Soluble and exosomal glycopeptides detected in human plasma using PUC-ERLIC method

Click the link below to view data in Mascot Peptide View OR "ALT + <- " (ALT+arrow) to return

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Spectrum_00572_Q96PD5_RLYHFLLGAWSLN#ATELDPCPLSPELLGLTKE
Spectrum_00573_Q96PD5_RLEPVHLQLQCMSQ#EQLAQVAAN#ATKE
Spectrum_00574_Q96PD5_RLEPVHLQLQCMSQEQ#LAQVAAN#ATKE
Spectrum_00575_Q96PD5_RLEPVHLQLQ#CMSQEQLAQVAAN#ATKE
Spectrum_00576_Q96PD5_RLEPVHLQ#LQCMSQEQLAQVAAN#ATKE
Spectrum_00577_Q96PD5_RLEPVHLQ#LQCM#SQEQLAQVAAN#ATKE
Spectrum_00578_Q96PD5_RLEPVHLQLQCM#SQEQ#LAQVAAN#ATKE
Spectrum_00579_Q96PD5_RLEPVHLQLQCM#SQ#EQLAQVAAN#ATKE
Spectrum_00580_Q9NZP8_KDRQDGEEVLQCM#PVCGRPVTPIAQN#QTTLGSSRA
Spectrum_00581_Q9NZP8_KDRQDGEEVLQCMPVCGRPVTPIAQN#QTTLGSSRA
Spectrum_00582_Q9ULI3_KSHAASDAPEN#LTLLAETADARG
Spectrum_00583_Q9Y5Y7_KANQQLN#FTEAKE
Spectrum_00584_Q9Y6R7_RYLPVN#SSLLTSDCSERC
Spectrum_00585_Q9Y6R7_RLLISSLSESPASVSILSQADN#TSKK
Spectrum_00586_Q9Y6R7_RGLCVLSVGAN#LTTFDGARG
Spectrum_00587_S4R471_RYFYN#GTSMACETFQYGGCM#GNGNN#FVTVRG
Spectrum_00588_S4R471_RYFYN#GTSM#ACETFQ#YGGCM#GN#GNN#FVTVRG
Spectrum_00589_S4R471_RYFYN#GTSM#ACETFQ#YGGCMGNGNN#FVTVRG
Spectrum_00590_S4R471_RYFYN#GTSM#ACETFQYGGCMGNGN#N#FVTVRG
Spectrum_00591_S4R471_RYFYN#GTSMACETFQ#YGGCMGNGN#N#FVTVRG
Spectrum_00592_S4R471_RYFYN#GTSM#ACETFQ#YGGCMGNGNNFVTVRG
Spectrum_00593_S4R471_RYFYN#GTSM#ACETFQYGGCM#GN#GNNFVTVRG
Spectrum_00594_S4R471_RYFYN#GTSM#ACETFQYGGCM#GNGN#N#FVTVRG
Spectrum_00595_S4R471_RYFYN#GTSM#ACETFQYGGCM#GN#GNN#FVTVRG
Spectrum_00596_S4R471_RYFYN#GTSMACETFQYGGCMGNGN#N#FVTVRG
Spectrum_00597_S4R471_RYFYN#GTSMACETFQYGGCM#GNGN#N#FVTVRG
Spectrum_00598_S4R471_RYFYN#GTSM#ACETFQYGGCM#GNGNN#FVTVRG
Spectrum_00599_S4R471_RYFYN#GTSM#ACETFQ#YGGCM#GNGNN#FVTVRG

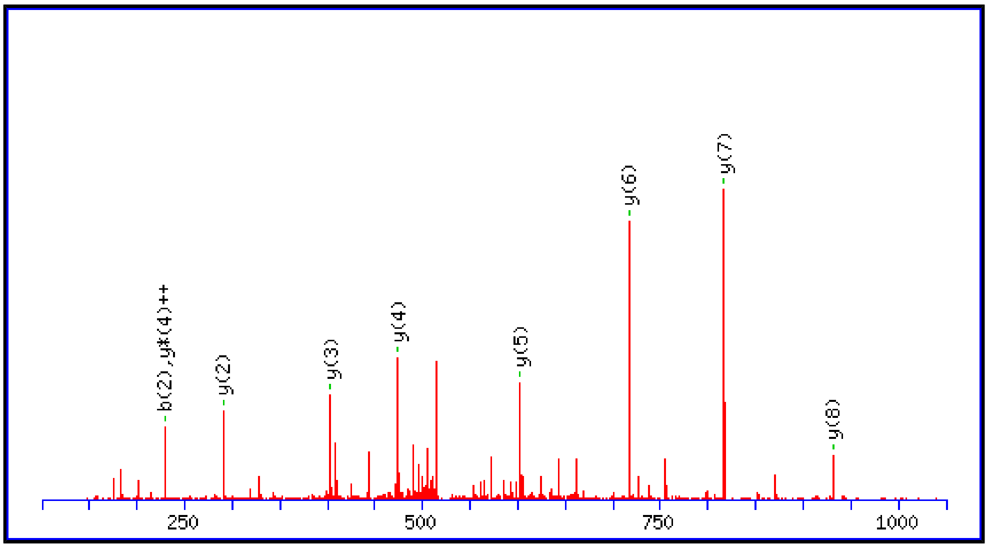
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDVDQALNR**
Found in **B0FWH6** in **con_Xuniprot_HUMAN3**, B0FWH6_HUMAN Sex hormone binding globulin (Fragment) OS=Homo sapiens GN=SHBG PE=2 SV=1

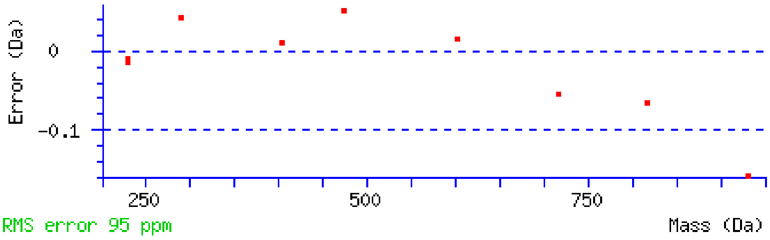
Match to Query 189: 1043.529368 from(522.771960,2+) intensity(67120.6875) rtinseconds(888) scans(2023) index(26488)
Title: 111019_Est_MI_YS_G_09Spectrum1726_scans__2023
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

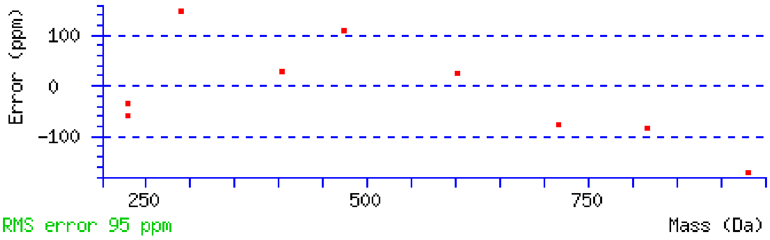
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1050 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1043.5247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 70 **Expect:** 1.5e-005
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	114.0913	57.5493					L							9
2	229.1183	115.0628			211.1077	106.0575	D	***931.4480***	466.2276	914.4214	457.7143	913.4374	457.2223	8
3	328.1867	164.5970			310.1761	155.5917	V	***816.4210***	408.7141	799.3945	400.2009	798.4104	399.7089	7
4	443.2136	222.1105			425.2031	213.1052	D	***717.3526***	359.1799	700.3260	350.6667	699.3420	350.1747	6
5	571.2722	286.1397	554.2457	277.6265	553.2617	277.1345	Q	***602.3257***	301.6665	585.2991	293.1532			5
6	642.3093	321.6583	625.2828	313.1450	624.2988	312.6530	A	***474.2671***	237.6372	457.2405	229.1239			4
7	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	L	***403.2300***	202.1186	386.2034	193.6053			3
8	870.4203	435.7138	853.3938	427.2005	852.4098	426.7085	N	***290.1459***	145.5766	273.1193	137.0633			2
9							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.2	1043.5247	0.0046	LDVDQALNR	Deamidated N8 100.00%
22.2	1043.5247	0.0046	LDVDQALNR	Deamidated Q5 0.00%
21.6	1043.5247	0.0046	VDLQGELDR	
15.0	1043.5247	0.0046	IDVADIDAGR	
14.2	1043.5247	0.0046	TSPSTAPLDR	
13.8	1043.5247	0.0046	ISQLPSQDR	
12.7	1043.5247	0.0046	DVVEGADLAR	
12.7	1043.5247	0.0046	LDSSPVSSPR	
11.5	1043.5247	0.0046	LDQGNIEVR	
11.5	1043.5247	0.0046	LDQGNIEVR	

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

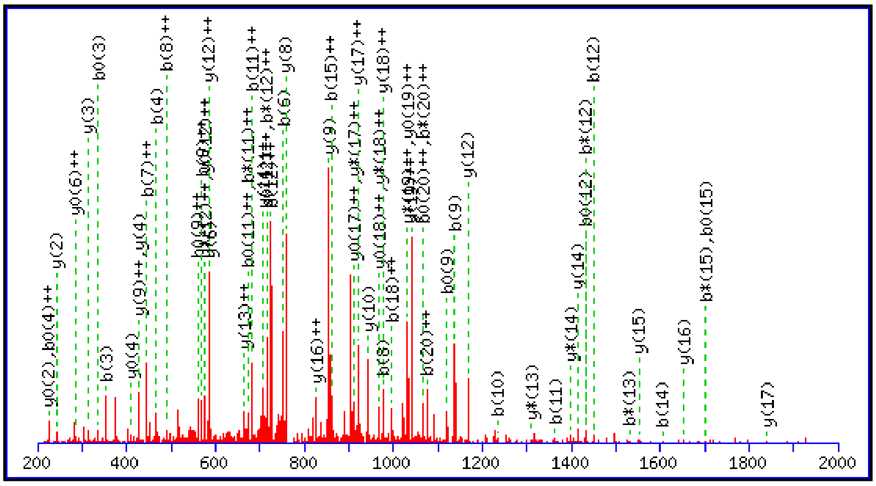
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHEIWTHSCPQSPGNGTDASH**
Found in **B0FWH6** in **con_Xuniprot_HUMAN3**, B0FWH6_HUMAN Sex hormone binding globulin (Fragment) OS=Homo sapiens GN=SHBG PE=2 SV=1

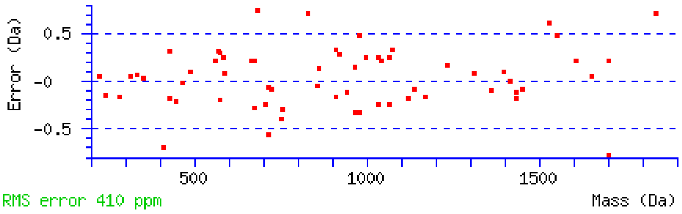
Match to Query 15144: 2304.951792 from(769.324540,3+) intensity(20358.0137) rtinseconds(436) scans(846) index(25162)
Title: 111019_Est_MI_YS_G_07Spectrum675_scans__846
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

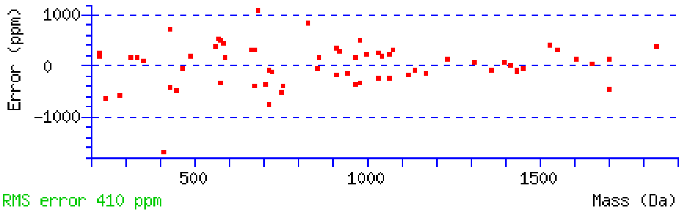
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2304.9454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15     : Deamidated (NQ)
Ions Score: 56  Expect: 8.5e-005
Matches : 67/206 fragment ions using 131 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							21
2	***225.0982***	113.0527			207.0877	104.0475	H	2218.9207	1109.9640	2201.8941	1101.4507	2200.9101	1100.9587	20
3	***354.1408***	177.5740			336.1302	168.5688	E	2081.8618	1041.4345	2064.8352	1032.9212	2063.8512	1032.4292	19
4	***467.2249***	234.1161			449.2143	225.1108	I	1952.8192	976.9132	1935.7926	968.3999	1934.8086	967.9079	18
5	653.3042	327.1557			635.2936	318.1504	W	***1839.7351***	920.3712	1822.7086	911.8579	1821.7245	911.3659	17
6	***754.3519***	377.6796			736.3413	368.6743	T	***1653.6558***	827.3315	1636.6292	818.8183	1635.6452	818.3263	16
7	891.4108	**446.2090**			873.4002	437.2037	H	***1552.6081***	776.8077	1535.5816	768.2944	1534.5975	767.8024	15
8	***978.4428***	**489.7250**			960.4322	480.7198	S	***1415.5492***	708.2782	1398.5227	699.7650	1397.5386	699.2730	14
9	***1138.4735***	**569.7404**			1120.4629	560.7351	C	1328.5172	664.7622	1311.4906	656.2489	1310.5066	655.7569	13
10	***1235.5262***	618.2667			1217.5157	609.2615	P	***1168.4865***	584.7469	1151.4600	576.2336	1150.4760	575.7416	12
11	***1363.5848***	**682.2960**	1346.5582	673.7828	1345.5742	673.2908	Q	1071.4338	536.2205	1054.4072	527.7072	1053.4232	527.2152	11
12	***1450.6168***	**725.8121**	1433.5903	717.2988	1432.6063	716.8068	S	***943.3752***	472.1912	926.3486	463.6780	925.3646	463.1859	10
13	1547.6696	774.3384	1530.6430	765.8252	1529.6590	765.3331	P	***856.3432***	428.6752	839.3166	420.1619	838.3326	419.6699	9
14	***1604.6911***	802.8492	1587.6645	794.3359	1586.6805	793.8439	G	***759.2904***	380.1488	742.2638	371.6356	741.2798	371.1435	8
15	1719.7180	**860.3626**	1702.6914	851.8494	1701.7074	851.3574	N	702.2689	351.6381	685.2424	343.1248	684.2584	342.6328	7
16	1776.7395	888.8734	1759.7129	880.3601	1758.7289	879.8681	G	***587.2420***	294.1246			569.2314	285.1193	6
17	1877.7871	939.3972	1860.7606	930.8839	1859.7766	930.3919	T	530.2205	265.6139			512.2100	256.6086	5
18	1992.8141	**996.9107**	1975.7875	988.3974	1974.8035	987.9054	D	***429.1728***	215.0901			411.1623	206.0848	4
19	2063.8512	**1032.4292**	2046.8246	1023.9160	2045.8406	1023.4240	A	***314.1459***	157.5766			296.1353	148.5713	3
20	2150.8832	**1075.9452**	2133.8567	1067.4320	2132.8727	1066.9400	S	***243.1088***	122.0580			225.0982	113.0527	2
21							H	156.0768	78.5420					1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.6	2304.9454	0.0064	SHEIWTHSCPQSPGNGTDASH	Deamidated N15 72.73%
51.4	2304.9454	0.0064	SHEIWTHSCPQSPGNGTDASH	Deamidated Q11 27.27%

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

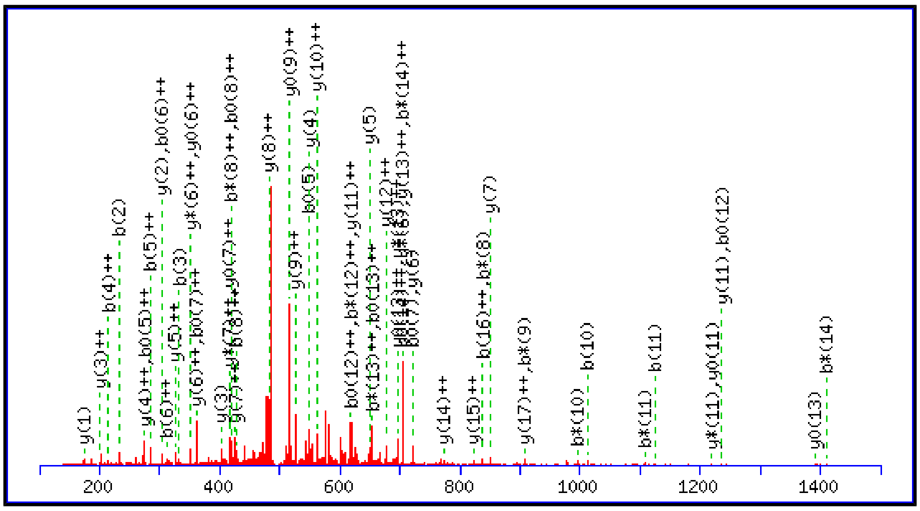
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CATPHGDNASLEATFVKR**
Found in **B1AHL2** in **con_Xuniprot_HUMAN3**, B1AHL2_HUMAN Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=2 SV=1

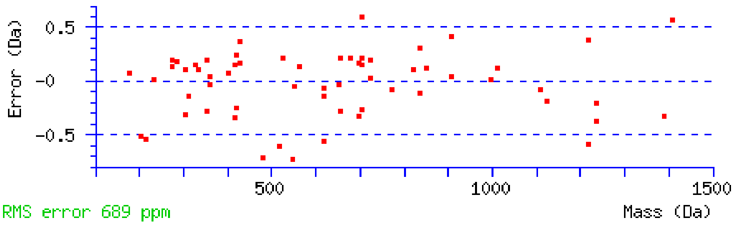
Match to Query 11881: 1973.934056 from(494.490790,4+) intensity(32052.8047) rtinseconds(719) scans(1553) index(10776)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum1291_scans__1553
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

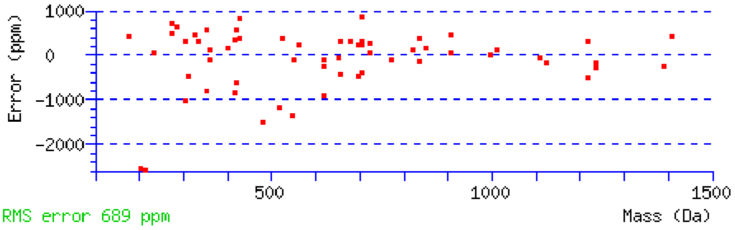
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1973.9265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 84 **Expect:** 8.3e-007
Matches : 61/178 fragment ions using 91 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							18
2	**232.0750**	116.5412					A	1814.9032	907.9552	1797.8766	899.4419	1796.8926	898.9499	17
3	**333.1227**	167.0650			315.1122	158.0597	T	1743.8660	872.4367	1726.8395	863.9234	1725.8555	863.4314	16
4	430.1755	**215.5914**			412.1649	206.5861	P	1642.8184	821.9128	1625.7918	813.3995	1624.8078	812.9075	15
5	567.2344	**284.1208**			549.2238	275.1156	H	1545.7656	773.3864	1528.7390	764.8732	1527.7550	764.3812	14
6	624.2559	**312.6316**			606.2453	303.6263	G	1408.7067	704.8570	1391.6801	696.3437	1390.6961	695.8517	13
7	739.2828	370.1450			721.2722	361.1398	D	1351.6852	676.3462	1334.6587	667.8330	1333.6747	667.3410	12
8	854.3097	**427.6585**	837.2832	419.1452	836.2992	418.6532	N	**1236.6583**	618.8328	1219.6317	610.3195	1218.6477	609.8275	11
9	925.3469	463.1771	908.3203	454.6638	907.3363	454.1718	A	1121.6313	561.3193	1104.6048	552.8060	1103.6208	552.3140	10
10	**1012.3789**	506.6931	995.3523	498.1798	994.3683	497.6878	S	1050.5942	525.8007	1033.5677	517.2875	1032.5837	516.7955	9
11	**1125.4629**	563.2351	1108.4364	554.7218	1107.4524	554.2298	L	963.5622	482.2847	946.5356	473.7715	945.5516	473.2795	8
12	1254.5055	627.7564	1237.4790	619.2431	1236.4950	618.7511	E	**850.4781**	425.7427	833.4516	417.2294	832.4676	416.7374	7
13	1325.5427	663.2750	1308.5161	654.7617	1307.5321	654.2697	A	**721.4355**	361.2214	704.4090	352.7081	703.4250	352.2161	6
14	1426.5903	713.7988	1409.5638	705.2855	1408.5798	704.7935	T	**650.3984**	325.7028	633.3719	317.1896	632.3879	316.6976	5
15	1573.6588	787.3330	1556.6322	778.8197	1555.6482	778.3277	F	**549.3507**	275.1790	532.3242	266.6657			4
16	1672.7272	**836.8672**	1655.7006	828.3539	1654.7166	827.8619	V	**402.2823**	201.6448	385.2558	193.1315			3
17	1800.8221	900.9147	1783.7956	892.4014	1782.8116	891.9094	K	**303.2139**	152.1106	286.1874	143.5973			2
18							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.0	1973.9265	0.0075	CATPHGDNASLEATFVKR
7.4	1971.9326	2.0014	SHPDQVASFADLAGKWDK
6.3	1972.9272	1.0068	HLADMALVGAEQERSSSR
6.0	1973.9438	-0.0097	MEIKDQGAQMEPLLPTR
4.7	1971.9287	2.0054	EGPSGPHGNEGKVGPPGDKGV
4.4	1973.9357	-0.0016	NEWHGRWNAAESHPRK
4.3	1971.9333	2.0007	EERSHQRNVMGGLTWR
4.1	1971.9360	1.9981	SQASEASFLSLFVAGCAAR
4.0	1971.9247	2.0093	LIDYISMNSTENYHKK
3.9	1972.9239	1.0102	SYRSVGGSGGGSFGDNLVTR

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

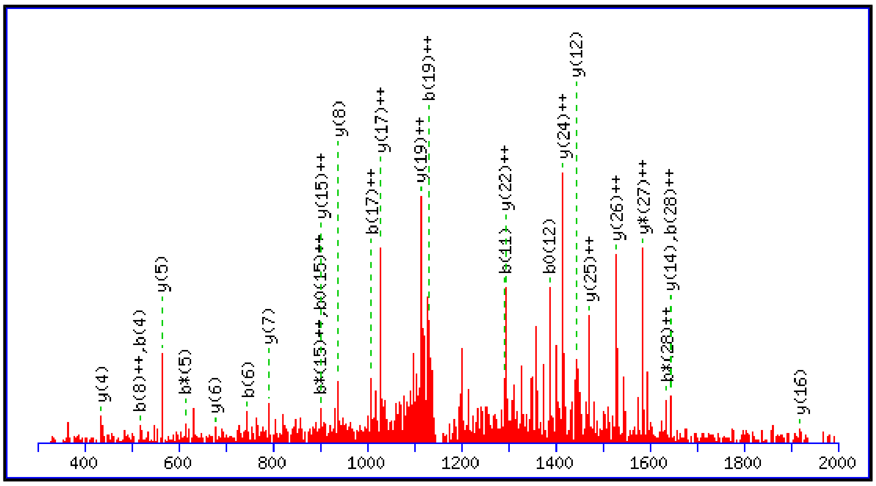
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NCQDIDECVTGIHNCSINETCFNIQGGFR**
Found in **B1AHL2** in **con_Xuniprot_HUMAN3**, B1AHL2_HUMAN Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=2 SV=1

Match to Query 27785: 3461.446692 from(1154.822840,3+) intensity(7200.7026) rtinseconds(3201) scans(8491) index(20053)
Title: 111019_Est_MI_YP_G_09Spectrum7540_scans__8491
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

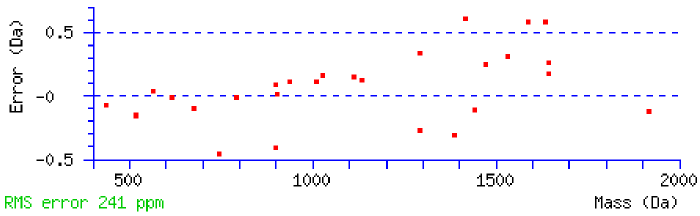
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

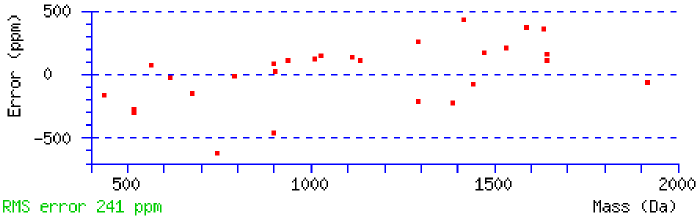


Monoisotopic mass of neutral peptide Mr(calc): 3459.4224
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
N18 : Deamidated (NQ)
Ions Score: 59 **Expect:** 4.7e-005
Matches : 28/312 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							29
2	275.0809	138.0441	258.0543	129.5308			C	3346.3868	1673.6970	3329.3602	1665.1838	3328.3762	1664.6917	28
3	403.1394	202.0734	386.1129	193.5601			Q	3186.3561	1593.6817	3169.3296	1585.1684	3168.3456	1584.6764	27
4	**518.1664**	259.5868	501.1398	251.0736	500.1558	250.5815	D	3058.2975	1529.6524	3041.2710	1521.1391	3040.2870	1520.6471	26
5	631.2504	316.1289	614.2239	307.6156	613.2399	307.1236	I	2943.2706	1472.1389	2926.2441	1463.6257	2925.2600	1463.1337	25
6	**746.2774**	373.6423	729.2508	365.1291	728.2668	364.6370	D	2830.1865	1415.5969	2813.1600	1407.0836	2812.1760	1406.5916	24
7	875.3200	438.1636	858.2934	429.6504	857.3094	429.1583	E	2715.1596	1358.0834	2698.1331	1349.5702	2697.1490	1349.0782	23
8	1035.3506	**518.1789**	1018.3241	509.6657	1017.3401	509.1737	C	2586.1170	1293.5621	2569.0905	1285.0489	2568.1064	1284.5569	22
9	1134.4190	567.7132	1117.3925	559.1999	1116.4085	558.7079	V	2426.0864	1213.5468	2409.0598	1205.0335	2408.0758	1204.5415	21
10	1235.4667	618.2370	1218.4402	609.7237	1217.4562	609.2317	T	2327.0179	1164.0126	2309.9914	1155.4993	2309.0074	1155.0073	20
11	**1292.4882**	646.7477	1275.4616	638.2345	1274.4776	637.7424	G	2225.9703	1113.4888	2208.9437	1104.9755	2207.9597	1104.4835	19
12	1405.5722	703.2898	1388.5457	694.7765	1387.5617	694.2845	I	2168.9488	1084.9780	2151.9223	1076.4648	2150.9382	1075.9728	18
13	1542.6312	771.8192	1525.6046	763.3059	1524.6206	762.8139	H	2055.8647	1028.4360	2038.8382	1019.9227	2037.8542	1019.4307	17
14	1657.6581	829.3327	1640.6315	820.8194	1639.6475	820.3274	N	***1918.8058***	959.9066	1901.7793	951.3933	1900.7953	950.9013	16
15	1817.6887	909.3480	1800.6622	900.8347	1799.6782	900.3427	C	1803.7789	902.3931	1786.7523	893.8798	1785.7683	893.3878	15
16	1904.7208	952.8640	1887.6942	944.3508	1886.7102	943.8587	S	***1643.7482***	822.3778	1626.7217	813.8645	1625.7377	813.3725	14
17	2017.8048	**1009.4061**	2000.7783	1000.8928	1999.7943	1000.4008	I	1556.7162	778.8617	1539.6897	770.3485	1538.7056	769.8565	13
18	2132.8318	1066.9195	2115.8052	1058.4063	2114.8212	1057.9142	N	***1443.6321***	722.3197	1426.6056	713.8064	1425.6216	713.3144	12
19	2261.8744	**1131.4408**	2244.8478	1122.9276	2243.8638	1122.4355	E	1328.6052	664.8062	1311.5786	656.2930	1310.5946	655.8010	11
20	2362.9221	1181.9647	2345.8955	1173.4514	2344.9115	1172.9594	T	1199.5626	600.2849	1182.5361	591.7717	1181.5520	591.2797	10
21	2522.9527	1261.9800	2505.9262	1253.4667	2504.9421	1252.9747	C	1098.5149	549.7611	1081.4884	541.2478			9
22	2670.0211	1335.5142	2652.9946	1327.0009	2652.0106	1326.5089	F	***938.4843***	469.7458	921.4577	461.2325			8

23	2784.0640	1392.5357	2767.0375	1384.0224	2766.0535	1383.5304	**N**	***791.4159***	396.2116	774.3893	387.6983			**7**
24	2897.1481	1449.0777	2880.1216	1440.5644	2879.1375	1440.0724	**I**	***677.3729***	339.1901	660.3464	330.6768			**6**
25	3025.2067	1513.1070	3008.1801	1504.5937	3007.1961	1504.1017	**Q**	***564.2889***	282.6481	547.2623	274.1348			**5**
26	3082.2281	1541.6177	3065.2016	1533.1044	3064.2176	1532.6124	**G**	***436.2303***	218.6188	419.2037	210.1055			**4**
27	3139.2496	1570.1284	3122.2231	1561.6152	3121.2390	1561.1232	**G**	379.2088	190.1081	362.1823	181.5948			**3**
28	3286.3180	**1643.6627**	3269.2915	1635.1494	3268.3075	1634.6574	**F**	322.1874	161.5973	305.1608	153.0840			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.4	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, N18 57.89%
56.0	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, N23 26.77%
53.3	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N18, N23 14.41%
39.1	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, Q25 0.54%
36.9	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N18, Q25 0.33%
25.4	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N23, Q25 0.02%
22.4	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated Q3, N18 0.01%
20.5	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N1, N18 0.01%
19.7	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated Q3, N23 0.01%
18.3	3459.4224	2.0243	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N1, N23 0.00%

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

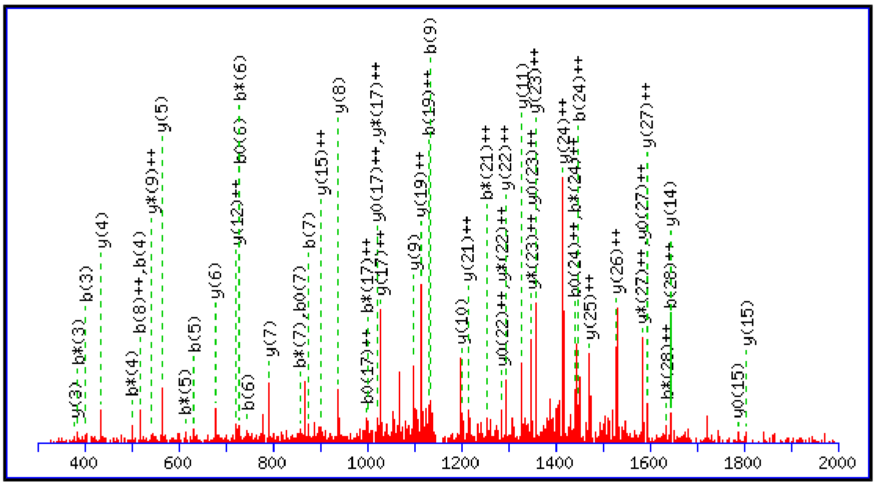
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NCQDIDECVTGIHNCSINETCFNIQGGFR**
Found in **B1AHL2** in **con_Xuniprot_HUMAN3**, B1AHL2_HUMAN Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=2 SV=1

Match to Query 27784: 3461.446422 from(1154.822750,3+) intensity(0.0000) rtinseconds(1783) scans(4645) index(19666)
Title: 111019_Est_MI_YP_G_09Spectrum4101_scans__4645
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

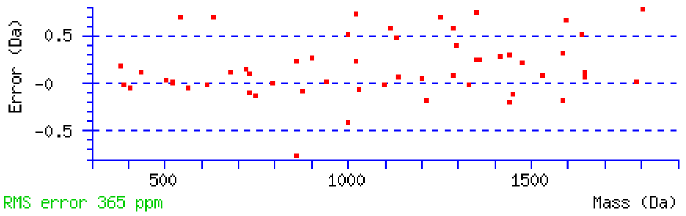
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

