GASGIQGLAR
23.0	928.509018	0.003190	GNTPKKPR
22.9	928.509018	0.003190	QGPSQLKR
21.6	928.509018	0.003190	GASGGALPKR
19.5	928.516403	-0.004195	KTPMLPAR
12.9	928.516403	-0.004195	KTPMLPAR
12.9	928.516403	-0.004195	KTPMLPAR
11.9	928.520233	-0.008025	QSIAQRAR
11.9	928.520233	-0.008025	QVSRAAAAR
11.3	928.509003	0.003205	QAKADQLR

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

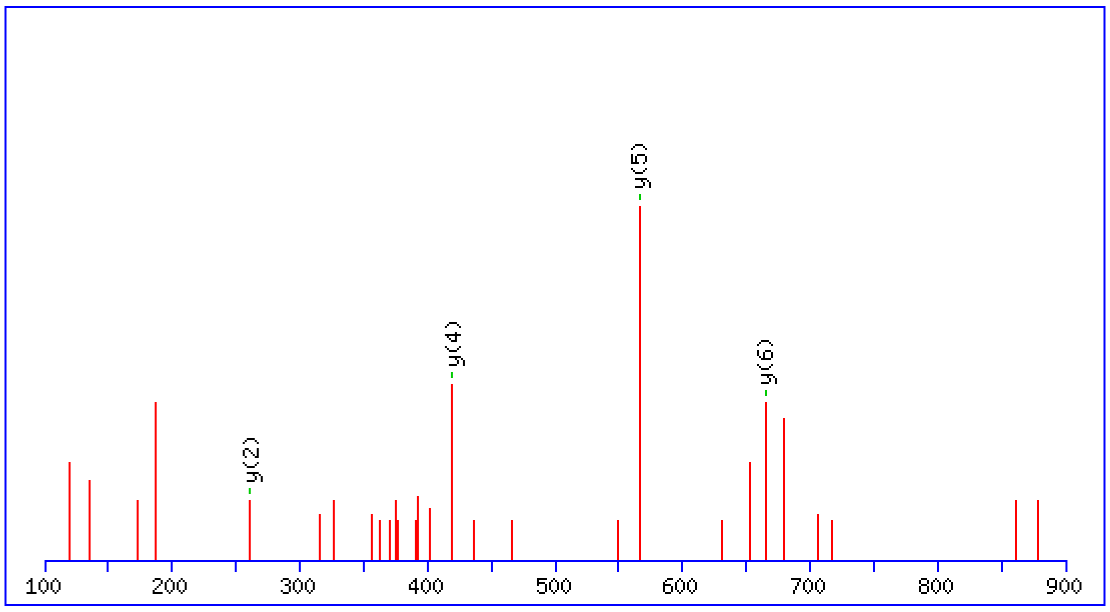
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLVFASNK**
Found in **CALI_HUMAN**, Calicin OS=Homo sapiens GN=CCIN PE=2 SV=3

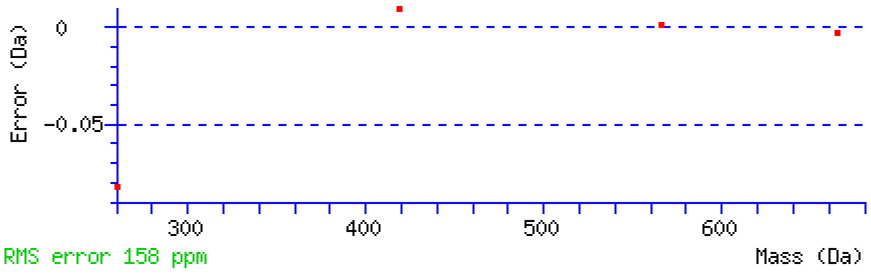
Match to Query 4868: 878.483128 from(440.248840,2+) rtinseconds(1854) index(16829)
Title: Locus:1.1.1.2237.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

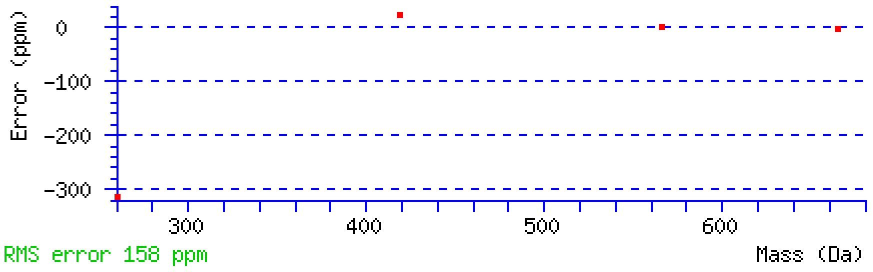
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 878.486160
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0092
Matches : 4/68 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							8
2	215.139019	108.073147			197.128454	99.067865	L	778.445765	389.726520	761.419216	381.213246	760.435200	380.721238	7
3	314.207433	157.607354			296.196868	148.602072	V	***665.361701***	333.184488	648.335152	324.671214	647.351136	324.179206	6
4	461.275847	231.141561			443.265282	222.136279	F	***566.293287***	283.650282	549.266738	275.137007	548.282722	274.644999	5
5	532.312961	266.660119			514.302396	257.654836	A	***419.224873***	210.116074	402.198324	201.602800	401.214308	201.110792	4
6	619.344989	310.176132			601.334424	301.170850	S	348.187759	174.597517	331.161210	166.084243	330.177194	165.592235	3
7	733.387916	367.197596	716.361367	358.684321	715.377351	358.192313	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 TLVFASNK
(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	878.486160	-0.003032	TLVFASNK

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

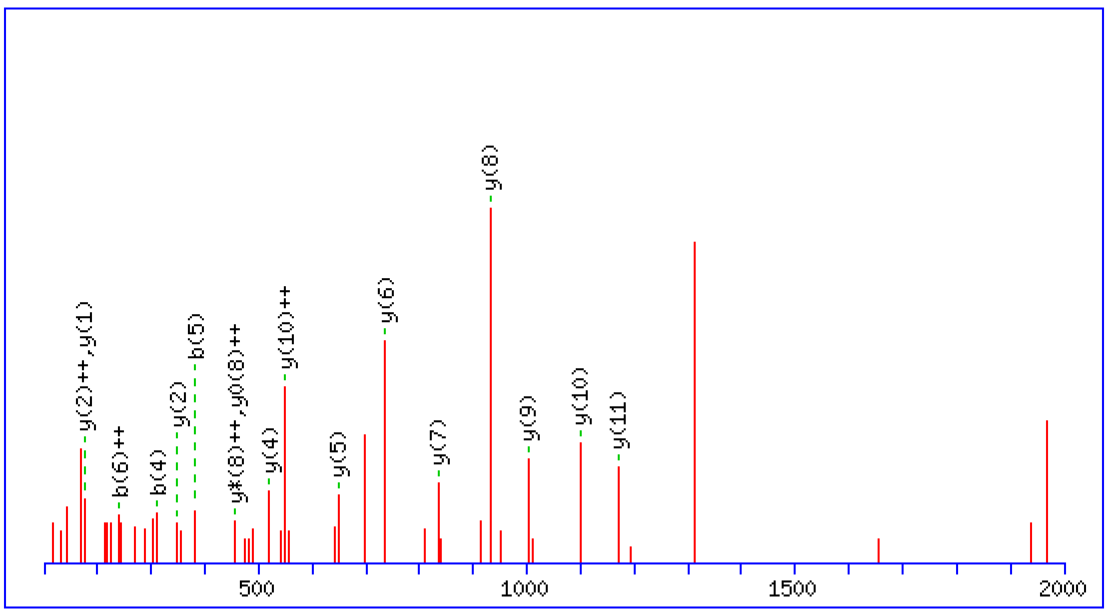
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAAPAPVSEAVCR**
Found in **ICAL_HUMAN**, Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4

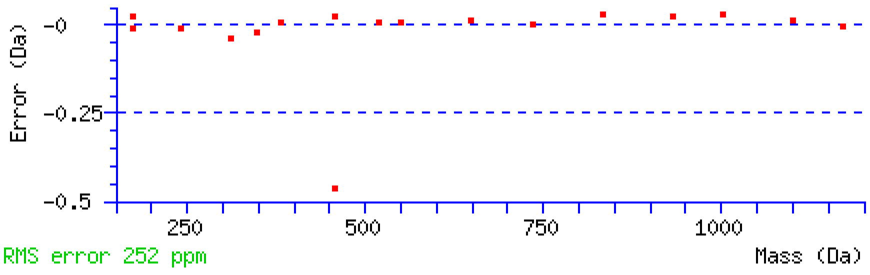
Match to Query 24940: 1311.669668 from(656.842110,2+) rtinseconds(1654) index(16249)
Title: Locus:1.1.1.2031.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

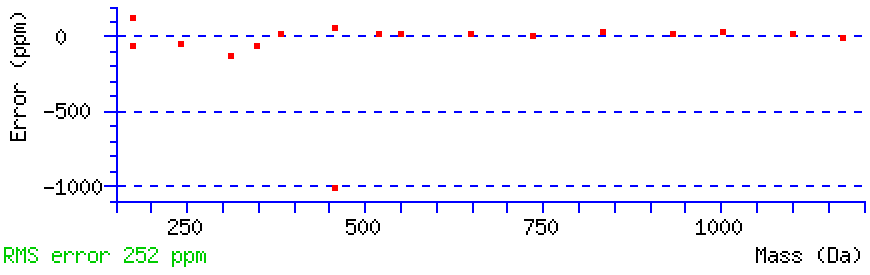
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1311.660492
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83  Expect: 4.9e-008
Matches : 17/98 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	143.081504	72.044390			A	1241.630684	621.318980	1224.604135	612.805706	1223.620119	612.313697	12
3	214.118618	107.562947			A	***1170.593570***	585.800423	1153.567021	577.287149	1152.583005	576.795141	11
4	**311.171382**	156.089329			P	***1099.556456***	550.281866	1082.529907	541.768592	1081.545891	541.276584	10
5	**382.208496**	191.607886			A	***1002.503692***	501.755484	985.477143	493.242210	984.493127	492.750202	9
6	479.261260	240.134268			P	***931.466578***	466.236927	914.440029	457.723652	913.456013	457.231644	8
7	578.329674	289.668475			V	***834.413814***	417.710545	817.387265	409.197270	816.403249	408.705262	7
8	665.361702	333.184489	647.351137	324.179207	S	***735.345400***	368.176338	718.318851	359.663063	717.334835	359.171055	6
9	794.404295	397.705786	776.393730	388.700503	E	***648.313372***	324.660324	631.286823	316.147049	630.302807	315.655041	5
10	865.441409	433.224343	847.430844	424.219060	A	***519.270779***	260.139028	502.244230	251.625753			4
11	964.509823	482.758550	946.499258	473.753267	V	448.233665	224.620470	431.207116	216.107196			3
12	1138.556122	569.781699	1120.545557	560.776416	C	***349.165251***	175.086263	332.138702	166.572989			2
13					R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.7	1311.660492	0.009176	AAAPAPVSEAVCR
4.5	1311.678268	-0.008600	AAAPSGPAPTTSIR
4.2	1311.678268	-0.008600	AAAPSGPAPTTSIR
2.5	1311.657150	0.012518	VNGKFSTEFQR
2.4	1311.667038	0.002630	IVEGDTPSLPER
0.3	1311.678284	-0.008616	NVTPKVGDPETR
0.0	1311.668350	0.001318	HNPEQKQIYR

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

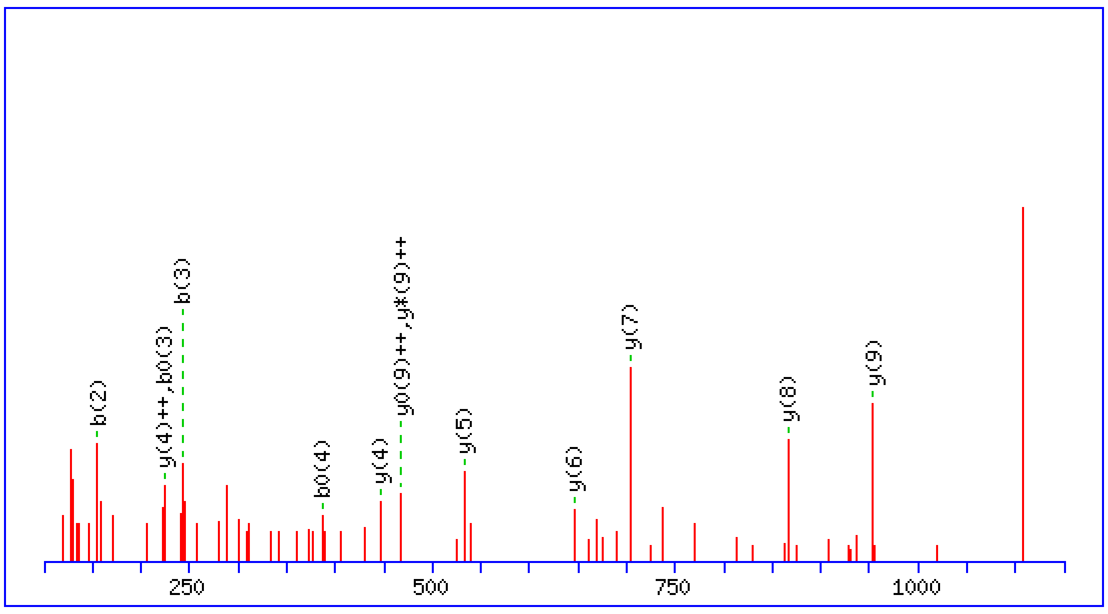
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPSYGLSAEVK**
Found in **CNN2_HUMAN**, Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4

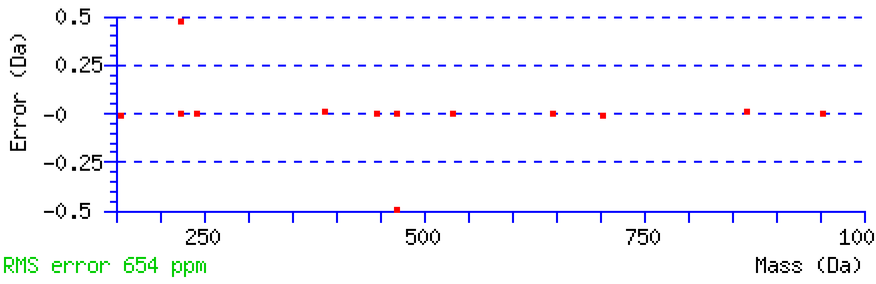
Match to Query 312083: 1106.564628 from(554.289590,2+) rtinseconds(1662) index(410362)
Title: Locus:1.1.1.1229.13
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

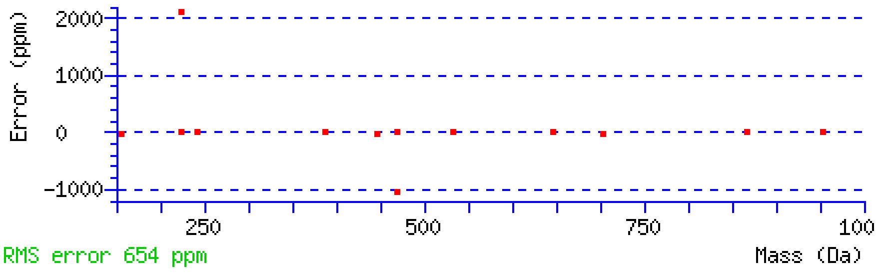
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1106.560776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0019
Matches : 13/92 fragment ions using 18 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							11
2	**155.081504**	78.044390			P	1050.546602	525.776939	1033.520053	517.263665	1032.536037	516.771657	10
3	**242.113532**	121.560404	224.102967	112.555121	S	***953.493838***	477.250557	936.467289	468.737283	935.483273	468.245275	9
4	405.176861	203.092068	387.166296	194.086786	Y	***866.461810***	433.734543	849.435261	425.221269	848.451245	424.729261	8
5	462.198325	231.602800	444.187760	222.597518	G	***703.398481***	352.202879	686.371932	343.689604	685.387916	343.197596	7
6	575.282389	288.144833	557.271824	279.139550	L	***646.377017***	323.692147	629.350468	315.178872	628.366452	314.686864	6
7	662.314417	331.660846	644.303852	322.655564	S	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	5
8	733.351531	367.179403	715.340966	358.174121	A	***446.260925***	223.634101	429.234376	215.120826	428.250360	214.628818	4
9	862.394124	431.700700	844.383559	422.695417	E	375.223811	188.115544	358.197262	179.602269	357.213246	179.110261	3
10	961.462538	481.234907	943.451973	472.229624	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 GPSYGLSAEVK
(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	1106.560776	0.003852	GPSYGLSAEVK
26.7	1106.560776	0.003852	GPAYGLSAEVK
3.9	1106.560745	0.003883	IKEPENYSK
2.3	1106.560791	0.003837	EAGFDLTQVK
2.1	1106.572021	-0.007393	KPESFGTIGR

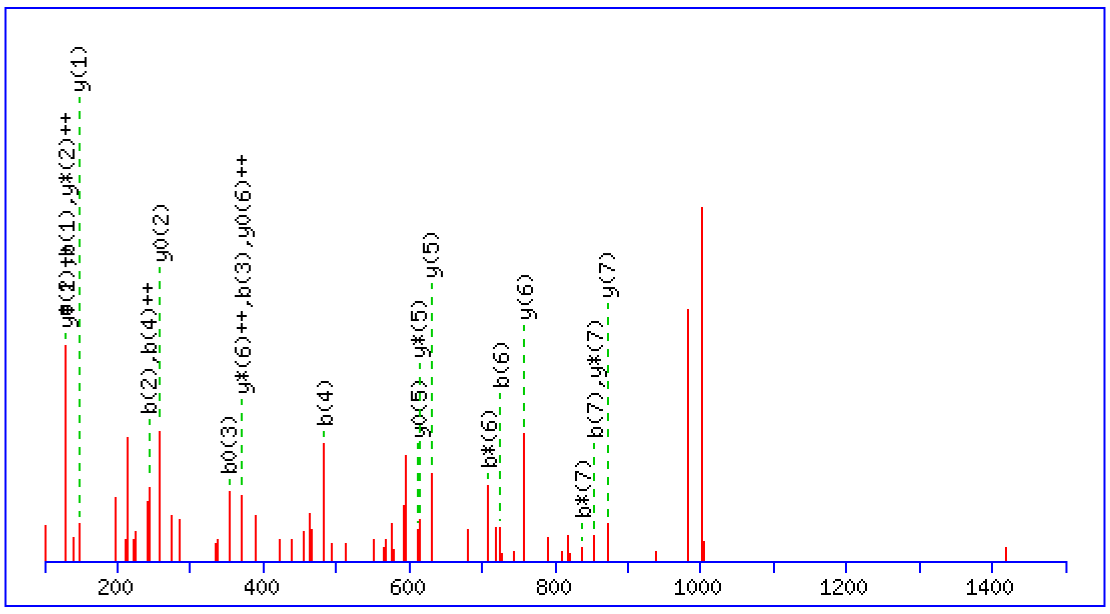
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELQILKEK**
Found in **CLIP1_HUMAN**, CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=1 SV=2

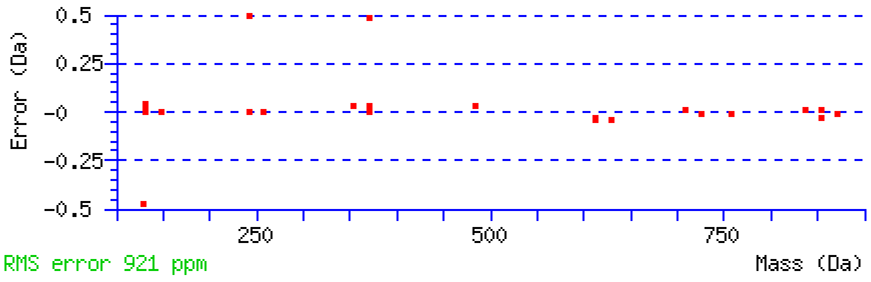
Match to Query 7341: 999.595688 from(500.805120,2+) rtinseconds(1606) index(1509)
Title: Locus:1.1.1.2668.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-8.mgf

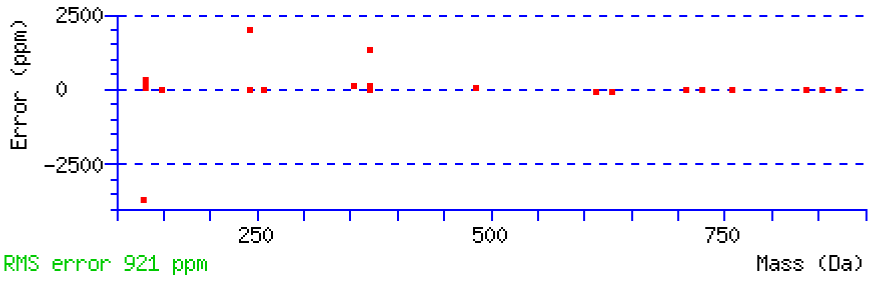
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 999.596405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0016
Matches : 23/78 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	***130.049869***	65.528572			112.039304	56.523290	**E**							8
2	***243.133933***	122.070605			225.123368	113.065322	**L**	**871.561130**	436.284203	854.534581	427.770929	853.550565	427.278921	7
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**Q**	**758.477066**	379.742171	741.450517	371.228897	740.466501	370.736889	6
4	***484.276575***	242.641926	467.250026	234.128651	466.266010	233.636643	**I**	**630.418488**	315.712882	613.391939	307.199608	612.407923	306.707600	5
5	597.360639	299.183958	580.334090	290.670683	579.350074	290.178675	**L**	517.334424	259.170850	500.307875	250.657576	499.323859	250.165568	4
6	***725.455602***	363.231439	708.429053	354.718165	707.445037	354.226157	**K**	404.250360	202.628818	387.223811	194.115544	386.239795	193.623536	3
7	***854.498195***	427.752736	837.471646	419.239461	836.487630	418.747453	**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 ELQILKEK
(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	999.596405	-0.000717	ELQILKEK
33.5	999.596405	-0.000717	ELKELIQK
30.6	999.596405	-0.000717	EQLELLKK
27.8	999.596405	-0.000717	QLELEIKK
24.4	999.596405	-0.000717	LQELKIEK
23.8	999.596405	-0.000717	IEKELLQK
17.6	999.596405	-0.000717	EKEILQIK
16.1	999.596405	-0.000717	EEIAVALKK
15.7	999.596436	-0.000748	GITVPEKLK
15.7	999.596405	-0.000717	LQELEKIK

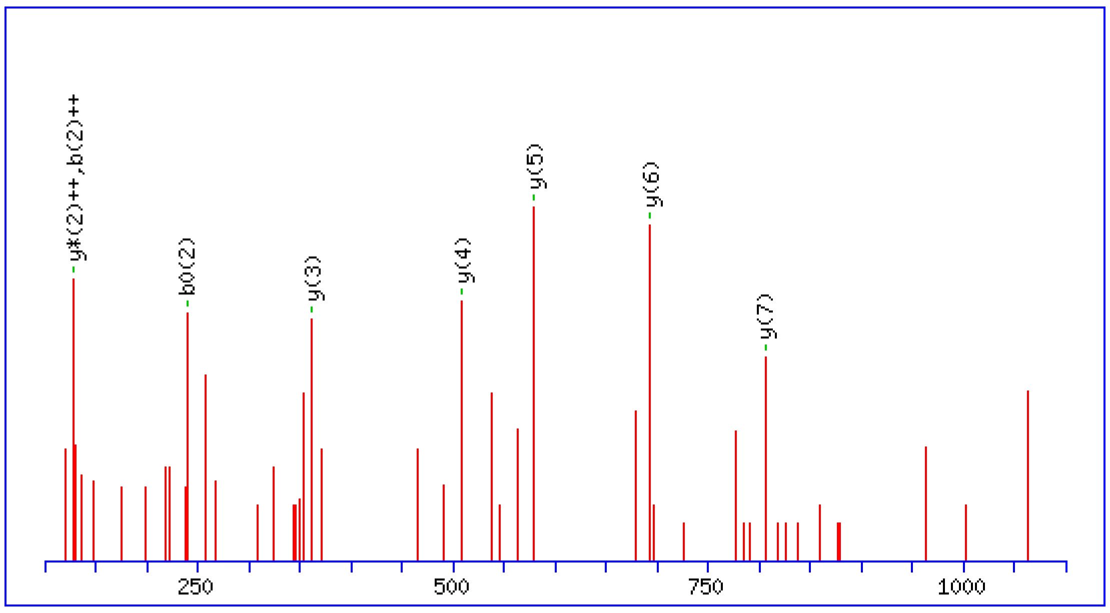
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQILAFSQK**
Found in **CAH4_HUMAN**, Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2

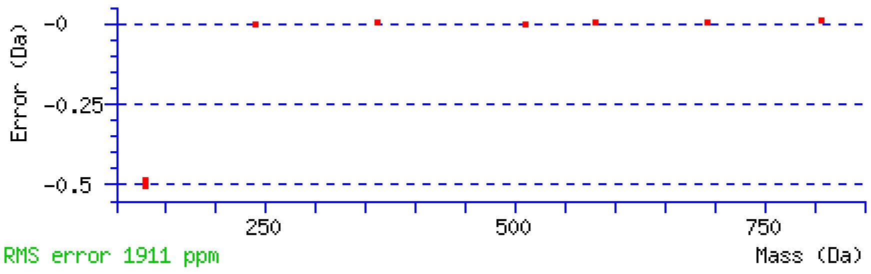
Match to Query 15455: 1062.567908 from(532.291230,2+) rtinseconds(2253) index(27304)
Title: Locus:1.1.1.2243.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

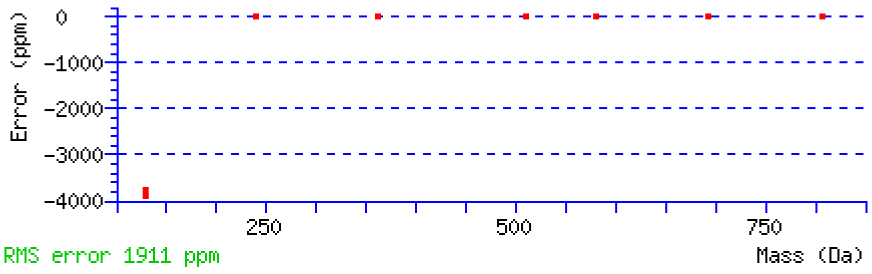
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1062.570938
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0014
Matches : 8/90 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							9
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	934.535644	467.771460	917.509095	459.258185	916.525079	458.766177	8
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	I	***806.477066***	403.742171	789.450517	395.228896	788.466501	394.736888	7
4	484.276575	242.641926	467.250026	234.128651	466.266010	233.636643	L	***693.393002***	347.200139	676.366453	338.686864	675.382437	338.194856	6
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	A	***580.308938***	290.658107	563.282389	282.144832	562.298373	281.652824	5
6	702.382103	351.694690	685.355554	343.181415	684.371538	342.689407	F	***509.271824***	255.139550	492.245275	246.626275	491.261259	246.134267	4
7	789.414131	395.210704	772.387582	386.697429	771.403566	386.205421	S	***362.203410***	181.605343	345.176861	173.092068	344.192845	172.600060	3
8	917.472709	459.239993	900.446160	450.726718	899.462144	450.234710	Q	275.171382	138.089329	258.144833	129.576054			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EQILAFSQK
(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	1062.570938	-0.003030	EQILAFSQK
5.6	1062.572266	-0.004358	ALWRAYQR
2.5	1062.574295	-0.006387	QEMAKSLLK

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

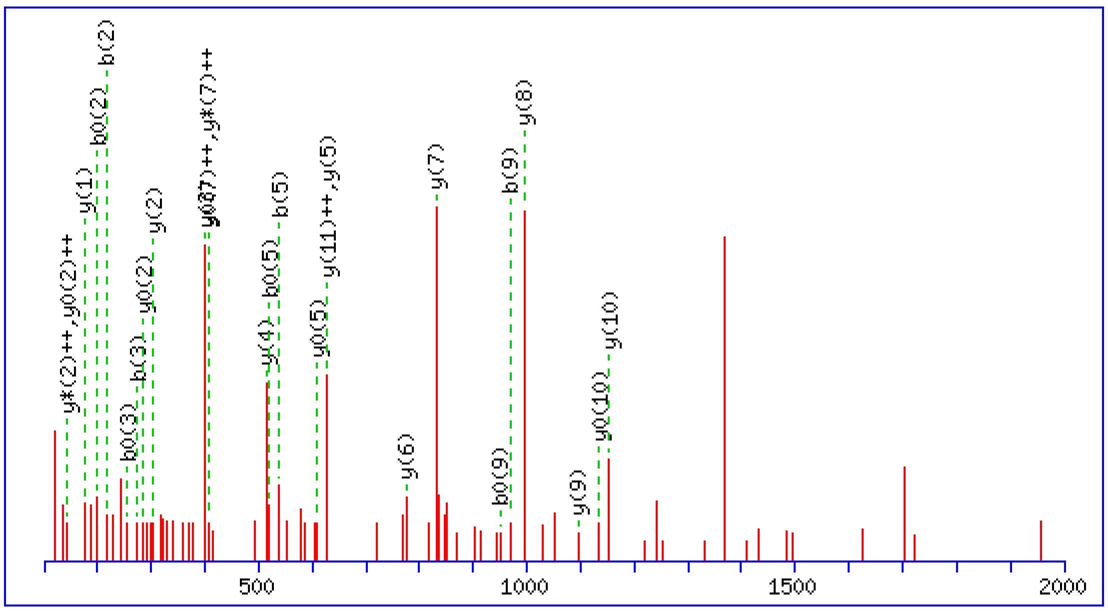
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTGTYGFLLPER**
Found in **CBPB2_HUMAN**, Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

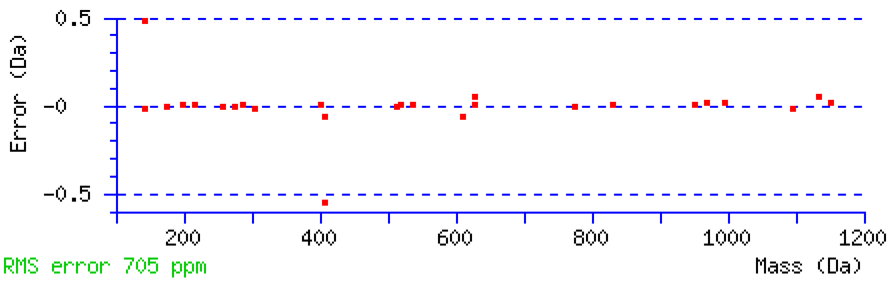
Match to Query 29883: 1367.680888 from(684.847720,2+) rtinseconds(3083) index(40911)
Title: Locus:1.1.1.2712.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

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 ●

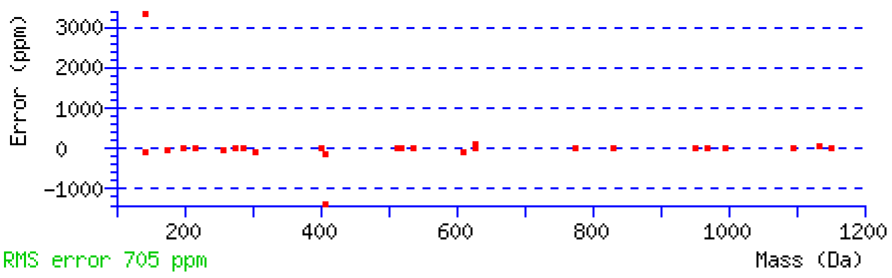


```
Monoisotopic mass of neutral peptide Mr(calc): 1367.672134
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00026
Matches : 26/108 fragment ions using 65 most intense peaks   (help)
```

#	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							12
2	**217.081898**	109.044587	199.071333	100.039304	T	1253.652466	627.329871	1236.625917	618.816597	1235.641901	618.324589	11
3	**274.103362**	137.555319	256.092797	128.550037	G	***1152.604787***	576.806032	1135.578238	568.292757	1134.594222	567.800749	10
4	375.151041	188.079159	357.140476	179.073876	T	***1095.583323***	548.295300	1078.556774	539.782025	1077.572758	539.290017	9
5	**538.214370**	269.610823	520.203805	260.605541	Y	***994.535644***	497.771460	977.509095	489.258186	976.525079	488.766178	8
6	595.235834	298.121555	577.225269	289.116273	G	***831.472315***	416.239796	814.445766	407.726521	813.461750	407.234513	7
7	742.304248	371.655762	724.293683	362.650480	F	***774.450851***	387.729064	757.424302	379.215789	756.440286	378.723781	6
8	855.388312	428.197794	837.377747	419.192512	L	***627.382437***	314.194857	610.355888	305.681582	609.371872	305.189574	5
9	**968.472376**	484.739826	950.461811	475.734544	L	***514.298373***	257.652825	497.271824	249.139550	496.287808	248.647542	4
10	1065.525140	533.266208	1047.514575	524.260926	P	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	3
11	1194.567733	597.787505	1176.557168	588.782222	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



RMS error 705 ppm



RMS error 705 ppm

NCBI **BLAST** search of DTGTYGFLLPER
(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	1367.672134	0.008754	DTGTYGFLLPER

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

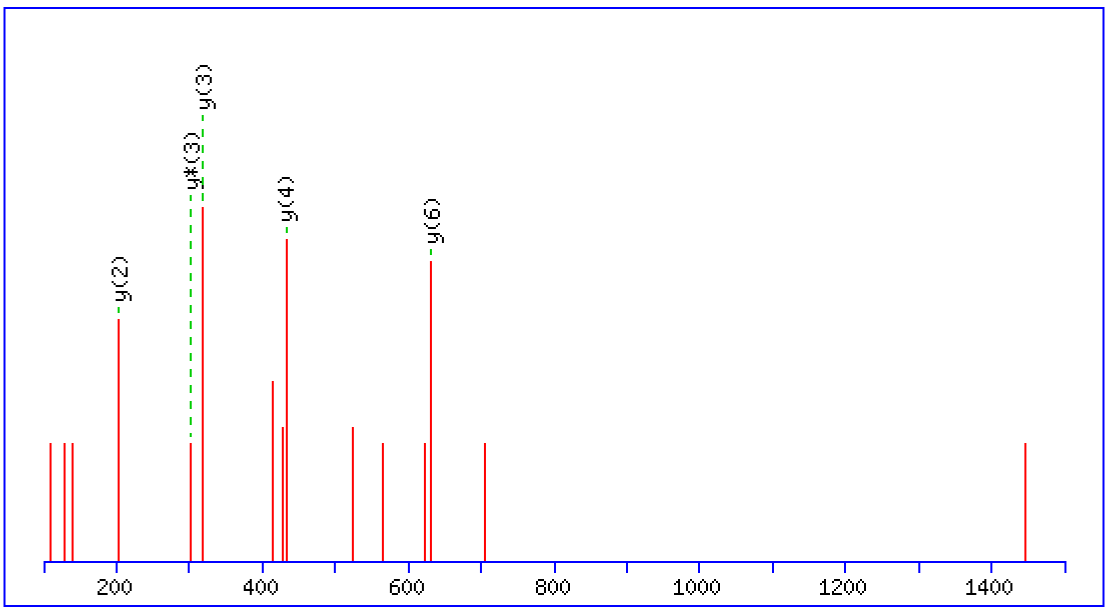
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MTISPDGK**
Found in **CEA18_HUMAN**, Carcinoembryonic antigen-related cell adhesion molecule 18 OS=Homo sapiens GN=CEACAM18 PE=2 SV=3

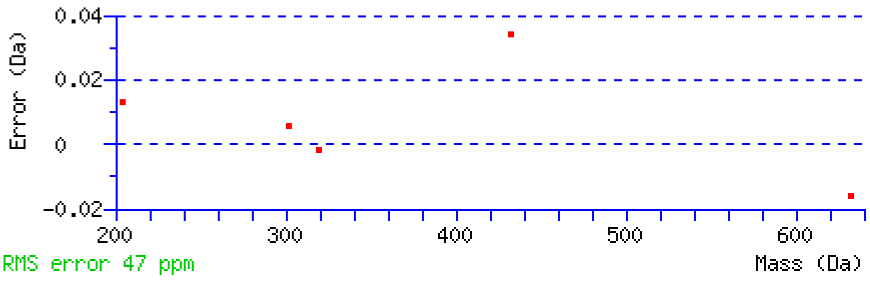
Match to Query 4256: 879.400948 from(440.707750,2+) rtinseconds(1878) index(10739)
Title: Locus:1.1.1.2213.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

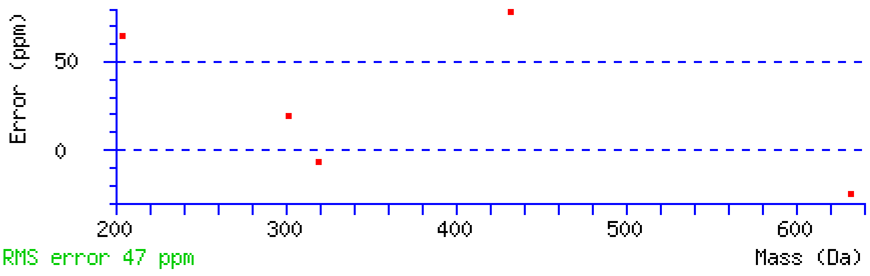
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 879.400787
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
P5 : Oxidation (P)
Ions Score: 35 **Expect:** 0.0027
Matches : 5/90 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							8
2	249.090355	125.048815	231.079790	116.043533	T	733.372661	367.189969	716.346112	358.676694	715.362096	358.184686	7
3	362.174419	181.590848	344.163854	172.585565	I	***632.324982***	316.666129	615.298433	308.152855	614.314417	307.660847	6
4	449.206447	225.106861	431.195882	216.101579	S	519.240918	260.124097	502.214369	251.610823	501.230353	251.118815	5
5	562.254126	281.630701	544.243561	272.625419	P	***432.208890***	216.608083	415.182341	208.094809	414.198325	207.602801	4
6	677.281069	339.144173	659.270504	330.138890	D	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
7	734.302533	367.654905	716.291968	358.649622	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 MTISPDGK
(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	879.400787	0.000161	MTISPDGK
19.6	879.397430	0.003518	FTSPPGDK
9.6	879.408646	-0.007698	EDLGFSGR
5.5	879.394241	0.006707	QEVAMMR
5.5	879.394241	0.006707	QEVAMMR
1.1	879.404617	-0.003669	TTNNSTSR
0.3	879.398743	0.002205	NGFYHSR
0.0	879.393387	0.007561	VSSNSVSNS

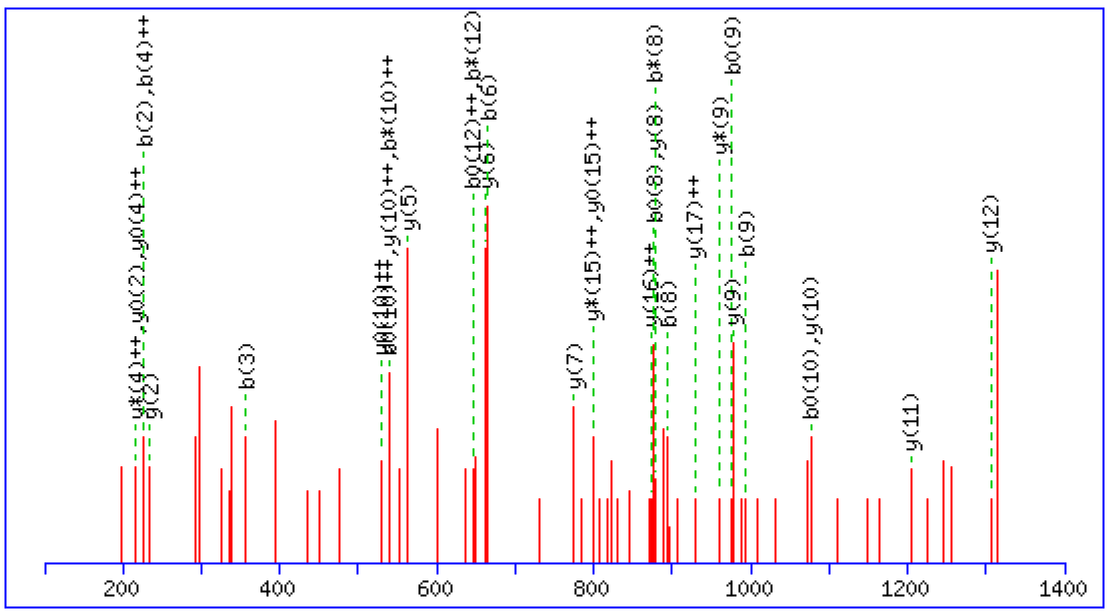
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEPLVTQVTTLVNTNSK**
Found in **CTNA1_HUMAN**, Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1

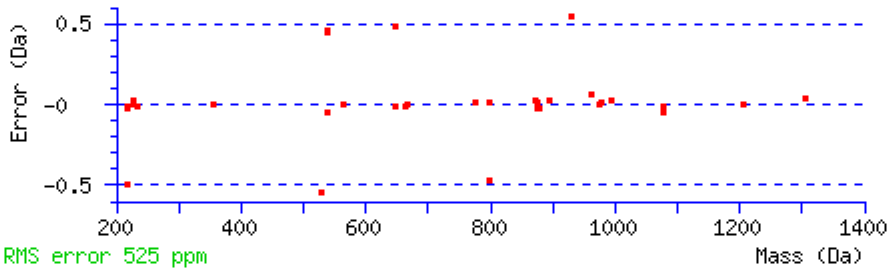
Match to Query 47374: 1969.107642 from(657.376490,3+) rtinseconds(3803) index(47543)
Title: Locus:1.1.1.3381.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

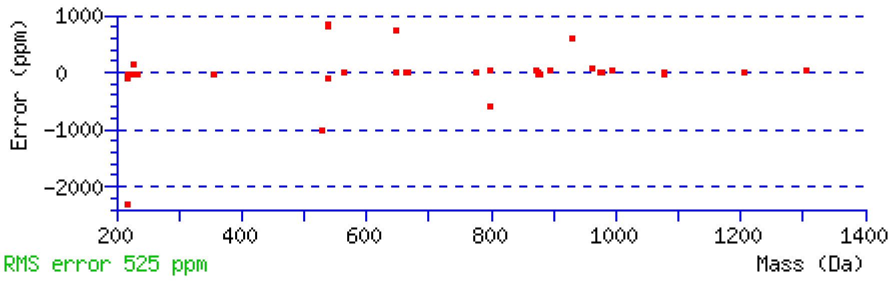
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1400 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1969.109558
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00091
Matches : 33/184 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							18
2	**227.175404**	114.091340					L	1857.032771	929.020024	1840.006222	920.506749	1839.022206	920.014741	17
3	**356.217997**	178.612637			338.207432	169.607354	E	1743.948707	872.477992	1726.922158	863.964717	1725.938142	863.472709	16
4	453.270761	227.139019			435.260196	218.133736	P	1614.906114	807.956695	1597.879565	799.443421	1596.895549	798.951413	15
5	566.354825	283.681051			548.344260	274.675768	L	1517.853350	759.430313	1500.826801	750.917039	1499.842785	750.425031	14
6	**665.423239**	333.215258			647.412674	324.209975	V	1404.769286	702.888281	1387.742737	694.375007	1386.758721	693.882998	13
7	766.470918	383.739097			748.460353	374.733815	T	***1305.700872***	653.354074	1288.674323	644.840800	1287.690307	644.348792	12
8	**894.529496**	447.768386	877.502947	439.255112	876.518931	438.763104	Q	***1204.653193***	602.830234	1187.626644	594.316960	1186.642628	593.824952	11
9	**993.597910**	497.302593	976.571361	488.789319	975.587345	488.297311	V	***1076.594615***	538.800946	1059.568066	530.287671	1058.584050	529.795663	10
10	1094.645589	547.826433	1077.619040	539.313158	1076.635024	538.821150	T	***977.526201***	489.266739	960.499652	480.753464	959.515636	480.261456	9
11	1195.693268	598.350272	1178.666719	589.836998	1177.682703	589.344990	T	***876.478522***	438.742899	859.451973	430.229625	858.467957	429.737617	8
12	1308.777332	654.892304	1291.750783	646.379030	1290.766767	645.887021	L	***775.430843***	388.219060	758.404294	379.705785	757.420278	379.213777	7
13	1407.845746	704.426511	1390.819197	695.913237	1389.835181	695.421228	V	***662.346779***	331.677028	645.320230	323.163753	644.336214	322.671745	6
14	1521.888673	761.447974	1504.862124	752.934700	1503.878108	752.442692	N	***563.278365***	282.142821	546.251816	273.629546	545.267800	273.137538	5
15	1622.936352	811.971814	1605.909803	803.458540	1604.925787	802.966531	T	449.235438	225.121357	432.208889	216.608083	431.224873	216.116075	4
16	1736.979279	868.993277	1719.952730	860.480003	1718.968714	859.987995	N	348.187759	174.597518	331.161210	166.084243	330.177194	165.592235	3
17	1824.011307	912.509292	1806.984758	903.996017	1806.000742	903.504009	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 LLEPLVTQVTTLVNTNSK
(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	1969.109558	-0.001916	LLEPLVTQVTTLVNTNSK
33.7	1969.109558	-0.001916	LLEPLVTQVTTLVNTSNK
0.6	1969.126144	-0.018502	HIIAQVLPHRDPALVFK

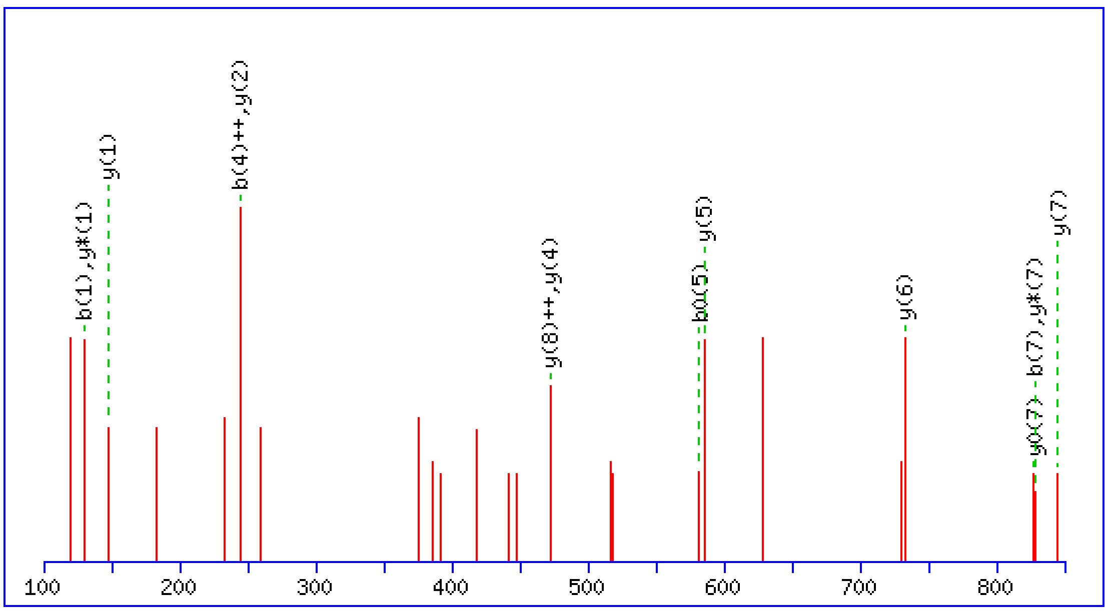
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPLFLDLPK**
Found in **CATL2_HUMAN**, Cathepsin L2 OS=Homo sapiens GN=CTSL2 PE=1 SV=2

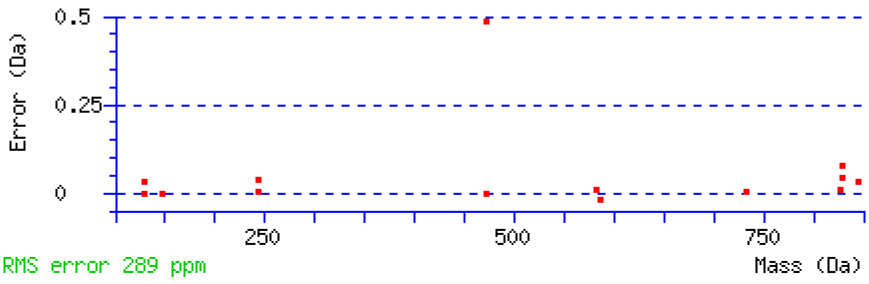
Match to Query 13660: 1070.599128 from(536.306840,2+) rtinseconds(3280) index(39654)
Title: Locus:1.1.1.2818.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

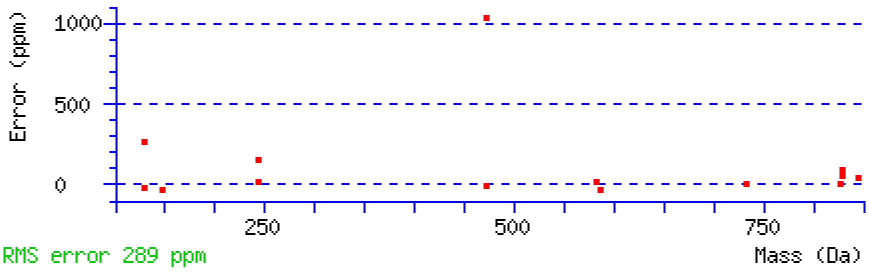
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1070.601181
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0039
Matches : 14/74 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	**130.049869**	65.528572	112.039304	56.523290	E							9
2	227.102633	114.054954	209.092068	105.049672	P	942.565881	471.786579	925.539332	463.273304	924.555316	462.781296	8
3	340.186697	170.596986	322.176132	161.591704	L	***845.513117***	423.260197	828.486568	414.746922	827.502552	414.254914	7
4	487.255111	244.131193	469.244546	235.125911	F	***732.429053***	366.718165	715.402504	358.204890	714.418488	357.712882	6
5	600.339175	300.673226	582.328610	291.667943	L	***585.360639***	293.183958	568.334090	284.670683	567.350074	284.178675	5
6	715.366118	358.186697	697.355553	349.181415	D	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
7	**828.450182**	414.728729	810.439617	405.723447	L	357.249632	179.128454	340.223083	170.615180			3
8	925.502946	463.255111	907.492381	454.249829	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 EPLFLDLPK
(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	1070.601181	-0.002053	EPLFLDLPK
9.0	1070.604538	-0.005410	IILEPMDLK
7.3	1070.608368	-0.009240	ENELLLGRK
6.2	1070.597153	0.001975	DQLDNLLLK
5.7	1070.608368	-0.009240	ENVREALLK
3.2	1070.608398	-0.009270	TAVAPLDRTK
2.4	1070.608383	-0.009255	VQDIKNNLK
0.9	1070.608383	-0.009255	ALEGTLPSKR
0.9	1070.601852	-0.002724	MARLLSPGAR
0.4	1070.608398	-0.009270	VNKTLPAGQK

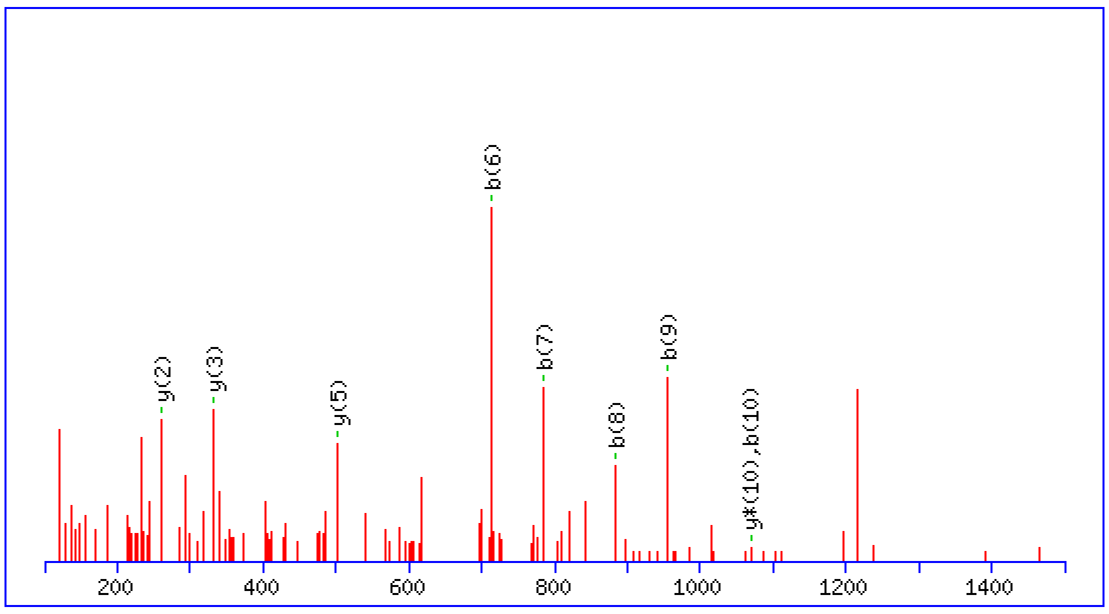
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDVLKEAVANK**
Found in **CATS_HUMAN**, Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3

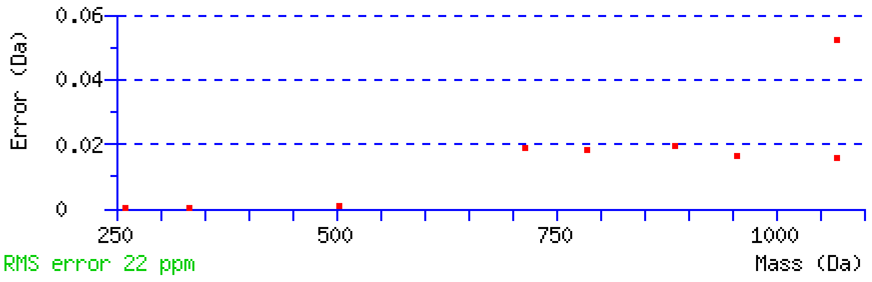
Match to Query 22677: 1214.661148 from(608.337850,2+) rtinseconds(2387) index(29278)
Title: Locus:1.1.1.2391.22
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

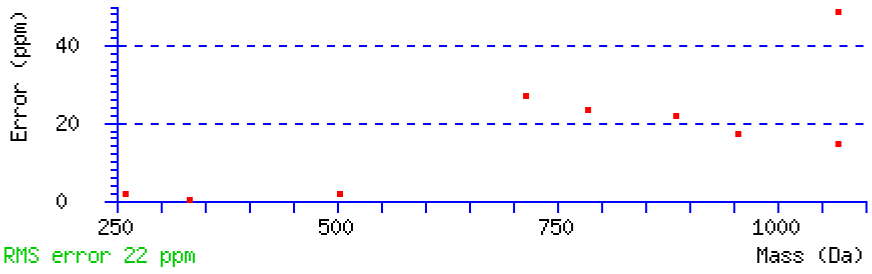
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1214.650635
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0018
Matches : 9/102 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	130.049869	65.528572			112.039304	56.523290	E							11
2	245.076812	123.042044			227.066247	114.036762	D	1086.615350	543.811313	1069.588801	535.298039	1068.604785	534.806031	10
3	344.145226	172.576251			326.134661	163.570969	V	971.588407	486.297842	954.561858	477.784567	953.577842	477.292559	9
4	457.229290	229.118283			439.218725	220.113001	L	872.519993	436.763635	855.493444	428.250360	854.509428	427.758352	8
5	585.324253	293.165765	568.297704	284.652490	567.313688	284.160482	K	759.435929	380.221603	742.409380	371.708328	741.425364	371.216320	7
6	*714.366846*	357.687061	697.340297	349.173787	696.356281	348.681779	E	631.340966	316.174121	614.314417	307.660847	613.330401	307.168839	6
7	*785.403960*	393.205618	768.377411	384.692344	767.393395	384.200336	A	**502.298373**	251.652824	485.271824	243.139550			5
8	*884.472374*	442.739825	867.445825	434.226551	866.461809	433.734543	V	431.261259	216.134267	414.234710	207.620993			4
9	*955.509488*	478.258382	938.482939	469.745108	937.498923	469.253100	A	**332.192845**	166.600061	315.166296	158.086786			3
10	*1069.552415*	535.279846	1052.525866	526.766571	1051.541850	526.274563	N	**261.155731**	131.081504	244.129182	122.568229			2
11							K	147.112804	74.060040	130.086255	65.546765			1

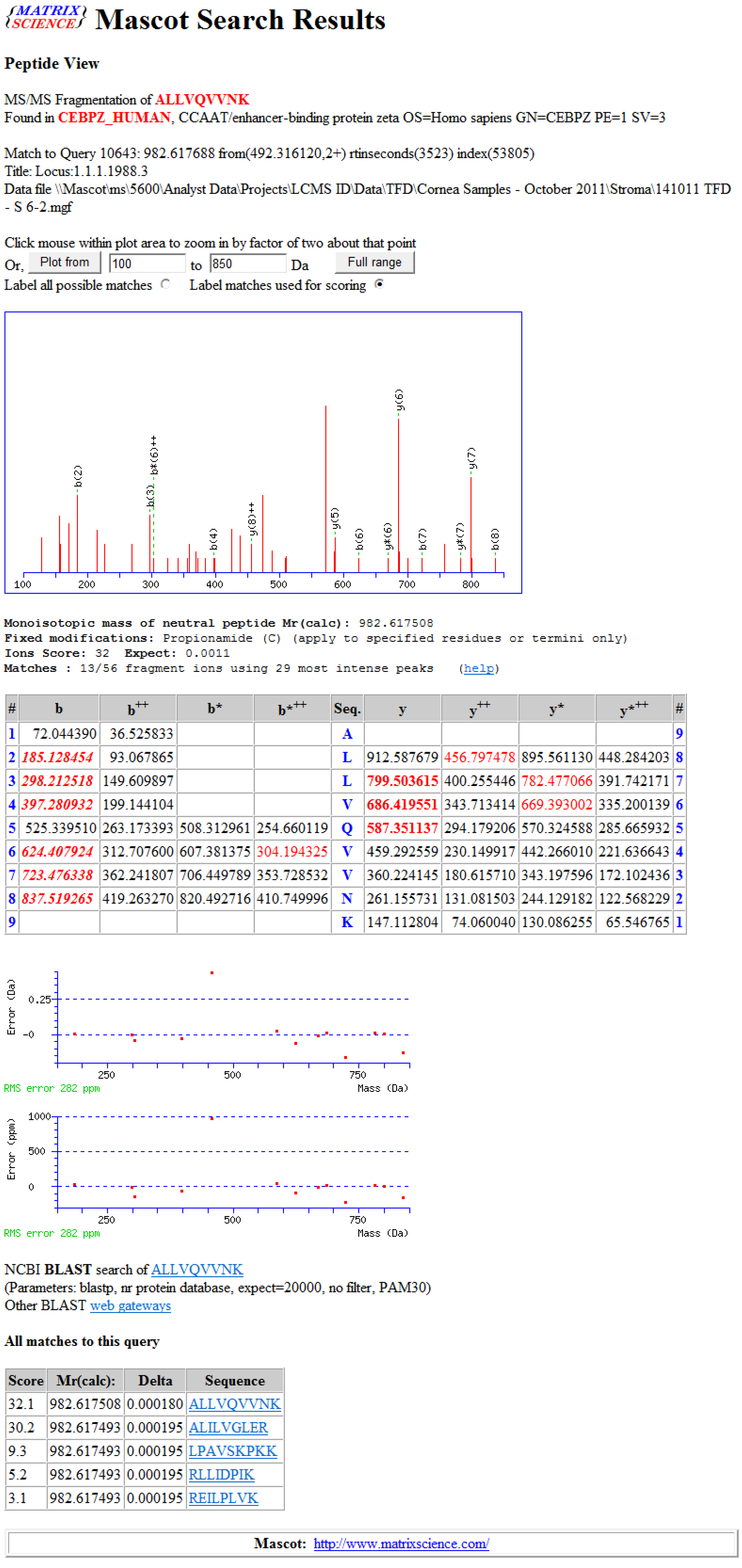




NCBI **BLAST** search of EDVLKEAVANK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.8	1214.650635	0.010513	EDVLKEAVANK
10.2	1214.650635	0.010513	GQEIETILANK
5.0	1214.650681	0.010467	VQTPEVDVKGK
4.2	1214.650650	0.010498	IKEDLDQVQK
1.6	1214.650650	0.010498	AVVVSPKEENK



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLVQVVNK**
Found in **CEBPZ_HUMAN**, CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3

Match to Query 10643: 982.617688 from(492.316120,2+) rtinseconds(3523) index(53805)
Title: Locus:1.1.1.1988.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.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): 982.617508
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0011
Matches : 13/56 fragment ions using 29 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			L	912.587679	456.797478	895.561130	448.284203	8
3	***298.212518***	149.609897			L	**799.503615**	400.255446	782.477066	391.742171	7
4	***397.280932***	199.144104			V	**686.419551**	343.713414	669.393002	335.200139	6
5	525.339510	263.173393	508.312961	254.660119	Q	**587.351137**	294.179206	570.324588	285.665932	5
6	***624.407924***	312.707600	607.381375	304.194325	V	459.292559	230.149917	442.266010	221.636643	4
7	***723.476338***	362.241807	706.449789	353.728532	V	360.224145	180.615710	343.197596	172.102436	3
8	***837.519265***	419.263270	820.492716	410.749996	N	261.155731	131.081503	244.129182	122.568229	2
9					K	147.112804	74.060040	130.086255	65.546765	1

RMS error 282 ppm

RMS error 282 ppm

NCBI **BLAST** search of ALLVQVVNK
(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	982.617508	0.000180	ALLVQVVNK
30.2	982.617493	0.000195	ALILVGLER
9.3	982.617493	0.000195	LPAVSKPKK
5.2	982.617493	0.000195	RLLIDPIK
3.1	982.617493	0.000195	REILPLVK

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

{MATRIX SCIENCE}

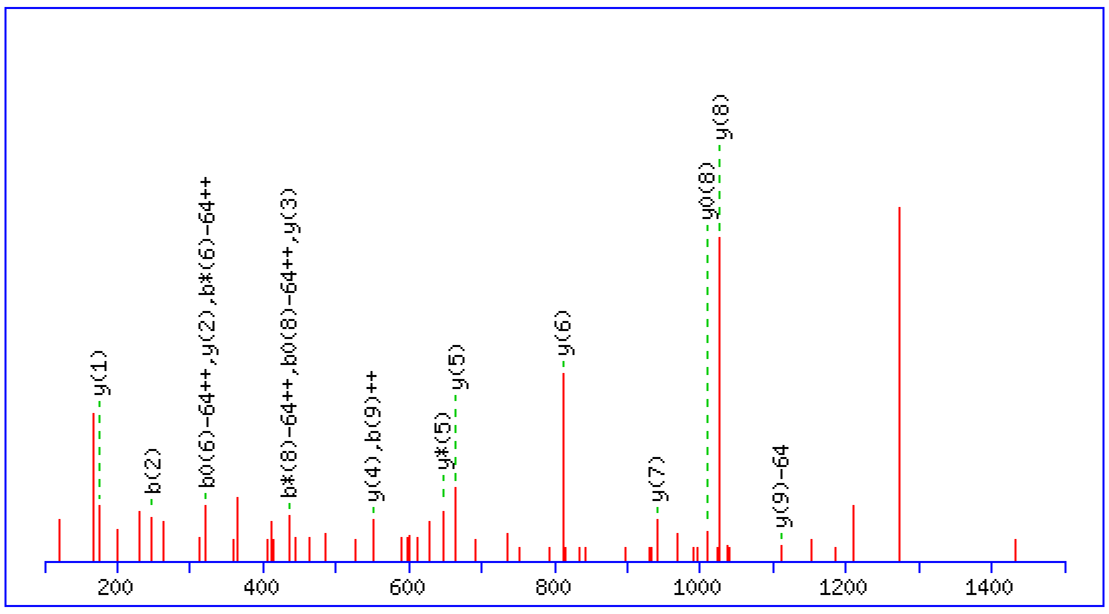
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMSEFNNNFR**
Found in **CD63_HUMAN**, CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2

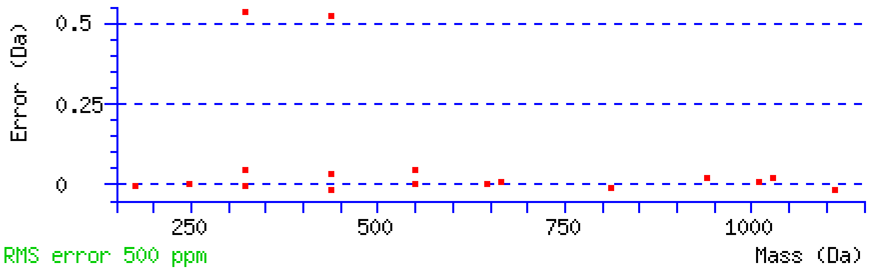
Match to Query 28897: 1272.555608 from(637.285080,2+) rtinseconds(1861) index(17671)
Title: Locus:1.1.1.2108.41
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

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 ●

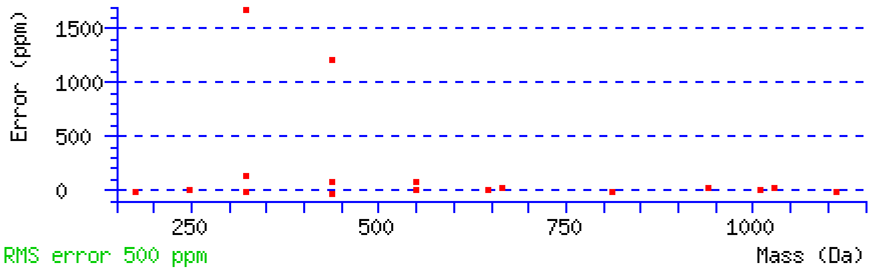


Monoisotopic mass of neutral peptide Mr(calc): 1272.555710
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 66 **Expect:** 9.3e-007
Matches : 17/126 fragment 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	100.075690	50.541483					V							10
2	183.112805	92.060040					M	***1110.496297***	555.751786	1093.469748	547.238512	1092.485732	546.746504	9
3	270.144833	135.576055			252.134268	126.570772	S	***1027.459182***	514.233229	1010.432633	505.719954	1009.448617	505.227946	8
4	399.187426	200.097351			381.176861	191.092069	E	***940.427154***	470.717215	923.400605	462.203940	922.416589	461.711932	7
5	546.255840	273.631558			528.245275	264.626276	F	***811.384561***	406.195918	794.358012	397.682644			6
6	660.298767	330.653022	643.272218	322.139747	642.288202	321.647739	N	***664.316147***	332.661711	647.289598	324.148437			5
7	774.341694	387.674485	757.315145	379.161210	756.331129	378.669202	N	***550.273220***	275.640248	533.246671	267.126973			4
8	888.384621	444.695948	871.358072	436.182674	870.374056	435.690666	N	***436.230293***	218.618784	419.203744	210.105510			3
9	1035.453035	518.230156	1018.426486	509.716881	1017.442470	509.224873	F	***322.187366***	161.597321	305.160817	153.084046			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 500 ppm



RMS error 500 ppm

NCBI **BLAST** search of VMSEFNNNFR
(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	1272.555710	-0.000102	VMSEFNNNFR
3.1	1272.555695	-0.000087	YSSYLNSHMR
2.1	1272.555511	0.000097	SRDHNSSNNSR
0.8	1272.555725	-0.000117	SPGMEPPFSHR

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

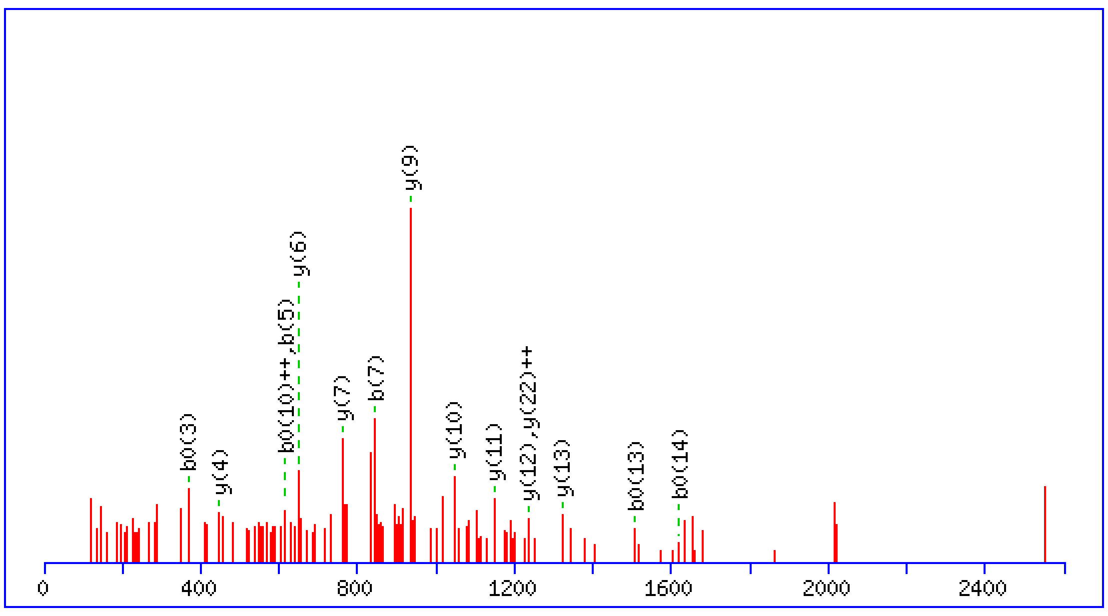
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFHETLDCCGSSTLTALTTSVLK**
Found in **CD81_HUMAN**, CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1

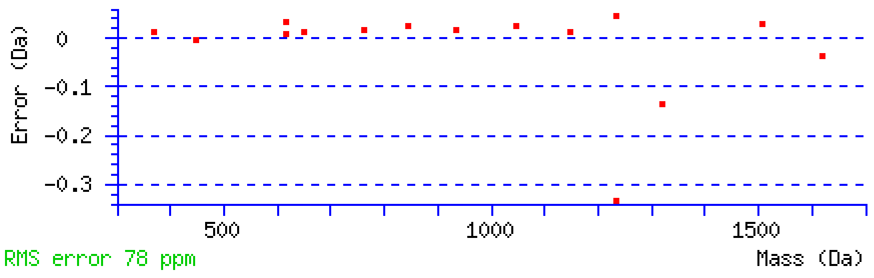
Match to Query 39779: 2569.256712 from(857.426180,3+) rtinseconds(3426) index(48811)
Title: Locus:1.1.1.2755.32
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

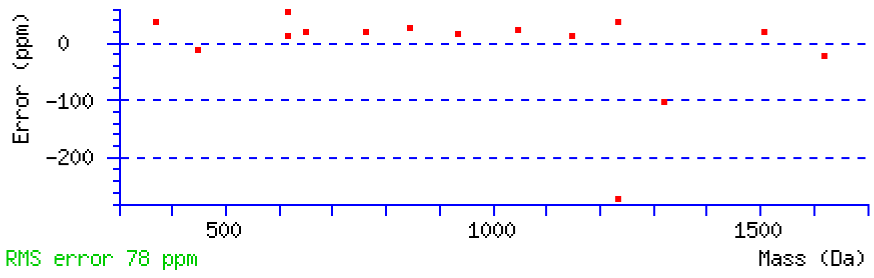
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2569.240402
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 2.7e-005
Matches : 15/214 fragment ions using 19 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							23
2	249.123369	125.065322	231.112804	116.060040	F	2469.199991	1235.103633	2452.173442	1226.590359	2451.189426	1226.098351	22
3	386.182281	193.594778	368.171716	184.589496	H	2322.131577	1161.569426	2305.105028	1153.056152	2304.121012	1152.564144	21
4	515.224874	258.116075	497.214309	249.110793	E	2185.072665	1093.039970	2168.046116	1084.526696	2167.062100	1084.034688	20
5	**616.272553**	308.639915	598.261988	299.634632	T	2056.030072	1028.518674	2039.003523	1020.005399	2038.019507	1019.513391	19
6	729.356617	365.181947	711.346052	356.176664	L	1954.982393	977.994835	1937.955844	969.481560	1936.971828	968.989552	18
7	**844.383560**	422.695418	826.372995	413.690136	D	1841.898329	921.452802	1824.871780	912.939528	1823.887764	912.447520	17
8	1018.429859	509.718568	1000.419294	500.713285	C	1726.871386	863.939331	1709.844837	855.426057	1708.860821	854.934049	16
9	1192.476158	596.741717	1174.465593	587.736434	C	1552.825087	776.916181	1535.798538	768.402907	1534.814522	767.910899	15
10	1249.497622	625.252449	1231.487057	616.247166	G	1378.778788	689.893032	1361.752239	681.379758	1360.768223	680.887750	14
11	1336.529650	668.768463	1318.519085	659.763180	S	***1321.757324***	661.382300	1304.730775	652.869026	1303.746759	652.377018	13
12	1423.561678	712.284477	1405.551113	703.279195	S	***1234.725296***	617.866286	1217.698747	609.353012	1216.714731	608.861004	12
13	1524.609357	762.808317	1506.598792	753.803034	T	***1147.693268***	574.350272	1130.666719	565.836998	1129.682703	565.344990	11
14	1637.693421	819.350349	1619.682856	810.345066	L	***1046.645589***	523.826433	1029.619040	515.313158	1028.635024	514.821150	10
15	1738.741100	869.874188	1720.730535	860.868905	T	***933.561525***	467.284401	916.534976	458.771126	915.550960	458.279118	9
16	1809.778214	905.392745	1791.767649	896.387462	A	832.513846	416.760561	815.487297	408.247287	814.503281	407.755279	8
17	1922.862278	961.934777	1904.851713	952.929494	L	***761.476732***	381.242004	744.450183	372.728730	743.466167	372.236722	7
18	2023.909957	1012.458616	2005.899392	1003.453334	T	***648.392668***	324.699972	631.366119	316.186698	630.382103	315.694690	6
19	2124.957636	1062.982456	2106.947071	1053.977173	T	547.344989	274.176133	530.318440	265.662858	529.334424	265.170850	5
20	2211.989664	1106.498470	2193.979099	1097.493187	S	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
21	2311.058078	1156.032677	2293.047513	1147.027394	V	359.265282	180.136279	342.238733	171.623004			3
22	2424.142142	1212.574709	2406.131577	1203.569426	L	260.196868	130.602072	243.170319	122.088798			2
23					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TFHETLDCCGSSTLTALTTSVLK
(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	2569.240402	0.016310	TFHETLDCCGSSTLTALTTSVLK
1.8	2569.237015	0.019697	TPILEDFELEGVCQLPDQSPPR

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

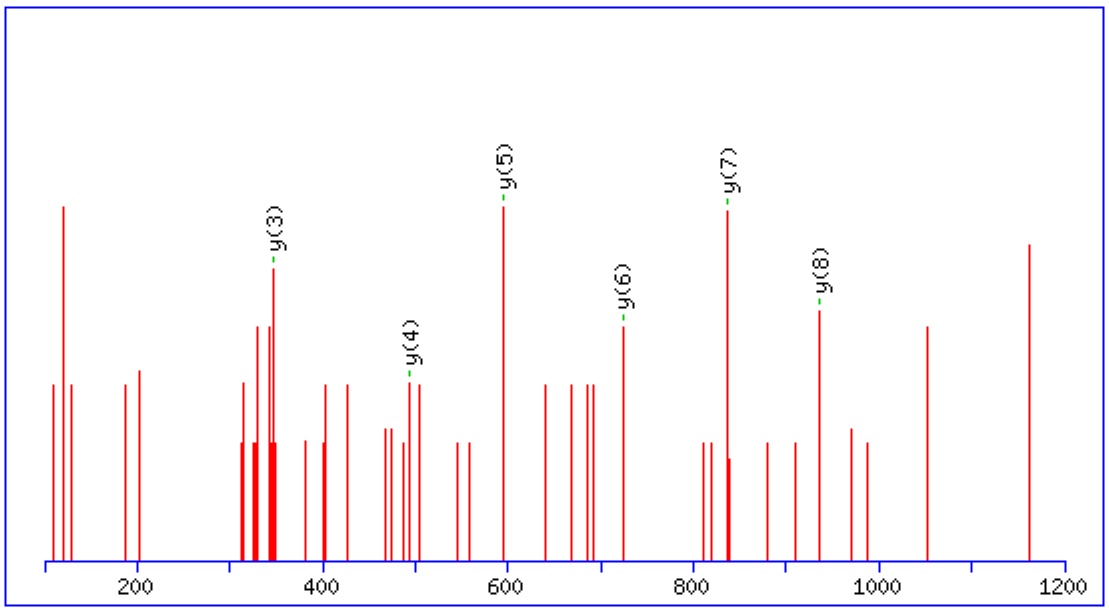
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDVLETFTVK**
Found in **CD9_HUMAN**, CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4

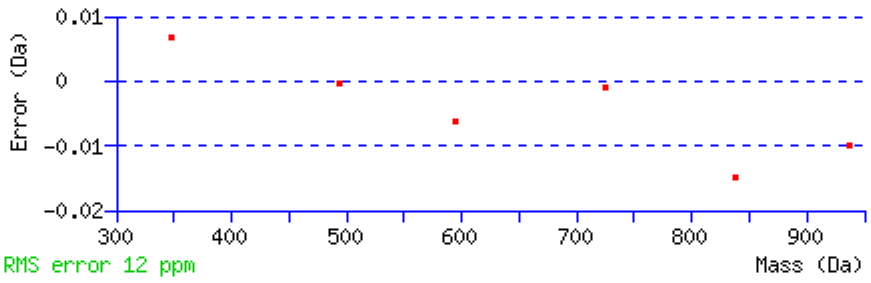
Match to Query 382567: 1178.656288 from(590.335420,2+) rtinseconds(2382) index(959005)
Title: Locus:1.1.1.1421.21
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

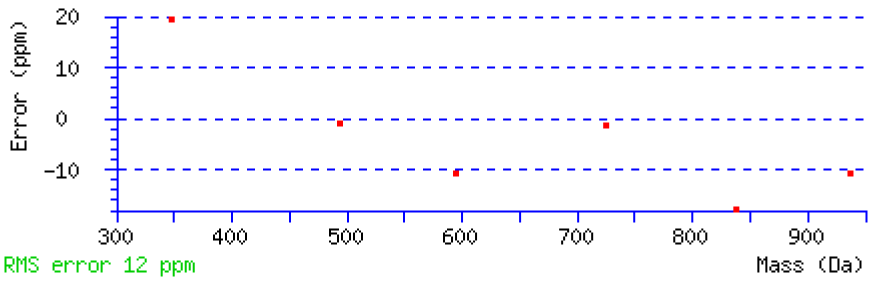
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1178.654694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.0002
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	129.102239	65.054757	112.075690	56.541483			K							10
2	244.129182	122.568229	227.102633	114.054955	226.118617	113.562947	D	1051.567004	526.287140	1034.540455	517.773866	1033.556439	517.281858	9
3	343.197596	172.102436	326.171047	163.589162	325.187031	163.097154	V	***936.540061***	468.773669	919.513512	460.260394	918.529496	459.768386	8
4	456.281660	228.644468	439.255111	220.131194	438.271095	219.639186	L	***837.471647***	419.239462	820.445098	410.726187	819.461082	410.234179	7
5	585.324253	293.165765	568.297704	284.652490	567.313688	284.160482	E	***724.387583***	362.697430	707.361034	354.184155	706.377018	353.692147	6
6	686.371932	343.689604	669.345383	335.176330	668.361367	334.684322	T	***595.344990***	298.176133	578.318441	289.662859	577.334425	289.170851	5
7	833.440346	417.223811	816.413797	408.710537	815.429781	408.218529	F	***494.297311***	247.652294	477.270762	239.139019	476.286746	238.647011	4
8	934.488025	467.747651	917.461476	459.234376	916.477460	458.742368	T	***347.228897***	174.118087	330.202348	165.604812	329.218332	165.112804	3
9	1033.556439	517.281858	1016.529890	508.768583	1015.545874	508.276575	V	246.181218	123.594247	229.154669	115.080973			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KDVLETFTVK
(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	1178.654694	0.001594	KDVLETFTVK

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

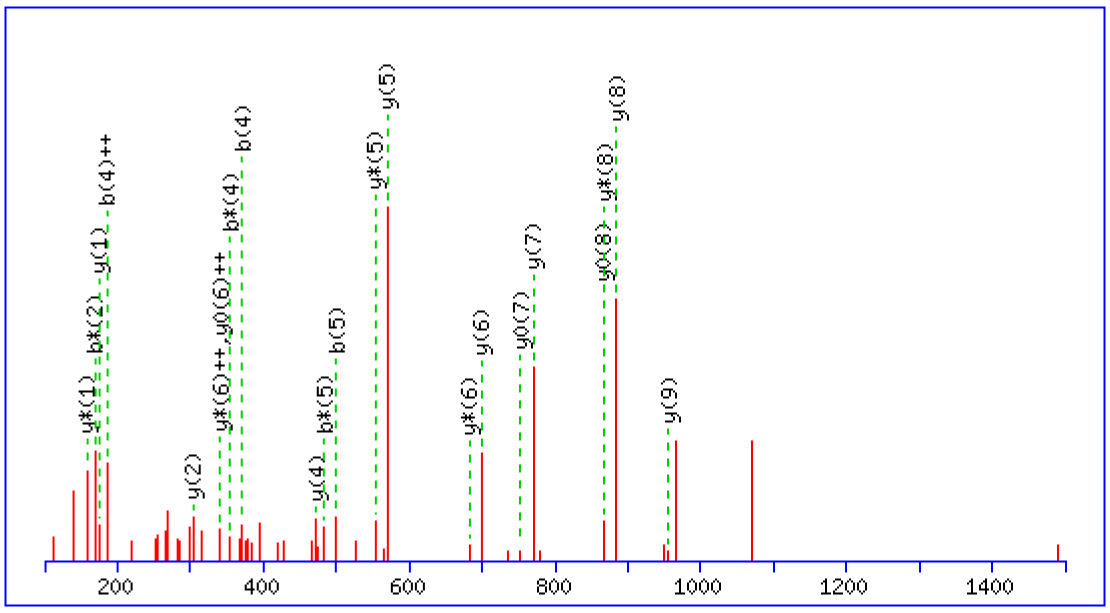
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NANAEPAVQR**
Found in **CD99_HUMAN**, CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1

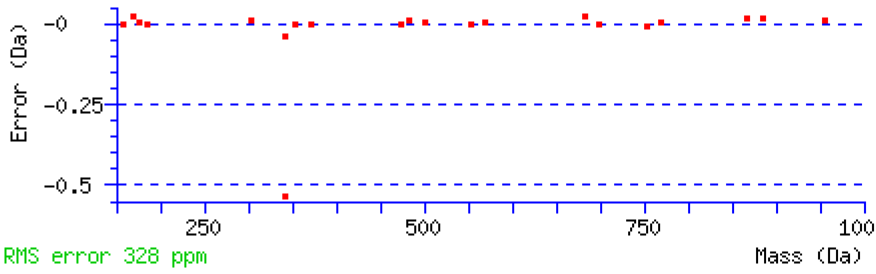
Match to Query 16797: 1068.529368 from(535.271960,2+) rtinseconds(864) index(638)
Title: Locus:1.1.1.1729.9
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

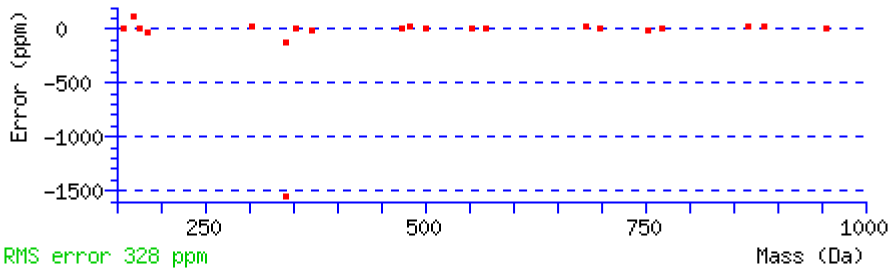
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1068.531189
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 5.8e-006
Matches : 23/90 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							10
2	**186.087317**	93.547296	169.060768	85.034022			A	***955.495570***	478.251423	938.469021	469.738149	937.485005	469.246141	9
3	300.130244	150.568760	283.103695	142.055486			N	***884.458456***	442.732866	867.431907	434.219592	866.447891	433.727584	8
4	**371.167358**	186.087317	354.140809	177.574042			A	***770.415529***	385.711403	753.388980	377.198128	752.404964	376.706120	7
5	**500.209951**	250.608613	483.183402	242.095339	482.199386	241.603331	E	***699.378415***	350.192846	682.351866	341.679571	681.367850	341.187563	6
6	597.262715	299.134996	580.236166	290.621721	579.252150	290.129713	P	***570.335822***	285.671549	553.309273	277.158275			5
7	668.299829	334.653553	651.273280	326.140278	650.289264	325.648270	A	***473.283058***	237.145167	456.256509	228.631892			4
8	767.368243	384.187760	750.341694	375.674485	749.357678	375.182477	V	402.245944	201.626610	385.219395	193.113335			3
9	895.426821	448.217049	878.400272	439.703774	877.416256	439.211766	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 NANAEPAVQR
(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	1068.531189	-0.001821	NANAEPAVQR
3.5	1068.538605	-0.009237	NMPVQDLPR

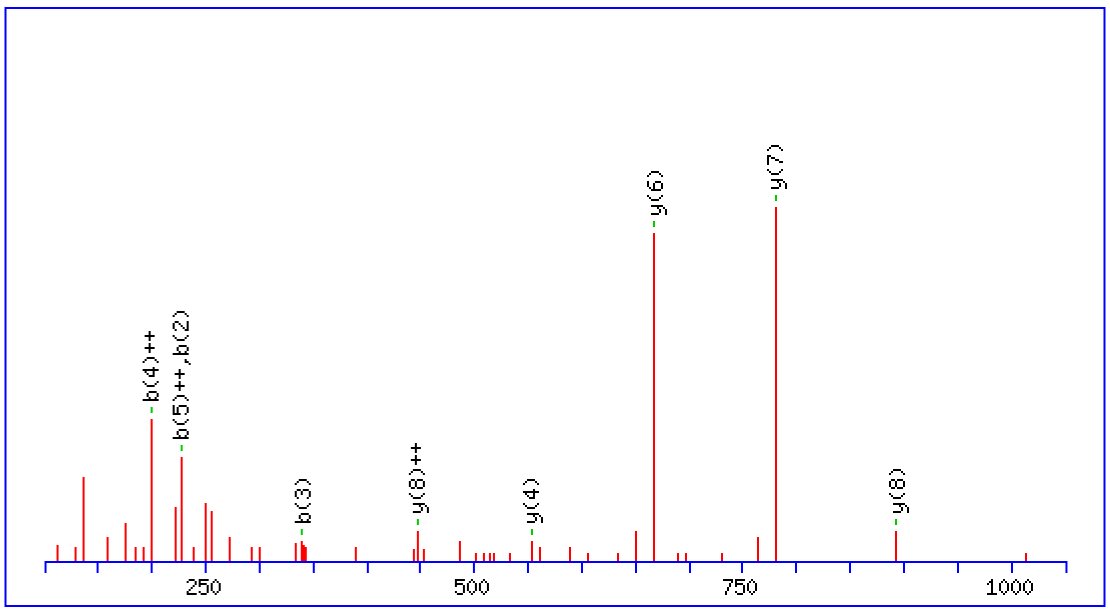
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLGGYQSR**
Found in **CDC5L_HUMAN**, Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2

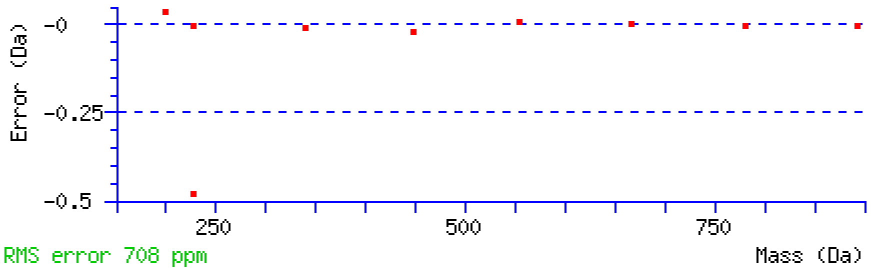
Match to Query 210830: 1005.563168 from(503.788860,2+) rtinseconds(1985) index(952482)
Title: Locus:1.1.1.1267.16
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

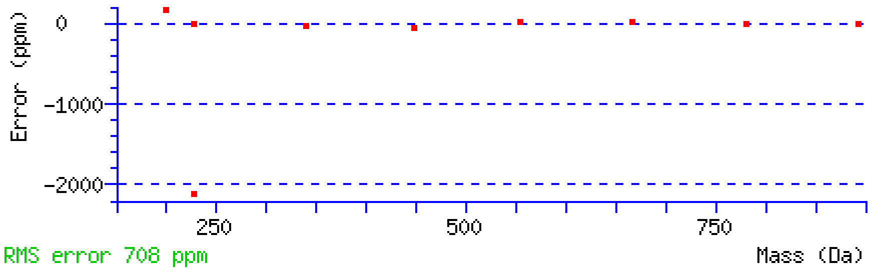
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1005.560715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.003
Matches : 9/68 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							9
2	**227.175404**	114.091340					L	*893.483943*	447.245610	876.457394	438.732335	875.473378	438.240327	8
3	**340.259468**	170.633372					L	*780.399879*	390.703578	763.373330	382.190303	762.389314	381.698295	7
4	397.280932	**199.144104**					G	*667.315815*	334.161546	650.289266	325.648271	649.305250	325.156263	6
5	454.302396	**227.654836**					G	610.294351	305.650814	593.267802	297.137539	592.283786	296.645531	5
6	617.365725	309.186501					Y	*553.272887*	277.140082	536.246338	268.626807	535.262322	268.134799	4
7	745.424303	373.215790	728.397754	364.702515			Q	390.209558	195.608417	373.183009	187.095143	372.198993	186.603135	3
8	832.456331	416.731804	815.429782	408.218529	814.445766	407.726521	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 ILLGGYQSR
(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	1005.560715	0.002453	ILLGGYQSR
17.4	1005.556885	0.006283	LLPALLFGM
14.6	1005.560715	0.002453	LIGYSQGIR
13.2	1005.560715	0.002453	LIFQDKSR
10.8	1005.553528	0.009640	LLFWVTEV
8.4	1005.560745	0.002423	PPQVVTPPR
7.9	1005.571945	-0.008777	LLHGSPNLR
7.4	1005.560745	0.002423	PPQVVTPPR
2.8	1005.571945	-0.008777	RPAPALPPR

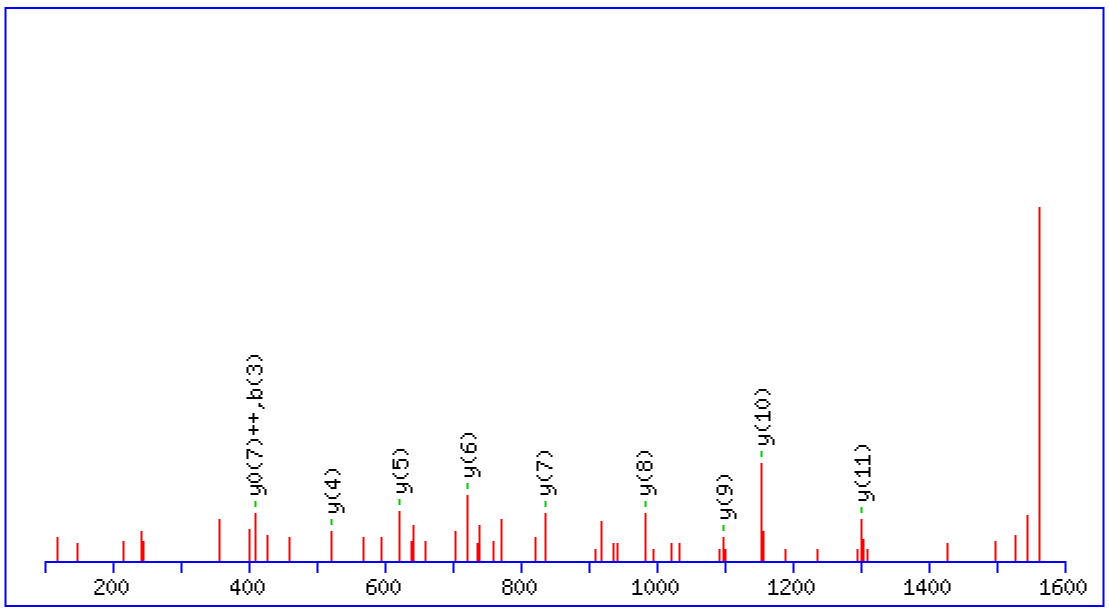
{MATRIX} *{SCIENCE}* Mascot Search Results

Peptide View

MS/MS Fragmentation of **MNFGDFLTVMTQK**
Found in **CETN2_HUMAN**, Centrin-2 OS=Homo sapiens GN=CETN2 PE=1 SV=1

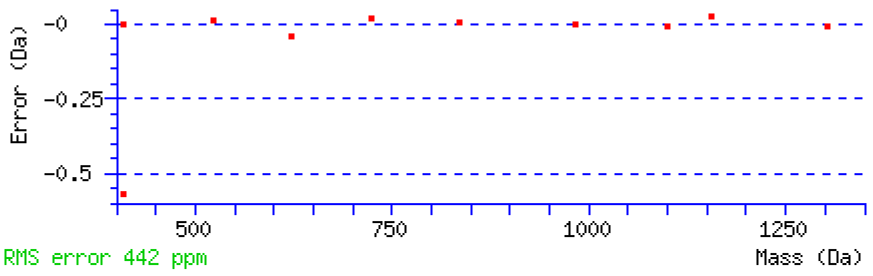
Match to Query 31425: 1562.721928 from(782.368240,2+) rtinseconds(3043) index(31599)
Title: Locus:1.1.1.2655.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

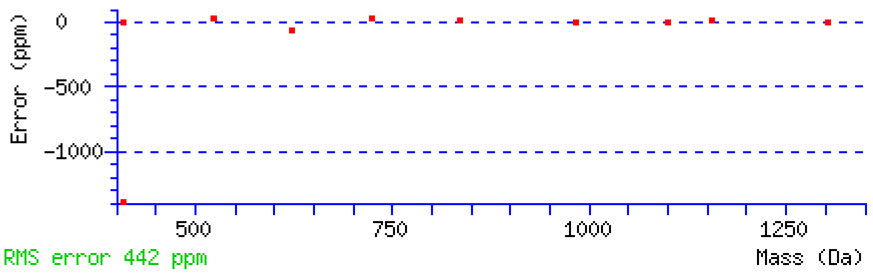
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 62  Expect: 5.7e-006
Matches : 10/246 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	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
62.1	1562.710922	0.011006	MNFGDFLTVMTQK
4.7	1562.714035	0.007893	LYTEDEFEKFDK

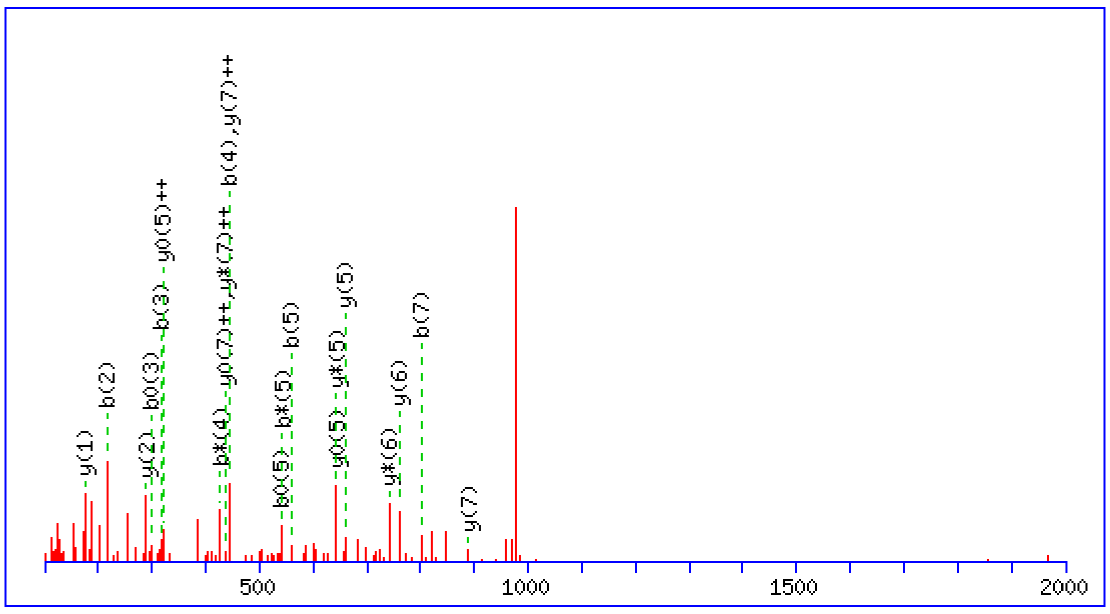
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEVKDEIR**
Found in **CNTRL_HUMAN**, Centriolin OS=Homo sapiens GN=CNTRL PE=1 SV=2

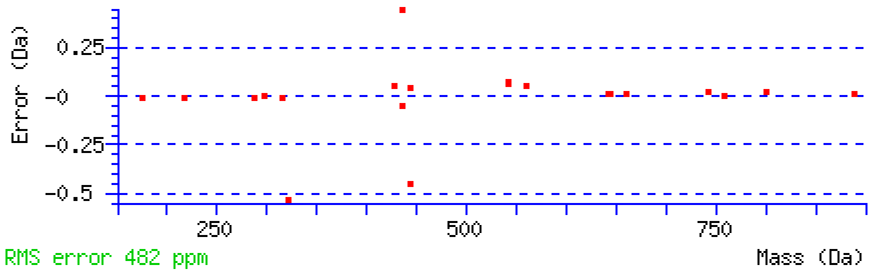
Match to Query 6834: 974.510788 from(488.262670,2+) rtinseconds(1003) index(4471)
Title: Locus:1.1.1.1858.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

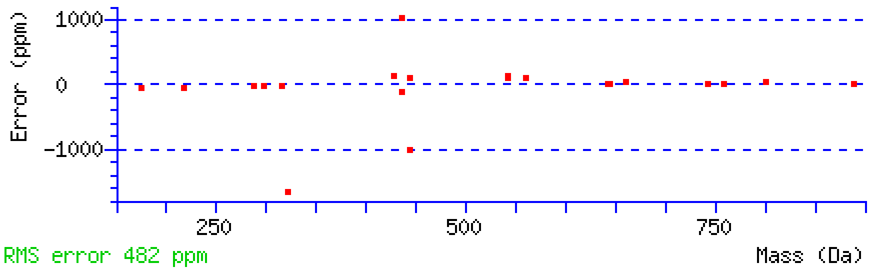
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 974.503250
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0054
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	***888.478522***	444.742899	871.451973	436.229625	870.467957	435.737617	7
3	***316.150311***	158.578793			298.139746	149.573511	V	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.216320	6
4	***444.245274***	222.626275	427.218725	214.113001	426.234709	213.620993	K	***660.367515***	330.687396	643.340966	322.174121	642.356950	321.682113	5
5	***559.272217***	280.139747	542.245668	271.626472	541.261652	271.134464	D	532.272552	266.639914	515.246003	258.126640	514.261987	257.634632	4
6	688.314810	344.661043	671.288261	336.147769	670.304245	335.655761	E	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
7	***801.398874***	401.203075	784.372325	392.689801	783.388309	392.197793	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 SEVKDEIR
(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	974.514496	-0.003708	SEVTDLRR
34.2	974.503250	0.007538	SEVKDEIR
13.0	974.514481	-0.003693	SVEERSLR
10.9	974.503250	0.007538	KLSDEDIR
8.1	974.514496	-0.003708	SSSGGRAPIK
7.6	974.514496	-0.003708	DTVLSRER
7.4	974.503250	0.007538	SVEDLKER
5.3	974.503265	0.007523	TVDKLEDR
5.2	974.503265	0.007523	DTLTEQLR
4.4	974.518524	-0.007736	FGKPELPR

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

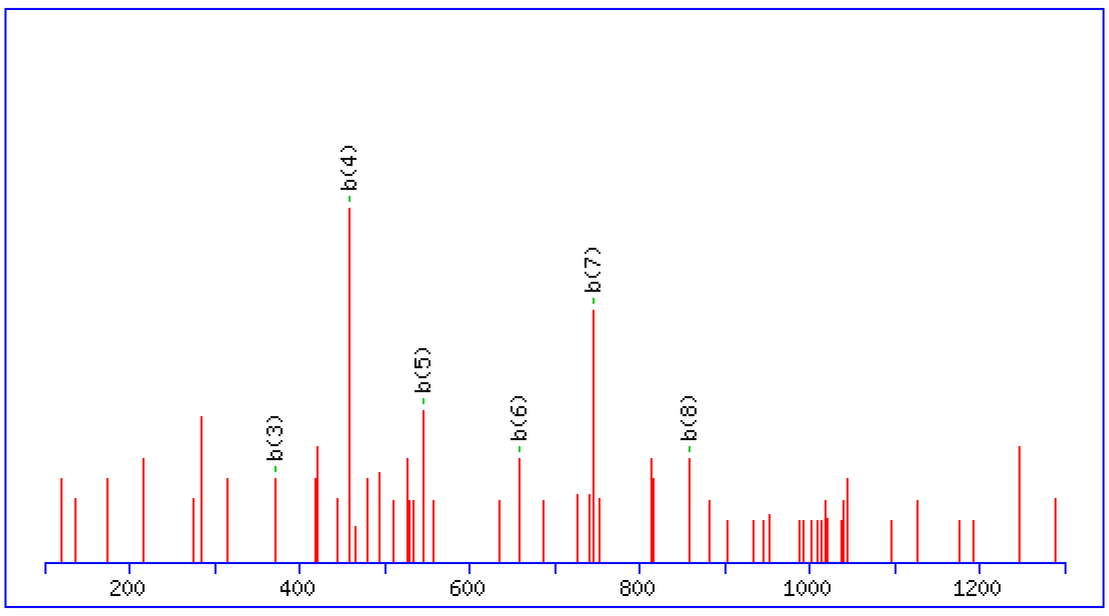
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNQSSLSPVLLPRNQR**
Found in **CER1_HUMAN**, Cerberus OS=Homo sapiens GN=CER1 PE=1 SV=1

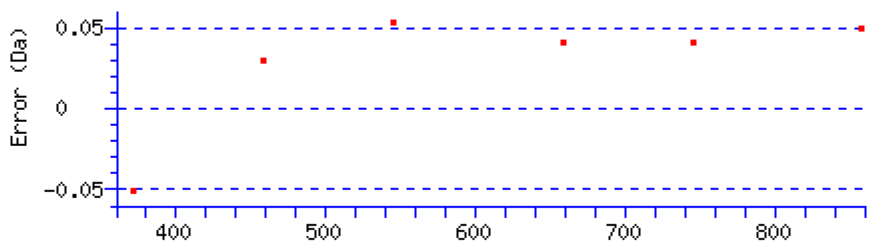
Match to Query 46653: 1867.987302 from(623.669710,3+) rtinseconds(3168) index(40925)
Title: Locus:1.1.1.2701.15
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

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 ●

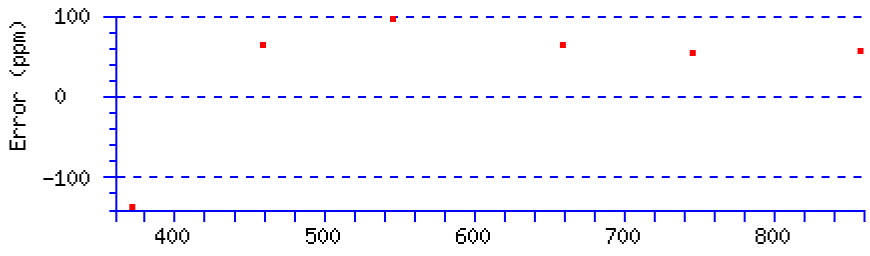


Monoisotopic mass of neutral peptide Mr(calc): 1867.986404
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P8 : Oxidation (P)
P12 : Oxidation (P)
Ions Score: 30 **Expect:** 0.0081
Matches : 6/156 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							16
2	243.108781	122.058029	226.082232	113.544754			N	1740.935121	870.971198	1723.908572	862.457924	1722.924556	861.965916	15
3	***371.167359***	186.087318	354.140810	177.574043			Q	1626.892194	813.949735	1609.865645	805.436460	1608.881629	804.944452	14
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	S	1498.833616	749.920446	1481.807067	741.407172	1480.823051	740.915163	13
5	***545.231415***	273.119346	528.204866	264.606071	527.220850	264.114063	S	1411.801588	706.404432	1394.775039	697.891157	1393.791023	697.399149	12
6	***658.315479***	329.661378	641.288930	321.148103	640.304914	320.656095	L	1324.769560	662.888418	1307.743011	654.375144	1306.758995	653.883135	11
7	***745.347507***	373.177392	728.320958	364.664117	727.336942	364.172109	S	1211.685496	606.346386	1194.658947	597.833111	1193.674931	597.341103	10
8	***858.395186***	429.701231	841.368637	421.187957	840.384621	420.695949	P	1124.653468	562.830372	1107.626919	554.317097			9
9	957.463600	479.235438	940.437051	470.722164	939.453035	470.230156	V	1011.605789	506.306532	994.579240	497.793258			8
10	1070.547664	535.777470	1053.521115	527.264196	1052.537099	526.772187	L	912.537375	456.772325	895.510826	448.259051			7
11	1183.631728	592.319502	1166.605179	583.806227	1165.621163	583.314219	L	799.453311	400.230294	782.426762	391.717019			6
12	1296.679407	648.843341	1279.652858	640.330067	1278.668842	639.838059	P	686.369247	343.688262	669.342698	335.174987			5
13	1452.780518	726.893897	1435.753969	718.380622	1434.769953	717.888614	R	573.321568	287.164422	556.295019	278.651148			4
14	1566.823445	783.915360	1549.796896	775.402086	1548.812880	774.910078	N	417.220457	209.113867	400.193908	200.600592			3
15	1694.882023	847.944649	1677.855474	839.431375	1676.871458	838.939367	Q	303.177530	152.092403	286.150981	143.579129			2
16							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 83 ppm



RMS error 83 ppm

NCBI **BLAST** search of QNQSSLSPVLLPRNQR
(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	1867.986404	0.000898	QNQSSLSPVLLPRNQR
12.4	1867.982544	0.004758	SMLLSNPHDLSLLKER
12.4	1867.982544	0.004758	SMLLSNPHDLSLLKER
10.1	1867.994446	-0.007144	IPASWTNPSGKYHIGIK
3.0	1867.986420	0.000882	SGPGSGSVNRIAKPSPGIR
2.0	1868.005676	-0.018374	LEHSLYKPQKGLFHR
1.6	1868.000305	-0.013003	QSEPLEITLLAPERTR
0.4	1867.986420	0.000882	SGPGSGSVNRIAKPSPGIR

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

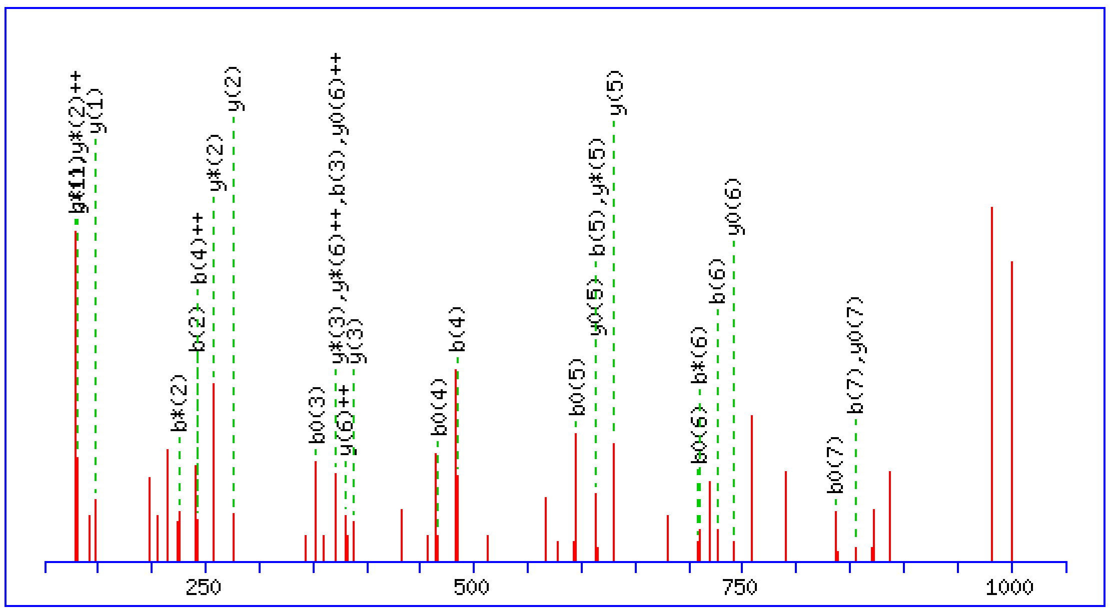
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLELEIKK**
Found in **CHM2B_HUMAN**, Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1

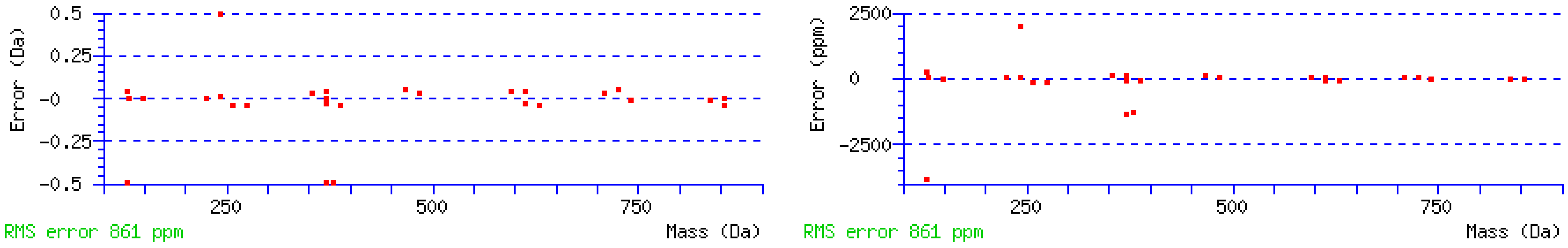
Match to Query 3582: 999.595448 from(500.805000,2+) rtinseconds(1638) index(1154)
Title: Locus:1.1.1.2932.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

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: 37 **Expect:** 0.0014
Matches : 30/74 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	***129.065854***	65.036565	112.039305	56.523291			**Q**							8
2	***242.149918***	121.578597	225.123369	113.065323			**L**	872.545145	436.776211	855.518596	428.262936	854.534580	427.770928	7
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	759.461081	380.234179	742.434532	371.720904	741.450516	371.228896	6
4	***484.276575***	242.641926	467.250026	234.128651	466.266010	233.636643	**L**	**630.418488**	315.712882	613.391939	307.199608	612.407923	306.707600	5
5	***613.319168***	307.163222	596.292619	298.649948	595.308603	298.157940	**E**	517.334424	259.170850	500.307875	250.657576	499.323859	250.165568	4
6	***726.403232***	363.705254	709.376683	355.191980	708.392667	354.699972	**I**	**388.291831**	194.649554	371.265282	186.136279			3
7	***854.498195***	427.752736	837.471646	419.239461	836.487630	418.747453	**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 QLELEIKK
(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	999.596405	-0.000957	QLELEIKK
36.4	999.596405	-0.000957	IEKELLQK
35.2	999.596405	-0.000957	ELKELIQK
33.9	999.596405	-0.000957	EQLELLKK
24.1	999.596405	-0.000957	LQELEKIK
22.2	999.596405	-0.000957	EKEILQIK
21.5	999.596436	-0.000988	GITVPEKLK
21.2	999.596405	-0.000957	ELQILKEK
18.6	999.596405	-0.000957	LQELKIEK
14.2	999.596405	-0.000957	LQLEEKLK

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

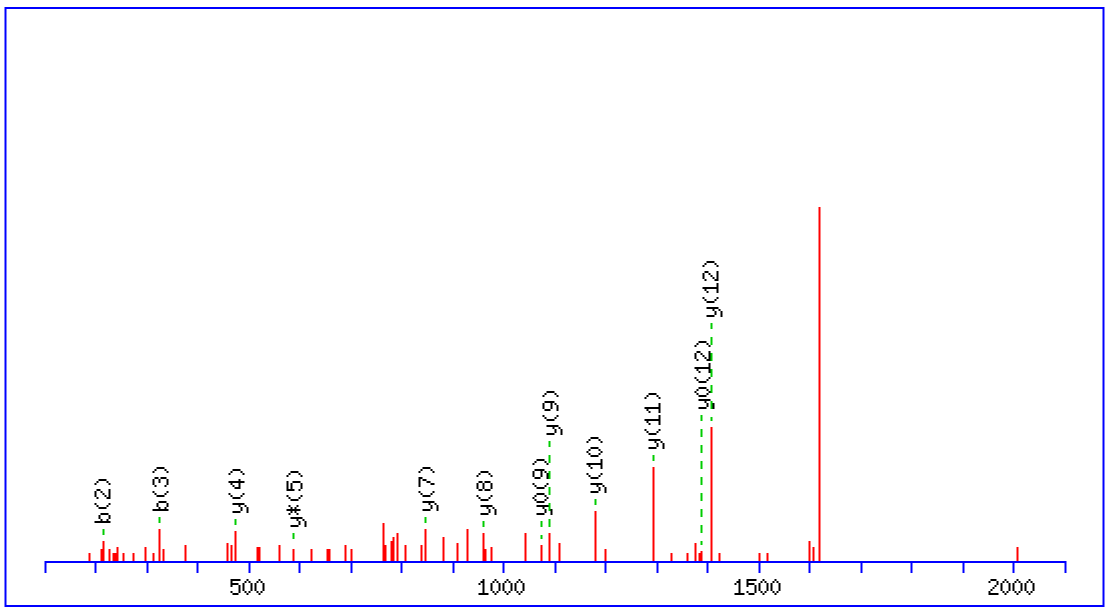
{MATRIX SCIENCE} Mascot Search Results

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

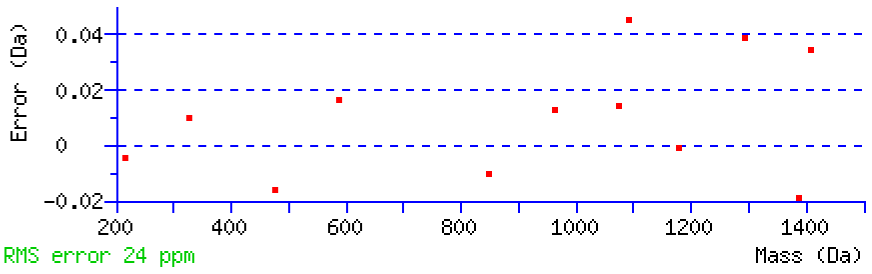
Match to Query 45360: 1618.770948 from(810.392750,2+) rtinseconds(2887) index(37016)
Title: Locus:1.1.1.2497.41
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

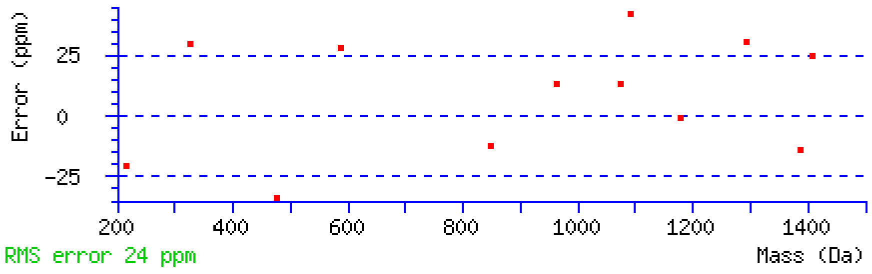
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1618.757339
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.00086
Matches : 12/148 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	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
34.1	1618.757339	0.013609	NVLDSEDEIEELSK
1.5	1618.766113	0.004835	SPFEVQVGPEAGMQK

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

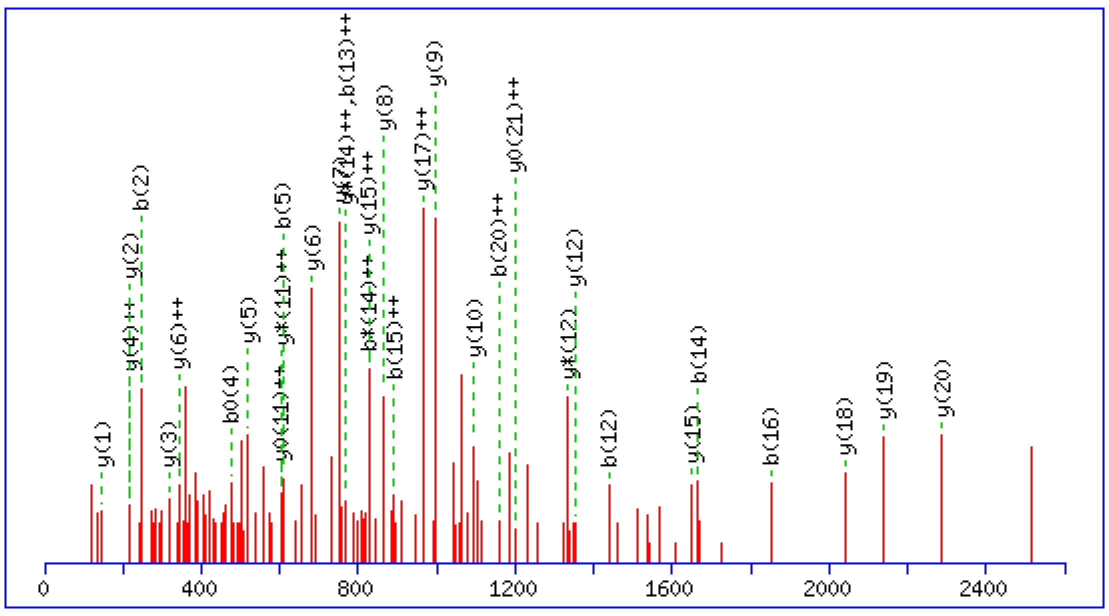
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DEFTNTCPSDKEVEIAYSDVAK**
Found in **CLIC4_HUMAN**, Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4

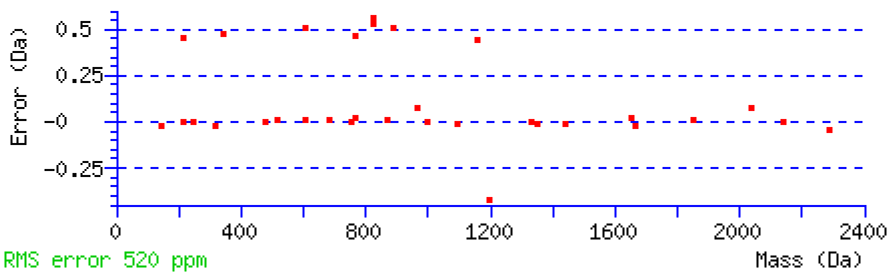
Match to Query 61916: 2531.136432 from(844.719420,3+) rtinseconds(2847) index(36742)
Title: Locus:1.1.1.2525.47
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

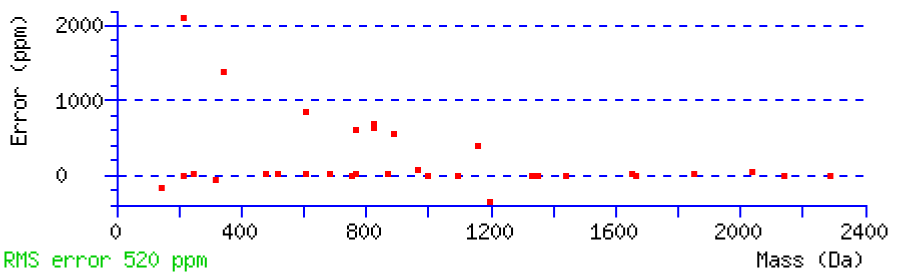
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2531.137344
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.6e-007
Matches : 33/238 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	116.034219	58.520748			98.023654	49.515465	D							22
2	**245.076812**	123.042044			227.066247	114.036762	E	2417.117699	1209.062487	2400.091150	1200.549213	2399.107134	1200.057205	21
3	392.145226	196.576251			374.134661	187.570969	F	***2288.075106***	1144.541191	2271.048557	1136.027916	2270.064541	1135.535908	20
4	493.192905	247.100091			475.182340	238.094808	T	***2141.006692***	1071.006984	2123.980143	1062.493709	2122.996127	1062.001701	19
5	**607.235832**	304.121554	590.209283	295.608280	589.225267	295.116272	N	***2039.959013***	1020.483145	2022.932464	1011.969870	2021.948448	1011.477862	18
6	708.283511	354.645394	691.256962	346.132119	690.272946	345.640111	T	1925.916086	963.461681	1908.889537	954.948407	1907.905521	954.456398	17
7	882.329810	441.668543	865.303261	433.155269	864.319245	432.663261	C	1824.868407	912.937841	1807.841858	904.424567	1806.857842	903.932559	16
8	979.382574	490.194925	962.356025	481.681651	961.372009	481.189643	P	***1650.822108***	825.914692	1633.795559	817.401418	1632.811543	816.909410	15
9	1066.414602	533.710939	1049.388053	525.197665	1048.404037	524.705657	S	1553.769344	777.388310	1536.742795	768.875036	1535.758779	768.383028	14
10	1181.441545	591.224411	1164.414996	582.711136	1163.430980	582.219128	D	1466.737316	733.872296	1449.710767	725.359022	1448.726751	724.867013	13
11	1309.536508	655.271892	1292.509959	646.758618	1291.525943	646.266610	K	***1351.710373***	676.358824	1334.683824	667.845550	1333.699808	667.353542	12
12	**1438.579101**	719.793189	1421.552552	711.279914	1420.568536	710.787906	E	1223.615410	612.311343	1206.588861	603.798069	1205.604845	603.306060	11
13	1537.647515	**769.327396**	1520.620966	760.814121	1519.636950	760.322113	V	***1094.572817***	547.790047	1077.546268	539.276772	1076.562252	538.784764	10
14	**1666.690108**	833.848692	1649.663559	825.335418	1648.679543	824.843410	E	***995.504403***	498.255839	978.477854	489.742565	977.493838	489.250557	9
15	1779.774172	**890.390724**	1762.747623	881.877450	1761.763607	881.385441	I	***866.461810***	433.734543	849.435261	425.221269	848.451245	424.729261	8
16	**1850.811286**	925.909281	1833.784737	917.396007	1832.800721	916.903998	A	***753.377746***	377.192511	736.351197	368.679237	735.367181	368.187229	7
17	2013.874615	1007.440946	1996.848066	998.927671	1995.864050	998.435663	Y	***682.340632***	341.673954	665.314083	333.160680	664.330067	332.668672	6
18	2100.906643	1050.956959	2083.880094	1042.443685	2082.896078	1041.951677	S	***519.277303***	260.142290	502.250754	251.629015	501.266738	251.137007	5
19	2215.933586	1108.470431	2198.907037	1099.957156	2197.923021	1099.465148	D	432.245275	216.626275	415.218726	208.113001	414.234710	207.620993	4
20	2315.002000	**1158.004638**	2297.975451	1149.491363	2296.991435	1148.999355	V	***317.218332***	159.112804	300.191783	150.599530			3
21	2386.039114	1193.523195	2369.012565	1185.009920	2368.028549	1184.517912	A	***218.149918***	109.578597	201.123369	101.065323			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.0	2531.137344	-0.000912	DEFTNTCPSDKEVEIAYSDVAK
5.2	2531.157288	-0.020856	DEFSYQEMIANLPLCSHPNPR

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

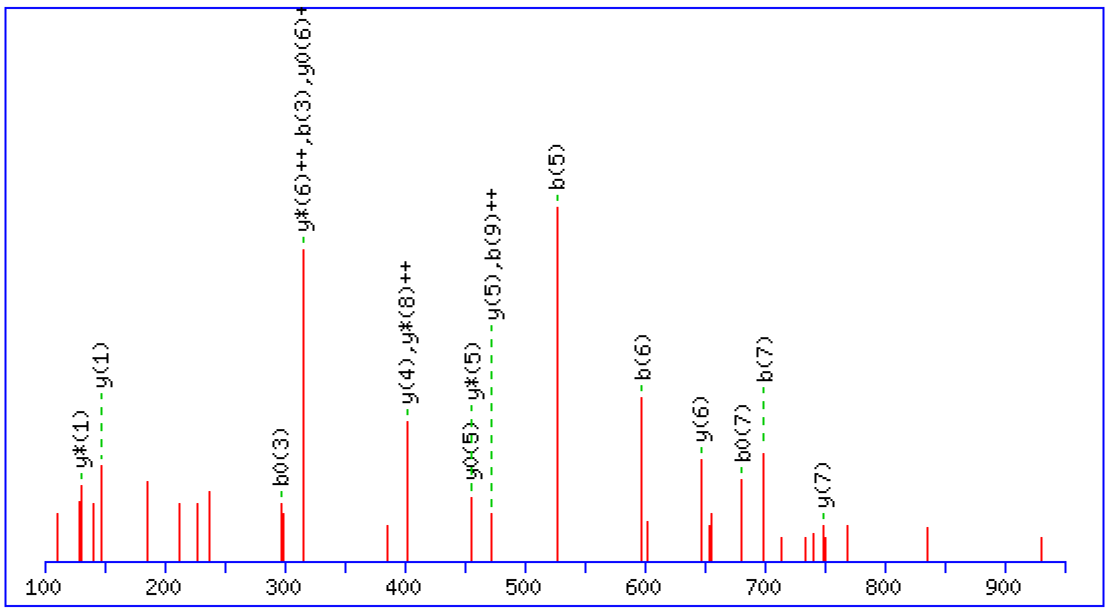
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASRPDATCASPAK**
Found in **CHAD_HUMAN**, Chondroadherin OS=Homo sapiens GN=CHAD PE=2 SV=2

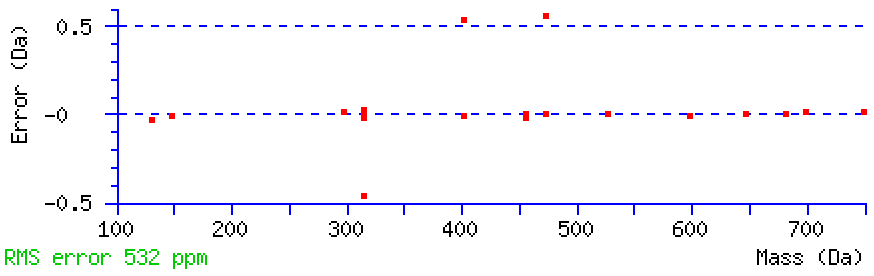
Match to Query 32284: 1344.640182 from(449.220670,3+) rtinseconds(799) index(845)
Title: Locus:1.1.1.1687.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

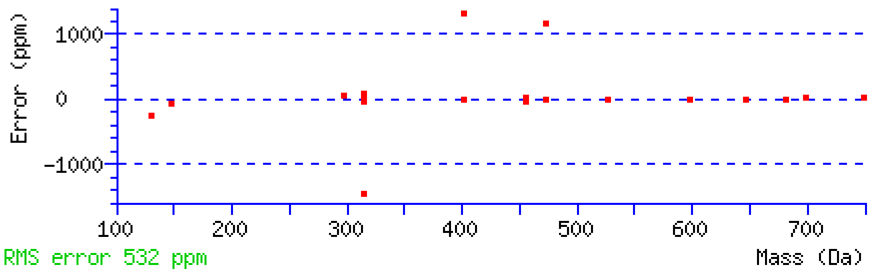
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1344.645569
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0023
Matches : 19/132 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							13
2	159.076418	80.041847			141.065853	71.036564	S	1274.615762	637.811519	1257.589213	629.298245	1256.605197	628.806237	12
3	**315.177529**	158.092402	298.150980	149.579128	297.166964	149.087120	R	1187.583734	594.295505	1170.557185	585.782231	1169.573169	585.290223	11
4	412.230293	206.618785	395.203744	198.105510	394.219728	197.613502	P	1031.482623	516.244950	1014.456074	507.731675	1013.472058	507.239667	10
5	**527.257236**	264.132256	510.230687	255.618982	509.246671	255.126974	D	934.429859	467.718568	917.403310	459.205293	916.419294	458.713285	9
6	**598.294350**	299.650813	581.267801	291.137539	580.283785	290.645531	A	819.402916	410.205096	802.376367	401.691822	801.392351	401.199814	8
7	**699.342029**	350.174653	682.315480	341.661378	681.331464	341.169370	T	***748.365802***	374.686539	731.339253	366.173265	730.355237	365.681257	7
8	873.388328	437.197802	856.361779	428.684528	855.377763	428.192520	C	***647.318123***	324.162700	630.291574	315.649425	629.307558	315.157417	6
9	944.425442	472.716359	927.398893	464.203084	926.414877	463.711076	A	***473.271824***	237.139550	456.245275	228.626276	455.261259	228.134268	5
10	1031.457470	516.232373	1014.430921	507.719099	1013.446905	507.227091	S	***402.234710***	201.620993	385.208161	193.107719	384.224145	192.615711	4
11	1128.510234	564.758755	1111.483685	556.245481	1110.499669	555.753473	P	***315.202682***	158.104979	298.176133	149.591704			3
12	1199.547348	600.277312	1182.520799	591.764038	1181.536783	591.272030	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 ASRPDATCASPAK
(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	1344.645569	-0.005387	ASRPDATCASPAK
8.3	1344.627121	0.013061	SMYLDIEYAPK
6.9	1344.626953	0.013229	NSPSPGGKEAETR
4.0	1344.634354	0.005828	VACKSSQPDPDK
0.2	1344.645584	-0.005402	KSVSHNMTAPNK

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

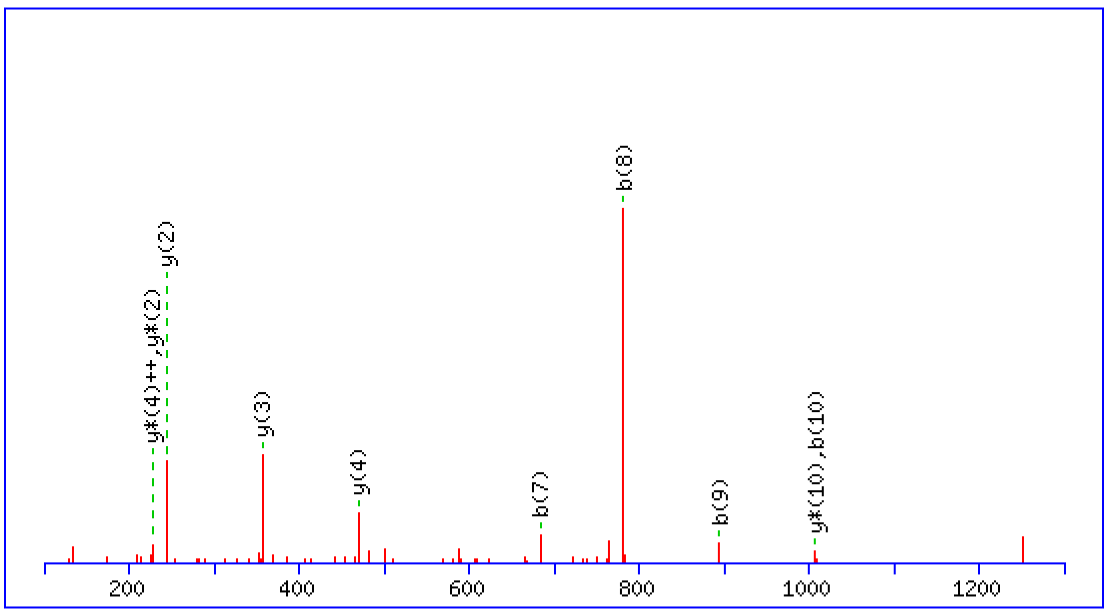
{MATRIX SCIENCE} Mascot Search Results

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

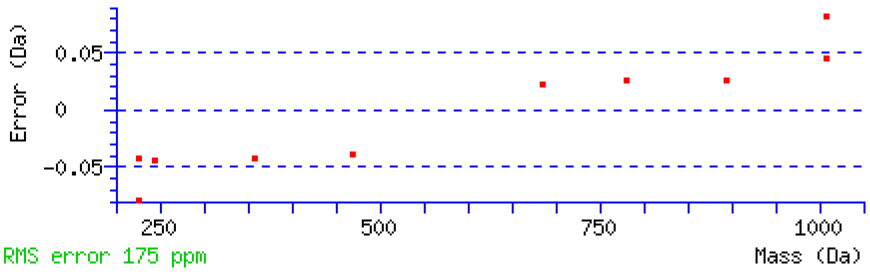
Match to Query 28359: 1249.645188 from(625.829870,2+) rtinseconds(1862) index(17897)
Title: Locus:1.1.1.2200.40
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

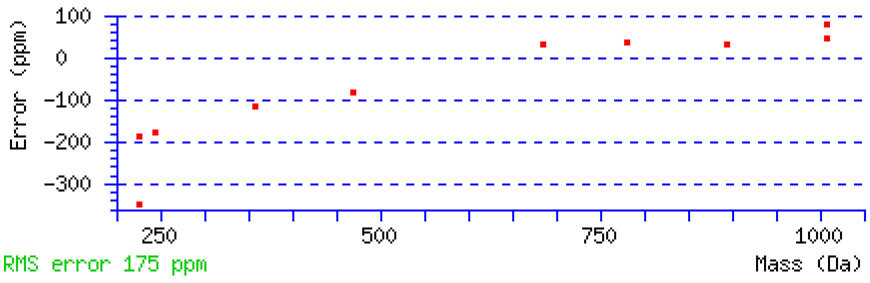
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1249.655426
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 45  Expect: 0.00043
Matches : 11/92 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							12
2	*227.139019*	114.073147			P	1137.578632	569.292954	1120.552083	560.779680	1119.568067	560.287672	11
3	284.160483	142.583879			G	1024.530953	512.769115	1007.504404	504.255840	1006.520388	503.763832	10
4	381.213247	191.110261			P	967.509489	484.258383	950.482940	475.745108	949.498924	475.253100	9
5	468.245275	234.626275	450.234710	225.620993	S	870.456725	435.732001	853.430176	427.218726	852.446160	426.726718	8
6	583.272218	292.139747	565.261653	283.134464	D	783.424697	392.215987	766.398148	383.702712	765.414132	383.210704	7
7	*684.319897*	342.663587	666.309332	333.658304	T	668.397754	334.702515	651.371205	326.189241	650.387189	325.697233	6
8	*781.372661*	391.189969	763.362096	382.184686	P	567.350075	284.178676	550.323526	275.665401			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
50.6	1249.641479	0.003709	DQLLPPSPNNR
44.6	1249.655426	-0.010238	LPGPSDTPILPQ
33.5	1249.655426	-0.010238	LPGPSDTPILPQ
33.5	1249.655426	-0.010238	LPGPSDTPILPQ
9.2	1249.652756	-0.007568	KGPGPGGPGGAGVAR
5.3	1249.652756	-0.007568	KGPGPGGPGGAGVAR
4.8	1249.652908	-0.007720	WMVFKGEIPK
3.2	1249.656754	-0.011566	GKPHFTLEGHK
2.5	1249.652710	-0.007522	LPRSEKPHDR
1.0	1249.633636	0.011552	VLVASATMDTAR

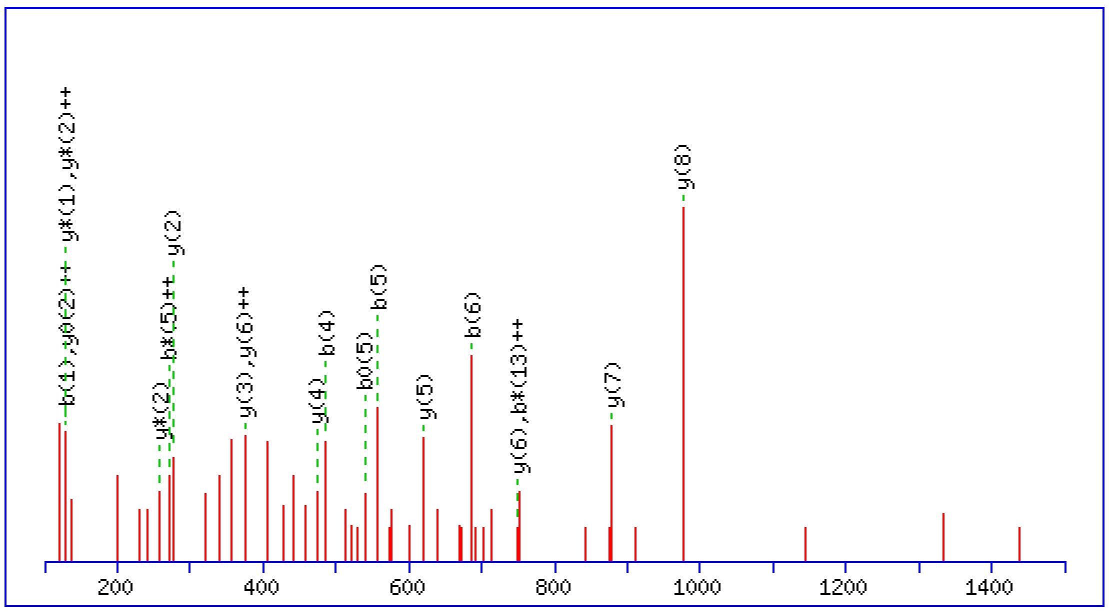
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVEEAEPEEFVVEK**
Found in **CBX3_HUMAN**, Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4

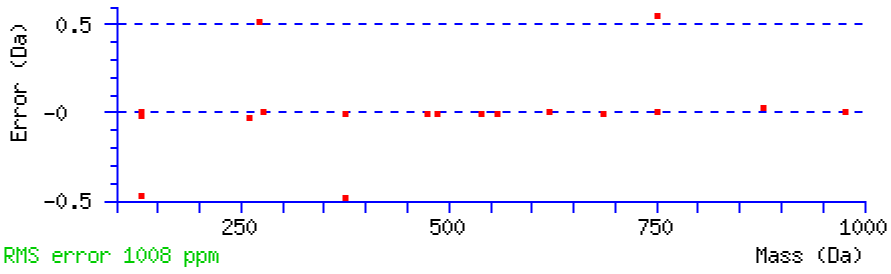
Match to Query 33448: 1660.819272 from(554.613700,3+) rtinseconds(2088) index(14304)
Title: Locus:1.1.1.2293.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

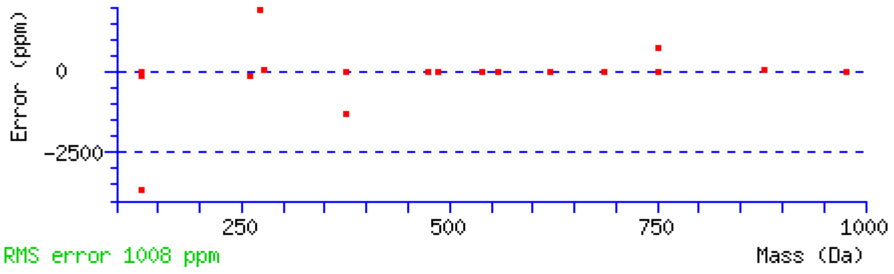
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1660.819550
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00029
Matches : 19/150 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	***129.102239***	65.054757	112.075690	56.541483			K							14
2	228.170653	114.588965	211.144104	106.075690			V	1533.731896	767.369586	1516.705347	758.856312	1515.721331	758.364304	13
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	1434.663482	717.835379	1417.636933	709.322105	1416.652917	708.830097	12
4	***486.255839***	243.631558	469.229290	235.118283	468.245274	234.626275	E	1305.620889	653.314083	1288.594340	644.800808	1287.610324	644.308800	11
5	***557.292953***	279.150115	540.266404	270.636840	539.282388	270.144832	A	1176.578296	588.792786	1159.551747	580.279512	1158.567731	579.787504	10
6	***686.335546***	343.671411	669.308997	335.158137	668.324981	334.666129	E	1105.541182	553.274229	1088.514633	544.760955	1087.530617	544.268947	9
7	783.388310	392.197793	766.361761	383.684519	765.377745	383.192511	P	***976.498589***	488.752933	959.472040	480.239658	958.488024	479.747650	8
8	912.430903	456.719090	895.404354	448.205815	894.420338	447.713807	E	***879.445825***	440.226551	862.419276	431.713276	861.435260	431.221268	7
9	1041.473496	521.240386	1024.446947	512.727112	1023.462931	512.235104	E	***750.403232***	375.705254	733.376683	367.191980	732.392667	366.699972	6
10	1188.541910	594.774593	1171.515361	586.261319	1170.531345	585.769311	F	***621.360639***	311.183958	604.334090	302.670683	603.350074	302.178675	5
11	1287.610324	644.308800	1270.583775	635.795526	1269.599759	635.303518	V	***474.292225***	237.649751	457.265676	229.136476	456.281660	228.644468	4
12	1386.678738	693.843007	1369.652189	685.329733	1368.668173	684.837725	V	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
13	1515.721331	758.364304	1498.694782	749.851029	1497.710766	749.359021	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





NCBI **BLAST** search of KVEEAEPEEFVVEK
(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	1660.819550	-0.000278	KVEEAEPEEFVVEK
3.4	1660.813034	0.006238	EQMSESILSFHIPK
2.0	1660.813034	0.006238	EQMSESILSFHIPK
1.6	1660.813019	0.006253	YLGEMEPPALPREK
0.1	1660.820938	-0.001666	ITSGNPQGFFSIHPK

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

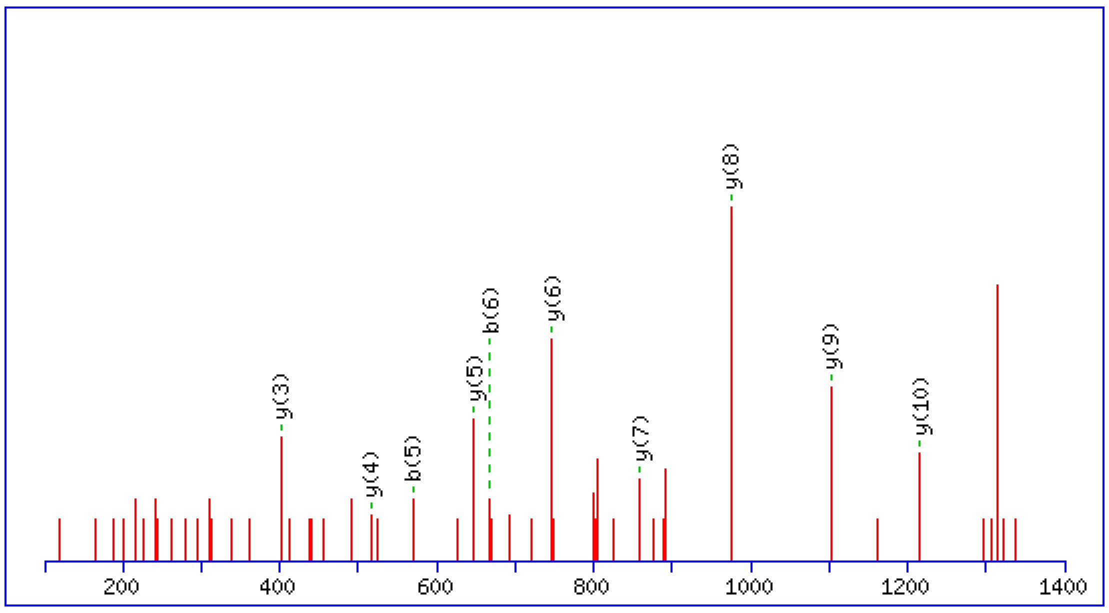
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLQDLVMDILR**
Found in **COPB_HUMAN**, Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3

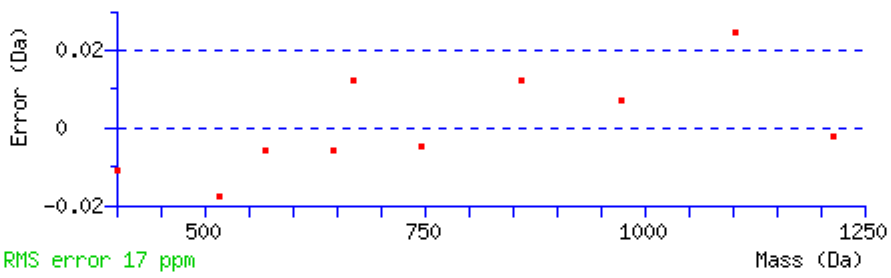
Match to Query 22957: 1313.740408 from(657.877480,2+) rtinseconds(4191) index(54133)
Title: Locus:1.1.1.3529.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

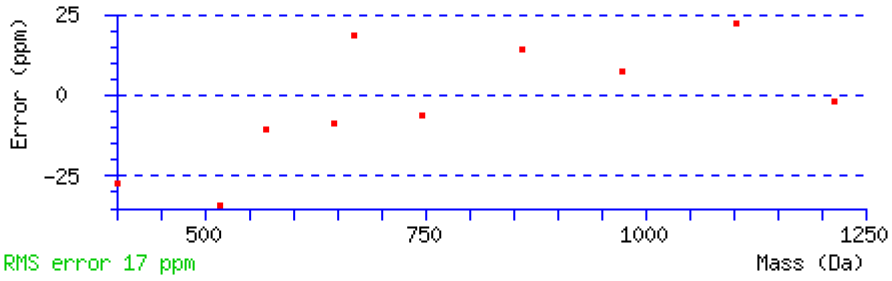
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1313.737701
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 4.8e-005
Matches : 10/104 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	100.075690	50.541483					V							11
2	213.159754	107.083515					L	***1215.676571***	608.341923	1198.650022	599.828649	1197.666006	599.336641	10
3	341.218332	171.112804	324.191783	162.599529			Q	***1102.592507***	551.799891	1085.565958	543.286617	1084.581942	542.794609	9
4	456.245275	228.626275	439.218726	220.113001	438.234710	219.620993	D	***974.533929***	487.770602	957.507380	479.257328	956.523364	478.765320	8
5	**569.329339**	285.168308	552.302790	276.655033	551.318774	276.163025	L	***859.506986***	430.257131	842.480437	421.743856	841.496421	421.251848	7
6	**668.397753**	334.702515	651.371204	326.189240	650.387188	325.697232	V	***746.422922***	373.715099	729.396373	365.201824	728.412357	364.709816	6
7	799.438238	400.222757	782.411689	391.709482	781.427673	391.217474	M	***647.354508***	324.180892	630.327959	315.667617	629.343943	315.175609	5
8	914.465181	457.736228	897.438632	449.222954	896.454616	448.730946	D	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	4
9	1027.549245	514.278260	1010.522696	505.764986	1009.538680	505.272978	I	***401.287080***	201.147178	384.260531	192.633903			3
10	1140.633309	570.820292	1123.606760	562.307018	1122.622744	561.815010	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 VLQDLVMDILR
(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	1313.737701	0.002707	VLQDLVMDILR

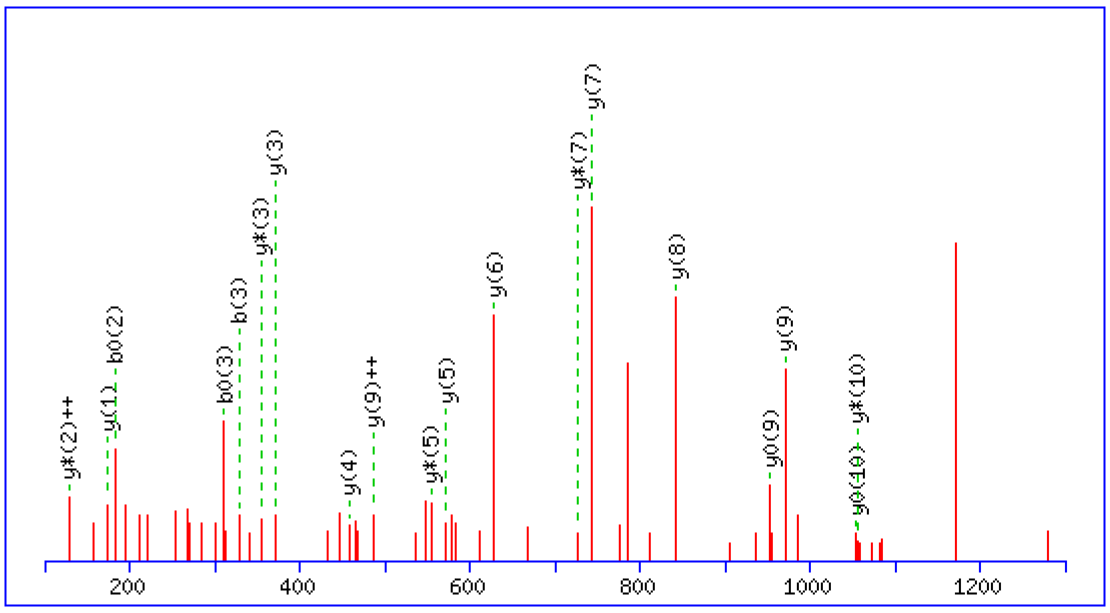
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTQVDGNSPVR**
Found in **COPD_HUMAN**, Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1

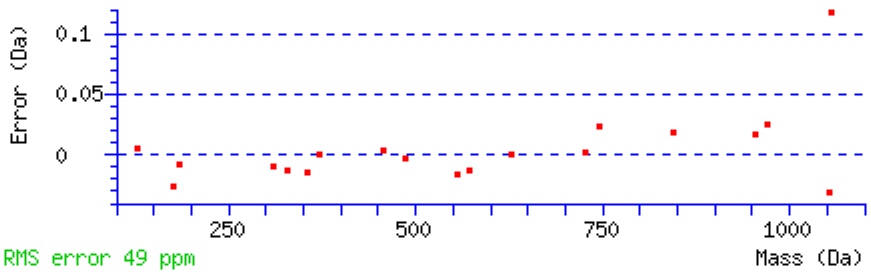
Match to Query 15450: 1170.600308 from(586.307430,2+) rtinseconds(1121) index(6495)
Title: Locus:1.1.1.1904.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

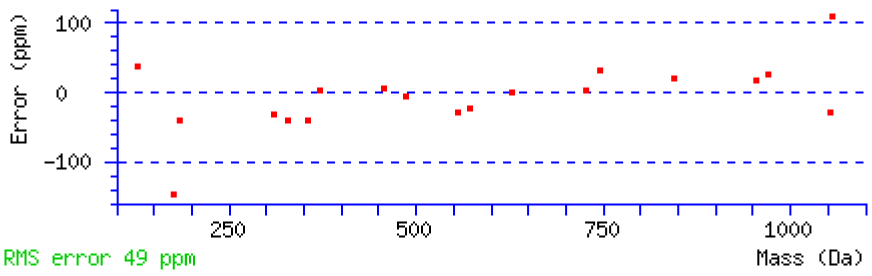
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1170.599319`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 45  Expect: 0.0002`
`Matches : 19/108 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	100.075690	50.541483					V							11
2	201.123369	101.065322			183.112804	92.060040	T	1072.538163	536.772719	1055.511614	528.259445	1054.527598	527.767437	10
3	329.181947	165.094611	312.155398	156.581337	311.171382	156.089329	Q	***971.490484***	486.248880	954.463935	477.735606	953.479919	477.243598	9
4	428.250361	214.628818	411.223812	206.115544	410.239796	205.623536	V	***843.431906***	422.219591	826.405357	413.706317	825.421341	413.214309	8
5	543.277304	272.142290	526.250755	263.629016	525.266739	263.137008	D	***744.363492***	372.685384	727.336943	364.172109	726.352927	363.680101	7
6	600.298768	300.653022	583.272219	292.139748	582.288203	291.647740	G	***629.336549***	315.171913	612.310000	306.658638	611.325984	306.166630	6
7	714.341695	357.674486	697.315146	349.161211	696.331130	348.669203	N	***572.315085***	286.661181	555.288536	278.147906	554.304520	277.655898	5
8	801.373723	401.190500	784.347174	392.677225	783.363158	392.185217	S	***458.272158***	229.639717	441.245609	221.126442	440.261593	220.634434	4
9	898.426487	449.716882	881.399938	441.203607	880.415922	440.711599	P	***371.240130***	186.123703	354.213581	177.610428			3
10	997.494901	499.251089	980.468352	490.737814	979.484336	490.245806	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 VTQVDGNSPVR
(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	1170.599319	0.000989	VTQVDGNSPVR
5.0	1170.599289	0.001019	AEAGPLGVAGSAR
4.8	1170.606689	-0.006381	MAPQLIDPVR

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

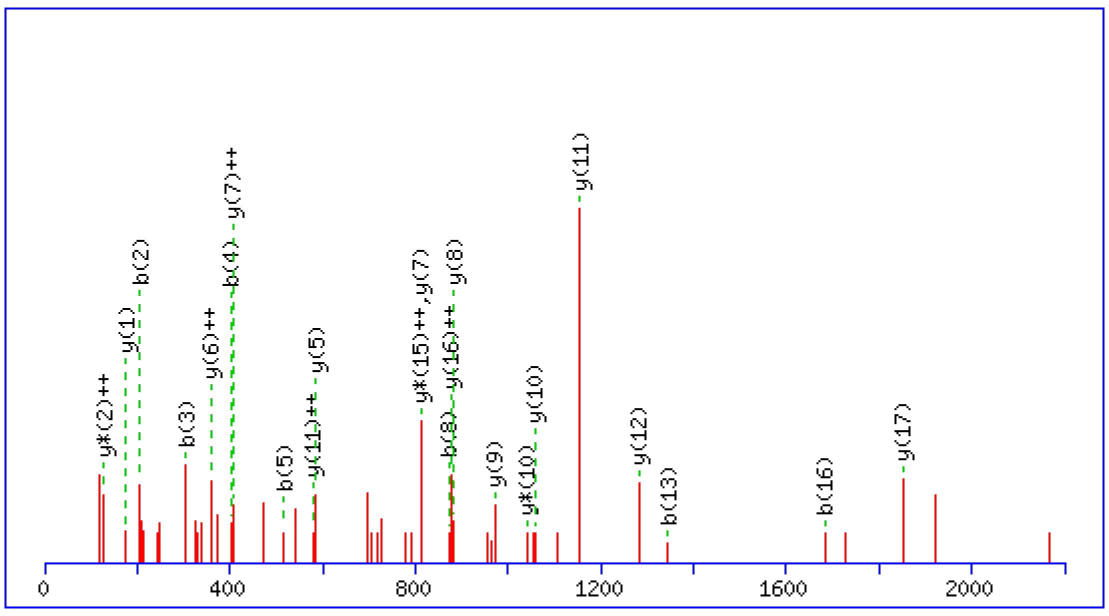
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGVVLDEIKPSSAPELQAVR**
Found in **COPE_HUMAN**, Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3

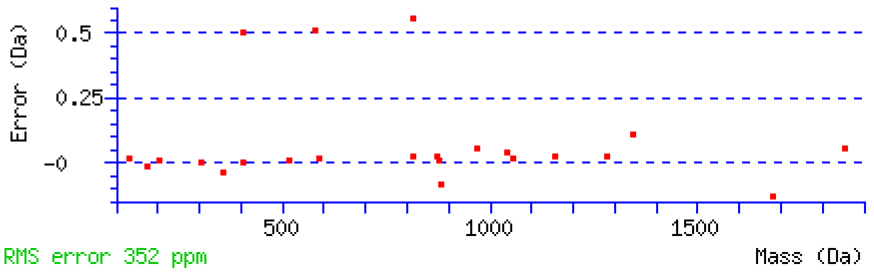
Match to Query 63368: 2154.181092 from(719.067640,3+) rtinseconds(3122) index(41598)
Title: Locus:1.1.1.2678.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

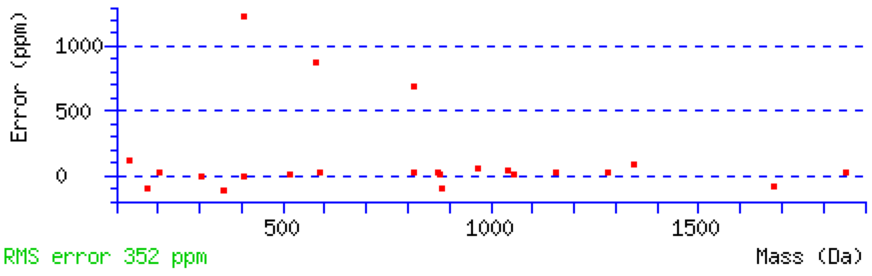
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2154.168457
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 3.9e-005
Matches : 23/192 fragment ions using 47 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							20
2	***205.097154***	103.052215					G	2008.107332	1004.557304	1991.080783	996.044030	1990.096767	995.552022	19
3	***304.165568***	152.586422					V	1951.085868	976.046572	1934.059319	967.533298	1933.075303	967.041290	18
4	***403.233982***	202.120629					V	***1852.017454***	926.512365	1834.990905	917.999091	1834.006889	917.507083	17
5	***516.318046***	258.662661					L	1752.949040	876.978158	1735.922491	868.464884	1734.938475	867.972876	16
6	631.344989	316.176133			613.334424	307.170850	D	1639.864976	820.436126	1622.838427	811.922852	1621.854411	811.430844	15
7	760.387582	380.697429			742.377017	371.692147	E	1524.838033	762.922655	1507.811484	754.409380	1506.827468	753.917372	14
8	***873.471646***	437.239461			855.461081	428.234179	I	1395.795440	698.401358	1378.768891	689.888084	1377.784875	689.396076	13
9	1001.566609	501.286943	984.540060	492.773668	983.556044	492.281660	K	***1282.711376***	641.859326	1265.684827	633.346052	1264.700811	632.854043	12
10	1098.619373	549.813325	1081.592824	541.300050	1080.608808	540.808042	P	***1154.616413***	577.811845	1137.589864	569.298570	1136.605848	568.806562	11
11	1185.651401	593.329339	1168.624852	584.816064	1167.640836	584.324056	S	***1057.563649***	529.285463	1040.537100	520.772188	1039.553084	520.280180	10
12	1272.683429	636.845353	1255.656880	628.332078	1254.672864	627.840070	S	***970.531621***	485.769449	953.505072	477.256174	952.521056	476.764166	9
13	***1343.720543***	672.363910	1326.693994	663.850635	1325.709978	663.358627	A	***883.499593***	442.253435	866.473044	433.740160	865.489028	433.248152	8
14	1440.773307	720.890292	1423.746758	712.377017	1422.762742	711.885009	P	***812.462479***	406.734878	795.435930	398.221603	794.451914	397.729595	7
15	1569.815900	785.411588	1552.789351	776.898314	1551.805335	776.406306	E	715.409715	358.208496	698.383166	349.695221	697.399150	349.203213	6
16	***1682.899964***	841.953620	1665.873415	833.440346	1664.889399	832.948338	L	***586.367122***	293.687199	569.340573	285.173924			5
17	1810.958542	905.982909	1793.931993	897.469635	1792.947977	896.977627	Q	473.283058	237.145167	456.256509	228.631892			4
18	1881.995656	941.501466	1864.969107	932.988192	1863.985091	932.496184	A	345.224480	173.115878	328.197931	164.602603			3
19	1981.064070	991.035673	1964.037521	982.522399	1963.053505	982.030391	V	274.187366	137.597321	257.160817	129.084047			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FGVVLDEIKPSSAPELQAVR
(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	2154.168457	0.012635	FGVVLDEIKPSSAPELQAVR
0.7	2154.175659	0.005433	QVSSSIDLLSIQQPRLSGAR

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

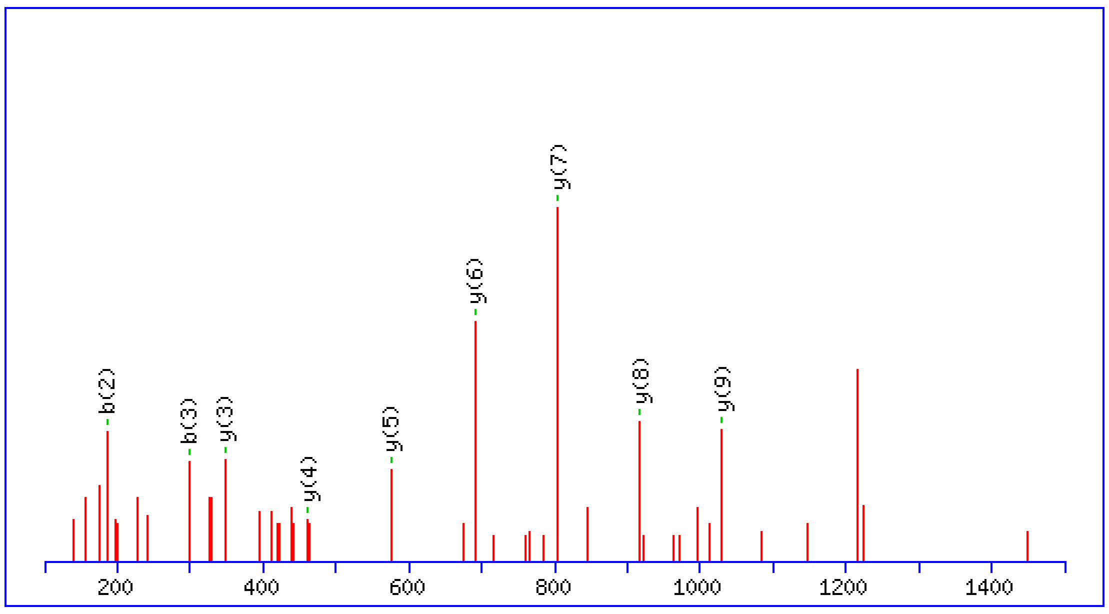
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AILILDNDGDR**
Found in **COPZ1_HUMAN**, Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=1 SV=1

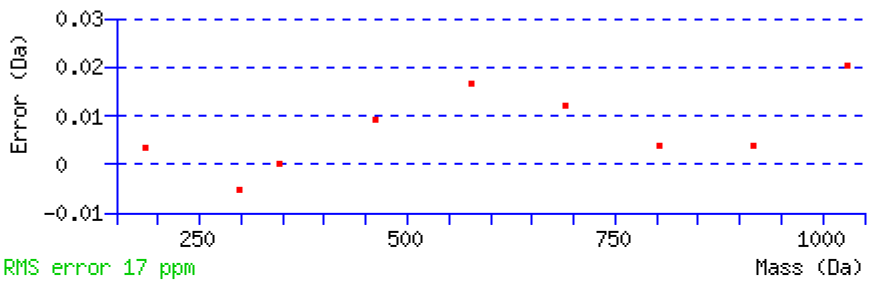
Match to Query 13257: 1213.629248 from(607.821900,2+) rtinseconds(2542) index(16207)
Title: Locus:1.1.1.2553.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

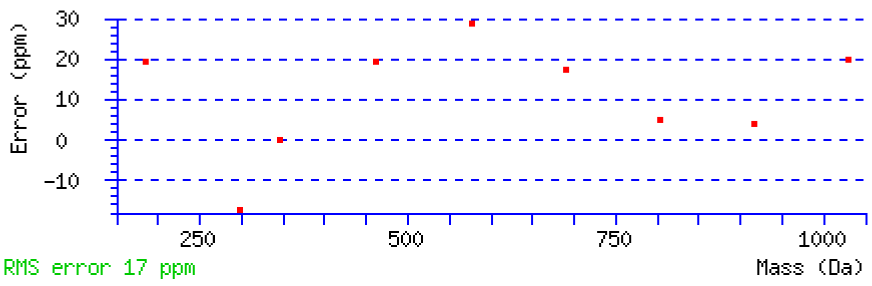
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1213.630249
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 2.4e-006
Matches : 9/96 fragment ions using 11 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					I	1143.600428	572.303852	1126.573879	563.790578	1125.589863	563.298569	10
3	**298.212518**	149.609897					L	***1030.516364***	515.761820	1013.489815	507.248546	1012.505799	506.756538	9
4	411.296582	206.151929					I	***917.432300***	459.219788	900.405751	450.706513	899.421735	450.214505	8
5	524.380646	262.693961					L	***804.348236***	402.677756	787.321687	394.164481	786.337671	393.672473	7
6	639.407589	320.207433			621.397024	311.202150	D	***691.264172***	346.135724	674.237623	337.622449	673.253607	337.130441	6
7	753.450516	377.228896	736.423967	368.715622	735.439951	368.223614	N	***576.237229***	288.622253	559.210680	280.108978	558.226664	279.616970	5
8	868.477459	434.742368	851.450910	426.229093	850.466894	425.737085	D	***462.194302***	231.600789	445.167753	223.087514	444.183737	222.595506	4
9	925.498923	463.253100	908.472374	454.739825	907.488358	454.247817	G	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	3
10	1040.525866	520.766571	1023.499317	512.253296	1022.515301	511.761288	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 AILILDNDGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.9	1213.630249	-0.001001	AILILDNDGDR
4.7	1213.620346	0.008902	APAPFRPASER
1.6	1213.623718	0.005530	KLQSHMDALR
1.6	1213.634918	-0.005670	MAAARAAPAAAAR
1.1	1213.620361	0.008887	ALVSAGNPGAWR

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

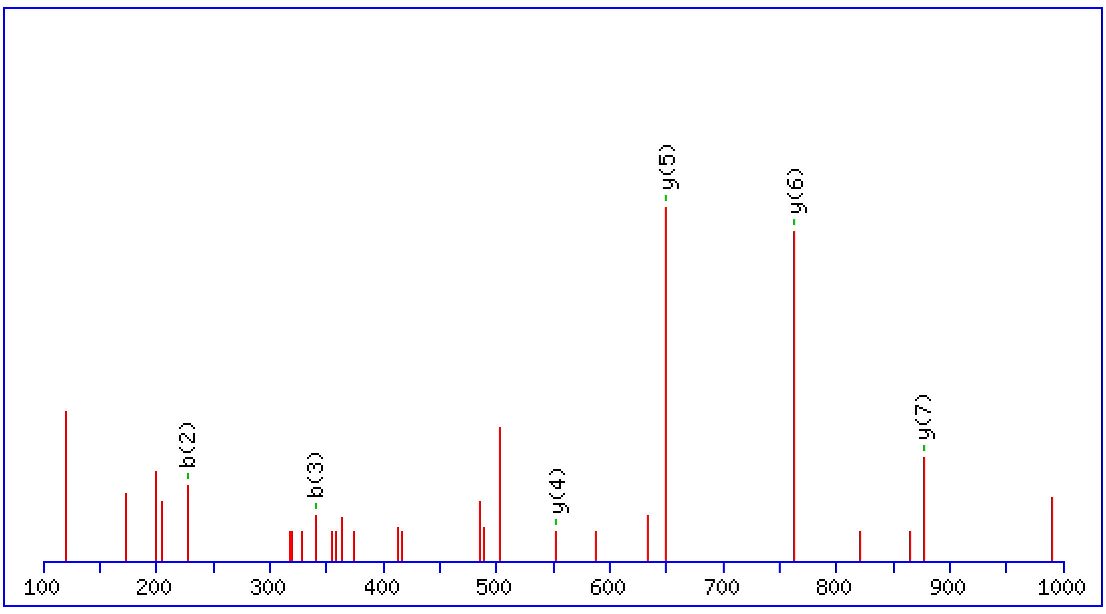
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPLPLHRK**
Found in **CC105_HUMAN**, Coiled-coil domain-containing protein 105 OS=Homo sapiens GN=CCDC105 PE=2 SV=3

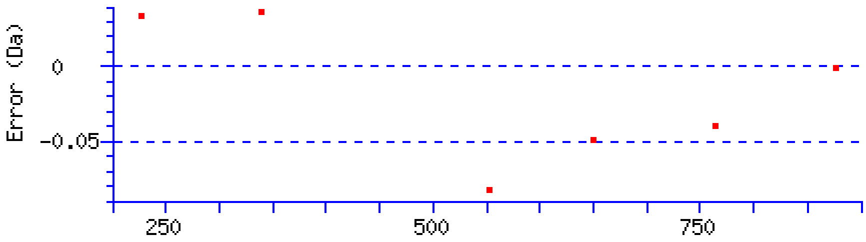
Match to Query 10602: 988.608588 from(495.311570,2+) rtinseconds(3297) index(40332)
Title: Locus:1.1.1.3063.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

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 ●

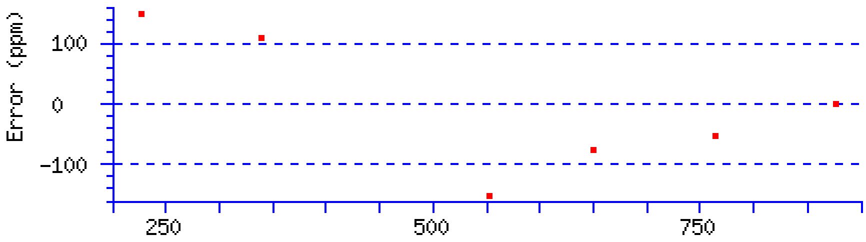


```
Monoisotopic mass of neutral peptide Mr(calc): 988.618164
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 31  Expect: 0.0016
Matches : 6/44 fragment ions using 8 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			L					8
2	**227.139019**	114.073147			P	***876.541398***	438.774337	859.514849	430.261062	7
3	**340.223083**	170.615179			L	***763.493719***	382.250498	746.467170	373.737223	6
4	437.275847	219.141561			P	***650.409655***	325.708465	633.383106	317.195191	5
5	550.359911	275.683594			L	***553.356891***	277.182084	536.330342	268.668809	4
6	687.418823	344.213050			H	440.272827	220.640051	423.246278	212.126777	3
7	843.519934	422.263605	826.493385	413.750330	R	303.213915	152.110595	286.187366	143.597321	2
8					K	147.112804	74.060040	130.086255	65.546765	1



RMS error 104 ppm



RMS error 104 ppm

NCBI **BLAST** search of LPLPLHRK
(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	988.618164	-0.009576	LPLPLHRK
17.7	988.606918	0.001670	ILLLQAYR
10.5	988.606934	0.001654	LLQFISLR
3.5	988.606934	0.001654	GFLGLNKIK
2.0	988.610962	-0.002374	LLGWLLFK
0.5	988.599060	0.009528	LLELMKVK
0.5	988.618164	-0.009576	LLGLVRYR
0.5	988.599060	0.009528	LLVLKMEK
0.5	988.606934	0.001654	LPFSIKIR

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

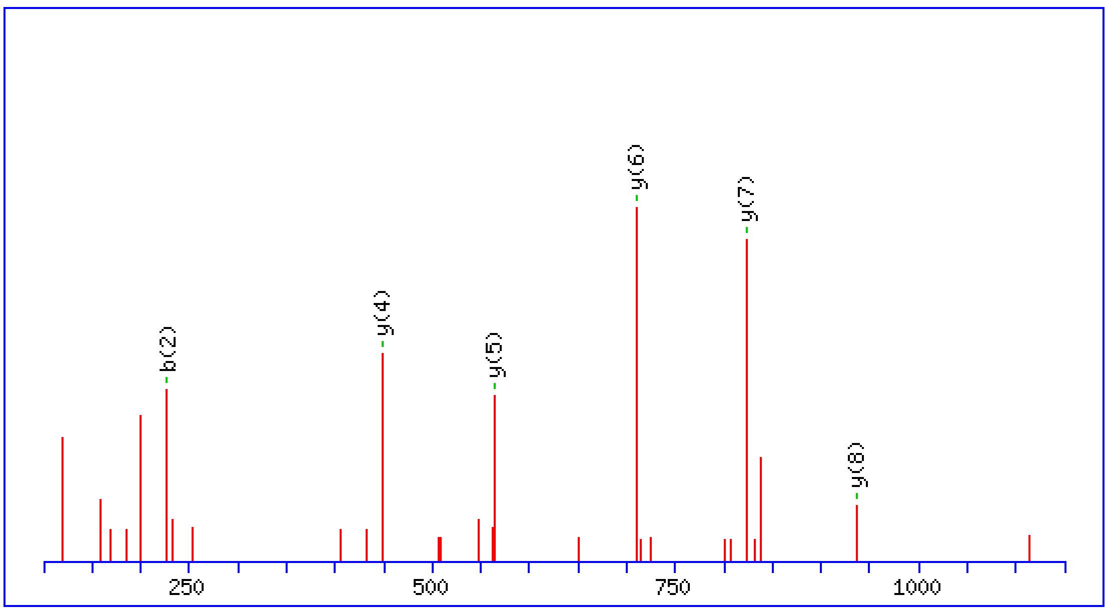
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPIMDTSLK**
Found in **CCD33_HUMAN**, Coiled-coil domain-containing protein 33 OS=Homo sapiens GN=CCDC33 PE=1 SV=3

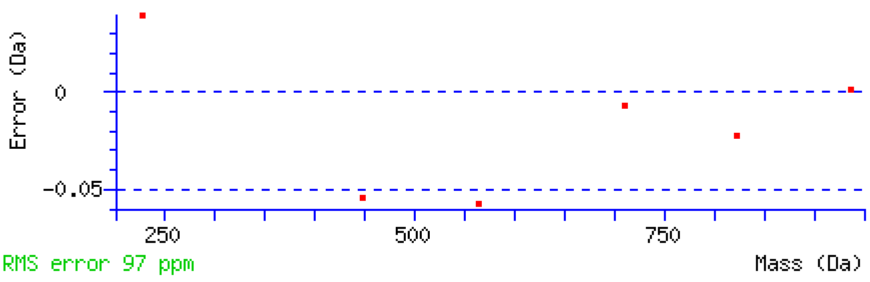
Match to Query 11327: 1048.551928 from(525.283240,2+) rtinseconds(2852) index(30342)
Title: Locus:1.1.1.2733.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

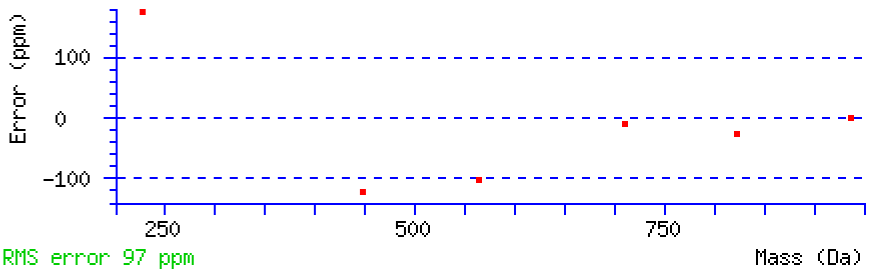
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1048.547440
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
M4      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 35  Expect: 0.0032
Matches : 6/104 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							9
2	227.139019	114.073147			P	***936.470661***	468.738969	919.444112	460.225694	918.460096	459.733686	8
3	340.223083	170.615179			I	***823.422982***	412.215129	806.396433	403.701855	805.412417	403.209847	7
4	487.258483	244.132879			M	***710.338918***	355.673097	693.312369	347.159823	692.328353	346.667815	6
5	602.285426	301.646351	584.274861	292.641069	D	***563.303518***	282.155397	546.276969	273.642123	545.292953	273.150115	5
6	703.333105	352.170191	685.322540	343.164908	T	***448.276575***	224.641926	431.250026	216.128651	430.266010	215.636643	4
7	790.365133	395.686205	772.354568	386.680922	S	347.228896	174.118086	330.202347	165.604812	329.218331	165.112804	3
8	903.449197	452.228237	885.438632	443.222954	L	260.196868	130.602072	243.170319	122.088798			2
9					K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of LPIMDTSLK
(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	1048.547440	0.004488	LPIMDTSLK
12.8	1048.555313	-0.003385	LIPTHPPDK
12.8	1048.555313	-0.003385	LIPTHPPDK
10.8	1048.555313	-0.003385	LPPITYTGR
2.4	1048.555313	-0.003385	LIPTHPPDK
1.5	1048.545425	0.006503	HTTFFGAIR

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

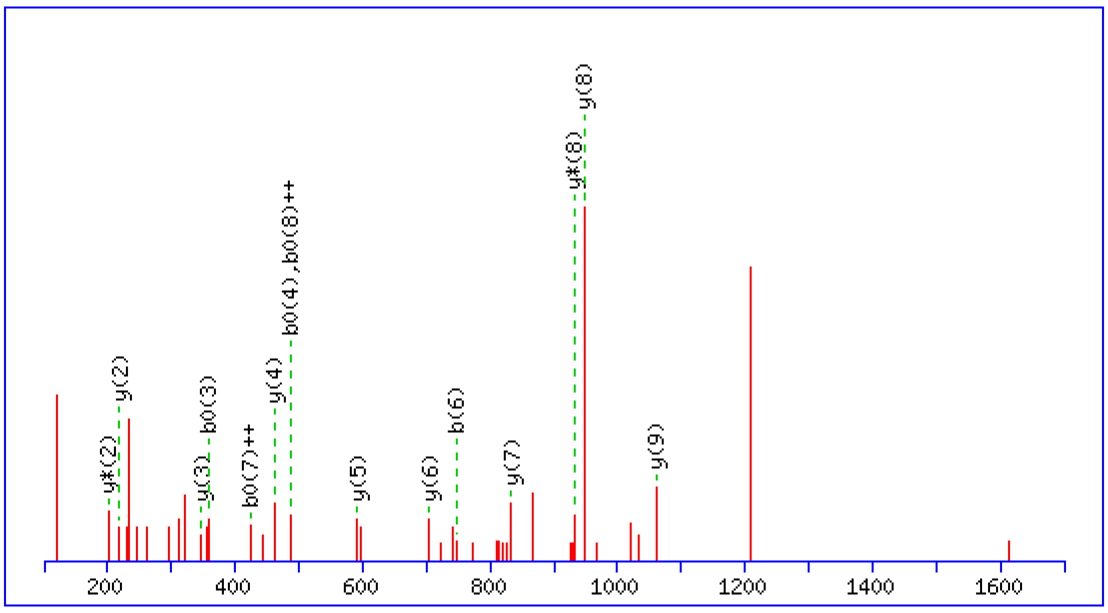
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLDELEDEAK**
Found in **CCD56_HUMAN**, Coiled-coil domain-containing protein 56 OS=Homo sapiens GN=CCDC56 PE=1 SV=1

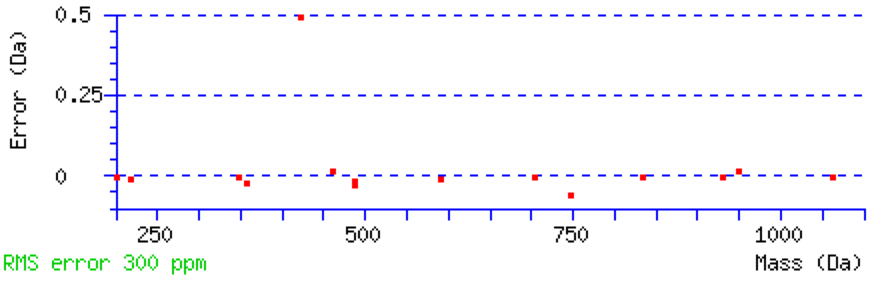
Match to Query 11552: 1207.568548 from(604.791550,2+) rtinseconds(2558) index(8199)
Title: Locus:1.1.1.2992.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

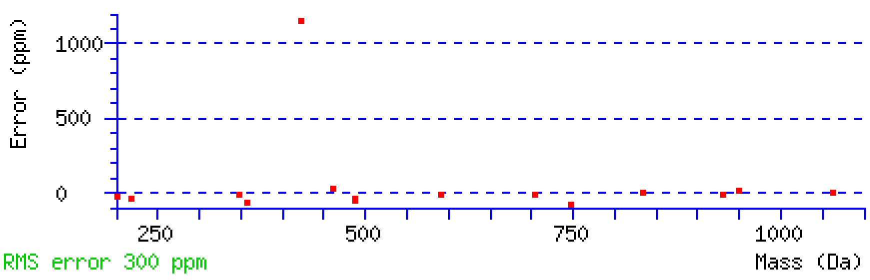
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1207.560822
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0008
Matches : 15/82 fragment ions using 32 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							10
2	261.159754	131.083515			L	***1061.499711***	531.253493	1044.473162	522.740219	1043.489146	522.248211	9
3	376.186697	188.596986	358.176132	179.591704	D	***948.415647***	474.711462	931.389098	466.198187	930.405082	465.706179	8
4	505.229290	253.118283	487.218725	244.113001	E	***833.388704***	417.197990	816.362155	408.684715	815.378139	408.192707	7
5	618.313354	309.660315	600.302789	300.655033	L	***704.346111***	352.676694	687.319562	344.163419	686.335546	343.671411	6
6	747.355947	374.181612	729.345382	365.176329	E	***591.262047***	296.134662	574.235498	287.621387	573.251482	287.129379	5
7	862.382890	431.695083	844.372325	422.689800	D	***462.219454***	231.613365	445.192905	223.100090	444.208889	222.608082	4
8	991.425483	496.216380	973.414918	487.211097	E	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	1062.462597	531.734937	1044.452032	522.729654	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 FLDELEDEAK
(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	1207.560822	0.007726	FLDELEDEAK
7.0	1207.565552	0.002996	MLLSWGGGESR
1.6	1207.572083	-0.003535	FPDDLDTNKK
1.6	1207.557678	0.010870	MPDMNIKAPK

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

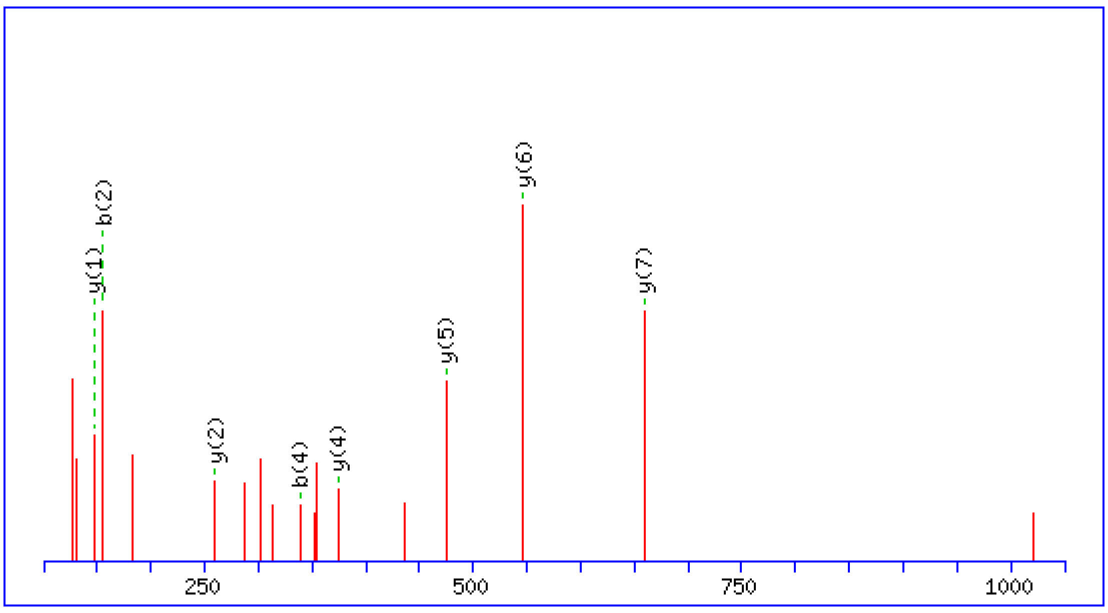
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPLATGGIK**
Found in **CCD72_HUMAN**, Coiled-coil domain-containing protein 72 OS=Homo sapiens GN=CCDC72 PE=1 SV=1

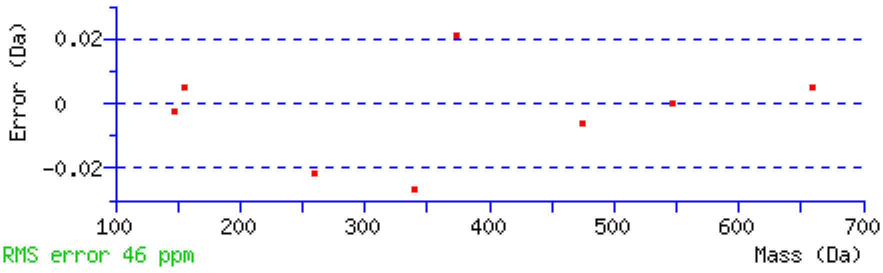
Match to Query 539: 812.474848 from(407.244700,2+) rtinseconds(1510) index(1138)
Title: Locus:1.1.1.2425.2
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

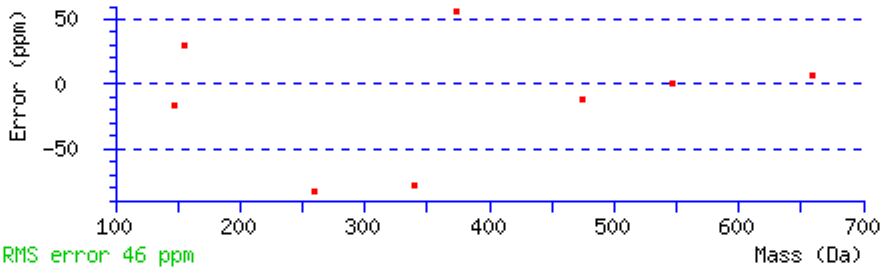
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 812.475601
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 8.9e-005
Matches : 8/64 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							9
2	**155.081504**	78.044390			P	756.461417	378.734347	739.434868	370.221072	738.450852	369.729064	8
3	268.165568	134.586422			L	***659.408653***	330.207965	642.382104	321.694690	641.398088	321.202682	7
4	**339.202682**	170.104979			A	***546.324589***	273.665933	529.298040	265.152658	528.314024	264.660650	6
5	440.250361	220.628819	422.239796	211.623536	T	***475.287475***	238.147375	458.260926	229.634101	457.276910	229.142093	5
6	497.271825	249.139551	479.261260	240.134268	G	***374.239796***	187.623536	357.213247	179.110261			4
7	554.293289	277.650283	536.282724	268.645000	G	317.218332	159.112804	300.191783	150.599529			3
8	667.377353	334.192315	649.366788	325.187032	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 GPLATGGIK
(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	812.475601	-0.000753	GPLATGGIK
17.4	812.475586	-0.000738	GPISAQLK
8.5	812.475601	-0.000753	GPLTVAQK
3.3	812.475586	-0.000738	QTLPNLK
0.7	812.475586	-0.000738	QLNPTLK

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

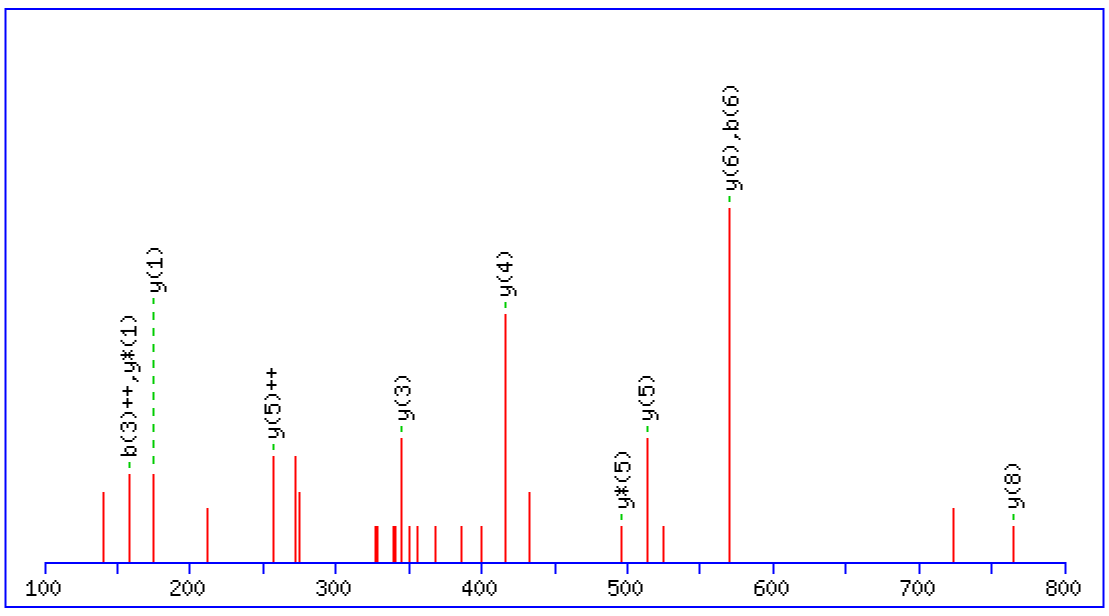
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEQGTPGPPGPAGPR**
Found in **COAA1_HUMAN**, Collagen alpha-1(X) chain OS=Homo sapiens GN=COL10A1 PE=1 SV=2

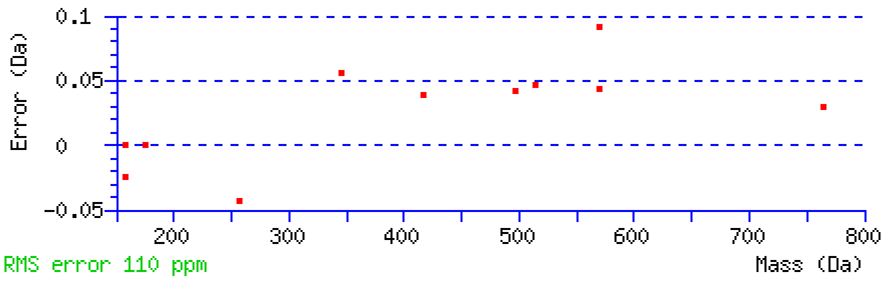
Match to Query 24342: 1389.672462 from(464.231430,3+) rtinseconds(1635) index(4964)
Title: Locus:1.1.1.2148.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

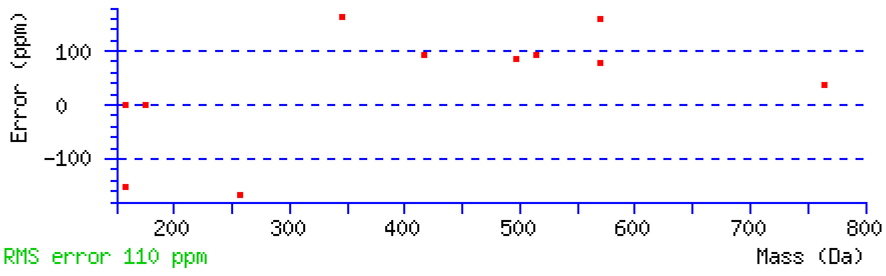
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1389.663712
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P14 : Oxidation (P)
Ions Score: 45 **Expect:** 0.00041
Matches : 11/142 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							15
2	187.071333	94.039305			169.060768	85.034022	E	1333.649507	667.328392	1316.622958	658.815117	1315.638942	658.323109	14
3	315.129911	158.068594	298.103362	149.555319	297.119346	149.063311	Q	1204.606914	602.807095	1187.580365	594.293821	1186.596349	593.801813	13
4	372.151375	186.579326	355.124826	178.066051	354.140810	177.574043	G	1076.548336	538.777806	1059.521787	530.264532	1058.537771	529.772524	12
5	473.199054	237.103165	456.172505	228.589891	455.188489	228.097883	T	1019.526872	510.267074	1002.500323	501.753800	1001.516307	501.261792	11
6	570.251818	285.629547	553.225269	277.116273	552.241253	276.624265	P	918.479193	459.743235	901.452644	451.229960			10
7	627.273282	314.140279	610.246733	305.627005	609.262717	305.134997	G	821.426429	411.216853	804.399880	402.703578			9
8	724.326046	362.666661	707.299497	354.153387	706.315481	353.661379	P	***764.404965***	382.706121	747.378416	374.192846			8
9	821.378810	411.193043	804.352261	402.679769	803.368245	402.187761	P	667.352201	334.179739	650.325652	325.666464			7
10	878.400274	439.703775	861.373725	431.190501	860.389709	430.698493	G	***570.299437***	285.653357	553.272888	277.140082			6
11	975.453038	488.230157	958.426489	479.716883	957.442473	479.224875	P	***513.277973***	257.142625	496.251424	248.629350			5
12	1046.490152	523.748714	1029.463603	515.235440	1028.479587	514.743432	A	***416.225209***	208.616242	399.198660	200.102968			4
13	1103.511616	552.259446	1086.485067	543.746172	1085.501051	543.254164	G	***345.188095***	173.097685	328.161546	164.584411			3
14	1216.559295	608.783286	1199.532746	600.270011	1198.548730	599.778003	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 GEQGTPGPPGPAGPR
(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	1389.663712	0.008750	GEQGTPGPPGPAGPR
30.8	1389.663712	0.008750	GEQGTPGPPGPAGPR
12.7	1389.663712	0.008750	GEQGTPGPPGPAGPR
12.7	1389.663712	0.008750	GEQGTPGPPGPAGPR
12.7	1389.663712	0.008750	VPPGDSPPGNGSGPR
11.1	1389.674927	-0.002465	DHPVNATKSPHR
6.1	1389.663712	0.008750	GHPDPTLPQPQR
4.8	1389.671082	0.001380	FPPMTRDELPR
4.7	1389.685699	-0.013237	DVLGRVGMTCPR
4.3	1389.664551	0.007911	AGPPHTCPLCPR

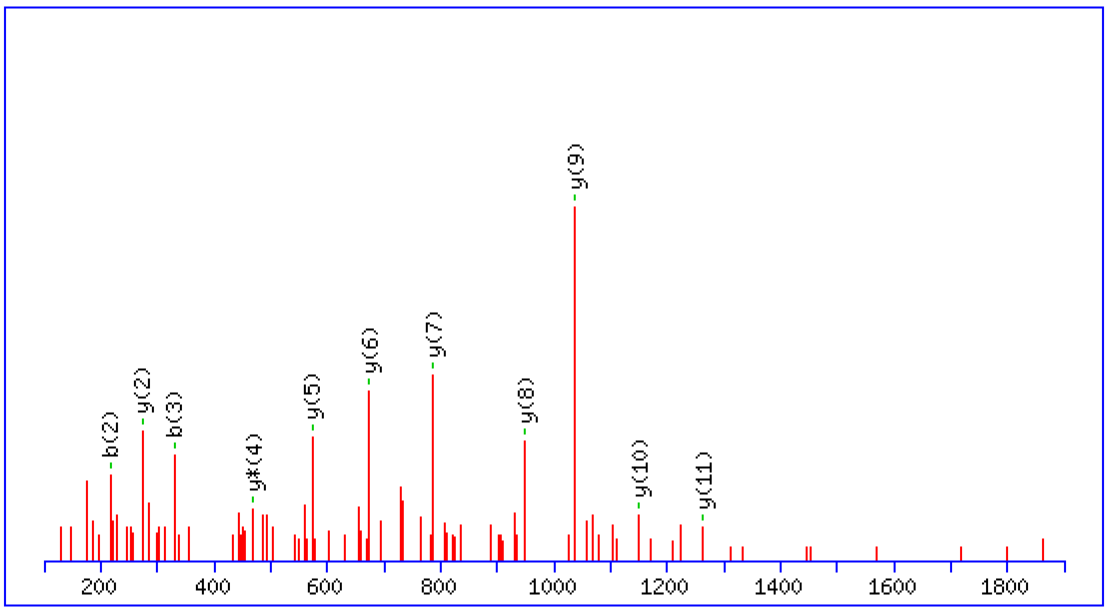
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SELISYLTSPDVR**
Found in **COHA1_HUMAN**, Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3

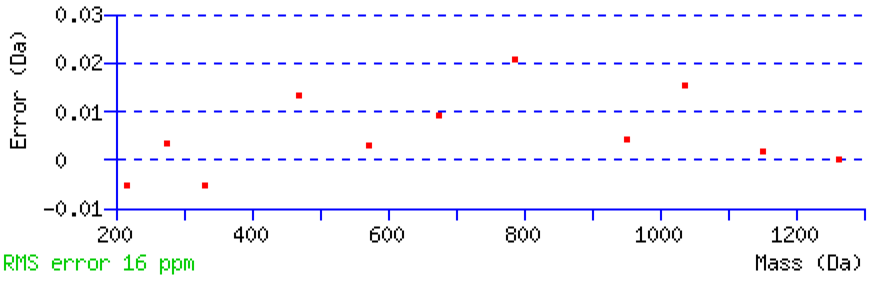
Match to Query 38702: 1478.775648 from(740.395100,2+) rtinseconds(3155) index(46807)
Title: Locus:1.1.1.1847.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

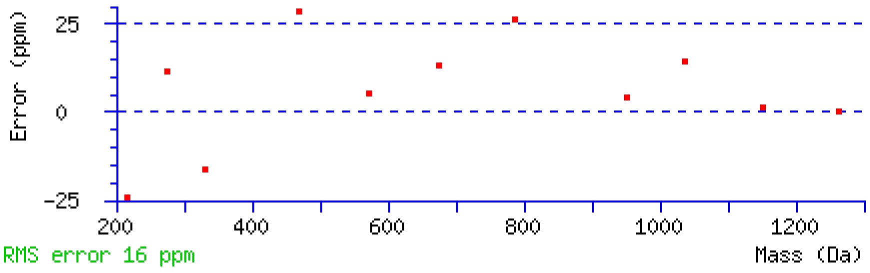
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1478.761658
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 2e-006
Matches : 11/116 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							13
2	**217.081897**	109.044586	199.071332	100.039304	E	1392.736922	696.872099	1375.710373	688.358825	1374.726357	687.866817	12
3	**330.165961**	165.586618	312.155396	156.581336	L	***1263.694329***	632.350803	1246.667780	623.837528	1245.683764	623.345520	11
4	443.250025	222.128650	425.239460	213.123368	I	***1150.610265***	575.808771	1133.583716	567.295496	1132.599700	566.803488	10
5	530.282053	265.644665	512.271488	256.639382	S	***1037.526201***	519.266739	1020.499652	510.753464	1019.515636	510.261456	9
6	693.345382	347.176329	675.334817	338.171046	Y	***950.494173***	475.750725	933.467624	467.237450	932.483608	466.745442	8
7	806.429446	403.718361	788.418881	394.713078	L	***787.430844***	394.219060	770.404295	385.705786	769.420279	385.213778	7
8	907.477125	454.242201	889.466560	445.236918	T	***674.346780***	337.677028	657.320231	329.163754	656.336215	328.671746	6
9	994.509153	497.758215	976.498588	488.752932	S	***573.299101***	287.153189	556.272552	278.639914	555.288536	278.147906	5
10	1091.561917	546.284597	1073.551352	537.279314	P	486.267073	243.637175	469.240524	235.123900	468.256508	234.631892	4
11	1206.588860	603.798068	1188.578295	594.792786	D	389.214309	195.110793	372.187760	186.597518	371.203744	186.105510	3
12	1305.657274	653.332275	1287.646709	644.326993	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 SELISYLTSPDVR
(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	1478.761658	0.013990	SELISYLTSPDVR

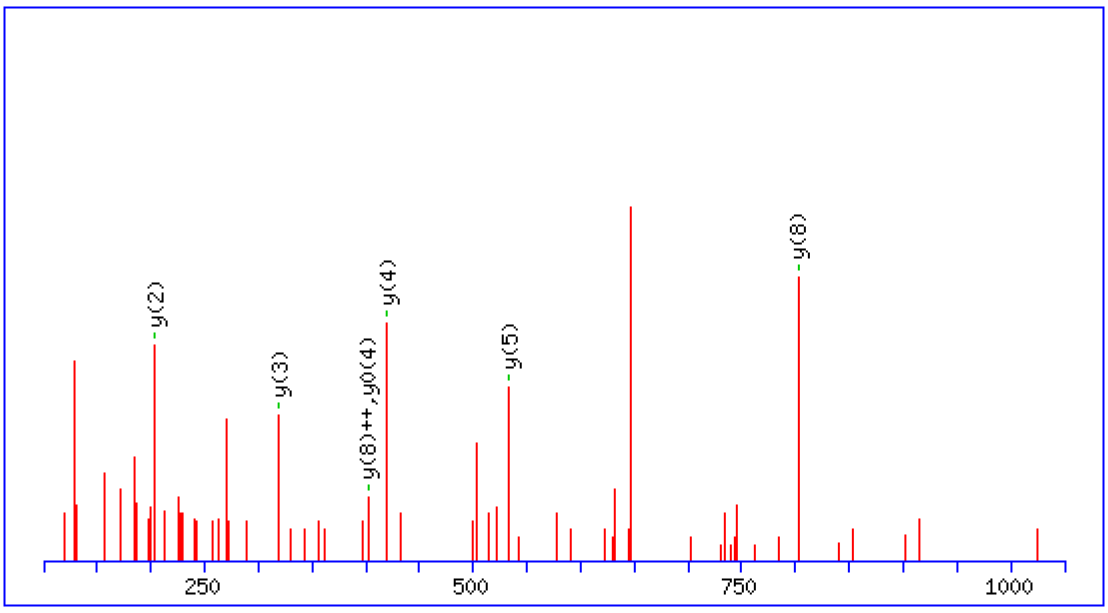
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAVVLTDGK**
Found in **COLA1_HUMAN**, Collagen alpha-1(XXI) chain OS=Homo sapiens GN=COL21A1 PE=2 SV=1

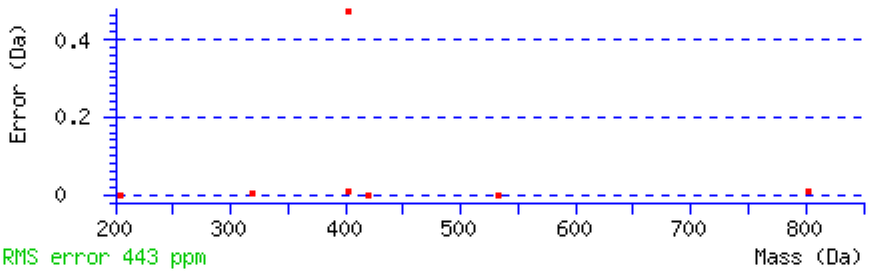
Match to Query 6207: 914.542588 from(458.278570,2+) rtinseconds(2054) index(25685)
Title: Locus:1.1.1.1425.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

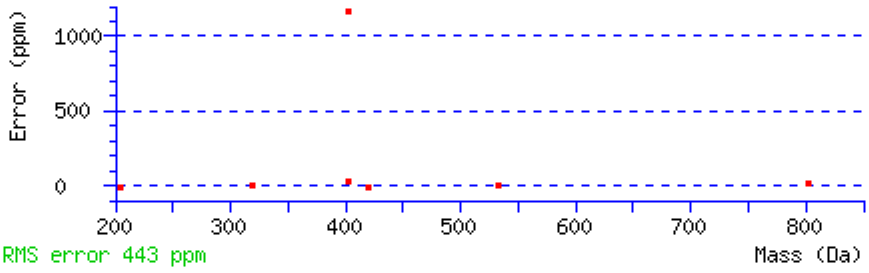
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 914.543686
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.00075
Matches : 7/66 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							9
2	185.128454	93.067865			A	***802.466896***	401.737086	785.440347	393.223812	784.456331	392.731804	8
3	284.196868	142.602072			V	731.429782	366.218529	714.403233	357.705255	713.419217	357.213247	7
4	383.265282	192.136279			V	632.361368	316.684322	615.334819	308.171048	614.350803	307.679040	6
5	496.349346	248.678311			L	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	5
6	597.397025	299.202151	579.386460	290.196868	T	***420.208890***	210.608083	403.182341	202.094809	402.198325	201.602801	4
7	712.423968	356.715622	694.413403	347.710340	D	***319.161211***	160.084243	302.134662	151.570969	301.150646	151.078961	3
8	769.445432	385.226354	751.434867	376.221072	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 IAVVLTDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.3	914.543686	-0.001098	IGVLITDGK
39.8	914.543686	-0.001098	IAVVLTDGK
17.9	914.543686	-0.001098	IGLETVGVK

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

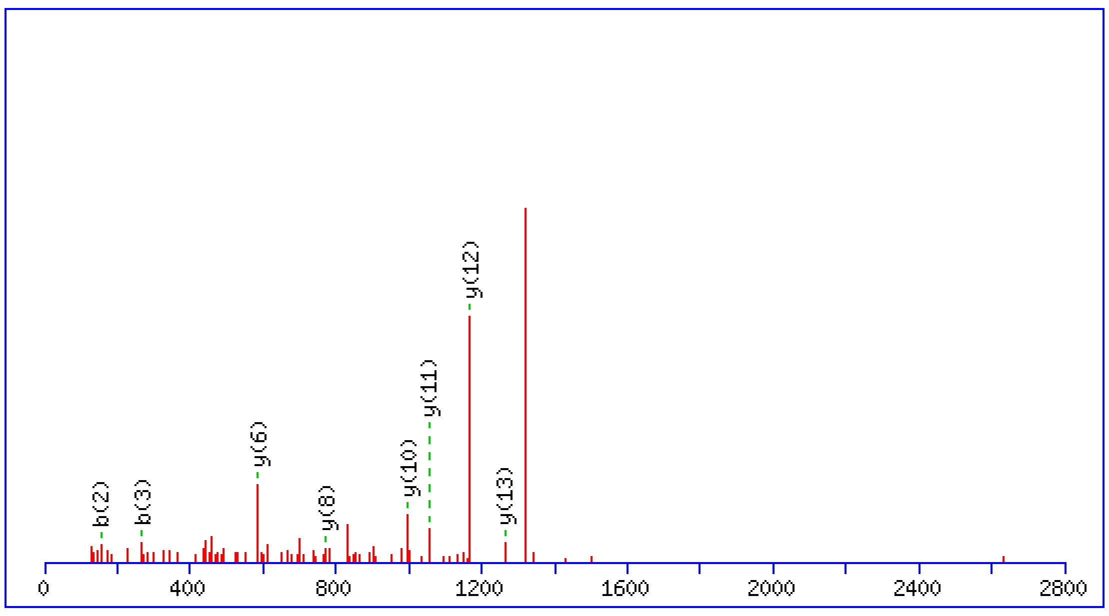
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPPGPKGEPGVPGK**
Found in **CONA1_HUMAN**, Collagen alpha-1(XXIII) chain OS=Homo sapiens GN=COL23A1 PE=2 SV=1

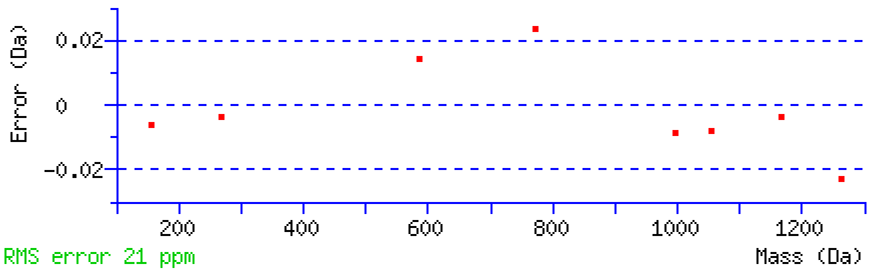
Match to Query 25522: 1320.654968 from(661.334760,2+) rtinseconds(1349) index(10708)
Title: Locus:1.1.1.1913.40
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

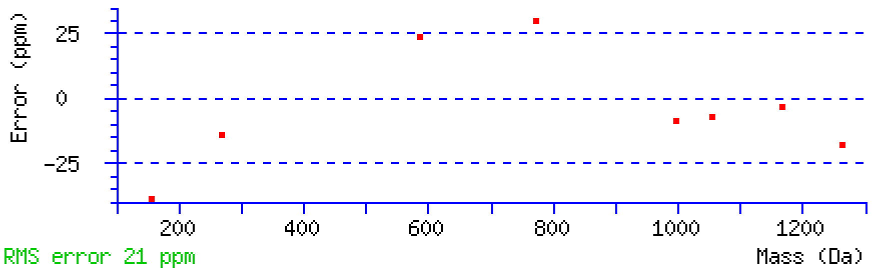
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1320.667404
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
P9      : Oxidation (P)
P12     : Oxidation (P)
Ions Score: 41  Expect: 0.00093
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	58.028740	29.518008					G							14
2	**155.081504**	78.044390					P	***1264.653195***	632.830236	1247.626646	624.316961	1246.642630	623.824953	13
3	**268.129183**	134.568230					P	***1167.600431***	584.303854	1150.573882	575.790579	1149.589866	575.298571	12
4	325.150647	163.078961					G	***1054.552752***	527.780014	1037.526203	519.266740	1036.542187	518.774732	11
5	422.203411	211.605344					P	***997.531288***	499.269282	980.504739	490.756008	979.520723	490.264000	10
6	550.298374	275.652825	533.271825	267.139551			K	900.478524	450.742900	883.451975	442.229626	882.467959	441.737618	9
7	607.319838	304.163557	590.293289	295.650283			G	***772.383561***	386.695419	755.357012	378.182144	754.372996	377.690136	8
8	736.362431	368.684854	719.335882	360.171579	718.351866	359.679571	E	715.362097	358.184687	698.335548	349.671412	697.351532	349.179404	7
9	849.410110	425.208693	832.383561	416.695419	831.399545	416.203411	P	***586.319504***	293.663390	569.292955	285.150115			6
10	906.431574	453.719425	889.405025	445.206151	888.421009	444.714143	G	473.271825	237.139550	456.245276	228.626276			5
11	1005.499988	503.253632	988.473439	494.740358	987.489423	494.248350	V	416.250361	208.628818	399.223812	200.115544			4
12	1118.547667	559.777472	1101.521118	551.264197	1100.537102	550.772189	P	317.181947	159.094611	300.155398	150.581337			3
13	1175.569131	588.288204	1158.542582	579.774929	1157.558566	579.282921	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 GPPGPKGEPGVPGK
(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	1320.667404	-0.012436	GPPGPKGEPGVPGK
24.4	1320.667404	-0.012436	GPPGPKGEPGVPGK
20.2	1320.667389	-0.012421	GPPGPPGSAALPGSK
19.5	1320.667404	-0.012436	GPPGPKGEPGVPGK
19.5	1320.667404	-0.012436	GPPGPKGEPGVPGK
19.2	1320.667389	-0.012421	GPPGPPGSAALPGSK
18.6	1320.667389	-0.012421	GPPGPPGSAALPGSK
17.4	1320.667389	-0.012421	GPPGEPGEKGVPGK
13.4	1320.667404	-0.012436	GPPGPKGEPGVPGK
7.8	1320.667389	-0.012421	GPPGPPGSAALPGSK

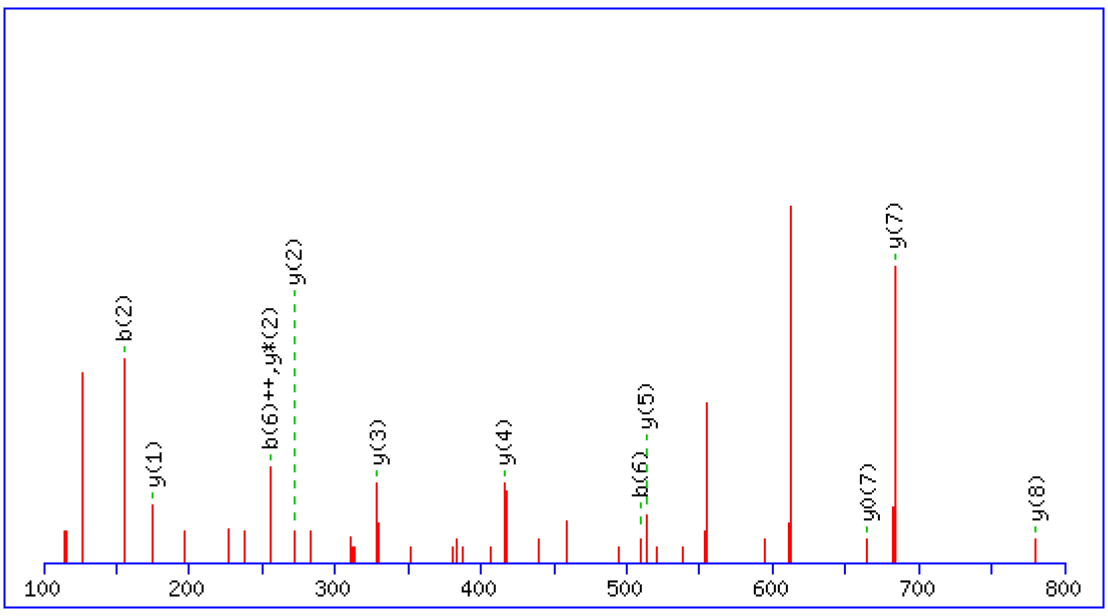
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPPGPSGPR**
Found in **COSA1_HUMAN**, Collagen alpha-1(XXVIII) chain OS=Homo sapiens GN=COL28A1 PE=2 SV=2

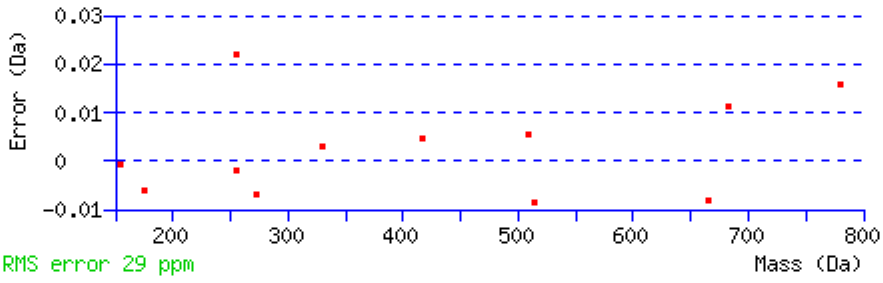
Match to Query 1815: 836.421568 from(419.218060,2+) rtinseconds(5062) index(26736)
Title: Locus:1.1.1.1986.5
Data file 120106_TFD_Pellet_S1.mgf

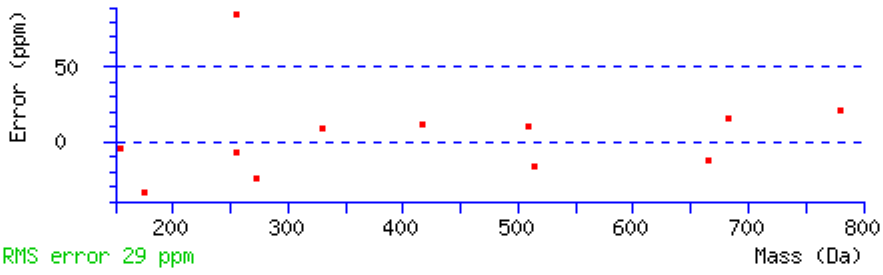
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 836.414078
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 38  Expect: 0.0021
Matches : 12/64 fragment ions using 29 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							9
2	**155.081504**	78.044390			P	***780.399879***	390.703578	763.373330	382.190303	762.389314	381.698295	8
3	268.129183	134.568230			P	***683.347115***	342.177196	666.320566	333.663921	665.336550	333.171913	7
4	325.150647	163.078961			G	570.299436	285.653356	553.272887	277.140082	552.288871	276.648074	6
5	422.203411	211.605344			P	***513.277972***	257.142624	496.251423	248.629350	495.267407	248.137342	5
6	**509.235439**	255.121357	491.224874	246.116075	S	***416.225208***	208.616242	399.198659	200.102968	398.214643	199.610960	4
7	566.256903	283.632090	548.246338	274.626807	G	***329.193180***	165.100228	312.166631	156.586954			3
8	663.309667	332.158472	645.299102	323.153189	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 GPPGPSGPR
(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	836.414078	0.007490	GPPGPSGPR
32.1	836.414078	0.007490	GPPGPSGPR
22.5	836.414078	0.007490	GAPGPPGPR
17.9	836.414078	0.007490	GPPGPSGPR
17.8	836.414078	0.007490	GPPGAPPGR
12.6	836.414078	0.007490	GAPGPPGPR
11.2	836.414078	0.007490	GPPGAPPGR
8.8	836.414078	0.007490	GPPGPSGPR
8.4	836.414078	0.007490	GPPGAPPGR
8.2	836.414078	0.007490	GAPGPPGPR

{MATRIX SCIENCE}

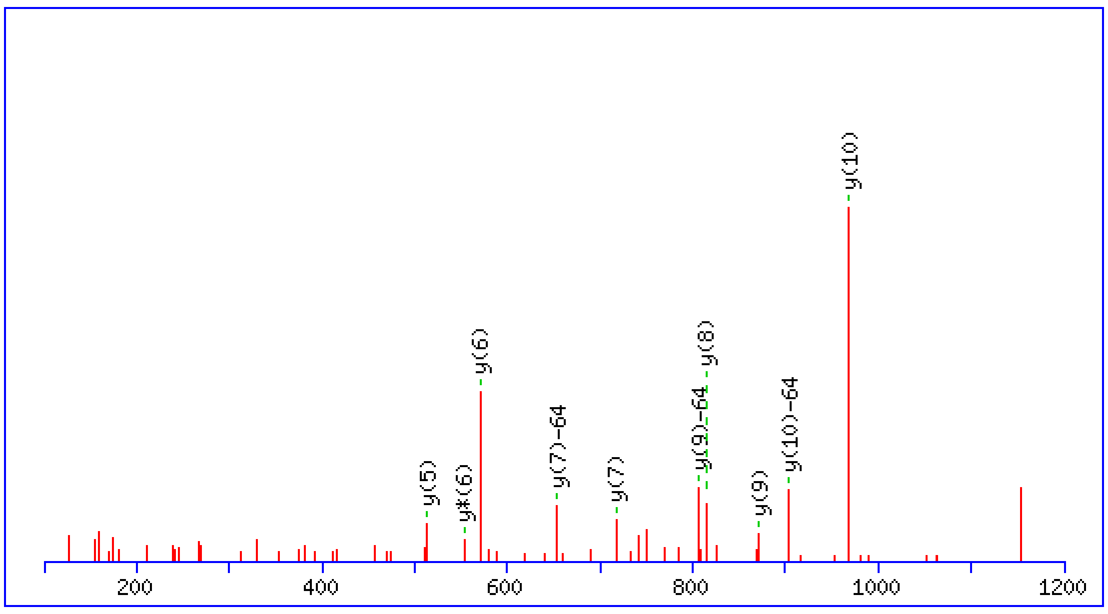
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEPGPMGIPGVK**
Found in **CO9A2_HUMAN**, Collagen alpha-2(IX) chain OS=Homo sapiens GN=COL9A2 PE=1 SV=2

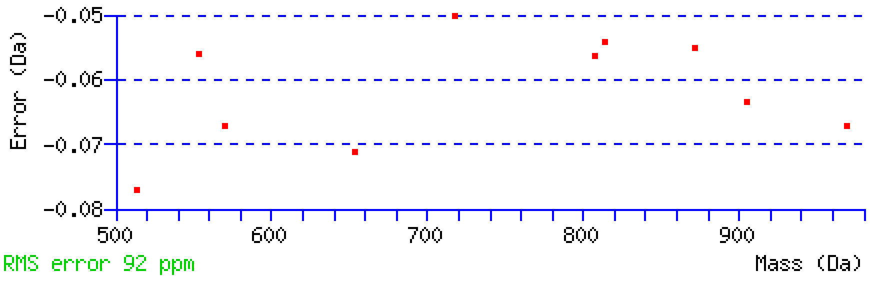
Match to Query 358534: 1153.571828 from(577.793190,2+) rtinseconds(1077) index(315755)
Title: Locus:1.1.1.769.17
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

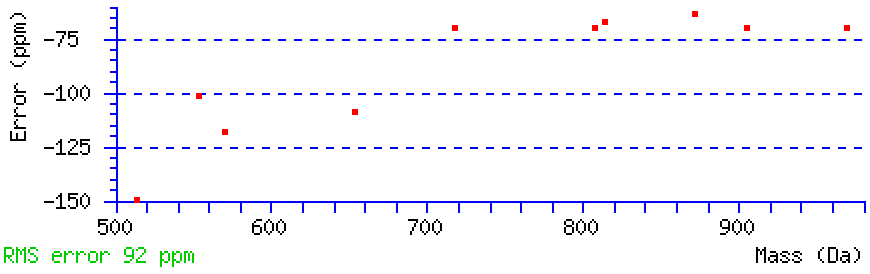
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1153.580154
Fixed modifications: Carbamidomethyl (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: 35  Expect: 0.00089
Matches : 10/134 fragment ions using 20 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							12
2	187.071333	94.039305	169.060768	85.034022	E	1097.565959	549.286618	1080.539410	540.773343	1079.555394	540.281335	11
3	284.124097	142.565687	266.113532	133.560404	P	***968.523366***	484.765321	951.496817	476.252047			10
4	341.145561	171.076418	323.134996	162.071136	G	***871.470602***	436.238939	854.444053	427.725665			9
5	438.198325	219.602801	420.187760	210.597518	P	***814.449138***	407.728207	797.422589	399.214933			8
6	585.233725	293.120501	567.223160	284.115218	M	***717.396374***	359.201825	700.369825	350.688551			7
7	642.255189	321.631233	624.244624	312.625950	G	***570.360974***	285.684125	553.334425	277.170851			6
8	755.339253	378.173265	737.328688	369.167982	I	***513.339510***	257.173393	496.312961	248.660119			5
9	852.392017	426.699647	834.381452	417.694364	P	400.255446	200.631361	383.228897	192.118087			4
10	909.413481	455.210379	891.402916	446.205096	G	303.202682	152.104979	286.176133	143.591704			3
11	1008.481895	504.744586	990.471330	495.739303	V	246.181218	123.594247	229.154669	115.080972			2
12					K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1153.580154	-0.008326	GEPGPMGIPGVK
17.6	1153.580154	-0.008326	GEPGPMGIPGVK
8.9	1153.580154	-0.008326	GEPGPMGIPGVK
5.6	1153.580154	-0.008326	GEPGPMGIPGVK
2.0	1153.568909	0.002919	GEVLSVLYQM

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

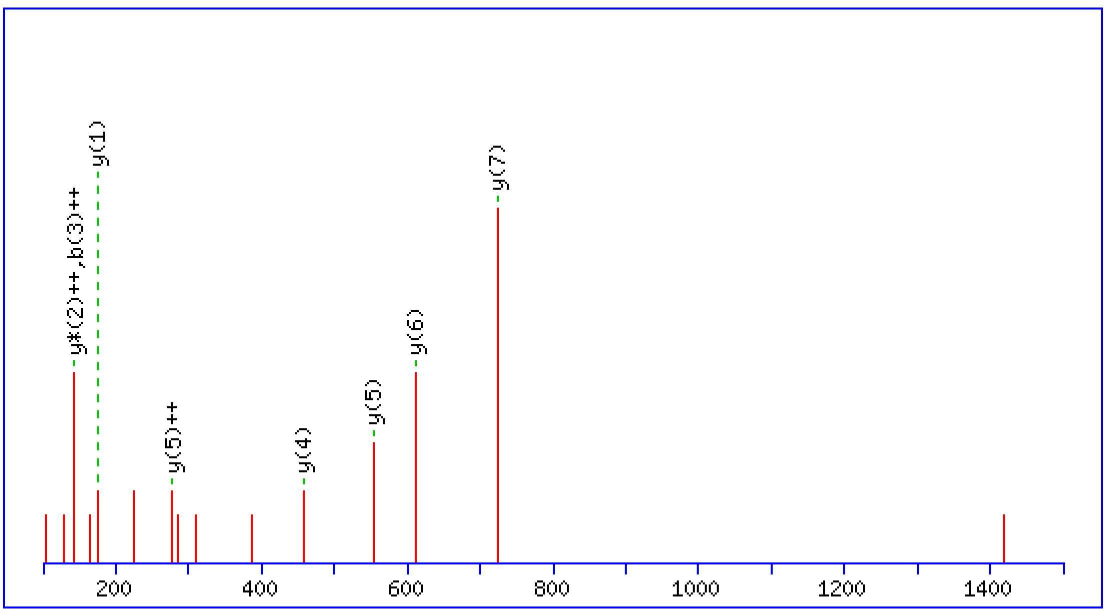
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLPGPPGQR**
Found in **CO6A5_HUMAN**, Collagen alpha-5(VI) chain OS=Homo sapiens GN=COL6A5 PE=1 SV=1

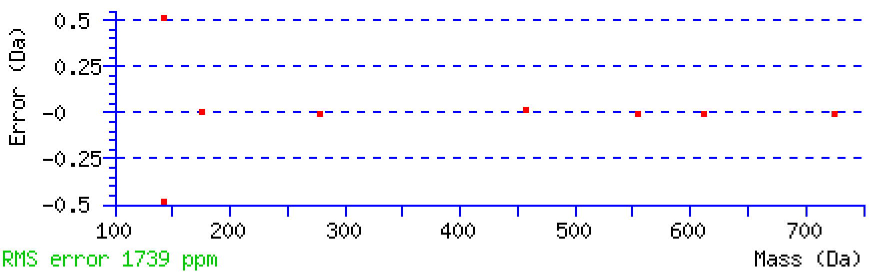
Match to Query 3722: 893.473088 from(447.743820,2+) rtinseconds(1122) index(3330)
Title: Locus:1.1.1.1947.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

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 ●

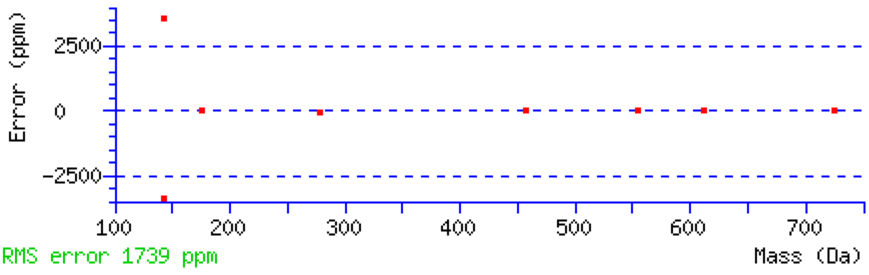


```
Monoisotopic mass of neutral peptide Mr(calc): 893.471924
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 38  Expect: 0.0029
Matches : 8/50 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					9
2	171.112804	86.060040			L	837.457729	419.232503	820.431180	410.719228	8
3	284.160483	142.583879			P	***724.373665***	362.690471	707.347116	354.177196	7
4	341.181947	171.094611			G	***611.325986***	306.166631	594.299437	297.653357	6
5	438.234711	219.620993			P	***554.304522***	277.655899	537.277973	269.142625	5
6	535.287475	268.147376			P	***457.251758***	229.129517	440.225209	220.616243	4
7	592.308939	296.658108			G	360.198994	180.603135	343.172445	172.089861	3
8	720.367517	360.687397	703.340968	352.174122	Q	303.177530	152.092403	286.150981	143.579129	2
9					R	***175.118952***	88.063114	158.092403	79.549840	1



RMS error 1739 ppm



RMS error 1739 ppm

NCBI **BLAST** search of GLPGPPGQR
(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	893.471924	0.001164	GLPGPPGQR
34.8	893.471924	0.001164	GLPGPQGPR
18.4	893.464706	0.008382	GPLPGYFK
16.8	893.471924	0.001164	GLPGPQGPR
15.1	893.471924	0.001164	GLPGPPGQR
12.4	893.471909	0.001179	GEPGKPGPR
10.3	893.471924	0.001164	VPAGGAGPPR
3.2	893.471924	0.001164	GLPGPPGQR
2.4	893.471909	0.001179	AVGPAQSHK
1.4	893.471924	0.001164	GLPGPQGPR

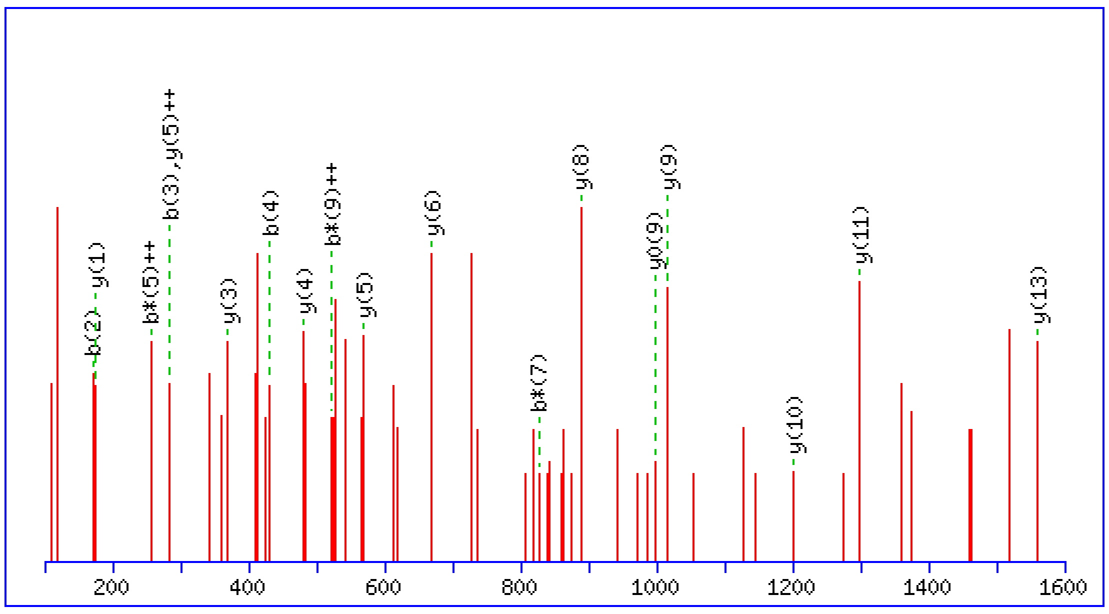
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNFPWQAFTSIHGR**
Found in **C1RL_HUMAN**, Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

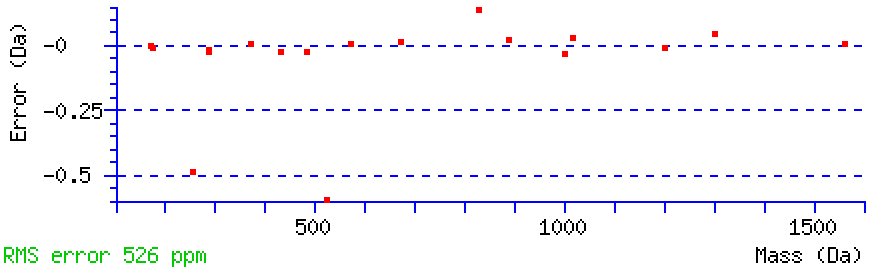
Match to Query 44755: 1729.875282 from(577.632370,3+) rtinseconds(3432) index(50059)
Title: Locus:1.1.1.2712.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

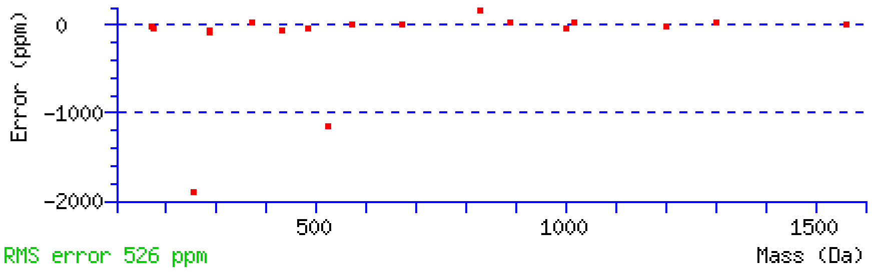
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1729.868881
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00064
Matches : 18/138 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	114.091340	57.549308					L							15
2	**171.112804**	86.060040					G	1617.792087	809.399682	1600.765538	800.886407	1599.781522	800.394399	14
3	**285.155731**	143.081504	268.129182	134.568229			N	***1560.770623***	780.888949	1543.744074	772.375675	1542.760058	771.883667	13
4	**432.224145**	216.615710	415.197596	208.102436			F	1446.727696	723.867486	1429.701147	715.354212	1428.717131	714.862203	12
5	529.276909	265.142093	512.250360	256.628818			P	***1299.659282***	650.333279	1282.632733	641.820004	1281.648717	641.327996	11
6	715.356222	358.181749	698.329673	349.668475			W	***1202.606518***	601.806897	1185.579969	593.293622	1184.595953	592.801614	10
7	843.414800	422.211038	826.388251	413.697764			Q	***1016.527205***	508.767240	999.500656	500.253966	998.516640	499.761958	9
8	914.451914	457.729595	897.425365	449.216321			A	***888.468627***	444.737951	871.442078	436.224677	870.458062	435.732669	8
9	1061.520328	531.263802	1044.493779	522.750528			F	817.431513	409.219394	800.404964	400.706120	799.420948	400.214112	7
10	1162.568007	581.787642	1145.541458	573.274367	1144.557442	572.782359	T	***670.363099***	335.685187	653.336550	327.171913	652.352534	326.679905	6
11	1249.600035	625.303656	1232.573486	616.790381	1231.589470	616.298373	S	***569.315420***	285.161348	552.288871	276.648073	551.304855	276.156065	5
12	1362.684099	681.845688	1345.657550	673.332413	1344.673534	672.840405	I	***482.283392***	241.645334	465.256843	233.132059			4
13	1499.743011	750.375144	1482.716462	741.861869	1481.732446	741.369861	H	***369.199328***	185.103302	352.172779	176.590027			3
14	1556.764475	778.885876	1539.737926	770.372601	1538.753910	769.880593	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 LGNFPWQAFTSIHGR
(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	1729.868881	0.006401	LGNFPWQAFTSIHGR

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

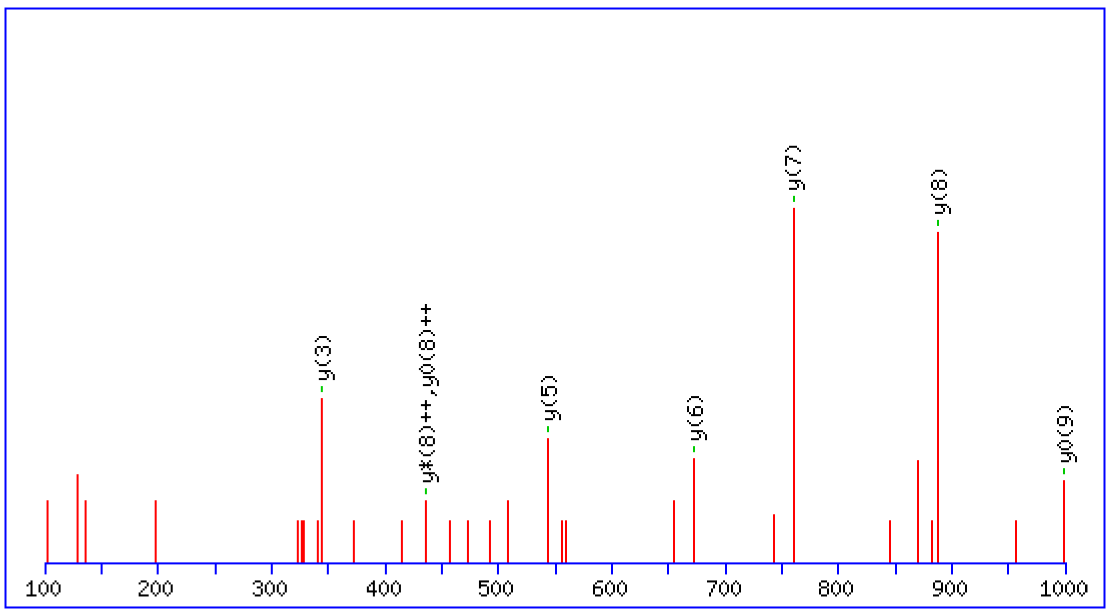
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEQSEAQLGR**
Found in **CSN5_HUMAN**, COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4

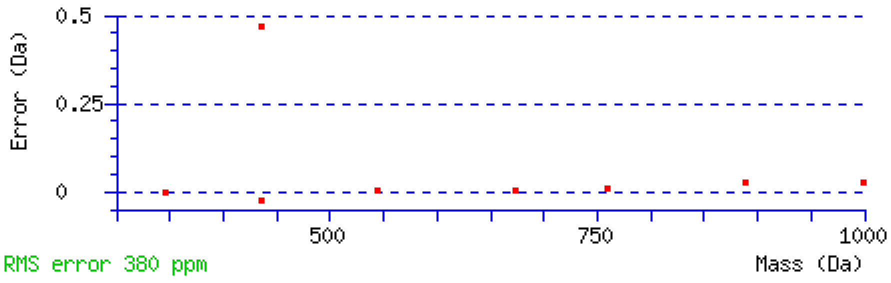
Match to Query 19584: 1129.578028 from(565.796290,2+) rtinseconds(1286) index(9018)
Title: Locus:1.1.1.1873.32
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

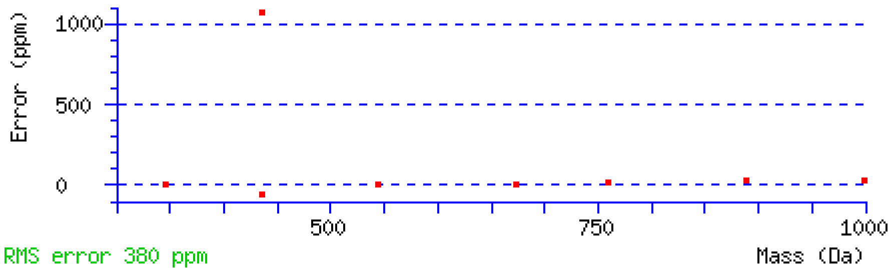
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1129.572723
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0005
Matches : 8/92 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							10
2	243.133933	122.070605			225.123368	113.065322	E	1017.495964	509.251620	1000.469415	500.738346	999.485399	500.246338	9
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	***888.453371***	444.730324	871.426822	436.217049	870.442806	435.725041	8
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	S	***760.394793***	380.701035	743.368244	372.187760	742.384228	371.695752	7
5	587.267132	294.137204	570.240583	285.623930	569.256567	285.131922	E	***673.362765***	337.185021	656.336216	328.671746	655.352200	328.179738	6
6	658.304246	329.655761	641.277697	321.142487	640.293681	320.650479	A	***544.320172***	272.663724	527.293623	264.150450			5
7	786.362824	393.685050	769.336275	385.171776	768.352259	384.679768	Q	473.283058	237.145167	456.256509	228.631892			4
8	899.446888	450.227082	882.420339	441.713808	881.436323	441.221800	L	***345.224480***	173.115878	328.197931	164.602603			3
9	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	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 LEQSEAQLGR
(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	1129.572723	0.005305	LEQSEAQLGR
8.4	1129.583954	-0.005926	ELQAEAGRTR
5.6	1129.572723	0.005305	KASPEAASTPR
3.0	1129.583969	-0.005941	NQKLDAGTQR
2.9	1129.572739	0.005289	NTPERSGLPK
2.1	1129.577454	0.000574	LVNGGGRCAGR
1.7	1129.580139	-0.002111	VLDLCAAPGGK
1.3	1129.580154	-0.002126	KNMPPPGVVK
0.8	1129.587997	-0.009969	QNPSITWIR
0.8	1129.580124	-0.002096	AVSPPASNMLK

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

MATRIX SCIENCE

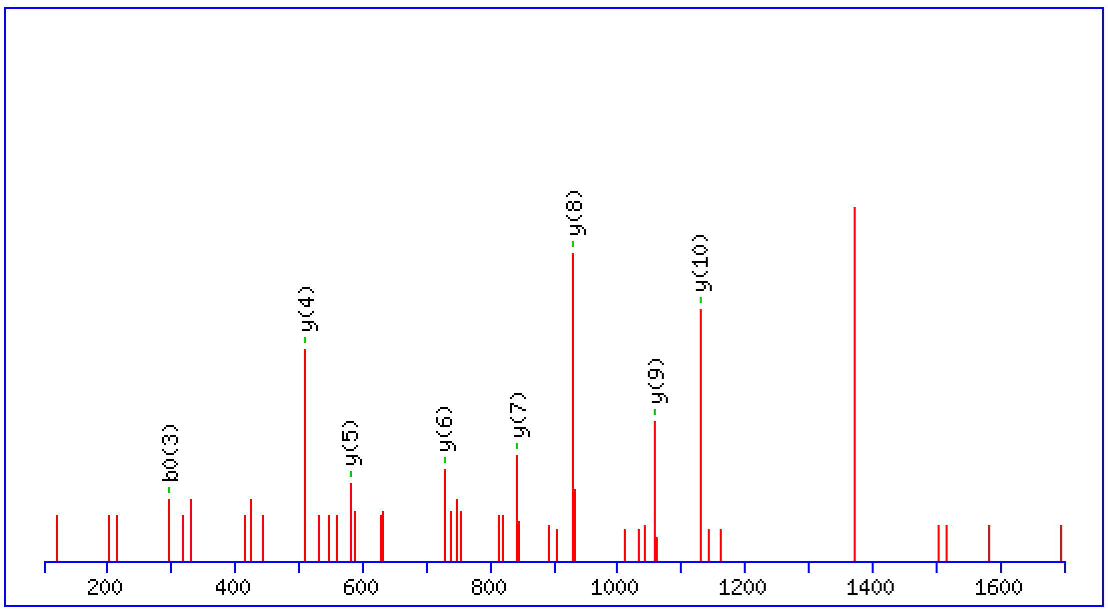
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAESDFASTFR**
Found in **CSN7A_HUMAN**, COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1

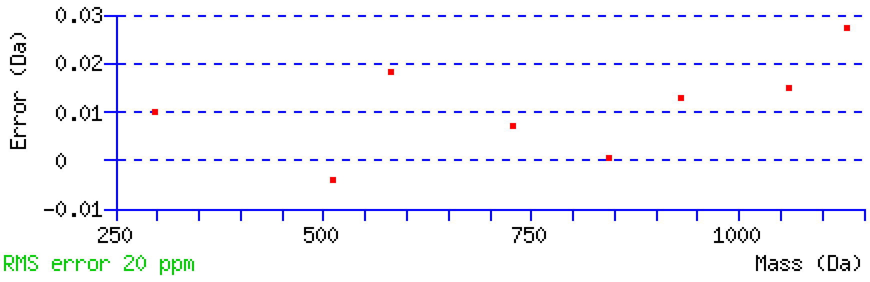
Match to Query 33703: 1371.643908 from(686.829230,2+) rtinseconds(2791) index(34064)
Title: Locus:1.1.1.2648.29
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

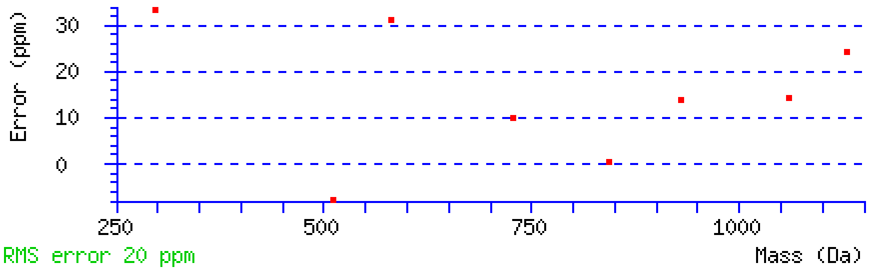
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1371.630646
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 1.5e-005
Matches : 8/106 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							12
2	243.133933	122.070605	225.123368	113.065322	L	1243.595343	622.301309	1226.568794	613.788035	1225.584778	613.296027	11
3	314.171047	157.589161	296.160482	148.583879	A	***1130.511279***	565.759277	1113.484730	557.246003	1112.500714	556.753995	10
4	443.213640	222.110458	425.203075	213.105176	E	***1059.474165***	530.240720	1042.447616	521.727446	1041.463600	521.235438	9
5	530.245668	265.626472	512.235103	256.621190	S	***930.431572***	465.719424	913.405023	457.206149	912.421007	456.714141	8
6	645.272611	323.139944	627.262046	314.134661	D	***843.399544***	422.203410	826.372995	413.690135	825.388979	413.198127	7
7	792.341025	396.674151	774.330460	387.668868	F	***728.372601***	364.689938	711.346052	356.176664	710.362036	355.684656	6
8	863.378139	432.192707	845.367574	423.187425	A	***581.304187***	291.155732	564.277638	282.642457	563.293622	282.150449	5
9	950.410167	475.708721	932.399602	466.703439	S	***510.267073***	255.637174	493.240524	247.123900	492.256508	246.631892	4
10	1051.457846	526.232561	1033.447281	517.227278	T	423.235045	212.121160	406.208496	203.607886	405.224480	203.115878	3
11	1198.526260	599.766768	1180.515695	590.761485	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 ELAESDFASTFR
(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	1371.630646	0.013262	ELAESDFASTFR
1.3	1371.653290	-0.009382	EPAPFNLYMFK
0.4	1371.656494	-0.012586	IPGSPPESMGRGR
0.4	1371.656494	-0.012586	IPGSPPESMGRGR

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

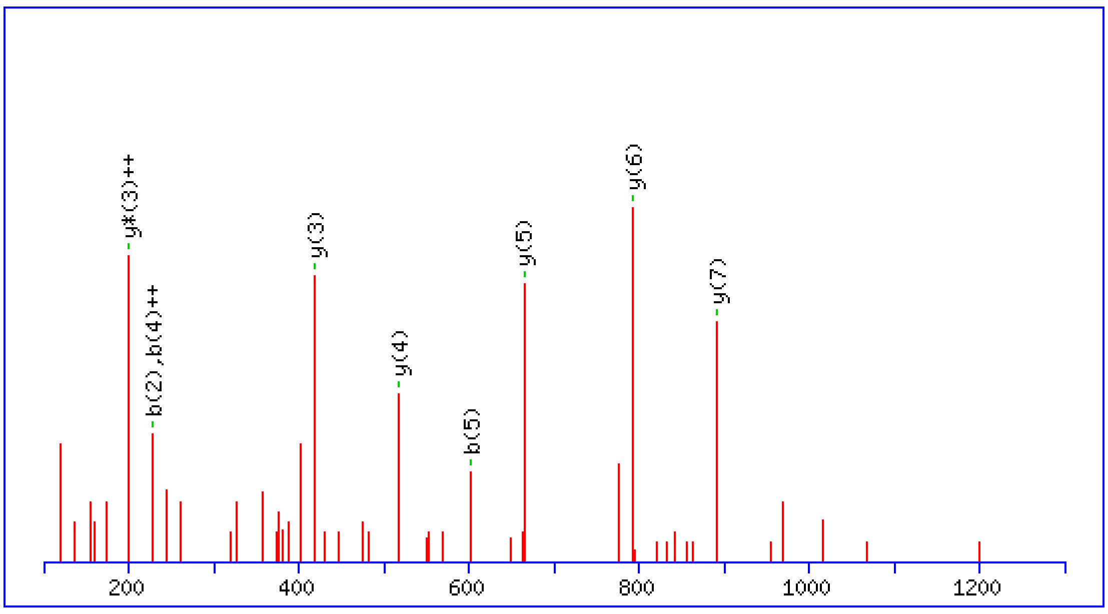
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIVQFVPFR**
Found in **CPNE2_HUMAN**, Copine-2 OS=Homo sapiens GN=CPNE2 PE=1 SV=3

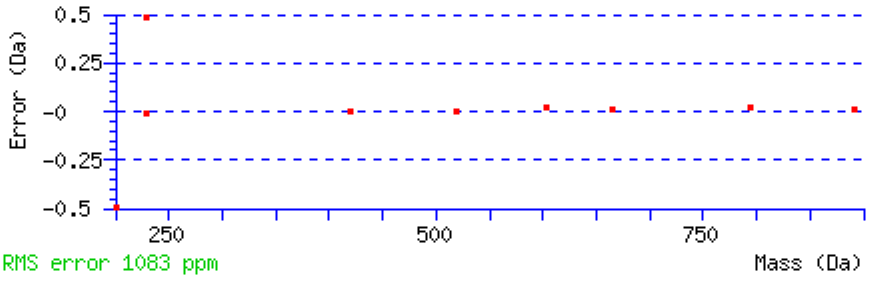
Match to Query 13434: 1119.617708 from(560.816130,2+) rtinseconds(3321) index(48174)
Title: Locus:1.1.1.2746.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

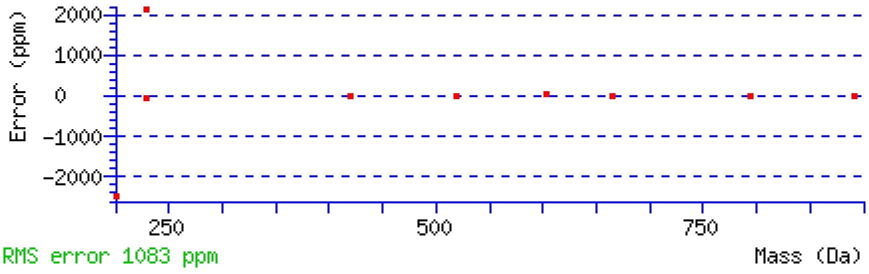
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1119.607697
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00024
Matches : 9/74 fragment ions using 10 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	116.034219	58.520748			98.023654	49.515465	**D**					9
2	**229.118283**	115.062779			211.107718	106.057497	**I**	1005.588014	503.297645	988.561465	494.784371	8
3	328.186697	164.596986			310.176132	155.591704	**V**	***892.503950***	446.755613	875.477401	438.242339	7
4	456.245275	228.626275	439.218726	220.113001	438.234710	219.620993	**Q**	***793.435536***	397.221406	776.408987	388.708131	6
5	**603.313689**	302.160483	586.287140	293.647208	585.303124	293.155200	**F**	***665.376958***	333.192117	648.350409	324.678843	5
6	702.382103	351.694690	685.355554	343.181415	684.371538	342.689407	**V**	***518.308544***	259.657910	501.281995	251.144635	4
7	799.434867	400.221072	782.408318	391.707797	781.424302	391.215789	**P**	***419.240130***	210.123703	402.213581	201.610428	3
8	946.503281	473.755279	929.476732	465.242004	928.492716	464.749996	**F**	322.187366	161.597321	305.160817	153.084046	2
9							**R**	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.5	1119.607697	0.010011	DIVQFVPFR
2.0	1119.617584	0.000124	FGVITEVDIK

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

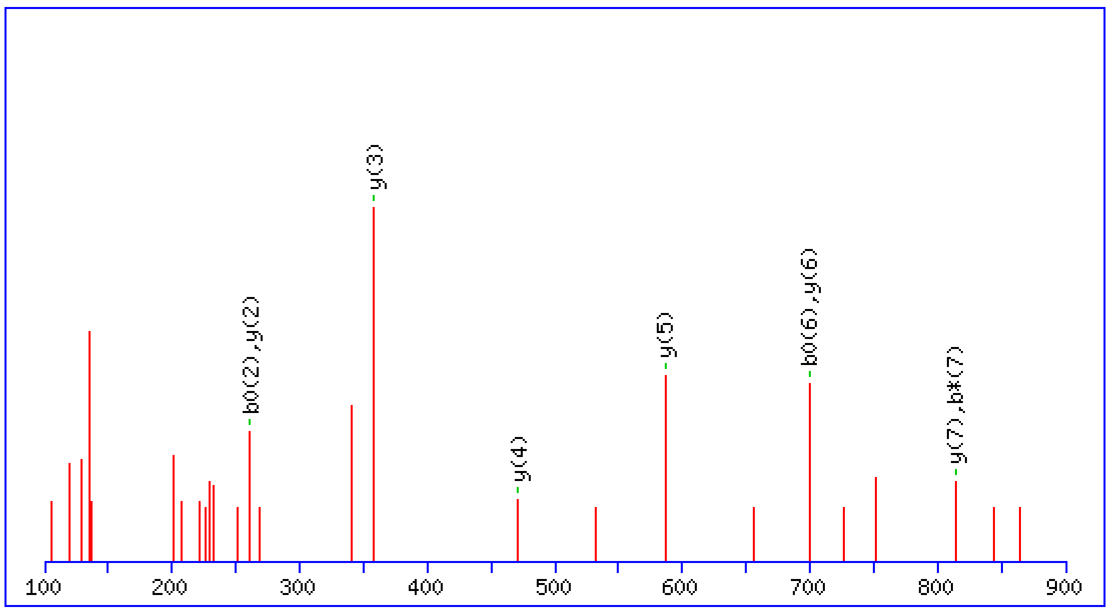
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDIDLPNK**
Found in **ATOX1_HUMAN**, Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1 PE=1 SV=1

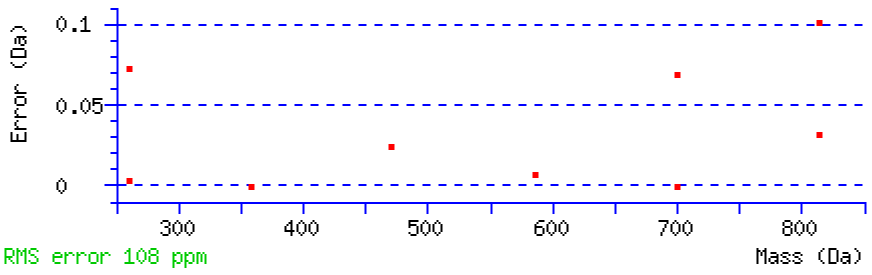
Match to Query 7104: 976.491408 from(489.252980,2+) rtinseconds(2140) index(5302)
Title: Locus:1.1.1.2917.7
Data file 2011-11-10 - TFD - S 9-8.mgf

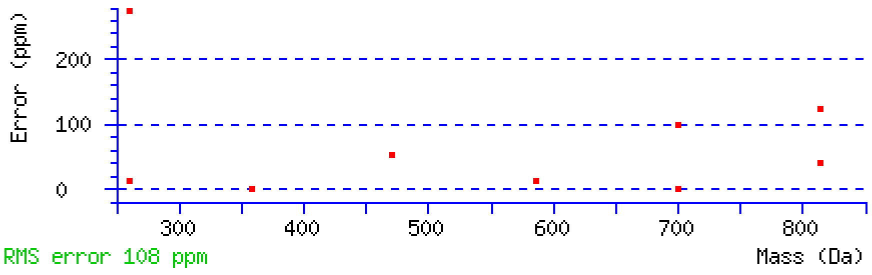
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 976.486542
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.8e-005
Matches : 9/62 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	164.070605	82.538940					Y							8
2	279.097548	140.052412			261.086983	131.047130	D	***814.430509***	407.718893	797.403960	399.205618	796.419944	398.713610	7
3	392.181612	196.594444			374.171047	187.589162	I	***699.403566***	350.205421	682.377017	341.692147	681.393001	341.200139	6
4	507.208555	254.107916			489.197990	245.102633	D	***586.319502***	293.663389	569.292953	285.150115	568.308937	284.658107	5
5	620.292619	310.649948			602.282054	301.644665	L	***471.292559***	236.149917	454.266010	227.636643			4
6	717.345383	359.176330			699.334818	350.171047	P	***358.208495***	179.607885	341.181946	171.094611			3
7	831.388310	416.197793	814.361761	407.684519	813.377745	407.192511	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 YDIDLPNK
(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	976.486542	0.004866	YDIDLPNK
5.8	976.483368	0.008040	INIMNMNK
2.4	976.482513	0.008895	QELSKSNTA
0.8	976.501129	-0.009721	SAKACDLAK
0.7	976.497772	-0.006364	AEAPALFSR
0.6	976.497787	-0.006379	YPPGTSLSR
0.6	976.501129	-0.009721	KASAVNMEK
0.3	976.501160	-0.009752	NVPKTQMK

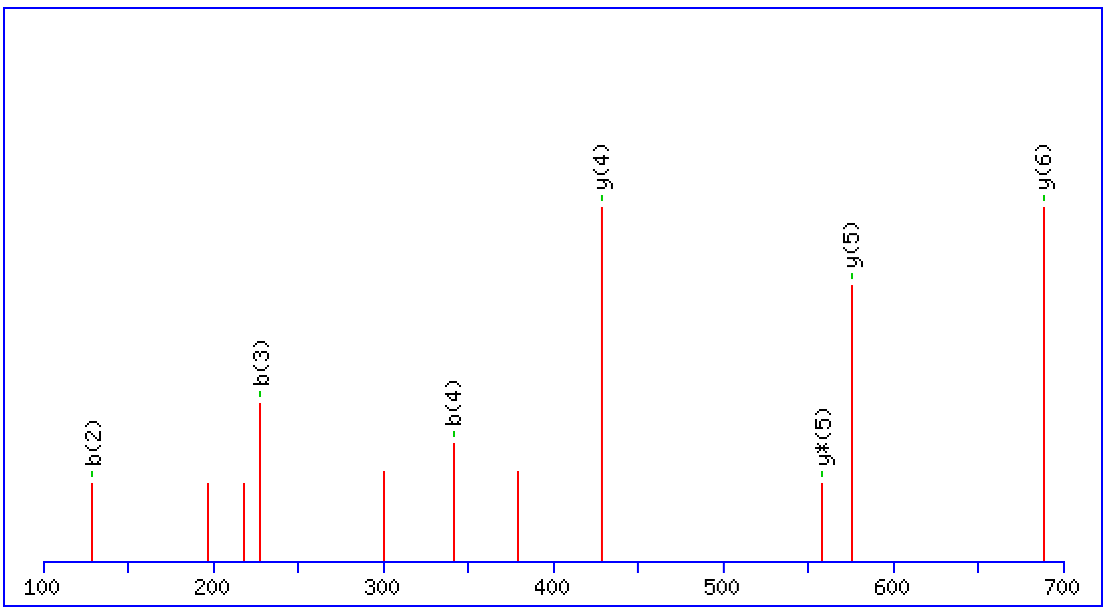
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGVIFPVGR**
Found in **H2AW_HUMAN**, Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3

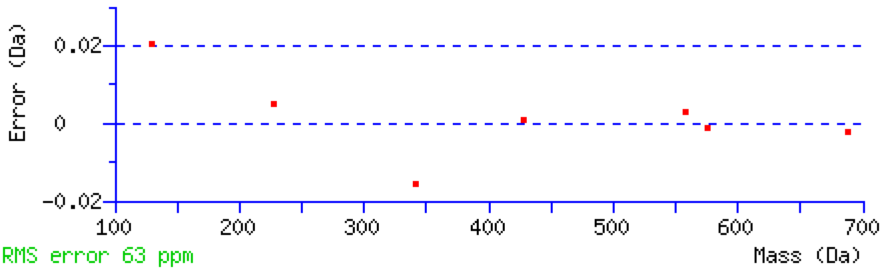
Match to Query 6848: 914.536128 from(458.275340,2+) rtinseconds(2537) index(23358)
Title: Locus:1.1.1.2429.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

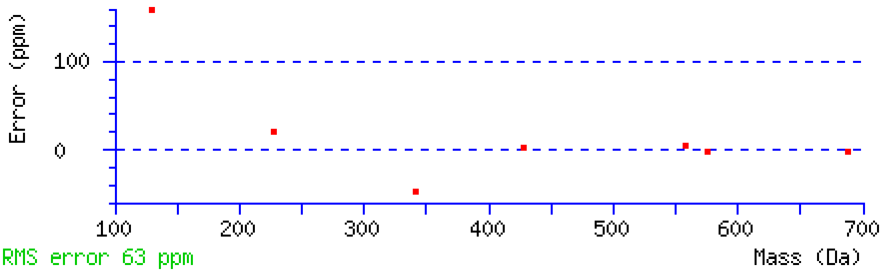
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 914.533798
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0083
Matches : 7/48 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	72.044390	36.525833	A					9
2	***129.065854***	65.036565	G	844.503950	422.755613	827.477401	414.242339	8
3	***228.134268***	114.570772	V	787.482486	394.244881	770.455937	385.731607	7
4	***341.218332***	171.112804	I	***688.414072***	344.710674	671.387523	336.197400	6
5	488.286746	244.647011	F	***575.330008***	288.168642	558.303459	279.655368	5
6	585.339510	293.173393	P	***428.261594***	214.634435	411.235045	206.121161	4
7	684.407924	342.707600	V	331.208830	166.108053	314.182281	157.594779	3
8	741.429388	371.218332	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 AGVIFPVGR
(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	914.533798	0.002330	AGVIFPVGR
21.2	914.543671	-0.007543	KVLDIPSK
13.5	914.533783	0.002345	VKLWDVR
11.4	914.543655	-0.007527	NLLISDLK
11.4	914.533768	0.002360	NLLLTWR
11.4	914.529724	0.006404	RAILASER
9.1	914.543655	-0.007527	KVDELIAK
1.6	914.529755	0.006373	QVASRVQK

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

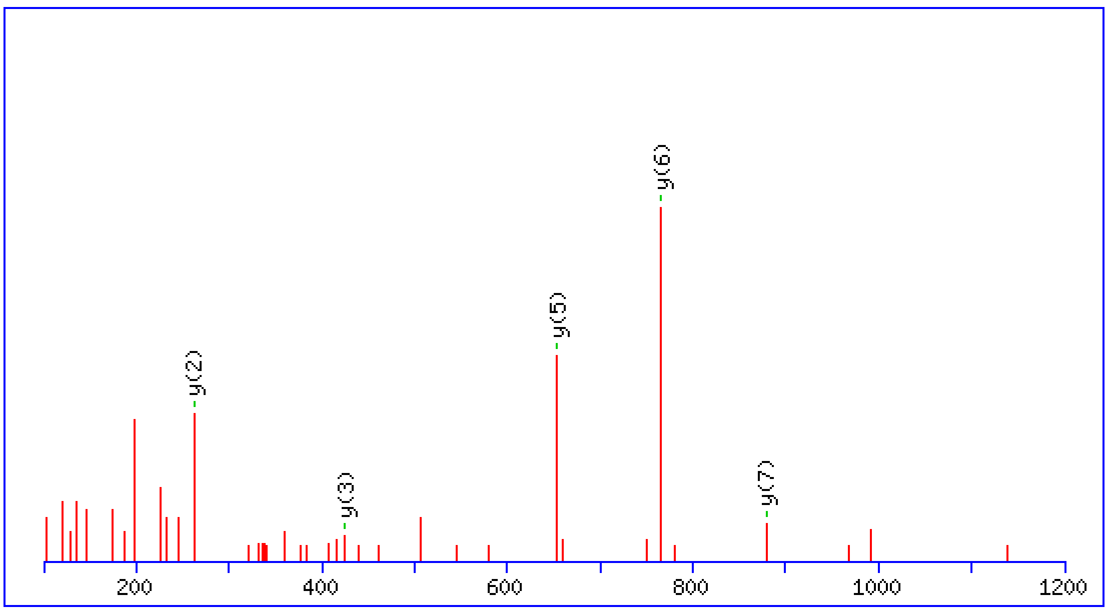
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLDPYSR**
Found in **CTXN1_HUMAN**, Cortexin-1 OS=Homo sapiens GN=CTXN1 PE=2 SV=1

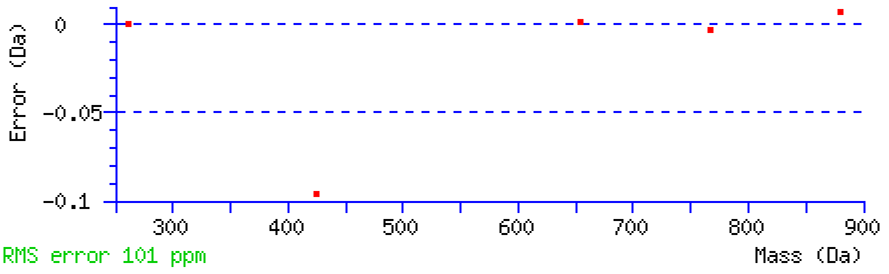
Match to Query 10771: 991.534448 from(496.774500,2+) rtinseconds(2609) index(27622)
Title: Locus:1.1.1.2804.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

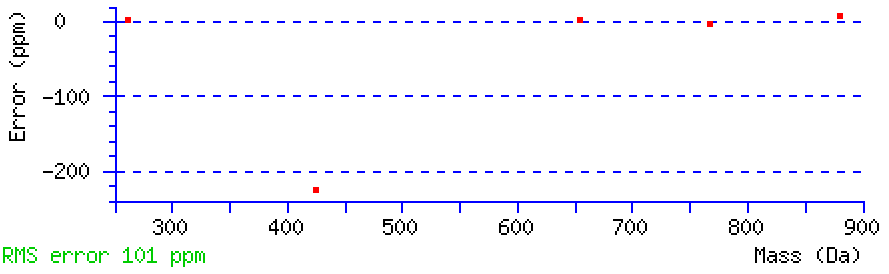
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 991.533829
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 35 **Expect:** 0.0027
Matches : 5/62 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							8
2	227.175404	114.091340			L	***879.457059***	440.232168	862.430510	431.718893	861.446494	431.226885	7
3	340.259468	170.633372			L	***766.372995***	383.690136	749.346446	375.176861	748.362430	374.684853	6
4	455.286411	228.146843	437.275846	219.141561	D	***653.288931***	327.148104	636.262382	318.634829	635.278366	318.142821	5
5	568.334090	284.670683	550.323525	275.665401	P	538.261988	269.634632	521.235439	261.121358	520.251423	260.629350	4
6	731.397419	366.202348	713.386854	357.197065	Y	***425.214309***	213.110793	408.187760	204.597518	407.203744	204.105510	3
7	818.429447	409.718362	800.418882	400.713079	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 ILLDPYSR
(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	991.533829	0.000619	ILLDPYSR
10.5	991.533813	0.000635	LLIYDNNK
8.4	991.541214	-0.006766	LIMLDPYK
5.7	991.533829	0.000619	LLQAADSFK
3.8	991.541031	-0.006583	IRSLSSSSR

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

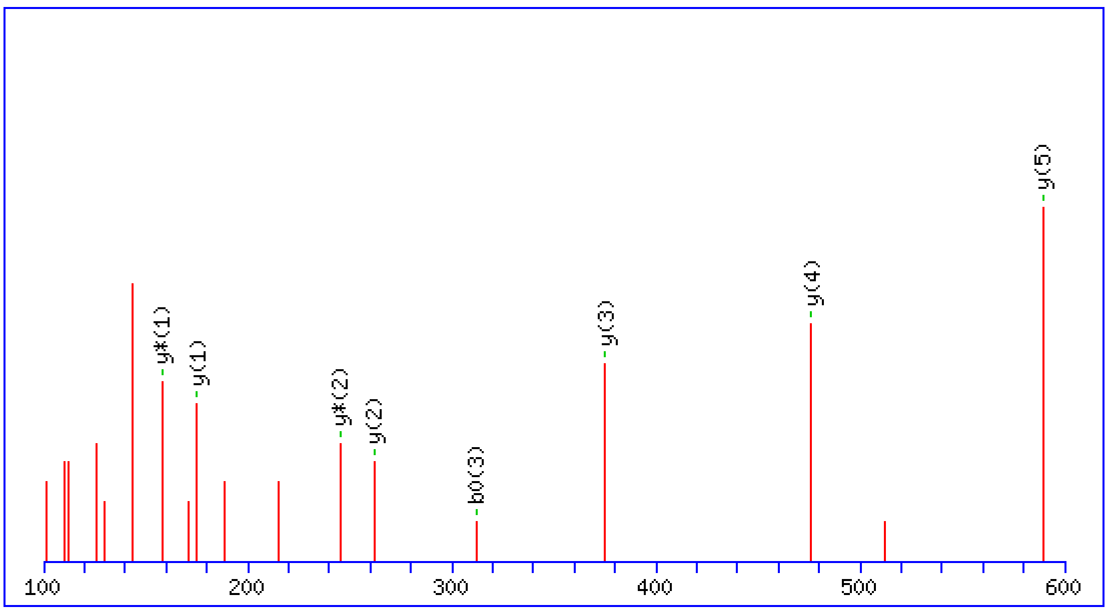
MATRIX SCIENCE Mascot Search Results

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

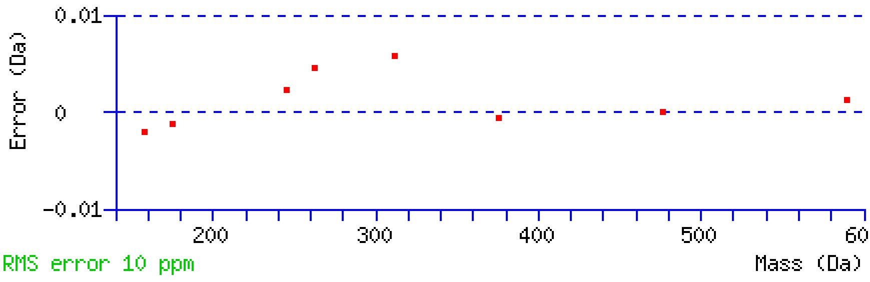
Match to Query 7339: 804.434208 from(403.224380,2+) rtinseconds(1215) index(401801)
Title: Locus:1.1.1.1058.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

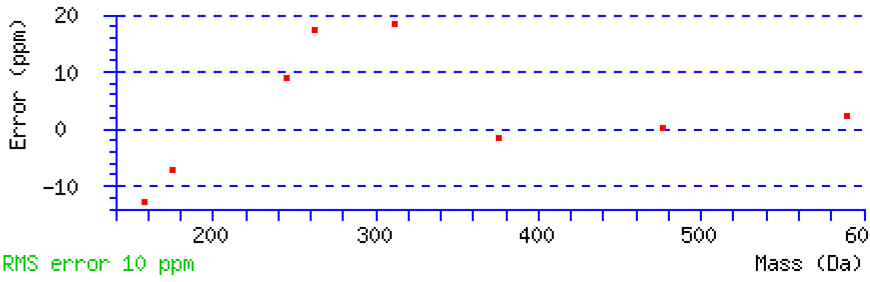
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 804.434128
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0039
Matches : 8/58 fragment ions using 11 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							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
38.9	804.434128	0.000080	TDLTLSR
12.4	804.434113	0.000095	LSELTSR
12.2	804.434113	0.000095	TESLISR
11.6	804.431610	0.002598	MWLSLR
11.4	804.434113	0.000095	SELISTR
7.5	804.434128	0.000080	SLDLTTR
6.4	804.434113	0.000095	SSSLGNLK
3.9	804.434113	0.000095	SSSNILGK
2.2	804.434113	0.000095	DTISNKK
0.5	804.434113	0.000095	KSADSLGK

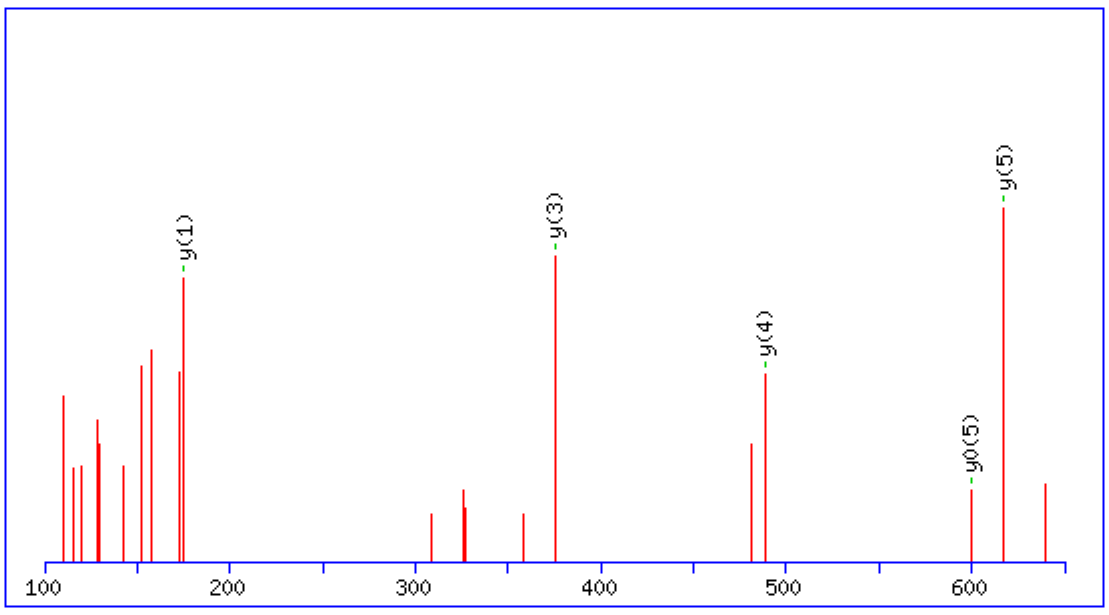
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MEPAREPPSR**
Found in **CLC2L_HUMAN**, C-type lectin domain family 2 member L OS=Homo sapiens GN=CLEC2L PE=2 SV=1

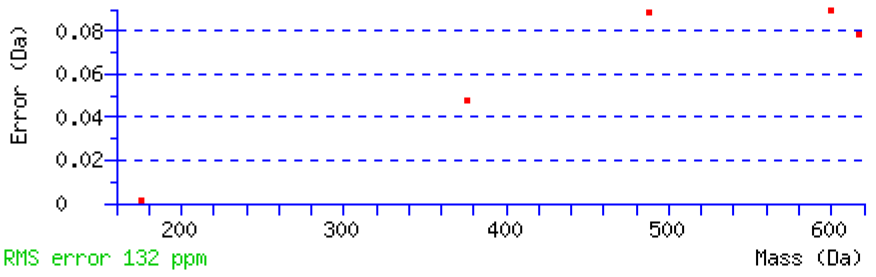
Match to Query 24090: 1200.564192 from(401.195340,3+) rtinseconds(979) index(5116)
Title: Locus:1.1.1.1651.2
Data file 2011-11-14 - TFD - S 2-1.mgf

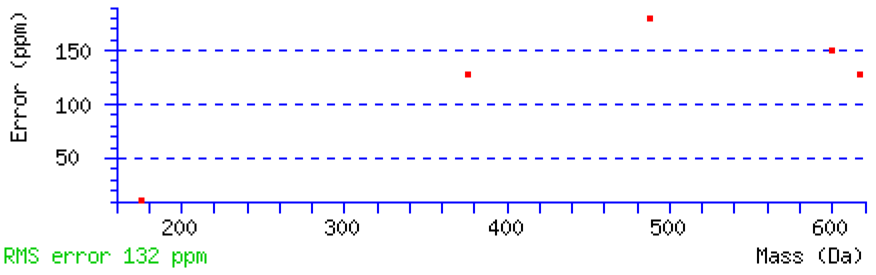
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.555695
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 31  Expect: 0.0097
Matches : 5/96 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	132.047761	66.527518					M							10
2	261.090354	131.048815			243.079789	122.043533	E	1070.522513	535.764895	1053.495964	527.251620	1052.511948	526.759612	9
3	358.143118	179.575197			340.132553	170.569915	P	941.479920	471.243598	924.453371	462.730324	923.469355	462.238316	8
4	429.180232	215.093754			411.169667	206.088472	A	844.427156	422.717216	827.400607	414.203942	826.416591	413.711934	7
5	585.281343	293.144310	568.254794	284.631035	567.270778	284.139027	R	773.390042	387.198659	756.363493	378.685385	755.379477	378.193377	6
6	714.323936	357.665606	697.297387	349.152332	696.313371	348.660324	E	***617.288931***	309.148104	600.262382	300.634829	599.278366	300.142821	5
7	827.371615	414.189446	810.345066	405.676171	809.361050	405.184163	P	***488.246338***	244.626807	471.219789	236.113532	470.235773	235.621524	4
8	940.419294	470.713285	923.392745	462.200011	922.408729	461.708003	P	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
9	1027.451322	514.229299	1010.424773	505.716025	1009.440757	505.224017	S	262.150980	131.579128	245.124431	123.065853	244.140415	122.573845	2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of MEPAREPPSR
(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	1200.555695	0.008497	MEPAREPPSR
17.0	1200.573486	-0.009294	SPTVPSQNPSR
17.0	1200.573486	-0.009294	SPTVPSQNPSR
13.4	1200.573471	-0.009279	SSEAPVQSPQR
12.7	1200.573486	-0.009294	VQAVDSGGPAER
7.5	1200.562241	0.001951	DLSSPTPSEPR
3.0	1200.562241	0.001951	DLSSPTPSEPR
2.1	1200.562225	0.001967	EVLQDSPEER
1.6	1200.552338	0.011854	GWDPNEQSLR
1.3	1200.555695	0.008497	LKEDCHTER

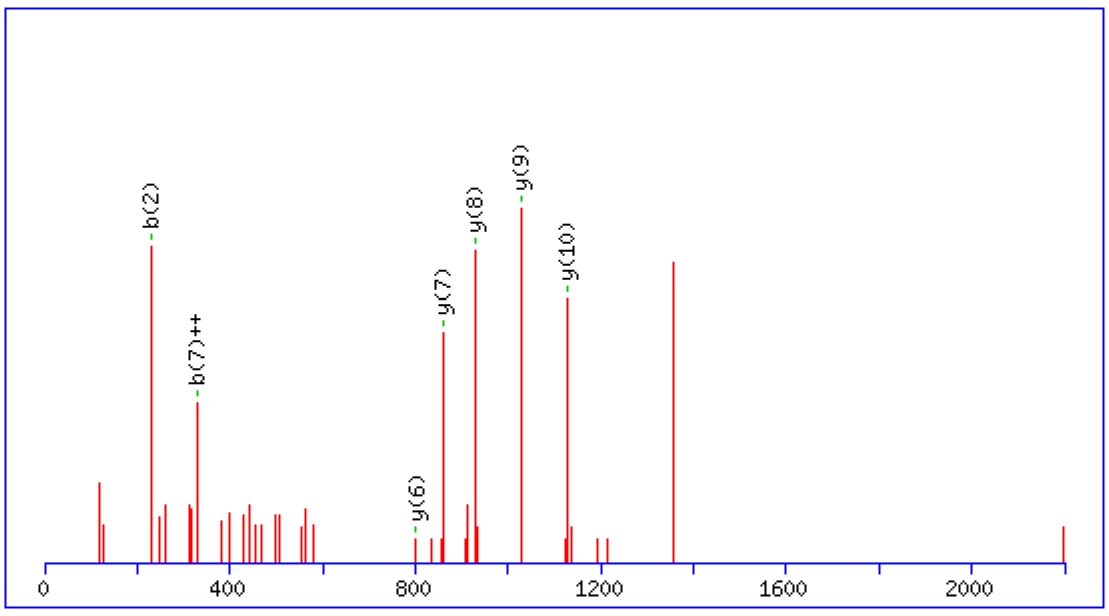
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVVAGTNYYIK**
Found in **CYTA_HUMAN**, Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1

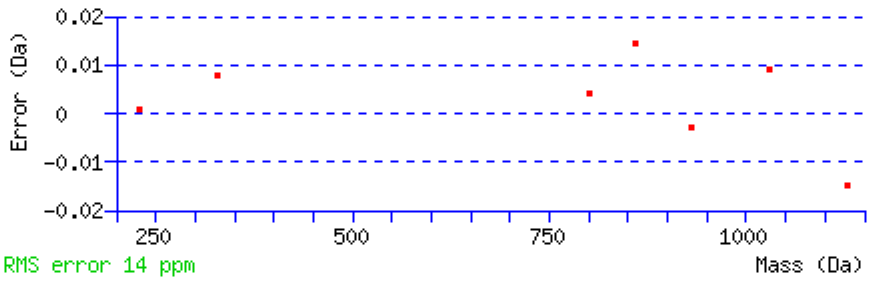
Match to Query 14660: 1355.703588 from(678.859070,2+) rtinseconds(2149) index(5322)
Title: Locus:1.1.1.2840.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

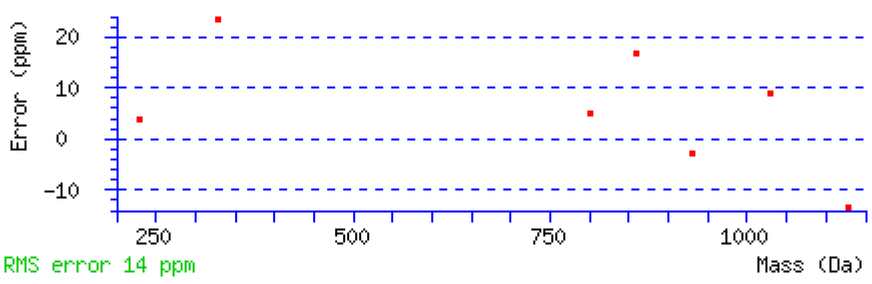
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1355.708511
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0035
Matches : 8/120 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							12
2	**230.113533**	115.560405	213.086984	107.047130	212.102968	106.555122	Q	1255.668116	628.337696	1238.641567	619.824422	1237.657551	619.332414	11
3	**329.181947**	165.094612	312.155398	156.581337	311.171382	156.089329	V	***1127.609538***	564.308407	1110.582989	555.795133	1109.598973	555.303124	10
4	428.250361	214.628819	411.223812	206.115544	410.239796	205.623536	V	***1028.541124***	514.774200	1011.514575	506.260926	1010.530559	505.768918	9
5	499.287475	250.147376	482.260926	241.634101	481.276910	241.142093	A	***929.472710***	465.239993	912.446161	456.726719	911.462145	456.234711	8
6	556.308939	278.658108	539.282390	270.144833	538.298374	269.652825	G	***858.435596***	429.721436	841.409047	421.208162	840.425031	420.716154	7
7	657.356618	329.181947	640.330069	320.668673	639.346053	320.176665	T	***801.414132***	401.210704	784.387583	392.697430	783.403567	392.205422	6
8	771.399545	386.203411	754.372996	377.690136	753.388980	377.198128	N	700.366453	350.686865	683.339904	342.173590			5
9	934.462874	467.735075	917.436325	459.221801	916.452309	458.729793	Y	586.323526	293.665401	569.296977	285.152127			4
10	1097.526203	549.266740	1080.499654	540.753465	1079.515638	540.261457	Y	423.260197	212.133736	406.233648	203.620462			3
11	1210.610267	605.808772	1193.583718	597.295497	1192.599702	596.803489	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 TQVVAGTNYYIK
(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	1355.708511	-0.004923	TQVVAGTNYYIK
12.2	1355.715714	-0.012126	QTLRSPEAGPIR
8.0	1355.708511	-0.004923	TLNFSNYGVTLK
5.1	1355.709183	-0.005595	QTLRCNPRPGK
4.3	1355.709183	-0.005595	QTLRCNPRPGK
4.0	1355.715683	-0.012095	QEAEQLKNQIR
2.9	1355.711899	-0.008311	KMTVNGAPVPPLT
2.3	1355.690750	0.012838	GISAALVYPFMR
1.2	1355.697235	0.006353	KSLEEAEIYFK
0.8	1355.704468	-0.000880	QEAGLIPRTEDK

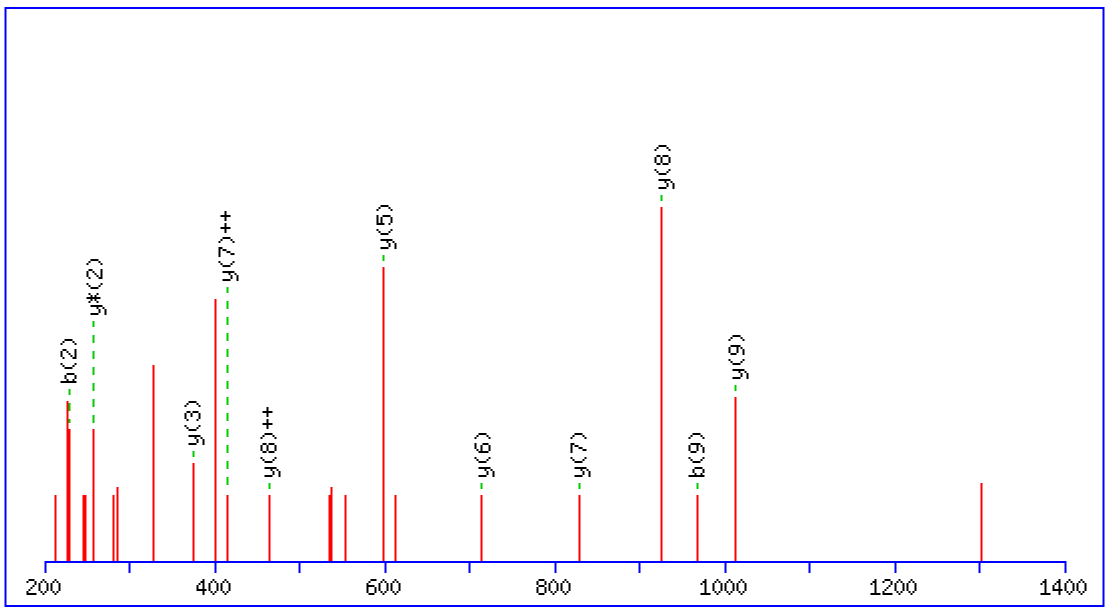
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLSPDDPQVQK**
Found in **CYTM_HUMAN**, Cystatin-M OS=Homo sapiens GN=CST6 PE=1 SV=1

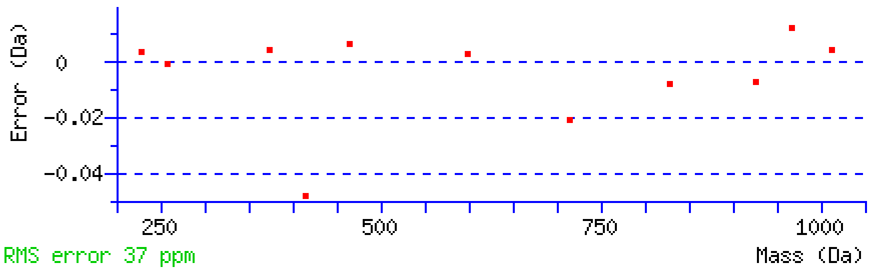
Match to Query 7877: 1240.600708 from(621.307630,2+) rtinseconds(1539) index(2132)
Title: Locus:1.1.1.2487.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

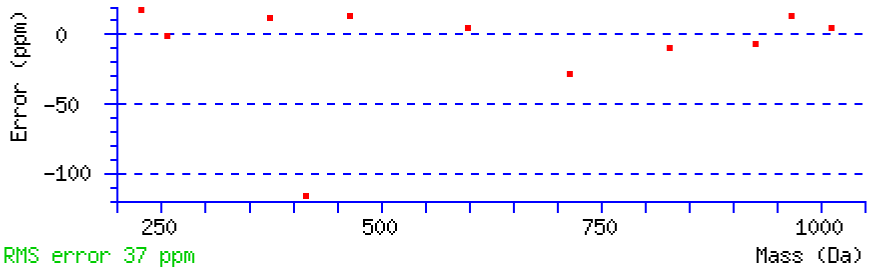
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1240.593552
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0005
Matches : 11/96 fragment ions using 16 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							11
2	**229.118283**	115.062779			211.107718	106.057497	L	1126.573880	563.790578	1109.547331	555.277304	1108.563315	554.785295	10
3	316.150311	158.578793			298.139746	149.573511	S	***1013.489816***	507.248546	996.463267	498.735272	995.479251	498.243264	9
4	413.203075	207.105175			395.192510	198.099893	P	***926.457788***	463.732532	909.431239	455.219257	908.447223	454.727249	8
5	528.230018	264.618647			510.219453	255.613364	D	***829.405024***	415.206150	812.378475	406.692876	811.394459	406.200868	7
6	643.256961	322.132118			625.246396	313.126836	D	***714.378081***	357.692679	697.351532	349.179404	696.367516	348.687396	6
7	740.309725	370.658501			722.299160	361.653218	P	***599.351138***	300.179207	582.324589	291.665933			5
8	868.368303	434.687790	851.341754	426.174515	850.357738	425.682507	Q	502.298374	251.652825	485.271825	243.139550			4
9	**967.436717**	484.221996	950.410168	475.708722	949.426152	475.216714	V	***374.239796***	187.623536	357.213247	179.110261			3
10	1095.495295	548.251285	1078.468746	539.738011	1077.484730	539.246003	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 DLSPDDPQVQK
(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	1240.593552	0.007156	DLSPDDPQVQK
9.6	1240.612152	-0.011444	MPDPAKSAPAPK
5.4	1240.612152	-0.011444	MPDPSKSAPAPK
3.4	1240.612152	-0.011444	MPDPAKSAPAPK
0.7	1240.604767	-0.004059	GAKGEAGAEGPPGK
0.3	1240.612152	-0.011444	MPDPAKSAPAPK
0.3	1240.612152	-0.011444	MPDPAKSAPAPK

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

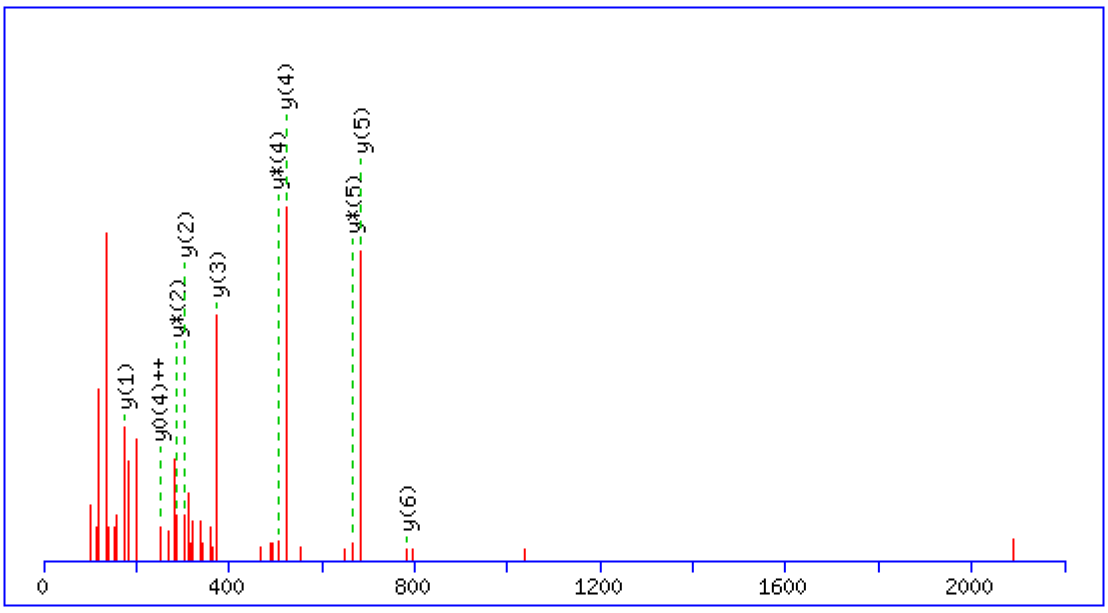
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVYFAER**
Found in **CRIP1_HUMAN**, Cysteine-rich protein 1 OS=Homo sapiens GN=CRIP1 PE=1 SV=3

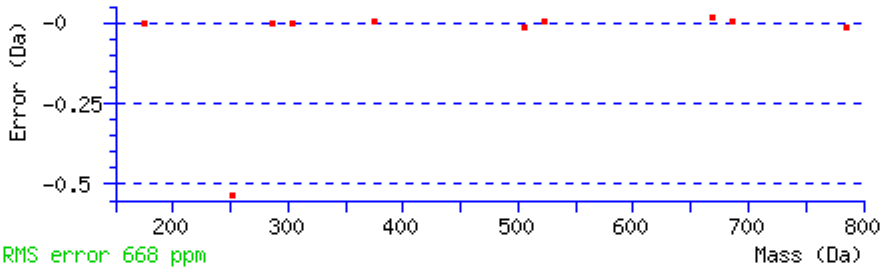
Match to Query 4056: 912.433948 from(457.224250,2+) rtinseconds(1868) index(2584)
Title: Locus:1.1.1.2416.9
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-7.mgf

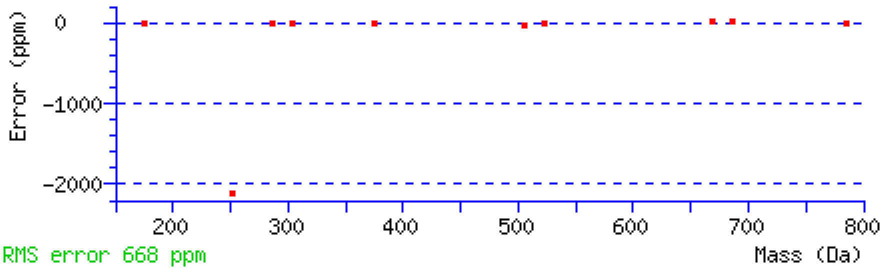
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 912.434113
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0011
Matches : 10/58 fragment ions using 20 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							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
37.7	912.434113	-0.000165	EVYFAER
16.6	912.430084	0.003864	EAAGPPEAR
11.0	912.430084	0.003864	EAAGPPEAR
7.3	912.437485	-0.003537	YLDMISR
6.2	912.434128	-0.000180	YPDFLSR
5.2	912.441330	-0.007382	EVSSHAQR
3.4	912.430954	0.002994	MPHLMER

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

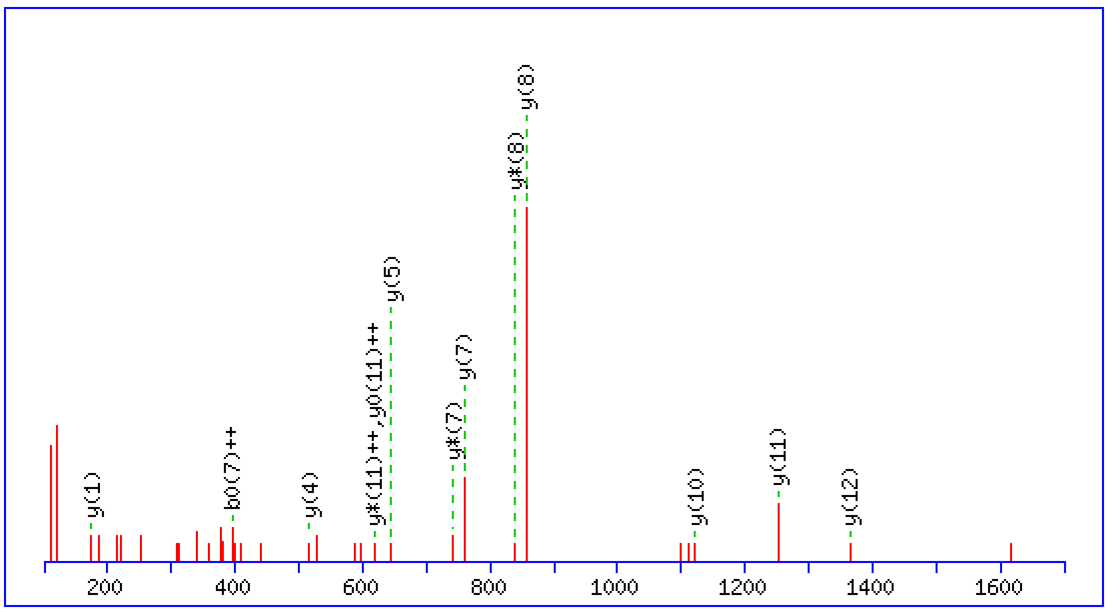
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLEEHPGGEEVLR**
Found in **CYB5_HUMAN**, Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2

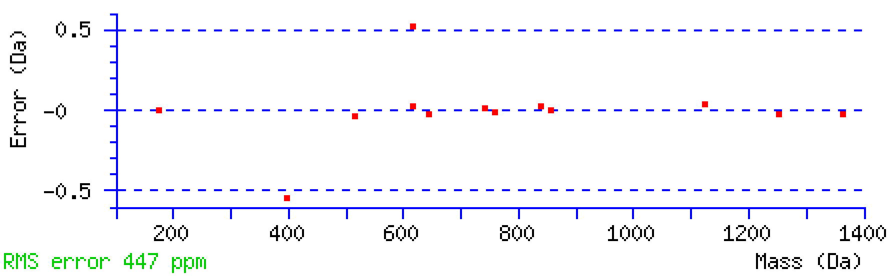
Match to Query 20094: 1510.738392 from(504.586740,3+) rtinseconds(2049) index(9075)
Title: Locus:1.1.1.2367.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

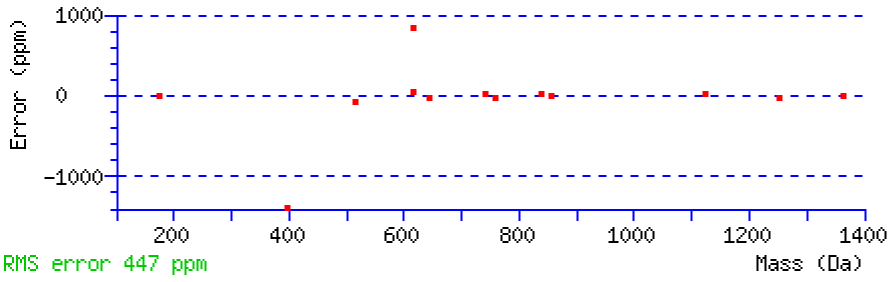
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1510.741592
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 8.8e-005
Matches : 13/110 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							13
2	261.159754	131.083515			L	***1364.680470***	682.843873	1347.653921	674.330599	1346.669905	673.838591	12
3	390.202347	195.604811	372.191782	186.599529	E	***1251.596406***	626.301841	1234.569857	617.788567	1233.585841	617.296559	11
4	519.244940	260.126108	501.234375	251.120826	E	***1122.553813***	561.780545	1105.527264	553.267270	1104.543248	552.775262	10
5	656.303852	328.655564	638.293287	319.650282	H	993.511220	497.259248	976.484671	488.745974	975.500655	488.253966	9
6	753.356616	377.181946	735.346051	368.176664	P	***856.452308***	428.729792	839.425759	420.216518	838.441743	419.724510	8
7	810.378080	405.692678	792.367515	396.687396	G	***759.399544***	380.203410	742.372995	371.690136	741.388979	371.198128	7
8	867.399544	434.203410	849.388979	425.198128	G	702.378080	351.692678	685.351531	343.179404	684.367515	342.687396	6
9	996.442137	498.724707	978.431572	489.719424	E	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
10	1125.484730	563.246003	1107.474165	554.240721	E	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
11	1224.553144	612.780210	1206.542579	603.774928	V	387.271430	194.139353	370.244881	185.626078			3
12	1337.637208	669.322242	1319.626643	660.316960	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 FLEEHPGGEEVLR
(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	1510.741592	-0.003200	FLEEHPGGEEVLR
0.8	1510.730362	0.008030	FSSGLFNKPEEPK
0.8	1510.727188	0.011204	EMNPALGIDCLHK
0.1	1510.745819	-0.007427	FLCALCVSALCR

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

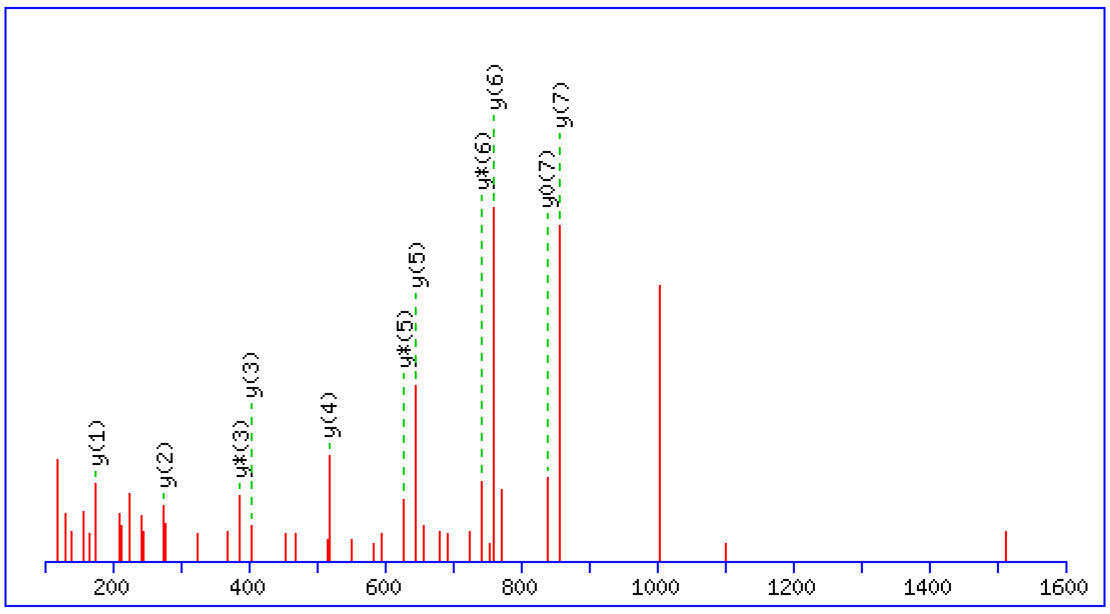
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPNQNQTR**
Found in **CX6B1_HUMAN**, Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2

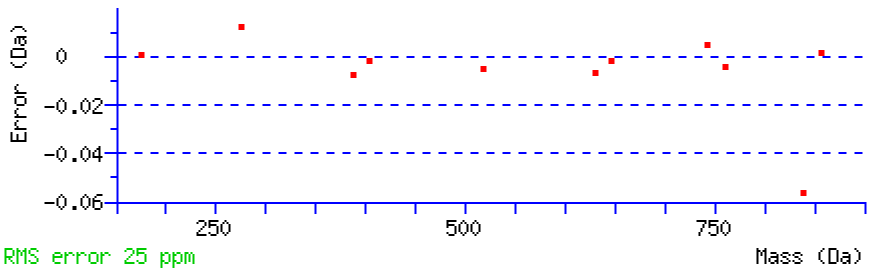
Match to Query 6396: 1003.483348 from(502.748950,2+) rtinseconds(992) index(317)
Title: Locus:1.1.1.2122.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

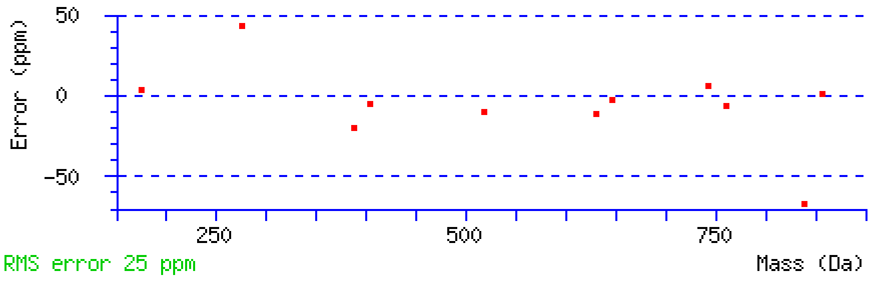
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1003.483536
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.4e-005
Matches : 11/66 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	148.075690	74.541483					F							8
2	245.128454	123.067865					P	*857.422405*	429.214841	840.395856	420.701566	839.411840	420.209558	7
3	359.171381	180.089328	342.144832	171.576054			N	*760.369641*	380.688459	743.343092	372.175184	742.359076	371.683176	6
4	487.229959	244.118618	470.203410	235.605343			Q	*646.326714*	323.666995	629.300165	315.153721	628.316149	314.661713	5
5	601.272886	301.140081	584.246337	292.626807			N	*518.268136*	259.637706	501.241587	251.124432	500.257571	250.632424	4
6	729.331464	365.169370	712.304915	356.656096			Q	*404.225209*	202.616242	387.198660	194.102968	386.214644	193.610960	3
7	830.379143	415.693210	813.352594	407.179935	812.368578	406.687927	T	*276.166631*	138.586953	259.140082	130.073679	258.156066	129.581671	2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FPNQNQTR
(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	1003.483536	-0.000188	FPNQNQTR
6.4	1003.489563	-0.006215	MIPEELEK
6.4	1003.489563	-0.006215	MIPEELEK
2.6	1003.483063	0.000285	CGMLIGPDK
2.5	1003.482193	0.001155	EPKAPTSDK
1.0	1003.483704	-0.000356	FPYLCYK
0.3	1003.490921	-0.007573	FHGKMEQK
0.0	1003.475662	0.007686	EDCLQGIR

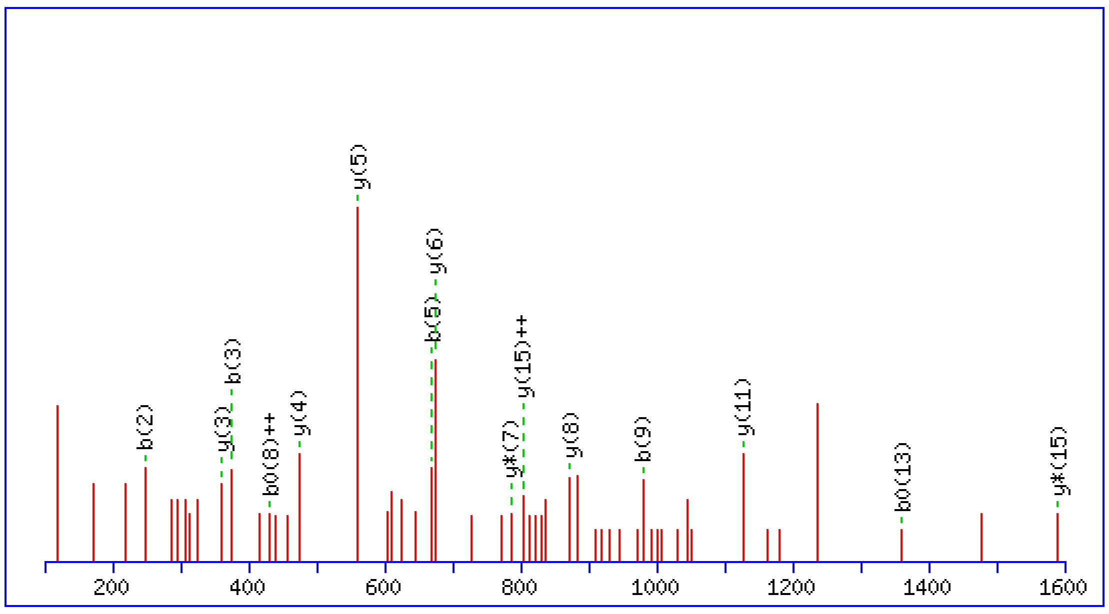
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVEFFGPGVAQLSIADR**
Found in **ACOC_HUMAN**, Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3

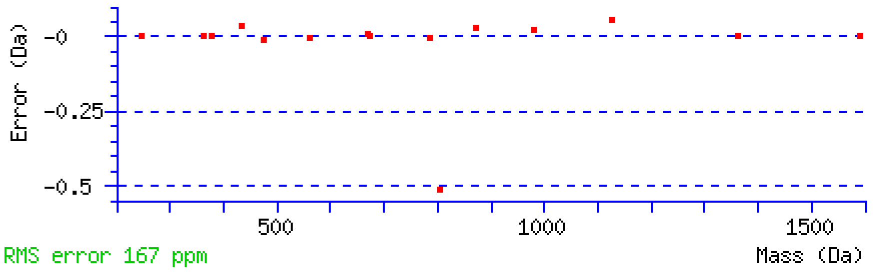
Match to Query 55309: 1851.959712 from(618.327180,3+) rtinseconds(3803) index(59101)
Title: Locus:1.1.1.2095.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

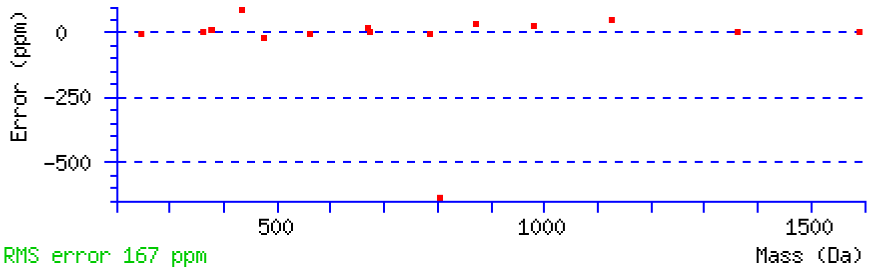
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1851.951950
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0051
Matches : 15/166 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	148.075690	74.541483					F							17
2	***247.144104***	124.075690					V	1705.890798	853.449037	1688.864249	844.935763	1687.880233	844.443754	16
3	***376.186697***	188.596986			358.176132	179.591704	E	1606.822384	803.914830	1589.795835	795.401556	1588.811819	794.909548	15
4	523.255111	262.131194			505.244546	253.125911	F	1477.779791	739.393533	1460.753242	730.880259	1459.769226	730.388251	14
5	***670.323525***	335.665401			652.312960	326.660118	F	1330.711377	665.859326	1313.684828	657.346052	1312.700812	656.854044	13
6	727.344989	364.176133			709.334424	355.170850	G	1183.642963	592.325120	1166.616414	583.811845	1165.632398	583.319837	12
7	824.397753	412.702515			806.387188	403.697232	P	***1126.621499***	563.814388	1109.594950	555.301113	1108.610934	554.809105	11
8	881.419217	441.213247			863.408652	432.207964	G	1029.568735	515.288006	1012.542186	506.774731	1011.558170	506.282723	10
9	***980.487631***	490.747454			962.477066	481.742171	V	972.547271	486.777273	955.520722	478.263999	954.536706	477.771991	9
10	1051.524745	526.266011			1033.514180	517.260728	A	***873.478857***	437.243067	856.452308	428.729792	855.468292	428.237784	8
11	1179.583323	590.295300	1162.556774	581.782025	1161.572758	581.290017	Q	802.441743	401.724509	785.415194	393.211235	784.431178	392.719227	7
12	1292.667387	646.837332	1275.640838	638.324057	1274.656822	637.832049	L	***674.383165***	337.695221	657.356616	329.181946	656.372600	328.689938	6
13	1379.699415	690.353346	1362.672866	681.840071	1361.688850	681.348063	S	***561.299101***	281.153189	544.272552	272.639914	543.288536	272.147906	5
14	1492.783479	746.895378	1475.756930	738.382103	1474.772914	737.890095	I	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
15	1563.820593	782.413934	1546.794044	773.900660	1545.810028	773.408652	A	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
16	1678.847536	839.927406	1661.820987	831.414132	1660.836971	830.922124	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of FVEFFGPGVAQLSIADR
(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	1851.951950	0.007762	FVEFFGPGVAQLSIADR

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

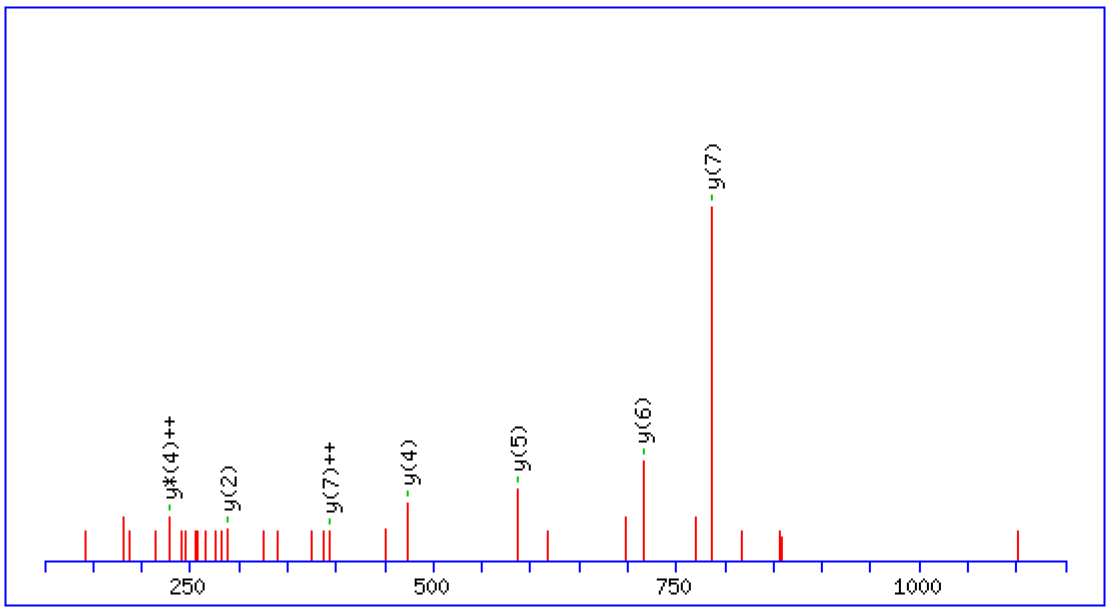
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLAEINANR**
Found in **DC1I2_HUMAN**, Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3

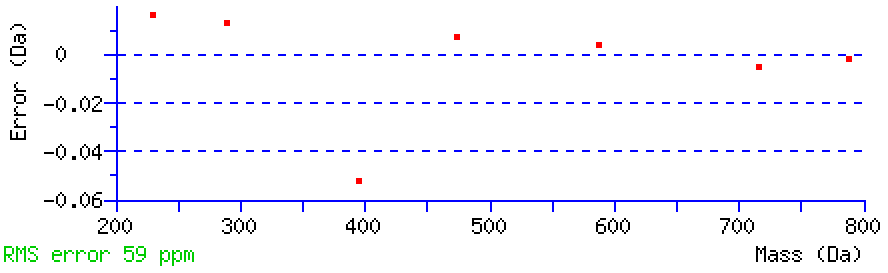
Match to Query 10389: 1000.529208 from(501.271880,2+) rtinseconds(1416) index(11633)
Title: Locus:1.1.1.2052.19
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-2.mgf

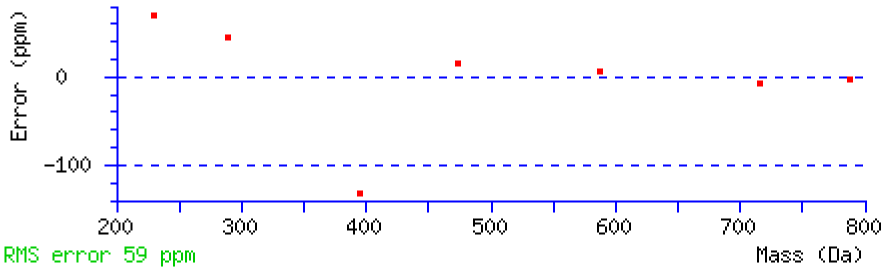
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1000.530121
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0007
Matches : 7/76 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**							9
2	215.139019	108.073147			197.128454	99.067865	**L**	900.489755	450.748516	883.463206	442.235241	882.479190	441.743233	8
3	286.176133	143.591704			268.165568	134.586422	**A**	***787.405691***	394.206484	770.379142	385.693209	769.395126	385.201201	7
4	415.218726	208.113001			397.208161	199.107719	**E**	***716.368577***	358.687927	699.342028	350.174652	698.358012	349.682644	6
5	528.302790	264.655033			510.292225	255.649751	**I**	***587.325984***	294.166630	570.299435	285.653356			5
6	642.345717	321.676497	625.319168	313.163222	624.335152	312.671214	**N**	***474.241920***	237.624598	457.215371	229.111323			4
7	713.382831	357.195054	696.356282	348.681779	695.372266	348.189771	**A**	360.198993	180.603134	343.172444	172.089860			3
8	827.425758	414.216517	810.399209	405.703242	809.415193	405.211234	**N**	***289.161879***	145.084577	272.135330	136.571303			2
9							**R**	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TLAEINANR
(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	1000.530121	-0.000913	TLAEINANR
6.8	1000.520248	0.008960	DVAAWGRAR
5.9	1000.530151	-0.000943	RNSGPVVEK

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

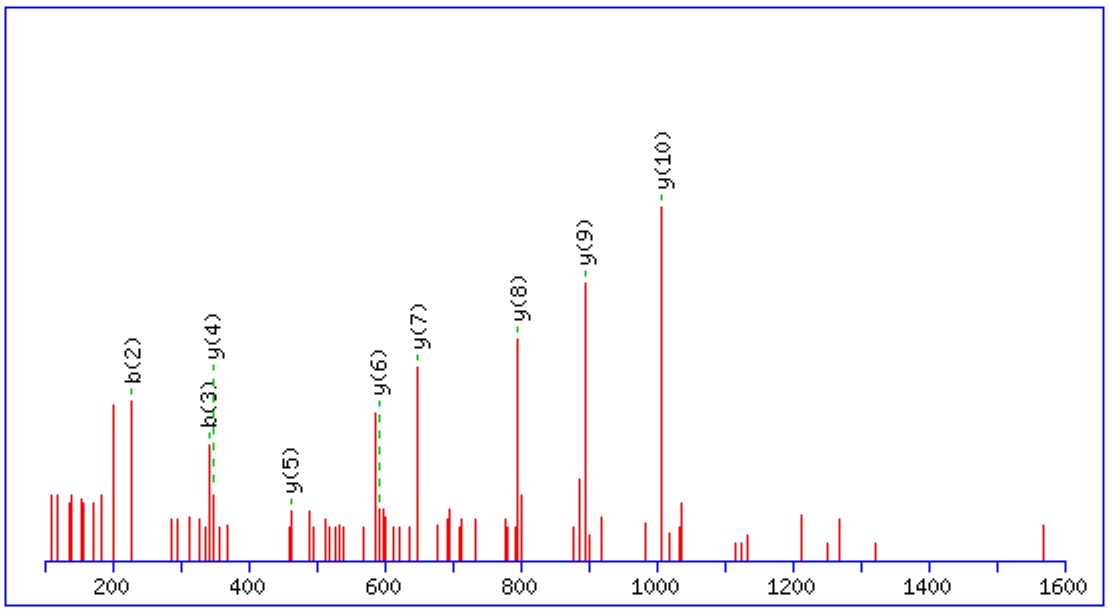
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NILVFGEDGSGK**
Found in **DC1L2_HUMAN**, Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1

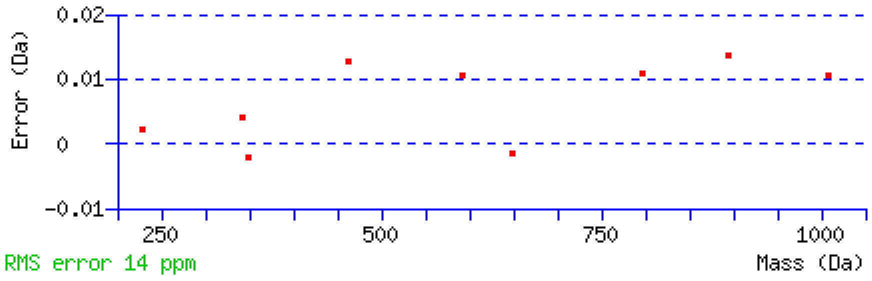
Match to Query 19612: 1234.624148 from(618.319350,2+) rtinseconds(2463) index(31261)
Title: Locus:1.1.1.2462.22
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

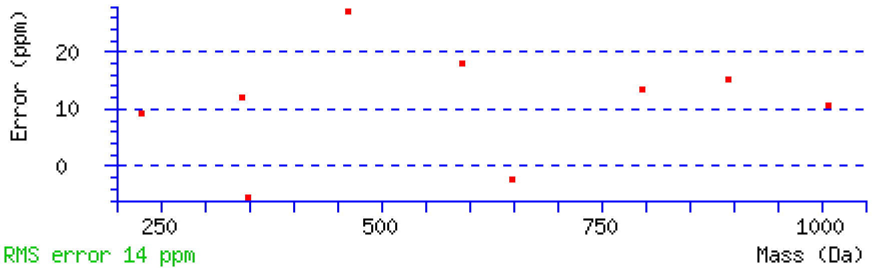
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1234.619370
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.00063
Matches : 9/116 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							12
2	**228.134267**	114.570771	211.107718	106.057497			I	1121.583716	561.295496	1104.557167	552.782222	1103.573151	552.290214	11
3	**341.218331**	171.112803	324.191782	162.599529			L	***1008.499652***	504.753464	991.473103	496.240190	990.489087	495.748182	10
4	440.286745	220.647010	423.260196	212.133736			V	***895.415588***	448.211432	878.389039	439.698158	877.405023	439.206150	9
5	587.355159	294.181218	570.328610	285.667943			F	***796.347174***	398.677225	779.320625	390.163951	778.336609	389.671943	8
6	644.376623	322.691950	627.350074	314.178675			G	***649.278760***	325.143018	632.252211	316.629744	631.268195	316.137736	7
7	773.419216	387.213246	756.392667	378.699972	755.408651	378.207964	E	***592.257296***	296.632286	575.230747	288.119012	574.246731	287.627004	6
8	888.446159	444.726718	871.419610	436.213443	870.435594	435.721435	D	***463.214703***	232.110989	446.188154	223.597715	445.204138	223.105707	5
9	945.467623	473.237450	928.441074	464.724175	927.457058	464.232167	G	***348.187760***	174.597518	331.161211	166.084243	330.177195	165.592235	4
10	1032.499651	516.753464	1015.473102	508.240189	1014.489086	507.748181	S	291.166296	146.086786	274.139747	137.573511	273.155731	137.081503	3
11	1089.521115	545.264196	1072.494566	536.750921	1071.510550	536.258913	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 NILVFGEDGSGK
(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	1234.619370	0.004778	NILVFGEDGSGK
0.9	1234.630585	-0.006437	LNLPPSPHANK

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

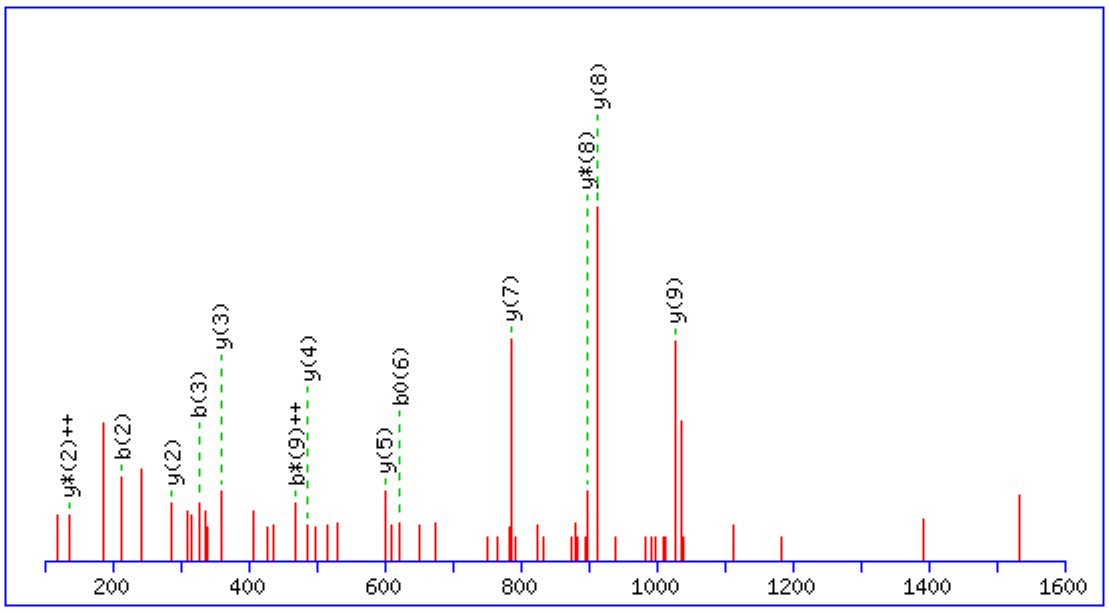
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVIQSVLQAIR**
Found in **CYFP1_HUMAN**, Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1

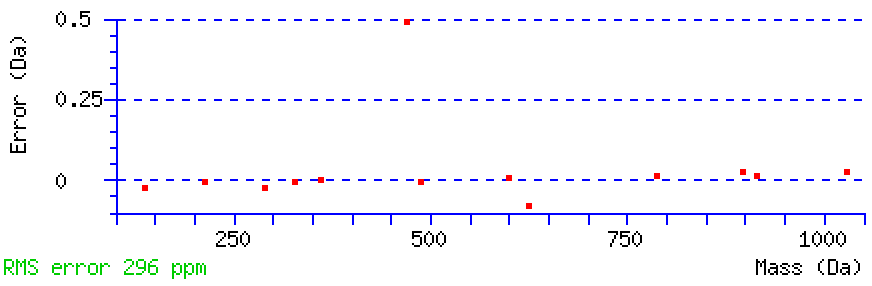
Match to Query 25831: 1239.739108 from(620.876830,2+) rtinseconds(4044) index(63431)
Title: Locus:1.1.1.2187.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

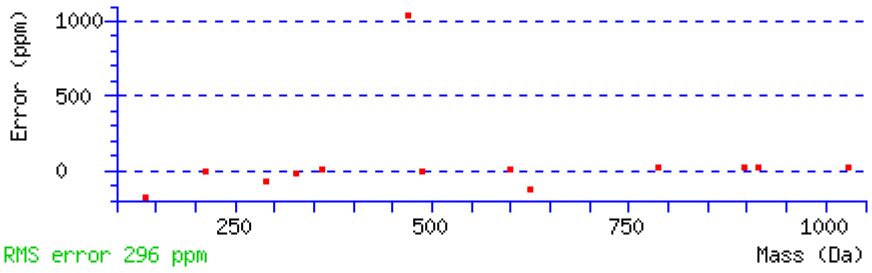
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1239.729904
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0011
Matches : 13/100 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	115.050203	58.028740	98.023654	49.515465			N							11
2	**214.118617**	107.562947	197.092068	99.049672			V	1126.694270	563.850773	1109.667721	555.337499	1108.683705	554.845490	10
3	**327.202681**	164.104978	310.176132	155.591704			I	***1027.625856***	514.316566	1010.599307	505.803291	1009.615291	505.311283	9
4	455.261259	228.134267	438.234710	219.620993			Q	***914.541792***	457.774534	897.515243	449.261259	896.531227	448.769252	8
5	542.293287	271.650282	525.266738	263.137007	524.282722	262.644999	S	***786.483214***	393.745245	769.456665	385.231970	768.472649	384.739962	7
6	641.361701	321.184489	624.335152	312.671214	623.351136	312.179206	V	699.451186	350.229231	682.424637	341.715956			6
7	754.445765	377.726521	737.419216	369.213246	736.435200	368.721238	L	***600.382772***	300.695024	583.356223	292.181749			5
8	882.504343	441.755810	865.477794	433.242535	864.493778	432.750527	Q	***487.298708***	244.152992	470.272159	235.639717			4
9	953.541457	477.274367	936.514908	468.761092	935.530892	468.269084	A	***359.240130***	180.123703	342.213581	171.610428			3
10	1066.625521	533.816398	1049.598972	525.303124	1048.614956	524.811116	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 NVIQSVLQAIR
(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	1239.729904	0.009204	NVIQSVLQAIR
8.3	1239.741150	-0.002042	GRLQQVLTGLR

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

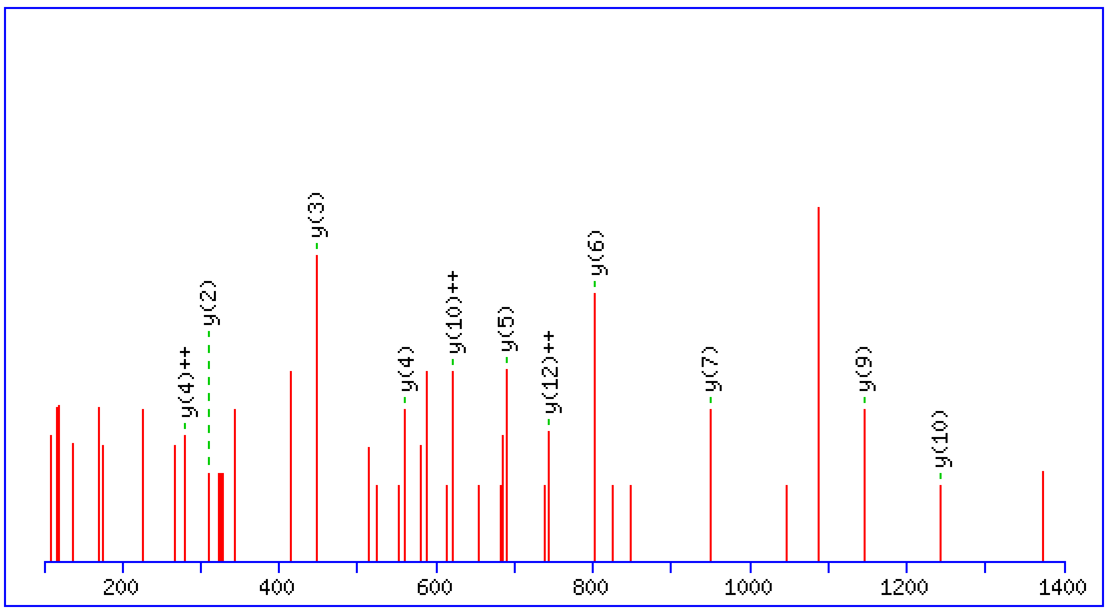
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSDEPPVFLEIHYK**
Found in **AMPL_HUMAN**, Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3

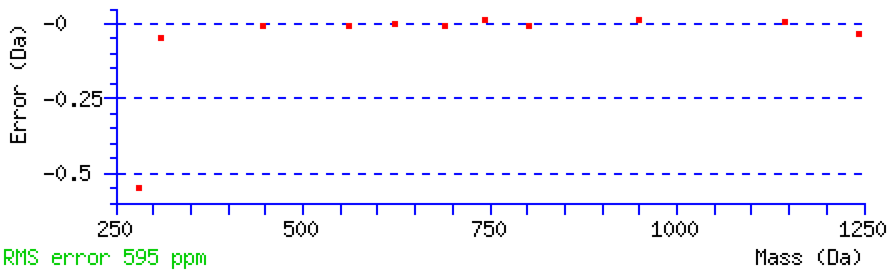
Match to Query 39403: 1629.811002 from(544.277610,3+) rtinseconds(2888) index(35274)
Title: Locus:1.1.1.2627.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

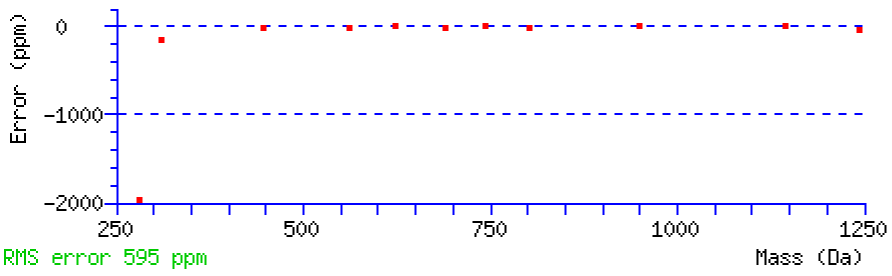
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1629.803864
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00027
Matches : 11/120 fragment ions using 22 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**							**14**
2	145.060768	73.034022	127.050203	64.028740	**S**	1573.789686	787.398481	1556.763137	778.885207	1555.779121	778.393199	**13**
3	260.087711	130.547494	242.077146	121.542211	**D**	1486.757658	743.882467	1469.731109	735.369193	1468.747093	734.877185	**12**
4	389.130304	195.068790	371.119739	186.063508	**E**	1371.730715	686.368995	1354.704166	677.855721	1353.720150	677.363713	**11**
5	486.183068	243.595172	468.172503	234.589890	**P**	***1242.688122***	621.847699	1225.661573	613.334425	1224.677557	612.842417	**10**
6	583.235832	292.121554	565.225267	283.116272	**P**	***1145.635358***	573.321317	1128.608809	564.808043	1127.624793	564.316035	**9**
7	682.304246	341.655761	664.293681	332.650479	**V**	1048.582594	524.794935	1031.556045	516.281661	1030.572029	515.789652	**8**
8	829.372660	415.189968	811.362095	406.184686	**F**	***949.514180***	475.260728	932.487631	466.747454	931.503615	466.255446	**7**
9	942.456724	471.732000	924.446159	462.726718	**L**	***802.445766***	401.726521	785.419217	393.213247	784.435201	392.721239	**6**
10	1071.499317	536.253297	1053.488752	527.248014	**E**	***689.361702***	345.184489	672.335153	336.671215	671.351137	336.179207	**5**
11	1184.583381	592.795328	1166.572816	583.790046	**I**	***560.319109***	280.663193	543.292560	272.149918			**4**
12	1321.642293	661.324784	1303.631728	652.319502	**H**	***447.235045***	224.121161	430.208496	215.607886			**3**
13	1484.705622	742.856449	1466.695057	733.851166	**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 GSDEPPVFLEIHYK
(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	1629.803864	0.007138	GSDEPPVFLEIHYK
7.7	1629.822296	-0.011294	RPWLSATPSSGASAAR
0.3	1629.819809	-0.008807	HCRDVFLAWVASR

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

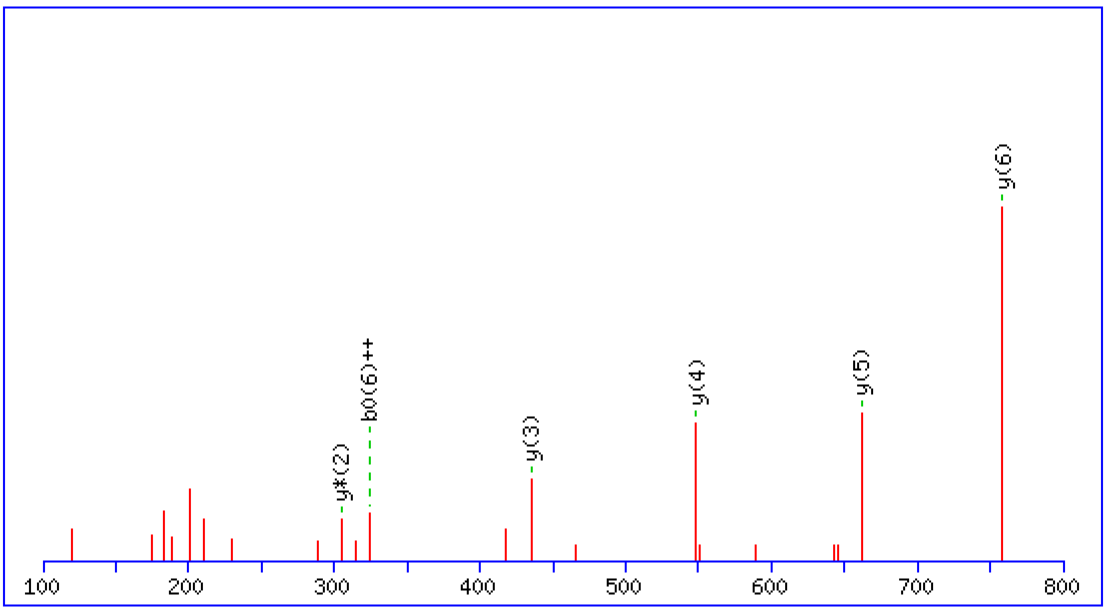
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLPLLLFR**
Found in **SERA_HUMAN**, D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4

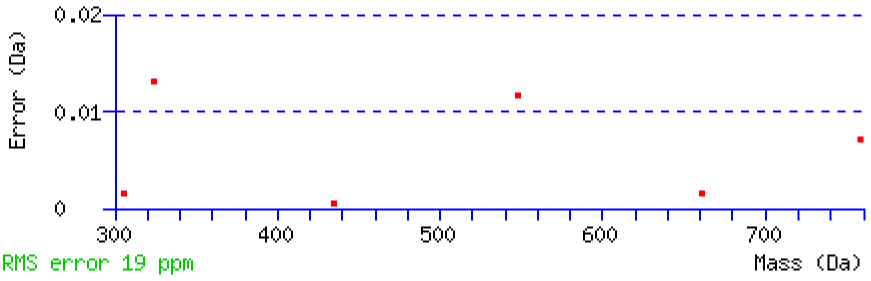
Match to Query 8595: 985.593388 from(493.803970,2+) rtinseconds(3967) index(56244)
Title: Locus:1.1.1.3052.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

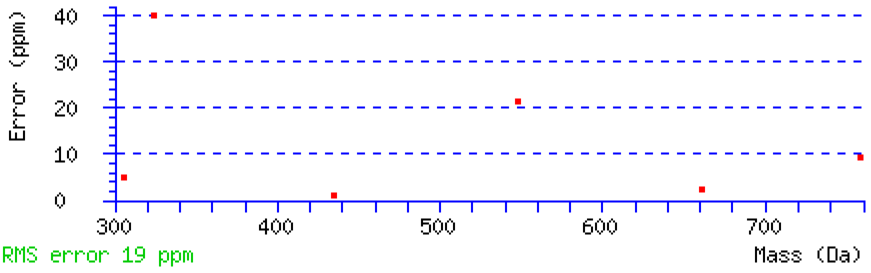
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 985.596039
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0035
Matches : 6/56 fragment ions using 7 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					8
2	229.118283	115.062779	211.107718	106.057497	L	871.576386	436.291831	854.549837	427.778557	7
3	326.171047	163.589161	308.160482	154.583879	P	***758.492322***	379.749799	741.465773	371.236525	6
4	439.255111	220.131193	421.244546	211.125911	L	***661.439558***	331.223417	644.413009	322.710143	5
5	552.339175	276.673226	534.328610	267.667943	L	***548.355494***	274.681385	531.328945	266.168111	4
6	665.423239	333.215258	647.412674	324.209975	L	***435.271430***	218.139353	418.244881	209.626078	3
7	812.491653	406.749465	794.481088	397.744182	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 DLPLLLFR
(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	985.596039	-0.002651	DLPLLLFR
12.8	985.596054	-0.002666	VPLLPFLR
5.5	985.599396	-0.006008	EVMLILIR
4.8	985.596039	-0.002651	VLEPFLLR

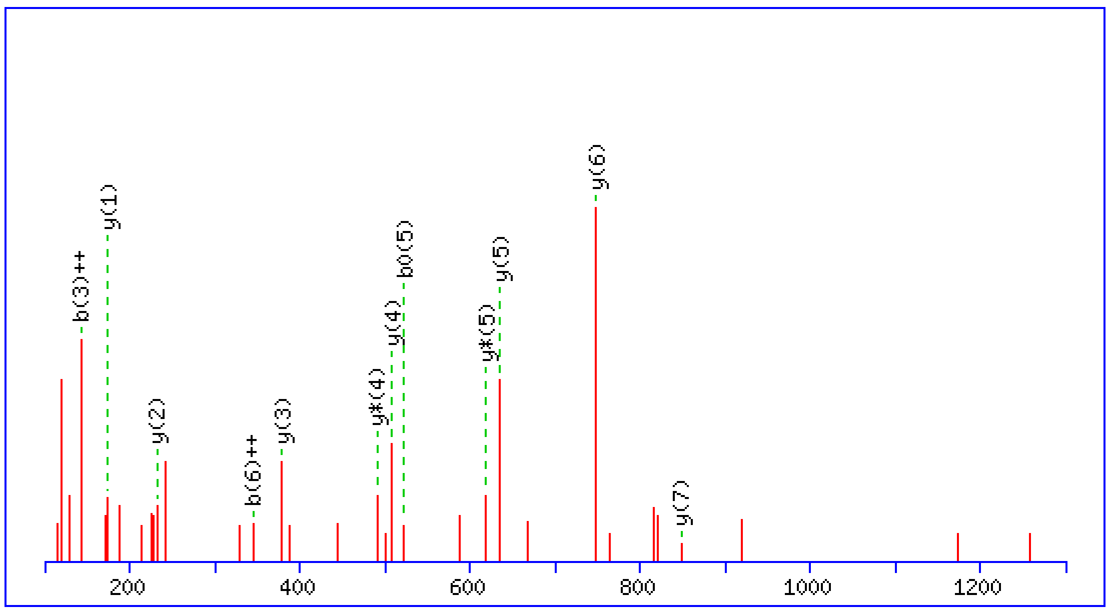
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLQEFGR**
Found in **DHRS7_HUMAN**, Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1

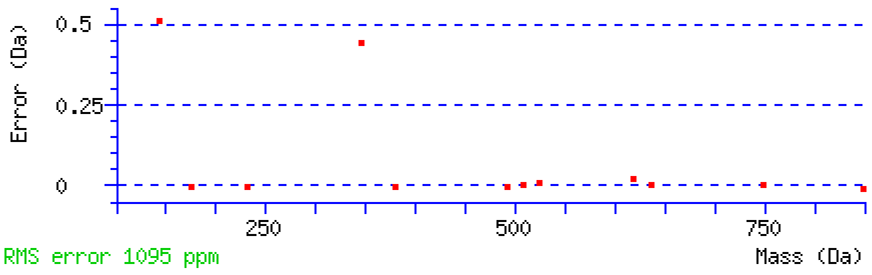
Match to Query 7700: 918.487308 from(460.250930,2+) rtinseconds(2052) index(21287)
Title: Locus:1.1.1.2181.7
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

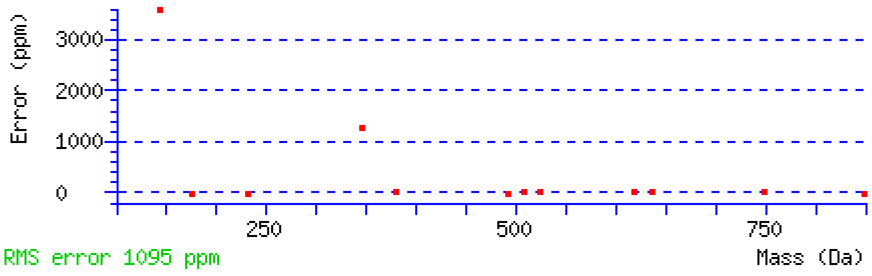
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 918.492310
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00032
Matches : 12/64 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							8
2	171.112804	86.060040					V	***848.462479***	424.734878	831.435930	416.221603	830.451914	415.729595	7
3	284.196868	**142.602072**					L	***749.394065***	375.200671	732.367516	366.687396	731.383500	366.195388	6
4	412.255446	206.631361	395.228897	198.118087			Q	***636.310001***	318.658639	619.283452	310.145364	618.299436	309.653356	5
5	541.298039	271.152658	524.271490	262.639383	523.287474	262.147375	E	***508.251423***	254.629349	491.224874	246.116075	490.240858	245.624067	4
6	688.366453	**344.686865**	671.339904	336.173590	670.355888	335.681582	F	***379.208830***	190.108053	362.182281	181.594778			3
7	745.387917	373.197597	728.361368	364.684322	727.377352	364.192314	G	***232.140416***	116.573846	215.113867	108.060571			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



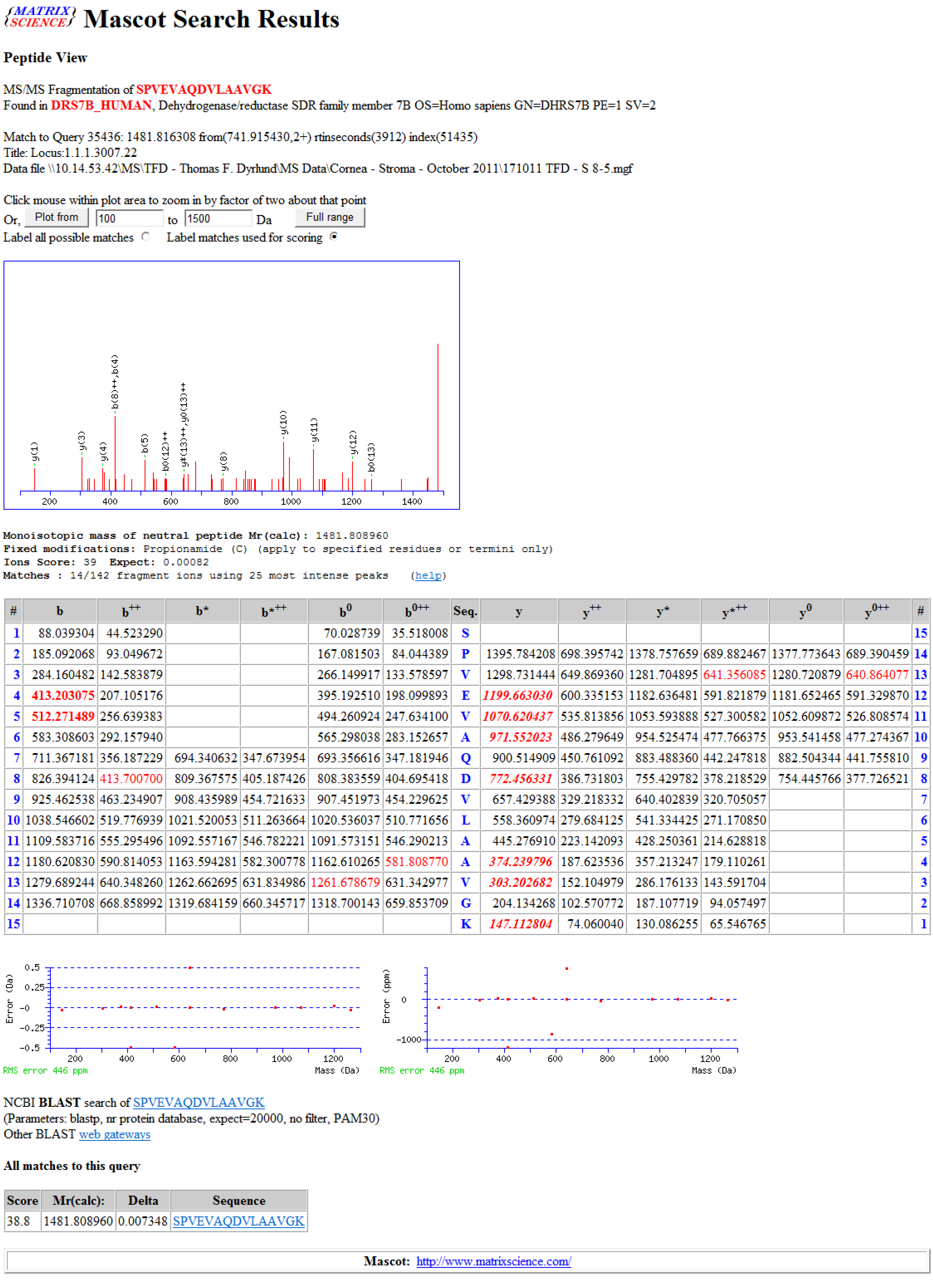


NCBI **BLAST** search of AVLQEFGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.7	918.492310	-0.005002	AVLQEFGR
4.2	918.492310	-0.005002	VLAQFGER
3.8	918.481079	0.006229	FSNDPVLK
3.4	918.484451	0.002857	GLLDVTCK
3.3	918.492310	-0.005002	EVTRTWK
0.9	918.484436	0.002872	MVLNSLDK
0.4	918.482422	0.004886	WNHVVHK
0.2	918.484421	0.002887	EKDLCIK

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPVEVAQDVLAAVGK**
Found in **DRS7B_HUMAN**, Dehydrogenase/reductase SDR family member 7B OS=Homo sapiens GN=DHRS7B PE=1 SV=2

Match to Query 35436: 1481.816308 from(741.915430,2+) rtinseconds(3912) index(51435)
Title: Locus:1.1.1.3007.22
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.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): 1481.808960
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.00082
Matches : 14/142 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							15
2	185.092068	93.049672			167.081503	84.044389	P	1395.784208	698.395742	1378.757659	689.882467	1377.773643	689.390459	14
3	284.160482	142.583879			266.149917	133.578597	V	1298.731444	649.869360	1281.704895	641.356085	1280.720879	640.864077	13
4	**413.203075**	207.105176			395.192510	198.099893	E	***1199.663030***	600.335153	1182.636481	591.821879	1181.652465	591.329870	12
5	**512.271489**	256.639383			494.260924	247.634100	V	***1070.620437***	535.813856	1053.593888	527.300582	1052.609872	526.808574	11
6	583.308603	292.157940			565.298038	283.152657	A	***971.552023***	486.279649	954.525474	477.766375	953.541458	477.274367	10
7	711.367181	356.187229	694.340632	347.673954	693.356616	347.181946	Q	900.514909	450.761092	883.488360	442.247818	882.504344	441.755810	9
8	826.394124	413.700700	809.367575	405.187426	808.383559	404.695418	D	***772.456331***	386.731803	755.429782	378.218529	754.445766	377.726521	8
9	925.462538	463.234907	908.435989	454.721633	907.451973	454.229625	V	657.429388	329.218332	640.402839	320.705057			7
10	1038.546602	519.776939	1021.520053	511.263664	1020.536037	510.771656	L	558.360974	279.684125	541.334425	271.170850			6
11	1109.583716	555.295496	1092.557167	546.782221	1091.573151	546.290213	A	445.276910	223.142093	428.250361	214.628818			5
12	1180.620830	590.814053	1163.594281	582.300778	1162.610265	581.808770	A	***374.239796***	187.623536	357.213247	179.110261			4
13	1279.689244	640.348260	1262.662695	631.834986	1261.678679	631.342977	V	***303.202682***	152.104979	286.176133	143.591704			3
14	1336.710708	668.858992	1319.684159	660.345717	1318.700143	659.853709	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 SPVEVAQDVLAAVGK
(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	1481.808960	0.007348	SPVEVAQDVLAAVGK

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

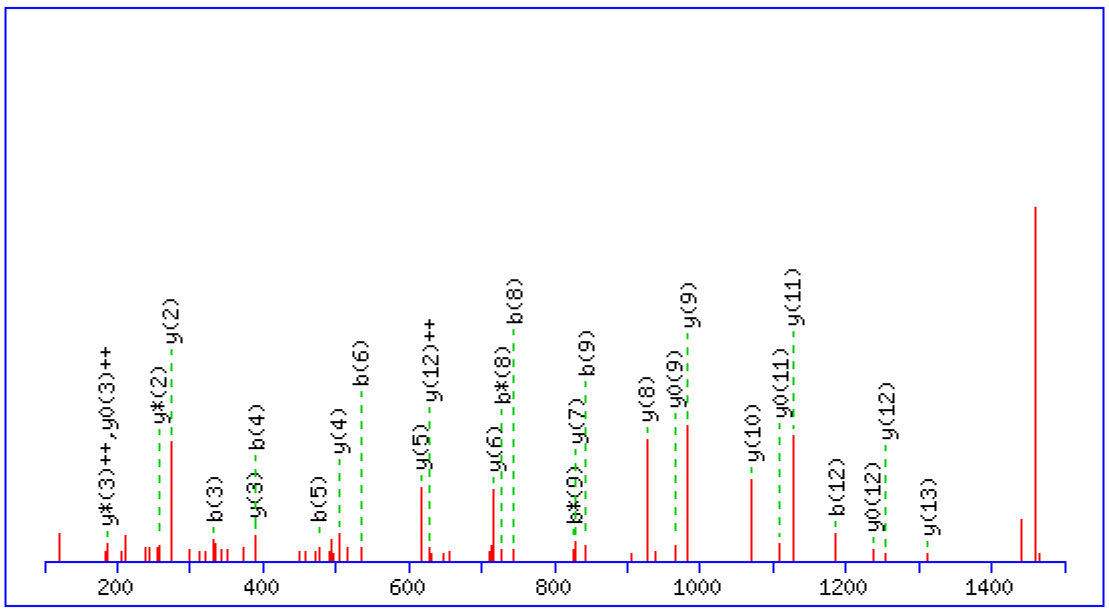
{MATRIX SCIENCE} Mascot Search Results

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

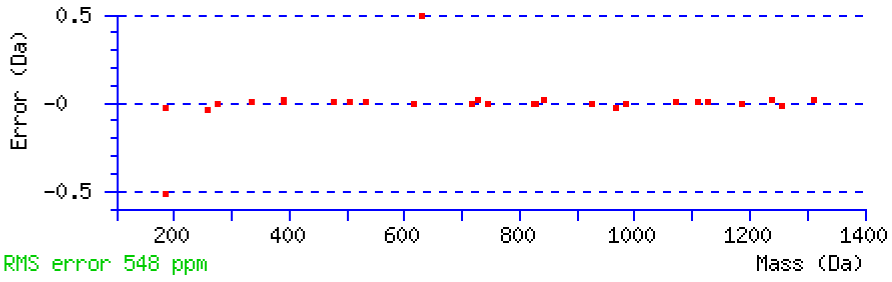
Match to Query 8317: 1458.744108 from(730.379330,2+) rtinseconds(2765) index(5725)
Title: Locus:1.1.1.3359.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

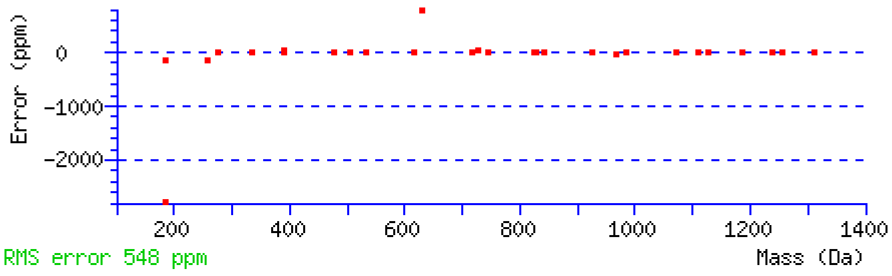
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1458.746719
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 122 **Expect:** 1e-011
Matches : 28/140 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	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
121.5	1458.746719	-0.002611	FGQGSGPIVLDDVR
6.9	1458.731415	0.012693	NPSGIINLGTSENK
5.4	1458.738831	0.005277	EVPTCVIDIIDR
5.4	1458.754089	-0.009981	MGFPEIILPGDVR

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

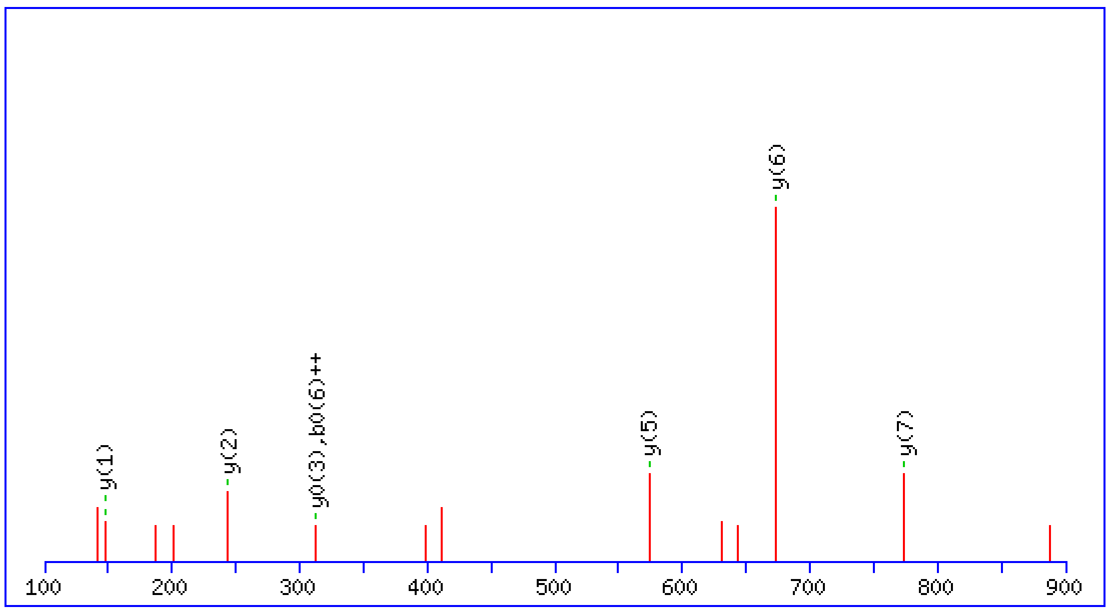
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTVENSPK**
Found in **DENR_HUMAN**, Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=2

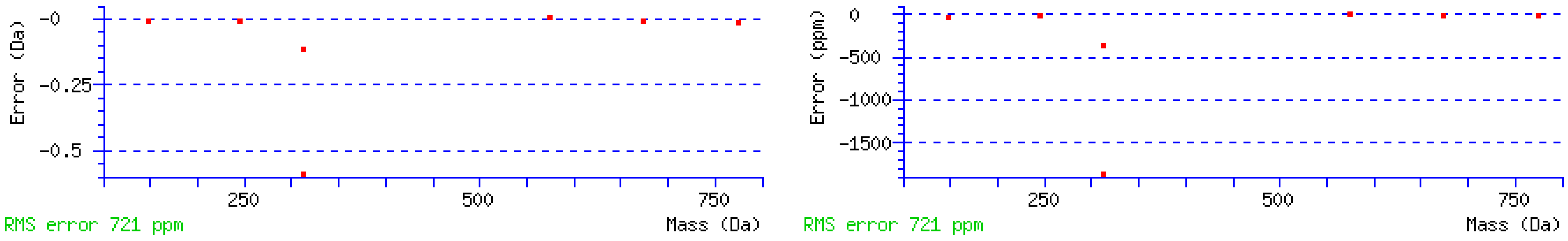
Match to Query 5252: 886.476628 from(444.245590,2+) rtinseconds(1046) index(3440)
Title: Locus:1.1.1.1839.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

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): 886.475983
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0025
Matches : 7/70 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							8
2	215.139019	108.073147			197.128454	99.067865	T	*774.399209*	387.703243	757.372660	379.189968	756.388644	378.697960	7
3	314.207433	157.607354			296.196868	148.602072	V	*673.351530*	337.179403	656.324981	328.666129	655.340965	328.174121	6
4	443.250026	222.128651			425.239461	213.123369	E	*574.283116*	287.645196	557.256567	279.131922	556.272551	278.639914	5
5	557.292953	279.150115	540.266404	270.636840	539.282388	270.144832	N	445.240523	223.123899	428.213974	214.610625	427.229958	214.118617	4
6	644.324981	322.666129	627.298432	314.152854	626.314416	313.660846	S	331.197596	166.102436	314.171047	157.589161	313.187031	157.097153	3
7	741.377745	371.192511	724.351196	362.679236	723.367180	362.187228	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 LTVENSPK
(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	886.475983	0.000645	LTVENSPK
20.9	886.475983	0.000645	ITVNPESK
11.6	886.475967	0.000661	LLSPSNEK
10.5	886.475998	0.000630	TPTQSLPK
10.5	886.475998	0.000630	VDSQTIPK
9.9	886.475967	0.000661	LAKSDEPK
9.1	886.475998	0.000630	IGTSTSPPK
8.2	886.469452	0.007176	MLQRDPK
5.5	886.473480	0.003148	AWCVIPK
4.1	886.469467	0.007161	LTTLHMR

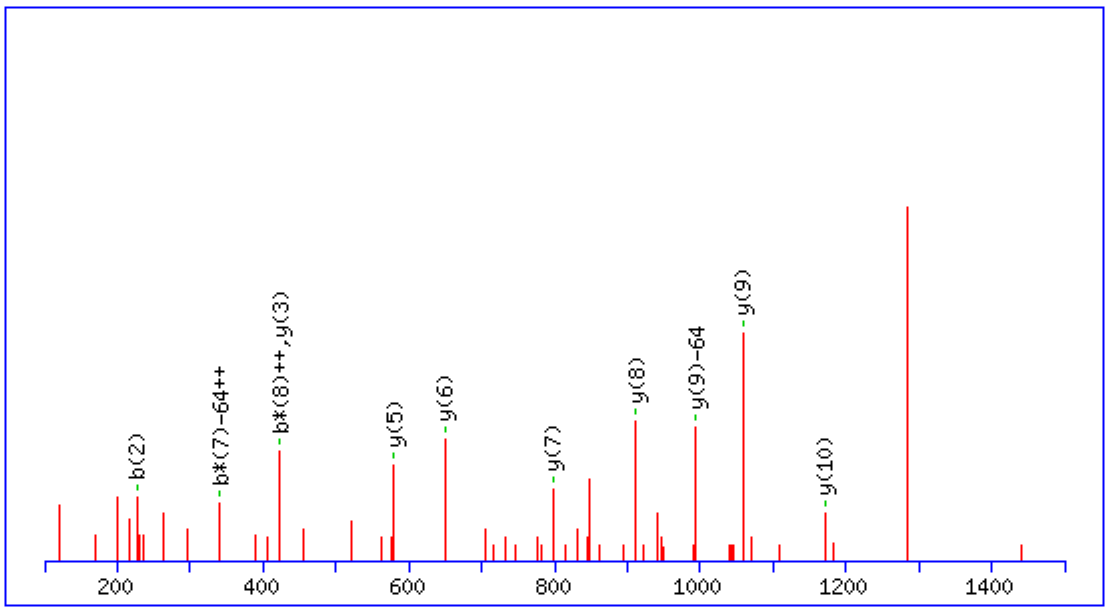
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLFNMAGVTFR**
Found in **DCTD_HUMAN**, Deoxycytidylate deaminase OS=Homo sapiens GN=DCTD PE=1 SV=2

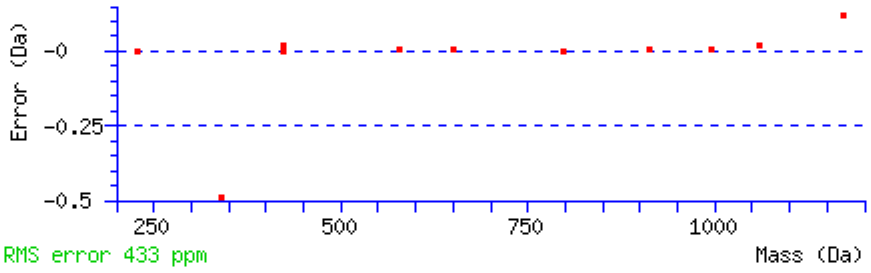
Match to Query 22467: 1283.672068 from(642.843310,2+) rtinseconds(3099) index(32344)
Title: Locus:1.1.1.2676.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

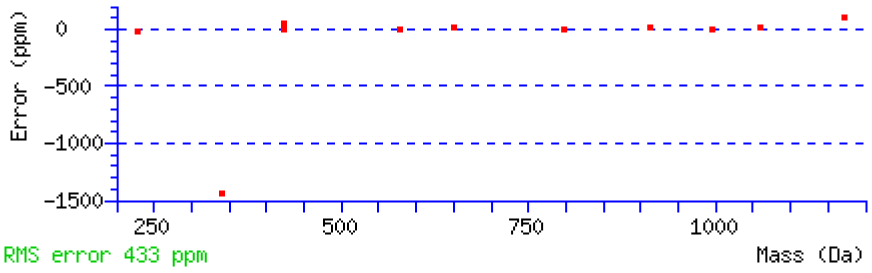
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1283.669632
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: 58  Expect: 1.4e-005
Matches : 11/146 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	227.175404	114.091340					L	***1171.592842***	586.300059	1154.566293	577.786785	1153.582277	577.294777	10
3	374.243818	187.625547					F	***1058.508778***	529.758027	1041.482229	521.244753	1040.498213	520.752745	9
4	488.286745	244.647010	471.260196	236.133736			N	***911.440364***	456.223820	894.413815	447.710546	893.429799	447.218538	8
5	635.322145	318.164711	618.295596	309.651436			M	***797.397437***	399.202357	780.370888	390.689082	779.386872	390.197074	7
6	706.359259	353.683268	689.332710	345.169993			A	***650.362037***	325.684657	633.335488	317.171382	632.351472	316.679374	6
7	763.380723	382.194000	746.354174	373.680725			G	***579.324923***	290.166100	562.298374	281.652825	561.314358	281.160817	5
8	862.449137	431.728207	845.422588	423.214932			V	522.303459	261.655368	505.276910	253.142093	504.292894	252.650085	4
9	963.496816	482.252046	946.470267	473.738772	945.486251	473.246764	T	***423.235045***	212.121161	406.208496	203.607886	405.224480	203.115878	3
10	1110.565230	555.786253	1093.538681	547.272979	1092.554665	546.780971	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 LLFNMAGVTFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	1283.669632	0.002436	LLFNMAGVTFR

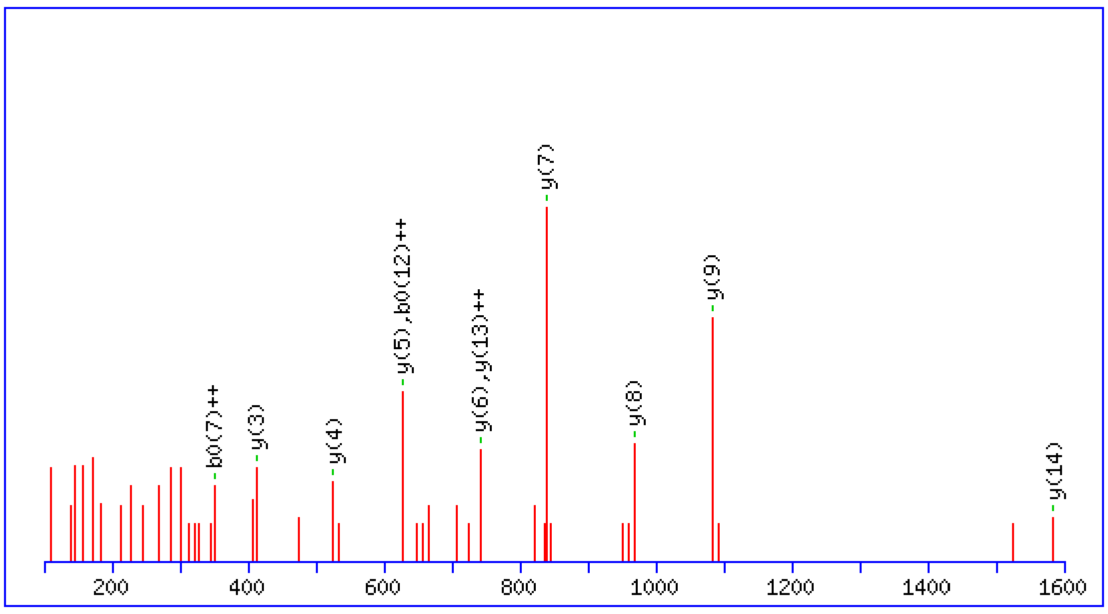
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTATDLDEPDTLHTR**
Found in **DSC1_HUMAN**, Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2

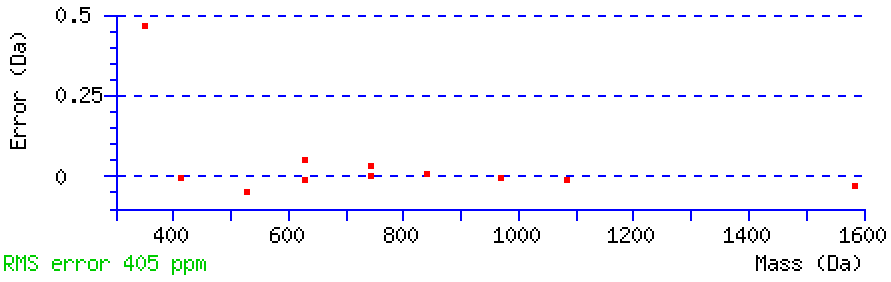
Match to Query 8955: 1682.806662 from(561.942830,3+) rtinseconds(1925) index(2408)
Title: Locus:1.1.1.3042.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

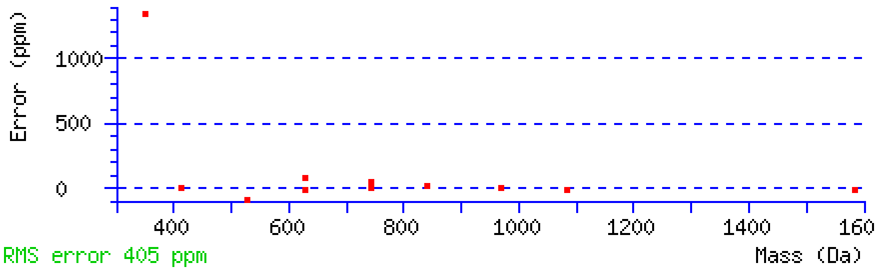
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1682.811157
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 5.1e-006
Matches : 11/136 fragment ions using 11 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							15
2	201.123369	101.065322	183.112804	92.060040	T	***1584.750008***	792.878642	1567.723459	784.365368	1566.739443	783.873359	14
3	272.160483	136.583879	254.149918	127.578597	A	1483.702329	742.354803	1466.675780	733.841528	1465.691764	733.349520	13
4	373.208162	187.107719	355.197597	178.102437	T	1412.665215	706.836246	1395.638666	698.322971	1394.654650	697.830963	12
5	488.235105	244.621191	470.224540	235.615908	D	1311.617536	656.312406	1294.590987	647.799132	1293.606971	647.307123	11
6	601.319169	301.163223	583.308604	292.157940	L	1196.590593	598.798935	1179.564044	590.285660	1178.580028	589.793652	10
7	716.346112	358.676694	698.335547	349.671412	D	***1083.506529***	542.256903	1066.479980	533.743628	1065.495964	533.251620	9
8	845.388705	423.197991	827.378140	414.192708	E	***968.479586***	484.743431	951.453037	476.230157	950.469021	475.738149	8
9	942.441469	471.724373	924.430904	462.719090	P	***839.436993***	420.222135	822.410444	411.708860	821.426428	411.216852	7
10	1057.468412	529.237844	1039.457847	520.232562	D	***742.384229***	371.695753	725.357680	363.182478	724.373664	362.690470	6
11	1158.516091	579.761684	1140.505526	570.756401	T	***627.357286***	314.182281	610.330737	305.669006	609.346721	305.176998	5
12	1271.600155	636.303716	1253.589590	627.298433	L	***526.309607***	263.658441	509.283058	255.145167	508.299042	254.653159	4
13	1408.659067	704.833172	1390.648502	695.827889	H	***413.225543***	207.116409	396.198994	198.603135	395.214978	198.111127	3
14	1509.706746	755.357011	1491.696181	746.351729	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 VTATDLDEPDTLHTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.6	1682.811157	-0.004495	VTATDLDEPDTLHTR
8.3	1682.812012	-0.005350	MVSAVLNGMLDQSFR
0.2	1682.808655	-0.001993	GQFVMEHHTLPEVK

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

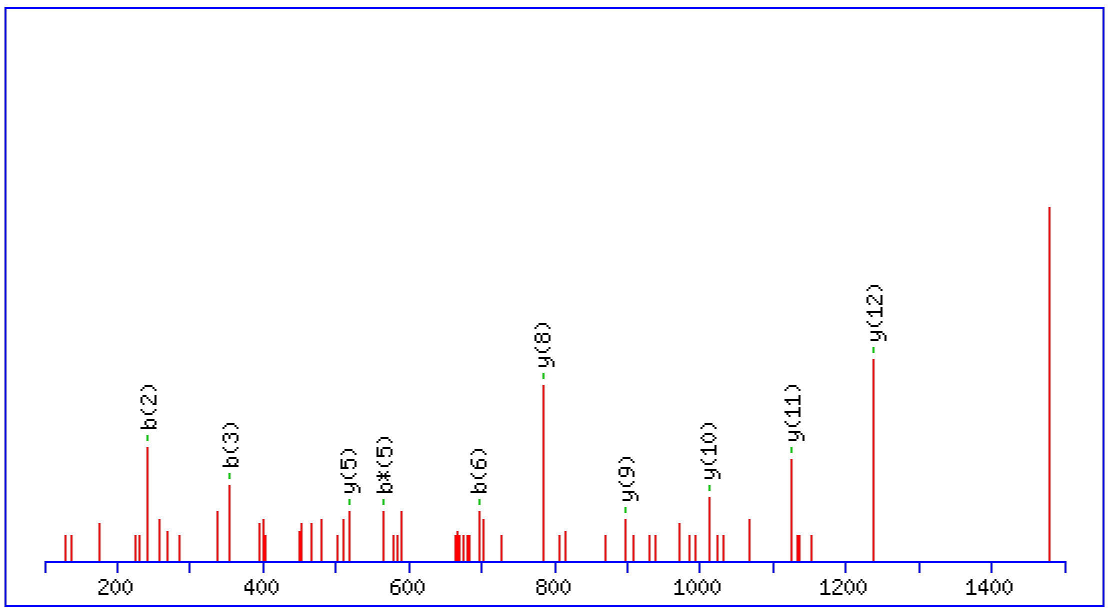
Mascot Search Results

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

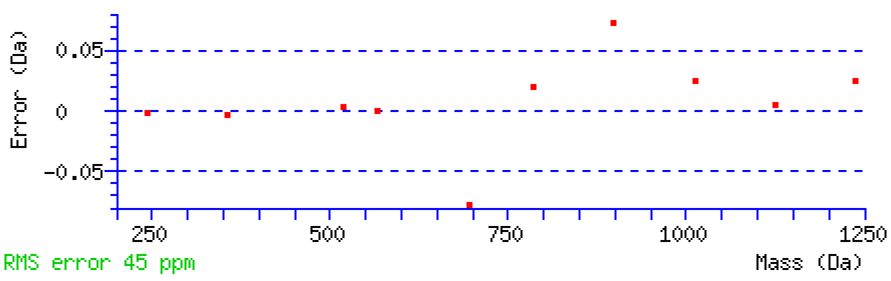
Match to Query 40059: 1478.884568 from(740.449560,2+) rtinseconds(4063) index(58448)
Title: Locus:1.1.1.3033.35
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

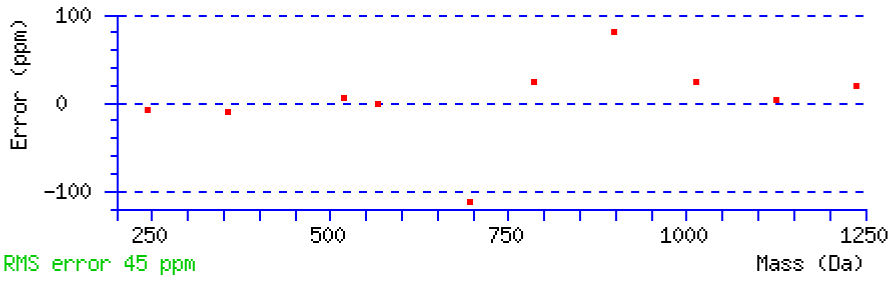
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1478.870804
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 2.1e-005
Matches : 10/140 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	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
47.7	1478.870804	0.013764	IQLLDLPGIIEGAK

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

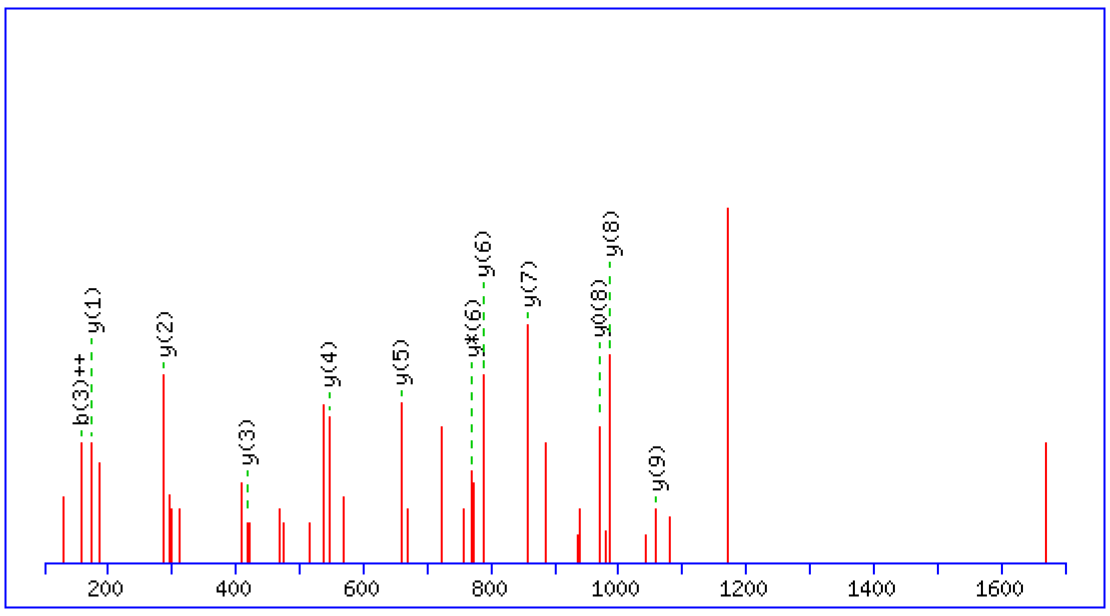
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAEAQIEELR**
Found in **DBLOH_HUMAN**, Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1

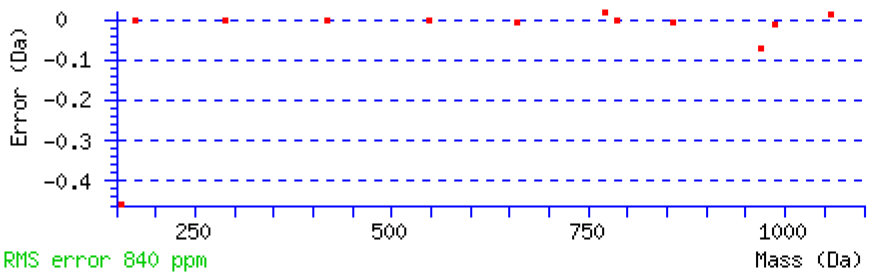
Match to Query 14875: 1170.623108 from(586.318830,2+) rtinseconds(2279) index(15112)
Title: Locus:1.1.1.2379.34
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

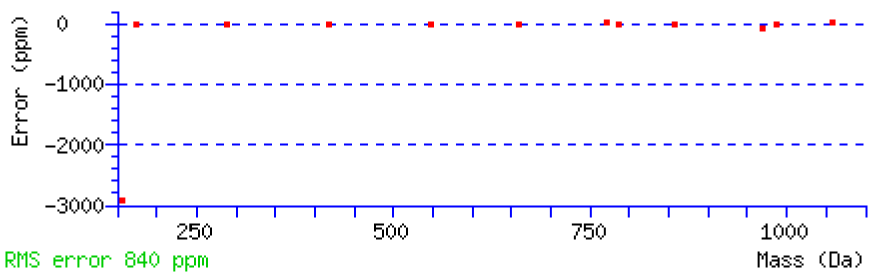
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1170.624405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71  Expect: 8.4e-007
Matches : 12/92 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							10
2	185.128454	93.067865					A	***1058.547665***	529.777471	1041.521116	521.264196	1040.537100	520.772188	9
3	314.171047	157.589161			296.160482	148.583879	E	***987.510551***	494.258914	970.484002	485.745639	969.499986	485.253631	8
4	385.208161	193.107718			367.197596	184.102436	A	***858.467958***	429.737617	841.441409	421.224343	840.457393	420.732335	7
5	513.266739	257.137008	496.240190	248.623733	495.256174	248.131725	Q	***787.430844***	394.219060	770.404295	385.705786	769.420279	385.213778	6
6	626.350803	313.679040	609.324254	305.165765	608.340238	304.673757	I	***659.372266***	330.189771	642.345717	321.676497	641.361701	321.184489	5
7	755.393396	378.200336	738.366847	369.687062	737.382831	369.195054	E	***546.288202***	273.647739	529.261653	265.134465	528.277637	264.642457	4
8	884.435989	442.721633	867.409440	434.208358	866.425424	433.716350	E	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
9	997.520053	499.263665	980.493504	490.750390	979.509488	490.258382	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 LAEAQIEELR
(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	1170.624405	-0.001297	LAEAQIEELR
14.5	1170.624451	-0.001343	IPSSTTLSPPR
7.1	1170.617905	0.005203	IRQPEMIPR
5.7	1170.624451	-0.001343	SLPLDQTLPR
5.1	1170.631851	-0.008743	LVTADGVPILC
4.7	1170.624451	-0.001343	LEPSDKVVPR
4.4	1170.624451	-0.001343	IPSSTTLSPPR
3.9	1170.624451	-0.001343	IPSSTTLSPPR
3.9	1170.614563	0.008545	IQSHFGTLPR
3.9	1170.617905	0.005203	IRQPEMIPR

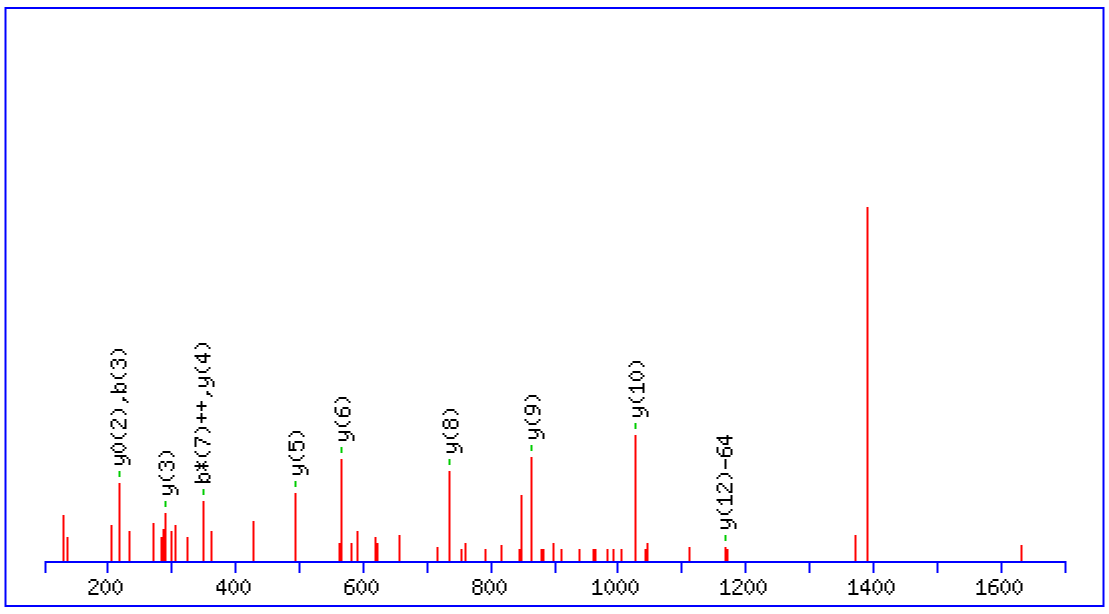
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAGMYQGLAFGGSK**
Found in **DKK2_HUMAN**, Dickkopf-related protein 2 OS=Homo sapiens GN=DKK2 PE=1 SV=1

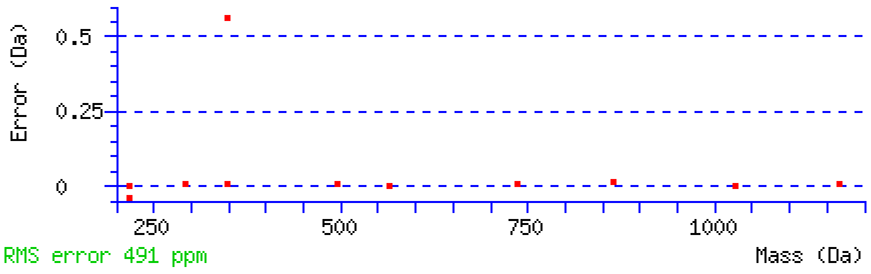
Match to Query 24334: 1388.644308 from(695.329430,2+) rtinseconds(2207) index(13689)
Title: Locus:1.1.1.2364.33
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

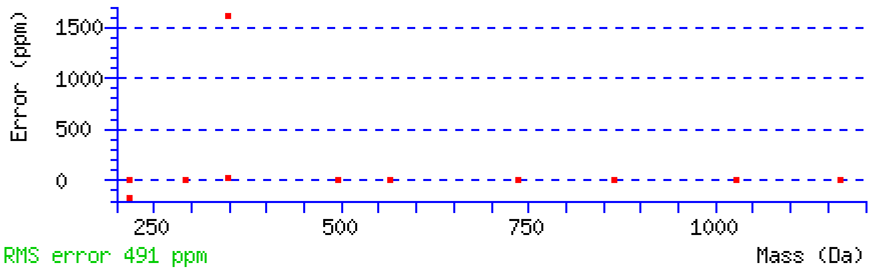
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1388.639450
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: 72 **Expect:** 5.7e-007
Matches : 11/218 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							14
2	159.076418	80.041847			141.065853	71.036564	A	1238.616416	619.811846	1221.589867	611.298572	1220.605851	610.806564	13
3	216.097882	108.552579			198.087317	99.547296	G	***1167.579302***	584.293289	1150.552753	575.780015	1149.568737	575.288007	12
4	299.134997	150.071136			281.124432	141.065854	M	1110.557838	555.782557	1093.531289	547.269283	1092.547273	546.777275	11
5	462.198326	231.602801			444.187761	222.597519	Y	***1027.520723***	514.264000	1010.494174	505.750725	1009.510158	505.258717	10
6	590.256904	295.632090	573.230355	287.118816	572.246339	286.626808	Q	***864.457394***	432.732335	847.430845	424.219061	846.446829	423.727053	9
7	647.278368	324.142822	630.251819	315.629548	629.267803	315.137540	G	***736.398816***	368.703046	719.372267	360.189772	718.388251	359.697764	8
8	760.362432	380.684854	743.335883	372.171580	742.351867	371.679572	L	679.377352	340.192314	662.350803	331.679039	661.366787	331.187031	7
9	831.399546	416.203411	814.372997	407.690137	813.388981	407.198129	A	***566.293288***	283.650282	549.266739	275.137007	548.282723	274.644999	6
10	978.467960	489.737618	961.441411	481.224343	960.457395	480.732335	F	***495.256174***	248.131725	478.229625	239.618450	477.245609	239.126442	5
11	1035.489424	518.248350	1018.462875	509.735076	1017.478859	509.243068	G	***348.187760***	174.597518	331.161211	166.084243	330.177195	165.592235	4
12	1092.510888	546.759082	1075.484339	538.245808	1074.500323	537.753800	G	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
13	1179.542916	590.275096	1162.516367	581.761822	1161.532351	581.269814	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 SAGMYQGLAFGGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	1388.639450	0.004858	SAGMYQGLAFGGSK

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

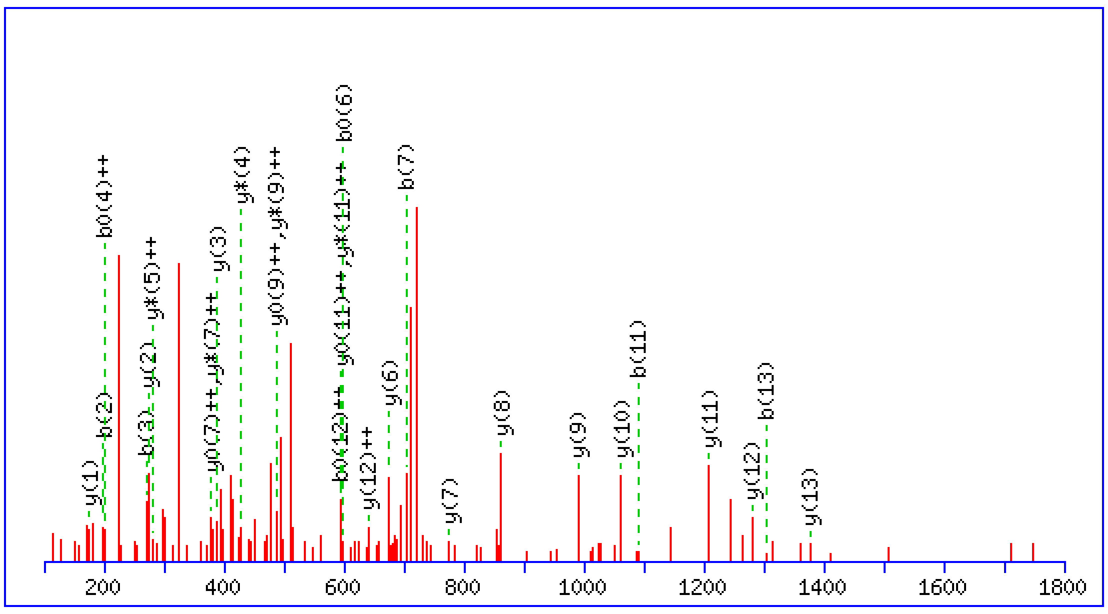
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPAFAESVTEGDVR**
Found in **ODO2_HUMAN**, Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4

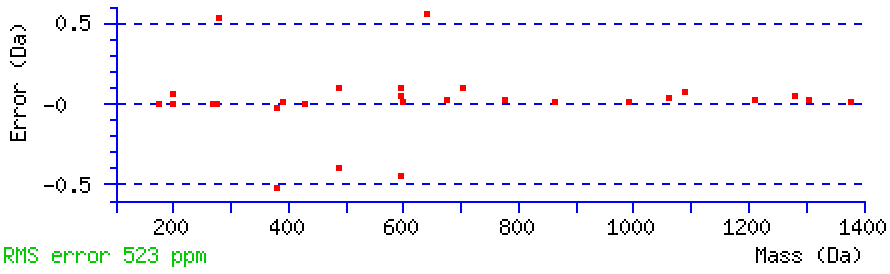
Match to Query 32795: 1477.711388 from(739.862970,2+) rtinseconds(2203) index(26603)
Title: Locus:1.1.1.2340.45
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

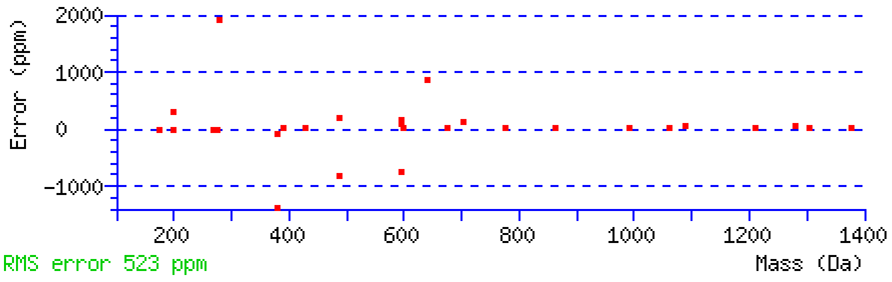
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1477.704895
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00016
Matches : 28/126 fragment ions using 79 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							14
2	**199.107719**	100.057497	181.097154	91.052215	P	***1377.664486***	689.335881	1360.637937	680.822607	1359.653921	680.330599	13
3	**270.144833**	135.576055	252.134268	126.570772	A	***1280.611722***	640.809499	1263.585173	632.296225	1262.601157	631.804217	12
4	417.213247	209.110261	399.202682	200.104979	F	***1209.574608***	605.290942	1192.548059	596.777668	1191.564043	596.285660	11
5	488.250361	244.628818	470.239796	235.623536	A	***1062.506194***	531.756735	1045.479645	523.243461	1044.495629	522.751453	10
6	617.292954	309.150115	599.282389	300.144833	E	***991.469080***	496.238178	974.442531	487.724904	973.458515	487.232896	9
7	**704.324982**	352.666129	686.314417	343.660846	S	***862.426487***	431.716882	845.399938	423.203607	844.415922	422.711599	8
8	803.393396	402.200336	785.382831	393.195053	V	***775.394459***	388.200868	758.367910	379.687593	757.383894	379.195585	7
9	904.441075	452.724176	886.430510	443.718893	T	***676.326045***	338.666661	659.299496	330.153386	658.315480	329.661378	6
10	1033.483668	517.245472	1015.473103	508.240190	E	575.278366	288.142821	558.251817	279.629547	557.267801	279.137539	5
11	**1090.505132**	545.756204	1072.494567	536.750922	G	446.235773	223.621524	429.209224	215.108250	428.225208	214.616242	4
12	1205.532075	603.269676	1187.521510	594.264393	D	***389.214309***	195.110793	372.187760	186.597518	371.203744	186.105510	3
13	**1304.600489**	652.803883	1286.589924	643.798600	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 TPAFAESVTEGDVR
(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	1477.704895	0.006493	TPAFAESVTEGDVR
6.2	1477.723480	-0.012092	TPAQAAFEKMQEK

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

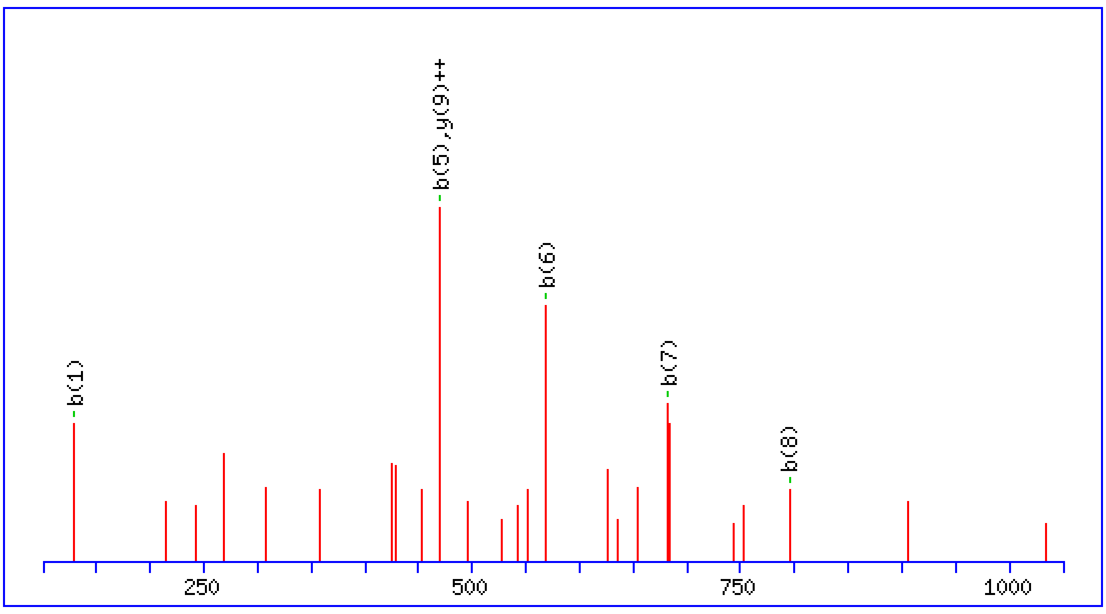
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVGNAVPPPLAK**
Found in **DNMT1_HUMAN**, DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2

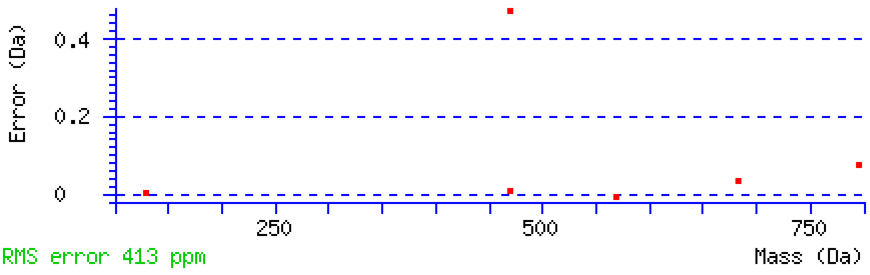
Match to Query 11804: 1221.667768 from(611.841160,2+) rtinseconds(3573) index(13837)
Title: Locus:1.1.1.3370.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

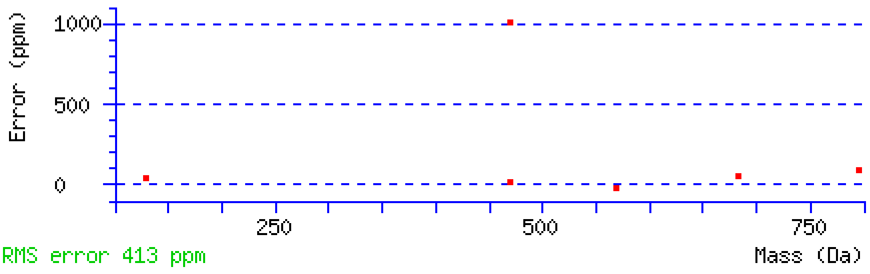
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1221.671738
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 31  Expect: 0.0042
Matches : 6/88 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	***129.065854***	65.036565	112.039305	56.523291	Q					12
2	228.134268	114.570772	211.107719	106.057498	V	1094.620437	547.813857	1077.593888	539.300582	11
3	285.155732	143.081504	268.129183	134.568230	G	995.552023	498.279650	978.525474	489.766375	10
4	399.198659	200.102968	382.172110	191.589693	N	938.530559	469.768918	921.504010	461.255643	9
5	***470.235773***	235.621525	453.209224	227.108250	A	824.487632	412.747454	807.461083	404.234180	8
6	***569.304187***	285.155732	552.277638	276.642457	V	753.450518	377.228897	736.423969	368.715623	7
7	***682.351866***	341.679571	665.325317	333.166297	P	654.382104	327.694690	637.355555	319.181416	6
8	***795.399545***	398.203411	778.372996	389.690136	P	541.334425	271.170851	524.307876	262.657576	5
9	892.452309	446.729793	875.425760	438.216518	P	428.286746	214.647011	411.260197	206.133737	4
10	1005.536373	503.271825	988.509824	494.758550	L	331.233982	166.120629	314.207433	157.607354	3
11	1076.573487	538.790382	1059.546938	530.277107	A	218.149918	109.578597	201.123369	101.065322	2
12					K	147.112804	74.060040	130.086255	65.546765	1



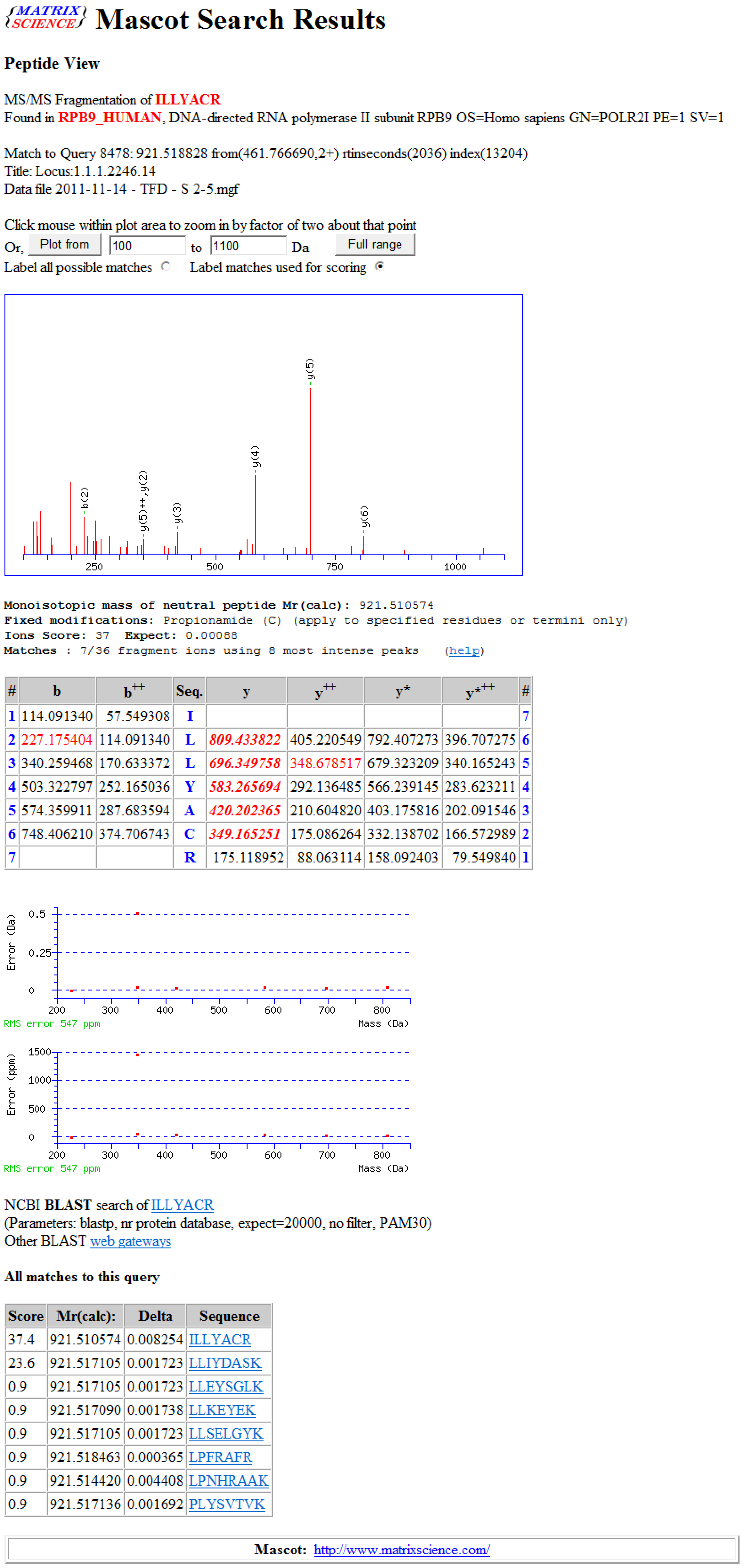


NCBI **BLAST** search of QVGNAVPPPLAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.1	1221.671738	-0.003970	QVGNAVPPPLAK
19.0	1221.671738	-0.003970	QVGNAVPPPLAK
9.1	1221.671738	-0.003970	QVGNAVPPPLAK
5.7	1221.657806	0.009962	QVAPGAPSAPRR
5.3	1221.657806	0.009962	KVAEIQGHAGGR

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLYACR**
Found in **RPB9_HUMAN**, DNA-directed RNA polymerase II subunit RPB9 OS=Homo sapiens GN=POLR2I PE=1 SV=1

Match to Query 8478: 921.518828 from(461.766690,2+) rtinseconds(2036) index(13204)
Title: Locus:1.1.1.2246.14
Data file 2011-11-14 - TFD - S 2-5.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): 921.510574
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00088
Matches : 7/36 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308	I					7
2	227.175404	114.091340	L	*809.433822*	405.220549	792.407273	396.707275	6
3	340.259468	170.633372	L	*696.349758*	348.678517	679.323209	340.165243	5
4	503.322797	252.165036	Y	*583.265694*	292.136485	566.239145	283.623211	4
5	574.359911	287.683594	A	*420.202365*	210.604820	403.175816	202.091546	3
6	748.406210	374.706743	C	*349.165251*	175.086264	332.138702	166.572989	2
7			R	175.118952	88.063114	158.092403	79.549840	1

NCBI **BLAST** search of ILLYACR
(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	921.510574	0.008254	ILLYACR
23.6	921.517105	0.001723	LLIYDASK
0.9	921.517105	0.001723	LLEYSGLK
0.9	921.517090	0.001738	LLKEYEK
0.9	921.517105	0.001723	LLSELGYK
0.9	921.518463	0.000365	LPFRAFR
0.9	921.514420	0.004408	LPNHRAAK
0.9	921.517136	0.001692	PLYSVTVK

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

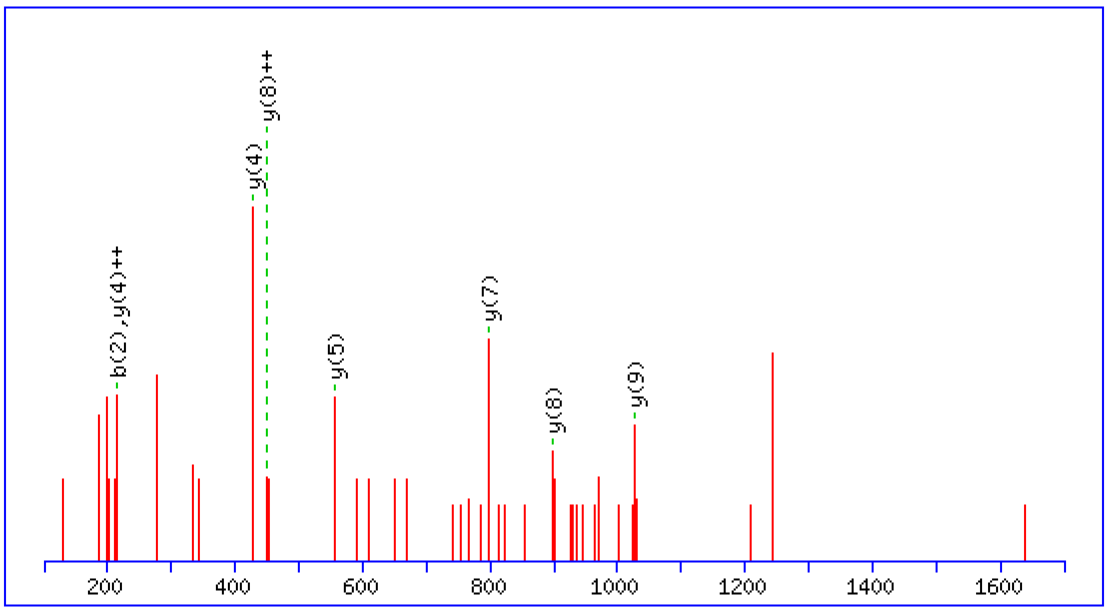
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLEVEIEPGVR**
Found in **DJB11_HUMAN**, DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1

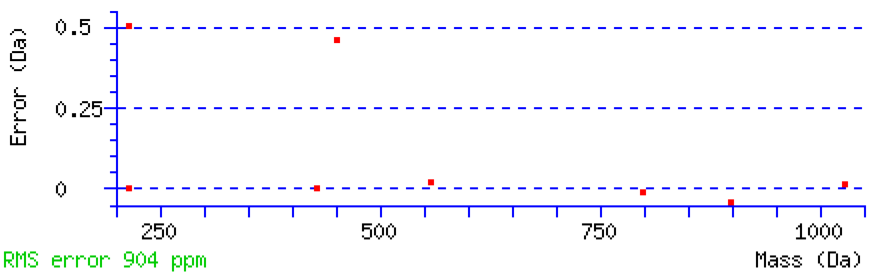
Match to Query 21879: 1240.668268 from(621.341410,2+) rtinseconds(2445) index(24220)
Title: Locus:1.1.1.2501.35
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

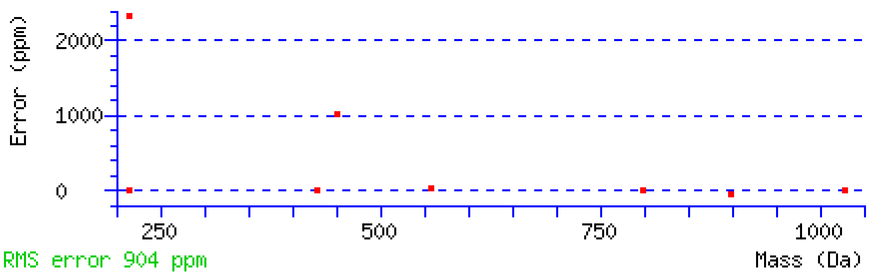
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1240.666306
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0018
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	102.054955	51.531116	84.044390	42.525833	T							11
2	215.139019	108.073147	197.128454	99.067865	L	1140.625915	570.816596	1123.599366	562.303321	1122.615350	561.811313	10
3	344.181612	172.594444	326.171047	163.589162	E	***1027.541851***	514.274564	1010.515302	505.761289	1009.531286	505.269281	9
4	443.250026	222.128651	425.239461	213.123369	V	***898.499258***	449.753267	881.472709	441.239993	880.488693	440.747985	8
5	572.292619	286.649948	554.282054	277.644665	E	***799.430844***	400.219060	782.404295	391.705785	781.420279	391.213777	7
6	685.376683	343.191980	667.366118	334.186697	I	670.388251	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	814.419276	407.713276	796.408711	398.707994	E	***557.304187***	279.155732	540.277638	270.642457	539.293622	270.150449	5
8	911.472040	456.239658	893.461475	447.234376	P	***428.261594***	214.634435	411.235045	206.121160			4
9	968.493504	484.750390	950.482939	475.745108	G	331.208830	166.108053	314.182281	157.594778			3
10	1067.561918	534.284597	1049.551353	525.279315	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 TLEVEIEPGVR
(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	1240.666306	0.001962	TLEVEIEPGVR
2.3	1240.666306	0.001962	ETLPELPSVTR
2.1	1240.666321	0.001947	LTEVLTDSHVK

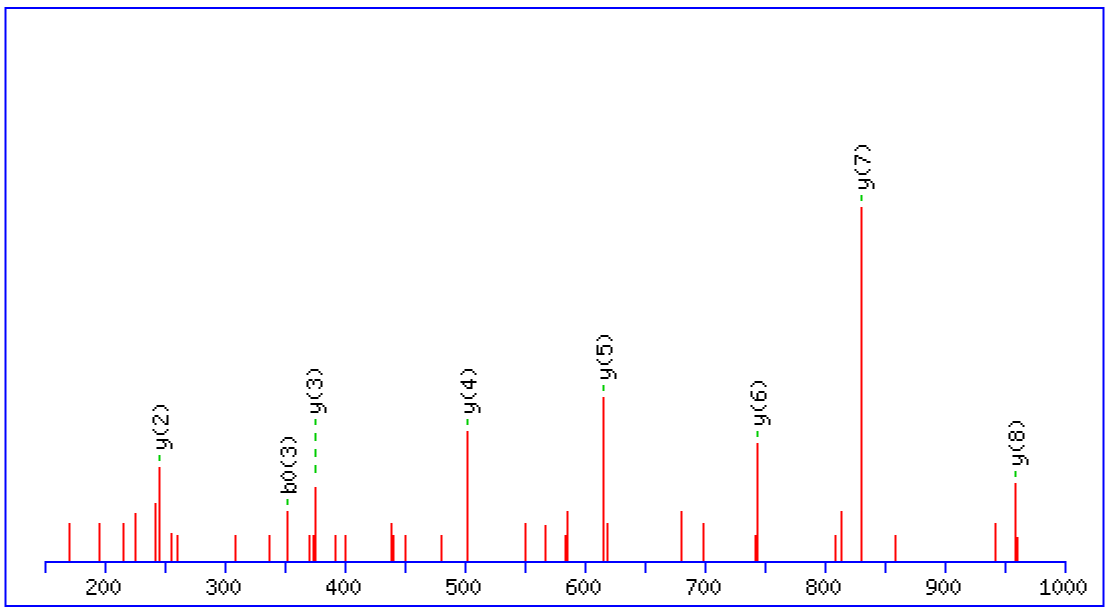
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELQSQIQEAR**
Found in **DPM3_HUMAN**, Dolichol-phosphate mannosyltransferase subunit 3 OS=Homo sapiens GN=DPM3 PE=1 SV=2

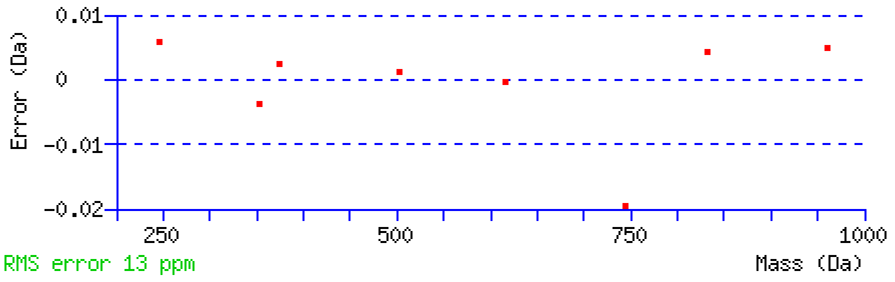
Match to Query 10441: 1200.610868 from(601.312710,2+) rtinseconds(1490) index(1126)
Title: Locus:1.1.1.2623.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-8.mgf

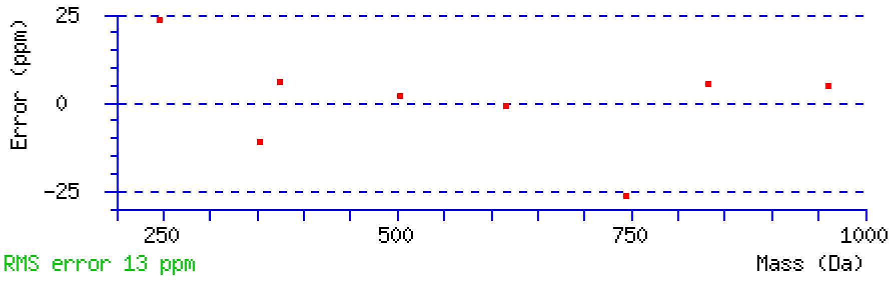
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.609833
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 8.3e-007
Matches : 8/100 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	130.049869	65.528572			112.039304	56.523290	E							10
2	243.133933	122.070605			225.123368	113.065322	L	1072.574549	536.790913	1055.548000	528.277638	1054.563984	527.785630	9
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	Q	***959.490485***	480.248881	942.463936	471.735606	941.479920	471.243598	8
4	458.224539	229.615907	441.197990	221.102633	440.213974	220.610625	S	***831.431907***	416.219592	814.405358	407.706317	813.421342	407.214309	7
5	586.283117	293.645197	569.256568	285.131922	568.272552	284.639914	Q	***744.399879***	372.703578	727.373330	364.190303	726.389314	363.698295	6
6	699.367181	350.187229	682.340632	341.673954	681.356616	341.181946	I	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	5
7	827.425759	414.216518	810.399210	405.703243	809.415194	405.211235	Q	***503.257237***	252.132256	486.230688	243.618982	485.246672	243.126974	4
8	956.468352	478.737814	939.441803	470.224540	938.457787	469.732532	E	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
9	1027.505466	514.256371	1010.478917	505.743097	1009.494901	505.251089	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 ELQSQIQEAR
(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	1200.609833	0.001035	ELQSQIQEAR
4.0	1200.609848	0.001020	QSLQELPAGSR
3.3	1200.603333	0.007535	MAKRPGPPGSR
2.4	1200.603333	0.007535	MAKRPGPPGSR
2.0	1200.621078	-0.010210	QNVGVSNRAEK
1.8	1200.613892	-0.003024	TPATQAIHIFS

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

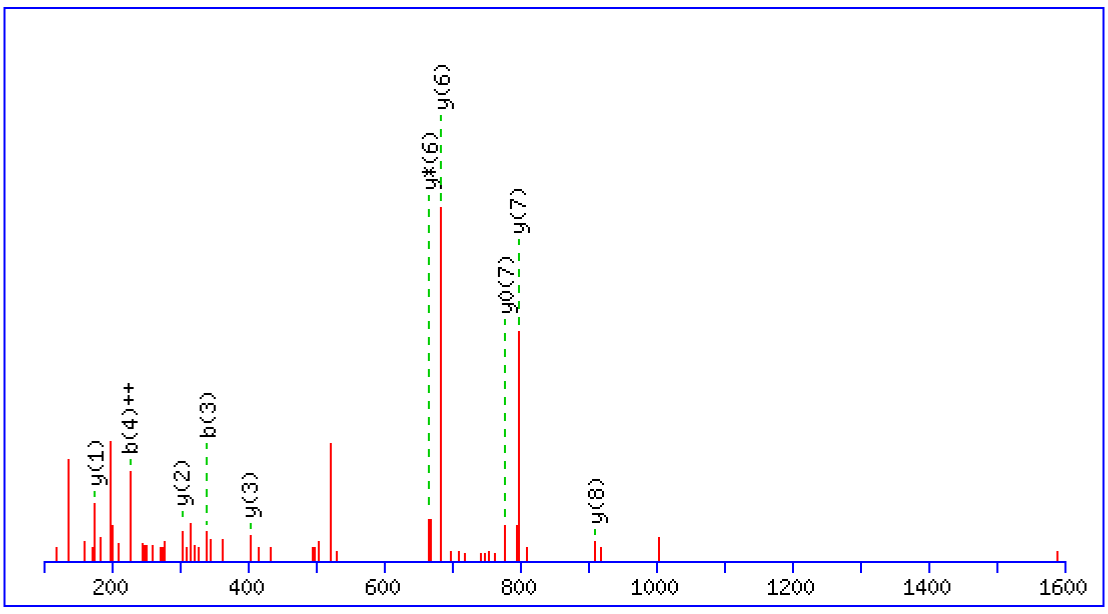
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPLPAVER**
Found in **STAU1_HUMAN**, Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2

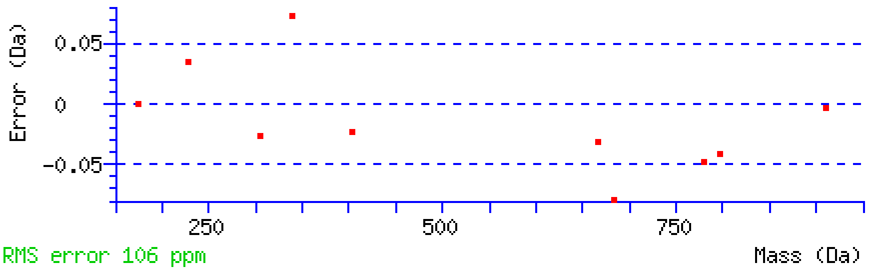
Match to Query 13570: 1022.575108 from(512.294830,2+) rtinseconds(2190) index(22597)
Title: Locus:1.1.1.2334.15
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

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 ●

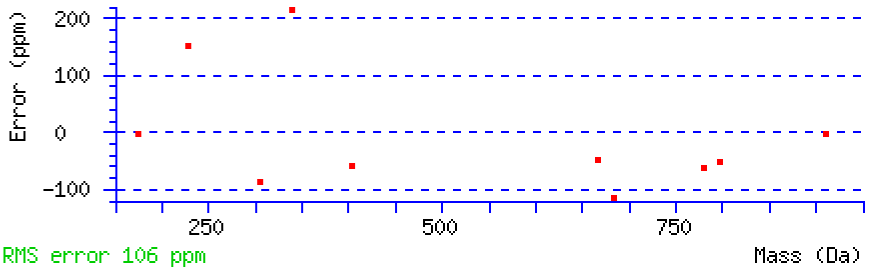


```
Monoisotopic mass of neutral peptide Mr(calc): 1022.576035
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P3      : Oxidation (P)
Ions Score: 36  Expect: 0.001
Matches : 11/64 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							9
2	**227.139019**	114.073147			P	***910.499259***	455.753268	893.472710	447.239993	892.488694	446.747985	8
3	**340.186698**	170.596987			P	***797.451580***	399.229428	780.425031	390.716154	779.441015	390.224146	7
4	453.270762	227.139019			L	***684.403901***	342.705589	667.377352	334.192314	666.393336	333.700306	6
5	550.323526	275.665401			P	571.319837	286.163557	554.293288	277.650282	553.309272	277.158274	5
6	621.360640	311.183958			A	474.267073	237.637174	457.240524	229.123900	456.256508	228.631892	4
7	720.429054	360.718165			V	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
8	849.471647	425.239462	831.461082	416.234179	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



RMS error 106 ppm



RMS error 106 ppm

NCBI **BLAST** search of LPPLPAVER
(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	1022.576035	-0.000927	LPPLPAVER
18.9	1022.576035	-0.000927	LPLVPESPR
17.0	1022.576035	-0.000927	LPPLPAVER
5.2	1022.576035	-0.000927	LPPLPAVER
4.2	1022.576050	-0.000942	IPQTQPVPK

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

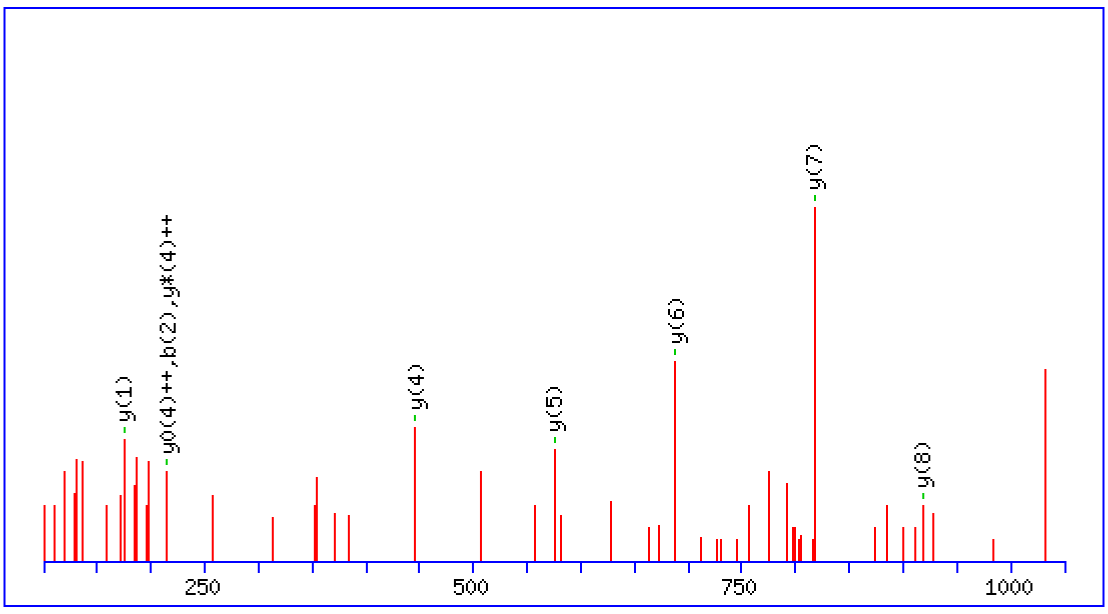
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTELETAVR**
Found in **DCTN2_HUMAN**, Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4

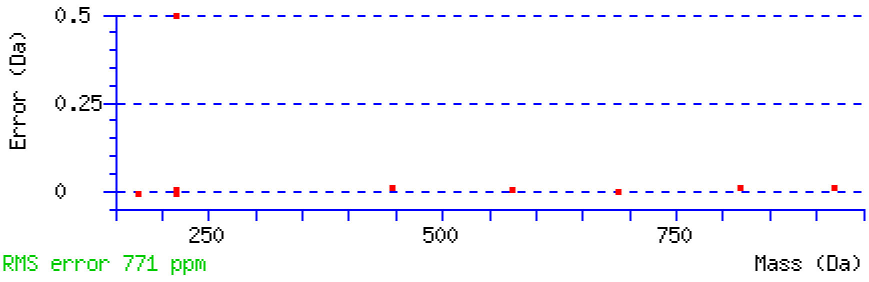
Match to Query 10243: 1030.570448 from(516.292500,2+) rtinseconds(1814) index(15592)
Title: Locus:1.1.1.2214.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

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 ●

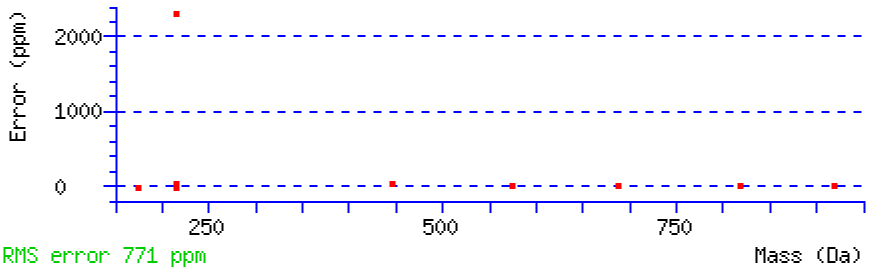


Monoisotopic mass of neutral peptide Mr(calc): 1030.565857
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 7.3e-005
Matches : 9/72 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	215.139019	108.073147	197.128454	99.067865	T	***918.489088***	459.748182	901.462539	451.234908	900.478523	450.742900	8
3	344.181612	172.594444	326.171047	163.589162	E	***817.441409***	409.224343	800.414860	400.711068	799.430844	400.219060	7
4	457.265676	229.136476	439.255111	220.131194	L	***688.398816***	344.703046	671.372267	336.189772	670.388251	335.697764	6
5	586.308269	293.657773	568.297704	284.652490	E	***575.314752***	288.161014	558.288203	279.647740	557.304187	279.155732	5
6	687.355948	344.181612	669.345383	335.176330	T	***446.272159***	223.639717	429.245610	215.126443	428.261594	214.634435	4
7	758.393062	379.700169	740.382497	370.694887	A	345.224480	173.115878	328.197931	164.602603			3
8	857.461476	429.234376	839.450911	420.229094	V	274.187366	137.597321	257.160817	129.084047			2
9					R	***175.118952***	88.063114	158.092403	79.549840			1



RMS error 771 ppm



RMS error 771 ppm

NCBI **BLAST** search of LTELETAVR
(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	1030.565857	0.004591	LTELETAVR
19.0	1030.565842	0.004606	TLELSEALR
8.9	1030.573242	-0.002794	ITEMPSIIK
8.2	1030.563354	0.007094	IMVLGANWK
8.0	1030.577103	-0.006655	VGTKPSASLR
7.6	1030.567200	0.003248	ITHRYSVR
7.6	1030.577103	-0.006655	ITTQITAGAR
7.3	1030.565887	0.004561	SAVTTVVNPK
6.0	1030.565872	0.004576	DDIITVISR
5.5	1030.565857	0.004591	ITVQKGEEK

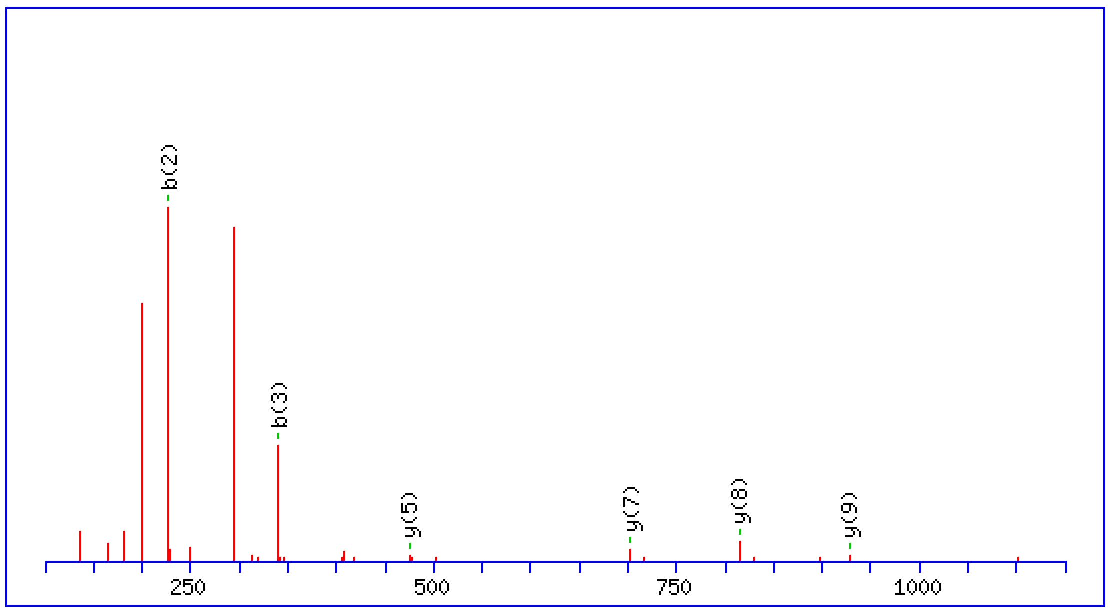
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IILQVGVATK**
Found in **DYH3_HUMAN**, Dynein heavy chain 3, axonemal OS=Homo sapiens GN=DNAH3 PE=2 SV=1

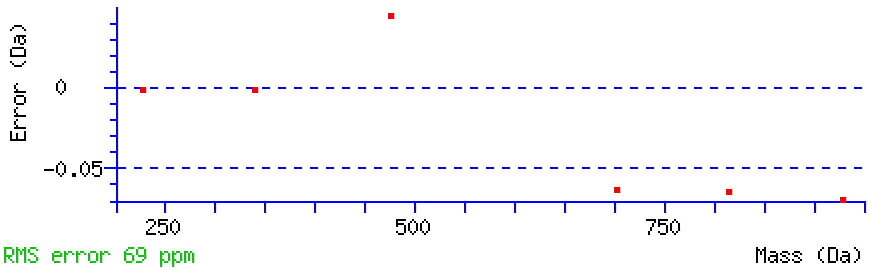
Match to Query 16325: 1040.658848 from(521.336700,2+) rtinseconds(2752) index(26649)
Title: Locus:1.1.1.2515.11
Data file 2011-11-14 - TFD - S 2-5.mgf

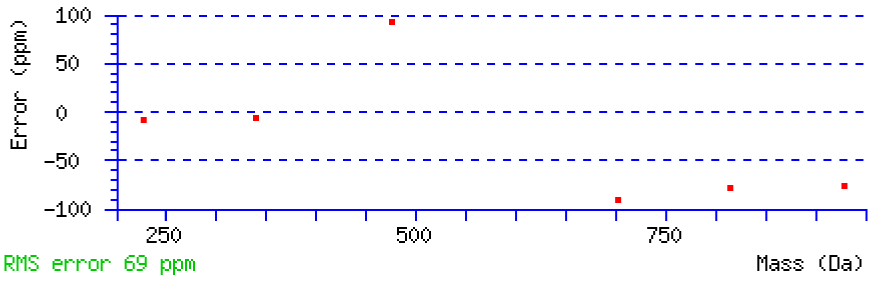
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1040.659378
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.00065
Matches : 6/84 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					I							10
2	**227.175404**	114.091340					I	***928.582595***	464.794936	911.556046	456.281661	910.572030	455.789653	9
3	**340.259468**	170.633372					L	***815.498531***	408.252904	798.471982	399.739629	797.487966	399.247621	8
4	468.318046	234.662661	451.291497	226.149386			Q	***702.414467***	351.710872	685.387918	343.197597	684.403902	342.705589	7
5	567.386460	284.196868	550.359911	275.683594			V	574.355889	287.681583	557.329340	279.168308	556.345324	278.676300	6
6	624.407924	312.707600	607.381375	304.194326			G	***475.287475***	238.147375	458.260926	229.634101	457.276910	229.142093	5
7	723.476338	362.241807	706.449789	353.728533			V	418.266011	209.636643	401.239462	201.123369	400.255446	200.631361	4
8	794.513452	397.760364	777.486903	389.247090			A	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
9	895.561131	448.284204	878.534582	439.770929	877.550566	439.278921	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 IILQVGVATK
(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	1040.659378	-0.000530	IILQVGVATK
20.6	1040.659348	-0.000500	LLLLEATIR
18.4	1040.659363	-0.000515	LLPSALGVKK
5.4	1040.659348	-0.000500	LLVEQAKLK
4.2	1040.659363	-0.000515	LKPLDKVTK

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

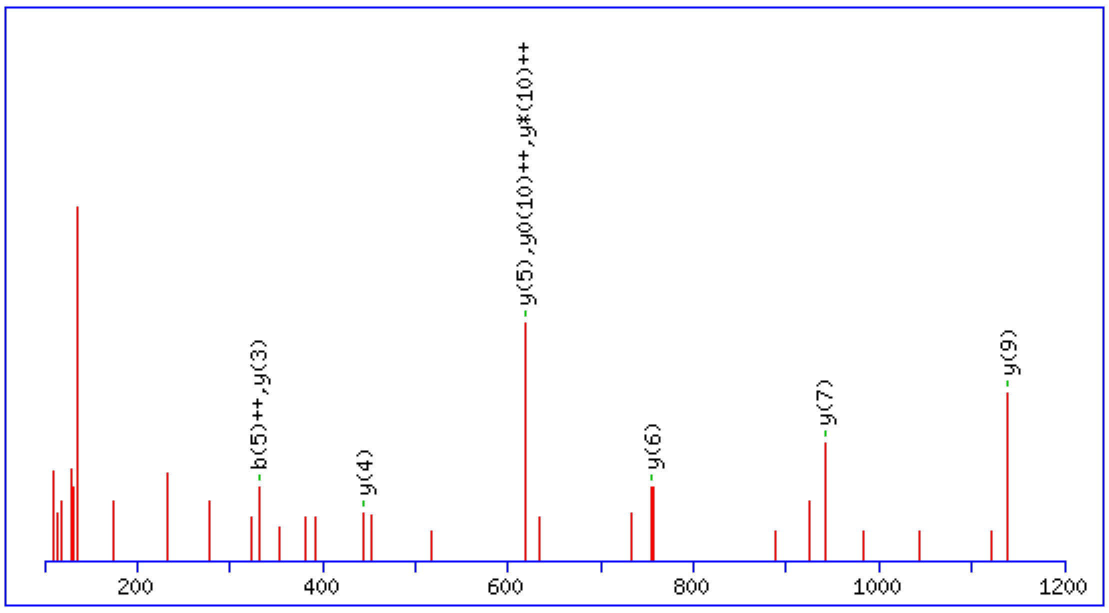
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNPTWHCIVGR**
Found in **DYL1_HUMAN**, Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1

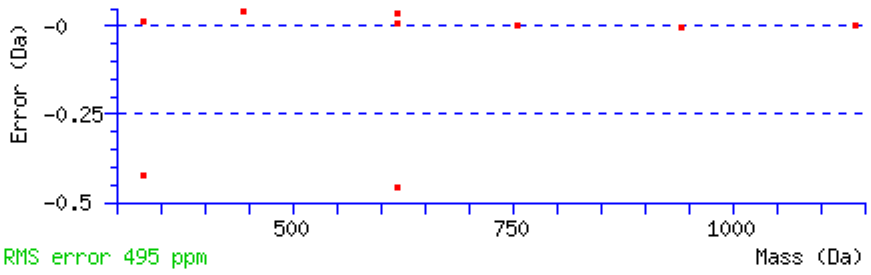
Match to Query 15610: 1415.678532 from(472.900120,3+) rtinseconds(2286) index(6320)
Title: Locus:1.1.1.2891.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

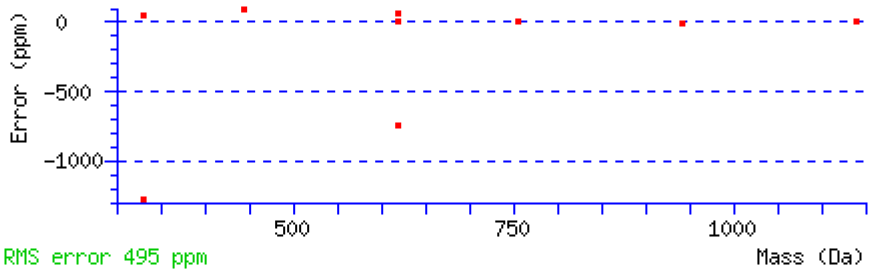
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1415.676834
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0022
Matches : 9/98 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	164.070605	82.538940					Y							11
2	278.113532	139.560404	261.086983	131.047130			N	1253.620788	627.314032	1236.594239	618.800758	1235.610223	618.308749	10
3	375.166296	188.086786	358.139747	179.573512			P	***1139.577861***	570.292569	1122.551312	561.779294	1121.567296	561.287286	9
4	476.213975	238.610626	459.187426	230.097351	458.203410	229.605343	T	1042.525097	521.766187	1025.498548	513.252912	1024.514532	512.760904	8
5	662.293288	331.650282	645.266739	323.137008	644.282723	322.645000	W	***941.477418***	471.242347	924.450869	462.729072			7
6	799.352200	400.179738	782.325651	391.666464	781.341635	391.174456	H	***755.398105***	378.202691	738.371556	369.689416			6
7	973.398499	487.202888	956.371950	478.689613	955.387934	478.197605	C	***618.339193***	309.673235	601.312644	301.159960			5
8	1086.482563	543.744920	1069.456014	535.231645	1068.471998	534.739637	I	***444.292894***	222.650085	427.266345	214.136810			4
9	1185.550977	593.279127	1168.524428	584.765852	1167.540412	584.273844	V	***331.208830***	166.108053	314.182281	157.594778			3
10	1242.572441	621.789859	1225.545892	613.276584	1224.561876	612.784576	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 YNPTWHCIVGR
(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	1415.676834	0.001698	YNPTWHCIVGR
9.4	1415.671478	0.007054	FGSRSLSTADMTK
1.1	1415.671494	0.007038	TADMPLTPNPVGR

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

{MATRIX SCIENCE}

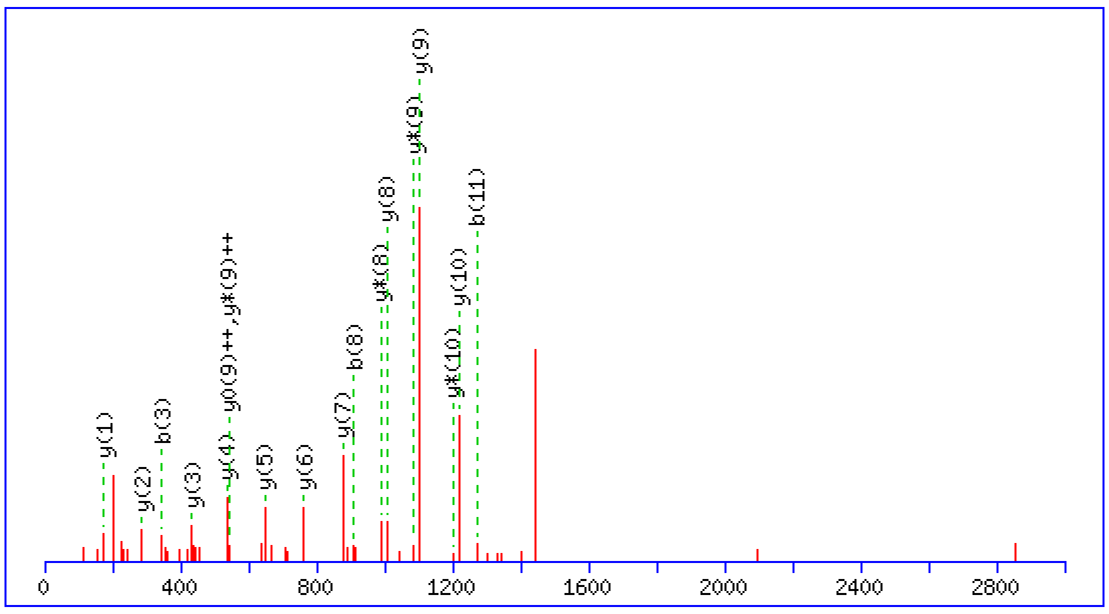
Mascot Search Results

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

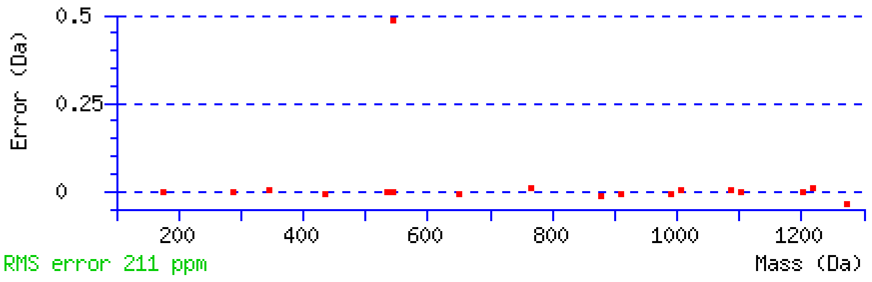
Match to Query 16156: 1445.713508 from(723.864030,2+) rtinseconds(3247) index(12544)
Title: Locus:1.1.1.3249.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

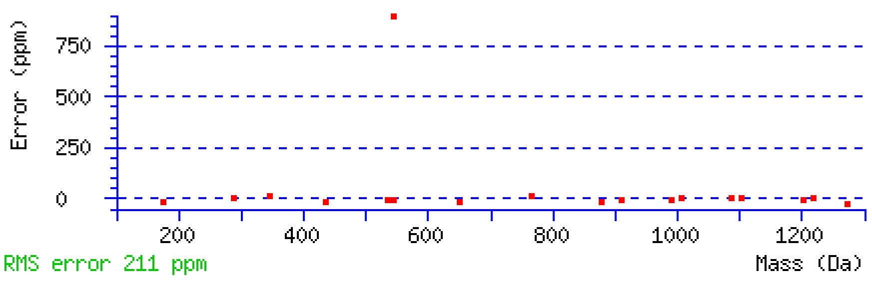
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1445.715057
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 86 **Expect:** 3.2e-008
Matches : 18/118 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	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
85.7	1445.715057	-0.001549	DIDPQNDLTFLR
6.8	1445.699783	0.013725	NLDDTIDDEKLR
3.4	1445.727142	-0.013634	CLAVHECFVKR

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

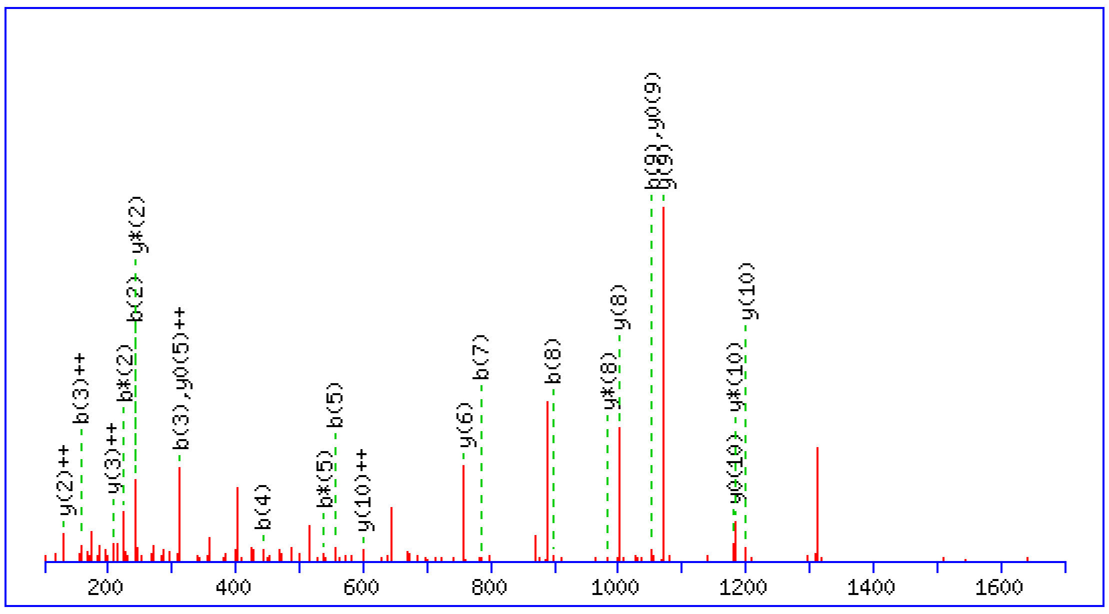
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKAELNDIRPK**
Found in **DMD_HUMAN**, Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3

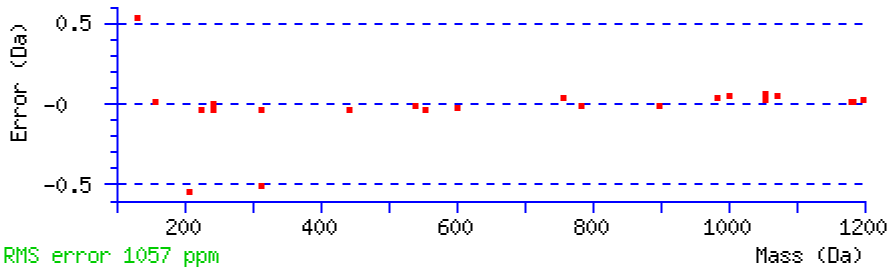
Match to Query 24234: 1311.756988 from(656.885770,2+) rtinseconds(3673) index(53841)
Title: Locus:1.1.1.2900.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

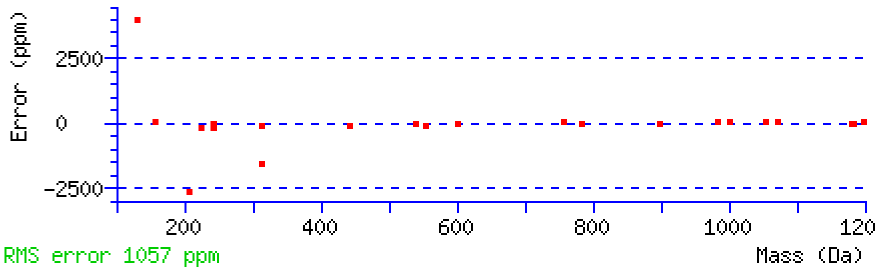
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1311.751007
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P10 : Oxidation (P)
Ions Score: 33 **Expect:** 0.0023
Matches : 23/104 fragment ions using 47 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	**1199.674262**	600.340769	1182.647713	591.827495	1181.663697	591.335487	10
3	***313.223417***	157.115346	296.196868	148.602072			A	**1071.579299**	536.293288	1054.552750	527.780013	1053.568734	527.288005	9
4	***442.266010***	221.636643	425.239461	213.123369	424.255445	212.631361	E	**1000.542185**	500.774731	983.515636	492.261456	982.531620	491.769448	8
5	***555.350074***	278.178675	538.323525	269.665401	537.339509	269.173393	L	871.499592	436.253434	854.473043	427.740160	853.489027	427.248152	7
6	669.393001	335.200139	652.366452	326.686864	651.382436	326.194856	N	**758.415528**	379.711402	741.388979	371.198128	740.404963	370.706120	6
7	***784.419944***	392.713610	767.393395	384.200335	766.409379	383.708328	D	644.372601	322.689939	627.346052	314.176664	626.362036	313.684656	5
8	***897.504008***	449.255642	880.477459	440.742368	879.493443	440.250360	I	529.345658	265.176467	512.319109	256.663193			4
9	***1053.605119***	527.306198	1036.578570	518.792923	1035.594554	518.300915	R	416.261594	208.634435	399.235045	200.121161			3
10	1166.652798	583.830037	1149.626249	575.316763	1148.642233	574.824755	P	260.160483	130.583879	243.133934	122.070605			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LKAELNDIRPK
(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	1311.751007	0.005981	LKAELNDIRPK
12.2	1311.744492	0.012496	ICILPNRGLAR
11.3	1311.755051	0.001937	FPPQAELLLLR
6.0	1311.755051	0.001937	FPPQAELLLLR
4.2	1311.751022	0.005966	GNLPAESVKILR
0.6	1311.769653	-0.012665	LQPMLVQALRK
0.3	1311.751038	0.005950	ASPLVAIGQTLAR

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

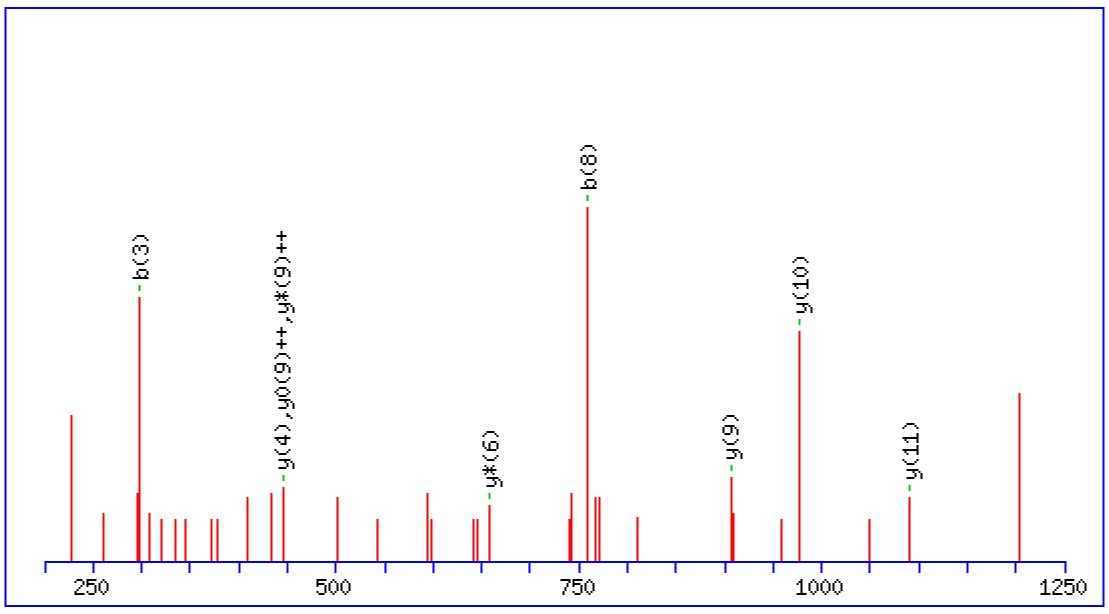
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLASGSDDAKVK**
Found in **RFWD2_HUMAN**, E3 ubiquitin-protein ligase RFWD2 OS=Homo sapiens GN=RFWD2 PE=1 SV=1

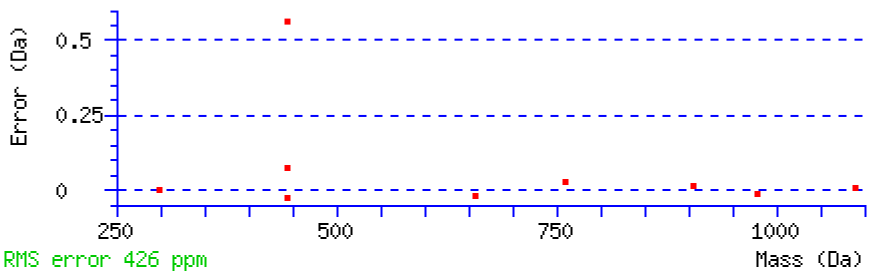
Match to Query 12993: 1202.645668 from(602.330110,2+) rtinseconds(2995) index(21122)
Title: Locus:1.1.1.2724.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

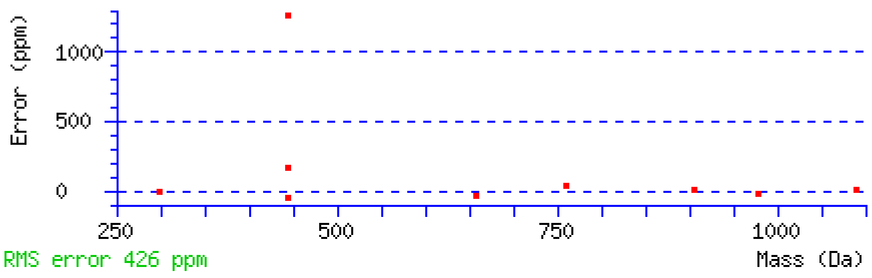
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1250 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1202.650650
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0071
Matches : 9/100 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	114.091340	57.549308					L							12
2	227.175404	114.091340					L	***1090.573879***	545.790578	1073.547330	537.277303	1072.563314	536.785295	11
3	**298.212518**	149.609897					A	***977.489815***	489.248545	960.463266	480.735271	959.479250	480.243263	10
4	385.244546	193.125911			367.233981	184.120628	S	***906.452701***	453.729988	889.426152	445.216714	888.442136	444.724706	9
5	442.266010	221.636643			424.255445	212.631360	G	819.420673	410.213975	802.394124	401.700700	801.410108	401.208692	8
6	529.298038	265.152657			511.287473	256.147375	S	762.399209	381.703242	745.372660	373.189968	744.388644	372.697960	7
7	644.324981	322.666129			626.314416	313.660846	D	675.367181	338.187229	658.340632	329.673954	657.356616	329.181946	6
8	**759.351924**	380.179600			741.341359	371.174317	D	560.340238	280.673757	543.313689	272.160483	542.329673	271.668475	5
9	830.389038	415.698157			812.378473	406.692874	A	***445.313295***	223.160285	428.286746	214.647011			4
10	958.484001	479.745638	941.457452	471.232364	940.473436	470.740356	K	374.276181	187.641728	357.249632	179.128454			3
11	1057.552415	529.279845	1040.525866	520.766571	1039.541850	520.274563	V	246.181218	123.594247	229.154669	115.080972			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LLASGSDDAKVK
(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	1202.650650	-0.004982	LLASGSDDAKVK
11.3	1202.655350	-0.009682	IITRMQAQAR
2.5	1202.640732	0.004936	INFSKPEAAAR
1.9	1202.650650	-0.004982	TDLDNSIGIKK

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

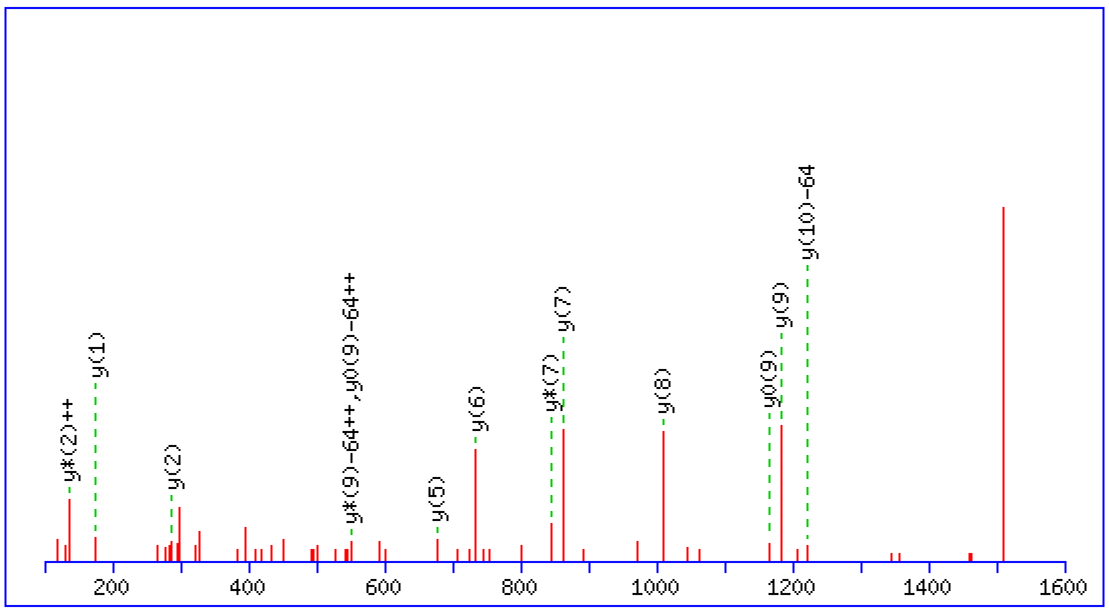
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILTCMQGMEEIR**
Found in **UBR1_HUMAN**, E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens GN=UBR1 PE=1 SV=1

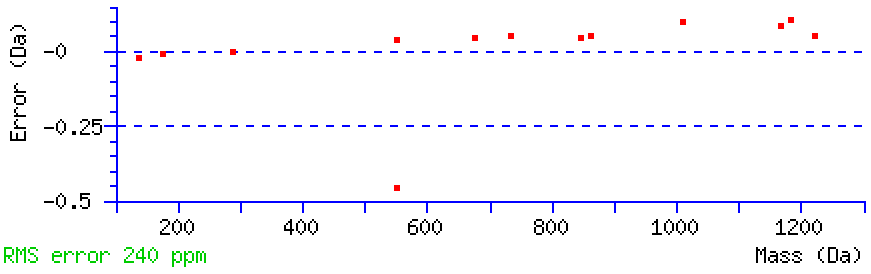
Match to Query 41156: 1509.697908 from(755.856230,2+) rtinseconds(2898) index(37404)
Title: Locus:1.1.1.2594.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

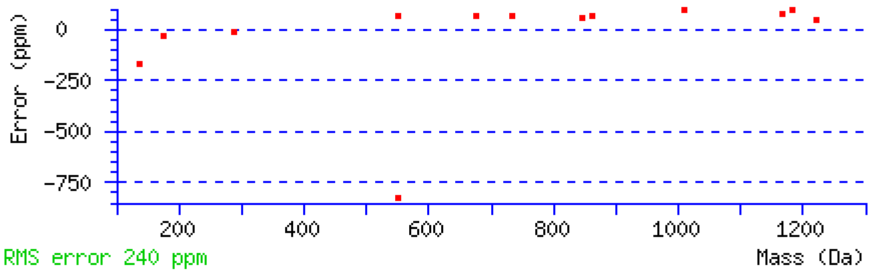
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1509.698929
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: 33  Expect: 0.0028
Matches : 13/178 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					I							12
2	227.175404	114.091340					L	1397.622171	699.314724	1380.595622	690.801449	1379.611606	690.309441	11
3	328.223083	164.615179			310.212518	155.609897	T	1284.538107	642.772692	1267.511558	634.259417	1266.527542	633.767409	10
4	502.269382	251.638329			484.258817	242.633047	C	***1183.490428***	592.248852	1166.463879	583.735578	1165.479863	583.243570	9
5	649.304782	325.156029			631.294217	316.150747	M	***1009.444129***	505.225703	992.417580	496.712428	991.433564	496.220420	8
6	777.363360	389.185318	760.336811	380.672044	759.352795	380.180036	Q	***862.408729***	431.708003	845.382180	423.194728	844.398164	422.702720	7
7	834.384824	417.696050	817.358275	409.182776	816.374259	408.690768	G	***734.350151***	367.678714	717.323602	359.165439	716.339586	358.673431	6
8	965.425309	483.216293	948.398760	474.703018	947.414744	474.211010	M	***677.328687***	339.167982	660.302138	330.654707	659.318122	330.162699	5
9	1094.467902	547.737589	1077.441353	539.224315	1076.457337	538.732307	E	546.288202	273.647739	529.261653	265.134465	528.277637	264.642457	4
10	1223.510495	612.258886	1206.483946	603.745611	1205.499930	603.253603	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
11	1336.594559	668.800918	1319.568010	660.287643	1318.583994	659.795635	I	***288.203016***	144.605146	271.176467	136.091871			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILTCMQGMEEIR
(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	1509.698929	-0.001021	ILTCMQGMEEIR
7.3	1509.698929	-0.001021	ILTCMQGMEEIR

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

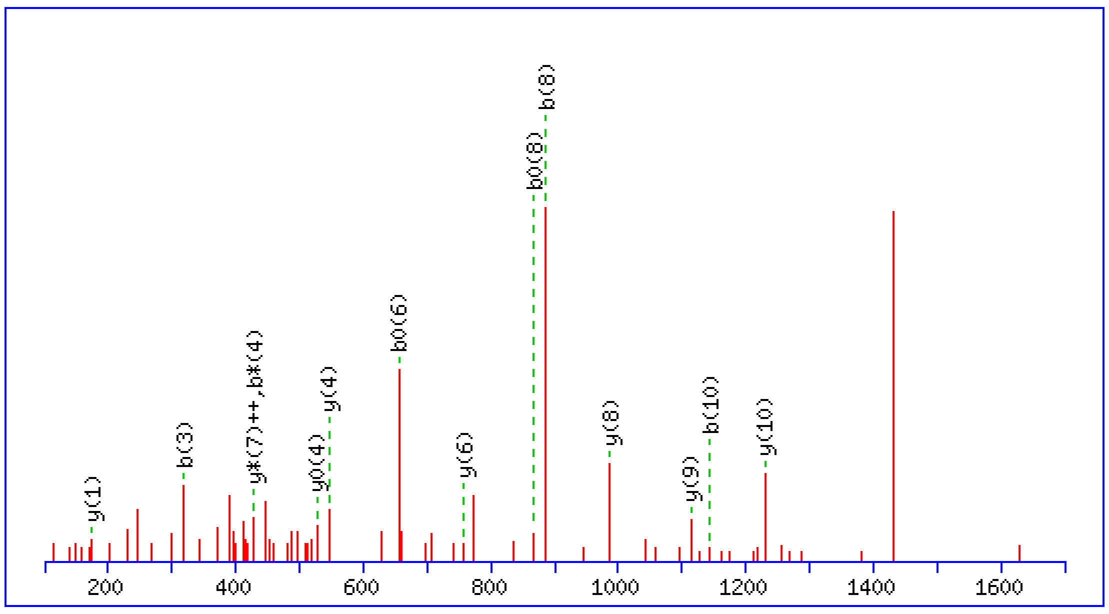
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSDQLDVIQENR**
Found in **UBR4_HUMAN**, E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1

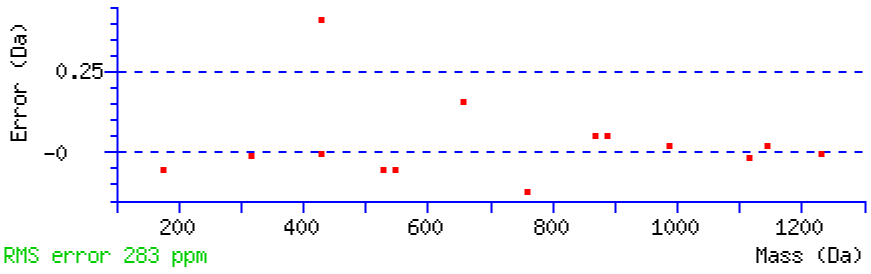
Match to Query 30328: 1430.661628 from(716.338090,2+) rtinseconds(2051) index(23824)
Title: Locus:1.1.1.2183.37
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

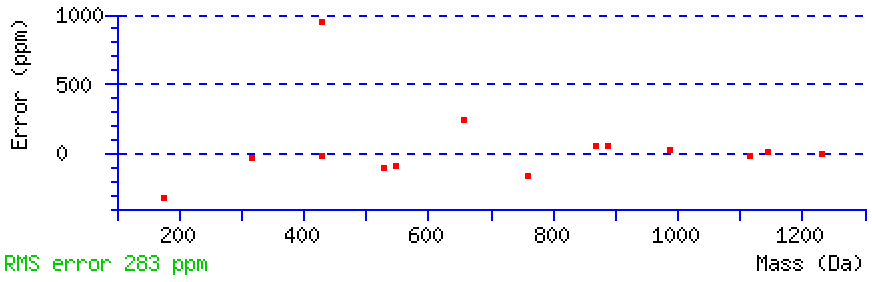
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1430.663742`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 31 Expect: 0.0071`
`Matches : 14/122 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	116.034219	58.520748			98.023654	49.515465	D							12
2	203.066247	102.036761			185.055682	93.031479	S	1316.644084	658.825680	1299.617535	650.312406	1298.633519	649.820398	11
3	**318.093190**	159.550233			300.082625	150.544951	D	***1229.612056***	615.309666	1212.585507	606.796392	1211.601491	606.304384	10
4	446.151768	223.579522	429.125219	215.066248	428.141203	214.574240	Q	***1114.585113***	557.796195	1097.558564	549.282920	1096.574548	548.790912	9
5	559.235832	280.121554	542.209283	271.608280	541.225267	271.116272	L	***986.526535***	493.766906	969.499986	485.253631	968.515970	484.761623	8
6	674.262775	337.635026	657.236226	329.121751	656.252210	328.629743	D	873.442471	437.224874	856.415922	428.711599	855.431906	428.219591	7
7	773.331189	387.169233	756.304640	378.655958	755.320624	378.163950	V	***758.415528***	379.711402	741.388979	371.198128	740.404963	370.706120	6
8	**886.415253**	443.711265	869.388704	435.197990	868.404688	434.705982	I	659.347114	330.177195	642.320565	321.663921	641.336549	321.171913	5
9	1014.473831	507.740554	997.447282	499.227279	996.463266	498.735271	Q	***546.263050***	273.635163	529.236501	265.121889	528.252485	264.629881	4
10	**1143.516424**	572.261850	1126.489875	563.748576	1125.505859	563.256568	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
11	1257.559351	629.283314	1240.532802	620.770039	1239.548786	620.278031	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 DSDQLDVIQENR
(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	1430.663742	-0.002114	DSDQLDVIQENR
8.1	1430.661224	0.000404	TSEACATHLHYK
0.5	1430.663742	-0.002114	TGEKPNGSVEPER
0.2	1430.674942	-0.013314	QQEATAEQENKR
0.1	1430.664612	-0.002984	LVEDGMHALGAMR

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

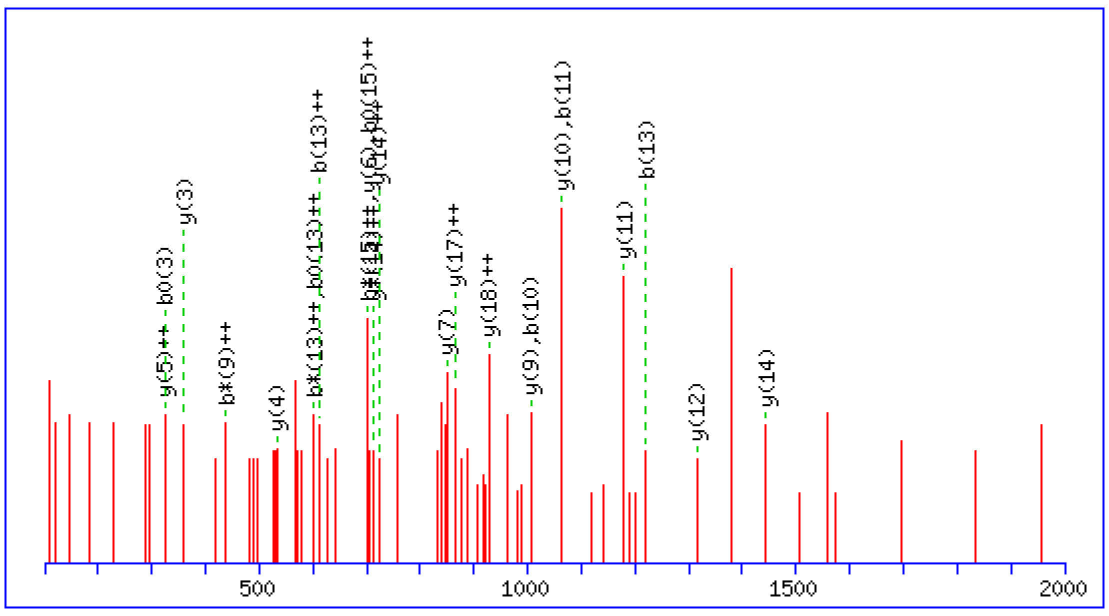
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITQAVLGAHDGGVFGLCALR**
Found in **EMAL2_HUMAN**, Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=2 SV=1

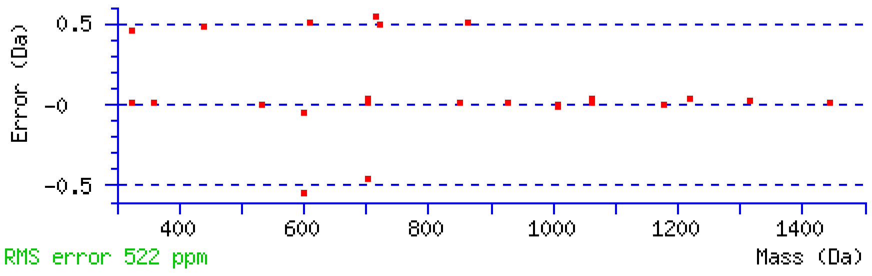
Match to Query 28975: 2068.076382 from(690.366070,3+) rtinseconds(3130) index(39465)
Title: Locus:1.1.1.2719.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

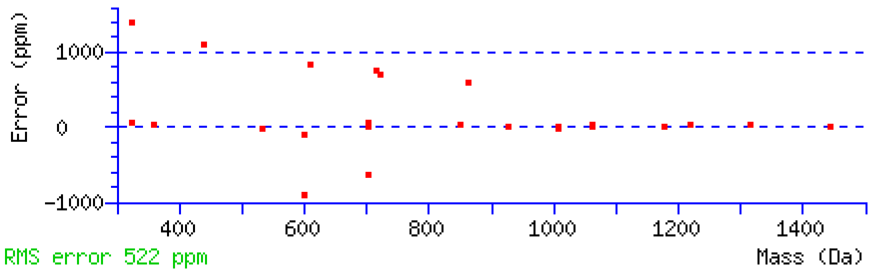
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2068.088791
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0043
Matches : 24/202 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	114.091340	57.549308					I							20
2	215.139019	108.073147			197.128454	99.067865	T	1956.011995	978.509635	1938.985446	969.996361	1938.001430	969.504353	19
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	Q	1854.964316	927.985796	1837.937767	919.472521	1836.953751	918.980513	18
4	414.234711	207.620994	397.208162	199.107719	396.224146	198.615711	A	1726.905738	863.956507	1709.879189	855.443232	1708.895173	854.951224	17
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	V	1655.868624	828.437950	1638.842075	819.924675	1637.858059	819.432667	16
6	626.387189	313.697233	609.360640	305.183958	608.376624	304.691950	L	1556.800210	778.903743	1539.773661	770.390468	1538.789645	769.898460	15
7	683.408653	342.207965	666.382104	333.694690	665.398088	333.202682	G	***1443.716146***	722.361711	1426.689597	713.848436	1425.705581	713.356428	14
8	754.445767	377.726522	737.419218	369.213247	736.435202	368.721239	A	1386.694682	693.850979	1369.668133	685.337704	1368.684117	684.845696	13
9	891.504679	446.255978	874.478130	437.742703	873.494114	437.250695	H	***1315.657568***	658.332422	1298.631019	649.819147	1297.647003	649.327139	12
10	**1006.531622**	503.769449	989.505073	495.256174	988.521057	494.764166	D	***1178.598656***	589.802966	1161.572107	581.289692	1160.588091	580.797683	11
11	**1063.553086**	532.280181	1046.526537	523.766907	1045.542521	523.274898	G	***1063.571713***	532.289494	1046.545164	523.776220			10
12	1120.574550	560.790913	1103.548001	552.277638	1102.563985	551.785630	G	***1006.550249***	503.778762	989.523700	495.265488			9
13	**1219.642964**	610.325120	1202.616415	601.811846	1201.632399	601.319837	V	949.528785	475.268031	932.502236	466.754756			8
14	1366.711378	683.859327	1349.684829	675.346053	1348.700813	674.854044	F	***850.460371***	425.733823	833.433822	417.220549			7
15	1423.732842	712.370059	1406.706293	703.856785	1405.722277	703.364776	G	***703.391957***	352.199616	686.365408	343.686342			6
16	1536.816906	768.912091	1519.790357	760.398816	1518.806341	759.906808	L	646.370493	323.688884	629.343944	315.175610			5
17	1710.863205	855.935240	1693.836656	847.421966	1692.852640	846.929958	C	***533.286429***	267.146853	516.259880	258.633578			4
18	1781.900319	891.453797	1764.873770	882.940523	1763.889754	882.448515	A	***359.240130***	180.123703	342.213581	171.610428			3
19	1894.984383	947.995829	1877.957834	939.482555	1876.973818	938.990547	L	288.203016	144.605146	271.176467	136.091871			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ITQAVLGAHDGGVFGLCALR
(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	2068.088791	-0.012409	ITQAVLGAHDGGVFGLCALR

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

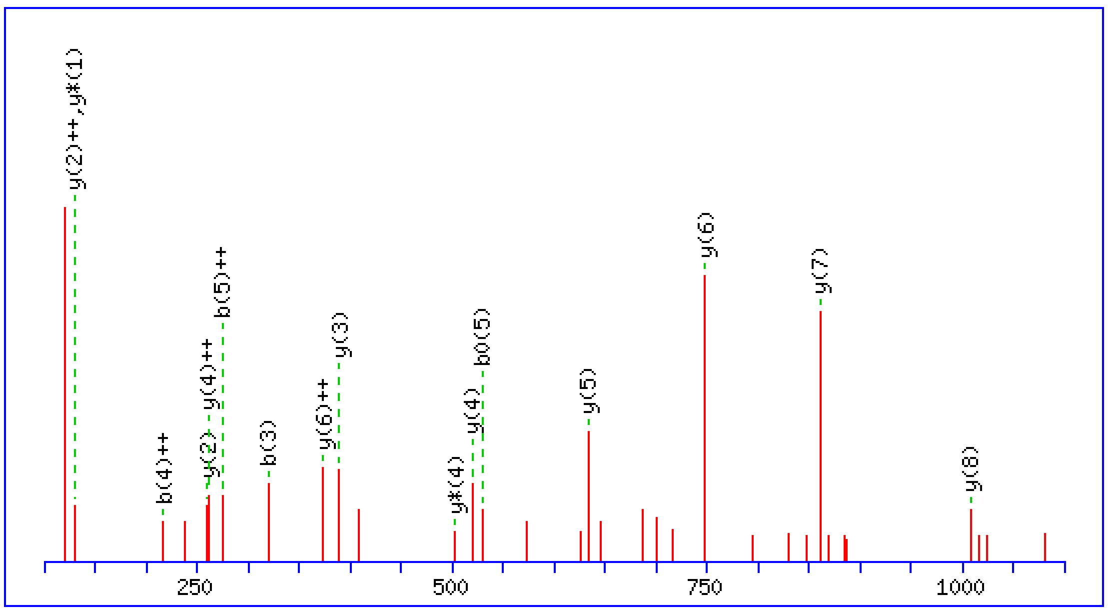
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGFIDLMELK**
Found in **EFHD1_HUMAN**, EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1

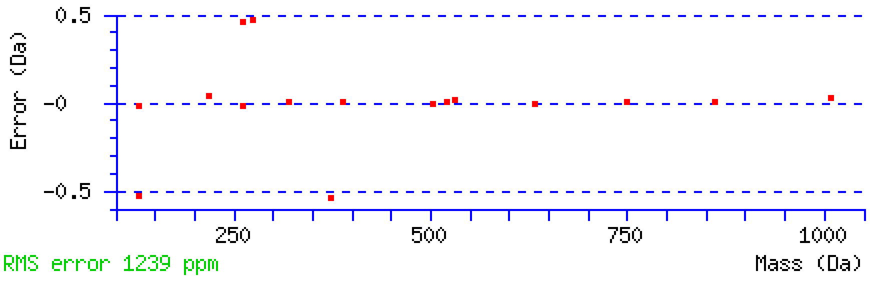
Match to Query 23236: 1179.585428 from(590.799990,2+) rtinseconds(3884) index(51200)
Title: Locus:1.1.1.2997.10
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

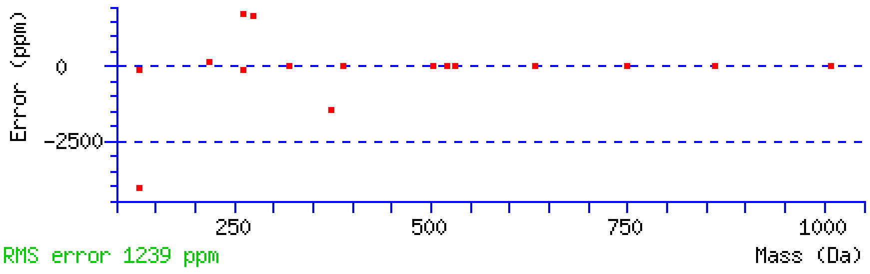
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1179.584549
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00046
Matches : 16/86 fragment ions using 25 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	173.055683	87.031479	155.045118	78.026197	G	1065.564895	533.286086	1048.538346	524.772811	1047.554330	524.280803	9
3	320.124097	160.565686	302.113532	151.560404	F	***1008.543431***	504.775354	991.516882	496.262079	990.532866	495.770071	8
4	433.208161	**217.107718**	415.197596	208.102436	I	***861.475017***	431.241147	844.448468	422.727872	843.464452	422.235864	7
5	548.235104	**274.621190**	530.224539	265.615907	D	***748.390953***	374.699115	731.364404	366.185840	730.380388	365.693832	6
6	661.319168	331.163222	643.308603	322.157940	L	***633.364010***	317.185643	616.337461	308.672369	615.353445	308.180361	5
7	792.359653	396.683465	774.349088	387.678182	M	***520.279946***	260.643611	503.253397	252.130337	502.269381	251.638329	4
8	921.402246	461.204761	903.391681	452.199479	E	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
9	1034.486310	517.746793	1016.475745	508.741511	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 DGFIDLMELK
(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	1179.584549	0.000879	DGFIDLMELK
12.7	1179.587921	-0.002493	MPSTDLLMLK
12.7	1179.587921	-0.002493	MPSTDLLMLK
5.7	1179.592438	-0.007010	GLDFDPLTFR
0.0	1179.578522	0.006906	FDGLHGQPGPR

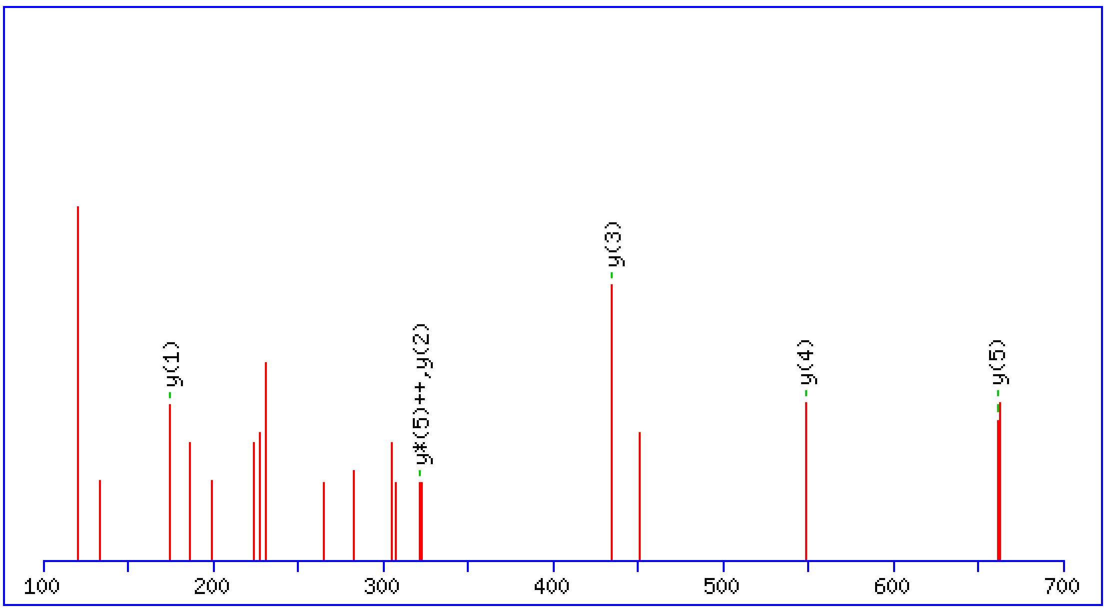
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFLLIFR**
Found in **EFHD2_HUMAN**, EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1

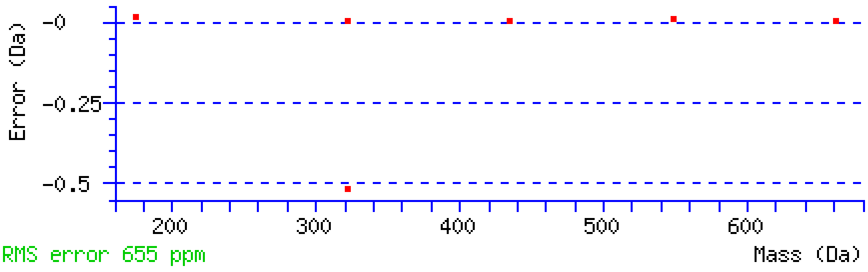
Match to Query 7593: 936.545228 from(469.279890,2+) rtinseconds(3803) index(48603)
Title: Locus:1.1.1.3253.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

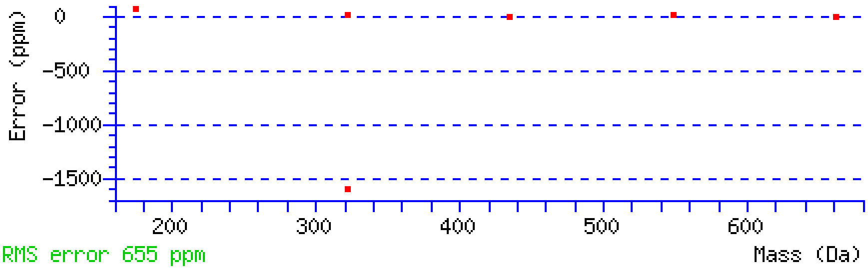
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 936.543274
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0025
Matches : 6/48 fragment ions using 11 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	277.118283	139.062779	259.107718	130.057497	F	808.507972	404.757624	791.481423	396.244350	6
3	390.202347	195.604811	372.191782	186.599529	L	***661.439558***	331.223417	644.413009	322.710143	5
4	503.286411	252.146843	485.275846	243.141561	L	***548.355494***	274.681385	531.328945	266.168111	4
5	616.370475	308.688876	598.359910	299.683593	I	***435.271430***	218.139353	418.244881	209.626078	3
6	763.438889	382.223083	745.428324	373.217800	F	***322.187366***	161.597321	305.160817	153.084046	2
7					R	***175.118952***	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of EFLLIFR
(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	936.543274	0.001954	EFLLIFR
5.9	936.539246	0.005982	YTGIRSLK

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

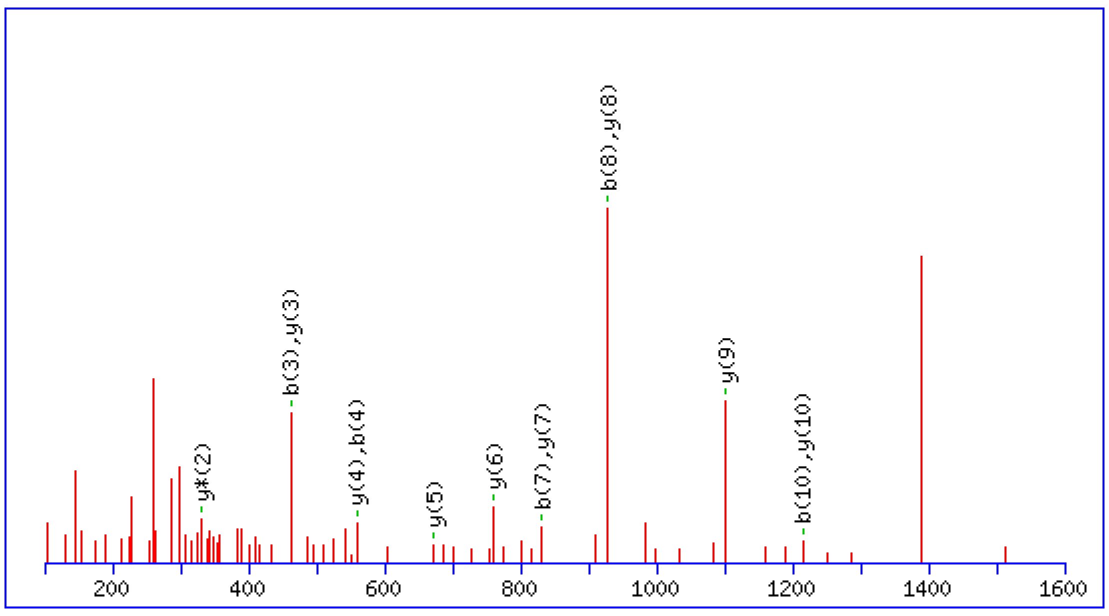
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLCPASNPLCR**
Found in **FBLN4_HUMAN**, EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3

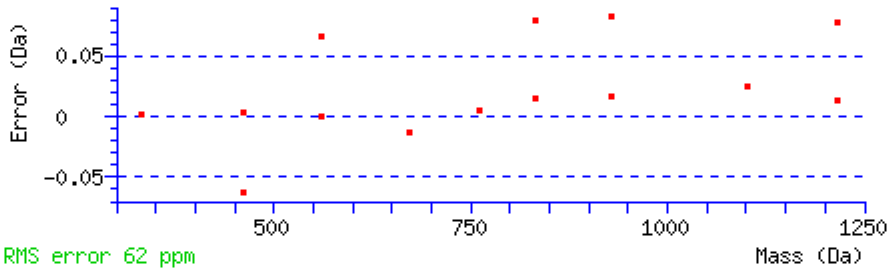
Match to Query 28767: 1388.641948 from(695.328250,2+) rtinseconds(1894) index(20386)
Title: Locus:1.1.1.2244.40
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

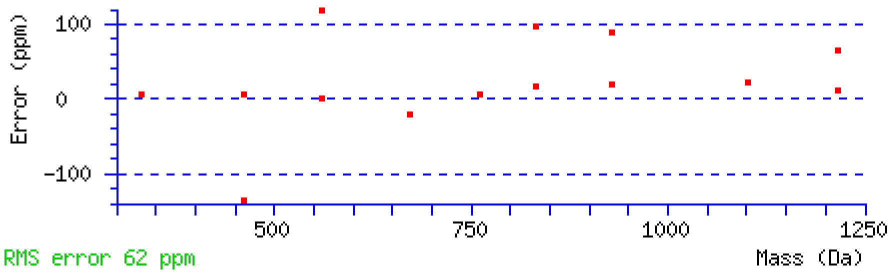
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1388.636261
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 1.2e-006
Matches : 14/88 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	175.053575	88.030425					C							11
2	288.137639	144.572457					L	***1215.597275***	608.302275	1198.570726	599.789001	1197.586710	599.296993	10
3	**462.183938**	231.595607					C	***1102.513211***	551.760244	1085.486662	543.246969	1084.502646	542.754961	9
4	**559.236702**	280.121989					P	***928.466912***	464.737094	911.440363	456.223819	910.456347	455.731811	8
5	630.273816	315.640546					A	***831.414148***	416.210712	814.387599	407.697437	813.403583	407.205429	7
6	717.305844	359.156560			699.295279	350.151277	S	***760.377034***	380.692155	743.350485	372.178880	742.366469	371.686872	6
7	**831.348771**	416.178023	814.322222	407.664749	813.338206	407.172741	N	***673.345006***	337.176141	656.318457	328.662867			5
8	**928.401535**	464.704406	911.374986	456.191131	910.390970	455.699123	P	***559.302079***	280.154678	542.275530	271.641403			4
9	1041.485599	521.246437	1024.459050	512.733163	1023.475034	512.241155	L	***462.249315***	231.628295	445.222766	223.115021			3
10	**1215.531898**	608.269587	1198.505349	599.756313	1197.521333	599.264304	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 CLCPASNPLCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.3	1388.636261	0.005687	CLCPASNPLCR
4.7	1388.641937	0.000011	SPEAATEGGAGEVSK
4.6	1388.641907	0.000041	KQEEDEENKPK
3.8	1388.653137	-0.011189	AQASPSEENKANK
3.8	1388.628220	0.013728	DYCPTNFTTLK
2.8	1388.646835	-0.004887	SSCLFCLPSFK
1.9	1388.646637	-0.004689	APICSQEEGRGR
0.5	1388.645935	-0.003987	WSEPNEEELIK
0.0	1388.639450	0.002498	SAGMYQGLAFGGSK

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

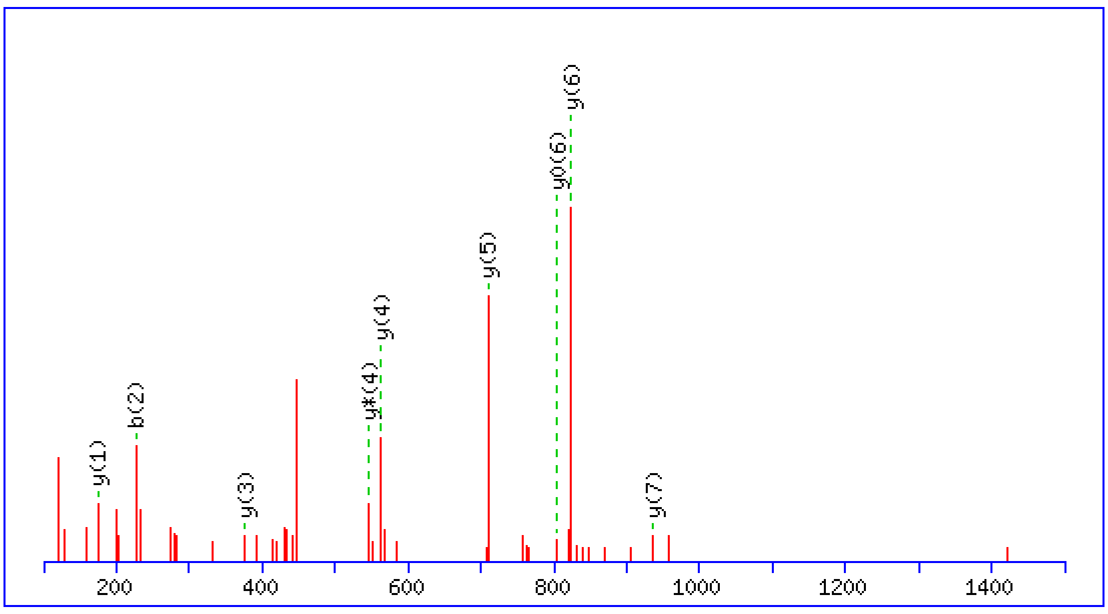
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIFWSDR**
Found in **EGLN2_HUMAN**, Egl nine homolog 2 OS=Homo sapiens GN=EGLN2 PE=1 SV=1

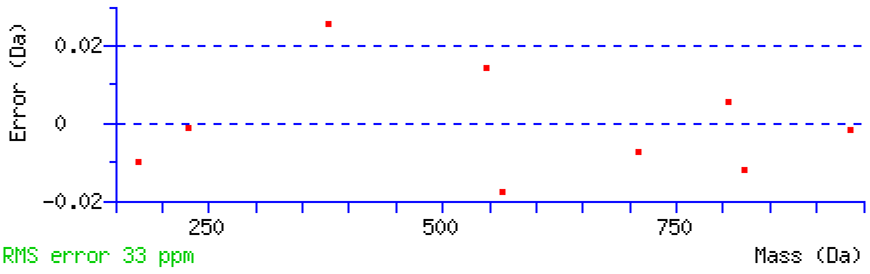
Match to Query 15106: 1048.560208 from(525.287380,2+) rtinseconds(2858) index(36954)
Title: Locus:1.1.1.2530.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

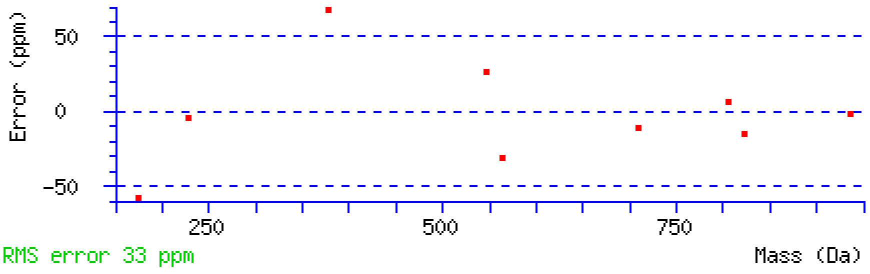
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1048.570557
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0038
Matches : 9/58 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							8
2	227.175404	114.091340			L	*936.493778*	468.750527	919.467229	460.237252	918.483213	459.745244	7
3	340.259468	170.633372			I	*823.409714*	412.208495	806.383165	403.695220	805.399149	403.203212	6
4	487.327882	244.167579			F	*710.325650*	355.666463	693.299101	347.153189	692.315085	346.661181	5
5	673.407195	337.207236			W	*563.257236*	282.132256	546.230687	273.618981	545.246671	273.126973	4
6	760.439223	380.723250	742.428658	371.717967	S	*377.177923*	189.092599	360.151374	180.579325	359.167358	180.087317	3
7	875.466166	438.236721	857.455601	429.231438	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
8					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIFWSDR
(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	1048.570557	-0.010349	LLIFWSDR
14.1	1048.566528	-0.006320	IIFGKNSDR
12.2	1048.555313	0.004895	LPPITYTGR
6.7	1048.552124	0.008084	LICNTMKR
6.6	1048.555313	0.004895	LIPTHPPDK
6.6	1048.555313	0.004895	LIPTHPPDK
4.6	1048.566544	-0.006336	SGGFDVKALR
1.7	1048.566559	-0.006351	LLGPPPPGGGR
1.4	1048.566559	-0.006351	LLGPPPPGGGR
1.4	1048.566559	-0.006351	LLGPPPPGGGR

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

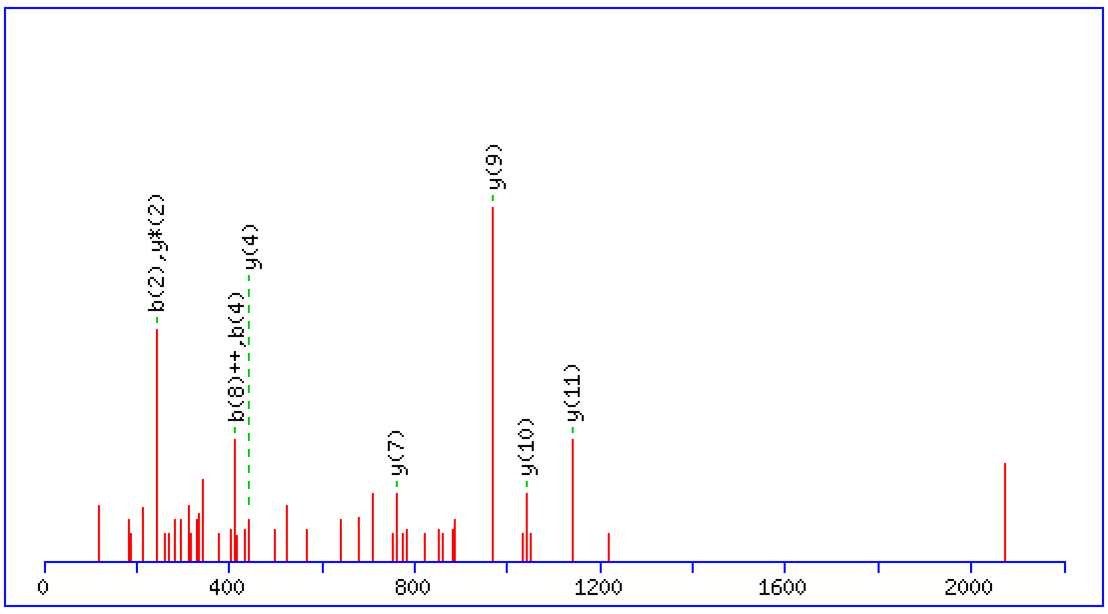
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEVAPISDIIAIK**
Found in **ETFA_HUMAN**, Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1

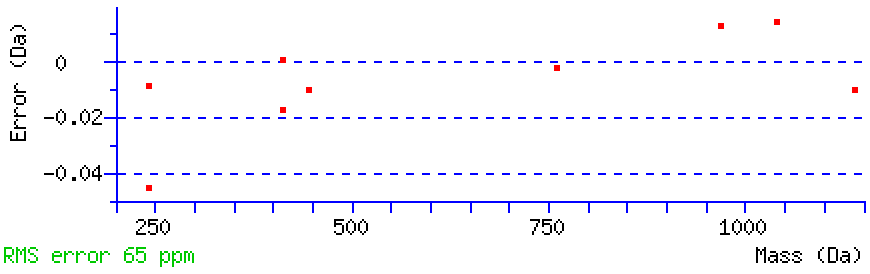
Match to Query 28679: 1380.827668 from(691.421110,2+) rtinseconds(3609) index(45826)
Title: Locus:1.1.1.2941.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

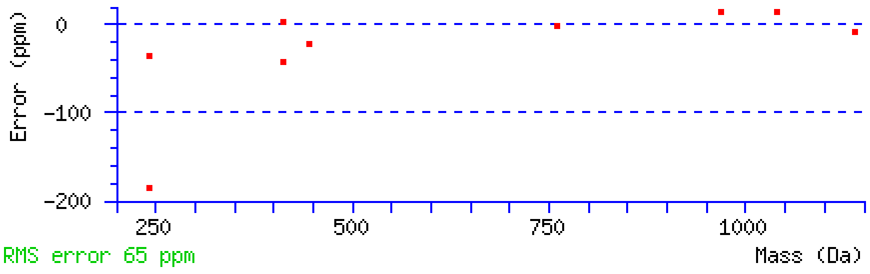
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1380.822784
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0012
Matches : 9/108 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							13
2	**243.133933**	122.070605	225.123368	113.065322	E	1268.746030	634.876653	1251.719481	626.363379	1250.735465	625.871371	12
3	342.202347	171.604812	324.191782	162.599529	V	***1139.703437***	570.355356	1122.676888	561.842082	1121.692872	561.350074	11
4	**413.239461**	207.123369	395.228896	198.118086	A	***1040.635023***	520.821149	1023.608474	512.307875	1022.624458	511.815867	10
5	510.292225	255.649751	492.281660	246.644468	P	***969.597909***	485.302592	952.571360	476.789318	951.587344	476.297310	9
6	623.376289	312.191783	605.365724	303.186500	I	872.545145	436.776210	855.518596	428.262936	854.534580	427.770928	8
7	710.408317	355.707797	692.397752	346.702514	S	***759.461081***	380.234178	742.434532	371.720904	741.450516	371.228896	7
8	825.435260	413.221268	807.424695	404.215986	D	672.429053	336.718164	655.402504	328.204890	654.418488	327.712882	6
9	938.519324	469.763300	920.508759	460.758018	I	557.402110	279.204693	540.375561	270.691418			5
10	1051.603388	526.305332	1033.592823	517.300050	I	***444.318046***	222.662661	427.291497	214.149386			4
11	1122.640502	561.823889	1104.629937	552.818606	A	331.233982	166.120629	314.207433	157.607354			3
12	1235.724566	618.365921	1217.714001	609.360638	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 LEVAPISDIIAIK
(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	1380.822784	0.004884	LEVAPISDIIAIK

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

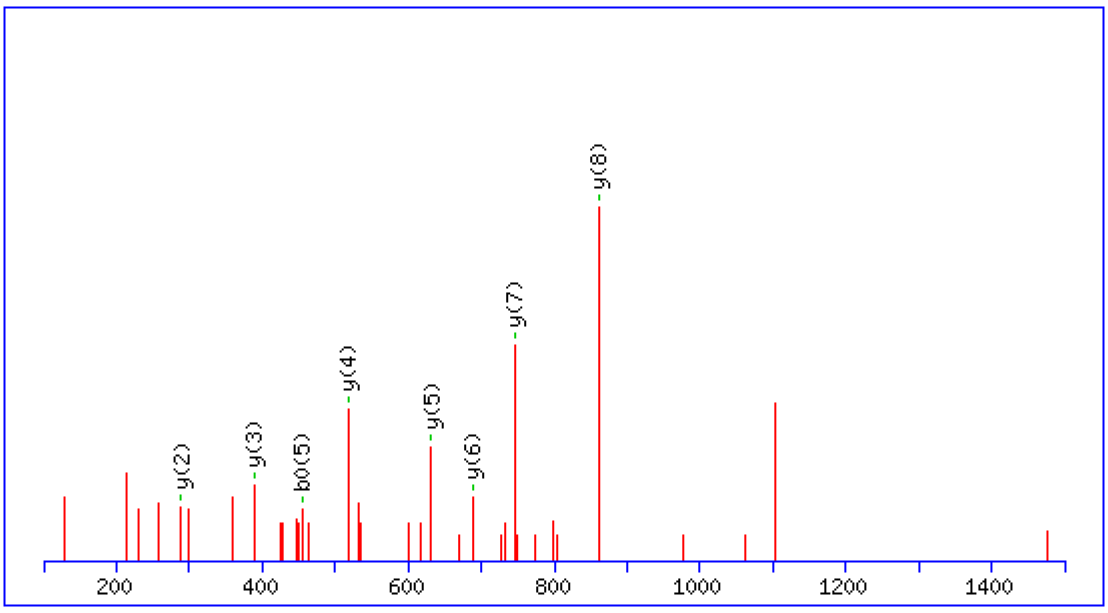
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIDGGLETLR**
Found in **ETFB_HUMAN**, Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3

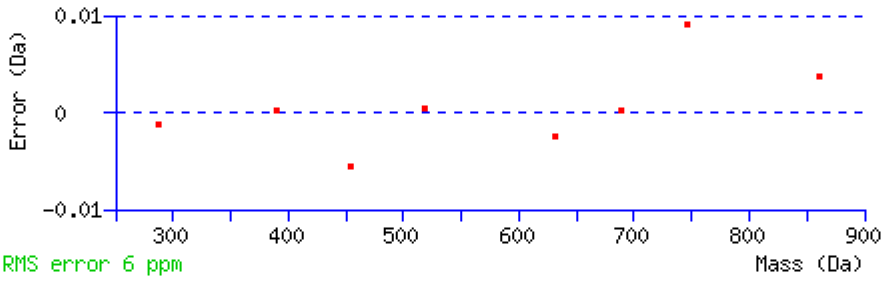
Match to Query 19038: 1101.564888 from(551.789720,2+) rtinseconds(2226) index(23622)
Title: Locus:1.1.1.2378.22
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

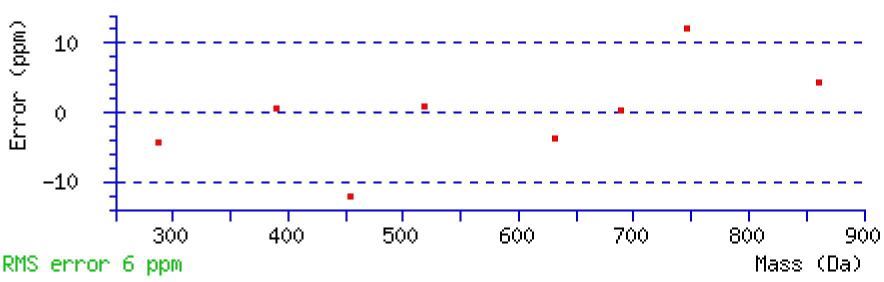
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1101.566589
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00049
Matches : 8/86 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							10
2	243.133933	122.070605	225.123368	113.065322	I	973.531287	487.269282	956.504738	478.756007	955.520722	478.263999	9
3	358.160876	179.584076	340.150311	170.578794	D	***860.447223***	430.727250	843.420674	422.213975	842.436658	421.721967	8
4	415.182340	208.094808	397.171775	199.089526	G	***745.420280***	373.213778	728.393731	364.700504	727.409715	364.208496	7
5	472.203804	236.605540	454.193239	227.600258	G	***688.398816***	344.703046	671.372267	336.189772	670.388251	335.697764	6
6	585.287868	293.147572	567.277303	284.142290	L	***631.377352***	316.192314	614.350803	307.679040	613.366787	307.187032	5
7	714.330461	357.668869	696.319896	348.663586	E	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
8	815.378140	408.192708	797.367575	399.187426	T	***389.250695***	195.128986	372.224146	186.615711	371.240130	186.123703	3
9	928.462204	464.734740	910.451639	455.729458	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 EIDGGLETLR
(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	1101.566589	-0.001701	EIDGGLETLR
8.5	1101.575317	-0.010429	YHGNVMLLR
7.9	1101.555344	0.009544	LETQELEPK
5.9	1101.570618	-0.005730	GGFLPPEEIK

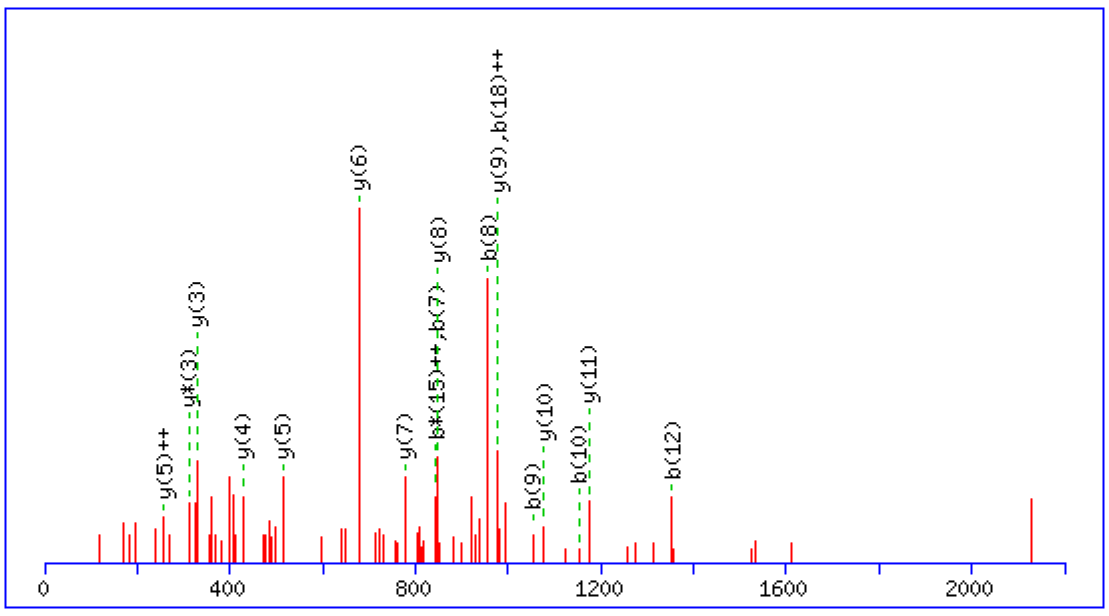
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLEKPFLLPVEAVYSVPGR**
Found in **EFTU_HUMAN**, Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2

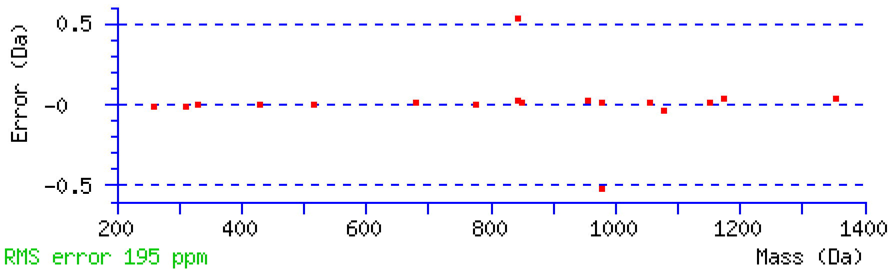
Match to Query 57202: 2128.172682 from(710.398170,3+) rtinseconds(3748) index(49998)
Title: Locus:1.1.1.2956.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

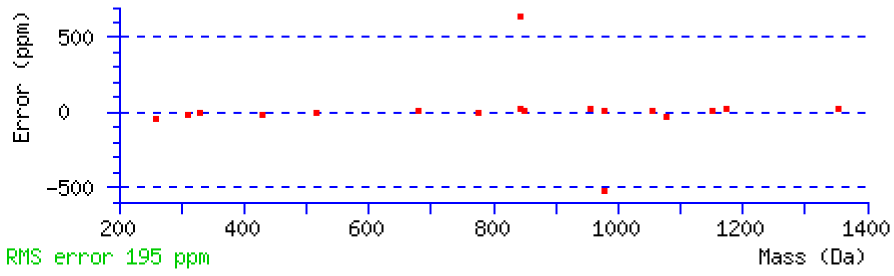
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2128.156830
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52  Expect: 3.1e-005
Matches : 18/202 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	116.034219	58.520748			98.023654	49.515465	D							19
2	229.118283	115.062779			211.107718	106.057497	L	2014.137176	1007.572226	1997.110627	999.058952	1996.126611	998.566944	18
3	358.160876	179.584076			340.150311	170.578793	E	1901.053112	951.030194	1884.026563	942.516920	1883.042547	942.024912	17
4	486.255839	243.631557	469.229290	235.118283	468.245274	234.626275	K	1772.010519	886.508898	1754.983970	877.995623	1753.999954	877.503615	16
5	583.308603	292.157940	566.282054	283.644665	565.298038	283.152657	P	1643.915556	822.461416	1626.889007	813.948142	1625.904991	813.456134	15
6	730.377017	365.692147	713.350468	357.178872	712.366452	356.686864	F	1546.862792	773.935034	1529.836243	765.421760	1528.852227	764.929752	14
7	**843.461081**	422.234179	826.434532	413.720904	825.450516	413.228896	L	1399.794378	700.400827	1382.767829	691.887553	1381.783813	691.395545	13
8	**956.545145**	478.776211	939.518596	470.262936	938.534580	469.770928	L	1286.710314	643.858795	1269.683765	635.345521	1268.699749	634.853513	12
9	**1053.597909**	527.302593	1036.571360	518.789318	1035.587344	518.297310	P	***1173.626250***	587.316763	1156.599701	578.803489	1155.615685	578.311481	11
10	**1152.666323**	576.836800	1135.639774	568.323525	1134.655758	567.831517	V	***1076.573486***	538.790381	1059.546937	530.277107	1058.562921	529.785099	10
11	1281.708916	641.358096	1264.682367	632.844822	1263.698351	632.352814	E	***977.505072***	489.256174	960.478523	480.742900	959.494507	480.250892	9
12	**1352.746030**	676.876653	1335.719481	668.363379	1334.735465	667.871371	A	***848.462479***	424.734878	831.435930	416.221603	830.451914	415.729595	8
13	1451.814444	726.410860	1434.787895	717.897586	1433.803879	717.405578	V	***777.425365***	389.216321	760.398816	380.703046	759.414800	380.211038	7
14	1614.877773	807.942525	1597.851224	799.429250	1596.867208	798.937242	Y	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	6
15	1701.909801	851.458539	1684.883252	842.945264	1683.899236	842.453256	S	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
16	1800.978215	900.992746	1783.951666	892.479471	1782.967650	891.987463	V	***428.261594***	214.634435	411.235045	206.121161			4
17	1898.030979	949.519128	1881.004430	941.005853	1880.020414	940.513845	P	***329.193180***	165.100228	312.166631	156.586954			3
18	1955.052443	978.029860	1938.025894	969.516585	1937.041878	969.024577	G	232.140416	116.573846	215.113867	108.060572			2
19							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of DLEKPFLLPVEAVYSVPGR
(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	2128.156830	0.015852	DLEKPFLLPVEAVYSVPGR

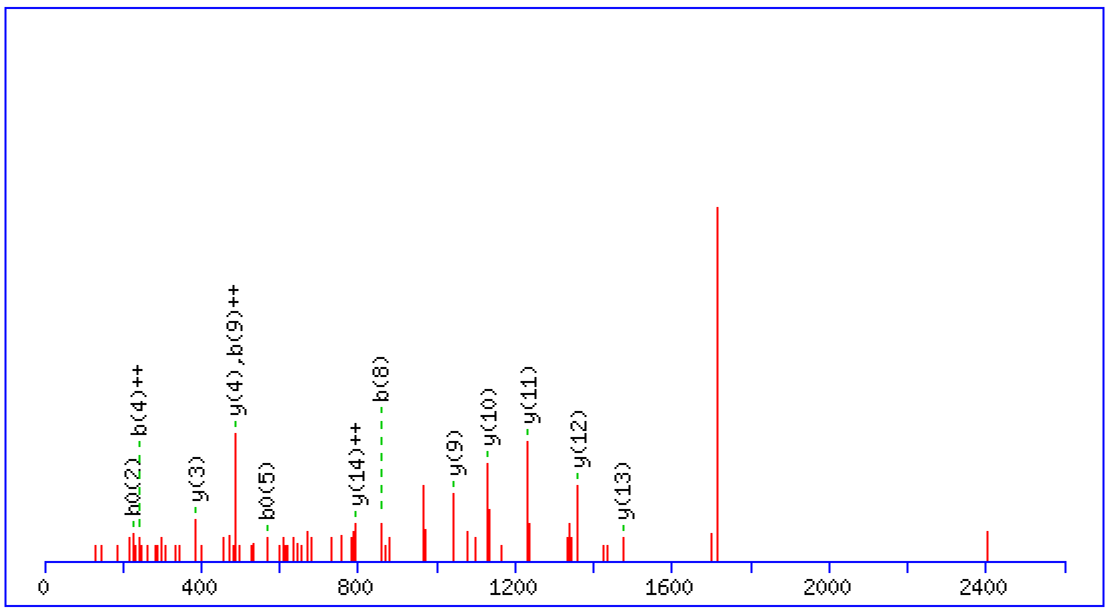
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELIQTSALNFLTPLR**
Found in **SHLB1_HUMAN**, Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1

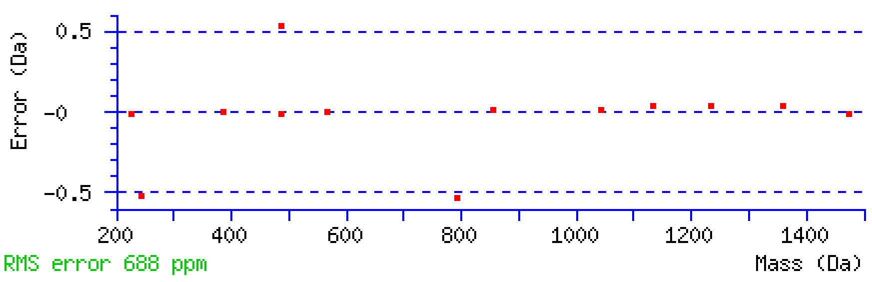
Match to Query 39603: 1714.974448 from(858.494500,2+) rtinseconds(3989) index(51555)
Title: Locus:1.1.1.3086.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

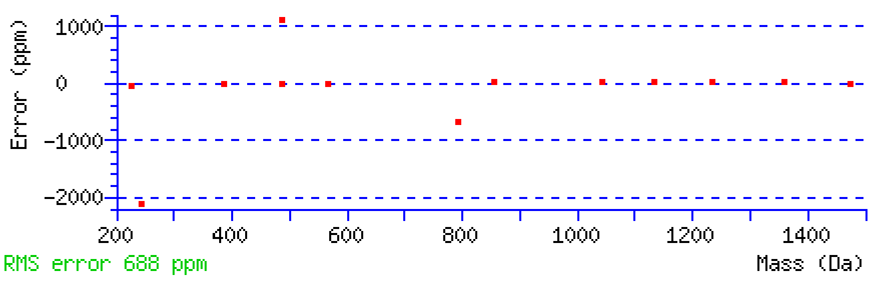
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1714.961746
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00026
Matches : 13/156 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**							15
2	243.133933	122.070605			225.123368	113.065322	**L**	1586.926455	793.966866	1569.899906	785.453591	1568.915890	784.961583	14
3	356.217997	178.612637			338.207432	169.607354	**I**	***1473.842391***	737.424833	1456.815842	728.911559	1455.831826	728.419551	13
4	484.276575	**242.641926**	467.250026	234.128651	466.266010	233.636643	**Q**	***1360.758327***	680.882801	1343.731778	672.369527	1342.747762	671.877519	12
5	585.324254	293.165765	568.297705	284.652491	567.313689	284.160483	**T**	***1232.699749***	616.853512	1215.673200	608.340238	1214.689184	607.848230	11
6	672.356282	336.681779	655.329733	328.168505	654.345717	327.676497	**S**	***1131.652070***	566.329673	1114.625521	557.816398	1113.641505	557.324390	10
7	743.393396	372.200336	726.366847	363.687062	725.382831	363.195054	**A**	***1044.620042***	522.813659	1027.593493	514.300384	1026.609477	513.808376	9
8	856.477460	428.742368	839.450911	420.229094	838.466895	419.737086	**L**	973.582928	487.295102	956.556379	478.781827	955.572363	478.289819	8
9	970.520387	**485.763832**	953.493838	477.250557	952.509822	476.758549	**N**	860.498864	430.753070	843.472315	422.239795	842.488299	421.747787	7
10	1117.588801	559.298039	1100.562252	550.784764	1099.578236	550.292756	**F**	746.455937	373.731607	729.429388	365.218332	728.445372	364.726324	6
11	1230.672865	615.840071	1213.646316	607.326796	1212.662300	606.834788	**L**	599.387523	300.197399	582.360974	291.684125	581.376958	291.192117	5
12	1331.720544	666.363910	1314.693995	657.850636	1313.709979	657.358628	**T**	***486.303459***	243.655367	469.276910	235.142093	468.292894	234.650085	4
13	1428.773308	714.890292	1411.746759	706.377018	1410.762743	705.885010	**P**	***385.255780***	193.131528	368.229231	184.618253			3
14	1541.857372	771.432324	1524.830823	762.919050	1523.846807	762.427041	**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 ELIQTSALNFLTPLR
(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	1714.961746	0.012702	ELIQTSALNFLTPLR

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

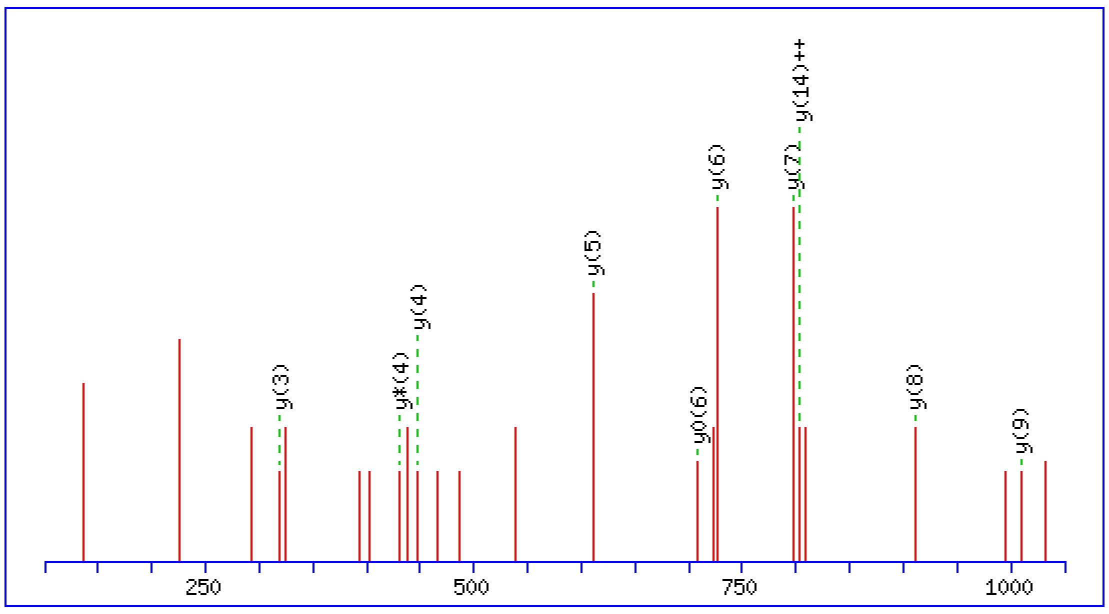
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **INEKPQVIADYESGR**
Found in **EDF1_HUMAN**, Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1 PE=1 SV=1

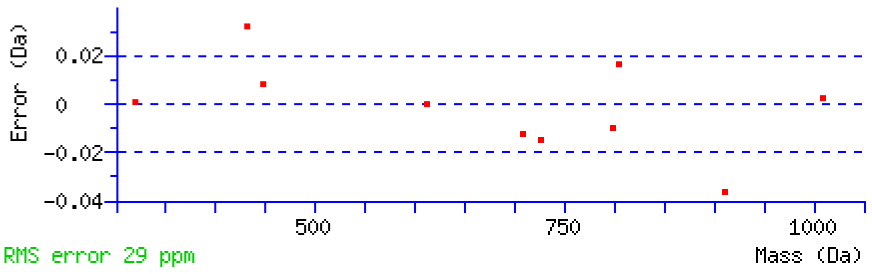
Match to Query 34453: 1717.859832 from(573.627220,3+) rtinseconds(1977) index(12349)
Title: Locus:1.1.1.2251.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

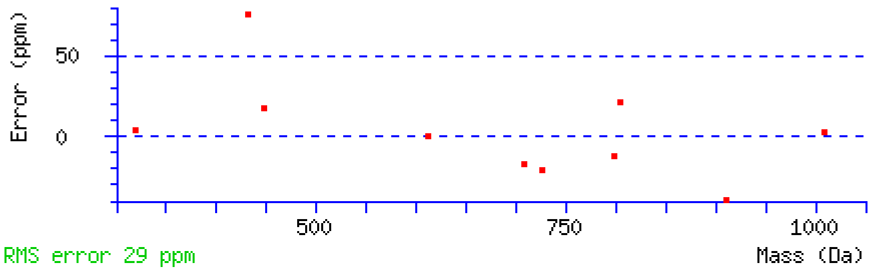
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1717.863480
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.011
Matches : 10/158 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							15
2	228.134267	114.570771	211.107718	106.057497			N	1605.786726	803.397001	1588.760177	794.883727	1587.776161	794.391719	14
3	357.176860	179.092068	340.150311	170.578793	339.166295	170.086785	E	1491.743799	746.375538	1474.717250	737.862263	1473.733234	737.370255	13
4	485.271823	243.139549	468.245274	234.626275	467.261258	234.134267	K	1362.701206	681.854241	1345.674657	673.340967	1344.690641	672.848959	12
5	582.324587	291.665932	565.298038	283.152657	564.314022	282.660649	P	1234.606243	617.806760	1217.579694	609.293485	1216.595678	608.801477	11
6	710.383165	355.695221	693.356616	347.181946	692.372600	346.689938	Q	1137.553479	569.280378	1120.526930	560.767103	1119.542914	560.275095	10
7	809.451579	405.229428	792.425030	396.716153	791.441014	396.224145	V	***1009.494901***	505.251089	992.468352	496.737814	991.484336	496.245806	9
8	922.535643	461.771460	905.509094	453.258185	904.525078	452.766177	I	***910.426487***	455.716882	893.399938	447.203607	892.415922	446.711599	8
9	993.572757	497.290017	976.546208	488.776742	975.562192	488.284734	A	***797.342423***	399.174850	780.315874	390.661575	779.331858	390.169567	7
10	1108.599700	554.803488	1091.573151	546.290214	1090.589135	545.798205	D	***726.305309***	363.656293	709.278760	355.143018	708.294744	354.651010	6
11	1271.663029	636.335153	1254.636480	627.821878	1253.652464	627.329870	Y	***611.278366***	306.142821	594.251817	297.629547	593.267801	297.137539	5
12	1400.705622	700.856449	1383.679073	692.343175	1382.695057	691.851167	E	***448.215037***	224.611157	431.188488	216.097882	430.204472	215.605874	4
13	1487.737650	744.372463	1470.711101	735.859189	1469.727085	735.367181	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
14	1544.759114	772.883195	1527.732565	764.369921	1526.748549	763.877913	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 INEKPQVIADYESGR
(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	1717.863480	-0.003648	INEKPQVIADYESGR

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

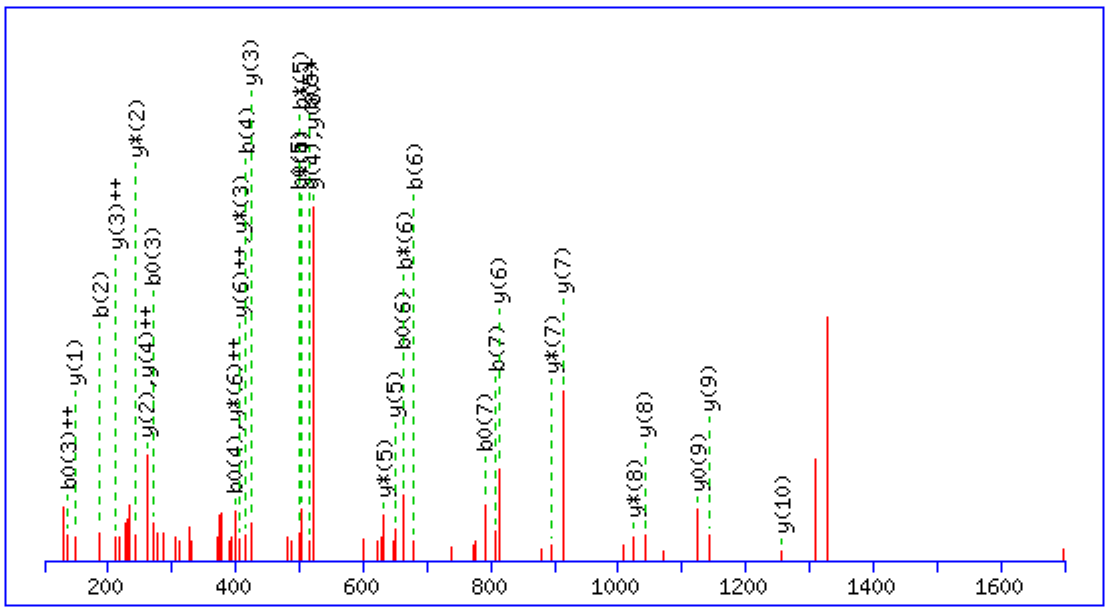
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADTQTYQPYNK**
Found in **ERH_HUMAN**, Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1

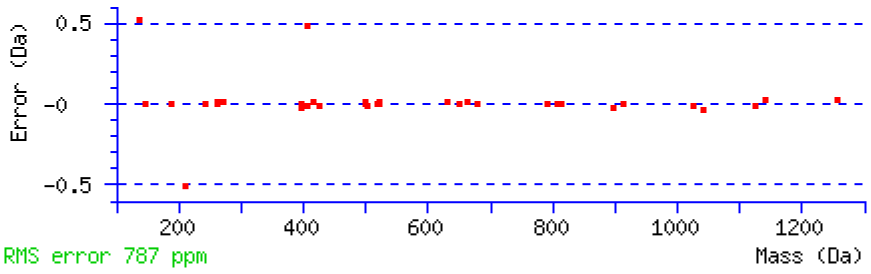
Match to Query 11820: 1327.607488 from(664.811020,2+) rtinseconds(1355) index(1264)
Title: Locus:1.1.1.2272.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

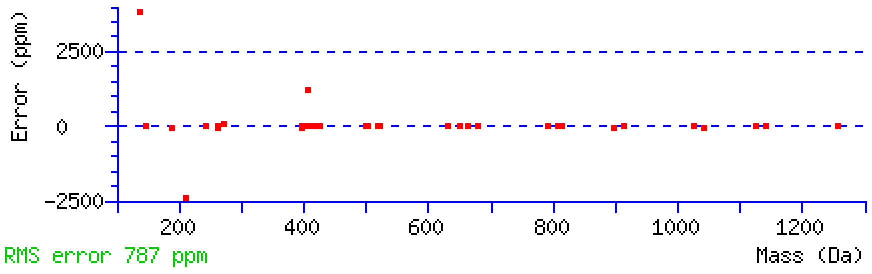
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1327.604431
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 1.4e-006
Matches : 35/100 fragment ions using 60 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	**187.071333**	94.039304			169.060768	85.034022	D	***1257.574610***	629.290943	1240.548061	620.777669	1239.564045	620.285661	10
3	288.119012	144.563144			270.108447	135.557862	T	***1142.547667***	571.777472	1125.521118	563.264197	1124.537102	562.772189	9
4	**416.177590**	208.592433	399.151041	200.079159	398.167025	199.587151	Q	***1041.499988***	521.253632	1024.473439	512.740358	1023.489423	512.248350	8
5	**517.225269**	259.116273	500.198720	250.602998	499.214704	250.110990	T	***913.441410***	457.224343	896.414861	448.711069	895.430845	448.219061	7
6	**680.288598**	340.647937	663.262049	332.134663	662.278033	331.642655	Y	***812.393731***	406.700504	795.367182	398.187229			6
7	**808.347176**	404.677226	791.320627	396.163952	790.336611	395.671944	Q	***649.330402***	325.168839	632.303853	316.655565			5
8	905.399940	453.203608	888.373391	444.690334	887.389375	444.198326	P	***521.271824***	261.139550	504.245275	252.626276			4
9	1068.463269	534.735273	1051.436720	526.221998	1050.452704	525.729990	Y	***424.219060***	212.613168	407.192511	204.099893			3
10	1182.506196	591.756736	1165.479647	583.243462	1164.495631	582.751454	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 ADTQTYQPYNK
(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	1327.604431	0.003057	ADTQTYQPYNK

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

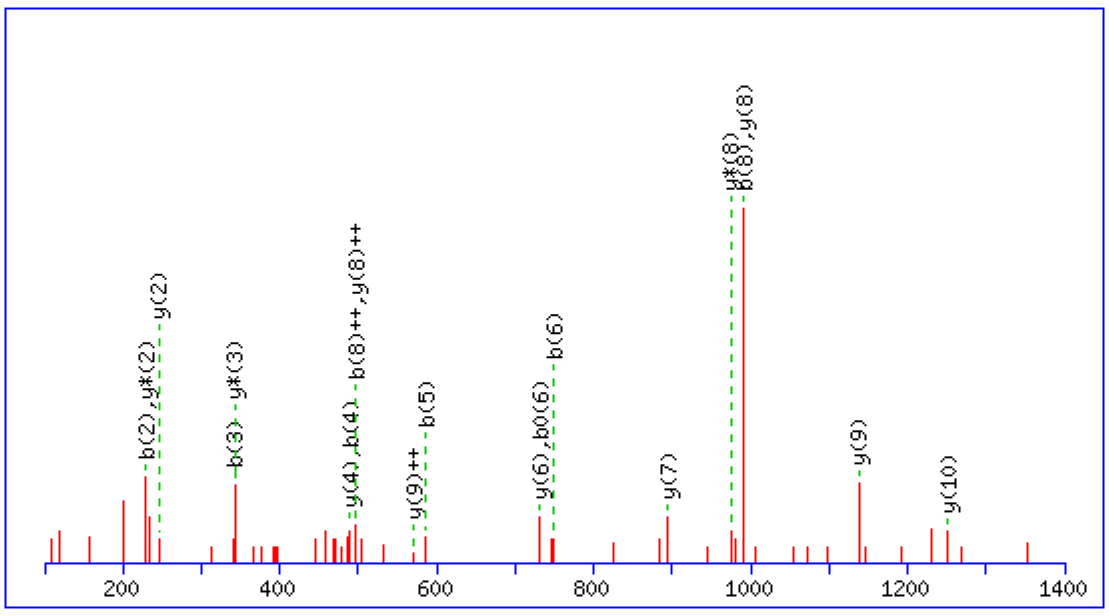
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DILFPYIEENVK**
Found in **ENOPH_HUMAN**, Enolase-phosphatase E1 OS=Homo sapiens GN=ENOPH1 PE=1 SV=1

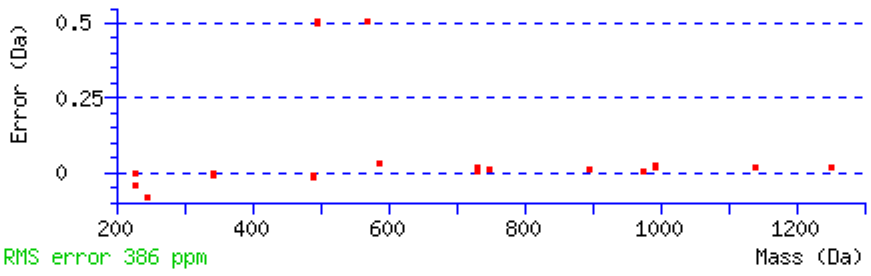
Match to Query 40040: 1478.778768 from(740.396660,2+) rtinseconds(3676) index(51803)
Title: Locus:1.1.1.2887.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

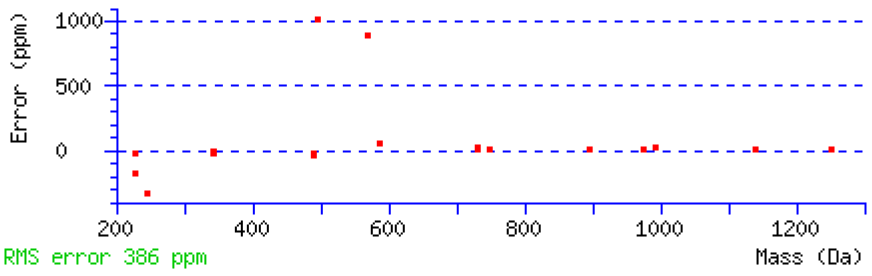
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1478.765671
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0059
Matches : 20/108 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							12
2	**229.118283**	115.062779			211.107718	106.057497	I	1364.746030	682.876653	1347.719481	674.363379	1346.735465	673.871371	11
3	**342.202347**	171.604811			324.191782	162.599529	L	***1251.661966***	626.334621	1234.635417	617.821347	1233.651401	617.329339	10
4	**489.270761**	245.139018			471.260196	236.133736	F	***1138.577902***	569.792589	1121.551353	561.279315	1120.567337	560.787307	9
5	**586.323525**	293.665401			568.312960	284.660118	P	***991.509488***	496.258382	974.482939	487.745108	973.498923	487.253100	8
6	**749.386854**	375.197065			731.376289	366.191783	Y	***894.456724***	447.732000	877.430175	439.218726	876.446159	438.726718	7
7	862.470918	431.739097			844.460353	422.733815	I	***731.393395***	366.200336	714.366846	357.687061	713.382830	357.195053	6
8	**991.513511**	496.260394			973.502946	487.255111	E	618.309331	309.658304	601.282782	301.145029	600.298766	300.653021	5
9	1120.556104	560.781690			1102.545539	551.776408	E	***489.266738***	245.137007	472.240189	236.623732	471.256173	236.131724	4
10	1234.599031	617.803154	1217.572482	609.289879	1216.588466	608.797871	N	360.224145	180.615711	343.197596	172.102436			3
11	1333.667445	667.337361	1316.640896	658.824086	1315.656880	658.332078	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 DILFPYIEENVK
(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	1478.765671	0.013097	DILFPYIEENVK
10.8	1478.772919	0.005849	SQSVSPPPVLSPPR
9.0	1478.772919	0.005849	SQSVSPPPVLSPPR
9.0	1478.772919	0.005849	SQSVSPPPVLSPPR
8.5	1478.784119	-0.005351	SLQEEHVAVAQLR
6.9	1478.772919	0.005849	SQSVSPPPVLSPPR
6.3	1478.772919	0.005849	SQSVSPPPVLSPPR
6.3	1478.772919	0.005849	SQSVSPPPVLSPPR
0.3	1478.772919	0.005849	SQSVSPPPVLSPPR
0.3	1478.772919	0.005849	SQSVSPPPVLSPPR

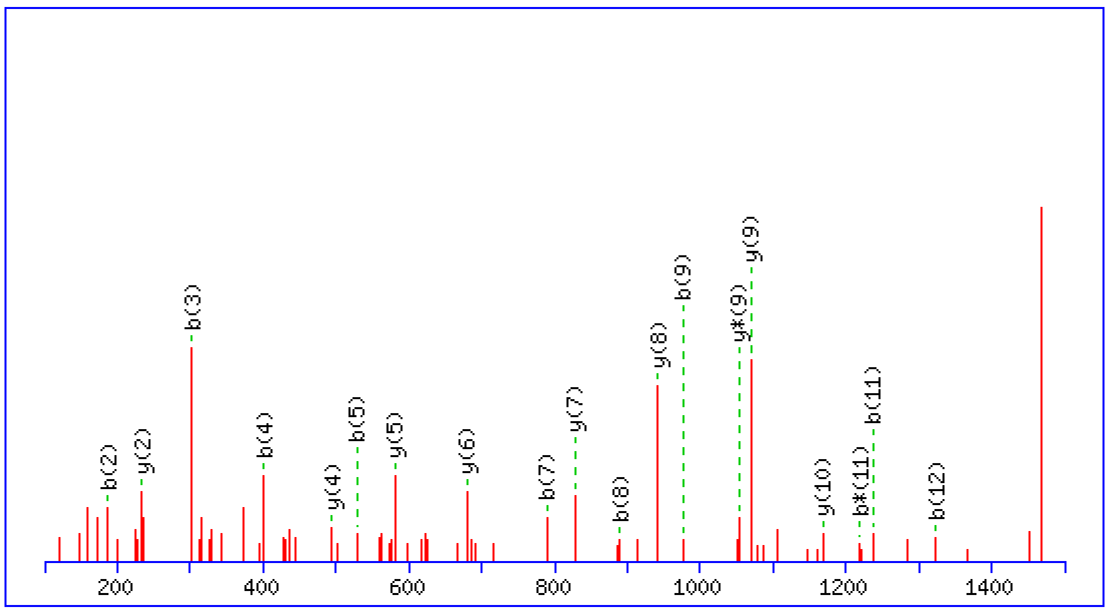
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DADVQNFVSFISK**
Found in **ECI1_HUMAN**, Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1

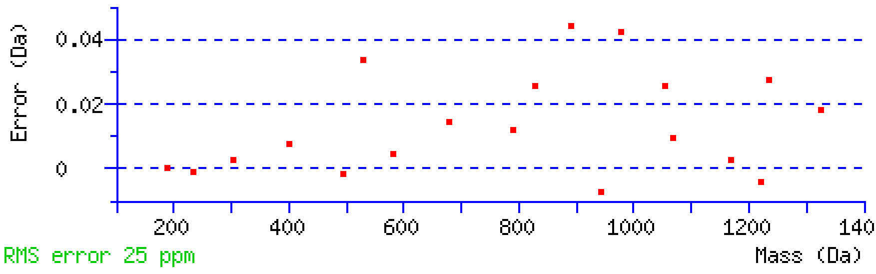
Match to Query 35114: 1468.726748 from(735.370650,2+) rtinseconds(3679) index(48926)
Title: Locus:1.1.1.2921.28
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

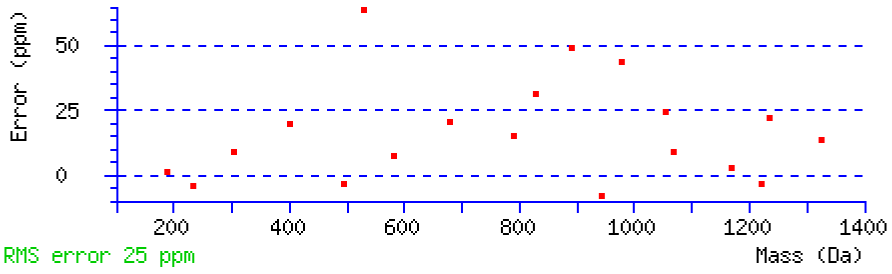
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1468.719818
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 77  Expect: 1.8e-007
Matches : 19/134 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							13
2	***187.071333***	94.039304			169.060768	85.034022	A	1354.700142	677.853709	1337.673593	669.340435	1336.689577	668.848426	12
3	***302.098276***	151.552776			284.087711	142.547494	D	1283.663028	642.335152	1266.636479	633.821878	1265.652463	633.329869	11
4	***401.166690***	201.086983			383.156125	192.081701	V	***1168.636085***	584.821680	1151.609536	576.308406	1150.625520	575.816398	10
5	***529.225268***	265.116272	512.198719	256.602998	511.214703	256.110990	Q	***1069.567671***	535.287474	1052.541122	526.774199	1051.557106	526.282191	9
6	643.268195	322.137736	626.241646	313.624461	625.257630	313.132453	N	***941.509093***	471.258184	924.482544	462.744910	923.498528	462.252902	8
7	***790.336609***	395.671943	773.310060	387.158668	772.326044	386.666660	F	***827.466166***	414.236721	810.439617	405.723446	809.455601	405.231438	7
8	***889.405023***	445.206150	872.378474	436.692875	871.394458	436.200867	V	***680.397752***	340.702514	663.371203	332.189239	662.387187	331.697231	6
9	***976.437051***	488.722164	959.410502	480.208889	958.426486	479.716881	S	***581.329338***	291.168307	564.302789	282.655033	563.318773	282.163025	5
10	1123.505465	562.256371	1106.478916	553.743096	1105.494900	553.251088	F	***494.297310***	247.652293	477.270761	239.139018	476.286745	238.647010	4
11	***1236.589529***	618.798402	1219.562980	610.285128	1218.578964	609.793120	I	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
12	***1323.621557***	662.314416	1306.595008	653.801142	1305.610992	653.309134	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 DADVQNFVSFISK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.2	1468.719818	0.006930	DADVQNFVSFISK
5.0	1468.738434	-0.011686	GFPALSQKMSPFK
4.5	1468.713257	0.013491	WEQAMKELHPGK
3.9	1468.740921	-0.014173	EAPSPEKTLPPQK
3.2	1468.740921	-0.014173	EAPSPEKTLPPQK
0.7	1468.727036	-0.000288	LSTVPSTQSQHPR

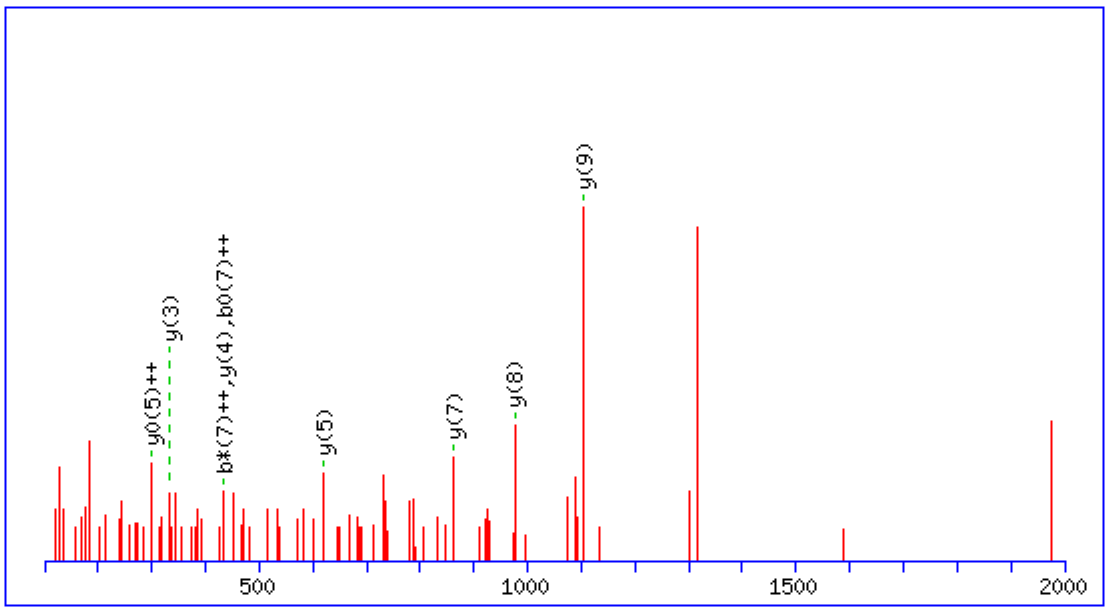
Mascot Search Results

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

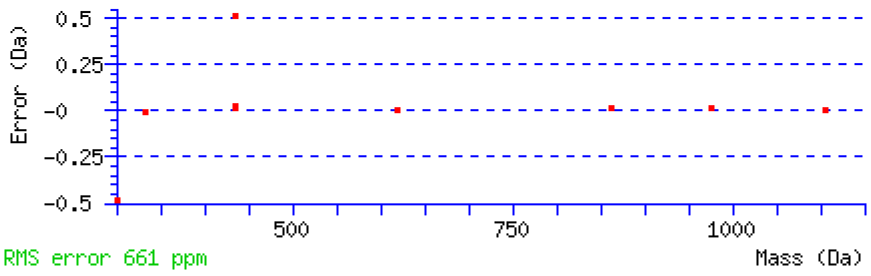
Match to Query 28330: 1316.663728 from(659.339140,2+) rtinseconds(2807) index(35975)
Title: Locus:1.1.1.2510.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

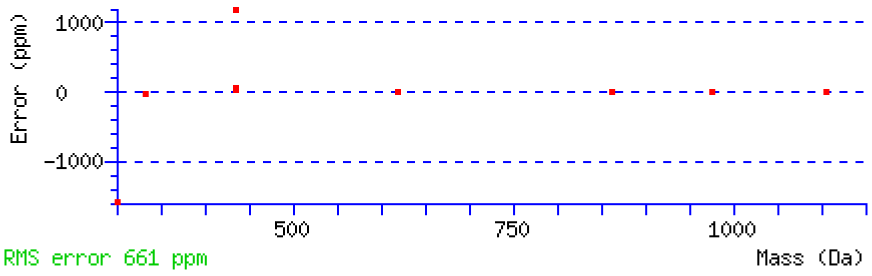
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1316.661209
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00016
Matches : 9/102 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	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
41.3	1316.661209	0.002519	VIELENWTEGK
0.9	1316.650650	0.013078	ALAQQGCALSER

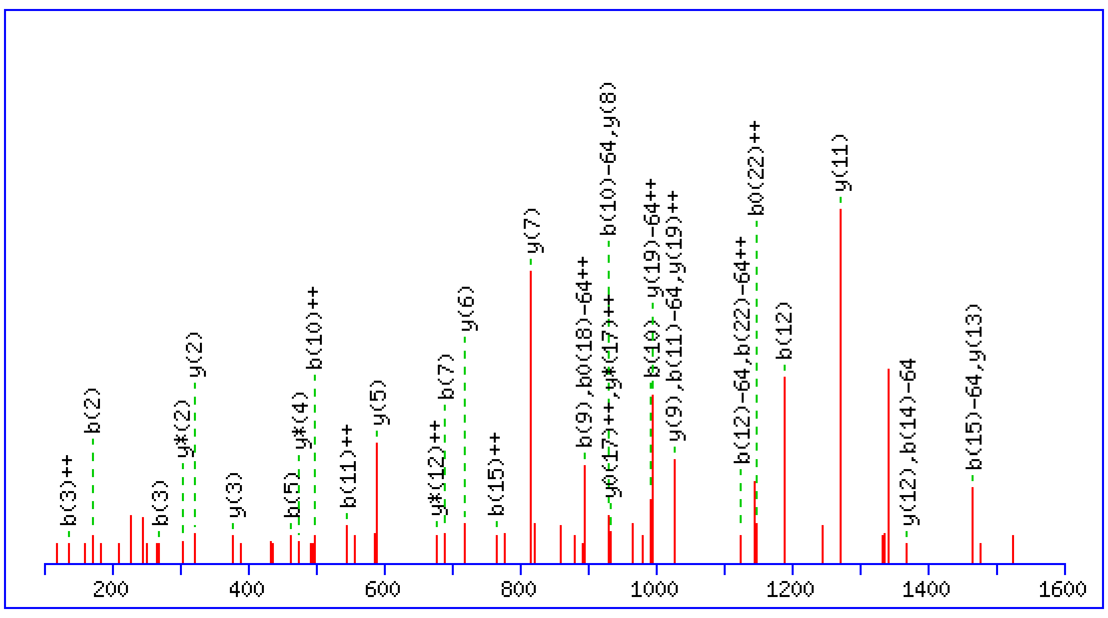
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of AVVHGILMGVPVPFPIPEPDGCK
Found in NPC2_HUMAN, Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1

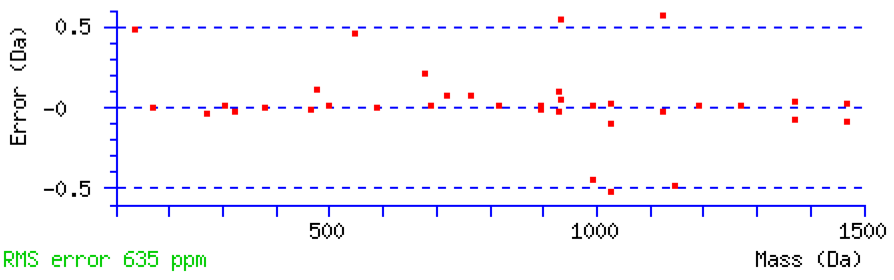
Match to Query 57857: 2458.277772 from(820.433200,3+) rtinseconds(3694) index(46623)
Title: Locus:1.1.1.3212.41
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

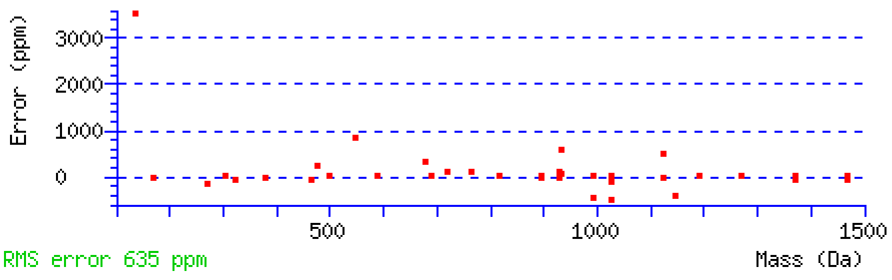
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2458.275284
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: 55  Expect: 2.3e-005
Matches : 36/262 fragment ions using 57 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							23
2	***171.112804***	86.060040			V	2388.245425	1194.626350	2371.218876	1186.113076	2370.234860	1185.621068	22
3	***270.181218***	**135.594247**			V	2289.177011	1145.092143	2272.150462	1136.578869	2271.166446	1136.086861	21
4	407.240130	204.123703			H	2190.108597	1095.557936	2173.082048	1087.044662	2172.098032	1086.552654	20
5	***464.261594***	232.634435			G	2053.049685	1027.028480	2036.023136	1018.515206	2035.039120	1018.023198	19
6	577.345658	289.176467			I	1996.028221	998.517749	1979.001672	990.004474	1978.017656	989.512466	18
7	***690.429722***	345.718499			L	1882.944157	941.975717	1865.917608	933.462442	1864.933592	932.970434	17
8	837.465122	419.236199			M	1769.860093	885.433685	1752.833544	876.920410	1751.849528	876.428402	16
9	***894.486586***	447.746931			G	1622.824693	811.915985	1605.798144	803.402710	1604.814128	802.910702	15
10	***993.555000***	**497.281138**			V	1565.803229	783.405253	1548.776680	774.891978	1547.792664	774.399970	14
11	1090.607764	**545.807520**			P	***1466.734815***	733.871046	1449.708266	725.357771	1448.724250	724.865763	13
12	***1189.676178***	595.341727			V	***1369.682051***	685.344664	1352.655502	676.831389	1351.671486	676.339381	12
13	1286.728942	643.868109			P	***1270.613637***	635.810457	1253.587088	627.297182	1252.603072	626.805174	11
14	1433.797356	717.402316			F	1173.560873	587.284075	1156.534324	578.770800	1155.550308	578.278792	10
15	1530.850120	**765.928698**			P	***1026.492459***	513.749868	1009.465910	505.236593	1008.481894	504.744585	9
16	1643.934184	822.470730			I	***929.439695***	465.223486	912.413146	456.710211	911.429130	456.218203	8
17	1740.986948	870.997112			P	***816.355631***	408.681454	799.329082	400.168179	798.345066	399.676171	7
18	1870.029541	935.518409	1852.018976	926.513126	E	***719.302867***	360.155072	702.276318	351.641797	701.292302	351.149789	6
19	1967.082305	984.044791	1949.071740	975.039508	P	***590.260274***	295.633775	573.233725	287.120500	572.249709	286.628492	5
20	2082.109248	1041.558262	2064.098683	1032.552979	D	493.207510	247.107393	476.180961	238.594118	475.196945	238.102110	4
21	2139.130712	1070.068994	2121.120147	1061.063711	G	***378.180567***	189.593921	361.154018	181.080647			3
22	2313.177011	1157.092143	2295.166446	1148.086861	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 AVVHGILMGVPVPFPIPEPDGCK
(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	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
33.6	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
21.1	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
16.4	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
14.1	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
5.5	2458.275284	0.002488	AVVHGILMGVPVPFPIPEPDGCK
4.9	2458.253296	0.024476	TTVFQYPVGWPPVQELPPSLR
0.9	2458.277725	0.000047	LLSSLLLTMSNNNPELFSPPQK
0.8	2458.300385	-0.022613	MVSAFYTILTPMLNPLIYSLR
0.6	2458.296356	-0.018584	LLPHAVSSLLCIELFQSLSCK

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

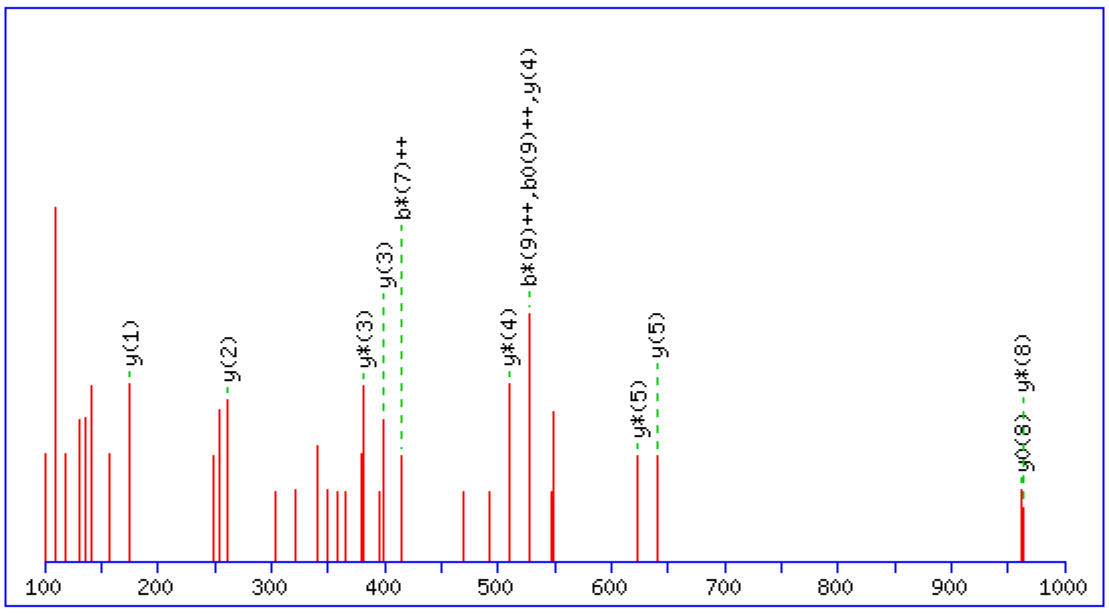
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQNFKVLLQHSR**
Found in **ERO1B_HUMAN**, ERO1-like protein beta OS=Homo sapiens GN=ERO1LB PE=1 SV=2

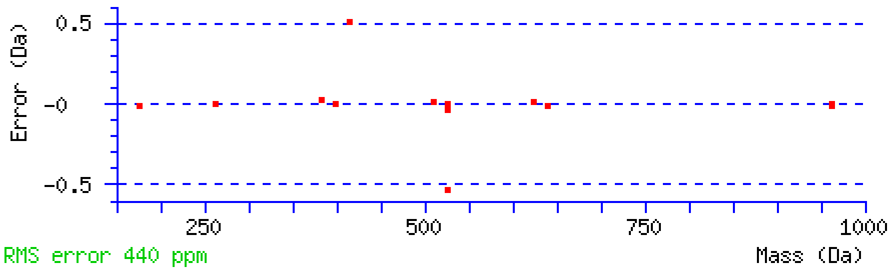
Match to Query 38228: 1596.865376 from(400.223620,4+) rtinseconds(1852) index(16309)
Title: Locus:1.1.1.2229.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

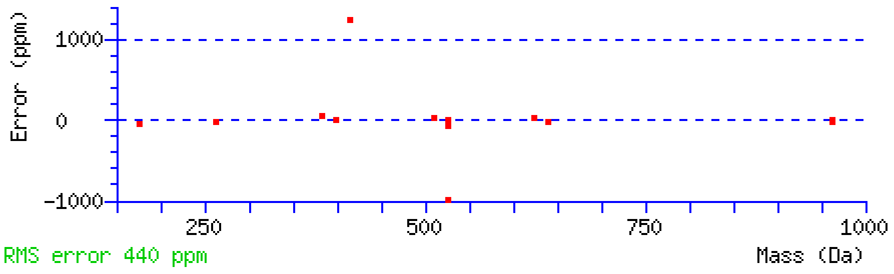
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1596.873611
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0059
Matches : 13/138 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	116.034219	58.520748			98.023654	49.515465	D							13
2	229.118283	115.062779			211.107718	106.057497	L	1482.853958	741.930617	1465.827409	733.417343	1464.843393	732.925335	12
3	357.176861	179.092068	340.150312	170.578794	339.166296	170.086786	Q	1369.769894	685.388585	1352.743345	676.875311	1351.759329	676.383303	11
4	471.219788	236.113532	454.193239	227.600258	453.209223	227.108250	N	1241.711316	621.359296	1224.684767	612.846022	1223.700751	612.354014	10
5	618.288202	309.647739	601.261653	301.134465	600.277637	300.642457	F	1127.668389	564.337833	1110.641840	555.824558	1109.657824	555.332550	9
6	746.383165	373.695221	729.356616	365.181946	728.372600	364.689938	K	980.599975	490.803626	963.573426	482.290351	962.589410	481.798343	8
7	845.451579	423.229428	828.425030	414.716153	827.441014	414.224145	V	852.505012	426.756144	835.478463	418.242870	834.494447	417.750862	7
8	958.535643	479.771460	941.509094	471.258185	940.525078	470.766177	L	753.436598	377.221937	736.410049	368.708663	735.426033	368.216655	6
9	1071.619707	536.313492	1054.593158	527.800217	1053.609142	527.308209	L	***640.352534***	320.679905	623.325985	312.166631	622.341969	311.674623	5
10	1199.678285	600.342781	1182.651736	591.829506	1181.667720	591.337498	Q	***527.268470***	264.137873	510.241921	255.624599	509.257905	255.132591	4
11	1336.737197	668.872237	1319.710648	660.358962	1318.726632	659.866954	H	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	3
12	1423.769225	712.388251	1406.742676	703.874976	1405.758660	703.382968	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 DLQNFKVLLQHSR
(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	1596.873611	-0.008235	DLQNFKVLLQHSR
6.5	1596.862396	0.002980	SSSVFAGKQGFITLR
3.1	1596.863266	0.002110	MSVIFFACVVRVR
2.9	1596.854523	0.010853	VPGLPTPIENMILR
2.7	1596.854523	0.010853	VPGLPTPIENMILR
0.5	1596.876984	-0.011608	VTNMKTSKPIVHSR

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

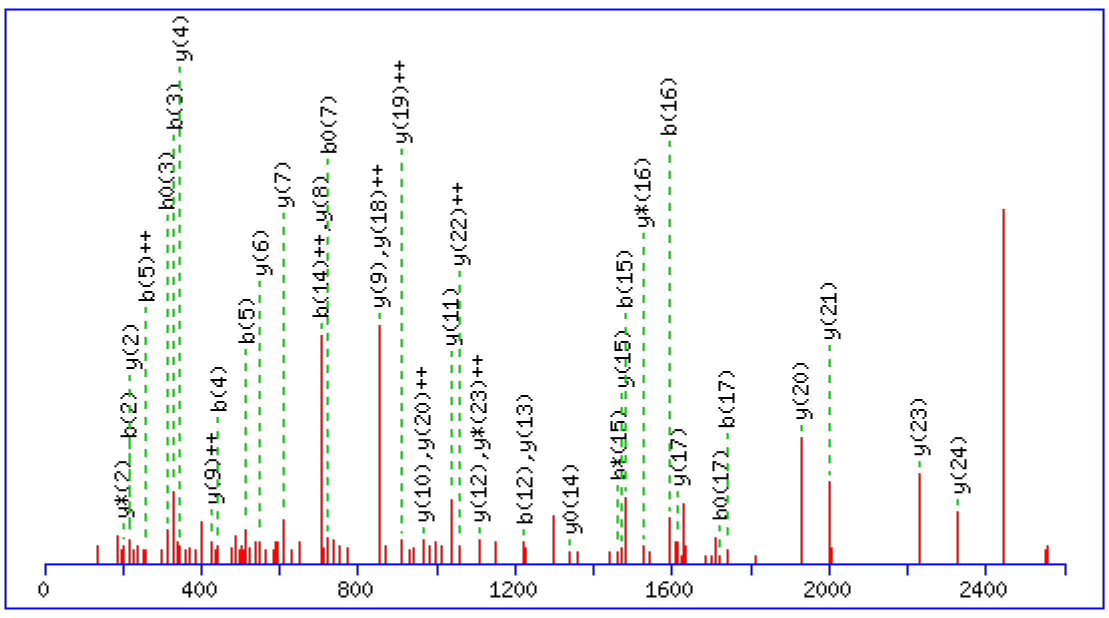
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITDLANLSAANHDAAIFPGGFGAAK**
Found in **ES1_HUMAN**, ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3

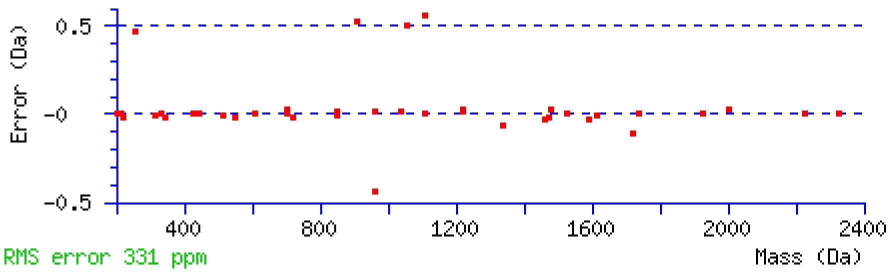
Match to Query 57755: 2441.235492 from(814.752440,3+) rtinseconds(3255) index(39565)
Title: Locus:1.1.1.3047.37
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

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 ●

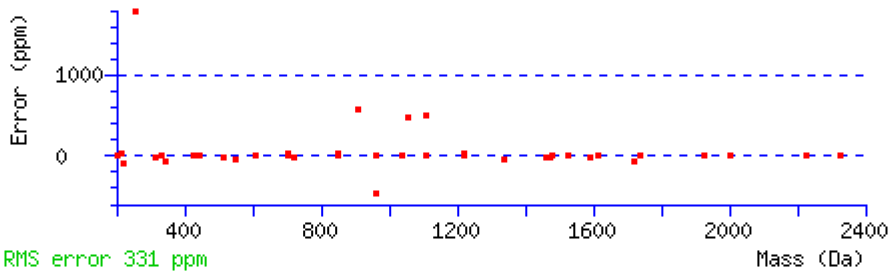


```
Monoisotopic mass of neutral peptide Mr(calc): 2441.233902
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 99  Expect: 1.4e-009
Matches : 39/252 fragment ions using 63 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							25
2	**215.139019**	108.073147			197.128454	99.067865	T	***2329.157137***	1165.082206	2312.130588	1156.568932	2311.146572	1156.076924	24
3	**330.165962**	165.586619			312.155397	156.581336	D	***2228.109458***	1114.558367	2211.082909	1106.045092	2210.098893	1105.553084	23
4	**443.250026**	222.128651			425.239461	213.123369	L	2113.082515	1057.044895	2096.055966	1048.531621	2095.071950	1048.039613	22
5	**514.287140**	257.647208			496.276575	248.641926	A	***1999.998451***	1000.502864	1982.971902	991.989589	1981.987886	991.497581	21
6	628.330067	314.668672	611.303518	306.155397	610.319502	305.663389	N	***1928.961337***	964.984307	1911.934788	956.471032	1910.950772	955.979024	20
7	741.414131	371.210704	724.387582	362.697429	723.403566	362.205421	L	1814.918410	907.962843	1797.891861	899.449569	1796.907845	898.957561	19
8	828.446159	414.726718	811.419610	406.213443	810.435594	405.721435	S	1701.834346	851.420811	1684.807797	842.907537	1683.823781	842.415529	18
9	899.483273	450.245274	882.456724	441.732000	881.472708	441.239992	A	***1614.802318***	807.904797	1597.775769	799.391523	1596.791753	798.899515	17
10	970.520387	485.763831	953.493838	477.250557	952.509822	476.758549	A	1543.765204	772.386240	1526.738655	763.872966	1525.754639	763.380958	16
11	1084.563314	542.785295	1067.536765	534.272021	1066.552749	533.780013	N	***1472.728090***	736.867683	1455.701541	728.354409	1454.717525	727.862401	15
12	**1221.622226**	611.314751	1204.595677	602.801477	1203.611661	602.309468	H	1358.685163	679.846220	1341.658614	671.332945	1340.674598	670.840937	14
13	1336.649169	668.828223	1319.622620	660.314948	1318.638604	659.822940	D	***1221.626251***	611.316764	1204.599702	602.803489	1203.615686	602.311481	13
14	1407.686283	704.346780	1390.659734	695.833505	1389.675718	695.341497	A	***1106.599308***	553.803292	1089.572759	545.290018			12
15	**1478.723397**	739.865337	1461.696848	731.352062	1460.712832	730.860054	A	***1035.562194***	518.284735	1018.535645	509.771461			11
16	**1591.807461**	796.407368	1574.780912	787.894094	1573.796896	787.402086	I	***964.525080***	482.766178	947.498531	474.252904			10
17	**1738.875875**	869.941576	1721.849326	861.428301	1720.865310	860.936293	F	***851.441016***	426.224146	834.414467	417.710872			9
18	1835.928639	918.467958	1818.902090	909.954683	1817.918074	909.462675	P	***704.372602***	352.689939	687.346053	344.176665			8
19	1892.950103	946.978689	1875.923554	938.465415	1874.939538	937.973407	G	***607.319838***	304.163557	590.293289	295.650283			7
20	1949.971567	975.489421	1932.945018	966.976147	1931.961002	966.484139	G	***550.298374***	275.652825	533.271825	267.139551			6
21	2097.039981	1049.023628	2080.013432	1040.510354	2079.029416	1040.018346	F	493.276910	247.142093	476.250361	238.628819			5
22	2154.061445	1077.534360	2137.034896	1069.021086	2136.050880	1068.529078	G	***346.208496***	173.607886	329.181947	165.094612			4
23	2225.098559	1113.052917	2208.072010	1104.539643	2207.087994	1104.047635	A	289.187032	145.097154	272.160483	136.583880			3
24	2296.135673	1148.571474	2279.109124	1140.058200	2278.125108	1139.566192	A	***218.149918***	109.578597	201.123369	101.065323			2
25							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 331 ppm



RMS error 331 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
99.5	2441.233902	0.001590	ITDLANLSAANHDAAIFPGGFGAAK
9.6	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR
9.6	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR
4.4	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR
4.2	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR
3.2	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR
1.7	2441.237305	-0.001813	LSLSPGAQPAPPPGPLPPPRPMR

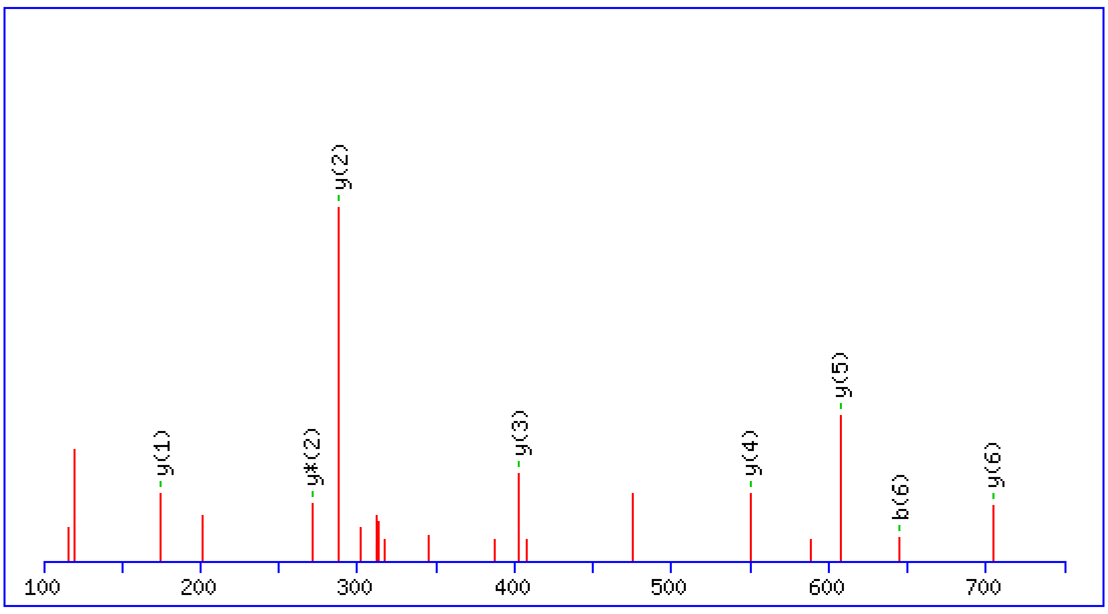
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPGFDLR**
Found in **CK054_HUMAN**, Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1

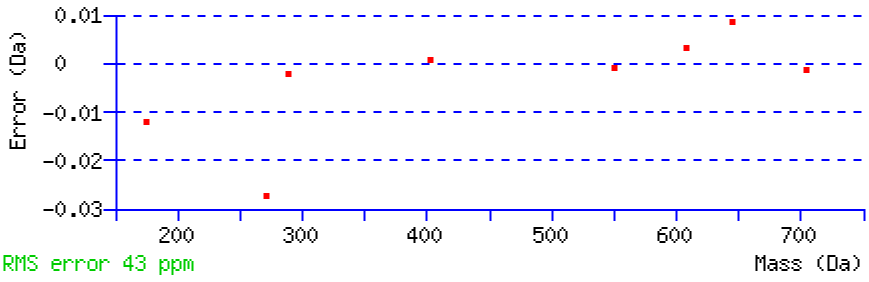
Match to Query 1173: 818.385188 from(410.199870,2+) rtinseconds(2096) index(24350)
Title: Locus:1.1.1.2183.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

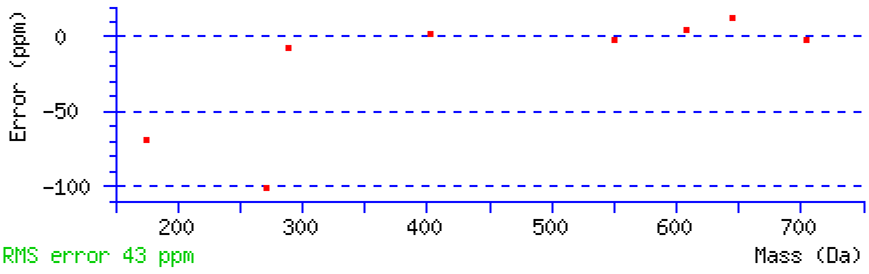
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 818.392273
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 6.4e-005
Matches : 8/56 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748	98.023654	49.515465	**D**							7
2	213.086983	107.047129	195.076418	98.041847	**P**	***704.372601***	352.689939	687.346052	344.176664	686.362036	343.684656	6
3	270.108447	135.557861	252.097882	126.552579	**G**	***607.319837***	304.163557	590.293288	295.650282	589.309272	295.158274	5
4	417.176861	209.092068	399.166296	200.086786	**F**	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
5	532.203804	266.605540	514.193239	257.600258	**D**	***403.229959***	202.118618	386.203410	193.605343	385.219394	193.113335	3
6	645.287868	323.147572	627.277303	314.142290	**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 DPGFDLR
(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	818.392273	-0.007085	DPGFDLR
25.7	818.392273	-0.007085	DPDGFLR
24.9	818.376999	0.008189	DATEDLR
11.6	818.377014	0.008174	DDSDLVR
10.6	818.392258	-0.007070	WDTEIR
9.8	818.388229	-0.003041	DDKASGAR
9.6	818.381699	0.003489	DRQCAR
9.4	818.377014	0.008174	TTSPEPR
8.8	818.384415	0.000773	MPPPTTK
8.8	818.381699	0.003489	CPRSNR

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

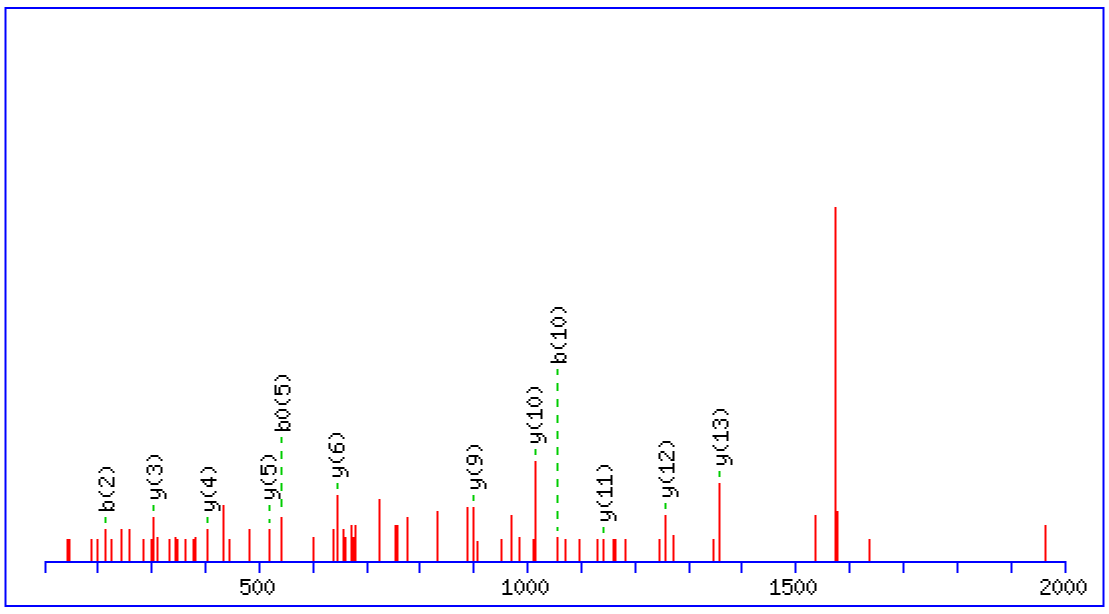
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLTDELAALQITGVK**
Found in **DHB11_HUMAN**, Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=1 SV=3

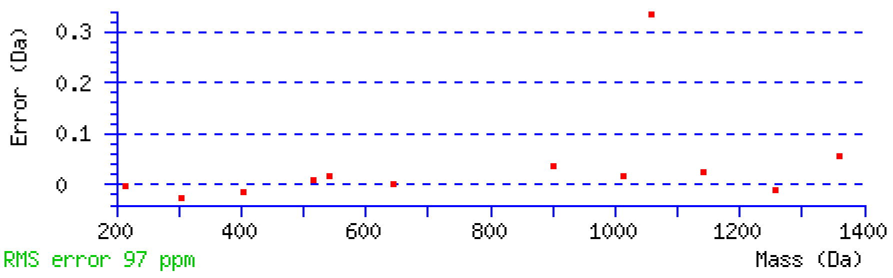
Match to Query 35245: 1571.884968 from(786.949760,2+) rtinseconds(3588) index(45438)
Title: Locus:1.1.1.2933.41
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

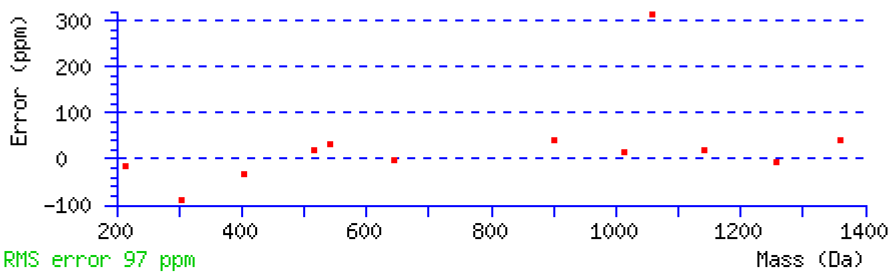
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1571.877029
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.7e-005
Matches : 12/144 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	102.054955	51.531116			84.044390	42.525833	T							15
2	**215.139019**	108.073147			197.128454	99.067865	L	1471.836638	736.421957	1454.810089	727.908683	1453.826073	727.416675	14
3	316.186698	158.596987			298.176133	149.591704	T	***1358.752574***	679.879925	1341.726025	671.366651	1340.742009	670.874643	13
4	431.213641	216.110458			413.203076	207.105176	D	***1257.704895***	629.356086	1240.678346	620.842811	1239.694330	620.350803	12
5	560.256234	280.631755			542.245669	271.626473	E	***1142.677952***	571.842614	1125.651403	563.329340	1124.667387	562.837332	11
6	673.340298	337.173787			655.329733	328.168505	L	***1013.635359***	507.321318	996.608810	498.808043	995.624794	498.316035	10
7	744.377412	372.692344			726.366847	363.687062	A	***900.551295***	450.779286	883.524746	442.266011	882.540730	441.774003	9
8	815.414526	408.210901			797.403961	399.205619	A	829.514181	415.260729	812.487632	406.747454	811.503616	406.255446	8
9	928.498590	464.752933			910.488025	455.747651	L	758.477067	379.742172	741.450518	371.228897	740.466502	370.736889	7
10	**1056.557168**	528.782222	1039.530619	520.268948	1038.546603	519.776940	Q	***645.393003***	323.200140	628.366454	314.686865	627.382438	314.194857	6
11	1169.641232	585.324254	1152.614683	576.810980	1151.630667	576.318971	I	***517.334425***	259.170851	500.307876	250.657576	499.323860	250.165568	5
12	1270.688911	635.848094	1253.662362	627.334819	1252.678346	626.842811	T	***404.250361***	202.628818	387.223812	194.115544	386.239796	193.623536	4
13	1327.710375	664.358825	1310.683826	655.845551	1309.699810	655.353543	G	***303.202682***	152.104979	286.176133	143.591704			3
14	1426.778789	713.893033	1409.752240	705.379758	1408.768224	704.887750	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 TLTDELAALQITGVK
(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	1571.877029	0.007939	TLTDELAALQITGVK
0.5	1571.870499	0.014469	QPGMKPIKGITNLK

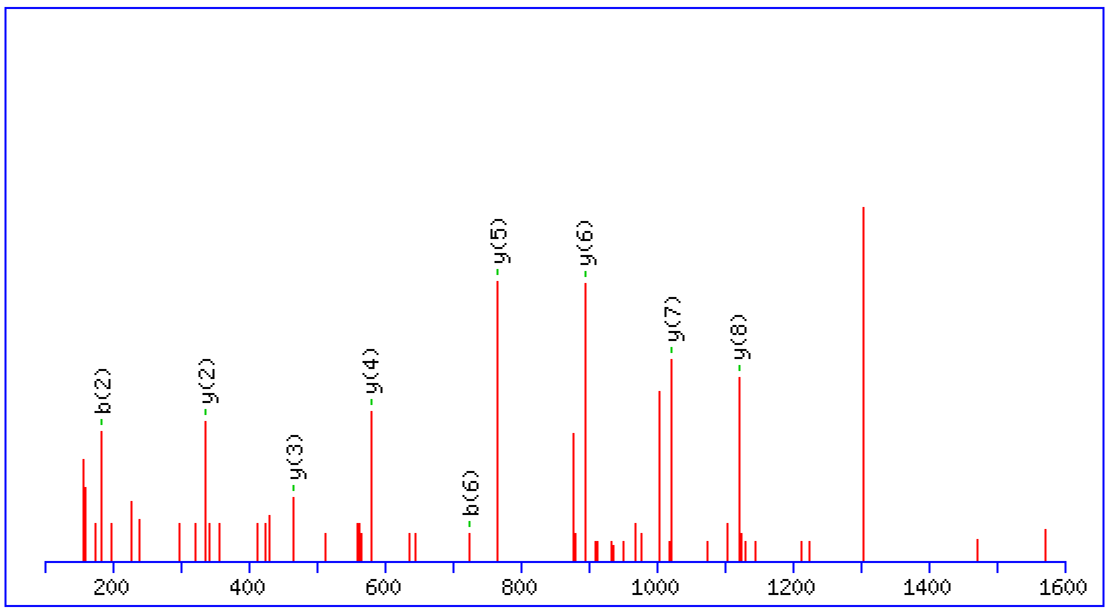
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIVQQWLEYR**
Found in **MCA3_HUMAN**, Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1

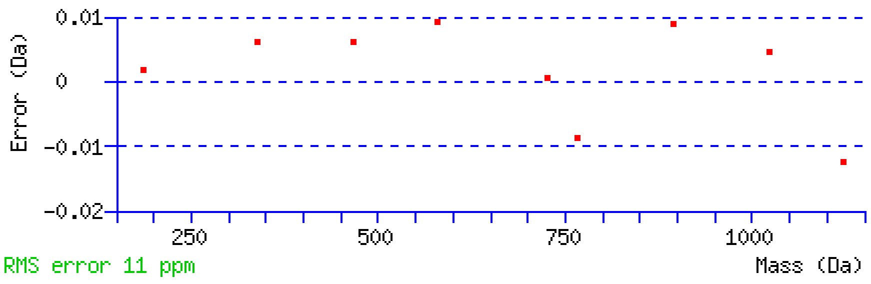
Match to Query 23318: 1304.691788 from(653.353170,2+) rtinseconds(3155) index(33175)
Title: Locus:1.1.1.2697.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

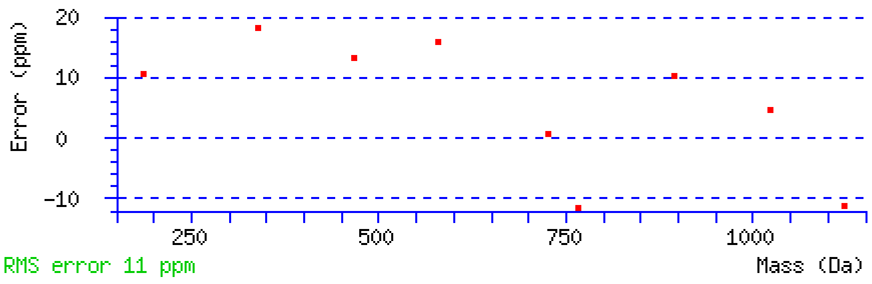
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1304.687698
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 5.8e-006
Matches : 9/84 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							10
2	**185.128454**	93.067865					I	1234.657885	617.832581	1217.631336	609.319306	1216.647320	608.827298	9
3	284.196868	142.602072					V	***1121.573821***	561.290549	1104.547272	552.777274	1103.563256	552.285266	8
4	412.255446	206.631361	395.228897	198.118087			Q	***1022.505407***	511.756342	1005.478858	503.243067	1004.494842	502.751059	7
5	540.314024	270.660650	523.287475	262.147376			Q	***894.446829***	447.727053	877.420280	439.213778	876.436264	438.721770	6
6	**726.393337**	363.700307	709.366788	355.187032			W	***766.388251***	383.697764	749.361702	375.184489	748.377686	374.692481	5
7	839.477401	420.242339	822.450852	411.729064			L	***580.308938***	290.658107	563.282389	282.144833	562.298373	281.652825	4
8	968.519994	484.763635	951.493445	476.250361	950.509429	475.758353	E	***467.224874***	234.116075	450.198325	225.602801	449.214309	225.110793	3
9	1131.583323	566.295300	1114.556774	557.782025	1113.572758	557.290017	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 AIVQQWLEYR
(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	1304.687698	0.004090	AIVQQWLEYR
10.2	1304.683670	0.008118	ALRASYTPSPAR
7.0	1304.683670	0.008118	ALRASYTPSPAR
4.6	1304.679810	0.011978	IAMAPLLEYER
4.2	1304.694931	-0.003143	SPGGPVAGPRAAPR
3.5	1304.683670	0.008118	SPRNNPVPPEAK
0.1	1304.687057	0.004731	ALVTLSSGDMRR

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

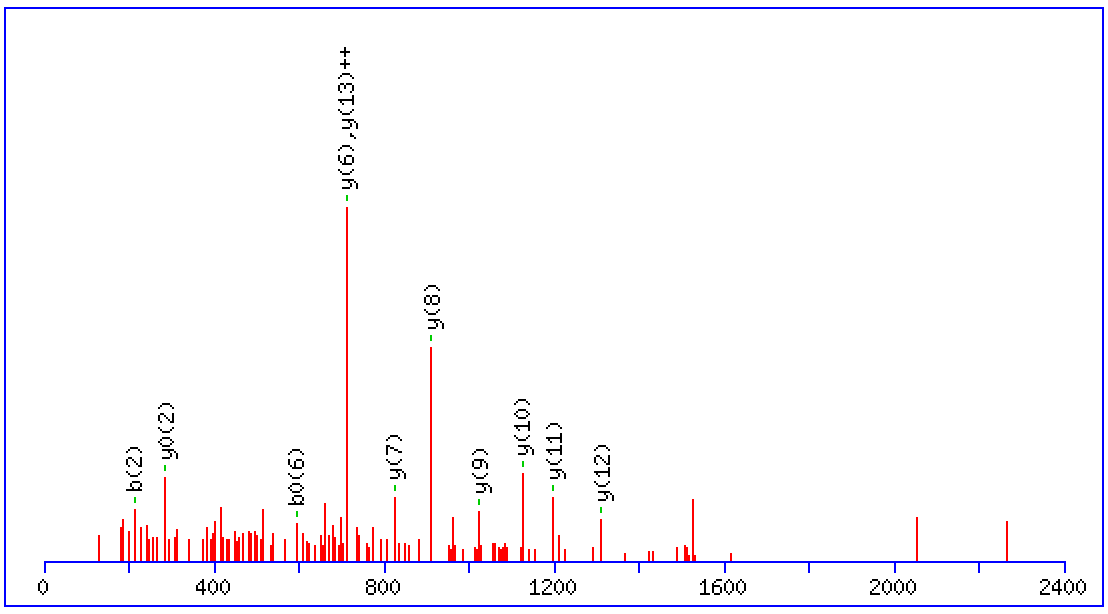
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLATLSIPITPER**
Found in **EIF3A_HUMAN**, Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1

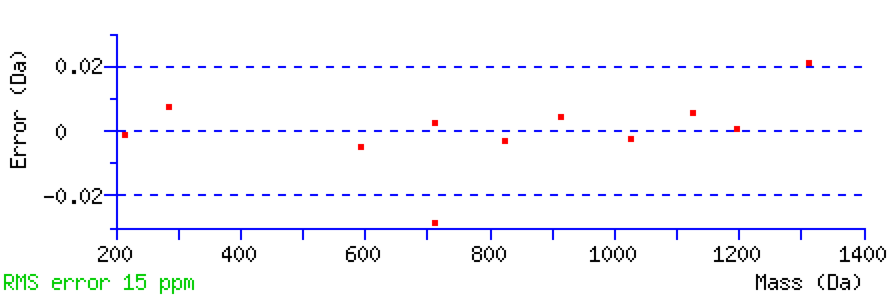
Match to Query 29743: 1521.920668 from(761.967610,2+) rtinseconds(3498) index(50153)
Title: Locus:1.1.1.2782.24
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

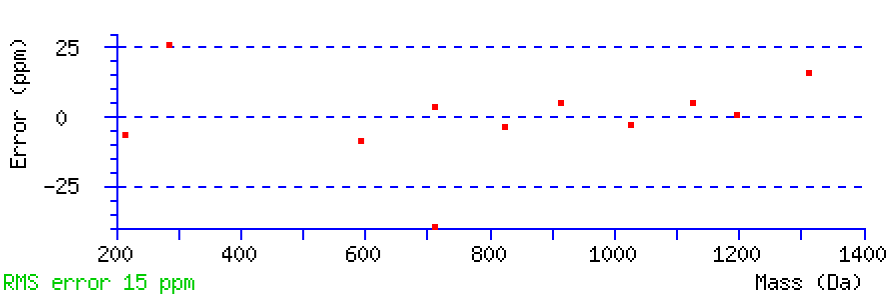
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1521.913010
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 3e-005
Matches : 11/120 fragment ions using 14 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	1423.851893	712.429585	1406.825344	703.916310	1405.841328	703.424302	13
3	326.243818	163.625547			L	***1310.767829***	655.887553	1293.741280	647.374278	1292.757264	646.882270	12
4	397.280932	199.144104			A	***1197.683765***	599.345521	1180.657216	590.832246	1179.673200	590.340238	11
5	498.328611	249.667943	480.318046	240.662661	T	***1126.646651***	563.826964	1109.620102	555.313689	1108.636086	554.821681	10
6	611.412675	306.209976	593.402110	297.204693	L	***1025.598972***	513.303124	1008.572423	504.789850	1007.588407	504.297842	9
7	698.444703	349.725990	680.434138	340.720707	S	***912.514908***	456.761092	895.488359	448.247818	894.504343	447.755810	8
8	811.528767	406.268022	793.518202	397.262739	I	***825.482880***	413.245078	808.456331	404.731804	807.472315	404.239796	7
9	908.581531	454.794404	890.570966	445.789121	P	***712.398816***	356.703046	695.372267	348.189772	694.388251	347.697764	6
10	1021.665595	511.336436	1003.655030	502.331153	I	615.346052	308.176664	598.319503	299.663390	597.335487	299.171382	5
11	1122.713274	561.860275	1104.702709	552.854992	T	502.261988	251.634632	485.235439	243.121357	484.251423	242.629349	4
12	1219.766038	610.386657	1201.755473	601.381374	P	401.214309	201.110793	384.187760	192.597518	383.203744	192.105510	3
13	1348.808631	674.907954	1330.798066	665.902671	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 VLLATLSIPITPER
(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	1521.913010	0.007658	VLLATLSIPITPER

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

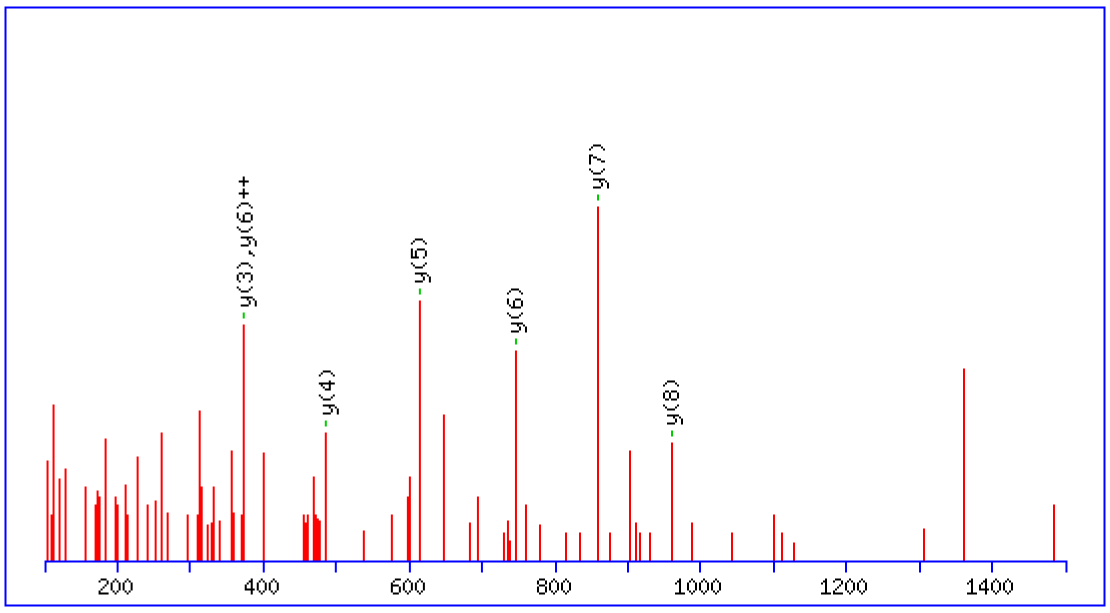
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLMQLPTR**
Found in **EIF3B_HUMAN**, Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3

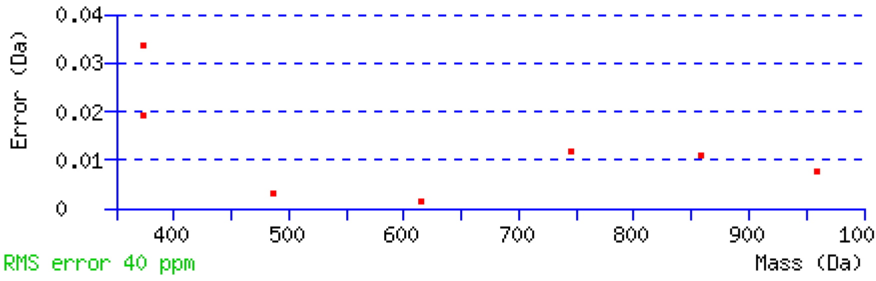
Match to Query 15813: 1057.601268 from(529.807910,2+) rtinseconds(2545) index(35143)
Title: Locus:1.1.1.1614.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

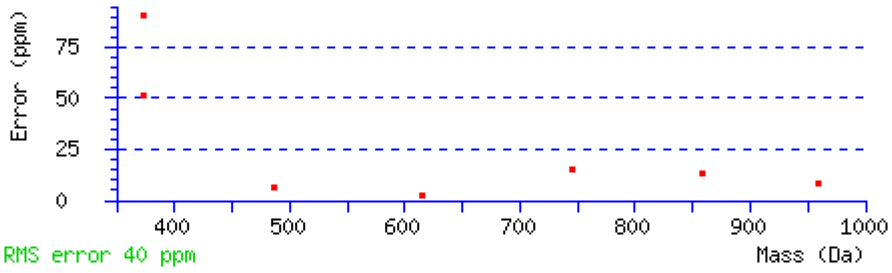
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1057.595398
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00043
Matches : 7/84 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	201.123369	101.065322			183.112804	92.060040	T	***959.534265***	480.270771	942.507716	471.757496	941.523700	471.265488	8
3	314.207433	157.607354			296.196868	148.602072	L	***858.486586***	429.746931	841.460037	421.233657	840.476021	420.741649	7
4	445.247918	223.127597			427.237353	214.122314	M	***745.402522***	373.204899	728.375973	364.691625	727.391957	364.199617	6
5	573.306496	287.156886	556.279947	278.643612	555.295931	278.151604	Q	***614.362037***	307.684657	597.335488	299.171382	596.351472	298.679374	5
6	686.390560	343.698918	669.364011	335.185644	668.379995	334.693636	L	***486.303459***	243.655367	469.276910	235.142093	468.292894	234.650085	4
7	783.443324	392.225300	766.416775	383.712026	765.432759	383.220018	P	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
8	884.491003	442.749140	867.464454	434.235865	866.480438	433.743857	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 VTLMQLPTR
(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	1057.595398	0.005870	VTLMQLPTR
7.8	1057.601883	-0.000615	KLDEEALLK
4.7	1057.601913	-0.000645	DTVELQLLK
1.3	1057.606613	-0.005345	KMVNQLAVR
0.1	1057.601898	-0.000630	LSLLQEVEK

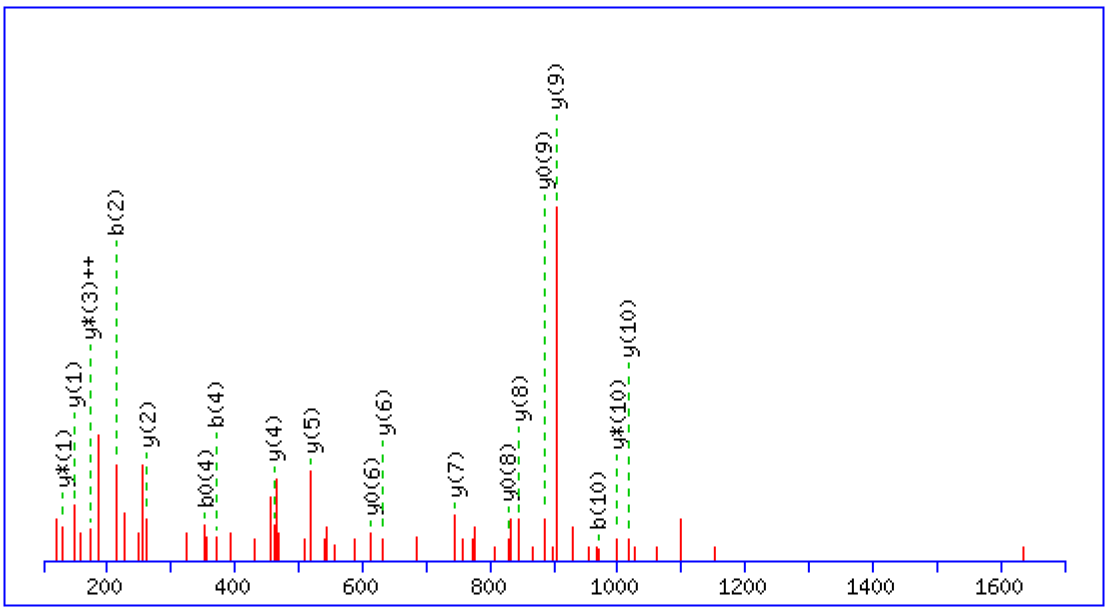
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIGTLLGTVDK**
Found in **EIF3F_HUMAN**, Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1

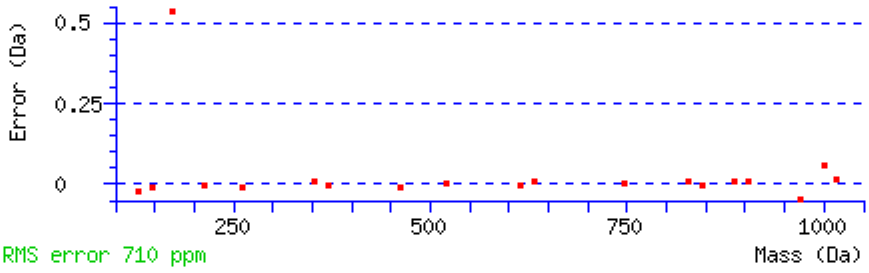
Match to Query 15004: 1114.654908 from(558.334730,2+) rtinseconds(2558) index(31066)
Title: Locus:1.1.1.2512.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

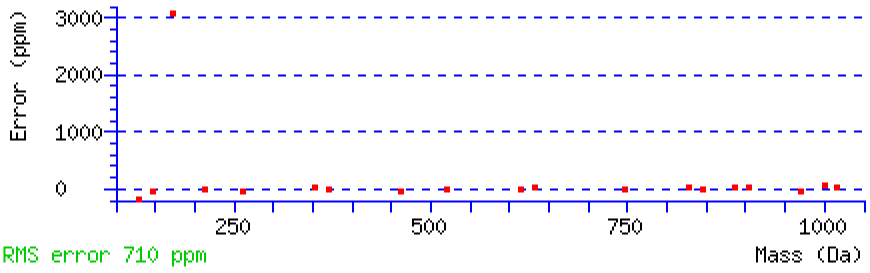
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1114.659790
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 6.7e-005
Matches : 19/92 fragment ions using 52 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	**213.159754**	107.083515			I	***1016.598639***	508.802958	999.572090	500.289683	998.588074	499.797675	10
3	270.181218	135.594247			G	***903.514575***	452.260926	886.488026	443.747651	885.504010	443.255643	9
4	**371.228897**	186.118087	353.218332	177.112804	T	***846.493111***	423.750194	829.466562	415.236919	828.482546	414.744911	8
5	484.312961	242.660119	466.302396	233.654836	L	***745.445432***	373.226354	728.418883	364.713080	727.434867	364.221072	7
6	597.397025	299.202151	579.386460	290.196868	L	***632.361368***	316.684322	615.334819	308.171048	614.350803	307.679040	6
7	654.418489	327.712883	636.407924	318.707600	G	***519.277304***	260.142290	502.250755	251.629016	501.266739	251.137008	5
8	755.466168	378.236722	737.455603	369.231440	T	***462.255840***	231.631558	445.229291	223.118283	444.245275	222.626275	4
9	854.534582	427.770929	836.524017	418.765647	V	361.208161	181.107718	344.181612	172.594444	343.197596	172.102436	3
10	**969.561525**	485.284401	951.550960	476.279118	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 VIGTLLGTVDK
(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	1114.659790	-0.004882	VIGTLLGTVDK
9.2	1114.659760	-0.004852	VLAITSSSIPK

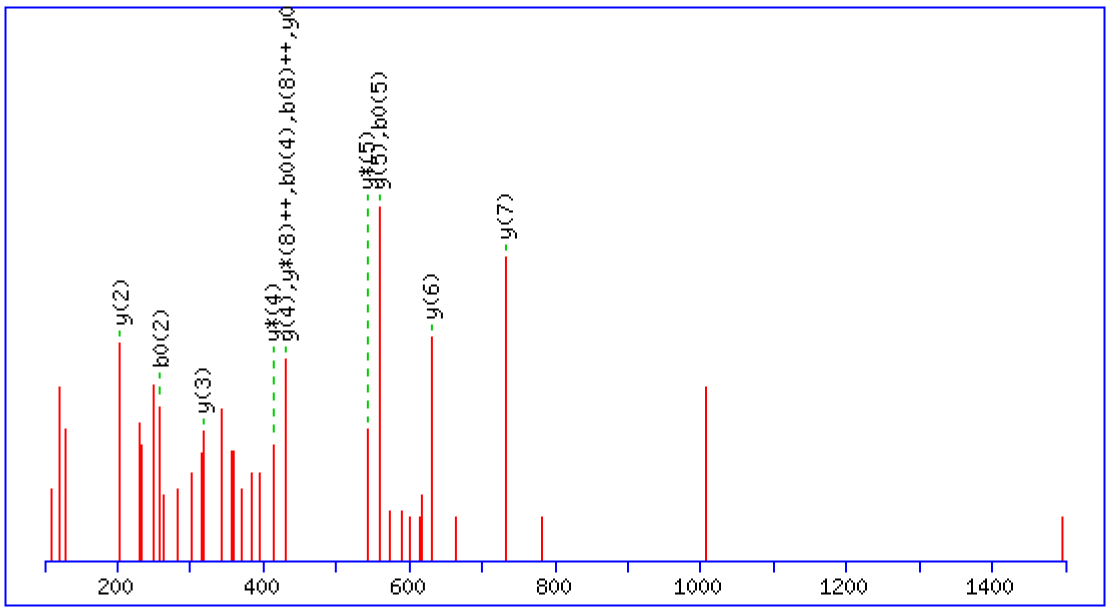
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFTAQNLGK**
Found in **EIF3H_HUMAN**, Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1

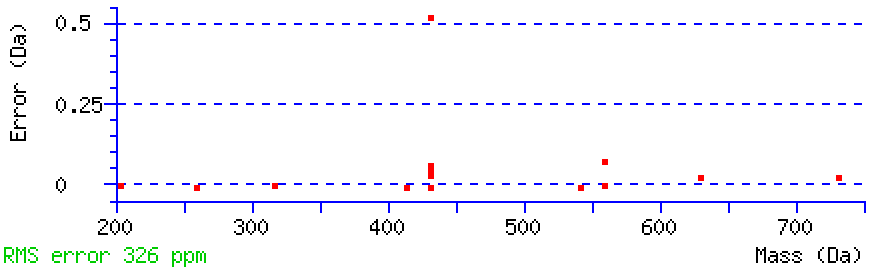
Match to Query 12108: 1006.509688 from(504.262120,2+) rtinseconds(1676) index(16363)
Title: Locus:1.1.1.2023.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

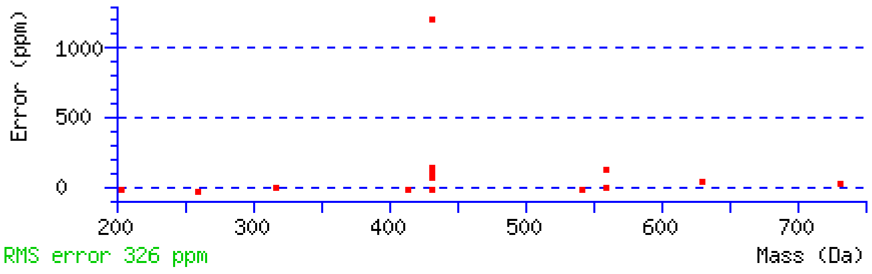
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1006.508347
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.0003
Matches : 14/76 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							9
2	277.118283	139.062779			259.107718	130.057497	F	878.473044	439.740160	861.446495	431.226886	860.462479	430.734878	8
3	378.165962	189.586619			360.155397	180.581336	T	***731.404630***	366.205953	714.378081	357.692679	713.394065	357.200671	7
4	449.203076	225.105176			431.192511	216.099893	A	***630.356951***	315.682114	613.330402	307.168839			6
5	577.261654	289.134465	560.235105	280.621191	559.251089	280.129183	Q	***559.319837***	280.163557	542.293288	271.650282			5
6	691.304581	346.155929	674.278032	337.642654	673.294016	337.150646	N	***431.261259***	216.134267	414.234710	207.620993			4
7	804.388645	402.697961	787.362096	394.184686	786.378080	393.692678	L	***317.218332***	159.112804	300.191783	150.599530			3
8	861.410109	431.208693	844.383560	422.695418	843.399544	422.203410	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 EFTAQNLGK
(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	1006.508347	0.001341	EFTAQNLGK
3.9	1006.505173	0.004515	MMQLNRAK
3.9	1006.505173	0.004515	MMQLNRAK

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

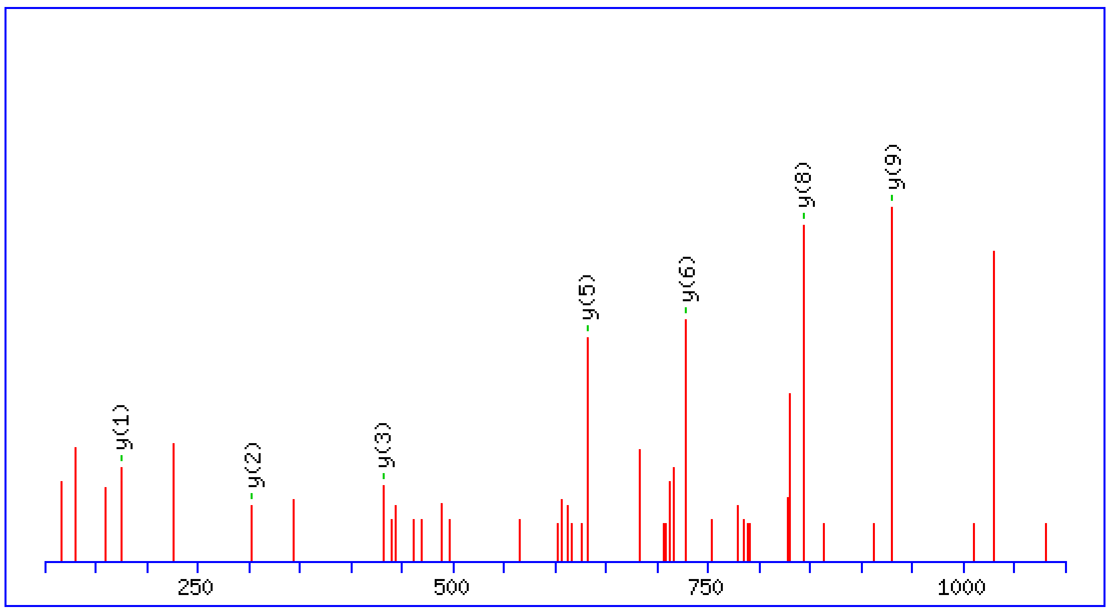
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSGGPSLEQR**
Found in **EIF3L_HUMAN**, Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1

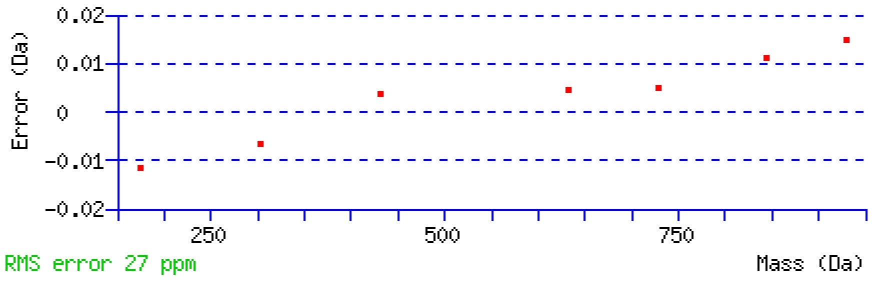
Match to Query 9252: 1028.531388 from(515.272970,2+) rtinseconds(1162) index(7287)
Title: Locus:1.1.1.1920.25
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

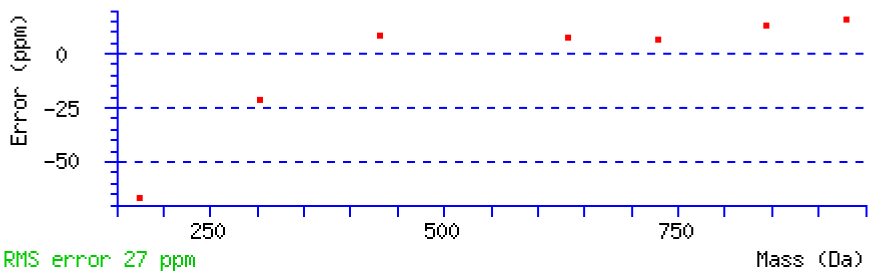
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1028.525070
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00031
Matches : 7/86 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							10
2	187.107718	94.057497			169.097153	85.052214	S	*930.463935*	465.735606	913.437386	457.222331	912.453370	456.730323	9
3	244.129182	122.568229			226.118617	113.562946	G	*843.431907*	422.219592	826.405358	413.706317	825.421342	413.214309	8
4	301.150646	151.078961			283.140081	142.073679	G	786.410443	393.708860	769.383894	385.195585	768.399878	384.703577	7
5	398.203410	199.605343			380.192845	190.600061	P	*729.388979*	365.198128	712.362430	356.684853	711.378414	356.192845	6
6	485.235438	243.121357			467.224873	234.116075	S	*632.336215*	316.671746	615.309666	308.158471	614.325650	307.666463	5
7	598.319502	299.663389			580.308937	290.658107	L	545.304187	273.155732	528.277638	264.642457	527.293622	264.150449	4
8	727.362095	364.184686			709.351530	355.179403	E	*432.220123*	216.613699	415.193574	208.100425	414.209558	207.608417	3
9	855.420673	428.213975	838.394124	419.700700	837.410108	419.208692	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 VSGGPSLEQR
(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	1028.525070	0.006318	VSGGPSLEQR
9.7	1028.525070	0.006318	VNVADEVQR
9.0	1028.536270	-0.004882	EAVNQANKR
8.5	1028.536270	-0.004882	QRLEAEAGR
4.2	1028.536285	-0.004897	AKPEGSPRR
3.9	1028.525055	0.006333	VAPEEGSGKR
1.5	1028.536270	-0.004882	AQEQELRR
1.5	1028.536270	-0.004882	QAEQERLR
0.7	1028.533783	-0.002395	WPRCLQR

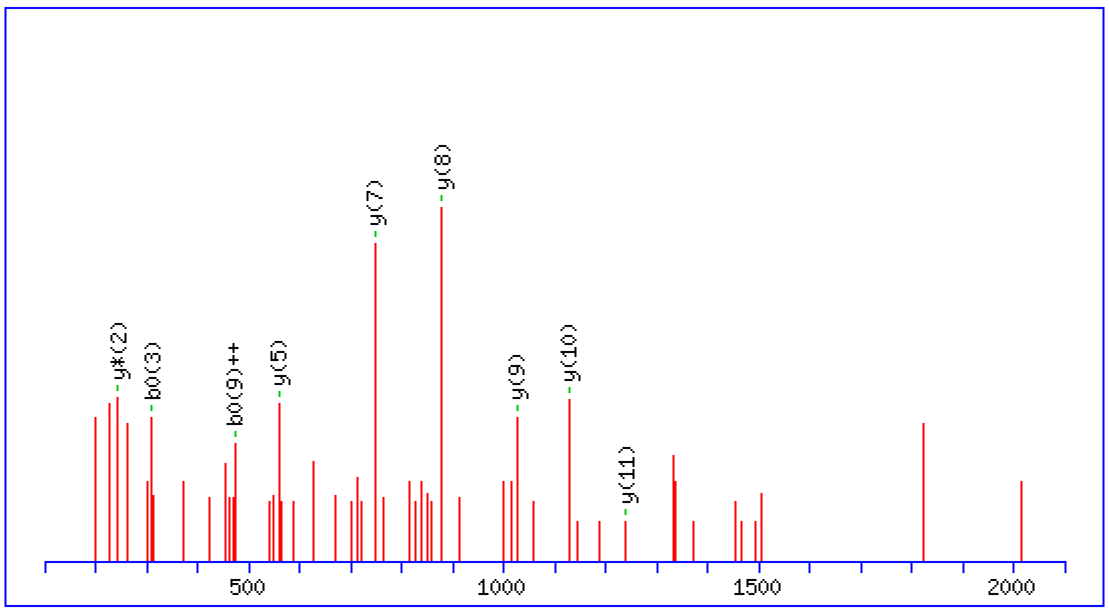
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLTFMGMAVENK**
Found in **EIF3M_HUMAN**, Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1

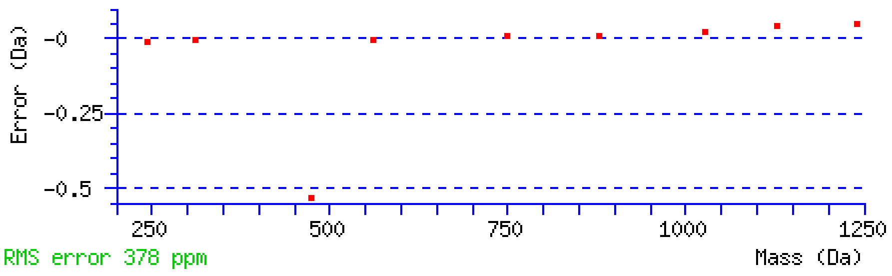
Match to Query 33899: 1352.683428 from(677.348990,2+) rtinseconds(3371) index(45963)
Title: Locus:1.1.1.2678.13
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

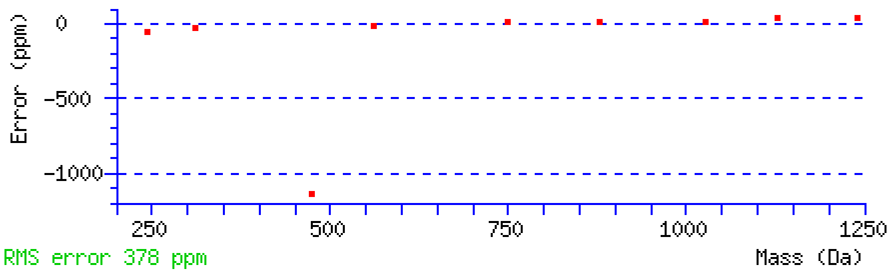
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1352.683212
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00082
Matches : 9/104 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	114.091340	57.549308					L							12
2	227.175404	114.091340					L	***1240.606443***	620.806860	1223.579894	612.293585	1222.595878	611.801577	11
3	328.223083	164.615179			310.212518	155.609897	T	***1127.522379***	564.264828	1110.495830	555.751553	1109.511814	555.259545	10
4	475.291497	238.149386			457.280932	229.144104	F	***1026.474700***	513.740988	1009.448151	505.227713	1008.464135	504.735705	9
5	606.331982	303.669629			588.321417	294.664347	M	***879.406286***	440.206781	862.379737	431.693507	861.395721	431.201499	8
6	663.353446	332.180361			645.342881	323.175079	G	***748.365801***	374.686539	731.339252	366.173264	730.355236	365.681256	7
7	794.393931	397.700604			776.383366	388.695321	M	691.344337	346.175807	674.317788	337.662532	673.333772	337.170524	6
8	865.431045	433.219161			847.420480	424.213878	A	***560.303852***	280.655564	543.277303	272.142290	542.293287	271.650282	5
9	964.499459	482.753368			946.488894	473.748085	V	489.266738	245.137007	472.240189	236.623732	471.256173	236.131724	4
10	1093.542052	547.274664			1075.531487	538.269382	E	390.198324	195.602800	373.171775	187.089525	372.187759	186.597517	3
11	1207.584979	604.296128	1190.558430	595.782853	1189.574414	595.290845	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 LLTFMGMAVENK
(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	1352.683212	0.000216	LLTFMGMAVENK
4.7	1352.687042	-0.003614	AQQMYAATKGLR
4.4	1352.693588	-0.010160	LPTTAFTRSSEK

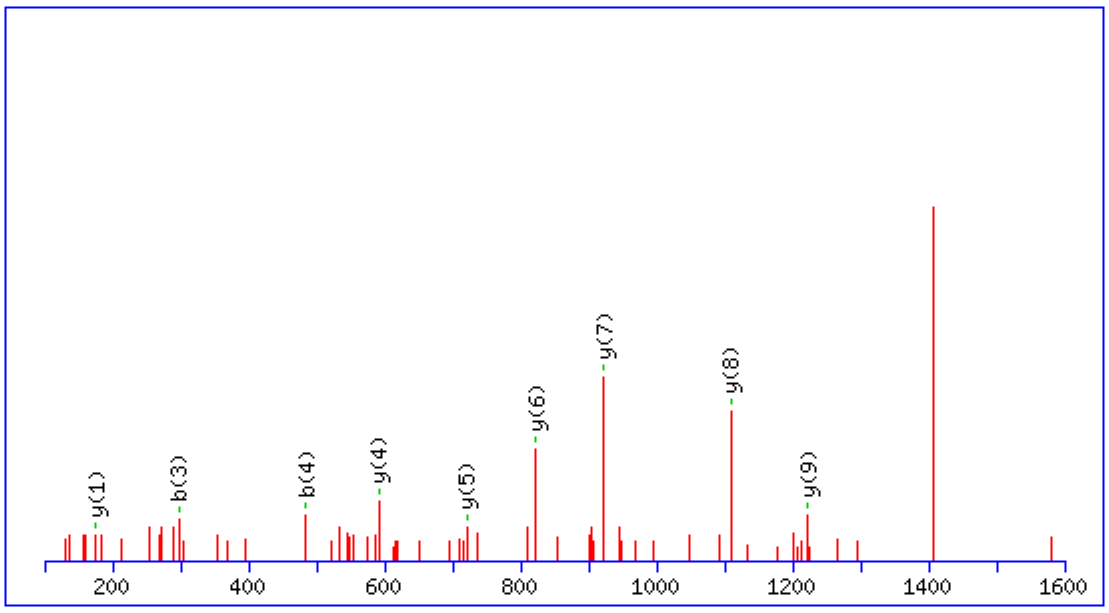
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAIWTTECENR**
Found in **IF4E_HUMAN**, Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2

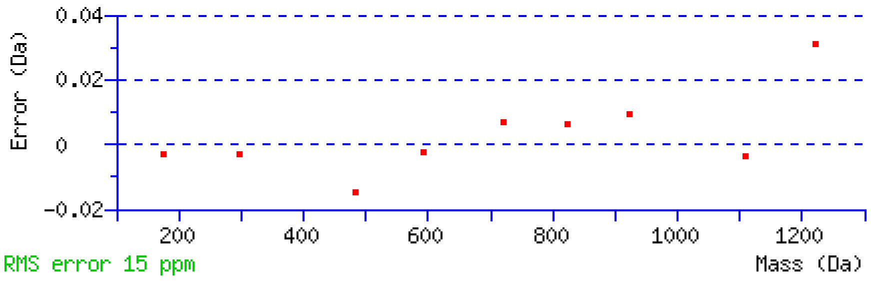
Match to Query 31473: 1405.672148 from(703.843350,2+) rtinseconds(2469) index(27868)
Title: Locus:1.1.1.2439.40
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

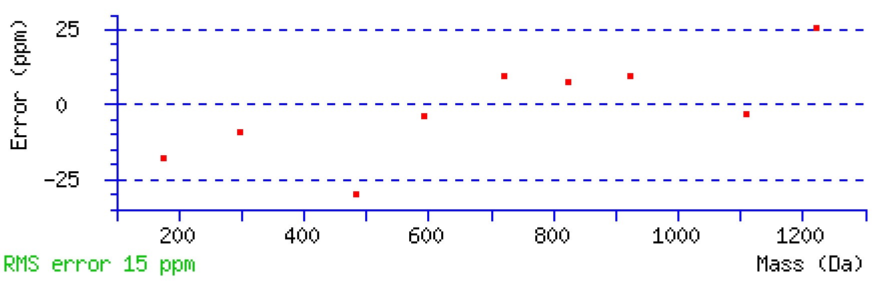
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1405.665970
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 2.5e-005
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	114.091340	57.549308					I							11
2	185.128454	93.067865					A	1293.589213	647.298245	1276.562664	638.784970	1275.578648	638.292962	10
3	298.212518	149.609897					I	1222.552099	611.779688	1205.525550	603.266413	1204.541534	602.774405	9
4	484.291831	242.649554					W	1109.468035	555.237656	1092.441486	546.724381	1091.457470	546.232373	8
5	585.339510	293.173393			567.328945	284.168111	T	923.388722	462.197999	906.362173	453.684725	905.378157	453.192717	7
6	686.387189	343.697233			668.376624	334.691950	T	822.341043	411.674160	805.314494	403.160885	804.330478	402.668877	6
7	815.429782	408.218529			797.419217	399.213247	E	721.293364	361.150320	704.266815	352.637046	703.282799	352.145038	5
8	989.476081	495.241679			971.465516	486.236396	C	592.250771	296.629024	575.224222	288.115749	574.240206	287.623741	4
9	1118.518674	559.762975			1100.508109	550.757693	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
10	1232.561601	616.784439	1215.535052	608.271164	1214.551036	607.779156	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 IAIWTTECENR
(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	1405.665970	0.006178	IAIWTTECENR

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

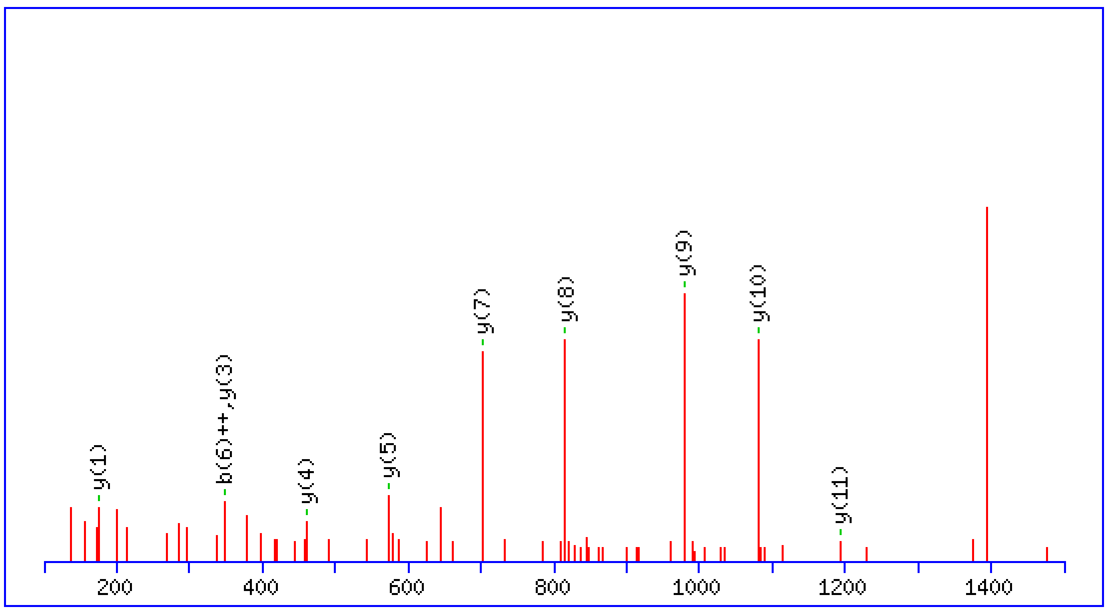
{MATRIX SCIENCE} Mascot Search Results

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

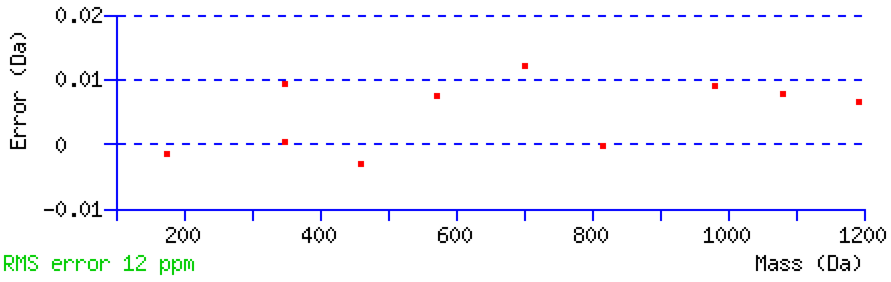
Match to Query 32607: 1392.691668 from(697.353110,2+) rtinseconds(2712) index(32684)
Title: Locus:1.1.1.2559.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

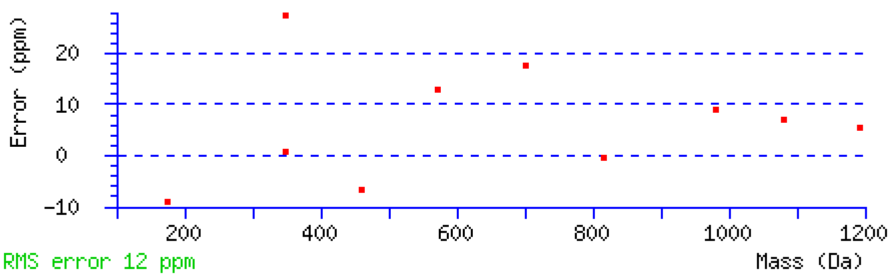
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1392.688492
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 88  Expect: 1.6e-008
Matches : 10/118 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
87.5	1392.688492	0.003176	EALTYDGALLGDR
4.1	1392.703766	-0.012098	SPLAYVPFSAGPR
4.1	1392.703766	-0.012098	SPLAYVPFSAGPR
4.1	1392.703110	-0.011442	SPLSVRSTDMIR
0.1	1392.699692	-0.008024	ALYESELADARR

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

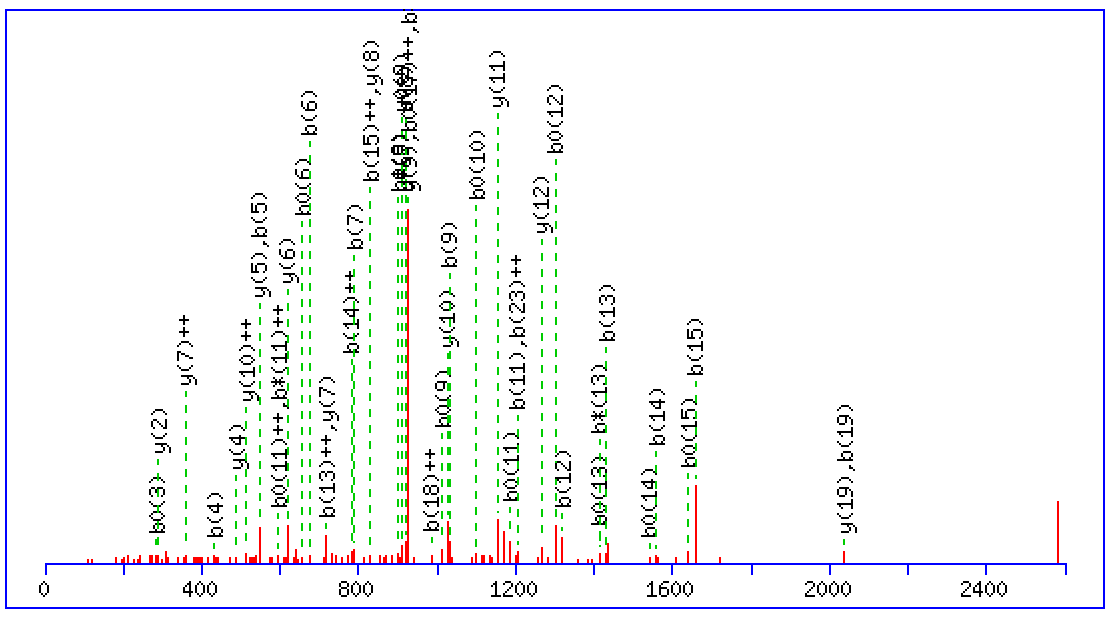
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TSIEDQDELSSLLQVPLVAGTVNR**
Found in **IF6_HUMAN**, Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1

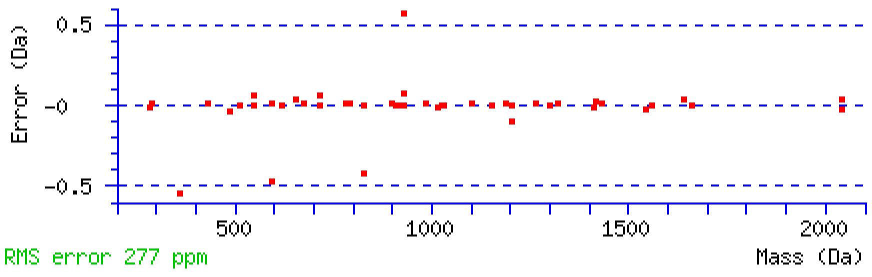
Match to Query 50133: 2583.334782 from(862.118870,3+) rtinseconds(4197) index(47626)
Title: Locus:1.1.1.3240.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

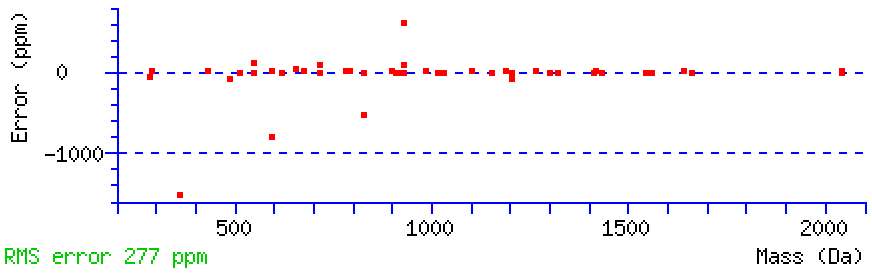
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2583.339172
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 77  Expect: 1.5e-007
Matches : 47/260 fragment ions using 64 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							24
2	189.086983	95.047129			171.076418	86.041847	S	2483.298774	1242.153025	2466.272225	1233.639750	2465.288209	1233.147742	23
3	302.171047	151.589161			284.160482	142.583879	I	2396.266746	1198.637011	2379.240197	1190.123736	2378.256181	1189.631728	22
4	***431.213640***	216.110458			413.203075	207.105176	E	2283.182682	1142.094979	2266.156133	1133.581704	2265.172117	1133.089696	21
5	***546.240583***	273.623930			528.230018	264.618647	D	2154.140089	1077.573682	2137.113540	1069.060408	2136.129524	1068.568400	20
6	***674.299161***	337.653219	657.272612	329.139944	656.288596	328.647936	Q	***2039.113146***	1020.060211	2022.086597	1011.546936	2021.102581	1011.054928	19
7	***789.326104***	395.166690	772.299555	386.653415	771.315539	386.161408	D	1911.054568	956.030922	1894.028019	947.517647	1893.044003	947.025639	18
8	***918.368697***	459.687987	901.342148	451.174712	900.358132	450.682704	E	1796.027625	898.517450	1779.001076	890.004176	1778.017060	889.512168	17
9	***1031.452761***	516.230019	1014.426212	507.716744	1013.442196	507.224736	L	1666.985032	833.996154	1649.958483	825.482879	1648.974467	824.990871	16
10	1118.484789	559.746033	1101.458240	551.232758	1100.474224	550.740750	S	1553.900968	777.454122	1536.874419	768.940847	1535.890403	768.448839	15
11	***1205.516817***	603.262047	1188.490268	594.748772	1187.506252	594.256764	S	1466.868940	733.938108	1449.842391	725.424833	1448.858375	724.932825	14
12	***1318.600881***	659.804079	1301.574332	651.290804	1300.590316	650.798796	L	1379.836912	690.422094	1362.810363	681.908819	1361.826347	681.416811	13
13	***1431.684945***	**716.346111**	1414.658396	707.832836	1413.674380	707.340828	L	***1266.752848***	633.880062	1249.726299	625.366787	1248.742283	624.874779	12
14	***1559.743523***	**780.375399**	1542.716974	771.862125	1541.732958	771.370117	Q	***1153.668784***	577.338030	1136.642235	568.824755	1135.658219	568.332747	11
15	***1658.811937***	**829.909607**	1641.785388	821.396332	1640.801372	820.904324	V	***1025.610206***	513.308741	1008.583657	504.795466	1007.599641	504.303458	10
16	1755.864701	878.435989	1738.838152	869.922714	1737.854136	869.430706	P	***926.541792***	463.774534	909.515243	455.261259	908.531227	454.769251	9
17	1868.948765	934.978020	1851.922216	926.464746	1850.938200	925.972738	L	***829.489028***	415.248152	812.462479	406.734877	811.478463	406.242869	8
18	1968.017179	**984.512227**	1950.990630	975.998953	1950.006614	975.506945	V	***716.404964***	358.706120	699.378415	350.192845	698.394399	349.700837	7
19	***2039.054293***	1020.030785	2022.027744	1011.517510	2021.043728	1011.025502	A	***617.336550***	309.171913	600.310001	300.658638	599.325985	300.166630	6
20	2096.075757	1048.541516	2079.049208	1040.028242	2078.065192	1039.536234	G	***546.299436***	273.653356	529.272887	265.140081	528.288871	264.648073	5
21	2197.123436	1099.065356	2180.096887	1090.552081	2179.112871	1090.060073	T	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	4
22	2296.191850	1148.599563	2279.165301	1140.086288	2278.181285	1139.594280	V	388.230293	194.618784	371.203744	186.105510			3
23	2410.234777	**1205.621026**	2393.208228	1197.107752	2392.224212	1196.615744	N	***289.161879***	145.084577	272.135330	136.571303			2
24							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.0	2583.339172	-0.004390	TSIEDQDELSSLLQVPLVAGTVNR
4.1	2583.354431	-0.019649	ELELGQVPLSAPPLPPRPDLPPR
4.0	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
4.0	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
3.8	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
3.8	2583.340027	-0.005245	IPQQNSESAMAKPQVVVAPVLMSK
3.5	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
2.8	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
2.7	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK
2.6	2583.321381	0.013401	AELASSSSKLGLKPASPGPPSAGPSMK

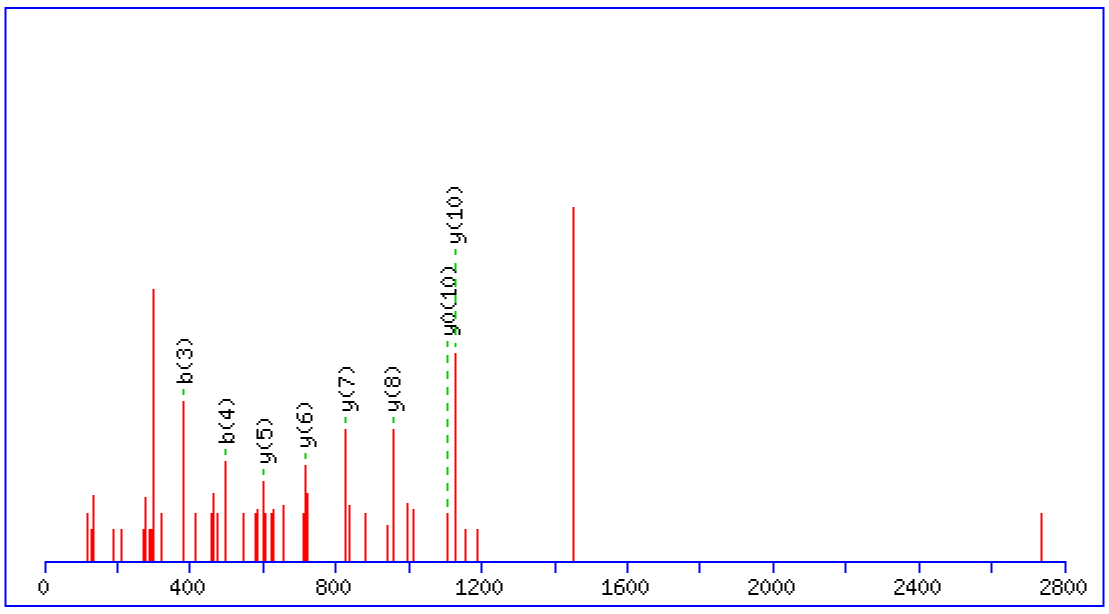
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YYGLQILENVIK**
Found in **XPO1_HUMAN**, Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1

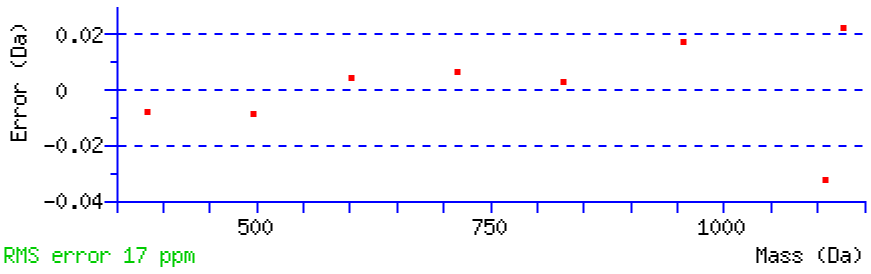
Match to Query 33954: 1451.811868 from(726.913210,2+) rtinseconds(4090) index(58481)
Title: Locus:1.1.1.3157.17
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

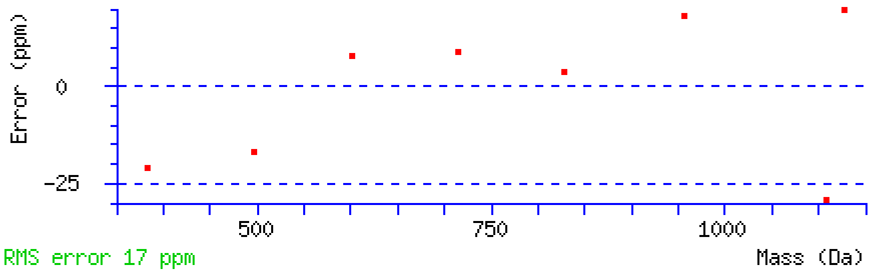
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1451.802383
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0023
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	164.070605	82.538940					Y							12
2	327.133934	164.070605					Y	1289.746365	645.376821	1272.719816	636.863546	1271.735800	636.371538	11
3	**384.155398**	192.581337					G	***1126.683036***	563.845156	1109.656487	555.331882	1108.672471	554.839874	10
4	**497.239462**	249.123369					L	1069.661572	535.334424	1052.635023	526.821150	1051.651007	526.329142	9
5	625.298040	313.152658	608.271491	304.639384			Q	***956.577508***	478.792392	939.550959	470.279118	938.566943	469.787110	8
6	738.382104	369.694690	721.355555	361.181416			I	***828.518930***	414.763103	811.492381	406.249829	810.508365	405.757821	7
7	851.466168	426.236722	834.439619	417.723448			L	***715.434866***	358.221071	698.408317	349.707797	697.424301	349.215789	6
8	980.508761	490.758019	963.482212	482.244744	962.498196	481.752736	E	***602.350802***	301.679039	585.324253	293.165765	584.340237	292.673757	5
9	1094.551688	547.779482	1077.525139	539.266208	1076.541123	538.774200	N	473.308209	237.157743	456.281660	228.644468			4
10	1193.620102	597.313689	1176.593553	588.800415	1175.609537	588.308407	V	359.265282	180.136279	342.238733	171.623004			3
11	1306.704166	653.855721	1289.677617	645.342447	1288.693601	644.850439	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 YYGLQILENVIK
(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	1451.802383	0.009485	YYGLQILENVIK
4.7	1451.803101	0.008767	VVIQGQKTCHIR
1.4	1451.807098	0.004770	DMHLLLWLQKR

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

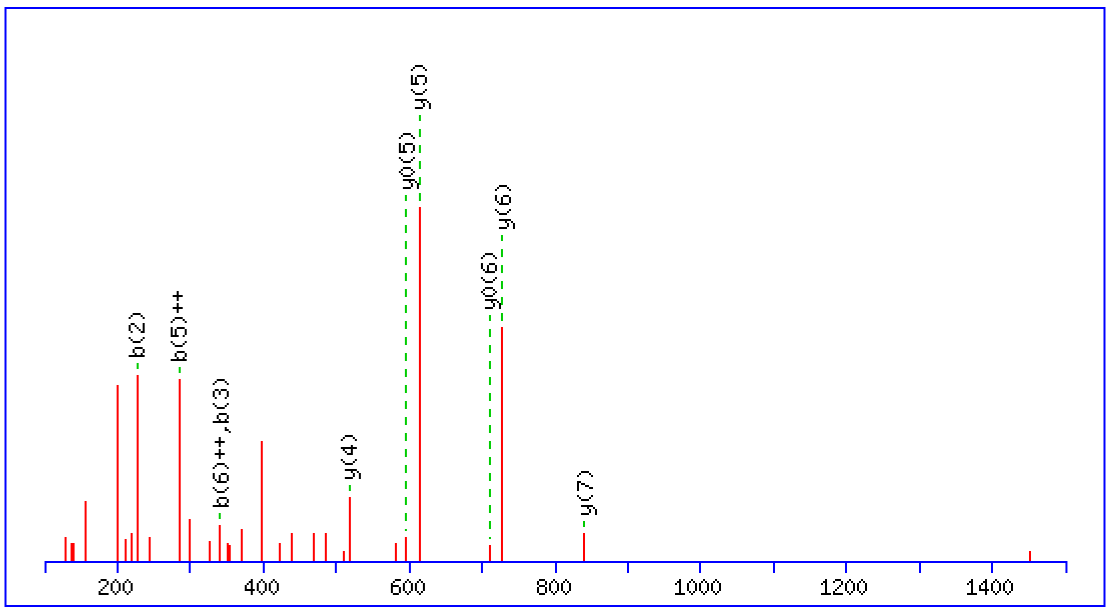
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIIPEIQK**
Found in **XPO2_HUMAN**, Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3

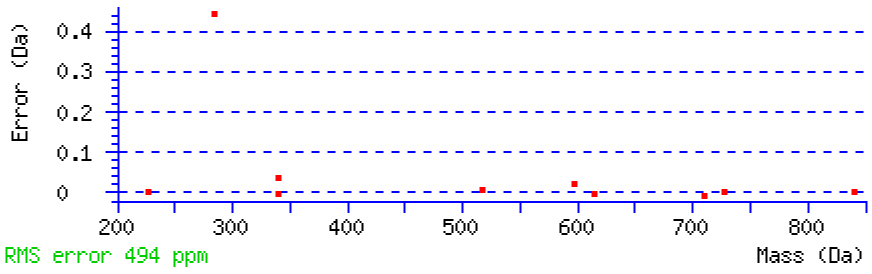
Match to Query 6783: 952.594748 from(477.304650,2+) rtinseconds(2752) index(21659)
Title: Locus:1.1.1.2559.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

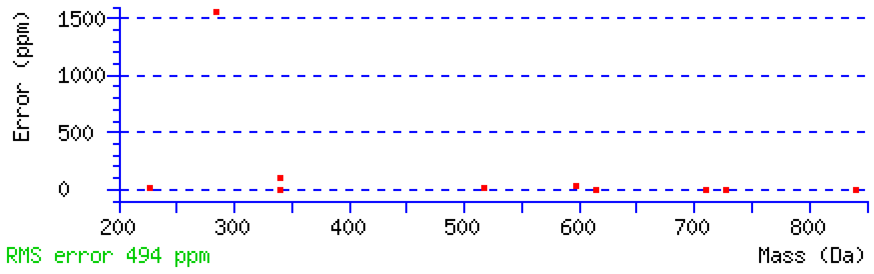
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 952.595688
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0013
Matches : 10/58 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							8
2	**227.175404**	114.091340					I	***840.518931***	420.763104	823.492382	412.249829	822.508366	411.757821	7
3	**340.259468**	170.633372					I	***727.434867***	364.221072	710.408318	355.707797	709.424302	355.215789	6
4	437.312232	219.159754					P	***614.350803***	307.679040	597.324254	299.165765	596.340238	298.673757	5
5	566.354825	***283.681051***			548.344260	274.675768	E	***517.298039***	259.152658	500.271490	250.639383	499.287474	250.147375	4
6	679.438889	***340.223083***			661.428324	331.217800	I	388.255446	194.631361	371.228897	186.118087			3
7	807.497467	404.252372	790.470918	395.739097	789.486902	395.247089	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 IIIPEIQK
(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	952.595688	-0.000940	IIIPEIQK
26.6	952.597031	-0.002283	LLIPRWR
26.6	952.595688	-0.000940	LLLPGELAK
20.7	952.595703	-0.000955	ILGILPPSK
20.7	952.595703	-0.000955	ILGILPPSK
20.3	952.595688	-0.000940	ILLLEAGPK
16.9	952.595688	-0.000940	LLIKEPPK
16.8	952.595688	-0.000940	LLIKEPPK
9.0	952.595688	-0.000940	LPEIKLPK
8.5	952.595688	-0.000940	LEPLKPLK

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

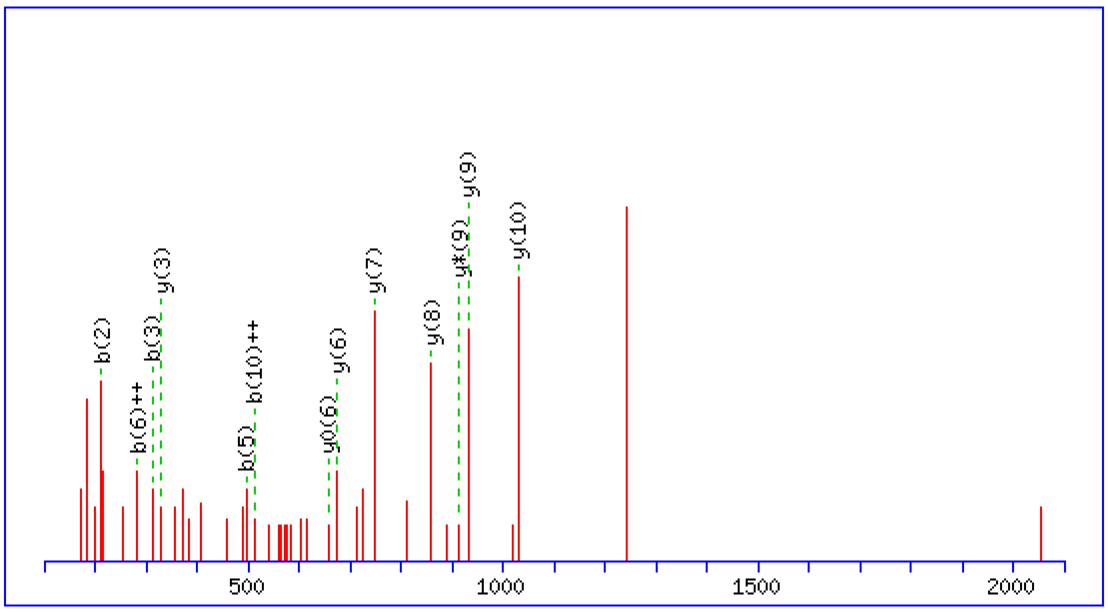
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLVALASEELAK**
Found in **ESYT2_HUMAN**, Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1

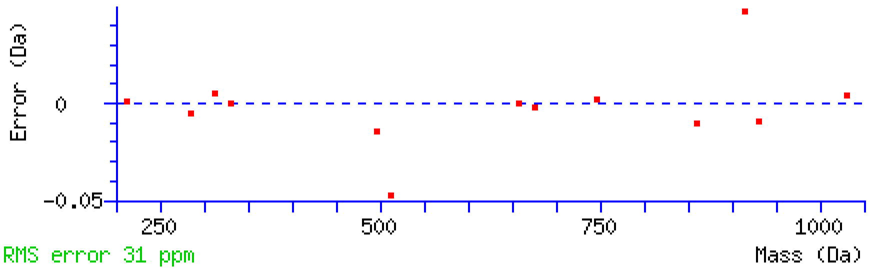
Match to Query 20742: 1241.724888 from(621.869720,2+) rtinseconds(2761) index(26485)
Title: Locus:1.1.1.2548.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

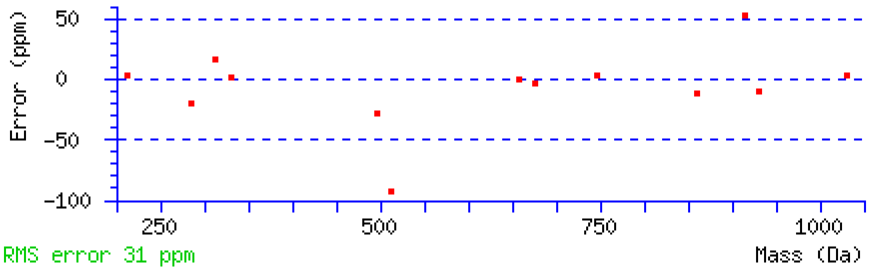
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 2100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1241.723068
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0028
Matches : 13/92 fragment ions using 26 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	1143.661966	572.334621	1126.635417	563.821347	1125.651401	563.329338	11
3	**312.228168**	156.617722			V	***1030.577902***	515.792589	1013.551353	507.279315	1012.567337	506.787307	10
4	383.265282	192.136279			A	***931.509488***	466.258382	914.482939	457.745107	913.498923	457.253099	9
5	**496.349346**	248.678311			L	***860.472374***	430.739825	843.445825	422.226550	842.461809	421.734542	8
6	567.386460	**284.196868**			A	***747.388310***	374.197793	730.361761	365.684518	729.377745	365.192510	7
7	654.418488	327.712882	636.407923	318.707600	S	***676.351196***	338.679236	659.324647	330.165961	658.340631	329.673953	6
8	783.461081	392.234179	765.450516	383.228896	E	589.319168	295.163222	572.292619	286.649948	571.308603	286.157940	5
9	912.503674	456.755475	894.493109	447.750193	E	460.276575	230.641925	443.250026	222.128651	442.266010	221.636643	4
10	1025.587738	**513.297507**	1007.577173	504.292224	L	***331.233982***	166.120629	314.207433	157.607354			3
11	1096.624852	548.816064	1078.614287	539.810781	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 VLVALASEELAK
(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	1241.723068	0.001820	VLVALASEELAK

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

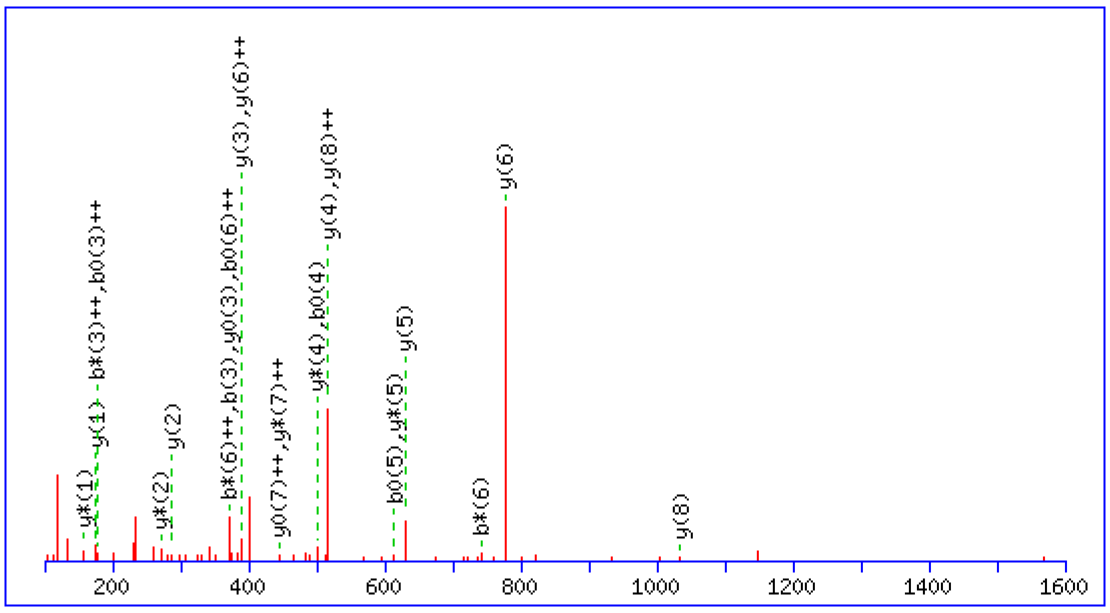
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQEFLQTLR**
Found in **FANCI_HUMAN**, Fanconi anemia group I protein OS=Homo sapiens GN=FANCI PE=1 SV=4

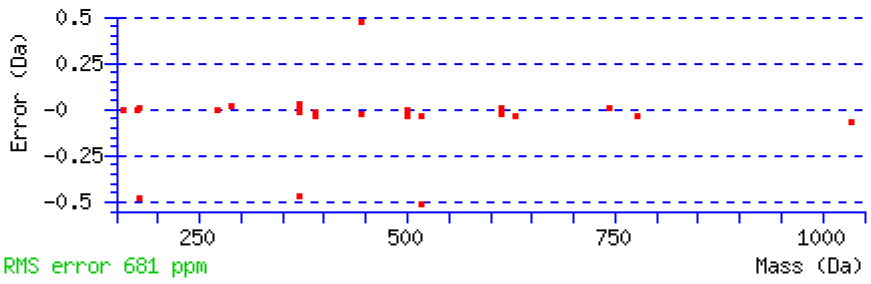
Match to Query 352151: 1146.640688 from(574.327620,2+) rtinseconds(1713) index(877750)
Title: Locus:1.1.1.951.30
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

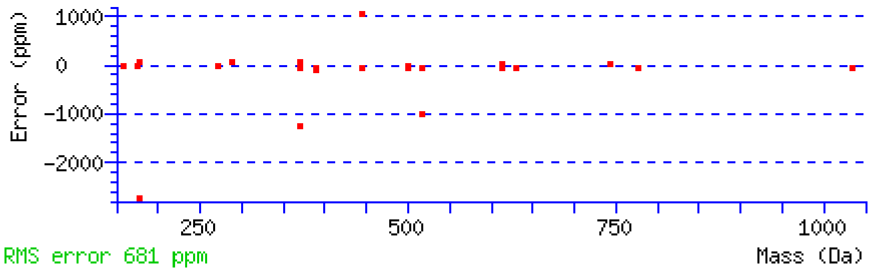
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1146.639694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0045
Matches : 24/86 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							9
2	242.149918	121.578597	225.123369	113.065323			Q	***1034.562922***	517.785099	1017.536373	509.271825	1016.552357	508.779817	8
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	906.504344	453.755810	889.477795	445.242536	888.493779	444.750528	7
4	518.260925	259.634101	501.234376	251.120826	500.250360	250.628818	F	***777.461751***	389.234514	760.435202	380.721239	759.451186	380.229231	6
5	631.344989	316.176133	614.318440	307.662858	613.334424	307.170850	L	***630.393337***	315.700307	613.366788	307.187032	612.382772	306.695024	5
6	759.403567	380.205422	742.377018	371.692147	741.393002	371.200139	Q	***517.309273***	259.158275	500.282724	250.645000	499.298708	250.152992	4
7	860.451246	430.729261	843.424697	422.215987	842.440681	421.723979	T	***389.250695***	195.128986	372.224146	186.615711	371.240130	186.123703	3
8	973.535310	487.271293	956.508761	478.758019	955.524745	478.266011	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 LQEFLQTLR
(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	1146.639694	0.000994	LQEFLQTLR
6.8	1146.629791	0.010897	SWPAAIPHLR
4.8	1146.639679	0.001009	LEDFIKNLR
2.2	1146.639694	0.000994	ISSVFASPALR
1.1	1146.631821	0.008867	IGISKSELVAM

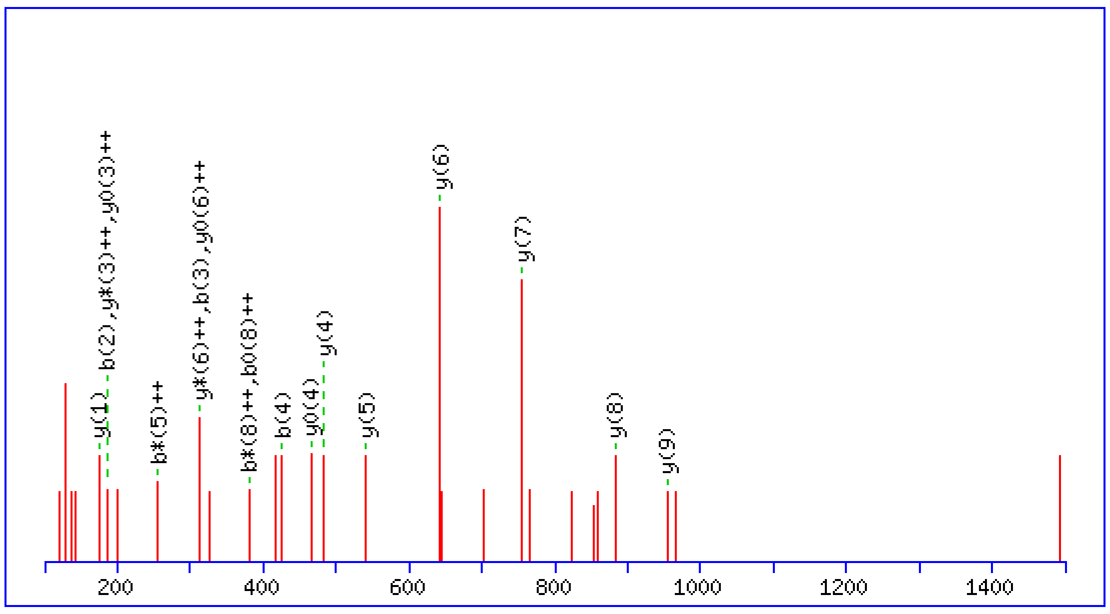
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAQITGPPDR**
Found in **FUBP1_HUMAN**, Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3

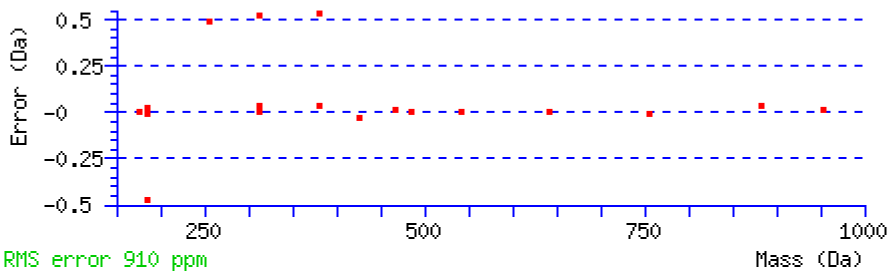
Match to Query 13108: 1066.577388 from(534.295970,2+) rtinseconds(1558) index(14421)
Title: Locus:1.1.1.1994.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

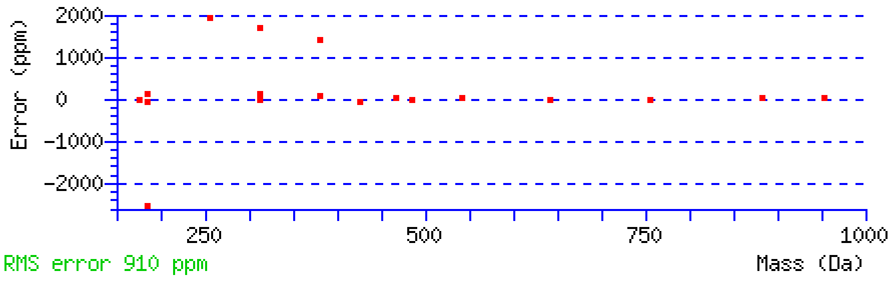
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1066.577103
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 0.00015
Matches : 18/94 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	114.091340	57.549308					I							10
2	**185.128454**	93.067865					A	***954.500322***	477.753799	937.473773	469.240525	936.489757	468.748517	9
3	**313.187032**	157.097154	296.160483	148.583879			Q	***883.463208***	442.235242	866.436659	433.721968	865.452643	433.229960	8
4	**426.271096**	213.639186	409.244547	205.125912			I	***755.404630***	378.205953	738.378081	369.692679	737.394065	369.200671	7
5	527.318775	264.163026	510.292226	255.649751	509.308210	255.157743	T	***642.320566***	321.663921	625.294017	313.150647	624.310001	312.658639	6
6	584.340239	292.673758	567.313690	284.160483	566.329674	283.668475	G	***541.272887***	271.140082	524.246338	262.626807	523.262322	262.134799	5
7	681.393003	341.200140	664.366454	332.686865	663.382438	332.194857	P	***484.251423***	242.629350	467.224874	234.116075	466.240858	233.624067	4
8	778.445767	389.726522	761.419218	381.213247	760.435202	380.721239	P	387.198659	194.102968	370.172110	185.589693	369.188094	185.097685	3
9	893.472710	447.239993	876.446161	438.726719	875.462145	438.234711	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IAQITGPPDR
(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	1066.577103	0.000285	IAQITGPPDR
7.7	1066.577103	0.000285	QAPSLPLPGR
7.2	1066.577103	0.000285	PPASGPSVLAR
6.2	1066.577103	0.000285	SPKAPPPVAR
4.7	1066.577103	0.000285	QAPSLPLPGR
2.5	1066.577103	0.000285	PPASGPSVLAR
0.5	1066.581131	-0.003743	NVVLQYGFK
0.2	1066.578445	-0.001057	TLGHHHPIR

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

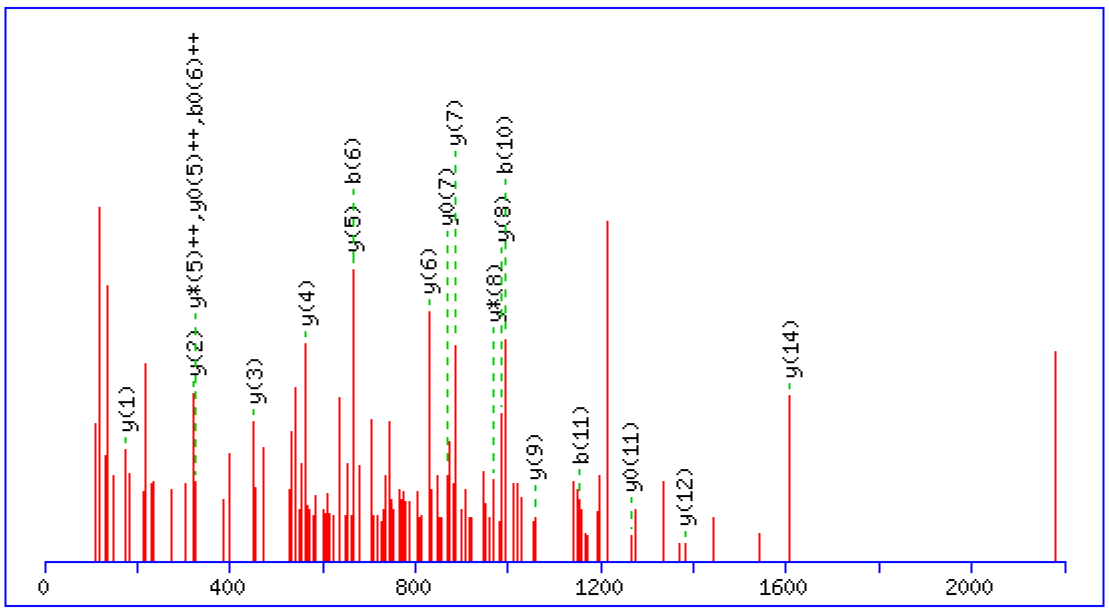
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVARPEPATGYTLEFR**
Found in **FSCN1_HUMAN**, Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3

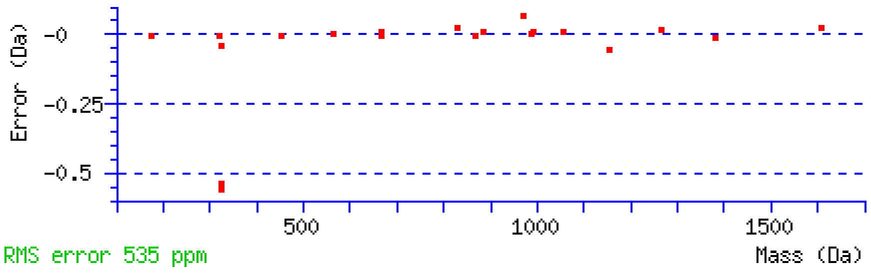
Match to Query 47296: 1818.974352 from(607.332060,3+) rtinseconds(2413) index(30310)
Title: Locus:1.1.1.2443.21
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

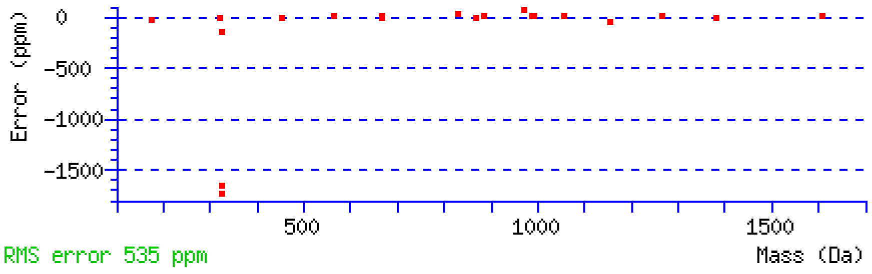
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1818.962814
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0003
Matches : 20/160 fragment ions using 62 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	1706.886048	853.946662	1689.859499	845.433388	1688.875483	844.941380	15
3	284.196868	142.602072					A	***1607.817634***	804.412455	1590.791085	795.899181	1589.807069	795.407173	14
4	440.297979	220.652627	423.271430	212.139353			R	1536.780520	768.893898	1519.753971	760.380624	1518.769955	759.888616	13
5	537.350743	269.179010	520.324194	260.665735			P	***1380.679409***	690.843343	1363.652860	682.330068	1362.668844	681.838060	12
6	**666.393336**	333.700306	649.366787	325.187032	648.382771	324.695024	E	1283.626645	642.316961	1266.600096	633.803686	1265.616080	633.311678	11
7	763.446100	382.226688	746.419551	373.713414	745.435535	373.221406	P	1154.584052	577.795664	1137.557503	569.282390	1136.573487	568.790381	10
8	834.483214	417.745245	817.456665	409.231971	816.472649	408.739963	A	***1057.531288***	529.269282	1040.504739	520.756008	1039.520723	520.263999	9
9	935.530893	468.269085	918.504344	459.755810	917.520328	459.263802	T	***986.494174***	493.750725	969.467625	485.237450	968.483609	484.745442	8
10	**992.552357**	496.779817	975.525808	488.266542	974.541792	487.774534	G	***885.446495***	443.226885	868.419946	434.713611	867.435930	434.221603	7
11	**1155.615686**	578.311481	1138.589137	569.798207	1137.605121	569.306199	Y	***828.425031***	414.716153	811.398482	406.202879	810.414466	405.710871	6
12	1256.663365	628.835321	1239.636816	620.322046	1238.652800	619.830038	T	***665.361702***	333.184489	648.335153	324.671214	647.351137	324.179206	5
13	1369.747429	685.377353	1352.720880	676.864078	1351.736864	676.372070	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
14	1498.790022	749.898649	1481.763473	741.385375	1480.779457	740.893366	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
15	1645.858436	823.432856	1628.831887	814.919582	1627.847871	814.427573	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 LVARPEPATGYTLEFR
(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	1818.962814	0.011538	LVARPEPATGYTLEFR
1.1	1818.963028	0.011324	FFMLLTFPLSFPISK

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

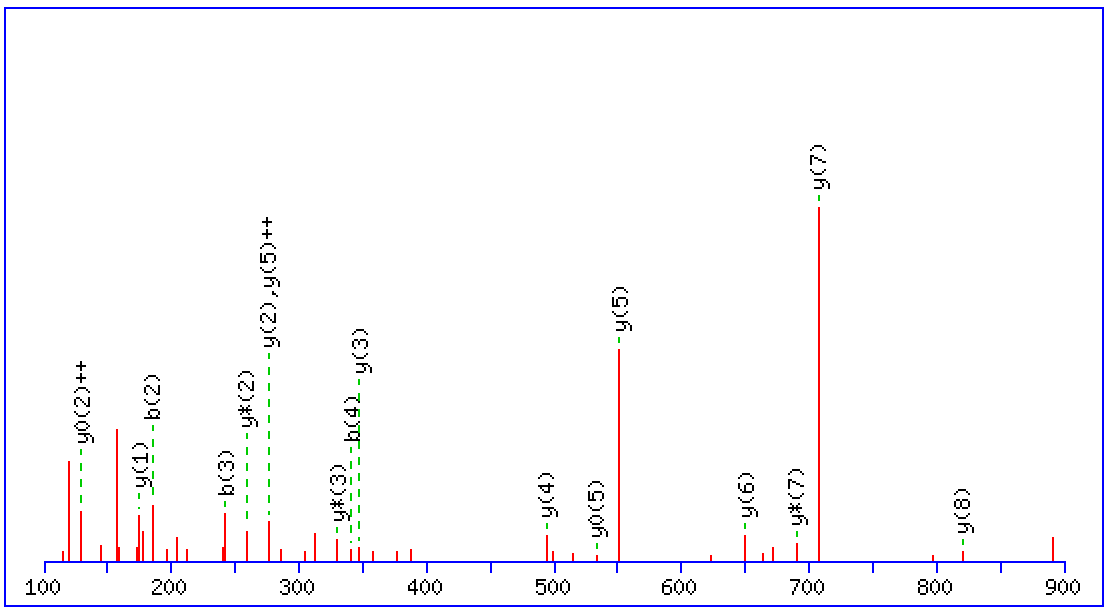
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGVGFATR**
Found in **FABP7_HUMAN**, Fatty acid-binding protein, brain OS=Homo sapiens GN=FABP7 PE=1 SV=3

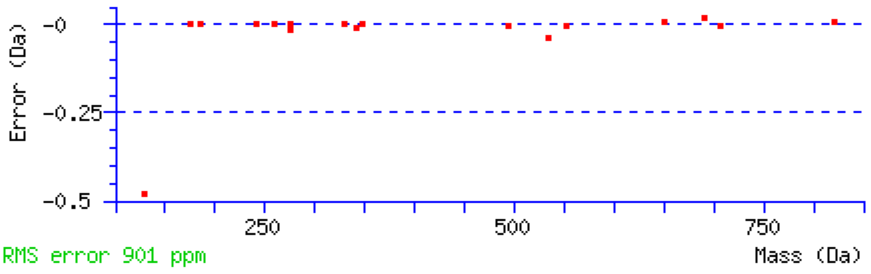
Match to Query 3203: 890.496268 from(446.255410,2+) rtinseconds(2199) index(5860)
Title: Locus:1.1.1.2595.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

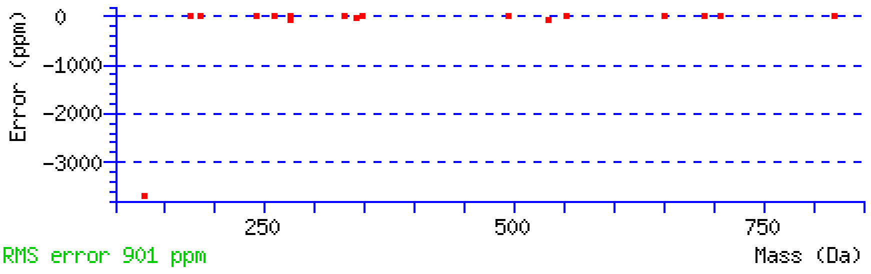
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 890.497406
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 3.1e-006
Matches : 17/64 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							9
2	**185.128454**	93.067865			L	***820.467565***	410.737421	803.441016	402.224146	802.457000	401.732138	8
3	**242.149918**	121.578597			G	***707.383501***	354.195389	690.356952	345.682114	689.372936	345.190106	7
4	**341.218332**	171.112804			V	***650.362037***	325.684657	633.335488	317.171382	632.351472	316.679374	6
5	398.239796	199.623536			G	***551.293623***	276.150450	534.267074	267.637175	533.283058	267.145167	5
6	545.308210	273.157743			F	***494.272159***	247.639718	477.245610	239.126443	476.261594	238.634435	4
7	616.345324	308.676300			A	***347.203745***	174.105511	330.177196	165.592236	329.193180	165.100228	3
8	717.393003	359.200140	699.382438	350.194857	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 ALGVGFATR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.8	890.497406	-0.001138	ALGVGFATR
8.4	890.500748	-0.004480	NLLKMTR
7.7	890.497406	-0.001138	AVGLAGTFR
6.8	890.489517	0.006751	IQVKMEK
4.9	890.489517	0.006751	ALINSVMK
1.3	890.497391	-0.001123	APPVPAPAR
1.1	890.497391	-0.001123	SPGPPAPLR
0.7	890.489502	0.006766	IAAISMASK
0.6	890.497375	-0.001107	ALYAVAQR
0.4	890.501404	-0.005136	ALHYFLK

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

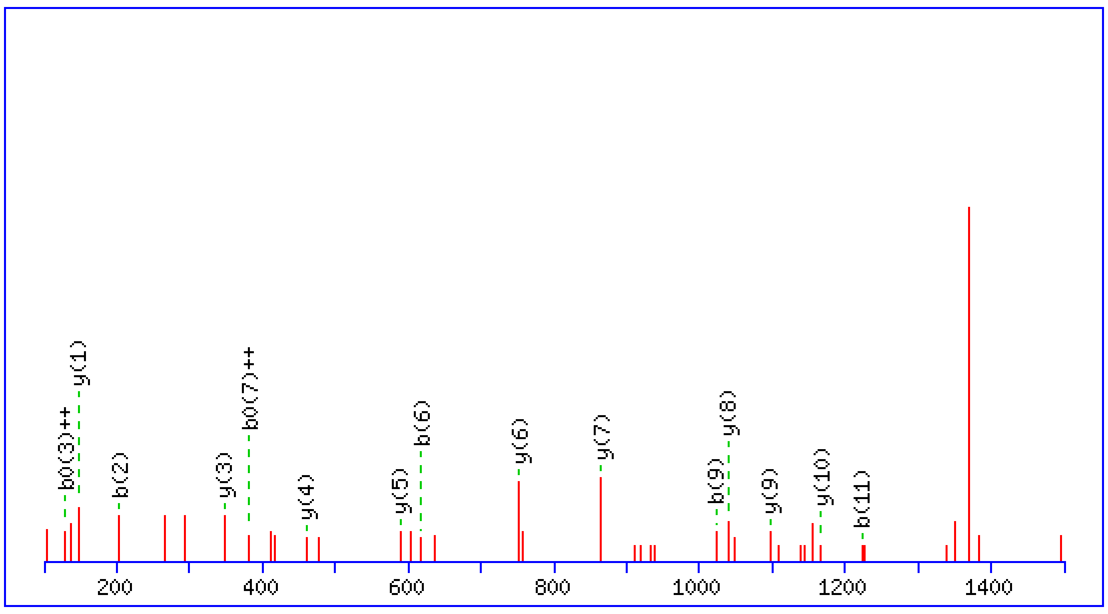
Mascot Search Results

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

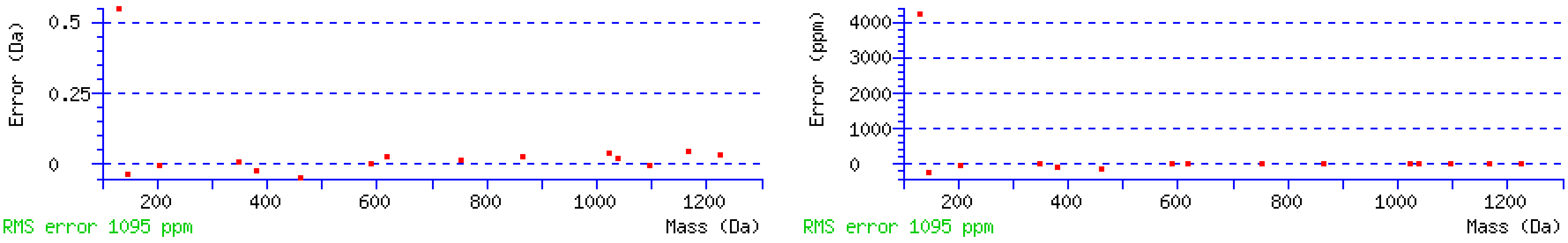
Match to Query 34682: 1368.664948 from(685.339750,2+) rtinseconds(2667) index(32927)
Title: Locus:1.1.1.2414.30
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

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): 1368.659500
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00019
Matches : 15/106 fragment ions using 39 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
48.2	1368.659500	0.005448	SDAGCLYELTVK
9.0	1368.652985	0.011963	GGDEVMFMRIAK
8.4	1368.652985	0.011963	GGDEVMFMRIAK
7.3	1368.670746	-0.005798	TTQSKIFQCDK
3.8	1368.678116	-0.013168	MLKSCFPESLK
3.7	1368.659500	0.005448	SDGSKYPEMVLK
0.7	1368.656128	0.008820	STSLFETAWEAK

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

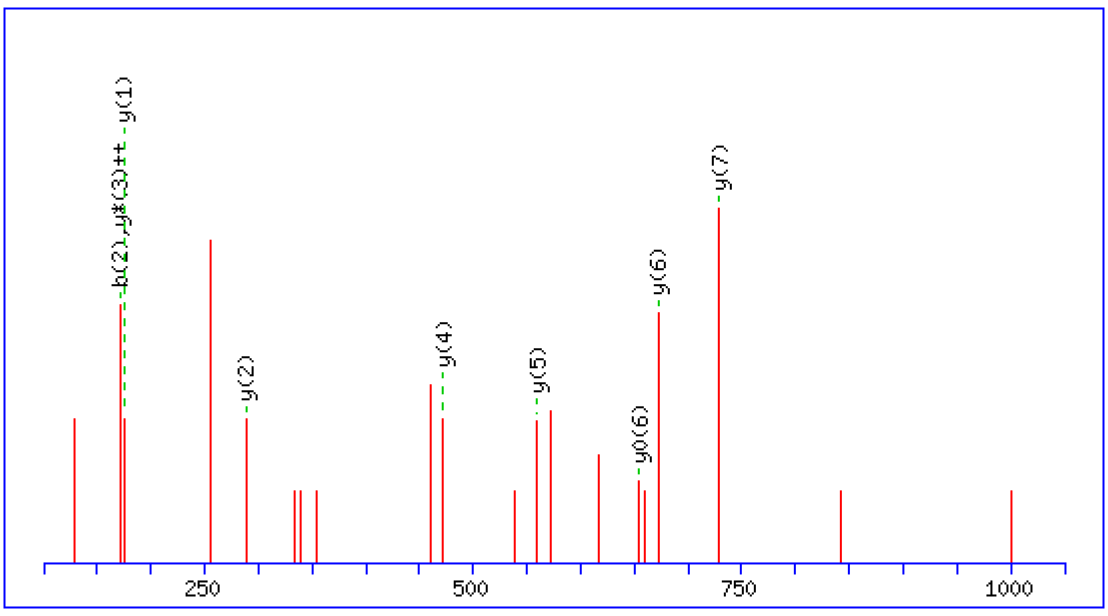
{MATRIX SCIENCE} Mascot Search Results

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

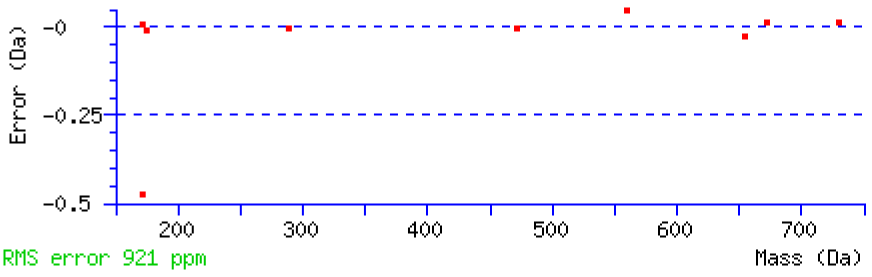
Match to Query 2770: 841.497688 from(421.756120,2+) rtinseconds(1945) index(19461)
Title: Locus:1.1.1.2232.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

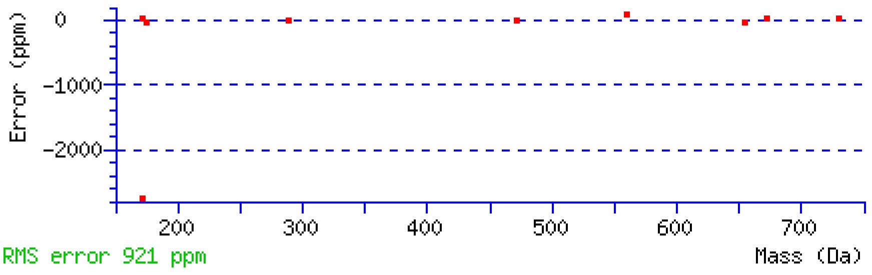
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 841.502136
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7 : Oxidation (P)
Ions Score: 39 **Expect:** 0.0013
Matches : 9/56 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			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
39.1	841.502136	-0.004448	IGLSLAPR
12.8	841.502136	-0.004448	LIGVANQK
11.3	841.502136	-0.004448	LLLSQPR
11.3	841.502136	-0.004448	LPNTLLR
10.0	841.502136	-0.004448	IPKSPLR
10.0	841.502136	-0.004448	ILGLAPSR
9.8	841.502136	-0.004448	LEKTVPR
6.0	841.502151	-0.004463	AVSVTPIR
5.5	841.502121	-0.004433	IVAEAIAR
5.3	841.502136	-0.004448	ILAVSPSR

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

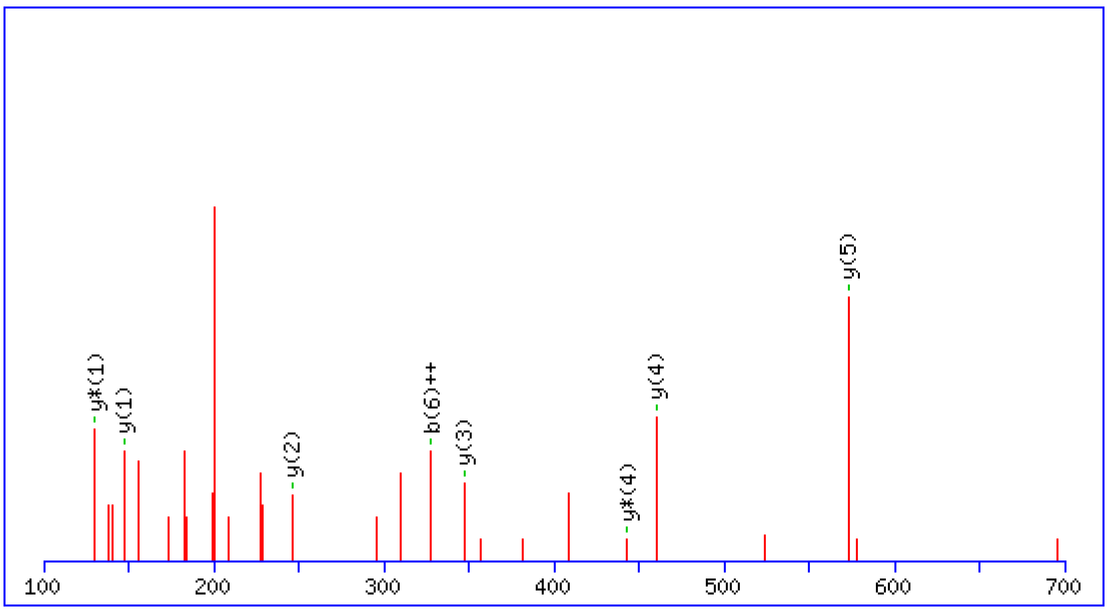
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIILTVK**
Found in **FRPD1_HUMAN**, FERM and PDZ domain-containing protein 1 OS=Homo sapiens GN=FRMPD1 PE=1 SV=1

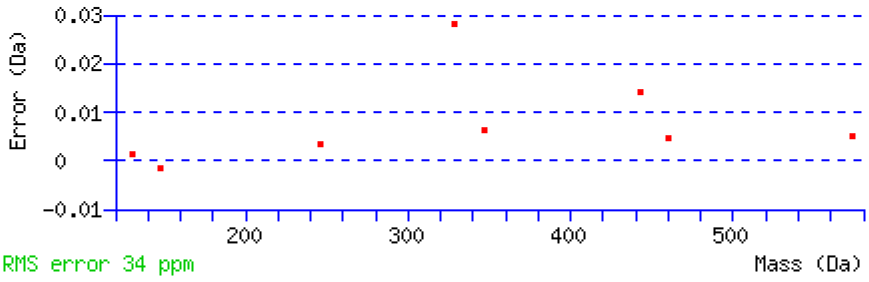
Match to Query 153: 800.495968 from(401.255260,2+) rtinseconds(2501) index(23819)
Title: Locus:1.1.1.2885.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

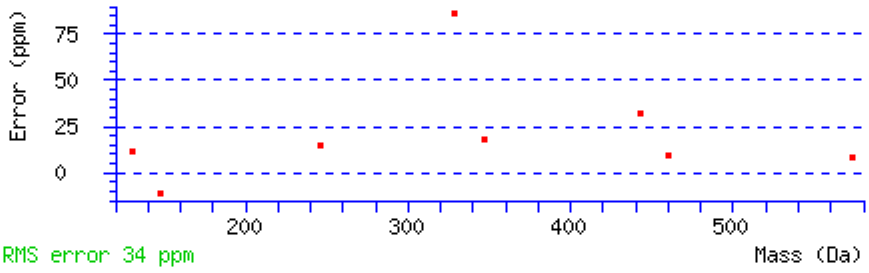
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 800.500748
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0023
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	116.034219	58.520748	98.023654	49.515465	**D**							7
2	229.118283	115.062779	211.107718	106.057497	**I**	686.481089	343.744183	669.454540	335.230908	668.470524	334.738900	6
3	342.202347	171.604811	324.191782	162.599529	**I**	***573.397025***	287.202151	556.370476	278.688876	555.386460	278.196868	5
4	455.286411	228.146843	437.275846	219.141561	**L**	***460.312961***	230.660118	443.286412	222.146844	442.302396	221.654836	4
5	556.334090	278.670683	538.323525	269.665401	**T**	***347.228897***	174.118086	330.202348	165.604812	329.218332	165.112804	3
6	655.402504	328.204890	637.391939	319.199608	**V**	***246.181218***	123.594247	229.154669	115.080972			2
7					**K**	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.0	800.500748	-0.004780	DIILTVK
18.4	800.500732	-0.004764	LDLLSLK
5.4	800.500732	-0.004764	ELISLVK
0.3	800.490829	0.005139	LHKLYK
0.3	800.490829	0.005139	LIKHYK

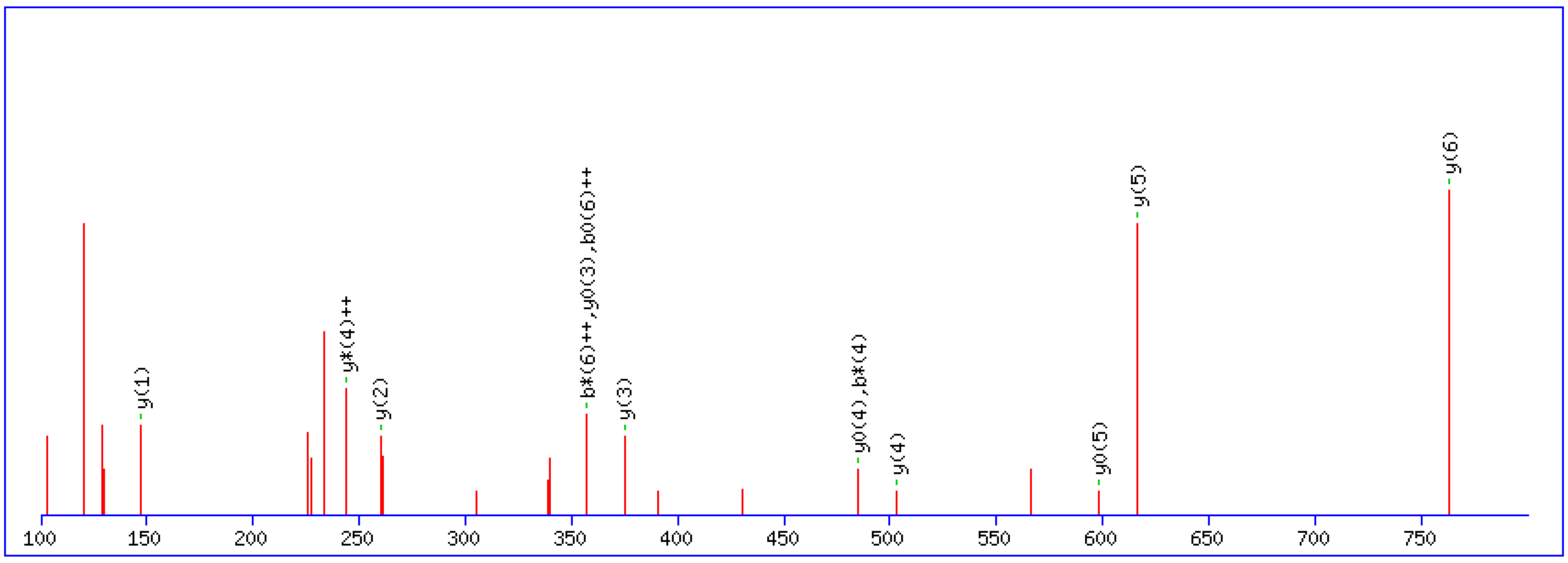
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFLQDIK**
Found in **FRIH_HUMAN**, Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2

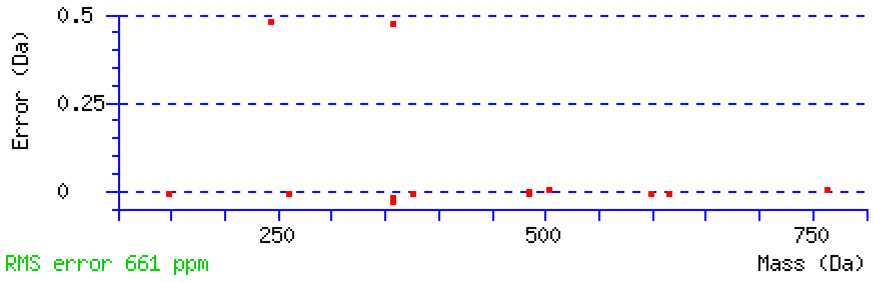
Match to Query 860: 875.510608 from(438.762580,2+) rtinseconds(2085) index(20584)
Title: Locus:1.1.1.1235.2
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 2.mgf

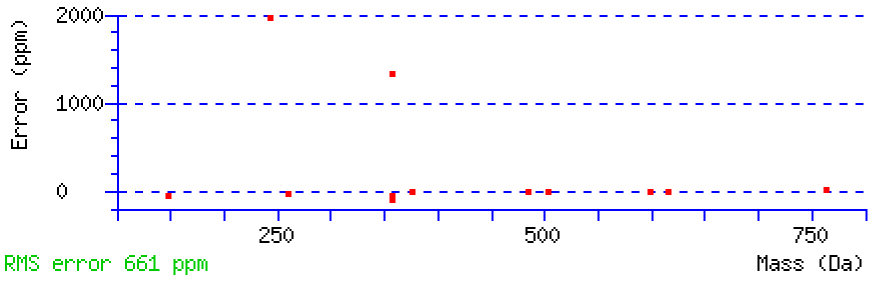
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 875.511642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00019
Matches : 13/54 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	114.091340	57.549308					I							7
2	261.159754	131.083515					F	*763.434867*	382.221072	746.408318	373.707797	745.424302	373.215789	6
3	374.243818	187.625547					L	*616.366453*	308.686865	599.339904	300.173590	598.355888	299.681582	5
4	502.302396	251.654836	485.275847	243.141561			Q	*503.282389*	252.144832	486.255840	243.631558	485.271824	243.139550	4
5	617.329339	309.168308	600.302790	300.655033	599.318774	300.163025	D	*375.223811*	188.115543	358.197262	179.602269	357.213246	179.110261	3
6	730.413403	365.710340	713.386854	357.197065	712.402838	356.705057	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 IFLQDIK
(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	875.511642	-0.001034	IFLQDIK
25.0	875.511627	-0.001019	LILYPNK
17.0	875.511627	-0.001019	ENIIFLK
15.7	875.511627	-0.001019	LELFLNK
15.0	875.511642	-0.001034	LKFIDPK
14.2	875.511642	-0.001034	FLLLQDK
14.2	875.511658	-0.001050	LFVGSIPK
14.0	875.511627	-0.001019	IYIPLNK
13.4	875.511642	-0.001034	LPPPPDIK
13.4	875.511642	-0.001034	VGSLYPIK

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

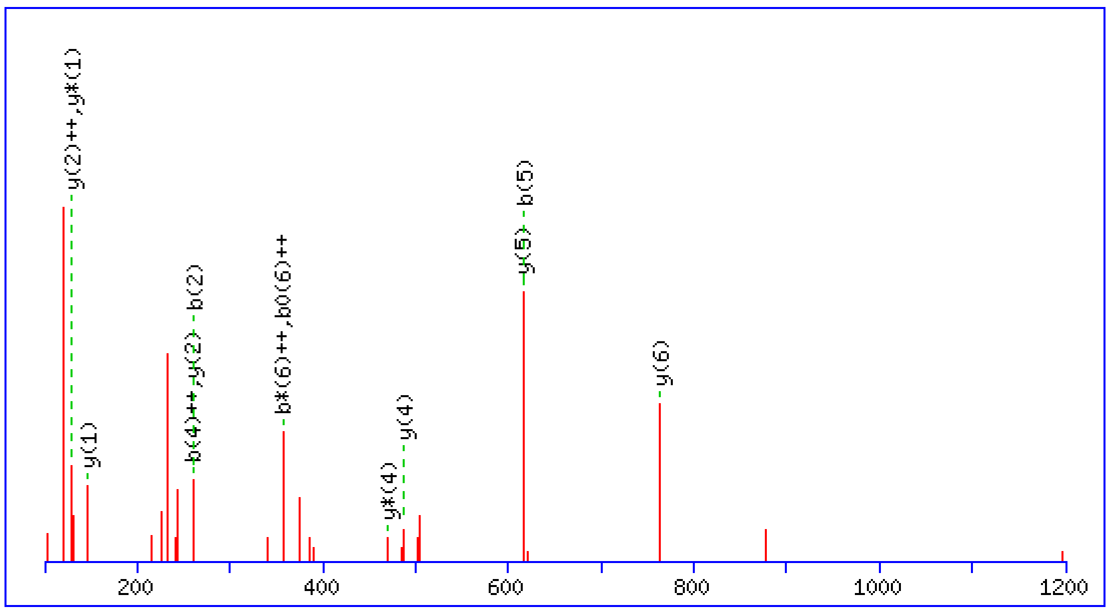
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMEKVIK**
Found in **FSIP2_HUMAN**, Fibrous sheath-interacting protein 2 OS=Homo sapiens GN=FSIP2 PE=1 SV=4

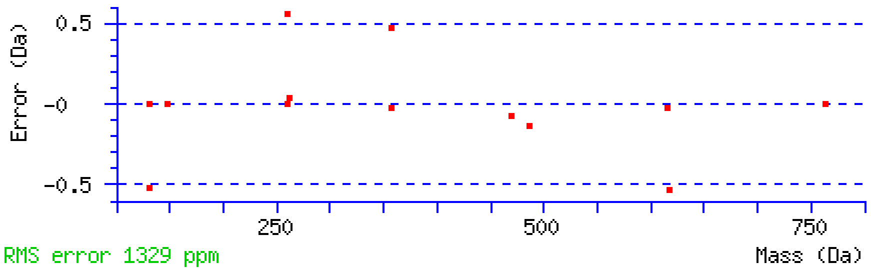
Match to Query 4654: 875.513608 from(438.764080,2+) rtinseconds(2570) index(23997)
Title: Locus:1.1.1.2442.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

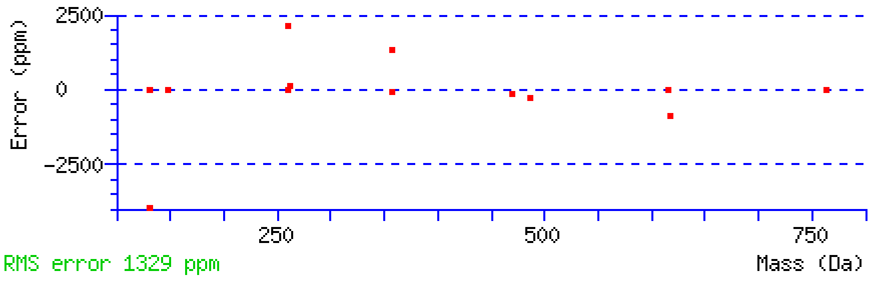
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 32  Expect: 0.0029
Matches : 13/84 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	**261.126740**	131.067008					M	***763.438238***	382.222757	746.411689	373.709483	745.427673	373.217475	6
3	390.169333	195.588304			372.158768	186.583022	E	***616.402838***	308.705057	599.376289	300.191783	598.392273	299.699775	5
4	518.264296	259.635786	501.237747	251.122512	500.253731	250.630504	K	***487.360245***	244.183760	470.333696	235.670486			4
5	**617.332710**	309.169993	600.306161	300.656719	599.322145	300.164711	V	359.265282	180.136279	342.238733	171.623004			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 IMEKVIK
(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	875.511642	0.001966	IFLQDIK
32.0	875.514999	-0.001391	IMEKVIK
31.5	875.514999	-0.001391	MIIKDLK
30.2	875.514999	-0.001391	IMKDLIK
30.1	875.511627	0.001981	ENIIFLK
24.7	875.511627	0.001981	FLNELIK
23.5	875.511658	0.001950	LFVGSIPK
22.3	875.511627	0.001981	LILYPNK
21.9	875.511627	0.001981	IYIPLNK
21.0	875.511642	0.001966	LKFIDPK

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

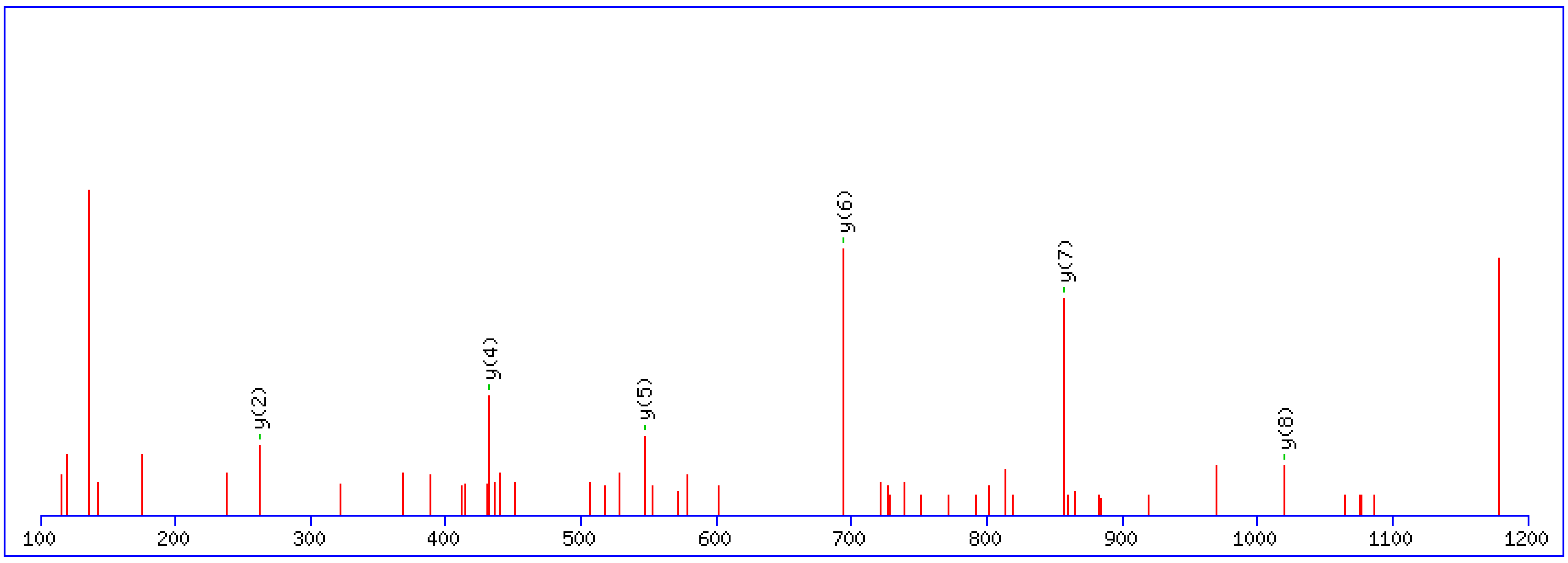
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGYYFDGISR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

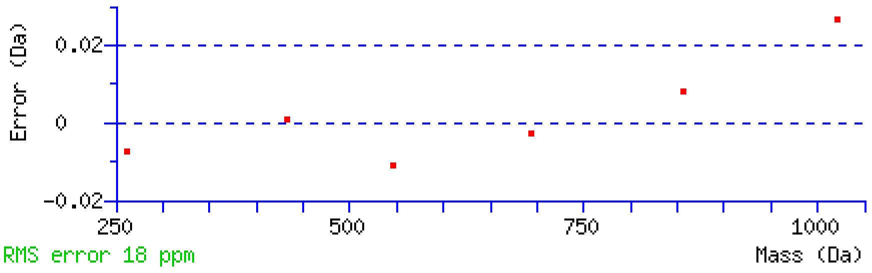
Match to Query 10874: 1177.547168 from(589.780860,2+) rtinseconds(2170) index(23162)
Title: Locus:1.1.1.1532.10
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

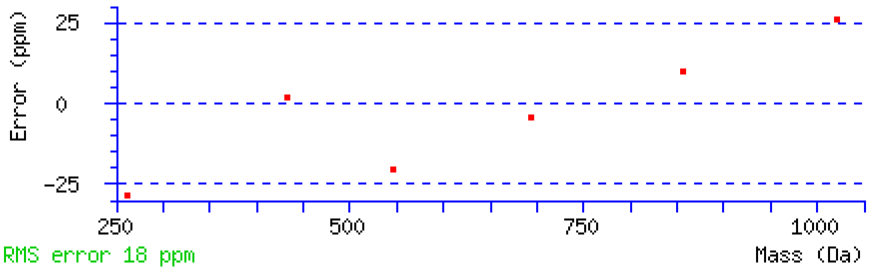
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1177.540390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00077
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	102.054955	51.531116	84.044390	42.525833	T							10
2	159.076419	80.041847	141.065854	71.036565	G	1077.499987	539.253632	1060.473438	530.740357	1059.489422	530.248349	9
3	322.139748	161.573512	304.129183	152.568230	Y	*1020.478523*	510.742900	1003.451974	502.229625	1002.467958	501.737617	8
4	485.203077	243.105177	467.192512	234.099894	Y	*857.415194*	429.211235	840.388645	420.697961	839.404629	420.205953	7
5	632.271491	316.639384	614.260926	307.634101	F	*694.351865*	347.679571	677.325316	339.166296	676.341300	338.674288	6
6	747.298434	374.152855	729.287869	365.147573	D	*547.283451*	274.145364	530.256902	265.632089	529.272886	265.140081	5
7	804.319898	402.663587	786.309333	393.658305	G	*432.256508*	216.631892	415.229959	208.118618	414.245943	207.626610	4
8	917.403962	459.205619	899.393397	450.200337	I	375.235044	188.121160	358.208495	179.607886	357.224479	179.115878	3
9	1004.435990	502.721633	986.425425	493.716351	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 TGYYFDGISR
(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	1177.540390	0.006778	TGYYFDGISR

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

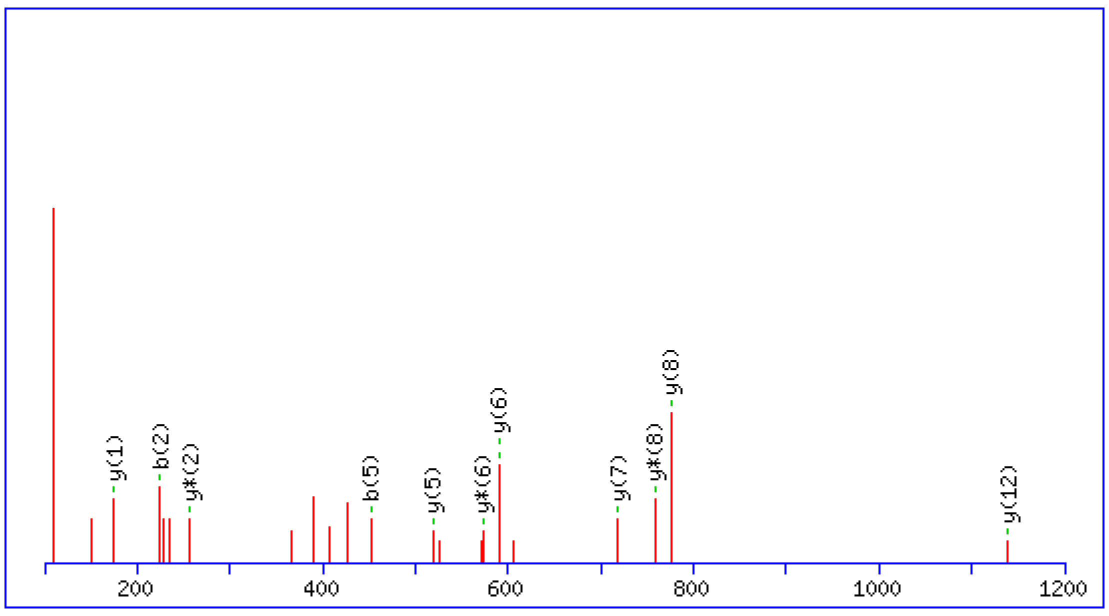
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HSGIGHGQASSAVR**
Found in **FILA_HUMAN**, Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3

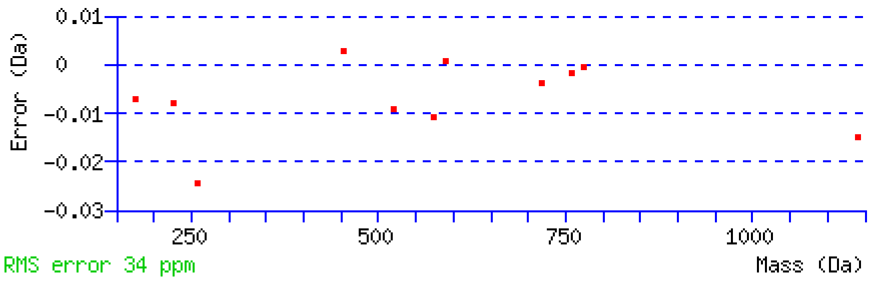
Match to Query 5874: 1362.682572 from(455.234800,3+) rtinseconds(668) index(488)
Title: Locus:1.1.1.891.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

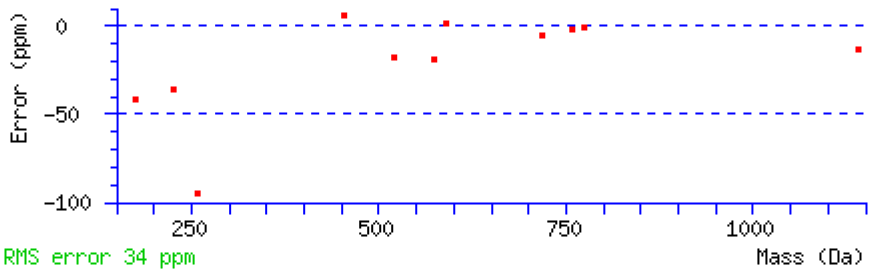
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1362.675262
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0083
Matches : 11/134 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	138.066188	69.536732					H							14
2	**225.098216**	113.052746			207.087651	104.047463	S	1226.623624	613.815450	1209.597075	605.302176	1208.613059	604.810168	13
3	282.119680	141.563478			264.109115	132.558195	G	***1139.591596***	570.299436	1122.565047	561.786162	1121.581031	561.294153	12
4	395.203744	198.105510			377.193179	189.100227	I	1082.570132	541.788704	1065.543583	533.275430	1064.559567	532.783422	11
5	**452.225208**	226.616242			434.214643	217.610959	G	969.486068	485.246672	952.459519	476.733398	951.475503	476.241390	10
6	589.284120	295.145698			571.273555	286.140416	H	912.464604	456.735940	895.438055	448.222666	894.454039	447.730658	9
7	646.305584	323.656430			628.295019	314.651148	G	***775.405692***	388.206484	758.379143	379.693210	757.395127	379.201202	8
8	774.364162	387.685719	757.337613	379.172445	756.353597	378.680437	Q	***718.384228***	359.695752	701.357679	351.182478	700.373663	350.690470	7
9	845.401276	423.204276	828.374727	414.691002	827.390711	414.198994	A	***590.325650***	295.666463	573.299101	287.153189	572.315085	286.661181	6
10	932.433304	466.720290	915.406755	458.207016	914.422739	457.715008	S	***519.288536***	260.147906	502.261987	251.634632	501.277971	251.142624	5
11	1019.465332	510.236304	1002.438783	501.723030	1001.454767	501.231022	S	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
12	1090.502446	545.754861	1073.475897	537.241587	1072.491881	536.749578	A	345.224480	173.115878	328.197931	164.602603			3
13	1189.570860	595.289068	1172.544311	586.775794	1171.560295	586.283786	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 HSGIGHGQASSAVR
(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	1362.675262	0.007310	HSGIGHGQASSAVR
16.0	1362.674774	0.007798	QGQMDAVRIMAK
8.0	1362.689133	-0.006561	RAAGYAQEEQLK
4.7	1362.674774	0.007798	QGQMDAVRIMAK
2.5	1362.688644	-0.006072	MKELEAELAMAK
2.0	1362.693863	-0.011291	ETPSPRPMRHR
1.8	1362.692520	-0.009948	MSTEEIIQRTR
1.7	1362.688705	-0.006133	MSIPMDGTAVITK
0.9	1362.681946	0.000626	ETEEIHLFFAK
0.3	1362.689148	-0.006576	QPSLNAYNSLTR

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

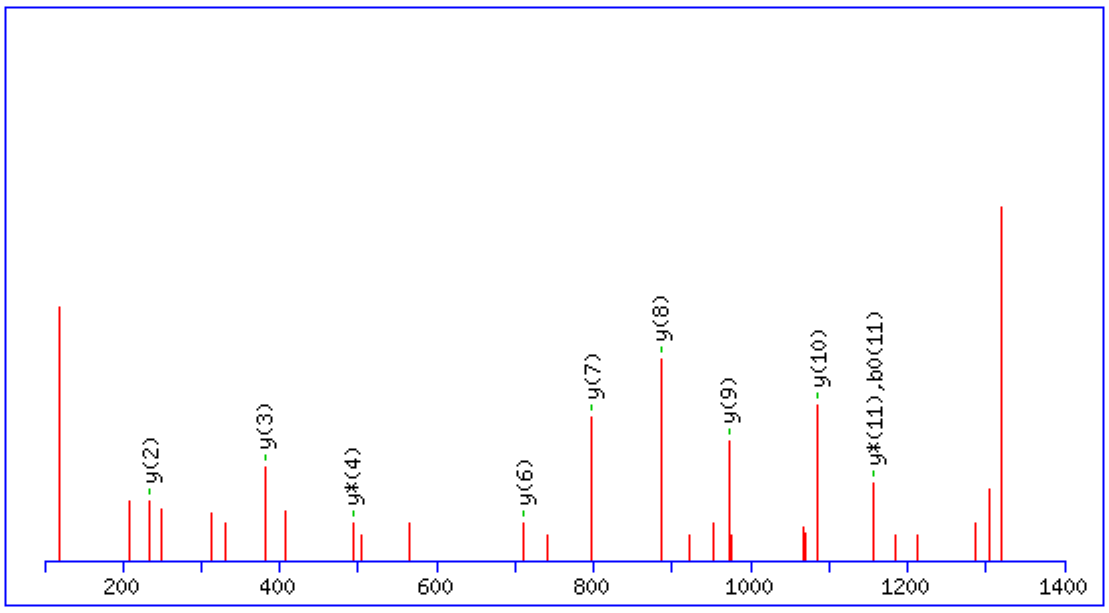
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSNSSSSNEFSK**
Found in **FILA2_HUMAN**, Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1

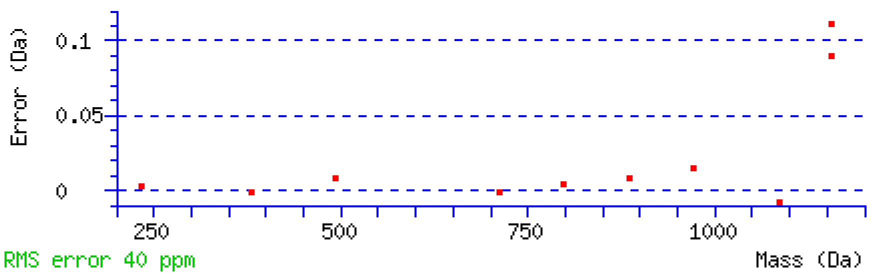
Match to Query 9900: 1319.560068 from(660.787310,2+) rtinseconds(1334) index(691)
Title: Locus:1.1.1.2335.14
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-8.mgf

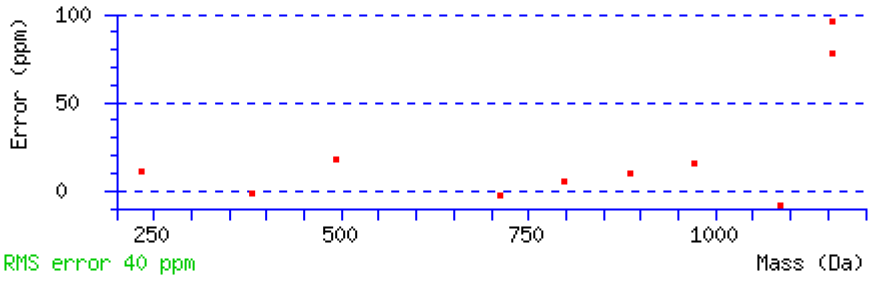
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1319.562958
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 1.9e-006
Matches : 10/124 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							12
2	235.107718	118.057497			217.097153	109.052214	S	1173.501833	587.254555	1156.475284	578.741280	1155.491268	578.249272	11
3	349.150645	175.078960	332.124096	166.565686	331.140080	166.073678	N	***1086.469805***	543.738541	1069.443256	535.225266	1068.459240	534.733258	10
4	436.182673	218.594974	419.156124	210.081700	418.172108	209.589692	S	***972.426878***	486.717077	955.400329	478.203803	954.416313	477.711795	9
5	523.214701	262.110989	506.188152	253.597714	505.204136	253.105706	S	***885.394850***	443.201063	868.368301	434.687789	867.384285	434.195781	8
6	610.246729	305.627003	593.220180	297.113728	592.236164	296.621720	S	***798.362822***	399.685049	781.336273	391.171775	780.352257	390.679767	7
7	697.278757	349.143016	680.252208	340.629742	679.268192	340.137734	S	***711.330794***	356.169035	694.304245	347.655761	693.320229	347.163753	6
8	811.321684	406.164480	794.295135	397.651205	793.311119	397.159197	N	624.298766	312.653021	607.272217	304.139747	606.288201	303.647739	5
9	940.364277	470.685776	923.337728	462.172502	922.353712	461.680494	E	510.255839	255.631558	493.229290	247.118283	492.245274	246.626275	4
10	1087.432691	544.219984	1070.406142	535.706709	1069.422126	535.214701	F	***381.213246***	191.110261	364.186697	182.596987	363.202681	182.104979	3
11	1174.464719	587.735998	1157.438170	579.222723	1156.454154	578.730715	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 FSNSSSSNEFSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.6	1319.562958	-0.002890	FSNSSSSNEFSK
0.5	1319.563843	-0.003775	FSCATCGQSFK

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

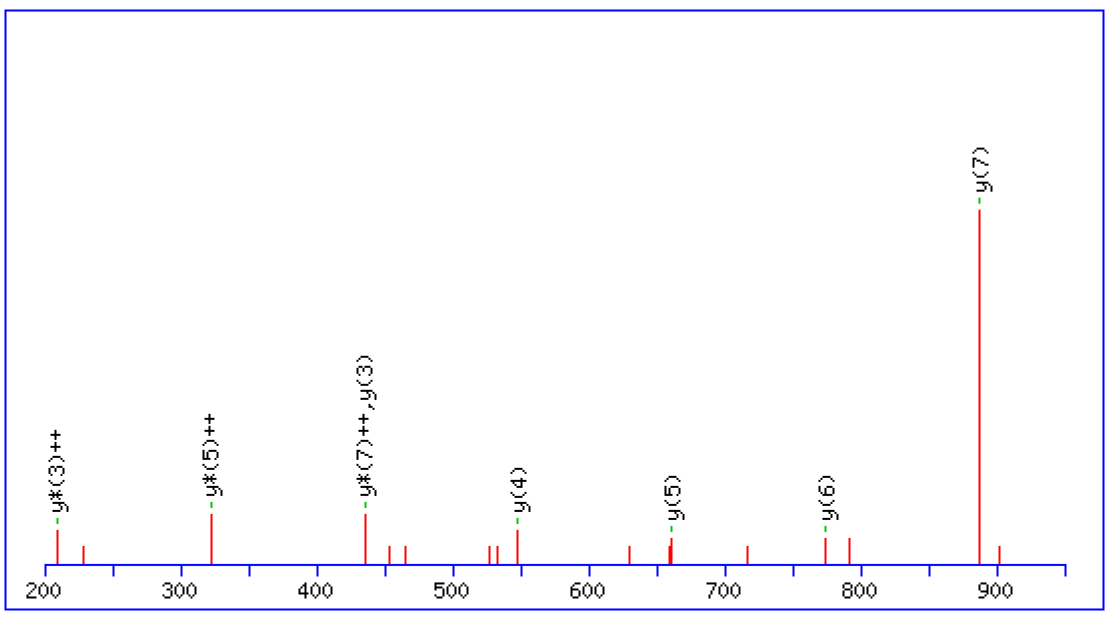
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SISDSDELASGFFVFPYPYPFRPLPPIPFPR**
Found in **FDSCP_HUMAN**, Follicular dendritic cell secreted peptide OS=Homo sapiens GN=FDCSP PE=1 SV=1

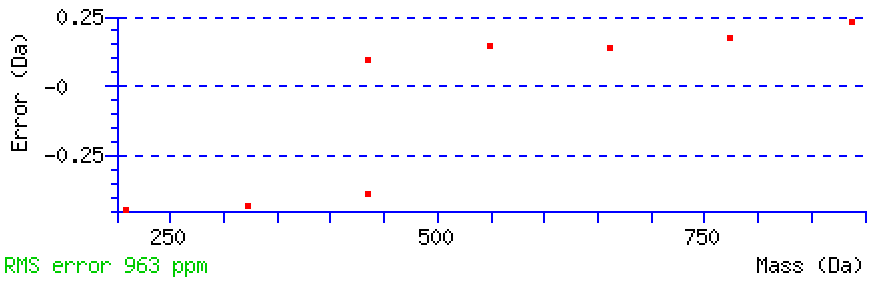
Match to Query 814549: 3618.774376 from(905.700870,4+) rtinseconds(3345) index(133313)
Title: Locus:1.1.1.1672.49
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

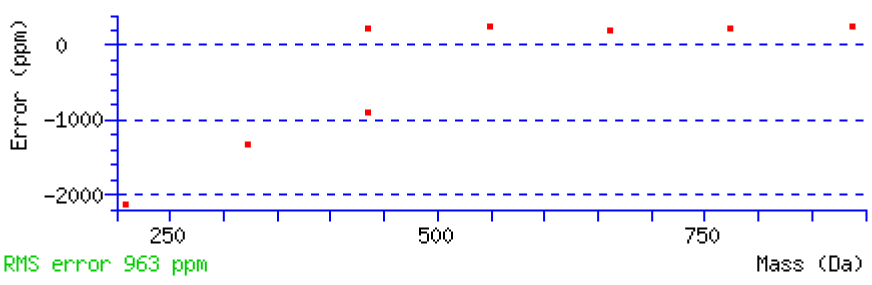
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3618.771149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P25    : Oxidation (P)
P26    : Oxidation (P)
P28    : Oxidation (P)
P30    : Oxidation (P)
Ions Score: 40  Expect: 0.00087
Matches : 8/276 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	88.039304	44.523290			70.028739	35.518008	S							31
2	201.123368	101.065322			183.112803	92.060039	I	3532.746374	1766.876825	3515.719825	1758.363551	3514.735809	1757.871543	30
3	288.155396	144.581336			270.144831	135.576053	S	3419.662310	1710.334793	3402.635761	1701.821518	3401.651745	1701.329511	29
4	403.182339	202.094807			385.171774	193.089525	D	3332.630282	1666.818779	3315.603733	1658.305505	3314.619717	1657.813497	28
5	490.214367	245.610821			472.203802	236.605539	S	3217.603339	1609.305308	3200.576790	1600.792033	3199.592774	1600.300025	27
6	605.241310	303.124293			587.230745	294.119011	D	3130.571311	1565.789294	3113.544762	1557.276019	3112.560746	1556.784011	26
7	734.283903	367.645590			716.273338	358.640307	E	3015.544368	1508.275822	2998.517819	1499.762548	2997.533803	1499.270540	25
8	847.367967	424.187622			829.357402	415.182339	L	2886.501775	1443.754526	2869.475226	1435.241251	2868.491210	1434.749243	24
9	918.405081	459.706179			900.394516	450.700896	A	2773.417711	1387.212494	2756.391162	1378.699219	2755.407146	1378.207211	23
10	1005.437109	503.222193			987.426544	494.216910	S	2702.380597	1351.693937	2685.354048	1343.180662	2684.370032	1342.688654	22
11	1062.458573	531.732924			1044.448008	522.727642	G	2615.348569	1308.177923	2598.322020	1299.664648			21
12	1209.526987	605.267132			1191.516422	596.261849	F	2558.327105	1279.667191	2541.300556	1271.153916			20
13	1356.595401	678.801339			1338.584836	669.796056	F	2411.258691	1206.132984	2394.232142	1197.619709			19
14	1455.663815	728.335546			1437.653250	719.330263	V	2264.190277	1132.598777	2247.163728	1124.085502			18
15	1602.732229	801.869753			1584.721664	792.864470	F	2165.121863	1083.064570	2148.095314	1074.551295			17
16	1699.784993	850.396135			1681.774428	841.390852	P	2018.053449	1009.530363	2001.026900	1001.017088			16
17	1862.848322	931.927799			1844.837757	922.922517	Y	1921.000685	961.003981	1903.974136	952.490706			15
18	1959.901086	980.454181			1941.890521	971.448899	P	1757.937356	879.472316	1740.910807	870.959042			14
19	2122.964415	1061.985845			2104.953850	1052.980563	Y	1660.884592	830.945934	1643.858043	822.432660			13
20	2220.017179	1110.512227			2202.006614	1101.506945	P	1497.821263	749.414270	1480.794714	740.900995			12
21	2367.085593	1184.046434			2349.075028	1175.041152	F	1400.768499	700.887888	1383.741950	692.374613			11
22	2523.186704	1262.096990	2506.160155	1253.583715	2505.176139	1253.091707	R	1253.700085	627.353681	1236.673536	618.840406			10
23	2620.239468	1310.623372	2603.212919	1302.110097	2602.228903	1301.618089	P	1097.598974	549.303125	1080.572425	540.789851			9
24	2733.323532	1367.165404	2716.296983	1358.652129	2715.312967	1358.160121	L	1000.546210	500.776743	983.519661	492.263469			8
25	2846.371211	1423.689244	2829.344662	1415.175969	2828.360646	1414.683961	P	***887.462146***	444.234711	870.435597	435.721437			7
26	2959.418890	1480.213083	2942.392341	1471.699809	2941.408325	1471.207801	P	***774.414467***	387.710872	757.387918	379.197597			6
27	3072.502954	1536.755115	3055.476405	1528.241841	3054.492389	1527.749833	I	***661.366788***	331.187032	644.340239	322.673758			5
28	3185.550633	1593.278955	3168.524084	1584.765680	3167.540068	1584.273672	P	***548.282724***	274.645000	531.256175	266.131726			4
29	3332.619047	1666.813162	3315.592498	1658.299887	3314.608482	1657.807879	F	***435.235045***	218.121161	418.208496	209.607886			3
30	3445.666726	1723.337001	3428.640177	1714.823727	3427.656161	1714.331719	P	288.166631	144.586954	271.140082	136.073679			2
31							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.6	3618.771149	0.003227	SISDSDELASGFFVFPYPYPFRPLPPIPFPR
22.2	3618.771149	0.003227	SISDSDELASGFFVFPYPYPFRPLPPIPFPR
12.8	3618.781601	-0.007225	GFTGLQGLPGPPGPSGDQGASGPAGPSGPRGPPGPVGPSGK
11.6	3618.761749	0.012627	SLNSQPLNLALSPQQSAQLLVSETSCQVSNRAM
8.6	3618.771149	0.003227	SISDSDELASGFFVFPYPYPFRPLPPIPFPR
7.6	3618.740005	0.034371	AQSSPASATFPVSVQEPPTKPRFTTGLVYDTLM
6.4	3618.769836	0.004540	NLQAHLIPGLNLNALGLFPPTSGMPPPTSGPPSAM
6.1	3618.803497	-0.029121	YSPIPPSLPPPAPQPPLYYPVDGYRVYQPVR
6.0	3618.781601	-0.007225	GFTGLQGLPGPPGPSGDQGASGPAGPSGPRGPPGPVGPSGK
6.0	3618.781601	-0.007225	GFTGLQGLPGPPGPSGDQGASGPAGPSGPRGPPGPVGPSGK

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

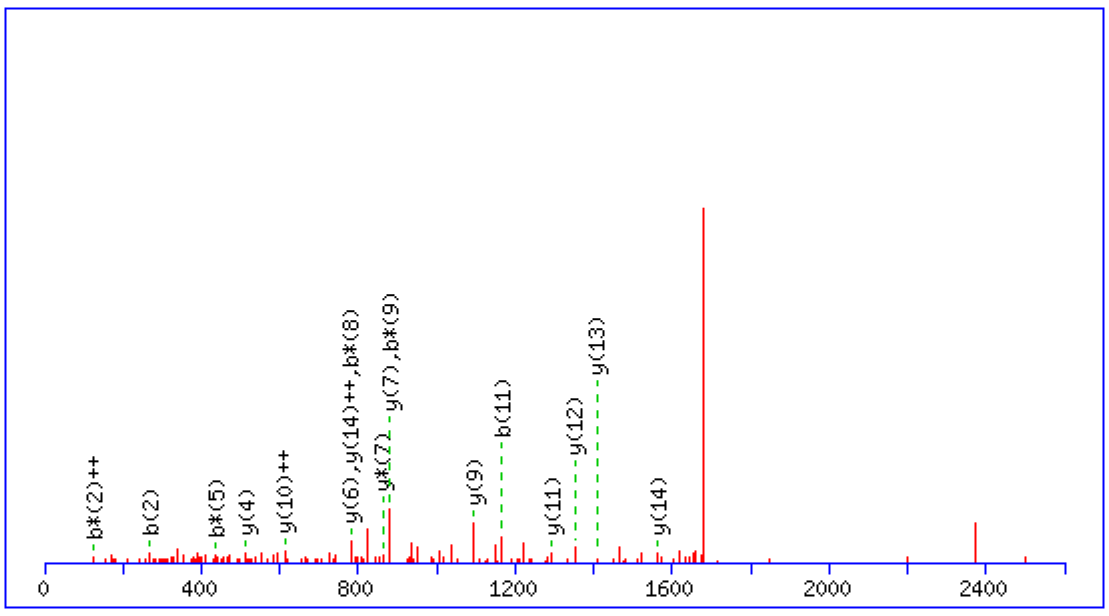
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IRGGAENTPPRPSFM**
Found in **FREM3_HUMAN**, FRAS1-related extracellular matrix protein 3 OS=Homo sapiens GN=FREM3 PE=2 SV=1

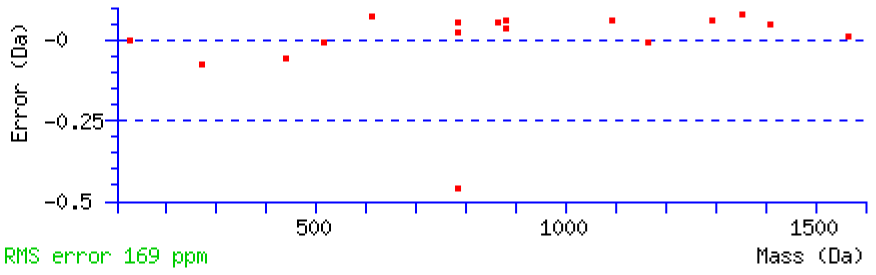
Match to Query 759193: 1676.781048 from(839.397800,2+) rtinseconds(1351) index(237163)
Title: Locus:1.1.1.1279.25
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

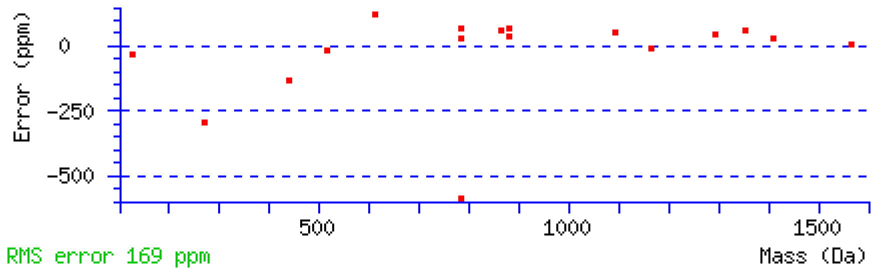
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1676.794052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P10     : Oxidation (P)
P12     : Oxidation (P)
M15     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 40  Expect: 0.0011
Matches : 17/216 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					I							15
2	**270.192451**	135.599864	253.165902	127.086589			R	***1564.717268***	782.862272	1547.690719	774.348998	1546.706703	773.856990	14
3	327.213915	164.110595	310.187366	155.597321			G	***1408.616157***	704.811717	1391.589608	696.298442	1390.605592	695.806434	13
4	384.235379	192.621327	367.208830	184.108053			G	***1351.594693***	676.300985	1334.568144	667.787710	1333.584128	667.295702	12
5	455.272493	228.139884	438.245944	219.626610			A	***1294.573229***	647.790253	1277.546680	639.276978	1276.562664	638.784970	11
6	584.315086	292.661181	567.288537	284.147907	566.304521	283.655899	E	1223.536115	612.271696	1206.509566	603.758421	1205.525550	603.266413	10
7	698.358013	349.682645	681.331464	341.169370	680.347448	340.677362	N	***1094.493522***	547.750399	1077.466973	539.237125	1076.482957	538.745117	9
8	799.405692	400.206484	782.379143	391.693210	781.395127	391.201202	T	980.450595	490.728936	963.424046	482.215661	962.440030	481.723653	8
9	896.458456	448.732866	879.431907	440.219592	878.447891	439.727584	P	***879.402916***	440.205096	862.376367	431.691822	861.392351	431.199814	7
10	1009.506135	505.256706	992.479586	496.743431	991.495570	496.251423	P	***782.350152***	391.678714	765.323603	383.165440	764.339587	382.673432	6
11	**1165.607246**	583.307261	1148.580697	574.793987	1147.596681	574.301979	R	669.302473	335.154875	652.275924	326.641600	651.291908	326.149592	5
12	1278.654925	639.831101	1261.628376	631.317826	1260.644360	630.825818	P	***513.201362***	257.104319			495.190797	248.099037	4
13	1365.686953	683.347115	1348.660404	674.833840	1347.676388	674.341832	S	400.153683	200.580480			382.143118	191.575197	3
14	1512.755367	756.881322	1495.728818	748.368047	1494.744802	747.876039	F	313.121655	157.064466					2
15							M	166.053241	83.530258					1





NCBI **BLAST** search of IRGGAENTPPRPSFM
(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	1676.794052	-0.013004	IRGGAENTPPRPSFM
31.8	1676.794052	-0.013004	IRGGAENTPPRPSFM
21.1	1676.794052	-0.013004	IRGGAENTPPRPSFM
16.1	1676.794052	-0.013004	IRGGAENTPPRPSFM

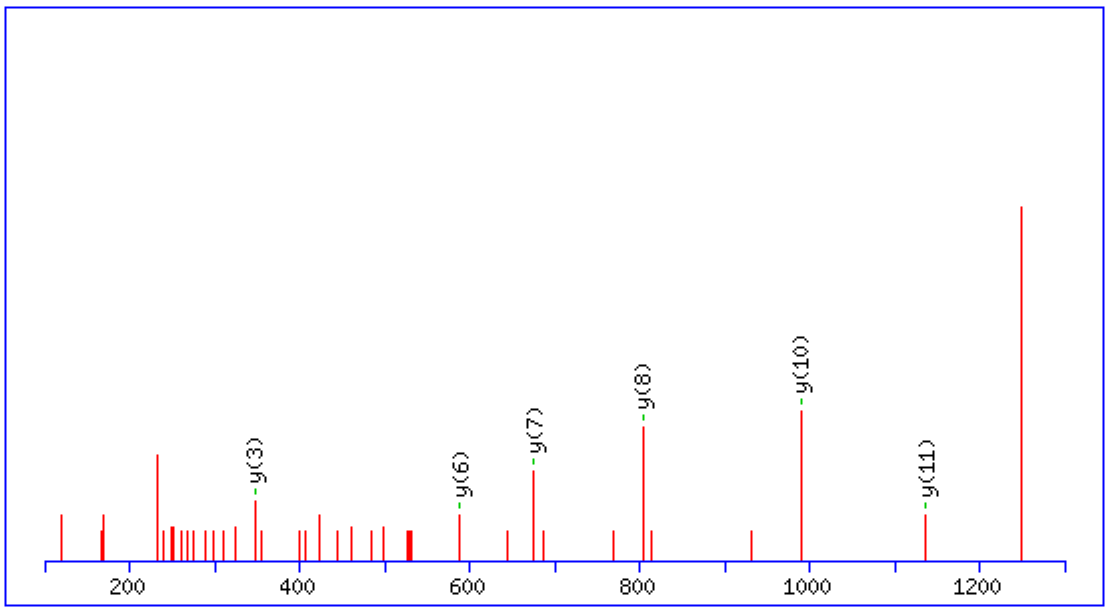
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFGQESGPSAEK**
Found in **FUND2_HUMAN**, FUN14 domain-containing protein 2 OS=Homo sapiens GN=FUNDC2 PE=1 SV=2

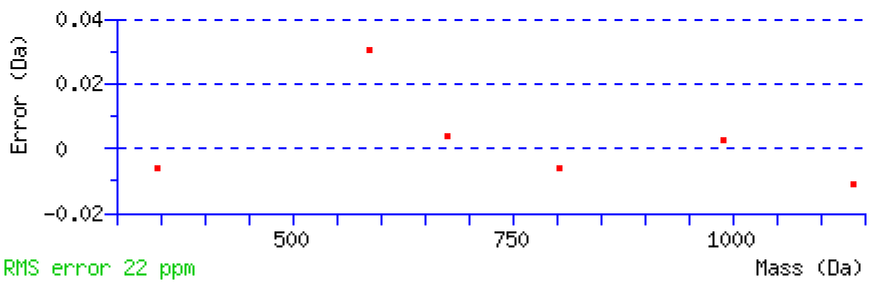
Match to Query 17502: 1248.599948 from(625.307250,2+) rtinseconds(1681) index(5920)
Title: Locus:1.1.1.2151.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

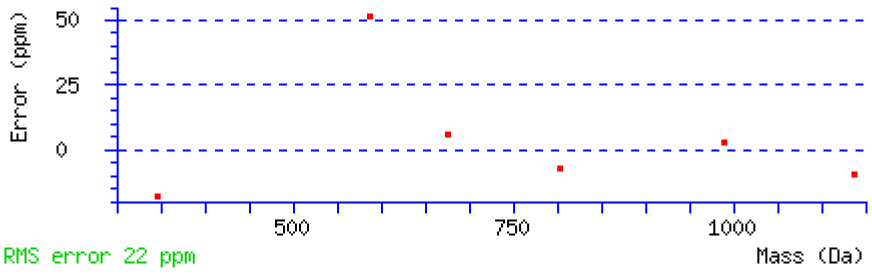
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1248.598618
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00043
Matches : 6/116 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**							12
2	261.159754	131.083515					**F**	*1136.521844*	568.764560	1119.495295	560.251286	1118.511279	559.759278	11
3	318.181218	159.594247					**G**	*989.453430*	495.230353	972.426881	486.717079	971.442865	486.225071	10
4	446.239796	223.623536	429.213247	215.110261			**Q**	932.431966	466.719621	915.405417	458.206347	914.421401	457.714339	9
5	575.282389	288.144833	558.255840	279.631558	557.271824	279.139550	**E**	*804.373388*	402.690332	787.346839	394.177057	786.362823	393.685049	8
6	662.314417	331.660846	645.287868	323.147572	644.303852	322.655564	**S**	*675.330795*	338.169036	658.304246	329.655761	657.320230	329.163753	7
7	719.335881	360.171579	702.309332	351.658304	701.325316	351.166296	**G**	*588.298767*	294.653022	571.272218	286.139747	570.288202	285.647739	6
8	816.388645	408.697961	799.362096	400.184686	798.378080	399.692678	**P**	531.277303	266.142290	514.250754	257.629015	513.266738	257.137007	5
9	903.420673	452.213975	886.394124	443.700700	885.410108	443.208692	**S**	434.224539	217.615907	417.197990	209.102633	416.213974	208.610625	4
10	974.457787	487.732531	957.431238	479.219257	956.447222	478.727249	**A**	*347.192511*	174.099893	330.165962	165.586619	329.181946	165.094611	3
11	1103.500380	552.253828	1086.473831	543.740554	1085.489815	543.248545	**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 LFGQESGPSAEK
(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	1248.598618	0.001330	LFGQESGPSAEK

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

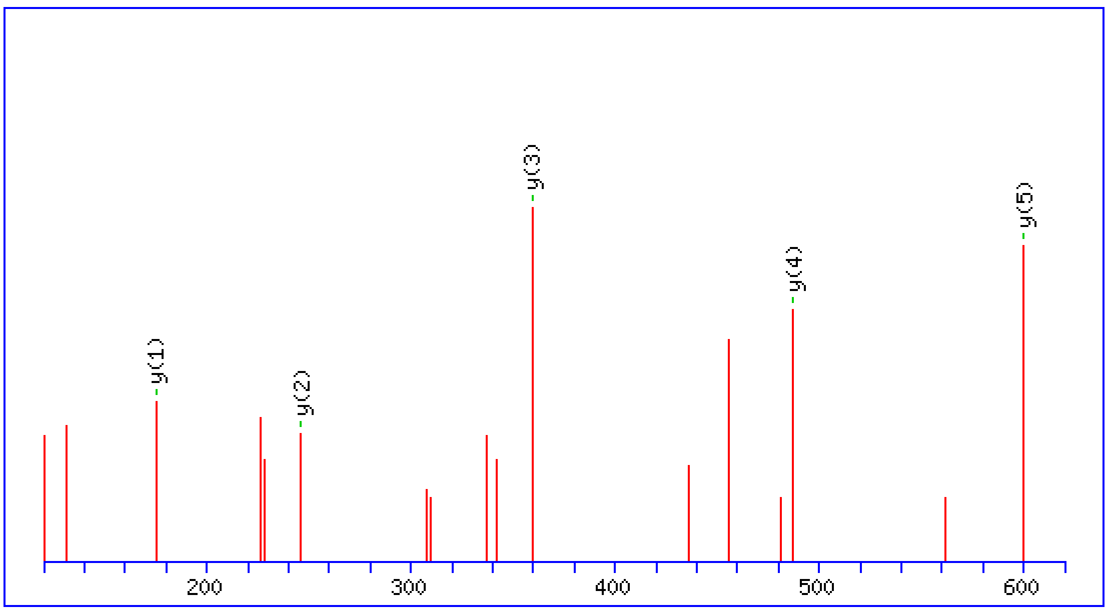
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPLKPAR**
Found in **FYB_HUMAN**, FYN-binding protein OS=Homo sapiens GN=FYB PE=1 SV=2

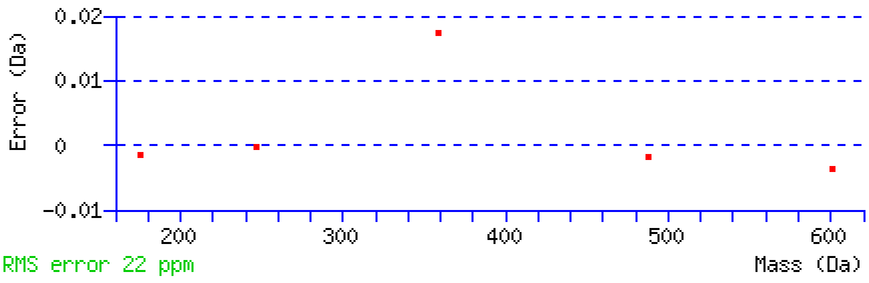
Match to Query 3224: 856.479488 from(429.247020,2+) rtinseconds(2130) index(27249)
Title: Locus:1.1.1.2094.6
Data file 2011-11-14 - TFD - S 2-1.mgf

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 ●

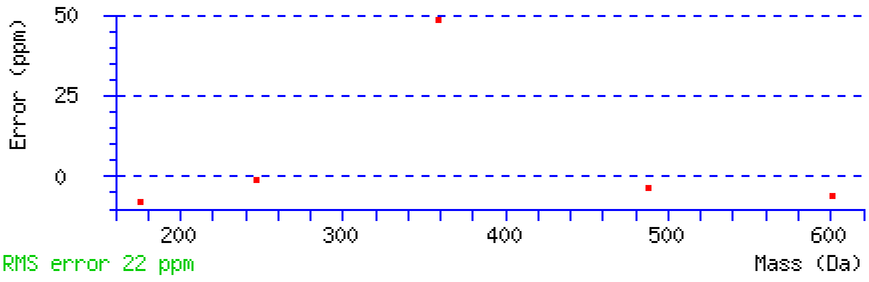


Monoisotopic mass of neutral peptide Mr(calc): 856.476654
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3 : Oxidation (P)
P6 : Oxidation (P)
Ions Score: 34 **Expect:** 0.0056
Matches : 5/62 fragment ions using 10 most intense peaks (help)

#	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	145.060768	73.034022			127.050203	64.028740	**G**	770.451915	385.729596	753.425366	377.216321	7
3	258.108447	129.557862			240.097882	120.552579	**P**	713.430451	357.218864	696.403902	348.705589	6
4	371.192511	186.099894			353.181946	177.094611	**L**	***600.382772***	300.695024	583.356223	292.181750	5
5	499.287474	250.147375	482.260925	241.634101	481.276909	241.142093	**K**	***487.298708***	244.152992	470.272159	235.639718	4
6	612.335153	306.671215	595.308604	298.157940	594.324588	297.665932	**P**	***359.203745***	180.105511	342.177196	171.592236	3
7	683.372267	342.189772	666.345718	333.676497	665.361702	333.184489	**A**	***246.156066***	123.581671	229.129517	115.068397	2
8							**R**	***175.118952***	88.063114	158.092403	79.549840	1



RMS error 22 ppm



RMS error 22 ppm

NCBI **BLAST** search of SGPLKPAR
(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	856.476654	0.002834	SGPLKPAR
34.0	856.487885	-0.008397	TRPKSPR
20.0	856.476639	0.002849	EQLLQAR
18.0	856.476639	0.002849	EQAIGAIR
18.0	856.476654	0.002834	ISGQLSPR
17.5	856.476669	0.002819	GVTIPSQR
17.5	856.487885	-0.008397	TRLAPGSR
12.5	856.476654	0.002834	SPVTNIAR
11.9	856.476654	0.002834	GLVNDLAR
9.5	856.476624	0.002864	NELAALAR

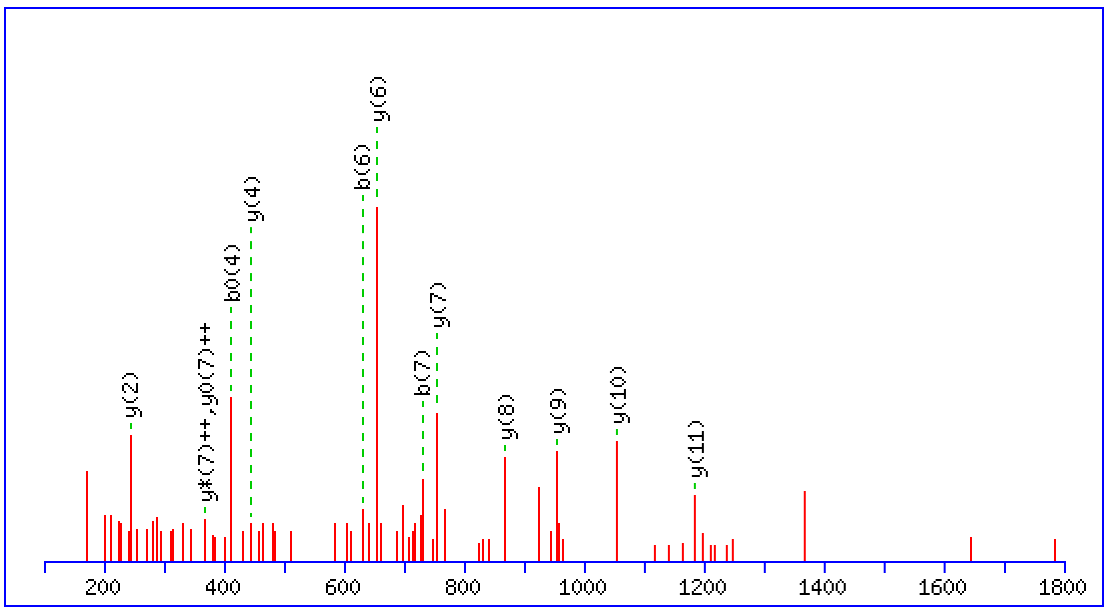
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLETSLVPLSDPK**
Found in **GALK1_HUMAN**, Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1

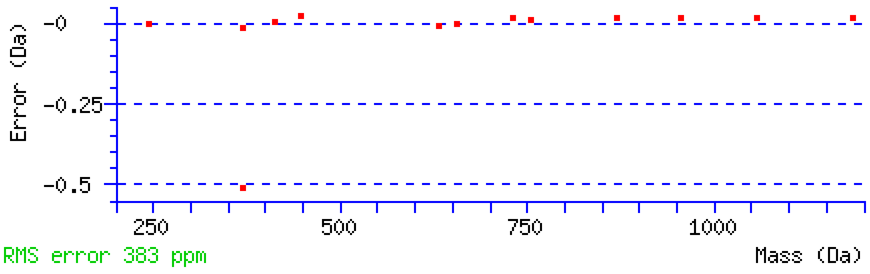
Match to Query 35317: 1384.750108 from(693.382330,2+) rtinseconds(2809) index(35557)
Title: Locus:1.1.1.2468.32
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

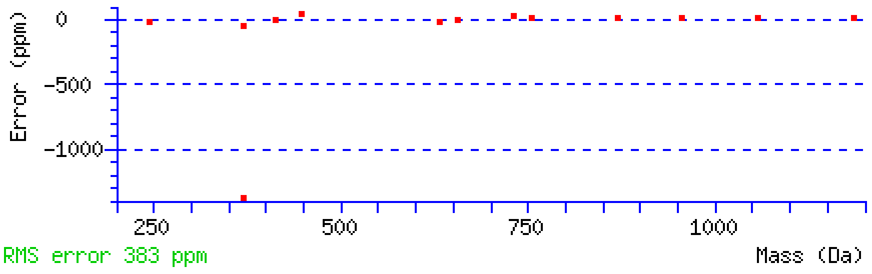
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1384.744949
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.4e-005
Matches : 13/116 fragment ions using 22 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	1298.720209	649.863743	1281.693660	641.350468	1280.709644	640.858460	12
3	330.165961	165.586618	312.155396	156.581336	E	***1185.636145***	593.321711	1168.609596	584.808436	1167.625580	584.316428	11
4	431.213640	216.110458	413.203075	207.105176	T	***1056.593552***	528.800414	1039.567003	520.287140	1038.582987	519.795132	10
5	518.245668	259.626472	500.235103	250.621190	S	***955.545873***	478.276575	938.519324	469.763300	937.535308	469.271292	9
6	**631.329732**	316.168504	613.319167	307.163222	L	***868.513845***	434.760561	851.487296	426.247286	850.503280	425.755278	8
7	**730.398146**	365.702711	712.387581	356.697429	V	***755.429781***	378.218529	738.403232	369.705254	737.419216	369.213246	7
8	827.450910	414.229093	809.440345	405.223811	P	***656.361367***	328.684322	639.334818	320.171047	638.350802	319.679039	6
9	940.534974	470.771125	922.524409	461.765843	L	559.308603	280.157940	542.282054	271.644665	541.298038	271.152657	5
10	1027.567002	514.287139	1009.556437	505.281857	S	***446.224539***	223.615908	429.197990	215.102633	428.213974	214.610625	4
11	1142.593945	571.800611	1124.583380	562.795328	D	359.192511	180.099894	342.165962	171.586619	341.181946	171.094611	3
12	1239.646709	620.326993	1221.636144	611.321710	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 SLETSLVPLSDPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.2	1384.744949	0.005159	SLETSLVPLSDPK
3.2	1384.738403	0.011705	LKEMIPKPEPR
3.2	1384.738403	0.011705	LKEMIPKPEPR
0.5	1384.756195	-0.006087	EVTVTTLAGLPER

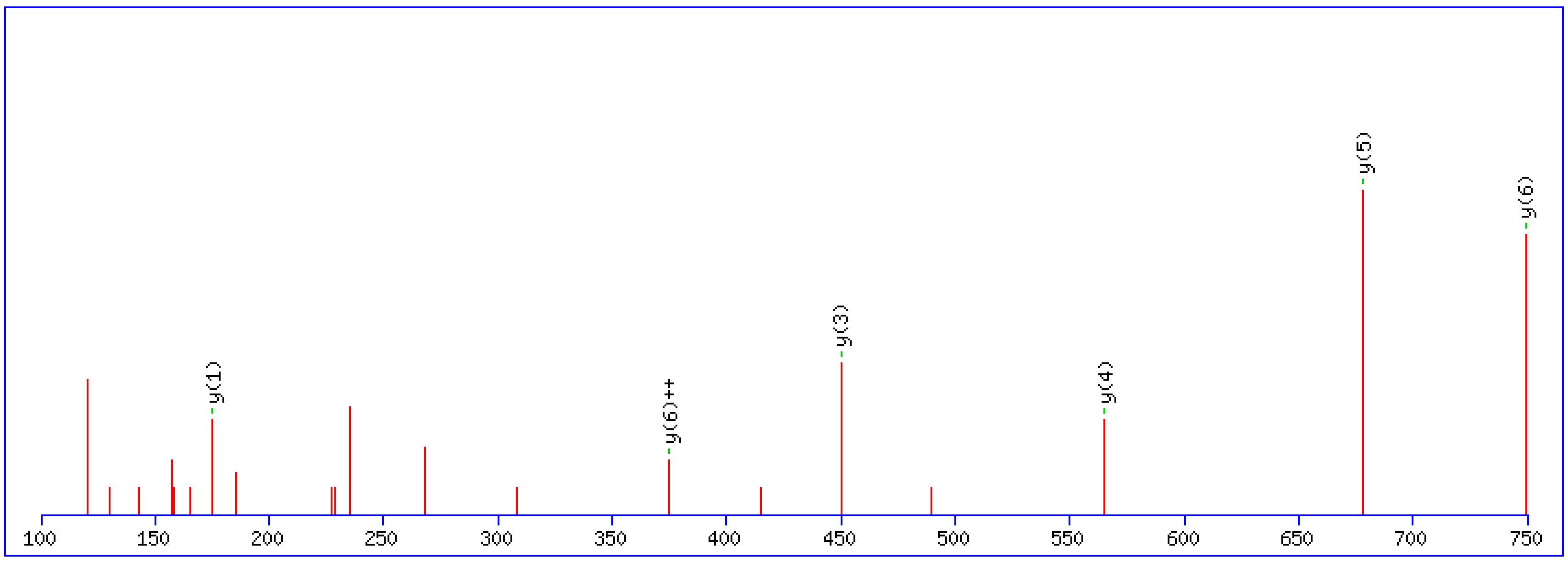
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IALDFQR**
Found in **LEG3_HUMAN**, Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5

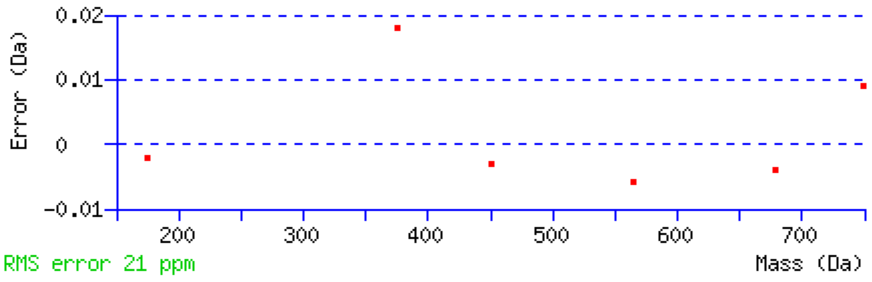
Match to Query 722: 861.469468 from(431.742010,2+) rtinseconds(1857) index(16237)
Title: Locus:1.1.1.1148.4
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 2.mgf

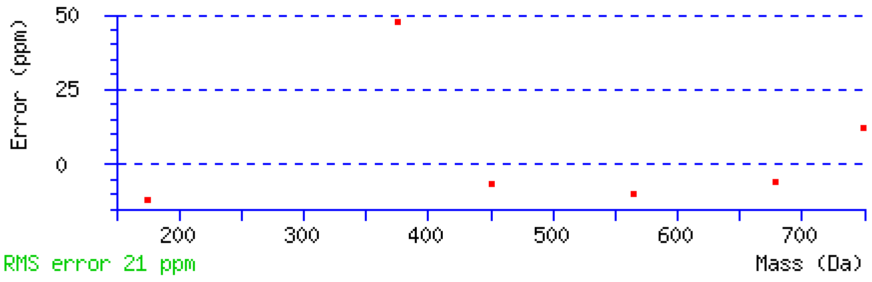
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 861.470840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0075
Matches : 6/50 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					I							7
2	185.128454	93.067865					A	***749.394065***	375.200671	732.367516	366.687396	731.383500	366.195388	6
3	298.212518	149.609897					L	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	5
4	413.239461	207.123369			395.228896	198.118086	D	***565.272887***	283.140082	548.246338	274.626807	547.262322	274.134799	4
5	560.307875	280.657576			542.297310	271.652293	F	***450.245944***	225.626610	433.219395	217.113335			3
6	688.366453	344.686865	671.339904	336.173590	670.355888	335.681582	Q	303.177530	152.092403	286.150981	143.579128			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IALDFQR
(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	861.470840	-0.001372	IALDFQR
20.3	861.470825	-0.001357	LAPYNIR
10.6	861.474197	-0.004729	LMNLISR
10.4	861.470840	-0.001372	IADFGLAR
10.4	861.470840	-0.001372	LADFGLAR
10.2	861.470825	-0.001357	IAEFLNR
8.4	861.474213	-0.004745	LLTQMTR
8.0	861.470840	-0.001372	LLFPSNR
8.0	861.474213	-0.004745	LMLSVAGR
5.1	861.462967	0.006501	LIMDNIK

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

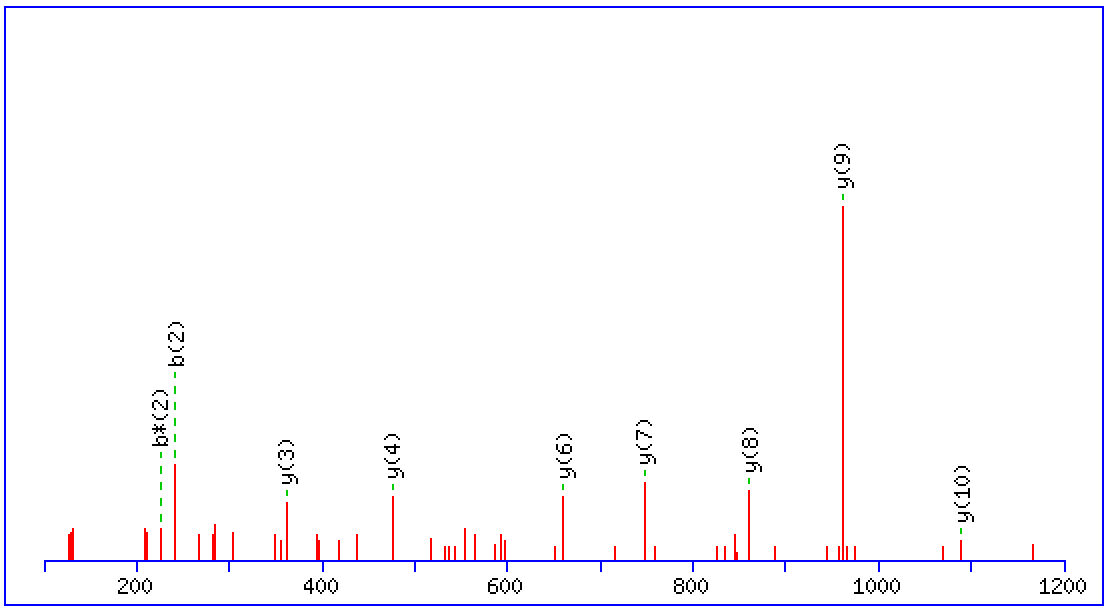
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQTLSAIDTIK**
Found in **LEGL_HUMAN**, Galectin-related protein OS=Homo sapiens GN=GRP PE=1 SV=2

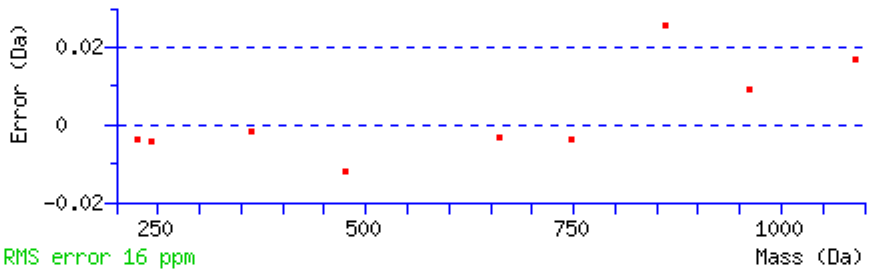
Match to Query 19083: 1201.693668 from(601.854110,2+) rtinseconds(2536) index(22521)
Title: Locus:1.1.1.2463.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

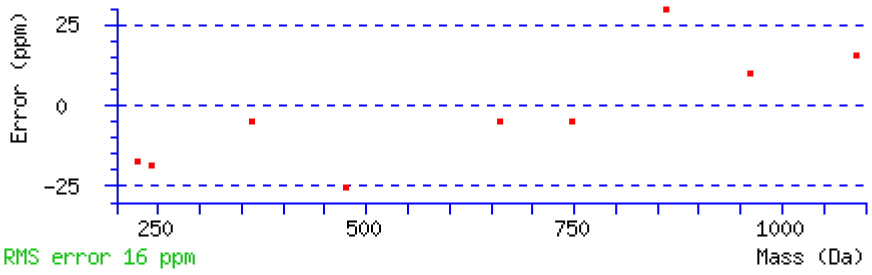
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1201.691788
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 6e-006
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	114.091340	57.549308					I							11
2	242.149918	121.578597	225.123369	113.065323			Q	*1089.615017*	545.311147	1072.588468	536.797872	1071.604452	536.305864	10
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	T	*961.556439*	481.281858	944.529890	472.768583	943.545874	472.276575	9
4	456.281661	228.644469	439.255112	220.131194	438.271096	219.639186	L	*860.508760*	430.758018	843.482211	422.244743	842.498195	421.752735	8
5	543.313689	272.160483	526.287140	263.647208	525.303124	263.155200	S	*747.424696*	374.215986	730.398147	365.702711	729.414131	365.210703	7
6	614.350803	307.679040	597.324254	299.165765	596.340238	298.673757	A	*660.392668*	330.699972	643.366119	322.186697	642.382103	321.694689	6
7	727.434867	364.221072	710.408318	355.707797	709.424302	355.215789	I	589.355554	295.181415	572.329005	286.668140	571.344989	286.176132	5
8	842.461810	421.734543	825.435261	413.221269	824.451245	412.729261	D	*476.271490*	238.639383	459.244941	230.126108	458.260925	229.634100	4
9	943.509489	472.258383	926.482940	463.745108	925.498924	463.253100	T	*361.244547*	181.125911	344.217998	172.612637	343.233982	172.120629	3
10	1056.593553	528.800414	1039.567004	520.287140	1038.582988	519.795132	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 IQTLSAIDTIK
(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	1201.691788	0.001880	IQTLSAIDTIK
0.7	1201.681900	0.011768	LKPVADRFPK
0.4	1201.681885	0.011783	QLDVLYPKAR

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

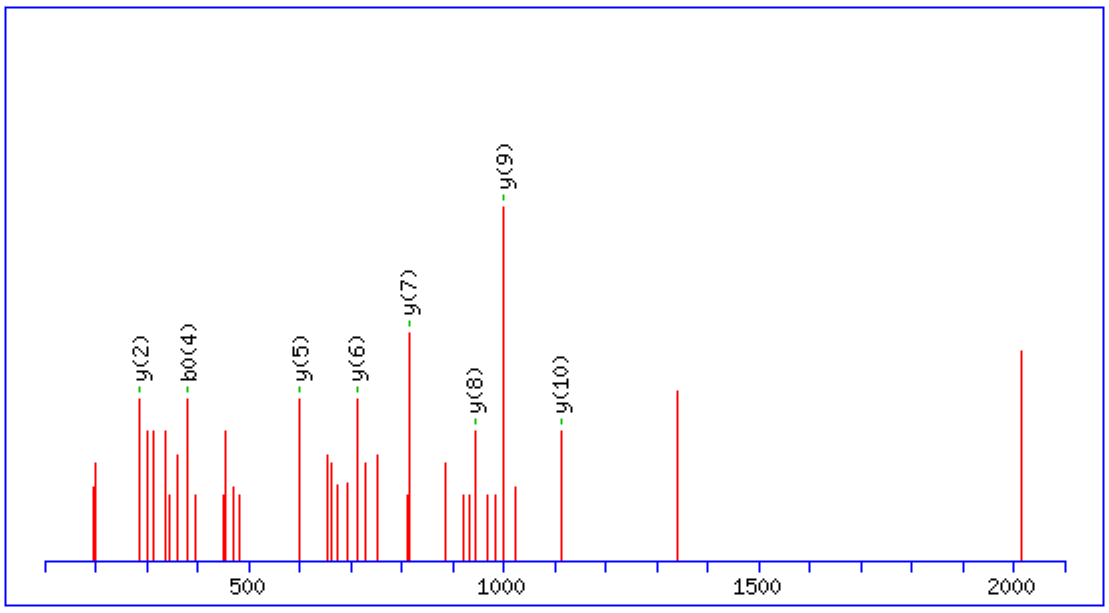
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLLGETLAQLIR**
Found in **GGT5_HUMAN**, Gamma-glutamyltransferase 5 OS=Homo sapiens GN=GGT5 PE=1 SV=2