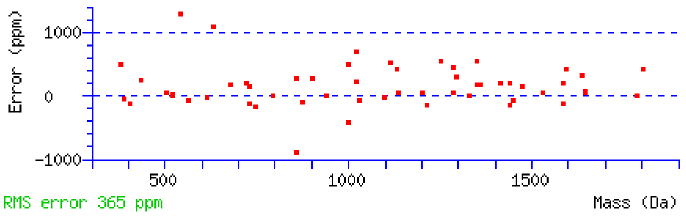


```
Monoisotopic mass of neutral peptide Mr(calc): 3459.4224
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N18     : Deamidated (NQ)
N23     : Deamidated (NQ)
Ions Score: 57  Expect: 8.5e-005
Matches : 55/312 fragment ions using 119 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							29
2	275.0809	138.0441	258.0543	129.5308			C	3346.3868	1673.6970	3329.3602	1665.1838	3328.3762	1664.6917	28
3	**403.1394**	202.0734	386.1129	193.5601			Q	3186.3561	1593.6817	3169.3296	1585.1684	3168.3456	1584.6764	27
4	**518.1664**	259.5868	501.1398	251.0736	500.1558	250.5815	D	3058.2975	1529.6524	3041.2710	1521.1391	3040.2870	1520.6471	26
5	**631.2504**	316.1289	614.2239	307.6156	613.2399	307.1236	I	2943.2706	1472.1389	2926.2441	1463.6257	2925.2600	1463.1337	25
6	**746.2774**	373.6423	729.2508	365.1291	728.2668	364.6370	D	2830.1865	1415.5969	2813.1600	1407.0836	2812.1760	1406.5916	24
7	**875.3200**	438.1636	858.2934	429.6504	857.3094	429.1583	E	2715.1596	1358.0834	2698.1331	1349.5702	2697.1490	1349.0782	23
8	1035.3506	518.1789	1018.3241	509.6657	1017.3401	509.1737	C	2586.1170	1293.5621	2569.0905	1285.0489	2568.1064	1284.5569	22
9	**1134.4190**	567.7132	1117.3925	559.1999	1116.4085	558.7079	V	2426.0864	1213.5468	2409.0598	1205.0335	2408.0758	1204.5415	21
10	1235.4667	618.2370	1218.4402	609.7237	1217.4562	609.2317	T	2327.0179	1164.0126	2309.9914	1155.4993	2309.0074	1155.0073	20
11	1292.4882	646.7477	1275.4616	638.2345	1274.4776	637.7424	G	2225.9703	1113.4888	2208.9437	1104.9755	2207.9597	1104.4835	19
12	1405.5722	703.2898	1388.5457	694.7765	1387.5617	694.2845	I	2168.9488	1084.9780	2151.9223	1076.4648	2150.9382	1075.9728	18
13	1542.6312	771.8192	1525.6046	763.3059	1524.6206	762.8139	H	2055.8647	1028.4360	2038.8382	1019.9227	2037.8542	1019.4307	17
14	1656.6741	828.8407	1639.6475	820.3274	1638.6635	819.8354	N	1918.8058	959.9066	1901.7793	951.3933	1900.7953	950.9013	16
15	1816.7047	908.8560	1799.6782	900.3427	1798.6942	899.8507	C	***1804.7629***	902.8851	1787.7363	894.3718	1786.7523	893.8798	15
16	1903.7368	952.3720	1886.7102	943.8587	1885.7262	943.3667	S	***1644.7322***	822.8698	1627.7057	814.3565	1626.7217	813.8645	14
17	2016.8208	1008.9140	1999.7943	1000.4008	1998.8103	999.9088	I	1557.7002	779.3537	1540.6737	770.8405	1539.6897	770.3485	13
18	2131.8478	1066.4275	2114.8212	1057.9142	2113.8372	1057.4222	N	1444.6162	722.8117	1427.5896	714.2984	1426.6056	713.8064	12
19	2260.8904	1130.9488	2243.8638	1122.4355	2242.8798	1121.9435	E	***1329.5892***	665.2982	1312.5627	656.7850	1311.5786	656.2930	11
20	2361.9380	1181.4727	2344.9115	1172.9594	2343.9275	1172.4674	T	***1200.5466***	600.7769	1183.5201	592.2637	1182.5361	591.7717	10
21	2521.9687	1261.4880	2504.9421	1252.9747	2503.9581	1252.4827	C	***1099.4989***	550.2531	1082.4724	541.7398			9
22	2669.0371	1335.0222	2652.0106	1326.5089	2651.0265	1326.0169	F	***939.4683***	470.2378	922.4417	461.7245			8

23	2784.0640	1392.5357	2767.0375	1384.0224	2766.0535	1383.5304	**N**	***792.3999***	396.7036	775.3733	388.1903			**7**
24	2897.1481	1449.0777	2880.1216	1440.5644	2879.1375	1440.0724	**I**	***677.3729***	339.1901	660.3464	330.6768			**6**
25	3025.2067	1513.1070	3008.1801	1504.5937	3007.1961	1504.1017	**Q**	***564.2889***	282.6481	547.2623	274.1348			**5**
26	3082.2281	1541.6177	3065.2016	1533.1044	3064.2176	1532.6124	**G**	***436.2303***	218.6188	419.2037	210.1055			**4**
27	3139.2496	1570.1284	3122.2231	1561.6152	3121.2390	1561.1232	**G**	***379.2088***	190.1081	362.1823	181.5948			**3**
28	3286.3180	1643.6627	3269.2915	1635.1494	3268.3075	1634.6574	**F**	322.1874	161.5973	305.1608	153.0840			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
56.7	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N18, N23 29.71%
54.8	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, N18 19.14%
54.6	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, N23 18.32%
50.6	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N18, Q25 7.24%
49.2	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated Q3, N18 5.33%
48.6	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N14, Q25 4.56%
48.5	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N1, N18 4.44%
47.4	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated Q3, N23 3.50%
46.5	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated N1, N23 2.83%
41.9	3459.4224	2.0240	NCQDIDECVTGIHNCSINETCFNIQGGFR	Deamidated Q3, N14 0.99%

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

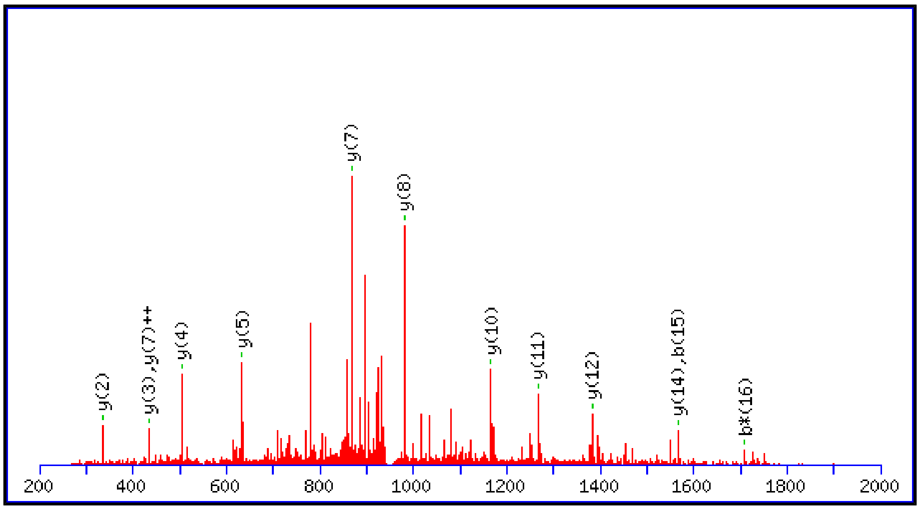
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGYNANTSVLSFQAVCR**
Found in **B1ALQ8** in **con_Xuniprot_HUMAN3**, B1ALQ8_HUMAN Complement factor H-related protein 4 OS=Homo sapiens GN=CFHR4 PE=2 SV=1

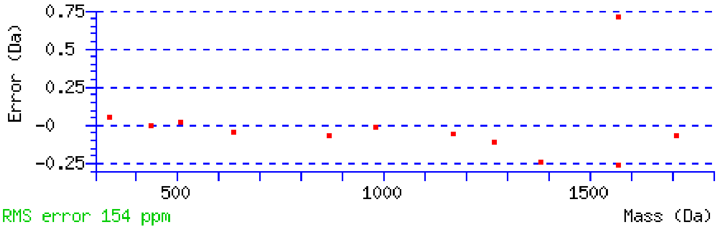
Match to Query 11308: 1899.921948 from(950.968250,2+) intensity(22541.6016) rtinseconds(1702) scans(4450) index(4435)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3777_scans__4450
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

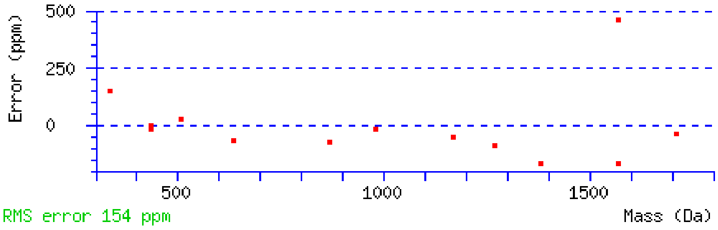
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1899.9149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 71 **Expect:** 1.8e-005
Matches : 13/162 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	114.0913	57.5493					L							17
2	171.1128	86.0600					G	1787.8381	894.4227	1770.8116	885.9094	1769.8275	885.4174	16
3	334.1761	167.5917					Y	1730.8166	865.9120	1713.7901	857.3987	1712.8061	856.9067	15
4	448.2191	224.6132	431.1925	216.0999			N	***1567.7533***	784.3803	1550.7268	775.8670	1549.7428	775.3750	14
5	519.2562	260.1317	502.2296	251.6185			A	1453.7104	727.3588	1436.6838	718.8456	1435.6998	718.3536	13
6	634.2831	317.6452	617.2566	309.1319			N	***1382.6733***	691.8403	1365.6467	683.3270	1364.6627	682.8350	12
7	735.3308	368.1690	718.3042	359.6558	717.3202	359.1638	T	***1267.6463***	634.3268	1250.6198	625.8135	1249.6358	625.3215	11
8	822.3628	411.6851	805.3363	403.1718	804.3523	402.6798	S	***1166.5987***	583.8030	1149.5721	575.2897	1148.5881	574.7977	10
9	921.4312	461.2193	904.4047	452.7060	903.4207	452.2140	V	1079.5666	540.2870	1062.5401	531.7737	1061.5561	531.2817	9
10	1034.5153	517.7613	1017.4888	509.2480	1016.5047	508.7560	L	***980.4982***	490.7527	963.4717	482.2395	962.4876	481.7475	8
11	1121.5473	561.2773	1104.5208	552.7640	1103.5368	552.2720	S	***867.4141***	434.2107	850.3876	425.6974	849.4036	425.2054	7
12	1268.6157	634.8115	1251.5892	626.2982	1250.6052	625.8062	F	780.3821	390.6947	763.3556	382.1814			6
13	1396.6743	698.8408	1379.6478	690.3275	1378.6638	689.8355	Q	***633.3137***	317.1605	616.2872	308.6472			5
14	1467.7114	734.3594	1450.6849	725.8461	1449.7009	725.3541	A	***505.2551***	253.1312	488.2286	244.6179			4
15	1566.7799	783.8936	1549.7533	775.3803	1548.7693	774.8883	V	***434.2180***	217.6126	417.1915	209.0994			3
16	1726.8105	863.9089	1709.7840	855.3956	1708.7999	854.9036	C	***335.1496***	168.0784	318.1231	159.5652			2
17							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.2	1899.9149	0.0071	LGYNANTSVLSFQAVCR	Deamidated N6 49.91%
71.2	1899.9149	0.0071	LGYNANTSVLSFQAVCR	Deamidated N4 49.91%
46.9	1899.9149	0.0071	LGYNANTSVLSFQAVCR	Deamidated Q13 0.18%
4.7	1898.9196	1.0023	DKGFAPNHLNVEKMALD	
4.7	1898.9196	1.0023	DKGFAPNHLNVEKMALN	
3.3	1897.9125	2.0095	TSLKNALKNMMGLNSDK	
2.9	1897.9125	2.0095	TSLKNALKNMMGLNSDK	
2.0	1897.9244	1.9976	VMTNKKTVNPYTNGWK	
0.9	1897.9058	2.0162	DQGTPEVQPTPAKDTWK	

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

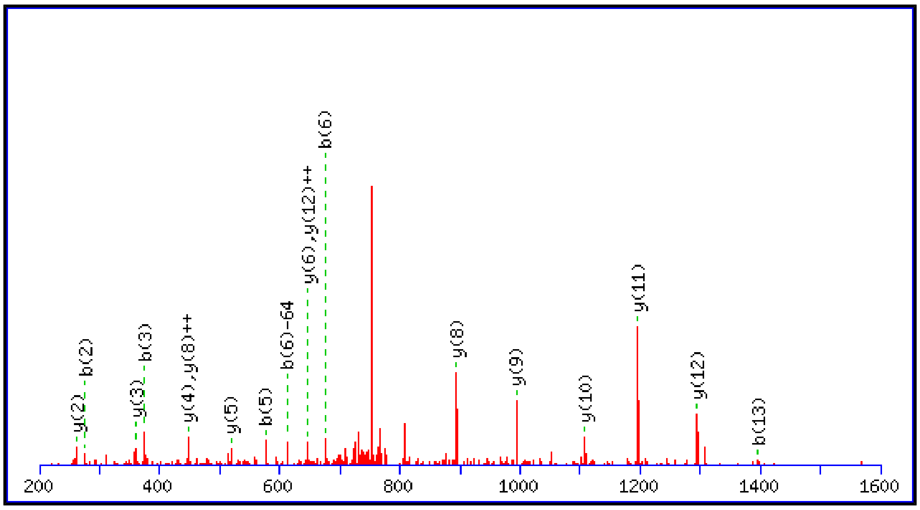
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKVSNVSCQASVSR**
Found in **B3KUE5** in **con_Xuniprot_HUMAN3**, B3KUE5_HUMAN Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=2 SV=1

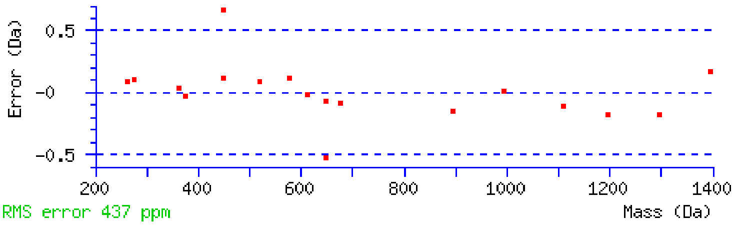
Match to Query 7403: 1568.732908 from(785.373730,2+) intensity(7423.2842) rtinseconds(250) scans(386) index(25154)
Title: 111019_Est_MI_YS_G_07Spectrum289_scans__386
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

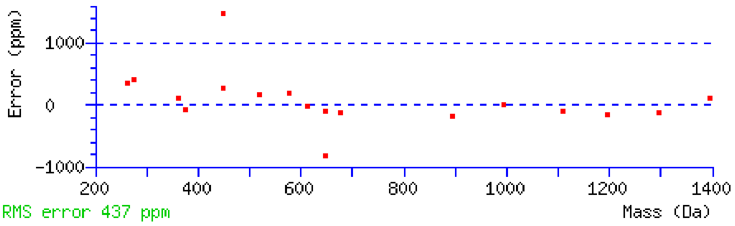
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1568.7287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N5 : Deamidated (NQ)
Ions Score: 82 **Expect:** 1.1e-006
Matches : 18/216 fragment ions using 26 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0427	74.5250					M							14
2	**276.1376**	138.5725	259.1111	130.0592			K	1422.7006	711.8539	1405.6740	703.3406	1404.6900	702.8486	13
3	**375.2061**	188.1067	358.1795	179.5934			V	***1294.6056***	647.8064	1277.5790	639.2932	1276.5950	638.8012	12
4	462.2381	231.6227	445.2115	223.1094	444.2275	222.6174	S	***1195.5372***	598.2722	1178.5106	589.7590	1177.5266	589.2669	11
5	**577.2650**	289.1362	560.2385	280.6229	559.2545	280.1309	N	***1108.5051***	554.7562	1091.4786	546.2429	1090.4946	545.7509	10
6	**676.3334**	338.6704	659.3069	330.1571	658.3229	329.6651	V	***993.4782***	497.2427	976.4517	488.7295	975.4676	488.2375	9
7	763.3655	382.1864	746.3389	373.6731	745.3549	373.1811	S	***894.4098***	447.7085	877.3832	439.1953	876.3992	438.7033	8
8	923.3961	462.2017	906.3696	453.6884	905.3855	453.1964	C	807.3778	404.1925	790.3512	395.6792	789.3672	395.1872	7
9	1051.4547	526.2310	1034.4281	517.7177	1033.4441	517.2257	Q	***647.3471***	324.1772	630.3206	315.6639	629.3365	315.1719	6
10	1122.4918	561.7495	1105.4653	553.2363	1104.4812	552.7443	A	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	5
11	1209.5238	605.2656	1192.4973	596.7523	1191.5133	596.2603	S	***448.2514***	224.6293	431.2249	216.1161	430.2409	215.6241	4
12	1308.5922	654.7998	1291.5657	646.2865	1290.5817	645.7945	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
13	1395.6243	698.3158	1378.5977	689.8025	1377.6137	689.3105	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.9	1568.7287	0.0042	MKVSNVSCQASVSR	Deamidated N5 99.44%
59.5	1568.7287	0.0042	MKVSNVSCQASVSR	Deamidated Q9 0.56%
15.5	1568.7392	-0.0063	LQDKMNFDVSNLK	
15.5	1568.7392	-0.0063	LQDKMNFDVSNLK	
12.3	1568.7293	0.0036	HMQFDSLRYLNK	
11.2	1566.7274	2.0055	NEESDLERGYTVR	
10.3	1568.7327	0.0002	NCVYKNIDCLLR	
9.3	1568.7327	0.0002	KMVDMLQDSFPAR	
9.3	1568.7352	-0.0023	MKLESASTSSLEDR	
7.1	1568.7327	0.0002	KFSNCNKLMPGEK	

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

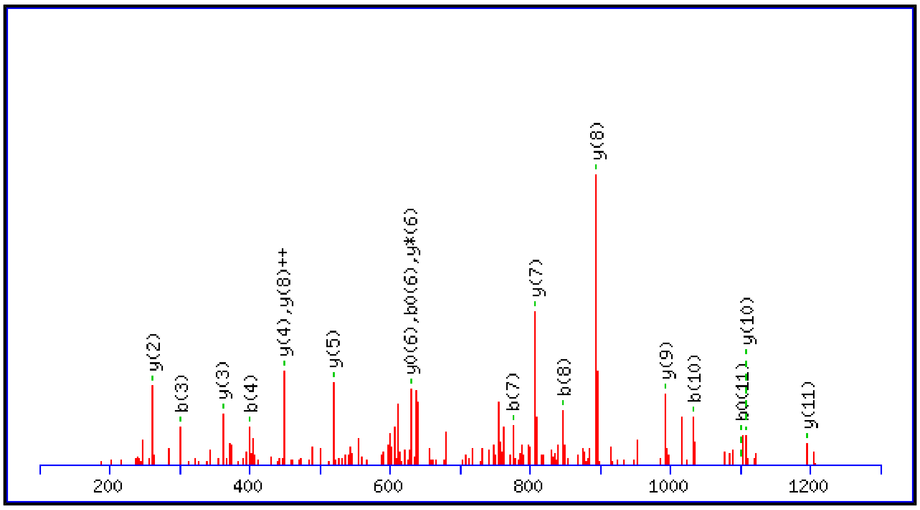
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSNVSCQASVSR**
Found in **B3KUE5** in **con_Xuniprot_HUMAN3**, B3KUE5_HUMAN Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=2 SV=1

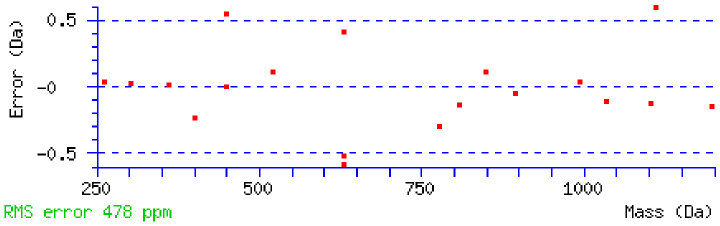
Match to Query 1940: 1293.600248 from(647.807400,2+) intensity(1695.7581) rtinseconds(205) scans(294) index(1818)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum214_scans__294
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

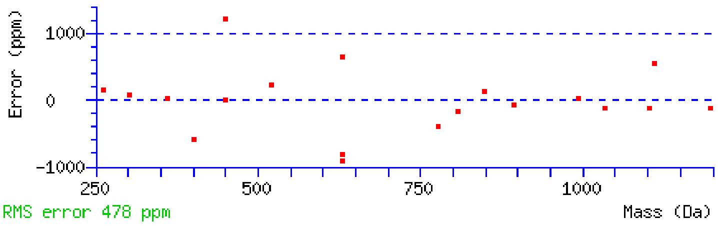
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1293.5983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 80 **Expect:** 1.7e-006
Matches : 19/124 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	100.0757	50.5415					V							12
2	187.1077	94.0575			169.0972	85.0522	S	***1195.5372***	598.2722	1178.5106	589.7590	1177.5266	589.2669	11
3	**302.1347**	151.5710	285.1081	143.0577	284.1241	142.5657	N	***1108.5051***	554.7562	1091.4786	546.2429	1090.4946	545.7509	10
4	**401.2031**	201.1052	384.1765	192.5919	383.1925	192.0999	V	***993.4782***	497.2427	976.4517	488.7295	975.4676	488.2375	9
5	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	S	***894.4098***	447.7085	877.3832	439.1953	876.3992	438.7033	8
6	648.2658	324.6365	631.2392	316.1232	630.2552	315.6312	C	***807.3778***	404.1925	790.3512	395.6792	789.3672	395.1872	7
7	**776.3243**	388.6658	759.2978	380.1525	758.3138	379.6605	Q	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
8	**847.3614**	424.1844	830.3349	415.6711	829.3509	415.1791	A	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	5
9	934.3935	467.7004	917.3669	459.1871	916.3829	458.6951	S	***448.2514***	224.6293	431.2249	216.1161	430.2409	215.6241	4
10	**1033.4619**	517.2346	1016.4353	508.7213	1015.4513	508.2293	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
11	1120.4939	560.7506	1103.4674	552.2373	1102.4833	551.7453	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.8	1293.5983	0.0019	VSNVSCQASVSR	Deamidated N3 99.84%
51.9	1293.5983	0.0019	VSNVSCQASVSR	Deamidated Q7 0.16%
12.2	1293.5983	0.0020	SSSVGCLAEASAR	
9.0	1293.5983	0.0020	RMGESDDSILR	
5.7	1293.5949	0.0053	TSDPSLHAHSDK	
5.7	1293.5983	0.0020	VMDRSLGEESR	
5.3	1291.5979	2.0023	SGGPVTSMGSAWR	
5.2	1292.5918	1.0085	MIKEEQEQNK	
4.2	1293.6048	-0.0045	LTSNASKSQNNK	
4.2	1293.6048	-0.0045	LTSNASKSQNNK	

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

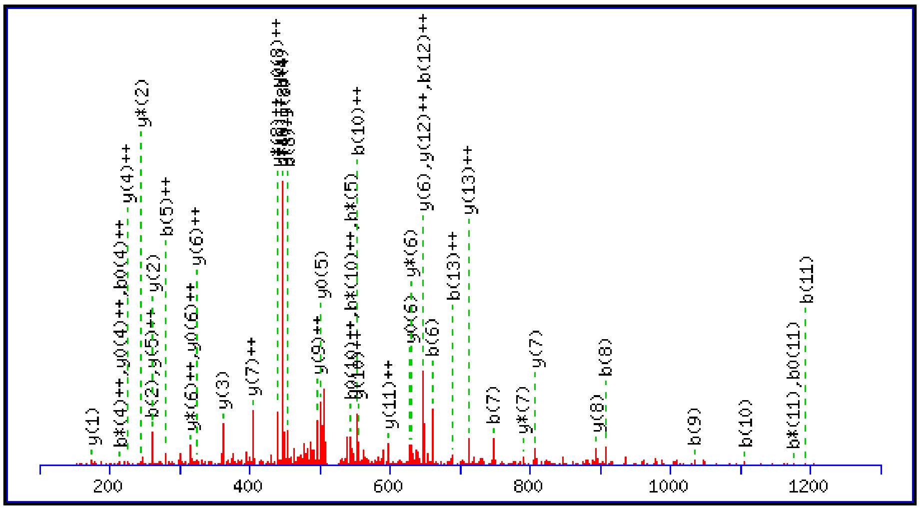
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MKVSNVSCQASVSR**
Found in **B3KUE5** in **con_Xuniprot_HUMAN3**, B3KUE5_HUMAN Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=2 SV=1

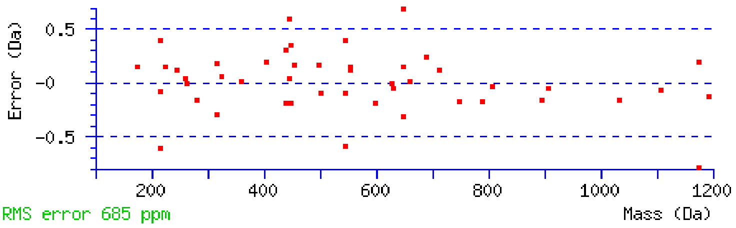
Match to Query 7016: 1552.736892 from(518.586240,3+) intensity(5994.3398) rtinseconds(381) scans(701) index(2461)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum570_scans__701
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

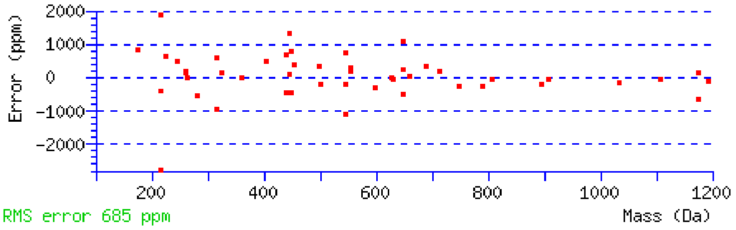
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1552.7337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.001
Matches : 48/146 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	132.0478	66.5275					M							14
2	**260.1427**	130.5750	243.1162	122.0617			K	1422.7006	711.8539	1405.6740	703.3406	1404.6900	702.8486	13
3	359.2111	180.1092	342.1846	171.5959			V	1294.6056	647.8064	1277.5790	639.2932	1276.5950	638.8012	12
4	**446.2432**	223.6252	429.2166	215.1119	428.2326	214.6199	S	1195.5372	598.2722	1178.5106	589.7590	1177.5266	589.2669	11
5	561.2701	**281.1387**	544.2436	272.6254	543.2595	272.1334	N	1108.5051	554.7562	1091.4786	546.2429	1090.4946	545.7509	10
6	**660.3385**	330.6729	643.3120	322.1596	642.3280	321.6676	V	993.4782	497.2427	976.4517	488.7295	975.4676	488.2375	9
7	**747.3706**	374.1889	730.3440	365.6756	729.3600	365.1836	S	**894.4098**	447.7085	877.3832	439.1953	876.3992	438.7033	8
8	**907.4012**	**454.2042**	890.3747	445.6910	889.3906	445.1990	C	**807.3778**	404.1925	790.3512	395.6792	789.3672	395.1872	7
9	**1035.4598**	518.2335	1018.4332	509.7203	1017.4492	509.2282	Q	**647.3471**	324.1772	630.3206	315.6639	629.3365	315.1719	6
10	**1106.4969**	**553.7521**	1089.4703	545.2388	1088.4863	544.7468	A	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
11	**1193.5289**	597.2681	1176.5024	588.7548	1175.5184	588.2628	S	**448.2514**	224.6293	431.2249	216.1161	430.2409	215.6241	4
12	1292.5973	**646.8023**	1275.5708	638.2890	1274.5868	637.7970	V	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
13	1379.6294	**690.3183**	1362.6028	681.8050	1361.6188	681.3130	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.6	1552.7337	0.0031	MKVSNVSCQASVSR	Deamidated N5 57.88%
51.2	1552.7337	0.0031	MKVSNVSCQASVSR	Deamidated Q9 42.12%
11.2	1550.7246	2.0123	MDSPSATVVSAVQSR	
9.2	1552.7369	0.0000	NESYLLQKEADSR	
9.0	1552.7344	0.0025	WFNTVNMALTQAR	
8.2	1551.7351	1.0018	EMELRFQEGKQR	
8.2	1552.7403	-0.0034	MKLESASTSSLEDR	
7.2	1550.7226	2.0143	KWASHHQINDASR	
6.9	1552.7304	0.0065	LVRYGAVECDESR	
6.9	1551.7311	1.0058	MQNVSSARQSSVDK	

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

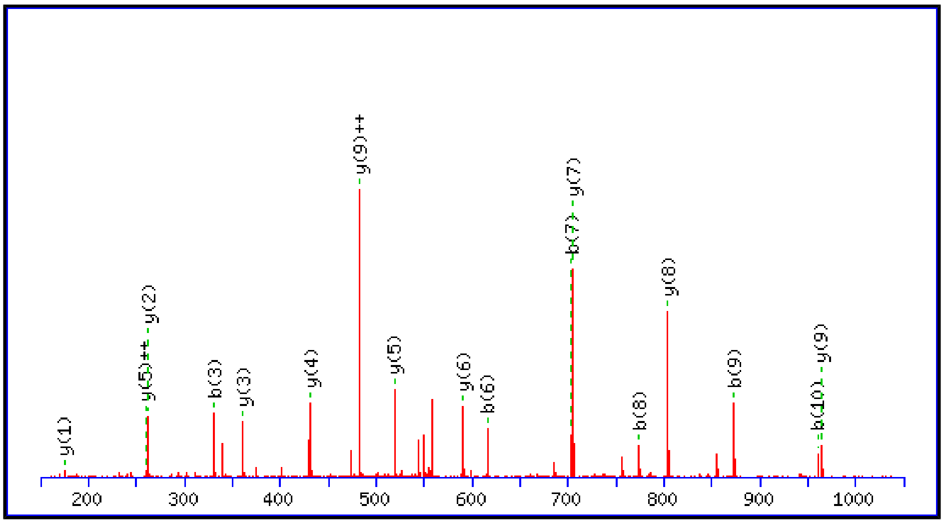
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLCVNASAVSR**
Found in **B3KWK7** in **con_Xuniprot_HUMAN3**, B3KWK7_HUMAN Insulin-like growth factor binding protein 3, isoform CRA_b OS=Homo sapiens GN=IGFBP3 PE=2 SV=1

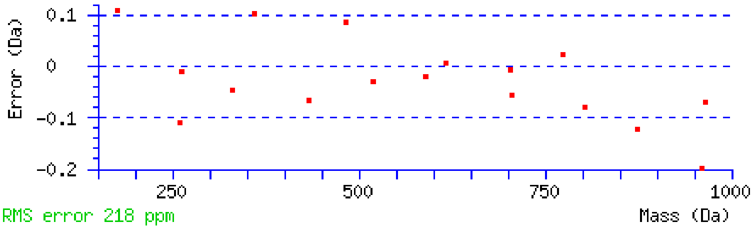
Match to Query 1448: 1133.551668 from(567.783110,2+) intensity(64951.5000) rtinseconds(674) scans(1386) index(12334)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum1184_scans__1386
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

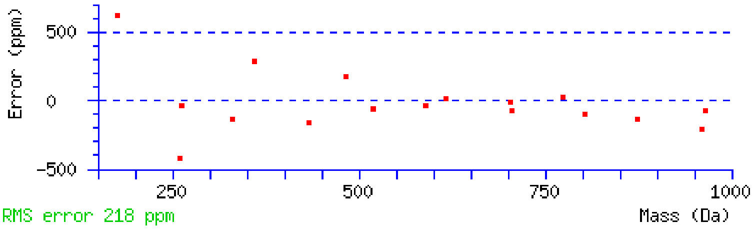
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1050 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1133.5499
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 99 **Expect:** 2.1e-008
Matches : 17/98 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							11
2	171.1128	86.0600					L	1077.5357	539.2715	1060.5092	530.7582	1059.5252	530.2662	10
3	**331.1435**	166.0754					C	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	9
4	430.2119	215.6096					V	***804.4210***	402.7141	787.3945	394.2009	786.4104	393.7089	8
5	545.2388	273.1230	528.2123	264.6098			N	***705.3526***	353.1799	688.3260	344.6667	687.3420	344.1747	7
6	**616.2759**	308.6416	599.2494	300.1283			A	***590.3257***	295.6665	573.2991	287.1532	572.3151	286.6612	6
7	**703.3080**	352.1576	686.2814	343.6443	685.2974	343.1523	S	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	5
8	**774.3451**	387.6762	757.3185	379.1629	756.3345	378.6709	A	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	4
9	**873.4135**	437.2104	856.3869	428.6971	855.4029	428.2051	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	**960.4455**	480.7264	943.4190	472.2131	942.4349	471.7211	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLCVNASAVSR
(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	1133.5499	0.0018	GLCVNASAVSR
24.0	1133.5499	0.0018	CATVSAAVAER
14.4	1133.5499	0.0018	DVCGSLLQSR
13.7	1133.5564	-0.0047	LESVDLQSSR
13.1	1132.5481	1.0036	NKIGMASPCR
12.7	1133.5499	0.0018	SSRMGPENKK
11.5	1133.5564	-0.0047	IQSVNNTISR
11.5	1133.5499	0.0018	QMAQKVADSR
10.9	1133.5564	-0.0048	TLGQSQSTSPK
10.9	1133.5564	-0.0048	TLGQSQSTSPK

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

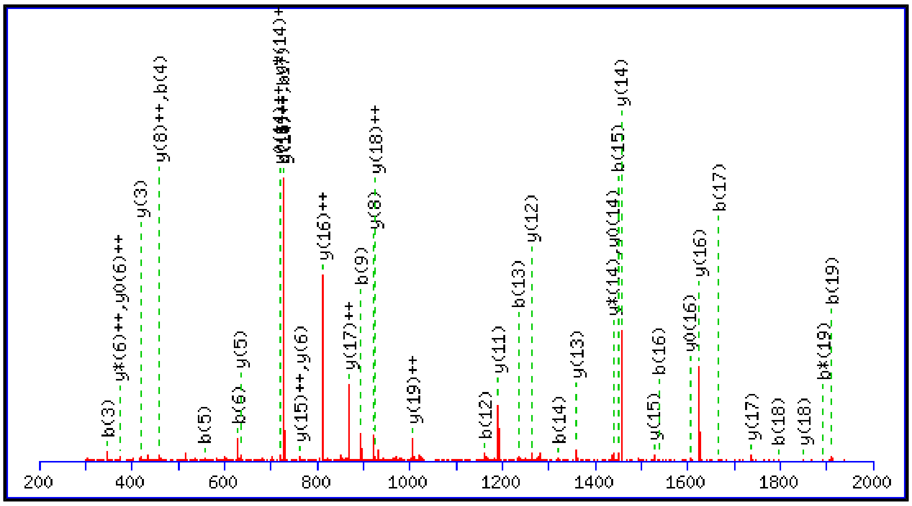
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AYLLPAPPAPGNASESEEDR**
Found in **B3KWK7** in **con_Xuniprot_HUMAN3**, B3KWK7_HUMAN Insulin-like growth factor binding protein 3, isoform CRA_b OS=Homo sapiens GN=IGFBP3 PE=2 SV=1

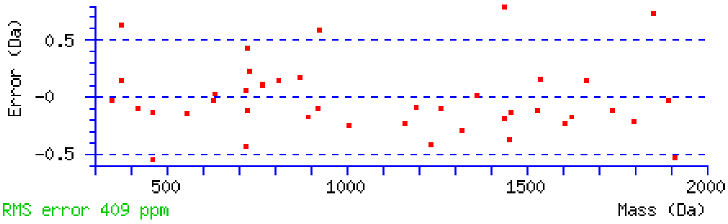
Match to Query 13159: 2083.978468 from(1042.996510,2+) intensity(96197.7266) rtinseconds(1154) scans(2793) index(24448)
Title: 111019_Est_MI_YS_G_06Spectrum2415_scans__2793
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

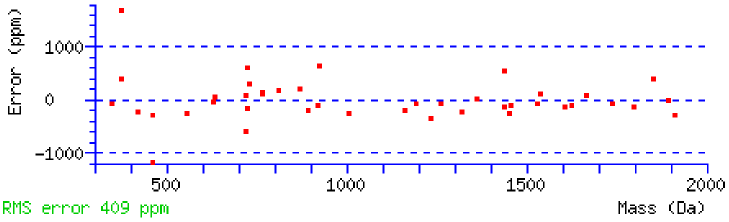
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9698
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 76 **Expect:** 5.1e-006
Matches : 42/178 fragment ions using 83 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							20
2	235.1077	118.0575					Y	2013.9400	1007.4736	1996.9134	998.9604	1995.9294	998.4684	19
3	***348.1918***	174.5995					L	**1850.8767**	925.9420	1833.8501	917.4287	1832.8661	916.9367	18
4	***461.2758***	231.1416					L	**1737.7926**	869.3999	1720.7661	860.8867	1719.7820	860.3947	17
5	***558.3286***	279.6679					P	**1624.7085**	812.8579	1607.6820	804.3446	1606.6980	803.8526	16
6	***629.3657***	315.1865					A	**1527.6558**	764.3315	1510.6292	755.8182	1509.6452	755.3262	15
7	***726.4185***	363.7129					P	**1456.6187**	728.8130	1439.5921	720.2997	1438.6081	719.8077	14
8	823.4713	412.2393					P	**1359.5659**	680.2866	1342.5393	671.7733	1341.5553	671.2813	13
9	***894.5084***	447.7578					A	**1262.5131**	631.7602	1245.4866	623.2469	1244.5026	622.7549	12
10	991.5611	496.2842					P	**1191.4760**	596.2416	1174.4495	587.7284	1173.4655	587.2364	11
11	1048.5826	524.7949					G	1094.4233	547.7153	1077.3967	539.2020	1076.4127	538.7100	10
12	***1163.6095***	582.3084	1146.5830	573.7951			N	1037.4018	519.2045	1020.3752	510.6913	1019.3912	510.1992	9
13	***1234.6467***	617.8270	1217.6201	609.3137			A	**922.3748**	461.6911	905.3483	453.1778	904.3643	452.6858	8
14	***1321.6787***	661.3430	1304.6521	652.8297	1303.6681	652.3377	S	851.3377	426.1725	834.3112	417.6592	833.3272	417.1672	7
15	***1450.7213***	725.8643	1433.6947	717.3510	1432.7107	716.8590	E	**764.3057**	382.6565	747.2792	374.1432	746.2951	373.6512	6
16	***1537.7533***	769.3803	1520.7268	760.8670	1519.7427	760.3750	S	**635.2631**	318.1352	618.2366	309.6219	617.2525	309.1299	5
17	***1666.7959***	833.9016	1649.7693	825.3883	1648.7853	824.8963	E	548.2311	274.6192	531.2045	266.1059	530.2205	265.6139	4
18	***1795.8385***	898.4229	1778.8119	889.9096	1777.8279	889.4176	E	**419.1885**	210.0979	402.1619	201.5846	401.1779	201.0926	3
19	***1910.8654***	955.9364	1893.8389	947.4231	1892.8549	946.9311	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.0	2083.9698	0.0087	AYLLPAPPAPGNASESEEDR
12.7	2083.9857	-0.0073	AIYNVSQCPGHQATPRQR
11.9	2083.9857	-0.0073	AIYNVSQCPGHQATPRQR
9.7	2083.9857	-0.0073	AIYNVSQCPGHQATPRQR
8.3	2081.9761	2.0023	ANCIMQEDESYLLQVLR
4.8	2082.9779	1.0005	SGESSCPLEQSVPPEPALAK
3.8	2082.9793	0.9992	TDMNEYHQVHVVINLDR
3.6	2083.9853	-0.0068	EIRINMSCAVFITMNPR
3.1	2082.9680	1.0105	QERLYEANERMWLEAK
3.0	2081.9687	2.0097	TNELFQTMQRAQELAQR

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

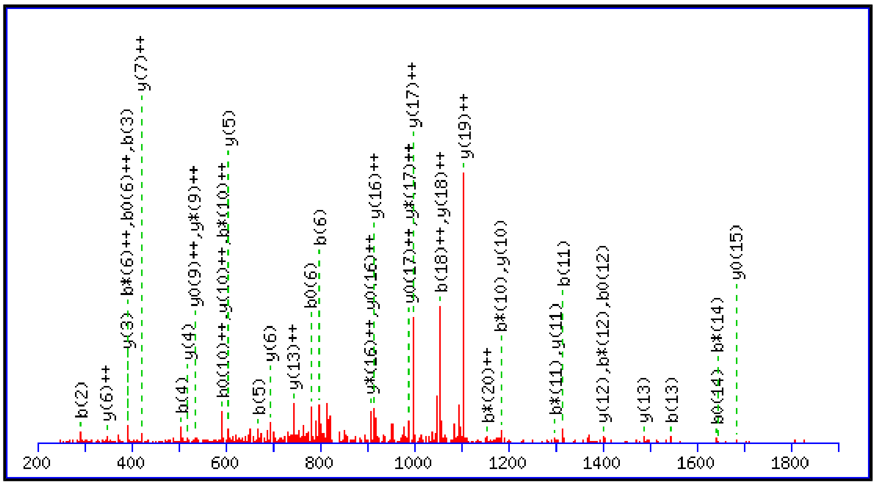
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YKVDYESQSTDTQNFSSESKR**
Found in **B3KWK7** in **con_Xuniprot_HUMAN3**, B3KWK7_HUMAN Insulin-like growth factor binding protein 3, isoform CRA_b OS=Homo sapiens GN=IGFBP3 PE=2 SV=1

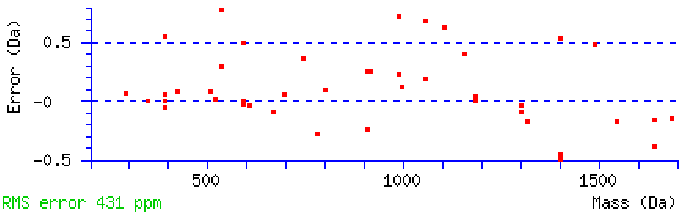
Match to Query 21524: 2499.112812 from(834.044880,3+) intensity(8821.7275) rtinseconds(579) scans(1178) index(1874)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum967_scans__1178
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

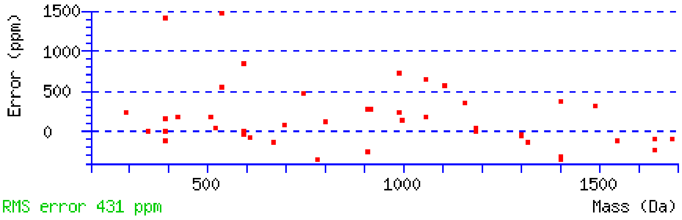
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2499.1037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 62 **Expect:** 6.9e-005
Matches : 43/228 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	164.0706	82.5389					Y							21
2	***292.1656***	146.5864	275.1390	138.0731			K	2337.0477	1169.0275	2320.0212	1160.5142	2319.0371	1160.0222	20
3	***391.2340***	196.1206	374.2074	187.6074			V	2208.9527	1104.9800	2191.9262	1096.4667	2190.9422	1095.9747	19
4	***506.2609***	253.6341	489.2344	245.1208	488.2504	244.6288	D	2109.8843	1055.4458	2092.8578	1046.9325	2091.8738	1046.4405	18
5	***669.3243***	335.1658	652.2977	326.6525	651.3137	326.1605	Y	1994.8574	997.9323	1977.8308	989.4191	1976.8468	988.9270	17
6	***798.3668***	399.6871	781.3403	391.1738	780.3563	390.6818	E	1831.7941	916.4007	1814.7675	907.8874	1813.7835	907.3954	16
7	885.3989	443.2031	868.3723	434.6898	867.3883	434.1978	S	1702.7515	851.8794	1685.7249	843.3661	1684.7409	842.8741	15
8	1013.4575	507.2324	996.4309	498.7191	995.4469	498.2271	Q	1615.7194	808.3634	1598.6929	799.8501	1597.7089	799.3581	14
9	1100.4895	550.7484	1083.4629	542.2351	1082.4789	541.7431	S	***1487.6609***	744.3341	1470.6343	735.8208	1469.6503	735.3288	13
10	1201.5372	601.2722	1184.5106	592.7589	1183.5266	592.2669	T	***1400.6288***	700.8181	1383.6023	692.3048	1382.6183	691.8128	12
11	***1316.5641***	658.7857	1299.5376	650.2724	1298.5535	649.7804	D	***1299.5811***	650.2942	1282.5546	641.7809	1281.5706	641.2889	11
12	1417.6118	709.3095	1400.5852	700.7963	1399.6012	700.3042	T	***1184.5542***	592.7807	1167.5277	584.2675	1166.5436	583.7755	10
13	***1545.6704***	773.3388	1528.6438	764.8255	1527.6598	764.3335	Q	1083.5065	542.2569	1066.4800	533.7436	1065.4960	533.2516	9
14	1660.6973	830.8523	1643.6708	822.3390	1642.6867	821.8470	N	955.4479	478.2276	938.4214	469.7143	937.4374	469.2223	8
15	1807.7657	904.3865	1790.7392	895.8732	1789.7552	895.3812	F	840.4210	420.7141	823.3945	412.2009	822.4104	411.7089	7
16	1894.7977	947.9025	1877.7712	939.3892	1876.7872	938.8972	S	***693.3526***	347.1799	676.3260	338.6667	675.3420	338.1747	6
17	1981.8298	991.4185	1964.8032	982.9053	1963.8192	982.4132	S	***606.3206***	303.6639	589.2940	295.1506	588.3100	294.6586	5
18	2110.8724	1055.9398	2093.8458	1047.4265	2092.8618	1046.9345	E	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	4
19	2197.9044	1099.4558	2180.8778	1090.9426	2179.8938	1090.4506	S	***390.2459***	195.6266	373.2194	187.1133	372.2354	186.6213	3
20	2325.9994	1163.5033	2308.9728	1154.9900	2307.9888	1154.4980	K	303.2139	152.1106	286.1874	143.5973			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.5	2499.1037	0.0091	YKVDYESQSTDTQNFSSESKR	Deamidated N14 66.84%
59.3	2499.1037	0.0091	YKVDYESQSTDTQNFSSESKR	Deamidated Q13 32.14%
44.3	2499.1037	0.0091	YKVDYESQSTDTQNFSSESKR	Deamidated Q8 1.02%
40.2	2498.1197	0.9931	YKVDYESQSTDTQNFSSESKR	
10.4	2497.1026	2.0102	EGCNLHREETSSSQYSIKNEK	
7.6	2497.1026	2.0102	EGCNLHREETSSSQYSIKNEK	
7.5	2499.1086	0.0042	FPTQPFASHNMGGEEIVMYESK	
7.1	2499.1078	0.0050	ESSTFTKSSGIYLWTYDDEDR	
6.8	2499.1145	-0.0016	EYDEMLQENEQNVALVKCIR	
6.8	2499.1145	-0.0016	EYDEMLQENEQNVALVKCIR	

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

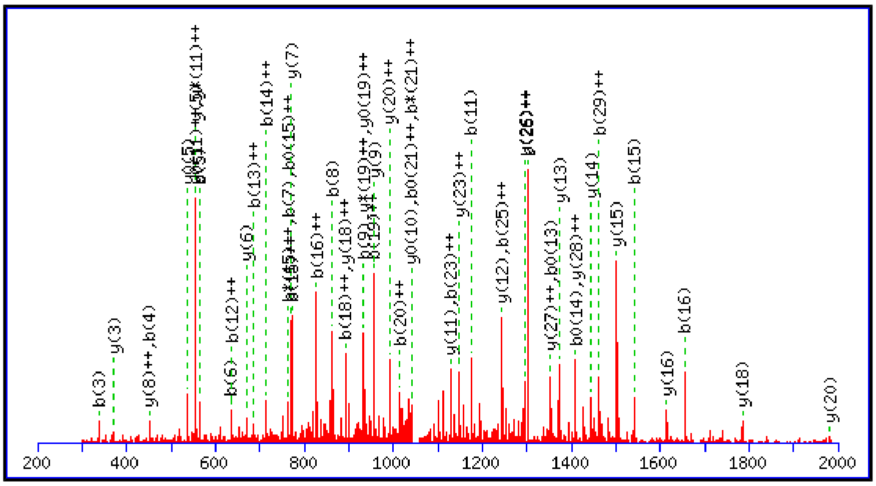
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHLIIAQVAKNPVGLIGAENATGETDPSHSK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 27336: 3154.639302 from(1052.553710,3+) intensity(61745.7422) rtinseconds(1474) scans(3631) index(9451)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum3098_scans__3631
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

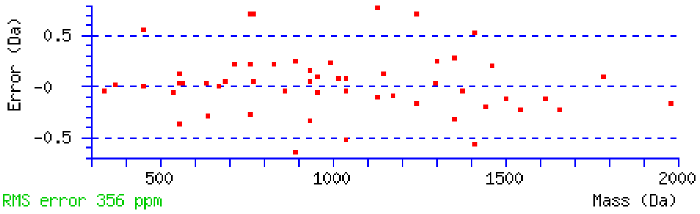
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

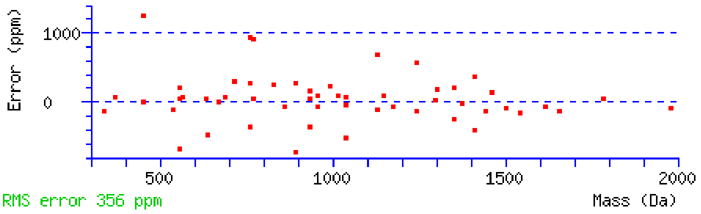


Monoisotopic mass of neutral peptide Mr(calc): 3154.6258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 92 **Expect:** 1.1e-007
Matches : 54/346 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							31
2	225.0982	113.0527			207.0877	104.0475	H	3068.6011	1534.8042	3051.5746	1526.2909	3050.5905	1525.7989	30
3	***338.1823***	169.5948			320.1717	160.5895	L	2931.5422	1466.2747	2914.5156	1457.7615	2913.5316	1457.2695	29
4	***451.2663***	226.1368			433.2558	217.1315	I	2818.4581	1409.7327	2801.4316	1401.2194	2800.4476	1400.7274	28
5	***564.3504***	282.6788			546.3398	273.6736	I	2705.3741	1353.1907	2688.3475	1344.6774	2687.3635	1344.1854	27
6	***635.3875***	318.1974			617.3770	309.1921	A	2592.2900	1296.6486	2575.2635	1288.1354	2574.2794	1287.6434	26
7	***763.4461***	382.2267	746.4196	373.7134	745.4355	373.2214	Q	2521.2529	1261.1301	2504.2263	1252.6168	2503.2423	1252.1248	25
8	***862.5145***	431.7609	845.4880	423.2476	844.5039	422.7556	V	2393.1943	1197.1008	2376.1678	1188.5875	2375.1837	1188.0955	24
9	***933.5516***	467.2795	916.5251	458.7662	915.5411	458.2742	A	2294.1259	1147.5666	2277.0993	1139.0533	2276.1153	1138.5613	23
10	1061.6466	531.3269	1044.6200	522.8137	1043.6360	522.3217	K	2223.0888	1112.0480	2206.0622	1103.5348	2205.0782	1103.0427	22
11	***1175.6895***	588.3484	1158.6630	579.8351	1157.6790	579.3431	N	2094.9938	1048.0005	2077.9673	1039.4873	2076.9833	1038.9953	21
12	1272.7423	***636.8748***	1255.7157	628.3615	1254.7317	627.8695	P	***1980.9509***	990.9791	1963.9243	982.4658	1962.9403	981.9738	20
13	1371.8107	***686.4090***	1354.7841	677.8957	1353.8001	677.4037	V	1883.8981	942.4527	1866.8716	933.9394	1865.8876	933.4474	19
14	1428.8322	***714.9197***	1411.8056	706.4064	1410.8216	705.9144	G	***1784.8297***	892.9185	1767.8032	884.4052	1766.8191	883.9132	18
15	***1541.9162***	***771.4617***	1524.8897	762.9485	1523.9057	762.4565	L	1727.8082	864.4078	1710.7817	855.8945	1709.7977	855.4025	17
16	***1655.0003***	***828.0038***	1637.9737	819.4905	1636.9897	818.9985	I	***1614.7242***	807.8657	1597.6976	799.3525	1596.7136	798.8604	16
17	1712.0218	856.5145	1694.9952	848.0012	1694.0112	847.5092	G	***1501.6401***	751.3237	1484.6136	742.8104	1483.6296	742.3184	15
18	1783.0589	***892.0331***	1766.0323	883.5198	1765.0483	883.0278	A	***1444.6187***	722.8130	1427.5921	714.2997	1426.6081	713.8077	14
19	1912.1015	***956.5544***	1895.0749	948.0411	1894.0909	947.5491	E	***1373.5815***	687.2944	1356.5550	678.7811	1355.5710	678.2891	13
20	2027.1284	***1014.0678***	2010.1019	1005.5546	2009.1178	1005.0626	N	***1244.5390***	622.7731	1227.5124	614.2598	1226.5284	613.7678	12
21	2098.1655	1049.5864	2081.1390	1041.0731	2080.1550	1040.5811	A	***1129.5120***	565.2596	1112.4855	556.7464	1111.5014	556.2544	11
22	2199.2132	1100.1102	2182.1866	1091.5970	2181.2026	1091.1050	T	1058.4749	529.7411	1041.4483	521.2278	1040.4643	520.7358	10
23	2256.2347	***1128.6210***	2239.2081	1120.1077	2238.2241	1119.6157	G	***957.4272***	479.2172	940.4007	470.7040	939.4166	470.2120	9

24	2385.2773	1193.1423	2368.2507	1184.6290	2367.2667	1184.1370	**E**	900.4058	450.7065	883.3792	442.1932	882.3952	441.7012	**8**
25	2486.3249	***1243.6661***	2469.2984	1235.1528	2468.3144	1234.6608	**T**	***771.3632***	386.1852	754.3366	377.6719	753.3526	377.1799	**7**
26	2601.3519	***1301.1796***	2584.3253	1292.6663	2583.3413	1292.1743	**D**	***670.3155***	335.6614	653.2889	327.1481	652.3049	326.6561	**6**
27	2698.4046	1349.7060	2681.3781	1341.1927	2680.3941	1340.7007	**P**	***555.2885***	278.1479	538.2620	269.6346	537.2780	269.1426	**5**
28	2785.4367	1393.2220	2768.4101	1384.7087	2767.4261	1384.2167	**S**	458.2358	229.6215	441.2092	221.1082	440.2252	220.6162	**4**
29	2922.4956	***1461.7514***	2905.4690	1453.2382	2904.4850	1452.7461	**H**	***371.2037***	186.1055	354.1772	177.5922	353.1932	177.1002	**3**
30	3009.5276	1505.2674	2992.5011	1496.7542	2991.5170	1496.2622	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
91.8	3154.6258	0.0135	SHLIIAQVAKNPVGLIGAENATGETDPSHSK	Deamidated N20 74.67%
85.1	3154.6258	0.0135	SHLIIAQVAKNPVGLIGAENATGETDPSHSK	Deamidated Q7 16.04%
82.7	3154.6258	0.0135	SHLIIAQVAKNPVGLIGAENATGETDPSHSK	Deamidated N11 9.29%
66.1	3153.6418	0.9975	SHLIIAQVAKNPVGLIGAENATGETDPSHSK	
10.3	3153.6346	1.0047	QLLSAAYLQPSAQGALPLHAEEPPPSPLTR	
9.7	3153.6346	1.0047	QLLSAAYLQPSAQGALPLHAEEPPPSPLTR	
8.7	3153.6346	1.0047	QLLSAAYLQPSAQGALPLHAEEPPPSPLTR	
8.3	3152.6375	2.0018	MISRHLPSVSSLPFHPQLHPQQMIISR	
8.3	3152.6375	2.0018	MISRHLPSVSSLPFHPQLHPQQMIISR	
6.4	3153.6227	1.0166	QQEIAAAAATGGSVLNVAALLASGTQVTPQIAM	

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

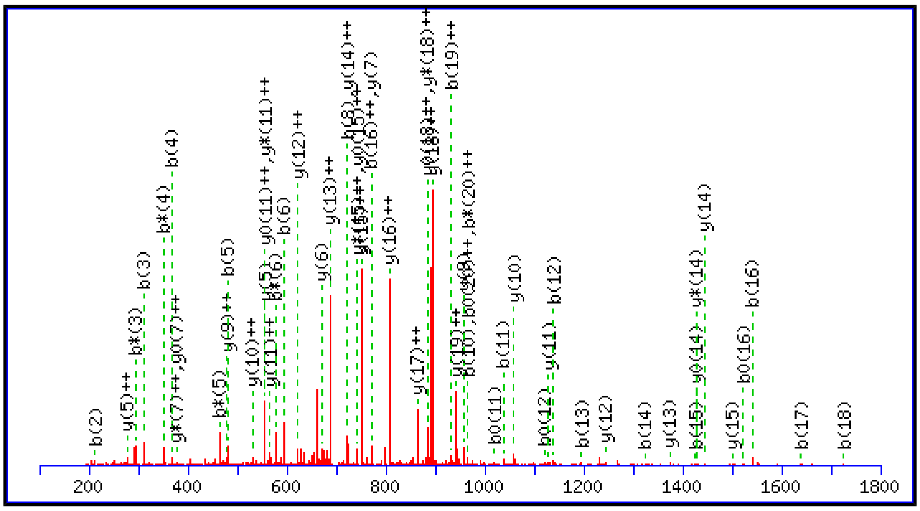
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPVGLIGAENATGETDPSHSK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 13540: 2093.992002 from(699.004610,3+) intensity(104071.2266) rtinseconds(789) scans(1877) index(4265)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum1634_scans__1877
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

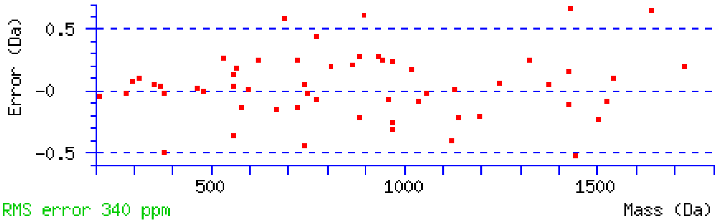
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

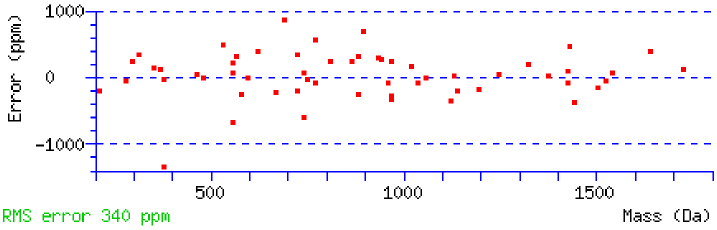


Monoisotopic mass of neutral peptide Mr(calc): 2093.9865
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 85 **Expect:** 6.6e-007
Matches : 58/222 fragment ions using 101 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**21**
2	***212.1030***	106.5551	195.0764	98.0418			**P**	1980.9509	990.9791	1963.9243	982.4658	1962.9403	981.9738	**20**
3	***311.1714***	156.0893	294.1448	147.5761			**V**	1883.8981	942.4527	1866.8716	933.9394	1865.8876	933.4474	**19**
4	***368.1928***	184.6001	351.1663	176.0868			**G**	1784.8297	892.9185	1767.8032	884.4052	1766.8191	883.9132	**18**
5	***481.2769***	241.1421	464.2504	232.6288			**L**	1727.8083	864.4078	1710.7817	855.8945	1709.7977	855.4025	**17**
6	***594.3610***	297.6841	577.3344	289.1709			**I**	1614.7242	807.8657	1597.6976	799.3525	1596.7136	798.8604	**16**
7	651.3824	326.1949	634.3559	317.6816			**G**	**1501.6401**	751.3237	1484.6136	742.8104	1483.6296	742.3184	**15**
8	***722.4196***	361.7134	705.3930	353.2001			**A**	**1444.6187**	722.8130	1427.5921	714.2997	1426.6081	713.8077	**14**
9	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	**E**	**1373.5815**	687.2944	1356.5550	678.7811	1355.5710	678.2891	**13**
10	***966.4891***	483.7482	949.4625	475.2349	948.4785	474.7429	**N**	**1244.5390**	622.7731	1227.5124	614.2598	1226.5284	613.7678	**12**
11	***1037.5262***	519.2667	1020.4997	510.7535	1019.5156	510.2615	**A**	**1129.5120**	565.2596	1112.4855	556.7464	1111.5014	556.2544	**11**
12	***1138.5739***	569.7906	1121.5473	561.2773	1120.5633	560.7853	**T**	**1058.4749**	529.7411	1041.4483	521.2278	1040.4643	520.7358	**10**
13	***1195.5953***	598.3013	1178.5688	589.7880	1177.5848	589.2960	**G**	**957.4272**	479.2172	940.4007	470.7040	939.4167	470.2120	**9**
14	***1324.6379***	662.8226	1307.6114	654.3093	1306.6274	653.8173	**E**	900.4058	450.7065	883.3792	442.1932	882.3952	441.7012	**8**
15	***1425.6856***	713.3464	1408.6591	704.8332	1407.6751	704.3412	**T**	**771.3632**	386.1852	754.3366	377.6719	753.3526	377.1799	**7**
16	***1540.7126***	770.8599	1523.6860	762.3466	1522.7020	761.8546	**D**	**670.3155**	335.6614	653.2889	327.1481	652.3049	326.6561	**6**
17	***1637.7653***	819.3863	1620.7388	810.8730	1619.7548	810.3810	**P**	**555.2885**	278.1479	538.2620	269.6346	537.2780	269.1426	**5**
18	***1724.7974***	862.9023	1707.7708	854.3890	1706.7868	853.8970	**S**	458.2358	229.6215	441.2092	221.1082	440.2252	220.6162	**4**
19	1861.8563	931.4318	1844.8297	922.9185	1843.8457	922.4265	**H**	371.2037	186.1055	354.1772	177.5922	353.1932	177.1002	**3**
20	1948.8883	974.9478	1931.8617	966.4345	1930.8777	965.9425	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**

21							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.5	2093.9865	0.0055	NPVGLIGAENATGETDPSHSK	Deamidated N10 98.33%
67.8	2093.9865	0.0055	NPVGLIGAENATGETDPSHSK	Deamidated N1 1.67%
6.0	2092.9921	0.9999	KGYAEALVEPTMMKTGHSQ	
6.0	2092.9921	0.9999	KGYAEALVEPTMMKTGHSQ	
5.9	2091.9928	1.9992	CMQVGGNANALGAKKGLGAQK	
2.2	2091.9904	2.0016	FPGPQVSADMRVVTMPGMR	
1.4	2092.9834	1.0086	KLTEGEQDEASNAAMLLEK	
1.2	2092.9926	0.9994	HGNFSTIAEEAESRKDFR	
1.1	2091.9904	2.0016	FPGPQVSADMRVVTMPGMR	
1.1	2092.9834	1.0086	KLTEGEQDEASNAAMLLEK	

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

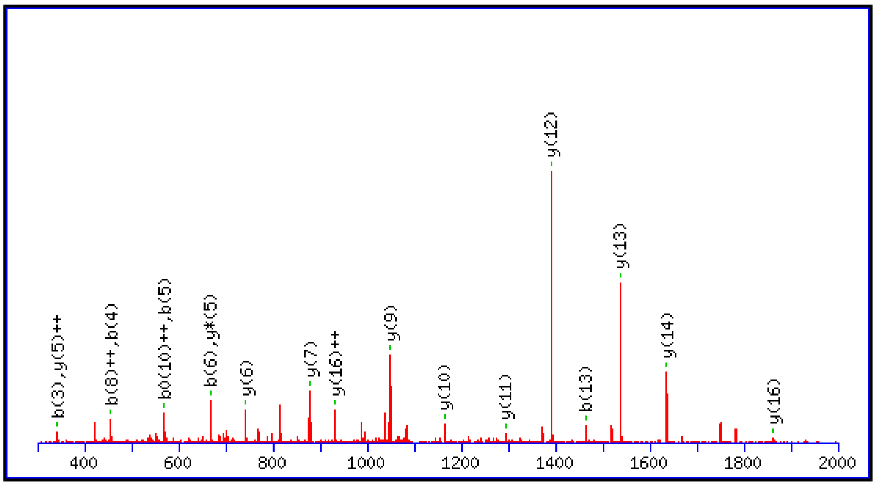
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DVQIIVFPEDGIHGFNFTR**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

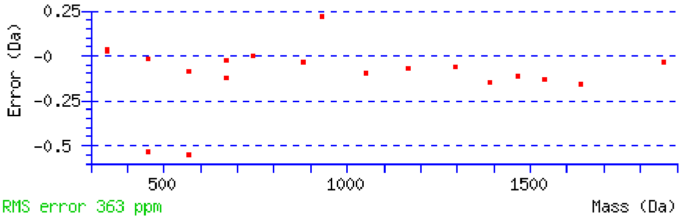
Match to Query 14867: 2204.098448 from(1103.056500,2+) intensity(46144.2344) rtinseconds(2305) scans(6088) index(16183)
Title: 111019_Est_MI_YP_G_05Spectrum5202_scans__6088
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

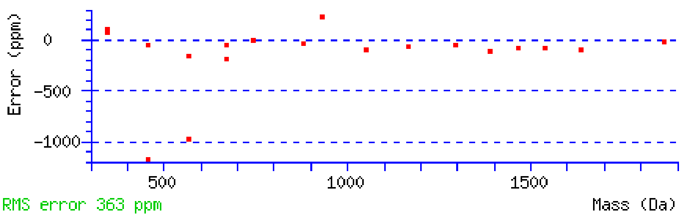
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2204.0902
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
Ions Score: 76 **Expect:** 7.2e-006
Matches : 19/210 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	116.0342	58.5207			98.0237	49.5155	D							19
2	215.1026	108.0550			197.0921	99.0497	V	2090.0706	1045.5389	2073.0440	1037.0256	2072.0600	1036.5336	18
3	**343.1612**	172.0842	326.1347	163.5710	325.1506	163.0790	Q	1991.0021	996.0047	1973.9756	987.4914	1972.9916	986.9994	17
4	**456.2453**	228.6263	439.2187	220.1130	438.2347	219.6210	I	***1862.9436***	931.9754	1845.9170	923.4621	1844.9330	922.9701	16
5	**569.3293**	285.1683	552.3028	276.6550	551.3188	276.1630	I	1749.8595	875.4334	1732.8329	866.9201	1731.8489	866.4281	15
6	**668.3978**	334.7025	651.3712	326.1892	650.3872	325.6972	V	***1636.7754***	818.8914	1619.7489	810.3781	1618.7649	809.8861	14
7	815.4662	408.2367	798.4396	399.7234	797.4556	399.2314	F	***1537.7070***	769.3571	1520.6805	760.8439	1519.6965	760.3519	13
8	912.5189	456.7631	895.4924	448.2498	894.5084	447.7578	P	***1390.6386***	695.8229	1373.6121	687.3097	1372.6280	686.8177	12
9	1041.5615	521.2844	1024.5350	512.7711	1023.5510	512.2791	E	***1293.5858***	647.2966	1276.5593	638.7833	1275.5753	638.2913	11
10	1156.5885	578.7979	1139.5619	570.2846	1138.5779	569.7926	D	***1164.5432***	582.7753	1147.5167	574.2620	1146.5327	573.7700	10
11	1213.6099	607.3086	1196.5834	598.7953	1195.5994	598.3033	G	***1049.5163***	525.2618	1032.4898	516.7485	1031.5057	516.2565	9
12	1326.6940	663.8506	1309.6674	655.3374	1308.6834	654.8454	I	992.4948	496.7511	975.4683	488.2378	974.4843	487.7458	8
13	**1463.7529**	732.3801	1446.7264	723.8668	1445.7423	723.3748	H	***879.4108***	440.2090	862.3842	431.6958	861.4002	431.2037	7
14	1520.7744	760.8908	1503.7478	752.3775	1502.7638	751.8855	G	***742.3519***	371.6796	725.3253	363.1663	724.3413	362.6743	6
15	1667.8428	834.4250	1650.8162	825.9118	1649.8322	825.4197	F	685.3304	343.1688	668.3039	334.6556	667.3198	334.1636	5
16	1782.8697	891.9385	1765.8432	883.4252	1764.8592	882.9332	N	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
17	1929.9381	965.4727	1912.9116	956.9594	1911.9276	956.4674	F	423.2350	212.1212	406.2085	203.6079	405.2245	203.1159	3
18	2030.9858	1015.9965	2013.9593	1007.4833	2012.9753	1006.9913	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.8	2204.0902	0.0082	DVQIIVFPEDGIHGFNFTR	Deamidated N16 100.00%
18.0	2204.0902	0.0082	DVQIIVFPEDGIHGFNFTR	Deamidated Q3 0.00%
10.2	2203.1062	0.9922	DVQIIVFPEDGIHGFNFTR	
5.4	2203.0952	1.0033	LVKNLLGEMPLWVCQSCR	
5.3	2204.0936	0.0049	DEFLVKIYGAQHPMGLDVR	
3.9	2203.0952	1.0033	LVKNLLGEMPLWVCQSCR	
1.5	2202.0838	2.0147	DNTVGDLSKAKPINPQSKAAM	
1.5	2202.0838	2.0147	DNTVGDLSKAKPINPQSKAAM	
1.4	2202.0986	1.9999	SEMLEIVQAIYKMVSSVMK	
1.2	2202.0986	1.9999	AEMLEIVQAIYKMVSSVMK	

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

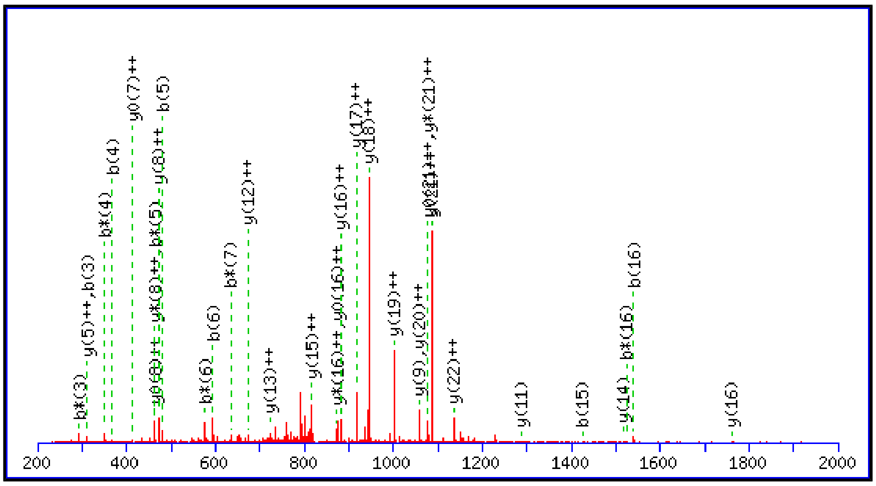
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPVGLIGAENATGETDPSHSKFLK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 21519: 2482.246362 from(828.422730,3+) intensity(24984.1797) rtinseconds(1306) scans(3047) index(26044)
Title: 111019_Est_MI_YS_G_08Spectrum2629_scans__3047
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

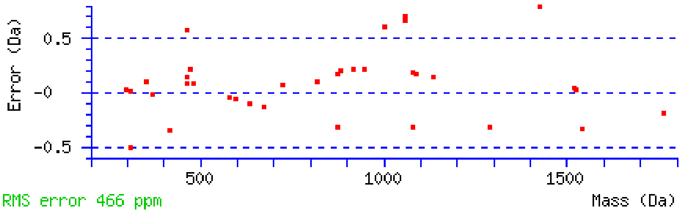
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

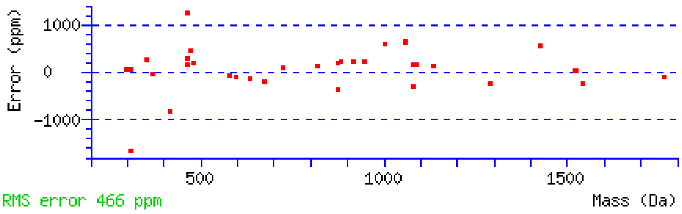


Monoisotopic mass of neutral peptide Mr(calc): 2482.2340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.0012
Matches : 35/252 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							24
2	212.1030	106.5551	195.0764	98.0418			P	2369.1983	1185.1028	2352.1718	1176.5895	2351.1878	1176.0975	23
3	**311.1714**	156.0893	294.1448	147.5761			V	2272.1456	1136.5764	2255.1190	1128.0631	2254.1350	1127.5711	22
4	**368.1928**	184.6001	351.1663	176.0868			G	2173.0772	1087.0422	2156.0506	1078.5289	2155.0666	1078.0369	21
5	**481.2769**	241.1421	464.2504	232.6288			L	2116.0557	1058.5315	2099.0291	1050.0182	2098.0451	1049.5262	20
6	**594.3610**	297.6841	577.3344	289.1709			I	2002.9716	1001.9895	1985.9451	993.4762	1984.9611	992.9842	19
7	651.3824	326.1949	634.3559	317.6816			G	1889.8876	945.4474	1872.8610	936.9341	1871.8770	936.4421	18
8	722.4196	361.7134	705.3930	353.2001			A	1832.8661	916.9367	1815.8396	908.4234	1814.8555	907.9314	17
9	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	E	**1761.8290**	881.4181	1744.8024	872.9049	1743.8184	872.4128	16
10	966.4891	483.7482	949.4625	475.2349	948.4785	474.7429	N	1632.7864	816.8968	1615.7598	808.3836	1614.7758	807.8916	15
11	1037.5262	519.2667	1020.4997	510.7535	1019.5156	510.2615	A	**1517.7594**	759.3834	1500.7329	750.8701	1499.7489	750.3781	14
12	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	T	1446.7223	723.8648	1429.6958	715.3515	1428.7118	714.8595	13
13	1195.5953	598.3013	1178.5688	589.7880	1177.5848	589.2960	G	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12
14	1324.6379	662.8226	1307.6114	654.3093	1306.6274	653.8173	E	**1288.6532**	644.8302	1271.6266	636.3170	1270.6426	635.8250	11
15	**1425.6856**	713.3464	1408.6591	704.8332	1407.6751	704.3412	T	1159.6106	580.3089	1142.5841	571.7957	1141.6000	571.3037	10
16	**1540.7126**	770.8599	1523.6860	762.3466	1522.7020	761.8546	D	**1058.5629**	529.7851	1041.5364	521.2718	1040.5524	520.7798	9
17	1637.7653	819.3863	1620.7388	810.8730	1619.7548	810.3810	P	943.5360	472.2716	926.5094	463.7584	925.5254	463.2663	8
18	1724.7974	862.9023	1707.7708	854.3890	1706.7868	853.8970	S	846.4832	423.7452	829.4567	415.2320	828.4726	414.7400	7
19	1861.8563	931.4318	1844.8297	922.9185	1843.8457	922.4265	H	759.4512	380.2292	742.4246	371.7160	741.4406	371.2239	6
20	1948.8883	974.9478	1931.8617	966.4345	1930.8777	965.9425	S	622.3923	311.6998	605.3657	303.1865	604.3817	302.6945	5
21	2076.9833	1038.9953	2059.9567	1030.4820	2058.9727	1029.9900	K	535.3602	268.1838	518.3337	259.6705			4
22	2224.0517	1112.5295	2207.0251	1104.0162	2206.0411	1103.5242	F	407.2653	204.1363	390.2387	195.6230			3
23	2337.1357	1169.0715	2320.1092	1160.5582	2319.1252	1160.0662	L	260.1969	130.6021	243.1703	122.0888			2

24							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.5	2482.2340	0.0124	NPVGLIGAENATGETDPSHSKFLK	Deamidated N10 91.21%
46.3	2481.2500	0.9964	NPVGLIGAENATGETDPSHSKFLK	
43.3	2482.2340	0.0124	NPVGLIGAENATGETDPSHSKFLK	Deamidated N1 8.79%
8.7	2482.2526	-0.0062	NVPVLFNDTETNLAGMYGKVRK	
5.8	2482.2526	-0.0062	NVPVLFNDTETNLAGMYGKVRK	
5.6	2480.2509	1.9955	LPVLAPAPASPPSPDPPTEVTPAEM	
5.0	2480.2324	2.0139	RAVSAAMLMATSANQITAVPLVTM	
4.5	2482.2526	-0.0062	NVPVLFNDTETNLAGMYGKVRK	
2.8	2480.2506	1.9957	LHGVKLEALNQSINIEQSQSDR	
2.8	2480.2506	1.9957	LHGVKLEALNQSINIEQSQSDR	

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

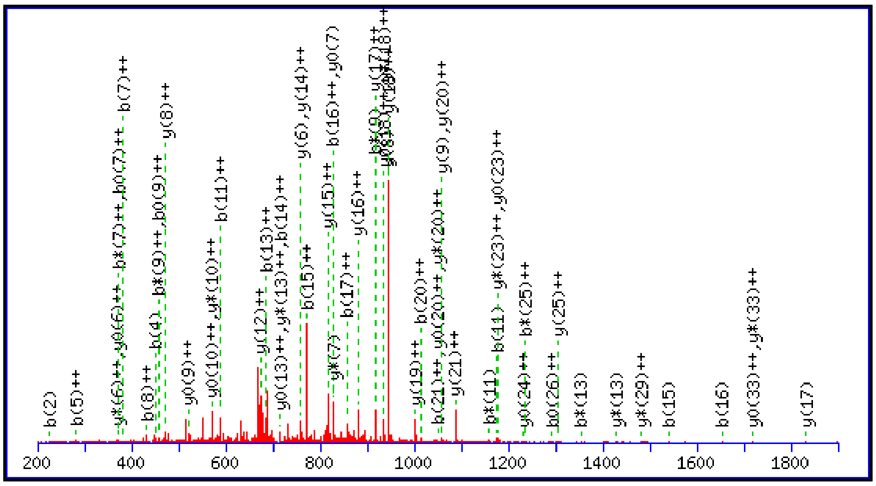
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHLIIAQVAKNPVGLIGAENATGETDPSHSKFLK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 27811: 3542.874820 from(709.582240,5+) intensity(36290.4102) rtinseconds(1653) scans(4108) index(25355)
Title: 111019_Est_MI_YS_G_07Spectrum3496_scans__4108
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

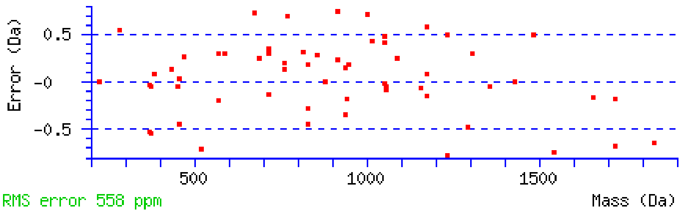
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

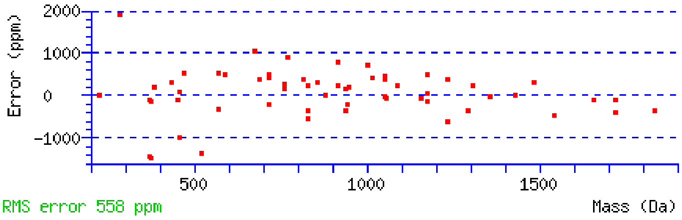


Monoisotopic mass of neutral peptide Mr(calc): 3542.8733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.00089
Matches : 60/376 fragment ions using 97 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							34
2	**225.0982**	113.0527			207.0877	104.0475	H	3456.8485	1728.9279	3439.8220	1720.4146	3438.8380	1719.9226	33
3	338.1823	169.5948			320.1717	160.5895	L	3319.7896	1660.3985	3302.7631	1651.8852	3301.7791	1651.3932	32
4	**451.2663**	226.1368			433.2558	217.1315	I	3206.7056	1603.8564	3189.6790	1595.3431	3188.6950	1594.8511	31
5	564.3504	***282.6788***			546.3398	273.6736	I	3093.6215	1547.3144	3076.5950	1538.8011	3075.6109	1538.3091	30
6	635.3875	318.1974			617.3770	309.1921	A	2980.5374	1490.7724	2963.5109	1482.2591	2962.5269	1481.7671	29
7	763.4461	***382.2267***	746.4196	373.7134	745.4355	373.2214	Q	2909.5003	1455.2538	2892.4738	1446.7405	2891.4898	1446.2485	28
8	862.5145	***431.7609***	845.4880	423.2476	844.5039	422.7556	V	2781.4418	1391.2245	2764.4152	1382.7112	2763.4312	1382.2192	27
9	933.5516	467.2795	916.5251	458.7662	915.5411	458.2742	A	2682.3733	1341.6903	2665.3468	1333.1770	2664.3628	1332.6850	26
10	1061.6466	531.3269	1044.6200	522.8137	1043.6360	522.3217	K	2611.3362	1306.1717	2594.3097	1297.6585	2593.3257	1297.1665	25
11	**1175.6895**	***588.3484***	1158.6630	579.8351	1157.6790	579.3431	N	2483.2413	1242.1243	2466.2147	1233.6110	2465.2307	1233.1190	24
12	1272.7423	636.8748	1255.7157	628.3615	1254.7317	627.8695	P	2369.1983	1185.1028	2352.1718	1176.5895	2351.1878	1176.0975	23
13	1371.8107	***686.4090***	1354.7841	677.8957	1353.8001	677.4037	V	2272.1456	1136.5764	2255.1190	1128.0631	2254.1350	1127.5711	22
14	1428.8322	***714.9197***	1411.8056	706.4064	1410.8216	705.9144	G	2173.0772	1087.0422	2156.0506	1078.5289	2155.0666	1078.0369	21
15	**1541.9162**	***771.4617***	1524.8897	762.9485	1523.9057	762.4565	L	2116.0557	1058.5315	2099.0291	1050.0182	2098.0451	1049.5262	20
16	**1655.0003**	***828.0038***	1637.9737	819.4905	1636.9897	818.9985	I	2002.9716	1001.9895	1985.9451	993.4762	1984.9611	992.9842	19
17	1712.0218	***856.5145***	1694.9952	848.0012	1694.0112	847.5092	G	1889.8876	945.4474	1872.8610	936.9341	1871.8770	936.4421	18
18	1783.0589	892.0331	1766.0323	883.5198	1765.0483	883.0278	A	**1832.8661**	916.9367	1815.8395	908.4234	1814.8555	907.9314	17
19	1912.1015	956.5544	1895.0749	948.0411	1894.0909	947.5491	E	1761.8290	881.4181	1744.8024	872.9049	1743.8184	872.4128	16
20	2027.1284	***1014.0678***	2010.1019	1005.5546	2009.1178	1005.0626	N	1632.7864	816.8968	1615.7598	808.3836	1614.7758	807.8916	15
21	2098.1655	***1049.5864***	2081.1390	1041.0731	2080.1550	1040.5811	A	1517.7594	759.3834	1500.7329	750.8701	1499.7489	750.3781	14
22	2199.2132	1100.1102	2182.1866	1091.5970	2181.2026	1091.1050	T	1446.7223	723.8648	1429.6958	715.3515	1428.7118	714.8595	13
23	2256.2347	1128.6210	2239.2081	1120.1077	2238.2241	1119.6157	G	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12

24	2385.2773	1193.1423	2368.2507	1184.6290	2367.2667	1184.1370	E	1288.6532	644.8302	1271.6266	636.3170	1270.6426	635.8250	11
25	2486.3249	1243.6661	2469.2984	1235.1528	2468.3144	1234.6608	T	1159.6106	580.3089	1142.5840	571.7957	1141.6000	571.3037	10
26	2601.3519	1301.1796	2584.3253	1292.6663	2583.3413	1292.1743	D	**1058.5629**	529.7851	1041.5364	521.2718	1040.5524	520.7798	9
27	2698.4046	1349.7060	2681.3781	1341.1927	2680.3941	1340.7007	P	**943.5360**	472.2716	926.5094	463.7584	925.5254	463.2663	8
28	2785.4367	1393.2220	2768.4101	1384.7087	2767.4261	1384.2167	S	846.4832	423.7452	829.4567	415.2320	828.4726	414.7400	7
29	2922.4956	1461.7514	2905.4690	1453.2382	2904.4850	1452.7461	H	**759.4512**	380.2292	742.4246	371.7160	741.4406	371.2239	6
30	3009.5276	1505.2674	2992.5011	1496.7542	2991.5170	1496.2622	S	622.3923	311.6998	605.3657	303.1865	604.3817	302.6945	5
31	3137.6226	1569.3149	3120.5960	1560.8016	3119.6120	1560.3096	K	535.3602	268.1838	518.3337	259.6705			4
32	3284.6910	1642.8491	3267.6644	1634.3359	3266.6804	1633.8438	F	407.2653	204.1363	390.2387	195.6230			3
33	3397.7750	1699.3912	3380.7485	1690.8779	3379.7645	1690.3859	L	260.1969	130.6021	243.1703	122.0888			2
34							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.2	3542.8733	0.0016	SHLIIAQVAKNPVGLIGAENATGETDPSHSKFLK	Deamidated N20 56.65%
46.5	3542.8733	0.0016	SHLIIAQVAKNPVGLIGAENATGETDPSHSKFLK	Deamidated Q7 24.11%
45.5	3542.8733	0.0016	SHLIIAQVAKNPVGLIGAENATGETDPSHSKFLK	Deamidated N11 19.24%
38.4	3541.8893	0.9856	SHLIIAQVAKNPVGLIGAENATGETDPSHSKFLK	
7.5	3541.8598	1.0150	MQPVTIASLQASVLPMVSMVGVQLSPPVTFQLR	
5.9	3540.8659	2.0089	AVISLLFLAVMYVVHHPLMVSDRMDLDTLAR	
5.8	3540.8690	2.0058	VPLYAVMYPVFNELERVNLSAAQTLRAAFIK	
5.2	3542.8845	-0.0097	VTELTEATGKLIRTSHIGKPHPQSFQPAAATQK	
5.2	3541.8766	0.9982	LQLTNDNEGKGNLWVTTILATQSGLIERVLLK	
4.8	3541.8637	1.0112	VMQLLSPTVLPAGVDERPPGGGKSCGVPEKQPLK	

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

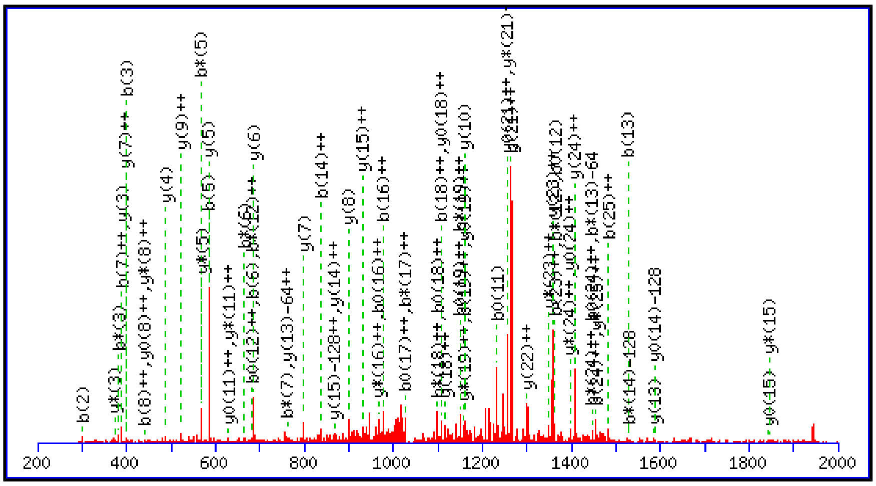
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WNVNAPPTFHSEMMYDNFTLVPVWGK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 27322: 3112.421802 from(1038.481210,3+) intensity(18124.8027) rtinseconds(2303) scans(5686) index(12021)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum4930_scans__5686
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

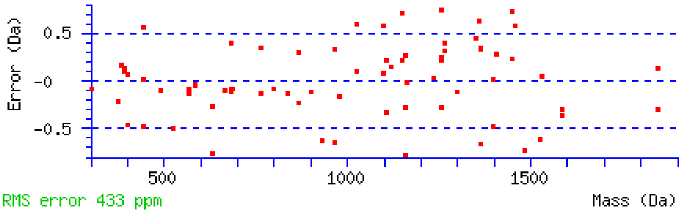
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

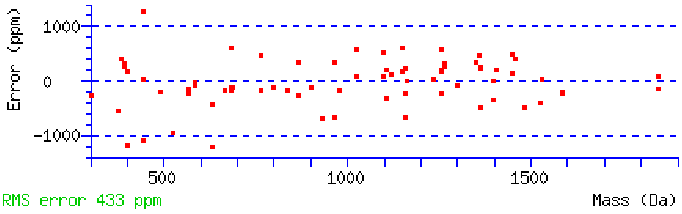


Monoisotopic mass of neutral peptide Mr(calc): 3112.4099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N17 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.0082
Matches : 75/426 fragment ions using 120 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							26
2	**301.1295**	151.0684	284.1030	142.5551			N	2927.3379	1464.1726	2910.3113	1455.6593	2909.3273	1455.1673	25
3	**400.1979**	200.6026	383.1714	192.0893			V	2813.2950	1407.1511	2796.2684	1398.6378	2795.2844	1398.1458	24
4	514.2409	257.6241	497.2143	249.1108			N	2714.2265	1357.6169	2697.2000	1349.1036	2696.2160	1348.6116	23
5	**585.2780**	293.1426	568.2514	284.6293			A	2600.1836	1300.5954	2583.1571	1292.0822	2582.1730	1291.5902	22
6	**682.3307**	341.6690	665.3042	333.1557			P	2529.1465	1265.0769	2512.1199	1256.5636	2511.1359	1256.0716	21
7	779.3835	***390.1954***	762.3570	381.6821			P	2432.0937	1216.5505	2415.0672	1208.0372	2414.0832	1207.5452	20
8	880.4312	***440.7192***	863.4046	432.2060	862.4206	431.7139	T	2335.0410	1168.0241	2318.0144	1159.5108	2317.0304	1159.0188	19
9	1027.4996	514.2534	1010.4730	505.7402	1009.4890	505.2482	F	2233.9933	1117.5003	2216.9667	1108.9870	2215.9827	1108.4950	18
10	1164.5585	582.7829	1147.5320	574.2696	1146.5479	573.7776	H	2086.9249	1043.9661	2069.8983	1035.4528	2068.9143	1034.9608	17
11	1251.5905	626.2989	1234.5640	617.7856	1233.5800	617.2936	S	1949.8660	975.4366	1932.8394	966.9233	1931.8554	966.4313	16
12	1380.6331	690.8202	1363.6066	682.3069	1362.6226	681.8149	E	1862.8339	931.9206	1845.8074	923.4073	1844.8234	922.9153	15
13	**1527.6685**	764.3379	1510.6420	755.8246	1509.6580	755.3326	M	1733.7913	867.3993	1716.7648	858.8860	1715.7808	858.3940	14
14	1674.7039	***837.8556***	1657.6774	829.3423	1656.6934	828.8503	M	***1586.7559***	793.8816	1569.7294	785.3683	1568.7454	784.8763	13
15	1837.7673	919.3873	1820.7407	910.8740	1819.7567	910.3820	Y	1439.7205	720.3639	1422.6940	711.8506	1421.7100	711.3586	12
16	1952.7942	***976.9007***	1935.7676	968.3875	1934.7836	967.8955	D	1276.6572	638.8322	1259.6307	630.3190	1258.6467	629.8270	11
17	2067.8211	1034.4142	2050.7946	1025.9009	2049.8106	1025.4089	N	***1161.6303***	581.3188	1144.6037	572.8055	1143.6197	572.3135	10
18	2214.8896	***1107.9484***	2197.8630	1099.4351	2196.8790	1098.9431	F	1046.6033	523.8053	1029.5768	515.2920	1028.5928	514.8000	9
19	2315.9372	***1158.4723***	2298.9107	1149.9590	2297.9267	1149.4670	T	***899.5349***	450.2711	882.5084	441.7578	881.5244	441.2658	8
20	2429.0213	1215.0143	2411.9947	1206.5010	2411.0107	1206.0090	L	***798.4872***	399.7473	781.4607	391.2340			7
21	2528.0897	***1264.5485***	2511.0632	1256.0352	2510.0791	1255.5432	V	***685.4032***	343.2052	668.3766	334.6919			6
22	2625.1425	1313.0749	2608.1159	1304.5616	2607.1319	1304.0696	P	***586.3348***	293.6710	569.3082	285.1577			5

23	2724.2109	***1362.6091***	2707.1843	1354.0958	2706.2003	1353.6038	**V**	***489.2820***	245.1446	472.2554	236.6314			**4**
24	2910.2902	***1455.6487***	2893.2637	1447.1355	2892.2796	1446.6435	**W**	***390.2136***	195.6104	373.1870	187.0972			**3**
25	2967.3117	***1484.1595***	2950.2851	1475.6462	2949.3011	1475.1542	**G**	204.1343	102.5708	187.1077	94.0575			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.3	3112.4099	0.0119	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N17 96.83%
30.3	3111.4259	0.9959	WNVNAPPTFHSEMMYDNFTLVPVWGK	