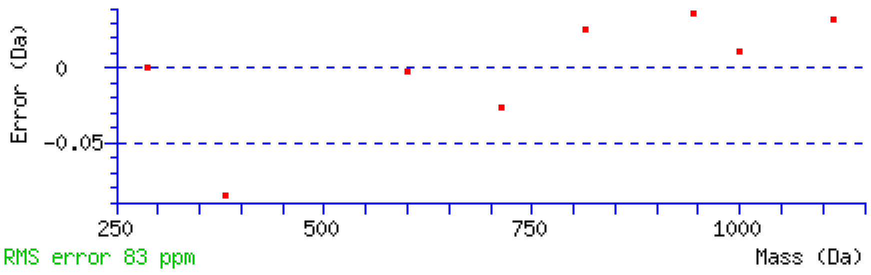
Match to Query 38834: 1340.776568 from(671.395560,2+) rtinseconds(4607) index(72096)
Title: Locus:1.1.1.3085.17
Data file 2011-11-14 - TFD - S 2-3.mgf

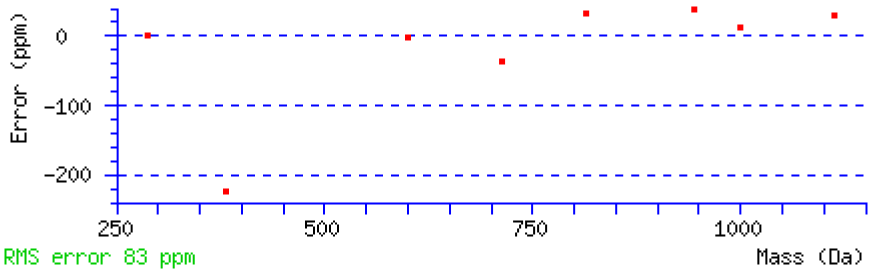
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1340.766342
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 6.9e-006
Matches : 8/104 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	116.034219	58.520748			98.023654	49.515465	D							12
2	229.118283	115.062779			211.107718	106.057497	L	1226.746700	613.876988	1209.720151	605.363713	1208.736135	604.871705	11
3	342.202347	171.604811			324.191782	162.599529	L	***1113.662636***	557.334956	1096.636087	548.821681	1095.652071	548.329673	10
4	399.223811	200.115543			381.213246	191.110261	G	***1000.578572***	500.792924	983.552023	492.279649	982.568007	491.787641	9
5	528.266404	264.636840			510.255839	255.631557	E	***943.557108***	472.282192	926.530559	463.768917	925.546543	463.276909	8
6	629.314083	315.160680			611.303518	306.155397	T	***814.514515***	407.760895	797.487966	399.247621	796.503950	398.755613	7
7	742.398147	371.702712			724.387582	362.697429	L	***713.466836***	357.237056	696.440287	348.723781			6
8	813.435261	407.221269			795.424696	398.215986	A	***600.382772***	300.695024	583.356223	292.181749			5
9	941.493839	471.250558	924.467290	462.737283	923.483274	462.245275	Q	529.345658	265.176467	512.319109	256.663192			4
10	1054.577903	527.792589	1037.551354	519.279315	1036.567338	518.787307	L	401.287080	201.147178	384.260531	192.633903			3
11	1167.661967	584.334621	1150.635418	575.821347	1149.651402	575.329339	I	***288.203016***	144.605146	271.176467	136.091871			2
12							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DLLGETLAQLIR
(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	1340.766342	0.010226	DLLGETLAQLIR

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

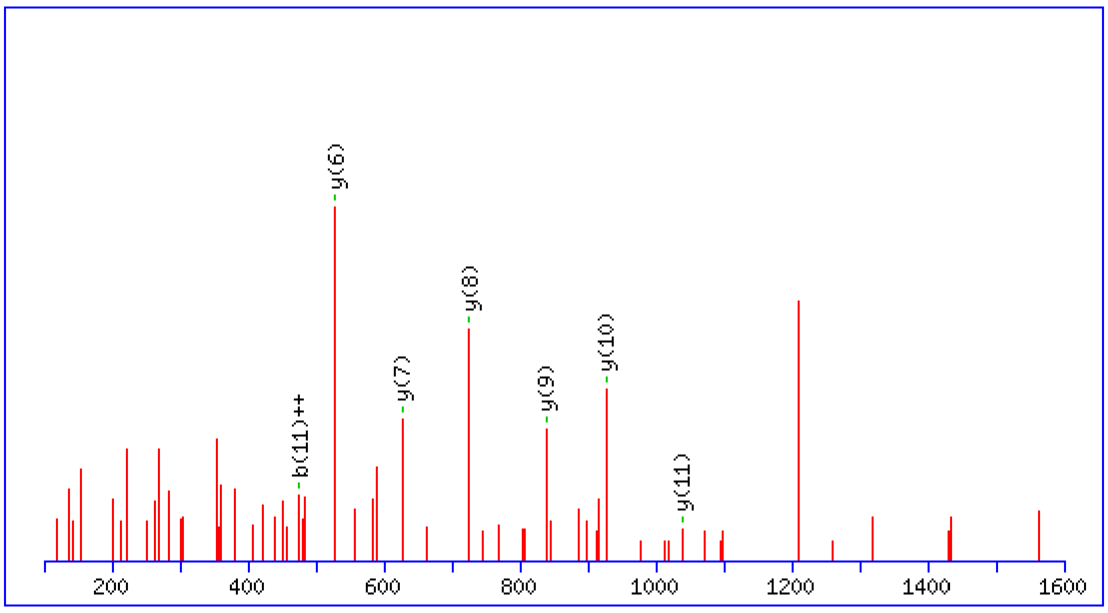
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGLSLVVPGGGIK**
Found in **SNAG_HUMAN**, Gamma-soluble NSF attachment protein OS=Homo sapiens GN=NAPG PE=1 SV=1

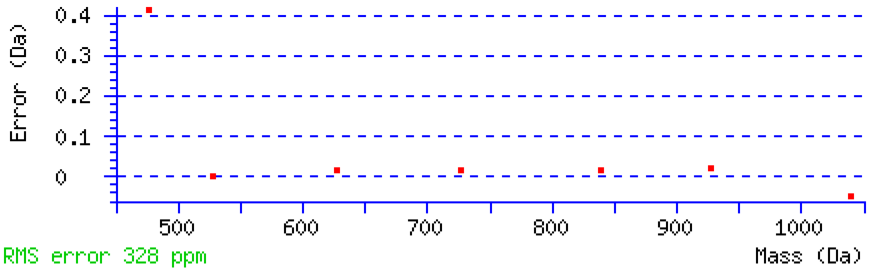
Match to Query 24485: 1208.753908 from(605.384230,2+) rtinseconds(3256) index(42698)
Title: Locus:1.1.1.2823.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

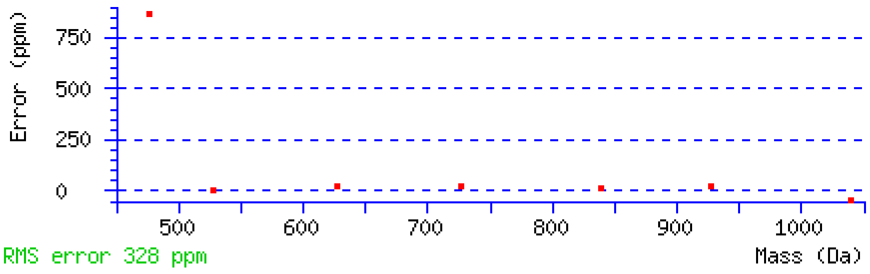
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1208.749268
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00011
Matches : 7/96 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			L							13
2	171.112804	86.060040			G	1096.672472	548.839874	1079.645923	540.326600	1078.661907	539.834592	12
3	284.196868	142.602072			L	***1039.651008***	520.329142	1022.624459	511.815868	1021.640443	511.323860	11
4	371.228896	186.118086	353.218331	177.112804	S	***926.566944***	463.787110	909.540395	455.273836	908.556379	454.781828	10
5	484.312960	242.660118	466.302395	233.654836	L	***839.534916***	420.271096	822.508367	411.757822			9
6	583.381374	292.194325	565.370809	283.189043	V	***726.450852***	363.729064	709.424303	355.215790			8
7	682.449788	341.728532	664.439223	332.723250	V	***627.382438***	314.194857	610.355889	305.681583			7
8	779.502552	390.254914	761.491987	381.249632	P	***528.314024***	264.660650	511.287475	256.147376			6
9	836.524016	418.765646	818.513451	409.760364	G	431.261260	216.134268	414.234711	207.620994			5
10	893.545480	447.276378	875.534915	438.271096	G	374.239796	187.623536	357.213247	179.110261			4
11	950.566944	475.787110	932.556379	466.781828	G	317.218332	159.112804	300.191783	150.599529			3
12	1063.651008	532.329142	1045.640443	523.323860	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 LGLSLVVPGGGIK
(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	1208.749268	0.004640	LGLSLVVPGGGIK

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

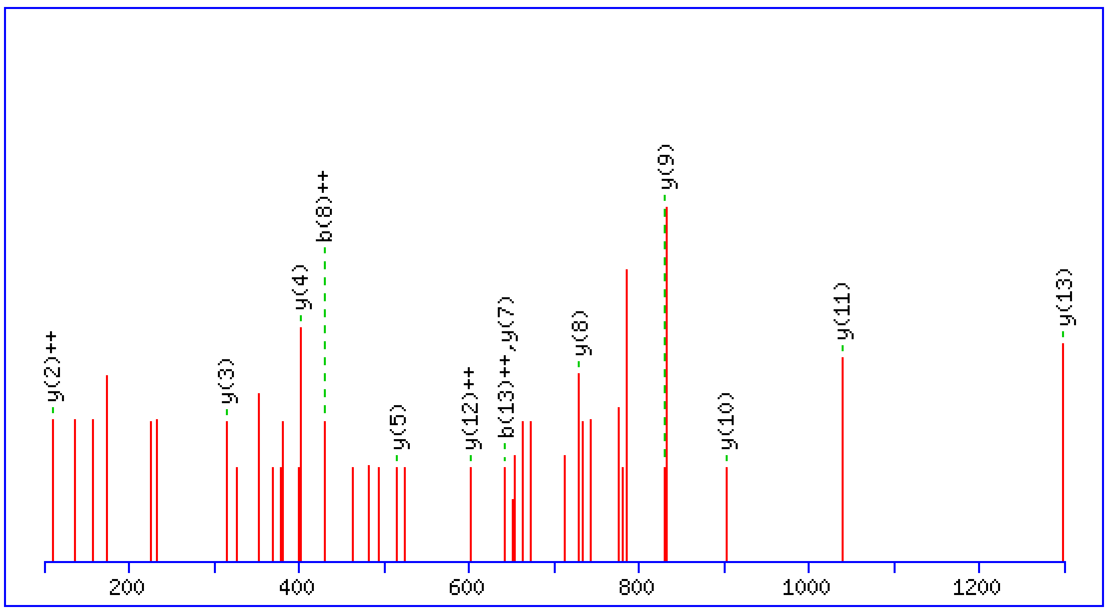
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDPYHATSGALSPAK**
Found in **CXA1_HUMAN**, Gap junction alpha-1 protein OS=Homo sapiens GN=GJA1 PE=1 SV=2

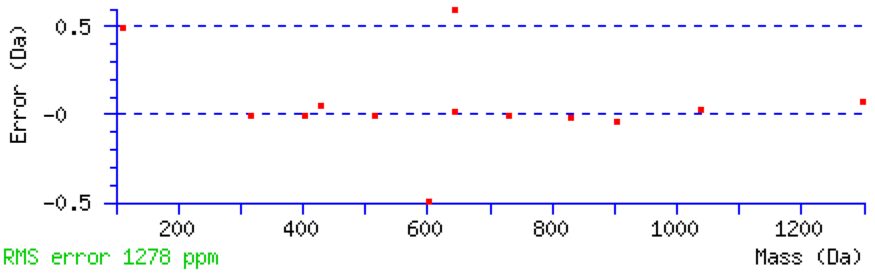
Match to Query 50959: 1500.720042 from(501.247290,3+) rtinseconds(1499) index(11894)
Title: Locus:1.1.1.1935.26
Data file 2011-11-14 - TFD - S 2-4.mgf

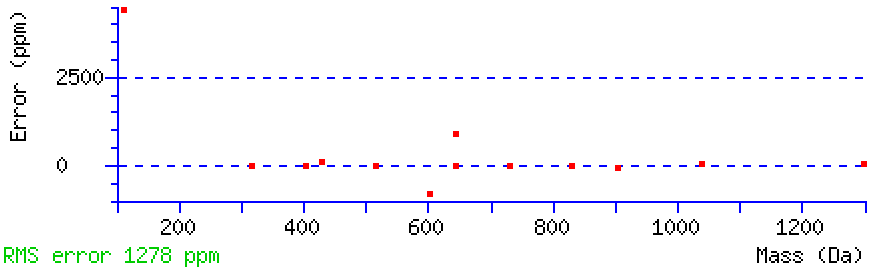
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1500.720856
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00016
Matches : 13/134 fragment ions using 30 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							15
2	203.066247	102.036761	185.055682	93.031479	D	1414.696121	707.851699	1397.669572	699.338424	1396.685556	698.846416	14
3	300.119011	150.563143	282.108446	141.557861	P	***1299.669178***	650.338227	1282.642629	641.824953	1281.658613	641.332945	13
4	463.182340	232.094808	445.171775	223.089525	Y	1202.616414	601.811845	1185.589865	593.298571	1184.605849	592.806563	12
5	600.241252	300.624264	582.230687	291.618982	H	***1039.553085***	520.280181	1022.526536	511.766906	1021.542520	511.274898	11
6	671.278366	336.142821	653.267801	327.137539	A	***902.494173***	451.750725	885.467624	443.237450	884.483608	442.745442	10
7	772.326045	386.666661	754.315480	377.661378	T	***831.457059***	416.232168	814.430510	407.718893	813.446494	407.226885	9
8	859.358073	**430.182675**	841.347508	421.177392	S	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	8
9	916.379537	458.693407	898.368972	449.688124	G	***643.377352***	322.192314	626.350803	313.679040	625.366787	313.187032	7
10	987.416651	494.211964	969.406086	485.206681	A	586.355888	293.681582	569.329339	285.168308	568.345323	284.676300	6
11	1100.500715	550.753995	1082.490150	541.748713	L	***515.318774***	258.163025	498.292225	249.649751	497.308209	249.157743	5
12	1187.532743	594.270010	1169.522178	585.264727	S	***402.234710***	201.620993	385.208161	193.107719	384.224145	192.615711	4
13	1284.585507	**642.796392**	1266.574942	633.791109	P	***315.202682***	158.104979	298.176133	149.591704			3
14	1355.622621	678.314949	1337.612056	669.309666	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 SDPYHATSGALSPAK
(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	1500.720856	-0.000814	SDPYHATSGALSPAK
8.3	1500.716812	0.003230	QPEEEETAVARAR

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

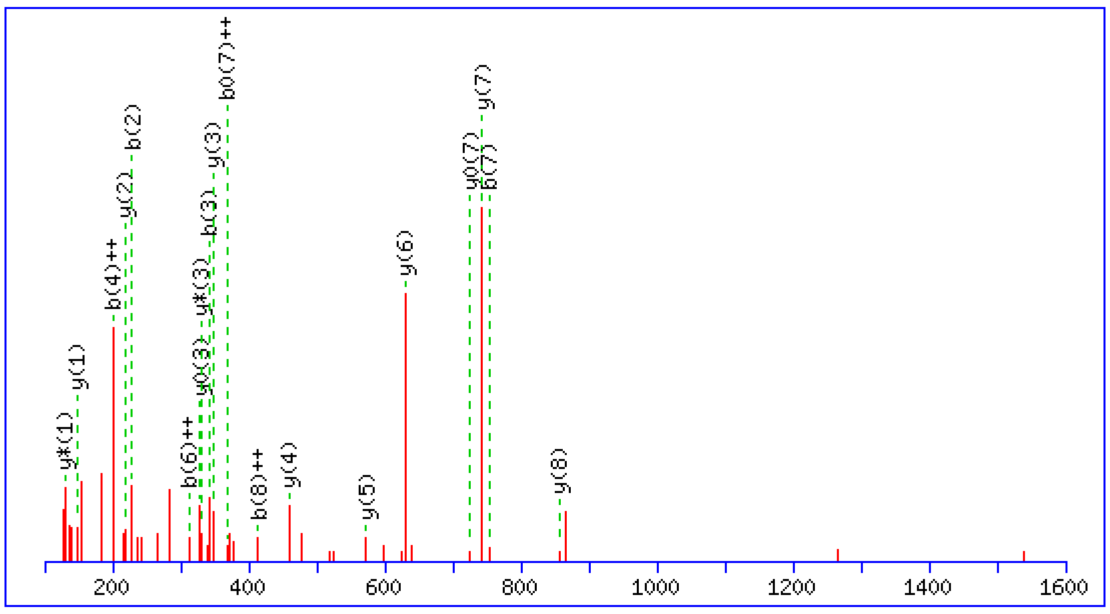
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLLGLIEAK**
Found in **GRP_HUMAN**, Gastrin-releasing peptide OS=Homo sapiens GN=GRP PE=1 SV=2

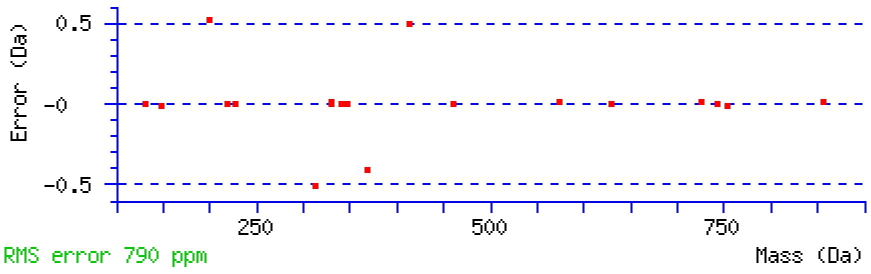
Match to Query 5226: 969.584088 from(485.799320,2+) rtinseconds(3292) index(12752)
Title: Locus:1.1.1.3266.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

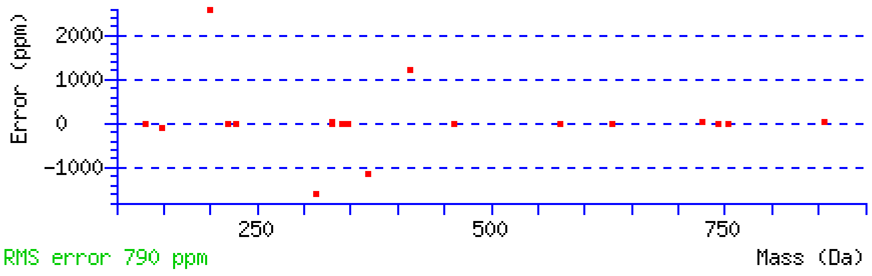
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 969.585846
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 1.1e-005
Matches : 19/80 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	115.050203	58.028740	98.023654	49.515465			N							9
2	**228.134267**	114.570771	211.107718	106.057497			L	***856.550231***	428.778754	839.523682	420.265479	838.539666	419.773471	8
3	**341.218331**	171.112803	324.191782	162.599529			L	***743.466167***	372.236722	726.439618	363.723447	725.455602	363.231439	7
4	398.239795	**199.623535**	381.213246	191.110261			G	***630.382103***	315.694690	613.355554	307.181415	612.371538	306.689407	6
5	511.323859	256.165568	494.297310	247.652293			L	***573.360639***	287.183958	556.334090	278.670683	555.350074	278.178675	5
6	624.407923	**312.707600**	607.381374	304.194325			I	***460.276575***	230.641925	443.250026	222.128651	442.266010	221.636643	4
7	**753.450516**	377.228896	736.423967	368.715622	735.439951	368.223614	E	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
8	824.487630	**412.747453**	807.461081	404.234178	806.477065	403.742170	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 NLLGLIEAK
(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	969.585846	-0.001758	NLLGLIEAK
16.2	969.585861	-0.001773	NILPITTAK
9.3	969.585861	-0.001773	KIVVEAPAK
2.4	969.585846	-0.001758	ELKNLIPK
1.4	969.585861	-0.001773	QTALAPLIK
0.7	969.585861	-0.001773	EKPIVKPK
0.3	969.585876	-0.001788	QLSVPVIAK

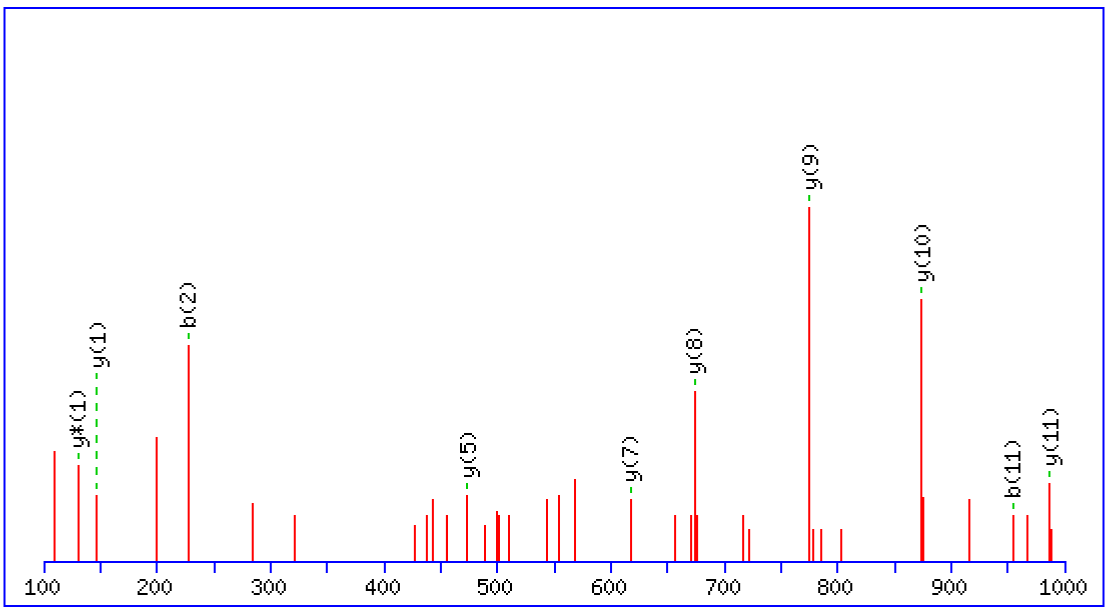
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILVTGGSGLVGK**
Found in **FCL_HUMAN**, GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1

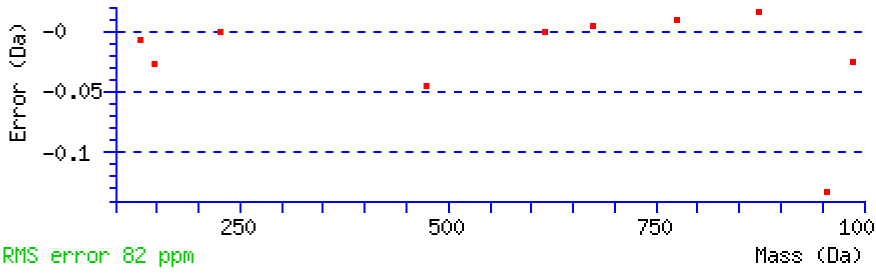
Match to Query 18839: 1099.663848 from(550.839200,2+) rtinseconds(2112) index(22444)
Title: Locus:1.1.1.2204.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

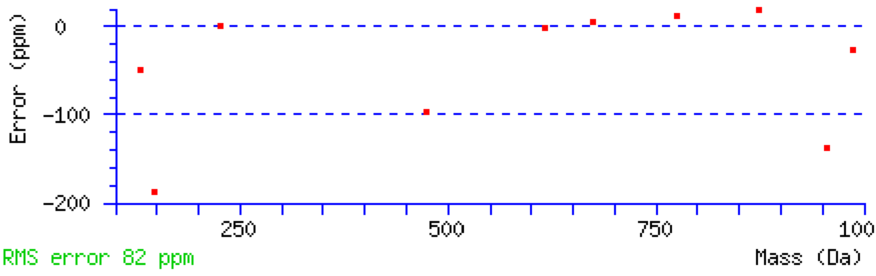
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1099.660126
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0026
Matches : 10/94 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			I							12
2	**227.175404**	114.091340			L	***987.583323***	494.295300	970.556774	485.782025	969.572758	485.290017	11
3	326.243818	163.625547			V	***874.499259***	437.753268	857.472710	429.239993	856.488694	428.747985	10
4	427.291497	214.149386	409.280932	205.144104	T	***775.430845***	388.219061	758.404296	379.705786	757.420280	379.213778	9
5	484.312961	242.660118	466.302396	233.654836	G	***674.383166***	337.695221	657.356617	329.181947	656.372601	328.689939	8
6	541.334425	271.170851	523.323860	262.165568	G	***617.361702***	309.184489	600.335153	300.671215	599.351137	300.179207	7
7	628.366453	314.686865	610.355888	305.681582	S	560.340238	280.673757	543.313689	272.160483	542.329673	271.668475	6
8	685.387917	343.197597	667.377352	334.192314	G	***473.308210***	237.157743	456.281661	228.644469			5
9	798.471981	399.739629	780.461416	390.734346	L	416.286746	208.647011	399.260197	200.133737			4
10	897.540395	449.273836	879.529830	440.268553	V	303.202682	152.104979	286.176133	143.591705			3
11	**954.561859**	477.784568	936.551294	468.779285	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 ILVTGGSGLVGK
(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	1099.660126	0.003722	ILVTGGSGLVGK
4.3	1099.660095	0.003753	ILIIGNSSVGK
4.3	1099.660095	0.003753	LLIIGNSSVGK
4.3	1099.660095	0.003753	LLLIGNSSVGK
3.8	1099.660080	0.003768	LLTKQAGEIK

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

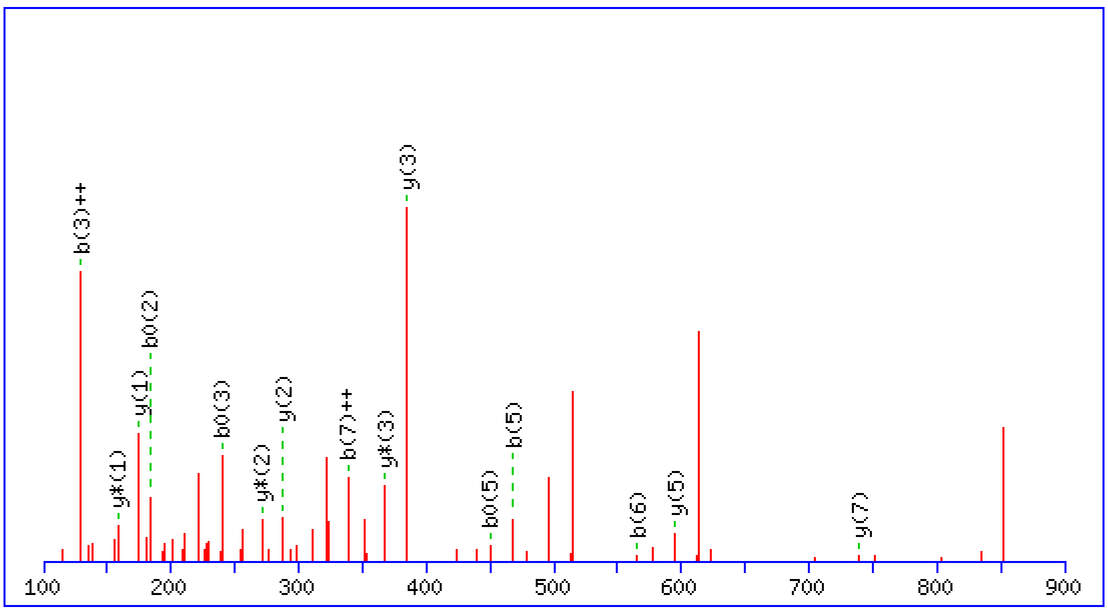
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSGPLPPR**
Found in **GMIP_HUMAN**, GEM-interacting protein OS=Homo sapiens GN=GMIP PE=1 SV=2

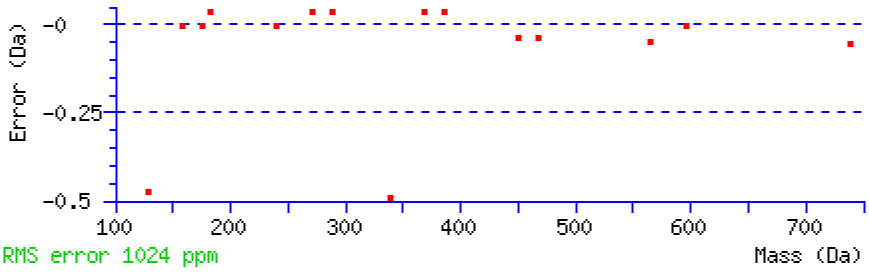
Match to Query 2865: 851.486508 from(426.750530,2+) rtinseconds(1409) index(8306)
Title: Locus:1.1.1.2035.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

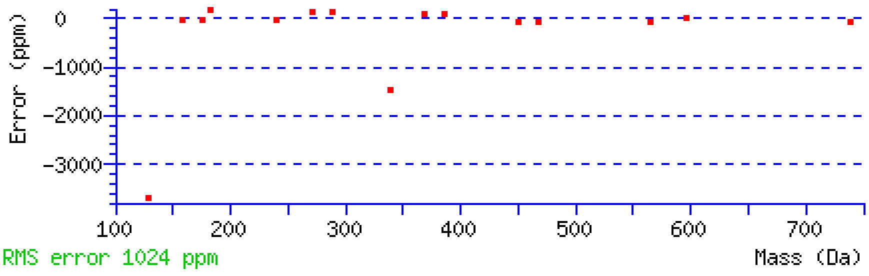
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 851.486496
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
Ions Score: 32  Expect: 0.0017
Matches : 15/56 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							8
2	201.123368	101.065322	183.112803	92.060039	S	***739.409715***	370.208496	722.383166	361.695221	721.399150	361.203213	7
3	258.144832	**129.576054**	240.134267	120.570771	G	652.377687	326.692482	635.351138	318.179207			6
4	355.197596	178.102436	337.187031	169.097153	P	***595.356223***	298.181750	578.329674	289.668475			5
5	**468.281660**	234.644468	450.271095	225.639185	L	498.303459	249.655368	481.276910	241.142093			4
6	**565.334424**	283.170850	547.323859	274.165568	P	***385.219395***	193.113336	368.192846	184.600061			3
7	678.382103	**339.694690**	660.371538	330.689407	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 LSGPLPPR
(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	851.486496	0.000012	LSGPLPPR
15.7	851.486496	0.000012	LSGPLPPR
14.0	851.486496	0.000012	LPQLPPR
11.7	851.486496	0.000012	LPQLPPR
11.3	851.486496	0.000012	AAVPLPPR
8.3	851.486496	0.000012	AAVPLPPR
4.9	851.486496	0.000012	LSGPLPPR
0.5	851.486496	0.000012	LPQLPPR

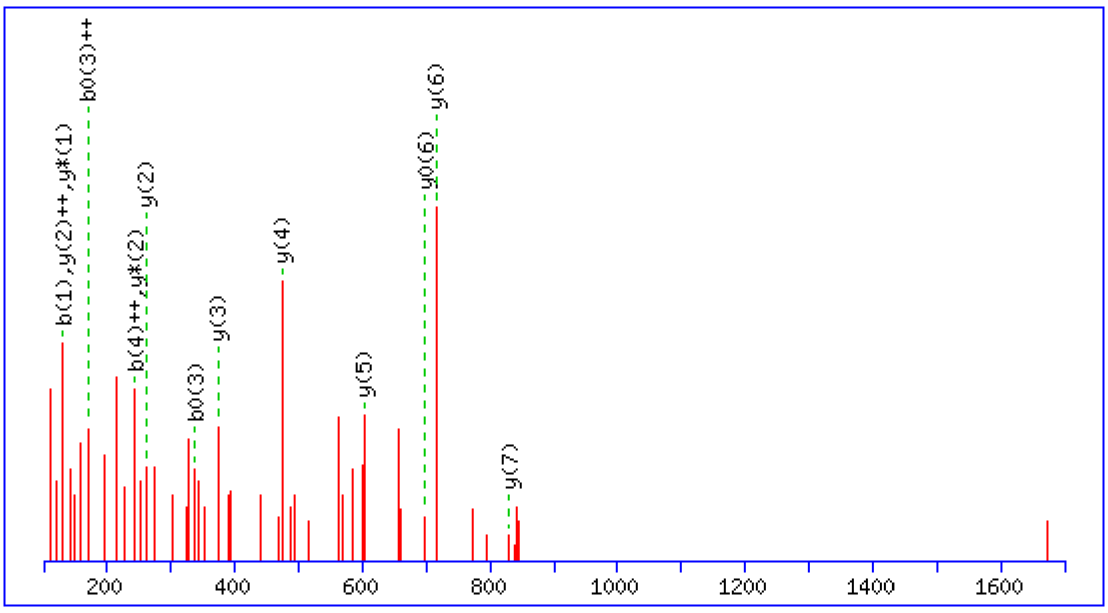
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILETLIK**
Found in **GFPT1_HUMAN**, Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3

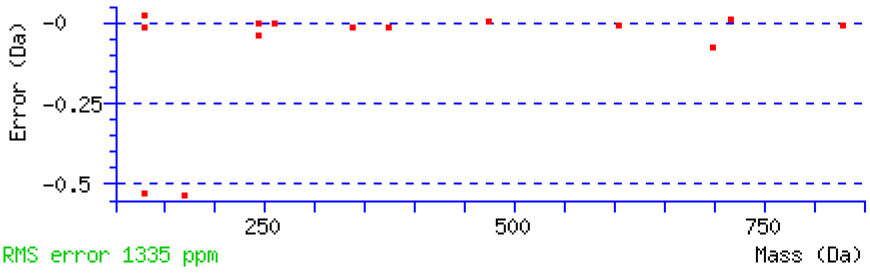
Match to Query 8907: 957.569068 from(479.791810,2+) rtinseconds(2814) index(40284)
Title: Locus:1.1.1.1717.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

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 ●

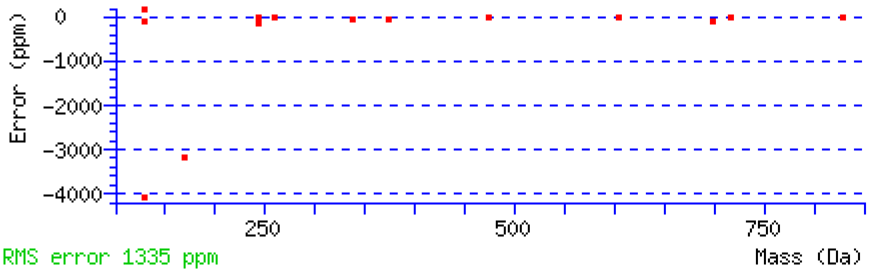


Monoisotopic mass of neutral peptide Mr(calc): 957.574615
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0031
Matches : 15/64 fragment ions using 24 most intense peaks (help)

#	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	**243.133933**	122.070605	225.123368	113.065322	I	***829.539332***	415.273304	812.512783	406.760030	811.528767	406.268022	7
3	356.217997	178.612637	338.207432	169.607354	L	***716.455268***	358.731272	699.428719	350.217998	698.444703	349.725990	6
4	485.260590	243.133933	467.250025	234.128651	E	***603.371204***	302.189240	586.344655	293.675966	585.360639	293.183958	5
5	586.308269	293.657773	568.297704	284.652490	T	***474.328611***	237.667944	457.302062	229.154669	456.318046	228.662661	4
6	699.392333	350.199805	681.381768	341.194522	L	***373.280932***	187.144104	356.254383	178.630830			3
7	812.476397	406.741837	794.465832	397.736554	I	***260.196868***	130.602072	243.170319	122.088798			2
8					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1335 ppm



RMS error 1335 ppm

NCBI **BLAST** search of EILETLIK
(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	957.574615	-0.005547	EILETLIK
8.6	957.574615	-0.005547	ELITILEK
3.2	957.560715	0.008353	RALGSPTLK
1.9	957.560715	0.008353	QGTNKGLIK
0.1	957.568115	0.000953	VPIKMQVK

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

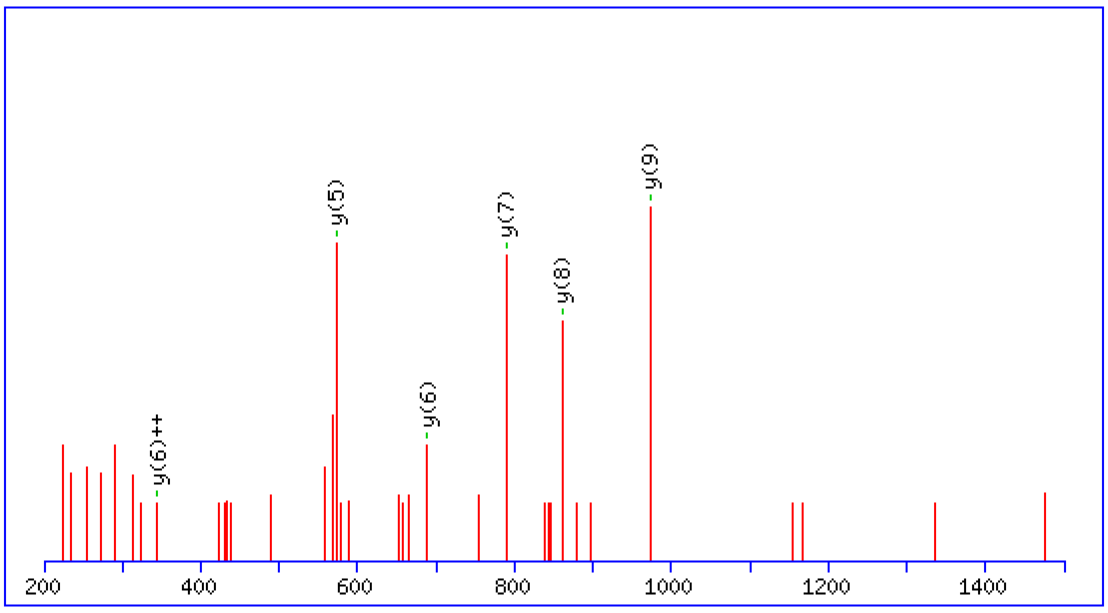
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLATDPDADR**
Found in **PGM2L_HUMAN**, Glucose 1,6-bisphosphate synthase OS=Homo sapiens GN=PGM2L1 PE=1 SV=3

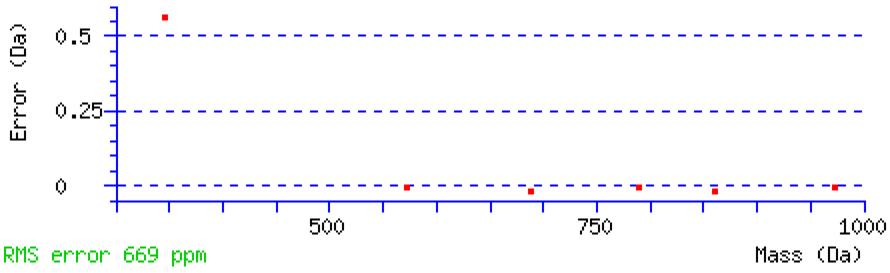
Match to Query 20229: 1170.587468 from(586.301010,2+) rtinseconds(1555) index(13920)
Title: Locus:1.1.1.2072.26
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

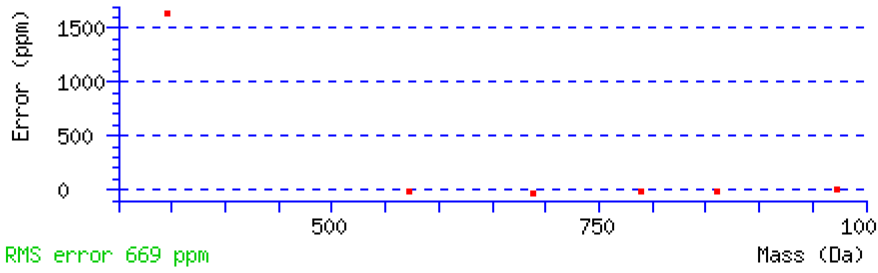
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1170.588074
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00071
Matches : 6/90 fragment ions using 9 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	1072.526930	536.767103	1055.500381	528.253829	1054.516365	527.761821	10
3	312.228168	156.617722			L	***973.458516***	487.232896	956.431967	478.719622	955.447951	478.227614	9
4	383.265282	192.136279			A	***860.374452***	430.690864	843.347903	422.177590	842.363887	421.685582	8
5	484.312961	242.660119	466.302396	233.654836	T	***789.337338***	395.172307	772.310789	386.659033	771.326773	386.167025	7
6	599.339904	300.173590	581.329339	291.168308	D	***688.289659***	344.648468	671.263110	336.135193	670.279094	335.643185	6
7	696.392668	348.699972	678.382103	339.694690	P	***573.262716***	287.134996	556.236167	278.621722	555.252151	278.129714	5
8	811.419611	406.213444	793.409046	397.208161	D	476.209952	238.608614	459.183403	230.095339	458.199387	229.603331	4
9	882.456725	441.732001	864.446160	432.726718	A	361.183009	181.095142	344.156460	172.581868	343.172444	172.089860	3
10	997.483668	499.245472	979.473103	490.240189	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VVLATDPDADR
(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	1170.588074	-0.000606	VVLATDPDADR

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

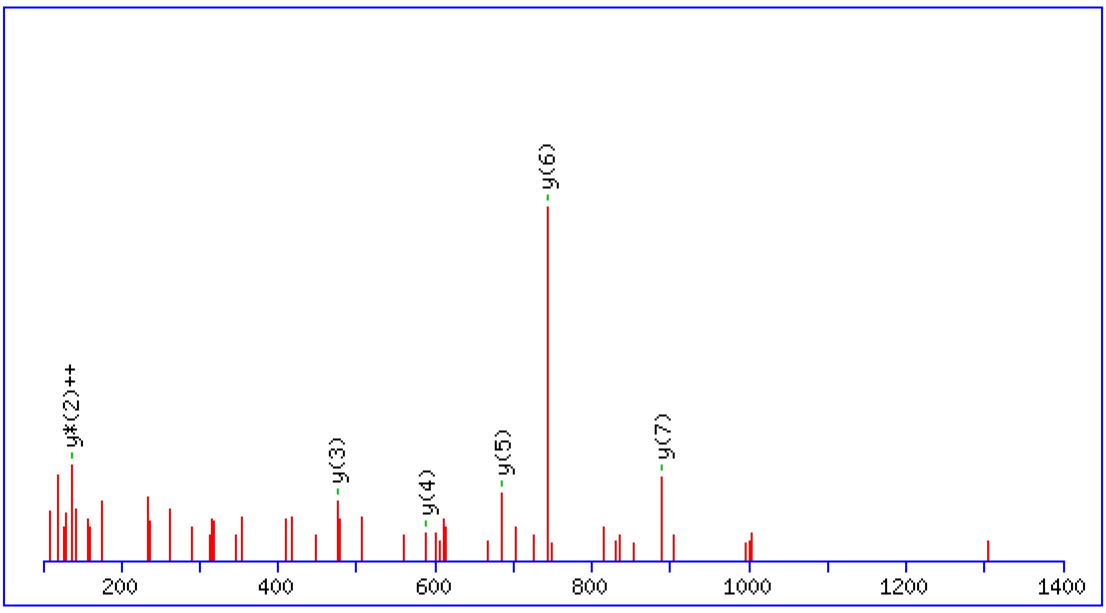
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFGPIWNR**
Found in **G6PD_HUMAN**, Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4

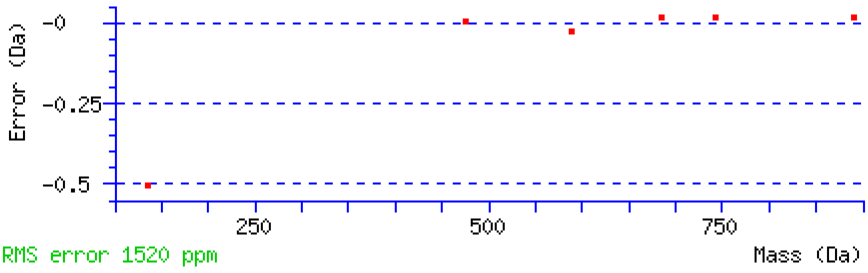
Match to Query 8066: 1001.549268 from(501.781910,2+) rtinseconds(2826) index(38939)
Title: Locus:1.1.1.2558.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

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 ●

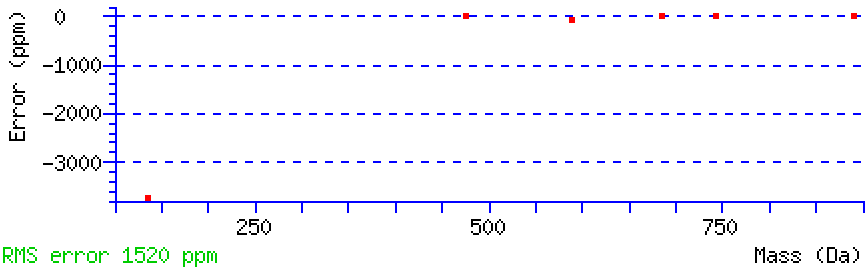


```
Monoisotopic mass of neutral peptide Mr(calc): 1001.544678
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.00069
Matches : 6/44 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			I					8
2	261.159754	131.083515			F	***889.467898***	445.237587	872.441349	436.724313	7
3	318.181218	159.594247			G	***742.399484***	371.703380	725.372935	363.190106	6
4	415.233982	208.120629			P	***685.378020***	343.192648	668.351471	334.679374	5
5	528.318046	264.662661			I	***588.325256***	294.666266	571.298707	286.152992	4
6	714.397359	357.702318			W	***475.241192***	238.124234	458.214643	229.610959	3
7	828.440286	414.723781	811.413737	406.210507	N	289.161879	145.084577	272.135330	136.571303	2
8					R	175.118952	88.063114	158.092403	79.549839	1



RMS error 1520 ppm



RMS error 1520 ppm

NCBI **BLAST** search of IFGPIWNR
(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	1001.544678	0.004590	IFGPIWNR
2.1	1001.540665	0.008603	GLFPGPSRR

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

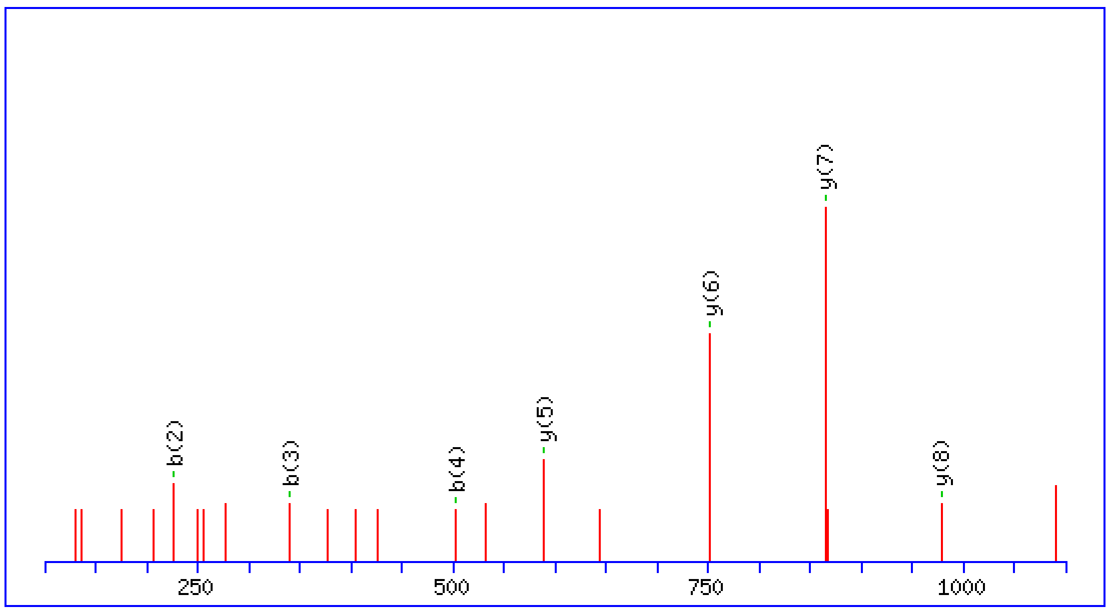
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIIYTNNLK**
Found in **GRCR2_HUMAN**, Glutaredoxin domain-containing cysteine-rich protein 2 OS=Homo sapiens GN=GRXCR2 PE=3 SV=1

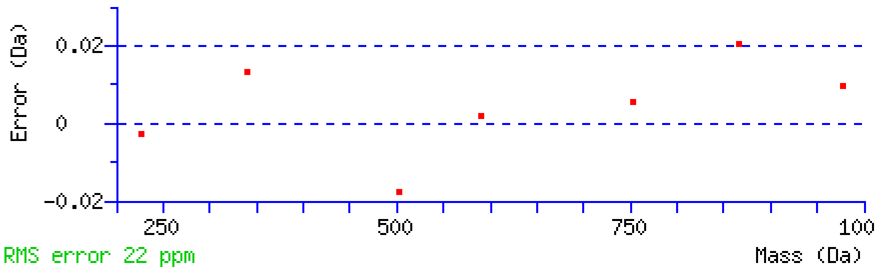
Match to Query 13347: 1090.632568 from(546.323560,2+) rtinseconds(3132) index(35571)
Title: Locus:1.1.1.2838.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

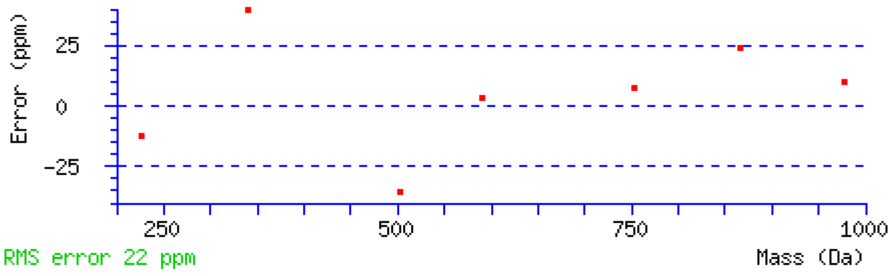
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1090.638611
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0038
Matches : 7/70 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					I							9
2	**227.175404**	114.091340					I	***978.561858***	489.784567	961.535309	481.271292	960.551293	480.779284	8
3	**340.259468**	170.633372					I	***865.477794***	433.242535	848.451245	424.729260	847.467229	424.237252	7
4	**503.322797**	252.165036					Y	***752.393730***	376.700503	735.367181	368.187229	734.383165	367.695221	6
5	604.370476	302.688876			586.359911	293.683594	T	***589.330401***	295.168838	572.303852	286.655564	571.319836	286.163556	5
6	718.413403	359.710340	701.386854	351.197065	700.402838	350.705057	N	488.282722	244.644999	471.256173	236.131724			4
7	832.456330	416.731803	815.429781	408.218528	814.445765	407.726520	N	374.239795	187.623535	357.213246	179.110261			3
8	945.540394	473.273835	928.513845	464.760561	927.529829	464.268553	L	260.196868	130.602072	243.170319	122.088797			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IIIYTNNLK
(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	1090.638611	-0.006043	IIIYTNNLK
15.6	1090.627396	0.005172	ILIEFDTLK
15.6	1090.638626	-0.006058	ILPEIIHPK
14.8	1090.638626	-0.006058	LLSQFLKDK
10.1	1090.638626	-0.006058	EPPPVLAKPK
10.0	1090.632767	-0.000199	ILWFIPFR
2.2	1090.624710	0.007858	LLSQHLPQR
1.7	1090.642014	-0.009446	ILSGVVTKMK
0.8	1090.638626	-0.006058	LLSAVLQGYK

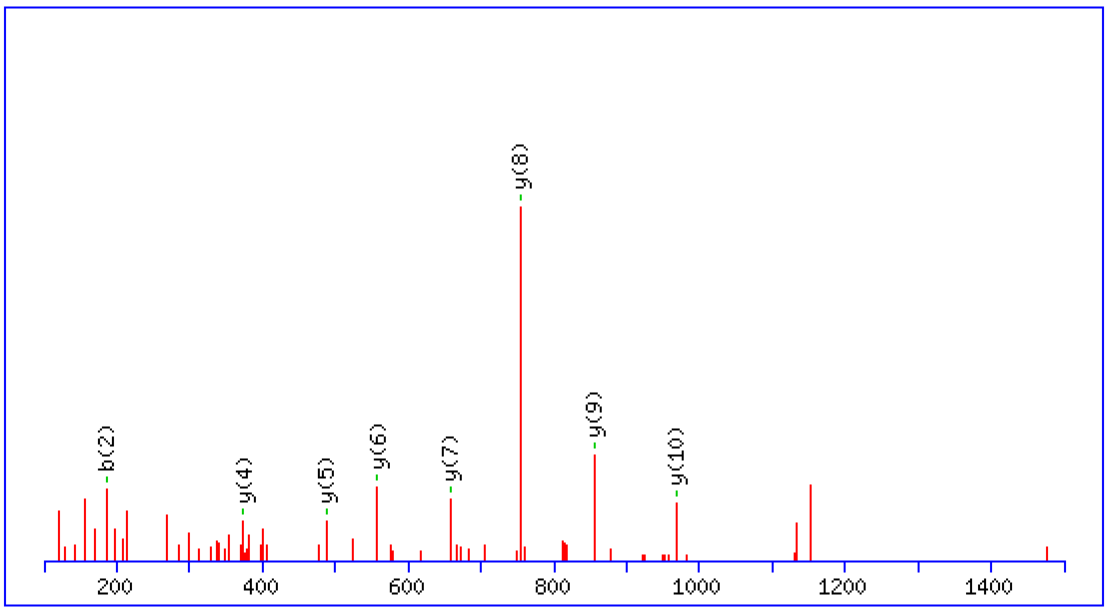
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLTPVAIAAGR**
Found in **GSHR_HUMAN**, Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2

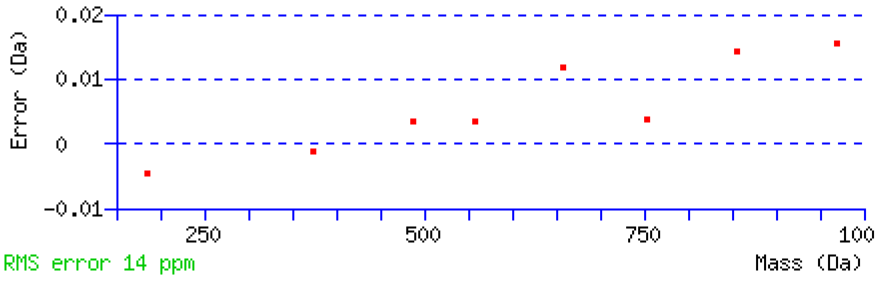
Match to Query 25111: 1151.711908 from(576.863230,2+) rtinseconds(2724) index(37701)
Title: Locus:1.1.1.2373.16
Data file 2011-11-14 - TFD - S 2-3.mgf

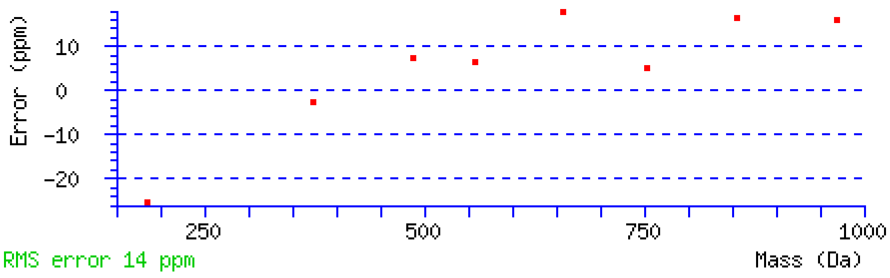
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1151.702621
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 9e-007
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	72.044390	36.525833			A							12
2	185.128454	93.067865			L	1081.672807	541.340042	1064.646258	532.826767	1063.662242	532.334759	11
3	298.212518	149.609897			L	*968.588743*	484.798010	951.562194	476.284735	950.578178	475.792727	10
4	399.260197	200.133737	381.249632	191.128454	T	*855.504679*	428.255978	838.478130	419.742703	837.494114	419.250695	9
5	496.312961	248.660119	478.302396	239.654836	P	*754.457000*	377.732138	737.430451	369.218864			8
6	595.381375	298.194326	577.370810	289.189043	V	*657.404236*	329.205756	640.377687	320.692482			7
7	666.418489	333.712883	648.407924	324.707600	A	*558.335822*	279.671549	541.309273	271.158275			6
8	779.502553	390.254915	761.491988	381.249632	I	*487.298708*	244.152992	470.272159	235.639718			5
9	850.539667	425.773472	832.529102	416.768189	A	*374.214644*	187.610960	357.188095	179.097686			4
10	921.576781	461.292029	903.566216	452.286746	A	303.177530	152.092403	286.150981	143.579129			3
11	978.598245	489.802761	960.587680	480.797478	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 ALLTPVAIAAGR
(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	1151.702621	0.009287	ALLTPVAIAAGR

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

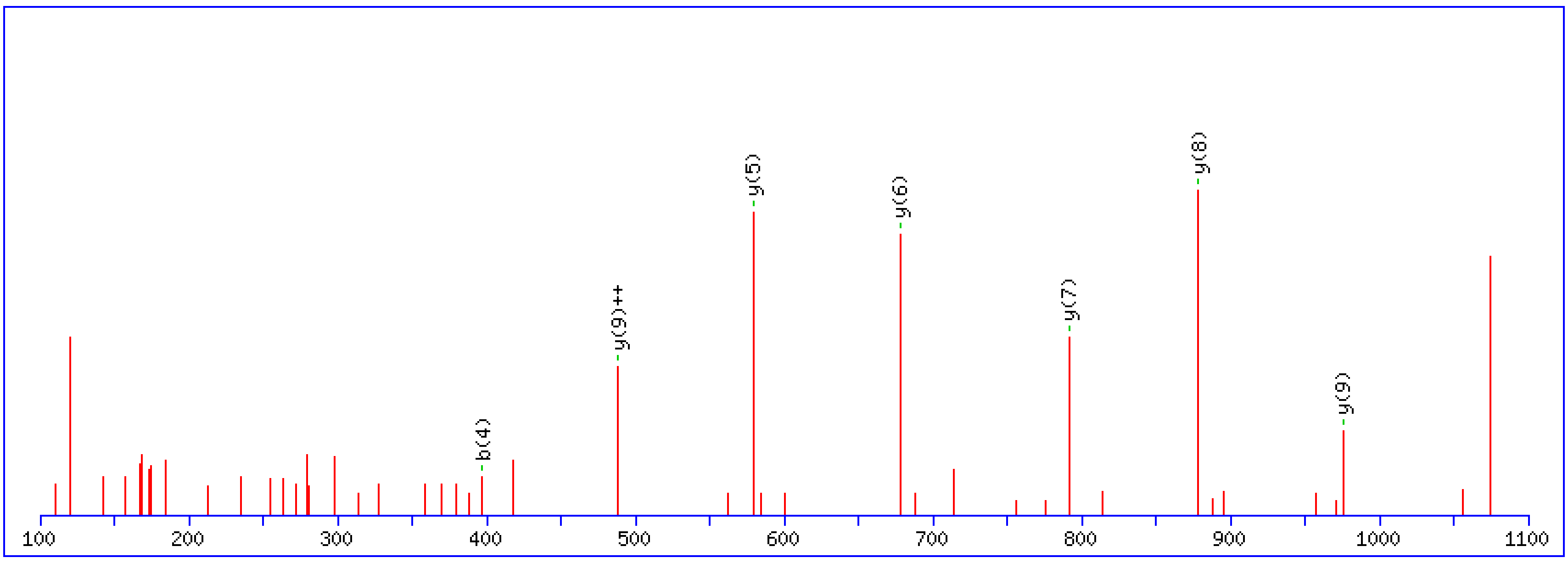
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPSLVGSFIR**
Found in **GSTO1_HUMAN**, Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2

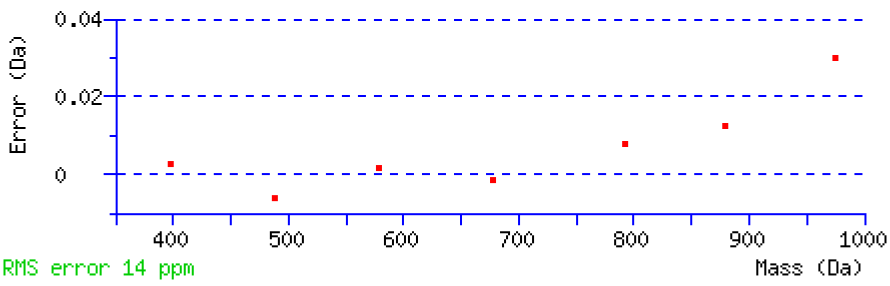
Match to Query 5027: 1073.620328 from(537.817440,2+) rtinseconds(2935) index(36737)
Title: Locus:1.1.1.1558.7
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 2.mgf

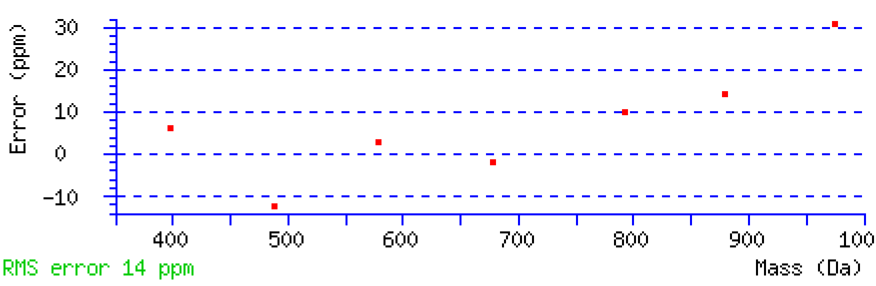
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1073.623337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 35   Expect: 0.00082
Matches : 7/80 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							10
2	197.128454	99.067865			P	***975.562192***	488.284734	958.535643	479.771459	957.551627	479.279451	9
3	284.160482	142.583879	266.149917	133.578596	S	***878.509428***	439.758352	861.482879	431.245077	860.498863	430.753069	8
4	397.244546	199.125911	379.233981	190.120628	L	***791.477400***	396.242338	774.450851	387.729064	773.466835	387.237056	7
5	496.312960	248.660118	478.302395	239.654835	V	***678.393336***	339.700306	661.366787	331.187031	660.382771	330.695023	6
6	553.334424	277.170850	535.323859	268.165568	G	***579.324922***	290.166099	562.298373	281.652825	561.314357	281.160817	5
7	640.366452	320.686864	622.355887	311.681581	S	522.303458	261.655367	505.276909	253.142092	504.292893	252.650084	4
8	787.434866	394.221071	769.424301	385.215788	F	435.271430	218.139353	418.244881	209.626078			3
9	900.518930	450.763103	882.508365	441.757820	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 VPSLVGSFIR
(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	1073.623337	-0.003009	VPSLVGSFIR
2.0	1073.619293	0.001035	VSTTAKQALR

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

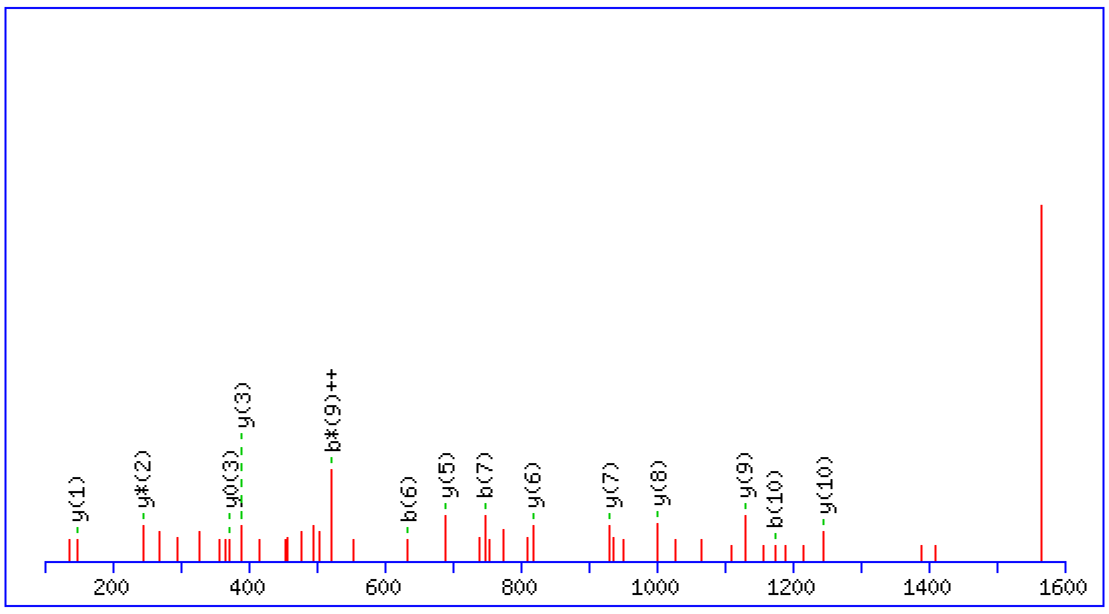
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAMDQALQWLEDK**
Found in **GST2_HUMAN**, Glutathione S-transferase theta-2 OS=Homo sapiens GN=GSTT2 PE=1 SV=1

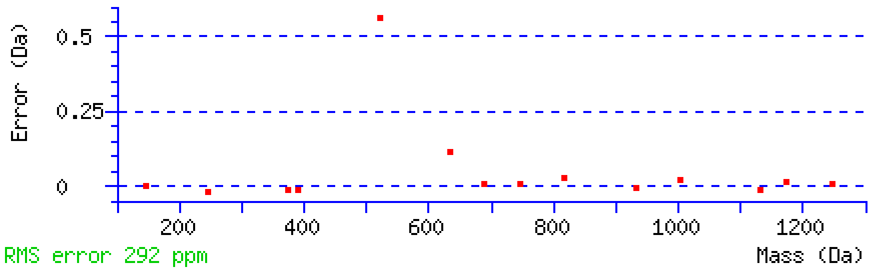
Match to Query 37043: 1563.736408 from(782.875480,2+) rtinseconds(3210) index(43578)
Title: Locus:1.1.1.2662.34
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

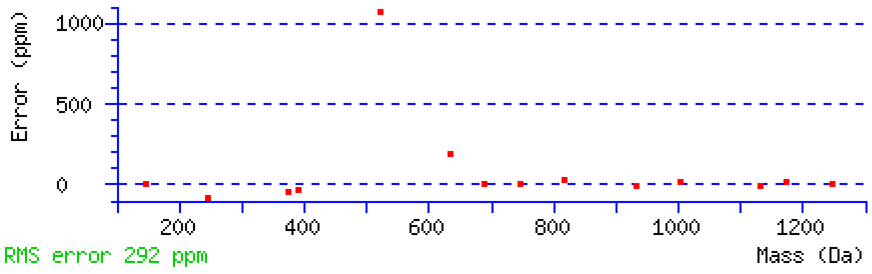
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1563.723892
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:** 1.4e-005
Matches : 14/202 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	1463.683508	732.345392	1446.656959	723.832117	1445.672943	723.340109	12
3	320.127469	160.567372			302.116904	151.562090	M	1392.646394	696.826835	1375.619845	688.313560	1374.635829	687.821552	11
4	435.154412	218.080844			417.143847	209.075561	D	***1245.610994***	623.309135	1228.584445	614.795861	1227.600429	614.303852	10
5	563.212990	282.110133	546.186441	273.596859	545.202425	273.104851	Q	***1130.584051***	565.795663	1113.557502	557.282389	1112.573486	556.790381	9
6	**634.250104**	317.628690	617.223555	309.115415	616.239539	308.623407	A	***1002.525473***	501.766374	985.498924	493.253100	984.514908	492.761092	8
7	**747.334168**	374.170722	730.307619	365.657447	729.323603	365.165439	L	***931.488359***	466.247818	914.461810	457.734543	913.477794	457.242535	7
8	875.392746	438.200011	858.366197	429.686736	857.382181	429.194729	Q	***818.404295***	409.705785	801.377746	401.192511	800.393730	400.700503	6
9	1061.472059	531.239668	1044.445510	522.726393	1043.461494	522.234385	W	***690.345717***	345.676496	673.319168	337.163222	672.335152	336.671214	5
10	**1174.556123**	587.781699	1157.529574	579.268425	1156.545558	578.776417	L	504.266404	252.636840	487.239855	244.123565	486.255839	243.631557	4
11	1303.598716	652.302996	1286.572167	643.789721	1285.588151	643.297713	E	***391.182340***	196.094808	374.155791	187.581533	373.171775	187.089525	3
12	1418.625659	709.816467	1401.599110	701.303193	1400.615094	700.811185	D	262.139747	131.573512	245.113198	123.060237	244.129182	122.568229	2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TAMDQALQWLEDK
(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	1563.723892	0.012516	TAMDQALQWLEDK
0.7	1563.738464	-0.002056	LQGEMMKLSEENR
0.5	1563.735123	0.001285	ELQEQMSRGDPFK

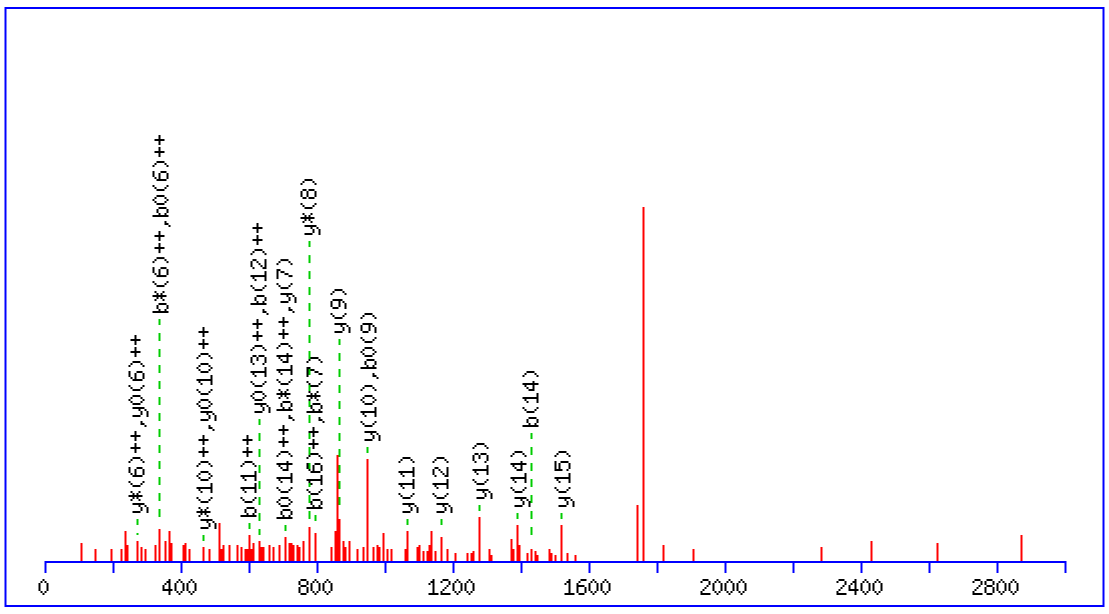
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIEINTISASFGGLASR**
Found in **GSHB_HUMAN**, Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1

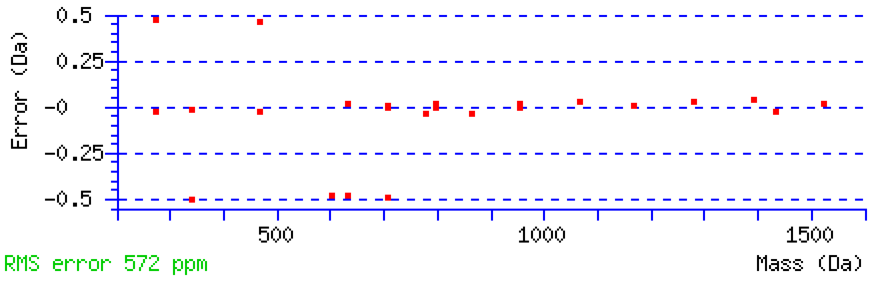
Match to Query 44887: 1762.920548 from(882.467550,2+) rtinseconds(3236) index(45218)
Title: Locus:1.1.1.2755.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

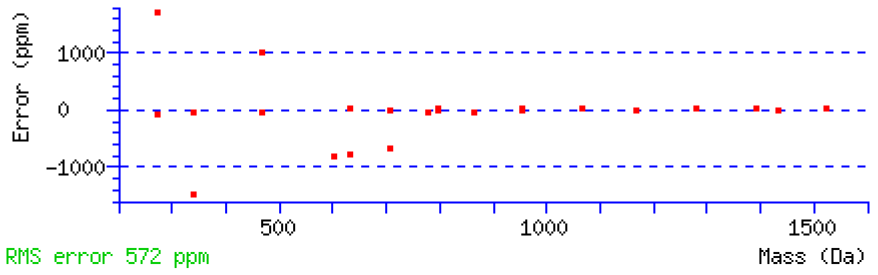
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1762.921341
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00041
Matches : 24/186 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							17
2	242.149918	121.578597	225.123369	113.065323			I	1635.870061	818.438668	1618.843512	809.925394	1617.859496	809.433386	16
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***1522.785997***	761.896637	1505.759448	753.383362	1504.775432	752.891354	15
4	484.276575	242.641926	467.250026	234.128651	466.266010	233.636643	I	***1393.743404***	697.375340	1376.716855	688.862066	1375.732839	688.370058	14
5	598.319502	299.663389	581.292953	291.150115	580.308937	290.658107	N	***1280.659340***	640.833308	1263.632791	632.320034	1262.648775	631.828025	13
6	699.367181	350.187229	682.340632	341.673954	681.356616	341.181946	T	***1166.616413***	583.811845	1149.589864	575.298570	1148.605848	574.806562	12
7	812.451245	406.729261	795.424696	398.215986	794.440680	397.723978	I	***1065.568734***	533.288005	1048.542185	524.774731	1047.558169	524.282722	11
8	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	S	***952.484670***	476.745973	935.458121	468.232698	934.474105	467.740690	10
9	970.520387	485.763832	953.493838	477.250557	952.509822	476.758549	A	***865.452642***	433.229959	848.426093	424.716684	847.442077	424.224676	9
10	1057.552415	529.279846	1040.525866	520.766571	1039.541850	520.274563	S	794.415528	397.711402	777.388979	389.198128	776.404963	388.706120	8
11	1204.620829	**602.814053**	1187.594280	594.300778	1186.610264	593.808770	F	***707.383500***	354.195388	690.356951	345.682113	689.372935	345.190105	7
12	1261.642293	**631.324785**	1244.615744	622.811510	1243.631728	622.319502	G	560.315086	280.661181	543.288537	272.147906	542.304521	271.655898	6
13	1318.663757	659.835517	1301.637208	651.322242	1300.653192	650.830234	G	503.293622	252.150449	486.267073	243.637174	485.283057	243.145166	5
14	1431.747821	716.377548	1414.721272	707.864274	1413.737256	707.372266	L	446.272158	223.639717	429.245609	215.126442	428.261593	214.634434	4
15	1502.784935	751.896105	1485.758386	743.382831	1484.774370	742.890823	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
16	1589.816963	**795.412120**	1572.790414	786.898845	1571.806398	786.406837	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of QIEINTISASFGGLASR
(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	1762.921341	-0.000793	QIEINTISASFGGLASR
2.8	1762.922684	-0.002136	LQEPRGVRPSDWAPR

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

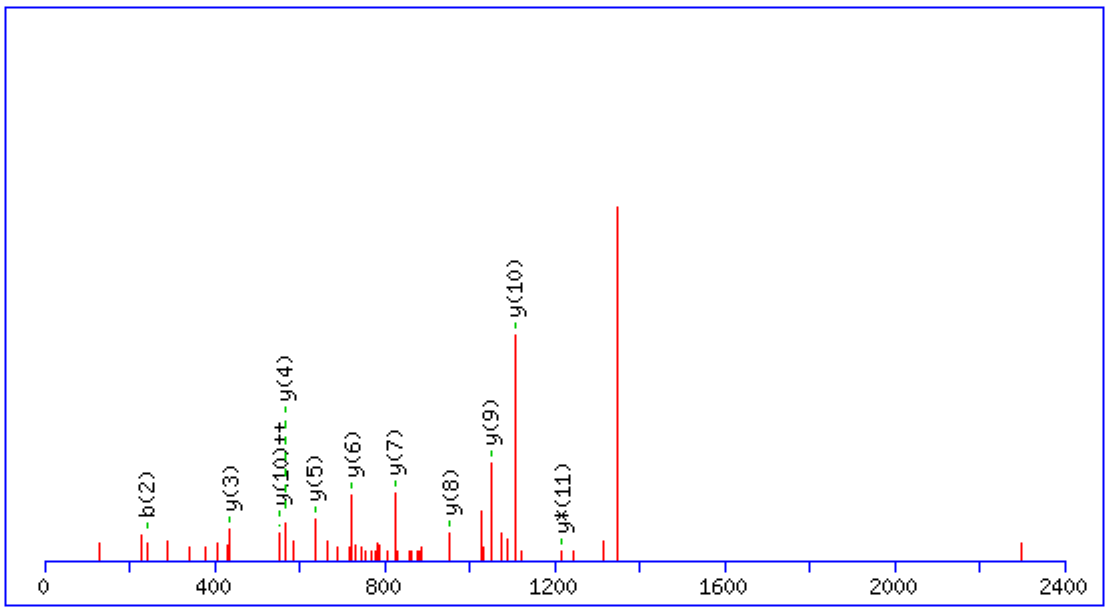
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQGPQTSAEVYR**
Found in **GPD1L_HUMAN**, Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1

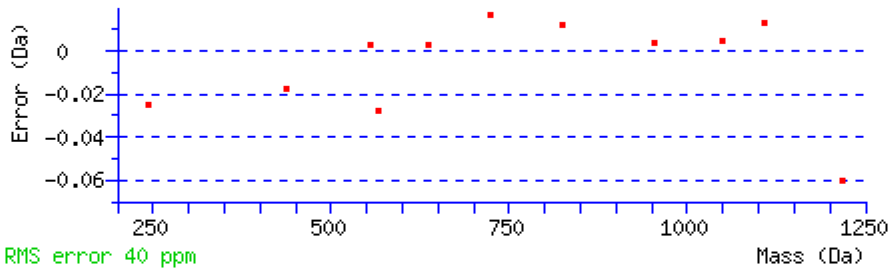
Match to Query 33655: 1347.680788 from(674.847670,2+) rtinseconds(1687) index(14373)
Title: Locus:1.1.1.2042.43
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

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 ●

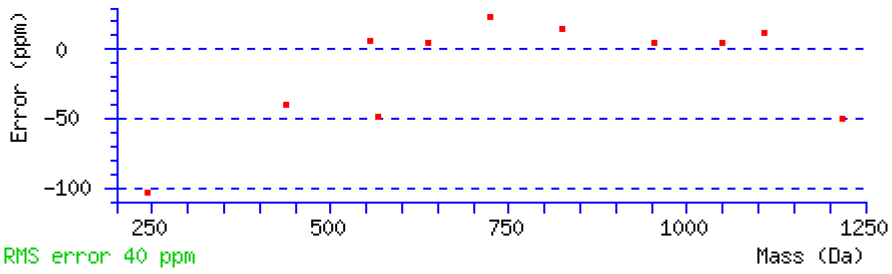


Monoisotopic mass of neutral peptide Mr(calc): 1347.678268
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00012
Matches : 11/114 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							12
2	242.149918	121.578597	225.123369	113.065323			Q	1235.601493	618.304385	1218.574944	609.791110	1217.590928	609.299102	11
3	299.171382	150.089329	282.144833	141.576055			G	***1107.542915***	554.275096	1090.516366	545.761821	1089.532350	545.269813	10
4	396.224146	198.615711	379.197597	190.102436			P	***1050.521451***	525.764364	1033.494902	517.251089	1032.510886	516.759081	9
5	524.282724	262.645000	507.256175	254.131726			Q	***953.468687***	477.237982	936.442138	468.724707	935.458122	468.232699	8
6	625.330403	313.168840	608.303854	304.655565	607.319838	304.163557	T	***825.410109***	413.208693	808.383560	404.695418	807.399544	404.203410	7
7	712.362431	356.684854	695.335882	348.171579	694.351866	347.679571	S	***724.362430***	362.684853	707.335881	354.171579	706.351865	353.679571	6
8	783.399545	392.203411	766.372996	383.690136	765.388980	383.198128	A	***637.330402***	319.168839	620.303853	310.655565	619.319837	310.163557	5
9	912.442138	456.724707	895.415589	448.211433	894.431573	447.719425	E	***566.293288***	283.650282	549.266739	275.137008	548.282723	274.645000	4
10	1011.510552	506.258914	994.484003	497.745639	993.499987	497.253631	V	***437.250695***	219.128985	420.224146	210.615711			3
11	1174.573881	587.790579	1157.547332	579.277304	1156.563316	578.785296	Y	338.182281	169.594778	321.155732	161.081504			2
12							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 40 ppm



RMS error 40 ppm

NCBI **BLAST** search of LQGPQTSAEVYR
(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	1347.678268	0.002520	LQGPQTSAEVYR
4.1	1347.671753	0.009035	KPVPHPNPTCR

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

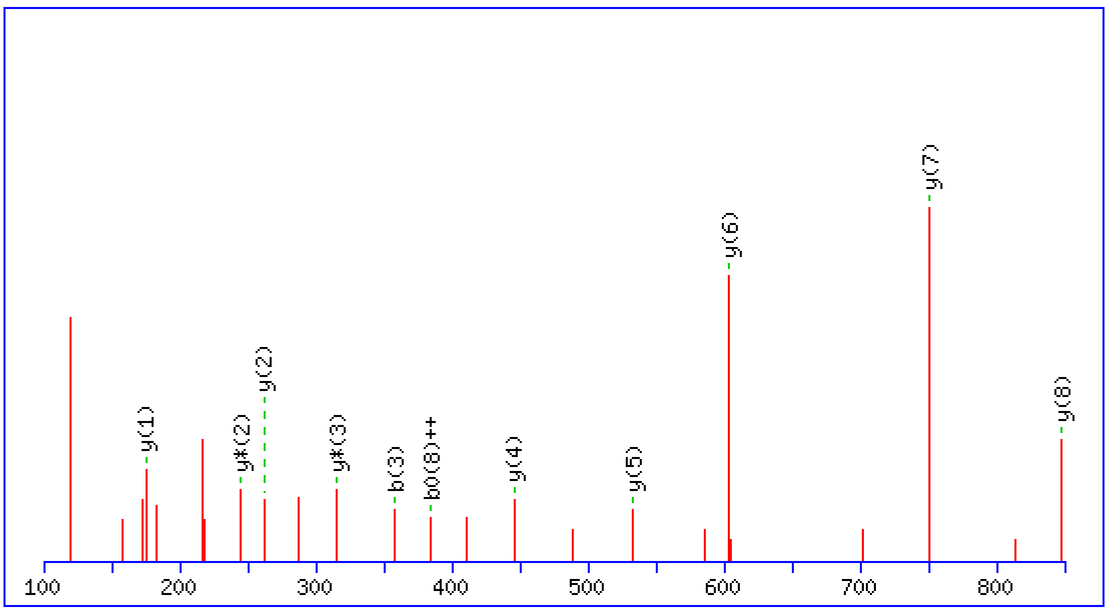
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPFASLASR**
Found in **GDE_HUMAN**, Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3

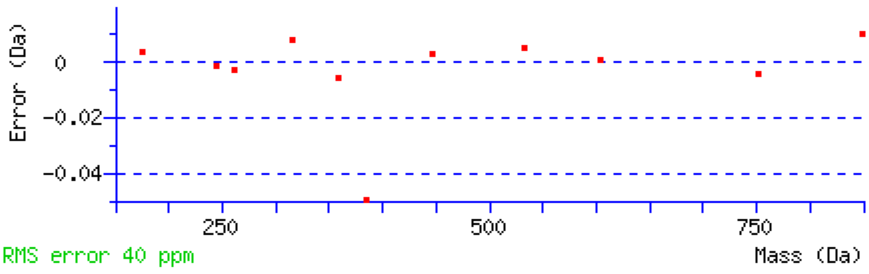
Match to Query 164269: 960.535648 from(481.275100,2+) rtinseconds(2459) index(890532)
Title: Locus:1.1.1.1240.12
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

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 ●

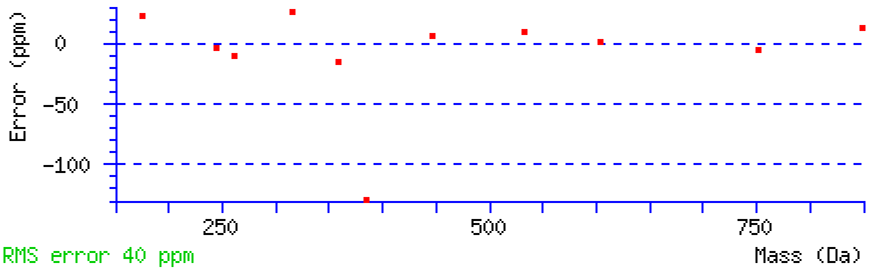


Monoisotopic mass of neutral peptide Mr(calc): 960.539246
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00027
Matches : 11/70 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	211.144104	106.075690			P	***848.462478***	424.734877	831.435929	416.221603	830.451913	415.729595	8
3	358.212518	179.609897			F	***751.409714***	376.208495	734.383165	367.695221	733.399149	367.203213	7
4	429.249632	215.128454			A	***604.341300***	302.674288	587.314751	294.161014	586.330735	293.669006	6
5	516.281660	258.644468	498.271095	249.639186	S	***533.304186***	267.155731	516.277637	258.642457	515.293621	258.150449	5
6	629.365724	315.186500	611.355159	306.181218	L	***446.272158***	223.639717	429.245609	215.126443	428.261593	214.634435	4
7	700.402838	350.705057	682.392273	341.699774	A	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
8	787.434866	394.221071	769.424301	385.215788	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



RMS error 40 ppm



RMS error 40 ppm

NCBI **BLAST** search of IPFASLASR
(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	960.539246	-0.003598	IPFASLASR
11.5	960.539261	-0.003613	IFPVDKSR
8.8	960.539261	-0.003613	FLNVLSPR
4.4	960.542618	-0.006970	ILSAMAVTR
3.4	960.535217	0.000431	IRELTSSR
0.5	960.539276	-0.003628	VFVSLGAPR
0.4	960.531387	0.004261	LPMASTITK

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

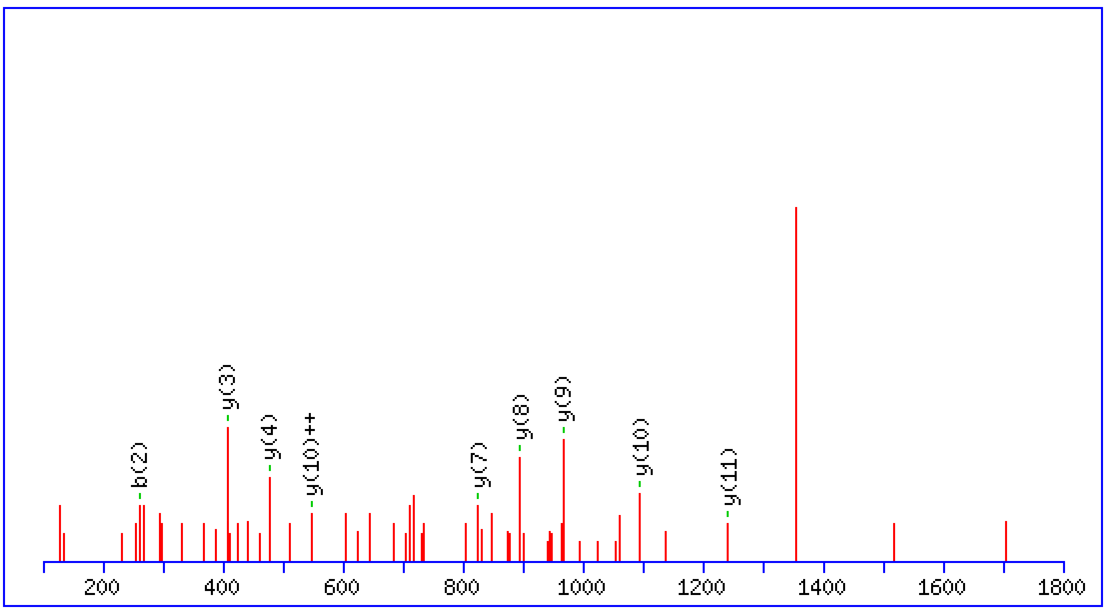
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFQAALYAAPYK**
Found in **GLTP_HUMAN**, Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3

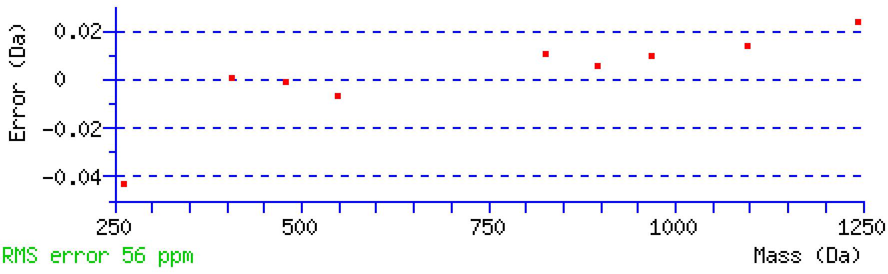
Match to Query 30130: 1354.738928 from(678.376740,2+) rtinseconds(2780) index(35479)
Title: Locus:1.1.1.2500.34
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

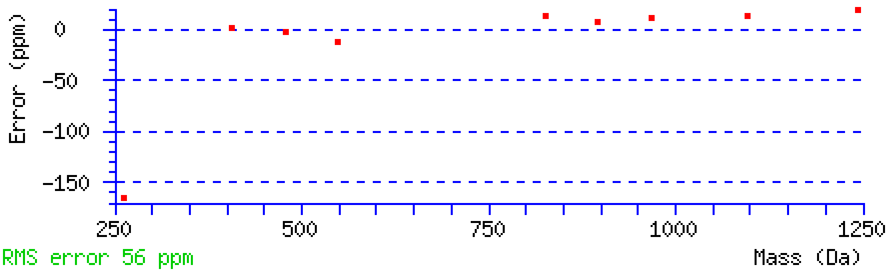
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1354.728485
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00014
Matches : 9/84 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308			I					12
2	261.159754	131.083515			F	*1242.651738*	621.829507	1225.625189	613.316233	11
3	389.218332	195.112804	372.191783	186.599529	Q	*1095.583324*	548.295300	1078.556775	539.782026	10
4	460.255446	230.631361	443.228897	222.118086	A	*967.524746*	484.266011	950.498197	475.752737	9
5	531.292560	266.149918	514.266011	257.636643	A	*896.487632*	448.747454	879.461083	440.234180	8
6	644.376624	322.691950	627.350075	314.178676	L	*825.450518*	413.228897	808.423969	404.715623	7
7	807.439953	404.223615	790.413404	395.710340	Y	712.366454	356.686865	695.339905	348.173591	6
8	878.477067	439.742172	861.450518	431.228897	A	549.303125	275.155201	532.276576	266.641926	5
9	949.514181	475.260729	932.487632	466.747454	A	*478.266011*	239.636644	461.239462	231.123369	4
10	1046.566945	523.787111	1029.540396	515.273836	P	*407.228897*	204.118087	390.202348	195.604812	3
11	1209.630274	605.318775	1192.603725	596.805501	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 IFQAALYAAPYK
(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	1354.728485	0.010443	IFQAALYAAPYK
9.7	1354.735718	0.003210	GEAFDRHLLGLK
3.6	1354.735733	0.003195	IHQKPEFVSVR
1.7	1354.728531	0.010397	QPYTLVVFFNK

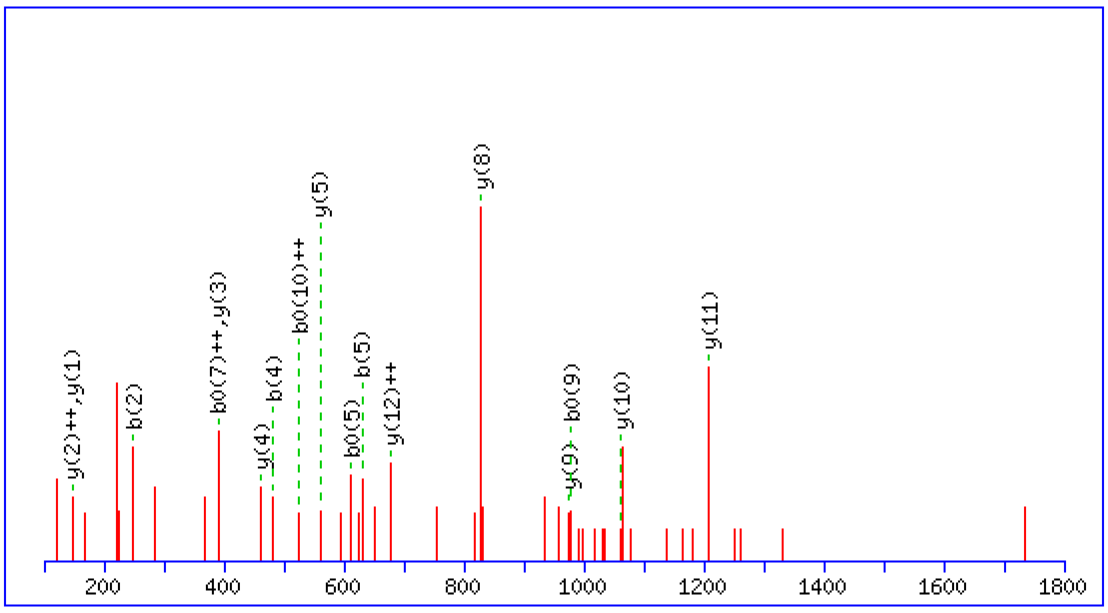
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFFSFPAVVAPFK**
Found in **SYG_HUMAN**, Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3

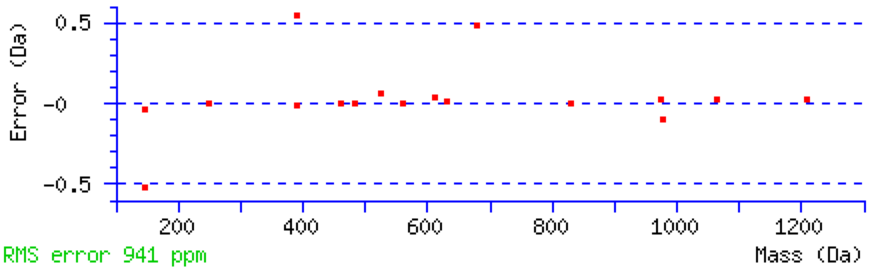
Match to Query 28713: 1456.785228 from(729.399890,2+) rtinseconds(4091) index(52253)
Title: Locus:1.1.1.3491.25
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

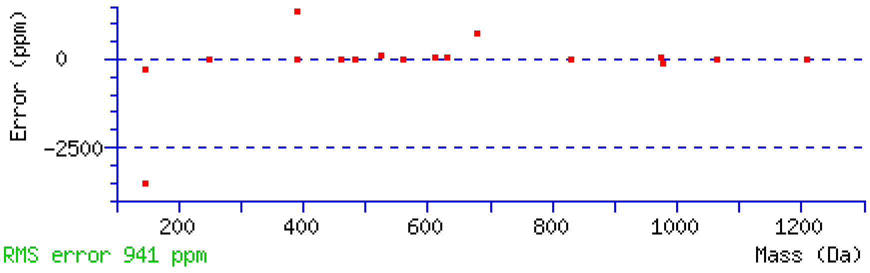
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1456.775497
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0071
Matches : 17/102 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							13
2	**249.123369**	125.065322	231.112804	116.060040	F	1356.735072	678.871174	1339.708523	670.357900	1338.724507	669.865891	12
3	396.191783	198.599529	378.181218	189.594247	F	***1209.666658***	605.336967	1192.640109	596.823692	1191.656093	596.331684	11
4	**483.223811**	242.115543	465.213246	233.110261	S	***1062.598244***	531.802760	1045.571695	523.289486	1044.587679	522.797478	10
5	**630.292225**	315.649750	612.281660	306.644468	F	***975.566216***	488.286746	958.539667	479.773472			9
6	727.344989	364.176132	709.334424	355.170850	P	***828.497802***	414.752539	811.471253	406.239265			8
7	798.382103	399.694689	780.371538	390.689407	A	731.445038	366.226157	714.418489	357.712883			7
8	897.450517	449.228896	879.439952	440.223614	V	660.407924	330.707600	643.381375	322.194326			6
9	996.518931	498.763103	978.508366	489.757821	V	***561.339510***	281.173393	544.312961	272.660119			5
10	1067.556045	534.281660	1049.545480	525.276378	A	***462.271096***	231.639186	445.244547	223.125912			4
11	1164.608809	582.808042	1146.598244	573.802760	P	***391.233982***	196.120629	374.207433	187.607355			3
12	1311.677223	656.342249	1293.666658	647.336967	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 TFFSFPAVVAPFK
(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	1456.775497	0.009731	TFFSFPAVVAPFK

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

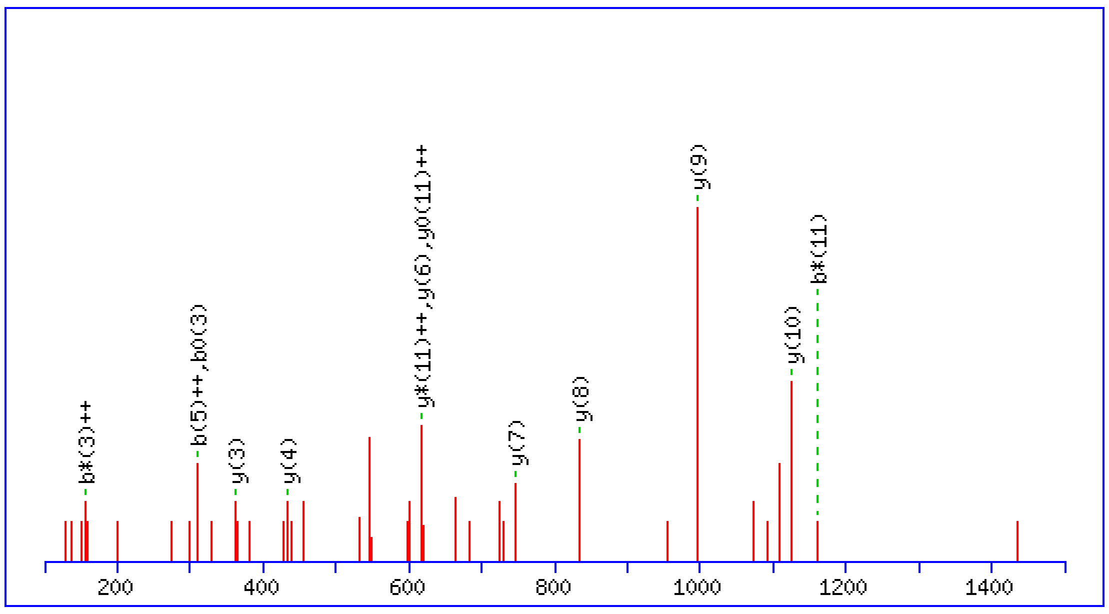
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQQYSEALASTR**
Found in **GAPR1_HUMAN**, Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3

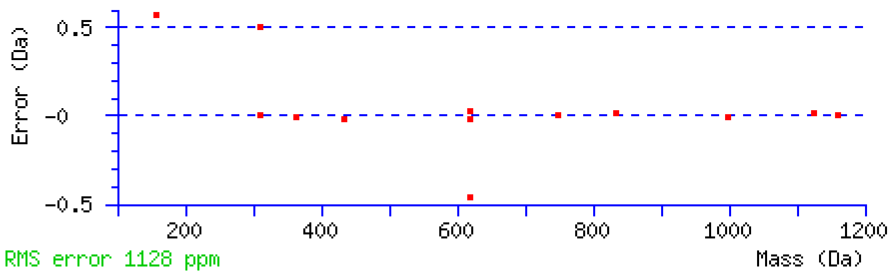
Match to Query 19015: 1452.685248 from(727.349900,2+) rtinseconds(1821) index(5967)
Title: Locus:1.1.1.2279.24
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

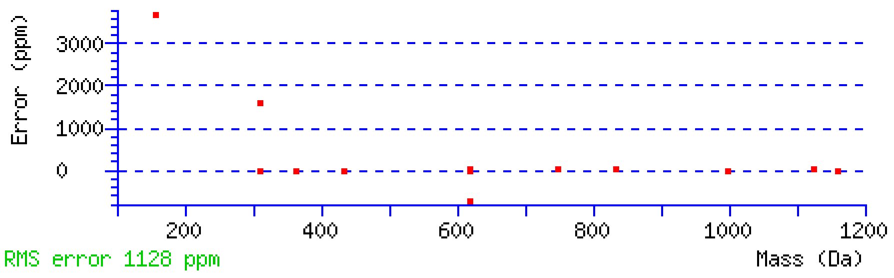
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1452.684448
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 1.6e-005
Matches : 13/138 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	130.049869	65.528572			112.039304	56.523290	E							13
2	201.086983	101.047130			183.076418	92.041847	A	1324.649171	662.828224	1307.622622	654.314949	1306.638606	653.822941	12
3	329.145561	165.076418	312.119012	156.563144	311.134996	156.071136	Q	1253.612057	627.309667	1236.585508	618.796392	1235.601492	618.304384	11
4	457.204139	229.105707	440.177590	220.592433	439.193574	220.100425	Q	***1125.553479***	563.280378	1108.526930	554.767103	1107.542914	554.275095	10
5	620.267468	310.637372	603.240919	302.124098	602.256903	301.632090	Y	***997.494901***	499.251089	980.468352	490.737814	979.484336	490.245806	9
6	707.299496	354.153386	690.272947	345.640111	689.288931	345.148103	S	***834.431572***	417.719424	817.405023	409.206150	816.421007	408.714142	8
7	836.342089	418.674683	819.315540	410.161408	818.331524	409.669400	E	***747.399544***	374.203410	730.372995	365.690136	729.388979	365.198128	7
8	907.379203	454.193240	890.352654	445.679965	889.368638	445.187957	A	***618.356951***	309.682114	601.330402	301.168839	600.346386	300.676831	6
9	1020.463267	510.735272	1003.436718	502.221997	1002.452702	501.729989	L	547.319837	274.163557	530.293288	265.650282	529.309272	265.158274	5
10	1091.500381	546.253829	1074.473832	537.740554	1073.489816	537.248546	A	***434.235773***	217.621525	417.209224	209.108250	416.225208	208.616242	4
11	1178.532409	589.769843	1161.505860	581.256568	1160.521844	580.764560	S	***363.198659***	182.102968	346.172110	173.589693	345.188094	173.097685	3
12	1279.580088	640.293682	1262.553539	631.780408	1261.569523	631.288400	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 EAQQYSEALASTR
(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	1452.684448	0.000800	EAQQYSEALASTR
1.3	1452.670761	0.014487	WESFDVTPAVMR

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

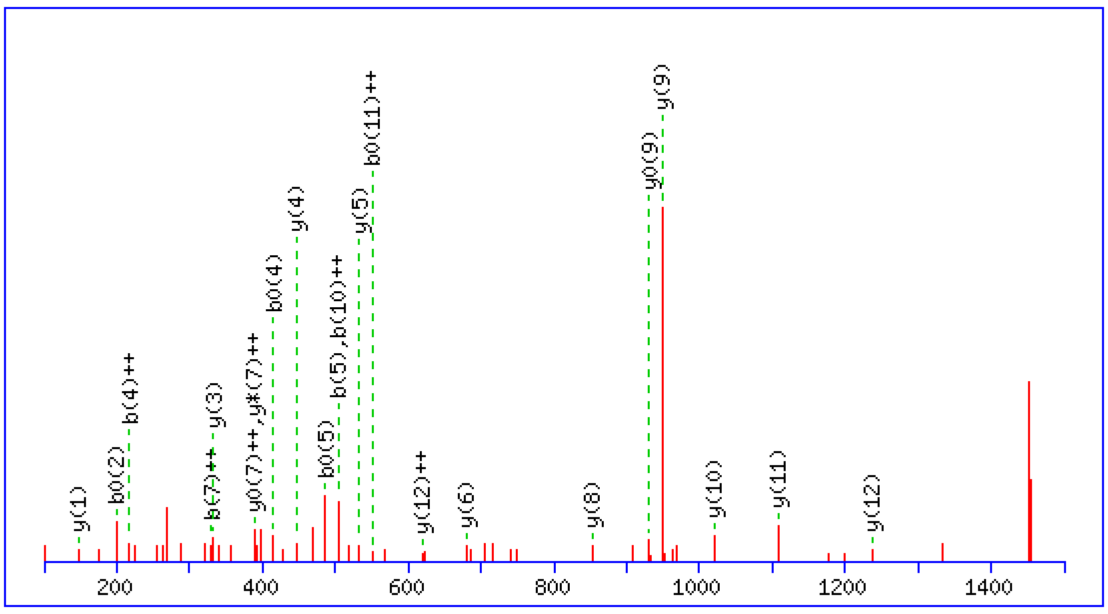
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESESAPGDFSLSVK**
Found in **GRB2_HUMAN**, Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1

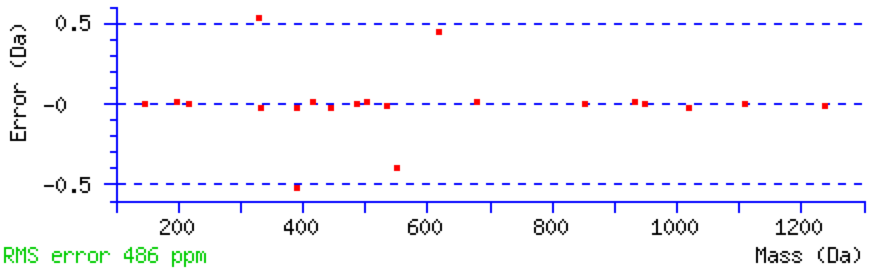
Match to Query 34541: 1451.687668 from(726.851110,2+) rtinseconds(2432) index(27493)
Title: Locus:1.1.1.2455.43
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

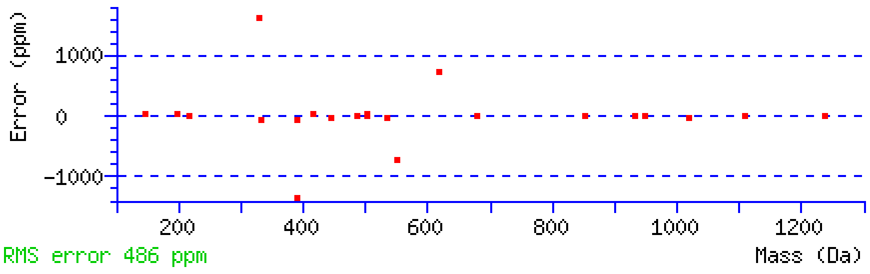
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1451.677994
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 7e-005
Matches : 23/126 fragment ions using 44 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							14
2	217.081897	109.044586	199.071332	100.039304	S	1323.642686	662.324981	1306.616137	653.811707	1305.632121	653.319698	13
3	346.124490	173.565883	328.113925	164.560600	E	***1236.610658***	618.808967	1219.584109	610.295693	1218.600093	609.803685	12
4	433.156518	**217.081897**	415.145953	208.076614	S	***1107.568065***	554.287671	1090.541516	545.774396	1089.557500	545.282388	11
5	504.193632	252.600454	486.183067	243.595171	A	***1020.536037***	510.771657	1003.509488	502.258382	1002.525472	501.766374	10
6	601.246396	301.126836	583.235831	292.121554	P	***949.498923***	475.253100	932.472374	466.739825	931.488358	466.247817	9
7	658.267860	**329.637568**	640.257295	320.632286	G	***852.446159***	426.726718	835.419610	418.213443	834.435594	417.721435	8
8	773.294803	387.151040	755.284238	378.145757	D	795.424695	398.215986	778.398146	389.702711	777.414130	389.210703	7
9	920.363217	460.685247	902.352652	451.679964	F	***680.397752***	340.702514	663.371203	332.189240	662.387187	331.697232	6
10	1007.395245	**504.201260**	989.384680	495.195978	S	***533.329338***	267.168307	516.302789	258.655033	515.318773	258.163025	5
11	1120.479309	560.743292	1102.468744	551.738010	L	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
12	1207.511337	604.259306	1189.500772	595.254024	S	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	3
13	1306.579751	653.793514	1288.569186	644.788231	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 ESESAPGDFSLSVK
(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	1451.677994	0.009674	ESESAPGDFSLSVK
9.2	1451.692581	-0.004913	ESLDTTCKEISR
1.3	1451.682724	0.004944	FPRSTSMQDPVR
0.5	1451.682693	0.004975	EICSEFRDQVR
0.2	1451.697983	-0.010315	MPGTVHSSWHSVK

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

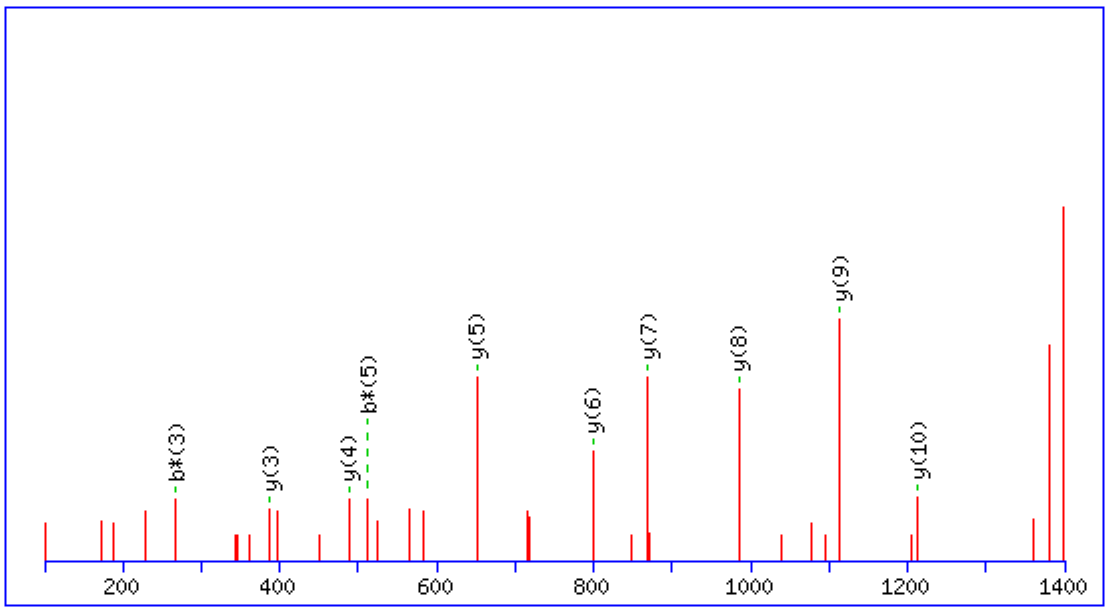
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGVEDAFYTLVR**
Found in **RASH_HUMAN**, GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1

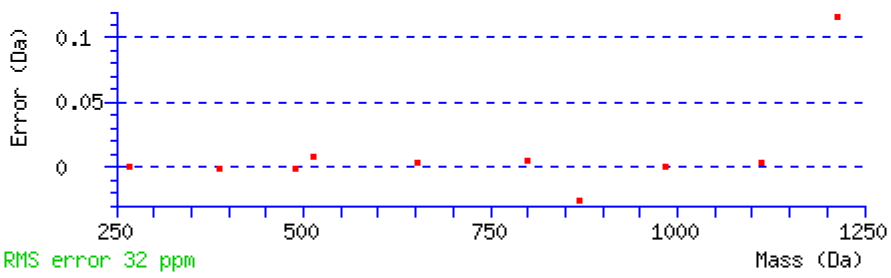
Match to Query 26570: 1396.706268 from(699.360410,2+) rtinseconds(3437) index(35951)
Title: Locus:1.1.1.2802.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

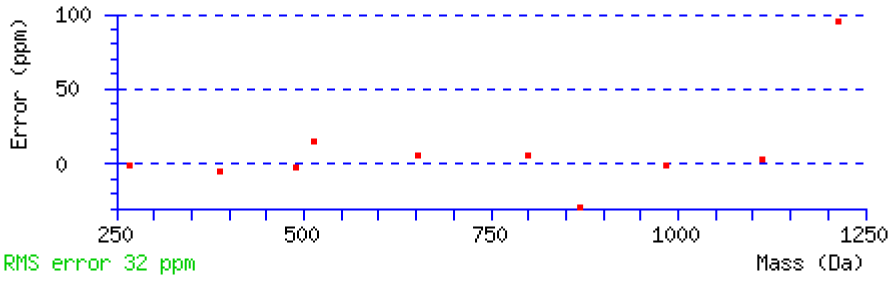
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1396.698685
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 1.1e-006
Matches : 10/120 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	186.087318	93.547297	169.060769	85.034023			G	1269.647380	635.327328	1252.620831	626.814054	1251.636815	626.322046	11
3	285.155732	143.081504	268.129183	134.568230			V	***1212.625916***	606.816596	1195.599367	598.303322	1194.615351	597.811313	10
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	E	***1113.557502***	557.282389	1096.530953	548.769115	1095.546937	548.277106	9
5	529.225268	265.116272	512.198719	256.602998	511.214703	256.110990	D	***984.514909***	492.761093	967.488360	484.247818	966.504344	483.755810	8
6	600.262382	300.634829	583.235833	292.121555	582.251817	291.629547	A	***869.487966***	435.247621	852.461417	426.734347	851.477401	426.242339	7
7	747.330796	374.169036	730.304247	365.655761	729.320231	365.163753	F	***798.450852***	399.729064	781.424303	391.215790	780.440287	390.723782	6
8	910.394125	455.700701	893.367576	447.187426	892.383560	446.695418	Y	***651.382438***	326.194857	634.355889	317.681583	633.371873	317.189575	5
9	1011.441804	506.224540	994.415255	497.711266	993.431239	497.219258	T	***488.319109***	244.663192	471.292560	236.149918	470.308544	235.657910	4
10	1124.525868	562.766572	1107.499319	554.253298	1106.515303	553.761289	L	***387.271430***	194.139353	370.244881	185.626078			3
11	1223.594282	612.300779	1206.567733	603.787505	1205.583717	603.295497	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 QGVEDAFYTLVR
(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	1396.698685	0.007583	QGVEDAFYTLVR
3.0	1396.699356	0.006912	GSMNRHVAAIGPR

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

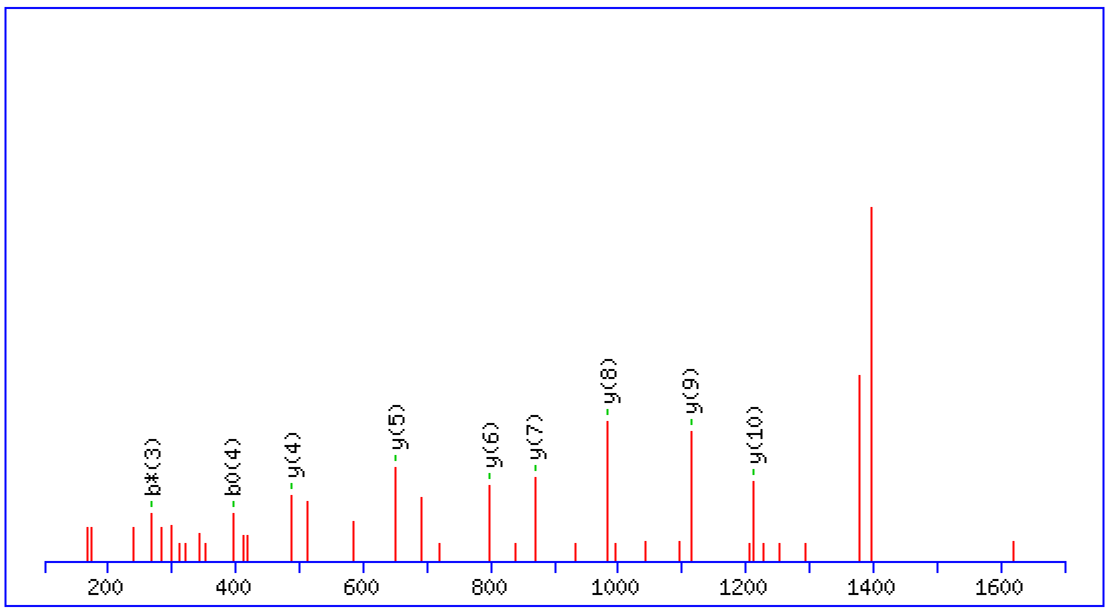
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGVEDAFYTLVR**
Found in **RASH_HUMAN**, GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1

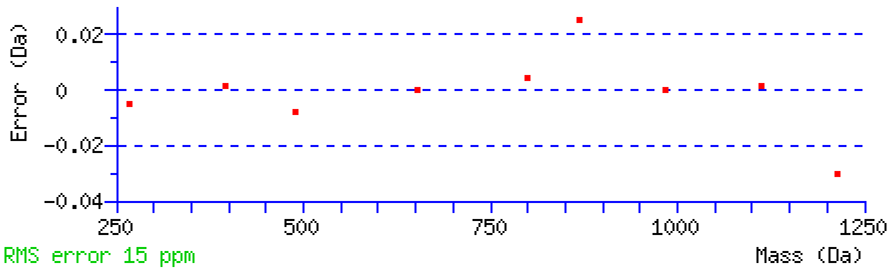
Match to Query 18067: 1396.701168 from(699.357860,2+) rtinseconds(3423) index(23140)
Title: Locus:1.1.1.2882.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

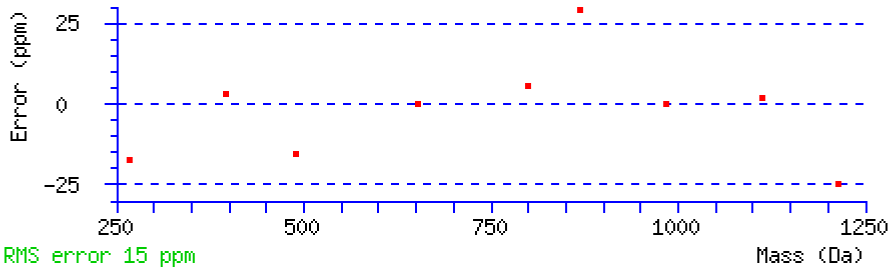
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1396.698685
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 2.7e-005
Matches : 9/120 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	186.087318	93.547297	169.060769	85.034023			G	1269.647380	635.327328	1252.620831	626.814054	1251.636815	626.322046	11
3	285.155732	143.081504	268.129183	134.568230			V	***1212.625916***	606.816596	1195.599367	598.303322	1194.615351	597.811313	10
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	E	***1113.557502***	557.282389	1096.530953	548.769115	1095.546937	548.277106	9
5	529.225268	265.116272	512.198719	256.602998	511.214703	256.110990	D	***984.514909***	492.761093	967.488360	484.247818	966.504344	483.755810	8
6	600.262382	300.634829	583.235833	292.121555	582.251817	291.629547	A	***869.487966***	435.247621	852.461417	426.734347	851.477401	426.242339	7
7	747.330796	374.169036	730.304247	365.655761	729.320231	365.163753	F	***798.450852***	399.729064	781.424303	391.215790	780.440287	390.723782	6
8	910.394125	455.700701	893.367576	447.187426	892.383560	446.695418	Y	***651.382438***	326.194857	634.355889	317.681583	633.371873	317.189575	5
9	1011.441804	506.224540	994.415255	497.711266	993.431239	497.219258	T	***488.319109***	244.663192	471.292560	236.149918	470.308544	235.657910	4
10	1124.525868	562.766572	1107.499319	554.253298	1106.515303	553.761289	L	387.271430	194.139353	370.244881	185.626078			3
11	1223.594282	612.300779	1206.567733	603.787505	1205.583717	603.295497	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 QGVEDAFYTLVR
(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	1396.698685	0.002483	QGVEDAFYTLVR
5.9	1396.713913	-0.012745	NGIPYAFAFELR
0.0	1396.698685	0.002483	DFAAEVVHPGDLK

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

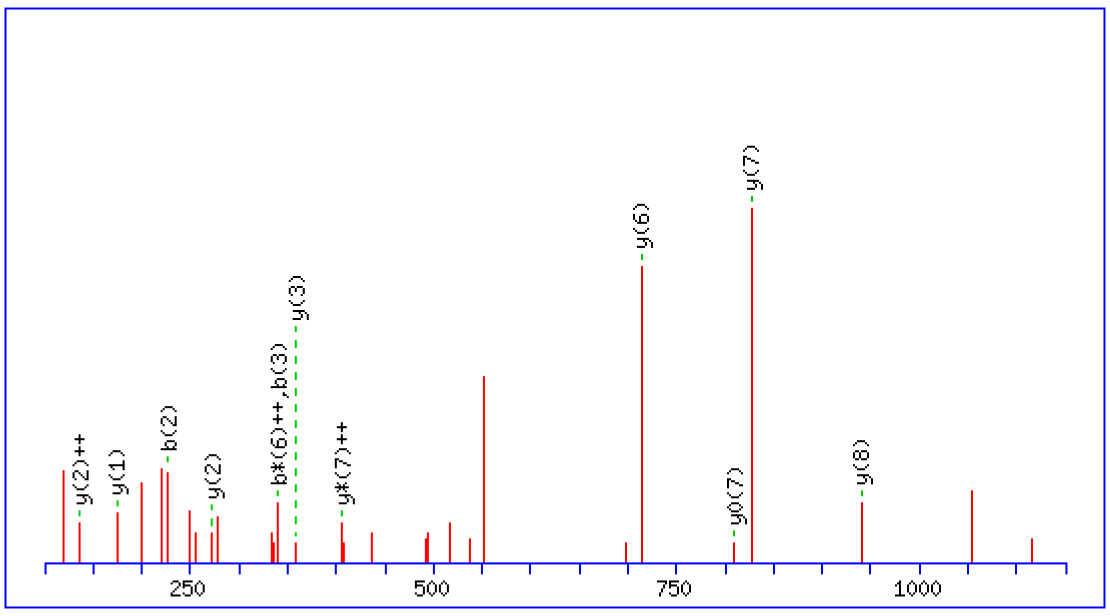
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPQRASPR**
Found in **GTPB5_HUMAN**, GTP-binding protein 5 OS=Homo sapiens GN=GTPBP5 PE=2 SV=1

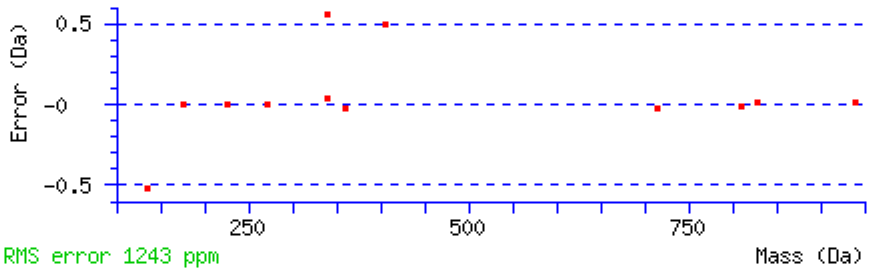
Match to Query 16958: 1052.604088 from(527.309320,2+) rtinseconds(2987) index(31086)
Title: Locus:1.1.1.2604.9
Data file 2011-11-14 - TFD - S 2-5.mgf

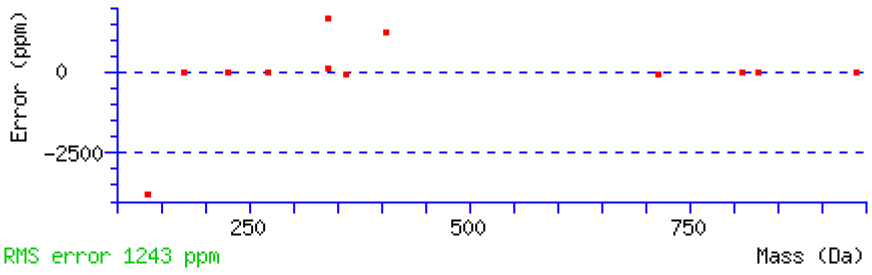
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1052.609055
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3 : Oxidation (P)
Ions Score: 31 **Expect:** 0.0049
Matches : 12/74 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							9
2	**227.175404**	114.091340					L	***940.532290***	470.769783	923.505741	462.256509	922.521725	461.764501	8
3	**340.223083**	170.615179					P	***827.448226***	414.227751	810.421677	405.714476	809.437661	405.222468	7
4	468.281661	234.644468	451.255112	226.131194			Q	***714.400547***	357.703912	697.373998	349.190637	696.389982	348.698629	6
5	624.382772	312.695024	607.356223	304.181750			R	586.341969	293.674623	569.315420	285.161348	568.331404	284.669340	5
6	695.419886	348.213581	678.393337	339.700307			A	430.240858	215.624067	413.214309	207.110792	412.230293	206.618784	4
7	782.451914	391.729595	765.425365	383.216320	764.441349	382.724313	S	***359.203744***	180.105510	342.177195	171.592235	341.193179	171.100227	3
8	879.504678	440.255977	862.478129	431.742703	861.494113	431.250695	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 LLPQRASPR
(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	1052.609055	-0.004967	LLPQRASPR
19.7	1052.613083	-0.008995	LLLPHAFSR
15.4	1052.597839	0.006249	IPLPQAQVR
10.9	1052.597839	0.006249	LLPPQRPGK
10.9	1052.609055	-0.004967	LLPQRASPR
10.4	1052.597824	0.006264	LPARPQVEK
8.8	1052.609055	-0.004967	IRQSPSPLR
7.7	1052.609039	-0.004951	LERSAPKPR
3.6	1052.597839	0.006249	LQGSPVPSLR
1.5	1052.613083	-0.008995	LLQLPQWR

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

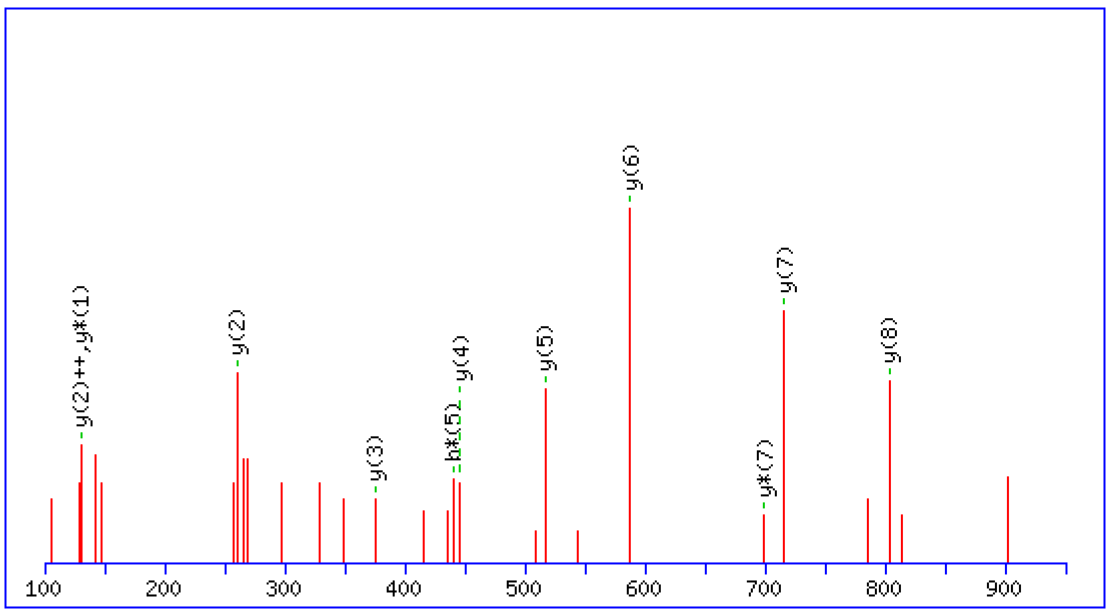
Mascot Search Results

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

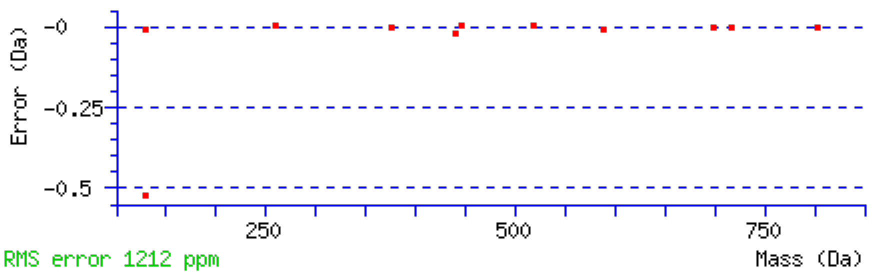
Match to Query 4261: 901.485608 from(451.750080,2+) rtinseconds(1057) index(107)
Title: Locus:1.1.1.2456.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-8.mgf

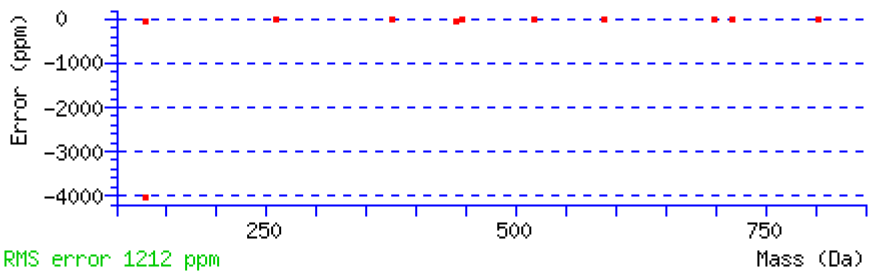
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 901.486877
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 2e-005
Matches : 11/86 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	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
59.6	901.486877	-0.001269	VSQAAADLK
10.3	901.486877	-0.001269	QEQSAVIK
7.7	901.486893	-0.001285	GSPGASLGIK
7.7	901.476974	0.008634	KWAAGQNK
5.8	901.486877	-0.001269	VSEQLQAK
5.6	901.486877	-0.001269	VNASAPSLK
3.9	901.486908	-0.001300	VQGTPVASK
3.9	901.486862	-0.001254	VEEELRK
3.3	901.486877	-0.001269	QEKAPVSK
2.2	901.490921	-0.005313	AFVPPDLK

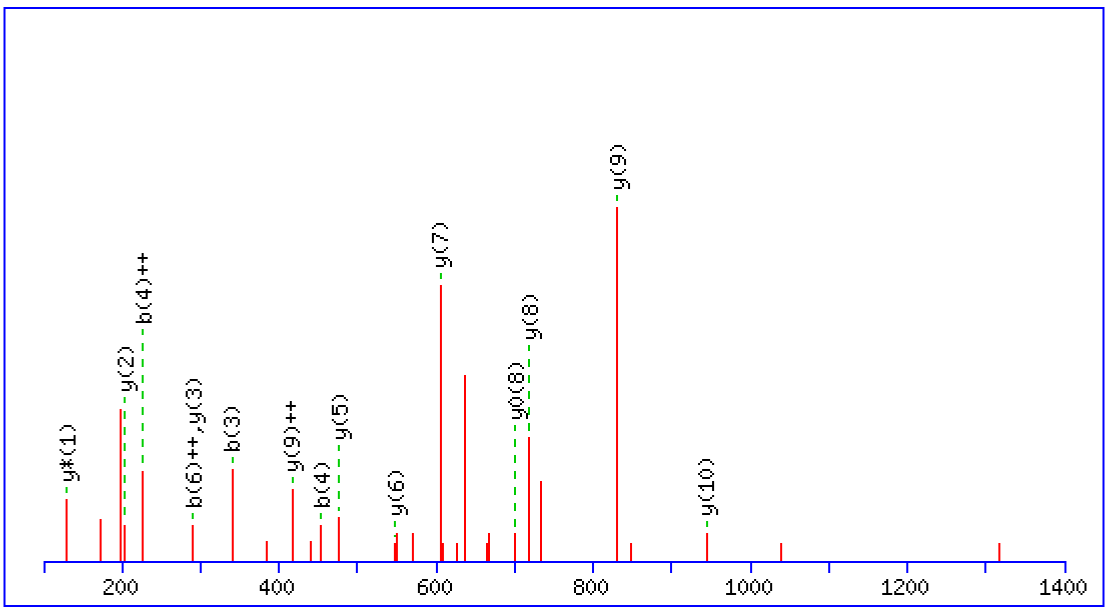
Mascot Search Results

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

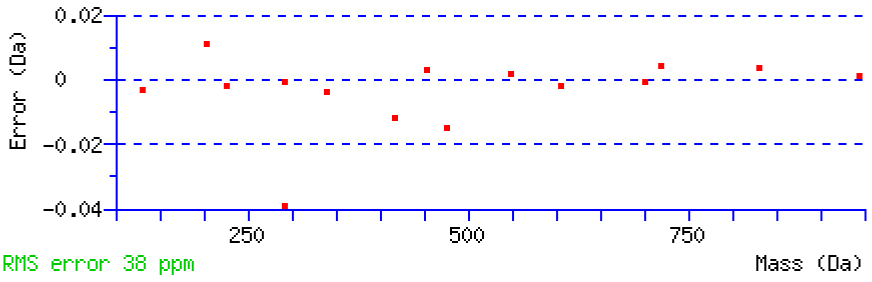
Match to Query 265945: 1056.616188 from(529.315370,2+) rtinseconds(2473) index(960670)
Title: Locus:1.1.1.1456.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

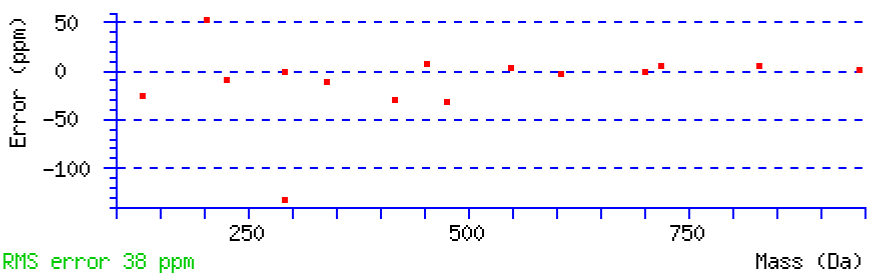
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1056.617889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 8.5e-005
Matches : 16/82 fragment ions using 31 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
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
48.9	1056.617889	-0.001701	ILLLGAGESGK
48.9	1056.617889	-0.001701	LLLLGAGESGK
20.6	1056.608002	0.008186	ILPVGAANFR
8.8	1056.606659	0.009529	LLPDTILEK
8.8	1056.606659	0.009529	LPLTDLEIK

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

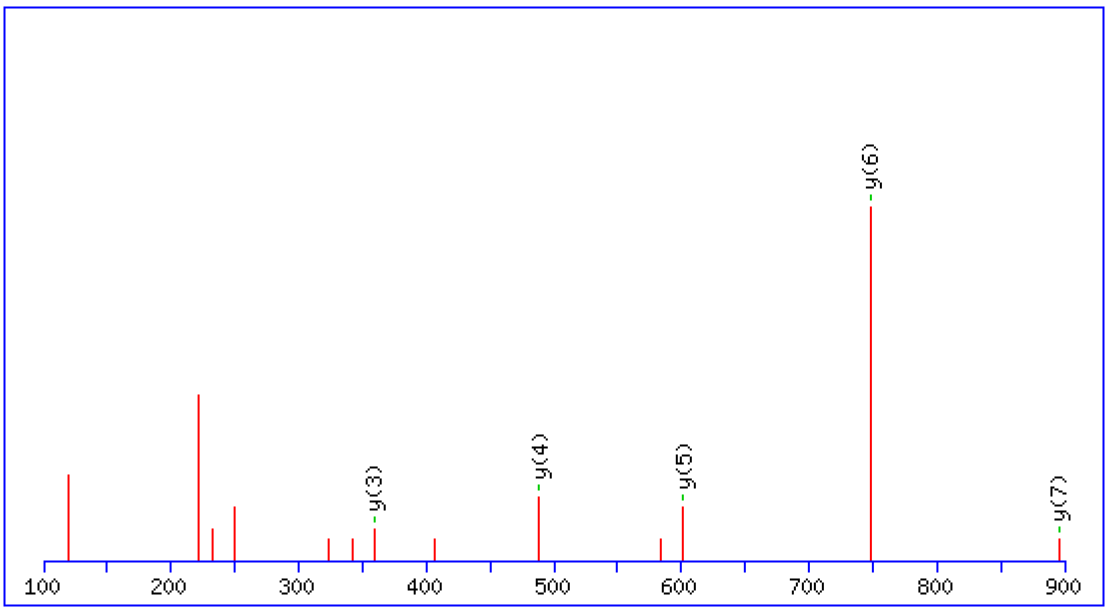
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFFLEALR**
Found in **HDHD2_HUMAN**, Haloacid dehalogenase-like hydrolase domain-containing protein 2 OS=Homo sapiens GN=HDHD2 PE=1 SV=1

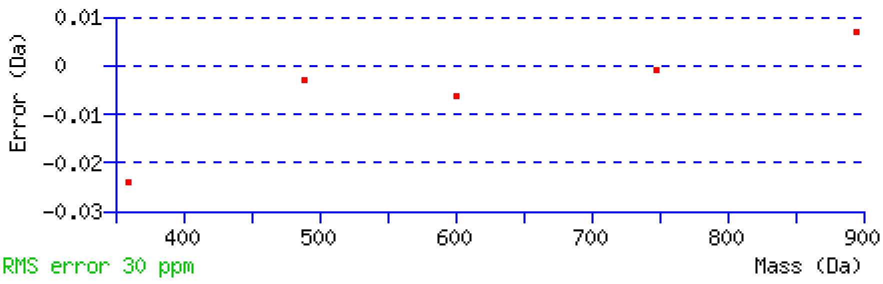
Match to Query 11015: 995.543288 from(498.778920,2+) rtinseconds(3404) index(42335)
Title: Locus:1.1.1.3103.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

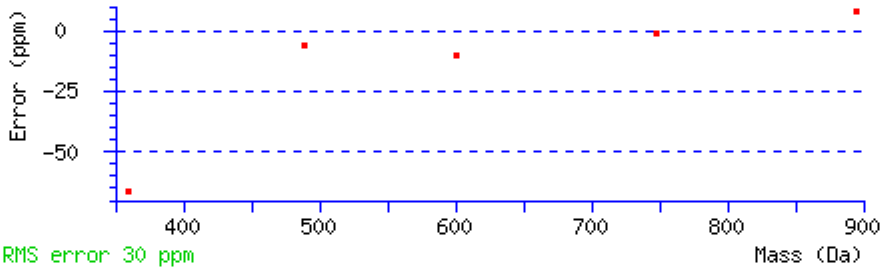
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 995.544006
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00014
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	102.054955	51.531116	84.044390	42.525833	T							8
2	249.123369	125.065322	231.112804	116.060040	F	***895.503615***	448.255446	878.477066	439.742171	877.493050	439.250163	7
3	396.191783	198.599529	378.181218	189.594247	F	***748.435201***	374.721239	731.408652	366.207964	730.424636	365.715956	6
4	509.275847	255.141561	491.265282	246.136279	L	***601.366787***	301.187032	584.340238	292.673757	583.356222	292.181749	5
5	638.318440	319.662858	620.307875	310.657576	E	***488.282723***	244.645000	471.256174	236.131725	470.272158	235.639717	4
6	709.355554	355.181415	691.344989	346.176132	A	***359.240130***	180.123703	342.213581	171.610429			3
7	822.439618	411.723447	804.429053	402.718165	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 TFFLEALR
(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	995.544006	-0.000718	TFFLEALR
1.1	995.539993	0.003295	TPATAPVPAR

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

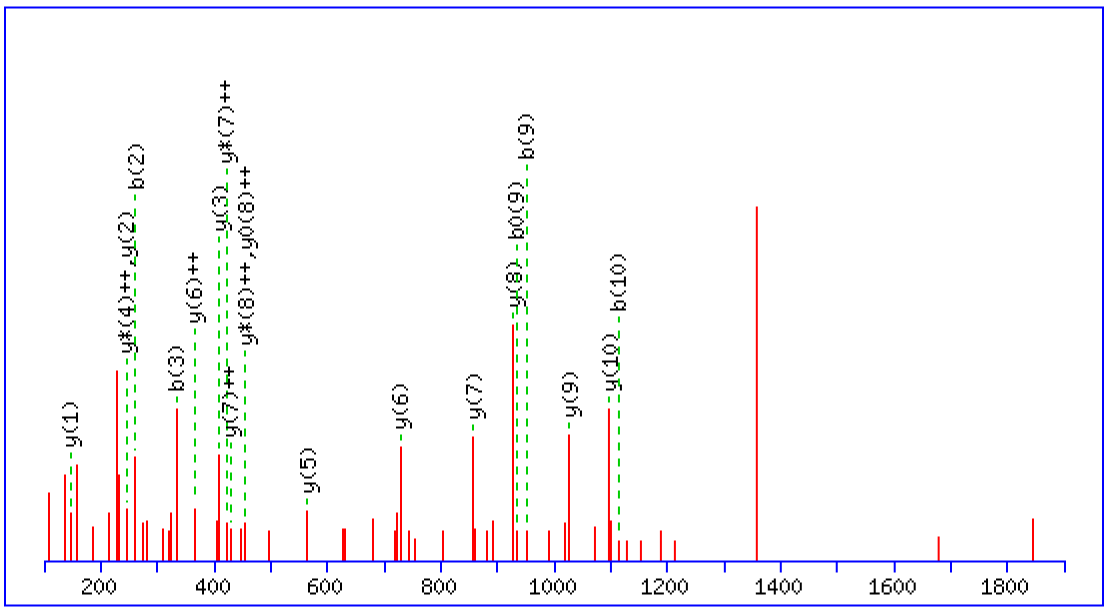
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SCAVAEYGVYVK**
Found in **HPTR_HUMAN**, Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2

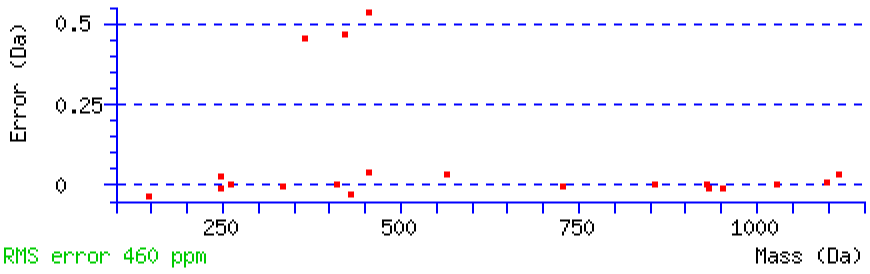
Match to Query 27208: 1358.658128 from(680.336340,2+) rtinseconds(2322) index(22254)
Title: Locus:1.1.1.2696.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

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 ●

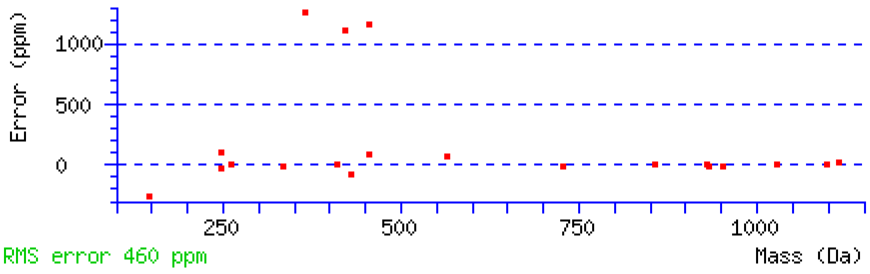


```
Monoisotopic mass of neutral peptide Mr(calc): 1358.654022
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00032
Matches : 20/98 fragment ions using 41 most intense peaks    (help)
```

#	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	**262.085603**	131.546439	244.075038	122.541157	C	1272.629288	636.818282	1255.602739	628.305008	1254.618723	627.813000	11
3	**333.122717**	167.064997	315.112152	158.059714	A	***1098.582989***	549.795133	1081.556440	541.281858	1080.572424	540.789850	10
4	432.191131	216.599204	414.180566	207.593921	V	***1027.545875***	514.276576	1010.519326	505.763301	1009.535310	505.271293	9
5	503.228245	252.117761	485.217680	243.112478	A	***928.477461***	464.742369	911.450912	456.229094	910.466896	455.737086	8
6	632.270838	316.639057	614.260273	307.633775	E	***857.440347***	429.223812	840.413798	420.710537	839.429782	420.218529	7
7	795.334167	398.170722	777.323602	389.165439	Y	***728.397754***	364.702515	711.371205	356.189241			6
8	852.355631	426.681454	834.345066	417.676171	G	***565.334425***	283.170851	548.307876	274.657576			5
9	**951.424045**	476.215661	933.413480	467.210378	V	508.312961	254.660119	491.286412	246.146844			4
10	**1114.487374**	557.747325	1096.476809	548.742043	Y	***409.244547***	205.125912	392.217998	196.612637			3
11	1213.555788	607.281532	1195.545223	598.276250	V	***246.181218***	123.594247	229.154669	115.080973			2
12					K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 460 ppm



RMS error 460 ppm

NCBI **BLAST** search of SCAVAEYGVYVK
(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	1358.654022	0.004106	SCAVAEYGVYVK

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

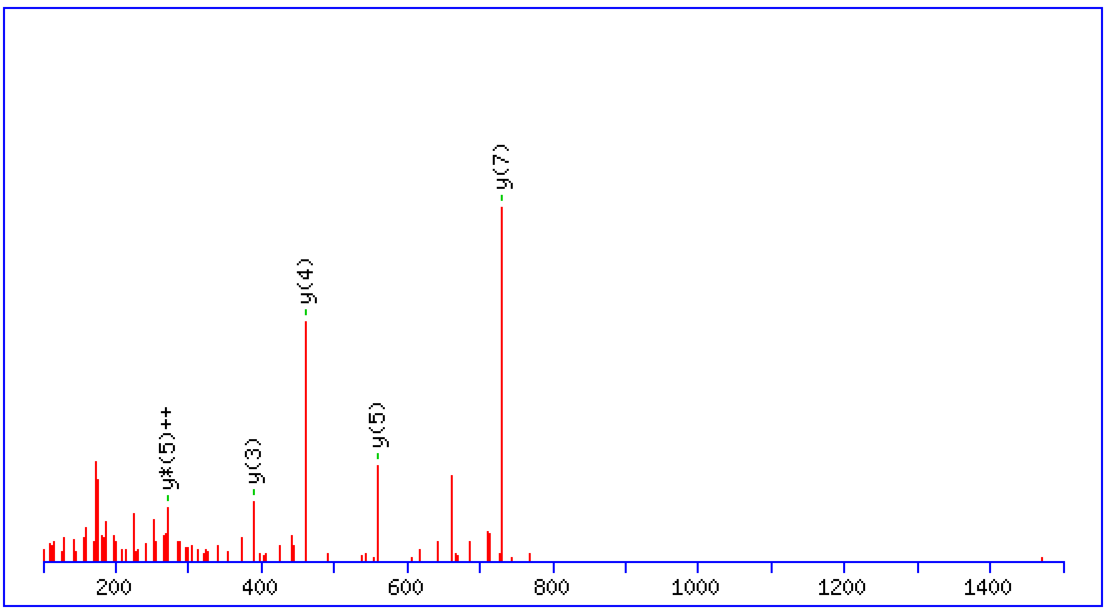
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIGVANQK**
Found in **HEAT1_HUMAN**, HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3

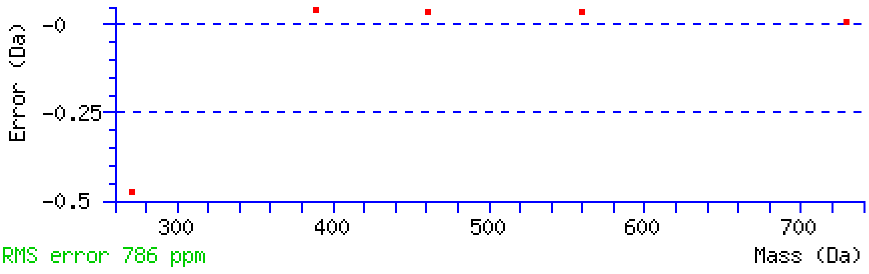
Match to Query 1327: 841.498388 from(421.756470,2+) rtinseconds(1844) index(11946)
Title: Locus:1.1.1.2632.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

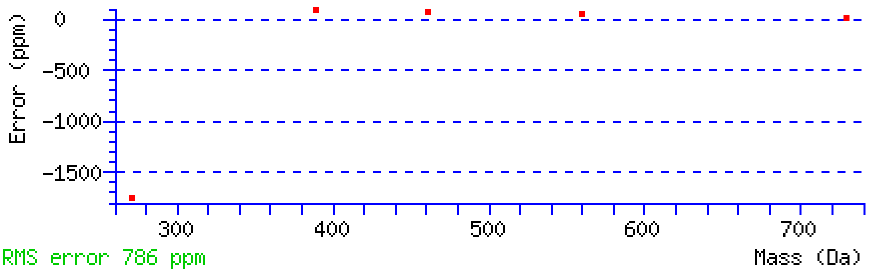
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 841.502136
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0087
Matches : 5/46 fragment ions using 7 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	***729.425365***	365.216321	712.398816	356.703046	7
3	284.196868	142.602072			G	616.341301	308.674289	599.314752	300.161014	6
4	383.265282	192.136279			V	***559.319837***	280.163557	542.293288	271.650282	5
5	454.302396	227.654836			A	***460.251423***	230.629349	443.224874	222.116075	4
6	568.345323	284.676300	551.318774	276.163025	N	***389.214309***	195.110792	372.187760	186.597518	3
7	696.403901	348.705589	679.377352	340.192314	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 LIGVANQK
(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	841.502136	-0.003748	LIGVANQK
12.4	841.502136	-0.003748	LPNTLLR
12.2	841.502136	-0.003748	ILGLAPSR
10.9	841.502136	-0.003748	IGLSLAPR
10.9	841.502121	-0.003733	IVAEAIAR
10.7	841.502136	-0.003748	LKDPTLR
10.7	841.502136	-0.003748	LNLLTPR
7.0	841.502151	-0.003763	ISGLPVTR
4.7	841.502151	-0.003763	ILVVQDR
4.7	841.502136	-0.003748	IPKSPLR

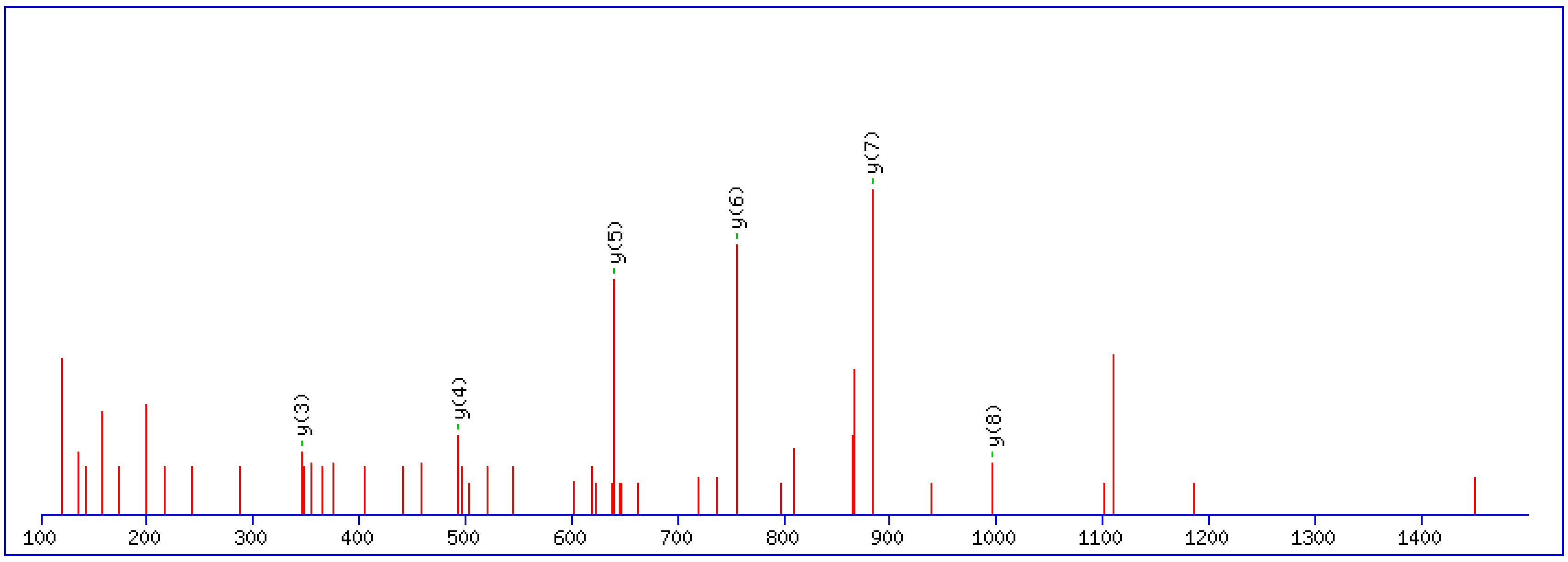
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQDFFNGR**
Found in **HSP71_HUMAN**, Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5

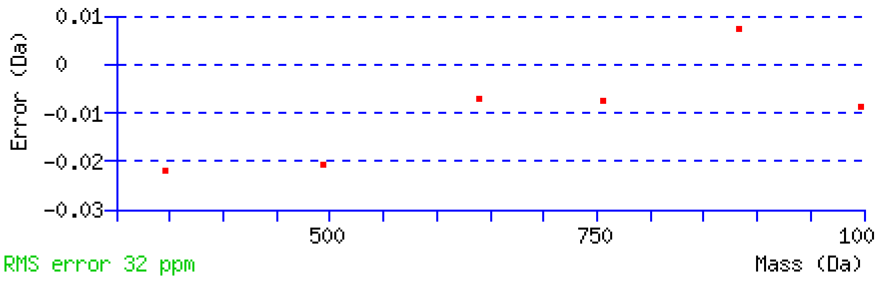
Match to Query 8202: 1108.574208 from(555.294380,2+) rtinseconds(2840) index(35917)
Title: Locus:1.1.1.1787.15
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

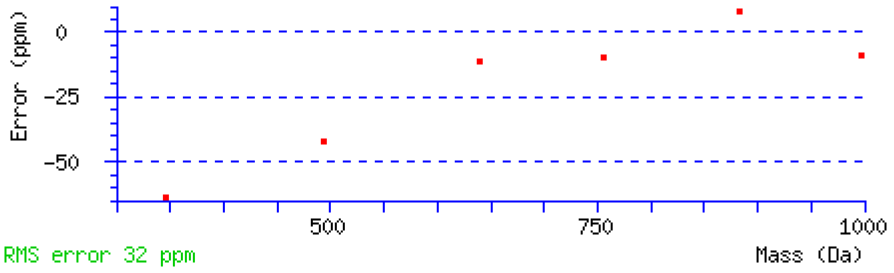
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1108.566544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.00015
Matches : 6/76 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					**L**	***996.489756***	498.748516	979.463207	490.235242	978.479191	489.743234	8
3	355.233982	178.120629	338.207433	169.607355			**Q**	***883.405692***	442.206484	866.379143	433.693210	865.395127	433.201202	7
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**D**	***755.347114***	378.177195	738.320565	369.663921	737.336549	369.171913	6
5	617.329339	309.168308	600.302790	300.655033	599.318774	300.163025	**F**	***640.320171***	320.663724	623.293622	312.150449			5
6	764.397753	382.702515	747.371204	374.189240	746.387188	373.697232	**F**	***493.251757***	247.129516	476.225208	238.616242			4
7	878.440680	439.723978	861.414131	431.210704	860.430115	430.718696	**N**	***346.183343***	173.595309	329.156794	165.082035			3
8	935.462144	468.234710	918.435595	459.721436	917.451579	459.229428	**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 LLQDFFNGR
(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	1108.566544	0.007664	LLQDFFNGR
3.6	1108.576431	-0.002223	LLEYDTVTR
3.1	1108.581131	-0.006923	LQLSGHAMPR

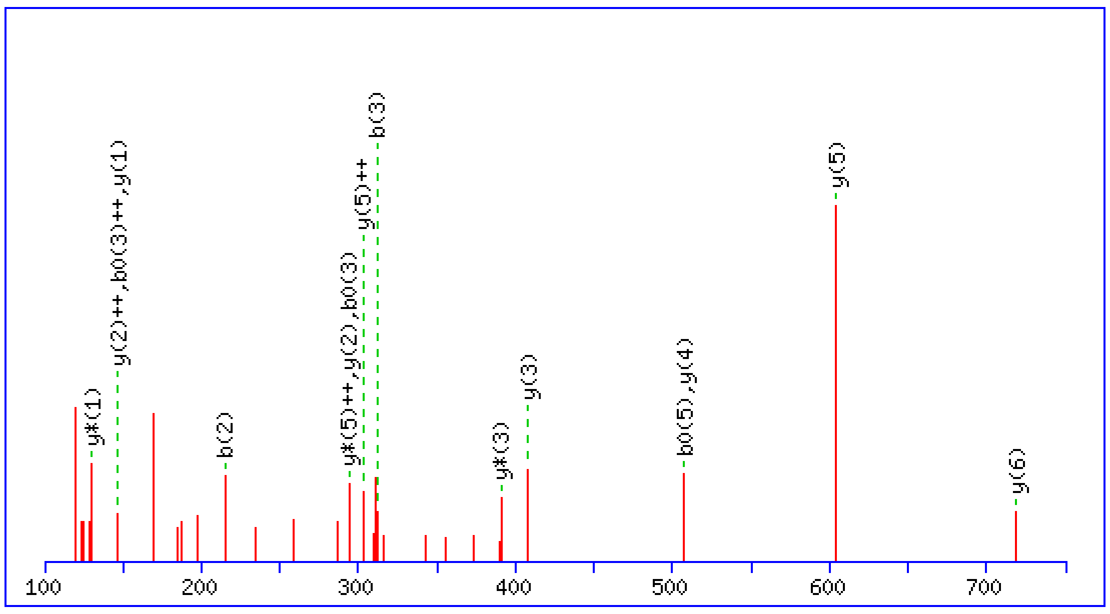
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDPVNFK**
Found in **HBAZ_HUMAN**, Hemoglobin subunit zeta OS=Homo sapiens GN=HBZ PE=1 SV=2

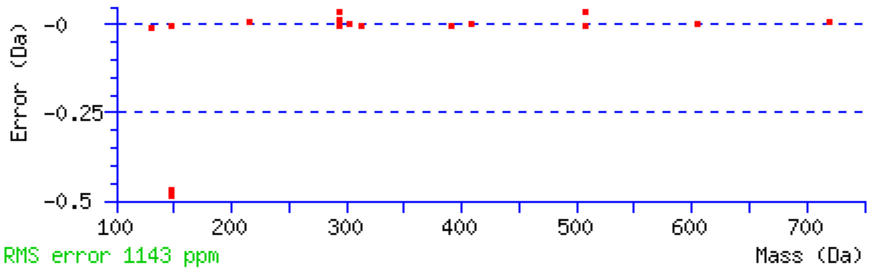
Match to Query 727: 817.433488 from(409.724020,2+) rtinseconds(1817) index(3382)
Title: Locus:1.1.1.2449.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

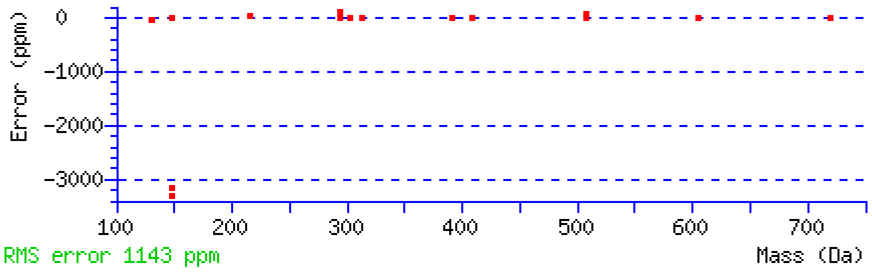
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 817.433411
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00036
Matches : 16/52 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	100.075690	50.541483					V							7
2	**215.102633**	108.054954			197.092068	99.049672	D	***719.372266***	360.189771	702.345717	351.676497	701.361701	351.184489	6
3	**312.155397**	156.581336			294.144832	147.576054	P	***604.345323***	302.676300	587.318774	294.163025			5
4	411.223811	206.115544			393.213246	197.110261	V	***507.292559***	254.149917	490.266010	245.636643			4
5	525.266738	263.137007	508.240189	254.623733	507.256173	254.131725	N	***408.224145***	204.615710	391.197596	196.102436			3
6	672.335152	336.671214	655.308603	328.157940	654.324587	327.665932	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 VDPVNFK
(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	817.433411	0.000077	VDPVNFK
25.0	817.436783	-0.003295	VPMTSGVK
19.0	817.429382	0.004106	TPPTSRK
13.6	817.433395	0.000093	VDSIAWK
7.2	817.436768	-0.003280	TLCPAVK
5.1	817.440598	-0.007110	NVTNRSK
4.7	817.436768	-0.003280	VQMPSLK
4.6	817.433395	0.000093	WDASVLK
3.7	817.429367	0.004121	DADRTLK
1.9	817.429382	0.004106	GEKGGVGSK

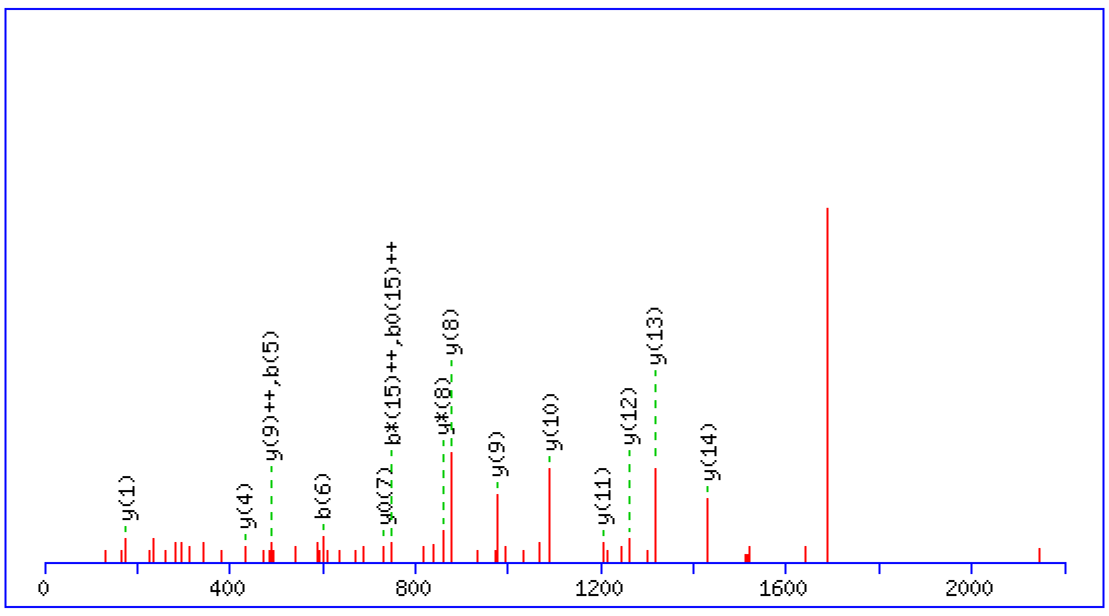
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFIGGLNVQTSESGLR**
Found in **ROA0_HUMAN**, Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1

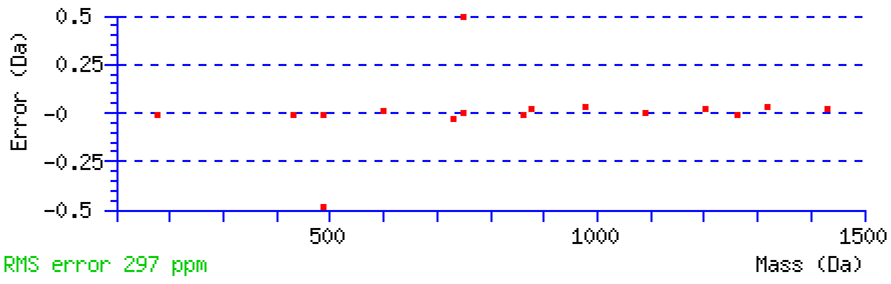
Match to Query 48086: 1689.917688 from(845.966120,2+) rtinseconds(3194) index(42694)
Title: Locus:1.1.1.2612.44
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

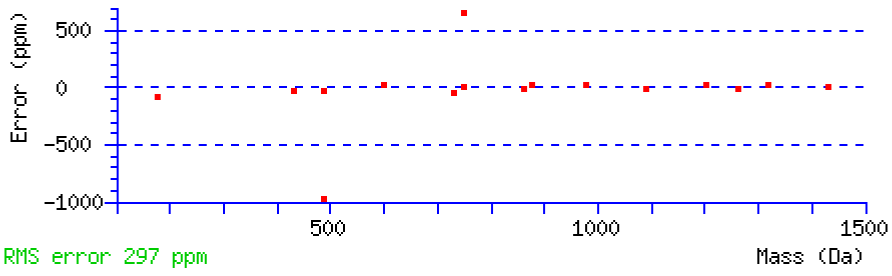
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1689.904984
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 2.5e-005
Matches : 16/144 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							16
2	261.159754	131.083515					F	1577.828197	789.417737	1560.801648	780.904462	1559.817632	780.412454	15
3	374.243818	187.625547					I	*1430.759783*	715.883530	1413.733234	707.370255	1412.749218	706.878247	14
4	431.265282	216.136279					G	*1317.675719*	659.341498	1300.649170	650.828223	1299.665154	650.336215	13
5	**488.286746**	244.647011					G	*1260.654255*	630.830765	1243.627706	622.317491	1242.643690	621.825483	12
6	**601.370810**	301.189043					L	*1203.632791*	602.320034	1186.606242	593.806759	1185.622226	593.314751	11
7	715.413737	358.210507	698.387188	349.697232			N	*1090.548727*	545.778002	1073.522178	537.264727	1072.538162	536.772719	10
8	814.482151	407.744713	797.455602	399.231439			V	*976.505800*	488.756538	959.479251	480.243264	958.495235	479.751256	9
9	942.540729	471.774002	925.514180	463.260728			Q	*877.437386*	439.222331	860.410837	430.709057	859.426821	430.217049	8
10	1043.588408	522.297842	1026.561859	513.784567	1025.577843	513.292559	T	749.378808	375.193042	732.352259	366.679768	731.368243	366.187760	7
11	1130.620436	565.813856	1113.593887	557.300582	1112.609871	556.808573	S	648.331129	324.669203	631.304580	316.155928	630.320564	315.663920	6
12	1259.663029	630.335153	1242.636480	621.821878	1241.652464	621.329870	E	561.299101	281.153189	544.272552	272.639914	543.288536	272.147906	5
13	1346.695057	673.851167	1329.668508	665.337892	1328.684492	664.845884	S	*432.256508*	216.631892	415.229959	208.118617	414.245943	207.626609	4
14	1403.716521	702.361899	1386.689972	693.848624	1385.705956	693.356616	G	345.224480	173.115878	328.197931	164.602603			3
15	1516.800585	758.903931	1499.774036	750.390656	1498.790020	749.898648	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 LFIGGLNVQTSESGLR
(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	1689.904984	0.012704	LFIGGLNVQTSESGLR
9.0	1689.923615	-0.005927	HMPPLKPKPLVTPR
5.3	1689.904968	0.012720	DIVDSFIRGSILEAR
5.3	1689.923615	-0.005927	HMPPLKPKPLVTPR
5.3	1689.923615	-0.005927	HMPPLKPKPLVTPR
5.3	1689.923615	-0.005927	HMPPLKPKPLVTPR
5.3	1689.923615	-0.005927	HMPPLKPKPLVTPR
2.1	1689.931458	-0.013770	FLNLIHHAAQGPTKK
1.0	1689.915695	0.001993	LEMMLEQKLALLSR
0.3	1689.923569	-0.005881	LFLDLACRLISEAR

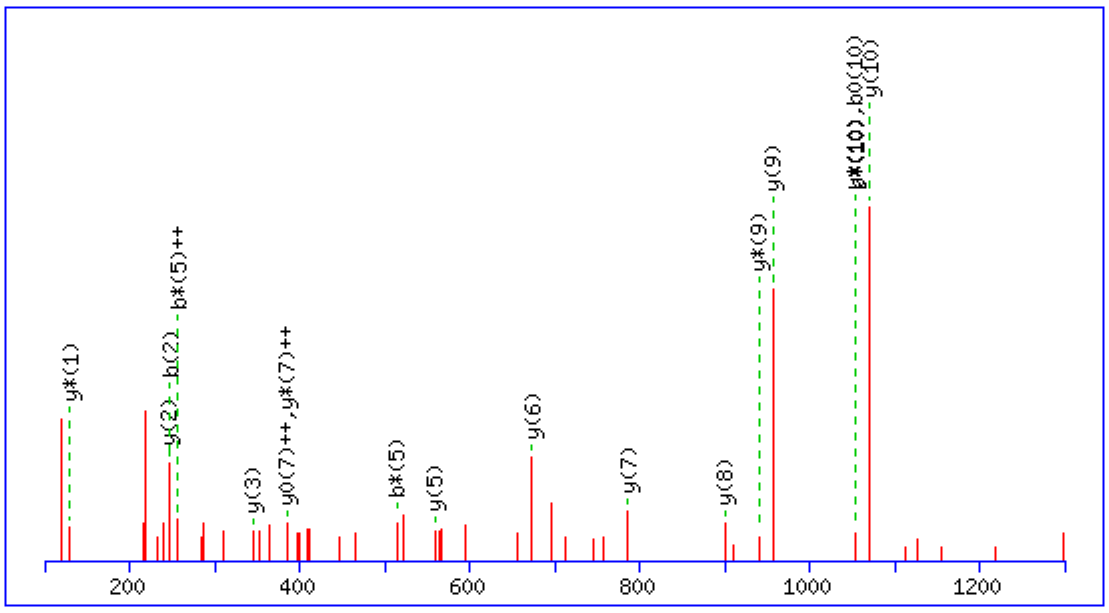
{MATRIX SCIENCE} Mascot Search Results

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

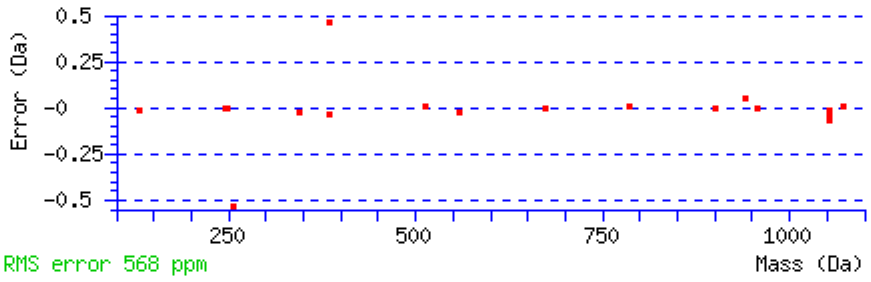
Match to Query 13919: 1315.785068 from(658.899810,2+) rtinseconds(3234) index(12489)
Title: Locus:1.1.1.3244.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

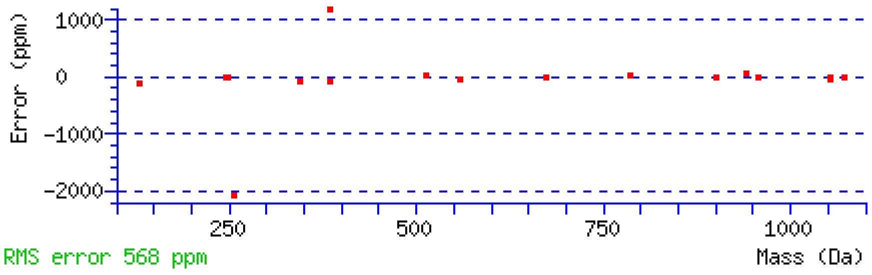
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1315.786377
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0014
Matches : 18/102 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	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
31.0	1315.786377	-0.001309	VFIGNLNTLVVK

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

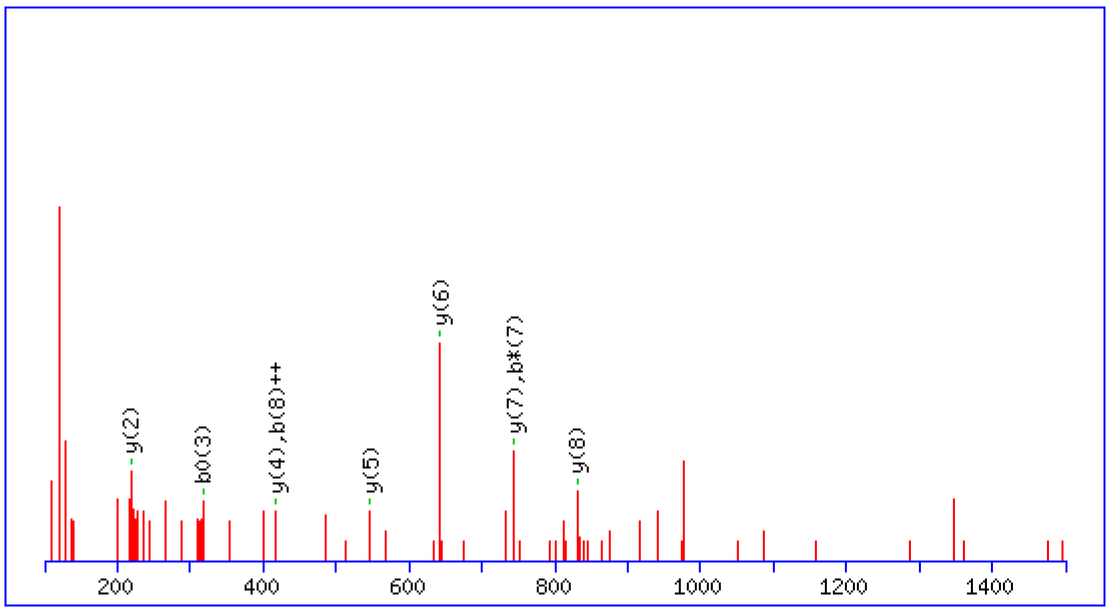
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSTPEQAAK**
Found in **HNRPL_HUMAN**, Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2

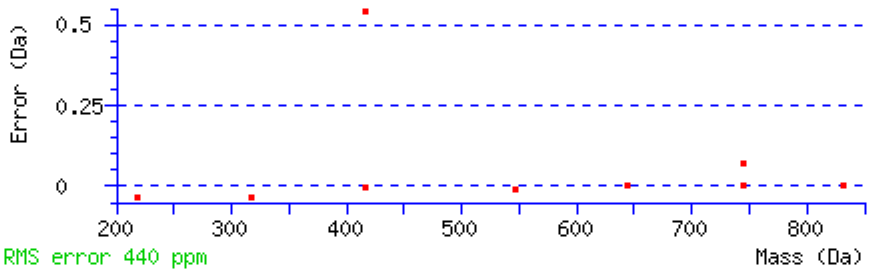
Match to Query 7068: 977.478808 from(489.746680,2+) rtinseconds(1157) index(7182)
Title: Locus:1.1.1.1918.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

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 ●

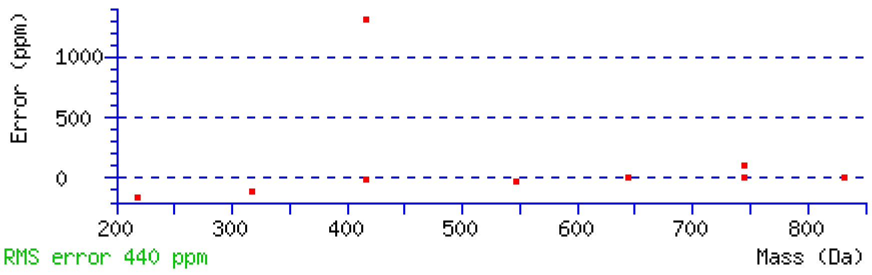


```
Monoisotopic mass of neutral peptide Mr(calc): 977.481796
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00025
Matches : 9/76 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							9
2	235.107718	118.057497			217.097153	109.052214	S	***831.420674***	416.213975	814.394125	407.700701	813.410109	407.208693	8
3	336.155397	168.581336			318.144832	159.576054	T	***744.388646***	372.697961	727.362097	364.184687	726.378081	363.692679	7
4	433.208161	217.107718			415.197596	208.102436	P	***643.340967***	322.174122	626.314418	313.660847	625.330402	313.168839	6
5	562.250754	281.629015			544.240189	272.623733	E	***546.288203***	273.647740	529.261654	265.134465	528.277638	264.642457	5
6	690.309332	345.658304	673.282783	337.145030	672.298767	336.653022	Q	***417.245610***	209.126443	400.219061	200.613168			4
7	761.346446	381.176861	744.319897	372.663587	743.335881	372.171579	A	289.187032	145.097154	272.160483	136.583879			3
8	832.383560	416.695418	815.357011	408.182144	814.372995	407.690136	A	***218.149918***	109.578597	201.123369	101.065322			2
9							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 440 ppm



RMS error 440 ppm

NCBI **BLAST** search of FSTPEQAAK
(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	977.481796	-0.002988	FSTPEQAAK

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

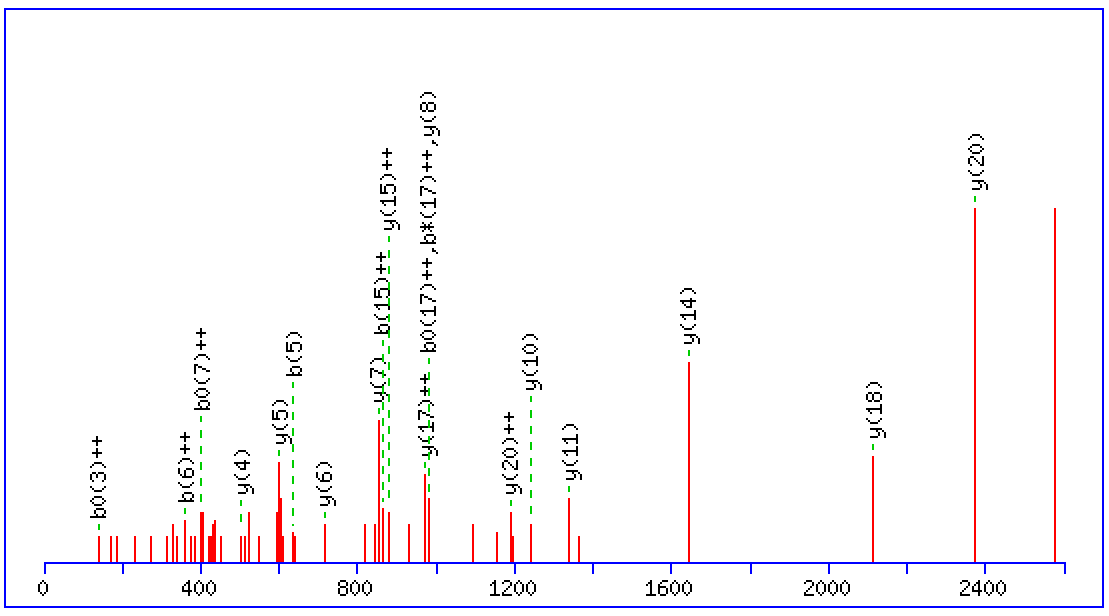
{MATRIX SCIENCE} Mascot Search Results

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

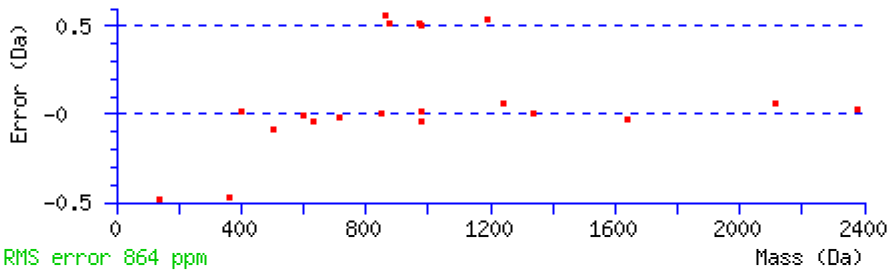
Match to Query 59969: 2574.319692 from(859.113840,3+) rtinseconds(4097) index(52364)
Title: Locus:1.1.1.3493.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

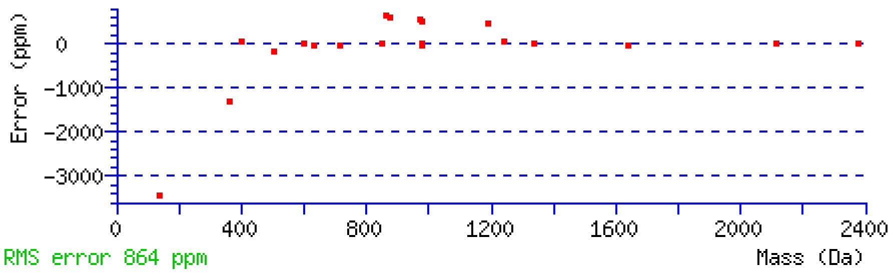
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2574.294067
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00039
Matches : 20/220 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	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
36.8	2574.294067	0.025625	AEPYCSVLPGFTFIQHLPLSER
0.5	2574.311157	0.008535	SIQGPSLSSWRNVMSEASLDVLAK

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

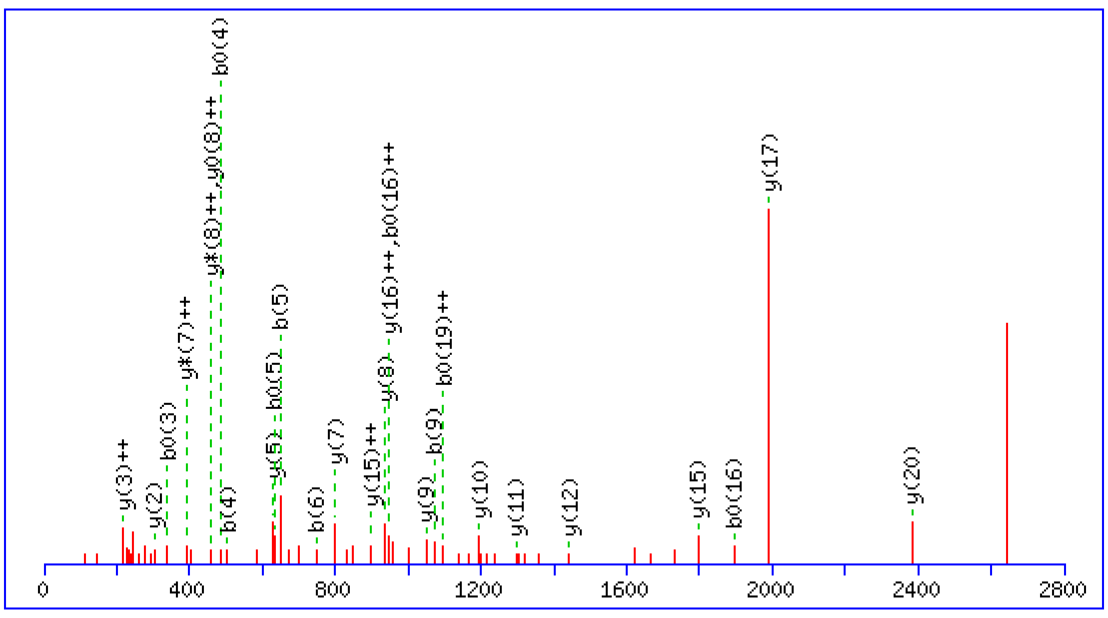
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEPFFPPPEEFVFIHAVPVEER**
Found in **HNRL2_HUMAN**, Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1

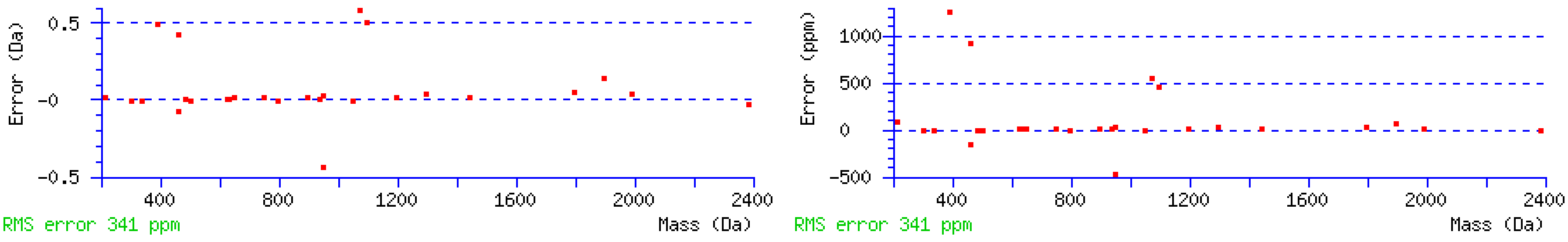
Match to Query 61006: 2640.313662 from(881.111830,3+) rtinseconds(4094) index(52313)
Title: Locus:1.1.1.3492.35
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

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): 2640.290039
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.5e-005
Matches : 27/208 fragment ions using 55 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							22
2	259.092462	130.049869	241.081897	121.044587	E	2512.254725	1256.631000	2495.228176	1248.117726	2494.244160	1247.625718	21
3	356.145226	178.576251	338.134661	169.570969	P	*2383.212132*	1192.109704	2366.185583	1183.596429	2365.201567	1183.104421	20
4	**503.213640**	252.110458	485.203075	243.105176	F	2286.159368	1143.583322	2269.132819	1135.070047	2268.148803	1134.578039	19
5	**650.282054**	325.644665	632.271489	316.639383	F	2139.090954	1070.049115	2122.064405	1061.535840	2121.080389	1061.043832	18
6	**747.334818**	374.171047	729.324253	365.165765	P	*1992.022540*	996.514908	1974.995991	988.001634	1974.011975	987.509626	17
7	844.387582	422.697429	826.377017	413.692147	P	1894.969776	947.988526	1877.943227	939.475252	1876.959211	938.983244	16
8	941.440346	471.223811	923.429781	462.218529	P	*1797.917012*	899.462144	1780.890463	890.948870	1779.906447	890.456862	15
9	**1070.482939**	535.745108	1052.472374	526.739825	E	1700.864248	850.935762	1683.837699	842.422488	1682.853683	841.930480	14
10	1199.525532	600.266404	1181.514967	591.261122	E	1571.821655	786.414466	1554.795106	777.901191	1553.811090	777.409183	13
11	1346.593946	673.800611	1328.583381	664.795329	F	*1442.779062*	721.893169	1425.752513	713.379895	1424.768497	712.887887	12
12	1445.662360	723.334818	1427.651795	714.329536	V	*1295.710648*	648.358962	1278.684099	639.845688	1277.700083	639.353680	11
13	1592.730774	796.869025	1574.720209	787.863743	F	*1196.642234*	598.824755	1179.615685	590.311481	1178.631669	589.819473	10
14	1705.814838	853.411057	1687.804273	844.405775	I	*1049.573820*	525.290548	1032.547271	516.777274	1031.563255	516.285266	9
15	1842.873750	921.940513	1824.863185	912.935231	H	*936.489756*	468.748516	919.463207	460.235242	918.479191	459.743234	8
16	1913.910864	957.459070	1895.900299	948.453788	A	*799.430844*	400.219060	782.404295	391.705786	781.420279	391.213778	7
17	2012.979278	1006.993277	1994.968713	997.987995	V	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	6
18	2110.032042	1055.519659	2092.021477	1046.514377	P	*629.325316*	315.166296	612.298767	306.653022	611.314751	306.161014	5
19	2209.100456	1105.053866	2191.089891	1096.048583	V	532.272552	266.639914	515.246003	258.126640	514.261987	257.634632	4
20	2338.143049	1169.575163	2320.132484	1160.569880	E	433.204138	217.105707	416.177589	208.592433	415.193573	208.100425	3
21	2467.185642	1234.096459	2449.175077	1225.091177	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 EEPFFPPPEEFVFIHAVPVEER
(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	2640.290039	0.023623	EEPFFPPPEEFVFIHAVPVEER
2.4	2640.326447	-0.012785	SGRMGPAMLRPALPAGPVGASSWQAK
2.0	2640.326447	-0.012785	SGRMGPAMLRPALPAGPVGASSWQAK
1.9	2640.326447	-0.012785	SGRMGPAMLRPALPAGPVGASSWQAK
1.3	2640.301300	0.012362	LHGMLEFLRPSSSNHSVGPMRTR
1.3	2640.301300	0.012362	LHGMLEFLRPSSSNHSVGPMRTR
0.6	2640.292755	0.020907	VCAKPWAPDMTLPGISPPPEKQK
0.6	2640.292755	0.020907	VCAKPWAPDMTLPGISPPPEKQK

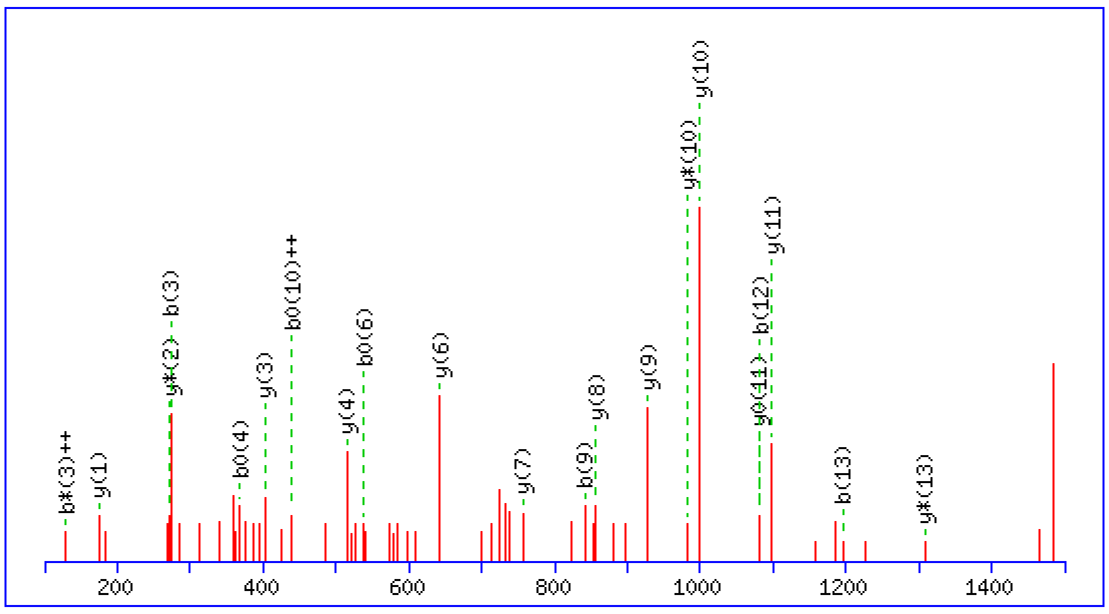
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SANLVAATLGAILNR**
Found in **HXK1_HUMAN**, Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3

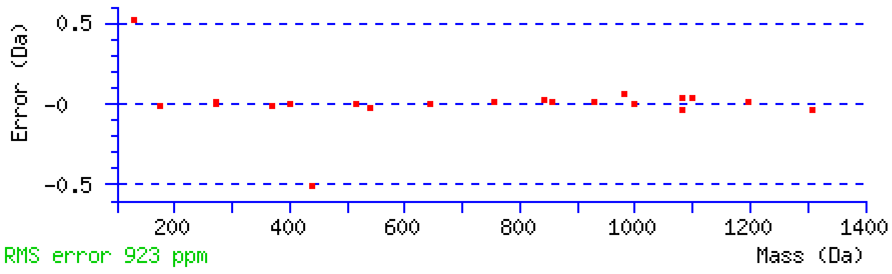
Match to Query 35427: 1482.862088 from(742.438320,2+) rtinseconds(4477) index(65153)
Title: Locus:1.1.1.3304.21
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

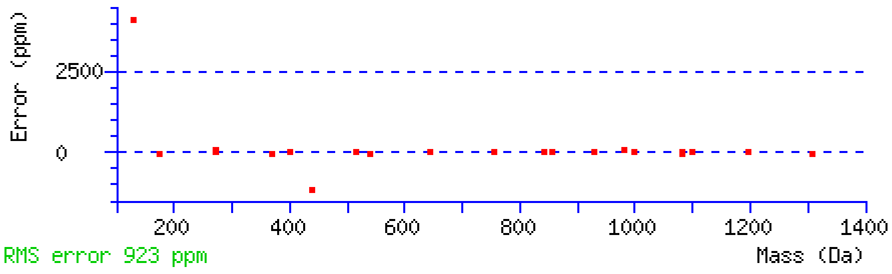
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1482.851791
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66  Expect: 6.6e-007
Matches : 21/150 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	88.039304	44.523290			70.028739	35.518008	S							15
2	159.076418	80.041847			141.065853	71.036564	A	1396.827075	698.917175	1379.800526	690.403901	1378.816510	689.911893	14
3	**273.119345**	137.063311	256.092796	128.550036	255.108780	128.058028	N	1325.789961	663.398619	1308.763412	654.885344	1307.779396	654.393336	13
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	L	1211.747034	606.377155	1194.720485	597.863881	1193.736469	597.371872	12
5	485.271823	243.139550	468.245274	234.626275	467.261258	234.134267	V	***1098.662970***	549.835123	1081.636421	541.321849	1080.652405	540.829841	11
6	556.308937	278.658107	539.282388	270.144832	538.298372	269.652824	A	***999.594556***	500.300916	982.568007	491.787642	981.583991	491.295634	10
7	627.346051	314.176664	610.319502	305.663389	609.335486	305.171381	A	***928.557442***	464.782359	911.530893	456.269084	910.546877	455.777076	9
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	T	***857.520328***	429.263802	840.493779	420.750527	839.509763	420.258519	8
9	**841.477794**	421.242535	824.451245	412.729261	823.467229	412.237253	L	***756.472649***	378.739962	739.446100	370.226688			7
10	898.499258	449.753267	881.472709	441.239993	880.488693	440.747985	G	***643.388585***	322.197930	626.362036	313.684656			6
11	969.536372	485.271824	952.509823	476.758550	951.525807	476.266542	A	586.367121	293.687198	569.340572	285.173924			5
12	**1082.620436**	541.813856	1065.593887	533.300582	1064.609871	532.808574	I	***515.330007***	258.168641	498.303458	249.655367			4
13	**1195.704500**	598.355888	1178.677951	589.842614	1177.693935	589.350606	L	***402.245943***	201.626609	385.219394	193.113335			3
14	1309.747427	655.377352	1292.720878	646.864077	1291.736862	646.372069	N	289.161879	145.084577	272.135330	136.571303			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.1	1482.851791	0.010297	SANLVAATLGAILNR
6.2	1482.847946	0.014142	MALVLEALPQIAAK
2.8	1482.851822	0.010266	LALVTGASGGIGAAVAR

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

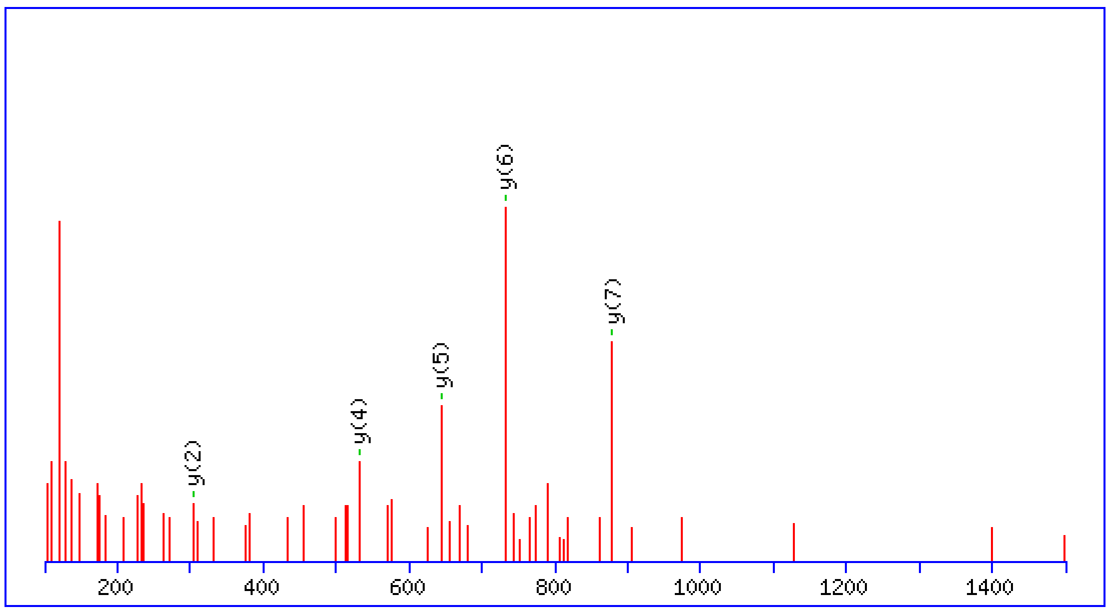
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IFSIVEQR**
Found in **SYHC_HUMAN**, Histidyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2

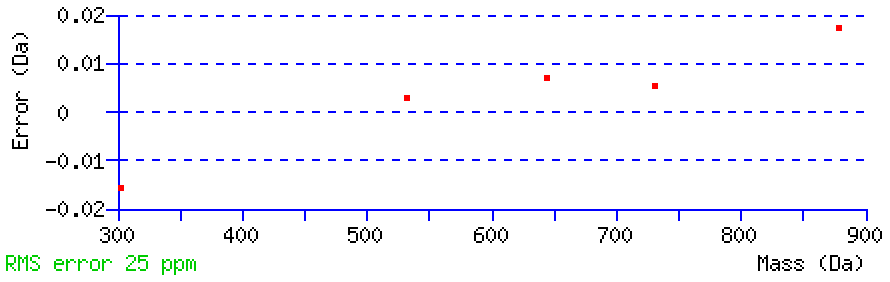
Match to Query 7638: 990.548088 from(496.281320,2+) rtinseconds(2227) index(27568)
Title: Locus:1.1.1.2330.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

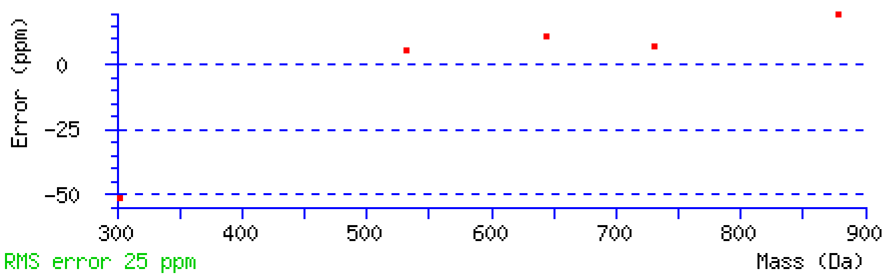
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 990.549820
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0024
Matches : 5/64 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					I							8
2	261.159754	131.083515					F	*878.473043*	439.740160	861.446494	431.226885	860.462478	430.734877	7
3	348.191782	174.599529			330.181217	165.594246	S	*731.404629*	366.205953	714.378080	357.692678	713.394064	357.200670	6
4	461.275846	231.141561			443.265281	222.136278	I	*644.372601*	322.689939	627.346052	314.176664	626.362036	313.684656	5
5	560.344260	280.675768			542.333695	271.670485	V	*531.288537*	266.147907	514.261988	257.634632	513.277972	257.142624	4
6	689.386853	345.197065			671.376288	336.191782	E	432.220123	216.613700	415.193574	208.100425	414.209558	207.608417	3
7	817.445431	409.226354	800.418882	400.713079	799.434866	400.221071	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 IFSIVEQR
(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	990.549820	-0.001732	IFSIVEQR
10.6	990.549820	-0.001732	IFSQLDIR
9.6	990.549820	-0.001732	FLSVLERQ
8.0	990.539917	0.008171	LFHYQKR
7.9	990.549835	-0.001747	LVFTDLQR
7.2	990.549820	-0.001732	SFLPLDRK
5.7	990.549820	-0.001732	LLSGFGLER
4.3	990.549835	-0.001747	LITQDFVR
2.9	990.549850	-0.001762	SLFVVVGDR
2.1	990.549820	-0.001732	KVTIYDPR

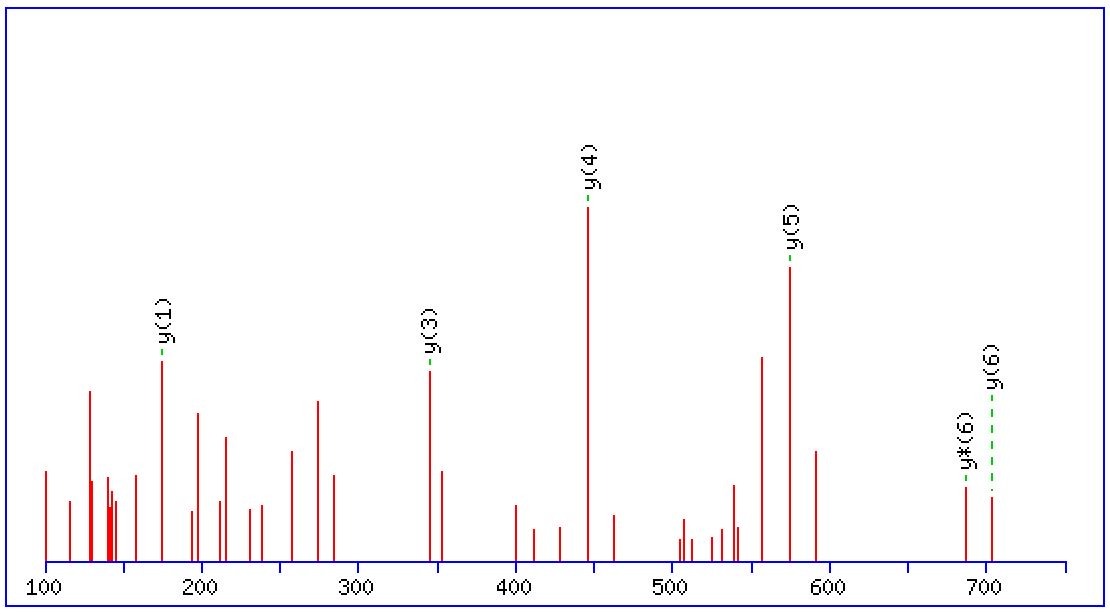
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQETGLR**
Found in **HDAC4_HUMAN**, Histone deacetylase 4 OS=Homo sapiens GN=HDAC4 PE=1 SV=3

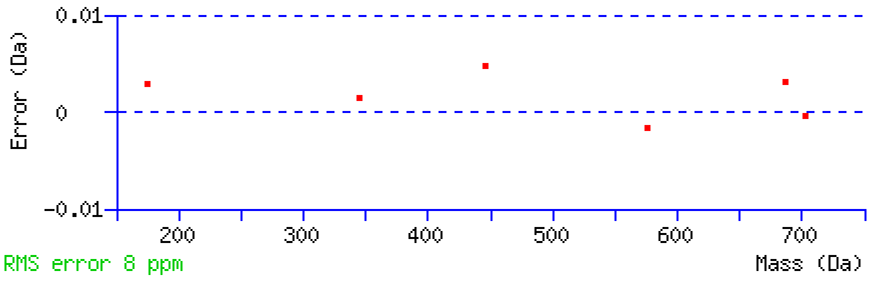
Match to Query 1797: 815.446368 from(408.730460,2+) rtinseconds(964) index(325)
Title: Locus:1.1.1.1807.3
Data file 2011-11-14 - TFD - S 2-7.mgf

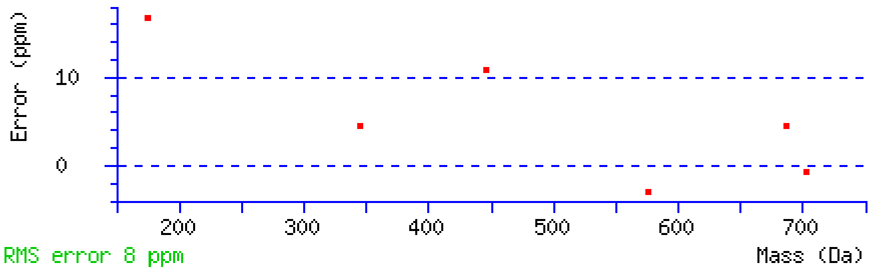
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 815.450104
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00063
Matches : 6/60 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**	*703.373330*	352.190303	686.346781	343.677029	685.362765	343.185021	6
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	**E**	*575.314752*	288.161014	558.288203	279.647740	557.304187	279.155732	5
4	472.240190	236.623733	455.213641	228.110459	454.229625	227.618451	**T**	*446.272159*	223.639718	429.245610	215.126443	428.261594	214.634435	4
5	529.261654	265.134465	512.235105	256.621191	511.251089	256.129183	**G**	*345.224480*	173.115878	328.197931	164.602604			3
6	642.345718	321.676497	625.319169	313.163223	624.335153	312.671215	**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 LQETGLR
(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	815.450104	-0.003736	LQETGLR
35.8	815.450104	-0.003736	EIQTAVR
27.7	815.450104	-0.003736	LQATEVR
24.5	815.450104	-0.003736	AAVTEAVR
20.8	815.450073	-0.003705	LEKAEAR
20.8	815.450073	-0.003705	LEKEAAR
20.8	815.450089	-0.003721	LEQLASR
14.4	815.438858	0.007510	LKEPGEK
14.4	815.454117	-0.007749	LQELWK
13.8	815.438858	0.007510	KLEPSDK

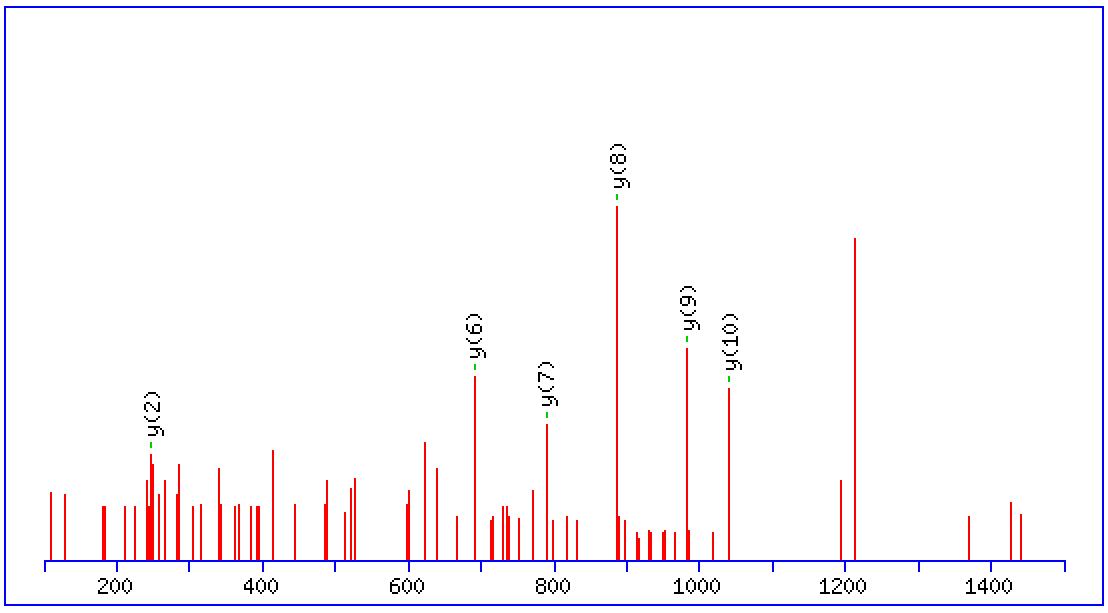
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATGPPVSELITK**
Found in **H15_HUMAN**, Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3

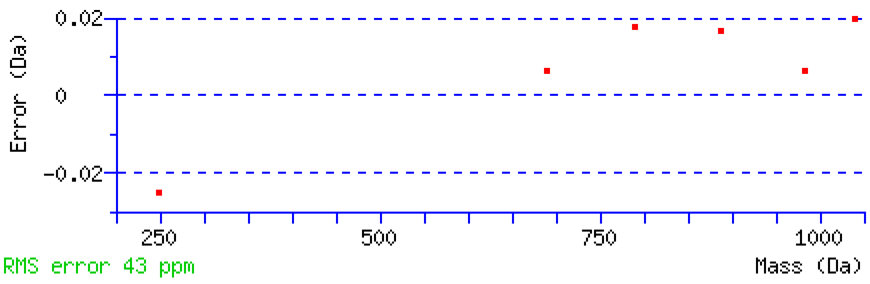
Match to Query 23739: 1211.686428 from(606.850490,2+) rtinseconds(2362) index(29358)
Title: Locus:1.1.1.2284.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

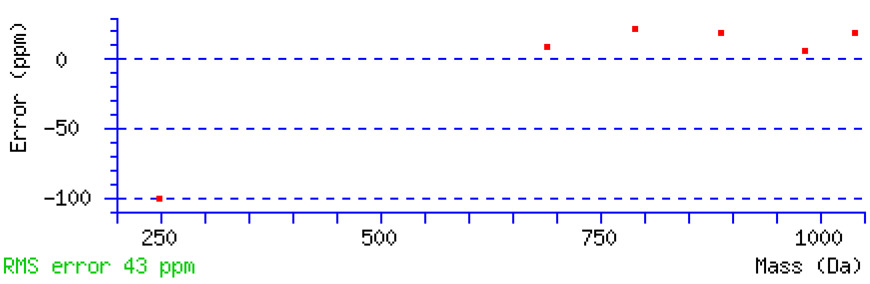
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1211.676147
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00046
Matches : 6/106 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	173.092069	87.049672	155.081504	78.044390	T	1141.646317	571.326797	1124.619768	562.813522	1123.635752	562.321514	11
3	230.113533	115.560404	212.102968	106.555122	G	*1040.598638*	520.802957	1023.572089	512.289682	1022.588073	511.797674	10
4	327.166297	164.086786	309.155732	155.081504	P	*983.577174*	492.292225	966.550625	483.778950	965.566609	483.286942	9
5	424.219061	212.613168	406.208496	203.607886	P	*886.524410*	443.765843	869.497861	435.252569	868.513845	434.760561	8
6	523.287475	262.147376	505.276910	253.142093	V	*789.471646*	395.239461	772.445097	386.726186	771.461081	386.234178	7
7	610.319503	305.663389	592.308938	296.658107	S	*690.403232*	345.705254	673.376683	337.191980	672.392667	336.699972	6
8	739.362096	370.184686	721.351531	361.179403	E	603.371204	302.189240	586.344655	293.675966	585.360639	293.183958	5
9	852.446160	426.726718	834.435595	417.721435	L	474.328611	237.667943	457.302062	229.154669	456.318046	228.662661	4
10	965.530224	483.268750	947.519659	474.263467	I	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
11	1066.577903	533.792589	1048.567338	524.787307	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 ATGPPVSELITK
(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	1211.676147	0.010281	ATGPPVSELITK

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

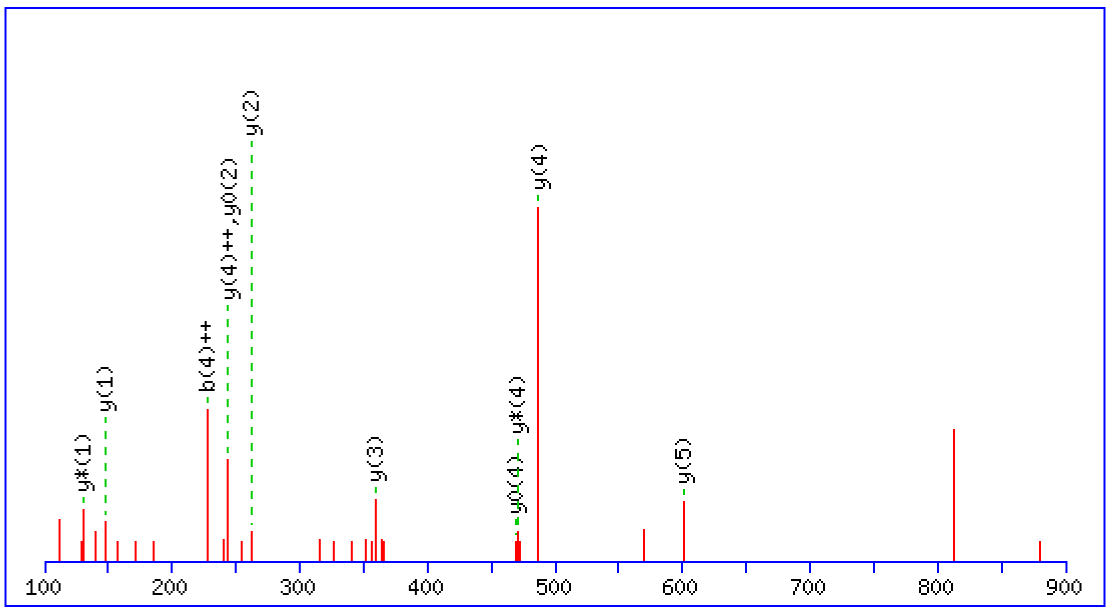
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPPKPDK**
Found in **H1FOO_HUMAN**, Histone H1oo OS=Homo sapiens GN=H1FOO PE=2 SV=1

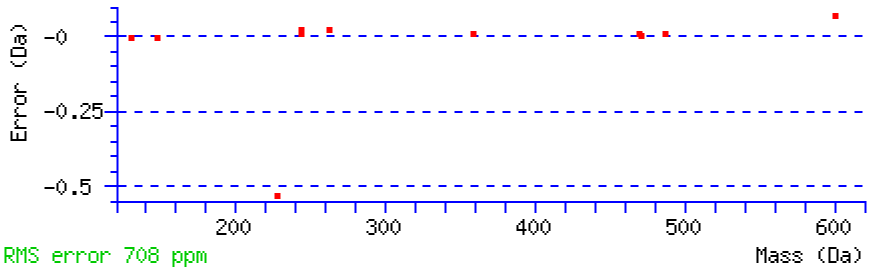
Match to Query 585: 811.450188 from(406.732370,2+) rtinseconds(1022) index(4586)
Title: Locus:1.1.1.1788.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

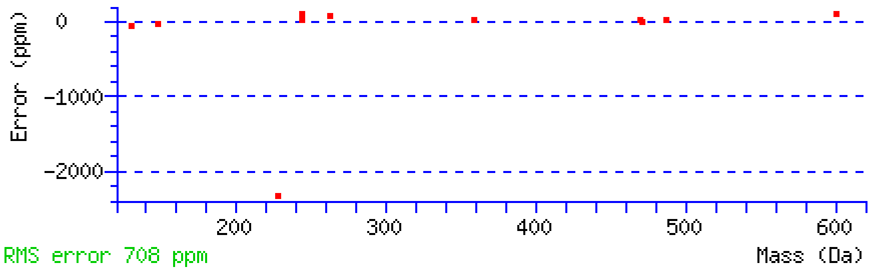
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 811.443970
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
P3      : Oxidation (P)
Ions Score: 39  Expect: 0.001
Matches : 11/54 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**							7
2	213.123369	107.065322					**P**	713.382832	357.195054	696.356283	348.681780	695.372267	348.189772	6
3	326.171048	163.589162					**P**	***600.335153***	300.671215	583.308604	292.157940	582.324588	291.665932	5
4	454.266011	227.636643	437.239462	219.123369			**K**	***487.287474***	244.147375	470.260925	235.634100	469.276909	235.142092	4
5	551.318775	276.163026	534.292226	267.649751			**P**	***359.192511***	180.099893	342.165962	171.586619	341.181946	171.094611	3
6	666.345718	333.676497	649.319169	325.163223	648.335153	324.671215	**D**	***262.139747***	131.573511	245.113198	123.060237	244.129182	122.568229	2
7							**K**	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPPKPDK
(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	811.443970	0.006218	VPPKPDK
19.8	811.455185	-0.004997	DPLQALR
13.7	811.443954	0.006234	DPLNPIK
12.2	811.443970	0.006218	VPEQPVK
11.4	811.443970	0.006218	IQTPPPK
10.4	811.443970	0.006218	VPQDPLK
7.7	811.443970	0.006218	VPPKPDK
6.2	811.443970	0.006218	VPNLPPK
5.2	811.445297	0.004891	QFRHPK
3.7	811.443970	0.006218	IQTPPPK

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

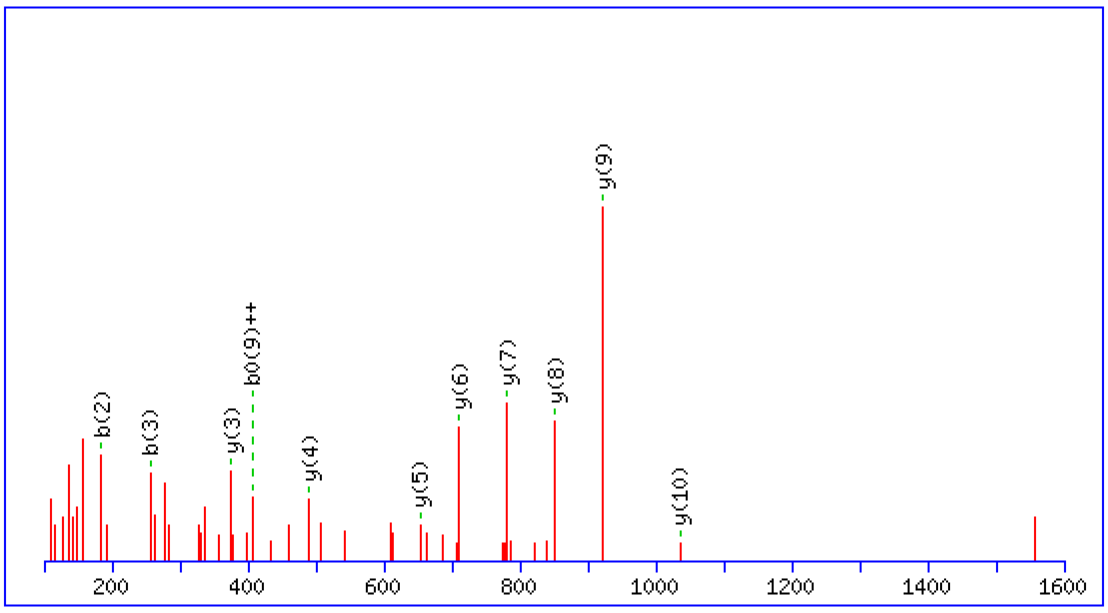
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALAAAGYDVEK**
Found in **H11_HUMAN**, Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3

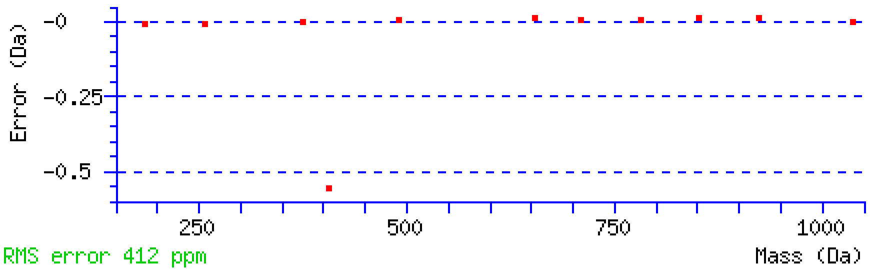
Match to Query 14578: 1106.560428 from(554.287490,2+) rtinseconds(1698) index(14805)
Title: Locus:1.1.1.2181.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

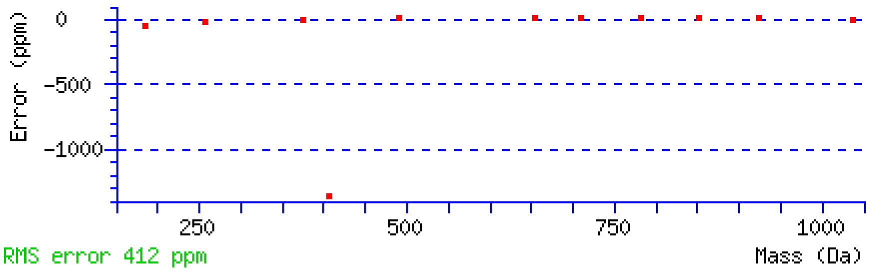
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1106.560760
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 3.7e-006
Matches : 11/84 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							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
65.4	1106.560760	-0.000332	ALAAAGYDVEK

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

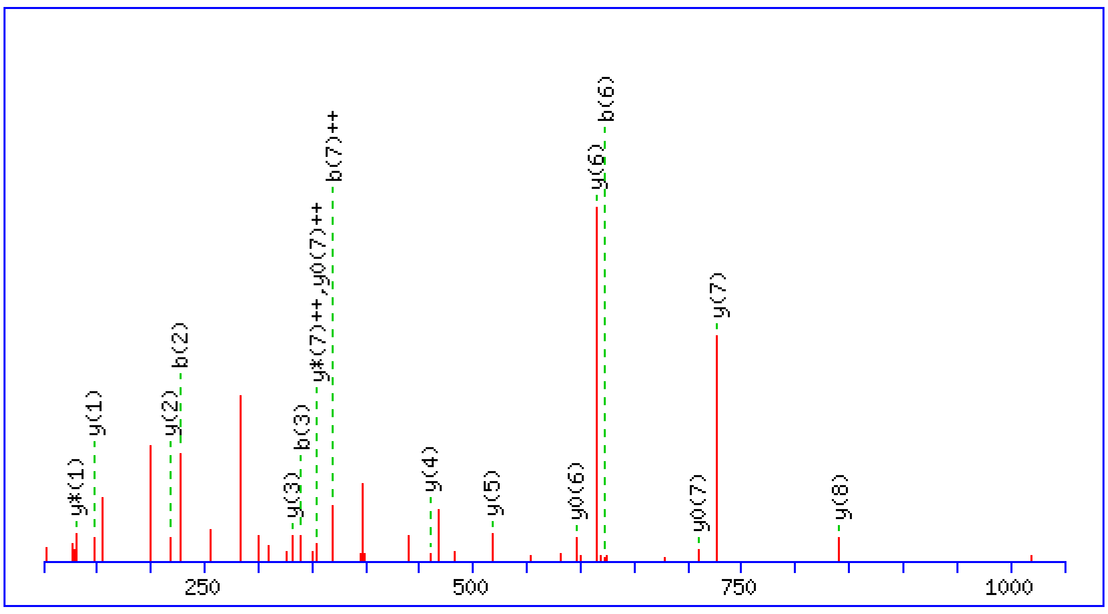
Mascot Search Results

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

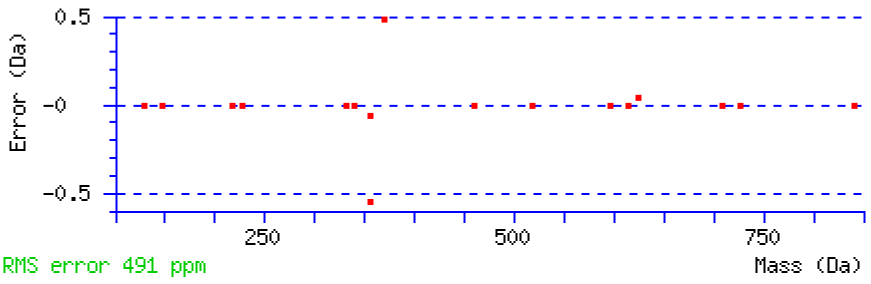
Match to Query 2909: 952.594628 from(477.304590,2+) rtinseconds(2721) index(5606)
Title: Locus:1.1.1.3343.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

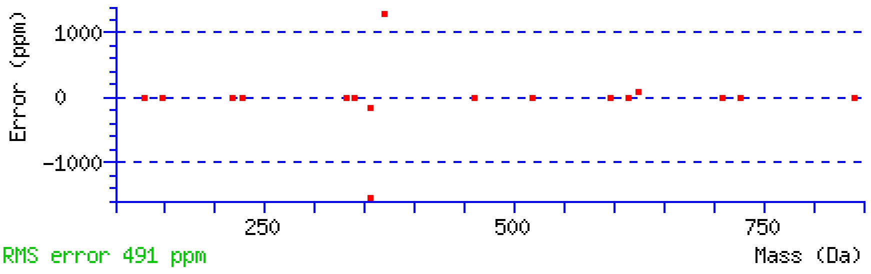
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 952.595688
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 3e-006
Matches : 17/64 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**							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
57.1	952.595688	-0.001060	LLLPGELAK
29.0	952.595688	-0.001060	IIIPEIQK
26.7	952.597031	-0.002403	LLIPRWR
22.6	952.595703	-0.001075	ILGILPPSK
17.9	952.595688	-0.001060	ILLLEAGPK
15.4	952.595688	-0.001060	LLIKEPPK
15.4	952.595688	-0.001060	LLIKEPPK
15.3	952.595703	-0.001075	ILGILPPSK
5.7	952.595688	-0.001060	LEPLKPLK
5.7	952.595688	-0.001060	LPEIKLPK

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

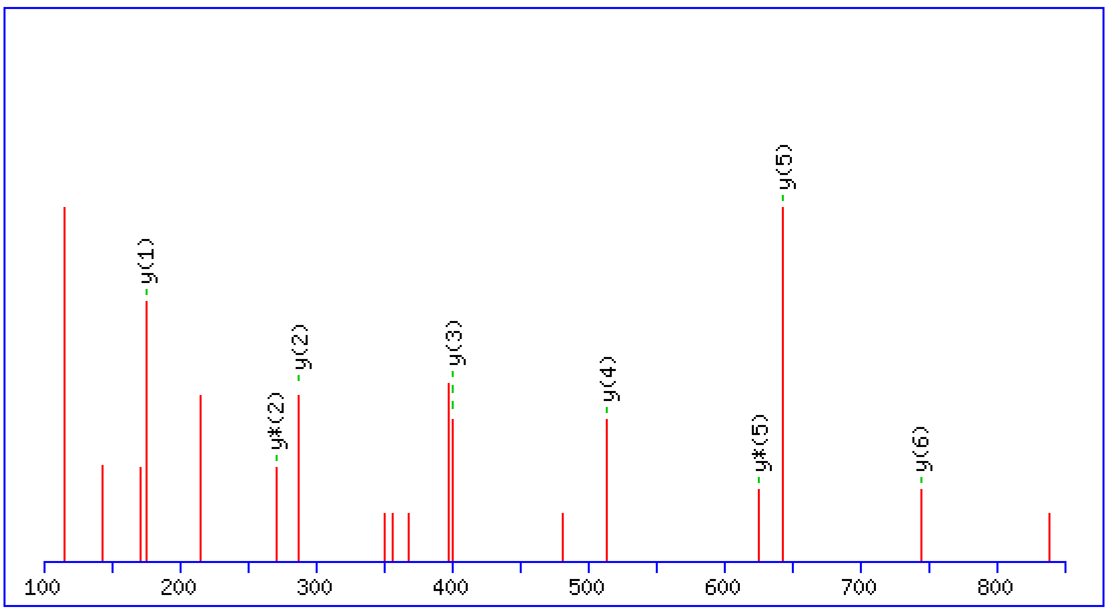
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STELLIR**
Found in **H31T_HUMAN**, Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3

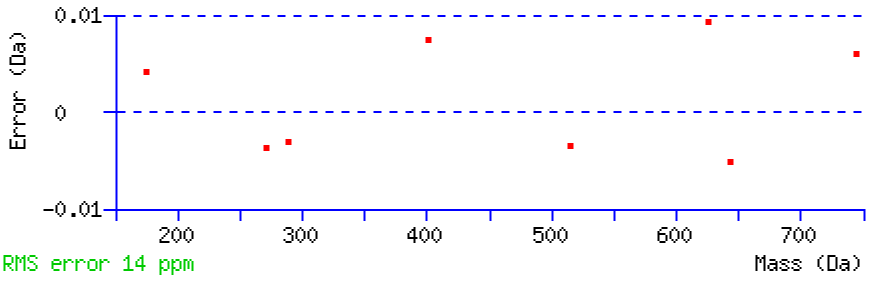
Match to Query 1515: 830.486248 from(416.250400,2+) rtinseconds(2011) index(16347)
Title: Locus:1.1.1.2578.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

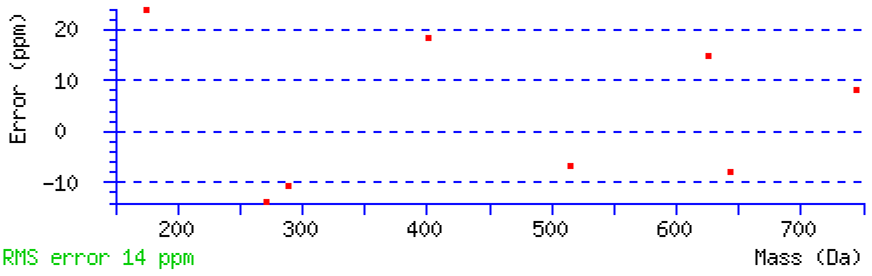
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 830.486145
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
54.5	830.486145	0.000103	STELLIR
11.8	830.486145	0.000103	TELSLLR
9.9	830.486145	0.000103	ESLTLLR
9.9	830.487503	-0.001255	HVGHLLR
9.9	830.479614	0.006634	KQCLLR
7.5	830.486160	0.000088	STAPVKTK
0.1	830.486160	0.000088	IITTDLR
0.1	830.486145	0.000103	LTELSLR
0.0	830.486160	0.000088	STLNGVLK

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

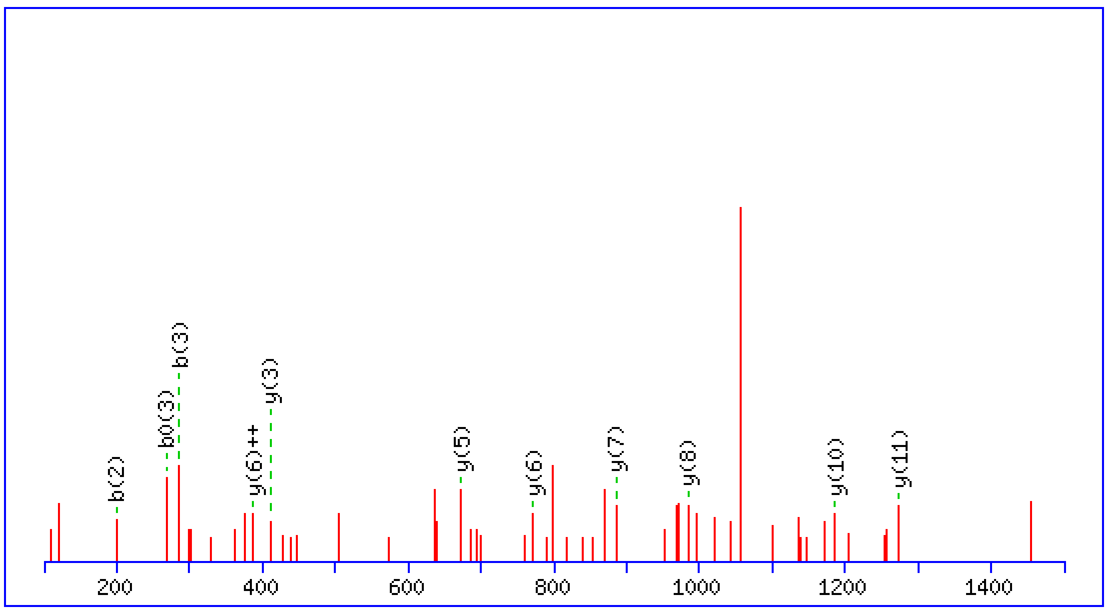
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPSSDVLVFDYTK**
Found in **RBBP4_HUMAN**, Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3

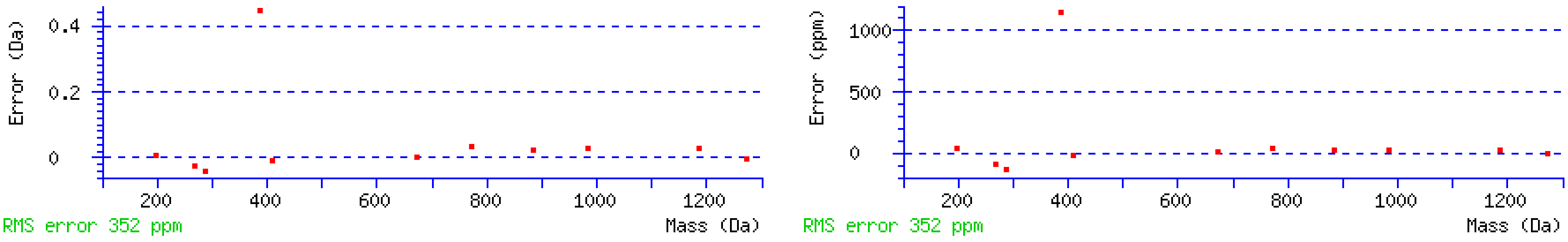
Match to Query 32685: 1470.730308 from(736.372430,2+) rtinseconds(2878) index(35103)
Title: Locus:1.1.1.2623.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

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): 1470.724243
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0048
Matches : 11/118 fragment ions using 24 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	**199.107719**	100.057497	181.097154	91.052215	P	1370.683824	685.845550	1353.657275	677.332276	1352.673259	676.840268	12
3	**286.139747**	143.573512	268.129182	134.568229	S	***1273.631060***	637.319168	1256.604511	628.805894	1255.620495	628.313886	11
4	373.171775	187.089525	355.161210	178.084243	S	***1186.599032***	593.803154	1169.572483	585.289880	1168.588467	584.797872	10
5	488.198718	244.602997	470.188153	235.597715	D	1099.567004	550.287140	1082.540455	541.773866	1081.556439	541.281858	9
6	587.267132	294.137204	569.256567	285.131922	V	***984.540061***	492.773669	967.513512	484.260394	966.529496	483.768386	8
7	700.351196	350.679236	682.340631	341.673954	L	***885.471647***	443.239462	868.445098	434.726187	867.461082	434.234179	7
8	799.419610	400.213443	781.409045	391.208161	V	***772.387583***	386.697430	755.361034	378.184155	754.377018	377.692147	6
9	946.488024	473.747650	928.477459	464.742368	F	***673.319169***	337.163223	656.292620	328.649948	655.308604	328.157940	5
10	1061.514967	531.261122	1043.504402	522.255839	D	526.250755	263.629016	509.224206	255.115741	508.240190	254.623733	4
11	1224.578296	612.792786	1206.567731	603.787504	Y	***411.223812***	206.115544	394.197263	197.602270	393.213247	197.110262	3
12	1325.625975	663.316626	1307.615410	654.311343	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 TPSSDVLVFDYTK
(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	1470.724243	0.006065	TPSSDVLVFDYTK
9.0	1470.731430	-0.001122	GEVDTAPQGNKDLK
3.3	1470.738831	-0.008523	VVSTSGEQMKVYK

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

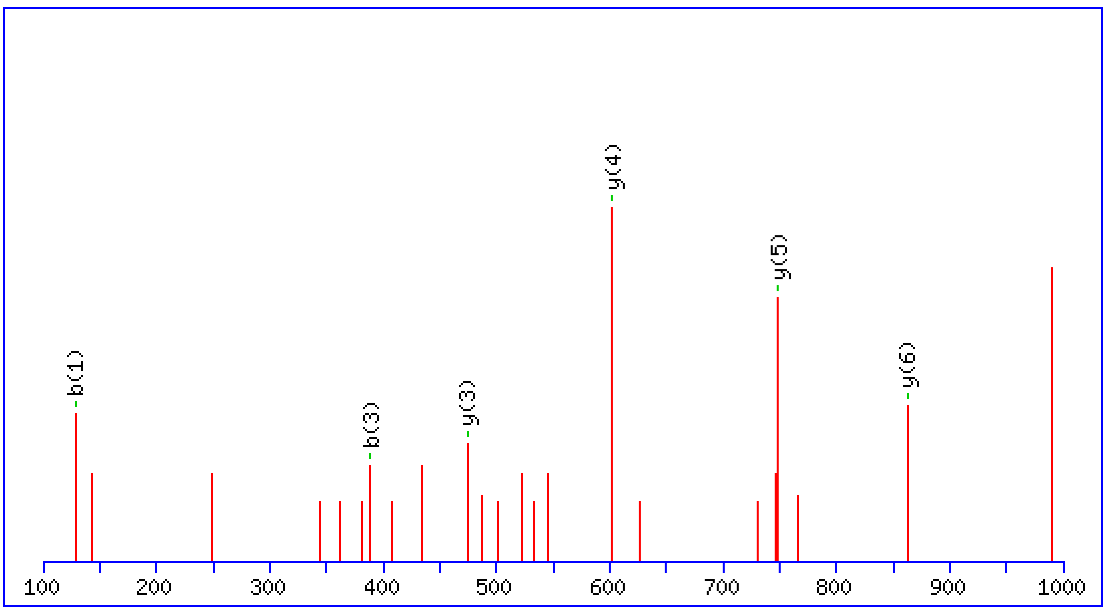
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIMKLWR**
Found in **MLL2_HUMAN**, Histone-lysine N-methyltransferase MLL2 OS=Homo sapiens GN=MLL2 PE=1 SV=2

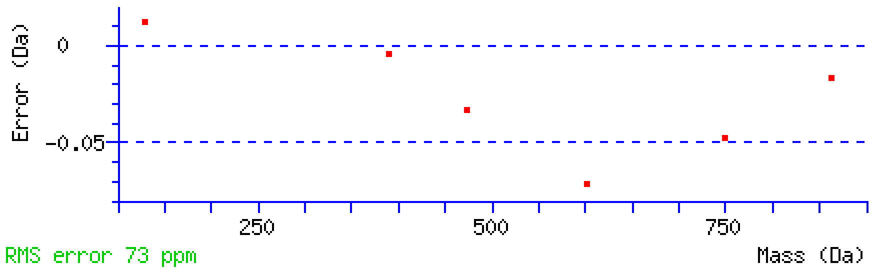
Match to Query 13033: 989.553228 from(495.783890,2+) rtinseconds(1738) index(15533)
Title: Locus:1.1.1.2153.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

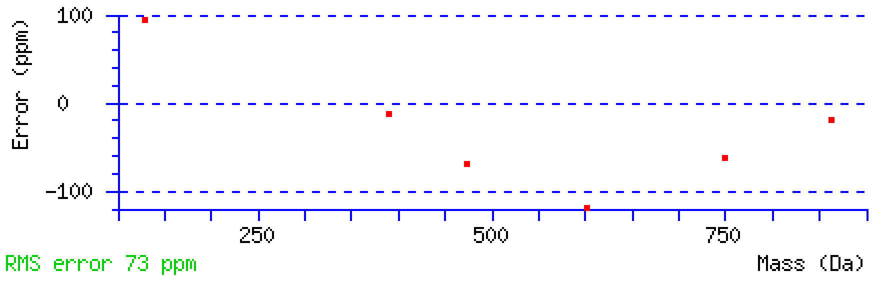
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 989.548035
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: 34 **Expect:** 0.0028
Matches : 6/72 fragment ions using 7 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	**I**	***862.496756***	431.752016	845.470207	423.238742	6
3	**389.185318**	195.096297	372.158769	186.583023	**M**	***749.412692***	375.209984	732.386143	366.696710	5
4	517.280281	259.143779	500.253732	250.630504	**K**	***602.377292***	301.692284	585.350743	293.179010	4
5	630.364345	315.685811	613.337796	307.172536	**L**	***474.282329***	237.644803	457.255780	229.131528	3
6	816.443658	408.725467	799.417109	400.212193	**W**	361.198265	181.102770	344.171716	172.589496	2
7					**R**	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of QIMKLWR
(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	989.548035	0.005193	QIMKLWR
19.5	989.557922	-0.004694	KLMLDLNK
8.9	989.544662	0.008566	KYPWAGLR
2.7	989.557938	-0.004710	KCVDTILK
1.7	989.557922	-0.004694	IKMEVLNK
0.9	989.557922	-0.004694	KEVLNMLK
0.9	989.554565	-0.001337	QELVNFLK
0.7	989.557922	-0.004694	KIMSSPLSK
0.7	989.557922	-0.004694	KLLENMVK
0.4	989.550552	0.002676	KTGTELVSR

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

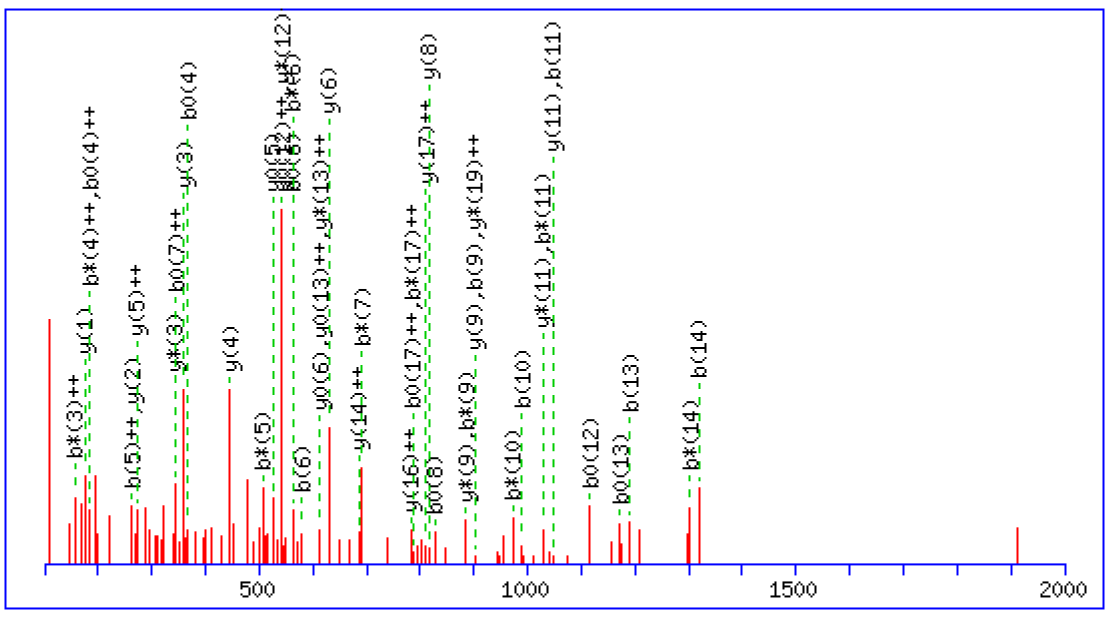
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSLGHGQHGSGSGQSPSPSR**
Found in **HORN_HUMAN**, Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2

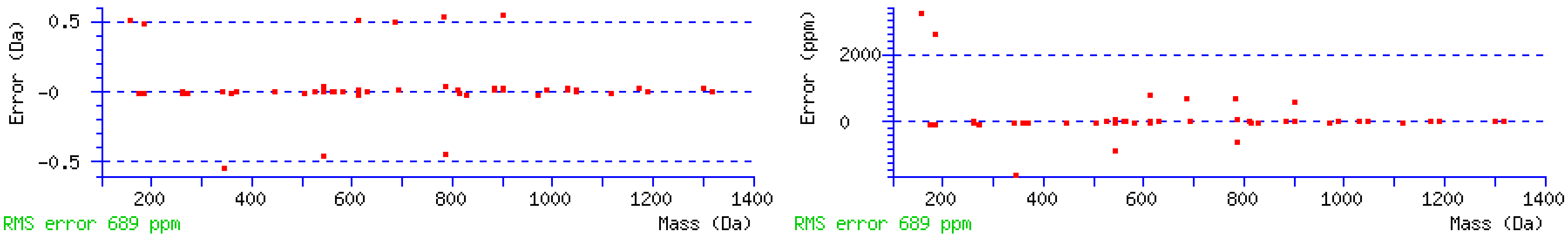
Match to Query 58851: 1946.886496 from(487.728900,4+) rtinseconds(672) index(146)
Title: Locus:1.1.1.1638.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

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): 1946.894333
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00047
Matches : 48/224 fragment ions using 69 most intense peaks   (help)
```

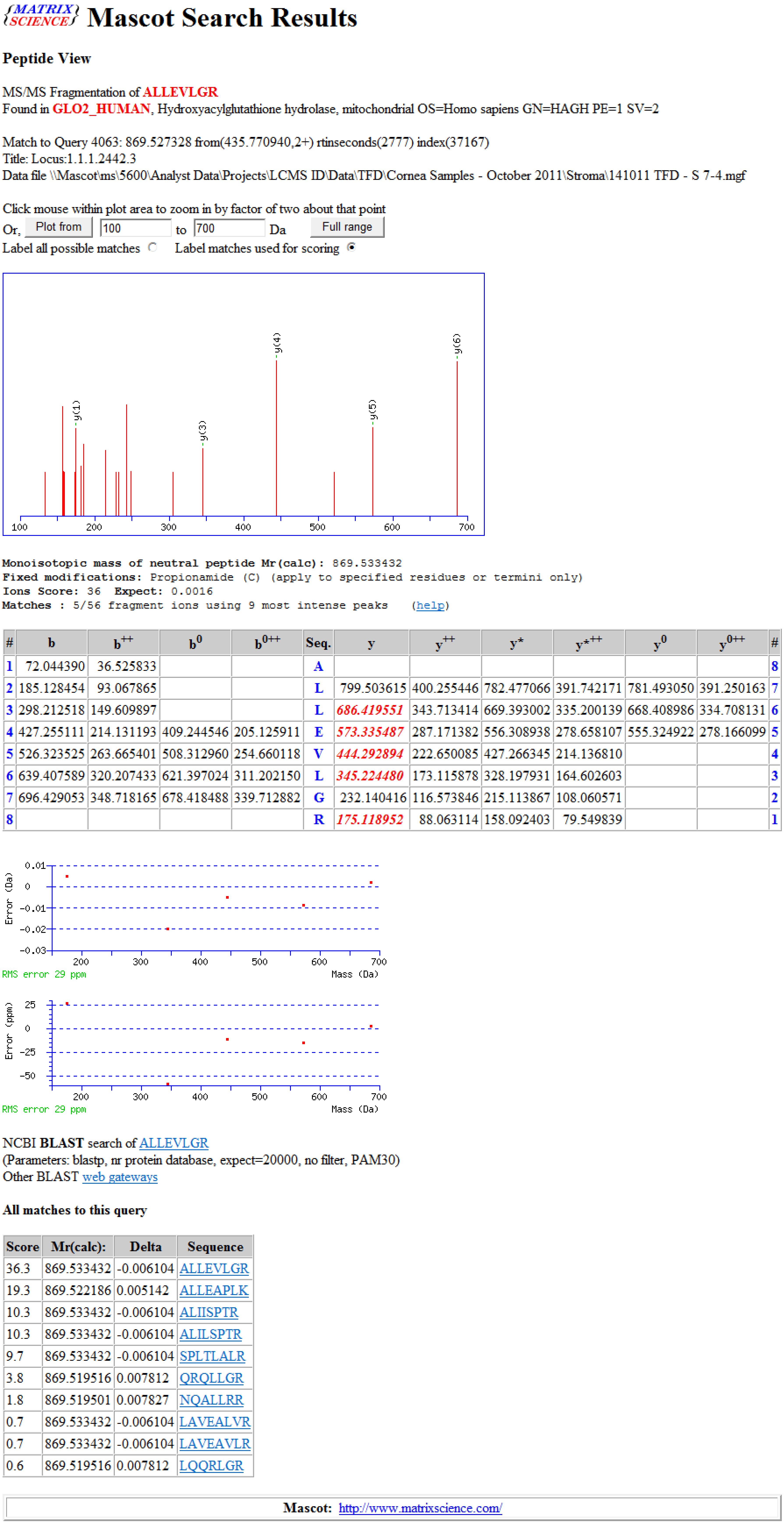
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							20
2	216.097882	108.552579	199.071333	100.039305	198.087317	99.547296	S	1819.843012	910.425144	1802.816463	901.911870	1801.832447	901.419862	19
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	L	1732.810984	866.909130	1715.784435	858.395856	1714.800419	857.903848	18
4	386.203410	193.605343	369.176861	185.092068	368.192845	184.600060	G	1619.726920	810.367098	1602.700371	801.853824	1601.716355	801.361816	17
5	523.262322	262.134799	506.235773	253.621525	505.251757	253.129517	H	1562.705456	781.856366	1545.678907	773.343092	1544.694891	772.851084	16
6	**580.283786**	290.645531	563.257237	282.132257	562.273221	281.640249	G	1425.646544	713.326910	1408.619995	704.813636	1407.635979	704.321628	15
7	708.342364	354.674820	691.315815	346.161546	690.331799	345.669538	Q	1368.625080	684.816178	1351.598531	676.302904	1350.614515	675.810896	14
8	845.401276	423.204276	828.374727	414.691002	827.390711	414.198994	H	1240.566502	620.786889	1223.539953	612.273615	1222.555937	611.781607	13
9	**902.422740**	451.715008	885.396191	443.201734	884.412175	442.709726	G	1103.507590	552.257433	1086.481041	543.744159	1085.497025	543.252151	12
10	**989.454768**	495.231022	972.428219	486.717748	971.444203	486.225740	S	***1046.486126***	523.746701	1029.459577	515.233427	1028.475561	514.741419	11
11	**1046.476232**	523.741754	1029.449683	515.228480	1028.465667	514.736471	G	959.454098	480.230687	942.427549	471.717413	941.443533	471.225405	10
12	1133.508260	567.257768	1116.481711	558.744494	1115.497695	558.252486	S	***902.432634***	451.719955	885.406085	443.206681	884.422069	442.714673	9
13	**1190.529724**	595.768500	1173.503175	587.255226	1172.519159	586.763218	G	***815.400606***	408.203941	798.374057	399.690667	797.390041	399.198659	8
14	**1318.588302**	659.797789	1301.561753	651.284515	1300.577737	650.792506	Q	758.379142	379.693209	741.352593	371.179935	740.368577	370.687927	7
15	1405.620330	703.313803	1388.593781	694.800529	1387.609765	694.308520	S	***630.320564***	315.663920	613.294015	307.150646	612.309999	306.658638	6
16	1502.673094	751.840185	1485.646545	743.326911	1484.662529	742.834903	P	***543.288536***	272.147906	526.261987	263.634632	525.277971	263.142624	5
17	1589.705122	795.356199	1572.678573	786.842925	1571.694557	786.350917	S	***446.235772***	223.621524	429.209223	215.108250	428.225207	214.616242	4
18	1686.757886	843.882581	1669.731337	835.369307	1668.747321	834.877299	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
19	1773.789914	887.398595	1756.763365	878.885321	1755.779349	878.393313	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	***175.118952***	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of QSLGHGQHGSGSGQSPSPSR
(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	1946.894333	-0.007837	QSLGHGQHGSGSGQSPSPSR
4.0	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
2.9	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
2.8	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
2.3	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
1.9	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
1.7	1946.882584	0.003912	EVSPMSAPNMPSIERDR
1.7	1946.882584	0.003912	EVSPMSAPNMPSIERDR
1.5	1946.897858	-0.011362	CQDPDEPPPPPRPMLR
1.5	1946.897858	-0.011362	CQDPDEPPPPPRPMLR



Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLEVLGR**
Found in **GLO2_HUMAN**, Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2

Match to Query 4063: 869.527328 from(435.770940,2+) rtinseconds(2777) index(37167)
Title: Locus:1.1.1.2442.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.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): 869.533432
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0016
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	72.044390	36.525833			A							8
2	185.128454	93.067865			L	799.503615	400.255446	782.477066	391.742171	781.493050	391.250163	7
3	298.212518	149.609897			L	686.419551	343.713414	669.393002	335.200139	668.408986	334.708131	6
4	427.255111	214.131193	409.244546	205.125911	E	573.335487	287.171382	556.308938	278.658107	555.324922	278.166099	5
5	526.323525	263.665401	508.312960	254.660118	V	444.292894	222.650085	427.266345	214.136810			4
6	639.407589	320.207433	621.397024	311.202150	L	345.224480	173.115878	328.197931	164.602603			3
7	696.429053	348.718165	678.418488	339.712882	G	232.140416	116.573846	215.113867	108.060571			2
8					R	175.118952	88.063114	158.092403	79.549839			1

RMS error 29 ppm

RMS error 29 ppm

NCBI **BLAST** search of ALLEVLGR
(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	869.533432	-0.006104	ALLEVLGR
19.3	869.522186	0.005142	ALLEAPLK
10.3	869.533432	-0.006104	ALIISPTR
10.3	869.533432	-0.006104	ALILSPTR
9.7	869.533432	-0.006104	SPLTLALR
3.8	869.519516	0.007812	QRQLLGR
1.8	869.519501	0.007827	NQALLRR
0.7	869.533432	-0.006104	LAVEALVR
0.7	869.533432	-0.006104	LAVEAVLR
0.6	869.519516	0.007812	LQQRLGR

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

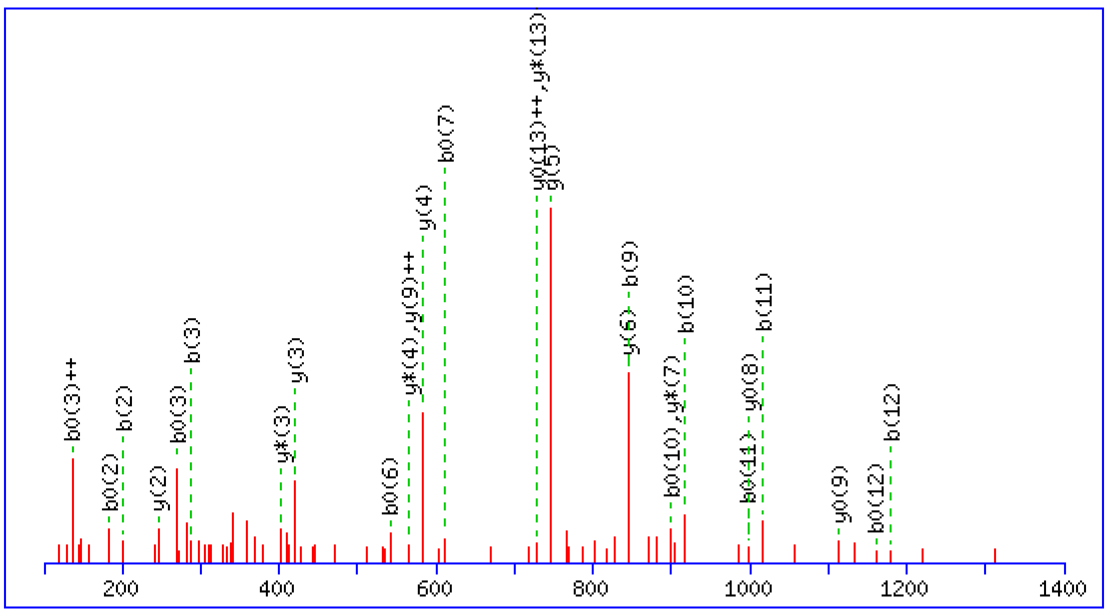
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSSVTAADTAVYYCAR**
Found in **HV207_HUMAN**, Ig heavy chain V-II region NEWM OS=Homo sapiens PE=1 SV=1

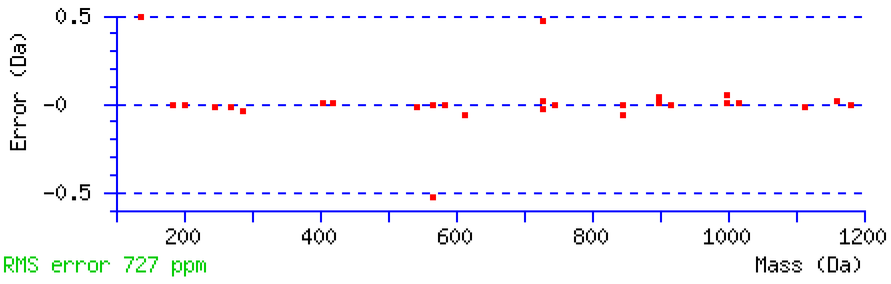
Match to Query 41125: 1760.836332 from(587.952720,3+) rtinseconds(2490) index(7715)
Title: Locus:1.1.1.3042.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-8.mgf

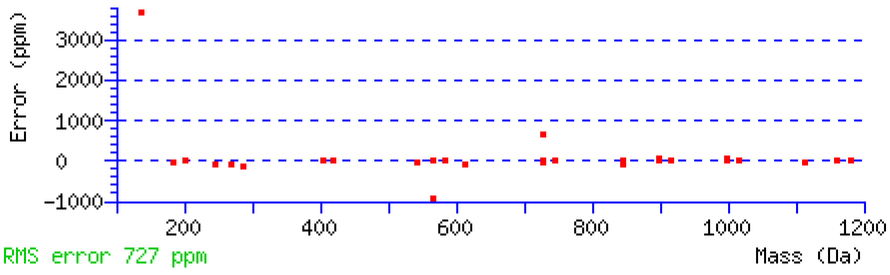
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1760.840317
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.0026
Matches : 28/134 fragment ions using 41 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							16
2	***201.123368***	101.065322	183.112803	92.060039	S	1648.763550	824.885413	1631.737001	816.372139	1630.752985	815.880131	15
3	***288.155396***	144.581336	270.144831	135.576053	S	1561.731522	781.369399	1544.704973	772.856125	1543.720957	772.364117	14
4	387.223810	194.115543	369.213245	185.110260	V	1474.699494	737.853385	1457.672945	729.340111	1456.688929	728.848103	13
5	488.271489	244.639382	470.260924	235.634100	T	1375.631080	688.319178	1358.604531	679.805904	1357.620515	679.313896	12
6	559.308603	280.157940	541.298038	271.152657	A	1274.583401	637.795339	1257.556852	629.282064	1256.572836	628.790056	11
7	630.345717	315.676497	612.335152	306.671214	A	1203.546287	602.276781	1186.519738	593.763507	1185.535722	593.271499	10
8	745.372660	373.189968	727.362095	364.184686	D	1132.509173	566.758225	1115.482624	558.244950	1114.498608	557.752942	9
9	***846.420339***	423.713808	828.409774	414.708525	T	1017.482230	509.244753	1000.455681	500.731479	999.471665	500.239471	8
10	***917.457453***	459.232365	899.446888	450.227082	A	916.434551	458.720914	899.408002	450.207639			7
11	***1016.525867***	508.766572	998.515302	499.761289	V	***845.397437***	423.202357	828.370888	414.689082			6
12	***1179.589196***	590.298236	1161.578631	581.292953	Y	***746.329023***	373.668150	729.302474	365.154875			5
13	1342.652525	671.829901	1324.641960	662.824618	Y	***583.265694***	292.136485	566.239145	283.623211			4
14	1516.698824	758.853050	1498.688259	749.847768	C	***420.202365***	210.604820	403.175816	202.091546			3
15	1587.735938	794.371607	1569.725373	785.366325	A	***246.156066***	123.581671	229.129517	115.068396			2
16					R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSSVTAADTAVYYCAR
(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	1760.840317	-0.003985	LSSVTAADTAVYYCAR
4.1	1760.836304	0.000028	AAQQTPDMTGPSSKQAK
4.1	1760.836304	0.000028	AAQQTPDMTGPSSKQAK
2.0	1760.832474	0.003858	NPVVMVDEIMSSSPPK
0.9	1760.844193	-0.007861	GDDGEVGPRGLPGEPGPR
0.5	1760.847519	-0.011187	SSSIASMPRSPSSAGSPR

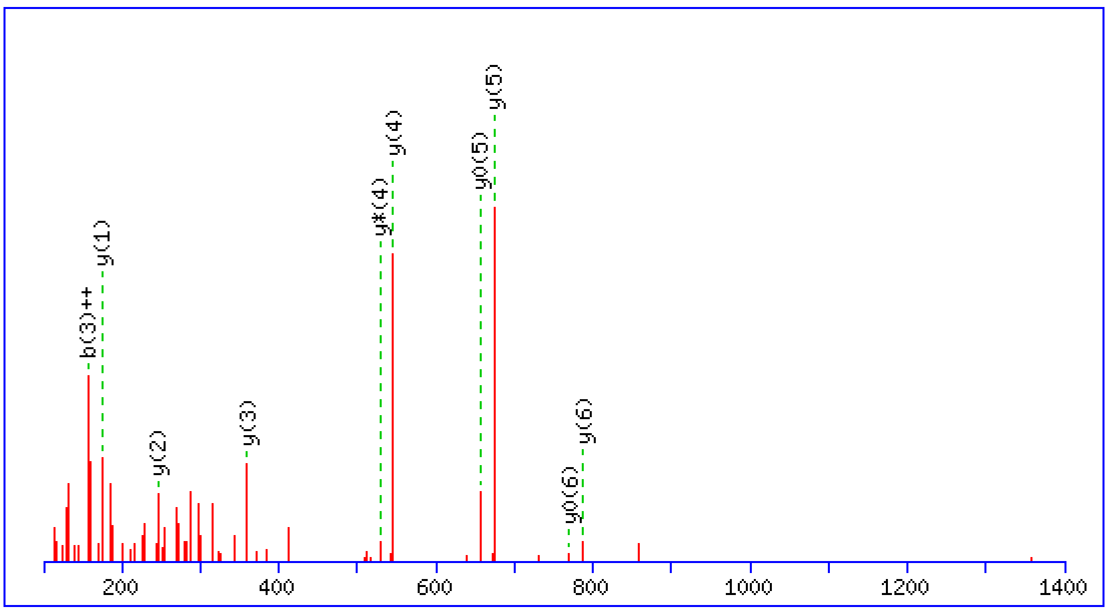
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALEWLAR**
Found in **HV201_HUMAN**, Ig heavy chain V-II region OU OS=Homo sapiens PE=1 SV=1

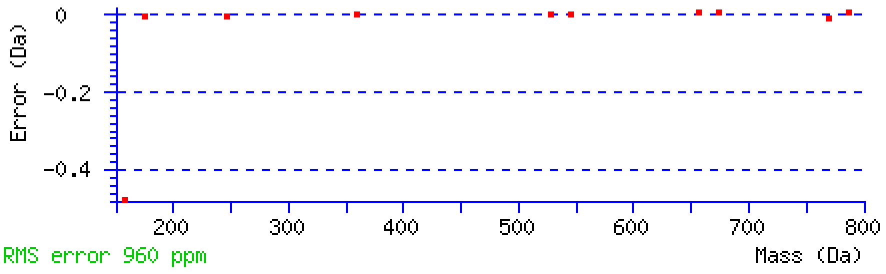
Match to Query 4371: 857.476888 from(429.745720,2+) rtinseconds(2570) index(34738)
Title: Locus:1.1.1.2314.3
Data file 2011-11-14 - TFD - S 2-3.mgf

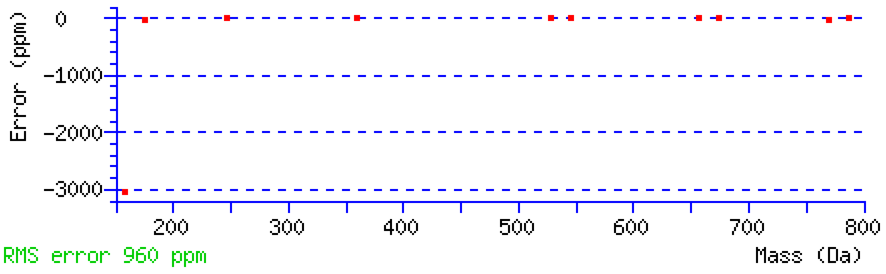
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 857.475906
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00016
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	72.044390	36.525833			A							7
2	185.128454	93.067865			L	***787.446100***	394.226688	770.419551	385.713414	769.435535	385.221406	6
3	314.171047	157.589161	296.160482	148.583879	E	***674.362036***	337.684656	657.335487	329.171382	656.351471	328.679374	5
4	500.250360	250.628818	482.239795	241.623536	W	***545.319443***	273.163360	528.292894	264.650085			4
5	613.334424	307.170850	595.323859	298.165568	L	***359.240130***	180.123703	342.213581	171.610428			3
6	684.371538	342.689407	666.360973	333.684125	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 ALEWLAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.4	857.475906	0.000982	ALEWLAR
13.7	857.479279	-0.002391	LAAMPALR
13.7	857.479279	-0.002391	LAAMPALR
11.7	857.471878	0.005010	AQAASAALR
10.6	857.483124	-0.006236	ANKPRTR
10.3	857.479279	-0.002391	AAPMLIAR
10.3	857.479279	-0.002391	AAPMLIAR
10.1	857.483124	-0.006236	RGQSLAAR
9.5	857.471893	0.004995	IAPETRR
8.6	857.475906	0.000982	EWIAALR

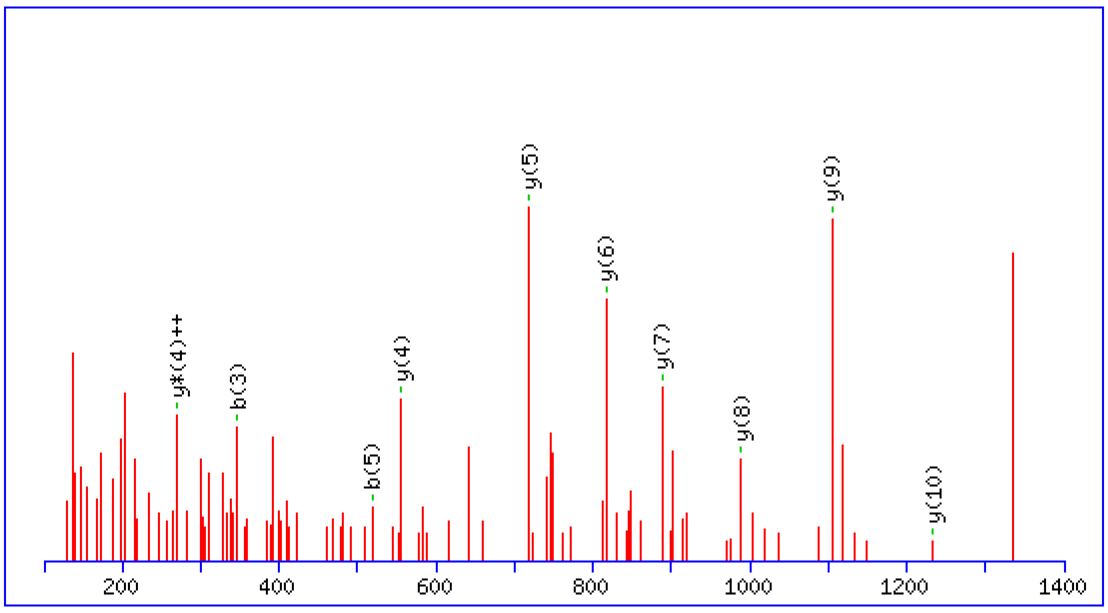
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEDTAVYYCAK**
Found in **HV312_HUMAN**, Ig heavy chain V-III region BUR OS=Homo sapiens PE=1 SV=1

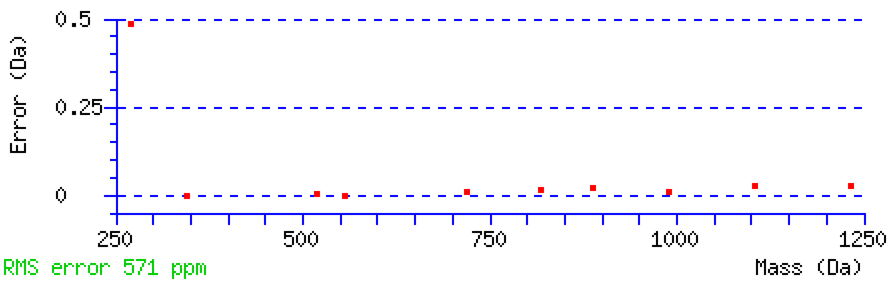
Match to Query 26224: 1333.588028 from(667.801290,2+) rtinseconds(1581) index(14730)
Title: Locus:1.1.1.2102.44
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

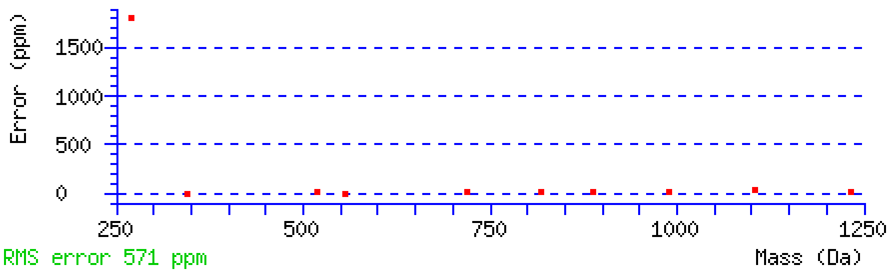
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1333.585999`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 59  Expect: 5.1e-006`
`Matches : 10/86 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	231.097548	116.052412	213.086983	107.047130	E	***1233.545618***	617.276447	1216.519069	608.763173	1215.535053	608.271165	10
3	**346.124491**	173.565884	328.113926	164.560601	D	***1104.503025***	552.755151	1087.476476	544.241876	1086.492460	543.749868	9
4	447.172170	224.089723	429.161605	215.084441	T	***989.476082***	495.241679	972.449533	486.728405	971.465517	486.236397	8
5	**518.209284**	259.608280	500.198719	250.602998	A	***888.428403***	444.717840	871.401854	436.204565			7
6	617.277698	309.142487	599.267133	300.137205	V	***817.391289***	409.199283	800.364740	400.686008			6
7	780.341027	390.674152	762.330462	381.668869	Y	***718.322875***	359.665076	701.296326	351.151801			5
8	943.404356	472.205816	925.393791	463.200534	Y	***555.259546***	278.133411	538.232997	269.620137			4
9	1117.450655	559.228966	1099.440090	550.223683	C	392.196217	196.601747	375.169668	188.088472			3
10	1188.487769	594.747523	1170.477204	585.742240	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 TEDTAVYYCAK
(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	1333.585999	0.002029	TEDTAVYYCAK

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

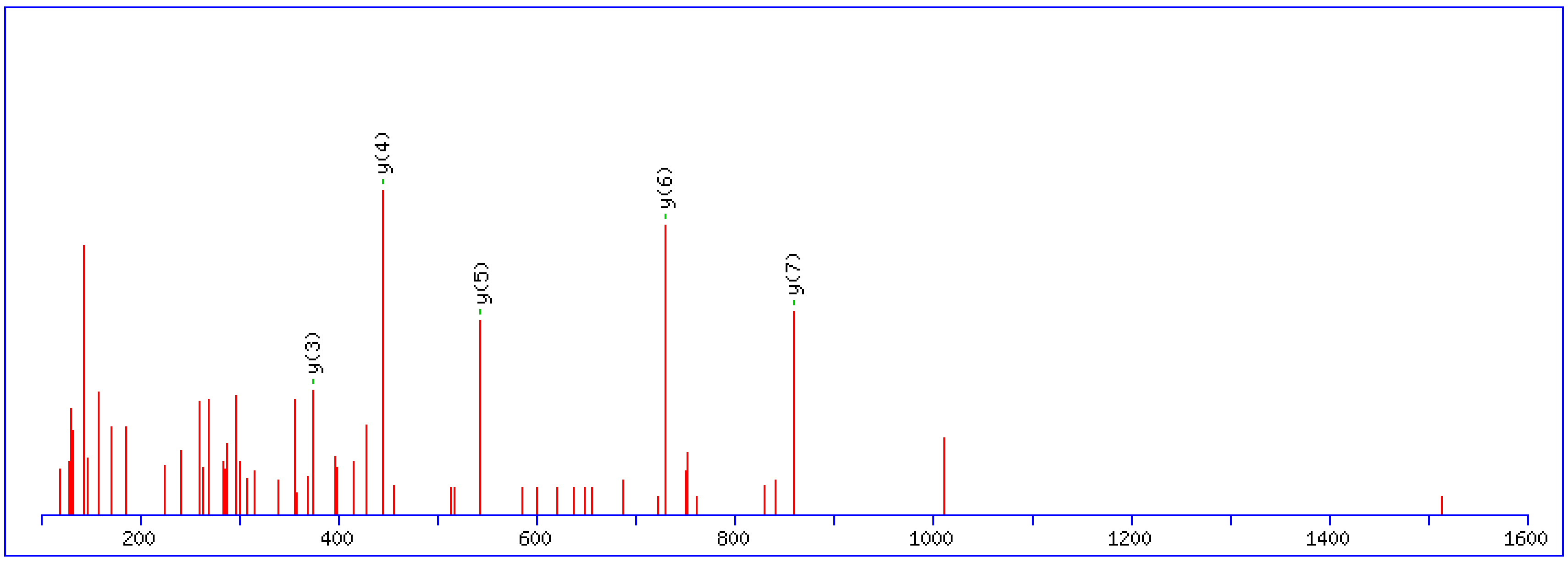
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEWVANIK**
Found in **HV320_HUMAN**, Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1

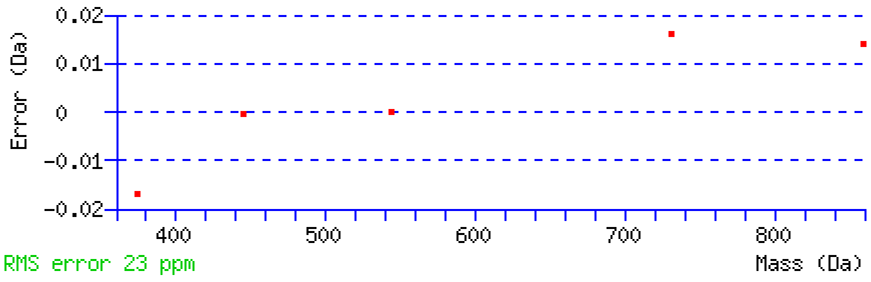
Match to Query 3820: 1028.565268 from(515.289910,2+) rtinseconds(2618) index(30689)
Title: Locus:1.1.1.1437.8
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 2.mgf

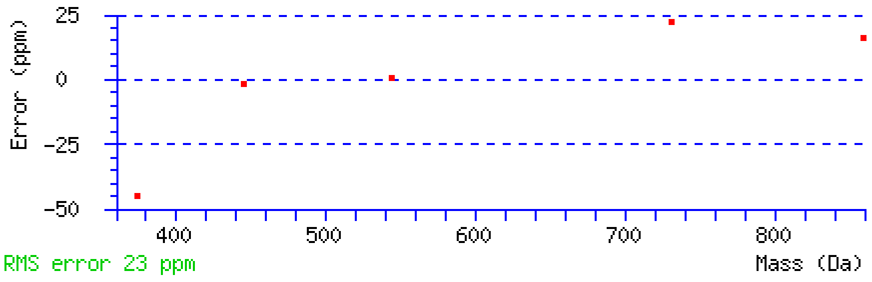
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1028.565460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 36  Expect: 0.0038
Matches : 5/68 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							9
2	171.112804	86.060040					L	972.551293	486.779285	955.524744	478.266010	954.540728	477.774002	8
3	300.155397	150.581336			282.144832	141.576054	E	***859.467229***	430.237253	842.440680	421.723978	841.456664	421.231970	7
4	486.234710	243.620993			468.224145	234.615711	W	***730.424636***	365.715956	713.398087	357.202681			6
5	585.303124	293.155200			567.292559	284.149918	V	***544.345323***	272.676300	527.318774	264.163025			5
6	656.340238	328.673757			638.329673	319.668475	A	***445.276909***	223.142092	428.250360	214.628818			4
7	770.383165	385.695221	753.356616	377.181946	752.372600	376.689938	N	***374.239795***	187.623535	357.213246	179.110261			3
8	883.467229	442.237253	866.440680	433.723978	865.456664	433.231970	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 GLEWVANIK
(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	1028.565460	-0.000192	GLEWVANIK
9.8	1028.561432	0.003836	GEEVAVKAAR
6.2	1028.568848	-0.003580	IGVKPCIDK
5.5	1028.561432	0.003836	EQVAEVRAK
5.2	1028.565475	-0.000207	TSLPWQGLK
2.5	1028.561447	0.003821	TGTAPLDRAK

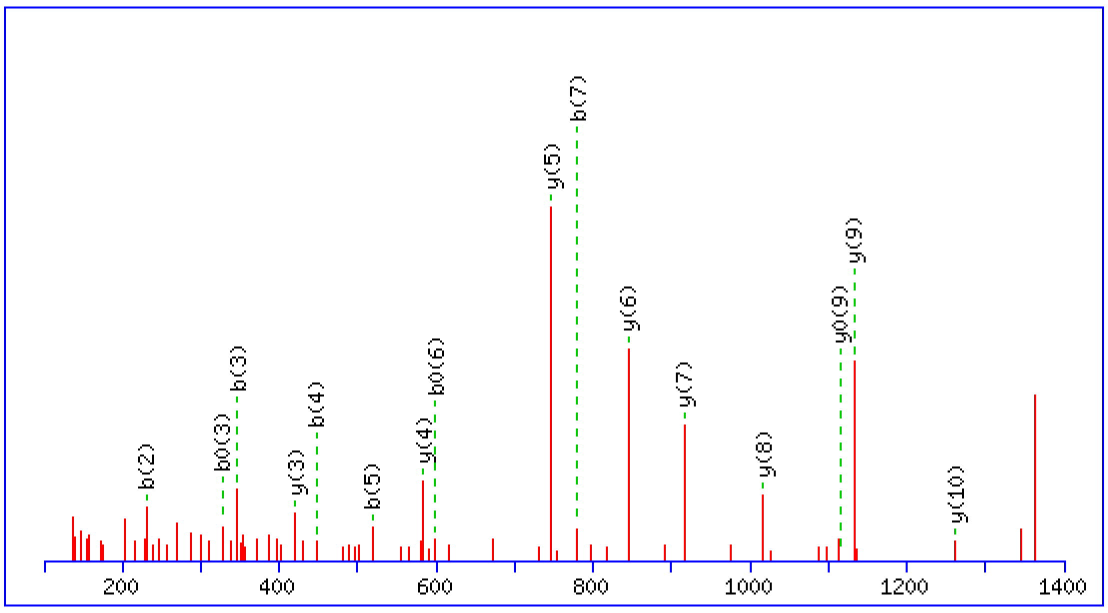
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEDTAVYYCAR**
Found in **HV310_HUMAN**, Ig heavy chain V-III region HIL OS=Homo sapiens PE=1 SV=1

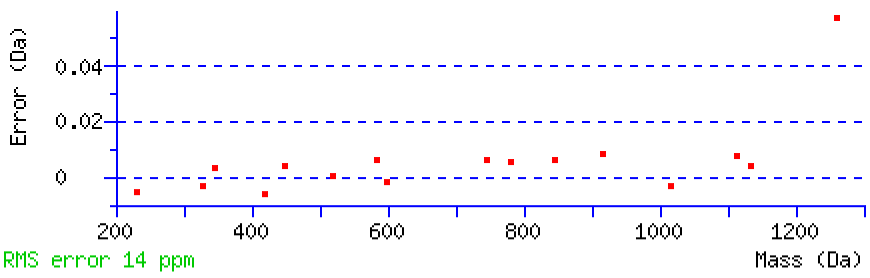
Match to Query 29600: 1361.600648 from(681.807600,2+) rtinseconds(1725) index(15319)
Title: Locus:1.1.1.2191.43
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

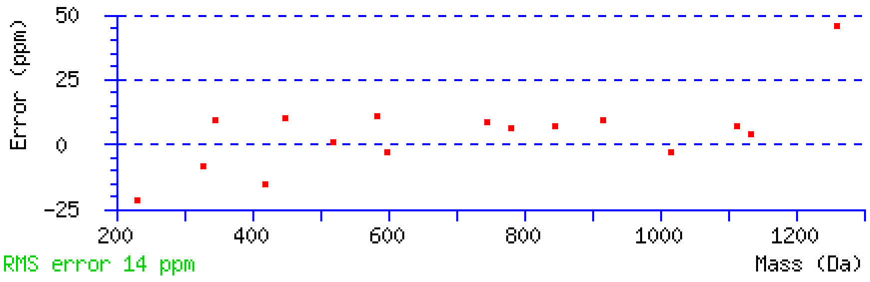
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1361.592148
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 9.4e-007
Matches : 16/86 fragment ions using 23 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	**231.097548**	116.052412	213.086983	107.047130	E	***1261.551766***	631.279521	1244.525217	622.766247	1243.541201	622.274239	10
3	**346.124491**	173.565884	328.113926	164.560601	D	***1132.509173***	566.758225	1115.482624	558.244950	1114.498608	557.752942	9
4	**447.172170**	224.089723	429.161605	215.084441	T	***1017.482230***	509.244753	1000.455681	500.731479	999.471665	500.239471	8
5	**518.209284**	259.608280	500.198719	250.602998	A	***916.434551***	458.720914	899.408002	450.207639			7
6	617.277698	309.142487	599.267133	300.137205	V	***845.397437***	423.202357	828.370888	414.689082			6
7	**780.341027**	390.674152	762.330462	381.668869	Y	***746.329023***	373.668150	729.302474	365.154875			5
8	943.404356	472.205816	925.393791	463.200534	Y	***583.265694***	292.136485	566.239145	283.623211			4
9	1117.450655	559.228966	1099.440090	550.223683	C	***420.202365***	210.604820	403.175816	202.091546			3
10	1188.487769	594.747523	1170.477204	585.742240	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 TEDTAVYYCAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.2	1361.592148	0.008500	TEDTAVYYCAR
11.7	1361.592163	0.008485	SDDTVVYYCAR
3.0	1361.592148	0.008500	VEDTATYYCAR

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

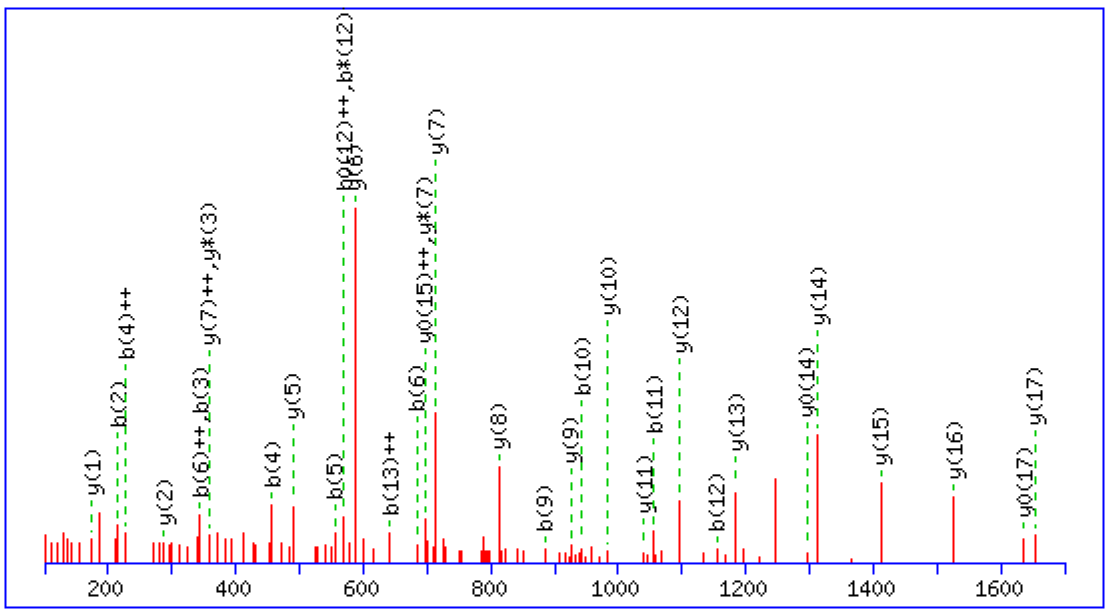
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVQLVESGGGLVKPGGSLR**
Found in **HV319_HUMAN**, Ig heavy chain V-III region JON OS=Homo sapiens PE=1 SV=1

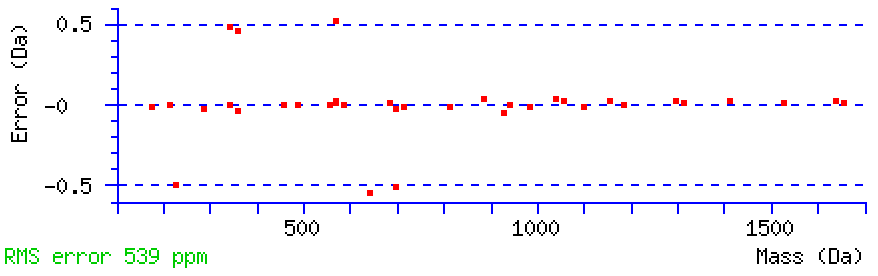
Match to Query 48882: 1867.021902 from(623.347910,3+) rtinseconds(2389) index(29864)
Title: Locus:1.1.1.2434.25
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

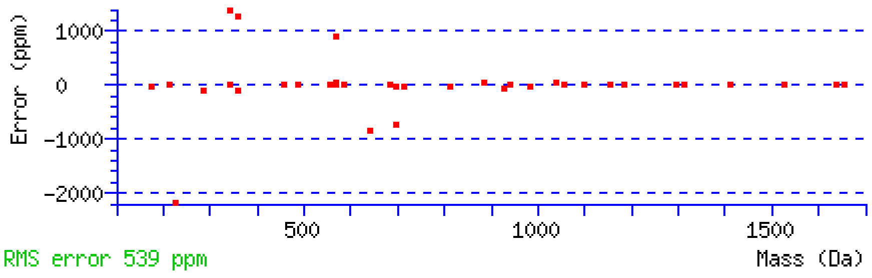
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1867.016342
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 109 **Expect:** 5.6e-011
Matches : 36/208 fragment ions using 53 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							19
2	**215.102633**	108.054954			197.092068	99.049672	V	1752.996660	877.001968	1735.970111	868.488694	1734.986095	867.996686	18
3	**343.161211**	172.084244	326.134662	163.570969	325.150646	163.078961	Q	***1653.928246***	827.467761	1636.901697	818.954487	1635.917681	818.462479	17
4	**456.245275**	**228.626276**	439.218726	220.113001	438.234710	219.620993	L	***1525.869668***	763.438472	1508.843119	754.925198	1507.859103	754.433190	16
5	**555.313689**	278.160483	538.287140	269.647208	537.303124	269.155200	V	***1412.785604***	706.896440	1395.759055	698.383166	1394.775039	697.891157	15
6	**684.356282**	**342.681779**	667.329733	334.168505	666.345717	333.676497	E	***1313.717190***	657.362233	1296.690641	648.848959	1295.706625	648.356951	14
7	771.388310	386.197793	754.361761	377.684519	753.377745	377.192511	S	***1184.674597***	592.840937	1167.648048	584.327662	1166.664032	583.835654	13
8	828.409774	414.708525	811.383225	406.195251	810.399209	405.703243	G	***1097.642569***	549.324923	1080.616020	540.811648	1079.632004	540.319640	12
9	**885.431238**	443.219257	868.404689	434.705983	867.420673	434.213975	G	***1040.621105***	520.814191	1023.594556	512.300916	1022.610540	511.808908	11
10	**942.452702**	471.729989	925.426153	463.216715	924.442137	462.724707	G	***983.599641***	492.303459	966.573092	483.790184	965.589076	483.298176	10
11	**1055.536766**	528.272021	1038.510217	519.758747	1037.526201	519.266739	L	***926.578177***	463.792727	909.551628	455.279452	908.567612	454.787444	9
12	**1154.605180**	577.806228	1137.578631	569.292954	1136.594615	568.800946	V	***813.494113***	407.250695	796.467564	398.737420	795.483548	398.245412	8
13	1282.700143	**641.853710**	1265.673594	633.340435	1264.689578	632.848427	K	***714.425699***	357.716487	697.399150	349.203213	696.415134	348.711205	7
14	1379.752907	690.380092	1362.726358	681.866817	1361.742342	681.374809	P	***586.330736***	293.669006	569.304187	285.155731	568.320171	284.663723	6
15	1436.774371	718.890824	1419.747822	710.377549	1418.763806	709.885541	G	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	5
16	1493.795835	747.401556	1476.769286	738.888281	1475.785270	738.396273	G	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
17	1580.827863	790.917570	1563.801314	782.404295	1562.817298	781.912287	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
18	1693.911927	847.459602	1676.885378	838.946327	1675.901362	838.454319	L	***288.203016***	144.605146	271.176467	136.091871			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
109.3	1867.016342	0.005560	DVQLVESGGGLVKPGGSLR
4.7	1867.020309	0.001593	YIPSLPDRILDAPEIR
4.2	1867.031555	-0.009653	FNLRLPSLDEQVIPAR

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

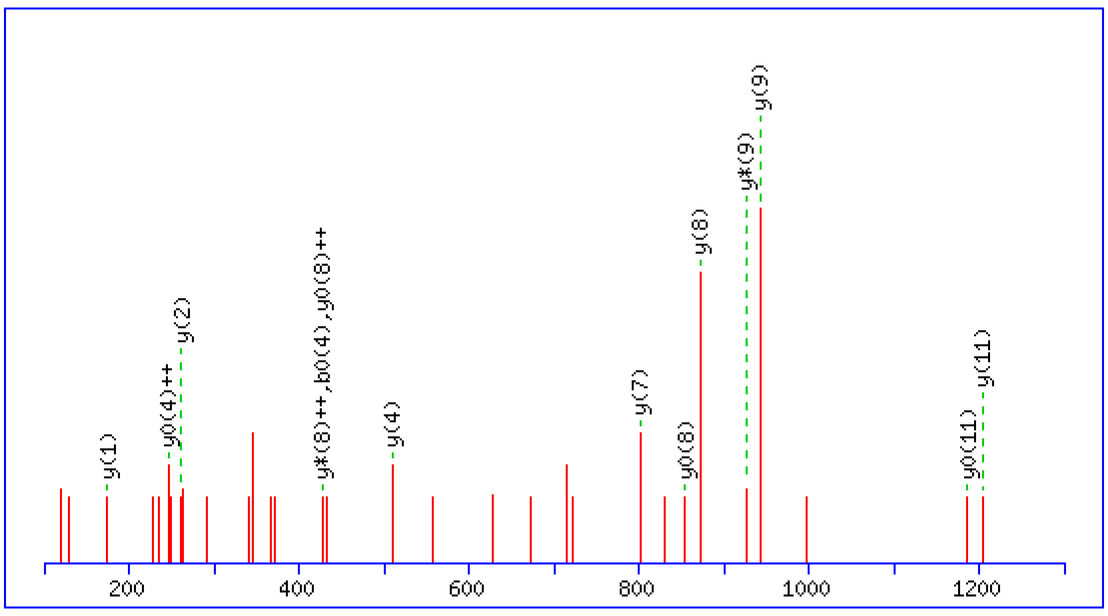
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSCAASGFTFSR**
Found in **HV309_HUMAN**, Ig heavy chain V-III region NIE OS=Homo sapiens PE=1 SV=1

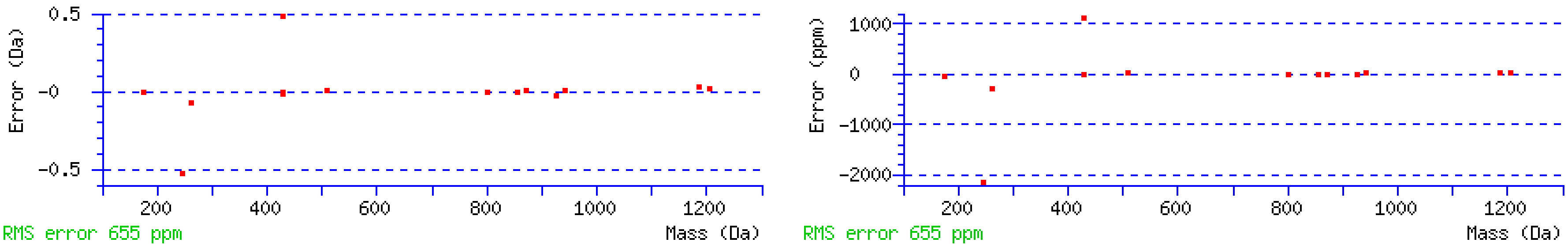
Match to Query 19760: 1316.629708 from(659.322130,2+) rtinseconds(2452) index(17825)
Title: Locus:1.1.1.2444.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

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): 1316.618317
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0075
Matches : 14/106 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							12
2	201.123368	101.065322	183.112803	92.060039	S	***1204.541534***	602.774405	1187.514985	594.261131	1186.530969	593.769123	11
3	375.169667	188.088471	357.159102	179.083189	C	1117.509506	559.258391	1100.482957	550.745117	1099.498941	550.253109	10
4	446.206781	223.607028	428.196216	214.601746	A	***943.463207***	472.235242	926.436658	463.721967	925.452642	463.229959	9
5	517.243895	259.125586	499.233330	250.120303	A	***872.426093***	436.716685	855.399544	428.203410	854.415528	427.711402	8
6	604.275923	302.641599	586.265358	293.636317	S	***801.388979***	401.198128	784.362430	392.684853	783.378414	392.192845	7
7	661.297387	331.152332	643.286822	322.147049	G	714.356951	357.682114	697.330402	349.168839	696.346386	348.676831	6
8	808.365801	404.686538	790.355236	395.681256	F	657.335487	329.171382	640.308938	320.658107	639.324922	320.166099	5
9	909.413480	455.210378	891.402915	446.205095	T	***510.267073***	255.637175	493.240524	247.123900	492.256508	246.631892	4
10	1056.481894	528.744585	1038.471329	519.739303	F	409.219394	205.113335	392.192845	196.600061	391.208829	196.108053	3
11	1143.513922	572.260599	1125.503357	563.255317	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 LSCAASGFTFSR
(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	1316.618317	0.011391	LSCAASGFTFSR
8.7	1316.618317	0.011391	LASCPDSWVPR
8.1	1316.629562	0.000146	MGWKEGQGVGPR
6.1	1316.621658	0.008050	HIMAEMIATER
6.0	1316.620819	0.008889	EEISGSGTQPGGAK
2.9	1316.621643	0.008065	MCNPEEAALLR
2.5	1316.624802	0.004906	EEEKNPEWLK
2.0	1316.636063	-0.006355	NQWQLSADDLK
0.7	1316.625488	0.004220	CEAANVAEQRR

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

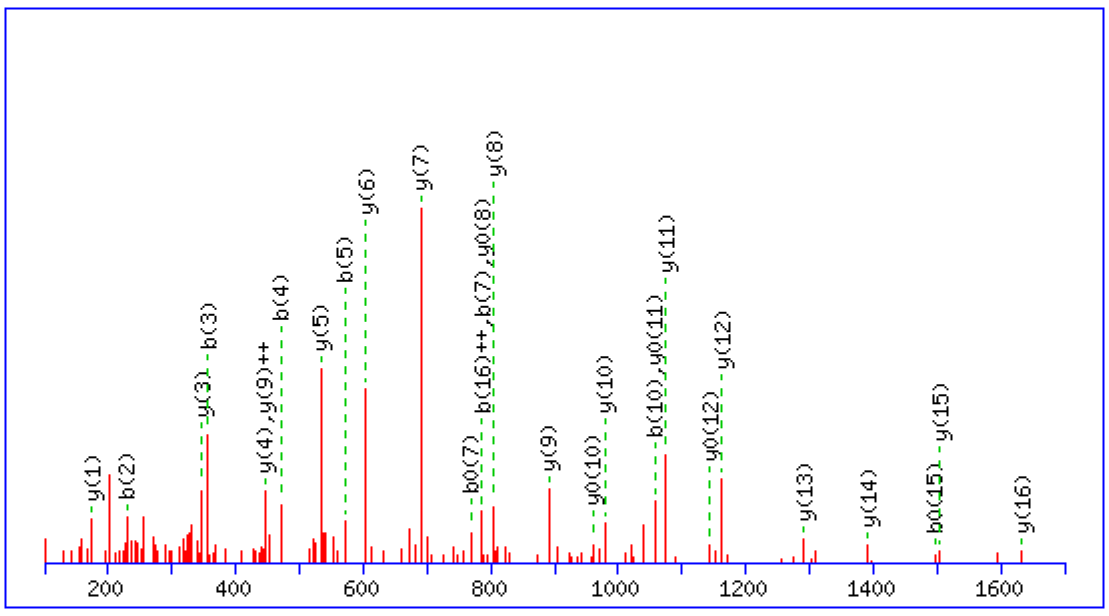
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIQLTQSPSSLSASVGDR**
Found in **KV122_HUMAN**, Ig kappa chain V-I region BAN OS=Homo sapiens PE=1 SV=1

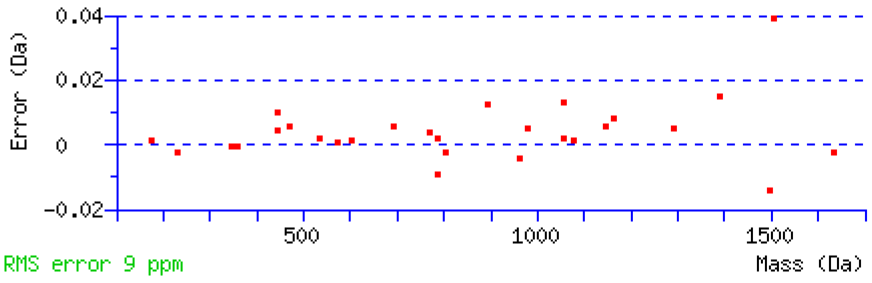
Match to Query 45179: 1859.921712 from(620.981180,3+) rtinseconds(2581) index(27096)
Title: Locus:1.1.1.2793.35
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

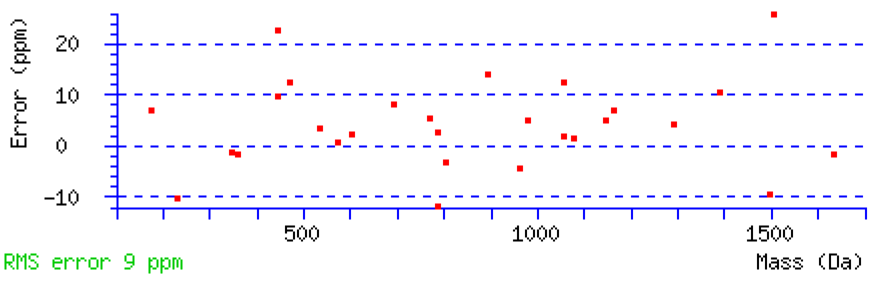
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1859.922485
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 151 **Expect:** 1.1e-014
Matches : 29/198 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	1745.902818	873.455047	1728.876269	864.941773	1727.892253	864.449765	17
3	**357.176861**	179.092068	340.150312	170.578794	339.166296	170.086786	Q	***1632.818754***	816.913015	1615.792205	808.399741	1614.808189	807.907733	16
4	**470.260925**	235.634100	453.234376	227.120826	452.250360	226.628818	L	***1504.760176***	752.883726	1487.733627	744.370452	1486.749611	743.878444	15
5	**571.308604**	286.157940	554.282055	277.644666	553.298039	277.152658	T	***1391.676112***	696.341694	1374.649563	687.828420	1373.665547	687.336412	14
6	699.367182	350.187229	682.340633	341.673955	681.356617	341.181947	Q	***1290.628433***	645.817855	1273.601884	637.304580	1272.617868	636.812572	13
7	**786.399210**	393.703243	769.372661	385.189969	768.388645	384.697961	S	***1162.569855***	581.788566	1145.543306	573.275291	1144.559290	572.783283	12
8	883.451974	442.229625	866.425425	433.716351	865.441409	433.224343	P	***1075.537827***	538.272552	1058.511278	529.759277	1057.527262	529.267269	11
9	970.484002	485.745639	953.457453	477.232365	952.473437	476.740357	S	***978.485063***	489.746170	961.458514	481.232895	960.474498	480.740887	10
10	**1057.516030**	529.261653	1040.489481	520.748379	1039.505465	520.256371	S	***891.453035***	446.230156	874.426486	437.716881	873.442470	437.224873	9
11	1170.600094	585.803685	1153.573545	577.290411	1152.589529	576.798402	L	***804.421007***	402.714142	787.394458	394.200867	786.410442	393.708859	8
12	1257.632122	629.319699	1240.605573	620.806425	1239.621557	620.314416	S	***691.336943***	346.172110	674.310394	337.658835	673.326378	337.166827	7
13	1328.669236	664.838256	1311.642687	656.324982	1310.658671	655.832973	A	***604.304915***	302.656096	587.278366	294.142821	586.294350	293.650813	6
14	1415.701264	708.354270	1398.674715	699.840996	1397.690699	699.348988	S	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.132256	5
15	1514.769678	757.888477	1497.743129	749.375203	1496.759113	748.883195	V	***446.235773***	223.621524	429.209224	215.108250	428.225208	214.616242	4
16	1571.791142	786.399209	1554.764593	777.885935	1553.780577	777.393927	G	***347.167359***	174.087317	330.140810	165.574043	329.156794	165.082035	3
17	1686.818085	843.912681	1669.791536	835.399406	1668.807520	834.907398	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 DIQLTQSPSSLSASVGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
150.7	1859.922485	-0.000773	DIQLTQSPSSLSASVGDR
17.7	1859.919968	0.001744	DSPGKPPMAPPSKEPPGR
17.7	1859.919968	0.001744	DSPGKPPMAPPSKEPPGR
6.1	1859.912552	0.009160	AENLRPSEPAPQPPEGR
5.5	1859.912552	0.009160	AENLRPSEPAPQPPEGR
0.4	1859.937744	-0.016032	TIDNADSSTLHAVTFLR

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

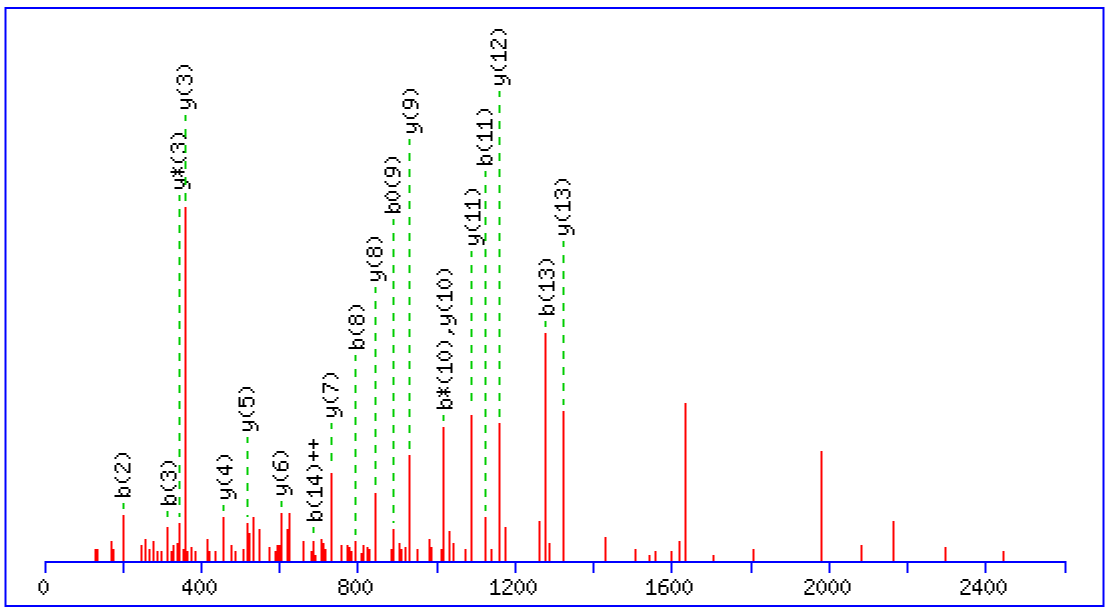
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLIYAASSLQSGVPSR**
Found in **KV109_HUMAN**, Ig kappa chain V-I region HK101 (Fragment) OS=Homo sapiens PE=4 SV=1

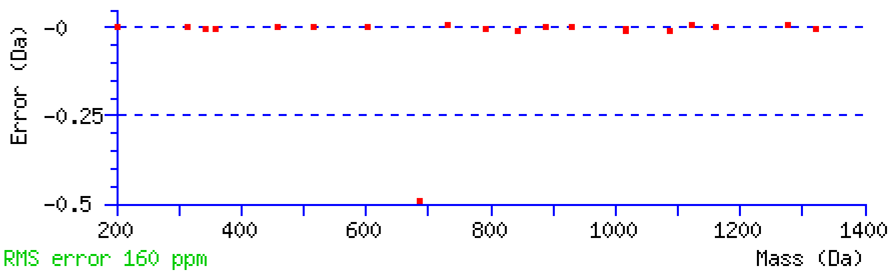
Match to Query 36005: 1634.863408 from(818.438980,2+) rtinseconds(2670) index(28754)
Title: Locus:1.1.1.2826.43
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

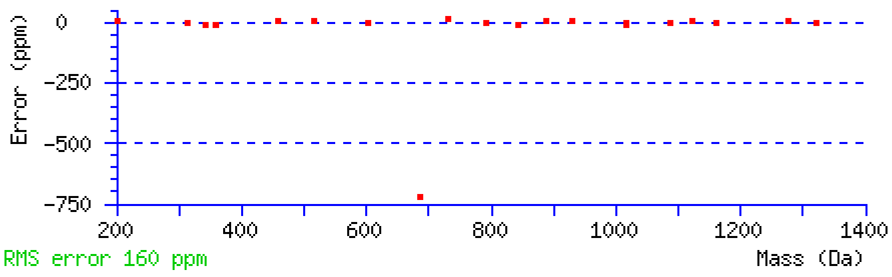
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1634.862762
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 88 **Expect:** 1.6e-008
Matches : 20/160 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	88.039304	44.523290			70.028739	35.518008	S							16
2	**201.123368**	101.065322			183.112803	92.060039	L	1548.838033	774.922655	1531.811484	766.409380	1530.827468	765.917372	15
3	**314.207432**	157.607354			296.196867	148.602071	I	1435.753969	718.380623	1418.727420	709.867348	1417.743404	709.375340	14
4	477.270761	239.139018			459.260196	230.133736	Y	***1322.669905***	661.838591	1305.643356	653.325316	1304.659340	652.833308	13
5	548.307875	274.657576			530.297310	265.652293	A	***1159.606576***	580.306926	1142.580027	571.793652	1141.596011	571.301644	12
6	619.344989	310.176133			601.334424	301.170850	A	***1088.569462***	544.788369	1071.542913	536.275095	1070.558897	535.783087	11
7	706.377017	353.692147			688.366452	344.686864	S	***1017.532348***	509.269812	1000.505799	500.756538	999.521783	500.264530	10
8	**793.409045**	397.208161			775.398480	388.202878	S	***930.500320***	465.753798	913.473771	457.240524	912.489755	456.748516	9
9	906.493109	453.750193			888.482544	444.744910	L	***843.468292***	422.237784	826.441743	413.724510	825.457727	413.232502	8
10	1034.551687	517.779481	1017.525138	509.266207	1016.541122	508.774199	Q	***730.384228***	365.695752	713.357679	357.182478	712.373663	356.690470	7
11	**1121.583715**	561.295496	1104.557166	552.782221	1103.573150	552.290213	S	***602.325650***	301.666463	585.299101	293.153189	584.315085	292.661181	6
12	1178.605179	589.806227	1161.578630	581.292953	1160.594614	580.800945	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1277.673593**	639.340435	1260.647044	630.827160	1259.663028	630.335152	V	***458.272158***	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1374.726357	687.866817	1357.699808	679.353542	1356.715792	678.861534	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	1461.758385	731.382831	1444.731836	722.869556	1443.747820	722.377548	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 SLIYAASSLQSGVPSR
(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	1634.862762	0.000646	SLIYAASSLQSGVPSR
7.5	1634.854904	0.008504	ALELTTTTMELGALR

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

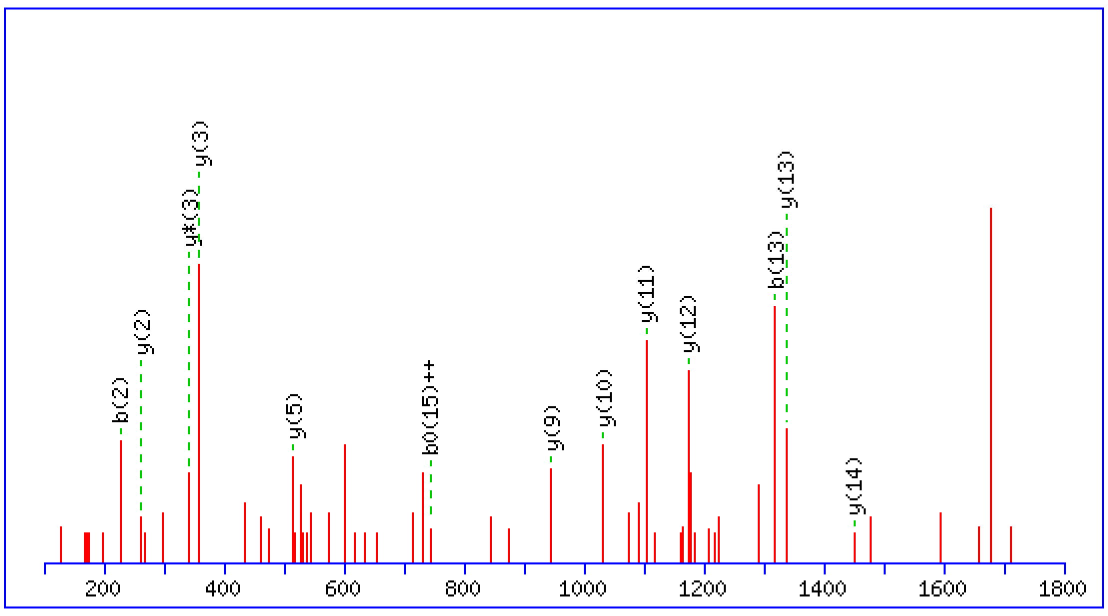
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYAASSLETGVPSR**
Found in **KV111_HUMAN**, Ig kappa chain V-I region Ka OS=Homo sapiens PE=1 SV=1

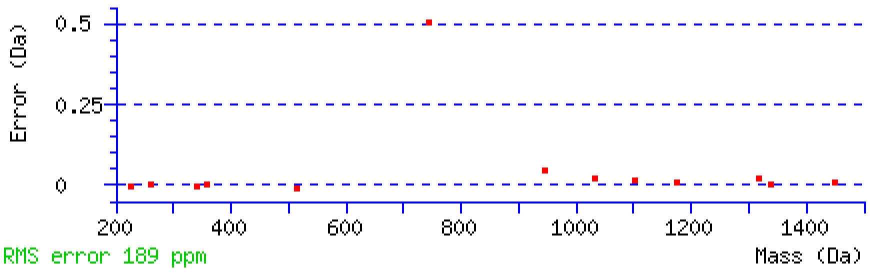
Match to Query 33719: 1675.927308 from(838.970930,2+) rtinseconds(3097) index(32321)
Title: Locus:1.1.1.2675.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

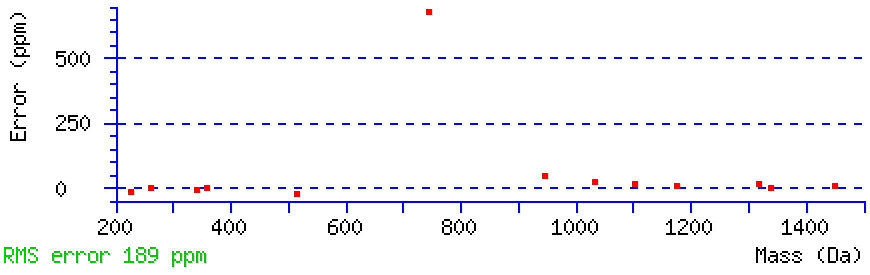
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1675.914459
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 2.3e-005
Matches : 13/136 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							16
2	**227.175404**	114.091340			L	1563.837699	782.422488	1546.811150	773.909213	1545.827134	773.417205	15
3	340.259468	170.633372			I	***1450.753635***	725.880456	1433.727086	717.367181	1432.743070	716.875173	14
4	503.322797	252.165036			Y	***1337.669571***	669.338424	1320.643022	660.825149	1319.659006	660.333141	13
5	574.359911	287.683594			A	***1174.606242***	587.806759	1157.579693	579.293485	1156.595677	578.801477	12
6	645.397025	323.202151			A	***1103.569128***	552.288202	1086.542579	543.774928	1085.558563	543.282920	11
7	732.429053	366.718165	714.418488	357.712882	S	***1032.532014***	516.769645	1015.505465	508.256371	1014.521449	507.764363	10
8	819.461081	410.234178	801.450516	401.228896	S	***945.499986***	473.253631	928.473437	464.740357	927.489421	464.248349	9
9	932.545145	466.776210	914.534580	457.770928	L	858.467958	429.737617	841.441409	421.224343	840.457393	420.732335	8
10	1061.587738	531.297507	1043.577173	522.292224	E	745.383894	373.195585	728.357345	364.682311	727.373329	364.190303	7
11	1162.635417	581.821347	1144.624852	572.816064	T	616.341301	308.674289	599.314752	300.161014	598.330736	299.669006	6
12	1219.656881	610.332078	1201.646316	601.326796	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
13	**1318.725295**	659.866286	1300.714730	650.861003	V	458.272158	229.639717	441.245609	221.126443	440.261593	220.634435	4
14	1415.778059	708.392668	1397.767494	699.387385	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
15	1502.810087	751.908682	1484.799522	742.903399	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 LLIYAASSLETGVPSR
(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	1675.914459	0.012849	LLIYAASSLETGVPSR
21.5	1675.914474	0.012834	LLIYGASTLETGVPSR
2.1	1675.915817	0.011491	ALSWGRYQLVVTQR
1.8	1675.911957	0.015351	QELFLIMAWLLQR
0.7	1675.940979	-0.013671	RLVDVAGFSIFIPSR

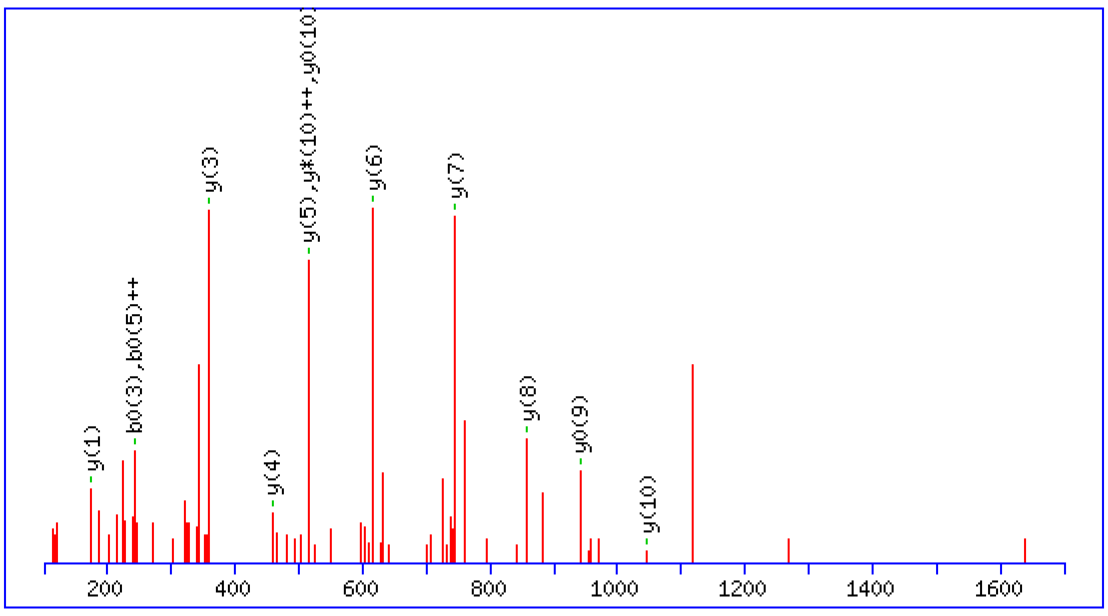
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASTLETGVPSR**
Found in **KV112_HUMAN**, Ig kappa chain V-I region Kue OS=Homo sapiens PE=1 SV=1

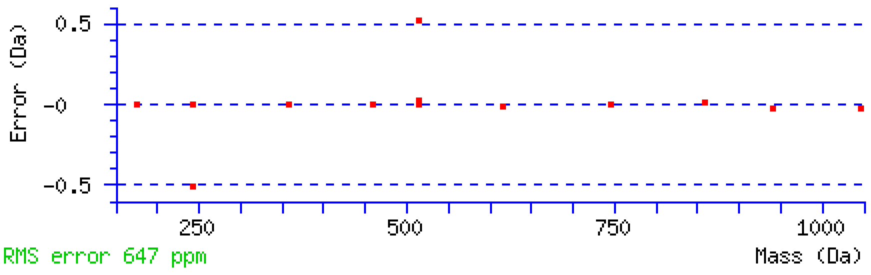
Match to Query 14349: 1116.575128 from(559.294840,2+) rtinseconds(1492) index(5443)
Title: Locus:1.1.1.2217.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

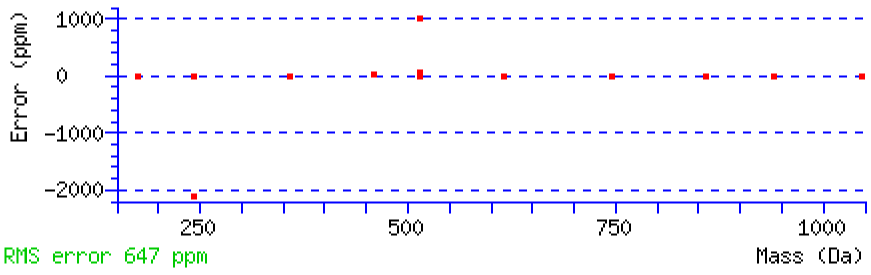
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1116.577499
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83  Expect: 1.8e-007
Matches : 13/96 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	159.076418	80.041847	141.065853	71.036564	S	***1046.547665***	523.777471	1029.521116	515.264196	1028.537100	514.772188	10
3	260.124097	130.565687	242.113532	121.560404	T	959.515637	480.261457	942.489088	471.748182	941.505072	471.256174	9
4	373.208161	187.107719	355.197596	178.102436	L	***858.467958***	429.737617	841.441409	421.224342	840.457393	420.732334	8
5	502.250754	251.629015	484.240189	242.623733	E	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	7
6	603.298433	302.152855	585.287868	293.147572	T	***616.341301***	308.674288	599.314752	300.161014	598.330736	299.669006	6
7	660.319897	330.663587	642.309332	321.658304	G	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	5
8	759.388311	380.197794	741.377746	371.192511	V	***458.272158***	229.639717	441.245609	221.126442	440.261593	220.634434	4
9	856.441075	428.724176	838.430510	419.718893	P	***359.203744***	180.105510	342.177195	171.592235	341.193179	171.100227	3
10	943.473103	472.240190	925.462538	463.234907	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 ASTLETGVPSR
(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	1116.577499	-0.002371	ASTLETGVPSR
8.0	1116.567596	0.007532	ATRDPFAPSR
6.8	1116.584854	-0.009726	MQNEIEILK
5.2	1116.577469	-0.002341	RSEDQIELK
5.0	1116.584885	-0.009757	CDQPLTLLK
4.5	1116.570969	0.004159	AGASIVGVNCR
3.4	1116.577469	-0.002341	SEVEKGEALR
2.3	1116.577484	-0.002356	VGVASSEELAR
1.8	1116.577469	-0.002341	ADIEEIKSGR
1.6	1116.578354	-0.003226	MAGAGPTMLLR

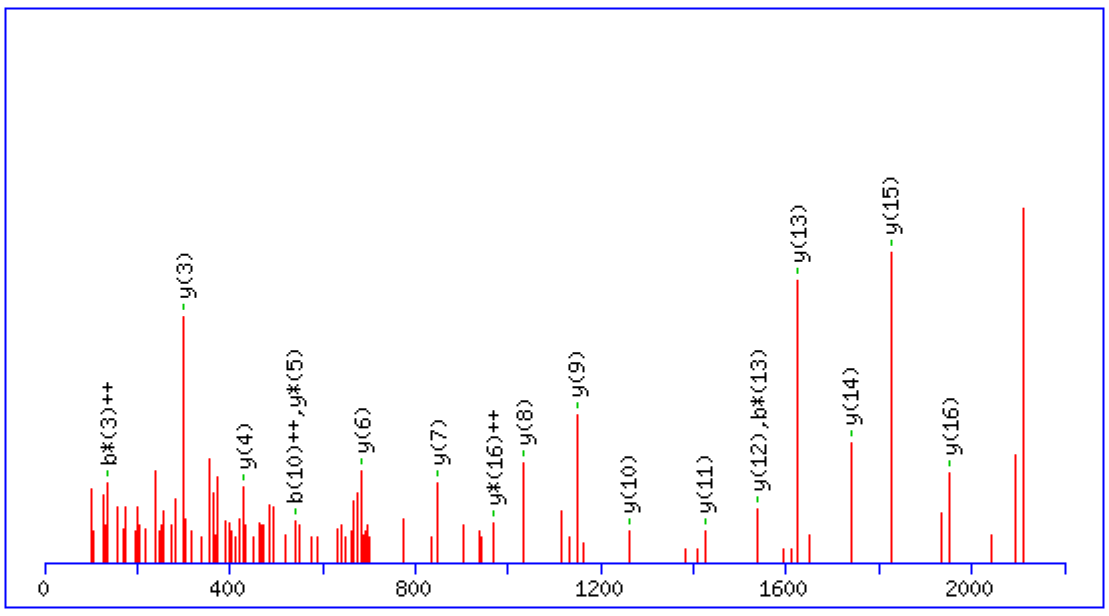
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASQSISNYLNWYQQKPGK**
Found in **KV123_HUMAN**, Ig kappa chain V-I region Walker OS=Homo sapiens PE=4 SV=1

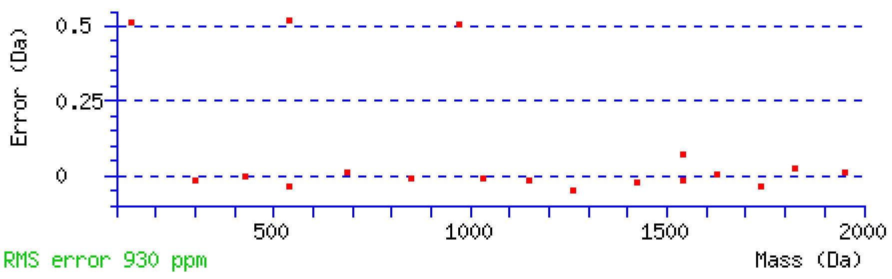
Match to Query 46826: 2111.033052 from(704.684960,3+) rtinseconds(2927) index(31768)
Title: Locus:1.1.1.2761.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

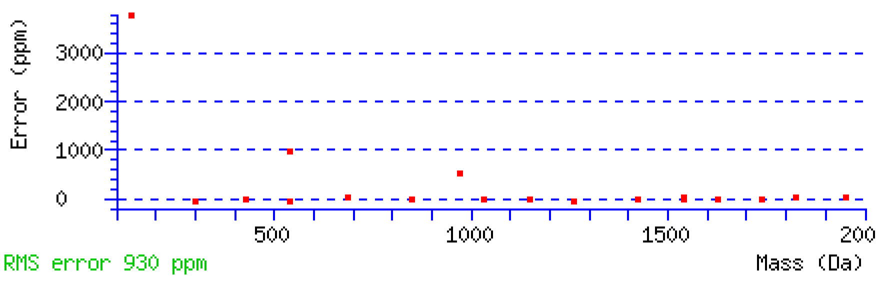
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2111.043564
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 118 **Expect:** 2e-011
Matches : 18/174 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							18
2	159.076418	80.041847			141.065853	71.036564	S	2041.013766	1021.010521	2023.987217	1012.497247	2023.003201	1012.005239	17
3	287.134996	144.071136	270.108447	135.557862	269.124431	135.065854	Q	***1953.981738***	977.494507	1936.955189	968.981233	1935.971173	968.489225	16
4	374.167024	187.587150	357.140475	179.073876	356.156459	178.581868	S	***1825.923160***	913.465218	1808.896611	904.951944	1807.912595	904.459936	15
5	487.251088	244.129182	470.224539	235.615908	469.240523	235.123900	I	***1738.891132***	869.949204	1721.864583	861.435930	1720.880567	860.943922	14
6	574.283116	287.645196	557.256567	279.131922	556.272551	278.639914	S	***1625.807068***	813.407172	1608.780519	804.893898	1607.796503	804.401890	13
7	688.326043	344.666660	671.299494	336.153385	670.315478	335.661377	N	***1538.775040***	769.891158	1521.748491	761.377884			12
8	851.389372	426.198324	834.362823	417.685050	833.378807	417.193042	Y	***1424.732113***	712.869695	1407.705564	704.356420			11
9	964.473436	482.740356	947.446887	474.227082	946.462871	473.735074	L	***1261.668784***	631.338030	1244.642235	622.824756			10
10	1078.516363	539.761820	1061.489814	531.248545	1060.505798	530.756537	N	***1148.584720***	574.795998	1131.558171	566.282724			9
11	1264.595676	632.801476	1247.569127	624.288202	1246.585111	623.796194	W	***1034.541793***	517.774535	1017.515244	509.261260			8
12	1427.659005	714.333141	1410.632456	705.819866	1409.648440	705.327858	Y	***848.462480***	424.734878	831.435931	416.221604			7
13	1555.717583	778.362430	1538.691034	769.849155	1537.707018	769.357147	Q	***685.399151***	343.203214	668.372602	334.689939			6
14	1683.776161	842.391719	1666.749612	833.878444	1665.765596	833.386436	Q	557.340573	279.173925	540.314024	270.660650			5
15	1811.871124	906.439200	1794.844575	897.925926	1793.860559	897.433918	K	***429.281995***	215.144635	412.255446	206.631361			4
16	1908.923888	954.965582	1891.897339	946.452308	1890.913323	945.960300	P	***301.187032***	151.097154	284.160483	142.583879			3
17	1965.945352	983.476314	1948.918803	974.963040	1947.934787	974.471032	G	204.134268	102.570772	187.107719	94.057497			2
18							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
117.8	2111.043564	-0.010512	ASQSISNYLNWYQQKPGK
9.2	2111.021851	0.011201	ALGVQGGQAGVPEGPGFCPQR
8.6	2111.021851	0.011201	ALGVQGGQAGVPEGPGFCPQR
6.1	2111.021851	0.011201	ALGVQGGQAGVPEGPGFCPQR
3.3	2111.036392	-0.003340	QQDAPKPTPAACRCSGLAR

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

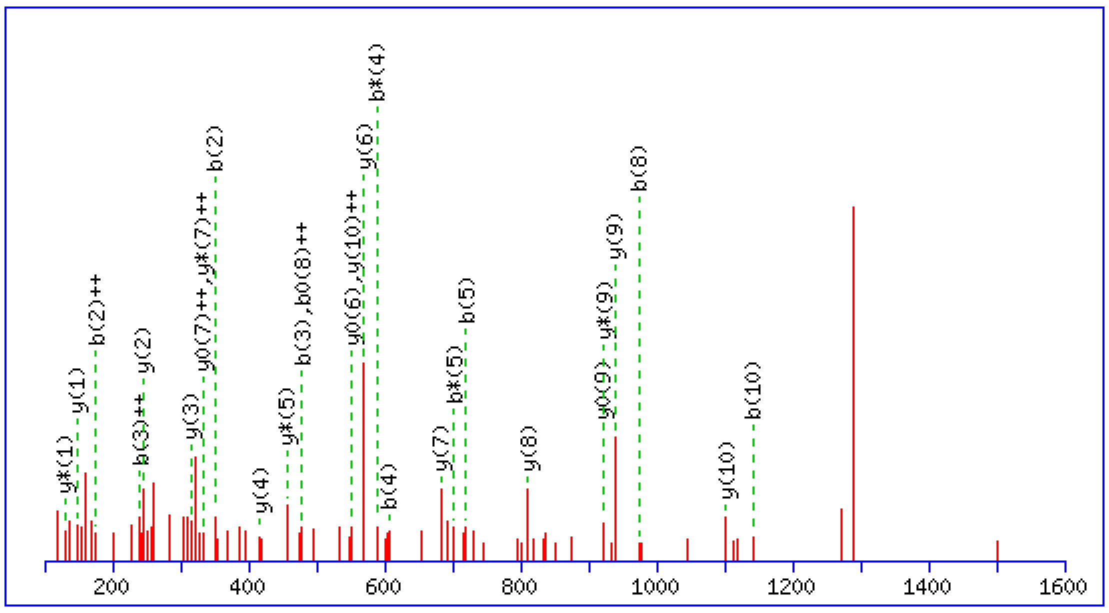
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WYQQLPGTAPK**
Found in **LV105_HUMAN**, Ig lambda chain V-I region NEWM OS=Homo sapiens PE=1 SV=1

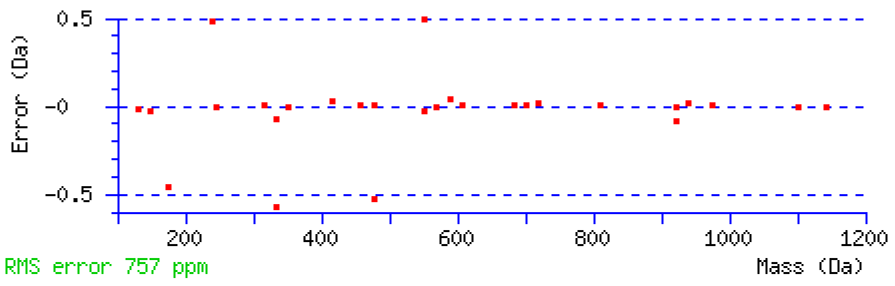
Match to Query 28170: 1287.662468 from(644.838510,2+) rtinseconds(2213) index(23386)
Title: Locus:1.1.1.2373.36
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

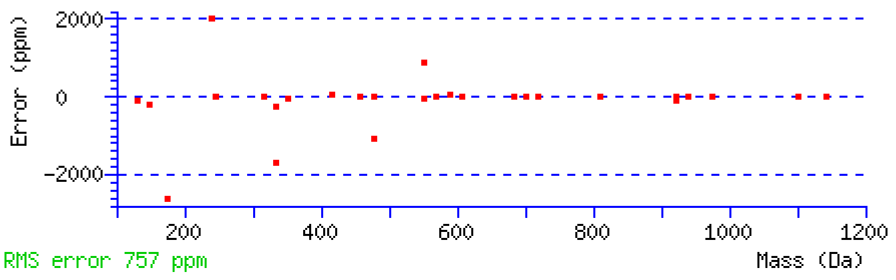
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1287.661163
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.00062
Matches : 28/96 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	187.086589	94.046932					W							11
2	**350.149918**	175.578597					Y	***1102.589138***	551.798207	1085.562589	543.284933	1084.578573	542.792925	10
3	**478.208496**	239.607886	461.181947	231.094612			Q	***939.525809***	470.266543	922.499260	461.753268	921.515244	461.261260	9
4	**606.267074**	303.637175	589.240525	295.123901			Q	***811.467231***	406.237254	794.440682	397.723979	793.456666	397.231971	8
5	**719.351138**	360.179207	702.324589	351.665933			L	***683.408653***	342.207965	666.382104	333.694690	665.398088	333.202682	7
6	816.403902	408.705589	799.377353	400.192315			P	***570.324589***	285.665933	553.298040	277.152658	552.314024	276.660650	6
7	873.425366	437.216321	856.398817	428.703047			G	473.271825	237.139551	456.245276	228.626276	455.261260	228.134268	5
8	**974.473045**	487.740161	957.446496	479.226886	956.462480	478.734878	T	***416.250361***	208.628818	399.223812	200.115544	398.239796	199.623536	4
9	1045.510159	523.258718	1028.483610	514.745443	1027.499594	514.253435	A	***315.202682***	158.104979	298.176133	149.591704			3
10	**1142.562923**	571.785100	1125.536374	563.271825	1124.552358	562.779817	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 WYQQLPGTAPK
(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	1287.661163	0.001305	WYQQLPGTAPK
4.8	1287.667007	-0.004539	ELDLVERESAK
1.7	1287.668350	-0.005882	NLEIQSWRSR

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

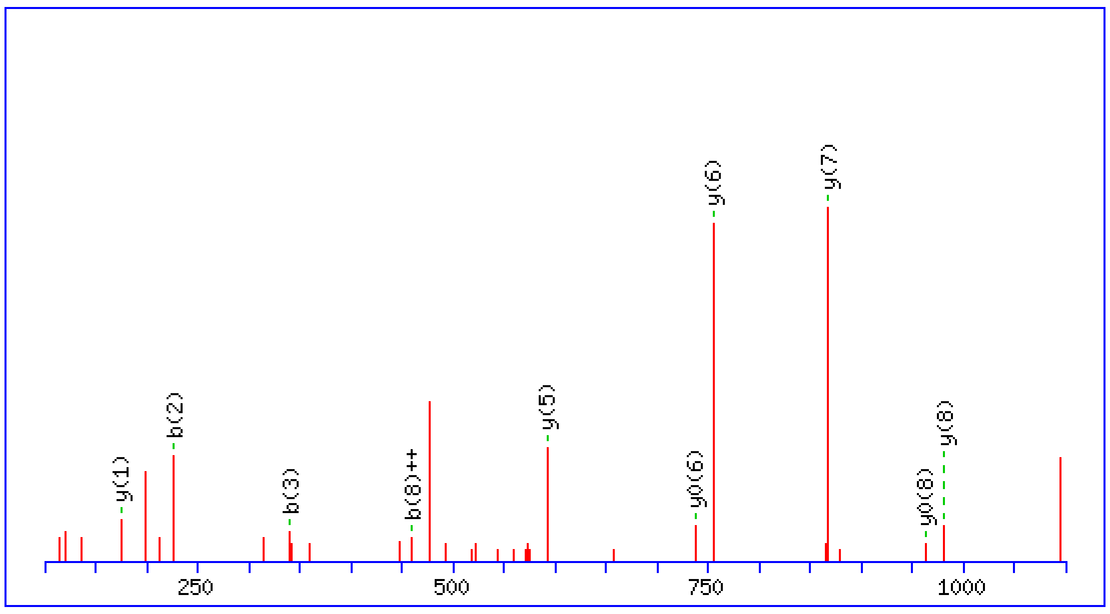
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYSSDQR**
Found in **LV101_HUMAN**, Ig lambda chain V-I region VOR OS=Homo sapiens PE=1 SV=1

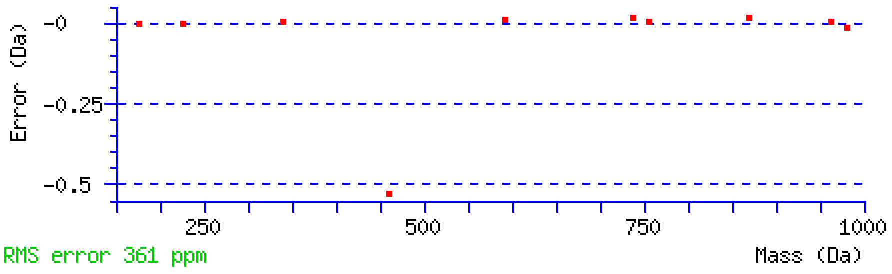
Match to Query 19201: 1093.578428 from(547.796490,2+) rtinseconds(2077) index(13965)
Title: Locus:1.1.1.2261.25
Data file 2011-11-14 - TFD - S 2-5.mgf

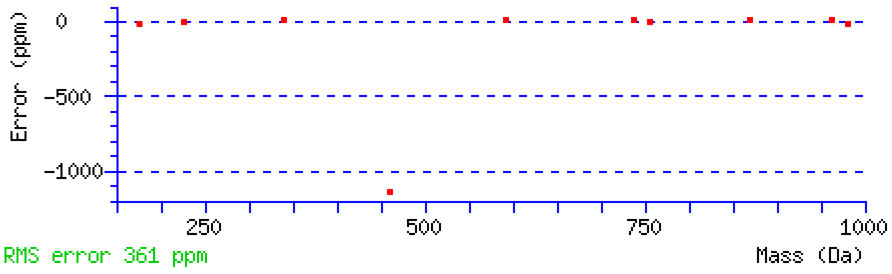
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1093.576752
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0034
Matches : 10/70 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	114.091340	57.549308					L							9
2	**227.175404**	114.091340					L	***981.499986***	491.253631	964.473437	482.740356	963.489421	482.248348	8
3	**340.259468**	170.633372					I	***868.415922***	434.711599	851.389373	426.198324	850.405357	425.706316	7
4	503.322797	252.165036					Y	***755.331858***	378.169567	738.305309	369.656293	737.321293	369.164285	6
5	590.354825	295.681051			572.344260	286.675768	S	***592.268529***	296.637903	575.241980	288.124628	574.257964	287.632620	5
6	677.386853	339.197065			659.376288	330.191782	S	505.236501	253.121888	488.209952	244.608614	487.225936	244.116606	4
7	792.413796	396.710536			774.403231	387.705253	D	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
8	920.472374	460.739825	903.445825	452.226550	902.461809	451.734542	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 LLIYSSDQR
(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	1093.576752	0.001676	LLIYSSDQR
3.7	1093.587997	-0.009569	LHLPDNTLR
2.9	1093.576752	0.001676	LPADSPIPER
2.5	1093.576767	0.001661	IPYTLSQTR
2.5	1093.587997	-0.009569	LLDVVHNER
2.5	1093.587997	-0.009569	LLTVNPEHR
1.9	1093.568924	0.009504	LPTTGMTITK
0.6	1093.576752	0.001676	LIEHINPDK
0.4	1093.587997	-0.009569	DSHPPLRLK

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

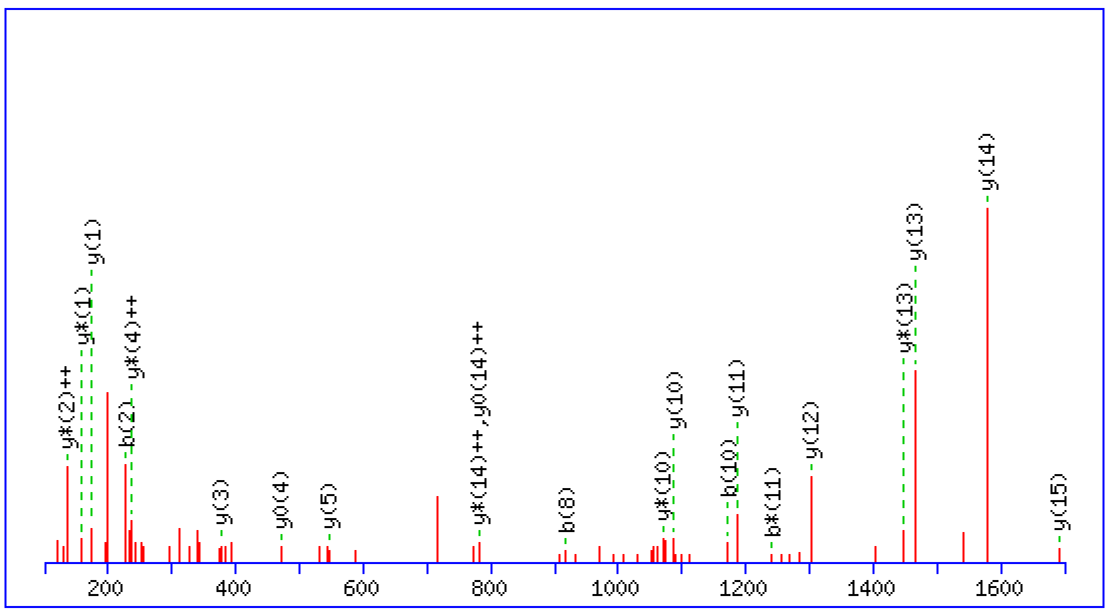
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIYDVNSRPSGISNR**
Found in **LV211_HUMAN**, Ig lambda chain V-II region NIG-84 OS=Homo sapiens PE=1 SV=1

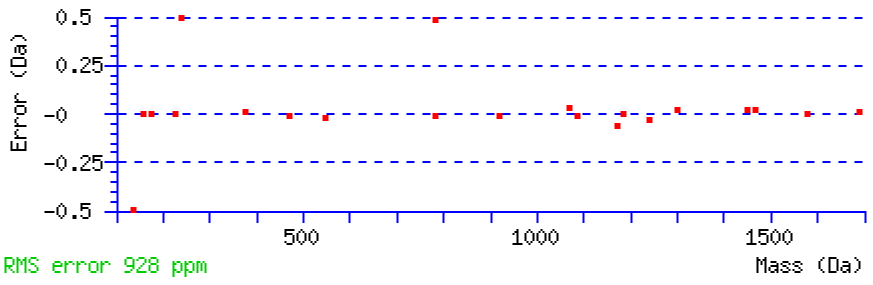
Match to Query 43666: 1802.961972 from(601.994600,3+) rtinseconds(2369) index(26002)
Title: Locus:1.1.1.2402.23
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

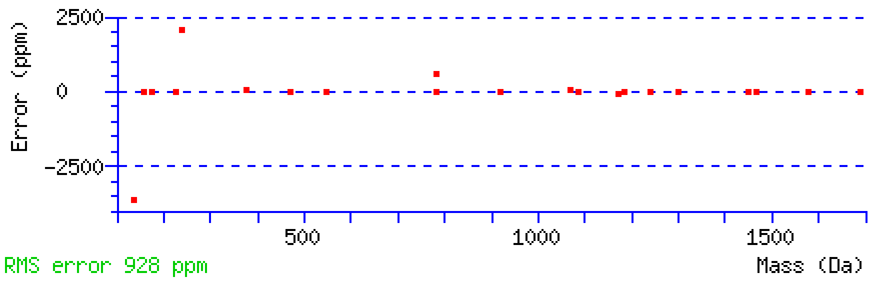
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1802.963867
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00035
Matches : 21/156 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							16
2	**227.175404**	114.091340					L	***1690.887107***	845.947192	1673.860558	837.433917	1672.876542	836.941909	15
3	340.259468	170.633372					I	***1577.803043***	789.405159	1560.776494	780.891885	1559.792478	780.399877	14
4	503.322797	252.165036					Y	***1464.718979***	732.863128	1447.692430	724.349853	1446.708414	723.857845	13
5	618.349740	309.678508			600.339175	300.673226	D	***1301.655650***	651.331463	1284.629101	642.818189	1283.645085	642.326180	12
6	717.418154	359.212715			699.407589	350.207432	V	***1186.628707***	593.817992	1169.602158	585.304717	1168.618142	584.812709	11
7	831.461081	416.234178	814.434532	407.720904	813.450516	407.228896	N	***1087.560293***	544.283785	1070.533744	535.770510	1069.549728	535.278502	10
8	**918.493109**	459.750192	901.466560	451.236918	900.482544	450.744910	S	973.517366	487.262321	956.490817	478.749047	955.506801	478.257039	9
9	1074.594220	537.800748	1057.567671	529.287474	1056.583655	528.795465	R	886.485338	443.746307	869.458789	435.233033	868.474773	434.741025	8
10	**1171.646984**	586.327130	1154.620435	577.813856	1153.636419	577.321847	P	730.384227	365.695752	713.357678	357.182477	712.373662	356.690469	7
11	1258.679012	629.843144	1241.652463	621.329870	1240.668447	620.837862	S	633.331463	317.169370	616.304914	308.656095	615.320898	308.164087	6
12	1315.700476	658.353876	1298.673927	649.840602	1297.689911	649.348593	G	***546.299435***	273.653355	529.272886	265.140081	528.288870	264.648073	5
13	1428.784540	714.895908	1411.757991	706.382634	1410.773975	705.890625	I	489.277971	245.142623	472.251422	236.629349	471.267406	236.137341	4
14	1515.816568	758.411922	1498.790019	749.898648	1497.806003	749.406639	S	***376.193907***	188.600591	359.167358	180.087317	358.183342	179.595309	3
15	1629.859495	815.433385	1612.832946	806.920111	1611.848930	806.428103	N	289.161879	145.084577	272.135330	136.571303			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LLIYDVNSRPSGISNR
(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	1802.963867	-0.001895	LLIYDVNSRPSGISNR
12.4	1802.952652	0.009320	LIIYEVSSRPSGVPDR
12.4	1802.952652	0.009320	LIIYEVSSRPSGVPDR
9.5	1802.977814	-0.015842	IPIPPSPLTPPDLNLR
9.5	1802.977814	-0.015842	IPIPPSPLTPPDLNLR
9.5	1802.977814	-0.015842	IPIPPSPLTPPDLNLR
7.7	1802.977768	-0.015796	IINEPTAAAIAYGLDKK
6.9	1802.977814	-0.015842	IPIPPSPLTPPDLNLR
6.9	1802.977814	-0.015842	IPIPPSPLTPPDLNLR
6.8	1802.977814	-0.015842	IPIPPSPLTPPDLNLR

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

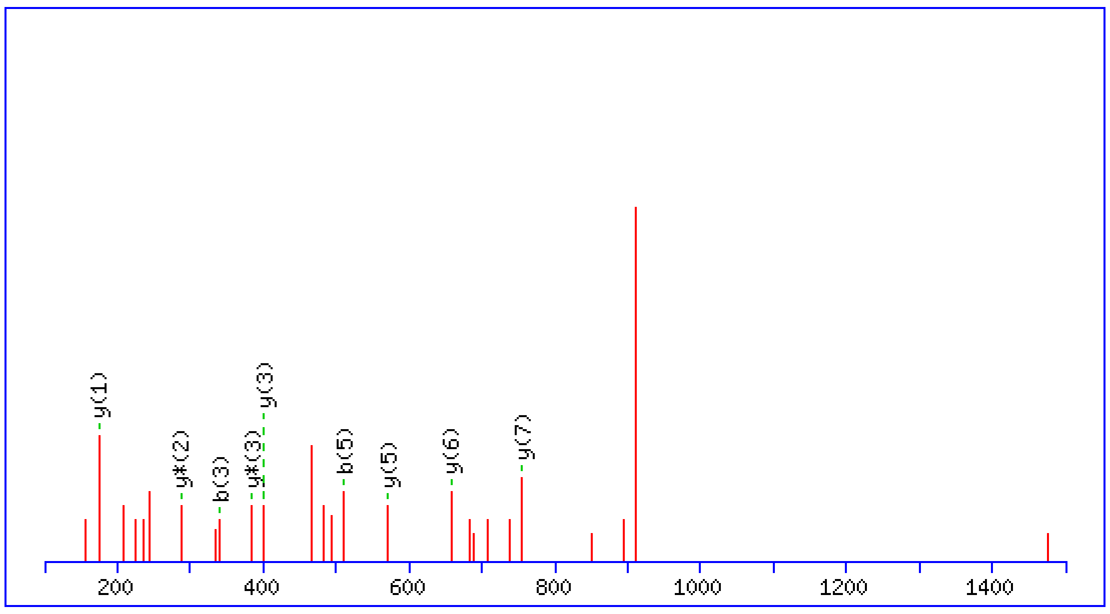
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **RPSGIPER**
Found in **LV401_HUMAN**, Ig lambda chain V-IV region Bau OS=Homo sapiens PE=1 SV=1

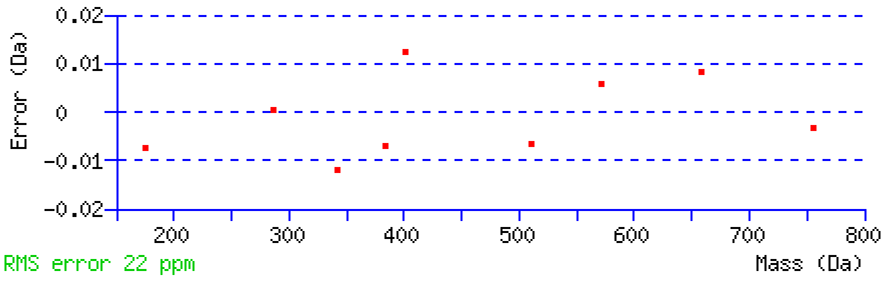
Match to Query 5967: 910.495268 from(456.254910,2+) rtinseconds(881) index(3278)
Title: Locus:1.1.1.973.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

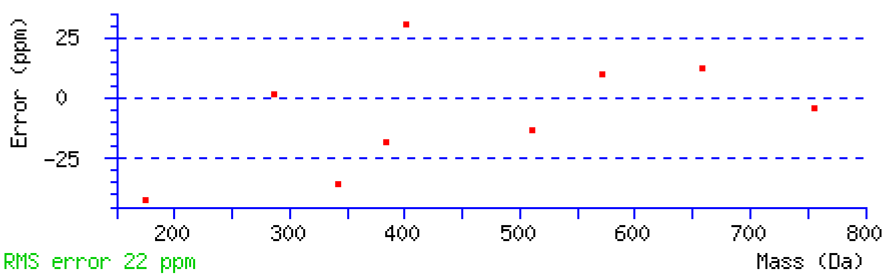
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 910.498444
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00097
Matches : 9/78 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	157.108387	79.057831	140.081838	70.544557			R							8
2	254.161151	127.584213	237.134602	119.070939			P	**755.404629**	378.205953	738.378080	369.692678	737.394064	369.200670	7
3	**341.193179**	171.100227	324.166630	162.586953	323.182614	162.094945	S	**658.351865**	329.679571	641.325316	321.166296	640.341300	320.674288	6
4	398.214643	199.610959	381.188094	191.097685	380.204078	190.605677	G	**571.319837**	286.163557	554.293288	277.650282	553.309272	277.158274	5
5	**511.298707**	256.152991	494.272158	247.639717	493.288142	247.147709	I	514.298373	257.652825	497.271824	249.139550	496.287808	248.647542	4
6	608.351471	304.679374	591.324922	296.166099	590.340906	295.674091	P	**401.214309**	201.110792	384.187760	192.597518	383.203744	192.105510	3
7	737.394064	369.200670	720.367515	360.687396	719.383499	360.195388	E	304.161545	152.584410	287.134996	144.071136	286.150980	143.579128	2
8							R	**175.118952**	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of RPSGIPER
(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	910.498444	-0.003176	RPSGIPER
40.2	910.498444	-0.003176	RPSGIPZR
20.7	910.498444	-0.003176	RPQELPR
5.4	910.498444	-0.003176	SILSAHQR
3.7	910.498428	-0.003160	AHESKLAR
1.7	910.498474	-0.003206	GPTRVPPR
1.5	910.487228	0.008040	DLPGAGPLR
1.3	910.487213	0.008055	AASPSPPLR
1.2	910.491928	0.003340	RGCVHLR
0.9	910.498459	-0.003191	RGPPPLAR

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

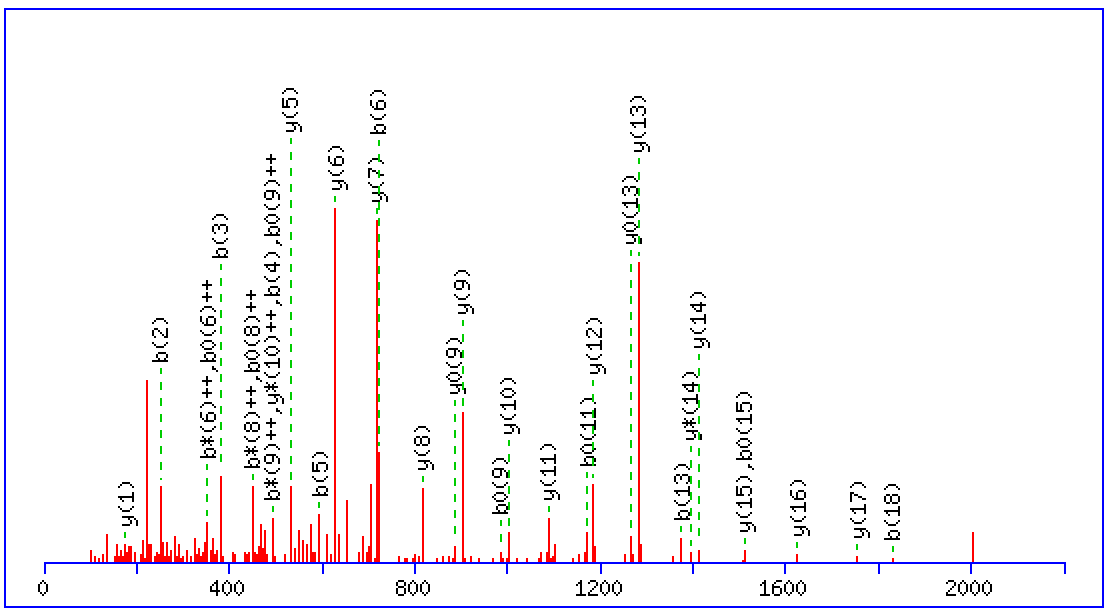
Mascot Search Results

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

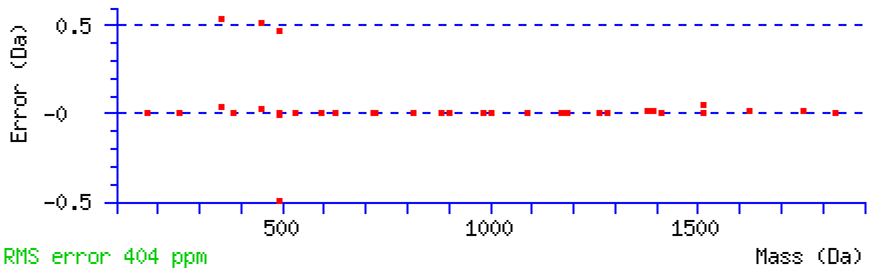
Match to Query 55669: 2003.001222 from(668.674350,3+) rtinseconds(2397) index(28332)
Title: Locus:1.1.1.2357.37
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

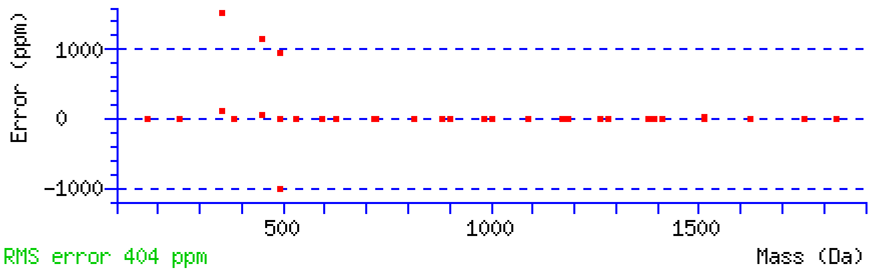
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2002.995987
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 138 **Expect:** 2.4e-013
Matches : 34/202 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							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
137.8	2002.995987	0.005235	SYELTQPPSVSVSPGQTAR
6.1	2003.001312	-0.000090	ASGKPNPWYTWLKNGER
4.3	2002.989426	0.011796	SAAKIALMNSVFNEHPSR
3.7	2002.984741	0.016481	TPLTDTSVYTELPNAEPR
3.6	2003.005890	-0.004668	ASIDPVPTSIDESSSVVLR
1.0	2002.999344	0.001878	TDLRTDLSTLMELSHQK
0.6	2002.982086	0.019136	APRRPSGPGPPSPTPPAPR
0.0	2002.990295	0.010927	RMMLDQCLELQLFHR

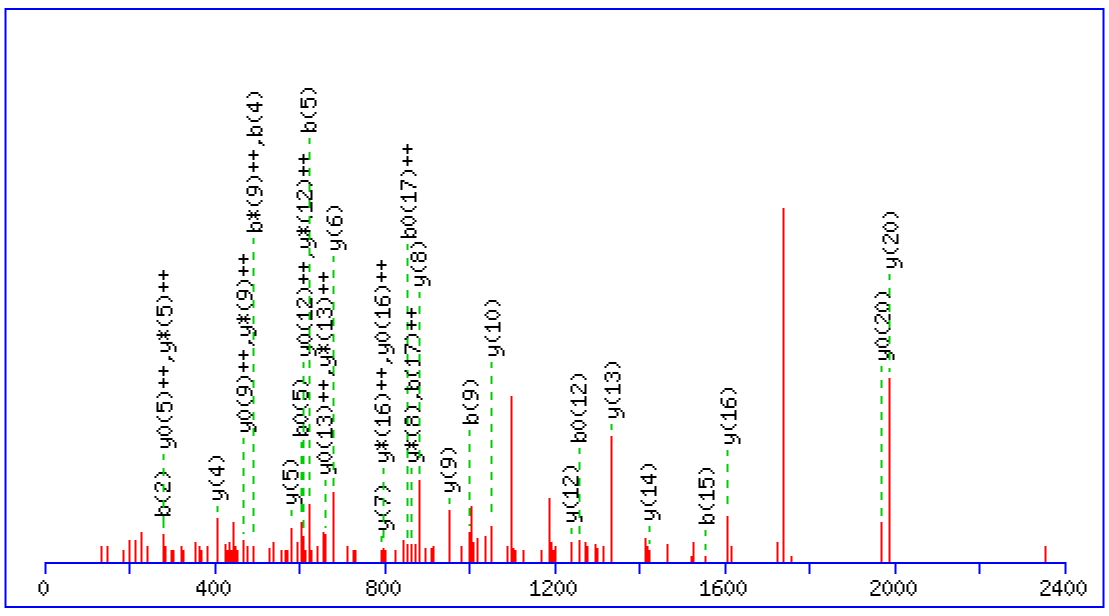
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YDLTQPPSVSVSPGQTASITCSGDK**
Found in **LV402_HUMAN**, Ig lambda chain V-IV region X OS=Homo sapiens PE=1 SV=1

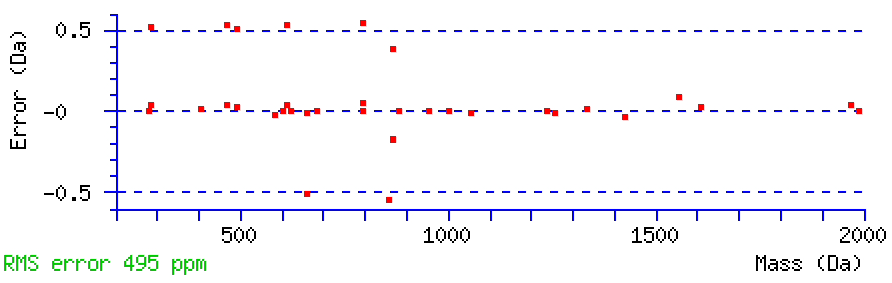
Match to Query 62773: 2608.244262 from(870.422030,3+) rtinseconds(2706) index(34093)
Title: Locus:1.1.1.2472.48
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

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 ●

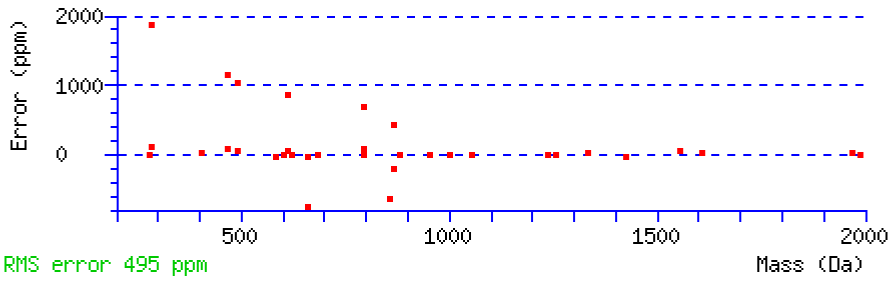


Monoisotopic mass of neutral peptide Mr(calc): 2608.232681
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00017
Matches : 34/276 fragment ions using 63 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							25
2	**279.097548**	140.052412			261.086983	131.047130	D	2446.176612	1223.591944	2429.150063	1215.078669	2428.166047	1214.586661	24
3	392.181612	196.594444			374.171047	187.589162	L	2331.149669	1166.078472	2314.123120	1157.565198	2313.139104	1157.073190	23
4	**493.229291**	247.118284			475.218726	238.113001	T	2218.065605	1109.536440	2201.039056	1101.023166	2200.055040	1100.531158	22
5	**621.287869**	311.147573	604.261320	302.634298	603.277304	302.142290	Q	2117.017926	1059.012601	2099.991377	1050.499326	2099.007361	1050.007318	21
6	718.340633	359.673955	701.314084	351.160680	700.330068	350.668672	P	***1988.959348***	994.983312	1971.932799	986.470038	1970.948783	985.978030	20
7	815.393397	408.200337	798.366848	399.687062	797.382832	399.195054	P	1891.906584	946.456930	1874.880035	937.943656	1873.896019	937.451648	19
8	902.425425	451.716351	885.398876	443.203076	884.414860	442.711068	S	1794.853820	897.930548	1777.827271	889.417274	1776.843255	888.925266	18
9	**1001.493839**	501.250558	984.467290	492.737283	983.483274	492.245275	V	1707.821792	854.414534	1690.795243	845.901260	1689.811227	845.409251	17
10	1088.525867	544.766572	1071.499318	536.253297	1070.515302	535.761289	S	***1608.753378***	804.880327	1591.726829	796.367053	1590.742813	795.875045	16
11	1187.594281	594.300779	1170.567732	585.787504	1169.583716	585.295496	V	1521.721350	761.364313	1504.694801	752.851039	1503.710785	752.359031	15
12	1274.626309	637.816793	1257.599760	629.303518	1256.615744	628.811510	S	***1422.652936***	711.830106	1405.626387	703.316832	1404.642371	702.824823	14
13	1371.679073	686.343175	1354.652524	677.829900	1353.668508	677.337892	P	***1335.620908***	668.314092	1318.594359	659.800817	1317.610343	659.308809	13
14	1428.700537	714.853907	1411.673988	706.340632	1410.689972	705.848624	G	***1238.568144***	619.787710	1221.541595	611.274435	1220.557579	610.782427	12
15	**1556.759115**	778.883196	1539.732566	770.369921	1538.748550	769.877913	Q	1181.546680	591.276978	1164.520131	582.763704	1163.536115	582.271695	11
16	1657.806794	829.407035	1640.780245	820.893761	1639.796229	820.401753	T	***1053.488102***	527.247689	1036.461553	518.734415	1035.477537	518.242407	10
17	1728.843908	864.925592	1711.817359	856.412318	1710.833343	855.920310	A	***952.440423***	476.723850	935.413874	468.210575	934.429858	467.718567	9
18	1815.875936	908.441606	1798.849387	899.928332	1797.865371	899.436324	S	***881.403309***	441.205293	864.376760	432.692018	863.392744	432.200010	8
19	1928.960000	964.983638	1911.933451	956.470364	1910.949435	955.978356	I	***794.371281***	397.689279	777.344732	389.176004	776.360716	388.683996	7
20	2030.007679	1015.507478	2012.981130	1006.994203	2011.997114	1006.502195	T	***681.287217***	341.147247	664.260668	332.633972	663.276652	332.141964	6
21	2204.053978	1102.530627	2187.027429	1094.017352	2186.043413	1093.525344	C	***580.239538***	290.623407	563.212989	282.110133	562.228973	281.618125	5
22	2291.086006	1146.046641	2274.059457	1137.533366	2273.075441	1137.041358	S	***406.193239***	203.600257	389.166690	195.086983	388.182674	194.594975	4
23	2348.107470	1174.557373	2331.080921	1166.044098	2330.096905	1165.552090	G	319.161211	160.084243	302.134662	151.570969	301.150646	151.078961	3
24	2463.134413	1232.070844	2446.107864	1223.557570	2445.123848	1223.065562	D	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
25							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 495 ppm



RMS error 495 ppm

NCBI **BLAST** search of YDLTQPPSVSVSPGQTASITCSGDK
(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	2608.232681	0.011581	YDLTQPPSVSVSPGQTASITCSGDK

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

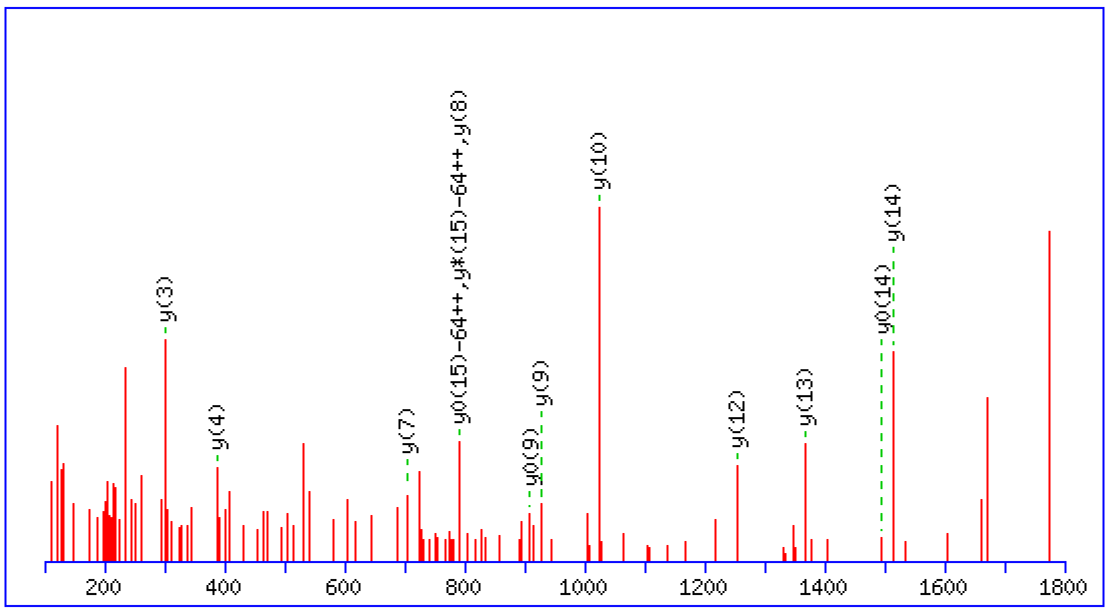
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFMLTQPHSVSESPGK**
Found in **LV601_HUMAN**, Ig lambda chain V-VI region AR OS=Homo sapiens PE=1 SV=1

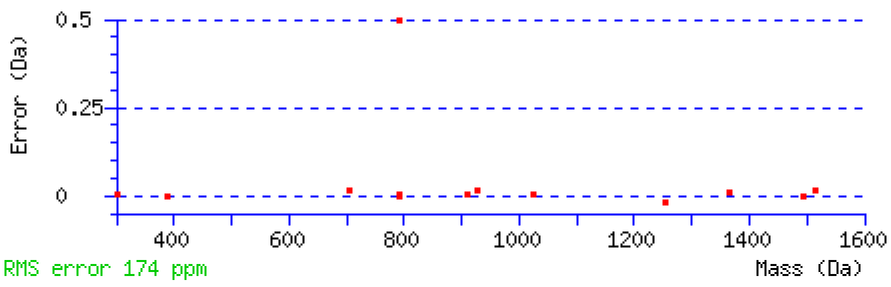
Match to Query 43443: 1774.835622 from(592.619150,3+) rtinseconds(1883) index(10526)
Title: Locus:1.1.1.2187.17
Data file 2011-11-14 - TFD - S 2-5.mgf

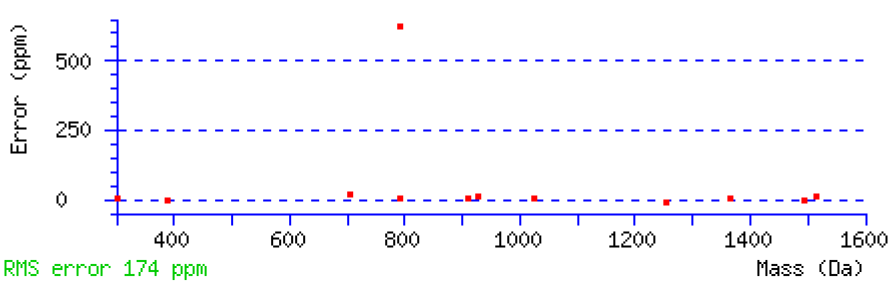
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1774.819611
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: 1.8e-006
Matches : 13/248 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							16
2	263.102633	132.054954			245.092068	123.049672	F	1660.799934	830.903605	1643.773385	822.390331	1642.789369	821.898323	15
3	410.138033	205.572654			392.127468	196.567372	M	***1513.731520***	757.369398	1496.704971	748.856124	1495.720955	748.364116	14
4	523.222097	262.114687			505.211532	253.109404	L	***1366.696120***	683.851698	1349.669571	675.338424	1348.685555	674.846416	13
5	624.269776	312.638526			606.259211	303.633243	T	***1253.612056***	627.309666	1236.585507	618.796392	1235.601491	618.304384	12
6	752.328354	376.667815	735.301805	368.154541	734.317789	367.662533	Q	1152.564377	576.785827	1135.537828	568.272552	1134.553812	567.780544	11
7	849.381118	425.194197	832.354569	416.680923	831.370553	416.188915	P	***1024.505799***	512.756538	1007.479250	504.243263	1006.495234	503.751255	10
8	986.440030	493.723653	969.413481	485.210378	968.429465	484.718370	H	***927.453035***	464.230156	910.426486	455.716881	909.442470	455.224873	9
9	1073.472058	537.239667	1056.445509	528.726393	1055.461493	528.234385	S	***790.394123***	395.700700	773.367574	387.187425	772.383558	386.695417	8
10	1172.540472	586.773874	1155.513923	578.260600	1154.529907	577.768592	V	***703.362095***	352.184686	686.335546	343.671411	685.351530	343.179403	7
11	1259.572500	630.289888	1242.545951	621.776614	1241.561935	621.284606	S	604.293681	302.650479	587.267132	294.137204	586.283116	293.645196	6
12	1388.615093	694.811185	1371.588544	686.297910	1370.604528	685.805902	E	517.261653	259.134465	500.235104	250.621190	499.251088	250.129182	5
13	1475.647121	738.327199	1458.620572	729.813924	1457.636556	729.321916	S	***388.219060***	194.613168	371.192511	186.099894	370.208495	185.607886	4
14	1572.699885	786.853581	1555.673336	778.340306	1554.689320	777.848298	P	***301.187032***	151.097154	284.160483	142.583879			3
15	1629.721349	815.364313	1612.694800	806.851038	1611.710784	806.359030	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 DFMLTQPHSVSESPGK
(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	1774.819611	0.016011	DFMLTQPHSVSESPGK
38.4	1774.819611	0.016011	DFMLTQPHSVSESPGK

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

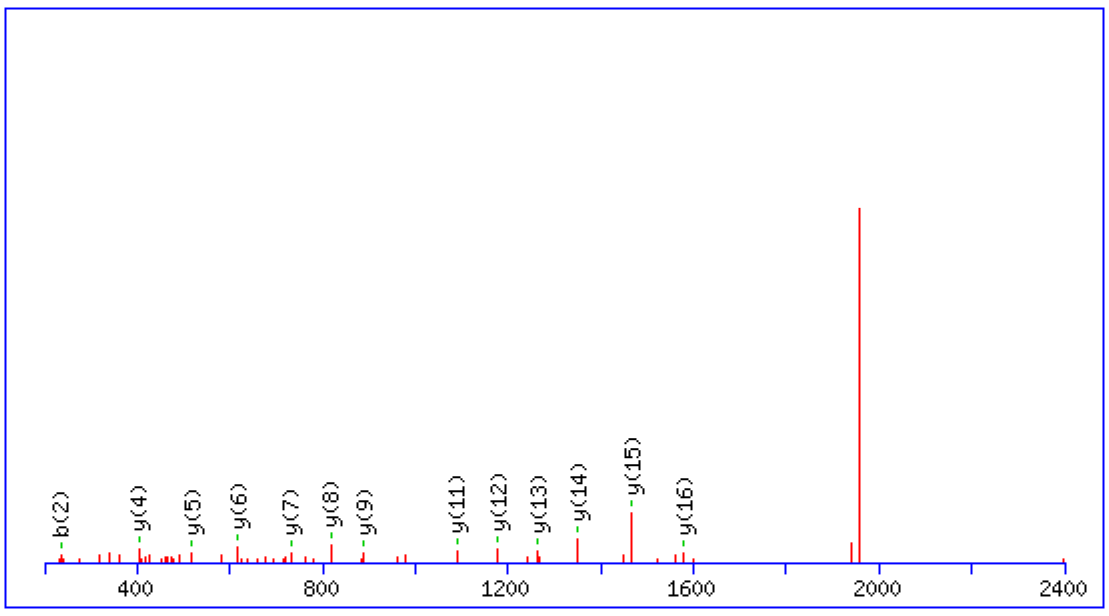
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSGSIDSSSNSASLTISGLK**
Found in **LV604_HUMAN**, Ig lambda chain V-VI region WLT OS=Homo sapiens PE=1 SV=1

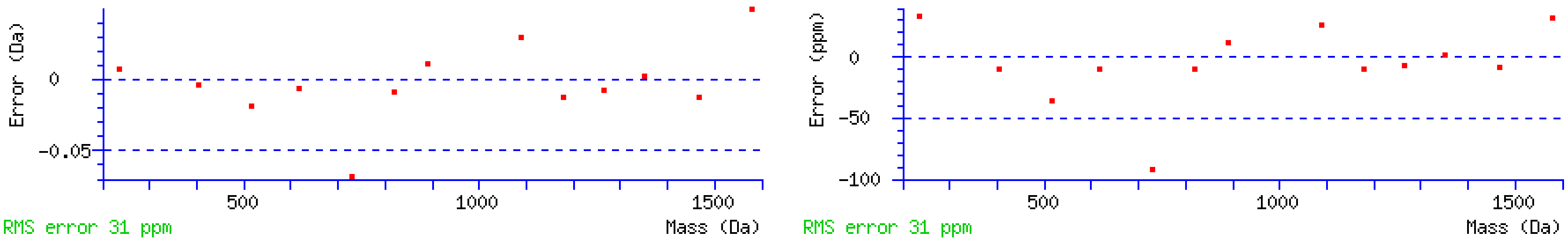
Match to Query 50762: 1956.963688 from(979.489120,2+) rtinseconds(2777) index(30762)
Title: Locus:1.1.1.2866.51
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

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): 1956.964005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 114 **Expect:** 2e-011
Matches : 13/202 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							20
2	235.107718	118.057497			217.097153	109.052214	S	1810.902875	905.955075	1793.876326	897.441801	1792.892310	896.949793	19
3	292.129182	146.568229			274.118617	137.562946	G	1723.870847	862.439061	1706.844298	853.925787	1705.860282	853.433779	18
4	379.161210	190.084243			361.150645	181.078960	S	1666.849383	833.928329	1649.822834	825.415055	1648.838818	824.923047	17
5	492.245274	246.626275			474.234709	237.620992	I	***1579.817355***	790.412315	1562.790806	781.899041	1561.806790	781.407033	16
6	607.272217	304.139747			589.261652	295.134464	D	***1466.733291***	733.870283	1449.706742	725.357009	1448.722726	724.865001	15
7	694.304245	347.655760			676.293680	338.650478	S	***1351.706348***	676.356812	1334.679799	667.843537	1333.695783	667.351529	14
8	781.336273	391.171774			763.325708	382.166492	S	***1264.674320***	632.840798	1247.647771	624.327523	1246.663755	623.835515	13
9	868.368301	434.687788			850.357736	425.682506	S	***1177.642292***	589.324784	1160.615743	580.811509	1159.631727	580.319501	12
10	982.411228	491.709252	965.384679	483.195977	964.400663	482.703969	N	***1090.610264***	545.808770	1073.583715	537.295495	1072.599699	536.803487	11
11	1069.443256	535.225266	1052.416707	526.711991	1051.432691	526.219983	S	976.567337	488.787306	959.540788	480.274032	958.556772	479.782024	10
12	1140.480370	570.743823	1123.453821	562.230548	1122.469805	561.738540	A	***889.535309***	445.271292	872.508760	436.758018	871.524744	436.266010	9
13	1227.512398	614.259837	1210.485849	605.746562	1209.501833	605.254554	S	***818.498195***	409.752735	801.471646	401.239461	800.487630	400.747453	8
14	1340.596462	670.801869	1323.569913	662.288594	1322.585897	661.796586	L	***731.466167***	366.236721	714.439618	357.723447	713.455602	357.231439	7
15	1441.644141	721.325708	1424.617592	712.812434	1423.633576	712.320426	T	***618.382103***	309.694689	601.355554	301.181415	600.371538	300.689407	6
16	1554.728205	777.867740	1537.701656	769.354466	1536.717640	768.862458	I	***517.334424***	259.170850	500.307875	250.657575	499.323859	250.165567	5
17	1641.760233	821.383754	1624.733684	812.870480	1623.749668	812.378472	S	***404.250360***	202.628818	387.223811	194.115543	386.239795	193.623535	4
18	1698.781697	849.894486	1681.755148	841.381212	1680.771132	840.889204	G	317.218332	159.112804	300.191783	150.599529			3
19	1811.865761	906.436518	1794.839212	897.923244	1793.855196	897.431236	L	260.196868	130.602072	243.170319	122.088797			2
20							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
114.4	1956.964005	-0.000317	FSGSIDSSSNSASLTISGLK
0.2	1956.979279	-0.015591	KHPPAEAPVPIPPSPDTK
0.1	1956.964005	-0.000317	LLLPGSSPSSPEDEVKDR
0.0	1956.979279	-0.015591	KHPPAEAPVPIPPSPDTK

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

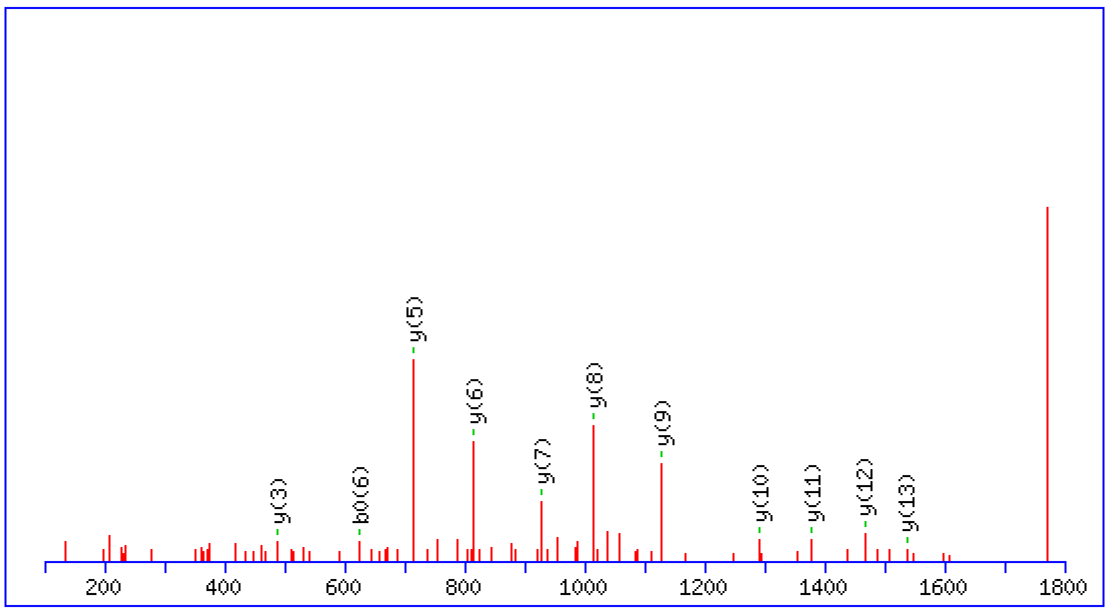
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAASSYLSLTPEQWR**
Found in **IGLL1_HUMAN**, Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens GN=IGLL1 PE=1 SV=1

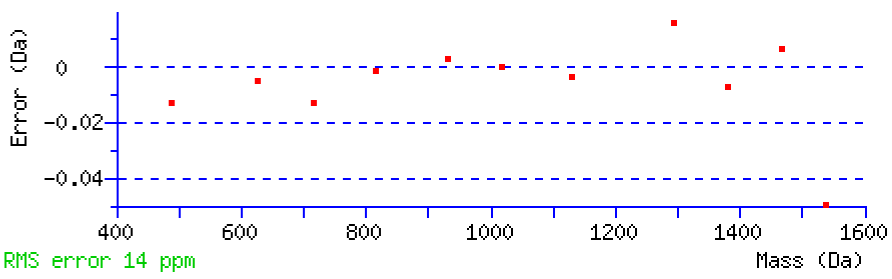
Match to Query 41038: 1770.870148 from(886.442350,2+) rtinseconds(3280) index(40024)
Title: Locus:1.1.1.3056.46
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

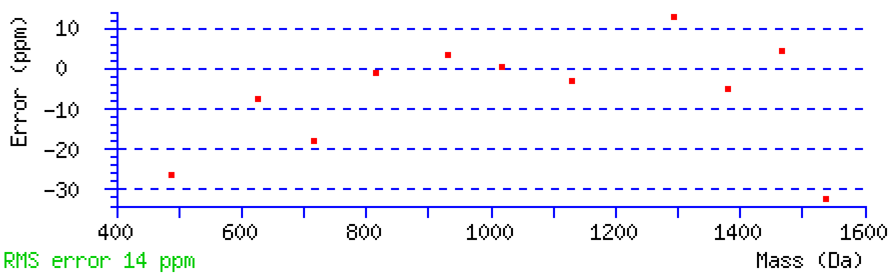
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1770.857666
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82 **Expect:** 2.7e-008
Matches : 11/132 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	164.070605	82.538940					Y							15
2	235.107719	118.057498					A	1608.801648	804.904462	1591.775099	796.391188	1590.791083	795.899180	14
3	306.144833	153.576055					A	***1537.764534***	769.385905	1520.737985	760.872631	1519.753969	760.380623	13
4	393.176861	197.092068			375.166296	188.086786	S	***1466.727420***	733.867348	1449.700871	725.354074	1448.716855	724.862066	12
5	480.208889	240.608082			462.198324	231.602800	S	***1379.695392***	690.351334	1362.668843	681.838060	1361.684827	681.346052	11
6	643.272218	322.139747			625.261653	313.134465	Y	***1292.663364***	646.835320	1275.636815	638.322046	1274.652799	637.830038	10
7	756.356282	378.681779			738.345717	369.676497	L	***1129.600035***	565.303656	1112.573486	556.790381	1111.589470	556.298373	9
8	843.388310	422.197793			825.377745	413.192511	S	***1016.515971***	508.761624	999.489422	500.248349	998.505406	499.756341	8
9	956.472374	478.739825			938.461809	469.734543	L	***929.483943***	465.245610	912.457394	456.732335	911.473378	456.240327	7
10	1057.520053	529.263665			1039.509488	520.258382	T	***816.399879***	408.703578	799.373330	400.190303	798.389314	399.698295	6
11	1154.572817	577.790047			1136.562252	568.784764	P	***715.352200***	358.179738	698.325651	349.666464	697.341635	349.174456	5
12	1283.615410	642.311343			1265.604845	633.306061	E	618.299436	309.653356	601.272887	301.140082	600.288871	300.648074	4
13	1411.673988	706.340632	1394.647439	697.827358	1393.663423	697.335350	Q	***489.256843***	245.132060	472.230294	236.618785			3
14	1597.753301	799.380289	1580.726752	790.867014	1579.742736	790.375006	W	361.198265	181.102770	344.171716	172.589496			2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
82.0	1770.857666	0.012482	YAASSYLSLTPEQWR
1.2	1770.854080	0.016068	LTPMFLMVMPGMISR
0.3	1770.854080	0.016068	LTPMFLMVMPGMISR

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

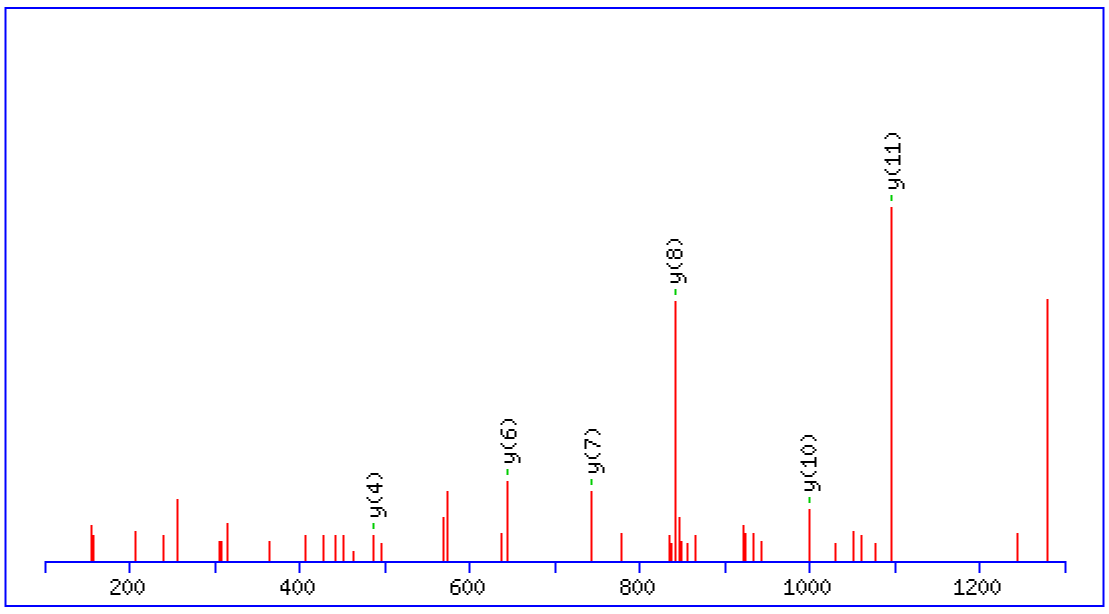
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPGTPVASSQPR**
Found in **ISLR_HUMAN**, Immunoglobulin superfamily containing leucine-rich repeat protein OS=Homo sapiens GN=ISLR PE=1 SV=1

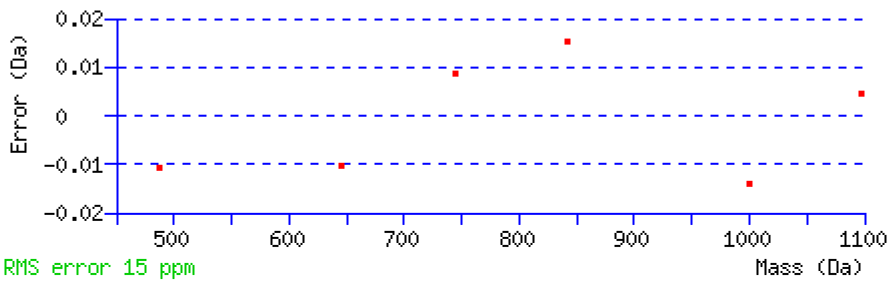
Match to Query 23964: 1279.693008 from(640.853780,2+) rtinseconds(1567) index(12534)
Title: Locus:1.1.1.2130.40
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

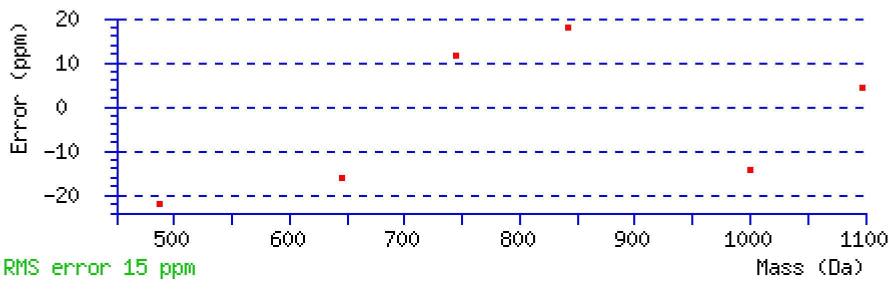
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1279.688446
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.002
Matches : 6/110 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							13
2	185.128454	93.067865					L	1209.658613	605.332944	1192.632064	596.819670	1191.648048	596.327662	12
3	282.181218	141.594247					P	*1096.574549*	548.790912	1079.548000	540.277638	1078.563984	539.785630	11
4	339.202682	170.104979					G	*999.521785*	500.264530	982.495236	491.751256	981.511220	491.259248	10
5	440.250361	220.628818			422.239796	211.623536	T	942.500321	471.753798	925.473772	463.240524	924.489756	462.748516	9
6	537.303125	269.155201			519.292560	260.149918	P	*841.452642*	421.229959	824.426093	412.716684	823.442077	412.224676	8
7	636.371539	318.689408			618.360974	309.684125	V	*744.399878*	372.703577	727.373329	364.190302	726.389313	363.698294	7
8	707.408653	354.207965			689.398088	345.202682	A	*645.331464*	323.169370	628.304915	314.656095	627.320899	314.164087	6
9	794.440681	397.723978			776.430116	388.718696	S	574.294350	287.650813	557.267801	279.137538	556.283785	278.645530	5
10	881.472709	441.239992			863.462144	432.234710	S	*487.262322*	244.134799	470.235773	235.621524	469.251757	235.129516	4
11	1009.531287	505.269281	992.504738	496.756007	991.520722	496.263999	Q	400.230294	200.618785	383.203745	192.105510			3
12	1106.584051	553.795663	1089.557502	545.282389	1088.573486	544.790381	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 ALPGTPVASSQPR
(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	1279.688446	0.004562	ALPGTPVASSQPR

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

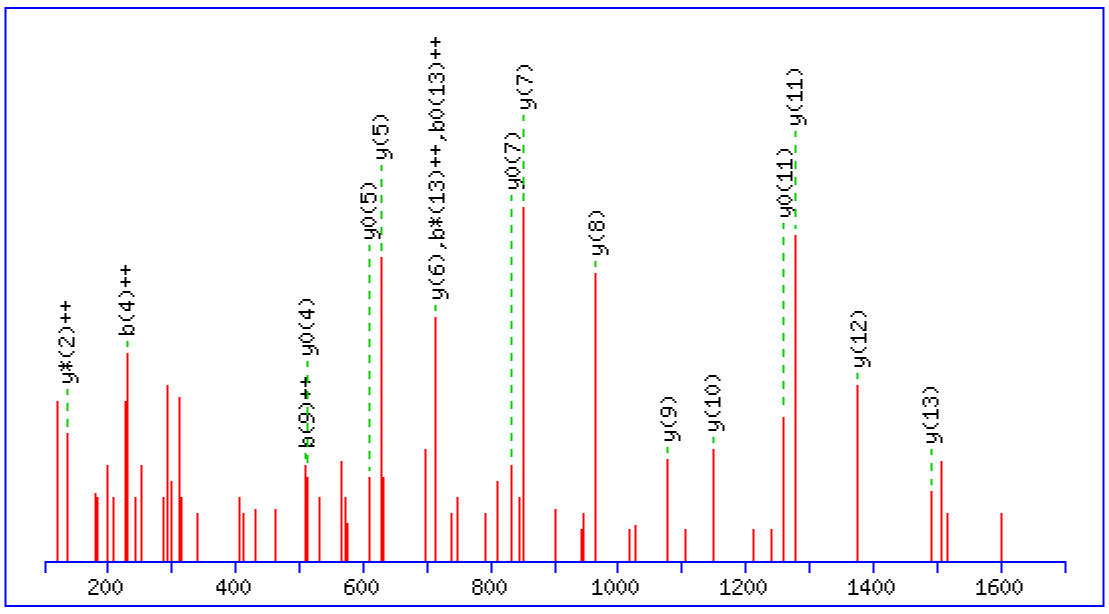
Mascot Search Results

Peptide View

MS/MS Fragmentation of ENIVEAIIHSPELIR
Found in IPO7_HUMAN, Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1

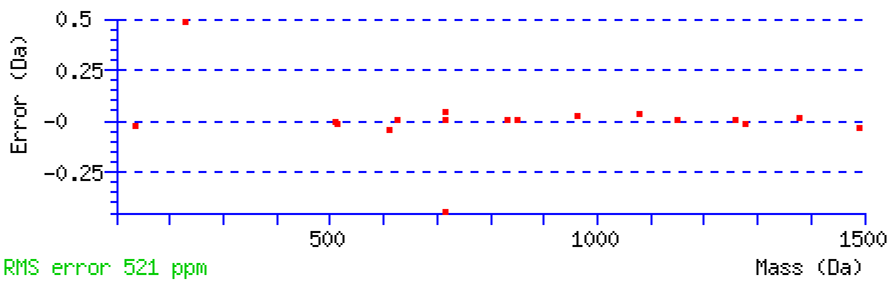
Match to Query 21039: 1731.956382 from(578.326070,3+) rtinseconds(3970) index(62023)
Title: Locus:1.1.1.2159.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

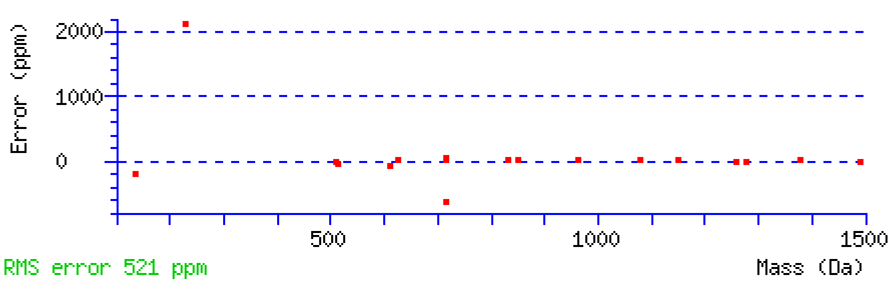
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1731.951889
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 5.2e-006
Matches : 18/160 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	130.049869	65.528572			112.039304	56.523290	E							15
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	1603.916617	802.461946	1586.890068	793.948672	1585.906052	793.456664	14
3	357.176860	179.092068	340.150311	170.578794	339.166295	170.086786	I	***1489.873690***	745.440483	1472.847141	736.927208	1471.863125	736.435200	13
4	456.245274	**228.626275**	439.218725	220.113001	438.234709	219.620993	V	***1376.789626***	688.898451	1359.763077	680.385176	1358.779061	679.893168	12
5	585.287867	293.147572	568.261318	284.634297	567.277302	284.142289	E	***1277.721212***	639.364244	1260.694663	630.850969	1259.710647	630.358961	11
6	656.324981	328.666129	639.298432	320.152854	638.314416	319.660846	A	***1148.678619***	574.842947	1131.652070	566.329673	1130.668054	565.837665	10
7	769.409045	385.208161	752.382496	376.694886	751.398480	376.202878	I	***1077.641505***	539.324390	1060.614956	530.811116	1059.630940	530.319108	9
8	882.493109	441.750193	865.466560	433.236918	864.482544	432.744910	I	***964.557441***	482.782358	947.530892	474.269084	946.546876	473.777076	8
9	1019.552021	**510.279649**	1002.525472	501.766374	1001.541456	501.274366	H	***851.473377***	426.240326	834.446828	417.727052	833.462812	417.235044	7
10	1106.584049	553.795663	1089.557500	545.282388	1088.573484	544.790380	S	***714.414465***	357.710870	697.387916	349.197596	696.403900	348.705588	6
11	1203.636813	602.322045	1186.610264	593.808770	1185.626248	593.316762	P	***627.382437***	314.194856	610.355888	305.681582	609.371872	305.189574	5
12	1332.679406	666.843341	1315.652857	658.330067	1314.668841	657.838058	E	530.329673	265.668474	513.303124	257.155200	512.319108	256.663192	4
13	1445.763470	723.385373	1428.736921	714.872098	1427.752905	714.380090	L	401.287080	201.147178	384.260531	192.633903			3
14	1558.847534	779.927405	1541.820985	771.414130	1540.836969	770.922122	I	288.203016	144.605146	271.176467	136.091871			2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.2	1731.951889	0.004493	ENIVEAIIHSPELIR
0.8	1731.940674	0.015708	EKEPHLVEEVSVLPK

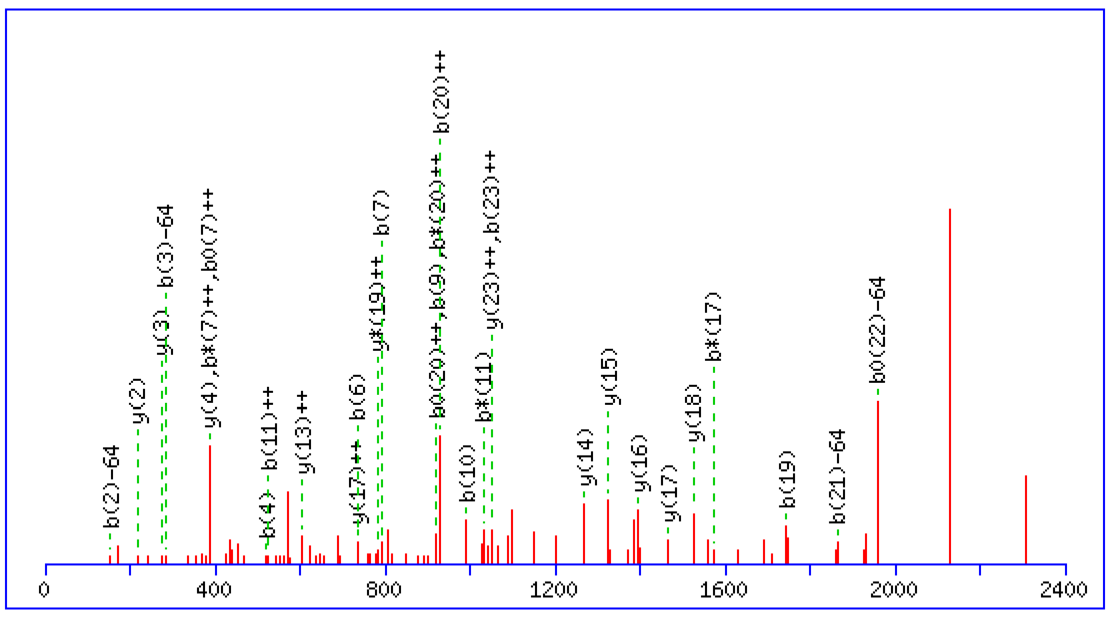
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAECGRGGAAGGALPTSPGPALGAK**
Found in **PLCL2_HUMAN**, Inactive phospholipase C-like protein 2 OS=Homo sapiens GN=PLCL2 PE=1 SV=2

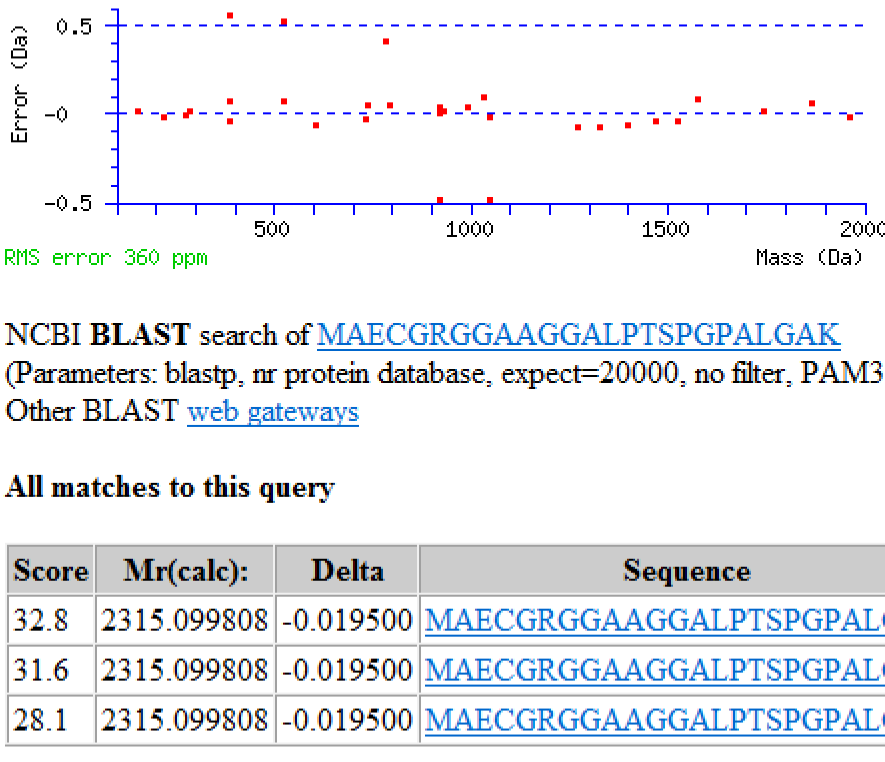
Match to Query 69364: 2315.080308 from(1158.547430,2+) rtinseconds(1264) index(10493)
Title: Locus:1.1.1.1120.51
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

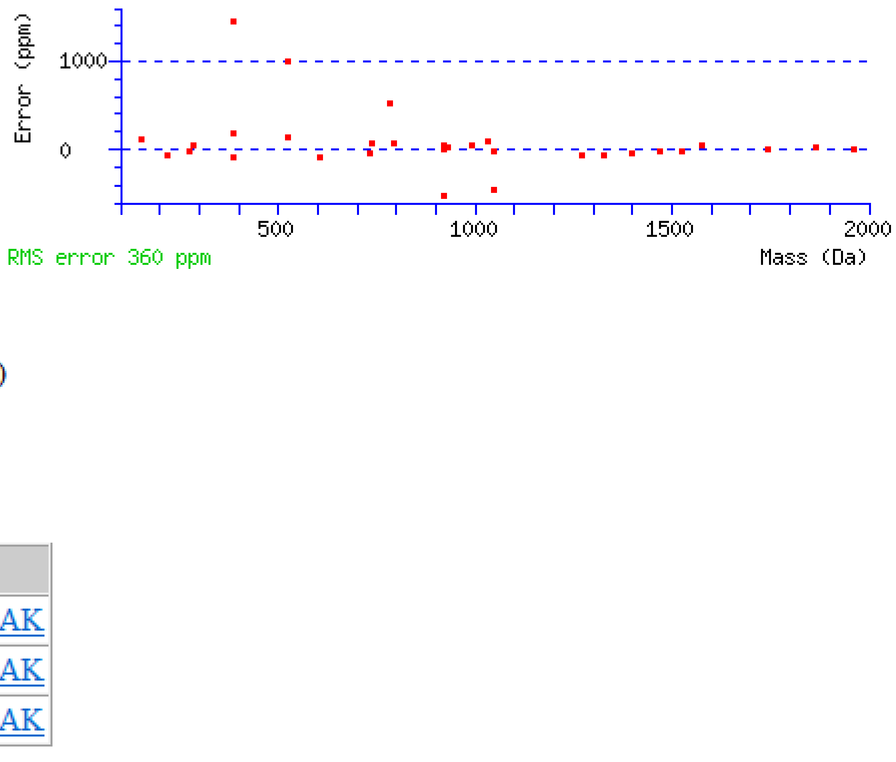
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2315.099808
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
P15 : Oxidation (P)
P20 : Oxidation (P)
Ions Score: 33 **Expect:** 0.0054
Matches : 31/388 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	148.042676	74.524976					M							25
2	219.079790	110.043533					A	2169.071696	1085.039486	2152.045147	1076.526211	2151.061131	1076.034203	24
3	348.122383	174.564829			330.111818	165.559547	E	2098.034582	1049.520929	2081.008033	1041.007654	2080.024017	1040.515646	23
4	***522.168682***	261.587979			504.158117	252.582697	C	1968.991989	984.999632	1951.965440	976.486358	1950.981424	975.994350	22
5	579.190146	290.098711			561.179581	281.093429	G	1794.945690	897.976483	1777.919141	889.463209	1776.935125	888.971201	21
6	***735.291257***	368.149267	718.264708	359.635992	717.280692	359.143984	R	1737.924226	869.465751	1720.897677	860.952476	1719.913661	860.460468	20
7	***792.312721***	396.659999	775.286172	388.146724	774.302156	387.654716	G	1581.823115	791.415195	1564.796566	782.901921	1563.812550	782.409913	19
8	849.334185	425.170731	832.307636	416.657456	831.323620	416.165448	G	***1524.801651***	762.904464	1507.775102	754.391189	1506.791086	753.899181	18
9	***920.371299***	460.689288	903.344750	452.176013	902.360734	451.684005	A	***1467.780187***	734.393731	1450.753638	725.880457	1449.769622	725.388449	17
10	***991.408413***	496.207845	974.381864	487.694570	973.397848	487.202562	A	***1396.743073***	698.875174	1379.716524	690.361900	1378.732508	689.869892	16
11	1048.429877	**524.718577**	1031.403328	516.205302	1030.419312	515.713294	G	***1325.705959***	663.356617	1308.679410	654.843343	1307.695394	654.351335	15
12	1105.451341	553.229309	1088.424792	544.716034	1087.440776	544.224026	G	***1268.684495***	634.845886	1251.657946	626.332611	1250.673930	625.840603	14
13	1176.488455	588.747865	1159.461906	580.234591	1158.477890	579.742583	A	1211.663031	606.335154	1194.636482	597.821879	1193.652466	597.329871	13
14	1289.572519	645.289897	1272.545970	636.776623	1271.561954	636.284615	L	1140.625917	570.816597	1123.599368	562.303322	1122.615352	561.811314	12
15	1402.620198	701.813737	1385.593649	693.300462	1384.609633	692.808454	P	1027.541853	514.274565	1010.515304	505.761290	1009.531288	505.269282	11
16	1503.667877	752.337576	1486.641328	743.824302	1485.657312	743.332294	T	914.494174	457.750725	897.467625	449.237451	896.483609	448.745443	10
17	1590.699905	795.853591	1573.673356	787.340316	1572.689340	786.848308	S	813.446495	407.226886	796.419946	398.713611	795.435930	398.221603	9
18	1687.752669	844.379973	1670.726120	835.866698	1669.742104	835.374690	P	726.414467	363.710872	709.387918	355.197597			8
19	***1744.774133***	872.890704	1727.747584	864.377430	1726.763568	863.885422	G	629.361703	315.184490	612.335154	306.671215			7
20	1857.821812	**929.414544**	1840.795263	920.901270	1839.811247	920.409261	P	572.340239	286.673758	555.313690	278.160483			6
21	1928.858926	964.933101	1911.832377	956.419827	1910.848361	955.927818	A	459.292560	230.149918	442.266011	221.636643			5
22	2041.942990	1021.475133	2024.916441	1012.961858	2023.932425	1012.469850	L	***388.255446***	194.631361	371.228897	186.118087			4
23	2098.964454	**1049.985865**	2081.937905	1041.472590	2080.953889	1040.980582	G	***275.171382***	138.089329	258.144833	129.576055			3
24	2170.001568	1085.504422	2152.975019	1076.991147	2151.991003	1076.499139	A	***218.149918***	109.578597	201.123369	101.065323			2
25							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of MAECGRGGAAGGALPTSPGPALGAK
(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	2315.099808	-0.019500	MAECGRGGAAGGALPTSPGPALGAK
31.6	2315.099808	-0.019500	MAECGRGGAAGGALPTSPGPALGAK
28.1	2315.099808	-0.019500	MAECGRGGAAGGALPTSPGPALGAK

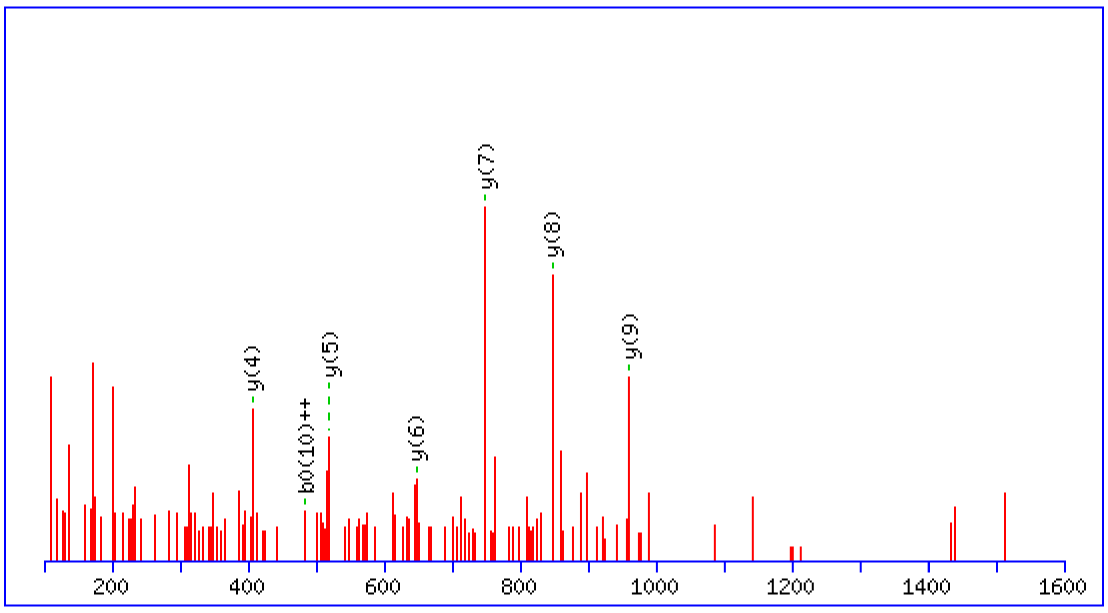
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLLVTELGSSR**
Found in **IMPA1_HUMAN**, Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1

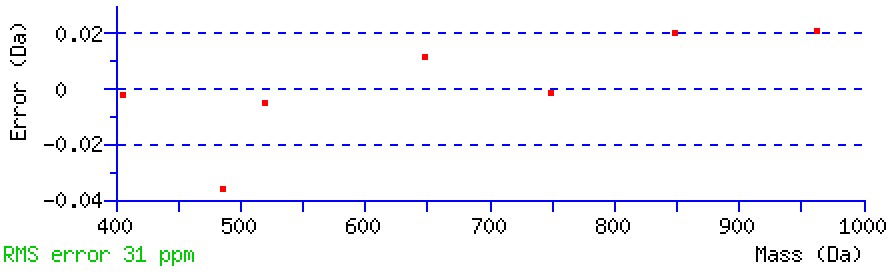
Match to Query 21150: 1160.642668 from(581.328610,2+) rtinseconds(2586) index(33601)
Title: Locus:1.1.1.2369.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

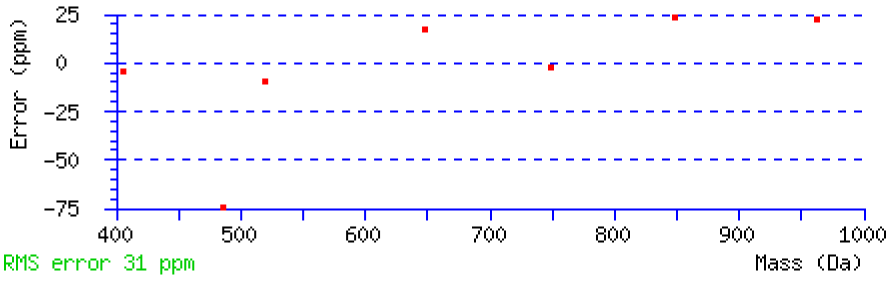
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1160.640091
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00042
Matches : 7/98 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	201.123368	101.065322	183.112803	92.060039	L	1074.615350	537.811313	1057.588801	529.298039	1056.604785	528.806031	10
3	314.207432	157.607354	296.196867	148.602071	L	***961.531286***	481.269281	944.504737	472.756007	943.520721	472.263999	9
4	413.275846	207.141561	395.265281	198.136279	V	***848.447222***	424.727249	831.420673	416.213975	830.436657	415.721967	8
5	514.323525	257.665401	496.312960	248.660118	T	***749.378808***	375.193042	732.352259	366.679768	731.368243	366.187760	7
6	643.366118	322.186697	625.355553	313.181415	E	***648.331129***	324.669203	631.304580	316.155928	630.320564	315.663920	6
7	756.450182	378.728729	738.439617	369.723447	L	***519.288536***	260.147906	502.261987	251.634632	501.277971	251.142624	5
8	813.471646	407.239461	795.461081	398.234179	G	***406.204472***	203.605874	389.177923	195.092600	388.193907	194.600592	4
9	900.503674	450.755475	882.493109	441.750193	S	349.183008	175.095142	332.156459	166.581867	331.172443	166.089859	3
10	987.535702	494.271489	969.525137	485.266207	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of SLLVTELGSSR
(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	1160.640091	0.002577	SLLVTELGSSR

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

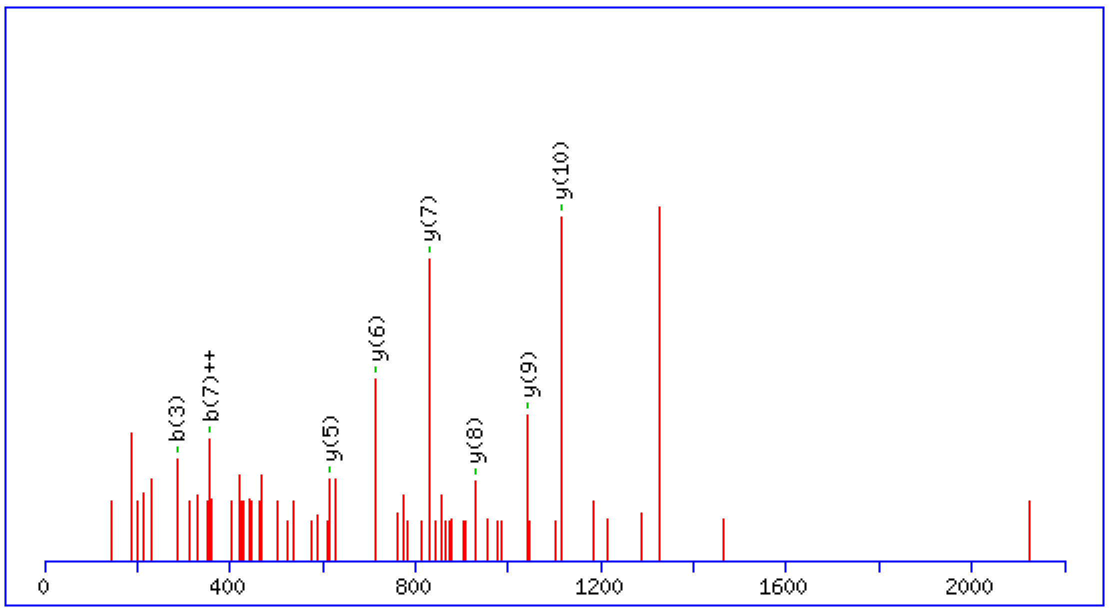
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLADVLVQEVIK**
Found in **INPP_HUMAN**, Inositol polyphosphate 1-phosphatase OS=Homo sapiens GN=INPP1 PE=1 SV=1

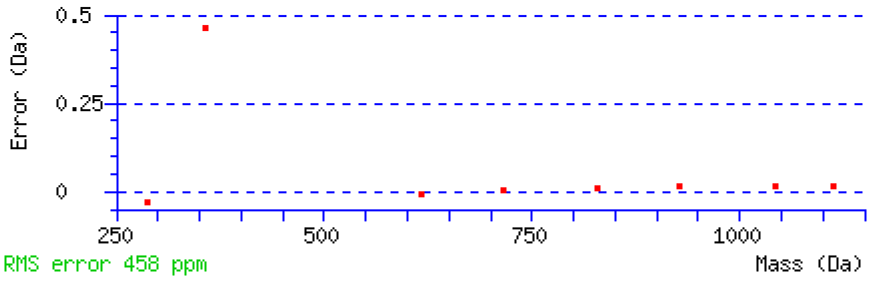
Match to Query 33446: 1326.786608 from(664.400580,2+) rtinseconds(3906) index(56045)
Title: Locus:1.1.1.2974.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

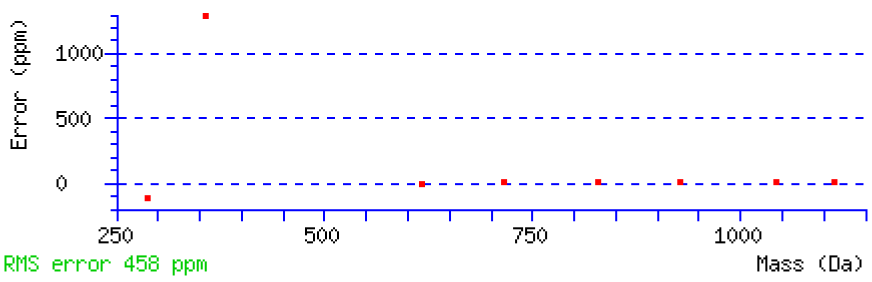
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1326.775864
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00071
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	102.054955	51.531116			84.044390	42.525833	T							12
2	215.139019	108.073147			197.128454	99.067865	L	1226.735466	613.871371	1209.708917	605.358097	1208.724901	604.866089	11
3	286.176133	143.591704			268.165568	134.586422	A	***1113.651402***	557.329339	1096.624853	548.816065	1095.640837	548.324057	10
4	401.203076	201.105176			383.192511	192.099894	D	***1042.614288***	521.810782	1025.587739	513.297508	1024.603723	512.805500	9
5	500.271490	250.639383			482.260925	241.634101	V	***927.587345***	464.297311	910.560796	455.784036	909.576780	455.292028	8
6	613.355554	307.181415			595.344989	298.176133	L	***828.518931***	414.763104	811.492382	406.249829	810.508366	405.757821	7
7	712.423968	356.715622			694.413403	347.710340	V	***715.434867***	358.221072	698.408318	349.707797	697.424302	349.215789	6
8	840.482546	420.744911	823.455997	412.231637	822.471981	411.739629	Q	***616.366453***	308.686865	599.339904	300.173590	598.355888	299.681582	5
9	969.525139	485.266208	952.498590	476.752933	951.514574	476.260925	E	488.307875	244.657575	471.281326	236.144301	470.297310	235.652293	4
10	1068.593553	534.800415	1051.567004	526.287140	1050.582988	525.795132	V	359.265282	180.136279	342.238733	171.623004			3
11	1181.677617	591.342447	1164.651068	582.829172	1163.667052	582.337164	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 TLADVLVQEVIK
(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	1326.775864	0.010744	TLADVLVQEVIK
1.3	1326.777191	0.009417	ALFRQPDLVLR

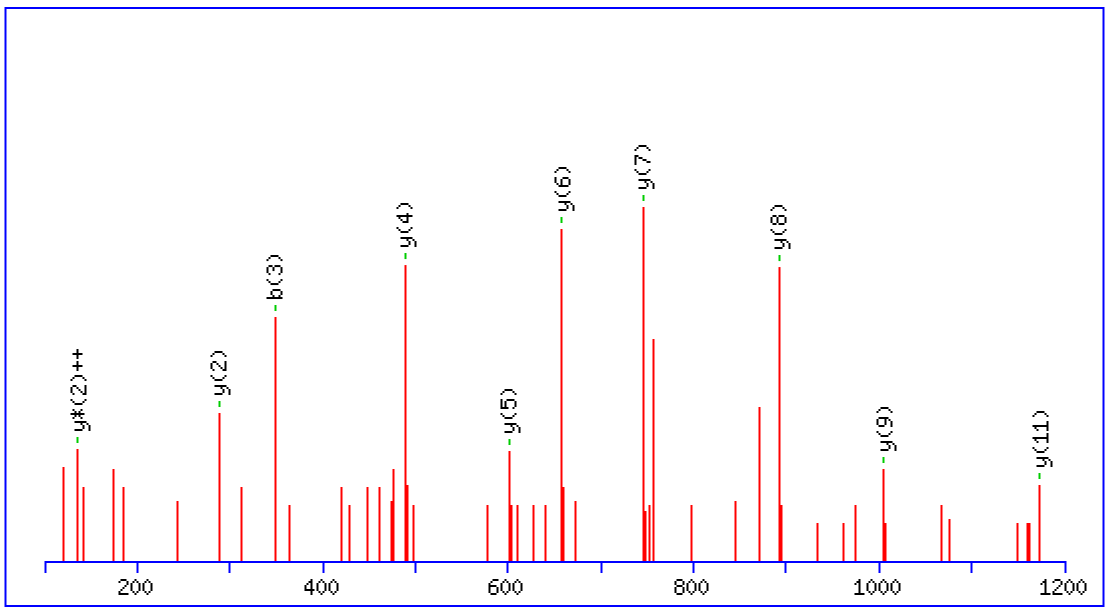
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAYLQPALFSGLAELR**
Found in **ALS_HUMAN**, Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

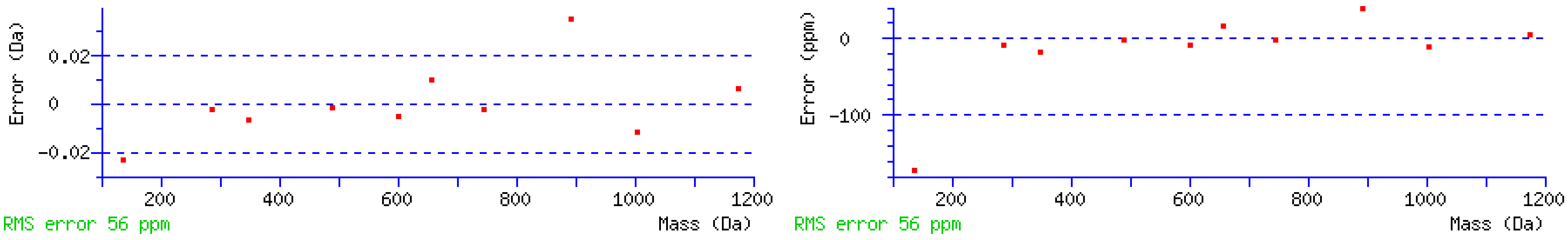
Match to Query 52335: 1760.984082 from(588.001970,3+) rtinseconds(4203) index(66436)
Title: Locus:1.1.1.2247.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

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): 1760.982468
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 4.5e-007
Matches : 10/150 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							16
2	185.128454	93.067865					A	1648.905720	824.956498	1631.879171	816.443224	1630.895155	815.951215	15
3	348.191783	174.599529					Y	1577.868606	789.437941	1560.842057	780.924666	1559.858041	780.432658	14
4	461.275847	231.141561					L	1414.805277	707.906276	1397.778728	699.393002	1396.794712	698.900994	13
5	589.334425	295.170851	572.307876	286.657576			Q	1301.721213	651.364244	1284.694664	642.850970	1283.710648	642.358962	12
6	686.387189	343.697233	669.360640	335.183958			P	***1173.662635***	587.334955	1156.636086	578.821681	1155.652070	578.329673	11
7	757.424303	379.215790	740.397754	370.702515			A	1076.609871	538.808573	1059.583322	530.295299	1058.599306	529.803291	10
8	870.508367	435.757822	853.481818	427.244547			L	***1005.572757***	503.290016	988.546208	494.776742	987.562192	494.284734	9
9	1017.576781	509.292029	1000.550232	500.778754			F	***892.488693***	446.747984	875.462144	438.234710	874.478128	437.742702	8
10	1104.608809	552.808043	1087.582260	544.294768	1086.598244	543.802760	S	***745.420279***	373.213777	728.393730	364.700503	727.409714	364.208495	7
11	1161.630273	581.318775	1144.603724	572.805500	1143.619708	572.313492	G	***658.388251***	329.697763	641.361702	321.184489	640.377686	320.692481	6
12	1274.714337	637.860806	1257.687788	629.347532	1256.703772	628.855524	L	***601.366787***	301.187031	584.340238	292.673757	583.356222	292.181749	5
13	1345.751451	673.379363	1328.724902	664.866089	1327.740886	664.374081	A	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	4
14	1474.794044	737.900660	1457.767495	729.387386	1456.783479	728.895378	E	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
15	1587.878108	794.442692	1570.851559	785.929418	1569.867543	785.437409	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 LAYLQPALFSGLAELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.9	1760.982468	0.001614	LAYLQPALFSGLAELR
2.2	1760.970627	0.013455	VTAAMVLTSLSTSPLVR

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

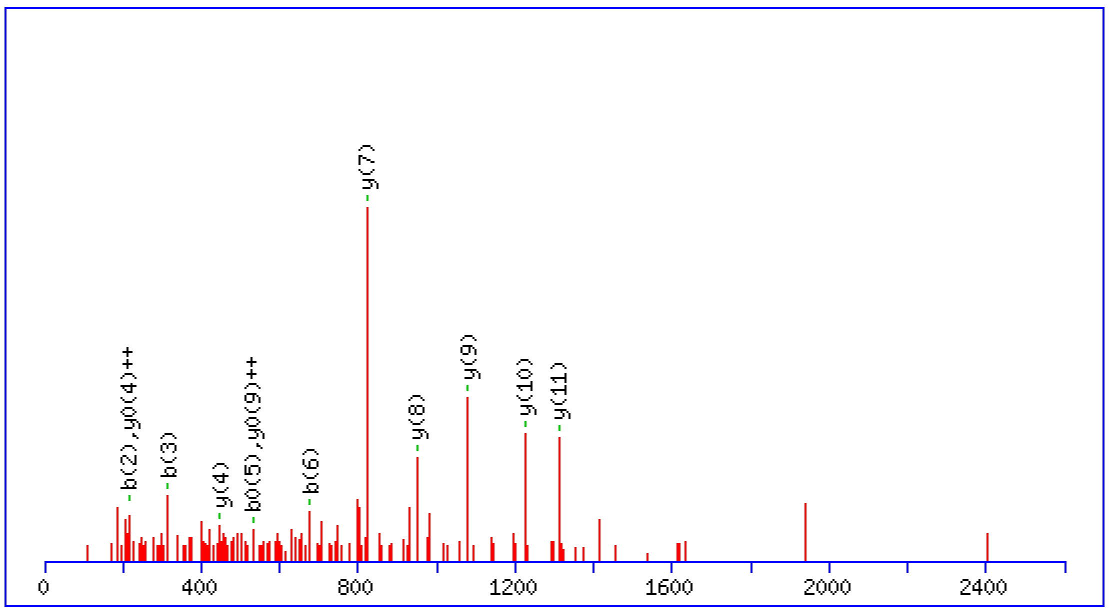
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVVSFEQPEFSVSR**
Found in **ITB4_HUMAN**, Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5

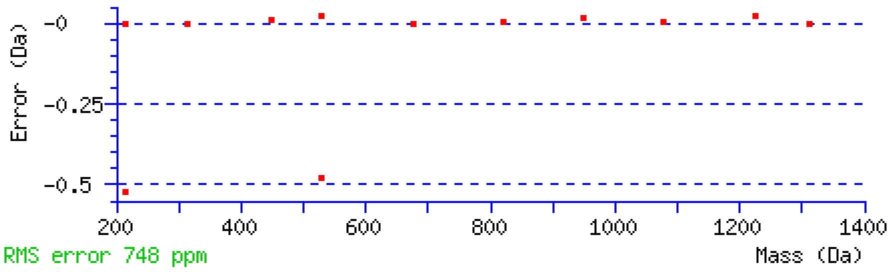
Match to Query 33869: 1624.776928 from(813.395740,2+) rtinseconds(2903) index(35988)
Title: Locus:1.1.1.2889.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

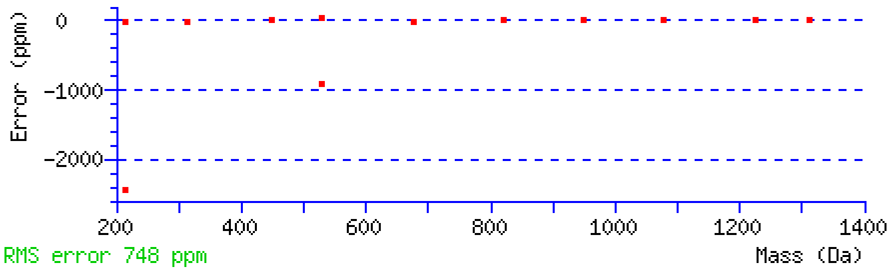
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1624.773315
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0033
Matches : 12/142 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	116.034219	58.520748			98.023654	49.515465	D							14
2	**215.102633**	108.054954			197.092068	99.049672	V	1510.753634	755.880455	1493.727085	747.367181	1492.743069	746.875173	13
3	**314.171047**	157.589161			296.160482	148.583879	V	1411.685220	706.346248	1394.658671	697.832974	1393.674655	697.340966	12
4	401.203075	201.105175			383.192510	192.099893	S	***1312.616806***	656.812041	1295.590257	648.298767	1294.606241	647.806759	11
5	548.271489	274.639383			530.260924	265.634100	F	***1225.584778***	613.296027	1208.558229	604.782753	1207.574213	604.290745	10
6	**677.314082**	339.160679			659.303517	330.155396	E	***1078.516364***	539.761820	1061.489815	531.248546	1060.505799	530.756538	9
7	805.372660	403.189968	788.346111	394.676694	787.362095	394.184686	Q	***949.473771***	475.240524	932.447222	466.727249	931.463206	466.235241	8
8	902.425424	451.716350	885.398875	443.203076	884.414859	442.711068	P	***821.415193***	411.211235	804.388644	402.697960	803.404628	402.205952	7
9	1031.468017	516.237646	1014.441468	507.724372	1013.457452	507.232364	E	724.362429	362.684853	707.335880	354.171578	706.351864	353.679570	6
10	1178.536431	589.771854	1161.509882	581.258579	1160.525866	580.766571	F	595.319836	298.163556	578.293287	289.650282	577.309271	289.158274	5
11	1265.568459	633.287868	1248.541910	624.774593	1247.557894	624.282585	S	***448.251422***	224.629349	431.224873	216.116075	430.240857	215.624067	4
12	1364.636873	682.822075	1347.610324	674.308800	1346.626308	673.816792	V	361.219394	181.113335	344.192845	172.600061	343.208829	172.108053	3
13	1451.668901	726.338089	1434.642352	717.824814	1433.658336	717.332806	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 DVVSFEQPEFSVSR
(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	1624.773315	0.003613	DVVSFEQPEFSVSR

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

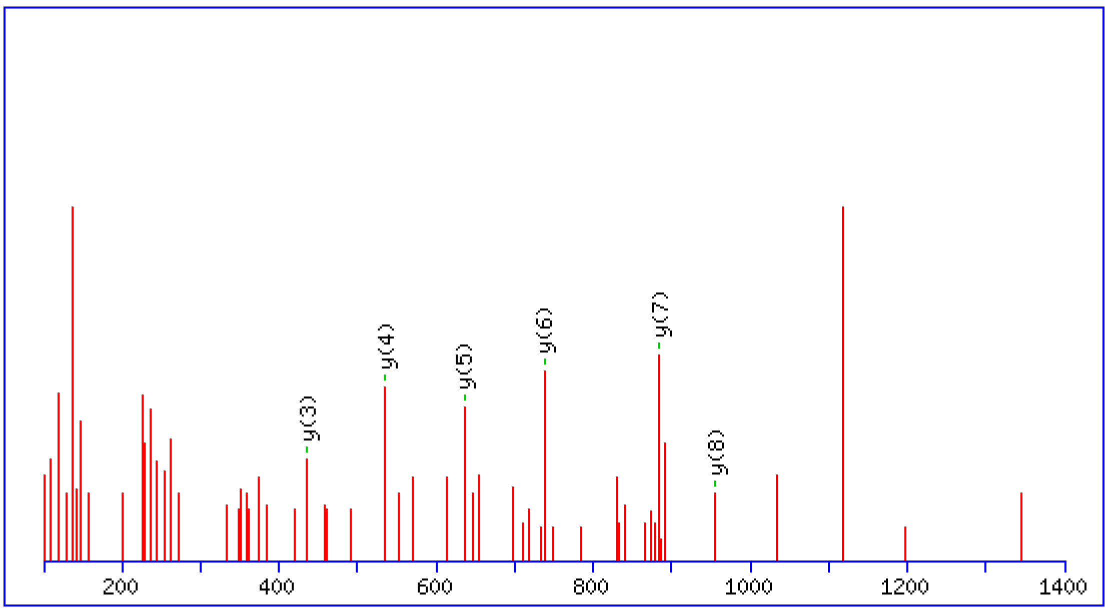
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAFTTVSCR**
Found in **ITIH5_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H5 OS=Homo sapiens GN=ITIH5 PE=2 SV=2

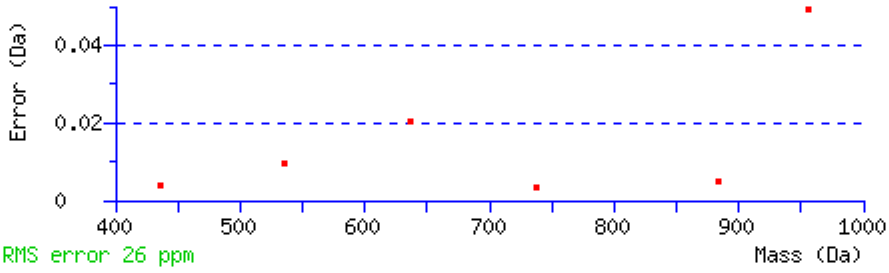
Match to Query 19171: 1117.531028 from(559.772790,2+) rtinseconds(1947) index(23655)
Title: Locus:1.1.1.1384.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

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 ●

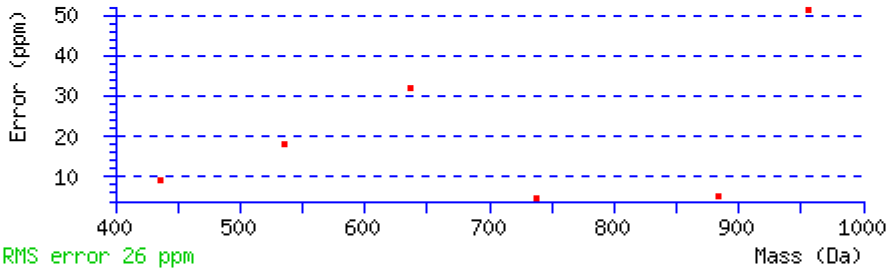


Monoisotopic mass of neutral peptide Mr(calc): 1117.522629
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0011
Matches : 6/70 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							9
2	235.107719	118.057498			A	*955.466579*	478.236927	938.440030	469.723653	937.456014	469.231645	8
3	382.176133	191.591704			F	*884.429465*	442.718370	867.402916	434.205096	866.418900	433.713088	7
4	483.223812	242.115544	465.213247	233.110262	T	*737.361051*	369.184164	720.334502	360.670889	719.350486	360.178881	6
5	584.271491	292.639384	566.260926	283.634101	T	*636.313372*	318.660324	619.286823	310.147049	618.302807	309.655041	5
6	683.339905	342.173591	665.329340	333.168308	V	*535.265693*	268.136484	518.239144	259.623210	517.255128	259.131202	4
7	770.371933	385.689605	752.361368	376.684322	S	*436.197279*	218.602277	419.170730	210.089003	418.186714	209.596995	3
8	944.418232	472.712754	926.407667	463.707472	C	349.165251	175.086263	332.138702	166.572989			2
9					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 26 ppm



RMS error 26 ppm

NCBI **BLAST** search of YAFTTVSCR
(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	1117.522629	0.008399	YAFTTVSCR

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

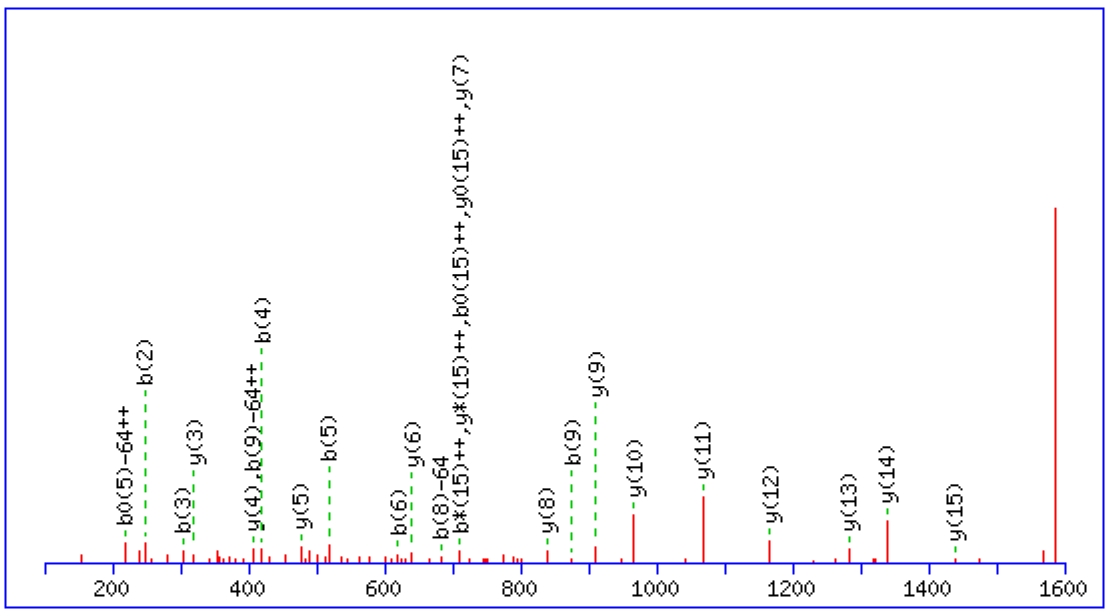
{MATRIX SCIENCE} Mascot Search Results

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

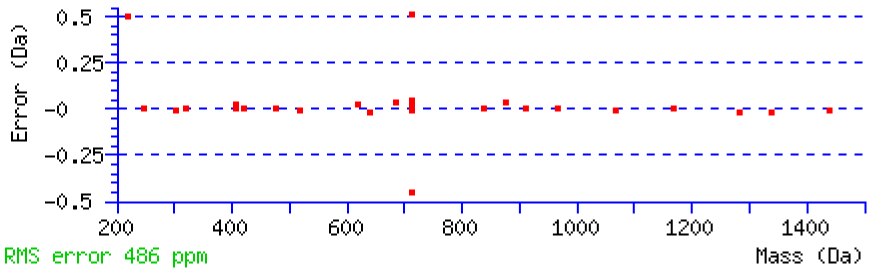
Match to Query 28020: 1584.748928 from(793.381740,2+) rtinseconds(1805) index(7184)
Title: Locus:1.1.1.2211.36
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

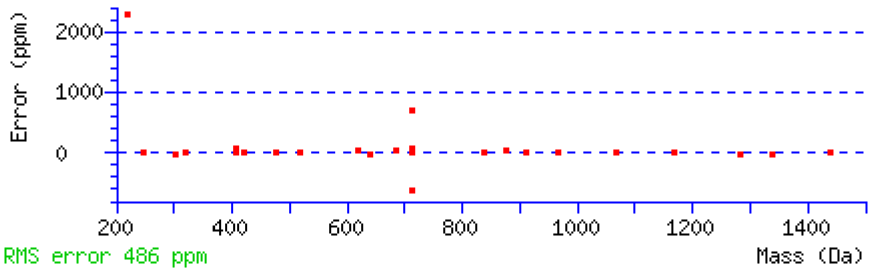
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 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: 131  Expect: 6.8e-013
Matches : 26/222 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	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
131.5	1584.745377	0.003551	MVGDVTGAQAYASTAK
10.0	1584.738846	0.010082	FVRVLCGMSSDER
0.2	1584.738861	0.010067	SMSTVIRMPDGGFR

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

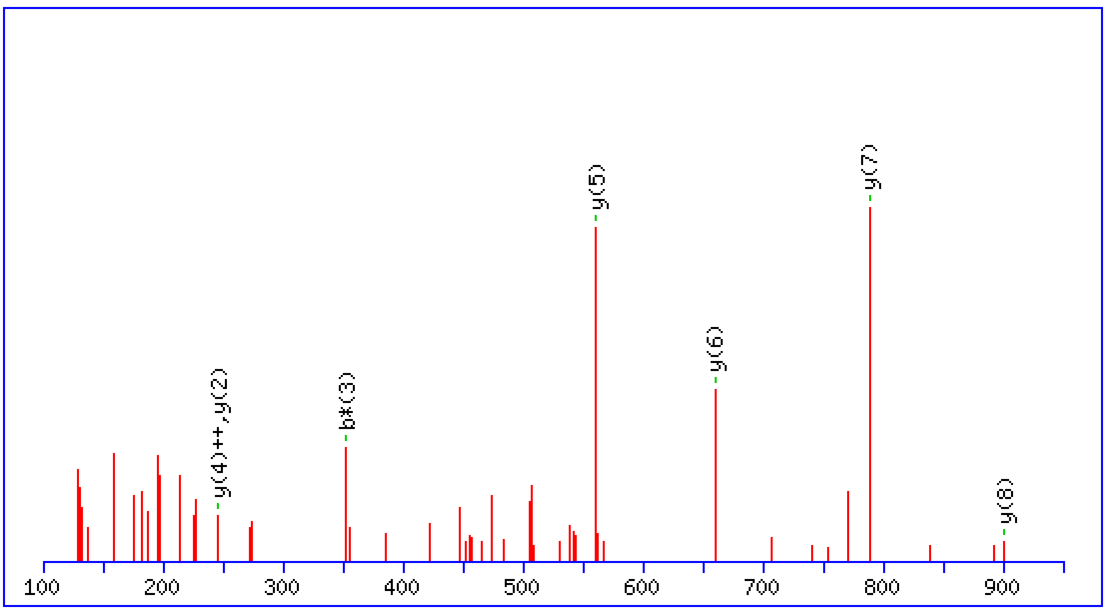
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLQVAMPVK**
Found in **IL1AP_HUMAN**, Interleukin-1 receptor accessory protein OS=Homo sapiens GN=IL1RAP PE=1 SV=2

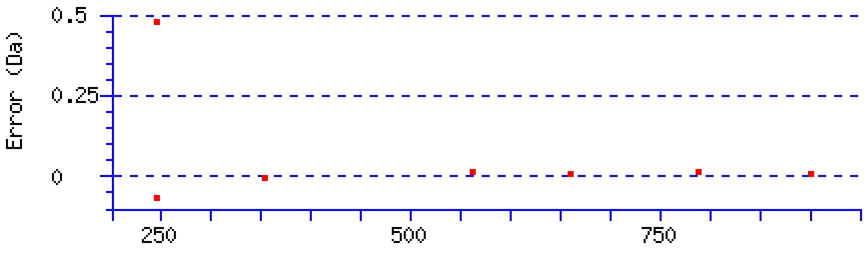
Match to Query 12805: 1028.575888 from(515.295220,2+) rtinseconds(2747) index(35035)
Title: Locus:1.1.1.2648.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

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 ●

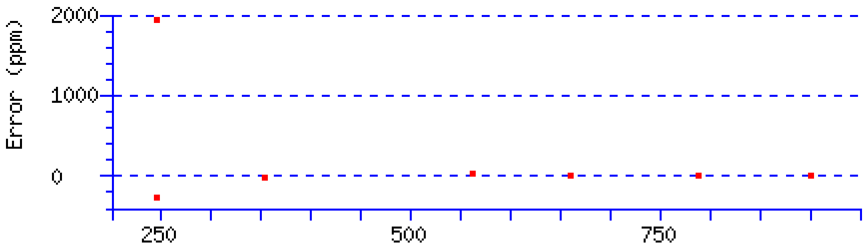


```
Monoisotopic mass of neutral peptide Mr(calc): 1028.568848
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
Ions Score: 39  Expect: 0.00093
Matches : 7/64 fragment ions using 8 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	#
1	129.065854	65.036565	112.039305	56.523291	Q					9
2	242.149918	121.578597	225.123369	113.065323	L	***901.517552***	451.262414	884.491003	442.749140	8
3	370.208496	185.607886	353.181947	177.094612	Q	***788.433488***	394.720382	771.406939	386.207108	7
4	469.276910	235.142093	452.250361	226.628819	V	***660.374910***	330.691093	643.348361	322.177819	6
5	540.314024	270.660650	523.287475	262.147376	A	***561.306496***	281.156886	544.279947	272.643612	5
6	671.354509	336.180893	654.327960	327.667618	M	490.269382	245.638329	473.242833	237.125054	4
7	784.402188	392.704732	767.375639	384.191458	P	359.228897	180.118086	342.202348	171.604812	3
8	883.470602	442.238939	866.444053	433.725665	V	***246.181218***	123.594247	229.154669	115.080972	2
9					K	147.112804	74.060040	130.086255	65.546765	1



RMS error 740 ppm



RMS error 740 ppm

NCBI **BLAST** search of QLQVAMPVK
(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	1028.568848	0.007040	QLQVAMPVK
39.4	1028.568848	0.007040	QLQVAMPVK
25.4	1028.576706	-0.000818	QIQVSWLR
6.7	1028.576691	-0.000803	KIIPWNSR
3.2	1028.568832	0.007056	QILTPMAQK
2.8	1028.572678	0.003210	QLLRTDQR

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

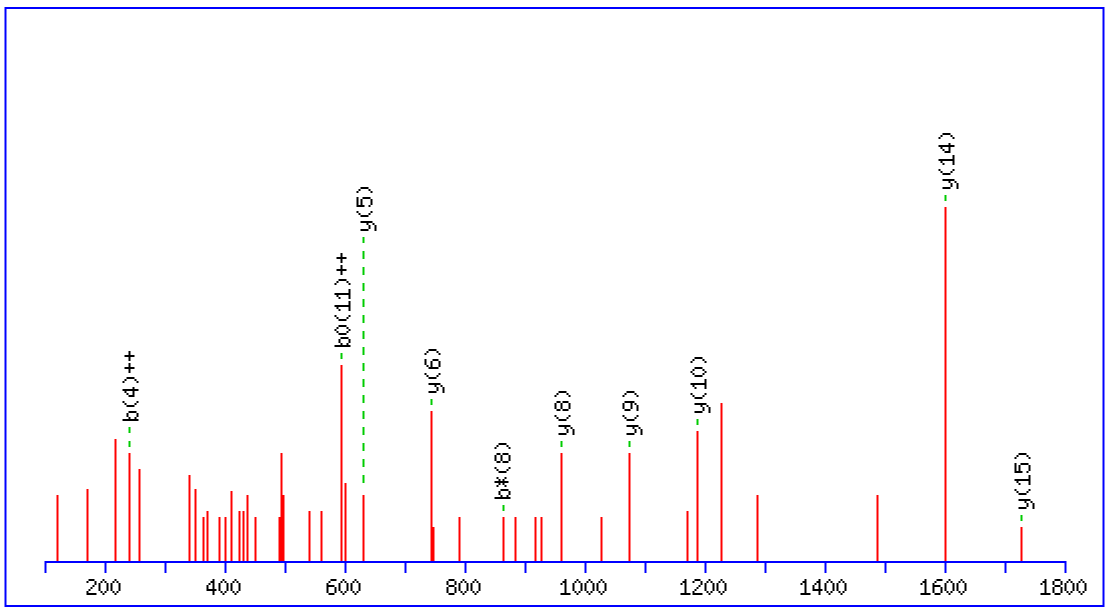
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQLEAVNITDLSENRK**
Found in **IL1RA_HUMAN**, Interleukin-1 receptor antagonist protein OS=Homo sapiens GN=IL1RN PE=1 SV=1

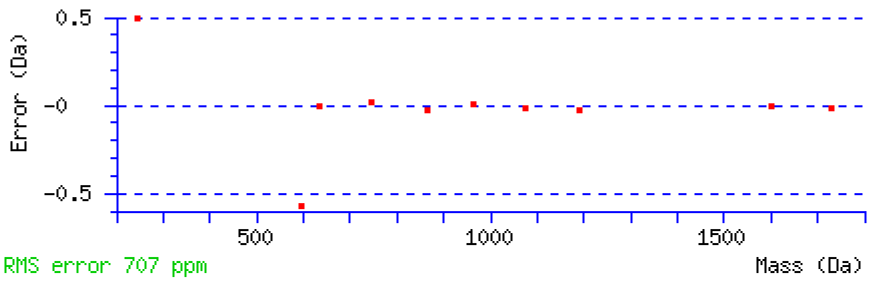
Match to Query 36633: 1841.981292 from(615.001040,3+) rtinseconds(2857) index(28324)
Title: Locus:1.1.1.2585.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

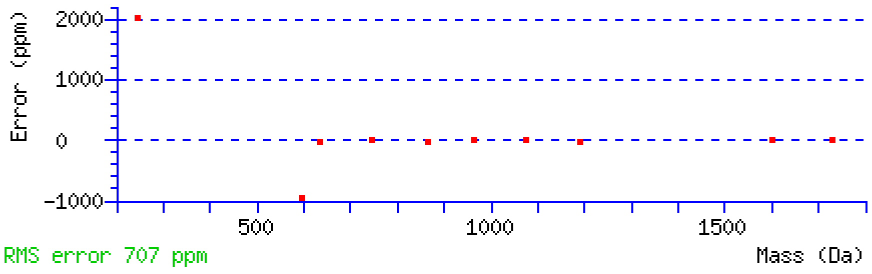
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1841.984650
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0022
Matches : 10/166 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							16
2	242.149918	121.578597	225.123369	113.065323			Q	***1729.907903***	865.457590	1712.881354	856.944315	1711.897338	856.452307	15
3	355.233982	178.120629	338.207433	169.607355			L	***1601.849325***	801.428301	1584.822776	792.915026	1583.838760	792.423018	14
4	484.276575	242.641926	467.250026	234.128651	466.266010	233.636643	E	1488.765261	744.886269	1471.738712	736.372994	1470.754696	735.880986	13
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	A	1359.722668	680.364972	1342.696119	671.851698	1341.712103	671.359690	12
6	654.382103	327.694690	637.355554	319.181415	636.371538	318.689407	V	1288.685554	644.846415	1271.659005	636.333141	1270.674989	635.841133	11
7	768.425030	384.716153	751.398481	376.202879	750.414465	375.710871	N	***1189.617140***	595.312208	1172.590591	586.798934	1171.606575	586.306926	10
8	881.509094	441.258185	864.482545	432.744911	863.498529	432.252903	I	***1075.574213***	538.290745	1058.547664	529.777470	1057.563648	529.285462	9
9	982.556773	491.782025	965.530224	483.268750	964.546208	482.776742	T	***962.490149***	481.748713	945.463600	473.235438	944.479584	472.743430	8
10	1097.583716	549.295496	1080.557167	540.782222	1079.573151	540.290214	D	861.442470	431.224873	844.415921	422.711599	843.431905	422.219591	7
11	1210.667780	605.837528	1193.641231	597.324254	1192.657215	596.832246	L	***746.415527***	373.711402	729.388978	365.198127	728.404962	364.706119	6
12	1297.699808	649.353542	1280.673259	640.840268	1279.689243	640.348260	S	***633.331463***	317.169370	616.304914	308.656095	615.320898	308.164087	5
13	1426.742401	713.874839	1409.715852	705.361564	1408.731836	704.869556	E	546.299435	273.653356	529.272886	265.140081	528.288870	264.648073	4
14	1540.785328	770.896302	1523.758779	762.383028	1522.774763	761.891020	N	417.256842	209.132059	400.230293	200.618784			3
15	1696.886439	848.946858	1679.859890	840.433583	1678.875874	839.941575	R	303.213915	152.110595	286.187366	143.597321			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LQLEAVNITDLSENRK
(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	1841.984650	-0.003358	LQLEAVNITDLSENRK

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

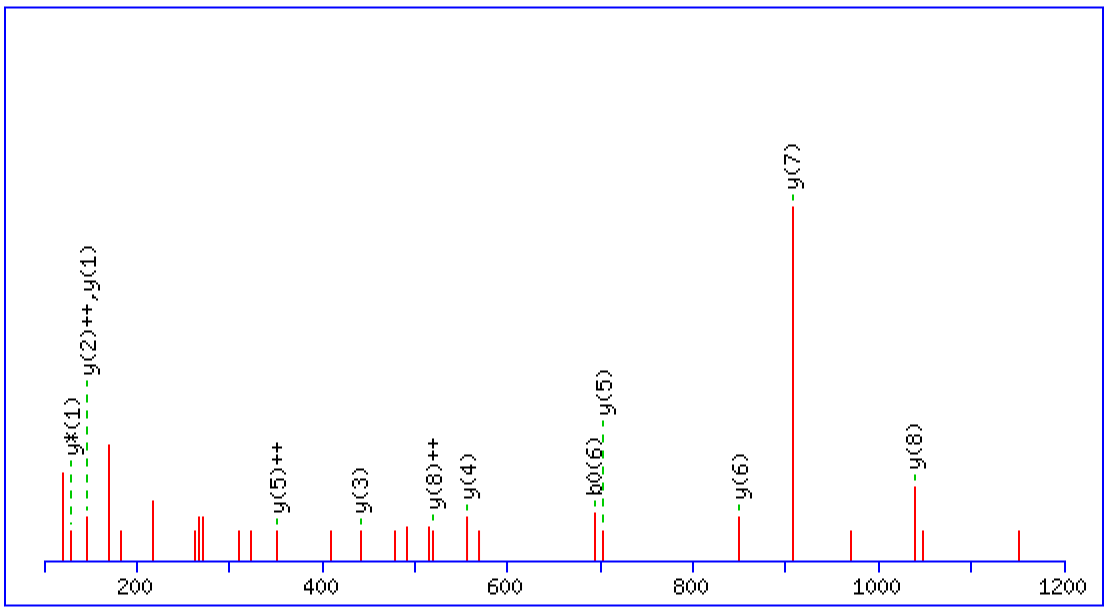
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LMGFFDFFK**
Found in **KDEL2_HUMAN**, KDEL motif-containing protein 2 OS=Homo sapiens GN=KDELC2 PE=1 SV=2

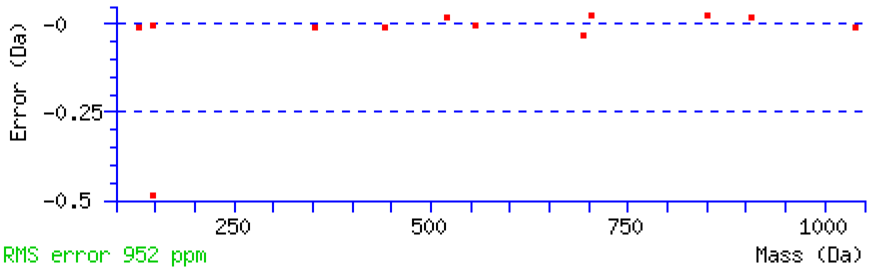
Match to Query 16646: 1150.558808 from(576.286680,2+) rtinseconds(4473) index(64860)
Title: Locus:1.1.1.3242.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

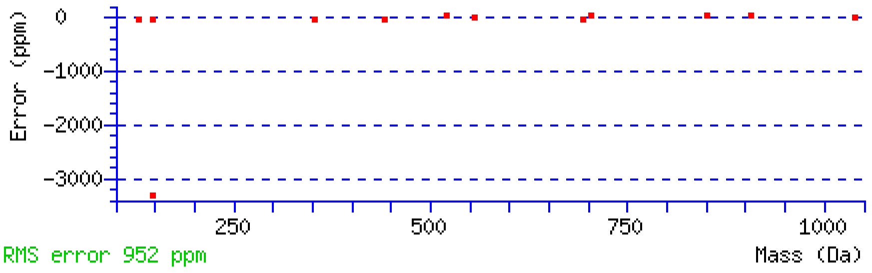
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1150.552155
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00057
Matches : 12/64 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							9
2	245.131825	123.069550			M	***1038.475352***	519.741314	1021.448803	511.228039	1020.464787	510.736031	8
3	302.153289	151.580282			G	***907.434867***	454.221071	890.408318	445.707797	889.424302	445.215789	7
4	449.221703	225.114489			F	***850.413403***	425.710339	833.386854	417.197065	832.402838	416.705057	6
5	596.290117	298.648697			F	***703.344989***	352.176132	686.318440	343.662858	685.334424	343.170850	5
6	711.317060	356.162168	693.306495	347.156885	D	***556.276575***	278.641925	539.250026	270.128651	538.266010	269.636643	4
7	858.385474	429.696375	840.374909	420.691092	F	***441.249632***	221.128454	424.223083	212.615179			3
8	1005.453888	503.230582	987.443323	494.225299	F	294.181218	147.594247	277.154669	139.080972			2
9					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LMGFFDFFK
(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	1150.552155	0.006653	LMGFFDFFK
1.7	1150.569214	-0.010406	LLQCAEPYK
0.7	1150.547455	0.011353	MLAVGAMEGTR

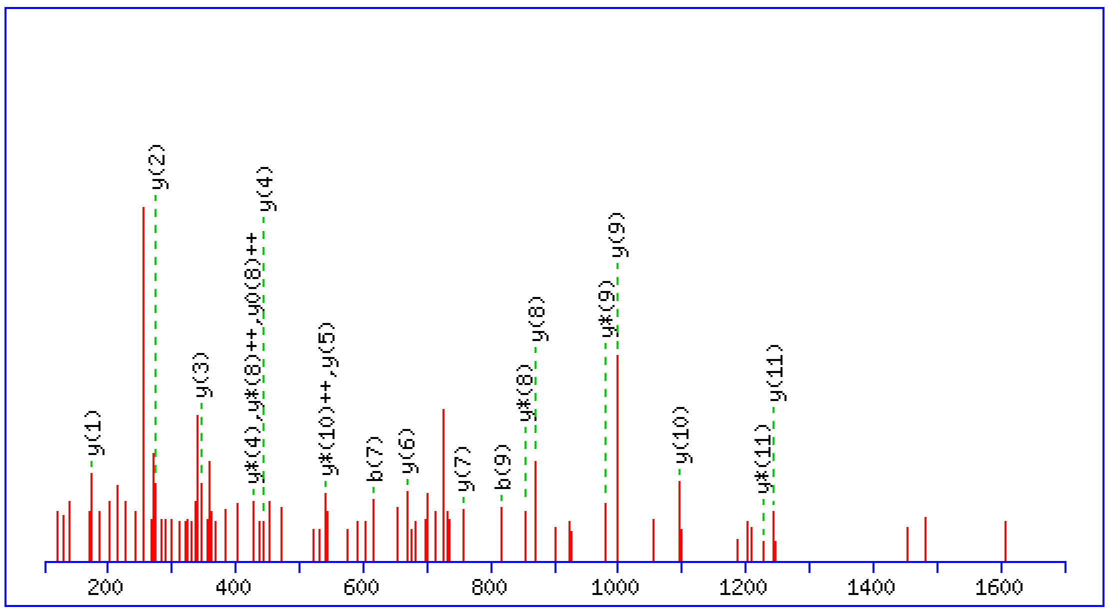
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGGAFVQNSQPVAVR**
Found in **KINH_HUMAN**, Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1

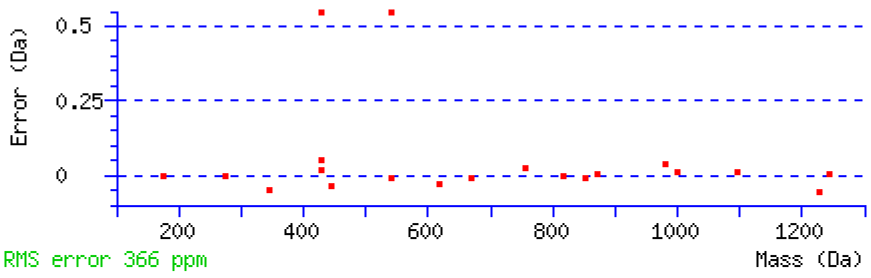
Match to Query 39127: 1485.768428 from(743.891490,2+) rtinseconds(1831) index(21424)
Title: Locus:1.1.1.1339.46
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

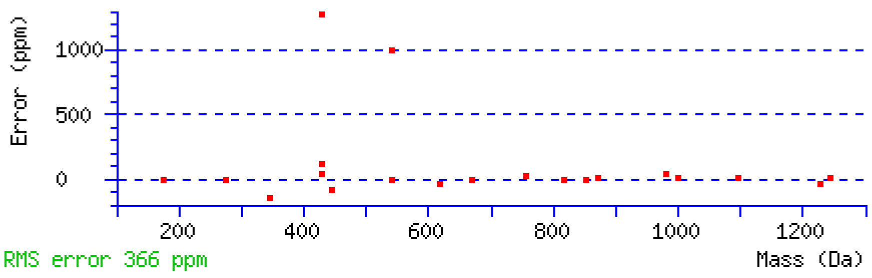
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1485.768845
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 2.6e-005
Matches : 20/128 fragment ions using 47 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	115.050204	58.028740					G	1429.754639	715.380958	1412.728090	706.867683	1411.744074	706.375675	14
3	172.071668	86.539472					G	1372.733175	686.870226	1355.706626	678.356951	1354.722610	677.864943	13
4	243.108782	122.058029					A	1315.711711	658.359494	1298.685162	649.846219	1297.701146	649.354211	12
5	390.177196	195.592236					F	***1244.674597***	622.840937	1227.648048	614.327662	1226.664032	613.835654	11
6	489.245610	245.126443					V	***1097.606183***	549.306730	1080.579634	540.793455	1079.595618	540.301447	10
7	617.304188	309.155732	600.277639	300.642458			Q	***998.537769***	499.772523	981.511220	491.259248	980.527204	490.767240	9
8	731.347115	366.177196	714.320566	357.663921			N	***870.479191***	435.743234	853.452642	427.229959	852.468626	426.737951	8
9	818.379143	409.693210	801.352594	401.179935	800.368578	400.687927	S	***756.436264***	378.721770	739.409715	370.208496	738.425699	369.716488	7
10	946.437721	473.722499	929.411172	465.209224	928.427156	464.717216	Q	***669.404236***	335.205756	652.377687	326.692482			6
11	1043.490485	522.248881	1026.463936	513.735606	1025.479920	513.243598	P	***541.345658***	271.176467	524.319109	262.663193			5
12	1142.558899	571.783088	1125.532350	563.269813	1124.548334	562.777805	V	***444.292894***	222.650085	427.266345	214.136811			4
13	1213.596013	607.301645	1196.569464	598.788370	1195.585448	598.296362	A	***345.224480***	173.115878	328.197931	164.602603			3
14	1312.664427	656.835852	1295.637878	648.322577	1294.653862	647.830569	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 GGGAFVQNSQPVAVR
(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	1485.768845	-0.000417	GGGAFVQNSQPVAVR
1.4	1485.776199	-0.007771	NLLPYLGPHKMR

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

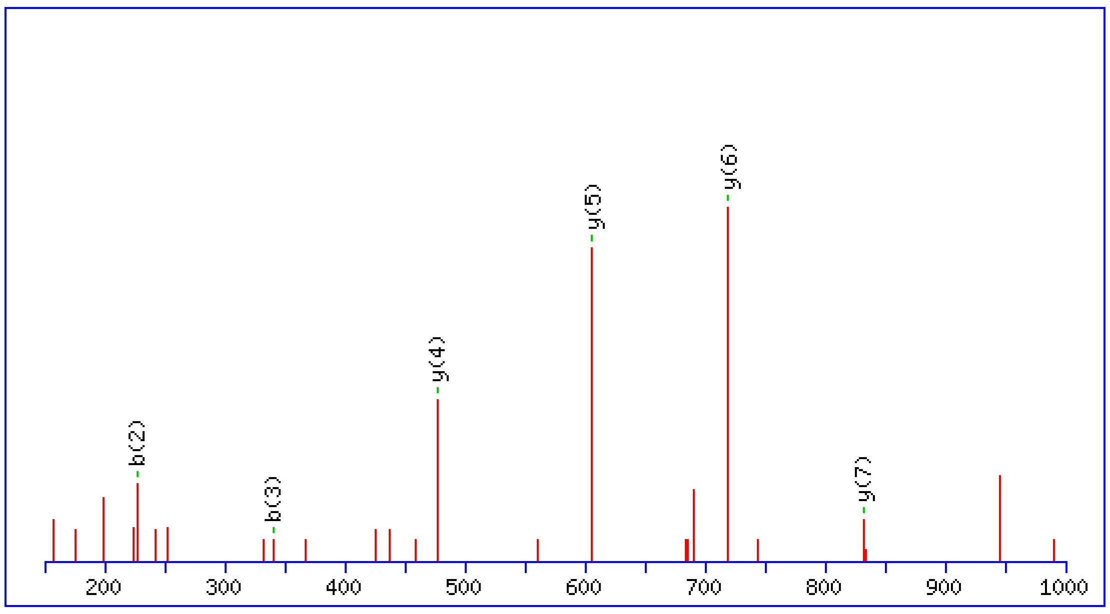
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LILENTSR**
Found in **KIF25_HUMAN**, Kinesin-like protein KIF25 OS=Homo sapiens GN=KIF25 PE=2 SV=2

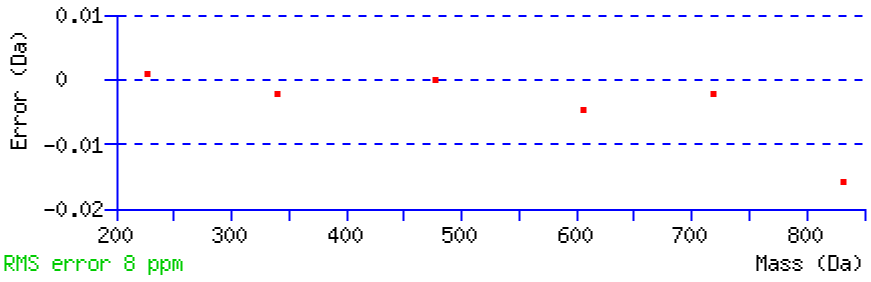
Match to Query 8666: 944.530408 from(473.272480,2+) rtinseconds(1736) index(14316)
Title: Locus:1.1.1.2160.16
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

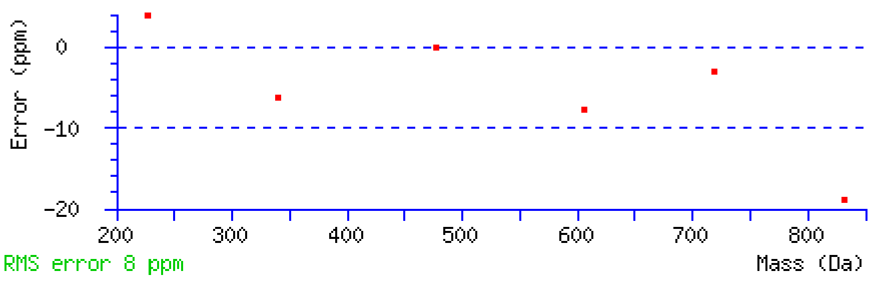
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 944.529068
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0033
Matches : 6/68 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							8
2	**227.175404**	114.091340					I	*832.452307*	416.729792	815.425758	408.216517	814.441742	407.724509	7
3	**340.259468**	170.633372					L	*719.368243*	360.187760	702.341694	351.674485	701.357678	351.182477	6
4	469.302061	235.154668			451.291496	226.149386	E	*606.284179*	303.645728	589.257630	295.132453	588.273614	294.640445	5
5	583.344988	292.176132	566.318439	283.662858	565.334423	283.170850	N	*477.241586*	239.124431	460.215037	230.611157	459.231021	230.119149	4
6	684.392667	342.699972	667.366118	334.186697	666.382102	333.694689	T	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
7	771.424695	386.215986	754.398146	377.702711	753.414130	377.210703	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 LILENTSR
(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	944.529068	0.001340	LILENTSR
20.5	944.536453	-0.006045	LLLMQEAK
12.4	944.529068	0.001340	ILASIEGSR
8.7	944.529068	0.001340	IPSEKLSR
3.3	944.529068	0.001340	LLTAERDK
2.5	944.533112	-0.002704	LLVNFDPK
1.9	944.529083	0.001325	ILTDSIQR
1.9	944.536453	-0.006045	LLAMLEQK
1.9	944.529068	0.001340	LLDEATKR
1.9	944.522537	0.007871	LLKCQNR

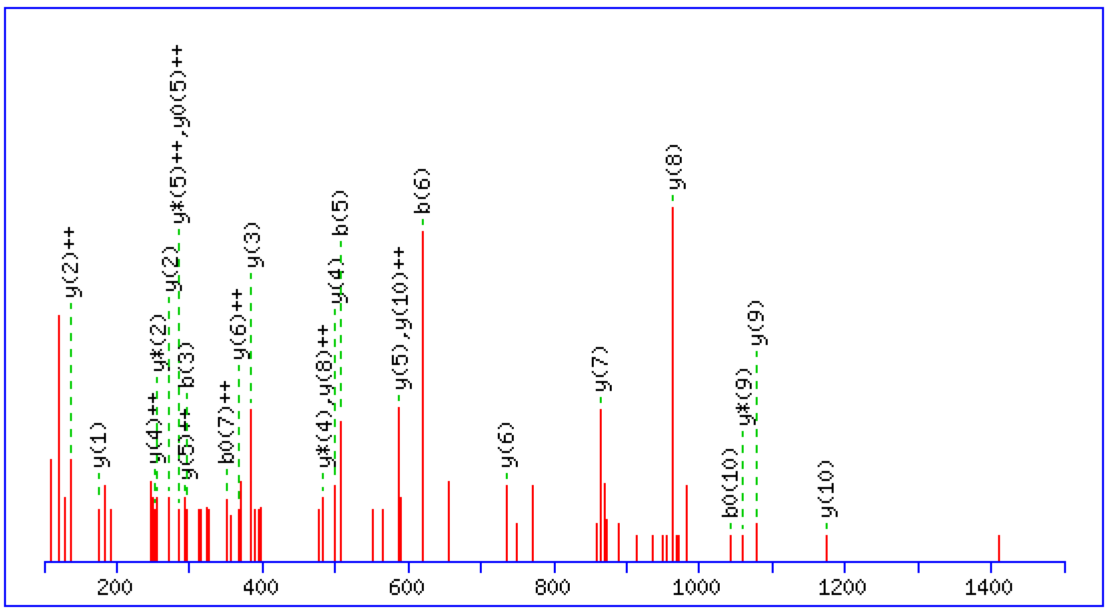
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HASPILPITEFSDIPR**
Found in **LAP2B_HUMAN**, Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2

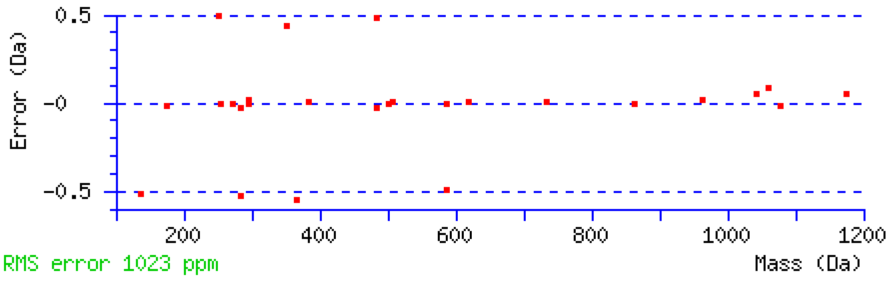
Match to Query 51996: 1791.950892 from(598.324240,3+) rtinseconds(3303) index(44914)
Title: Locus:1.1.1.2747.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

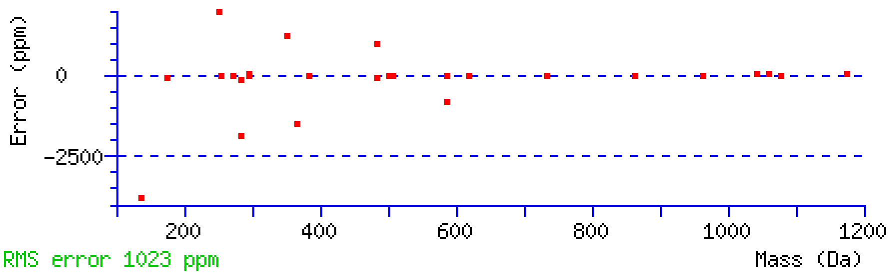
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1791.951920
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00034
Matches : 26/140 fragment ions using 57 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							16
2	209.103302	105.055289			A	1655.900299	828.453788	1638.873750	819.940513	1637.889734	819.448505	15
3	**296.135330**	148.571303	278.124765	139.566021	S	1584.863185	792.935231	1567.836636	784.421956	1566.852620	783.929948	14
4	393.188094	197.097685	375.177529	188.092403	P	1497.831157	749.419217	1480.804608	740.905942	1479.820592	740.413934	13
5	**506.272158**	253.639717	488.261593	244.634435	I	1400.778393	700.892835	1383.751844	692.379560	1382.767828	691.887552	12
6	**619.356222**	310.181749	601.345657	301.176467	L	1287.694329	644.350803	1270.667780	635.837528	1269.683764	635.345520	11
7	716.408986	358.708131	698.398421	349.702849	P	***1174.610265***	587.808771	1157.583716	579.295496	1156.599700	578.803488	10
8	829.493050	415.250163	811.482485	406.244881	I	***1077.557501***	539.282389	1060.530952	530.769114	1059.546936	530.277106	9
9	930.540729	465.774003	912.530164	456.768720	T	***964.473437***	482.740357	947.446888	474.227082	946.462872	473.735074	8
10	1059.583322	530.295299	1041.572757	521.290017	E	***863.425758***	432.216517	846.399209	423.703243	845.415193	423.211235	7
11	1206.651736	603.829506	1188.641171	594.824224	F	***734.383165***	367.695221	717.356616	359.181946	716.372600	358.689938	6
12	1293.683764	647.345520	1275.673199	638.340238	S	***587.314751***	294.161014	570.288202	285.647739	569.304186	285.155731	5
13	1408.710707	704.858992	1390.700142	695.853709	D	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4
14	1521.794771	761.401024	1503.784206	752.395741	I	***385.255780***	193.131528	368.229231	184.618253			3
15	1618.847535	809.927406	1600.836970	800.922123	P	***272.171716***	136.589496	255.145167	128.076221			2
16					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HASPILPITEFSDIPR
(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	1791.951920	-0.001028	HASPILPITEFSDIPR

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

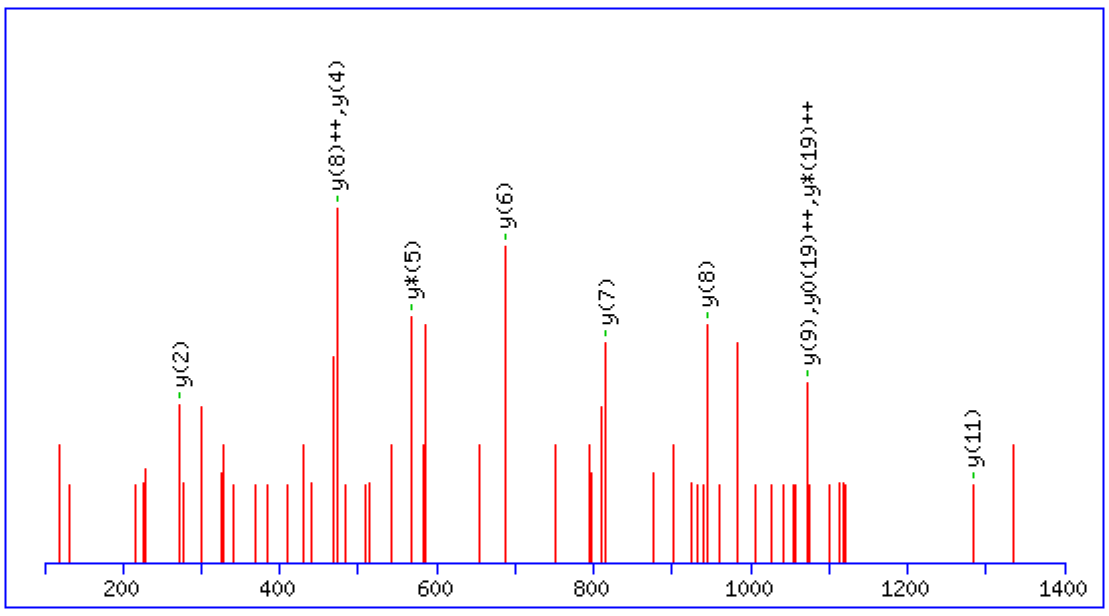
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLQGLQLDLPLEEETLSLPR**
Found in **LAMB3_HUMAN**, Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1

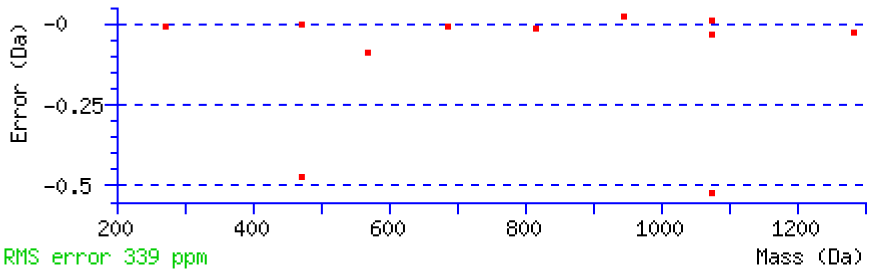
Match to Query 55172: 2264.240682 from(755.754170,3+) rtinseconds(4083) index(52106)
Title: Locus:1.1.1.3488.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

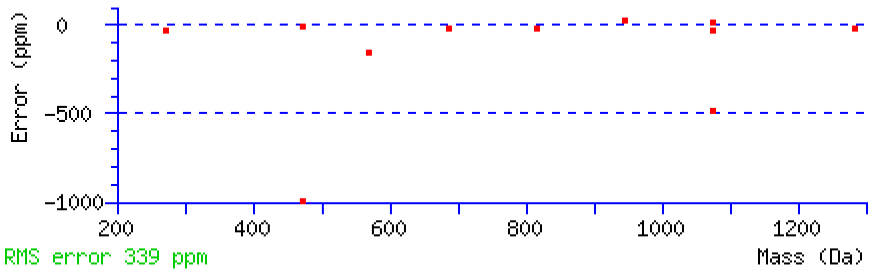
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2264.226349
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41 **Expect:** 0.00026
Matches : 11/218 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							20
2	215.139019	108.073147			197.128454	99.067865	L	2164.185977	1082.596626	2147.159428	1074.083352	2146.175412	1073.591344	19
3	343.197597	172.102437	326.171048	163.589162	325.187032	163.097154	Q	2051.101913	1026.054594	2034.075364	1017.541320	2033.091348	1017.049312	18
4	400.219061	200.613169	383.192512	192.099894	382.208496	191.607886	G	1923.043335	962.025305	1906.016786	953.512031	1905.032770	953.020023	17
5	513.303125	257.155201	496.276576	248.641926	495.292560	248.149918	L	1866.021871	933.514573	1848.995322	925.001299	1848.011306	924.509291	16
6	641.361703	321.184490	624.335154	312.671215	623.351138	312.179207	Q	1752.937807	876.972541	1735.911258	868.459267	1734.927242	867.967259	15
7	754.445767	377.726522	737.419218	369.213247	736.435202	368.721239	L	1624.879229	812.943252	1607.852680	804.429978	1606.868664	803.937970	14
8	869.472710	435.239993	852.446161	426.726719	851.462145	426.234711	D	1511.795165	756.401220	1494.768616	747.887946	1493.784600	747.395938	13
9	982.556774	491.782025	965.530225	483.268751	964.546209	482.776743	L	1396.768222	698.887749	1379.741673	690.374474	1378.757657	689.882466	12
10	1079.609538	540.308407	1062.582989	531.795133	1061.598973	531.303124	P	***1283.684158***	642.345717	1266.657609	633.832442	1265.673593	633.340434	11
11	1192.693602	596.850439	1175.667053	588.337164	1174.683037	587.845156	L	1186.631394	593.819335	1169.604845	585.306060	1168.620829	584.814052	10
12	1321.736195	661.371735	1304.709646	652.858461	1303.725630	652.366453	E	***1073.547330***	537.277303	1056.520781	528.764028	1055.536765	528.272020	9
13	1450.778788	725.893032	1433.752239	717.379757	1432.768223	716.887749	E	***944.504737***	472.756007	927.478188	464.242732	926.494172	463.750724	8
14	1579.821381	790.414329	1562.794832	781.901054	1561.810816	781.409046	E	***815.462144***	408.234710	798.435595	399.721435	797.451579	399.229427	7
15	1680.869060	840.938168	1663.842511	832.424894	1662.858495	831.932886	T	***686.419551***	343.713413	669.393002	335.200139	668.408986	334.708131	6
16	1793.953124	897.480200	1776.926575	888.966926	1775.942559	888.474917	L	585.371872	293.189574	568.345323	284.676299	567.361307	284.184291	5
17	1880.985152	940.996214	1863.958603	932.482940	1862.974587	931.990931	S	***472.287808***	236.647542	455.261259	228.134267	454.277243	227.642259	4
18	1994.069216	997.538246	1977.042667	989.024971	1976.058651	988.532963	L	385.255780	193.131528	368.229231	184.618253			3
19	2091.121980	1046.064628	2074.095431	1037.551353	2073.111415	1037.059345	P	***272.171716***	136.589496	255.145167	128.076221			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of TLQGLQLDLPLEEETLSLPR
(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	2264.226349	0.014333	TLQGLQLDLPLEEETLSLPR

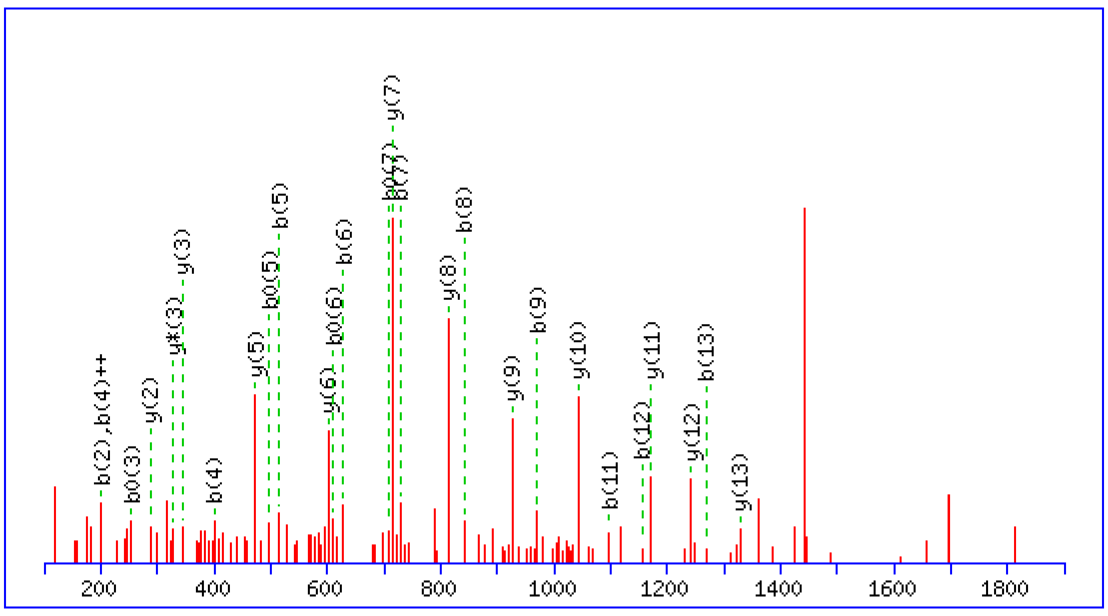
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSAEDLVLEGAGLR**
Found in **LAMC1_HUMAN**, Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3

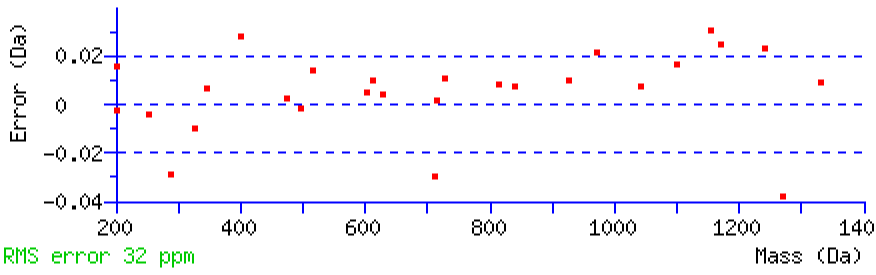
Match to Query 25756: 1441.786488 from(721.900520,2+) rtinseconds(3490) index(49998)
Title: Locus:1.1.1.2779.19
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

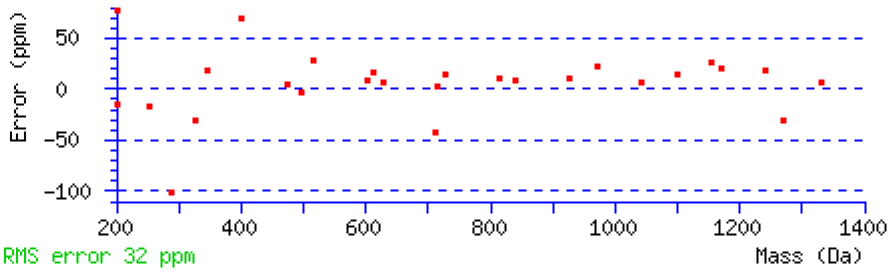
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1441.777634
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 89  Expect: 1.1e-008
Matches : 27/118 fragment ions using 39 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	***1329.700871***	665.354073	1312.674322	656.840799	1311.690306	656.348791	13
3	272.160482	136.583879	254.149917	127.578596	A	***1242.668843***	621.838059	1225.642294	613.324785	1224.658278	612.832777	12
4	**401.203075**	201.105175	383.192510	192.099893	E	***1171.631729***	586.319502	1154.605180	577.806228	1153.621164	577.314220	11
5	**516.230018**	258.618647	498.219453	249.613364	D	***1042.589136***	521.798206	1025.562587	513.284931	1024.578571	512.792923	10
6	**629.314082**	315.160679	611.303517	306.155396	L	***927.562193***	464.284734	910.535644	455.771460	909.551628	455.279452	9
7	**728.382496**	364.694886	710.371931	355.689603	V	***814.478129***	407.742702	797.451580	399.229428	796.467564	398.737420	8
8	**841.466560**	421.236918	823.455995	412.231635	L	***715.409715***	358.208495	698.383166	349.695221	697.399150	349.203213	7
9	**970.509153**	485.758215	952.498588	476.752932	E	***602.325651***	301.666463	585.299102	293.153189	584.315086	292.661181	6
10	1027.530617	514.268946	1009.520052	505.263664	G	***473.283058***	237.145167	456.256509	228.631892			5
11	**1098.567731**	549.787503	1080.557166	540.782221	A	416.261594	208.634435	399.235045	200.121160			4
12	**1155.589195**	578.298235	1137.578630	569.292953	G	***345.224480***	173.115878	328.197931	164.602603			3
13	**1268.673259**	634.840267	1250.662694	625.834985	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 LSAEDLVLEGAGLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
89.0	1441.777634	0.008854	LSAEDLVLEGAGLR
17.4	1441.788879	-0.002391	RVLGDSGELDILR
10.6	1441.792892	-0.006404	LPDIFEAQIAGLR
2.5	1441.790207	-0.003719	FQAPGARSSRPIR
1.9	1441.788864	-0.002376	TGLEKAAAGAVGLER
1.4	1441.789734	-0.003246	KLLCGLCPGALGR
1.0	1441.796249	-0.009761	MNVLNLLEEVLR
0.8	1441.777649	0.008839	LSPKSDISPLTPR
0.2	1441.779007	0.007481	TSVGVHSFSRLPR

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

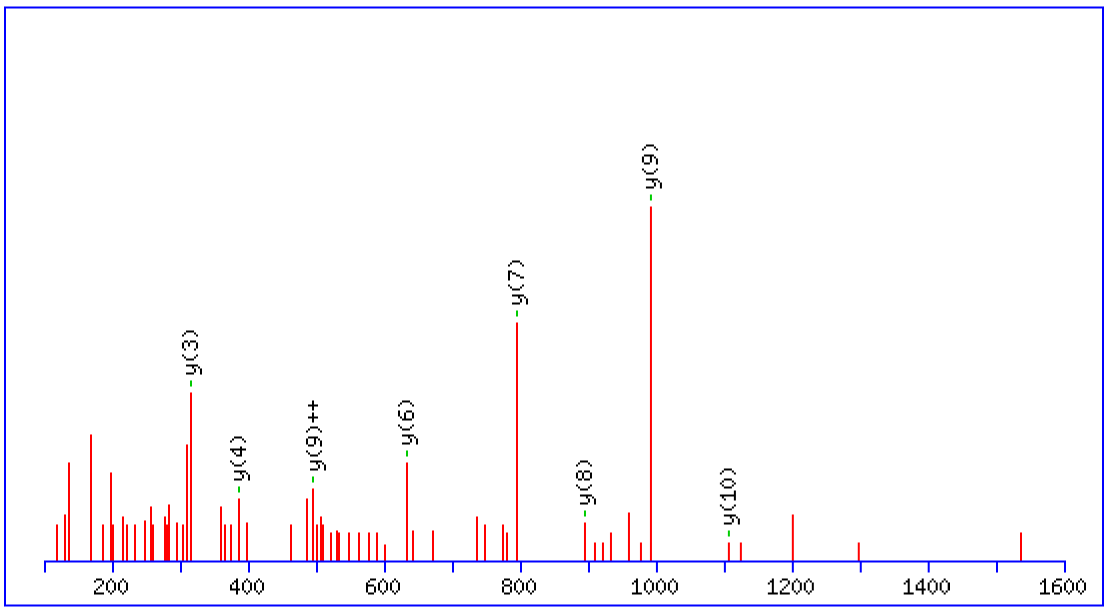
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDPVYFVAPAK**
Found in **LAMC2_HUMAN**, Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2

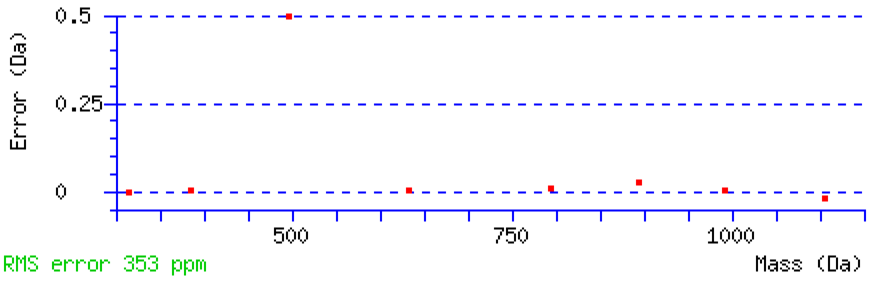
Match to Query 25431: 1218.664628 from(610.339590,2+) rtinseconds(2860) index(36504)
Title: Locus:1.1.1.2487.29
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

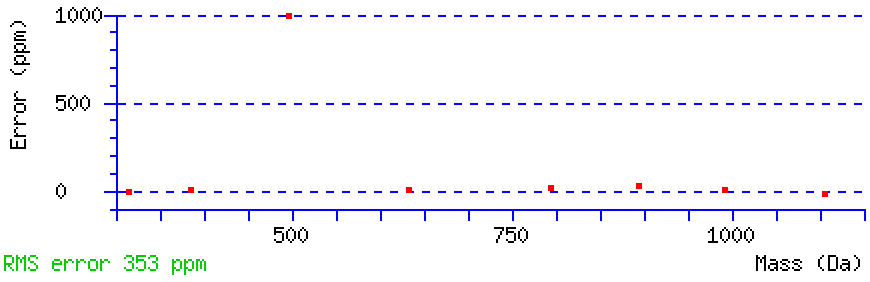
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1218.664856
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 6.1e-006
Matches : 8/80 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	229.118283	115.062779	211.107718	106.057497	D	*1106.588074*	553.797675	1089.561525	545.284401	1088.577509	544.792393	10
3	326.171047	163.589161	308.160482	154.583879	P	*991.561131*	496.284204	974.534582	487.770929			9
4	425.239461	213.123369	407.228896	204.118086	V	*894.508367*	447.757822	877.481818	439.244547			8
5	588.302790	294.655033	570.292225	285.649751	Y	*795.439953*	398.223615	778.413404	389.710340			7
6	735.371204	368.189240	717.360639	359.183958	F	*632.376624*	316.691950	615.350075	308.178676			6
7	834.439618	417.723447	816.429053	408.718165	V	485.308210	243.157743	468.281661	234.644469			5
8	905.476732	453.242004	887.466167	444.236721	A	*386.239796*	193.623536	369.213247	185.110262			4
9	1002.529496	501.768386	984.518931	492.763104	P	*315.202682*	158.104979	298.176133	149.591705			3
10	1073.566610	537.286943	1055.556045	528.281661	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 LDPVYFVAPAK
(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	1218.664856	-0.000228	LDPVYFVAPAK
3.4	1218.660812	0.003816	IKAVYDTNPAK
2.1	1218.654312	0.010316	FLPGGTLCRGK

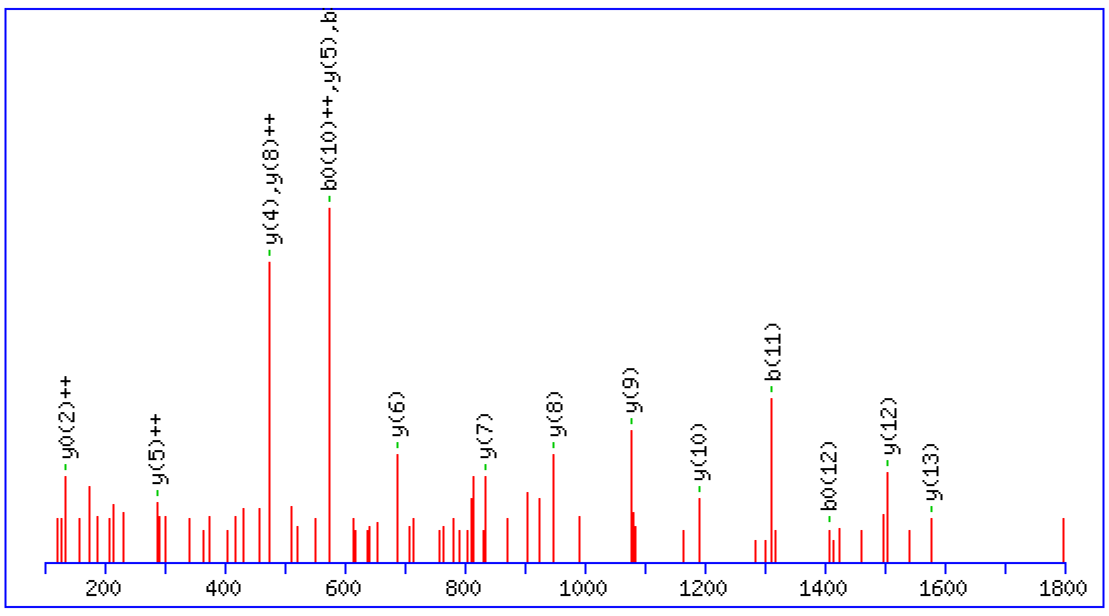
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGSYAWEIKDFLVGQDR**
Found in **MESD_HUMAN**, LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2

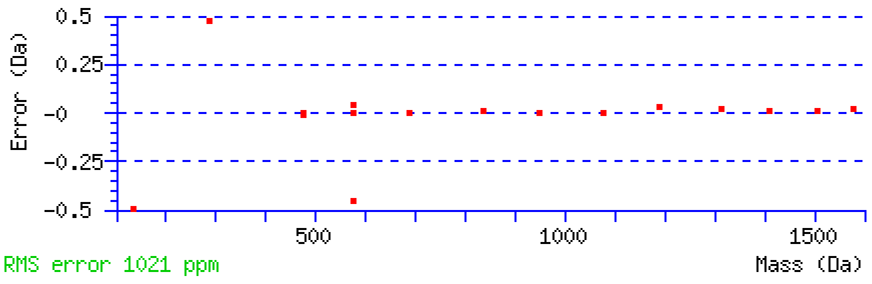
Match to Query 52138: 1997.950542 from(666.990790,3+) rtinseconds(3780) index(48207)
Title: Locus:1.1.1.3244.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

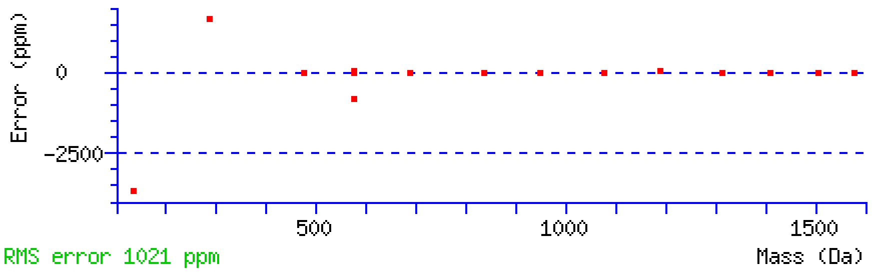
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1997.948303
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 2.4e-006
Matches : 16/174 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							17
2	173.055683	87.031479			155.045118	78.026197	G	1883.928640	942.467958	1866.902091	933.954684	1865.918075	933.462676	16
3	260.087711	130.547493			242.077146	121.542211	S	1826.907176	913.957226	1809.880627	905.443952	1808.896611	904.951944	15
4	423.151040	212.079158			405.140475	203.073875	Y	1739.875148	870.441212	1722.848599	861.927938	1721.864583	861.435930	14
5	494.188154	247.597715			476.177589	238.592433	A	***1576.811819***	788.909548	1559.785270	780.396273	1558.801254	779.904265	13
6	680.267467	340.637372			662.256902	331.632089	W	***1505.774705***	753.390991	1488.748156	744.877716	1487.764140	744.385708	12
7	809.310060	405.158668			791.299495	396.153386	E	1319.695392	660.351334	1302.668843	651.838060	1301.684827	651.346052	11
8	922.394124	461.700700			904.383559	452.695418	I	***1190.652799***	595.830038	1173.626250	587.316763	1172.642234	586.824755	10
9	1050.489087	525.748182	1033.462538	517.234907	1032.478522	516.742899	K	***1077.568735***	539.288006	1060.542186	530.774731	1059.558170	530.282723	9
10	1165.516030	583.261653	1148.489481	574.748379	1147.505465	574.256371	D	***949.473772***	475.240524	932.447223	466.727250	931.463207	466.235242	8
11	1312.584444	656.795860	1295.557895	648.282586	1294.573879	647.790578	F	***834.446829***	417.727053	817.420280	409.213778	816.436264	408.721770	7
12	1425.668508	713.337892	1408.641959	704.824618	1407.657943	704.332610	L	***687.378415***	344.192846	670.351866	335.679571	669.367850	335.187563	6
13	1524.736922	762.872099	1507.710373	754.358825	1506.726357	753.866817	V	***574.294351***	287.650814	557.267802	279.137539	556.283786	278.645531	5
14	1581.758386	791.382831	1564.731837	782.869557	1563.747821	782.377549	G	***475.225937***	238.116607	458.199388	229.603332	457.215372	229.111324	4
15	1709.816964	855.412120	1692.790415	846.898846	1691.806399	846.406838	Q	418.204473	209.605875	401.177924	201.092600	400.193908	200.600592	3
16	1824.843907	912.925592	1807.817358	904.412317	1806.833342	903.920309	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.2	1997.948303	0.002239	DGSYAWEIKDFLVGQDR
9.8	1997.948303	0.002239	AYPDVAALSDGYWVVSNR
6.5	1997.947662	0.002880	TSDGKSPTSPTSPHMPALR
6.5	1997.947662	0.002880	TSDGKSPTSPTSPHMPALR
6.5	1997.947662	0.002880	TSDGKSPTSPTSPHMPALR
5.7	1997.955551	-0.005009	GGRAAPGPPPPPPPGQAPR
5.4	1997.955551	-0.005009	GGRAAPGPPPPPPPGQAPR
5.4	1997.955551	-0.005009	GGRAAPGPPPPPPPGQAPR
0.7	1997.947647	0.002895	GEPGSKQSPPMASSPIQPR
0.7	1997.947647	0.002895	GEPGSKQSPPMASSPIQPR

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

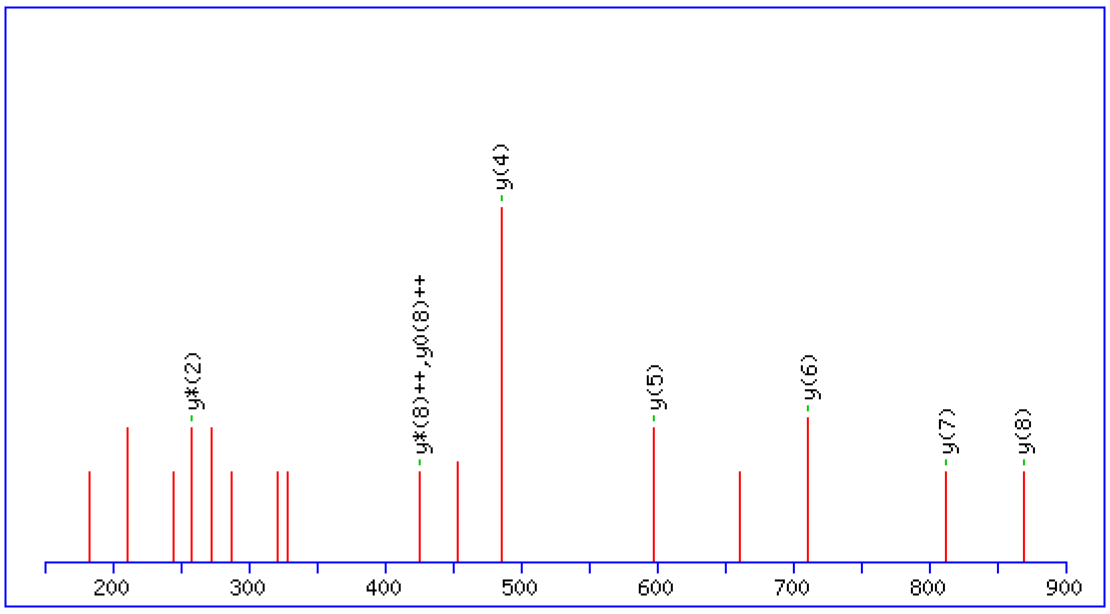
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGTLLPLQK**
Found in **LECT2_HUMAN**, Leukocyte cell-derived chemotaxin-2 OS=Homo sapiens GN=LECT2 PE=1 SV=2

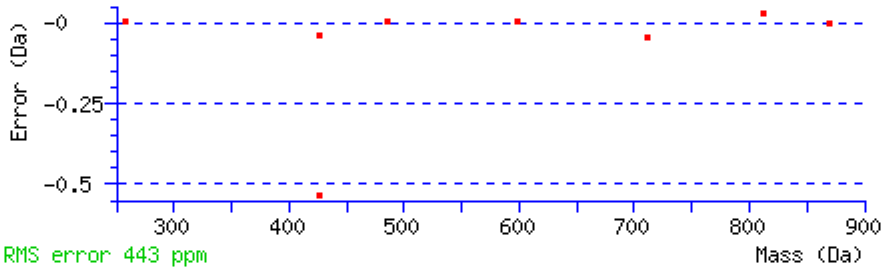
Match to Query 9686: 981.622668 from(491.818610,2+) rtinseconds(2649) index(24608)
Title: Locus:1.1.1.2506.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

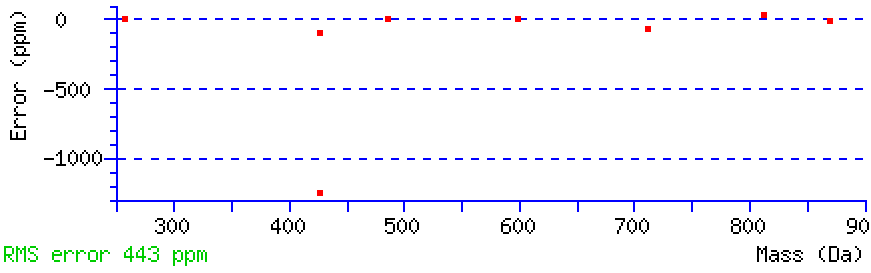
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 981.622253
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.00033
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	114.091340	57.549308					L							9
2	171.112804	86.060040					G	***869.545481***	435.276379	852.518932	426.763104	851.534916	426.271096	8
3	272.160483	136.583879			254.149918	127.578597	T	***812.524017***	406.765647	795.497468	398.252372	794.513452	397.760364	7
4	385.244547	193.125912			367.233982	184.120629	L	***711.476338***	356.241807	694.449789	347.728533			6
5	498.328611	249.667944			480.318046	240.662661	L	***598.392274***	299.699775	581.365725	291.186501			5
6	595.381375	298.194326			577.370810	289.189043	P	***485.308210***	243.157743	468.281661	234.644468			4
7	708.465439	354.736358			690.454874	345.731075	L	388.255446	194.631361	371.228897	186.118087			3
8	836.524017	418.765647	819.497468	410.252372	818.513452	409.760364	Q	275.171382	138.089329	258.144833	129.576055			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LGTLLPLQK
(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	981.622253	0.000415	LGTLLPLQK
13.1	981.615707	0.006961	KMKPLLPR

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

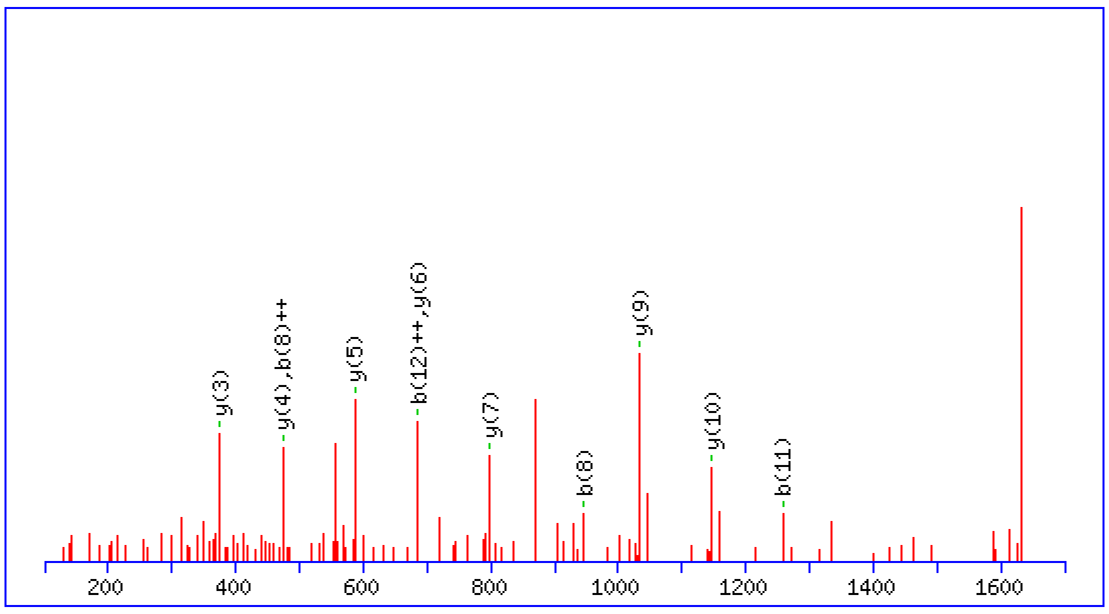
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESLRLHPPVPVISR**
Found in **CP4F2_HUMAN**, Leukotriene-B(4) omega-hydroxylase 1 OS=Homo sapiens GN=CYP4F2 PE=1 SV=1

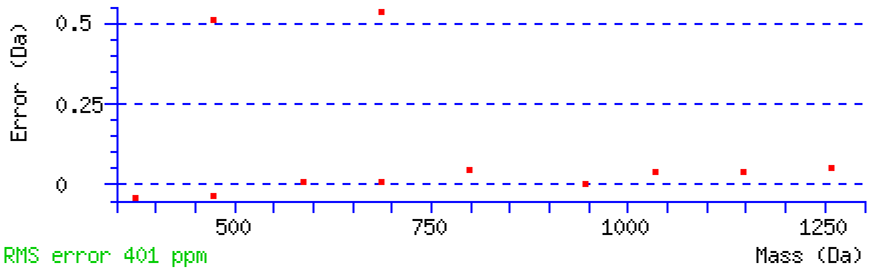
Match to Query 46119: 1630.923028 from(816.468790,2+) rtinseconds(4201) index(60733)
Title: Locus:1.1.1.3084.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

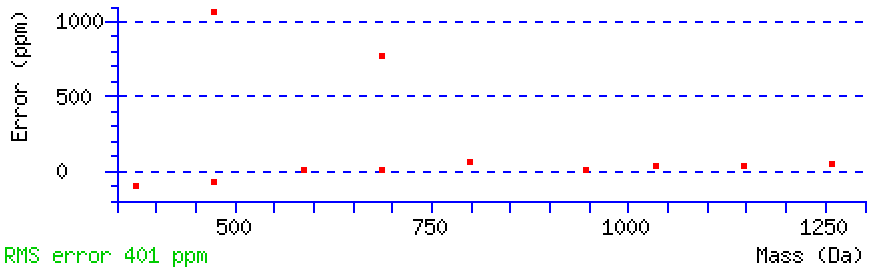
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1630.915482
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P8      : Oxidation (P)
P10     : Oxidation (P)
Ions Score: 48  Expect: 5.4e-005
Matches : 11/148 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	130.049869	65.528572			112.039304	56.523290	E							14
2	217.081897	109.044586			199.071332	100.039304	S	1502.880173	751.943725	1485.853624	743.430450	1484.869608	742.938442	13
3	330.165961	165.586618			312.155396	156.581336	L	1415.848145	708.427711	1398.821596	699.914436	1397.837580	699.422428	12
4	486.267072	243.637174	469.240523	235.123899	468.256507	234.631891	R	1302.764081	651.885679	1285.737532	643.372404	1284.753516	642.880396	11
5	599.351136	300.179206	582.324587	291.665932	581.340571	291.173924	L	***1146.662970***	573.835123	1129.636421	565.321849	1128.652405	564.829841	10
6	736.410048	368.708662	719.383499	360.195387	718.399483	359.703379	H	***1033.578906***	517.293091	1016.552357	508.779817	1015.568341	508.287809	9
7	833.462812	417.235044	816.436263	408.721769	815.452247	408.229762	P	896.519994	448.763635	879.493445	440.250361	878.509429	439.758353	8
8	**946.510491**	**473.758884**	929.483942	465.245609	928.499926	464.753601	P	***799.467230***	400.237253	782.440681	391.723979	781.456665	391.231971	7
9	1045.578905	523.293091	1028.552356	514.779816	1027.568340	514.287808	V	***686.419551***	343.713414	669.393002	335.200139	668.408986	334.708131	6
10	1158.626584	579.816930	1141.600035	571.303656	1140.616019	570.811648	P	***587.351137***	294.179207	570.324588	285.665932	569.340572	285.173924	5
11	**1257.694998**	629.351137	1240.668449	620.837863	1239.684433	620.345855	V	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
12	1370.779062	**685.893169**	1353.752513	677.379895	1352.768497	676.887887	I	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1457.811090	729.409183	1440.784541	720.895909	1439.800525	720.403901	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 ESLRLHPPVPVISR
(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	1630.915482	0.007546	ESLRLHPPVPVISR
37.9	1630.915482	0.007546	ESLRLHPPVPVISR
11.0	1630.915482	0.007546	ESLRLHPPVPVISR

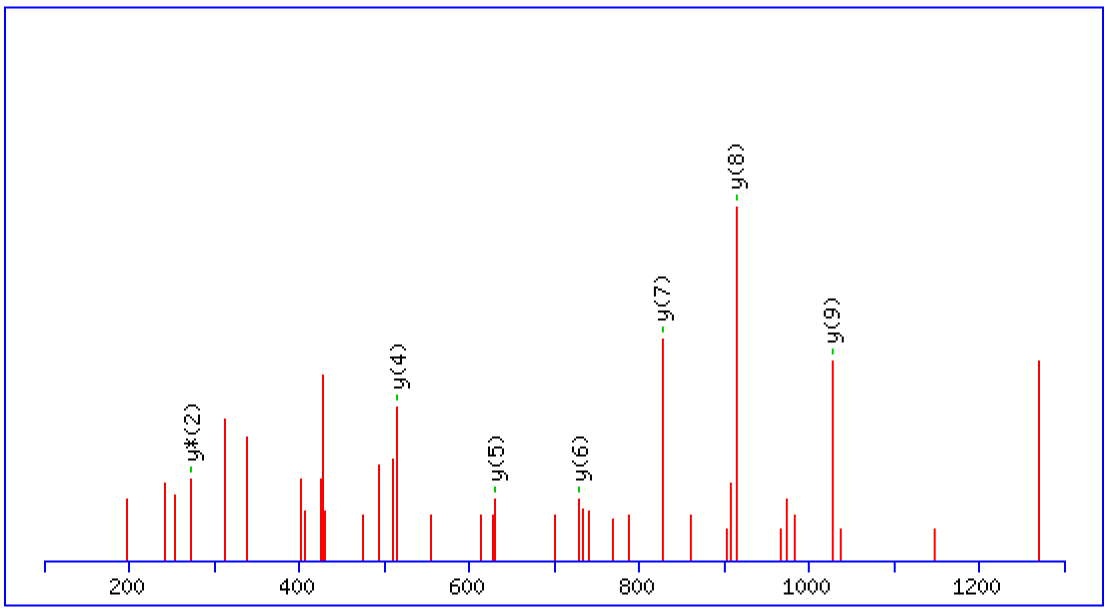
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILSPVDIIDR**
Found in **LPP3_HUMAN**, Lipid phosphate phosphohydrolase 3 OS=Homo sapiens GN=PPAP2B PE=1 SV=1

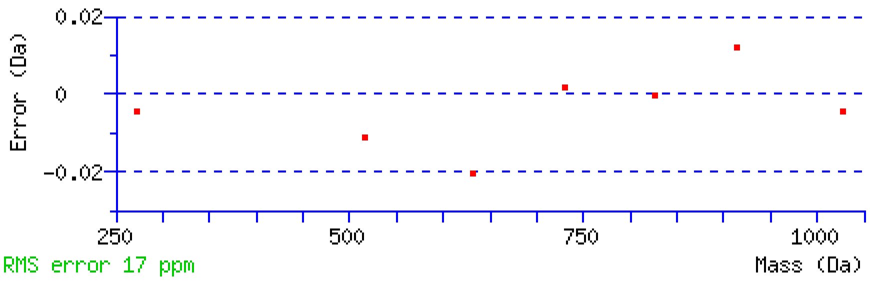
Match to Query 23352: 1268.695828 from(635.355190,2+) rtinseconds(3270) index(39469)
Title: Locus:1.1.1.2814.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

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 ●

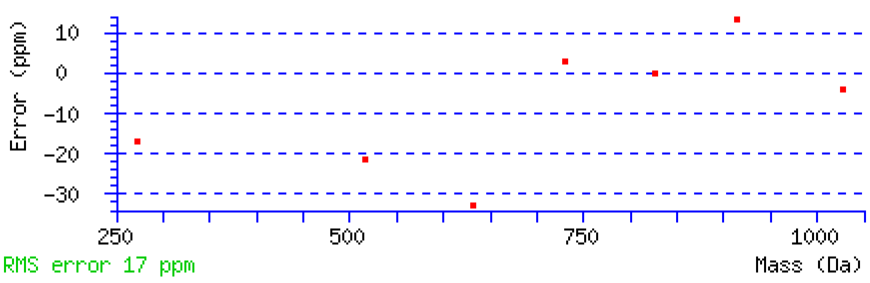


```
Monoisotopic mass of neutral peptide Mr(calc): 1268.697601
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00024
Matches : 7/98 fragment ions using 10 most intense peaks   (help)
```

#	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							11
2	243.133933	122.070605	225.123368	113.065322	I	1140.662300	570.834788	1123.635751	562.321514	1122.651735	561.829506	10
3	356.217997	178.612637	338.207432	169.607354	L	***1027.578236***	514.292756	1010.551687	505.779482	1009.567671	505.287474	9
4	443.250025	222.128650	425.239460	213.123368	S	***914.494172***	457.750724	897.467623	449.237450	896.483607	448.745442	8
5	540.302789	270.655033	522.292224	261.649750	P	***827.462144***	414.234710	810.435595	405.721436	809.451579	405.229428	7
6	639.371203	320.189240	621.360638	311.183957	V	***730.409380***	365.708328	713.382831	357.195054	712.398815	356.703046	6
7	754.398146	377.702711	736.387581	368.697429	D	***631.340966***	316.174121	614.314417	307.660847	613.330401	307.168839	5
8	867.482210	434.244743	849.471645	425.239461	I	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
9	980.566274	490.786775	962.555709	481.781493	I	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
10	1095.593217	548.300247	1077.582652	539.294964	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 17 ppm



RMS error 17 ppm

NCBI **BLAST** search of EILSPVDIIDR
(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	1268.697601	-0.001773	EILSPVDIIDR

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

MATRIX SCIENCE

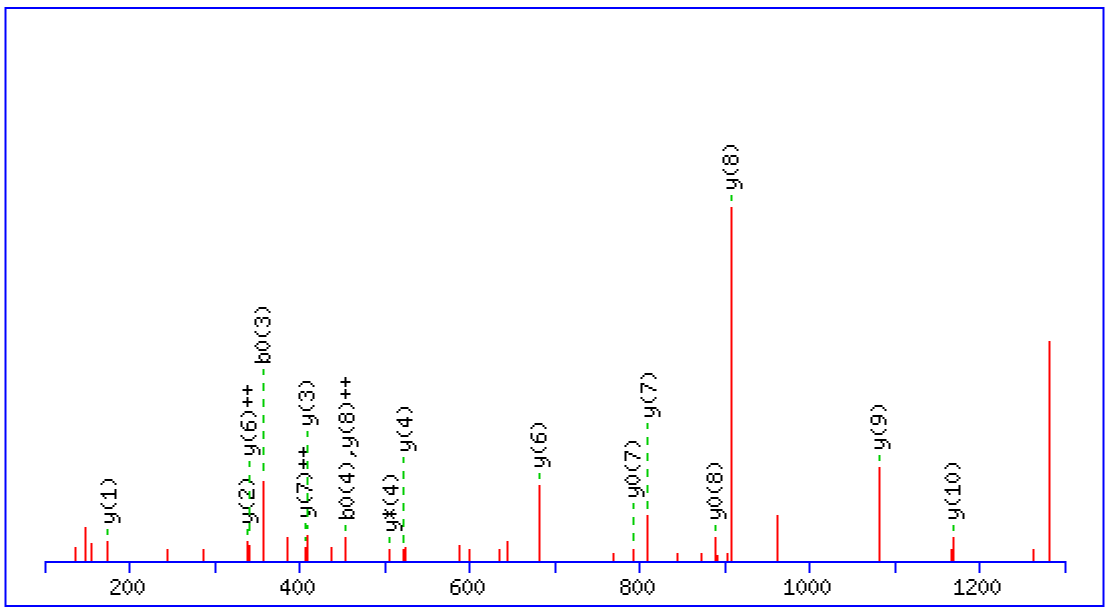
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISCPEGTNAYR**
Found in **REG1A_HUMAN**, Lithostathine-1-alpha OS=Homo sapiens GN=REG1A PE=1 SV=3

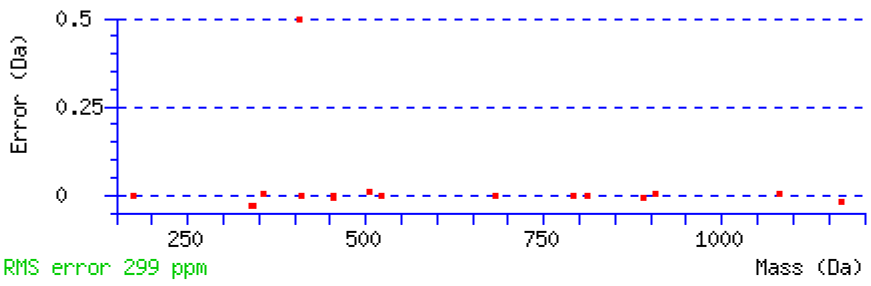
Match to Query 18626: 1280.583108 from(641.298830,2+) rtinseconds(1528) index(4382)
Title: Locus:1.1.1.2094.32
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

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 ●

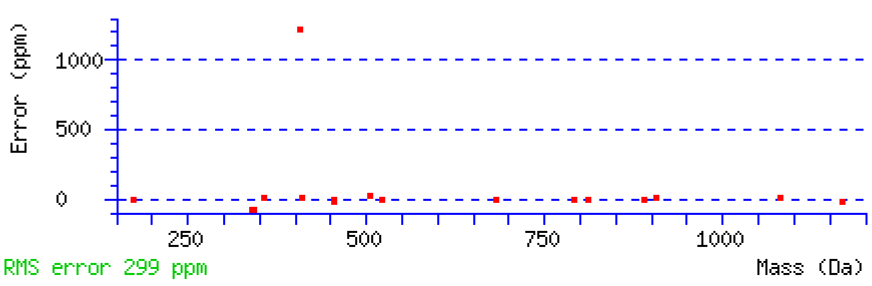


Monoisotopic mass of neutral peptide Mr(calc): 1280.581909
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 3.6e-005
Matches : 17/96 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							11
2	201.123368	101.065322			183.112803	92.060039	S	***1168.505149***	584.756213	1151.478600	576.242938	1150.494584	575.750930	10
3	375.169667	188.088471			357.159102	179.083189	C	***1081.473121***	541.240199	1064.446572	532.726924	1063.462556	532.234916	9
4	472.222431	236.614853			454.211866	227.609571	P	***907.426822***	454.217049	890.400273	445.703775	889.416257	445.211767	8
5	601.265024	301.136150			583.254459	292.130868	E	***810.374058***	405.690667	793.347509	397.177393	792.363493	396.685385	7
6	658.286488	329.646882			640.275923	320.641600	G	***681.331465***	341.169371	664.304916	332.656096	663.320900	332.164088	6
7	759.334167	380.170722			741.323602	371.165439	T	624.310001	312.658639	607.283452	304.145364	606.299436	303.653356	5
8	873.377094	437.192185	856.350545	428.678911	855.366529	428.186903	N	***523.262322***	262.134799	506.235773	253.621524			4
9	944.414208	472.710742	927.387659	464.197468	926.403643	463.705460	A	***409.219395***	205.113335	392.192846	196.600061			3
10	1107.477537	554.242407	1090.450988	545.729132	1089.466972	545.237124	Y	***338.182281***	169.594778	321.155732	161.081504			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 299 ppm



RMS error 299 ppm

NCBI **BLAST** search of ISCPEGTNAYR
(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	1280.581909	0.001199	ISCPEGTNAYR
9.8	1280.578766	0.004342	TVCAGGCARCK
6.7	1280.585938	-0.002829	MNEGFEWQLK
1.4	1280.581940	0.001168	WTSRDVGMADK
0.9	1280.591812	-0.008704	KMDETDASSAVK

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

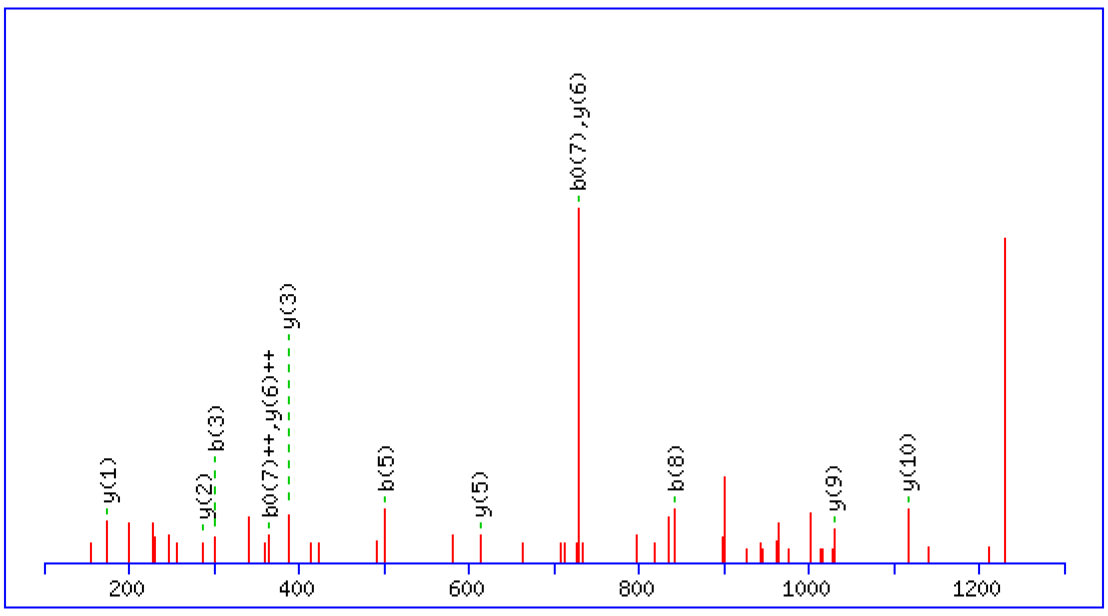
{MATRIX SCIENCE} Mascot Search Results

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

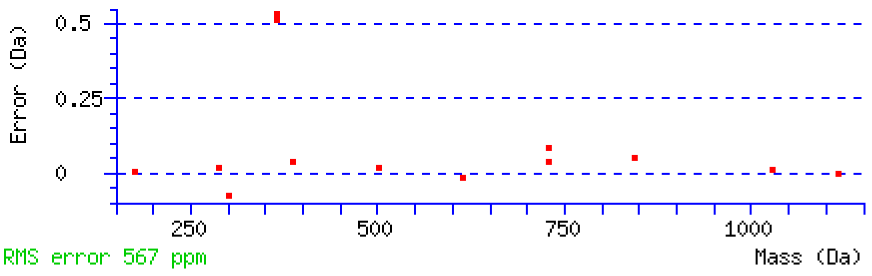
Match to Query 13616: 1228.596928 from(615.305740,2+) rtinseconds(2161) index(10696)
Title: Locus:1.1.1.2409.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

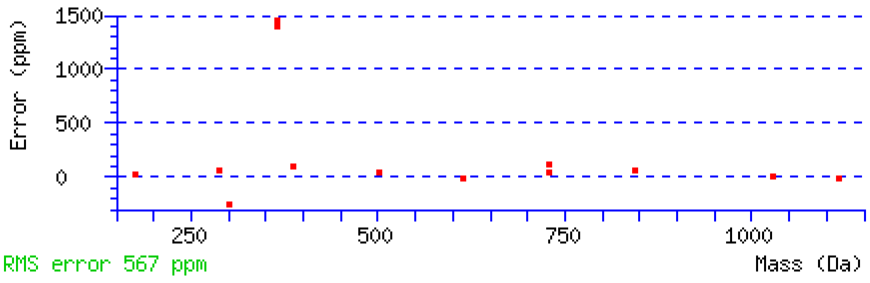
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1228.593552
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P10     : Oxidation (P)
Ions Score: 34  Expect: 0.0036
Matches : 13/90 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							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
34.3	1228.593552	0.003376	LSTSPDEPVPR
14.2	1228.593552	0.003376	LSTSPDEPVPR
9.9	1228.593552	0.003376	LSTSPDEPVPR
7.9	1228.598236	-0.001308	INVMNDRDPR
5.1	1228.591034	0.005894	ISEQFTAMFR
4.2	1228.586990	0.009938	ILASASHEMDR
0.5	1228.604752	-0.007824	LELQEAQDQR

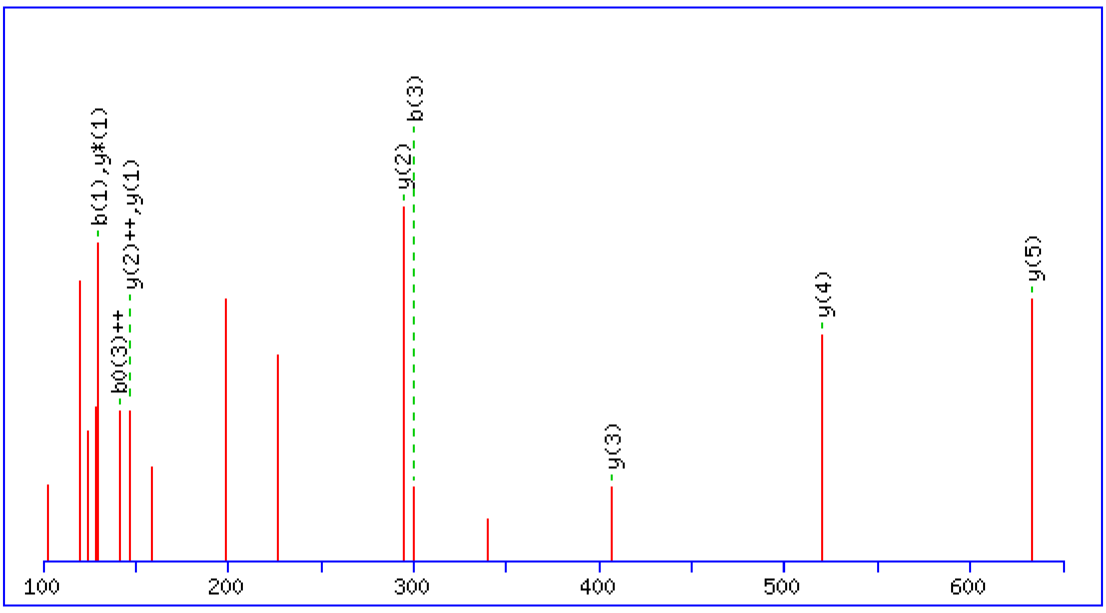
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGIILFK**
Found in **LA_HUMAN**, Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2

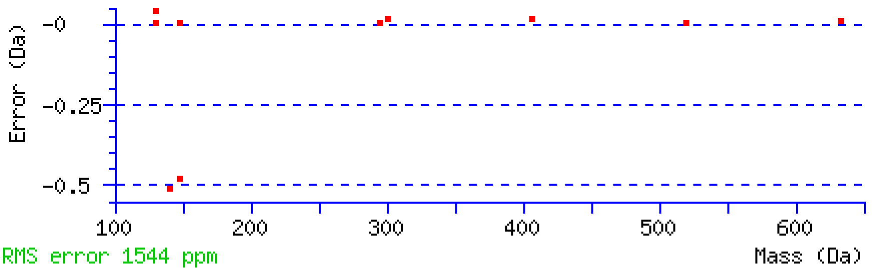
Match to Query 953: 818.487428 from(410.250990,2+) rtinseconds(2656) index(31005)
Title: Locus:1.1.1.2539.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

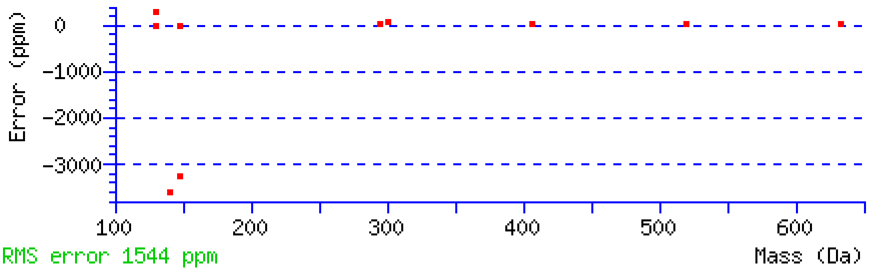
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 818.490173
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00047
Matches : 10/48 fragment ions using 13 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	690.454874	345.731075	673.428325	337.217801	6
3	**300.155397**	150.581336	282.144832	141.576054	I	***633.433410***	317.220343	616.406861	308.707068	5
4	413.239461	207.123369	395.228896	198.118086	I	***520.349346***	260.678311	503.322797	252.165036	4
5	526.323525	263.665401	508.312960	254.660118	L	***407.265282***	204.136279	390.238733	195.623004	3
6	673.391939	337.199608	655.381374	328.194325	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 EGIILFK
(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	818.490173	-0.002745	EGIILFK
34.4	818.490173	-0.002745	GEILIFK
9.5	818.490173	-0.002745	ILDAIFK
8.6	818.490173	-0.002745	IAIDLFK
8.3	818.490173	-0.002745	LEGLFLK
0.8	818.490173	-0.002745	LGLLEFK

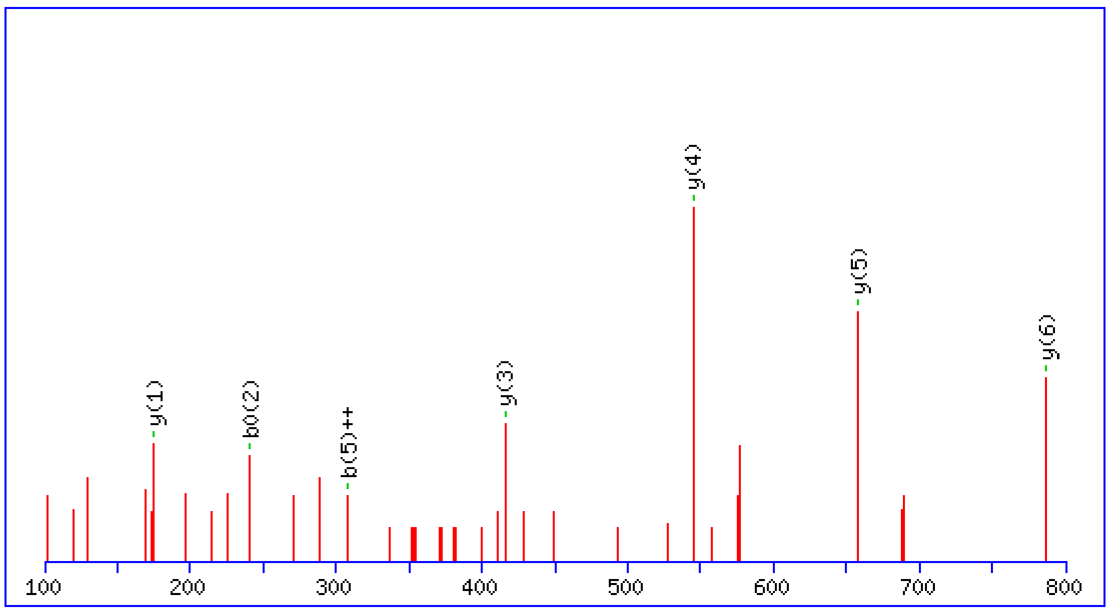
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EELEPKR**
Found in **KDM5C_HUMAN**, Lysine-specific demethylase 5C OS=Homo sapiens GN=KDM5C PE=1 SV=2

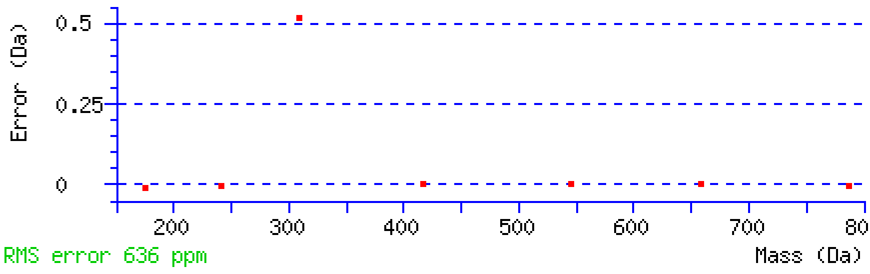
Match to Query 7207: 915.468588 from(458.741570,2+) rtinseconds(2483) index(28213)
Title: Locus:1.1.1.2531.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

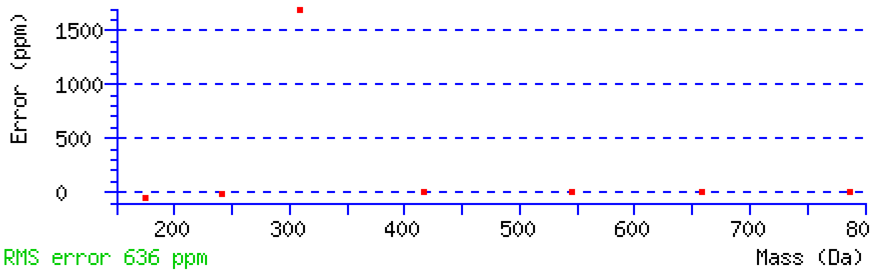
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 915.466125
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 41 **Expect:** 0.0023
Matches : 7/56 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	130.049869	65.528572			112.039304	56.523290	**E**							7
2	259.092462	130.049869			241.081897	121.044587	**E**	***787.430844***	394.219060	770.404295	385.705786	769.420279	385.213778	6
3	372.176526	186.591901			354.165961	177.586619	**L**	***658.388251***	329.697764	641.361702	321.184489	640.377686	320.692481	5
4	501.219119	251.113198			483.208554	242.107915	**E**	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
5	614.266798	307.637037			596.256233	298.631755	**P**	***416.261594***	208.634435	399.235045	200.121160			3
6	742.361761	371.684519	725.335212	363.171244	724.351196	362.679236	**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 EELEPKR
(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	915.466125	0.002463	EELEPKR
25.6	915.466141	0.002447	EELPSAVR
25.3	915.466125	0.002463	EIEEQLR
23.9	915.466125	0.002463	EEELAAVR
14.9	915.477356	-0.008768	EKNQELR
13.9	915.466125	0.002463	EEDLAALR
12.4	915.477371	-0.008783	EGLSNQLR
11.9	915.477371	-0.008783	QQDEIKR
11.7	915.477356	-0.008768	EAGNIKER
11.5	915.477371	-0.008783	EQDKLQR

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

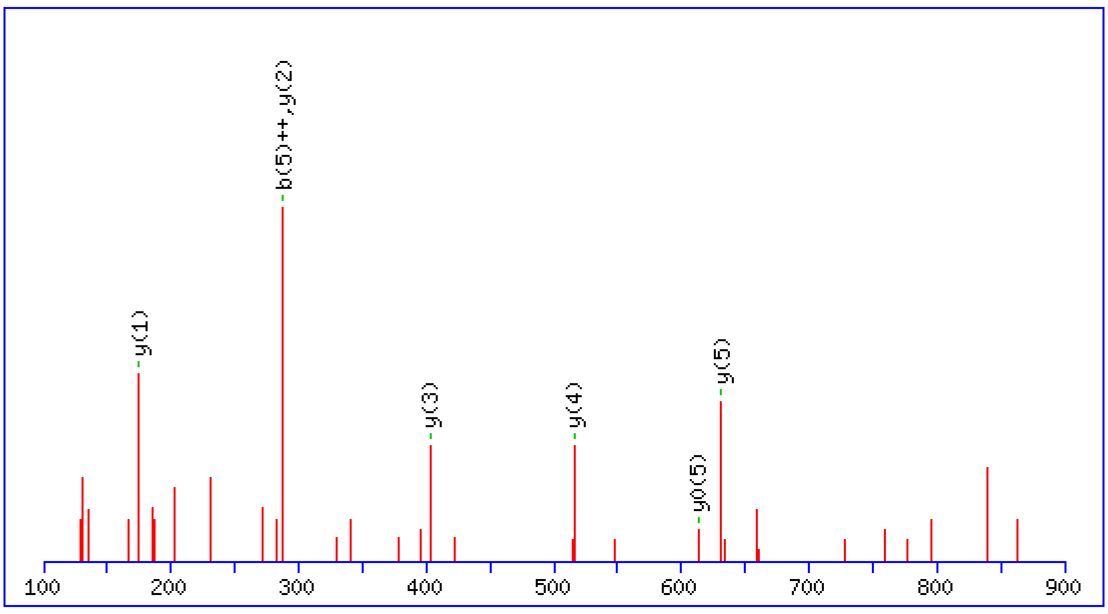
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEDPDLR**
Found in **KDM7_HUMAN**, Lysine-specific demethylase 7 OS=Homo sapiens GN=JHDM1D PE=1 SV=2

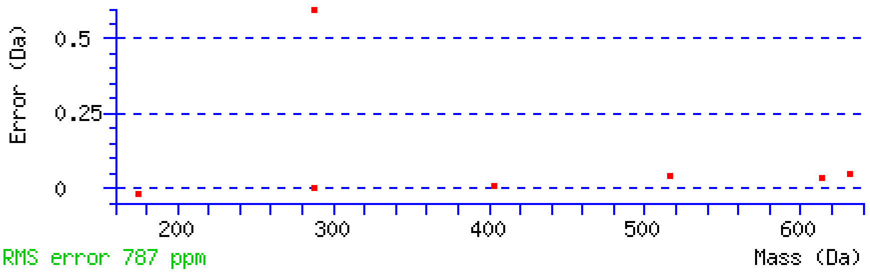
Match to Query 61186: 860.380928 from(431.197740,2+) rtinseconds(1645) index(494931)
Title: Locus:1.1.1.1245.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

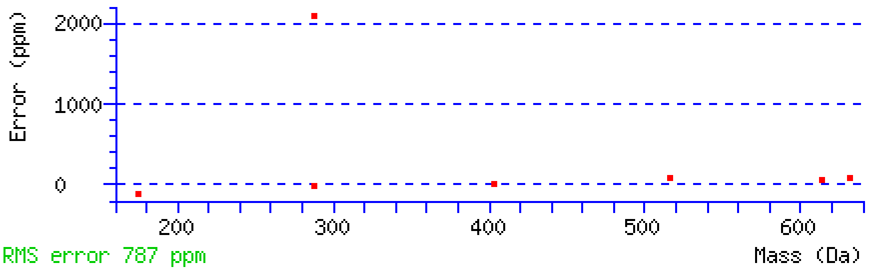
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 860.387573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 44 **Expect:** 0.0011
Matches : 7/56 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							7
2	231.097548	116.052412	213.086983	107.047130	E	760.347174	380.677225	743.320625	372.163951	742.336609	371.671943	6
3	346.124491	173.565884	328.113926	164.560601	D	***631.304581***	316.155929	614.278032	307.642654	613.294016	307.150646	5
4	459.172170	230.089723	441.161605	221.084441	P	***516.277638***	258.642457	499.251089	250.129182	498.267073	249.637174	4
5	574.199113	287.603195	556.188548	278.597912	D	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
6	687.283177	344.145227	669.272612	335.139944	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 TEDPDLR
(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	860.387573	-0.006645	TEDPDLR
10.2	860.387573	-0.006645	EDTPLDR
8.8	860.381042	-0.000114	GCELNPR
8.5	860.387558	-0.006630	EASPPSNK
6.2	860.381058	-0.000130	VPCSNPR
5.1	860.387558	-0.006630	SDPEELR
3.5	860.381042	-0.000114	AAGSGDMPR
1.5	860.381058	-0.000130	GSPGSMGPR
0.9	860.387543	-0.006615	EEEEGIR
0.7	860.387558	-0.006630	SLEDEPR

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

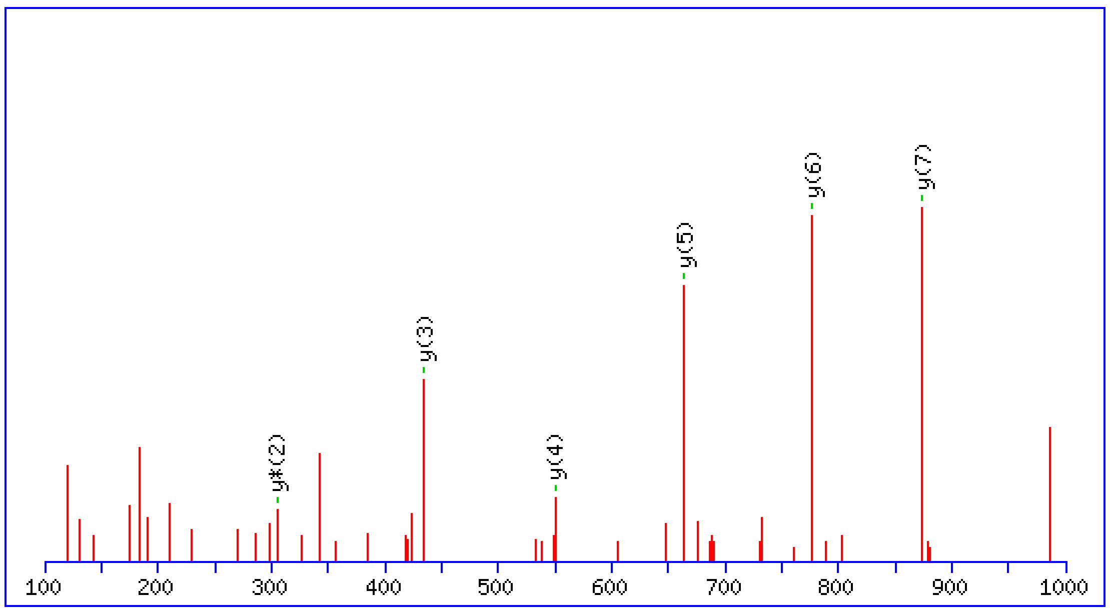
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPLNDLFR**
Found in **LAMP2_HUMAN**, Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2

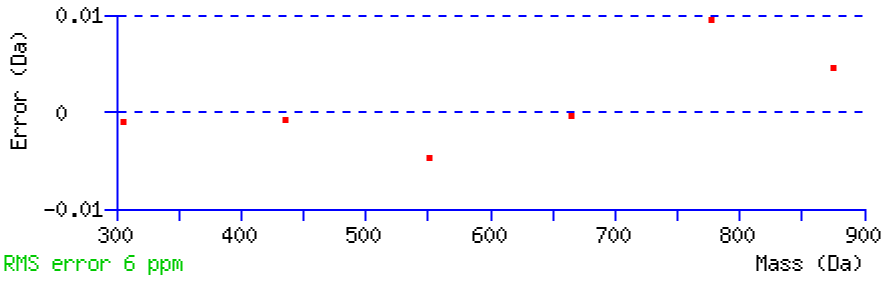
Match to Query 10863: 986.548048 from(494.281300,2+) rtinseconds(3102) index(45787)
Title: Locus:1.1.1.1827.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

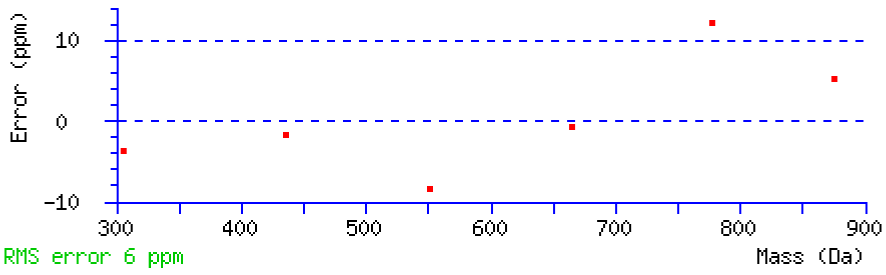
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 986.554901
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00014
Matches : 6/64 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**							8
2	211.144104	106.075690					**P**	*874.478128*	437.742702	857.451579	429.229428	856.467563	428.737420	7
3	324.228168	162.617722					**L**	*777.425364*	389.216320	760.398815	380.703046	759.414799	380.211038	6
4	438.271095	219.639186	421.244546	211.125911			**N**	*664.341300*	332.674288	647.314751	324.161014	646.330735	323.669006	5
5	553.298038	277.152657	536.271489	268.639383	535.287473	268.147375	**D**	*550.298373*	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	666.382102	333.694689	649.355553	325.181415	648.371537	324.689407	**L**	*435.271430*	218.139353	418.244881	209.626079			3
7	813.450516	407.228896	796.423967	398.715622	795.439951	398.223614	**F**	322.187366	161.597321	305.160817	153.084047			2
8							**R**	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of IPLNDLFR
(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	986.554901	-0.006853	IPLNDLFR
1.1	986.547043	0.001005	LILPQMPK
0.9	986.543686	0.004362	IPGFTDLPK
0.9	986.554901	-0.006853	IPPTYQIR
0.9	986.554886	-0.006838	LPEAAFLAR
0.9	986.540985	0.007063	LPNHLTHR
0.4	986.539658	0.008390	ILPSSDTVR
0.4	986.547028	0.001020	MPEKILPK

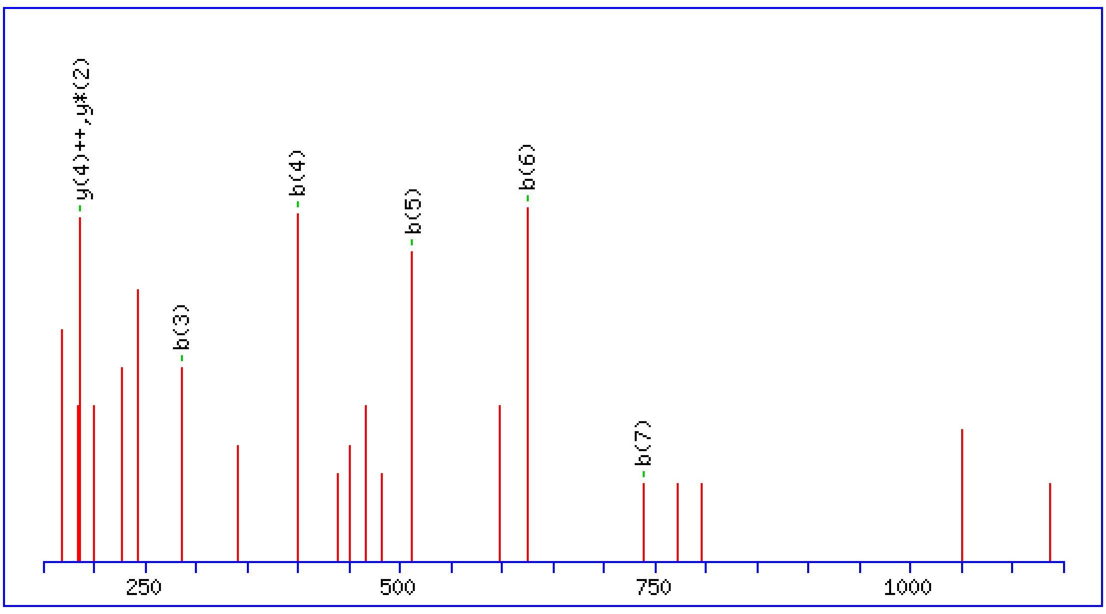
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TALPLLPGGK**
Found in **MFS6L_HUMAN**, Major facilitator superfamily domain-containing protein 6-like OS=Homo sapiens GN=MFSD6L PE=2 SV=2

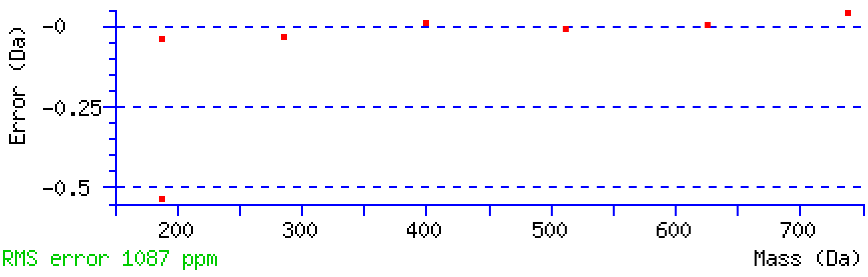
Match to Query 6633: 997.582868 from(499.798710,2+) rtinseconds(3272) index(22703)
Title: Locus:1.1.1.2827.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

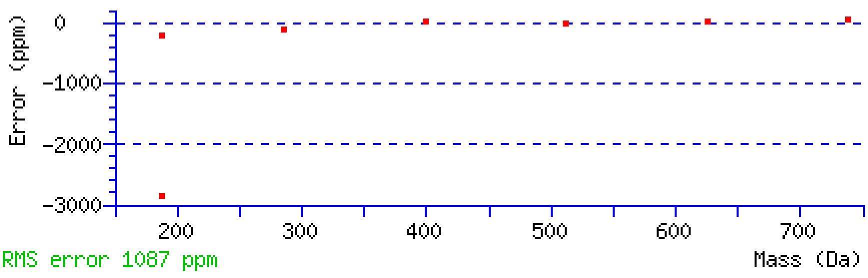
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 997.580795
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
P7 : Oxidation (P)
Ions Score: 40 **Expect:** 0.00079
Matches : 7/72 fragment ions using 7 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	173.092069	87.049672	155.081504	78.044390	A	897.540396	449.273836	880.513847	440.760562	9
3	*286.176133*	143.591704	268.165568	134.586422	L	826.503282	413.755279	809.476733	405.242005	8
4	*399.223812*	200.115544	381.213247	191.110262	P	713.419218	357.213247	696.392669	348.699973	7
5	*512.307876*	256.657576	494.297311	247.652294	L	600.371539	300.689408	583.344990	292.176133	6
6	*625.391940*	313.199608	607.381375	304.194326	L	487.287475	244.147376	470.260926	235.634101	5
7	*738.439619*	369.723448	720.429054	360.718165	P	374.203411	187.605344	357.176862	179.092069	4
8	795.461083	398.234180	777.450518	389.228897	G	261.155732	131.081504	244.129183	122.568230	3
9	852.482547	426.744912	834.471982	417.739629	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 TALPLLPGGK
(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	997.580795	0.002073	TALPLLPGGK
7.9	997.592010	-0.009142	GQIINVLNK
3.5	997.592010	-0.009142	LLLEQGGLR
2.4	997.578079	0.004789	LNRQLAQR
2.3	997.580780	0.002088	LLLAPGSSPK
0.7	997.574249	0.008619	MLAKGLPPR

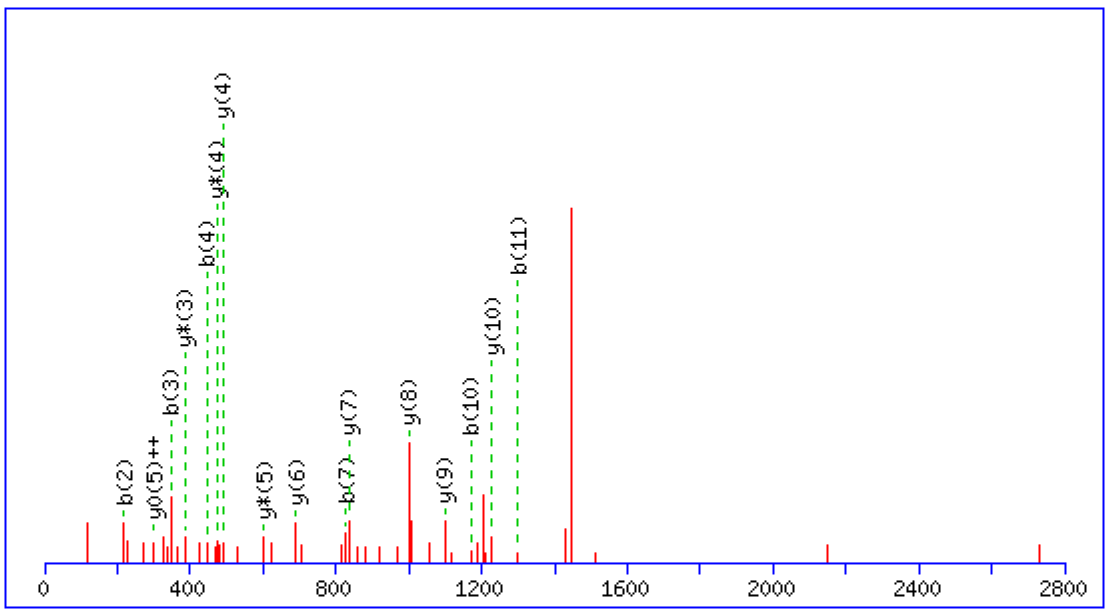
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAEVYFAQSQQK**
Found in **MLEC_HUMAN**, Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1

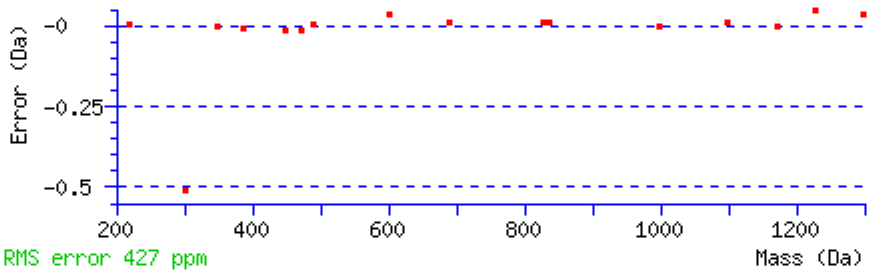
Match to Query 33203: 1444.706228 from(723.360390,2+) rtinseconds(2390) index(28185)
Title: Locus:1.1.1.2354.40
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

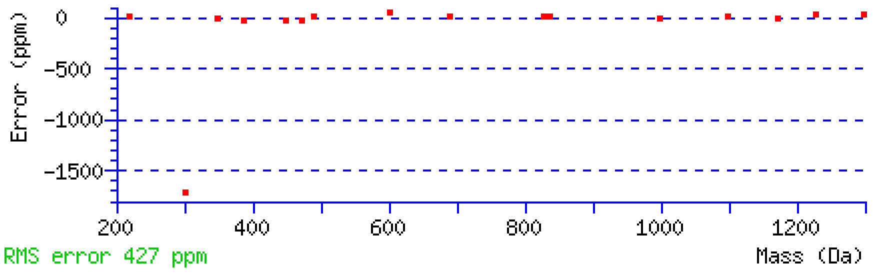
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1444.698669
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00066
Matches : 16/108 fragment ions using 32 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							12
2	***219.112804***	110.060040					A	1298.637544	649.822410	1281.610995	641.309136	1280.626979	640.817128	11
3	***348.155397***	174.581336			330.144832	165.576054	E	***1227.600430***	614.303853	1210.573881	605.790579	1209.589865	605.298571	10
4	***447.223811***	224.115544			429.213246	215.110261	V	***1098.557837***	549.782557	1081.531288	541.269282	1080.547272	540.777274	9
5	610.287140	305.647208			592.276575	296.641926	Y	***999.489423***	500.248350	982.462874	491.735075	981.478858	491.243067	8
6	757.355554	379.181415			739.344989	370.176133	F	***836.426094***	418.716685	819.399545	410.203411	818.415529	409.711403	7
7	***828.392668***	414.699972			810.382103	405.694690	A	***689.357680***	345.182478	672.331131	336.669204	671.347115	336.177196	6
8	956.451246	478.729261	939.424697	470.215987	938.440681	469.723979	Q	618.320566	309.663921	601.294017	301.150647	600.310001	300.658639	5
9	1043.483274	522.245275	1026.456725	513.732001	1025.472709	513.239993	S	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.629350	4
10	***1171.541852***	586.274564	1154.515303	577.761290	1153.531287	577.269282	Q	403.229960	202.118618	386.203411	193.605344			3
11	***1299.600430***	650.303853	1282.573881	641.790579	1281.589865	641.298571	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 FAEVYFAQSQQK
(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	1444.698669	0.007559	FAEVYFAQSQQK
7.0	1444.715759	-0.009531	GSPSSQSIPEKNSK
4.4	1444.694672	0.011556	TQPFQAQPPQQK
3.3	1444.719803	-0.013575	GGVAPAPEAPEPPPK
3.2	1444.715775	-0.009547	NGSTAVAESVASPQK
1.0	1444.704529	0.001699	LEGVAEETDNLQK
0.8	1444.698059	0.008169	AVPVPNMTPSGVGR
0.7	1444.699371	0.006857	CPGGLPGHAGGAAPGR

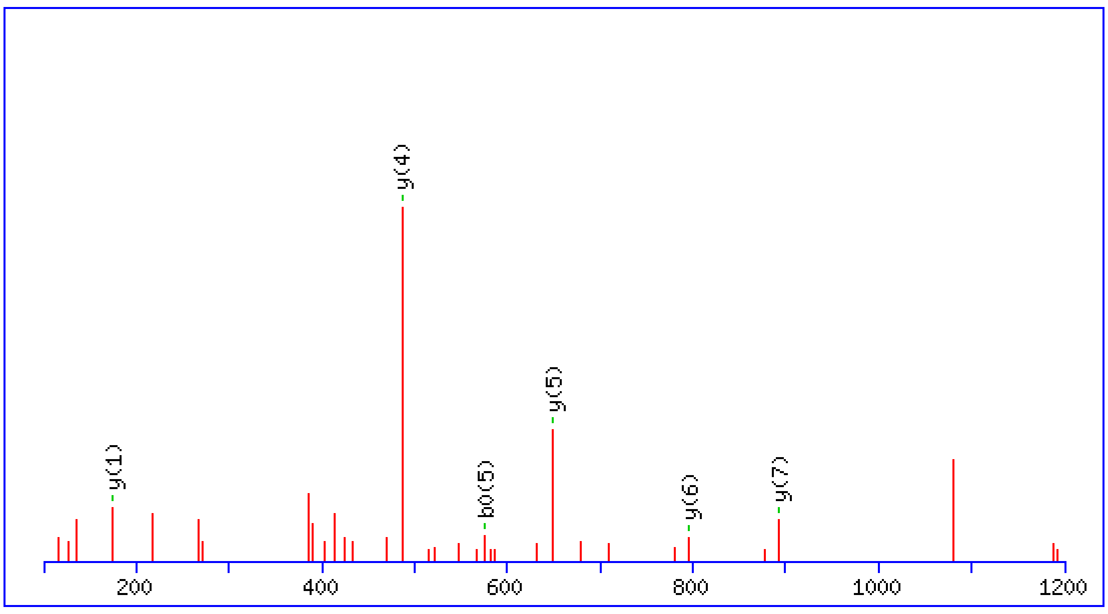
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGPFYPTLR**
Found in **MCTS1_HUMAN**, Malignant T cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1

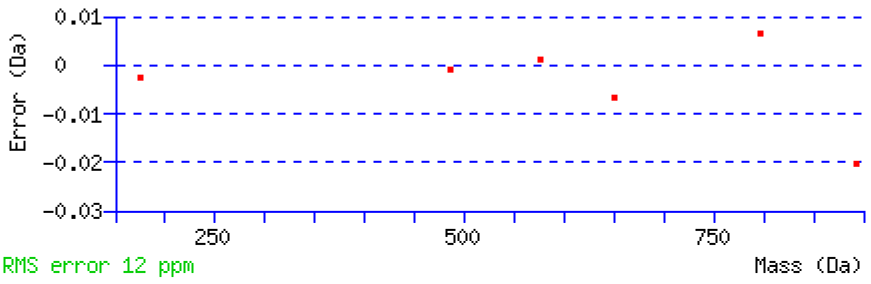
Match to Query 14012: 1078.546368 from(540.280460,2+) rtinseconds(2515) index(22135)
Title: Locus:1.1.1.2455.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

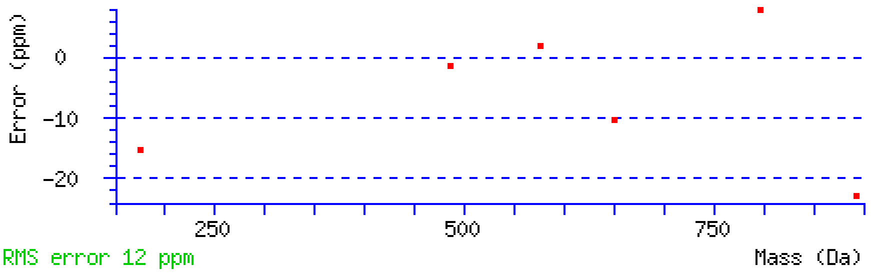
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1078.544739
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0025
Matches : 6/76 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							9
2	187.071333	94.039305	169.060768	85.034022	G	950.509430	475.758353	933.482881	467.245079	932.498865	466.753071	8
3	284.124097	142.565687	266.113532	133.560404	P	***893.487966***	447.247621	876.461417	438.734347	875.477401	438.242339	7
4	431.192511	216.099894	413.181946	207.094611	F	***796.435202***	398.721239	779.408653	390.207965	778.424637	389.715957	6
5	594.255840	297.631558	576.245275	288.626276	Y	***649.366788***	325.187032	632.340239	316.673758	631.356223	316.181750	5
6	691.308604	346.157940	673.298039	337.152658	P	***486.303459***	243.655368	469.276910	235.142093	468.292894	234.650085	4
7	792.356283	396.681780	774.345718	387.676497	T	389.250695	195.128986	372.224146	186.615711	371.240130	186.123703	3
8	905.440347	453.223812	887.429782	444.218529	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 EGPFYPTLR
(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	1078.544739	0.001629	EGPFYPTLR
9.8	1078.540726	0.005642	GEGGAPPLPPR
9.8	1078.540726	0.005642	GEGGAPPLPPR
8.4	1078.540710	0.005658	IGLFNSSADR
8.4	1078.538223	0.008145	ILGFWGGCR
8.1	1078.540726	0.005642	GEGGAPPLPPR
8.1	1078.540726	0.005642	GEGGAPPLPPR
7.1	1078.540726	0.005642	ADFVAGSLSGR
6.7	1078.540710	0.005658	EGKFNDTLR
2.5	1078.551956	-0.005588	EGFRSLGGTR

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

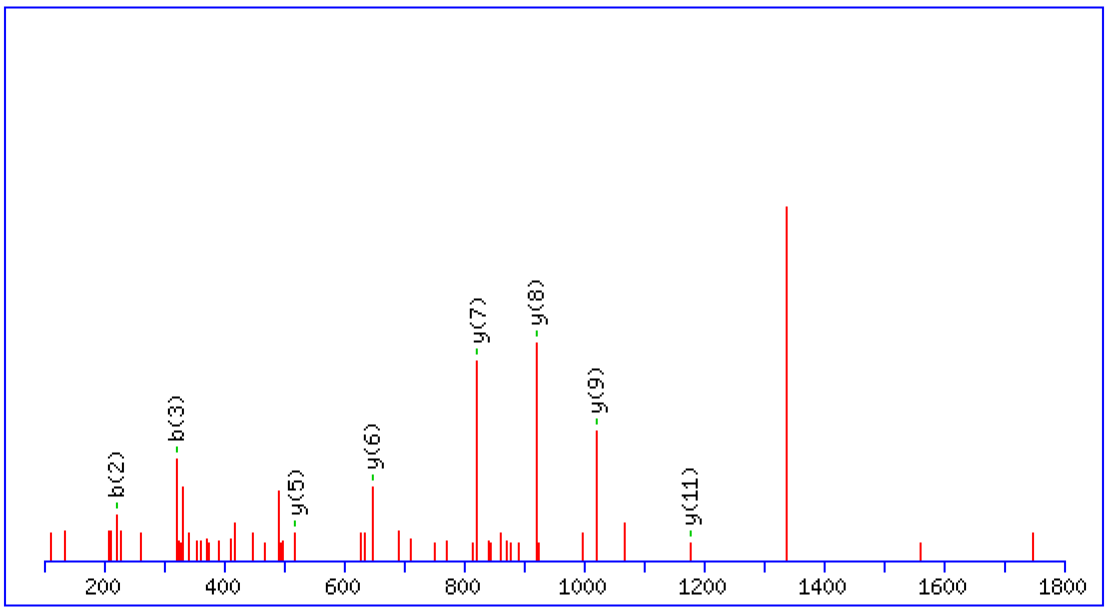
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGVVVCEADTGR**
Found in **GMPPB_HUMAN**, Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2

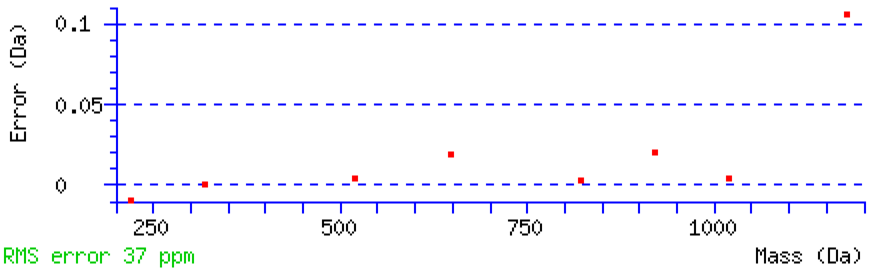
Match to Query 31953: 1338.636028 from(670.325290,2+) rtinseconds(1888) index(20390)
Title: Locus:1.1.1.2103.43
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

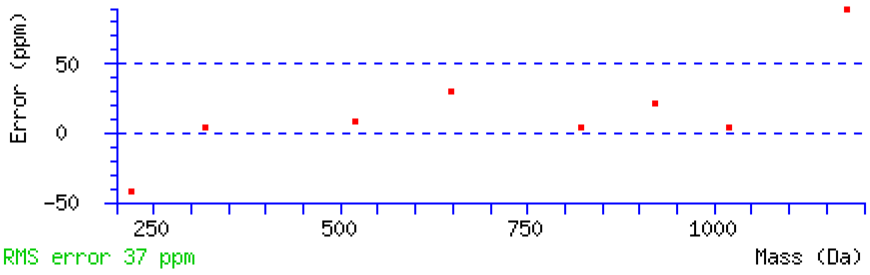
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1338.623810
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.0003
Matches : 8/94 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							12
2	**221.092069**	111.049673			G	***1176.567750***	588.787513	1159.541201	580.274238	1158.557185	579.782230	11
3	**320.160483**	160.583879			V	1119.546286	560.276781	1102.519737	551.763506	1101.535721	551.271498	10
4	419.228897	210.118087			V	***1020.477872***	510.742574	1003.451323	502.229299	1002.467307	501.737291	9
5	518.297311	259.652294			V	***921.409458***	461.208367	904.382909	452.695092	903.398893	452.203084	8
6	692.343610	346.675443			C	***822.341044***	411.674160	805.314495	403.160885	804.330479	402.668877	7
7	821.386203	411.196740	803.375638	402.191457	E	***648.294745***	324.651010	631.268196	316.137736	630.284180	315.645728	6
8	892.423317	446.715297	874.412752	437.710014	A	***519.252152***	260.129714	502.225603	251.616439	501.241587	251.124431	5
9	1007.450260	504.228768	989.439695	495.223485	D	448.215038	224.611157	431.188489	216.097882	430.204473	215.605874	4
10	1108.497939	554.752607	1090.487374	545.747325	T	333.188095	167.097685	316.161546	158.584411	315.177530	158.092403	3
11	1165.519403	583.263339	1147.508838	574.258057	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 YGVVVCEADTGR
(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	1338.623810	0.012218	YGVVVCEADTGR

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

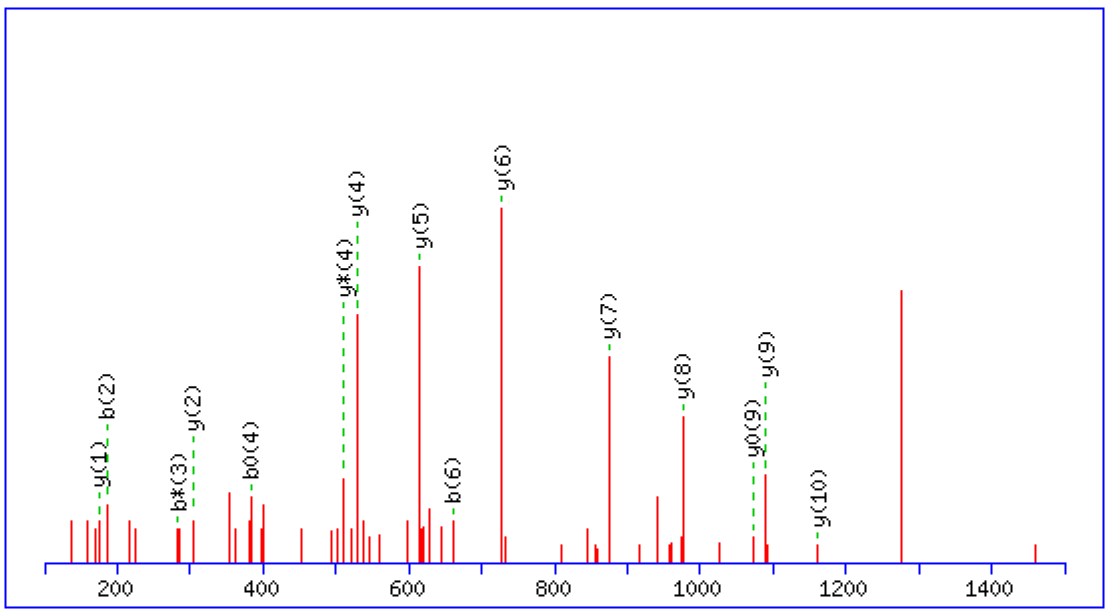
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NANTFISPQQR**
Found in **MGP_HUMAN**, Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2

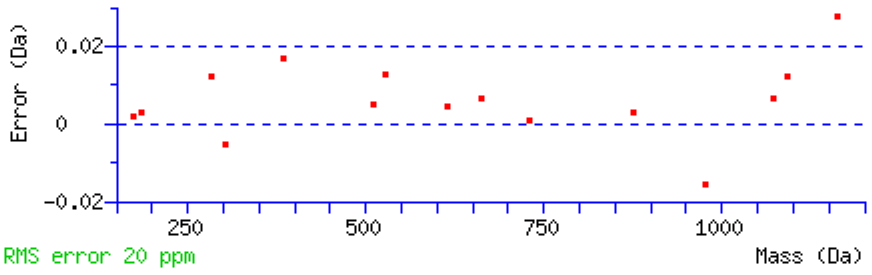
Match to Query 9569: 1274.637688 from(638.326120,2+) rtinseconds(1766) index(2259)
Title: Locus:1.1.1.2522.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

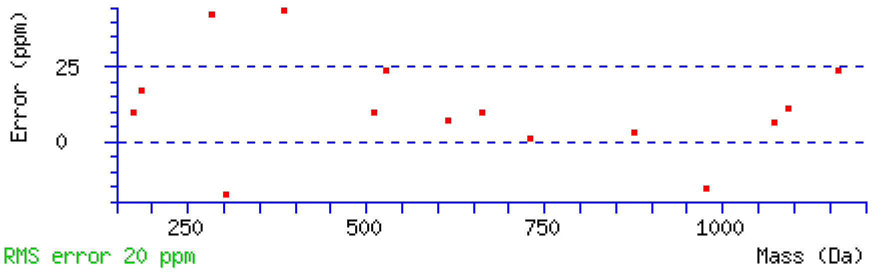
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1274.636734
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 85 **Expect:** 4.8e-008
Matches : 15/106 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	115.050203	58.028740	98.023654	49.515465			N							11
2	**186.087317**	93.547296	169.060768	85.034022			A	***1161.601098***	581.304187	1144.574549	572.790913	1143.590533	572.298905	10
3	300.130244	150.568760	283.103695	142.055486			N	***1090.563984***	545.785630	1073.537435	537.272356	1072.553419	536.780348	9
4	401.177923	201.092600	384.151374	192.579325	383.167358	192.087317	T	***976.521057***	488.764167	959.494508	480.250892	958.510492	479.758884	8
5	548.246337	274.626807	531.219788	266.113532	530.235772	265.621524	F	***875.473378***	438.240327	858.446829	429.727053	857.462813	429.235045	7
6	**661.330401**	331.168839	644.303852	322.655564	643.319836	322.163556	I	***728.404964***	364.706120	711.378415	356.192846	710.394399	355.700838	6
7	748.362429	374.684853	731.335880	366.171578	730.351864	365.679570	S	***615.320900***	308.164088	598.294351	299.650814	597.310335	299.158806	5
8	845.415193	423.211235	828.388644	414.697960	827.404628	414.205952	P	***528.288872***	264.648074	511.262323	256.134800			4
9	973.473771	487.240524	956.447222	478.727249	955.463206	478.235241	Q	431.236108	216.121692	414.209559	207.608417			3
10	1101.532349	551.269813	1084.505800	542.756538	1083.521784	542.264530	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 NANTFISPQQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.6	1274.636734	0.000954	NANTFISPQQR
12.0	1274.625504	0.012184	QSWNVLESQGK
10.2	1274.628860	0.008828	LGEGCEPISKR
7.3	1274.628876	0.008812	NANMVAVLDQGK
5.3	1274.628860	0.008828	CAGNEDIITLR
4.4	1274.628876	0.008812	CAGTVEVEIQR
4.2	1274.646652	-0.008964	SQSIDTPGVISR
1.3	1274.640778	-0.003090	GKPPPSFSWTR
1.3	1274.640778	-0.003090	GKPPPSFSWTR

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

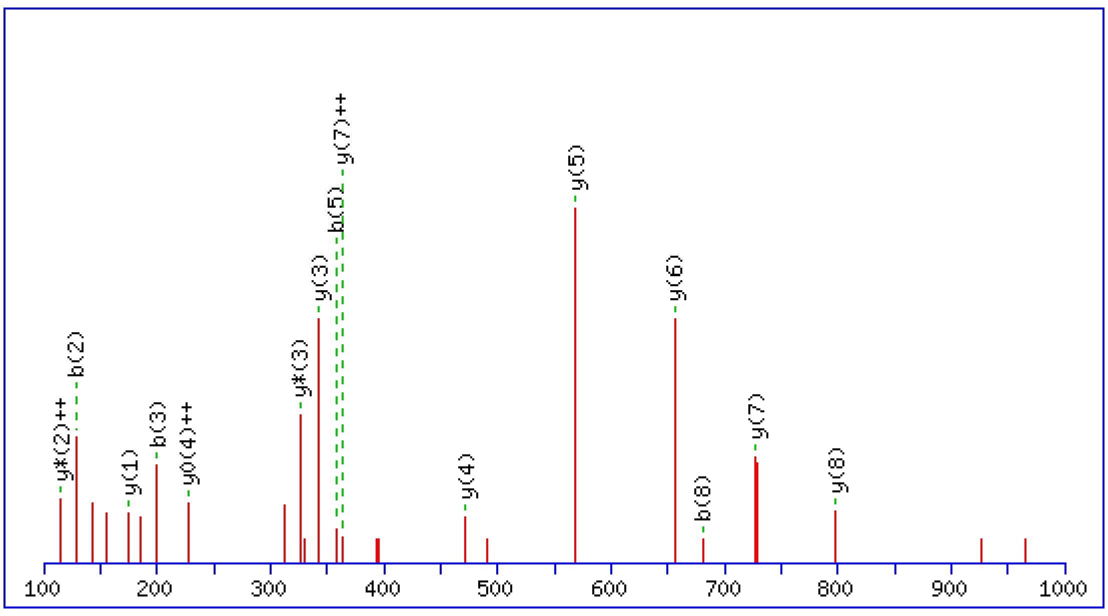
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAAASPEPAR**
Found in **MXRA7_HUMAN**, Matrix-remodeling-associated protein 7 OS=Homo sapiens GN=MXRA7 PE=1 SV=1

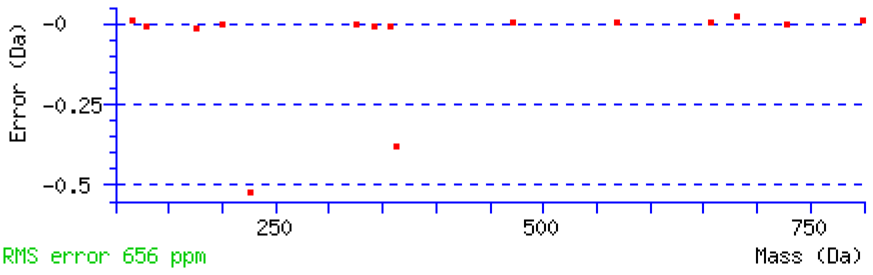
Match to Query 8692: 925.457288 from(463.735920,2+) rtinseconds(720) index(145)
Title: Locus:1.1.1.1763.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

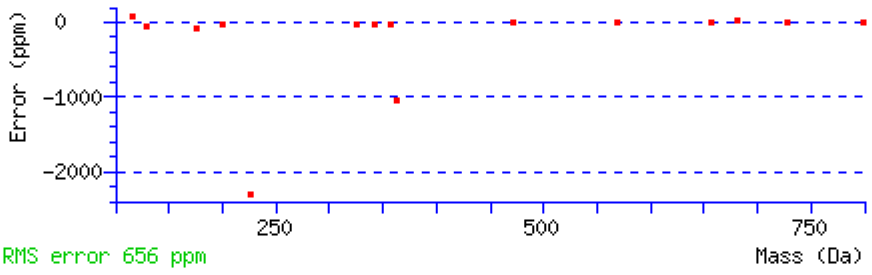
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 925.461716
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 3.1e-005
Matches : 15/76 fragment ions using 22 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	**129.065854**	65.036565			A	869.447557	435.227417	852.421008	426.714142	851.436992	426.222134	9
3	**200.102968**	100.555122			A	***798.410443***	399.708860	781.383894	391.195585	780.399878	390.703577	8
4	271.140082	136.073679			A	***727.373329***	364.190303	710.346780	355.677028	709.362764	355.185020	7
5	**358.172110**	179.589693	340.161545	170.584411	S	***656.336215***	328.671746	639.309666	320.158471	638.325650	319.666463	6
6	455.224874	228.116075	437.214309	219.110793	P	***569.304187***	285.155732	552.277638	276.642457	551.293622	276.150449	5
7	584.267467	292.637372	566.256902	283.632089	E	***472.251423***	236.629349	455.224874	228.116075	454.240858	227.624067	4
8	**681.320231**	341.163754	663.309666	332.158471	P	***343.208830***	172.108053	326.182281	163.594778			3
9	752.357345	376.682311	734.346780	367.677028	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 GAAASPEPAR
(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	925.461716	-0.004428	GAAASPEPAR
9.5	925.461746	-0.004458	QVPGSDPAR
9.4	925.461746	-0.004458	QTPAPGPAR
8.6	925.461746	-0.004458	QTPAPGPAR
4.8	925.461746	-0.004458	QTPAPGPAR
4.8	925.461746	-0.004458	QAPGSDPVR
4.5	925.461746	-0.004458	NGGLPGGPNK
3.6	925.451843	0.005445	QNHFPQR
2.5	925.461716	-0.004428	QPAAPAAER
0.5	925.457886	-0.000598	KIMDEFK

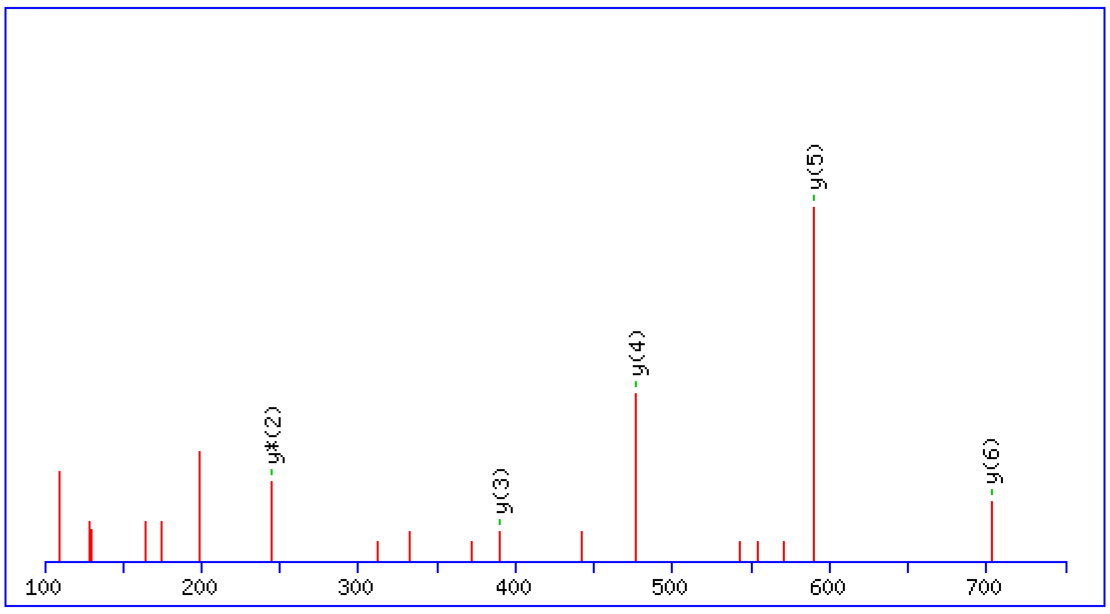
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIPSKDK**
Found in **MTBP_HUMAN**, Mdm2-binding protein OS=Homo sapiens GN=MTBP PE=1 SV=1

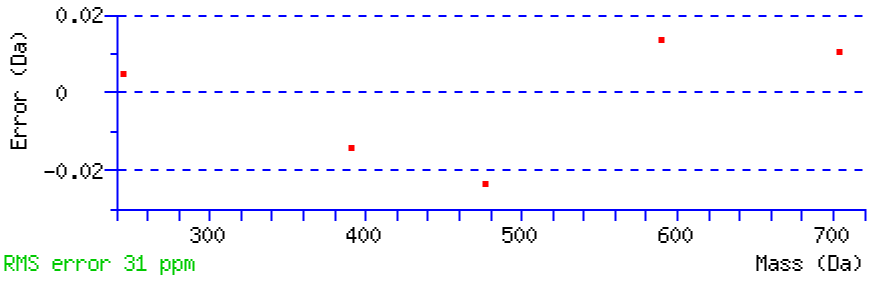
Match to Query 903: 815.482768 from(408.748660,2+) rtinseconds(1575) index(4712)
Title: Locus:1.1.1.2069.3
Data file 2011-11-14 - TFD - S 2-5.mgf

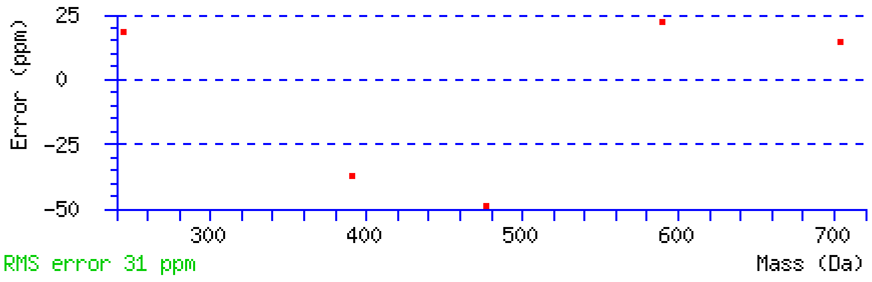
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [750] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 815.475250
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 36  Expect: 0.0047
Matches : 5/56 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					**I**							7
2	227.175404	114.091340					**I**	***703.398481***	352.202879	686.371932	343.689604	685.387916	343.197596	6
3	340.223083	170.615179					**P**	***590.314417***	295.660847	573.287868	287.147572	572.303852	286.655564	5
4	427.255111	214.131193			409.244546	205.125911	**S**	***477.266738***	239.137007	460.240189	230.623732	459.256173	230.131724	4
5	555.350074	278.178675	538.323525	269.665401	537.339509	269.173393	**K**	***390.234710***	195.620993	373.208161	187.107718	372.224145	186.615710	3
6	670.377017	335.692147	653.350468	327.178872	652.366452	326.686864	**D**	262.139747	131.573511	245.113198	123.060237	244.129182	122.568229	2
7							**K**	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IIPSKDK
(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	815.475250	0.007518	IIPSKDK
32.0	815.486481	-0.003713	IIPSSKR
21.5	815.486481	-0.003713	LLIGASSR
17.4	815.475266	0.007502	IILDGTGK
10.3	815.486481	-0.003713	LLNTLSR
10.3	815.486481	-0.003713	IIRTGEK
8.5	815.486481	-0.003713	ILTGEKR
8.1	815.486465	-0.003697	LLSKAER
7.2	815.475250	0.007518	KSLIDPK
7.2	815.475250	0.007518	QSIIDLK

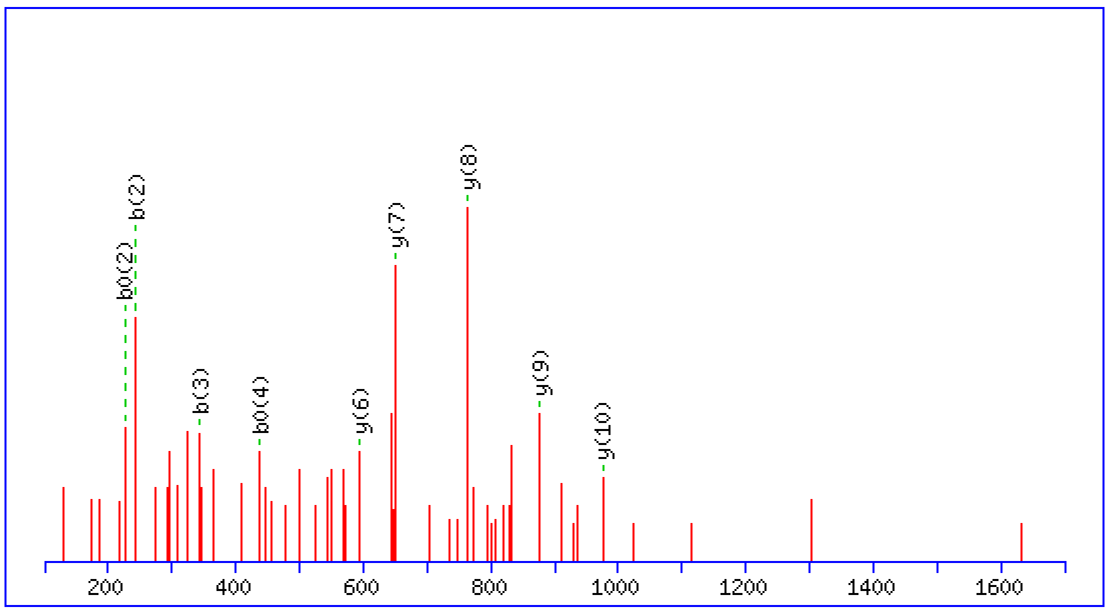
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENVLIGDGAGFK**
Found in **ACADM_HUMAN**, Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1

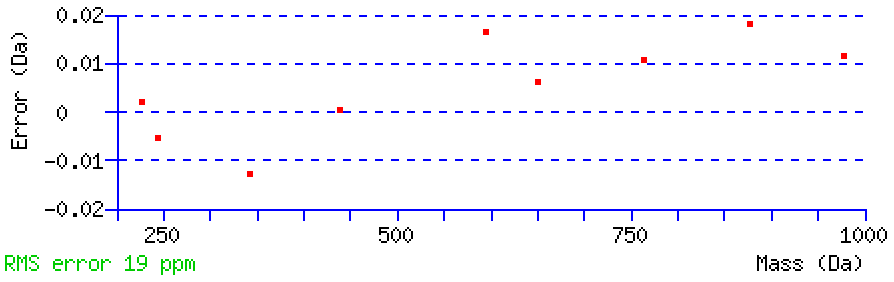
Match to Query 26535: 1218.627708 from(610.321130,2+) rtinseconds(2488) index(29679)
Title: Locus:1.1.1.2438.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

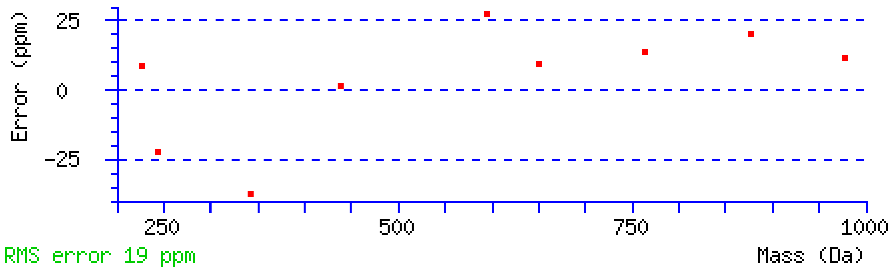
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1218.624451
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00074
Matches : 9/120 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	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	N	1090.589136	545.798206	1073.562587	537.284932	1072.578571	536.792924	11
3	**343.161210**	172.084243	326.134661	163.570969	325.150645	163.078961	V	***976.546209***	488.776743	959.519660	480.263468	958.535644	479.771460	10
4	456.245274	228.626275	439.218725	220.113001	438.234709	219.620993	L	***877.477795***	439.242536	860.451246	430.729261	859.467230	430.237253	9
5	569.329338	285.168307	552.302789	276.655033	551.318773	276.163025	I	***764.393731***	382.700504	747.367182	374.187229	746.383166	373.695221	8
6	626.350802	313.679039	609.324253	305.165765	608.340237	304.673757	G	***651.309667***	326.158472	634.283118	317.645197	633.299102	317.153189	7
7	741.377745	371.192511	724.351196	362.679236	723.367180	362.187228	D	***594.288203***	297.647740	577.261654	289.134465	576.277638	288.642457	6
8	798.399209	399.703243	781.372660	391.189968	780.388644	390.697960	G	479.261260	240.134268	462.234711	231.620994			5
9	869.436323	435.221800	852.409774	426.708525	851.425758	426.216517	A	422.239796	211.623536	405.213247	203.110261			4
10	926.457787	463.732532	909.431238	455.219257	908.447222	454.727249	G	351.202682	176.104979	334.176133	167.591704			3
11	1073.526201	537.266739	1056.499652	528.753464	1055.515636	528.261456	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 ENVLIGDGAGFK
(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	1218.624451	0.003257	ENVLIGDGAGFK
7.8	1218.639725	-0.012017	DQVGVLAGWFK
1.4	1218.624451	0.003257	NEVFLDVVER

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

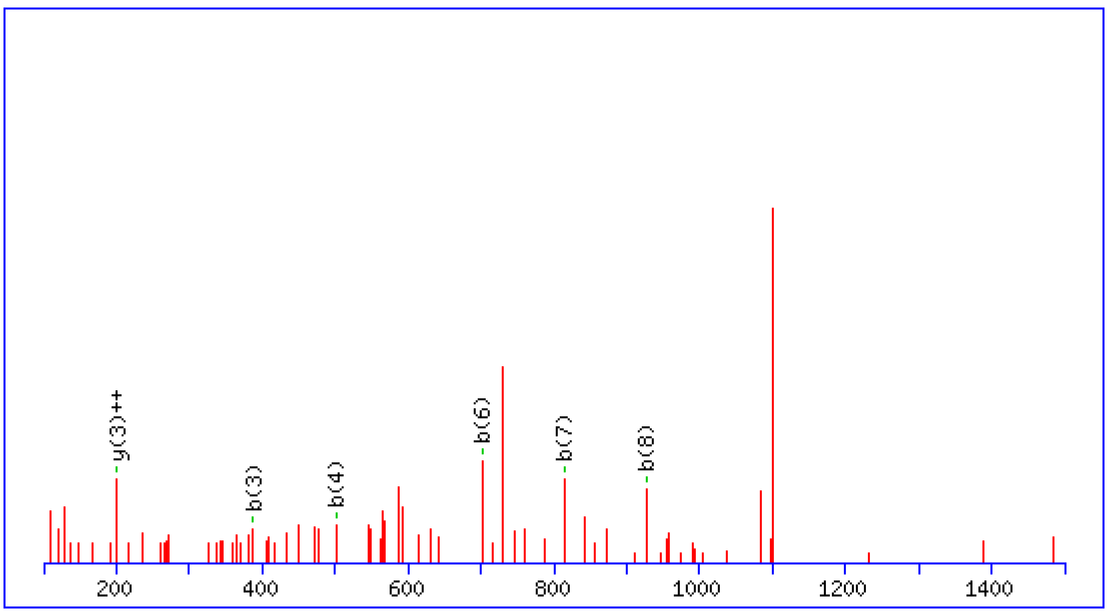
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YHSIVTLPR**
Found in **MSHR_HUMAN**, Melanocyte-stimulating hormone receptor OS=Homo sapiens GN=MC1R PE=1 SV=2

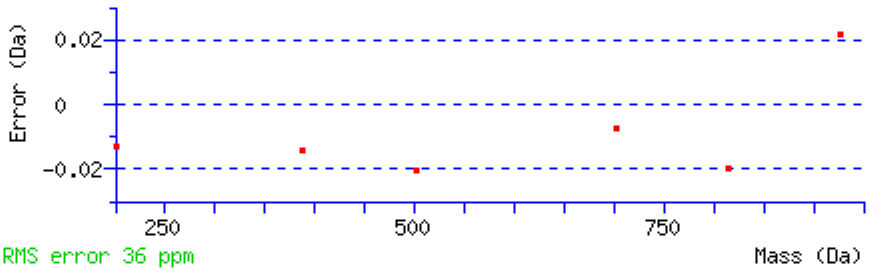
Match to Query 13051: 1100.598468 from(551.306510,2+) rtinseconds(2128) index(25175)
Title: Locus:1.1.1.2312.17
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