26.2	3112.4099	0.0119	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N4 1.92%
24.4	3112.4099	0.0119	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N2 1.26%
7.3	3111.4316	0.9902	QIGPDARPRNQSSTYTATSWLDMEQSR	
6.7	3111.4316	0.9902	QIGPDARPRNQSSTYTATSWLDMEQSR	
4.9	3111.4246	0.9972	VILALGDYMGATCHACIGGTNVRNEMQK	
4.3	3111.4317	0.9901	MKLNPQNSEVMPWDPPYYSGVIRAER	
3.9	3111.4316	0.9902	QIGPDARPRNQSSTYTATSWLDMEQSR	
1.6	3111.4059	1.0159	ANRNAEEFELTNIDMVQCDVCLLSNR	

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

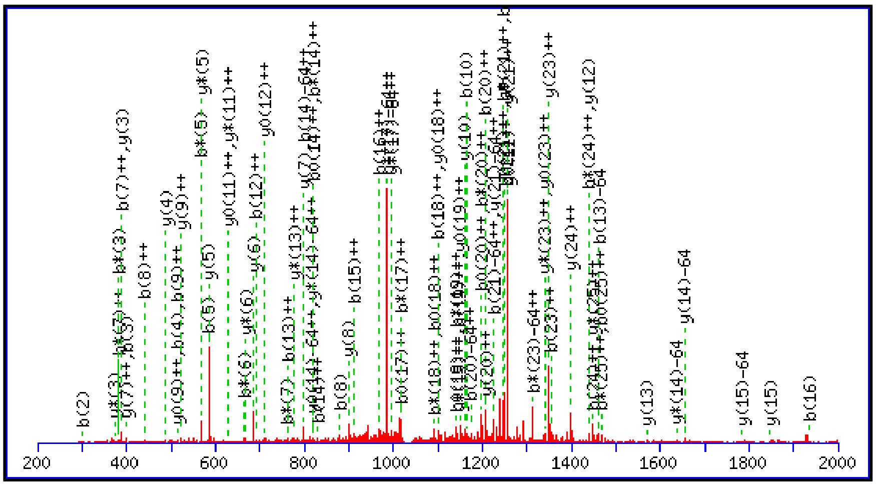
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WNVNAPPTFHSEMMYDNFTLVPVWGK**
Found in **A6NHF2** in **con_Xuniprot_HUMAN3**, A6NHF2_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=2 SV=3

Match to Query 27315: 3096.428472 from(1033.150100,3+) intensity(32956.5078) rtinseconds(2419) scans(6013) index(12057)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum5219_scans__6013
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

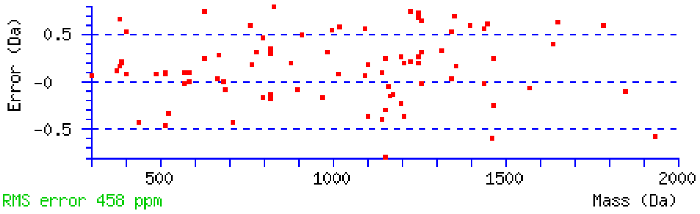
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

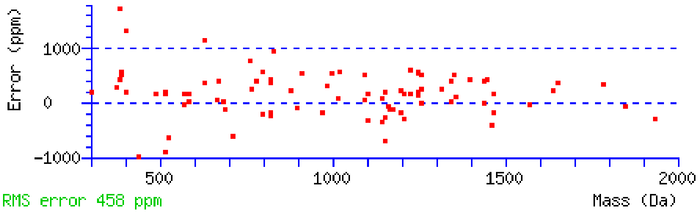


Monoisotopic mass of neutral peptide Mr(calc): 3096.4150
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N17 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.033
Matches : 87/420 fragment ions using 173 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					**W**							**26**
2	**301.1295**	151.0684	284.1030	142.5551			**N**	2911.3430	1456.1751	2894.3164	1447.6618	2893.3324	1447.1698	**25**
3	**400.1979**	200.6026	383.1714	192.0893			**V**	2797.3000	1399.1537	2780.2735	1390.6404	2779.2895	1390.1484	**24**
4	**514.2409**	257.6241	497.2143	249.1108			**N**	2698.2316	1349.6195	2681.2051	1341.1062	2680.2211	1340.6142	**23**
5	**585.2780**	293.1426	568.2514	284.6293			**A**	2584.1887	1292.5980	2567.1621	1284.0847	2566.1781	1283.5927	**22**
6	682.3307	341.6690	665.3042	333.1557			**P**	2513.1516	1257.0794	2496.1250	1248.5662	2495.1410	1248.0741	**21**
7	779.3835	***390.1954***	762.3570	381.6821			**P**	2416.0988	1208.5530	2399.0723	1200.0398	2398.0883	1199.5478	**20**
8	**880.4312**	***440.7192***	863.4046	432.2060	862.4206	431.7139	**T**	2319.0461	1160.0267	2302.0195	1151.5134	2301.0355	1151.0214	**19**
9	1027.4996	***514.2534***	1010.4730	505.7402	1009.4890	505.2482	**F**	2217.9984	1109.5028	2200.9718	1100.9896	2199.9878	1100.4975	**18**
10	**1164.5585**	582.7829	1147.5320	574.2696	1146.5479	573.7776	**H**	2070.9300	1035.9686	2053.9034	1027.4553	2052.9194	1026.9633	**17**
11	1251.5905	626.2989	1234.5640	617.7856	1233.5800	617.2936	**S**	1933.8711	967.4392	1916.8445	958.9259	1915.8605	958.4339	**16**
12	1380.6331	***690.8202***	1363.6066	682.3069	1362.6226	681.8149	**E**	**1846.8390**	923.9231	1829.8125	915.4099	1828.8285	914.9179	**15**
13	1527.6685	***764.3379***	1510.6420	755.8246	1509.6580	755.3326	**M**	1717.7964	859.4019	1700.7699	850.8886	1699.7859	850.3966	**14**
14	1658.7090	***829.8581***	1641.6825	821.3449	1640.6984	820.8529	**M**	**1570.7610**	785.8842	1553.7345	777.3709	1552.7505	776.8789	**13**
15	1821.7723	***911.3898***	1804.7458	902.8765	1803.7618	902.3845	**Y**	**1439.7205**	720.3639	1422.6940	711.8506	1421.7100	711.3586	**12**
16	**1936.7993**	***968.9033***	1919.7727	960.3900	1918.7887	959.8980	**D**	1276.6572	638.8322	1259.6307	630.3190	1258.6467	629.8270	**11**
17	2051.8262	1026.4168	2034.7997	1017.9035	2033.8157	1017.4115	**N**	**1161.6303**	581.3188	1144.6037	572.8055	1143.6197	572.3135	**10**
18	2198.8946	***1099.9510***	2181.8681	1091.4377	2180.8841	1090.9457	**F**	1046.6033	523.8053	1029.5768	515.2920	1028.5928	514.8000	**9**
19	2299.9423	***1150.4748***	2282.9158	1141.9615	2281.9318	1141.4695	**T**	**899.5349**	450.2711	882.5084	441.7578	881.5244	441.2658	**8**
20	2413.0264	***1207.0168***	2395.9998	1198.5036	2395.0158	1198.0115	**L**	**798.4872**	399.7473	781.4607	391.2340			**7**
21	2512.0948	***1256.5510***	2495.0682	1248.0378	2494.0842	1247.5458	**V**	**685.4032**	343.2052	668.3766	334.6919			**6**
22	2609.1476	1305.0774	2592.1210	1296.5641	2591.1370	1296.0721	**P**	**586.3348**	293.6710	569.3082	285.1577			**5**

23	2708.2160	***1354.6116***	2691.1894	1346.0984	2690.2054	1345.6063	**V**	**489.2820**	245.1446	472.2554	236.6314			**4**
24	2894.2953	***1447.6513***	2877.2687	1439.1380	2876.2847	1438.6460	**W**	**390.2136**	195.6104	373.1870	187.0972			**3**
25	2951.3168	1476.1620	2934.2902	1467.6487	2933.3062	1467.1567	**G**	204.1343	102.5708	187.1077	94.0575			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.7	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N17, Oxidation M13; 82.01%
30.1	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N17, Oxidation M14; 14.32%
23.4	3095.4310	0.9975	WNVNAPPTFHSEMMYDNFTLVPVWGK	
21.1	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N4, Oxidation M13; 1.77%
18.3	3095.4310	0.9975	WNVNAPPTFHSEMMYDNFTLVPVWGK	
17.7	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N2, Oxidation M13; 0.81%
17.4	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N4, Oxidation M14; 0.76%
13.8	3096.4150	0.0135	WNVNAPPTFHSEMMYDNFTLVPVWGK	Deamidated N2, Oxidation M14; 0.33%
8.5	3095.4366	0.9918	QIGPDARPRNQSSTYTATSWLDMEQSR	
5.6	3096.4294	-0.0009	VAQVRACLSTCPPEYEYQFASGDRHR	

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

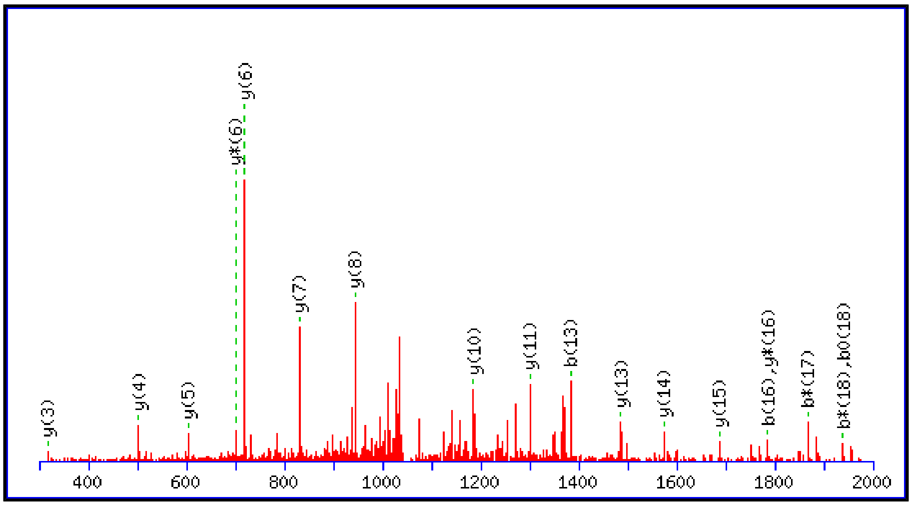
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSNNSDANLELINTWVAK**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

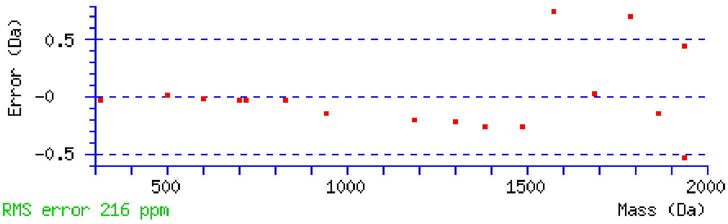
Match to Query 13693: 2101.075488 from(1051.545020,2+) intensity(37412.4961) rtinseconds(3166) scans(8074) index(12223)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum7057_scans__8074
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

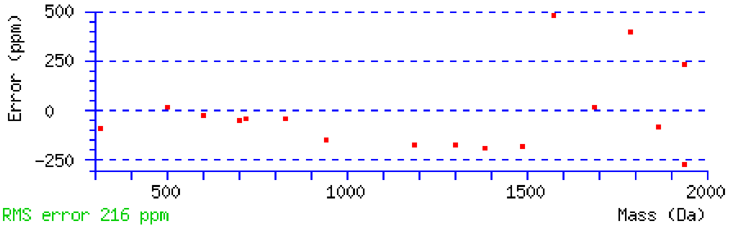
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2101.0691
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 112 **Expect:** 1.5e-009
Matches : 18/198 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	100.0757	50.5415					V							19
2	213.1598	107.0835					L	2003.0080	1002.0076	1985.9815	993.4944	1984.9974	993.0024	18
3	300.1918	150.5995			282.1812	141.5942	S	1889.9239	945.4656	1872.8974	936.9523	1871.9134	936.4603	17
4	415.2187	208.1130	398.1922	199.5997	397.2082	199.1077	N	1802.8919	901.9496	1785.8654	893.4363	1784.8814	892.9443	16
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	N	***1687.8650***	844.4361	1670.8384	835.9229	1669.8544	835.4308	15
6	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	S	***1573.8220***	787.4147	1556.7955	778.9014	1555.8115	778.4094	14
7	731.3206	366.1639	714.2941	357.6507	713.3101	357.1587	D	***1486.7900***	743.8986	1469.7635	735.3854	1468.7795	734.8934	13
8	802.3577	401.6825	785.3312	393.1692	784.3472	392.6772	A	1371.7631	686.3852	1354.7365	677.8719	1353.7525	677.3799	12
9	916.4007	458.7040	899.3741	450.1907	898.3901	449.6987	N	***1300.7260***	650.8666	1283.6994	642.3533	1282.7154	641.8613	11
10	1029.4847	515.2460	1012.4582	506.7327	1011.4742	506.2407	L	***1186.6830***	593.8452	1169.6565	585.3319	1168.6725	584.8399	10
11	1158.5273	579.7673	1141.5008	571.2540	1140.5168	570.7620	E	1073.5990	537.3031	1056.5724	528.7898	1055.5884	528.2978	9
12	1271.6114	636.3093	1254.5848	627.7961	1253.6008	627.3040	L	***944.5564***	472.7818	927.5298	464.2686	926.5458	463.7765	8
13	**1384.6954**	692.8514	1367.6689	684.3381	1366.6849	683.8461	I	***831.4723***	416.2398	814.4458	407.7265	813.4617	407.2345	7
14	1498.7384	749.8728	1481.7118	741.3596	1480.7278	740.8675	N	***718.3883***	359.6978	701.3617	351.1845	700.3777	350.6925	6
15	1599.7861	800.3967	1582.7595	791.8834	1581.7755	791.3914	T	***604.3453***	302.6763	587.3188	294.1630	586.3348	293.6710	5
16	**1785.8654**	893.4363	1768.8388	884.9230	1767.8548	884.4310	W	***503.2976***	252.1525	486.2711	243.6392			4
17	1884.9338	942.9705	1867.9072	934.4573	1866.9232	933.9652	V	***317.2183***	159.1128	300.1918	150.5995			3
18	1955.9709	978.4891	1938.9443	969.9758	1937.9603	969.4838	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
112.4	2101.0691	0.0064	VLSNNSDANLELINTWVAK	Deamidated N4 98.86%
92.8	2101.0691	0.0064	VLSNNSDANLELINTWVAK	Deamidated N5 1.09%
79.1	2101.0691	0.0064	VLSNNSDANLELINTWVAK	Deamidated N9 0.05%
55.0	2101.0691	0.0064	VLSNNSDANLELINTWVAK	Deamidated N14 0.00%
8.9	2100.0626	1.0129	TALELSWNIIPSEEELEK	
6.0	2100.0811	0.9944	EATGTRGELNLLQSAQADVK	
5.4	2101.0837	-0.0082	VLQLMNLTDSRLAQAGNEK	
5.4	2101.0837	-0.0082	VLQLMNLTDSRLAQAGNEK	
4.5	2101.0651	0.0104	EATGTRGELNLLQSAQADVK	
4.3	2101.0691	0.0064	EEIGNTGEPILAFNDKGVAK	

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

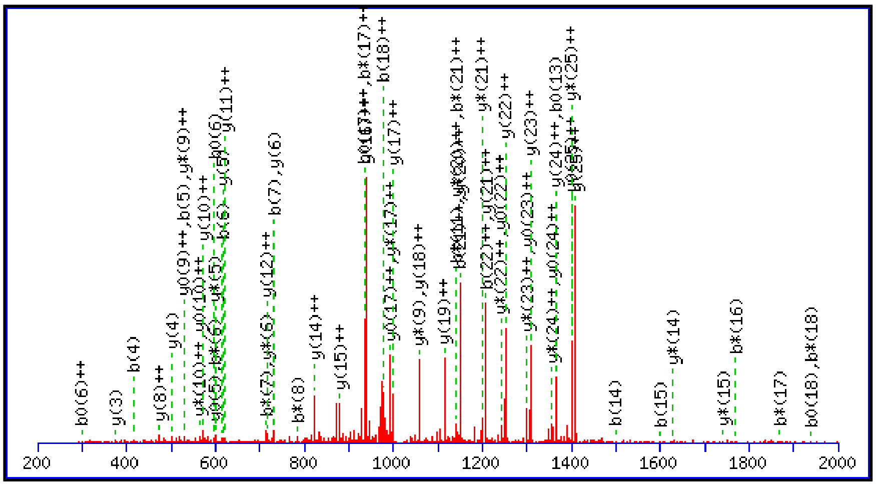
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSNNSDANLELINTWVAKNTNNKISR**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

Match to Query 27283: 3028.572162 from(1010.531330,3+) intensity(294941.0625) rtinseconds(1938) scans(4928) index(25471)
Title: 111019_Est_MI_YS_G_07Spectrum4204_scans__4928
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

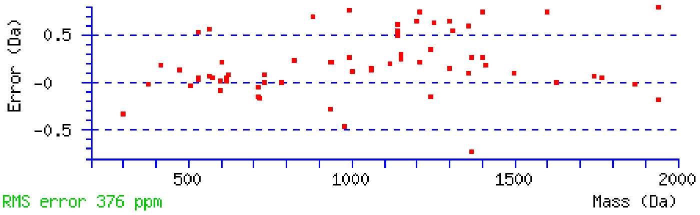
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

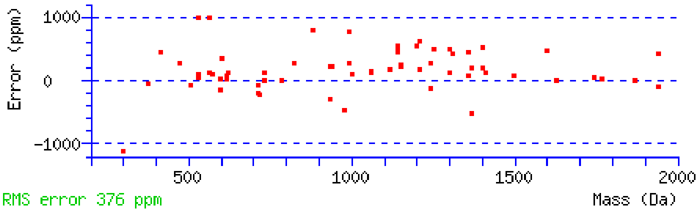


Monoisotopic mass of neutral peptide Mr(calc): 3028.5577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 76 **Expect:** 3.9e-006
Matches : 65/300 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							27
2	213.1598	107.0835					L	2930.4966	1465.7520	2913.4701	1457.2387	2912.4861	1456.7467	26
3	300.1918	150.5995			282.1812	141.5942	S	2817.4126	1409.2099	2800.3860	1400.6966	2799.4020	1400.2046	25
4	**415.2187**	208.1130	398.1922	199.5997	397.2082	199.1077	N	2730.3805	1365.6939	2713.3540	1357.1806	2712.3700	1356.6886	24
5	**529.2617**	265.1345	512.2351	256.6212	511.2511	256.1292	N	2615.3536	1308.1804	2598.3271	1299.6672	2597.3430	1299.1752	23
6	**616.2937**	308.6505	599.2671	300.1372	598.2831	299.6452	S	2501.3107	1251.1590	2484.2841	1242.6457	2483.3001	1242.1537	22
7	**731.3206**	366.1639	714.2941	357.6507	713.3101	357.1587	D	2414.2786	1207.6430	2397.2521	1199.1297	2396.2681	1198.6377	21
8	802.3577	401.6825	785.3312	393.1692	784.3472	392.6772	A	2299.2517	1150.1295	2282.2252	1141.6162	2281.2411	1141.1242	20
9	916.4007	458.7040	899.3741	450.1907	898.3901	449.6987	N	2228.2146	1114.6109	2211.1880	1106.0977	2210.2040	1105.6056	19
10	1029.4847	515.2460	1012.4582	506.7327	1011.4742	506.2407	L	2114.1717	1057.5895	2097.1451	1049.0762	2096.1611	1048.5842	18
11	1158.5273	579.7673	1141.5008	571.2540	1140.5168	570.7620	E	2001.0876	1001.0474	1984.0610	992.5342	1983.0770	992.0422	17
12	1271.6114	636.3093	1254.5848	627.7961	1253.6008	627.3040	L	1872.0450	936.5261	1855.0185	928.0129	1854.0344	927.5209	16
13	1384.6954	692.8514	1367.6689	684.3381	1366.6849	683.8461	I	1758.9609	879.9841	1741.9344	871.4708	1740.9504	870.9788	15
14	**1498.7384**	749.8728	1481.7118	741.3596	1480.7278	740.8675	N	1645.8769	823.4421	1628.8503	814.9288	1627.8663	814.4368	14
15	**1599.7861**	800.3967	1582.7595	791.8834	1581.7755	791.3914	T	1531.8340	766.4206	1514.8074	757.9073	1513.8234	757.4153	13
16	1785.8654	893.4363	1768.8388	884.9230	1767.8548	884.4310	W	1430.7863	715.8968	1413.7597	707.3835	1412.7757	706.8915	12
17	1884.9338	942.9705	1867.9072	934.4573	1866.9232	933.9652	V	1244.7070	622.8571	1227.6804	614.3438	1226.6964	613.8518	11
18	1955.9709	978.4891	1938.9443	969.9758	1937.9603	969.4838	A	1145.6385	573.3229	1128.6120	564.8096	1127.6280	564.3176	10
19	2084.0659	1042.5366	2067.0393	1034.0233	2066.0553	1033.5313	K	1074.6014	537.8044	1057.5749	529.2911	1056.5909	528.7991	9
20	2198.1088	1099.5580	2181.0822	1091.0448	2180.0982	1090.5527	N	946.5065	473.7569	929.4799	465.2436	928.4959	464.7516	8
21	2299.1565	1150.0819	2282.1299	1141.5686	2281.1459	1141.0766	T	832.4635	416.7354	815.4370	408.2221	814.4530	407.7301	7
22	2413.1994	1207.1033	2396.1728	1198.5901	2395.1888	1198.0981	N	**731.4159**	366.2116	714.3893	357.6983	713.4053	357.2063	6
23	2527.2423	1264.1248	2510.2158	1255.6115	2509.2318	1255.1195	N	**617.3729**	309.1901	600.3464	300.6768	599.3624	300.1848	5

24	2655.3373	1328.1723	2638.3107	1319.6590	2637.3267	1319.1670	**K**	**503.3300**	252.1686	486.3035	243.6554	485.3194	243.1634	**4**
25	2768.4213	1384.7143	2751.3948	1376.2010	2750.4108	1375.7090	**I**	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
26	2855.4534	1428.2303	2838.4268	1419.7171	2837.4428	1419.2250	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.4	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N4 27.59%
75.3	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N5 21.52%
75.2	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N20 20.84%
74.2	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N22 16.47%
70.3	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N14 6.71%
68.7	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N23 4.62%
65.5	3028.5577	0.0145	VLSNNSDANLELINTWVAKNTNNKISR	Deamidated N9 2.25%
60.3	3027.5737	0.9985	VLSNNSDANLELINTWVAKNTNNKISR	
5.3	3027.5793	0.9928	GPPVLSFFLSLGTLSFAPRPLWADRHM	
3.3	3026.5800	1.9921	RSPPSWFVSPLVRLPTGTNQPLFCLR	

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

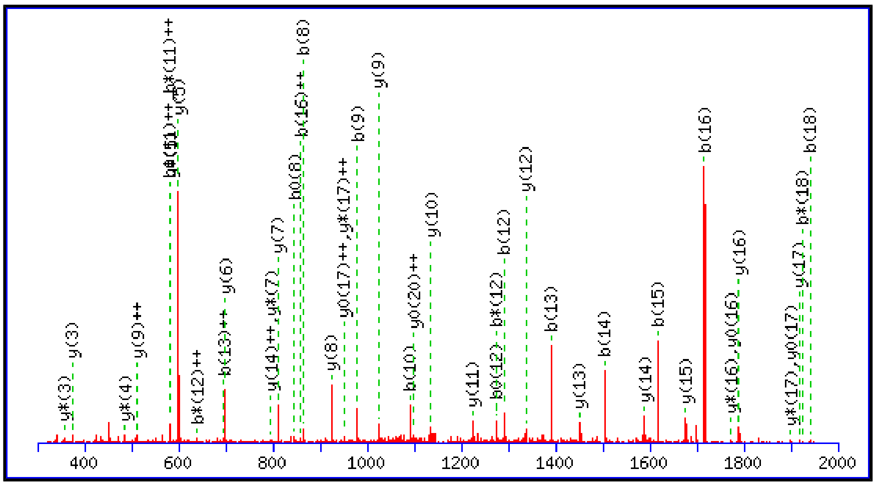
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGQLQLSHNLSLVILVPQNLK**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

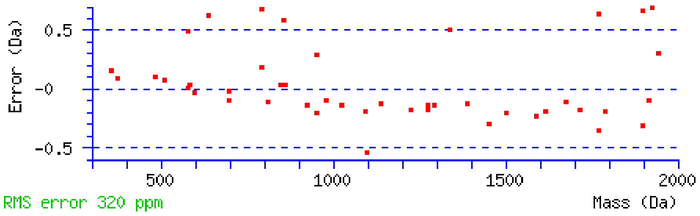
Match to Query 15170: 2313.351028 from(1157.682790,2+) intensity(124402.6172) rtinseconds(2424) scans(6061) index(9146)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum5234_scans__6061
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

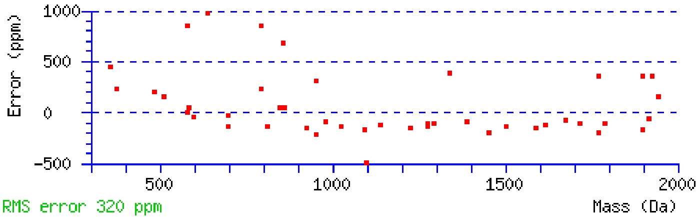
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2313.3420
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 71 **Expect:** 1.2e-006
Matches : 45/204 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							21
2	157.0972	79.0522					G	2215.2809	1108.1441	2198.2543	1099.6308	2197.2703	1099.1388	20
3	285.1557	143.0815	268.1292	134.5682			Q	2158.2594	1079.6333	2141.2329	1071.1201	2140.2489	1070.6281	19
4	398.2398	199.6235	381.2132	191.1103			L	2030.2008	1015.6041	2013.1743	1007.0908	2012.1903	1006.5988	18
5	526.2984	263.6528	509.2718	255.1396			Q	***1917.1168***	959.0620	1900.0902	950.5488	1899.1062	950.0567	17
6	639.3824	320.1949	622.3559	311.6816			L	***1789.0582***	895.0327	1772.0316	886.5195	1771.0476	886.0275	16
7	726.4145	363.7109	709.3879	355.1976	708.4039	354.7056	S	***1675.9741***	838.4907	1658.9476	829.9774	1657.9636	829.4854	15
8	**863.4734**	432.2403	846.4468	423.7271	845.4628	423.2350	H	***1588.9421***	794.9747	1571.9156	786.4614	1570.9315	785.9694	14
9	**978.5003**	489.7538	961.4738	481.2405	960.4898	480.7485	N	***1451.8832***	726.4452	1434.8566	717.9320	1433.8726	717.4400	13
10	**1091.5844**	546.2958	1074.5578	537.7826	1073.5738	537.2905	L	***1336.8562***	668.9318	1319.8297	660.4185	1318.8457	659.9265	12
11	1178.6164	589.8118	1161.5899	581.2986	1160.6058	580.8066	S	***1223.7722***	612.3897	1206.7456	603.8765	1205.7616	603.3844	11
12	**1291.7005**	646.3539	1274.6739	637.8406	1273.6899	637.3486	L	***1136.7402***	568.8737	1119.7136	560.3604			10
13	**1390.7689**	695.8881	1373.7423	687.3748	1372.7583	686.8828	V	***1023.6561***	512.3317	1006.6295	503.8184			9
14	**1503.8530**	752.4301	1486.8264	743.9168	1485.8424	743.4248	I	***924.5877***	462.7975	907.5611	454.2842			8
15	**1616.9370**	808.9721	1599.9105	800.4589	1598.9265	799.9669	L	***811.5036***	406.2554	794.4771	397.7422			7
16	**1716.0054**	858.5064	1698.9789	849.9931	1697.9949	849.5011	V	***698.4196***	349.7134	681.3930	341.2001			6
17	1813.0582	907.0327	1796.0316	898.5195	1795.0476	898.0275	P	***599.3511***	300.1792	582.3246	291.6659			5
18	**1941.1168**	971.0620	1924.0902	962.5488	1923.1062	962.0567	Q	502.2984	251.6528	485.2718	243.1395			4
19	2055.1597	1028.0835	2038.1332	1019.5702	2037.1491	1019.0782	N	***374.2398***	187.6235	357.2132	179.1103			3
20	2168.2438	1084.6255	2151.2172	1076.1122	2150.2332	1075.6202	L	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.1	2313.3420	0.0090	VGQLQLSHNLSLVILVPQNLK	Deamidated N9 93.34%
57.4	2313.3420	0.0090	VGQLQLSHNLSLVILVPQNLK	Deamidated Q5 4.03%
54.0	2313.3420	0.0090	VGQLQLSHNLSLVILVPQNLK	Deamidated Q3 1.82%
48.9	2313.3420	0.0090	VGQLQLSHNLSLVILVPQNLK	Deamidated Q18 0.57%
45.4	2313.3420	0.0090	VGQLQLSHNLSLVILVPQNLK	Deamidated N19 0.25%
41.3	2312.3580	0.9930	VGQLQLSHNLSLVILVPQNLK	

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

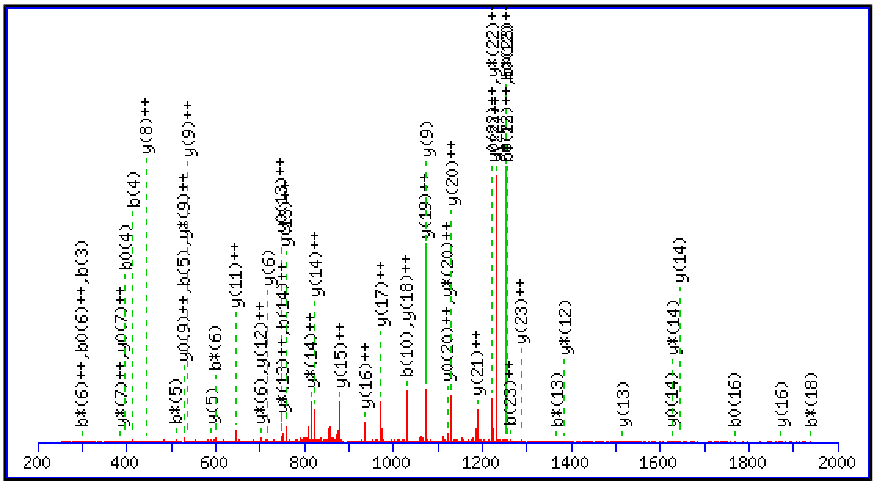
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLSNNSDANLELINTWVAKNTNNK**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

Match to Query 22468: 2672.351022 from(891.790950,3+) intensity(156419.8281) rtinseconds(1942) scans(4988) index(9640)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum4280_scans__4988
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

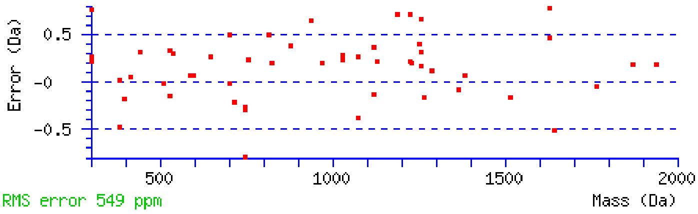
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

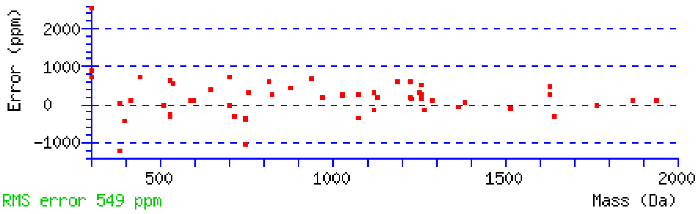


Monoisotopic mass of neutral peptide Mr(calc): 2672.3405
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 66 **Expect:** 5.9e-005
Matches : 54/260 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							24
2	213.1598	107.0835					L	2574.2794	1287.6434	2557.2529	1279.1301	2556.2689	1278.6381	23
3	**300.1918**	150.5995			282.1812	141.5942	S	2461.1954	1231.1013	2444.1688	1222.5880	2443.1848	1222.0960	22
4	**415.2187**	208.1130	398.1922	199.5997	397.2082	199.1077	N	2374.1633	1187.5853	2357.1368	1179.0720	2356.1528	1178.5800	21
5	**529.2617**	265.1345	512.2351	256.6212	511.2511	256.1292	N	2259.1364	1130.0718	2242.1098	1121.5586	2241.1258	1121.0666	20
6	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	S	2145.0935	1073.0504	2128.0669	1064.5371	2127.0829	1064.0451	19
7	731.3206	366.1639	714.2941	357.6507	713.3101	357.1587	D	2058.0614	1029.5344	2041.0349	1021.0211	2040.0509	1020.5291	18
8	802.3577	401.6825	785.3312	393.1692	784.3472	392.6772	A	1943.0345	972.0209	1926.0080	963.5076	1925.0239	963.0156	17
9	916.4007	458.7040	899.3741	450.1907	898.3901	449.6987	N	**1871.9974**	936.5023	1854.9708	927.9891	1853.9868	927.4970	16
10	**1029.4847**	515.2460	1012.4582	506.7327	1011.4742	506.2407	L	1757.9545	879.4809	1740.9279	870.9676	1739.9439	870.4756	15
11	1158.5273	579.7673	1141.5008	571.2540	1140.5168	570.7620	E	**1644.8704**	822.9388	1627.8438	814.4256	1626.8598	813.9336	14
12	1271.6114	636.3093	1254.5848	627.7961	1253.6008	627.3040	L	**1515.8278**	758.4175	1498.8013	749.9043	1497.8172	749.4123	13
13	1384.6954	692.8514	1367.6689	684.3381	1366.6849	683.8461	I	1402.7437	701.8755	1385.7172	693.3622	1384.7332	692.8702	12
14	1498.7384	749.8728	1481.7118	741.3596	1480.7278	740.8675	N	1289.6597	645.3335	1272.6331	636.8202	1271.6491	636.3282	11
15	1599.7861	800.3967	1582.7595	791.8834	1581.7755	791.3914	T	1175.6167	588.3120	1158.5902	579.7987	1157.6062	579.3067	10
16	1785.8654	893.4363	1768.8388	884.9230	1767.8548	884.4310	W	**1074.5691**	537.7882	1057.5425	529.2749	1056.5585	528.7829	9
17	1884.9338	942.9705	1867.9072	934.4573	1866.9232	933.9652	V	888.4898	444.7485	871.4632	436.2352	870.4792	435.7432	8
18	1955.9709	978.4891	1938.9443	969.9758	1937.9603	969.4838	A	789.4213	395.2143	772.3948	386.7010	771.4108	386.2090	7
19	2084.0659	1042.5366	2067.0393	1034.0233	2066.0553	1033.5313	K	**718.3842**	359.6958	701.3577	351.1825	700.3737	350.6905	6
20	2198.1088	1099.5580	2181.0822	1091.0448	2180.0982	1090.5527	N	**590.2893**	295.6483	573.2627	287.1350	572.2787	286.6430	5
21	2299.1565	1150.0819	2282.1299	1141.5686	2281.1459	1141.0766	T	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
22	2413.1994	1207.1033	2396.1728	1198.5901	2395.1888	1198.0981	N	375.1987	188.1030	358.1721	179.5897			3
23	2527.2423	1264.1248	2510.2158	1255.6115	2509.2318	1255.1195	N	261.1557	131.0815	244.1292	122.5682			2

24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.3	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N4 65.07%
59.2	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N14 12.69%
59.1	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N9 12.48%
57.6	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N5 8.88%
53.0	2671.3565	0.9945	VLSNNSDANLELINTWVAKNTNNK	
42.8	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N23 0.29%
42.8	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N22 0.29%
42.8	2672.3405	0.0105	VLSNNSDANLELINTWVAKNTNNK	Deamidated N20 0.29%
4.5	2671.3488	1.0022	LMNIFLKDSITTWEILAVSMSDK	
3.2	2672.3558	-0.0048	YSYDLNGNLHLLSPGNSARLTPLR	

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

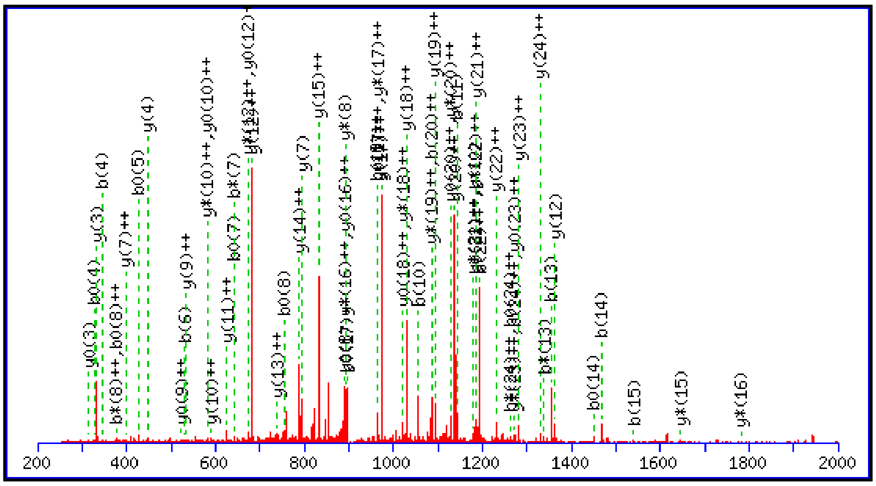
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIRDTFVNASR**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

Match to Query 25392: 2717.388342 from(906.803390,3+) intensity(130552.4375) rtinseconds(2038) scans(5245) index(22718)
Title: 111019_Est_MI_YS_G_03Spectrum4593_scans__5245
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

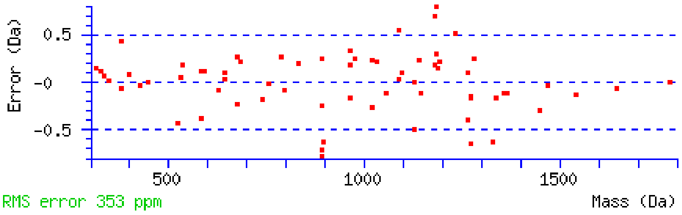
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

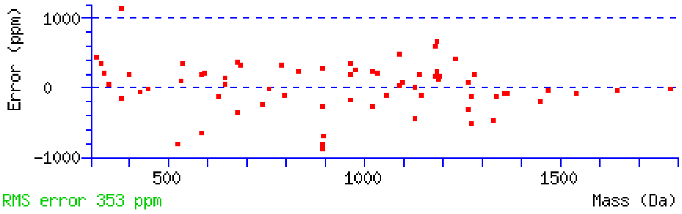


Monoisotopic mass of neutral peptide Mr(calc): 2717.3773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 65 **Expect:** 8.2e-005
Matches : 68/270 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					**G**							**25**
2	157.0972	79.0522					**V**	2661.3631	1331.1852	2644.3366	1322.6719	2643.3525	1322.1799	**24**
3	258.1448	129.5761			240.1343	120.5708	**T**	2562.2947	1281.6510	2545.2681	1273.1377	2544.2841	1272.6457	**23**
4	**345.1769**	173.0921			327.1663	164.0868	**S**	2461.2470	1231.1271	2444.2205	1222.6139	2443.2364	1222.1219	**22**
5	444.2453	222.6263			426.2347	213.6210	**V**	2374.2150	1187.6111	2357.1884	1179.0979	2356.2044	1178.6058	**21**
6	**531.2773**	266.1423			513.2667	257.1370	**S**	2275.1466	1138.0769	2258.1200	1129.5636	2257.1360	1129.0716	**20**
7	659.3359	330.1716	642.3093	321.6583	641.3253	321.1663	**Q**	2188.1145	1094.5609	2171.0880	1086.0476	2170.1040	1085.5556	**19**
8	772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	**I**	2060.0560	1030.5316	2043.0294	1022.0183	2042.0454	1021.5263	**18**
9	919.4884	460.2478	902.4618	451.7345	901.4778	451.2425	**F**	1946.9719	973.9896	1929.9454	965.4763	1928.9613	964.9843	**17**
10	**1056.5473**	528.7773	1039.5207	520.2640	1038.5367	519.7720	**H**	1799.9035	900.4554	1782.8769	891.9421	1781.8929	891.4501	**16**
11	**1143.5793**	572.2933	1126.5528	563.7800	1125.5687	563.2880	**S**	1662.8446	831.9259	1645.8180	823.4127	1644.8340	822.9206	**15**
12	1240.6321	620.8197	1223.6055	612.3064	1222.6215	611.8144	**P**	1575.8125	788.4099	1558.7860	779.8966	1557.8020	779.4046	**14**
13	**1355.6590**	678.3331	1338.6325	669.8199	1337.6484	669.3279	**D**	1478.7598	739.8835	1461.7332	731.3703	1460.7492	730.8782	**13**
14	**1468.7431**	734.8752	1451.7165	726.3619	1450.7325	725.8699	**L**	**1363.7328**	682.3701	1346.7063	673.8568	1345.7223	673.3648	**12**
15	**1539.7802**	770.3937	1522.7536	761.8805	1521.7696	761.3884	**A**	1250.6488	625.8280	1233.6222	617.3148	1232.6382	616.8227	**11**
16	1652.8642	826.9358	1635.8377	818.4225	1634.8537	817.9305	**I**	**1179.6117**	590.3095	1162.5851	581.7962	1161.6011	581.3042	**10**
17	1808.9654	904.9863	1791.9388	896.4730	1790.9548	895.9810	**R**	1066.5276	533.7674	1049.5010	525.2542	1048.5170	524.7622	**9**
18	1923.9923	962.4998	1906.9658	953.9865	1905.9817	953.4945	**D**	910.4265	455.7169	893.3999	447.2036	892.4159	446.7116	**8**
19	2025.0400	1013.0236	2008.0134	1004.5104	2007.0294	1004.0183	**T**	**795.3995**	398.2034	778.3730	389.6901	777.3890	389.1981	**7**
20	2172.1084	1086.5578	2155.0818	1078.0446	2154.0978	1077.5526	**F**	694.3519	347.6796	677.3253	339.1663	676.3413	338.6743	**6**
21	2271.1768	1136.0920	2254.1503	1127.5788	2253.1662	1127.0868	**V**	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	**5**
22	2386.2038	1193.6055	2369.1772	1185.0922	2368.1932	1184.6002	**N**	**448.2150**	224.6112	431.1885	216.0979	430.2045	215.6059	**4**
23	2457.2409	1229.1241	2440.2143	1220.6108	2439.2303	1220.1188	**A**	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	**3**

24	2544.2729	1272.6401	2527.2463	1264.1268	2526.2623	1263.6348	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.6	2717.3773	0.0110	GVTSVSQIFHSPDLAIRDTFVNASR	Deamidated N22 99.71%
39.2	2717.3773	0.0110	GVTSVSQIFHSPDLAIRDTFVNASR	Deamidated Q7 0.29%
38.7	2716.3933	0.9950	GVTSVSQIFHSPDLAIRDTFVNASR	
5.0	2715.3698	2.0186	LHRACVLGDGGNNGPGCIVLVTPPSR	
3.7	2717.3793	0.0091	AIQMAQEQATDTEILERKTVLPSK	
3.7	2717.3793	0.0091	AIQMAQEQATDTEILERKTVLPSK	
3.7	2717.3793	0.0091	AIQMAQEQATDTEILERKTVLPSK	
2.9	2715.3789	2.0095	KISIVTNWNAPQNIEEQDIVMKK	
2.9	2715.3789	2.0095	KISIVTNWNAPQNIEEQDIVMKK	
2.9	2715.3789	2.0095	KISIVTNWNAPQNIEEQDIVMKK	

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

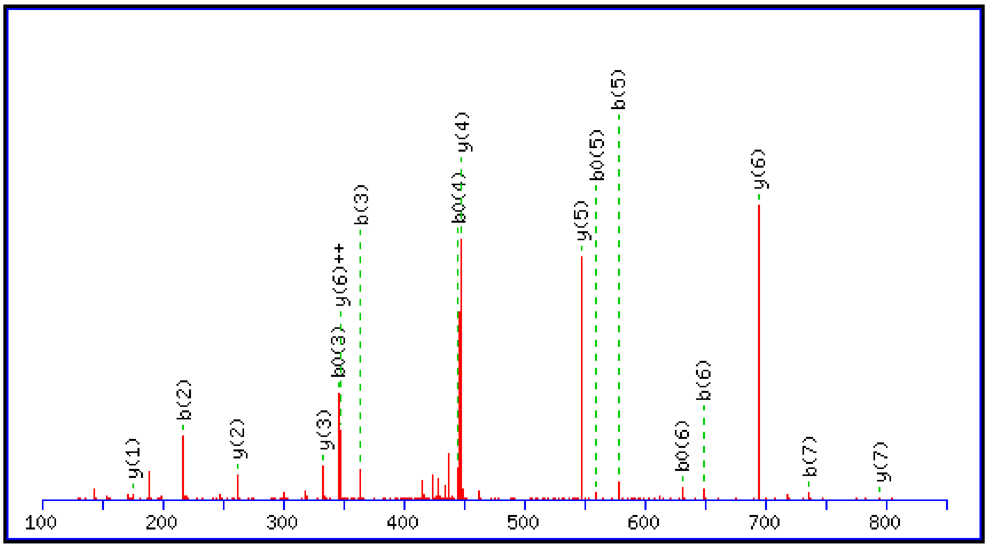
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTFVNASR**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

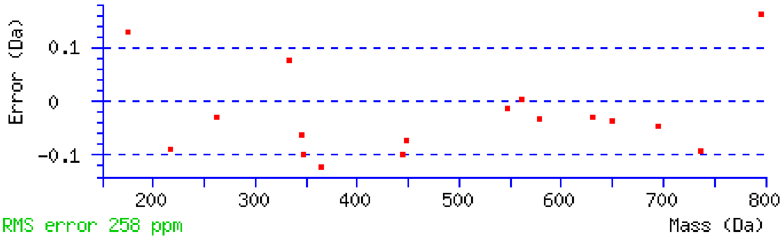
Match to Query 15: 909.419728 from(455.717140,2+) intensity(181831.8594) rtinseconds(434) scans(779) index(12274)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum644_scans__779
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

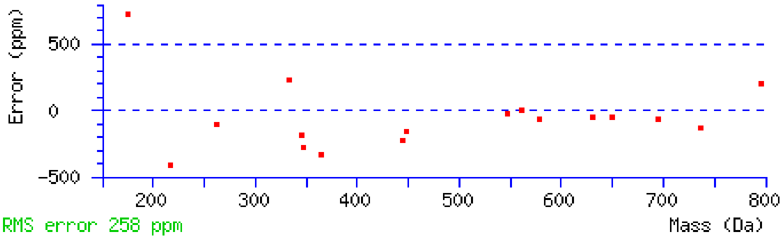
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 909.4192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00033
Matches : 17/74 fragment ions using 28 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							8
2	**217.0819**	109.0446			199.0713	100.0393	T	***795.3995***	398.2034	778.3730	389.6901	777.3890	389.1981	7
3	**364.1503**	182.5788			346.1397	173.5735	F	***694.3519***	347.6796	677.3253	339.1663	676.3413	338.6743	6
4	463.2187	232.1130			445.2082	223.1077	V	***547.2835***	274.1454	530.2569	265.6321	529.2729	265.1401	5
5	**578.2457**	289.6265	561.2191	281.1132	560.2351	280.6212	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
6	**649.2828**	325.1450	632.2562	316.6318	631.2722	316.1397	A	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
7	**736.3148**	368.6610	719.2883	360.1478	718.3042	359.6558	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.7	909.4192	0.0005	DTFVNASR
20.0	909.4192	0.0005	NFTPSTSR
14.2	909.4192	0.0005	DTFTRSPS
13.3	909.4152	0.0045	SGTSGSATSR
12.7	909.4192	0.0005	TDTPFSSR
5.6	908.4208	0.9989	IMAQMQR
5.2	907.4134	2.0063	SQQTLDSK
4.3	909.4192	0.0005	VFTTNNGR
4.0	909.4226	-0.0028	GMKTSGANK
4.0	909.4225	-0.0028	KSANAKGSM

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

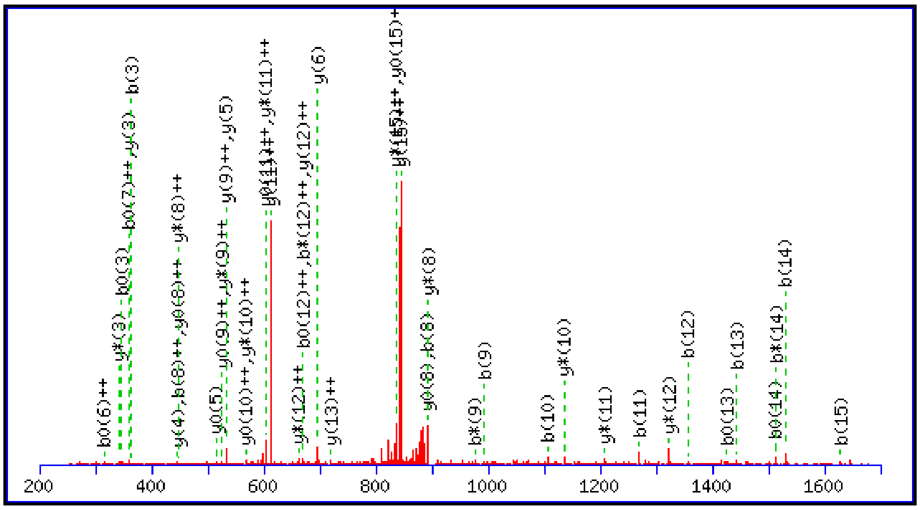
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTFVNASRTLYSSSPR**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

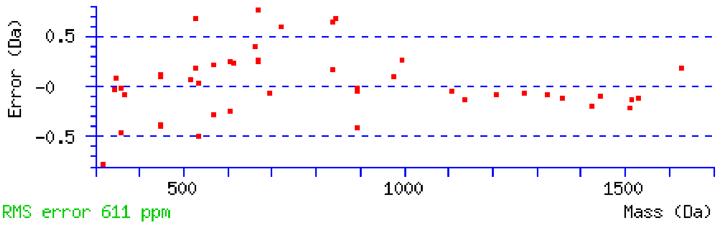
Match to Query 10896: 1800.872968 from(901.443760,2+) intensity(151624.7188) rtinseconds(1250) scans(2978) index(25267)
Title: 111019_Est_MI_YS_G_07Spectrum2519_scans__2978
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

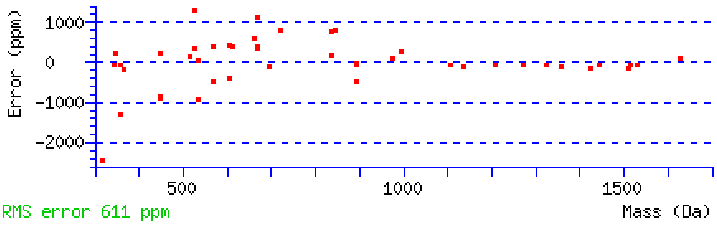
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1800.8642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
Ions Score: 50  Expect: 0.0021
Matches : 46/168 fragment ions using 72 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							16
2	217.0819	109.0446			199.0713	100.0393	T	1686.8446	843.9259	1669.8180	835.4127	1668.8340	834.9206	15
3	***364.1503***	182.5788			346.1397	173.5735	F	1585.7969	793.4021	1568.7703	784.8888	1567.7863	784.3968	14
4	463.2187	232.1130			445.2082	223.1077	V	1438.7285	719.8679	1421.7019	711.3546	1420.7179	710.8626	13
5	578.2457	289.6265	561.2191	281.1132	560.2351	280.6212	N	1339.6601	670.3337	1322.6335	661.8204	1321.6495	661.3284	12
6	649.2828	325.1450	632.2562	316.6318	631.2722	316.1397	A	1224.6331	612.8202	1207.6066	604.3069	1206.6226	603.8149	11
7	736.3148	368.6610	719.2883	360.1478	718.3042	359.6558	S	1153.5960	577.3016	1136.5695	568.7884	1135.5854	568.2964	10
8	***892.4159***	446.7116	875.3894	438.1983	874.4054	437.7063	R	1066.5640	533.7856	1049.5374	525.2724	1048.5534	524.7803	9
9	***993.4636***	497.2354	976.4371	488.7222	975.4530	488.2302	T	910.4629	455.7351	893.4363	447.2218	892.4523	446.7298	8
10	***1106.5477***	553.7775	1089.5211	545.2642	1088.5371	544.7722	L	809.4152	405.2112	792.3886	396.6980	791.4046	396.2060	7
11	***1269.6110***	635.3091	1252.5844	626.7959	1251.6004	626.3039	Y	**696.3311**	348.6692	679.3046	340.1559	678.3206	339.6639	6
12	***1356.6430***	678.8251	1339.6165	670.3119	1338.6325	669.8199	S	**533.2678**	267.1375	516.2413	258.6243	515.2572	258.1323	5
13	***1443.6751***	722.3412	1426.6485	713.8279	1425.6645	713.3359	S	**446.2358**	223.6215	429.2092	215.1082	428.2252	214.6162	4
14	***1530.7071***	765.8572	1513.6805	757.3439	1512.6965	756.8519	S	**359.2037**	180.1055	342.1772	171.5922	341.1932	171.1002	3
15	***1627.7598***	814.3836	1610.7333	805.8703	1609.7493	805.3783	P	272.1717	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.1	1800.8642	0.0087	DTFVNASRTLYSSSPR
10.9	1799.8611	1.0119	IVVYTACNNGSSSVISK
4.9	1799.8764	0.9966	IGCYVTIFQNISNLR
3.5	1800.8754	-0.0024	DEAQLYKEEHLRNR
3.2	1800.8741	-0.0011	ELQGAQEDLGISLSSPR
3.0	1800.8689	0.0040	NEGHHLKMHTSLSGPR
3.0	1800.8788	-0.0059	DSLRQLEAMVQQDPR
2.6	1799.8762	0.9967	ASSAQSGGSSGGPAVPTVQR
1.8	1799.8624	1.0105	LAQFDYGRKCSEVAR
1.6	1800.8676	0.0054	NLSPQSPKGQLAACSNK

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

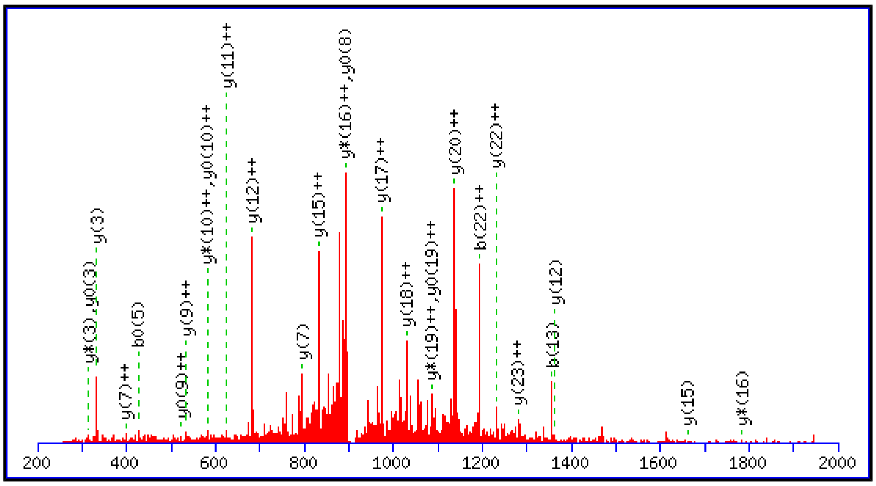
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVTSVSQIFHSPDLAIRDTFVNASR**
Found in **B4E1F0** in **con_Xuniprot_HUMAN3**, B4E1F0_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=2 SV=1

Match to Query 25401: 2718.365082 from(907.128970,3+) intensity(13913.7373) rtinseconds(3158) scans(8328) index(22947)
Title: 111019_Est_MI_YS_G_03Spectrum7334_scans__8328
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

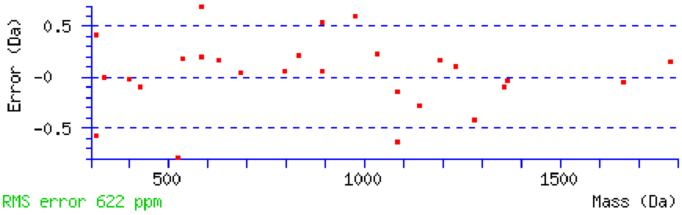
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

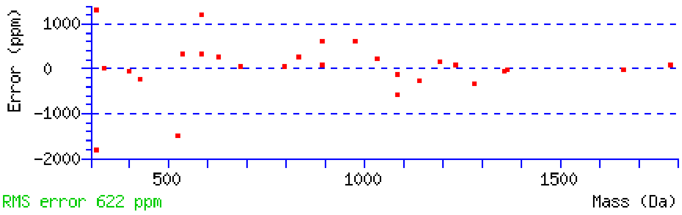


Monoisotopic mass of neutral peptide Mr(calc): 2718.3613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.053
Matches : 27/270 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							25
2	157.0972	79.0522					V	2662.3471	1331.6772	2645.3206	1323.1639	2644.3366	1322.6719	24
3	258.1448	129.5761			240.1343	120.5708	T	2563.2787	1282.1430	2546.2522	1273.6297	2545.2681	1273.1377	23
4	345.1769	173.0921			327.1663	164.0868	S	2462.2310	1231.6192	2445.2045	1223.1059	2444.2205	1222.6139	22
5	444.2453	222.6263			426.2347	213.6210	V	2375.1990	1188.1031	2358.1725	1179.5899	2357.1884	1179.0979	21
6	531.2773	266.1423			513.2667	257.1370	S	2276.1306	1138.5689	2259.1040	1130.0557	2258.1200	1129.5636	20
7	660.3199	330.6636	643.2933	322.1503	642.3093	321.6583	Q	2189.0986	1095.0529	2172.0720	1086.5396	2171.0880	1086.0476	19
8	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	I	2060.0560	1030.5316	2043.0294	1022.0183	2042.0454	1021.5263	18
9	920.4724	460.7398	903.4458	452.2266	902.4618	451.7345	F	1946.9719	973.9896	1929.9454	965.4763	1928.9613	964.9843	17
10	1057.5313	529.2693	1040.5047	520.7560	1039.5207	520.2640	H	1799.9035	900.4554	1782.8769	891.9421	1781.8929	891.4501	16
11	1144.5633	572.7853	1127.5368	564.2720	1126.5528	563.7800	S	**1662.8446**	831.9259	1645.8180	823.4127	1644.8340	822.9206	15
12	1241.6161	621.3117	1224.5895	612.7984	1223.6055	612.3064	P	1575.8125	788.4099	1558.7860	779.8966	1557.8020	779.4046	14
13	1356.6430	678.8251	1339.6165	670.3119	1338.6325	669.8199	D	1478.7598	739.8835	1461.7332	731.3703	1460.7492	730.8782	13
14	1469.7271	735.3672	1452.7005	726.8539	1451.7165	726.3619	L	**1363.7328**	682.3701	1346.7063	673.8568	1345.7223	673.3648	12
15	1540.7642	770.8857	1523.7377	762.3725	1522.7536	761.8805	A	1250.6488	625.8280	1233.6222	617.3148	1232.6382	616.8227	11
16	1653.8483	827.4278	1636.8217	818.9145	1635.8377	818.4225	I	1179.6117	590.3095	1162.5851	581.7962	1161.6011	581.3042	10
17	1809.9494	905.4783	1792.9228	896.9651	1791.9388	896.4730	R	1066.5276	533.7674	1049.5010	525.2542	1048.5170	524.7622	9
18	1924.9763	962.9918	1907.9498	954.4785	1906.9658	953.9865	D	910.4265	455.7169	893.3999	447.2036	892.4159	446.7116	8
19	2026.0240	1013.5156	2008.9974	1005.0024	2008.0134	1004.5104	T	**795.3995**	398.2034	778.3730	389.6901	777.3890	389.1981	7
20	2173.0924	1087.0498	2156.0659	1078.5366	2155.0818	1078.0446	F	694.3519	347.6796	677.3253	339.1663	676.3413	338.6743	6
21	2272.1608	1136.5841	2255.1343	1128.0708	2254.1503	1127.5788	V	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
22	2387.1878	1194.0975	2370.1612	1185.5842	2369.1772	1185.0922	N	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4

23	2458.2249	1229.6161	2441.1983	1221.1028	2440.2143	1220.6108	**A**	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	**3**
24	2545.2569	1273.1321	2528.2304	1264.6188	2527.2463	1264.1268	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GVTSVSQIFHSPDLAIRDTFVNASR
(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	2718.3613	0.0038	GVTSVSQIFHSPDLAIRDTFVNASR
9.2	2716.3629	2.0022	KISIVTNWNAPQNIEEQDIVMKK
7.5	2716.3663	1.9988	MAVVLPAVVEELLSEMAAAVQESARS
4.6	2717.3508	1.0143	QKSPEQQETVLDGNLIIRYDVDR
2.5	2717.3507	1.0143	QQAEARNAGLLSLLGQSVEEIDRFA
2.3	2718.3759	-0.0108	NKAGPLAEGQPNAVVLPQGCVRQDAK
2.2	2716.3602	2.0049	DRGLYVCAARNSAGQTLSAVQLHVK
2.0	2716.3629	2.0022	AKNYLSDVVKSMNQITELAAEYTK
2.0	2716.3629	2.0022	MQTSVSEIEQVLPVLITENIWNR
2.0	2716.3629	2.0022	MQTSVSEIEQVLPVLITENIWNR

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

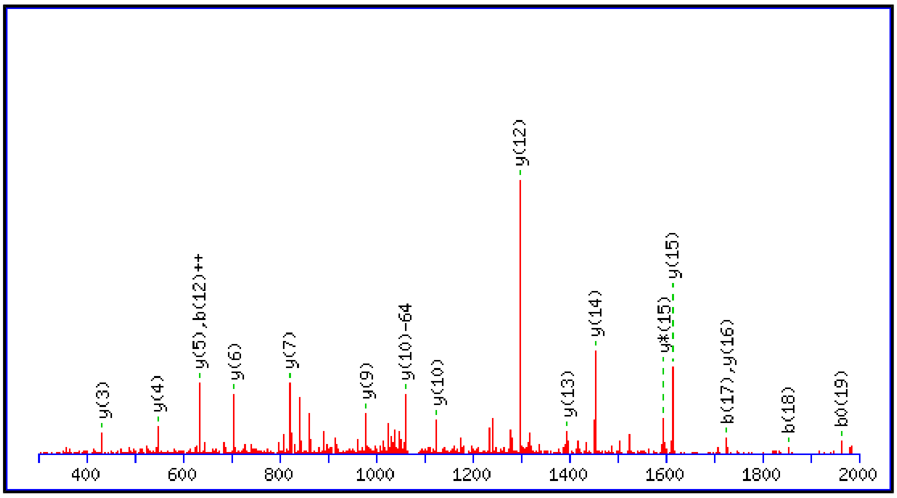
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

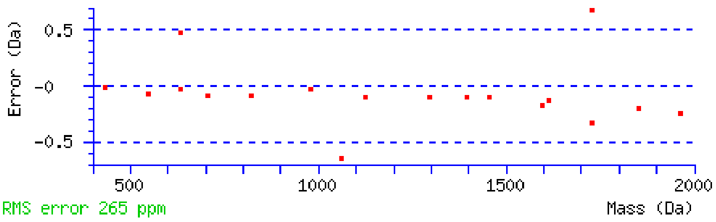
Match to Query 14427: 2155.910508 from(1078.962530,2+) intensity(40049.3516) rtinseconds(713) scans(1537) index(10775)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum1278_scans__1537
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

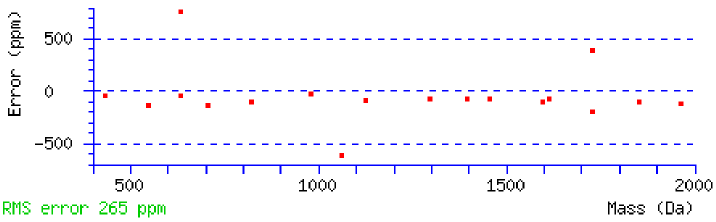
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2155.8998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N14 : Deamidated (NQ)
Ions Score: 118 **Expect:** 8e-011
Matches : 18/320 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	114.0913	57.5493					L							20
2	215.1390	108.0731			197.1285	99.0679	T	2043.8230	1022.4151	2026.7964	1013.9019	2025.8124	1013.4099	19
3	330.1660	165.5866			312.1554	156.5813	D	1942.7753	971.8913	1925.7488	963.3780	1924.7647	962.8860	18
4	431.2136	216.1105			413.2031	207.1052	T	1827.7484	914.3778	1810.7218	905.8645	1809.7378	905.3725	17
5	544.2977	272.6525			526.2871	263.6472	I	***1726.7007***	863.8540	1709.6741	855.3407	1708.6901	854.8487	16
6	704.3284	352.6678			686.3178	343.6625	C	***1613.6166***	807.3120	1596.5901	798.7987	1595.6061	798.3067	15
7	761.3498	381.1785			743.3393	372.1733	G	***1453.5860***	727.2966	1436.5594	718.7834	1435.5754	718.2913	14
8	860.4182	430.7128			842.4077	421.7075	V	***1396.5645***	698.7859	1379.5380	690.2726	1378.5539	689.7806	13
9	917.4397	459.2235			899.4291	450.2182	G	***1297.4961***	649.2517	1280.4696	640.7384	1279.4855	640.2464	12
10	1032.4666	516.7370	1015.4401	508.2237	1014.4561	507.7317	N	1240.4746	620.7410	1223.4481	612.2277	1222.4641	611.7357	11
11	1179.5020	590.2547	1162.4755	581.7414	1161.4915	581.2494	M	***1125.4477***	563.2275	1108.4211	554.7142	1107.4371	554.2222	10
12	1266.5341	633.7707	1249.5075	625.2574	1248.5235	624.7654	S	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	9
13	1337.5712	669.2892	1320.5446	660.7760	1319.5606	660.2839	A	891.3803	446.1938	874.3537	437.6805	873.3697	437.1885	8
14	1452.5981	726.8027	1435.5716	718.2894	1434.5876	717.7974	N	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	7
15	1523.6352	762.3213	1506.6087	753.8080	1505.6247	753.3160	A	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	6
16	1610.6673	805.8373	1593.6407	797.3240	1592.6567	796.8320	S	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	5
17	**1725.6942**	863.3507	1708.6677	854.8375	1707.6836	854.3455	D	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	4
18	**1853.7528**	927.3800	1836.7262	918.8668	1835.7422	918.3747	Q	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
19	1982.7954	991.9013	1965.7688	983.3881	1964.7848	982.8960	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
118.2	2155.8998	0.0107	LTDTICGVGNMSANASDQER	Deamidated N10, N14 99.87%
89.1	2155.8998	0.0107	LTDTICGVGNMSANASDQER	Deamidated N10, Q18 0.12%
73.6	2155.8998	0.0107	LTDTICGVGNMSANASDQER	Deamidated N14, Q18 0.00%
55.7	2154.9158	0.9948	LTDTICGVGNMSANASDQER	
43.8	2154.9158	0.9948	LTDTICGVGNMSANASDQER	
38.2	2154.9158	0.9948	LTDTICGVGNMSANASDQER	
6.7	2155.9141	-0.0036	EEEESVNASSFGQNTNKER	
2.3	2155.9141	-0.0036	EEEESVNASSFGQNTNKER	
2.0	2155.9141	-0.0036	EEEESVNASSFGQNTNKER	
1.9	2154.9099	1.0006	GNHSFDLCFCGREGANLSI	

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

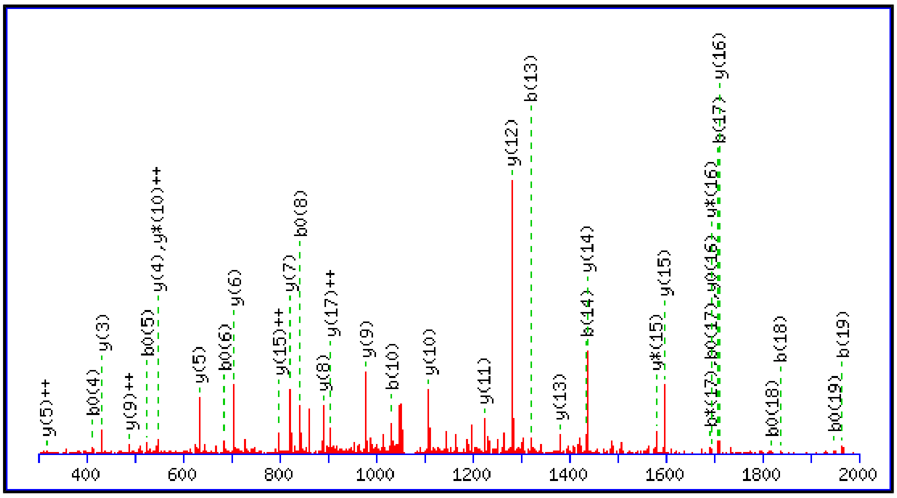
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

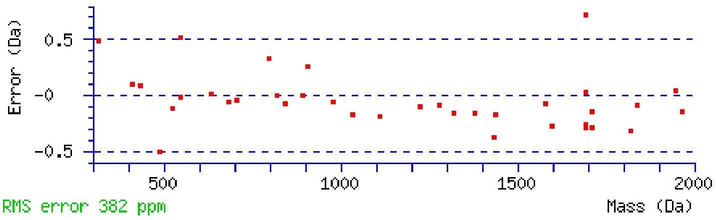
Match to Query 14389: 2139.913908 from(1070.964230,2+) intensity(13382.8516) rtinseconds(1149) scans(2650) index(12480)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2297_scans__2650
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

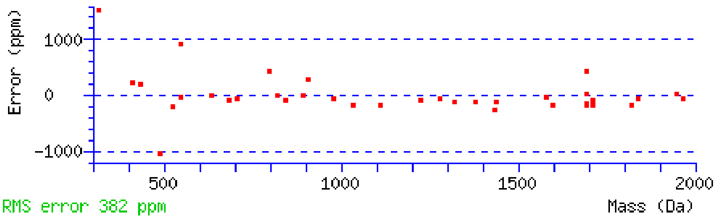
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2139.9048
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
N14 : Deamidated (NQ)
Ions Score: 104 **Expect:** 2.5e-009
Matches : 36/206 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							20
2	215.1390	108.0731			197.1285	99.0679	T	2027.8281	1014.4177	2010.8015	1005.9044	2009.8175	1005.4124	19
3	330.1660	165.5866			312.1554	156.5813	D	1926.7804	963.8938	1909.7538	955.3806	1908.7698	954.8886	18
4	431.2136	216.1105			413.2031	207.1052	T	1811.7535	906.3804	1794.7269	897.8671	1793.7429	897.3751	17
5	544.2977	272.6525			526.2871	263.6472	I	***1710.7058***	855.8565	1693.6792	847.3433	1692.6952	846.8512	16
6	704.3284	352.6678			686.3178	343.6625	C	***1597.6217***	799.3145	1580.5952	790.8012	1579.6111	790.3092	15
7	761.3498	381.1785			743.3393	372.1733	G	***1437.5911***	719.2992	1420.5645	710.7859	1419.5805	710.2939	14
8	860.4182	430.7128			842.4077	421.7075	V	***1380.5696***	690.7884	1363.5431	682.2752	1362.5590	681.7832	13
9	917.4397	459.2235			899.4291	450.2182	G	***1281.5012***	641.2542	1264.4746	632.7410	1263.4906	632.2489	12
10	**1032.4666**	516.7370	1015.4401	508.2237	1014.4561	507.7317	N	***1224.4797***	612.7435	1207.4532	604.2302	1206.4692	603.7382	11
11	1163.5071	582.2572	1146.4806	573.7439	1145.4966	573.2519	M	***1109.4528***	555.2300	1092.4262	546.7168	1091.4422	546.2247	10
12	1250.5392	625.7732	1233.5126	617.2599	1232.5286	616.7679	S	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	9
13	**1321.5763**	661.2918	1304.5497	652.7785	1303.5657	652.2865	A	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	8
14	**1436.6032**	718.8052	1419.5767	710.2920	1418.5926	709.8000	N	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	7
15	1507.6403	754.3238	1490.6138	745.8105	1489.6298	745.3185	A	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	6
16	1594.6724	797.8398	1577.6458	789.3265	1576.6618	788.8345	S	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	5
17	**1709.6993**	855.3533	1692.6727	846.8400	1691.6887	846.3480	D	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	4
18	**1837.7579**	919.3826	1820.7313	910.8693	1819.7473	910.3773	Q	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
19	**1966.8005**	983.9039	1949.7739	975.3906	1948.7899	974.8986	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.1	2139.9048	0.0091	LTDTICGVGNMSANASDQER	Deamidated N10, N14 99.44%
81.4	2139.9048	0.0091	LTDTICGVGNMSANASDQER	Deamidated N10, Q18 0.53%
69.5	2139.9048	0.0091	LTDTICGVGNMSANASDQER	Deamidated N14, Q18 0.03%
42.4	2138.9208	0.9931	LTDTICGVGNMSANASDQER	
23.4	2138.9208	0.9931	LTDTICGVGNMSANASDQER	
22.4	2138.9208	0.9931	LTDTICGVGNMSANASDQER	
1.5	2139.9167	-0.0028	DSGDGYGSHTLCAYNLGEPK	
1.2	2139.9201	-0.0062	DLDSCNSDPVAVASCFVER	
0.9	2139.9208	-0.0069	CDEVRCTGNTTSPGMAGRR	

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

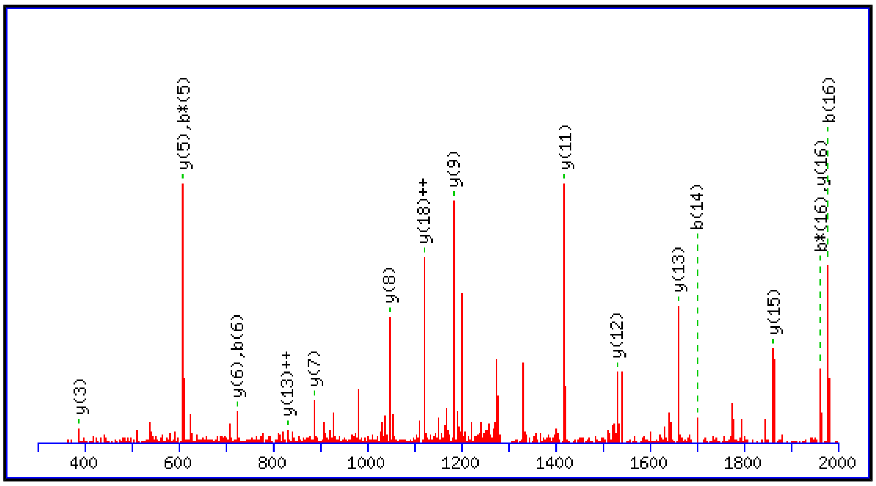
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYYNVSDEISFHCYDGYTLR**
Found in **B4E1Z4** in **con_Xuniprot_HUMAN3**, B4E1Z4_HUMAN Complement factor B OS=Homo sapiens GN=CFB PE=2 SV=1

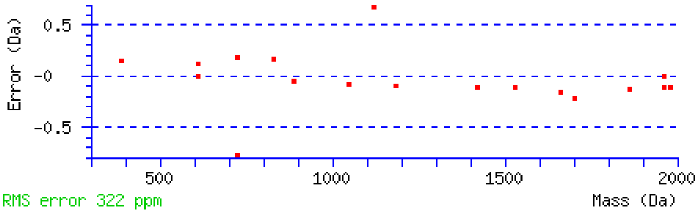
Match to Query 21973: 2586.106288 from(1294.060420,2+) intensity(42161.5117) rtinseconds(2080) scans(4958) index(16891)
Title: 111019_Est_MI_YP_G_06Spectrum4103_scans__4958
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

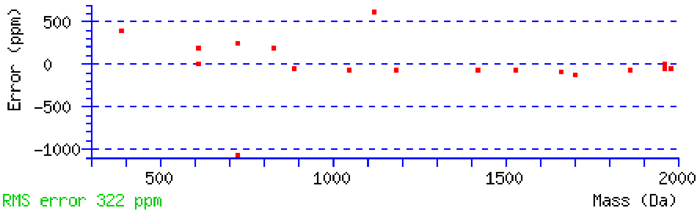
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2586.1009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 100 **Expect:** 6.7e-009
Matches : 18/228 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							21
2	185.0921	93.0497			167.0815	84.0444	P	2500.0762	1250.5417	2483.0496	1242.0284	2482.0656	1241.5364	20
3	348.1554	174.5813			330.1448	165.5761	Y	2403.0234	1202.0153	2385.9969	1193.5021	2385.0128	1193.0101	19
4	511.2187	256.1130			493.2082	247.1077	Y	2239.9601	1120.4837	2222.9335	1111.9704	2221.9495	1111.4784	18
5	626.2457	313.6265	609.2191	305.1132	608.2351	304.6212	N	2076.8967	1038.9520	2059.8702	1030.4387	2058.8862	1029.9467	17
6	**725.3141**	363.1607	708.2875	354.6474	707.3035	354.1554	V	***1961.8698***	981.4385	1944.8433	972.9253	1943.8592	972.4333	16
7	812.3461	406.6767	795.3196	398.1634	794.3355	397.6714	S	***1862.8014***	931.9043	1845.7748	923.3911	1844.7908	922.8991	15
8	927.3731	464.1902	910.3465	455.6769	909.3625	455.1849	D	1775.7694	888.3883	1758.7428	879.8750	1757.7588	879.3830	14
9	1056.4156	528.7115	1039.3891	520.1982	1038.4051	519.7062	E	***1660.7424***	830.8748	1643.7159	822.3616	1642.7319	821.8696	13
10	1169.4997	585.2535	1152.4732	576.7402	1151.4891	576.2482	I	***1531.6998***	766.3536	1514.6733	757.8403	1513.6893	757.3483	12
11	1256.5317	628.7695	1239.5052	620.2562	1238.5212	619.7642	S	***1418.6158***	709.8115	1401.5892	701.2982	1400.6052	700.8062	11
12	1403.6002	702.3037	1386.5736	693.7904	1385.5896	693.2984	F	1331.5837	666.2955	1314.5572	657.7822	1313.5732	657.2902	10
13	1540.6591	770.8332	1523.6325	762.3199	1522.6485	761.8279	H	***1184.5153***	592.7613	1167.4888	584.2480	1166.5048	583.7560	9
14	**1700.6897**	850.8485	1683.6632	842.3352	1682.6791	841.8432	C	***1047.4564***	524.2318	1030.4299	515.7186	1029.4458	515.2266	8
15	1863.7530	932.3802	1846.7265	923.8669	1845.7425	923.3749	Y	***887.4258***	444.2165	870.3992	435.7032	869.4152	435.2112	7
16	**1978.7800**	989.8936	1961.7534	981.3804	1960.7694	980.8883	D	***724.3624***	362.6849	707.3359	354.1716	706.3519	353.6796	6
17	2035.8015	1018.4044	2018.7749	1009.8911	2017.7909	1009.3991	G	***609.3355***	305.1714	592.3089	296.6581	591.3249	296.1661	5
18	2198.8648	1099.9360	2181.8382	1091.4228	2180.8542	1090.9307	Y	552.3140	276.6607	535.2875	268.1474	534.3035	267.6554	4
19	2299.9125	1150.4599	2282.8859	1141.9466	2281.9019	1141.4546	T	***389.2507***	195.1290	372.2241	186.6157	371.2401	186.1237	3
20	2412.9965	1207.0019	2395.9700	1198.4886	2394.9860	1197.9966	L	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.7	2586.1009	0.0054	SPYYNVSDEISFHCYDGYTLR
2.3	2584.0886	2.0177	ESKMSDWVNCNFDDYGAFLLR
1.9	2586.1093	-0.0030	ENTYTDNLDSTEELERGDDIQK
0.2	2586.1141	-0.0078	VQSTTENFMQYMKQFNSQNLK

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

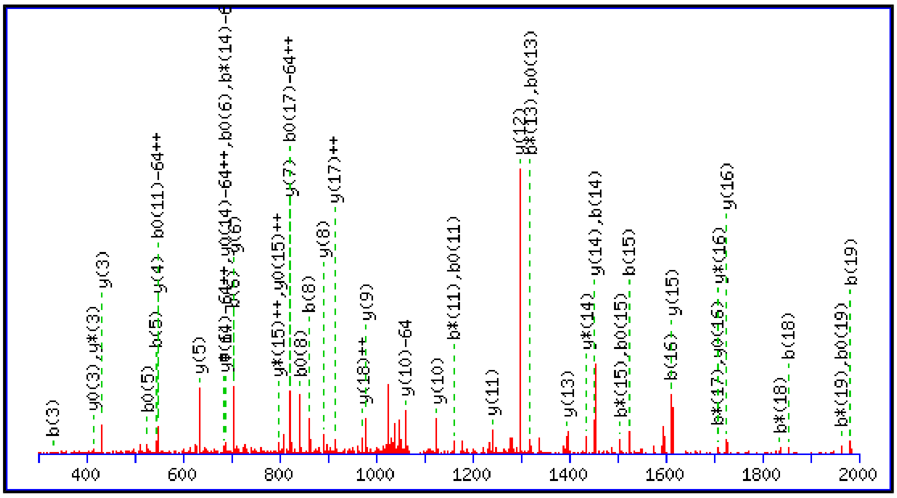
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

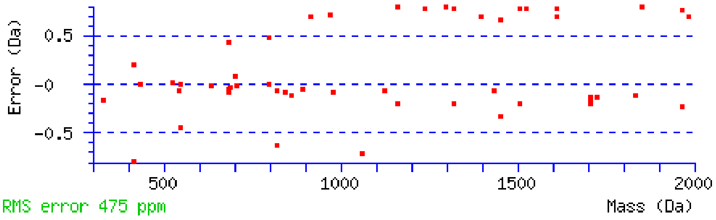
Match to Query 14432: 2155.920508 from(1078.967530,2+) intensity(19694.9141) rtinseconds(788) scans(1716) index(25990)
Title: 111019_Est_MI_YS_G_08Spectrum1471_scans__1716
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

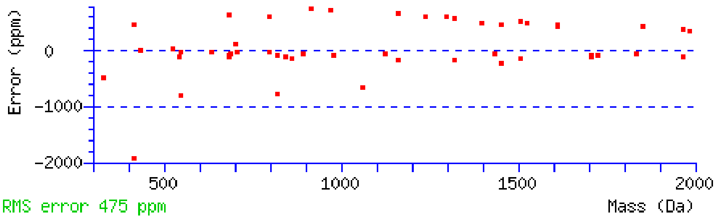
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2154.9158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N14 : Deamidated (NQ)
Ions Score: 74 **Expect:** 2.7e-006
Matches : 52/320 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							20
2	215.1390	108.0731			197.1285	99.0679	T	2042.8390	1021.9231	2025.8124	1013.4099	2024.8284	1012.9178	19
3	**330.1660**	165.5866			312.1554	156.5813	D	1941.7913	971.3993	1924.7647	962.8860	1923.7807	962.3940	18
4	431.2136	216.1105			413.2031	207.1052	T	1826.7644	913.8858	1809.7378	905.3725	1808.7538	904.8805	17
5	**544.2977**	272.6525			526.2871	263.6472	I	***1725.7167***	863.3620	1708.6901	854.8487	1707.7061	854.3567	16
6	**704.3284**	352.6678			686.3178	343.6625	C	***1612.6326***	806.8199	1595.6061	798.3067	1594.6220	797.8147	15
7	761.3498	381.1785			743.3393	372.1733	G	***1452.6020***	726.8046	1435.5754	718.2913	1434.5914	717.7993	14
8	**860.4182**	430.7128			842.4077	421.7075	V	***1395.5805***	698.2939	1378.5539	689.7806	1377.5699	689.2886	13
9	917.4397	459.2235			899.4291	450.2182	G	***1296.5121***	648.7597	1279.4855	640.2464	1278.5015	639.7544	12
10	1031.4826	516.2449	1014.4561	507.7317	1013.4721	507.2397	N	***1239.4906***	620.2489	1222.4641	611.7357	1221.4801	611.2437	11
11	1178.5180	589.7626	1161.4915	581.2494	1160.5075	580.7574	M	***1125.4477***	563.2275	1108.4211	554.7142	1107.4371	554.2222	10
12	1265.5501	633.2787	1248.5235	624.7654	1247.5395	624.2734	S	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	9
13	1336.5872	668.7972	1319.5606	660.2839	1318.5766	659.7919	A	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	8
14	**1451.6141**	726.3107	1434.5876	717.7974	1433.6035	717.3054	N	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	7
15	**1522.6512**	761.8292	1505.6247	753.3160	1504.6407	752.8240	A	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	6
16	**1609.6833**	805.3453	1592.6567	796.8320	1591.6727	796.3400	S	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	5
17	1724.7102	862.8587	1707.6836	854.3455	1706.6996	853.8535	D	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	4
18	**1852.7688**	926.8880	1835.7422	918.3747	1834.7582	917.8827	Q	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
19	**1981.8114**	991.4093	1964.7848	982.8960	1963.8008	982.4040	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
74.0	2154.9158	1.0048	LTDTICGVGNMSANASDQER	Deamidated N14 71.74%
69.8	2154.9158	1.0048	LTDTICGVGNMSANASDQER	Deamidated Q18 26.96%
56.6	2154.9158	1.0048	LTDTICGVGNMSANASDQER	Deamidated N10 1.30%
4.4	2155.9141	0.0064	EEEESVNASSFGQNTNKER	
3.1	2155.9141	0.0064	EEEESVNASSFGQNTNKER	
1.6	2155.9188	0.0017	ANMNSDSRHLGTSEVDHER	
1.5	2155.9141	0.0064	EEEESVNASSFGQNTNKER	
0.9	2155.9110	0.0096	QMEDEAKRSETMNAEQSR	
0.6	2154.9270	0.9936	KMASVNGSSQNCVSGQERGR	
0.6	2155.9150	0.0055	DMSSFMLPGSSHITDSEQR	

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

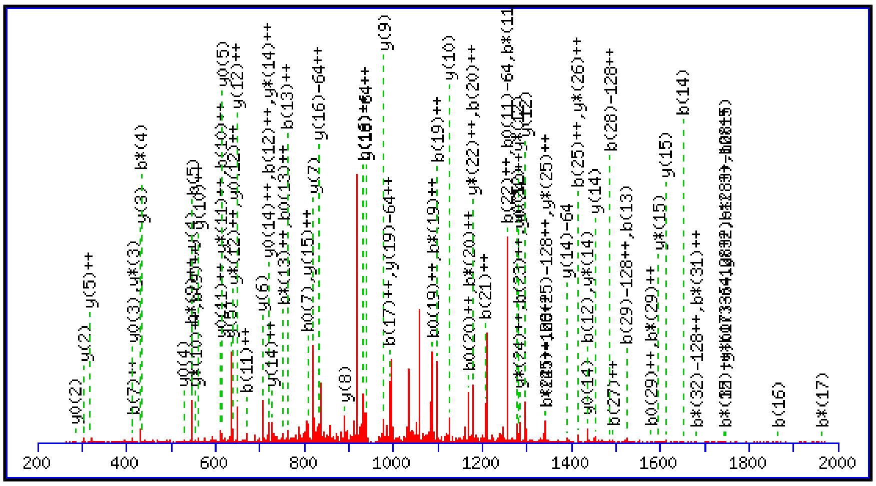
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28075: 3806.734096 from(952.690800,4+) intensity(68265.7891) rtinseconds(1718) scans(4502) index(23963)
Title: 111019_Est_MI_YS_G_05Spectrum3897_scans__4502
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

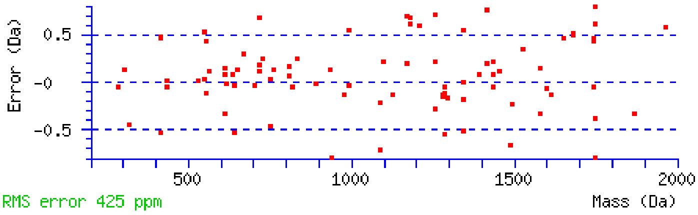
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

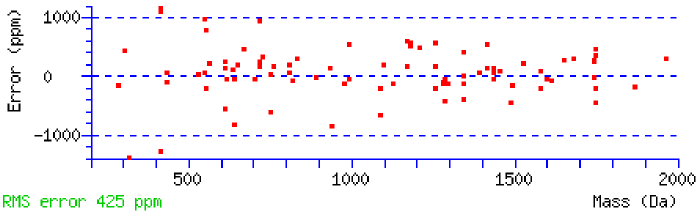


Monoisotopic mass of neutral peptide Mr(calc): 3806.7186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N24 : Deamidated (NQ)
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N28 : Deamidated (NQ)
Ions Score: 66 **Expect:** 3.8e-005
Matches : 91/670 fragment ions using 137 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**34**
2	185.1285	93.0679					**L**	3736.6888	1868.8480	3719.6622	1860.3347	3718.6782	1859.8427	**33**
3	322.1874	161.5973					**H**	3623.6047	1812.3060	3606.5781	1803.7927	3605.5941	1803.3007	**32**
4	450.2459	225.6266	433.2194	217.1133			**Q**	3486.5458	1743.7765	3469.5192	1735.2633	3468.5352	1734.7712	**31**
5	**549.3144**	275.1608	532.2878	266.6475			**V**	3358.4872	1679.7472	3341.4607	1671.2340	3340.4766	1670.7420	**30**
6	696.3828	348.6950	679.3562	340.1817			**F**	3259.4188	1630.2130	3242.3922	1621.6998	3241.4082	1621.2077	**29**
7	825.4254	***413.2163***	808.3988	404.7030	807.4148	404.2110	**E**	3112.3504	1556.6788	3095.3238	1548.1655	3094.3398	1547.6735	**28**
8	962.4843	481.7458	945.4577	473.2325	944.4737	472.7405	**H**	2983.3078	1492.1575	2966.2812	1483.6443	2965.2972	1483.1522	**27**
9	1109.5197	***555.2635***	1092.4931	546.7502	1091.5091	546.2582	**M**	2846.2489	1423.6281	2829.2223	1415.1148	2828.2383	1414.6228	**26**
10	1222.6037	***611.8055***	1205.5772	603.2922	1204.5932	602.8002	**L**	2699.2135	1350.1104	2682.1869	1341.5971	2681.2029	1341.1051	**25**
11	1337.6307	***669.3190***	1320.6041	660.8057	1319.6201	660.3137	**D**	2586.1294	1293.5683	2569.1029	1285.0551	2568.1188	1284.5631	**24**
12	**1436.6991**	***718.8532***	1419.6725	710.3399	1418.6885	709.8479	**V**	2471.1025	1236.0549	2454.0759	1227.5416	2453.0919	1227.0496	**23**
13	**1523.7311**	***762.3692***	1506.7046	753.8559	1505.7206	753.3639	**S**	2372.0340	1186.5207	2355.0075	1178.0074	2354.0235	1177.5154	**22**
14	**1651.8261**	826.4167	1634.7995	817.9034	1633.8155	817.4114	**K**	2285.0020	1143.0046	2267.9755	1134.4914	2266.9915	1133.9994	**21**
15	1764.9102	882.9587	1747.8836	874.4454	1746.8996	873.9534	**L**	2156.9071	1078.9572	2139.8805	1070.4439	2138.8965	1069.9519	**20**
16	**1865.9578**	***933.4826***	1848.9313	924.9693	1847.9473	924.4773	**T**	2043.8230	1022.4151	2026.7964	1013.9019	2025.8124	1013.4099	**19**
17	1980.9848	***990.9960***	1963.9582	982.4828	1962.9742	981.9907	**D**	1942.7753	971.8913	1925.7488	963.3780	1924.7647	962.8860	**18**
18	2082.0325	1041.5199	2065.0059	1033.0066	2064.0219	1032.5146	**T**	1827.7484	914.3778	1810.7218	905.8645	1809.7378	905.3725	**17**
19	2195.1165	***1098.0619***	2178.0900	1089.5486	2177.1060	1089.0566	**I**	1726.7007	863.8540	1709.6741	855.3407	1708.6901	854.8487	**16**
20	2355.1472	***1178.0772***	2338.1206	1169.5639	2337.1366	1169.0719	**C**	***1613.6166***	807.3120	1596.5901	798.7987	1595.6061	798.3067	**15**