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 ●

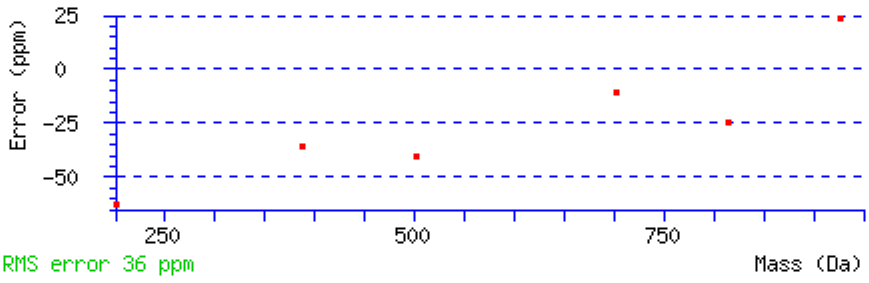


```
Monoisotopic mass of neutral peptide Mr(calc): 1100.597839
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P8      : Oxidation (P)
Ions Score: 31  Expect: 0.0098
Matches : 6/70 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			**Y**							9
2	301.129517	151.068397			**H**	938.541792	469.774534	921.515243	461.261259	920.531227	460.769252	8
3	***388.161545***	194.584410	370.150980	185.579128	**S**	801.482880	401.245078	784.456331	392.731804	783.472315	392.239796	7
4	***501.245609***	251.126443	483.235044	242.121160	**I**	714.450852	357.729064	697.424303	349.215790	696.440287	348.723782	6
5	600.314023	300.660650	582.303458	291.655367	**V**	601.366788	301.187032	584.340239	292.673758	583.356223	292.181750	5
6	***701.361702***	351.184489	683.351137	342.179207	**T**	502.298374	251.652825	485.271825	243.139550	484.287809	242.647542	4
7	***814.445766***	407.726521	796.435201	398.721239	**L**	401.250695	201.128985	384.224146	192.615711			3
8	***927.493445***	464.250361	909.482880	455.245078	**P**	288.166631	144.586953	271.140082	136.073679			2
9					**R**	175.118952	88.063114	158.092403	79.549839			1



RMS error 36 ppm



RMS error 36 ppm

NCBI **BLAST** search of YHSIVTLPR
(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	1100.597839	0.000629	YHSIVTLPR
18.8	1100.601196	-0.002728	LQVACDLLR
18.8	1100.597839	0.000629	NPKVFDPLR
14.8	1100.593811	0.004657	ASPTRTAPLR
13.3	1100.597839	0.000629	VGKETWLPR
10.2	1100.601196	-0.002728	DACQVLLLR
9.9	1100.605042	-0.006574	LSSPRTRPR
9.1	1100.607727	-0.009259	AEPTVTNILK
8.9	1100.601212	-0.002744	CAVVGNGGILK
8.4	1100.601196	-0.002728	MAAALQVLPR

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

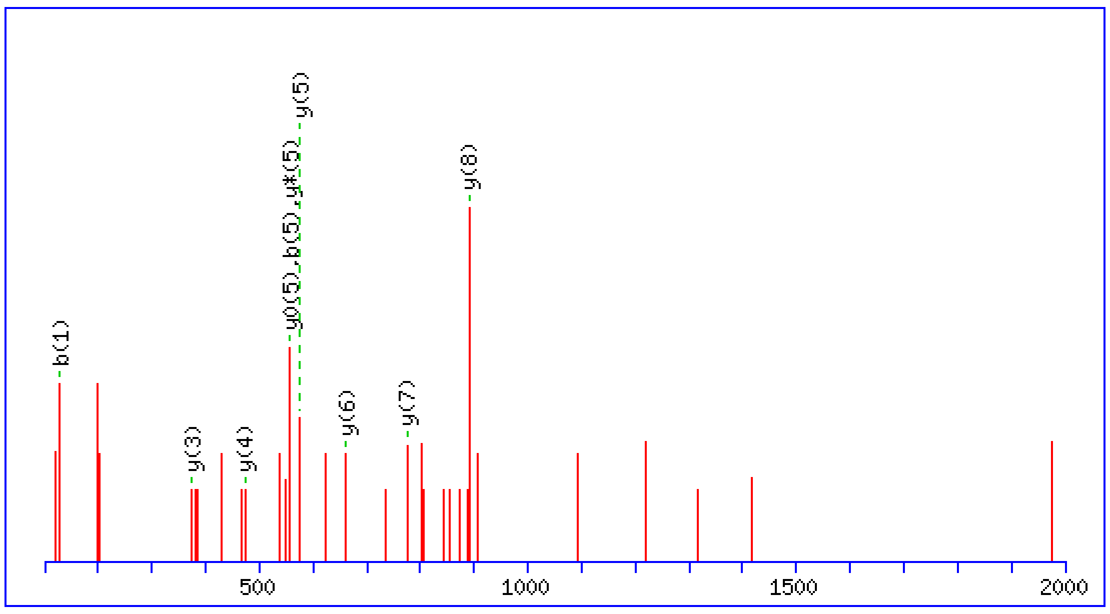
Mascot Search Results

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

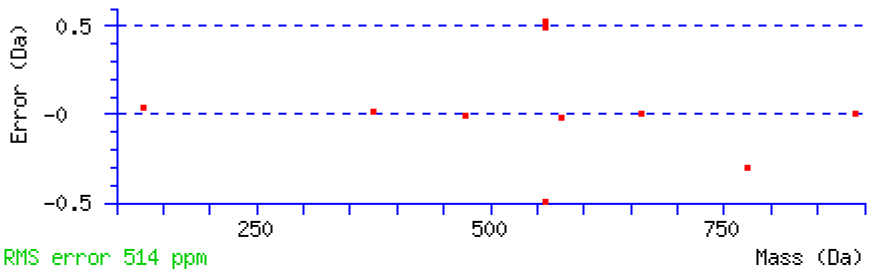
Match to Query 10878: 1130.623568 from(566.319060,2+) rtinseconds(2616) index(17109)
Title: Locus:1.1.1.2581.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

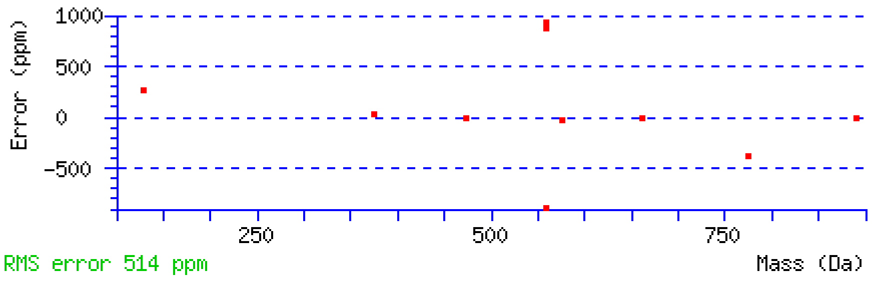
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1130.618301
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0086
Matches : 10/100 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							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
33.0	1130.618301	0.005267	QIDLSTVDLK
13.6	1130.629517	-0.005949	KLDLSNVQSK
6.0	1130.618271	0.005297	KLEADSLEVK
1.0	1130.633545	-0.009977	AVAAPVELFSK

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

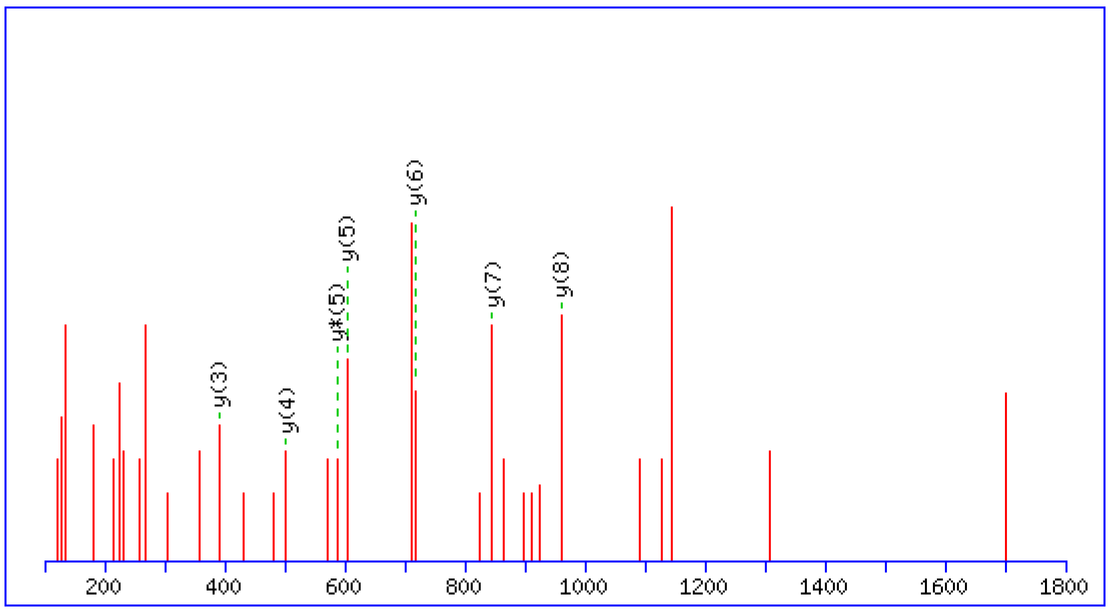
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDQLTLSQR**
Found in **TIMP3_HUMAN**, Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2

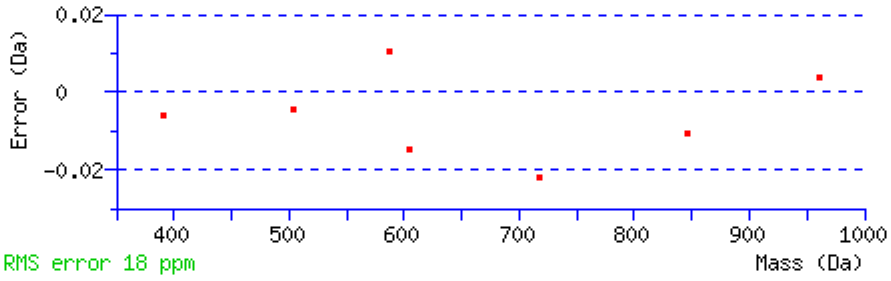
Match to Query 351540: 1145.587708 from(573.801130,2+) rtinseconds(2315) index(957811)
Title: Locus:1.1.1.1395.27
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

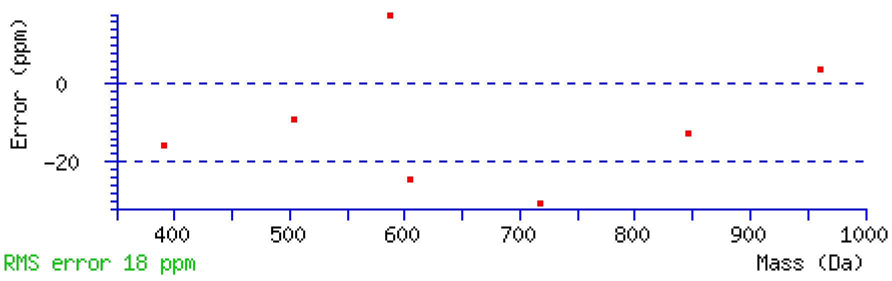
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1145.582916
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0018
Matches : 7/86 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	187.086589	94.046932					W							9
2	302.113532	151.560404			284.102967	142.555122	D	***960.510886***	480.759081	943.484337	472.245807	942.500321	471.753799	8
3	430.172110	215.589693	413.145561	207.076419	412.161545	206.584411	Q	***845.483943***	423.245610	828.457394	414.732335	827.473378	414.240327	7
4	543.256174	272.131725	526.229625	263.618451	525.245609	263.126443	L	***717.425365***	359.216321	700.398816	350.703046	699.414800	350.211038	6
5	644.303853	322.655565	627.277304	314.142290	626.293288	313.650282	T	***604.341301***	302.674289	587.314752	294.161014	586.330736	293.669006	5
6	757.387917	379.197597	740.361368	370.684322	739.377352	370.192314	L	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	4
7	844.419945	422.713611	827.393396	414.200336	826.409380	413.708328	S	***390.209558***	195.608417	373.183009	187.095143	372.198993	186.603135	3
8	972.478523	486.742900	955.451974	478.229625	954.467958	477.737617	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 WDQLTLSQR
(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	1145.582916	0.004792	WDQLTLSQR
2.6	1145.582901	0.004807	LRPDETPYR

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

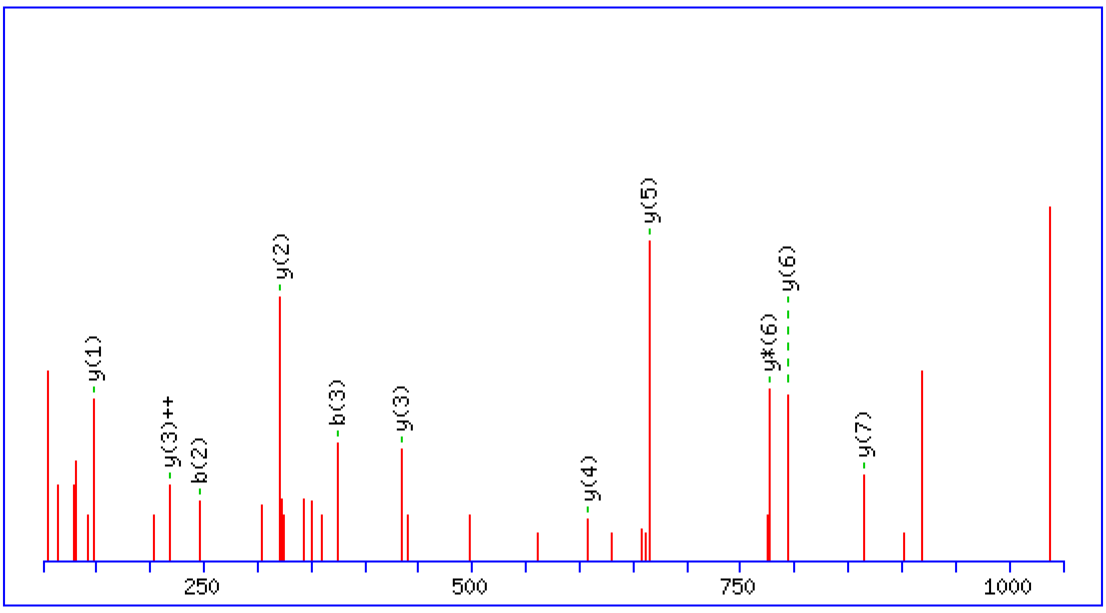
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAQGCICK**
Found in **MT1A_HUMAN**, Metallothionein-1A OS=Homo sapiens GN=MT1A PE=1 SV=2

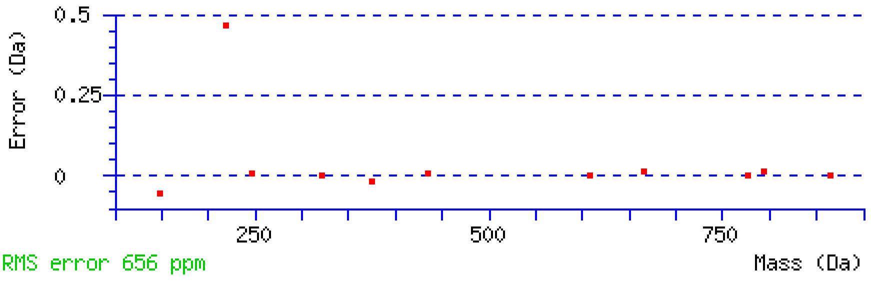
Match to Query 10235: 1037.447548 from(519.731050,2+) rtinseconds(906) index(489)
Title: Locus:1.1.1.1855.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

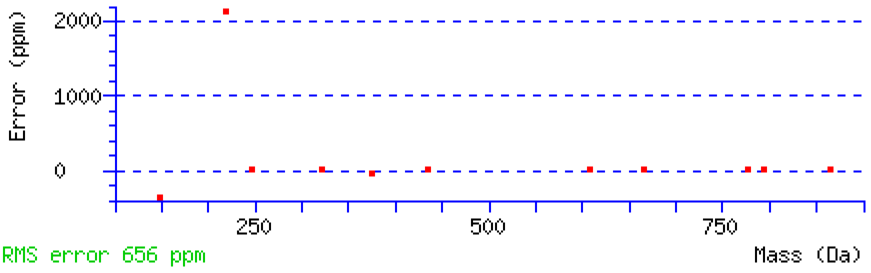
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1050] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1037.445618
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 2.2e-005
Matches : 11/52 fragment ions using 17 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





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
52.9	1037.445618	0.001930	CAQGCICK
3.7	1037.444748	0.002800	TCSATEEAR
1.9	1037.453491	-0.005943	NMGPHHSMK
0.5	1037.448792	-0.001244	TPENFPCK

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

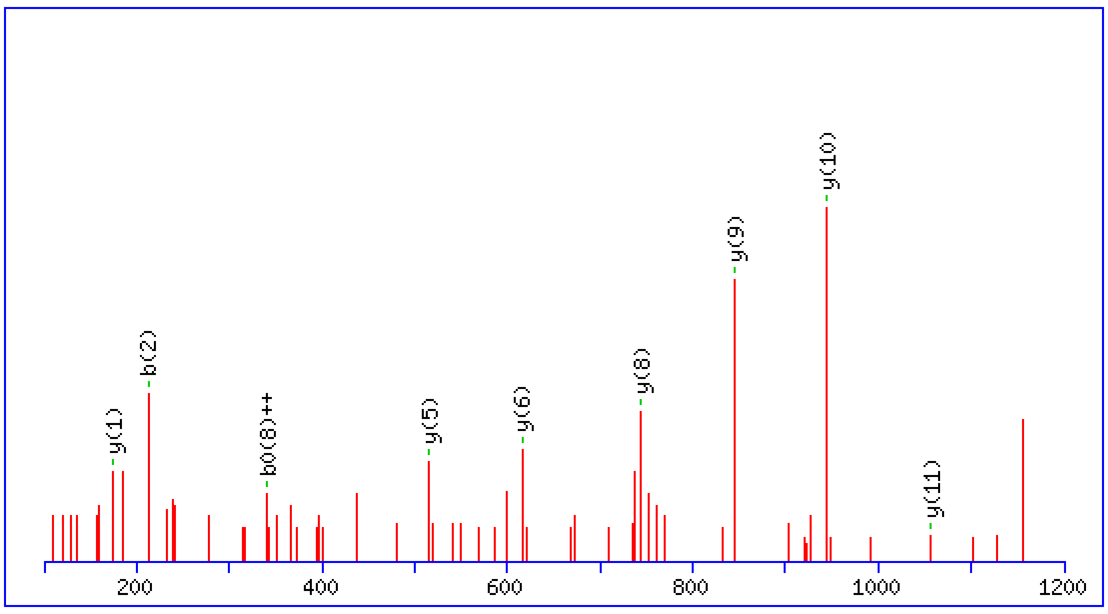
Mascot Search Results

Peptide View

MS/MS Fragmentation of VLVTGATGLLGR
Found in MAT2B_HUMAN, Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1

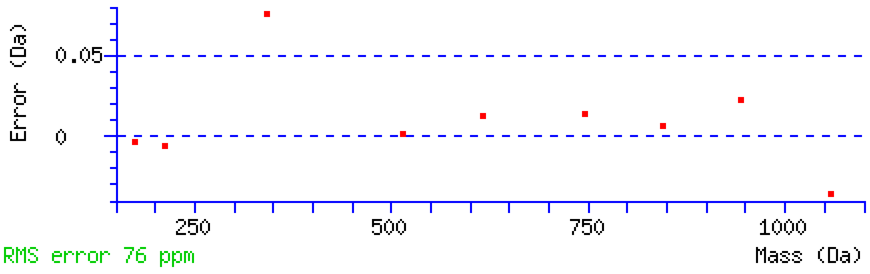
Match to Query 21808: 1155.700808 from(578.857680,2+) rtinseconds(2693) index(32229)
Title: Locus:1.1.1.2611.24
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

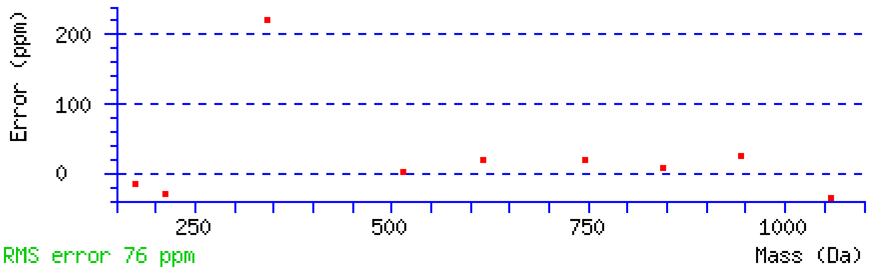
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1155.697571
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 8.6e-006
Matches : 9/94 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	213.159754	107.083515			L	*1057.636422*	529.321849	1040.609873	520.808575	1039.625857	520.316567	11
3	312.228168	156.617722			V	*944.552358*	472.779817	927.525809	464.266543	926.541793	463.774535	10
4	413.275847	207.141561	395.265282	198.136279	T	*845.483944*	423.245610	828.457395	414.732336	827.473379	414.240328	9
5	470.297311	235.652293	452.286746	226.647011	G	*744.436265*	372.721771	727.409716	364.208496	726.425700	363.716488	8
6	541.334425	271.170851	523.323860	262.165568	A	687.414801	344.211039	670.388252	335.697764	669.404236	335.205756	7
7	642.382104	321.694690	624.371539	312.689408	T	*616.377687*	308.692482	599.351138	300.179207	598.367122	299.687199	6
8	699.403568	350.205422	681.393003	341.200140	G	*515.330008*	258.168642	498.303459	249.655368			5
9	812.487632	406.747454	794.477067	397.742172	L	458.308544	229.657910	441.281995	221.144635			4
10	925.571696	463.289486	907.561131	454.284204	L	345.224480	173.115878	328.197931	164.602603			3
11	982.593160	491.800218	964.582595	482.794936	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 VLVTGATGLLGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	1155.697571	0.003237	VLVTGATGLLGR
14.7	1155.697540	0.003268	VLLQSALSLGR
6.1	1155.691010	0.009798	VLLRQQLMR
2.0	1155.708771	-0.007963	VLTLLQARSR

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

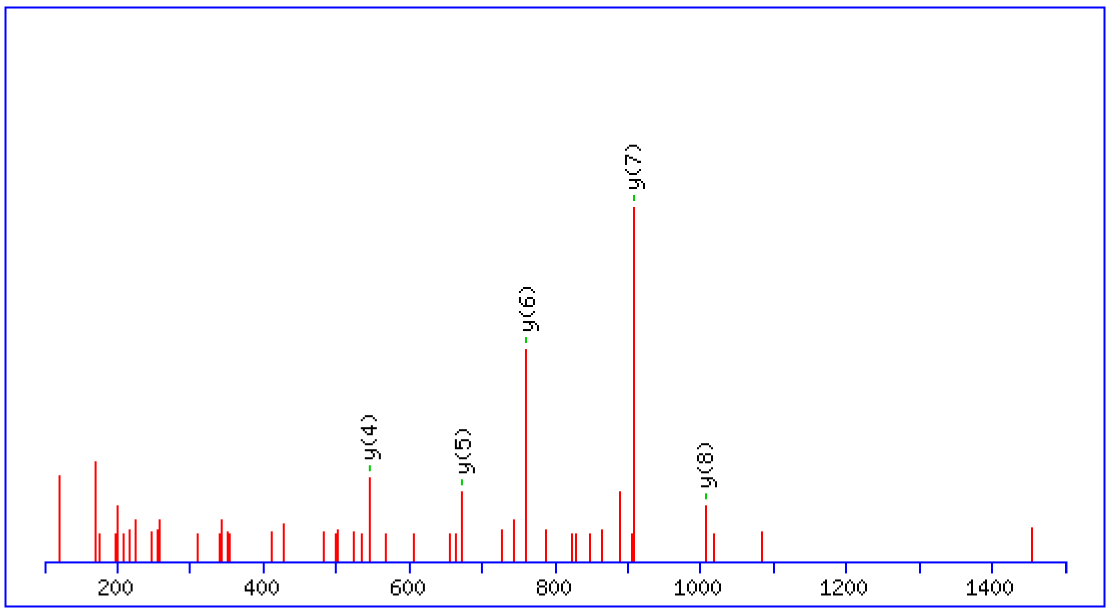
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVFSQQELR**
Found in **MSRB3_HUMAN**, Methionine-R-sulfoxide reductase B3 OS=Homo sapiens GN=MSRB3 PE=1 SV=2

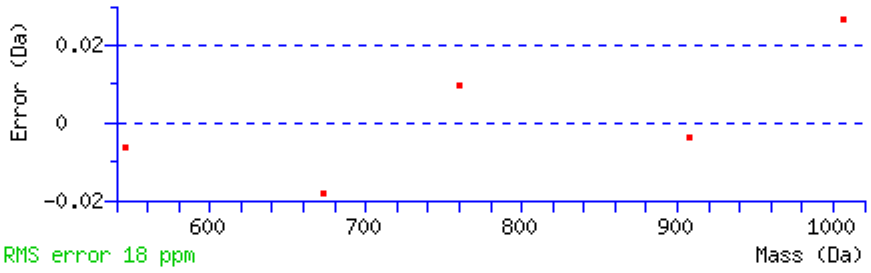
Match to Query 12526: 1104.591568 from(553.303060,2+) rtinseconds(2081) index(11928)
Title: Locus:1.1.1.2304.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

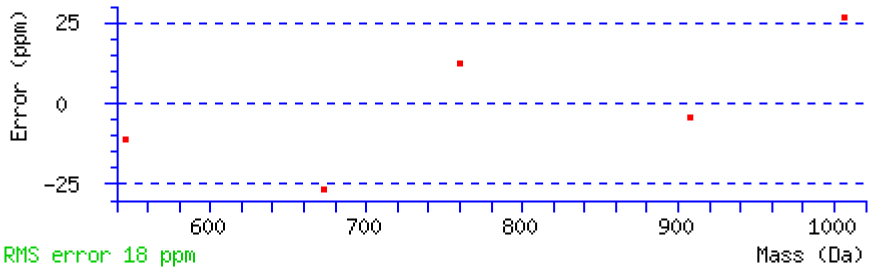
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1104.592758
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.012
Matches : 5/78 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	199.144104	100.075690					V	***1006.531621***	503.769449	989.505072	495.256174	988.521056	494.764166	8
3	346.212518	173.609897					F	***907.463207***	454.235242	890.436658	445.721967	889.452642	445.229959	7
4	433.244546	217.125911			415.233981	208.120628	S	***760.394793***	380.701035	743.368244	372.187760	742.384228	371.695752	6
5	561.303124	281.155200	544.276575	272.641926	543.292559	272.149918	Q	***673.362765***	337.185021	656.336216	328.671746	655.352200	328.179738	5
6	689.361702	345.184489	672.335153	336.671215	671.351137	336.179207	Q	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	4
7	818.404295	409.705786	801.377746	401.192511	800.393730	400.700503	E	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
8	931.488359	466.247818	914.461810	457.734543	913.477794	457.242535	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 VVFSQQELR
(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	1104.592758	-0.001190	VVFSQQELR
10.5	1104.584885	0.006683	TPMSVEIKGK

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

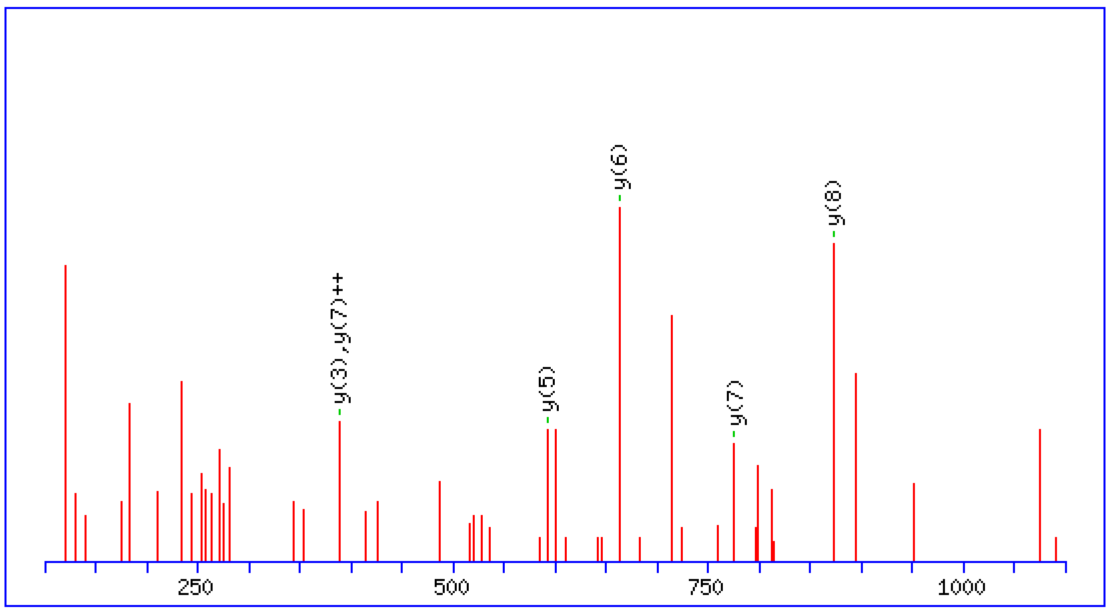
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSPIAGFLQK**
Found in **MCEE_HUMAN**, Methylmalonyl-CoA epimerase, mitochondrial OS=Homo sapiens GN=MCEE PE=1 SV=1

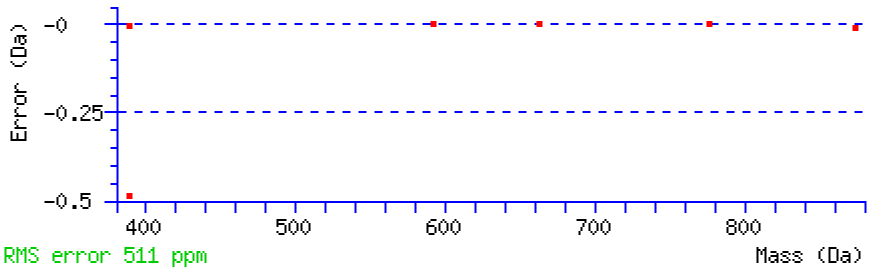
Match to Query 11538: 1074.575748 from(538.295150,2+) rtinseconds(2963) index(23540)
Title: Locus:1.1.1.2638.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

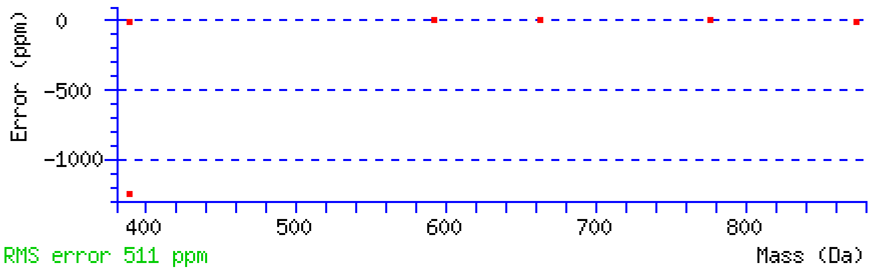
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1074.570953
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.012
Matches : 6/76 fragment ions using 9 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							10
2	203.066247	102.036761			185.055682	93.031479	S	960.551294	480.779285	943.524745	472.266010	942.540729	471.774002	9
3	300.119011	150.563143			282.108446	141.557861	P	***873.519266***	437.263271	856.492717	428.749997			8
4	413.203075	207.105175			395.192510	198.099893	I	***776.466502***	388.736889	759.439953	380.223615			7
5	484.240189	242.623732			466.229624	233.618450	A	***663.382438***	332.194857	646.355889	323.681582			6
6	541.261653	271.134465			523.251088	262.129182	G	***592.345324***	296.676300	575.318775	288.163026			5
7	688.330067	344.668672			670.319502	335.663389	F	535.323860	268.165568	518.297311	259.652293			4
8	801.414131	401.210704			783.403566	392.205421	L	***388.255446***	194.631361	371.228897	186.118086			3
9	929.472709	465.239993	912.446160	456.726718	911.462144	456.234710	Q	275.171382	138.089329	258.144833	129.576054			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of DSPIAGFLQK
(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	1074.570953	0.004795	DSPIAGFLQK
21.4	1074.566925	0.008823	ELGIKTDGSR
4.6	1074.585541	-0.009793	MLTINPSKR
4.3	1074.585541	-0.009793	MLTINPAKR
3.7	1074.566925	0.008823	IVSLDSANTR
1.8	1074.582169	-0.006421	WILSASKDR

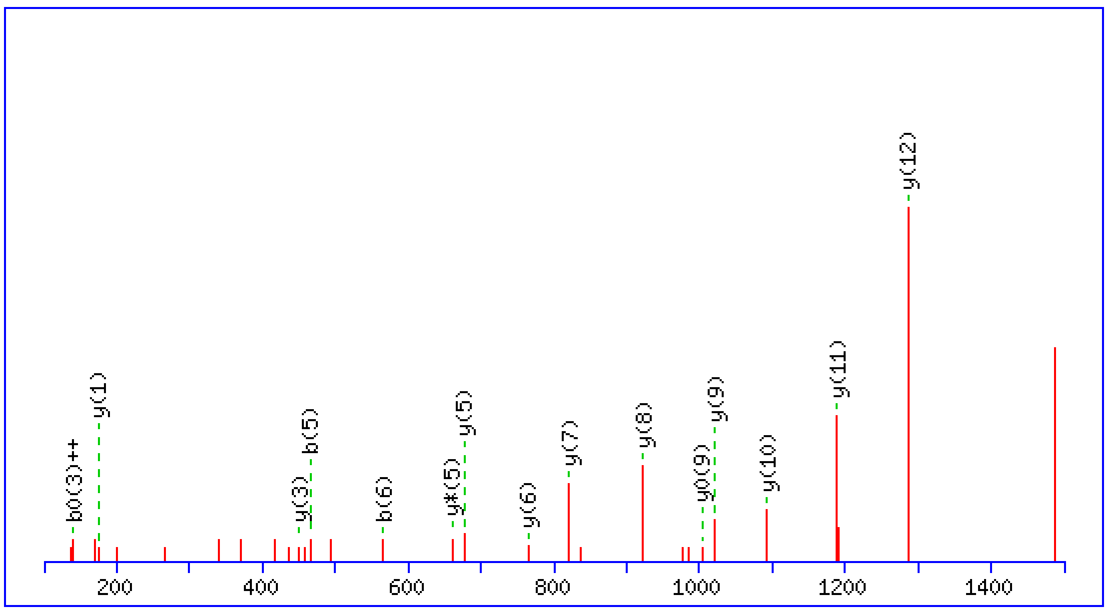
{MATRIX SCIENCE} Mascot Search Results

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

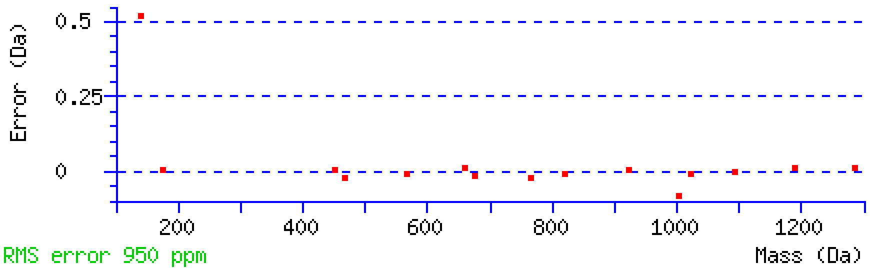
Match to Query 26218: 1485.751008 from(743.882780,2+) rtinseconds(2213) index(13780)
Title: Locus:1.1.1.2366.46
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

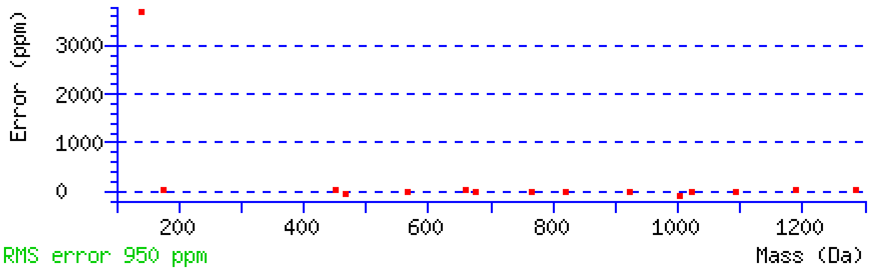
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1485.746368
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 2.7e-007
Matches : 15/126 fragment ions using 28 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
71.5	1485.746368	0.004640	VTPPAVTGSPEFER
1.4	1485.742340	0.008668	LSPSPTTEDPRVR
0.1	1485.743668	0.007340	SPLTQHFQNSRR

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

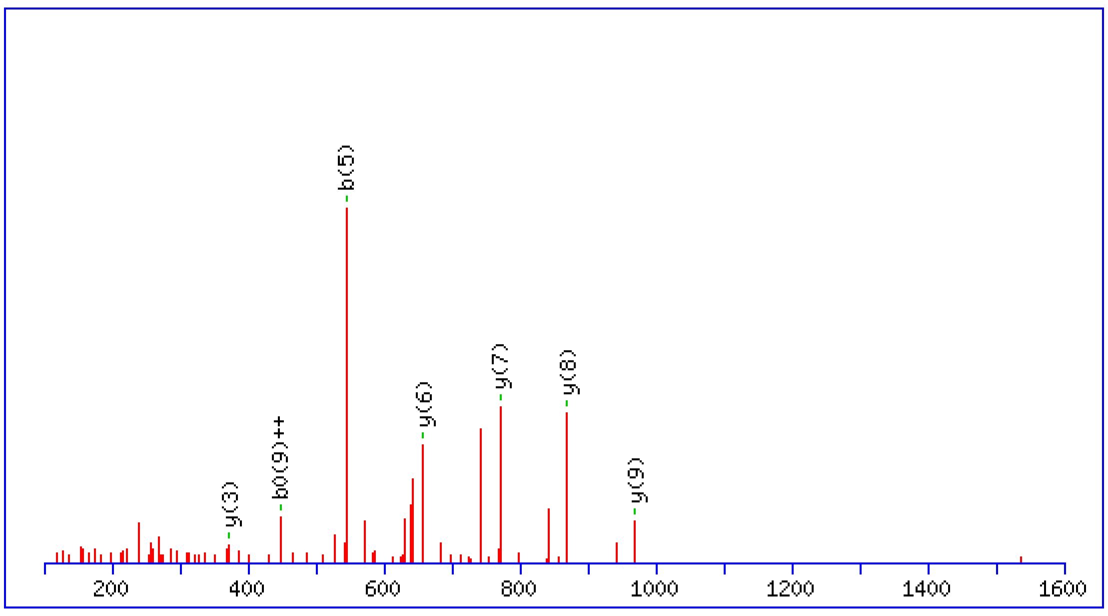
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEPSLVVPGIDLPK**
Found in **MAP2_HUMAN**, Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4

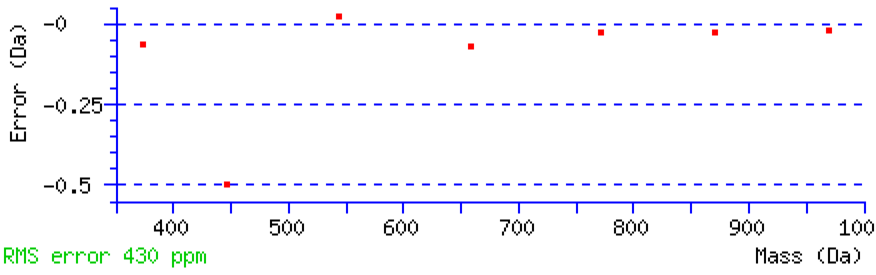
Match to Query 656679: 1511.807232 from(504.943020,3+) rtinseconds(1534) index(642481)
Title: Locus:1.1.1.773.17
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

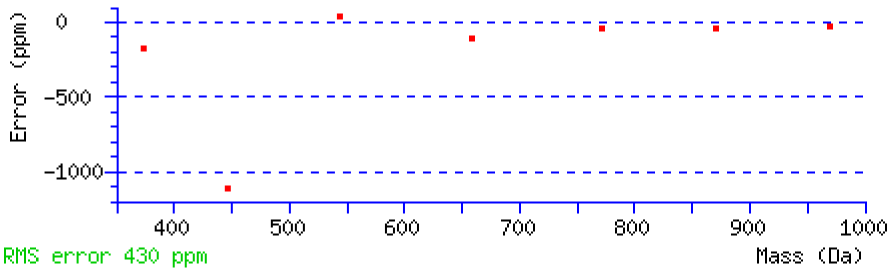
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1511.808304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
P8      : Oxidation (P)
P13     : Oxidation (P)
Ions Score: 30  Expect: 0.01
Matches : 7/124 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							14
2	231.097548	116.052412	213.086983	107.047130	E	1411.767889	706.387583	1394.741340	697.874308	1393.757324	697.382300	13
3	344.145227	172.576252	326.134662	163.570969	P	1282.725296	641.866286	1265.698747	633.353011	1264.714731	632.861003	12
4	431.177255	216.092266	413.166690	207.086983	S	1169.677617	585.342447	1152.651068	576.829172	1151.667052	576.337164	11
5	544.261319	272.634298	526.250754	263.629015	L	1082.645589	541.826433	1065.619040	533.313158	1064.635024	532.821150	10
6	643.329733	322.168505	625.319168	313.163222	V	***969.561525***	485.284401	952.534976	476.771126	951.550960	476.279118	9
7	742.398147	371.702712	724.387582	362.697429	V	***870.493111***	435.750194	853.466562	427.236919	852.482546	426.744911	8
8	855.445826	428.226551	837.435261	419.221269	P	***771.424697***	386.215987	754.398148	377.702712	753.414132	377.210704	7
9	912.467290	456.737283	894.456725	447.732001	G	***658.377018***	329.692147	641.350469	321.178873	640.366453	320.686865	6
10	1025.551354	513.279315	1007.540789	504.274032	I	601.355554	301.181415	584.329005	292.668140	583.344989	292.176132	5
11	1140.578297	570.792787	1122.567732	561.787504	D	488.271490	244.639383	471.244941	236.126108	470.260925	235.634100	4
12	1253.662361	627.334818	1235.651796	618.329536	L	***373.244547***	187.125911	356.217998	178.612637			3
13	1366.710040	683.858658	1348.699475	674.853375	P	260.160483	130.583879	243.133934	122.070605			2
14					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TEPSLVVPGIDLPK
(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	1511.808304	-0.001072	TEPSLVVPGIDLPK
9.3	1511.809662	-0.002430	GPFPLQVVSVGGPAR
4.1	1511.794342	0.012890	ELEGILLPSDRDR
3.5	1511.820847	-0.013615	GWTRALGPEQLLR
2.7	1511.819504	-0.012272	ELSTPDKVLIPER
1.6	1511.798401	0.008831	SGPLGDQPFAGLLPK
1.0	1511.820816	-0.013584	IDNLYERALHIR

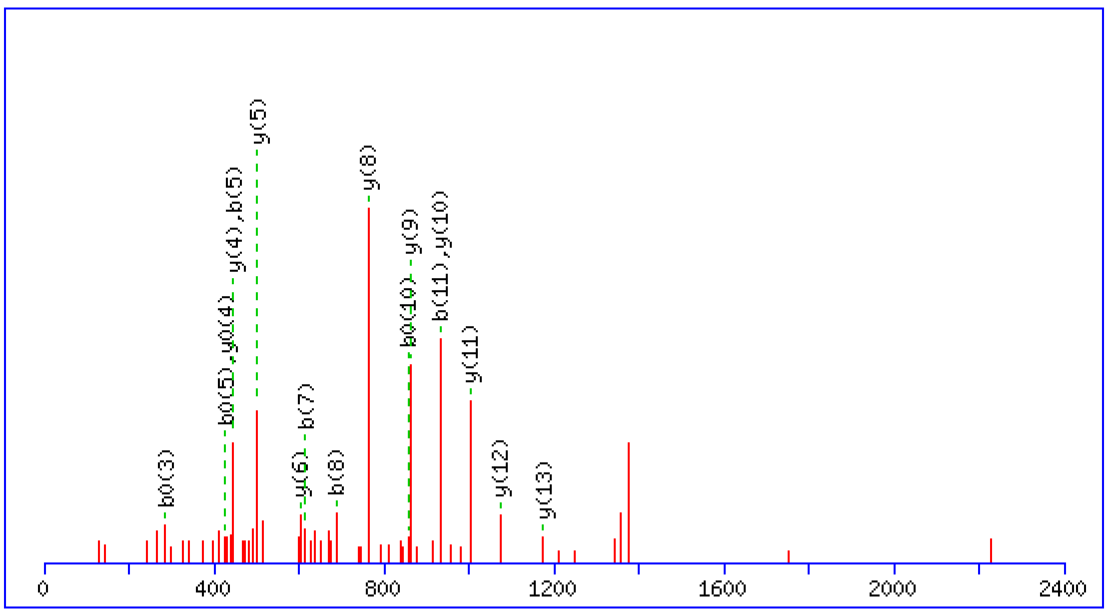
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTTAAAVASTGPSSR**
Found in **MAP4_HUMAN**, Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3

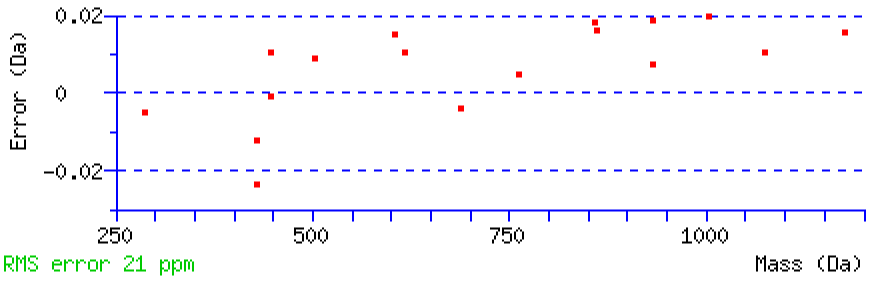
Match to Query 25810: 1376.696888 from(689.355720,2+) rtinseconds(1159) index(6836)
Title: Locus:1.1.1.1952.41
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-1.mgf

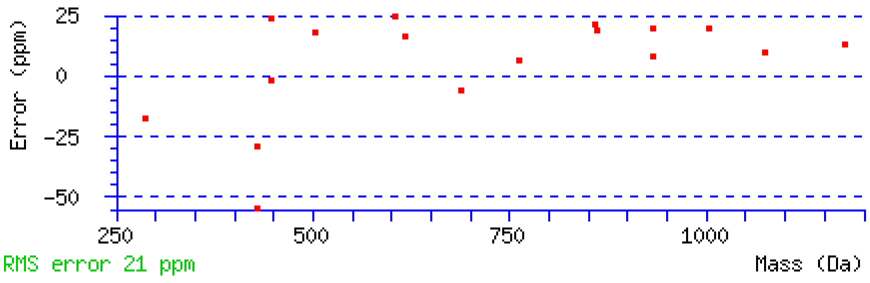
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1376.689575
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 71 **Expect:** 8.2e-007
Matches : 17/138 fragment ions using 24 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	203.102634	102.054955	185.092069	93.049672	T	1276.649171	638.828224	1259.622622	630.314949	1258.638606	629.822941	14
3	304.150313	152.578794	286.139748	143.573512	T	***1175.601492***	588.304384	1158.574943	579.791110	1157.590927	579.299102	13
4	375.187427	188.097352	357.176862	179.092069	A	***1074.553813***	537.780545	1057.527264	529.267270	1056.543248	528.775262	12
5	**446.224541**	223.615908	428.213976	214.610626	A	***1003.516699***	502.261988	986.490150	493.748713	985.506134	493.256705	11
6	517.261655	259.134466	499.251090	250.129183	A	***932.479585***	466.743431	915.453036	458.230156	914.469020	457.738148	10
7	**616.330069**	308.668673	598.319504	299.663390	V	***861.442471***	431.224874	844.415922	422.711599	843.431906	422.219591	9
8	**687.367183**	344.187230	669.356618	335.181947	A	***762.374057***	381.690667	745.347508	373.177392	744.363492	372.685384	8
9	774.399211	387.703243	756.388646	378.697961	S	691.336943	346.172110	674.310394	337.658835	673.326378	337.166827	7
10	875.446890	438.227083	857.436325	429.221800	T	***604.304915***	302.656096	587.278366	294.142821	586.294350	293.650813	6
11	**932.468354**	466.737815	914.457789	457.732532	G	***503.257236***	252.132256	486.230687	243.618982	485.246671	243.126974	5
12	1029.521118	515.264197	1011.510553	506.258914	P	***446.235772***	223.621524	429.209223	215.108250	428.225207	214.616242	4
13	1116.553146	558.780211	1098.542581	549.774928	S	349.183008	175.095142	332.156459	166.581868	331.172443	166.089860	3
14	1203.585174	602.296225	1185.574609	593.290943	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
15					R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.6	1376.689575	0.007313	TTTAAAVASTGPSSR
5.4	1376.690399	0.006489	SLCCRNLAVEK
3.9	1376.693573	0.003315	SRELEFVEQPK
2.6	1376.700790	-0.003902	TKPSSSSRQLDR
0.7	1376.685684	0.011204	LMELLEEISER

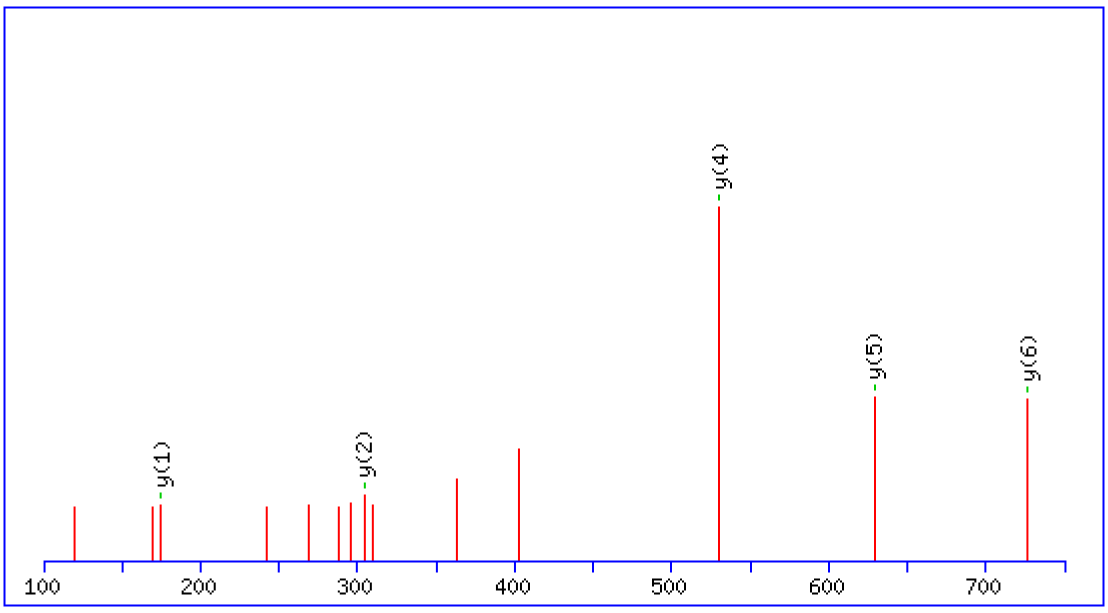
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPVIIER**
Found in **MLP3A_HUMAN**, Microtubule-associated proteins 1A/1B light chain 3A OS=Homo sapiens GN=MAP1LC3A PE=1 SV=2

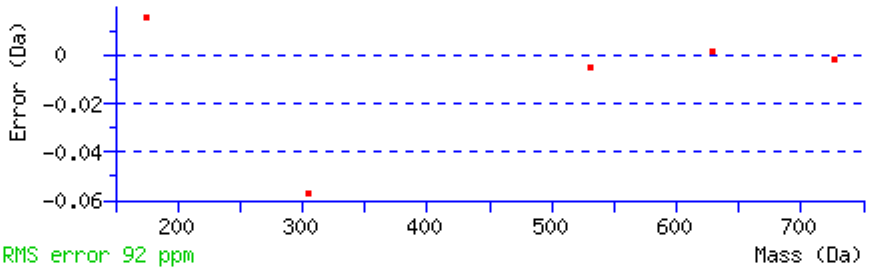
Match to Query 2250: 838.528868 from(420.271710,2+) rtinseconds(2190) index(16214)
Title: Locus:1.1.1.2332.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

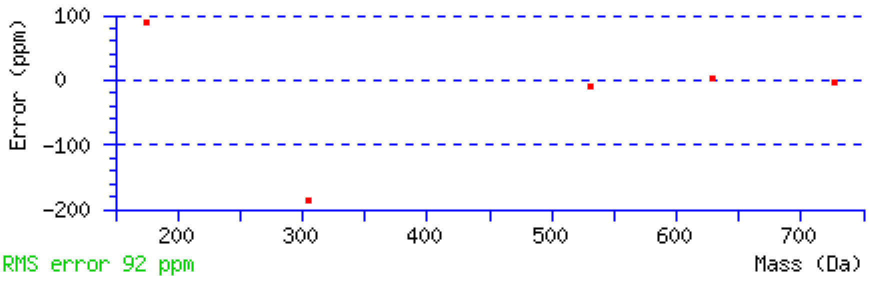
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 838.527618
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 1.5e-005
Matches : 5/48 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	211.144104	106.075690			P	726.450851	363.729064	709.424302	355.215789	708.440286	354.723781	6
3	310.212518	155.609897			V	629.398087	315.202682	612.371538	306.689407	611.387522	306.197399	5
4	423.296582	212.151929			I	530.329673	265.668475	513.303124	257.155200	512.319108	256.663192	4
5	536.380646	268.693961			I	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	665.423239	333.215258	647.412674	324.209975	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 IPVIIER
(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	838.527618	0.001250	IPVIIER
5.5	838.527618	0.001250	LLDPLLR
5.5	838.527618	0.001250	LLPEVLR
1.2	838.527618	0.001250	LPAVSKPK
1.2	838.527618	0.001250	LPKPPKK

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

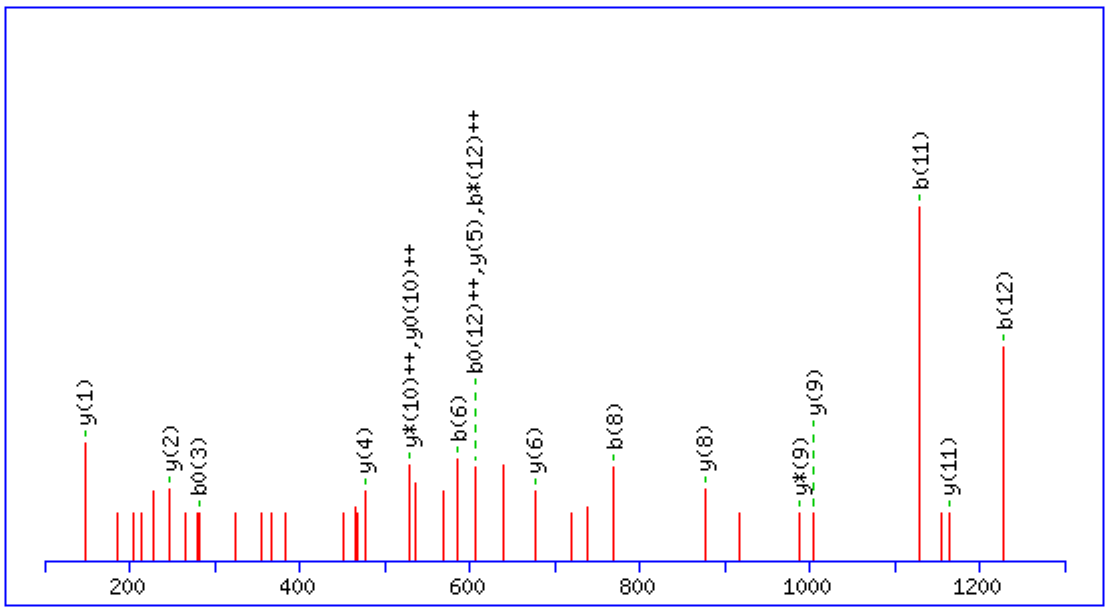
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVSAQSLAEDDVE**
Found in **TOM20_HUMAN**, Mitochondrial import receptor subunit TOM20 homolog OS=Homo sapiens GN=TOMM20 PE=1 SV=1

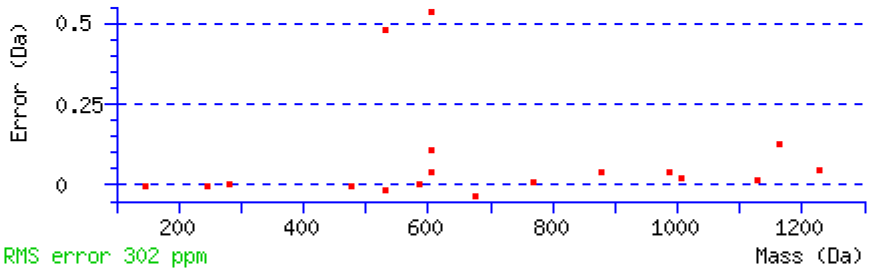
Match to Query 24068: 1374.655448 from(688.335000,2+) rtinseconds(2514) index(18898)
Title: Locus:1.1.1.2480.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

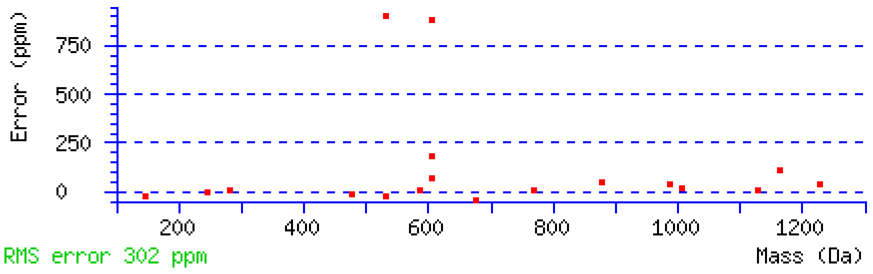
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1374.651443
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52   Expect: 0.0001
Matches : 18/116 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					I							13
2	213.159754	107.083515					V	1262.574667	631.790972	1245.548118	623.277697	1244.564102	622.785689	12
3	300.191782	150.599529			282.181217	141.594247	S	***1163.506253***	582.256765	1146.479704	573.743490	1145.495688	573.251482	11
4	371.228896	186.118086			353.218331	177.112804	A	1076.474225	538.740751	1059.447676	530.227476	1058.463660	529.735468	10
5	499.287474	250.147375	482.260925	241.634101	481.276909	241.142093	Q	***1005.437111***	503.222194	988.410562	494.708919	987.426546	494.216911	9
6	**586.319502**	293.663389	569.292953	285.150115	568.308937	284.658107	S	***877.378533***	439.192905			859.367968	430.187622	8
7	699.403566	350.205421	682.377017	341.692147	681.393001	341.200139	L	790.346505	395.676891			772.335940	386.671608	7
8	**770.440680**	385.723978	753.414131	377.210704	752.430115	376.718696	A	***677.262441***	339.134859			659.251876	330.129576	6
9	899.483273	450.245275	882.456724	441.732000	881.472708	441.239992	E	***606.225327***	303.616302			588.214762	294.611019	5
10	1014.510216	507.758746	997.483667	499.245472	996.499651	498.753464	D	***477.182734***	239.095005			459.172169	230.089723	4
11	**1129.537159**	565.272218	1112.510610	556.758943	1111.526594	556.266935	D	362.155791	181.581534			344.145226	172.576251	3
12	**1228.605573**	614.806425	1211.579024	606.293150	1210.595008	605.801142	V	***247.128848***	124.068062			229.118283	115.062780	2
13							E	***148.060434***	74.533855			130.049869	65.528573	1





NCBI **BLAST** search of IVSAQSLAEDDVE
(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	1374.651443	0.004005	IVSAQSLAEDDVE

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

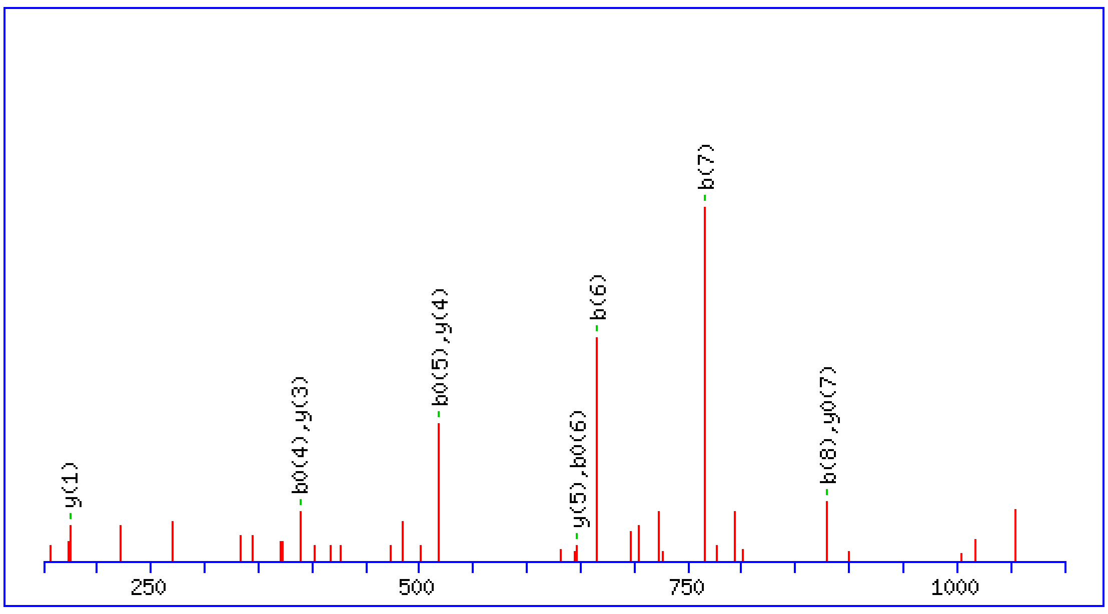
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVYSEETLR**
Found in **IMMT_HUMAN**, Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1

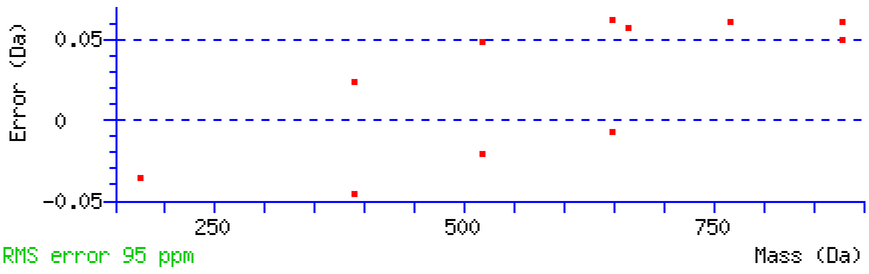
Match to Query 14203: 1052.524048 from(527.269300,2+) rtinseconds(1667) index(10201)
Title: Locus:1.1.1.2445.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

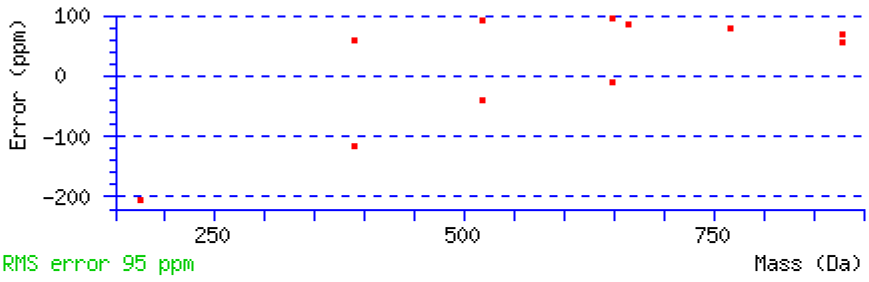
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1052.513824
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0038
Matches : 11/70 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							9
2	157.097154	79.052215			V	996.499652	498.753464	979.473103	490.240190	978.489087	489.748182	8
3	320.160483	160.583879			Y	897.431238	449.219257	880.404689	440.705983	879.420673	440.213975	7
4	407.192511	204.099894	389.181946	195.094611	S	734.367909	367.687593	717.341360	359.174318	716.357344	358.682310	6
5	536.235104	268.621190	518.224539	259.615908	E	***647.335881***	324.171579	630.309332	315.658304	629.325316	315.166296	5
6	**665.277697**	333.142487	647.267132	324.137204	E	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
7	**766.325376**	383.666326	748.314811	374.661044	T	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
8	**879.409440**	440.208358	861.398875	431.203076	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 GVYSEETLR
(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	1052.513824	0.010224	GVYSEETLR
20.8	1052.518082	0.005966	MVGTVIMMR
20.8	1052.518082	0.005966	MVGTVIMMR
14.8	1052.525101	-0.001053	GDPGVGLPGPR
11.6	1052.524567	-0.000519	KMLEEIMK
11.4	1052.517868	0.006180	SSVDPAIFAF
11.2	1052.525070	-0.001022	EEVIHGDVR
11.2	1052.532440	-0.008392	MPKEYITR
11.2	1052.532440	-0.008392	MPKEYITR
11.1	1052.532425	-0.008377	CGKAYAELK

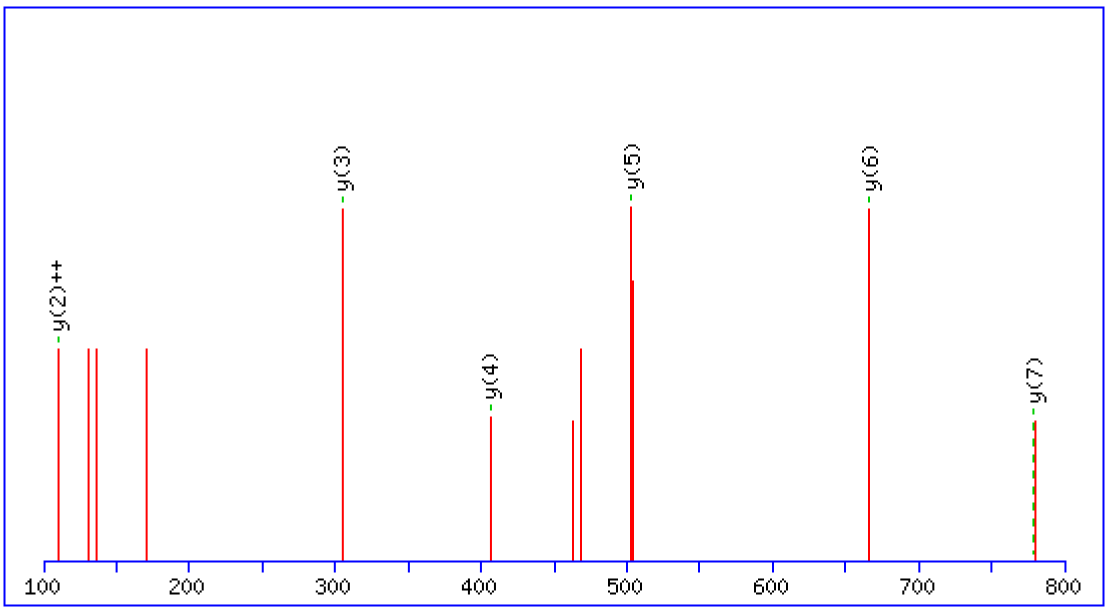
{MATRIX SCIENCE} Mascot Search Results

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

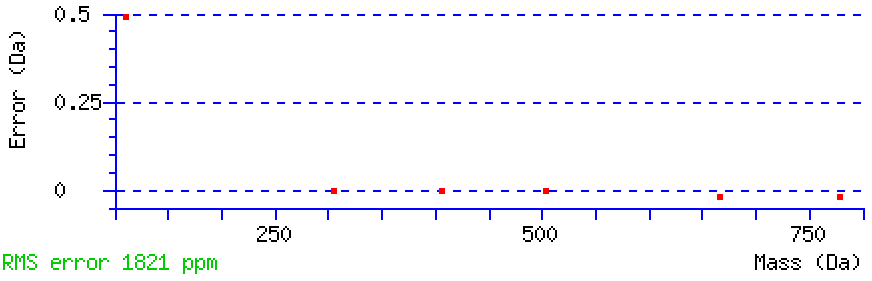
Match to Query 8289: 936.486768 from(469.250660,2+) rtinseconds(1347) index(7184)
Title: Locus:1.1.1.2011.14
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

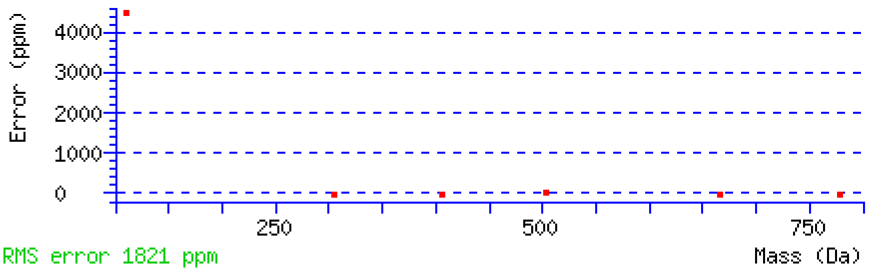
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 936.491623
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 8.3e-005
Matches : 6/76 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							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
46.3	936.491623	-0.004855	SAIYPTSAK
2.6	936.485123	0.001645	MAPVPPGPR
1.5	936.491653	-0.004885	TGISDVFAK
1.1	936.485107	0.001661	ASLPHGPMK
0.5	936.491623	-0.004855	SKIPYDAK

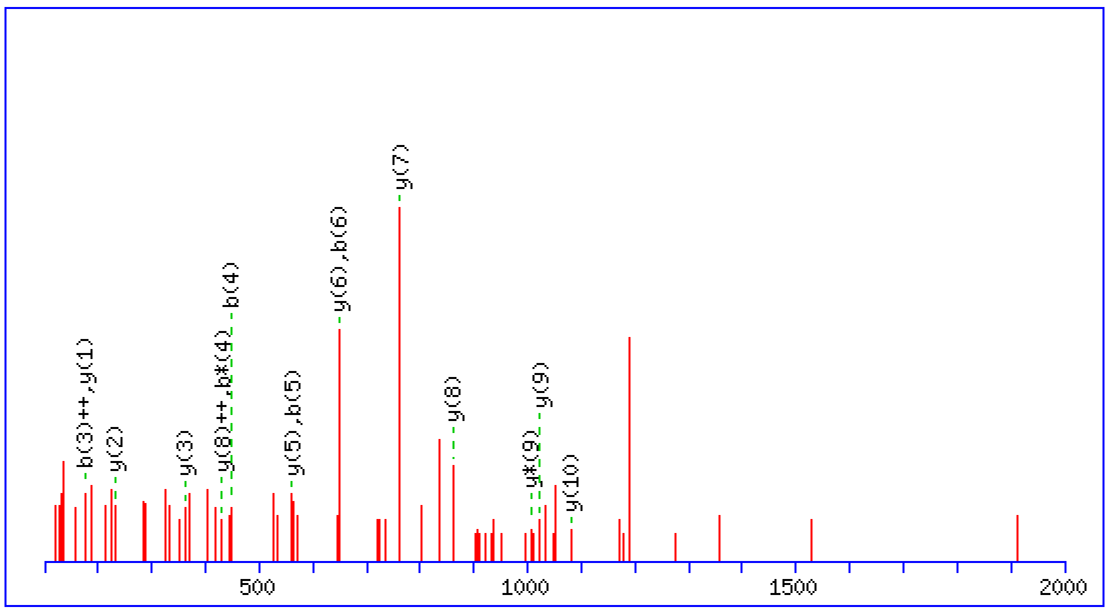
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGYVLSSIEGR**
Found in **BUB3_HUMAN**, Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1

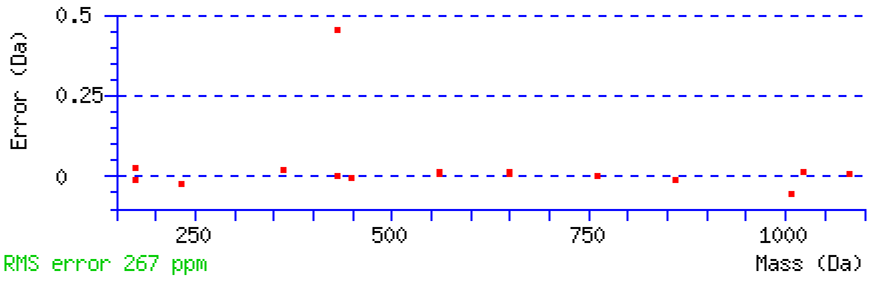
Match to Query 24749: 1207.610768 from(604.812660,2+) rtinseconds(2371) index(27327)
Title: Locus:1.1.1.2302.30
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

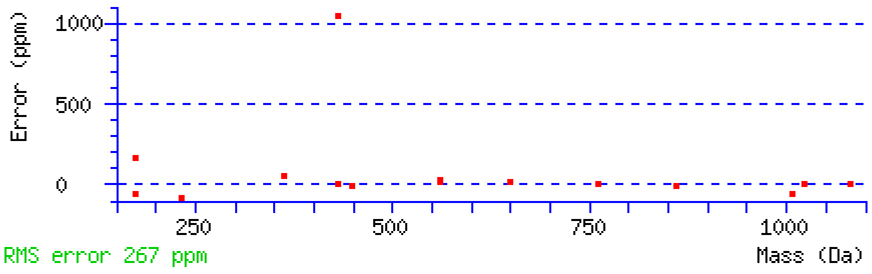
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1207.619690
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0019
Matches : 16/106 fragment ions using 47 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	186.087318	93.547297	169.060769	85.034023			G	***1080.568400***	540.787838	1063.541851	532.274564	1062.557835	531.782555	10
3	349.150647	175.078961	332.124098	166.565687			Y	***1023.546936***	512.277106	1006.520387	503.763831	1005.536371	503.271823	9
4	**448.219061**	224.613169	431.192512	216.099894			V	***860.483607***	430.745442	843.457058	422.232167	842.473042	421.740159	8
5	**561.303125**	281.155201	544.276576	272.641926			L	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	7
6	**648.335153**	324.671215	631.308604	316.157940	630.324588	315.665932	S	***648.331129***	324.669203	631.304580	316.155928	630.320564	315.663920	6
7	735.367181	368.187229	718.340632	359.673954	717.356616	359.181946	S	***561.299101***	281.153189	544.272552	272.639914	543.288536	272.147906	5
8	848.451245	424.729261	831.424696	416.215986	830.440680	415.723978	I	474.267073	237.637174	457.240524	229.123900	456.256508	228.631892	4
9	977.493838	489.250557	960.467289	480.737282	959.483273	480.245274	E	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
10	1034.515302	517.761289	1017.488753	509.248015	1016.504737	508.756007	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 QGYVLSSIEGR
(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	1207.619690	-0.008922	QGYVLSSIEGR
9.5	1207.608475	0.002293	ASVQFDITPSK
4.4	1207.613159	-0.002391	CEAPPVPPRR
3.8	1207.605774	0.004994	SDSLSPPRHGR
1.6	1207.605759	0.005009	QASAFSRASQR

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

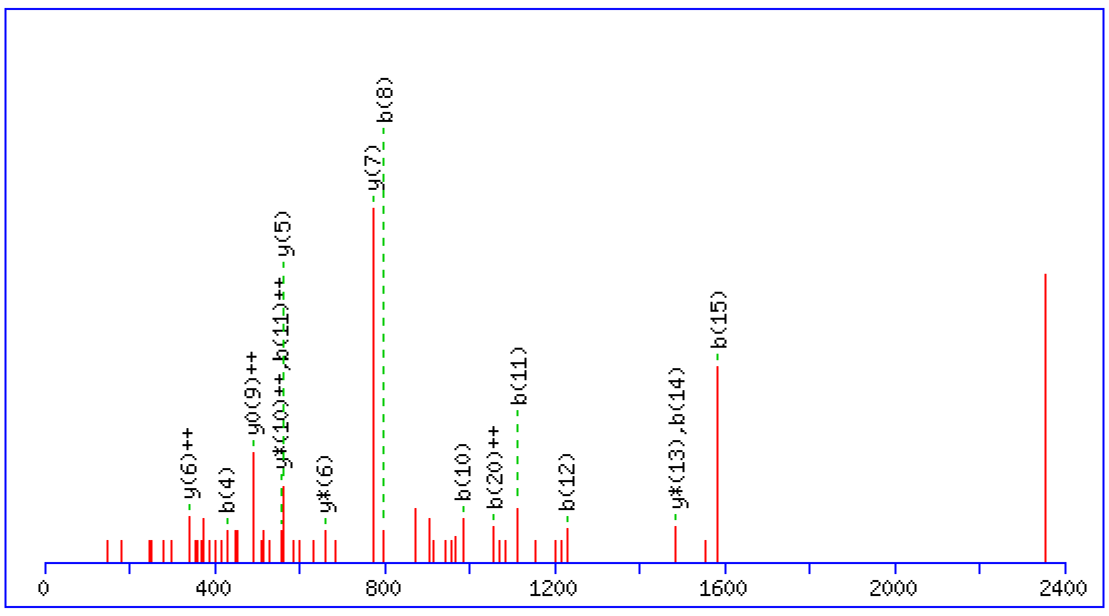
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGERPVTAGEEDEQVPDSIDAR**
Found in **MIP18_HUMAN**, Mitotic spindle-associated MMXD complex subunit MIP18 OS=Homo sapiens GN=FAM96B PE=1 SV=1

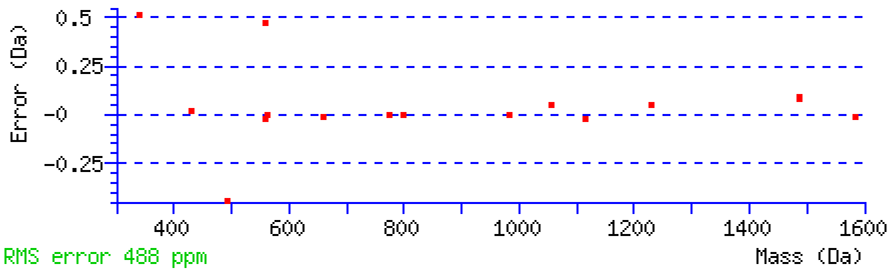
Match to Query 31576: 2356.064322 from(786.362050,3+) rtinseconds(1937) index(11805)
Title: Locus:1.1.1.2235.46
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

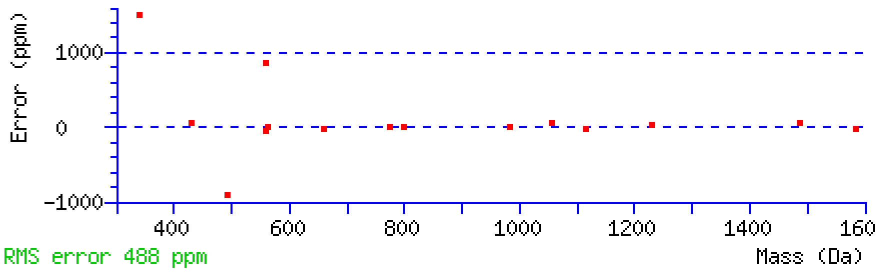
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2356.077866
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0013
Matches : 16/242 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							22
2	145.060768	73.034022			127.050203	64.028740	G	2270.053125	1135.530200	2253.026576	1127.016926	2252.042560	1126.524918	21
3	274.103361	137.555319			256.092796	128.550036	E	2213.031661	1107.019468	2196.005112	1098.506194	2195.021096	1098.014186	20
4	***430.204472***	215.605874	413.177923	207.092600	412.193907	206.600592	R	2083.989068	1042.498172	2066.962519	1033.984897	2065.978503	1033.492889	19
5	527.257236	264.132256	510.230687	255.618982	509.246671	255.126974	P	1927.887957	964.447617	1910.861408	955.934342	1909.877392	955.442334	18
6	626.325650	313.666463	609.299101	305.153189	608.315085	304.661181	V	1830.835193	915.921235	1813.808644	907.407960	1812.824628	906.915952	17
7	727.373329	364.190303	710.346780	355.677028	709.362764	355.185020	T	1731.766779	866.387028	1714.740230	857.873753	1713.756214	857.381745	16
8	***798.410443***	399.708860	781.383894	391.195585	780.399878	390.703577	A	1630.719100	815.863188	1613.692551	807.349914	1612.708535	806.857906	15
9	855.431907	428.219592	838.405358	419.706317	837.421342	419.214309	G	1559.681986	780.344631	1542.655437	771.831357	1541.671421	771.339349	14
10	***984.474500***	492.740888	967.447951	484.227614	966.463935	483.735606	E	1502.660522	751.833899	1485.633973	743.320625	1484.649957	742.828617	13
11	***1113.517093***	557.262185	1096.490544	548.748910	1095.506528	548.256902	E	1373.617929	687.312603	1356.591380	678.799328	1355.607364	678.307320	12
12	***1228.544036***	614.775656	1211.517487	606.262382	1210.533471	605.770374	D	1244.575336	622.791306	1227.548787	614.278032	1226.564771	613.786024	11
13	1357.586629	679.296953	1340.560080	670.783678	1339.576064	670.291670	E	1129.548393	565.277835	1112.521844	556.764560	1111.537828	556.272552	10
14	***1485.645207***	743.326242	1468.618658	734.812967	1467.634642	734.320959	Q	1000.505800	500.756538	983.479251	492.243264	982.495235	491.751256	9
15	***1584.713621***	792.860449	1567.687072	784.347174	1566.703056	783.855166	V	872.447222	436.727249	855.420673	428.213975	854.436657	427.721967	8
16	1681.766385	841.386831	1664.739836	832.873556	1663.755820	832.381548	P	**773.378808**	387.193042	756.352259	378.679768	755.368243	378.187760	7
17	1796.793328	898.900302	1779.766779	890.387028	1778.782763	889.895020	D	676.326044	338.666660	659.299495	330.153386	658.315479	329.661378	6
18	1883.825356	942.416316	1866.798807	933.903042	1865.814791	933.411034	S	**561.299101**	281.153189	544.272552	272.639914	543.288536	272.147906	5
19	1996.909420	998.958348	1979.882871	990.445074	1978.898855	989.953066	I	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
20	2111.936363	1056.471820	2094.909814	1047.958545	2093.925798	1047.466537	D	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
21	2182.973477	1091.990377	2165.946928	1083.477102	2164.962912	1082.985094	A	246.156066	123.581671	229.129517	115.068397			2
22							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of SGERPVTAGEEDEQVPDSIDAR
(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	2356.077866	-0.013544	SGERPVTAGEEDEQVPDSIDAR
2.1	2356.066605	-0.002283	TSGLAGEPEGELSKEDHENTEK
0.4	2356.078690	-0.014368	LSENAFDLEAMSMLNRAQER
0.2	2356.042984	0.021338	TGESSYRACFSFHSSYSEIK

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

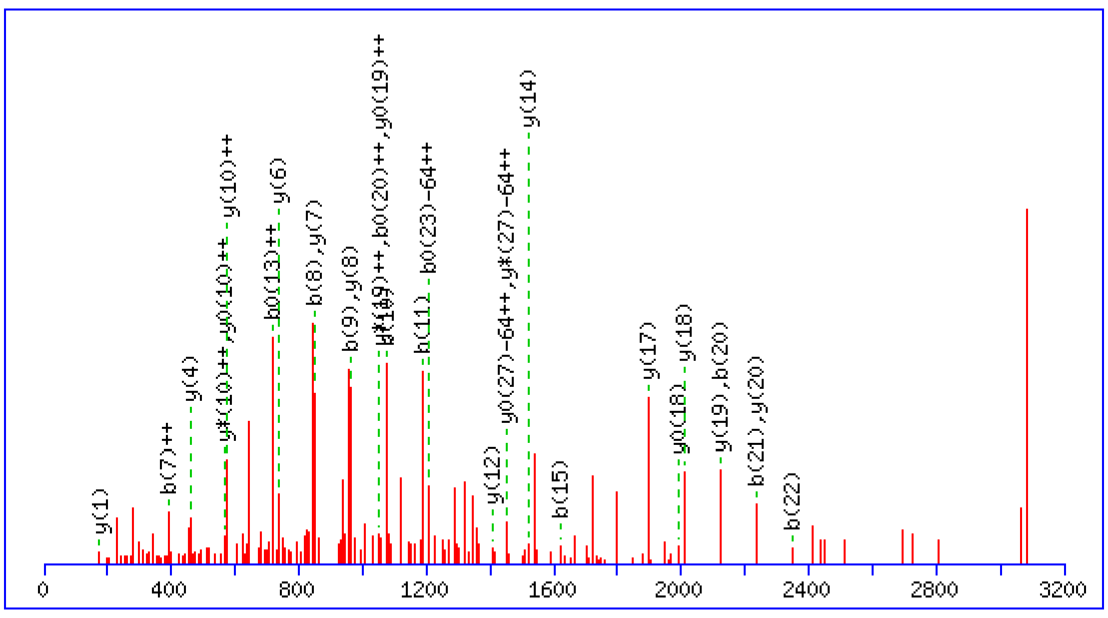
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFSALFIAILLFDIGGFPPSLLMEDVAR**
Found in **MOT9_HUMAN**, Monocarboxylate transporter 9 OS=Homo sapiens GN=SLC16A9 PE=2 SV=1

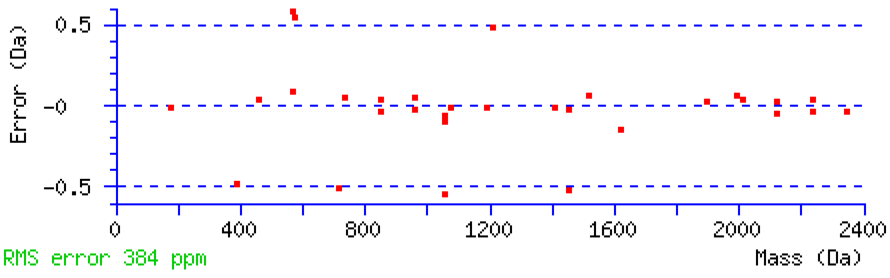
Match to Query 75507: 3082.648962 from(1028.556930,3+) rtinseconds(4848) index(76444)
Title: Locus:1.1.1.3369.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-1.mgf

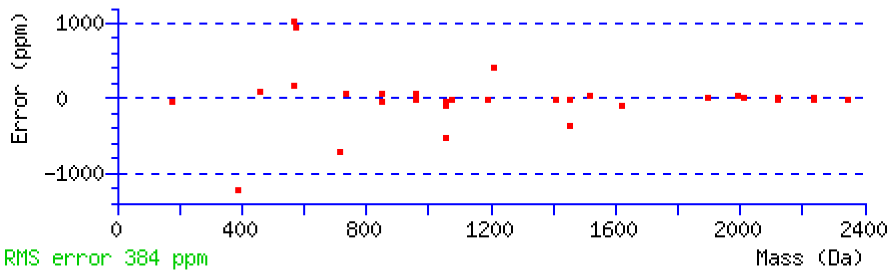
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3082.645325
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P18 : Oxidation (P)
M23 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 42 **Expect:** 0.00026
Matches : 31/412 fragment ions using 48 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							28
2	247.144104	124.075690			F	2984.584182	1492.795729	2967.557633	1484.282454	2966.573617	1483.790446	27
3	334.176132	167.591704	316.165567	158.586422	S	2837.515768	1419.261522	2820.489219	1410.748247	2819.505203	1410.256239	26
4	405.213246	203.110261	387.202681	194.104978	A	2750.483740	1375.745508	2733.457191	1367.232233	2732.473175	1366.740225	25
5	518.297310	259.652293	500.286745	250.647011	L	2679.446626	1340.226951	2662.420077	1331.713676	2661.436061	1331.221668	24
6	665.365724	333.186500	647.355159	324.181218	F	2566.362562	1283.684919	2549.336013	1275.171644	2548.351997	1274.679636	23
7	778.449788	389.728532	760.439223	380.723250	I	2419.294148	1210.150712	2402.267599	1201.637437	2401.283583	1201.145429	22
8	**849.486902**	425.247089	831.476337	416.241807	A	2306.210084	1153.608680	2289.183535	1145.095405	2288.199519	1144.603397	21
9	**962.570966**	481.789121	944.560401	472.783839	I	***2235.172970***	1118.090123	2218.146421	1109.576848	2217.162405	1109.084840	20
10	**1075.655030**	538.331153	1057.644465	529.325870	L	***2122.088906***	1061.548091	2105.062357	1053.034816	2104.078341	1052.542808	19
11	**1188.739094**	594.873185	1170.728529	585.867902	L	***2009.004842***	1005.006059	1991.978293	996.492785	1990.994277	996.000777	18
12	1335.807508	668.407392	1317.796943	659.402109	F	***1895.920778***	948.464027	1878.894229	939.950753	1877.910213	939.458745	17
13	1450.834451	725.920864	1432.823886	716.915581	D	1748.852364	874.929820	1731.825815	866.416546	1730.841799	865.924538	16
14	1563.918515	782.462895	1545.907950	773.457613	I	1633.825421	817.416349	1616.798872	808.903074	1615.814856	808.411066	15
15	**1620.939979**	810.973627	1602.929414	801.968345	G	***1520.741357***	760.874317	1503.714808	752.361042	1502.730792	751.869034	14
16	1677.961443	839.484359	1659.950878	830.479077	G	1463.719893	732.363585	1446.693344	723.850310	1445.709328	723.358302	13
17	1825.029857	913.018566	1807.019292	904.013284	F	***1406.698429***	703.852853	1389.671880	695.339578	1388.687864	694.847570	12
18	1938.077536	969.542406	1920.066971	960.537123	P	1259.630015	630.318646	1242.603466	621.805371	1241.619450	621.313363	11
19	2035.130300	1018.068788	2017.119735	1009.063505	P	1146.582336	573.794806	1129.555787	565.281532	1128.571771	564.789524	10
20	**2122.162328**	1061.584802	2104.151763	1052.579519	S	1049.529572	525.268424	1032.503023	516.755150	1031.519007	516.263142	9
21	**2235.246392**	1118.126834	2217.235827	1109.121551	L	***962.497544***	481.752410	945.470995	473.239136	944.486979	472.747128	8
22	**2348.330456**	1174.668866	2330.319891	1165.663583	L	***849.413480***	425.210378	832.386931	416.697104	831.402915	416.205096	7
23	2495.365856	1248.186566	2477.355291	1239.181283	M	***736.329416***	368.668346	719.302867	360.155072	718.318851	359.663064	6
24	2624.408449	1312.707862	2606.397884	1303.702580	E	589.294016	295.150646	572.267467	286.637372	571.283451	286.145364	5
25	2739.435392	1370.221334	2721.424827	1361.216051	D	***460.251423***	230.629349	443.224874	222.116075	442.240858	221.624067	4
26	2838.503806	1419.755541	2820.493241	1410.750258	V	345.224480	173.115878	328.197931	164.602603			3
27	2909.540920	1455.274098	2891.530355	1446.268815	A	246.156066	123.581671	229.129517	115.068397			2
28					R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VFSALFIAILLFDIGGFPPSLLMEDVAR
(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	3082.645325	0.003637	VFSALFIAILLFDIGGFPPSLLMEDVAR
40.0	3082.645325	0.003637	VFSALFIAILLFDIGGFPPSLLMEDVAR
20.4	3082.645325	0.003637	VFSALFIAILLFDIGGFPPSLLMEDVAR
3.6	3082.652283	-0.003321	EAASSAPALRPLGAAATSRAAPLAPLPAPSPR

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

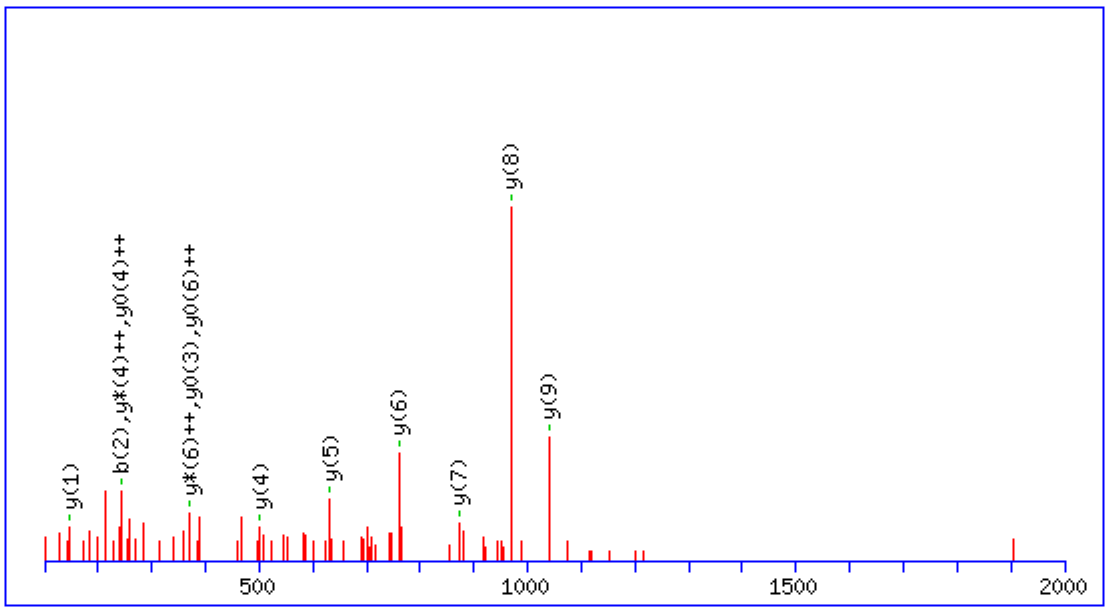
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAPLQELIEK**
Found in **MOL1A_HUMAN**, Mps one binder kinase activator-like 1A OS=Homo sapiens GN=MOBKL1A PE=1 SV=3

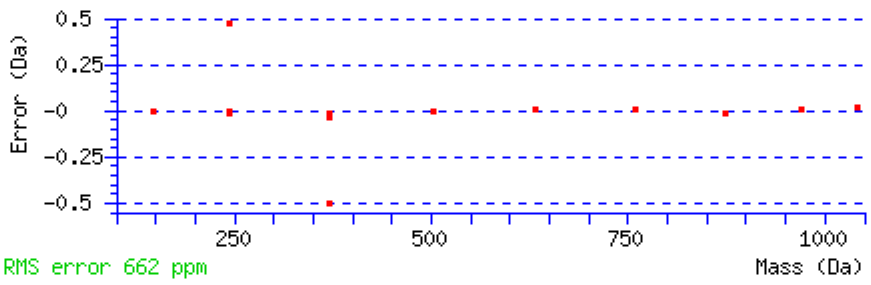
Match to Query 27934: 1281.721028 from(641.867790,2+) rtinseconds(3389) index(45045)
Title: Locus:1.1.1.2810.26
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

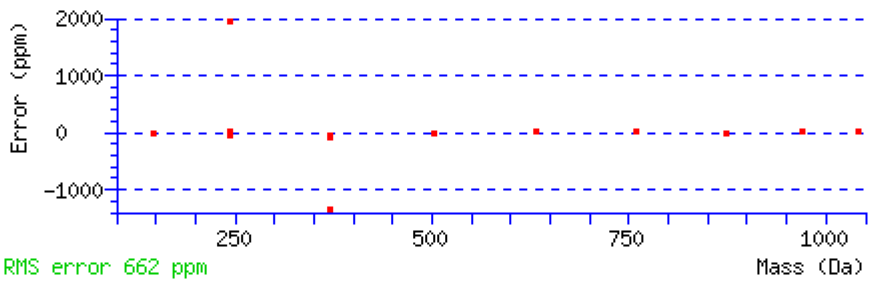
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1281.717972
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 7.5e-006
Matches : 13/108 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	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	L	1153.682702	577.344989	1136.656153	568.831715	1135.672137	568.339707	10
3	314.171047	157.589161			296.160482	148.583879	A	***1040.598638***	520.802957	1023.572089	512.289683	1022.588073	511.797675	9
4	411.223811	206.115544			393.213246	197.110261	P	***969.561524***	485.284400	952.534975	476.771126	951.550959	476.279118	8
5	524.307875	262.657576			506.297310	253.652293	L	***872.508760***	436.758018	855.482211	428.244744	854.498195	427.752736	7
6	652.366453	326.686865	635.339904	318.173590	634.355888	317.681582	Q	***759.424696***	380.215986	742.398147	371.702712	741.414131	371.210704	6
7	781.409046	391.208161	764.382497	382.694887	763.398481	382.202879	E	***631.366118***	316.186697	614.339569	307.673423	613.355553	307.181415	5
8	894.493110	447.750193	877.466561	439.236919	876.482545	438.744911	L	***502.323525***	251.665401	485.296976	243.152126	484.312960	242.660118	4
9	1007.577174	504.292225	990.550625	495.778951	989.566609	495.286943	I	389.239461	195.123369	372.212912	186.610094	371.228896	186.118086	3
10	1136.619767	568.813522	1119.593218	560.300247	1118.609202	559.808239	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 ELAPLQELIEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.2	1281.717972	0.003056	ELAPLQELIEK
3.3	1281.729218	-0.008190	VSNKALPAPIEK
0.8	1281.718033	0.002995	TLPPGLLTPTPK

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

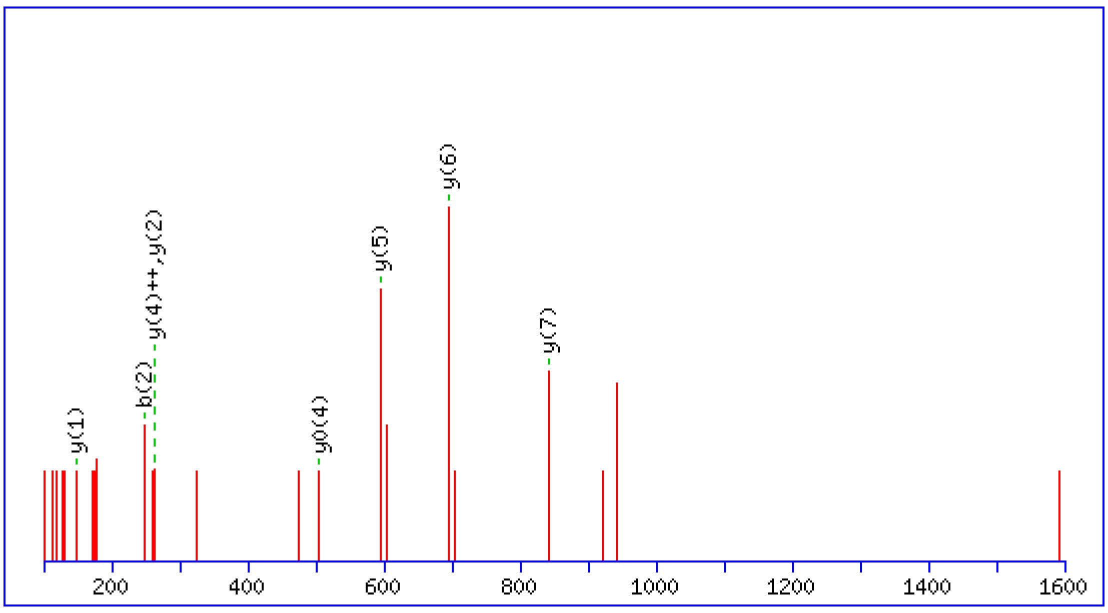
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFTASCDK**
Found in **RAE1L_HUMAN**, mRNA export factor OS=Homo sapiens GN=RAE1 PE=1 SV=1

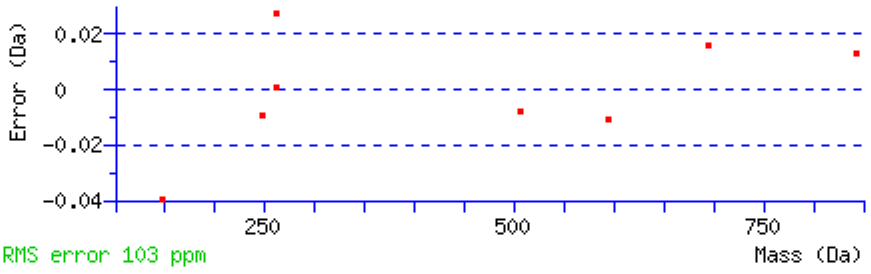
Match to Query 8264: 940.428508 from(471.221530,2+) rtinseconds(1083) index(5179)
Title: Locus:1.1.1.1795.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

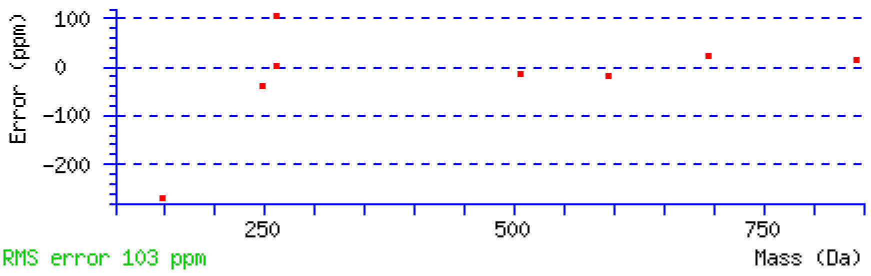
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 940.432419
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0044
Matches : 8/64 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							8
2	247.144104	124.075690			F	***842.371281***	421.689279	825.344732	413.176004	824.360716	412.683996	7
3	348.191783	174.599529	330.181218	165.594247	T	***695.302867***	348.155072	678.276318	339.641797	677.292302	339.149789	6
4	419.228897	210.118087	401.218332	201.112804	A	***594.255188***	297.631232	577.228639	289.117958	576.244623	288.625950	5
5	506.260925	253.634100	488.250360	244.628818	S	523.218074	262.112675	506.191525	253.599401	505.207509	253.107393	4
6	680.307224	340.657250	662.296659	331.651968	C	436.186046	218.596661	419.159497	210.083386	418.175481	209.591378	3
7	795.334167	398.170722	777.323602	389.165439	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 VFTASCDK
(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	940.432419	-0.003911	VFTASCDK
2.9	940.432404	-0.003896	YAPGSATMK
2.0	940.432419	-0.003911	SAVDFQMK
0.6	940.424988	0.003520	EEPENARP

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

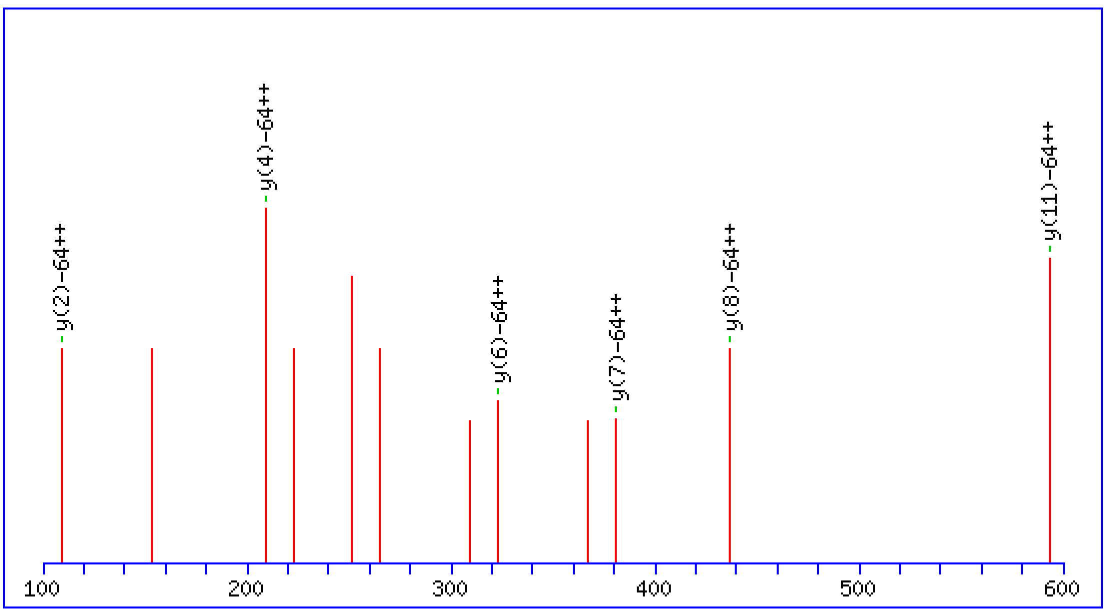
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITVLLDEVAEDM**
Found in **MALT1_HUMAN**, Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens GN=MALT1 PE=1 SV=1

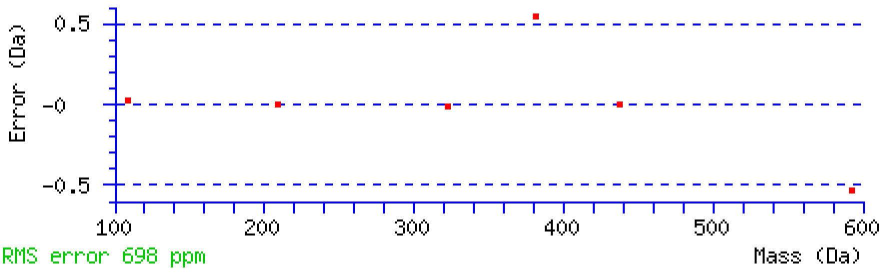
Match to Query 111072: 1362.660372 from(455.227400,3+) rtinseconds(3631) index(837527)
Title: Locus:1.1.1.1452.7
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

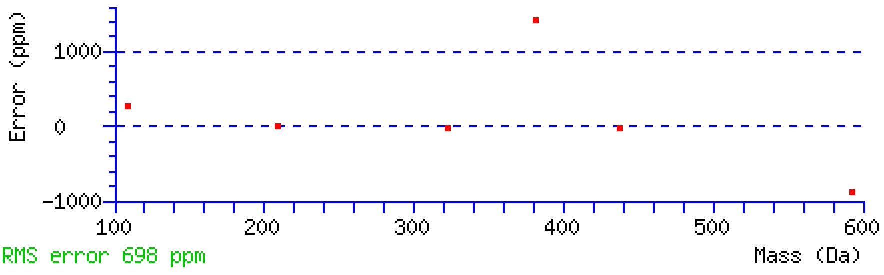
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1362.658844
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12     : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 49   Expect: 0.00054
Matches : 6/126 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^0	y^{0++}	#
1	114.091340	57.549308			I					12
2	215.139019	108.073147	197.128454	99.067865	T	1186.583777	593.795527	1168.573212	584.790244	11
3	314.207433	157.607354	296.196868	148.602072	V	1085.536098	543.271687	1067.525533	534.266405	10
4	427.291497	214.149386	409.280932	205.144104	L	986.467684	493.737480	968.457119	484.732197	9
5	540.375561	270.691419	522.364996	261.686136	L	873.383620	437.195448	855.373055	428.190166	8
6	655.402504	328.204890	637.391939	319.199608	D	760.299556	380.653416	742.288991	371.648134	7
7	784.445097	392.726187	766.434532	383.720904	E	645.272613	323.139945	627.262048	314.134662	6
8	883.513511	442.260394	865.502946	433.255111	V	516.230020	258.618648	498.219455	249.613366	5
9	954.550625	477.778951	936.540060	468.773668	A	417.161606	209.084441	399.151041	200.079159	4
10	1083.593218	542.300247	1065.582653	533.294964	E	346.124492	173.565884	328.113927	164.560602	3
11	1198.620161	599.813719	1180.609596	590.808436	D	217.081899	109.044588	199.071334	100.039305	2
12					M	102.054956	51.531116			1





NCBI **BLAST** search of ITVLLDEVAEDM
(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	1362.658844	0.001528	ITVLLDEVAEDM
14.8	1362.666672	-0.006300	IAEEFEVELER
13.0	1362.652786	0.007586	EVGHHASSIPDAK
10.3	1362.670105	-0.009733	DTVSLSGTIPVQM
10.0	1362.671417	-0.011045	LTLWRQQGTNM
9.6	1362.652786	0.007586	DTEADLQFRPR
9.0	1362.660202	0.000170	SAGDAVCTGWLVK
8.5	1362.670105	-0.009733	DTVSLSGTIPVQM
7.8	1362.660172	0.000200	MATNWGSLLQDK
6.8	1362.673904	-0.013532	RLSSGEDTTELR

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

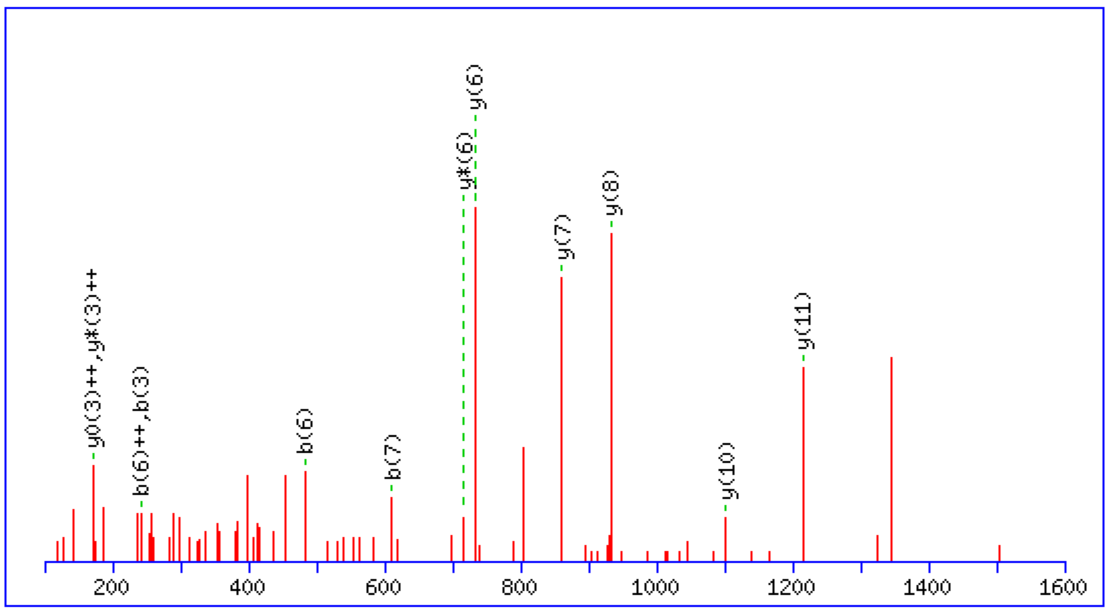
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLPGAQSLCPSR**
Found in **MIS_HUMAN**, Muellerian-inhibiting factor OS=Homo sapiens GN=AMH PE=1 SV=3

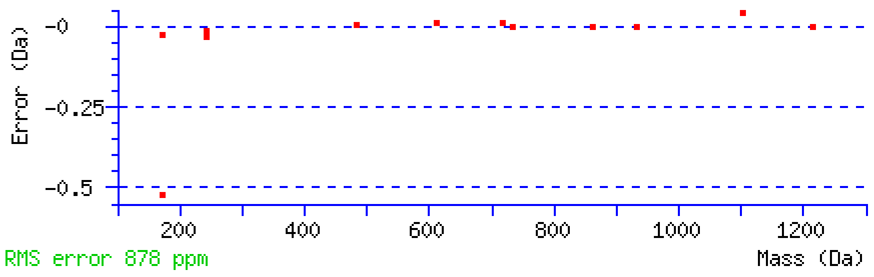
Match to Query 29690: 1342.662208 from(672.338380,2+) rtinseconds(1803) index(18559)
Title: Locus:1.1.1.2167.36
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

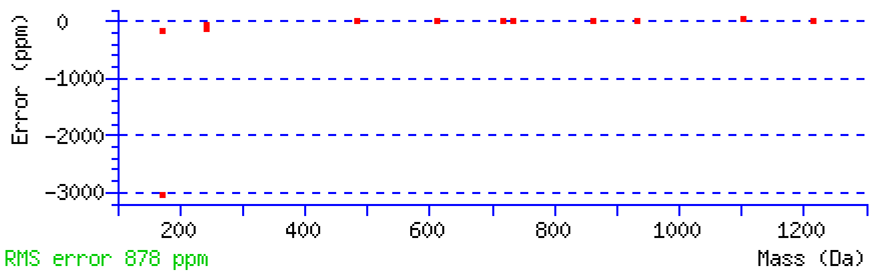
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1342.666321
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 42 **Expect:** 0.00013
Matches : 12/116 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							13
2	129.065854	65.036565					G	1272.636498	636.821887	1255.609949	628.308613	1254.625933	627.816605	12
3	**242.149918**	121.578597					L	***1215.615034***	608.311155	1198.588485	599.797881	1197.604469	599.305873	11
4	355.197597	178.102437					P	***1102.530970***	551.769123	1085.504421	543.255849	1084.520405	542.763841	10
5	412.219061	206.613169					G	989.483291	495.245284	972.456742	486.732009	971.472726	486.240001	9
6	**483.256175**	242.131726					A	***932.461827***	466.734552	915.435278	458.221277	914.451262	457.729269	8
7	**611.314753**	306.161015	594.288204	297.647740			Q	***861.424713***	431.215995	844.398164	422.702720	843.414148	422.210712	7
8	698.346781	349.677029	681.320232	341.163754	680.336216	340.671746	S	***733.366135***	367.186706	716.339586	358.673431	715.355570	358.181423	6
9	811.430845	406.219061	794.404296	397.705786	793.420280	397.213778	L	646.334107	323.670692	629.307558	315.157417	628.323542	314.665409	5
10	985.477144	493.242210	968.450595	484.728936	967.466579	484.236928	C	533.250043	267.128660	516.223494	258.615385	515.239478	258.123377	4
11	1082.529908	541.768592	1065.503359	533.255318	1064.519343	532.763309	P	359.203744	180.105510	342.177195	171.592235	341.193179	171.100227	3
12	1169.561936	585.284606	1152.535387	576.771332	1151.551371	576.279324	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 AGLPGAQSLCPSR
(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	1342.666321	-0.004113	AGLPGAQSLCPSR
1.0	1342.658936	0.003272	GTSLGDPRNSSPR

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

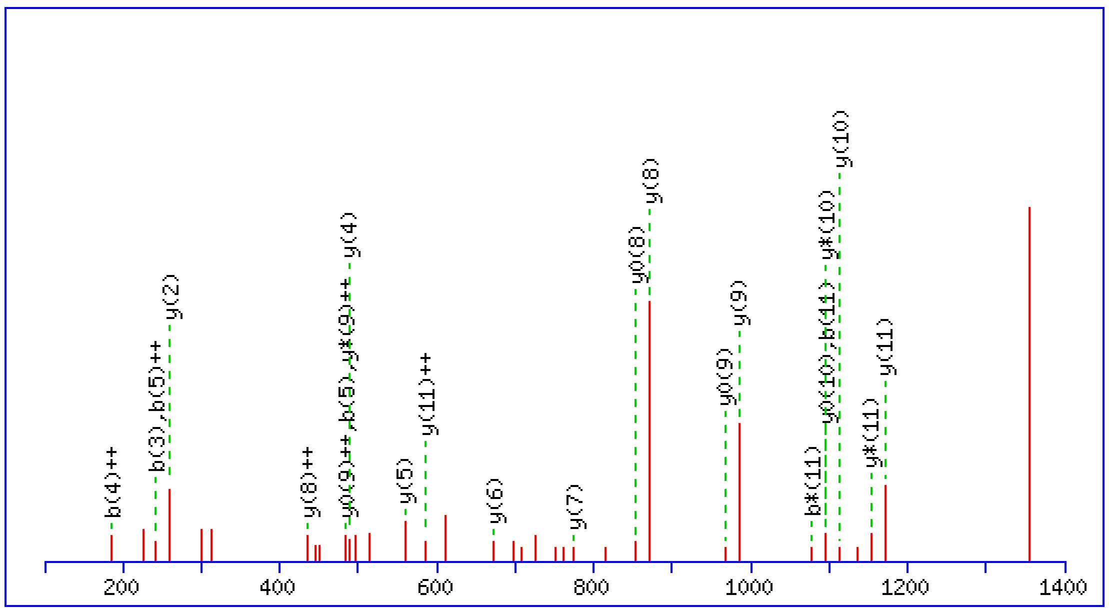
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGQNPTNAEVLK**
Found in **MYL6B_HUMAN**, Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1

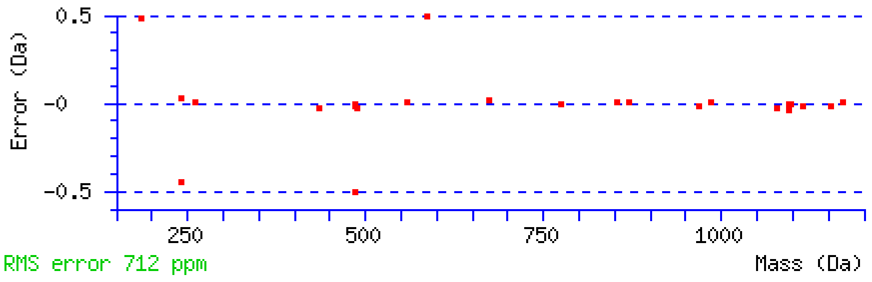
Match to Query 10385: 1353.729348 from(677.871950,2+) rtinseconds(1912) index(2941)
Title: Locus:1.1.1.2578.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

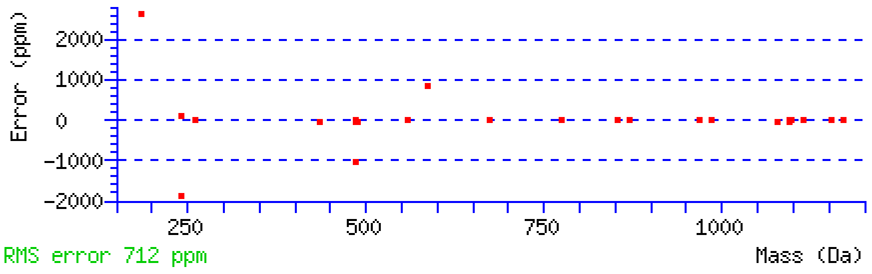
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1353.725204
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 7.6e-006
Matches : 24/120 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	72.044390	36.525833					A							13
2	185.128454	93.067865					L	1283.695392	642.351334	1266.668843	633.838060	1265.684827	633.346052	12
3	**242.149918**	121.578597					G	***1170.611328***	585.809302	1153.584779	577.296028	1152.600763	576.804020	11
4	370.208496	185.607886	353.181947	177.094612			Q	***1113.589864***	557.298570	1096.563315	548.785296	1095.579299	548.293288	10
5	**484.251423**	242.629350	467.224874	234.116075			N	***985.531286***	493.269281	968.504737	484.756007	967.520721	484.263999	9
6	581.304187	291.155732	564.277638	282.642457			P	***871.488359***	436.247818	854.461810	427.734543	853.477794	427.242535	8
7	682.351866	341.679571	665.325317	333.166297	664.341301	332.674289	T	***774.435595***	387.721436	757.409046	379.208161	756.425030	378.716153	7
8	796.394793	398.701035	779.368244	390.187760	778.384228	389.695752	N	***673.387916***	337.197596	656.361367	328.684322	655.377351	328.192314	6
9	867.431907	434.219592	850.405358	425.706317	849.421342	425.214309	A	***559.344989***	280.176133	542.318440	271.662858	541.334424	271.170850	5
10	996.474500	498.740888	979.447951	490.227614	978.463935	489.735606	E	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
11	**1095.542914**	548.275095	1078.516365	539.761821	1077.532349	539.269813	V	359.265282	180.136279	342.238733	171.623004			3
12	1208.626978	604.817127	1191.600429	596.303853	1190.616413	595.811845	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 ALGQNPTNAEVLK
(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	1353.725204	0.004144	ALGQNPTNAEVLK
0.1	1353.725204	0.004144	SILAKPSSSPDPR

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

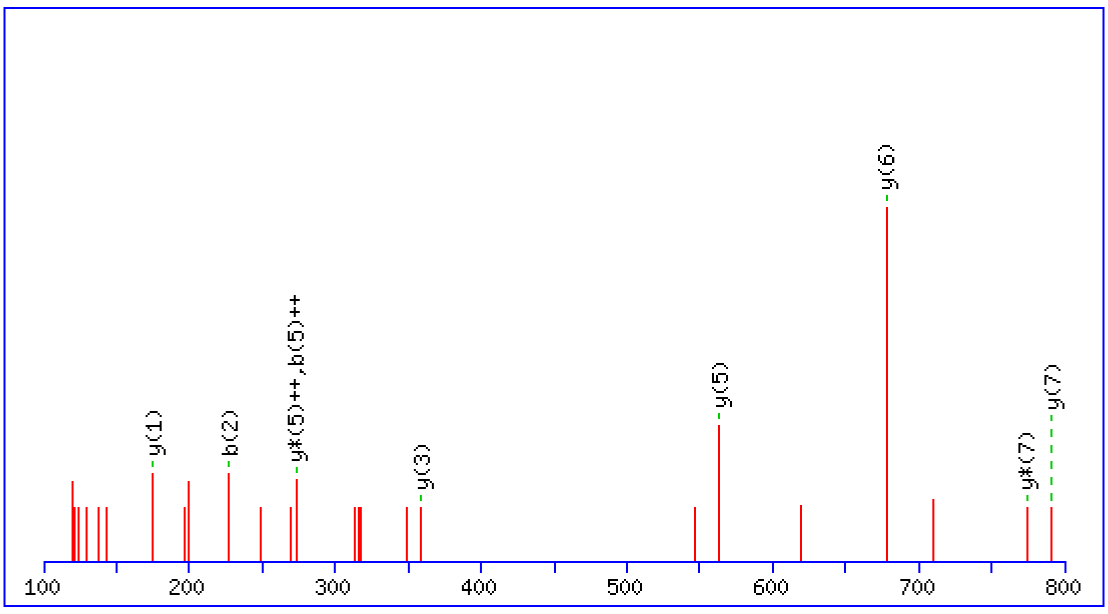
Mascot Search Results

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

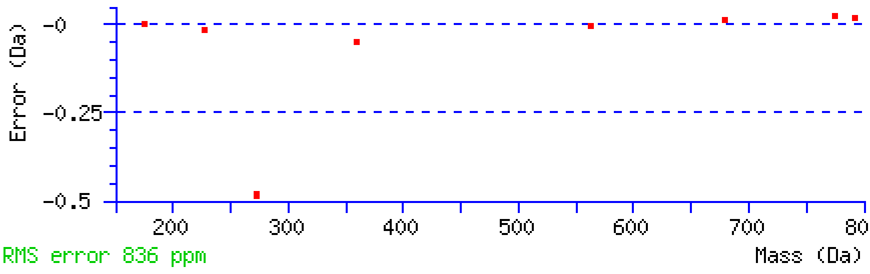
Match to Query 5005: 903.512288 from(452.763420,2+) rtinseconds(2880) index(32316)
Title: Locus:1.1.1.2667.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

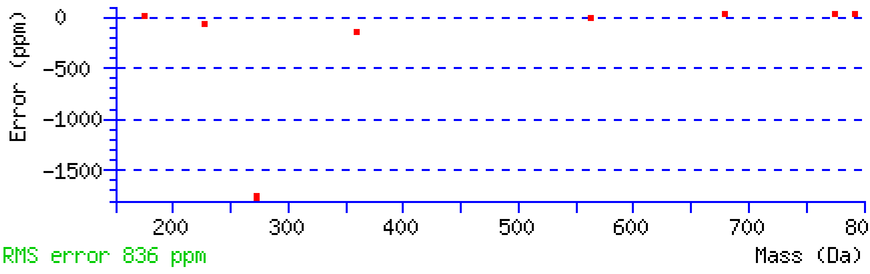
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 903.517792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0034
Matches : 9/56 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	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
34.4	903.517792	-0.005504	IIDFGLAR
34.4	903.517792	-0.005504	ILDFGLAR
34.4	903.517792	-0.005504	LIDFGLAR
11.2	903.513748	-0.001460	LISKSNSR
9.3	903.503387	0.008901	IILQMMR
9.3	903.521149	-0.008861	LLKMEVR
9.3	903.517776	-0.005488	LLKYDPR
9.3	903.517776	-0.005488	LLNLYPR
9.3	903.517776	-0.005488	LLPNYLR
8.9	903.521149	-0.008861	LDIMLKR

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

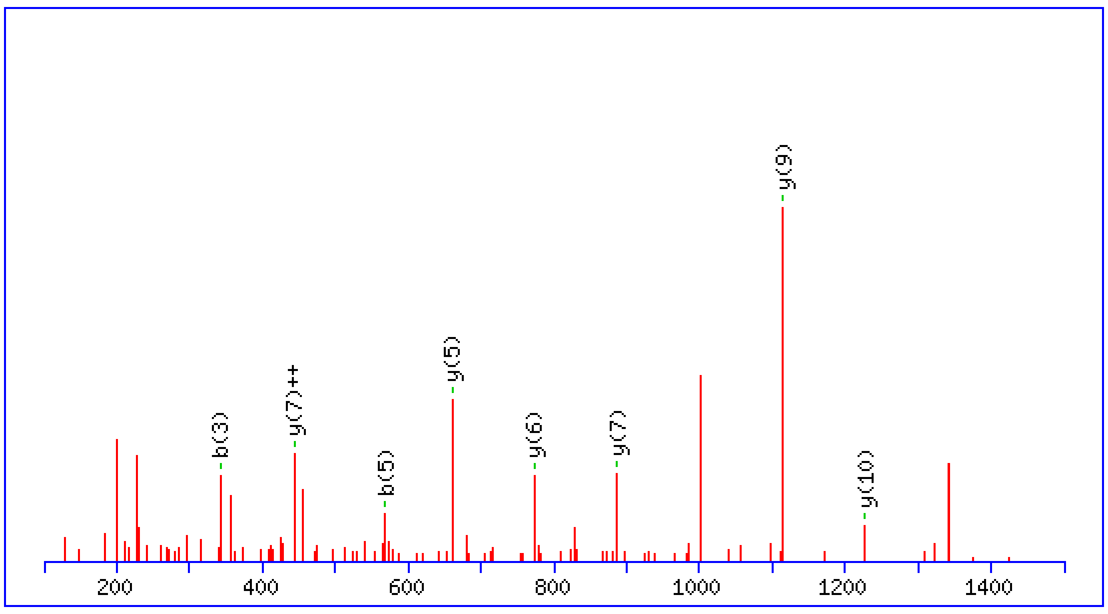
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILDPLLLLTWK**
Found in **MYO1H_HUMAN**, Myosin-Ih OS=Homo sapiens GN=MYO1H PE=2 SV=2

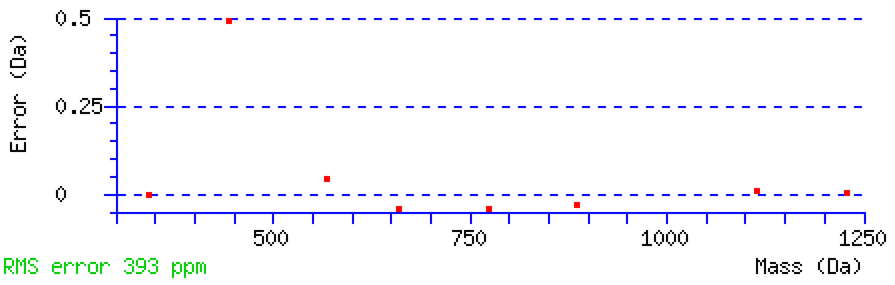
Match to Query 26680: 1339.814728 from(670.914640,2+) rtinseconds(3553) index(51676)
Title: Locus:1.1.1.2854.12
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

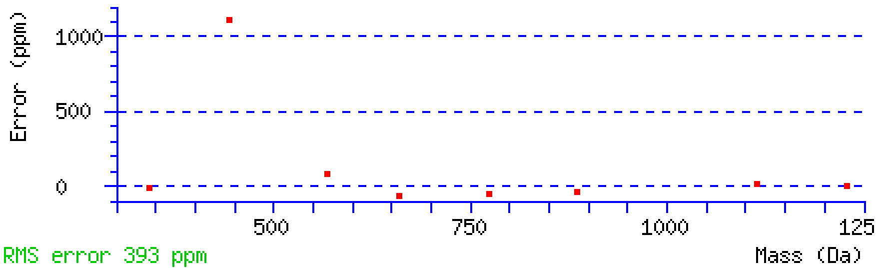
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1339.811508
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
Ions Score: 32  Expect: 0.001
Matches : 8/92 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							11
2	227.175404	114.091340			L	*1227.734738*	614.371007	1210.708189	605.857733	1209.724173	605.365725	10
3	**342.202347**	171.604811	324.191782	162.599529	D	*1114.650674*	557.828975	1097.624125	549.315701	1096.640109	548.823693	9
4	455.250026	228.128651	437.239461	219.123369	P	999.623731	500.315504	982.597182	491.802229	981.613166	491.310221	8
5	**568.334090**	284.670683	550.323525	275.665401	L	*886.576052*	443.791664	869.549503	435.278390	868.565487	434.786382	7
6	681.418154	341.212715	663.407589	332.207433	L	*773.491988*	387.249632	756.465439	378.736358	755.481423	378.244350	6
7	794.502218	397.754747	776.491653	388.749465	L	*660.407924*	330.707600	643.381375	322.194326	642.397359	321.702318	5
8	907.586282	454.296779	889.575717	445.291497	L	547.323860	274.165568	530.297311	265.652294	529.313295	265.160286	4
9	1008.633961	504.820619	990.623396	495.815336	T	434.239796	217.623536	417.213247	209.110262	416.229231	208.618254	3
10	1194.713274	597.860275	1176.702709	588.854993	W	333.192117	167.099697	316.165568	158.586422			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ILDPLLLLTWK
(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	1339.811508	0.003220	ILDPLLLLTWK
7.1	1339.807465	0.007263	LILEPTQAAKLK
1.5	1339.807465	0.007263	LLNPLVSKISEK
0.7	1339.807495	0.007233	IPVADIKAIVTGK

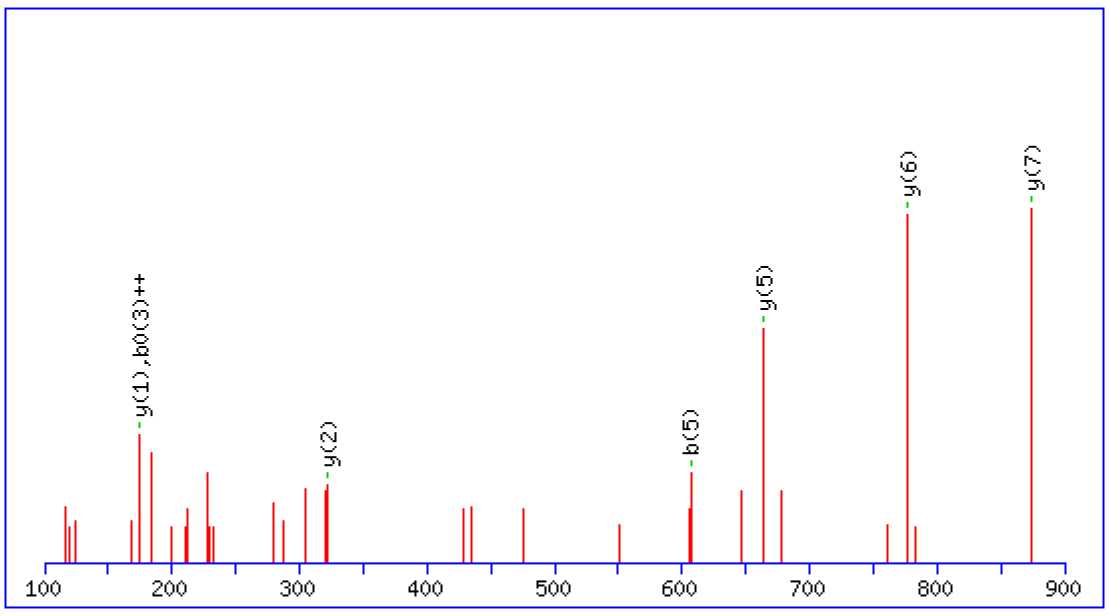
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MFSLKPPKPTFR**
Found in **MTMRA_HUMAN**, Myotubularin-related protein 10 OS=Homo sapiens GN=MTMR10 PE=1 SV=3

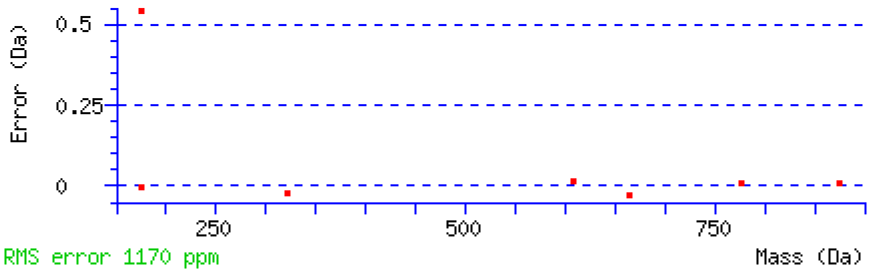
Match to Query 47272: 1479.780402 from(494.267410,3+) rtinseconds(3067) index(43874)
Title: Locus:1.1.1.2457.7
Data file 2011-11-14 - TFD - S 2-2.mgf

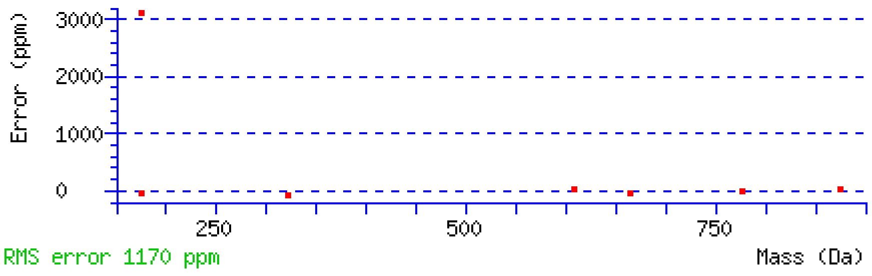
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1479.790802
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P7      : Oxidation (P)
P9      : Oxidation (P)
Ions Score: 33  Expect: 0.0055
Matches : 7/116 fragment ions using 8 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.047761	66.527518					M							12
2	279.116175	140.061725					F	1349.757599	675.382438	1332.731050	666.869163	1331.747034	666.377155	11
3	366.148203	183.577739			348.137638	174.572457	S	1202.689185	601.848231	1185.662636	593.334956	1184.678620	592.842948	10
4	479.232267	240.119771			461.221702	231.114489	L	1115.657157	558.332217	1098.630608	549.818942	1097.646592	549.326934	9
5	607.327230	304.167253	590.300681	295.653978	589.316665	295.161971	K	1002.573093	501.790185	985.546544	493.276910	984.562528	492.784902	8
6	704.379994	352.693635	687.353445	344.180361	686.369429	343.688353	P	*874.478130*	437.742703	857.451581	429.229429	856.467565	428.737421	7
7	817.427673	409.217475	800.401124	400.704200	799.417108	400.212192	P	*777.425366*	389.216321	760.398817	380.703047	759.414801	380.211039	6
8	945.522636	473.264956	928.496087	464.751682	927.512071	464.259674	K	*664.377687*	332.692482	647.351138	324.179207	646.367122	323.687199	5
9	1058.570315	529.788795	1041.543766	521.275521	1040.559750	520.783513	P	536.282724	268.645000	519.256175	260.131726	518.272159	259.639718	4
10	1159.617994	580.312635	1142.591445	571.799361	1141.607429	571.307352	T	423.235045	212.121161	406.208496	203.607886	405.224480	203.115878	3
11	1306.686408	653.846842	1289.659859	645.333568	1288.675843	644.841560	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 MFSLKPPKPTFR
(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	1479.790802	-0.010400	MFSLKPPKPTFR
19.5	1479.790802	-0.010400	MFSLKPPKPTFR
18.6	1479.775558	0.004844	TKGDFILVGDLMR
11.7	1479.790802	-0.010400	MFSLKPPKPTFR
8.9	1479.790802	-0.010400	MFSLKPPKPTFR
5.4	1479.776871	0.003531	HGLHYVNKPMLR
4.6	1479.790802	-0.010400	MFSLKPPKPTFR
4.6	1479.790802	-0.010400	MFSLKPPKPTFR
2.0	1479.786804	-0.006402	GIPGMVGLPGPPGRK
1.3	1479.790802	-0.010400	QFLAPPMLKFTR

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

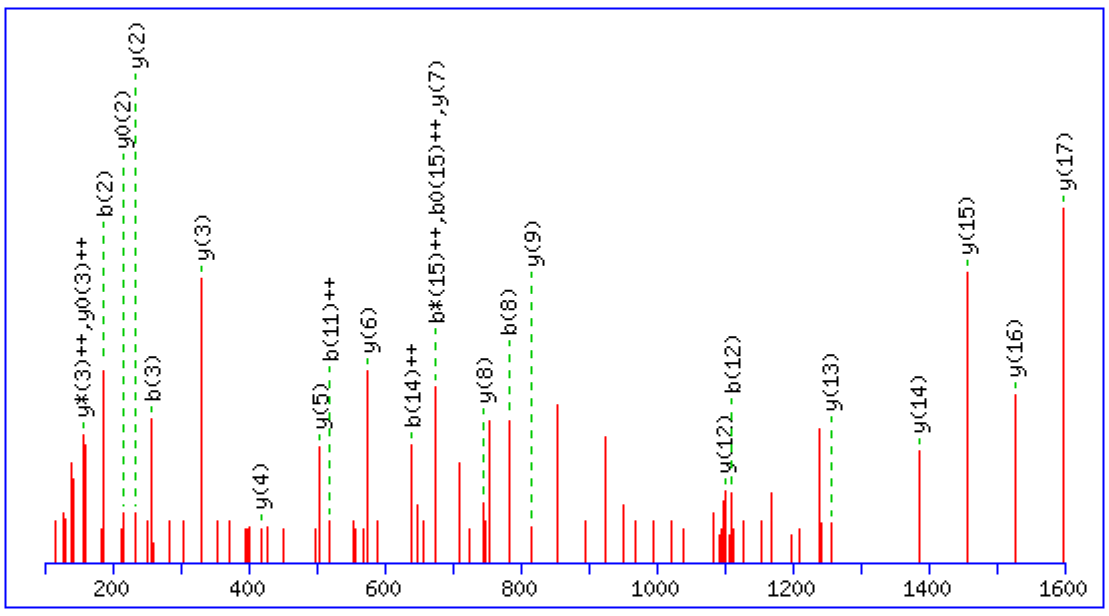
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEAAAERPGEAAVASSPSK**
Found in **MARCS_HUMAN**, Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4

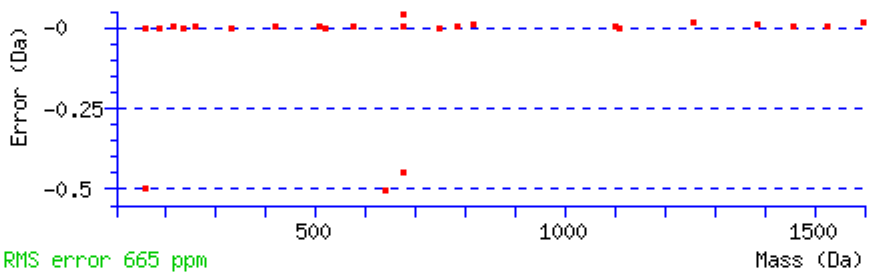
Match to Query 53079: 1783.872462 from(595.631430,3+) rtinseconds(1164) index(8578)
Title: Locus:1.1.1.1082.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

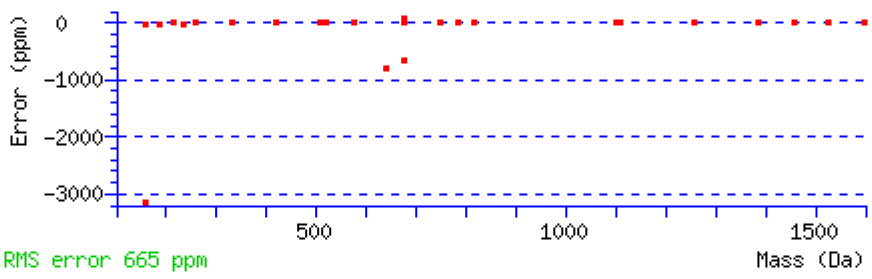
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1783.870010
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 2e-009
Matches : 25/200 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	58.028740	29.518008					G							19
2	**187.071333**	94.039305			169.060768	85.034022	E	1727.855868	864.431572	1710.829319	855.918298	1709.845303	855.426290	18
3	**258.108447**	129.557862			240.097882	120.552579	A	***1598.813275***	799.910276	1581.786726	791.397001	1580.802710	790.904993	17
4	329.145561	165.076418			311.134996	156.071136	A	***1527.776161***	764.391719	1510.749612	755.878444	1509.765596	755.386436	16
5	400.182675	200.594975			382.172110	191.589693	A	***1456.739047***	728.873162	1439.712498	720.359887	1438.728482	719.867879	15
6	529.225268	265.116272			511.214703	256.110990	E	***1385.701933***	693.354605	1368.675384	684.841330	1367.691368	684.349322	14
7	685.326379	343.166828	668.299830	334.653553	667.315814	334.161545	R	***1256.659340***	628.833308	1239.632791	620.320034	1238.648775	619.828026	13
8	**782.379143**	391.693210	765.352594	383.179935	764.368578	382.687927	P	***1100.558229***	550.782753	1083.531680	542.269478	1082.547664	541.777470	12
9	839.400607	420.203942	822.374058	411.690667	821.390042	411.198659	G	1003.505465	502.256371	986.478916	493.743096	985.494900	493.251088	11
10	968.443200	484.725238	951.416651	476.211964	950.432635	475.719956	E	946.484001	473.745639	929.457452	465.232364	928.473436	464.740356	10
11	1039.480314	520.243795	1022.453765	511.730521	1021.469749	511.238513	A	***817.441408***	409.224342	800.414859	400.711068	799.430843	400.219060	9
12	**1110.517428**	555.762352	1093.490879	547.249078	1092.506863	546.757070	A	***746.404294***	373.705785	729.377745	365.192511	728.393729	364.700503	8
13	1209.585842	605.296559	1192.559293	596.783285	1191.575277	596.291277	V	***675.367180***	338.187228	658.340631	329.673954	657.356615	329.181946	7
14	1280.622956	640.815116	1263.596407	632.301842	1262.612391	631.809834	A	***576.298766***	288.653021	559.272217	280.139747	558.288201	279.647739	6
15	1367.654984	684.331130	1350.628435	675.817856	1349.644419	675.325848	S	***505.261652***	253.134464	488.235103	244.621190	487.251087	244.129182	5
16	1454.687012	727.847144	1437.660463	719.333870	1436.676447	718.841862	S	***418.229624***	209.618450	401.203075	201.105176	400.219059	200.613168	4
17	1551.739776	776.373526	1534.713227	767.860252	1533.729211	767.368244	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
18	1638.771804	819.889540	1621.745255	811.376266	1620.761239	810.884258	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.2	1783.870010	0.002452	GEAAAERPGEAAVASSPSK
1.4	1783.888657	-0.016195	QEQIQAMPLADSQAVR
0.1	1783.884827	-0.012365	VGSGCTMKELYDLGLK

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

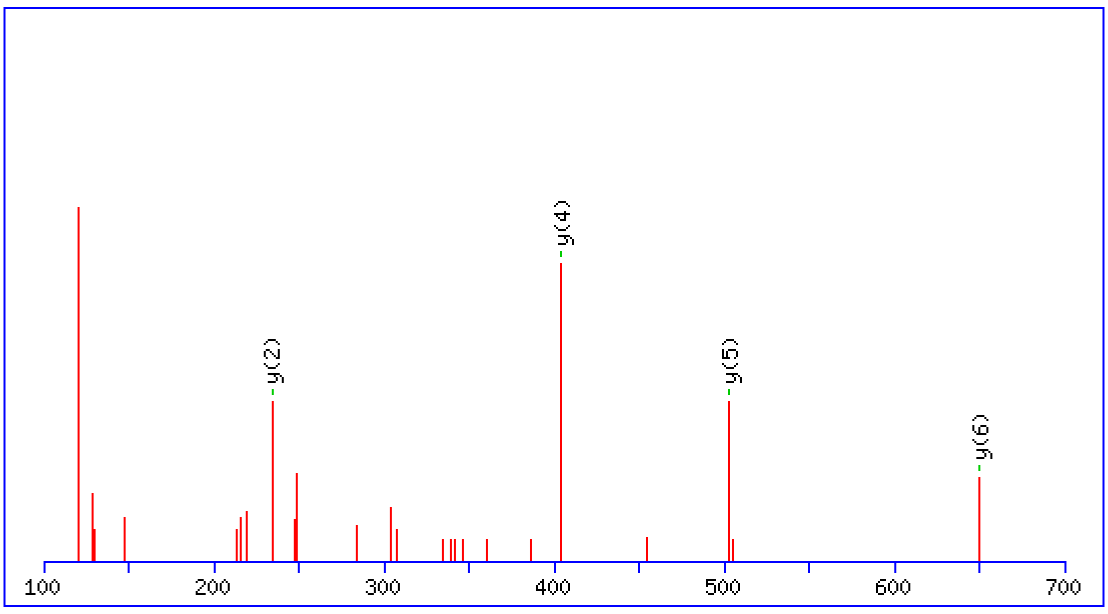
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFFVGLSK**
Found in **DDAH1_HUMAN**, N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3

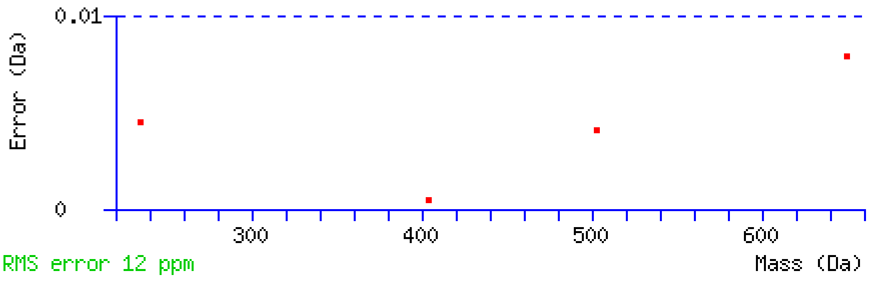
Match to Query 12428: 925.491228 from(463.752890,2+) rtinseconds(2659) index(33838)
Title: Locus:1.1.1.2375.4
Data file 2011-11-14 - TFD - S 2-4.mgf

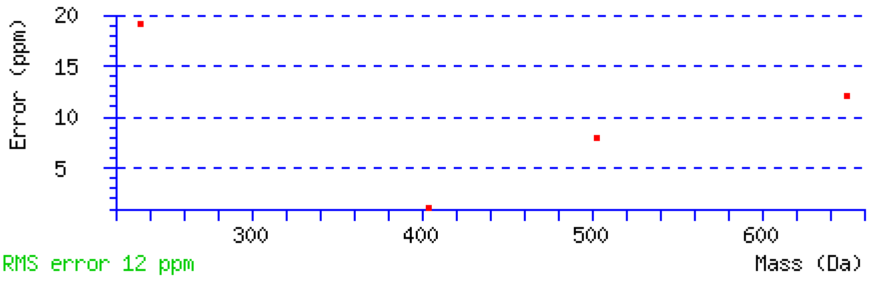
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 925.490921
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0044
Matches : 4/68 fragment ions using 5 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	277.118283	139.062779	259.107718	130.057497	F	797.455602	399.231439	780.429053	390.718165	779.445037	390.226157	7
3	424.186697	212.596986	406.176132	203.591704	F	***650.387188***	325.697232	633.360639	317.183958	632.376623	316.691950	6
4	523.255111	262.131193	505.244546	253.125911	V	***503.318774***	252.163025	486.292225	243.649750	485.308209	243.157742	5
5	580.276575	290.641926	562.266010	281.636643	G	***404.250360***	202.628818	387.223811	194.115544	386.239795	193.623536	4
6	693.360639	347.183958	675.350074	338.178675	L	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
7	780.392667	390.699972	762.382102	381.694689	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 EFFVGLSK
(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	925.490921	0.000307	EFFVGLSK
9.2	925.498108	-0.006880	EKAHSGGIK
4.2	925.486877	0.004351	ETEAVIHK
3.7	925.486877	0.004351	KYSSLSGGK
2.2	925.490921	0.000307	SFFDVALK
1.2	925.490936	0.000292	FGTFVAALT
0.0	925.486877	0.004351	AAPTSAPPSK

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

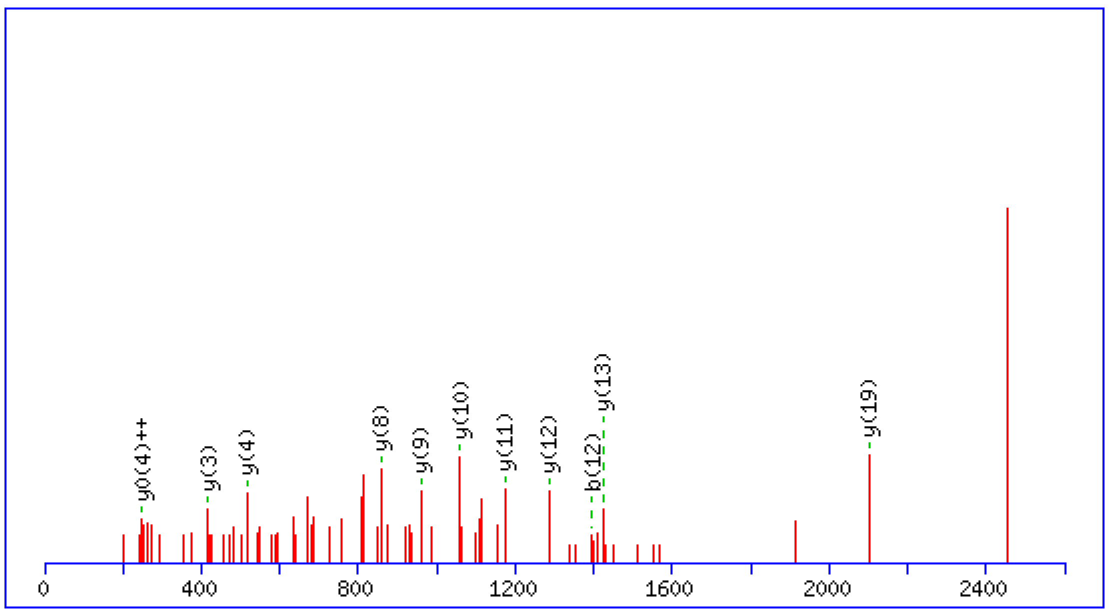
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQYSDALEHLLTTGQGVVLER**
Found in **NDUAA_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1

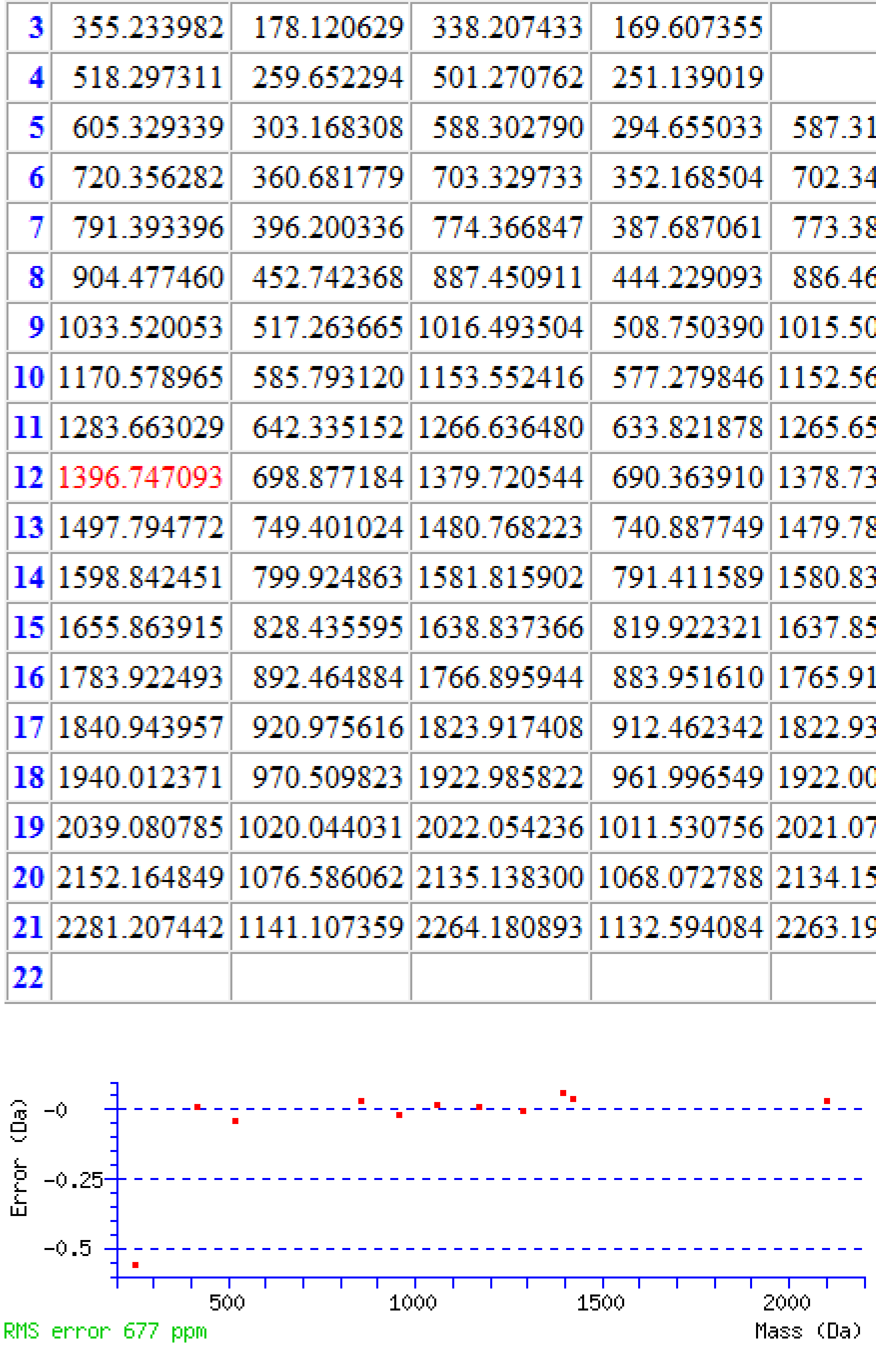
Match to Query 71941: 2454.309792 from(819.110540,3+) rtinseconds(4099) index(61543)
Title: Locus:1.1.1.2939.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

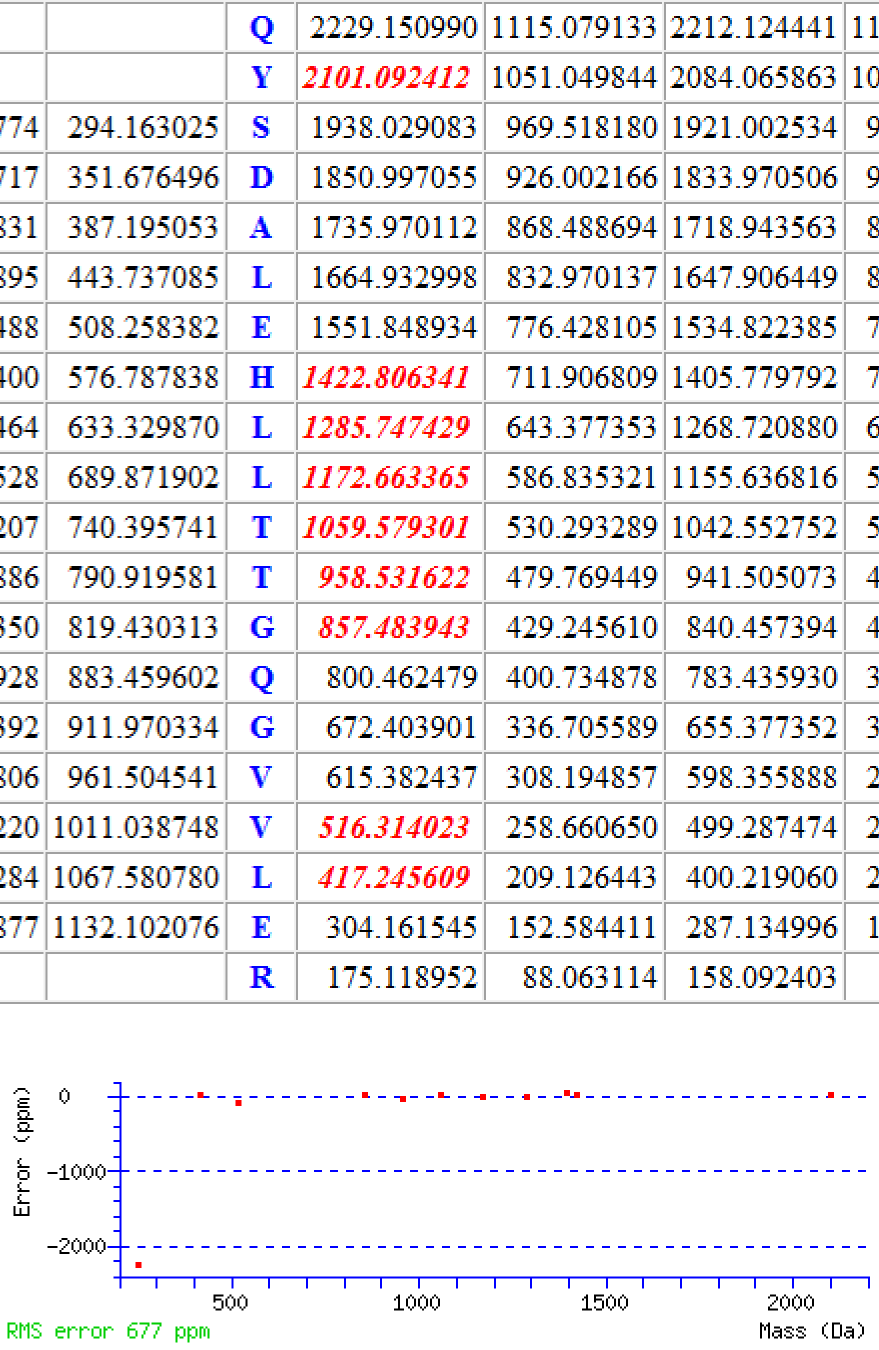
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2454.311829
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57 **Expect:** 1.1e-005
Matches : 11/238 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							22
2	227.175404	114.091340					L	2342.235054	1171.621165	2325.208505	1163.107890	2324.224489	1162.615882	21
3	355.233982	178.120629	338.207433	169.607355			Q	2229.150990	1115.079133	2212.124441	1106.565858	2211.140425	1106.073850	20
4	518.297311	259.652294	501.270762	251.139019			Y	***2101.092412***	1051.049844	2084.065863	1042.536569	2083.081847	1042.044561	19
5	605.329339	303.168308	588.302790	294.655033	587.318774	294.163025	S	1938.029083	969.518180	1921.002534	961.004905	1920.018518	960.512897	18
6	720.356282	360.681779	703.329733	352.168504	702.345717	351.676496	D	1850.997055	926.002166	1833.970506	917.488891	1832.986490	916.996883	17
7	791.393396	396.200336	774.366847	387.687061	773.382831	387.195053	A	1735.970112	868.488694	1718.943563	859.975420	1717.959547	859.483412	16
8	904.477460	452.742368	887.450911	444.229093	886.466895	443.737085	L	1664.932998	832.970137	1647.906449	824.456863	1646.922433	823.964855	15
9	1033.520053	517.263665	1016.493504	508.750390	1015.509488	508.258382	E	1551.848934	776.428105	1534.822385	767.914831	1533.838369	767.422823	14
10	1170.578965	585.793120	1153.552416	577.279846	1152.568400	576.787838	H	***1422.806341***	711.906809	1405.779792	703.393534	1404.795776	702.901526	13
11	1283.663029	642.335152	1266.636480	633.821878	1265.652464	633.329870	L	***1285.747429***	643.377353	1268.720880	634.864078	1267.736864	634.372070	12
12	1396.747093	698.877184	1379.720544	690.363910	1378.736528	689.871902	L	***1172.663365***	586.835321	1155.636816	578.322046	1154.652800	577.830038	11
13	1497.794772	749.401024	1480.768223	740.887749	1479.784207	740.395741	T	***1059.579301***	530.293289	1042.552752	521.780014	1041.568736	521.288006	10
14	1598.842451	799.924863	1581.815902	791.411589	1580.831886	790.919581	T	***958.531622***	479.769449	941.505073	471.256175	940.521057	470.764167	9
15	1655.863915	828.435595	1638.837366	819.922321	1637.853350	819.430313	G	***857.483943***	429.245610	840.457394	420.732335	839.473378	420.240327	8
16	1783.922493	892.464884	1766.895944	883.951610	1765.911928	883.459602	Q	800.462479	400.734878	783.435930	392.221603	782.451914	391.729595	7
17	1840.943957	920.975616	1823.917408	912.462342	1822.933392	911.970334	G	672.403901	336.705589	655.377352	328.192314	654.393336	327.700306	6
18	1940.012371	970.509823	1922.985822	961.996549	1922.001806	961.504541	V	615.382437	308.194857	598.355888	299.681582	597.371872	299.189574	5
19	2039.080785	1020.044031	2022.054236	1011.530756	2021.070220	1011.038748	V	***516.314023***	258.660650	499.287474	250.147375	498.303458	249.655367	4
20	2152.164849	1076.586062	2135.138300	1068.072788	2134.154284	1067.580780	L	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
21	2281.207442	1141.107359	2264.180893	1132.594084	2263.196877	1132.102076	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 LLQYSDALEHLLTTGQGVVLER
(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	2454.311829	-0.002037	LLQYSDALEHLLTTGQGVVLER

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

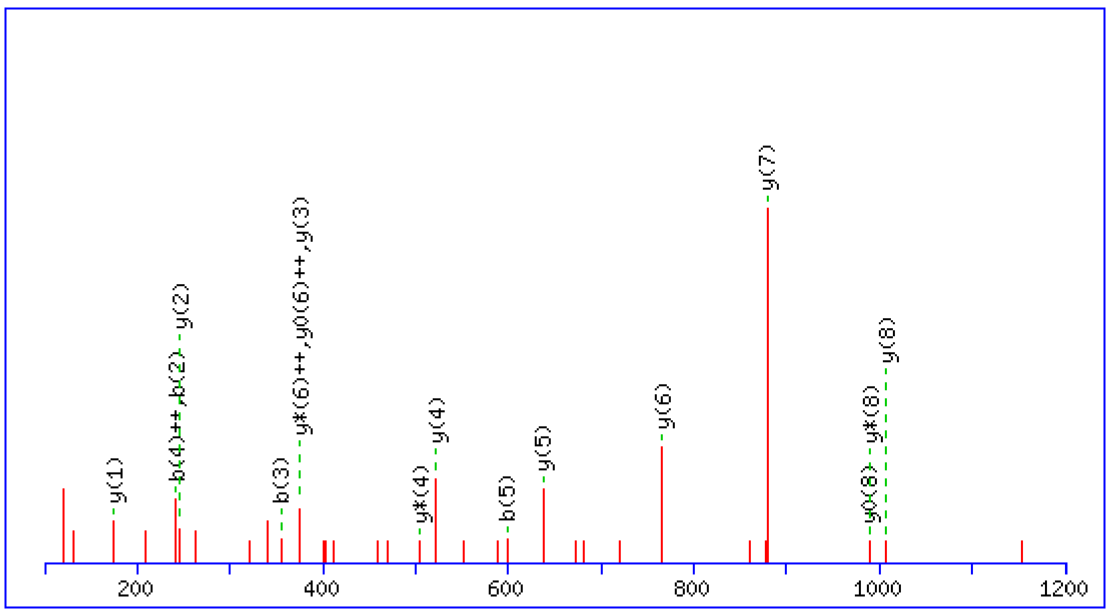
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQIEDFEAR**
Found in **NDUAD_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=1 SV=3

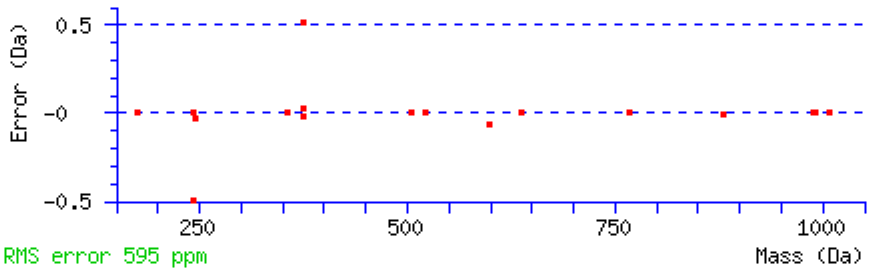
Match to Query 15652: 1119.558888 from(560.786720,2+) rtinseconds(2586) index(23424)
Title: Locus:1.1.1.2482.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

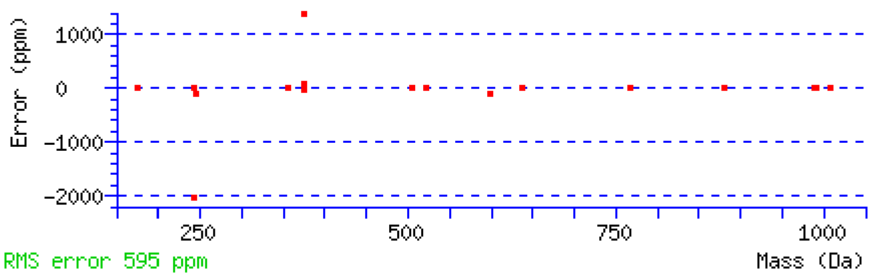
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1119.556015
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 0.00018
Matches : 17/84 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	**242.149918**	121.578597	225.123369	113.065323			Q	***1007.479251***	504.243264	990.452702	495.729989	989.468686	495.237981	8
3	**355.233982**	178.120629	338.207433	169.607355			I	***879.420673***	440.213975	862.394124	431.700700	861.410108	431.208692	7
4	484.276575	242.641926	467.250026	234.128651	466.266010	233.636643	E	***766.336609***	383.671943	749.310060	375.158668	748.326044	374.666660	6
5	**599.303518**	300.155397	582.276969	291.642123	581.292953	291.150115	D	***637.294016***	319.150646	620.267467	310.637372	619.283451	310.145364	5
6	746.371932	373.689604	729.345383	365.176330	728.361367	364.684322	F	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
7	875.414525	438.210901	858.387976	429.697626	857.403960	429.205618	E	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
8	946.451639	473.729458	929.425090	465.216183	928.441074	464.724175	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 LQIEDFEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	1119.556015	0.002873	LQIEDFEAR
13.9	1119.556046	0.002842	QIPDVETFR
6.6	1119.567261	-0.008373	QLIQQGDYR
6.3	1119.556030	0.002858	EPGLLPYGSR
6.1	1119.549500	0.009388	SHSMRFIDK
4.4	1119.552841	0.006047	NQEMKLAMR
2.4	1119.556015	0.002873	DPQLEIAYR
1.6	1119.556015	0.002873	NPLPEYLSR
1.3	1119.559387	-0.000499	LIECDTLSR
1.1	1119.559418	-0.000530	TVVAPMLDSR

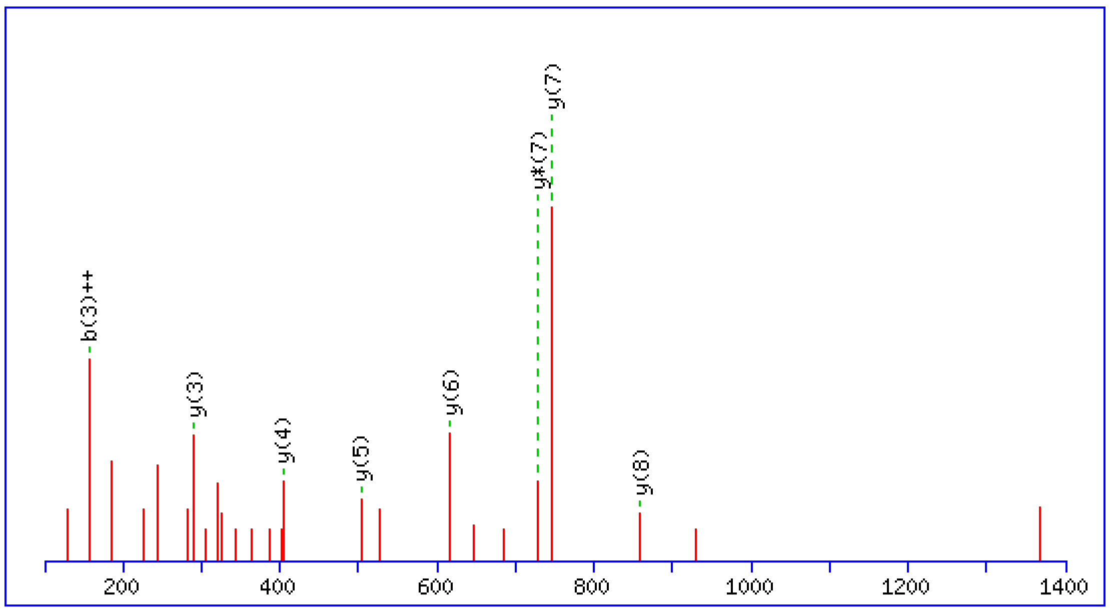
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALENVLSGK**
Found in **NDUA2_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3

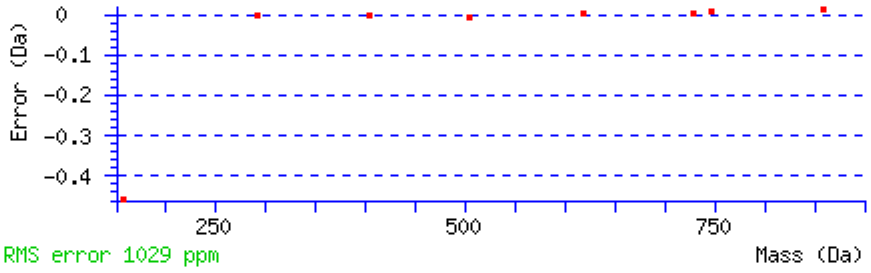
Match to Query 4387: 929.519368 from(465.766960,2+) rtinseconds(2119) index(5516)
Title: Locus:1.1.1.2565.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

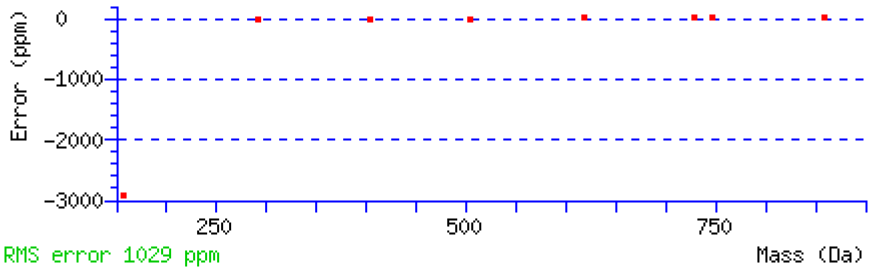
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 929.518173
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 6.3e-006
Matches : 8/82 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	72.044390	36.525833					A							9
2	185.128454	93.067865					L	***859.488358***	430.247817	842.461809	421.734543	841.477793	421.242535	8
3	314.171047	157.589161			296.160482	148.583879	E	***746.404294***	373.705785	729.377745	365.192511	728.393729	364.700503	7
4	428.213974	214.610625	411.187425	206.097351	410.203409	205.605343	N	***617.361701***	309.184489	600.335152	300.671214	599.351136	300.179206	6
5	527.282388	264.144832	510.255839	255.631558	509.271823	255.139550	V	***503.318774***	252.163025	486.292225	243.649751	485.308209	243.157743	5
6	640.366452	320.686864	623.339903	312.173590	622.355887	311.681582	L	***404.250360***	202.628818	387.223811	194.115544	386.239795	193.623536	4
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
8	784.419944	392.713610	767.393395	384.200336	766.409379	383.708328	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 ALENVLSGK
(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	929.518173	0.001195	ALENVLSGK
4.3	929.518173	0.001195	EDAQKVLK
3.0	929.518158	0.001210	LAELELSR
1.0	929.518143	0.001225	ALAEEAAKK

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

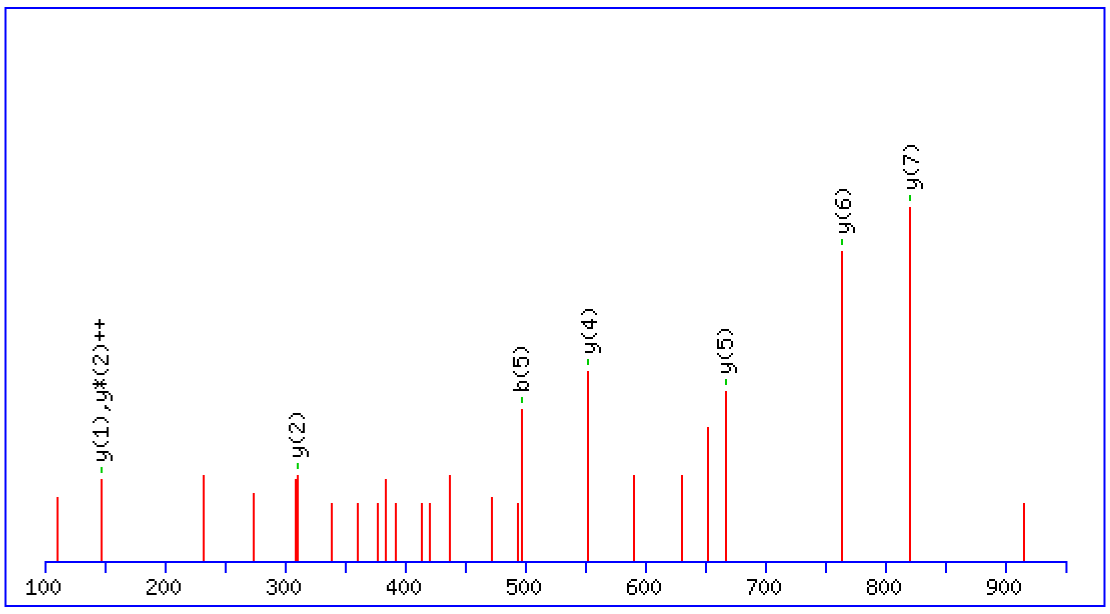
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGPNDQYK**
Found in **NDUA4_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1

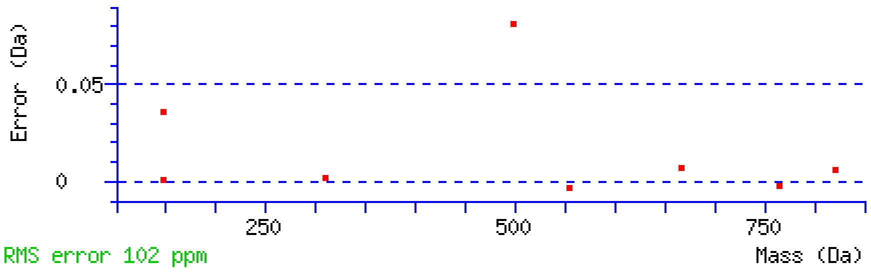
Match to Query 13114: 933.457808 from(467.736180,2+) rtinseconds(1192) index(1041)
Title: Locus:1.1.1.1898.4
Data file 2011-11-14 - TFD - S 2-7.mgf

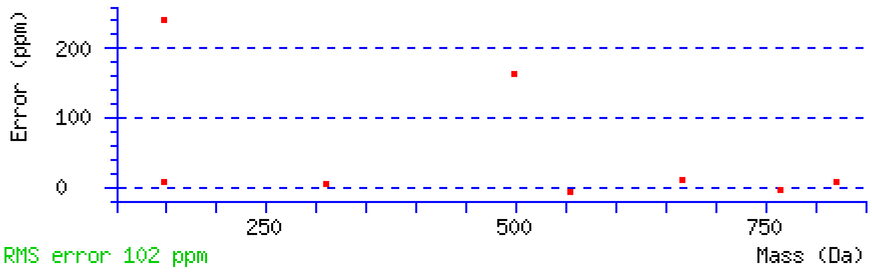
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 933.455582
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 4.4e-005
Matches : 8/64 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	171.112804	86.060040					G	***821.378809***	411.193043	804.352260	402.679768	803.368244	402.187760	7
3	268.165568	134.586422					P	***764.357345***	382.682311	747.330796	374.169036	746.346780	373.677028	6
4	382.208495	191.607885	365.181946	183.094611			N	***667.304581***	334.155929	650.278032	325.642654	649.294016	325.150646	5
5	497.235438	249.121357	480.208889	240.608082	479.224873	240.116075	D	***553.261654***	277.134465	536.235105	268.621191	535.251089	268.129183	4
6	625.294016	313.150646	608.267467	304.637372	607.283451	304.145364	Q	438.234711	219.620994	421.208162	211.107719			3
7	788.357345	394.682311	771.330796	386.169036	770.346780	385.677028	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 LGPNDQYK
(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	933.455582	0.002226	LGPNDQYK
11.6	933.458969	-0.001161	LGMGEGGVSK
6.1	933.466827	-0.009019	IHSPSPHK
4.9	933.465469	-0.007661	ISDEEITK
1.7	933.455612	0.002196	LGFDDPVR
0.8	933.466827	-0.009019	LGNNVDFR
0.3	933.462967	-0.005159	LWDELMK

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

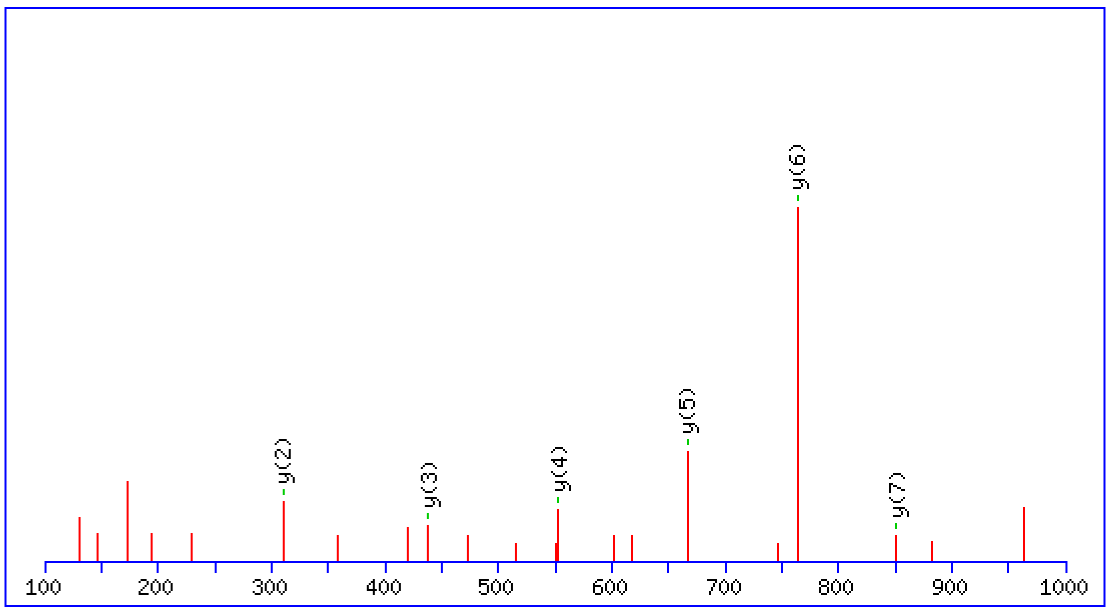
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSPNDQYK**
Found in **NUA4L_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4-like 2 OS=Homo sapiens GN=NDUFA4L2 PE=2 SV=1

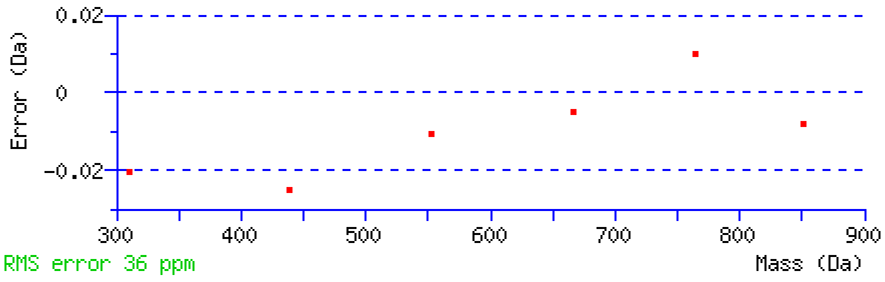
Match to Query 15249: 963.467048 from(482.740800,2+) rtinseconds(1067) index(599)
Title: Locus:1.1.1.1846.5
Data file 2011-11-14 - TFD - S 2-7.mgf

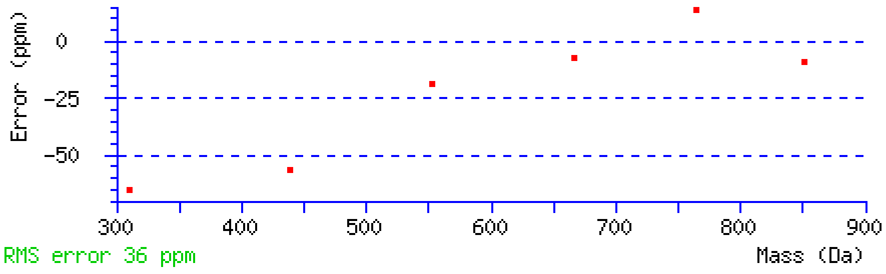
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 963.466141
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 3.2e-005
Matches : 6/70 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	201.123368	101.065322			183.112803	92.060039	S	***851.389373***	426.198325	834.362824	417.685050	833.378808	417.193042	7
3	298.176132	149.591704			280.165567	140.586422	P	***764.357345***	382.682311	747.330796	374.169036	746.346780	373.677028	6
4	412.219059	206.613168	395.192510	198.099893	394.208494	197.607885	N	***667.304581***	334.155929	650.278032	325.642654	649.294016	325.150646	5
5	527.246002	264.126639	510.219453	255.613365	509.235437	255.121357	D	***553.261654***	277.134465	536.235105	268.621191	535.251089	268.129183	4
6	655.304580	328.155928	638.278031	319.642654	637.294015	319.150646	Q	***438.234711***	219.620993	421.208162	211.107719			3
7	818.367909	409.687593	801.341360	401.174318	800.357344	400.682310	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 LSPNDQYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.4	963.466141	0.000907	LSPNDQYK
10.4	963.469528	-0.002480	SLNPTGTMK
9.6	963.458267	0.008781	LSVEEEMK
8.4	963.463638	0.003410	ISAWCWK
7.0	963.466156	0.000892	LHPPEDPK
3.9	963.469513	-0.002465	QAMTELQK
3.5	963.469513	-0.002465	ATQLEQMK
2.8	963.466156	0.000892	LHPPEDPK
1.6	963.469513	-0.002465	AQLTEQMK
1.0	963.466156	0.000892	LHPPEDPK

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

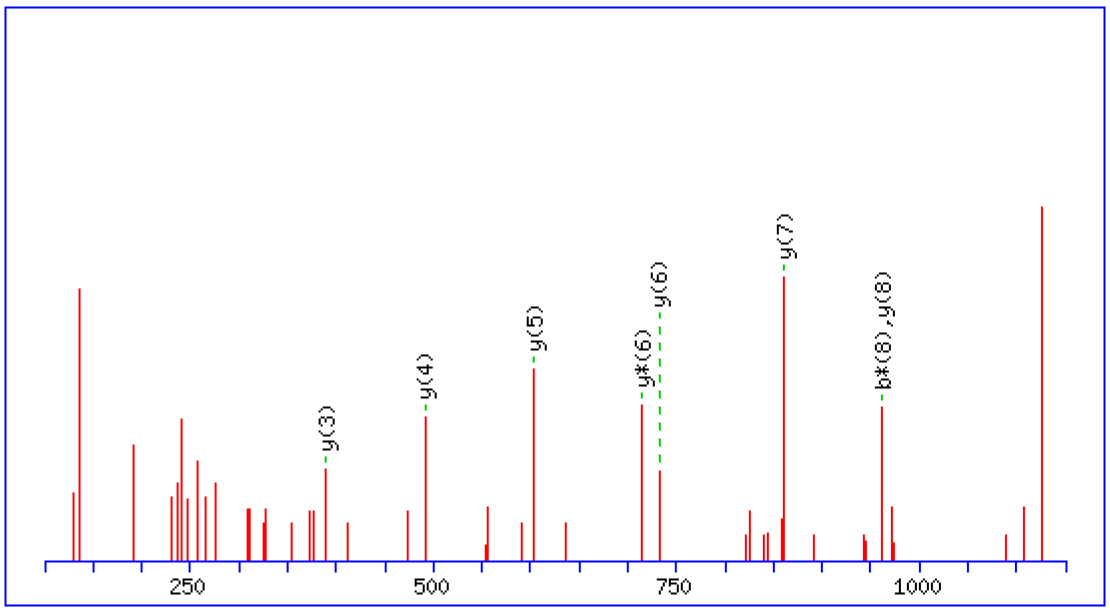
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTEQITNEK**
Found in **NDUA5_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3

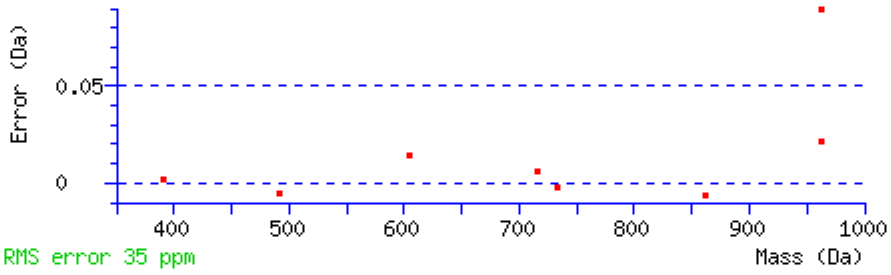
Match to Query 8750: 1124.534248 from(563.274400,2+) rtinseconds(1290) index(1004)
Title: Locus:1.1.1.2247.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

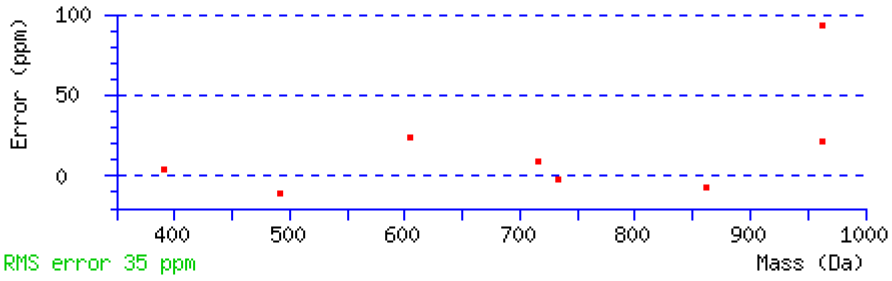
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1124.534943
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 4e-005
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	164.070605	82.538940					Y							9
2	265.118284	133.062780			247.107719	124.057498	T	***962.478917***	481.743097	945.452368	473.229822	944.468352	472.737814	8
3	394.160877	197.584077			376.150312	188.578794	E	***861.431238***	431.219257	844.404689	422.705983	843.420673	422.213975	7
4	522.219455	261.613366	505.192906	253.100091	504.208890	252.608083	Q	***732.388645***	366.697961	715.362096	358.184686	714.378080	357.692678	6
5	635.303519	318.155398	618.276970	309.642123	617.292954	309.150115	I	***604.330067***	302.668672	587.303518	294.155397	586.319502	293.663389	5
6	736.351198	368.679237	719.324649	360.165963	718.340633	359.673955	T	***491.246003***	246.126639	474.219454	237.613365	473.235438	237.121357	4
7	850.394125	425.700701	833.367576	417.187426	832.383560	416.695418	N	***390.198324***	195.602800	373.171775	187.089525	372.187759	186.597517	3
8	979.436718	490.221997	962.410169	481.708723	961.426153	481.216715	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 YTEQITNEK
(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	1124.534943	-0.000695	YTEQITNEK
3.8	1124.525070	0.009178	YRNGPDFPK

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

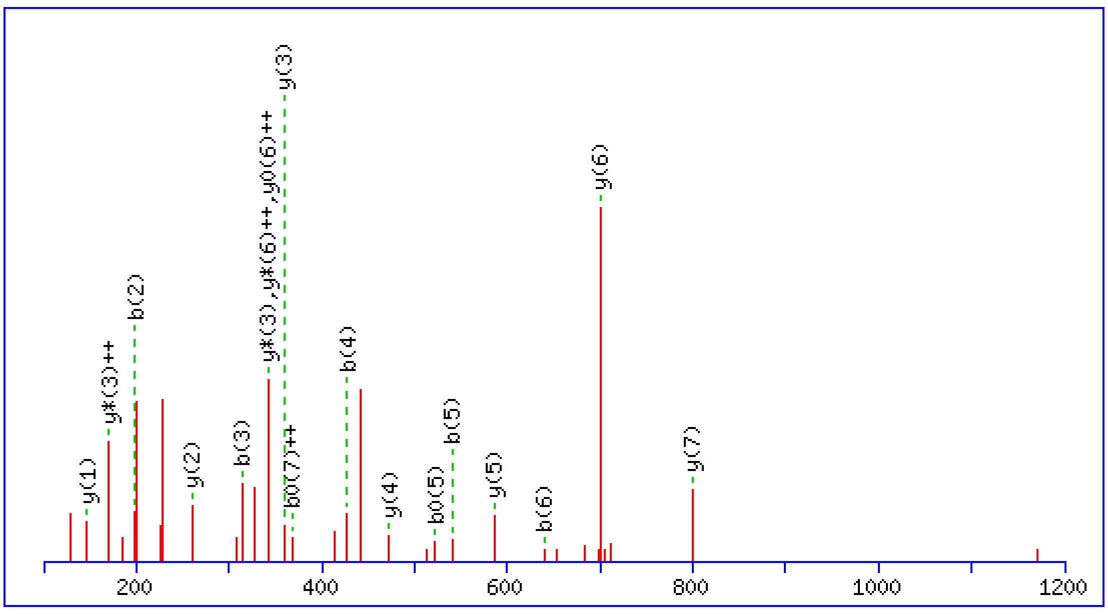
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVDLLVIK**
Found in **NDUA6_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens GN=NDUFA6 PE=1 SV=3

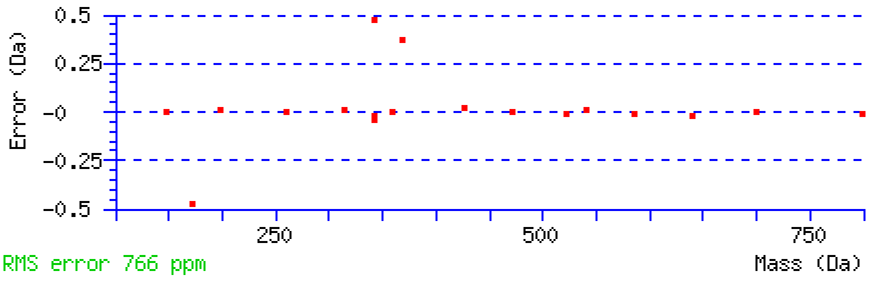
Match to Query 2117: 897.592988 from(449.803770,2+) rtinseconds(3020) index(10426)
Title: Locus:1.1.1.3054.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

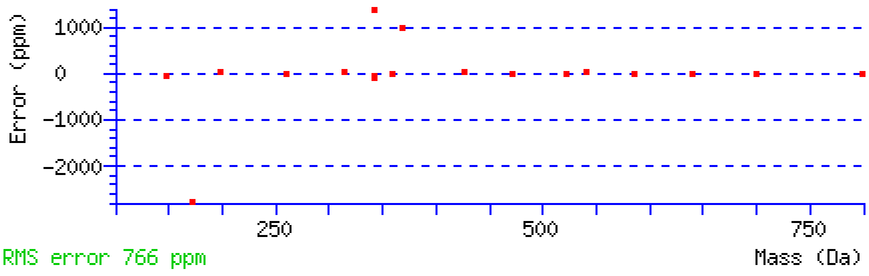
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 897.589905
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 4.1e-006
Matches : 18/56 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							8
2	**199.144104**	100.075690			V	***799.528767***	400.268022	782.502218	391.754747	781.518202	391.262739	7
3	**314.171047**	157.589161	296.160482	148.583879	D	***700.460353***	350.733815	683.433804	342.220540	682.449788	341.728532	6
4	**427.255111**	214.131193	409.244546	205.125911	L	***585.433410***	293.220343	568.406861	284.707069			5
5	**540.339175**	270.673226	522.328610	261.667943	L	***472.349346***	236.678311	455.322797	228.165036			4
6	**639.407589**	320.207433	621.397024	311.202150	V	***359.265282***	180.136279	342.238733	171.623004			3
7	752.491653	376.749465	734.481088	367.744182	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 VVDLLVIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	897.589905	0.003083	VVDLLVIK
15.0	897.601120	-0.008132	GKLKPVIK
12.2	897.589874	0.003114	DIIALLLK
10.0	897.601120	-0.008132	VQLKALVK
8.6	897.589905	0.003083	VVTIIPKI
2.2	897.589890	0.003098	VLSPLIIK

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

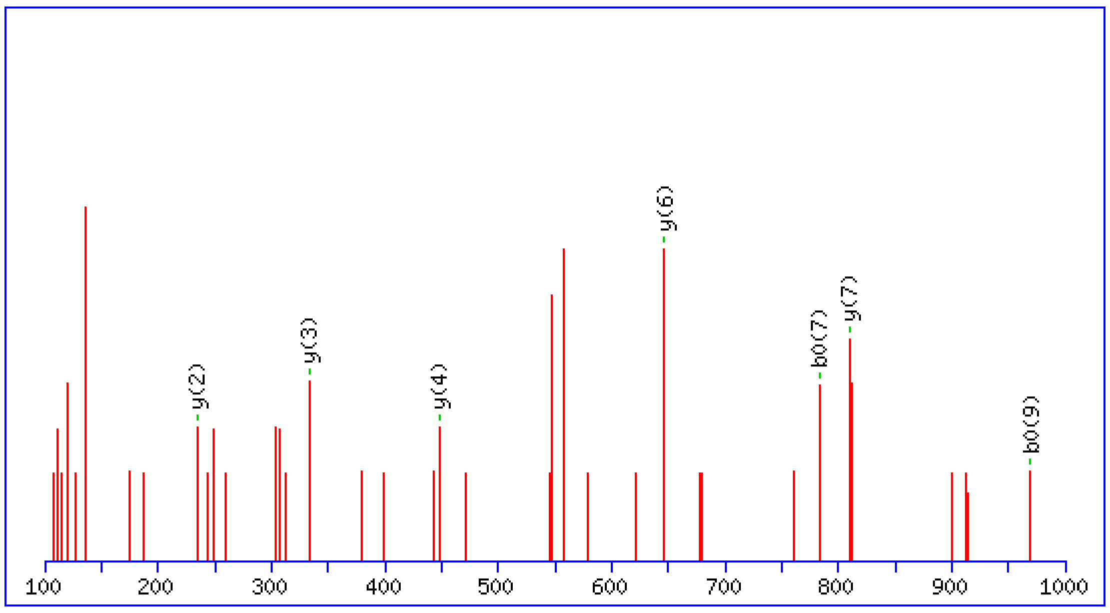
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QPVYVVDVSK**
Found in **NDUA9_HUMAN**, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDUFA9 PE=1 SV=2

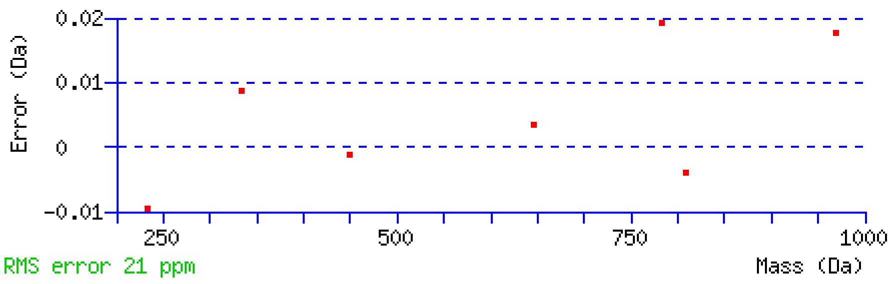
Match to Query 16910: 1132.608508 from(567.311530,2+) rtinseconds(2047) index(16778)
Title: Locus:1.1.1.2350.31
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

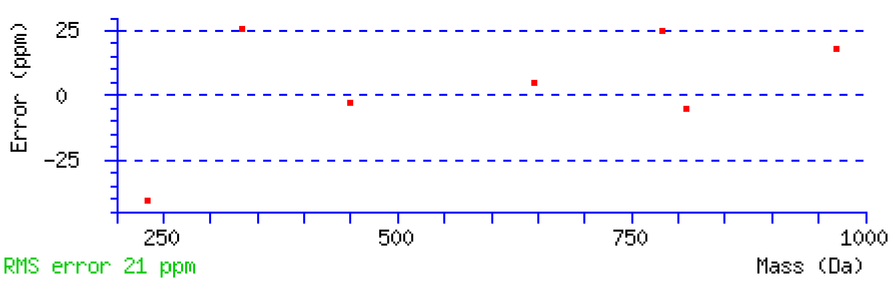
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1132.612839
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.00071
Matches : 7/94 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							10
2	226.118618	113.562947	209.092069	105.049673			P	1005.561524	503.284400	988.534975	494.771126	987.550959	494.279118	9
3	325.187032	163.097154	308.160483	154.583879			V	908.508760	454.758018	891.482211	446.244744	890.498195	445.752736	8
4	488.250361	244.628818	471.223812	236.115544			Y	***809.440346***	405.223811	792.413797	396.710537	791.429781	396.218529	7
5	587.318775	294.163026	570.292226	285.649751			V	***646.377017***	323.692147	629.350468	315.178872	628.366452	314.686864	6
6	686.387189	343.697233	669.360640	335.183958			V	547.308603	274.157940	530.282054	265.644665	529.298038	265.152657	5
7	801.414132	401.210704	784.387583	392.697430	783.403567	392.205422	D	***448.240189***	224.623732	431.213640	216.110458	430.229624	215.618450	4
8	900.482546	450.744911	883.455997	442.231636	882.471981	441.739628	V	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	3
9	987.514574	494.260925	970.488025	485.747650	969.504009	485.255642	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





NCBI **BLAST** search of QPVYVVDVSK
(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	1132.612839	-0.004331	QPVYVVDVSK
0.1	1132.598892	0.009616	IRAFAPETGR

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

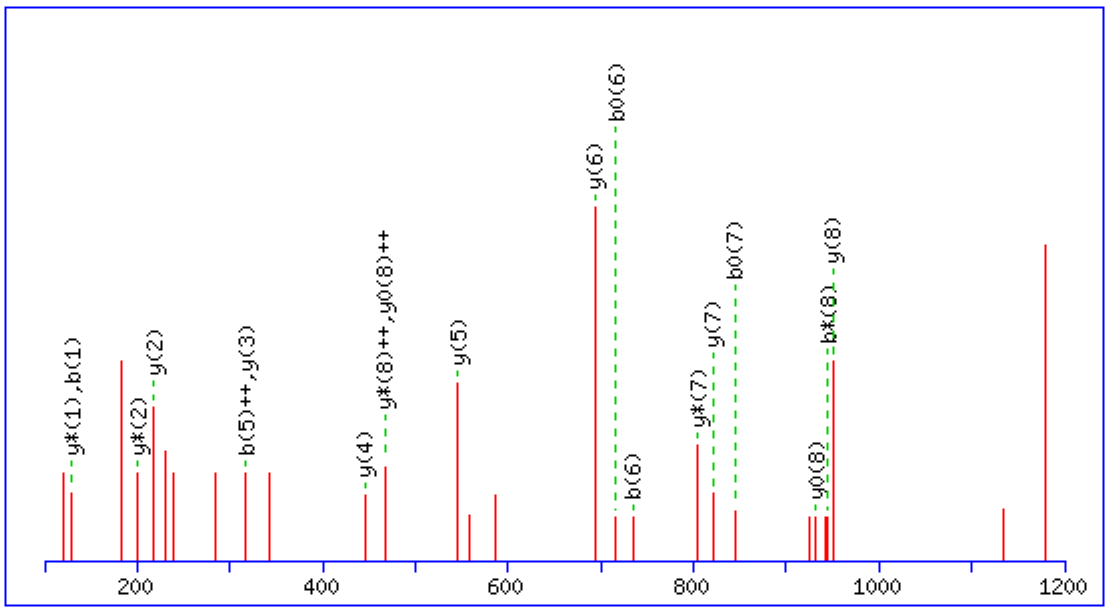
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVEQFTQVAK**
Found in **NDUBA_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3

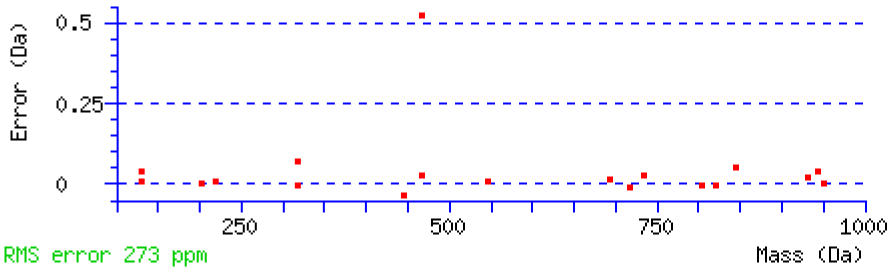
Match to Query 17342: 1177.602288 from(589.808420,2+) rtinseconds(1812) index(7278)
Title: Locus:1.1.1.2214.23
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

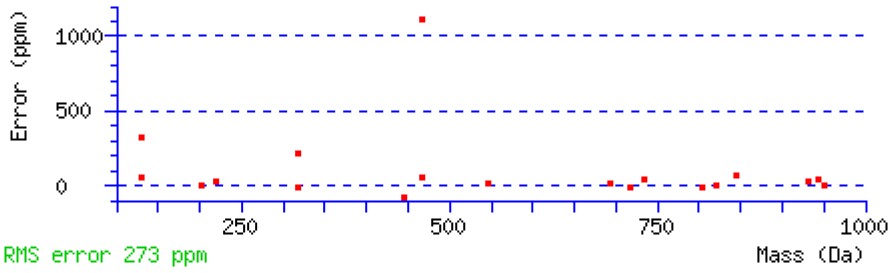
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1177.597900
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 8e-005
Matches : 19/94 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	**130.049869**	65.528572			112.039304	56.523290	E							10
2	229.118283	115.062780			211.107718	106.057497	V	1049.562588	525.284932	1032.536039	516.771658	1031.552023	516.279650	9
3	358.160876	179.584076			340.150311	170.578794	E	***950.494174***	475.750725	933.467625	467.237451	932.483609	466.745443	8
4	486.219454	243.613365	469.192905	235.100091	468.208889	234.608083	Q	***821.451581***	411.229429	804.425032	402.716154	803.441016	402.224146	7
5	633.287868	317.147572	616.261319	308.634298	615.277303	308.142290	F	***693.393003***	347.200140	676.366454	338.686865	675.382438	338.194857	6
6	**734.335547**	367.671412	717.308998	359.158137	716.324982	358.666129	T	***546.324589***	273.665933	529.298040	265.152658	528.314024	264.660650	5
7	862.394125	431.700701	845.367576	423.187426	844.383560	422.695418	Q	***445.276910***	223.142093	428.250361	214.628818			4
8	961.462539	481.234908	944.435990	472.721633	943.451974	472.229625	V	***317.218332***	159.112804	300.191783	150.599529			3
9	1032.499653	516.753465	1015.473104	508.240190	1014.489088	507.748182	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 EVEQFTQVAK
(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	1177.597900	0.004388	EVEQFTQVAK
2.2	1177.593872	0.008416	QTQSASSTLQK

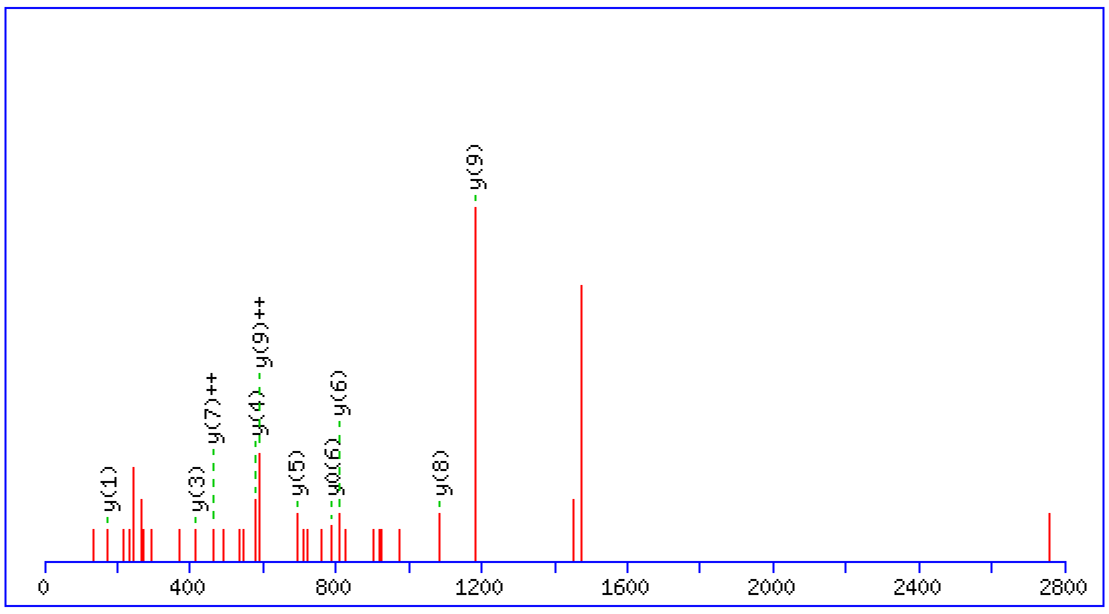
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QYPYNNLYLER**
Found in **NDUB8_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUFB8 PE=1 SV=1

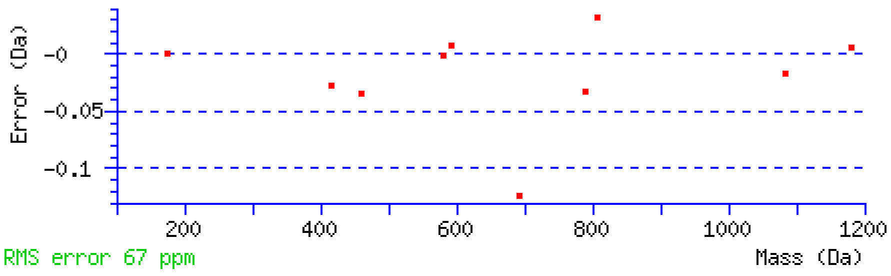
Match to Query 28645: 1471.714708 from(736.864630,2+) rtinseconds(2600) index(23696)
Title: Locus:1.1.1.2487.48
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

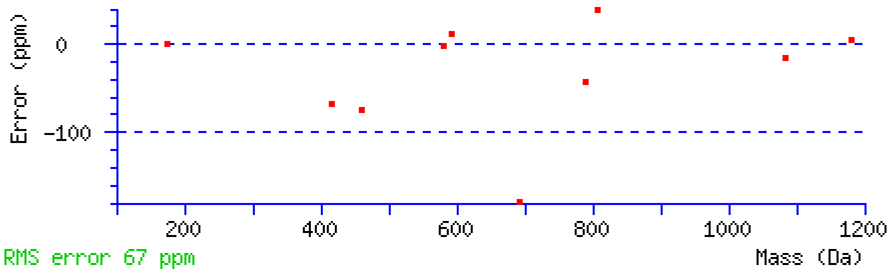
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.709534
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.001
Matches : 10/100 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							11
2	292.129183	146.568230	275.102634	138.054955			Y	1344.658278	672.832777	1327.631729	664.319502	1326.647713	663.827494	10
3	389.181947	195.094611	372.155398	186.581337			P	***1181.594949***	591.301112	1164.568400	582.787838	1163.584384	582.295830	9
4	552.245276	276.626276	535.218727	268.113002			Y	***1084.542185***	542.774730	1067.515636	534.261456	1066.531620	533.769448	8
5	666.288203	333.647740	649.261654	325.134465			N	921.478856	461.243066	904.452307	452.729791	903.468291	452.237783	7
6	780.331130	390.669203	763.304581	382.155929			N	***807.435929***	404.221602	790.409380	395.708328	789.425364	395.216320	6
7	893.415194	447.211235	876.388645	438.697961			L	***693.393002***	347.200139	676.366453	338.686864	675.382437	338.194856	5
8	1056.478523	528.742900	1039.451974	520.229625			Y	***580.308938***	290.658107	563.282389	282.144832	562.298373	281.652824	4
9	1169.562587	585.284931	1152.536038	576.771657			L	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
10	1298.605180	649.806228	1281.578631	641.292953	1280.594615	640.800945	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 QYPYNNLYLER
(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	1471.709534	0.005174	QYPYNNLYLER
8.8	1471.705536	0.009172	EGSDSYAITFRAR
0.1	1471.712936	0.001772	INSNPYFSLMVR

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

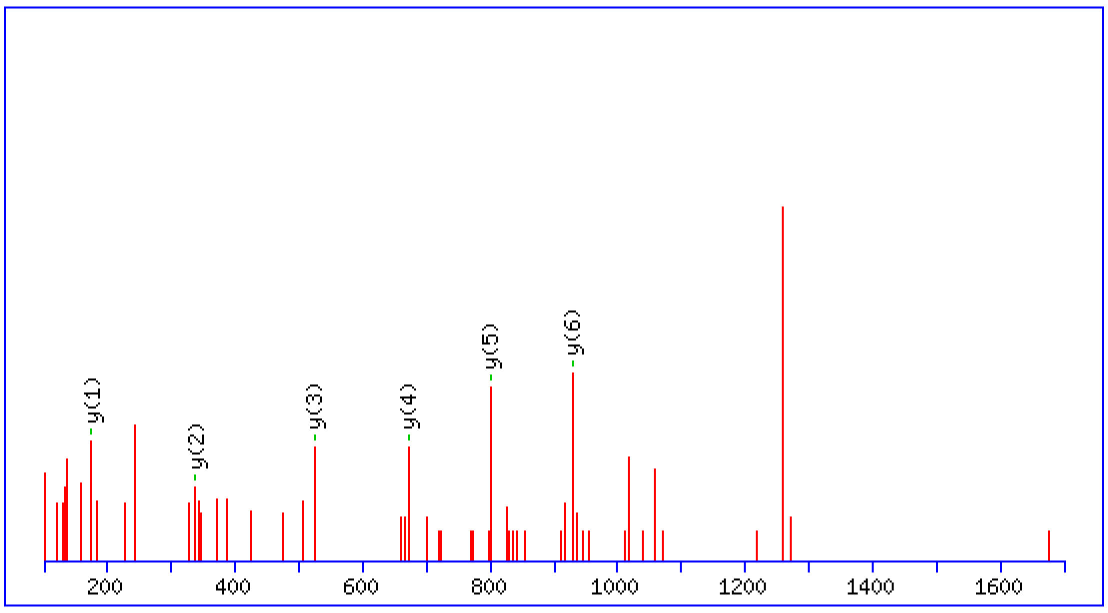
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAEEEFWYR**
Found in **NDUB9_HUMAN**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=1 SV=3

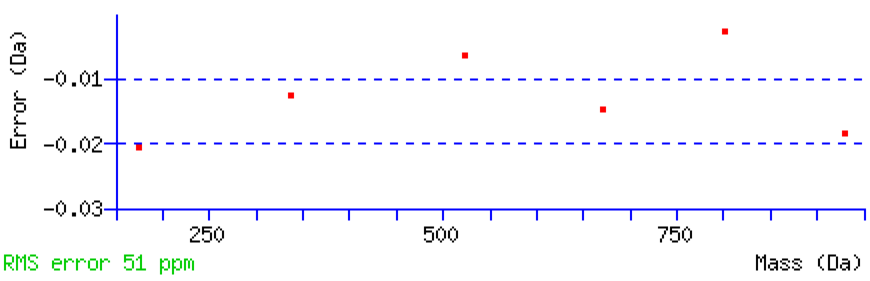
Match to Query 14470: 1257.529768 from(629.772160,2+) rtinseconds(2663) index(17540)
Title: Locus:1.1.1.2598.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

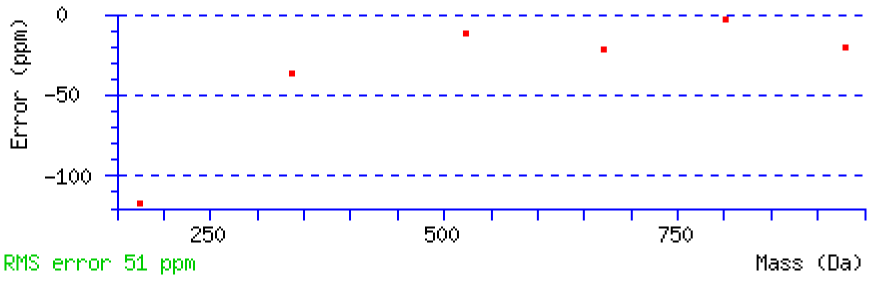
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1257.530182
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00064
Matches : 6/72 fragment ions using 11 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							9
2	201.086983	101.047130	183.076418	92.041847	A	1129.494901	565.251089	1112.468352	556.737814	1111.484336	556.245806	8
3	330.129576	165.568426	312.119011	156.563144	E	1058.457787	529.732532	1041.431238	521.219257	1040.447222	520.727249	7
4	459.172169	230.089722	441.161604	221.084440	E	*929.415194*	465.211235	912.388645	456.697961	911.404629	456.205953	6
5	588.214762	294.611019	570.204197	285.605737	E	*800.372601*	400.689939	783.346052	392.176664	782.362036	391.684656	5
6	735.283176	368.145226	717.272611	359.139944	F	*671.330008*	336.168642	654.303459	327.655368			4
7	921.362489	461.184883	903.351924	452.179600	W	*524.261594*	262.634435	507.235045	254.121161			3
8	1084.425818	542.716547	1066.415253	533.711265	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 EAEEEFWYR
(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	1257.530182	-0.000414	EAEEEFWYR

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

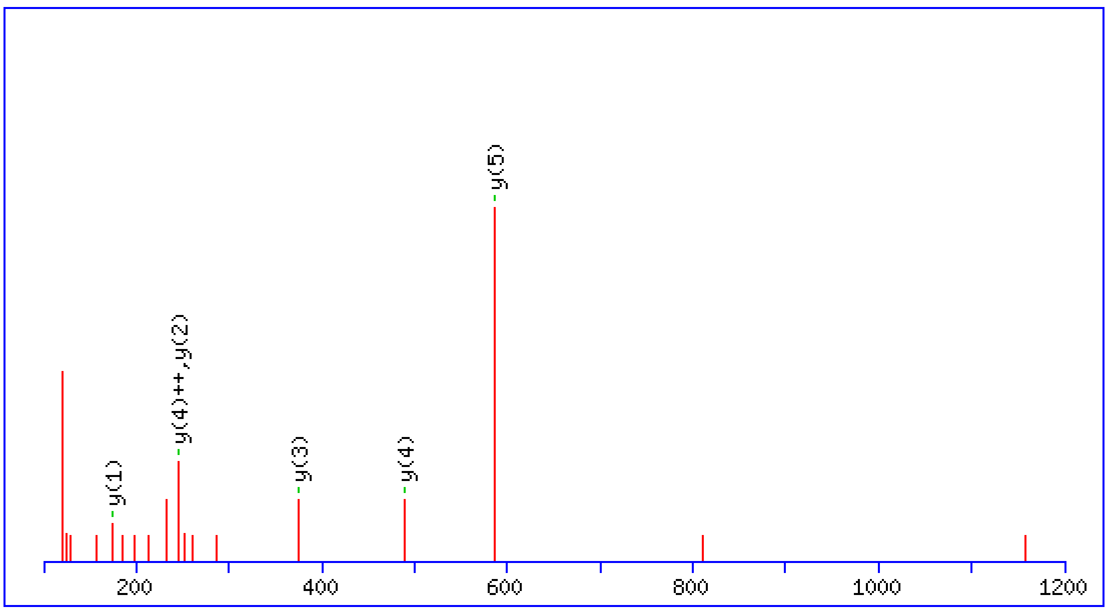
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLPDEAR**
Found in **NDUC2_HUMAN**, NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1

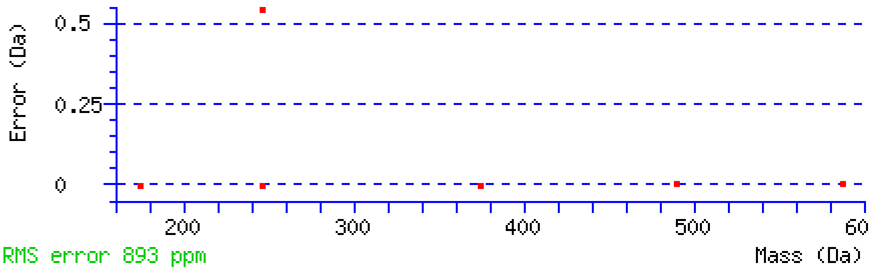
Match to Query 1740: 846.424408 from(424.219480,2+) rtinseconds(1638) index(2507)
Title: Locus:1.1.1.2381.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

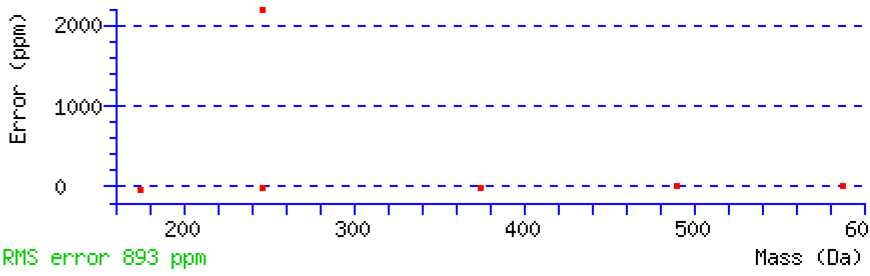
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 846.423553
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0012
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	148.075690	74.541483			F							7
2	261.159754	131.083515			L	700.362430	350.684853	683.335881	342.171579	682.351865	341.679571	6
3	358.212518	179.609897			P	***587.278366***	294.142821	570.251817	285.629547	569.267801	285.137539	5
4	473.239461	237.123369	455.228896	228.118086	D	***490.225602***	245.616439	473.199053	237.103164	472.215037	236.611156	4
5	602.282054	301.644665	584.271489	292.639383	E	***375.198659***	188.102967	358.172110	179.589693	357.188094	179.097685	3
6	673.319168	337.163222	655.308603	328.157940	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 FLPDEAR
(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	846.423553	0.000855	FLPDEAR
10.7	846.430756	-0.006348	SNRDSLR
10.7	846.419525	0.004883	SQAADSLR
9.6	846.423553	0.000855	VEFPEAR
9.5	846.419510	0.004898	ESQKEAR
8.3	846.426926	-0.002518	SCPVLNK
4.5	846.419525	0.004883	SAPASATAR
3.2	846.426926	-0.002518	NMIPVNK
3.0	846.426926	-0.002518	EIVMPSR
1.8	846.426926	-0.002518	LMLEPGR

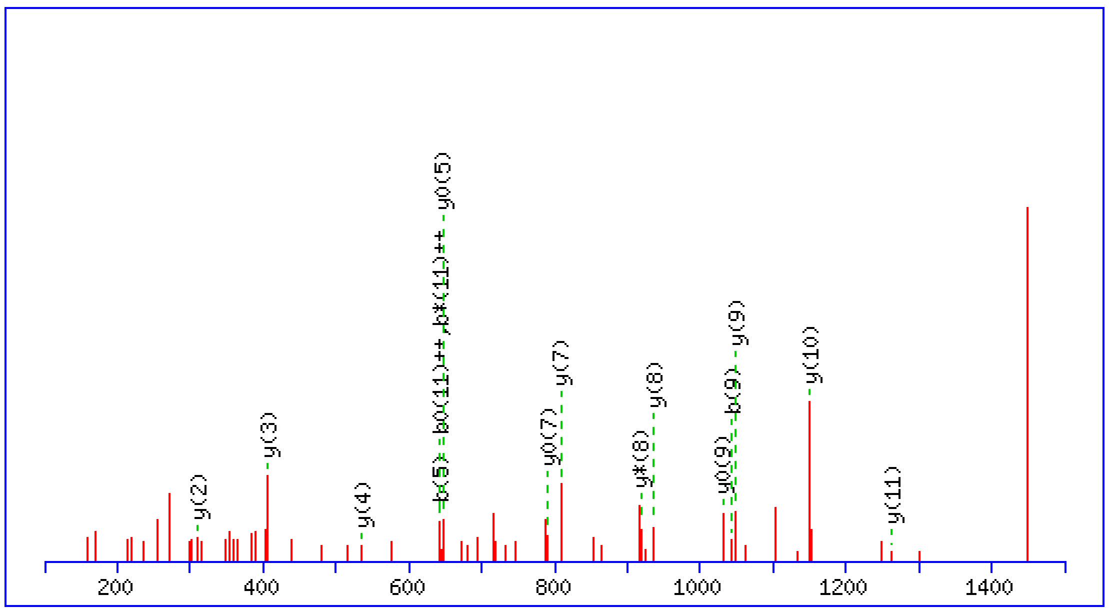
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLTIQSGEQPYK**
Found in **NDUS5_HUMAN**, NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens GN=NDUFS5 PE=1 SV=3

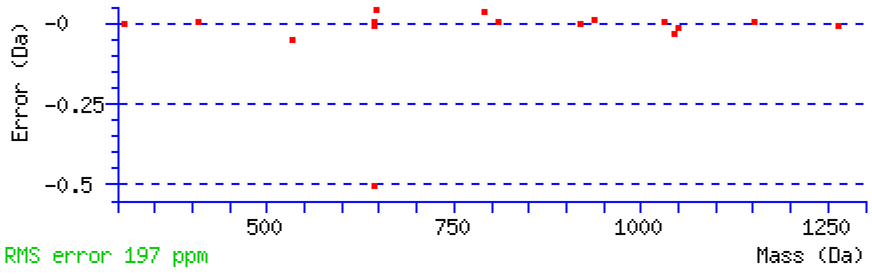
Match to Query 16196: 1448.717988 from(725.366270,2+) rtinseconds(2615) index(8597)
Title: Locus:1.1.1.3013.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

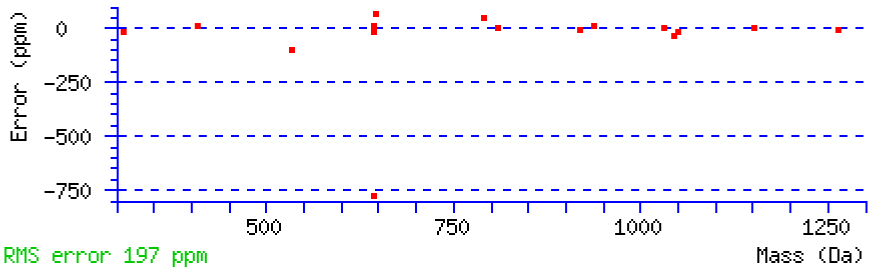
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1448.729965
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.0003
Matches : 16/112 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	187.086589	94.046932					W							12
2	300.170653	150.588965					L	***1263.657945***	632.332611	1246.631396	623.819336	1245.647380	623.327328	11
3	401.218332	201.112804			383.207767	192.107522	T	***1150.573881***	575.790579	1133.547332	567.277304	1132.563316	566.785296	10
4	514.302396	257.654836			496.291831	248.649554	I	***1049.526202***	525.266739	1032.499653	516.753465	1031.515637	516.261457	9
5	**642.360974**	321.684125	625.334425	313.170851	624.350409	312.678843	Q	***936.442138***	468.724707	919.415589	460.211433	918.431573	459.719425	8
6	729.393002	365.200139	712.366453	356.686865	711.382437	356.194857	S	***808.383560***	404.695418	791.357011	396.182144	790.372995	395.690136	7
7	786.414466	393.710871	769.387917	385.197597	768.403901	384.705589	G	721.351532	361.179404	704.324983	352.666130	703.340967	352.174122	6
8	915.457059	458.232168	898.430510	449.718893	897.446494	449.226885	E	664.330068	332.668672	647.303519	324.155398	646.319503	323.663390	5
9	**1043.515637**	522.261457	1026.489088	513.748182	1025.505072	513.256174	Q	***535.287475***	268.147376	518.260926	259.634101			4
10	1140.568401	570.787839	1123.541852	562.274564	1122.557836	561.782556	P	***407.228897***	204.118087	390.202348	195.604812			3
11	1303.631730	652.319503	1286.605181	643.806229	1285.621165	643.314221	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 WLTIQSGEQPYK
(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	1448.729965	-0.011977	WLTIQSGEQPYK
5.0	1448.714706	0.003282	EASLYSPPSTLPR
0.4	1448.714737	0.003251	GEPGLPGPEGPPGLK
0.0	1448.729309	-0.011321	SVPSEKLTTAMNR

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

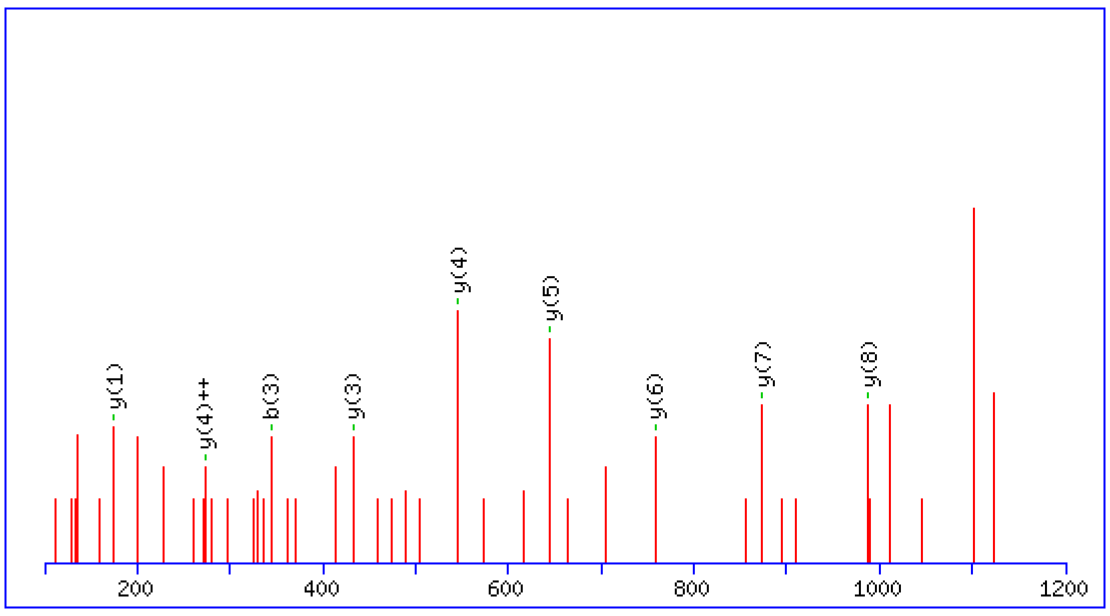
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDDLVNWAR**
Found in **NDUS7_HUMAN**, NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=1 SV=3

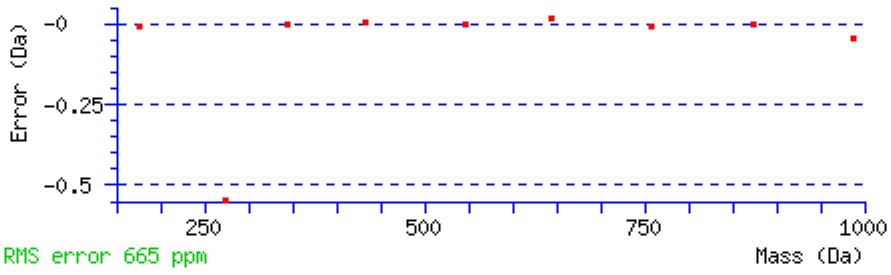
Match to Query 12390: 1100.565408 from(551.289980,2+) rtinseconds(2885) index(22987)
Title: Locus:1.1.1.2609.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

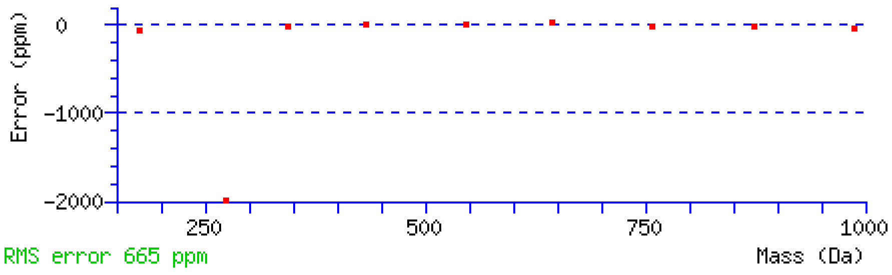
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1100.561447
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61  Expect: 1.1e-005
Matches : 9/72 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	114.091340	57.549308					L							9
2	229.118283	115.062779			211.107718	106.057497	D	***988.484670***	494.745973	971.458121	486.232698	970.474105	485.740690	8
3	344.145226	172.576251			326.134661	163.570968	D	***873.457727***	437.232502	856.431178	428.719227	855.447162	428.227219	7
4	457.229290	229.118283			439.218725	220.113001	L	***758.430784***	379.719030	741.404235	371.205755			6
5	556.297704	278.652490			538.287139	269.647208	V	***645.346720***	323.176998	628.320171	314.663724			5
6	670.340631	335.673954	653.314082	327.160679	652.330066	326.668671	N	***546.278306***	273.642791	529.251757	265.129516			4
7	856.419944	428.713610	839.393395	420.200335	838.409379	419.708328	W	***432.235379***	216.621327	415.208830	208.108053			3
8	927.457058	464.232167	910.430509	455.718892	909.446493	455.226884	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 LDDLVNWAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.7	1100.561447	0.003961	LDDLVNWAR
13.1	1100.557419	0.007989	DLDNSPLRR
8.9	1100.561462	0.003946	LYGPDVGQPR
7.4	1100.571304	-0.005896	IEELEAELR
7.1	1100.557434	0.007974	EVSPPGARTR
5.8	1100.557419	0.007989	EDVLEQRGR
5.4	1100.571304	-0.005896	IEELEEALR
5.4	1100.557419	0.007989	ITENPPSRR
4.8	1100.557434	0.007974	GQAPSSTPGKR
3.7	1100.571335	-0.005927	EAKVGEPEVK

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

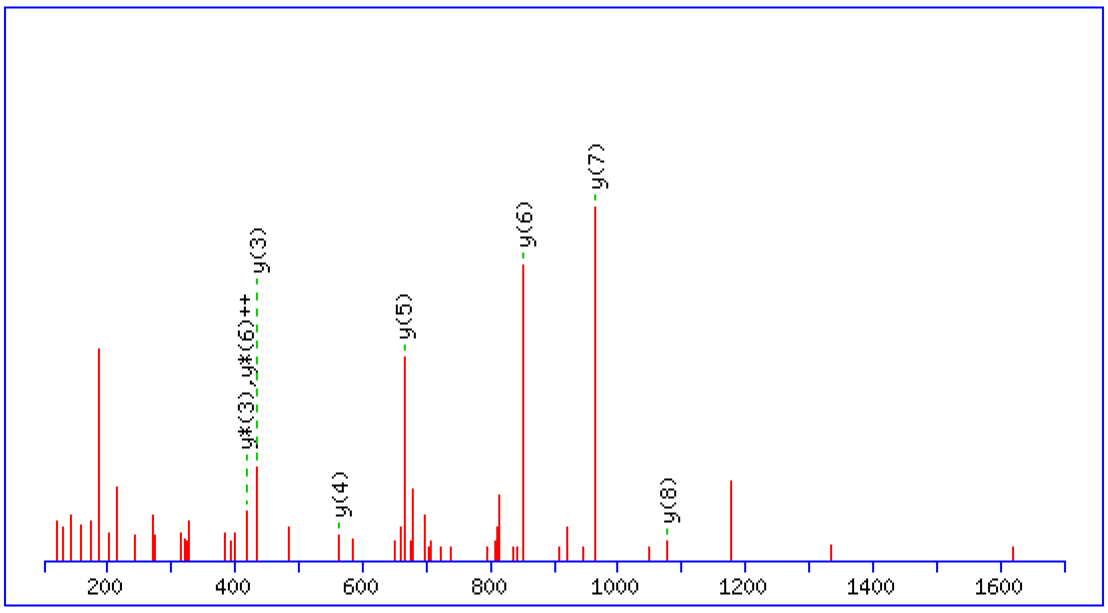
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLWTELFR**
Found in **NDUS8_HUMAN**, NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Homo sapiens GN=NDUFS8 PE=1 SV=1

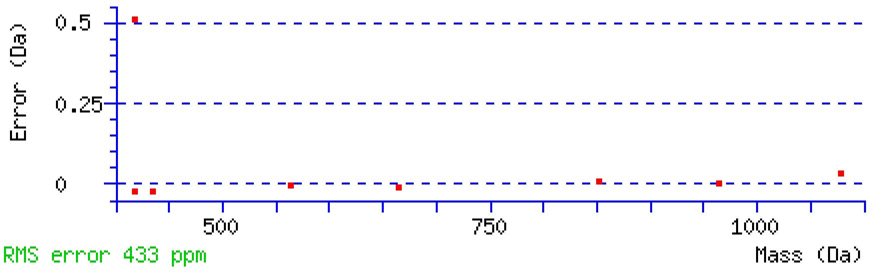
Match to Query 20093: 1177.650948 from(589.832750,2+) rtinseconds(4154) index(53886)
Title: Locus:1.1.1.3385.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

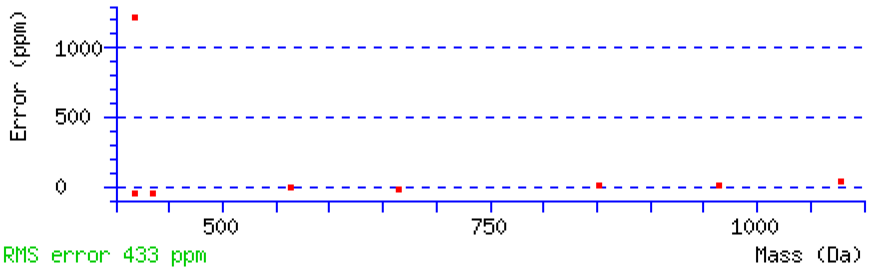
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1177.649536
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 5e-005
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	102.054955	51.531116	84.044390	42.525833	T							9
2	215.139019	108.073147	197.128454	99.067865	L	***1077.609143***	539.308210	1060.582594	530.794935	1059.598578	530.302927	8
3	328.223083	164.615179	310.212518	155.609897	L	***964.525079***	482.766178	947.498530	474.252903	946.514514	473.760895	7
4	514.302396	257.654836	496.291831	248.649554	W	***851.441015***	426.224146	834.414466	417.710871	833.430450	417.218863	6
5	615.350075	308.178676	597.339510	299.173393	T	***665.361702***	333.184489	648.335153	324.671215	647.351137	324.179207	5
6	744.392668	372.699972	726.382103	363.694690	E	***564.314023***	282.660650	547.287474	274.147375	546.303458	273.655367	4
7	857.476732	429.242004	839.466167	420.236722	L	***435.271430***	218.139353	418.244881	209.626079			3
8	1004.545146	502.776211	986.534581	493.770929	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 TLLWTELFR
(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	1177.649536	0.001412	TLLWTELFR
1.5	1177.652908	-0.001960	TGLKLTFCPK
1.1	1177.659424	-0.008476	ITIFEVLESK

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

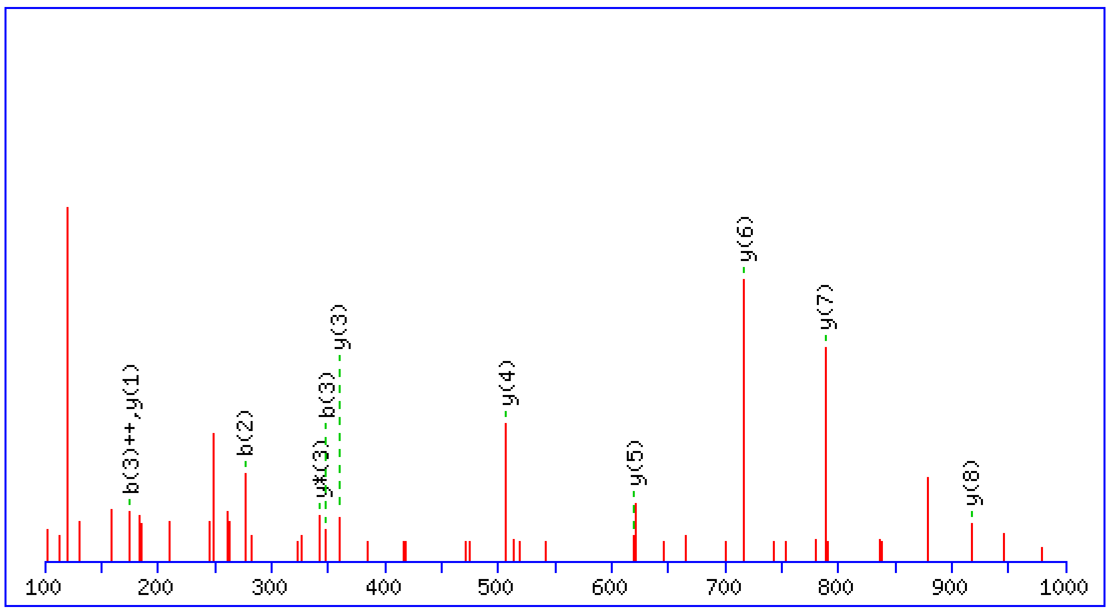
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEAPLFNAR**
Found in **NDUS1_HUMAN**, NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3

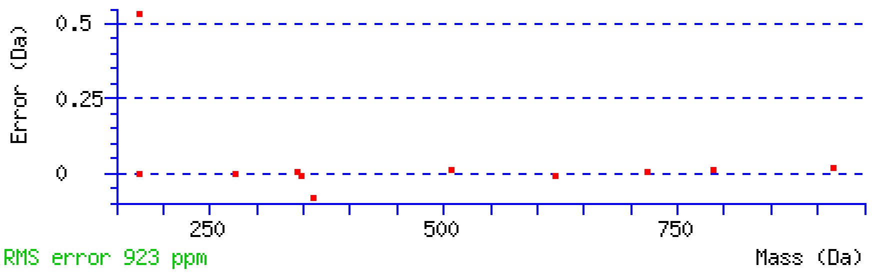
Match to Query 16173: 1063.546168 from(532.780360,2+) rtinseconds(2720) index(38490)
Title: Locus:1.1.1.1681.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

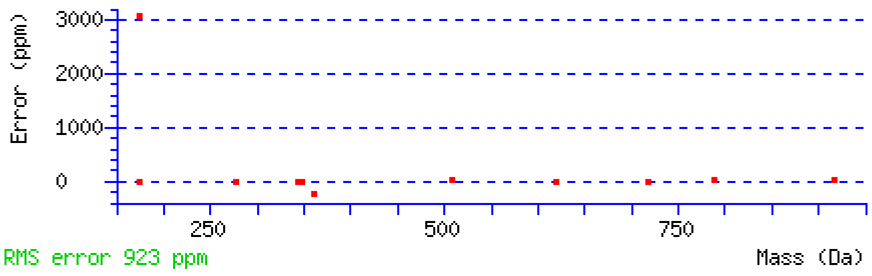
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1063.545059
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.00076
Matches : 11/68 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	148.075690	74.541483					F							9
2	**277.118283**	139.062779			259.107718	130.057497	E	***917.483942***	459.245609	900.457393	450.732334	899.473377	450.240326	8
3	**348.155397**	174.581336			330.144832	165.576054	A	***788.441349***	394.724313	771.414800	386.211038			7
4	445.208161	223.107718			427.197596	214.102436	P	***717.404235***	359.205756	700.377686	350.692481			6
5	558.292225	279.649751			540.281660	270.644468	L	***620.351471***	310.679374	603.324922	302.166099			5
6	705.360639	353.183958			687.350074	344.178675	F	***507.267407***	254.137341	490.240858	245.624067			4
7	819.403566	410.205421	802.377017	401.692146	801.393001	401.200138	N	***360.198993***	180.603134	343.172444	172.089860			3
8	890.440680	445.723978	873.414131	437.210703	872.430115	436.718695	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 FEAPLFNAR
(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	1063.545059	0.001109	FEAPLFNAR
2.7	1063.548447	-0.002279	MPPPPPKPR
2.7	1063.548447	-0.002279	MPPPPPKPR
2.7	1063.548447	-0.002279	MPPPPPKPR
2.7	1063.548447	-0.002279	MPPPPPKPR
2.2	1063.551804	-0.005636	MTLVLSMNR

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

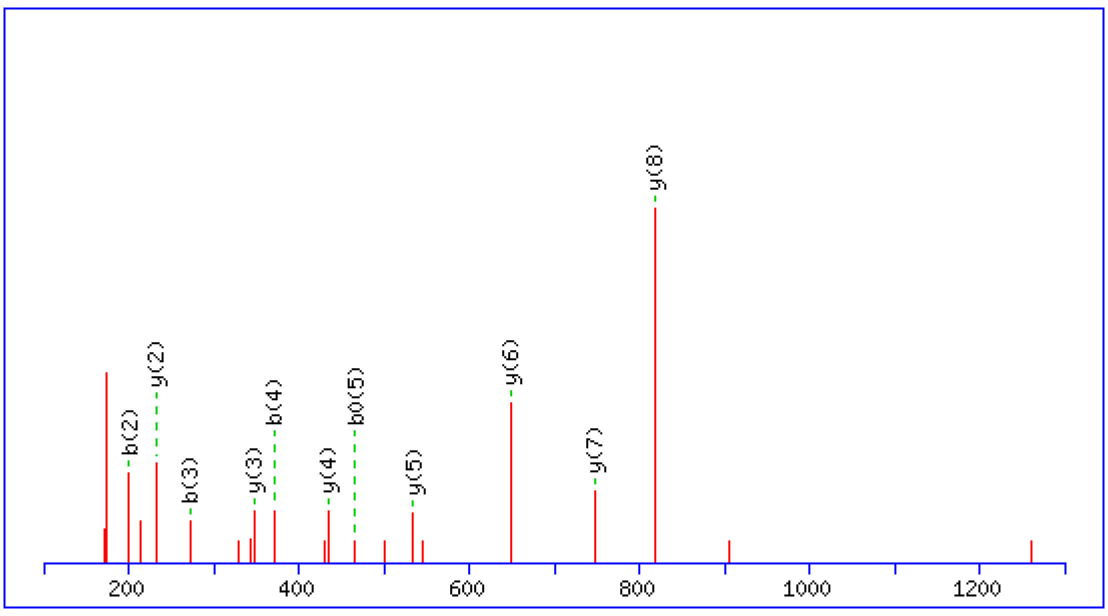
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVAVITSDGR**
Found in **NAA38_HUMAN**, N-alpha-acetyltransferase 38, NatC auxiliary subunit OS=Homo sapiens GN=NAA38 PE=1 SV=3

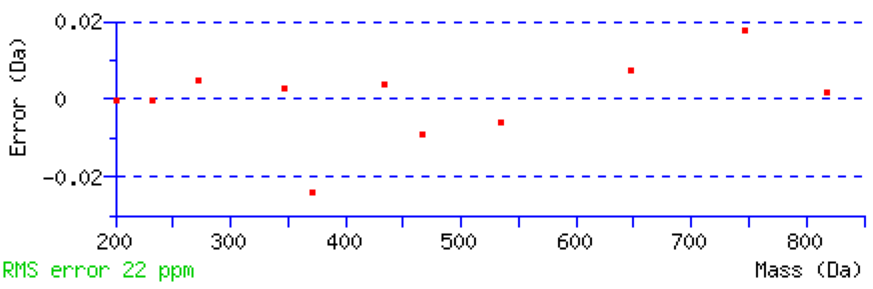
Match to Query 5907: 1017.543048 from(509.778800,2+) rtinseconds(1519) index(1177)
Title: Locus:1.1.1.2428.10
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

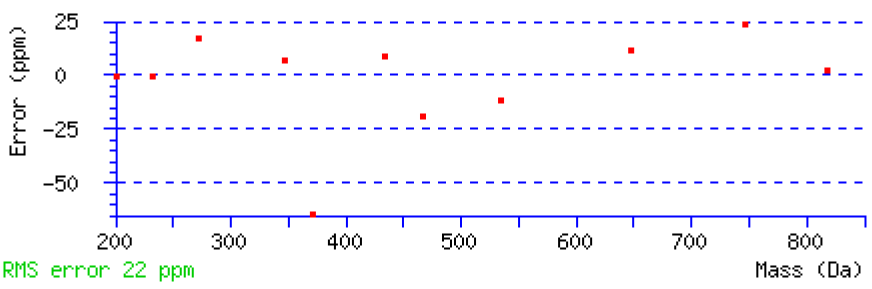
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1017.545486
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 8.7e-006
Matches : 11/86 fragment ions using 16 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	**201.123369**	101.065322	183.112804	92.060040	V	917.505072	459.256174	900.478523	450.742900	899.494507	450.250892	9
3	**272.160483**	136.583879	254.149918	127.578597	A	***818.436658***	409.721967	801.410109	401.208693	800.426093	400.716685	8
4	**371.228897**	186.118087	353.218332	177.112804	V	***747.399544***	374.203410	730.372995	365.690136	729.388979	365.198128	7
5	484.312961	242.660119	466.302396	233.654836	I	***648.331130***	324.669203	631.304581	316.155929	630.320565	315.663921	6
6	585.360640	293.183958	567.350075	284.178676	T	***535.247066***	268.127171	518.220517	259.613897	517.236501	259.121889	5
7	672.392668	336.699972	654.382103	327.694690	S	***434.199387***	217.603332	417.172838	209.090057	416.188822	208.598049	4
8	787.419611	394.213444	769.409046	385.208161	D	***347.167359***	174.087318	330.140810	165.574043	329.156794	165.082035	3
9	844.441075	422.724176	826.430510	413.718893	G	***232.140416***	116.573846	215.113867	108.060572			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of TVAVITSDGR
(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	1017.545486	-0.002438	TVAVITSDGR
12.5	1017.552826	-0.009778	EAAVMKEIK
12.5	1017.545441	-0.002393	LSAVEKESR
9.4	1017.534210	0.008838	SIKEVDEAK
8.5	1017.552841	-0.009793	QIEITICK
3.3	1017.552856	-0.009808	VPAKLSPMK
1.8	1017.538925	0.004123	EAMVRALGR
1.6	1017.538940	0.004108	GVLGMANKGR
0.8	1017.552826	-0.009778	EAVLAMEKK
0.6	1017.534241	0.008807	LPVTGTAESK

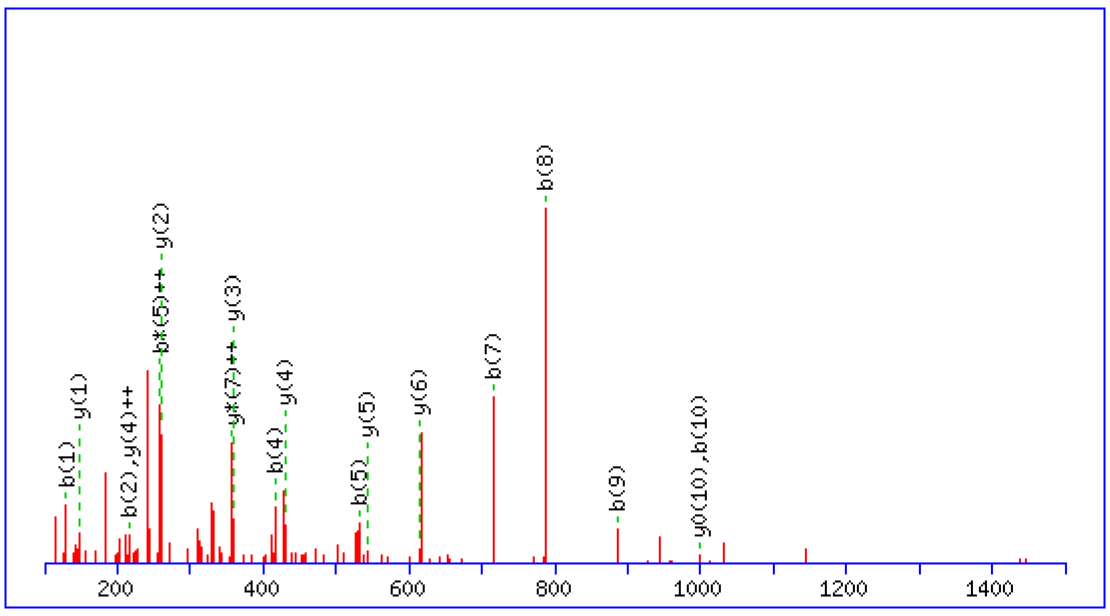
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSEADALAVLK**
Found in **SYNE1_HUMAN**, Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=3

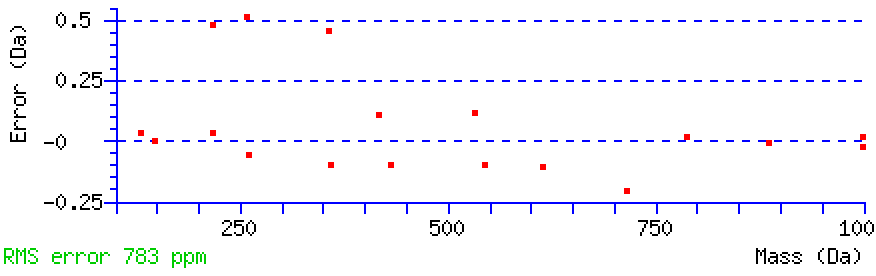
Match to Query 17981: 1143.617348 from(572.815950,2+) rtinseconds(2408) index(21167)
Title: Locus:1.1.1.2380.21
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

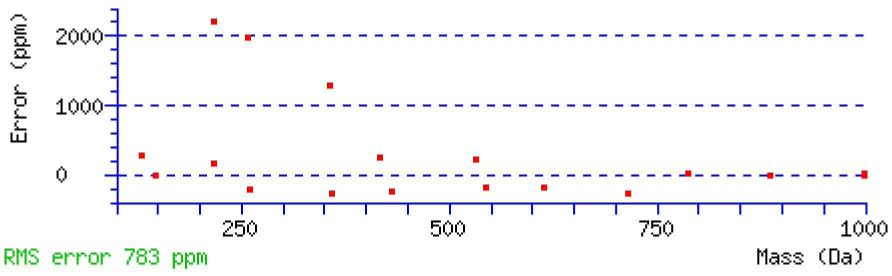
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1143.613525
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0057
Matches : 18/106 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	***129.065854***	65.036565	112.039305	56.523291			Q							11
2	***216.097882***	108.552579	199.071333	100.039305	198.087317	99.547296	S	1016.562252	508.784764	999.535703	500.271490	998.551687	499.779482	10
3	345.140475	173.073875	328.113926	164.560601	327.129910	164.068593	E	929.530224	465.268750	912.503675	456.755476	911.519659	456.263468	9
4	***416.177589***	208.592432	399.151040	200.079158	398.167024	199.587150	A	800.487631	400.747454	783.461082	392.234179	782.477066	391.742171	8
5	***531.204532***	266.105904	514.177983	257.592629	513.193967	257.100621	D	729.450517	365.228897	712.423968	356.715622	711.439952	356.223614	7
6	602.241646	301.624461	585.215097	293.111186	584.231081	292.619178	A	**614.423574**	307.715425	597.397025	299.202151			6
7	***715.325710***	358.166493	698.299161	349.653218	697.315145	349.161210	L	**543.386460**	272.196868	526.359911	263.683594			5
8	***786.362824***	393.685050	769.336275	385.171775	768.352259	384.679767	A	**430.302396**	215.654836	413.275847	207.141562			4
9	***885.431238***	443.219257	868.404689	434.705982	867.420673	434.213974	V	**359.265282**	180.136279	342.238733	171.623005			3
10	***998.515302***	499.761289	981.488753	491.248014	980.504737	490.756006	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 QSEADALAVLK
(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	1143.613525	0.003823	QSEADALAVLK
21.5	1143.613525	0.003823	EKAVTDEKPK
19.3	1143.624771	-0.007423	IDQRTAISPK
19.1	1143.613525	0.003823	KSLSPEQDIK
17.2	1143.613556	0.003792	QVTTPDVEKK
16.1	1143.613541	0.003807	SLQSALDVSPK
15.8	1143.613556	0.003792	ASPVTQTSPIK
14.5	1143.624771	-0.007423	SISASGRPPLK
14.4	1143.628784	-0.011436	EAKAPPPPPPK
13.9	1143.624786	-0.007438	QTTPVQGAKSK

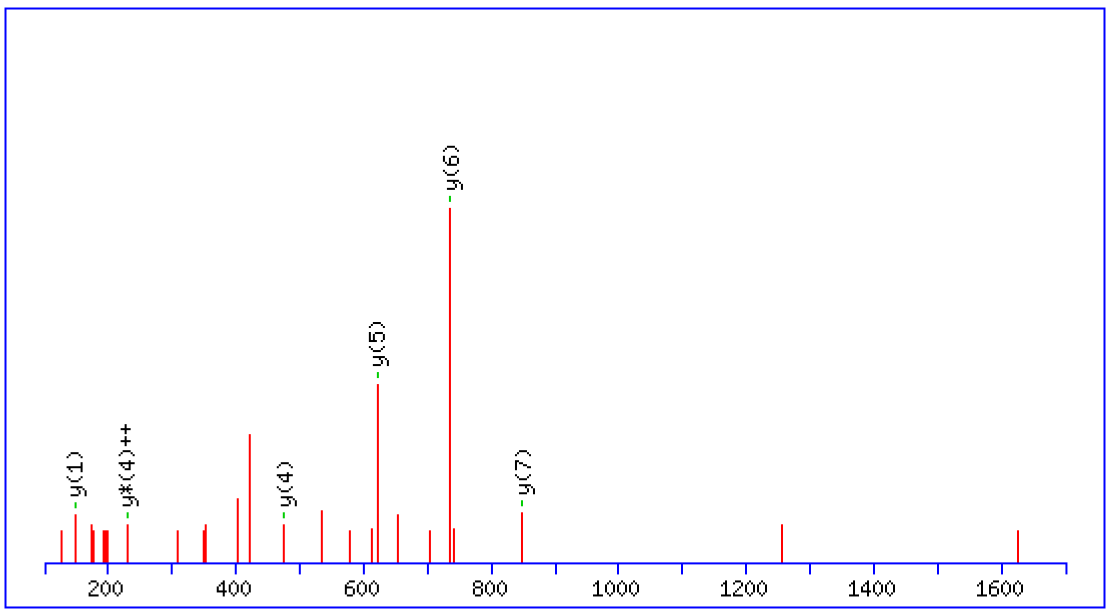
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLMQEAK**
Found in **NMUR1_HUMAN**, Neuromedin-U receptor 1 OS=Homo sapiens GN=NMUR1 PE=2 SV=1

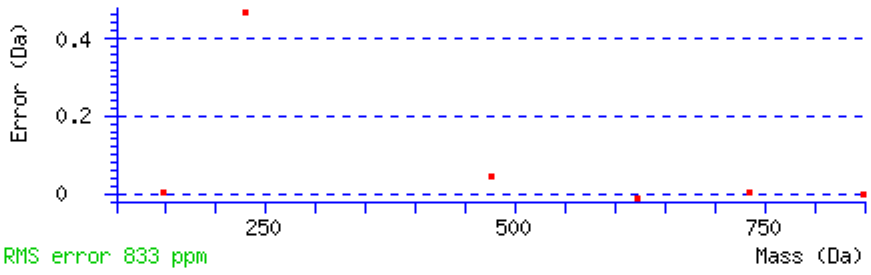
Match to Query 8891: 960.522688 from(481.268620,2+) rtinseconds(1742) index(11637)
Title: Locus:1.1.1.2474.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

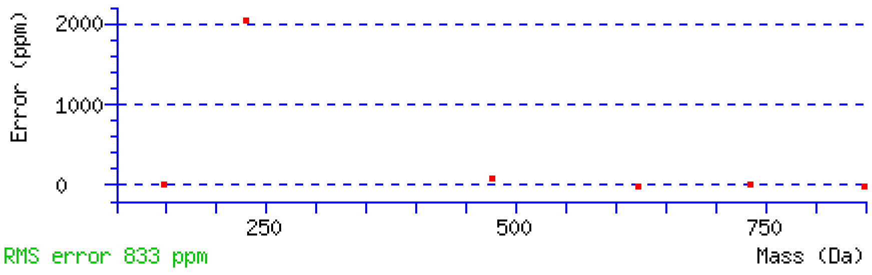
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 960.531372
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: 42  Expect: 0.00074
Matches : 6/98 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	227.175404	114.091340					L	*848.454617*	424.730947	831.428068	416.217672	830.444052	415.725664	7
3	340.259468	170.633372					L	*735.370553*	368.188915	718.344004	359.675640	717.359988	359.183632	6
4	487.294868	244.151072					M	*622.286489*	311.646883	605.259940	303.133608	604.275924	302.641600	5
5	615.353446	308.180361	598.326897	299.667087			Q	*475.251089*	238.129183	458.224540	229.615908	457.240524	229.123900	4
6	744.396039	372.701658	727.369490	364.188383	726.385474	363.696375	E	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
7	815.433153	408.220215	798.406604	399.706940	797.422588	399.214932	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 LLLMQEAK
(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	960.531372	-0.008684	LLLMQEAK
26.2	960.531372	-0.008684	LLEMLQSK
14.9	960.528015	-0.005327	EPPSFIKK
12.5	960.528030	-0.005342	EPPTFVKK
11.4	960.531372	-0.008684	ILSMAEGIK
11.4	960.531372	-0.008684	LLAMLEQK
11.4	960.531357	-0.008669	LLMAEEKK
11.4	960.528030	-0.005342	LLVNFDPK
8.4	960.531387	-0.008699	LDSIICVK
5.3	960.517456	0.005232	GLLRAMER

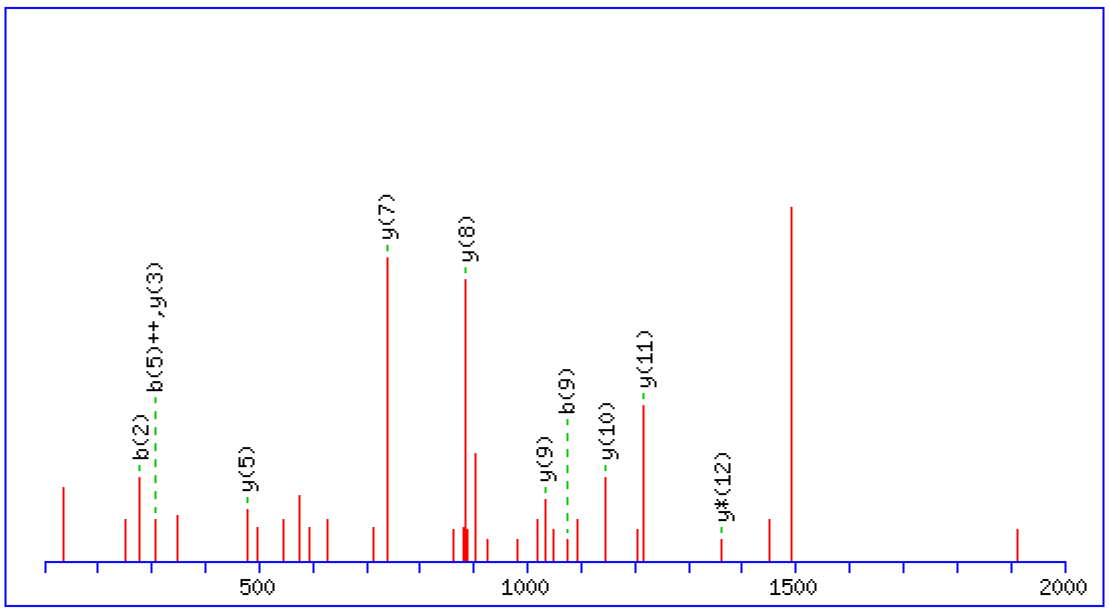
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYANFFPYGDASK**
Found in **HPCA_HUMAN**, Neuron-specific calcium-binding protein hippocalcin OS=Homo sapiens GN=HPCA PE=1 SV=2

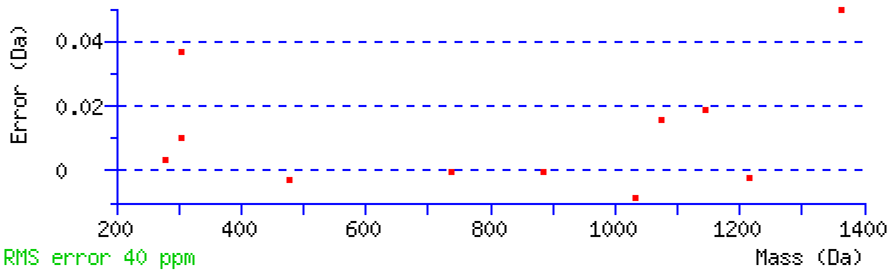
Match to Query 29158: 1491.716148 from(746.865350,2+) rtinseconds(3100) index(32354)
Title: Locus:1.1.1.2676.31
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

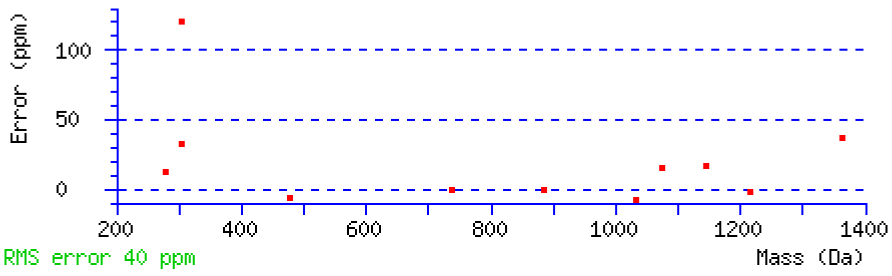
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1491.703415
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.0015
Matches : 11/118 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							13
2	**277.154669**	139.080973					Y	1379.626644	690.316960	1362.600095	681.803686	1361.616079	681.311678	12
3	348.191783	174.599530					A	***1216.563315***	608.785296	1199.536766	600.272021	1198.552750	599.780013	11
4	462.234710	231.620993	445.208161	223.107719			N	***1145.526201***	573.266739	1128.499652	564.753464	1127.515636	564.261456	10
5	609.303124	305.155200	592.276575	296.641926			F	***1031.483274***	516.245275	1014.456725	507.732001	1013.472709	507.239993	9
6	756.371538	378.689407	739.344989	370.176133			F	***884.414860***	442.711068	867.388311	434.197794	866.404295	433.705786	8
7	853.424302	427.215789	836.397753	418.702515			P	***737.346446***	369.176861	720.319897	360.663587	719.335881	360.171579	7
8	1016.487631	508.747454	999.461082	500.234179			Y	640.293682	320.650479	623.267133	312.137205	622.283117	311.645197	6
9	**1073.509095**	537.258186	1056.482546	528.744911			G	***477.230353***	239.118815	460.203804	230.605540	459.219788	230.113532	5
10	1188.536038	594.771657	1171.509489	586.258383	1170.525473	585.766375	D	420.208889	210.608083	403.182340	202.094808	402.198324	201.602800	4
11	1259.573152	630.290214	1242.546603	621.776940	1241.562587	621.284932	A	***305.181946***	153.094611	288.155397	144.581337	287.171381	144.089329	3
12	1346.605180	673.806228	1329.578631	665.292954	1328.594615	664.800946	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 IYANFFPYGDASK
(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	1491.703415	0.012733	IYANFFPYGDASK
2.2	1491.725235	-0.009087	MAAAPGGSAQPAGPGPR
0.6	1491.706665	0.009483	GDPGRPGPPGPVGPR
0.3	1491.706619	0.009529	RAPQASGPSTPGYR
0.2	1491.713989	0.002159	FEGMEPLPSRSSR

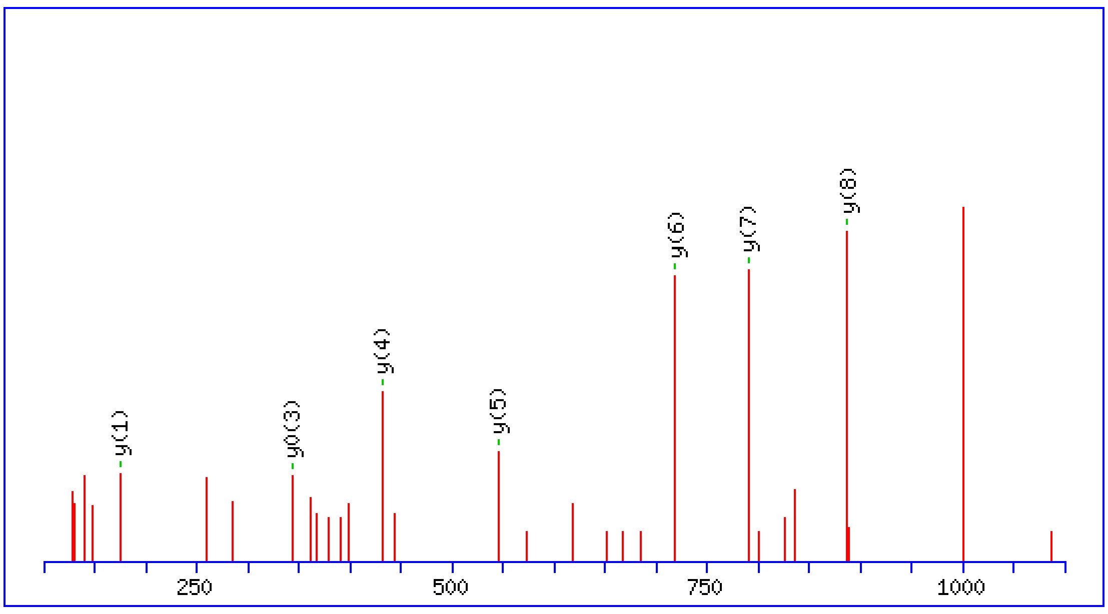
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPACIAGER**
Found in **DEF1_HUMAN**, Neutrophil defensin 1 OS=Homo sapiens GN=DEFA1 PE=1 SV=1

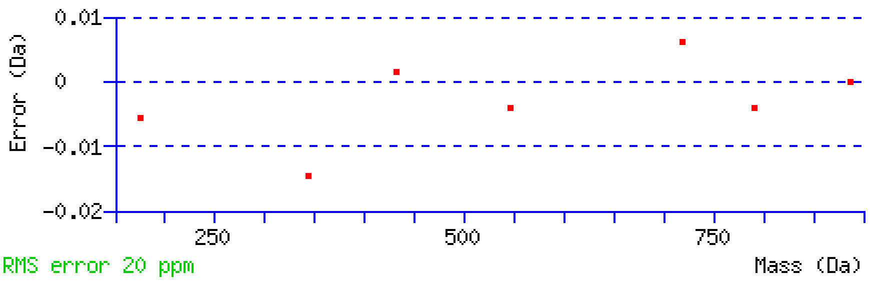
Match to Query 6294: 999.516948 from(500.765750,2+) rtinseconds(1646) index(2552)
Title: Locus:1.1.1.2384.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

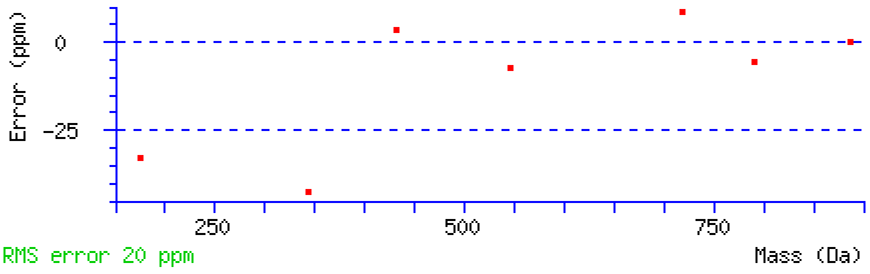
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 999.517120
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 1.7e-005
Matches : 7/64 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	211.144104	106.075690			P	***887.440364***	444.223820	870.413815	435.710546	869.429799	435.218538	8
3	282.181218	141.594247			A	***790.387600***	395.697438	773.361051	387.184164	772.377035	386.692156	7
4	456.227517	228.617396			C	***719.350486***	360.178881	702.323937	351.665607	701.339921	351.173599	6
5	569.311581	285.159429			I	***545.304187***	273.155732	528.277638	264.642457	527.293622	264.150449	5
6	640.348695	320.677986			A	***432.220123***	216.613700	415.193574	208.100425	414.209558	207.608417	4
7	697.370159	349.188718			G	361.183009	181.095143	344.156460	172.581868	343.172444	172.089860	3
8	826.412752	413.710014	808.402187	404.704732	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 IPACIAGER
(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	999.517120	-0.000172	IPACIAGER
17.4	999.517136	-0.000188	LPSSPLGCR
12.9	999.520981	-0.004033	LGRGQGAADR
7.8	999.517120	-0.000172	CLAPLEGAR
1.7	999.517120	-0.000172	LPPNREMK
0.5	999.517807	-0.000859	LPFHFDPK
0.5	999.517120	-0.000172	LPPNREMK
0.0	999.513763	0.003185	IAPNWDIR
0.0	999.520966	-0.004018	EGQNQLRR

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

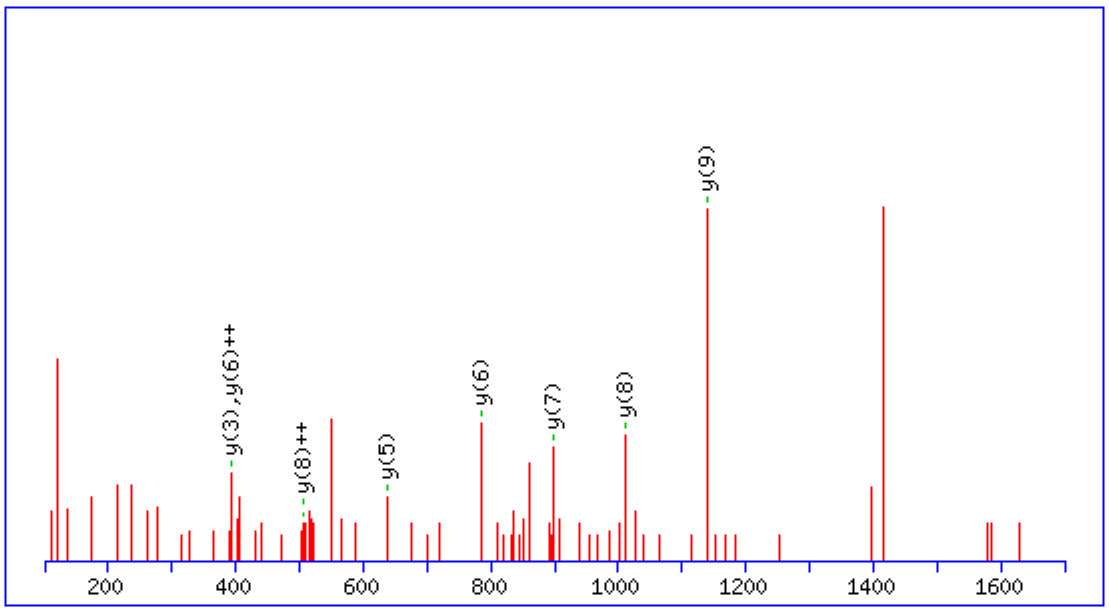
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQELIFEDFAR**
Found in **NIBL1_HUMAN**, Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3

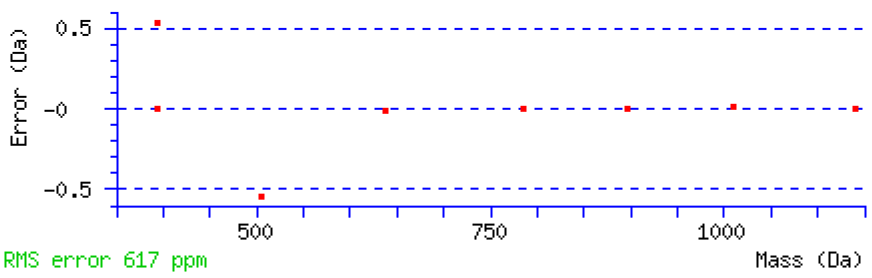
Match to Query 27312: 1413.698808 from(707.856680,2+) rtinseconds(3646) index(44751)
Title: Locus:1.1.1.3321.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

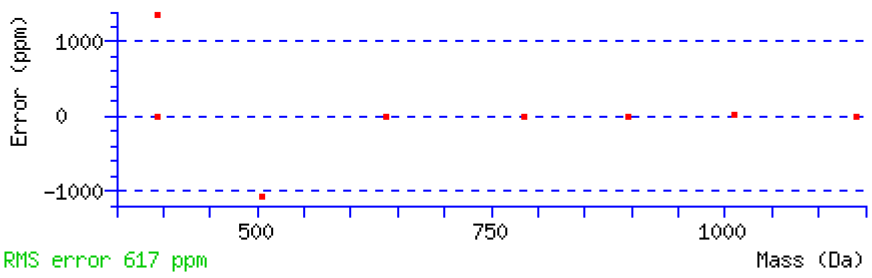
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1413.692856
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.00039
Matches : 8/108 fragment ions using 13 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	276.134268	138.570772	259.107719	130.057497			Q	1267.631729	634.319503	1250.605180	625.806228	1249.621164	625.314220	10
3	405.176861	203.092068	388.150312	194.578794	387.166296	194.086786	E	***1139.573151***	570.290214	1122.546602	561.776939	1121.562586	561.284931	9
4	518.260925	259.634101	501.234376	251.120826	500.250360	250.628818	L	***1010.530558***	505.768917	993.504009	497.255643	992.519993	496.763635	8
5	631.344989	316.176133	614.318440	307.662858	613.334424	307.170850	I	***897.446494***	449.226885	880.419945	440.713611	879.435929	440.221603	7
6	778.413403	389.710340	761.386854	381.197065	760.402838	380.705057	F	***784.362430***	392.684853	767.335881	384.171579	766.351865	383.679571	6
7	907.455996	454.231636	890.429447	445.718362	889.445431	445.226354	E	***637.294016***	319.150646	620.267467	310.637372	619.283451	310.145364	5
8	1022.482939	511.745108	1005.456390	503.231833	1004.472374	502.739825	D	508.251423	254.629349	491.224874	246.116075	490.240858	245.624067	4
9	1169.551353	585.279315	1152.524804	576.766040	1151.540788	576.274032	F	***393.224480***	197.115878	376.197931	188.602603			3
10	1240.588467	620.797872	1223.561918	612.284597	1222.577902	611.792589	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 FQELIFEDFAR
(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	1413.692856	0.005952	FQELIFEDFAR
2.0	1413.709961	-0.011153	EVAPGEKSVPETR

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

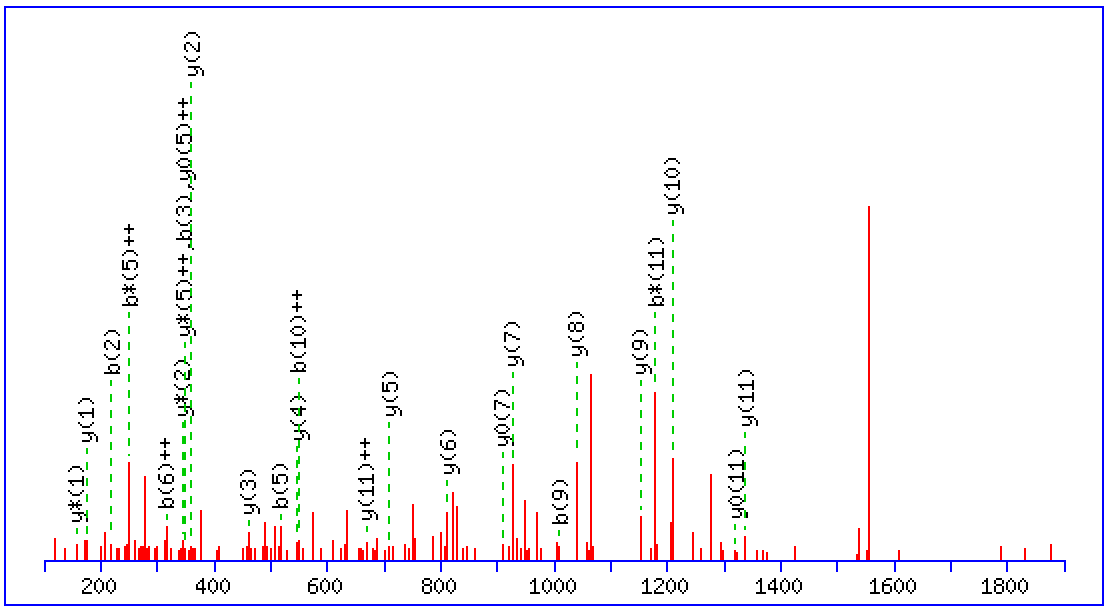
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFQGLLDTYSVWR**
Found in **PNCB_HUMAN**, Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1 PE=1 SV=2

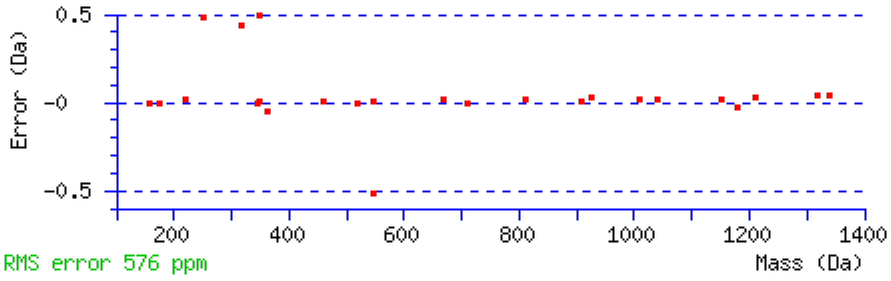
Match to Query 38350: 1554.782428 from(778.398490,2+) rtinseconds(3670) index(51528)
Title: Locus:1.1.1.2937.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

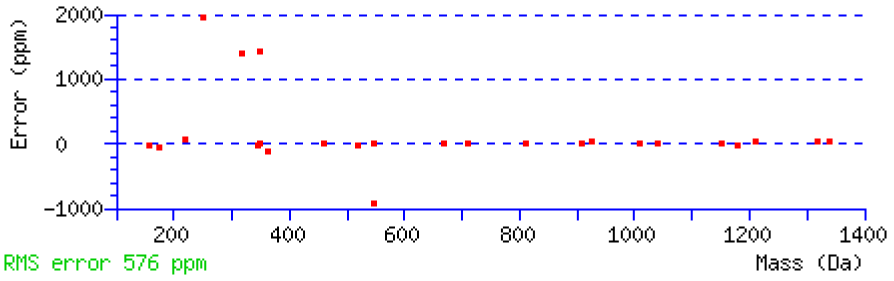
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1554.783081
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0051
Matches : 26/122 fragment ions using 82 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	**219.112804**	110.060040					F	1484.753242	742.880259	1467.726693	734.366985	1466.742677	733.874977	12
3	**347.171382**	174.089329	330.144833	165.576055			Q	***1337.684828***	669.346052	1320.658279	660.832778	1319.674263	660.340770	11
4	404.192846	202.600061	387.166297	194.086786			G	***1209.626250***	605.316763	1192.599701	596.803489	1191.615685	596.311481	10
5	**517.276910**	259.142093	500.250361	250.628819			L	***1152.604786***	576.806031	1135.578237	568.292757	1134.594221	567.800749	9
6	630.360974	315.684125	613.334425	307.170851			L	***1039.520722***	520.263999	1022.494173	511.750725	1021.510157	511.258717	8
7	745.387917	373.197597	728.361368	364.684322	727.377352	364.192314	D	***926.436658***	463.721967	909.410109	455.208693	908.426093	454.716685	7
8	846.435596	423.721436	829.409047	415.208162	828.425031	414.716154	T	***811.409715***	406.208496	794.383166	397.695221	793.399150	397.203213	6
9	**1009.498925**	505.253101	992.472376	496.739826	991.488360	496.247818	Y	***710.362036***	355.684656	693.335487	347.171382	692.351471	346.679374	5
10	1096.530953	548.769115	1079.504404	540.255840	1078.520388	539.763832	S	***547.298707***	274.152992	530.272158	265.639717	529.288142	265.147709	4
11	1195.599367	598.303322	1178.572818	589.790047	1177.588802	589.298039	V	***460.266679***	230.636977	443.240130	222.123703			3
12	1381.678680	691.342978	1364.652131	682.829704	1363.668115	682.337696	W	***361.198265***	181.102770	344.171716	172.589496			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AFQGLLDTYSVWR
(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	1554.783081	-0.000653	AFQGLLDTYSVWR

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

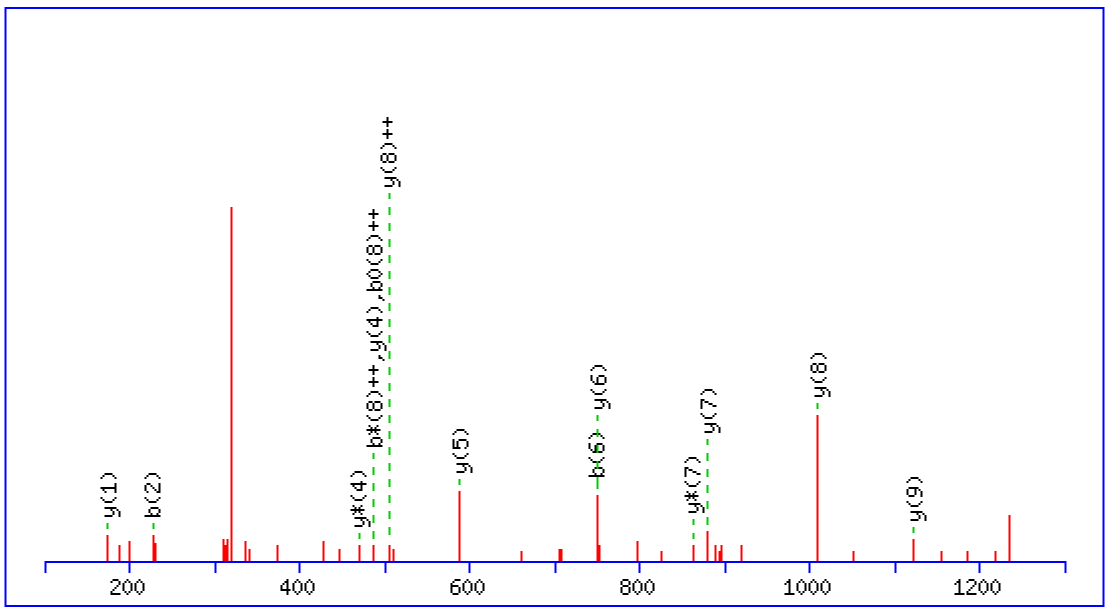
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEEYTQLAR**
Found in **NIT1_HUMAN**, Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2

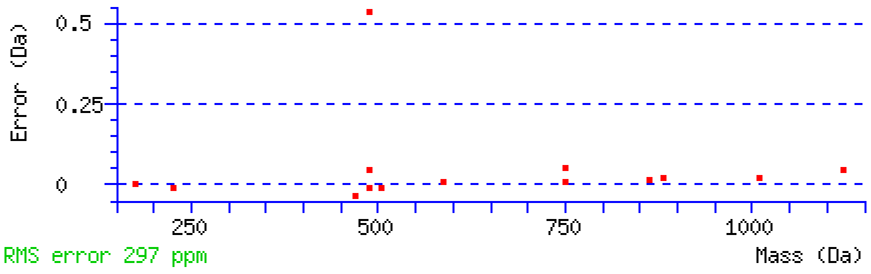
Match to Query 21589: 1234.657048 from(618.335800,2+) rtinseconds(2570) index(26608)
Title: Locus:1.1.1.2549.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

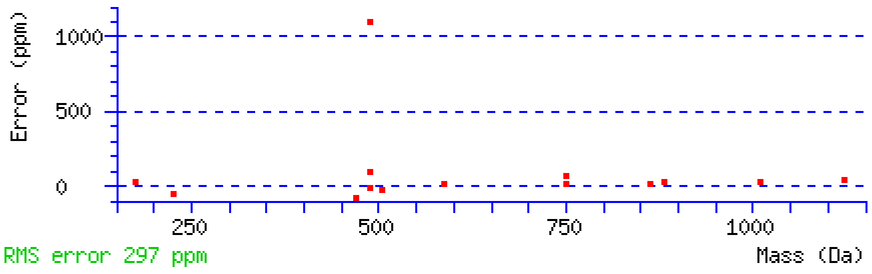
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1234.655716
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00042
Matches : 14/84 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							10
2	**227.175404**	114.091340					L	***1122.578966***	561.793121	1105.552417	553.279847	1104.568401	552.787839	9
3	356.217997	178.612637			338.207432	169.607354	E	***1009.494902***	505.251089	992.468353	496.737815	991.484337	496.245807	8
4	485.260590	243.133933			467.250025	234.128651	E	***880.452309***	440.729793	863.425760	432.216518	862.441744	431.724510	7
5	648.323919	324.665598			630.313354	315.660315	Y	***751.409716***	376.208496	734.383167	367.695222	733.399151	367.203214	6
6	**749.371598**	375.189437			731.361033	366.184155	T	***588.346387***	294.676832	571.319838	286.163557	570.335822	285.671549	5
7	877.430176	439.218726	860.403627	430.705452	859.419611	430.213444	Q	***487.298708***	244.152992	470.272159	235.639717			4
8	990.514240	495.760758	973.487691	487.247484	972.503675	486.755476	L	359.240130	180.123703	342.213581	171.610428			3
9	1061.551354	531.279315	1044.524805	522.766041	1043.540789	522.274033	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 LLEEYTQLAR
(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	1234.655716	0.001332	LLEEYTQLAR
14.6	1234.655716	0.001332	LLIIDYSENR
6.4	1234.655716	0.001332	EILETKAPYR
5.8	1234.666977	-0.009929	LSIVGDGKYGAR
3.3	1234.655716	0.001332	EPLETLKSYR

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

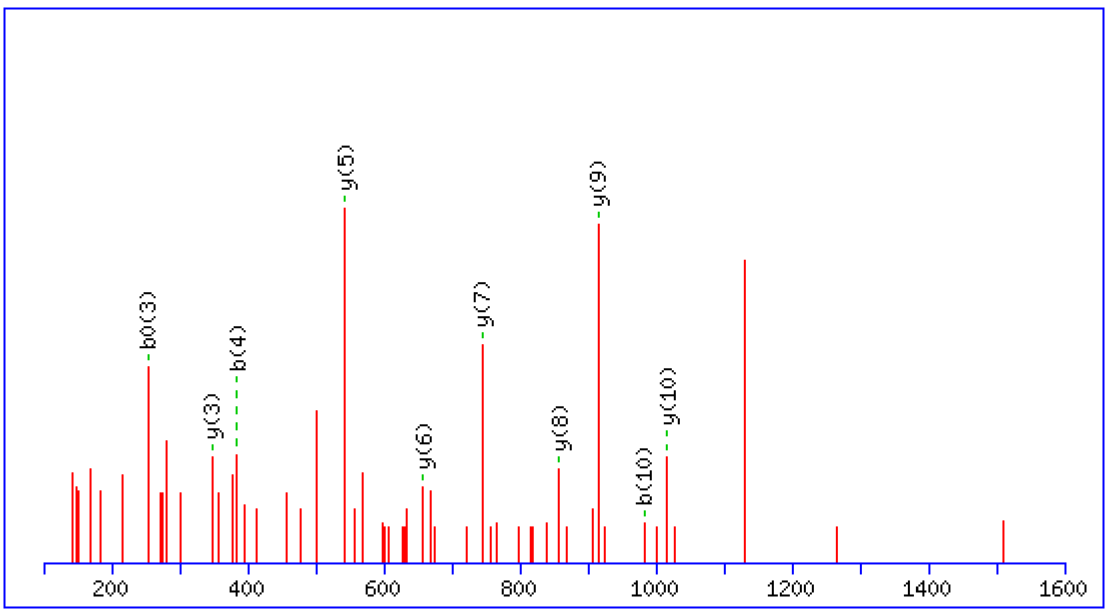
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTGISDPVTVK**
Found in **NOE1_HUMAN**, Noelin OS=Homo sapiens GN=OLFM1 PE=1 SV=4

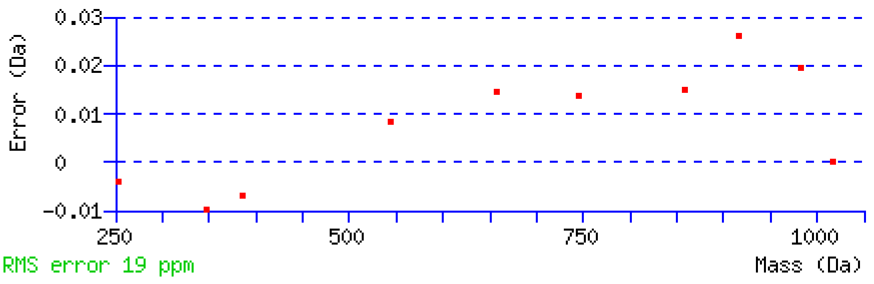
Match to Query 15953: 1128.639268 from(565.326910,2+) rtinseconds(2076) index(24270)
Title: Locus:1.1.1.2193.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

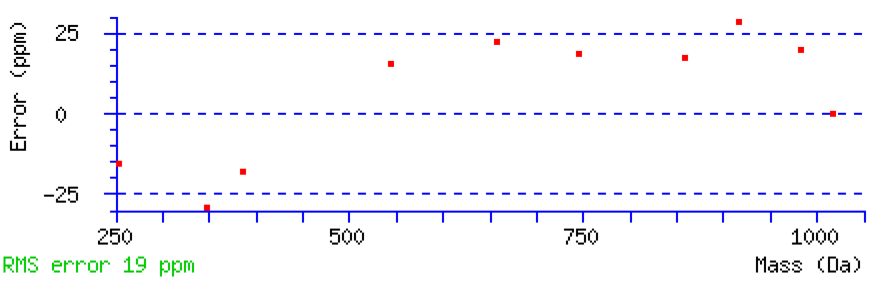
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1128.639053
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00017
Matches : 10/94 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							11
2	215.139019	108.073147	197.128454	99.067865	T	***1016.562253***	508.784764	999.535704	500.271490	998.551688	499.779482	10
3	272.160483	136.583879	254.149918	127.578597	G	***915.514574***	458.260925	898.488025	449.747650	897.504009	449.255642	9
4	**385.244547**	193.125912	367.233982	184.120629	I	***858.493110***	429.750193	841.466561	421.236918	840.482545	420.744910	8
5	472.276575	236.641926	454.266010	227.636643	S	***745.409046***	373.208161	728.382497	364.694887	727.398481	364.202879	7
6	587.303518	294.155397	569.292953	285.150115	D	***658.377018***	329.692147	641.350469	321.178872	640.366453	320.686864	6
7	684.356282	342.681779	666.345717	333.676497	P	***543.350075***	272.178676	526.323526	263.665401	525.339510	263.173393	5
8	783.424696	392.215986	765.414131	383.210704	V	446.297311	223.652293	429.270762	215.139019	428.286746	214.647011	4
9	884.472375	442.739826	866.461810	433.734543	T	***347.228897***	174.118086	330.202348	165.604812	329.218332	165.112804	3
10	**983.540789**	492.274033	965.530224	483.268750	V	246.181218	123.594247	229.154669	115.080972			2
11					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LTGISDPVTVK
(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	1128.639053	0.000215	LTGISDPVTVK
14.1	1128.650269	-0.011001	LTGTGPKNITK
6.0	1128.632492	0.006776	LTASKTHIMK
6.0	1128.629120	0.010148	TLGWEALLAR
3.9	1128.650238	-0.010970	EITLLEQRK
2.5	1128.639008	0.000260	AVEELQSIIK
2.4	1128.650238	-0.010970	LTELEQRIK
1.7	1128.639038	0.000230	KVPSDTLPLK
1.2	1128.639038	0.000230	NVDTLTPLIK

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

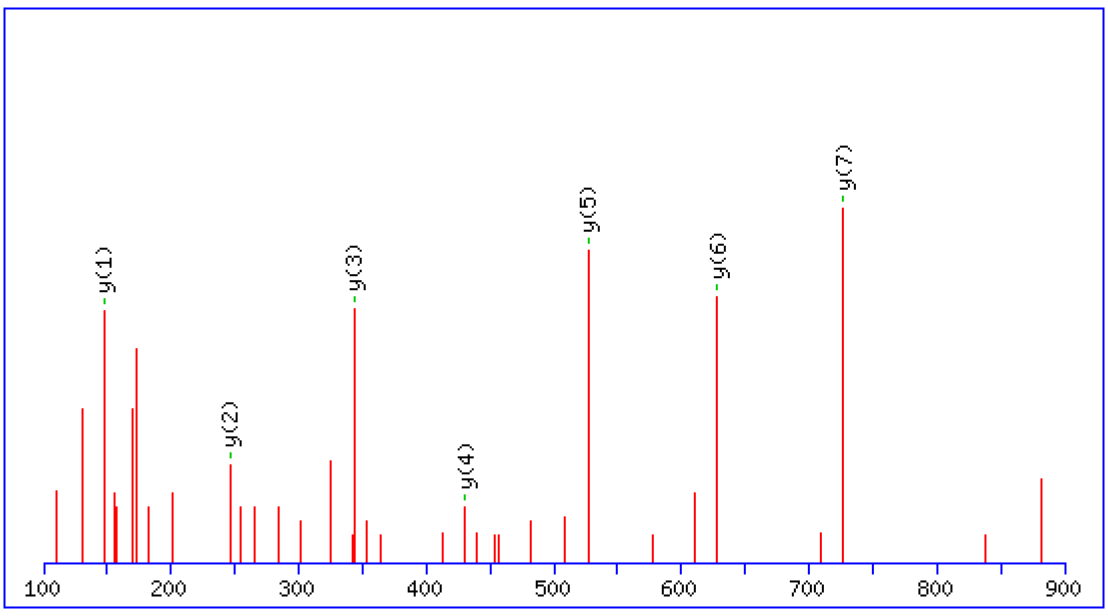
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATVTPSPVK**
Found in **NUCKS_HUMAN**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Homo sapiens GN=NUCKS1 PE=1 SV=1

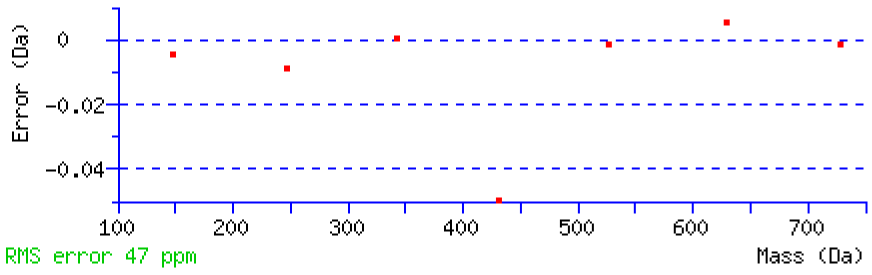
Match to Query 6725: 898.508508 from(450.261530,2+) rtinseconds(1126) index(3913)
Title: Locus:1.1.1.1918.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

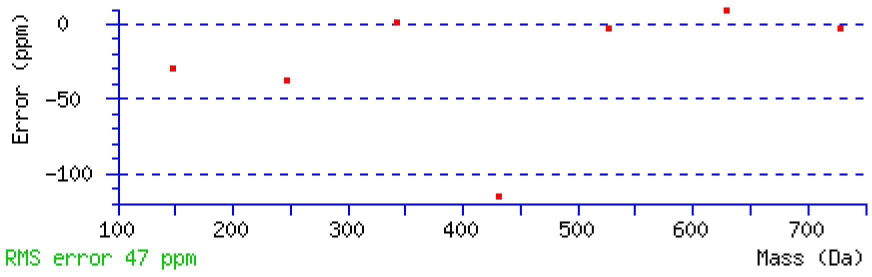
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 898.512390
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 6.8e-008
Matches : 7/72 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							9
2	173.092069	87.049672	155.081504	78.044390	T	828.482546	414.744911	811.455997	406.231637	810.471981	405.739629	8
3	272.160483	136.583879	254.149918	127.578597	V	*727.434867*	364.221072	710.408318	355.707797	709.424302	355.215789	7
4	373.208162	187.107719	355.197597	178.102437	T	*628.366453*	314.686865	611.339904	306.173590	610.355888	305.681582	6
5	470.260926	235.634101	452.250361	226.628818	P	*527.318774*	264.163025	510.292225	255.649750	509.308209	255.157742	5
6	557.292954	279.150115	539.282389	270.144833	S	*430.266010*	215.636643	413.239461	207.123368	412.255445	206.631360	4
7	654.345718	327.676497	636.335153	318.671215	P	*343.233982*	172.120629	326.207433	163.607354			3
8	753.414132	377.210704	735.403567	368.205422	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 ATVTPSPVK
(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	898.512390	-0.003882	ATVTPSPVK
24.7	898.512375	-0.003867	TAAPLAPVK
11.9	898.512375	-0.003867	NLLDTPVK
11.9	898.512375	-0.003867	VNTELPVK
9.7	898.502487	0.006021	QWKGGPVK
7.5	898.512360	-0.003852	EPKAIDVK
6.5	898.512375	-0.003867	DGKPLLPK
5.5	898.512390	-0.003882	DGPVVTALK
0.8	898.505844	0.002664	CPRVLPK
0.2	898.512375	-0.003867	ASTGPPLIK

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

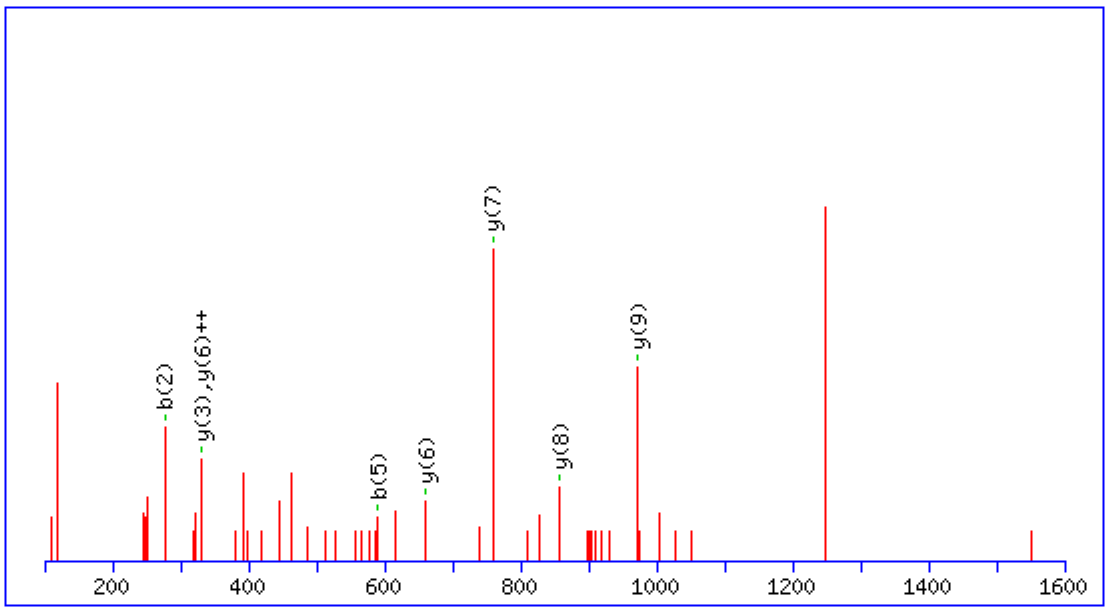
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEDVVNQSSPK**
Found in **TIAR_HUMAN**, Nucleolysin TIAR OS=Homo sapiens GN=TIAL1 PE=1 SV=1

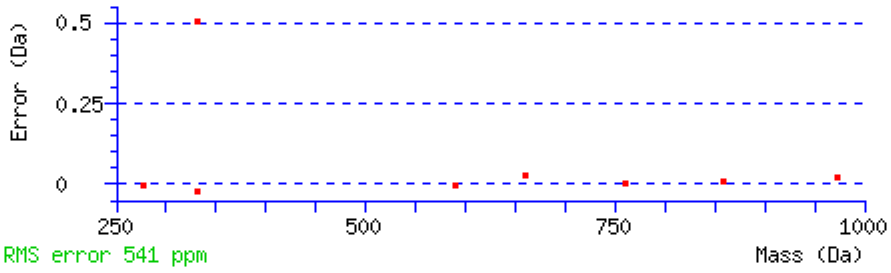
Match to Query 28249: 1248.610268 from(625.312410,2+) rtinseconds(1621) index(13303)
Title: Locus:1.1.1.2108.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

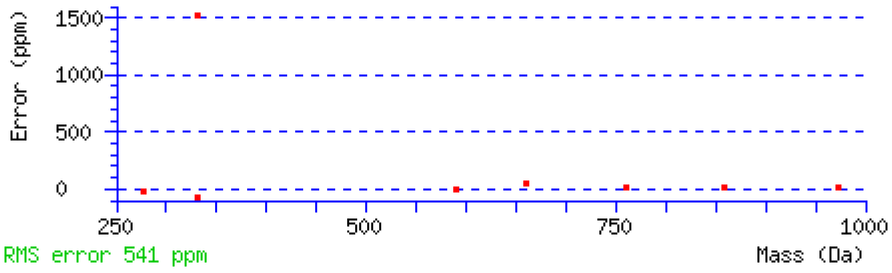
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1248.598633
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0049
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	148.075690	74.541483					F							11
2	**277.118283**	139.062779			259.107718	130.057497	E	1102.537493	551.772384	1085.510944	543.259110	1084.526928	542.767102	10
3	392.145226	196.576251			374.134661	187.570968	D	***973.494900***	487.251088	956.468351	478.737813	955.484335	478.245805	9
4	491.213640	246.110458			473.203075	237.105176	V	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	8
5	**590.282054**	295.644665			572.271489	286.639383	V	***759.399543***	380.203409	742.372994	371.690135	741.388978	371.198127	7
6	704.324981	352.666129	687.298432	344.152854	686.314416	343.660846	N	***660.331129***	330.669202	643.304580	322.155928	642.320564	321.663920	6
7	832.383559	416.695418	815.357010	408.182143	814.372994	407.690135	Q	546.288202	273.647739	529.261653	265.134464	528.277637	264.642456	5
8	919.415587	460.211432	902.389038	451.698157	901.405022	451.206149	S	418.229624	209.618450	401.203075	201.105175	400.219059	200.613167	4
9	1006.447615	503.727445	989.421066	495.214171	988.437050	494.722163	S	***331.197596***	166.102436	314.171047	157.589161	313.187031	157.097153	3
10	1103.500379	552.253827	1086.473830	543.740553	1085.489814	543.248545	P	244.165568	122.586422	227.139019	114.073147			2
11							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of FEDVVNQSSPK
(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	1248.598633	0.011635	FEDVVNQSSPK

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

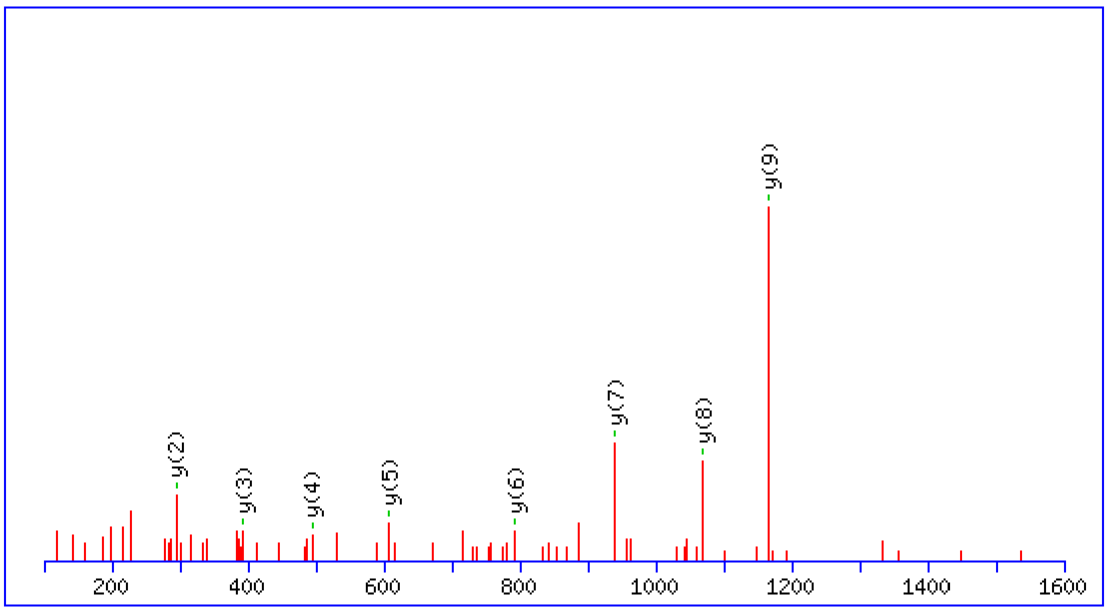
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GIPEFWLTVFK**
Found in **NP1L1_HUMAN**, Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1

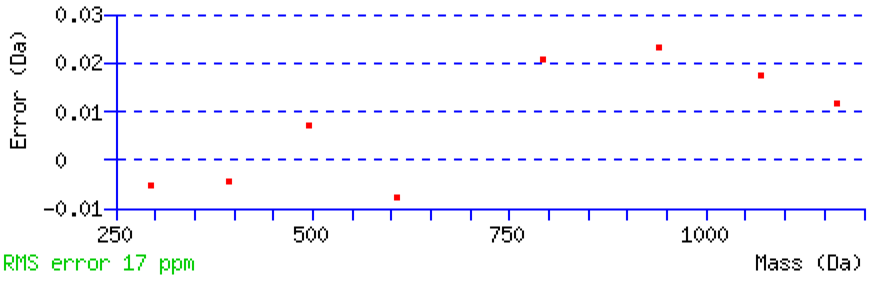
Match to Query 28130: 1335.731888 from(668.873220,2+) rtinseconds(4473) index(64866)
Title: Locus:1.1.1.3242.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

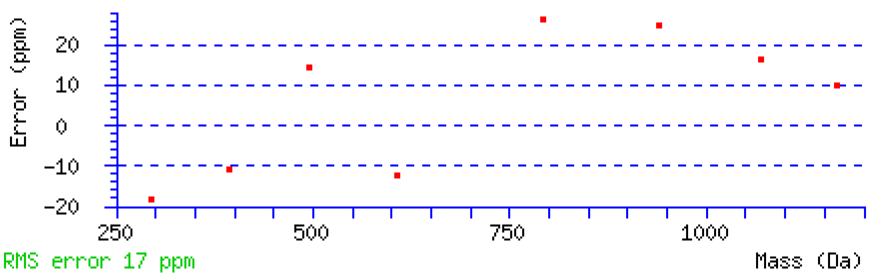
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1335.722717
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 2.3e-006
Matches : 8/88 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			**G**							11
2	171.112804	86.060040			**I**	1279.708523	640.357900	1262.681974	631.844625	1261.697958	631.352617	10
3	268.165568	134.586422			**P**	***1166.624459***	583.815868	1149.597910	575.302593	1148.613894	574.810585	9
4	397.208161	199.107718	379.197596	190.102436	**E**	***1069.571695***	535.289486	1052.545146	526.776211	1051.561130	526.284203	8
5	544.276575	272.641926	526.266010	263.636643	**F**	***940.529102***	470.768189	923.502553	462.254915	922.518537	461.762907	7
6	730.355888	365.681582	712.345323	356.676300	**W**	***793.460688***	397.233982	776.434139	388.720708	775.450123	388.228700	6
7	843.439952	422.223614	825.429387	413.218332	**L**	***607.381375***	304.194326	590.354826	295.681051	589.370810	295.189043	5
8	944.487631	472.747454	926.477066	463.742171	**T**	***494.297311***	247.652294	477.270762	239.139019	476.286746	238.647011	4
9	1043.556045	522.281661	1025.545480	513.276378	**V**	***393.249632***	197.128454	376.223083	188.615180			3
10	1190.624459	595.815868	1172.613894	586.810585	**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 GIPEFWLTVFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.1	1335.722717	0.009171	GIPEFWLTVFK

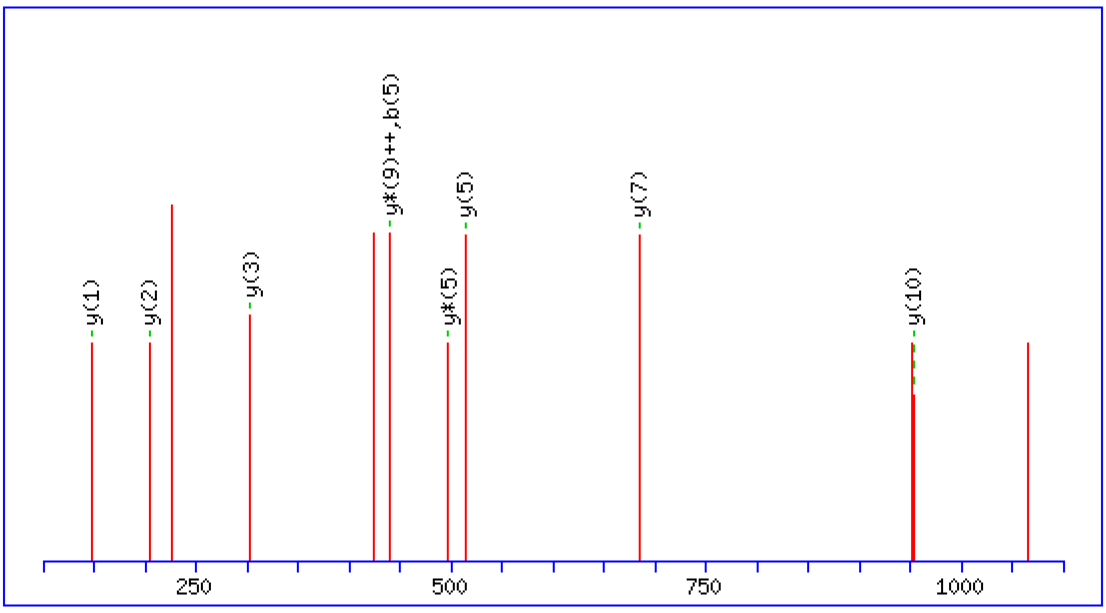
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGIVGLPNVGK**
Found in **OLA1_HUMAN**, Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2

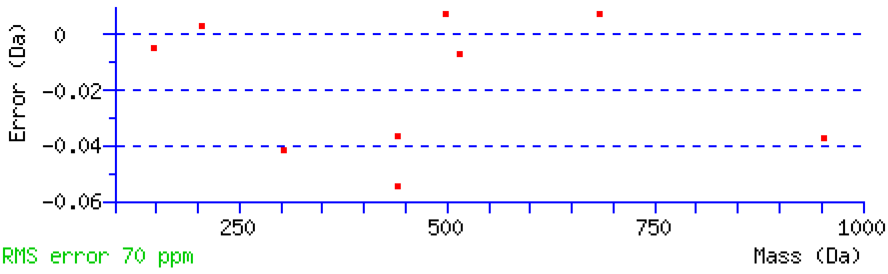
Match to Query 24729: 1065.661948 from(533.838250,2+) rtinseconds(2752) index(35595)
Title: Locus:1.1.1.2410.11
Data file 2011-11-14 - TFD - S 2-4.mgf

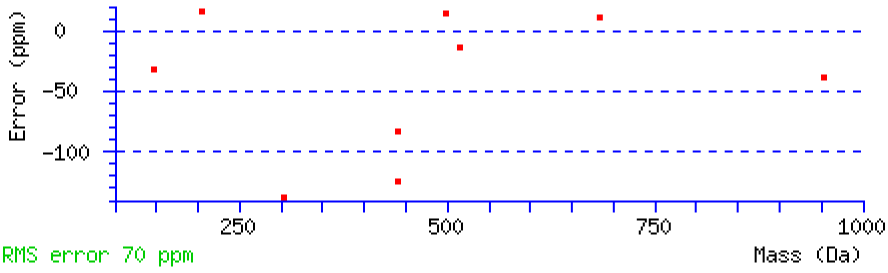
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1065.654633
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47   Expect: 3e-005
Matches : 9/66 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	114.091340	57.549308			I					11
2	171.112804	86.060040			G	953.577843	477.292559	936.551294	468.779285	10
3	284.196868	142.602072			I	896.556379	448.781827	879.529830	440.268553	9
4	383.265282	192.136279			V	783.472315	392.239796	766.445766	383.726521	8
5	440.286746	220.647011			G	684.403901	342.705588	667.377352	334.192314	7
6	553.370810	277.189043			L	627.382437	314.194857	610.355888	305.681582	6
7	650.423574	325.715425			P	514.298373	257.652825	497.271824	249.139550	5
8	764.466501	382.736889	747.439952	374.223614	N	417.245609	209.126442	400.219060	200.613168	4
9	863.534915	432.271096	846.508366	423.757821	V	303.202682	152.104979	286.176133	143.591704	3
10	920.556379	460.781828	903.529830	452.268553	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 IGIVGLPNVGK
(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	1065.654633	0.007315	IGIVGLPNVGK

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

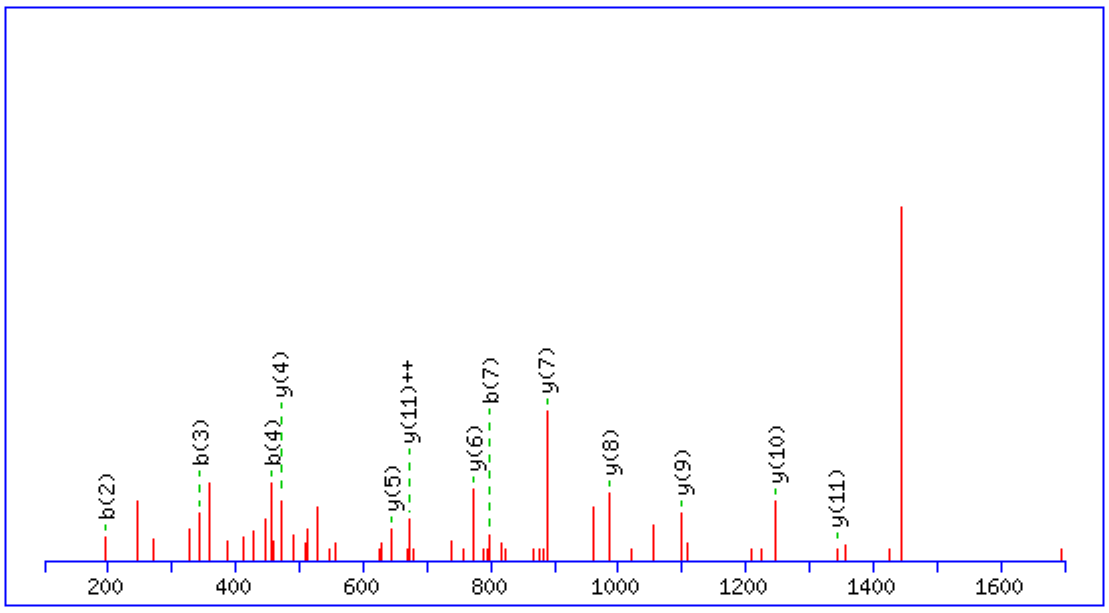
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFLVLECPNLK**
Found in **OSTC_HUMAN**, Oligosaccharyltransferase complex subunit OSTC OS=Homo sapiens GN=OSTC PE=1 SV=1

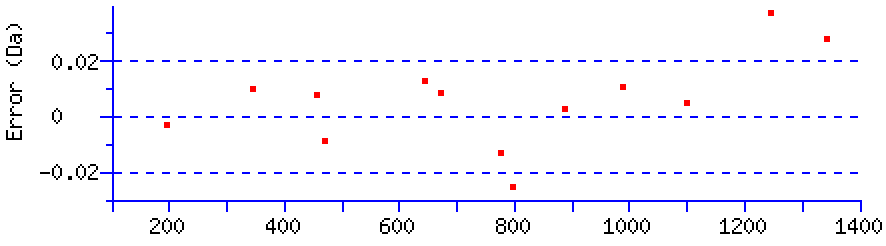
Match to Query 27848: 1441.803828 from(721.909190,2+) rtinseconds(3474) index(36269)
Title: Locus:1.1.1.2816.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

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 ●

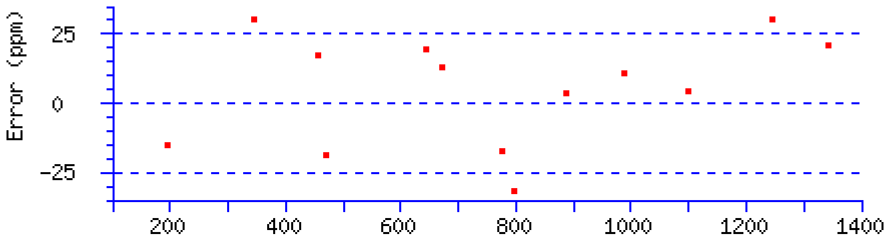


Monoisotopic mass of neutral peptide Mr(calc): 1441.800293
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00013
Matches : 13/92 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							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



RMS error 19 ppm



RMS error 19 ppm

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
47.6	1441.800293	0.003535	VPFLVLECPNLK

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

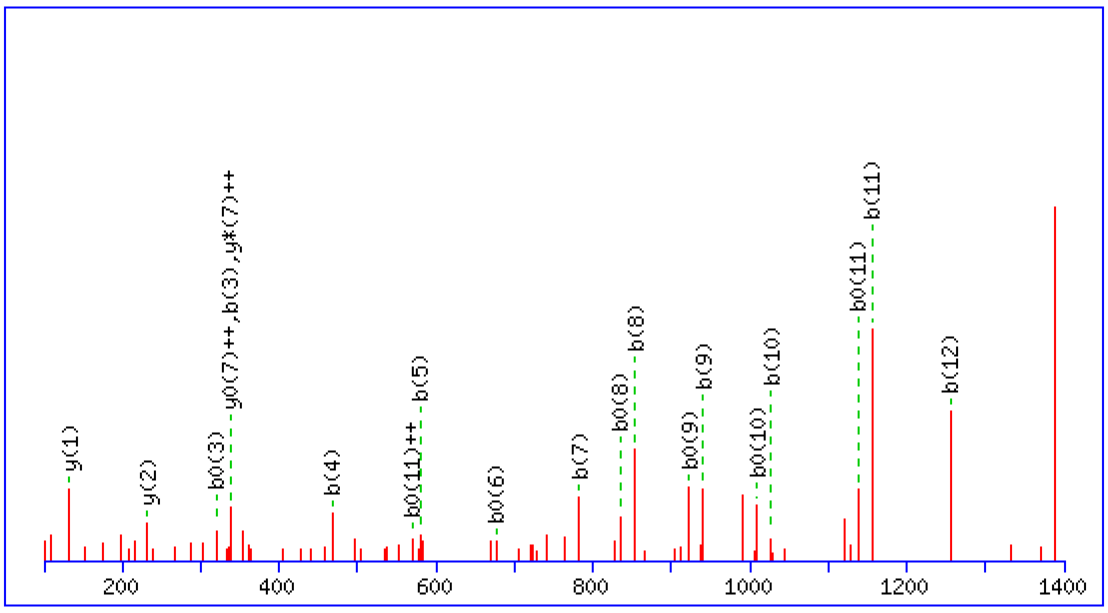
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISHELDSASSEVN**
Found in **OSTP_HUMAN**, Osteopontin OS=Homo sapiens GN=SPP1 PE=1 SV=1

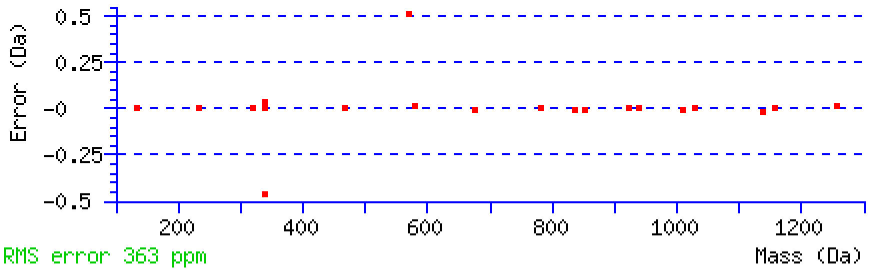
Match to Query 12275: 1386.627548 from(694.321050,2+) rtinseconds(1527) index(1255)
Title: Locus:1.1.1.2287.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-7.mgf

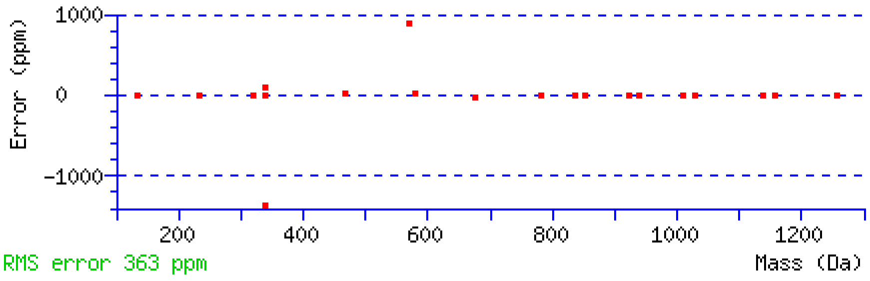
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1386.626282
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 2.2e-007
Matches : 20/114 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							13
2	201.123368	101.065322	183.112803	92.060039	S	1274.549513	637.778395	1257.522964	629.265120	1256.538948	628.773112	12
3	***338.182280***	169.594778	320.171715	160.589495	H	1187.517485	594.262381	1170.490936	585.749106	1169.506920	585.257098	11
4	***467.224873***	234.116074	449.214308	225.110792	E	1050.458573	525.732925	1033.432024	517.219650	1032.448008	516.727642	10
5	***580.308937***	290.658107	562.298372	281.652824	L	921.415980	461.211628	904.389431	452.698354	903.405415	452.206346	9
6	695.335880	348.171578	677.325315	339.166295	D	808.331916	404.669596	791.305367	396.156322	790.321351	395.664314	8
7	***782.367908***	391.687592	764.357343	382.682309	S	693.304973	347.156125	676.278424	338.642850	675.294408	338.150842	7
8	***853.405022***	427.206149	835.394457	418.200866	A	606.272945	303.640111	589.246396	295.126836	588.262380	294.634828	6
9	***940.437050***	470.722163	922.426485	461.716880	S	535.235831	268.121554	518.209282	259.608279	517.225266	259.116271	5
10	***1027.469078***	514.238177	1009.458513	505.232894	S	448.203803	224.605540	431.177254	216.092265	430.193238	215.600257	4
11	***1156.511671***	578.759474	1138.501106	569.754191	E	361.171775	181.089526	344.145226	172.576251	343.161210	172.084243	3
12	***1255.580085***	628.293681	1237.569520	619.288398	V	**232.129182**	116.568229	215.102633	108.054955			2
13					N	**133.060768**	67.034022	116.034219	58.520747			1





NCBI **BLAST** search of ISHELDSASSEVN
(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	1386.626282	0.001266	ISHELDSASSEVN

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

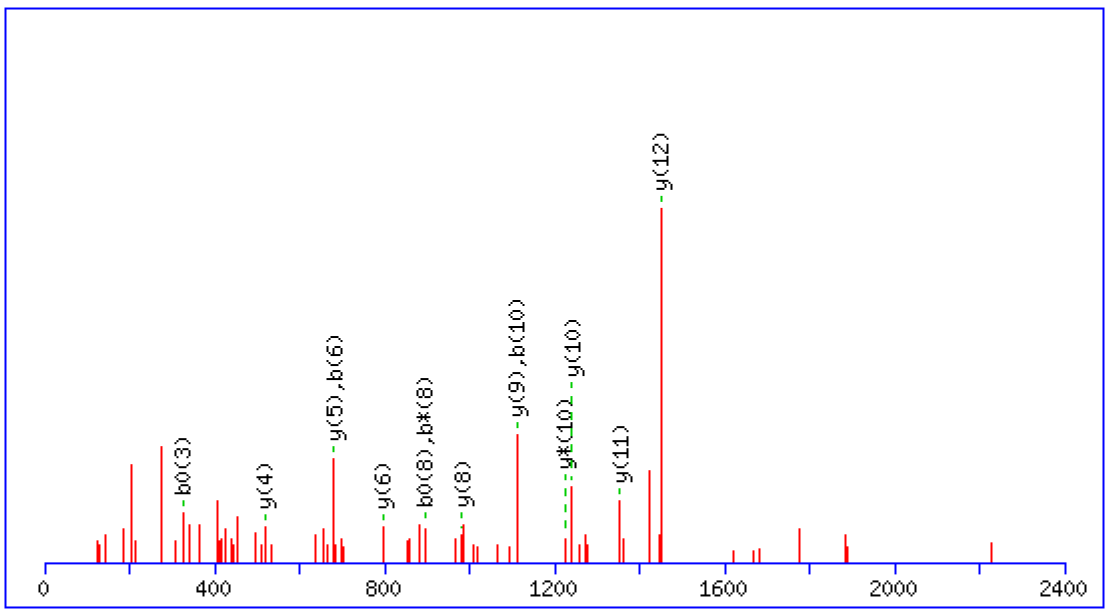
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETIPLQETSLYTQDR**
Found in **PPT1_HUMAN**, Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1

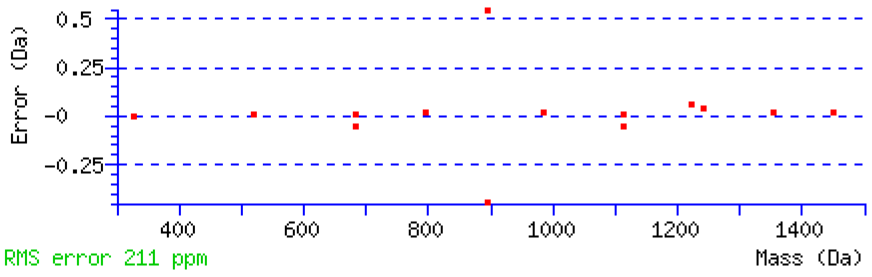
Match to Query 52006: 1792.900888 from(897.457720,2+) rtinseconds(2670) index(32997)
Title: Locus:1.1.1.2415.50
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

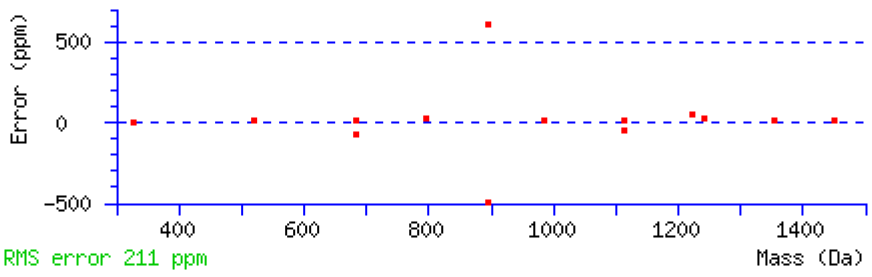
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1792.884293
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.00056
Matches : 14/156 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							15
2	231.097548	116.052412			213.086983	107.047130	T	1664.848994	832.928135	1647.822445	824.414861	1646.838429	823.922853	14
3	344.181612	172.594444			326.171047	163.589162	I	1563.801315	782.404295	1546.774766	773.891021	1545.790750	773.399013	13
4	441.234376	221.120826			423.223811	212.115544	P	***1450.717251***	725.862264	1433.690702	717.348989	1432.706686	716.856981	12
5	554.318440	277.662858			536.307875	268.657576	L	***1353.664487***	677.335882	1336.637938	668.822607	1335.653922	668.330599	11
6	**682.377018**	341.692147	665.350469	333.178873	664.366453	332.686865	Q	***1240.580423***	620.793850	1223.553874	612.280575	1222.569858	611.788567	10
7	811.419611	406.213444	794.393062	397.700169	793.409046	397.208161	E	***1112.521845***	556.764561	1095.495296	548.251286	1094.511280	547.759278	9
8	912.467290	456.737283	895.440741	448.224009	894.456725	447.732001	T	***983.479252***	492.243264	966.452703	483.729989	965.468687	483.237981	8
9	999.499318	500.253297	982.472769	491.740023	981.488753	491.248015	S	882.431573	441.719425	865.405024	433.206150	864.421008	432.714142	7
10	**1112.583382**	556.795329	1095.556833	548.282055	1094.572817	547.790047	L	***795.399545***	398.203411	778.372996	389.690136	777.388980	389.198128	6
11	1275.646711	638.326994	1258.620162	629.813719	1257.636146	629.321711	Y	***682.315481***	341.661379	665.288932	333.148104	664.304916	332.656096	5
12	1376.694390	688.850833	1359.667841	680.337559	1358.683825	679.845551	T	***519.252152***	260.129714	502.225603	251.616440	501.241587	251.124432	4
13	1504.752968	752.880122	1487.726419	744.366848	1486.742403	743.874840	Q	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
14	1619.779911	810.393594	1602.753362	801.880319	1601.769346	801.388311	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ETIPLQETSLYTQDR
(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	1792.884293	0.016595	ETIPLQETSLYTQDR
1.8	1792.908081	-0.007193	ALPYRISAHSQQHNR
1.6	1792.888977	0.011911	QIAKCQQLQQEYSR
0.2	1792.884323	0.016565	GESPPTPPGQPPISPKK
0.2	1792.884323	0.016565	GESPPTPPGQPPISPKK

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

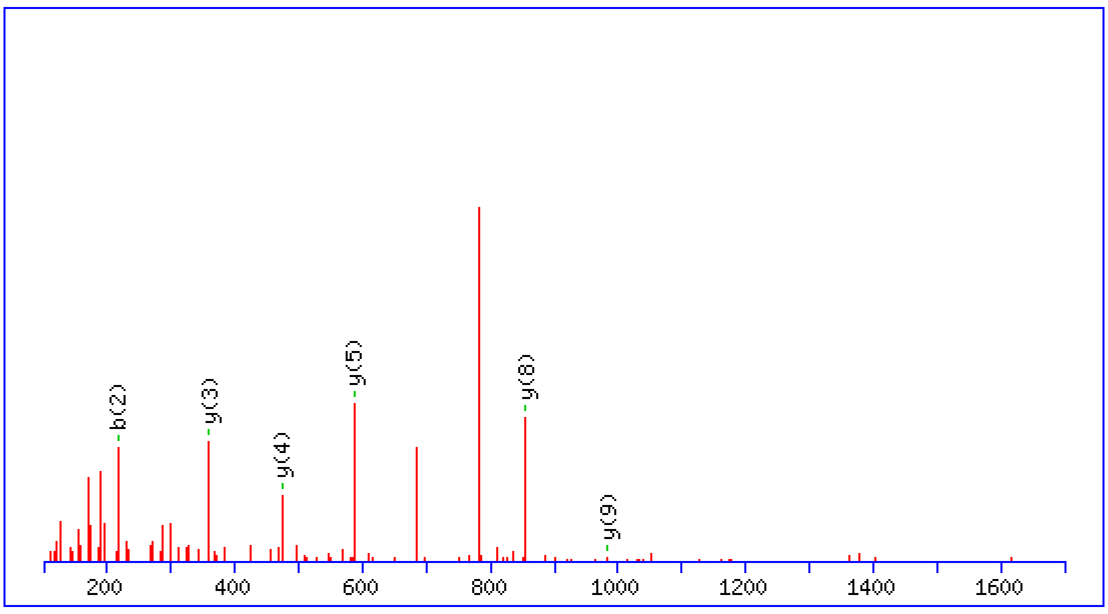
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEVPAIDLAR**
Found in **GP2_HUMAN**, Pancreatic secretory granule membrane major glycoprotein GP2 OS=Homo sapiens GN=GP2 PE=2 SV=3

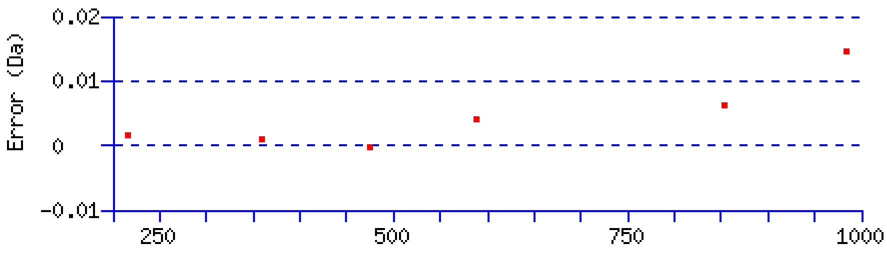
Match to Query 9448: 1069.581648 from(535.798100,2+) rtinseconds(2275) index(26890)
Title: Locus:1.1.1.2317.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

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 ●

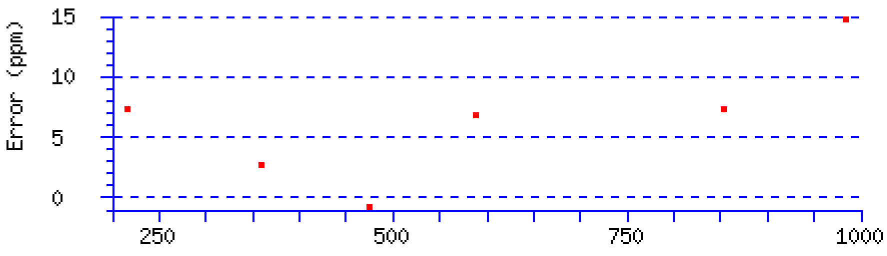


```
Monoisotopic mass of neutral peptide Mr(calc): 1069.576752
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0052
Matches : 6/84 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							10
2	217.081897	109.044586	199.071332	100.039304	E	***983.552022***	492.279649	966.525473	483.766374	965.541457	483.274366	9
3	316.150311	158.578793	298.139746	149.573511	V	***854.509429***	427.758353	837.482880	419.245078	836.498864	418.753070	8
4	413.203075	207.105175	395.192510	198.099893	P	755.441015	378.224145	738.414466	369.710871	737.430450	369.218863	7
5	484.240189	242.623732	466.229624	233.618450	A	658.388251	329.697764	641.361702	321.184489	640.377686	320.692481	6
6	597.324253	299.165765	579.313688	290.160482	I	***587.351137***	294.179207	570.324588	285.665932	569.340572	285.173924	5
7	712.351196	356.679236	694.340631	347.673953	D	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
8	825.435260	413.221268	807.424695	404.215985	L	***359.240130***	180.123703	342.213581	171.610428			3
9	896.472374	448.739825	878.461809	439.734542	A	246.156066	123.581671	229.129517	115.068396			2
10					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 7 ppm



RMS error 7 ppm

NCBI **BLAST** search of SEVPAIDLAR
(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	1069.576752	0.004896	SEVPAIDLAR
14.5	1069.576752	0.004896	SEKEPLPVR
11.4	1069.587997	-0.006349	DTLSLRPPR
8.1	1069.576752	0.004896	EPLKLDPSR
7.0	1069.576752	0.004896	SEKEPLPVR
7.0	1069.576767	0.004881	EPIQPSVLR
1.0	1069.587982	-0.006334	ISSVPAINNR

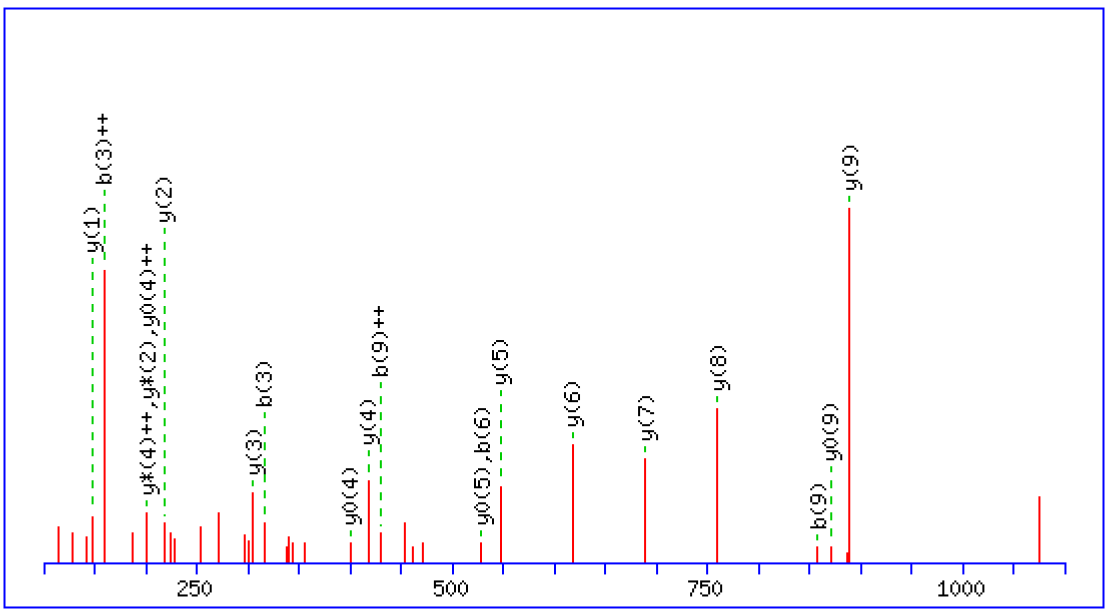
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVEAAAELSAK**
Found in **PTMS_HUMAN**, Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2

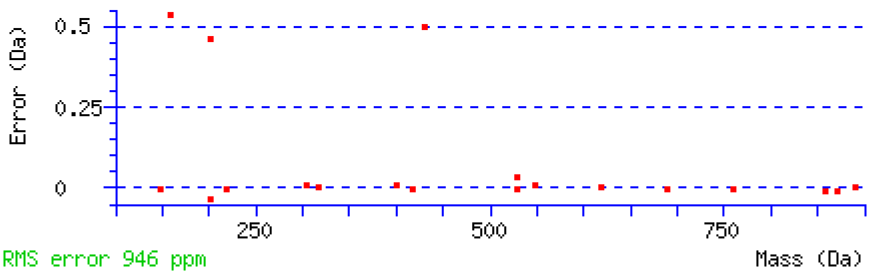
Match to Query 21943: 1074.556688 from(538.285620,2+) rtinseconds(1559) index(5775)
Title: Locus:1.1.1.2105.18
Data file 2011-11-14 - TFD - S 2-6.mgf

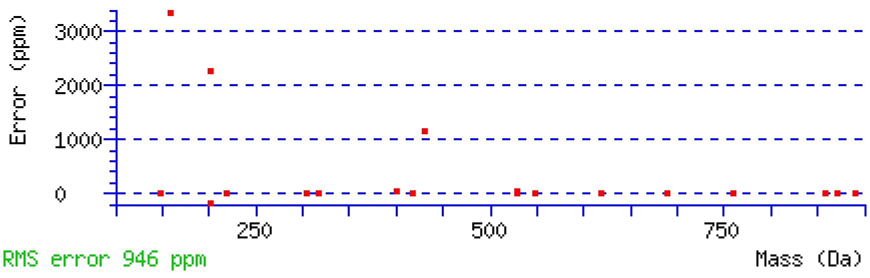
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1074.555664
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 92 **Expect:** 1e-008
Matches : 20/96 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							11
2	187.107718	94.057497	169.097153	85.052214	V	988.530952	494.769114	971.504403	486.255839	970.520387	485.763831	10
3	**316.150311**	**158.578793**	298.139746	149.573511	E	***889.462538***	445.234907	872.435989	436.721633	871.451973	436.229625	9
4	387.187425	194.097351	369.176860	185.092068	A	***760.419945***	380.713610	743.393396	372.200336	742.409380	371.708328	8
5	458.224539	229.615907	440.213974	220.610625	A	***689.382831***	345.195053	672.356282	336.681779	671.372266	336.189771	7
6	**529.261653**	265.134465	511.251088	256.129182	A	***618.345717***	309.676496	601.319168	301.163222	600.335152	300.671214	6
7	658.304246	329.655761	640.293681	320.650479	E	***547.308603***	274.157940	530.282054	265.644665	529.298038	265.152657	5
8	771.388310	386.197793	753.377745	377.192511	L	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
9	**858.420338**	**429.713807**	840.409773	420.708525	S	***305.181946***	153.094611	288.155397	144.581336	287.171381	144.089328	3
10	929.457452	465.232364	911.446887	456.227082	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 SVEAAAELSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
92.0	1074.555664	0.001024	SVEAAAELSAK
16.7	1074.555649	0.001039	ASEIKEAEAK
13.4	1074.566925	-0.010237	SLDTRGDLAK
12.4	1074.555695	0.000993	SIDDIGGALSK
7.6	1074.555664	0.001024	AEAAALTETAK
5.6	1074.566925	-0.010237	AQGDASKVTAK
4.1	1074.549149	0.007539	SAMPLRDAAK
3.9	1074.557037	-0.000349	EGFGRALGPR
3.6	1074.555695	0.000993	TDLDNSIGIK
3.1	1074.555664	0.001024	VSEEENLKK

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

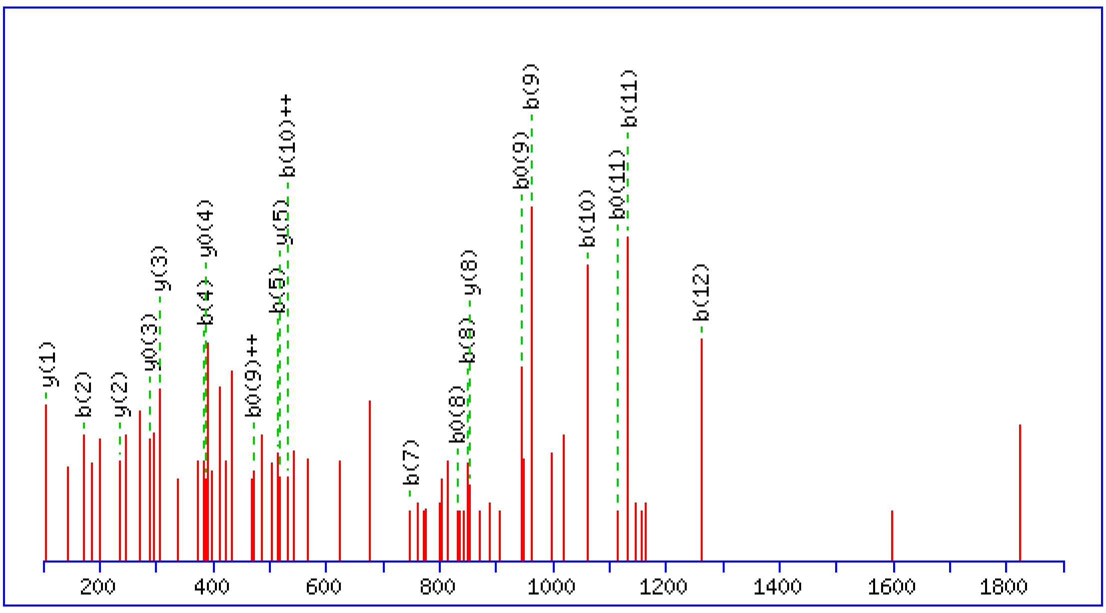
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGVDEFSTLVAES**
Found in **PRVA_HUMAN**, Parvalbumin alpha OS=Homo sapiens GN=PVALB PE=1 SV=2

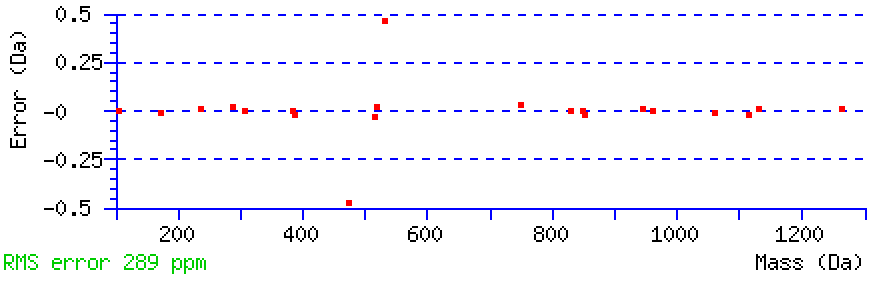
Match to Query 32427: 1365.673128 from(683.843840,2+) rtinseconds(3633) index(26513)
Title: Locus:1.1.1.2818.12
Data file 2011-11-14 - TFD - S 2-7.mgf

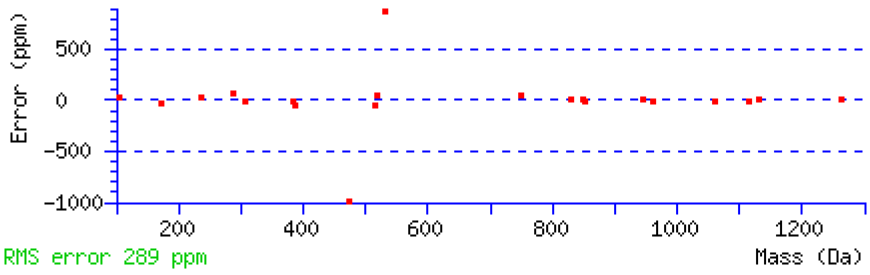
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1365.666382
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0012
Matches : 21/90 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I					13
2	***171.112804***	86.060040			G	1253.589589	627.298433	1235.579024	618.293150	12
3	270.181218	135.594247			V	1196.568125	598.787701	1178.557560	589.782418	11
4	***385.208161***	193.107719	367.197596	184.102436	D	1097.499711	549.253494	1079.489146	540.248211	10
5	***514.250754***	257.629015	496.240189	248.623733	E	982.472768	491.740022	964.462203	482.734740	9
6	661.319168	331.163222	643.308603	322.157940	F	**853.430175**	427.218726	835.419610	418.213443	8
7	***748.351196***	374.679236	730.340631	365.673954	S	706.361761	353.684519	688.351196	344.679236	7
8	***849.398875***	425.203076	831.388310	416.197793	T	619.329733	310.168505	601.319168	301.163222	6
9	***962.482939***	481.745108	944.472374	472.739825	L	**518.282054**	259.644665	500.271489	250.639383	5
10	***1061.551353***	531.279315	1043.540788	522.274032	V	405.197990	203.102633	387.187425	194.097350	4
11	***1132.588467***	566.797872	1114.577902	557.792589	A	**306.129576**	153.568426	288.119011	144.563143	3
12	***1261.631060***	631.319168	1243.620495	622.313885	E	**235.092462**	118.049869	217.081897	109.044586	2
13					S	**106.049869**	53.528573	88.039304	44.523290	1





NCBI **BLAST** search of IGVDEFSTLVAES
(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	1365.666382	0.006746	IGVDEFSTLVAES

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

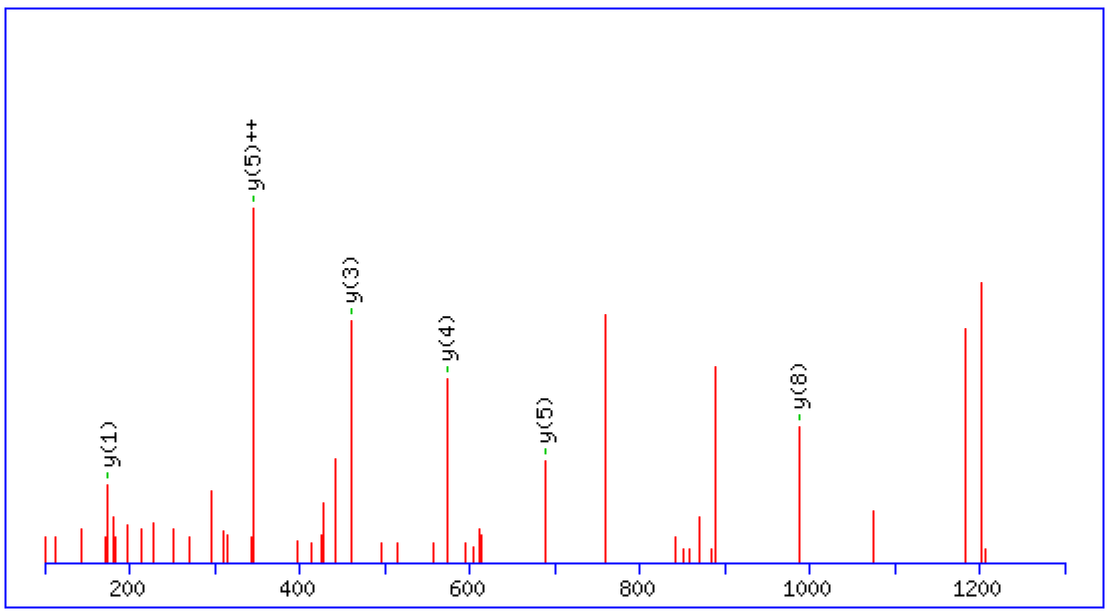
Mascot Search Results

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

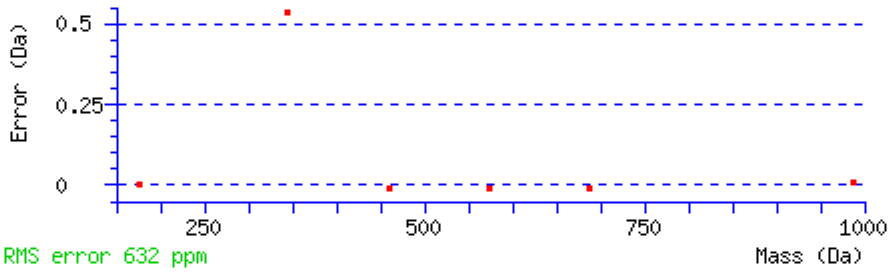
Match to Query 14451: 1201.596388 from(601.805470,2+) rtinseconds(1907) index(3952)
Title: Locus:1.1.1.2402.13
Data file 2011-11-14 - TFD - S 2-8.mgf

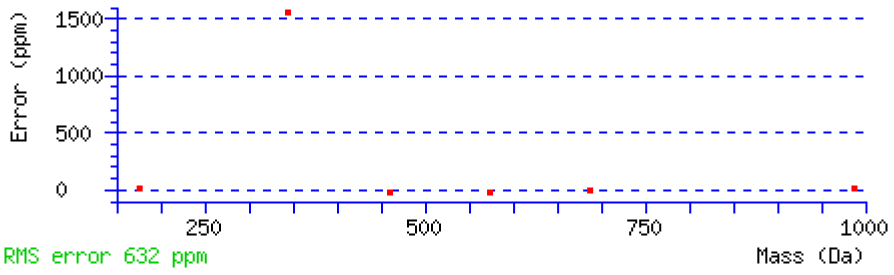
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1201.605087
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0088
Matches : 6/104 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							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
31.2	1201.605087	-0.008699	TNLADDIRER
9.7	1201.593872	0.002516	QDTVELQNQK
9.3	1201.605087	-0.008699	SQELDNKNVR
9.3	1201.593857	0.002531	GKEEELQDVR
7.4	1201.605118	-0.008730	QVTVEVSNNGR
7.0	1201.593872	0.002516	KGEDPLATDTR
6.5	1201.605087	-0.008699	KSQSENVPASR
5.0	1201.605103	-0.008715	SLQDEVSPRR
0.8	1201.587341	0.009047	QLGEKGPCQR
0.6	1201.602615	-0.006227	MRGFPLGGPDR

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

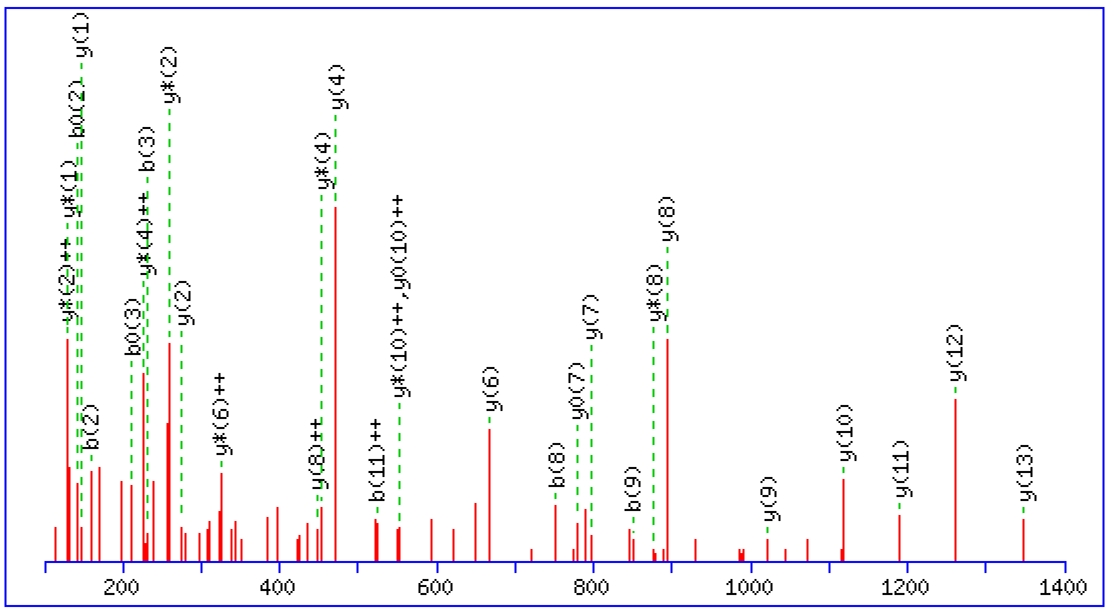
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAAPKPEPVPVQK**
Found in **PDLI5_HUMAN**, PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5

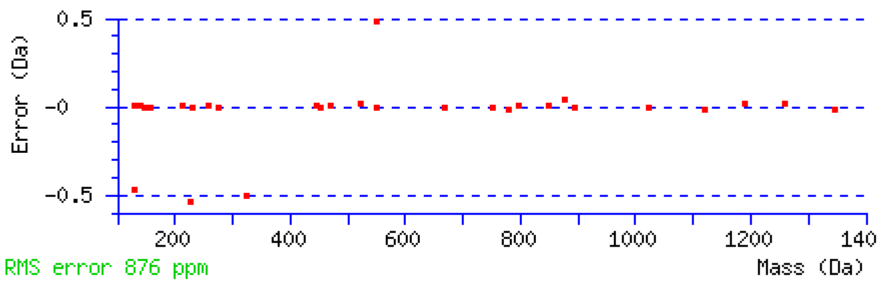
Match to Query 9911: 1417.790292 from(473.604040,3+) rtinseconds(1261) index(930)
Title: Locus:1.1.1.2381.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

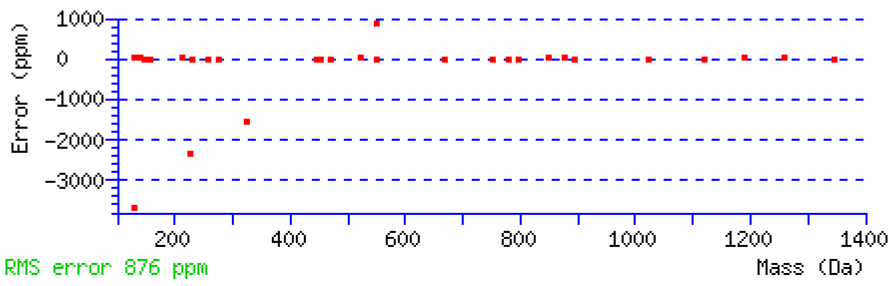
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1417.792892
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 2.2e-005
Matches : 29/132 fragment ions using 69 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	**159.076418**	80.041847			141.065853	71.036564	S	***1347.763078***	674.385177	1330.736529	665.871903	1329.752513	665.379895	13
3	**230.113532**	115.560404			212.102967	106.555121	A	***1260.731050***	630.869163	1243.704501	622.355889	1242.720485	621.863881	12
4	301.150646	151.078961			283.140081	142.073679	A	***1189.693936***	595.350606	1172.667387	586.837332	1171.683371	586.345324	11
5	398.203410	199.605343			380.192845	190.600061	P	***1118.656822***	559.832049	1101.630273	551.318775	1100.646257	550.826767	10
6	526.298373	263.652825	509.271824	255.139550	508.287808	254.647542	K	***1021.604058***	511.305667	1004.577509	502.792393	1003.593493	502.300385	9
7	623.351137	312.179207	606.324588	303.665932	605.340572	303.173924	P	***893.509095***	447.258186	876.482546	438.744911	875.498530	438.252903	8
8	**752.393730**	376.700503	735.367181	368.187229	734.383165	367.695221	E	***796.456331***	398.731804	779.429782	390.218529	778.445766	389.726521	7
9	**849.446494**	425.226885	832.419945	416.713611	831.435929	416.221603	P	***667.413738***	334.210507	650.387189	325.697233			6
10	948.514908	474.761092	931.488359	466.247818	930.504343	465.755810	V	570.360974	285.684125	553.334425	277.170851			5
11	1045.567672	523.287474	1028.541123	514.774200	1027.557107	514.282192	P	***471.292560***	236.149918	454.266011	227.636644			4
12	1144.636086	572.821681	1127.609537	564.308407	1126.625521	563.816399	V	374.239796	187.623536	357.213247	179.110262			3
13	1272.694664	636.850970	1255.668115	628.337696	1254.684099	627.845688	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 ASAAPKPEPVPVQK
(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	1417.792892	-0.002600	ASAAPKPEPVPVQK

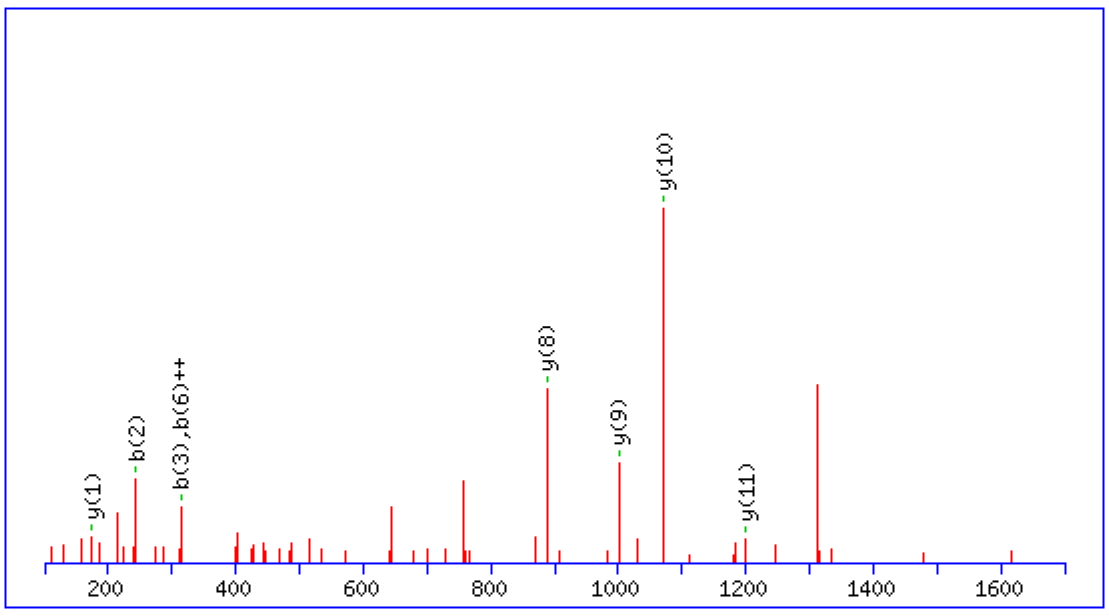
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEAPSPKAIVTR**
Found in **PDZD8_HUMAN**, PDZ domain-containing protein 8 OS=Homo sapiens GN=PDZD8 PE=1 SV=1

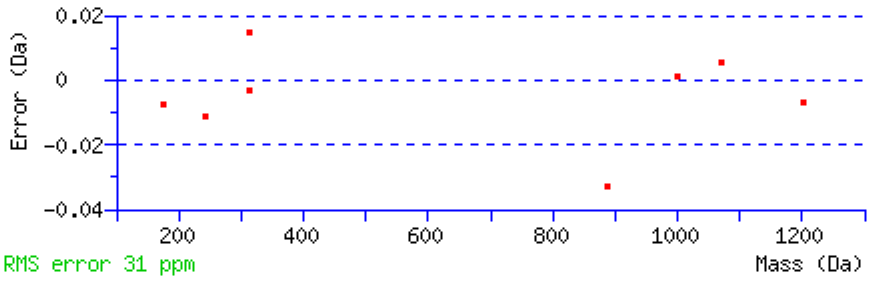
Match to Query 30115: 1312.738088 from(657.376320,2+) rtinseconds(3812) index(56525)
Title: Locus:1.1.1.2832.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

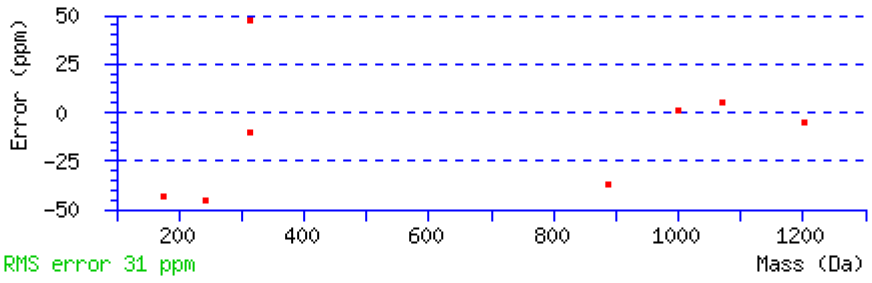
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1312.735046
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 31  Expect: 0.0061
Matches : 8/116 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	**243.133933**	122.070605			225.123368	113.065322	E	***1200.658279***	600.832778	1183.631730	592.319503	1182.647714	591.827495	11
3	**314.171047**	157.589161			296.160482	148.583879	A	***1071.615686***	536.311481	1054.589137	527.798207	1053.605121	527.306199	10
4	427.218726	214.113001			409.208161	205.107719	P	***1000.578572***	500.792924	983.552023	492.279650	982.568007	491.787642	9
5	514.250754	257.629015			496.240189	248.623733	S	***887.530893***	444.269085	870.504344	435.755810	869.520328	435.263802	8
6	627.298433	314.152855			609.287868	305.147572	P	800.498865	400.753071	783.472316	392.239796	782.488300	391.747788	7
7	755.393396	378.200336	738.366847	369.687062	737.382831	369.195054	K	687.451186	344.229231	670.424637	335.715957	669.440621	335.223949	6
8	826.430510	413.718893	809.403961	405.205619	808.419945	404.713611	A	559.356223	280.181750	542.329674	271.668475	541.345658	271.176467	5
9	939.514574	470.260925	922.488025	461.747651	921.504009	461.255643	I	488.319109	244.663193	471.292560	236.149918	470.308544	235.657910	4
10	1038.582988	519.795132	1021.556439	511.281858	1020.572423	510.789850	V	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
11	1139.630667	570.318972	1122.604118	561.805697	1121.620102	561.313689	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 LEAPSPKAIVTR
(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	1312.735046	0.003042	LEAPSPKAIVTR
18.7	1312.735016	0.003072	LEKINAEQQLK
10.3	1312.735046	0.003042	IISNVPADSLIR
7.0	1312.735077	0.003011	LVTVPSSPPTKR
6.0	1312.735031	0.003057	EALEKVDQILR
5.2	1312.750320	-0.012232	TPVAVTAWALLR
4.3	1312.746277	-0.008189	ILSVLRPQSER
4.3	1312.735077	0.003011	LVTVPSSPPTKR
4.3	1312.735077	0.003011	LVTVPSSPPTKR
0.5	1312.725128	0.012960	KNQALNIAWQK

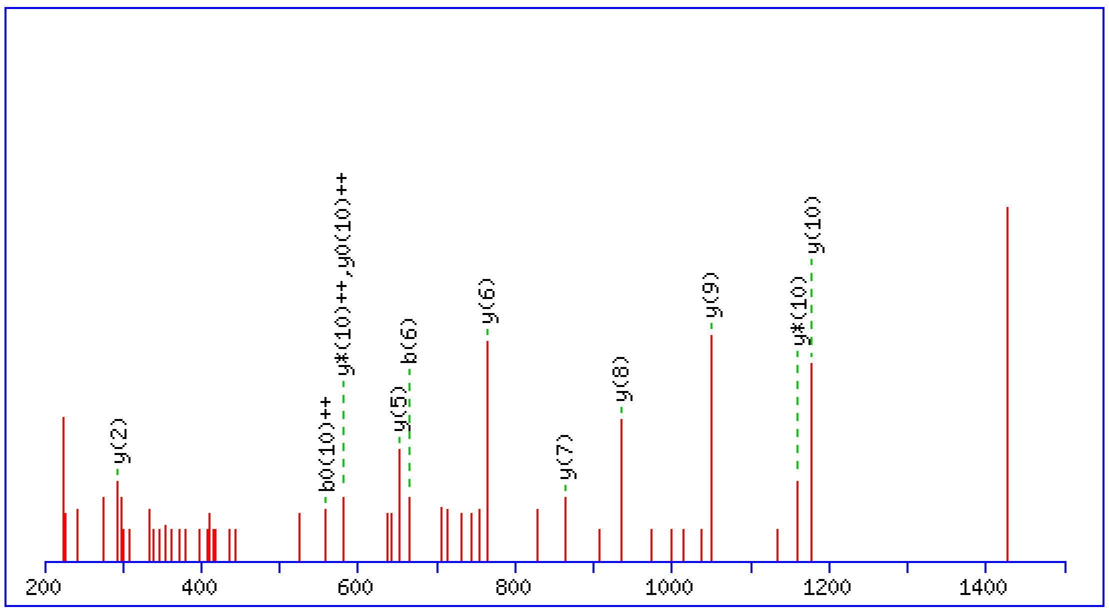
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYQDAVLEDIFK**
Found in **FKBP7_HUMAN**, Peptidyl-prolyl cis-trans isomerase FKBP7 OS=Homo sapiens GN=FKBP7 PE=1 SV=1

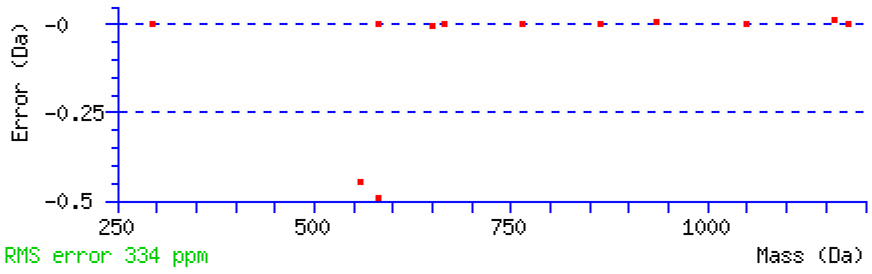
Match to Query 32673: 1426.709348 from(714.361950,2+) rtinseconds(3773) index(52188)
Title: Locus:1.1.1.2878.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

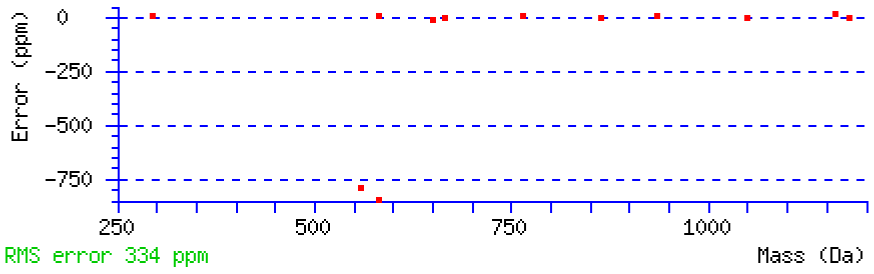
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1426.697998
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0013
Matches : 12/122 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							12
2	251.102633	126.054954			233.092068	117.049672	Y	1340.673260	670.840268	1323.646711	662.326994	1322.662695	661.834986	11
3	379.161211	190.084244	362.134662	181.570969	361.150646	181.078961	Q	***1177.609931***	589.308604	1160.583382	580.795329	1159.599366	580.303321	10
4	494.188154	247.597715	477.161605	239.084441	476.177589	238.592433	D	***1049.551353***	525.279315	1032.524804	516.766040	1031.540788	516.274032	9
5	565.225268	283.116272	548.198719	274.602998	547.214703	274.110990	A	***934.524410***	467.765843	917.497861	459.252569	916.513845	458.760561	8
6	664.293682	332.650479	647.267133	324.137205	646.283117	323.645197	V	***863.487296***	432.247286	846.460747	423.734012	845.476731	423.242004	7
7	777.377746	389.192511	760.351197	380.679237	759.367181	380.187229	L	***764.418882***	382.713079	747.392333	374.199805	746.408317	373.707797	6
8	906.420339	453.713808	889.393790	445.200533	888.409774	444.708525	E	***651.334818***	326.171047	634.308269	317.657773	633.324253	317.165765	5
9	1021.447282	511.227279	1004.420733	502.714005	1003.436717	502.221997	D	522.292225	261.649751	505.265676	253.136476	504.281660	252.644468	4
10	1134.531346	567.769311	1117.504797	559.256037	1116.520781	558.764028	I	407.265282	204.136279	390.238733	195.623004			3
11	1281.599760	641.303518	1264.573211	632.790244	1263.589195	632.298236	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 SYQDAVLEDIFK
(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	1426.697998	0.011350	SYQDAVLEDIFK
7.9	1426.706558	0.002790	HPQDPRSPGPAPR
6.8	1426.698669	0.010679	AQINHSIAMQNGK

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

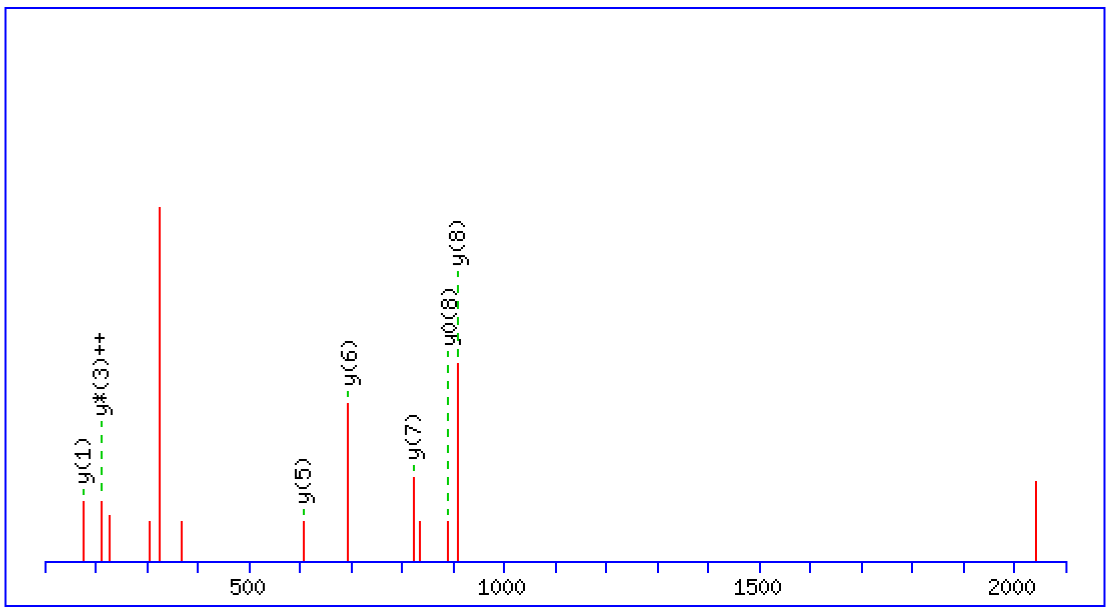
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISQSGDFLR**
Found in **FKBP9_HUMAN**, Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens GN=FKBP9 PE=1 SV=2

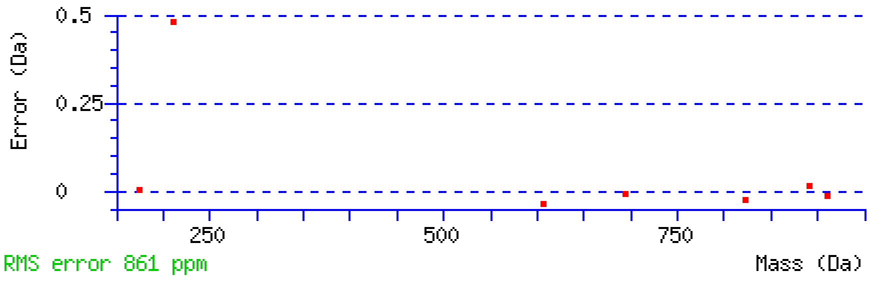
Match to Query 227233: 1021.517368 from(511.765960,2+) rtinseconds(1845) index(648202)
Title: Locus:1.1.1.892.9
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

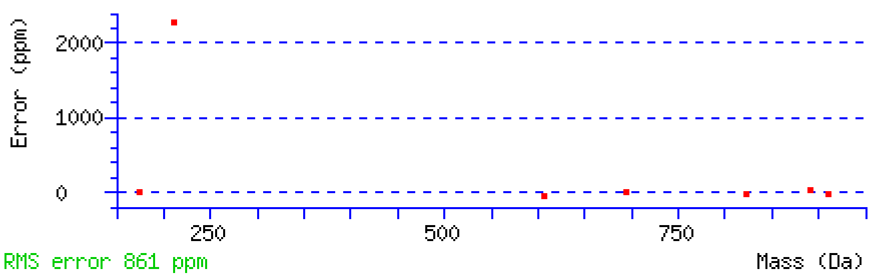
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1021.519257
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38  Expect: 0.0021
Matches : 7/84 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	201.123368	101.065322			183.112803	92.060039	S	***909.442471***	455.224874	892.415922	446.711599	891.431906	446.219591	8
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	Q	***822.410443***	411.708860	805.383894	403.195585	804.399878	402.703577	7
4	416.213974	208.610625	399.187425	200.097350	398.203409	199.605342	S	***694.351865***	347.679571	677.325316	339.166296	676.341300	338.674288	6
5	473.235438	237.121357	456.208889	228.608082	455.224873	228.116074	G	***607.319837***	304.163557	590.293288	295.650282	589.309272	295.158274	5
6	588.262381	294.634829	571.235832	286.121554	570.251816	285.629546	D	550.298373	275.652825	533.271824	267.139550	532.287808	266.647542	4
7	735.330795	368.169036	718.304246	359.655761	717.320230	359.163753	F	435.271430	218.139353	418.244881	209.626078			3
8	848.414859	424.711068	831.388310	416.197793	830.404294	415.705785	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 ISQSGDFLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.4	1021.519257	-0.001889	ISQSGDFLR
22.0	1021.519241	-0.001873	LSKFDEQR
14.5	1021.508011	0.009357	IQSSESFPK
11.3	1021.519226	-0.001858	LQSENLYR
10.0	1021.519257	-0.001889	ITSNAFPTR
9.7	1021.511368	0.006000	MSNAETLLK
4.4	1021.519257	-0.001889	TSVKYGPDR
3.6	1021.507996	0.009372	IYPEELSR
3.6	1021.519257	-0.001889	LNDFASTVR
3.3	1021.526642	-0.009274	LEMIFTPR

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

{MATRIX SCIENCE}

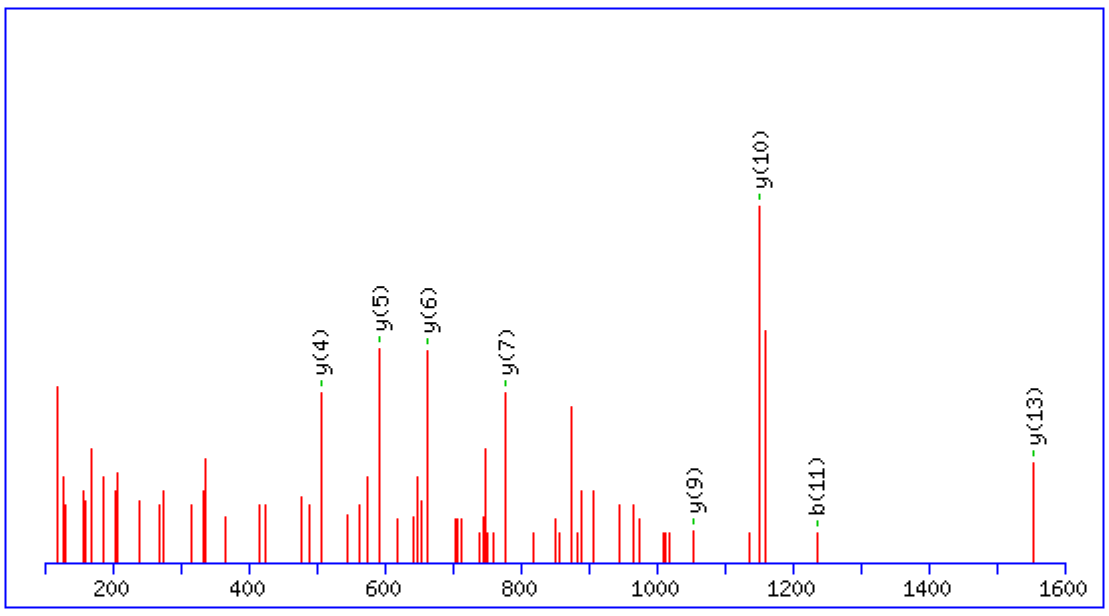
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQMQKPFEDASFALR**
Found in **PIN1_HUMAN**, Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Homo sapiens GN=PIN1 PE=1 SV=1

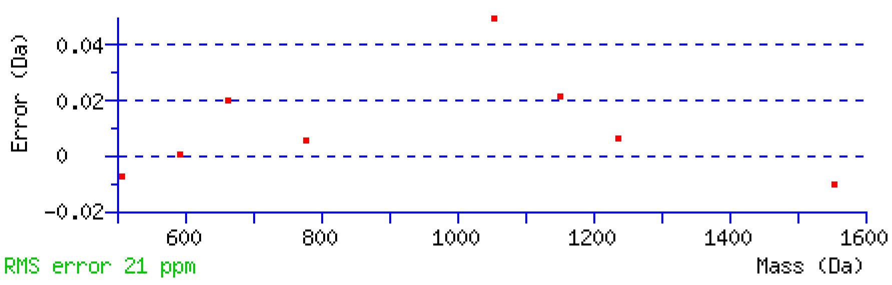
Match to Query 22982: 1739.827152 from(580.949660,3+) rtinseconds(2448) index(14775)
Title: Locus:1.1.1.2517.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

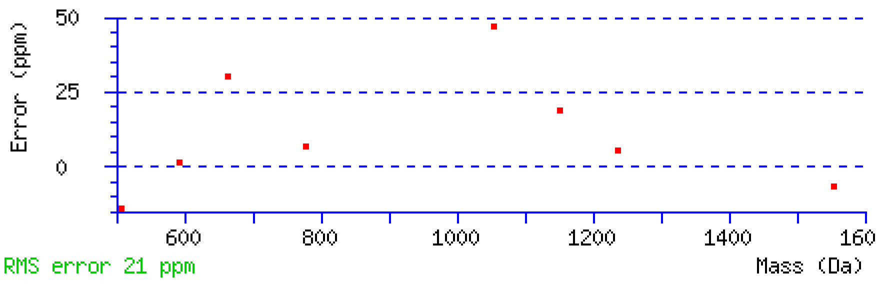
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1739.830093
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: 42 **Expect:** 0.00044
Matches : 8/218 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							15
2	186.087318	93.547297	169.060769	85.034023			Q	1683.815919	842.411598	1666.789370	833.898323	1665.805354	833.406315	14
3	333.122718	167.064997	316.096169	158.551723			M	***1555.757341***	778.382309	1538.730792	769.869034	1537.746776	769.377026	13
4	461.181296	231.094286	444.154747	222.581012			Q	1408.721941	704.864609	1391.695392	696.351334	1390.711376	695.859326	12
5	589.276259	295.141768	572.249710	286.628493			K	1280.663363	640.835319	1263.636814	632.322045	1262.652798	631.830037	11
6	686.329023	343.668150	669.302474	335.154875			P	***1152.568400***	576.787838	1135.541851	568.274564	1134.557835	567.782555	10
7	833.397437	417.202357	816.370888	408.689082			F	***1055.515636***	528.261456	1038.489087	519.748181	1037.505071	519.256173	9
8	962.440030	481.723653	945.413481	473.210379	944.429465	472.718371	E	908.447222	454.727249	891.420673	446.213975	890.436657	445.721967	8
9	1077.466973	539.237125	1060.440424	530.723850	1059.456408	530.231842	D	***779.404629***	390.205953	762.378080	381.692678	761.394064	381.200670	7
10	1148.504087	574.755682	1131.477538	566.242407	1130.493522	565.750399	A	***664.377686***	332.692481	647.351137	324.179207	646.367121	323.687199	6
11	1235.536115	618.271696	1218.509566	609.758421	1217.525550	609.266413	S	***593.340572***	297.173924	576.314023	288.660650	575.330007	288.168642	5
12	1382.604529	691.805903	1365.577980	683.292628	1364.593964	682.800620	F	***506.308544***	253.657910	489.281995	245.144635			4
13	1453.641643	727.324460	1436.615094	718.811185	1435.631078	718.319177	A	359.240130	180.123703	342.213581	171.610428			3
14	1566.725707	783.866492	1549.699158	775.353217	1548.715142	774.861209	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 GQMQKPFEDASFALR
(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	1739.830093	-0.002941	GQMQKPFEDASFALR
28.1	1739.830093	-0.002941	GQMQKPFEDASFALR
5.8	1739.830109	-0.002957	EKIPSHHFMPGSPTK

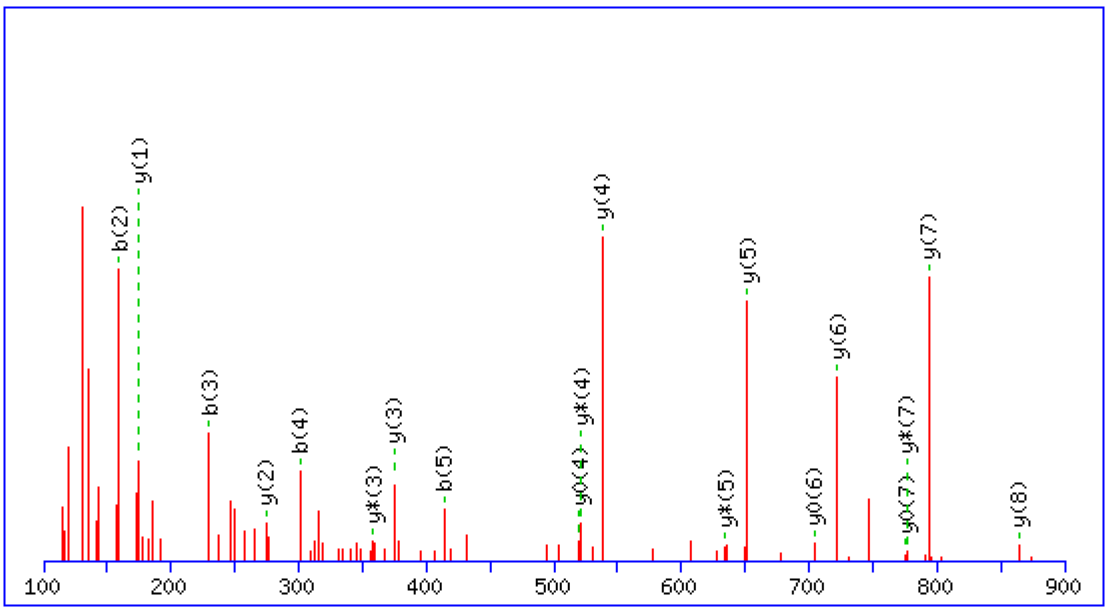
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAAAIYTVR**
Found in **PMP22_HUMAN**, Peripheral myelin protein 22 OS=Homo sapiens GN=PMP22 PE=1 SV=1

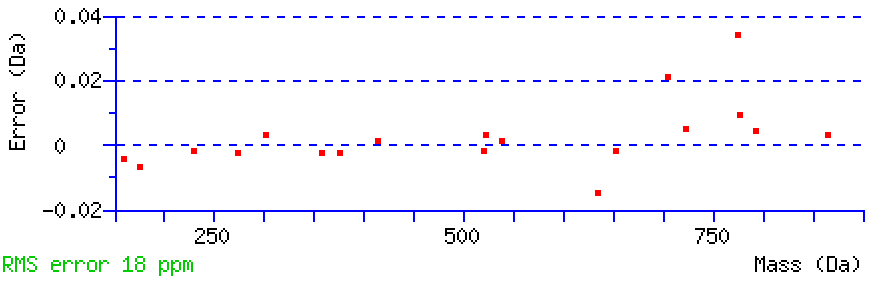
Match to Query 152775: 950.517208 from(476.265880,2+) rtinseconds(1510) index(492338)
Title: Locus:1.1.1.1193.12
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

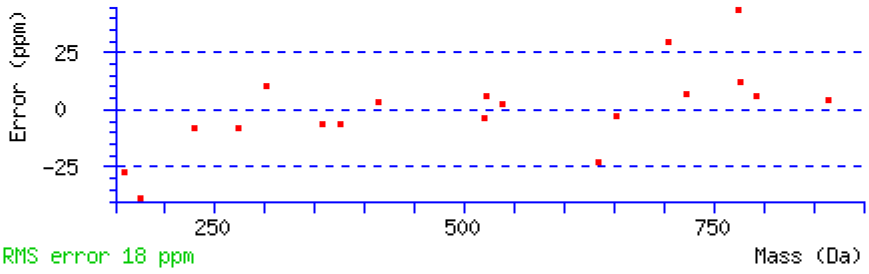
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 950.518509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 2.1e-005
Matches : 19/76 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							9
2	**159.076418**	80.041847	141.065853	71.036564	A	***864.493780***	432.750528	847.467231	424.237254	846.483215	423.745246	8
3	**230.113532**	115.560404	212.102967	106.555121	A	***793.456666***	397.231971	776.430117	388.718697	775.446101	388.226689	7
4	**301.150646**	151.078961	283.140081	142.073679	A	***722.419552***	361.713414	705.393003	353.200140	704.408987	352.708132	6
5	**414.234710**	207.620993	396.224145	198.615711	I	***651.382438***	326.194857	634.355889	317.681583	633.371873	317.189575	5
6	577.298039	289.152658	559.287474	280.147375	Y	***538.298374***	269.652825	521.271825	261.139551	520.287809	260.647543	4
7	678.345718	339.676497	660.335153	330.671215	T	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
8	777.414132	389.210704	759.403567	380.205422	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 SAAAIYTVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	950.518509	-0.001301	SAAAIYTVR
5.4	950.518524	-0.001316	VGSGLLYSR
0.2	950.518555	-0.001347	GVPPPPTVR

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

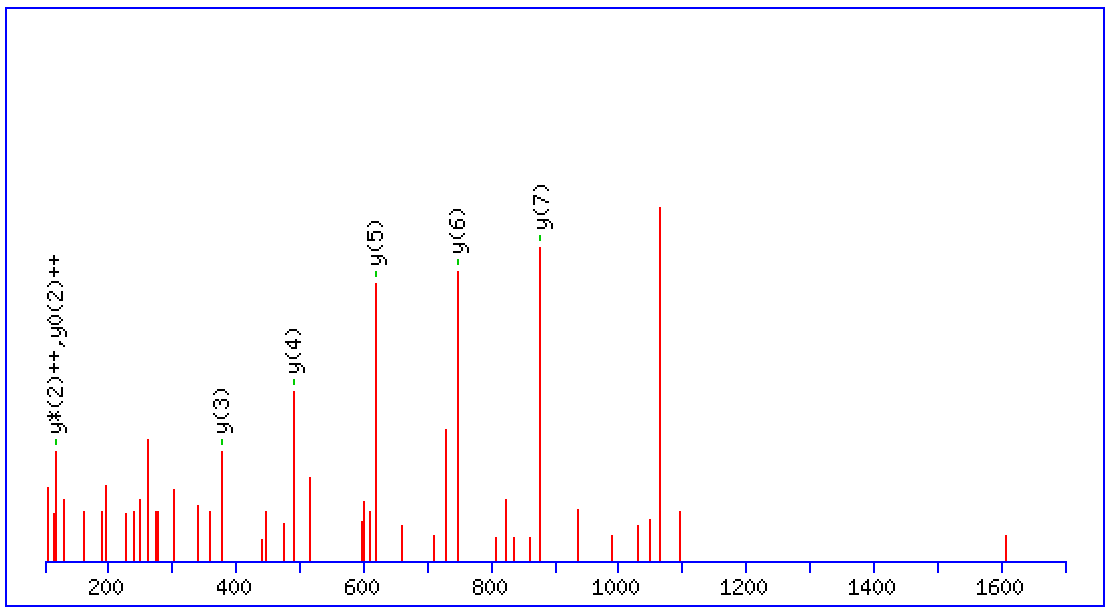
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMMKELQTK**
Found in **PEX1_HUMAN**, Peroxisome biogenesis factor 1 OS=Homo sapiens GN=PEX1 PE=1 SV=1

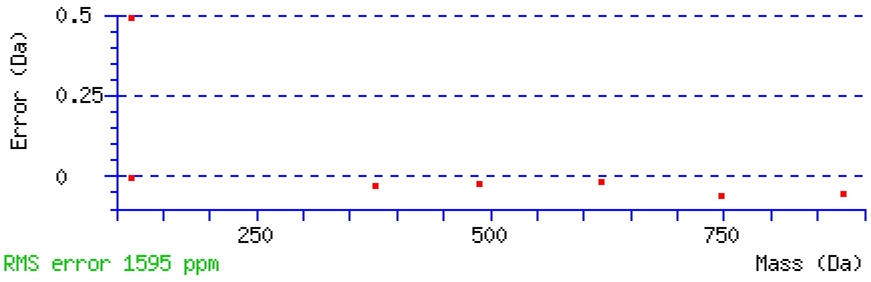
Match to Query 12304: 1064.527768 from(533.271160,2+) rtinseconds(1179) index(5089)
Title: Locus:1.1.1.1913.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-1.mgf

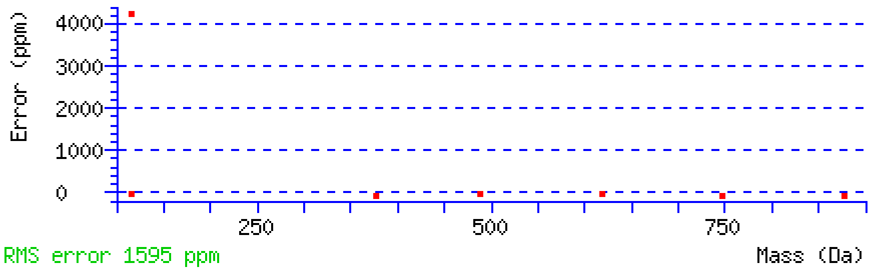
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1064.535812
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.0012
Matches : 7/80 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	58.028740	29.518008					G							9
2	189.069225	95.038250					M	1008.521651	504.764464	991.495102	496.251189	990.511086	495.759181	8
3	320.109710	160.558493					M	***877.481166***	439.244221	860.454617	430.730947	859.470601	430.238939	7
4	448.204673	224.605975	431.178124	216.092700			K	***746.440681***	373.723979	729.414132	365.210704	728.430116	364.718696	6
5	577.247266	289.127271	560.220717	280.613997	559.236701	280.121989	E	***618.345718***	309.676497	601.319169	301.163223	600.335153	300.671215	5
6	690.331330	345.669303	673.304781	337.156029	672.320765	336.664021	L	***489.303125***	245.155201	472.276576	236.641926	471.292560	236.149918	4
7	818.389908	409.698592	801.363359	401.185318	800.379343	400.693310	Q	***376.219061***	188.613169	359.192512	180.099894	358.208496	179.607886	3
8	919.437587	460.222432	902.411038	451.709157	901.427022	451.217149	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 GMMKELQTK
(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	1064.535812	-0.008044	GMMKELQTK
5.6	1064.517212	0.010556	STLGPKGMDK
5.0	1064.517212	0.010556	TSLGPKGMDK
4.8	1064.532455	-0.004687	EFVIIDCR
3.7	1064.532455	-0.004687	DALFVAAGCK
3.5	1064.525055	0.002713	DLPNSGKYR
0.8	1064.536301	-0.008533	QPLPSQHSR
0.7	1064.536301	-0.008533	YRDLAGGTGR
0.6	1064.536301	-0.008533	QTPHLGEQR
0.2	1064.517181	0.010587	ETASELLMR

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

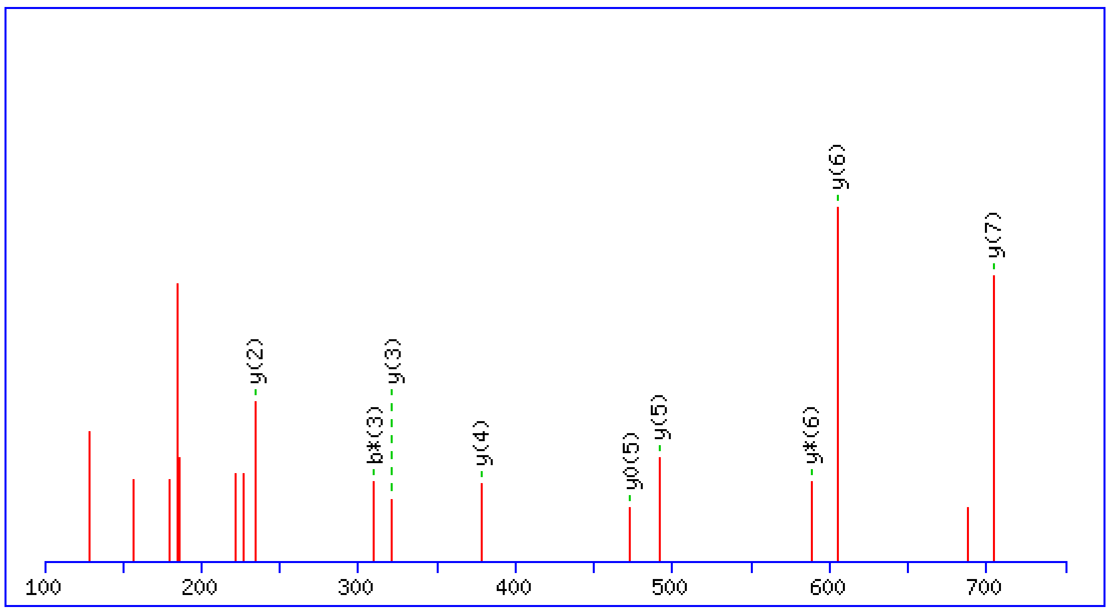
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVNLGSSK**
Found in **PHF5A_HUMAN**, PHD finger-like domain-containing protein 5A OS=Homo sapiens GN=PHF5A PE=1 SV=1

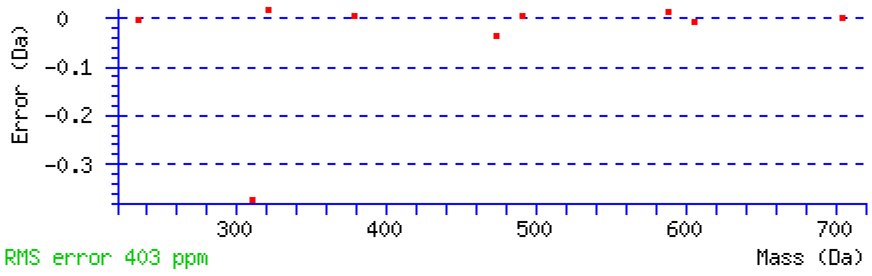
Match to Query 693: 816.468528 from(409.241540,2+) rtinseconds(1291) index(1009)
Title: Locus:1.1.1.2248.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

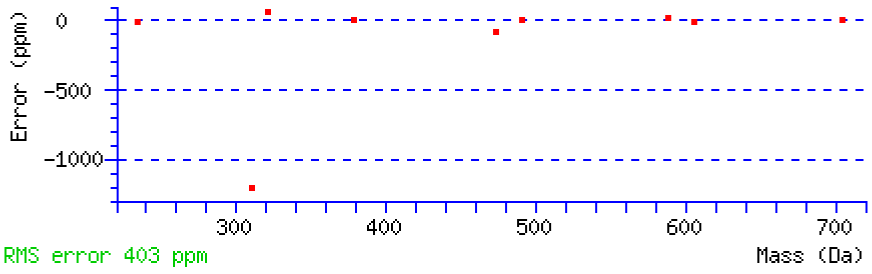
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 816.470505
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00014
Matches : 9/68 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							8
2	213.159754	107.083515					V	***704.393729***	352.700503	687.367180	344.187228	686.383164	343.695220	7
3	327.202681	164.104978	310.176132	155.591704			N	***605.325315***	303.166296	588.298766	294.653021	587.314750	294.161013	6
4	440.286745	220.647010	423.260196	212.133736			L	***491.282388***	246.144832	474.255839	237.631557	473.271823	237.139549	5
5	497.308209	249.157742	480.281660	240.644468			G	***378.198324***	189.602800	361.171775	181.089525	360.187759	180.597517	4
6	584.340237	292.673757	567.313688	284.160482	566.329672	283.668474	S	***321.176860***	161.092068	304.150311	152.578793	303.166295	152.086785	3
7	671.372265	336.189771	654.345716	327.676496	653.361700	327.184488	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 IVNLGSSK
(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	816.470505	-0.001977	IVNLGSSK
15.9	816.470505	-0.001977	LVNDTKK
14.6	816.470490	-0.001962	INVKESK
7.7	816.470490	-0.001962	LAALNTSK
3.1	816.470505	-0.001977	GSILATQK
2.2	816.470505	-0.001977	IVKESGGK
2.2	816.470505	-0.001977	IVSITER
2.2	816.470520	-0.001992	IVTTDLR
0.8	816.463974	0.004554	IPMLRR
0.7	816.474533	-0.006005	IPPFISK

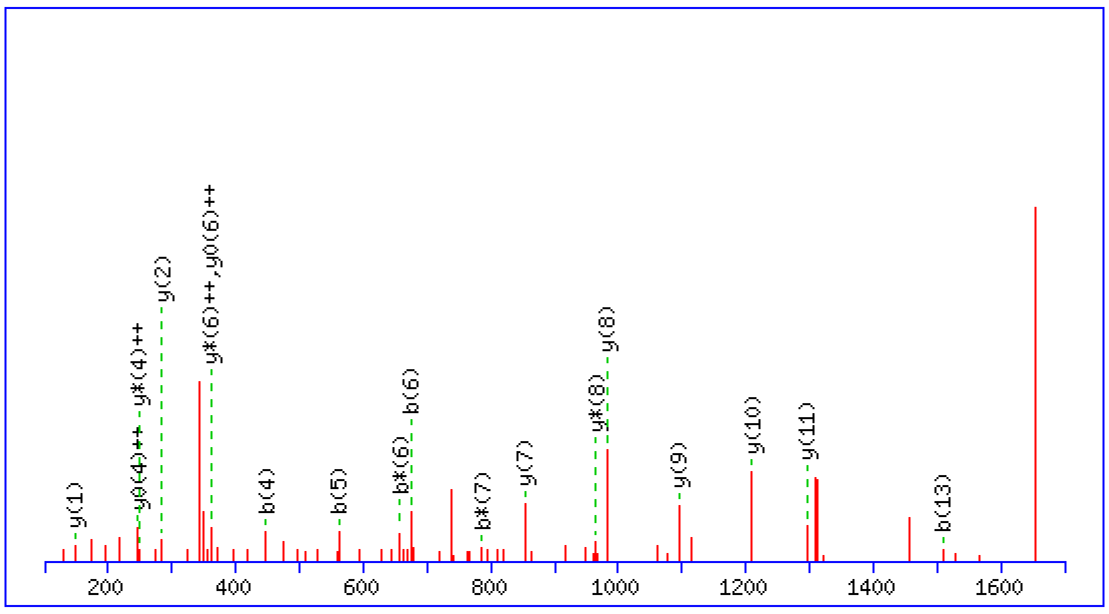
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLFSNIEDILEVHK**
Found in **PREX1_HUMAN**, Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein OS=Homo sapiens GN=PREX1 PE=1 SV=3

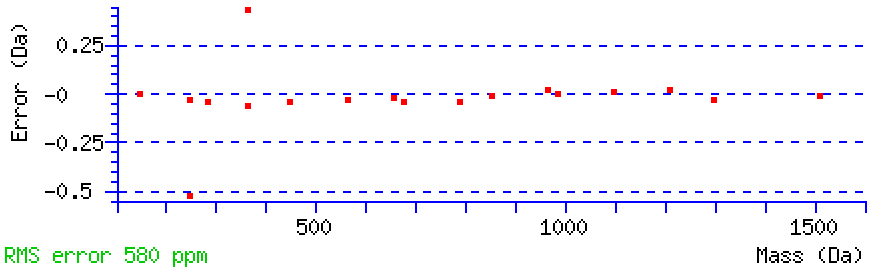
Match to Query 55804: 1654.878688 from(828.446620,2+) rtinseconds(2524) index(33570)
Title: Locus:1.1.1.2250.44
Data file 2011-11-14 - TFD - S 2-2.mgf

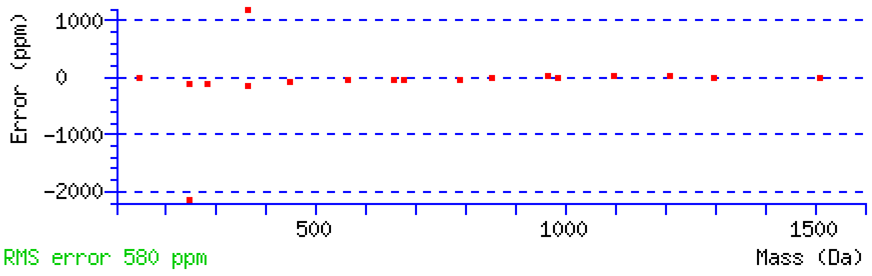
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1654.893005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0046
Matches : 18/136 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	100.075690	50.541483					V							14
2	213.159754	107.083515					L	1556.831884	778.919580	1539.805335	770.406306	1538.821319	769.914297	13
3	360.228168	180.617722					F	1443.747820	722.377548	1426.721271	713.864274	1425.737255	713.372266	12
4	**447.260196**	224.133736			429.249631	215.128454	S	***1296.679406***	648.843341	1279.652857	640.330067	1278.668841	639.838058	11
5	**561.303123**	281.155200	544.276574	272.641925	543.292558	272.149917	N	***1209.647378***	605.327327	1192.620829	596.814053	1191.636813	596.322044	10
6	**674.387187**	337.697232	657.360638	329.183957	656.376622	328.691949	I	***1095.604451***	548.305863	1078.577902	539.792589	1077.593886	539.300581	9
7	803.429780	402.218528	786.403231	393.705254	785.419215	393.213246	E	***982.520387***	491.763832	965.493838	483.250557	964.509822	482.758549	8
8	918.456723	459.732000	901.430174	451.218725	900.446158	450.726717	D	***853.477794***	427.242535	836.451245	418.729261	835.467229	418.237253	7
9	1031.540787	516.274031	1014.514238	507.760757	1013.530222	507.268749	I	738.450851	369.729064	721.424302	361.215789	720.440286	360.723781	6
10	1144.624851	572.816063	1127.598302	564.302789	1126.614286	563.810781	L	625.366787	313.187032	608.340238	304.673757	607.356222	304.181749	5
11	1273.667444	637.337360	1256.640895	628.824086	1255.656879	628.332077	E	512.282723	256.645000	495.256174	248.131725	494.272158	247.639717	4
12	1372.735858	686.871567	1355.709309	678.358293	1354.725293	677.866285	V	383.240130	192.123703	366.213581	183.610429			3
13	**1509.794770**	755.401023	1492.768221	746.887749	1491.784205	746.395740	H	***284.171716***	142.589496	267.145167	134.076221			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VLFSNIEDILEVHK
(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	1654.893005	-0.014317	VLFSNIEDILEVHK
5.3	1654.893036	-0.014348	SPQQTVPYVVPLSPK
4.2	1654.871246	0.007442	VRQILMASGSTTFTK
3.8	1654.885147	-0.006459	LLEPADMVLLSVPDK
0.3	1654.889008	-0.010320	SSQGSPSVVVAPSPKTK

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

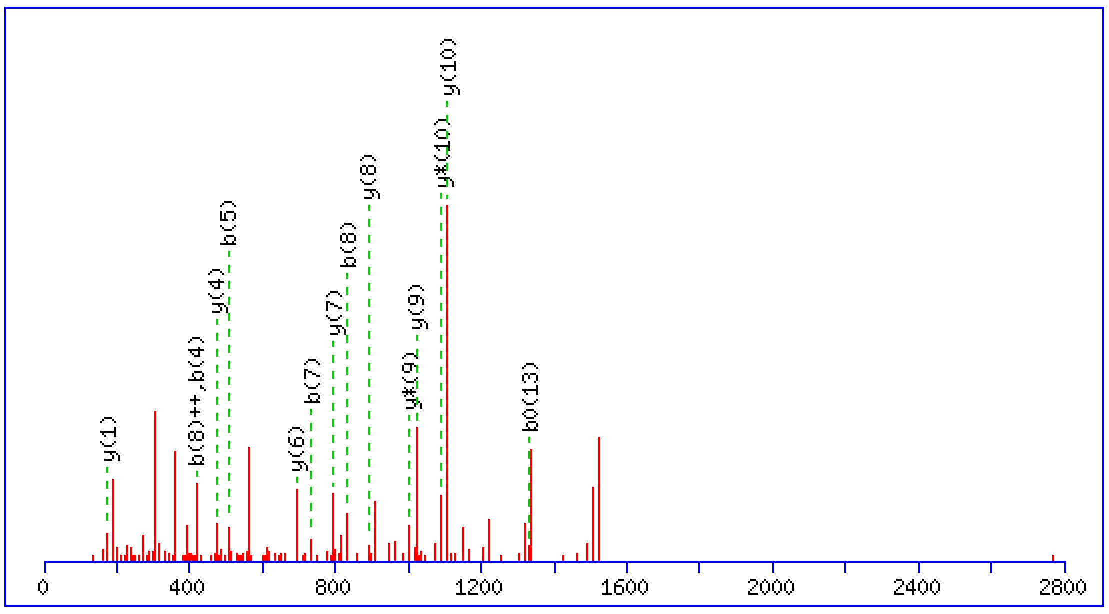
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGRSMPTSMALDR**
Found in **PGM5_HUMAN**, Phosphoglucomutase-like protein 5 OS=Homo sapiens GN=PGM5 PE=1 SV=2

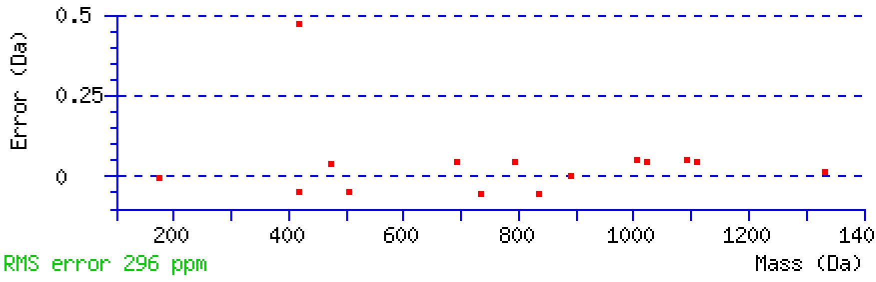
Match to Query 36562: 1524.704448 from(763.359500,2+) rtinseconds(2629) index(32404)
Title: Locus:1.1.1.2539.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

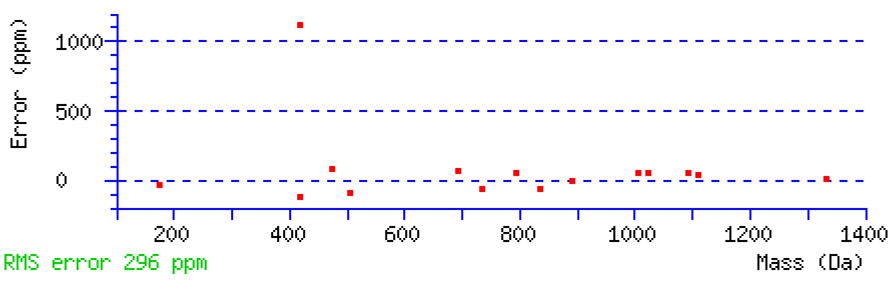
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1524.717712
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00077
Matches : 15/140 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							14
2	205.097154	103.052215					F	1468.703531	734.855404	1451.676982	726.342129	1450.692966	725.850121	13
3	262.118618	131.562947					G	1321.635117	661.321197	1304.608568	652.807922	1303.624552	652.315914	12
4	**418.219729**	209.613502	401.193180	201.100228			R	1264.613653	632.810465	1247.587104	624.297190	1246.603088	623.805182	11
5	**505.251757**	253.129516	488.225208	244.616242	487.241192	244.124234	S	***1108.512542***	554.759909	1091.485993	546.246635	1090.501977	545.754627	10
6	636.292242	318.649759	619.265693	310.136484	618.281677	309.644477	M	***1021.480514***	511.243895	1004.453965	502.730621	1003.469949	502.238613	9
7	**733.345006**	367.176141	716.318457	358.662867	715.334441	358.170859	P	***890.440029***	445.723653	873.413480	437.210378	872.429464	436.718370	8
8	**834.392685**	417.699981	817.366136	409.186706	816.382120	408.694698	T	***793.387265***	397.197271	776.360716	388.683996	775.376700	388.191988	7
9	921.424713	461.215995	904.398164	452.702720	903.414148	452.210712	S	***692.339586***	346.673431	675.313037	338.160157	674.329021	337.668149	6
10	1052.465198	526.736237	1035.438649	518.222963	1034.454633	517.730955	M	605.307558	303.157417	588.281009	294.644143	587.296993	294.152135	5
11	1123.502312	562.254794	1106.475763	553.741520	1105.491747	553.249512	A	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
12	1236.586376	618.796826	1219.559827	610.283552	1218.575811	609.791543	L	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
13	1351.613319	676.310298	1334.586770	667.797023	1333.602754	667.305015	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





NCBI **BLAST** search of GFGRSMPTSMALDR
(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	1524.717712	-0.013264	GFGRSMPTSMALDR

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

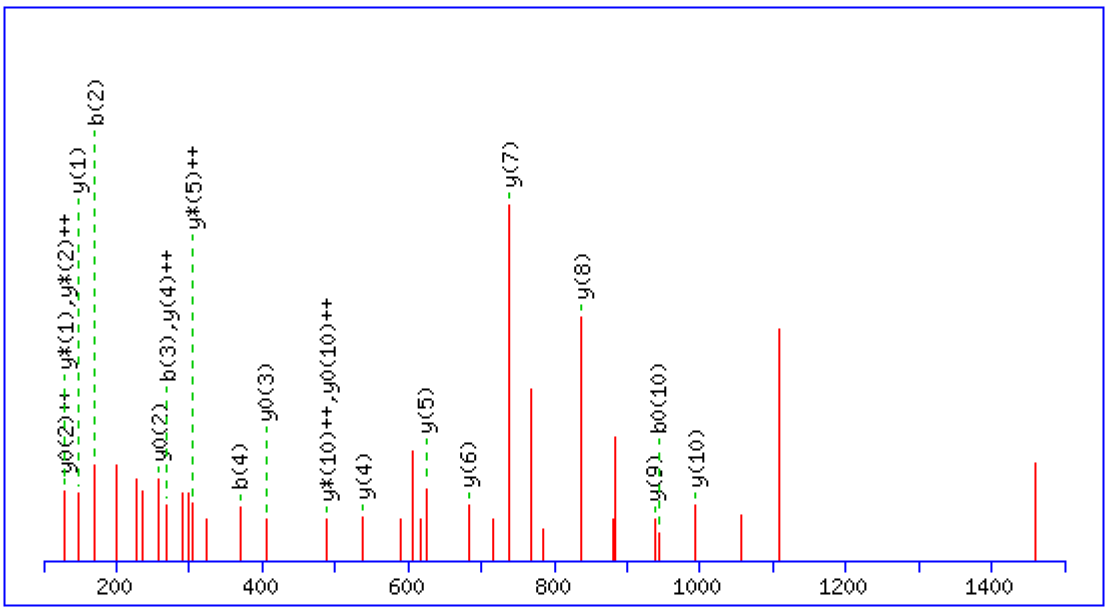
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGVVGGSDFEK**
Found in **PMM2_HUMAN**, Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=1 SV=1

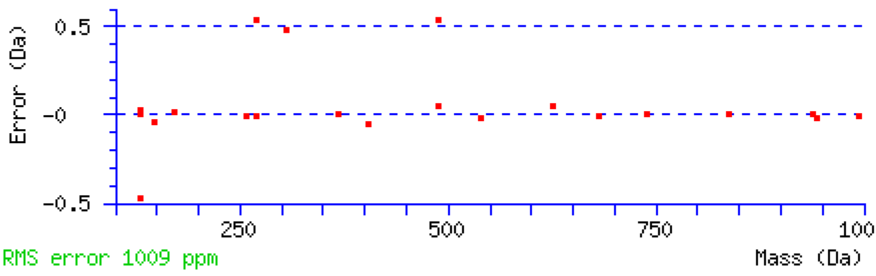
Match to Query 16871: 1106.560328 from(554.287440,2+) rtinseconds(2020) index(16518)
Title: Locus:1.1.1.2581.25
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

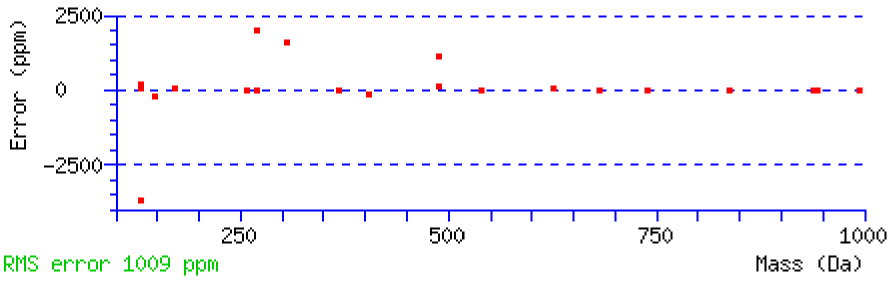
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1106.560806
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 7.9e-005
Matches : 21/86 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			I							11
2	**171.112804**	86.060040			G	***994.484002***	497.745639	977.457453	489.232365	976.473437	488.740357	10
3	**270.181218**	135.594247			V	***937.462538***	469.234907	920.435989	460.721633	919.451973	460.229625	9
4	**369.249632**	185.128454			V	***838.394124***	419.700700	821.367575	411.187426	820.383559	410.695418	8
5	426.271096	213.639186			G	***739.325710***	370.166493	722.299161	361.653219	721.315145	361.161211	7
6	483.292560	242.149918			G	***682.304246***	341.655761	665.277697	333.142487	664.293681	332.650479	6
7	570.324588	285.665932	552.314023	276.660650	S	***625.282782***	313.145029	608.256233	304.631755	607.272217	304.139747	5
8	685.351531	343.179404	667.340966	334.174121	D	***538.250754***	269.629015	521.224205	261.115741	520.240189	260.623733	4
9	832.419945	416.713611	814.409380	407.708328	F	423.223811	212.115543	406.197262	203.602269	405.213246	203.110261	3
10	961.462538	481.234907	943.451973	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 IGVVGGSDFEK
(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	1106.560806	-0.000478	IGVVGGSDFEK
5.9	1106.552902	0.007426	LLEMLDTEK

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

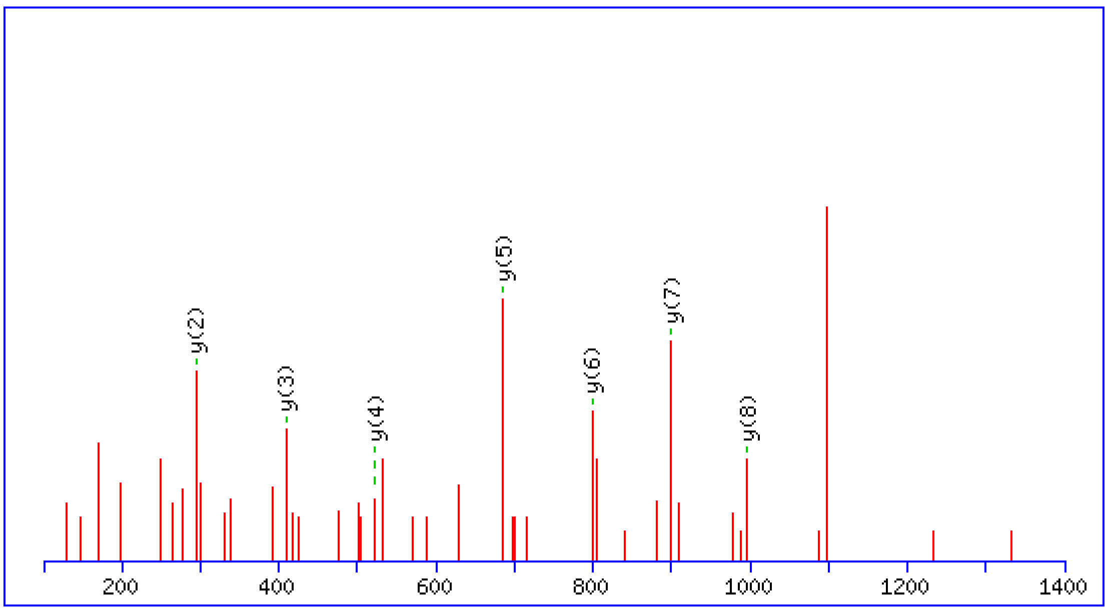
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPTLYLDFK**
Found in **PIR_HUMAN**, Pirin OS=Homo sapiens GN=PIR PE=1 SV=1

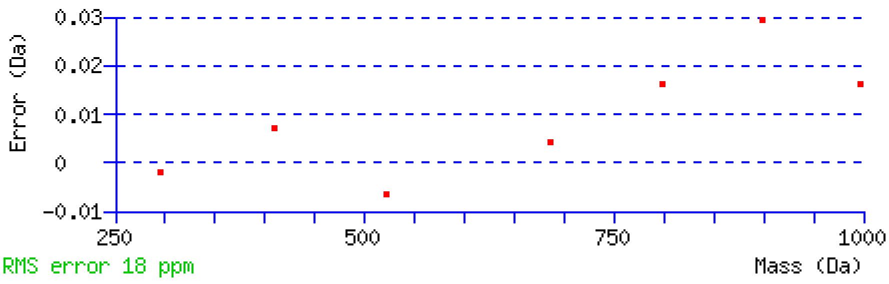
Match to Query 18562: 1096.585008 from(549.299780,2+) rtinseconds(3065) index(39176)
Title: Locus:1.1.1.2751.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

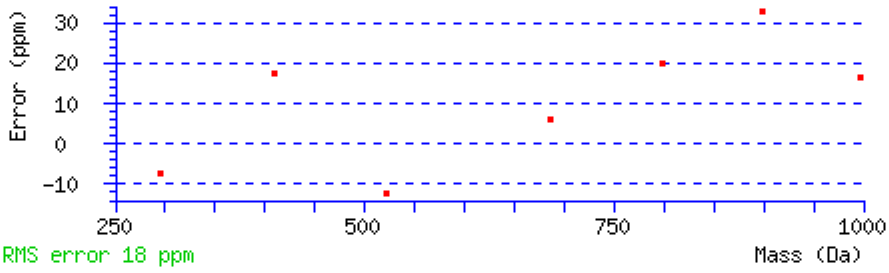
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1096.580460
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 61 **Expect:** 3.5e-006
Matches : 7/76 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	199.107719	100.057497	181.097154	91.052215	P	***996.540061***	498.773669	979.513512	490.260394	978.529496	489.768386	8
3	300.155398	150.581337	282.144833	141.576055	T	***899.487297***	450.247287	882.460748	441.734012	881.476732	441.242004	7
4	413.239462	207.123369	395.228897	198.118087	L	***798.439618***	399.723447	781.413069	391.210173	780.429053	390.718165	6
5	576.302791	288.655034	558.292226	279.649751	Y	***685.355554***	343.181415	668.329005	334.668141	667.344989	334.176133	5
6	689.386855	345.197066	671.376290	336.191783	L	***522.292225***	261.649751	505.265676	253.136476	504.281660	252.644468	4
7	804.413798	402.710537	786.403233	393.705255	D	***409.208161***	205.107719	392.181612	196.594444	391.197596	196.102436	3
8	951.482212	476.244744	933.471647	467.239462	F	***294.181218***	147.594247	277.154669	139.080973			2
9					K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of TPTLYLDFK
(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	1096.580460	0.004548	TPTLYLDFK
2.7	1096.577759	0.007249	VAERNFPHK

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

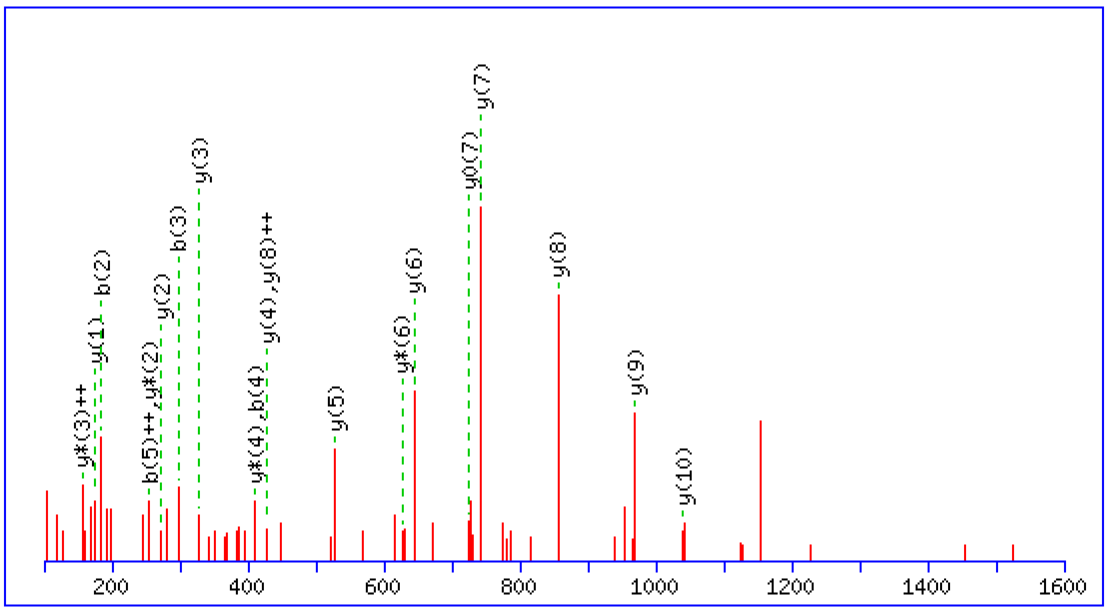
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LALLVDTVGPR**
Found in **PGCP_HUMAN**, Plasma glutamate carboxypeptidase OS=Homo sapiens GN=PGCP PE=1 SV=1

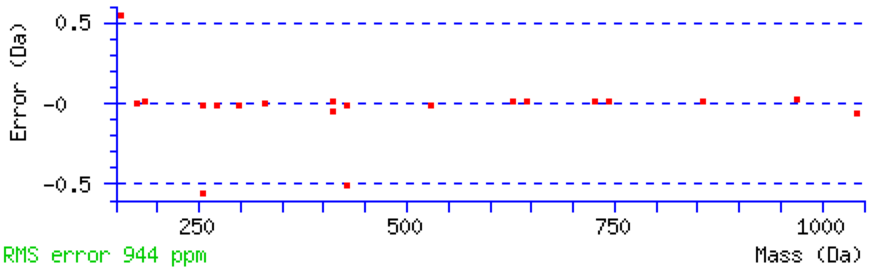
Match to Query 16742: 1152.680088 from(577.347320,2+) rtinseconds(2861) index(36749)
Title: Locus:1.1.1.2628.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

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 ●

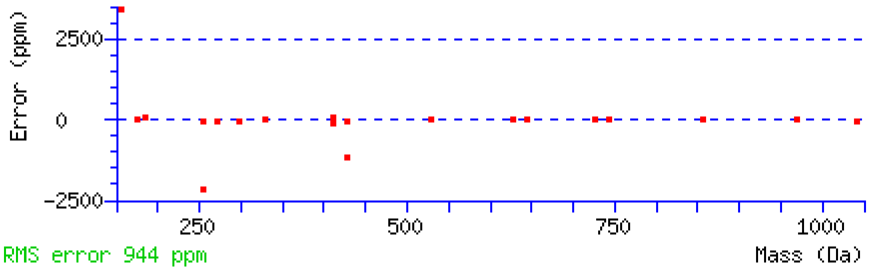


```
Monoisotopic mass of neutral peptide Mr(calc): 1152.686661
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 8.2e-006
Matches : 20/82 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			L							11
2	**185.128454**	93.067865			A	***1040.609872***	520.808574	1023.583323	512.295300	1022.599307	511.803292	10
3	**298.212518**	149.609897			L	***969.572758***	485.290017	952.546209	476.776743	951.562193	476.284735	9
4	**411.296582**	206.151929			L	***856.488694***	428.747985	839.462145	420.234711	838.478129	419.742703	8
5	510.364996	255.686136			V	***743.404630***	372.205953	726.378081	363.692679	725.394065	363.200671	7
6	625.391939	313.199608	607.381374	304.194325	D	***644.336216***	322.671746	627.309667	314.158472	626.325651	313.666464	6
7	726.439618	363.723447	708.429053	354.718165	T	***529.309273***	265.158275	512.282724	256.645000	511.298708	256.152992	5
8	825.508032	413.257654	807.497467	404.252372	V	***428.261594***	214.634435	411.235045	206.121160			4
9	882.529496	441.768386	864.518931	432.763104	G	***329.193180***	165.100228	312.166631	156.586953			3
10	979.582260	490.294768	961.571695	481.289486	P	***272.171716***	136.589496	255.145167	128.076221			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 944 ppm



RMS error 944 ppm

NCBI **BLAST** search of LALLVDTVGPR
(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	1152.686661	-0.006573	LALLVDTVGPR

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

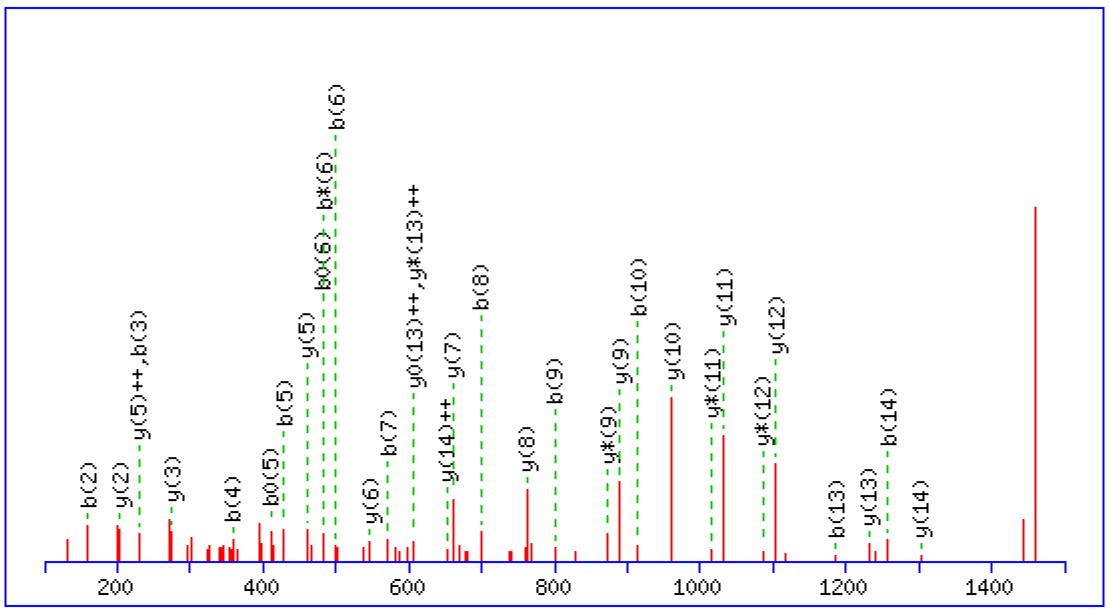
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAAQAAAQTNSNAAGK**
Found in **PAIRB_HUMAN**, Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2

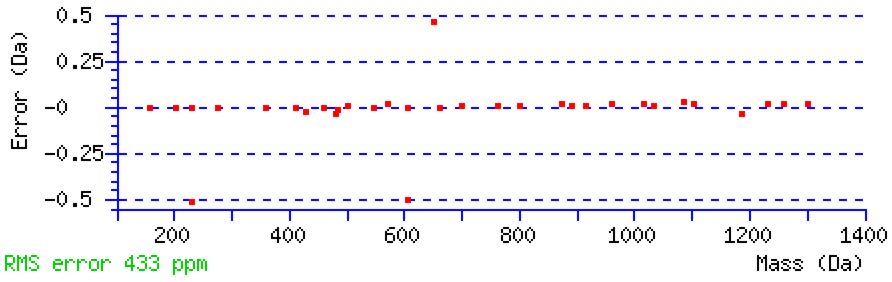
Match to Query 31747: 1459.707188 from(730.860870,2+) rtinseconds(729) index(133)
Title: Locus:1.1.1.1795.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

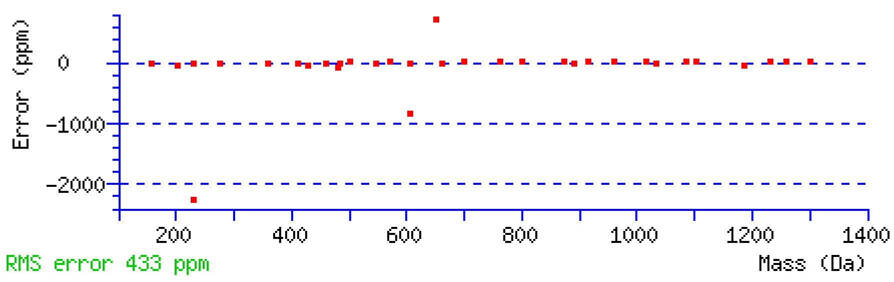
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1459.701492
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 98 **Expect:** 7.8e-010
Matches : 33/164 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	88.039304	44.523290			70.028739	35.518008	S							16
2	**159.076418**	80.041847			141.065853	71.036564	A	1373.676783	687.342029	1356.650234	678.828755	1355.666218	678.336747	15
3	**230.113532**	115.560404			212.102967	106.555121	A	***1302.639669***	651.823472	1285.613120	643.310198	1284.629104	642.818190	14
4	**358.172110**	179.589693	341.145561	171.076419	340.161545	170.584411	Q	***1231.602555***	616.304915	1214.576006	607.791641	1213.591990	607.299633	13
5	**429.209224**	215.108250	412.182675	206.594976	411.198659	206.102968	A	***1103.543977***	552.275627	1086.517428	543.762352	1085.533412	543.270344	12
6	**500.246338**	250.626807	483.219789	242.113532	482.235773	241.621524	A	***1032.506863***	516.757070	1015.480314	508.243795	1014.496298	507.751787	11
7	**571.283452**	286.145364	554.256903	277.632090	553.272887	277.140082	A	***961.469749***	481.238513	944.443200	472.725238	943.459184	472.233230	10
8	**699.342030**	350.174653	682.315481	341.661379	681.331465	341.169371	Q	***890.432635***	445.719956	873.406086	437.206681	872.422070	436.714673	9
9	**800.389709**	400.698493	783.363160	392.185218	782.379144	391.693210	T	***762.374057***	381.690667	745.347508	373.177392	744.363492	372.685384	8
10	**914.432636**	457.719956	897.406087	449.206682	896.422071	448.714674	N	***661.326378***	331.166827	644.299829	322.653552	643.315813	322.161544	7
11	1001.464664	501.235970	984.438115	492.722695	983.454099	492.230687	S	***547.283451***	274.145364	530.256902	265.632089	529.272886	265.140081	6
12	1115.507591	558.257434	1098.481042	549.744159	1097.497026	549.252151	N	***460.251423***	230.629349	443.224874	222.116075			5
13	**1186.544705**	593.775991	1169.518156	585.262716	1168.534140	584.770708	A	346.208496	173.607886	329.181947	165.094611			4
14	**1257.581819**	629.294548	1240.555270	620.781273	1239.571254	620.289265	A	***275.171382***	138.089329	258.144833	129.576054			3
15	1314.603283	657.805279	1297.576734	649.292005	1296.592718	648.799997	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 SAAQAAAQTNSNAAGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
98.4	1459.701492	0.005696	SAAQAAAQTNSNAAGK
1.3	1459.697662	0.009526	MDANSKDKPPETK

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

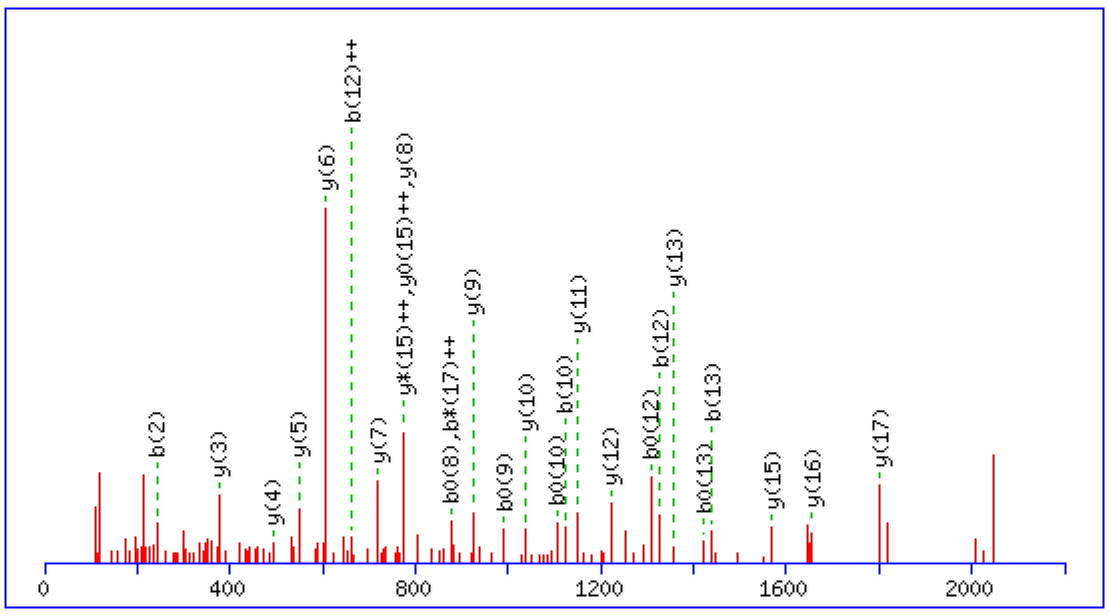
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELFSPLHALNFGIGGDTTR**
Found in **PA1B2_HUMAN**, Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1

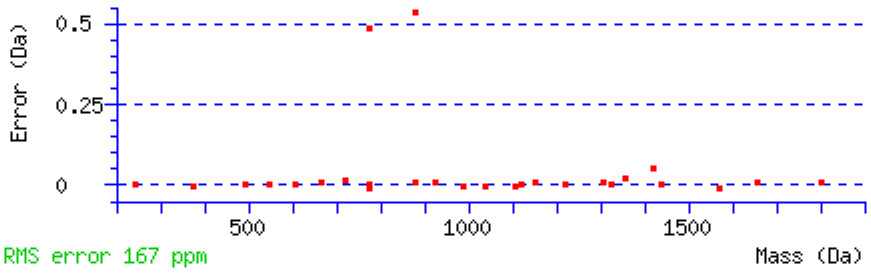
Match to Query 45764: 2044.033212 from(682.351680,3+) rtinseconds(3687) index(43825)
Title: Locus:1.1.1.3049.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

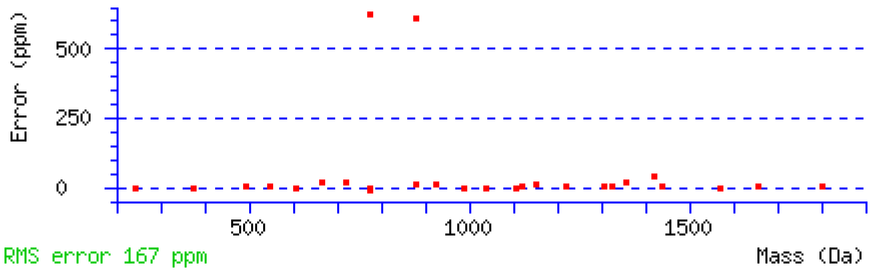
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2044.037796
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 115 **Expect:** 3.6e-011
Matches : 27/196 fragment ions using 36 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							19
2	**243.133933**	122.070605			225.123368	113.065322	L	1916.002474	958.504875	1898.975925	949.991600	1897.991909	949.499592	18
3	390.202347	195.604811			372.191782	186.599529	F	***1802.918410***	901.962843	1785.891861	893.449568	1784.907845	892.957560	17
4	477.234375	239.120825			459.223810	230.115543	S	***1655.849996***	828.428636	1638.823447	819.915361	1637.839431	819.423353	16
5	574.287139	287.647208			556.276574	278.641925	P	***1568.817968***	784.912622	1551.791419	776.399347	1550.807403	775.907339	15
6	687.371203	344.189240			669.360638	335.183957	L	1471.765204	736.386240	1454.738655	727.872965	1453.754639	727.380957	14
7	824.430115	412.718696			806.419550	403.713413	H	***1358.681140***	679.844208	1341.654591	671.330934	1340.670575	670.838925	13
8	895.467229	448.237253			877.456664	439.231970	A	***1221.622228***	611.314752	1204.595679	602.801478	1203.611663	602.309469	12
9	1008.551293	504.779285			990.540728	495.774002	L	***1150.585114***	575.796195	1133.558565	567.282920	1132.574549	566.790912	11
10	**1122.594220**	561.800748	1105.567671	553.287474	1104.583655	552.795465	N	***1037.501050***	519.254163	1020.474501	510.740888	1019.490485	510.248880	10
11	1269.662634	635.334955	1252.636085	626.821681	1251.652069	626.329673	F	***923.458123***	462.232699	906.431574	453.719425	905.447558	453.227417	9
12	**1326.684098**	663.845687	1309.657549	655.332413	1308.673533	654.840404	G	***776.389709***	388.698492	759.363160	380.185218	758.379144	379.693210	8
13	**1439.768162**	720.387719	1422.741613	711.874444	1421.757597	711.382436	I	***719.368245***	360.187760	702.341696	351.674486	701.357680	351.182478	7
14	1496.789626	748.898451	1479.763077	740.385176	1478.779061	739.893168	G	***606.284181***	303.645729	589.257632	295.132454	588.273616	294.640446	6
15	1553.811090	777.409183	1536.784541	768.895908	1535.800525	768.403900	G	***549.262717***	275.134997	532.236168	266.621722	531.252152	266.129714	5
16	1668.838033	834.922654	1651.811484	826.409380	1650.827468	825.917372	D	***492.241253***	246.624265	475.214704	238.110990	474.230688	237.618982	4
17	1769.885712	885.446494	1752.859163	876.933219	1751.875147	876.441211	T	***377.214310***	189.110793	360.187761	180.597518	359.203745	180.105510	3
18	1870.933391	935.970333	1853.906842	927.457059	1852.922826	926.965051	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
115.3	2044.037796	-0.004584	ELFSPLHALNFGIGGDTTR
4.5	2044.037292	-0.004080	LESFPELMTAAKFLLMR
0.3	2044.049026	-0.015814	HLGNPAKDGGNVTVSLFYR

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

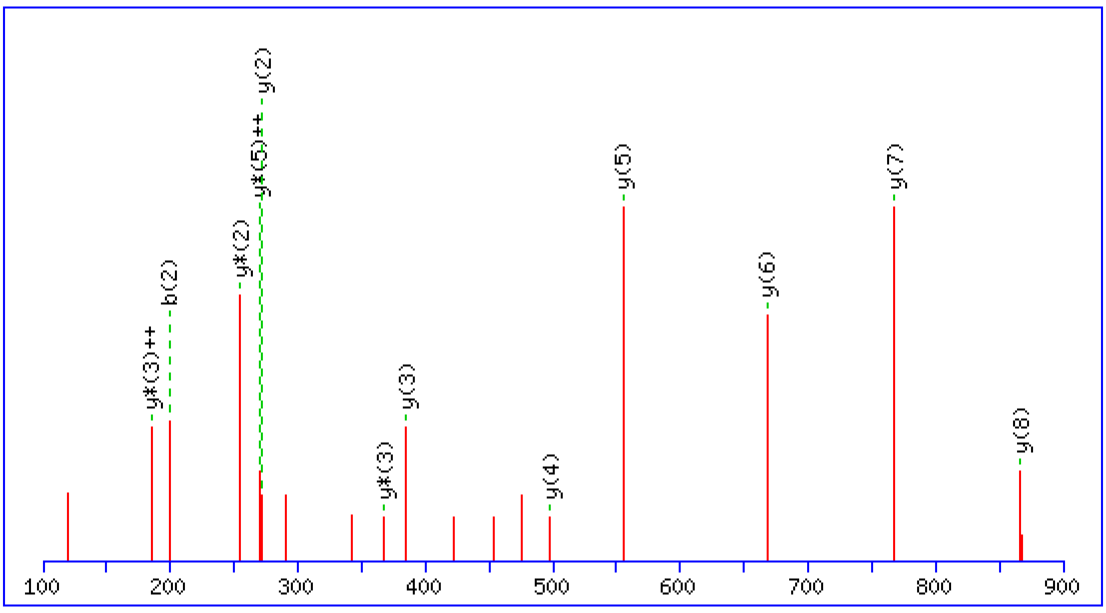
Mascot Search Results

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

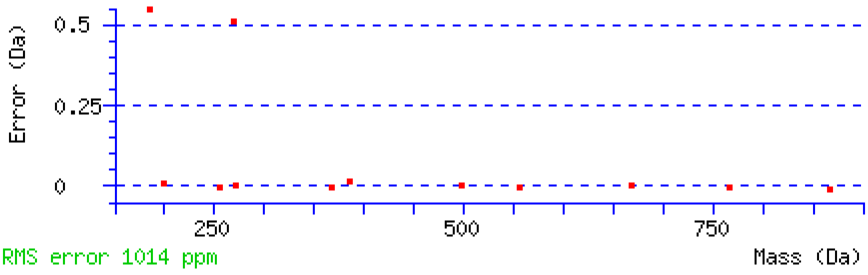
Match to Query 9285: 964.646388 from(483.330470,2+) rtinseconds(3186) index(38464)
Title: Locus:1.1.1.3021.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

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 ●

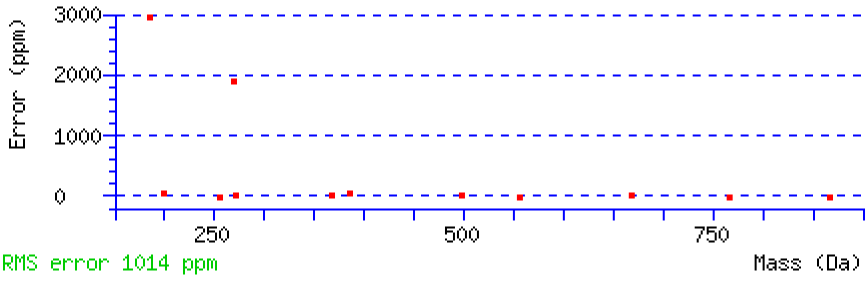


```
Monoisotopic mass of neutral peptide Mr(calc): 964.643341
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 2.6e-006
Matches : 12/48 fragment ions using 19 most intense peaks   (help)
```

#	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



RMS error 1014 ppm



RMS error 1014 ppm

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
55.8	964.643341	0.003047	VVVLGLLPR

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

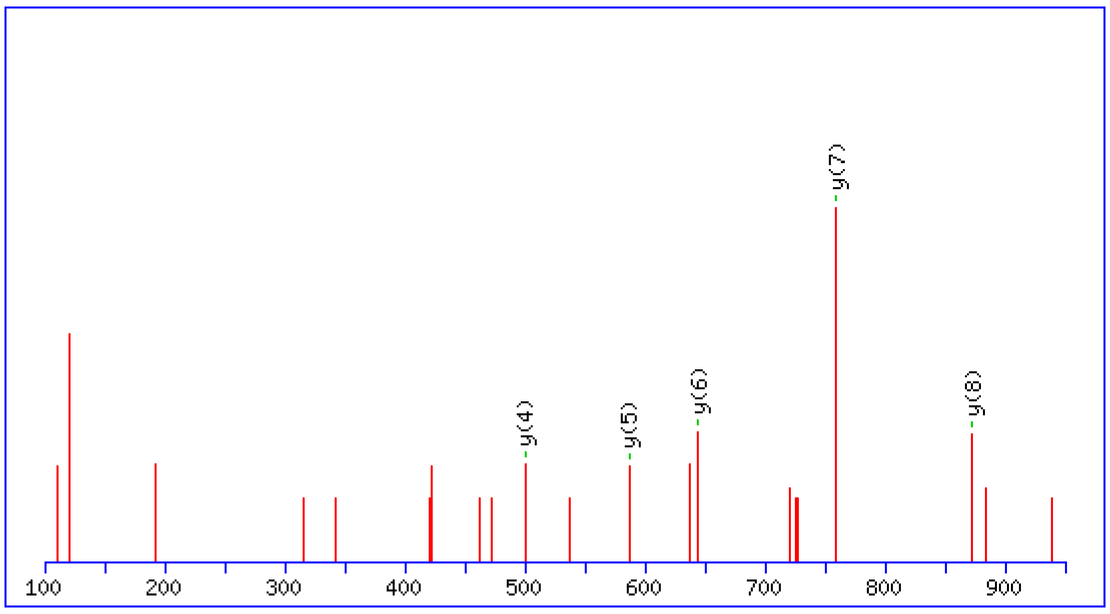
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPLDGSVLLR**
Found in **PVRL4_HUMAN**, Poliovirus receptor-related protein 4 OS=Homo sapiens GN=PVRL4 PE=1 SV=1

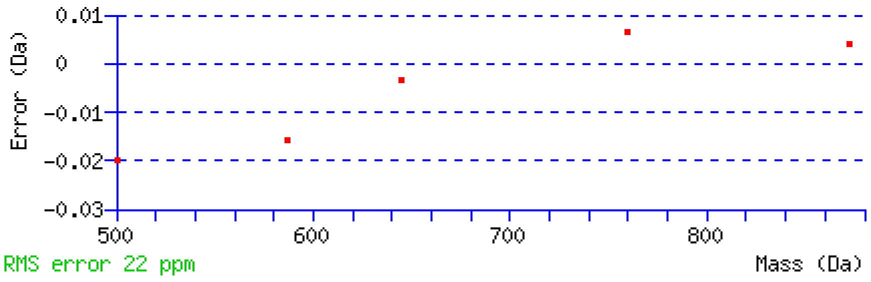
Match to Query 19075: 1082.610888 from(542.312720,2+) rtinseconds(2743) index(34475)
Title: Locus:1.1.1.2536.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

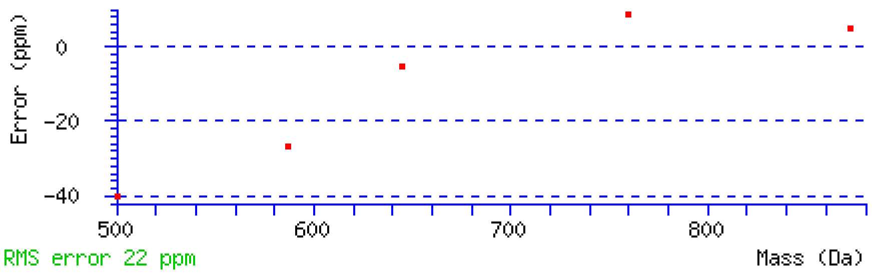
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1082.608398
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0018
Matches : 5/94 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							10
2	212.102967	106.555121	195.076418	98.041847			P	969.572757	485.290017	952.546208	476.776742	951.562192	476.284734	9
3	325.187031	163.097153	308.160482	154.583879			L	***872.519993***	436.763635	855.493444	428.250360	854.509428	427.758352	8
4	440.213974	220.610625	423.187425	212.097351	422.203409	211.605343	D	***759.435929***	380.221603	742.409380	371.708328	741.425364	371.216320	7
5	497.235438	249.121357	480.208889	240.608082	479.224873	240.116075	G	***644.408986***	322.708131	627.382437	314.194857	626.398421	313.702849	6
6	584.267466	292.637371	567.240917	284.124097	566.256901	283.632089	S	***587.387522***	294.197399	570.360973	285.684125	569.376957	285.192117	5
7	683.335880	342.171578	666.309331	333.658303	665.325315	333.166295	V	***500.355494***	250.681385	483.328945	242.168111			4
8	796.419944	398.713610	779.393395	390.200335	778.409379	389.708328	L	401.287080	201.147178	384.260531	192.633904			3
9	909.504008	455.255642	892.477459	446.742368	891.493443	446.250360	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 NPLDGSVLLR
(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	1082.608398	0.002490	NPLDGSVLLR

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

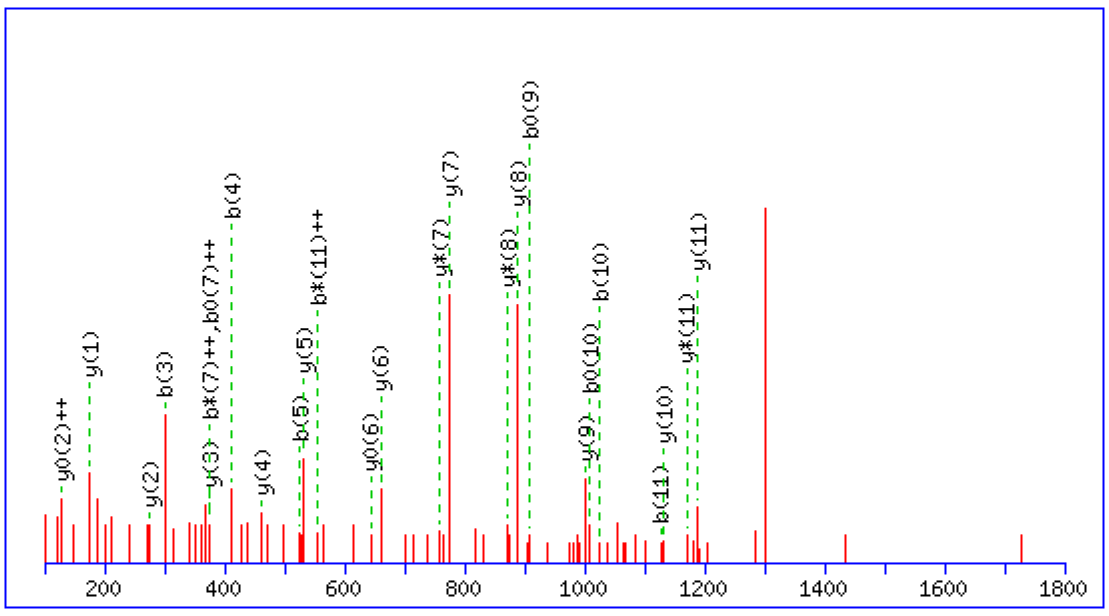
Mascot Search Results

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

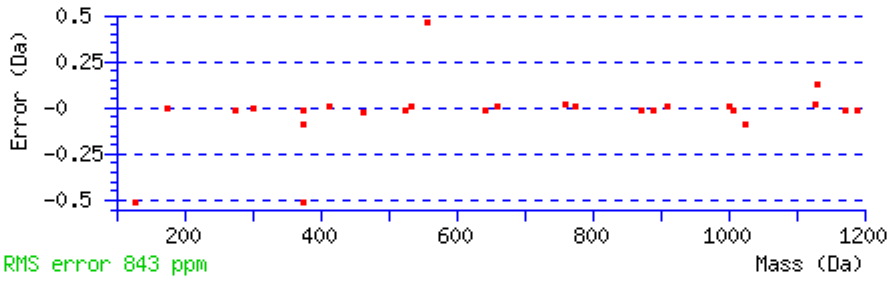
Match to Query 30340: 1300.704388 from(651.359470,2+) rtinseconds(2350) index(26932)
Title: Locus:1.1.1.2294.35
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

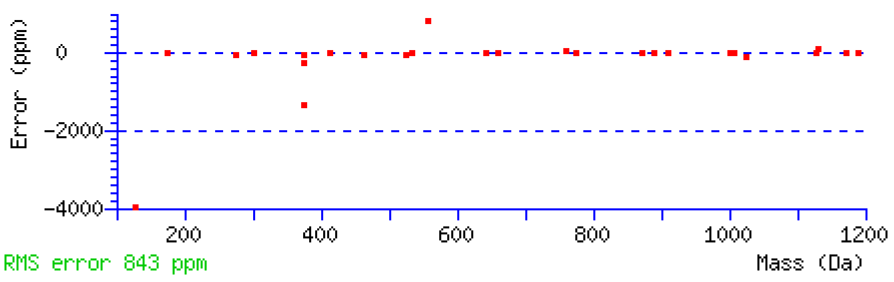
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1300.698669
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63  Expect: 7.5e-006
Matches : 26/114 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	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
62.5	1300.698669	0.005719	IGELLDQASVTR
9.1	1300.707397	-0.003009	WLLMVNPTRR
9.1	1300.707397	-0.003009	WLLMVNPTRR
6.5	1300.692154	0.012234	LPSVMAGVPARR
5.1	1300.702698	0.001690	LEIGFPPVLER
4.2	1300.709900	-0.005512	KAGRPGTSPLASK
2.3	1300.692108	0.012280	LAMNILAQNASR
1.8	1300.698654	0.005734	TLKSGLTPEEAR
0.8	1300.706055	-0.001667	DIAPVLDLKCK

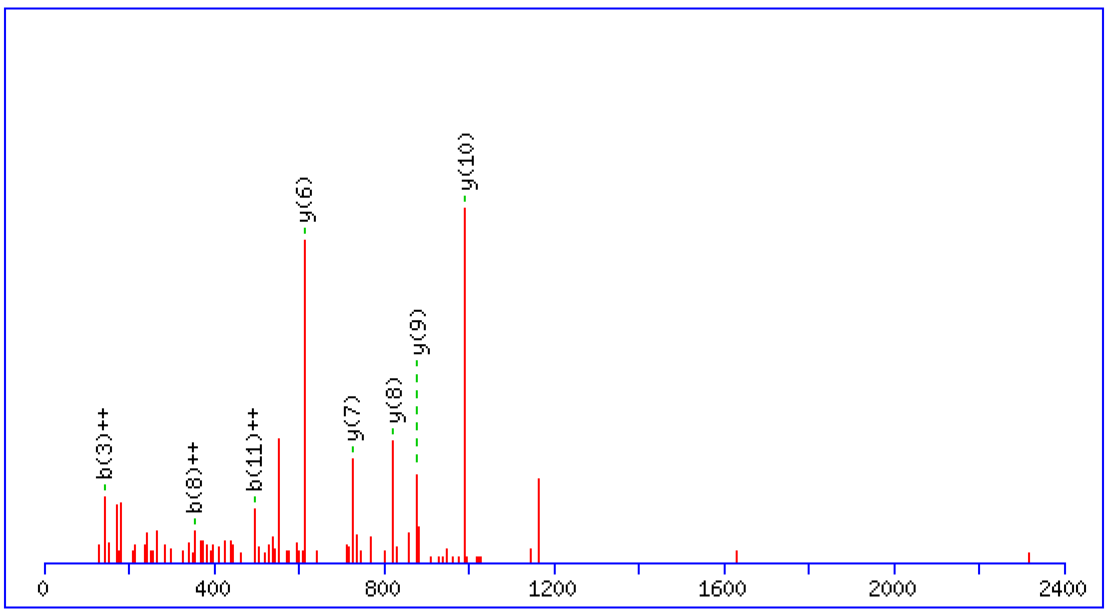
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGLGPPPGDAPR**
Found in **KCNQ4_HUMAN**, Potassium voltage-gated channel subfamily KQT member 4 OS=Homo sapiens GN=KCNQ4 PE=1 SV=2

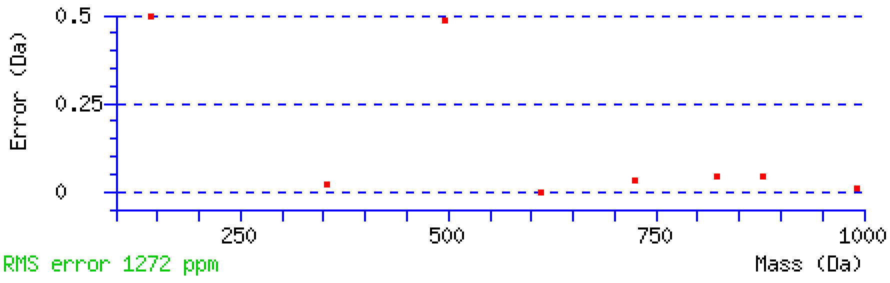
Match to Query 365656: 1161.618048 from(581.816300,2+) rtinseconds(1361) index(404618)
Title: Locus:1.1.1.1114.19
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

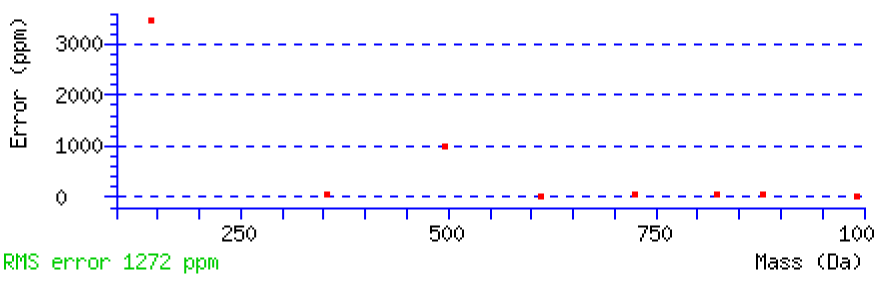
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1161.614227
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
Ions Score: 43  Expect: 0.0006
Matches : 8/88 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	171.112804	86.060040			G	1049.537436	525.272356	1032.510887	516.759082	1031.526871	516.267074	11
3	284.196868	***142.602072***			L	***992.515972***	496.761624	975.489423	488.248350	974.505407	487.756342	10
4	341.218332	171.112804			G	***879.431908***	440.219592	862.405359	431.706318	861.421343	431.214310	9
5	438.271096	219.639186			P	***822.410444***	411.708860	805.383895	403.195586	804.399879	402.703578	8
6	551.318775	276.163026			P	***725.357680***	363.182478	708.331131	354.669204	707.347115	354.177196	7
7	648.371539	324.689408			P	***612.310001***	306.658639	595.283452	298.145364	594.299436	297.653356	6
8	705.393003	***353.200140***			G	515.257237	258.132257	498.230688	249.618982	497.246672	249.126974	5
9	820.419946	410.713611	802.409381	401.708329	D	458.235773	229.621524	441.209224	221.108250	440.225208	220.616242	4
10	891.457060	446.232168	873.446495	437.226886	A	343.208830	172.108053	326.182281	163.594779			3
11	988.509824	***494.758550***	970.499259	485.753268	P	272.171716	136.589496	255.145167	128.076222			2
12					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LGLGPPPGDAPR
(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	1161.614227	0.003821	LGLGPPPGDAPR
41.6	1161.614227	0.003821	LGLGPPPGDAPR
31.6	1161.614227	0.003821	LGLGPPPGDAPR
30.5	1161.614227	0.003821	LGLGPPPGDAPR
9.1	1161.614243	0.003805	LPGIGPPPGGPR
5.2	1161.614243	0.003805	LPGIGPPPGGPR
4.4	1161.614243	0.003805	LPGIGPPPGGPR
4.4	1161.614243	0.003805	LPGIGPPPGGPR
3.8	1161.614243	0.003805	LPGIGPPPGGPR
3.1	1161.614243	0.003805	LPGIGPPPGGPR

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

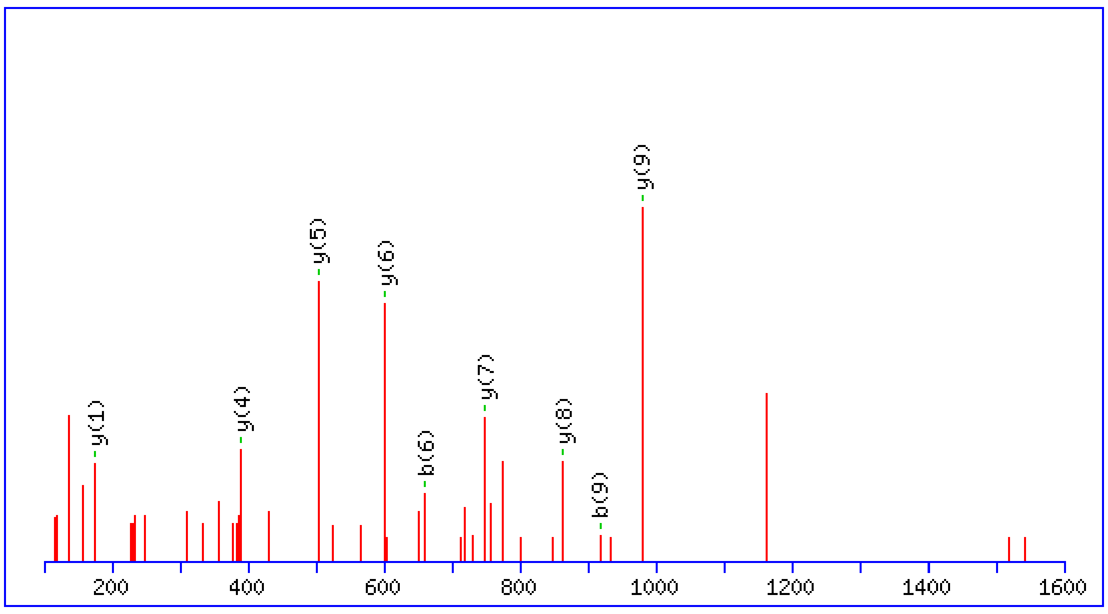
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDDFVLGSAR**
Found in **PRAF2_HUMAN**, PRA1 family protein 2 OS=Homo sapiens GN=PRAF2 PE=1 SV=1

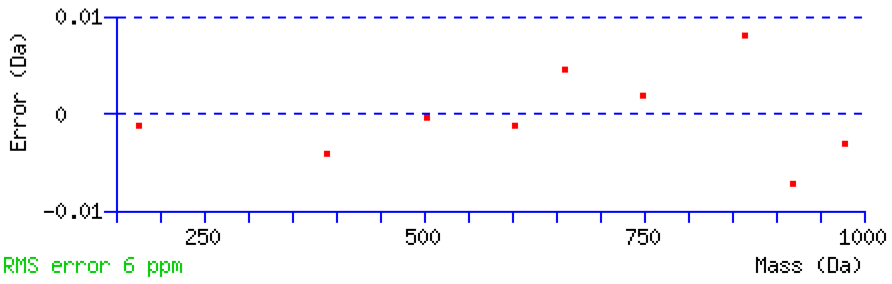
Match to Query 18812: 1162.600188 from(582.307370,2+) rtinseconds(2980) index(28725)
Title: Locus:1.1.1.2596.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

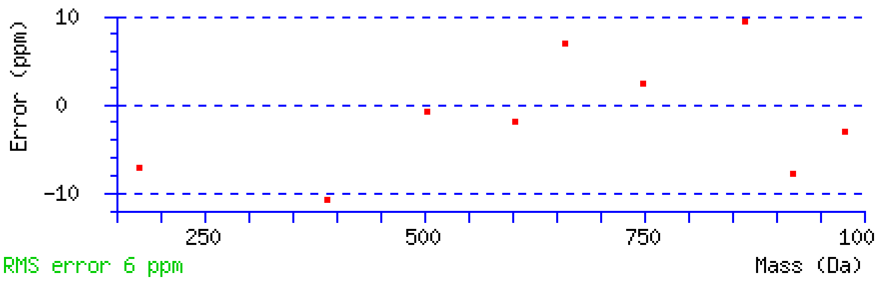
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1162.598236
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00017
Matches : 9/92 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							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
48.7	1162.598236	0.001952	ALDDFVLGSAR
9.6	1162.598206	0.001982	IATEAIENFR
4.8	1162.602951	-0.002763	LRQGFCGVGR
2.9	1162.609451	-0.009263	AFNQLSNLTR
0.7	1162.591690	0.008498	QLFNCQALR

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

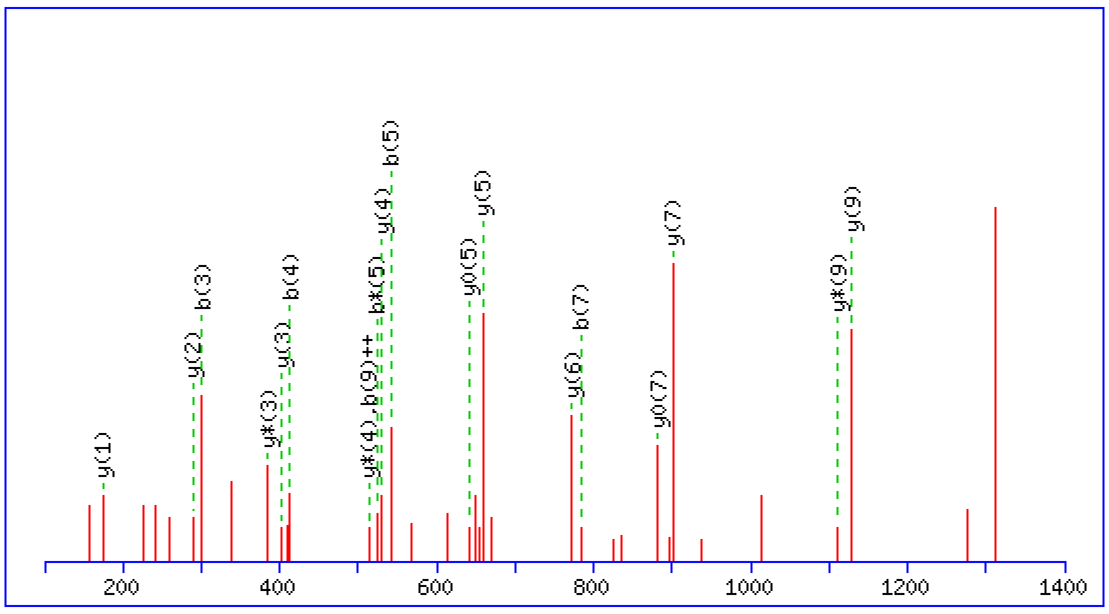
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LADIQIEQLNR**
Found in **PFD1_HUMAN**, Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2

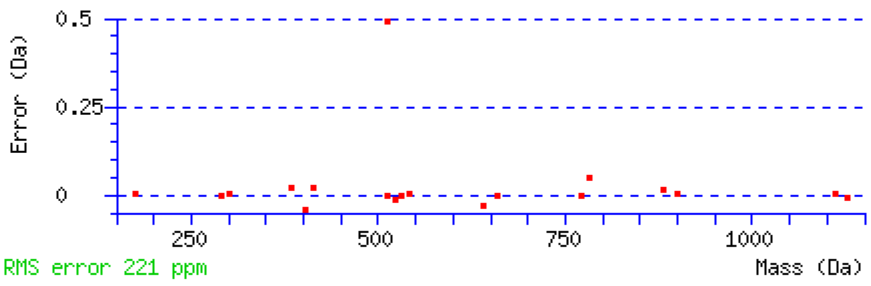
Match to Query 13768: 1311.709848 from(656.862200,2+) rtinseconds(2548) index(8100)
Title: Locus:1.1.1.2988.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

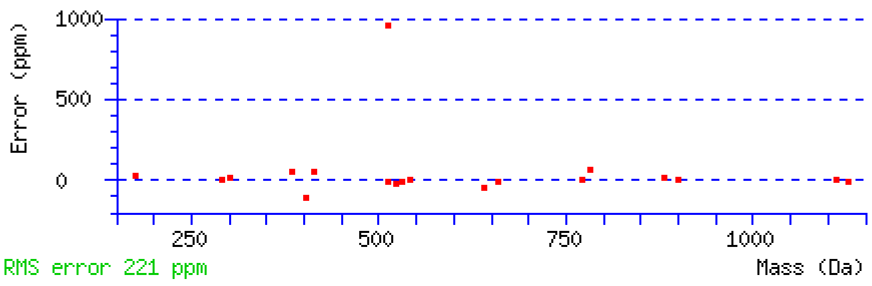
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1311.714630
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 3.6e-005
Matches : 19/100 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							11
2	185.128454	93.067865					A	1199.637877	600.322577	1182.611328	591.809302	1181.627312	591.317294	10
3	**300.155397**	150.581336			282.144832	141.576054	D	***1128.600763***	564.804020	1111.574214	556.290745	1110.590198	555.798737	9
4	**413.239461**	207.123369			395.228896	198.118086	I	1013.573820	507.290548	996.547271	498.777274	995.563255	498.285266	8
5	**541.298039**	271.152658	524.271490	262.639383	523.287474	262.147375	Q	***900.489756***	450.748516	883.463207	442.235241	882.479191	441.743233	7
6	654.382103	327.694690	637.355554	319.181415	636.371538	318.689407	I	***772.431178***	386.719227	755.404629	378.205953	754.420613	377.713945	6
7	**783.424696**	392.215986	766.398147	383.702712	765.414131	383.210704	E	***659.347114***	330.177195	642.320565	321.663921	641.336549	321.171913	5
8	911.483274	456.245275	894.456725	447.732001	893.472709	447.239993	Q	***530.304521***	265.655899	513.277972	257.142624			4
9	1024.567338	512.787307	1007.540789	504.274032	1006.556773	503.782024	L	***402.245943***	201.626609	385.219394	193.113335			3
10	1138.610265	569.808771	1121.583716	561.295496	1120.599700	560.803488	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 LADIQIEQLNR
(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	1311.714630	-0.004782	LADIQIEQLNR
7.4	1311.704758	0.005090	WPLGTPRAAATR
3.2	1311.714645	-0.004797	EVAPERTLPLR
1.6	1311.700729	0.009119	QVQEQVAQRAR
1.1	1311.712006	-0.002158	GRPSTGGGVVRGGR
0.6	1311.714630	-0.004782	SRISLIPPEER

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

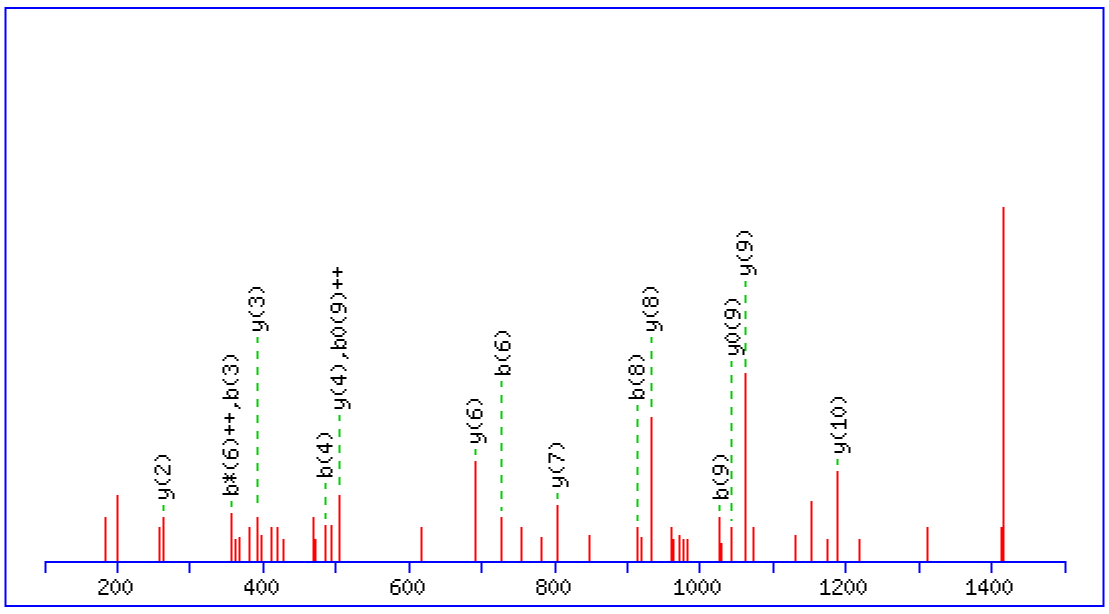
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLQEEIDALESR**
Found in **PFD4_HUMAN**, Prefoldin subunit 4 OS=Homo sapiens GN=PFDN4 PE=1 SV=1

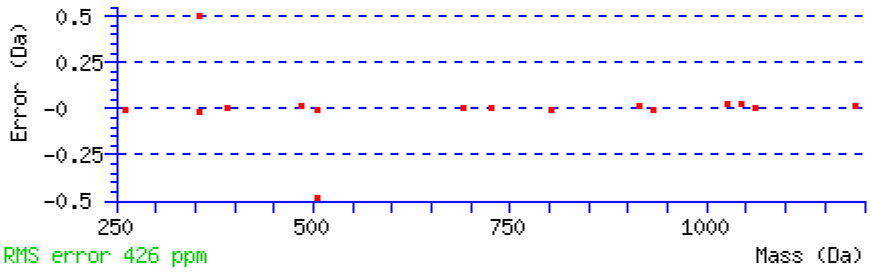
Match to Query 27127: 1415.693828 from(708.854190,2+) rtinseconds(3268) index(34677)
Title: Locus:1.1.1.2739.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

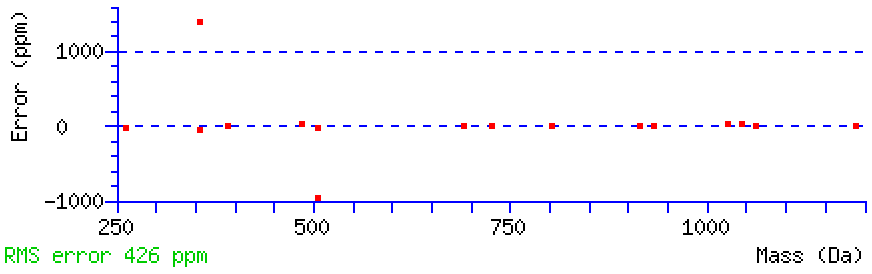
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1415.689194
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0007
Matches : 16/124 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	115.050203	58.028740	98.023654	49.515465			N							12
2	228.134267	114.570771	211.107718	106.057497			L	1302.653586	651.830431	1285.627037	643.317157	1284.643021	642.825149	11
3	**356.192845**	178.600060	339.166296	170.086786			Q	***1189.569522***	595.288399	1172.542973	586.775125	1171.558957	586.283117	10
4	**485.235438**	243.121357	468.208889	234.608082	467.224873	234.116075	E	***1061.510944***	531.259110	1044.484395	522.745836	1043.500379	522.253828	9
5	614.278031	307.642654	597.251482	299.129379	596.267466	298.637371	E	***932.468351***	466.737814	915.441802	458.224539	914.457786	457.732531	8
6	**727.362095**	364.184686	710.335546	355.671411	709.351530	355.179403	I	***803.425758***	402.216517	786.399209	393.703243	785.415193	393.211235	7
7	842.389038	421.698157	825.362489	413.184883	824.378473	412.692875	D	***690.341694***	345.674485	673.315145	337.161211	672.331129	336.669203	6
8	**913.426152**	457.216714	896.399603	448.703440	895.415587	448.211432	A	575.314751	288.161014	558.288202	279.647739	557.304186	279.155731	5
9	**1026.510216**	513.758746	1009.483667	505.245471	1008.499651	504.753463	L	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
10	1155.552809	578.280043	1138.526260	569.766768	1137.542244	569.274760	E	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
11	1242.584837	621.796057	1225.558288	613.282782	1224.574272	612.790774	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 NLQEEIDALESR
(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	1415.689194	0.004634	NLQEEIDALESR
14.3	1415.703140	-0.009312	EIPETTPIEEVK
1.8	1415.682678	0.011150	QAAKACPSTPESR

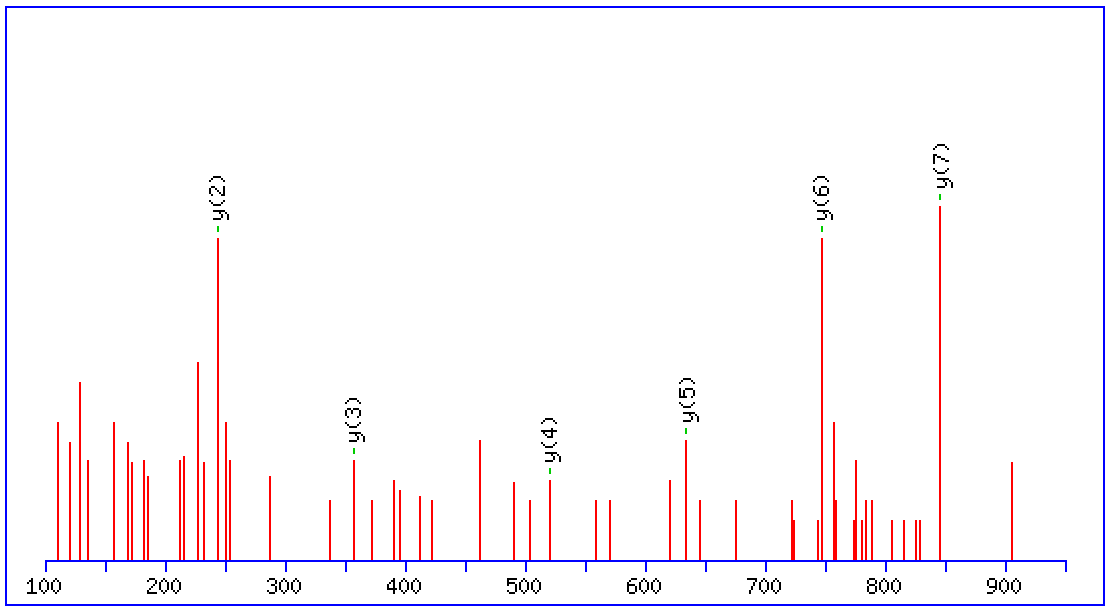
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATVLNYLPK**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

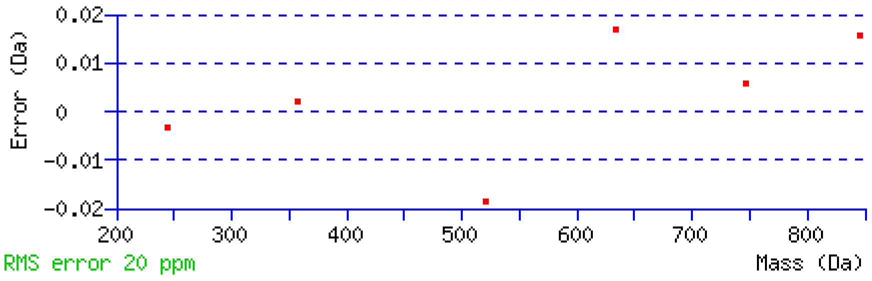
Match to Query 13149: 1017.591268 from(509.802910,2+) rtinseconds(2713) index(38400)
Title: Locus:1.1.1.2317.7
Data file 2011-11-14 - TFD - S 2-1.mgf

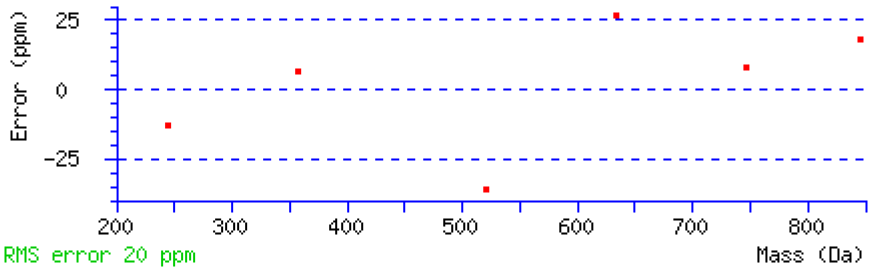
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [950] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1017.585861
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 6.1e-005
Matches : 6/72 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	72.044390	36.525833					A							9
2	173.092069	87.049672			155.081504	78.044390	T	947.556045	474.281661	930.529496	465.768386	929.545480	465.276378	8
3	272.160483	136.583879			254.149918	127.578597	V	***846.508366***	423.757821	829.481817	415.244547			7
4	385.244547	193.125912			367.233982	184.120629	L	***747.439952***	374.223614	730.413403	365.710340			6
5	499.287474	250.147375	482.260925	241.634101	481.276909	241.142093	N	***634.355888***	317.681582	617.329339	309.168308			5
6	662.350803	331.679040	645.324254	323.165765	644.340238	322.673757	Y	***520.312961***	260.660119	503.286412	252.146844			4
7	775.434867	388.221072	758.408318	379.707797	757.424302	379.215789	L	***357.249632***	179.128454	340.223083	170.615180			3
8	872.487631	436.747454	855.461082	428.234179	854.477066	427.742171	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 ATVLNYLPK
(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	1017.585861	0.005407	ATVLNYLPK
11.0	1017.597092	-0.005824	KYTIKPPR
9.6	1017.581848	0.009420	ATVLTTERK

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

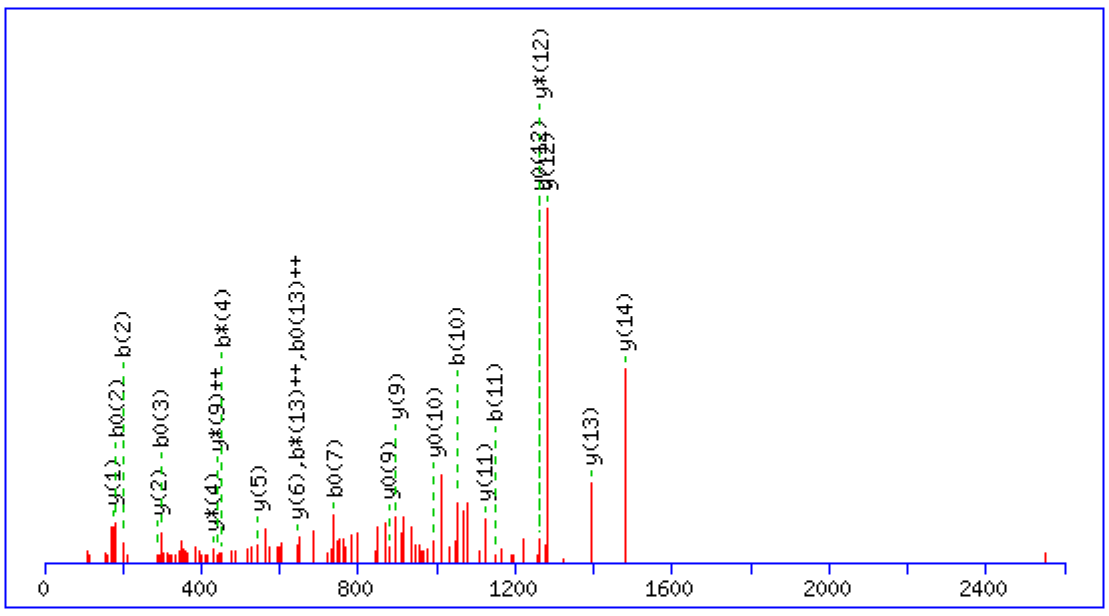
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSPRIDGPPTPASLR**
Found in **PCF11_HUMAN**, Pre-mRNA cleavage complex 2 protein Pcf11 OS=Homo sapiens GN=PCF11 PE=1 SV=3

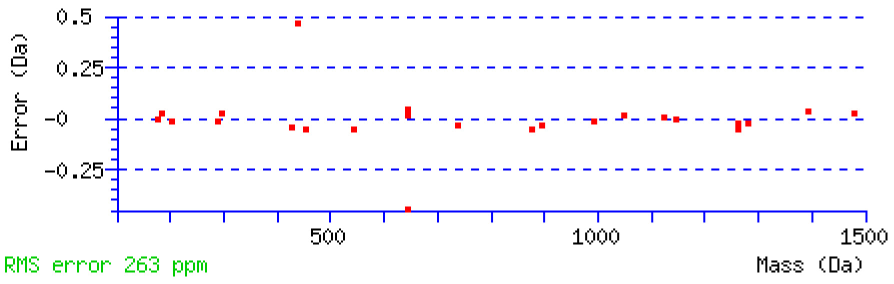
Match to Query 39980: 1591.868442 from(531.630090,3+) rtinseconds(3972) index(56345)
Title: Locus:1.1.1.3054.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

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 ●

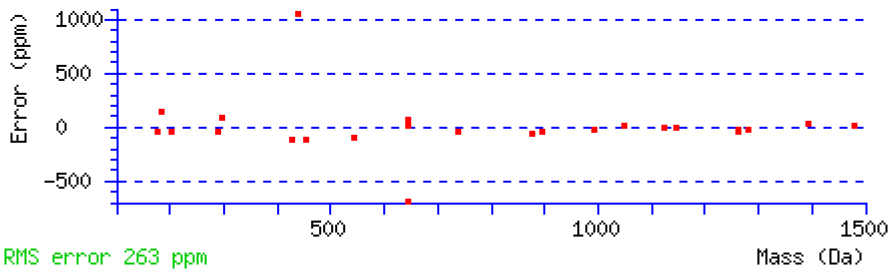


```
Monoisotopic mass of neutral peptide Mr(calc): 1591.868195
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 30  Expect: 0.0024
Matches : 24/156 fragment ions using 69 most intense peaks    (help)
```

#	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	***1479.791418***	740.399347	1462.764869	731.886073	1461.780853	731.394065	14
3	314.171047	157.589161			296.160482	148.583879	P	***1392.759390***	696.883333	1375.732841	688.370059	1374.748825	687.878050	13
4	470.272158	235.639717	453.245609	227.126443	452.261593	226.634435	R	***1279.711711***	640.359493	1262.685162	631.846219	1261.701146	631.354211	12
5	583.356222	292.181749	566.329673	283.668475	565.345657	283.176467	I	***1123.610600***	562.308938	1106.584051	553.795664	1105.600035	553.303655	11
6	698.383165	349.695221	681.356616	341.181946	680.372600	340.689938	D	1010.526536	505.766906	993.499987	497.253631	992.515971	496.761623	10
7	755.404629	378.205953	738.378080	369.692678	737.394064	369.200670	G	***895.499593***	448.253435	878.473044	439.740160	877.489028	439.248152	9
8	852.457393	426.732335	835.430844	418.219060	834.446828	417.727052	P	838.478129	419.742703	821.451580	411.229428	820.467564	410.737420	8
9	949.510157	475.258717	932.483608	466.745442	931.499592	466.253434	P	741.425365	371.216320	724.398816	362.703046	723.414800	362.211038	7
10	**1050.557836**	525.782556	1033.531287	517.269282	1032.547271	516.777273	T	***644.372601***	322.689938	627.346052	314.176664	626.362036	313.684656	6
11	**1147.610600**	574.308938	1130.584051	565.795664	1129.600035	565.303655	P	***543.324922***	272.166099	526.298373	263.652825	525.314357	263.160817	5
12	1218.647714	609.827495	1201.621165	601.314221	1200.637149	600.822212	A	446.272158	223.639717	429.245609	215.126442	428.261593	214.634434	4
13	1305.679742	653.343509	1288.653193	644.830235	1287.669177	644.338227	S	375.235044	188.121160	358.208495	179.607885	357.224479	179.115877	3
14	1418.763806	709.885541	1401.737257	701.372267	1400.753241	700.880258	L	***288.203016***	144.605146	271.176467	136.091871			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 263 ppm



RMS error 263 ppm

NCBI **BLAST** search of LSPRIDGPPTPASLR
(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	1591.868195	0.000247	LSPRIDGPPTPASLR
4.7	1591.868195	0.000247	LSPRIDGPPTPASLR
4.7	1591.868195	0.000247	LSPRIDGPPTPASLR
2.1	1591.883438	-0.014996	IISREHQWPIGLK
1.9	1591.875565	-0.007123	IISRYLLCQADVK

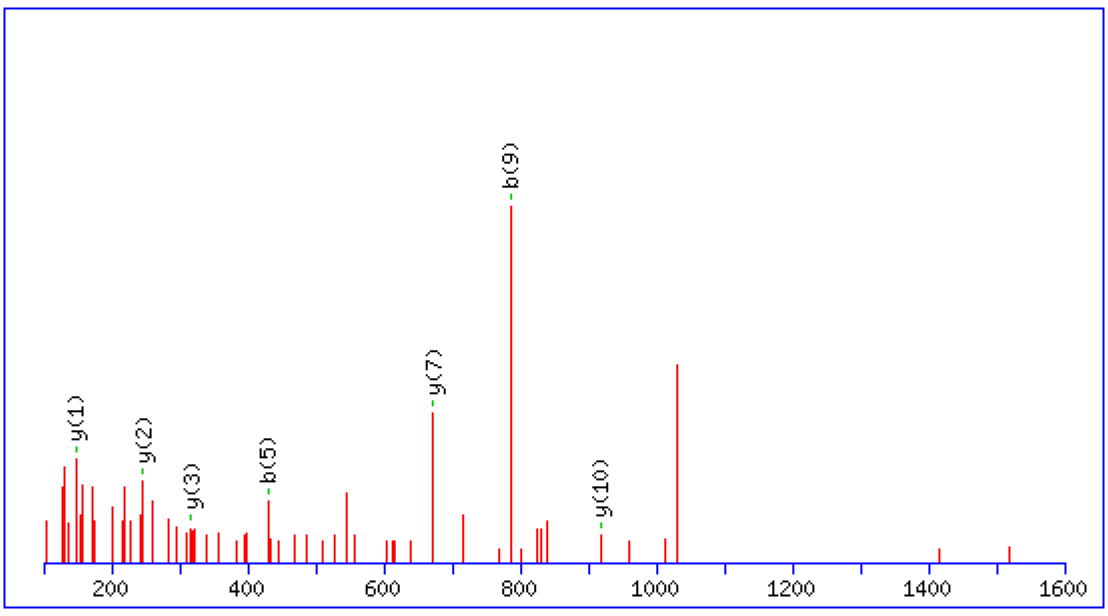
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITSGADLGAVK**
Found in **MARHA_HUMAN**, Probable E3 ubiquitin-protein ligase MARCH10 OS=Homo sapiens GN=MARCH10 PE=1 SV=3

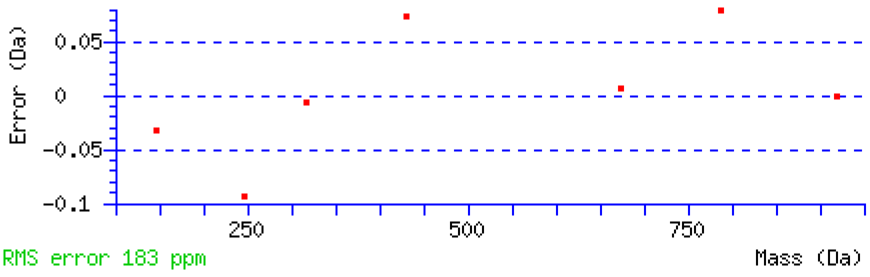
Match to Query 15657: 1030.563468 from(516.289010,2+) rtinseconds(2277) index(25720)
Title: Locus:1.1.1.2359.24
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

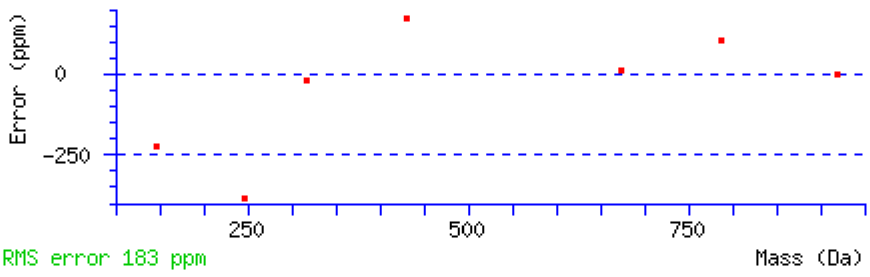
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1030.565872
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.0018
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	114.091340	57.549308			I							11
2	215.139019	108.073147	197.128454	99.067865	T	***918.489088***	459.748182	901.462539	451.234908	900.478523	450.742900	10
3	302.171047	151.589161	284.160482	142.583879	S	817.441409	409.224343	800.414860	400.711068	799.430844	400.219060	9
4	359.192511	180.099893	341.181946	171.094611	G	730.409381	365.708329	713.382832	357.195054	712.398816	356.703046	8
5	**430.229625**	215.618450	412.219060	206.613168	A	***673.387917***	337.197597	656.361368	328.684322	655.377352	328.192314	7
6	545.256568	273.131922	527.246003	264.126640	D	602.350803	301.679040	585.324254	293.165765	584.340238	292.673757	6
7	658.340632	329.673954	640.330067	320.668672	L	487.323860	244.165568	470.297311	235.652293			5
8	715.362096	358.184686	697.351531	349.179404	G	374.239796	187.623536	357.213247	179.110261			4
9	**786.399210**	393.703243	768.388645	384.697961	A	***317.218332***	159.112804	300.191783	150.599529			3
10	885.467624	443.237450	867.457059	434.232168	V	***246.181218***	123.594247	229.154669	115.080972			2
11					K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ITSGADLGAVK
(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	1030.565872	-0.002404	ITSGADLGAVK
14.7	1030.565842	-0.002374	INESLSQLK
9.5	1030.565857	-0.002389	DSLAKSPSVK
9.3	1030.565857	-0.002389	QDLTEKAVK
9.3	1030.565857	-0.002389	LSQLESQVK
9.0	1030.567200	-0.003732	HTPLHLAAR
8.9	1030.565842	-0.002374	ENTKEIVAK
8.2	1030.565842	-0.002374	NLSLESQIK
8.2	1030.559341	0.004127	ECRGGVLVK
8.1	1030.565842	-0.002374	INSSIEQLK

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

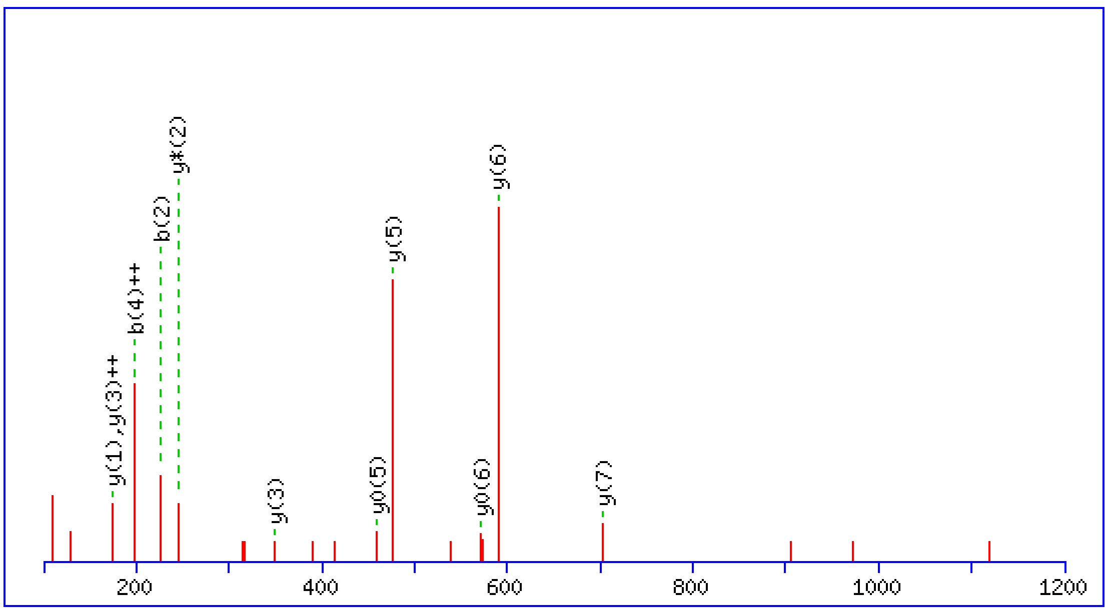
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLIGASSR**
Found in **AT10A_HUMAN**, Probable phospholipid-transporting ATPase VA OS=Homo sapiens GN=ATP10A PE=2 SV=2

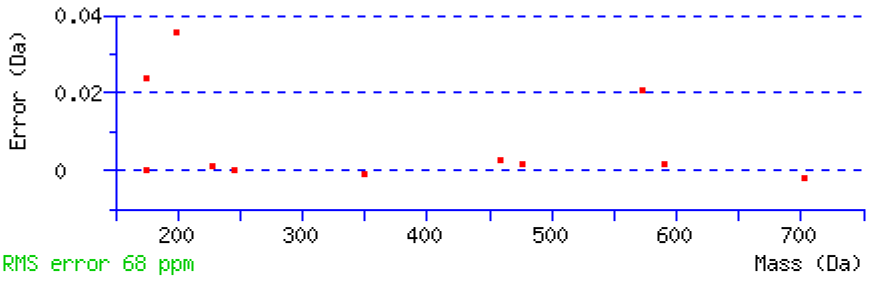
Match to Query 594: 815.484628 from(408.749590,2+) rtinseconds(1656) index(8303)
Title: Locus:1.1.1.2280.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

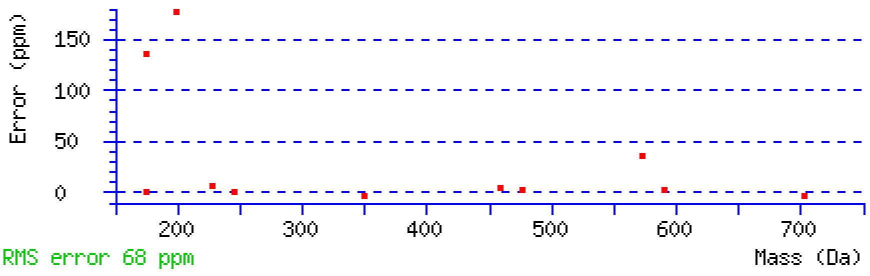
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 815.486481
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0032
Matches : 11/58 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							8
2	227.175404	114.091340			L	***703.409714***	352.208495	686.383165	343.695221	685.399149	343.203213	7
3	340.259468	170.633372			I	***590.325650***	295.666463	573.299101	287.153189	572.315085	286.661181	6
4	397.280932	199.144104			G	***477.241586***	239.124431	460.215037	230.611156	459.231021	230.119148	5
5	468.318046	234.662661			A	420.220122	210.613699	403.193573	202.100424	402.209557	201.608416	4
6	555.350074	278.178675	537.339509	269.173392	S	***349.183008***	175.095142	332.156459	166.581867	331.172443	166.089859	3
7	642.382102	321.694689	624.371537	312.689406	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 LLIGASSR
(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	815.486481	-0.001853	LLIGASSR
27.8	815.486481	-0.001853	IIPSSKR
12.2	815.486465	-0.001837	LLSKAER
11.7	815.486481	-0.001853	LLNTLSR
10.3	815.479950	0.004678	LMIRQR
8.9	815.486481	-0.001853	LPSSLRK
8.8	815.486481	-0.001853	ILTGEKR
8.0	815.486481	-0.001853	IIRTGEK
6.6	815.486481	-0.001853	LLADTRK
6.6	815.490509	-0.005881	LLWSLGK

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

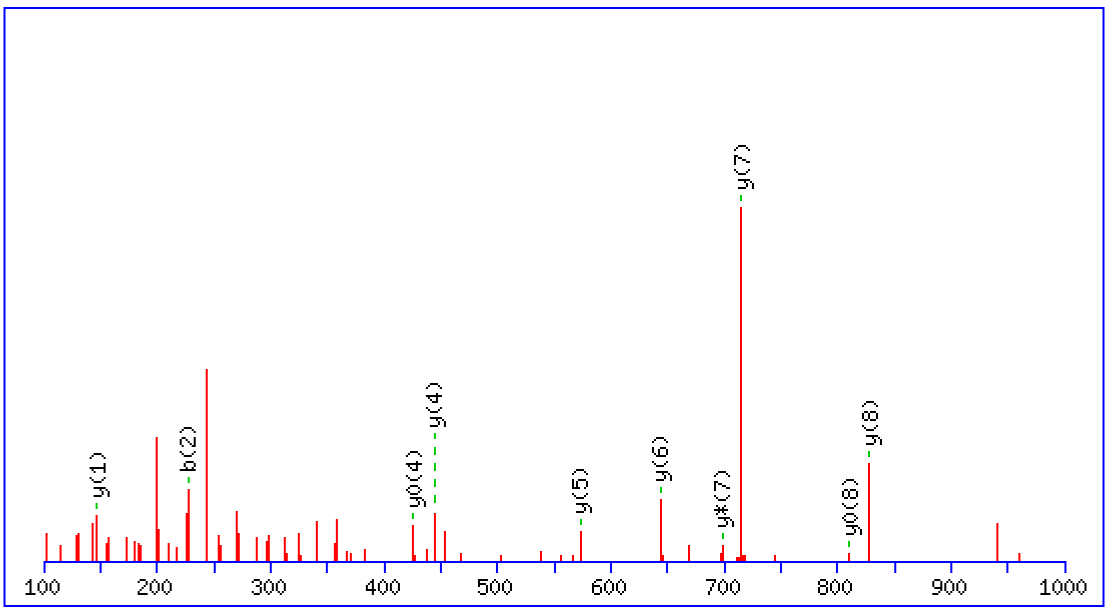
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLAAEPLSK**
Found in **GT251_HUMAN**, Procollagen galactosyltransferase 1 OS=Homo sapiens GN=GLT25D1 PE=1 SV=1

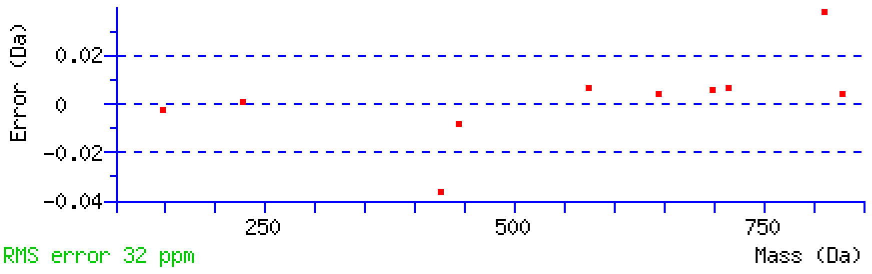
Match to Query 4852: 940.561108 from(471.287830,2+) rtinseconds(1810) index(15724)
Title: Locus:1.1.1.2470.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

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 ●

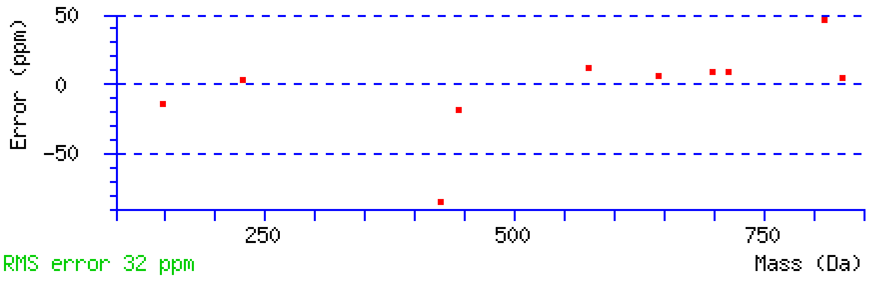


Monoisotopic mass of neutral peptide Mr(calc): 940.559296
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00018
Matches : 10/70 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			L							9
2	227.175404	114.091340			L	*828.482545*	414.744911	811.455996	406.231636	810.471980	405.739628	8
3	298.212518	149.609897			A	*715.398481*	358.202879	698.371932	349.689604	697.387916	349.197596	7
4	369.249632	185.128454			A	*644.361367*	322.684322	627.334818	314.171047	626.350802	313.679039	6
5	498.292225	249.649750	480.281660	240.644468	E	*573.324253*	287.165765	556.297704	278.652490	555.313688	278.160482	5
6	595.344989	298.176133	577.334424	289.170850	P	*444.281660*	222.644468	427.255111	214.131193	426.271095	213.639186	4
7	708.429053	354.718165	690.418488	345.712882	L	347.228896	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	795.461081	398.234179	777.450516	389.228896	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 32 ppm



RMS error 32 ppm

NCBI **BLAST** search of LLAAEPLSK
(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	940.559296	0.001812	LLAAEPLSK
14.2	940.559296	0.001812	LALSIPAEK
13.1	940.559311	0.001797	LLNILDPK
10.1	940.559326	0.001782	IPVLKDPK
9.9	940.559311	0.001797	IPIEIVNK
7.4	940.559311	0.001797	ENLPLVLK
6.3	940.559311	0.001797	KDLLEVPK

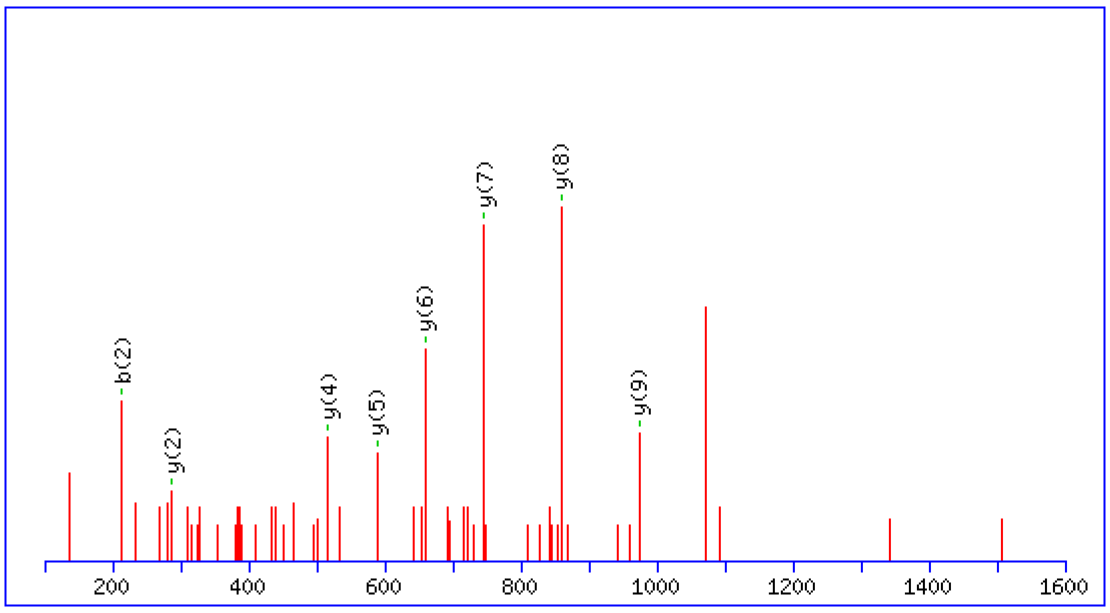
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNLSAAQTLR**
Found in **PDC10_HUMAN**, Programmed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1

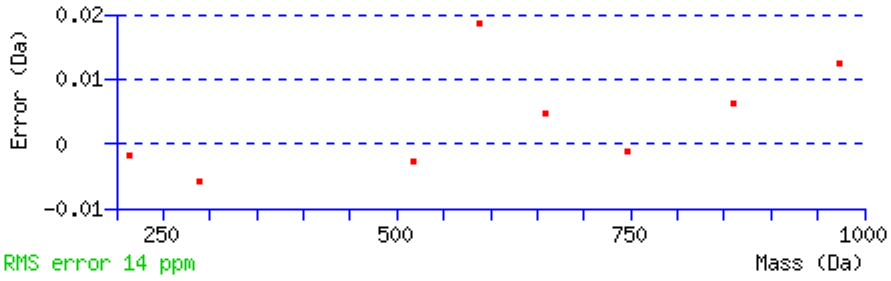
Match to Query 16465: 1071.605428 from(536.809990,2+) rtinseconds(1949) index(19843)
Title: Locus:1.1.1.2187.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

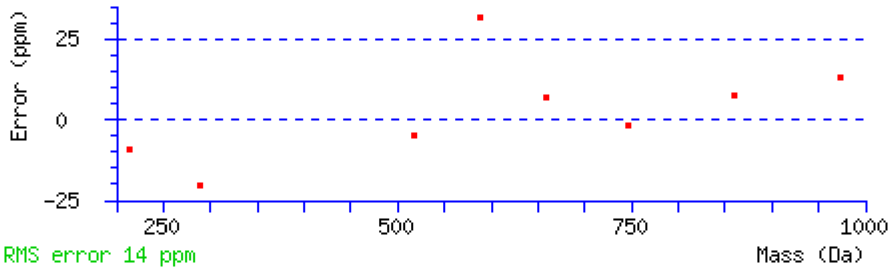
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1071.603638
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 2e-006
Matches : 8/96 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							10
2	214.118617	107.562947	197.092068	99.049672			N	***973.542520***	487.274898	956.515971	478.761624	955.531955	478.269616	9
3	327.202681	164.104978	310.176132	155.591704			L	***859.499593***	430.253435	842.473044	421.740160	841.489028	421.248152	8
4	414.234709	207.620993	397.208160	199.107718	396.224144	198.615710	S	***746.415529***	373.711403	729.388980	365.198128	728.404964	364.706120	7
5	485.271823	243.139549	468.245274	234.626275	467.261258	234.134267	A	***659.383501***	330.195389	642.356952	321.682114	641.372936	321.190106	6
6	556.308937	278.658107	539.282388	270.144832	538.298372	269.652824	A	***588.346387***	294.676832	571.319838	286.163557	570.335822	285.671549	5
7	684.367515	342.687396	667.340966	334.174121	666.356950	333.682113	Q	***517.309273***	259.158275	500.282724	250.645000	499.298708	250.152992	4
8	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	T	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	3
9	898.499258	449.753267	881.472709	441.239993	880.488693	440.747985	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 VNLSAAQTLR
(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	1071.603638	0.001790	VNLSAAQTLR
7.4	1071.603653	0.001775	AVGVSKQDIR

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

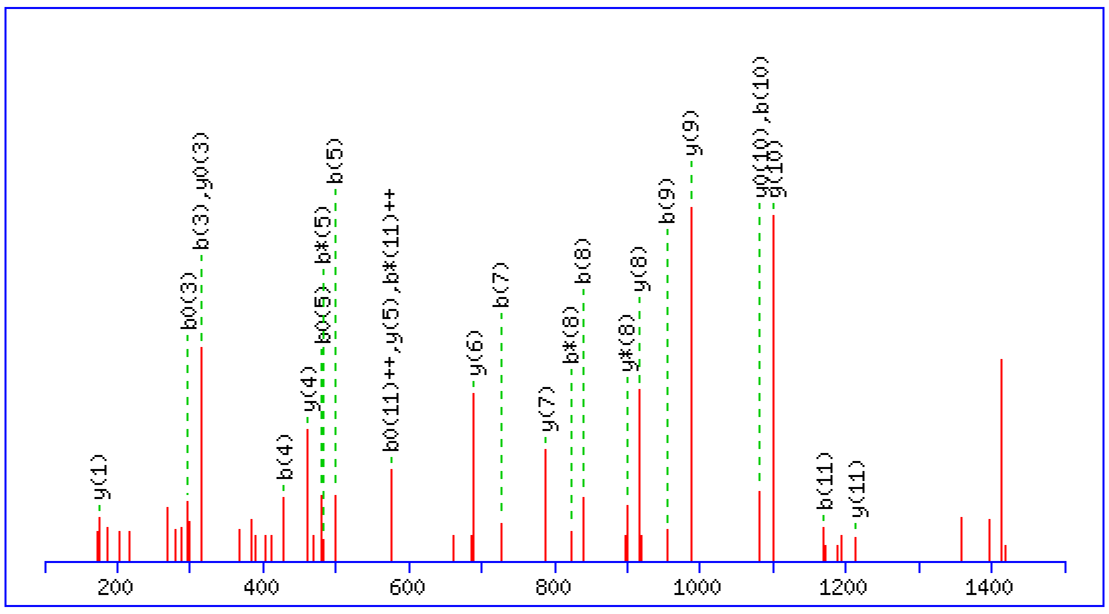
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSILAQVLDQSAR**
Found in **PDCD5_HUMAN**, Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3

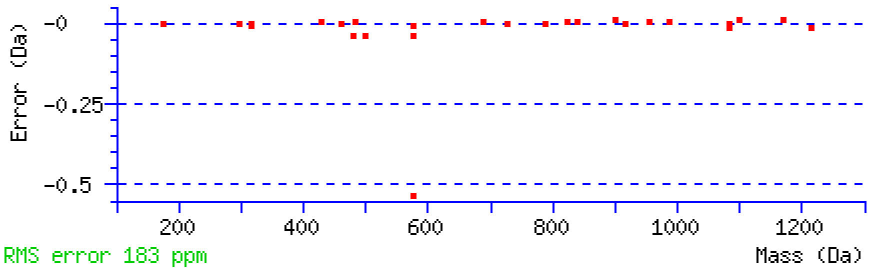
Match to Query 27065: 1413.763608 from(707.889080,2+) rtinseconds(3388) index(35582)
Title: Locus:1.1.1.2783.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

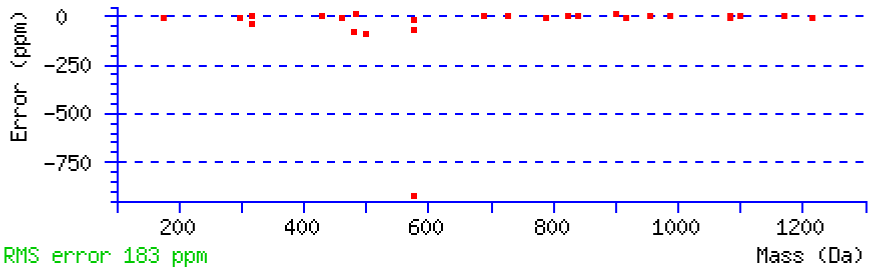
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1413.757568
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 82 **Expect:** 7.5e-008
Matches : 26/138 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							13
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	1300.721941	650.864609	1283.695392	642.351334	1282.711376	641.859326	12
3	***315.166295***	158.086785	298.139746	149.573511	297.155730	149.081503	I	***1213.689913***	607.348595	1196.663364	598.835320	1195.679348	598.343312	11
4	***428.250359***	214.628818	411.223810	206.115543	410.239794	205.623535	L	***1100.605849***	550.806563	1083.579300	542.293288	1082.595284	541.801280	10
5	***499.287473***	250.147375	482.260924	241.634100	481.276908	241.142092	A	***987.521785***	494.264531	970.495236	485.751256	969.511220	485.259248	9
6	627.346051	314.176664	610.319502	305.663389	609.335486	305.171381	Q	***916.484671***	458.745974	899.458122	450.232699	898.474106	449.740691	8
7	***726.414465***	363.710871	709.387916	355.197596	708.403900	354.705588	V	***788.426093***	394.716685	771.399544	386.203410	770.415528	385.711402	7
8	***839.498529***	420.252903	822.471980	411.739628	821.487964	411.247620	L	***689.357679***	345.182478	672.331130	336.669203	671.347114	336.177195	6
9	***954.525472***	477.766374	937.498923	469.253100	936.514907	468.761092	D	***576.273615***	288.640446	559.247066	280.127171	558.263050	279.635163	5
10	***1082.584050***	541.795663	1065.557501	533.282389	1064.573485	532.790381	Q	***461.246672***	231.126974	444.220123	222.613700	443.236107	222.121692	4
11	***1169.616078***	585.311677	1152.589529	576.798403	1151.605513	576.306395	S	333.188094	167.097685	316.161545	158.584410	315.177529	158.092402	3
12	1240.653192	620.830234	1223.626643	612.316960	1222.642627	611.824952	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 NSILAQVLDQSAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.5	1413.757568	0.006040	NSILAQVLDQSAR
5.4	1413.772858	-0.009250	RIPPPPPPVPAGR
0.4	1413.776840	-0.013232	AYFHLLNQIAPK

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

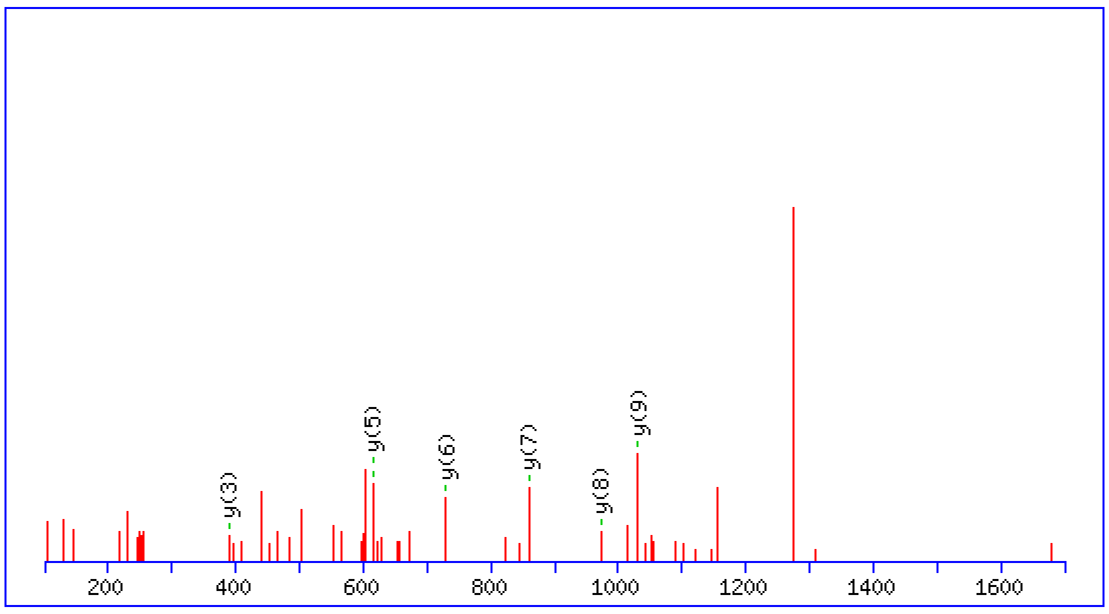
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CAGNEDIITLR**
Found in **PCNA_HUMAN**, Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1

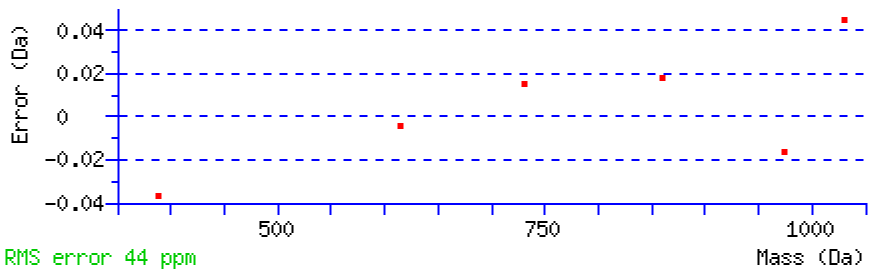
Match to Query 27837: 1274.635208 from(638.324880,2+) rtinseconds(2311) index(28412)
Title: Locus:1.1.1.2265.30
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

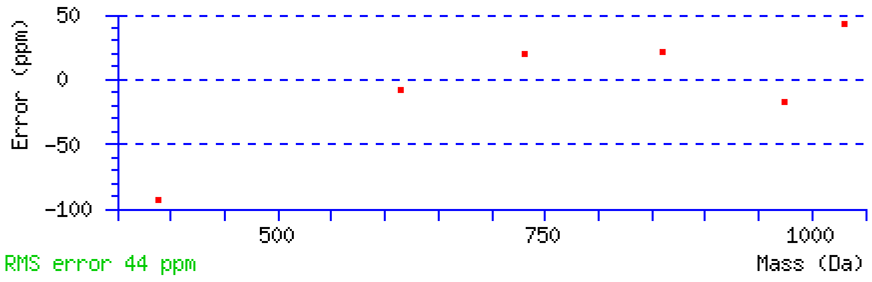
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1274.628860
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37  Expect: 0.00063
Matches : 6/102 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	175.053575	88.030425					C							11
2	246.090689	123.548982					A	1101.589864	551.298570	1084.563315	542.785296	1083.579299	542.293288	10
3	303.112153	152.059714					G	***1030.552750***	515.780013	1013.526201	507.266739	1012.542185	506.774731	9
4	417.155080	209.081178	400.128531	200.567904			N	***973.531286***	487.269281	956.504737	478.756007	955.520721	478.263999	8
5	546.197673	273.602475	529.171124	265.089200	528.187108	264.597192	E	***859.488359***	430.247818	842.461810	421.734543	841.477794	421.242535	7
6	661.224616	331.115946	644.198067	322.602672	643.214051	322.110664	D	***730.445766***	365.726521	713.419217	357.213247	712.435201	356.721239	6
7	774.308680	387.657978	757.282131	379.144704	756.298115	378.652696	I	***615.418823***	308.213050	598.392274	299.699775	597.408258	299.207767	5
8	887.392744	444.200010	870.366195	435.686736	869.382179	435.194728	I	502.334759	251.671017	485.308210	243.157743	484.324194	242.665735	4
9	988.440423	494.723850	971.413874	486.210575	970.429858	485.718567	T	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
10	1101.524487	551.265882	1084.497938	542.752607	1083.513922	542.260599	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 CAGNEDIITLR
(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	1274.628860	0.006348	CAGNEDIITLR
2.8	1274.632889	0.002319	MIWDGIVENAK
0.9	1274.628860	0.006348	GAMLENLSPTSR
0.7	1274.647522	-0.012314	MMQGGVGIPTIR

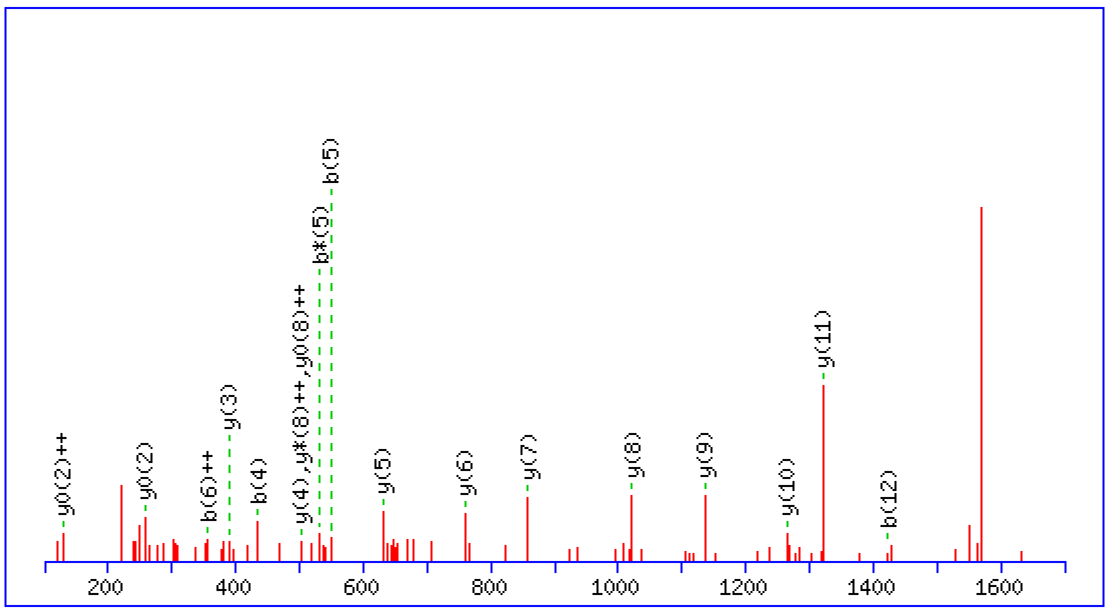
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TFGENYVQELLEK**
Found in **PROSC_HUMAN**, Proline synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=1

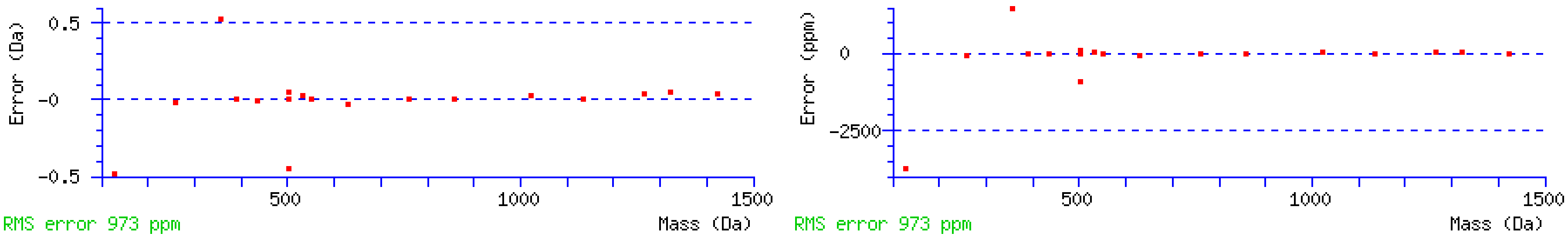
Match to Query 43586: 1568.786808 from(785.400680,2+) rtinseconds(3671) index(51712)
Title: Locus:1.1.1.2885.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

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): 1568.772217
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 4.9e-006
Matches : 18/134 fragment ions using 30 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							13
2	249.123369	125.065322			231.112804	116.060040	F	1468.731837	734.869556	1451.705288	726.356282	1450.721272	725.864274	12
3	306.144833	153.576054			288.134268	144.570772	G	***1321.663423***	661.335349	1304.636874	652.822075	1303.652858	652.330067	11
4	**435.187426**	218.097351			417.176861	209.092068	E	***1264.641959***	632.824617	1247.615410	624.311343	1246.631394	623.819335	10
5	**549.230353**	275.118815	532.203804	266.605540	531.219788	266.113532	N	***1135.599366***	568.303321	1118.572817	559.790047	1117.588801	559.298038	9
6	712.293682	356.650479	695.267133	348.137205	694.283117	347.645197	Y	***1021.556439***	511.281857	1004.529890	502.768583	1003.545874	502.276575	8
7	811.362096	406.184686	794.335547	397.671411	793.351531	397.179403	V	***858.493110***	429.750193	841.466561	421.236918	840.482545	420.744910	7
8	939.420674	470.213975	922.394125	461.700700	921.410109	461.208692	Q	***759.424696***	380.215986	742.398147	371.702711	741.414131	371.210703	6
9	1068.463267	534.735271	1051.436718	526.221997	1050.452702	525.729989	E	***631.366118***	316.186697	614.339569	307.673422	613.355553	307.181414	5
10	1181.547331	591.277303	1164.520782	582.764029	1163.536766	582.272021	L	***502.323525***	251.665400	485.296976	243.152126	484.312960	242.660118	4
11	1294.631395	647.819335	1277.604846	639.306061	1276.620830	638.814053	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
12	**1423.673988**	712.340632	1406.647439	703.827357	1405.663423	703.335349	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 TFGENYVQELLEK
(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	1568.772217	0.014591	TFGENYVQELLEK
0.9	1568.783493	0.003315	VVPSASTTFDNFLR

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

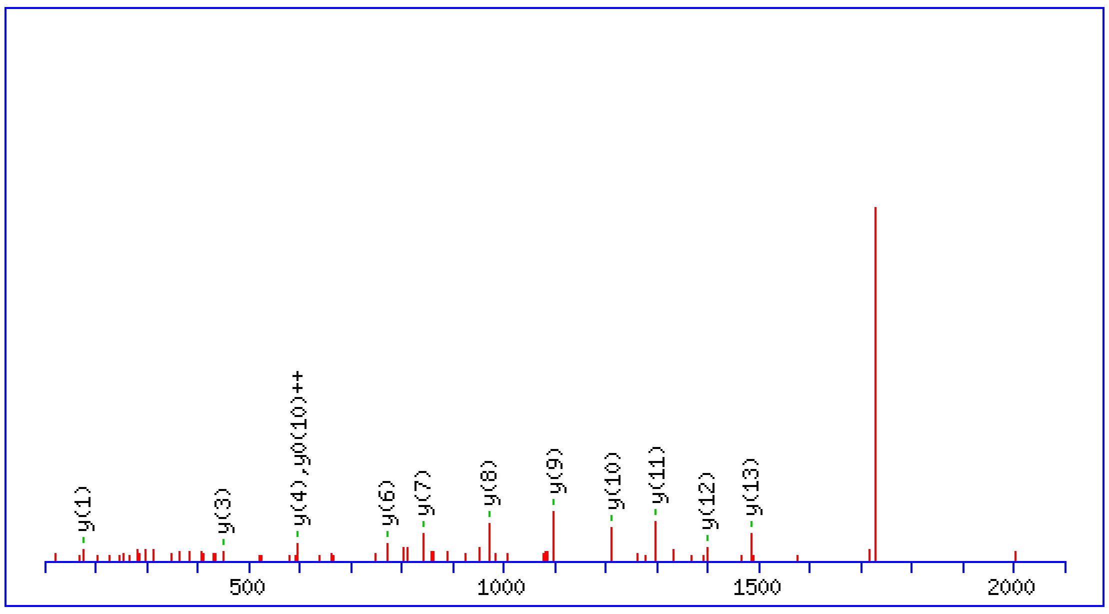
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPSVSLQEASSFFQR**
Found in **PROL4_HUMAN**, Proline-rich protein 4 OS=Homo sapiens GN=PRR4 PE=1 SV=3

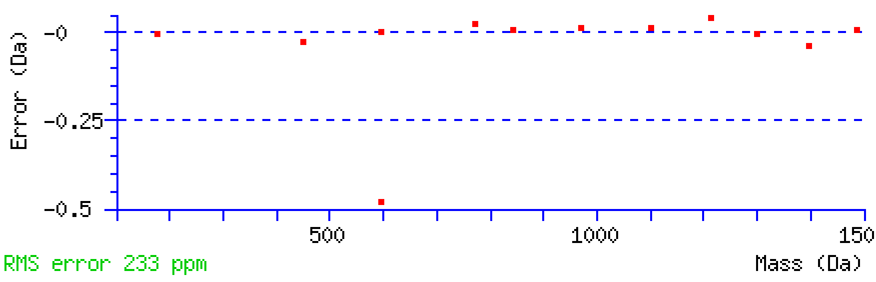
Match to Query 39299: 1728.860288 from(865.437420,2+) rtinseconds(3791) index(48423)
Title: Locus:1.1.1.3248.42
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

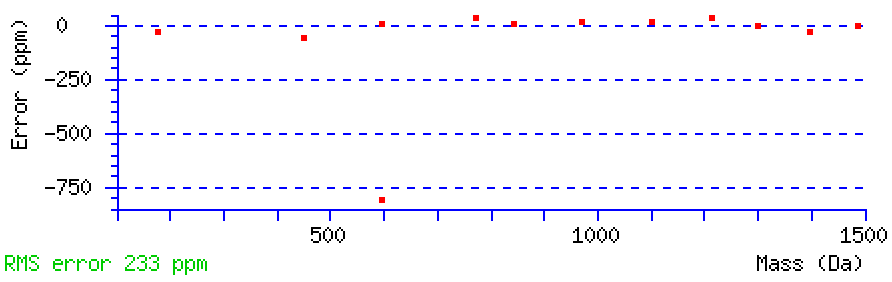
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1728.847137
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 94 **Expect:** 5.4e-009
Matches : 12/144 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	148.075690	74.541483					F							15
2	245.128454	123.067865					P	1582.785997	791.896637	1565.759448	783.383362	1564.775432	782.891354	14
3	332.160482	166.583879			314.149917	157.578596	S	*1485.733233*	743.370255	1468.706684	734.856980	1467.722668	734.364972	13
4	431.228896	216.118086			413.218331	207.112803	V	*1398.701205*	699.854241	1381.674656	691.340966	1380.690640	690.848958	12
5	518.260924	259.634100			500.250359	250.628818	S	*1299.632791*	650.320034	1282.606242	641.806759	1281.622226	641.314751	11
6	631.344988	316.176132			613.334423	307.170850	L	*1212.600763*	606.804020	1195.574214	598.290745	1194.590198	597.798737	10
7	759.403566	380.205421	742.377017	371.692147	741.393001	371.200139	Q	*1099.516699*	550.261988	1082.490150	541.748713	1081.506134	541.256705	9
8	888.446159	444.726718	871.419610	436.213443	870.435594	435.721435	E	*971.458121*	486.232699	954.431572	477.719424	953.447556	477.227416	8
9	959.483273	480.245275	942.456724	471.732000	941.472708	471.239992	A	*842.415528*	421.711402	825.388979	413.198128	824.404963	412.706120	7
10	1046.515301	523.761289	1029.488752	515.248014	1028.504736	514.756006	S	*771.378414*	386.192845	754.351865	377.679571	753.367849	377.187563	6
11	1133.547329	567.277303	1116.520780	558.764028	1115.536764	558.272020	S	684.346386	342.676831	667.319837	334.163557	666.335821	333.671549	5
12	1280.615743	640.811510	1263.589194	632.298235	1262.605178	631.806227	F	*597.314358*	299.160817	580.287809	290.647543			4
13	1427.684157	714.345717	1410.657608	705.832442	1409.673592	705.340434	F	*450.245944*	225.626610	433.219395	217.113336			3
14	1555.742735	778.375006	1538.716186	769.861731	1537.732170	769.369723	Q	303.177530	152.092403	286.150981	143.579129			2
15							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.3	1728.847137	0.013151	FPSVSLQEASSFFQR

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

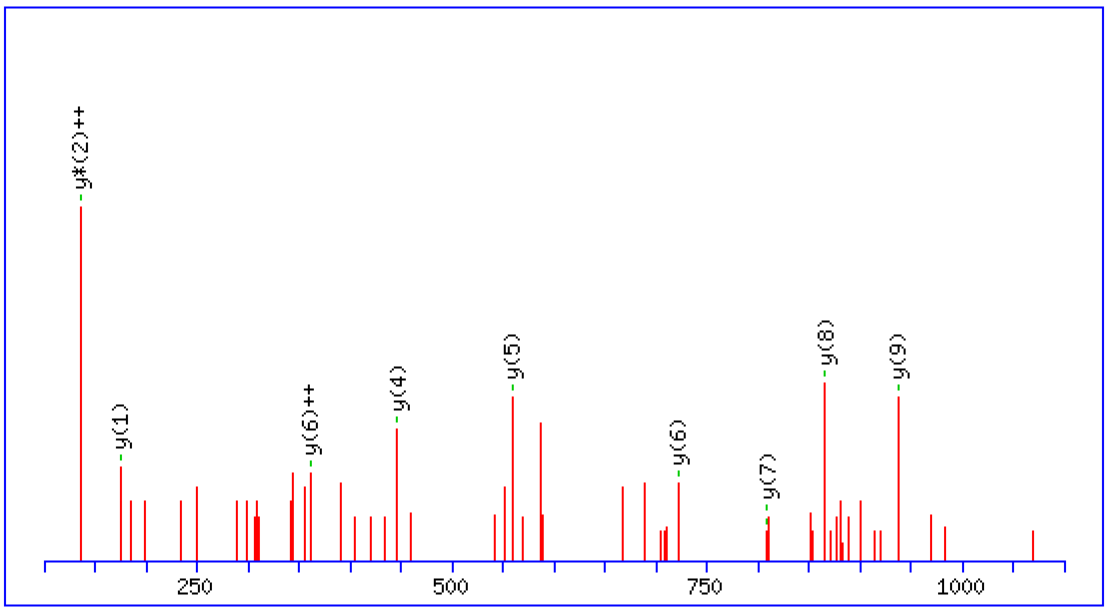
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASAGSYISALR**
Found in **PSB8_HUMAN**, Proteasome subunit beta type-8 OS=Homo sapiens GN=PSMB8 PE=1 SV=3

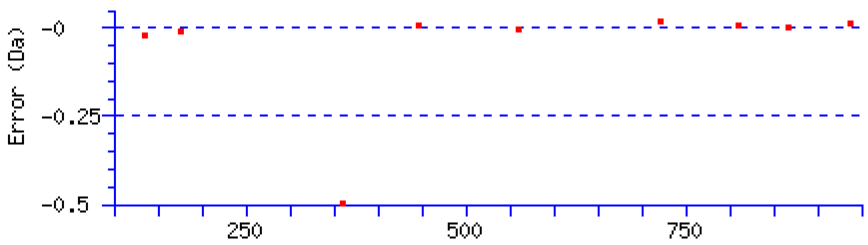
Match to Query 17757: 1094.582728 from(548.298640,2+) rtinseconds(2366) index(25947)
Title: Locus:1.1.1.2401.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

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 ●

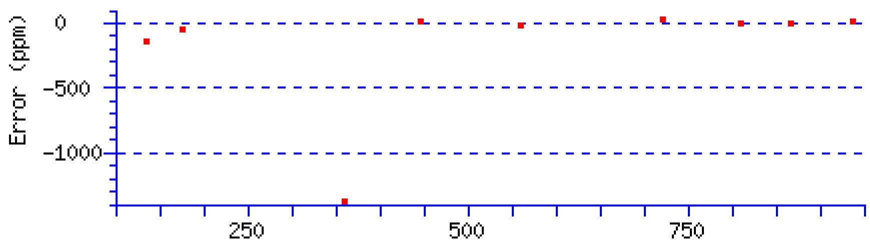


```
Monoisotopic mass of neutral peptide Mr(calc): 1094.571991
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.001
Matches : 9/92 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							11
2	159.076418	80.041847	141.065853	71.036564	S	1024.542185	512.774731	1007.515636	504.261456	1006.531620	503.769448	10
3	230.113532	115.560404	212.102967	106.555121	A	***937.510157***	469.258717	920.483608	460.745442	919.499592	460.253434	9
4	287.134996	144.071136	269.124431	135.065854	G	***866.473043***	433.740160	849.446494	425.226885	848.462478	424.734877	8
5	374.167024	187.587150	356.156459	178.581868	S	***809.451579***	405.229428	792.425030	396.716153	791.441014	396.224145	7
6	537.230353	269.118815	519.219788	260.113532	Y	***722.419551***	361.713414	705.393002	353.200139	704.408986	352.708131	6
7	650.314417	325.660847	632.303852	316.655564	I	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	5
8	737.346445	369.176861	719.335880	360.171578	S	***446.272158***	223.639717	429.245609	215.126443	428.261593	214.634435	4
9	808.383559	404.695418	790.372994	395.690135	A	359.240130	180.123703	342.213581	171.610429			3
10	921.467623	461.237450	903.457058	452.232167	L	288.203016	144.605146	271.176467	136.091872			2
11					R	***175.118952***	88.063114	158.092403	79.549840			1



RMS error 460 ppm



RMS error 460 ppm

NCBI **BLAST** search of ASAGSYISALR
(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	1094.571991	0.010737	ASAGSYISALR

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

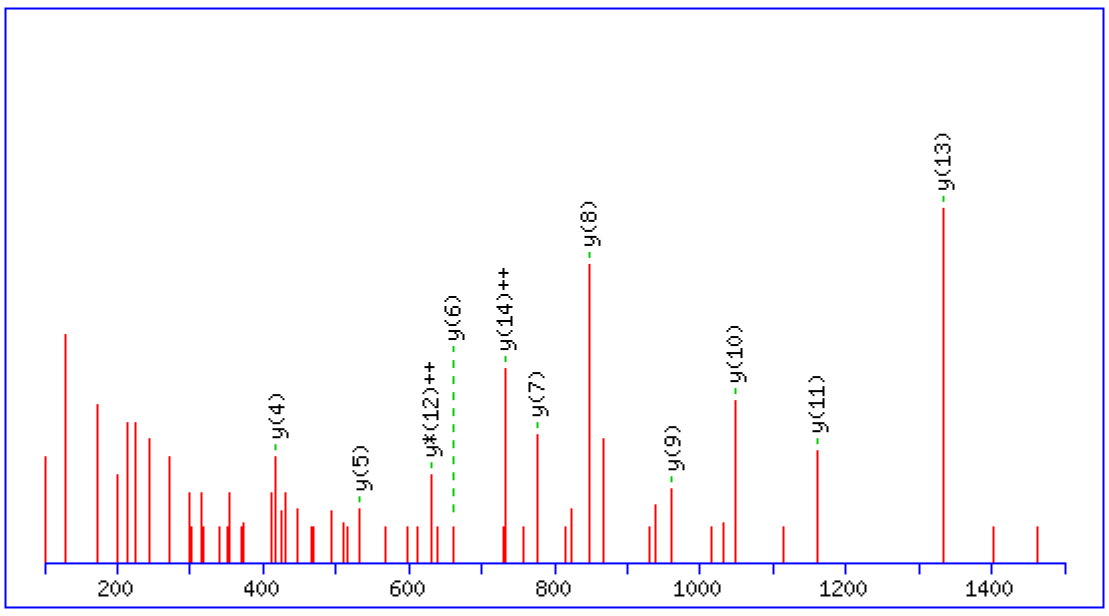
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEGDLSLADKDVTAK**
Found in **AHNK2_HUMAN**, Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2

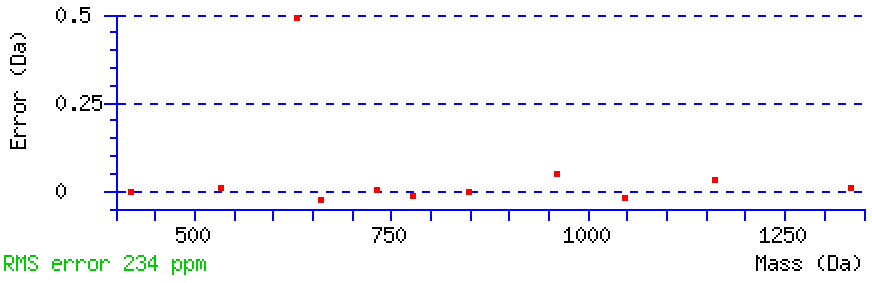
Match to Query 701433: 1573.820442 from(525.614090,3+) rtinseconds(1967) index(650557)
Title: Locus:1.1.1.939.14
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

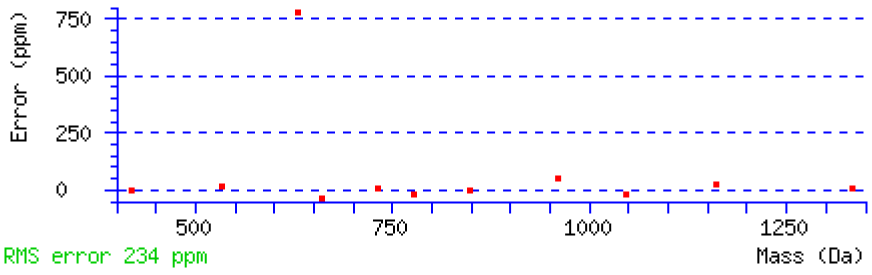
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1573.819901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 8.5e-005
Matches : 11/144 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	114.091340	57.549308					L							15
2	243.133933	122.070605			225.123368	113.065322	E	1461.743130	731.375203	1444.716581	722.861929	1443.732565	722.369921	14
3	300.155397	150.581336			282.144832	141.576054	G	***1332.700537***	666.853907	1315.673988	658.340632	1314.689972	657.848624	13
4	415.182340	208.094808			397.171775	199.089526	D	1275.679073	638.343175	1258.652524	629.829900	1257.668508	629.337892	12
5	528.266404	264.636840			510.255839	255.631558	L	***1160.652130***	580.829703	1143.625581	572.316429	1142.641565	571.824421	11
6	615.298432	308.152854			597.287867	299.147572	S	***1047.568066***	524.287671	1030.541517	515.774397	1029.557501	515.282389	10
7	728.382496	364.694886			710.371931	355.689604	L	***960.536038***	480.771657	943.509489	472.258383	942.525473	471.766375	9
8	799.419610	400.213443			781.409045	391.208161	A	***847.451974***	424.229625	830.425425	415.716351	829.441409	415.224343	8
9	914.446553	457.726915			896.435988	448.721632	D	***776.414860***	388.711068	759.388311	380.197794	758.404295	379.705786	7
10	1042.541516	521.774396	1025.514967	513.261122	1024.530951	512.769114	K	***661.387917***	331.197597	644.361368	322.684322	643.377352	322.192314	6
11	1157.568459	579.287868	1140.541910	570.774593	1139.557894	570.282585	D	***533.292954***	267.150115	516.266405	258.636841	515.282389	258.144833	5
12	1256.636873	628.822075	1239.610324	620.308800	1238.626308	619.816792	V	***418.266011***	209.636644	401.239462	201.123369	400.255446	200.631361	4
13	1357.684552	679.345914	1340.658003	670.832640	1339.673987	670.340632	T	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
14	1428.721666	714.864471	1411.695117	706.351197	1410.711101	705.859189	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 LEGDLSLADKDVTAK
(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	1573.819901	0.000541	LEGDLSLADKDVTAK
4.7	1573.807343	0.013099	AGPRPGPRPPGGAPAR
3.7	1573.807343	0.013099	AGPRPGPRPPGGAPAR
2.8	1573.807343	0.013099	AGPRPGPRPPGGAPAR
2.8	1573.807343	0.013099	AGPRPGPRPPGGAPAR
1.1	1573.821243	-0.000801	QNKPTGFALGSIEGR