21	2412.1686	***1206.5880***	2395.1421	1198.0747	2394.1581	1197.5827	**G**	***1453.5860***	727.2966	1436.5594	718.7834	1435.5754	718.2913	**14**

22	2511.2370	***1256.1222***	2494.2105	1247.6089	2493.2265	1247.1169	**V**	1396.5645	698.7859	1379.5380	690.2726	1378.5539	689.7806	**13**
23	2568.2585	***1284.6329***	2551.2320	1276.1196	2550.2479	1275.6276	**G**	***1297.4961***	649.2517	1280.4696	640.7384	1279.4855	640.2464	**12**
24	2683.2855	***1342.1464***	2666.2589	1333.6331	2665.2749	1333.1411	**N**	1240.4746	620.7410	1223.4481	612.2277	1222.4641	611.7357	**11**
25	2830.3209	***1415.6641***	2813.2943	1407.1508	2812.3103	1406.6588	**M**	***1125.4477***	563.2275	1108.4211	554.7142	1107.4371	554.2222	**10**
26	2917.3529	1459.1801	2900.3263	1450.6668	2899.3423	1450.1748	**S**	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2988.3900	***1494.6986***	2971.3634	1486.1854	2970.3794	1485.6934	**A**	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3103.4169	1552.2121	3086.3904	1543.6988	3085.4064	1543.2068	**N**	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3174.4541	1587.7307	3157.4275	1579.2174	3156.4435	1578.7254	**A**	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3261.4861	1631.2467	3244.4595	1622.7334	3243.4755	1622.2414	**S**	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3376.5130	1688.7601	3359.4865	1680.2469	3358.5025	1679.7549	**D**	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3504.5716	1752.7894	3487.5451	1744.2762	3486.5610	1743.7842	**Q**	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3633.6142	1817.3107	3616.5876	1808.7975	3615.6036	1808.3055	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.1	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28 71.64%
60.9	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Q32 21.54%
58.5	3805.7346	0.9995	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
54.2	3805.7346	0.9995	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
53.7	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Q32 4.06%
50.1	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28 1.77%
50.1	3805.7346	0.9995	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
45.4	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N24 0.60%
43.5	3806.7186	0.0155	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32 0.39%
41.8	3805.7346	0.9995	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	

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

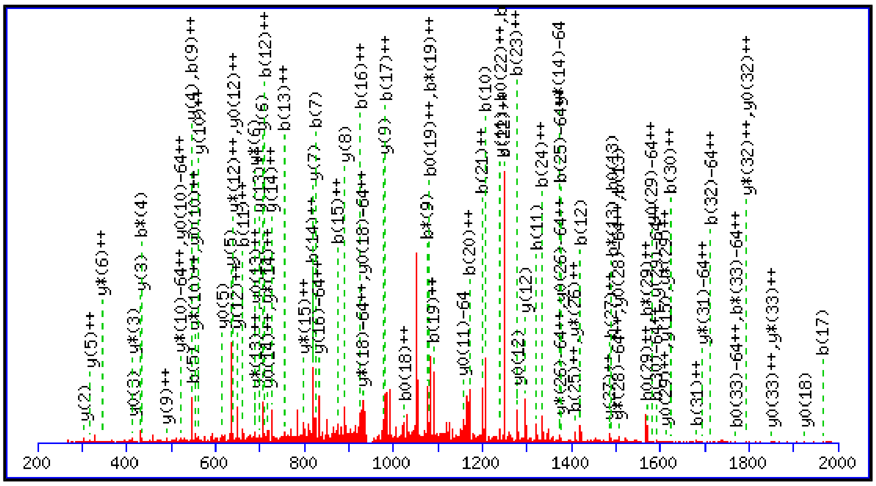
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28067: 3790.733896 from(948.690750,4+) intensity(24578.5723) rtinseconds(2078) scans(5380) index(9682)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum4631_scans__5380
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

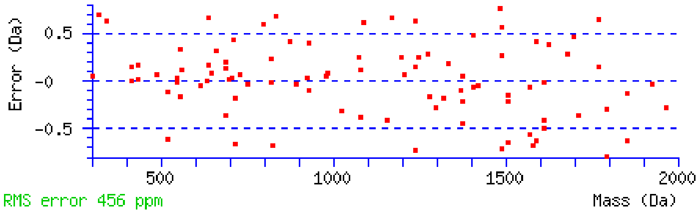
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

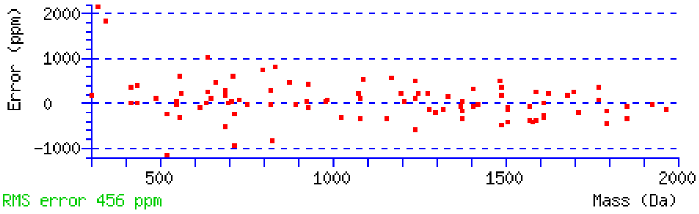


Monoisotopic mass of neutral peptide Mr(calc): 3790.7237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N24 : Deamidated (NQ)
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N28 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00014
Matches : 96/574 fragment ions using 171 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							34
2	185.1285	93.0679					L	3720.6938	1860.8506	3703.6673	1852.3373	3702.6833	1851.8453	33
3	322.1874	161.5973					H	3607.6098	1804.3085	3590.5832	1795.7953	3589.5992	1795.3032	32
4	450.2459	225.6266	433.2194	217.1133			Q	3470.5509	1735.7791	3453.5243	1727.2658	3452.5403	1726.7738	31
5	**549.3144**	275.1608	532.2878	266.6475			V	3342.4923	1671.7498	3325.4657	1663.2365	3324.4817	1662.7445	30
6	696.3828	348.6950	679.3562	340.1817			F	3243.4239	1622.2156	3226.3973	1613.7023	3225.4133	1613.2103	29
7	**825.4254**	413.2163	808.3988	404.7030	807.4148	404.2110	E	3096.3555	1548.6814	3079.3289	1540.1681	3078.3449	1539.6761	28
8	962.4843	481.7458	945.4577	473.2325	944.4737	472.7405	H	2967.3129	1484.1601	2950.2863	1475.6468	2949.3023	1475.1548	27
9	1093.5248	***547.2660***	1076.4982	538.7527	1075.5142	538.2607	M	2830.2540	1415.6306	2813.2274	1407.1173	2812.2434	1406.6253	26
10	**1206.6088**	603.8081	1189.5823	595.2948	1188.5983	594.8028	L	2699.2135	1350.1104	2682.1869	1341.5971	2681.2029	1341.1051	25
11	**1321.6358**	***661.3215***	1304.6092	652.8082	1303.6252	652.3162	D	2586.1294	1293.5683	2569.1029	1285.0551	2568.1188	1284.5631	24
12	**1420.7042**	***710.8557***	1403.6776	702.3425	1402.6936	701.8504	V	2471.1025	1236.0549	2454.0759	1227.5416	2453.0919	1227.0496	23
13	**1507.7362**	***754.3717***	1490.7097	745.8585	1489.7256	745.3665	S	2372.0340	1186.5207	2355.0075	1178.0074	2354.0235	1177.5154	22
14	1635.8312	***818.4192***	1618.8046	809.9060	1617.8206	809.4139	K	2285.0020	1143.0046	2267.9755	1134.4914	2266.9915	1133.9994	21
15	1748.9152	***874.9613***	1731.8887	866.4480	1730.9047	865.9560	L	2156.9071	1078.9572	2139.8805	1070.4439	2138.8965	1069.9519	20
16	1849.9629	***925.4851***	1832.9364	916.9718	1831.9524	916.4798	T	2043.8230	1022.4151	2026.7964	1013.9019	2025.8124	1013.4099	19
17	**1964.9899**	***982.9986***	1947.9633	974.4853	1946.9793	973.9933	D	1942.7753	971.8913	1925.7488	963.3780	1924.7647	962.8860	18
18	2066.0375	1033.5224	2049.0110	1025.0091	2048.0270	1024.5171	T	1827.7484	914.3778	1810.7218	905.8645	1809.7378	905.3725	17
19	2179.1216	***1090.0644***	2162.0951	1081.5512	2161.1110	1081.0592	I	1726.7007	863.8540	1709.6741	855.3407	1708.6901	854.8487	16
20	2339.1523	***1170.0798***	2322.1257	1161.5665	2321.1417	1161.0745	C	**1613.6166**	807.3120	1596.5901	798.7987	1595.6061	798.3067	15
21	2396.1737	***1198.5905***	2379.1472	1190.0772	2378.1632	1189.5852	G	1453.5860	727.2966	1436.5594	718.7834	1435.5754	718.2913	14
22	2495.2421	***1248.1247***	2478.2156	1239.6114	2477.2316	1239.1194	V	1396.5645	698.7859	1379.5380	690.2726	1378.5539	689.7806	13

23	2552.2636	***1276.6354***	2535.2370	1268.1222	2534.2530	1267.6302	**G**	**1297.4961**	649.2517	1280.4696	640.7384	1279.4855	640.2464	**12**
24	2667.2905	***1334.1489***	2650.2640	1325.6356	2649.2800	1325.1436	**N**	**1240.4746**	620.7410	1223.4481	612.2277	1222.4641	611.7357	**11**
25	2814.3259	***1407.6666***	2797.2994	1399.1533	2796.3154	1398.6613	**M**	1125.4477	563.2275	1108.4211	554.7142	1107.4371	554.2222	**10**
26	2901.3580	1451.1826	2884.3314	1442.6693	2883.3474	1442.1773	**S**	**978.4123**	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2972.3951	***1486.7012***	2955.3685	1478.1879	2954.3845	1477.6959	**A**	**891.3803**	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3087.4220	1544.2146	3070.3955	1535.7014	3069.4115	1535.2094	**N**	**820.3432**	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3158.4591	1579.7332	3141.4326	1571.2199	3140.4486	1570.7279	**A**	**705.3162**	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3245.4912	***1623.2492***	3228.4646	1614.7359	3227.4806	1614.2439	**S**	**634.2791**	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3360.5181	***1680.7627***	3343.4916	1672.2494	3342.5075	1671.7574	**D**	**547.2471**	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3488.5767	1744.7920	3471.5501	1736.2787	3470.5661	1735.7867	**Q**	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3617.6193	1809.3133	3600.5927	1800.8000	3599.6087	1800.3080	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.7	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28, Oxidation M25; 40.18%
58.3	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Q32, Oxidation M25; 23.23%
56.7	3789.7397	0.9942	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
55.7	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28, Oxidation M25; 12.71%
54.5	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32, Oxidation M25; 9.82%
52.9	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N24, Oxidation M25; 6.67%
52.5	3789.7397	0.9942	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
52.4	3789.7397	0.9942	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
50.1	3790.7237	0.0102	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Q32, Oxidation M25; 3.52%
43.7	3789.7397	0.9942	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28065: 3774.733176 from(944.690570,4+) intensity(14278.2158) rtinseconds(2307) scans(5716) index(9118)
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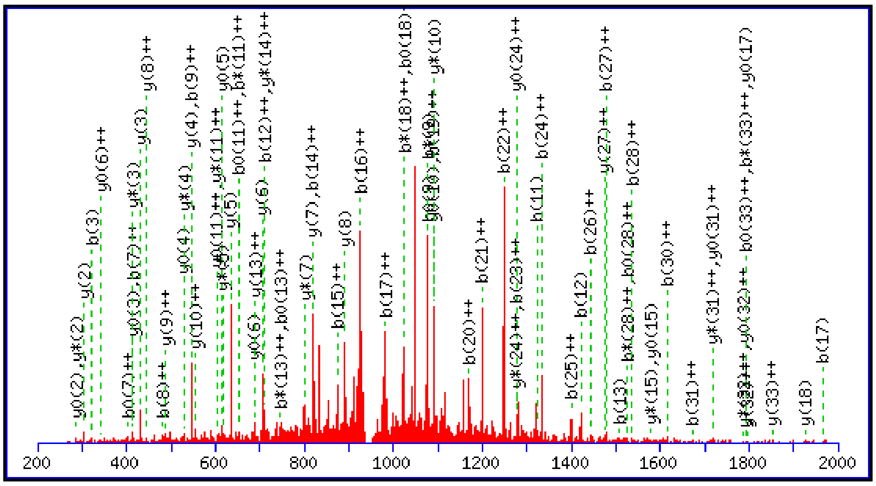
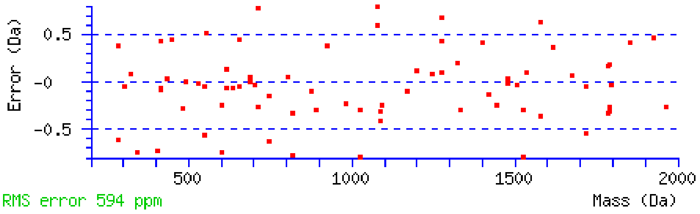
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

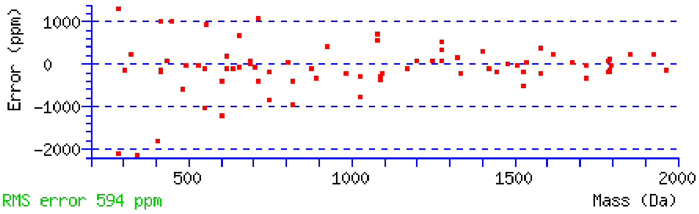


Monoisotopic mass of neutral peptide Mr(calc): 3774.7287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
N24 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00028
Matches : 78/376 fragment ions using 172 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					**A**							**34**
2	185.1285	93.0679					**L**	3704.6989	1852.8531	3687.6724	1844.3398	3686.6884	1843.8478	**33**
3	322.1874	161.5973					**H**	3591.6149	1796.3111	3574.5883	1787.7978	3573.6043	1787.3058	**32**
4	451.2300	226.1186	434.2034	217.6053			**Q**	3454.5559	1727.7816	3437.5294	1719.2683	3436.5454	1718.7763	**31**
5	550.2984	275.6528	533.2718	267.1396			**V**	3325.5134	1663.2603	3308.4868	1654.7470	3307.5028	1654.2550	**30**
6	697.3668	349.1870	680.3402	340.6738			**F**	3226.4449	1613.7261	3209.4184	1605.2128	3208.4344	1604.7208	**29**
7	826.4094	***413.7083***	809.3828	405.1951	808.3988	404.7030	**E**	3079.3765	1540.1919	3062.3500	1531.6786	3061.3660	1531.1866	**28**
8	963.4683	***482.2378***	946.4417	473.7245	945.4577	473.2325	**H**	2950.3339	1475.6706	2933.3074	1467.1573	2932.3234	1466.6653	**27**
9	1094.5088	***547.7580***	1077.4822	539.2448	1076.4982	538.7527	**M**	2813.2750	1407.1411	2796.2485	1398.6279	2795.2645	1398.1359	**26**
10	1207.5928	604.3001	1190.5663	595.7868	1189.5823	595.2948	**L**	2682.2345	1341.6209	2665.2080	1333.1076	2664.2240	1332.6156	**25**
11	1322.6198	661.8135	1305.5932	653.3003	1304.6092	652.8082	**D**	2569.1505	1285.0789	2552.1239	1276.5656	2551.1399	1276.0736	**24**
12	1421.6882	***711.3477***	1404.6617	702.8345	1403.6776	702.3425	**V**	2454.1235	1227.5654	2437.0970	1219.0521	2436.1130	1218.5601	**23**
13	1508.7202	754.8638	1491.6937	746.3505	1490.7097	745.8585	**S**	2355.0551	1178.0312	2338.0286	1169.5179	2337.0446	1169.0259	**22**
14	1636.8152	***818.9112***	1619.7886	810.3980	1618.8046	809.9060	**K**	2268.0231	1134.5152	2250.9965	1126.0019	2250.0125	1125.5099	**21**
15	1749.8993	***875.4533***	1732.8727	866.9400	1731.8887	866.4480	**L**	2139.9281	1070.4677	2122.9016	1061.9544	2121.9176	1061.4624	**20**
16	1850.9469	***925.9771***	1833.9204	917.4638	1832.9364	916.9718	**T**	2026.8441	1013.9257	2009.8175	1005.4124	2008.8335	1004.9204	**19**
17	1965.9739	***983.4906***	1948.9473	974.9773	1947.9633	974.4853	**D**	**1925.7964**	963.4018	1908.7698	954.8886	1907.7858	954.3965	**18**
18	2067.0216	1034.0144	2049.9950	1025.5011	2049.0110	1025.0091	**T**	1810.7694	905.8884	1793.7429	897.3751	1792.7589	896.8831	**17**
19	2180.1056	***1090.5564***	2163.0791	1082.0432	2162.0951	1081.5512	**I**	1709.7218	855.3645	1692.6952	846.8512	1691.7112	846.3592	**16**
20	2340.1363	***1170.5718***	2323.1097	1162.0585	2322.1257	1161.5665	**C**	1596.6377	798.8225	1579.6111	790.3092	1578.6271	789.8172	**15**
21	2397.1577	***1199.0825***	2380.1312	1190.5692	2379.1472	1190.0772	**G**	1436.6070	718.8072	1419.5805	710.2939	1418.5965	709.8019	**14**
22	2496.2261	***1248.6167***	2479.1996	1240.1034	2478.2156	1239.6114	**V**	1379.5856	690.2964	1362.5590	681.7832	1361.5750	681.2911	**13**

23	2553.2476	***1277.1274***	2536.2211	1268.6142	2535.2370	1268.1222	**G**	1280.5172	640.7622	1263.4906	632.2489	1262.5066	631.7569	**12**
24	2668.2746	***1334.6409***	2651.2480	1326.1276	2650.2640	1325.6356	**N**	1223.4957	612.2515	1206.4692	603.7382	1205.4851	603.2462	**11**
25	2799.3150	***1400.1612***	2782.2885	1391.6479	2781.3045	1391.1559	**M**	1108.4688	554.7380	1091.4422	546.2247	1090.4582	545.7327	**10**
26	2886.3471	***1443.6772***	2869.3205	1435.1639	2868.3365	1434.6719	**S**	977.4283	489.2178	960.4017	480.7045	959.4177	480.2125	**9**
27	2957.3842	***1479.1957***	2940.3576	1470.6825	2939.3736	1470.1904	**A**	**890.3962**	445.7018	873.3697	437.1885	872.3857	436.6965	**8**
28	3071.4271	***1536.2172***	3054.4006	1527.7039	3053.4165	1527.2119	**N**	**819.3591**	410.1832	802.3326	401.6699	801.3486	401.1779	**7**
29	3142.4642	1571.7357	3125.4377	1563.2225	3124.4537	1562.7305	**A**	**705.3162**	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3229.4962	***1615.2518***	3212.4697	1606.7385	3211.4857	1606.2465	**S**	**634.2791**	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3344.5232	***1672.7652***	3327.4966	1664.2520	3326.5126	1663.7600	**D**	**547.2471**	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3472.5818	1736.7945	3455.5552	1728.2812	3454.5712	1727.7892	**Q**	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3601.6244	1801.3158	3584.5978	1792.8025	3583.6138	1792.3105	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.0	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N24 40.80%
57.4	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28 35.62%
54.4	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28 17.85%
49.0	3773.7447	0.9884	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
47.2	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32 3.44%
45.2	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Q32 2.14%
42.3	3773.7447	0.9884	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
38.1	3773.7447	0.9884	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
33.8	3774.7287	0.0044	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Q32 0.16%
31.8	3773.7447	0.9884	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	

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

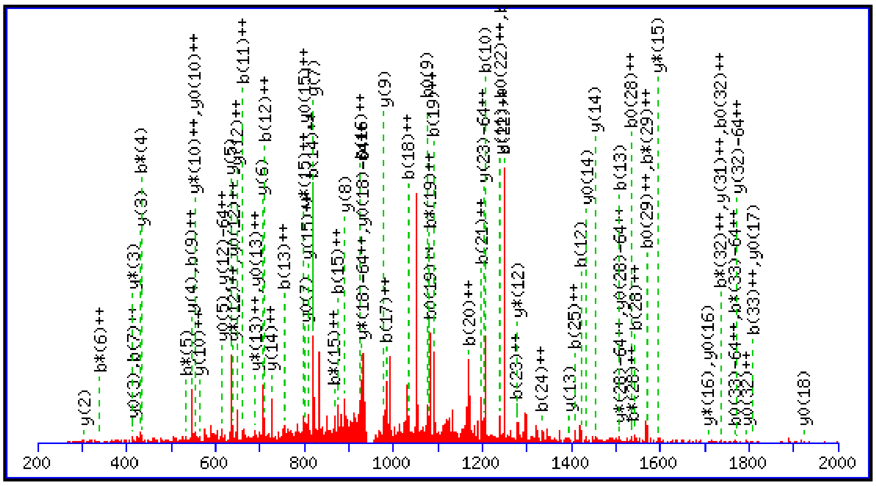
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28071: 3792.743176 from(949.193070,4+) intensity(21352.9277) rtinseconds(2181) scans(5361) index(9085)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum4616_scans__5361
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

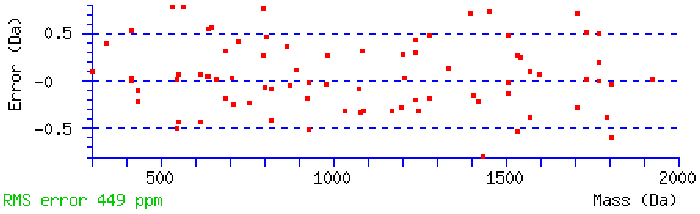
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

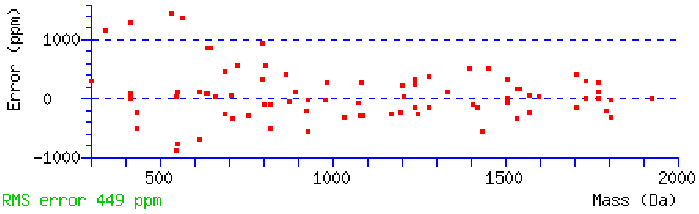


Monoisotopic mass of neutral peptide Mr(calc): 3790.7237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N28 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.00087
Matches : 82/574 fragment ions using 172 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							34
2	185.1285	93.0679					L	3720.6938	1860.8506	3703.6673	1852.3373	3702.6833	1851.8453	33
3	322.1874	161.5973					H	3607.6098	1804.3085	3590.5832	1795.7953	3589.5992	1795.3032	32
4	451.2300	226.1186	434.2034	217.6053			Q	3470.5509	1735.7791	3453.5243	1727.2658	3452.5403	1726.7738	31
5	550.2984	275.6528	533.2718	267.1396			V	3341.5083	1671.2578	3324.4817	1662.7445	3323.4977	1662.2525	30
6	697.3668	349.1870	680.3402	340.6738			F	3242.4399	1621.7236	3225.4133	1613.2103	3224.4293	1612.7183	29
7	826.4094	***413.7083***	809.3828	405.1951	808.3988	404.7030	E	3095.3714	1548.1894	3078.3449	1539.6761	3077.3609	1539.1841	28
8	963.4683	482.2378	946.4417	473.7245	945.4577	473.2325	H	2966.3288	1483.6681	2949.3023	1475.1548	2948.3183	1474.6628	27
9	1094.5088	***547.7580***	1077.4822	539.2448	1076.4982	538.7527	M	2829.2699	1415.1386	2812.2434	1406.6253	2811.2594	1406.1333	26
10	1207.5928	604.3001	1190.5663	595.7868	1189.5823	595.2948	L	2698.2295	1349.6184	2681.2029	1341.1051	2680.2189	1340.6131	25
11	1322.6198	***661.8135***	1305.5932	653.3003	1304.6092	652.8082	D	2585.1454	1293.0763	2568.1188	1284.5631	2567.1348	1284.0710	24
12	1421.6882	***711.3477***	1404.6617	702.8345	1403.6776	702.3425	V	2470.1184	1235.5629	2453.0919	1227.0496	2452.1079	1226.5576	23
13	1508.7202	***754.8638***	1491.6937	746.3505	1490.7097	745.8585	S	2371.0500	1186.0287	2354.0235	1177.5154	2353.0395	1177.0234	22
14	1636.8152	***818.9112***	1619.7886	810.3980	1618.8046	809.9060	K	2284.0180	1142.5126	2266.9915	1133.9994	2266.0074	1133.5074	21
15	1749.8993	***875.4533***	1732.8727	866.9400	1731.8887	866.4480	L	2155.9230	1078.4652	2138.8965	1069.9519	2137.9125	1069.4599	20
16	1850.9469	***925.9771***	1833.9204	917.4638	1832.9364	916.9718	T	2042.8390	1021.9231	2025.8124	1013.4099	2024.8284	1012.9178	19
17	1965.9739	***983.4906***	1948.9473	974.9773	1947.9633	974.4853	D	1941.7913	971.3993	1924.7647	962.8860	1923.7807	962.3940	18
18	2067.0216	***1034.0144***	2049.9950	1025.5011	2049.0110	1025.0091	T	1826.7644	913.8858	1809.7378	905.3725	1808.7538	904.8805	17
19	2180.1056	***1090.5564***	2163.0791	1082.0432	2162.0951	1081.5512	I	1725.7167	863.3620	1708.6901	854.8487	1707.7061	854.3567	16
20	2340.1363	***1170.5718***	2323.1097	1162.0585	2322.1257	1161.5665	C	1612.6326	806.8199	1595.6061	798.3067	1594.6220	797.8147	15
21	2397.1577	***1199.0825***	2380.1312	1190.5692	2379.1472	1190.0772	G	***1452.6020***	726.8046	1435.5754	718.2913	1434.5914	717.7993	14
22	2496.2261	***1248.6167***	2479.1996	1240.1034	2478.2156	1239.6114	V	***1395.5805***	698.2939	1378.5539	689.7806	1377.5699	689.2886	13

23	2553.2476	***1277.1274***	2536.2211	1268.6142	2535.2370	1268.1222	**G**	1296.5121	648.7597	1279.4855	640.2464	1278.5015	639.7544	**12**
24	2667.2905	***1334.1489***	2650.2640	1325.6356	2649.2800	1325.1436	**N**	***1239.4906***	620.2489	1222.4641	611.7357	1221.4801	611.2437	**11**
25	2814.3259	***1407.6666***	2797.2994	1399.1533	2796.3154	1398.6613	**M**	1125.4477	563.2275	1108.4211	554.7142	1107.4371	554.2222	**10**
26	2901.3580	1451.1826	2884.3314	1442.6693	2883.3474	1442.1773	**S**	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2972.3951	1486.7012	2955.3685	1478.1879	2954.3845	1477.6959	**A**	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3087.4220	***1544.2146***	3070.3955	1535.7014	3069.4115	1535.2094	**N**	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3158.4591	1579.7332	3141.4326	1571.2199	3140.4486	1570.7279	**A**	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3245.4912	1623.2492	3228.4646	1614.7359	3227.4806	1614.2439	**S**	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3360.5181	1680.7627	3343.4916	1672.2494	3342.5075	1671.7574	**D**	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3488.5767	1744.7920	3471.5501	1736.2787	3470.5661	1735.7867	**Q**	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3617.6193	***1809.3133***	3600.5927	1800.8000	3599.6087	1800.3080	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.1	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28, Oxidation M25; 32.59%
52.9	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32, Oxidation M25; 30.91%
52.2	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N24, Oxidation M25; 26.25%
45.5	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Q32, Oxidation M25; 5.66%
43.4	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28, Oxidation M25; 3.51%
38.3	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Q32, Oxidation M25; 1.07%
16.8	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28, Oxidation M9; 0.01%
15.6	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28, Oxidation M9; 0.01%
6.1	3790.7316	2.0116	GTEGRTGLPGNQGEPGSKGQPGDSGEMGFPGMAGLFGPK	
5.3	3790.7237	2.0195	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32, Oxidation M9; 0.00%

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

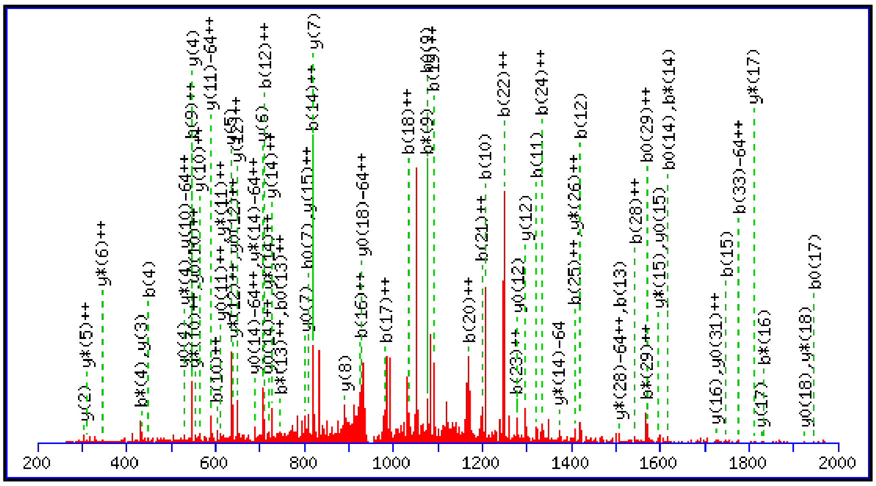
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28068: 3790.739096 from(948.692050,4+) intensity(22131.1035) rtinseconds(2175) scans(5344) index(9082)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum4600_scans__5344
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

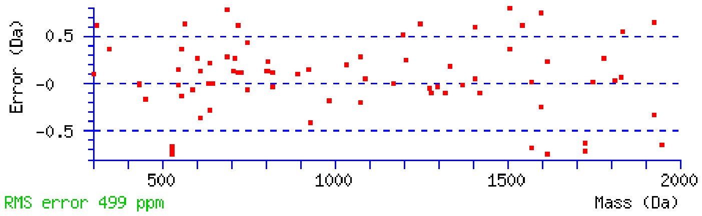
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

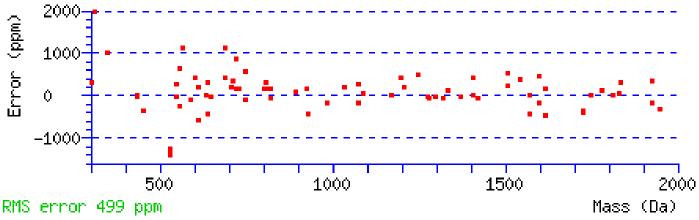


Monoisotopic mass of neutral peptide Mr(calc): 3790.7237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N24 : Deamidated (NQ)
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q32 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0015
Matches : 76/574 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							34
2	185.1285	93.0679					L	3720.6938	1860.8506	3703.6673	1852.3373	3702.6833	1851.8453	33
3	322.1874	161.5973					H	3607.6098	1804.3085	3590.5832	1795.7953	3589.5992	1795.3032	32
4	**450.2459**	225.6266	433.2194	217.1133			Q	3470.5509	1735.7791	3453.5243	1727.2658	3452.5403	1726.7738	31
5	549.3144	275.1608	532.2878	266.6475			V	3342.4923	1671.7498	3325.4657	1663.2365	3324.4817	1662.7445	30
6	696.3828	348.6950	679.3562	340.1817			F	3243.4239	1622.2156	3226.3973	1613.7023	3225.4133	1613.2103	29
7	825.4254	413.2163	808.3988	404.7030	807.4148	404.2110	E	3096.3555	1548.6814	3079.3289	1540.1681	3078.3449	1539.6761	28
8	962.4843	481.7458	945.4577	473.2325	944.4737	472.7405	H	2967.3129	1484.1601	2950.2863	1475.6468	2949.3023	1475.1548	27
9	1093.5248	***547.2660***	1076.4982	538.7527	1075.5142	538.2607	M	2830.2540	1415.6306	2813.2274	1407.1173	2812.2434	1406.6253	26
10	**1206.6088**	***603.8081***	1189.5823	595.2948	1188.5983	594.8028	L	2699.2135	1350.1104	2682.1869	1341.5971	2681.2029	1341.1051	25
11	**1321.6358**	661.3215	1304.6092	652.8082	1303.6252	652.3162	D	2586.1294	1293.5683	2569.1029	1285.0551	2568.1188	1284.5631	24
12	**1420.7042**	***710.8557***	1403.6776	702.3425	1402.6936	701.8504	V	2471.1025	1236.0549	2454.0759	1227.5416	2453.0919	1227.0496	23
13	**1507.7362**	754.3717	1490.7097	745.8585	1489.7256	745.3665	S	2372.0340	1186.5207	2355.0075	1178.0074	2354.0235	1177.5154	22
14	1635.8312	***818.4192***	1618.8046	809.9060	1617.8206	809.4139	K	2285.0020	1143.0046	2267.9755	1134.4914	2266.9915	1133.9994	21
15	**1748.9152**	874.9613	1731.8887	866.4480	1730.9047	865.9560	L	2156.9071	1078.9572	2139.8805	1070.4439	2138.8965	1069.9519	20
16	1849.9629	***925.4851***	1832.9364	916.9718	1831.9524	916.4798	T	2043.8230	1022.4151	2026.7964	1013.9019	2025.8124	1013.4099	19
17	1964.9899	***982.9986***	1947.9633	974.4853	1946.9793	973.9933	D	1942.7753	971.8913	1925.7488	963.3780	1924.7647	962.8860	18
18	2066.0375	***1033.5224***	2049.0110	1025.0091	2048.0270	1024.5171	T	***1827.7484***	914.3778	1810.7218	905.8645	1809.7378	905.3725	17
19	2179.1216	***1090.0644***	2162.0951	1081.5512	2161.1110	1081.0592	I	***1726.7007***	863.8540	1709.6741	855.3407	1708.6901	854.8487	16
20	2339.1523	***1170.0798***	2322.1257	1161.5665	2321.1417	1161.0745	C	1613.6166	807.3120	1596.5901	798.7987	1595.6061	798.3067	15
21	2396.1737	***1198.5905***	2379.1472	1190.0772	2378.1632	1189.5852	G	1453.5860	727.2966	1436.5594	718.7834	1435.5754	718.2913	14
22	2495.2421	***1248.1247***	2478.2156	1239.6114	2477.2316	1239.1194	V	1396.5645	698.7859	1379.5380	690.2726	1378.5539	689.7806	13

23	2552.2636	***1276.6354***	2535.2370	1268.1222	2534.2530	1267.6302	**G**	***1297.4961***	649.2517	1280.4696	640.7384	1279.4855	640.2464	**12**
24	2667.2905	***1334.1489***	2650.2640	1325.6356	2649.2800	1325.1436	**N**	1240.4746	620.7410	1223.4481	612.2277	1222.4641	611.7357	**11**
25	2814.3259	***1407.6666***	2797.2994	1399.1533	2796.3154	1398.6613	**M**	1125.4477	563.2275	1108.4211	554.7142	1107.4371	554.2222	**10**
26	2901.3580	1451.1826	2884.3314	1442.6693	2883.3474	1442.1773	**S**	978.4123	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2972.3951	1486.7012	2955.3685	1478.1879	2954.3845	1477.6959	**A**	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3086.4380	***1543.7226***	3069.4115	1535.2094	3068.4274	1534.7174	**N**	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3157.4751	1579.2412	3140.4486	1570.7279	3139.4646	1570.2359	**A**	***706.3002***	353.6538	689.2737	345.1405	688.2897	344.6485	**6**
30	3244.5071	1622.7572	3227.4806	1614.2439	3226.4966	1613.7519	**S**	***635.2631***	318.1352	618.2366	309.6219	617.2525	309.1299	**5**
31	3359.5341	1680.2707	3342.5075	1671.7574	3341.5235	1671.2654	**D**	***548.2311***	274.6192	531.2045	266.1059	530.2205	265.6139	**4**
32	3488.5767	1744.7920	3471.5501	1736.2787	3470.5661	1735.7867	**Q**	***433.2041***	217.1057	416.1776	208.5924	415.1936	208.1004	**3**
33	3617.6193	1809.3133	3600.5927	1800.8000	3599.6087	1800.3080	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.6	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Q32, Oxidation M25; 40.50%
49.4	3789.7397	0.9994	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
48.6	3789.7397	0.9994	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
48.2	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, N28, Oxidation M25; 23.41%
45.0	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Q32, Oxidation M25; 11.16%
44.6	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N28, Oxidation M25; 10.32%
43.0	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Q32, Oxidation M25; 7.05%
42.8	3789.7397	0.9994	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
41.6	3790.7237	0.0154	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, N24, Oxidation M25; 5.10%
31.6	3789.7397	0.9994	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	

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

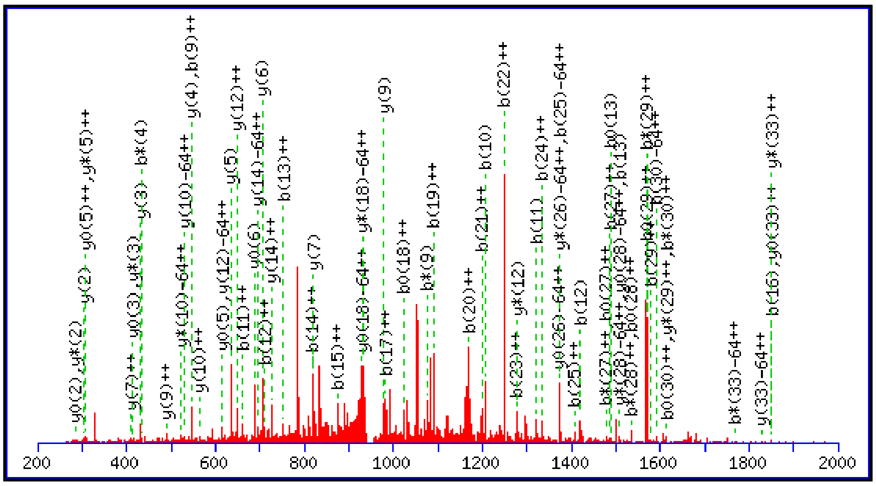
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28070: 3791.756776 from(948.946470,4+) intensity(0.0000) rtinseconds(2177) scans(5820) index(24126)
Title: 111019_Est_MI_YS_G_05Spectrum5036_scans__5820
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

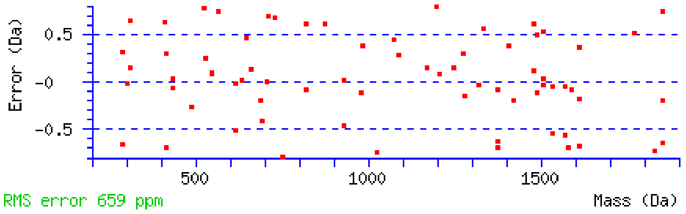
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

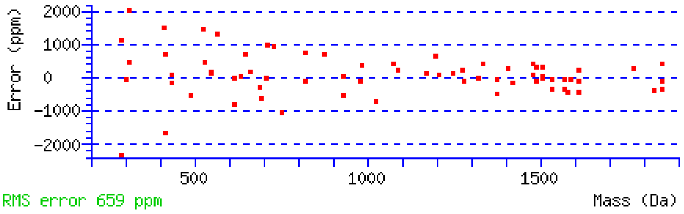


Monoisotopic mass of neutral peptide Mr(calc): 3789.7397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N28 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0017
Matches : 71/574 fragment ions using 133 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					**A**							**34**
2	185.1285	93.0679					**L**	3719.7098	1860.3585	3702.6833	1851.8453	3701.6993	1851.3533	**33**
3	322.1874	161.5973					**H**	3606.6258	1803.8165	3589.5992	1795.3032	3588.6152	1794.8112	**32**
4	450.2459	225.6266	433.2194	217.1133			**Q**	3469.5668	1735.2871	3452.5403	1726.7738	3451.5563	1726.2818	**31**
5	549.3144	275.1608	532.2878	266.6475			**V**	3341.5083	1671.2578	3324.4817	1662.7445	3323.4977	1662.2525	**30**
6	696.3828	348.6950	679.3562	340.1817			**F**	3242.4399	1621.7236	3225.4133	1613.2103	3224.4293	1612.7183	**29**
7	825.4254	413.2163	808.3988	404.7030	807.4148	404.2110	**E**	3095.3714	1548.1894	3078.3449	1539.6761	3077.3609	1539.1841	**28**
8	962.4843	481.7458	945.4577	473.2325	944.4737	472.7405	**H**	2966.3288	1483.6681	2949.3023	1475.1548	2948.3183	1474.6628	**27**
9	1093.5248	***547.2660***	1076.4982	538.7527	1075.5142	538.2607	**M**	2829.2699	1415.1386	2812.2434	1406.6253	2811.2594	1406.1333	**26**
10	**1206.6088**	603.8081	1189.5823	595.2948	1188.5983	594.8028	**L**	2698.2295	1349.6184	2681.2029	1341.1051	2680.2189	1340.6131	**25**
11	**1321.6358**	***661.3215***	1304.6092	652.8082	1303.6252	652.3162	**D**	2585.1454	1293.0763	2568.1188	1284.5631	2567.1348	1284.0710	**24**
12	**1420.7042**	***710.8557***	1403.6776	702.3425	1402.6936	701.8504	**V**	2470.1184	1235.5629	2453.0919	1227.0496	2452.1079	1226.5576	**23**
13	**1507.7362**	***754.3717***	1490.7097	745.8585	1489.7256	745.3665	**S**	2371.0500	1186.0287	2354.0235	1177.5154	2353.0395	1177.0234	**22**
14	1635.8312	***818.4192***	1618.8046	809.9060	1617.8206	809.4139	**K**	2284.0180	1142.5126	2266.9915	1133.9994	2266.0074	1133.5074	**21**
15	1748.9152	***874.9613***	1731.8887	866.4480	1730.9047	865.9560	**L**	2155.9230	1078.4652	2138.8965	1069.9519	2137.9125	1069.4599	**20**
16	**1849.9629**	925.4851	1832.9364	916.9718	1831.9524	916.4798	**T**	2042.8390	1021.9231	2025.8124	1013.4099	2024.8284	1012.9178	**19**
17	1964.9899	***982.9986***	1947.9633	974.4853	1946.9793	973.9933	**D**	1941.7913	971.3993	1924.7647	962.8860	1923.7807	962.3940	**18**
18	2066.0375	1033.5224	2049.0110	1025.0091	2048.0270	1024.5171	**T**	1826.7644	913.8858	1809.7378	905.3725	1808.7538	904.8805	**17**
19	2179.1216	***1090.0644***	2162.0951	1081.5512	2161.1110	1081.0592	**I**	1725.7167	863.3620	1708.6901	854.8487	1707.7061	854.3567	**16**
20	2339.1523	***1170.0798***	2322.1257	1161.5665	2321.1417	1161.0745	**C**	1612.6326	806.8199	1595.6061	798.3067	1594.6220	797.8147	**15**
21	2396.1737	***1198.5905***	2379.1472	1190.0772	2378.1632	1189.5852	**G**	1452.6020	726.8046	1435.5754	718.2913	1434.5914	717.7993	**14**
22	2495.2421	***1248.1247***	2478.2156	1239.6114	2477.2316	1239.1194	**V**	1395.5805	698.2939	1378.5539	689.7806	1377.5699	689.2886	**13**

23	2552.2636	***1276.6354***	2535.2370	1268.1222	2534.2530	1267.6302	**G**	1296.5121	648.7597	1279.4855	640.2464	1278.5015	639.7544	**12**
24	2666.3065	***1333.6569***	2649.2800	1325.1436	2648.2960	1324.6516	**N**	1239.4906	620.2489	1222.4641	611.7357	1221.4801	611.2437	**11**
25	2813.3419	***1407.1746***	2796.3154	1398.6613	2795.3314	1398.1693	**M**	1125.4477	563.2275	1108.4211	554.7142	1107.4371	554.2222	**10**
26	2900.3739	1450.6906	2883.3474	1442.1773	2882.3634	1441.6853	**S**	**978.4123**	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2971.4111	***1486.2092***	2954.3845	1477.6959	2953.4005	1477.2039	**A**	891.3803	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3086.4380	1543.7226	3069.4115	1535.2094	3068.4274	1534.7174	**N**	**820.3432**	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3157.4751	***1579.2412***	3140.4486	1570.7279	3139.4646	1570.2359	**A**	**705.3162**	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3244.5071	1622.7572	3227.4806	1614.2439	3226.4966	1613.7519	**S**	**634.2791**	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3359.5341	1680.2707	3342.5075	1671.7574	3341.5235	1671.2654	**D**	**547.2471**	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3487.5927	1744.3000	3470.5661	1735.7867	3469.5821	1735.2947	**Q**	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3616.6353	1808.8213	3599.6087	1800.3080	3598.6247	1799.8160	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.5	3789.7397	2.0171	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28, Oxidation M25; 49.59%
49.2	3789.7397	2.0171	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q32, Oxidation M25; 36.84%
43.6	3789.7397	2.0171	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24, Oxidation M25; 10.12%
38.9	3789.7397	2.0171	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4, Oxidation M25; 3.44%
5.8	3791.7497	0.0071	EQHLSENEPVDTNSDNNLFTDTDLKSIVKNSASK	
5.1	3790.7562	1.0006	TKVMQYTVITCVTSGSGMDYFMINQATTNIDKR	
4.7	3790.7528	1.0040	MEEVYLPDNINEGQVQVRTLYLSVDPYMRCR	
4.4	3791.7402	0.0165	TKVMQYTVITCVTSGSGMDYFMINQATTNIDKR	
4.4	3790.7562	1.0006	TKVMQYTVITCVTSGSGMDYFMINQATTNIDKR	
4.1	3790.7657	0.9911	EQHLSENEPVDTNSDNNLFTDTDLKSIVKNSASK	

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

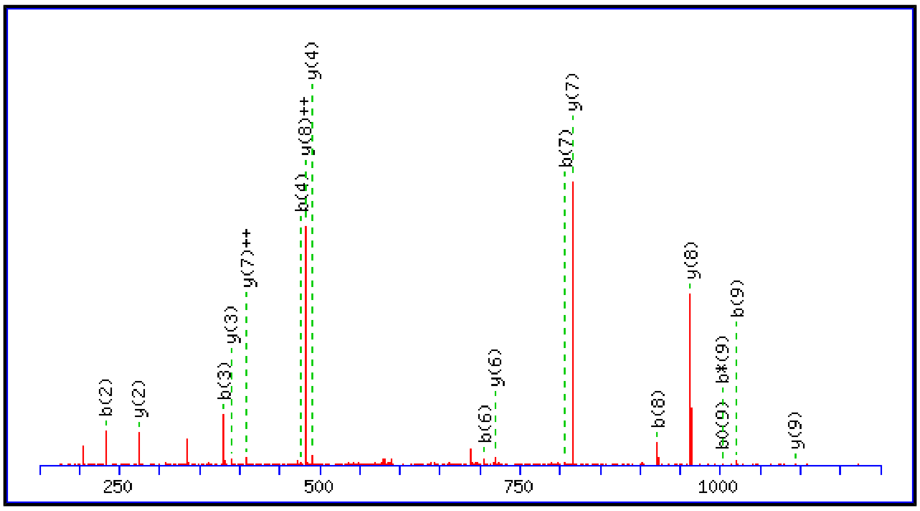
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMFPNLTDVR**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

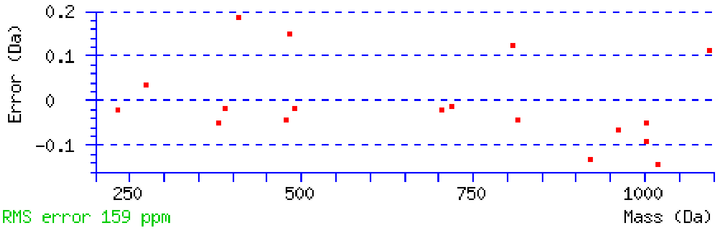
Match to Query 1626: 1193.577888 from(597.796220,2+) intensity(241547.7031) rtinseconds(1596) scans(3997) index(26668)
Title: 111019_Est_MI_YS_G_09Spectrum3463_scans__3997
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

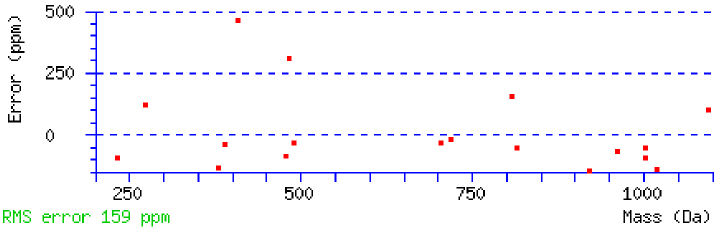
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1193.5751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0018
Matches : 18/96 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	***233.0954***	117.0514			215.0849	108.0461	M	***1093.5347***	547.2710	1076.5081	538.7577	1075.5241	538.2657	9
3	***380.1639***	190.5856			362.1533	181.5803	F	***962.4942***	481.7507	945.4676	473.2375	944.4836	472.7454	8
4	***477.2166***	239.1119			459.2061	230.1067	P	***815.4258***	408.2165	798.3992	399.7032	797.4152	399.2112	7
5	592.2436	296.6254	575.2170	288.1121	574.2330	287.6201	N	***718.3730***	359.6901	701.3464	351.1769	700.3624	350.6849	6
6	***705.3276***	353.1675	688.3011	344.6542	687.3171	344.1622	L	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
7	***806.3753***	403.6913	789.3488	395.1780	788.3647	394.6860	T	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	4
8	***921.4022***	461.2048	904.3757	452.6915	903.3917	452.1995	D	***389.2143***	195.1108	372.1878	186.5975	371.2037	186.1055	3
9	***1020.4707***	510.7390	1003.4441	502.2257	1002.4601	501.7337	V	***274.1874***	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.4	1193.5751	0.0028	TMFPNLTDVR
12.6	1191.5771	2.0007	NDFEPVKQSK
12.0	1193.5724	0.0055	KGGHTCEIHR
9.6	1193.5724	0.0055	GGFVGRGAGGMGR
9.4	1191.5740	2.0039	VMMGVQINER
7.5	1191.5772	2.0007	FPDDLDTNKK
6.8	1191.5772	2.0007	VLDNYPDTVR
4.8	1191.5731	2.0048	TQSSAGVQATNK
4.2	1193.5764	0.0015	HHPDLIFCR
4.0	1191.5731	2.0048	TQSSAGVQATNK

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

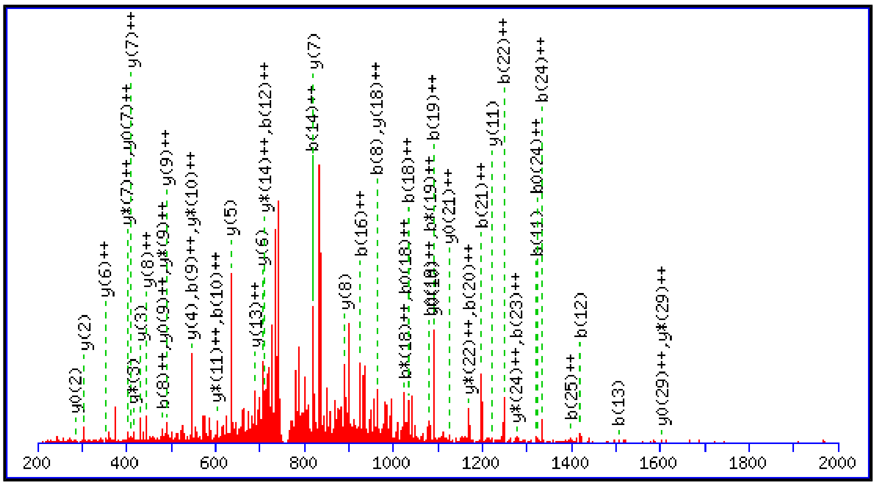
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

Match to Query 28066: 3775.742520 from(756.155780,5+) intensity(27890.1602) rtinseconds(2188) scans(5688) index(9718)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum4904_scans__5688
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

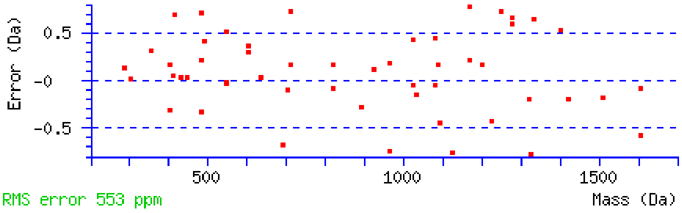
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

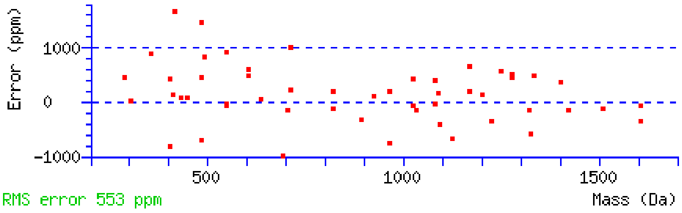


Monoisotopic mass of neutral peptide Mr(calc): 3773.7447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N28 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0046
Matches : 52/376 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**34**
2	185.1285	93.0679					**L**	3703.7149	1852.3611	3686.6884	1843.8478	3685.7043	1843.3558	**33**
3	322.1874	161.5973					**H**	3590.6308	1795.8191	3573.6043	1787.3058	3572.6203	1786.8138	**32**
4	450.2459	225.6266	433.2194	217.1133			**Q**	3453.5719	1727.2896	3436.5454	1718.7763	3435.5614	1718.2843	**31**
5	549.3144	275.1608	532.2878	266.6475			**V**	3325.5134	1663.2603	3308.4868	1654.7470	3307.5028	1654.2550	**30**
6	696.3828	348.6950	679.3562	340.1817			**F**	3226.4449	1613.7261	3209.4184	1605.2128	3208.4344	1604.7208	**29**
7	825.4254	413.2163	808.3988	404.7030	807.4148	404.2110	**E**	3079.3765	1540.1919	3062.3500	1531.6786	3061.3660	1531.1866	**28**
8	**962.4843**	***481.7458***	945.4577	473.2325	944.4737	472.7405	**H**	2950.3339	1475.6706	2933.3074	1467.1573	2932.3234	1466.6653	**27**
9	1093.5248	***547.2660***	1076.4982	538.7527	1075.5142	538.2607	**M**	2813.2750	1407.1411	2796.2485	1398.6279	2795.2645	1398.1359	**26**
10	1206.6088	***603.8081***	1189.5823	595.2948	1188.5983	594.8028	**L**	2682.2345	1341.6209	2665.2080	1333.1076	2664.2240	1332.6156	**25**
11	**1321.6358**	661.3215	1304.6092	652.8082	1303.6252	652.3162	**D**	2569.1505	1285.0789	2552.1239	1276.5656	2551.1399	1276.0736	**24**
12	**1420.7042**	***710.8557***	1403.6776	702.3425	1402.6936	701.8504	**V**	2454.1235	1227.5654	2437.0970	1219.0521	2436.1130	1218.5601	**23**
13	**1507.7362**	754.3717	1490.7097	745.8585	1489.7256	745.3665	**S**	2355.0551	1178.0312	2338.0286	1169.5179	2337.0446	1169.0259	**22**
14	1635.8312	***818.4192***	1618.8046	809.9060	1617.8206	809.4139	**K**	2268.0231	1134.5152	2250.9965	1126.0019	2250.0125	1125.5099	**21**
15	1748.9152	874.9613	1731.8887	866.4480	1730.9047	865.9560	**L**	2139.9281	1070.4677	2122.9016	1061.9544	2121.9176	1061.4624	**20**
16	1849.9629	***925.4851***	1832.9364	916.9718	1831.9524	916.4798	**T**	2026.8441	1013.9257	2009.8175	1005.4124	2008.8335	1004.9204	**19**
17	1964.9899	982.9986	1947.9633	974.4853	1946.9793	973.9933	**D**	1925.7964	963.4018	1908.7698	954.8886	1907.7858	954.3965	**18**
18	2066.0375	***1033.5224***	2049.0110	1025.0091	2048.0270	1024.5171	**T**	1810.7694	905.8884	1793.7429	897.3751	1792.7589	896.8831	**17**
19	2179.1216	***1090.0644***	2162.0951	1081.5512	2161.1110	1081.0592	**I**	1709.7218	855.3645	1692.6952	846.8512	1691.7112	846.3592	**16**
20	2339.1523	***1170.0798***	2322.1257	1161.5665	2321.1417	1161.0745	**C**	1596.6377	798.8225	1579.6111	790.3092	1578.6271	789.8172	**15**
21	2396.1737	***1198.5905***	2379.1472	1190.0772	2378.1632	1189.5852	**G**	1436.6070	718.8072	1419.5805	710.2939	1418.5965	709.8019	**14**
22	2495.2421	***1248.1247***	2478.2156	1239.6114	2477.2316	1239.1194	**V**	1379.5856	690.2964	1362.5590	681.7832	1361.5750	681.2911	**13**
23	2552.2636	***1276.6354***	2535.2370	1268.1222	2534.2530	1267.6302	**G**	1280.5172	640.7622	1263.4906	632.2489	1262.5066	631.7569	**12**

24	2666.3065	***1333.6569***	2649.2800	1325.1436	2648.2960	1324.6516	**N**	***1223.4957***	612.2515	1206.4692	603.7382	1205.4851	603.2462	**11**
25	2797.3470	***1399.1771***	2780.3205	1390.6639	2779.3364	1390.1719	**M**	1109.4528	555.2300	1092.4262	546.7168	1091.4422	546.2247	**10**
26	2884.3790	1442.6932	2867.3525	1434.1799	2866.3685	1433.6879	**S**	978.4123	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
27	2955.4161	1478.2117	2938.3896	1469.6984	2937.4056	1469.2064	**A**	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
28	3070.4431	1535.7252	3053.4165	1527.2119	3052.4325	1526.7199	**N**	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
29	3141.4802	1571.2437	3124.4537	1562.7305	3123.4696	1562.2385	**A**	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
30	3228.5122	1614.7598	3211.4857	1606.2465	3210.5017	1605.7545	**S**	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
31	3343.5392	1672.2732	3326.5126	1663.7600	3325.5286	1663.2679	**D**	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
32	3471.5978	1736.3025	3454.5712	1727.7892	3453.5872	1727.2972	**Q**	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
33	3600.6403	1800.8238	3583.6138	1792.3105	3582.6298	1791.8185	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.1	3773.7447	1.9978	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N28 56.45%
42.0	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
41.9	3773.7447	1.9978	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated N24 21.66%
40.6	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
39.5	3773.7447	1.9978	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q32 12.32%
38.4	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
38.4	3773.7447	1.9978	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	Deamidated Q4 9.56%
37.0	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
30.7	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	
24.5	3774.7287	1.0138	ALHQVFEHMLDVSKLTDTICGVGNMSANASDQER	

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

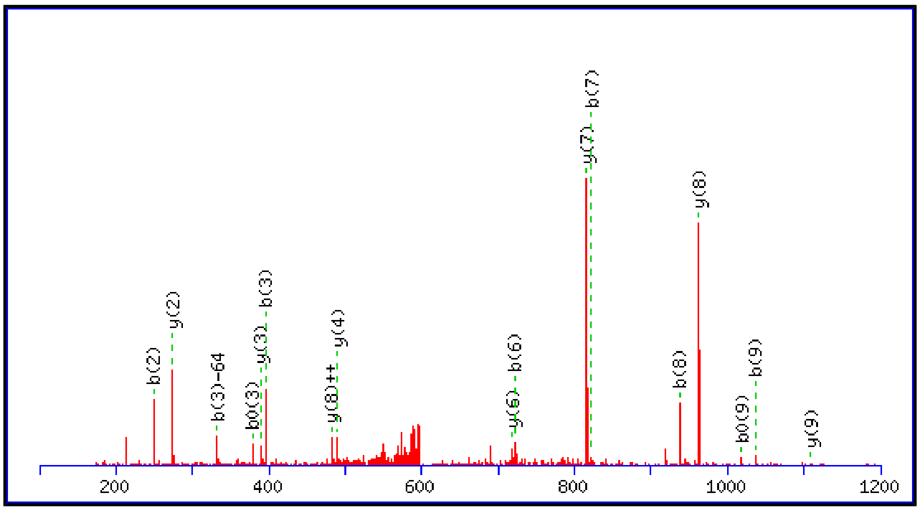
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMFPNLTDVR**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

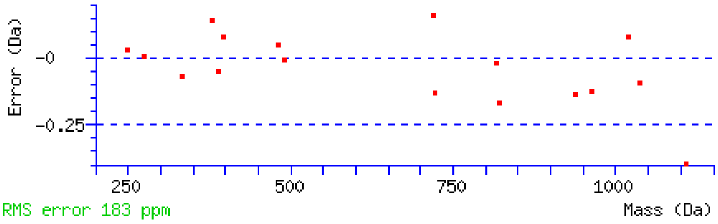
Match to Query 1699: 1209.575048 from(605.794800,2+) intensity(6849.5000) rtinseconds(1354) scans(3156) index(20707)
Title: 111019_Est_MI_YP_G_11Spectrum2762_scans__3156
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

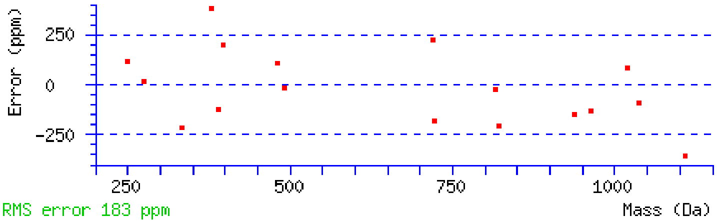
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1209.5700
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N5 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0048
Matches : 17/144 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	102.0550	51.5311			84.0444	42.5258	T							10
2	***249.0904***	125.0488			231.0798	116.0435	M	***1109.5296***	555.2684	1092.5030	546.7552	1091.5190	546.2631	9
3	***396.1588***	198.5830			378.1482	189.5777	F	***962.4942***	481.7507	945.4676	473.2375	944.4836	472.7454	8
4	493.2115	247.1094			475.2010	238.1041	P	***815.4258***	408.2165	798.3992	399.7032	797.4152	399.2112	7
5	608.2385	304.6229	591.2119	296.1096	590.2279	295.6176	N	***718.3730***	359.6901	701.3464	351.1769	700.3624	350.6849	6
6	***721.3225***	361.1649	704.2960	352.6516	703.3120	352.1596	L	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
7	***822.3702***	411.6887	805.3437	403.1755	804.3597	402.6835	T	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	4
8	***937.3972***	469.2022	920.3706	460.6889	919.3866	460.1969	D	***389.2143***	195.1108	372.1878	186.5975	371.2037	186.1055	3
9	***1036.4656***	518.7364	1019.4390	510.2232	1018.4550	509.7311	V	***274.1874***	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TMFPNLTDVR
(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	1209.5700	0.0051	TMFPNLTDVR
15.2	1209.5778	-0.0028	TFFDHSSLTR
7.6	1209.5812	-0.0062	GQFSQLMGAVR
7.4	1209.5699	0.0051	YTMVPESLNR
7.0	1207.5721	2.0030	TFEDNLIEAR
6.1	1209.5812	-0.0062	GQFSQLMGAVR
5.8	1209.5700	0.0051	AAMQFGDTEIK
4.8	1208.5673	1.0077	TEEGPTLSYGR
3.2	1209.5738	0.0013	YSRDQAESVR
3.0	1208.5747	1.0003	TQMPDPKTFK

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

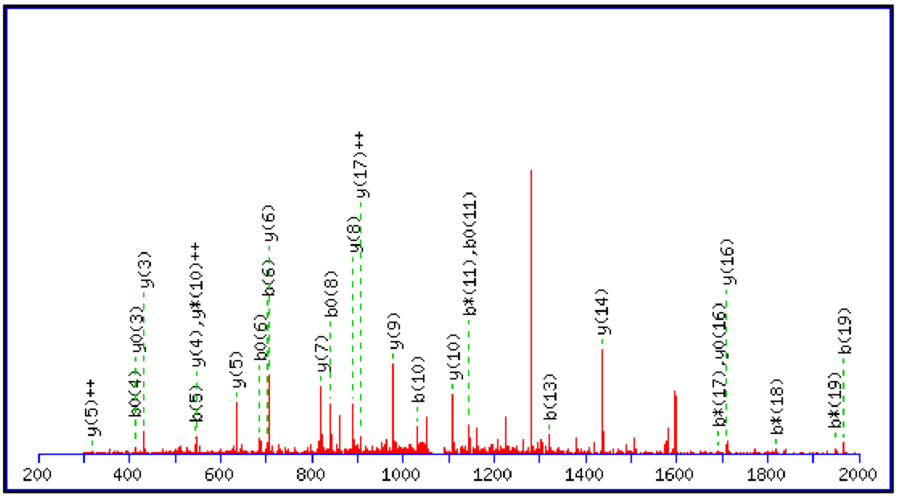
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTDTICGVGNMSANASDQER**
Found in **B4DQI1** in **con_Xuniprot_HUMAN3**, B4DQI1_HUMAN Complement C2b fragment OS=Homo sapiens GN=C2 PE=2 SV=1

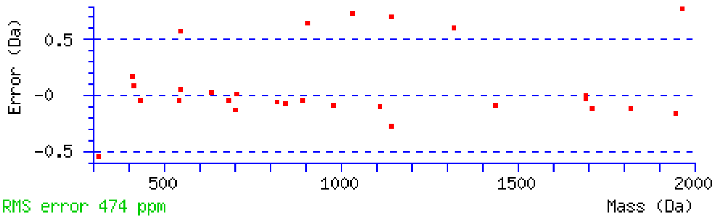
Match to Query 14392: 2139.921748 from(1070.968150,2+) intensity(18929.9277) rtinseconds(1114) scans(2590) index(10861)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum2182_scans__2590
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

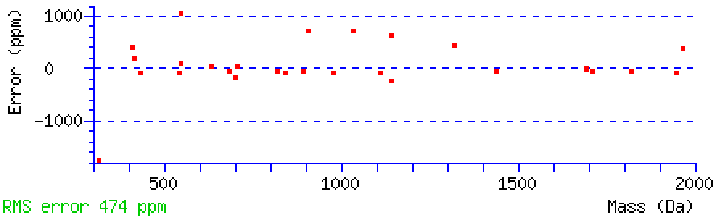
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2138.9208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0025
Matches : 28/206 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					**L**							**20**
2	215.1390	108.0731			197.1285	99.0679	**T**	2026.8441	1013.9257	2009.8175	1005.4124	2008.8335	1004.9204	**19**
3	330.1660	165.5866			312.1554	156.5813	**D**	1925.7964	963.4018	1908.7698	954.8886	1907.7858	954.3965	**18**
4	431.2136	216.1105			413.2031	207.1052	**T**	1810.7694	905.8884	1793.7429	897.3751	1792.7589	896.8831	**17**
5	**544.2977**	272.6525			526.2871	263.6472	**I**	***1709.7218***	855.3645	1692.6952	846.8512	1691.7112	846.3592	**16**
6	**704.3284**	352.6678			686.3178	343.6625	**C**	1596.6377	798.8225	1579.6111	790.3092	1578.6271	789.8172	**15**
7	761.3498	381.1785			743.3393	372.1733	**G**	***1436.6070***	718.8072	1419.5805	710.2939	1418.5965	709.8019	**14**
8	860.4182	430.7128			842.4077	421.7075	**V**	1379.5856	690.2964	1362.5590	681.7832	1361.5750	681.2911	**13**
9	917.4397	459.2235			899.4291	450.2182	**G**	1280.5172	640.7622	1263.4906	632.2489	1262.5066	631.7569	**12**
10	**1031.4826**	516.2449	1014.4561	507.7317	1013.4721	507.2397	**N**	1223.4957	612.2515	1206.4692	603.7382	1205.4851	603.2462	**11**
11	1162.5231	581.7652	1145.4966	573.2519	1144.5125	572.7599	**M**	***1109.4528***	555.2300	1092.4262	546.7168	1091.4422	546.2247	**10**
12	1249.5551	625.2812	1232.5286	616.7679	1231.5446	616.2759	**S**	***978.4123***	489.7098	961.3857	481.1965	960.4017	480.7045	**9**
13	**1320.5923**	660.7998	1303.5657	652.2865	1302.5817	651.7945	**A**	***891.3803***	446.1938	874.3537	437.6805	873.3697	437.1885	**8**
14	1435.6192	718.3132	1418.5926	709.8000	1417.6086	709.3080	**N**	***820.3432***	410.6752	803.3166	402.1619	802.3326	401.6699	**7**
15	1506.6563	753.8318	1489.6298	745.3185	1488.6457	744.8265	**A**	***705.3162***	353.1617	688.2897	344.6485	687.3056	344.1565	**6**
16	1593.6883	797.3478	1576.6618	788.8345	1575.6778	788.3425	**S**	***634.2791***	317.6432	617.2525	309.1299	616.2685	308.6379	**5**
17	1708.7153	854.8613	1691.6887	846.3480	1690.7047	845.8560	**D**	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	**4**
18	1836.7739	918.8906	1819.7473	910.3773	1818.7633	909.8853	**Q**	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	**3**
19	**1965.8164**	983.4119	1948.7899	974.8986	1947.8059	974.4066	**E**	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
20							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.6	2138.9208	1.0009	LTDTICGVGNMSANASDQER	Deamidated N14 84.75%
36.5	2138.9208	1.0009	LTDTICGVGNMSANASDQER	Deamidated Q18 13.10%
28.6	2138.9208	1.0009	LTDTICGVGNMSANASDQER	Deamidated N10 2.16%
6.3	2139.9167	0.0050	DSGDGYGSHTLCAYNLGEPK	
1.2	2139.9160	0.0057	QMEDEAKRSETMNAEQSR	
0.2	2138.9240	0.9978	SKTDWSNDEVVNRESDEK	
0.0	2139.9320	-0.0102	QASWGSNEDGVEFWPKMR	
0.0	2139.9320	-0.0102	QASWGSNEDGVEFWPKMR	

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

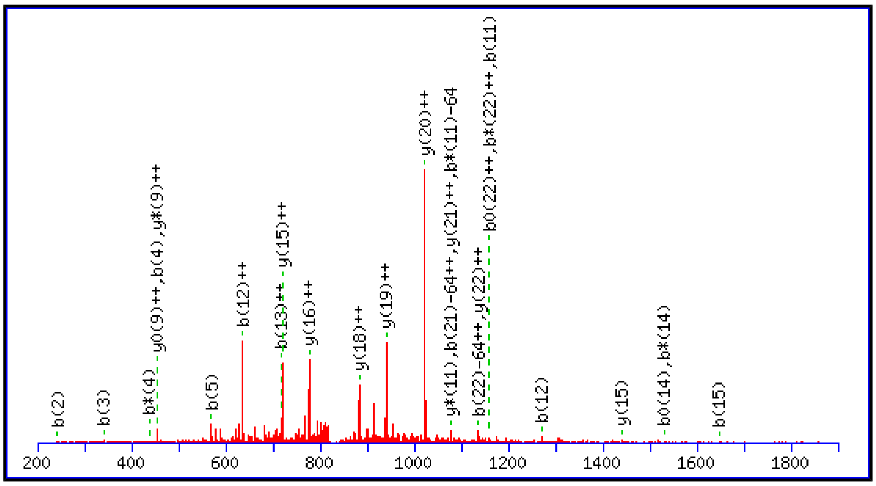
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KIVLDPSGSMNIYLVLDGSDSIGASNFTGAKK**
Found in **B4E1Z4** in **con_Xuniprot_HUMAN3**, B4E1Z4_HUMAN Complement factor B OS=Homo sapiens GN=CFB PE=2 SV=1

Match to Query 27415: 3313.689136 from(829.429560,4+) intensity(31022.5352) rtinseconds(2038) scans(5141) index(23396)
Title: 111019_Est_MI_YS_G_04Spectrum4438_scans__5141
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

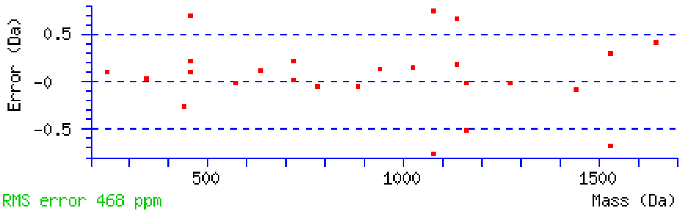
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

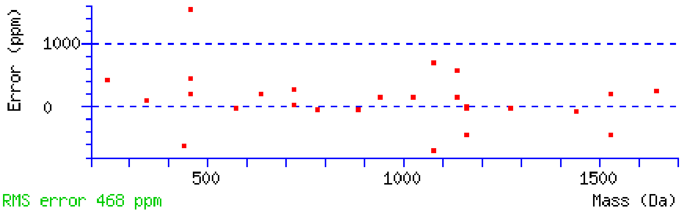


Monoisotopic mass of neutral peptide Mr(calc): 3313.6752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N26 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.031
Matches : 28/542 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							32
2	***242.1863***	121.5968	225.1598	113.0835			I	3186.5875	1593.7974	3169.5609	1585.2841	3168.5769	1584.7921	31
3	***341.2547***	171.1310	324.2282	162.6177			V	3073.5034	1537.2553	3056.4769	1528.7421	3055.4929	1528.2501	30
4	***454.3388***	227.6730	437.3122	219.1598			L	2974.4350	1487.7211	2957.4085	1479.2079	2956.4244	1478.7159	29
5	***569.3657***	285.1865	552.3392	276.6732	551.3552	276.1812	D	2861.3509	1431.1791	2844.3244	1422.6658	2843.3404	1422.1738	28
6	666.4185	333.7129	649.3919	325.1996	648.4079	324.7076	P	2746.3240	1373.6656	2729.2975	1365.1524	2728.3134	1364.6604	27
7	753.4505	377.2289	736.4240	368.7156	735.4400	368.2236	S	2649.2712	1325.1393	2632.2447	1316.6260	2631.2607	1316.1340	26
8	810.4720	405.7396	793.4454	397.2264	792.4614	396.7343	G	2562.2392	1281.6232	2545.2127	1273.1100	2544.2286	1272.6180	25
9	897.5040	449.2556	880.4775	440.7424	879.4934	440.2504	S	2505.2177	1253.1125	2488.1912	1244.5992	2487.2072	1244.1072	24
10	1044.5394	522.7733	1027.5129	514.2601	1026.5288	513.7681	M	2418.1857	1209.5965	2401.1592	1201.0832	2400.1752	1200.5912	23
11	***1158.5823***	579.7948	1141.5558	571.2815	1140.5718	570.7895	N	2271.1503	1136.0788	2254.1238	1127.5655	2253.1398	1127.0735	22
12	***1271.6664***	636.3368	1254.6399	627.8236	1253.6558	627.3316	I	2157.1074	1079.0573	2140.0808	1070.5441	2139.0968	1070.0521	21
13	1434.7297	717.8685	1417.7032	709.3552	1416.7192	708.8632	Y	2044.0233	1022.5153	2026.9968	1014.0020	2026.0128	1013.5100	20
14	1547.8138	774.4105	1530.7872	765.8973	1529.8032	765.4053	L	1880.9600	940.9836	1863.9335	932.4704	1862.9494	931.9784	19
15	***1646.8822***	823.9447	1629.8557	815.4315	1628.8716	814.9395	V	1767.8759	884.4416	1750.8494	875.9283	1749.8654	875.4363	18
16	1759.9663	880.4868	1742.9397	871.9735	1741.9557	871.4815	L	1668.8075	834.9074	1651.7810	826.3941	1650.7970	825.9021	17
17	1874.9932	938.0002	1857.9667	929.4870	1856.9826	928.9950	D	1555.7235	778.3654	1538.6969	769.8521	1537.7129	769.3601	16
18	1932.0147	966.5110	1914.9881	957.9977	1914.0041	957.5057	G	1440.6965	720.8519	1423.6700	712.3386	1422.6859	711.8466	15
19	2019.0467	1010.0270	2002.0202	1001.5137	2001.0361	1001.0217	S	1383.6751	692.3412	1366.6485	683.8279	1365.6645	683.3359	14
20	2134.0736	1067.5405	2117.0471	1059.0272	2116.0631	1058.5352	D	1296.6430	648.8251	1279.6165	640.3119	1278.6325	639.8199	13
21	2221.1057	1111.0565	2204.0791	1102.5432	2203.0951	1102.0512	S	1181.6161	591.3117	1164.5895	582.7984	1163.6055	582.3064	12
22	2334.1897	1167.5985	2317.1632	1159.0852	2316.1792	1158.5932	I	1094.5841	547.7957	1077.5575	539.2824	1076.5735	538.7904	11

23	2391.2112	1196.1092	2374.1847	1187.5960	2373.2006	1187.1040	**G**	981.5000	491.2536	964.4734	482.7404	963.4894	482.2483	**10**
24	2462.2483	1231.6278	2445.2218	1223.1145	2444.2378	1222.6225	**A**	924.4785	462.7429	907.4520	454.2296	906.4680	453.7376	**9**
25	2549.2803	1275.1438	2532.2538	1266.6305	2531.2698	1266.1385	**S**	853.4414	427.2243	836.4149	418.7111	835.4308	418.2191	**8**
26	2664.3073	1332.6573	2647.2807	1324.1440	2646.2967	1323.6520	**N**	766.4094	383.7083	749.3828	375.1951	748.3988	374.7030	**7**
27	2811.3757	1406.1915	2794.3492	1397.6782	2793.3651	1397.1862	**F**	651.3824	326.1949	634.3559	317.6816	633.3719	317.1896	**6**
28	2912.4234	1456.7153	2895.3968	1448.2021	2894.4128	1447.7100	**T**	504.3140	252.6606	487.2875	244.1474	486.3035	243.6554	**5**
29	2969.4448	1485.2261	2952.4183	1476.7128	2951.4343	1476.2208	**G**	403.2663	202.1368	386.2398	193.6235			**4**
30	3040.4820	1520.7446	3023.4554	1512.2313	3022.4714	1511.7393	**A**	346.2449	173.6261	329.2183	165.1128			**3**
31	3168.5769	1584.7921	3151.5504	1576.2788	3150.5664	1575.7868	**K**	275.2078	138.1075	258.1812	129.5942			**2**
32							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.4	3313.6752	0.0140	KIVLDPSGSMNIYLVLDGSDSIGASNFTGAKK	Deamidated N26 82.88%
36.4	3312.6911	0.9980	KIVLDPSGSMNIYLVLDGSDSIGASNFTGAKK	
31.5	3313.6752	0.0140	KIVLDPSGSMNIYLVLDGSDSIGASNFTGAKK	Deamidated N11 17.12%
14.4	3311.6972	1.9919	DPELFLGLASNILNFITSSMLNSRNNFIR	
14.4	3312.6812	1.0079	DPELFLGLASNILNFITSSMLNSRNNFIR	
14.4	3312.6812	1.0079	DPELFLGLASNILNFITSSMLNSRNNFIR	
14.4	3312.6812	1.0079	DPELFLGLASNILNFITSSMLNSRNNFIR	
12.1	3313.6874	0.0017	AWTGATMQMMLYINVFISMLPLLPLAPVK	
9.6	3312.6812	1.0079	DPELFLGLASNILNFITSSMLNSRNNFIR	
9.0	3312.6812	1.0079	DPELFLGLASNILNFITSSMLNSRNNFIR	

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

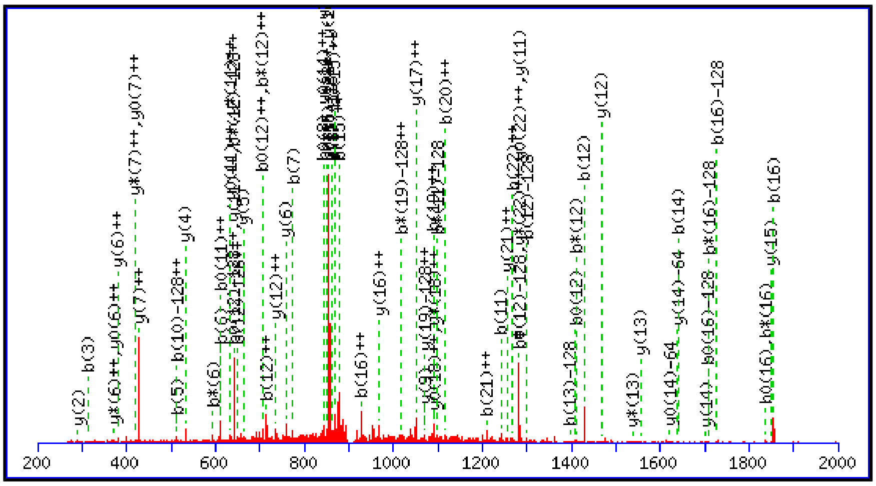
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KALQAVYSMMSWPDDVPPEGWNR**
Found in **B4E1Z4** in **con_Xuniprot_HUMAN3**, B4E1Z4_HUMAN Complement factor B OS=Homo sapiens GN=CFB PE=2 SV=1

Match to Query 25365: 2709.227352 from(904.083060,3+) intensity(9010.7939) rtinseconds(1555) scans(3894) index(24529)
Title: 111019_Est_MI_YS_G_06Spectrum3376_scans__3894
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

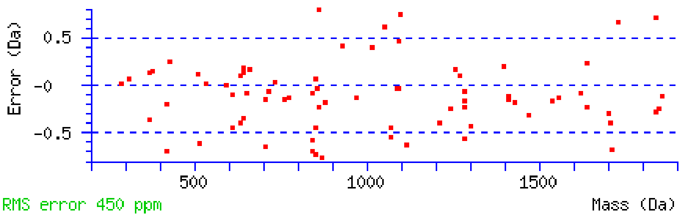
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

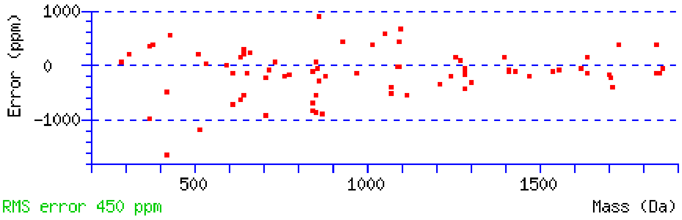


```
Monoisotopic mass of neutral peptide Mr(calc): 2709.2203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M10     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N22     : Deamidated (NQ)
Ions Score: 36  Expect: 0.043
Matches : 77/380 fragment ions using 163 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							23
2	200.1394	100.5733	183.1128	92.0600			A	2582.1326	1291.5700	2565.1061	1283.0567	2564.1221	1282.5647	22
3	***313.2234***	157.1153	296.1969	148.6021			L	2511.0955	1256.0514	2494.0690	1247.5381	2493.0850	1247.0461	21
4	441.2820	221.1446	424.2554	212.6314			Q	2398.0115	1199.5094	2380.9849	1190.9961	2380.0009	1190.5041	20
5	***512.3191***	256.6632	495.2926	248.1499			A	2269.9529	1135.4801	2252.9263	1126.9668	2251.9423	1126.4748	19
6	***611.3875***	306.1974	594.3610	297.6841			V	2198.9158	1099.9615	2181.8892	1091.4482	2180.9052	1090.9562	18
7	***774.4509***	387.7291	757.4243	379.2158			Y	2099.8474	1050.4273	2082.8208	1041.9140	2081.8368	1041.4220	17
8	***861.4829***	431.2451	844.4563	422.7318	843.4723	422.2398	S	1936.7840	968.8957	1919.7575	960.3824	1918.7735	959.8904	16
9	1008.5183	504.7628	991.4917	496.2495	990.5077	495.7575	M	***1849.7520***	925.3796	1832.7254	916.8664	1831.7414	916.3744	15
10	1155.5537	578.2805	1138.5271	569.7672	1137.5431	569.2752	M	***1702.7166***	851.8619	1685.6900	843.3487	1684.7060	842.8567	14
11	***1242.5857***	621.7965	1225.5592	613.2832	1224.5751	612.7912	S	***1555.6812***	778.3442	1538.6546	769.8310	1537.6706	769.3390	13
12	***1428.6650***	***714.8361***	1411.6385	706.3229	1410.6545	705.8309	W	***1468.6492***	734.8282	1451.6226	726.3149	1450.6386	725.8229	12
13	1525.7178	763.3625	1508.6912	754.8493	1507.7072	754.3572	P	***1282.5699***	641.7886	1265.5433	633.2753	1264.5593	632.7833	11
14	***1640.7447***	820.8760	1623.7182	812.3627	1622.7342	811.8707	D	1185.5171	593.2622	1168.4905	584.7489	1167.5065	584.2569	10
15	1755.7717	***878.3895***	1738.7451	869.8762	1737.7611	869.3842	D	***1070.4902***	535.7487	1053.4636	527.2354	1052.4796	526.7434	9
16	***1854.8401***	***927.9237***	1837.8135	919.4104	1836.8295	918.9184	V	955.4632	478.2352	938.4367	469.7220	937.4526	469.2300	8
17	1951.8928	976.4501	1934.8663	967.9368	1933.8823	967.4448	P	***856.3948***	428.7010	839.3682	420.1878	838.3842	419.6958	7
18	2048.9456	1024.9764	2031.9191	1016.4632	2030.9350	1015.9712	P	***759.3420***	380.1747	742.3155	371.6614	741.3315	371.1694	6
19	2177.9882	***1089.4977***	2160.9617	1080.9845	2159.9776	1080.4925	E	***662.2893***	331.6483	645.2627	323.1350	644.2787	322.6430	5
20	2235.0097	***1118.0085***	2217.9831	1109.4952	2216.9991	1109.0032	G	***533.2467***	267.1270	516.2201	258.6137			4
21	2421.0890	***1211.0481***	2404.0624	1202.5349	2403.0784	1202.0428	W	476.2252	238.6162	459.1987	230.1030			3
22	2536.1159	***1268.5616***	2519.0894	1260.0483	2518.1054	1259.5563	N	***290.1459***	145.5766	273.1193	137.0633			2