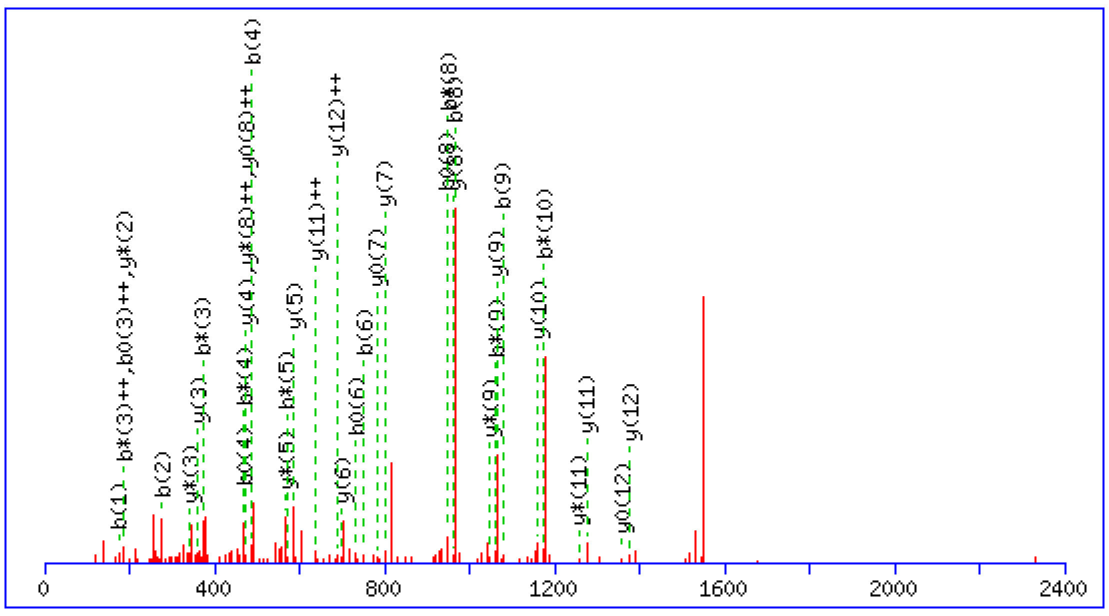
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CTNPTYTLIIRGK**
Found in **APCD1_HUMAN**, Protein APCDD1 OS=Homo sapiens GN=APCDD1 PE=1 SV=1

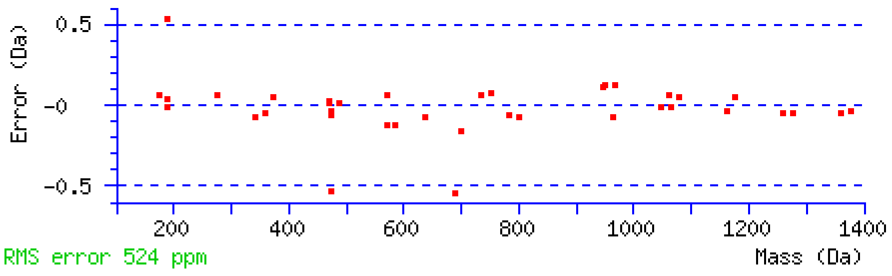
Match to Query 41460: 1549.832648 from(775.923600,2+) rtinseconds(3514) index(50898)
Title: Locus:1.1.1.2719.26
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

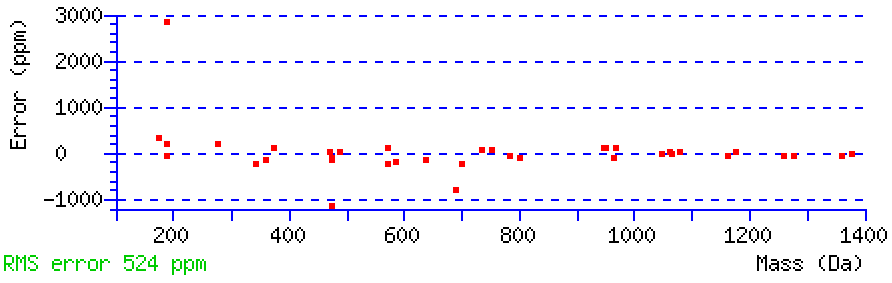
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1549.828629
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0026
Matches : 38/126 fragment ions using 106 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							13
2	**276.101254**	138.554265			258.090689	129.548982	T	***1376.789628***	688.898452	1359.763079	680.385177	1358.779063	679.893169	12
3	390.144181	195.575729	373.117632	187.062454	372.133616	186.570446	N	***1275.741949***	638.374613	1258.715400	629.861338	1257.731384	629.369330	11
4	**487.196945**	244.102110	470.170396	235.588836	469.186380	235.096828	P	***1161.699022***	581.353149	1144.672473	572.839874	1143.688457	572.347866	10
5	588.244624	294.625950	571.218075	286.112676	570.234059	285.620668	T	***1064.646258***	532.826767	1047.619709	524.313493	1046.635693	523.821485	9
6	**751.307953**	376.157615	734.281404	367.644340	733.297388	367.152332	Y	***963.598579***	482.302927	946.572030	473.789653	945.588014	473.297645	8
7	852.355632	426.681454	835.329083	418.168180	834.345067	417.676172	T	***800.535250***	400.771263	783.508701	392.257988	782.524685	391.765980	7
8	**965.439696**	483.223486	948.413147	474.710212	947.429131	474.218204	L	***699.487571***	350.247423	682.461022	341.734149			6
9	**1078.523760**	539.765518	1061.497211	531.252244	1060.513195	530.760236	I	***586.403507***	293.705391	569.376958	285.192117			5
10	1191.607824	596.307550	1174.581275	587.794276	1173.597259	587.302267	I	***473.319443***	237.163359	456.292894	228.650085			4
11	1347.708935	674.358105	1330.682386	665.844831	1329.698370	665.352823	R	***360.235379***	180.621327	343.208830	172.108053			3
12	1404.730399	702.868837	1387.703850	694.355563	1386.719834	693.863555	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 CTNPTYTLIIRGK
(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	1549.828629	0.004019	CTNPTYTLIIRGK
10.7	1549.832489	0.000159	ADGDKPRAHLTVVR
4.2	1549.821259	0.011389	TSSPGGKKPPPTPQR
4.1	1549.823914	0.008734	FDSKDEILLTLEK
4.0	1549.821259	0.011389	TSSPGGKKPPPTPQR
4.0	1549.821259	0.011389	TSSPGGKKPPPTPQR
3.4	1549.821259	0.011389	TSSPGGKKPPPTPQR
1.0	1549.823914	0.008734	DVLYPSLKEITEK

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

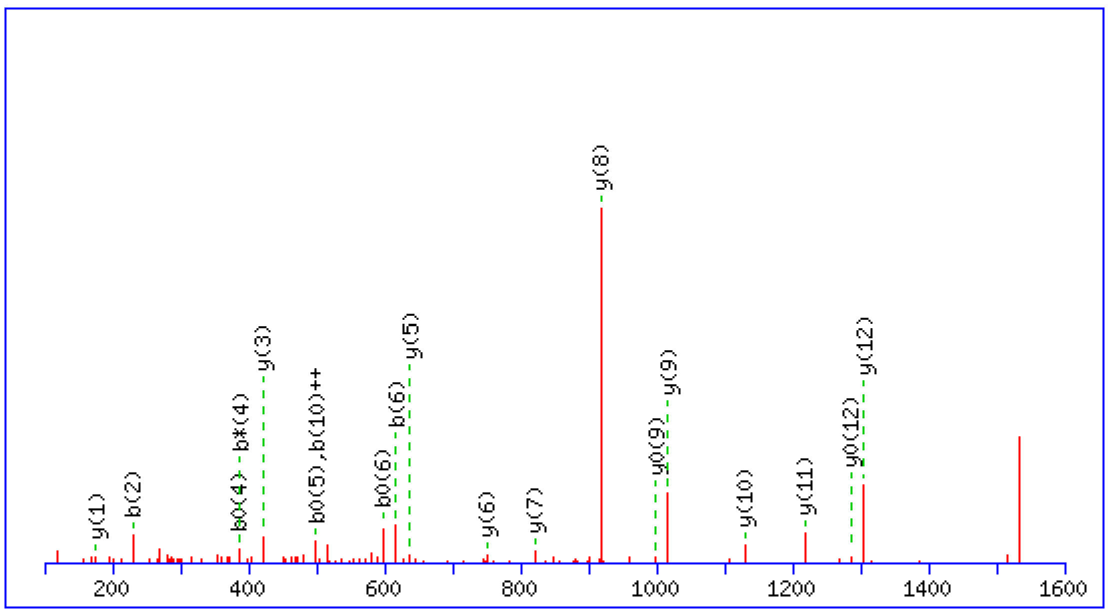
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQSSLVPALTDFVR**
Found in **CUTA_HUMAN**, Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2

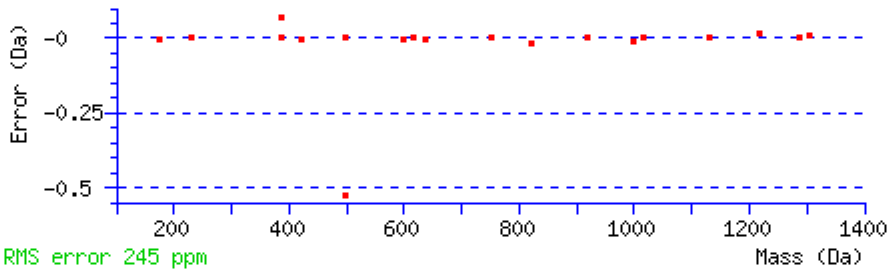
Match to Query 30601: 1532.824768 from(767.419660,2+) rtinseconds(3619) index(37345)
Title: Locus:1.1.1.2870.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

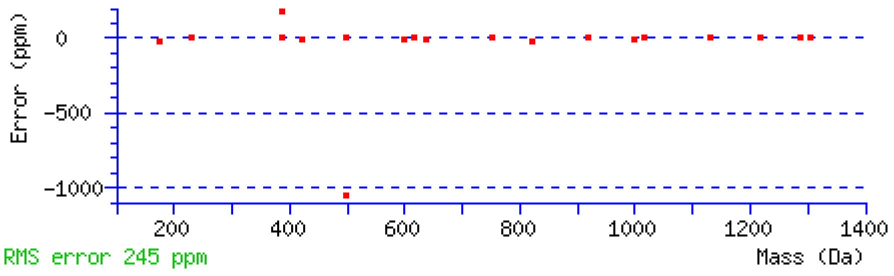
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1532.819870
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 89 **Expect:** 1.3e-008
Matches : 19/148 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	**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





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
88.6	1532.819870	0.004898	TQSSLVPALTDFVR
9.9	1532.823853	0.000915	IYYTGKYQSLGIK
4.2	1532.816666	0.008102	ELILMRNLMNVR
2.5	1532.816681	0.008087	LMDAVMLQLTRAR
2.3	1532.817352	0.007416	MHTKIVPPWAPPK
2.3	1532.816681	0.008087	LMDAVMLQLTRAR
2.1	1532.831100	-0.006332	VPSTDITFRPTRK
2.0	1532.817352	0.007416	MHTKIVPPWAPPK
1.0	1532.831055	-0.006287	NNSFVNEIISRIK
0.8	1532.811966	0.012802	VIASELGSMPELKK

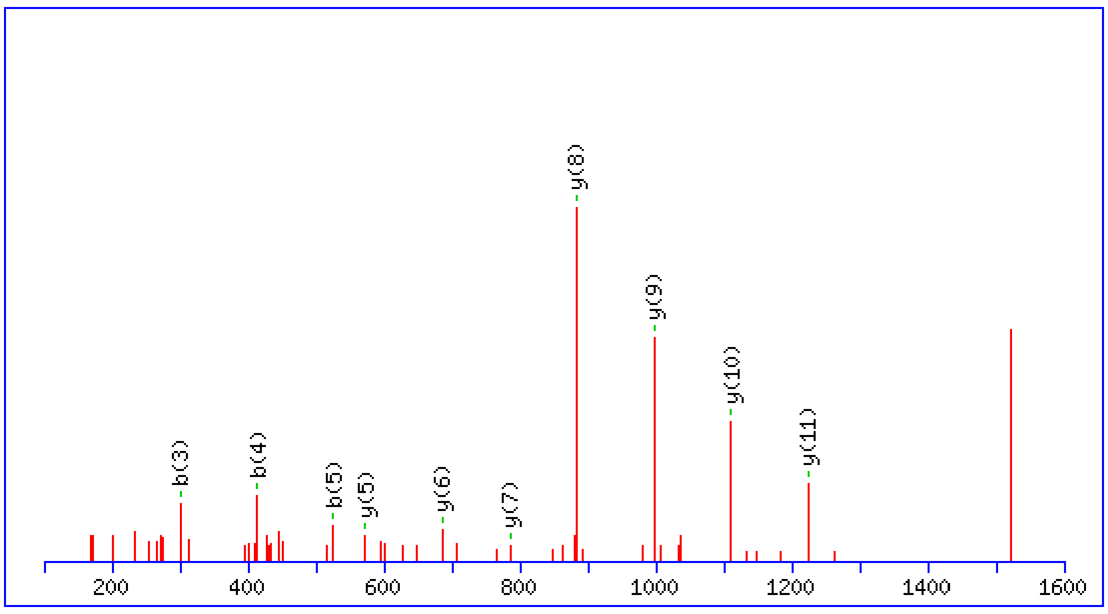
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAVLIDPVLETAPR**
Found in **ETHE1_HUMAN**, Protein ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2

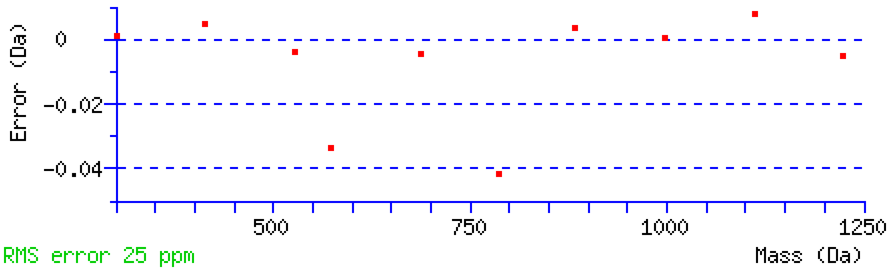
Match to Query 36660: 1521.843748 from(761.929150,2+) rtinseconds(3114) index(40134)
Title: Locus:1.1.1.2708.35
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

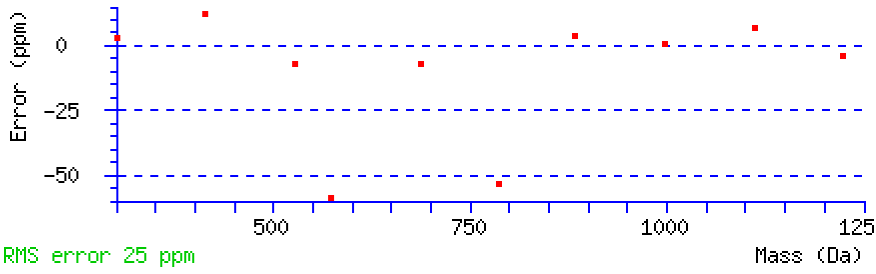
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1521.840240
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 8.7e-007
Matches : 10/124 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							14
2	201.086983	101.047130	183.076418	92.041847	A	1393.804943	697.406109	1376.778394	688.892835	1375.794378	688.400827	13
3	**300.155397**	150.581336	282.144832	141.576054	V	1322.767829	661.887552	1305.741280	653.374278	1304.757264	652.882270	12
4	**413.239461**	207.123369	395.228896	198.118086	L	***1223.699415***	612.353346	1206.672866	603.840071	1205.688850	603.348063	11
5	**526.323525**	263.665401	508.312960	254.660118	I	***1110.615351***	555.811313	1093.588802	547.298039	1092.604786	546.806031	10
6	641.350468	321.178872	623.339903	312.173589	D	***997.531287***	499.269282	980.504738	490.756007	979.520722	490.263999	9
7	738.403232	369.705254	720.392667	360.699972	P	***882.504344***	441.755810	865.477795	433.242536	864.493779	432.750528	8
8	837.471646	419.239461	819.461081	410.234178	V	***785.451580***	393.229428	768.425031	384.716154	767.441015	384.224146	7
9	950.555710	475.781493	932.545145	466.776210	L	***686.383166***	343.695221	669.356617	335.181947	668.372601	334.689939	6
10	1079.598303	540.302790	1061.587738	531.297507	E	***573.299102***	287.153189	556.272553	278.639915	555.288537	278.147907	5
11	1180.645982	590.826629	1162.635417	581.821347	T	444.256509	222.631892	427.229960	214.118618	426.245944	213.626610	4
12	1251.683096	626.345186	1233.672531	617.339903	A	343.208830	172.108053	326.182281	163.594778			3
13	1348.735860	674.871568	1330.725295	665.866286	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 EAVLIDPVLETAPR
(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	1521.840240	0.003508	EAVLIDPVLETAPR
0.8	1521.830338	0.013410	LWIEGPPEGQKLR

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

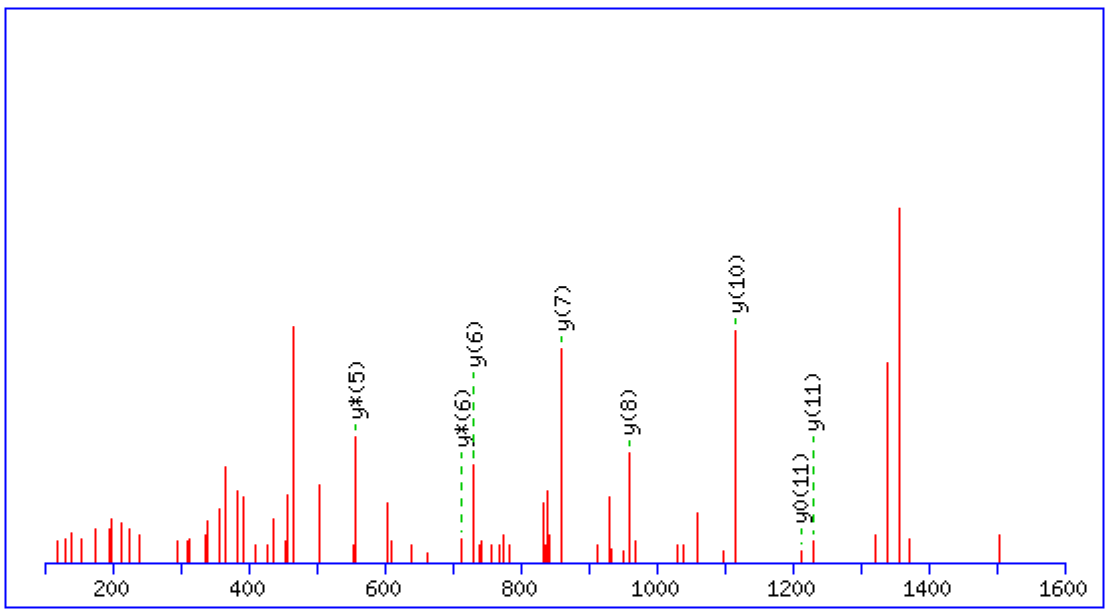
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPSAVERLEADK**
Found in **F110A_HUMAN**, Protein FAM110A OS=Homo sapiens GN=FAM110A PE=1 SV=1

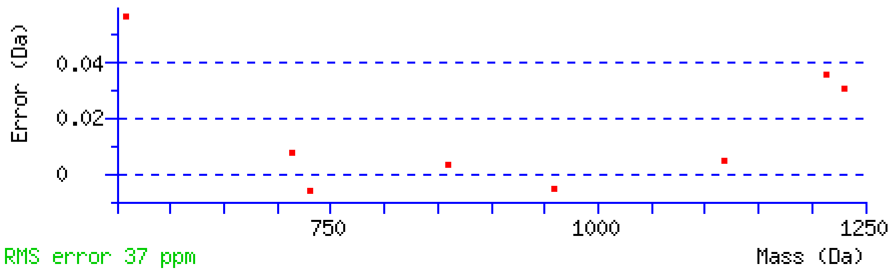
Match to Query 545286: 1357.724548 from(679.869550,2+) rtinseconds(2511) index(961389)
Title: Locus:1.1.1.1470.39
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

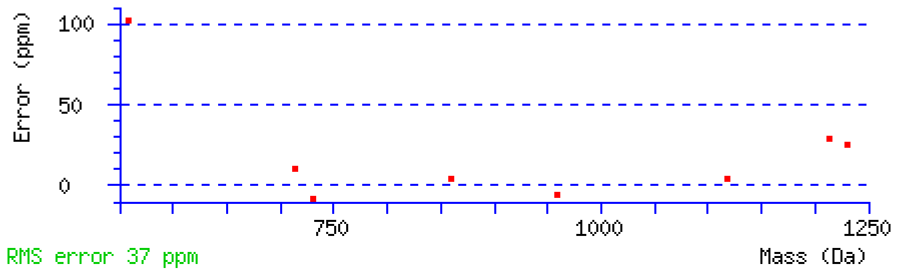
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1357.720108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 32  Expect: 0.0072
Matches : 9/126 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							12
2	242.149918	121.578597	225.123369	113.065322			P	***1230.632457***	615.819867	1213.605908	607.306592	1212.621892	606.814584	11
3	329.181946	165.094611	312.155397	156.581336	311.171381	156.089328	S	***1117.584778***	559.296027	1100.558229	550.782753	1099.574213	550.290745	10
4	400.219060	200.613168	383.192511	192.099893	382.208495	191.607885	A	1030.552750	515.780013	1013.526201	507.266739	1012.542185	506.774731	9
5	499.287474	250.147375	482.260925	241.634100	481.276909	241.142092	V	***959.515636***	480.261456	942.489087	471.748182	941.505071	471.256174	8
6	628.330067	314.668672	611.303518	306.155397	610.319502	305.663389	E	***860.447222***	430.727249	843.420673	422.213975	842.436657	421.721967	7
7	784.431178	392.719227	767.404629	384.205953	766.420613	383.713945	R	***731.404629***	366.205953	714.378080	357.692678	713.394064	357.200670	6
8	897.515242	449.261259	880.488693	440.747985	879.504677	440.255977	L	575.303518	288.155397	558.276969	279.642123	557.292953	279.150115	5
9	1026.557835	513.782556	1009.531286	505.269281	1008.547270	504.777273	E	462.219454	231.613365	445.192905	223.100091	444.208889	222.608083	4
10	1097.594949	549.301113	1080.568400	540.787838	1079.584384	540.295830	A	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
11	1212.621892	606.814584	1195.595343	598.301310	1194.611327	597.809302	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 KPSAVERLEADK
(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	1357.720108	0.004440	KPSAVERLEADK
8.6	1357.720123	0.004425	QIQEKTDIIDR
7.3	1357.720123	0.004425	KLLESGADVNQGK
6.8	1357.724182	0.000366	KPVPDLVPGNFK
4.6	1357.731339	-0.006791	ERQLSKPLSER
2.6	1357.720139	0.004409	EVTVQGLEPSRK
0.5	1357.724167	0.000381	EPVGPSSAPPVPPK

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

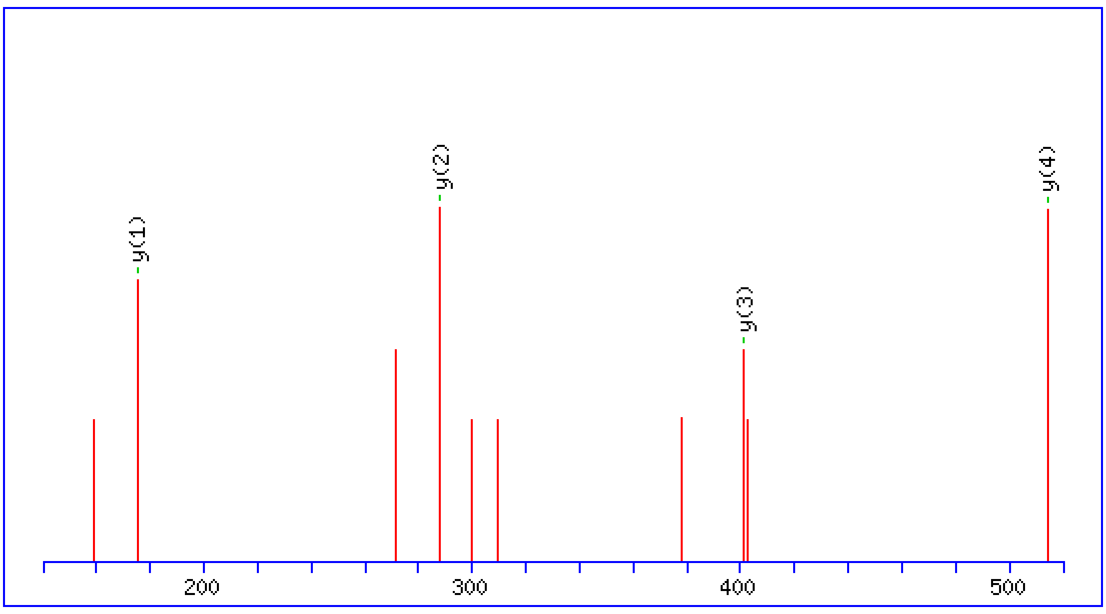
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGLLPLR**
Found in **F179A_HUMAN**, Protein FAM179A OS=Homo sapiens GN=FAM179A PE=2 SV=2

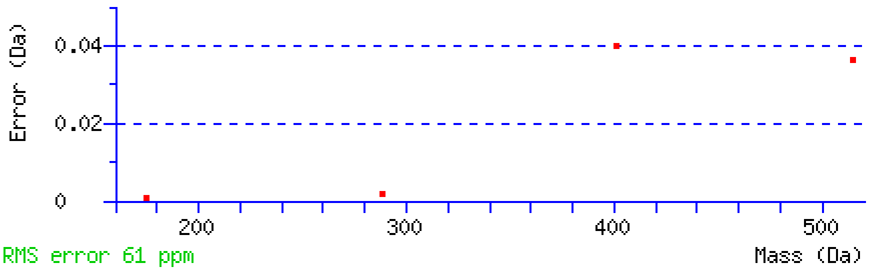
Match to Query 805: 812.476748 from(407.245650,2+) rtinseconds(2026) index(13159)
Title: Locus:1.1.1.2270.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 140 to 520 Da Full range
Label all possible matches ○ Label matches used for scoring ●

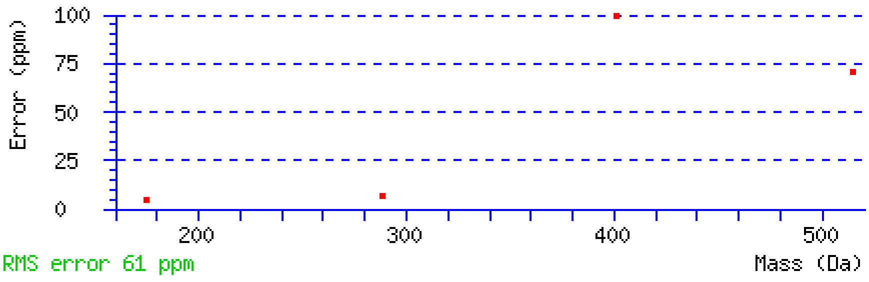


```
Monoisotopic mass of neutral peptide Mr(calc): 812.475586
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 40  Expect: 0.00043
Matches : 4/48 fragment ions using 4 most intense peaks   (help)
```

#	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



RMS error 61 ppm



RMS error 61 ppm

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
40.4	812.475586	0.001162	EGLLPLR
22.0	812.475586	0.001162	APEVLLR
22.0	812.475601	0.001147	TLTPPLR
8.1	812.475601	0.001147	DIVPTLR
8.1	812.475601	0.001147	DPVLTLR
8.1	812.475586	0.001162	EVLPAIR
8.1	812.469055	0.007693	HLKMLR
8.1	812.475586	0.001162	IAPEVLR
8.1	812.469055	0.007693	IMKHLR
8.1	812.475601	0.001147	IPSLVPR

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

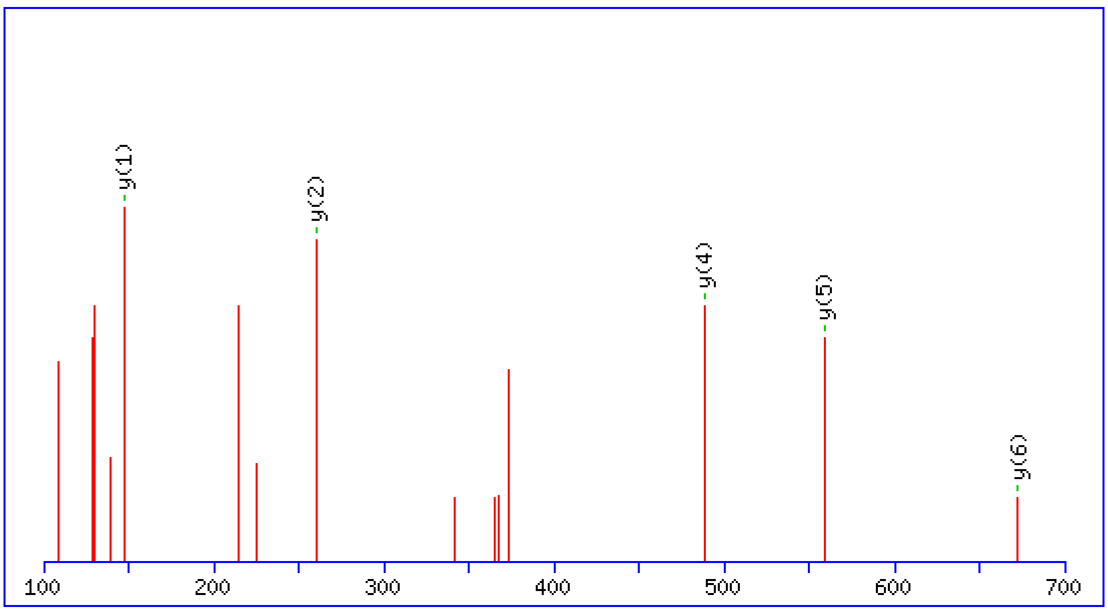
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAEVIK**
Found in **F190A_HUMAN**, Protein FAM190A OS=Homo sapiens GN=FAM190A PE=2 SV=2

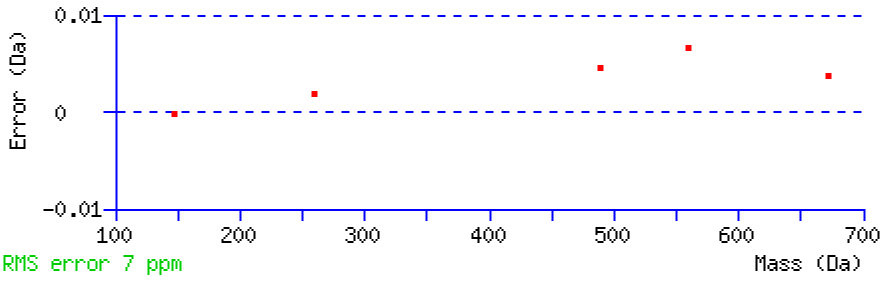
Match to Query 4364: 800.467328 from(401.240940,2+) rtinseconds(2452) index(960252)
Title: Locus:1.1.1.1448.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

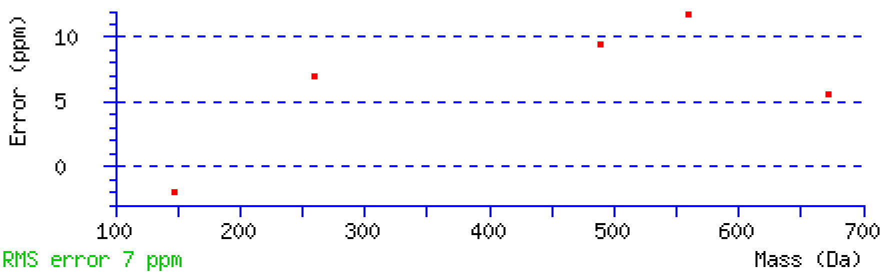
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 800.464340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00017
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	L	*672.429053*	336.718165	655.402504	328.204890	654.418488	327.712882	6
3	314.171047	157.589161	296.160482	148.583879	A	*559.344989*	280.176133	542.318440	271.662858	541.334424	271.170850	5
4	443.213640	222.110458	425.203075	213.105176	E	*488.307875*	244.657575	471.281326	236.144301	470.297310	235.652293	4
5	542.282054	271.644665	524.271489	262.639383	V	359.265282	180.136279	342.238733	171.623004			3
6	655.366118	328.186697	637.355553	319.181415	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 ELAEVIK
(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	800.464340	0.002988	ELAEVIK
29.3	800.464340	0.002988	EILGEIK
29.3	800.464355	0.002973	EIPVSIK
29.3	800.464340	0.002988	ELELGLK
29.3	800.464340	0.002988	ELVEALK
29.2	800.464340	0.002988	EAEVLLK
29.2	800.464340	0.002988	EGLELLK
29.2	800.464355	0.002973	EVLSPLK
29.0	800.464340	0.002988	ELAELVK
16.8	800.464340	0.002988	LEELGIK

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

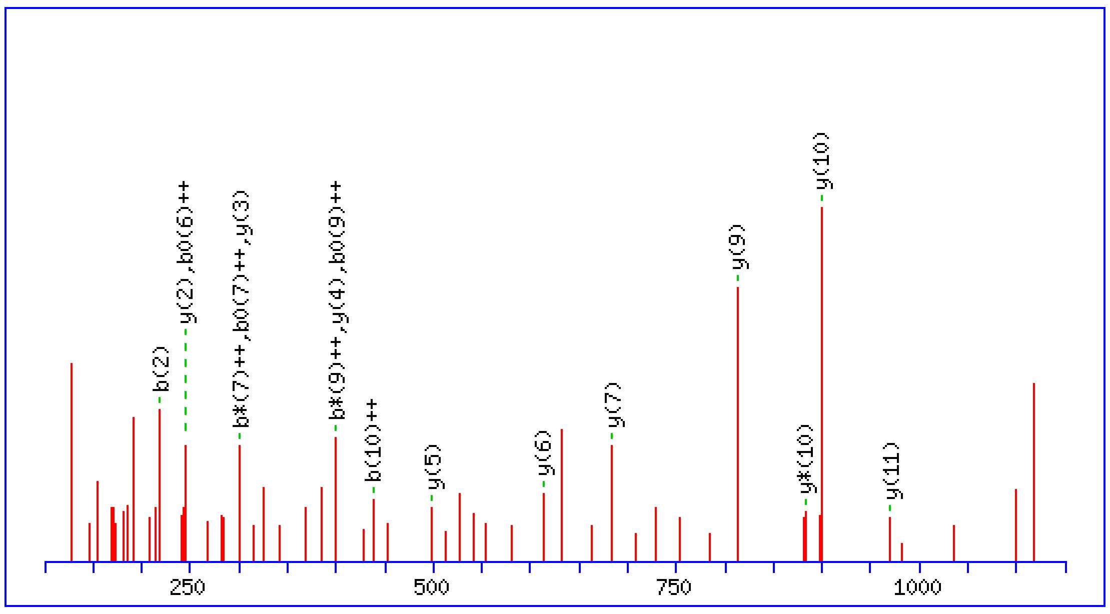
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MASGAANVVGPK**
Found in **FAM3C_HUMAN**, Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1

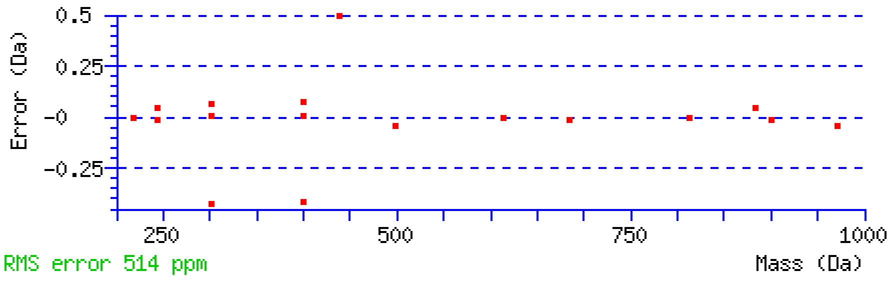
Match to Query 19788: 1116.557828 from(559.286190,2+) rtinseconds(1109) index(3197)
Title: Locus:1.1.1.1950.27
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

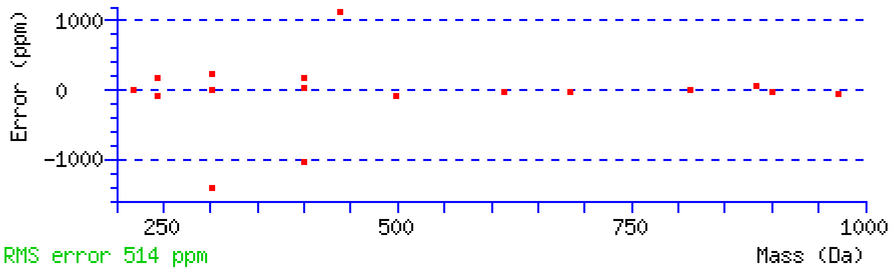
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 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: 71 **Expect:** 3.7e-007
Matches : 17/148 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	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
70.7	1116.559738	-0.001910	MASGAANVVGPK
2.1	1116.556366	0.001462	FSHDLTLER

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

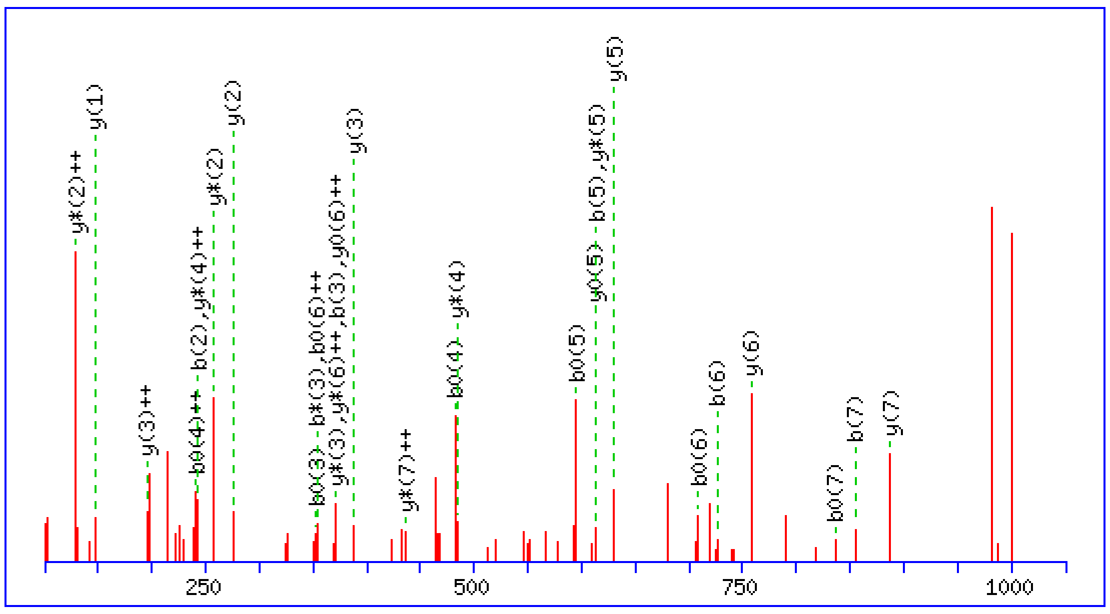
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEKELLQK**
Found in **FA81A_HUMAN**, Protein FAM81A OS=Homo sapiens GN=FAM81A PE=2 SV=3

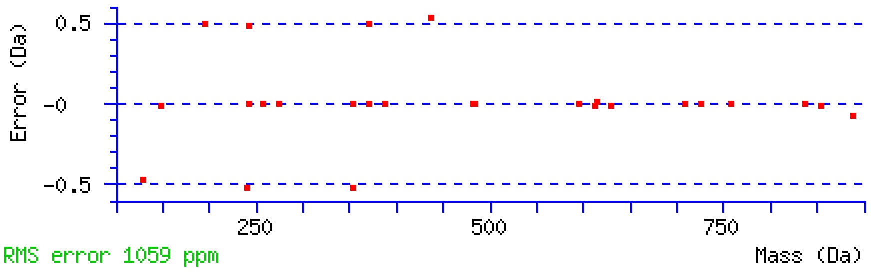
Match to Query 7342: 999.595688 from(500.805120,2+) rtinseconds(1616) index(1545)
Title: Locus:1.1.1.2672.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-8.mgf

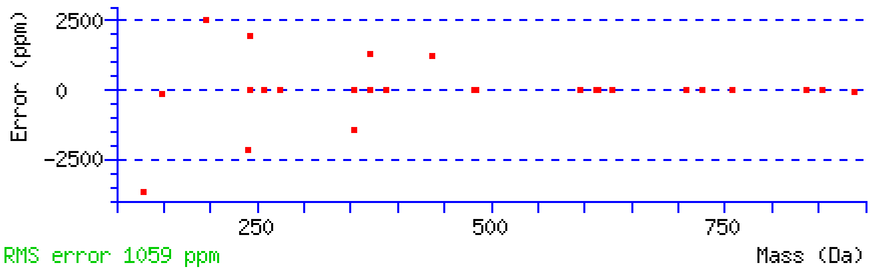
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 999.596405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0059
Matches : 30/70 fragment ions using 47 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
30.2	999.596405	-0.000717	IEKELLQK
27.6	999.596405	-0.000717	QLELEIKK
26.6	999.596405	-0.000717	ELKELIQK
25.6	999.596405	-0.000717	EQLELLKK
16.6	999.596405	-0.000717	ELQILKEK
15.9	999.596405	-0.000717	LQELEKIK
13.8	999.596405	-0.000717	LQELKIEK
13.3	999.596436	-0.000748	GITVPEKLK
12.1	999.596405	-0.000717	EELLKQLK
11.5	999.596405	-0.000717	EKEILQIK

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

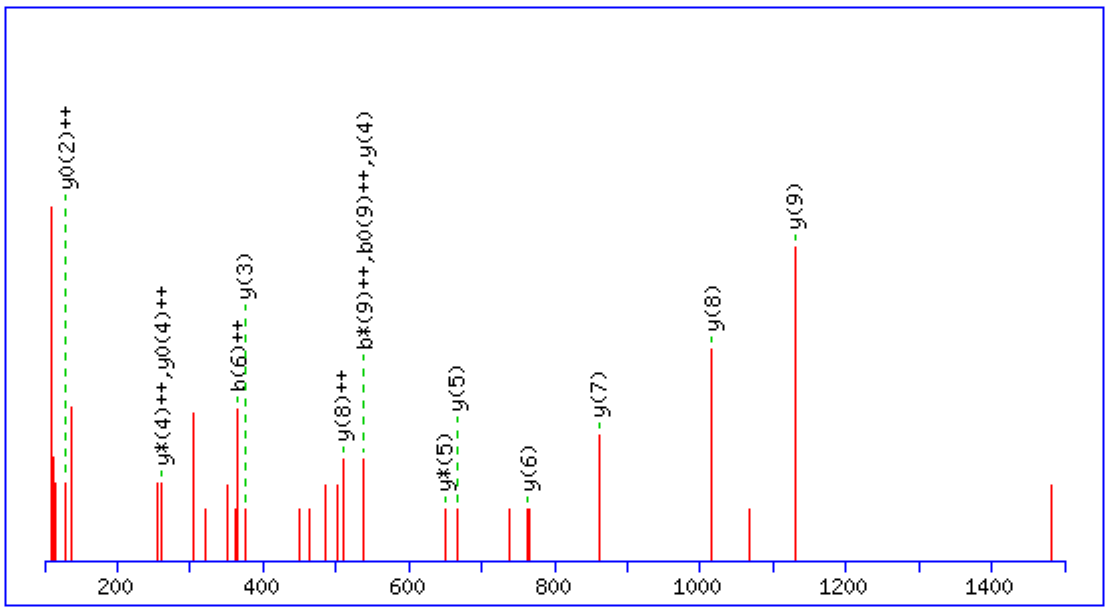
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLRPPQYVTR**
Found in **FA83H_HUMAN**, Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3

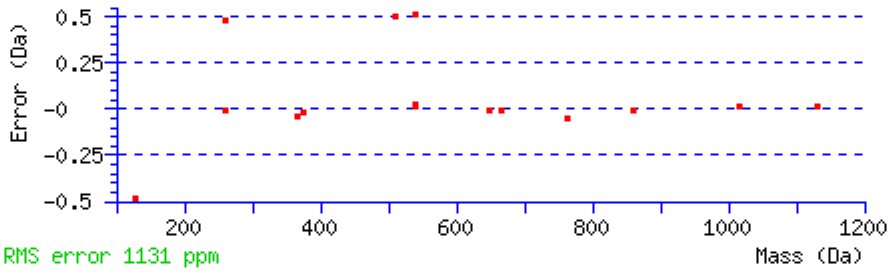
Match to Query 463087: 1265.696802 from(422.906210,3+) rtinseconds(1258) index(941451)
Title: Locus:1.1.1.986.6
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

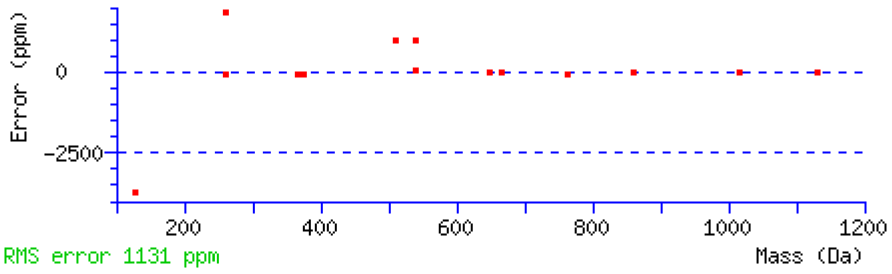
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1265.699280
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.0019
Matches : 15/86 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							10
2	251.150252	126.078764					L	*1129.647655*	565.327466	1112.621106	556.814191	1111.637090	556.322183	9
3	407.251363	204.129319	390.224814	195.616045			R	*1016.563591*	508.785434	999.537042	500.272159	998.553026	499.780151	8
4	504.304127	252.655701	487.277578	244.142427			P	*860.462480*	430.734878	843.435931	422.221603	842.451915	421.729595	7
5	601.356891	301.182084	584.330342	292.668809			P	*763.409716*	382.208496	746.383167	373.695222	745.399151	373.203214	6
6	729.415469	365.211373	712.388920	356.698098			Q	*666.356952*	333.682114	649.330403	325.168839	648.346387	324.676831	5
7	892.478798	446.743037	875.452249	438.229763			Y	*538.298374*	269.652825	521.271825	261.139550	520.287809	260.647542	4
8	991.547212	496.277244	974.520663	487.763970			V	*375.235045*	188.121160	358.208496	179.607886	357.224480	179.115878	3
9	1092.594891	546.801084	1075.568342	538.287809	1074.584326	537.795801	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of HLRPPQYVTR
(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	1265.699280	-0.002478	HLRPPQYVTR
2.0	1265.691422	0.005380	LHGVPRPLAMK

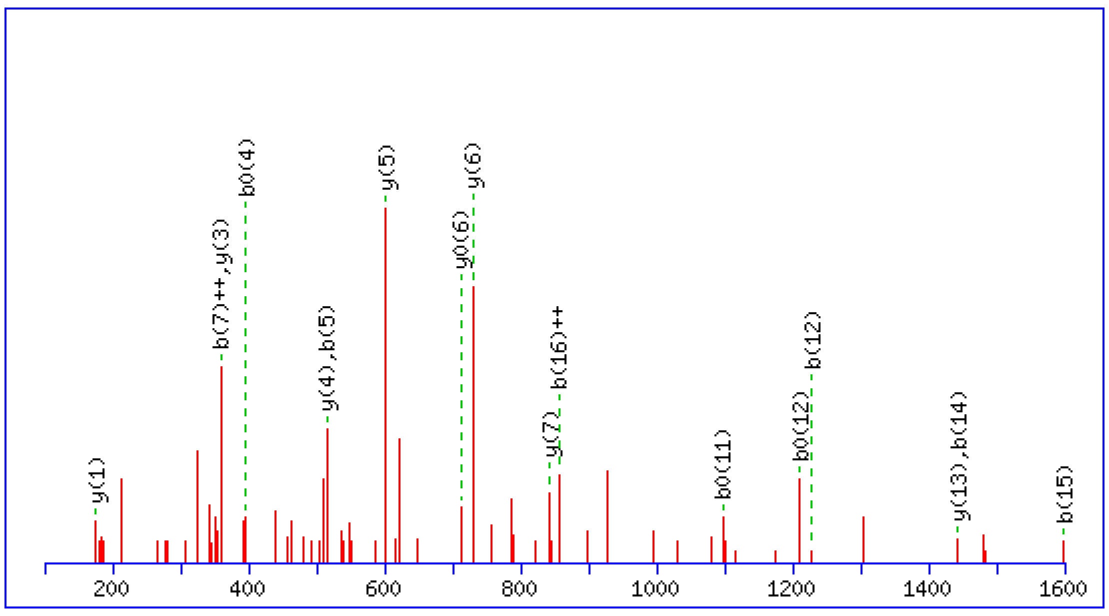
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDQTAMITAILQSRLAR**
Found in **FAN_HUMAN**, Protein FAN OS=Homo sapiens GN=NSMAF PE=1 SV=2

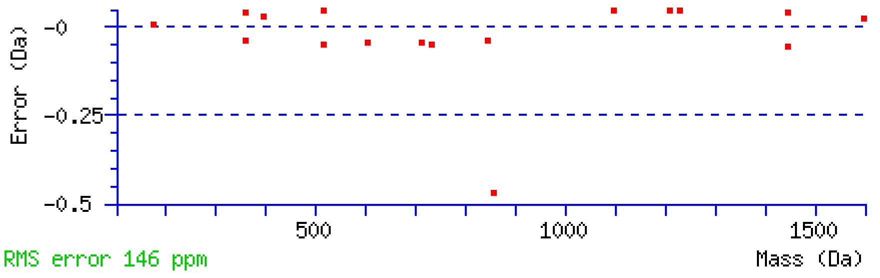
Match to Query 51401: 1957.071762 from(653.364530,3+) rtinseconds(4071) index(47302)
Title: Locus:1.1.1.3014.22
Data file 2011-11-14 - TFD - S 2-5.mgf

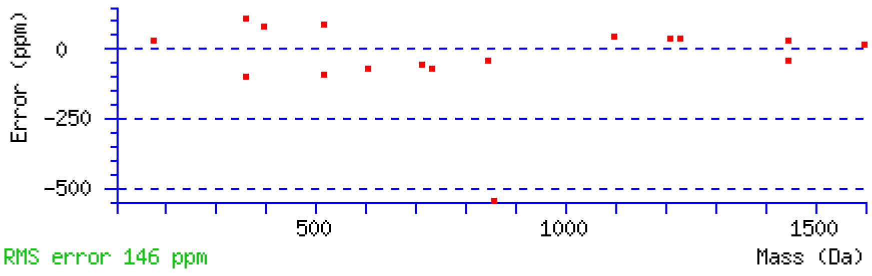
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1957.077850
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.00066
Matches : 17/186 fragment ions using 27 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							18
2	171.112804	86.060040					G	1845.001095	923.004186	1827.974546	914.490911	1826.990530	913.998903	17
3	286.139747	143.573512			268.129182	134.568229	D	1787.979631	894.493453	1770.953082	885.980179	1769.969066	885.488171	16
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	Q	1672.952688	836.979982	1655.926139	828.466708	1654.942123	827.974700	15
5	**515.246004**	258.126640	498.219455	249.613366	497.235439	249.121358	T	1544.894110	772.950693	1527.867561	764.437419	1526.883545	763.945410	14
6	586.283118	293.645197	569.256569	285.131923	568.272553	284.639915	A	***1443.846431***	722.426853	1426.819882	713.913579	1425.835866	713.421571	13
7	717.323603	**359.165440**	700.297054	350.652165	699.313038	350.160157	M	1372.809317	686.908297	1355.782768	678.395022	1354.798752	677.903014	12
8	830.407667	415.707472	813.381118	407.194197	812.397102	406.702189	I	1241.768832	621.388054	1224.742283	612.874780	1223.758267	612.382771	11
9	931.455346	466.231311	914.428797	457.718037	913.444781	457.226029	T	1128.684768	564.846022	1111.658219	556.332747	1110.674203	555.840739	10
10	1002.492460	501.749868	985.465911	493.236594	984.481895	492.744586	A	1027.637089	514.322183	1010.610540	505.808908	1009.626524	505.316900	9
11	1115.576524	558.291900	1098.549975	549.778626	1097.565959	549.286618	I	956.599975	478.803626	939.573426	470.290351	938.589410	469.798343	8
12	**1228.660588**	614.833932	1211.634039	606.320658	1210.650023	605.828649	L	***843.515911***	422.261594	826.489362	413.748319	825.505346	413.256311	7
13	1356.719166	678.863221	1339.692617	670.349947	1338.708601	669.857939	Q	***730.431847***	365.719562	713.405298	357.206287	712.421282	356.714279	6
14	**1443.751194**	722.379235	1426.724645	713.865961	1425.740629	713.373953	S	***602.373269***	301.690272	585.346720	293.176998	584.362704	292.684990	5
15	**1599.852305**	800.429791	1582.825756	791.916516	1581.841740	791.424508	R	***515.341241***	258.174258	498.314692	249.660984			4
16	1712.936369	**856.971823**	1695.909820	848.458548	1694.925804	847.966540	L	***359.240130***	180.123703	342.213581	171.610428			3
17	1783.973483	892.490380	1766.946934	883.977105	1765.962918	883.485097	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 LGDQTAMITAILQSRLAR
(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	1957.077850	-0.006088	LGDQTAMITAILQSRLAR
0.1	1957.073166	-0.001404	LTTPATLTLPEIAASGLTR

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

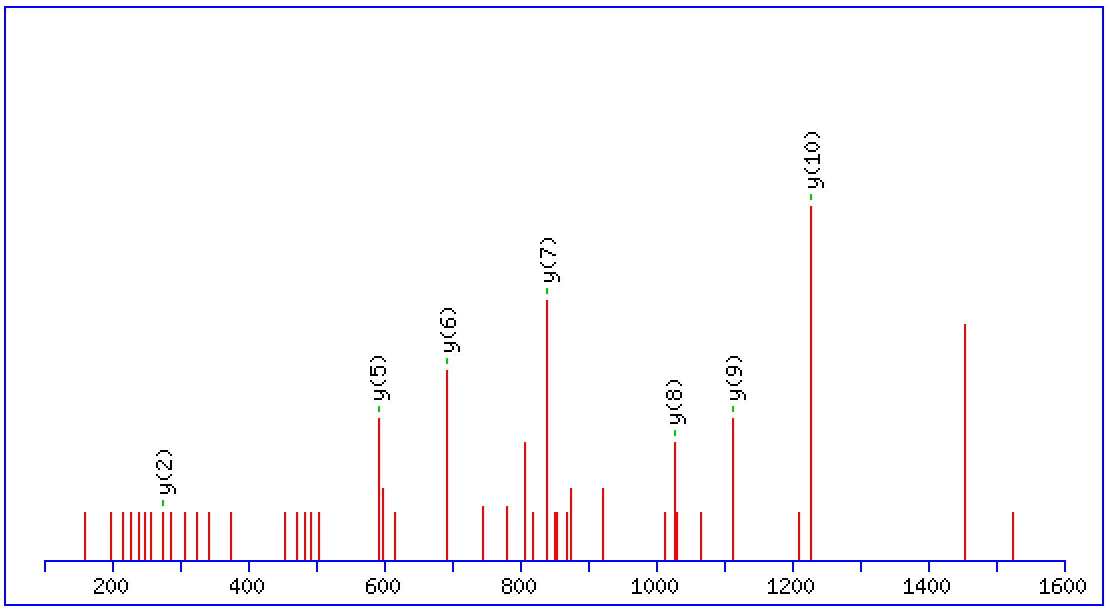
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLDSWFTSTQEK**
Found in **JAGN1_HUMAN**, Protein jagunal homolog 1 OS=Homo sapiens GN=JAGN1 PE=1 SV=1

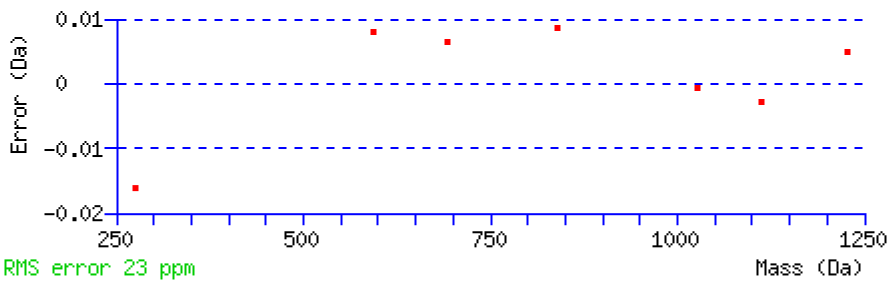
Match to Query 28115: 1453.712888 from(727.863720,2+) rtinseconds(3153) index(33135)
Title: Locus:1.1.1.2696.37
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

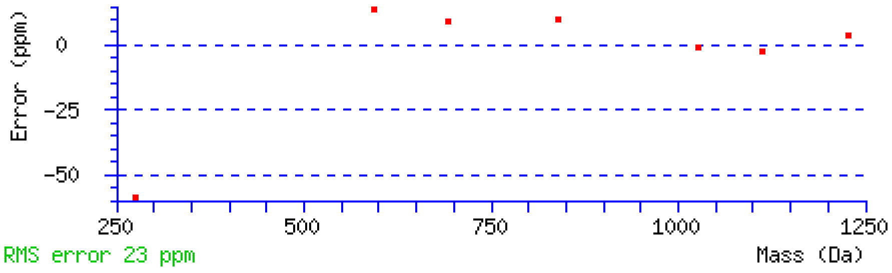
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1453.708908
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 9.4e-005
Matches : 7/108 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							12
2	227.175404	114.091340					L	1341.632123	671.319700	1324.605574	662.806425	1323.621558	662.314417	11
3	342.202347	171.604811			324.191782	162.599529	D	***1228.548059***	614.777668	1211.521510	606.264393	1210.537494	605.772385	10
4	429.234375	215.120825			411.223810	206.115543	S	***1113.521116***	557.264196	1096.494567	548.750922	1095.510551	548.258914	9
5	615.313688	308.160482			597.303123	299.155199	W	***1026.489088***	513.748182	1009.462539	505.234908	1008.478523	504.742900	8
6	762.382102	381.694689			744.371537	372.689406	F	***840.409775***	420.708526	823.383226	412.195251	822.399210	411.703243	7
7	863.429781	432.218528			845.419216	423.213246	T	***693.341361***	347.174319	676.314812	338.661044	675.330796	338.169036	6
8	950.461809	475.734542			932.451244	466.729260	S	***592.293682***	296.650479	575.267133	288.137205	574.283117	287.645197	5
9	1051.509488	526.258382			1033.498923	517.253099	T	505.261654	253.134465	488.235105	244.621191	487.251089	244.129183	4
10	1179.568066	590.287671	1162.541517	581.774397	1161.557501	581.282389	Q	404.213975	202.610626	387.187426	194.097351	386.203410	193.605343	3
11	1308.610659	654.808968	1291.584110	646.295693	1290.600094	645.803685	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 LLDSWFTSTQEK
(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	1453.708908	0.003980	LLDSWFTSTQEK

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

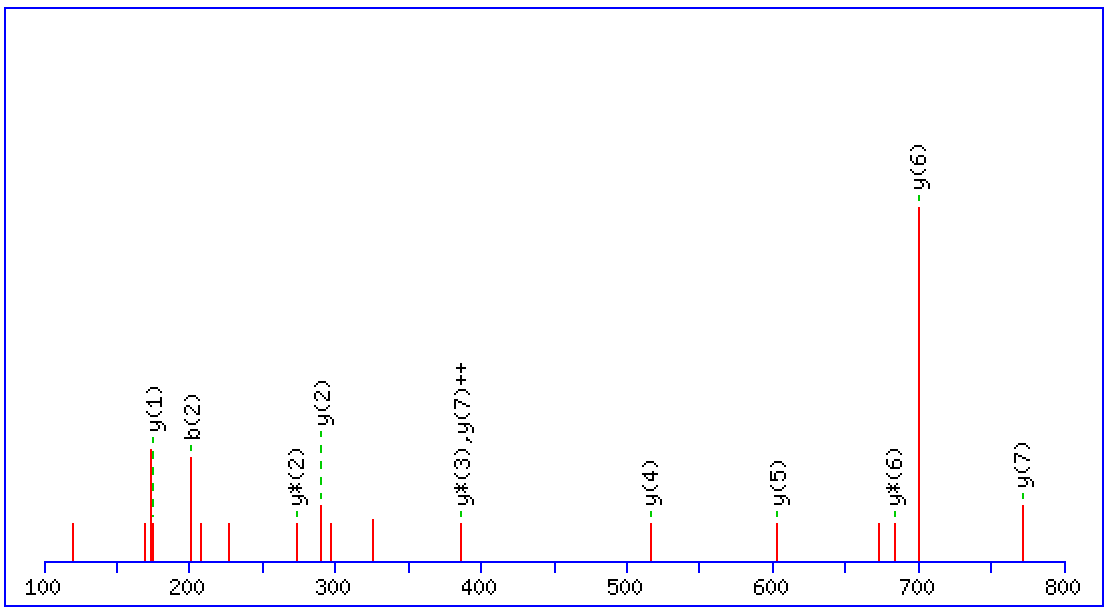
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAPSLLDR**
Found in **KISHA_HUMAN**, Protein kish-A OS=Homo sapiens GN=TMEM167A PE=2 SV=1

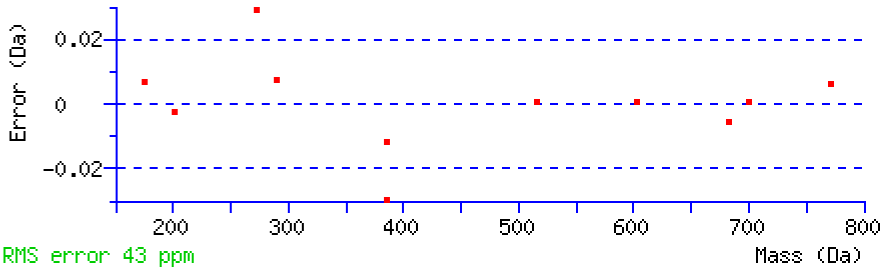
Match to Query 15905: 970.541788 from(486.278170,2+) rtinseconds(2314) index(11937)
Title: Locus:1.1.1.2324.16
Data file 2011-11-14 - TFD - S 2-7.mgf

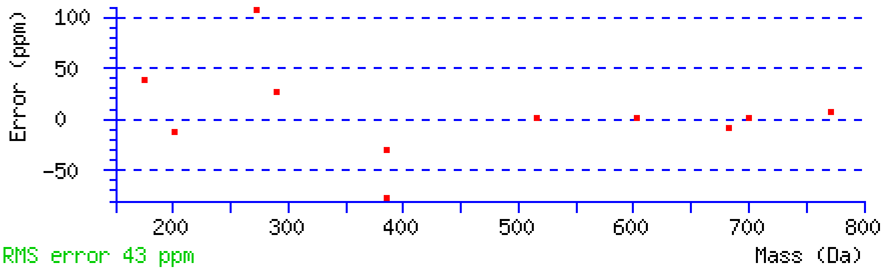
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 970.544724
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00031
Matches : 11/78 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**							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
48.2	970.544724	-0.002936	SLAPSLLDR
13.8	970.533493	0.008295	LSAPTIPEK
9.8	970.544724	-0.002936	AEILSPLGR
6.6	970.544739	-0.002951	LSVSPPSLR
4.1	970.544739	-0.002951	SLSPILPGR
3.4	970.534836	0.006952	WLRPEVR
2.3	970.533493	0.008295	LSAPTIPEK
1.5	970.544739	-0.002951	LSVSPPSLR
1.3	970.544739	-0.002951	SPGSPLLLR
1.3	970.544739	-0.002951	SSPSPVILR

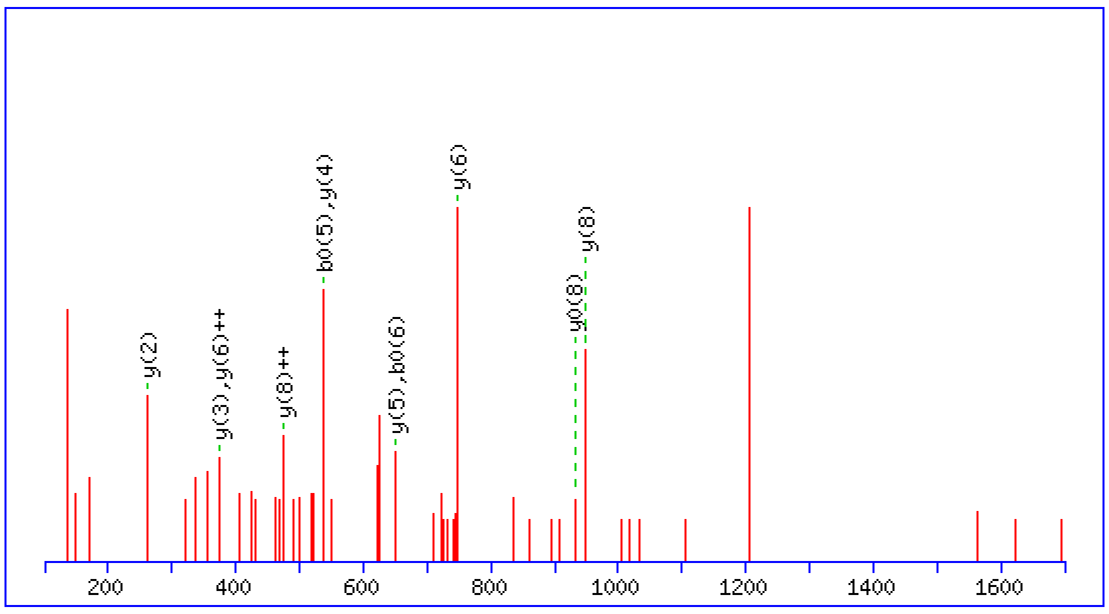
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQNSPIYISR**
Found in **LIN7A_HUMAN**, Protein lin-7 homolog A OS=Homo sapiens GN=LIN7A PE=1 SV=2

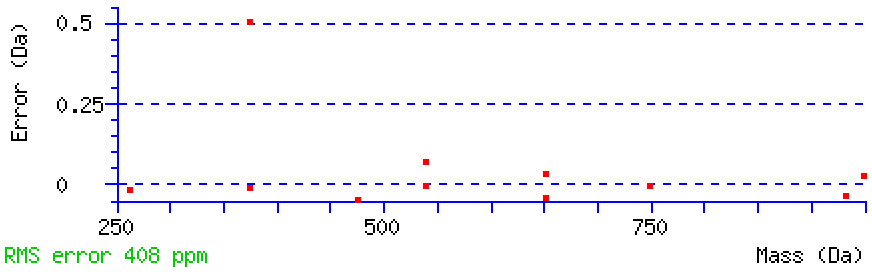
Match to Query 22949: 1205.601508 from(603.808030,2+) rtinseconds(1881) index(17075)
Title: Locus:1.1.1.2216.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

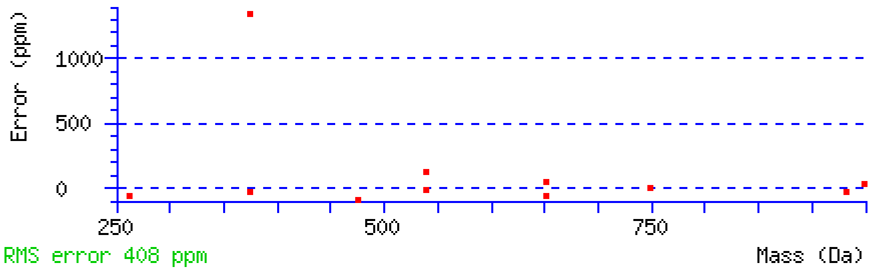
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1205.604019
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 4.6e-005
Matches : 11/104 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	130.049869	65.528572			112.039304	56.523290	E							10
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1077.568734	539.288005	1060.542185	530.774731	1059.558169	530.282723	9
3	372.151374	186.579325	355.124825	178.066051	354.140809	177.574043	N	***949.510156***	475.258716	932.483607	466.745442	931.499591	466.253434	8
4	459.183402	230.095339	442.156853	221.582065	441.172837	221.090057	S	835.467229	418.237253	818.440680	409.723978	817.456664	409.231970	7
5	556.236166	278.621721	539.209617	270.108447	538.225601	269.616439	P	***748.435201***	374.721239	731.408652	366.207964	730.424636	365.715956	6
6	669.320230	335.163753	652.293681	326.650479	651.309665	326.158471	I	***651.382437***	326.194857	634.355888	317.681582	633.371872	317.189574	5
7	832.383559	416.695418	815.357010	408.182143	814.372994	407.690135	Y	***538.298373***	269.652825	521.271824	261.139550	520.287808	260.647542	4
8	945.467623	473.237450	928.441074	464.724175	927.457058	464.232167	I	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
9	1032.499651	516.753464	1015.473102	508.240189	1014.489086	507.748181	S	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
10							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of EQNSPIYISR
(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	1205.604019	-0.002511	EQNSPIYISR
4.3	1205.607407	-0.005899	AEMLPKTSGTR
2.5	1205.596161	0.005347	VANSEAMILDK
0.4	1205.611435	-0.009927	LSWVQAMDLK
0.0	1205.590317	0.011191	CPHLLDFFK

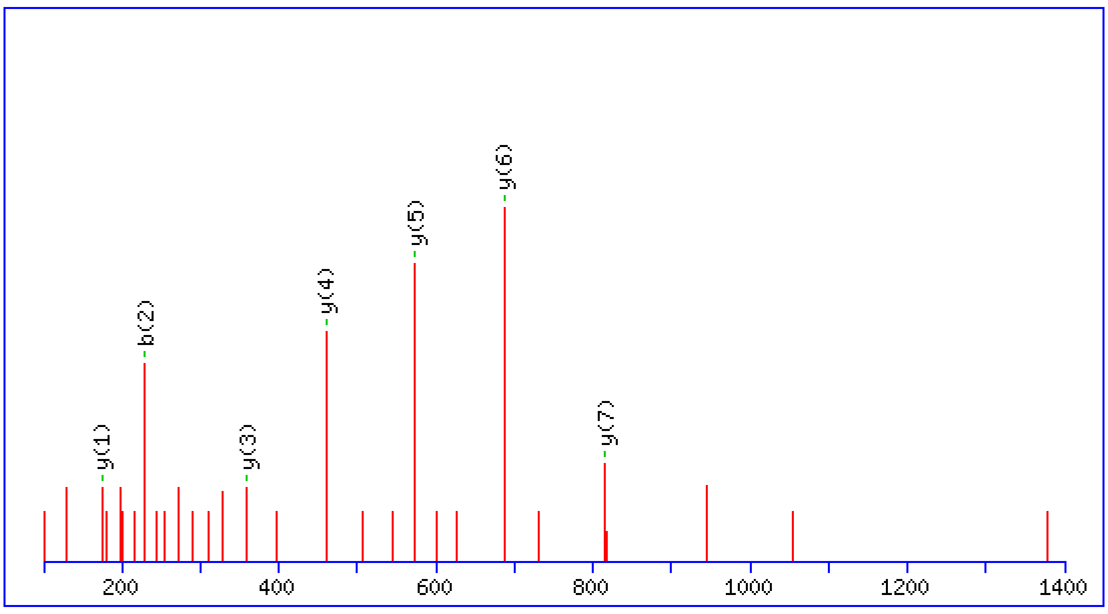
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEILTALR**
Found in **LZIC_HUMAN**, Protein LZIC OS=Homo sapiens GN=LZIC PE=1 SV=1

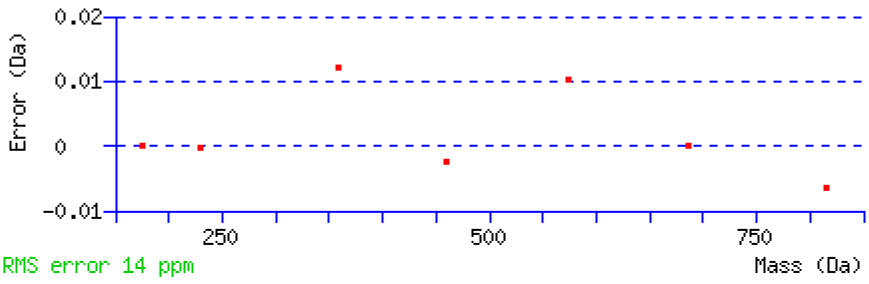
Match to Query 6237: 913.558708 from(457.786630,2+) rtinseconds(2673) index(25050)
Title: Locus:1.1.1.2515.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

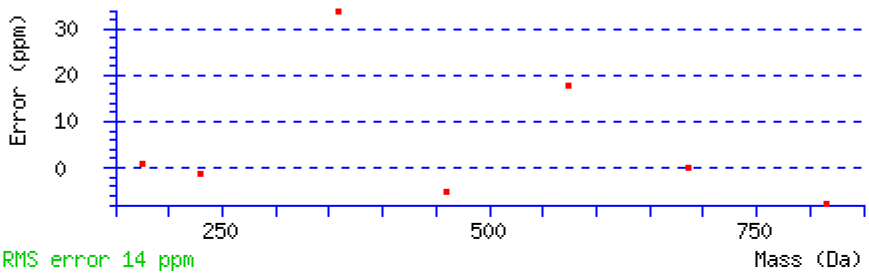
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 913.559647
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 1.7e-005
Matches : 7/62 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							8
2	229.118283	115.062780	211.107718	106.057497	E	***815.498530***	408.252903	798.471981	399.739629	797.487965	399.247621	7
3	342.202347	171.604812	324.191782	162.599529	I	***686.455937***	343.731607	669.429388	335.218332	668.445372	334.726324	6
4	455.286411	228.146844	437.275846	219.141561	L	***573.371873***	287.189575	556.345324	278.676300	555.361308	278.184292	5
5	556.334090	278.670683	538.323525	269.665401	T	***460.287809***	230.647542	443.261260	222.134268	442.277244	221.642260	4
6	627.371204	314.189240	609.360639	305.183958	A	***359.240130***	180.123703	342.213581	171.610429			3
7	740.455268	370.731272	722.444703	361.725990	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 VEILTALR
(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	913.559647	-0.000939	VEILTALR
26.1	913.559647	-0.000939	ELVITIAR
9.0	913.559647	-0.000939	TLILDALR
3.8	913.567032	-0.008324	MLPLSLLK
2.8	913.559647	-0.000939	ITVLEALR
1.8	913.559631	-0.000923	DLINLAKK
1.3	913.559647	-0.000939	LISLPLSR
0.8	913.559647	-0.000939	VEAGKVAIK
0.6	913.559631	-0.000923	VENLIAKK

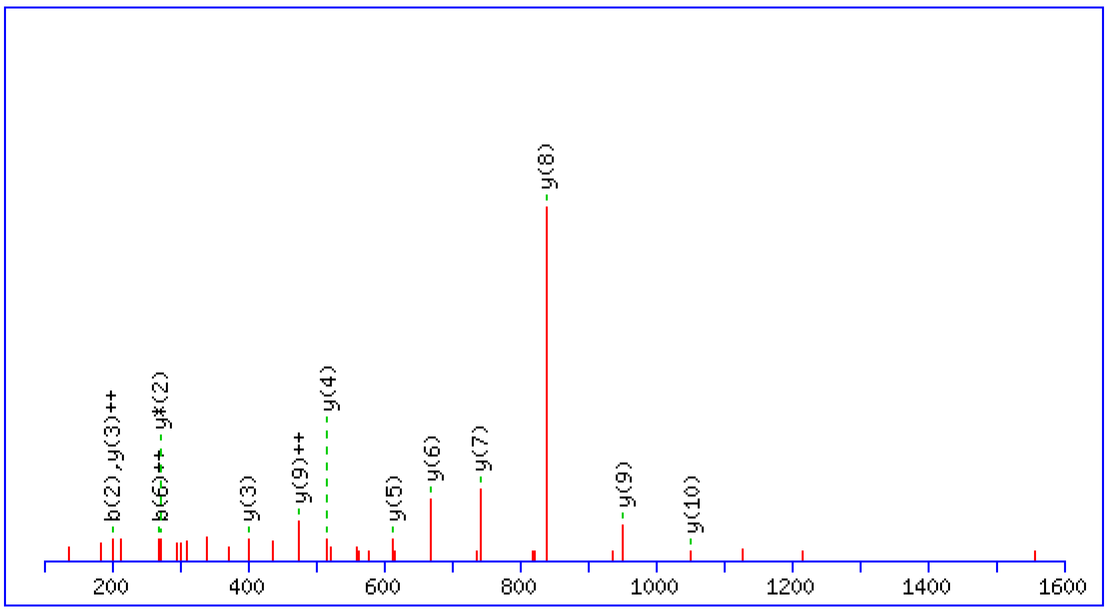
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLPAGPDILR**
Found in **MAL2_HUMAN**, Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1

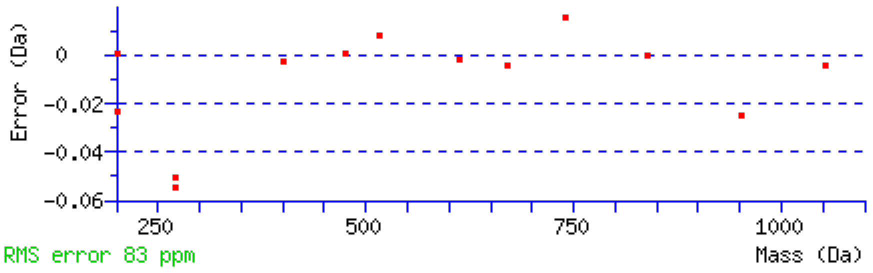
Match to Query 11549: 1150.670828 from(576.342690,2+) rtinseconds(2843) index(19668)
Title: Locus:1.1.1.2667.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

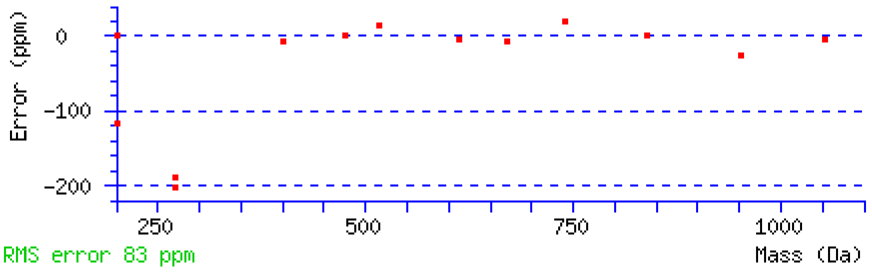
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1150.671005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 62  Expect: 2.2e-006
Matches : 13/92 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	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
62.2	1150.671005	-0.000177	VTLPAGPDILR
2.2	1150.659760	0.011068	SLLLTVSQYK
0.1	1150.682236	-0.011408	ELAVVTHRVK

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

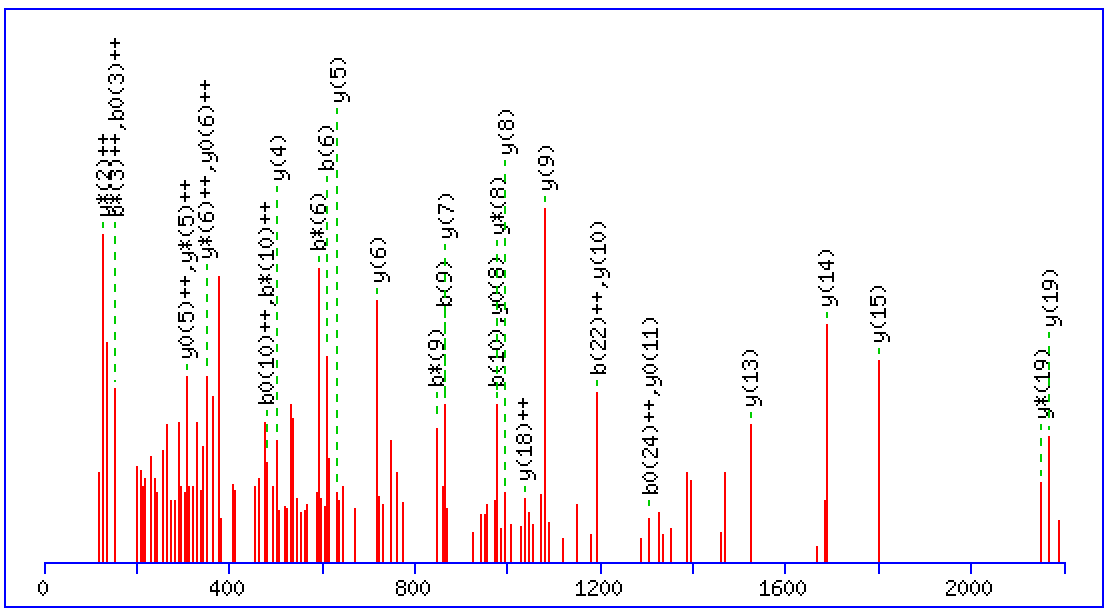
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TKPPLAPGTILYEAELSQFSEDIKK**
Found in **NIBAN_HUMAN**, Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1

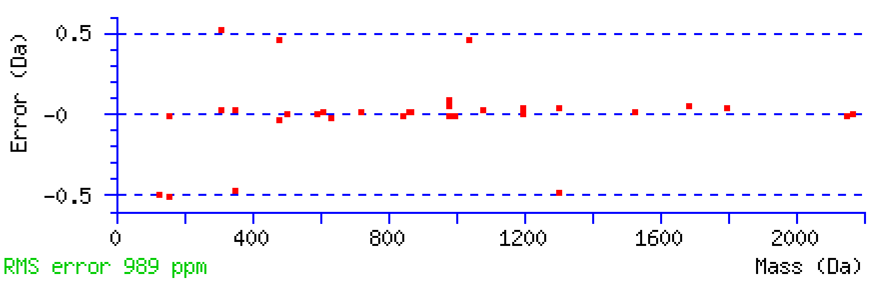
Match to Query 70437: 2774.484776 from(694.628470,4+) rtinseconds(3492) index(50041)
Title: Locus:1.1.1.2780.12
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

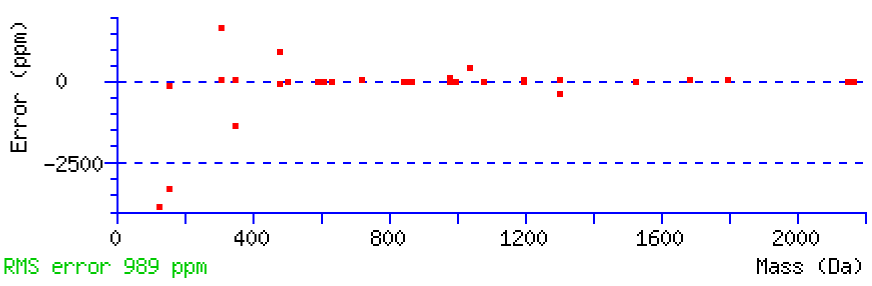
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2774.474167
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 4.5e-005
Matches : 32/280 fragment ions using 49 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							25
2	230.149918	115.578597	213.123369	107.065323	212.139353	106.573315	K	2674.433812	1337.720544	2657.407263	1329.207269	2656.423247	1328.715261	24
3	327.202682	164.104979	310.176133	155.591705	309.192117	155.099697	P	2546.338849	1273.673062	2529.312300	1265.159788	2528.328284	1264.667780	23
4	424.255446	212.631361	407.228897	204.118087	406.244881	203.626079	P	2449.286085	1225.146680	2432.259536	1216.633406	2431.275520	1216.141398	22
5	537.339510	269.173393	520.312961	260.660119	519.328945	260.168111	L	2352.233321	1176.620298	2335.206772	1168.107024	2334.222756	1167.615016	21
6	**608.376624**	304.691950	591.350075	296.178676	590.366059	295.686668	A	2239.149257	1120.078266	2222.122708	1111.564992	2221.138692	1111.072984	20
7	705.429388	353.218332	688.402839	344.705058	687.418823	344.213050	P	***2168.112143***	1084.559709	2151.085594	1076.046435	2150.101578	1075.554427	19
8	762.450852	381.729064	745.424303	373.215790	744.440287	372.723782	G	2071.059379	1036.033327	2054.032830	1027.520053	2053.048814	1027.028045	18
9	**863.498531**	432.252904	846.471982	423.739629	845.487966	423.247621	T	2014.037915	1007.522596	1997.011366	999.009321	1996.027350	998.517313	17
10	**976.582595**	488.794936	959.556046	480.281661	958.572030	479.789653	I	1912.990236	956.998756	1895.963687	948.485482	1894.979671	947.993474	16
11	1089.666659	545.336968	1072.640110	536.823693	1071.656094	536.331685	L	***1799.906172***	900.456724	1782.879623	891.943450	1781.895607	891.451442	15
12	1252.729988	626.868632	1235.703439	618.355358	1234.719423	617.863350	Y	***1686.822108***	843.914692	1669.795559	835.401418	1668.811543	834.909410	14
13	1381.772581	691.389929	1364.746032	682.876654	1363.762016	682.384646	E	***1523.758779***	762.383028	1506.732230	753.869753	1505.748214	753.377745	13
14	1452.809695	726.908486	1435.783146	718.395211	1434.799130	717.903203	A	1394.716186	697.861731	1377.689637	689.348457	1376.705621	688.856448	12
15	1581.852288	791.429782	1564.825739	782.916508	1563.841723	782.424500	E	1323.679072	662.343174	1306.652523	653.829900	1305.668507	653.337891	11
16	1694.936352	847.971814	1677.909803	839.458540	1676.925787	838.966532	L	***1194.636479***	597.821878	1177.609930	589.308603	1176.625914	588.816595	10
17	1781.968380	891.487828	1764.941831	882.974554	1763.957815	882.482546	S	***1081.552415***	541.279846	1064.525866	532.766571	1063.541850	532.274563	9
18	1910.026958	955.517117	1893.000409	947.003843	1892.016393	946.511835	Q	***994.520387***	497.763832	977.493838	489.250557	976.509822	488.758549	8
19	2057.095372	1029.051324	2040.068823	1020.538049	2039.084807	1020.046041	F	***866.461809***	433.734543	849.435260	425.221268	848.451244	424.729260	7
20	2144.127400	1072.567338	2127.100851	1064.054063	2126.116835	1063.562055	S	***719.393395***	360.200336	702.366846	351.687061	701.382830	351.195053	6
21	2273.169993	1137.088634	2256.143444	1128.575360	2255.159428	1128.083352	E	***632.361367***	316.684322	615.334818	308.171047	614.350802	307.679039	5
22	2388.196936	1194.602106	2371.170387	1186.088831	2370.186371	1185.596823	D	***503.318774***	252.163025	486.292225	243.649750	485.308209	243.157742	4
23	2501.281000	1251.144138	2484.254451	1242.630863	2483.270435	1242.138855	I	388.291831	194.649554	371.265282	186.136279			3
24	2629.375963	1315.191619	2612.349414	1306.678345	2611.365398	1306.186337	K	275.207767	138.107521	258.181218	129.594247			2
25							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of TKPPLAPGTILYEAELSQFSEDIKK
(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	2774.474167	0.010609	TKPPLAPGTILYEAELSQFSEDIKK
5.7	2774.471527	0.013249	LDALLSEPIPIHGRGNFPTLSVQPR

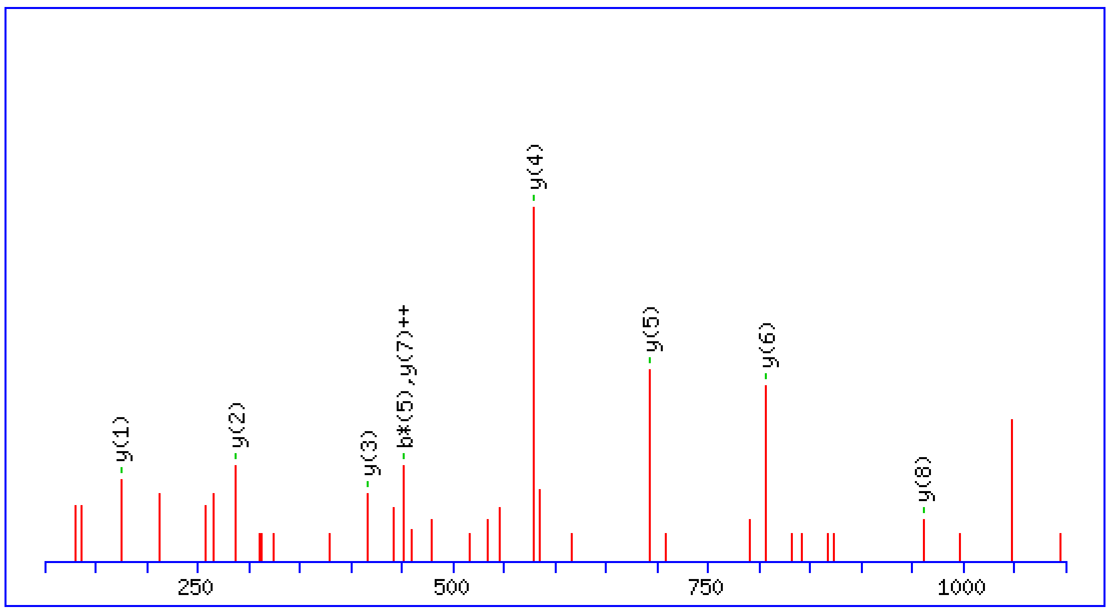
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGPNIYELR**
Found in **NIPS2_HUMAN**, Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1

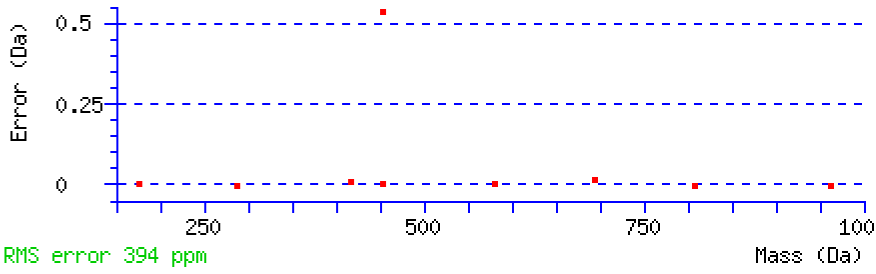
Match to Query 15845: 1047.536848 from(524.775700,2+) rtinseconds(2241) index(23916)
Title: Locus:1.1.1.2384.16
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

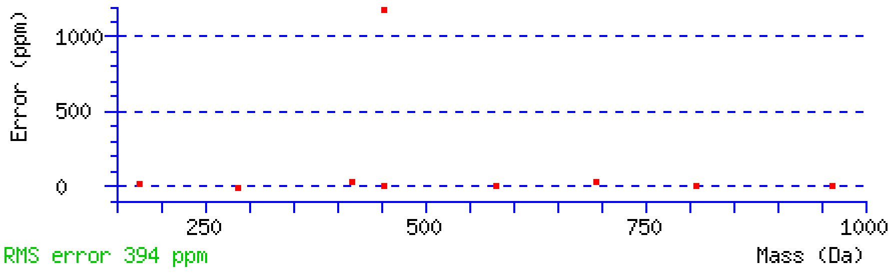
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1047.534882
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66  Expect: 3.9e-006
Matches : 9/86 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	88.039304	44.523290			70.028739	35.518008	**S**							9
2	145.060768	73.034022			127.050203	64.028740	**G**	***961.510157***	481.258717	944.483608	472.745442	943.499592	472.253434	8
3	242.113532	121.560404			224.102967	112.555121	**P**	904.488693	452.747985	887.462144	444.234710	886.478128	443.742702	7
4	356.156459	178.581867	339.129910	170.068593	338.145894	169.576585	**N**	***807.435929***	404.221603	790.409380	395.708328	789.425364	395.216320	6
5	469.240523	235.123899	452.213974	226.610625	451.229958	226.118617	**I**	***693.393002***	347.200139	676.366453	338.686865	675.382437	338.194857	5
6	632.303852	316.655564	615.277303	308.142290	614.293287	307.650282	**Y**	***580.308938***	290.658107	563.282389	282.144833	562.298373	281.652825	4
7	761.346445	381.176861	744.319896	372.663586	743.335880	372.171578	**E**	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
8	874.430509	437.718893	857.403960	429.205618	856.419944	428.713610	**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 SGPNIYELR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.3	1047.534882	0.001966	SGPNIYELR
10.1	1047.534882	0.001966	KLPEYNPR
10.1	1047.534897	0.001951	KPQDYIPR
9.8	1047.534897	0.001951	QLFQDLER
6.3	1047.538254	-0.001406	SKEEVMAVR
5.5	1047.538254	-0.001406	IMAKTSEPR
4.9	1047.538254	-0.001406	SLENLGMLR
4.9	1047.538254	-0.001406	SLGENMIIR
4.9	1047.534897	0.001951	SEVNLPFSR
3.7	1047.534897	0.001951	QAFLAETPR

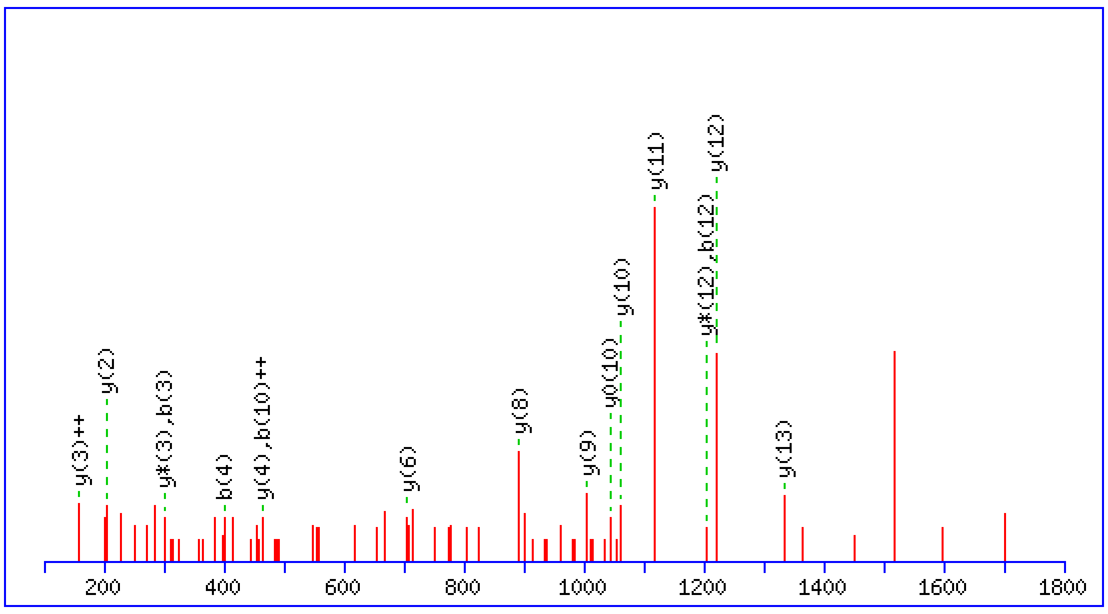
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVLTGGLDALEFIGK**
Found in **NXP20_HUMAN**, Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2

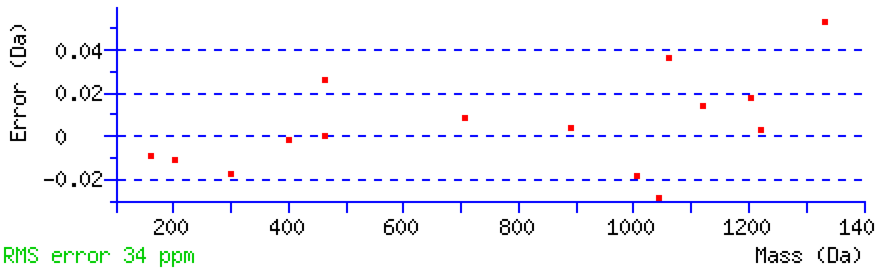
Match to Query 31538: 1518.835168 from(760.424860,2+) rtinseconds(3972) index(50198)
Title: Locus:1.1.1.3446.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

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 ●

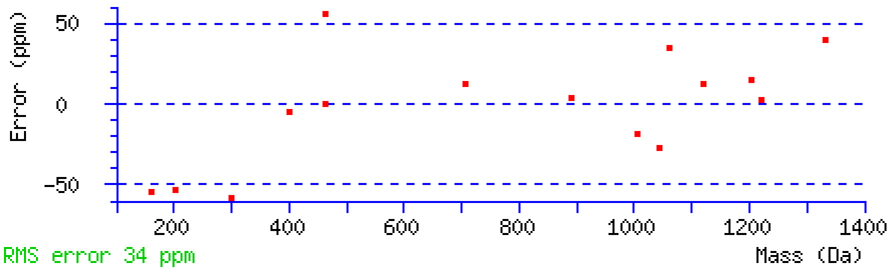


Monoisotopic mass of neutral peptide Mr(calc): 1518.829361
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.00018
Matches : 17/132 fragment ions using 33 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290	70.028739	35.518008	S							15
2	187.107718	94.057497	169.097153	85.052214	V	1432.804609	716.905943	1415.778060	708.392668	1414.794044	707.900660	14
3	**300.191782**	150.599529	282.181217	141.594247	L	***1333.736195***	667.371736	1316.709646	658.858461	1315.725630	658.366453	13
4	**401.239461**	201.123369	383.228896	192.118086	T	***1220.652131***	610.829704	1203.625582	602.316429	1202.641566	601.824421	12
5	458.260925	229.634100	440.250360	220.628818	G	***1119.604452***	560.305864	1102.577903	551.792590	1101.593887	551.300582	11
6	515.282389	258.144833	497.271824	249.139550	G	***1062.582988***	531.795132	1045.556439	523.281858	1044.572423	522.789850	10
7	628.366453	314.686865	610.355888	305.681582	L	***1005.561524***	503.284400	988.534975	494.771126	987.550959	494.279118	9
8	743.393396	372.200336	725.382831	363.195054	D	***892.477460***	446.742368	875.450911	438.229094	874.466895	437.737086	8
9	814.430510	407.718893	796.419945	398.713611	A	777.450517	389.228897	760.423968	380.715622	759.439952	380.223614	7
10	927.514574	464.260925	909.504009	455.255643	L	***706.413403***	353.710340	689.386854	345.197065	688.402838	344.705057	6
11	1056.557167	528.782222	1038.546602	519.776939	E	593.329339	297.168308	576.302790	288.655033	575.318774	288.163025	5
12	**1203.625581**	602.316429	1185.615016	593.311146	F	***464.286746***	232.647011	447.260197	224.133736			4
13	1316.709645	658.858461	1298.699080	649.853178	I	317.218332	159.112804	300.191783	150.599529			3
14	1373.731109	687.369193	1355.720544	678.363910	G	***204.134268***	102.570772	187.107719	94.057497			2
15					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 34 ppm



RMS error 34 ppm

NCBI **BLAST** search of SVLTGGLDALEFIGK
(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	1518.829361	0.005807	SVLTGGLDALEFIGK

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

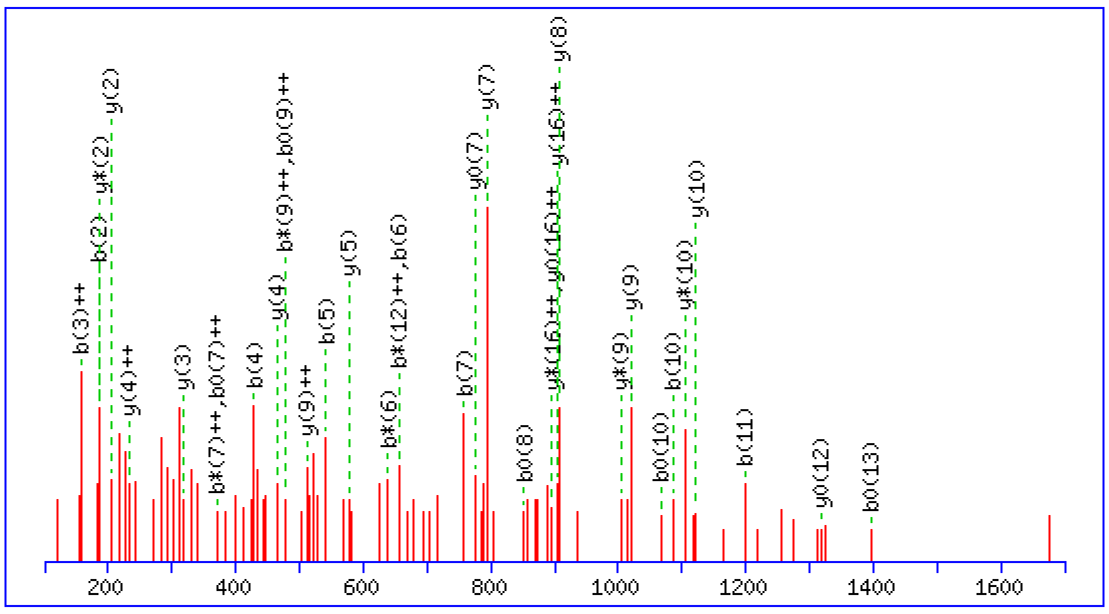
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AIENIDTLTNLESLFLGK**
Found in **PP1R7_HUMAN**, Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1

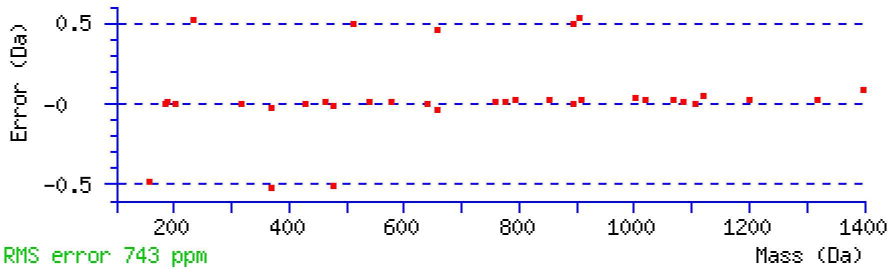
Match to Query 25732: 1990.076052 from(664.365960,3+) rtinseconds(4630) index(69995)
Title: Locus:1.1.1.3281.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

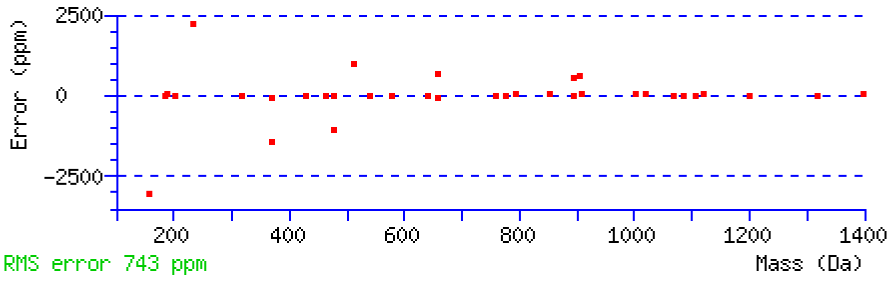
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1990.062241
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0014
Matches : 35/184 fragment ions using 84 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	***185.128454***	93.067865					I	1920.032435	960.519855	1903.005886	952.006581	1902.021870	951.514573	17
3	314.171047	157.589161			296.160482	148.583879	E	1806.948371	903.977823	1789.921822	895.464549	1788.937806	894.972541	16
4	***428.213974***	214.610625	411.187425	206.097351	410.203409	205.605343	N	1677.905778	839.456527	1660.879229	830.943252	1659.895213	830.451244	15
5	***541.298038***	271.152657	524.271489	262.639383	523.287473	262.147375	I	1563.862851	782.435063	1546.836302	773.921789	1545.852286	773.429781	14
6	***656.324981***	328.666129	639.298432	320.152854	638.314416	319.660846	D	1450.778787	725.893032	1433.752238	717.379757	1432.768222	716.887749	13
7	***757.372660***	379.189968	740.346111	370.676694	739.362095	370.184686	T	1335.751844	668.379560	1318.725295	659.866286	1317.741279	659.374277	12
8	870.456724	435.732000	853.430175	427.218726	852.446159	426.726718	L	1234.704165	617.855720	1217.677616	609.342446	1216.693600	608.850438	11
9	971.504403	486.255840	954.477854	477.742565	953.493838	477.250557	T	***1121.620101***	561.313688	1104.593552	552.800414	1103.609536	552.308406	10
10	***1085.547330***	543.277303	1068.520781	534.764029	1067.536765	534.272021	N	***1020.572422***	510.789849	1003.545873	502.276574	1002.561857	501.784566	9
11	***1198.631394***	599.819335	1181.604845	591.306061	1180.620829	590.814053	L	***906.529495***	453.768385	889.502946	445.255111	888.518930	444.763103	8
12	1327.673987	664.340631	1310.647438	655.827357	1309.663422	655.335349	E	***793.445431***	397.226353	776.418882	388.713079	775.434866	388.221071	7
13	1414.706015	707.856646	1397.679466	699.343371	1396.695450	698.851363	S	664.402838	332.705057	647.376289	324.191782	646.392273	323.699774	6
14	1527.790079	764.398677	1510.763530	755.885403	1509.779514	755.393395	L	***577.370810***	289.189043	560.344261	280.675768			5
15	1674.858493	837.932885	1657.831944	829.419610	1656.847928	828.927602	F	***464.286746***	232.647011	447.260197	224.133736			4
16	1787.942557	894.474916	1770.916008	885.961642	1769.931992	885.469634	L	***317.218332***	159.112804	300.191783	150.599529			3
17	1844.964021	922.985648	1827.937472	914.472374	1826.953456	913.980366	G	***204.134268***	102.570772	187.107719	94.057497			2
18							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of AIENIDTLTNLESLFLGK
(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	1990.062241	0.013811	AIENIDTLTNLESLFLGK

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

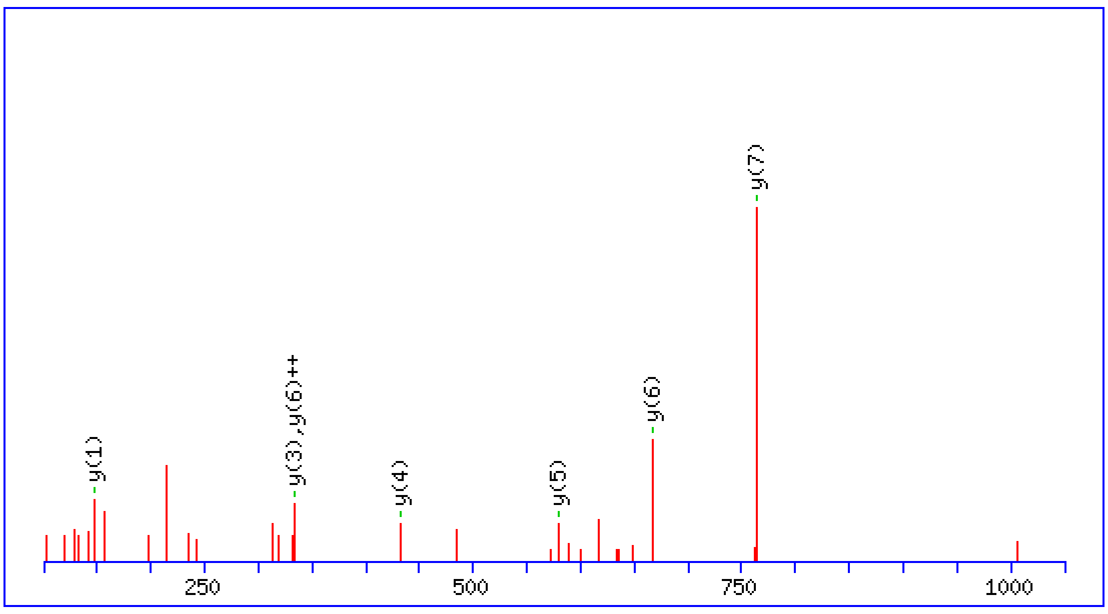
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELPSFVGEK**
Found in **S10A2_HUMAN**, Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3

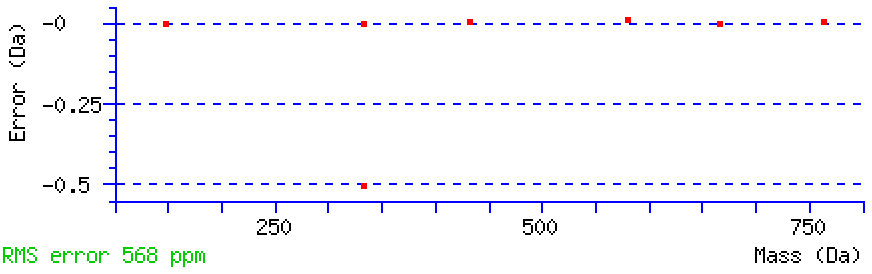
Match to Query 7425: 1004.518448 from(503.266500,2+) rtinseconds(2347) index(4707)
Title: Locus:1.1.1.2950.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-8.mgf

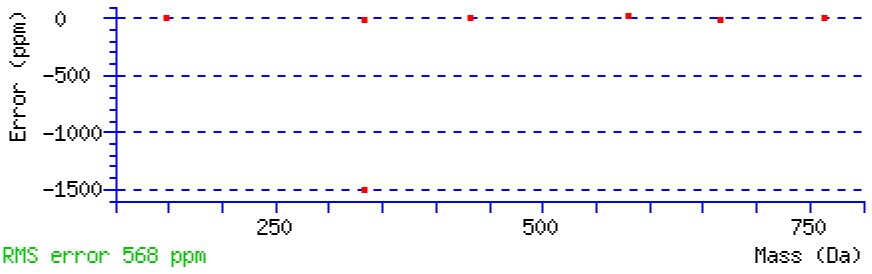
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1004.517853
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 1.5e-005
Matches : 7/78 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	243.133933	122.070605	225.123368	113.065322	L	876.482545	438.744911	859.455996	430.231636	858.471980	429.739628	8
3	340.186697	170.596987	322.176132	161.591704	P	***763.398481***	382.202879	746.371932	373.689604	745.387916	373.197596	7
4	427.218725	214.113001	409.208160	205.107718	S	***666.345717***	333.676497	649.319168	325.163222	648.335152	324.671214	6
5	574.287139	287.647208	556.276574	278.641925	F	***579.313689***	290.160483	562.287140	281.647208	561.303124	281.155200	5
6	673.355553	337.181415	655.344988	328.176132	V	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
7	730.377017	365.692147	712.366452	356.686864	G	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
8	859.419610	430.213443	841.409045	421.208161	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 ELPSFVGEK
(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	1004.517853	0.000595	ELPSFVGEK
8.5	1004.525055	-0.006607	KNATTQNTK
4.7	1004.521194	-0.002746	IEMDKLEK
4.4	1004.511978	0.006470	FPLEWWK
1.9	1004.517838	0.000610	IEPLNEFK
1.9	1004.517838	0.000610	LEKFPDEK
0.9	1004.515167	0.003281	GPAPRHADGK

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

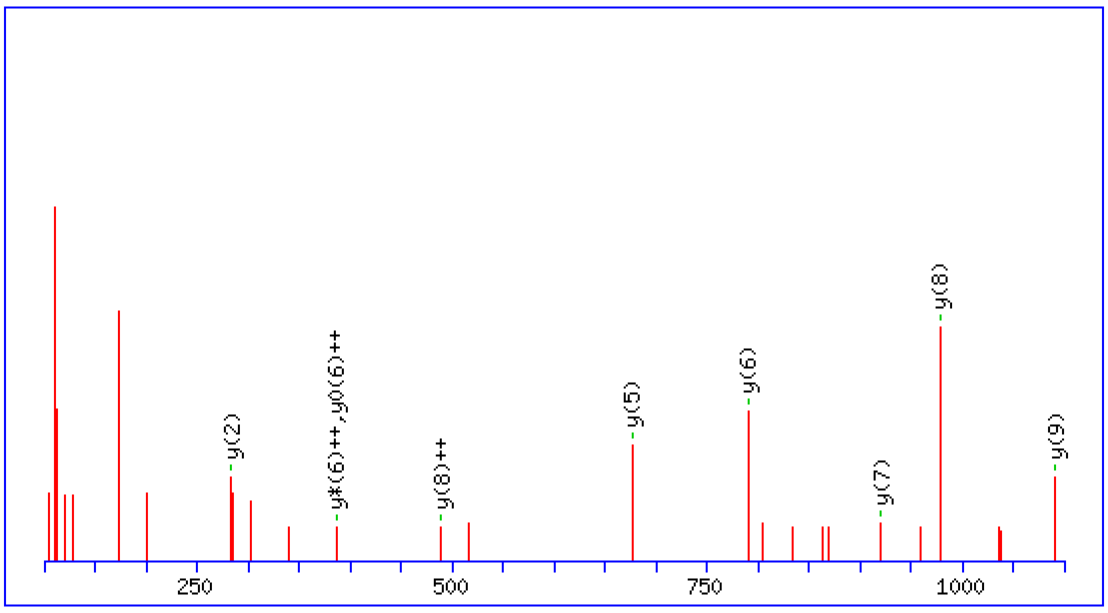
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIIGMIDMFHK**
Found in **S10A7_HUMAN**, Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4

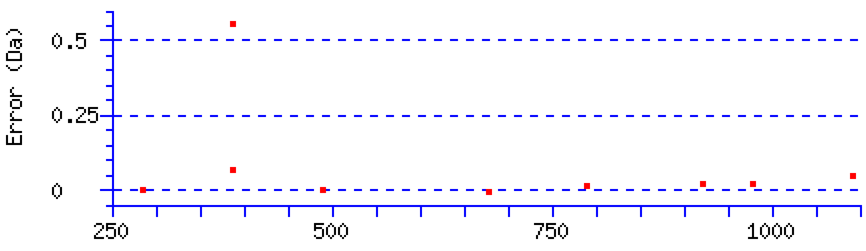
Match to Query 28925: 1290.641022 from(431.220950,3+) rtinseconds(3565) index(54604)
Title: Locus:1.1.1.2004.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

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 ●

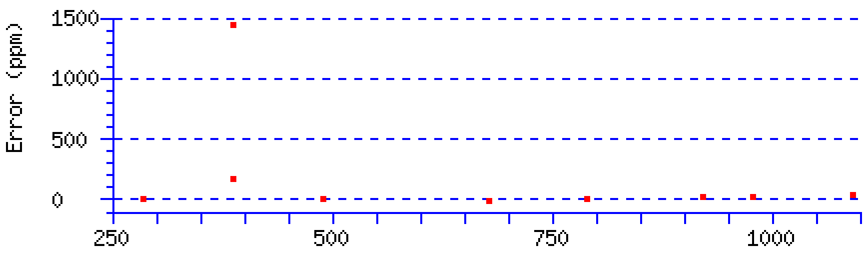


```
Monoisotopic mass of neutral peptide Mr(calc): 1290.646439
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0047
Matches : 9/92 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290	70.028739	35.518008	S							11
2	201.123368	101.065322	183.112803	92.060039	I	1204.621699	602.814487	1187.595150	594.301213	1186.611134	593.809205	10
3	314.207432	157.607354	296.196867	148.602071	I	***1091.537635***	546.272455	1074.511086	537.759181	1073.527070	537.267173	9
4	371.228896	186.118086	353.218331	177.112803	G	***978.453571***	489.730423	961.427022	481.217149	960.443006	480.725141	8
5	502.269381	251.638328	484.258816	242.633046	M	***921.432107***	461.219691	904.405558	452.706417	903.421542	452.214409	7
6	615.353445	308.180361	597.342880	299.175078	I	***790.391622***	395.699449	773.365073	387.186174	772.381057	386.694166	6
7	730.380388	365.693832	712.369823	356.688549	D	***677.307558***	339.157417	660.281009	330.644142	659.296993	330.152134	5
8	861.420873	431.214074	843.410308	422.208792	M	562.280615	281.643946	545.254066	273.130671			4
9	1008.489287	504.748281	990.478722	495.742999	F	431.240130	216.123703	414.213581	207.610428			3
10	1145.548199	573.277737	1127.537634	564.272455	H	***284.171716***	142.589496	267.145167	134.076221			2
11					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 483 ppm



RMS error 483 ppm

NCBI **BLAST** search of SIIGMIDMFHK
(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	1290.646439	-0.005417	SIIGMIDMFHK
6.2	1290.648941	-0.007919	SLGMAVEDTVAAK
1.7	1290.645569	-0.004547	KASETSPFPPAK

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

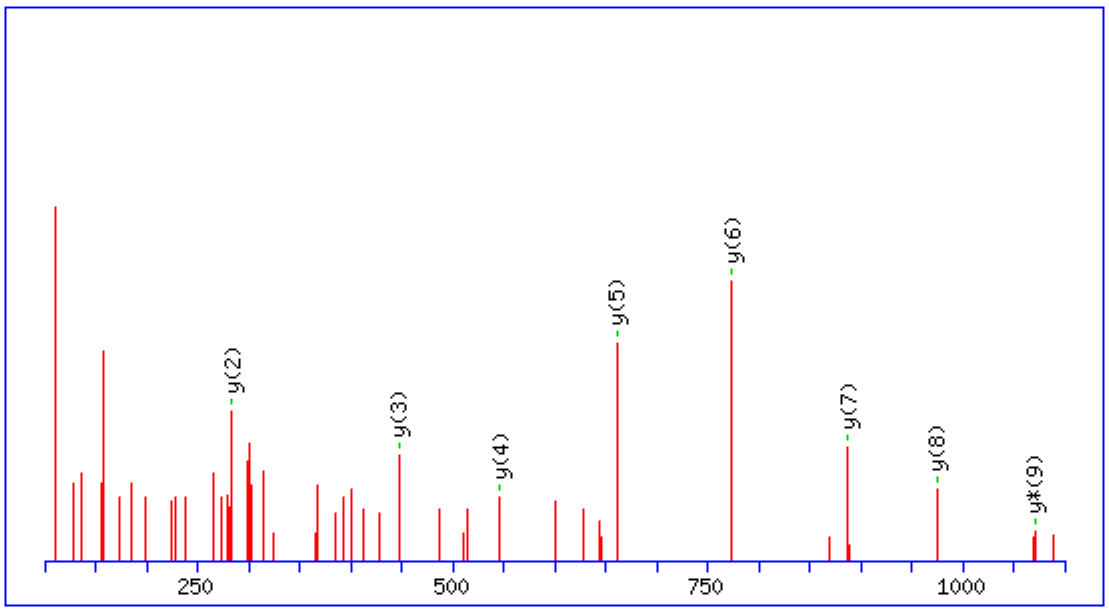
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALNSIIDVYHK**
Found in **S10A8_HUMAN**, Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1

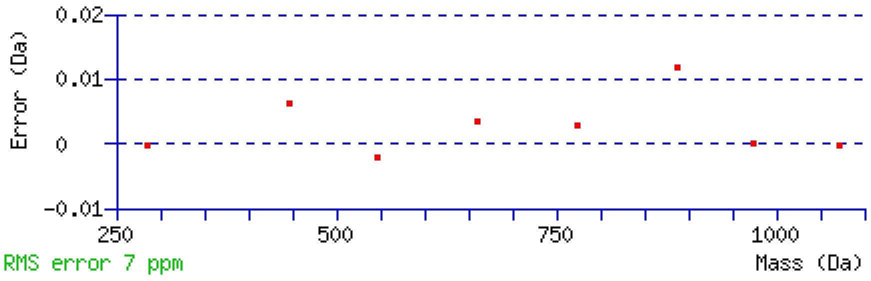
Match to Query 8359: 1271.688432 from(424.903420,3+) rtinseconds(2505) index(7919)
Title: Locus:1.1.1.2855.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

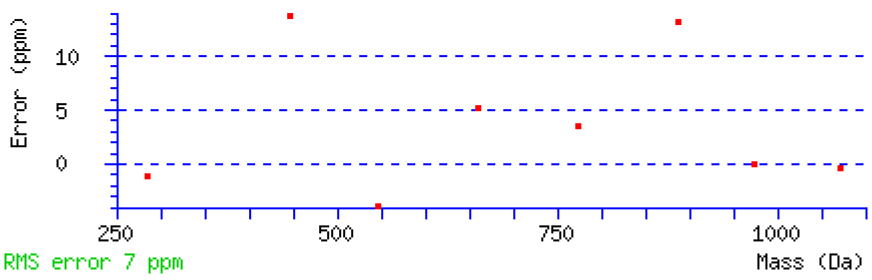
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1271.687363
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60  Expect: 3.8e-006
Matches : 8/102 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	72.044390	36.525833					A							11
2	185.128454	93.067865					L	1201.657549	601.332413	1184.631000	592.819138	1183.646984	592.327130	10
3	299.171381	150.089328	282.144832	141.576054			N	1088.573485	544.790381	1071.546936	536.277106	1070.562920	535.785098	9
4	386.203409	193.605343	369.176860	185.092068	368.192844	184.600060	S	***974.530558***	487.768917	957.504009	479.255642	956.519993	478.763634	8
5	499.287473	250.147375	482.260924	241.634100	481.276908	241.142092	I	***887.498530***	444.252903	870.471981	435.739628	869.487965	435.247620	7
6	612.371537	306.689407	595.344988	298.176132	594.360972	297.684124	I	***774.414466***	387.710871	757.387917	379.197596	756.403901	378.705588	6
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	D	***661.330402***	331.168839	644.303853	322.655564	643.319837	322.163556	5
8	826.466894	413.737085	809.440345	405.223811	808.456329	404.731803	V	***546.303459***	273.655368	529.276910	265.142093			4
9	989.530223	495.268750	972.503674	486.755475	971.519658	486.263467	Y	***447.235045***	224.121160	430.208496	215.607886			3
10	1126.589135	563.798205	1109.562586	555.284931	1108.578570	554.792923	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 ALNSIIDVYHK
(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	1271.687363	0.001069	ALNSIIDVYHK
2.1	1271.683334	0.005098	RTQLEEIQQK
1.8	1271.676804	0.011628	QQELLRQAMR

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

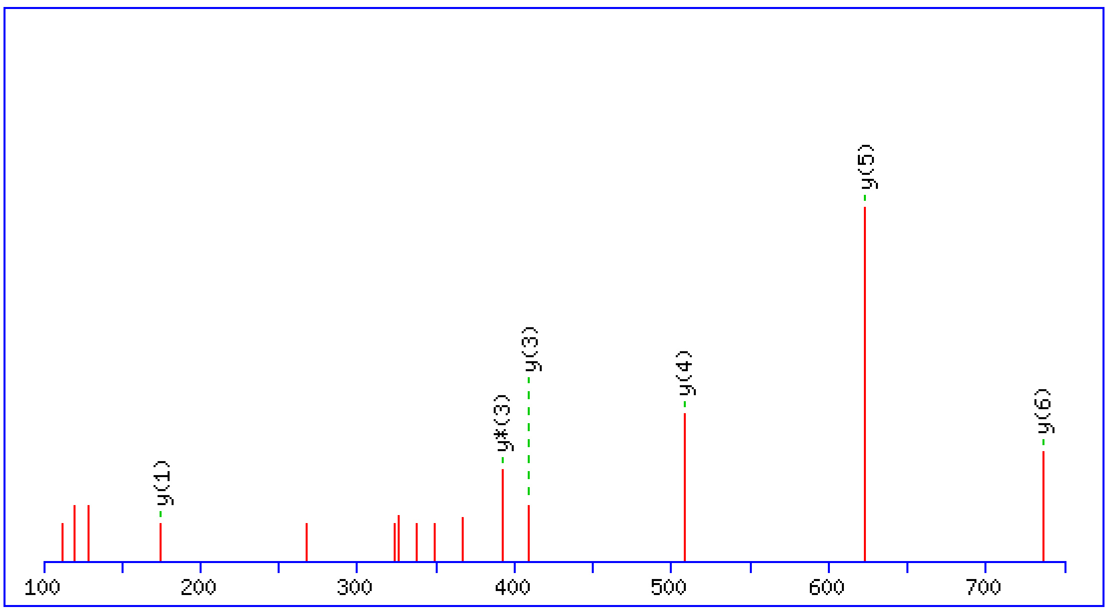
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIDVFSR**
Found in **S100P_HUMAN**, Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2

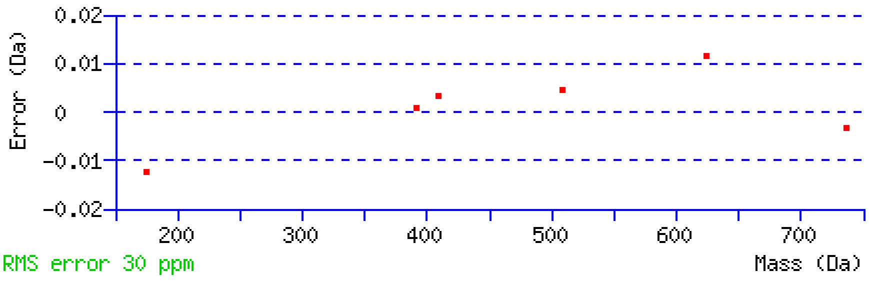
Match to Query 50180: 848.479068 from(425.246810,2+) rtinseconds(2527) index(961702)
Title: Locus:1.1.1.1477.2
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

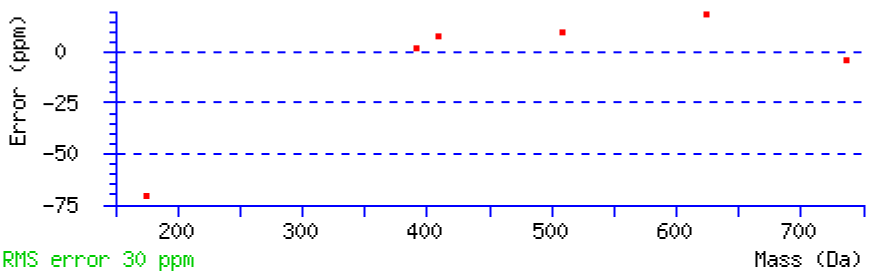
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 848.475601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0013
Matches : 6/54 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	227.175404	114.091340			I	***736.398815***	368.703046	719.372266	360.189771	718.388250	359.697763	6
3	342.202347	171.604811	324.191782	162.599529	D	***623.314751***	312.161014	606.288202	303.647739	605.304186	303.155731	5
4	441.270761	221.139018	423.260196	212.133736	V	***508.287808***	254.647542	491.261259	246.134268	490.277243	245.642260	4
5	588.339175	294.673226	570.328610	285.667943	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
6	675.371203	338.189240	657.360638	329.183957	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 IIDVFSR
(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	848.475601	0.003467	IIDVFSR
13.3	848.475601	0.003467	LPYSVVR
10.9	848.486801	-0.007733	ILREYR
10.9	848.486801	-0.007733	LLERYR
10.9	848.486801	-0.007733	LLREYR
10.9	848.475601	0.003467	LLSTFPR
9.8	848.475586	0.003482	KGYSPLGK
8.6	848.475586	0.003482	IEVGLYR
8.6	848.475601	0.003467	LVESVFR
3.5	848.478958	0.000110	LICTKSK

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

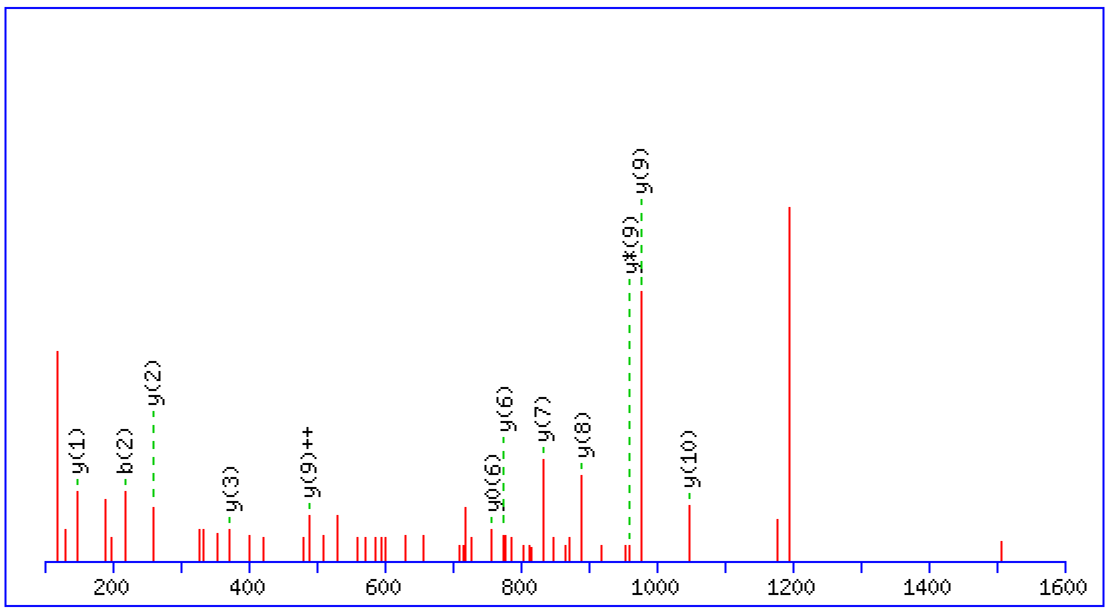
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FASGGCDNLIK**
Found in **SEC13_HUMAN**, Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3

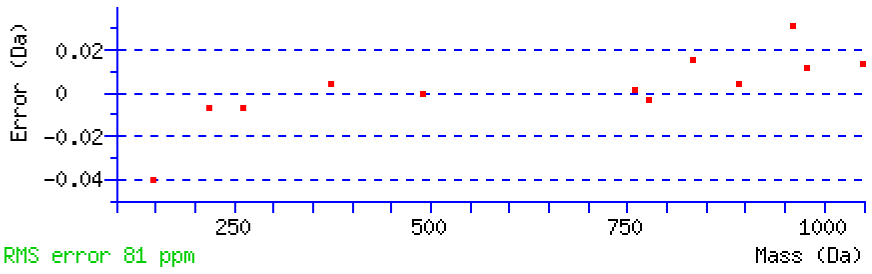
Match to Query 22749: 1194.580448 from(598.297500,2+) rtinseconds(1908) index(20778)
Title: Locus:1.1.1.2111.31
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

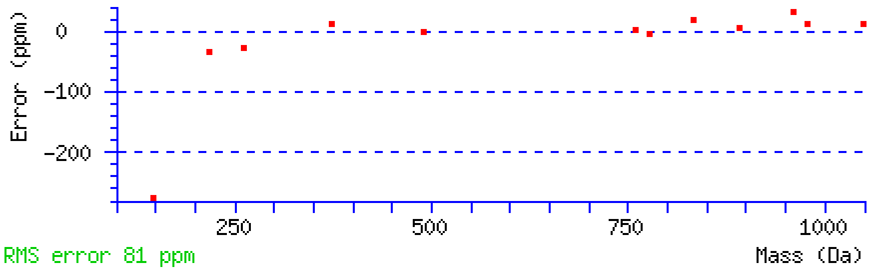
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1194.570297
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 7.9e-005
Matches : 12/94 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	148.075690	74.541483					F							11
2	219.112804	110.060040					A	***1048.509171***	524.758223	1031.482622	516.244949	1030.498606	515.752941	10
3	306.144832	153.576054			288.134267	144.570772	S	***977.472057***	489.239667	960.445508	480.726392	959.461492	480.234384	9
4	363.166296	182.086786			345.155731	173.081504	G	***890.440029***	445.723653	873.413480	437.210378	872.429464	436.718370	8
5	420.187760	210.597518			402.177195	201.592235	G	***833.418565***	417.212921	816.392016	408.699646	815.408000	408.207638	7
6	594.234059	297.620668			576.223494	288.615385	C	***776.397101***	388.702189	759.370552	380.188914	758.386536	379.696906	6
7	709.261002	355.134139			691.250437	346.128856	D	602.350802	301.679039	585.324253	293.165765	584.340237	292.673757	5
8	823.303929	412.155602	806.277380	403.642328	805.293364	403.150320	N	487.323859	244.165567	470.297310	235.652293			4
9	936.387993	468.697634	919.361444	460.184360	918.377428	459.692352	L	***373.280932***	187.144104	356.254383	178.630830			3
10	1049.472057	525.239667	1032.445508	516.726392	1031.461492	516.234384	I	***260.196868***	130.602072	243.170319	122.088798			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	1194.570297	0.010151	FASGGCDNLIK
2.7	1194.588043	-0.007595	EPENPSLHLK
2.4	1194.572784	0.007664	SSLNSISSSDAK
0.1	1194.575012	0.005436	MSRVHGMHPK

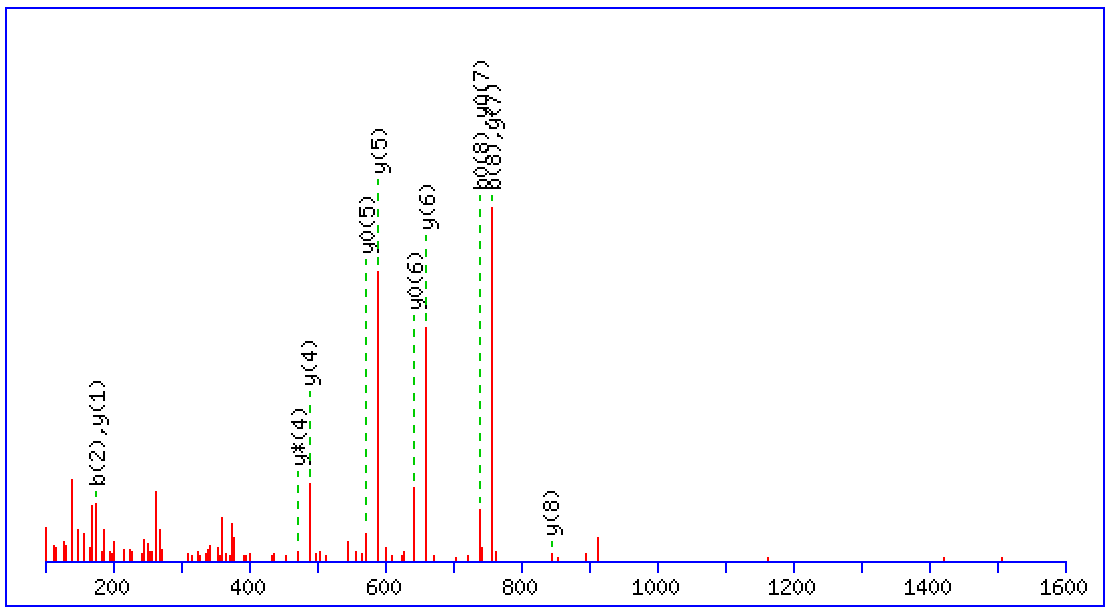
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SSPATADKR**
Found in **SHRM3_HUMAN**, Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2

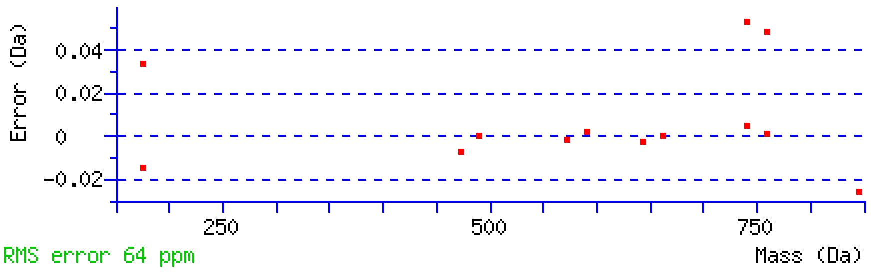
Match to Query 7536: 931.471748 from(466.743150,2+) rtinseconds(875) index(65)
Title: Locus:1.1.1.2005.4
Data file 2011-11-14 - TFD - S 2-8.mgf

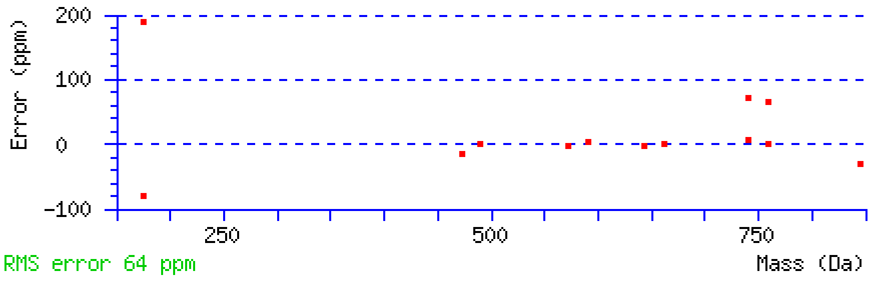
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 931.472290
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00017
Matches : 13/78 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	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
48.7	931.472290	-0.000542	SSPATADKR
23.1	931.479675	-0.007927	SLIMEAPR
17.5	931.465759	0.005989	CRPNLSR
13.0	931.479691	-0.007943	SLMPSIPR
12.2	931.479706	-0.007958	IMTTVDPR
12.2	931.472290	-0.000542	DQEAKVSR
11.0	931.466431	0.005317	NFPYHVR
9.4	931.472305	-0.000557	QSGIGLDSR
8.2	931.465775	0.005973	TQAGMRPR
8.1	931.472290	-0.000542	ASISPSSGAR

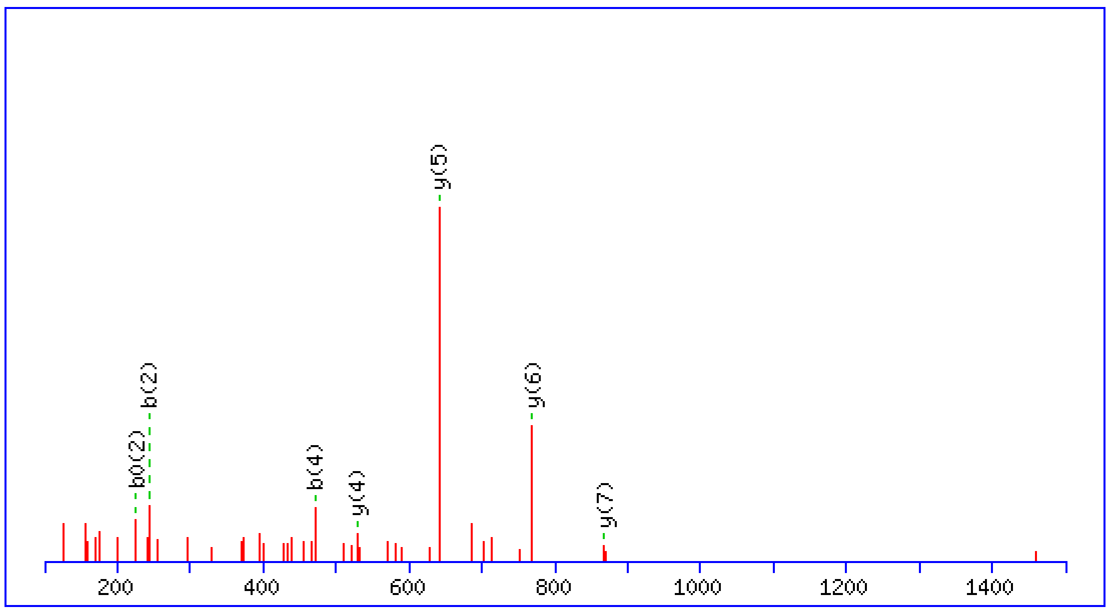
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENVQLMSYK**
Found in **SMG8_HUMAN**, Protein SMG8 OS=Homo sapiens GN=SMG8 PE=1 SV=1

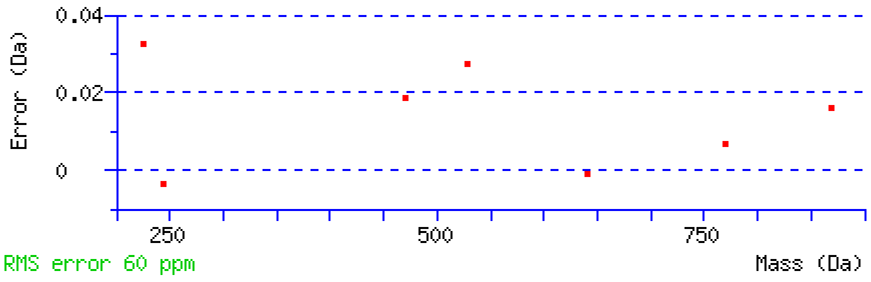
Match to Query 316338: 1110.544628 from(556.279590,2+) rtinseconds(895) index(172010)
Title: Locus:1.1.1.478.11
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

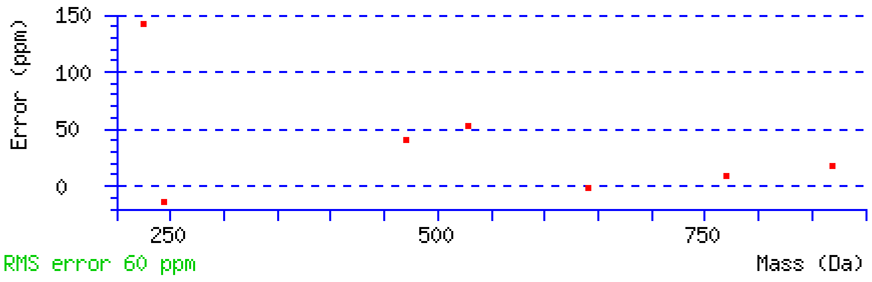
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1110.537918
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0072
Matches : 7/90 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	130.049869	65.528572			112.039304	56.523290	E							9
2	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	N	982.502629	491.754953	965.476080	483.241678	964.492064	482.749670	8
3	343.161210	172.084243	326.134661	163.570969	325.150645	163.078961	V	***868.459702***	434.733489	851.433153	426.220215	850.449137	425.728207	7
4	**471.219788**	236.113532	454.193239	227.600258	453.209223	227.108250	Q	***769.391288***	385.199282	752.364739	376.686008	751.380723	376.194000	6
5	584.303852	292.655564	567.277303	284.142290	566.293287	283.650282	L	***641.332710***	321.169993	624.306161	312.656719	623.322145	312.164711	5
6	715.344337	358.175807	698.317788	349.662532	697.333772	349.170524	M	***528.248646***	264.627961	511.222097	256.114687	510.238081	255.622679	4
7	802.376365	401.691821	785.349816	393.178546	784.365800	392.686538	S	397.208161	199.107719	380.181612	190.594444	379.197596	190.102436	3
8	965.439694	483.223485	948.413145	474.710211	947.429129	474.218203	Y	310.176133	155.591705	293.149584	147.078430			2
9							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ENVQLMSYK
(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	1110.537918	0.006710	ENVQLMSYK
13.7	1110.553009	-0.008381	EGAGPRGAGPAR
13.3	1110.537918	0.006710	NKDLIGSYAM
9.7	1110.541794	0.002834	GPVGGSDAAPQR
5.5	1110.549805	-0.005177	YGAWYLNPK
5.0	1110.541779	0.002849	RNEGAGGPPPK
1.9	1110.545822	-0.001194	GSVAGSSPFFR
1.7	1110.541779	0.002849	GALDGNSPPQR
1.5	1110.555695	-0.011067	GEDPELPGAVK
1.5	1110.541962	0.002666	LPLPYGFSAM

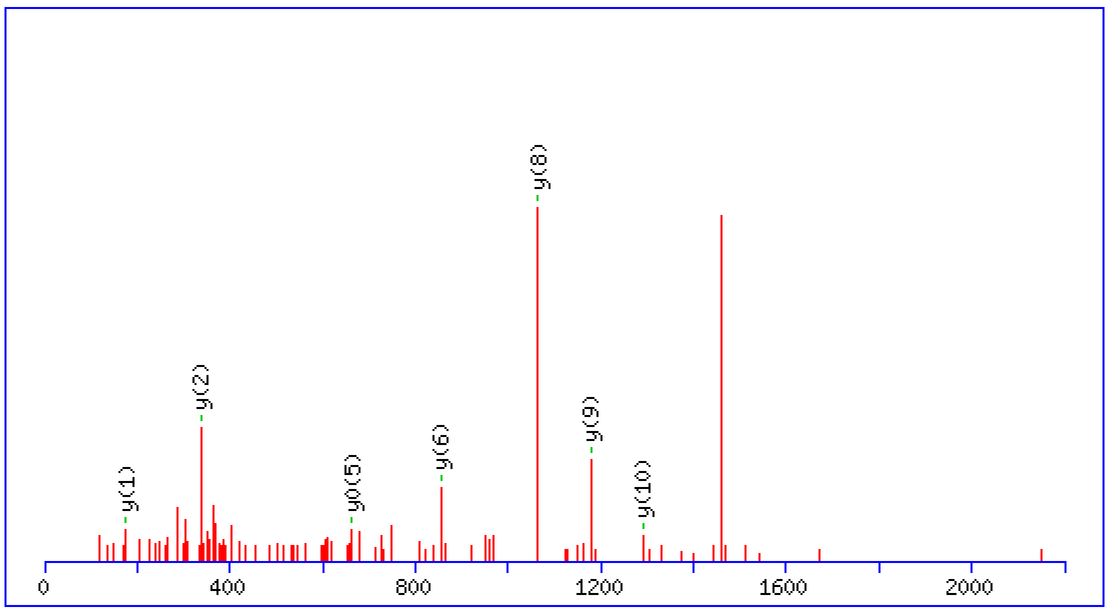
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLNPLCQVDYR**
Found in **SC23A_HUMAN**, Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2

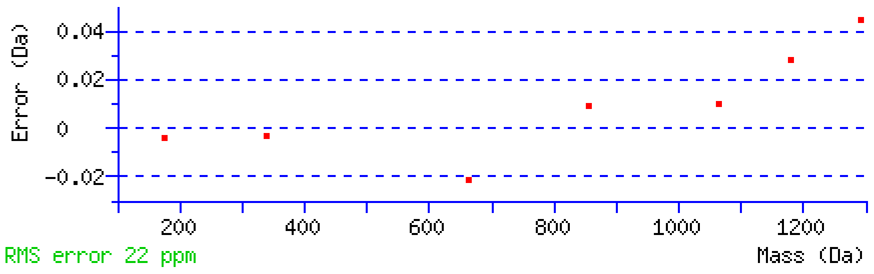
Match to Query 37485: 1460.749668 from(731.382110,2+) rtinseconds(2773) index(39514)
Title: Locus:1.1.1.1701.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

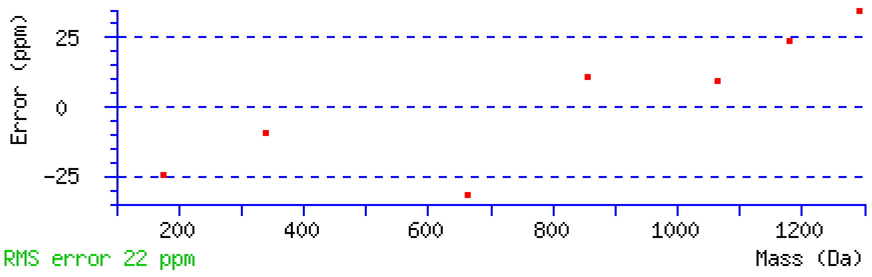
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1460.744568
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0027
Matches : 7/104 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							12
2	171.112804	86.060040					V	1390.714748	695.861012	1373.688199	687.347738	1372.704183	686.855730	11
3	284.196868	142.602072					L	***1291.646334***	646.326805	1274.619785	637.813531	1273.635769	637.321523	10
4	398.239795	199.623536	381.213246	191.110261			N	***1178.562270***	589.784773	1161.535721	581.271499	1160.551705	580.779491	9
5	495.292559	248.149918	478.266010	239.636643			P	***1064.519343***	532.763310	1047.492794	524.250035	1046.508778	523.758027	8
6	608.376623	304.691950	591.350074	296.178675			L	967.466579	484.236928	950.440030	475.723653	949.456014	475.231645	7
7	782.422922	391.715099	765.396373	383.201825			C	***854.382515***	427.694896	837.355966	419.181621	836.371950	418.689613	6
8	910.481500	455.744388	893.454951	447.231114			Q	680.336216	340.671746	663.309667	332.158472	662.325651	331.666464	5
9	1009.549914	505.278595	992.523365	496.765321			V	552.277638	276.642457	535.251089	268.129183	534.267073	267.637175	4
10	1124.576857	562.792067	1107.550308	554.278792	1106.566292	553.786784	D	453.209224	227.108250	436.182675	218.594975	435.198659	218.102967	3
11	1287.640186	644.323731	1270.613637	635.810457	1269.629621	635.318449	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 AVLNPLCQVDYR
(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	1460.744568	0.005100	AVLNPLCQVDYR
2.7	1460.762329	-0.012661	AVPPTYADLGKSAR
2.2	1460.752441	-0.002773	HQVPHIQQAFEK

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

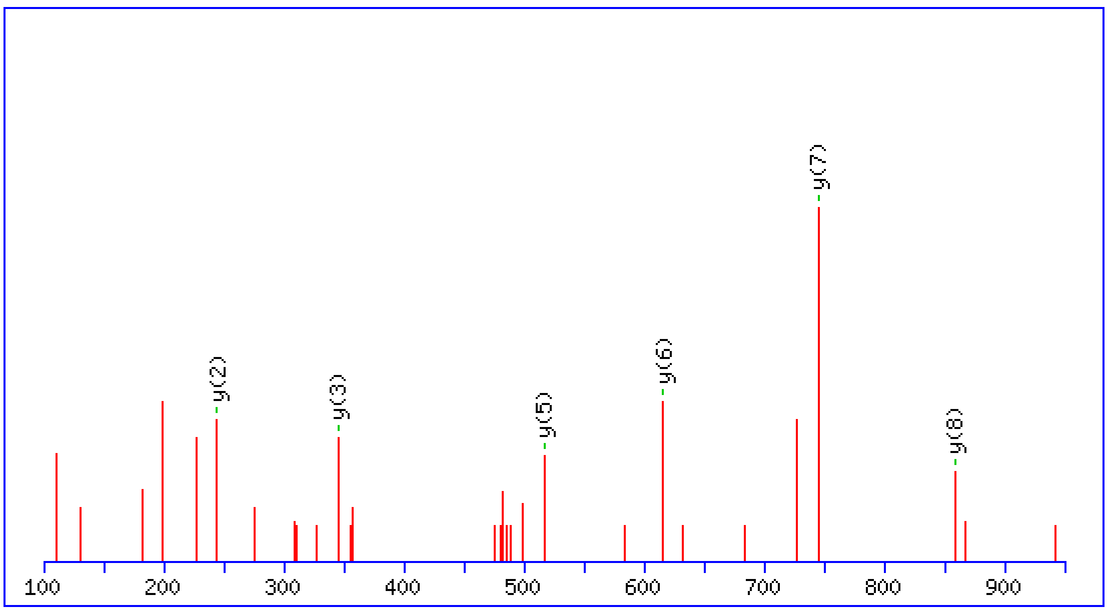
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIEVGDTPK**
Found in **S61A1_HUMAN**, Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2

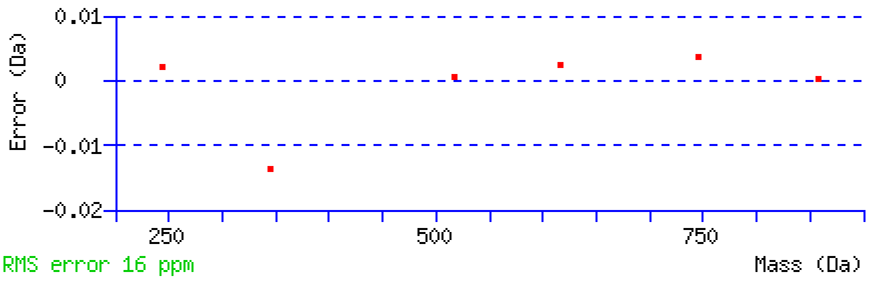
Match to Query 11767: 970.528068 from(486.271310,2+) rtinseconds(1636) index(13577)
Title: Locus:1.1.1.2114.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

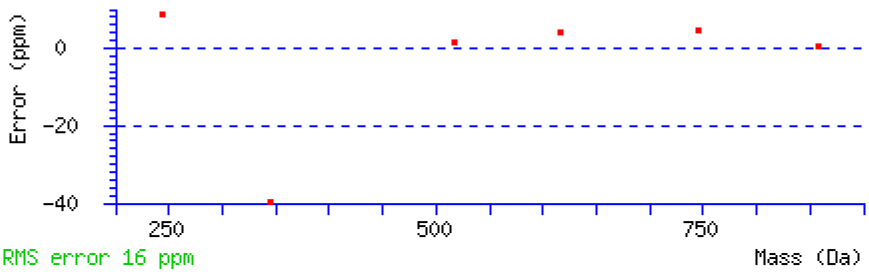
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 970.533508
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.00012
Matches : 6/72 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			I							9
2	227.175404	114.091340			I	*858.456725*	429.732001	841.430176	421.218726	840.446160	420.726718	8
3	356.217997	178.612637	338.207432	169.607354	E	*745.372661*	373.189969	728.346112	364.676694	727.362096	364.184686	7
4	455.286411	228.146844	437.275846	219.141561	V	*616.330068*	308.668672	599.303519	300.155398	598.319503	299.663390	6
5	512.307875	256.657576	494.297310	247.652293	G	*517.261654*	259.134465	500.235105	250.621191	499.251089	250.129183	5
6	627.334818	314.171047	609.324253	305.165765	D	460.240190	230.623733	443.213641	222.110458	442.229625	221.618450	4
7	728.382497	364.694887	710.371932	355.689604	T	*345.213247*	173.110262	328.186698	164.596987	327.202682	164.104979	3
8	825.435261	413.221269	807.424696	404.215986	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 IIEVGDTPK
(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	970.533508	-0.005440	IIEVGDTPK
8.9	970.523605	0.004463	IPGNWQIK
3.8	970.530807	-0.002739	LPAQRTNR
1.5	970.523590	0.004478	IPLYANHK
0.8	970.519577	0.008491	ILGNPASAGR
0.3	970.533493	-0.005425	LLQELPDK
0.3	970.519592	0.008476	LPNAGTQVR

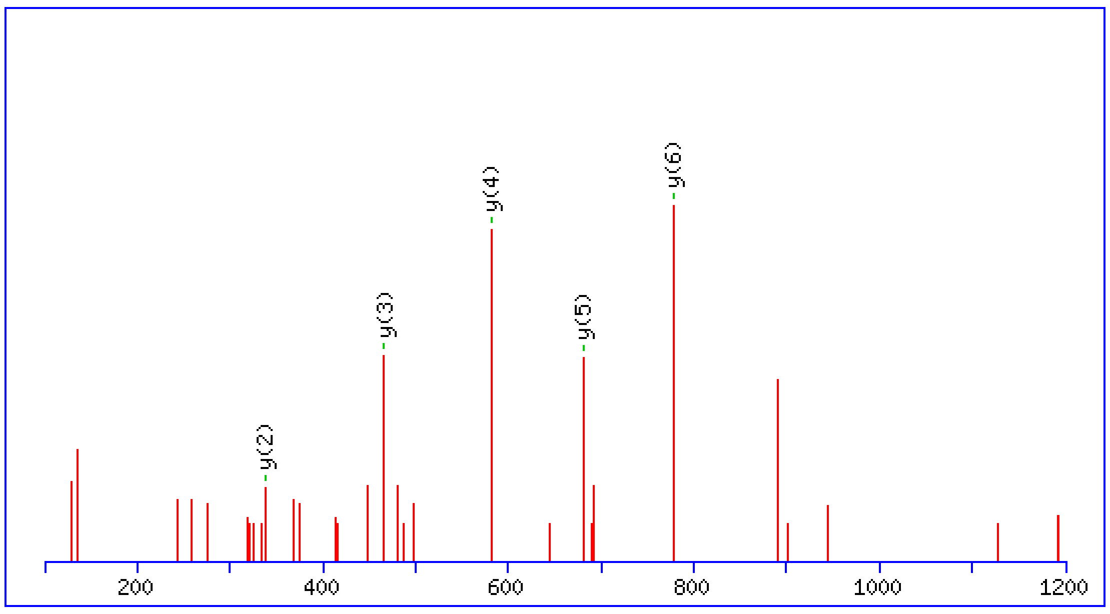
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPVDQYR**
Found in **TRIQK_HUMAN**, Protein TRIQK OS=Homo sapiens GN=C8orf83 PE=2 SV=1

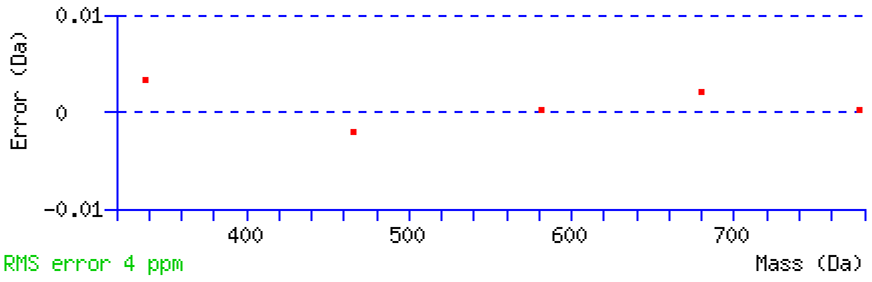
Match to Query 1979: 889.464348 from(445.739450,2+) rtinseconds(1646) index(2768)
Title: Locus:1.1.1.2528.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

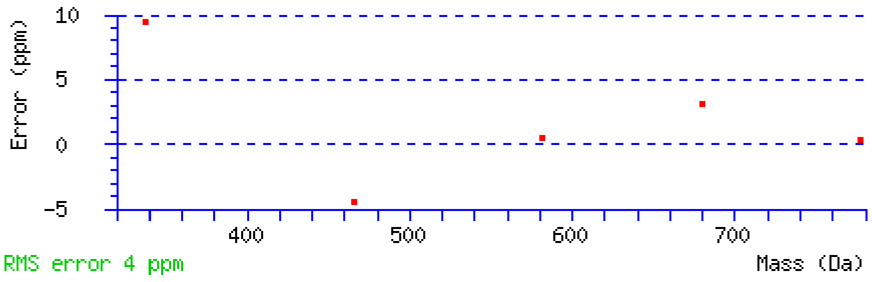
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 889.465759
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.001
Matches : 5/52 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	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
41.8	889.465759	-0.001411	LPVDQYR
9.9	889.457870	0.006478	KEPEIMK
6.4	889.457870	0.006478	KEELPMK
4.4	889.457886	0.006462	LAMAIPDK
1.8	889.465759	-0.001411	IPFDRDK
1.8	889.469116	-0.004768	LPKTEMR
1.5	889.469131	-0.004783	VTLQCQK
0.6	889.465775	-0.001427	IVGPGPYR
0.6	889.469131	-0.004783	RMIDPVK

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

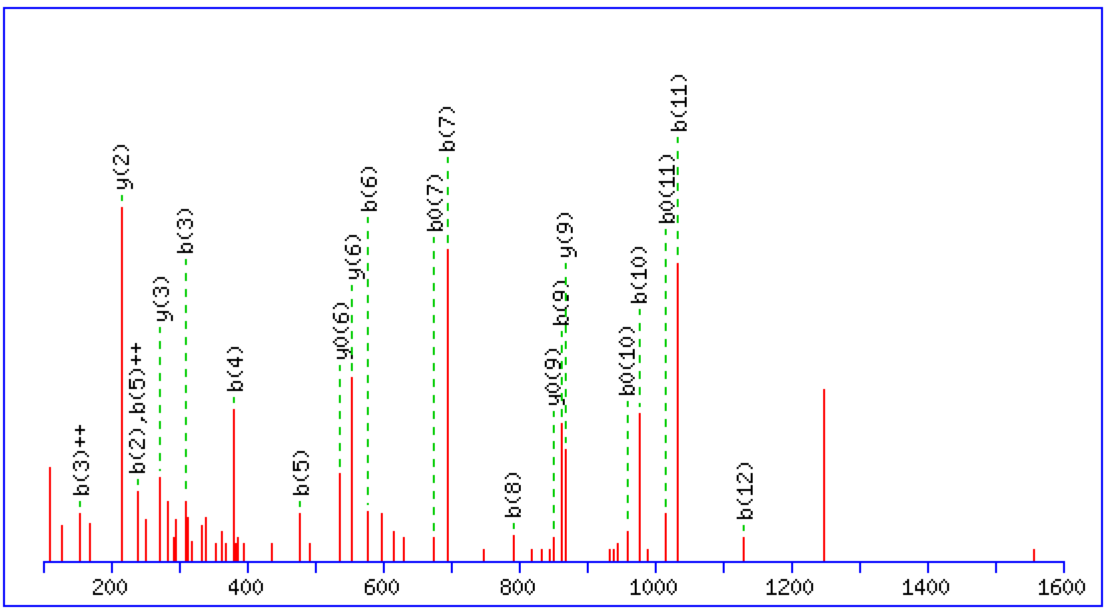
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HTAAPTDPADGPV**
Found in **PLP2_HUMAN**, Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1

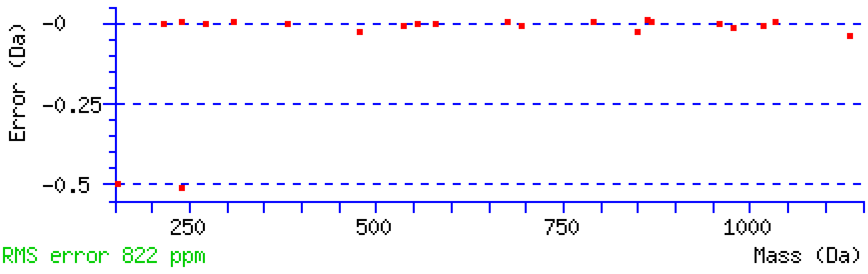
Match to Query 19867: 1247.578708 from(624.796630,2+) rtinseconds(1518) index(3752)
Title: Locus:1.1.1.2104.31
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

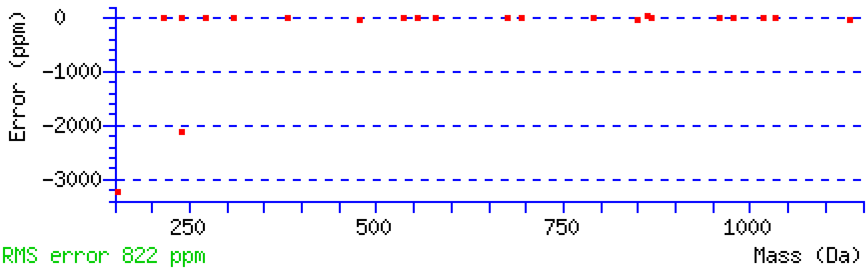
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1247.578247
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 103 **Expect:** 2.1e-010
Matches : 22/88 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	138.066188	69.536732			H					13
2	239.113867	120.060571	221.103302	111.055289	T	1111.526597	556.266937	1093.516032	547.261654	12
3	310.150981	155.579128	292.140416	146.573846	A	1010.478918	505.743097	992.468353	496.737815	11
4	381.188095	191.097685	363.177530	182.092403	A	939.441804	470.224540	921.431239	461.219258	10
5	478.240859	239.624067	460.230294	230.618785	P	868.404690	434.705983	850.394125	425.700701	9
6	579.288538	290.147907	561.277973	281.142625	T	771.351926	386.179601	753.341361	377.174319	8
7	694.315481	347.661379	676.304916	338.656096	D	670.304247	335.655762	652.293682	326.650479	7
8	791.368245	396.187761	773.357680	387.182478	P	555.277304	278.142290	537.266739	269.137008	6
9	862.405359	431.706318	844.394794	422.701035	A	458.224540	229.615908	440.213975	220.610625	5
10	977.432302	489.219789	959.421737	480.214506	D	387.187426	194.097351	369.176861	185.092068	4
11	1034.453766	517.730521	1016.443201	508.725238	G	272.160483	136.583879			3
12	1131.506530	566.256903	1113.495965	557.251620	P	215.139019	108.073148			2
13					V	118.086255	59.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
103.3	1247.578247	0.000461	HTAAPTDPADGPV
0.1	1247.567673	0.011035	TSCTRQDNPR

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

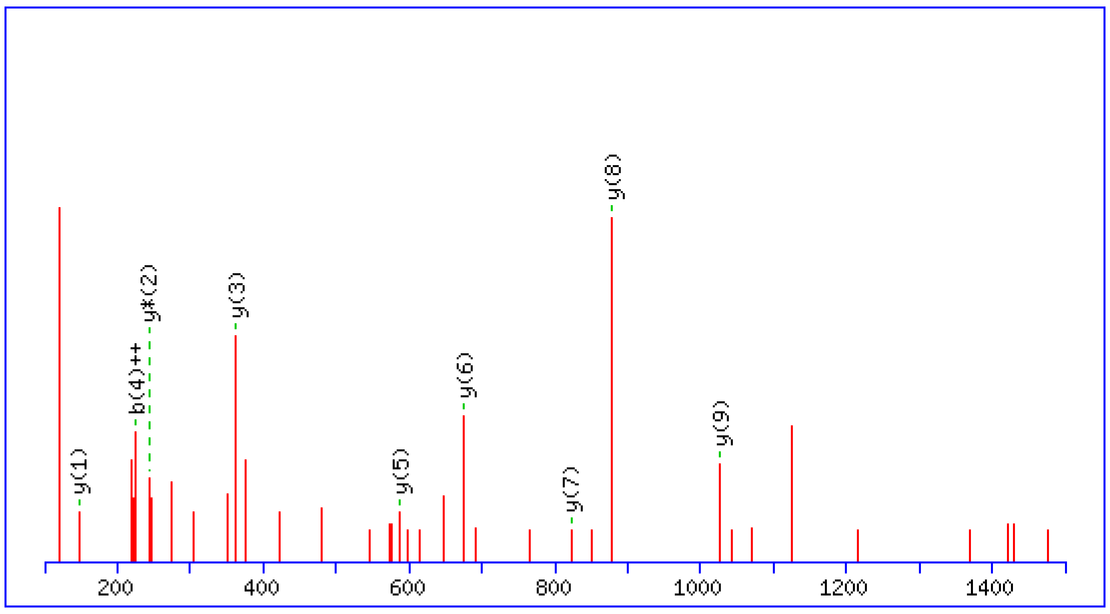
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFGFSLITNK**
Found in **PNPH_HUMAN**, Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2

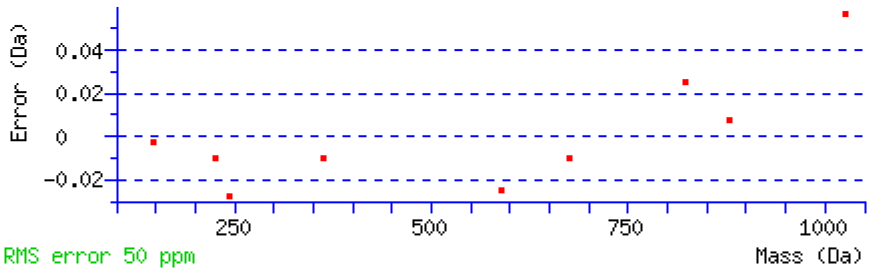
Match to Query 16571: 1124.618748 from(563.316650,2+) rtinseconds(3342) index(40803)
Title: Locus:1.1.1.2841.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

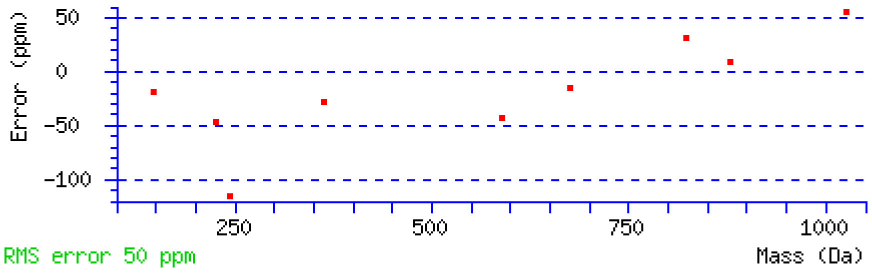
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1124.623001
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0039
Matches : 9/80 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							10
2	247.144104	124.075690					F	***1026.561858***	513.784567	1009.535309	505.271293	1008.551293	504.779285	9
3	304.165568	152.586422					G	***879.493444***	440.250360	862.466895	431.737086	861.482879	431.245078	8
4	451.233982	226.120629					F	***822.471980***	411.739628	805.445431	403.226354	804.461415	402.734346	7
5	538.266010	269.636643			520.255445	260.631360	S	***675.403566***	338.205421	658.377017	329.692147	657.393001	329.200139	6
6	651.350074	326.178675			633.339509	317.173392	L	***588.371538***	294.689407	571.344989	286.176133	570.360973	285.684125	5
7	764.434138	382.720707			746.423573	373.715424	I	475.287474	238.147375	458.260925	229.634101	457.276909	229.142093	4
8	865.481817	433.244547			847.471252	424.239264	T	***362.203410***	181.605343	345.176861	173.092069	344.192845	172.600061	3
9	979.524744	490.266010	962.498195	481.752735	961.514179	481.260727	N	261.155731	131.081504	244.129182	122.568229			2
10							K	***147.112804***	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of VFGFSLITNK
(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	1124.623001	-0.004253	VFGFSLITNK

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

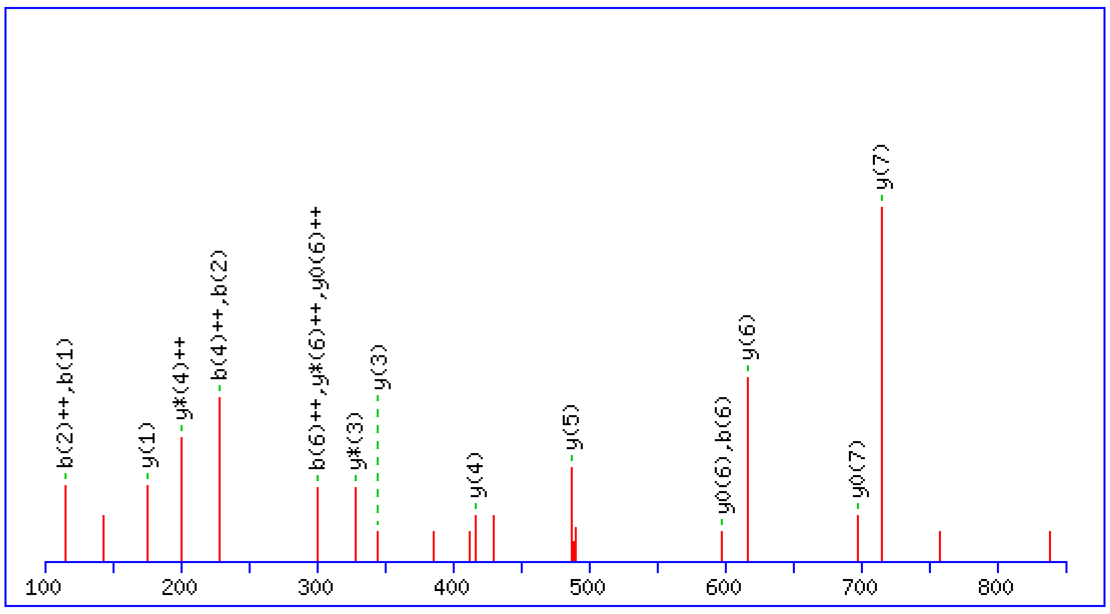
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIVEAAAVR**
Found in **RS26L_HUMAN**, Putative 40S ribosomal protein S26-like 1 OS=Homo sapiens GN=RPS26P11 PE=5 SV=1

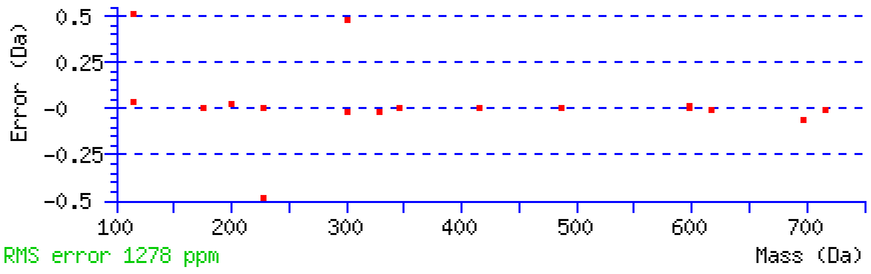
Match to Query 4746: 941.529488 from(471.772020,2+) rtinseconds(1697) index(4464)
Title: Locus:1.1.1.2233.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

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 ●

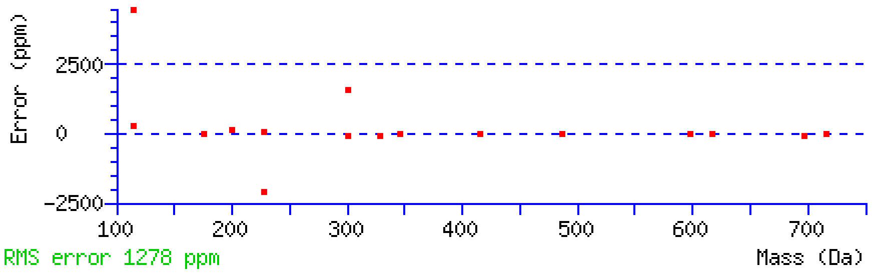


```
Monoisotopic mass of neutral peptide Mr(calc): 941.529404
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 3.9e-005
Matches : 18/80 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**115.050203**	58.028740	98.023654	49.515465			**N**							9
2	**228.134267**	**114.570771**	211.107718	106.057497			**I**	828.493779	414.750528	811.467230	406.237253	810.483214	405.745245	8
3	327.202681	164.104978	310.176132	155.591704			**V**	***715.409715***	358.208496	698.383166	349.695221	697.399150	349.203213	7
4	456.245274	**228.626275**	439.218725	220.113001	438.234709	219.620993	**E**	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
5	527.282388	264.144832	510.255839	255.631558	509.271823	255.139550	**A**	***487.298708***	244.152992	470.272159	235.639717			5
6	**598.319502**	**299.663389**	581.292953	291.150115	580.308937	290.658107	**A**	***416.261594***	208.634435	399.235045	200.121160			4
7	669.356616	335.181946	652.330067	326.668672	651.346051	326.176664	**A**	***345.224480***	173.115878	328.197931	164.602603			3
8	768.425030	384.716153	751.398481	376.202879	750.414465	375.710871	**V**	274.187366	137.597321	257.160817	129.084047			2
9							**R**	***175.118952***	88.063114	158.092403	79.549840			1



RMS error 1278 ppm



RMS error 1278 ppm

NCBI **BLAST** search of NIVEAAAVR
(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	941.529404	0.000084	NIVEAAAVR
24.4	941.529434	0.000054	AGVVPSQLR
12.2	941.529404	0.000084	LNPADIKR
11.5	941.529419	0.000069	VELQQGLR
8.5	941.522873	0.006615	MARGPLAAR
7.8	941.529419	0.000069	SPDGRIAVK
5.9	941.529419	0.000069	GILVASNPR
5.3	941.529419	0.000069	GATLAALGPR
5.2	941.529419	0.000069	ALQALTGPR
4.0	941.529419	0.000069	TQIPLQAR

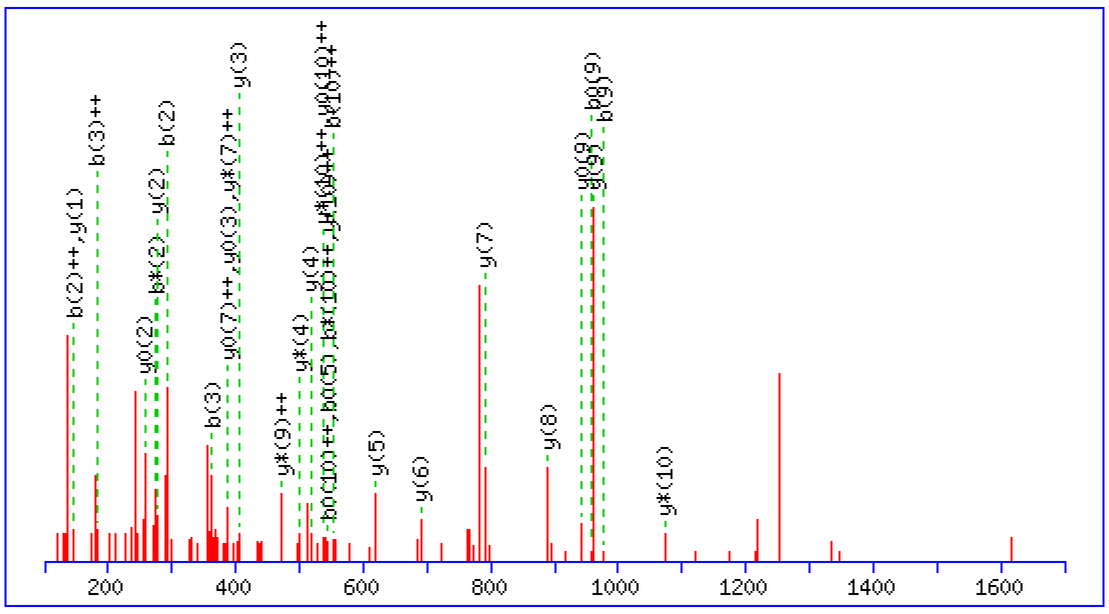
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YQAVTATLEEK**
Found in **R13AX_HUMAN**, Putative 60S ribosomal protein L13a-like MGC87657 OS=Homo sapiens PE=5 SV=1

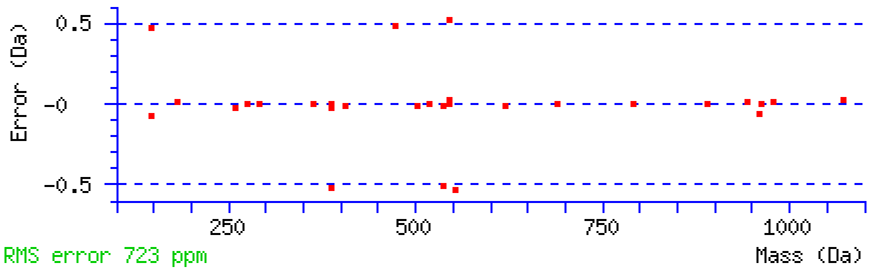
Match to Query 25464: 1251.640528 from(626.827540,2+) rtinseconds(1895) index(18961)
Title: Locus:1.1.1.2166.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

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 ●

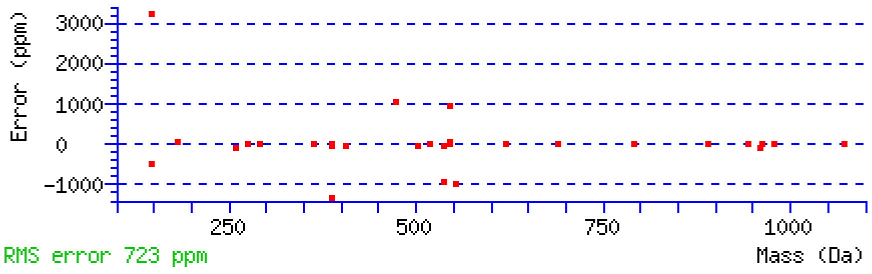


Monoisotopic mass of neutral peptide Mr(calc): 1251.634659
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48 **Expect:** 0.00012
Matches : 31/108 fragment ions using 55 most intense peaks (help)

#	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	**292.129183**	**146.568230**	275.102634	138.054955			Q	1089.578632	545.292954	1072.552083	536.779680	1071.568067	536.287671	10
3	**363.166297**	**182.086787**	346.139748	173.573512			A	***961.520054***	481.263665	944.493505	472.750391	943.509489	472.258383	9
4	462.234711	231.620994	445.208162	223.107719			V	***890.482940***	445.745108	873.456391	437.231833	872.472375	436.739825	8
5	563.282390	282.144833	546.255841	273.631559	545.271825	273.139551	T	***791.414526***	396.210901	774.387977	387.697627	773.403961	387.205619	7
6	634.319504	317.663390	617.292955	309.150116	616.308939	308.658108	A	***690.366847***	345.687062	673.340298	337.173787	672.356282	336.681779	6
7	735.367183	368.187230	718.340634	359.673955	717.356618	359.181947	T	***619.329733***	310.168505	602.303184	301.655230	601.319168	301.163222	5
8	848.451247	424.729262	831.424698	416.215987	830.440682	415.723979	L	***518.282054***	259.644665	501.255505	251.131391	500.271489	250.639383	4
9	**977.493840**	489.250558	960.467291	480.737284	959.483275	480.245276	E	***405.197990***	203.102633	388.171441	194.589358	387.187425	194.097350	3
10	1106.536433	**553.771855**	1089.509884	545.258580	1088.525868	544.766572	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



RMS error 723 ppm



RMS error 723 ppm

NCBI **BLAST** search of YQAVTATLEEK
(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	1251.634659	0.005869	YQAVTATLEEK
5.9	1251.643234	-0.002706	SGPPRARPGPGR
2.7	1251.634659	0.005869	AADVEPSLPEPK
1.9	1251.642059	-0.001531	VLLDFLMEEK
1.1	1251.645905	-0.005377	GVEAIPEGSHIK

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

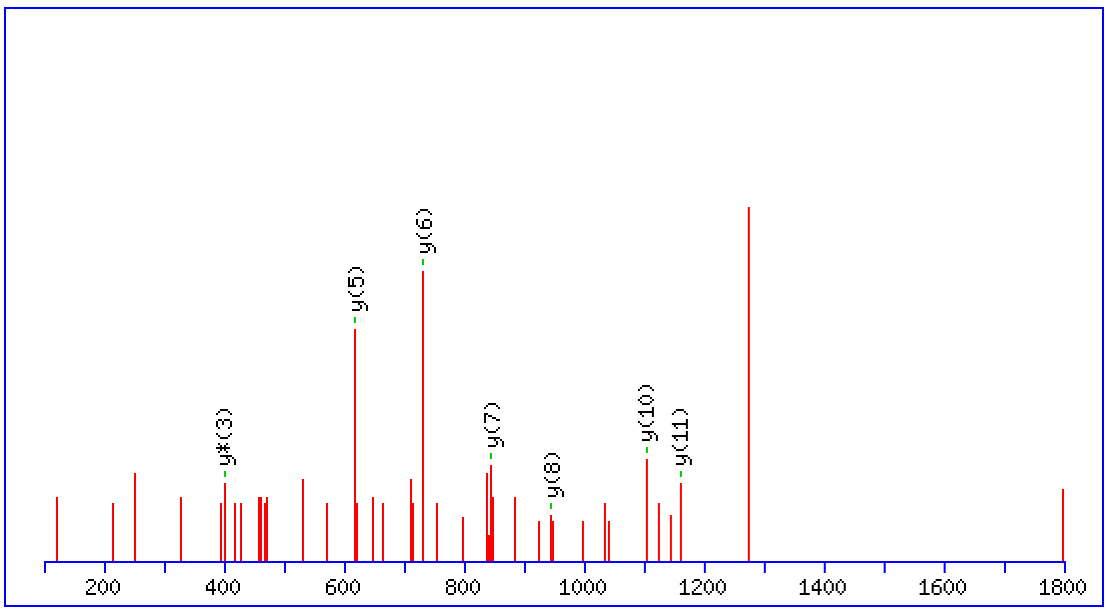
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGASTLLSDIER**
Found in **DEOC_HUMAN**, Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2

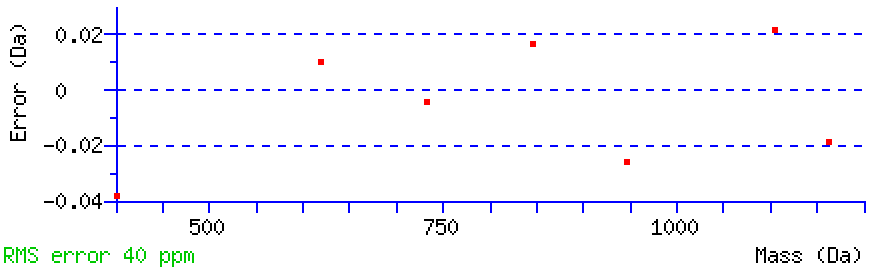
Match to Query 39160: 1273.696068 from(637.855310,2+) rtinseconds(3156) index(43157)
Title: Locus:1.1.1.2561.23
Data file 2011-11-14 - TFD - S 2-4.mgf

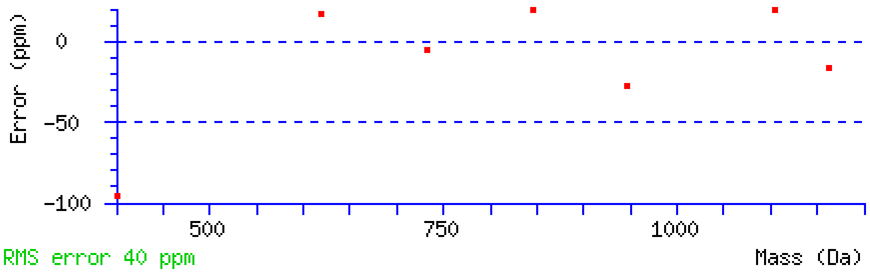
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1273.687759
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00028
Matches : 7/102 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308			I							12
2	171.112804	86.060040			G	***1161.610993***	581.309135	1144.584444	572.795860	1143.600428	572.303852	11
3	242.149918	121.578597			A	***1104.589529***	552.798403	1087.562980	544.285128	1086.578964	543.793120	10
4	329.181946	165.094611	311.171381	156.089328	S	1033.552415	517.279846	1016.525866	508.766571	1015.541850	508.274563	9
5	430.229625	215.618450	412.219060	206.613168	T	***946.520387***	473.763832	929.493838	465.250557	928.509822	464.758549	8
6	543.313689	272.160483	525.303124	263.155200	L	***845.472708***	423.239992	828.446159	414.726718	827.462143	414.234710	7
7	656.397753	328.702515	638.387188	319.697232	L	***732.388644***	366.697960	715.362095	358.184686	714.378079	357.692678	6
8	743.429781	372.218529	725.419216	363.213246	S	***619.304580***	310.155928	602.278031	301.642654	601.294015	301.150646	5
9	858.456724	429.732000	840.446159	420.726718	D	532.272552	266.639914	515.246003	258.126640	514.261987	257.634632	4
10	971.540788	486.274032	953.530223	477.268750	I	417.245609	209.126443	400.219060	200.613168	399.235044	200.121160	3
11	1100.583381	550.795329	1082.572816	541.790046	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 IGASTLLSDIER
(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	1273.687759	0.008309	IGASTLLSDIER
3.8	1273.689102	0.006966	ITNGAFPTRAAR
2.1	1273.706390	-0.010322	SAGILTLPIMSR
2.1	1273.706390	-0.010322	SAGILTLPIMSR

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

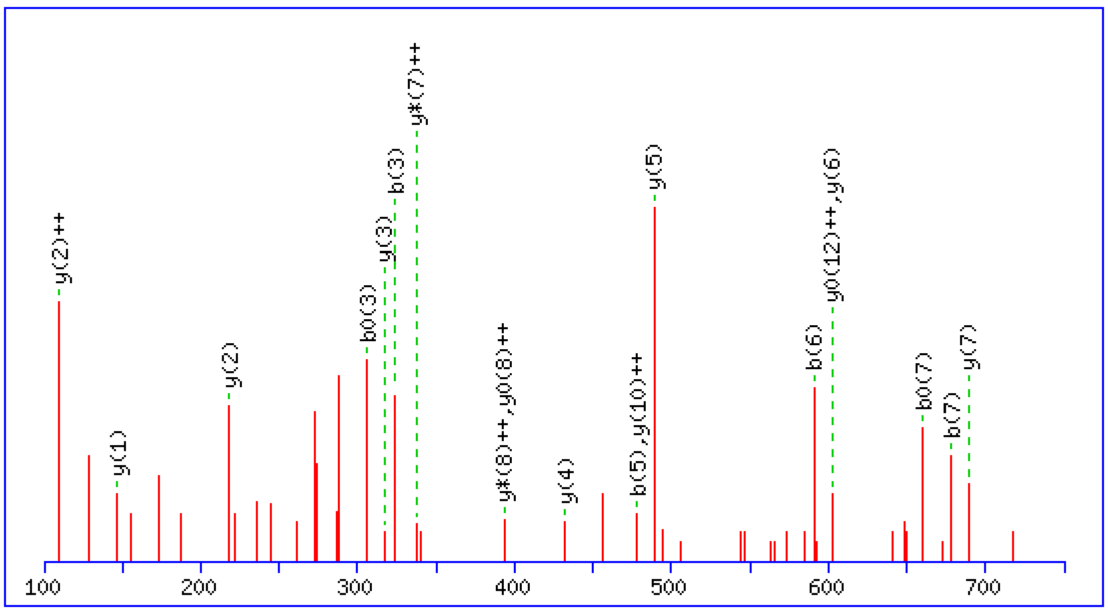
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEHPGLSIGDVAK**
Found in **HGB1A_HUMAN**, Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1

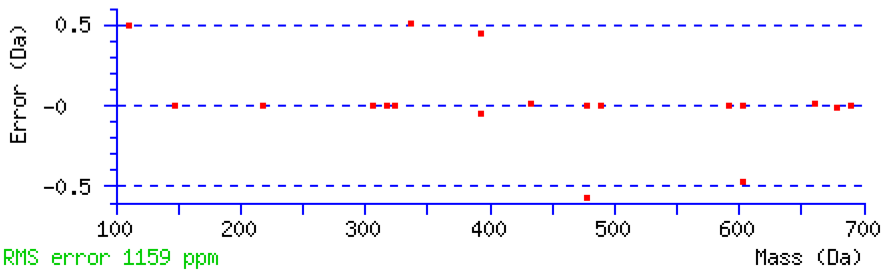
Match to Query 474157: 1278.655002 from(427.225610,3+) rtinseconds(1788) index(804546)
Title: Locus:1.1.1.748.5
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

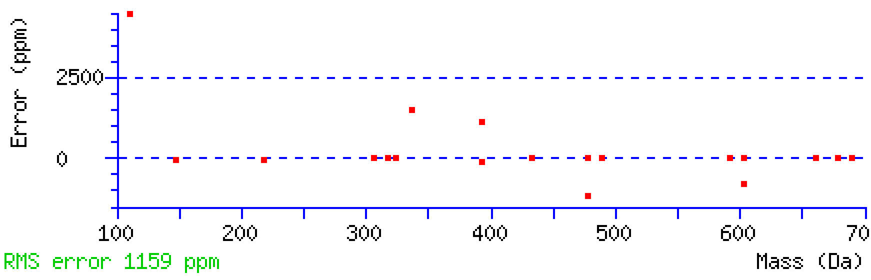
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1278.656815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.00013
Matches : 19/112 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							13
2	187.071333	94.039305	169.060768	85.034022	E	1222.642628	611.824952	1205.616079	603.311678	1204.632063	602.819670	12
3	***324.130245***	162.568761	306.119680	153.563478	H	1093.600035	547.303655	1076.573486	538.790381	1075.589470	538.298373	11
4	421.183009	211.095143	403.172444	202.089860	P	956.541123	478.774200	939.514574	470.260925	938.530558	469.768917	10
5	***478.204473***	239.605875	460.193908	230.600592	G	859.488359	430.247818	842.461810	421.734543	841.477794	421.242535	9
6	***591.288537***	296.147907	573.277972	287.142624	L	802.466895	401.737086	785.440346	393.223811	784.456330	392.731803	8
7	***678.320565***	339.663921	660.310000	330.658638	S	***689.382831***	345.195054	672.356282	336.681779	671.372266	336.189771	7
8	791.404629	396.205953	773.394064	387.200670	I	***602.350803***	301.679040	585.324254	293.165765	584.340238	292.673757	6
9	848.426093	424.716685	830.415528	415.711402	G	***489.266739***	245.137007	472.240190	236.623733	471.256174	236.131725	5
10	963.453036	482.230156	945.442471	473.224874	D	***432.245275***	216.626275	415.218726	208.113001	414.234710	207.620993	4
11	1062.521450	531.764363	1044.510885	522.759080	V	***317.218332***	159.112804	300.191783	150.599529			3
12	1133.558564	567.282920	1115.547999	558.277637	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 GEHPGLSIGDVAK
(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	1278.656815	-0.001813	GEHPGLSIGDVAK
5.7	1278.660828	-0.005826	WSKYPLDVQK
4.8	1278.656815	-0.001813	IPTHGGDINDIK
4.4	1278.656815	-0.001813	DPKHLNDDVVK
3.4	1278.656784	-0.001782	KGGLYSQEQAAK
2.3	1278.656815	-0.001813	DHPQLKTPPSK

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

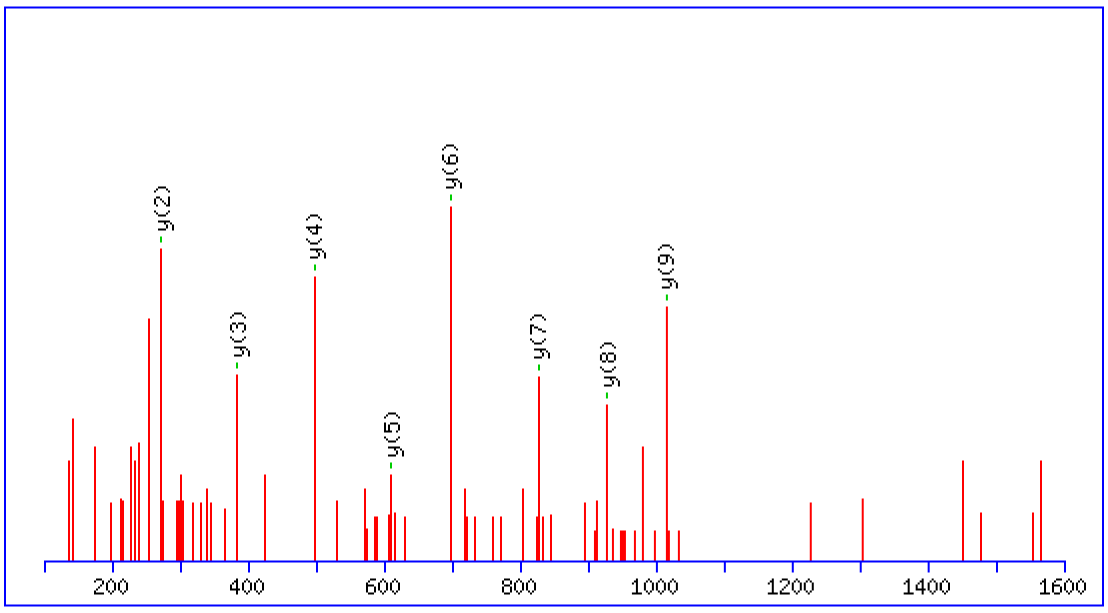
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSTESILIPR**
Found in **LC1L1_HUMAN**, Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1P1 PE=5 SV=1

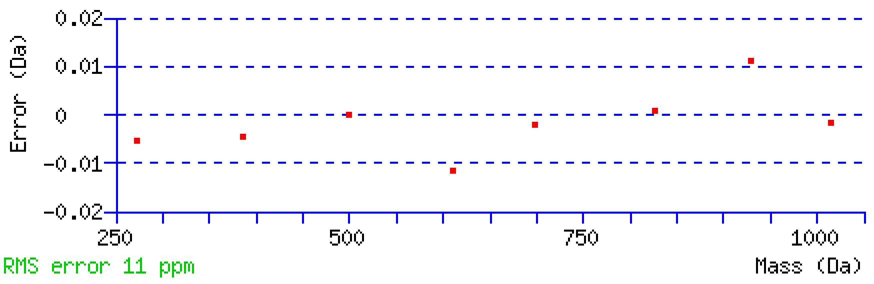
Match to Query 23504: 1184.679788 from(593.347170,2+) rtinseconds(2747) index(26565)
Title: Locus:1.1.1.2513.27
Data file 2011-11-14 - TFD - S 2-5.mgf

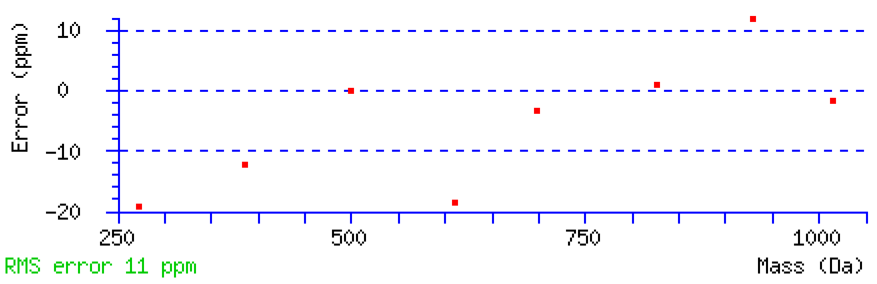
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1184.676468
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 81 **Expect:** 5.1e-008
Matches : 8/86 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							11
2	171.112804	86.060040			L	1128.662300	564.834788	1111.635751	556.321514	1110.651735	555.829506	10
3	258.144832	129.576054	240.134267	120.570772	S	***1015.578236***	508.292756	998.551687	499.779482	997.567671	499.287474	9
4	359.192511	180.099894	341.181946	171.094611	T	***928.546208***	464.776742	911.519659	456.263468	910.535643	455.771460	8
5	488.235104	244.621190	470.224539	235.615908	E	***827.498529***	414.252903	810.471980	405.739628	809.487964	405.247620	7
6	575.267132	288.137204	557.256567	279.131922	S	***698.455936***	349.731606	681.429387	341.218332	680.445371	340.726324	6
7	688.351196	344.679236	670.340631	335.673954	I	***611.423908***	306.215592	594.397359	297.702318			5
8	801.435260	401.221268	783.424695	392.215986	L	***498.339844***	249.673560	481.313295	241.160285			4
9	914.519324	457.763300	896.508759	448.758018	I	***385.255780***	193.131528	368.229231	184.618253			3
10	1011.572088	506.289682	993.561523	497.284400	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 GLSTESILIPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.5	1184.676468	0.003320	GLSTESILIPR

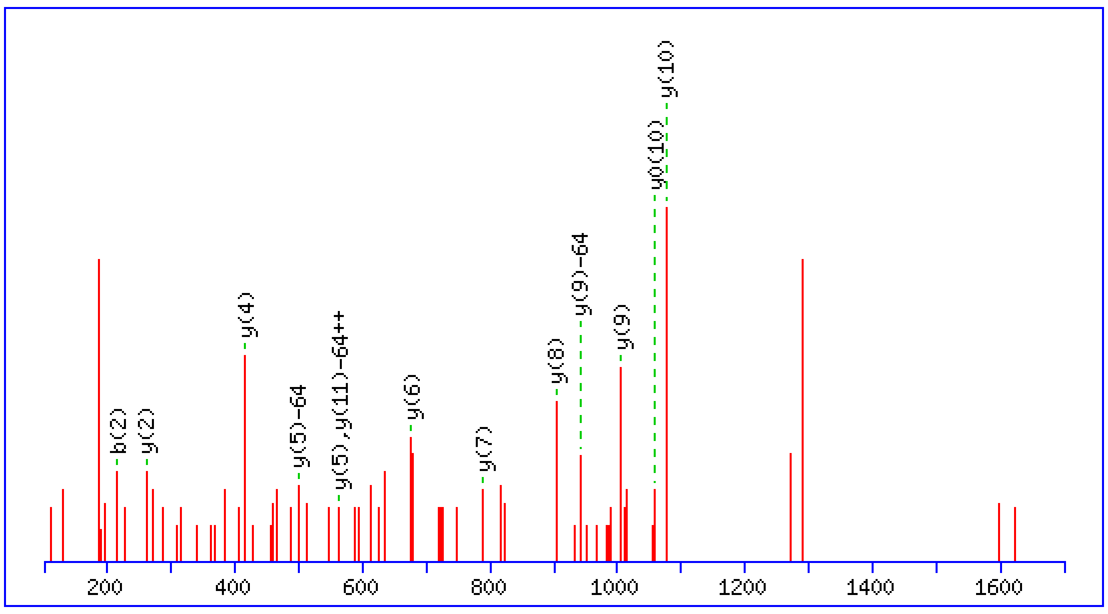
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLATDILMGVLK**
Found in **DHX15_HUMAN**, Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2

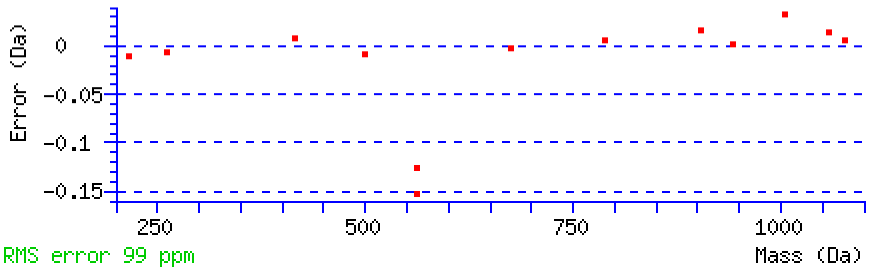
Match to Query 26634: 1289.731688 from(645.873120,2+) rtinseconds(4015) index(57072)
Title: Locus:1.1.1.3129.8
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

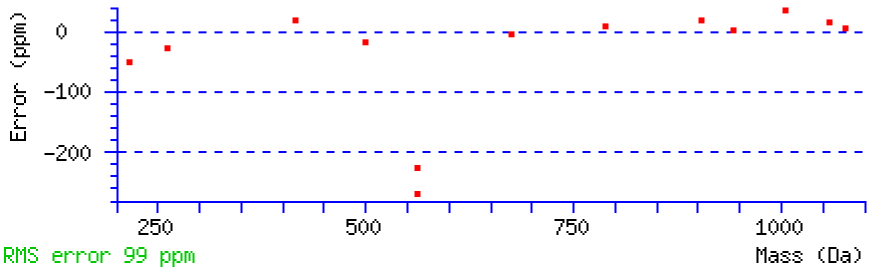
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1289.726471
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: 56  Expect: 1.2e-005
Matches : 13/148 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116	84.044390	42.525833	T							12
2	215.139019	108.073147	197.128454	99.067865	L	1189.686074	595.346675	1172.659525	586.833401	1171.675509	586.341392	11
3	286.176133	143.591704	268.165568	134.586422	A	***1076.602010***	538.804643	1059.575461	530.291369	1058.591445	529.799361	10
4	387.223812	194.115544	369.213247	185.110262	T	***1005.564896***	503.286086	988.538347	494.772811	987.554331	494.280803	9
5	502.250755	251.629016	484.240190	242.623733	D	***904.517217***	452.762247	887.490668	444.248972	886.506652	443.756964	8
6	615.334819	308.171048	597.324254	299.165765	I	***789.490274***	395.248775	772.463725	386.735501			7
7	728.418883	364.713080	710.408318	355.707797	L	***676.406210***	338.706743	659.379661	330.193468			6
8	875.454283	438.230780	857.443718	429.225497	M	***563.322146***	282.164711	546.295597	273.651436			5
9	932.475747	466.741512	914.465182	457.736229	G	***416.286746***	208.647011	399.260197	200.133736			4
10	1031.544161	516.275719	1013.533596	507.270436	V	359.265282	180.136279	342.238733	171.623004			3
11	1144.628225	572.817750	1126.617660	563.812468	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 TLATDILMGVLK
(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	1289.726471	0.005217	TLATDILMGVLK
5.7	1289.734314	-0.002626	LGEEVSLRFLK
0.7	1289.723099	0.008589	FDSKVDPILIK

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

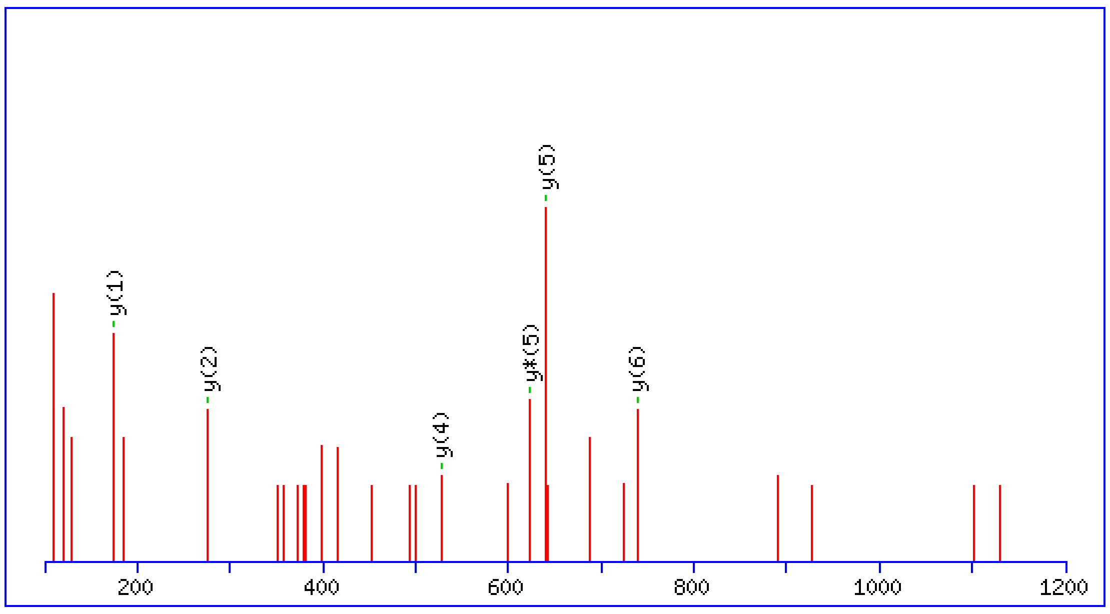
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVLNHTR**
Found in **CHK29_HUMAN**, Putative transmembrane protein C8orfK29 OS=Homo sapiens GN=C8orfK29 PE=2 SV=1

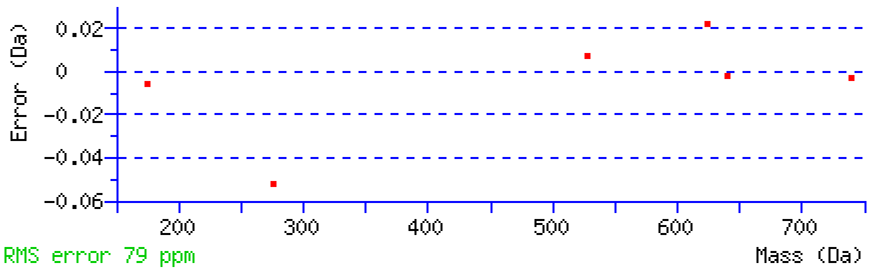
Match to Query 1934: 851.494448 from(426.754500,2+) rtinseconds(1736) index(15226)
Title: Locus:1.1.1.2129.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-1.mgf

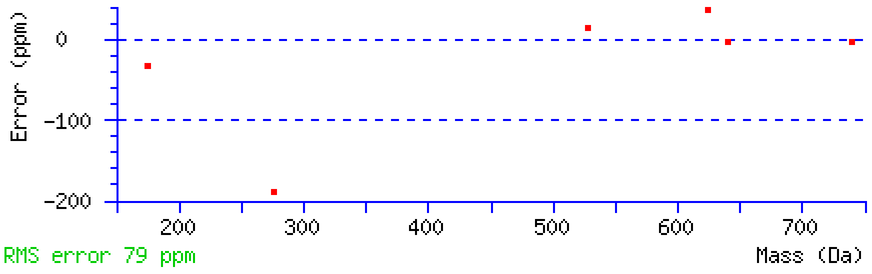
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 851.497726
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30 **Expect:** 0.0066
Matches : 6/54 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							7
2	213.159754	107.083515					V	*739.420948*	370.214112	722.394399	361.700838	721.410383	361.208830	6
3	326.243818	163.625547					L	*640.352534*	320.679905	623.325985	312.166631	622.341969	311.674623	5
4	440.286745	220.647010	423.260196	212.133736			N	*527.268470*	264.137873	510.241921	255.624599	509.257905	255.132591	4
5	577.345657	289.176467	560.319108	280.663192			H	413.225543	207.116409	396.198994	198.603135	395.214978	198.111127	3
6	678.393336	339.700306	661.366787	331.187032	660.382771	330.695024	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 LVLNHTR
(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	851.497726	-0.003278	LVLNHTR
17.9	851.497726	-0.003278	IVLTHNR
17.7	851.497726	-0.003278	VLLQHSR
17.7	851.497726	-0.003278	VLPKSHR
8.3	851.497726	-0.003278	LVTLNHR
7.9	851.486496	0.007952	VLPAPAPR
7.9	851.486496	0.007952	VLPAPAPR
7.5	851.497711	-0.003263	LEHGIKR
3.9	851.486481	0.007967	LPEPPRK
3.4	851.497726	-0.003278	GAVLLSHR

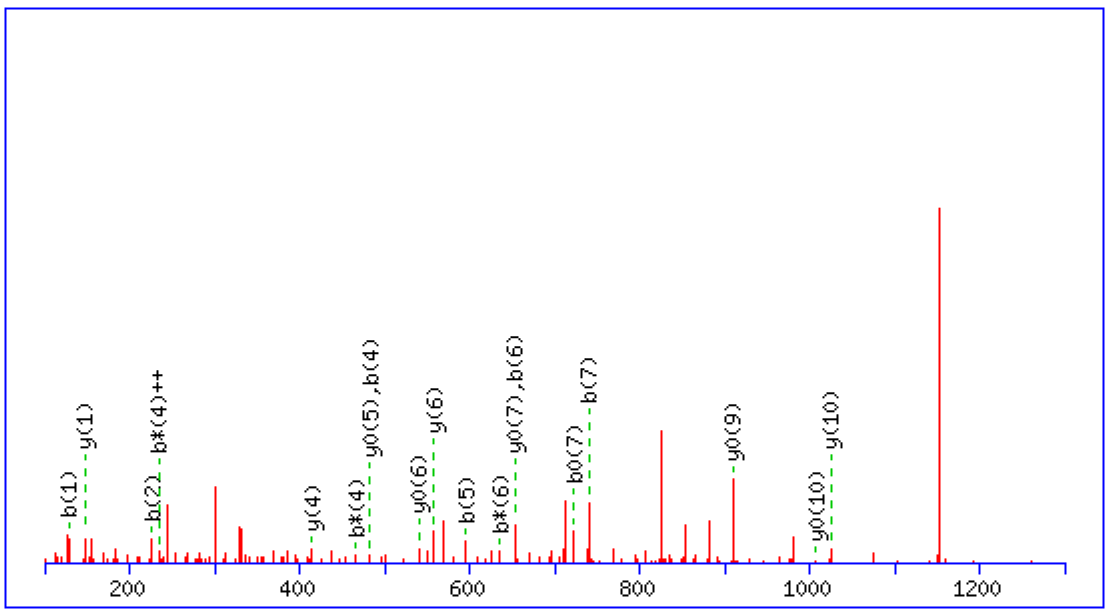
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPAWPGSPAVK**
Found in **CJ041_HUMAN**, Putative uncharacterized protein encoded by NCRNA00245 OS=Homo sapiens GN=NCRNA00245 PE=2 SV=1

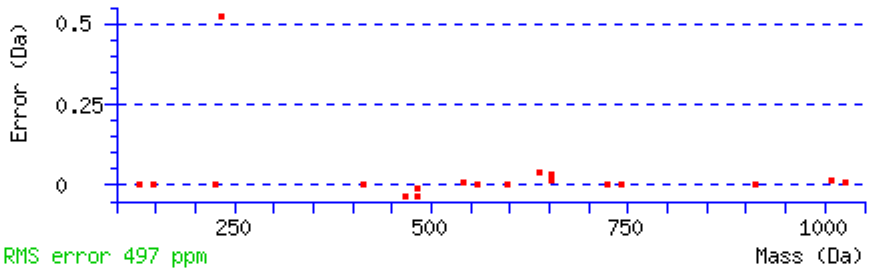
Match to Query 14360: 1152.638828 from(577.326690,2+) rtinseconds(1399) index(7837)
Title: Locus:1.1.1.2312.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

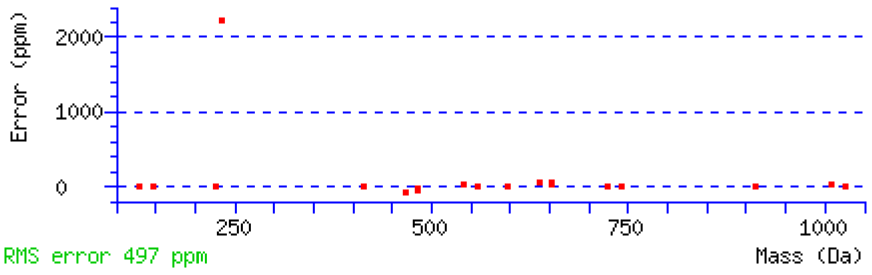
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1152.629135
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 31  Expect: 0.008
Matches : 20/100 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	***129.102239***	65.054757	112.075690	56.541483			K							11
2	***226.155003***	113.581139	209.128454	105.067865			P	**1025.541458**	513.274367	1008.514909	504.761092	1007.530893	504.269084	10
3	297.192117	149.099696	280.165568	140.586422			A	928.488694	464.747985	911.462145	456.234710	910.478129	455.742702	9
4	***483.271430***	242.139353	466.244881	233.626079			W	857.451580	429.229428	840.425031	420.716153	839.441015	420.224145	8
5	***596.319109***	298.663193	579.292560	290.149918			P	671.372267	336.189772	654.345718	327.676497	653.361702	327.184489	7
6	***653.340573***	327.173925	636.314024	318.660650			G	**558.324588**	279.665932	541.298039	271.152657	540.314023	270.660649	6
7	***740.372601***	370.689939	723.346052	362.176664	722.362036	361.684656	S	501.303124	251.155200	484.276575	242.641925	483.292559	242.149917	5
8	837.425365	419.216321	820.398816	410.703046	819.414800	410.211038	P	**414.271096**	207.639186	397.244547	199.125911			4
9	908.462479	454.734878	891.435930	446.221603	890.451914	445.729595	A	317.218332	159.112804	300.191783	150.599529			3
10	***1007.530893***	504.269085	990.504344	495.755810	989.520328	495.263802	V	246.181218	123.594247	229.154669	115.080972			2
11							K	**147.112804**	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of KPAWPGSPAVK
(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	1152.629135	0.009693	KPAWPGSPAVK
12.9	1152.629135	0.009693	KPAWPGSPAVK
8.0	1152.650238	-0.011410	ENGELLPILR
6.8	1152.629135	0.009693	HIFENVIGPK
6.6	1152.650284	-0.011456	QKPPAGVVTPK
5.7	1152.629135	0.009693	KPAWPGSPAVK
2.6	1152.650269	-0.011441	VKPASPVAQPK
0.3	1152.650253	-0.011425	IPVPINAELR

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

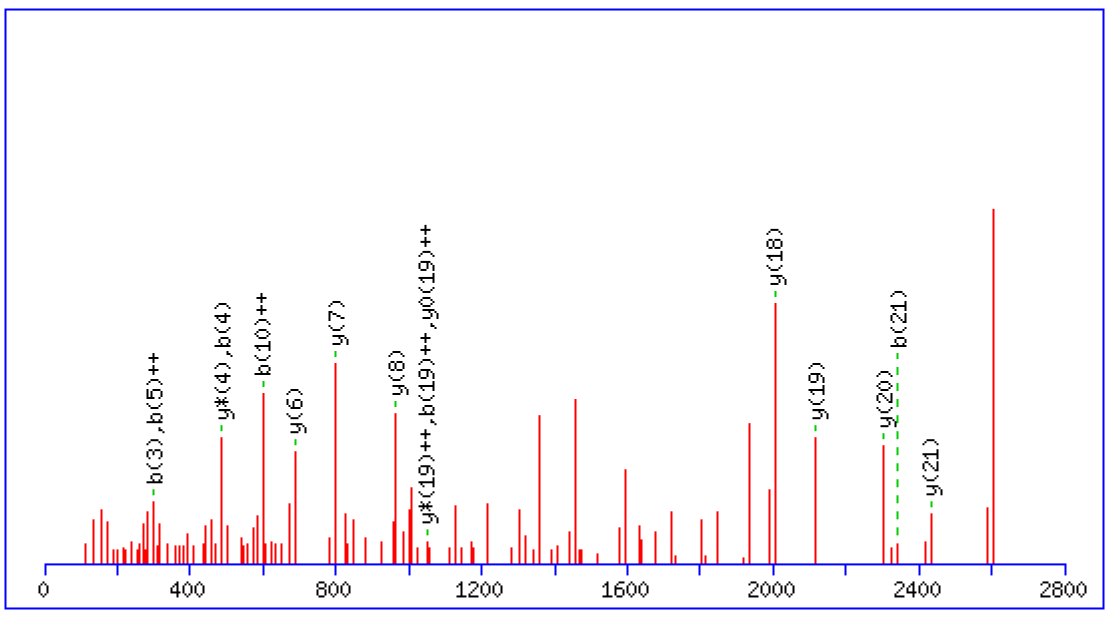
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEWIGEIYHSGSPNYNPSLKSR**
Found in **VSIG6_HUMAN**, Putative V-set and immunoglobulin domain-containing protein 6 OS=Homo sapiens GN=VSIG6 PE=5 SV=2

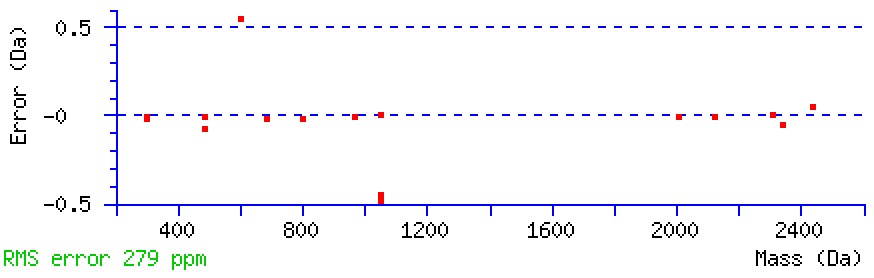
Match to Query 71733: 2603.274042 from(868.765290,3+) rtinseconds(3018) index(42573)
Title: Locus:1.1.1.2630.43
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

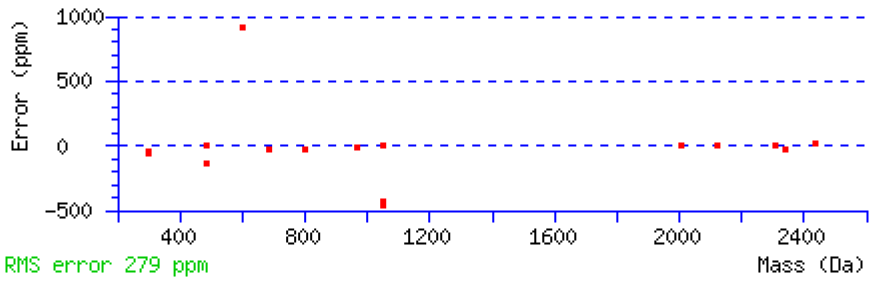
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2603.276810
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0039
Matches : 16/230 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							23
2	171.112804	86.060040					L	2547.262662	1274.134969	2530.236113	1265.621694	2529.252097	1265.129686	22
3	**300.155397**	150.581336			282.144832	141.576054	E	***2434.178598***	1217.592937	2417.152049	1209.079662	2416.168033	1208.587654	21
4	**486.234710**	243.620993			468.224145	234.615711	W	***2305.136005***	1153.071640	2288.109456	1144.558366	2287.125440	1144.066358	20
5	599.318774	**300.163025**			581.308209	291.157743	I	***2119.056692***	1060.031984	2102.030143	1051.518709	2101.046127	1051.026701	19
6	656.340238	328.673757			638.329673	319.668475	G	***2005.972628***	1003.489952	1988.946079	994.976678	1987.962063	994.484670	18
7	785.382831	393.195054			767.372266	384.189771	E	1948.951164	974.979220	1931.924615	966.465946	1930.940599	965.973938	17
8	898.466895	449.737086			880.456330	440.731803	I	1819.908571	910.457924	1802.882022	901.944649	1801.898006	901.452641	16
9	1061.530224	531.268750			1043.519659	522.263468	Y	1706.824507	853.915892	1689.797958	845.402617	1688.813942	844.910609	15
10	1198.589136	**599.798206**			1180.578571	590.792924	H	1543.761178	772.384227	1526.734629	763.870953	1525.750613	763.378945	14
11	1285.621164	643.314220			1267.610599	634.308938	S	1406.702266	703.854771	1389.675717	695.341497	1388.691701	694.849489	13
12	1342.642628	671.824952			1324.632063	662.819670	G	1319.670238	660.338757	1302.643689	651.825483	1301.659673	651.333475	12
13	1429.674656	715.340966			1411.664091	706.335684	S	1262.648774	631.828025	1245.622225	623.314751	1244.638209	622.822743	11
14	1526.727420	763.867348			1508.716855	754.862066	P	1175.616746	588.312011	1158.590197	579.798737	1157.606181	579.306729	10
15	1640.770347	820.888812	1623.743798	812.375537	1622.759782	811.883529	N	1078.563982	539.785629	1061.537433	531.272355	1060.553417	530.780347	9
16	1803.833676	902.420476	1786.807127	893.907202	1785.823111	893.415194	Y	***964.521055***	482.764166	947.494506	474.250891	946.510490	473.758883	8
17	1917.876603	959.441940	1900.850054	950.928665	1899.866038	950.436657	N	***801.457726***	401.232501	784.431177	392.719227	783.447161	392.227219	7
18	2014.929367	1007.968322	1997.902818	999.455047	1996.918802	998.963039	P	***687.414799***	344.211038	670.388250	335.697763	669.404234	335.205755	6
19	2101.961395	**1051.484335**	2084.934846	1042.971061	2083.950830	1042.479053	S	590.362035	295.684656	573.335486	287.171381	572.351470	286.679373	5
20	2215.045459	1108.026367	2198.018910	1099.513093	2197.034894	1099.021085	L	503.330007	252.168642	486.303458	243.655367	485.319442	243.163359	4
21	**2343.140422**	1172.073849	2326.113873	1163.560574	2325.129857	1163.068566	K	390.245943	195.626610	373.219394	187.113335	372.235378	186.621327	3
22	2430.172450	1215.589863	2413.145901	1207.076588	2412.161885	1206.584580	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
23							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLEWIGEIYHSGSPNYNPSLKSR
(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	2603.276810	-0.002768	GLEWIGEIYHSGSPNYNPSLKSR
5.0	2603.286758	-0.012716	QEVEATAGLLYVDDPNWSGIGVVR
4.2	2603.253723	0.020319	ESTCSPTPDSTASLPPPPAPGLASPR
4.0	2603.271545	0.002497	EGIPGPLGPPGPPGSVGPPGASGLKGDK
3.7	2603.271545	0.002497	EGIPGPLGPPGPPGSVGPPGASGLKGDK
3.7	2603.271545	0.002497	EGIPGPLGPPGPPGSVGPPGASGLKGDK
3.6	2603.271545	0.002497	EGIPGPLGPPGPPGSVGPPGASGLKGDK

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

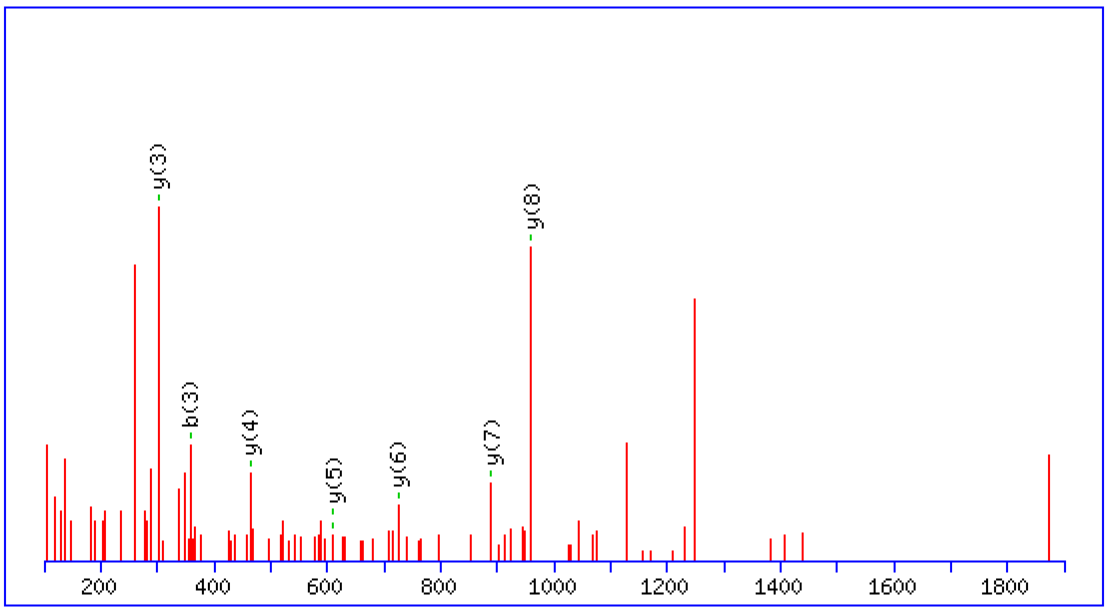
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CLAYDFYPGK**
Found in **ZA2G_HUMAN**, Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2

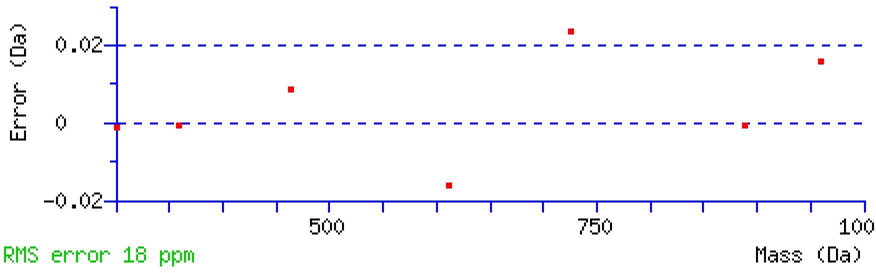
Match to Query 31409: 1246.574468 from(624.294510,2+) rtinseconds(2659) index(36459)
Title: Locus:1.1.1.2348.24
Data file 2011-11-14 - TFD - S 2-3.mgf

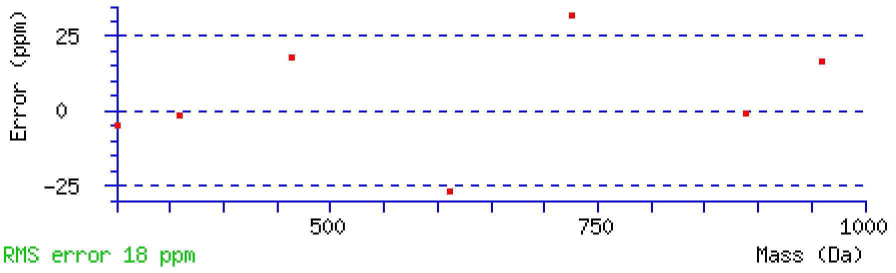
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1246.569229
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00054
Matches : 7/72 fragment ions using 12 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							10
2	288.137639	144.572457			L	1073.530225	537.268751	1056.503676	528.755476	1055.519660	528.263468	9
3	359.174753	180.091014			A	***960.446161***	480.726719	943.419612	472.213444	942.435596	471.721436	8
4	522.238082	261.622679			Y	***889.409047***	445.208162	872.382498	436.694887	871.398482	436.202879	7
5	637.265025	319.136151	619.254460	310.130868	D	***726.345718***	363.676497	709.319169	355.163223	708.335153	354.671215	6
6	784.333439	392.670358	766.322874	383.665075	F	***611.318775***	306.163026	594.292226	297.649751			5
7	947.396768	474.202022	929.386203	465.196740	Y	***464.250361***	232.628818	447.223812	224.115544			4
8	1044.449532	522.728404	1026.438967	513.723122	P	***301.187032***	151.097154	284.160483	142.583879			3
9	1101.470996	551.239136	1083.460431	542.233854	G	204.134268	102.570772	187.107719	94.057497			2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of CLAYDFYPGK
(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	1246.569229	0.005239	CLAYDFYPGK

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

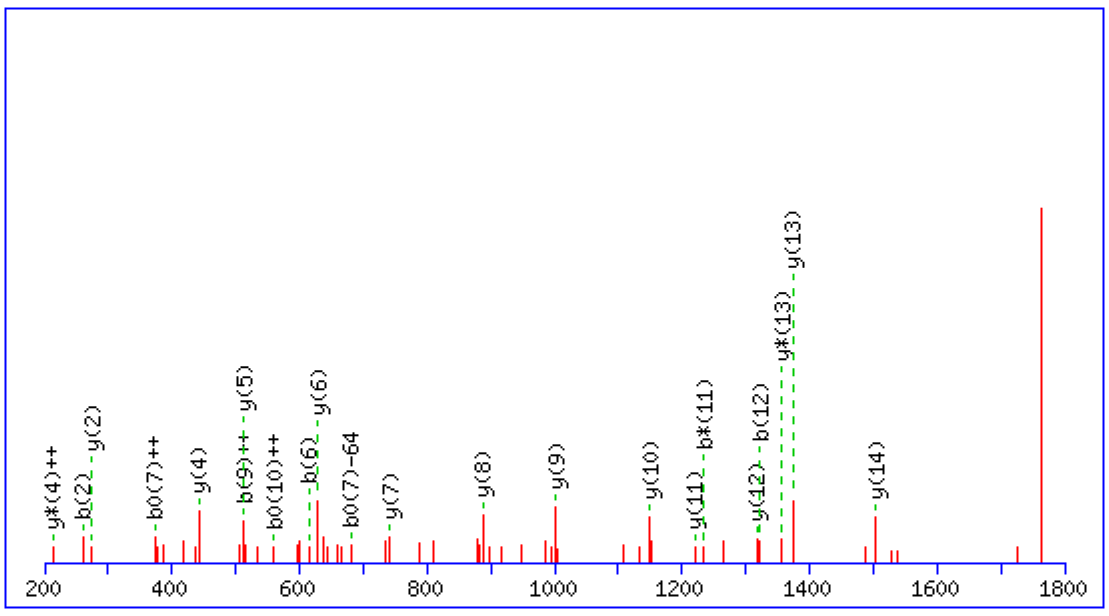
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMEGPAFNFLDAPAVR**
Found in **ODPB_HUMAN**, Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3

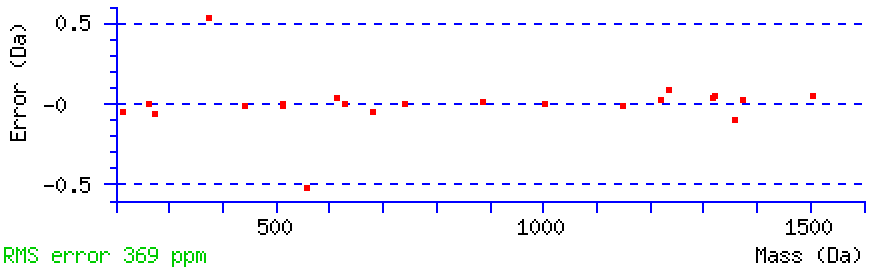
Match to Query 51063: 1762.887008 from(882.450780,2+) rtinseconds(3446) index(47593)
Title: Locus:1.1.1.2800.41
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

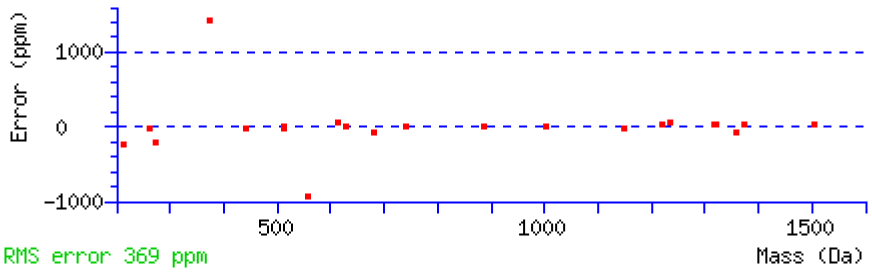
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1762.871231
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: 66 **Expect:** 3e-006
Matches : 22/228 fragment ions using 52 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	**261.126740**	131.067008					M	1650.794455	825.900866	1633.767906	817.387591	1632.783890	816.895583	15
3	390.169333	195.588304			372.158768	186.583022	E	***1503.759055***	752.383165	1486.732506	743.869891	1485.748490	743.377883	14
4	447.190797	224.099036			429.180232	215.093754	G	***1374.716462***	687.861869	1357.689913	679.348594	1356.705897	678.856586	13
5	544.243561	272.625419			526.232996	263.620136	P	***1317.694998***	659.351137	1300.668449	650.837863	1299.684433	650.345854	12
6	**615.280675**	308.143976			597.270110	299.138693	A	***1220.642234***	610.824755	1203.615685	602.311481	1202.631669	601.819472	11
7	762.349089	381.678182			744.338524	372.672900	F	***1149.605120***	575.306198	1132.578571	566.792924	1131.594555	566.300915	10
8	876.392016	438.699646	859.365467	430.186371	858.381451	429.694363	N	***1002.536706***	501.771991	985.510157	493.258716	984.526141	492.766708	9
9	1023.460430	512.233853	1006.433881	503.720578	1005.449865	503.228570	F	***888.493779***	444.750528	871.467230	436.237253	870.483214	435.745245	8
10	1136.544494	568.775885	1119.517945	560.262610	1118.533929	559.770602	L	***741.425365***	371.216321	724.398816	362.703046	723.414800	362.211038	7
11	1251.571437	626.289356	1234.544888	617.776082	1233.560872	617.284074	D	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
12	**1322.608551**	661.807913	1305.582002	653.294639	1304.597986	652.802631	A	***513.314358***	257.160817	496.287809	248.647543			5
13	1419.661315	710.334295	1402.634766	701.821021	1401.650750	701.329013	P	***442.277244***	221.642260	425.250695	213.128986			4
14	1490.698429	745.852852	1473.671880	737.339578	1472.687864	736.847570	A	345.224480	173.115878	328.197931	164.602603			3
15	1589.766843	795.387059	1572.740294	786.873785	1571.756278	786.381777	V	***274.187366***	137.597321	257.160817	129.084047			2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IMEGPAFNFLDAPAVR
(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	1762.871231	0.015777	IMEGPAFNFLDAPAVR
36.7	1762.871231	0.015777	IMEGPAFNFLDAPAVR

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

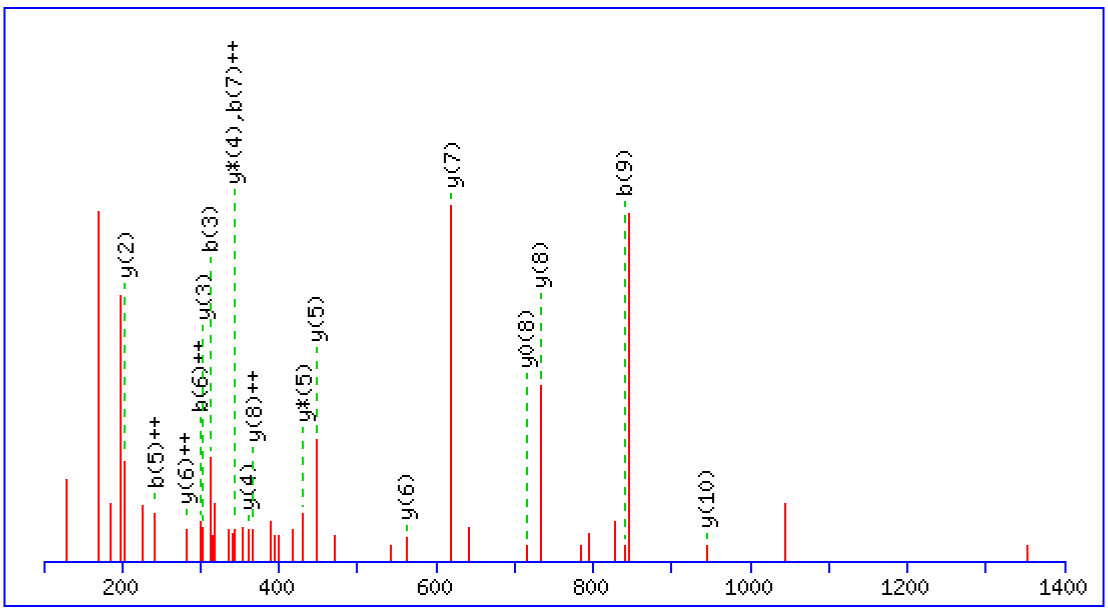
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLVLGDSGVGK**
Found in **RABL3_HUMAN**, Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1

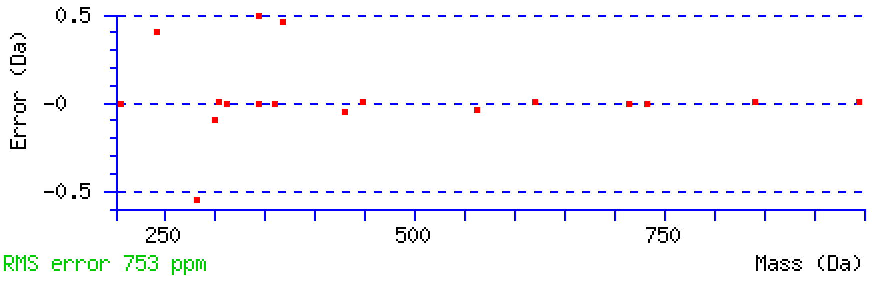
Match to Query 14853: 1042.606108 from(522.310330,2+) rtinseconds(2046) index(21692)
Title: Locus:1.1.1.2224.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

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 ●

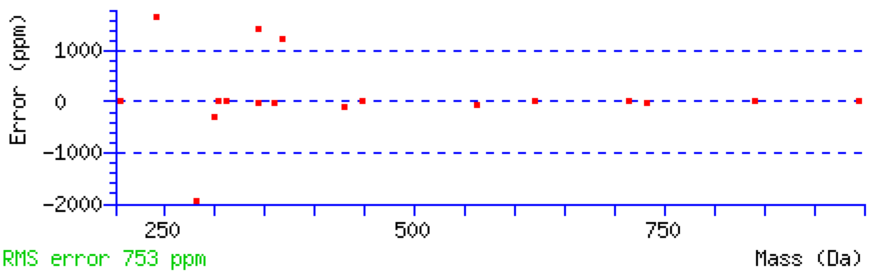


Monoisotopic mass of neutral peptide Mr(calc): 1042.602280
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 0.00014
Matches : 18/82 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	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 753 ppm



RMS error 753 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
68.2	1042.602280	0.003828	VVLIGDSGVGK
48.8	1042.602280	0.003828	VLVLGDSGVGK
5.9	1042.613495	-0.007387	KKPVSGGSVGK
3.1	1042.602234	0.003874	QEVEKLLGK
2.2	1042.595718	0.010390	VAMTPALRGK

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

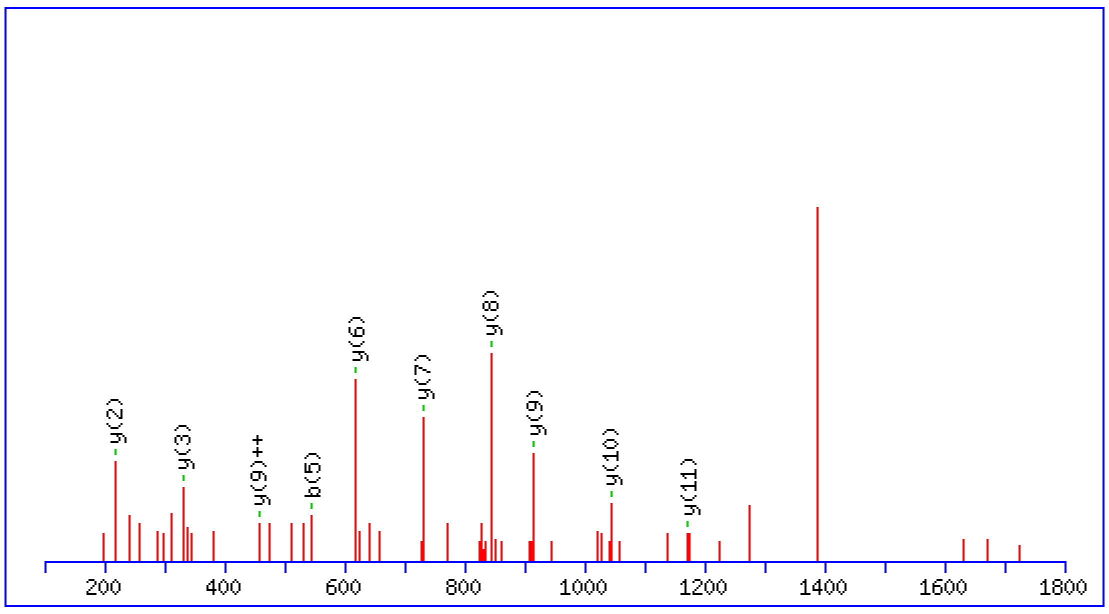
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDEQALLSSILAK**
Found in **LTOR1_HUMAN**, Ragulator complex protein LAMTOR1 OS=Homo sapiens GN=LAMTOR1 PE=1 SV=2

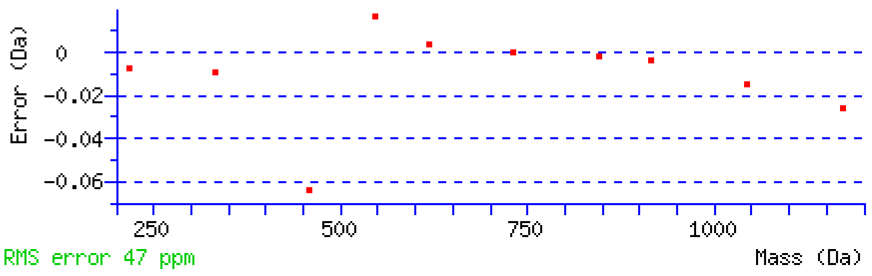
Match to Query 26375: 1387.759388 from(694.886970,2+) rtinseconds(3521) index(36813)
Title: Locus:1.1.1.2834.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

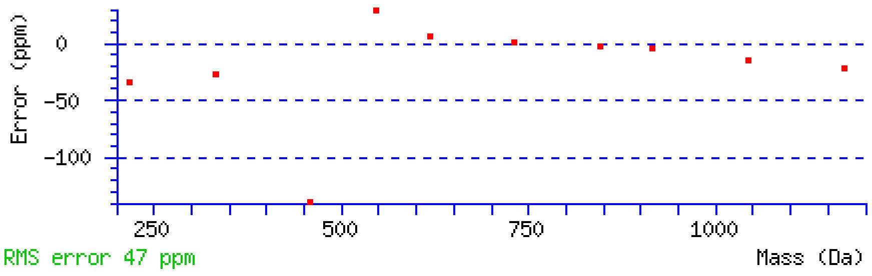
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1387.755829
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 7.3e-007
Matches : 10/130 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							13
2	217.081898	109.044587			199.071333	100.039304	D	1287.715458	644.361367	1270.688909	635.848093	1269.704893	635.356084	12
3	346.124491	173.565883			328.113926	164.560601	E	***1172.688515***	586.847895	1155.661966	578.334621	1154.677950	577.842613	11
4	474.183069	237.595172	457.156520	229.081898	456.172504	228.589890	Q	***1043.645922***	522.326599	1026.619373	513.813325	1025.635357	513.321316	10
5	545.220183	273.113730	528.193634	264.600455	527.209618	264.108447	A	***915.587344***	458.297310	898.560795	449.784035	897.576779	449.292027	9
6	658.304247	329.655762	641.277698	321.142487	640.293682	320.650479	L	***844.550230***	422.778753	827.523681	414.265478	826.539665	413.773470	8
7	771.388311	386.197794	754.361762	377.684519	753.377746	377.192511	L	***731.466166***	366.236721	714.439617	357.723446	713.455601	357.231438	7
8	858.420339	429.713808	841.393790	421.200533	840.409774	420.708525	S	***618.382102***	309.694689	601.355553	301.181414	600.371537	300.689406	6
9	945.452367	473.229822	928.425818	464.716547	927.441802	464.224539	S	531.350074	266.178675	514.323525	257.665400	513.339509	257.173392	5
10	1058.536431	529.771854	1041.509882	521.258579	1040.525866	520.766571	I	444.318046	222.662661	427.291497	214.149386			4
11	1171.620495	586.313885	1154.593946	577.800611	1153.609930	577.308603	L	***331.233982***	166.120629	314.207433	157.607354			3
12	1242.657609	621.832442	1225.631060	613.319168	1224.647044	612.827160	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 TDEQALLSSILAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.9	1387.755829	0.003559	TDEQALLSSILAK
3.4	1387.767090	-0.007702	LGSRVITDPSLSK
2.5	1387.749313	0.010075	EKDCALTVVALR

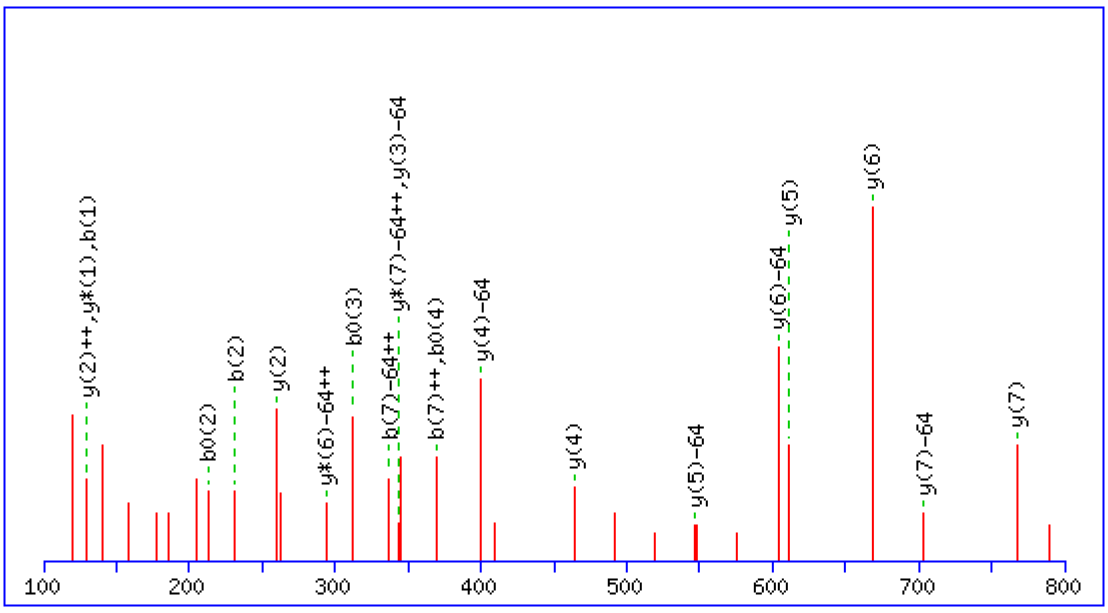
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETVGFGMLK**
Found in **LTOR2_HUMAN**, Ragulator complex protein LAMTOR2 OS=Homo sapiens GN=LAMTOR2 PE=1 SV=1

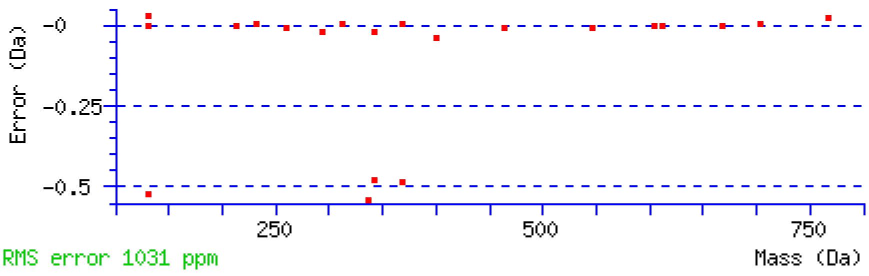
Match to Query 6239: 996.494968 from(499.254760,2+) rtinseconds(2205) index(5886)
Title: Locus:1.1.1.2597.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

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 ●

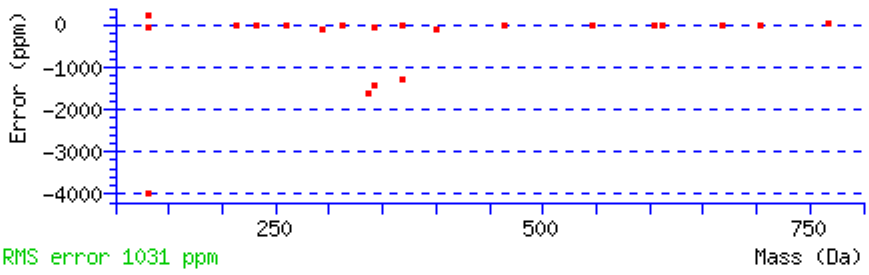


Monoisotopic mass of neutral peptide Mr(calc): 996.495026
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 34 **Expect:** 0.0017
Matches : 21/100 fragment ions using 27 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	804.461418	402.734347	787.434869	394.221073	786.450853	393.729065	8
3	330.165962	165.586619	312.155397	156.581337	V	***703.413739***	352.210508	686.387190	343.697233			7
4	387.187426	194.097351	369.176861	185.092069	G	***604.345325***	302.676301	587.318776	294.163026			6
5	534.255840	267.631558	516.245275	258.626276	F	***547.323861***	274.165569	530.297312	265.652294			5
6	591.277304	296.142290	573.266739	287.137008	G	***400.255447***	200.631362	383.228898	192.118087			4
7	674.314419	337.660848	656.303854	328.655565	M	***343.233983***	172.120629	326.207434	163.607355			3
8	787.398483	394.202880	769.387918	385.197597	L	***260.196868***	130.602072	243.170319	122.088798			2
9					K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1031 ppm



RMS error 1031 ppm

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
34.2	996.495026	-0.000058	ETVGFGMLK
4.7	996.502853	-0.007885	AKFENFNK

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

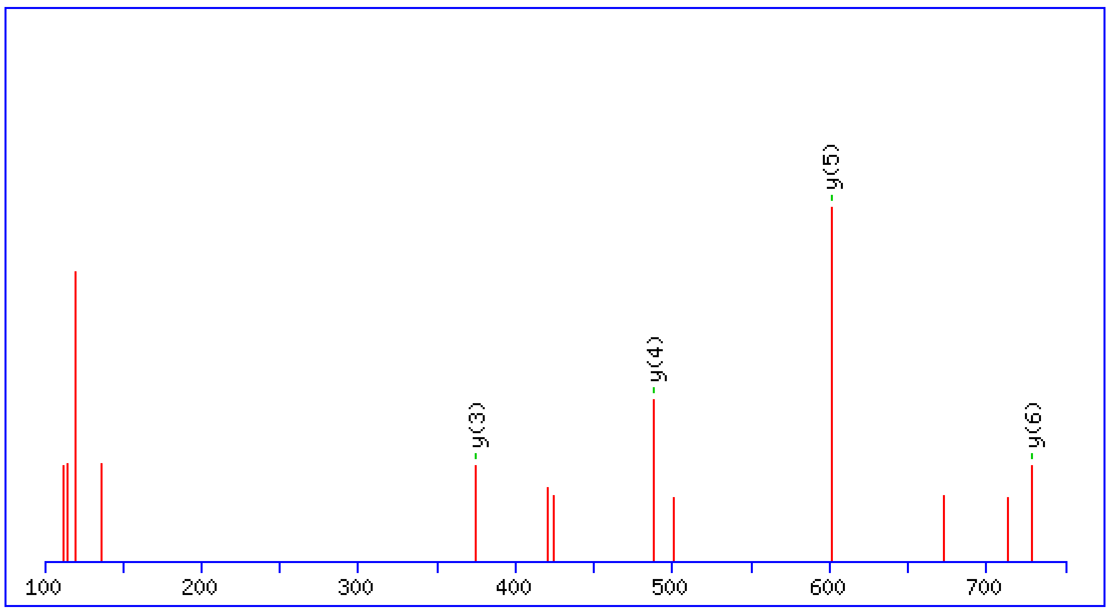
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKLPDLK**
Found in **TRPM6_HUMAN**, Transient receptor potential cation channel subfamily M member 6 OS=Homo sapiens GN=TRPM6 PE=1 SV=2

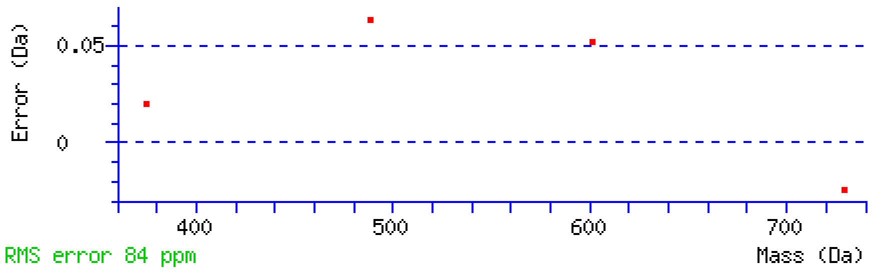
Match to Query 2344: 841.531708 from(421.773130,2+) rtinseconds(2790) index(33831)
Title: Locus:1.1.1.2559.3
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

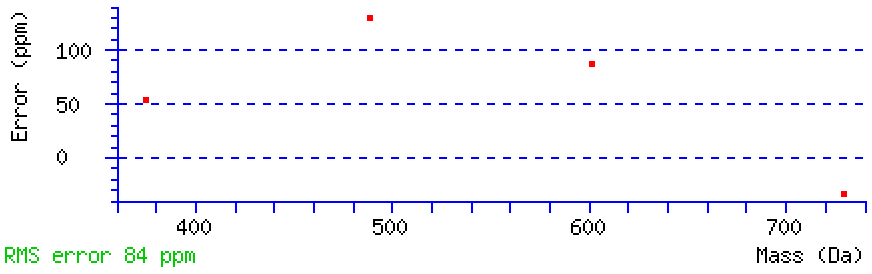
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 841.527283
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 30 **Expect:** 0.0069
Matches : 4/58 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							7
2	242.186303	121.596790	225.159754	113.083515			K	*729.450517*	365.228897	712.423968	356.715622	711.439952	356.223614	6
3	355.270367	178.138822	338.243818	169.625547			L	*601.355554*	301.181415	584.329005	292.668141	583.344989	292.176133	5
4	468.318046	234.662661	451.291497	226.149387			P	*488.271490*	244.639383	471.244941	236.126108	470.260925	235.634100	4
5	583.344989	292.176133	566.318440	283.662858	565.334424	283.170850	D	*375.223811*	188.115543	358.197262	179.602269	357.213246	179.110261	3
6	696.429053	348.718165	679.402504	340.204890	678.418488	339.712882	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 LKLPDLK
(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	841.527283	0.004425	LKLPDLK
30.4	841.538513	-0.006805	LQILSLR
16.3	841.538513	-0.006805	LKLSPLR
16.3	841.527283	0.004425	LKPVLEK
13.9	841.527283	0.004425	LLQIIDK
2.5	841.538528	-0.006820	KLLVVDR
2.5	841.527283	0.004425	QILEVLK
2.5	841.538513	-0.006805	QLINVKK
2.5	841.538513	-0.006805	QLLNKVK
1.9	841.538498	-0.006790	IKALLER

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

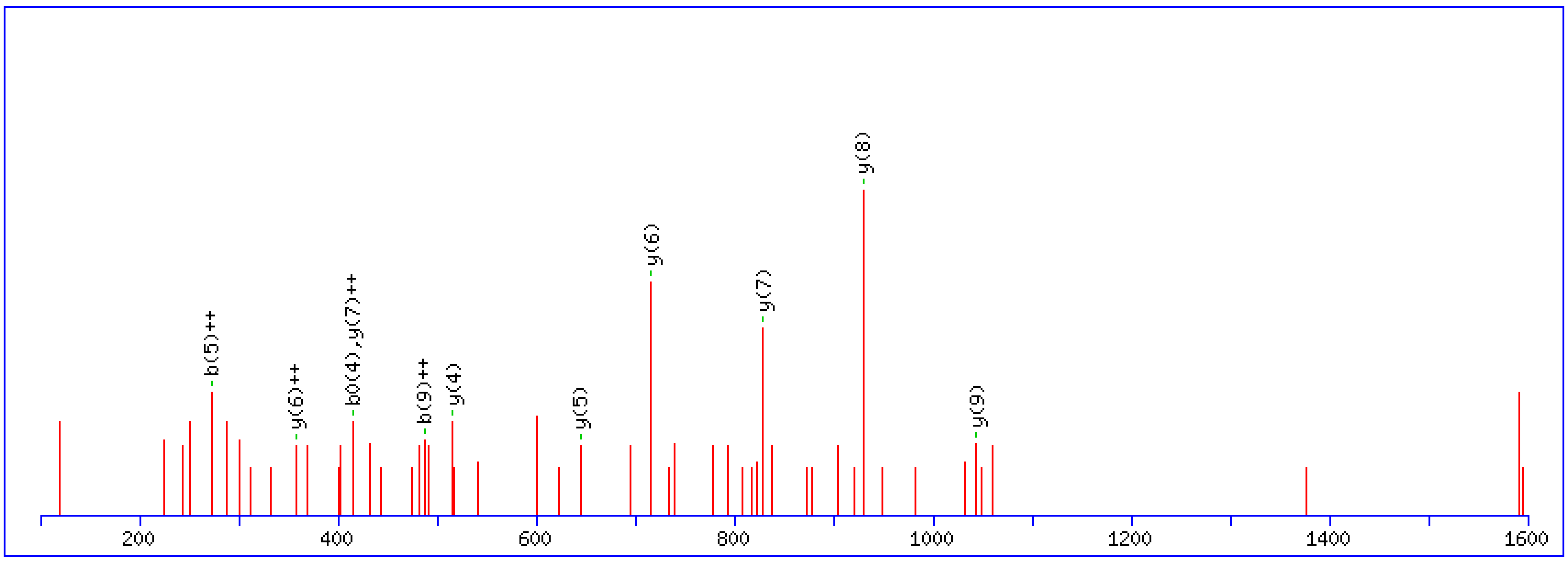
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFLTLAEDILR**
Found in **RAB10_HUMAN**, Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1

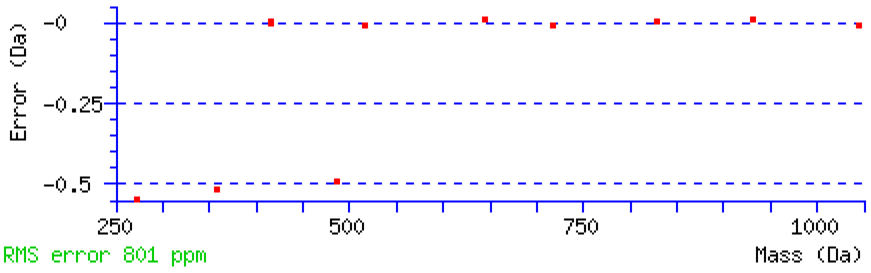
Match to Query 14979: 1260.713208 from(631.363880,2+) rtinseconds(4082) index(58815)
Title: Locus:1.1.1.2261.14
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

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 ●

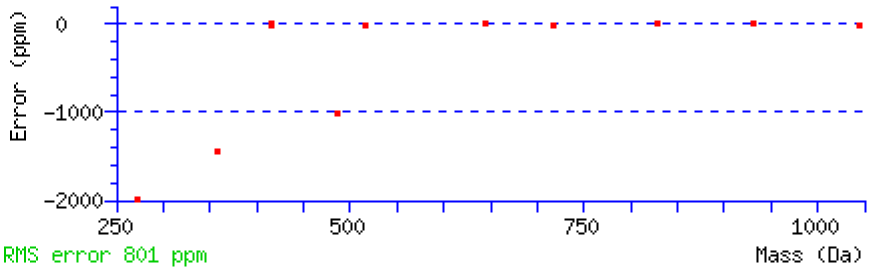


```
Monoisotopic mass of neutral peptide Mr(calc): 1260.707764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0029
Matches : 11/88 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833			A							11
2	219.112804	110.060040			F	1190.677951	595.842613	1173.651402	587.329339	1172.667386	586.837331	10
3	332.196868	166.602072			L	***1043.609537***	522.308406	1026.582988	513.795132	1025.598972	513.303124	9
4	433.244547	217.125912	415.233982	208.120629	T	***930.525473***	465.766374	913.498924	457.253100	912.514908	456.761092	8
5	546.328611	**273.667944**	528.318046	264.662661	L	***829.477794***	415.242535	812.451245	406.729260	811.467229	406.237252	7
6	617.365725	309.186501	599.355160	300.181218	A	***716.393730***	358.700503	699.367181	350.187228	698.383165	349.695220	6
7	746.408318	373.707797	728.397753	364.702515	E	***645.356616***	323.181946	628.330067	314.668671	627.346051	314.176663	5
8	861.435261	431.221269	843.424696	422.215986	D	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	4
9	974.519325	**487.763301**	956.508760	478.758018	I	401.287080	201.147178	384.260531	192.633903			3
10	1087.603389	544.305332	1069.592824	535.300050	L	288.203016	144.605146	271.176467	136.091871			2
11					R	175.118952	88.063114	158.092403	79.549839			1



RMS error 801 ppm



RMS error 801 ppm

NCBI **BLAST** search of AFLTLAEDILR
(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	1260.707764	0.005444	AFLTLAEDILR

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

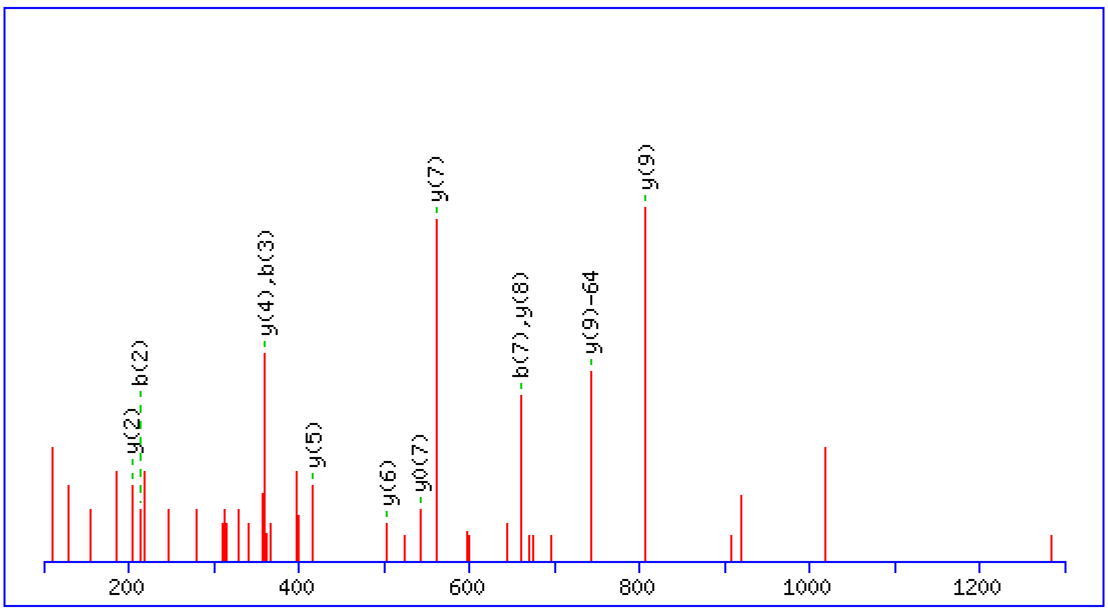
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIMVGSGGVGK**
Found in **RALA_HUMAN**, Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1

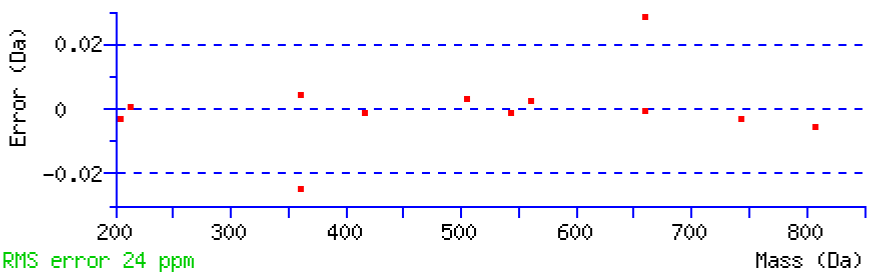
Match to Query 13346: 1018.543548 from(510.279050,2+) rtinseconds(1498) index(11602)
Title: Locus:1.1.1.2013.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

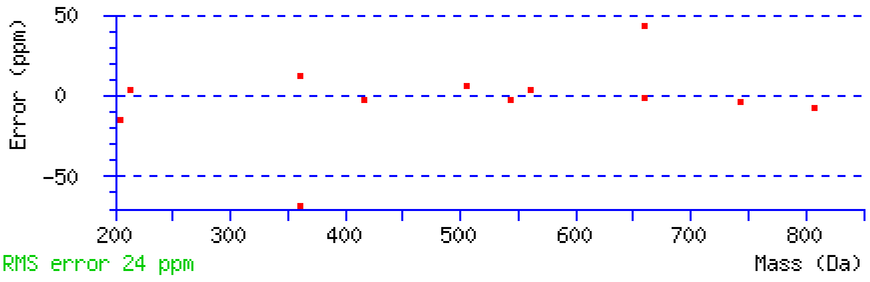
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1018.548141
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: 44  Expect: 0.0001
Matches : 12/118 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	**213.159754**	107.083515			I	920.486980	460.747128	903.460431	452.233854	902.476415	451.741846	10
3	**360.195154**	180.601215			M	***807.402916***	404.205096	790.376367	395.691822	789.392351	395.199814	9
4	459.263568	230.135422			V	***660.367516***	330.687396	643.340967	322.174122	642.356951	321.682114	8
5	516.285032	258.646154			G	***561.299102***	281.153189	544.272553	272.639915	543.288537	272.147907	7
6	603.317060	302.162168	585.306495	293.156885	S	***504.277638***	252.642457	487.251089	244.129183	486.267073	243.637175	6
7	**660.338524**	330.672900	642.327959	321.667618	G	***417.245610***	209.126443	400.219061	200.613169			5
8	717.359988	359.183632	699.349423	350.178350	G	***360.224146***	180.615711	343.197597	172.102437			4
9	816.428402	408.717839	798.417837	399.712557	V	303.202682	152.104979	286.176133	143.591704			3
10	873.449866	437.228571	855.439301	428.223289	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 VIMVGSGGVGK
(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	1018.548141	-0.004593	VIMVGSGGVGK
1.0	1018.533493	0.010055	IVFSPEEAK

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

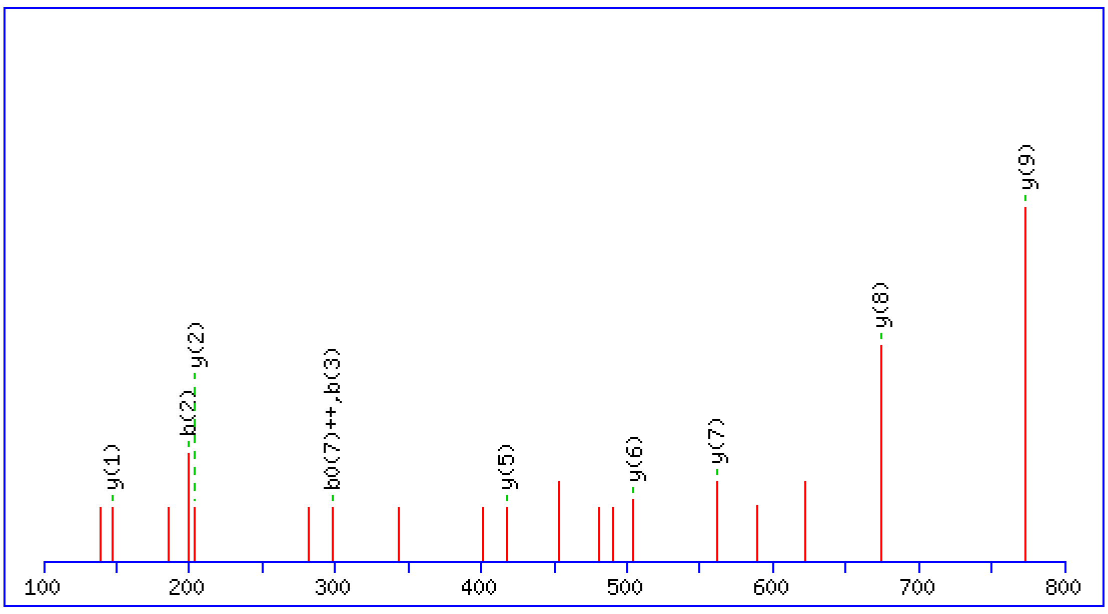
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVLGSGGVGK**
Found in **RAP2A_HUMAN**, Ras-related protein Rap-2a OS=Homo sapiens GN=RAP2A PE=1 SV=1

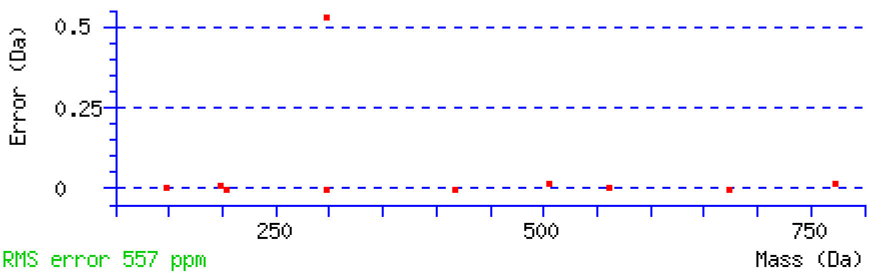
Match to Query 9084: 970.583668 from(486.299110,2+) rtinseconds(1774) index(8990)
Title: Locus:1.1.1.2173.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

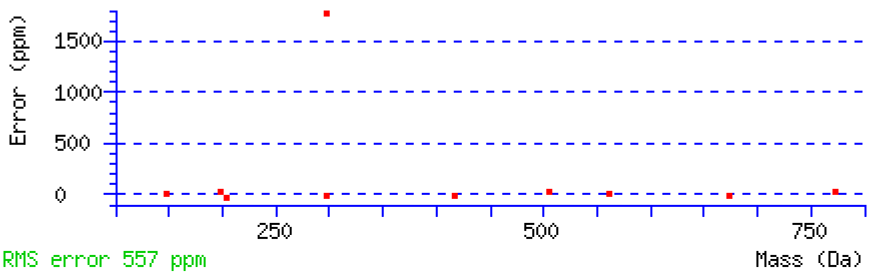
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 970.581161
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00026
Matches : 10/80 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	**199.144104**	100.075690			V	872.519994	436.763635	855.493445	428.250361	854.509429	427.758353	10
3	**298.212518**	149.609897			V	***773.451580***	387.229428	756.425031	378.716154	755.441015	378.224146	9
4	411.296582	206.151929			L	***674.383166***	337.695221	657.356617	329.181947	656.372601	328.689939	8
5	468.318046	234.662661			G	***561.299102***	281.153189	544.272553	272.639915	543.288537	272.147907	7
6	555.350074	278.178675	537.339509	269.173393	S	***504.277638***	252.642457	487.251089	244.129183	486.267073	243.637175	6
7	612.371538	306.689407	594.360973	297.684125	G	***417.245610***	209.126443	400.219061	200.613169			5
8	669.393002	335.200139	651.382437	326.194857	G	360.224146	180.615711	343.197597	172.102437			4
9	768.461416	384.734346	750.450851	375.729064	V	303.202682	152.104979	286.176133	143.591704			3
10	825.482880	413.245078	807.472315	404.239796	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 VVVLGSGGVGK
(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	970.581161	0.002507	VVVLGSGGVGK
10.2	970.592377	-0.008709	VVVSGGRGLK
2.3	970.581116	0.002552	IGIGELITR
0.8	970.585159	-0.001491	VPTGLPFIK

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

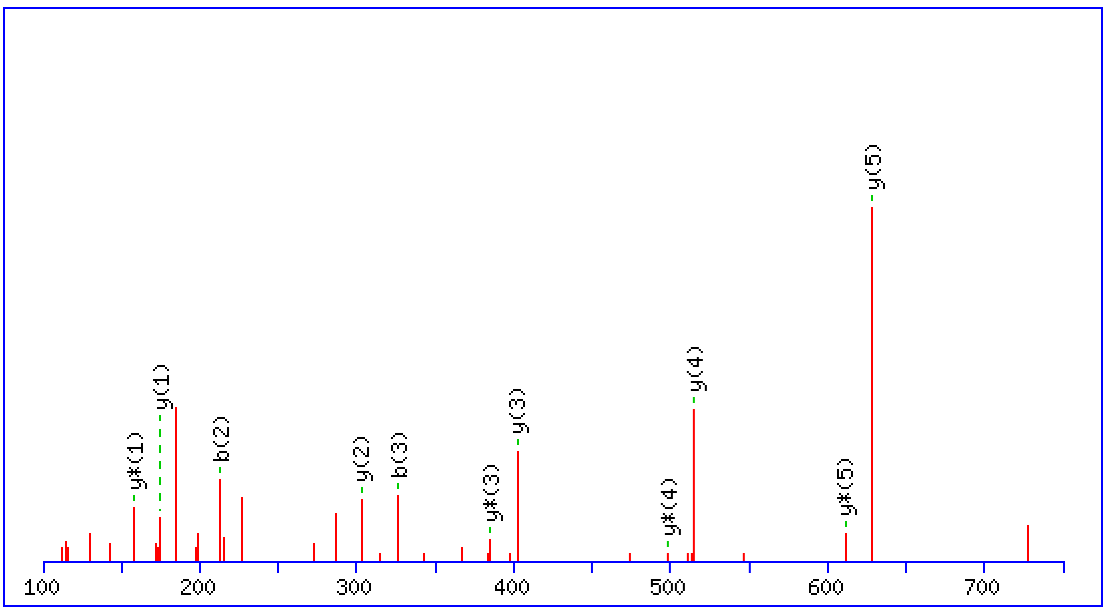
Mascot Search Results

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

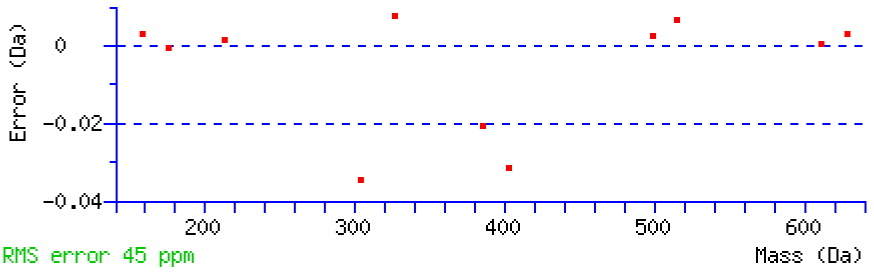
Match to Query 1281: 839.559428 from(420.786990,2+) rtinseconds(2384) index(26660)
Title: Locus:1.1.1.2689.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

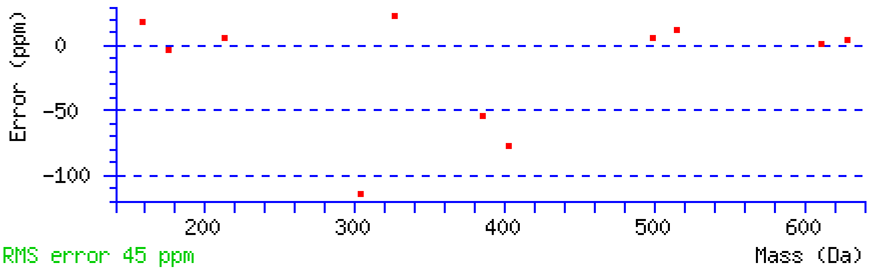
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 839.559265
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 35 **Expect:** 0.00035
Matches : 11/38 fragment ions using 18 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
35.4	839.559265	0.000163	VIIPVKR
23.4	839.559265	0.000163	VLLLGAVR
21.5	839.559265	0.000163	VLPVIKR
19.7	839.559265	0.000163	LPVLKVR
15.7	839.559265	0.000163	IVVLLQR
10.0	839.559265	0.000163	LVQLLVR
7.5	839.559265	0.000163	IVGLGLLR
6.3	839.559250	0.000178	LKITIPR
4.7	839.559250	0.000178	LLTLKPR
0.8	839.559265	0.000163	VIVGALLR

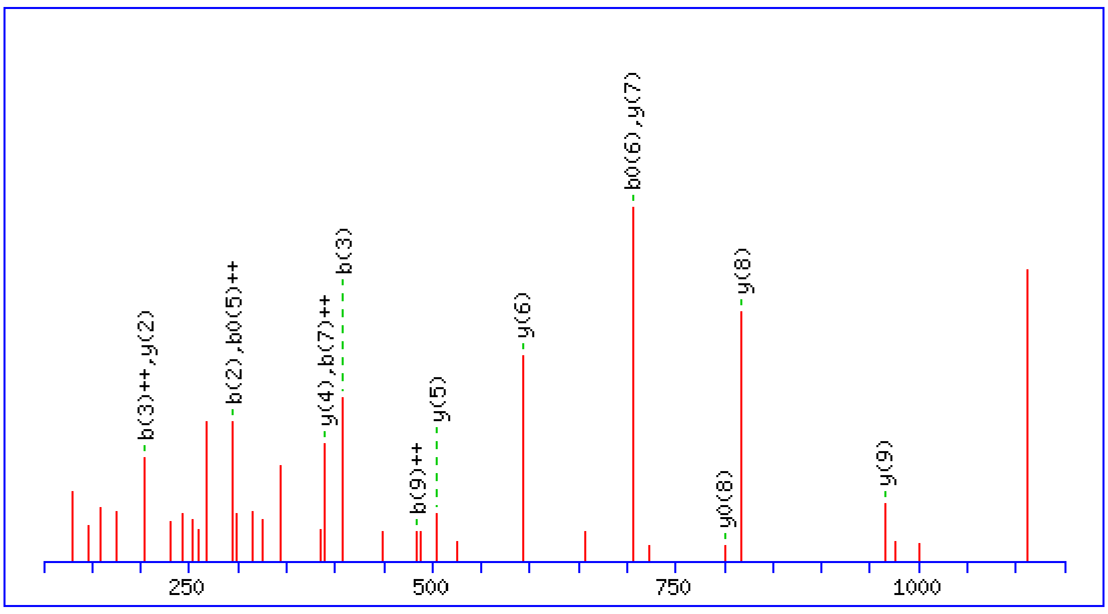
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MFILSDGEGK**
Found in **RFA3_HUMAN**, Replication protein A 14 kDa subunit OS=Homo sapiens GN=RPA3 PE=1 SV=1

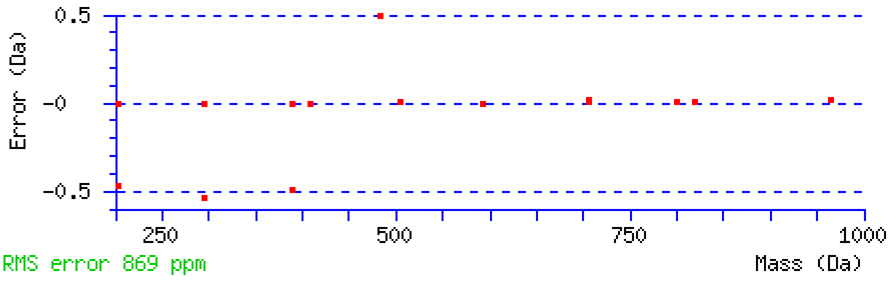
Match to Query 7462: 1111.522348 from(556.768450,2+) rtinseconds(2179) index(4046)
Title: Locus:1.1.1.2680.4
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

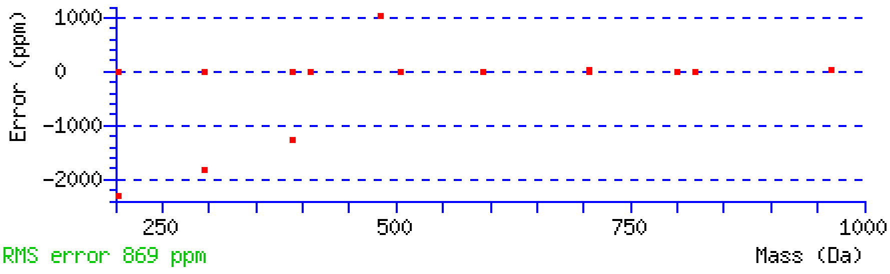
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1111.521957
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: 59 **Expect:** 1.2e-005
Matches : 15/106 fragment ions using 15 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							10
2	**295.111090**	148.059183			F	***965.493838***	483.250557	948.467289	474.737283	947.483273	474.245275	9
3	**408.195154**	**204.601215**			I	***818.425424***	409.716350	801.398875	401.203076	800.414859	400.711068	8
4	521.279218	261.143247			L	***705.341360***	353.174318	688.314811	344.661044	687.330795	344.169036	7
5	608.311246	304.659261	590.300681	295.653978	S	***592.257296***	296.632286	575.230747	288.119012	574.246731	287.627004	6
6	723.338189	362.172733	705.327624	353.167450	D	***505.225268***	253.116272	488.198719	244.602998	487.214703	244.110990	5
7	780.359653	**390.683465**	762.349088	381.678182	G	***390.198325***	195.602801	373.171776	187.089526	372.187760	186.597518	4
8	909.402246	455.204761	891.391681	446.199479	E	333.176861	167.092069	316.150312	158.578794	315.166296	158.086786	3
9	966.423710	**483.715493**	948.413145	474.710211	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 MFILSDGEGK
(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	1111.521957	0.000391	MFILSDGEGK
14.4	1111.533157	-0.010809	KYGNEIMNK
13.1	1111.518768	0.003580	MMEIAKAMR
7.0	1111.518768	0.003580	MMEIAKAMR
6.9	1111.518768	0.003580	MMEIAKAMR
3.2	1111.529831	-0.007483	FPSPHPSPAK
0.9	1111.518600	0.003748	ASVFYGPDPK
0.5	1111.525818	-0.003470	GSQGPPGPTGNK

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

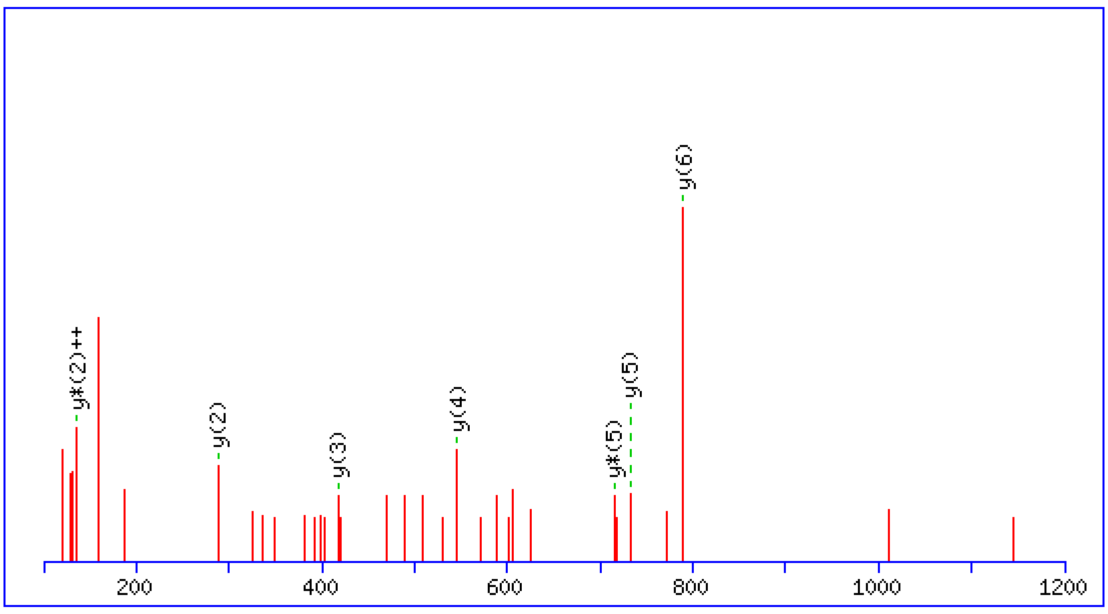
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGWEELR**
Found in **RCN3_HUMAN**, Reticulocalbin-3 OS=Homo sapiens GN=RCN3 PE=1 SV=1

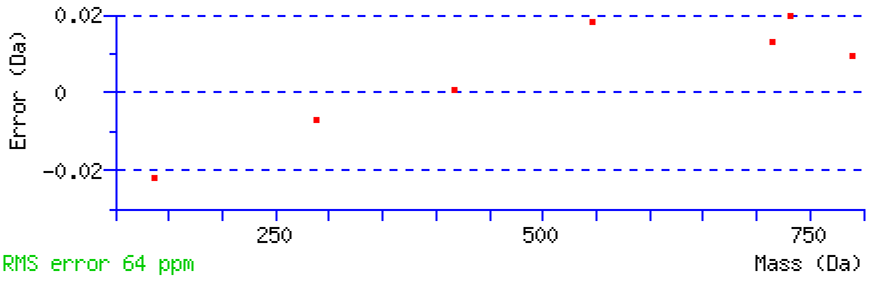
Match to Query 3716: 887.452028 from(444.733290,2+) rtinseconds(2241) index(25098)
Title: Locus:1.1.1.2391.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

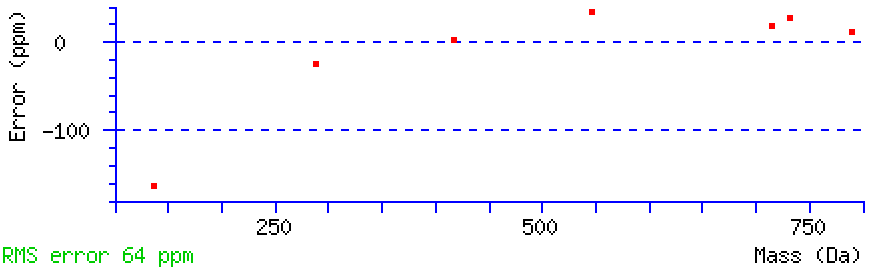
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 887.450104
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.008
Matches : 7/50 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**							7
2	157.097154	79.052215			**G**	***789.388979***	395.198128	772.362430	386.684853	771.378414	386.192845	6
3	343.176467	172.091872			**W**	***732.367515***	366.687396	715.340966	358.174121	714.356950	357.682113	5
4	472.219060	236.613168	454.208495	227.607886	**E**	***546.288202***	273.647739	529.261653	265.134465	528.277637	264.642457	4
5	601.261653	301.134465	583.251088	292.129182	**E**	***417.245609***	209.126443	400.219060	200.613168	399.235044	200.121160	3
6	714.345717	357.676497	696.335152	348.671214	**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 VGWEELR
(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	887.450104	0.001924	VGWEELR
18.3	887.446075	0.005953	RSVEEPR
7.8	887.450134	0.001894	VPSPFGPR
5.6	887.450134	0.001894	VPSPFGPR
4.4	887.453476	-0.001448	VAVEAPMR
4.2	887.453476	-0.001448	VAVEAPMR
3.3	887.453461	-0.001433	MINPELR
3.2	887.460007	-0.007979	VADPTLEK

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

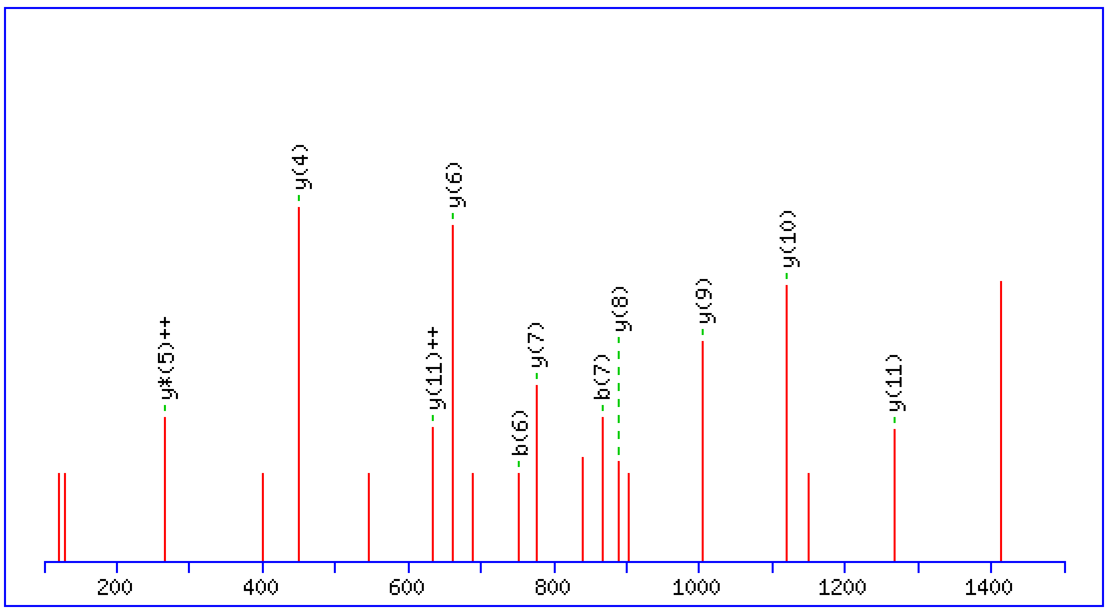
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFDDDLLVSTSR**
Found in **PDE6D_HUMAN**, Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta OS=Homo sapiens GN=PDE6D PE=1 SV=1

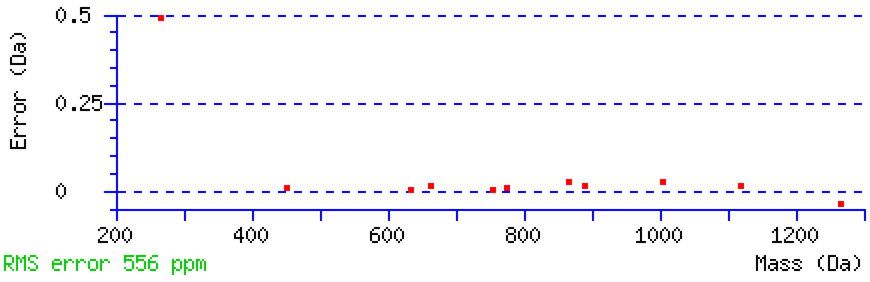
Match to Query 27063: 1413.684228 from(707.849390,2+) rtinseconds(3179) index(33613)
Title: Locus:1.1.1.2706.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

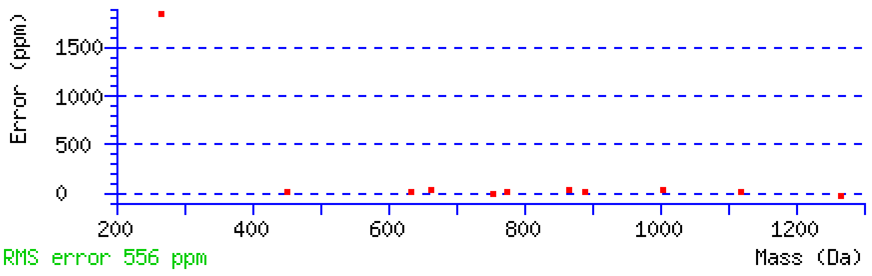
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1413.677628
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 6.1e-005
Matches : 11/104 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							12
2	295.144104	148.075690			F	***1267.616472***	634.311874	1250.589923	625.798600	1249.605907	625.306591	11
3	410.171047	205.589161	392.160482	196.583879	D	***1120.548058***	560.777667	1103.521509	552.264393	1102.537493	551.772385	10
4	525.197990	263.102633	507.187425	254.097351	D	***1005.521115***	503.264196	988.494566	494.750921	987.510550	494.258913	9
5	640.224933	320.616105	622.214368	311.610822	D	***890.494172***	445.750724	873.467623	437.237450	872.483607	436.745442	8
6	**753.308997**	377.158137	735.298432	368.152854	L	***775.467229***	388.237253	758.440680	379.723978	757.456664	379.231970	7
7	**866.393061**	433.700169	848.382496	424.694886	L	***662.383165***	331.695221	645.356616	323.181946	644.372600	322.689938	6
8	965.461475	483.234376	947.450910	474.229093	V	549.299101	275.153189	532.272552	266.639914	531.288536	266.147906	5
9	1052.493503	526.750389	1034.482938	517.745107	S	***450.230687***	225.618981	433.204138	217.105707	432.220122	216.613699	4
10	1153.541182	577.274229	1135.530617	568.268946	T	363.198659	182.102968	346.172110	173.589693	345.188094	173.097685	3
11	1240.573210	620.790243	1222.562645	611.784961	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 FFDDDLLVSTSR
(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	1413.677628	0.006600	FFDDDLLVSTSR
2.0	1413.684799	-0.000571	ERNPLTPASEPR
1.7	1413.674454	0.009774	MSVKSPFNVMSR

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

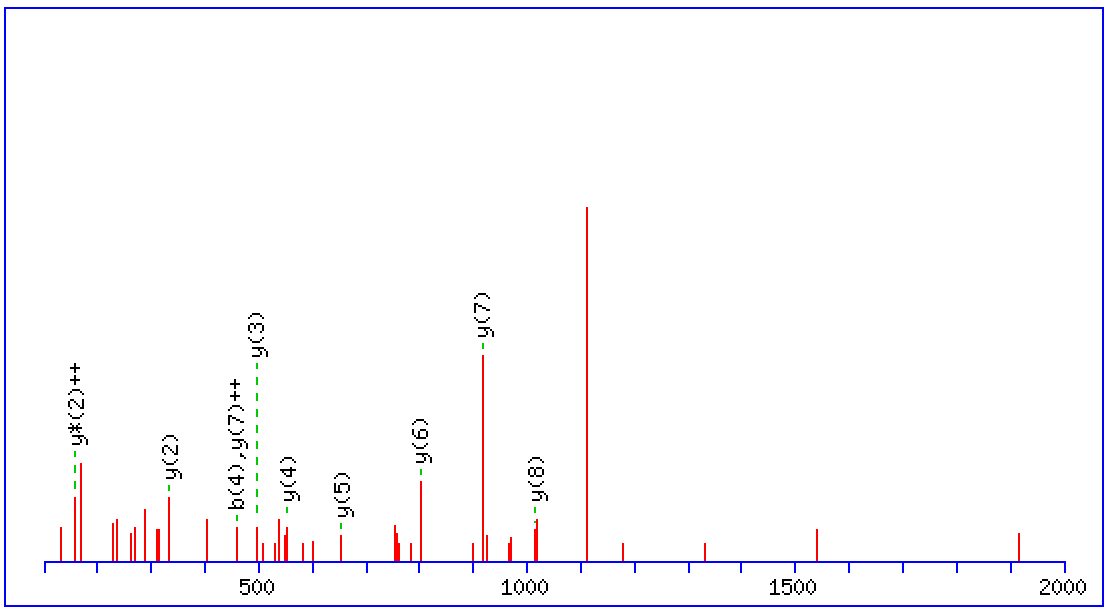
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **PVDFTGYWK**
Found in **RET1_HUMAN**, Retinol-binding protein 1 OS=Homo sapiens GN=RBP1 PE=1 SV=2

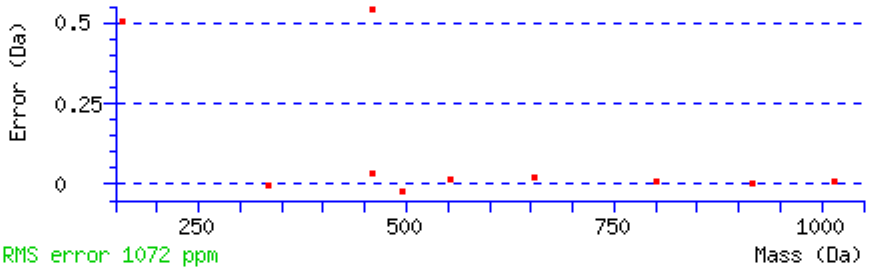
Match to Query 6175: 1111.535268 from(556.774910,2+) rtinseconds(2976) index(10289)
Title: Locus:1.1.1.3037.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

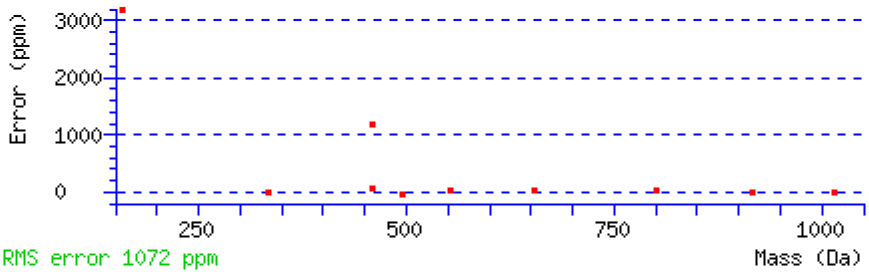
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1111.533859
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 7.6e-005
Matches : 10/68 fragment ions using 17 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	98.060040	49.533658			P							9
2	197.128454	99.067865			V	***1015.488360***	508.247818	998.461811	499.734544	997.477795	499.242536	8
3	312.155397	156.581336	294.144832	147.576054	D	***916.419946***	458.713611	899.393397	450.200337	898.409381	449.708329	7
4	459.223811	230.115544	441.213246	221.110261	F	***801.393003***	401.200140	784.366454	392.686865	783.382438	392.194857	6
5	560.271490	280.639383	542.260925	271.634101	T	***654.324589***	327.665933	637.298040	319.152658	636.314024	318.660650	5
6	617.292954	309.150115	599.282389	300.144833	G	***553.276910***	277.142093	536.250361	268.628819			4
7	780.356283	390.681780	762.345718	381.676497	Y	***496.255446***	248.631361	479.228897	240.118086			3
8	966.435596	483.721436	948.425031	474.716154	W	***333.192117***	167.099696	316.165568	158.586422			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of PVDFTGYWK
(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	1111.533859	0.001409	PVDFTGYWK
0.4	1111.525803	0.009465	VPPDERDPR

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

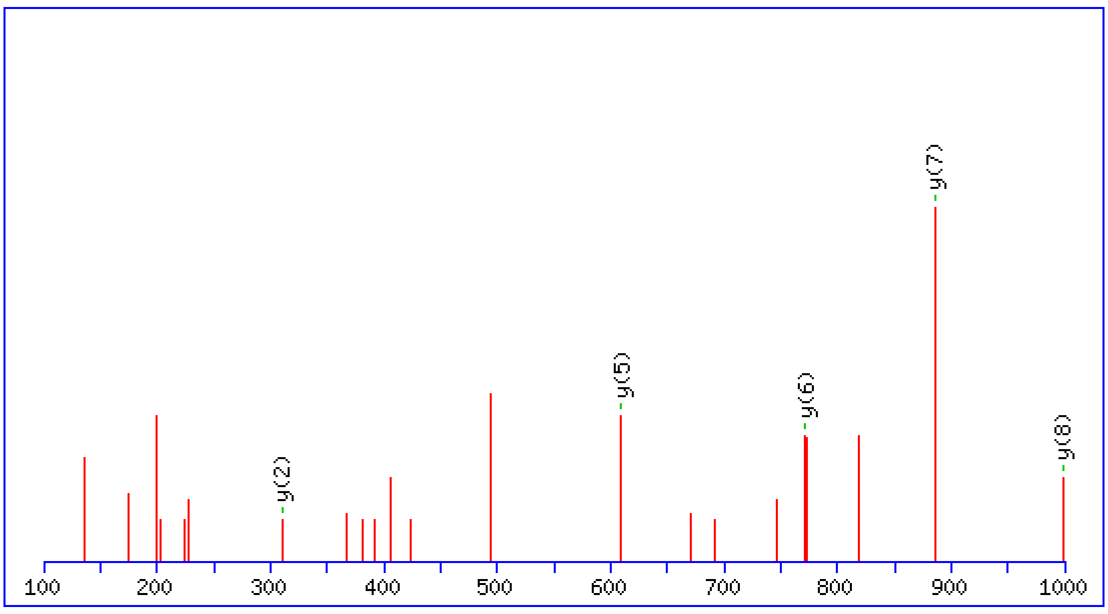
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIPYLDAYK**
Found in **RHG05_HUMAN**, Rho GTPase-activating protein 5 OS=Homo sapiens GN=ARHGAP5 PE=1 SV=2

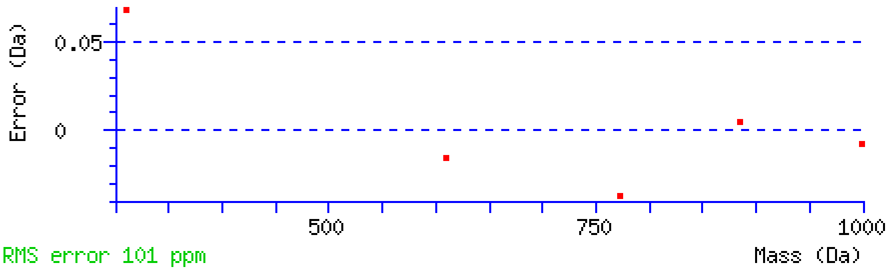
Match to Query 14135: 1110.606388 from(556.310470,2+) rtinseconds(3248) index(37538)
Title: Locus:1.1.1.2882.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

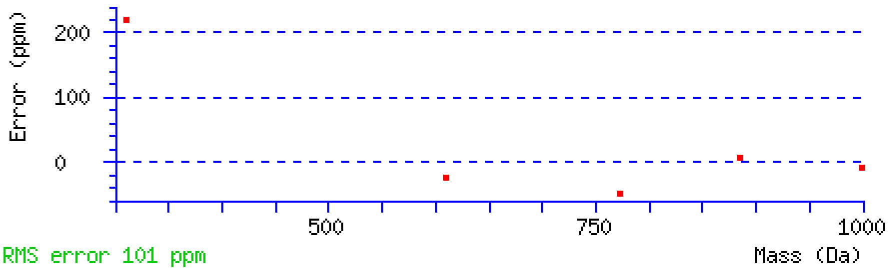
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1110.596085
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3      : Oxidation (P)
Ions Score: 32  Expect: 0.0052
Matches : 5/64 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			I							9
2	227.175404	114.091340			I	***998.519326***	499.763301	981.492777	491.250026	980.508761	490.758018	8
3	340.223083	170.615179			P	***885.435262***	443.221269	868.408713	434.707994	867.424697	434.215986	7
4	503.286412	252.146844			Y	***772.387583***	386.697430	755.361034	378.184155	754.377018	377.692147	6
5	616.370476	308.688876			L	***609.324254***	305.165765	592.297705	296.652491	591.313689	296.160483	5
6	731.397419	366.202348	713.386854	357.197065	D	496.240190	248.623733	479.213641	240.110458	478.229625	239.618450	4
7	802.434533	401.720905	784.423968	392.715622	A	381.213247	191.110261	364.186698	182.596987			3
8	965.497862	483.252569	947.487297	474.247286	Y	***310.176133***	155.591704	293.149584	147.078430			2
9					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IIPYLDAYK
(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	1110.596085	0.010303	IIPYLDAYK
10.9	1110.614731	-0.008343	IPMLFLFSK
10.5	1110.603302	0.003086	LLPPPKNER
2.5	1110.614548	-0.008160	LPTSAPRPTR
2.1	1110.603317	0.003071	LPGEAPVIQR
1.1	1110.607330	-0.000942	LLVPAYTYR
0.1	1110.603302	0.003086	ILPGGAAEQAGK

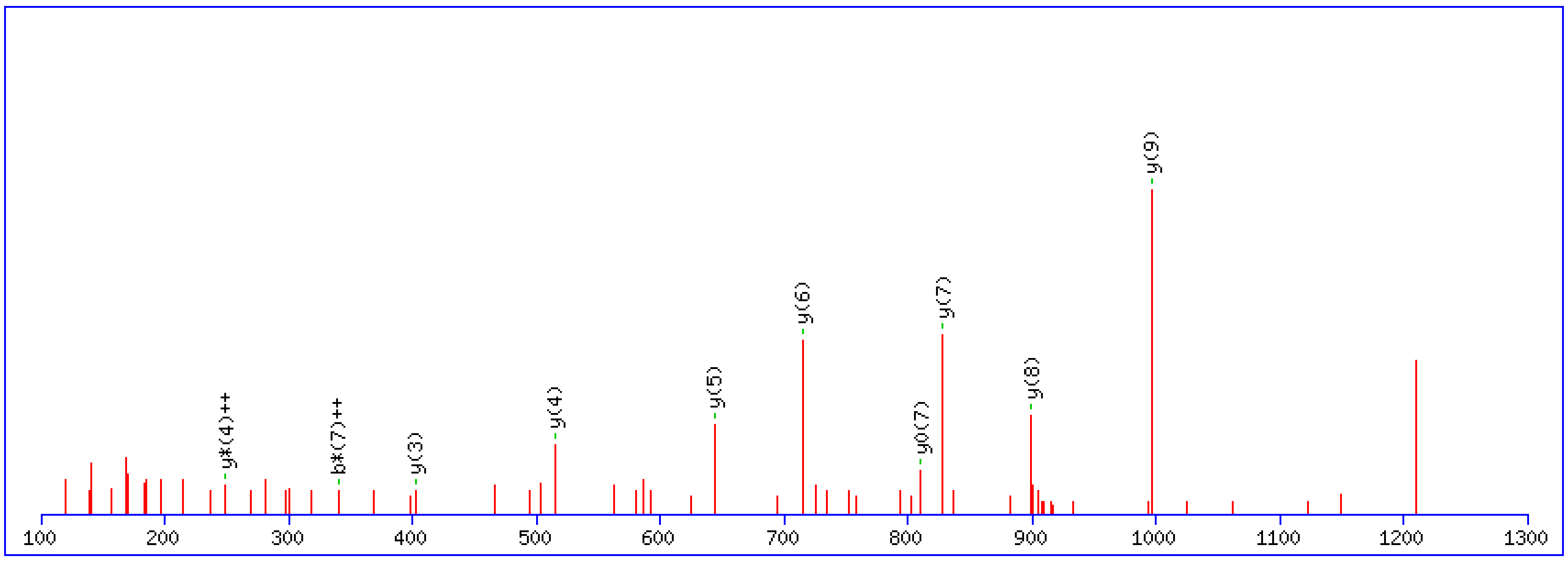
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNPALAELNLR**
Found in **RINI_HUMAN**, Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2

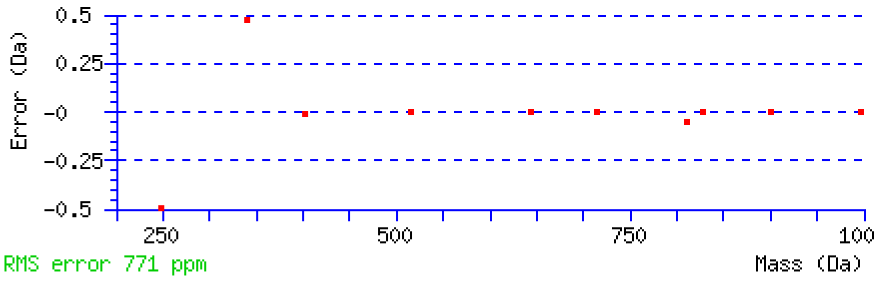
Match to Query 12435: 1208.693388 from(605.353970,2+) rtinseconds(2507) index(29566)
Title: Locus:1.1.1.1660.14
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

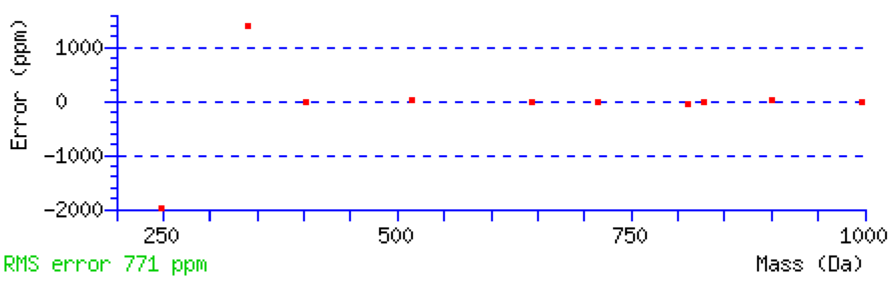
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1208.687683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00049
Matches : 10/98 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	100.075690	50.541483					V							11
2	214.118617	107.562947	197.092068	99.049672			N	1110.626583	555.816930	1093.600034	547.303655	1092.616018	546.811647	10
3	311.171381	156.089328	294.144832	147.576054			P	***996.583656***	498.795466	979.557107	490.282192	978.573091	489.790184	9
4	382.208495	191.607886	365.181946	183.094611			A	***899.530892***	450.269084	882.504343	441.755810	881.520327	441.263802	8
5	495.292559	248.149918	478.266010	239.636643			L	***828.493778***	414.750527	811.467229	406.237253	810.483213	405.745245	7
6	566.329673	283.668475	549.303124	275.155200			A	***715.409714***	358.208495	698.383165	349.695221	697.399149	349.203213	6
7	695.372266	348.189771	678.345717	339.676497	677.361701	339.184489	E	***644.372600***	322.689938	627.346051	314.176664	626.362035	313.684656	5
8	808.456330	404.731803	791.429781	396.218529	790.445765	395.726521	L	***515.330007***	258.168642	498.303458	249.655367			4
9	922.499257	461.753267	905.472708	453.239992	904.488692	452.747984	N	***402.245943***	201.626609	385.219394	193.113335			3
10	1035.583321	518.295299	1018.556772	509.782024	1017.572756	509.290016	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 VNPALAELNLR
(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	1208.687683	0.005705	VNPALAELNLR

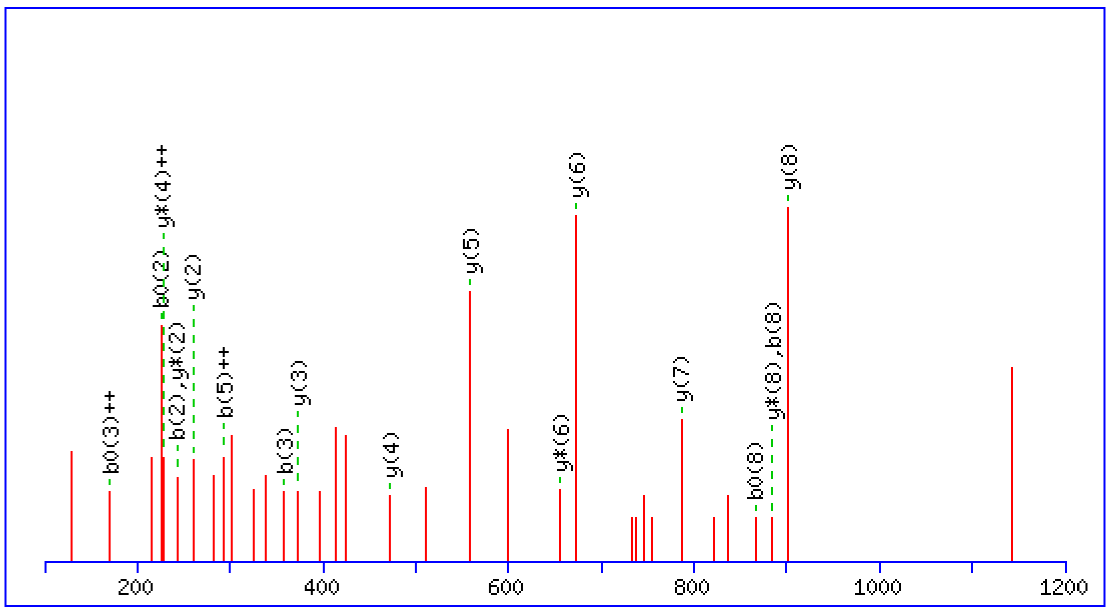
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELDLNSVLLK**
Found in **RNT2_HUMAN**, Ribonuclease T2 OS=Homo sapiens GN=RNASET2 PE=1 SV=2

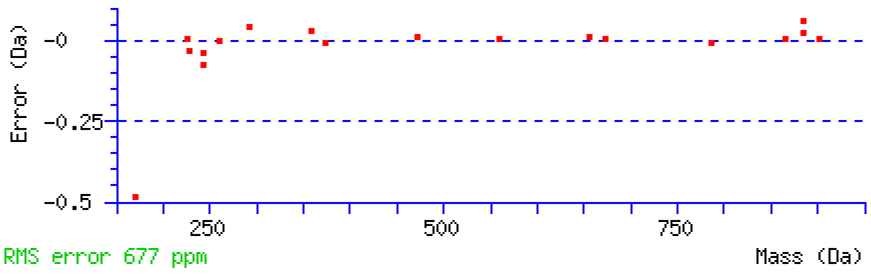
Match to Query 11206: 1142.656328 from(572.335440,2+) rtinseconds(3262) index(22665)
Title: Locus:1.1.1.2823.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

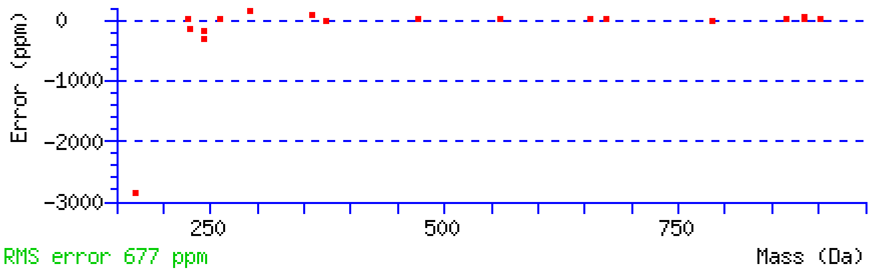
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1142.654663
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00053
Matches : 18/92 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							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
41.6	1142.654663	0.001665	ELDLNSVLLK
10.9	1142.654663	0.001665	LEDLATLIQK
7.3	1142.665909	-0.009581	TKQIQEGVIK
4.7	1142.665894	-0.009566	LEGEVRSLLK
4.1	1142.665894	-0.009566	NQEVTIKALK
3.1	1142.654694	0.001634	GTTLVVELAPK

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

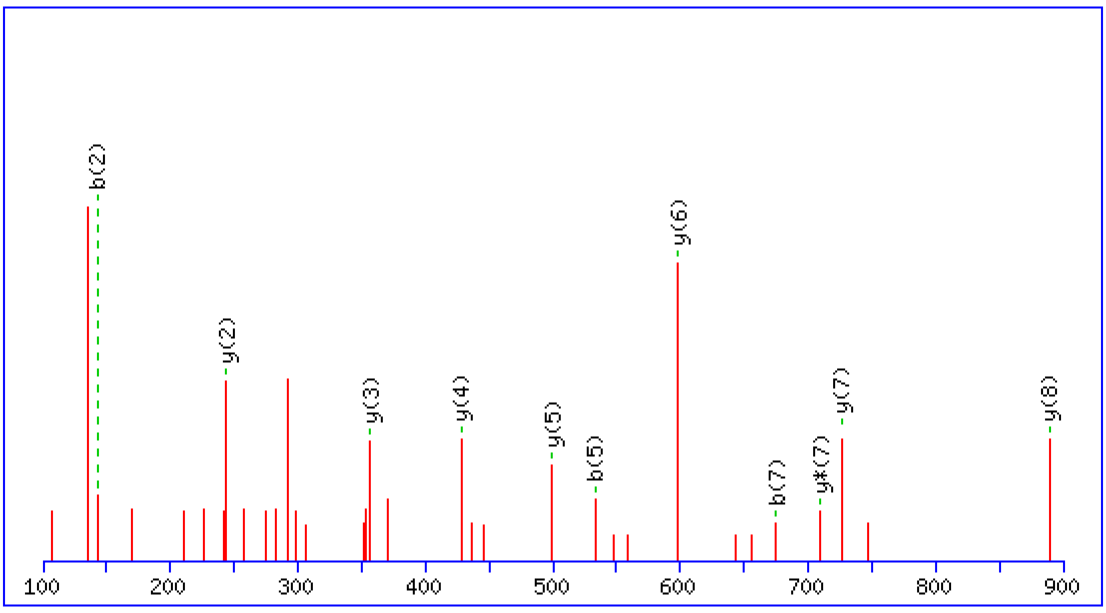
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAYQVAALPK**
Found in **UK114_HUMAN**, Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1

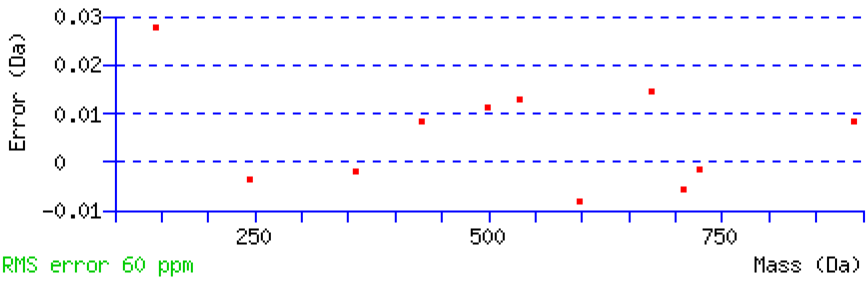
Match to Query 7043: 1030.580688 from(516.297620,2+) rtinseconds(2072) index(5304)
Title: Locus:1.1.1.2547.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

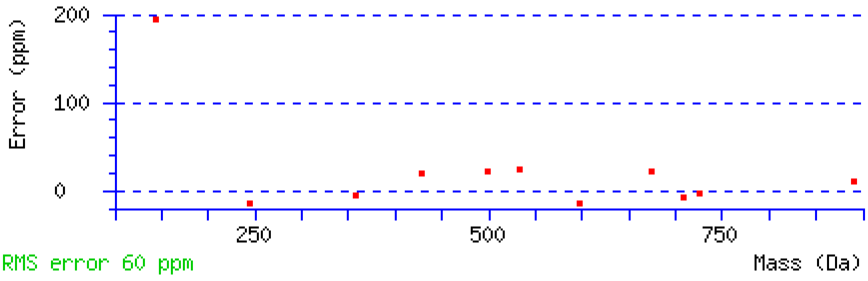
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1030.581100
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 7.4e-006
Matches : 11/66 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.044390	36.525833			A					10
2	**143.081504**	72.044390			A	960.551295	480.779286	943.524746	472.266011	9
3	306.144833	153.576055			Y	***889.514181***	445.260729	872.487632	436.747454	8
4	434.203411	217.605344	417.176862	209.092069	Q	***726.450852***	363.729064	709.424303	355.215790	7
5	**533.271825**	267.139551	516.245276	258.626276	V	***598.392274***	299.699775	581.365725	291.186501	6
6	604.308939	302.658108	587.282390	294.144833	A	***499.323860***	250.165568	482.297311	241.652293	5
7	**675.346053**	338.176665	658.319504	329.663390	A	***428.286746***	214.647011	411.260197	206.133737	4
8	788.430117	394.718697	771.403568	386.205422	L	***357.249632***	179.128454	340.223083	170.615180	3
9	885.482881	443.245079	868.456332	434.731804	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 AAYQVAALPK
(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	1030.581100	-0.000412	AAYQVAALPK
6.2	1030.577072	0.003616	SRLATLNEK

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

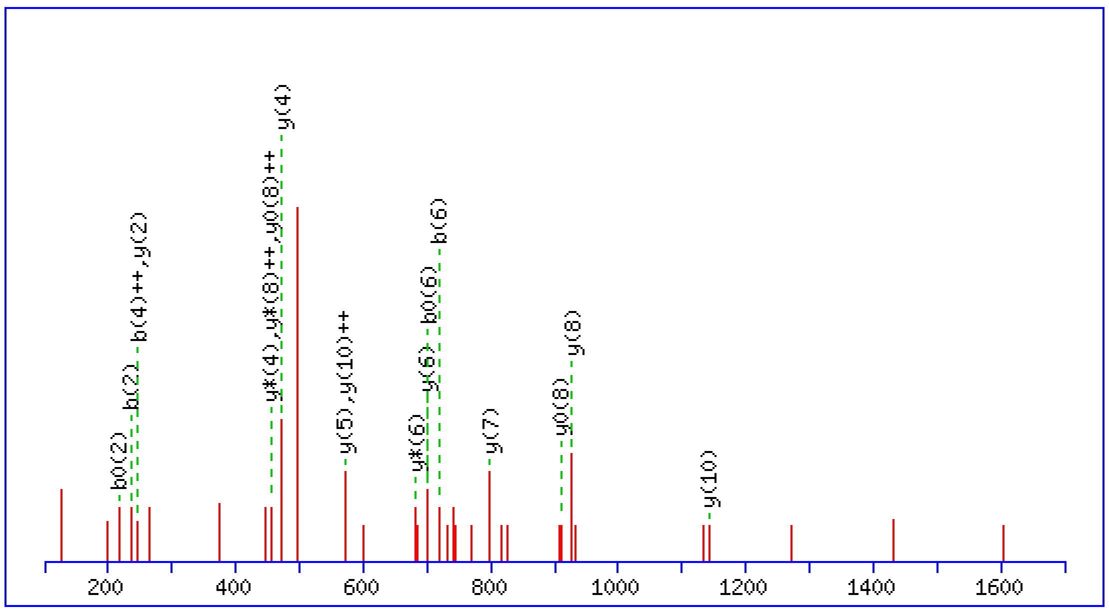
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSQEVQVPEAR**
Found in **RIR2B_HUMAN**, Ribonucleoside-diphosphate reductase subunit M2 B OS=Homo sapiens GN=RRM2B PE=1 SV=1

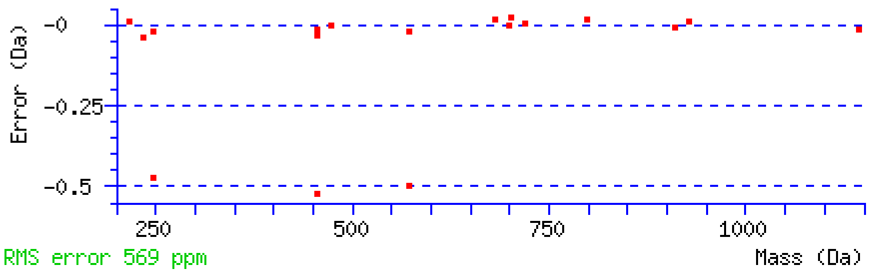
Match to Query 30910: 1288.652768 from(645.333660,2+) rtinseconds(1936) index(19294)
Title: Locus:1.1.1.2228.37
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

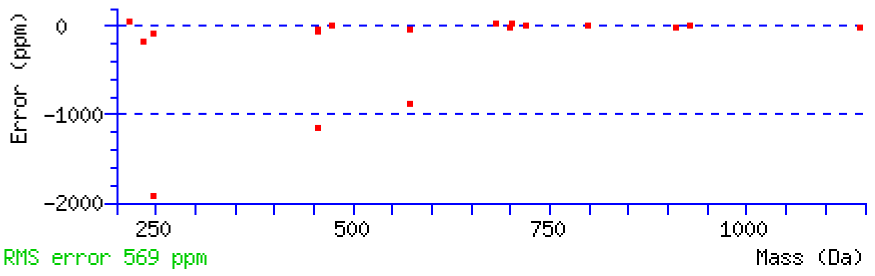
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1288.641159
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0022
Matches : 18/110 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							11
2	**235.107718**	118.057497			217.097153	109.052214	S	***1142.580028***	571.793652	1125.553479	563.280378	1124.569463	562.788370	10
3	363.166296	182.086786	346.139747	173.573512	345.155731	173.081504	Q	1055.548000	528.277638	1038.521451	519.764364	1037.537435	519.272356	9
4	492.208889	246.608082	475.182340	238.094808	474.198324	237.602800	E	***927.489422***	464.248349	910.462873	455.735075	909.478857	455.243067	8
5	591.277303	296.142290	574.250754	287.629015	573.266738	287.137007	V	***798.446829***	399.727053	781.420280	391.213778	780.436264	390.721770	7
6	**719.335881**	360.171579	702.309332	351.658304	701.325316	351.166296	Q	***699.378415***	350.192846	682.351866	341.679571	681.367850	341.187563	6
7	818.404295	409.705786	801.377746	401.192511	800.393730	400.700503	V	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
8	915.457059	458.232168	898.430510	449.718893	897.446494	449.226885	P	***472.251423***	236.629350	455.224874	228.116075	454.240858	227.624067	4
9	1044.499652	522.753464	1027.473103	514.240190	1026.489087	513.748182	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
10	1115.536766	558.272021	1098.510217	549.758747	1097.526201	549.266739	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 FSQEVQVPEAR
(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	1288.641159	0.011609	FSQEVQVPEAR
13.3	1288.655731	-0.002963	MEALQKQQAAR
0.5	1288.662262	-0.009494	IKQELGEESTR

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

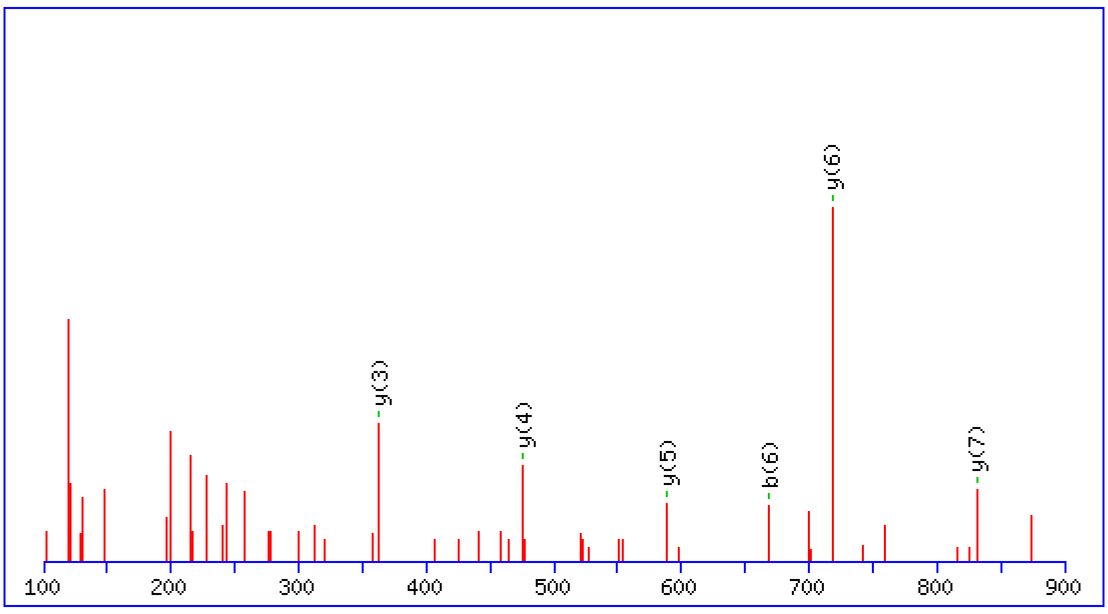
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIEILSEK**
Found in **RRBP1_HUMAN**, Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4

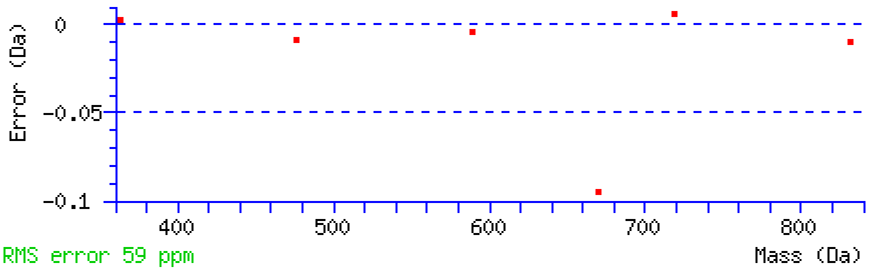
Match to Query 4984: 943.561668 from(472.788110,2+) rtinseconds(2372) index(26419)
Title: Locus:1.1.1.2684.11
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

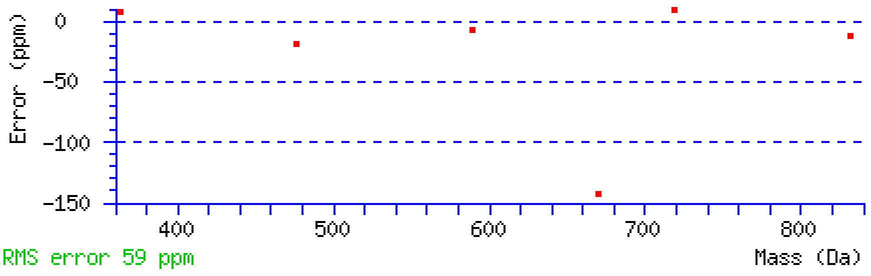
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 943.558960
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0013
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	114.091340	57.549308			L							8
2	227.175404	114.091340			I	*831.482210*	416.244743	814.455661	407.731469	813.471645	407.239461	7
3	356.217997	178.612637	338.207432	169.607354	E	*718.398146*	359.702711	701.371597	351.189437	700.387581	350.697429	6
4	469.302061	235.154669	451.291496	226.149386	I	*589.355553*	295.181415	572.329004	286.668140	571.344988	286.176132	5
5	582.386125	291.696701	564.375560	282.691418	L	*476.271489*	238.639382	459.244940	230.126108	458.260924	229.634100	4
6	669.418153	335.212715	651.407588	326.207432	S	*363.187425*	182.097350	346.160876	173.584076	345.176860	173.092068	3
7	798.460746	399.734011	780.450181	390.728729	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 LIEILSEK
(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	943.558960	0.002708	LIEILSEK
21.6	943.570190	-0.008522	ILKNLESK
14.7	943.570206	-0.008538	AVGKILSEK
12.4	943.558960	0.002708	LLIESLEK
5.7	943.558960	0.002708	ILLLSEEK
5.4	943.552460	0.009208	ILGLPLMR
3.6	943.570221	-0.008553	LLSVKGSPK
2.8	943.570206	-0.008538	LIKSDQLK
0.1	943.552460	0.009208	KPPKVTMK

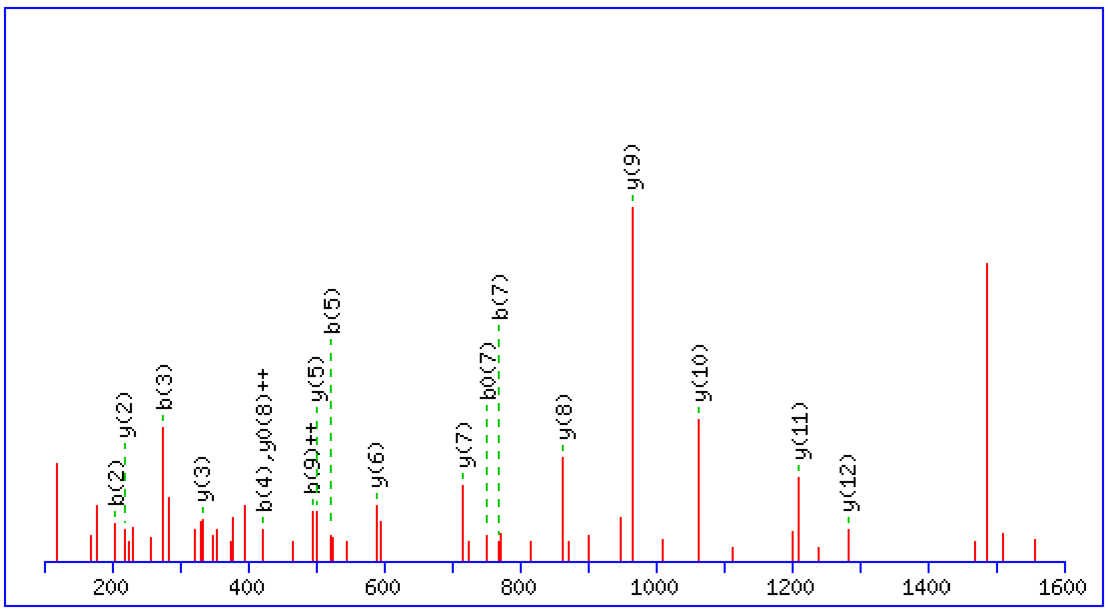
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFAFVTFESPADAK**
Found in **HNRGT_HUMAN**, RNA-binding motif protein, X-linked-like-2 OS=Homo sapiens GN=RBMXL2 PE=1 SV=3

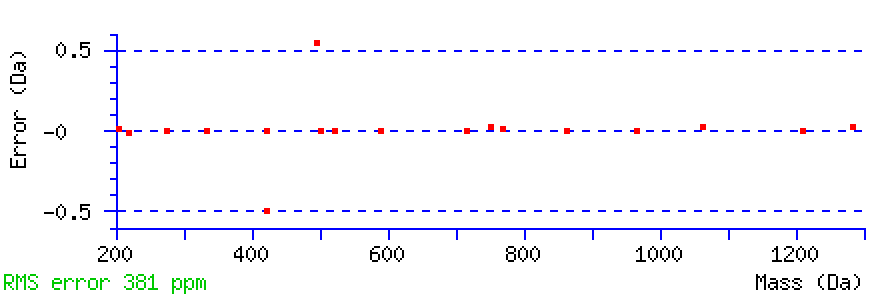
Match to Query 29035: 1485.718868 from(743.866710,2+) rtinseconds(3320) index(35044)
Title: Locus:1.1.1.2758.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

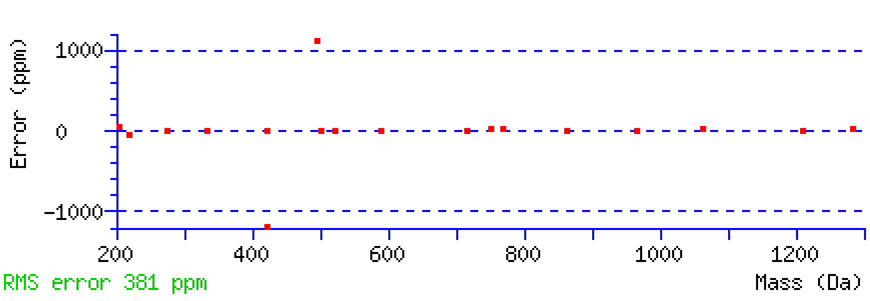
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1485.714005
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59 **Expect:** 1.4e-005
Matches : 18/116 fragment ions using 40 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							14
2	**205.097154**	103.052215			F	1429.699809	715.353543	1412.673260	706.840268	1411.689244	706.348260	13
3	**276.134268**	138.570772			A	***1282.631395***	641.819335	1265.604846	633.306061	1264.620830	632.814053	12
4	**423.202682**	212.104979			F	***1211.594281***	606.300778	1194.567732	597.787504	1193.583716	597.295496	11
5	**522.271096**	261.639186			V	***1064.525867***	532.766572	1047.499318	524.253297	1046.515302	523.761289	10
6	623.318775	312.163026	605.308210	303.157743	T	***965.457453***	483.232365	948.430904	474.719090	947.446888	474.227082	9
7	**770.387189**	385.697232	752.376624	376.691950	F	***864.409774***	432.708525	847.383225	424.195250	846.399209	423.703242	8
8	899.429782	450.218529	881.419217	441.213246	E	***717.341360***	359.174318	700.314811	350.661044	699.330795	350.169036	7
9	986.461810	493.734543	968.451245	484.729260	S	***588.298767***	294.653022	571.272218	286.139747	570.288202	285.647739	6
10	1083.514574	542.260925	1065.504009	533.255642	P	***501.266739***	251.137007	484.240190	242.623733	483.256174	242.131725	5
11	1154.551688	577.779482	1136.541123	568.774199	A	404.213975	202.610626	387.187426	194.097351	386.203410	193.605343	4
12	1269.578631	635.292953	1251.568066	626.287671	D	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
13	1340.615745	670.811510	1322.605180	661.806228	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 GFAFVTFESPADAK
(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	1485.714005	0.004863	GFAFVTFESPADAK

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

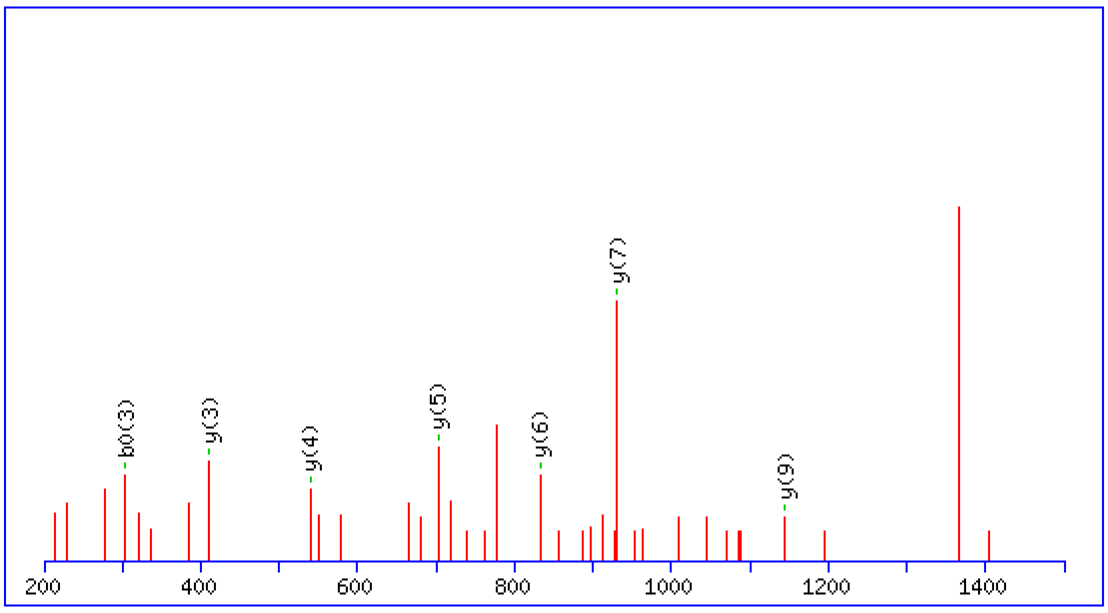
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYTLVEYETYK**
Found in **RBM8A_HUMAN**, RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1

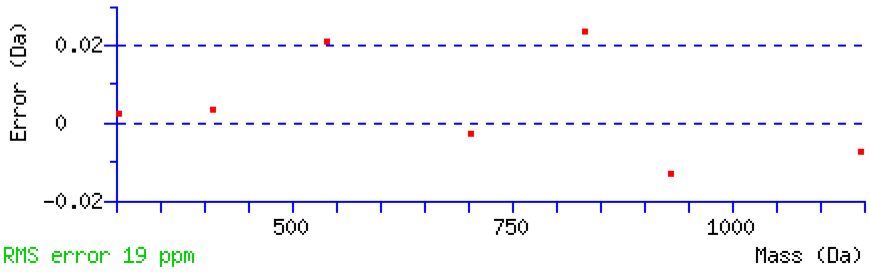
Match to Query 23524: 1364.651028 from(683.332790,2+) rtinseconds(2553) index(24791)
Title: Locus:1.1.1.2620.46
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-5.mgf

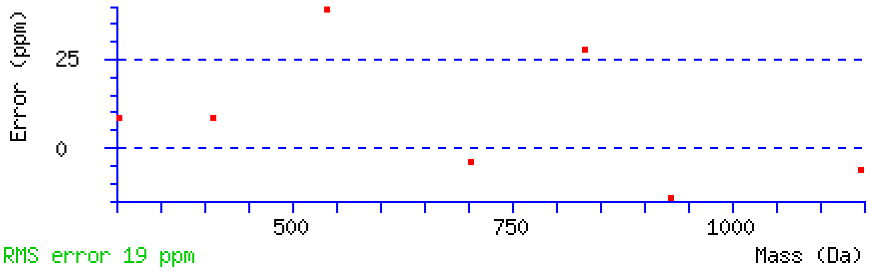
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1364.649979
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00056
Matches : 7/92 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							11
2	221.092069	111.049673			Y	1308.635813	654.821545	1291.609264	646.308270	1290.625248	645.816262	10
3	322.139748	161.573512	304.129183	152.568230	T	*1145.572484*	573.289880	1128.545935	564.776606	1127.561919	564.284598	9
4	435.223812	218.115544	417.213247	209.110262	L	1044.524805	522.766041	1027.498256	514.252766	1026.514240	513.760758	8
5	534.292226	267.649751	516.281661	258.644469	V	*931.440741*	466.224009	914.414192	457.710734	913.430176	457.218726	7
6	663.334819	332.171048	645.324254	323.165765	E	*832.372327*	416.689802	815.345778	408.176527	814.361762	407.684519	6
7	826.398148	413.702712	808.387583	404.697430	Y	*703.329734*	352.168505	686.303185	343.655231	685.319169	343.163223	5
8	955.440741	478.224009	937.430176	469.218726	E	*540.266405*	270.636841	523.239856	262.123566	522.255840	261.631558	4
9	1056.488420	528.747848	1038.477855	519.742565	T	*411.223812*	206.115544	394.197263	197.602269	393.213247	197.110261	3
10	1219.551749	610.279513	1201.541184	601.274230	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 GYTLVEYETYK
(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	1364.649979	0.001049	GYTLVEYETYK

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

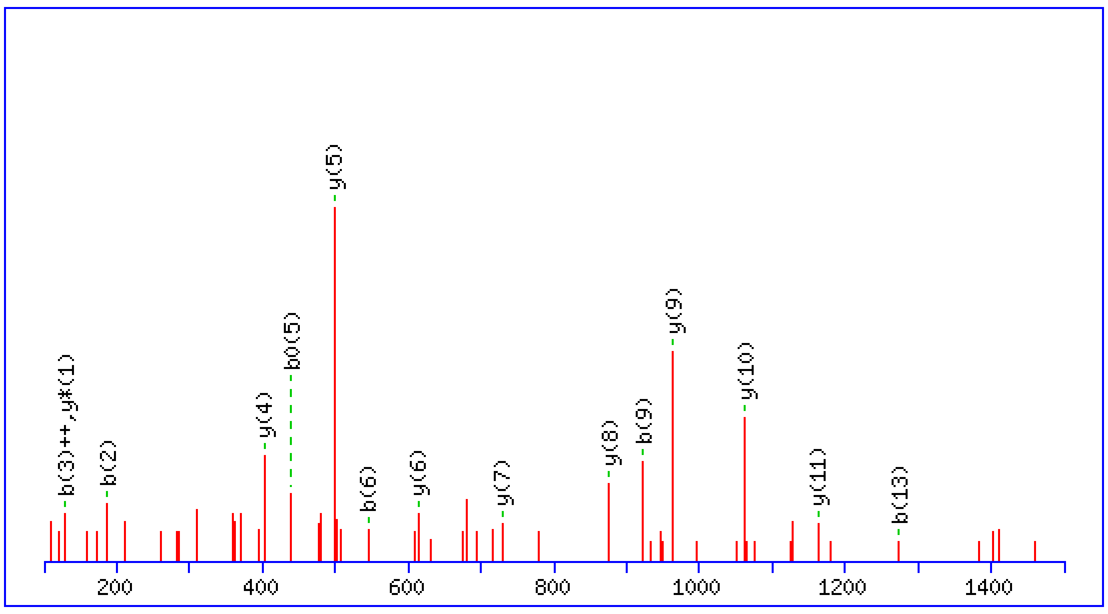
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEATVSFDDPPSAK**
Found in **FUS_HUMAN**, RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1

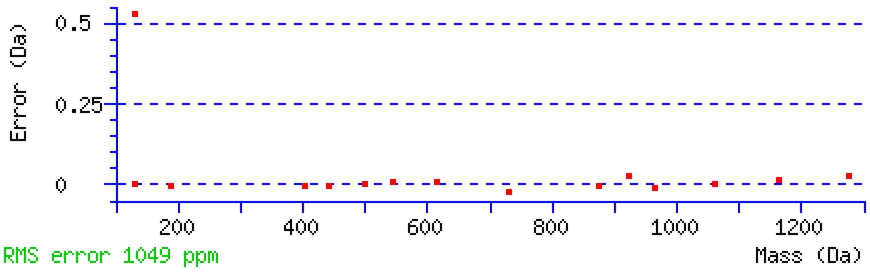
Match to Query 32878: 1419.656068 from(710.835310,2+) rtinseconds(1831) index(19108)
Title: Locus:1.1.1.2178.37
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

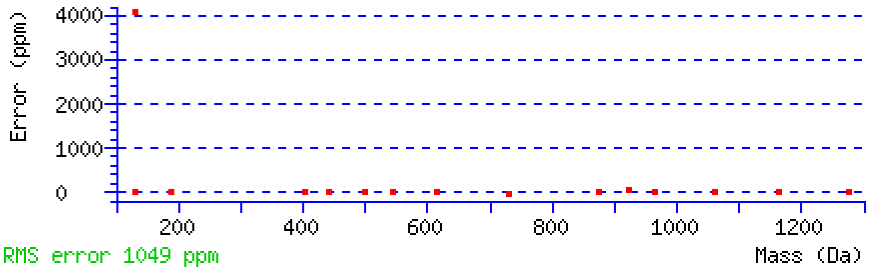
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1419.651794
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55 **Expect:** 1.2e-005
Matches : 15/124 fragment ions using 24 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008			G							14
2	**187.071333**	94.039305	169.060768	85.034022	E	1363.637602	682.322439	1346.611053	673.809165	1345.627037	673.317157	13
3	258.108447	129.557862	240.097882	120.552579	A	1234.595009	617.801143	1217.568460	609.287868	1216.584444	608.795860	12
4	359.156126	180.081701	341.145561	171.076419	T	***1163.557895***	582.282586	1146.531346	573.769311	1145.547330	573.277303	11
5	458.224540	229.615908	440.213975	220.610626	V	***1062.510216***	531.758746	1045.483667	523.245472	1044.499651	522.753464	10
6	**545.256568**	273.131922	527.246003	264.126640	S	***963.441802***	482.224539	946.415253	473.711265	945.431237	473.219257	9
7	692.324982	346.666129	674.314417	337.660847	F	***876.409774***	438.708525	859.383225	430.195251	858.399209	429.703243	8
8	807.351925	404.179601	789.341360	395.174318	D	***729.341360***	365.174318	712.314811	356.661044	711.330795	356.169036	7
9	**922.378868**	461.693072	904.368303	452.687790	D	***614.314417***	307.660847	597.287868	299.147572	596.303852	298.655564	6
10	1019.431632	510.219454	1001.421067	501.214172	P	***499.287474***	250.147375	482.260925	241.634101	481.276909	241.142093	5
11	1116.484396	558.745836	1098.473831	549.740554	P	***402.234710***	201.620993	385.208161	193.107719	384.224145	192.615711	4
12	1203.516424	602.261850	1185.505859	593.256568	S	305.181946	153.094611	288.155397	144.581337	287.171381	144.089329	3
13	**1274.553538**	637.780407	1256.542973	628.775125	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 GEATVSFDDPPSAK
(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	1419.651794	0.004274	GEATVSFDDPPSAK
2.7	1419.670258	-0.014190	ASSSGGSGGGSGGRVPK

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

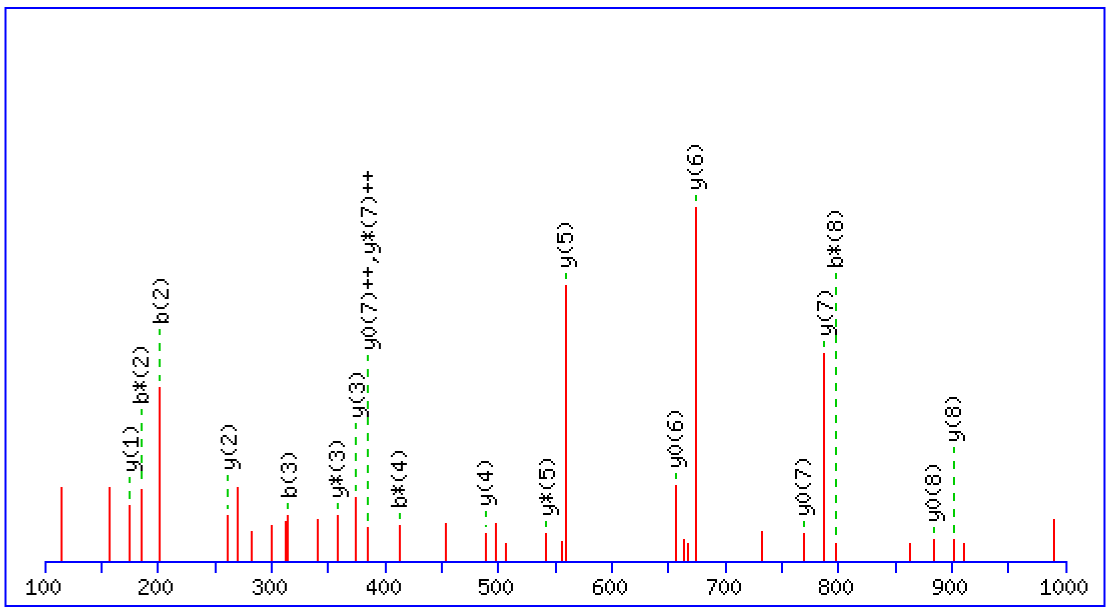
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SNIDALLSR**
Found in **RALY_HUMAN**, RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1

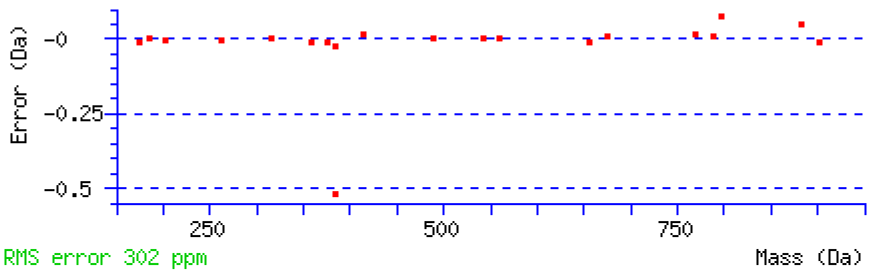
Match to Query 11033: 987.535188 from(494.774870,2+) rtinseconds(2460) index(31195)
Title: Locus:1.1.1.2321.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

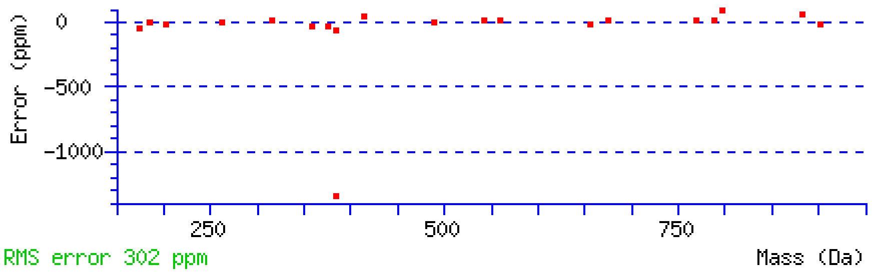
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 987.534882
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 59  Expect: 1.8e-005
Matches : 20/92 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	88.039304	44.523290			70.028739	35.518008	S							9
2	**202.082231**	101.544753	185.055682	93.031479	184.071666	92.539471	N	***901.510156***	451.258716	884.483607	442.745442	883.499591	442.253434	8
3	**315.166295**	158.086785	298.139746	149.573511	297.155730	149.081503	I	***787.467229***	394.237253	770.440680	385.723978	769.456664	385.231970	7
4	430.193238	215.600257	413.166689	207.086983	412.182673	206.594975	D	***674.383165***	337.695221	657.356616	329.181946	656.372600	328.689938	6
5	501.230352	251.118814	484.203803	242.605539	483.219787	242.113531	A	***559.356222***	280.181749	542.329673	271.668475	541.345657	271.176467	5
6	614.314416	307.660846	597.287867	299.147572	596.303851	298.655564	L	***488.319108***	244.663192	471.292559	236.149918	470.308543	235.657910	4
7	727.398480	364.202878	710.371931	355.689604	709.387915	355.197596	L	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
8	814.430508	407.718892	797.403959	399.205618	796.419943	398.713610	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 SNIDALLSR
(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	987.534882	0.000306	SNIDALLSR
16.6	987.534897	0.000291	SQVIEGISR
8.4	987.534866	0.000322	SNIREIEK
7.5	987.534897	0.000291	SNSIIVSPR
6.2	987.534882	0.000306	SLAASSPSIR
3.5	987.534882	0.000306	SRAEDLGLK

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

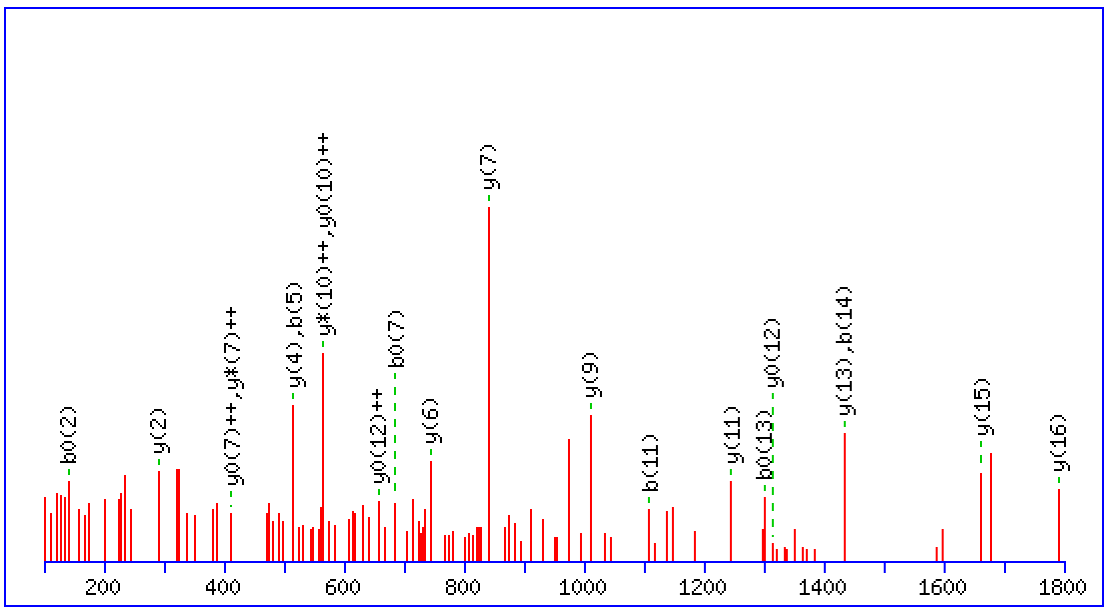
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTEDITSPHGIPLDLLDR**
Found in **RUVB1_HUMAN**, RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1

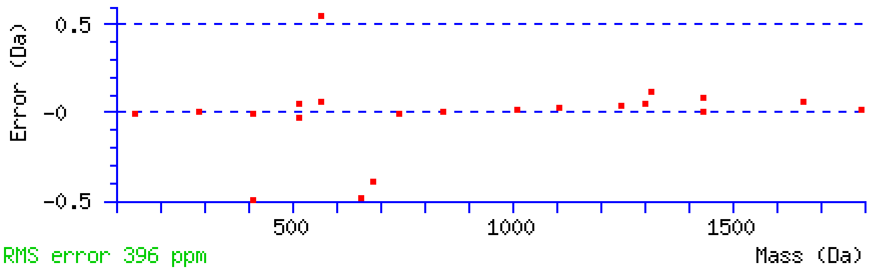
Match to Query 53250: 1948.004292 from(650.342040,3+) rtinseconds(3117) index(42969)
Title: Locus:1.1.1.2710.11
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

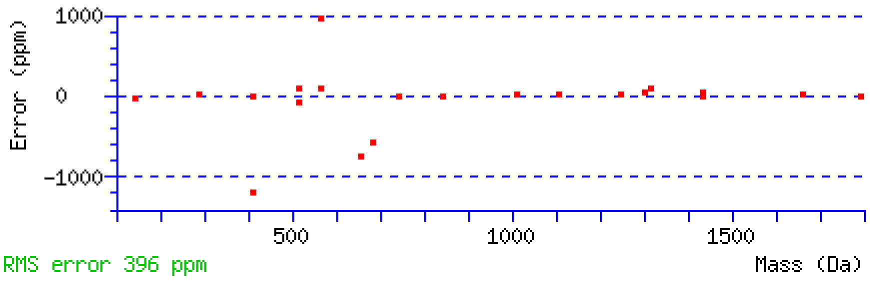
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1947.990173
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 0.00012
Matches : 21/166 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							18
2	159.076419	80.041847	141.065854	71.036565	T	1891.975984	946.491630	1874.949435	937.978356	1873.965419	937.486347	17
3	288.119012	144.563144	270.108447	135.557862	E	***1790.928305***	895.967790	1773.901756	887.454516	1772.917740	886.962508	16
4	403.145955	202.076616	385.135390	193.071333	D	***1661.885712***	831.446494	1644.859163	822.933219	1643.875147	822.441211	15
5	**516.230019**	258.618648	498.219454	249.613365	I	1546.858769	773.933022	1529.832220	765.419748	1528.848204	764.927740	14
6	617.277698	309.142487	599.267133	300.137205	T	***1433.774705***	717.390990	1416.748156	708.877716	1415.764140	708.385708	13
7	704.309726	352.658501	686.299161	343.653219	S	1332.727026	666.867151	1315.700477	658.353876	1314.716461	657.861868	12
8	801.362490	401.184883	783.351925	392.179601	P	***1245.694998***	623.351137	1228.668449	614.837862	1227.684433	614.345854	11
9	938.421402	469.714339	920.410837	460.709057	H	1148.642234	574.824755	1131.615685	566.311480	1130.631669	565.819472	10
10	995.442866	498.225071	977.432301	489.219789	G	***1011.583322***	506.295299	994.556773	497.782024	993.572757	497.290016	9
11	**1108.526930**	554.767103	1090.516365	545.761821	I	954.561858	477.784567	937.535309	469.271292	936.551293	468.779284	8
12	1205.579694	603.293485	1187.569129	594.288203	P	***841.477794***	421.242535	824.451245	412.729260	823.467229	412.237252	7
13	1318.663758	659.835517	1300.653193	650.830234	L	***744.425030***	372.716153	727.398481	364.202878	726.414465	363.710870	6
14	**1433.690701**	717.348989	1415.680136	708.343706	D	631.340966	316.174121	614.314417	307.660846	613.330401	307.168838	5
15	1546.774765	773.891020	1528.764200	764.885738	L	***516.314023***	258.660649	499.287474	250.147375	498.303458	249.655367	4
16	1659.858829	830.433052	1641.848264	821.427770	L	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
17	1774.885772	887.946524	1756.875207	878.941241	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 GTEDITSPHGIPLDLLDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.7	1947.990173	0.014119	GTEDITSPHGIPLDLLDR

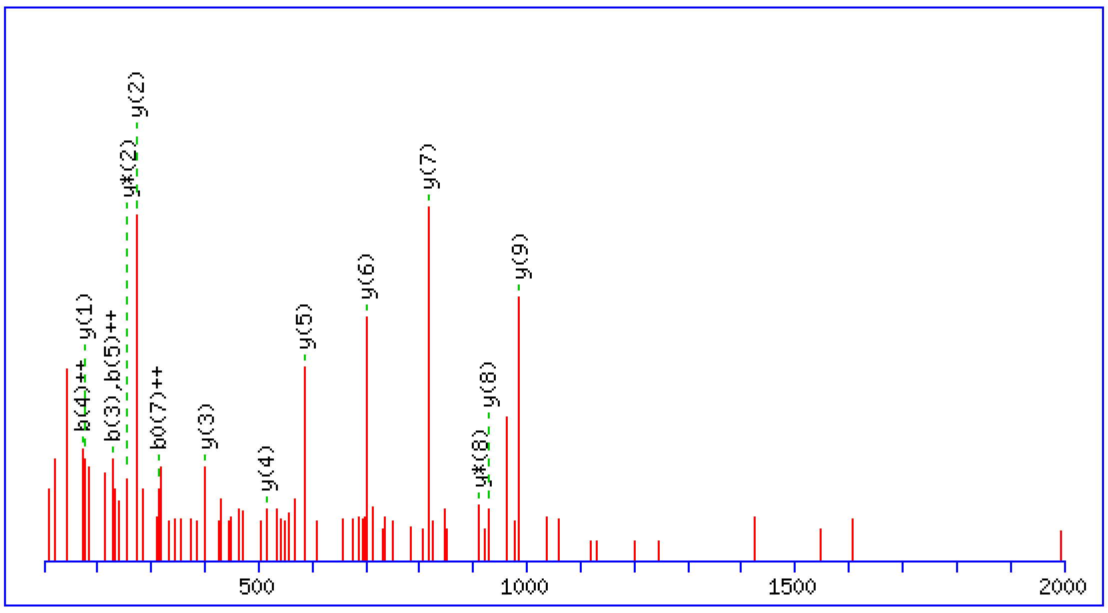
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLGLDDALEPR**
Found in **RUVB2_HUMAN**, RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3

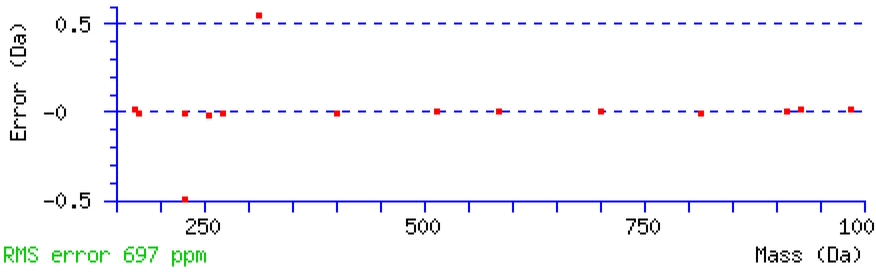
Match to Query 15280: 1154.603768 from(578.309160,2+) rtinseconds(2466) index(31308)
Title: Locus:1.1.1.2463.19
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

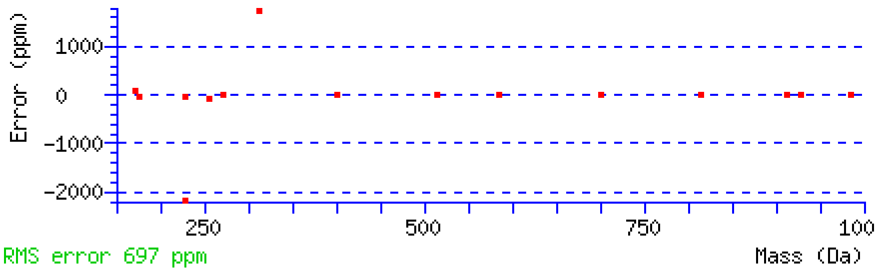
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1154.593140
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00016
Matches : 16/88 fragment ions using 40 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	171.112804	86.060040			**L**	1098.578965	549.793121	1081.552416	541.279846	1080.568400	540.787838	10
3	228.134268	114.570772			**G**	***985.494901***	493.251089	968.468352	484.737814	967.484336	484.245806	9
4	341.218332	171.112804			**L**	***928.473437***	464.740357	911.446888	456.227082	910.462872	455.735074	8
5	456.245275	228.626275	438.234710	219.620993	**D**	***815.389373***	408.198325	798.362824	399.685050	797.378808	399.193042	7
6	571.272218	286.139747	553.261653	277.134465	**D**	***700.362430***	350.684853	683.335881	342.171579	682.351865	341.679571	6
7	642.309332	321.658304	624.298767	312.653022	**A**	***585.335487***	293.171382	568.308938	284.658107	567.324922	284.166099	5
8	755.393396	378.200336	737.382831	369.195054	**L**	***514.298373***	257.652825	497.271824	249.139550	496.287808	248.647542	4
9	884.435989	442.721633	866.425424	433.716350	**E**	***401.214309***	201.110792	384.187760	192.597518	383.203744	192.105510	3
10	981.488753	491.248015	963.478188	482.242732	**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 GLGLDDALEPR
(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	1154.593140	0.010628	GLGLDDALEPR
3.4	1154.593155	0.010613	GLPGPPGSKGEK
2.0	1154.593155	0.010613	LTGELHDGVSK

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

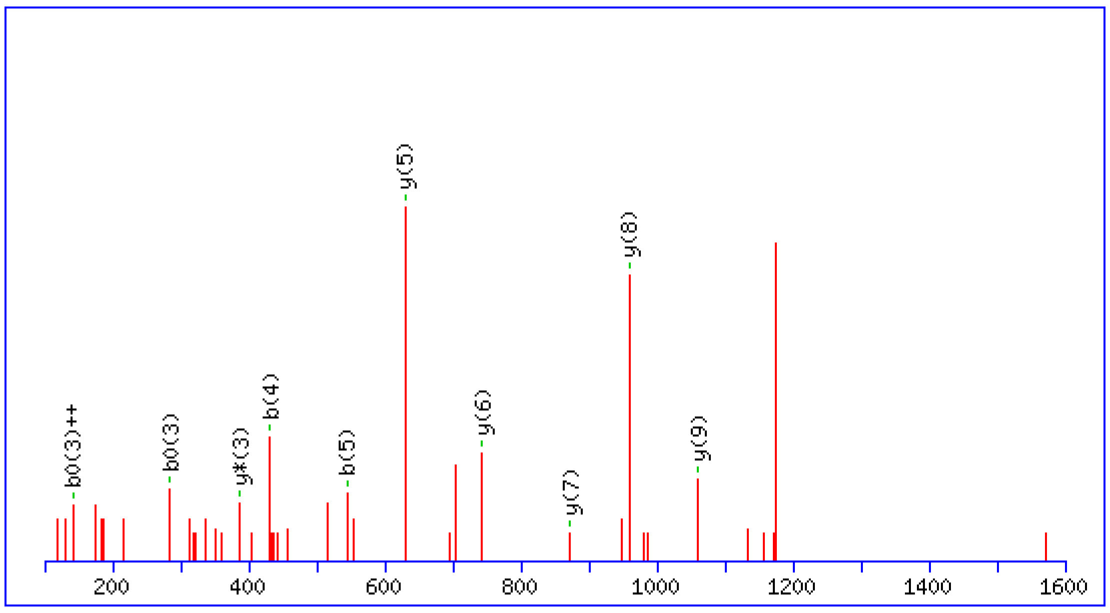
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITSEIPQTER**
Found in **SARNP_HUMAN**, SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3

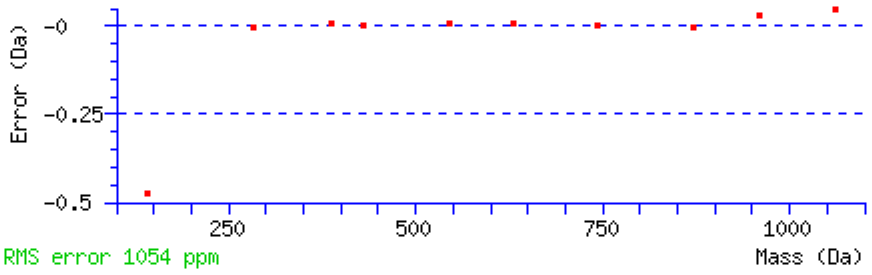
Match to Query 21704: 1172.605468 from(587.310010,2+) rtinseconds(1510) index(13182)
Title: Locus:1.1.1.1959.32
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

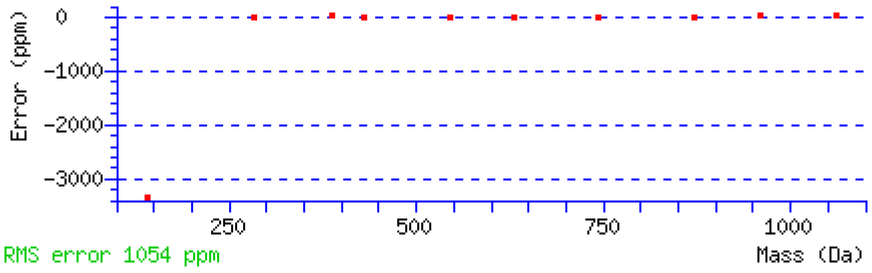
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1172.603699
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.0002
Matches : 10/92 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	114.091340	57.549308					I							10
2	215.139019	108.073147			197.128454	99.067865	T	***1060.526930***	530.767103	1043.500381	522.253829	1042.516365	521.761821	9
3	302.171047	151.589161			284.160482	142.583879	S	***959.479251***	480.243264	942.452702	471.729989	941.468686	471.237981	8
4	**431.213640**	216.110458			413.203075	207.105176	E	***872.447223***	436.727250	855.420674	428.213975	854.436658	427.721967	7
5	**544.297704**	272.652490			526.287139	263.647208	I	***743.404630***	372.205953	726.378081	363.692679	725.394065	363.200671	6
6	641.350468	321.178872			623.339903	312.173590	P	***630.320566***	315.663921	613.294017	307.150647	612.310001	306.658639	5
7	769.409046	385.208161	752.382497	376.694887	751.398481	376.202879	Q	533.267802	267.137539	516.241253	258.624265	515.257237	258.132257	4
8	870.456725	435.732001	853.430176	427.218726	852.446160	426.726718	T	405.209224	203.108250	388.182675	194.594975	387.198659	194.102967	3
9	999.499318	500.253297	982.472769	491.740023	981.488753	491.248015	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 ITSEIPQTER
(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	1172.603699	0.001769	ITSEIPQTER
5.1	1172.603729	0.001739	TTVEVKPDPR
3.6	1172.614944	-0.009476	ALTNGSLPAGTR

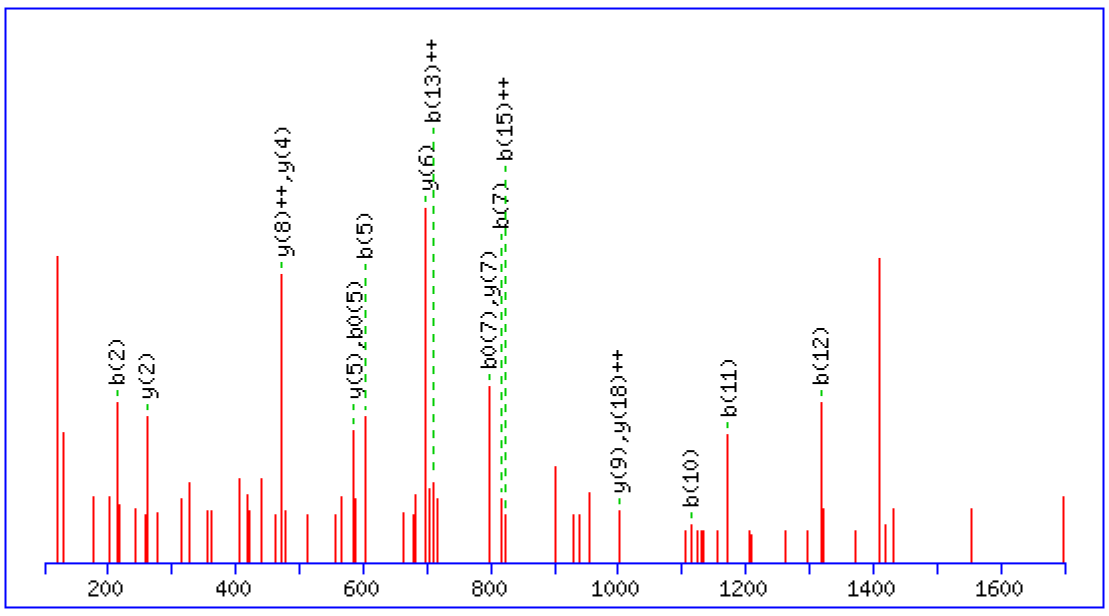
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVFENPDPSDGFVLIPDLK**
Found in **DCPS_HUMAN**, Scavenger mRNA-decapping enzyme DcpS OS=Homo sapiens GN=DCPS PE=1 SV=2

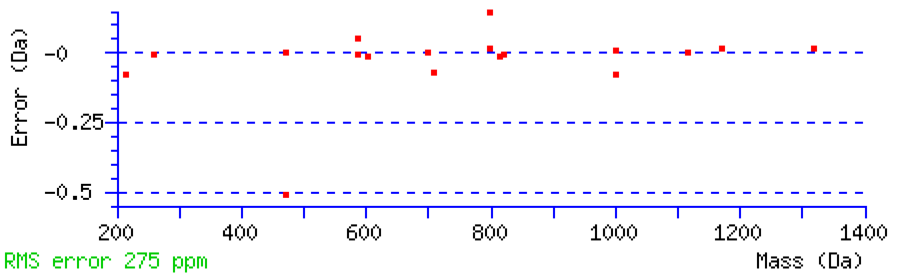
Match to Query 62525: 2114.105022 from(705.708950,3+) rtinseconds(4054) index(58300)
Title: Locus:1.1.1.3030.29
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

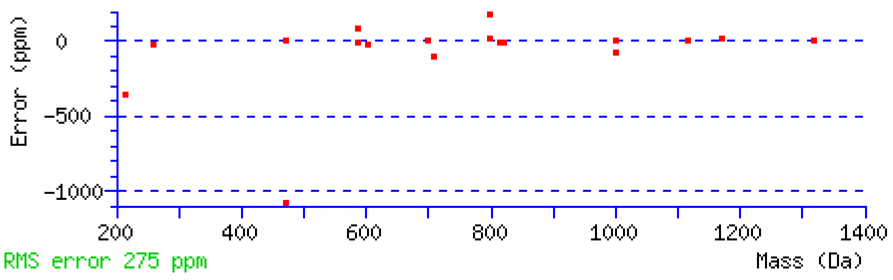
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2114.093582
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0032
Matches : 18/198 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	114.091340	57.549308					I							19
2	***213.159754***	107.083515					V	2002.016785	1001.512030	1984.990236	992.998756	1984.006220	992.506748	18
3	360.228168	180.617722					F	1902.948371	951.977823	1885.921822	943.464549	1884.937806	942.972541	17
4	489.270761	245.139018			471.260196	236.133736	E	1755.879957	878.443616	1738.853408	869.930342	1737.869392	869.438334	16
5	***603.313688***	302.160482	586.287139	293.647208	585.303123	293.155200	N	1626.837364	813.922320	1609.810815	805.409045	1608.826799	804.917037	15
6	700.366452	350.686864	683.339903	342.173590	682.355887	341.681582	P	1512.794437	756.900856	1495.767888	748.387582	1494.783872	747.895574	14
7	***815.393395***	408.200336	798.366846	399.687061	797.382830	399.195053	D	1415.741673	708.374474	1398.715124	699.861200	1397.731108	699.369192	13
8	912.446159	456.726718	895.419610	448.213443	894.435594	447.721435	P	1300.714730	650.861003	1283.688181	642.347728	1282.704165	641.855720	12
9	999.478187	500.242732	982.451638	491.729457	981.467622	491.237449	S	1203.661966	602.334621	1186.635417	593.821346	1185.651401	593.329338	11
10	***1114.505130***	557.756203	1097.478581	549.242929	1096.494565	548.750921	D	1116.629938	558.818607	1099.603389	550.305332	1098.619373	549.813324	10
11	***1171.526594***	586.266935	1154.500045	577.753661	1153.516029	577.261652	G	***1001.602995***	501.305135	984.576446	492.791861	983.592430	492.299853	9
12	***1318.595008***	659.801142	1301.568459	651.287868	1300.584443	650.795860	F	944.581531	472.794403	927.554982	464.281129	926.570966	463.789121	8
13	1417.663422	**709.335349**	1400.636873	700.822075	1399.652857	700.330067	V	***797.513117***	399.260196	780.486568	390.746922	779.502552	390.254914	7
14	1530.747486	765.877381	1513.720937	757.364107	1512.736921	756.872098	L	***698.444703***	349.725989	681.418154	341.212715	680.434138	340.720707	6
15	1643.831550	**822.419413**	1626.805001	813.906139	1625.820985	813.414130	I	***585.360639***	293.183957	568.334090	284.670683	567.350074	284.178675	5
16	1740.884314	870.945795	1723.857765	862.432521	1722.873749	861.940512	P	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
17	1855.911257	928.459267	1838.884708	919.945992	1837.900692	919.453984	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
18	1968.995321	985.001298	1951.968772	976.488024	1950.984756	975.996016	L	***260.196868***	130.602072	243.170319	122.088797			2
19							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of IVFENPDPSDGFVLIPDLK
(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	2114.093582	0.011440	IVFENPDPSDGFVLIPDLK

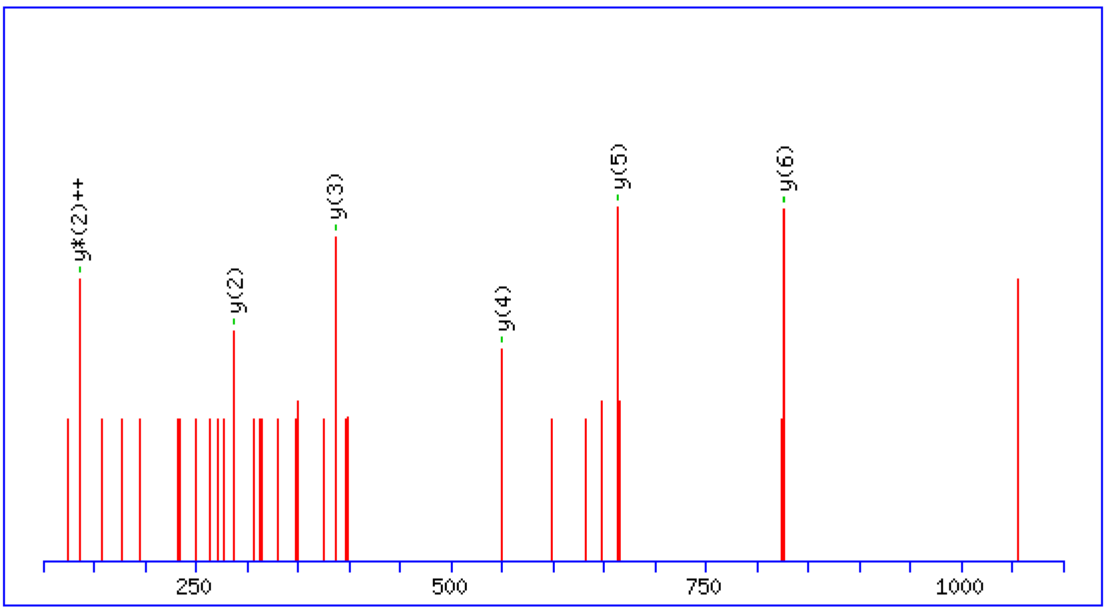
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNYNYVIR**
Found in **SFRP3_HUMAN**, Secreted frizzled-related protein 3 OS=Homo sapiens GN=FRZB PE=1 SV=2

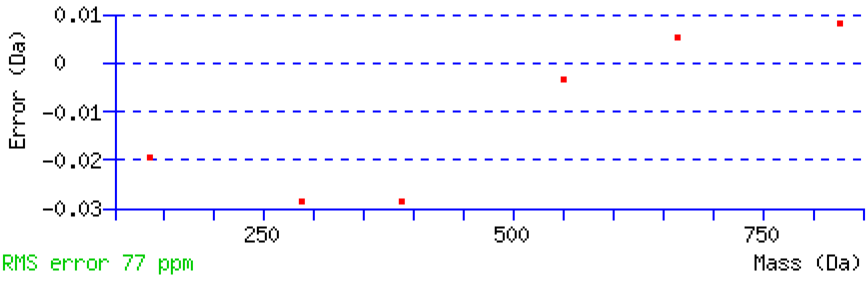
Match to Query 12716: 1054.518348 from(528.266450,2+) rtinseconds(1873) index(13471)
Title: Locus:1.1.1.2284.22
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

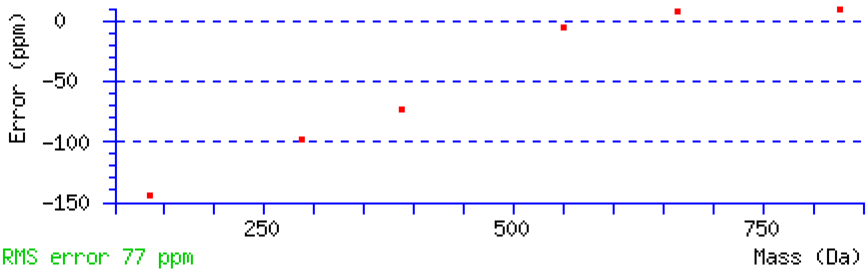
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1054.519562
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00047
Matches : 6/56 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.050203	58.028740	98.023654	49.515465	N					8
2	229.093130	115.050203	212.066581	106.536929	N	941.483942	471.245609	924.457393	462.732335	7
3	392.156459	196.581867	375.129910	188.068593	Y	***827.441015***	414.224146	810.414466	405.710871	6
4	506.199386	253.603331	489.172837	245.090057	N	***664.377686***	332.692481	647.351137	324.179207	5
5	669.262715	335.134996	652.236166	326.621721	Y	***550.334759***	275.671018	533.308210	267.157743	4
6	768.331129	384.669203	751.304580	376.155928	V	***387.271430***	194.139353	370.244881	185.626078	3
7	881.415193	441.211235	864.388644	432.697960	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 NNYNYVIR
(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	1054.519562	-0.001214	NNYNYVIR
13.1	1054.508347	0.010001	IDNYFDLR

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

{MATRIX SCIENCE}

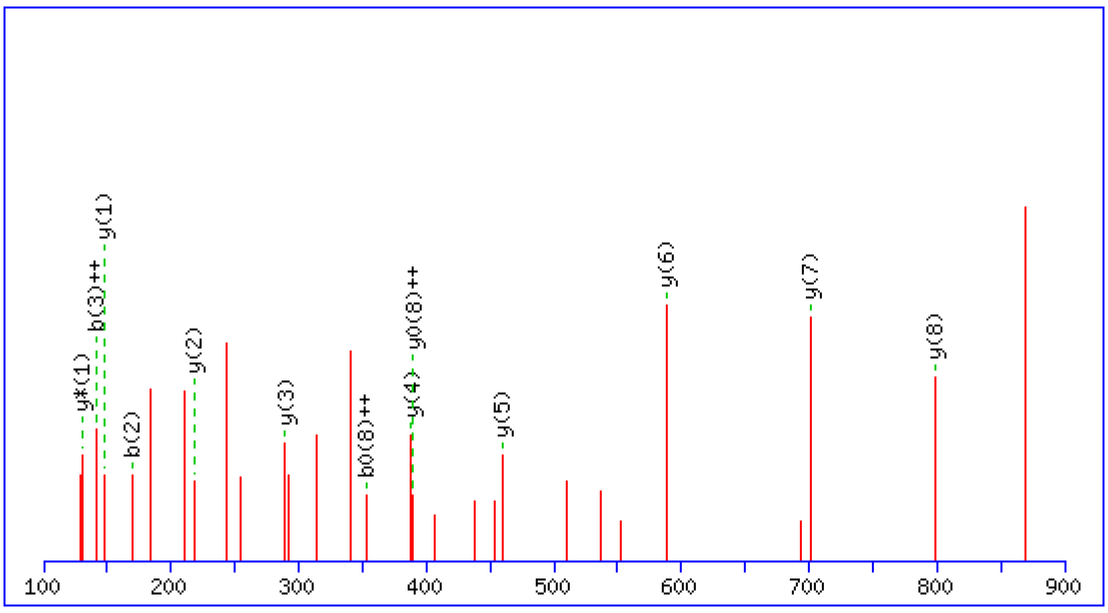
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APLEAVAAK**
Found in **SG1D1_HUMAN**, Secretoglobin family 1D member 1 OS=Homo sapiens GN=SCGB1D1 PE=1 SV=1

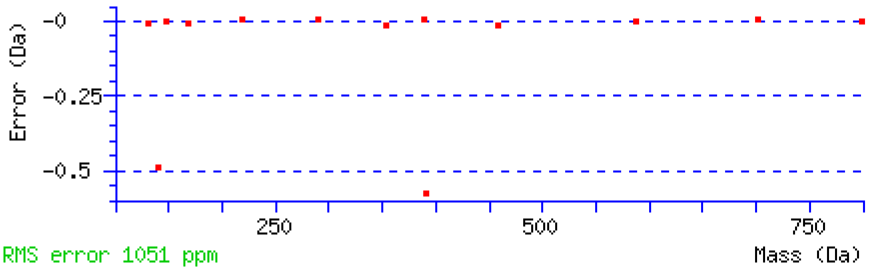
Match to Query 4329: 868.503468 from(435.259010,2+) rtinseconds(1323) index(981)
Title: Locus:1.1.1.2178.3
Data file 2011-11-14 - TFD - S 2-8.mgf

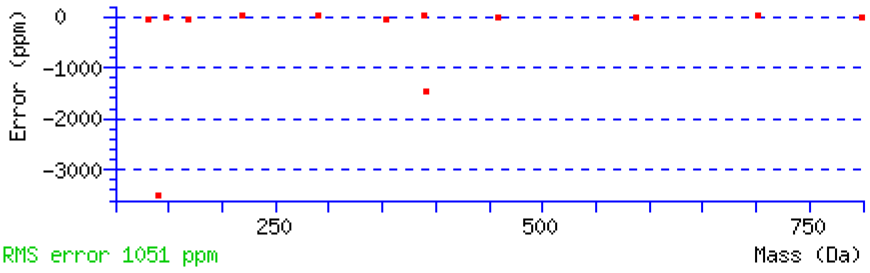
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 868.501785
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49  Expect: 4.1e-005
Matches : 13/64 fragment ions using 28 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	169.097154	85.052215			P	*798.471981*	399.739629	781.445432	391.226354	780.461416	390.734346	8
3	282.181218	141.594247			L	*701.419217*	351.213247	684.392668	342.699972	683.408652	342.207964	7
4	411.223811	206.115544	393.213246	197.110261	E	*588.335153*	294.671215	571.308604	286.157940	570.324588	285.665932	6
5	482.260925	241.634100	464.250360	232.628818	A	*459.292560*	230.149918	442.266011	221.636643			5
6	581.329339	291.168308	563.318774	282.163025	V	*388.255446*	194.631361	371.228897	186.118086			4
7	652.366453	326.686865	634.355888	317.681582	A	*289.187032*	145.097154	272.160483	136.583879			3
8	723.403567	362.205422	705.393002	353.200139	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 APLEAVAAK
(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	868.501785	0.001683	APLEAVAAK
3.6	868.495270	0.008198	ALPRGMPK

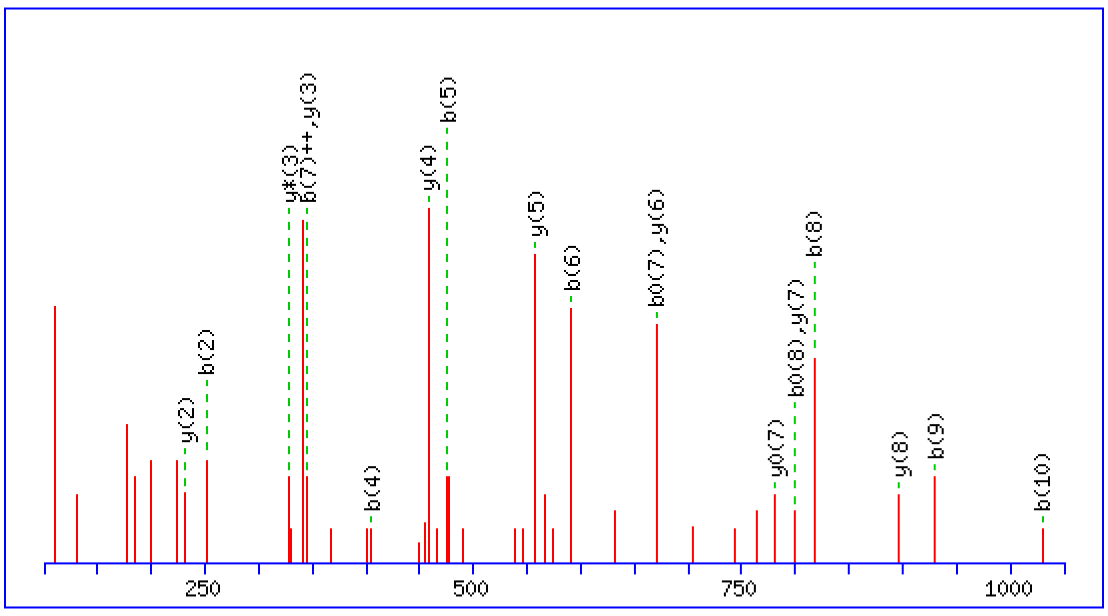
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HLPGADPELVLLGR**
Found in **SELM_HUMAN**, Selenoprotein M OS=Homo sapiens GN=SELM PE=1 SV=3

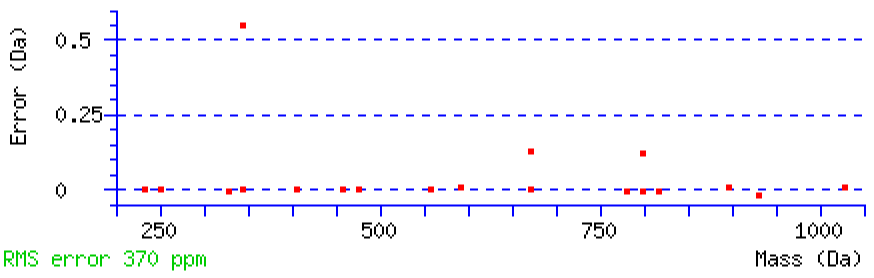
Match to Query 19629: 1485.832242 from(496.284690,3+) rtinseconds(3005) index(21215)
Title: Locus:1.1.1.2728.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

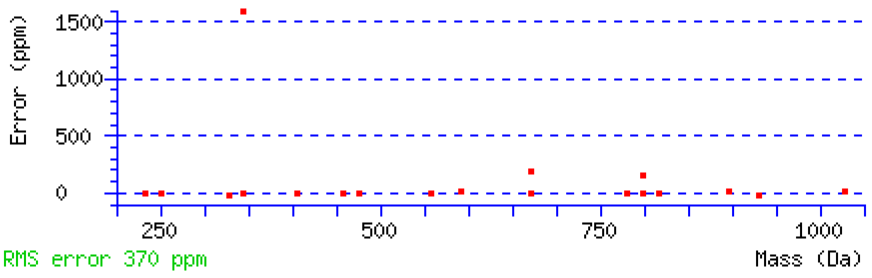
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1485.830353
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46  Expect: 0.00014
Matches : 19/108 fragment ions using 30 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							14
2	***251.150252***	126.078764			L	1349.778728	675.393002	1332.752179	666.879727	1331.768163	666.387719	13
3	348.203016	174.605146			P	1236.694664	618.850970	1219.668115	610.337696	1218.684099	609.845687	12
4	***405.224480***	203.115878			G	1139.641900	570.324588	1122.615351	561.811313	1121.631335	561.319305	11
5	***476.261594***	238.634435			A	1082.620436	541.813856	1065.593887	533.300581	1064.609871	532.808573	10
6	***591.288537***	296.147907	573.277972	287.142624	D	1011.583322	506.295299	994.556773	497.782024	993.572757	497.290016	9
7	688.341301	344.674289	670.330736	335.669006	P	***896.556379***	448.781827	879.529830	440.268553	878.545814	439.776545	8
8	***817.383894***	409.195585	799.373329	400.190303	E	***799.503615***	400.255445	782.477066	391.742171	781.493050	391.250163	7
9	***930.467958***	465.737617	912.457393	456.732335	L	***670.461022***	335.734149	653.434473	327.220874			6
10	***1029.536372***	515.271824	1011.525807	506.266542	V	***557.376958***	279.192117	540.350409	270.678842			5
11	1142.620436	571.813856	1124.609871	562.808573	L	***458.308544***	229.657910	441.281995	221.144635			4
12	1255.704500	628.355888	1237.693935	619.350605	L	***345.224480***	173.115878	328.197931	164.602603			3
13	1312.725964	656.866620	1294.715399	647.861337	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 HLPGADPELVLLGR
(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	1485.830353	0.001889	HLPGADPELVLLGR
12.9	1485.822479	0.009763	GTMPKEVNLGLLAK
2.5	1485.833694	-0.001452	QIQLAQKLEIMR
2.0	1485.844254	-0.012012	LFPSEAVIAEGILK
1.8	1485.830353	0.001889	ATFSPIVTLEPRR
0.5	1485.840240	-0.007998	LQILVSPNSSLSTK

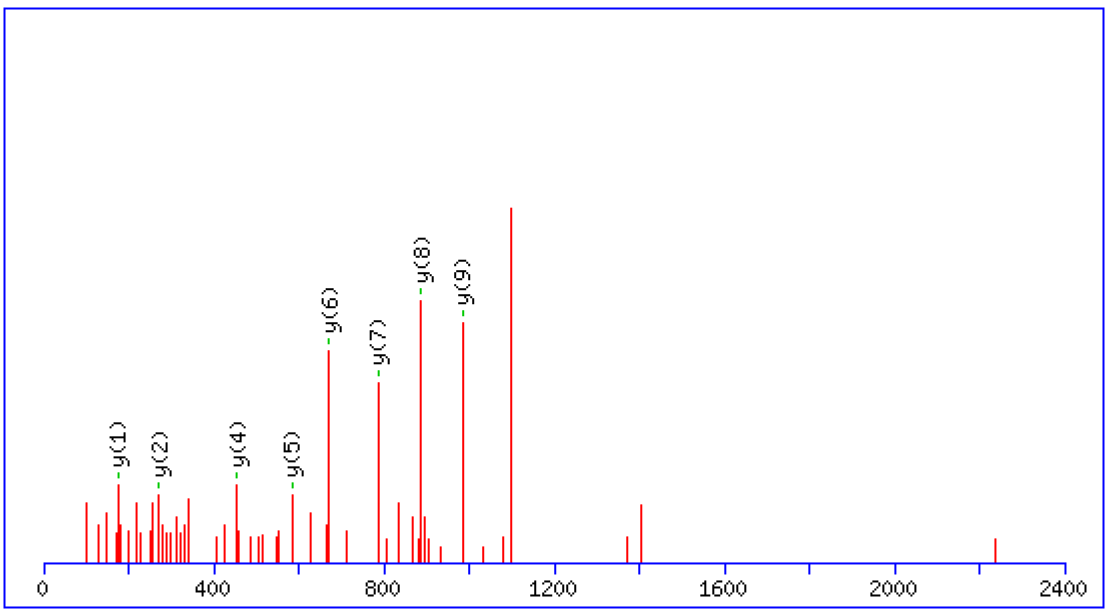
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPTDSELAPR**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

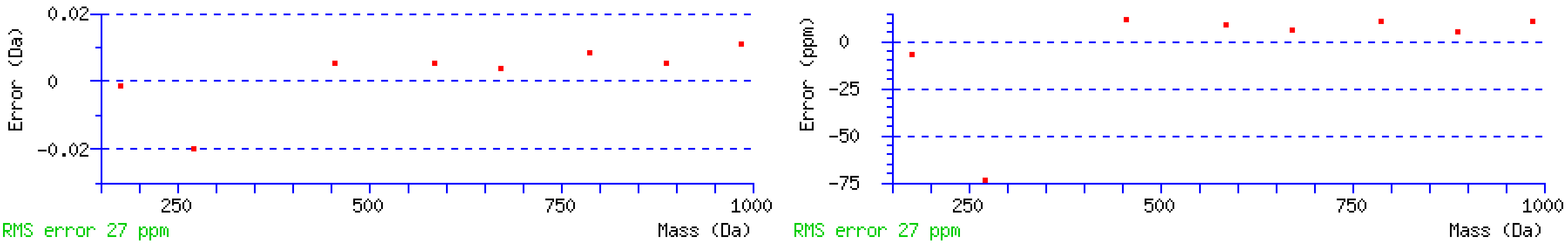
Match to Query 21730: 1097.576968 from(549.795760,2+) rtinseconds(1746) index(18964)
Title: Locus:1.1.1.1998.29
Data file 2011-11-14 - TFD - S 2-3.mgf

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): 1097.571671
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 85  Expect: 2.7e-008
Matches : 8/78 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							10
2	211.144104	106.075690			P	***985.494901***	493.251089	968.468352	484.737814	967.484336	484.245806	9
3	312.191783	156.599529	294.181218	147.594247	T	***888.442137***	444.724707	871.415588	436.211432	870.431572	435.719424	8
4	427.218726	214.113001	409.208161	205.107719	D	***787.394458***	394.200867	770.367909	385.687593	769.383893	385.195585	7
5	514.250754	257.629015	496.240189	248.623733	S	***672.367515***	336.687396	655.340966	328.174121	654.356950	327.682113	6
6	643.293347	322.150312	625.282782	313.145029	E	***585.335487***	293.171382	568.308938	284.658107	567.324922	284.166099	5
7	756.377411	378.692344	738.366846	369.687061	L	***456.292894***	228.650085	439.266345	220.136811			4
8	827.414525	414.210901	809.403960	405.205618	A	343.208830	172.108053	326.182281	163.594779			3
9	924.467289	462.737283	906.456724	453.732000	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 LPTDSELAPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.4	1097.571671	0.005297	LPTDSELAPR
19.3	1097.571671	0.005297	ILAESPPPAR
14.7	1097.576385	0.000583	LGAGTPCRPR
13.9	1097.582901	-0.005933	IPAAGASQLDR
10.5	1097.586945	-0.009977	IGVWEPLPR
9.3	1097.571671	0.005297	SLPSSPELPR
9.2	1097.586945	-0.009977	LPPDPLFQR
9.2	1097.586945	-0.009977	LPPDPLFQR
8.3	1097.586960	-0.009992	VVLDPWDVR
7.6	1097.576385	0.000583	MGGRPGSLAPR

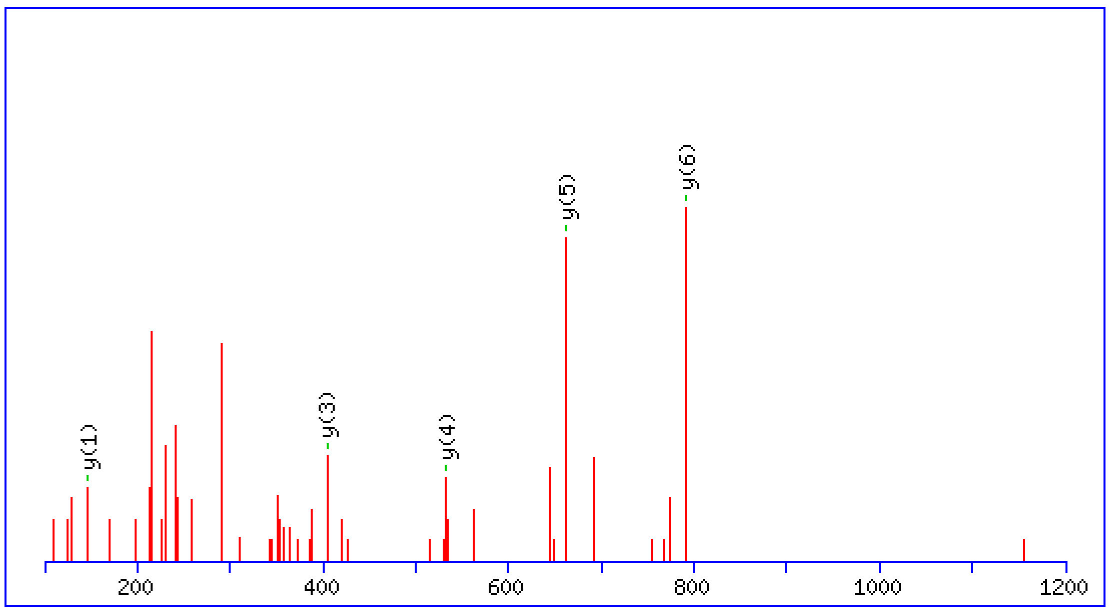
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEEEKEK**
Found in **CA114_HUMAN**, Uncharacterized protein C1orf114 OS=Homo sapiens GN=C1orf114 PE=2 SV=1

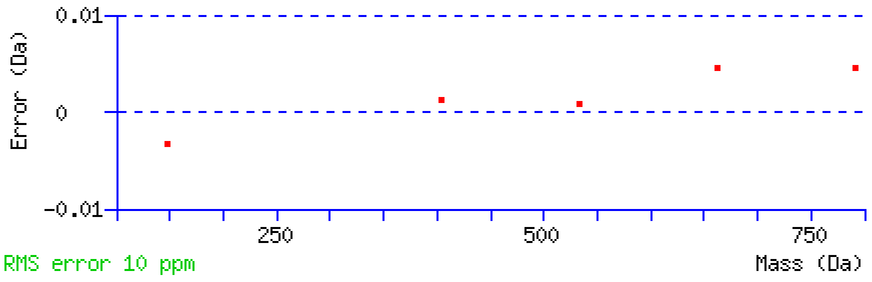
Match to Query 7537: 903.453508 from(452.734030,2+) rtinseconds(1044) index(5566)
Title: Locus:1.1.1.1727.21
Data file 2011-11-14 - TFD - S 2-3.mgf

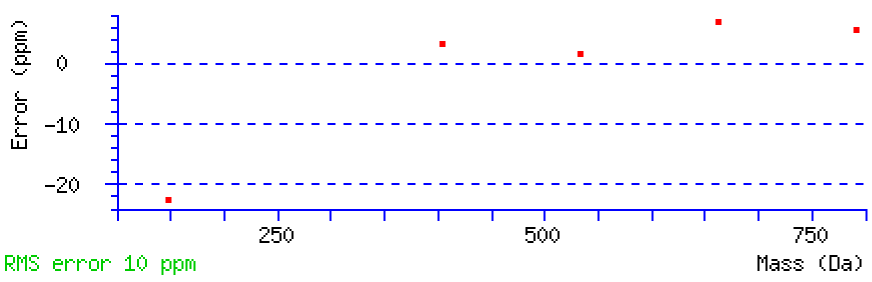
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 903.454880
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40 **Expect:** 0.0017
Matches : 5/60 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					**I**							7
2	243.133933	122.070605			225.123368	113.065322	**E**	***791.378139***	396.192708	774.351590	387.679433	773.367574	387.187425	6
3	372.176526	186.591901			354.165961	177.586619	**E**	***662.335546***	331.671411	645.308997	323.158137	644.324981	322.666129	5
4	501.219119	251.113198			483.208554	242.107915	**E**	***533.292953***	267.150115	516.266404	258.636840	515.282388	258.144832	4
5	629.314082	315.160679	612.287533	306.647405	611.303517	306.155397	**K**	***404.250360***	202.628818	387.223811	194.115544	386.239795	193.623536	3
6	758.356675	379.681976	741.330126	371.168701	740.346110	370.676693	**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 IEEEKEK
(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	903.454895	-0.001387	IEEELGSK
39.6	903.454880	-0.001372	IEEEKEK
39.6	903.454880	-0.001372	LEEEEKK
22.8	903.454880	-0.001372	ELEEEKK
14.2	903.454910	-0.001402	ELESVPSK
9.9	903.445023	0.008485	LWDATNGK
8.0	903.448395	0.005113	LVEPMAGR
7.1	903.448395	0.005113	IVGGQECK
5.2	903.445023	0.008485	IVEWDSR
4.6	903.448395	0.005113	ITGCASPGK

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

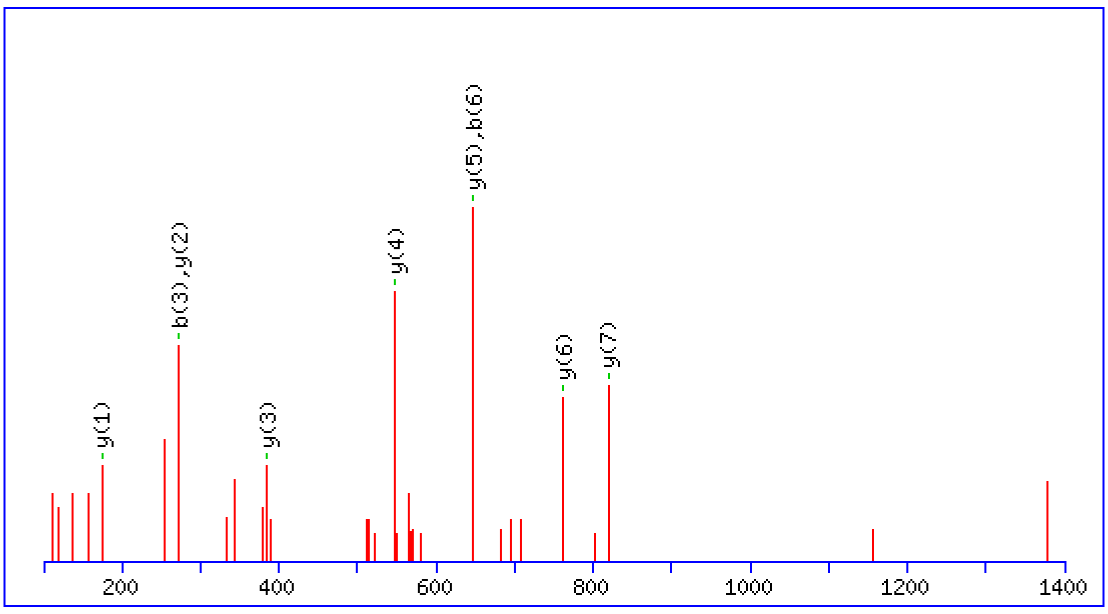
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGDVYIPR**
Found in **SRSF2_HUMAN**, Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4

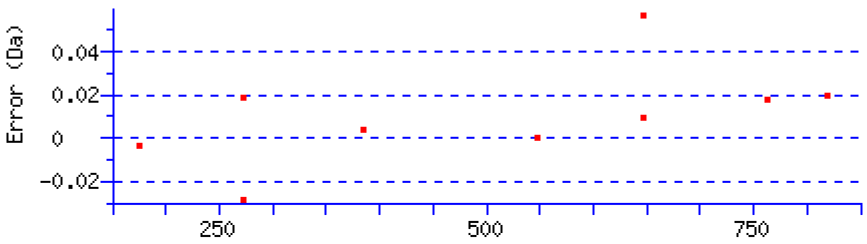
Match to Query 8156: 917.495148 from(459.754850,2+) rtinseconds(2013) index(20747)
Title: Locus:1.1.1.2258.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

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 ●

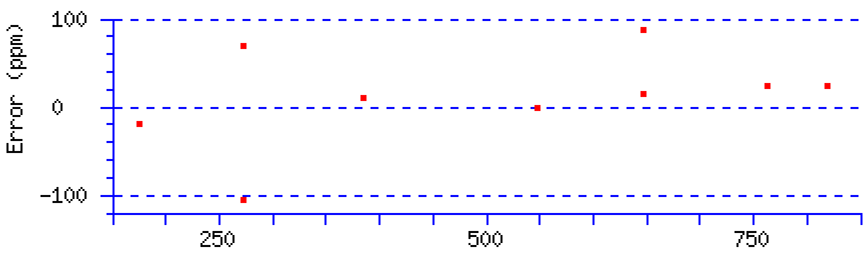