23							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.8	2709.2203	0.0070	KALQAVYSMMSWPDDVPPEGWNR	Deamidated N22 98.98%
20.5	2708.2363	0.9911	KALQAVYSMMSWPDDVPPEGWNR	
16.0	2709.2203	0.0070	KALQAVYSMMSWPDDVPPEGWNR	Deamidated Q4 1.02%
4.8	2708.2118	1.0155	YGRPCVCRYSGRTNECIQNYR	
3.9	2707.2258	2.0015	TGCSLMGASVDSTLAFNTYVHFQGK	
2.8	2709.2329	-0.0055	QYQHLNASFWFQRGCAGCTHLK	
2.8	2709.2329	-0.0055	QYQHLNASFWFQRGCAGCTHLK	
2.3	2709.2329	-0.0055	QYQHLNASFWFQRGCAGCTHLK	
2.1	2709.2203	0.0070	RYYDEVEAEGYVKHDCVGYVMK	
1.5	2708.2301	0.9973	QQEETHVQVADPVIGPTSEQGNVDK	

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

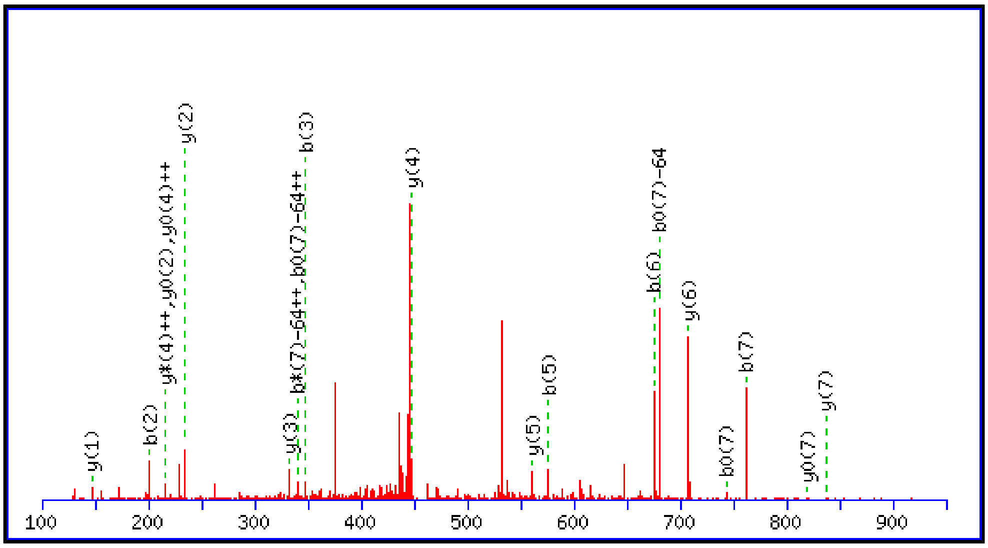
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEMLNVSK**
Found in **B5MCY1** in **con_Xuniprot_HUMAN3**, TDR15_HUMAN Tudor domain-containing protein 15 OS=Homo sapiens GN=TDRD15 PE=2 SV=1