```
Monoisotopic mass of neutral peptide Mr(calc): 917.497070
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74  Expect: 4.9e-007
Matches : 9/56 fragment ions using 8 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483			V							8
2	157.097154	79.052215			G	*819.435930*	410.221603	802.409381	401.708329	801.425365	401.216321	7
3	**272.124097**	136.565687	254.113532	127.560404	D	*762.414466*	381.710871	745.387917	373.197597	744.403901	372.705589	6
4	371.192511	186.099894	353.181946	177.094611	V	*647.387523*	324.197400	630.360974	315.684125			5
5	534.255840	267.631558	516.245275	258.626276	Y	*548.319109*	274.663193	531.292560	266.149918			4
6	**647.339904**	324.173590	629.329339	315.168308	I	*385.255780*	193.131528	368.229231	184.618254			3
7	744.392668	372.699972	726.382103	363.694690	P	*272.171716*	136.589496	255.145167	128.076222			2
8					R	*175.118952*	88.063114	158.092403	79.549840			1



RMS error 53 ppm



RMS error 53 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.9	917.497070	-0.001922	VGDVYIPR
11.8	917.497055	-0.001907	VSLPSYPR
11.4	917.497070	-0.001922	FGITDLPR
11.4	917.497040	-0.001892	KIYEPPR
9.9	917.500443	-0.005295	VVGDLMLR
9.2	917.493027	0.002121	SSPAVSRSK
3.8	917.487152	0.007996	YFAKHPR
1.5	917.497055	-0.001907	ELFGLSPR
0.7	917.500412	-0.005264	ASLDLMIR
0.7	917.487167	0.007981	KWGFQPR

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

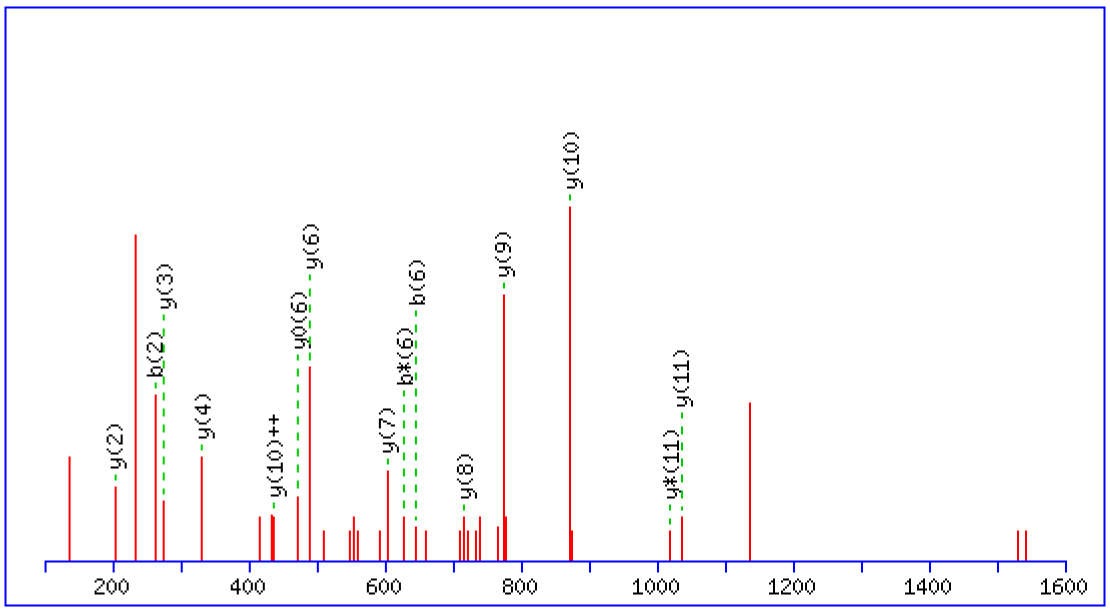
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYVGNLGTGAGK**
Found in **SRSF7_HUMAN**, Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1

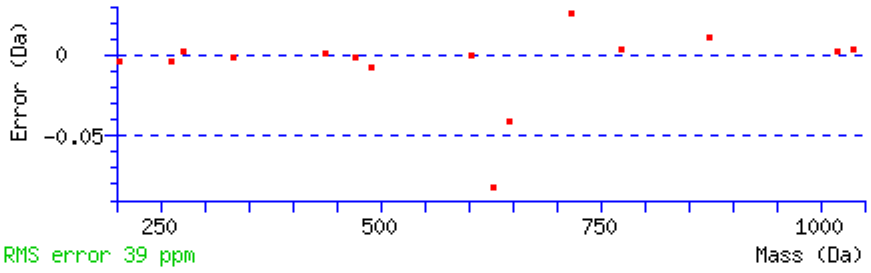
Match to Query 20885: 1134.601368 from(568.307960,2+) rtinseconds(1747) index(15504)
Title: Locus:1.1.1.2065.24
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

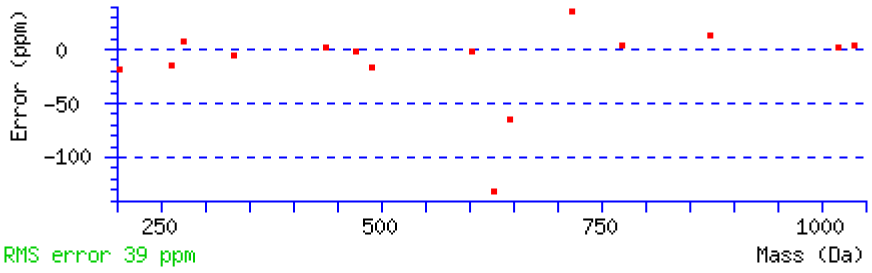
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1134.603333
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 9.4e-007
Matches : 15/102 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	100.075690	50.541483					V							12
2	**263.139019**	132.073148					Y	***1036.542187***	518.774732	1019.515638	510.261457	1018.531622	509.769449	11
3	362.207433	181.607355					V	***873.478858***	437.243067	856.452309	428.729793	855.468293	428.237785	10
4	419.228897	210.118087					G	***774.410444***	387.708860	757.383895	379.195586	756.399879	378.703578	9
5	533.271824	267.139550	516.245275	258.626276			N	***717.388980***	359.198128	700.362431	350.684854	699.378415	350.192846	8
6	**646.355888**	323.681582	629.329339	315.168308			L	***603.346053***	302.176665	586.319504	293.663390	585.335488	293.171382	7
7	703.377352	352.192314	686.350803	343.679040			G	***490.261989***	245.634632	473.235440	237.121358	472.251424	236.629350	6
8	804.425031	402.716154	787.398482	394.202879	786.414466	393.710871	T	433.240525	217.123900	416.213976	208.610626	415.229960	208.118618	5
9	861.446495	431.226886	844.419946	422.713611	843.435930	422.221603	G	***332.192846***	166.600061	315.166297	158.086786			4
10	932.483609	466.745443	915.457060	458.232168	914.473044	457.740160	A	***275.171382***	138.089329	258.144833	129.576054			3
11	989.505073	495.256175	972.478524	486.742900	971.494508	486.250892	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 VYVGNLGTGAGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.8	1134.603333	-0.001965	VYVGNLGTGAGK
4.5	1134.606674	-0.005306	IQMVSSSQKK

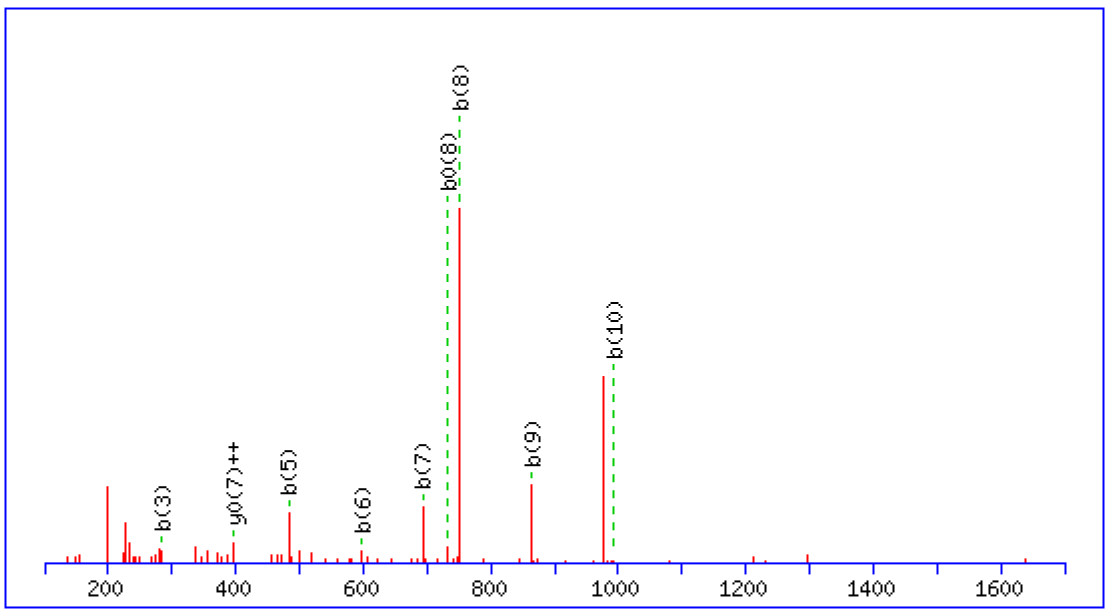
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPASPLPGLERK**
Found in **MARK2_HUMAN**, Serine/threonine-protein kinase MARK2 OS=Homo sapiens GN=MARK2 PE=1 SV=2

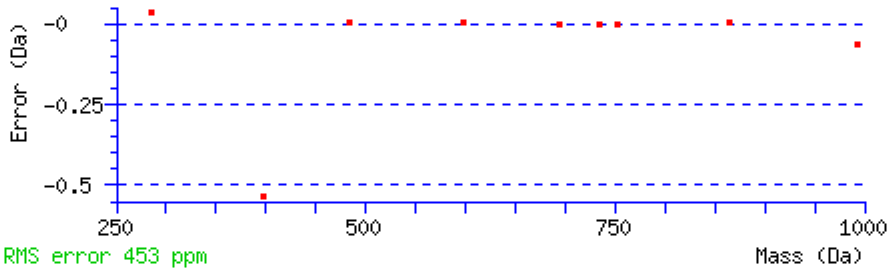
Match to Query 488897: 1294.727308 from(648.370930,2+) rtinseconds(2250) index(956712)
Title: Locus:1.1.1.1370.20
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

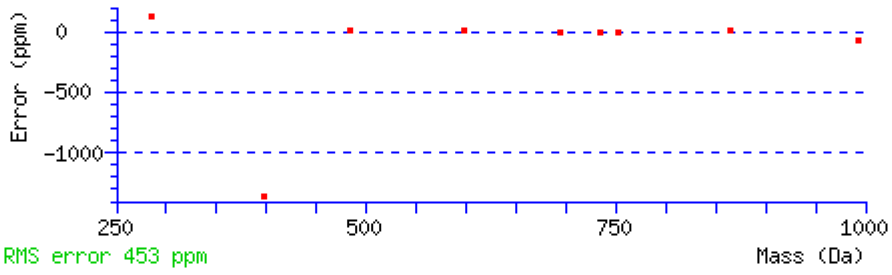
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1294.724487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P2 : Oxidation (P)
P5 : Oxidation (P)
Ions Score: 37 **Expect:** 0.0011
Matches : 9/102 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							12
2	213.123369	107.065322					P	1196.663364	598.835320	1179.636815	590.322046	1178.652799	589.830038	11
3	***284.160483***	142.583879					A	1083.615685	542.311481	1066.589136	533.798206	1065.605120	533.306198	10
4	371.192511	186.099893			353.181946	177.094611	S	1012.578571	506.792924	995.552022	498.279649	994.568006	497.787641	9
5	***484.240190***	242.623733			466.229625	233.618450	P	925.546543	463.276910	908.519994	454.763635	907.535978	454.271627	8
6	***597.324254***	299.165765			579.313689	290.160483	L	812.498864	406.753070	795.472315	398.239796	794.488299	397.747788	7
7	***694.377018***	347.692147			676.366453	338.686865	P	699.414800	350.211038	682.388251	341.697764	681.404235	341.205756	6
8	***751.398482***	376.202879			733.387917	367.197597	G	602.362036	301.684656	585.335487	293.171382	584.351471	292.679374	5
9	***864.482546***	432.744911			846.471981	423.739629	L	545.340572	273.173924	528.314023	264.660650	527.330007	264.168642	4
10	***993.525139***	497.266208			975.514574	488.260925	E	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	3
11	1149.626250	575.316763	1132.599701	566.803489	1131.615685	566.311481	R	303.213915	152.110595	286.187366	143.597321			2
12							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VPASPLPGLERK
(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	1294.724487	0.002821	VPASPLPGLERK
16.7	1294.724487	0.002821	VPASPLPGLERK
16.5	1294.717972	0.009336	CRDLPGLPLVR
13.7	1294.724487	0.002821	VPASPLPGLERK
8.9	1294.724472	0.002836	IKIEPGIEPQR
2.6	1294.724472	0.002836	IKIEPGIEPQR
1.4	1294.739731	-0.012423	QKAYFILSLGR

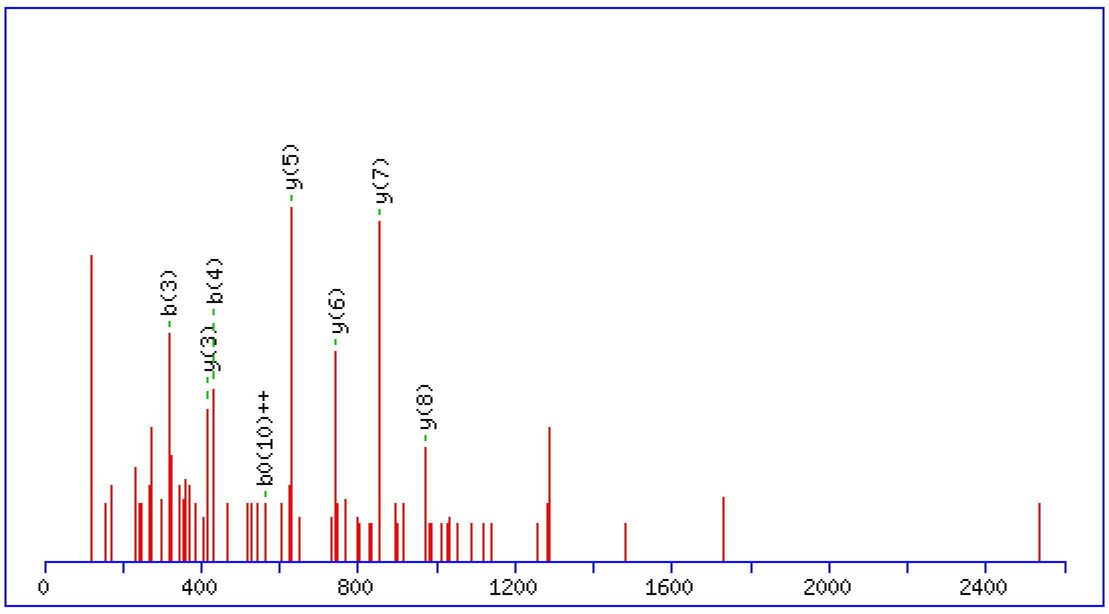
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VMSIPDVIRLK**
Found in **PRKX_HUMAN**, Serine/threonine-protein kinase PRKX OS=Homo sapiens GN=PRKX PE=2 SV=1

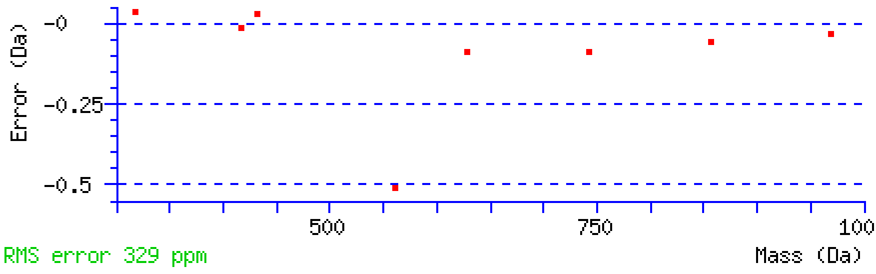
Match to Query 24232: 1285.731728 from(643.873140,2+) rtinseconds(3667) index(46099)
Title: Locus:1.1.1.3202.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

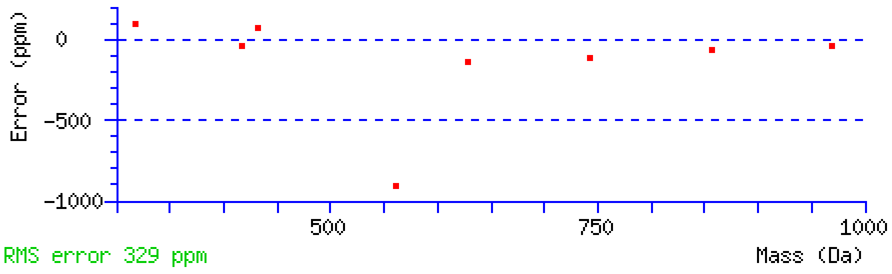
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.742783
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
Ions Score: 32  Expect: 0.0015
Matches : 8/90 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
32.4	1285.742783	-0.011055	VMSIPDVIRLK
2.1	1285.735367	-0.003639	SLELSVNLQRK
0.7	1285.742783	-0.011055	VMSIPDVIRLK

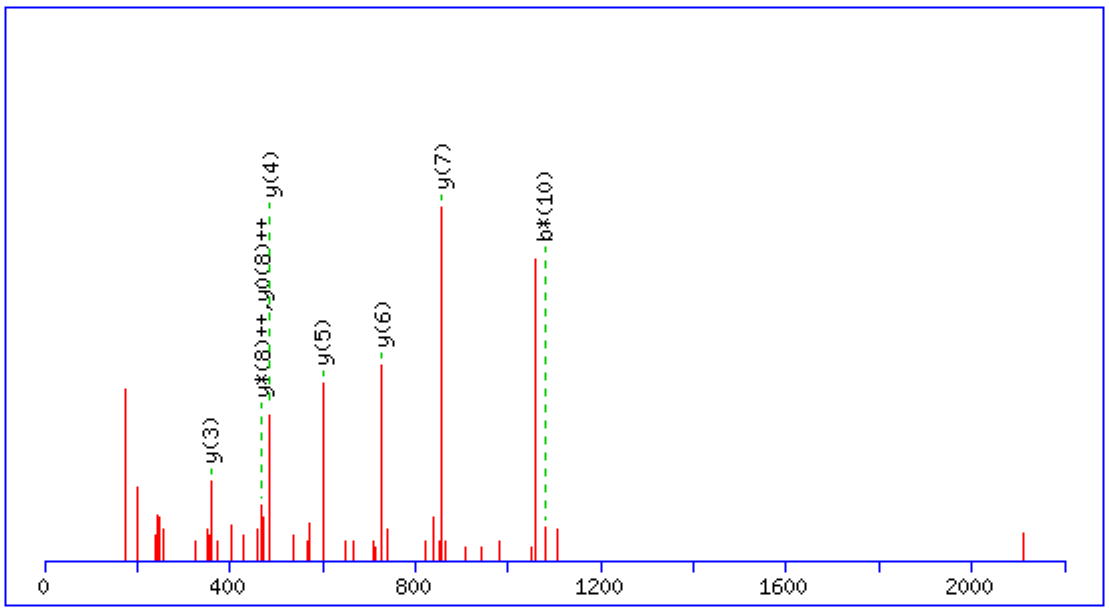
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISNSPEKPKVIQ**
Found in **ACVL1_HUMAN**, Serine/threonine-protein kinase receptor R3 OS=Homo sapiens GN=ACVRL1 PE=1 SV=2

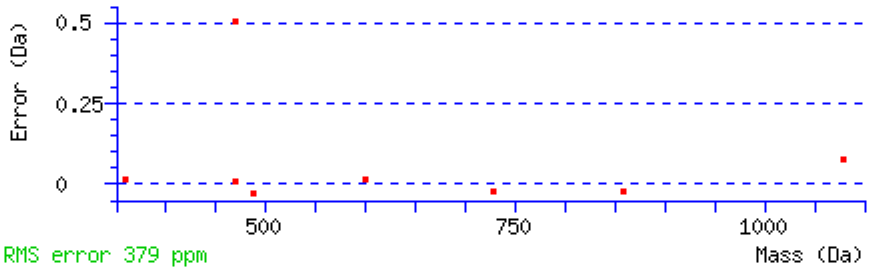
Match to Query 541681: 1354.734388 from(678.374470,2+) rtinseconds(2189) index(733935)
Title: Locus:1.1.1.1090.23
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

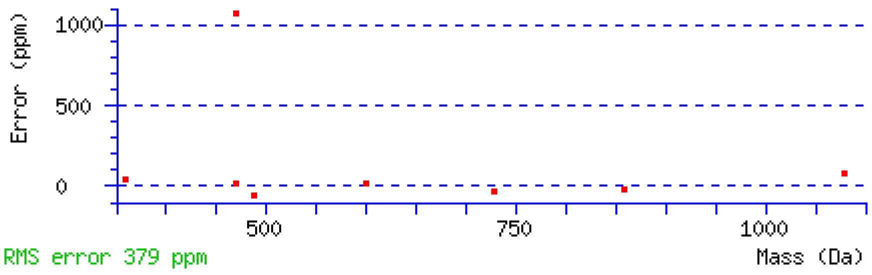
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1354.745605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P8 : Oxidation (P)
Ions Score: 31 **Expect:** 0.0093
Matches : 8/114 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							12
2	201.123368	101.065322			183.112803	92.060039	S	1242.668842	621.838059	1225.642293	613.324785	1224.658277	612.832777	11
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	N	1155.636814	578.322045	1138.610265	569.808771	1137.626249	569.316762	10
4	402.198323	201.602800	385.171774	193.089525	384.187758	192.597517	S	1041.593887	521.300582	1024.567338	512.787307	1023.583322	512.295299	9
5	499.251087	250.129182	482.224538	241.615907	481.240522	241.123899	P	954.561859	477.784567	937.535310	469.271293	936.551294	468.779285	8
6	628.293680	314.650478	611.267131	306.137204	610.283115	305.645196	E	***857.509095***	429.258185	840.482546	420.744911	839.498530	420.252903	7
7	756.388643	378.697960	739.362094	370.184685	738.378078	369.692677	K	***728.466502***	364.736889	711.439953	356.223614			6
8	869.436322	435.221799	852.409773	426.708525	851.425757	426.216517	P	***600.371539***	300.689407	583.344990	292.176133			5
9	997.531285	499.269281	980.504736	490.756006	979.520720	490.263998	K	***487.323860***	244.165568	470.297311	235.652293			4
10	1096.599699	548.803488	1079.573150	540.290213	1078.589134	539.798205	V	***359.228897***	180.118086	342.202348	171.604812			3
11	1209.683763	605.345520	1192.657214	596.832245	1191.673198	596.340237	I	260.160483	130.583879	243.133934	122.070605			2
12							Q	147.076419	74.041847	130.049870	65.528573			1





NCBI **BLAST** search of ISNSPEKPKVIQ
(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	1354.745605	-0.011217	ISNSPEKPKVIQ

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

{MATRIX SCIENCE}

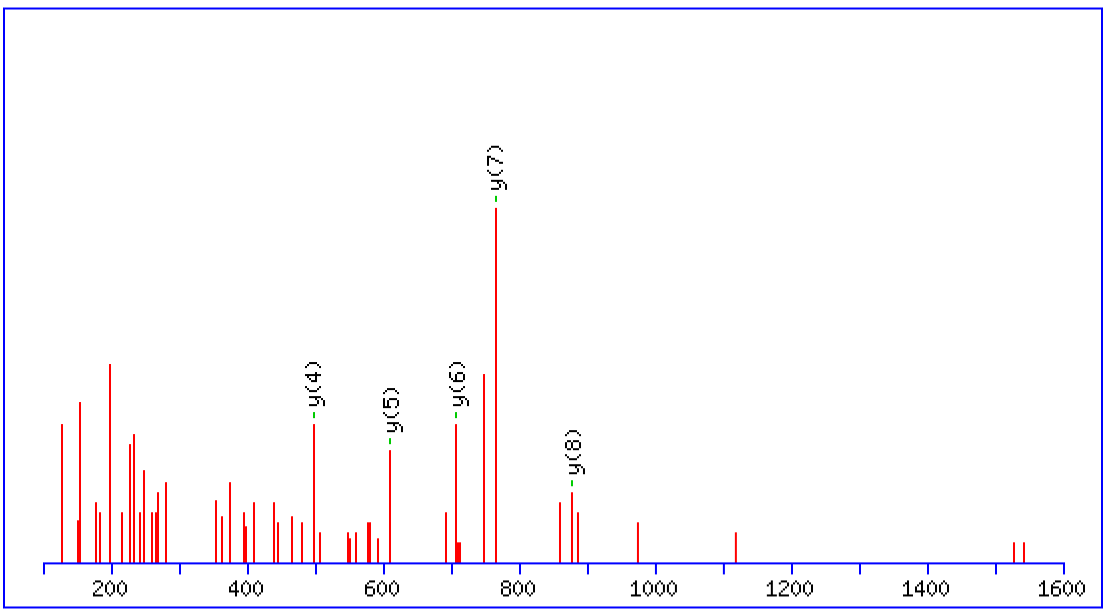
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLGPPPPPR**
Found in **PP1RA_HUMAN**, Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens GN=PPP1R10 PE=1 SV=1

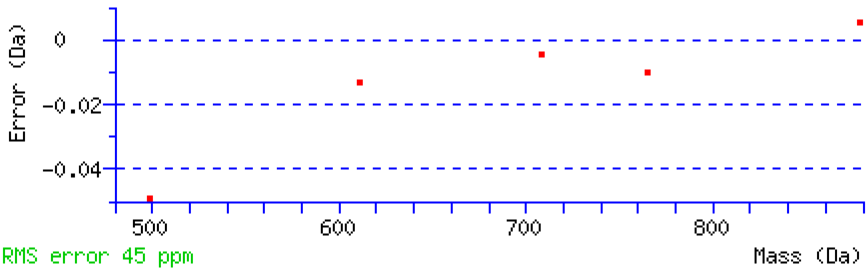
Match to Query 7302: 990.540588 from(496.277570,2+) rtinseconds(2130) index(21820)
Title: Locus:1.1.1.2592.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

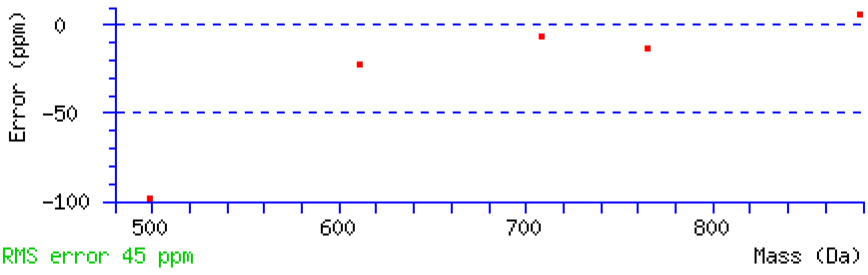
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 990.549835
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P5      : Oxidation (P)
P7      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 32  Expect: 0.0034
Matches : 5/48 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308	L					9
2	227.175404	114.091340	L	*878.473045*	439.740161	861.446496	431.226886	8
3	284.196868	142.602072	G	*765.388981*	383.198129	748.362432	374.684854	7
4	381.249632	191.128454	P	*708.367517*	354.687397	691.340968	346.174122	6
5	494.297311	247.652293	P	*611.314753*	306.161015	594.288204	297.647740	5
6	591.350075	296.178676	P	*498.267074*	249.637175	481.240525	241.123900	4
7	704.397754	352.702515	P	401.214310	201.110793	384.187761	192.597518	3
8	817.445433	409.226355	P	288.166631	144.586953	271.140082	136.073679	2
9			R	175.118952	88.063114	158.092403	79.549839	1





NCBI **BLAST** search of LLGPPPPPR
(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	990.549835	-0.009247	LLGPPPPPR
32.2	990.549835	-0.009247	LLGPPPPPR
32.2	990.549835	-0.009247	LLGPPPPPR
19.7	990.549835	-0.009247	LLGPPPPPR
19.7	990.549835	-0.009247	LLGPPPPPR
19.7	990.549835	-0.009247	LLGPPPPPR
18.5	990.549835	-0.009247	LLGPPPPPR
8.7	990.549835	-0.009247	LLGPPPPPR
8.7	990.549835	-0.009247	LLGPPPPPR
8.7	990.549835	-0.009247	LLGPPPPPR

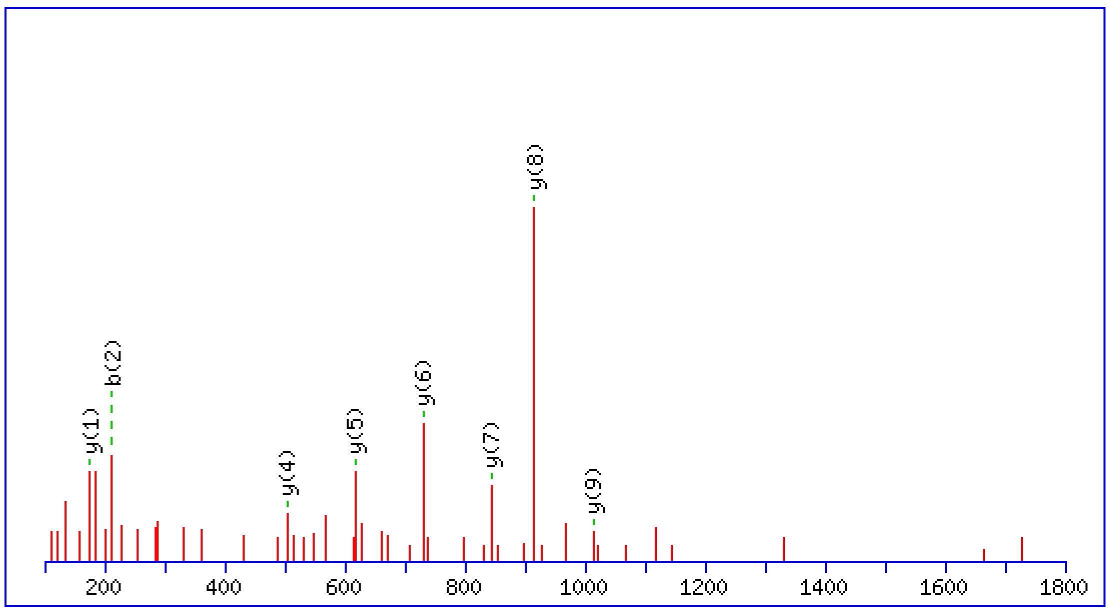
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVALLNTLDR**
Found in **PTPA_HUMAN**, Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3

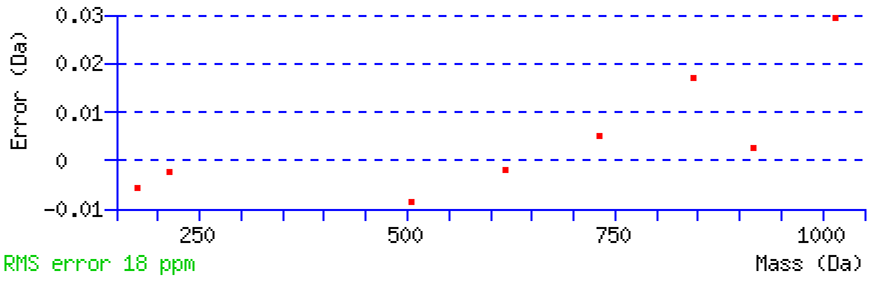
Match to Query 16667: 1126.666108 from(564.340330,2+) rtinseconds(3055) index(35548)
Title: Locus:1.1.1.2733.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

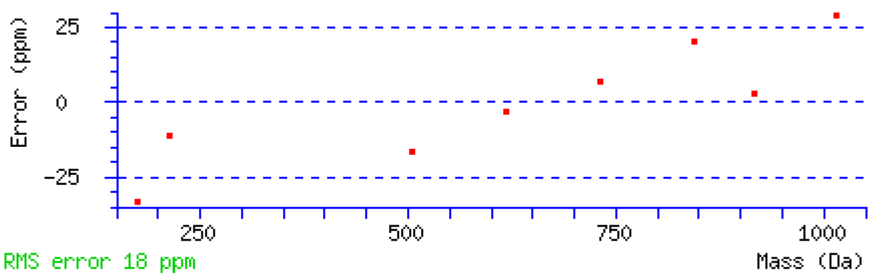
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1126.670990
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 1.2e-005
Matches : 8/84 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							10
2	213.159754	107.083515					V	***1014.594221***	507.800749	997.567672	499.287474	996.583656	498.795466	9
3	284.196868	142.602072					A	***915.525807***	458.266542	898.499258	449.753267	897.515242	449.261259	8
4	397.280932	199.144104					L	***844.488693***	422.747985	827.462144	414.234710	826.478128	413.742702	7
5	510.364996	255.686136					L	***731.404629***	366.205953	714.378080	357.692678	713.394064	357.200670	6
6	624.407923	312.707600	607.381374	304.194325			N	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	5
7	725.455602	363.231439	708.429053	354.718165	707.445037	354.226157	T	***504.277638***	252.642457	487.251089	244.129183	486.267073	243.637175	4
8	838.539666	419.773471	821.513117	411.260197	820.529101	410.768189	L	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
9	953.566609	477.286943	936.540060	468.773668	935.556044	468.281660	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
10							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of LVALLNTLDR
(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	1126.670990	-0.004882	LVALLNTLDR
4.5	1126.670990	-0.004882	VLAPKQSLQK
4.2	1126.670975	-0.004867	VLAEVEALKR
3.9	1126.671021	-0.004913	IVNTVPITVR
3.9	1126.671021	-0.004913	IVTTPQTVLR
1.5	1126.661087	0.005021	VALLHQKYR
1.1	1126.672333	-0.006225	AVLIPHHKGR

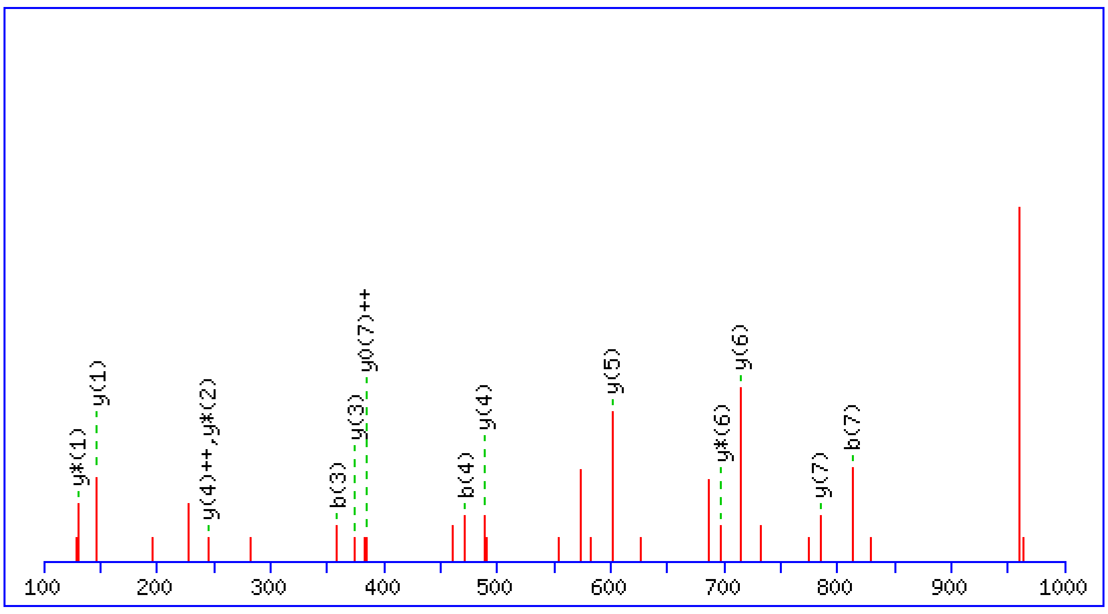
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CALLILDK**
Found in **ANR44_HUMAN**, Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B OS=Homo sapiens GN=ANKRD44 PE=1 SV=3

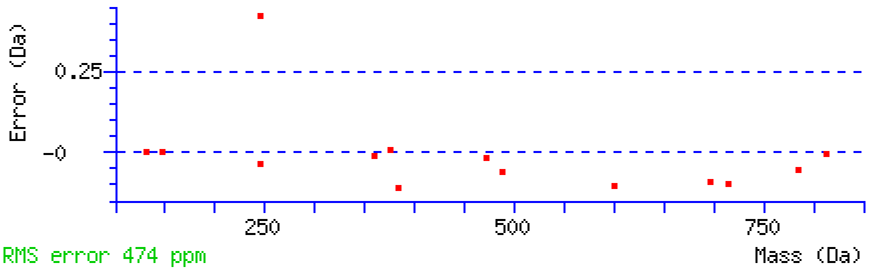
Match to Query 8458: 958.545228 from(480.279890,2+) rtinseconds(1212) index(3197)
Title: Locus:1.1.1.1967.11
Data file 2011-11-10 - TFD - S 8-1.mgf

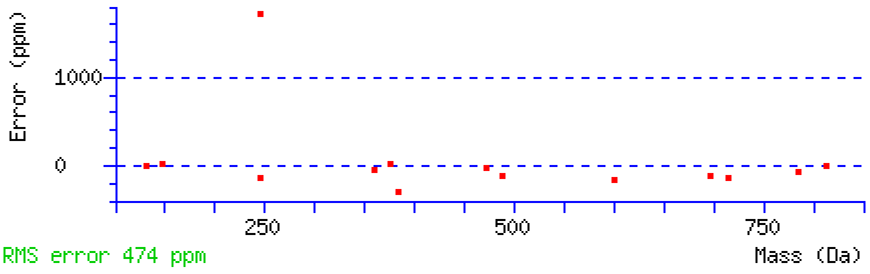
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 958.552109
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00047
Matches : 14/56 fragment ions using 21 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	246.090689	123.548982			A	***785.513117***	393.260197	768.486568	384.746922	767.502552	384.254914	7
3	**359.174753**	180.091015			L	***714.476003***	357.741640	697.449454	349.228365	696.465438	348.736357	6
4	**472.258817**	236.633047			L	***601.391939***	301.199608	584.365390	292.686333	583.381374	292.194325	5
5	585.342881	293.175079			I	***488.307875***	244.657575	471.281326	236.144301	470.297310	235.652293	4
6	698.426945	349.717111			L	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
7	**813.453888**	407.230582	795.443323	398.225300	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 CALLILDK
(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	958.552109	-0.006881	CALLILDK
37.0	958.544739	0.000489	ELQTTLVR
29.8	958.544724	0.000504	LSRDELVK
19.3	958.544724	0.000504	NTDAAKIVK
19.3	958.544739	0.000489	SATVQINVK
18.9	958.538193	0.007035	ERCIIVR
13.8	958.544739	0.000489	TLATTLAPR
12.3	958.552124	-0.006896	CIIPSVIK
11.8	958.544708	0.000520	KTLEEAIR
8.7	958.544724	0.000504	EDLVSLRK

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

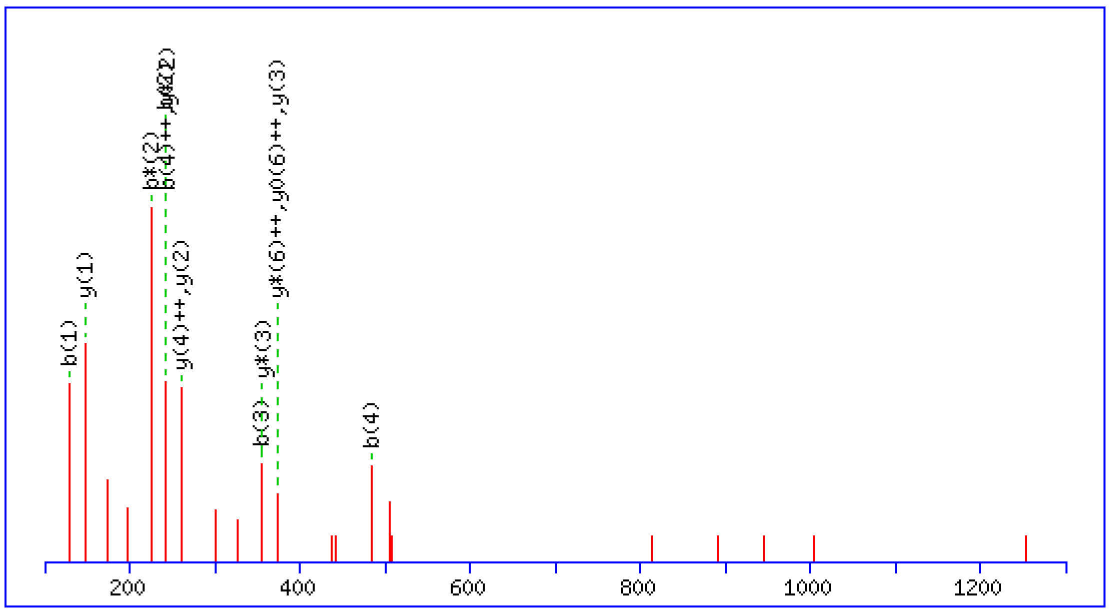
Mascot Search Results

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

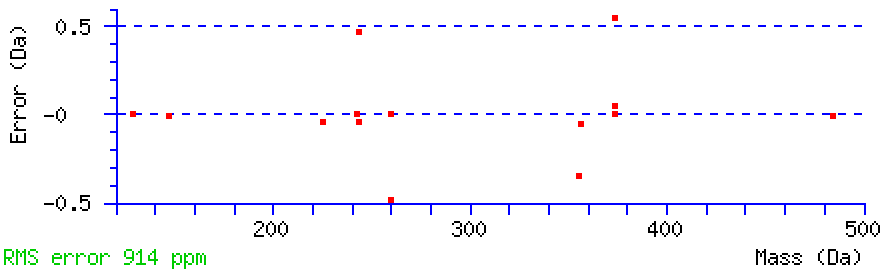
Match to Query 5581: 1002.638948 from(502.326750,2+) rtinseconds(1828) index(2472)
Title: Locus:1.1.1.2546.7
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-7.mgf

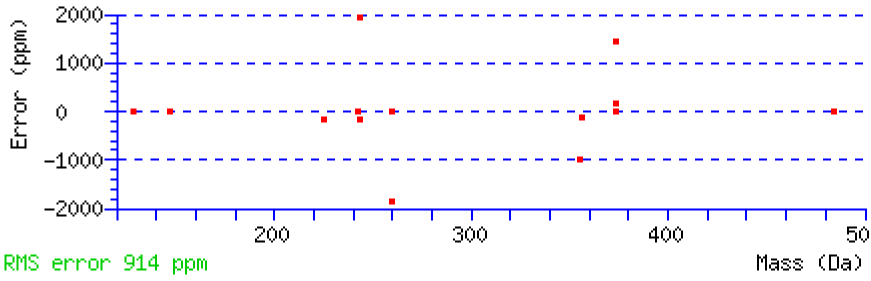
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1002.647720
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32  Expect: 0.00067
Matches : 15/70 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	***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
31.7	1002.647720	-0.008772	KLIEFLLK
16.5	1002.647720	-0.008772	LKLFEILK
0.6	1002.647736	-0.008788	IFLLGLSIK

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

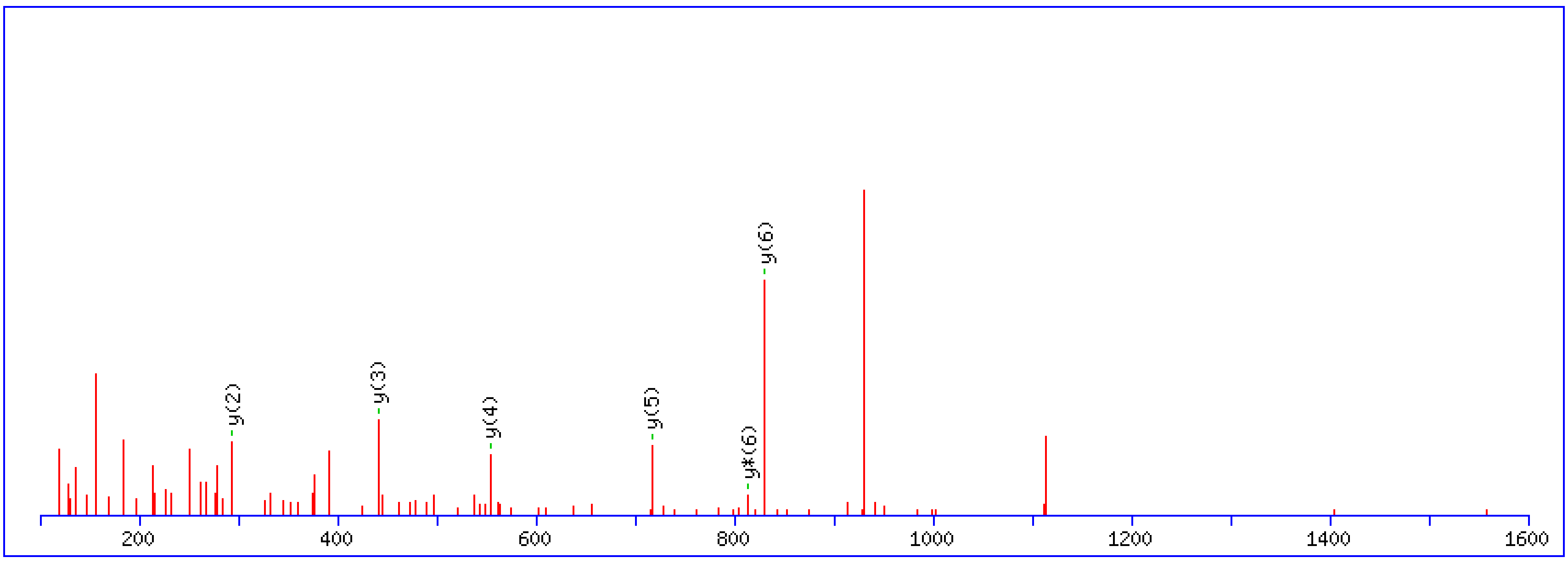
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLANYIFFK**
Found in **SPA11_HUMAN**, Serpin A11 OS=Homo sapiens GN=SERPINA11 PE=2 SV=2

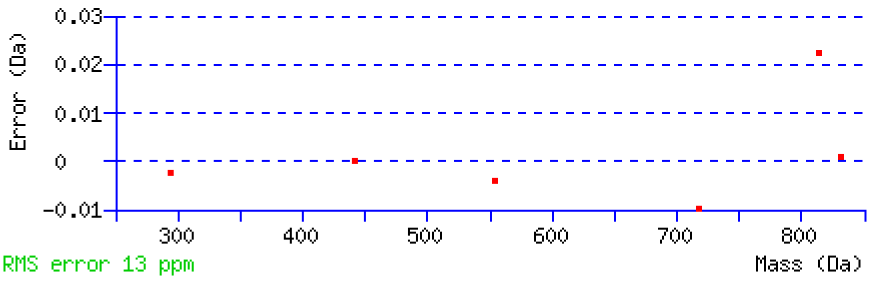
Match to Query 8426: 1113.624248 from(557.819400,2+) rtinseconds(3533) index(49109)
Title: Locus:1.1.1.2051.7
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

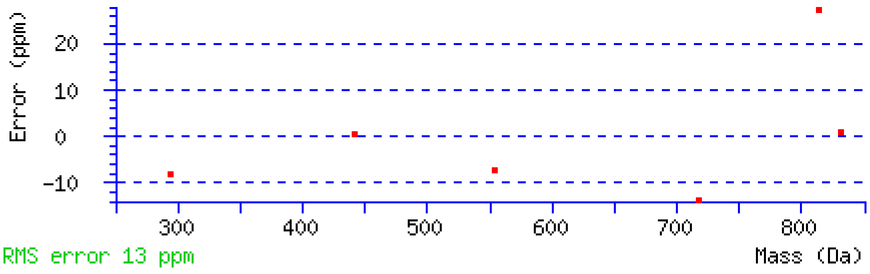
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1113.622253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0055
Matches : 6/58 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	100.075690	50.541483			V					9
2	213.159754	107.083515			L	1015.561130	508.284203	998.534581	499.770929	8
3	284.196868	142.602072			A	902.477066	451.742171	885.450517	443.228897	7
4	398.239795	199.623536	381.213246	191.110261	N	***831.439952***	416.223614	814.413403	407.710340	6
5	561.303124	281.155200	544.276575	272.641926	Y	***717.397025***	359.202151	700.370476	350.688876	5
6	674.387188	337.697232	657.360639	329.183958	I	***554.333696***	277.670486	537.307147	269.157212	4
7	821.455602	411.231439	804.429053	402.718165	F	***441.249632***	221.128454	424.223083	212.615180	3
8	968.524016	484.765646	951.497467	476.252371	F	***294.181218***	147.594247	277.154669	139.080973	2
9					K	147.112804	74.060040	130.086255	65.546766	1





NCBI **BLAST** search of VLANYIFFK
(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	1113.622253	0.001995	VLANYIFFK
6.6	1113.618240	0.006008	AIVGHVDLYK
2.9	1113.626770	-0.002522	RPHAPGRPAR

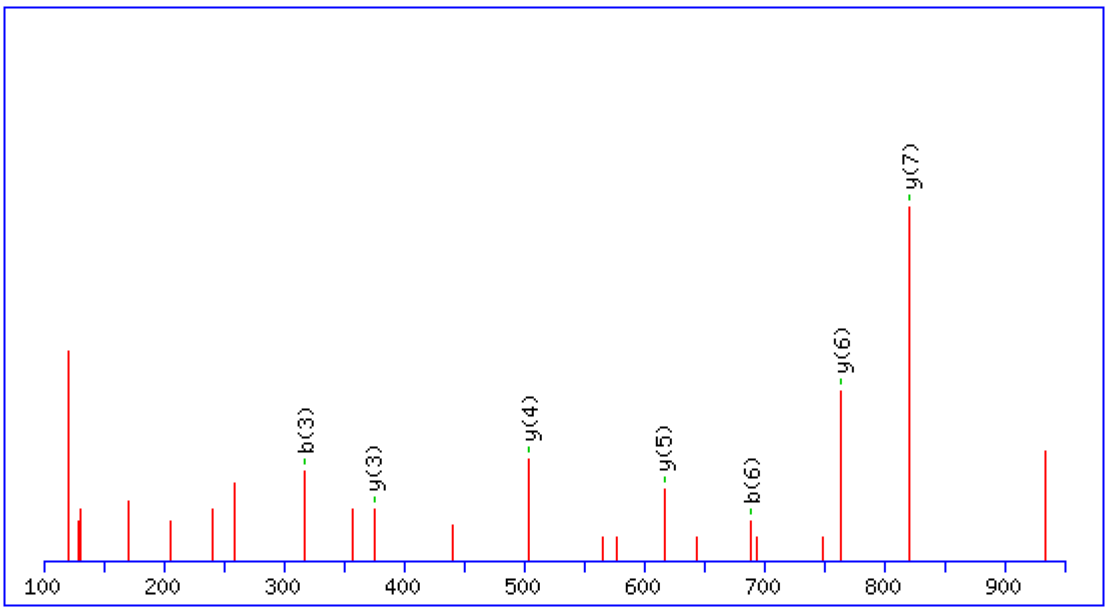
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGFIEEVK**
Found in **SPB12_HUMAN**, Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1

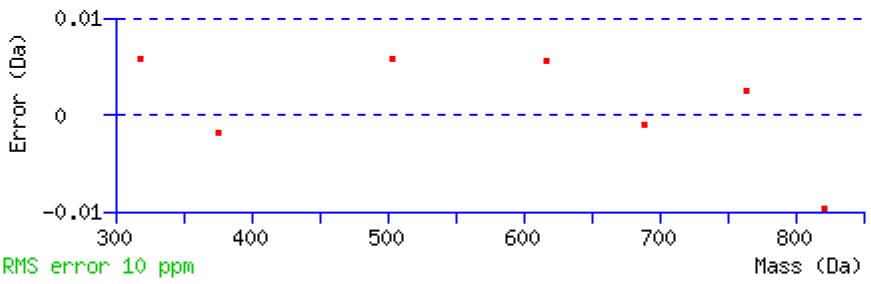
Match to Query 2632: 933.516708 from(467.765630,2+) rtinseconds(2526) index(5064)
Title: Locus:1.1.1.3270.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

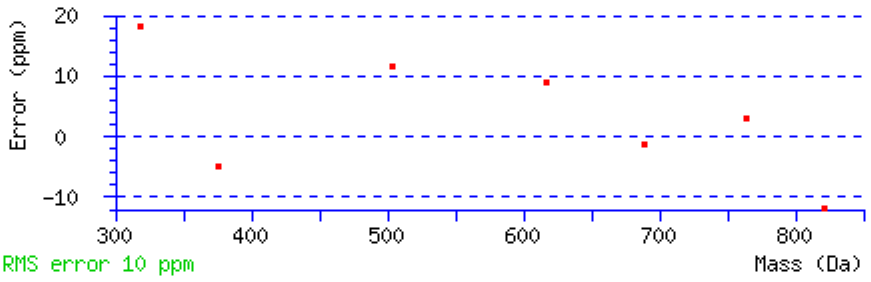
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 933.517120
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 0.0001
Matches : 7/58 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	171.112804	86.060040			G	***821.440346***	411.223811	804.413797	402.710537	803.429781	402.218529	7
3	**318.181218**	159.594247			F	***764.418882***	382.713079	747.392333	374.199805	746.408317	373.707797	6
4	431.265282	216.136279			I	***617.350468***	309.178872	600.323919	300.665598	599.339903	300.173590	5
5	560.307875	280.657576	542.297310	271.652293	E	***504.266404***	252.636840	487.239855	244.123565	486.255839	243.631557	4
6	**689.350468**	345.178872	671.339903	336.173590	E	***375.223811***	188.115543	358.197262	179.602269	357.213246	179.110261	3
7	788.418882	394.713079	770.408317	385.707797	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 IGFIEEVK
(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	933.517120	-0.000412	IGFIEEVK
12.6	933.524338	-0.007630	LGKSSSVTR
10.7	933.517120	-0.000412	VAFLLDEK
1.5	933.525665	-0.008957	LGGPAARHR

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

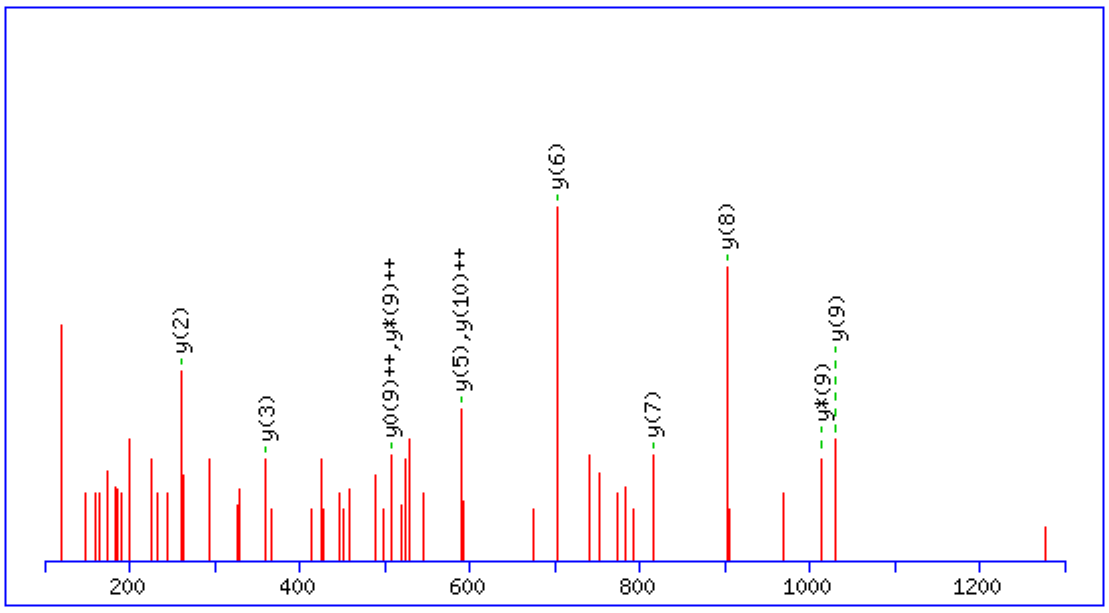
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFQSLLTEVNK**
Found in **SPB9_HUMAN**, Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1

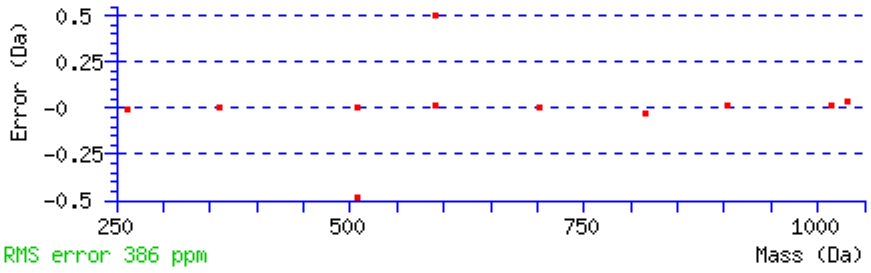
Match to Query 27242: 1248.677868 from(625.346210,2+) rtinseconds(2804) index(35451)
Title: Locus:1.1.1.2466.26
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

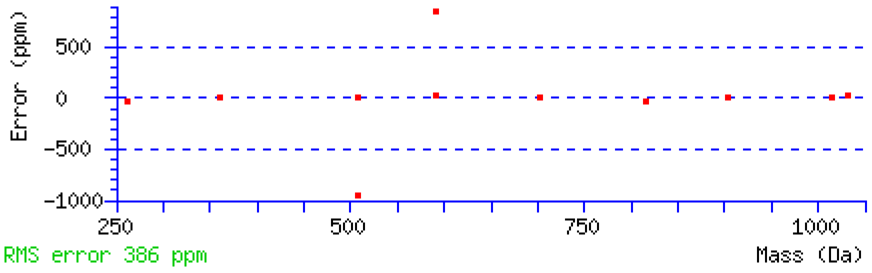
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1248.671387
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 66 **Expect:** 4.2e-006
Matches : 11/104 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	219.112804	110.060040					F	1178.641565	589.824421	1161.615016	581.311146	1160.631000	580.819138	10
3	347.171382	174.089329	330.144833	165.576055			Q	***1031.573151***	516.290214	1014.546602	507.776939	1013.562586	507.284931	9
4	434.203410	217.605343	417.176861	209.092069	416.192845	208.600061	S	***903.514573***	452.260925	886.488024	443.747650	885.504008	443.255642	8
5	547.287474	274.147375	530.260925	265.634101	529.276909	265.142093	L	***816.482545***	408.744911	799.455996	400.231636	798.471980	399.739628	7
6	660.371538	330.689407	643.344989	322.176133	642.360973	321.684125	L	***703.398481***	352.202879	686.371932	343.689604	685.387916	343.197596	6
7	761.419217	381.213247	744.392668	372.699972	743.408652	372.207964	T	***590.314417***	295.660847	573.287868	287.147572	572.303852	286.655564	5
8	890.461810	445.734543	873.435261	437.221269	872.451245	436.729261	E	489.266738	245.137007	472.240189	236.623732	471.256173	236.131724	4
9	989.530224	495.268750	972.503675	486.755476	971.519659	486.263468	V	***360.224145***	180.615710	343.197596	172.102436			3
10	1103.573151	552.290214	1086.546602	543.776939	1085.562586	543.284931	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 AFQSLLTEVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.6	1248.671387	0.006481	AFQSLLTEVNK
0.9	1248.682617	-0.004749	NGVYLLSLSQR

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

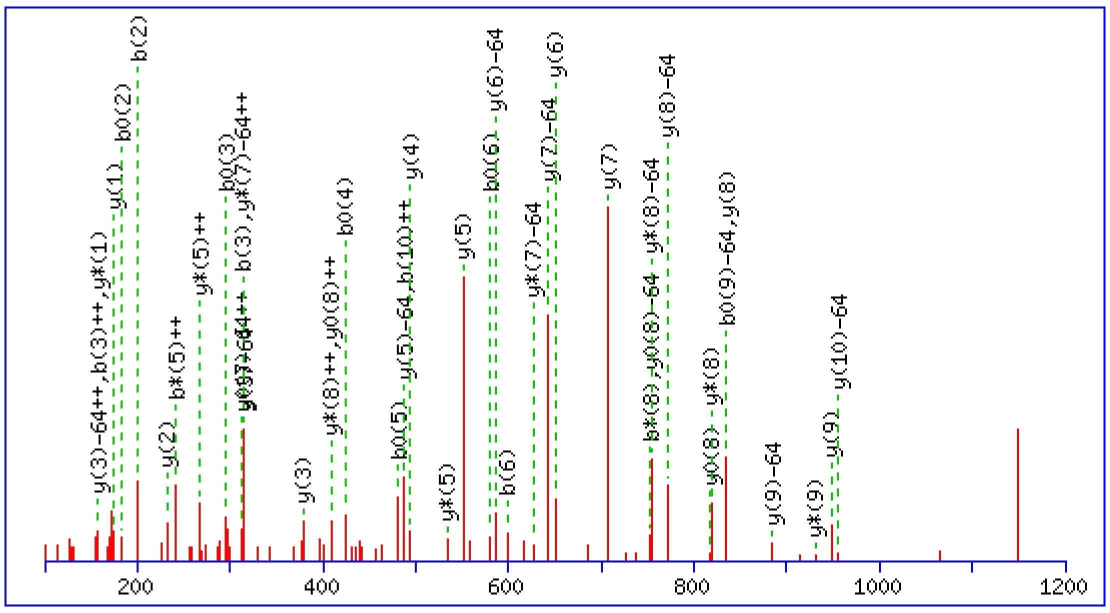
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALQGVGDMGR**
Found in **SAA4_HUMAN**, Serum amyloid A-4 protein OS=Homo sapiens GN=SAA4 PE=1 SV=2

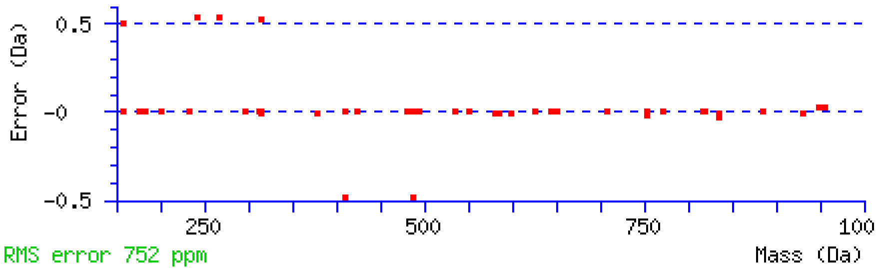
Match to Query 9326: 1147.527928 from(574.771240,2+) rtinseconds(1364) index(711)
Title: Locus:1.1.1.2225.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-7.mgf

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 ●

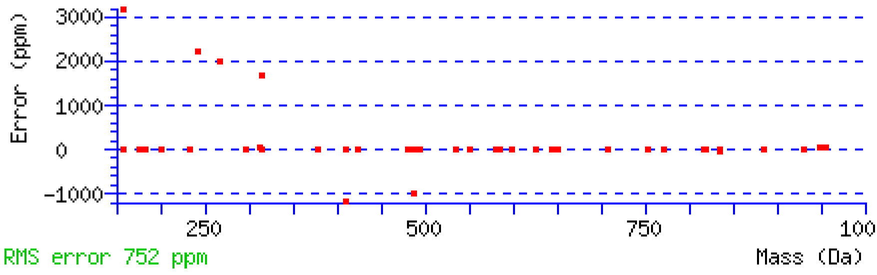


```
Monoisotopic mass of neutral peptide Mr(calc): 1147.529175
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 76  Expect: 7.2e-008
Matches : 43/166 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							11
2	**201.086983**	101.047130			183.076418	92.041847	A	1019.493857	510.250567	1002.467308	501.737292	1001.483292	501.245284	10
3	**314.171047**	157.589161			296.160482	148.583879	L	***948.456743***	474.732010	931.430194	466.218735	930.446178	465.726727	9
4	442.229625	221.618450	425.203076	213.105176	424.219060	212.613168	Q	***835.372679***	418.189978	818.346130	409.676703	817.362114	409.184695	8
5	499.251089	250.129182	482.224540	241.615908	481.240524	241.123900	G	***707.314101***	354.160689	690.287552	345.647414	689.303536	345.155406	7
6	**598.319503**	299.663390	581.292954	291.150115	580.308938	290.658107	V	***650.292637***	325.649957	633.266088	317.136682	632.282072	316.644674	6
7	655.340967	328.174122	638.314418	319.660847	637.330402	319.168839	G	***551.224223***	276.115750	534.197674	267.602475	533.213658	267.110467	5
8	770.367910	385.687593	753.341361	377.174319	752.357345	376.682311	D	***494.202759***	247.605017	477.176210	239.091743	476.192194	238.599735	4
9	917.403310	459.205293	900.376761	450.692019	899.392745	450.200011	M	***379.175816***	190.091546	362.149267	181.578271			3
10	974.424774	487.716025	957.398225	479.202751	956.414209	478.710743	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 752 ppm



RMS error 752 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.2	1147.529175	-0.001247	EALQGVGDMGR
0.0	1147.521774	0.006154	QTEPRGDSSR

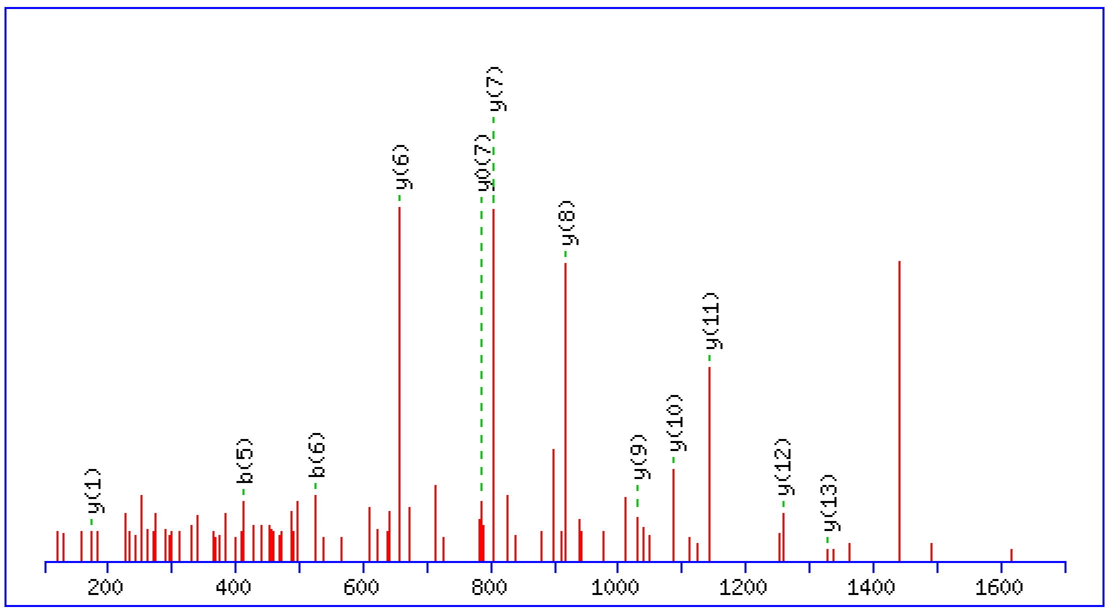
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IALGGLLFPASNLR**
Found in **SHBG_HUMAN**, Sex hormone-binding globulin OS=Homo sapiens GN=SHBG PE=1 SV=2

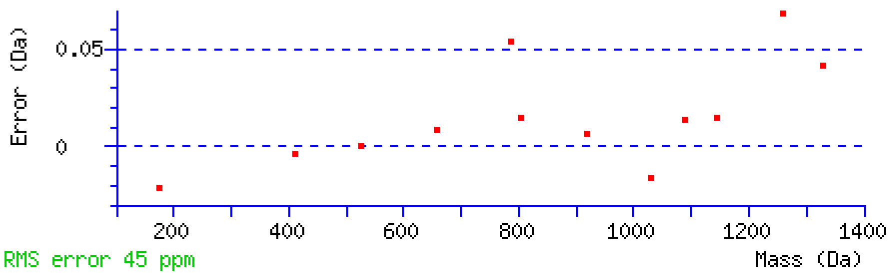
Match to Query 31138: 1440.855828 from(721.435190,2+) rtinseconds(3766) index(54901)
Title: Locus:1.1.1.2958.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

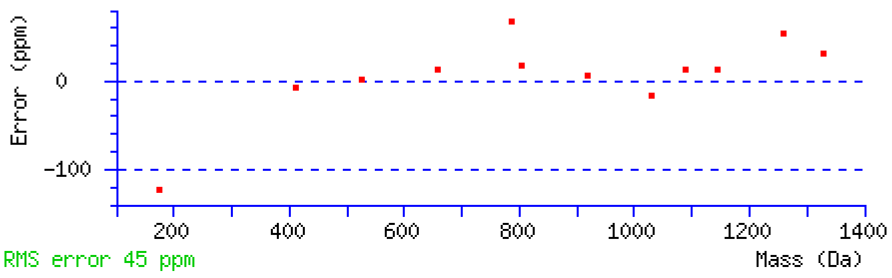
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1440.845261
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 3.1e-006
Matches : 12/108 fragment ions using 26 most intense peaks    (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					I							14
2	185.128454	93.067865					A	***1328.768497***	664.887887	1311.741948	656.374612	1310.757932	655.882604	13
3	298.212518	149.609897					L	***1257.731383***	629.369330	1240.704834	620.856055	1239.720818	620.364047	12
4	355.233982	178.120629					G	***1144.647319***	572.827297	1127.620770	564.314023	1126.636754	563.822015	11
5	**412.255446**	206.631361					G	***1087.625855***	544.316566	1070.599306	535.803291	1069.615290	535.311283	10
6	**525.339510**	263.173393					L	***1030.604391***	515.805834	1013.577842	507.292559	1012.593826	506.800551	9
7	638.423574	319.715425					L	***917.520327***	459.263802	900.493778	450.750527	899.509762	450.258519	8
8	785.491988	393.249632					F	***804.436263***	402.721769	787.409714	394.208495	786.425698	393.716487	7
9	882.544752	441.776014					P	***657.367849***	329.187563	640.341300	320.674288	639.357284	320.182280	6
10	953.581866	477.294571					A	560.315085	280.661181	543.288536	272.147906	542.304520	271.655898	5
11	1040.613894	520.810585			1022.603329	511.805303	S	489.277971	245.142623	472.251422	236.629349	471.267406	236.137341	4
12	1154.656821	577.832049	1137.630272	569.318774	1136.646256	568.826766	N	402.245943	201.626609	385.219394	193.113335			3
13	1267.740885	634.374080	1250.714336	625.860806	1249.730320	625.368798	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 IALGGLLFPASNLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.6	1440.845261	0.010567	IALGGLLFPASNLR

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

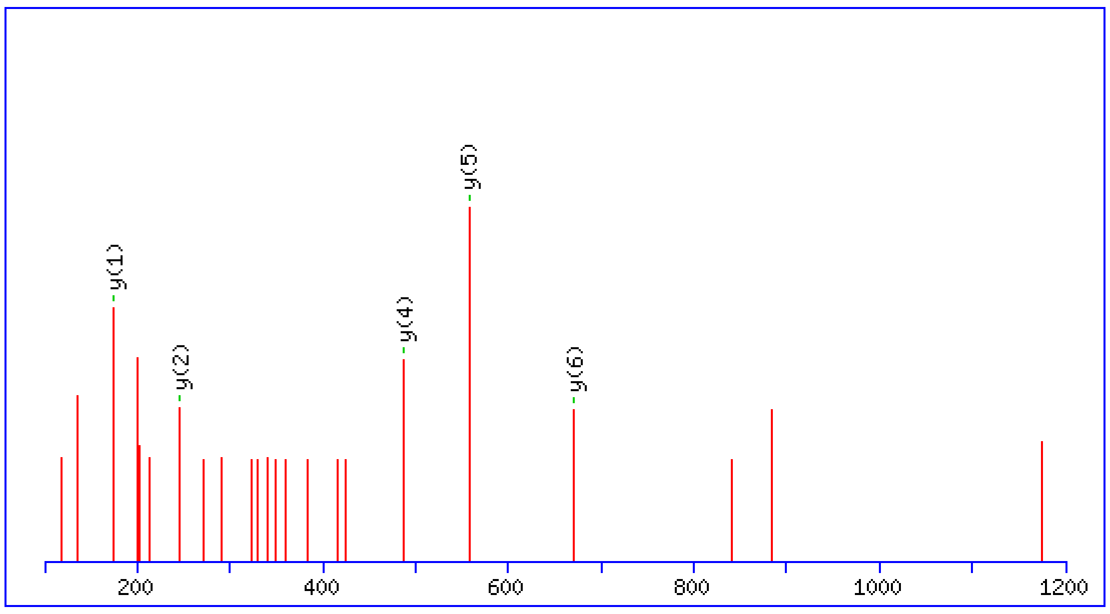
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEIAQLAR**
Found in **SGMR1_HUMAN**, Sigma non-opioid intracellular receptor 1 OS=Homo sapiens GN=SIGMAR1 PE=1 SV=1

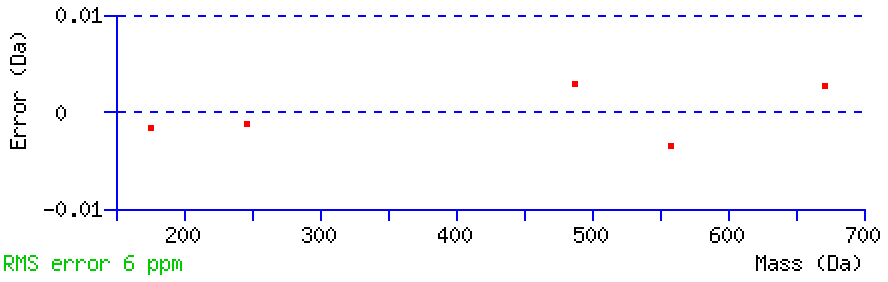
Match to Query 7157: 928.489448 from(465.252000,2+) rtinseconds(1742) index(11634)
Title: Locus:1.1.1.2474.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

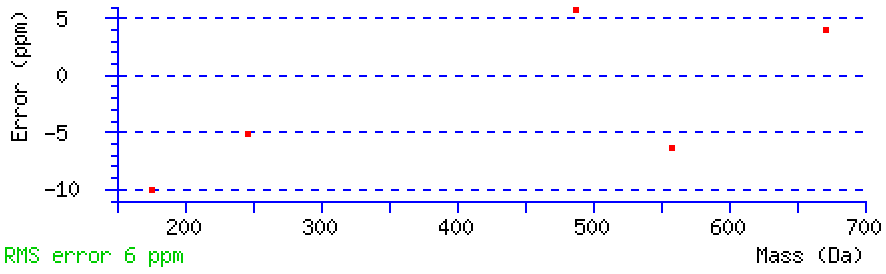
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 928.497757
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^{*}	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**	800.462479	400.734878	783.435930	392.221603	782.451914	391.729595	7
3	372.176526	186.591901			354.165961	177.586619	**I**	*671.419886*	336.213581	654.393337	327.700307			6
4	443.213640	222.110458			425.203075	213.105176	**A**	*558.335822*	279.671549	541.309273	271.158275			5
5	571.272218	286.139747	554.245669	277.626473	553.261653	277.134465	**Q**	*487.298708*	244.152992	470.272159	235.639718			4
6	684.356282	342.681779	667.329733	334.168505	666.345717	333.676497	**L**	359.240130	180.123703	342.213581	171.610429			3
7	755.393396	378.200336	738.366847	369.687062	737.382831	369.195054	**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 EEIAQLAR
(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	928.497757	-0.008309	EEIAQLAR
24.8	928.497757	-0.008309	EIEALQAR
11.8	928.483856	0.005592	RAGSQSPAR
11.6	928.483887	0.005561	GGPGSARGVR
7.7	928.497787	-0.008339	VDGELGALR
6.2	928.497757	-0.008309	AELAEGALR
5.8	928.487885	0.001563	SWPRLDR
5.8	928.497772	-0.008324	ALSPEGALR
5.3	928.497772	-0.008324	VNGEIEIR
4.2	928.487885	0.001563	FNKHLDR

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

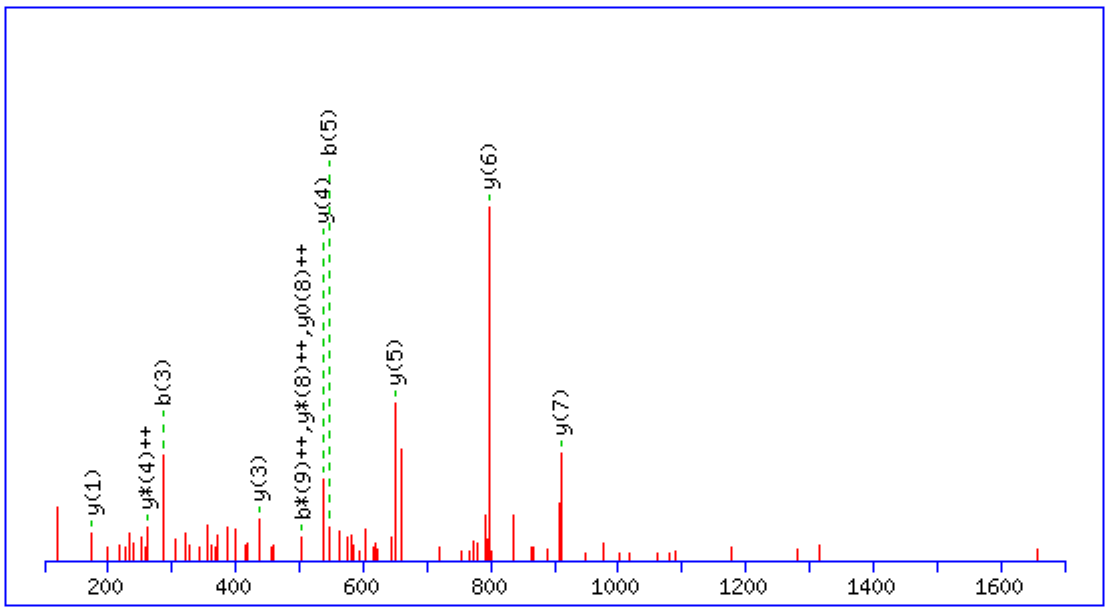
{MATRIX SCIENCE} Mascot Search Results

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

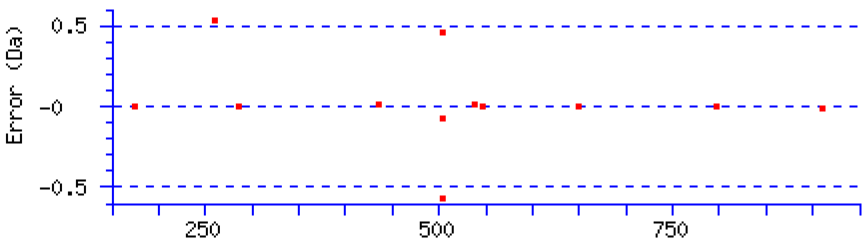
Match to Query 18836: 1194.644848 from(598.329700,2+) rtinseconds(3756) index(37696)
Title: Locus:1.1.1.2921.3
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

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 ●

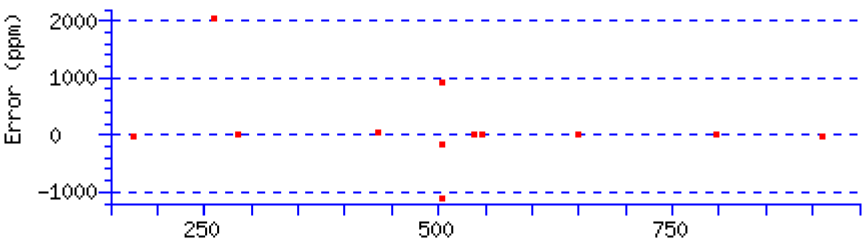


```
Monoisotopic mass of neutral peptide Mr(calc): 1194.639709
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35  Expect: 0.0028
Matches : 12/86 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	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



RMS error 726 ppm



RMS error 726 ppm

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
35.1	1194.639709	0.005139	GDLLFLTNFR
10.2	1194.639709	0.005139	DVIAFPKSFR
1.1	1194.635696	0.009152	GDLGLPGQPGLR

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

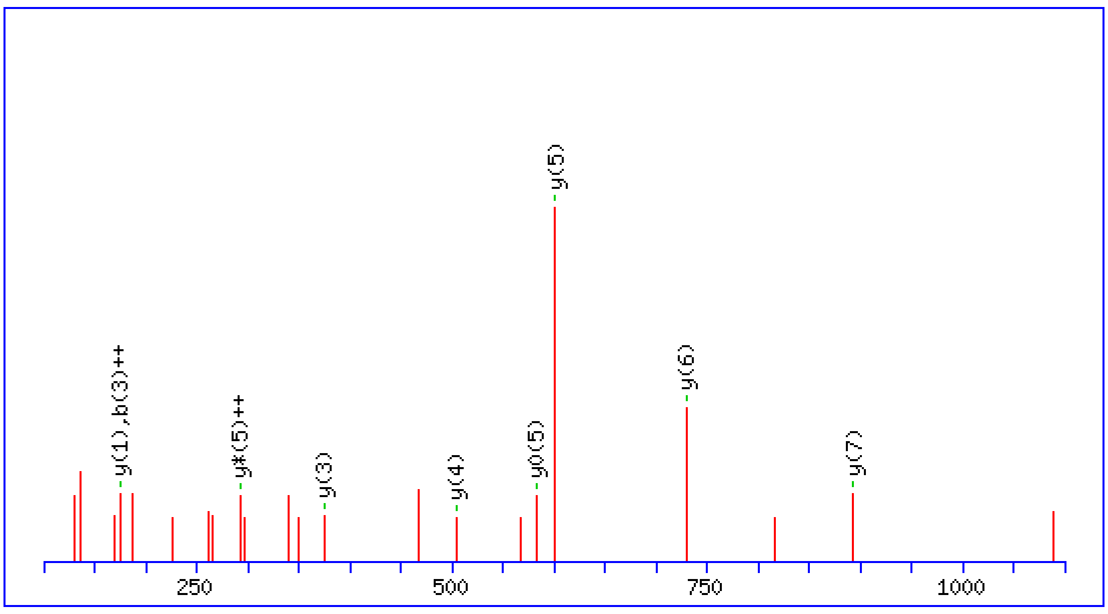
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DAYEPEISR**
Found in **SPCS2_HUMAN**, Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3

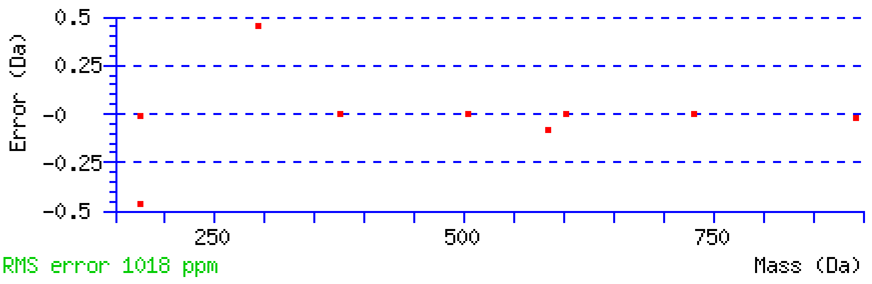
Match to Query 285081: 1078.503248 from(540.258900,2+) rtinseconds(1536) index(407964)
Title: Locus:1.1.1.1181.15
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

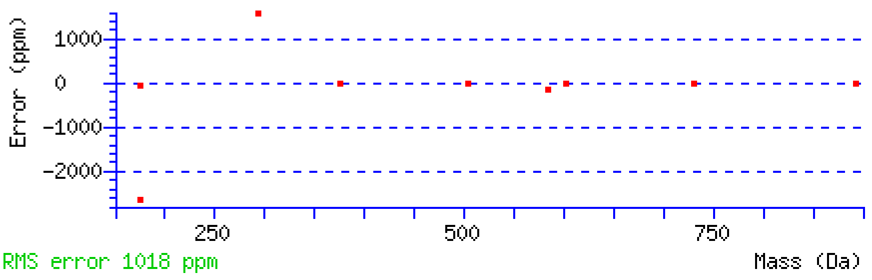
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1078.493073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.00038
Matches : 9/78 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							9
2	187.071333	94.039304	169.060768	85.034022	A	964.473437	482.740357	947.446888	474.227082	946.462872	473.735074	8
3	350.134662	175.570969	332.124097	166.565687	Y	***893.436323***	447.221800	876.409774	438.708525	875.425758	438.216517	7
4	479.177255	240.092266	461.166690	231.086983	E	***730.372994***	365.690135	713.346445	357.176861	712.362429	356.684853	6
5	576.230019	288.618648	558.219454	279.613365	P	***601.330401***	301.168839	584.303852	292.655564	583.319836	292.163556	5
6	705.272612	353.139944	687.262047	344.134662	E	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
7	818.356676	409.681976	800.346111	400.676694	I	***375.235044***	188.121160	358.208495	179.607886	357.224479	179.115878	3
8	905.388704	453.197990	887.378139	444.192708	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 DAYEPEISR
(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	1078.493073	0.010175	DAYEPEISR
10.9	1078.496460	0.006788	MDSETPKQK
8.5	1078.496445	0.006803	ANSSLQEISM
8.2	1078.493103	0.010145	GPTEQGPYAK
7.7	1078.500488	0.002760	SMYPPLDPK
5.2	1078.507690	-0.004442	AGASIPAMSSR
4.8	1078.504318	-0.001070	FINQDSAER
4.1	1078.500504	0.002744	GPVPSFSELM
3.2	1078.511734	-0.008486	HPVMSVSYK
3.1	1078.493103	0.010145	SFDEQNVPK

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

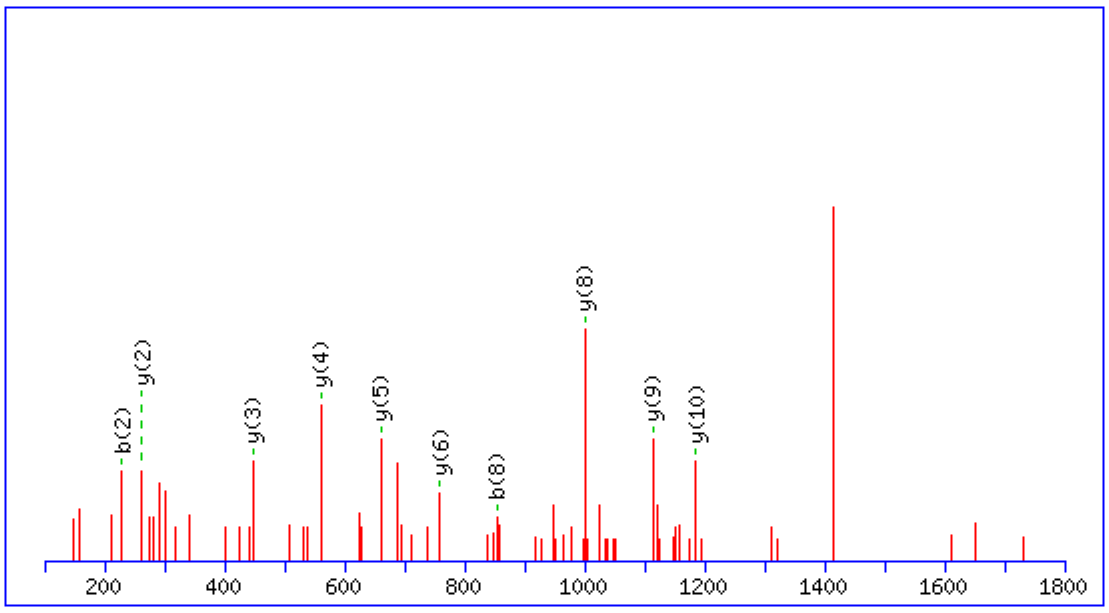
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNALNQVVLWDK**
Found in **SPCS3_HUMAN**, Signal peptidase complex subunit 3 OS=Homo sapiens GN=SPCS3 PE=1 SV=1

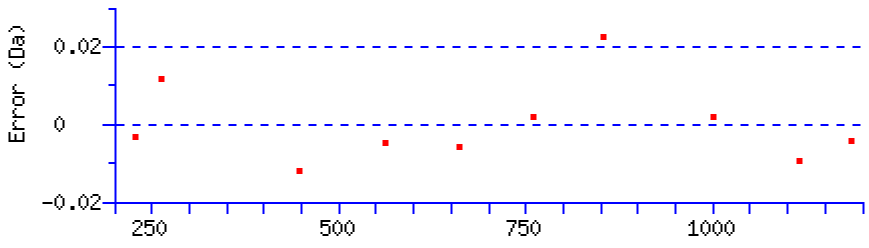
Match to Query 32154: 1412.749768 from(707.382160,2+) rtinseconds(2978) index(39230)
Title: Locus:1.1.1.2575.35
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

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 ●

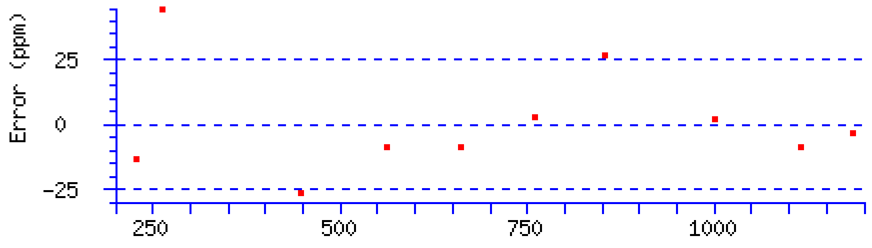


Monoisotopic mass of neutral peptide Mr(calc): 1412.741196
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 73 **Expect:** 1.5e-007
Matches : 10/110 fragment ions using 12 most intense peaks (help)

#	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							12
2	**229.093130**	115.050203	212.066581	106.536929			N	1299.705562	650.356419	1282.679013	641.843145	1281.694997	641.351137	11
3	300.130244	150.568760	283.103695	142.055486			A	***1185.662635***	593.334956	1168.636086	584.821681	1167.652070	584.329673	10
4	413.214308	207.110792	396.187759	198.597518			L	***1114.625521***	557.816399	1097.598972	549.303124	1096.614956	548.811116	9
5	527.257235	264.132256	510.230686	255.618981			N	***1001.541457***	501.274367	984.514908	492.761092	983.530892	492.269084	8
6	655.315813	328.161545	638.289264	319.648270			Q	887.498530	444.252903	870.471981	435.739629	869.487965	435.247621	7
7	754.384227	377.695752	737.357678	369.182477			V	***759.439952***	380.223614	742.413403	371.710340	741.429387	371.218332	6
8	**853.452641**	427.229959	836.426092	418.716684			V	***660.371538***	330.689407	643.344989	322.176133	642.360973	321.684125	5
9	966.536705	483.771991	949.510156	475.258716			L	***561.303124***	281.155200	544.276575	272.641926	543.292559	272.149918	4
10	1152.616018	576.811647	1135.589469	568.298373			W	***448.219060***	224.613168	431.192511	216.099894	430.208495	215.607886	3
11	1267.642961	634.325119	1250.616412	625.811844	1249.632396	625.319836	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



RMS error 19 ppm



RMS error 19 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.2	1412.741196	0.008572	NNALNQVVLWDK
0.5	1412.762314	-0.012546	VSPLQNLASINNK

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

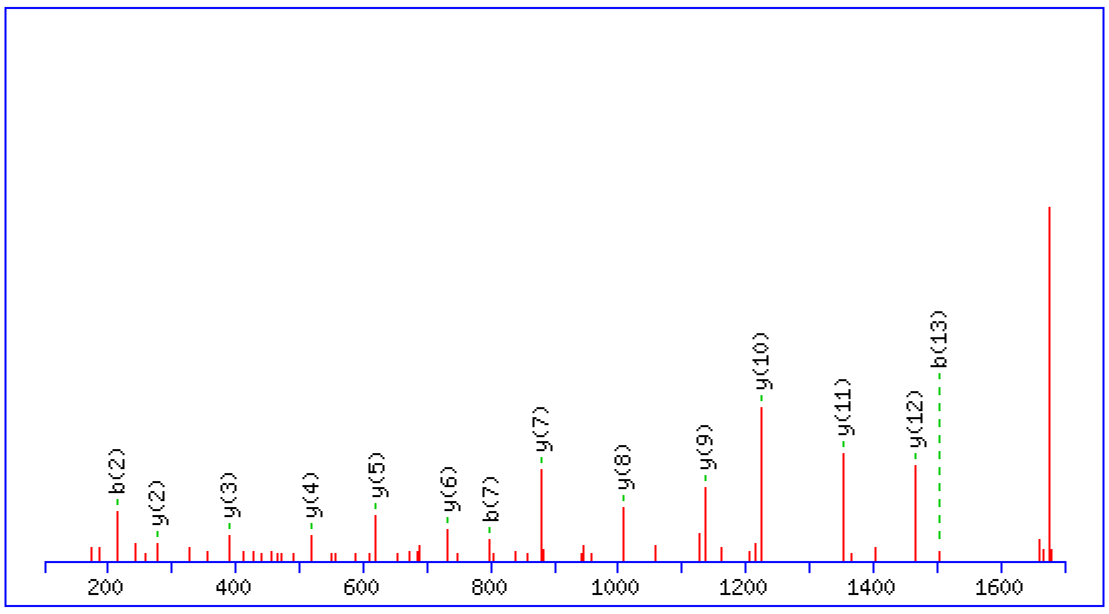
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLESEQFLTELTR**
Found in **SRP14_HUMAN**, Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2

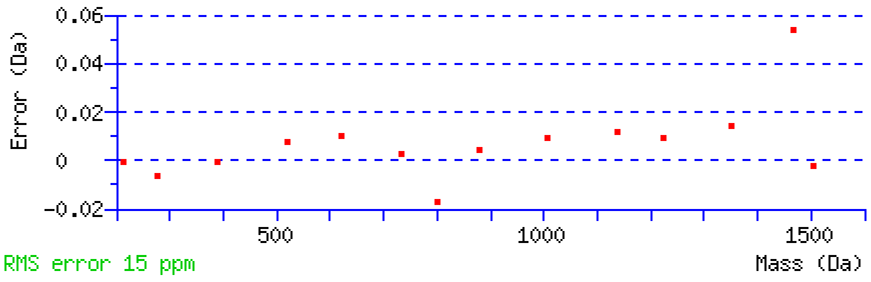
Match to Query 44905: 1676.906968 from(839.460760,2+) rtinseconds(3839) index(39615)
Title: Locus:1.1.1.2964.12
Data file 2011-11-14 - TFD - S 2-6.mgf

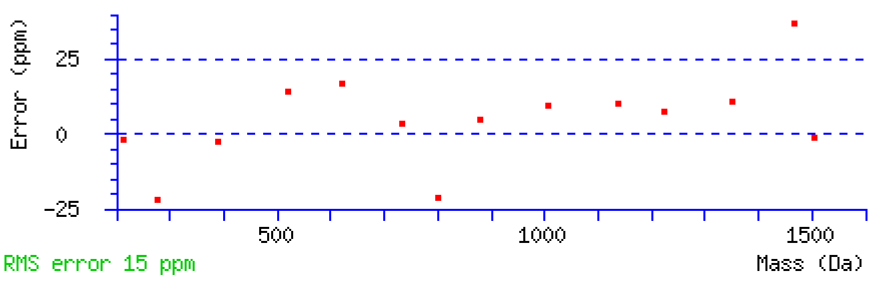
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1676.898483
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 123 **Expect:** 3.8e-012
Matches : 14/136 fragment ions using 15 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	100.075690	50.541483					V							14
2	**213.159754**	107.083515					L	1578.837365	789.922320	1561.810816	781.409046	1560.826800	780.917038	13
3	326.243818	163.625547					L	***1465.753301***	733.380289	1448.726752	724.867014	1447.742736	724.375006	12
4	455.286411	228.146843			437.275846	219.141561	E	***1352.669237***	676.838256	1335.642688	668.324982	1334.658672	667.832974	11
5	542.318439	271.662858			524.307874	262.657575	S	***1223.626644***	612.316960	1206.600095	603.803686	1205.616079	603.311677	10
6	671.361032	336.184154			653.350467	327.178872	E	***1136.594616***	568.800946	1119.568067	560.287672	1118.584051	559.795664	9
7	**799.419610**	400.213443	782.393061	391.700169	781.409045	391.208161	Q	***1007.552023***	504.279650	990.525474	495.766375	989.541458	495.274367	8
8	946.488024	473.747650	929.461475	465.234376	928.477459	464.742368	F	***879.493445***	440.250361	862.466896	431.737086	861.482880	431.245078	7
9	1059.572088	530.289682	1042.545539	521.776408	1041.561523	521.284399	L	***732.425031***	366.716154	715.398482	358.202879	714.414466	357.710871	6
10	1160.619767	580.813521	1143.593218	572.300247	1142.609202	571.808239	T	***619.340967***	310.174122	602.314418	301.660847	601.330402	301.168839	5
11	1289.662360	645.334818	1272.635811	636.821544	1271.651795	636.329536	E	***518.293288***	259.650282	501.266739	251.137008	500.282723	250.645000	4
12	1402.746424	701.876850	1385.719875	693.363576	1384.735859	692.871567	L	***389.250695***	195.128985	372.224146	186.615711	371.240130	186.123703	3
13	**1503.794103**	752.400690	1486.767554	743.887415	1485.783538	743.395407	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 VLLESEQFLTELTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
122.6	1676.898483	0.008485	VLLESEQFLTELTR
9.4	1676.891968	0.015000	VIPELNGKLTGMAFR
3.3	1676.921158	-0.014190	VLMPTVPIFPKEFK

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

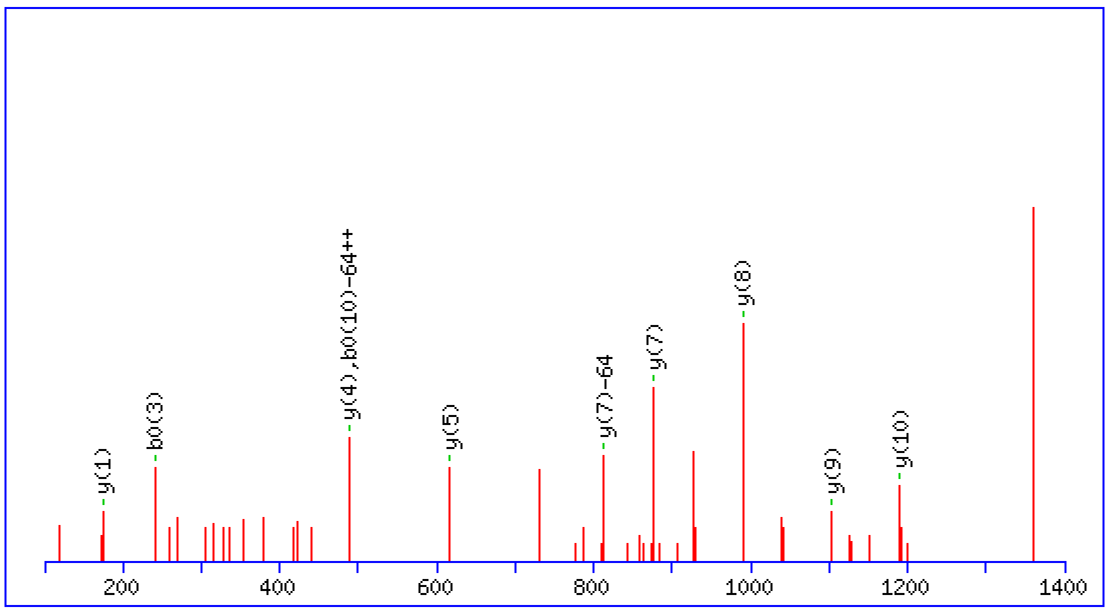
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNSIIMLEALER**
Found in **RUXGL_HUMAN**, Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens PE=3 SV=2

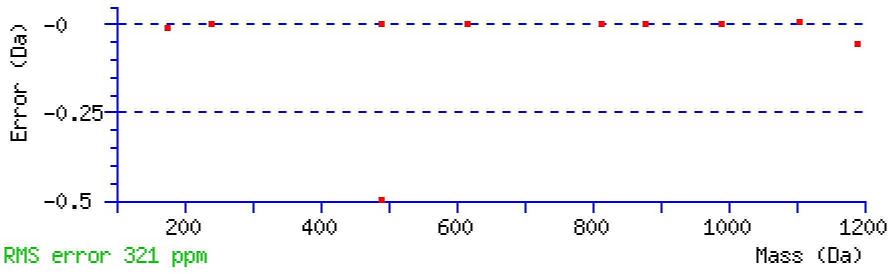
Match to Query 14444: 1360.705528 from(681.360040,2+) rtinseconds(2988) index(8638)
Title: Locus:1.1.1.3232.9
Data file 2011-11-10 - TFD - S 9-8.mgf

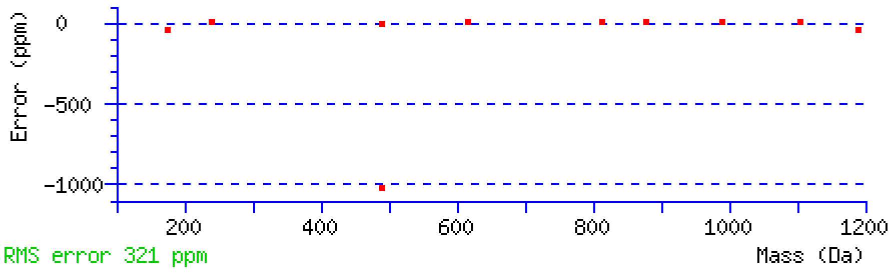
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1360.702011
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: 60 **Expect:** 7.6e-006
Matches : 10/190 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							12
2	172.071667	86.539471	155.045118	78.026197			N	1304.687863	652.847569	1287.661314	644.334295	1286.677298	643.842287	11
3	259.103695	130.055485	242.077146	121.542211	241.093130	121.050203	S	***1190.644936***	595.826106	1173.618387	587.312832	1172.634371	586.820823	10
4	372.187759	186.597517	355.161210	178.084243	354.177194	177.592235	I	***1103.612908***	552.310092	1086.586359	543.796817	1085.602343	543.304809	9
5	485.271823	243.139549	468.245274	234.626275	467.261258	234.134267	I	***990.528844***	495.768060	973.502295	487.254785	972.518279	486.762777	8
6	632.307223	316.657250	615.280674	308.143975	614.296658	307.651967	M	***877.444780***	439.226028	860.418231	430.712753	859.434215	430.220745	7
7	745.391287	373.199282	728.364738	364.686007	727.380722	364.193999	L	730.409380	365.708328	713.382831	357.195053	712.398815	356.703045	6
8	874.433880	437.720578	857.407331	429.207304	856.423315	428.715296	E	***617.325316***	309.166296	600.298767	300.653021	599.314751	300.161013	5
9	945.470994	473.239135	928.444445	464.725861	927.460429	464.233853	A	***488.282723***	244.644999	471.256174	236.131725	470.272158	235.639717	4
10	1058.555058	529.781167	1041.528509	521.267893	1040.544493	520.775884	L	417.245609	209.126442	400.219060	200.613168	399.235044	200.121160	3
11	1187.597651	594.302463	1170.571102	585.789189	1169.587086	585.297181	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 GNSIIMLEALER
(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	1360.702011	0.003517	GNSIIMLEALER
5.6	1360.713257	-0.007729	CTNIGGLELSRK
2.8	1360.702011	0.003517	EEGAKLSMEVLR

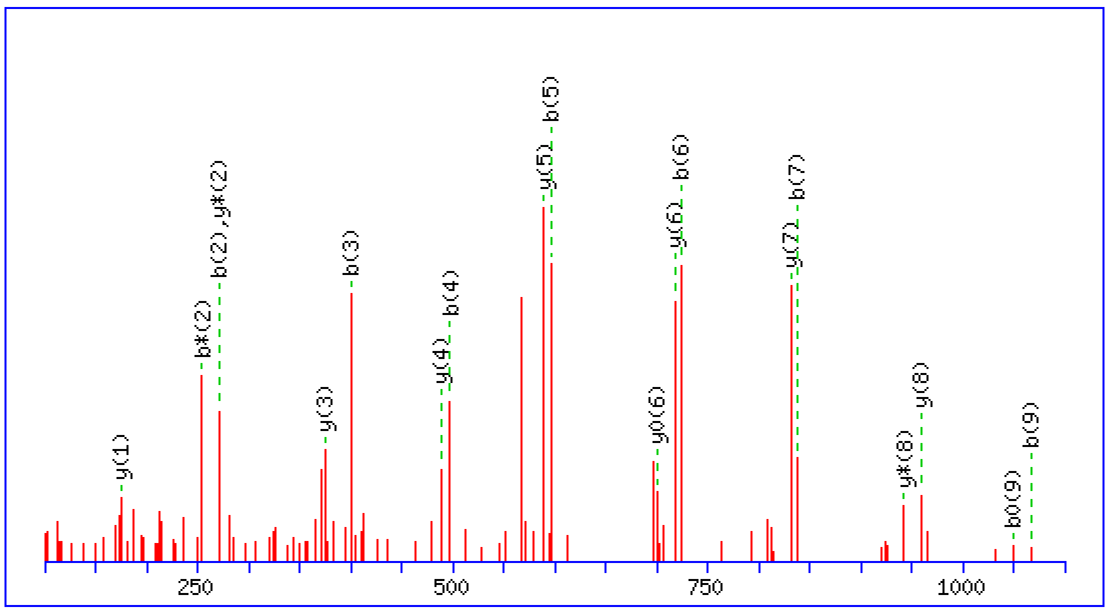
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NREPVQLETLSIR**
Found in **SMD1_HUMAN**, Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1

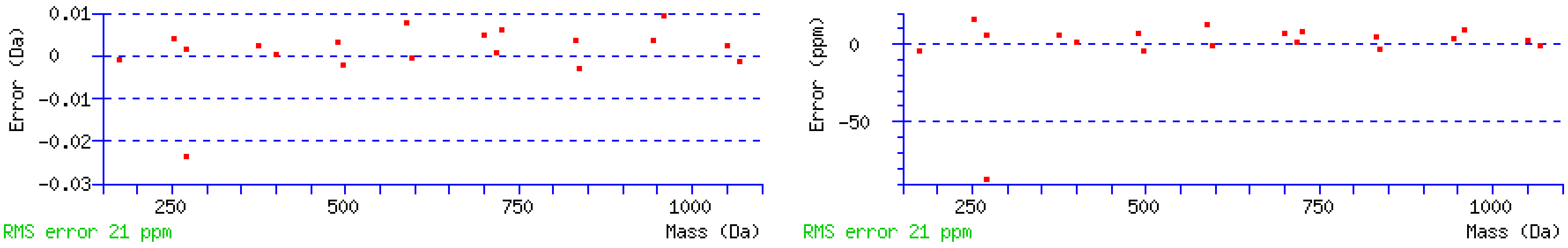
Match to Query 10853: 1553.850852 from(518.957560,3+) rtinseconds(2468) index(7676)
Title: Locus:1.1.1.2841.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-7.mgf

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): 1553.852524
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 80 **Expect:** 4.5e-008
Matches : 19/136 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	***271.151314***	136.079295	254.124765	127.566021			R	1440.816904	720.912090	1423.790355	712.398816	1422.806339	711.906808	12
3	***400.193907***	200.600592	383.167358	192.087317	382.183342	191.595309	E	1284.715793	642.861535	1267.689244	634.348260	1266.705228	633.856252	11
4	***497.246671***	249.126974	480.220122	240.613699	479.236106	240.121691	P	1155.673200	578.340238	1138.646651	569.826964	1137.662635	569.334955	10
5	***596.315085***	298.661181	579.288536	290.147906	578.304520	289.655898	V	1058.620436	529.813856	1041.593887	521.300582	1040.609871	520.808573	9
6	***724.373663***	362.690470	707.347114	354.177195	706.363098	353.685187	Q	***959.552022***	480.279649	942.525473	471.766374	941.541457	471.274366	8
7	***837.457727***	419.232502	820.431178	410.719227	819.447162	410.227219	L	***831.493444***	416.250360	814.466895	407.737085	813.482879	407.245077	7
8	966.500320	483.753798	949.473771	475.240524	948.489755	474.748516	E	***718.409380***	359.708328	701.382831	351.195053	700.398815	350.703045	6
9	***1067.547999***	534.277638	1050.521450	525.764363	1049.537434	525.272355	T	***589.366787***	295.187031	572.340238	286.673757	571.356222	286.181749	5
10	1180.632063	590.819670	1163.605514	582.306395	1162.621498	581.814387	L	***488.319108***	244.663192	471.292559	236.149917	470.308543	235.657909	4
11	1267.664091	634.335684	1250.637542	625.822409	1249.653526	625.330401	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
12	1380.748155	690.877716	1363.721606	682.364441	1362.737590	681.872433	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 NREPVQLETLSIR
(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	1553.852524	-0.001672	NREPVQLETLSIR
1.4	1553.845322	0.005530	YEAIQLTFKQVSK

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

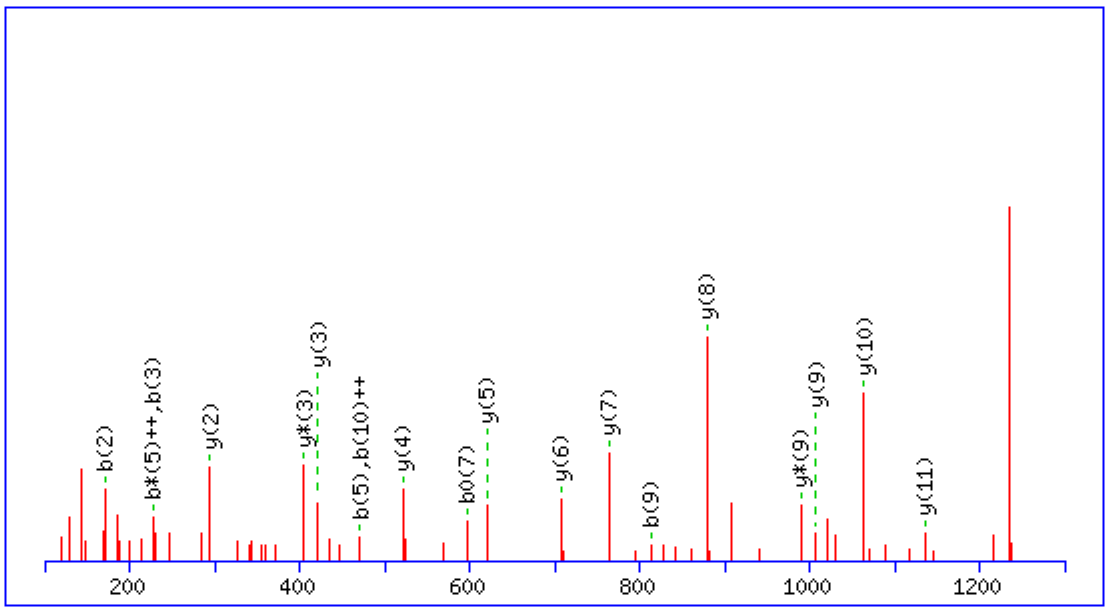
{MATRIX SCIENCE} Mascot Search Results

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

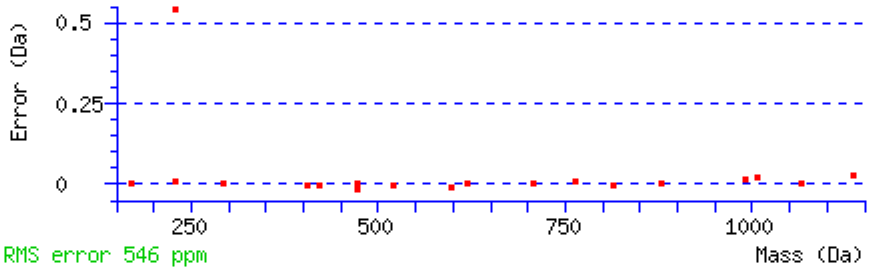
Match to Query 21914: 1233.636928 from(617.825740,2+) rtinseconds(1933) index(12503)
Title: Locus:1.1.1.2200.29
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

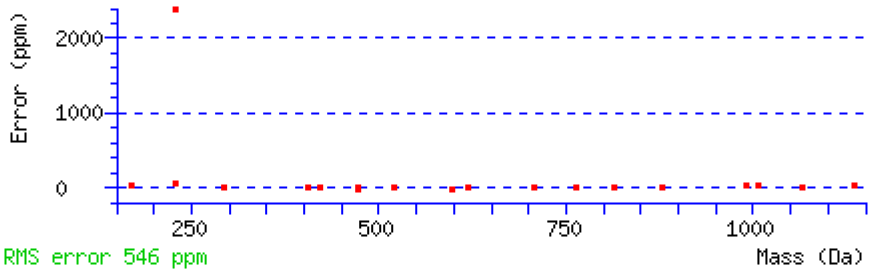
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1233.635376
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 99 **Expect:** 9.7e-010
Matches : 19/108 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	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
99.0	1233.635376	0.001552	VAGQDGSVVQFK
2.9	1233.635330	0.001598	NISNTGEKPFK

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

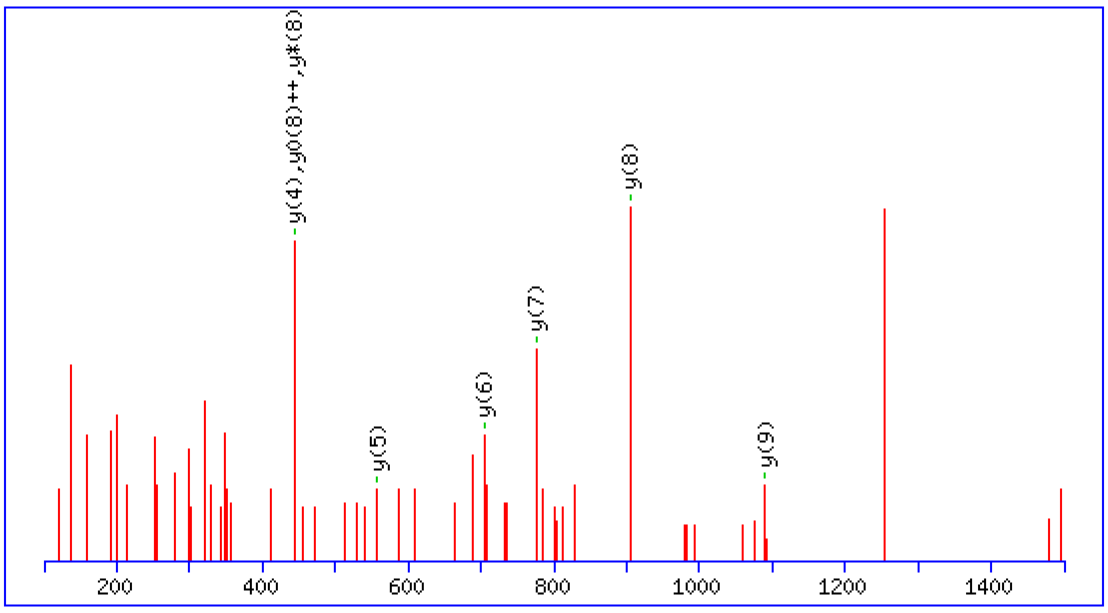
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YWEAFLPEAK**
Found in **SNX1_HUMAN**, Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3

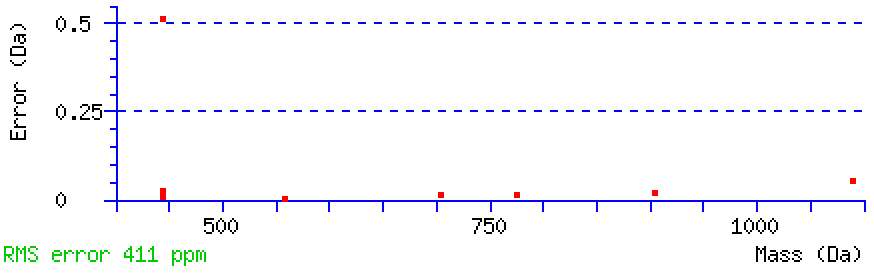
Match to Query 24001: 1252.621168 from(627.317860,2+) rtinseconds(3233) index(46167)
Title: Locus:1.1.1.2744.10
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-2.mgf

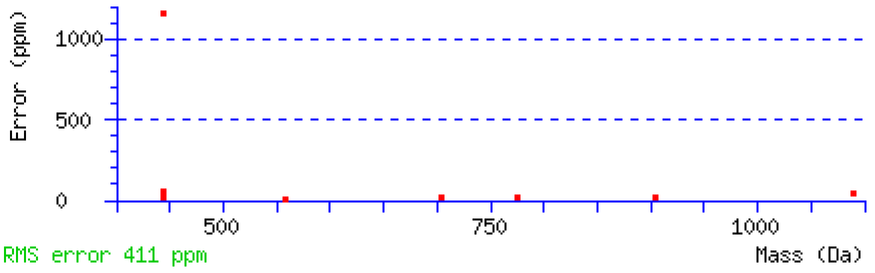
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1252.612793
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.0012
Matches : 8/82 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940			Y							10
2	350.149918	175.578597			W	***1090.556773***	545.782025	1073.530224	537.268750	1072.546208	536.776742	9
3	479.192511	240.099894	461.181946	231.094611	E	***904.477460***	452.742368	887.450911	444.229094	886.466895	443.737086	8
4	550.229625	275.618451	532.219060	266.613168	A	***775.434867***	388.221072	758.408318	379.707797	757.424302	379.215789	7
5	697.298039	349.152658	679.287474	340.147375	F	***704.397753***	352.702515	687.371204	344.189240	686.387188	343.697232	6
6	810.382103	405.694690	792.371538	396.689407	L	***557.329339***	279.168308	540.302790	270.655033	539.318774	270.163025	5
7	907.434867	454.221072	889.424302	445.215789	P	***444.245275***	222.626275	427.218726	214.113001	426.234710	213.620993	4
8	1036.477460	518.742368	1018.466895	509.737086	E	347.192511	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	1107.514574	554.260925	1089.504009	545.255643	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 YWEAFLPEAK
(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	1252.612793	0.008375	YWEAFLPEAK

Mascot: http://www.matrixscience.com/

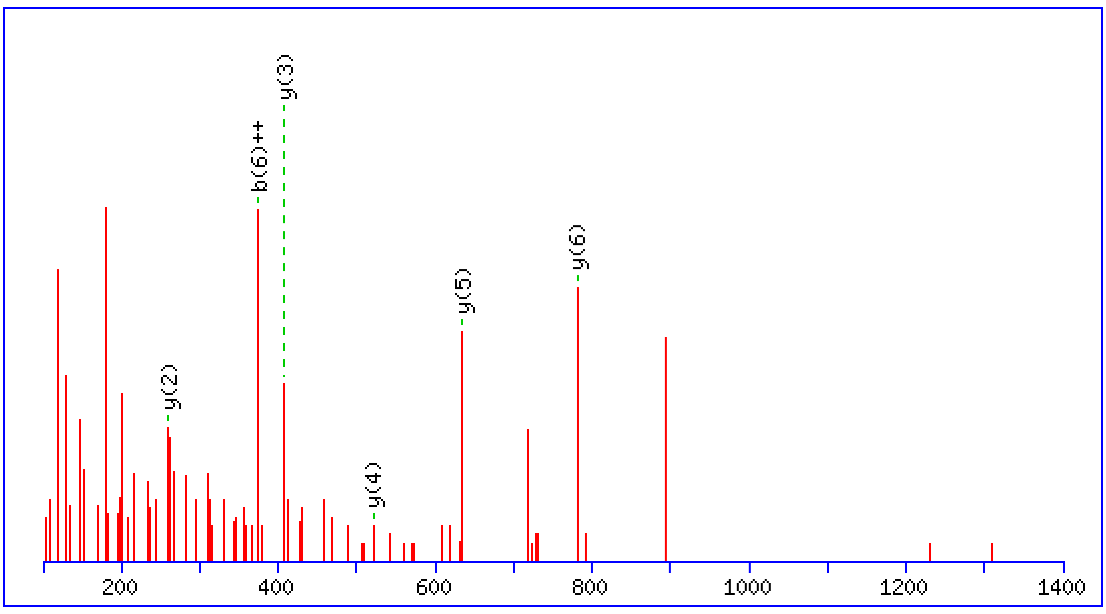
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFPNFLK**
Found in **SPDYA_HUMAN**, Speedy protein A OS=Homo sapiens GN=SPDYA PE=1 SV=2

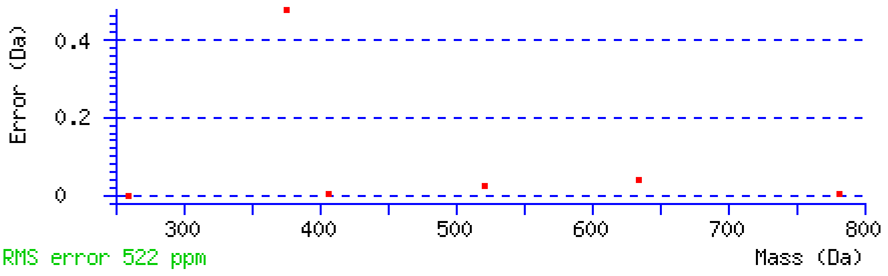
Match to Query 3073: 893.504888 from(447.759720,2+) rtinseconds(2429) index(27518)
Title: Locus:1.1.1.2706.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-1.mgf

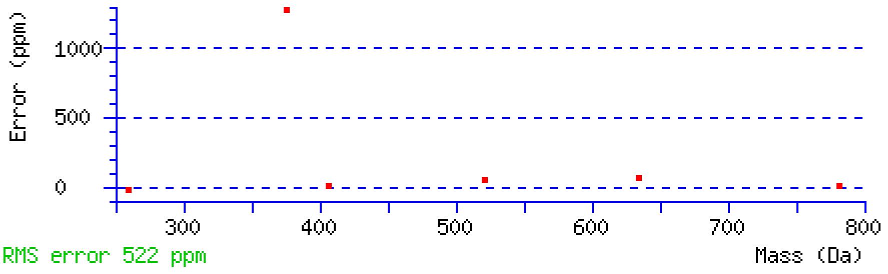
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 893.501083
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P3 : Oxidation (P)
Ions Score: 39 **Expect:** 0.00091
Matches : 6/42 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.091340	57.549308			L					7
2	261.159754	131.083515			F	***781.424302***	391.215789	764.397753	382.702515	6
3	374.207433	187.607354			P	***634.355888***	317.681582	617.329339	309.168308	5
4	488.250360	244.628818	471.223811	236.115544	N	***521.308209***	261.157743	504.281660	252.644468	4
5	635.318774	318.163025	618.292225	309.649751	F	***407.265282***	204.136279	390.238733	195.623005	3
6	748.402838	374.705057	731.376289	366.191783	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 LFPNFLK
(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	893.501083	0.003805	LFPNFLK
25.1	893.504440	0.000448	LMNIFLK
10.8	893.504456	0.000432	LFIGMVSK
9.3	893.504456	0.000432	KVMFLPK
5.2	893.497040	0.007848	EKPAPPQK
3.9	893.497070	0.007818	TGPPPALGGK
3.4	893.497040	0.007848	SYRLDIK
2.0	893.508301	-0.003413	GVHGGILNK
1.3	893.497055	0.007833	LPDPPSLR
0.6	893.497055	0.007833	FSTKGNLK

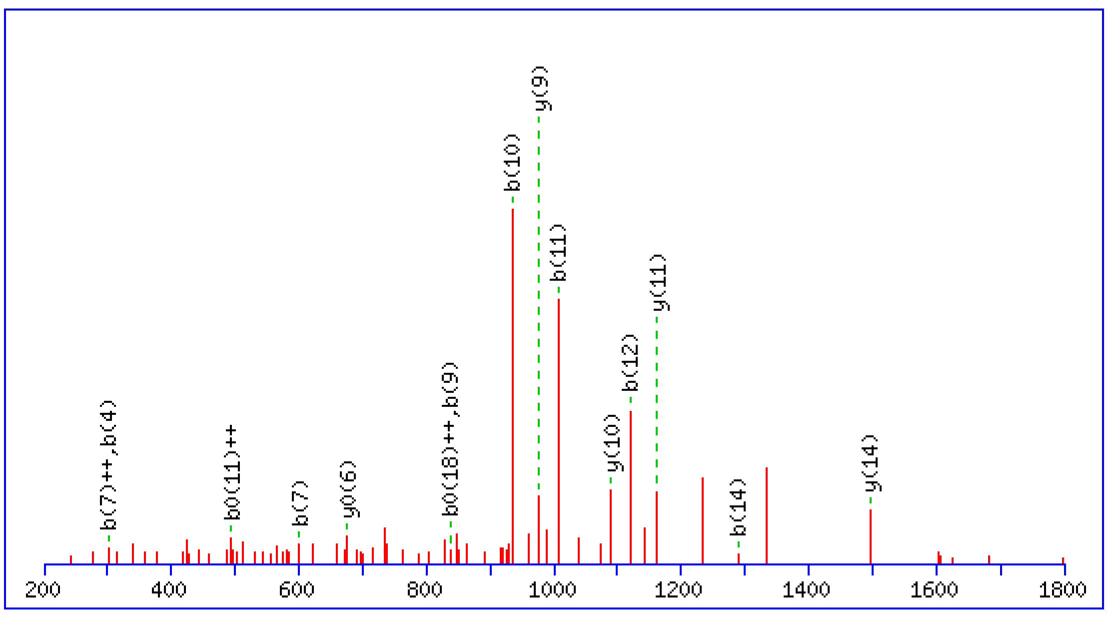
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGGEAVETHPAPGPLPPPEVR**
Found in **SPT21_HUMAN**, Spermatogenesis-associated protein 21 OS=Homo sapiens GN=SPATA21 PE=2 SV=3

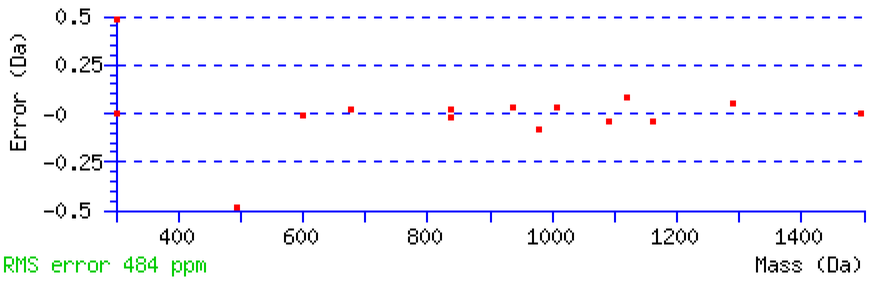
Match to Query 886284: 2095.047648 from(1048.531100,2+) rtinseconds(3057) index(520826)
Title: Locus:1.1.1.1788.49
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

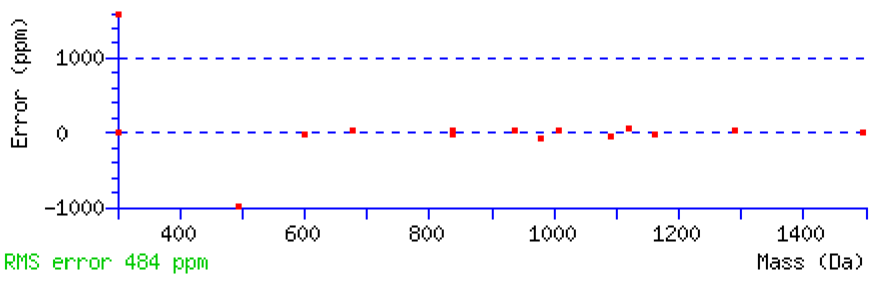
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2095.033447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P12     : Oxidation (P)
P14     : Oxidation (P)
Ions Score: 31  Expect: 0.0097
Matches : 15/190 fragment ions using 27 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							21
2	115.050204	58.028740			G	2039.019248	1020.013262	2021.992699	1011.499988	2021.008683	1011.007980	20
3	172.071668	86.539472			G	1981.997784	991.502530	1964.971235	982.989256	1963.987219	982.497248	19
4	***301.114261***	151.060768	283.103696	142.055486	E	1924.976320	962.991798	1907.949771	954.478524	1906.965755	953.986516	18
5	372.151375	186.579325	354.140810	177.574043	A	1795.933727	898.470502	1778.907178	889.957227	1777.923162	889.465219	17
6	471.219789	236.113532	453.209224	227.108250	V	1724.896613	862.951945	1707.870064	854.438670	1706.886048	853.946662	16
7	***600.262382***	300.634829	582.251817	291.629547	E	1625.828199	813.417738	1608.801650	804.904463	1607.817634	804.412455	15
8	701.310061	351.158669	683.299496	342.153386	T	**1496.785606**	748.896441	1479.759057	740.383167	1478.775041	739.891159	14
9	***838.368973***	419.688125	820.358408	410.682842	H	1395.737927	698.372602	1378.711378	689.859327	1377.727362	689.367319	13
10	***935.421737***	468.214507	917.411172	459.209224	P	1258.679015	629.843146	1241.652466	621.329871	1240.668450	620.837863	12
11	***1006.458851***	503.733064	988.448286	494.727781	A	**1161.626251**	581.316764	1144.599702	572.803489	1143.615686	572.311481	11
12	***1119.506530***	560.256903	1101.495965	551.251621	P	**1090.589137**	545.798207	1073.562588	537.284932	1072.578572	536.792924	10
13	1176.527994	588.767635	1158.517429	579.762353	G	**977.541458**	489.274367	960.514909	480.761093	959.530893	480.269085	9
14	***1289.575673***	645.291475	1271.565108	636.286192	P	920.519994	460.763635	903.493445	452.250361	902.509429	451.758353	8
15	1402.659737	701.833507	1384.649172	692.828224	L	807.472315	404.239796	790.445766	395.726521	789.461750	395.234513	7
16	1499.712501	750.359889	1481.701936	741.354606	P	694.388251	347.697764	677.361702	339.184489	676.377686	338.692481	6
17	1596.765265	798.886271	1578.754700	789.880988	P	597.335487	299.171382	580.308938	290.658107	579.324922	290.166099	5
18	1693.818029	847.412653	1675.807464	838.407370	P	500.282723	250.645000	483.256174	242.131725	482.272158	241.639717	4
19	1822.860622	911.933949	1804.850057	902.928666	E	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
20	1921.929036	961.468156	1903.918471	952.462874	V	274.187366	137.597321	257.160817	129.084047			2
21					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of GGGEAVETHPAPGPLPPPEVR
(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	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
21.0	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
21.0	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
21.0	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
13.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
13.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
13.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
12.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
12.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR
12.4	2095.033447	0.014201	GGGEAVETHPAPGPLPPPEVR

Mascot: http://www.matrixscience.com/

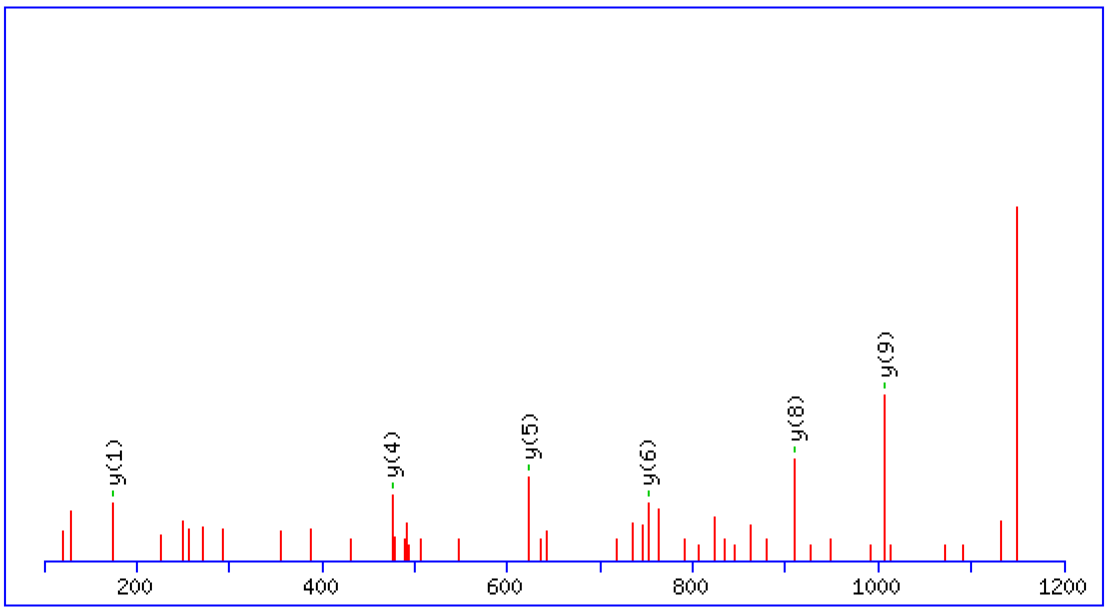
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAPSAEFSVDR**
Found in **SPON1_HUMAN**, Spondin-1 OS=Homo sapiens GN=SPON1 PE=1 SV=2

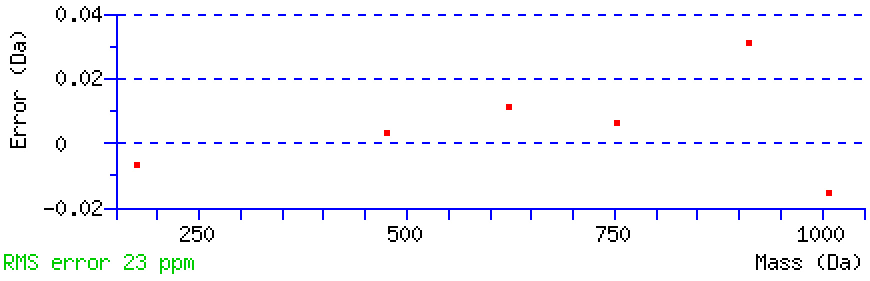
Match to Query 20566: 1148.544248 from(575.279400,2+) rtinseconds(1784) index(20506)
Title: Locus:1.1.1.1321.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

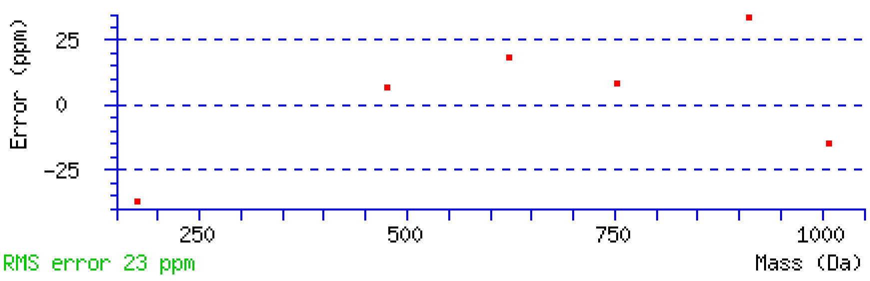
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1148.546188
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44 **Expect:** 0.0011
Matches : 6/92 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833			A							11
2	143.081504	72.044390			A	1078.516364	539.761820	1061.489815	531.248546	1060.505799	530.756538	10
3	240.134268	120.570772			P	***1007.479250***	504.243263	990.452701	495.729989	989.468685	495.237981	9
4	327.166296	164.086786	309.155731	155.081504	S	***910.426486***	455.716881	893.399937	447.203607	892.415921	446.711599	8
5	398.203410	199.605343	380.192845	190.600061	A	823.394458	412.200867	806.367909	403.687592	805.383893	403.195585	7
6	527.246003	264.126640	509.235438	255.121357	E	***752.357344***	376.682310	735.330795	368.169036	734.346779	367.677028	6
7	674.314417	337.660847	656.303852	328.655564	F	***623.314751***	312.161014	606.288202	303.647739	605.304186	303.155731	5
8	761.346445	381.176861	743.335880	372.171578	S	***476.246337***	238.626806	459.219788	230.113532	458.235772	229.621524	4
9	860.414859	430.711068	842.404294	421.705785	V	389.214309	195.110792	372.187760	186.597518	371.203744	186.105510	3
10	975.441802	488.224539	957.431237	479.219256	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
11					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AAPSAEFSVDR
(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	1148.546188	-0.001940	AAPSAEFSVDR
6.7	1148.546188	-0.001940	ASEVQEPFSR

Mascot: http://www.matrixscience.com/

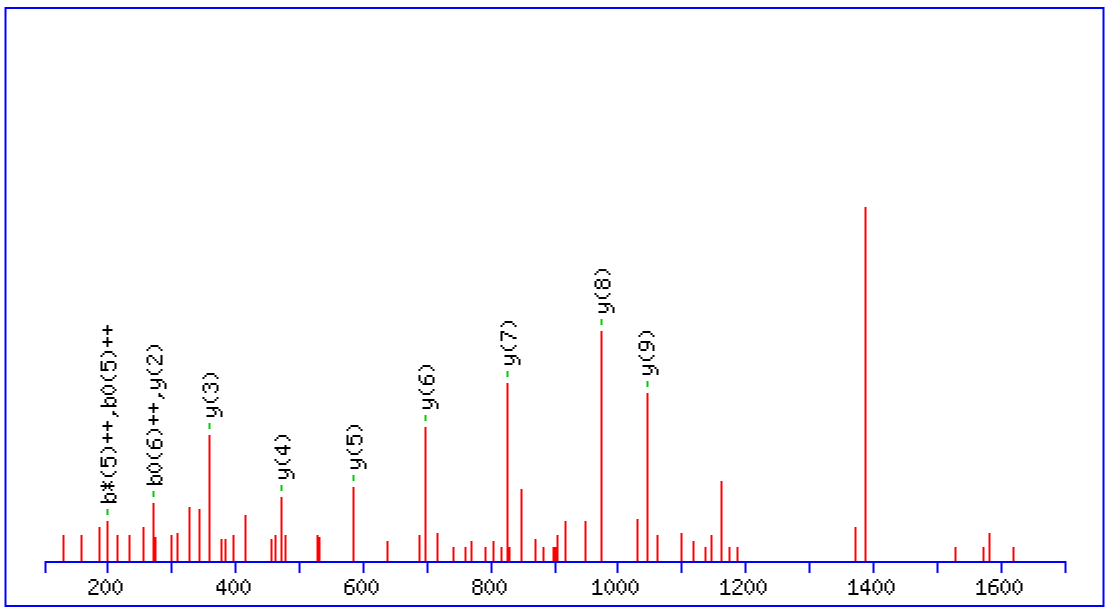
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASGQAFELILSPR**
Found in **STMN1_HUMAN**, Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3

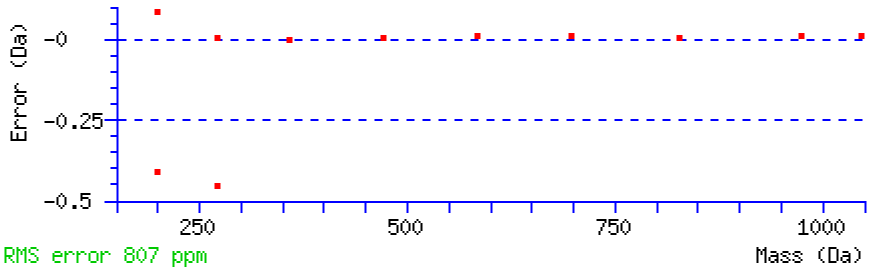
Match to Query 26372: 1387.751248 from(694.882900,2+) rtinseconds(3238) index(34348)
Title: Locus:1.1.1.2728.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

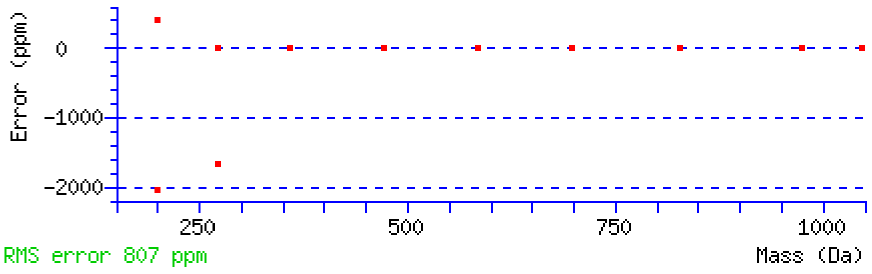
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1387.745941
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69  Expect: 1.3e-006
Matches : 11/132 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							13
2	159.076418	80.041847			141.065853	71.036564	S	1317.716127	659.361702	1300.689578	650.848427	1299.705562	650.356419	12
3	216.097882	108.552579			198.087317	99.547296	G	1230.684099	615.845688	1213.657550	607.332413	1212.673534	606.840405	11
4	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	1173.662635	587.334956	1156.636086	578.821681	1155.652070	578.329673	10
5	415.193574	208.100425	398.167025	199.587150	397.183009	199.095142	A	***1045.604057***	523.305667	1028.577508	514.792392	1027.593492	514.300384	9
6	562.261988	281.634632	545.235439	273.121357	544.251423	272.629349	F	***974.566943***	487.787110	957.540394	479.273835	956.556378	478.781827	8
7	691.304581	346.155929	674.278032	337.642654	673.294016	337.150646	E	***827.498529***	414.252903	810.471980	405.739628	809.487964	405.247620	7
8	804.388645	402.697961	787.362096	394.184686	786.378080	393.692678	L	***698.455936***	349.731606	681.429387	341.218332	680.445371	340.726324	6
9	917.472709	459.239993	900.446160	450.726718	899.462144	450.234710	I	***585.371872***	293.189574	568.345323	284.676300	567.361307	284.184292	5
10	1030.556773	515.782025	1013.530224	507.268750	1012.546208	506.776742	L	***472.287808***	236.647542	455.261259	228.134268	454.277243	227.642260	4
11	1117.588801	559.298039	1100.562252	550.784764	1099.578236	550.292756	S	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
12	1214.641565	607.824421	1197.615016	599.311146	1196.631000	598.819138	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 ASGQAFELILSPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.3	1387.745941	0.005307	ASGQAFELILSPR
12.3	1387.738083	0.013165	TAVEAPLGMKLDK
7.6	1387.745956	0.005292	ANPDRTFDLVLK
3.1	1387.745941	0.005307	LLTSLWEKQDR
2.2	1387.738083	0.013165	ILTLESMNPQVK
0.1	1387.745987	0.005261	VSDGSKVSVFHVK

Mascot: http://www.matrixscience.com/

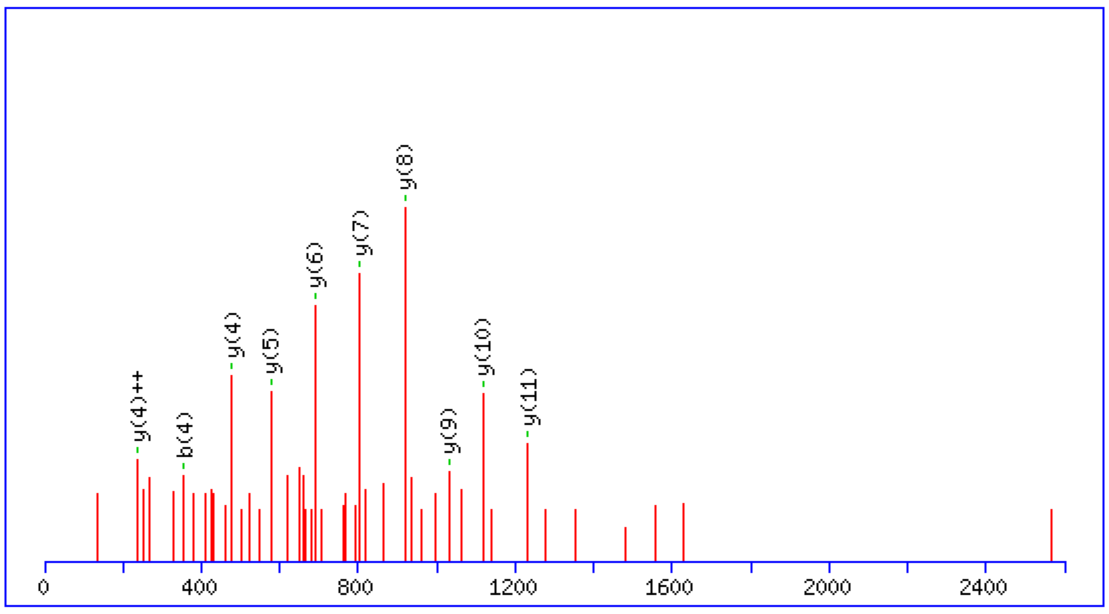
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGANSLLDLVVFGR**
Found in **DHSA_HUMAN**, Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2

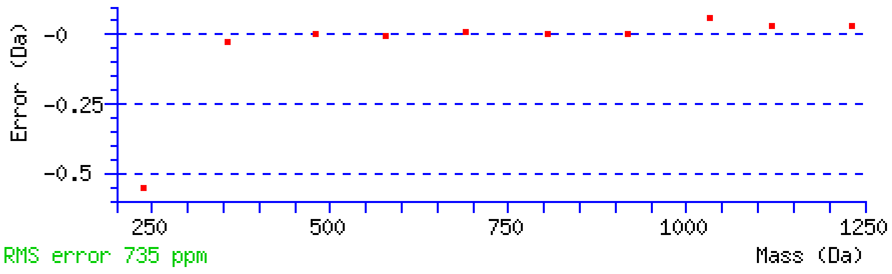
Match to Query 34370: 1472.846868 from(737.430710,2+) rtinseconds(4463) index(64676)
Title: Locus:1.1.1.3238.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

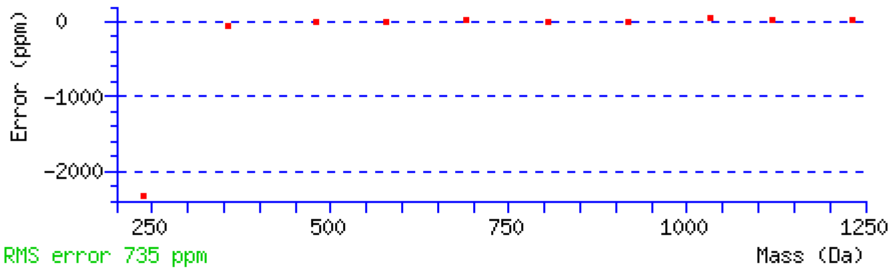
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1472.835114
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 60 **Expect:** 3.8e-006
Matches : 10/130 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	114.091340	57.549308					L							14
2	171.112804	86.060040					G	1360.758326	680.882801	1343.731777	672.369527	1342.747761	671.877519	13
3	242.149918	121.578597					A	1303.736862	652.372069	1286.710313	643.858795	1285.726297	643.366786	12
4	356.192845	178.600060	339.166296	170.086786			N	***1232.699748***	616.853512	1215.673199	608.340238	1214.689183	607.848230	11
5	443.224873	222.116074	426.198324	213.602800	425.214308	213.110792	S	***1118.656821***	559.832049	1101.630272	551.318774	1100.646256	550.826766	10
6	556.308937	278.658107	539.282388	270.144832	538.298372	269.652824	L	***1031.624793***	516.316035	1014.598244	507.802760	1013.614228	507.310752	9
7	669.393001	335.200139	652.366452	326.686864	651.382436	326.194856	L	***918.540729***	459.774003	901.514180	451.260728	900.530164	450.768720	8
8	784.419944	392.713610	767.393395	384.200335	766.409379	383.708328	D	***805.456665***	403.231971	788.430116	394.718696	787.446100	394.226688	7
9	897.504008	449.255642	880.477459	440.742368	879.493443	440.250360	L	***690.429722***	345.718499	673.403173	337.205225			6
10	996.572422	498.789849	979.545873	490.276574	978.561857	489.784566	V	***577.345658***	289.176467	560.319109	280.663193			5
11	1095.640836	548.324056	1078.614287	539.810782	1077.630271	539.318774	V	***478.277244***	239.642260	461.250695	231.128986			4
12	1242.709250	621.858263	1225.682701	613.344989	1224.698685	612.852981	F	379.208830	190.108053	362.182281	181.594778			3
13	1299.730714	650.368995	1282.704165	641.855721	1281.720149	641.363713	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 LGANSLLDLVVFGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.1	1472.835114	0.011754	LGANSLLDLVVFGR

Mascot: http://www.matrixscience.com/

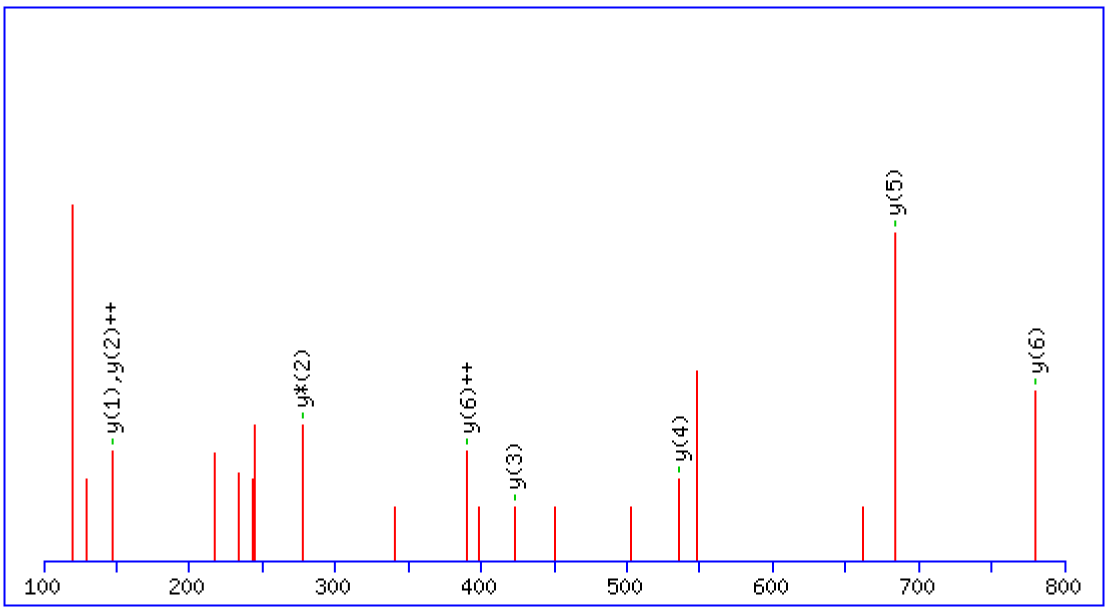
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFLEFK**
Found in **ST1A1_HUMAN**, Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3

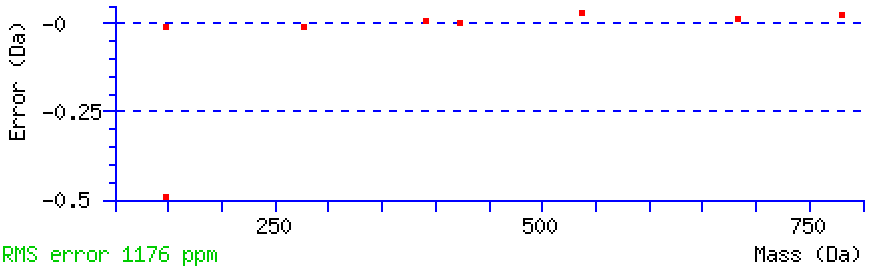
Match to Query 5063: 878.490288 from(440.252420,2+) rtinseconds(3056) index(40362)
Title: Locus:1.1.1.2654.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

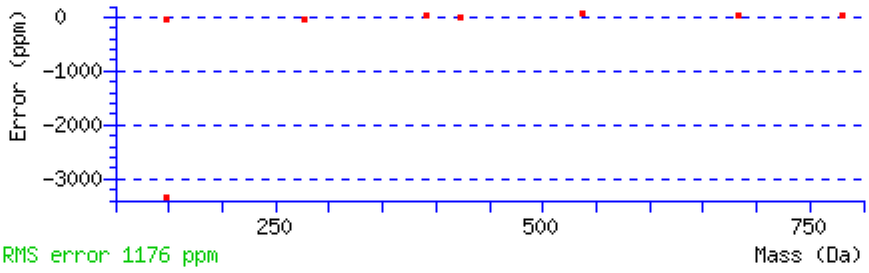
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 878.490189
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0028
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	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
33.3	878.490189	0.000099	VPFLEFK
5.7	878.486145	0.004143	VLIYESR
4.2	878.497391	-0.007103	VQAPHLSK
3.7	878.486160	0.004128	VYQTPKK
2.0	878.497391	-0.007103	VPAATPAPR
1.5	878.497391	-0.007103	TPPPPSRK
1.2	878.486130	0.004158	ALAYAKDK

Mascot: http://www.matrixscience.com/

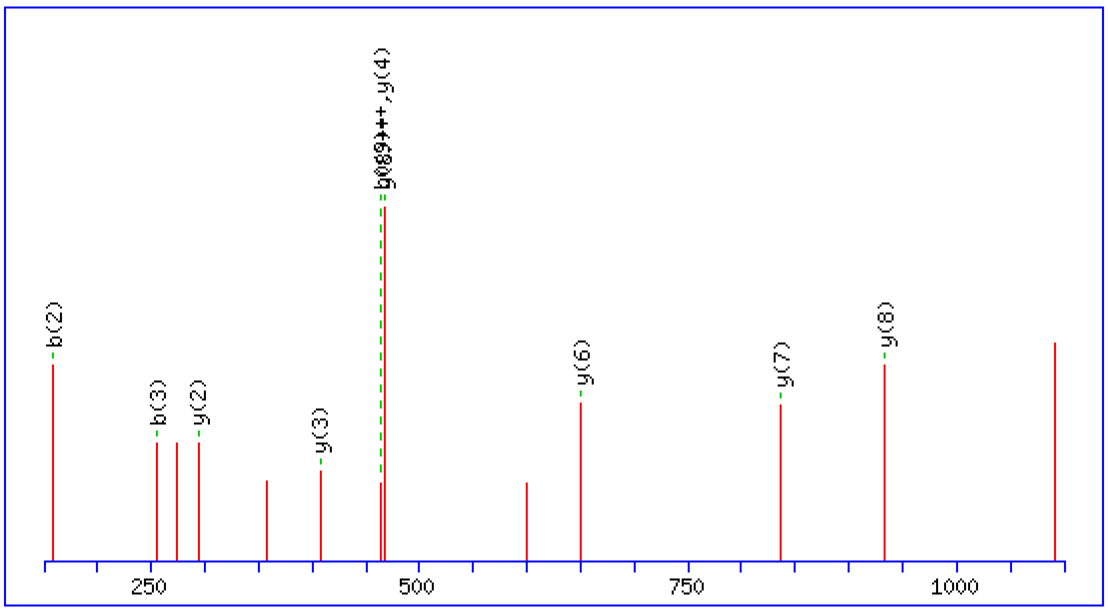
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTPWEGGLFK**
Found in **UBC9_HUMAN**, SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1

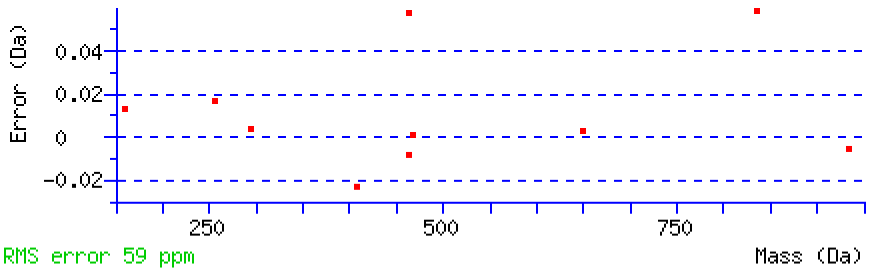
Match to Query 22935: 1090.548068 from(546.281310,2+) rtinseconds(2948) index(30677)
Title: Locus:1.1.1.2633.23
Data file 2011-11-14 - TFD - S 2-6.mgf

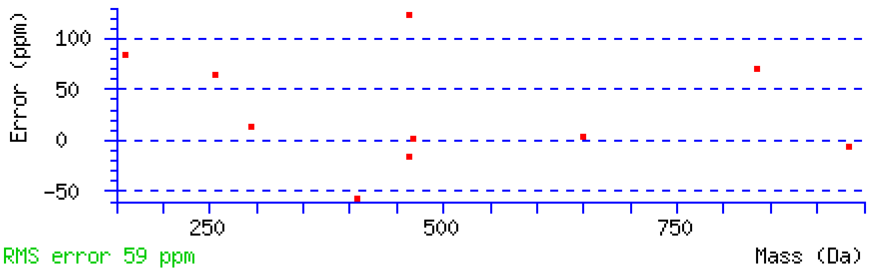
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1090.544754
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2e-005
Matches : 10/78 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							10
2	**159.076419**	80.041847	141.065854	71.036565	T	1034.530559	517.768918	1017.504010	509.255643	1016.519994	508.763635	9
3	**256.129183**	128.568230	238.118618	119.562947	P	*933.482880*	467.245078	916.456331	458.731804	915.472315	458.239796	8
4	442.208496	221.607886	424.197931	212.602604	W	*836.430116*	418.718696	819.403567	410.205422	818.419551	409.713414	7
5	571.251089	286.129183	553.240524	277.123900	E	*650.350803*	325.679040	633.324254	317.165765	632.340238	316.673757	6
6	628.272553	314.639915	610.261988	305.634632	G	521.308210	261.157743	504.281661	252.644469			5
7	685.294017	343.150647	667.283452	334.145364	G	*464.286746*	232.647011	447.260197	224.133737			4
8	798.378081	399.692679	780.367516	390.687396	L	*407.265282*	204.136279	390.238733	195.623004			3
9	945.446495	473.226886	927.435930	464.221603	F	*294.181218*	147.594247	277.154669	139.080972			2
10					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of GTPWEGGLFK
(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	1090.544754	0.003314	GTPWEGGLFK
2.2	1090.550598	-0.002530	ASSPSDIISSK

Mascot: http://www.matrixscience.com/

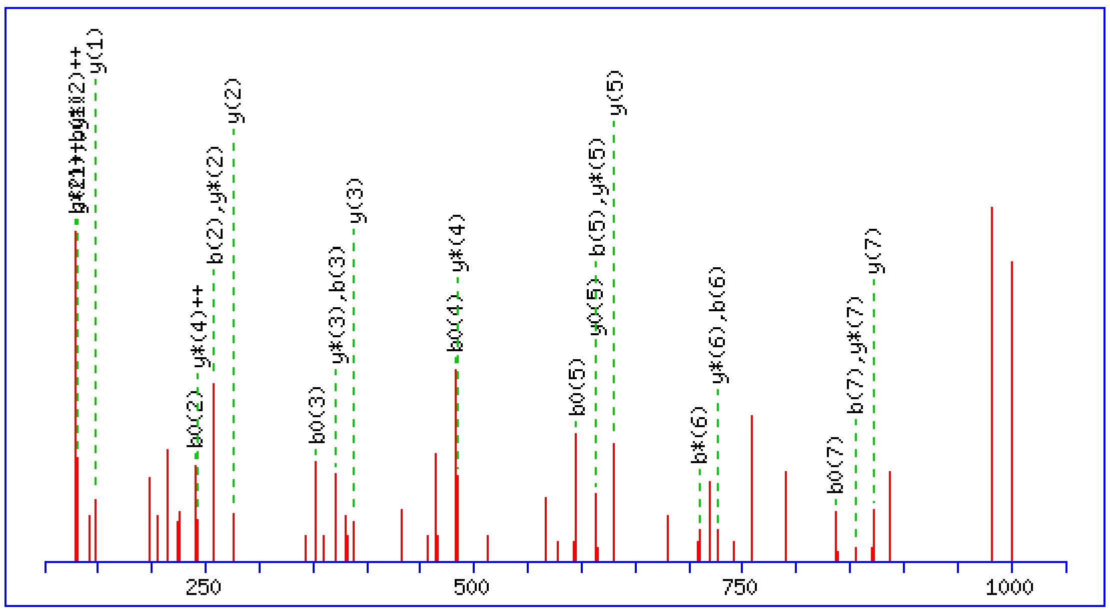
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLELLKK**
Found in **SUN3_HUMAN**, SUN domain-containing protein 3 OS=Homo sapiens GN=SUN3 PE=2 SV=4

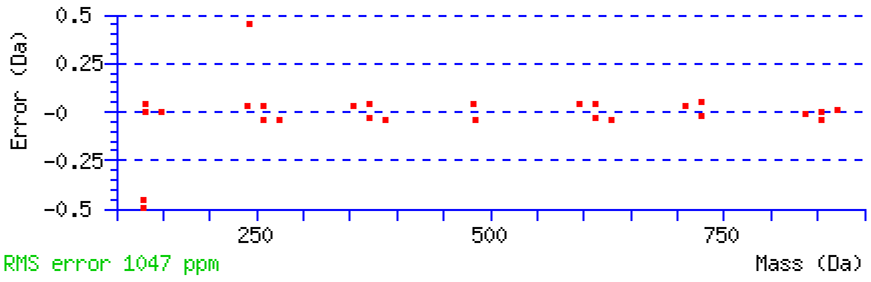
Match to Query 3582: 999.595448 from(500.805000,2+) rtinseconds(1638) index(1154)
Title: Locus:1.1.1.2932.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

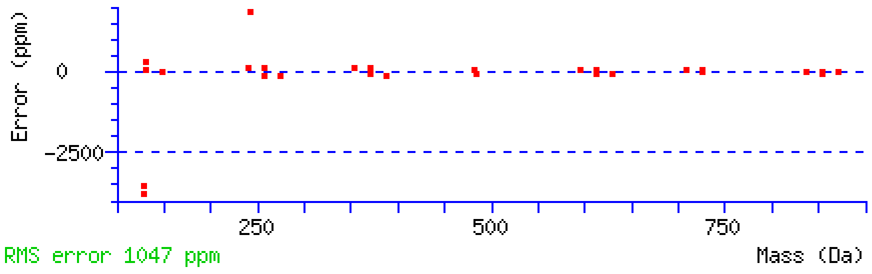
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 999.596405
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0025
Matches : 28/74 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	***130.049869***	65.528572			112.039304	56.523290	**E**							8
2	***258.108447***	129.557862	241.081898	121.044587	240.097882	120.552579	**Q**	**871.561130**	436.284203	854.534581	427.770929	853.550565	427.278921	7
3	***371.192511***	186.099894	354.165962	177.586619	353.181946	177.094611	**L**	743.502552	372.254914	726.476003	363.741640	725.491987	363.249632	6
4	500.235104	250.621190	483.208555	242.107916	482.224539	241.615908	**E**	**630.418488**	315.712882	613.391939	307.199608	612.407923	306.707600	5
5	***613.319168***	307.163222	596.292619	298.649948	595.308603	298.157940	**L**	501.375895	251.191586	484.349346	242.678311			4
6	***726.403232***	363.705254	709.376683	355.191980	708.392667	354.699972	**L**	**388.291831**	194.649554	371.265282	186.136279			3
7	***854.498195***	427.752736	837.471646	419.239461	836.487630	418.747453	**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 EQLELLKK
(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	999.596405	-0.000957	QLELEIKK
36.4	999.596405	-0.000957	IEKELLQK
35.2	999.596405	-0.000957	ELKELIQK
33.9	999.596405	-0.000957	EQLELLKK
24.1	999.596405	-0.000957	LQELEKIK
22.2	999.596405	-0.000957	EKEILQIK
21.5	999.596436	-0.000988	GITVPEKLK
21.2	999.596405	-0.000957	ELQILKEK
18.6	999.596405	-0.000957	LQELKIEK
14.2	999.596405	-0.000957	LQLEEKLK

Mascot: http://www.matrixscience.com/

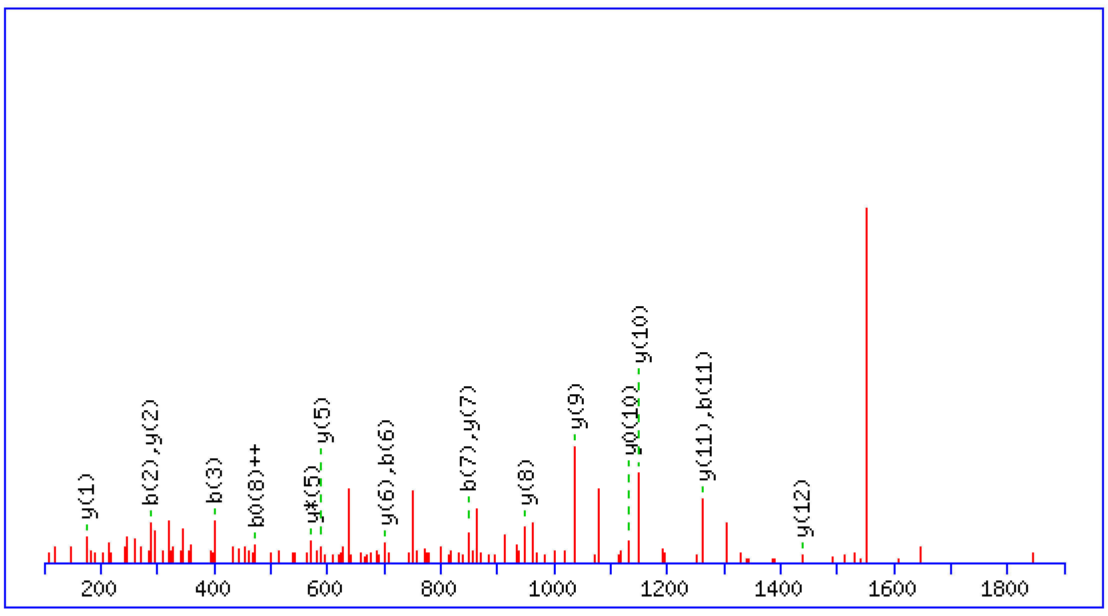
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LCLISTFLEDGIR**
Found in **SURF4_HUMAN**, Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3

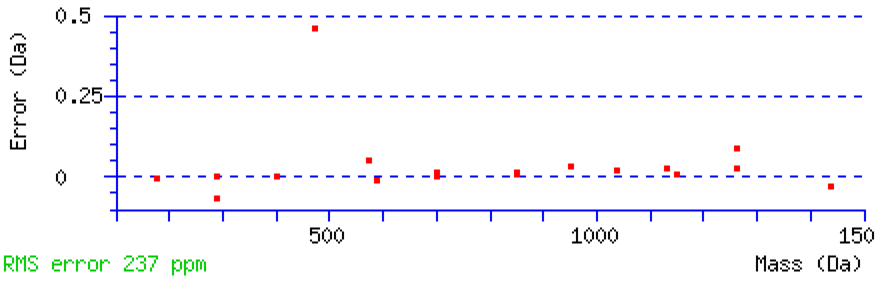
Match to Query 31454: 1549.808568 from(775.911560,2+) rtinseconds(4047) index(60570)
Title: Locus:1.1.1.2991.10
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

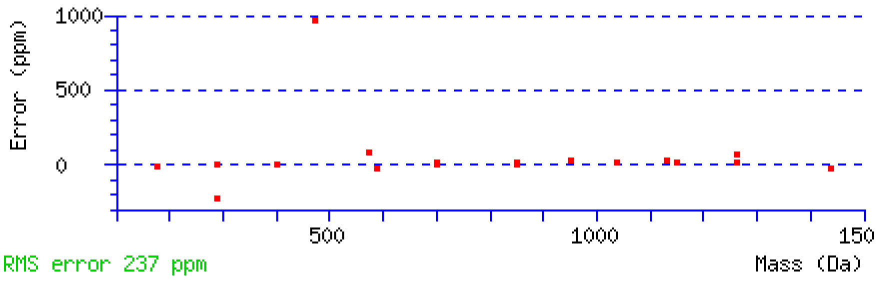
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1549.817398
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 4.5e-006
Matches : 18/106 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			L							13
2	**288.137639**	144.572457			C	***1437.740628***	719.373952	1420.714079	710.860678	1419.730063	710.368670	12
3	**401.221703**	201.114489			L	***1263.694329***	632.350802	1246.667780	623.837528	1245.683764	623.345520	11
4	514.305767	257.656522			I	***1150.610265***	575.808771	1133.583716	567.295496	1132.599700	566.803488	10
5	601.337795	301.172536	583.327230	292.167253	S	***1037.526201***	519.266738	1020.499652	510.753464	1019.515636	510.261456	9
6	**702.385474**	351.696375	684.374909	342.691093	T	***950.494173***	475.750724	933.467624	467.237450	932.483608	466.745442	8
7	**849.453888**	425.230582	831.443323	416.225300	F	***849.446494***	425.226885	832.419945	416.713610	831.435929	416.221602	7
8	962.537952	481.772614	944.527387	472.767332	L	***702.378080***	351.692678	685.351531	343.179403	684.367515	342.687395	6
9	1091.580545	546.293911	1073.569980	537.288628	E	***589.294016***	295.150646	572.267467	286.637371	571.283451	286.145363	5
10	1206.607488	603.807382	1188.596923	594.802100	D	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
11	**1263.628952**	632.318114	1245.618387	623.312832	G	345.224480	173.115878	328.197931	164.602603			3
12	1376.713016	688.860146	1358.702451	679.854863	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 LCLISTFLEDGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.8	1549.817398	-0.008830	LCLISTFLEDGIR
14.0	1549.821213	-0.012645	SSLLNRYLNDSLR
9.9	1549.796280	0.012288	WPVSMFEKLLPR
9.2	1549.810013	-0.001445	SPTPPPSSKPSSIPR
8.0	1549.806183	0.002385	YIVLMDIVPVDNK
6.2	1549.800110	0.008458	QLHEFSSPSHLLR
5.5	1549.803482	0.005086	RFSQMLQDKPLR
4.2	1549.810043	-0.001475	GAPGPPGLPGSVDLLR
4.2	1549.810043	-0.001475	GAPGPPGLPGSVDLLR
4.2	1549.810043	-0.001475	GAPGPPGLPGSVDLLR

Mascot: http://www.matrixscience.com/

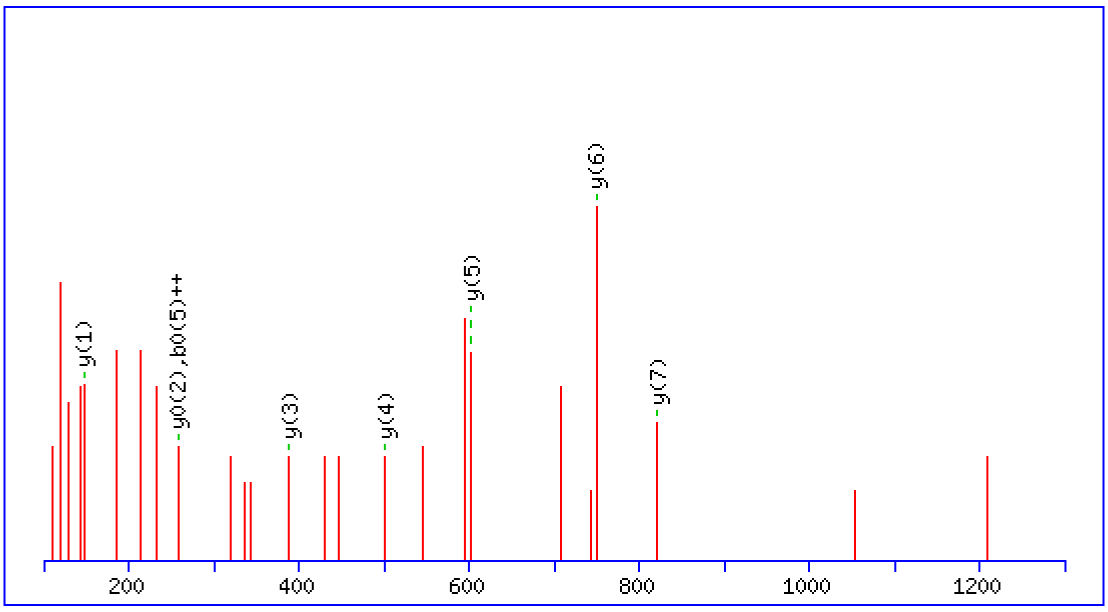
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAFTLLEK**
Found in **YKT6_HUMAN**, Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1

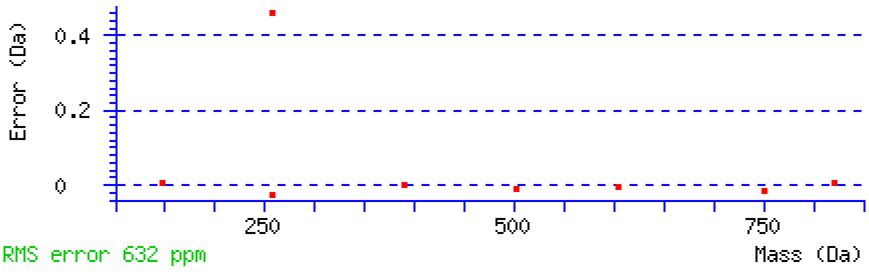
Match to Query 7819: 919.537488 from(460.776020,2+) rtinseconds(2807) index(34405)
Title: Locus:1.1.1.2594.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

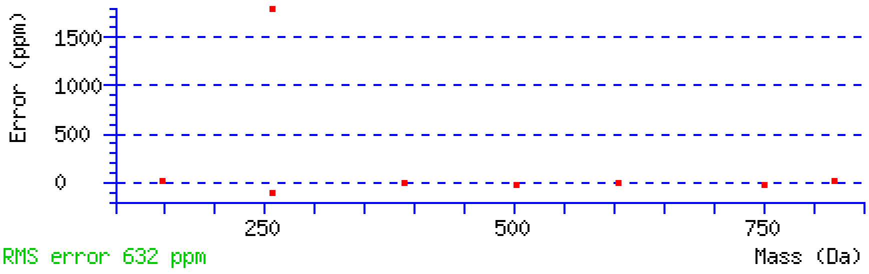
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 919.537857
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0014
Matches : 8/62 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							8
2	171.112804	86.060040			A	***821.476732***	411.242004	804.450183	402.728730	803.466167	402.236722	7
3	318.181218	159.594247			F	***750.439618***	375.723447	733.413069	367.210173	732.429053	366.718165	6
4	419.228897	210.118087	401.218332	201.112804	T	***603.371204***	302.189240	586.344655	293.675966	585.360639	293.183958	5
5	532.312961	266.660119	514.302396	257.654836	L	***502.323525***	251.665401	485.296976	243.152126	484.312960	242.660118	4
6	645.397025	323.202151	627.386460	314.196868	L	***389.239461***	195.123369	372.212912	186.610094	371.228896	186.118086	3
7	774.439618	387.723447	756.429053	378.718165	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 VAFTLLEK
(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	919.537857	-0.000369	VAFTLLEK

Mascot: http://www.matrixscience.com/

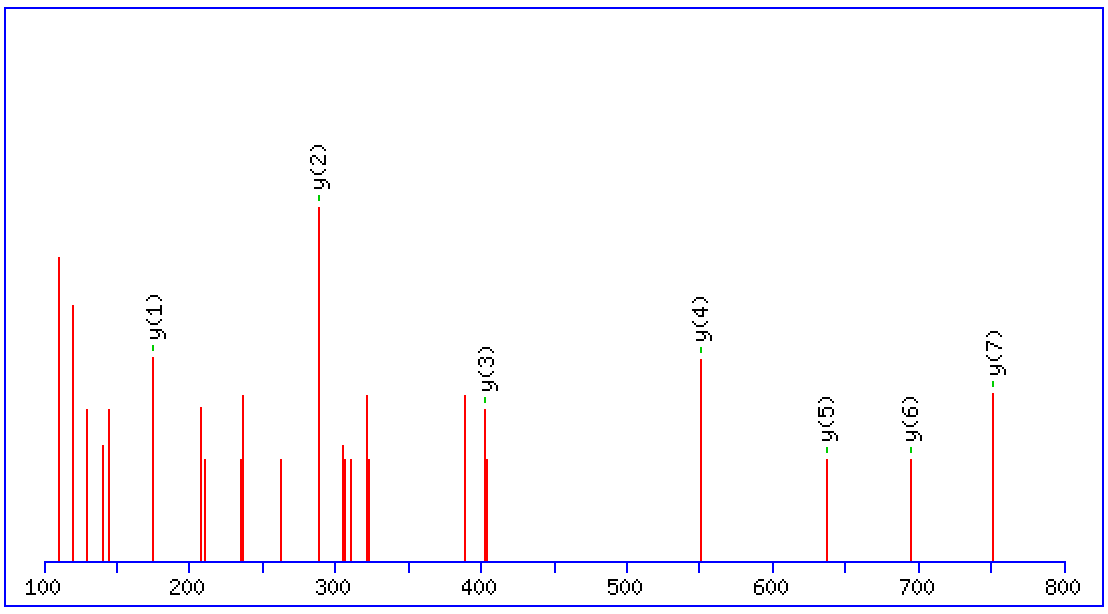
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGGSFDLR**
Found in **SNG2_HUMAN**, Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1

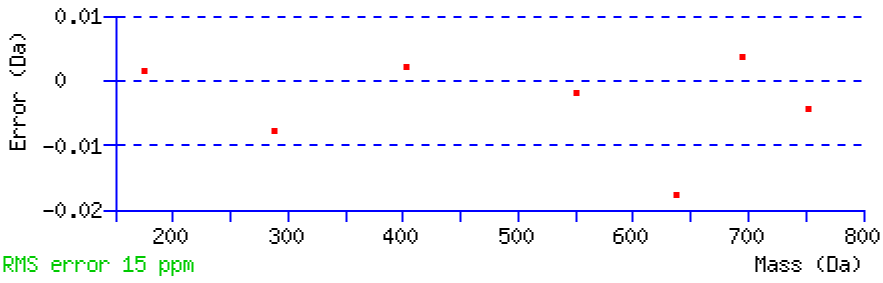
Match to Query 1136: 821.406888 from(411.710720,2+) rtinseconds(1756) index(14703)
Title: Locus:1.1.1.2168.3
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

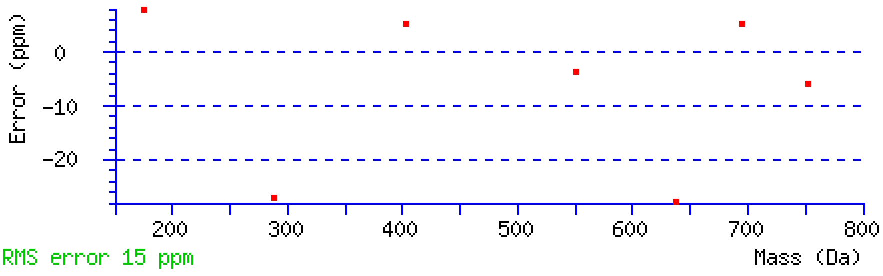
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 821.403168
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 2.3e-005
Matches : 7/60 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							8
2	129.065854	65.036565			G	***751.373329***	376.190303	734.346780	367.677028	733.362764	367.185020	7
3	186.087318	93.547297			G	***694.351865***	347.679571	677.325316	339.166296	676.341300	338.674288	6
4	273.119346	137.063311	255.108781	128.058029	S	***637.330401***	319.168838	620.303852	310.655564	619.319836	310.163556	5
5	420.187760	210.597518	402.177195	201.592235	F	***550.298373***	275.652825	533.271824	267.139550	532.287808	266.647542	4
6	535.214703	268.110990	517.204138	259.105707	D	***403.229959***	202.118617	386.203410	193.605343	385.219394	193.113335	3
7	648.298767	324.653022	630.288202	315.647739	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 AGGSFDLR
(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	821.403168	0.003720	AGGSFDLR
8.0	821.406525	0.000363	KISGDMR
6.9	821.414383	-0.007495	QYRSPR
5.1	821.403168	0.003720	SPTQSFR
4.8	821.410568	-0.003680	TWMVGTK
4.7	821.406525	0.000363	TMTNALR
4.3	821.406525	0.000363	REVMGSK
4.1	821.414398	-0.007510	HPSVNPR
3.1	821.403152	0.003736	ALSFDNR
3.0	821.403152	0.003736	YGEQGLR

Mascot: http://www.matrixscience.com/

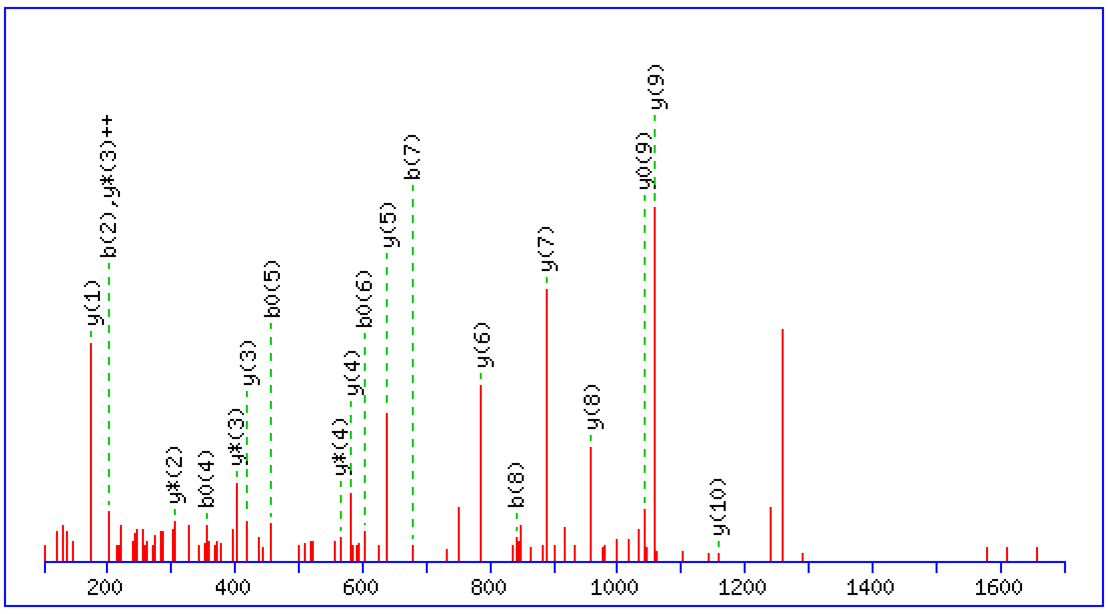
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVTATFGYPFR**
Found in **SYPL1_HUMAN**, Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1

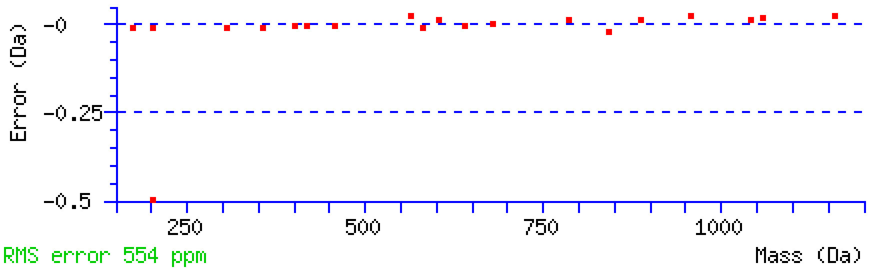
Match to Query 26731: 1258.640908 from(630.327730,2+) rtinseconds(2947) index(40345)
Title: Locus:1.1.1.2506.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

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 ●

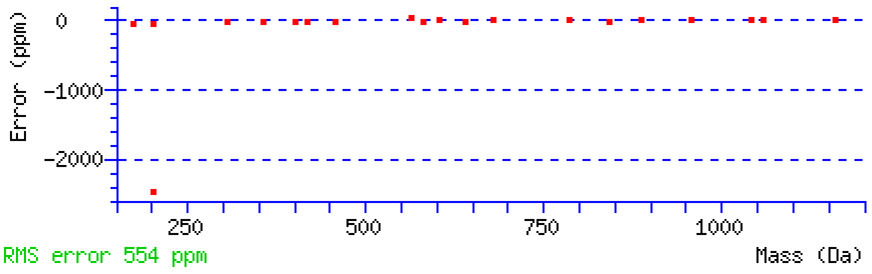


```
Monoisotopic mass of neutral peptide Mr(calc): 1258.634644
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64   Expect: 2.7e-006
Matches : 20/88 fragment ions using 34 most intense peaks   (help)
```

#	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	***1158.594223***	579.800750	1141.567674	571.287475	1140.583658	570.795467	10
3	302.171048	151.589162	284.160483	142.583879	T	***1059.525809***	530.266543	1042.499260	521.753268	1041.515244	521.261260	9
4	373.208162	187.107719	355.197597	178.102436	A	***958.478130***	479.742703	941.451581	471.229429	940.467565	470.737421	8
5	474.255841	237.631558	456.245276	228.626276	T	***887.441016***	444.224146	870.414467	435.710872	869.430451	435.218864	7
6	621.324255	311.165766	603.313690	302.160483	F	***786.393337***	393.700307	769.366788	385.187032			6
7	**678.345719**	339.676498	660.335154	330.671215	G	***639.324923***	320.166100	622.298374	311.652825			5
8	**841.409048**	421.208162	823.398483	412.202879	Y	***582.303459***	291.655368	565.276910	283.142093			4
9	938.461812	469.734544	920.451247	460.729262	P	***419.240130***	210.123703	402.213581	201.610429			3
10	1085.530226	543.268751	1067.519661	534.263469	F	322.187366	161.597321	305.160817	153.084047			2
11					R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 554 ppm



RMS error 554 ppm

NCBI **BLAST** search of TVTATFGYPFR
(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	1258.634644	0.006264	TVTATFGYPFR
4.0	1258.649216	-0.008308	LSSGPCWLVAR
3.7	1258.651703	-0.010795	QSQLEALDSLR
2.4	1258.651733	-0.010825	TVSALGLDPSGAR
2.3	1258.641815	-0.000907	SVGEGAREWIR

Mascot: http://www.matrixscience.com/

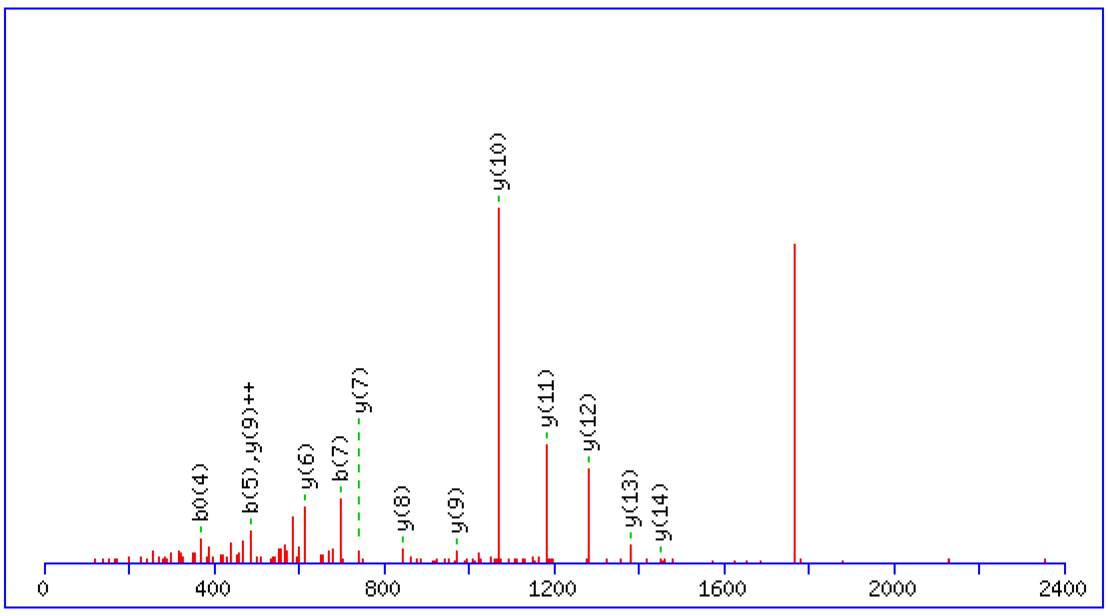
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGEAVVLPEVEPGLTAR**
Found in **SDC1_HUMAN**, Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3

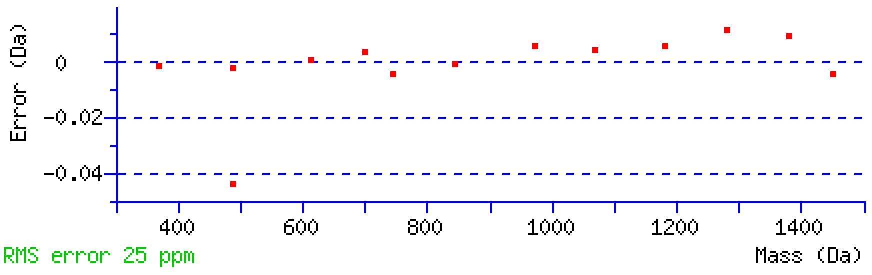
Match to Query 45100: 1764.933848 from(883.474200,2+) rtinseconds(2876) index(36140)
Title: Locus:1.1.1.2568.21
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-1.mgf

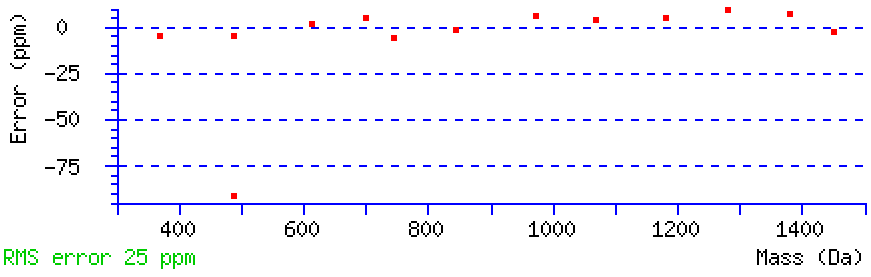
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1764.925766
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74 **Expect:** 3.3e-007
Matches : 13/156 fragment ions using 16 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	187.071333	94.039305	169.060768	85.034022	G	1636.890464	818.948870	1619.863915	810.435595	1618.879899	809.943587	16
3	316.113926	158.560601	298.103361	149.555319	E	1579.869000	790.438138	1562.842451	781.924864	1561.858435	781.432855	15
4	387.151040	194.079158	369.140475	185.073876	A	***1450.826407***	725.916841	1433.799858	717.403567	1432.815842	716.911559	14
5	**486.219454**	243.613365	468.208889	234.608083	V	***1379.789293***	690.398285	1362.762744	681.885010	1361.778728	681.393002	13
6	585.287868	293.147572	567.277303	284.142290	V	***1280.720879***	640.864078	1263.694330	632.350803	1262.710314	631.858795	12
7	**698.371932**	349.689604	680.361367	340.684322	L	***1181.652465***	591.329870	1164.625916	582.816596	1163.641900	582.324588	11
8	795.424696	398.215986	777.414131	389.210704	P	***1068.568401***	534.787838	1051.541852	526.274564	1050.557836	525.782556	10
9	924.467289	462.737283	906.456724	453.732000	E	***971.515637***	486.261456	954.489088	477.748182	953.505072	477.256174	9
10	1023.535703	512.271490	1005.525138	503.266207	V	***842.473044***	421.740160	825.446495	413.226885	824.462479	412.734877	8
11	1152.578296	576.792786	1134.567731	567.787504	E	***743.404630***	372.205953	726.378081	363.692678	725.394065	363.200670	7
12	1249.631060	625.319168	1231.620495	616.313886	P	***614.362037***	307.684656	597.335488	299.171382	596.351472	298.679374	6
13	1306.652524	653.829900	1288.641959	644.824618	G	517.309273	259.158274	500.282724	250.645000	499.298708	250.152992	5
14	1419.736588	710.371932	1401.726023	701.366649	L	460.287809	230.647542	443.261260	222.134268	442.277244	221.642260	4
15	1520.784267	760.895772	1502.773702	751.890489	T	347.203745	174.105510	330.177196	165.592236	329.193180	165.100228	3
16	1591.821381	796.414329	1573.810816	787.409046	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 EGEAVVLPEVEPGLTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.8	1764.925766	0.008082	EGEAVVLPEVEPGLTAR
15.0	1764.944412	-0.010564	LPPQSCLLLPPTPVR
9.3	1764.944412	-0.010564	LPPQSCLLLPPTPVR
3.7	1764.944412	-0.010564	LPPQSCLLLPPTPVR

Mascot: http://www.matrixscience.com/

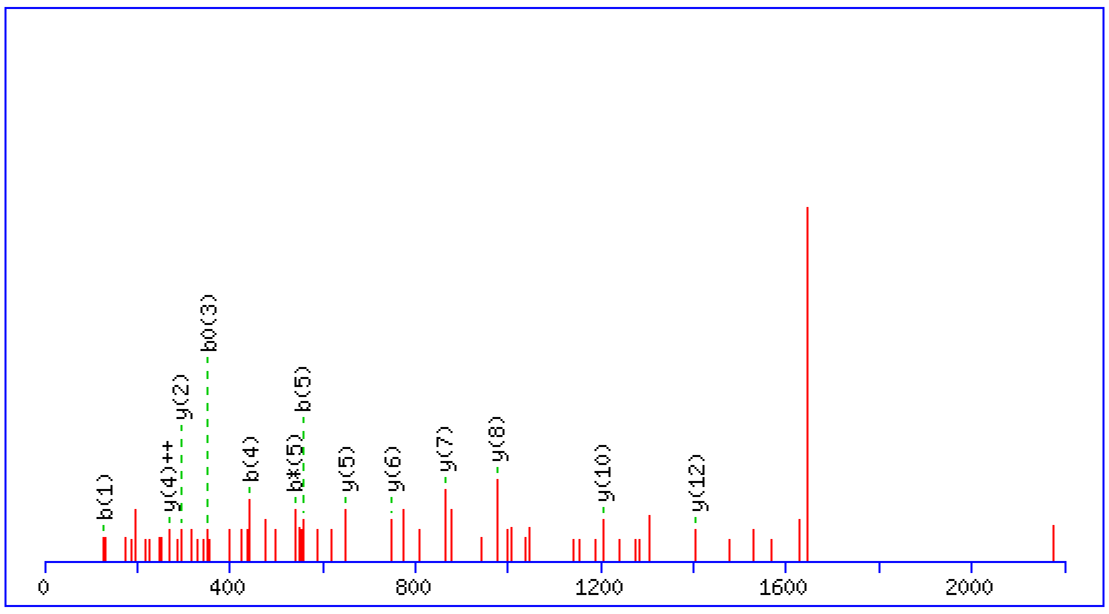
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEADILDVNQIFK**
Found in **STX12_HUMAN**, Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1

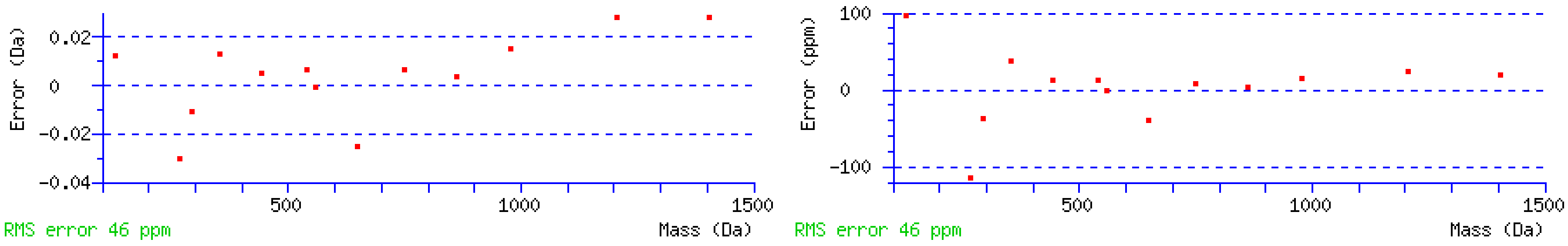
Match to Query 37397: 1644.887748 from(823.451150,2+) rtinseconds(3855) index(50148)
Title: Locus:1.1.1.3035.34
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

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): 1644.872269
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.004
Matches : 13/140 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	**129.065854**	65.036565	112.039305	56.523291			Q							14
2	242.149918	121.578597	225.123369	113.065323			L	1517.820986	759.414131	1500.794437	750.900857	1499.810421	750.408848	13
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***1404.736922***	702.872099	1387.710373	694.358825	1386.726357	693.866817	12
4	**442.229625**	221.618450	425.203076	213.105176	424.219060	212.613168	A	1275.694329	638.350803	1258.667780	629.837528	1257.683764	629.345520	11
5	**557.256568**	279.131922	540.230019	270.618648	539.246003	270.126640	D	***1204.657215***	602.832246	1187.630666	594.318971	1186.646650	593.826963	10
6	670.340632	335.673954	653.314083	327.160680	652.330067	326.668672	I	1089.630272	545.318774	1072.603723	536.805500	1071.619707	536.313492	9
7	783.424696	392.215986	766.398147	383.702712	765.414131	383.210704	L	***976.546208***	488.776742	959.519659	480.263468	958.535643	479.771460	8
8	898.451639	449.729458	881.425090	441.216183	880.441074	440.724175	D	***863.462144***	432.234710	846.435595	423.721436	845.451579	423.229428	7
9	997.520053	499.263665	980.493504	490.750390	979.509488	490.258382	V	***748.435201***	374.721239	731.408652	366.207964			6
10	1111.562980	556.285128	1094.536431	547.771854	1093.552415	547.279845	N	***649.366787***	325.187032	632.340238	316.673757			5
11	1239.621558	620.314417	1222.595009	611.801143	1221.610993	611.309135	Q	535.323860	268.165568	518.297311	259.652294			4
12	1352.705622	676.856449	1335.679073	668.343175	1334.695057	667.851166	I	407.265282	204.136279	390.238733	195.623004			3
13	1499.774036	750.390656	1482.747487	741.877382	1481.763471	741.385374	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 QLEADILDVNQIFK
(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	1644.872269	0.015479	QLEADILDVNQIFK
7.0	1644.875610	0.012138	QLEEGMKEILQAIK

Mascot: http://www.matrixscience.com/

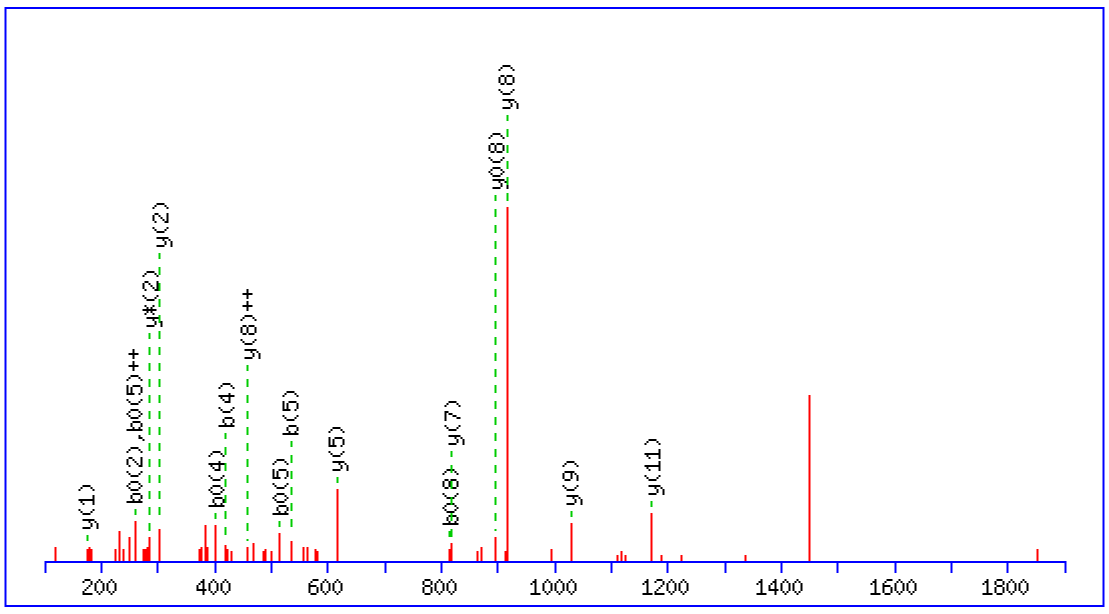
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFGSLPTTPSEQR**
Found in **STX7_HUMAN**, Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4

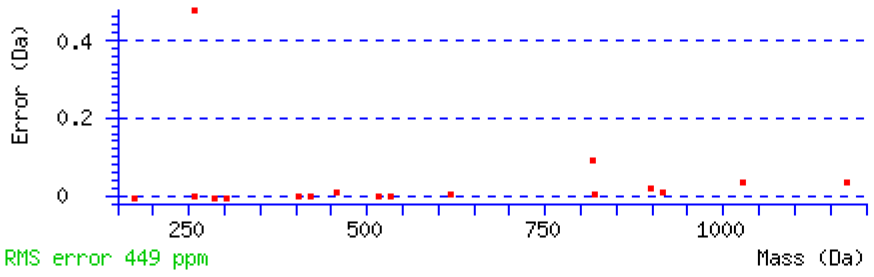
Match to Query 38640: 1447.703068 from(724.858810,2+) rtinseconds(2147) index(23251)
Title: Locus:1.1.1.2309.36
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

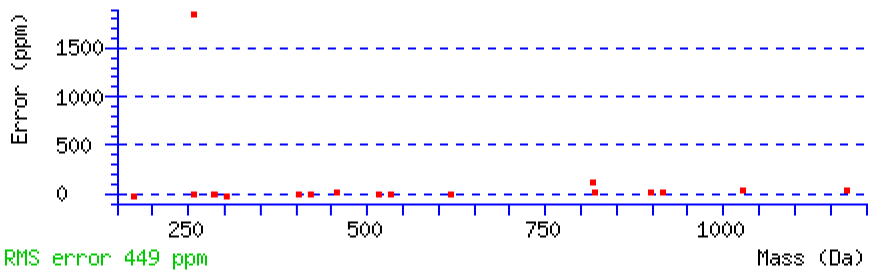
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1447.694321
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0031
Matches : 17/118 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	130.049869	65.528572			112.039304	56.523290	E							13
2	277.118283	139.062779			259.107718	130.057497	F	1319.659007	660.333142	1302.632458	651.819867	1301.648442	651.327859	12
3	334.139747	167.573511			316.129182	158.568229	G	***1172.590593***	586.798935	1155.564044	578.285660	1154.580028	577.793652	11
4	**421.171775**	211.089525			403.161210	202.084243	S	1115.569129	558.288203	1098.542580	549.774928	1097.558564	549.282920	10
5	**534.255839**	267.631558			516.245274	258.626275	L	***1028.537101***	514.772189	1011.510552	506.258914	1010.526536	505.766906	9
6	631.308603	316.157940			613.298038	307.152657	P	***915.453037***	458.230157	898.426488	449.716882	897.442472	449.224874	8
7	732.356282	366.681779			714.345717	357.676497	T	***818.400273***	409.703775	801.373724	401.190500	800.389708	400.698492	7
8	833.403961	417.205619			815.393396	408.200336	T	717.352594	359.179935	700.326045	350.666661	699.342029	350.174653	6
9	930.456725	465.732001			912.446160	456.726718	P	***616.304915***	308.656096	599.278366	300.142821	598.294350	299.650813	5
10	1017.488753	509.248015			999.478188	500.242732	S	519.252151	260.129714	502.225602	251.616439	501.241586	251.124431	4
11	1146.531346	573.769311			1128.520781	564.764028	E	432.220123	216.613699	415.193574	208.100425	414.209558	207.608417	3
12	1274.589924	637.798600	1257.563375	629.285326	1256.579359	628.793318	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 EFGSLPTTPSEQR
(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	1447.694321	0.008747	EFGSLPTTPSEQR
6.7	1447.709549	-0.006481	YADAIFTNSYRK
0.9	1447.695175	0.007893	VCFPAAQAPAMQK

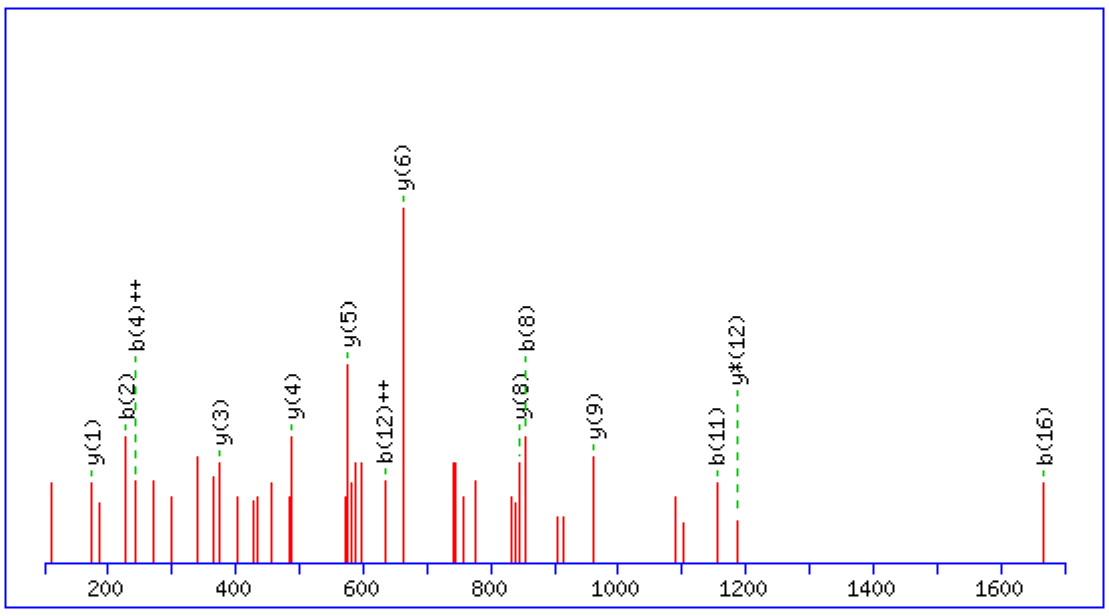
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIQEQDAGLDALSSIISR**
Found in **STX8_HUMAN**, Syntaxin-8 OS=Homo sapiens GN=STX8 PE=1 SV=2

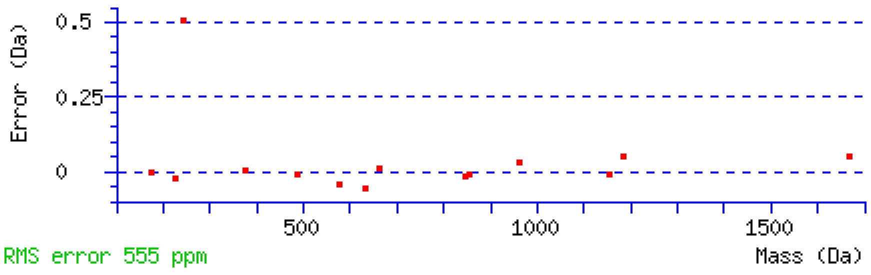
Match to Query 50612: 1928.021022 from(643.680950,3+) rtinseconds(3836) index(50851)
Title: Locus:1.1.1.2955.5
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-5.mgf

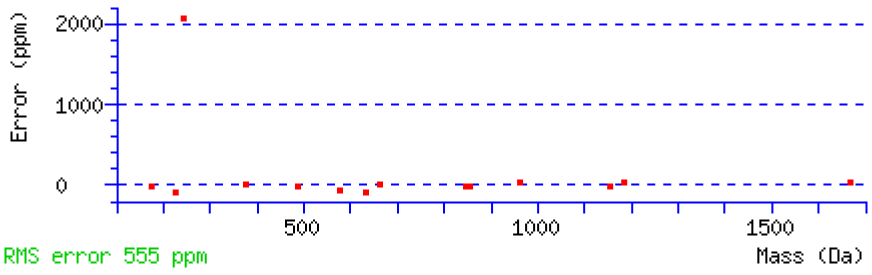
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1928.021439
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 6.4e-005
Matches : 14/192 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							18
2	***227.175404***	114.091340					I	1815.944683	908.475980	1798.918134	899.962705	1797.934118	899.470697	17
3	355.233982	178.120629	338.207433	169.607355			Q	1702.860619	851.933948	1685.834070	843.420673	1684.850054	842.928665	16
4	484.276575	**242.641926**	467.250026	234.128651	466.266010	233.636643	E	1574.802041	787.904659	1557.775492	779.391384	1556.791476	778.899376	15
5	612.335153	306.671215	595.308604	298.157940	594.324588	297.665932	Q	1445.759448	723.383362	1428.732899	714.870088	1427.748883	714.378080	14
6	727.362096	364.184686	710.335547	355.671412	709.351531	355.179404	D	1317.700870	659.354073	1300.674321	650.840799	1299.690305	650.348790	13
7	798.399210	399.703243	781.372661	391.189969	780.388645	390.697961	A	1202.673927	601.840602	1185.647378	593.327327	1184.663362	592.835319	12
8	***855.420674***	428.213975	838.394125	419.700701	837.410109	419.208693	G	1131.636813	566.322045	1114.610264	557.808770	1113.626248	557.316762	11
9	968.504738	484.756007	951.478189	476.242733	950.494173	475.750725	L	1074.615349	537.811312	1057.588800	529.298038	1056.604784	528.806030	10
10	1083.531681	542.269479	1066.505132	533.756204	1065.521116	533.264196	D	***961.531285***	481.269281	944.504736	472.756006	943.520720	472.263998	9
11	***1154.568795***	577.788036	1137.542246	569.274761	1136.558230	568.782753	A	***846.504342***	423.755809	829.477793	415.242534	828.493777	414.750526	8
12	1267.652859	**634.330068**	1250.626310	625.816793	1249.642294	625.324785	L	775.467228	388.237252	758.440679	379.723977	757.456663	379.231969	7
13	1354.684887	677.846082	1337.658338	669.332807	1336.674322	668.840799	S	***662.383164***	331.695220	645.356615	323.181946	644.372599	322.689938	6
14	1441.716915	721.362096	1424.690366	712.848821	1423.706350	712.356813	S	***575.351136***	288.179206	558.324587	279.665932	557.340571	279.173924	5
15	1554.800979	777.904128	1537.774430	769.390853	1536.790414	768.898845	I	***488.319108***	244.663192	471.292559	236.149917	470.308543	235.657909	4
16	***1667.885043***	834.446160	1650.858494	825.932885	1649.874478	825.440877	I	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
17	1754.917071	877.962174	1737.890522	869.448899	1736.906506	868.956891	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IIQEQDAGLDALSSIISR
(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	1928.021439	-0.000417	IIQEQDAGLDALSSIISR
2.6	1928.014923	0.006099	KINQNVAALPVASSVMDR
2.0	1928.003708	0.017314	NLPVTGPQAPTIKELMR
1.8	1928.032715	-0.011693	TTLQRQVEPTVTISPSR
0.1	1928.015594	0.005428	DPTWIVKQPEYAVVQR

Mascot: http://www.matrixscience.com/

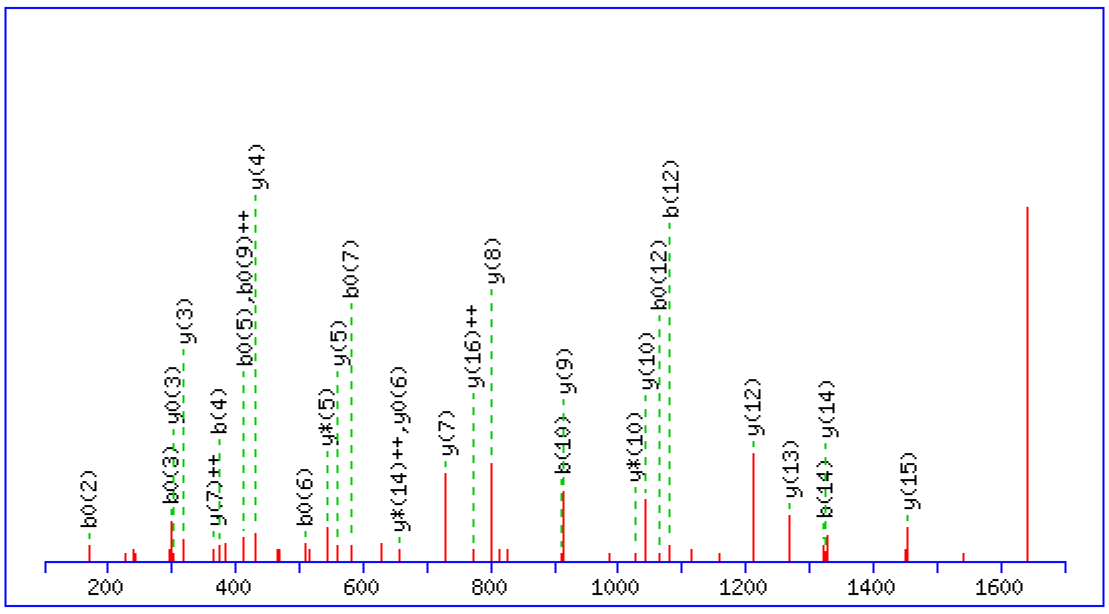
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSEGGPAEIAGLQIGDK**
Found in **TX1B3_HUMAN**, Tax1-binding protein 3 OS=Homo sapiens GN=TAX1BP3 PE=1 SV=2

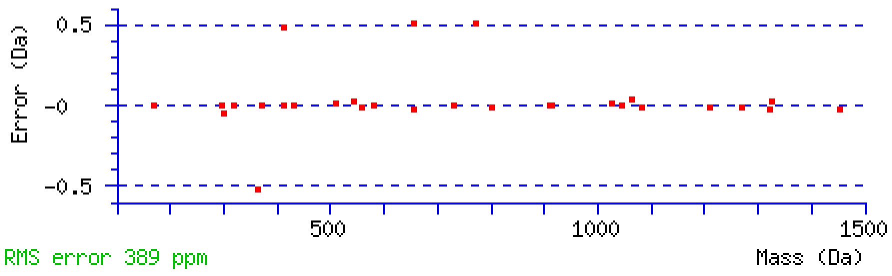
Match to Query 18036: 1639.837528 from(820.926040,2+) rtinseconds(2738) index(9479)
Title: Locus:1.1.1.3059.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

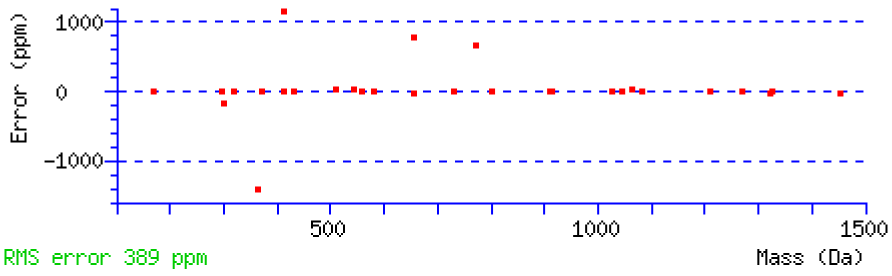
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1639.841705
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 74  Expect: 5.1e-007
Matches : 29/164 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	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
73.5	1639.841705	-0.004177	VSEGGPAEIAGLQIGDK

Mascot: http://www.matrixscience.com/

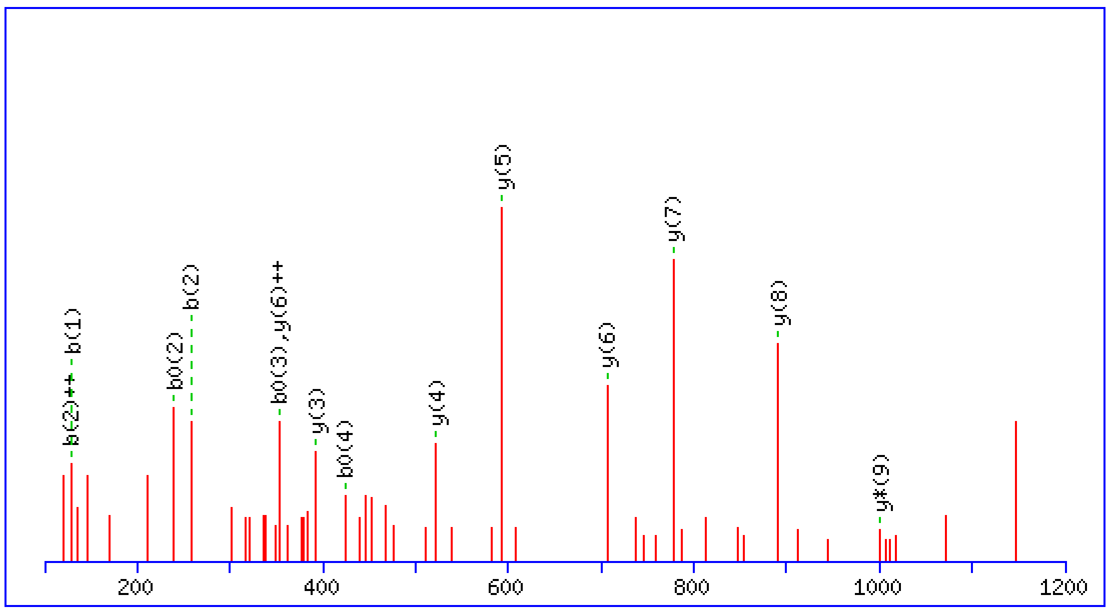
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQLAIAEFAR**
Found in **TCPA_HUMAN**, T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1

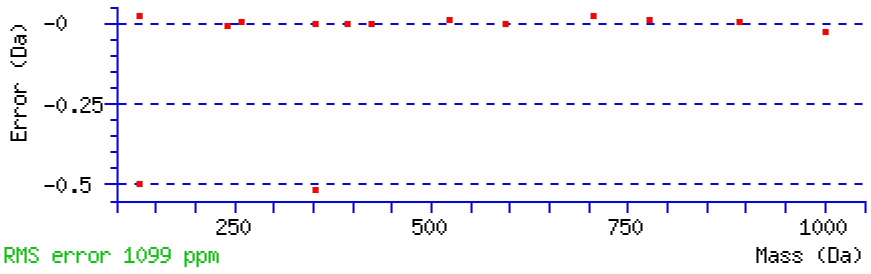
Match to Query 16434: 1146.607948 from(574.311250,2+) rtinseconds(2750) index(34640)
Title: Locus:1.1.1.2586.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

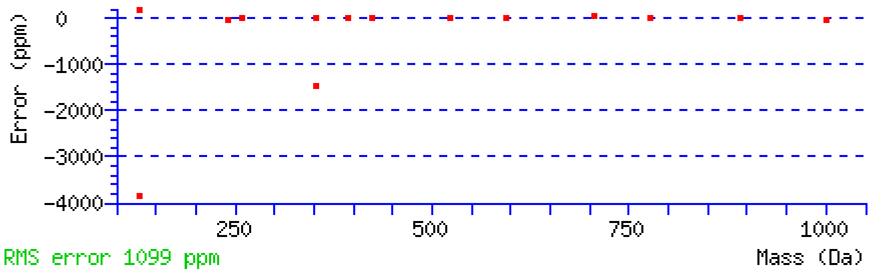
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1146.603287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43  Expect: 0.00039
Matches : 14/100 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	**258.108447**	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1018.568007	509.787642	1001.541458	501.274367	1000.557442	500.782359	9
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	L	***890.509429***	445.758353	873.482880	437.245078	872.498864	436.753070	8
4	442.229625	221.618450	425.203076	213.105176	424.219060	212.613168	A	***777.425365***	389.216320	760.398816	380.703046	759.414800	380.211038	7
5	555.313689	278.160483	538.287140	269.647208	537.303124	269.155200	I	***706.388251***	353.697764	689.361702	345.184489	688.377686	344.692481	6
6	626.350803	313.679040	609.324254	305.165765	608.340238	304.673757	A	***593.304187***	297.155732	576.277638	288.642457	575.293622	288.150449	5
7	755.393396	378.200336	738.366847	369.687062	737.382831	369.195054	E	***522.267073***	261.637175	505.240524	253.123900	504.256508	252.631892	4
8	902.461810	451.734543	885.435261	443.221269	884.451245	442.729261	F	***393.224480***	197.115878	376.197931	188.602603			3
9	973.498924	487.253100	956.472375	478.739825	955.488359	478.247818	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 EQLAIAEFAR
(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	1146.603287	0.004661	EQLAIAEFAR
6.5	1146.599274	0.008674	RTISQQSAEK
4.5	1146.617905	-0.009957	RTLQSLACGK
3.1	1146.614532	-0.006584	QEFNKRPTK
2.9	1146.613190	-0.005242	GSITISAEEIK

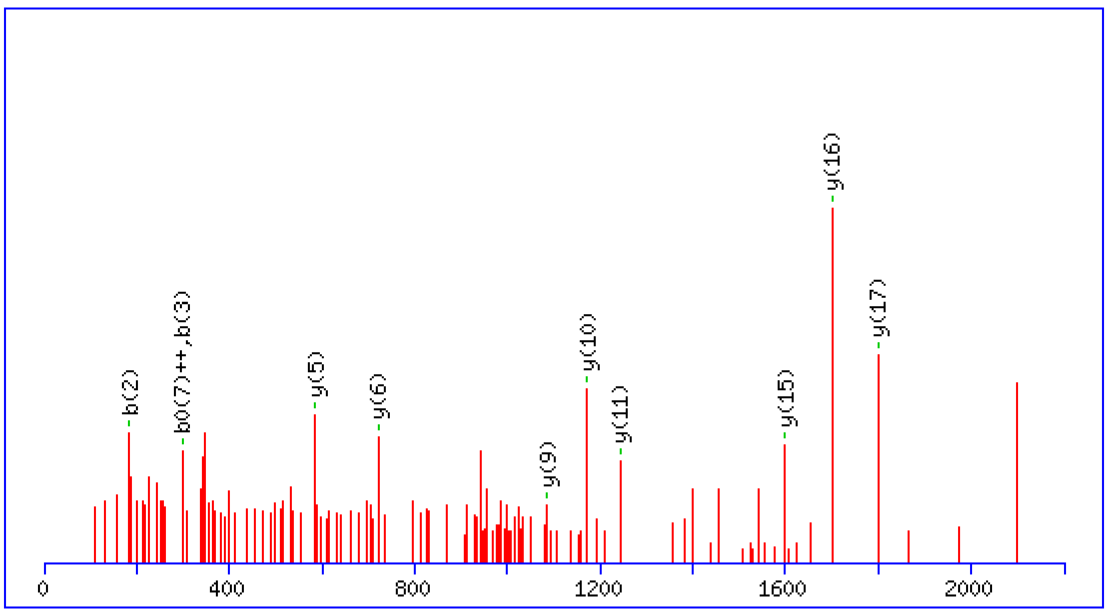
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LALVTGGEIASTFDHPELVK**
Found in **TCPB_HUMAN**, T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4

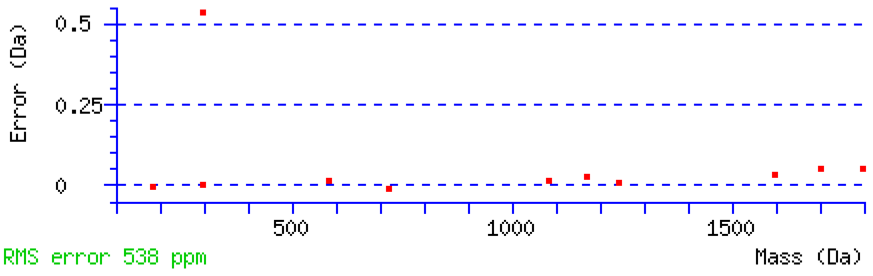
Match to Query 29125: 2096.104722 from(699.708850,3+) rtinseconds(3220) index(44898)
Title: Locus:1.1.1.2749.14
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

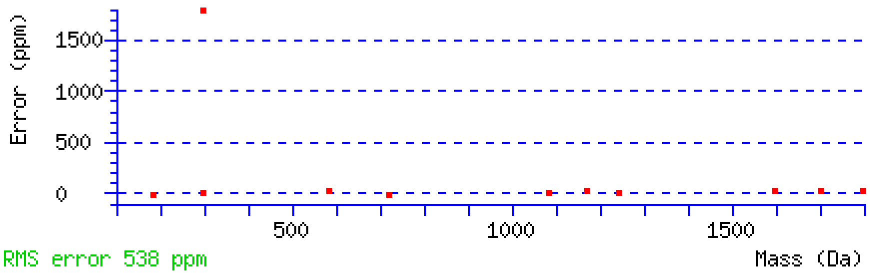
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2096.115372
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42  Expect: 0.00017
Matches : 11/176 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							20
2	**185.128454**	93.067865			A	1984.038585	992.522931	1967.012036	984.009656	1966.028020	983.517648	19
3	**298.212518**	149.609897			L	1913.001471	957.004374	1895.974922	948.491099	1894.990906	947.999091	18
4	397.280932	199.144104			V	***1799.917407***	900.462342	1782.890858	891.949067	1781.906842	891.457059	17
5	498.328611	249.667944	480.318046	240.662661	T	***1700.848993***	850.928135	1683.822444	842.414860	1682.838428	841.922852	16
6	555.350075	278.178676	537.339510	269.173393	G	***1599.801314***	800.404295	1582.774765	791.891021	1581.790749	791.399013	15
7	612.371539	306.689408	594.360974	297.684125	G	1542.779850	771.893563	1525.753301	763.380289	1524.769285	762.888281	14
8	741.414132	371.210704	723.403567	362.205422	E	1485.758386	743.382831	1468.731837	734.869557	1467.747821	734.377549	13
9	854.498196	427.752736	836.487631	418.747454	I	1356.715793	678.861535	1339.689244	670.348260	1338.705228	669.856252	12
10	925.535310	463.271293	907.524745	454.266011	A	***1243.631729***	622.319503	1226.605180	613.806228	1225.621164	613.314220	11
11	1012.567338	506.787307	994.556773	497.782025	S	***1172.594615***	586.800946	1155.568066	578.287671	1154.584050	577.795663	10
12	1113.615017	557.311147	1095.604452	548.305864	T	***1085.562587***	543.284932	1068.536038	534.771657	1067.552022	534.279649	9
13	1260.683431	630.845354	1242.672866	621.840071	F	984.514908	492.761092	967.488359	484.247818	966.504343	483.755810	8
14	1375.710374	688.358825	1357.699809	679.353543	D	837.446494	419.226885	820.419945	410.713611	819.435929	410.221603	7
15	1512.769286	756.888281	1494.758721	747.882999	H	***722.419551***	361.713414	705.393002	353.200139	704.408986	352.708131	6
16	1609.822050	805.414663	1591.811485	796.409381	P	***585.360639***	293.183958	568.334090	284.670683	567.350074	284.178675	5
17	1738.864643	869.935960	1720.854078	860.930677	E	488.307875	244.657575	471.281326	236.144301	470.297310	235.652293	4
18	1851.948707	926.477992	1833.938142	917.472709	L	359.265282	180.136279	342.238733	171.623004			3
19	1951.017121	976.012199	1933.006556	967.006916	V	246.181218	123.594247	229.154669	115.080973			2
20					K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LALVTGGEIASTFDHPELVK
(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	2096.115372	-0.010650	LALVTGGEIASTFDHPELVK
1.9	2096.115387	-0.010665	VPSPVLPGVSSPAYPIPALR
1.1	2096.115387	-0.010665	VPSPVLPGVSSPAYPIPALR

Mascot: http://www.matrixscience.com/

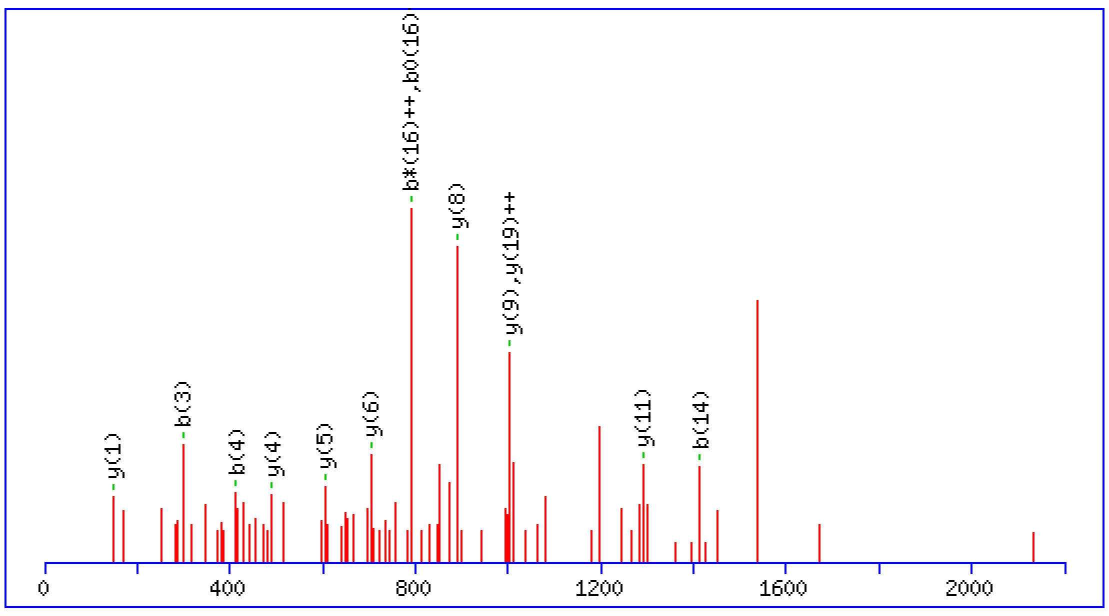
Mascot Search Results

Peptide View

MS/MS Fragmentation of **INALTAASEAACLIVSVDETIK**
Found in **TCPH_HUMAN**, T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2

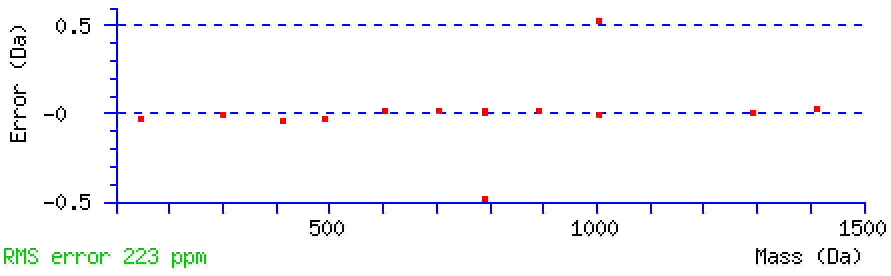
Match to Query 67054: 2302.228722 from(768.416850,3+) rtinseconds(5116) index(74049)
Title: Locus:1.1.1.3334.18
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

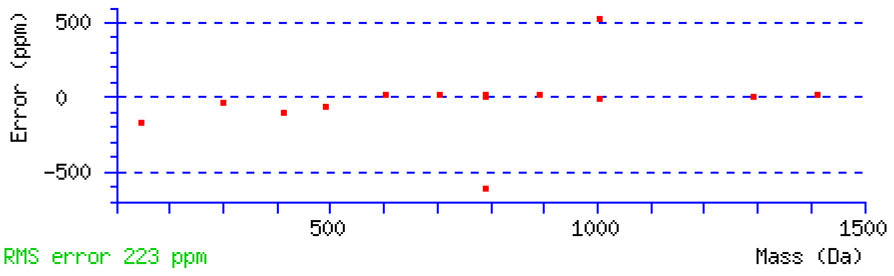
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2302.208969
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 52 **Expect:** 2.5e-005
Matches : 14/238 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							22
2	228.134267	114.570771	211.107718	106.057497			N	2190.132227	1095.569751	2173.105678	1087.056477	2172.121662	1086.564469	21
3	**299.171381**	150.089328	282.144832	141.576054			A	2076.089300	1038.548288	2059.062751	1030.035013	2058.078735	1029.543005	20
4	**412.255445**	206.631361	395.228896	198.118086			L	2005.052186	1003.029731	1988.025637	994.516457	1987.041621	994.024448	19
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	T	1891.968122	946.487699	1874.941573	937.974425	1873.957557	937.482417	18
6	584.340238	292.673757	567.313689	284.160483	566.329673	283.668475	A	1790.920443	895.963860	1773.893894	887.450585	1772.909878	886.958577	17
7	655.377352	328.192314	638.350803	319.679039	637.366787	319.187031	A	1719.883329	860.445303	1702.856780	851.932028	1701.872764	851.440020	16
8	742.409380	371.708328	725.382831	363.195053	724.398815	362.703045	S	1648.846215	824.926746	1631.819666	816.413471	1630.835650	815.921463	15
9	871.451973	436.229625	854.425424	427.716350	853.441408	427.224342	E	1561.814187	781.410732	1544.787638	772.897457	1543.803622	772.405449	14
10	942.489087	471.748181	925.462538	463.234907	924.478522	462.742899	A	1432.771594	716.889435	1415.745045	708.376161	1414.761029	707.884153	13
11	1013.526201	507.266738	996.499652	498.753464	995.515636	498.261456	A	1361.734480	681.370878	1344.707931	672.857604	1343.723915	672.365596	12
12	1187.572500	594.289888	1170.545951	585.776614	1169.561935	585.284606	C	***1290.697366***	645.852321	1273.670817	637.339047	1272.686801	636.847039	11
13	1300.656564	650.831920	1283.630015	642.318646	1282.645999	641.826637	L	1116.651067	558.829172	1099.624518	550.315897	1098.640502	549.823889	10
14	**1413.740628**	707.373952	1396.714079	698.860677	1395.730063	698.368669	I	***1003.567003***	502.287140	986.540454	493.773865	985.556438	493.281857	9
15	1512.809042	756.908159	1495.782493	748.394884	1494.798477	747.902876	V	***890.482939***	445.745108	873.456390	437.231833	872.472374	436.739825	8
16	1599.841070	800.424173	1582.814521	791.910899	1581.830505	791.418890	S	***791.414525***	396.210901	774.387976	387.697626	773.403960	387.205618	7
17	1698.909484	849.958380	1681.882935	841.445106	1680.898919	840.953098	V	***704.382497***	352.694887	687.355948	344.181612	686.371932	343.689604	6
18	1813.936427	907.471852	1796.909878	898.958577	1795.925862	898.466569	D	***605.314083***	303.160680	588.287534	294.647405	587.303518	294.155397	5
19	1942.979020	971.993148	1925.952471	963.479874	1924.968455	962.987866	E	***490.287140***	245.647208	473.260591	237.133933	472.276575	236.641925	4
20	2044.026699	1022.516988	2027.000150	1014.003713	2026.016134	1013.511705	T	361.244547	181.125911	344.217998	172.612637	343.233982	172.120629	3
21	2157.110763	1079.059019	2140.084214	1070.545745	2139.100198	1070.053737	I	260.196868	130.602072	243.170319	122.088797			2
22							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of INALTAASEAACLIVSVDETIK
(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	2302.208969	0.019753	INALTAASEAACLIVSVDETIK
3.0	2302.206512	0.022210	MTDPSLGLTVPMAPPLAPLPPR
0.2	2302.232132	-0.003410	LPVPESITGFARLTVSEWLR

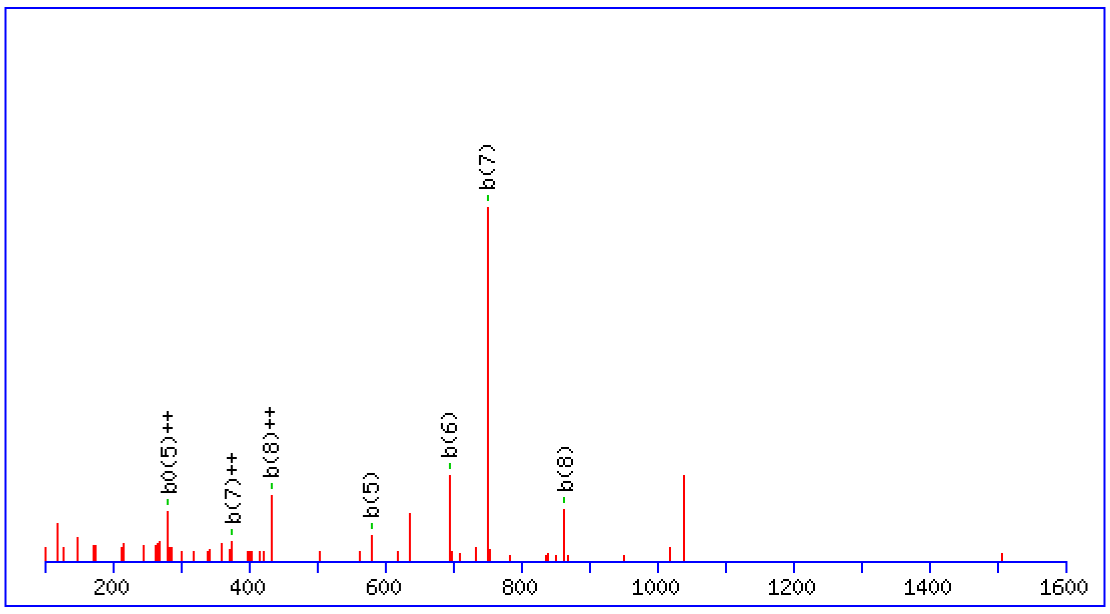
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VFMDSNGIR**
Found in **TECT3_HUMAN**, Tectonic-3 OS=Homo sapiens GN=TCTN3 PE=2 SV=2

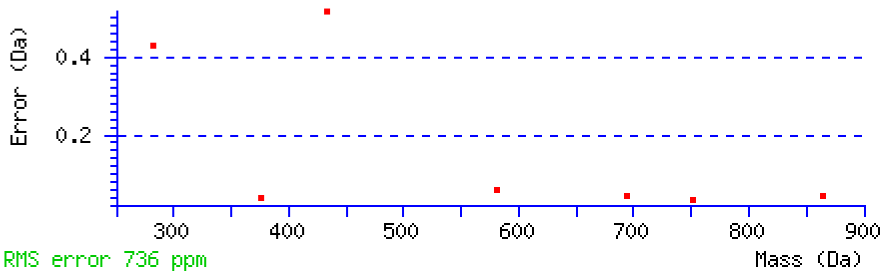
Match to Query 4146: 1037.490468 from(519.752510,2+) rtinseconds(1599) index(1068)
Title: Locus:1.1.1.2917.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

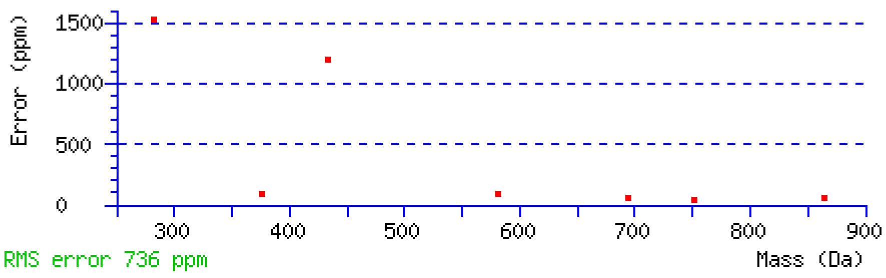
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1037.496414
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31 **Expect:** 0.008
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	247.144104	124.075690					F	939.435277	470.221277	922.408728	461.708002	921.424712	461.215994	8
3	378.184589	189.595932					M	792.366863	396.687070	775.340314	388.173795	774.356298	387.681787	7
4	493.211532	247.109404			475.200967	238.104121	D	661.326378	331.166827	644.299829	322.653553	643.315813	322.161545	6
5	***580.243560***	290.625418			562.232995	281.620136	S	546.299435	273.653356	529.272886	265.140081	528.288870	264.648073	5
6	***694.286487***	347.646882	677.259938	339.133607	676.275922	338.641599	N	459.267407	230.137342	442.240858	221.624067			4
7	***751.307951***	**376.157614**	734.281402	367.644339	733.297386	367.152331	G	345.224480	173.115878	328.197931	164.602604			3
8	***864.392015***	**432.699646**	847.365466	424.186371	846.381450	423.694363	I	288.203016	144.605146	271.176467	136.091872			2
9							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of VFMDSNGIR
(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	1037.496414	-0.005946	VFMDSNGIR
21.0	1037.488998	0.001470	YSTNNGNIR
19.0	1037.499756	-0.009288	CLSNCTKK
18.2	1037.493042	-0.002574	GTYWEGGIR
16.1	1037.496399	-0.005931	EMFQSAGIR
16.1	1037.481155	0.009313	MDSIGSSGLR
15.3	1037.489014	0.001454	SNKEGSGGFR
13.6	1037.485184	0.005284	DPFLDMIR
12.4	1037.496414	-0.005946	CPPIPAHGK
10.4	1037.485153	0.005315	CLSPEYAGK

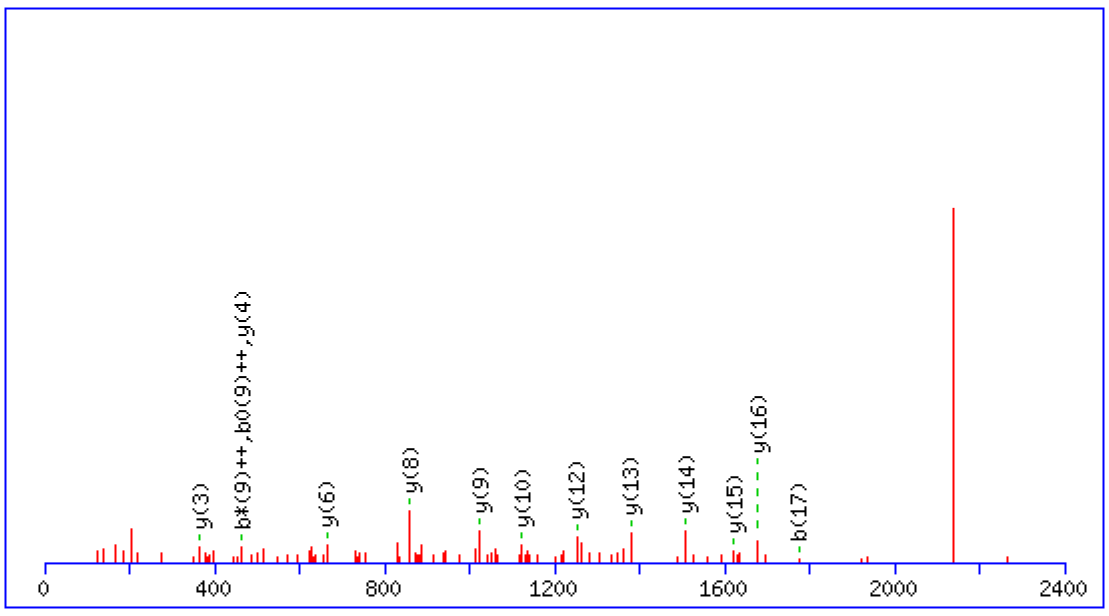
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FALQGLEQGATYPVSLVAFK**
Found in **TENN_HUMAN**, Tenascin-N OS=Homo sapiens GN=TNN PE=1 SV=2

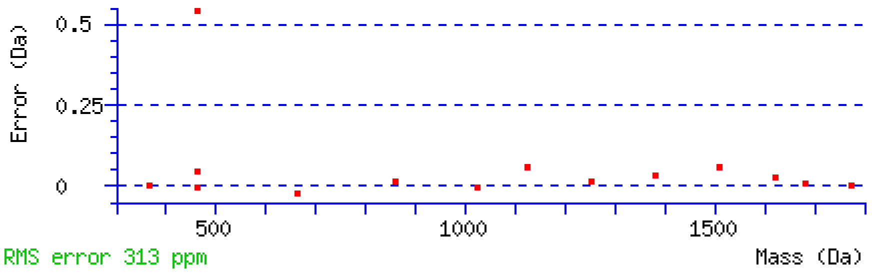
Match to Query 55804: 2138.160888 from(1070.087720,2+) rtinseconds(4006) index(59798)
Title: Locus:1.1.1.2975.38
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-1.mgf

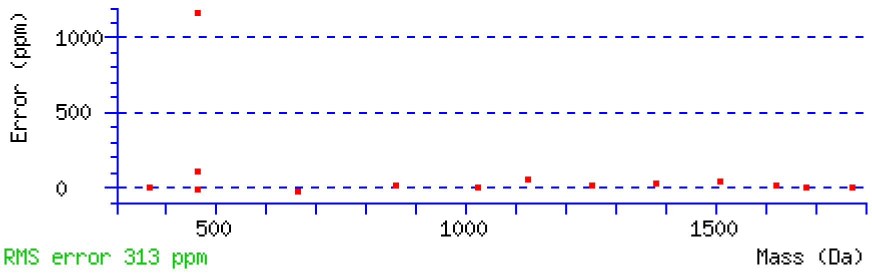
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2138.141190
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 76  Expect: 1.5e-007
Matches : 14/200 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	148.075690	74.541483					F							20
2	219.112804	110.060040					A	1992.080057	996.543667	1975.053508	988.030392	1974.069492	987.538384	19
3	332.196868	166.602072					L	1921.042943	961.025110	1904.016394	952.511835	1903.032378	952.019827	18
4	460.255446	230.631361	443.228897	222.118087			Q	1807.958879	904.483078	1790.932330	895.969803	1789.948314	895.477795	17
5	517.276910	259.142093	500.250361	250.628819			G	***1679.900301***	840.453789	1662.873752	831.940514	1661.889736	831.448506	16
6	630.360974	315.684125	613.334425	307.170851			L	***1622.878837***	811.943057	1605.852288	803.429782	1604.868272	802.937774	15
7	759.403567	380.205422	742.377018	371.692147	741.393002	371.200139	E	***1509.794773***	755.401025	1492.768224	746.887750	1491.784208	746.395742	14
8	887.462145	444.234711	870.435596	435.721436	869.451580	435.229428	Q	***1380.752180***	690.879728	1363.725631	682.366454	1362.741615	681.874446	13
9	944.483609	472.745443	927.457060	464.232168	926.473044	463.740160	G	***1252.693602***	626.850439	1235.667053	618.337165	1234.683037	617.845157	12
10	1015.520723	508.264000	998.494174	499.750725	997.510158	499.258717	A	1195.672138	598.339707	1178.645589	589.826433	1177.661573	589.334425	11
11	1116.568402	558.787839	1099.541853	550.274565	1098.557837	549.782557	T	***1124.635024***	562.821150	1107.608475	554.307876	1106.624459	553.815868	10
12	1279.631731	640.319504	1262.605182	631.806229	1261.621166	631.314221	Y	***1023.587345***	512.297311	1006.560796	503.784036	1005.576780	503.292028	9
13	1376.684495	688.845886	1359.657946	680.332611	1358.673930	679.840603	P	***860.524016***	430.765646	843.497467	422.252372	842.513451	421.760364	8
14	1475.752909	738.380093	1458.726360	729.866818	1457.742344	729.374810	V	763.471252	382.239264	746.444703	373.725990	745.460687	373.233982	7
15	1562.784937	781.896107	1545.758388	773.382832	1544.774372	772.890824	S	***664.402838***	332.705057	647.376289	324.191783	646.392273	323.699775	6
16	1675.869001	838.438139	1658.842452	829.924864	1657.858436	829.432856	L	577.370810	289.189043	560.344261	280.675769			5
17	1774.937415	887.972346	1757.910866	879.459071	1756.926850	878.967063	V	***464.286746***	232.647011	447.260197	224.133737			4
18	1845.974529	923.490903	1828.947980	914.977628	1827.963964	914.485620	A	***365.218332***	183.112804	348.191783	174.599530			3
19	1993.042943	997.025110	1976.016394	988.511835	1975.032378	988.019827	F	294.181218	147.594247	277.154669	139.080973			2
20							K	147.112804	74.060040	130.086255	65.546766			1





NCBI **BLAST** search of FALQGLEQGATYPVSLVAFK
(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	2138.141190	0.019698	FALQGLEQGATYPVSLVAFK

Mascot: http://www.matrixscience.com/

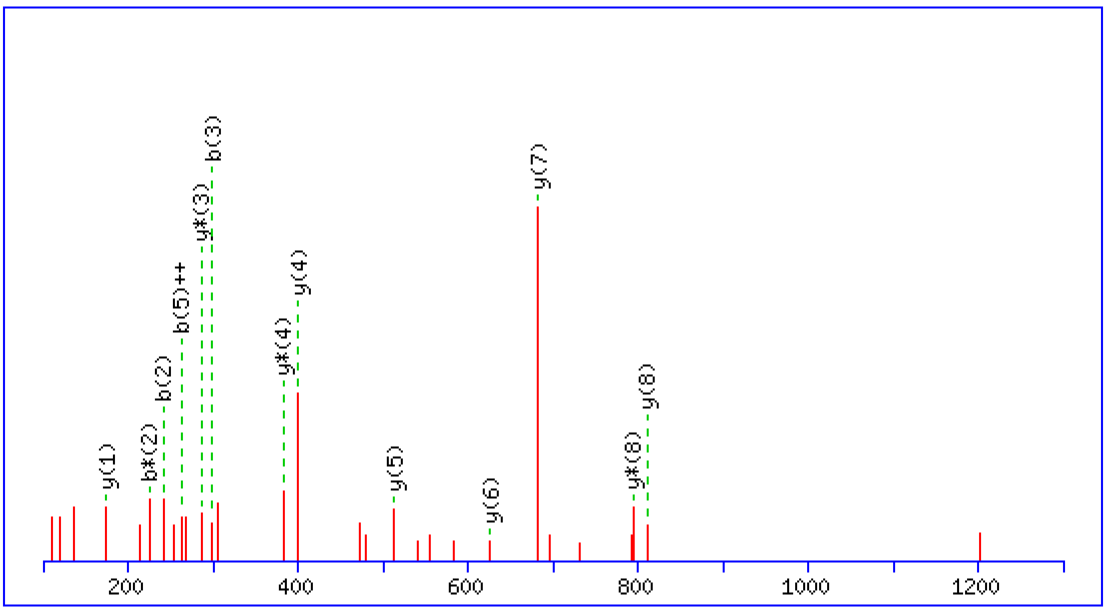
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQGLIPGAR**
Found in **TENX_HUMAN**, Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3

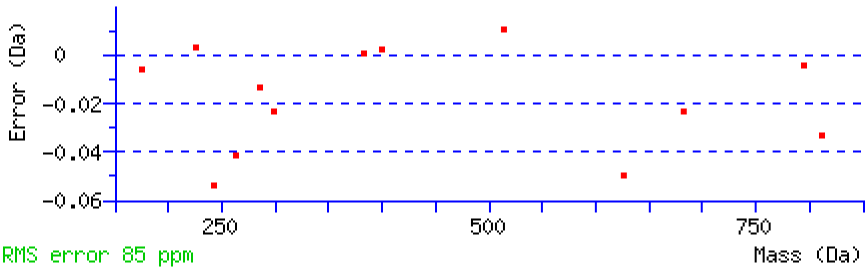
Match to Query 6724: 923.553148 from(462.783850,2+) rtinseconds(2091) index(26387)
Title: Locus:1.1.1.1439.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

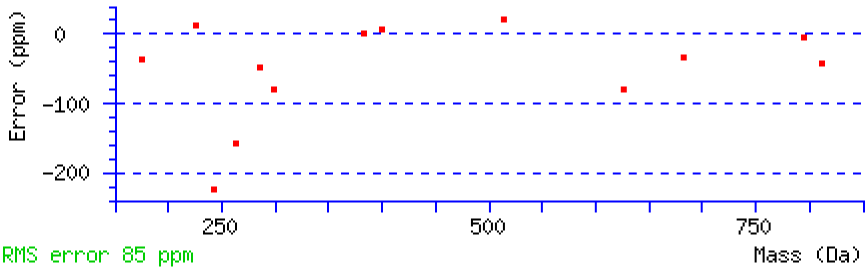
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 923.555237
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33 **Expect:** 0.0016
Matches : 13/62 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.091340	57.549308			L					9
2	**242.149918**	121.578597	225.123369	113.065323	Q	***811.478464***	406.242870	794.451915	397.729596	8
3	**299.171382**	150.089329	282.144833	141.576055	G	***683.419886***	342.213581	666.393337	333.700307	7
4	412.255446	206.631361	395.228897	198.118087	L	***626.398422***	313.702849	609.371873	305.189575	6
5	525.339510	263.173393	508.312961	254.660119	I	***513.314358***	257.160817	496.287809	248.647543	5
6	622.392274	311.699775	605.365725	303.186501	P	***400.230294***	200.618785	383.203745	192.105511	4
7	679.413738	340.210507	662.387189	331.697233	G	303.177530	152.092403	286.150981	143.579129	3
8	750.450852	375.729064	733.424303	367.215790	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 LQGLIPGAR
(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	923.555237	-0.002089	LQGLIPGAR
9.7	923.555222	-0.002074	NLLSPKPR
5.5	923.555222	-0.002074	NISPKIPR

Mascot: http://www.matrixscience.com/

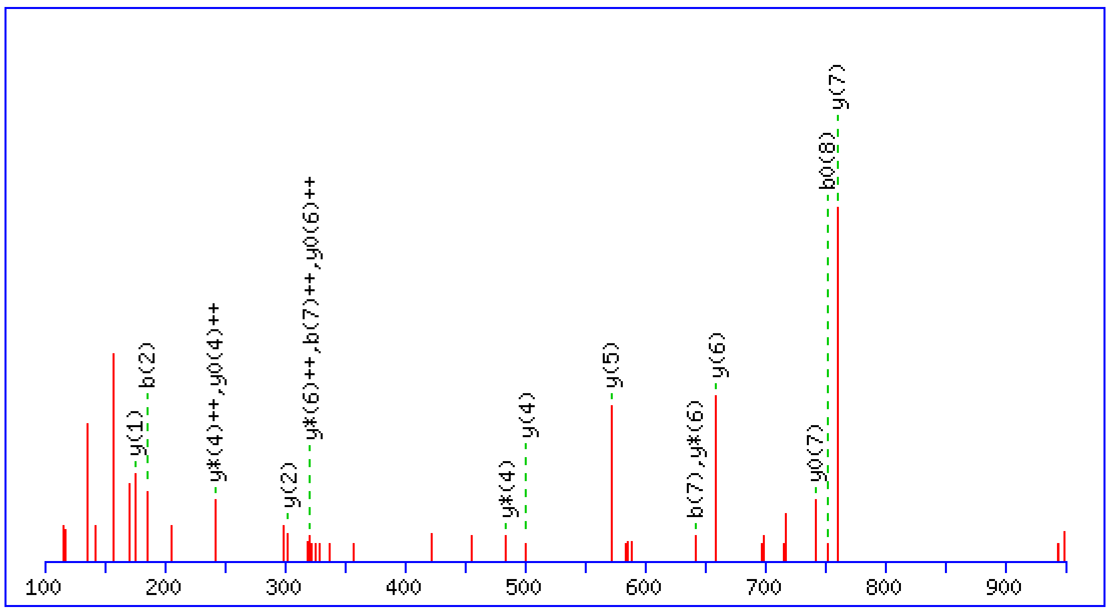
Mascot Search Results

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

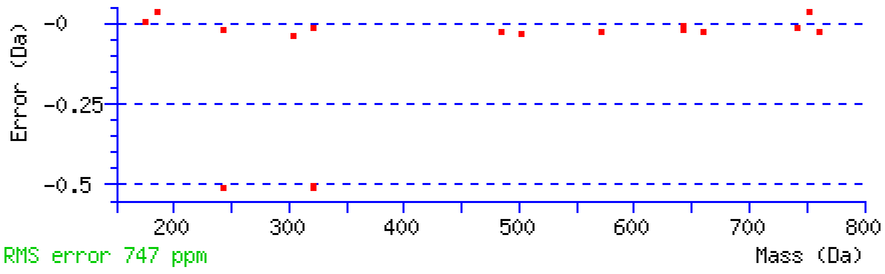
Match to Query 9080: 943.476368 from(472.745460,2+) rtinseconds(1644) index(12861)
Title: Locus:1.1.1.2156.14
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

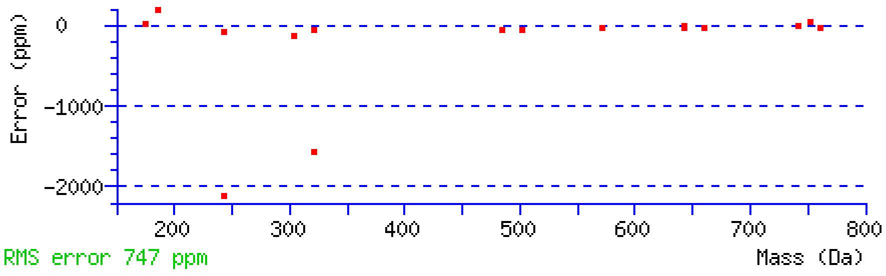
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 943.472305
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33   Expect: 0.0064
Matches : 17/78 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	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
32.5	943.472305	0.004063	SPTSAPTQR
25.9	943.476303	0.000065	AITSAYYR
11.7	943.483521	-0.007153	REVADAQR
10.8	943.483521	-0.007153	ALGDRDAAR
8.6	943.473633	0.002735	RWQNGGAR
8.2	943.472290	0.004078	SPSPKESGR
8.1	943.472305	0.004063	SPPGPASKR
5.4	943.472305	0.004063	QDIDLGAGR
5.2	943.472305	0.004063	SPGQPSSLR
5.0	943.472305	0.004063	TSPADGKPR

Mascot: http://www.matrixscience.com/

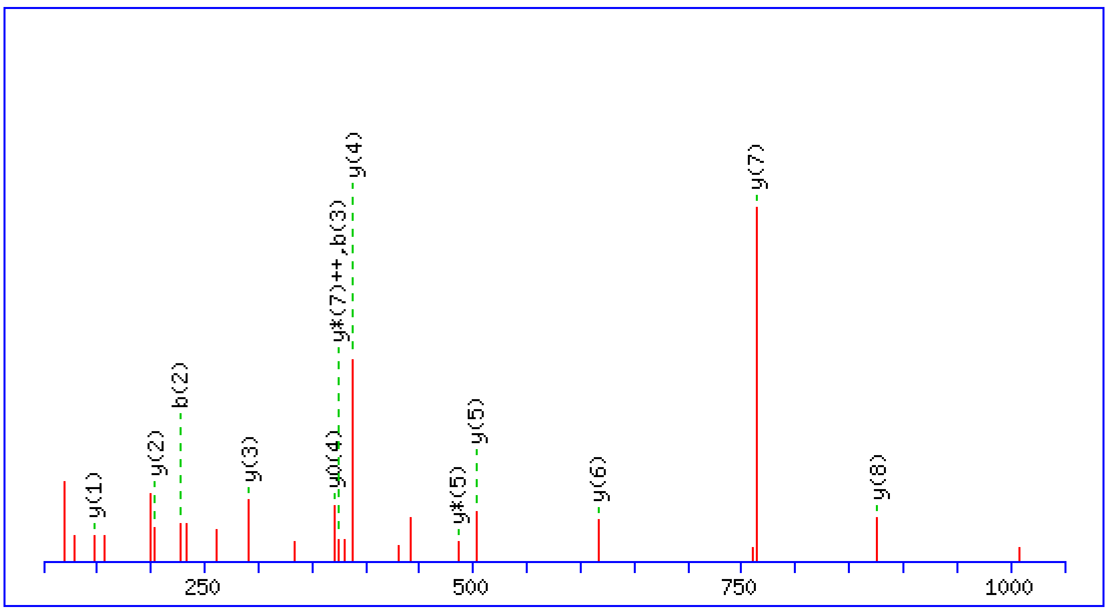
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILFLDPSGK**
Found in **TXD12_HUMAN**, Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1

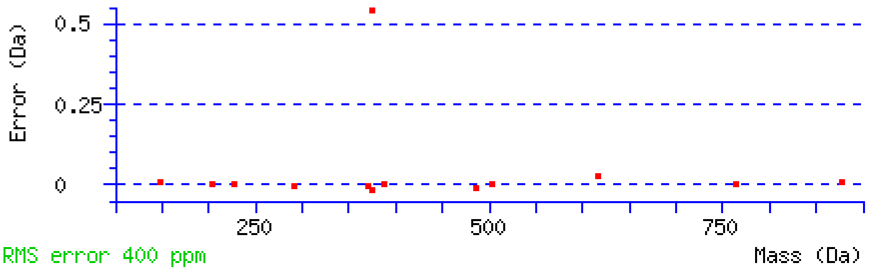
Match to Query 9610: 988.560168 from(495.287360,2+) rtinseconds(3005) index(24185)
Title: Locus:1.1.1.2664.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

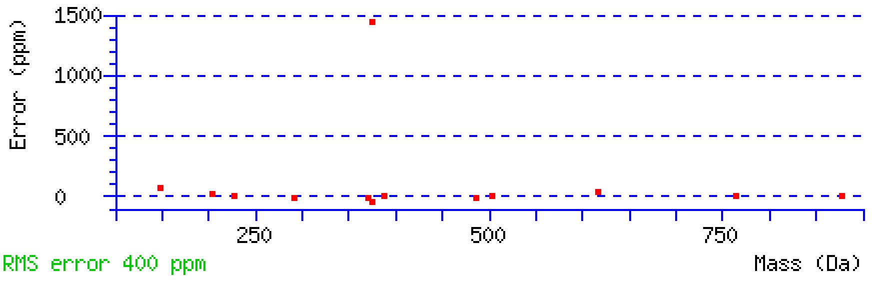
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 988.559326
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69  Expect: 8.4e-007
Matches : 13/68 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I							9
2	**227.175404**	114.091340			L	***876.482545***	438.744911	859.455996	430.231636	858.471980	429.739628	8
3	**374.243818**	187.625547			F	***763.398481***	382.202879	746.371932	373.689604	745.387916	373.197596	7
4	487.327882	244.167579			L	***616.330067***	308.668672	599.303518	300.155397	598.319502	299.663389	6
5	602.354825	301.681051	584.344260	292.675768	D	***503.246003***	252.126639	486.219454	243.613365	485.235438	243.121357	5
6	699.407589	350.207433	681.397024	341.202150	P	***388.219060***	194.613168	371.192511	186.099894	370.208495	185.607886	4
7	786.439617	393.723447	768.429052	384.718164	S	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
8	843.461081	422.234179	825.450516	413.228896	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 ILFLDPSGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.8	988.559326	0.000842	ILFLDPSGK
13.3	988.559326	0.000842	LLQDLFPK
7.6	988.566528	-0.006360	ILSRGSQTK
6.3	988.559326	0.000842	LPTAFLPSK
6.1	988.555283	0.004885	IISSSPNKK
6.0	988.562668	-0.002500	ILKEDMLK
6.0	988.559311	0.000857	LLTSLWEK
4.1	988.552795	0.007373	IFLCLGPR
4.1	988.566528	-0.006360	LLRTTETR
4.1	988.555283	0.004885	LLTKETER

Mascot: http://www.matrixscience.com/

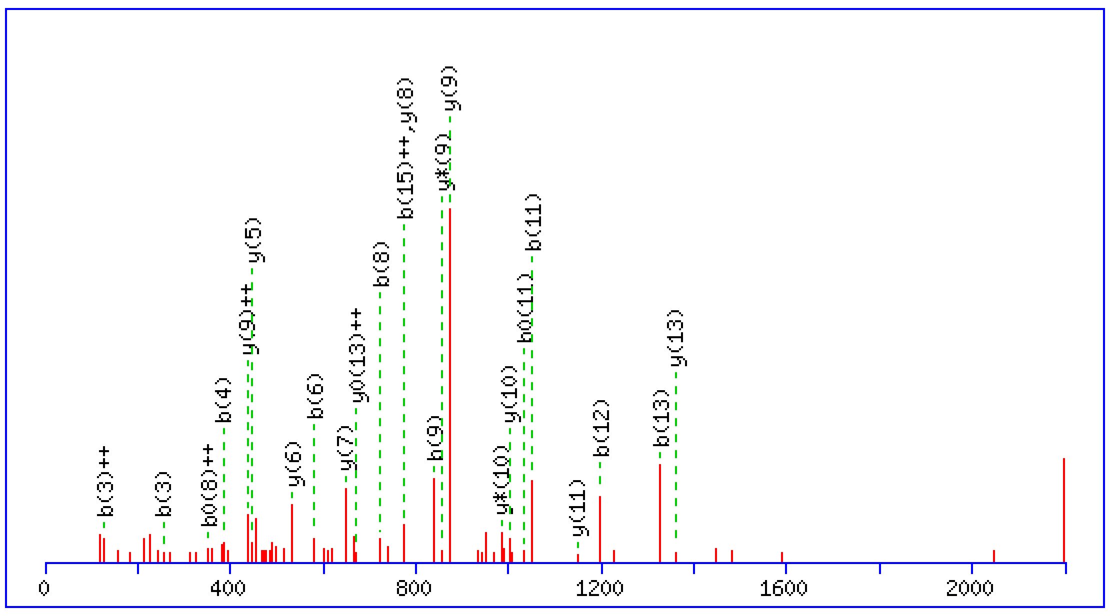
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGVKPVGSDPDFQPELSGAGSR**
Found in **TXNL1_HUMAN**, Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3

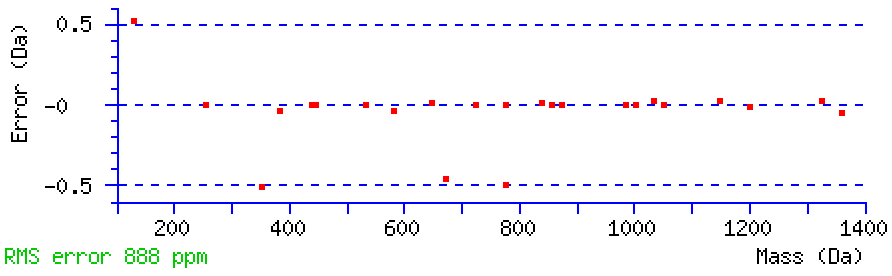
Match to Query 65230: 2198.104062 from(733.708630,3+) rtinseconds(2318) index(26340)
Title: Locus:1.1.1.2282.43
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

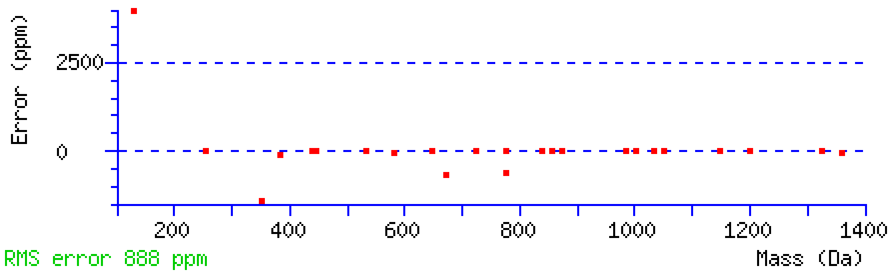
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2198.096786
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.0003
Matches : 24/230 fragment ions using 47 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	157.097154	79.052215					G	2100.035624	1050.521450	2083.009075	1042.008175	2082.025059	1041.516167	21
3	***256.165568***	128.586422					V	2043.014160	1022.010718	2025.987611	1013.497444	2025.003595	1013.005436	20
4	***384.260531***	192.633904	367.233982	184.120629			K	1943.945746	972.476511	1926.919197	963.963237	1925.935181	963.471229	19
5	481.313295	241.160285	464.286746	232.647011			P	1815.850783	908.429030	1798.824234	899.915755	1797.840218	899.423747	18
6	***580.381709***	290.694493	563.355160	282.181218			V	1718.798019	859.902648	1701.771470	851.389373	1700.787454	850.897365	17
7	637.403173	319.205225	620.376624	310.691950			G	1619.729605	810.368441	1602.703056	801.855166	1601.719040	801.363158	16
8	***724.435201***	362.721239	707.408652	354.207964	706.424636	353.715956	S	1562.708141	781.857709	1545.681592	773.344434	1544.697576	772.852426	15
9	***839.462144***	420.234710	822.435595	411.721435	821.451579	411.229427	D	1475.676113	738.341695	1458.649564	729.828420	1457.665548	729.336412	14
10	936.514908	468.761092	919.488359	460.247818	918.504343	459.755810	P	***1360.649170***	680.828223	1343.622621	672.314949	1342.638605	671.822941	13
11	***1051.541851***	526.274564	1034.515302	517.761289	1033.531286	517.269281	D	1263.596406	632.301841	1246.569857	623.788567	1245.585841	623.296559	12
12	***1198.610265***	599.808771	1181.583716	591.295496	1180.599700	590.803488	F	***1148.569463***	574.788370	1131.542914	566.275095	1130.558898	565.783087	11
13	***1326.668843***	663.838060	1309.642294	655.324785	1308.658278	654.832777	Q	***1001.501049***	501.254163	984.474500	492.740888	983.490484	492.248880	10
14	1423.721607	712.364442	1406.695058	703.851167	1405.711042	703.359159	P	***873.442471***	437.224874	856.415922	428.711599	855.431906	428.219591	9
15	1552.764200	776.885738	1535.737651	768.372464	1534.753635	767.880456	E	***776.389707***	388.698492	759.363158	380.185217	758.379142	379.693209	8
16	1665.848264	833.427770	1648.821715	824.914496	1647.837699	824.422488	L	***647.347114***	324.177195	630.320565	315.663920	629.336549	315.171912	7
17	1752.880292	876.943784	1735.853743	868.430510	1734.869727	867.938502	S	***534.263050***	267.635163	517.236501	259.121889	516.252485	258.629881	6
18	1809.901756	905.454516	1792.875207	896.941242	1791.891191	896.449234	G	***447.231022***	224.119149	430.204473	215.605874	429.220457	215.113866	5
19	1880.938870	940.973073	1863.912321	932.459799	1862.928305	931.967791	A	390.209558	195.608417	373.183009	187.095142	372.198993	186.603134	4
20	1937.960334	969.483805	1920.933785	960.970531	1919.949769	960.478523	G	319.172444	160.089860	302.145895	151.576585	301.161879	151.084577	3
21	2024.992362	1012.999819	2007.965813	1004.486545	2006.981797	1003.994537	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
22							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of VGVKPVGSDPDFQPELSGAGSR
(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	2198.096786	0.007276	VGVKPVGSDPDFQPELSGAGSR
4.7	2198.118744	-0.014682	AAIVVNGHGMTPLKVAAESCK
1.9	2198.123260	-0.019198	IAPRPARPPPVFADSPFQR
0.3	2198.111359	-0.007297	VGMADANSPPKPLSKPRTPR
0.3	2198.111359	-0.007297	VGMADANSPPKPLSKPRTPR
0.2	2198.103973	0.000089	IPLEKPGSGGSSPGATSGSGRAGR

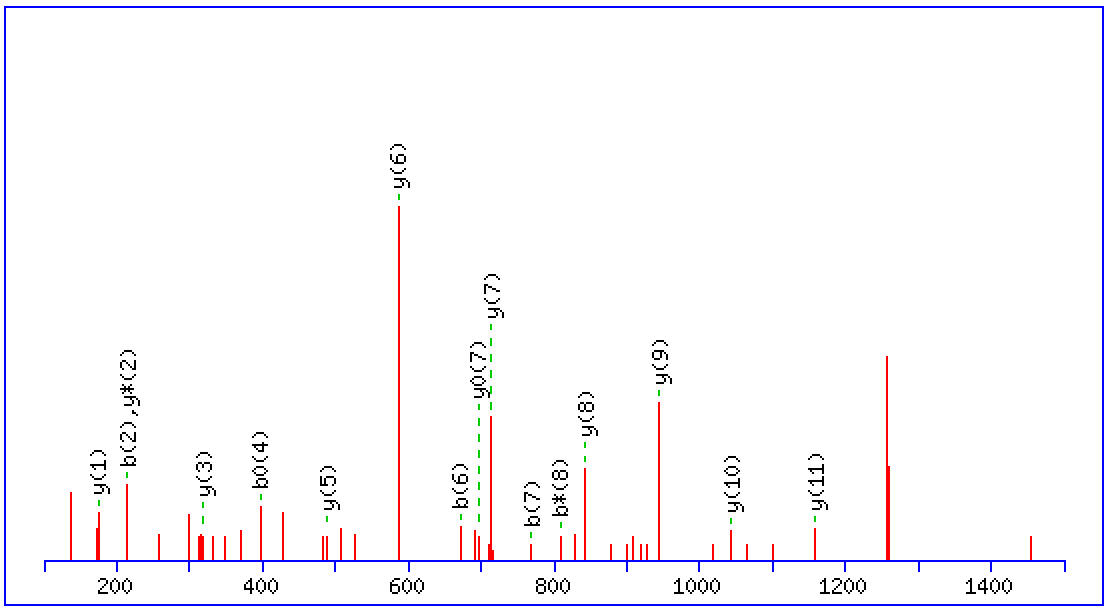
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDVTEQPGLSGR**
Found in **TMX1_HUMAN**, Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1

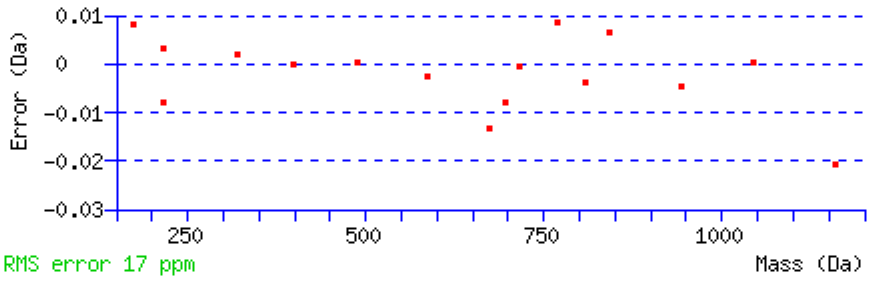
Match to Query 26902: 1256.630928 from(629.322740,2+) rtinseconds(1697) index(13881)
Title: Locus:1.1.1.2176.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

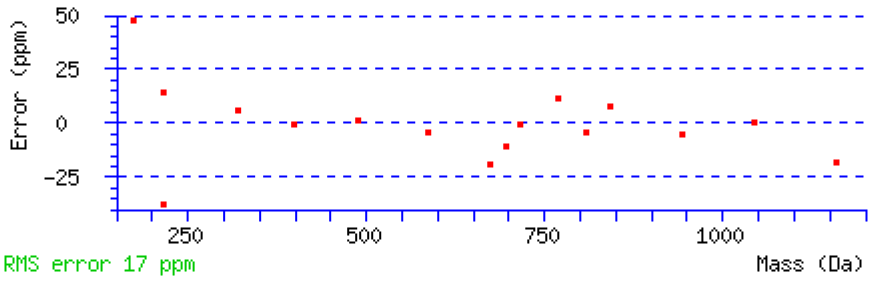
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1256.636093
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54  Expect: 4.3e-005
Matches : 16/116 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	100.075690	50.541483					V							12
2	**215.102633**	108.054954			197.092068	99.049672	D	***1158.574943***	579.791110	1141.548394	571.277835	1140.564378	570.785827	11
3	314.171047	157.589161			296.160482	148.583879	V	***1043.548000***	522.277638	1026.521451	513.764364	1025.537435	513.272356	10
4	415.218726	208.113001			397.208161	199.107719	T	***944.479586***	472.743431	927.453037	464.230157	926.469021	463.738149	9
5	544.261319	272.634298			526.250754	263.629015	E	***843.431907***	422.219592	826.405358	413.706317	825.421342	413.214309	8
6	**672.319897**	336.663587	655.293348	328.150312	654.309332	327.658304	Q	***714.389314***	357.698295	697.362765	349.185021	696.378749	348.693013	7
7	**769.372661**	385.189969	752.346112	376.676694	751.362096	376.184686	P	***586.330736***	293.669006	569.304187	285.155732	568.320171	284.663724	6
8	826.394125	413.700701	809.367576	405.187426	808.383560	404.695418	G	***489.277972***	245.142624	472.251423	236.629349	471.267407	236.137341	5
9	939.478189	470.242733	922.451640	461.729458	921.467624	461.237450	L	432.256508	216.631892	415.229959	208.118617	414.245943	207.626609	4
10	1026.510217	513.758747	1009.483668	505.245472	1008.499652	504.753464	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
11	1083.531681	542.269479	1066.505132	533.756204	1065.521116	533.264196	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 VDVTEQPGLSGR
(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	1256.636093	-0.005165	VDVTEQPGLSGR

Mascot: http://www.matrixscience.com/

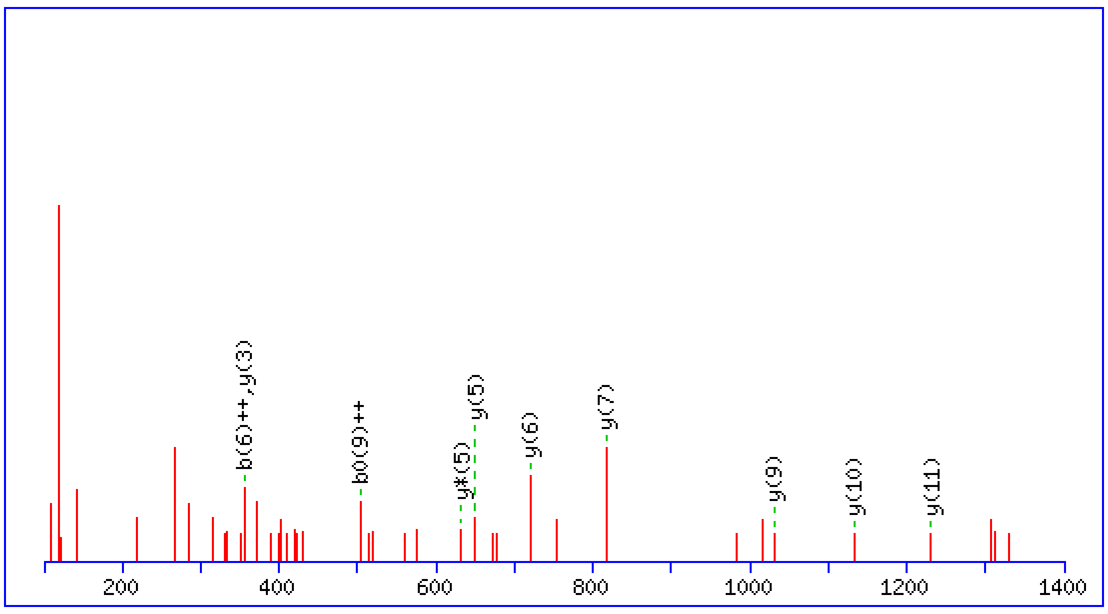
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFVTTLPAFFHAK**
Found in **TMX4_HUMAN**, Thioredoxin-related transmembrane protein 4 OS=Homo sapiens GN=TMX4 PE=1 SV=1

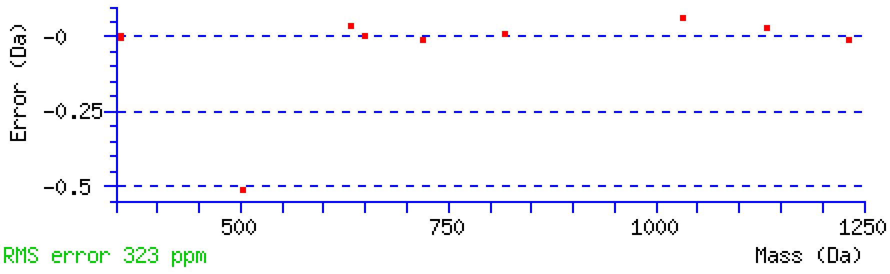
Match to Query 33432: 1524.804942 from(509.275590,3+) rtinseconds(3634) index(46301)
Title: Locus:1.1.1.2951.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

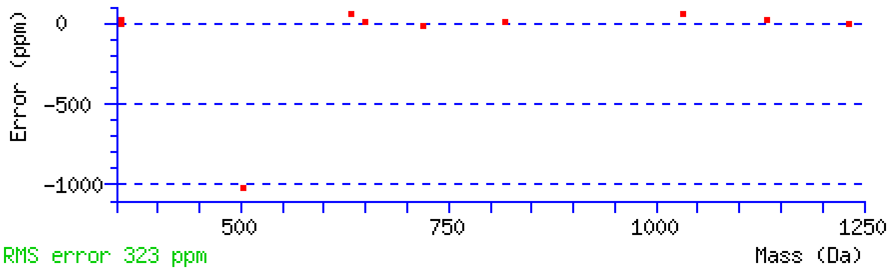
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1524.812943
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 30  Expect: 0.0015
Matches : 10/98 fragment ions using 23 most intense peaks   (help)
```

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483			F							13
2	295.144104	148.075690			F	1378.751786	689.879531	1361.725237	681.366257	1360.741221	680.874249	12
3	394.212518	197.609897			V	***1231.683372***	616.345324	1214.656823	607.832050	1213.672807	607.340042	11
4	495.260197	248.133737	477.249632	239.128454	T	***1132.614958***	566.811117	1115.588409	558.297843	1114.604393	557.805835	10
5	596.307876	298.657576	578.297311	289.652294	T	***1031.567279***	516.287278	1014.540730	507.774003	1013.556714	507.281995	9
6	709.391940	355.199608	691.381375	346.194326	L	930.519600	465.763438	913.493051	457.250164			8
7	806.444704	403.725990	788.434139	394.720708	P	***817.435536***	409.221406	800.408987	400.708132			7
8	877.481818	439.244547	859.471253	430.239265	A	***720.382772***	360.695024	703.356223	352.181750			6
9	1024.550232	512.778754	1006.539667	503.773471	F	***649.345658***	325.176467	632.319109	316.663193			5
10	1171.618646	586.312961	1153.608081	577.307679	F	502.277244	251.642260	485.250695	243.128986			4
11	1308.677558	654.842417	1290.666993	645.837135	H	***355.208830***	178.108053	338.182281	169.594778			3
12	1379.714672	690.360974	1361.704107	681.355692	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 FFVTTLPAFFHAK
(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	1524.812943	-0.008001	FFVTTLPAFFHAK
0.1	1524.804871	0.000071	GSPSPAAPGPPAGPLPR

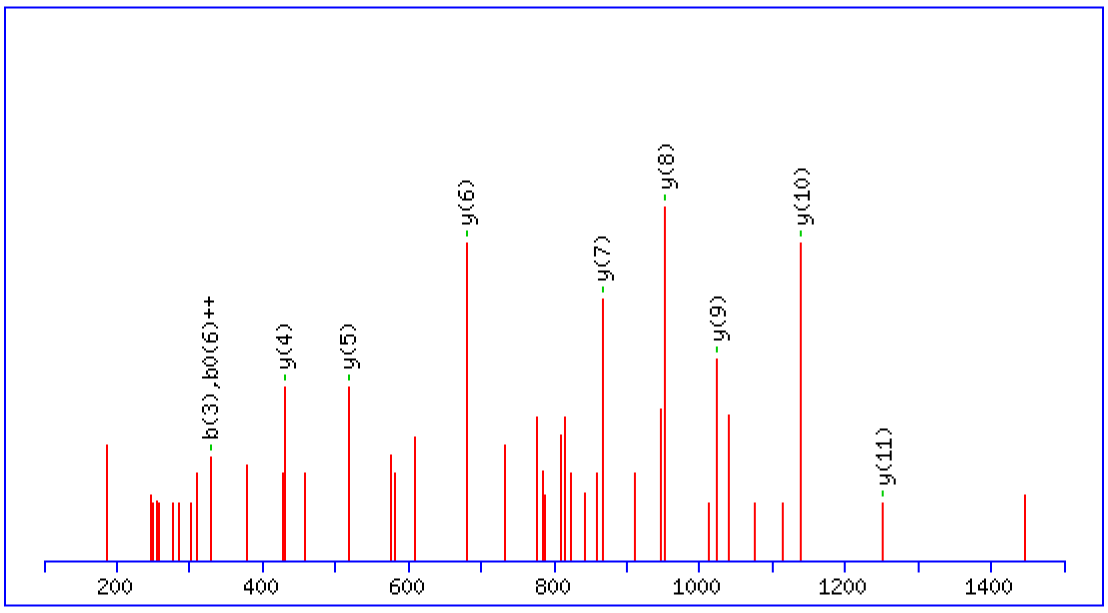
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLDASWYSPGTR**
Found in **THTR_HUMAN**, Thiosulfate sulfurtransferase OS=Homo sapiens GN=TST PE=1 SV=4

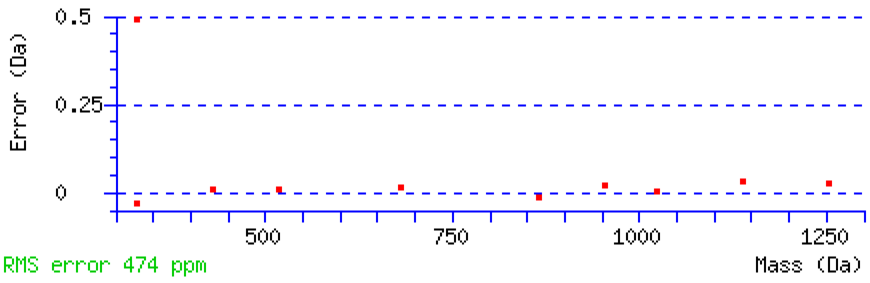
Match to Query 33765: 1350.665708 from(676.340130,2+) rtinseconds(2536) index(30437)
Title: Locus:1.1.1.2364.40
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

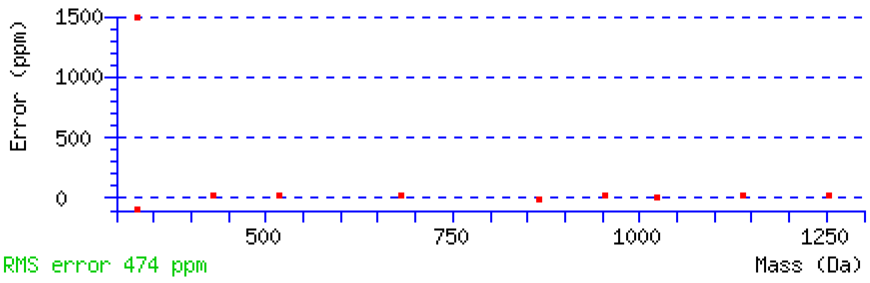
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1350.656815
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 68 **Expect:** 5.2e-006
Matches : 10/104 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							12
2	213.159754	107.083515			L	***1252.595678***	626.801477	1235.569129	618.288203	1234.585113	617.796195	11
3	328.186697	164.596986	310.176132	155.591704	D	***1139.511614***	570.259445	1122.485065	561.746171	1121.501049	561.254163	10
4	399.223811	200.115544	381.213246	191.110261	A	***1024.484671***	512.745973	1007.458122	504.232699	1006.474106	503.740691	9
5	486.255839	243.631557	468.245274	234.626275	S	***953.447557***	477.227417	936.421008	468.714142	935.436992	468.222134	8
6	672.335152	336.671214	654.324587	327.665932	W	***866.415529***	433.711403	849.388980	425.198128	848.404964	424.706120	7
7	835.398481	418.202879	817.387916	409.197596	Y	***680.336216***	340.671746	663.309667	332.158472	662.325651	331.666464	6
8	922.430509	461.718893	904.419944	452.713610	S	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	5
9	1019.483273	510.245275	1001.472708	501.239992	P	***430.240859***	215.624068	413.214310	207.110793	412.230294	206.618785	4
10	1076.504737	538.756007	1058.494172	529.750724	G	333.188095	167.097685	316.161546	158.584411	315.177530	158.092403	3
11	1177.552416	589.279846	1159.541851	580.274564	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 VLDASWYSPGTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.3	1350.656815	0.008893	VLDASWYSPGTR
0.9	1350.656830	0.008878	VDPAAFQAVFDR

Mascot: http://www.matrixscience.com/

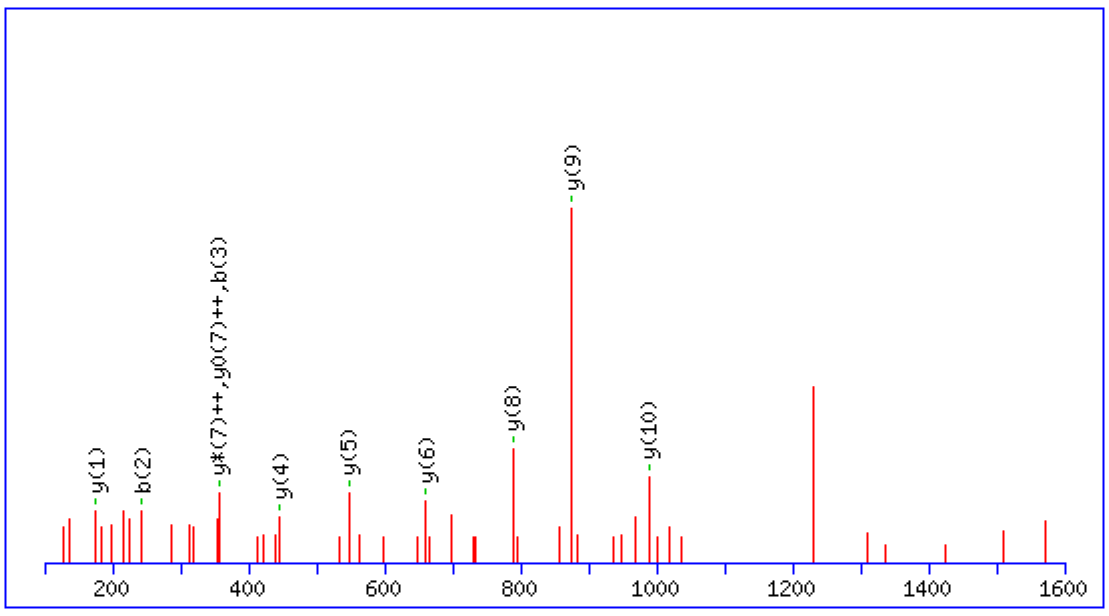
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NELSGALTGLTR**
Found in **SYTC_HUMAN**, Threonyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3

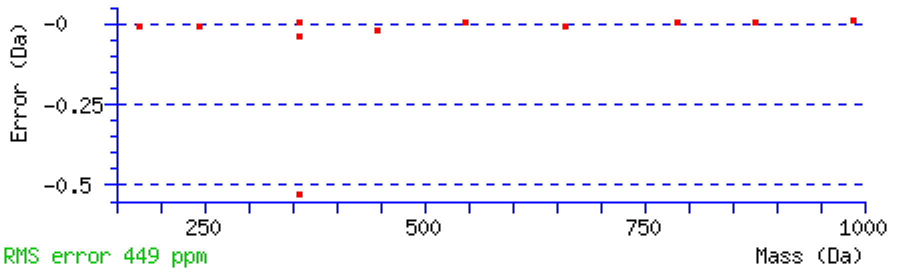
Match to Query 19087: 1230.651948 from(616.333250,2+) rtinseconds(2692) index(27405)
Title: Locus:1.1.1.2958.25
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-2.mgf

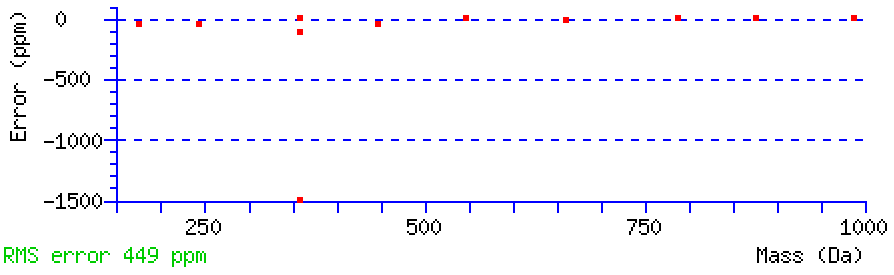
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1230.656799
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 67  Expect: 5.4e-006
Matches : 11/128 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	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	E	1117.621165	559.314221	1100.594616	550.800946	1099.610600	550.308938	11
3	**357.176860**	179.092068	340.150311	170.578794	339.166295	170.086786	L	***988.578572***	494.792924	971.552023	486.279650	970.568007	485.787642	10
4	444.208888	222.608082	427.182339	214.094808	426.198323	213.602800	S	***875.494508***	438.250892	858.467959	429.737618	857.483943	429.245610	9
5	501.230352	251.118814	484.203803	242.605540	483.219787	242.113532	G	***788.462480***	394.734878	771.435931	386.221604	770.451915	385.729596	8
6	572.267466	286.637371	555.240917	278.124097	554.256901	277.632089	A	731.441016	366.224146	714.414467	357.710872	713.430451	357.218864	7
7	685.351530	343.179403	668.324981	334.666129	667.340965	334.174121	L	***660.403902***	330.705589	643.377353	322.192315	642.393337	321.700307	6
8	786.399209	393.703243	769.372660	385.189968	768.388644	384.697960	T	***547.319838***	274.163557	530.293289	265.650283	529.309273	265.158275	5
9	843.420673	422.213975	826.394124	413.700700	825.410108	413.208692	G	***446.272159***	223.639717	429.245610	215.126443	428.261594	214.634435	4
10	956.504737	478.756007	939.478188	470.242732	938.494172	469.750724	L	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	3
11	1057.552416	529.279846	1040.525867	520.766572	1039.541851	520.274564	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 NELSGALTGLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.2	1230.656799	-0.004851	NELSGALTGLTR
35.0	1230.645584	0.006364	DTKTPTQSLPK
22.3	1230.664215	-0.012267	QTVDKVMGIPK
11.9	1230.664185	-0.012237	KTMQIGESLPK
11.5	1230.646896	0.005052	SRLGYAAPPAGR
11.5	1230.646896	0.005052	SRLGYAAPPAGR
7.6	1230.660797	-0.008849	ENPVYEKKPK
6.2	1230.656799	-0.004851	AIATDTVANLSR
4.6	1230.656784	-0.004836	EINSLSGKLDR
3.1	1230.664185	-0.012237	LTTCKQELPK

Mascot: http://www.matrixscience.com/

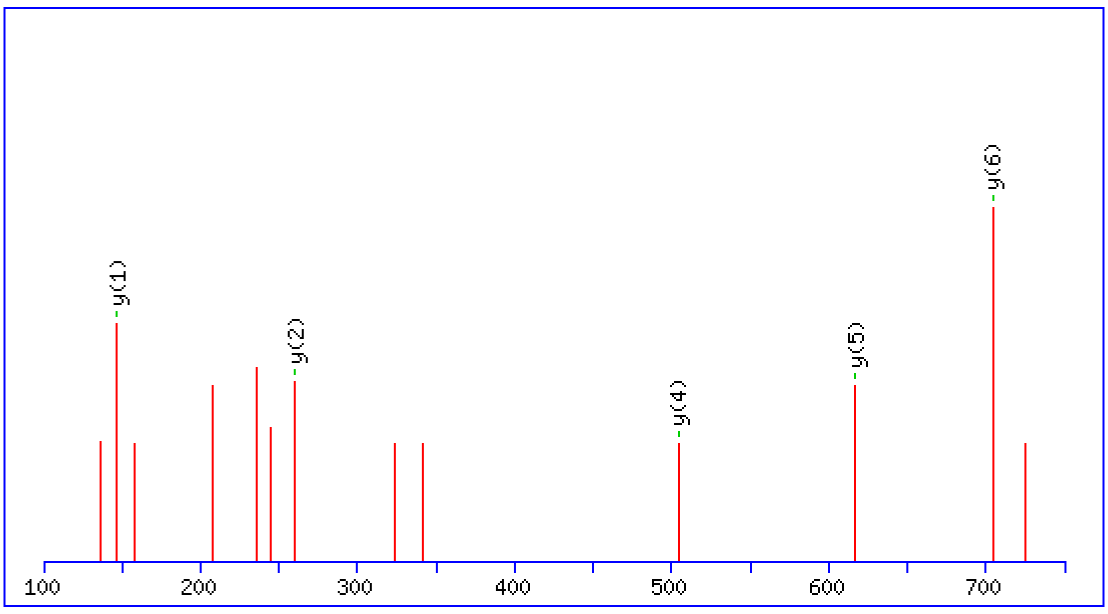
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSIEDLK**
Found in **THYN1_HUMAN**, Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1

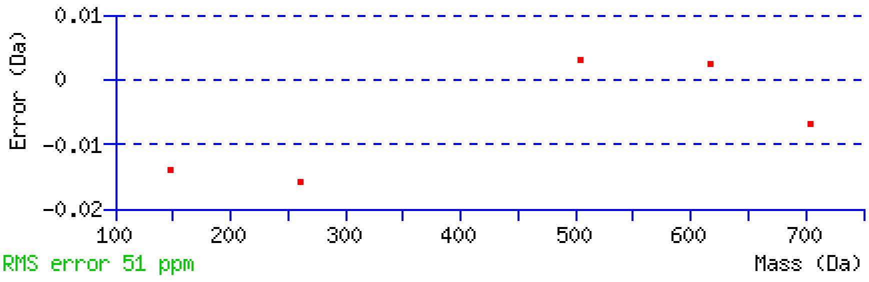
Match to Query 3186: 850.443128 from(426.228840,2+) rtinseconds(2660) index(24941)
Title: Locus:1.1.1.2481.3
Data file 2011-11-14 - TFD - S 2-5.mgf

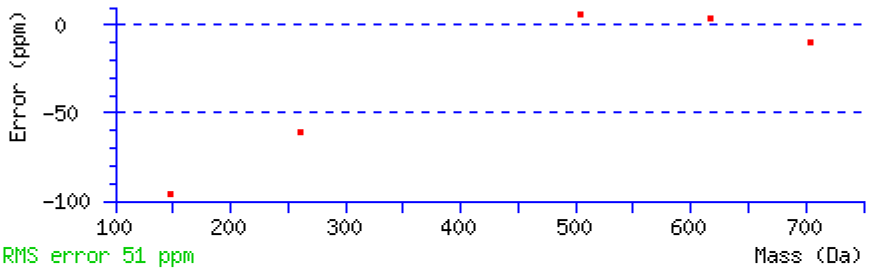
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 850.443619
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00059
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	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
47.4	850.443619	-0.000491	FSIEDLK
29.1	850.443604	-0.000476	AYIEDLK
29.1	850.443619	-0.000491	SFLDELK
29.1	850.443604	-0.000476	YAIEDLK
16.0	850.444962	-0.001834	FSRWQK
14.9	850.443619	-0.000491	SFEVELK
7.8	850.443619	-0.000491	EEFVSIK
7.8	850.443619	-0.000491	ELVSYPK
6.7	850.443619	-0.000491	SEVEFLK
6.3	850.437119	0.006009	GCVFGGLK

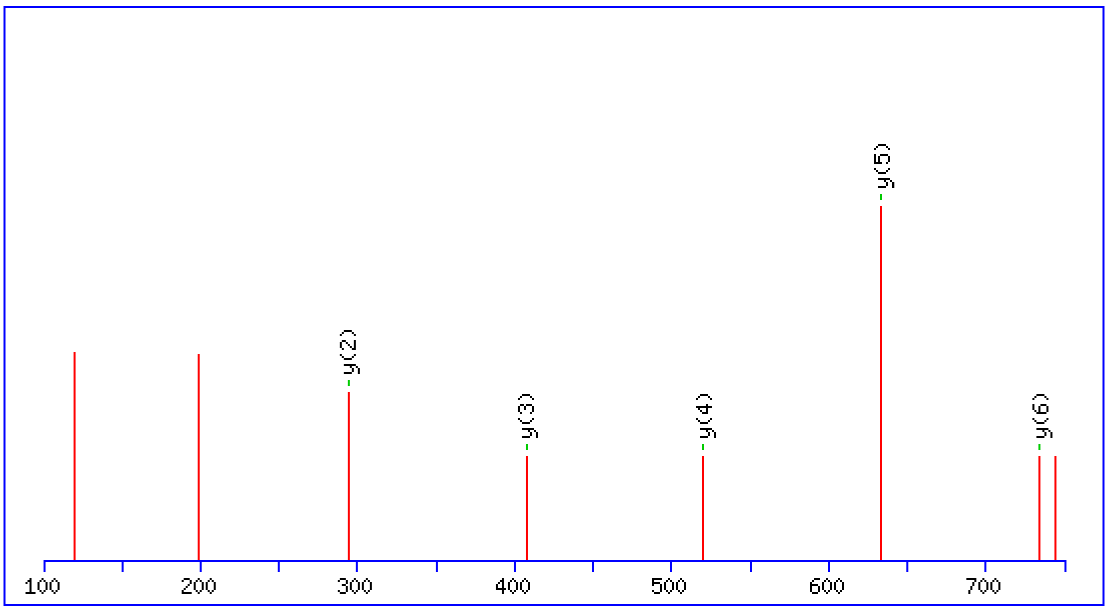
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTLLLFK**
Found in **TPRKB_HUMAN**, TP53RK-binding protein OS=Homo sapiens GN=TPRKB PE=1 SV=1

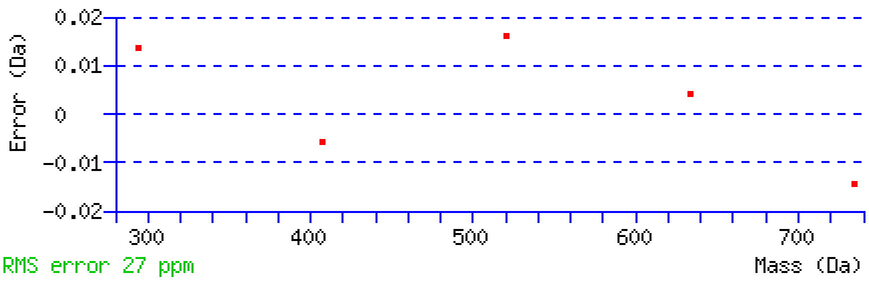
Match to Query 2015: 832.542748 from(417.278650,2+) rtinseconds(3291) index(34880)
Title: Locus:1.1.1.2748.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

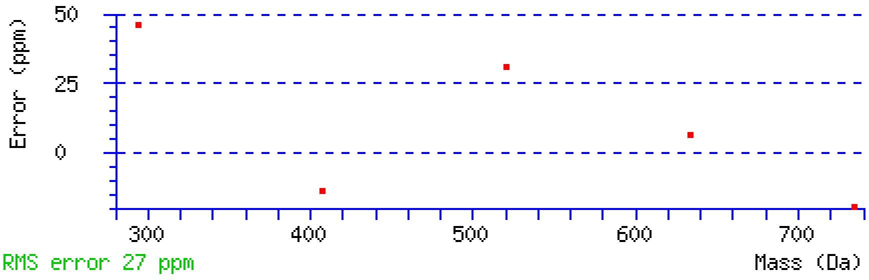
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 832.542221
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 1.5e-005
Matches : 5/48 fragment ions using 6 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	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
48.4	832.542221	0.000527	VTLLLFK

Mascot: http://www.matrixscience.com/

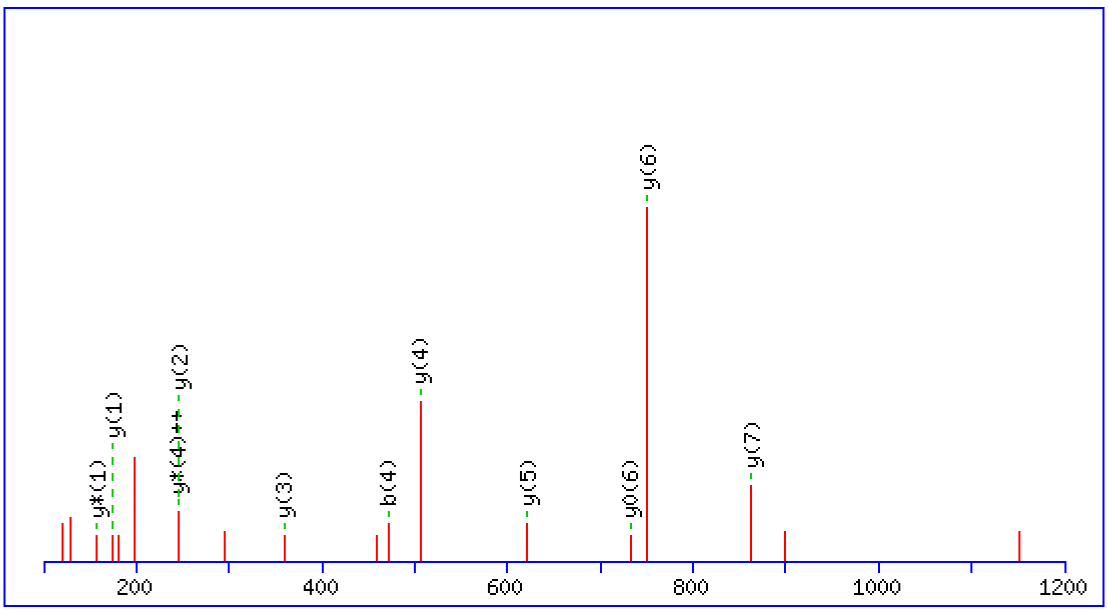
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIEDFLAR**
Found in **TPPC3_HUMAN**, Trafficking protein particle complex subunit 3 OS=Homo sapiens GN=TRAPPC3 PE=1 SV=1

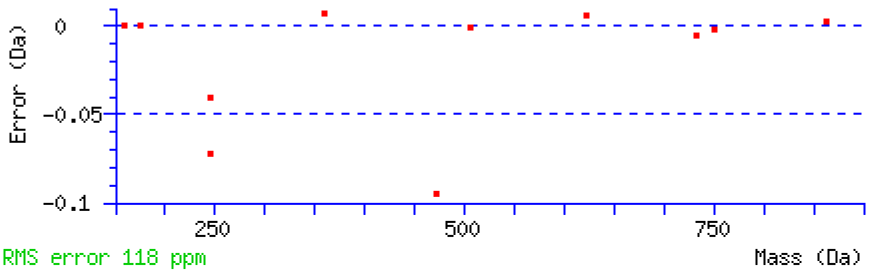
Match to Query 7872: 975.540608 from(488.777580,2+) rtinseconds(2933) index(23390)
Title: Locus:1.1.1.2627.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

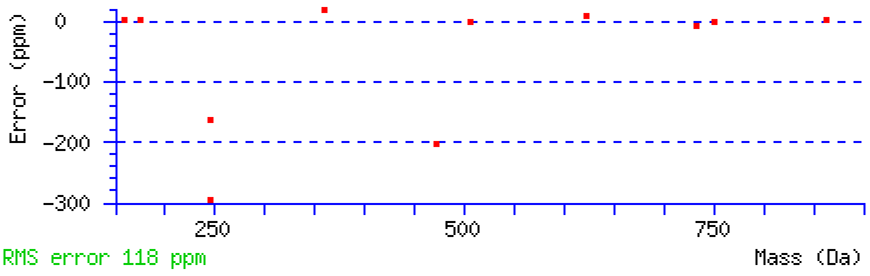
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 975.538910
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 55  Expect: 3.8e-005
Matches : 11/58 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							8
2	227.175404	114.091340			I	863.462144	432.234710	846.435595	423.721436	845.451579	423.229428	7
3	356.217997	178.612637	338.207432	169.607354	E	750.378080	375.692678	733.351531	367.179404	732.367515	366.687396	6
4	471.244940	236.126108	453.234375	227.120826	D	621.335487	311.171382	604.308938	302.658107	603.324922	302.166099	5
5	618.313354	309.660315	600.302789	300.655033	F	506.308544	253.657910	489.281995	245.144636			4
6	731.397418	366.202347	713.386853	357.197065	L	359.240130	180.123703	342.213581	171.610429			3
7	802.434532	401.720904	784.423967	392.715622	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 LIEDFLAR
(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	975.538910	0.001698	LIEDFLAR
9.6	975.531052	0.009556	IIMEEVVK
9.2	975.550156	-0.009548	RAGGEFLVK
9.0	975.538910	0.001698	ILLDPYSR
8.6	975.542282	-0.001674	ETQMVKIK
7.3	975.542282	-0.001674	LMQTDKLK
6.2	975.538910	0.001698	LDLEALFR
5.6	975.550156	-0.009548	QTIQIFAR
2.8	975.542267	-0.001659	LKMQAEIK
2.6	975.531052	0.009556	ILLDDLMK

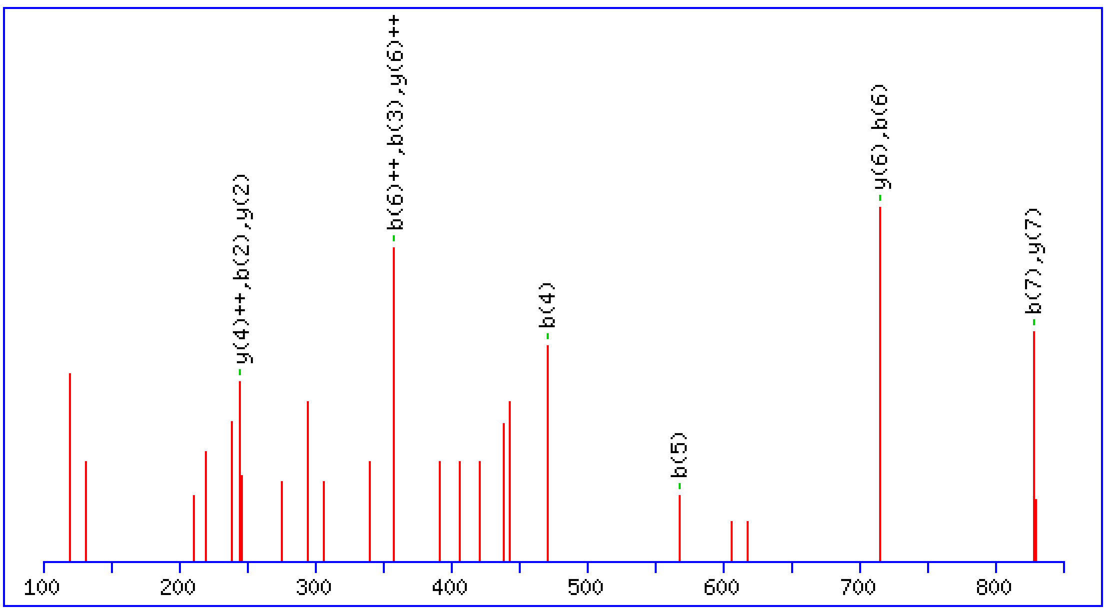
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPIIPFLL**
Found in **TECR_HUMAN**, Trans-2,3-enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1

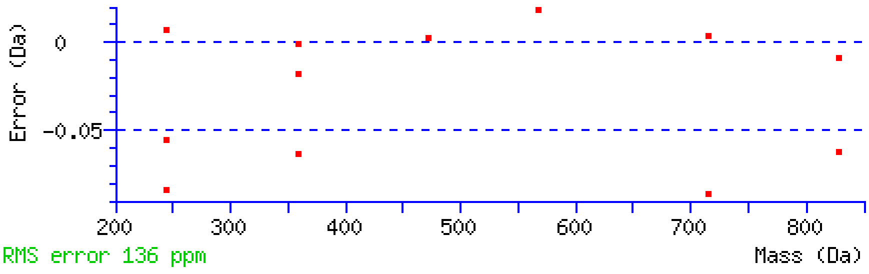
Match to Query 9497: 958.559708 from(480.287130,2+) rtinseconds(4684) index(61046)
Title: Locus:1.1.1.3220.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

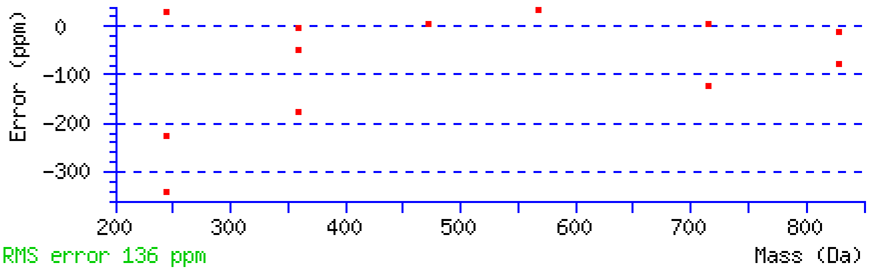
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 958.556152
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P2      : Oxidation (P)
Ions Score: 58  Expect: 8.6e-006
Matches : 12/28 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	#
1	132.047761	66.527518	M			8
2	***245.095440***	123.051358	P	**828.522954**	414.765115	7
3	***358.179504***	179.593390	I	**715.475275**	358.241276	6
4	***471.263568***	236.135422	I	602.391211	301.699244	5
5	***568.316332***	284.661804	P	489.307147	245.157211	4
6	***715.384746***	358.196011	F	392.254383	196.630829	3
7	***828.468810***	414.738043	L	**245.185969**	123.096623	2
8			L	132.101905	66.554590	1





NCBI **BLAST** search of MPIIPFLL
(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	958.556152	0.003556	MPIIPFLL
58.4	958.556152	0.003556	MPIIPFLL
25.1	958.556152	0.003556	MPIIPFLL
14.1	958.552124	0.007584	MPIVDKLK
8.9	958.563339	-0.003631	MLSQKPKK
7.7	958.552109	0.007599	MLVENILK
5.7	958.552109	0.007599	CALLILDK
4.0	958.552124	0.007584	MPIVDKLK
0.9	958.559998	-0.000290	VPPPPPIAR

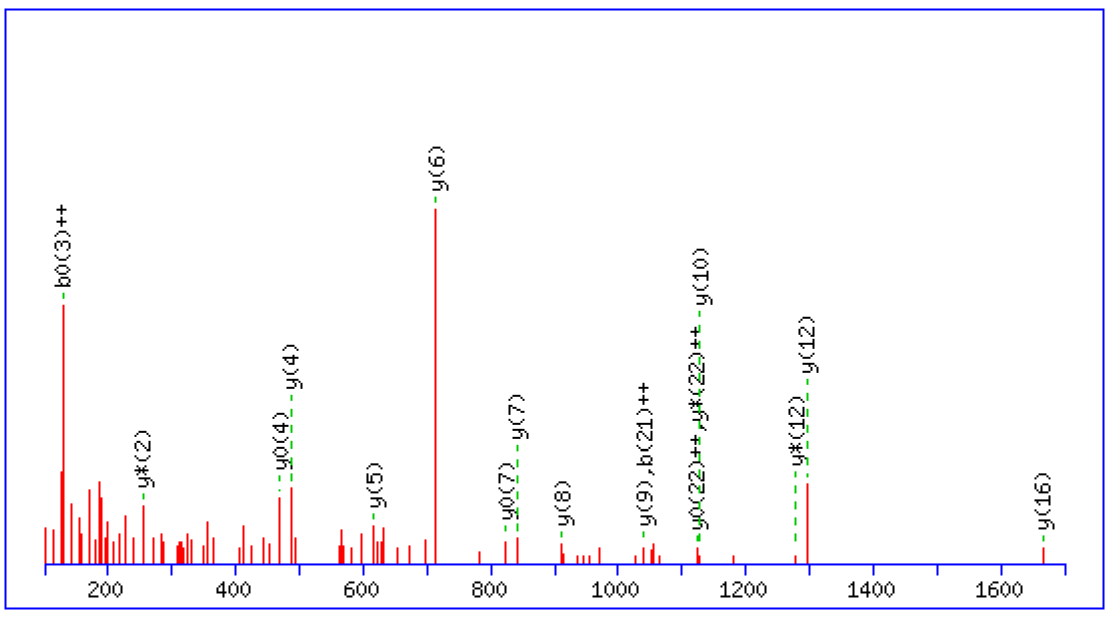
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGEGKPQGEGKPASQAKPESQPR**
Found in **TCAL3_HUMAN**, Transcription elongation factor A protein-like 3 OS=Homo sapiens GN=TCEAL3 PE=1 SV=1

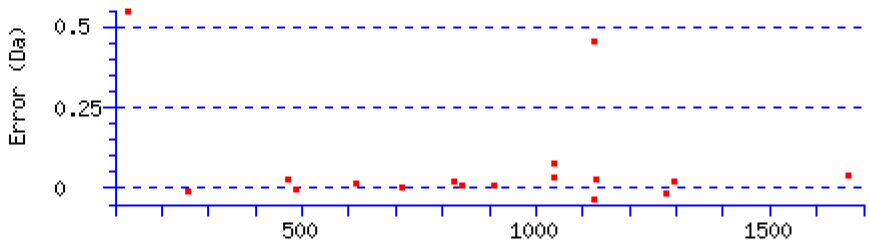
Match to Query 67222: 2478.190070 from(496.645290,5+) rtinseconds(712) index(122)
Title: Locus:1.1.1.1760.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

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 ●

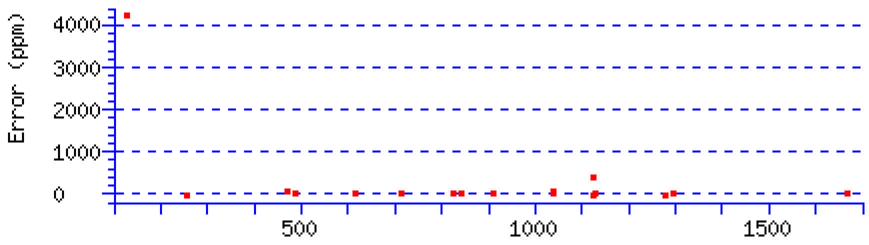


Monoisotopic mass of neutral peptide Mr(calc): 2478.209854
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 7.6e-005
Matches : 17/260 fragment ions using 25 most intense peaks (help)

#	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							24
2	217.081897	109.044586			199.071332	100.039304	E	2392.185143	1196.596209	2375.158594	1188.082935	2374.174578	1187.590927	23
3	274.103361	137.555319			256.092796	128.550036	G	2263.142550	1132.074913	2246.116001	1123.561638	2245.131985	1123.069630	22
4	403.145954	202.076615			385.135389	193.071333	E	2206.121086	1103.564181	2189.094537	1095.050906	2188.110521	1094.558898	21
5	460.167418	230.587347			442.156853	221.582065	G	2077.078493	1039.042884	2060.051944	1030.529610	2059.067928	1030.037602	20
6	588.262381	294.634829	571.235832	286.121554	570.251816	285.629546	K	2020.057029	1010.532153	2003.030480	1002.018878	2002.046464	1001.526870	19
7	685.315145	343.161211	668.288596	334.647936	667.304580	334.155928	P	1891.962066	946.484671	1874.935517	937.971397	1873.951501	937.479389	18
8	813.373723	407.190500	796.347174	398.677225	795.363158	398.185217	Q	1794.909302	897.958289	1777.882753	889.445015	1776.898737	888.953007	17
9	870.395187	435.701232	853.368638	427.187957	852.384622	426.695949	G	***1666.850724***	833.929000	1649.824175	825.415726	1648.840159	824.923718	16
10	999.437780	500.222528	982.411231	491.709254	981.427215	491.217246	E	1609.829260	805.418268	1592.802711	796.904994	1591.818695	796.412986	15
11	1056.459244	528.733260	1039.432695	520.219986	1038.448679	519.727978	G	1480.786667	740.896972	1463.760118	732.383697	1462.776102	731.891689	14
12	1184.554207	592.780742	1167.527658	584.267467	1166.543642	583.775459	K	1423.765203	712.386240	1406.738654	703.872965	1405.754638	703.380957	13
13	1281.606971	641.307124	1264.580422	632.793849	1263.596406	632.301841	P	***1295.670240***	648.338758	1278.643691	639.825484	1277.659675	639.333476	12
14	1352.644085	676.825681	1335.617536	668.312406	1334.633520	667.820398	A	1198.617476	599.812376	1181.590927	591.299102	1180.606911	590.807094	11
15	1439.676113	720.341695	1422.649564	711.828420	1421.665548	711.336412	S	***1127.580362***	564.293819	1110.553813	555.780545	1109.569797	555.288537	10
16	1567.734691	784.370984	1550.708142	775.857709	1549.724126	775.365701	Q	***1040.548334***	520.777805	1023.521785	512.264531	1022.537769	511.772523	9
17	1638.771805	819.889541	1621.745256	811.376266	1620.761240	810.884258	A	***912.489756***	456.748516	895.463207	448.235242	894.479191	447.743234	8
18	1766.866768	883.937022	1749.840219	875.423748	1748.856203	874.931740	K	***841.452642***	421.229959	824.426093	412.716685	823.442077	412.224677	7
19	1863.919532	932.463404	1846.892983	923.950130	1845.908967	923.458122	P	***713.357679***	357.182478	696.331130	348.669203	695.347114	348.177195	6
20	1992.962125	996.984701	1975.935576	988.471426	1974.951560	987.979418	E	***616.304915***	308.656096	599.278366	300.142821	598.294350	299.650813	5
21	2079.994153	1040.500715	2062.967604	1031.987440	2061.983588	1031.495432	S	***487.262322***	244.134799	470.235773	235.621525	469.251757	235.129517	4
22	2208.052731	1104.530004	2191.026182	1096.016729	2190.042166	1095.524721	Q	400.230294	200.618785	383.203745	192.105511			3
23	2305.105495	1153.056386	2288.078946	1144.543111	2287.094930	1144.051103	P	272.171716	136.589496	255.145167	128.076221			2
24							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 1032 ppm



RMS error 1032 ppm

NCBI **BLAST** search of SEGEGKPQGEGKPASQAKPESQPR
(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	2478.209854	-0.019784	SEGEGKPQGEGKPASQAKPESQPR
3.1	2478.173004	0.017066	IQVQDLMQQLEKQNSEMEQK
1.9	2478.188934	0.001136	QGLLGAYHDEACFSLAIPFDPK
1.8	2478.188934	0.001136	QGLLGAYHDEACFSLAIPFDPK
1.5	2478.177536	0.012534	GEAGDPGPPGLPAYSPHPSLAKGAR
1.5	2478.180878	0.009192	GLPPSSPMVSSAHNPNKAEIPER
1.3	2478.206711	-0.016641	FPLEEPGPRPLPWPPGSDEVAK
1.1	2478.206711	-0.016641	FPLEEPGPRPLPWPPGSDEVAK
1.1	2478.206711	-0.016641	FPLEEPGPRPLPWPPGSDEVAK
0.6	2478.180878	0.009192	GLPPSSPMVSSAHNPNKAEIPER

Mascot: http://www.matrixscience.com/

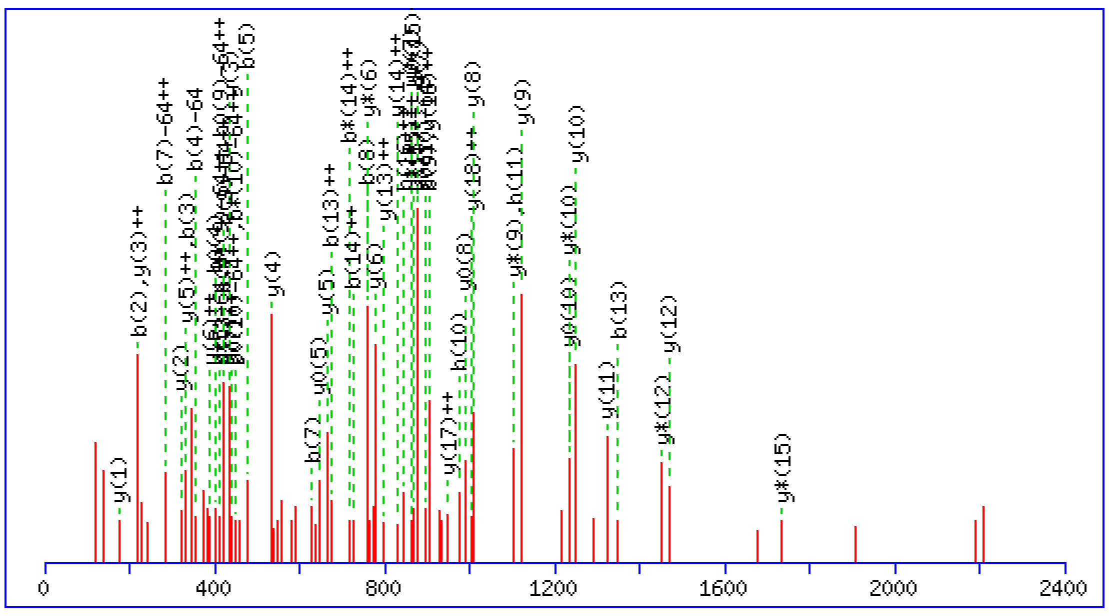
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AMLSGPGQFAENETNEVNFR**
Found in **ELOC_HUMAN**, Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1

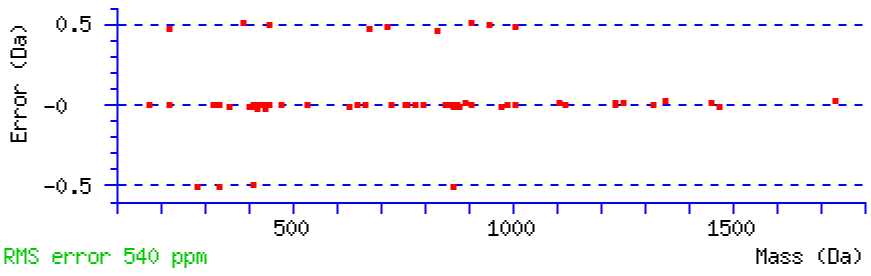
Match to Query 20586: 2225.992812 from(743.004880,3+) rtinseconds(2795) index(9767)
Title: Locus:1.1.1.3080.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

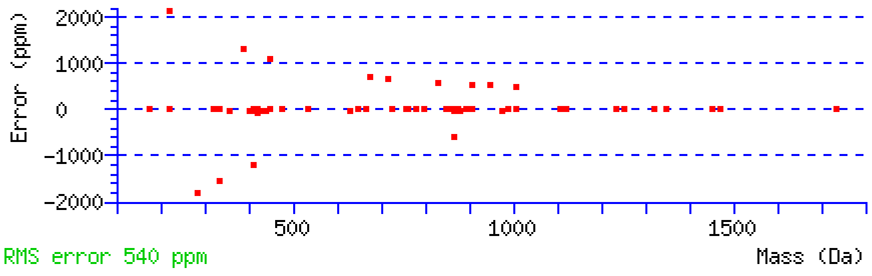
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2226.001129
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: 85  Expect: 1.6e-008
Matches : 58/298 fragment ions using 78 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	**219.079790**	110.043533					M	2155.971309	1078.489292	2138.944760	1069.976018	2137.960744	1069.484010	19
3	**332.163854**	166.585565					L	2008.935909	1004.971593	1991.909360	996.458318	1990.925344	995.966310	18
4	**419.195882**	210.101579			401.185317	201.096296	S	1895.851845	948.429560	1878.825296	939.916286	1877.841280	939.424278	17
5	**476.217346**	238.612311			458.206781	229.607028	G	1808.819817	904.913547	1791.793268	896.400272	1790.809252	895.908264	16
6	573.270110	287.138693			555.259545	278.133410	P	1751.798353	876.402815	1734.771804	867.889540	1733.787788	867.397532	15
7	**630.291574**	315.649425			612.281009	306.644142	G	1654.745589	827.876433	1637.719040	819.363158	1636.735024	818.871150	14
8	**758.350152**	379.678714	741.323603	371.165439	740.339587	370.673431	Q	1597.724125	799.365701	1580.697576	790.852426	1579.713560	790.360418	13
9	**905.418566**	453.212921	888.392017	444.699646	887.408001	444.207638	F	***1469.665547***	735.336412	1452.638998	726.823137	1451.654982	726.331129	12
10	**976.455680**	488.731478	959.429131	480.218203	958.445115	479.726195	A	***1322.597133***	661.802205	1305.570584	653.288930	1304.586568	652.796922	11
11	**1105.498273**	553.252774	1088.471724	544.739500	1087.487708	544.247492	E	***1251.560019***	626.283648	1234.533470	617.770373	1233.549454	617.278365	10
12	1219.541200	610.274238	1202.514651	601.760964	1201.530635	601.268955	N	***1122.517426***	561.762351	1105.490877	553.249077	1104.506861	552.757069	9
13	**1348.583793**	**674.795535**	1331.557244	666.282260	1330.573228	665.790252	E	***1008.474499***	504.740888	991.447950	496.227613	990.463934	495.735605	8
14	1449.631472	**725.319374**	1432.604923	716.806100	1431.620907	716.314092	T	***879.431906***	440.219591	862.405357	431.706317	861.421341	431.214309	7
15	1563.674399	782.340838	1546.647850	773.827563	1545.663834	773.335555	N	***778.384227***	389.695752	761.357678	381.182477	760.373662	380.690469	6
16	1692.716992	**846.862134**	1675.690443	838.348860	1674.706427	837.856851	E	***664.341300***	332.674288	647.314751	324.161014	646.330735	323.669006	5
17	1791.785406	896.396341	1774.758857	887.883067	1773.774841	887.391058	V	***535.298707***	268.152992	518.272158	259.639717			4
18	1905.828333	953.417804	1888.801784	944.904530	1887.817768	944.412522	N	***436.230293***	218.618784	419.203744	210.105510			3
19	2052.896747	1026.952011	2035.870198	1018.438737	2034.886182	1017.946729	F	***322.187366***	161.597321	305.160817	153.084047			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of AMLSGPGQFAENETNEVNFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
85.2	2226.001129	-0.008317	AMLSGPGQFAENETNEVNFR
63.1	2226.001129	-0.008317	AMLSGPGQFAENETNEVNFR
2.1	2225.992416	0.000396	DSDTGDDQPDILEPPEVAAAR
1.4	2225.992416	0.000396	DSDTGDDQPDILEPPEVAAAR

Mascot: http://www.matrixscience.com/

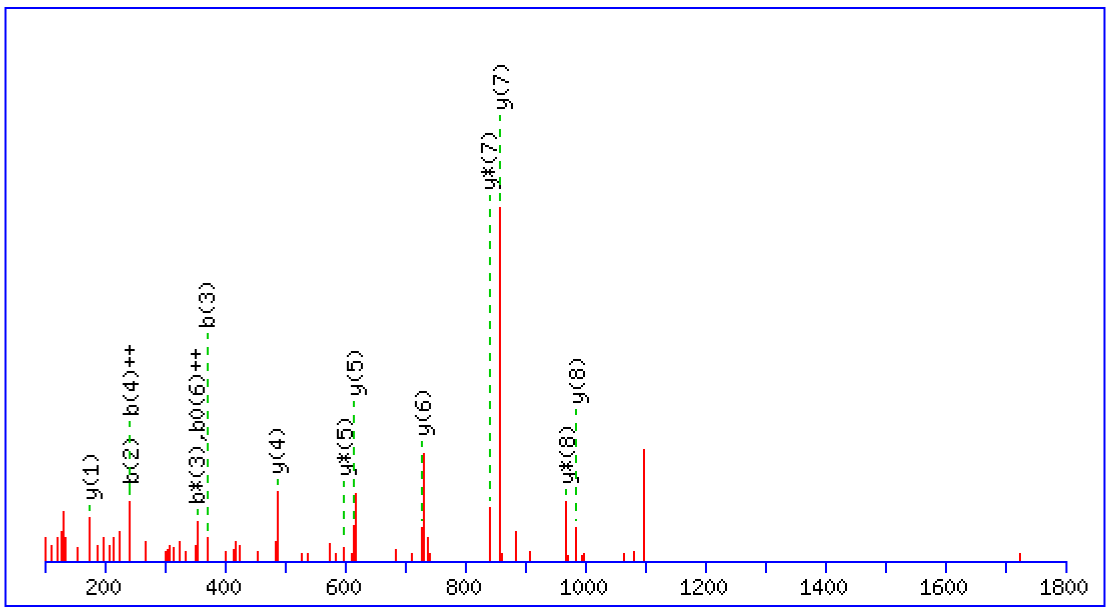
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQELEIQAR**
Found in **TFEC_HUMAN**, Transcription factor EC OS=Homo sapiens GN=TFEC PE=1 SV=1

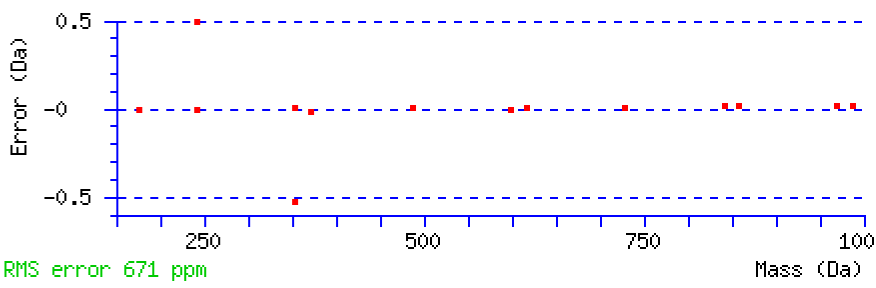
Match to Query 12995: 1098.608648 from(550.311600,2+) rtinseconds(1975) index(22225)
Title: Locus:1.1.1.2253.17
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-3.mgf

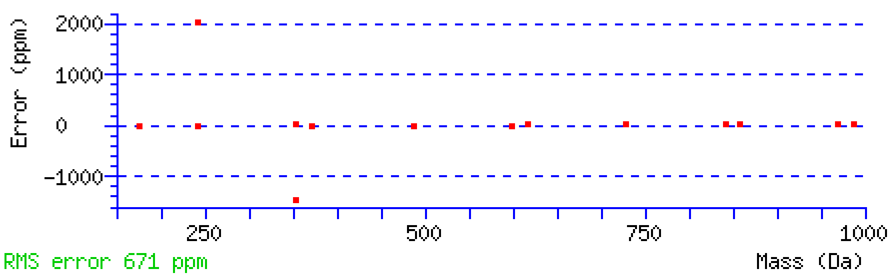
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1098.603287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00044
Matches : 14/82 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							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
44.1	1098.603287	0.005361	IQELEIQAR
21.8	1098.614517	-0.005869	IQQAKNEIR
8.2	1098.614532	-0.005884	KLQPSLNSGR
7.7	1098.614548	-0.005900	KPSRIPTPR
7.1	1098.610703	-0.002055	IQPLDVCIK
6.9	1098.603302	0.005346	LKPTNPAAQK
6.9	1098.614532	-0.005884	LRTELPAGAR
6.3	1098.614517	-0.005869	KLQALNADAR
6.2	1098.603302	0.005346	LQQQINEVK
5.8	1098.603317	0.005331	LQGTLPVEAR

Mascot: http://www.matrixscience.com/

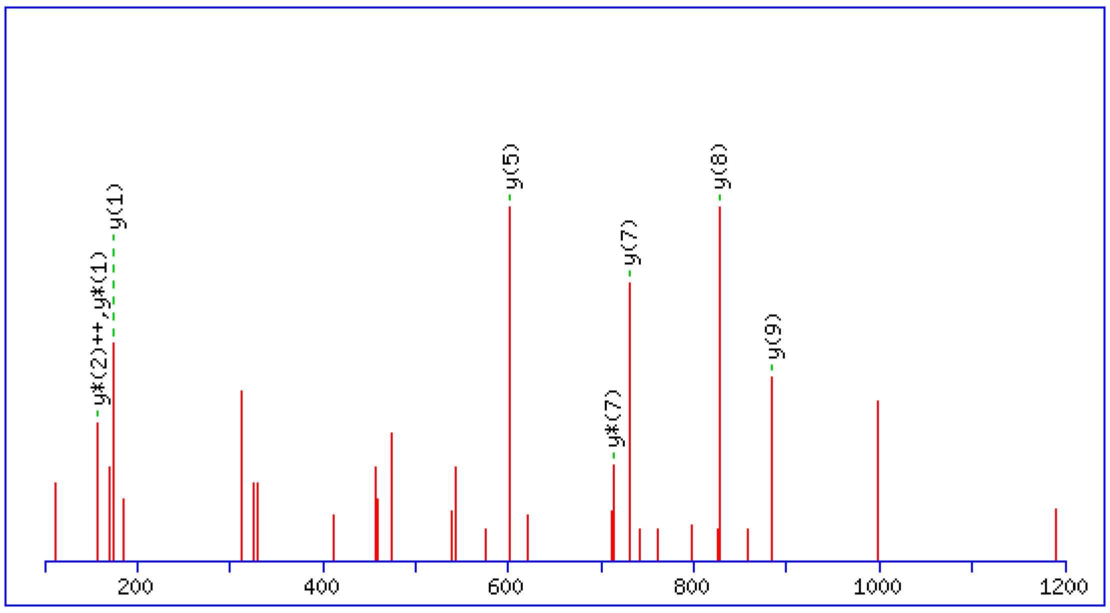
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGPAGASLRR**
Found in **SP8_HUMAN**, Transcription factor Sp8 OS=Homo sapiens GN=SP8 PE=2 SV=3

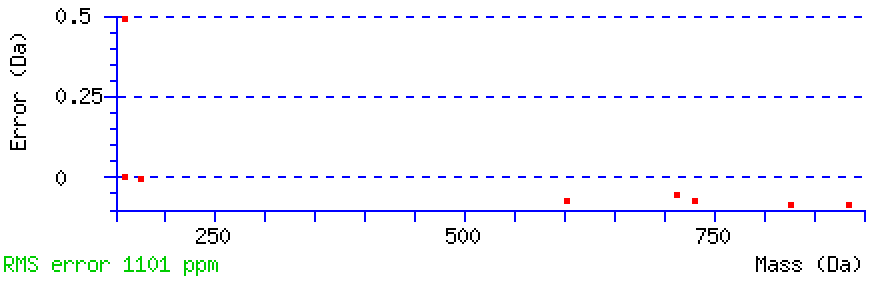
Match to Query 12070: 996.587488 from(499.301020,2+) rtinseconds(1017) index(2933)
Title: Locus:1.1.1.1828.16
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

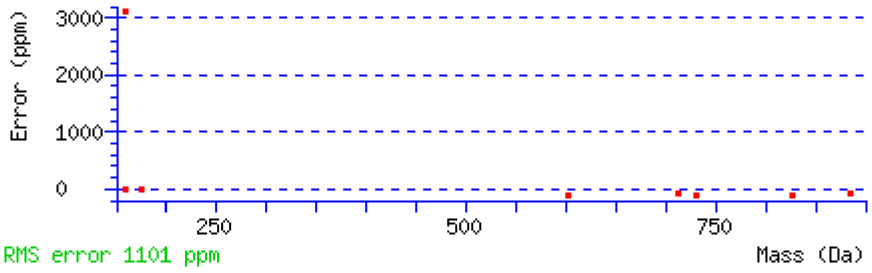
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 996.582840
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 31  Expect: 0.0053
Matches : 8/74 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							10
2	171.112804	86.060040					G	***884.506075***	442.756675	867.479526	434.243401	866.495510	433.751393	9
3	268.165568	134.586422					P	***827.484611***	414.245943	810.458062	405.732669	809.474046	405.240661	8
4	339.202682	170.104979					A	***730.431847***	365.719562	713.405298	357.206287	712.421282	356.714279	7
5	396.224146	198.615711					G	659.394733	330.201005	642.368184	321.687730	641.384168	321.195722	6
6	467.261260	234.134268					A	***602.373269***	301.690272	585.346720	293.176998	584.362704	292.684990	5
7	554.293288	277.650282			536.282723	268.644999	S	531.336155	266.171716	514.309606	257.658441	513.325590	257.166433	4
8	667.377352	334.192314			649.366787	325.187031	L	444.304127	222.655701	427.277578	214.142427			3
9	823.478463	412.242869	806.451914	403.729595	805.467898	403.237587	R	331.220063	166.113669	314.193514	157.600395			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LGPAGASLRR
(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	996.582840	0.004648	LGPAGASLRR
17.5	996.582855	0.004633	LGQPLTGRR
3.4	996.596771	-0.009283	IPLITATPR

Mascot: http://www.matrixscience.com/

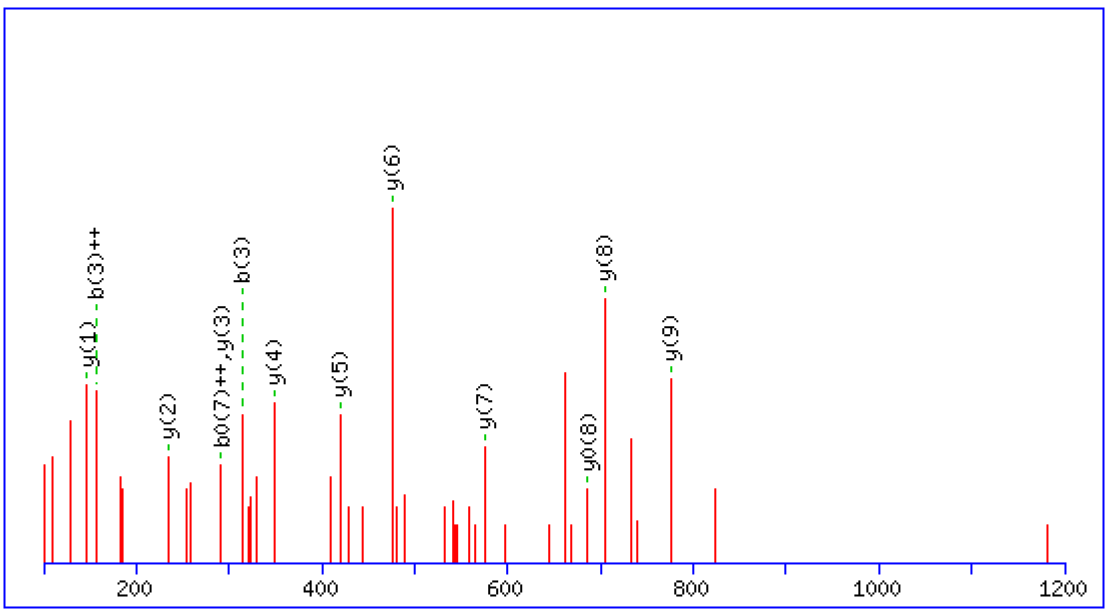
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAEVGAGGSK**
Found in **PURB_HUMAN**, Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3

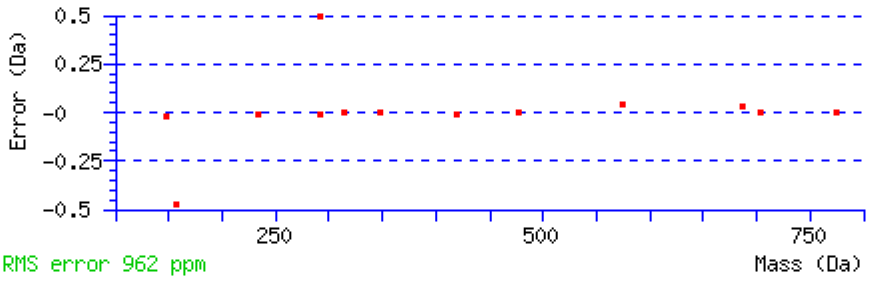
Match to Query 5476: 887.466308 from(444.740430,2+) rtinseconds(895) index(484)
Title: Locus:1.1.1.1928.2
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

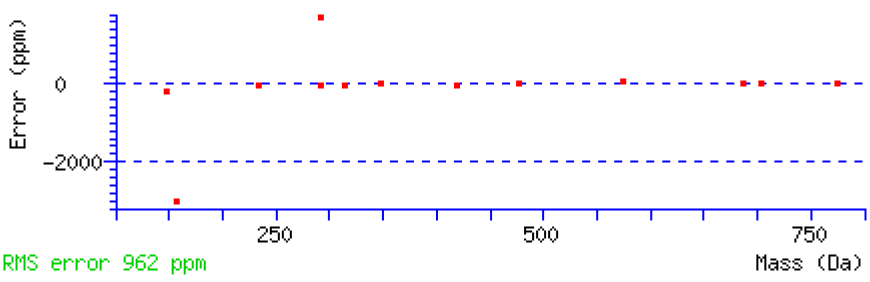
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 887.471237
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 84  Expect: 6.3e-008
Matches : 13/84 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							10
2	185.128454	93.067865			A	*775.394459*	388.200868	758.367910	379.687593	757.383894	379.195585	9
3	314.171047	157.589161	296.160482	148.583879	E	*704.357345*	352.682311	687.330796	344.169036	686.346780	343.677028	8
4	413.239461	207.123369	395.228896	198.118086	V	*575.314752*	288.161014	558.288203	279.647740	557.304187	279.155732	7
5	470.260925	235.634100	452.250360	226.628818	G	*476.246338*	238.626807	459.219789	230.113532	458.235773	229.621524	6
6	541.298039	271.152658	523.287474	262.147375	A	*419.224874*	210.116075	402.198325	201.602801	401.214309	201.110793	5
7	598.319503	299.663390	580.308938	290.658107	G	*348.187760*	174.597518	331.161211	166.084244	330.177195	165.592236	4
8	655.340967	328.174122	637.330402	319.168839	G	*291.166296*	146.086786	274.139747	137.573512	273.155731	137.081504	3
9	742.372995	371.690136	724.362430	362.684853	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 IAEVGAGGSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
84.2	887.471237	-0.004929	IAEVGAGGSK
11.6	887.471222	-0.004914	ILSNNPSK
8.2	887.459976	0.006332	AIEADIEK
6.7	887.471222	-0.004914	ELANQVSK
6.7	887.471222	-0.004914	LAANISGDK
4.9	887.471222	-0.004914	LISDANQK
4.8	887.460007	0.006301	IPSSPDLK
4.3	887.459976	0.006332	IAGLEEEK
4.0	887.471237	-0.004929	LATPGNTAK
3.5	887.459991	0.006317	ISPEGLEK

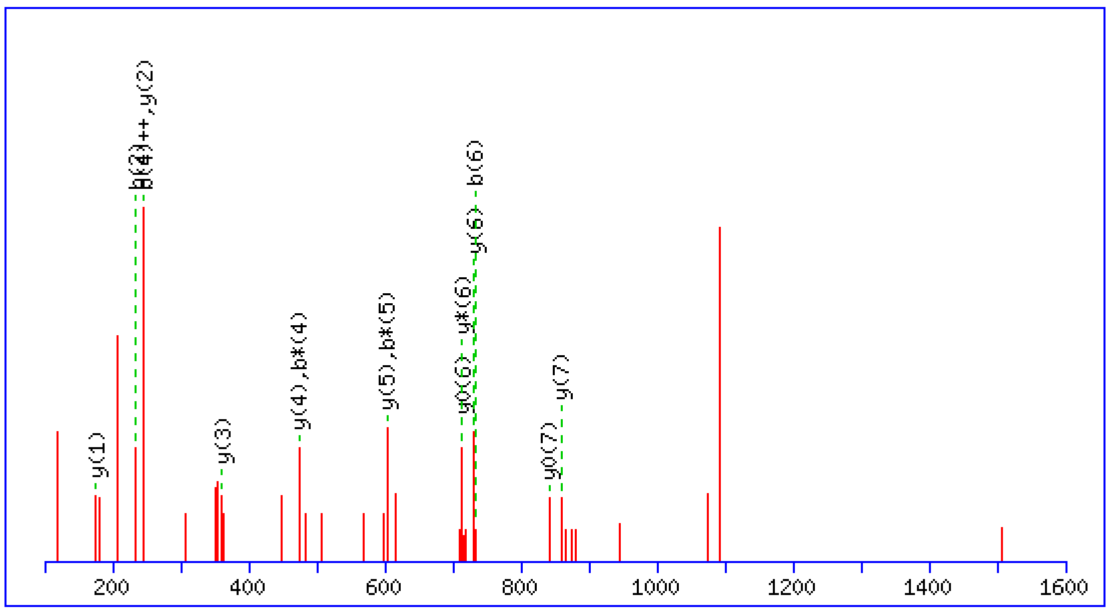
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFQQELDAR**
Found in **TSNAX_HUMAN**, Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1

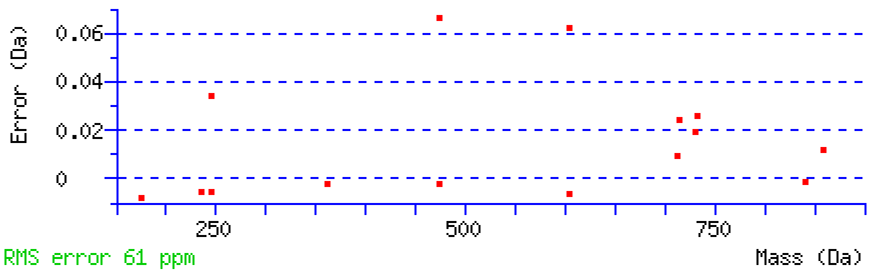
Match to Query 17416: 1092.524308 from(547.269430,2+) rtinseconds(1921) index(21025)
Title: Locus:1.1.1.2116.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

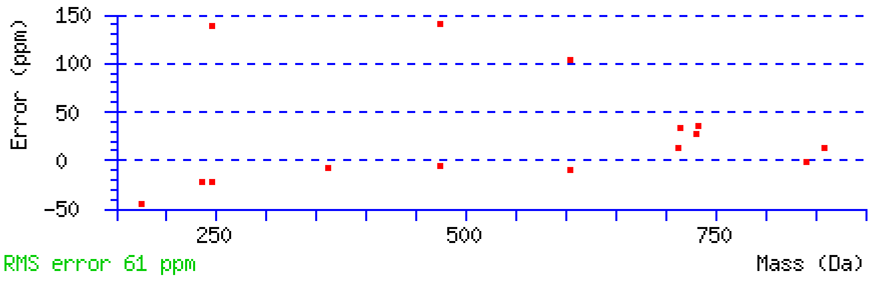
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1092.519974
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 46 **Expect:** 0.00035
Matches : 15/88 fragment ions using 25 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							9
2	**235.107718**	118.057497			217.097153	109.052214	F	1006.495236	503.751256	989.468687	495.237982	988.484671	494.745974	8
3	363.166296	182.086786	346.139747	173.573512	345.155731	173.081504	Q	***859.426822***	430.217049	842.400273	421.703775	841.416257	421.211767	7
4	491.224874	246.116075	474.198325	237.602801	473.214309	237.110793	Q	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.182478	6
5	620.267467	310.637372	603.240918	302.124097	602.256902	301.632089	E	***603.309666***	302.158471	586.283117	293.645197	585.299101	293.153189	5
6	**733.351531**	367.179404	716.324982	358.666129	715.340966	358.174121	L	***474.267073***	237.637174	457.240524	229.123900	456.256508	228.631892	4
7	848.378474	424.692875	831.351925	416.179601	830.367909	415.687593	D	***361.183009***	181.095142	344.156460	172.581868	343.172444	172.089860	3
8	919.415588	460.211432	902.389039	451.698158	901.405023	451.206150	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 SFQQELDAR
(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	1092.519974	0.004334	SFQQELDAR
26.1	1092.523331	0.000977	MNTQEAKQK
10.1	1092.523346	0.000962	QMSQQNLTK
9.4	1092.524002	0.000306	EPYPDFVAR
8.5	1092.534576	-0.010268	MSSQKGNVAR
5.3	1092.519958	0.004350	AQYEDIAQR
4.9	1092.523331	0.000977	MAAAETQSLR
4.6	1092.534561	-0.010253	MSALQESRR
1.3	1092.520844	0.003464	MRYHMPVK
1.3	1092.520844	0.003464	MRYHMPVK

Mascot: http://www.matrixscience.com/

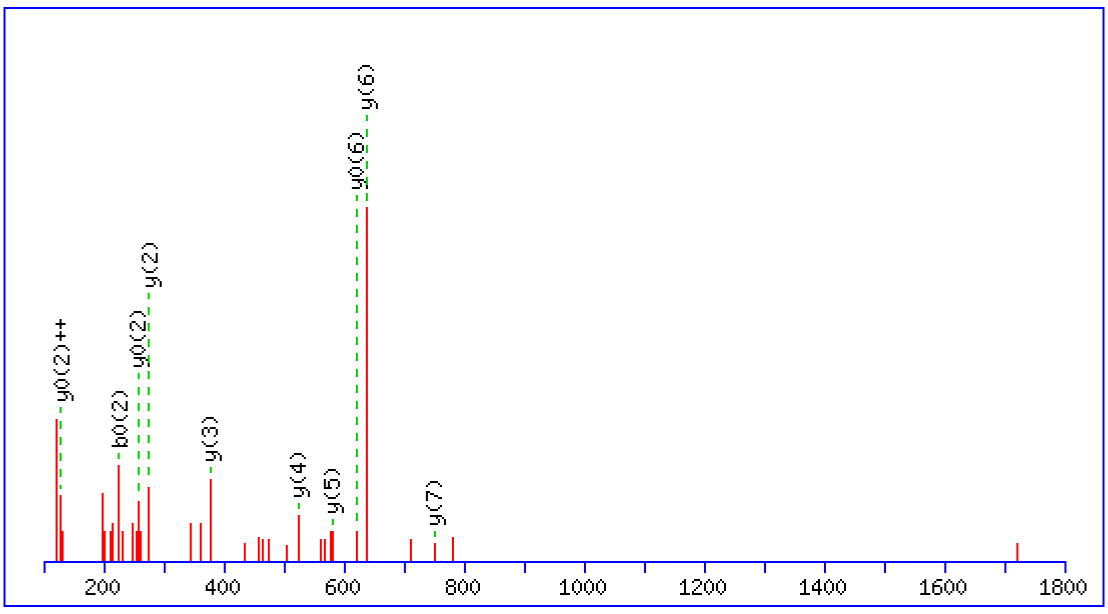
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGGFTEK**
Found in **TSPOA_HUMAN**, Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3

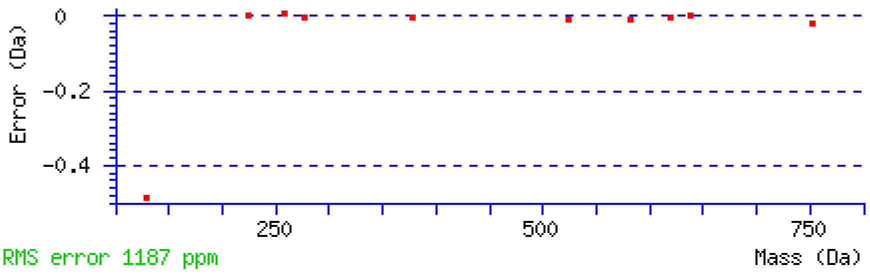
Match to Query 4262: 879.432548 from(440.723550,2+) rtinseconds(1673) index(7343)
Title: Locus:1.1.1.2135.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

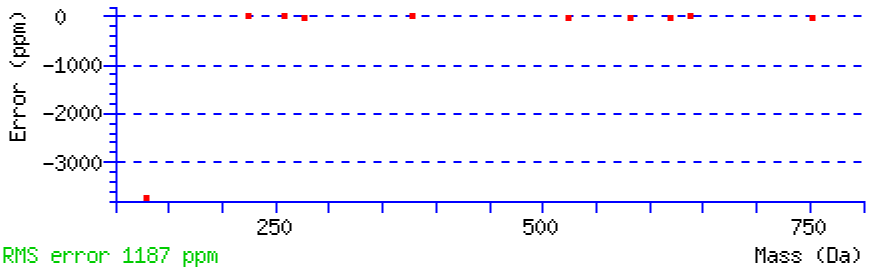
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 879.433792
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0021
Matches : 10/68 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							8
2	243.133933	122.070605	225.123368	113.065322	L	***751.398482***	376.202879	734.371933	367.689605	733.387917	367.197597	7
3	300.155397	150.581336	282.144832	141.576054	G	***638.314418***	319.660847	621.287869	311.147573	620.303853	310.655565	6
4	357.176861	179.092068	339.166296	170.086786	G	***581.292954***	291.150115	564.266405	282.636841	563.282389	282.144833	5
5	504.245275	252.626275	486.234710	243.620993	F	***524.271490***	262.639383	507.244941	254.126109	506.260925	253.634101	4
6	605.292954	303.150115	587.282389	294.144833	T	***377.203076***	189.105176	360.176527	180.591902	359.192511	180.099894	3
7	734.335547	367.671412	716.324982	358.666129	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 ELGGFTEK
(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	879.433792	-0.001244	ELGGFTEK
9.4	879.433777	-0.001229	ELNETFK
5.8	879.427246	0.005302	EIFNMAR
5.7	879.430618	0.001930	ELGKMMR
4.6	879.433777	-0.001229	EKSPPYK
4.3	879.433762	-0.001214	EKEAFEK
3.5	879.433777	-0.001229	QFSLEEK
1.8	879.430634	0.001914	QMVMSLR
0.5	879.433777	-0.001229	ELGPYSSK
0.3	879.433762	-0.001214	EEAFKEK

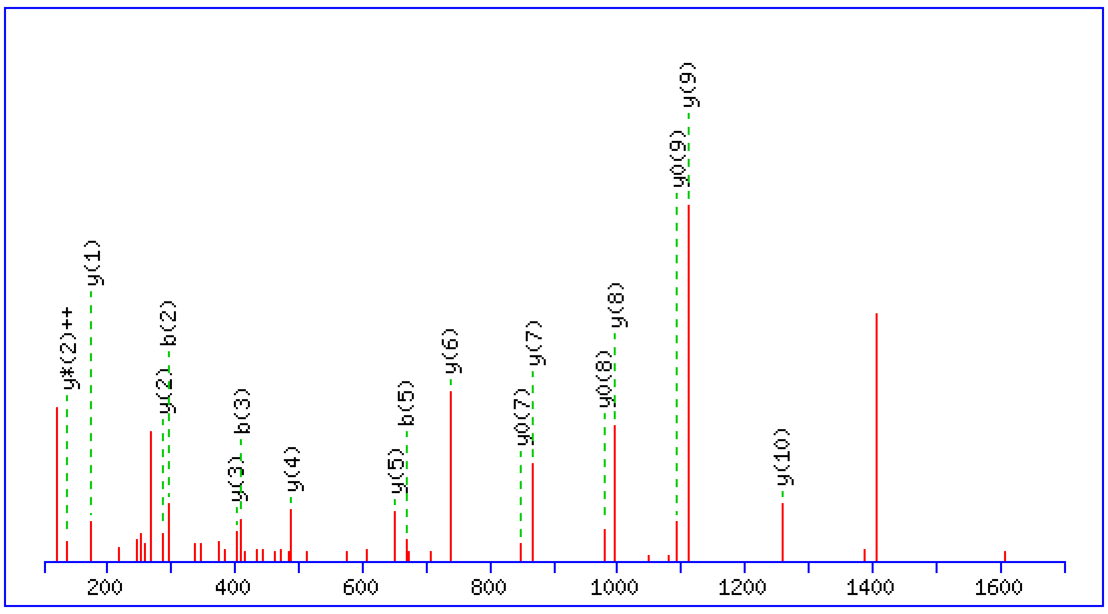
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FFDEESYSLLR**
Found in **SSRD_HUMAN**, Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1

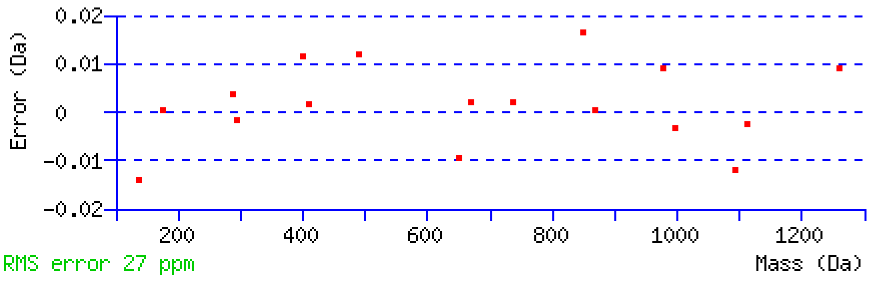
Match to Query 18218: 1404.657528 from(703.336040,2+) rtinseconds(3192) index(22395)
Title: Locus:1.1.1.2797.14
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

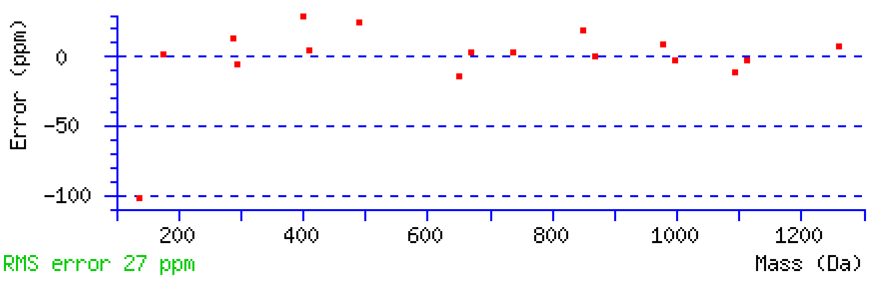
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1404.656128
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83  Expect: 3.5e-008
Matches : 17/90 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							11
2	**295.144104**	148.075690			F	***1258.595008***	629.801142	1241.568459	621.287867	1240.584443	620.795859	10
3	**410.171047**	205.589161	392.160482	196.583879	D	***1111.526594***	556.266935	1094.500045	547.753661	1093.516029	547.261652	9
4	539.213640	270.110458	521.203075	261.105176	E	***996.499651***	498.753463	979.473102	490.240189	978.489086	489.748181	8
5	**668.256233**	334.631755	650.245668	325.626472	E	***867.457058***	434.232167	850.430509	425.718892	849.446493	425.226884	7
6	755.288261	378.147769	737.277696	369.142486	S	***738.414465***	369.710870	721.387916	361.197596	720.403900	360.705588	6
7	918.351590	459.679433	900.341025	450.674151	Y	***651.382437***	326.194856	634.355888	317.681582	633.371872	317.189574	5
8	1005.383618	503.195447	987.373053	494.190164	S	***488.319108***	244.663192	471.292559	236.149917	470.308543	235.657909	4
9	1118.467682	559.737479	1100.457117	550.732196	L	***401.287080***	201.147178	384.260531	192.633903			3
10	1231.551746	616.279511	1213.541181	607.274228	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 FFDEESYSLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.2	1404.656128	0.001400	FFDEESYSLLR
3.5	1404.660172	-0.002644	MSQARQICPER
2.2	1404.655487	0.002041	MAAVDSDVESLPR
1.2	1404.666718	-0.009190	TEPDGAGTMNKLR
1.1	1404.653641	0.003887	IYFMPWTPYR
1.1	1404.653625	0.003903	IYYMPWTPYR
1.0	1404.656815	0.000713	FHADSVCKASNR
0.8	1404.653641	0.003887	IYFMPWTPYR

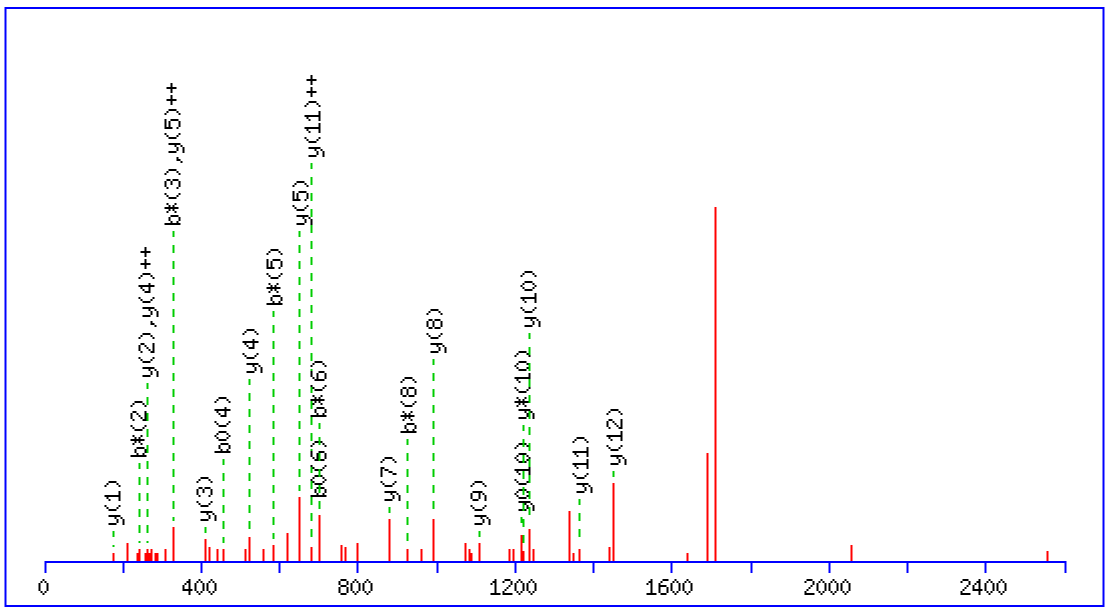
Mascot Search Results

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

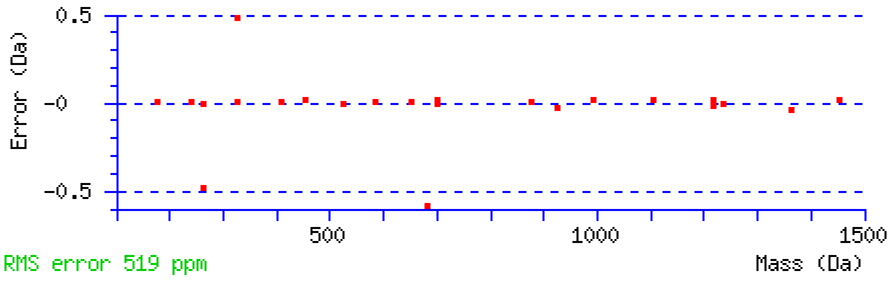
Match to Query 34206: 1706.822288 from(854.418420,2+) rtinseconds(3377) index(35520)
Title: Locus:1.1.1.2779.24
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

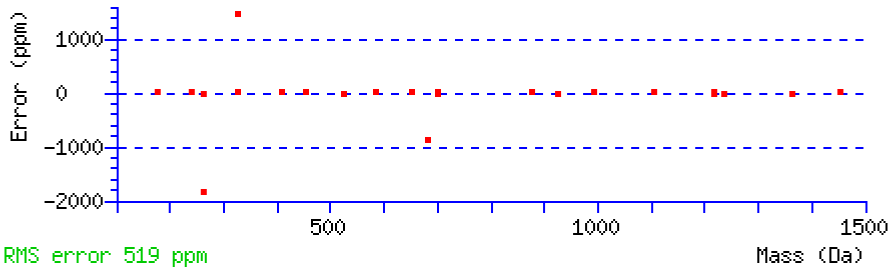
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1706.811127
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 6.9e-005
Matches : 23/150 fragment ions using 50 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
49.4	1706.811127	0.011161	QQSEEDLLLQDFSR
5.1	1706.829773	-0.007485	VVLASQPDLECGFSR

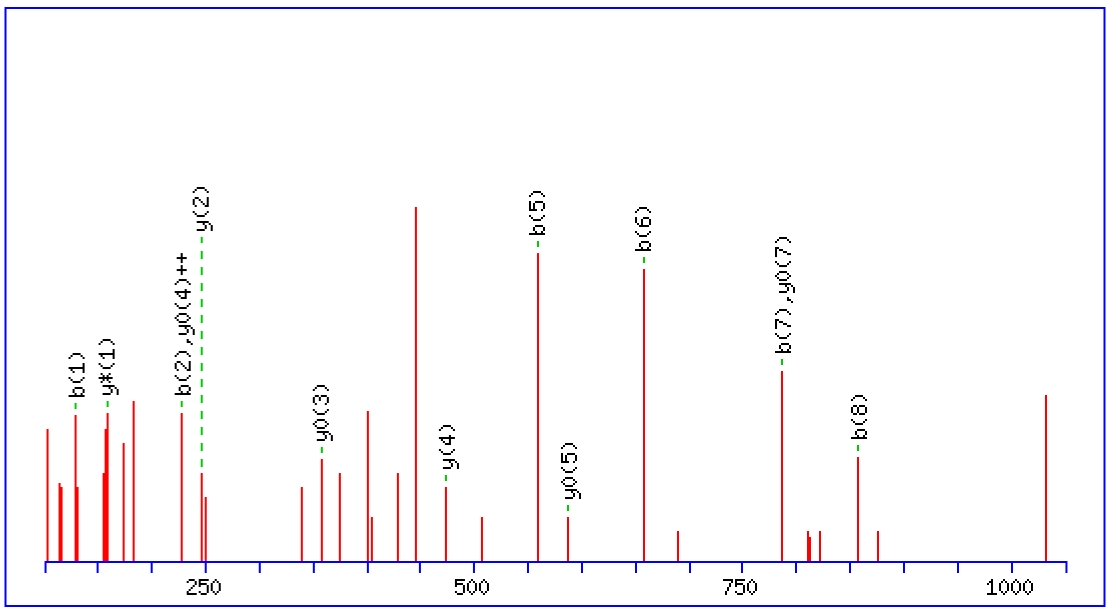
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVAQMVEAR**
Found in **TMC3_HUMAN**, Transmembrane channel-like protein 3 OS=Homo sapiens GN=TMC3 PE=1 SV=3

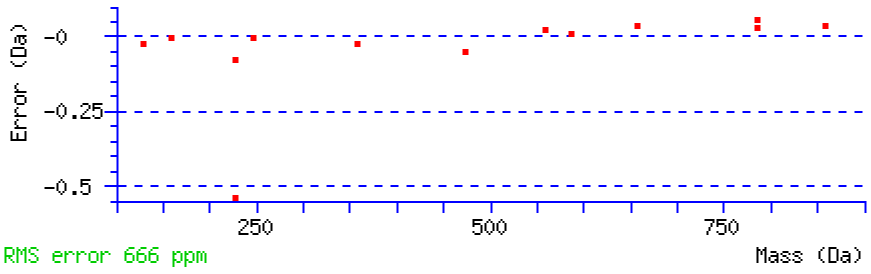
Match to Query 9446: 1030.551128 from(516.282840,2+) rtinseconds(1177) index(7061)
Title: Locus:1.1.1.1968.28
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

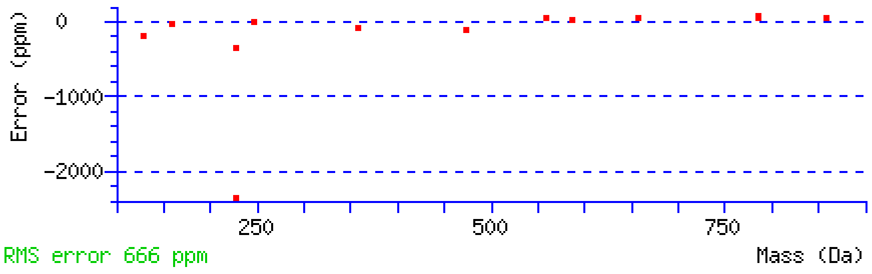
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1030.559326
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0042
Matches : 13/80 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	***129.102239***	65.054757	112.075690	56.541483			K							9
2	***228.170653***	114.588965	211.144104	106.075690			V	903.471664	452.239470	886.445115	443.726196	885.461099	443.234188	8
3	299.207767	150.107522	282.181218	141.594247			A	804.403250	402.705263	787.376701	394.191989	786.392685	393.699981	7
4	427.266345	214.136811	410.239796	205.623536			Q	733.366136	367.186706	716.339587	358.673432	715.355571	358.181424	6
5	***558.306830***	279.657053	541.280281	271.143779			M	605.307558	303.157417	588.281009	294.644143	587.296993	294.152135	5
6	***657.375244***	329.191260	640.348695	320.677986			V	**474.267073**	237.637174	457.240524	229.123900	456.256508	228.631892	4
7	***786.417837***	393.712557	769.391288	385.199282	768.407272	384.707274	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
8	***857.454951***	429.231114	840.428402	420.717839	839.444386	420.225831	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 KVAQMVEAR
(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	1030.559326	-0.008198	KVAQMVEAR
22.2	1030.551941	-0.000813	TSEGVLRNR
11.9	1030.559326	-0.008198	KVPSLCSAR
10.2	1030.551941	-0.000813	IGTEAGTRAR
6.6	1030.559311	-0.008183	KICELQAR
6.3	1030.551941	-0.000813	RASLSVQDR
6.1	1030.545410	0.005718	MSRPVRNR
5.1	1030.559326	-0.008198	INMISGPKR
3.3	1030.551941	-0.000813	RPSVSKEGR
3.1	1030.549423	0.001705	RCINIWR

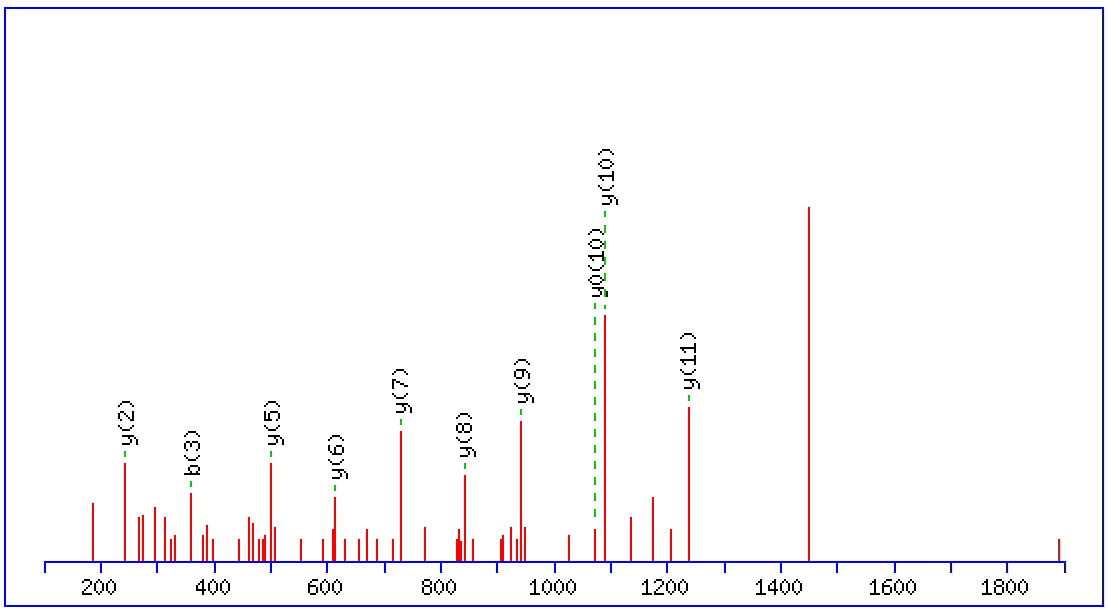
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVMFTIDIGEAPK**
Found in **TMED2_HUMAN**, Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1

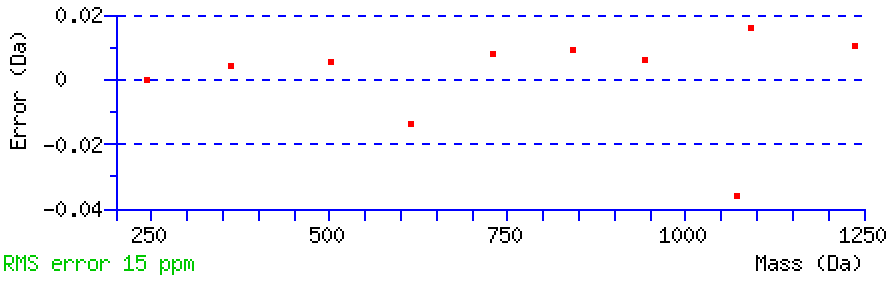
Match to Query 39112: 1448.767168 from(725.390860,2+) rtinseconds(3207) index(34642)
Title: Locus:1.1.1.2729.29
Data file 2011-11-14 - TFD - S 2-6.mgf

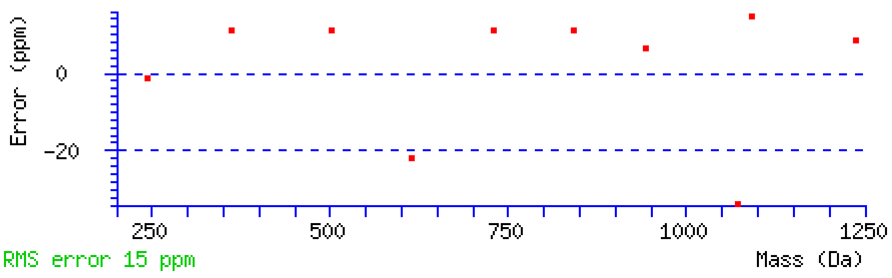
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1448.758499
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: 72  Expect: 2e-007
Matches : 10/154 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							13
2	213.159754	107.083515			V	1336.681717	668.844497	1319.655168	660.331222	1318.671152	659.839214	12
3	360.195154	180.601215			M	***1237.613303***	619.310290	1220.586754	610.797015	1219.602738	610.305007	11
4	507.263568	254.135422			F	***1090.577903***	545.792590	1073.551354	537.279315	1072.567338	536.787307	10
5	608.311247	304.659262	590.300682	295.653979	T	***943.509489***	472.258383	926.482940	463.745108	925.498924	463.253100	9
6	721.395311	361.201294	703.384746	352.196011	I	***842.461810***	421.734543	825.435261	413.221269	824.451245	412.729261	8
7	836.422254	418.714765	818.411689	409.709482	D	***729.377746***	365.192511	712.351197	356.679237	711.367181	356.187229	7
8	949.506318	475.256797	931.495753	466.251514	I	***614.350803***	307.679040	597.324254	299.165765	596.340238	298.673757	6
9	1006.527782	503.767529	988.517217	494.762247	G	***501.266739***	251.137008	484.240190	242.623733	483.256174	242.131725	5
10	1135.570375	568.288826	1117.559810	559.283543	E	444.245275	222.626275	427.218726	214.113001	426.234710	213.620993	4
11	1206.607489	603.807383	1188.596924	594.802100	A	315.202682	158.104979	298.176133	149.591704			3
12	1303.660253	652.333765	1285.649688	643.328482	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 IVMFTIDIGEAPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.9	1448.758499	0.008669	IVMFTIDIGEAPK
0.6	1448.755798	0.011370	VLGNYCRLGEVR

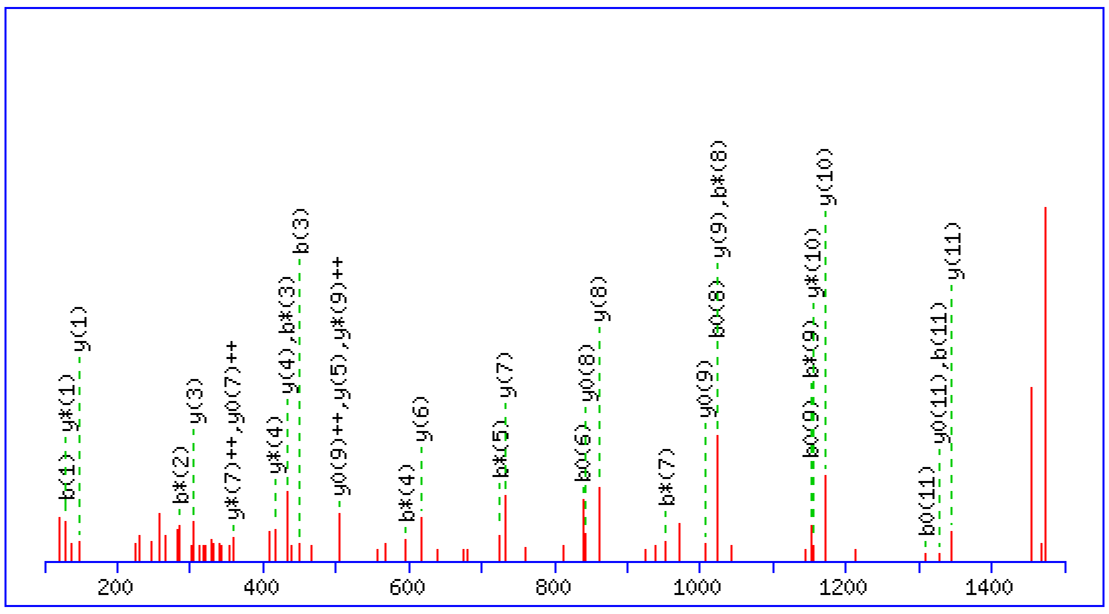
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCFYEDIAQGTK**
Found in **TMED7_HUMAN**, Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2

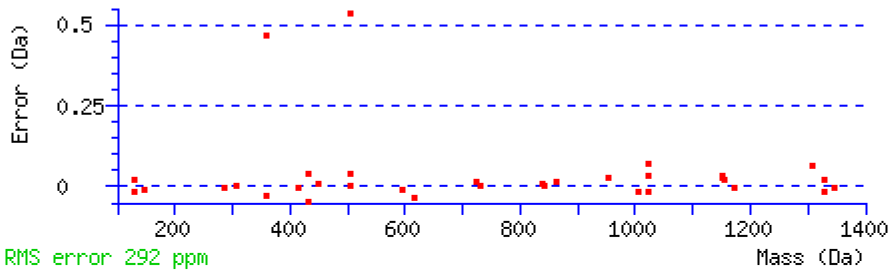
Match to Query 34129: 1472.673288 from(737.343920,2+) rtinseconds(2408) index(28535)
Title: Locus:1.1.1.2361.40
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

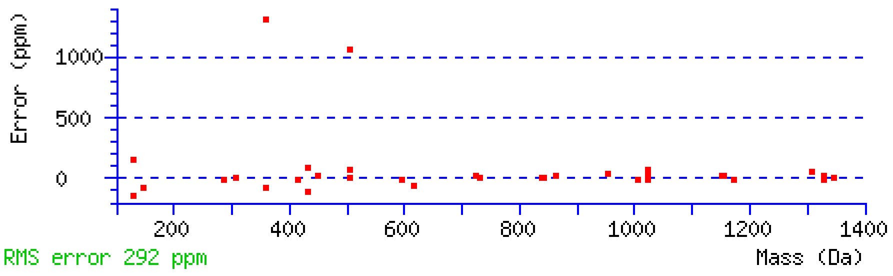
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1472.660568
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 69 **Expect:** 1.1e-006
Matches : 34/122 fragment ions using 47 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	303.112153	152.059714	286.085604	143.546440			C	***1345.609281***	673.308279	1328.582732	664.795004	1327.598716	664.302996	11
3	**450.180567**	225.593921	433.154018	217.080647			F	***1171.562982***	586.285129	1154.536433	577.771855	1153.552417	577.279847	10
4	613.243896	307.125586	596.217347	298.612311			Y	***1024.494568***	512.750922	1007.468019	504.237648	1006.484003	503.745640	9
5	742.286489	371.646883	725.259940	363.133608	724.275924	362.641600	E	***861.431239***	431.219258	844.404690	422.705983	843.420674	422.213975	8
6	857.313432	429.160354	840.286883	420.647079	839.302867	420.155071	D	***732.388646***	366.697961	715.362097	358.184687	714.378081	357.692679	7
7	970.397496	485.702386	953.370947	477.189111	952.386931	476.697103	I	***617.361703***	309.184490	600.335154	300.671215	599.351138	300.179207	6
8	1041.434610	521.220943	1024.408061	512.707669	1023.424045	512.215661	A	***504.277639***	252.642458	487.251090	244.129183	486.267074	243.637175	5
9	1169.493188	585.250232	1152.466639	576.736958	1151.482623	576.244950	Q	***433.240525***	217.123901	416.213976	208.610626	415.229960	208.118618	4
10	1226.514652	613.760964	1209.488103	605.247690	1208.504087	604.755682	G	***305.181947***	153.094611	288.155398	144.581337	287.171382	144.089329	3
11	**1327.562331**	664.284804	1310.535782	655.771529	1309.551766	655.279521	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 QCFYEDIAQGTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.7	1472.660568	0.012720	QCFYEDIAQGTK
6.2	1472.663910	0.009378	EKPYKCSTCEK
2.1	1472.685501	-0.012213	QEERIQEQEER
1.4	1472.685699	-0.012411	KEPQYLEMEFK

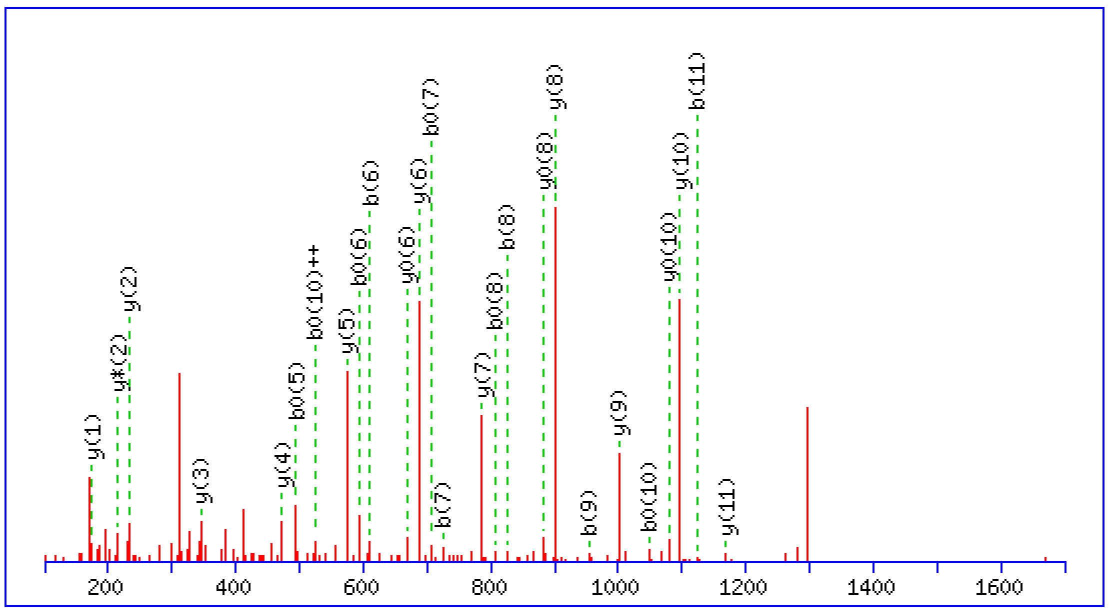
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAPVDVLTQIGR**
Found in **TM109_HUMAN**, Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1

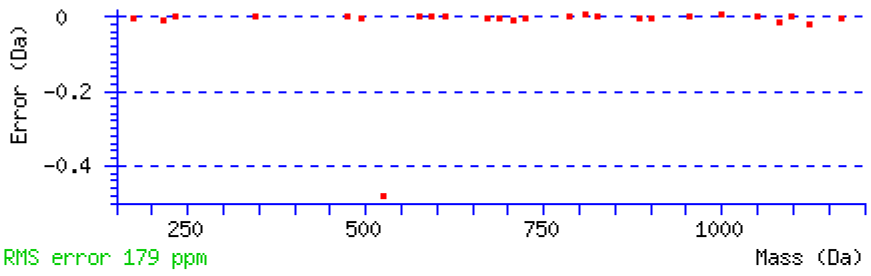
Match to Query 19136: 1296.707308 from(649.360930,2+) rtinseconds(3091) index(24083)
Title: Locus:1.1.1.2685.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-6.mgf

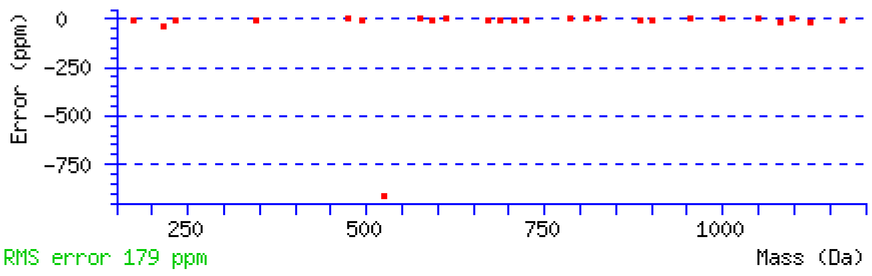
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1296.703766
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 108 **Expect:** 1.3e-010
Matches : 26/108 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	130.049869	65.528572			112.039304	56.523290	E							12
2	201.086983	101.047130			183.076418	92.041847	A	***1168.668450***	584.837863	1151.641901	576.324589	1150.657885	575.832580	11
3	298.139747	149.573512			280.129182	140.568229	P	***1097.631336***	549.319306	1080.604787	540.806032	1079.620771	540.314023	10
4	397.208161	199.107719			379.197596	190.102436	V	***1000.578572***	500.792924	983.552023	492.279650	982.568007	491.787642	9
5	512.235104	256.621190			494.224539	247.615908	D	***901.510158***	451.258717	884.483609	442.745443	883.499593	442.253435	8
6	**611.303518**	306.155397			593.292953	297.150115	V	***786.483215***	393.745246	769.456666	385.231971	768.472650	384.739963	7
7	**724.387582**	362.697429			706.377017	353.692147	L	***687.414801***	344.211039	670.388252	335.697764	669.404236	335.205756	6
8	**825.435261**	413.221269			807.424696	404.215986	T	***574.330737***	287.669007	557.304188	279.155732	556.320172	278.663724	5
9	**953.493839**	477.250558	936.467290	468.737283	935.483274	468.245275	Q	***473.283058***	237.145167	456.256509	228.631892			4
10	1066.577903	533.792590	1049.551354	525.279315	1048.567338	524.787307	I	***345.224480***	173.115878	328.197931	164.602603			3
11	**1123.599367**	562.303322	1106.572818	553.790047	1105.588802	553.298039	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 EAPVDVLTQIGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
107.9	1296.703766	0.003542	EAPVDVLTQIGR
8.4	1296.714966	-0.007658	EVLATPLENRR
3.8	1296.714966	-0.007658	SSHIVEASIRAK
1.8	1296.703751	0.003557	LLAEPAGGLVGER
0.1	1296.711151	-0.003843	MPLLSLHLDVK

Mascot: http://www.matrixscience.com/

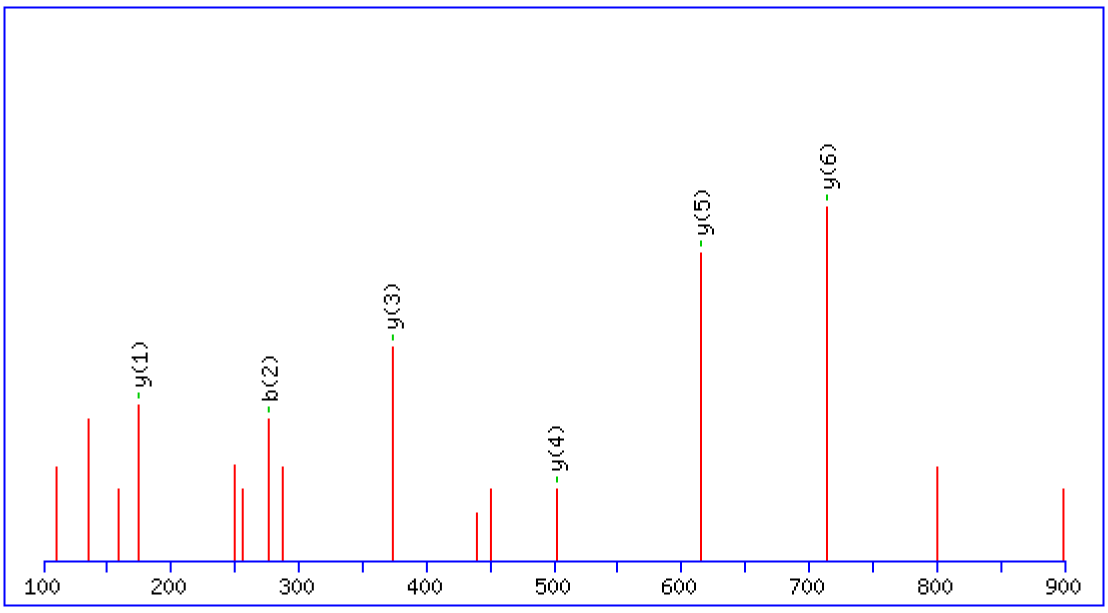
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YIVIEPTR**
Found in **TMM11_HUMAN**, Transmembrane protein 11, mitochondrial OS=Homo sapiens GN=TMEM11 PE=1 SV=1

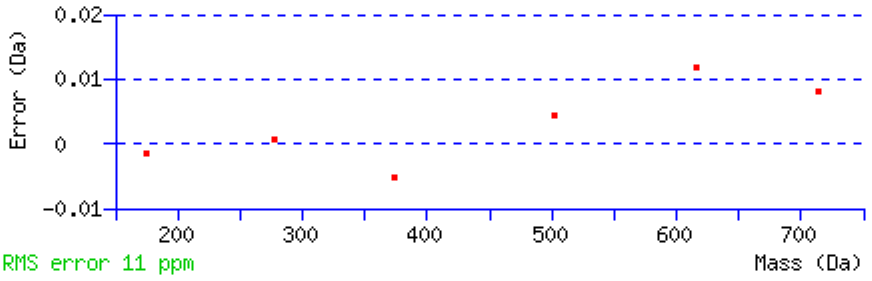
Match to Query 10071: 989.554828 from(495.784690,2+) rtinseconds(2060) index(13793)
Title: Locus:1.1.1.2283.12
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

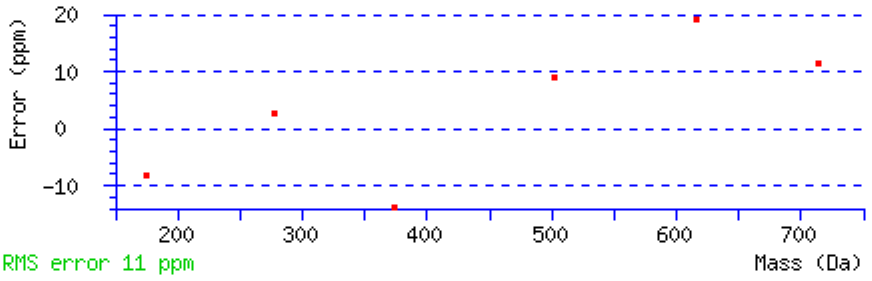
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 989.554565
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 42 **Expect:** 0.00036
Matches : 6/60 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940			Y							8
2	277.154669	139.080973			I	827.498530	414.252903	810.471981	405.739629	809.487965	405.247621	7
3	376.223083	188.615180			V	*714.414466*	357.710871	697.387917	349.197597	696.403901	348.705589	6
4	489.307147	245.157212			I	*615.346052*	308.176664	598.319503	299.663390	597.335487	299.171382	5
5	618.349740	309.678508	600.339175	300.673226	E	*502.261988*	251.634632	485.235439	243.121357	484.251423	242.629349	4
6	715.402504	358.204890	697.391939	349.199608	P	*373.219395*	187.113335	356.192846	178.600061	355.208830	178.108053	3
7	816.450183	408.728730	798.439618	399.723447	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
8					R	*175.118952*	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of YIVIEPTR
(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	989.554565	0.000263	YIVIEPTR
11.8	989.554581	0.000247	VEFTIPLR
6.3	989.554550	0.000278	IEYSIPLR
2.1	989.546692	0.008136	EMLDILIK
0.7	989.554565	0.000263	DFLKNLPK

Mascot: http://www.matrixscience.com/

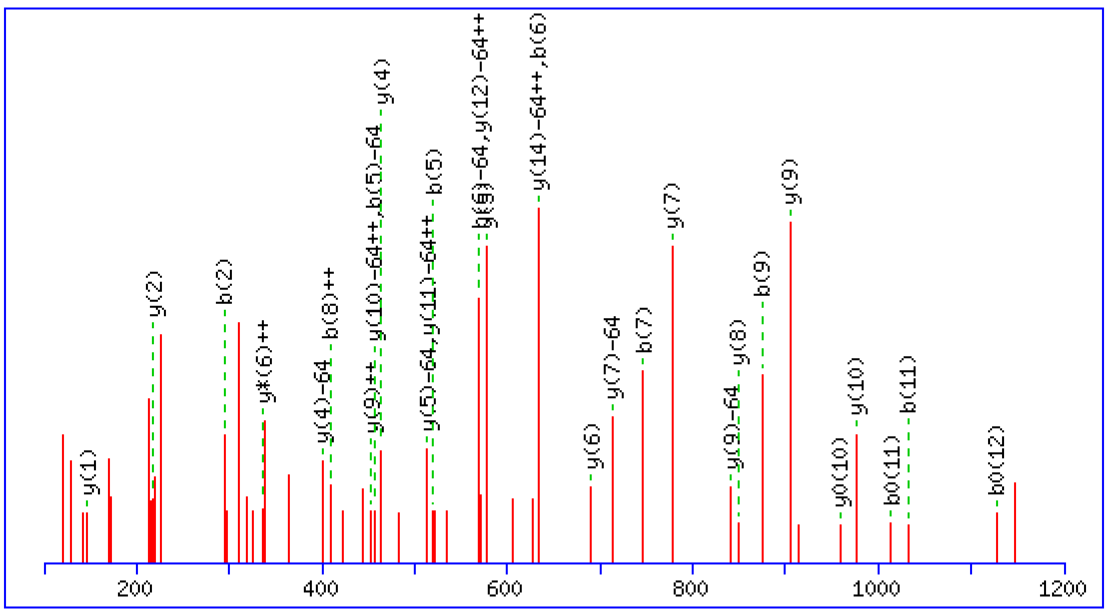
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FMPAGLIAGASLLMVAK**
Found in **TM14C_HUMAN**, Transmembrane protein 14C OS=Homo sapiens GN=TMEM14C PE=1 SV=1

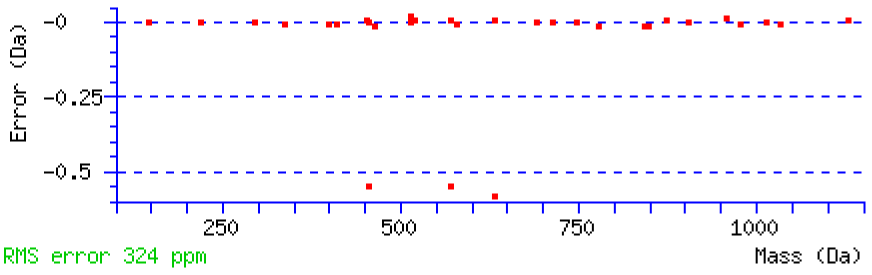
Match to Query 18461: 1720.919622 from(574.647150,3+) rtinseconds(3737) index(14274)
Title: Locus:1.1.1.3431.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

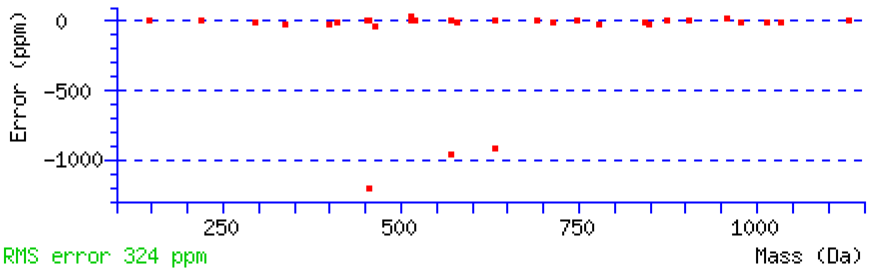
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1720.925568
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
M14 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 45 **Expect:** 0.00011
Matches : 31/242 fragment ions using 56 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	***295.111090***	148.059183			M	1574.864450	787.935863	1557.837901	779.422588	1556.853885	778.930580	16
3	392.163854	196.585565			P	1427.829050	714.418163	1410.802501	705.904889	1409.818485	705.412881	15
4	463.200968	232.104122			A	1330.776286	665.891781	1313.749737	657.378507	1312.765721	656.886499	14
5	***520.222432***	260.614854			G	1259.739172	630.373224	1242.712623	621.859949	1241.728607	621.367941	13
6	***633.306496***	317.156886			L	1202.717708	601.862492	1185.691159	593.349218	1184.707143	592.857209	12
7	***746.390560***	373.698918			I	1089.633644	545.320460	1072.607095	536.807185	1071.623079	536.315177	11
8	817.427674	409.217475			A	***976.549580***	488.778428	959.523031	480.265153	958.539015	479.773145	10
9	***874.449138***	437.728207			G	***905.512466***	453.259871	888.485917	444.746596	887.501901	444.254588	9
10	945.486252	473.246764			A	***848.491002***	424.749139	831.464453	416.235864	830.480437	415.743856	8
11	***1032.518280***	516.762778	1014.507715	507.757496	S	***777.453888***	389.230582	760.427339	380.717307	759.443323	380.225299	7
12	1145.602344	573.304810	1127.591779	564.299527	L	***690.421860***	345.714568	673.395311	337.201293			6
13	1258.686408	629.846842	1240.675843	620.841559	L	***577.337796***	289.172536	560.311247	280.659262			5
14	1405.721808	703.364542	1387.711243	694.359259	M	***464.253732***	232.630504	447.227183	224.117230			4
15	1504.790222	752.898749	1486.779657	743.893466	V	317.218332	159.112804	300.191783	150.599530			3
16	1575.827336	788.417306	1557.816771	779.412023	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 FMPAGLIAGASLLMVAK
(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	1720.925568	-0.005946	FMPAGLIAGASLLMVAK
39.6	1720.925568	-0.005946	FMPAGLIAGASLLMVAK
2.5	1720.935944	-0.016322	LLGQPSLDSLPIPAPR
0.6	1720.910782	0.008840	AGGALELLLAEGPGPAGGR

Mascot: http://www.matrixscience.com/

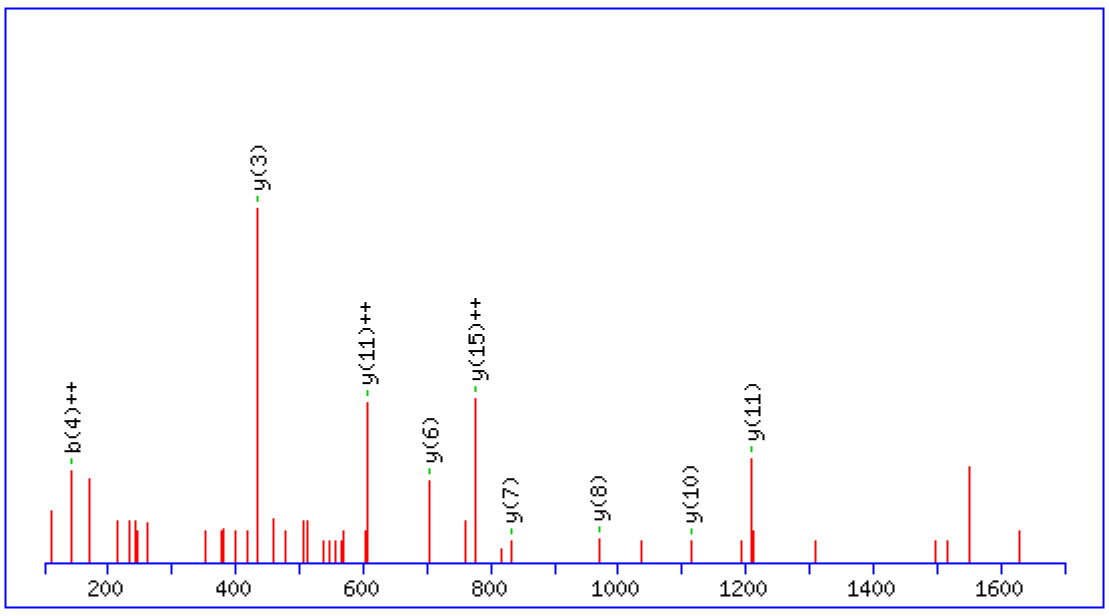
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLGGEVPGSHQGPDPYR**
Found in **TM205_HUMAN**, Transmembrane protein 205 OS=Homo sapiens GN=TMEM205 PE=1 SV=1

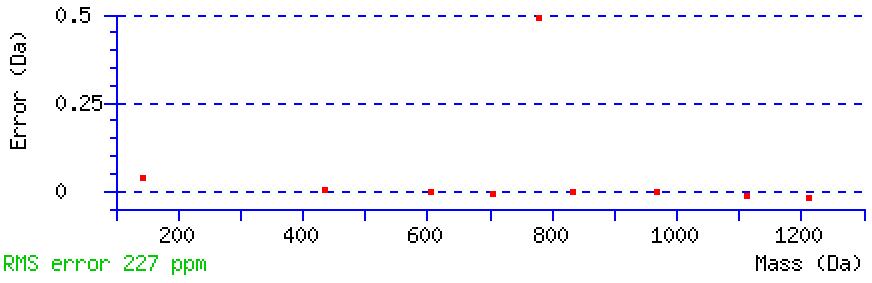
Match to Query 22807: 1721.808762 from(574.943530,3+) rtinseconds(1798) index(5741)
Title: Locus:1.1.1.2271.15
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-6.mgf

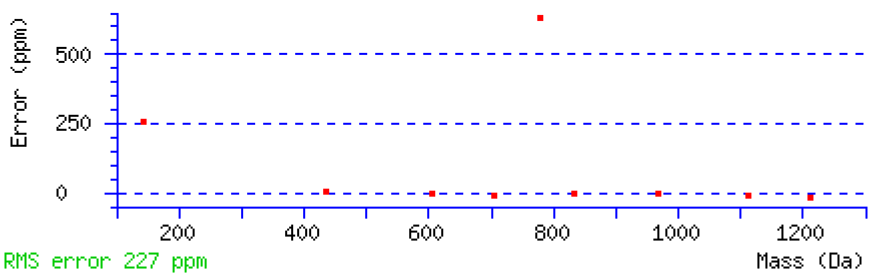
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 1721.812164`
`Fixed modifications: Propionamide (C) (apply to specified residues or termini only)`
`Ions Score: 33  Expect: 0.00099`
`Matches : 9/158 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	58.028740	29.518008					G							17
2	171.112804	86.060040					L	1665.797961	833.402619	1648.771412	824.889344	1647.787396	824.397336	16
3	228.134268	114.570772					G	1552.713897	776.860587	1535.687348	768.347312	1534.703332	767.855304	15
4	285.155732	143.081504					G	1495.692433	748.349855	1478.665884	739.836580	1477.681868	739.344572	14
5	414.198325	207.602801			396.187760	198.597518	E	1438.670969	719.839123	1421.644420	711.325848	1420.660404	710.833840	13
6	513.266739	257.137008			495.256174	248.131725	V	1309.628376	655.317826	1292.601827	646.804552	1291.617811	646.312544	12
7	610.319503	305.663390			592.308938	296.658107	P	***1210.559962***	605.783619	1193.533413	597.270345	1192.549397	596.778337	11
8	667.340967	334.174122			649.330402	325.168839	G	***1113.507198***	557.257237	1096.480649	548.743963	1095.496633	548.251955	10
9	754.372995	377.690136			736.362430	368.684853	S	1056.485734	528.746505	1039.459185	520.233231	1038.475169	519.741223	9
10	891.431907	446.219592			873.421342	437.214309	H	***969.453706***	485.230491	952.427157	476.717217	951.443141	476.225209	8
11	1019.490485	510.248881	1002.463936	501.735606	1001.479920	501.243598	Q	***832.394794***	416.701035	815.368245	408.187761	814.384229	407.695753	7
12	1076.511949	538.759613	1059.485400	530.246338	1058.501384	529.754330	G	***704.336216***	352.671746	687.309667	344.158472	686.325651	343.666464	6
13	1173.564713	587.285995	1156.538164	578.772720	1155.554148	578.280712	P	647.314752	324.161014	630.288203	315.647740	629.304187	315.155732	5
14	1288.591656	644.799466	1271.565107	636.286192	1270.581091	635.794184	D	550.261988	275.634632	533.235439	267.121358	532.251423	266.629350	4
15	1385.644420	693.325848	1368.617871	684.812574	1367.633855	684.320566	P	***435.235045***	218.121161	418.208496	209.607886			3
16	1548.707749	774.857513	1531.681200	766.344238	1530.697184	765.852230	Y	338.182281	169.594778	321.155732	161.081504			2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of GLGGEVPGSHQGPDPYR
(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	1721.812164	-0.003402	GLGGEVPGSHQGPDPYR
0.6	1721.822037	-0.013275	GPSPSAGLPEEGPTAAPR
0.1	1721.822037	-0.013275	GPSPSAGLPEEGPTAAPR

Mascot: http://www.matrixscience.com/

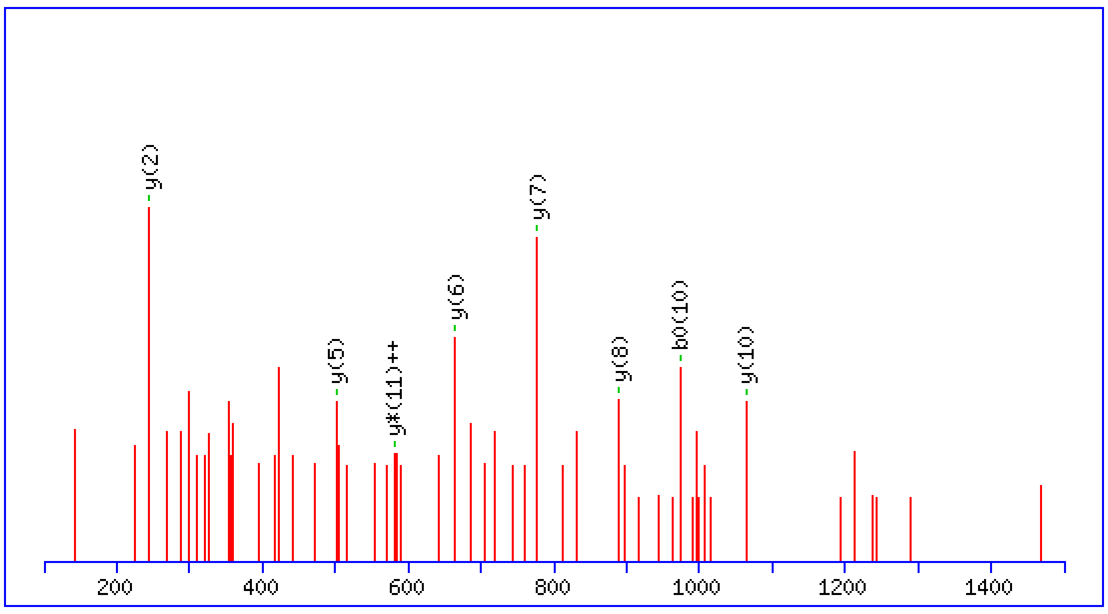
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLSSLLYGSIPK**
Found in **TXTP_HUMAN**, Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2

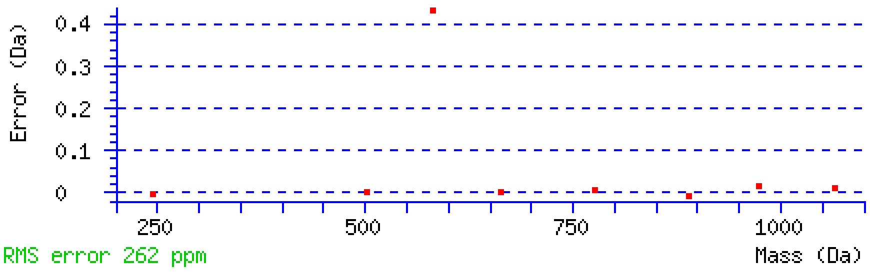
Match to Query 27360: 1233.701828 from(617.858190,2+) rtinseconds(3325) index(45313)
Title: Locus:1.1.1.2755.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

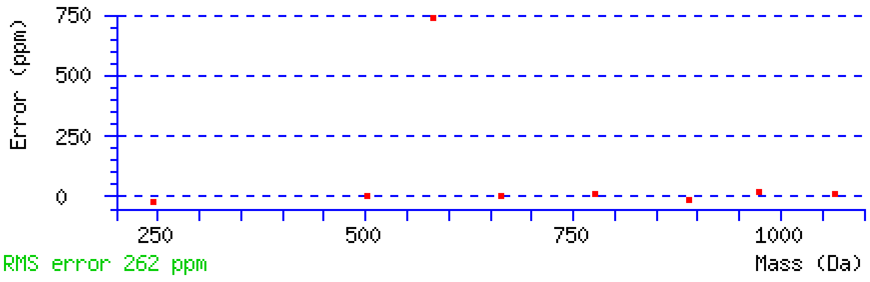
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1233.696869
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 0.00019
Matches : 8/100 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008			G							12
2	171.112804	86.060040			L	1177.682701	589.344989	1160.656152	580.831714	1159.672136	580.339706	11
3	258.144832	129.576054	240.134267	120.570772	S	***1064.598637***	532.802957	1047.572088	524.289682	1046.588072	523.797674	10
4	345.176860	173.092068	327.166295	164.086785	S	977.566609	489.286943	960.540060	480.773668	959.556044	480.281660	9
5	458.260924	229.634100	440.250359	220.628818	L	***890.534581***	445.770929	873.508032	437.257654	872.524016	436.765646	8
6	571.344988	286.176132	553.334423	277.170850	L	***777.450517***	389.228897	760.423968	380.715622	759.439952	380.223614	7
7	734.408317	367.707797	716.397752	358.702514	Y	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	6
8	791.429781	396.218529	773.419216	387.213246	G	***501.303124***	251.155200	484.276575	242.641925	483.292559	242.149917	5
9	878.461809	439.734543	860.451244	430.729260	S	444.281660	222.644468	427.255111	214.131193	426.271095	213.639185	4
10	991.545873	496.276575	973.535308	487.271292	I	357.249632	179.128454	340.223083	170.615179			3
11	1088.598637	544.802957	1070.588072	535.797674	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 GLSSLLYGSIPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.5	1233.696869	0.004959	GLSSLLYGSIPK
0.8	1233.708099	-0.006271	ELTNLLGLHPK
0.1	1233.708099	-0.006271	AATIVLQSYLR

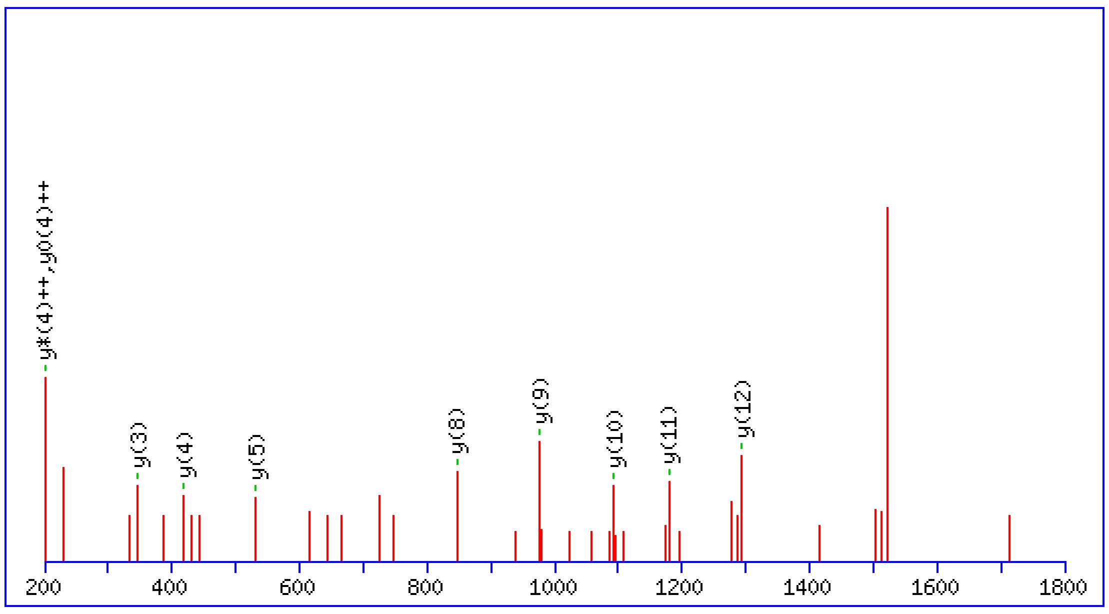
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLNSDMDSILASLK**
Found in **ECHA_HUMAN**, Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2

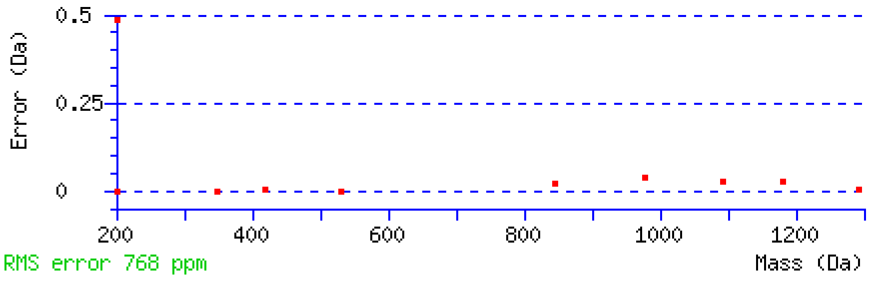
Match to Query 37011: 1520.743988 from(761.379270,2+) rtinseconds(4360) index(63097)
Title: Locus:1.1.1.3259.29
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-2.mgf

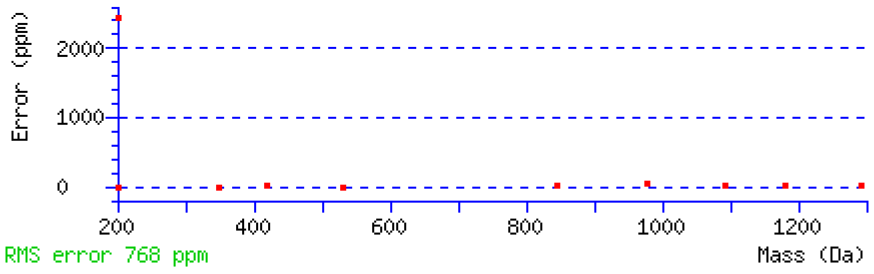
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1520.739197
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 6e-006
Matches : 10/148 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	116.034219	58.520748			98.023654	49.515465	D							14
2	229.118283	115.062779			211.107718	106.057497	L	1406.719556	703.863416	1389.693007	695.350141	1388.708991	694.858133	13
3	343.161210	172.084243	326.134661	163.570968	325.150645	163.078960	N	***1293.635492***	647.321384	1276.608943	638.808110	1275.624927	638.316101	12
4	430.193238	215.600257	413.166689	207.086983	412.182673	206.594975	S	***1179.592565***	590.299920	1162.566016	581.786646	1161.582000	581.294638	11
5	545.220181	273.113729	528.193632	264.600454	527.209616	264.108446	D	***1092.560537***	546.783906	1075.533988	538.270632	1074.549972	537.778624	10
6	676.260666	338.633971	659.234117	330.120697	658.250101	329.628689	M	***977.533594***	489.270435	960.507045	480.757160	959.523029	480.265152	9
7	791.287609	396.147443	774.261060	387.634168	773.277044	387.142160	D	***846.493109***	423.750192	829.466560	415.236918	828.482544	414.744910	8
8	878.319637	439.663457	861.293088	431.150182	860.309072	430.658174	S	731.466166	366.236721	714.439617	357.723446	713.455601	357.231438	7
9	991.403701	496.205489	974.377152	487.692214	973.393136	487.200206	I	644.434138	322.720707	627.407589	314.207432	626.423573	313.715424	6
10	1104.487765	552.747520	1087.461216	544.234246	1086.477200	543.742238	L	***531.350074***	266.178675	514.323525	257.665400	513.339509	257.173392	5
11	1175.524879	588.266077	1158.498330	579.752803	1157.514314	579.260795	A	***418.266010***	209.636643	401.239461	201.123368	400.255445	200.631360	4
12	1262.556907	631.782091	1245.530358	623.268817	1244.546342	622.776809	S	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
13	1375.640971	688.324123	1358.614422	679.810849	1357.630406	679.318841	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 DLNSDMDSILASLK
(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	1520.739197	0.004791	DLNSDMDSILASLK
7.5	1520.735855	0.008133	VENSLDASPFSVPK

Mascot: http://www.matrixscience.com/

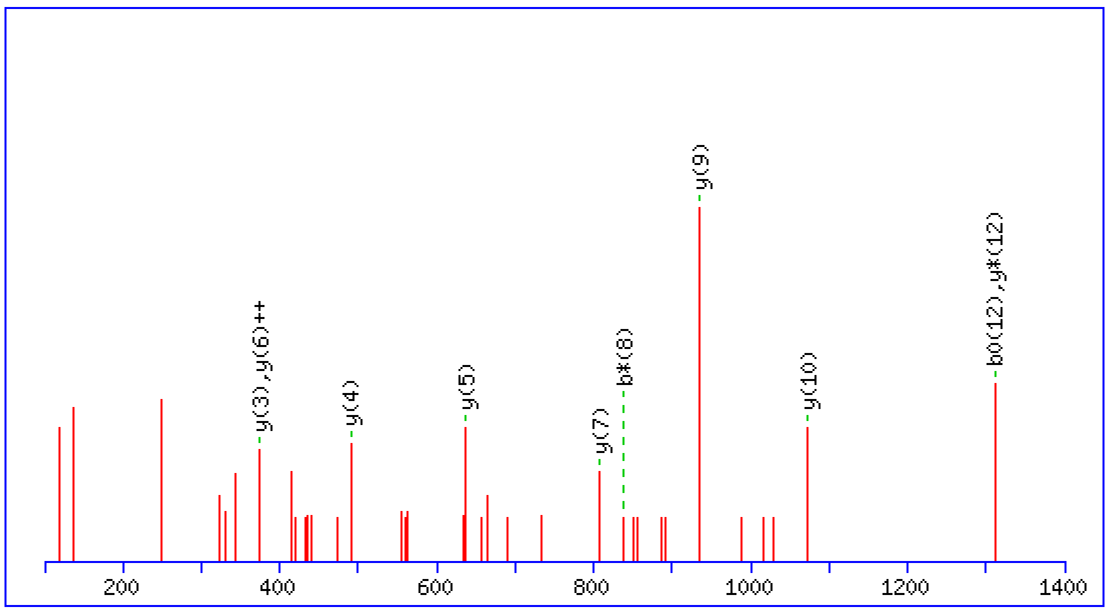
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYQQHGAGLFDVTR**
Found in **TPP1_HUMAN**, Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2

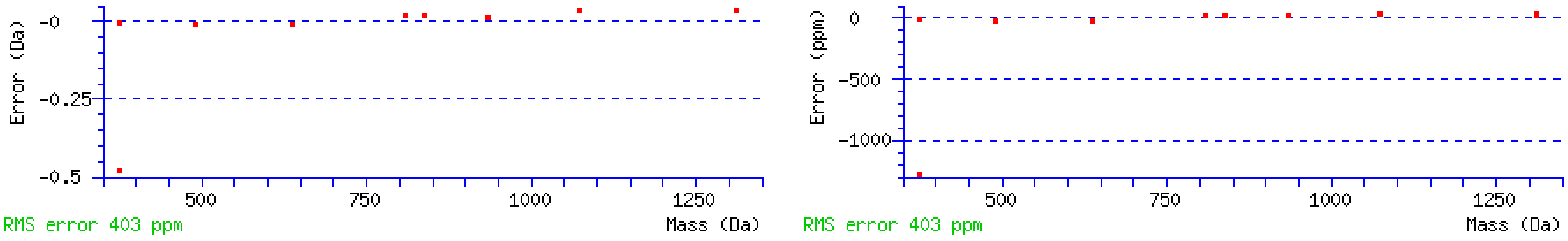
Match to Query 45233: 1603.805082 from(535.608970,3+) rtinseconds(2369) index(27463)
Title: Locus:1.1.1.2394.17
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

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): 1603.810699
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39  Expect: 0.00044
Matches : 10/130 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							14
2	277.154669	139.080973					Y	1491.733905	746.370591	1474.707356	737.857316	1473.723340	737.365308	13
3	405.213247	203.110262	388.186698	194.596987			Q	1328.670576	664.838926	1311.644027	656.325652	1310.660011	655.833644	12
4	533.271825	267.139551	516.245276	258.626276			Q	1200.611998	600.809637	1183.585449	592.296363	1182.601433	591.804355	11
5	670.330737	335.669007	653.304188	327.155732			H	***1072.553420***	536.780348	1055.526871	528.267074	1054.542855	527.775066	10
6	727.352201	364.179739	710.325652	355.666464			G	***935.494508***	468.250892	918.467959	459.737618	917.483943	459.245610	9
7	798.389315	399.698296	781.362766	391.185021			A	878.473044	439.740160	861.446495	431.226886	860.462479	430.734878	8
8	855.410779	428.209028	838.384230	419.695753			G	***807.435930***	404.221603	790.409381	395.708329	789.425365	395.216321	7
9	968.494843	484.751060	951.468294	476.237785			L	750.414466	375.710871	733.387917	367.197597	732.403901	366.705589	6
10	1115.563257	558.285267	1098.536708	549.771992			F	***637.330402***	319.168839	620.303853	310.655565	619.319837	310.163557	5
11	1230.590200	615.798738	1213.563651	607.285464	1212.579635	606.793456	D	***490.261988***	245.634632	473.235439	237.121358	472.251423	236.629350	4
12	1329.658614	665.332945	1312.632065	656.819671	1311.648049	656.327663	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
13	1430.706293	715.856785	1413.679744	707.343510	1412.695728	706.851502	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 LYQQHGAGLFDVTR
(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	1603.810699	-0.005617	LYQQHGAGLFDVTR
3.4	1603.798767	0.006315	MTENSTSAPAAKPKR
0.0	1603.798981	0.006101	MSTYLVAFIVGEMK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

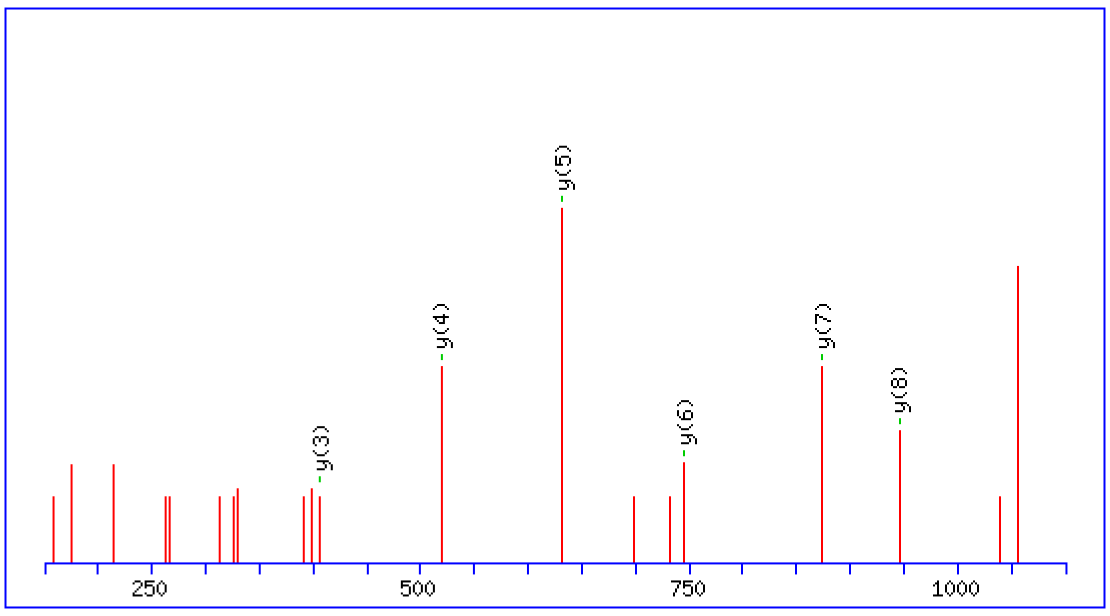
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAEPIPKMK**
Found in **TRIO_HUMAN**, Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2

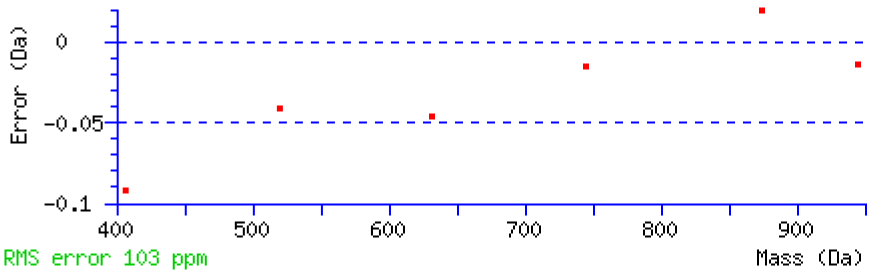
Match to Query 13772: 1073.548608 from(537.781580,2+) rtinseconds(1467) index(4567)
Title: Locus:1.1.1.2057.20
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

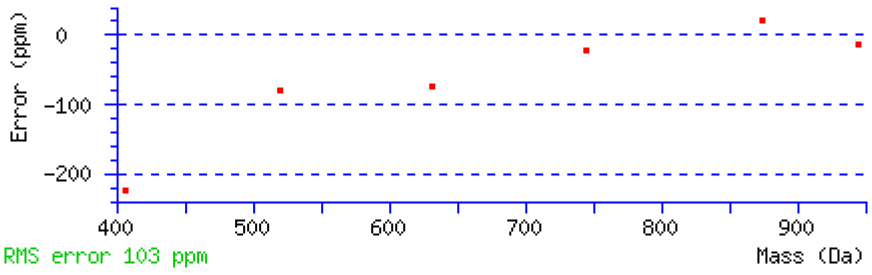
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1073.542664
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
P6      : Oxidation (P)
Ions Score: 36  Expect: 0.0052
Matches : 6/72 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**							**9**
2	201.086983	101.047130			183.076418	92.041847	**A**	*945.507381*	473.257329	928.480832	464.744054	927.496816	464.252046	**8**
3	330.129576	165.568426			312.119011	156.563144	**E**	*874.470267*	437.738772	857.443718	429.225497	856.459702	428.733489	**7**
4	443.177255	222.092266			425.166690	213.086983	**P**	*745.427674*	373.217475	728.401125	364.704201			**6**
5	556.261319	278.634298			538.250754	269.629015	**I**	*632.379995*	316.693636	615.353446	308.180361			**5**
6	669.308998	335.158137			651.298433	326.152855	**P**	*519.295931*	260.151604	502.269382	251.638329			**4**
7	797.403961	399.205619	780.377412	390.692344	779.393396	390.200336	**K**	*406.248252*	203.627764	389.221703	195.114490			**3**
8	928.444446	464.725861	911.417897	456.212587	910.433881	455.720579	**M**	278.153289	139.580283	261.126740	131.067008			**2**
9							**K**	147.112804	74.060040	130.086255	65.546766			**1**





NCBI **BLAST** search of EAEPIPKMK
(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	1073.542664	0.005944	EAEPIPKMK
26.7	1073.542664	0.005944	EAEPIPKMK
12.3	1073.546524	0.002084	ISQQVEQSR
8.1	1073.546509	0.002099	QTNINLESR
6.6	1073.557770	-0.009162	GGSQLSVDRR
5.4	1073.542664	0.005944	EAEPIPKMK
4.0	1073.550537	-0.001929	DFLAPLENR
3.5	1073.550552	-0.001944	EFVNPSLPR
3.5	1073.550552	-0.001944	EFVNPSLPR
3.1	1073.551895	-0.003287	EIHFHVHR

Mascot: http://www.matrixscience.com/

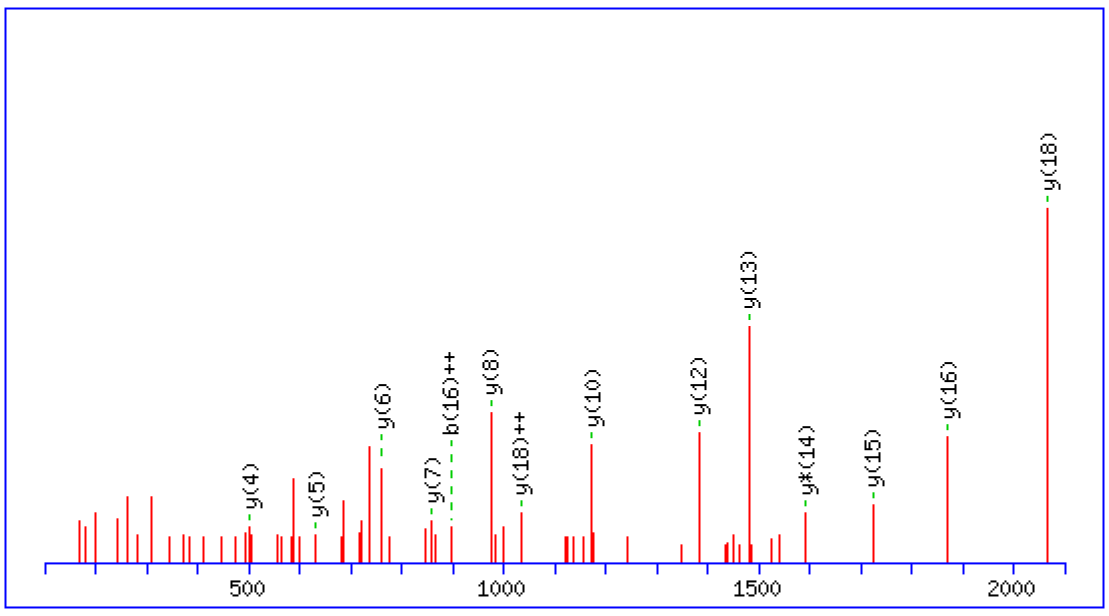
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILPVFDEPPNPTNVEESLKR**
Found in **TMOD3_HUMAN**, Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1

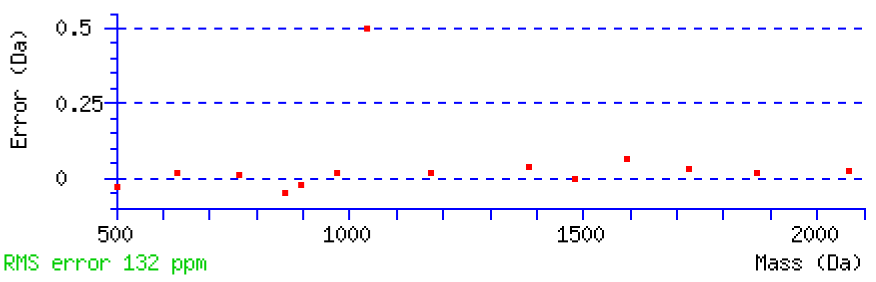
Match to Query 65473: 2293.209972 from(765.410600,3+) rtinseconds(3235) index(43637)
Title: Locus:1.1.1.2721.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

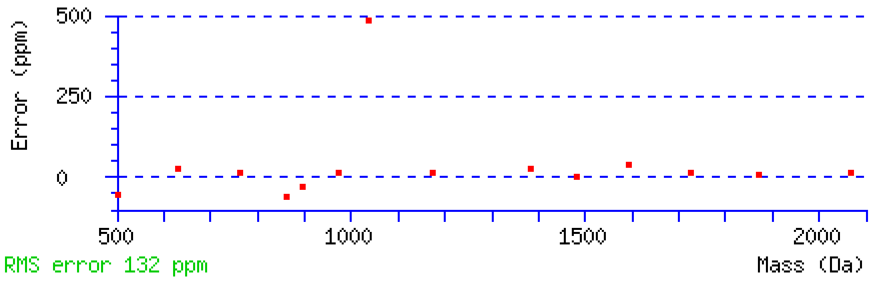
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2293.195389
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 57  Expect: 9e-006
Matches : 14/194 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					I							20
2	227.175404	114.091340					L	2181.118624	1091.062950	2164.092075	1082.549675	2163.108059	1082.057667	19
3	324.228168	162.617722					P	***2068.034560***	1034.520918	2051.008011	1026.007643	2050.023995	1025.515635	18
4	423.296582	212.151929					V	1970.981796	985.994536	1953.955247	977.481262	1952.971231	976.989254	17
5	570.364996	285.686136					F	***1871.913382***	936.460329	1854.886833	927.947055	1853.902817	927.455047	16
6	685.391939	343.199608			667.381374	334.194325	D	***1724.844968***	862.926122	1707.818419	854.412848	1706.834403	853.920840	15
7	814.434532	407.720904			796.423967	398.715622	E	1609.818025	805.412651	1592.791476	796.899376	1591.807460	796.407368	14
8	911.487296	456.247286			893.476731	447.242004	P	***1480.775432***	740.891354	1463.748883	732.378080	1462.764867	731.886072	13
9	1008.540060	504.773668			990.529495	495.768386	P	***1383.722668***	692.364972	1366.696119	683.851698	1365.712103	683.359690	12
10	1122.582987	561.795132	1105.556438	553.281857	1104.572422	552.789849	N	1286.669904	643.838590	1269.643355	635.325316	1268.659339	634.833308	11
11	1219.635751	610.321514	1202.609202	601.808239	1201.625186	601.316231	P	***1172.626977***	586.817127	1155.600428	578.303852	1154.616412	577.811844	10
12	1320.683430	660.845353	1303.656881	652.332079	1302.672865	651.840071	T	1075.574213	538.290745	1058.547664	529.777470	1057.563648	529.285462	9
13	1434.726357	717.866817	1417.699808	709.353542	1416.715792	708.861534	N	***974.526534***	487.766905	957.499985	479.253631	956.515969	478.761623	8
14	1533.794771	767.401024	1516.768222	758.887749	1515.784206	758.395741	V	***860.483607***	430.745442	843.457058	422.232167	842.473042	421.740159	7
15	1662.837364	831.922320	1645.810815	823.409046	1644.826799	822.917038	E	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	6
16	1791.879957	896.443617	1774.853408	887.930342	1773.869392	887.438334	E	***632.372600***	316.689938	615.346051	308.176664	614.362035	307.684656	5
17	1878.911985	939.959631	1861.885436	931.446356	1860.901420	930.954348	S	***503.330007***	252.168642	486.303458	243.655367	485.319442	243.163359	4
18	1991.996049	996.501663	1974.969500	987.988388	1973.985484	987.496380	L	416.297979	208.652628	399.271430	200.139353			3
19	2120.091012	1060.549144	2103.064463	1052.035870	2102.080447	1051.543862	K	303.213915	152.110596	286.187366	143.597321			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ILPVFDEPPNPTNVEESLKR
(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	2293.195389	0.014583	ILPVFDEPPNPTNVEESLKR
2.7	2293.206635	0.003337	LIIYEVSSRPSGVPDRFSGSK

Mascot: http://www.matrixscience.com/

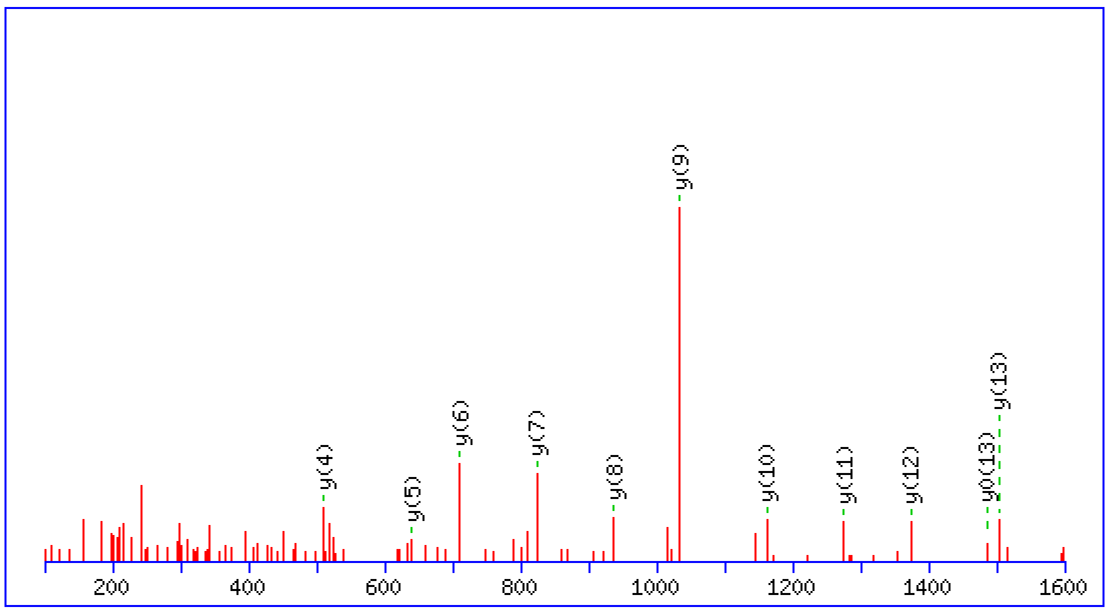
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALIEVLQPLIAEHQAR**
Found in **SYWC_HUMAN**, Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2

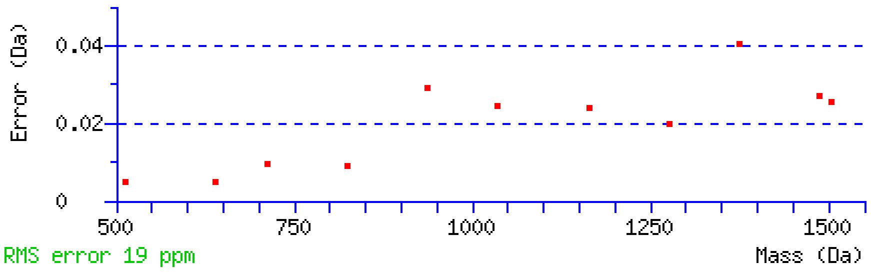
Match to Query 46187: 1800.040482 from(601.020770,3+) rtinseconds(3302) index(47826)
Title: Locus:1.1.1.2739.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-3.mgf

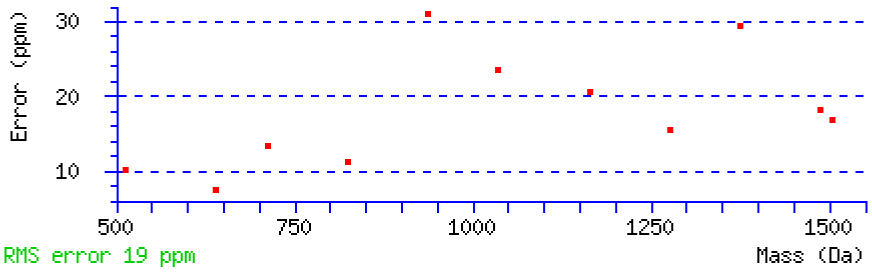
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1800.025726
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 83 **Expect:** 7.3e-009
Matches : 11/154 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	72.044390	36.525833					A							16
2	185.128454	93.067865					L	1729.995932	865.501604	1712.969383	856.988330	1711.985367	856.496322	15
3	298.212518	149.609897					I	1616.911868	808.959572	1599.885319	800.446298	1598.901303	799.954289	14
4	427.255111	214.131193			409.244546	205.125911	E	***1503.827804***	752.417540	1486.801255	743.904266	1485.817239	743.412258	13
5	526.323525	263.665401			508.312960	254.660118	V	***1374.785211***	687.896244	1357.758662	679.382969	1356.774646	678.890961	12
6	639.407589	320.207433			621.397024	311.202150	L	***1275.716797***	638.362037	1258.690248	629.848762	1257.706232	629.356754	11
7	767.466167	384.236722	750.439618	375.723447	749.455602	375.231439	Q	***1162.632733***	581.820005	1145.606184	573.306730	1144.622168	572.814722	10
8	864.518931	432.763104	847.492382	424.249829	846.508366	423.757821	P	***1034.574155***	517.790716	1017.547606	509.277441	1016.563590	508.785433	9
9	977.602995	489.305136	960.576446	480.791861	959.592430	480.299853	L	***937.521391***	469.264334	920.494842	460.751059	919.510826	460.259051	8
10	1090.687059	545.847168	1073.660510	537.333893	1072.676494	536.841885	I	***824.437327***	412.722302	807.410778	404.209027	806.426762	403.717019	7
11	1161.724173	581.365725	1144.697624	572.852450	1143.713608	572.360442	A	***711.353263***	356.180270	694.326714	347.666995	693.342698	347.174987	6
12	1290.766766	645.887021	1273.740217	637.373747	1272.756201	636.881738	E	***640.316149***	320.661713	623.289600	312.148438	622.305584	311.656430	5
13	1427.825678	714.416477	1410.799129	705.903203	1409.815113	705.411194	H	***511.273556***	256.140416	494.247007	247.627141			4
14	1555.884256	778.445766	1538.857707	769.932492	1537.873691	769.440484	Q	374.214644	187.610960	357.188095	179.097686			3
15	1626.921370	813.964323	1609.894821	805.451049	1608.910805	804.959041	A	246.156066	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of ALIEVLQPLIAEHQAR
(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	1800.025726	0.014756	ALIEVLQPLIAEHQAR

Mascot: http://www.matrixscience.com/

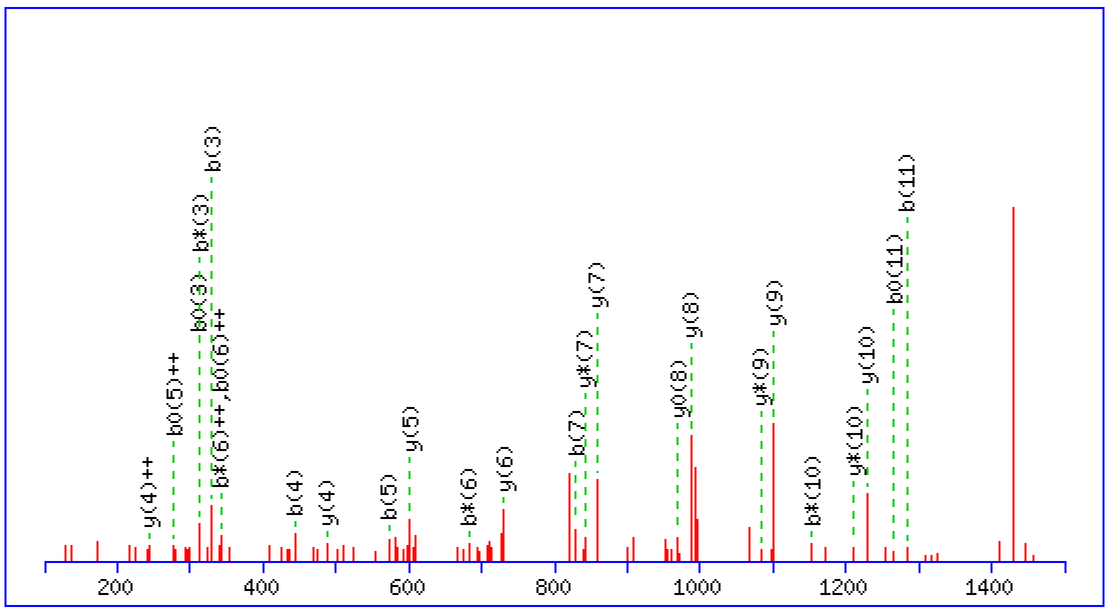
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSQLEQENNLLK**
Found in **T22D1_HUMAN**, TSC22 domain family protein 1 OS=Homo sapiens GN=TSC22D1 PE=1 SV=3

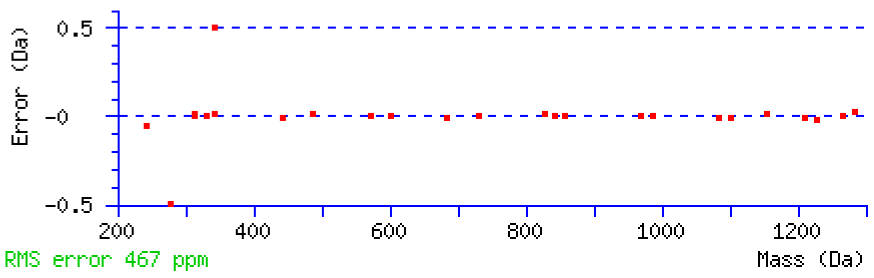
Match to Query 12525: 1428.719508 from(715.367030,2+) rtinseconds(2107) index(5449)
Title: Locus:1.1.1.2560.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

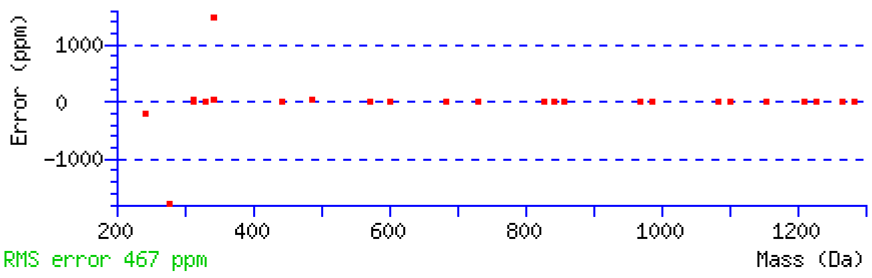
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1428.720825
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 35 **Expect:** 0.0031
Matches : 25/120 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	115.050203	58.028740	98.023654	49.515465			N							12
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	1315.685220	658.346248	1298.658671	649.832973	1297.674655	649.340965	11
3	**330.140809**	165.574042	313.114260	157.060768	312.130244	156.568760	Q	***1228.653192***	614.830234	1211.626643	606.316959	1210.642627	605.824951	10
4	**443.224873**	222.116075	426.198324	213.602800	425.214308	213.110792	L	***1100.594614***	550.800945	1083.568065	542.287670	1082.584049	541.795662	9
5	**572.267466**	286.637371	555.240917	278.124097	554.256901	277.632089	E	***987.510550***	494.258913	970.484001	485.745638	969.499985	485.253630	8
6	700.326044	350.666660	683.299495	342.153386	682.315479	341.661378	Q	***858.467957***	429.737616	841.441408	421.224342	840.457392	420.732334	7
7	**829.368637**	415.187957	812.342088	406.674682	811.358072	406.182674	E	***730.409379***	365.708327	713.382830	357.195053	712.398814	356.703045	6
8	943.411564	472.209420	926.385015	463.696146	925.400999	463.204138	N	***601.366786***	301.187031	584.340237	292.673756			5
9	1057.454491	529.230884	1040.427942	520.717609	1039.443926	520.225601	N	***487.323859***	244.165567	470.297310	235.652293			4
10	1170.538555	585.772915	1153.512006	577.259641	1152.527990	576.767633	L	373.280932	187.144104	356.254383	178.630829			3
11	**1283.622619**	642.314947	1266.596070	633.801673	1265.612054	633.309665	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 NSQLEQENNLLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1428.720825	-0.001317	NSQLEQENNLLK
7.4	1428.710968	0.008540	QSNVIADHRDFK
6.8	1428.732086	-0.012578	SQPLTSPESRTAR
1.9	1428.720856	-0.001348	LTDLLQQEEQGR

Mascot: http://www.matrixscience.com/

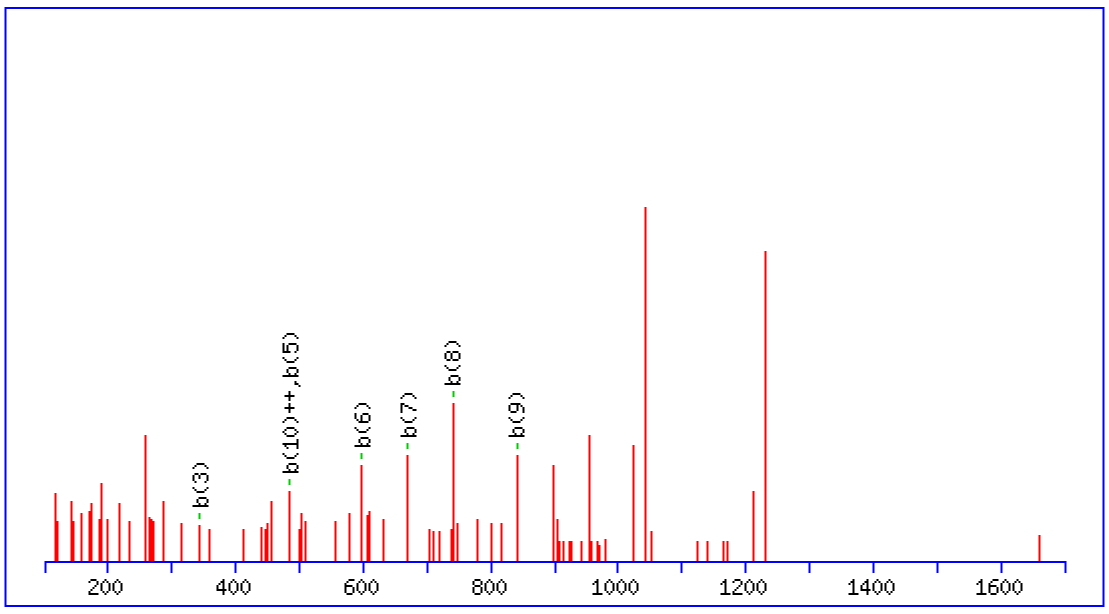
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVNAAIAATKSR**
Found in **TBAL3_HUMAN**, Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2

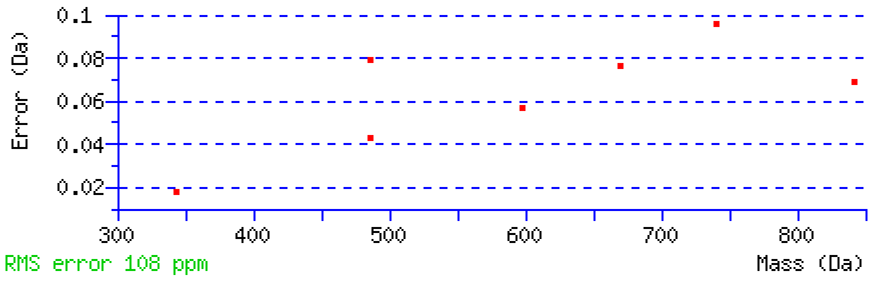
Match to Query 20726: 1229.671828 from(615.843190,2+) rtinseconds(2786) index(37856)
Title: Locus:1.1.1.2466.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

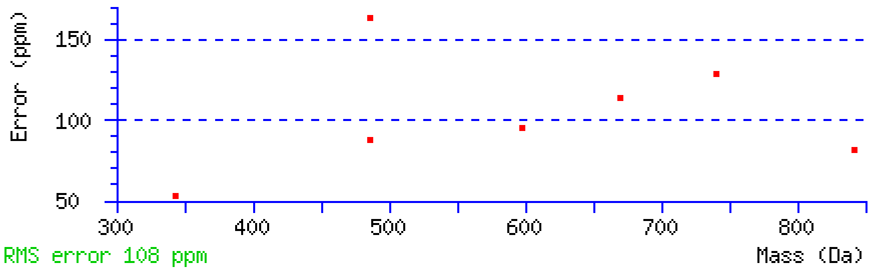
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1229.672760
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.00052
Matches : 7/126 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							12
2	229.118283	115.062780			211.107718	106.057497	V	1101.637483	551.322380	1084.610934	542.809105	1083.626918	542.317097	11
3	***343.161210***	172.084243	326.134661	163.570969	325.150645	163.078961	N	1002.569069	501.788173	985.542520	493.274898	984.558504	492.782890	10
4	414.198324	207.602800	397.171775	199.089526	396.187759	198.597518	A	888.526142	444.766709	871.499593	436.253435	870.515577	435.761427	9
5	***485.235438***	243.121357	468.208889	234.608082	467.224873	234.116075	A	817.489028	409.248152	800.462479	400.734878	799.478463	400.242870	8
6	***598.319502***	299.663389	581.292953	291.150115	580.308937	290.658107	I	746.451914	373.729595	729.425365	365.216321	728.441349	364.724313	7
7	***669.356616***	335.181946	652.330067	326.668672	651.346051	326.176664	A	633.367850	317.187563	616.341301	308.674289	615.357285	308.182281	6
8	***740.393730***	370.700503	723.367181	362.187229	722.383165	361.695221	A	562.330736	281.669006	545.304187	273.155732	544.320171	272.663724	5
9	***841.441409***	421.224343	824.414860	412.711068	823.430844	412.219060	T	491.293622	246.150449	474.267073	237.637175	473.283057	237.145167	4
10	969.536372	485.271824	952.509823	476.758550	951.525807	476.266542	K	390.245943	195.626610	373.219394	187.113335	372.235378	186.621327	3
11	1056.568400	528.787838	1039.541851	520.274564	1038.557835	519.782556	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 EVNAAIAATKSR
(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	1229.672760	-0.000932	EVNAAIAATKSR
4.0	1229.672775	-0.000947	NQELLSVGSKR
1.3	1229.672791	-0.000963	GATNPGLKSLTR

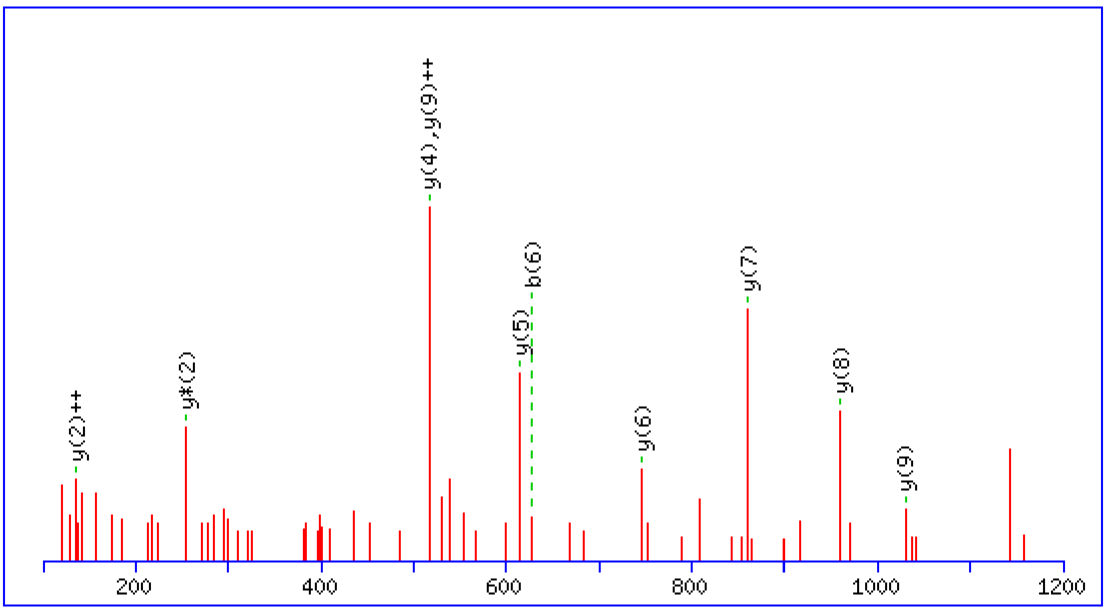
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVNMVPFPR**
Found in **TBB1_HUMAN**, Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1

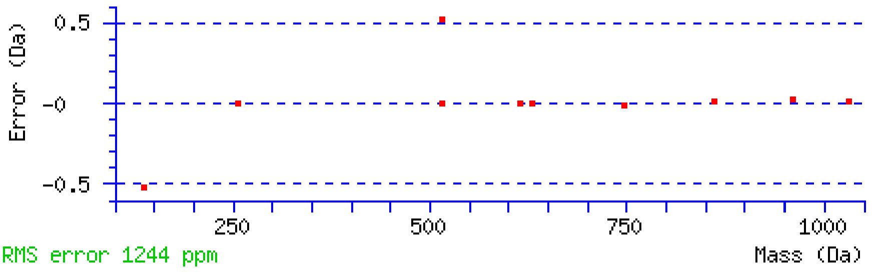
Match to Query 20267: 1142.626208 from(572.320380,2+) rtinseconds(2989) index(43646)
Title: Locus:1.1.1.1784.18
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

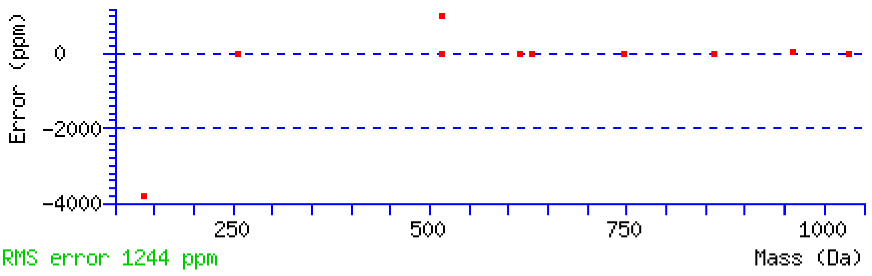
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1142.627029
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51  Expect: 9.5e-005
Matches : 10/66 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	185.128454	93.067865			A	***1030.550248***	515.778762	1013.523699	507.265488	9
3	284.196868	142.602072			V	***959.513134***	480.260205	942.486585	471.746931	8
4	398.239795	199.623536	381.213246	191.110261	N	***860.444720***	430.725998	843.418171	422.212724	7
5	529.280280	265.143778	512.253731	256.630504	M	***746.401793***	373.704535	729.375244	365.191260	6
6	628.348694	314.677985	611.322145	306.164711	V	***615.361308***	308.184292	598.334759	299.671018	5
7	725.401458	363.204367	708.374909	354.691093	P	***516.292894***	258.650085	499.266345	250.136811	4
8	872.469872	436.738574	855.443323	428.225300	F	419.240130	210.123703	402.213581	201.610429	3
9	969.522636	485.264956	952.496087	476.751682	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 LAVNMVPFPR
(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	1142.627029	-0.000821	LAVNMVPFPR
7.8	1142.623016	0.003192	APVLRVMGPR
0.1	1142.629517	-0.003309	LIGIDEVSAAR

Mascot: http://www.matrixscience.com/

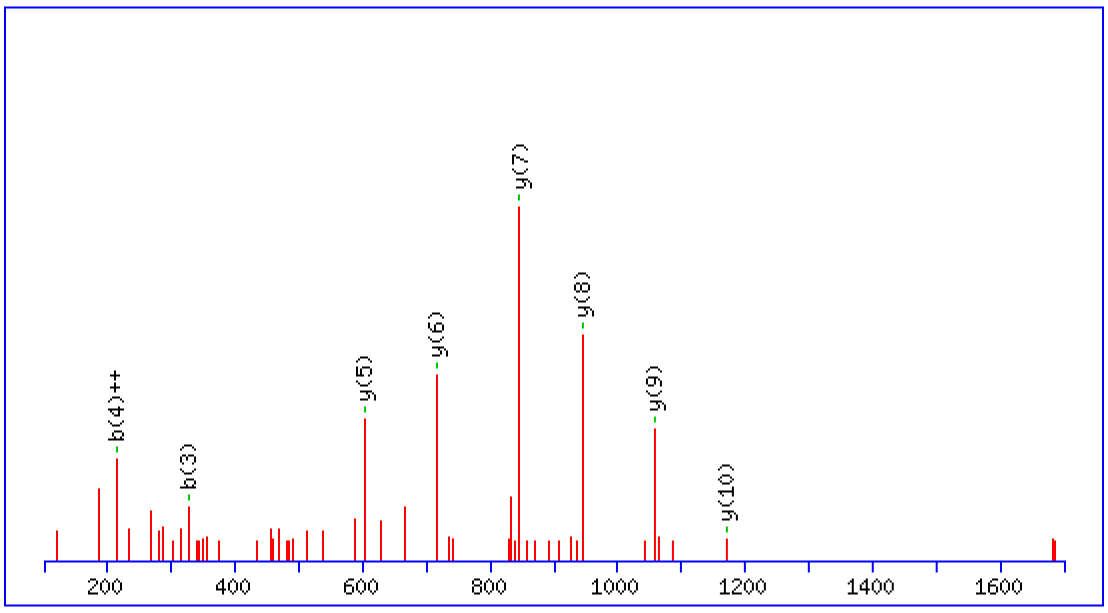
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLLVELPAFLR**
Found in **TNAP2_HUMAN**, Tumor necrosis factor alpha-induced protein 2 OS=Homo sapiens GN=TNFAIP2 PE=1 SV=2

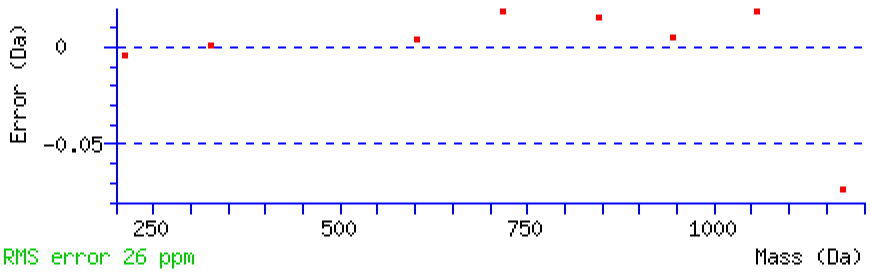
Match to Query 33020: 1268.793928 from(635.404240,2+) rtinseconds(4209) index(64829)
Title: Locus:1.1.1.2938.12
Data file 2011-11-14 - TFD - S 2-3.mgf

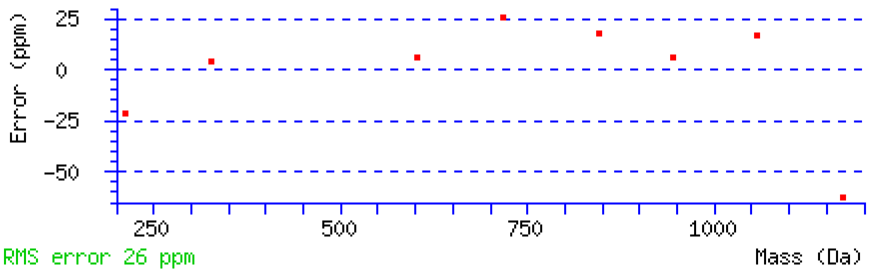
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1268.785629
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 2.7e-005
Matches : 9/80 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483			V							11
2	**213.159754**	107.083515			L	***1170.724507***	585.865891	1153.697958	577.352617	1152.713942	576.860609	10
3	**326.243818**	163.625547			L	***1057.640443***	529.323860	1040.613894	520.810585	1039.629878	520.318577	9
4	425.312232	213.159754			V	***944.556379***	472.781828	927.529830	464.268553	926.545814	463.776545	8
5	554.354825	277.681051	536.344260	268.675768	E	***845.487965***	423.247621	828.461416	414.734346	827.477400	414.242338	7
6	667.438889	334.223083	649.428324	325.217800	L	***716.445372***	358.726324	699.418823	350.213049			6
7	764.491653	382.749465	746.481088	373.744182	P	***603.361308***	302.184292	586.334759	293.671017			5
8	835.528767	418.268022	817.518202	409.262739	A	506.308544	253.657910	489.281995	245.144635			4
9	982.597181	491.802229	964.586616	482.796946	F	435.271430	218.139353	418.244881	209.626078			3
10	1095.681245	548.344261	1077.670680	539.338978	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 VLLVELPAFLR
(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	1268.785629	0.008299	VLLVELPAFLR
2.2	1268.781616	0.012312	LVLSTLSGRPVK

Mascot: http://www.matrixscience.com/

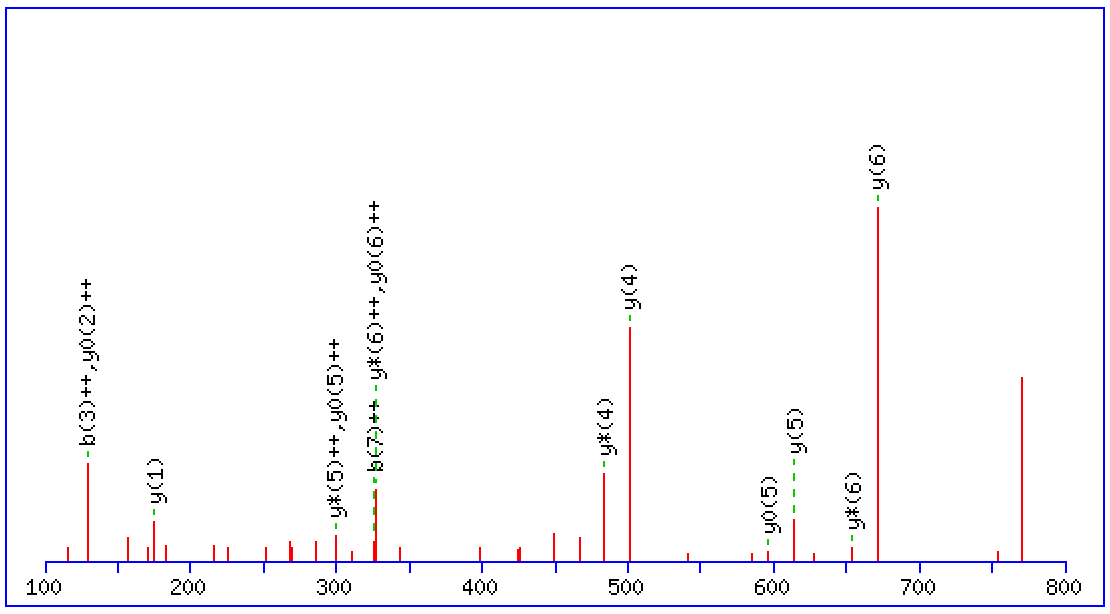
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALGPQPTR**
Found in **P5I13_HUMAN**, Tumor protein p53-inducible protein 13 OS=Homo sapiens GN=TP53I13 PE=2 SV=1

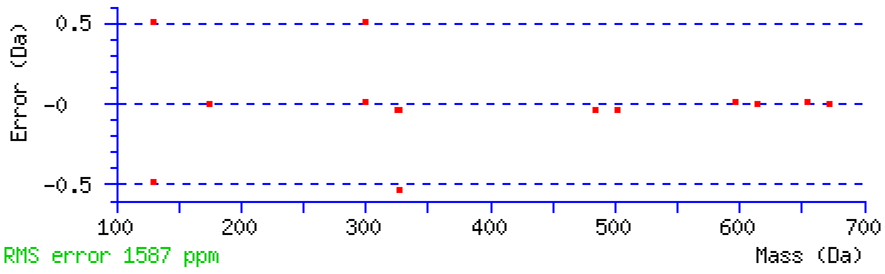
Match to Query 127838: 925.499168 from(463.756860,2+) rtinseconds(1439) index(406106)
Title: Locus:1.1.1.1144.7
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

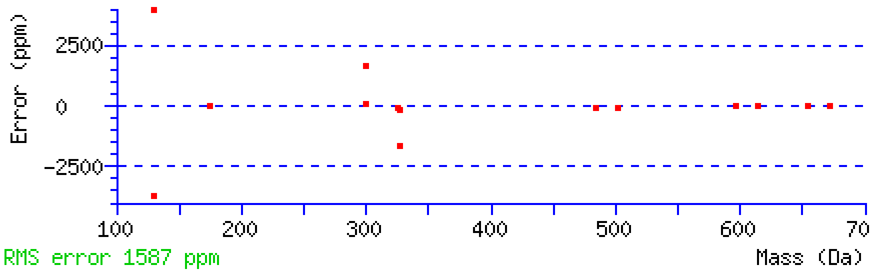
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 925.498123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P5 : Oxidation (P)
Ions Score: 31 **Expect:** 0.0077
Matches : 14/70 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	72.044390	36.525833					A							9
2	143.081504	72.044390					A	855.468294	428.237785	838.441745	419.724511	837.457729	419.232503	8
3	256.165568	**128.586422**					L	784.431180	392.719228	767.404631	384.205954	766.420615	383.713946	7
4	313.187032	157.097154					G	***671.347116***	336.177196	654.320567	327.663922	653.336551	327.171914	6
5	426.234711	213.620994					P	***614.325652***	307.666464	597.299103	299.153190	596.315087	298.661182	5
6	554.293289	277.650283	537.266740	269.137008			Q	***501.277973***	251.142625	484.251424	242.629350	483.267408	242.137342	4
7	651.346053	**326.176665**	634.319504	317.663390			P	373.219395	187.113336	356.192846	178.600061	355.208830	178.108053	3
8	752.393732	376.700504	735.367183	368.187230	734.383167	367.695222	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 AALGPQPTR
(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	925.498123	0.001045	AALGPQPTR
16.8	925.498123	0.001045	AALGPQPTR
15.2	925.498123	0.001045	APSVANPVR
2.8	925.502151	-0.002983	YALTFGVR
2.2	925.498108	0.001060	KPADIPNR
1.7	925.498123	0.001045	LVETHATR
0.6	925.494293	0.004875	FTLLMTGK

Mascot: http://www.matrixscience.com/

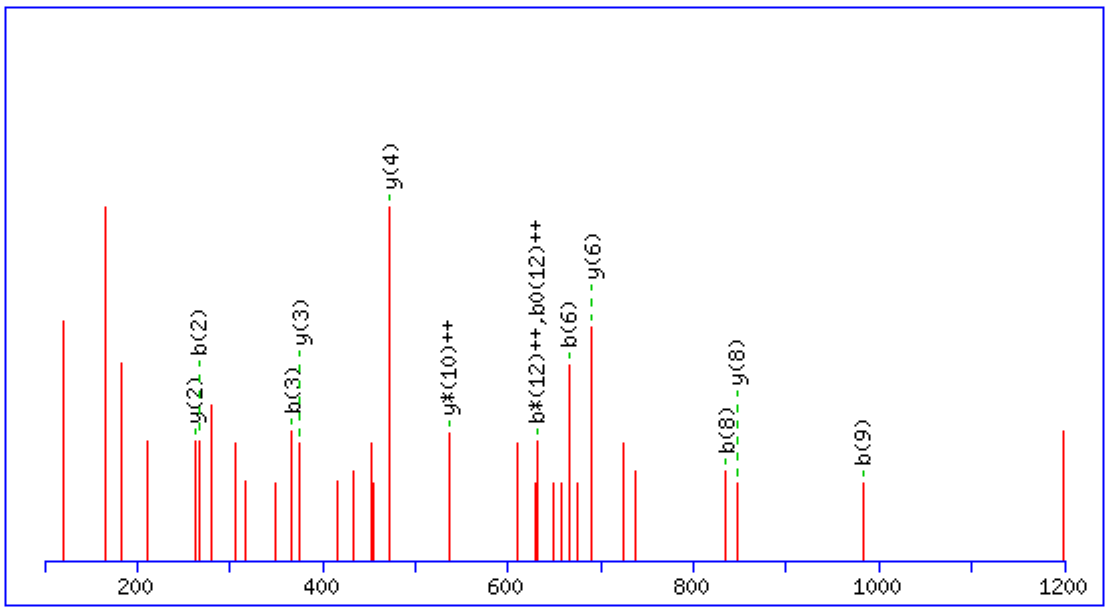
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTLQGVAFPISR**
Found in **TWF1_HUMAN**, Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3

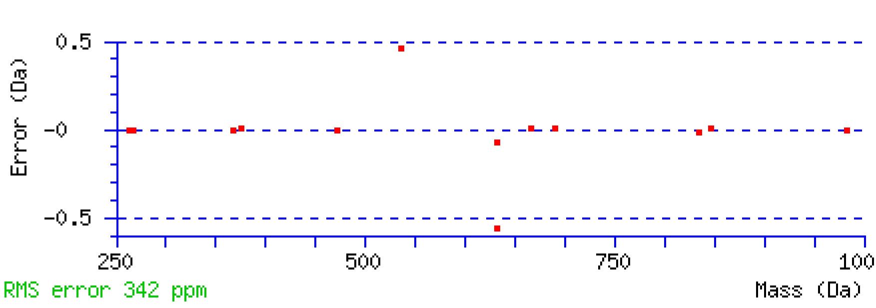
Match to Query 31056: 1452.778842 from(485.266890,3+) rtinseconds(2398) index(23345)
Title: Locus:1.1.1.2484.10
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

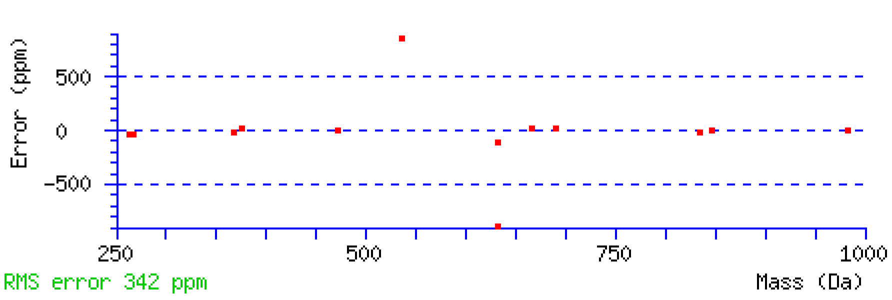
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1200 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1452.783752
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 37 **Expect:** 0.0016
Matches : 13/136 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	138.066188	69.536732					H							13
2	*266.124766*	133.566021	249.098217	125.052746			Q	1316.732113	658.869695	1299.705564	650.356420	1298.721548	649.864412	12
3	*367.172445*	184.089860	350.145896	175.576586	349.161880	175.084578	T	1188.673535	594.840406	1171.646986	586.327131	1170.662970	585.835123	11
4	480.256509	240.631892	463.229960	232.118618	462.245944	231.626610	L	1087.625856	544.316566	1070.599307	535.803292	1069.615291	535.311283	10
5	608.315087	304.661182	591.288538	296.147907	590.304522	295.655899	Q	974.541792	487.774534	957.515243	479.261259	956.531227	478.769252	9
6	*665.336551*	333.171914	648.310002	324.658639	647.325986	324.166631	G	*846.483214*	423.745245	829.456665	415.231970	828.472649	414.739962	8
7	764.404965	382.706121	747.378416	374.192846	746.394400	373.700838	V	789.461750	395.234513	772.435201	386.721238	771.451185	386.229230	7
8	*835.442079*	418.224678	818.415530	409.711403	817.431514	409.219395	A	*690.393336*	345.700306	673.366787	337.187031	672.382771	336.695023	6
9	*982.510493*	491.758885	965.483944	483.245610	964.499928	482.753602	F	619.356222	310.181749	602.329673	301.668475	601.345657	301.176467	5
10	1079.563257	540.285267	1062.536708	531.771992	1061.552692	531.279984	P	*472.287808*	236.647542	455.261259	228.134267	454.277243	227.642259	4
11	1192.647321	596.827298	1175.620772	588.314024	1174.636756	587.822016	I	*375.235044*	188.121160	358.208495	179.607885	357.224479	179.115877	3
12	1279.679349	640.343313	1262.652800	631.830038	1261.668784	631.338030	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 HQTLQGVAFPISR
(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	1452.783752	-0.004910	HQTLQGVAFPISR

Mascot: http://www.matrixscience.com/

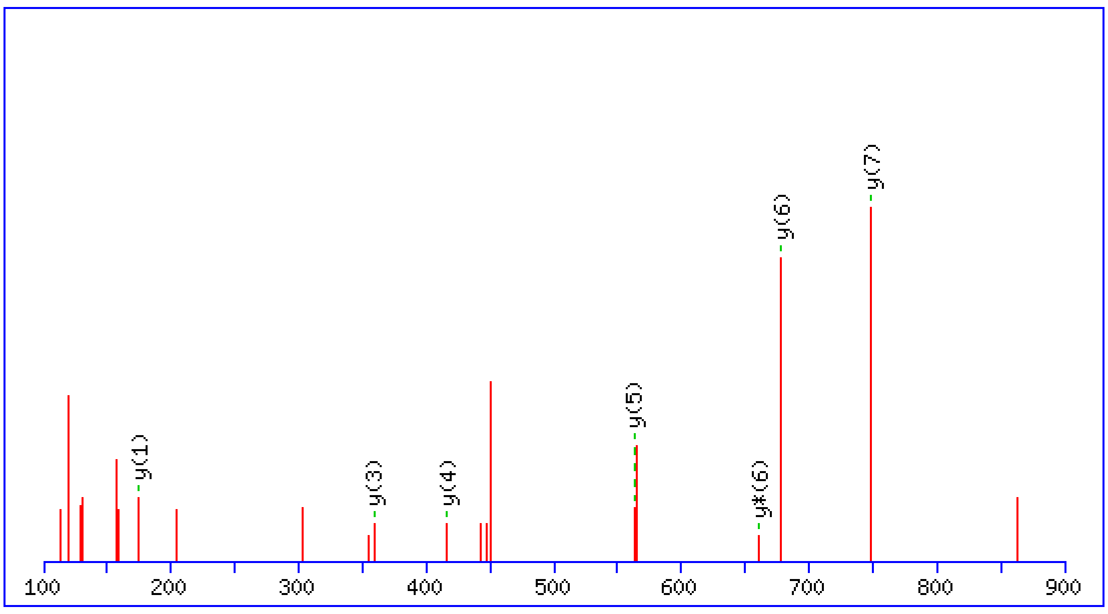
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IADFGLAR**
Found in **BLK_HUMAN**, Tyrosine-protein kinase Blk OS=Homo sapiens GN=BLK PE=1 SV=3

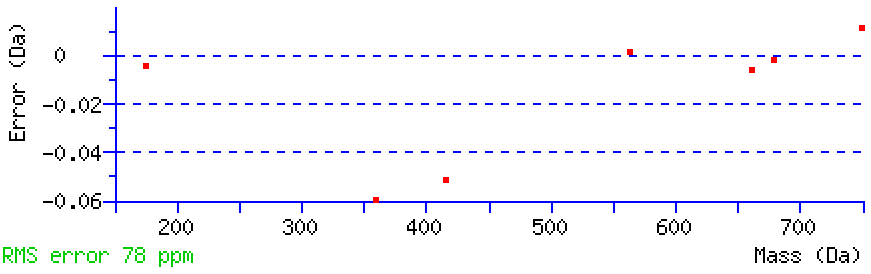
Match to Query 3917: 861.468648 from(431.741600,2+) rtinseconds(2380) index(26311)
Title: Locus:1.1.1.2493.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

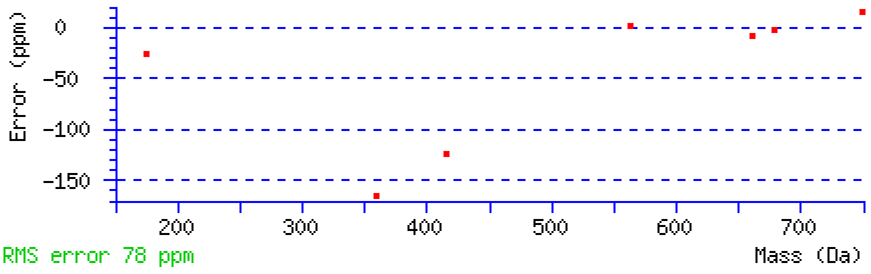
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 861.470840
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 43 **Expect:** 0.00079
Matches : 7/56 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			I							8
2	185.128454	93.067865			A	***749.394065***	375.200671	732.367516	366.687396	731.383500	366.195388	7
3	300.155397	150.581336	282.144832	141.576054	D	***678.356951***	339.682114	661.330402	331.168839	660.346386	330.676831	6
4	447.223811	224.115544	429.213246	215.110261	F	***563.330008***	282.168642	546.303459	273.655368			5
5	504.245275	252.626275	486.234710	243.620993	G	***416.261594***	208.634435	399.235045	200.121160			4
6	617.329339	309.168308	599.318774	300.163025	L	***359.240130***	180.123703	342.213581	171.610428			3
7	688.366453	344.686865	670.355888	335.681582	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 IADFGLAR
(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	861.470840	-0.002192	IALDFQR
43.0	861.470840	-0.002192	IADFGLAR
43.0	861.470840	-0.002192	LADFGLAR
18.2	861.470825	-0.002177	LAPYNIR
13.9	861.474197	-0.005549	LLEGMRK
9.4	861.470825	-0.002177	IAEFLNR
7.2	861.470840	-0.002192	IGADFLAR
6.9	861.474197	-0.005549	LGEMRLK
5.4	861.474213	-0.005565	LMLSVAGR
3.4	861.470856	-0.002208	VPLSFQR

Mascot: http://www.matrixscience.com/

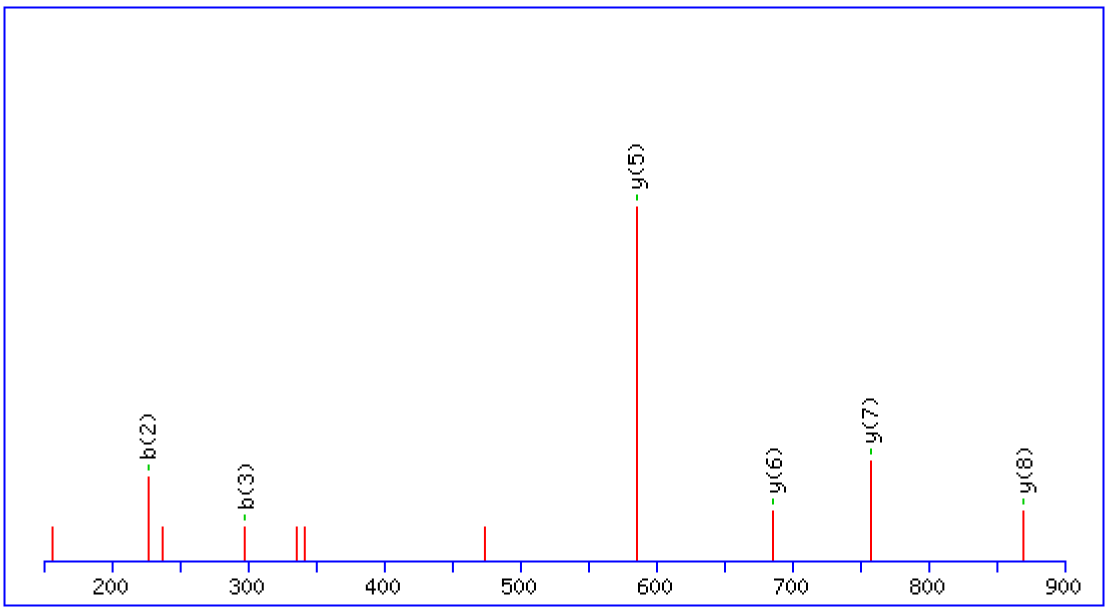
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LIATTAHEK**
Found in **KSYK_HUMAN**, Tyrosine-protein kinase SYK OS=Homo sapiens GN=SYK PE=1 SV=1

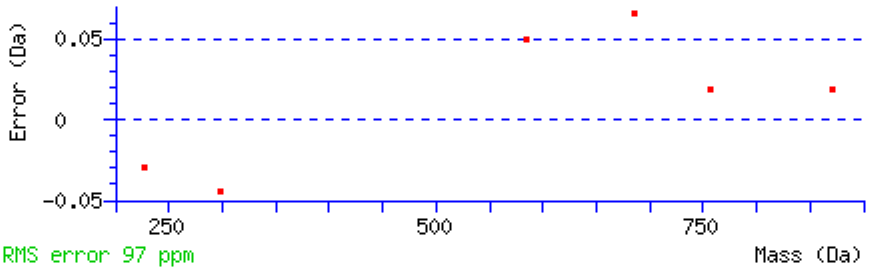
Match to Query 8370: 982.541528 from(492.278040,2+) rtinseconds(5116) index(74643)
Title: Locus:1.1.1.3488.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

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 ●

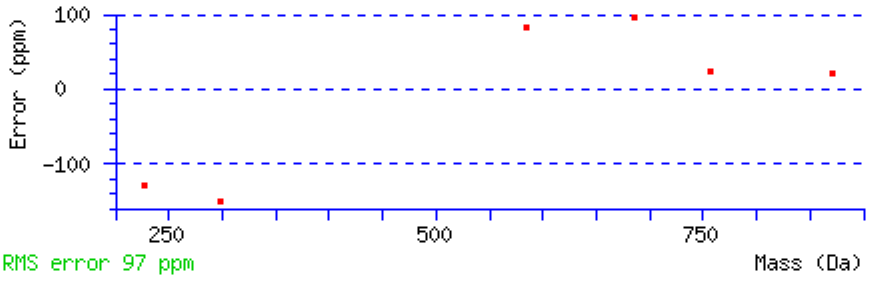


```
Monoisotopic mass of neutral peptide Mr(calc): 982.544724
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 41  Expect: 0.00051
Matches : 6/72 fragment ions using 7 most intense peaks   (help)
```

#	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			I	***870.467959***	435.737618	853.441410	427.224343	852.457394	426.732335	8
3	**298.212518**	149.609897			A	***757.383895***	379.195586	740.357346	370.682311	739.373330	370.190303	7
4	399.260197	200.133737	381.249632	191.128454	T	***686.346781***	343.677029	669.320232	335.163754	668.336216	334.671746	6
5	500.307876	250.657576	482.297311	241.652294	T	***585.299102***	293.153189	568.272553	284.639915	567.288537	284.147907	5
6	571.344990	286.176133	553.334425	277.170851	A	484.251423	242.629349	467.224874	234.116075	466.240858	233.624067	4
7	708.403902	354.705589	690.393337	345.700307	H	413.214309	207.110792	396.187760	198.597518	395.203744	198.105510	3
8	837.446495	419.226886	819.435930	410.221603	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



RMS error 97 ppm



RMS error 97 ppm

NCBI **BLAST** search of LIATTAHEK
(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	982.544724	-0.003196	LIATTAHEK
16.4	982.544724	-0.003196	ILGDPEALR
2.3	982.544739	-0.003211	EGIVLHSTK
1.3	982.544724	-0.003196	ILPQDLER
1.3	982.544724	-0.003196	LLQPEDLR

Mascot: http://www.matrixscience.com/

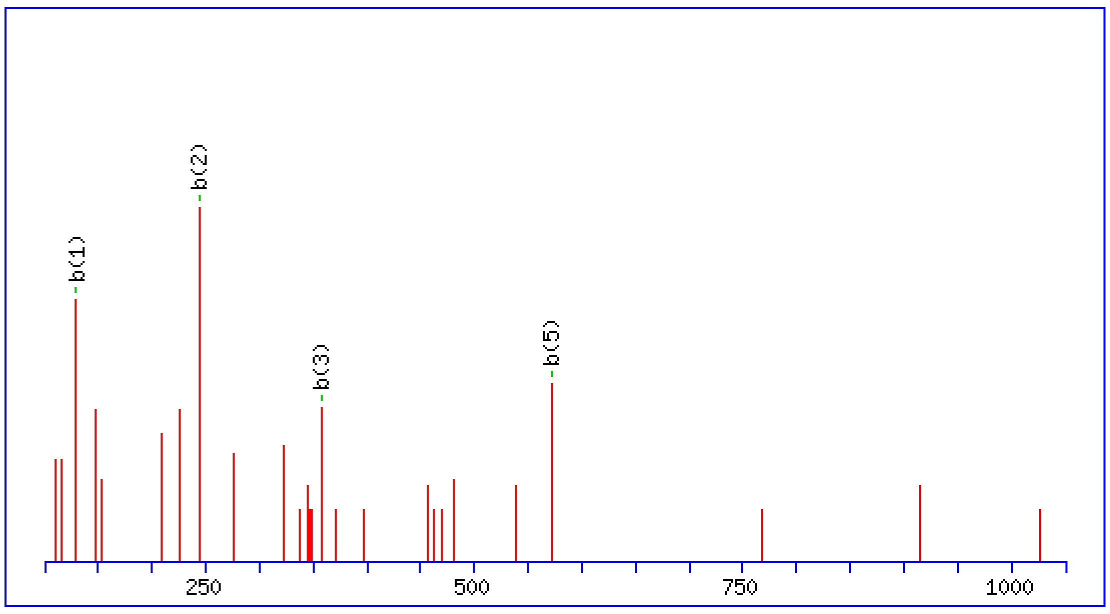
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDILTGR**
Found in **PTN4_HUMAN**, Tyrosine-protein phosphatase non-receptor type 4 OS=Homo sapiens GN=PTPN4 PE=1 SV=1

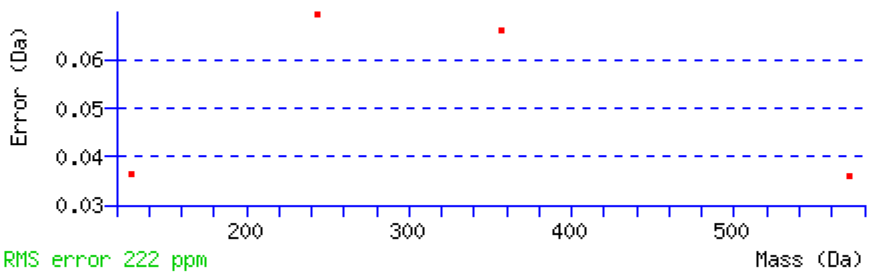
Match to Query 295: 801.437868 from(401.726210,2+) rtinseconds(1422) index(8635)
Title: Locus:1.1.1.2063.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

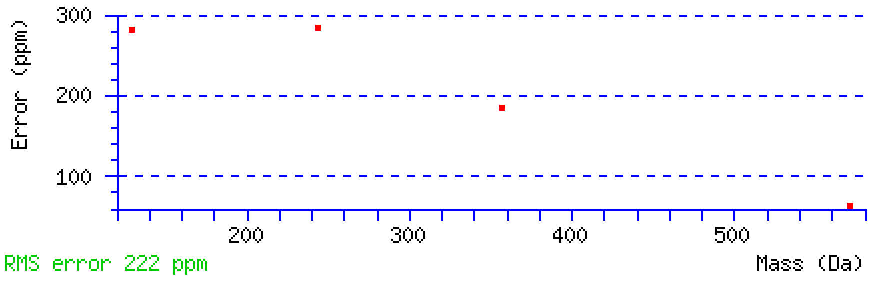
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 801.434464
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0047
Matches : 4/66 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	***129.065854***	65.036565	112.039305	56.523291			**Q**							7
2	***244.092797***	122.550037	227.066248	114.036762	226.082232	113.544754	**D**	674.383166	337.695221	657.356617	329.181947	656.372601	328.689939	6
3	***357.176861***	179.092069	340.150312	170.578794	339.166296	170.086786	**I**	559.356223	280.181750	542.329674	271.668475	541.345658	271.176467	5
4	470.260925	235.634101	453.234376	227.120826	452.250360	226.628818	**L**	446.272159	223.639718	429.245610	215.126443	428.261594	214.634435	4
5	***571.308604***	286.157940	554.282055	277.644666	553.298039	277.152658	**T**	333.188095	167.097686	316.161546	158.584411	315.177530	158.092403	3
6	628.330068	314.668672	611.303519	306.155398	610.319503	305.663390	**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 QDILTGR
(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	801.434464	0.003404	QDILTGR
8.5	801.438477	-0.000609	KVEPWK
8.0	801.438477	-0.000609	QWLVEK
7.7	801.438492	-0.000624	GPPPPPPK
7.0	801.434479	0.003389	GVPSLTGR
7.0	801.434464	0.003404	VQELTGR
6.1	801.434464	0.003404	KGVQGGEK
6.0	801.441849	-0.003981	AGPVAIMK
5.6	801.445694	-0.007826	RSLTGPR
5.6	801.434448	0.003420	SRLDPAK

Mascot: http://www.matrixscience.com/

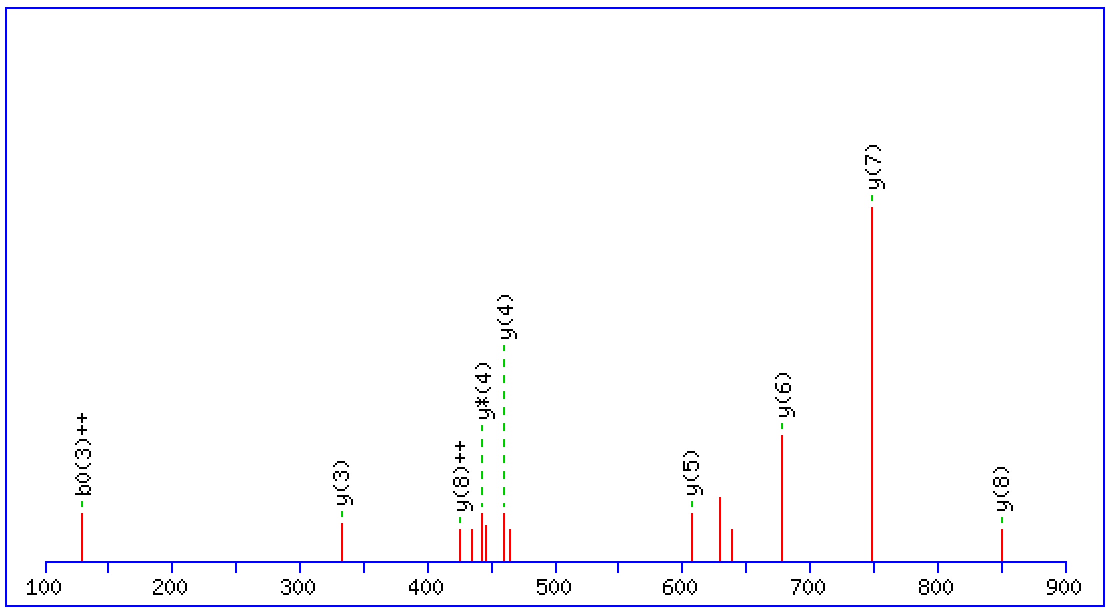
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTAAFQQGK**
Found in **RU1C_HUMAN**, U1 small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1

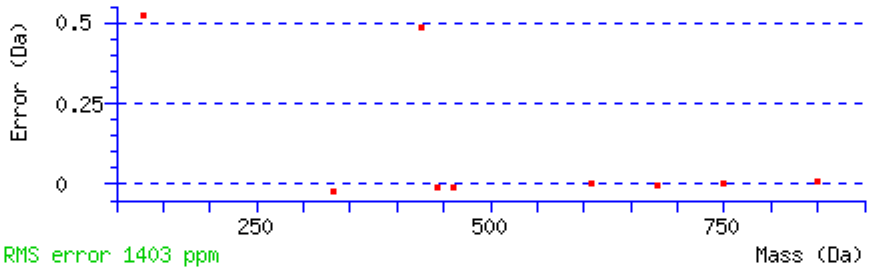
Match to Query 8631: 950.482248 from(476.248400,2+) rtinseconds(975) index(806)
Title: Locus:1.1.1.1837.6
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

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 ●

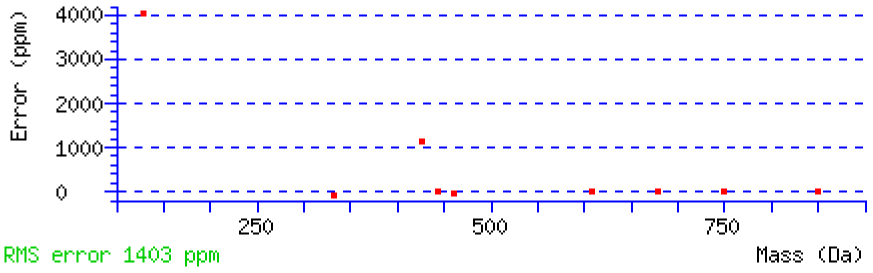


Monoisotopic mass of neutral peptide Mr(calc): 950.482147
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 4.9e-005
Matches : 9/72 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							9
2	203.102634	102.054955			185.092069	93.049672	T	*850.441745*	425.724511	833.415196	417.211236	832.431180	416.719228	8
3	274.139748	137.573512			256.129183	128.568230	A	*749.394066*	375.200671	732.367517	366.687397			7
4	345.176862	173.092069			327.166297	164.086786	A	*678.356952*	339.682114	661.330403	331.168840			6
5	492.245276	246.626276			474.234711	237.620993	F	*607.319838*	304.163557	590.293289	295.650283			5
6	620.303854	310.655565	603.277305	302.142291	602.293289	301.650283	Q	*460.251424*	230.629350	443.224875	222.116076			4
7	748.362432	374.684854	731.335883	366.171580	730.351867	365.679572	Q	*332.192846*	166.600061	315.166297	158.086787			3
8	805.383896	403.195586	788.357347	394.682312	787.373331	394.190304	G	204.134268	102.570772	187.107719	94.057498			2
9							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 1403 ppm



RMS error 1403 ppm

NCBI **BLAST** search of TTAAFQQGK
(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	950.482147	0.000101	TTAAFQQGK

Mascot: http://www.matrixscience.com/

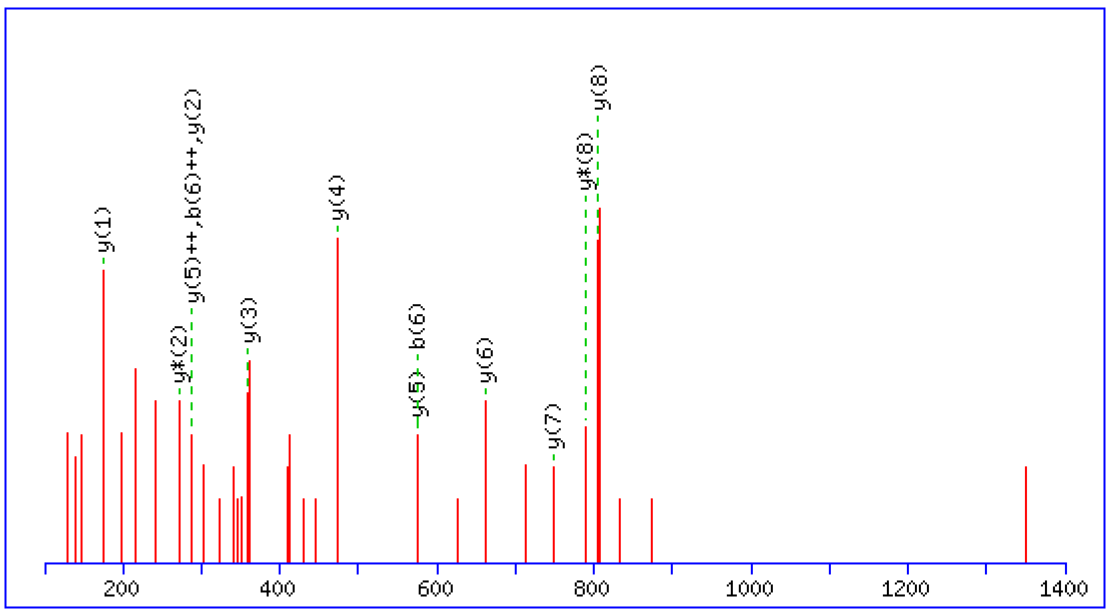
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELGSSTNALR**
Found in **RU2B_HUMAN**, U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1

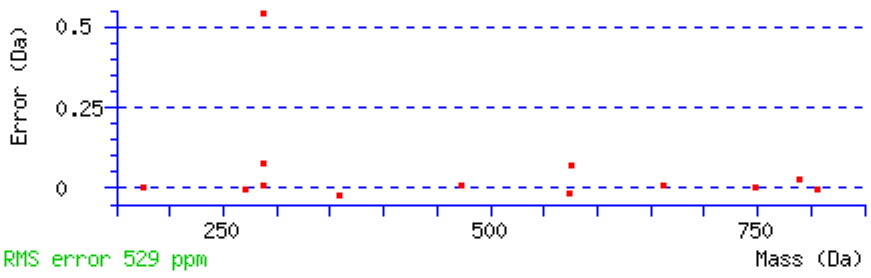
Match to Query 15029: 1046.534908 from(524.274730,2+) rtinseconds(1423) index(10226)
Title: Locus:1.1.1.1984.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-5.mgf

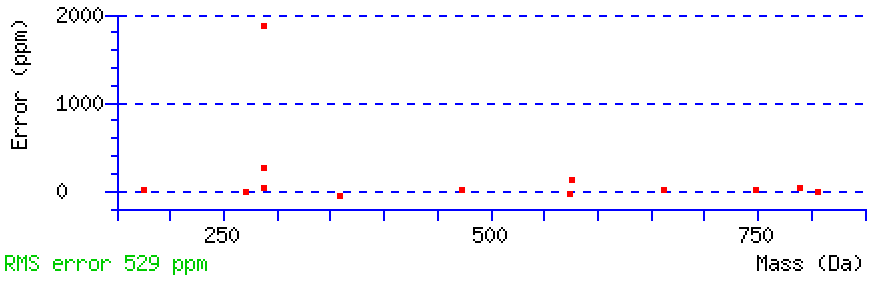
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1046.535614
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 48  Expect: 0.00062
Matches : 13/88 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							10
2	243.133933	122.070605			225.123368	113.065322	L	918.500320	459.753798	901.473771	451.240523	900.489755	450.748516	9
3	300.155397	150.581336			282.144832	141.576054	G	***805.416256***	403.211766	788.389707	394.698491	787.405691	394.206483	8
4	387.187425	194.097351			369.176860	185.092068	S	***748.394792***	374.701034	731.368243	366.187760	730.384227	365.695752	7
5	474.219453	237.613364			456.208888	228.608082	S	***661.362764***	331.185020	644.336215	322.671745	643.352199	322.179737	6
6	575.267132	288.137204			557.256567	279.131922	T	***574.330736***	287.669006	557.304187	279.155732	556.320171	278.663724	5
7	689.310059	345.158668	672.283510	336.645393	671.299494	336.153385	N	***473.283057***	237.145166	456.256508	228.631892			4
8	760.347173	380.677225	743.320624	372.163950	742.336608	371.671942	A	***359.240130***	180.123703	342.213581	171.610428			3
9	873.431237	437.219257	856.404688	428.705982	855.420672	428.213974	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 ELGSSTNALR
(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	1046.535614	-0.000706	ELGSSTNALR
15.7	1046.535614	-0.000706	EVSSATNALR
15.1	1046.529099	0.005809	MAGRTTAAPR
8.5	1046.539642	-0.004734	EPGEFALLR
8.4	1046.533127	0.001781	LTCWQAVR
6.3	1046.543030	-0.008122	TPMAGVSPKK
4.8	1046.535614	-0.000706	SATAAAAATGQK
4.8	1046.542999	-0.008091	LEAAVMELR
4.6	1046.525269	0.009639	CLCIGPGVK
4.3	1046.539642	-0.004734	EFDSLPALR

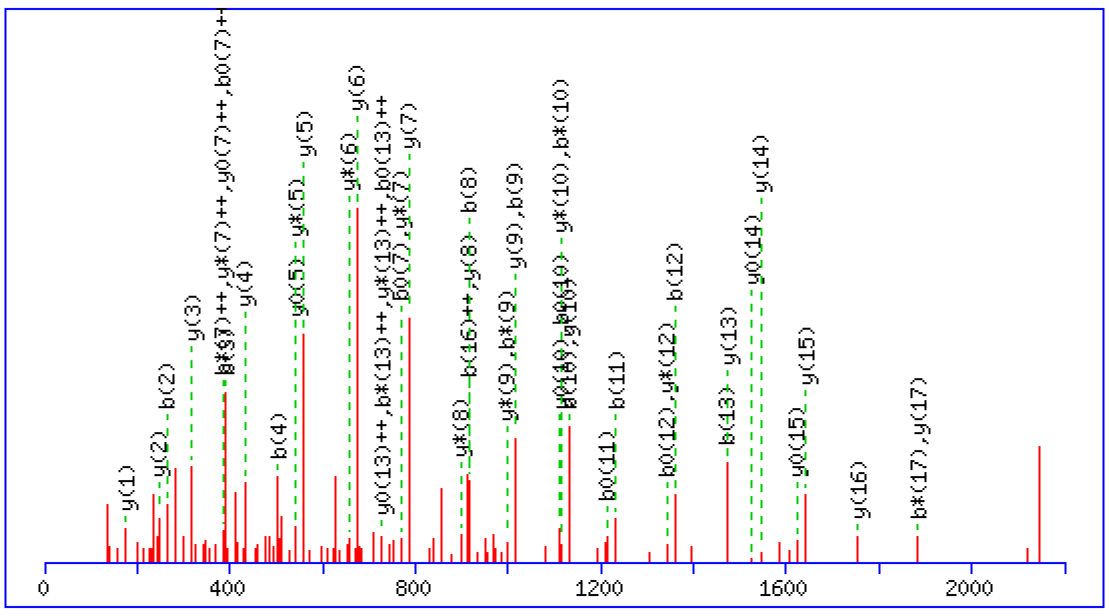
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YVQLPADEVDTQLLQDAAR**
Found in **LSM2_HUMAN**, U6 snRNA-associated Sm-like protein LSm2 OS=Homo sapiens GN=LSM2 PE=1 SV=1

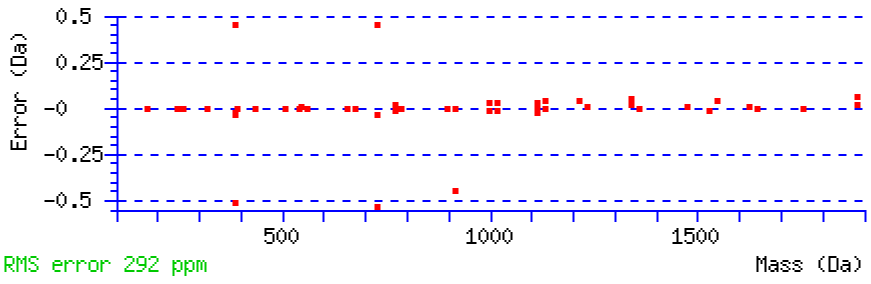
Match to Query 20385: 2144.069502 from(715.697110,3+) rtinseconds(3367) index(12994)
Title: Locus:1.1.1.3293.4
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

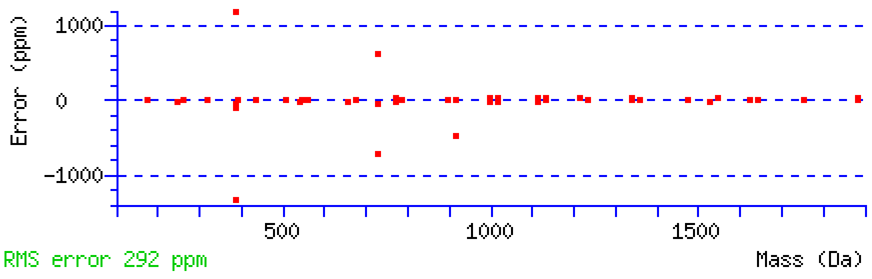
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2144.074951
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 106  Expect: 3.4e-010
Matches : 51/194 fragment ions using 60 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							19
2	**263.139019**	132.073148					V	1982.018913	991.513095	1964.992364	982.999820	1964.008348	982.507812	18
3	**391.197597**	196.102437	374.171048	187.589162			Q	***1882.950499***	941.978888	1865.923950	933.465613	1864.939934	932.973605	17
4	**504.281661**	252.644469	487.255112	244.131194			L	***1754.891921***	877.949599	1737.865372	869.436324	1736.881356	868.944316	16
5	601.334425	301.170851	584.307876	292.657576			P	***1641.807857***	821.407567	1624.781308	812.894292	1623.797292	812.402284	15
6	672.371539	336.689408	655.344990	328.176133			A	***1544.755093***	772.881185	1527.728544	764.367910	1526.744528	763.875902	14
7	787.398482	394.202879	770.371933	385.689605	769.387917	385.197597	D	***1473.717979***	737.362628	1456.691430	728.849353	1455.707414	728.357345	13
8	**916.441075**	458.724176	899.414526	450.210901	898.430510	449.718893	E	1358.691036	679.849156	1341.664487	671.335882	1340.680471	670.843874	12
9	**1015.509489**	508.258383	998.482940	499.745108	997.498924	499.253100	V	1229.648443	615.327860	1212.621894	606.814585	1211.637878	606.322577	11
10	**1130.536432**	565.771854	1113.509883	557.258580	1112.525867	556.766572	D	***1130.580029***	565.793653	1113.553480	557.280378	1112.569464	556.788370	10
11	**1231.584111**	616.295694	1214.557562	607.782419	1213.573546	607.290411	T	***1015.553086***	508.280181	998.526537	499.766907	997.542521	499.274899	9
12	**1359.642689**	680.324983	1342.616140	671.811708	1341.632124	671.319700	Q	***914.505407***	457.756342	897.478858	449.243067	896.494842	448.751059	8
13	**1472.726753**	736.867014	1455.700204	728.353740	1454.716188	727.861732	L	***786.446829***	393.727053	769.420280	385.213778	768.436264	384.721770	7
14	1585.810817	793.409046	1568.784268	784.895772	1567.800252	784.403764	L	***673.362765***	337.185021	656.336216	328.671746	655.352200	328.179738	6
15	1713.869395	857.438335	1696.842846	848.925061	1695.858830	848.433053	Q	***560.278701***	280.642989	543.252152	272.129714	542.268136	271.637706	5
16	1828.896338	914.951807	1811.869789	906.438533	1810.885773	905.946525	D	***432.220123***	216.613700	415.193574	208.100425	414.209558	207.608417	4
17	1899.933452	950.470364	1882.906903	941.957090	1881.922887	941.465082	A	***317.193180***	159.100228	300.166631	150.586954			3
18	1970.970566	985.988921	1953.944017	977.475647	1952.960001	976.983638	A	***246.156066***	123.581671	229.129517	115.068397			2
19							R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of YVQLPADEVDTQLLQDAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
105.7	2144.074951	-0.005449	YVQLPADEVDTQLLQDAAR
6.4	2144.086227	-0.016725	GPPGPSGLAGEPGKPGIPGLPGR
5.5	2144.068420	0.001082	TFPAAQCPEESKPPVRIR
3.8	2144.086166	-0.016664	VPRLPATAAEPEAAVISNGEH
1.3	2144.051163	0.018339	GGLSPFHAPAQSPGLHGGAAGSR
1.2	2144.065918	0.003584	SAPNCILLAMFLVHYGHR

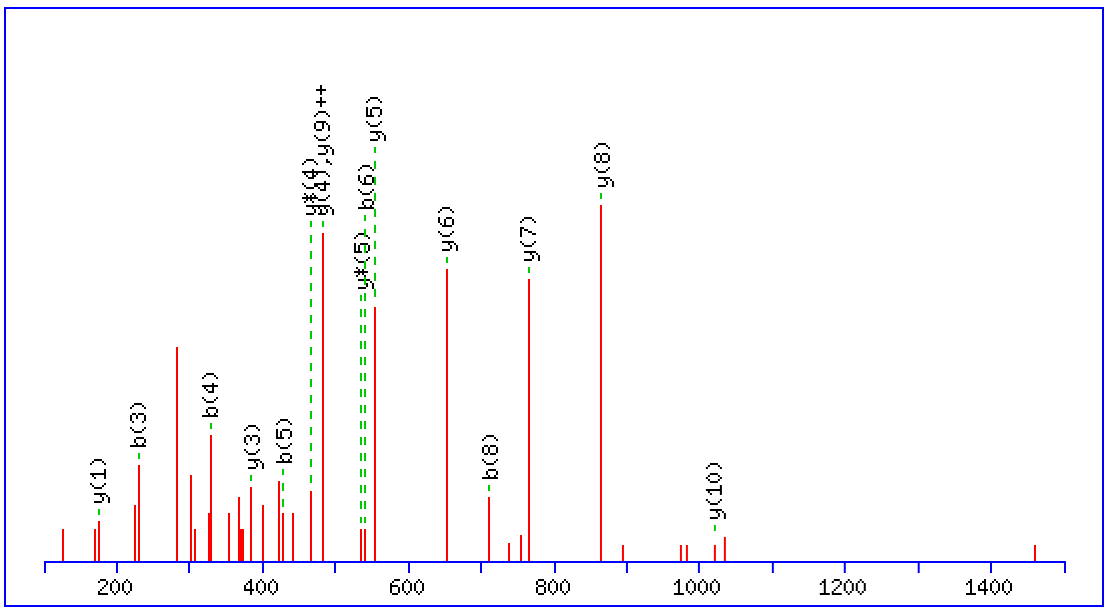
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GDGVVLVAPPLR**
Found in **LSM3_HUMAN**, U6 snRNA-associated Sm-like protein LSm3 OS=Homo sapiens GN=LSM3 PE=1 SV=2

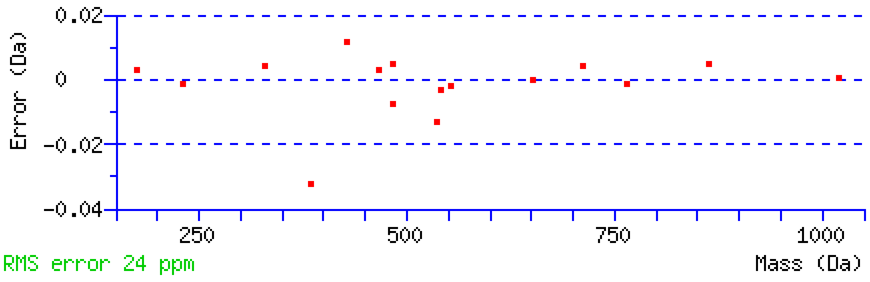
Match to Query 20231: 1191.700848 from(596.857700,2+) rtinseconds(2790) index(26915)
Title: Locus:1.1.1.2525.13
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-6.mgf

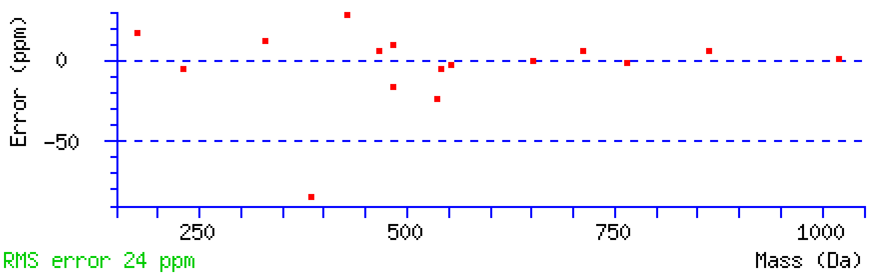
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1191.697571
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56 **Expect:** 4.4e-006
Matches : 16/88 fragment ions using 26 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	173.055683	87.031479	155.045118	78.026197	D	1135.683371	568.345324	1118.656822	559.832049	1117.672806	559.340041	11
3	**230.077147**	115.542211	212.066582	106.536929	G	***1020.656428***	510.831852	1003.629879	502.318578			10
4	**329.145561**	165.076418	311.134996	156.071136	V	963.634964	482.321120	946.608415	473.807845			9
5	**428.213975**	214.610626	410.203410	205.605343	V	***864.566550***	432.786913	847.540001	424.273639			8
6	**541.298039**	271.152658	523.287474	262.147375	L	***765.498136***	383.252706	748.471587	374.739431			7
7	640.366453	320.686865	622.355888	311.681582	V	***652.414072***	326.710674	635.387523	318.197400			6
8	**711.403567**	356.205422	693.393002	347.200139	A	***553.345658***	277.176467	536.319109	268.663193			5
9	808.456331	404.731804	790.445766	395.726521	P	***482.308544***	241.657910	465.281995	233.144635			4
10	905.509095	453.258186	887.498530	444.252903	P	***385.255780***	193.131528	368.229231	184.618253			3
11	1018.593159	509.800218	1000.582594	500.794935	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 GDGVVLVAPPLR
(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	1191.697571	0.003277	GDGVVLVAPPLR
4.6	1191.708755	-0.007907	DPLALAALPRR
0.9	1191.708786	-0.007938	GVPIRLEVGPR

Mascot: http://www.matrixscience.com/

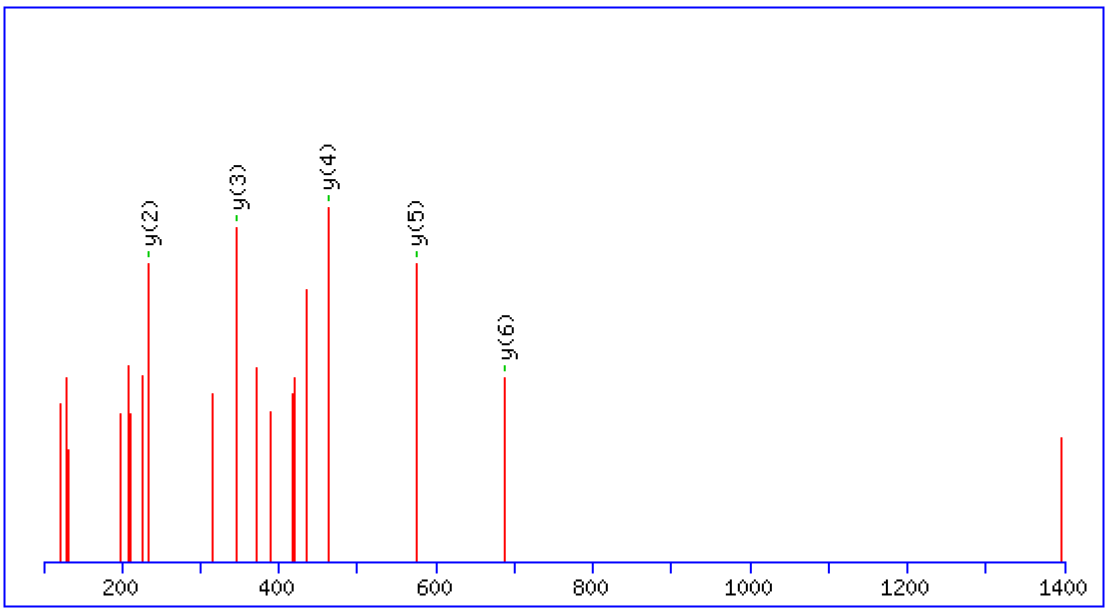
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ESILDLSK**
Found in **LSM7_HUMAN**, U6 snRNA-associated Sm-like protein LSm7 OS=Homo sapiens GN=LSM7 PE=1 SV=1

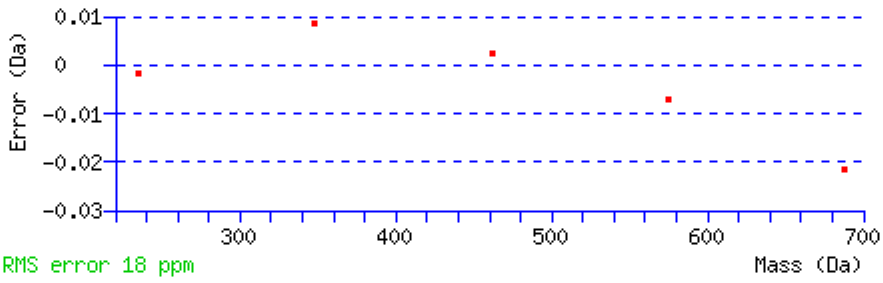
Match to Query 3193: 903.491168 from(452.752860,2+) rtinseconds(2461) index(7414)
Title: Locus:1.1.1.2956.5
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

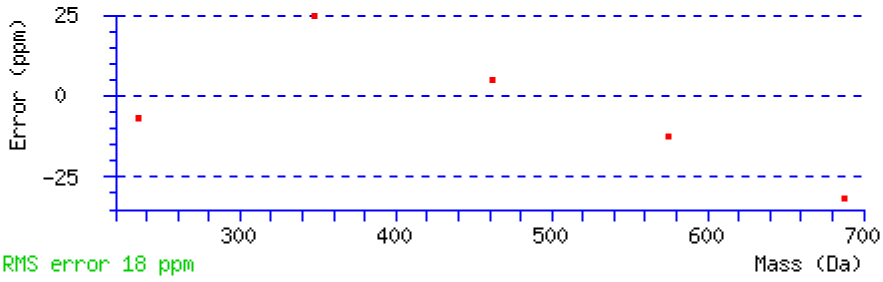
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 903.491287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 45  Expect: 0.0004
Matches : 5/68 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							8
2	217.081897	109.044586	199.071332	100.039304	S	775.455995	388.231636	758.429446	379.718361	757.445430	379.226353	7
3	330.165961	165.586618	312.155396	156.581336	I	*688.423967*	344.715622	671.397418	336.202347	670.413402	335.710339	6
4	443.250025	222.128650	425.239460	213.123368	L	*575.339903*	288.173590	558.313354	279.660315	557.329338	279.168307	5
5	558.276968	279.642122	540.266403	270.636840	D	*462.255839*	231.631557	445.229290	223.118283	444.245274	222.626275	4
6	671.361032	336.184154	653.350467	327.178872	L	*347.228896*	174.118086	330.202347	165.604811	329.218331	165.112803	3
7	758.393060	379.700168	740.382495	370.694886	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 ESILDLSK
(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	903.491287	-0.000119	ESILDLSK
13.8	903.491287	-0.000119	LELSDLSK
4.9	903.492630	-0.001462	EIQHHLK

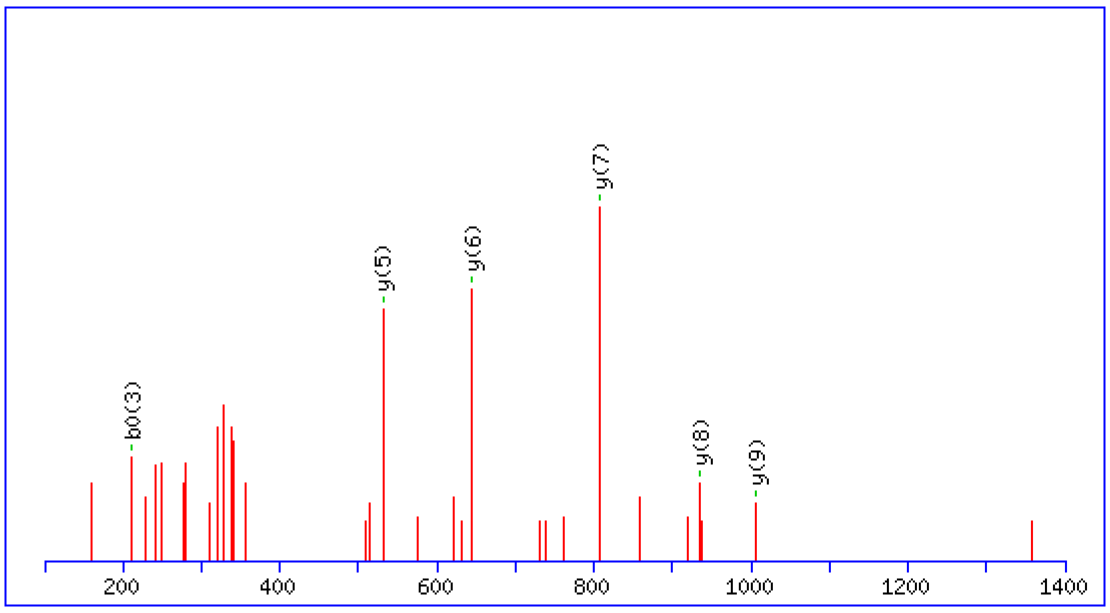
{MATRIX SCIENCE} Mascot Search Results

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

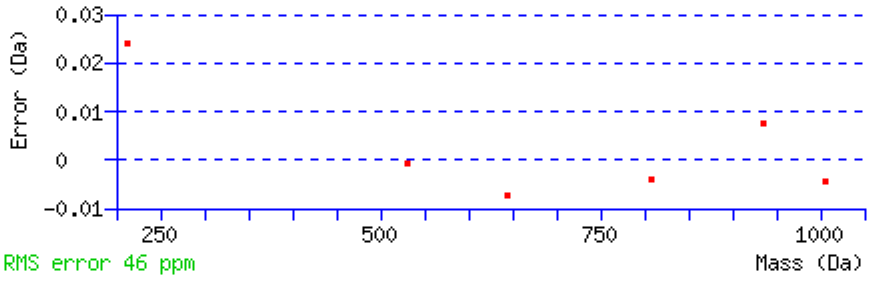
Match to Query 366548: 1163.631388 from(582.822970,2+) rtinseconds(2289) index(813525)
Title: Locus:1.1.1.941.22
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

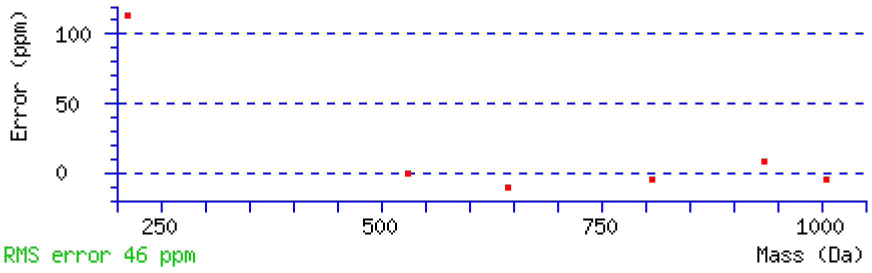
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1163.629837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 34  Expect: 0.0019
Matches : 6/104 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	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
34.2	1163.629837	0.001551	ASAQYITAALR

Mascot: http://www.matrixscience.com/

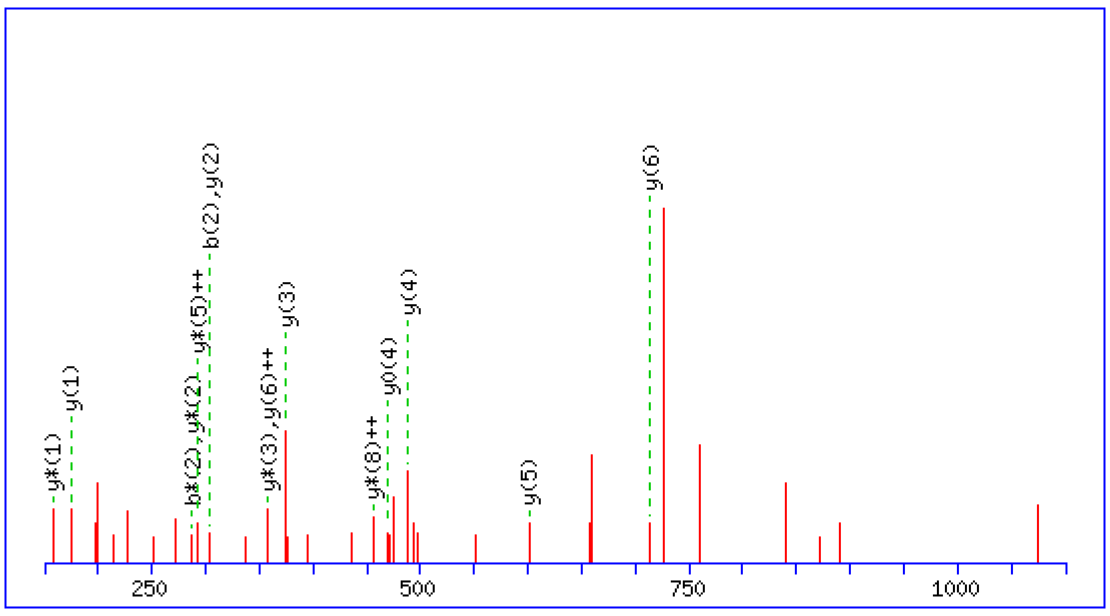
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FRGPLLAER**
Found in **CYLD_HUMAN**, Ubiquitin carboxyl-terminal hydrolase CYLD OS=Homo sapiens GN=CYLD PE=1 SV=1

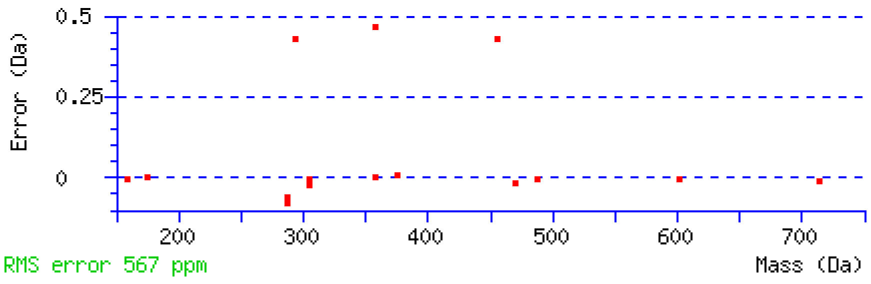
Match to Query 8236: 1073.587528 from(537.801040,2+) rtinseconds(2700) index(9056)
Title: Locus:1.1.1.3045.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

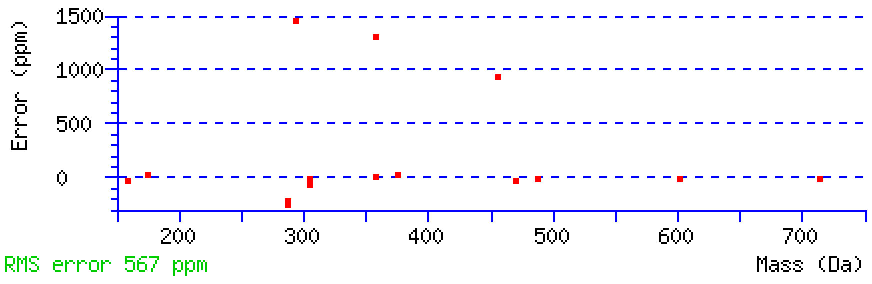
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1073.598160
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4 : Oxidation (P)
Ions Score: 32 **Expect:** 0.01
Matches : 15/78 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	148.075690	74.541483					F							9
2	304.176801	152.592039	287.150252	144.078764			R	927.537041	464.272159	910.510492	455.758884	909.526476	455.266876	8
3	361.198265	181.102770	344.171716	172.589496			G	771.435930	386.221603	754.409381	377.708329	753.425365	377.216321	7
4	474.245944	237.626610	457.219395	229.113335			P	***714.414466***	357.710871	697.387917	349.197597	696.403901	348.705589	6
5	587.330008	294.168642	570.303459	285.655368			L	***601.366787***	301.187032	584.340238	292.673757	583.356222	292.181749	5
6	700.414072	350.710674	683.387523	342.197400			L	***488.282723***	244.645000	471.256174	236.131725	470.272158	235.639717	4
7	771.451186	386.229231	754.424637	377.715957			A	***375.198659***	188.102968	358.172110	179.589693	357.188094	179.097685	3
8	900.493779	450.750528	883.467230	442.237253	882.483214	441.745245	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 FRGPLLAER
(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	1073.598160	-0.010632	FRGPLLAER
17.9	1073.590302	-0.002774	VVKMSPIER
9.4	1073.577042	0.010486	SFPWRLPR
9.1	1073.586945	0.000583	VIFQLPGER
7.7	1073.590302	-0.002774	VVKMSPIER
6.5	1073.582916	0.004612	VSSGKKPPSR
5.0	1073.590271	-0.002743	MARLAELAAL
4.6	1073.582901	0.004627	SDLSELRVR
4.5	1073.586945	0.000583	LALPGFSTPR
3.4	1073.586945	0.000583	LALPGFSTPR

Mascot: http://www.matrixscience.com/

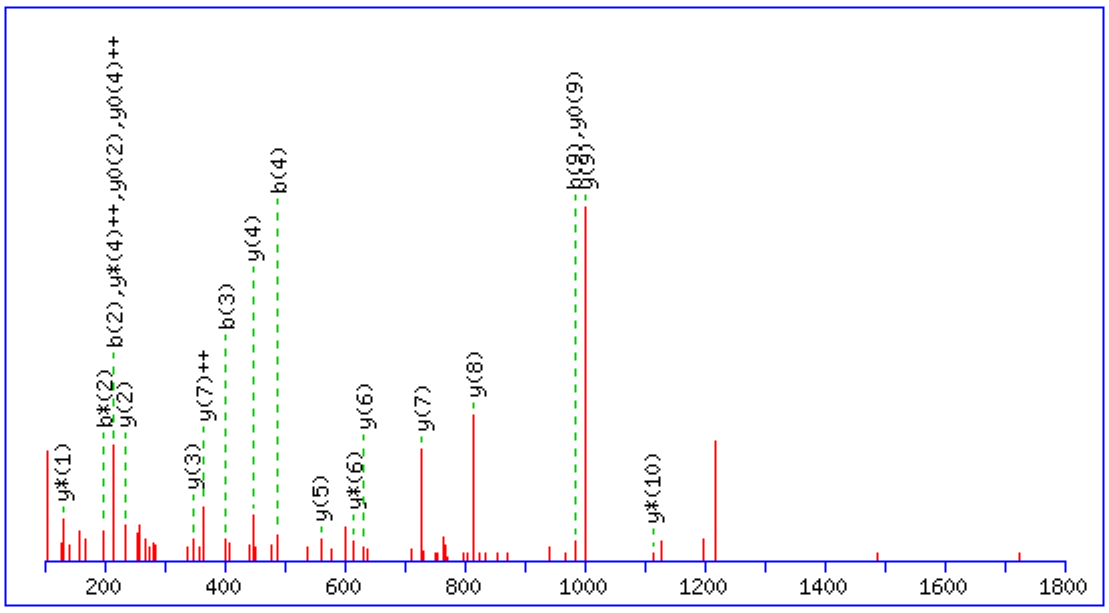
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQWSPALTISK**
Found in **UB2D2_HUMAN**, Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1

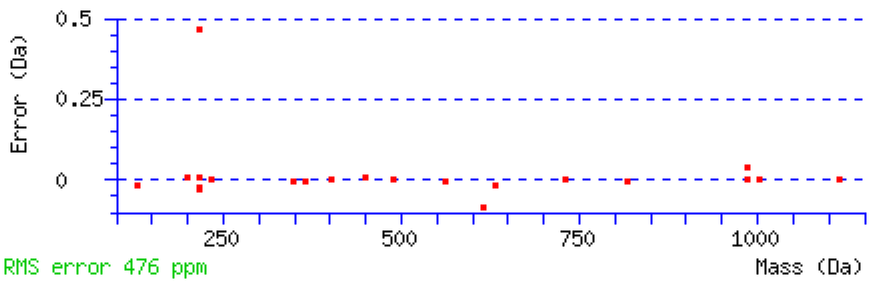
Match to Query 19654: 1216.647408 from(609.330980,2+) rtinseconds(2523) index(22289)
Title: Locus:1.1.1.2458.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

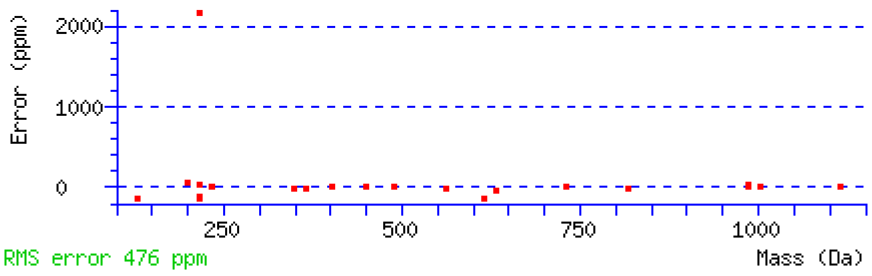
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1216.645172
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 58 **Expect:** 2e-005
Matches : 21/116 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	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	1130.620436	565.813856	1113.593887	557.300582	1112.609871	556.808574	10
3	**402.177195**	201.592236	385.150646	193.078961	384.166630	192.586953	W	***1002.561858***	501.784567	985.535309	493.271293	984.551293	492.779285	9
4	**489.209223**	245.108250	472.182674	236.594975	471.198658	236.102967	S	***816.482545***	408.744911	799.455996	400.231636	798.471980	399.739628	8
5	586.261987	293.634632	569.235438	285.121357	568.251422	284.629349	P	***729.450517***	365.228897	712.423968	356.715622	711.439952	356.223614	7
6	657.299101	329.153189	640.272552	320.639914	639.288536	320.147906	A	***632.397753***	316.702515	615.371204	308.189240	614.387188	307.697232	6
7	770.383165	385.695221	753.356616	377.181946	752.372600	376.689938	L	***561.360639***	281.183958	544.334090	272.670683	543.350074	272.178675	5
8	871.430844	436.219060	854.404295	427.705786	853.420279	427.213778	T	***448.276575***	224.641926	431.250026	216.128651	430.266010	215.636643	4
9	**984.514908**	492.761092	967.488359	484.247818	966.504343	483.755810	I	***347.228896***	174.118086	330.202347	165.604812	329.218331	165.112804	3
10	1071.546936	536.277106	1054.520387	527.763832	1053.536371	527.271824	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 SQWSPALTISK
(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	1216.645172	0.002236	SQWSPALTISK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

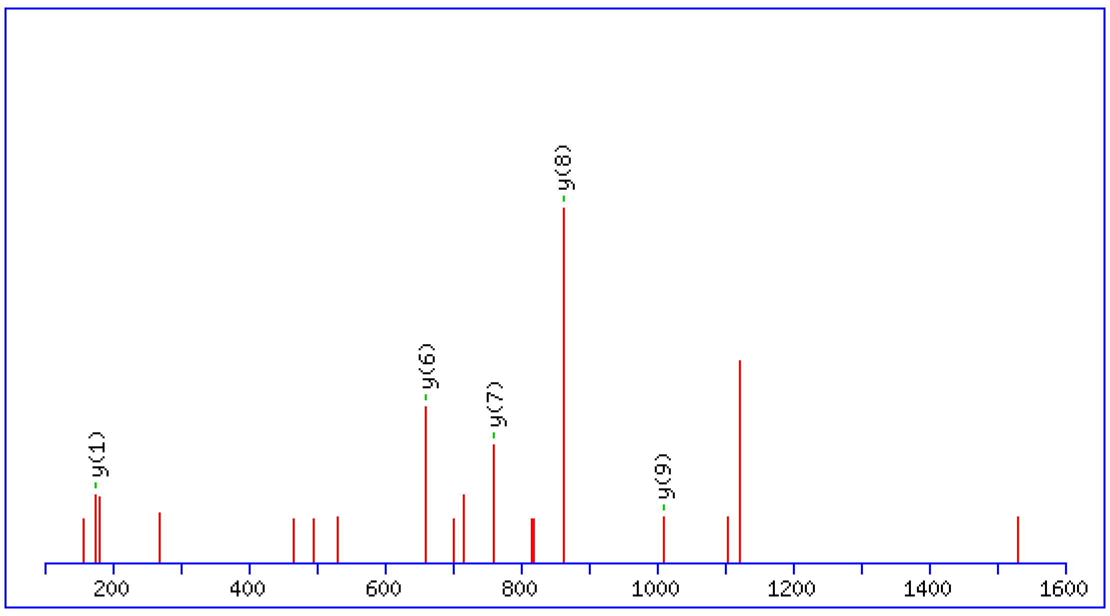
Mascot Search Results

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

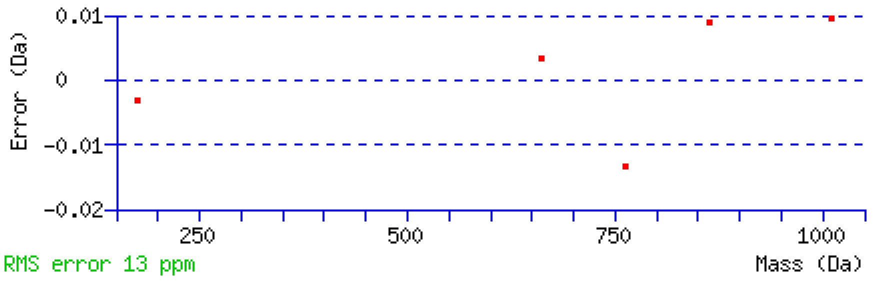
Match to Query 19090: 1121.553768 from(561.784160,2+) rtinseconds(899) index(1824)
Title: Locus:1.1.1.1725.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

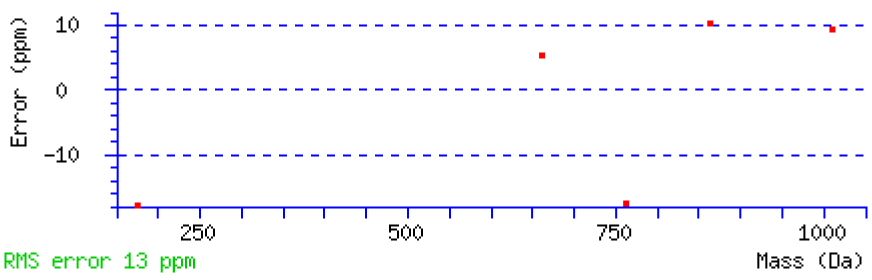
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1121.549911
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: 41 **Expect:** 0.0011
Matches : 5/134 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							10
2	261.126740	131.067008					M	***1009.473121***	505.240199	992.446572	496.726924	991.462556	496.234916	9
3	362.174419	181.590848			344.163854	172.585565	T	***862.437721***	431.722499	845.411172	423.209224	844.427156	422.717216	8
4	463.222098	232.114687			445.211533	223.109405	T	***761.390042***	381.198659	744.363493	372.685385	743.379477	372.193377	7
5	520.243562	260.625419			502.232997	251.620137	G	***660.342363***	330.674820	643.315814	322.161545	642.331798	321.669537	6
6	634.286489	317.646883	617.259940	309.133608	616.275924	308.641600	N	603.320899	302.164088	586.294350	293.650813	585.310334	293.158805	5
7	748.329416	374.668346	731.302867	366.155072	730.318851	365.663064	N	489.277972	245.142624	472.251423	236.629349	471.267407	236.137341	4
8	849.377095	425.192186	832.350546	416.678911	831.366530	416.186903	T	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
9	948.445509	474.726393	931.418960	466.213118	930.434944	465.721110	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
40.5	1121.549911	0.003857	LMTTGNNTVR
25.8	1121.561783	-0.008015	LFTDWRER
25.3	1121.553925	-0.000157	LFPMSALDGR
25.3	1121.553925	-0.000157	LFPMSALDGR
13.8	1121.557739	-0.003971	LFSNSRENR
13.8	1121.550552	0.003216	LFWADSDLR
5.6	1121.553940	-0.000172	CLVSGWGTTK
4.8	1121.561142	-0.007374	STMTLGRSGGR
2.5	1121.553925	-0.000157	MLIPFSNPR
2.3	1121.560440	-0.006672	LFLTEEDQK

Mascot: http://www.matrixscience.com/

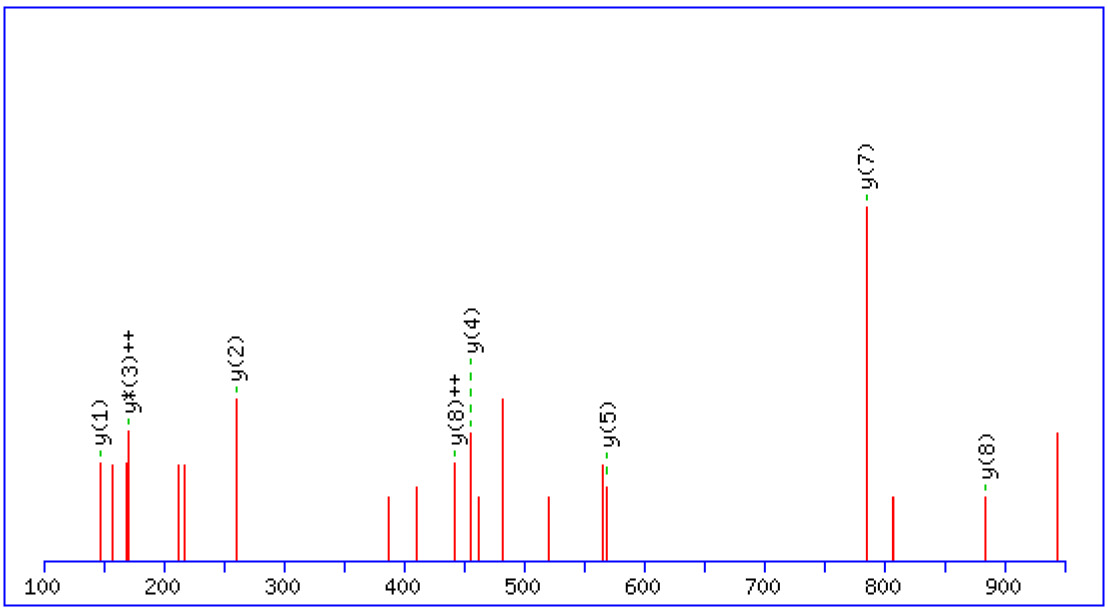
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVSEIPVLK**
Found in **UFC1_HUMAN**, Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens GN=UFC1 PE=1 SV=3

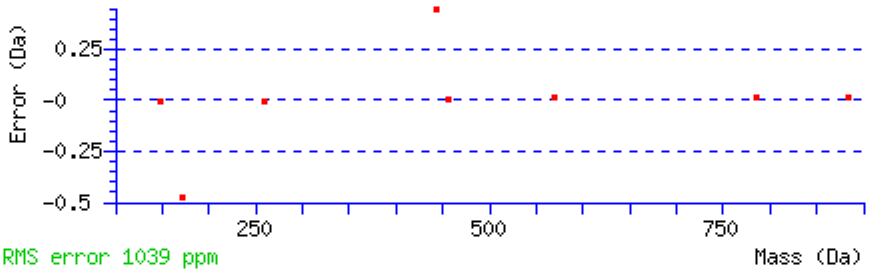
Match to Query 9778: 982.607068 from(492.310810,2+) rtinseconds(2432) index(20695)
Title: Locus:1.1.1.2423.7
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

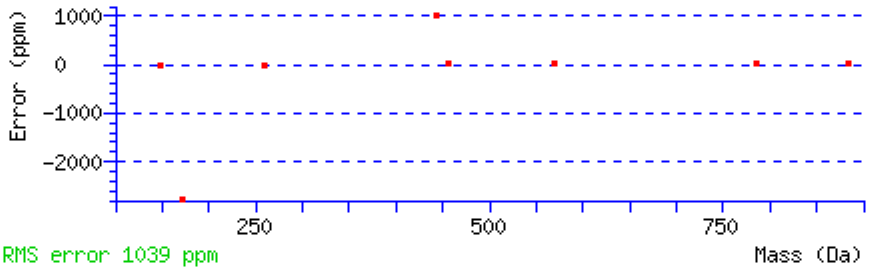
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 982.606277
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47   Expect: 2.4e-005
Matches : 8/66 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							9
2	199.144104	100.075690			V	***884.545145***	442.776211	867.518596	434.262936	866.534580	433.770928	8
3	286.176132	143.591704	268.165567	134.586422	S	***785.476731***	393.242004	768.450182	384.728729	767.466166	384.236721	7
4	415.218725	208.113001	397.208160	199.107718	E	698.444703	349.725990	681.418154	341.212715	680.434138	340.720707	6
5	528.302789	264.655033	510.292224	255.649750	I	***569.402110***	285.204693	552.375561	276.691419			5
6	625.355553	313.181415	607.344988	304.176132	P	***456.318046***	228.662661	439.291497	220.149386			4
7	724.423967	362.715622	706.413402	353.710339	V	359.265282	180.136279	342.238733	171.623004			3
8	837.508031	419.257654	819.497466	410.252371	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 VVSEIPVLK
(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	982.606277	0.000791	VVSEIPVLK
5.9	982.606262	0.000806	TPLILAVEK
0.8	982.603577	0.003491	VVAAAGRALR

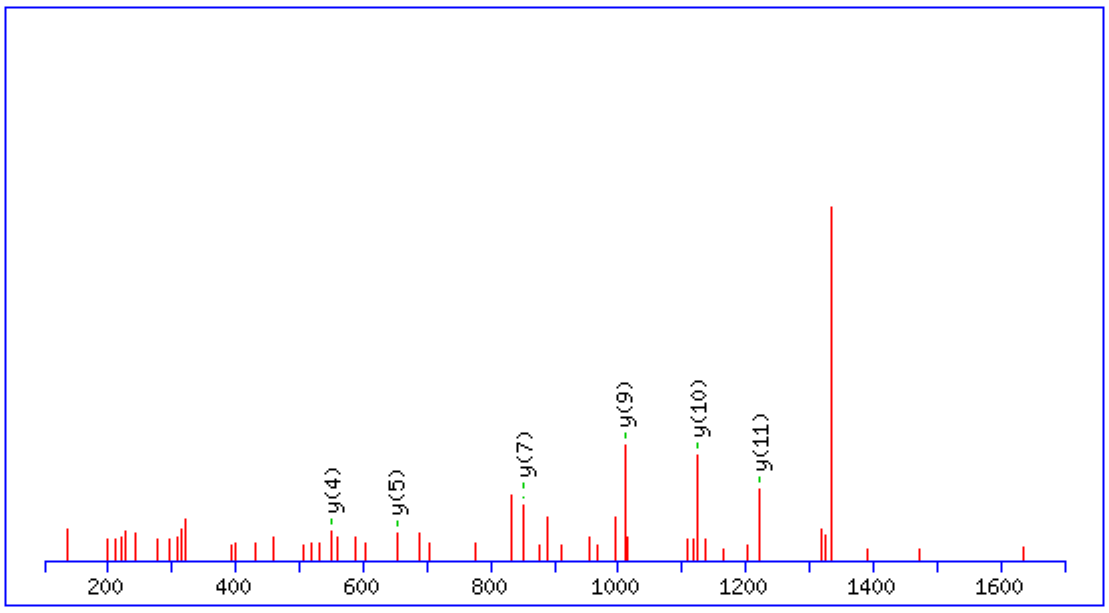
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPDGTSLTQTFR**
Found in **UBXN1_HUMAN**, UBX domain-containing protein 1 OS=Homo sapiens GN=UBXN1 PE=1 SV=2

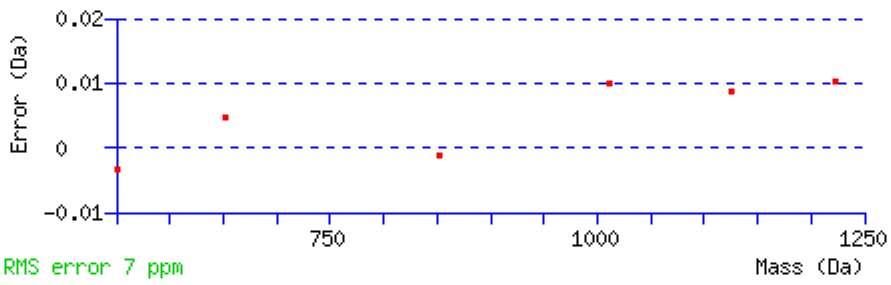
Match to Query 32948: 1334.685728 from(668.350140,2+) rtinseconds(2578) index(31231)
Title: Locus:1.1.1.2380.34
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

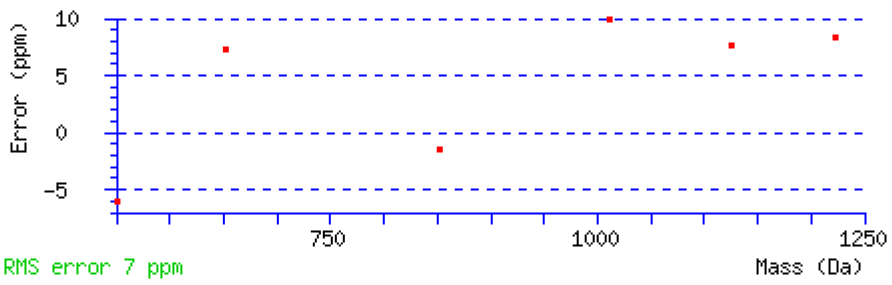
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1334.683044
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0027
Matches : 6/108 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	211.144104	106.075690					P	*1222.606244*	611.806760	1205.579695	603.293486	1204.595679	602.801478	11
3	326.171047	163.589161			308.160482	154.583879	D	*1125.553480*	563.280378	1108.526931	554.767104	1107.542915	554.275096	10
4	383.192511	192.099893			365.181946	183.094611	G	*1010.526537*	505.766907	993.499988	497.253632	992.515972	496.761624	9
5	484.240190	242.623733			466.229625	233.618450	T	953.505073	477.256175	936.478524	468.742900	935.494508	468.250892	8
6	571.272218	286.139747			553.261653	277.134465	S	*852.457394*	426.732335	835.430845	418.219061	834.446829	417.727053	7
7	684.356282	342.681779			666.345717	333.676497	L	765.425366	383.216321	748.398817	374.703047	747.414801	374.211039	6
8	785.403961	393.205619			767.393396	384.200336	T	*652.341302*	326.674289	635.314753	318.161015	634.330737	317.669007	5
9	913.462539	457.234908	896.435990	448.721633	895.451974	448.229625	Q	*551.293623*	276.150450	534.267074	267.637175	533.283058	267.145167	4
10	1014.510218	507.758747	997.483669	499.245473	996.499653	498.753465	T	423.235045	212.121161	406.208496	203.607886	405.224480	203.115878	3
11	1161.578632	581.292954	1144.552083	572.779680	1143.568067	572.287672	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 LPDGTSLTQTFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1334.683044	0.002684	LPDGTSLTQTFR
1.5	1334.675140	0.010588	IKQDVESLMEK

Mascot: http://www.matrixscience.com/

{MATRIX SCIENCE}

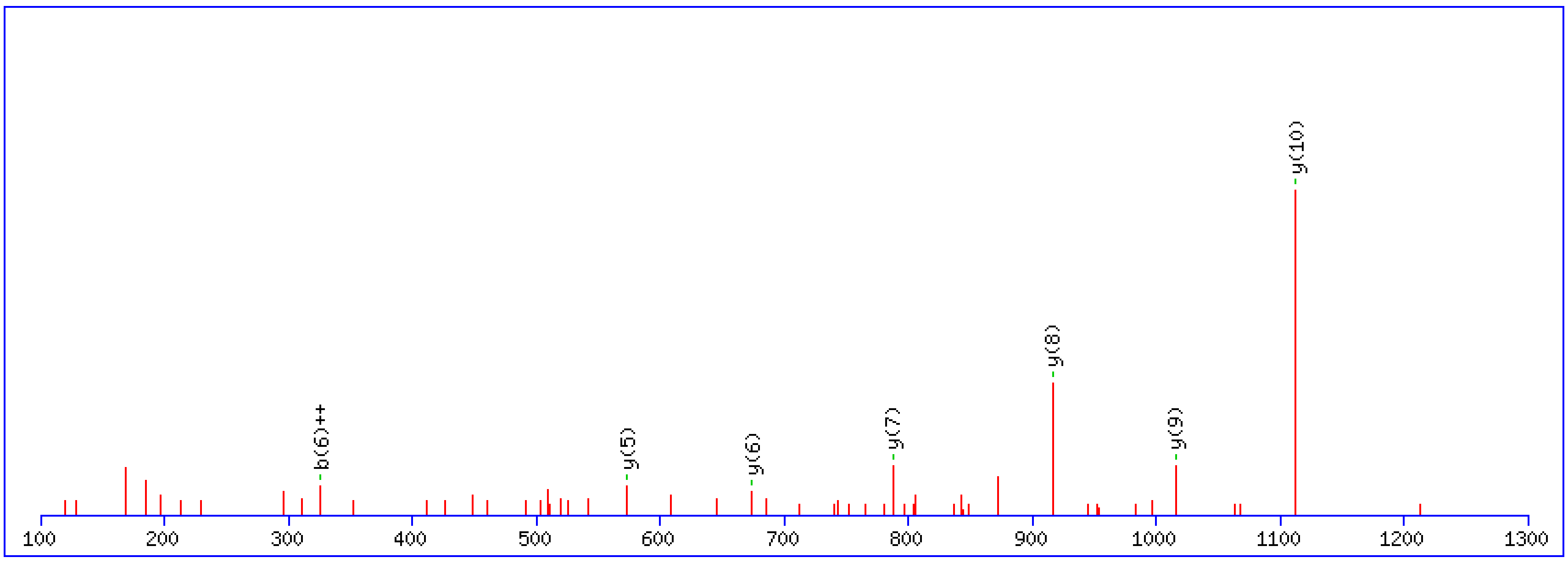
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVPVEITISLLK**
Found in **KCY_HUMAN**, UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3

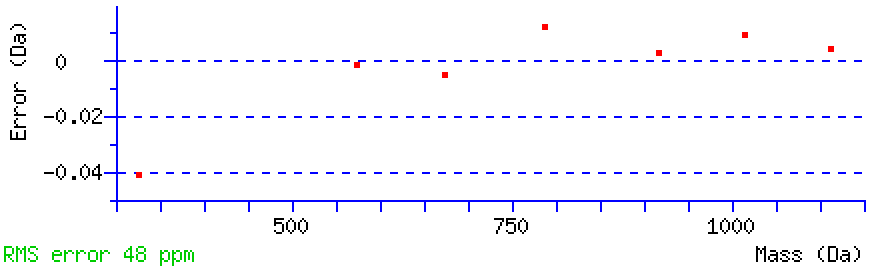
Match to Query 18208: 1323.837748 from(662.926150,2+) rtinseconds(3785) index(53921)
Title: Locus:1.1.1.2147.20
Data file 2012-01-27 - TFD - Stroma - IEC - 10ul - 1.mgf

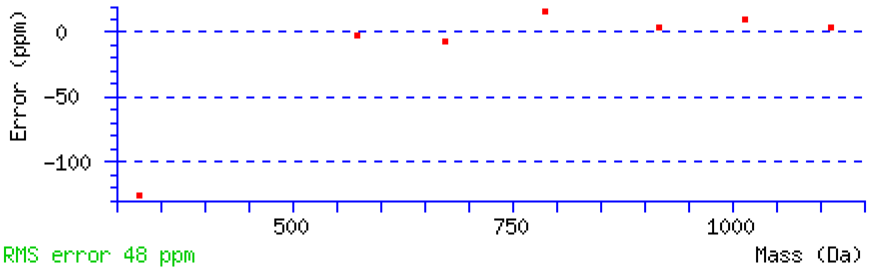
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1323.837723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 40  Expect: 9.8e-005
Matches : 7/96 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	213.159754	107.083515			V	1211.760952	606.384114	1194.734403	597.870840	1193.750387	597.378832	11
3	310.212518	155.609897			P	***1112.692538***	556.849907	1095.665989	548.336633	1094.681973	547.844625	10
4	409.280932	205.144104			V	***1015.639774***	508.323525	998.613225	499.810251	997.629209	499.318243	9
5	538.323525	269.665401	520.312960	260.660118	E	***916.571360***	458.789318	899.544811	450.276043	898.560795	449.784035	8
6	651.407589	326.207433	633.397024	317.202150	I	***787.528767***	394.268022	770.502218	385.754747	769.518202	385.262739	7
7	752.455268	376.731272	734.444703	367.725990	T	***674.444703***	337.725990	657.418154	329.212715	656.434138	328.720707	6
8	865.539332	433.273304	847.528767	424.268022	I	***573.397024***	287.202150	556.370475	278.688875	555.386459	278.196868	5
9	952.571360	476.789318	934.560795	467.784036	S	460.312960	230.660118	443.286411	222.146843	442.302395	221.654835	4
10	1065.655424	533.331350	1047.644859	524.326068	L	373.280932	187.144104	356.254383	178.630829			3
11	1178.739488	589.873382	1160.728923	580.868099	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 IVPVEITISLLK
(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	1323.837723	0.000025	IVPVEITISLLK

Mascot: http://www.matrixscience.com/

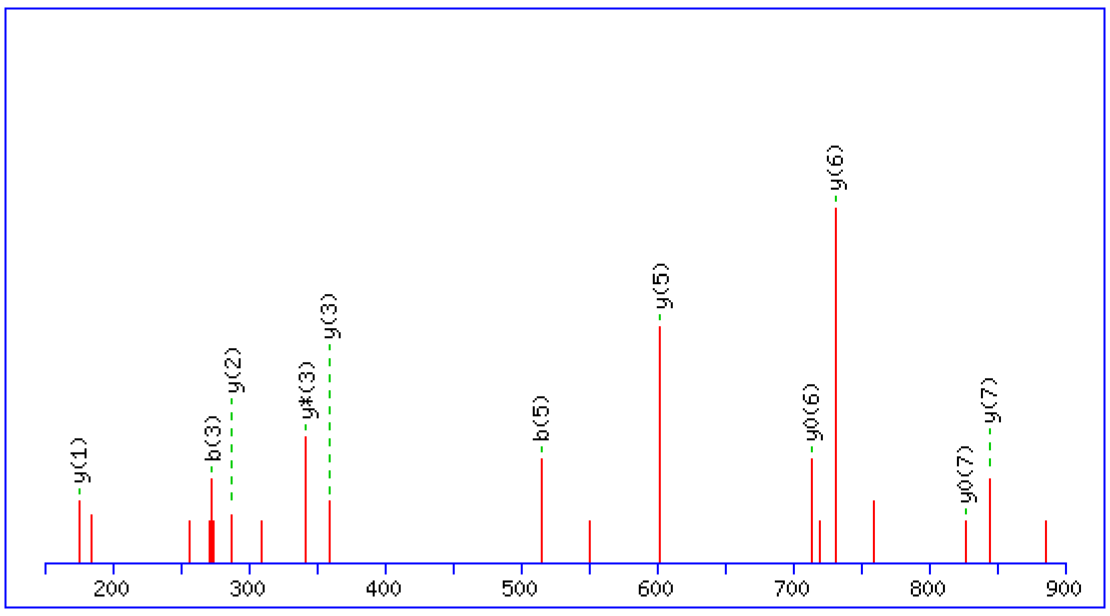
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSQLEDQALR**
Found in **CS068_HUMAN**, Uncharacterized protein C19orf68 OS=Homo sapiens GN=C19orf68 PE=1 SV=2

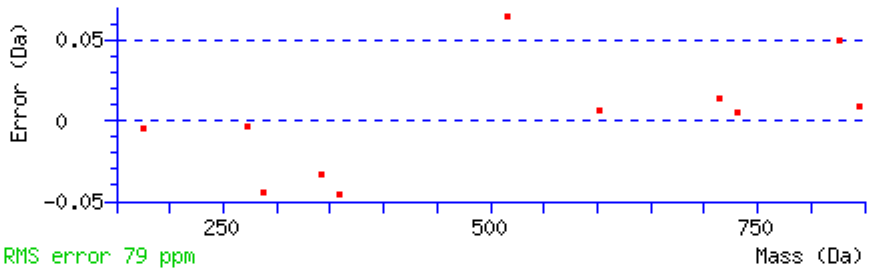
Match to Query 20983: 1115.554248 from(558.784400,2+) rtinseconds(1378) index(8735)
Title: Locus:1.1.1.2015.28
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-4.mgf

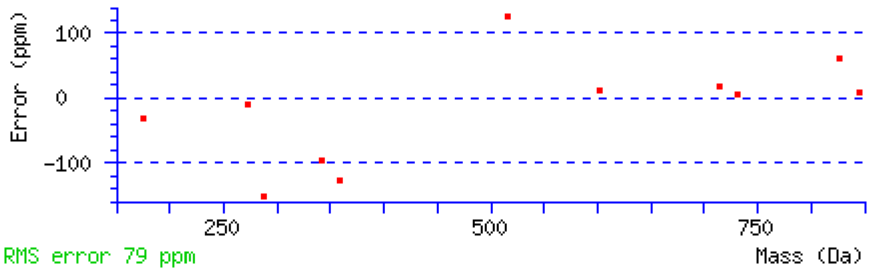
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1115.557083
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 51 **Expect:** 9.6e-005
Matches : 11/94 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	58.028740	29.518008					G							10
2	145.060768	73.034022			127.050203	64.028740	S	1059.542914	530.275095	1042.516365	521.761821	1041.532349	521.269813	9
3	**273.119346**	137.063311	256.092797	128.550037	255.108781	128.058029	Q	972.510886	486.759081	955.484337	478.245807	954.500321	477.753799	8
4	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	L	***844.452308***	422.729792	827.425759	414.216518	826.441743	413.724510	7
5	**515.246003**	258.126640	498.219454	249.613365	497.235438	249.121357	E	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.182478	6
6	630.272946	315.640111	613.246397	307.126837	612.262381	306.634829	D	***602.325651***	301.666464	585.299102	293.153189	584.315086	292.661181	5
7	758.331524	379.669400	741.304975	371.156126	740.320959	370.664118	Q	487.298708	244.152992	470.272159	235.639717			4
8	829.368638	415.187957	812.342089	406.674683	811.358073	406.182675	A	***359.240130***	180.123703	342.213581	171.610428			3
9	942.452702	471.729989	925.426153	463.216715	924.442137	462.724707	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 GSQLEDQALR
(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	1115.557083	-0.002835	GSQLEDQALR
10.8	1115.557098	-0.002850	TNGVAISDPSR
6.7	1115.557083	-0.002835	ATLSAAPSNPR
5.3	1115.543335	0.010913	IYYGMNALR
3.6	1115.550552	0.003696	APRCAQVER
3.4	1115.543350	0.010898	AQWEMPQVK
3.3	1115.564468	-0.010220	MVLNEEIPR
3.3	1115.545883	0.008365	SPPSLTPTPR
2.9	1115.543335	0.010913	SNAQFKMYK
2.7	1115.545868	0.008380	DPDITSSPIR

Mascot: http://www.matrixscience.com/

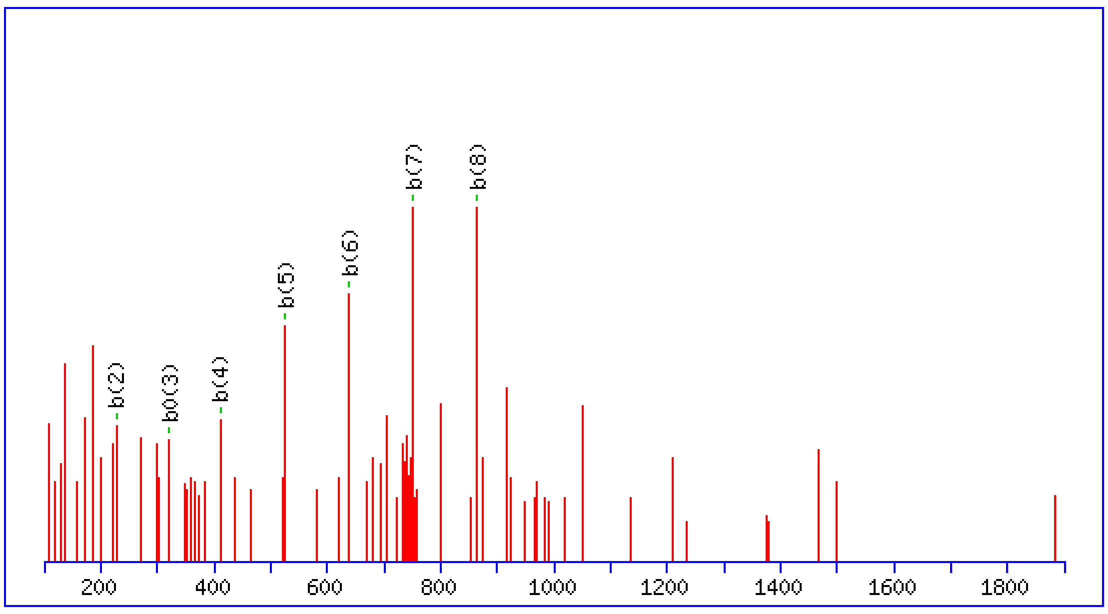
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPLADPPPMR**
Found in **CA172_HUMAN**, Uncharacterized protein C1orf172 OS=Homo sapiens GN=C1orf172 PE=2 SV=2

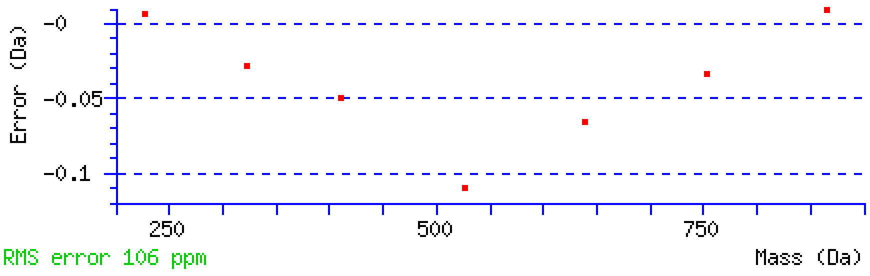
Match to Query 21523: 1169.531428 from(585.772990,2+) rtinseconds(3070) index(42636)
Title: Locus:1.1.1.2552.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.mgf

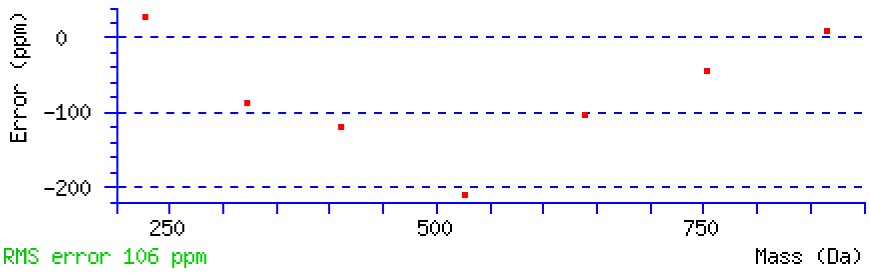
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1169.538666
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
P7      : Oxidation (P)
P8      : Oxidation (P)
Ions Score: 46  Expect: 0.00019
Matches : 7/80 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572	112.039304	56.523290	E							10
2	*227.102633*	114.054954	209.092068	105.049672	P	1041.503359	521.255318	1024.476810	512.742043	1023.492794	512.250035	9
3	340.186697	170.596986	322.176132	161.591704	L	944.450595	472.728936	927.424046	464.215661	926.440030	463.723653	8
4	*411.223811*	206.115544	393.213246	197.110261	A	831.366531	416.186904	814.339982	407.673629	813.355966	407.181621	7
5	*526.250754*	263.629015	508.240189	254.623733	D	760.329417	380.668347	743.302868	372.155072	742.318852	371.663064	6
6	*639.298433*	320.152855	621.287868	311.147572	P	645.302474	323.154875	628.275925	314.641601			5
7	*752.346112*	376.676694	734.335547	367.671412	P	532.254795	266.631036	515.228246	258.117761			4
8	*865.393791*	433.200534	847.383226	424.195251	P	419.207116	210.107196	402.180567	201.593922			3
9	996.434276	498.720776	978.423711	489.715494	M	306.159437	153.583357	289.132888	145.070082			2
10					R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of EPLADPPPMR
(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	1169.538666	-0.007238	EPLADPPPMR
30.4	1169.538666	-0.007238	EPLADPPPMR
17.0	1169.538666	-0.007238	EPLADPPPMR
6.1	1169.538666	-0.007238	EPLADPPPMR
5.9	1169.538666	-0.007238	EPLADPPPMR

Mascot: http://www.matrixscience.com/

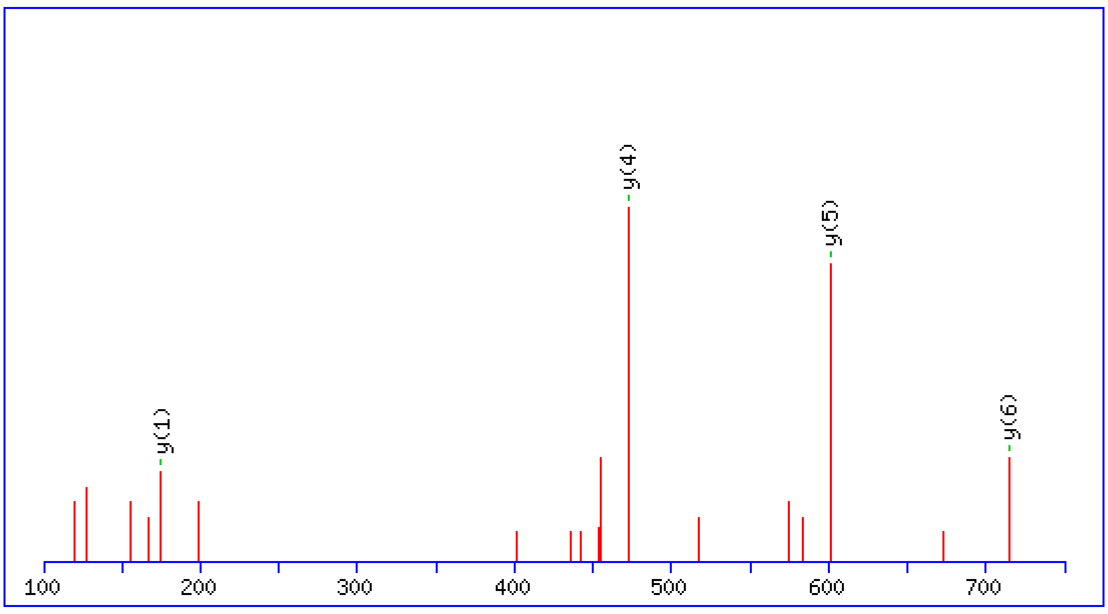
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLEPALR**
Found in **CA087_HUMAN**, Uncharacterized protein C1orf87 OS=Homo sapiens GN=C1orf87 PE=2 SV=1

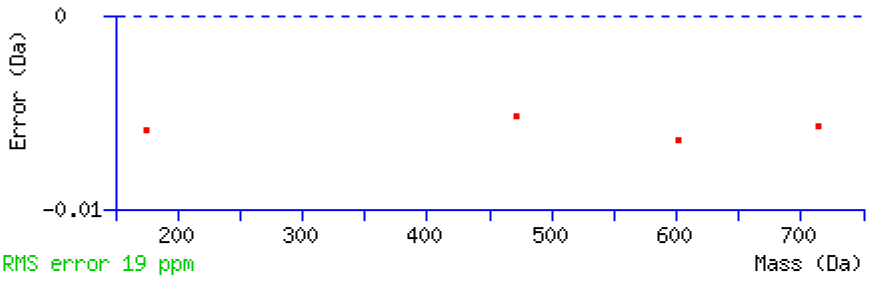
Match to Query 27857: 826.492268 from(414.253410,2+) rtinseconds(1769) index(646749)
Title: Locus:1.1.1.863.3
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

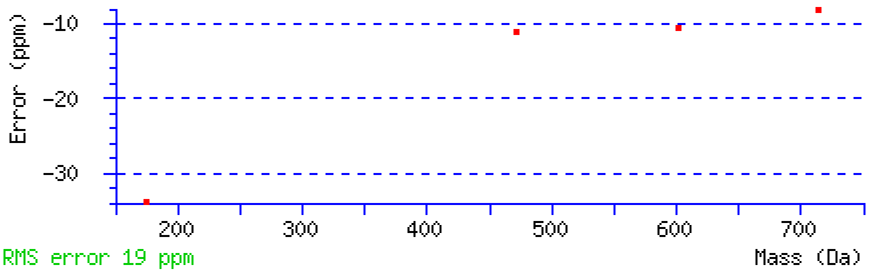
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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: 35 **Expect:** 0.0014
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	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





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
35.0	826.491226	0.001042	LLEPALR
32.9	826.491226	0.001042	ILLSPER
32.9	826.491241	0.001027	LIPSPLR
18.3	826.491226	0.001042	LELPLSR
17.8	826.491241	0.001027	ILTPEVR
17.8	826.491257	0.001011	IPVVVER
17.8	826.491226	0.001042	LPLEALR
17.8	826.491257	0.001011	LPTPVLR
17.7	826.491226	0.001042	EPIALIR
14.4	826.491241	0.001027	LDTPLLR

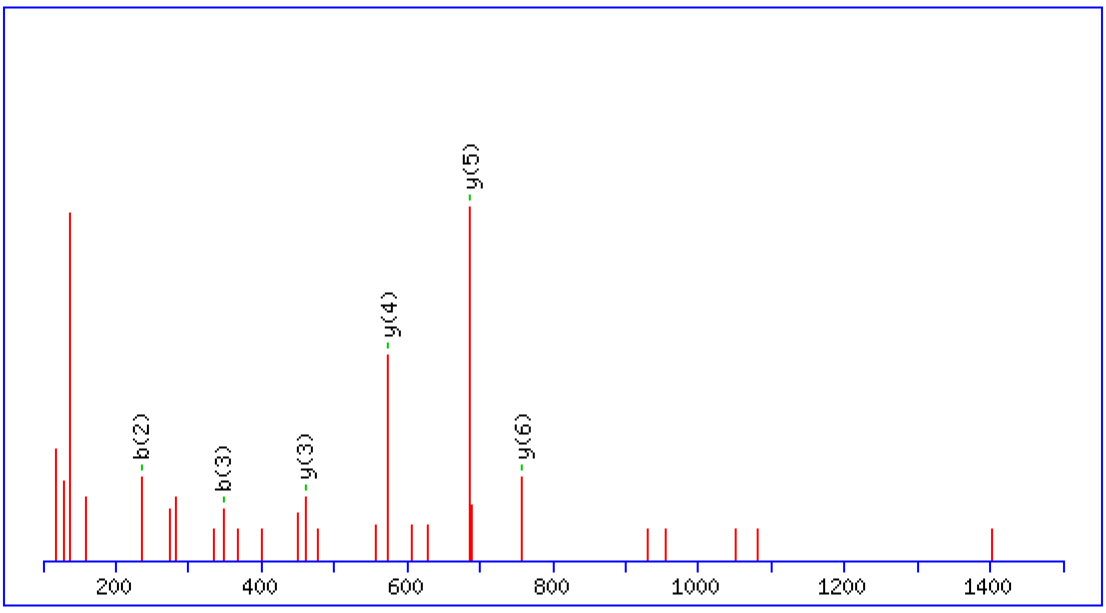
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YALNVWR**
Found in **K1958_HUMAN**, Uncharacterized protein KIAA1958 OS=Homo sapiens GN=KIAA1958 PE=1 SV=1

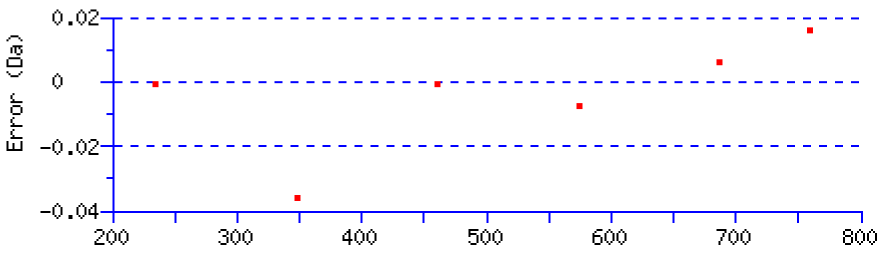
Match to Query 5312: 920.483528 from(461.249040,2+) rtinseconds(2486) index(29710)
Title: Locus:1.1.1.2485.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-3.mgf

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 ●

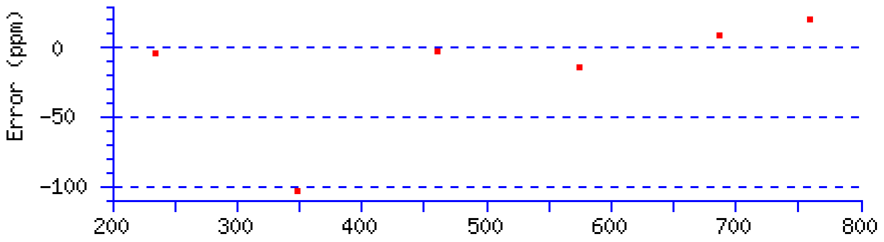


```
Monoisotopic mass of neutral peptide Mr(calc): 920.486816
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 33  Expect: 0.0012
Matches : 6/42 fragment ions using 7 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	164.070605	82.538940			Y					7
2	**235.107719**	118.057498			A	***758.430784***	379.719030	741.404235	371.205755	6
3	**348.191783**	174.599529			L	***687.393670***	344.200473	670.367121	335.687198	5
4	462.234710	231.620993	445.208161	223.107719	N	***574.309606***	287.658441	557.283057	279.145167	4
5	561.303124	281.155200	544.276575	272.641926	V	***460.266679***	230.636977	443.240130	222.123703	3
6	747.382437	374.194857	730.355888	365.681582	W	361.198265	181.102770	344.171716	172.589496	2
7					R	175.118952	88.063114	158.092403	79.549839	1



RMS error 43 ppm



RMS error 43 ppm

NCBI **BLAST** search of YALNVWR
(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	920.486816	-0.003288	YALNVWR
2.1	920.475586	0.007942	YAPLGWSK
0.1	920.474930	0.008598	RLEATGMK

Mascot: http://www.matrixscience.com/

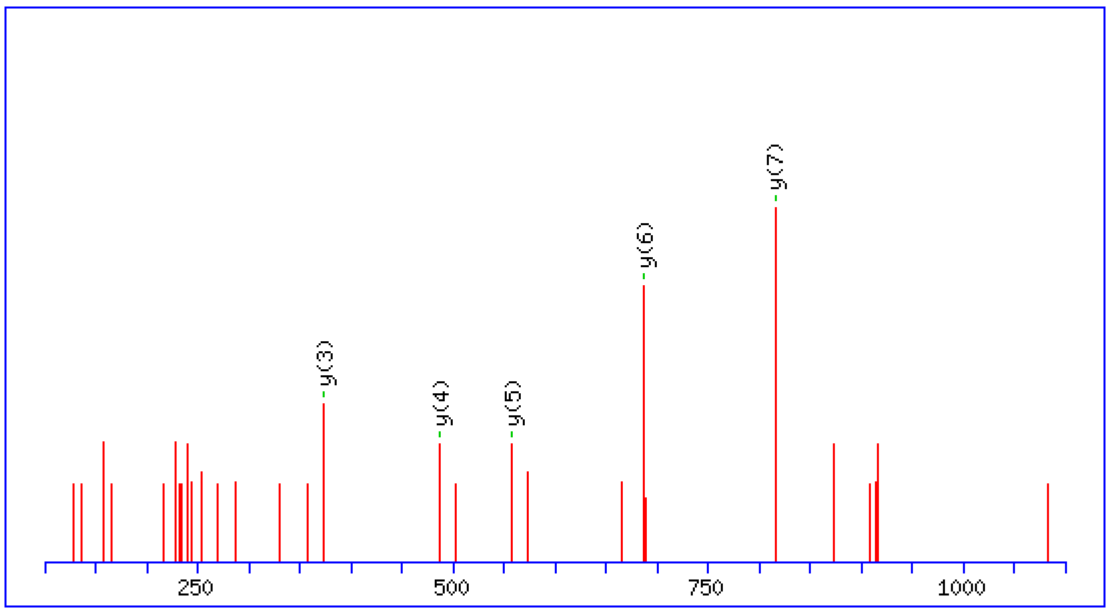
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVEEALAQR**
Found in **MYG1_HUMAN**, UPF0160 protein MYG1, mitochondrial OS=Homo sapiens GN=C12orf10 PE=1 SV=2

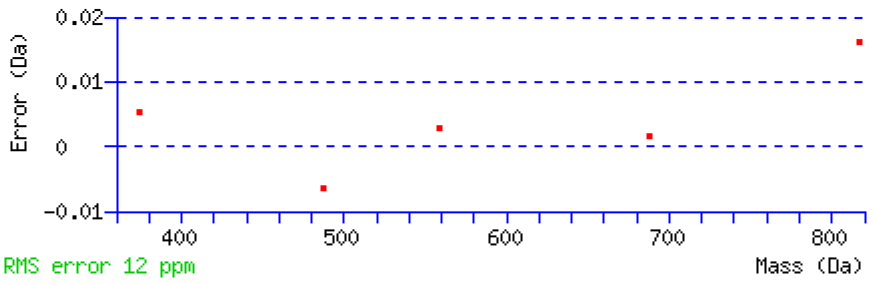
Match to Query 15238: 1098.601188 from(550.307870,2+) rtinseconds(2210) index(19811)
Title: Locus:1.1.1.2413.23
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

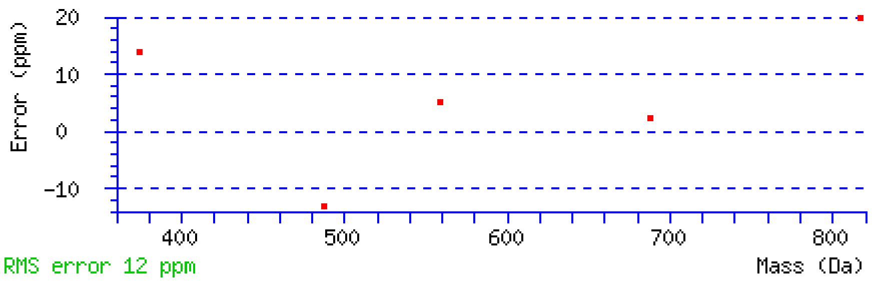
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1098.603287
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 36 **Expect:** 0.0026
Matches : 5/76 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	72.044390	36.525833					A							10
2	185.128454	93.067865					L	1028.573486	514.790381	1011.546937	506.277107	1010.562921	505.785099	9
3	284.196868	142.602072					V	915.489422	458.248349	898.462873	449.735075	897.478857	449.243067	8
4	413.239461	207.123369			395.228896	198.118086	E	***816.421008***	408.714142	799.394459	400.200868	798.410443	399.708860	7
5	542.282054	271.644665			524.271489	262.639383	E	***687.378415***	344.192845	670.351866	335.679571	669.367850	335.187563	6
6	613.319168	307.163222			595.308603	298.157940	A	***558.335822***	279.671549	541.309273	271.158275			5
7	726.403232	363.705254			708.392667	354.699972	L	***487.298708***	244.152992	470.272159	235.639717			4
8	797.440346	399.223811			779.429781	390.218528	A	***374.214644***	187.610960	357.188095	179.097685			3
9	925.498924	463.253100	908.472375	454.739825	907.488359	454.247818	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 ALVEEALAQR
(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	1098.603287	-0.002099	ALVEEALAQR

Mascot: http://www.matrixscience.com/

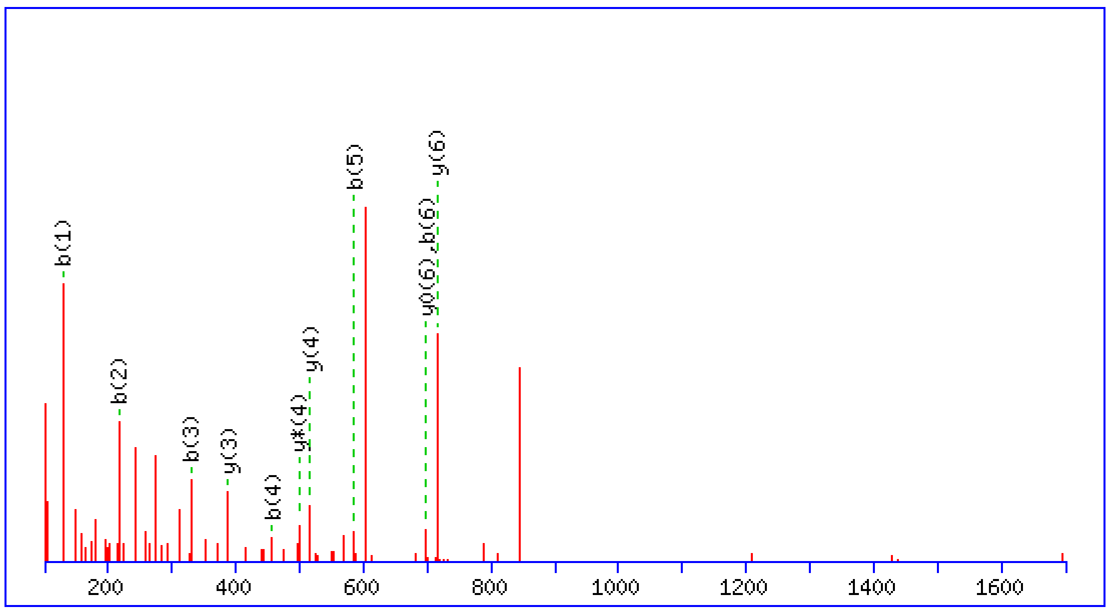
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSLKKPK**
Found in **CF057_HUMAN**, UPF0369 protein C6orf57 OS=Homo sapiens GN=C6orf57 PE=2 SV=1

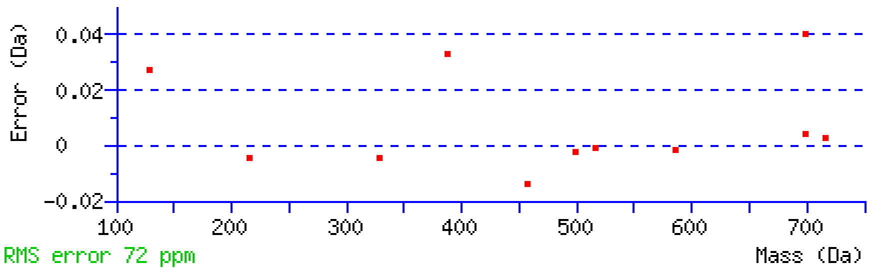
Match to Query 2370: 843.514188 from(422.764370,2+) rtinseconds(997) index(5445)
Title: Locus:1.1.1.1018.8
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-2.mgf

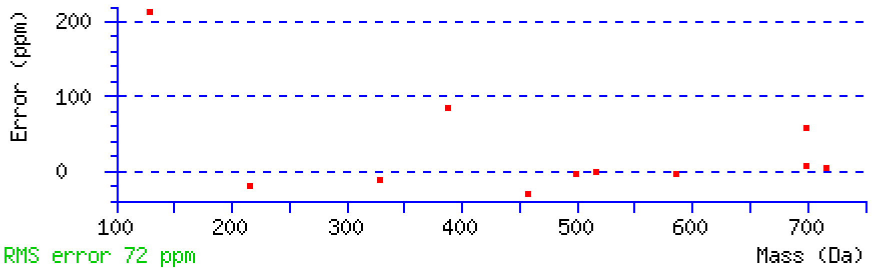
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 843.517776
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
Ions Score: 51  Expect: 8.6e-005
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	***129.065854***	65.036565	112.039305	56.523291			**Q**							7
2	***216.097882***	108.552579	199.071333	100.039305	198.087317	99.547296	**S**	**716.466501**	358.736889	699.439952	350.223614	698.455936	349.731606	6
3	***329.181946***	165.094611	312.155397	156.581336	311.171381	156.089328	**L**	629.434473	315.220875	612.407924	306.707600			5
4	***457.276909***	229.142092	440.250360	220.628818	439.266344	220.136810	**K**	**516.350409**	258.678843	499.323860	250.165568			4
5	***585.371872***	293.189574	568.345323	284.676300	567.361307	284.184292	**K**	**388.255446**	194.631361	371.228897	186.118087			3
6	***698.419551***	349.713414	681.393002	341.200139	680.408986	340.708131	**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 QSLKKPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.3	843.517776	-0.003588	GALSQLKK
51.3	843.517776	-0.003588	QSLKKPK
35.8	843.517792	-0.003604	QTVKQLK
23.9	843.517776	-0.003588	KPKPSKK
23.9	843.517776	-0.003588	QLKLSQK
23.3	843.517776	-0.003588	LSQKPKK
21.8	843.517776	-0.003588	QLLSKQK
20.5	843.506546	0.007642	KIVEDIK
20.5	843.506546	0.007642	KLLDDIK
20.5	843.506546	0.007642	KLTLEPK

Mascot: http://www.matrixscience.com/

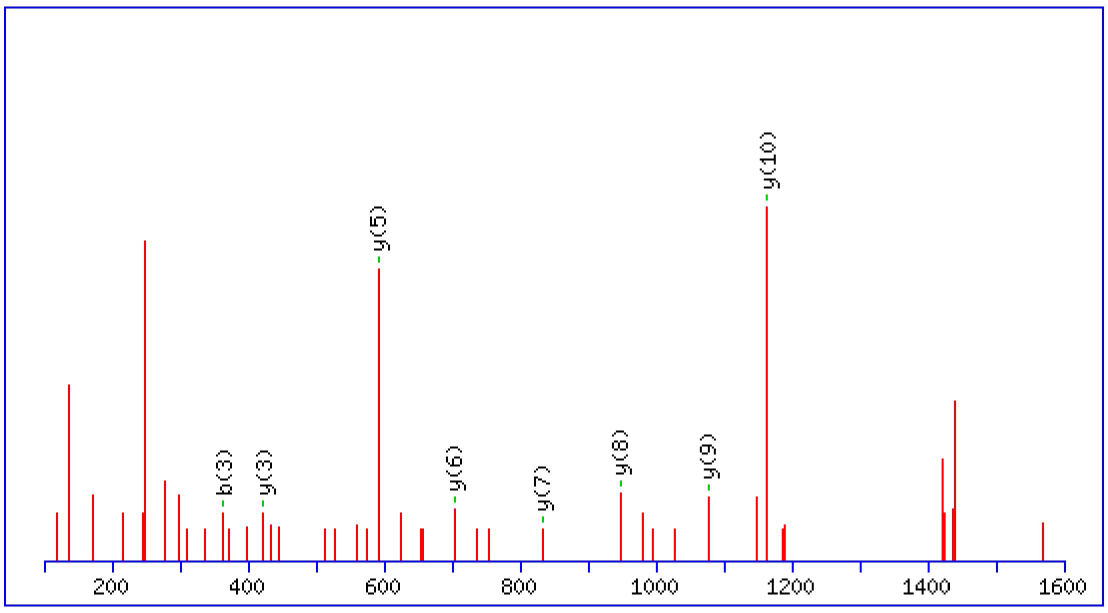
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYSEDELPAEFK**
Found in **CP080_HUMAN**, UPF0468 protein C16orf80 OS=Homo sapiens GN=C16orf80 PE=1 SV=1

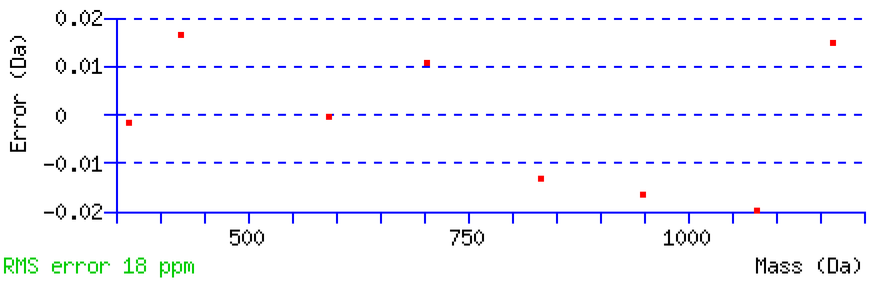
Match to Query 27784: 1439.684868 from(720.849710,2+) rtinseconds(2734) index(25990)
Title: Locus:1.1.1.2538.38
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

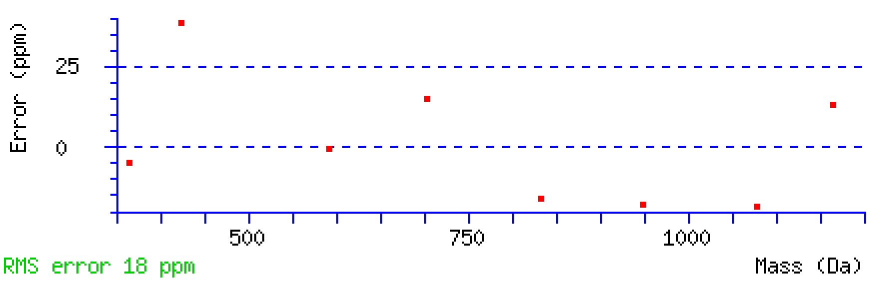
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1439.681992
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53  Expect: 5.7e-005
Matches : 8/102 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							12
2	277.154669	139.080973			Y	1327.605239	664.306258	1310.578690	655.792983	1309.594674	655.300975	11
3	364.186697	182.596987	346.176132	173.591704	S	***1164.541910***	582.774593	1147.515361	574.261319	1146.531345	573.769311	10
4	493.229290	247.118283	475.218725	238.113001	E	***1077.509882***	539.258579	1060.483333	530.745305	1059.499317	530.253297	9
5	608.256233	304.631755	590.245668	295.626472	D	***948.467289***	474.737283	931.440740	466.224008	930.456724	465.732000	8
6	737.298826	369.153051	719.288261	360.147769	E	***833.440346***	417.223811	816.413797	408.710537	815.429781	408.218529	7
7	850.382890	425.695083	832.372325	416.689801	L	***704.397753***	352.702515	687.371204	344.189240	686.387188	343.697232	6
8	947.435654	474.221465	929.425089	465.216183	P	***591.313689***	296.160483	574.287140	287.647208	573.303124	287.155200	5
9	1018.472768	509.740022	1000.462203	500.734740	A	494.260925	247.634100	477.234376	239.120826	476.250360	238.628818	4
10	1147.515361	574.261319	1129.504796	565.256036	E	***423.223811***	212.115543	406.197262	203.602269	405.213246	203.110261	3
11	1294.583775	647.795526	1276.573210	638.790243	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 LYSEDELPAEFK
(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	1439.681992	0.002876	LYSEDELPAEFK

Mascot: http://www.matrixscience.com/

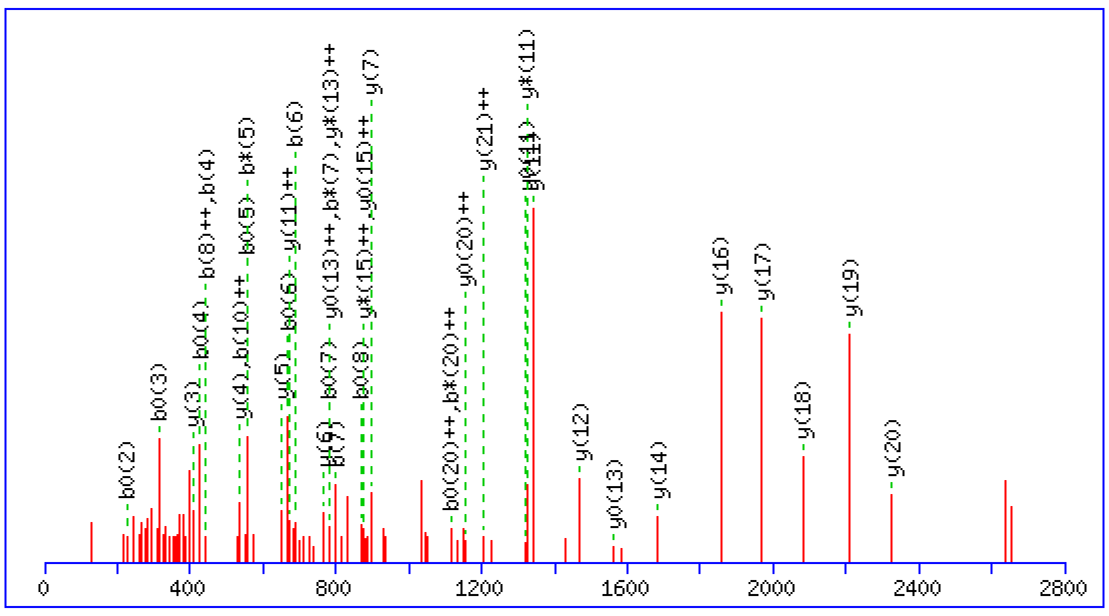
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENSIEILSSTIKPYNAEDNENFK**
Found in **CA123_HUMAN**, UPF0587 protein C1orf123 OS=Homo sapiens GN=C1orf123 PE=1 SV=1

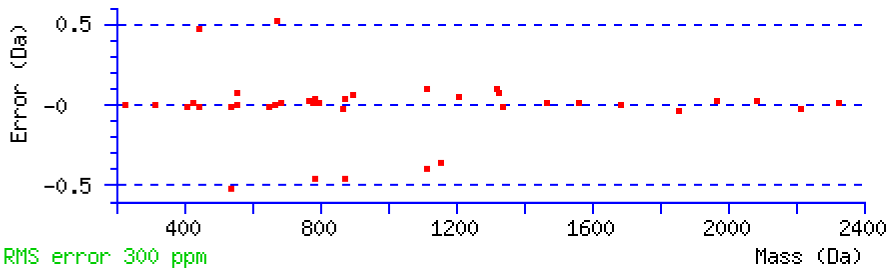
Match to Query 60986: 2654.272782 from(885.764870,3+) rtinseconds(3190) index(41545)
Title: Locus:1.1.1.2736.46
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

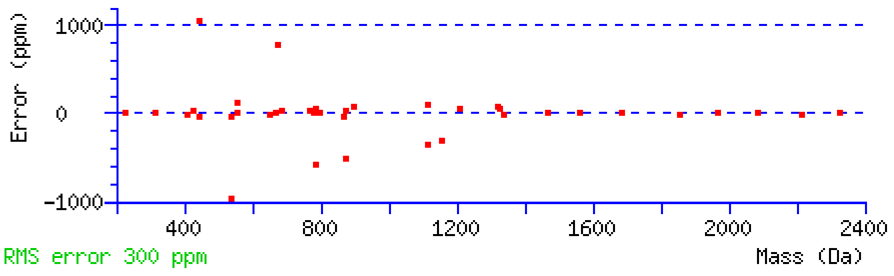
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2654.271088
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 75  Expect: 1.7e-007
Matches : 39/256 fragment ions using 56 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							23
2	244.092796	122.550036	227.066247	114.036762	226.082231	113.544754	N	2526.235837	1263.621556	2509.209288	1255.108282	2508.225272	1254.616274	22
3	331.124824	166.066050	314.098275	157.552776	313.114259	157.060768	S	2412.192910	1206.600093	2395.166361	1198.086818	2394.182345	1197.594810	21
4	**444.208888**	222.608082	427.182339	214.094808	426.198323	213.602800	I	***2325.160882***	1163.084079	2308.134333	1154.570804	2307.150317	1154.078796	20
5	573.251481	287.129379	556.224932	278.616104	555.240916	278.124096	E	***2212.076818***	1106.542047	2195.050269	1098.028772	2194.066253	1097.536764	19
6	**686.335545**	343.671411	669.308996	335.158136	668.324980	334.666128	I	***2083.034225***	1042.020750	2066.007676	1033.507476	2065.023660	1033.015468	18
7	**799.419609**	400.213443	782.393060	391.700168	781.409044	391.208160	L	***1969.950161***	985.478719	1952.923612	976.965444	1951.939596	976.473436	17
8	886.451637	443.729457	869.425088	435.216182	868.441072	434.724174	S	***1856.866097***	928.936686	1839.839548	920.423412	1838.855532	919.931404	16
9	973.483665	487.245471	956.457116	478.732196	955.473100	478.240188	S	1769.834069	885.420673	1752.807520	876.907398	1751.823504	876.415390	15
10	1074.531344	537.769310	1057.504795	529.256036	1056.520779	528.764028	T	***1682.802041***	841.904659	1665.775492	833.391384	1664.791476	832.899376	14
11	1187.615408	594.311342	1170.588859	585.798068	1169.604843	585.306059	I	1581.754362	791.380819	1564.727813	782.867545	1563.743797	782.375537	13
12	1315.710371	658.358823	1298.683822	649.845549	1297.699806	649.353541	K	***1468.670298***	734.838787	1451.643749	726.325513	1450.659733	725.833505	12
13	1412.763135	706.885205	1395.736586	698.371931	1394.752570	697.879923	P	***1340.575335***	670.791306	1323.548786	662.278031	1322.564770	661.786023	11
14	1575.826464	788.416870	1558.799915	779.903596	1557.815899	779.411588	Y	1243.522571	622.264924	1226.496022	613.751649	1225.512006	613.259641	10
15	1689.869391	845.438334	1672.842842	836.925059	1671.858826	836.433051	N	1080.459242	540.733259	1063.432693	532.219985	1062.448677	531.727977	9
16	1760.906505	880.956890	1743.879956	872.443616	1742.895940	871.951608	A	966.416315	483.711796	949.389766	475.198521	948.405750	474.706513	8
17	1889.949098	945.478187	1872.922549	936.964912	1871.938533	936.472904	E	***895.379201***	448.193239	878.352652	439.679964	877.368636	439.187956	7
18	2004.976041	1002.991659	1987.949492	994.478384	1986.965476	993.986376	D	***766.336608***	383.671942	749.310059	375.158668	748.326043	374.666660	6
19	2119.018968	1060.013122	2101.992419	1051.499847	2101.008403	1051.007839	N	***651.309665***	326.158471	634.283116	317.645196	633.299100	317.153188	5
20	2248.061561	1124.534418	2231.035012	1116.021144	2230.050996	1115.529136	E	***537.266738***	269.137007	520.240189	260.623733	519.256173	260.131725	4
21	2362.104488	1181.555882	2345.077939	1173.042607	2344.093923	1172.550599	N	***408.224145***	204.615710	391.197596	196.102436			3
22	2509.172902	1255.090089	2492.146353	1246.576814	2491.162337	1246.084806	F	294.181218	147.594247	277.154669	139.080972			2
23							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of ENSIEILSSTIKPYNAEDNENFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.3	2654.271088	0.001694	ENSIEILSSTIKPYNAEDNENFK
3.0	2654.275909	-0.003127	GPPGRAGLPGSDGAPGPPGTSLMLPFR
1.2	2654.275909	-0.003127	GPPGRAGLPGSDGAPGPPGTSLMLPFR

Mascot: http://www.matrixscience.com/

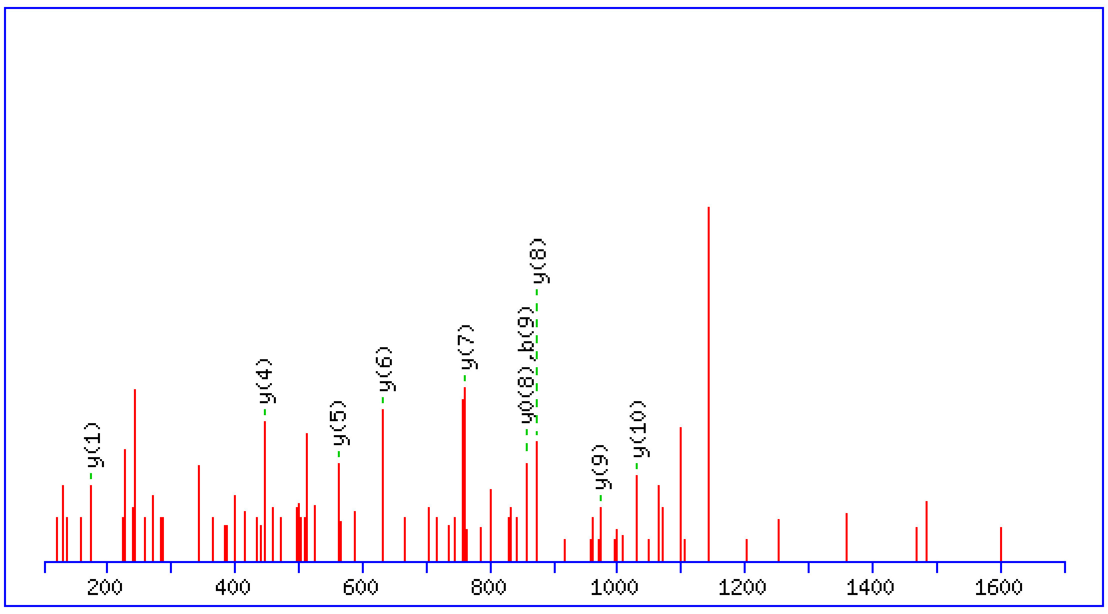
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGVLEADSAIR**
Found in **CK068_HUMAN**, UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68 PE=1 SV=2

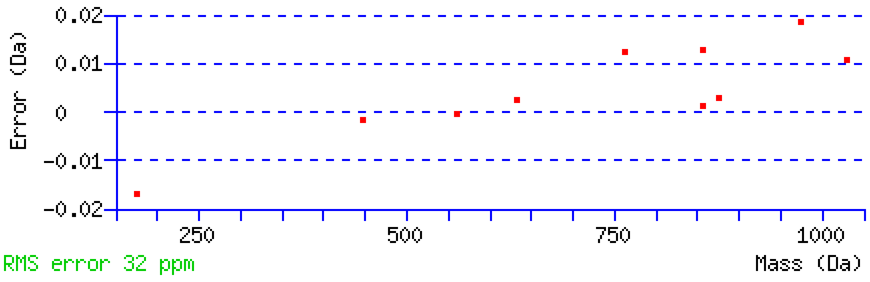
Match to Query 21157: 1142.622208 from(572.318380,2+) rtinseconds(2443) index(27477)
Title: Locus:1.1.1.2516.22
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 9-4.mgf

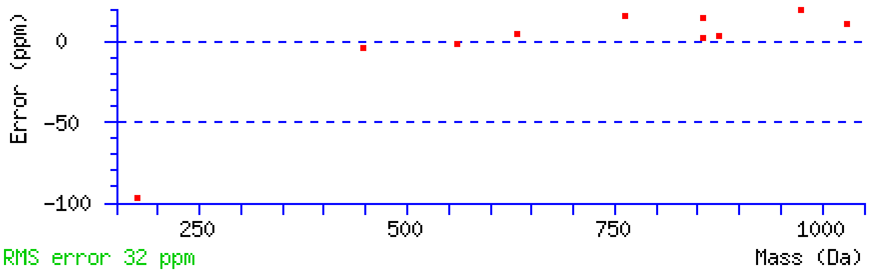
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1142.629517
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.00014
Matches : 10/86 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							11
2	171.112804	86.060040			G	*1030.552750*	515.780013	1013.526201	507.266739	1012.542185	506.774731	10
3	270.181218	135.594247			V	*973.531286*	487.269281	956.504737	478.756006	955.520721	478.263998	9
4	383.265282	192.136279			L	*874.462872*	437.735074	857.436323	429.221799	856.452307	428.729791	8
5	512.307875	256.657576	494.297310	247.652293	E	*761.378808*	381.193042	744.352259	372.679767	743.368243	372.187759	7
6	583.344989	292.176133	565.334424	283.170850	A	*632.336215*	316.671745	615.309666	308.158471	614.325650	307.666463	6
7	698.371932	349.689604	680.361367	340.684322	D	*561.299101*	281.153189	544.272552	272.639914	543.288536	272.147906	5
8	785.403960	393.205618	767.393395	384.200335	S	*446.272158*	223.639717	429.245609	215.126442	428.261593	214.634434	4
9	856.441074	428.724175	838.430509	419.718892	A	359.240130	180.123703	342.213581	171.610428			3
10	969.525138	485.266207	951.514573	476.260924	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 LGVLEADSAIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.0	1142.629517	-0.007309	LGVLEADSAIR
14.2	1142.629532	-0.007324	GLVPEDKTLR
7.8	1142.622986	-0.000778	LRLGPECLR
6.6	1142.615601	0.006607	RPLSPETRR
3.0	1142.618256	0.003952	LAELEEALQK
2.8	1142.611755	0.010453	LRLPSPSMDK
2.2	1142.619629	0.002579	RLWSSPLPR

Mascot: http://www.matrixscience.com/

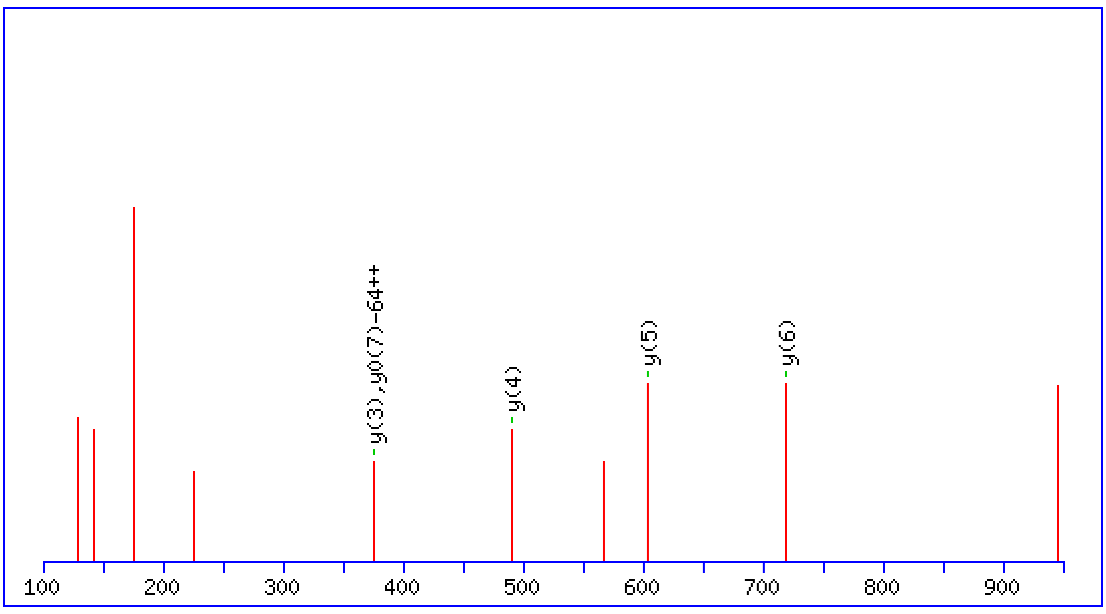
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILDIDIPM**
Found in **TFCP2_HUMAN**, Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2 PE=1 SV=2

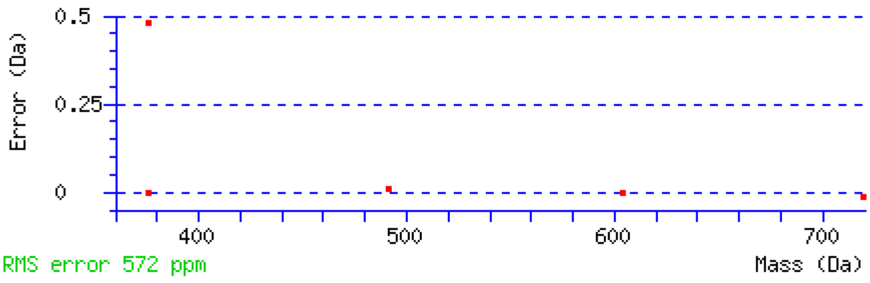
Match to Query 147488: 944.480028 from(473.247290,2+) rtinseconds(1301) index(488456)
Title: Locus:1.1.1.1112.7
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

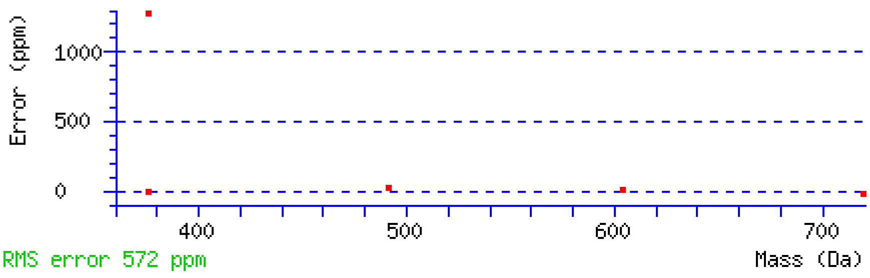
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 944.488861
Fixed modifications: Carbamidomethyl (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: 33  Expect: 0.0094
Matches : 5/68 fragment ions using 5 most intense peaks   (help)
```

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	114.091340	57.549308			I					8
2	227.175404	114.091340			L	832.412083	416.709680	814.401518	407.704397	7
3	342.202347	171.604811	324.191782	162.599529	D	*719.328019*	360.167648	701.317454	351.162365	6
4	455.286411	228.146843	437.275846	219.141561	I	*604.301076*	302.654176	586.290511	293.648894	5
5	570.313354	285.660315	552.302789	276.655033	D	*491.217012*	246.112144	473.206447	237.106861	4
6	683.397418	342.202347	665.386853	333.197065	I	*376.190069*	188.598672			3
7	780.450182	390.728729	762.439617	381.723447	P	263.106005	132.056640			2
8					M	166.053241	83.530258			1





NCBI **BLAST** search of ILDIDIPM
(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	944.488861	-0.008833	ILDIDIPM
32.7	944.488861	-0.008833	ILDIDIPM
32.7	944.488861	-0.008833	LLDLDIPM
32.7	944.488861	-0.008833	LLDLDIPM
18.9	944.474960	0.005068	VIEPGCVR
4.0	944.482803	-0.002775	DPIWRSR
4.0	944.474960	0.005068	LEVVPGCR
3.6	944.478760	0.001268	ALNRNSDR
3.4	944.482834	-0.002806	HVVFSGSGR
2.1	944.474945	0.005083	QPGLVMER

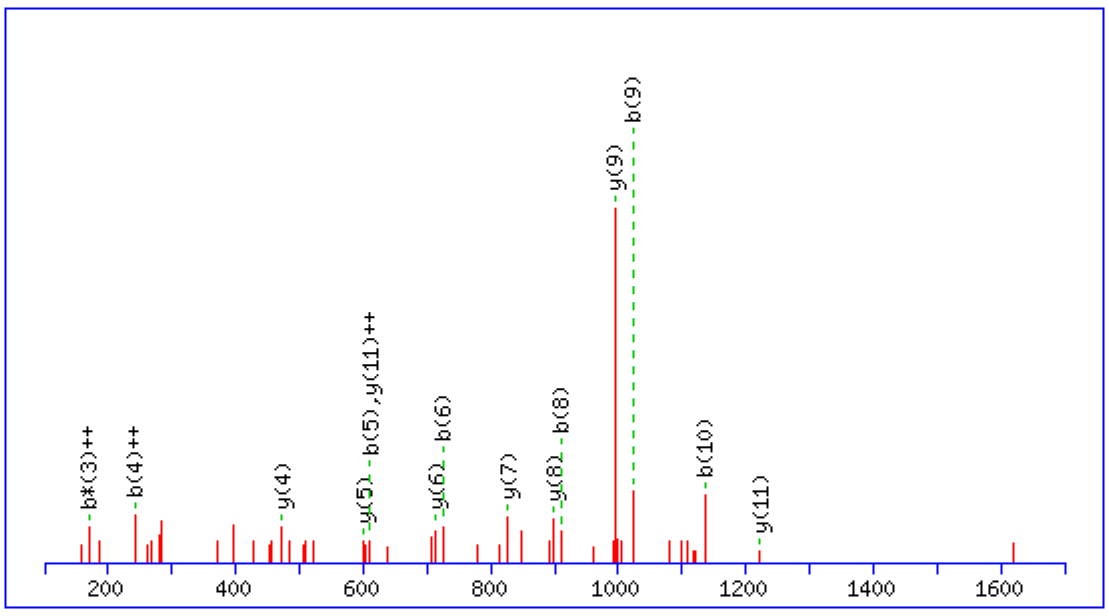
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QIIQQNPSLLPALLQQIGR**
Found in **RD23B_HUMAN**, UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1

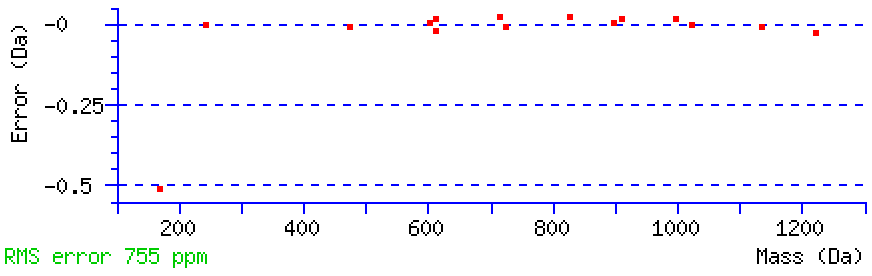
Match to Query 57221: 2129.247462 from(710.756430,3+) rtinseconds(4116) index(56028)
Title: Locus:1.1.1.3096.19
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-3.mgf

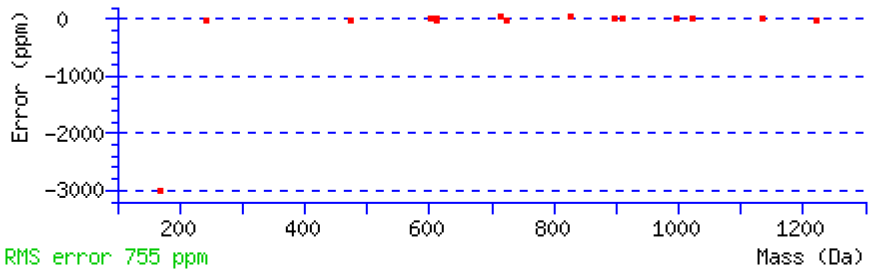
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2129.232040
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 4e-006
Matches : 16/180 fragment ions using 22 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.065854	65.036565	112.039305	56.523291			Q							19
2	***242.149918***	121.578597	225.123369	113.065323			I	2002.180773	1001.594024	1985.154224	993.080750	1984.170208	992.588742	18
3	355.233982	178.120629	338.207433	169.607355			I	1889.096709	945.051992	1872.070160	936.538718	1871.086144	936.046710	17
4	483.292560	242.149918	466.266011	233.636644			Q	1776.012645	888.509961	1758.986096	879.996686	1758.002080	879.504678	16
5	***611.351138***	306.179207	594.324589	297.665933			Q	1647.954067	824.480671	1630.927518	815.967397	1629.943502	815.475389	15
6	***725.394065***	363.200671	708.367516	354.687396			N	1519.895489	760.451382	1502.868940	751.938108	1501.884924	751.446100	14
7	822.446829	411.727053	805.420280	403.213778			P	1405.852562	703.429919	1388.826013	694.916644	1387.841997	694.424636	13
8	***909.478857***	455.243067	892.452308	446.729792	891.468292	446.237784	S	1308.799798	654.903537	1291.773249	646.390262	1290.789233	645.898254	12
9	***1022.562921***	511.785099	1005.536372	503.271824	1004.552356	502.779816	L	***1221.767770***	611.387523	1204.741221	602.874249			11
10	***1135.646985***	568.327131	1118.620436	559.813856	1117.636420	559.321848	L	1108.683706	554.845491	1091.657157	546.332217			10
11	1232.699749	616.853513	1215.673200	608.340238	1214.689184	607.848230	P	***995.599642***	498.303459	978.573093	489.790184			9
12	1303.736863	652.372070	1286.710314	643.858795	1285.726298	643.366787	A	***898.546878***	449.777077	881.520329	441.263802			8
13	1416.820927	708.914102	1399.794378	700.400827	1398.810362	699.908819	L	***827.509764***	414.258520	810.483215	405.745245			7
14	1529.904991	765.456133	1512.878442	756.942859	1511.894426	756.450851	L	***714.425700***	357.716488	697.399151	349.203214			6
15	1657.963569	829.485422	1640.937020	820.972148	1639.953004	820.480140	Q	***601.341636***	301.174456	584.315087	292.661182			5
16	1786.022147	893.514711	1768.995598	885.001437	1768.011582	884.509429	Q	***473.283058***	237.145167	456.256509	228.631893			4
17	1899.106211	950.056743	1882.079662	941.543469	1881.095646	941.051461	I	345.224480	173.115878	328.197931	164.602603			3
18	1956.127675	978.567475	1939.101126	970.054201	1938.117110	969.562193	G	232.140416	116.573846	215.113867	108.060572			2
19							R	175.118952	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of QIIQQNPSLLPALLQQIGR
(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	2129.232040	0.015422	QIIQQNPSLLPALLQQIGR

Mascot: http://www.matrixscience.com/

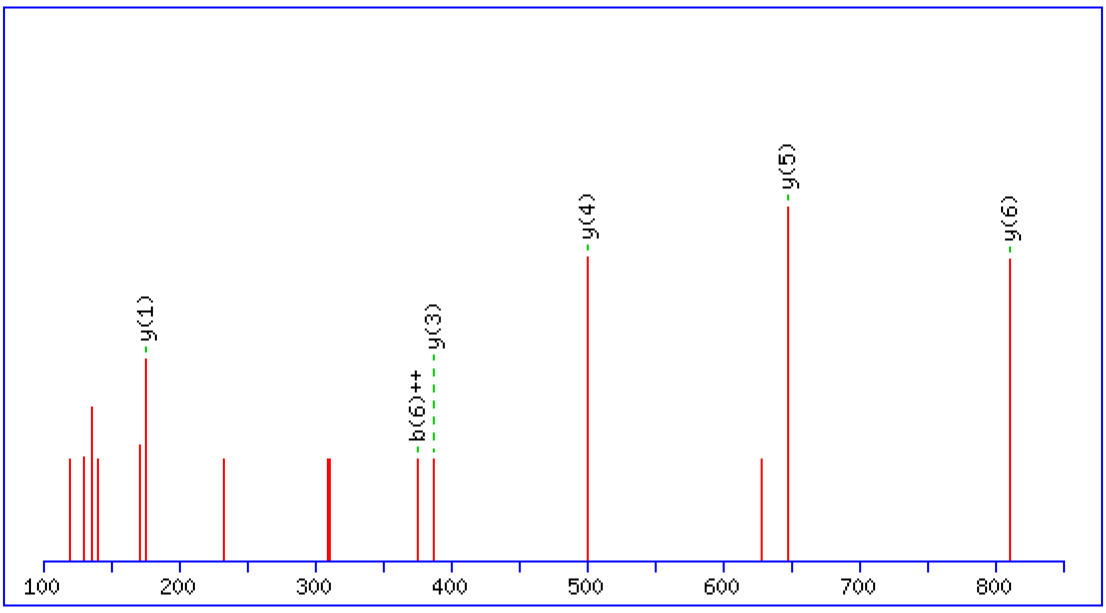
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYFLLVR**
Found in **VP26A_HUMAN**, Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=2

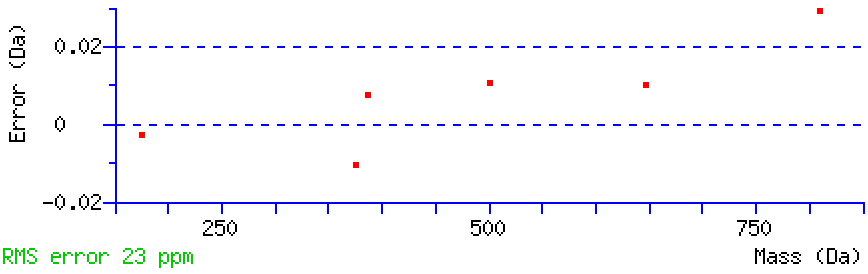
Match to Query 12243: 922.562368 from(462.288460,2+) rtinseconds(3359) index(46935)
Title: Locus:1.1.1.2637.3
Data file 2011-11-14 - TFD - S 2-4.mgf

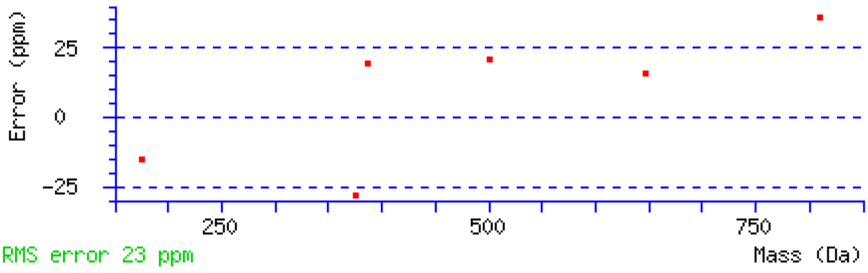
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 922.564011
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0012
Matches : 6/36 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	114.091340	57.549308	I					7
2	277.154669	139.080973	Y	***810.487237***	405.747257	793.460688	397.233982	6
3	424.223083	212.615180	F	***647.423908***	324.215592	630.397359	315.702318	5
4	537.307147	269.157212	L	***500.355494***	250.681385	483.328945	242.168111	4
5	650.391211	325.699244	L	***387.271430***	194.139353	370.244881	185.626079	3
6	749.459625	375.233451	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 IYFLLVR
(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	922.564011	-0.001643	IYFLLVR
10.6	922.571228	-0.008860	RAPVLPVR
1.5	922.571213	-0.008845	KHASVLLR
1.5	922.559998	0.002370	LATPPVVAR
1.5	922.559982	0.002386	LISIAPGPR
1.5	922.559967	0.002401	LKPALEPR
1.5	922.564011	-0.001643	LVFIIYR

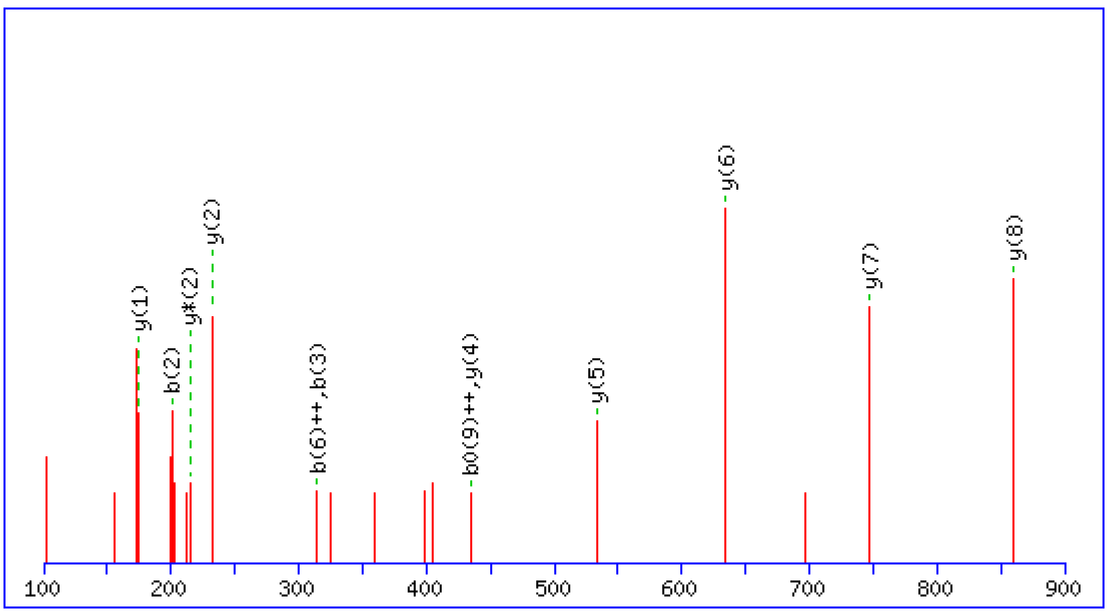
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEIITVSDGR**
Found in **VPS25_HUMAN**, Vacuolar protein-sorting-associated protein 25 OS=Homo sapiens GN=VPS25 PE=1 SV=1

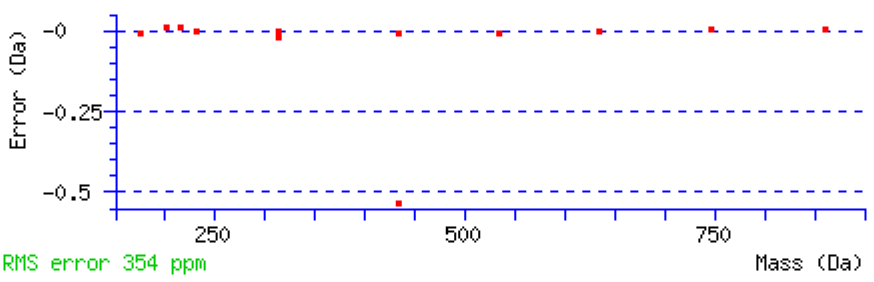
Match to Query 12654: 1059.548768 from(530.781660,2+) rtinseconds(1836) index(7628)
Title: Locus:1.1.1.2223.25
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

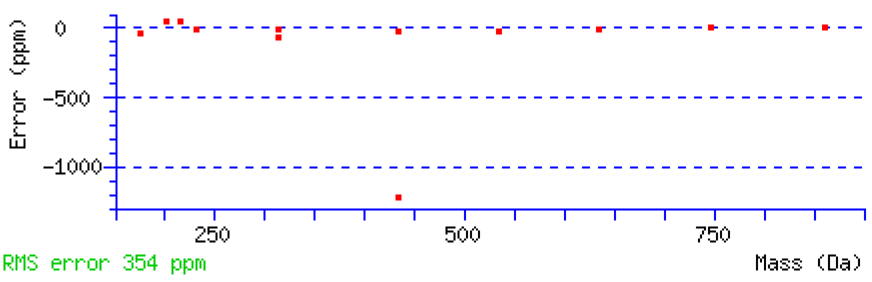
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1059.556030
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 56  Expect: 4.4e-005
Matches : 12/84 fragment ions using 16 most intense peaks   (help)
```

#	b	b⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.044390	36.525833			A							10
2	**201.086983**	101.047130	183.076418	92.041847	E	989.526201	495.266739	972.499652	486.753464	971.515636	486.261456	9
3	**314.171047**	157.589161	296.160482	148.583879	I	***860.483608***	430.745442	843.457059	422.232168	842.473043	421.740160	8
4	427.255111	214.131193	409.244546	205.125911	I	***747.399544***	374.203410	730.372995	365.690136	729.388979	365.198128	7
5	528.302790	264.655033	510.292225	255.649751	T	***634.315480***	317.661378	617.288931	309.148104	616.304915	308.656096	6
6	627.371204	314.189240	609.360639	305.183958	V	***533.267801***	267.137539	516.241252	258.624264	515.257236	258.132256	5
7	714.403232	357.705254	696.392667	348.699972	S	***434.199387***	217.603332	417.172838	209.090057	416.188822	208.598049	4
8	829.430175	415.218726	811.419610	406.213443	D	347.167359	174.087318	330.140810	165.574043	329.156794	165.082035	3
9	886.451639	443.729458	868.441074	434.724175	G	***232.140416***	116.573846	215.113867	108.060572			2
10					R	***175.118952***	88.063114	158.092403	79.549840			1





NCBI **BLAST** search of AEIITVSDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.0	1059.556030	-0.007262	AEIITVSDGR
21.7	1059.544769	0.003999	EPSITKEEK
18.0	1059.538269	0.010499	LSPPACTLR
17.1	1059.549515	-0.000747	TVLQGQMQR
8.2	1059.549500	-0.000732	LECGGKGLGR
5.3	1059.544800	0.003968	LTVSPEPSSK
4.0	1059.557404	-0.008636	TVPGGGFGGRR
3.3	1059.542130	0.006638	RSVAAGGGGGSGK
2.6	1059.556030	-0.007262	SPPTNKIGSK
2.2	1059.538284	0.010484	TVEACPVVR

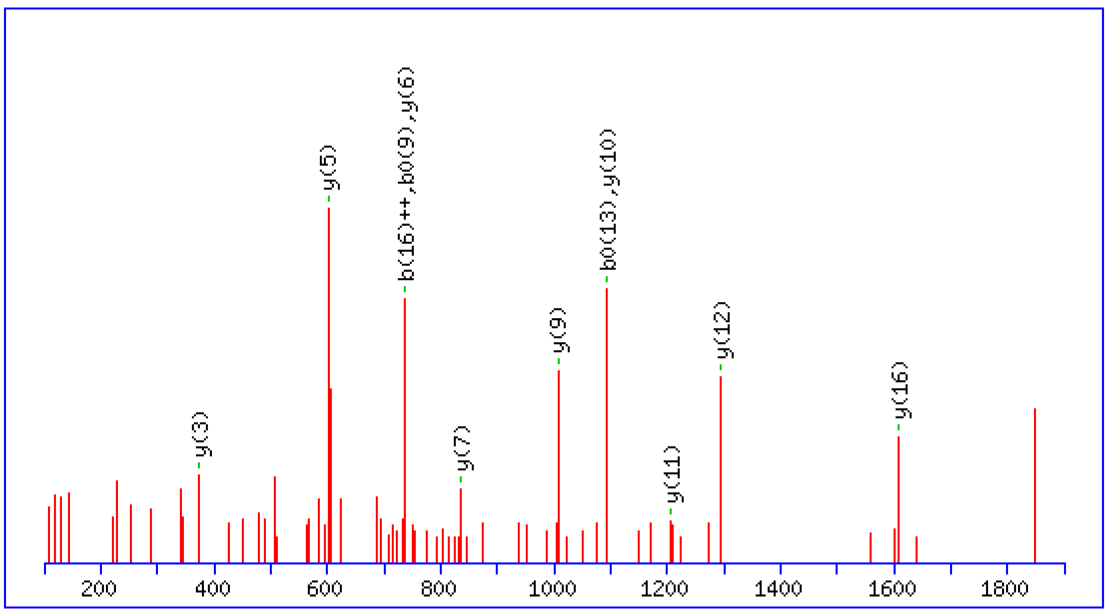
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLGSGLSLSGLVHPELSR**
Found in **ACADV_HUMAN**, Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1

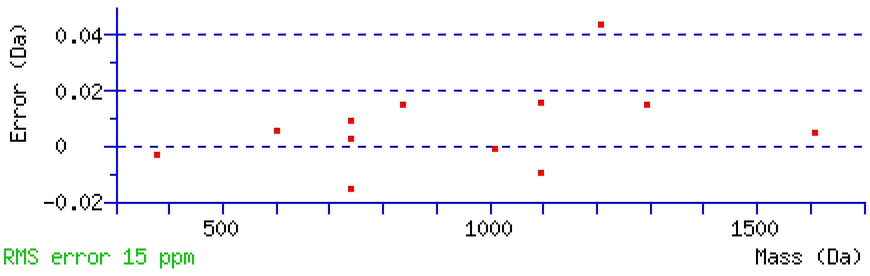
Match to Query 48285: 1849.018752 from(617.346860,3+) rtinseconds(3136) index(43318)
Title: Locus:1.1.1.2717.10
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-3.mgf

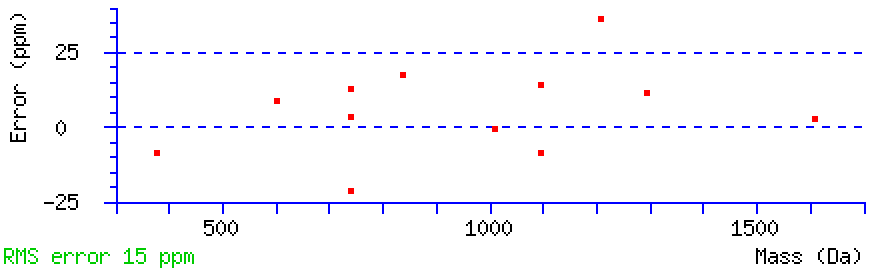
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1849.005753
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 65  Expect: 1.5e-006
Matches : 12/170 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							19
2	129.065854	65.036565			G	1778.975923	889.991600	1761.949374	881.478325	1760.965358	880.986317	18
3	242.149918	121.578597			L	1721.954459	861.480868	1704.927910	852.967593	1703.943894	852.475585	17
4	299.171382	150.089329			G	***1608.870395***	804.938836	1591.843846	796.425561	1590.859830	795.933553	16
5	386.203410	193.605343	368.192845	184.600061	S	1551.848931	776.428104	1534.822382	767.914829	1533.838366	767.422821	15
6	443.224874	222.116075	425.214309	213.110793	G	1464.816903	732.912090	1447.790354	724.398815	1446.806338	723.906807	14
7	556.308938	278.658107	538.298373	269.652825	L	1407.795439	704.401358	1390.768890	695.888083	1389.784874	695.396075	13
8	643.340966	322.174121	625.330401	313.168838	S	***1294.711375***	647.859326	1277.684826	639.346051	1276.700810	638.854043	12
9	756.425030	378.716153	738.414465	369.710871	L	***1207.679347***	604.343312	1190.652798	595.830037	1189.668782	595.338029	11
10	843.457058	422.232167	825.446493	413.226884	S	***1094.595283***	547.801280	1077.568734	539.288005	1076.584718	538.795997	10
11	900.478522	450.742899	882.467957	441.737617	G	***1007.563255***	504.285266	990.536706	495.771991	989.552690	495.279983	9
12	1013.562586	507.284931	995.552021	498.279649	L	950.541791	475.774534	933.515242	467.261259	932.531226	466.769251	8
13	1112.631000	556.819138	1094.620435	547.813856	V	***837.457727***	419.232502	820.431178	410.719227	819.447162	410.227219	7
14	1249.689912	625.348594	1231.679347	616.343312	H	***738.389313***	369.698295	721.362764	361.185020	720.378748	360.693012	6
15	1346.742676	673.874976	1328.732111	664.869694	P	***601.330401***	301.168839	584.303852	292.655564	583.319836	292.163556	5
16	1475.785269	738.396273	1457.774704	729.390990	E	504.277637	252.642457	487.251088	244.129182	486.267072	243.637174	4
17	1588.869333	794.938305	1570.858768	785.933022	L	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
18	1675.901361	838.454319	1657.890796	829.449036	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 AGLGSGLSLSGLVHPELSR
(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	1849.005753	0.012999	AGLGSGLSLSGLVHPELSR

Mascot: http://www.matrixscience.com/

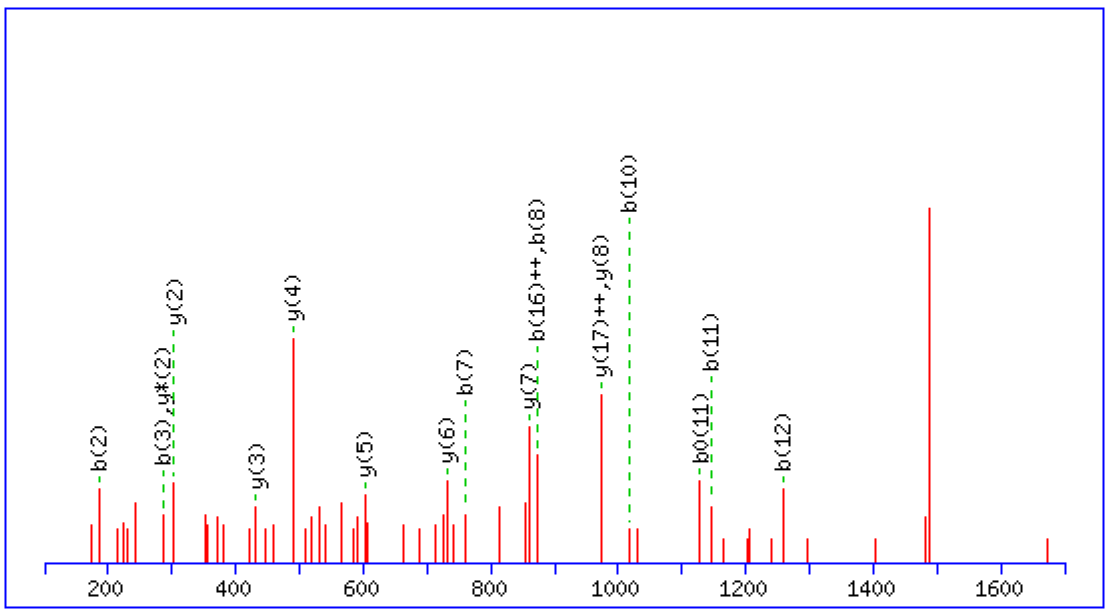
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IATETDQIGSEIIEELGEQR**
Found in **VTI1B_HUMAN**, Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=1 SV=3

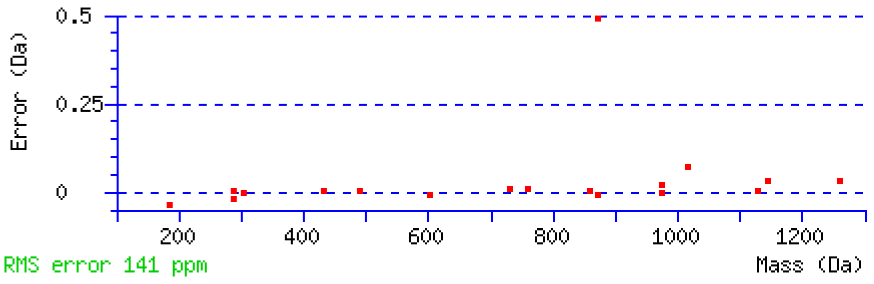
Match to Query 56403: 2230.101792 from(744.374540,3+) rtinseconds(3840) index(49262)
Title: Locus:1.1.1.3266.32
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-5.mgf

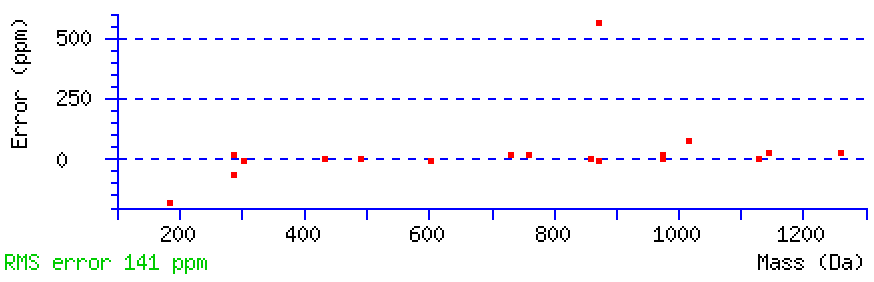
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2230.096451
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 50  Expect: 0.00013
Matches : 18/208 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							20
2	***185.128454***	93.067865					A	2118.019700	1059.513488	2100.993151	1051.000213	2100.009135	1050.508205	19
3	***286.176133***	143.591704			268.165568	134.586422	T	2046.982586	1023.994931	2029.956037	1015.481657	2028.972021	1014.989648	18
4	415.218726	208.113001			397.208161	199.107719	E	1945.934907	973.471091	1928.908358	964.957817	1927.924342	964.465809	17
5	516.266405	258.636841			498.255840	249.631558	T	1816.892314	908.949795	1799.865765	900.436520	1798.881749	899.944512	16
6	631.293348	316.150312			613.282783	307.145030	D	1715.844635	858.425955	1698.818086	849.912681	1697.834070	849.420673	15
7	***759.351926***	380.179601	742.325377	371.666327	741.341361	371.174319	Q	1600.817692	800.912484	1583.791143	792.399209	1582.807127	791.907201	14
8	***872.435990***	436.721633	855.409441	428.208359	854.425425	427.716351	I	1472.759114	736.883195	1455.732565	728.369920	1454.748549	727.877912	13
9	929.457454	465.232365	912.430905	456.719091	911.446889	456.227083	G	1359.675050	680.341163	1342.648501	671.827888	1341.664485	671.335880	12
10	***1016.489482***	508.748379	999.462933	500.235105	998.478917	499.743097	S	1302.653586	651.830431	1285.627037	643.317156	1284.643021	642.825148	11
11	***1145.532075***	573.269676	1128.505526	564.756401	1127.521510	564.264393	E	1215.621558	608.314417	1198.595009	599.801142	1197.610993	599.309134	10
12	***1258.616139***	629.811708	1241.589590	621.298433	1240.605574	620.806425	I	1086.578965	543.793120	1069.552416	535.279846	1068.568400	534.787838	9
13	1371.700203	686.353739	1354.673654	677.840465	1353.689638	677.348457	I	***973.494901***	487.251088	956.468352	478.737814	955.484336	478.245806	8
14	1500.742796	750.875036	1483.716247	742.361761	1482.732231	741.869753	E	***860.410837***	430.709056	843.384288	422.195782	842.400272	421.703774	7
15	1629.785389	815.396332	1612.758840	806.883058	1611.774824	806.391050	E	***731.368244***	366.187760	714.341695	357.674486	713.357679	357.182478	6
16	1742.869453	871.938364	1725.842904	863.425090	1724.858888	862.933082	L	***602.325651***	301.666463	585.299102	293.153189	584.315086	292.661181	5
17	1799.890917	900.449096	1782.864368	891.935822	1781.880352	891.443814	G	***489.241587***	245.124431	472.215038	236.611157	471.231022	236.119149	4
18	1928.933510	964.970393	1911.906961	956.457118	1910.922945	955.965110	E	***432.220123***	216.613699	415.193574	208.100425	414.209558	207.608417	3
19	2056.992088	1028.999682	2039.965539	1020.486407	2038.981523	1019.994399	Q	***303.177530***	152.092403	286.150981	143.579129			2
20							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IATETDQIGSEIIEELGEQR
(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	2230.096451	0.005341	IATETDQIGSEIIEELGEQR

Mascot: http://www.matrixscience.com/

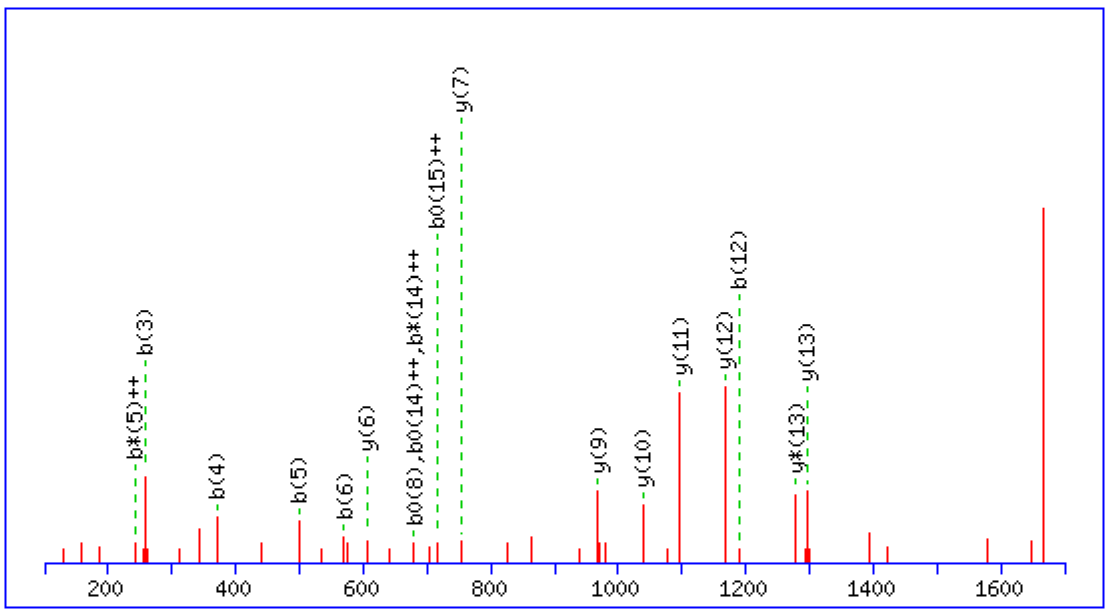
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADALQAGASQFETSAAK**
Found in **VAMP2_HUMAN**, Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=1 SV=3

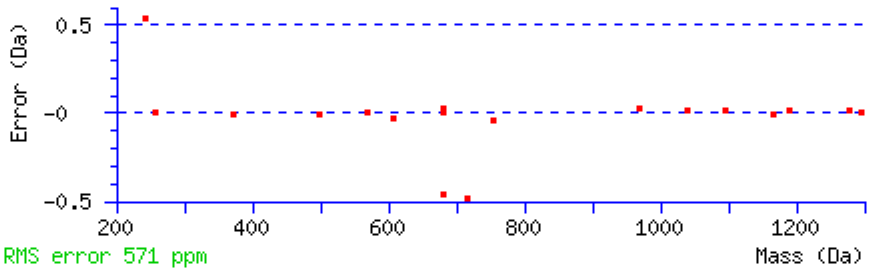
Match to Query 28999: 1664.807748 from(833.411150,2+) rtinseconds(2326) index(15829)
Title: Locus:1.1.1.2409.46
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-6.mgf

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 ●

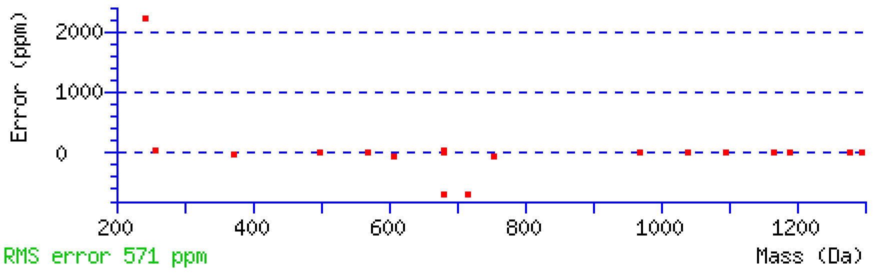


```
Monoisotopic mass of neutral peptide Mr(calc): 1664.800552
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47  Expect: 0.00028
Matches : 18/176 fragment ions using 27 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							17
2	187.071333	94.039304			169.060768	85.034022	D	1594.770743	797.889010	1577.744194	789.375735	1576.760178	788.883727	16
3	***258.108447***	129.557862			240.097882	120.552579	A	1479.743800	740.375538	1462.717251	731.862264	1461.733235	731.370256	15
4	***371.192511***	186.099894			353.181946	177.094611	L	1408.706686	704.856981	1391.680137	696.343707	1390.696121	695.851699	14
5	***499.251089***	250.129183	482.224540	241.615908	481.240524	241.123900	Q	***1295.622622***	648.314949	1278.596073	639.801675	1277.612057	639.309667	13
6	***570.288203***	285.647740	553.261654	277.134465	552.277638	276.642457	A	***1167.564044***	584.285660	1150.537495	575.772386	1149.553479	575.280378	12
7	627.309667	314.158472	610.283118	305.645197	609.299102	305.153189	G	***1096.526930***	548.767103	1079.500381	540.253829	1078.516365	539.761821	11
8	698.346781	349.677029	681.320232	341.163754	680.336216	340.671746	A	***1039.505466***	520.256371	1022.478917	511.743097	1021.494901	511.251089	10
9	785.378809	393.193043	768.352260	384.679768	767.368244	384.187760	S	***968.468352***	484.737814	951.441803	476.224540	950.457787	475.732532	9
10	913.437387	457.222332	896.410838	448.709057	895.426822	448.217049	Q	881.436324	441.221800	864.409775	432.708526	863.425759	432.216518	8
11	1060.505801	530.756539	1043.479252	522.243264	1042.495236	521.751256	F	***753.377746***	377.192511	736.351197	368.679237	735.367181	368.187229	7
12	***1189.548394***	595.277835	1172.521845	586.764561	1171.537829	586.272553	E	***606.309332***	303.658304	589.282783	295.145030	588.298767	294.653022	6
13	1290.596073	645.801675	1273.569524	637.288400	1272.585508	636.796392	T	477.266739	239.137008	460.240190	230.623733	459.256174	230.131725	5
14	1377.628101	689.317689	1360.601552	680.804414	1359.617536	680.312406	S	376.219060	188.613168	359.192511	180.099894	358.208495	179.607886	4
15	1448.665215	724.836246	1431.638666	716.322971	1430.654650	715.830963	A	289.187032	145.097154	272.160483	136.583879			3
16	1519.702329	760.354803	1502.675780	751.841528	1501.691764	751.349520	A	218.149918	109.578597	201.123369	101.065322			2
17							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 571 ppm



RMS error 571 ppm

NCBI **BLAST** search of ADALQAGASQFETSAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.6	1664.800552	0.007196	ADALQAGASQFETSAAK
11.9	1664.794052	0.013696	SPQSPGGNICHLGAPK
4.9	1664.794052	0.013696	SPQSPGGNICHLGAPK
2.0	1664.811859	-0.004111	GATGPVGPPGASVSGPPGR

Mascot: http://www.matrixscience.com/

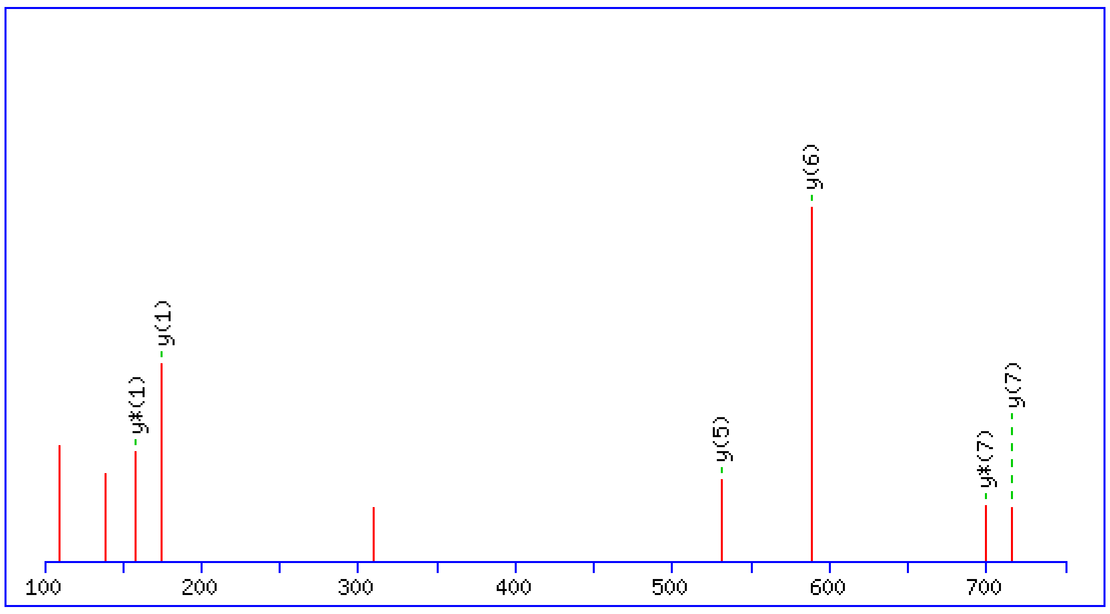
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQGDLAGR**
Found in **JAM3_HUMAN**, Junctional adhesion molecule C OS=Homo sapiens GN=JAM3 PE=1 SV=1

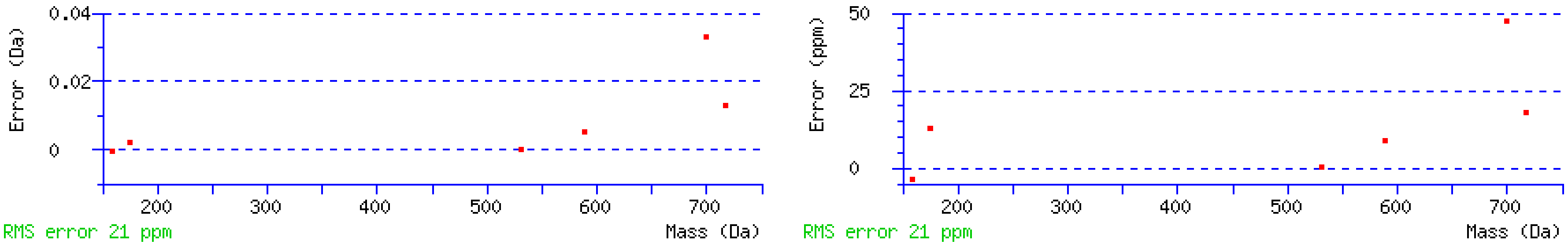
Match to Query 1777: 828.439968 from(415.227260,2+) rtinseconds(1097) index(3221)
Title: Locus:1.1.1.1817.4
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

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): 828.445358
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 34 **Expect:** 0.0055
Matches : 6/68 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							8
2	242.149918	121.578597	225.123369	113.065323			Q	***716.368579***	358.687928	699.342030	350.174653	698.358014	349.682645	7
3	299.171382	150.089329	282.144833	141.576055			G	***588.310001***	294.658639	571.283452	286.145364	570.299436	285.653356	6
4	414.198325	207.602801	397.171776	199.089526	396.187760	198.597518	D	***531.288537***	266.147907	514.261988	257.634632	513.277972	257.142624	5
5	527.282389	264.144833	510.255840	255.631558	509.271824	255.139550	L	416.261594	208.634435	399.235045	200.121160			4
6	598.319503	299.663390	581.292954	291.150115	580.308938	290.658107	A	303.177530	152.092403	286.150981	143.579128			3
7	655.340967	328.174122	638.314418	319.660847	637.330402	319.168839	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 IQGDLAGR
(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	828.445358	-0.005390	IQGDLAGR
33.7	828.445358	-0.005390	LQGEVQR
33.7	828.445358	-0.005390	LQGKDPR
24.1	828.445343	-0.005375	IQANVER
24.1	828.445343	-0.005375	IQNAEVR
24.1	828.445343	-0.005375	LQDIANR
19.4	828.434113	0.005855	LQGEAPSK
18.2	828.445328	-0.005360	LNALNER
10.1	828.434113	0.005855	IQSPQEK
10.1	828.434128	0.005840	LQPGDTAK

Mascot: http://www.matrixscience.com/

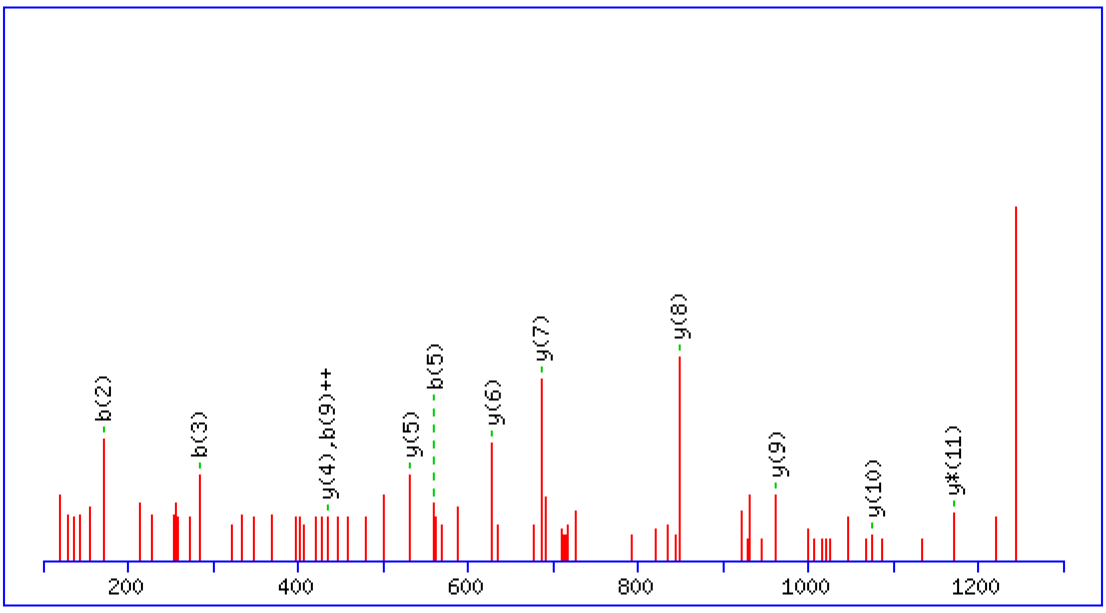
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GILLYGPPGCGK**
Found in **NSF_HUMAN**, Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3

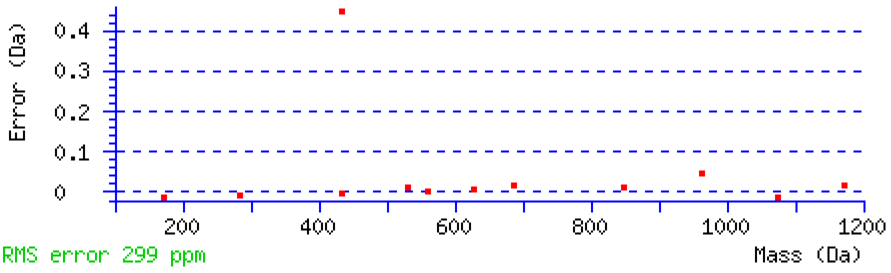
Match to Query 21469: 1244.665948 from(623.340250,2+) rtinseconds(2533) index(33020)
Title: Locus:1.1.1.2369.33
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-2.mgf

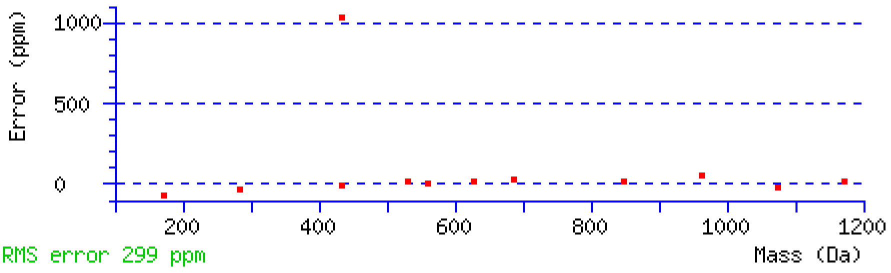
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1244.658722
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 39 **Expect:** 0.0007
Matches : 12/66 fragment ions using 23 most intense peaks (help)

#	b	b++	Seq.	y	y++	y*	y*++	#
1	58.028740	29.518008	G					12
2	**171.112804**	86.060040	I	1188.644544	594.825910	1171.617995	586.312636	11
3	**284.196868**	142.602072	L	***1075.560480***	538.283878	1058.533931	529.770604	10
4	397.280932	199.144104	L	***962.476416***	481.741846	945.449867	473.228572	9
5	**560.344261**	280.675769	Y	***849.392352***	425.199814	832.365803	416.686540	8
6	617.365725	309.186501	G	***686.329023***	343.668150	669.302474	335.154875	7
7	714.418489	357.712883	P	***629.307559***	315.157418	612.281010	306.644143	6
8	811.471253	406.239265	P	***532.254795***	266.631036	515.228246	258.117761	5
9	868.492717	434.749997	G	***435.202031***	218.104653	418.175482	209.591379	4
10	1042.539016	521.773146	C	378.180567	189.593921	361.154018	181.080647	3
11	1099.560480	550.283878	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 GILLYGPPGCGK
(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	1244.658722	0.007226	GILLYGPPGCGK

Mascot: http://www.matrixscience.com/

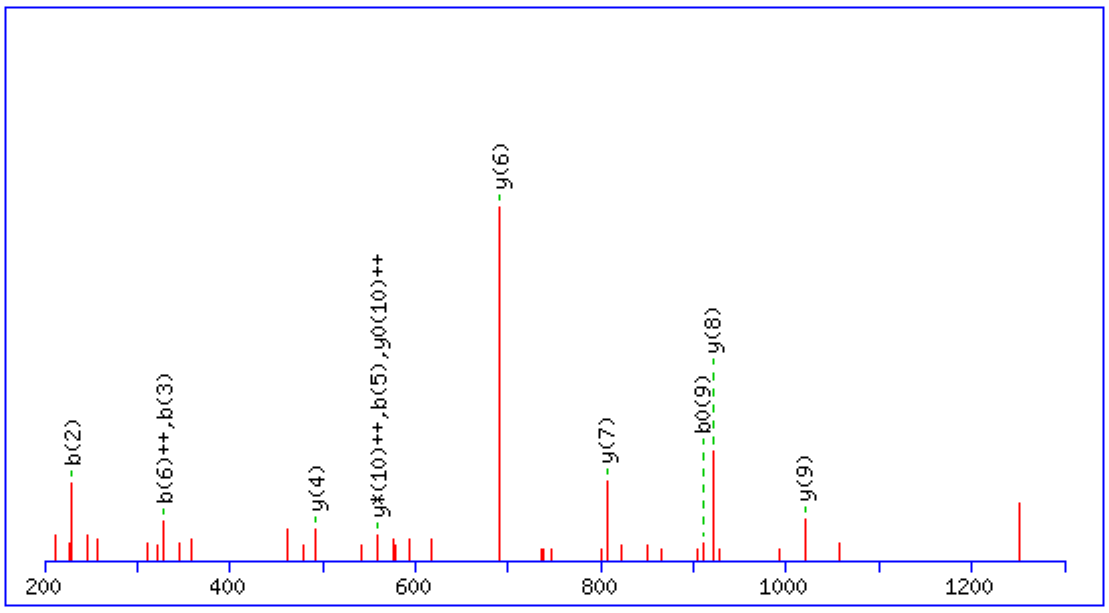
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNVDDPTGNFR**
Found in **LMAN2_HUMAN**, Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1

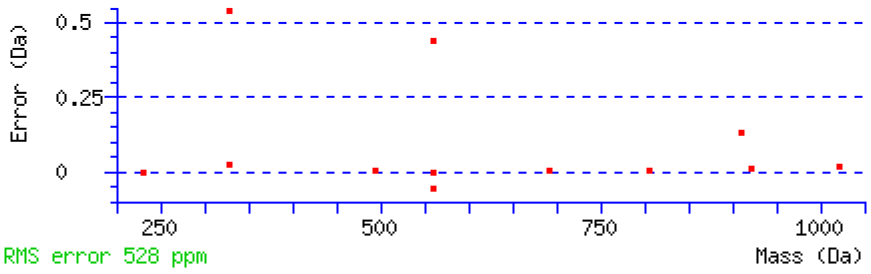
Match to Query 27187: 1248.538888 from(625.276720,2+) rtinseconds(1767) index(15871)
Title: Locus:1.1.1.2072.41
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

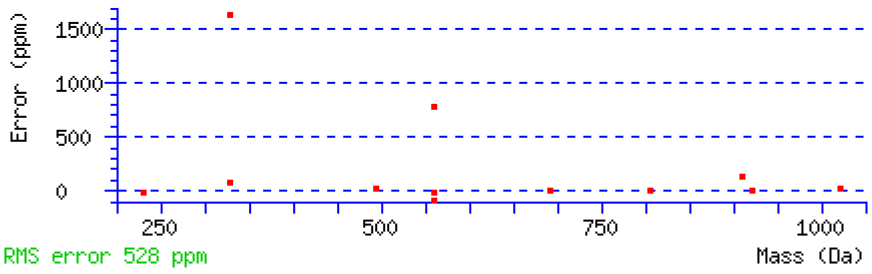
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1248.537109
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 49 **Expect:** 5.3e-005
Matches : 12/110 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	116.034219	58.520748			98.023654	49.515465	D							11
2	**230.077146**	115.542211	213.050597	107.028937	212.066581	106.536928	N	1134.517427	567.762352	1117.490878	559.249077	1116.506862	558.757069	10
3	**329.145560**	165.076418	312.119011	156.563144	311.134995	156.071136	V	***1020.474500***	510.740888	1003.447951	502.227614	1002.463935	501.735606	9
4	444.172503	222.589890	427.145954	214.076615	426.161938	213.584607	D	***921.406086***	461.206681	904.379537	452.693407	903.395521	452.201399	8
5	**559.199446**	280.103361	542.172897	271.590087	541.188881	271.098079	D	***806.379143***	403.693210	789.352594	395.179935	788.368578	394.687927	7
6	656.252210	328.629743	639.225661	320.116469	638.241645	319.624461	P	***691.352200***	346.179738	674.325651	337.666464	673.341635	337.174456	6
7	757.299889	379.153583	740.273340	370.640308	739.289324	370.148300	T	594.299436	297.653356	577.272887	289.140082	576.288871	288.648074	5
8	814.321353	407.664315	797.294804	399.151040	796.310788	398.659032	G	***493.251757***	247.129516	476.225208	238.616242			4
9	928.364280	464.685778	911.337731	456.172504	910.353715	455.680496	N	436.230293	218.618784	419.203744	210.105510			3
10	1075.432694	538.219985	1058.406145	529.706711	1057.422129	529.214703	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 DNVDDPTGNFR
(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	1248.537109	0.001779	DNVDDPTGNFR

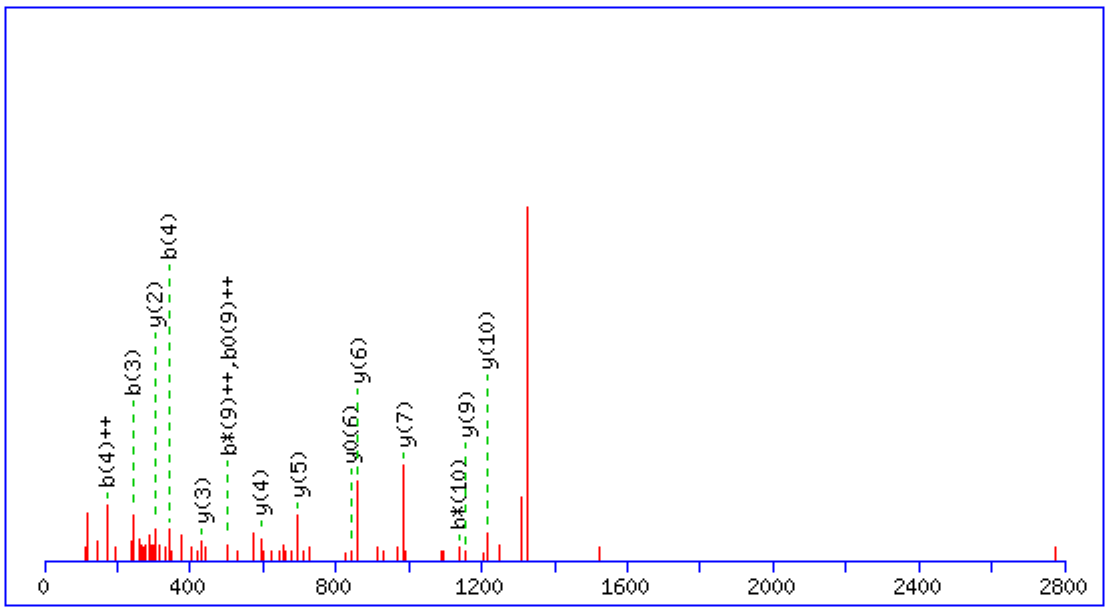
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGAVQYTYEQR**
Found in **VITRN_HUMAN**, Vitrin OS=Homo sapiens GN=VIT PE=2 SV=1

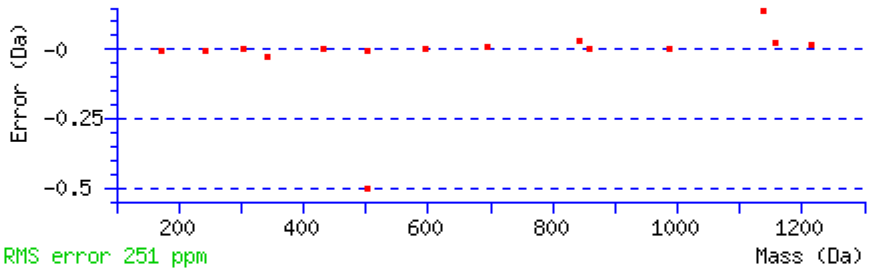
Match to Query 32514: 1326.654888 from(664.334720,2+) rtinseconds(1874) index(17919)
Title: Locus:1.1.1.2113.39
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-4.mgf

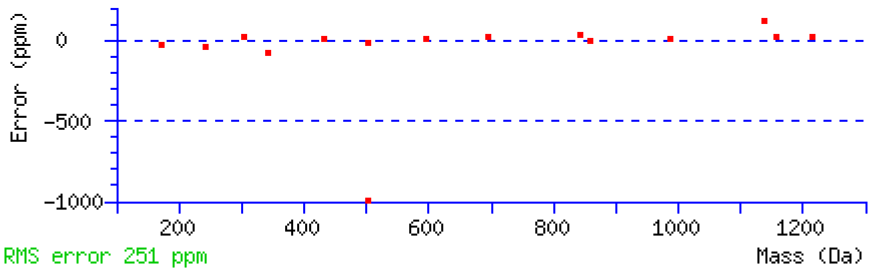
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1326.656799
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 2e-005
Matches : 16/96 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							11
2	**171.112804**	86.060040					G	***1214.580030***	607.793653	1197.553481	599.280379	1196.569465	598.788371	10
3	**242.149918**	121.578597					A	***1157.558566***	579.282921	1140.532017	570.769647	1139.548001	570.277639	9
4	**341.218332**	171.112804					V	1086.521452	543.764364	1069.494903	535.251090	1068.510887	534.759082	8
5	469.276910	235.142093	452.250361	226.628818			Q	***987.453038***	494.230157	970.426489	485.716883	969.442473	485.224875	7
6	632.340239	316.673758	615.313690	308.160483			Y	***859.394460***	430.200868	842.367911	421.687594	841.383895	421.195586	6
7	733.387918	367.197597	716.361369	358.684323	715.377353	358.192315	T	***696.331131***	348.669204	679.304582	340.155929	678.320566	339.663921	5
8	896.451247	448.729262	879.424698	440.215987	878.440682	439.723979	Y	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.140082	4
9	1025.493840	513.250558	1008.467291	504.737284	1007.483275	504.245276	E	***432.220123***	216.613700	415.193574	208.100425	414.209558	207.608417	3
10	1153.552418	577.279847	1136.525869	568.766573	1135.541853	568.274565	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 IGAVQYTYEQR
(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	1326.656799	-0.001911	IGAVQYTYEQR

Mascot: http://www.matrixscience.com/

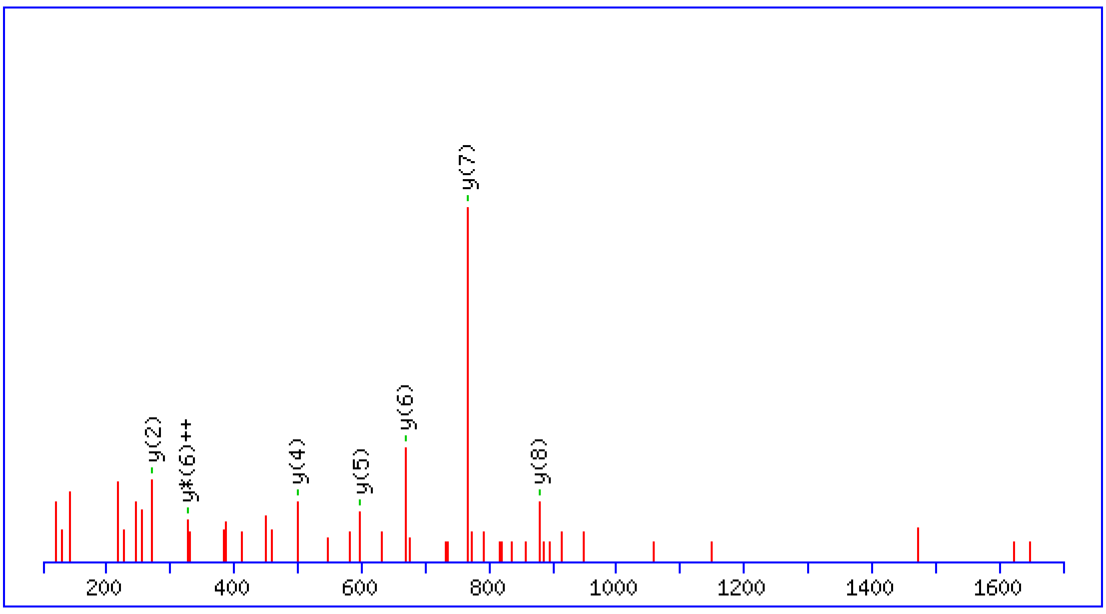
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVLPAVLNPR**
Found in **VMA5A_HUMAN**, von Willebrand factor A domain-containing protein 5A OS=Homo sapiens GN=VWA5A PE=2 SV=2

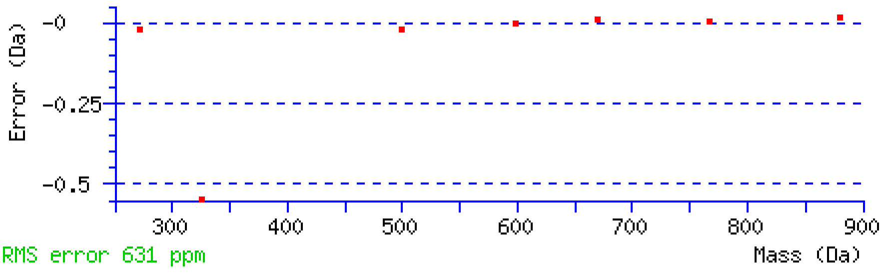
Match to Query 26549: 1124.671288 from(563.342920,2+) rtinseconds(3219) index(46732)
Title: Locus:1.1.1.2514.15
Data file 2011-11-14 - TFD - S 2-2.mgf

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 ●

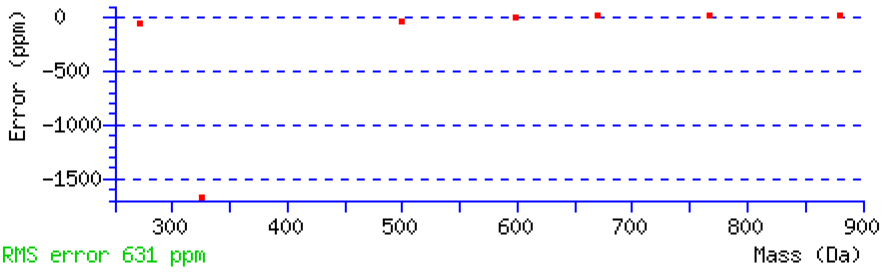


Monoisotopic mass of neutral peptide Mr(calc): 1124.670609
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 47 **Expect:** 5.3e-005
Matches : 7/58 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	148.075690	74.541483			F					10
2	247.144104	124.075690			V	978.609477	489.808377	961.582928	481.295102	9
3	360.228168	180.617722			L	***879.541063***	440.274170	862.514514	431.760895	8
4	457.280932	229.144104			P	***766.456999***	383.732138	749.430450	375.218863	7
5	528.318046	264.662661			A	***669.404235***	335.205756	652.377686	326.692481	6
6	627.386460	314.196868			V	***598.367121***	299.687199	581.340572	291.173924	5
7	740.470524	370.738900			L	***499.298707***	250.152992	482.272158	241.639717	4
8	854.513451	427.760363	837.486902	419.247089	N	386.214643	193.610960	369.188094	185.097685	3
9	951.566215	476.286745	934.539666	467.773471	P	***272.171716***	136.589496	255.145167	128.076222	2
10					R	175.118952	88.063114	158.092403	79.549840	1



RMS error 631 ppm



RMS error 631 ppm

NCBI **BLAST** search of FVLPAVLNPR
(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	1124.670609	0.000679	FVLPAVLNPR

Mascot: http://www.matrixscience.com/

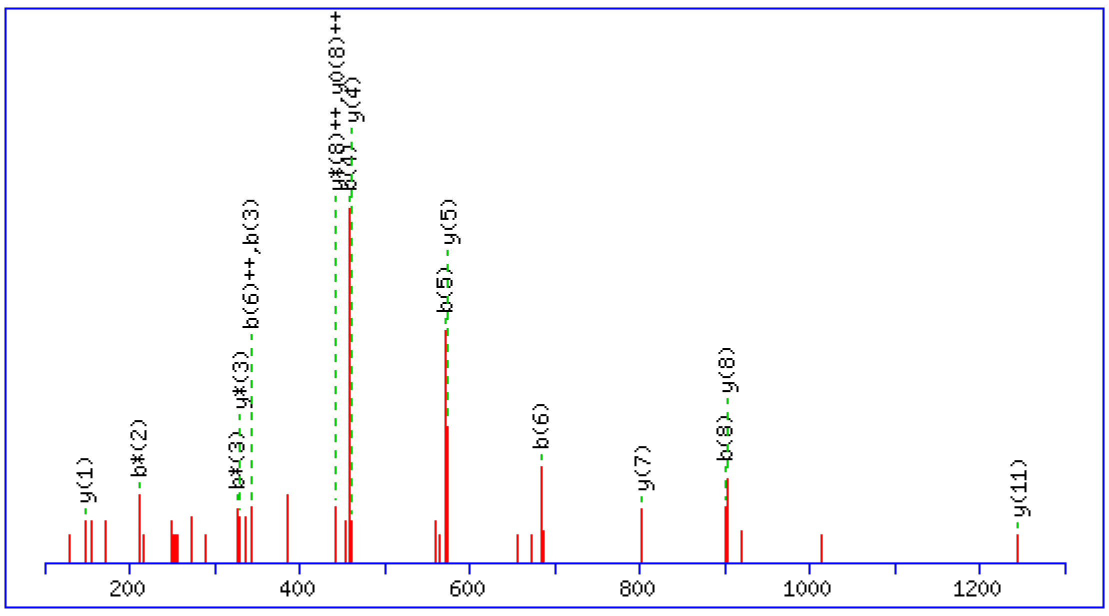
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ARDDLITDLLNEAK**
Found in **VATE1_HUMAN**, V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1

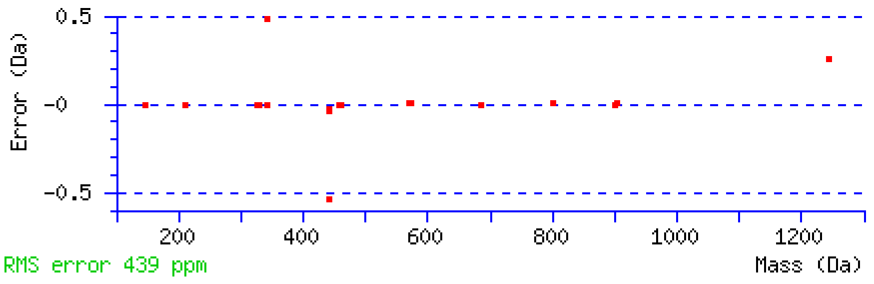
Match to Query 35741: 1585.823802 from(529.615210,3+) rtinseconds(3618) index(46003)
Title: Locus:1.1.1.2945.6
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-4.mgf

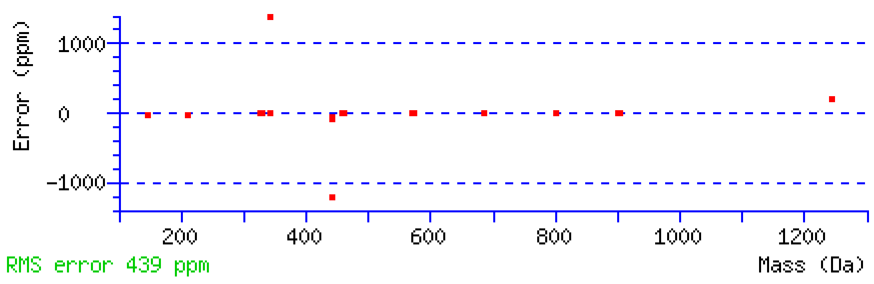
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.831116
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 44  Expect: 0.00035
Matches : 18/146 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	72.044390	36.525833					A							14
2	228.145501	114.576388	211.118952	106.063114			R	1515.801313	758.404295	1498.774764	749.891020	1497.790748	749.399012	13
3	***343.172444***	172.089860	326.145895	163.576585	325.161879	163.084577	D	1359.700202	680.353739	1342.673653	671.840465	1341.689637	671.348457	12
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	D	***1244.673259***	622.840268	1227.646710	614.326993	1226.662694	613.834985	11
5	***571.283451***	286.145364	554.256902	277.632089	553.272886	277.140081	L	1129.646316	565.326796	1112.619767	556.813522	1111.635751	556.321514	10
6	***684.367515***	342.687396	667.340966	334.174121	666.356950	333.682113	I	1016.562252	508.784764	999.535703	500.271490	998.551687	499.779482	9
7	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	T	***903.478188***	452.242732	886.451639	443.729458	885.467623	443.237450	8
8	***900.442137***	450.724707	883.415588	442.211432	882.431572	441.719424	D	***802.430509***	401.718893	785.403960	393.205618	784.419944	392.713610	7
9	1013.526201	507.266739	996.499652	498.753464	995.515636	498.261456	L	687.403566	344.205421	670.377017	335.692147	669.393001	335.200139	6
10	1126.610265	563.808771	1109.583716	555.295496	1108.599700	554.803488	L	***574.319502***	287.663389	557.292953	279.150115	556.308937	278.658107	5
11	1240.653192	620.830234	1223.626643	612.316960	1222.642627	611.824952	N	***461.235438***	231.121357	444.208889	222.608083	443.224873	222.116075	4
12	1369.695785	685.351531	1352.669236	676.838256	1351.685220	676.346248	E	347.192511	174.099894	330.165962	165.586619	329.181946	165.094611	3
13	1440.732899	720.870088	1423.706350	712.356813	1422.722334	711.864805	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 ARDDLITDLLNEAK
(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	1585.831116	-0.007314	ARDDLITDLLNEAK
6.9	1585.825287	-0.001485	EPSFIVVHYAGPVR
6.9	1585.808670	0.015132	ESETEPEPVTLLVK
6.1	1585.817398	0.006404	MVVPEKEQSWIPK
5.3	1585.831131	-0.007329	QVLEDSPAGKTNALK
4.8	1585.813354	0.010448	NLQLMEGKEPATGAK
3.7	1585.817398	0.006404	QKLGMVEWIEPPK
2.9	1585.813400	0.010402	SSQMPRPSVPPLVK
2.9	1585.813400	0.010402	SSQMPRPSVPPLVK
2.1	1585.817398	0.006404	MLVQNDITSYKFK

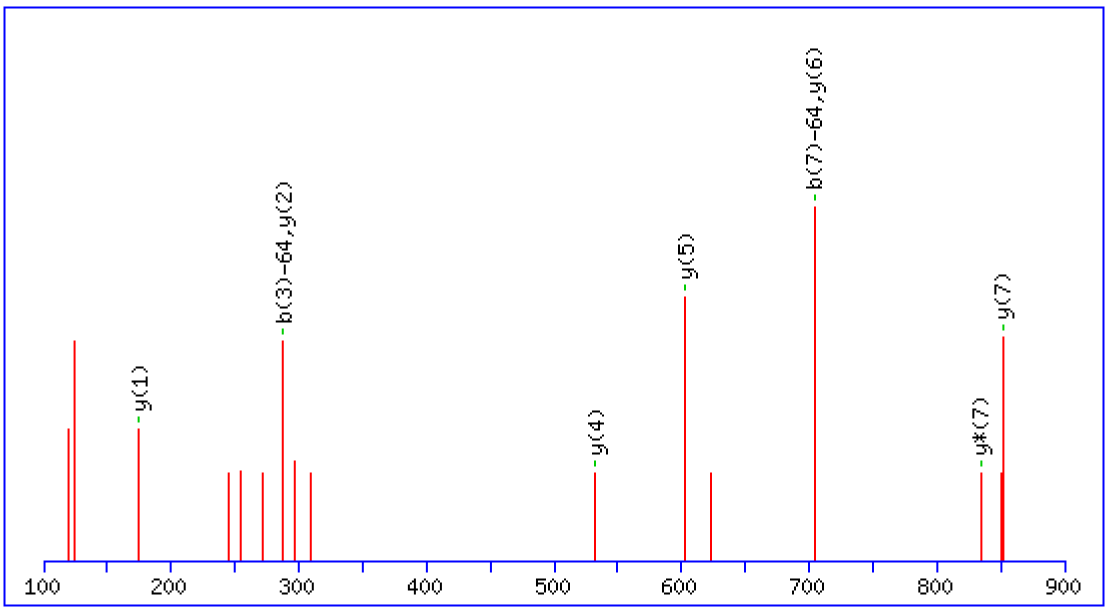
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMFTAEDLR**
Found in **VATF_HUMAN**, V-type proton ATPase subunit F OS=Homo sapiens GN=ATP6V1F PE=1 SV=2

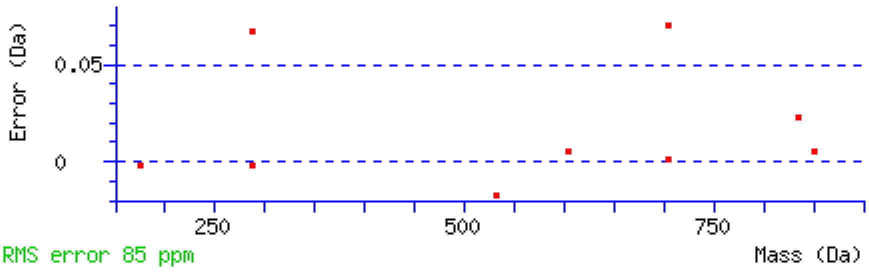
Match to Query 7512: 1054.475728 from(528.245140,2+) rtinseconds(2025) index(5080)
Title: Locus:1.1.1.2529.13
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-7.mgf

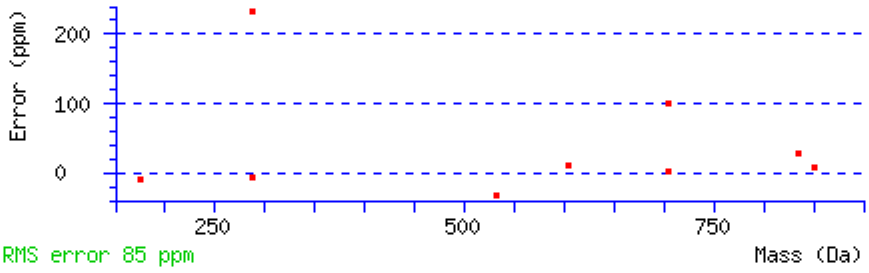
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1054.475342
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: 45 **Expect:** 0.0002
Matches : 9/100 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							9
2	205.064140	103.035708			M	998.461159	499.734218	981.434610	491.220943	980.450594	490.728935	8
3	352.132554	176.569915			F	***851.425759***	426.216518	834.399210	417.703243	833.415194	417.211235	7
4	453.180233	227.093754	435.169668	218.088472	T	***704.357345***	352.682311	687.330796	344.169036	686.346780	343.677028	6
5	524.217347	262.612312	506.206782	253.607029	A	***603.309666***	302.158471	586.283117	293.645197	585.299101	293.153189	5
6	653.259940	327.133608	635.249375	318.128326	E	***532.272552***	266.639914	515.246003	258.126640	514.261987	257.634632	4
7	768.286883	384.647080	750.276318	375.641797	D	403.229959	202.118618	386.203410	193.605343	385.219394	193.113335	3
8	881.370947	441.189112	863.360382	432.183829	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 GMFTAEDLR
(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	1054.475342	0.000386	GMFTAEDLR
9.3	1054.483215	-0.007487	GEPSHPFPR
0.5	1054.483215	-0.007487	GEPSHPFPR

Mascot: http://www.matrixscience.com/

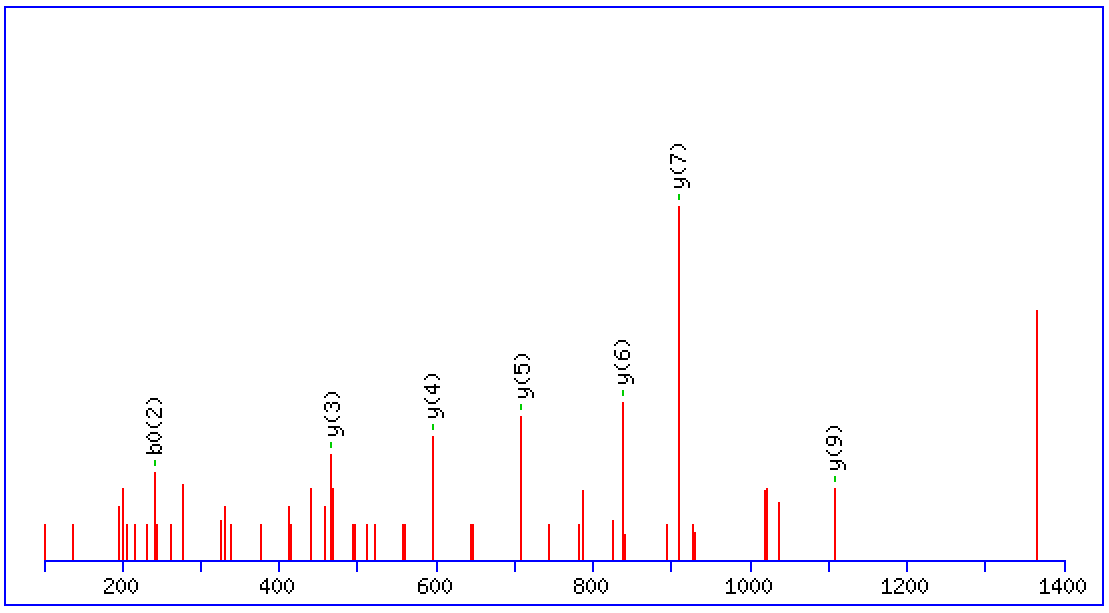
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEAQAEIEQYR**
Found in **VATG1_HUMAN**, V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3

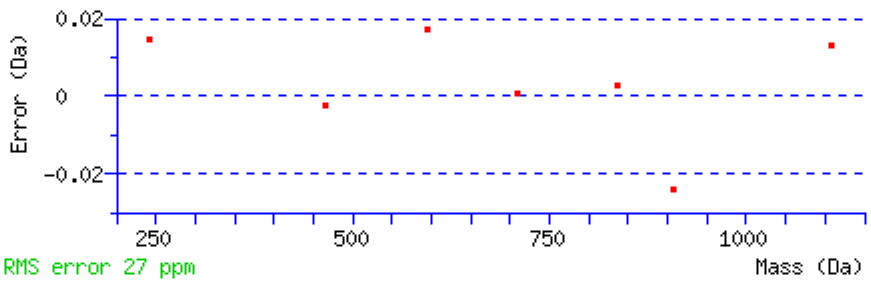
Match to Query 15025: 1364.621688 from(683.318120,2+) rtinseconds(1903) index(3486)
Title: Locus:1.1.1.2748.27
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-7.mgf

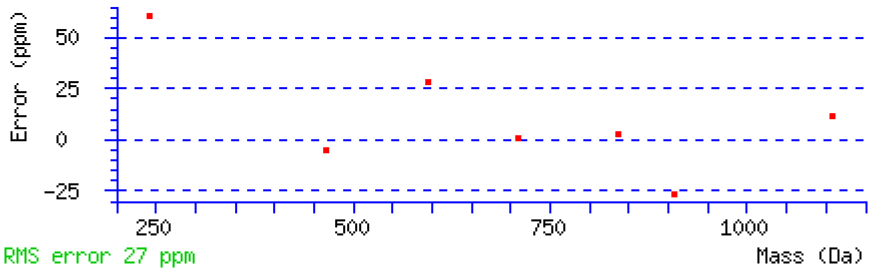
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1364.620773
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.0012
Matches : 7/108 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	130.049869	65.528572			112.039304	56.523290	E							11
2	259.092462	130.049869			241.081897	121.044587	E	1236.585508	618.796392	1219.558959	610.283118	1218.574943	609.791109	10
3	330.129576	165.568426			312.119011	156.563144	A	***1107.542915***	554.275096	1090.516366	545.761821	1089.532350	545.269813	9
4	458.188154	229.597715	441.161605	221.084441	440.177589	220.592433	Q	1036.505801	518.756539	1019.479252	510.243264	1018.495236	509.751256	8
5	529.225268	265.116272	512.198719	256.602998	511.214703	256.110990	A	***908.447223***	454.727250	891.420674	446.213975	890.436658	445.721967	7
6	658.267861	329.637569	641.241312	321.124294	640.257296	320.632286	E	***837.410109***	419.208693	820.383560	410.695418	819.399544	410.203410	6
7	771.351925	386.179601	754.325376	377.666326	753.341360	377.174318	I	***708.367516***	354.687396	691.340967	346.174122	690.356951	345.682114	5
8	900.394518	450.700897	883.367969	442.187623	882.383953	441.695615	E	***595.283452***	298.145364	578.256903	289.632090	577.272887	289.140082	4
9	1028.453096	514.730186	1011.426547	506.216911	1010.442531	505.724903	Q	***466.240859***	233.624067	449.214310	225.110793			3
10	1191.516425	596.261851	1174.489876	587.748576	1173.505860	587.256568	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 EEAQAEIEQYR
(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	1364.620773	0.000915	EEAQAEIEQYR

Mascot: http://www.matrixscience.com/

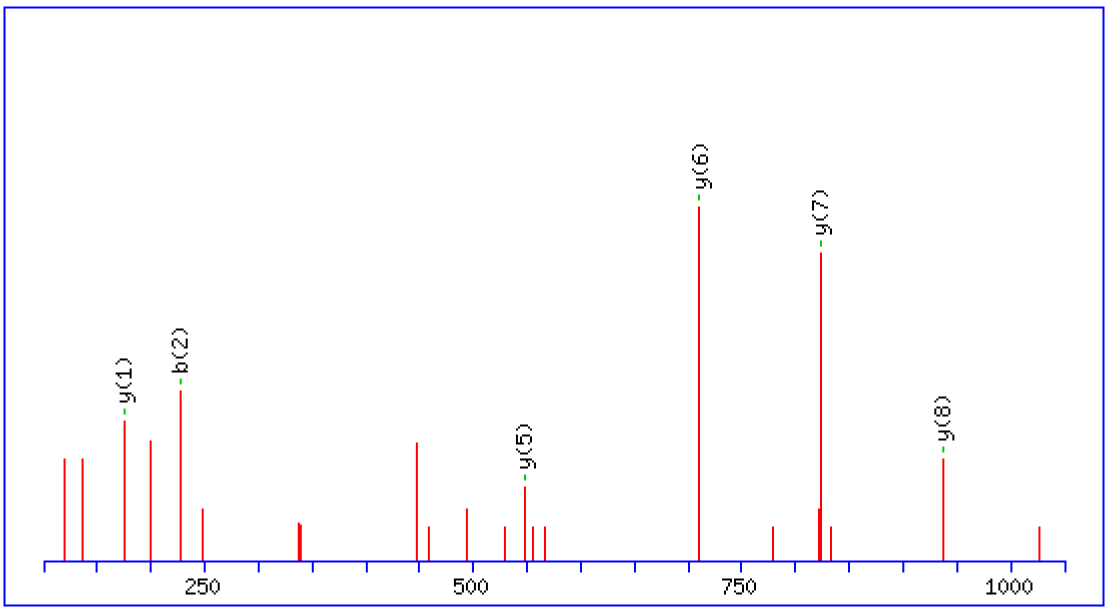
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLYSLDGR**
Found in **WRP73_HUMAN**, WD repeat-containing protein WRAP73 OS=Homo sapiens GN=WRAP73 PE=2 SV=1

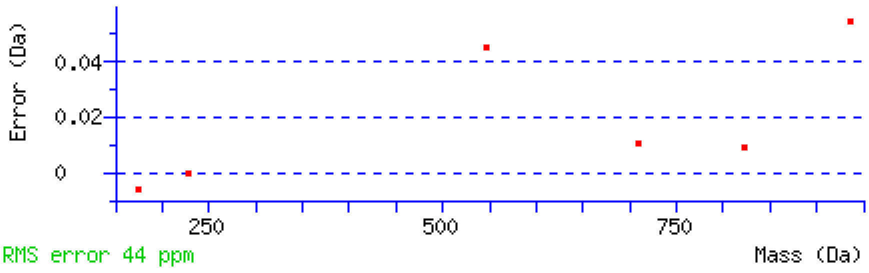
Match to Query 15917: 1048.588068 from(525.301310,2+) rtinseconds(2829) index(34809)
Title: Locus:1.1.1.2602.9
Data file \\10.14.53.42\MS\TFD - Thomas F. Dyrlund\MS Data\Cornea - Stroma - October 2011\171011 TFD - S 8-5.mgf

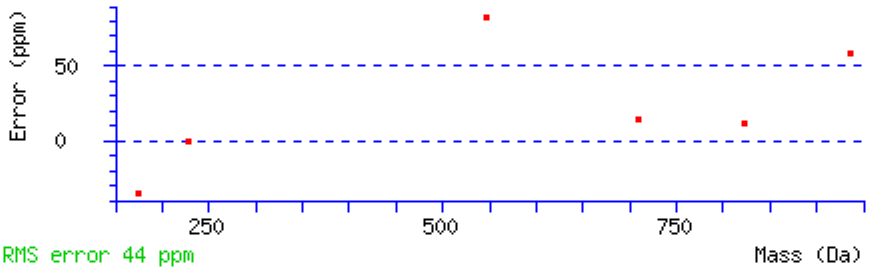
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1048.591675
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 32 **Expect:** 0.004
Matches : 6/68 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	*936.514908*	468.761092	919.488359	460.247818	918.504343	459.755810	8
3	340.259468	170.633372			L	*823.430844*	412.219060	806.404295	403.705785	805.420279	403.213777	7
4	503.322797	252.165036			Y	*710.346780*	355.677028	693.320231	347.163754	692.336215	346.671746	6
5	590.354825	295.681051	572.344260	286.675768	S	*547.283451*	274.145364	530.256902	265.632089	529.272886	265.140081	5
6	703.438889	352.223083	685.428324	343.217800	L	460.251423	230.629349	443.224874	222.116075	442.240858	221.624067	4
7	818.465832	409.736554	800.455267	400.731271	D	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
8	875.487296	438.247286	857.476731	429.242004	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 ILLYSLDGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.0	1048.591675	-0.003607	ILLYSLDGR
9.2	1048.577744	0.010324	LEPLEHRR

Mascot: http://www.matrixscience.com/

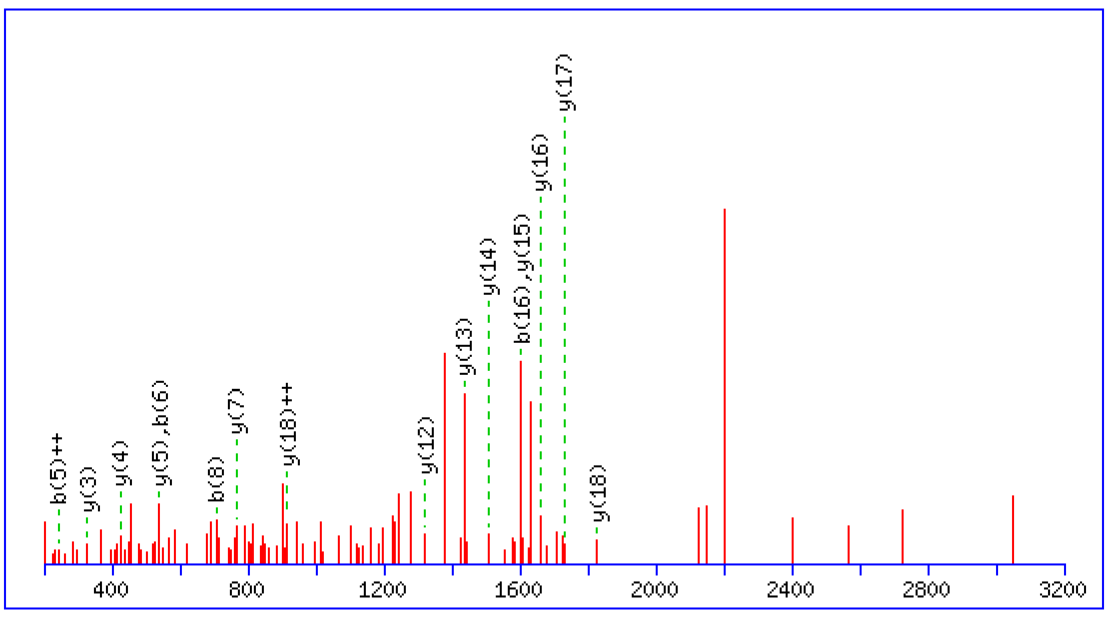
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPEPAGPAPFPLPALPLPPGR**
Found in **WTIP_HUMAN**, Wilms tumor protein 1-interacting protein OS=Homo sapiens GN=WTIP PE=2 SV=2

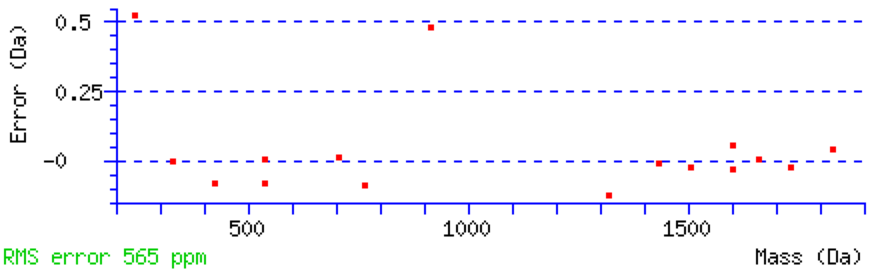
Match to Query 57594: 2141.115168 from(1071.564860,2+) rtinseconds(2603) index(34582)
Title: Locus:1.1.1.2509.48
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-1.mgf

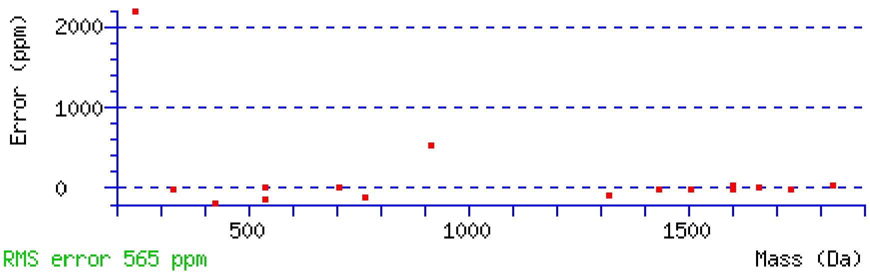
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2141.115707
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P9      : Oxidation (P)
P11     : Oxidation (P)
P13     : Oxidation (P)
P16     : Oxidation (P)
Ions Score: 33  Expect: 0.0036
Matches : 16/164 fragment ions using 50 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							21
2	185.092068	93.049672	167.081503	84.044389	P	2055.090957	1028.049116	2038.064408	1019.535842	2037.080392	1019.043834	20
3	314.134661	157.570968	296.124096	148.565686	E	1958.038193	979.522734	1941.011644	971.009460	1940.027628	970.517452	19
4	411.187425	206.097351	393.176860	197.092068	P	***1828.995600***	915.001438	1811.969051	906.488163			18
5	482.224539	241.615907	464.213974	232.610625	A	***1731.942836***	866.475056	1714.916287	857.961781			17
6	**539.246003**	270.126640	521.235438	261.121357	G	***1660.905722***	830.956499	1643.879173	822.443224			16
7	636.298767	318.653022	618.288202	309.647739	P	***1603.884258***	802.445767	1586.857709	793.932492			15
8	**707.335881**	354.171579	689.325316	345.166296	A	***1506.831494***	753.919385	1489.804945	745.406110			14
9	820.383560	410.695418	802.372995	401.690136	P	***1435.794380***	718.400828	1418.767831	709.887553			13
10	967.451974	484.229625	949.441409	475.224343	F	***1322.746701***	661.876988	1305.720152	653.363714			12
11	1080.499653	540.753465	1062.489088	531.748182	P	1175.678287	588.342781	1158.651738	579.829507			11
12	1193.583717	597.295497	1175.573152	588.290214	L	1062.630608	531.818942	1045.604059	523.305667			10
13	1306.631396	653.819336	1288.620831	644.814054	P	949.546544	475.276910	932.519995	466.763635			9
14	1377.668510	689.337893	1359.657945	680.332610	A	836.498865	418.753070	819.472316	410.239796			8
15	1490.752574	745.879925	1472.742009	736.874642	L	***765.461751***	383.234513	748.435202	374.721239			7
16	**1603.800253**	802.403764	1585.789688	793.398482	P	652.377687	326.692481	635.351138	318.179207			6
17	1716.884317	858.945796	1698.873752	849.940514	L	***539.330008***	270.168642	522.303459	261.655367			5
18	1813.937081	907.472178	1795.926516	898.466896	P	***426.245944***	213.626610	409.219395	205.113335			4
19	1910.989845	955.998560	1892.979280	946.993278	P	***329.193180***	165.100228	312.166631	156.586953			3
20	1968.011309	984.509292	1950.000744	975.504010	G	232.140416	116.573846	215.113867	108.060571			2
21					R	175.118952	88.063114	158.092403	79.549839			1



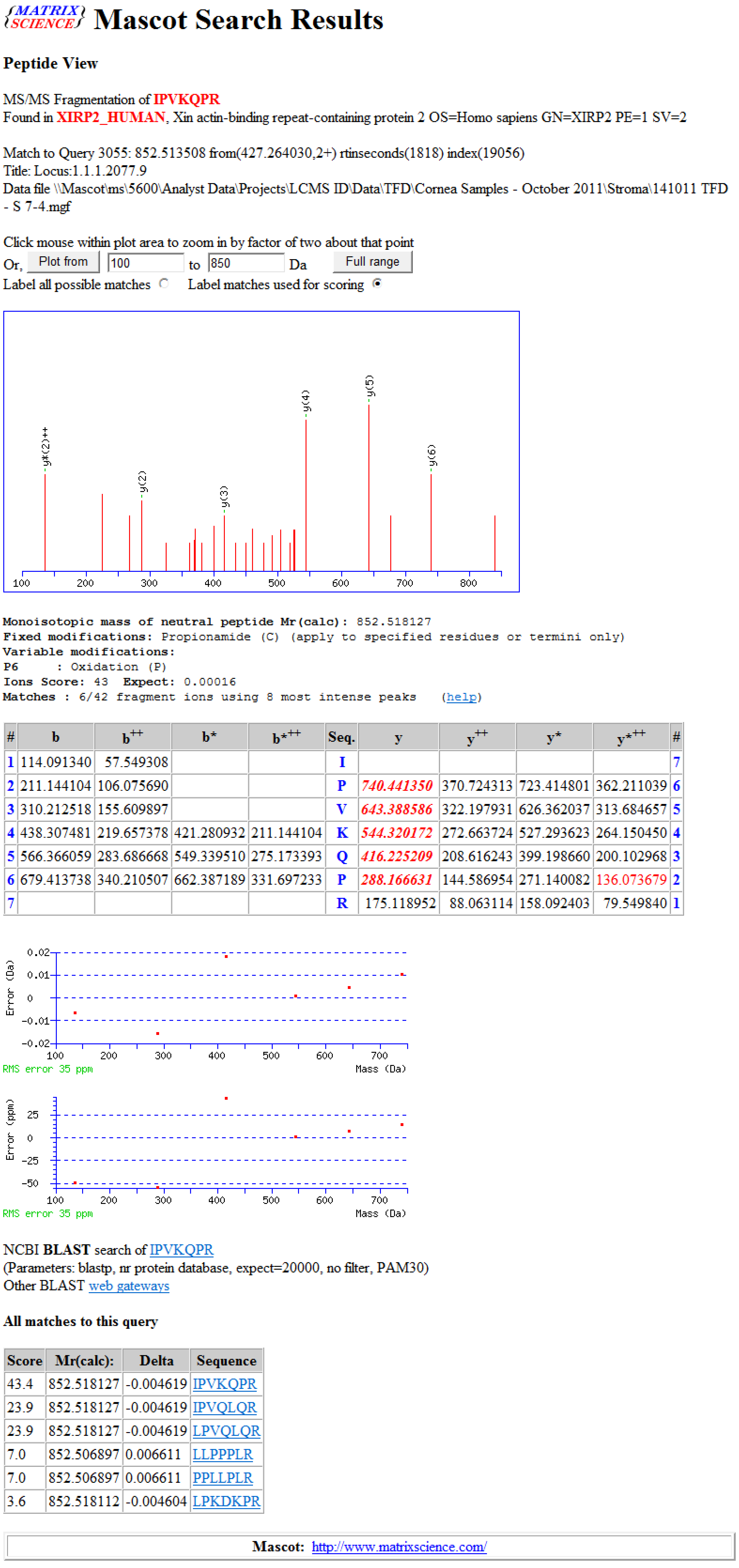


NCBI **BLAST** search of SPEPAGPAPFPLPALPLPPGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.3	2141.115707	-0.000539	SPEPAGPAPFPLPALPLPPGR
22.0	2141.115707	-0.000539	SPEPAGPAPFPLPALPLPPGR
9.7	2141.115707	-0.000539	SPEPAGPAPFPLPALPLPPGR
9.6	2141.115707	-0.000539	SPEPAGPAPFPLPALPLPPGR
7.2	2141.115707	-0.000539	SPEPAGPAPFPLPALPLPPGR

Mascot: http://www.matrixscience.com/



Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPVKQPR**
Found in **XIRP2_HUMAN**, Xin actin-binding repeat-containing protein 2 OS=Homo sapiens GN=XIRP2 PE=1 SV=2

Match to Query 3055: 852.513508 from(427.264030,2+) rtinseconds(1818) index(19056)
Title: Locus:1.1.1.2077.9
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 7-4.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): 852.518127
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P6      : Oxidation (P)
Ions Score: 43  Expect: 0.00016
Matches : 6/42 fragment ions using 8 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	438.307481	219.657378	421.280932	211.144104	K	*544.320172*	272.663724	527.293623	264.150450	4
5	566.366059	283.686668	549.339510	275.173393	Q	*416.225209*	208.616243	399.198660	200.102968	3
6	679.413738	340.210507	662.387189	331.697233	P	*288.166631*	144.586954	271.140082	136.073679	2
7					R	175.118952	88.063114	158.092403	79.549840	1

NCBI **BLAST** search of IPVKQPR
(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	-0.004619	IPVKQPR
23.9	852.518127	-0.004619	IPVQLQR
23.9	852.518127	-0.004619	LPVQLQR
7.0	852.506897	0.006611	LLPPPLR
7.0	852.506897	0.006611	PPLLPLR
3.6	852.518112	-0.004604	LPKDKPR

Mascot: http://www.matrixscience.com/

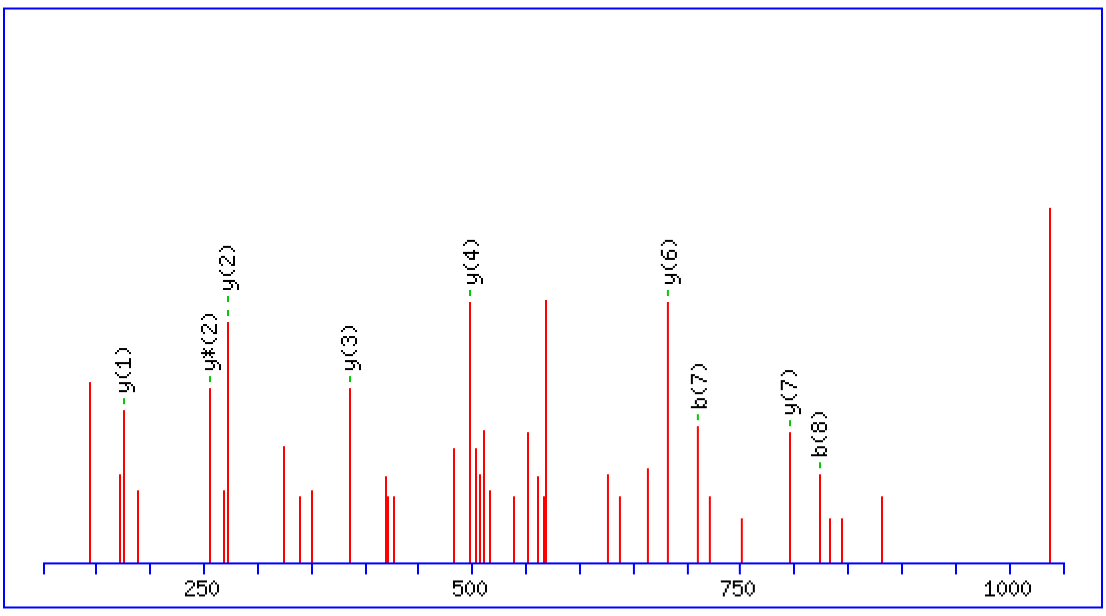
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MAPPLAPLPPR**
Found in **ZN764_HUMAN**, Zinc finger protein 764 OS=Homo sapiens GN=ZNF764 PE=1 SV=2

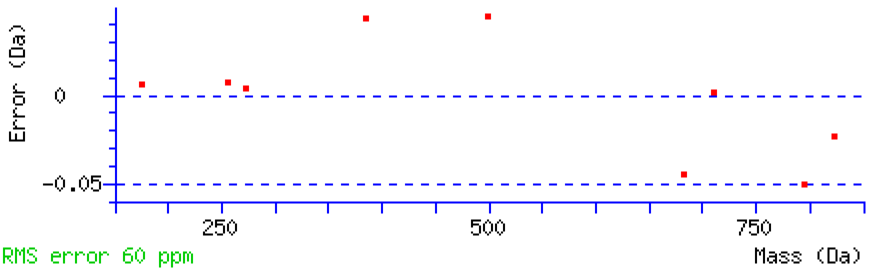
Match to Query 19239: 1206.654102 from(403.225310,3+) rtinseconds(2789) index(27004)
Title: Locus:1.1.1.2559.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 6-6.mgf

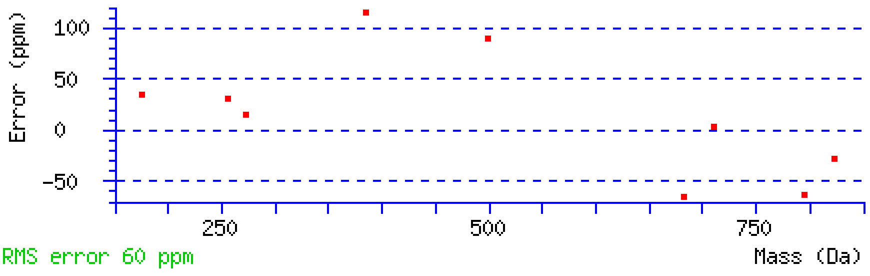
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1206.643066
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Variable modifications:
P4      : Oxidation (P)
P7      : Oxidation (P)
P9      : Oxidation (P)
Ions Score: 36  Expect: 0.0024
Matches : 9/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	132.047761	66.527518	M					11
2	203.084875	102.046075	A	1076.609873	538.808575	1059.583324	530.295300	10
3	300.137639	150.572457	P	1005.572759	503.290018	988.546210	494.776743	9
4	413.185318	207.096297	P	908.519995	454.763636	891.493446	446.250361	8
5	526.269382	263.638329	L	***795.472316***	398.239796	778.445767	389.726522	7
6	597.306496	299.156886	A	***682.388252***	341.697764	665.361703	333.184490	6
7	**710.354175**	355.680726	P	611.351138	306.179207	594.324589	297.665933	5
8	**823.438239**	412.222758	L	***498.303459***	249.655367	481.276910	241.142093	4
9	936.485918	468.746597	P	***385.219395***	193.113335	368.192846	184.600061	3
10	1033.538682	517.272979	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 MAPPLAPLPPR
(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	1206.643066	0.011036	MAPPLAPLPPR
36.1	1206.643066	0.011036	MAPPLAPLPPR
36.1	1206.643066	0.011036	MAPPLAPLPPR
21.4	1206.643066	0.011036	MAPPLAPLPPR
21.4	1206.643066	0.011036	MAPPLAPLPPR
21.4	1206.643066	0.011036	MAPPLAPLPPR
13.9	1206.643066	0.011036	MAPPLAPLPPR
13.9	1206.643066	0.011036	MAPPLAPLPPR
13.9	1206.643066	0.011036	MAPPLAPLPPR
13.9	1206.646927	0.007175	RTLPGGQPPPR

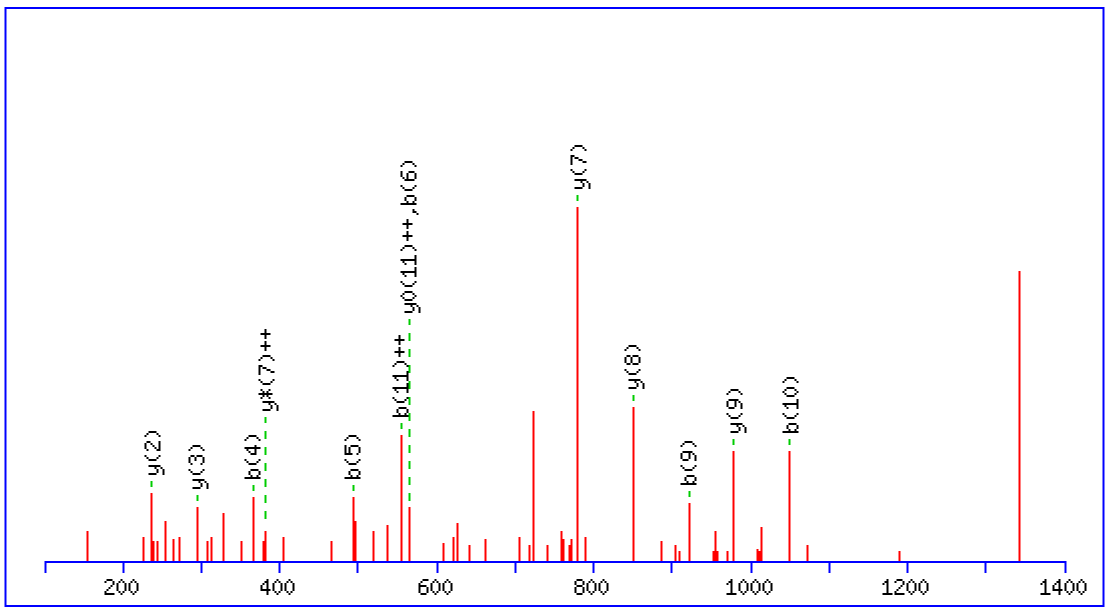
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPAPKAPDEQGSM**
Found in **ZN839_HUMAN**, Zinc finger protein 839 OS=Homo sapiens GN=ZNF839 PE=2 SV=1

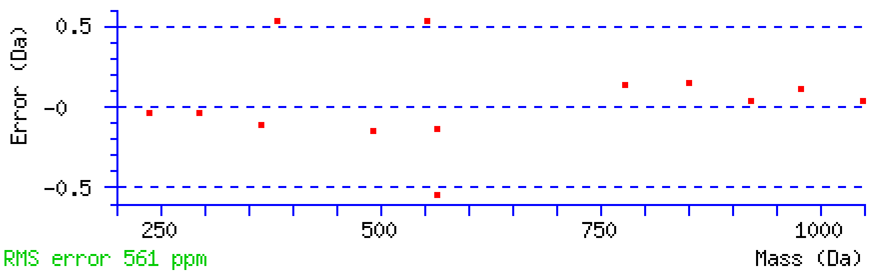
Match to Query 531941: 1341.625888 from(671.820220,2+) rtinseconds(1210) index(92840)
Title: Locus:1.1.1.863.24
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 TFD - Stroma - IEC R2\mascot_daemon_merge.mgf

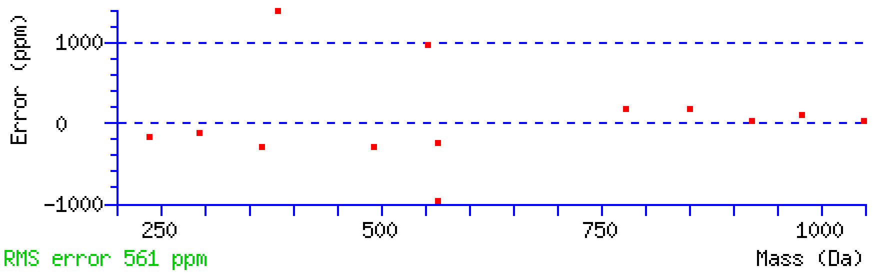
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1341.623459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
P7 : Oxidation (P)
Ions Score: 30 **Expect:** 0.0074
Matches : 13/114 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							13
2	197.128454	99.067865					P	1243.562330	622.284803	1226.535781	613.771529	1225.551765	613.279520	12
3	268.165568	134.586422					A	1146.509566	573.758421	1129.483017	565.245147	1128.499001	564.753138	11
4	***365.218332***	183.112804					P	1075.472452	538.239864	1058.445903	529.726590	1057.461887	529.234582	10
5	***493.313295***	247.160285	476.286746	238.647011			K	***978.419688***	489.713482	961.393139	481.200208	960.409123	480.708200	9
6	***564.350409***	282.678843	547.323860	274.165568			A	***850.324725***	425.666001	833.298176	417.152726	832.314160	416.660718	8
7	677.398088	339.202682	660.371539	330.689408			P	***779.287611***	390.147444	762.261062	381.634169	761.277046	381.142161	7
8	792.425031	396.716154	775.398482	388.202879	774.414466	387.710871	D	666.239932	333.623604	649.213383	325.110330	648.229367	324.618322	6
9	***921.467624***	461.237450	904.441075	452.724176	903.457059	452.232168	E	551.212989	276.110133	534.186440	267.596858	533.202424	267.104850	5
10	***1049.526202***	525.266739	1032.499653	516.753465	1031.515637	516.261457	Q	422.170396	211.588836	405.143847	203.075561	404.159831	202.583553	4
11	1106.547666	553.777471	1089.521117	545.264197	1088.537101	544.772188	G	***294.111818***	147.559547			276.101253	138.554264	3
12	1193.579694	597.293485	1176.553145	588.780211	1175.569129	588.288203	S	***237.090354***	119.048815			219.079789	110.043533	2
13							M	150.058326	75.532801					1





NCBI **BLAST** search of VPAPKAPDEQGSM
(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	1341.623459	0.002429	VPAPKAPDEQGSM
7.7	1341.623459	0.002429	VPAPKAPDEQGSM

Mascot: http://www.matrixscience.com/

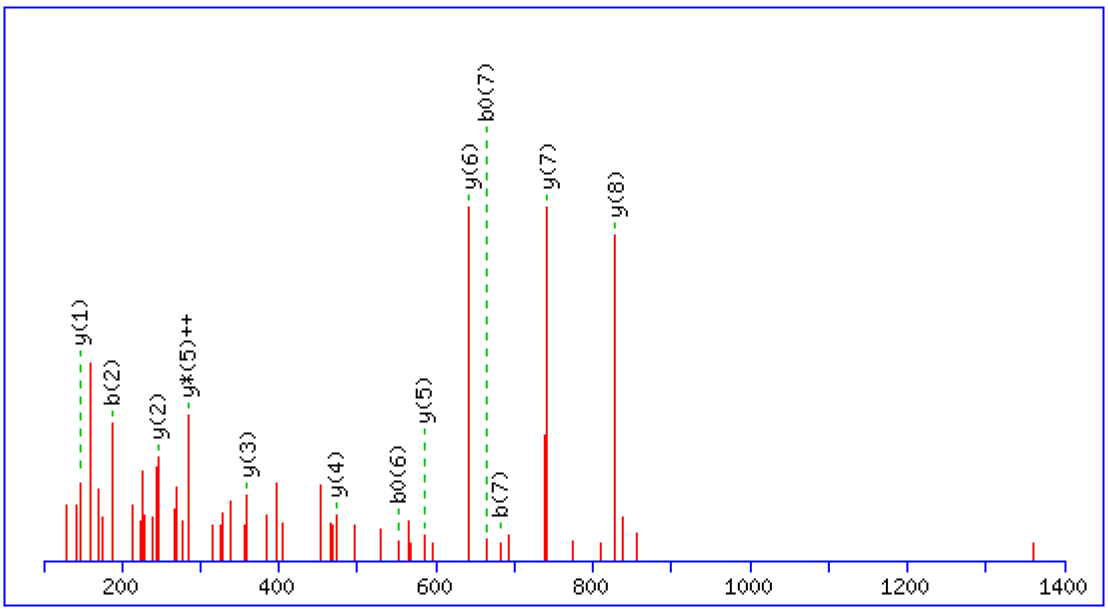
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVGLLLVK**
Found in **ZG16B_HUMAN**, Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3

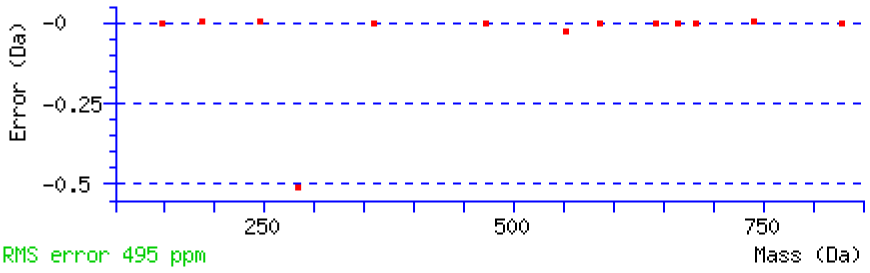
Match to Query 2515: 926.617728 from(464.316140,2+) rtinseconds(3033) index(6122)
Title: Locus:1.1.1.3467.2
Data file \\Mascot\ms\5600\Analyst Data\Projects\LCMS ID\Data\TFD\Cornea Samples - October 2011\Stroma\141011 TFD - S 3-8.mgf

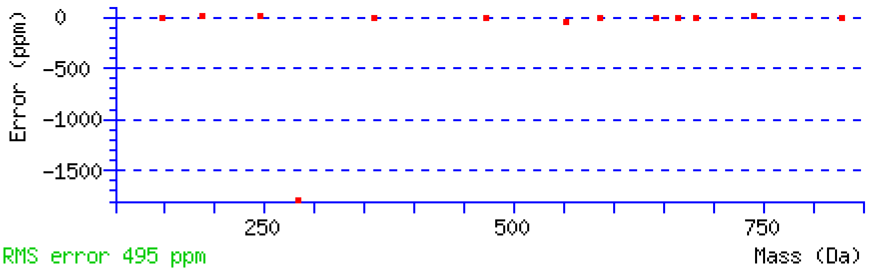
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 926.616455
Fixed modifications: Propionamide (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 5.3e-006
Matches : 13/64 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							9
2	**187.107718**	94.057497	169.097153	85.052214	S	***828.555316***	414.781296	811.528767	406.268022	810.544751	405.776014	8
3	286.176132	143.591704	268.165567	134.586422	V	***741.523288***	371.265282	724.496739	362.752008			7
4	343.197596	172.102436	325.187031	163.097153	G	***642.454874***	321.731075	625.428325	313.217801			6
5	456.281660	228.644468	438.271095	219.639186	L	***585.433410***	293.220343	568.406861	284.707069			5
6	569.365724	285.186500	551.355159	276.181218	L	***472.349346***	236.678311	455.322797	228.165036			4
7	**682.449788**	341.728532	664.439223	332.723250	L	***359.265282***	180.136279	342.238733	171.623004			3
8	781.518202	391.262739	763.507637	382.257456	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 VSVGLLLVK
(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	926.616455	0.001273	VSVGLLLVK

Mascot: http://www.matrixscience.com/