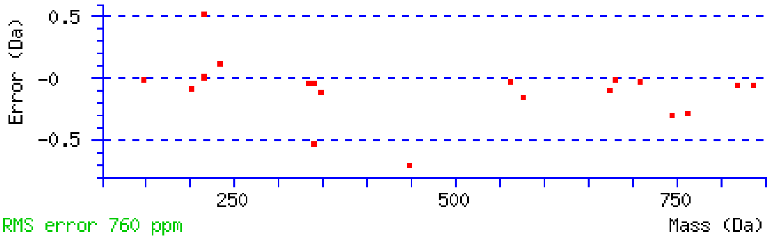
Match to Query 13: 907.431128 from(454.722840,2+) intensity(60855.0234) rtinseconds(804) scans(1833) index(13555)
Title: 111019_Est_ISCardio_NMI_YS_G_15Spectrum1581_scans__1833
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐

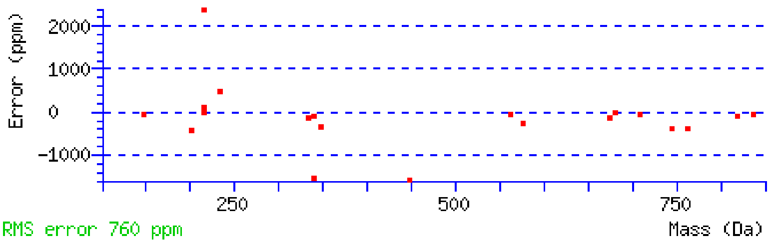


Monoisotopic mass of neutral peptide Mr(calc): 907.4321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N5 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0048
Matches : 20/110 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							8
2	**201.0870**	101.0471			183.0764	92.0418	E	***837.4022***	419.2048	820.3757	410.6915	819.3917	410.1995	7
3	**348.1224**	174.5648			330.1118	165.5595	M	***708.3597***	354.6835	691.3331	346.1702	690.3491	345.6782	6
4	461.2064	231.1069			443.1959	222.1016	L	***561.3243***	281.1658	544.2977	272.6525	543.3137	272.1605	5
5	**576.2334**	288.6203	559.2068	280.1071	558.2228	279.6151	N	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6184	4
6	**675.3018**	338.1545	658.2753	329.6413	657.2912	329.1493	V	***333.2132***	167.1103	316.1867	158.5970	315.2027	158.1050	3
7	**762.3338**	381.6706	745.3073	373.1573	744.3233	372.6653	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
8							K	***147.1128***	74.0600	130.0863	65.5468			1



RMS error 760 ppm



NCBI **BLAST** search of [AEMLNVSK]
(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	907.4321	-0.0009	AEMLNVSK
25.7	907.4287	0.0025	LNFEANAK
24.3	907.4321	-0.0009	DLMINASK
21.5	907.4287	0.0024	ANFIEADK
21.5	907.4321	-0.0009	AQMLTEAK
13.4	907.4321	-0.0009	DLMKEQK
13.3	907.4321	-0.0009	QVAEMSVK
13.0	905.4277	2.0035	SGPAQTAMK
12.4	907.4287	0.0024	INFQEEK
12.0	907.4295	0.0016	EAMMLWK

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

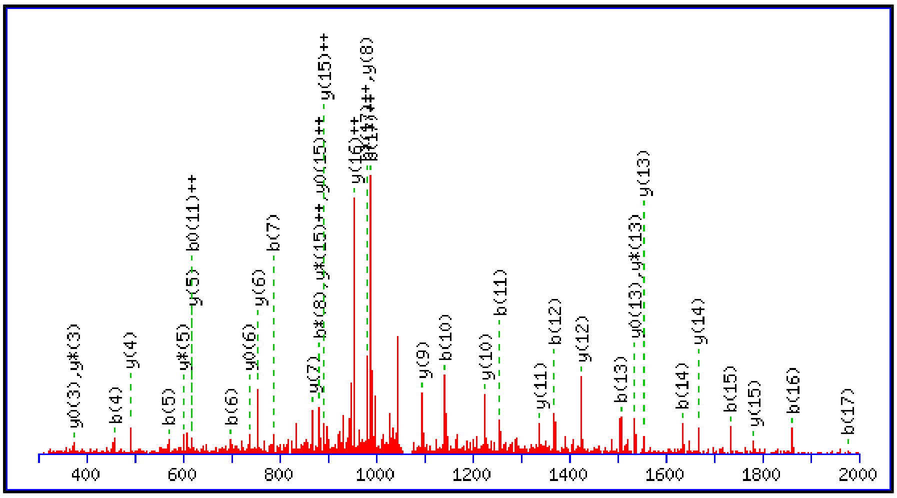
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDKDLQSLEDILHQVENK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

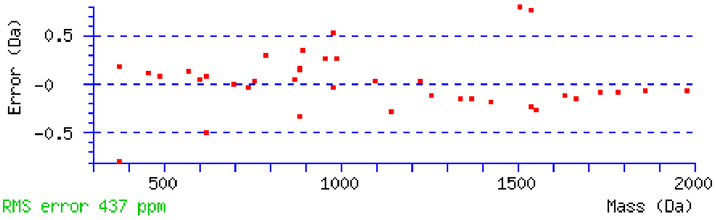
Match to Query 14239: 2123.084988 from(1062.549770,2+) intensity(28118.3418) rtinseconds(2326) scans(5660) index(16981)
Title: 111019_Est_MI_YP_G_06Spectrum4707_scans__5660
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

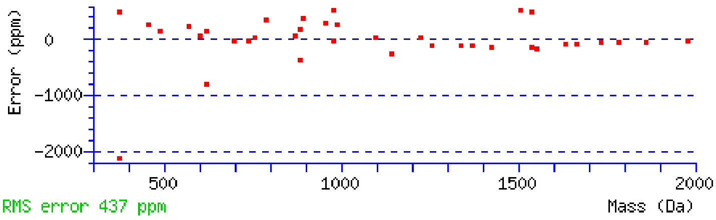
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2123.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 97 **Expect:** 5.1e-008
Matches : 38/194 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	100.0757	50.5415					V							18
2	215.1026	108.0550			197.0921	99.0497	D	2025.0135	1013.0104	2007.9869	1004.4971	2007.0029	1004.0051	17
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	K	1909.9865	955.4969	1892.9600	946.9836	1891.9760	946.4916	16
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	D	***1781.8916***	891.4494	1764.8650	882.9362	1763.8810	882.4441	15
5	***571.3086***	286.1579	554.2821	277.6447	553.2980	277.1527	L	***1666.8646***	833.9360	1649.8381	825.4227	1648.8541	824.9307	14
6	***699.3672***	350.1872	682.3406	341.6740	681.3566	341.1819	Q	***1553.7806***	777.3939	1536.7540	768.8807	1535.7700	768.3886	13
7	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	S	***1425.7220***	713.3646	1408.6955	704.8514	1407.7114	704.3594	12
8	899.4833	450.2453	882.4567	441.7320	881.4727	441.2400	L	***1338.6900***	669.8486	1321.6634	661.3353	1320.6794	660.8433	11
9	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	E	***1225.6059***	613.3066	1208.5794	604.7933	1207.5953	604.3013	10
10	***1143.5528***	572.2800	1126.5263	563.7668	1125.5422	563.2748	D	***1096.5633***	548.7853	1079.5368	540.2720	1078.5528	539.7800	9
11	***1256.6369***	628.8221	1239.6103	620.3088	1238.6263	619.8168	I	***981.5364***	491.2718	964.5098	482.7585	963.5258	482.2665	8
12	***1369.7209***	685.3641	1352.6944	676.8508	1351.7104	676.3588	L	***868.4523***	434.7298	851.4258	426.2165	850.4417	425.7245	7
13	***1506.7798***	753.8936	1489.7533	745.3803	1488.7693	744.8883	H	***755.3682***	378.1878	738.3417	369.6745	737.3577	369.1825	6
14	***1634.8384***	817.9229	1617.8119	809.4096	1616.8279	808.9176	Q	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
15	***1733.9068***	867.4571	1716.8803	858.9438	1715.8963	858.4518	V	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
16	***1862.9494***	931.9784	1845.9229	923.4651	1844.9389	922.9731	E	391.1823	196.0948	374.1558	187.5815	373.1718	187.0895	3
17	***1977.9764***	989.4918	1960.9498	980.9786	1959.9658	980.4865	N	262.1397	131.5735	245.1132	123.0602			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.0	2123.0746	0.0104	VDKDLQSLEDILHQVENK	Deamidated N17 96.93%
82.0	2123.0746	0.0104	VDKDLQSLEDILHQVENK	Deamidated Q14 3.07%
52.4	2123.0746	0.0104	VDKDLQSLEDILHQVENK	Deamidated Q6 0.00%
43.1	2122.0906	0.9944	VDKDLQSLEDILHQVENK	
17.3	2123.0932	-0.0082	QVETIRNLVDSYMSIINK	
10.6	2123.0755	0.0095	VQNVEAGKGCVAAVYSMVLK	
10.6	2123.0755	0.0095	VQNVEAGKGCVAAVYSMVLK	
7.3	2123.0899	-0.0049	SQYQTVRYDILPLSPVSR	
7.2	2123.0932	-0.0082	QVETIRNLVDSYMSIINK	
4.8	2122.0715	1.0135	TVATSGNMQAVELLLSTLEK	

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

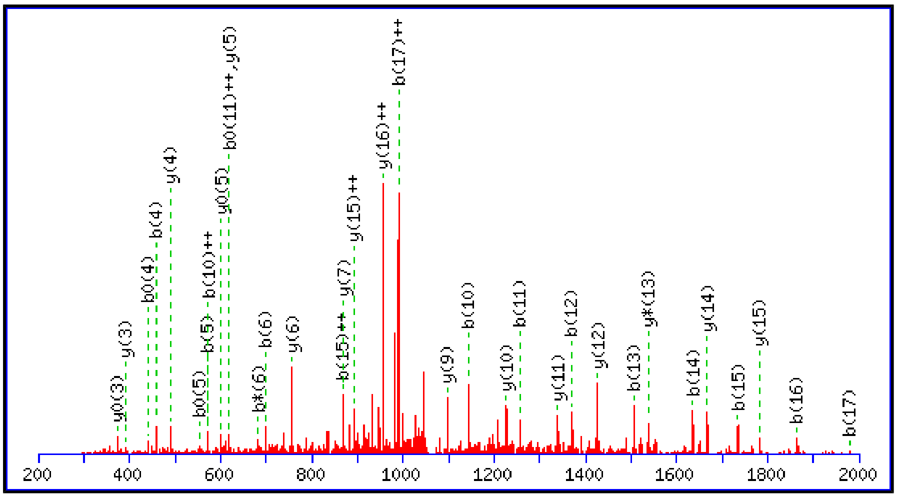
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDKDLQSLEDILHQVENK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

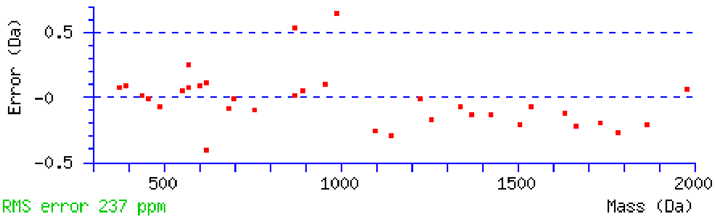
Match to Query 14253: 2124.065828 from(1063.040190,2+) intensity(32723.9844) rtinseconds(2212) scans(5507) index(15332)
Title: 111019_Est_MI_YP_G_04Spectrum4748_scans__5507
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

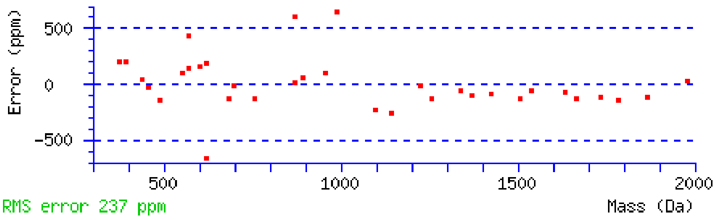
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2124.0586
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 89 **Expect:** 3.7e-007
Matches : 34/194 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							18
2	215.1026	108.0550			197.0921	99.0497	D	2025.9975	1013.5024	2008.9710	1004.9891	2007.9869	1004.4971	17
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	K	1910.9706	955.9889	1893.9440	947.4756	1892.9600	946.9836	16
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	D	***1782.8756***	891.9414	1765.8491	883.4282	1764.8650	882.9362	15
5	***571.3086***	286.1579	554.2821	277.6447	553.2980	277.1527	L	***1667.8487***	834.4280	1650.8221	825.9147	1649.8381	825.4227	14
6	***699.3672***	350.1872	682.3406	341.6740	681.3566	341.1819	Q	1554.7646	777.8859	1537.7380	769.3727	1536.7540	768.8807	13
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	S	***1426.7060***	713.8566	1409.6795	705.3434	1408.6955	704.8514	12
8	899.4833	450.2453	882.4567	441.7320	881.4727	441.2400	L	***1339.6740***	670.3406	1322.6474	661.8274	1321.6634	661.3353	11
9	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	E	***1226.5899***	613.7986	1209.5634	605.2853	1208.5794	604.7933	10
10	***1143.5528***	**572.2800**	1126.5263	563.7668	1125.5422	563.2748	D	***1097.5473***	549.2773	1080.5208	540.7640	1079.5368	540.2720	9
11	***1256.6369***	628.8221	1239.6103	620.3088	1238.6263	619.8168	I	982.5204	491.7638	965.4938	483.2506	964.5098	482.7585	8
12	***1369.7209***	685.3641	1352.6944	676.8508	1351.7104	676.3588	L	***869.4363***	435.2218	852.4098	426.7085	851.4258	426.2165	7
13	***1506.7798***	753.8936	1489.7533	745.3803	1488.7693	744.8883	H	***756.3523***	378.6798	739.3257	370.1665	738.3417	369.6745	6
14	***1635.8224***	818.4149	1618.7959	809.9016	1617.8119	809.4096	Q	***619.2933***	310.1503	602.2668	301.6370	601.2828	301.1450	5
15	***1734.8909***	**867.9491**	1717.8643	859.4358	1716.8803	858.9438	V	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
16	***1863.9335***	932.4704	1846.9069	923.9571	1845.9229	923.4651	E	***391.1823***	196.0948	374.1558	187.5815	373.1718	187.0895	3
17	***1978.9604***	**989.9838**	1961.9338	981.4706	1960.9498	980.9786	N	262.1397	131.5735	245.1132	123.0602			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.6	2124.0586	0.0072	VDKDLQSLEDILHQVENK	Deamidated Q14, N17 99.99%
47.0	2124.0586	0.0072	VDKDLQSLEDILHQVENK	Deamidated Q6, N17 0.01%
46.1	2124.0586	0.0072	VDKDLQSLEDILHQVENK	Deamidated Q6, Q14 0.01%
11.9	2124.0674	-0.0015	EHQDINHVGLLLSYDMIK	
9.5	2123.0577	1.0081	MQDMLKMAFDALAKIHTK	
8.5	2124.0595	0.0063	VQNVEAGKGCVAAVYSMVLK	
8.3	2124.0640	0.0018	NFFVNRTVQKHFDTLQK	
7.5	2124.0640	0.0018	NFFVNRTVQKHFDTLQK	
6.9	2124.0640	0.0018	NFFVNRTVQKHFDTLQK	
6.6	2124.0586	0.0072	NEVQHLIDELSQLDKDVK	

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

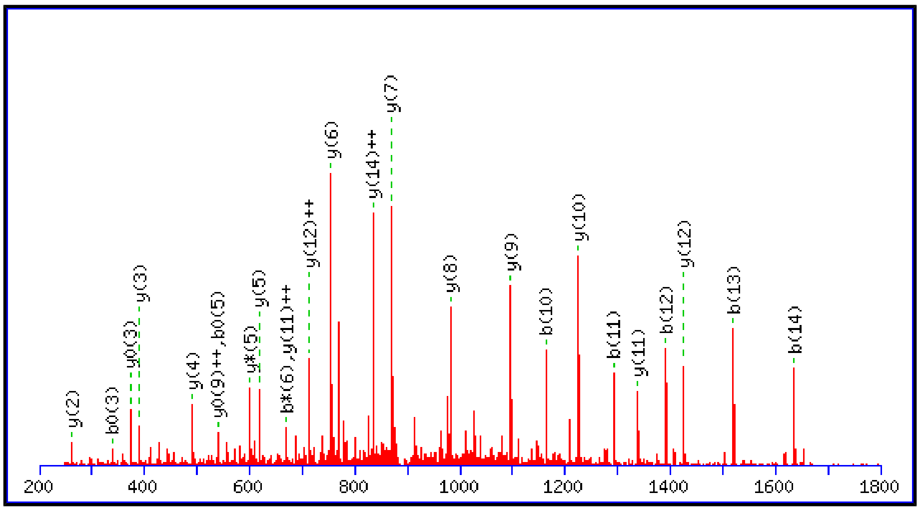
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSLEDILHQVENK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

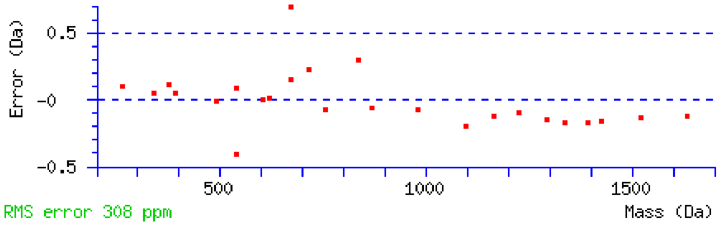
Match to Query 10144: 1780.890508 from(891.452530,2+) intensity(186271.0469) rtinseconds(2400) scans(5992) index(9135)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum5174_scans__5992
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

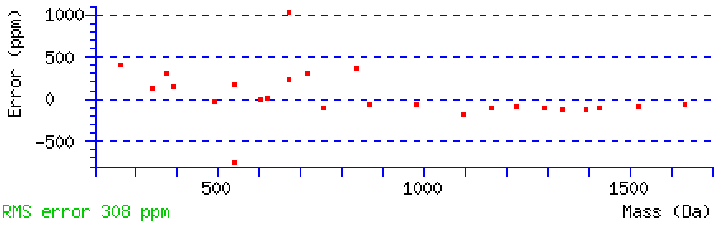
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1780.8843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 88 **Expect:** 3.9e-007
Matches : 25/160 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	229.1183	115.0628			211.1077	106.0575	L	1666.8646	833.9360	1649.8381	825.4227	1648.8541	824.9307	14
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	Q	1553.7806	777.3939	1536.7540	768.8807	1535.7700	768.3886	13
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	S	***1425.7220***	713.3646	1408.6955	704.8514	1407.7114	704.3594	12
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	L	***1338.6900***	669.8486	1321.6634	661.3353	1320.6794	660.8433	11
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	E	***1225.6059***	613.3066	1208.5794	604.7933	1207.5953	604.3013	10
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	D	***1096.5633***	548.7853	1079.5368	540.2720	1078.5527	539.7800	9
8	914.4466	457.7269	897.4200	449.2136	896.4360	448.7216	I	***981.5364***	491.2718	964.5098	482.7585	963.5258	482.2665	8
9	1027.5306	514.2689	1010.5041	505.7557	1009.5201	505.2637	L	***868.4523***	434.7298	851.4258	426.2165	850.4417	425.7245	7
10	**1164.5895**	582.7984	1147.5630	574.2851	1146.5790	573.7931	H	***755.3682***	378.1878	738.3417	369.6745	737.3577	369.1825	6
11	**1292.6481**	646.8277	1275.6216	638.3144	1274.6375	637.8224	Q	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
12	**1391.7165**	696.3619	1374.6900	687.8486	1373.7060	687.3566	V	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
13	**1520.7591**	760.8832	1503.7326	752.3699	1502.7485	751.8779	E	***391.1823***	196.0948	374.1558	187.5815	373.1718	187.0895	3
14	**1635.7861**	818.3967	1618.7595	809.8834	1617.7755	809.3914	N	***262.1397***	131.5735	245.1132	123.0602			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.1	1780.8843	0.0062	DLQSLEDILHQVENK	Deamidated N14 99.98%
51.1	1780.8843	0.0062	DLQSLEDILHQVENK	Deamidated Q11 0.02%
21.2	1780.8883	0.0022	QLNSIYGEYIPELNK	
21.0	1780.8883	0.0022	QLNSIYGEYIPELNK	
8.2	1780.8843	0.0062	DLQSLEDILHQVENK	Deamidated Q3 0.00%
6.5	1779.8825	1.0080	KMLNEKVSNQAFEDK	
6.0	1780.8843	0.0062	SLQKLDPHQKDDINK	
5.8	1780.8955	-0.0050	RESSQPLLQGENPTPK	
4.4	1780.8843	0.0062	NEVQHLIDELSQLDK	
3.8	1780.8843	0.0062	NEVQHLIDELSQLDK	

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

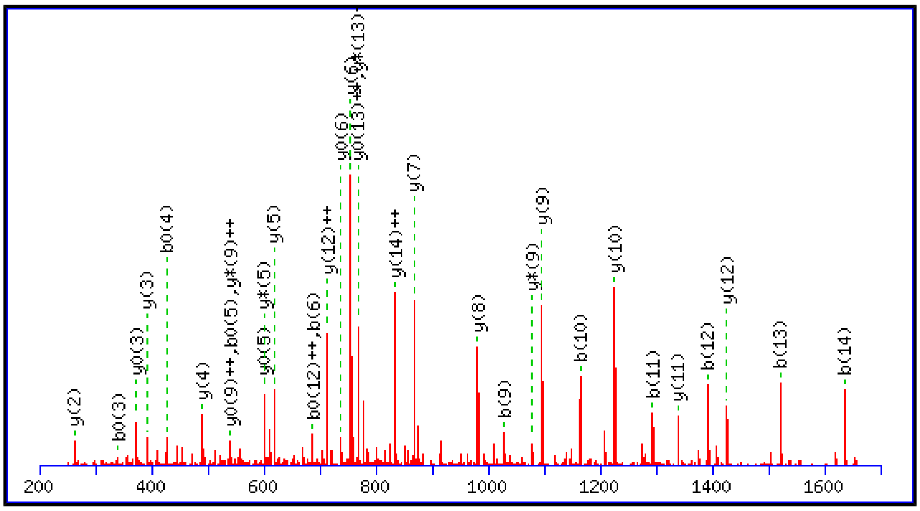
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSLEDILHQVENK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

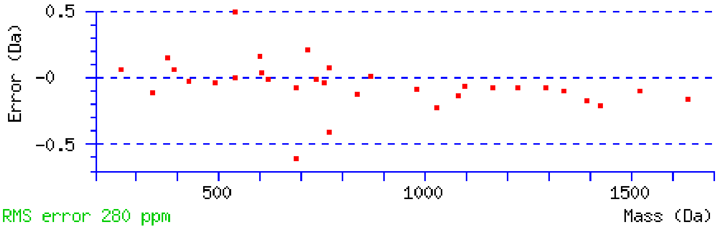
Match to Query 10178: 1781.871928 from(891.943240,2+) intensity(470838.0313) rtinseconds(2380) scans(6316) index(4626)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum5382_scans__6316
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

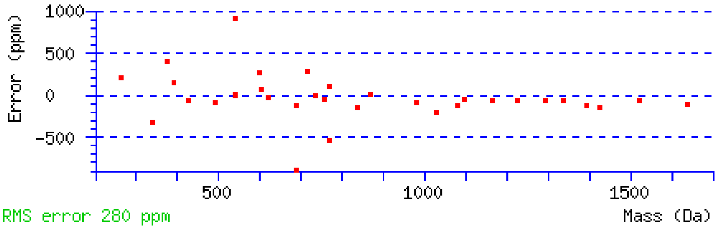
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1781.8683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N14 : Deamidated (NQ)
Ions Score: 75 **Expect:** 8.6e-006
Matches : 33/160 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	116.0342	58.5207			98.0237	49.5155	D							15
2	229.1183	115.0628			211.1077	106.0575	L	1667.8487	834.4280	1650.8221	825.9147	1649.8381	825.4227	14
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	Q	1554.7646	777.8859	1537.7380	769.3727	1536.7540	768.8807	13
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	S	***1425.7220***	713.3646	1408.6955	704.8514	1407.7114	704.3594	12
5	558.2770	279.6421	541.2504	271.1288	540.2664	270.6368	L	***1338.6900***	669.8486	1321.6634	661.3353	1320.6794	660.8433	11
6	**687.3196**	344.1634	670.2930	335.6501	669.3090	335.1581	E	***1225.6059***	613.3066	1208.5794	604.7933	1207.5953	604.3013	10
7	802.3465	401.6769	785.3200	393.1636	784.3359	392.6716	D	***1096.5633***	548.7853	1079.5368	540.2720	1078.5528	539.7800	9
8	915.4306	458.2189	898.4040	449.7056	897.4200	449.2136	I	***981.5364***	491.2718	964.5098	482.7585	963.5258	482.2665	8
9	**1028.5146**	514.7610	1011.4881	506.2477	1010.5041	505.7557	L	***868.4523***	434.7298	851.4258	426.2165	850.4417	425.7245	7
10	**1165.5735**	583.2904	1148.5470	574.7771	1147.5630	574.2851	H	***755.3682***	378.1878	738.3417	369.6745	737.3577	369.1825	6
11	**1293.6321**	647.3197	1276.6056	638.8064	1275.6216	638.3144	Q	***618.3093***	309.6583	601.2828	301.1450	600.2988	300.6530	5
12	**1392.7005**	696.8539	1375.6740	688.3406	1374.6900	687.8486	V	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
13	**1521.7431**	761.3752	1504.7166	752.8619	1503.7326	752.3699	E	***391.1823***	196.0948	374.1558	187.5815	373.1718	187.0895	3
14	**1636.7701**	818.8887	1619.7435	810.3754	1618.7595	809.8834	N	***262.1397***	131.5735	245.1132	123.0602			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
74.6	1781.8683	0.0036	DLQSLEDILHQVENK	Deamidated Q3, N14 98.78%
53.9	1781.8683	0.0036	DLQSLEDILHQVENK	Deamidated Q11, N14 0.84%
50.5	1781.8683	0.0036	DLQSLEDILHQVENK	Deamidated Q3, Q11 0.38%
23.2	1780.8665	1.0054	KMLNEKVSNQAFEDK	
18.7	1781.8723	-0.0004	QLNSIYGEYIPELNK	
14.7	1781.8723	-0.0004	QLNSIYGEYIPELNK	
14.1	1781.8631	0.0088	KVTCEHVRSTWHNK	
9.7	1781.8723	-0.0004	QLNSIYGEYIPELNK	
9.6	1780.8665	1.0054	KMLNEKVSNQAFEDK	
8.7	1781.8795	-0.0076	LQNPSESSEPIPLESR	

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

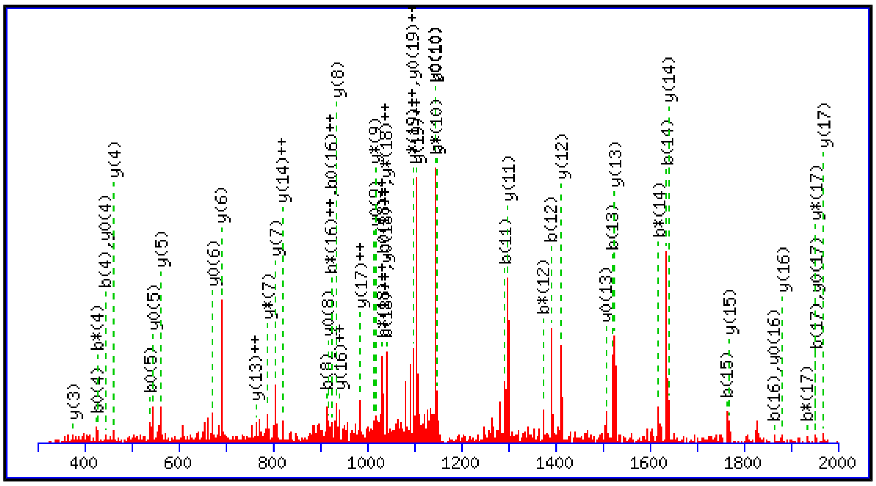
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSLEDILHQVENKTSEVK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

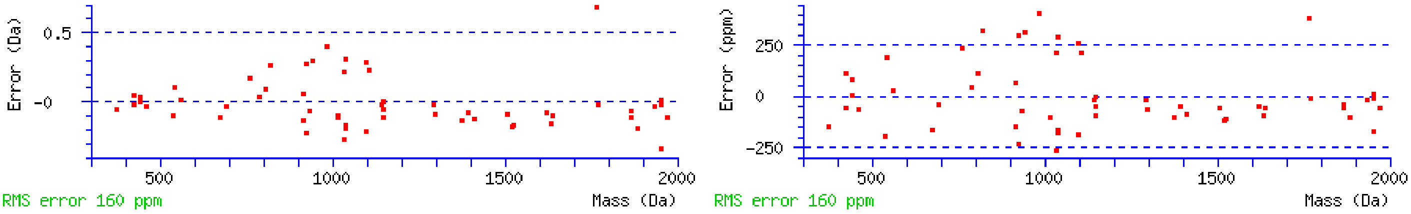
Match to Query 15467: 2325.180068 from(1163.597310,2+) intensity(45979.9414) rtinseconds(2389) scans(6199) index(14751)
Title: 111019_Est_MI_YP_G_03Spectrum5407_scans__6199
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2325.1700
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 74 **Expect:** 9.2e-006
Matches : 57/220 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							20
2	229.1183	115.0628			211.1077	106.0575	L	2211.1503	1106.0788	2194.1238	1097.5655	2193.1398	1097.0735	19
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	Q	2098.0663	1049.5368	2081.0397	1041.0235	2080.0557	1040.5315	18
4	**444.2089**	222.6081	427.1823	214.0948	426.1983	213.6028	S	***1970.0077***	985.5075	1952.9811	976.9942	1951.9971	976.5022	17
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	L	***1882.9756***	941.9915	1865.9491	933.4782	1864.9651	932.9862	16
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	E	***1769.8916***	885.4494	1752.8650	876.9362	1751.8810	876.4441	15
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	D	***1640.8490***	820.9281	1623.8224	812.4149	1622.8384	811.9229	14
8	**914.4466**	457.7269	897.4200	449.2136	896.4360	448.7216	I	***1525.8220***	763.4147	1508.7955	754.9014	1507.8115	754.4094	13
9	1027.5306	514.2689	1010.5041	505.7557	1009.5201	505.2637	L	***1412.7380***	706.8726	1395.7114	698.3594	1394.7274	697.8673	12
10	1164.5895	582.7984	1147.5630	574.2851	1146.5790	573.7931	H	***1299.6539***	650.3306	1282.6274	641.8173	1281.6434	641.3253	11
11	**1292.6481**	646.8277	1275.6216	638.3144	1274.6375	637.8224	Q	1162.5950	581.8011	1145.5685	573.2879	1144.5844	572.7959	10
12	**1391.7165**	696.3619	1374.6900	687.8486	1373.7060	687.3566	V	1034.5364	517.7719	1017.5099	509.2586	1016.5259	508.7666	9
13	**1520.7591**	760.8832	1503.7326	752.3699	1502.7485	751.8779	E	***935.4680***	468.2376	918.4415	459.7244	917.4575	459.2324	8
14	**1635.7861**	818.3967	1618.7595	809.8834	1617.7755	809.3914	N	***806.4254***	403.7164	789.3989	395.2031	788.4149	394.7111	7
15	**1763.8810**	882.4441	1746.8545	873.9309	1745.8705	873.4389	K	***691.3985***	346.2029	674.3719	337.6896	673.3879	337.1976	6
16	**1864.9287**	932.9680	1847.9021	924.4547	1846.9181	923.9627	T	***563.3035***	282.1554	546.2770	273.6421	545.2930	273.1501	5
17	**1951.9607**	976.4840	1934.9342	967.9707	1933.9502	967.4787	S	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	4
18	2081.0033	1041.0053	2063.9768	1032.4920	2062.9928	1032.0000	E	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
19	2180.0717	1090.5395	2163.0452	1082.0262	2162.0612	1081.5342	V	246.1812	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
74.2	2325.1700	0.0101	DLQSLEDILHQVENKTSEVK	Deamidated N14 97.90%
57.5	2325.1700	0.0101	DLQSLEDILHQVENKTSEVK	Deamidated Q11 2.09%
33.8	2325.1700	0.0101	DLQSLEDILHQVENKTSEVK	Deamidated Q3 0.01%
20.9	2324.1859	0.9941	DLQSLEDILHQVENKTSEVK	
11.1	2323.1691	2.0110	EIMAEDDQVFLMKLQSLLAK	
2.3	2324.1769	1.0031	KLRGTMLLTFMTQGVNFGHR	
1.9	2325.1827	-0.0027	DEPRSTNLFMKLDSVFIWK	

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

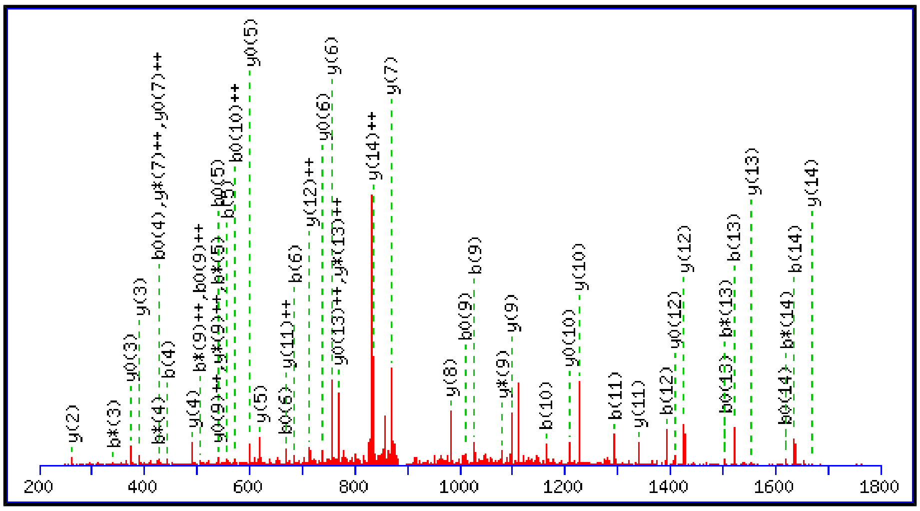
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSLEDILHQVENK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

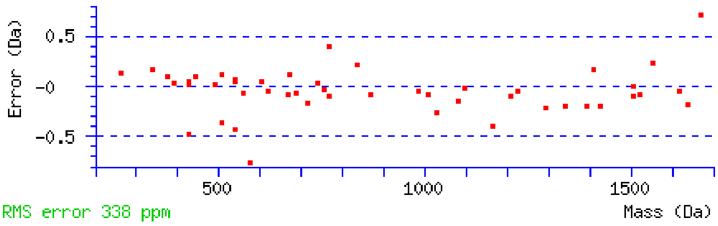
Match to Query 10182: 1781.874248 from(891.944400,2+) intensity(57212.0352) rtinseconds(2378) scans(6208) index(1545)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum5441_scans__6208
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

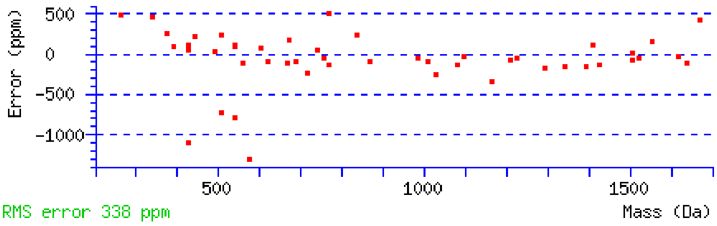
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1781.8683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Deamidated (NQ)
N14 : Deamidated (NQ)
Ions Score: 73 **Expect:** 1.4e-005
Matches : 51/160 fragment ions using 92 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	229.1183	115.0628			211.1077	106.0575	L	***1667.8487***	834.4280	1650.8221	825.9147	1649.8381	825.4227	14
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	Q	***1554.7646***	777.8859	1537.7380	769.3727	1536.7540	768.8807	13
4	**444.2089**	222.6081	427.1823	214.0948	426.1983	213.6028	S	***1426.7060***	713.8566	1409.6795	705.3434	1408.6955	704.8514	12
5	**557.2930**	279.1501	540.2664	270.6368	539.2824	270.1448	L	***1339.6740***	670.3406	1322.6474	661.8274	1321.6634	661.3353	11
6	**686.3355**	343.6714	669.3090	335.1581	668.3250	334.6661	E	***1226.5899***	613.7986	1209.5634	605.2853	1208.5794	604.7933	10
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	D	***1097.5473***	549.2773	1080.5208	540.7640	1079.5368	540.2720	9
8	914.4466	457.7269	897.4200	449.2136	896.4360	448.7216	I	***982.5204***	491.7638	965.4938	483.2506	964.5098	482.7585	8
9	**1027.5306**	514.2689	1010.5041	505.7557	1009.5201	505.2637	L	***869.4363***	435.2218	852.4098	426.7085	851.4258	426.2165	7
10	**1164.5895**	582.7984	1147.5630	574.2851	1146.5790	573.7931	H	***756.3523***	378.6798	739.3257	370.1665	738.3417	369.6745	6
11	**1293.6321**	647.3197	1276.6056	638.8064	1275.6216	638.3144	Q	***619.2933***	310.1503	602.2668	301.6370	601.2828	301.1450	5
12	**1392.7005**	696.8539	1375.6740	688.3406	1374.6900	687.8486	V	***490.2508***	245.6290	473.2242	237.1157	472.2402	236.6237	4
13	**1521.7431**	761.3752	1504.7166	752.8619	1503.7326	752.3699	E	***391.1823***	196.0948	374.1558	187.5815	373.1718	187.0895	3
14	**1636.7701**	818.8887	1619.7435	810.3754	1618.7595	809.8834	N	***262.1397***	131.5735	245.1132	123.0602			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.6	1781.8683	0.0060	DLQSLEDILHQVENK	Deamidated Q11, N14 100.00%
24.9	1781.8683	0.0060	DLQSLEDILHQVENK	Deamidated Q3, N14 0.00%
19.2	1781.8723	0.0020	QLNSIYGEYIPELNK	
18.2	1781.8683	0.0060	DLQSLEDILHQVENK	Deamidated Q3, Q11 0.00%
17.2	1781.8723	0.0020	QLNSIYGEYIPELNK	
11.0	1781.8795	-0.0053	LQNPSESSEPIPLESR	
6.4	1781.8804	-0.0062	QLAMIQNSSGMALFVR	
5.6	1781.8804	-0.0062	MMPLHGTLTKIHNEK	
5.4	1781.8723	0.0020	QLNSIYGEYIPELNK	
4.9	1780.8665	1.0077	KMLNEKVSNQAFEDK	

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

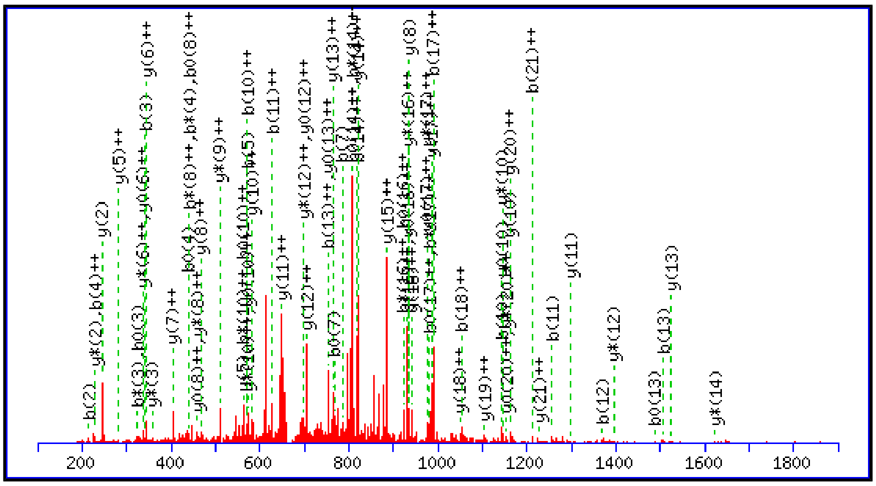
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDKDLQSLEDILHQVENKTSEVK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

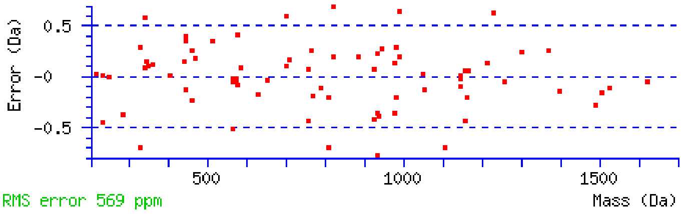
Match to Query 22428: 2667.365456 from(667.848640,4+) intensity(61773.1328) rtinseconds(2282) scans(5747) index(14198)
Title: 111019_Est_MI_YP_G_02Spectrum5019_scans__5747
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

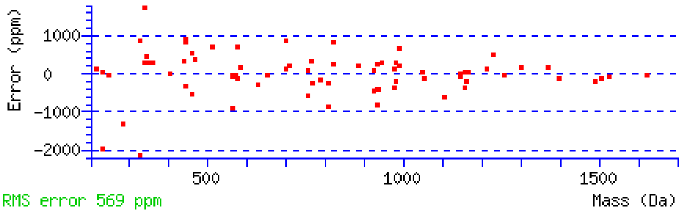
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2667.3603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 66 **Expect:** 6.1e-005
Matches : 77/254 fragment ions using 148 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							23
2	**215.1026**	108.0550			197.0921	99.0497	D	2569.2992	1285.1532	2552.2726	1276.6399	2551.2886	1276.1479	22
3	**343.1976**	172.1024	326.1710	163.5892	325.1870	163.0972	K	2454.2722	1227.6398	2437.2457	1219.1265	2436.2617	1218.6345	21
4	458.2245	**229.6159**	441.1980	221.1026	440.2140	220.6106	D	2326.1773	1163.5923	2309.1507	1155.0790	2308.1667	1154.5870	20
5	**571.3086**	286.1579	554.2821	277.6447	553.2980	277.1527	L	2211.1503	1106.0788	2194.1238	1097.5655	2193.1398	1097.0735	19
6	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	Q	2098.0663	1049.5368	2081.0397	1041.0235	2080.0557	1040.5315	18
7	**786.3992**	393.7032	769.3727	385.1900	768.3886	384.6980	S	1970.0077	985.5075	1952.9811	976.9942	1951.9971	976.5022	17
8	899.4833	450.2453	882.4567	441.7320	881.4727	441.2400	L	1882.9756	941.9915	1865.9491	933.4782	1864.9651	932.9862	16
9	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	E	1769.8916	885.4494	1752.8650	876.9362	1751.8810	876.4441	15
10	**1143.5528**	**572.2800**	1126.5263	563.7668	1125.5422	563.2748	D	1640.8490	820.9281	1623.8224	812.4149	1622.8384	811.9229	14
11	**1256.6369**	**628.8221**	1239.6103	620.3088	1238.6263	619.8168	I	**1525.8220**	763.4147	1508.7955	754.9014	1507.8115	754.4094	13
12	**1369.7209**	685.3641	1352.6944	676.8508	1351.7104	676.3588	L	1412.7380	706.8726	1395.7114	698.3594	1394.7274	697.8673	12
13	**1506.7798**	**753.8936**	1489.7533	745.3803	1488.7693	744.8883	H	**1299.6539**	650.3306	1282.6274	641.8173	1281.6434	641.3253	11
14	1634.8384	**817.9229**	1617.8119	809.4096	1616.8279	808.9176	Q	**1162.5950**	581.8011	1145.5685	573.2879	1144.5844	572.7959	10
15	1733.9068	867.4571	1716.8803	858.9438	1715.8963	858.4518	V	1034.5364	517.7719	1017.5099	509.2586	1016.5259	508.7666	9
16	1862.9494	**931.9784**	1845.9229	923.4651	1844.9389	922.9731	E	**935.4680**	468.2376	918.4415	459.7244	917.4575	459.2324	8
17	1977.9764	**989.4918**	1960.9498	980.9786	1959.9658	980.4865	N	806.4254	403.7164	789.3989	395.2031	788.4149	394.7111	7
18	2106.0713	**1053.5393**	2089.0448	1045.0260	2088.0608	1044.5340	K	691.3985	346.2029	674.3719	337.6896	673.3879	337.1976	6
19	2207.1190	1104.0631	2190.0925	1095.5499	2189.1085	1095.0579	T	**563.3035**	282.1554	546.2770	273.6421	545.2930	273.1501	5
20	2294.1510	1147.5792	2277.1245	1139.0659	2276.1405	1138.5739	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
21	2423.1936	**1212.1005**	2406.1671	1203.5872	2405.1831	1203.0952	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
22	2522.2621	1261.6347	2505.2355	1253.1214	2504.2515	1252.6294	V	**246.1812**	123.5942	229.1547	115.0810			2
23							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.8	2667.3603	0.0052	VDKDLQSLEDILHQVENKTSEVK	Deamidated N17 53.29%
64.9	2667.3603	0.0052	VDKDLQSLEDILHQVENKTSEVK	Deamidated Q14 43.82%
53.1	2667.3603	0.0052	VDKDLQSLEDILHQVENKTSEVK	Deamidated Q6 2.89%
3.7	2667.3560	0.0095	VNLLNHNIPKGPCILCGMGNFKR	
3.4	2666.3625	1.0029	NPFNTGMLFTSSLDLIKVNLDVAR	
3.4	2666.3625	1.0029	NPFNTGMLFTSSLDLIKVNLDVAR	
2.9	2665.3536	2.0119	MVDFPGYNLSGAVASFLFILLTMK	
2.7	2665.3633	2.0022	NLVQSMQVLSGVFTDVEASLKDIR	
2.7	2665.3601	2.0054	CSLDSSLRIMICLLKIPSTNATR	
2.7	2666.3625	1.0029	NPFNTGMLFTSSLDLIKVNLDVAR	

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

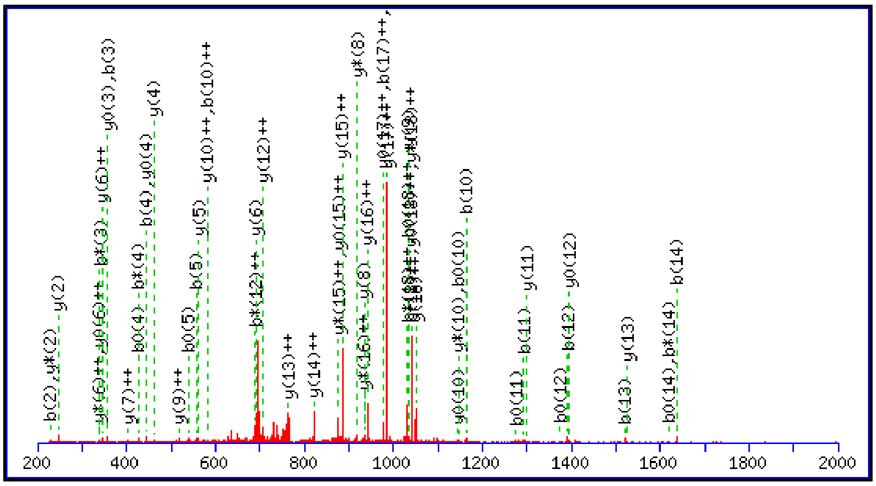
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLQSLEDILHQVENKTSEVK**
Found in **C9JC84** in **con_Xuniprot_HUMAN3**, C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1

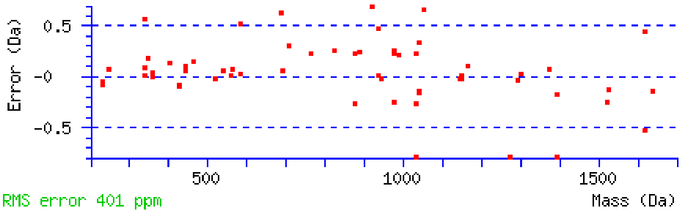
Match to Query 15471: 2326.156692 from(776.392840,3+) intensity(35456.7773) rtinseconds(2405) scans(6283) index(1554)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum5508_scans__6283
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

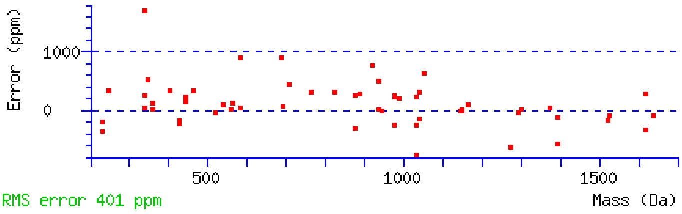
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2326.1540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Deamidated (NQ)
N14 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0017
Matches : 59/220 fragment ions using 110 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**20**
2	**229.1183**	115.0628			211.1077	106.0575	**L**	2212.1343	1106.5708	2195.1078	1098.0575	2194.1238	1097.5655	**19**
3	**357.1769**	179.0921	340.1503	170.5788	339.1663	170.0868	**Q**	2099.0503	1050.0288	2082.0237	1041.5155	2081.0397	1041.0235	**18**
4	**444.2089**	222.6081	427.1823	214.0948	426.1983	213.6028	**S**	1970.9917	985.9995	1953.9651	977.4862	1952.9811	976.9942	**17**
5	**557.2930**	279.1501	540.2664	270.6368	539.2824	270.1448	**L**	1883.9597	942.4835	1866.9331	933.9702	1865.9491	933.4782	**16**
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	**E**	1770.8756	885.9414	1753.8491	877.4282	1752.8650	876.9362	**15**
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	**D**	1641.8330	821.4201	1624.8065	812.9069	1623.8224	812.4149	**14**
8	914.4466	457.7269	897.4200	449.2136	896.4360	448.7216	**I**	***1526.8061***	763.9067	1509.7795	755.3934	1508.7955	754.9014	**13**
9	1027.5306	514.2689	1010.5041	505.7557	1009.5201	505.2637	**L**	1413.7220	707.3646	1396.6955	698.8514	1395.7114	698.3594	**12**
10	**1164.5895**	582.7984	1147.5630	574.2851	1146.5790	573.7931	**H**	***1300.6379***	650.8226	1283.6114	642.3093	1282.6274	641.8173	**11**
11	**1293.6321**	647.3197	1276.6056	638.8064	1275.6216	638.3144	**Q**	1163.5790	582.2932	1146.5525	573.7799	1145.5685	573.2879	**10**
12	**1392.7005**	696.8539	1375.6740	688.3406	1374.6900	687.8486	**V**	***1034.5364***	517.7719	1017.5099	509.2586	1016.5259	508.7666	**9**
13	**1521.7431**	761.3752	1504.7166	752.8619	1503.7326	752.3699	**E**	***935.4680***	468.2376	918.4415	459.7244	917.4575	459.2324	**8**
14	**1636.7701**	818.8887	1619.7435	810.3754	1618.7595	809.8834	**N**	806.4254	403.7164	789.3989	395.2031	788.4149	394.7111	**7**
15	1764.8650	882.9362	1747.8385	874.4229	1746.8545	873.9309	**K**	***691.3985***	346.2029	674.3719	337.6896	673.3879	337.1976	**6**
16	1865.9127	933.4600	1848.8862	924.9467	1847.9022	924.4547	**T**	***563.3035***	282.1554	546.2770	273.6421	545.2930	273.1501	**5**
17	1952.9447	976.9760	1935.9182	968.4627	1934.9342	967.9707	**S**	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	**4**
18	2081.9873	1041.4973	2064.9608	1032.9840	2063.9768	1032.4920	**E**	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
19	2181.0558	1091.0315	2164.0292	1082.5182	2163.0452	1082.0262	**V**	***246.1812***	123.5942	229.1547	115.0810			**2**
20							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.8	2326.1540	0.0027	DLQSLEDILHQVENKTSEVK	Deamidated Q11, N14 98.80%
30.6	2326.1540	0.0027	DLQSLEDILHQVENKTSEVK	Deamidated Q3, N14 0.75%
28.4	2326.1540	0.0027	DLQSLEDILHQVENKTSEVK	Deamidated Q3, Q11 0.45%
10.1	2326.1627	-0.0060	AYVFNLSCLGSQVERLLEAR	
7.4	2326.1627	-0.0060	DNTLMFEARFESGNLQKVVK	
6.4	2325.1457	1.0110	NEQKAKMEALLGSGMVQVGYR	
6.4	2325.1457	1.0110	NEQKAKMEALLGSGMVQVGYR	
6.1	2326.1614	-0.0047	QPPPHHGANNVVCDLRGFRR	
5.9	2325.1570	0.9997	TNCMLGEQQVVQDAGRPVPVK	
5.7	2324.1404	2.0163	NGAVSMGNRSAAPSVPGSDARPAR	

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

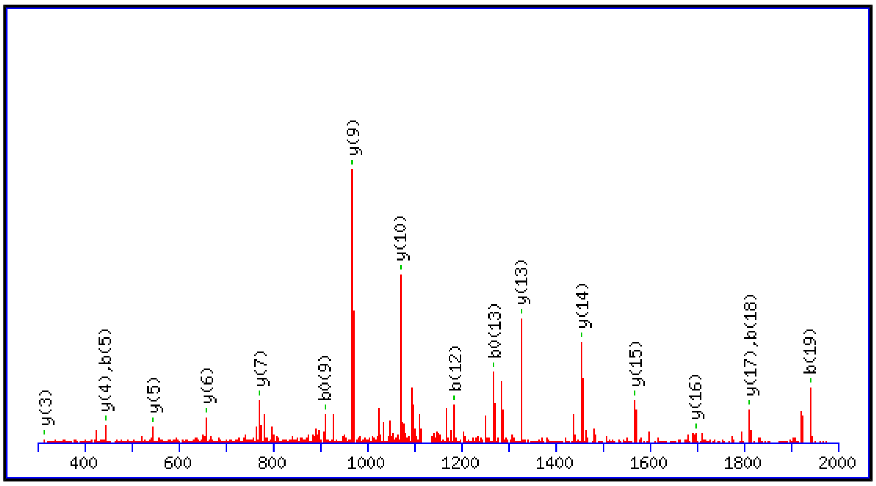
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADGTVNQIEGEATPVNLTEPAK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

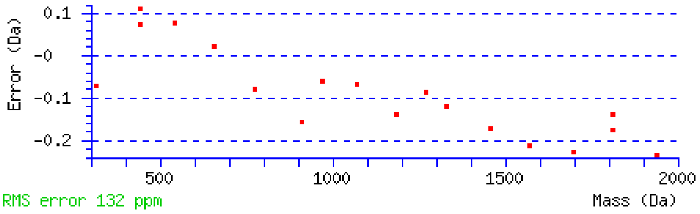
Match to Query 15109: 2254.107748 from(1128.061150,2+) intensity(46238.7109) rtinseconds(1290) scans(3297) index(19504)
Title: 111019_Est_MI_YP_G_09Spectrum2913_scans__3297
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

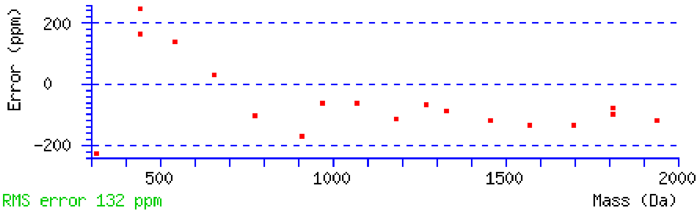
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2254.0965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
Ions Score: 115 **Expect:** 9.9e-010
Matches : 18/234 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							22
2	187.0713	94.0393			169.0608	85.0340	D	2184.0667	1092.5370	2167.0401	1084.0237	2166.0561	1083.5317	21
3	244.0928	122.5500			226.0822	113.5448	G	2069.0397	1035.0235	2052.0132	1026.5102	2051.0291	1026.0182	20
4	345.1405	173.0739			327.1299	164.0686	T	2012.0182	1006.5128	1994.9917	997.9995	1994.0077	997.5075	19
5	**444.2089**	222.6081			426.1983	213.6028	V	1910.9706	955.9889	1893.9440	947.4756	1892.9600	946.9836	18
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	N	***1811.9022***	906.4547	1794.8756	897.9414	1793.8916	897.4494	17
7	686.3104	343.6588	669.2838	335.1456	668.2998	334.6536	Q	***1697.8592***	849.4333	1680.8327	840.9200	1679.8487	840.4280	16
8	799.3945	400.2009	782.3679	391.6876	781.3839	391.1956	I	***1569.8006***	785.4040	1552.7741	776.8907	1551.7901	776.3987	15
9	928.4371	464.7222	911.4105	456.2089	910.4265	455.7169	E	***1456.7166***	728.8619	1439.6900	720.3487	1438.7060	719.8566	14
10	985.4585	493.2329	968.4320	484.7196	967.4480	484.2276	G	***1327.6740***	664.3406	1310.6474	655.8274	1309.6634	655.3354	13
11	1114.5011	557.7542	1097.4746	549.2409	1096.4905	548.7489	E	1270.6525	635.8299	1253.6260	627.3166	1252.6420	626.8246	12
12	**1185.5382**	593.2727	1168.5117	584.7595	1167.5277	584.2675	A	1141.6099	571.3086	1124.5834	562.7953	1123.5994	562.3033	11
13	1286.5859	643.7966	1269.5594	635.2833	1268.5753	634.7913	T	***1070.5728***	535.7900	1053.5463	527.2768	1052.5623	526.7848	10
14	1383.6387	692.3230	1366.6121	683.8097	1365.6281	683.3177	P	***969.5251***	485.2662	952.4986	476.7529	951.5146	476.2609	9
15	1482.7071	741.8572	1465.6805	733.3439	1464.6965	732.8519	V	872.4724	436.7398	855.4458	428.2266	854.4618	427.7345	8
16	1597.7340	799.3706	1580.7075	790.8574	1579.7235	790.3654	N	***773.4040***	387.2056	756.3774	378.6923	755.3934	378.2003	7
17	1710.8181	855.9127	1693.7915	847.3994	1692.8075	846.9074	L	***658.3770***	329.6921	641.3505	321.1789	640.3665	320.6869	6
18	**1811.8658**	906.4365	1794.8392	897.9232	1793.8552	897.4312	T	***545.2930***	273.1501	528.2664	264.6368	527.2824	264.1448	5
19	**1940.9084**	970.9578	1923.8818	962.4445	1922.8978	961.9525	E	***444.2453***	222.6263	427.2187	214.1130	426.2347	213.6210	4
20	2037.9611	1019.4842	2020.9346	1010.9709	2019.9506	1010.4789	P	***315.2027***	158.1050	298.1761	149.5917			3
21	2108.9982	1055.0028	2091.9717	1046.4895	2090.9877	1045.9975	A	218.1499	109.5786	201.1234	101.0653			2
22							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
114.6	2254.0965	0.0113	ADGTVNQIEGEATPVNLTEPAK	Deamidated N16 100.00%
31.3	2254.0965	0.0113	ADGTVNQIEGEATPVNLTEPAK	Deamidated Q7 0.00%
31.3	2254.0965	0.0113	ADGTVNQIEGEATPVNLTEPAK	Deamidated N6 0.00%
23.6	2253.1125	0.9953	ADGTVNQIEGEATPVNLTEPAK	
6.0	2254.1092	-0.0015	MPAGGQAPQLTPVIPAFWEAR	
1.1	2254.1025	0.0053	CRDLLDEARNYHLHLSSR	

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

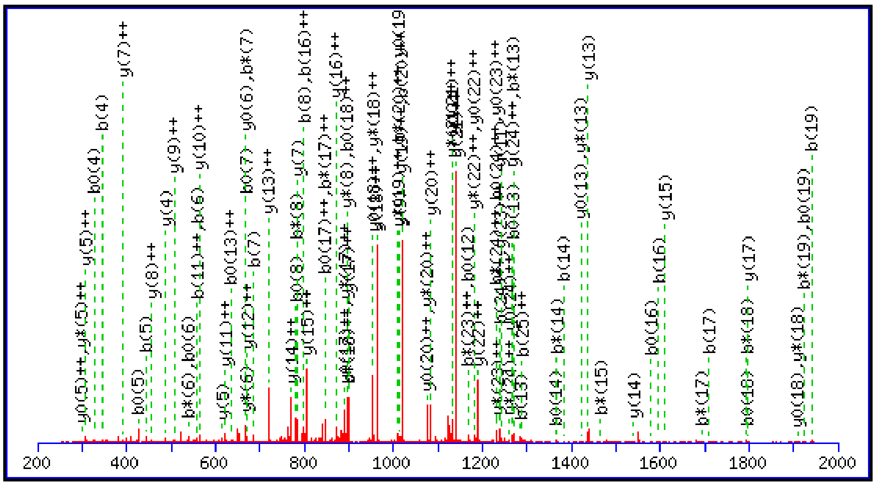
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADGTVNQIEGEATPVNLTEPAKLEVK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

Match to Query 25423: 2723.396172 from(908.806000,3+) intensity(1265734.1250) rtinseconds(1626) scans(3862) index(10157)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum3271_scans__3862
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

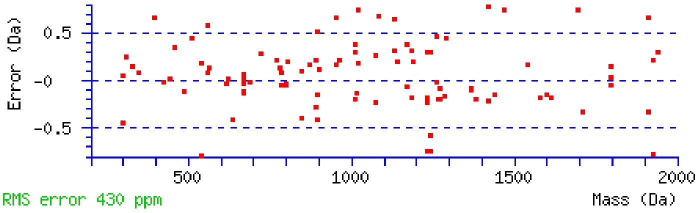
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

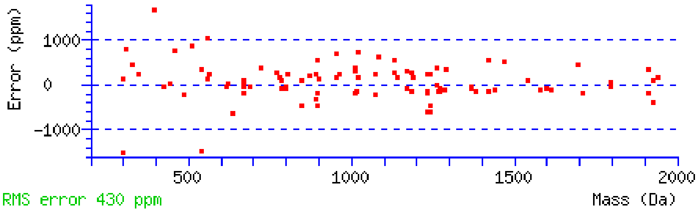


Monoisotopic mass of neutral peptide Mr(calc): 2723.3865
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
Ions Score: 104 **Expect:** 8.4e-009
Matches : 97/284 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							26
2	187.0713	94.0393			169.0608	85.0340	D	2653.3567	1327.1820	2636.3301	1318.6687	2635.3461	1318.1767	25
3	244.0928	122.5500			226.0822	113.5448	G	2538.3297	1269.6685	2521.3032	1261.1552	2520.3192	1260.6632	24
4	**345.1405**	173.0739			327.1299	164.0686	T	2481.3083	1241.1578	2464.2817	1232.6445	2463.2977	1232.1525	23
5	**444.2089**	222.6081			426.1983	213.6028	V	2380.2606	1190.6339	2363.2340	1182.1207	2362.2500	1181.6287	22
6	**558.2518**	279.6295	541.2253	271.1163	540.2413	270.6243	N	2281.1922	1141.0997	2264.1656	1132.5865	2263.1816	1132.0944	21
7	**686.3104**	343.6588	669.2838	335.1456	668.2998	334.6536	Q	2167.1493	1084.0783	2150.1227	1075.5650	2149.1387	1075.0730	20
8	**799.3945**	400.2009	782.3679	391.6876	781.3839	391.1956	I	2039.0907	1020.0490	2022.0641	1011.5357	2021.0801	1011.0437	19
9	928.4371	464.7222	911.4105	456.2089	910.4265	455.7169	E	1926.0066	963.5069	1908.9801	954.9937	1907.9961	954.5017	18
10	985.4585	493.2329	968.4320	484.7196	967.4480	484.2276	G	**1796.9640**	898.9856	1779.9375	890.4724	1778.9535	889.9804	17
11	1114.5011	**557.7542**	1097.4746	549.2409	1096.4905	548.7489	E	1739.9426	870.4749	1722.9160	861.9616	1721.9320	861.4696	16
12	1185.5382	593.2727	1168.5117	584.7595	1167.5277	584.2675	A	**1610.9000**	805.9536	1593.8734	797.4403	1592.8894	796.9483	15
13	**1286.5859**	643.7966	1269.5594	635.2833	1268.5753	634.7913	T	**1539.8629**	770.4351	1522.8363	761.9218	1521.8523	761.4298	14
14	**1383.6387**	692.3230	1366.6121	683.8097	1365.6281	683.3177	P	**1438.8152**	719.9112	1421.7886	711.3980	1420.8046	710.9059	13
15	1482.7071	741.8572	1465.6805	733.3439	1464.6965	732.8519	V	1341.7624	671.3848	1324.7359	662.8716	1323.7518	662.3796	12
16	**1597.7340**	**799.3706**	1580.7075	790.8574	1579.7235	790.3654	N	**1242.6940**	621.8506	1225.6674	613.3374	1224.6834	612.8454	11
17	**1710.8181**	855.9127	1693.7915	847.3994	1692.8075	846.9074	L	1127.6671	564.3372	1110.6405	555.8239	1109.6565	555.3319	10
18	1811.8658	906.4365	1794.8392	897.9232	1793.8552	897.4312	T	**1014.5830**	507.7951	997.5564	499.2819	996.5724	498.7898	9
19	**1940.9084**	970.9578	1923.8818	962.4445	1922.8978	961.9525	E	913.5353	457.2713	896.5088	448.7580	895.5247	448.2660	8
20	2037.9611	**1019.4842**	2020.9346	1010.9709	2019.9506	1010.4789	P	**784.4927**	392.7500	767.4662	384.2367	766.4822	383.7447	7
21	2108.9982	1055.0028	2091.9717	1046.4895	2090.9877	1045.9975	A	687.4400	344.2236	670.4134	335.7103	669.4294	335.2183	6
22	2237.0932	1119.0502	2220.0667	1110.5370	2219.0826	1110.0450	K	**616.4028**	308.7051	599.3763	300.1918	598.3923	299.6998	5
23	2350.1773	1175.5923	2333.1507	1167.0790	2332.1667	1166.5870	L	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	4

24	2479.2199	**1240.1136**	2462.1933	1231.6003	2461.2093	1231.1083	**E**	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
25	2578.2883	**1289.6478**	2561.2617	1281.1345	2560.2777	1280.6425	**V**	246.1812	123.5942	229.1547	115.0810			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.3	2723.3865	0.0097	ADGTVNQIEGEATPVNLTEPAKLEVK	Deamidated N16 41.22%
103.8	2723.3865	0.0097	ADGTVNQIEGEATPVNLTEPAKLEVK	Deamidated Q7 36.65%
101.6	2723.3865	0.0097	ADGTVNQIEGEATPVNLTEPAKLEVK	Deamidated N6 22.13%
99.7	2722.4025	0.9937	ADGTVNQIEGEATPVNLTEPAKLEVK	
11.6	2723.4024	-0.0063	ASNVASIKTMLPGEHQQVLSNLQSR	
10.9	2723.4071	-0.0109	LAQLLEGYARYSVSVFQPPFQPGR	
8.7	2722.3862	1.0100	DLFLQQMMDEWFLLPKELLRR	
7.8	2722.3894	1.0068	LTVQDIQALEHKPAKASMMQQPAR	
4.2	2723.4071	-0.0109	LAQLLEGYARYSVSVFQPPFQPGR	
3.2	2723.3912	0.0050	EITTAGKNNDMGGVAYLTGVTSKRPK	

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

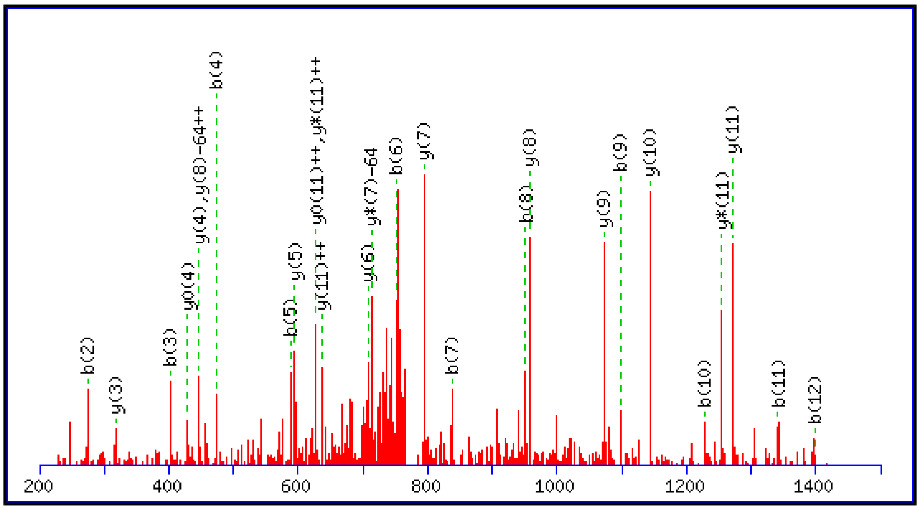
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

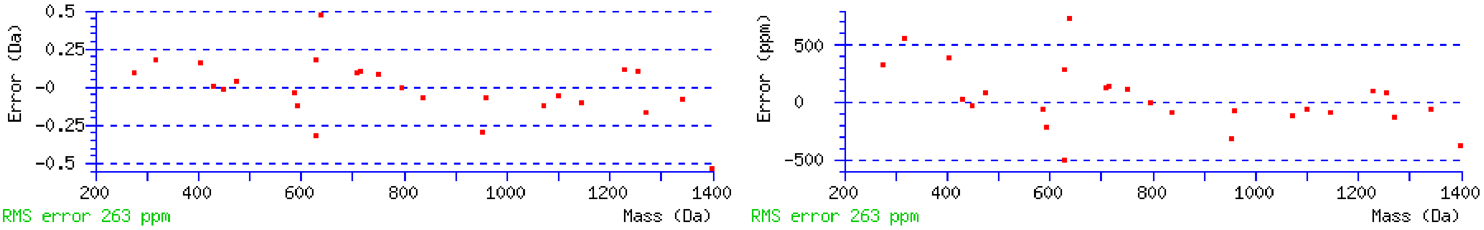
Match to Query 6928: 1543.669928 from(772.842240,2+) intensity(13099.6836) rtinseconds(568) scans(1276) index(24372)
Title: 111019_Est_MI_YS_G_06Spectrum1096_scans__1276
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1543.6646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 89 **Expect:** 9.9e-008
Matches : 27/194 fragment ions using 36 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	161.0379	81.0226					C							13
2	***274.1220***	137.5646					I	1384.6413	692.8243	1367.6148	684.3110	1366.6307	683.8190	12
3	***402.1806***	201.5939	385.1540	193.0806			Q	**1271.5572**	636.2823	1254.5307	627.7690	1253.5467	627.2770	11
4	***473.2177***	237.1125	456.1911	228.5992			A	**1143.4987**	572.2530	1126.4721	563.7397	1125.4881	563.2477	10
5	***588.2446***	294.6260	571.2181	286.1127			N	**1072.4616**	536.7344	1055.4350	528.2211	1054.4510	527.7291	9
6	***751.3080***	376.1576	734.2814	367.6443			Y	**957.4346**	479.2209	940.4081	470.7077	939.4240	470.2157	8
7	***838.3400***	419.6736	821.3134	411.1604	820.3294	410.6683	S	**794.3713**	397.6893	777.3447	389.1760	776.3607	388.6840	7
8	***951.4240***	476.2157	934.3975	467.7024	933.4135	467.2104	L	**707.3393**	354.1733	690.3127	345.6600	689.3287	345.1680	6
9	***1098.4594***	549.7334	1081.4329	541.2201	1080.4489	540.7281	M	**594.2552**	297.6312	577.2286	289.1180	576.2446	288.6259	5
10	***1227.5020***	614.2547	1210.4755	605.7414	1209.4915	605.2494	E	**447.2198**	224.1135	430.1932	215.6003	429.2092	215.1082	4
11	***1341.5450***	671.2761	1324.5184	662.7628	1323.5344	662.2708	N	**318.1772**	159.5922	301.1506	151.0790			3
12	***1398.5664***	699.7869	1381.5399	691.2736	1380.5559	690.7816	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.1	1543.6646	0.0053	CIQANYSLMENGK	Deamidated N5 98.92%
69.5	1543.6646	0.0053	CIQANYSLMENGK	Deamidated Q3 1.08%
26.1	1543.6646	0.0053	CIQANYSLMENGK	Deamidated N11 0.00%
7.4	1542.6741	0.9958	SPSTWMMSMRAAR	
5.8	1543.6725	-0.0026	SWTFGQSAQAMASR	
2.0	1542.6741	0.9958	SPSTWMMSMRAAR	
1.9	1542.6741	0.9958	SPSTWMMSMRAAR	

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

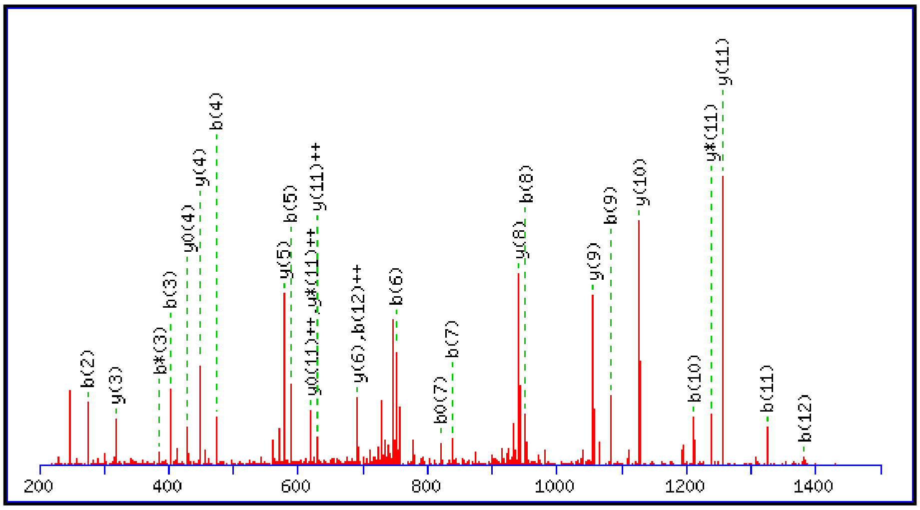
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

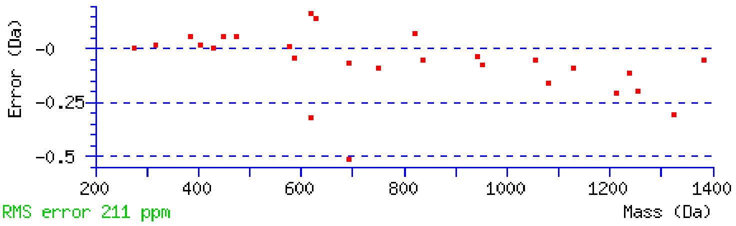
Match to Query 6896: 1527.674068 from(764.844310,2+) intensity(161547.2813) rtinseconds(990) scans(2222) index(12413)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum1920_scans__2222
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

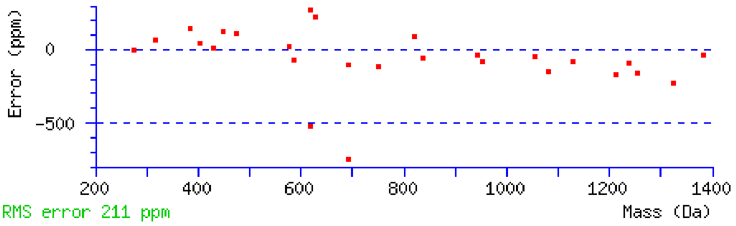
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1527.6697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 88 **Expect:** 1.5e-007
Matches : 27/122 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	161.0379	81.0226					C							13
2	***274.1220***	137.5646					I	1368.6464	684.8268	1351.6198	676.3136	1350.6358	675.8216	12
3	***402.1806***	201.5939	385.1540	193.0806			Q	**1255.5623**	628.2848	1238.5358	619.7715	1237.5518	619.2795	11
4	***473.2177***	237.1125	456.1911	228.5992			A	**1127.5038**	564.2555	1110.4772	555.7422	1109.4932	555.2502	10
5	***588.2446***	294.6260	571.2181	286.1127			N	**1056.4666**	528.7370	1039.4401	520.2237	1038.4561	519.7317	9
6	***751.3080***	376.1576	734.2814	367.6443			Y	**941.4397**	471.2235	924.4131	462.7102	923.4291	462.2182	8
7	***838.3400***	419.6736	821.3134	411.1604	820.3294	410.6683	S	778.3764	389.6918	761.3498	381.1785	760.3658	380.6865	7
8	***951.4240***	476.2157	934.3975	467.7024	933.4135	467.2104	L	**691.3443**	346.1758	674.3178	337.6625	673.3338	337.1705	6
9	***1082.4645***	541.7359	1065.4380	533.2226	1064.4540	532.7306	M	**578.2603**	289.6338	561.2337	281.1205	560.2497	280.6285	5
10	***1211.5071***	606.2572	1194.4806	597.7439	1193.4966	597.2519	E	**447.2198**	224.1135	430.1932	215.6003	429.2092	215.1082	4
11	***1325.5501***	663.2787	1308.5235	654.7654	1307.5395	654.2734	N	**318.1772**	159.5922	301.1506	151.0790			3
12	***1382.5715***	691.7894	1365.5450	683.2761	1364.5609	682.7841	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.0	1527.6697	0.0043	CIQANYSLMENGK	Deamidated N5 99.76%
61.7	1527.6697	0.0043	CIQANYSLMENGK	Deamidated Q3 0.24%
33.7	1527.6697	0.0043	CIQANYSLMENGK	Deamidated N11 0.00%
3.2	1527.6729	0.0012	VEAFDNEFEATQK	
1.9	1527.6697	0.0043	WQMKQNETTAMK	
1.1	1527.6689	0.0052	NSNEQINAFSTSSK	

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

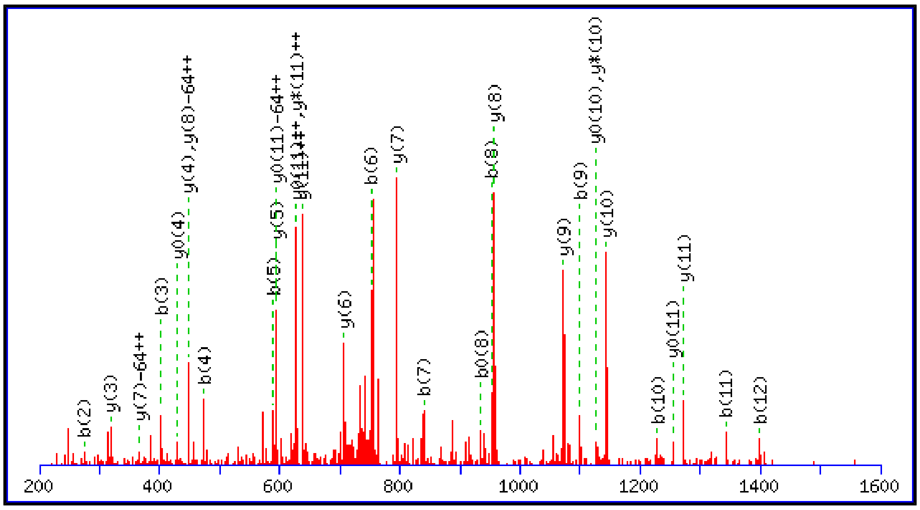
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

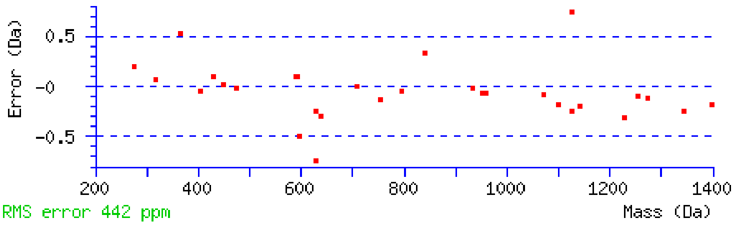
Match to Query 6931: 1544.648928 from(773.331740,2+) intensity(16872.2539) rtinseconds(716) scans(1528) index(6883)
Title: 111019_Est_ISCardio_NMI_YP_G_10Spectrum1298_scans__1528
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

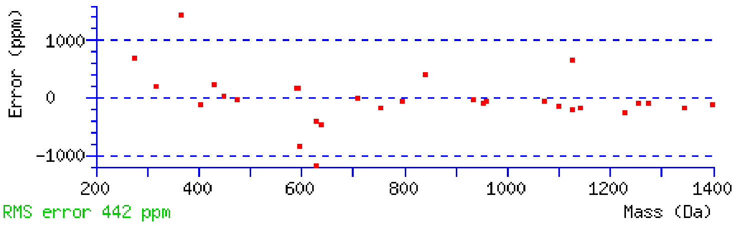
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1544.6487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N5 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 80 **Expect:** 5e-007
Matches : 31/194 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	161.0379	81.0226					C							13
2	274.1220	137.5646					I	1385.6253	693.3163	1368.5988	684.8030	1367.6148	684.3110	12
3	403.1646	202.0859	386.1380	193.5727			Q	1272.5413	636.7743	1255.5147	628.2610	1254.5307	627.7690	11
4	474.2017	237.6045	457.1751	229.0912			A	1143.4987	572.2530	1126.4721	563.7397	1125.4881	563.2477	10
5	589.2286	295.1180	572.2021	286.6047			N	1072.4616	536.7344	1055.4350	528.2211	1054.4510	527.7291	9
6	752.2920	376.6496	735.2654	368.1363			Y	957.4346	479.2209	940.4081	470.7077	939.4240	470.2157	8
7	839.3240	420.1656	822.2974	411.6524	821.3134	411.1604	S	794.3713	397.6893	777.3447	389.1760	776.3607	388.6840	7
8	952.4081	476.7077	935.3815	468.1944	934.3975	467.7024	L	707.3393	354.1733	690.3127	345.6600	689.3287	345.1680	6
9	1099.4435	550.2254	1082.4169	541.7121	1081.4329	541.2201	M	594.2552	297.6312	577.2286	289.1180	576.2446	288.6259	5
10	1228.4861	614.7467	1211.4595	606.2334	1210.4755	605.7414	E	447.2198	224.1135	430.1932	215.6003	429.2092	215.1082	4
11	1342.5290	671.7681	1325.5024	663.2549	1324.5184	662.7628	N	318.1772	159.5922	301.1506	151.0790			3
12	1399.5504	700.2789	1382.5239	691.7656	1381.5399	691.2736	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.1	1544.6487	0.0003	CIQANYSLMENGK	Deamidated Q3, N5 99.99%
36.0	1544.6487	0.0003	CIQANYSLMENGK	Deamidated Q3, N11 0.00%
31.2	1544.6487	0.0003	CIQANYSLMENGK	Deamidated N5, N11 0.00%
5.4	1544.6422	0.0068	KCNWKMGNTMDK	
2.5	1543.6395	1.0094	GSQCHTMHNLVNK	

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

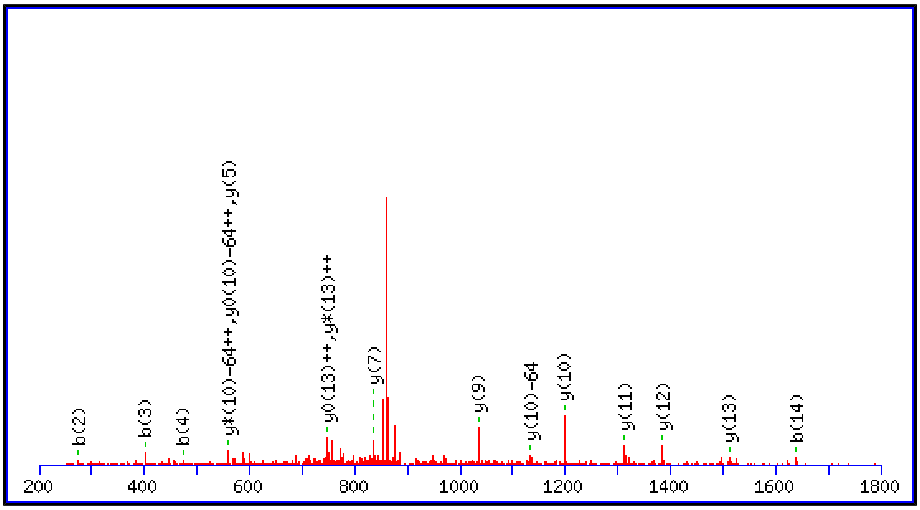
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGKIK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

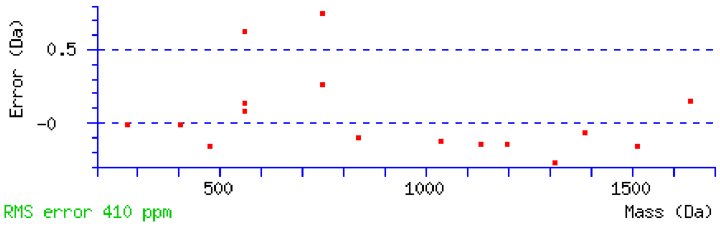
Match to Query 10191: 1784.851008 from(893.432780,2+) intensity(11588.9356) rtinseconds(694) scans(1511) index(25188)
Title: 111019_Est_MI_YS_G_07Spectrum1259_scans__1511
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

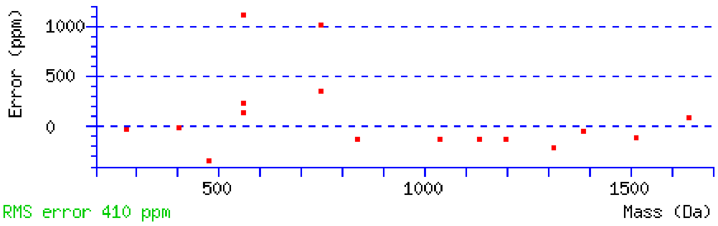
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1784.8437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 **Expect:** 0.00022
Matches : 16/226 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	161.0379	81.0226					C							15
2	**274.1220**	137.5646					I	1625.8203	813.4138	1608.7938	804.9005	1607.8098	804.4085	14
3	**402.1806**	201.5939	385.1540	193.0806			Q	***1512.7363***	756.8718	1495.7097	748.3585	1494.7257	747.8665	13
4	**473.2177**	237.1125	456.1911	228.5992			A	***1384.6777***	692.8425	1367.6511	684.3292	1366.6671	683.8372	12
5	588.2446	294.6260	571.2181	286.1127			N	***1313.6406***	657.3239	1296.6140	648.8107	1295.6300	648.3186	11
6	751.3080	376.1576	734.2814	367.6443			Y	***1198.6136***	599.8105	1181.5871	591.2972	1180.6031	590.8052	10
7	838.3400	419.6736	821.3134	411.1604	820.3294	410.6683	S	***1035.5503***	518.2788	1018.5238	509.7655	1017.5397	509.2735	9
8	951.4240	476.2157	934.3975	467.7024	933.4135	467.2104	L	948.5183	474.7628	931.4917	466.2495	930.5077	465.7575	8
9	1098.4594	549.7334	1081.4329	541.2201	1080.4489	540.7281	M	***835.4342***	418.2207	818.4077	409.7075	817.4236	409.2155	7
10	1227.5020	614.2547	1210.4755	605.7414	1209.4915	605.2494	E	688.3988	344.7030	671.3723	336.1898	670.3882	335.6978	6
11	1341.5450	671.2761	1324.5184	662.7628	1323.5344	662.2708	N	***559.3562***	280.1817	542.3297	271.6685			5
12	1398.5664	699.7869	1381.5399	691.2736	1380.5559	690.7816	G	445.3133	223.1603	428.2867	214.6470			4
13	1526.6614	763.8343	1509.6348	755.3211	1508.6508	754.8291	K	388.2918	194.6496	371.2653	186.1363			3
14	**1639.7455**	820.3764	1622.7189	811.8631	1621.7349	811.3711	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.9	1784.8437	0.0073	CIQANYSLMENGKIK	Deamidated N5 99.26%
38.5	1784.8437	0.0073	CIQANYSLMENGKIK	Deamidated Q3 0.72%
23.6	1784.8437	0.0073	CIQANYSLMENGKIK	Deamidated N11 0.02%
6.9	1784.8477	0.0033	ICQPIMAVYATYDPK	
2.1	1783.8563	0.9947	MLSFTGPDFNAVSIGGR	
1.7	1783.8561	0.9949	RASGAGGQHVNTTDSAVR	
0.9	1784.8549	-0.0039	MLDNDLDRYTMVRK	
0.8	1783.8410	1.0100	MEIYGSAVADKLDNSR	
0.3	1784.8590	-0.0080	LIMVQHWPETVCEK	

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

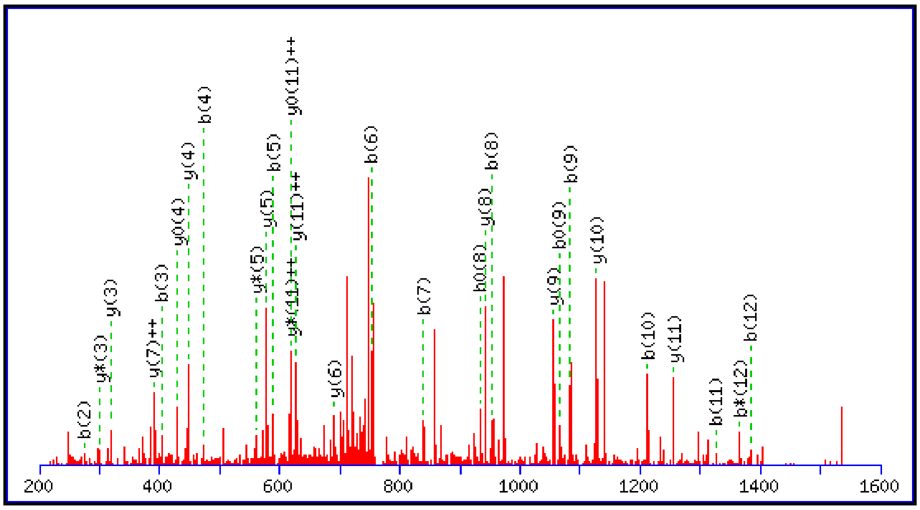
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

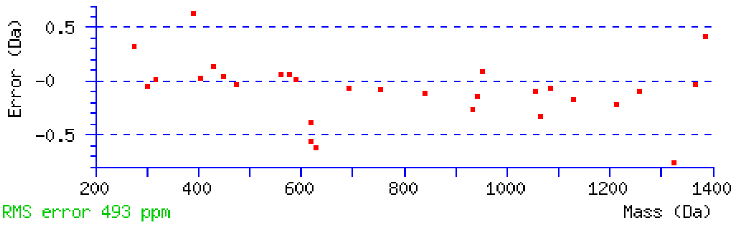
Match to Query 6904: 1528.657388 from(765.335970,2+) intensity(21894.1172) rtinseconds(1031) scans(2274) index(13166)
Title: 111019_Est_ISCardio_NMI_YS_G_11Spectrum1963_scans__2274
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

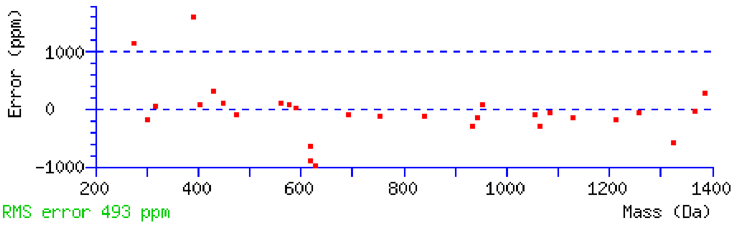
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1528.6537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.00055
Matches : 29/122 fragment ions using 79 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0379	81.0226					C							13
2	***274.1220***	137.5646					I	1369.6304	685.3188	1352.6039	676.8056	1351.6198	676.3136	12
3	***403.1646***	202.0859	386.1380	193.5727			Q	**1256.5463**	628.7768	1239.5198	620.2635	1238.5358	619.7715	11
4	***474.2017***	237.6045	457.1751	229.0912			A	**1127.5038**	564.2555	1110.4772	555.7422	1109.4932	555.2502	10
5	***589.2286***	295.1180	572.2021	286.6047			N	**1056.4666**	528.7370	1039.4401	520.2237	1038.4561	519.7317	9
6	***752.2920***	376.6496	735.2654	368.1363			Y	**941.4397**	471.2235	924.4131	462.7102	923.4291	462.2182	8
7	***839.3240***	420.1656	822.2974	411.6524	821.3134	411.1604	S	778.3764	389.6918	761.3498	381.1785	760.3658	380.6865	7
8	***952.4081***	476.7077	935.3815	468.1944	934.3975	467.7024	L	**691.3443**	346.1758	674.3178	337.6625	673.3338	337.1705	6
9	***1083.4485***	542.2279	1066.4220	533.7146	1065.4380	533.2226	M	**578.2603**	289.6338	561.2337	281.1205	560.2497	280.6285	5
10	***1212.4911***	606.7492	1195.4646	598.2359	1194.4806	597.7439	E	**447.2198**	224.1135	430.1932	215.6003	429.2092	215.1082	4
11	***1326.5341***	663.7707	1309.5075	655.2574	1308.5235	654.7654	N	**318.1772**	159.5922	301.1506	151.0790			3
12	***1383.5555***	692.2814	1366.5290	683.7681	1365.5450	683.2761	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.7	1528.6537	0.0037	CIQANYSLMENGK	Deamidated Q3, N5 99.95%
15.8	1528.6537	0.0037	CIQANYSLMENGK	Deamidated Q3, N11 0.03%
11.8	1528.6537	0.0037	CIQANYSLMENGK	Deamidated N5, N11 0.01%
8.2	1528.6650	-0.0076	FELGDGQNMCSKK	

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

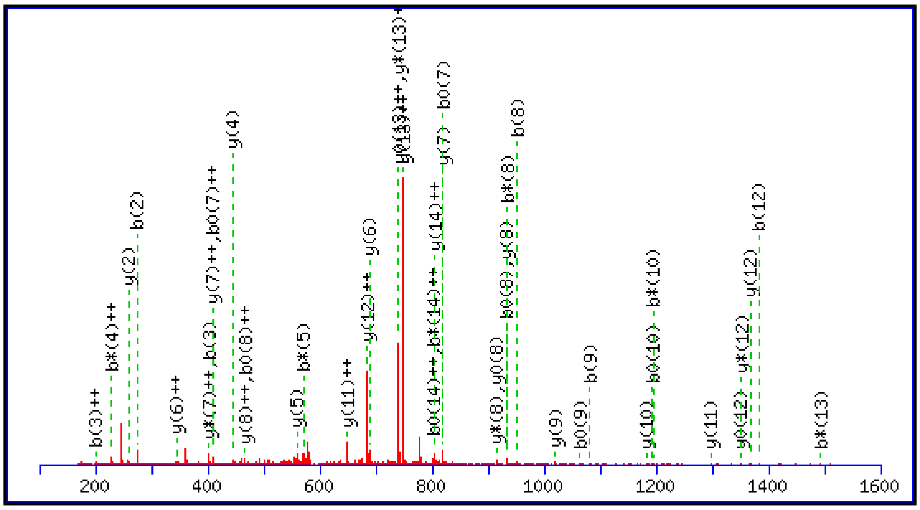
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGKIK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

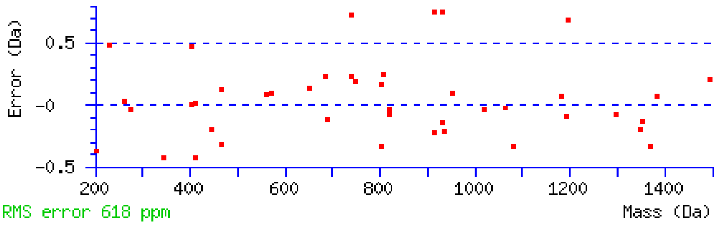
Match to Query 9876: 1768.853772 from(590.625200,3+) intensity(28630.2461) rtinseconds(1107) scans(2604) index(26524)
Title: 111019_Est_MI_YS_G_09Spectrum2237_scans__2604
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

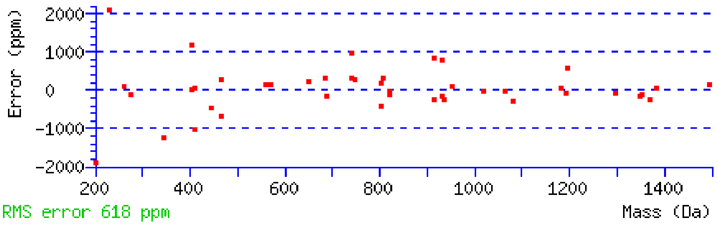
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1768.8487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0063
Matches : 43/142 fragment ions using 81 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							15
2	**274.1220**	137.5646					I	1609.8254	805.4163	1592.7989	796.9031	1591.8149	796.4111	14
3	**402.1806**	201.5939	385.1540	193.0806			Q	1496.7414	748.8743	1479.7148	740.3610	1478.7308	739.8690	13
4	473.2177	237.1125	456.1911	228.5992			A	***1368.6828***	684.8450	1351.6562	676.3318	1350.6722	675.8397	12
5	588.2446	294.6260	571.2181	286.1127			N	***1297.6457***	649.3265	1280.6191	640.8132	1279.6351	640.3212	11
6	751.3080	376.1576	734.2814	367.6443			Y	***1182.6187***	591.8130	1165.5922	583.2997	1164.6082	582.8077	10
7	838.3400	419.6736	821.3134	411.1604	820.3294	410.6683	S	***1019.5554***	510.2813	1002.5288	501.7681	1001.5448	501.2761	9
8	**951.4240**	476.2157	934.3975	467.7024	933.4135	467.2104	L	***932.5234***	466.7653	915.4968	458.2520	914.5128	457.7600	8
9	**1082.4645**	541.7359	1065.4380	533.2226	1064.4540	532.7306	M	***819.4393***	410.2233	802.4128	401.7100	801.4287	401.2180	7
10	1211.5071	606.2572	1194.4806	597.7439	1193.4966	597.2519	E	***688.3988***	344.7030	671.3723	336.1898	670.3882	335.6978	6
11	1325.5501	663.2787	1308.5235	654.7654	1307.5395	654.2734	N	***559.3562***	280.1817	542.3297	271.6685			5
12	**1382.5715**	691.7894	1365.5450	683.2761	1364.5609	682.7841	G	***445.3133***	223.1603	428.2867	214.6470			4
13	1510.6665	755.8369	1493.6399	747.3236	1492.6559	746.8316	K	388.2918	194.6496	371.2653	186.1363			3
14	1623.7505	812.3789	1606.7240	803.8656	1605.7400	803.3736	I	***260.1969***	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.7	1768.8487	0.0050	CIQANYSLMENGKIK	Deamidated N5 69.01%
42.0	1768.8487	0.0050	CIQANYSLMENGKIK	Deamidated Q3 29.44%
29.2	1768.8487	0.0050	CIQANYSLMENGKIK	Deamidated N11 1.55%
9.6	1767.8421	1.0117	NRLSLNDLSSSSTMAR	
8.4	1767.8421	1.0117	NRLSLNDLSSSSTMAR	
8.0	1767.8508	1.0029	LCQAMFDQALRSRR	
5.0	1768.8454	0.0084	ICSQLPHIDTIFNNP	
4.9	1768.8487	0.0050	DLLLAYMKGNANLCR	
4.9	1768.8487	0.0050	NLLLAYMKGNANLCR	
4.6	1767.8500	1.0038	EDAAEAPDGRAGGVAVGAR	

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

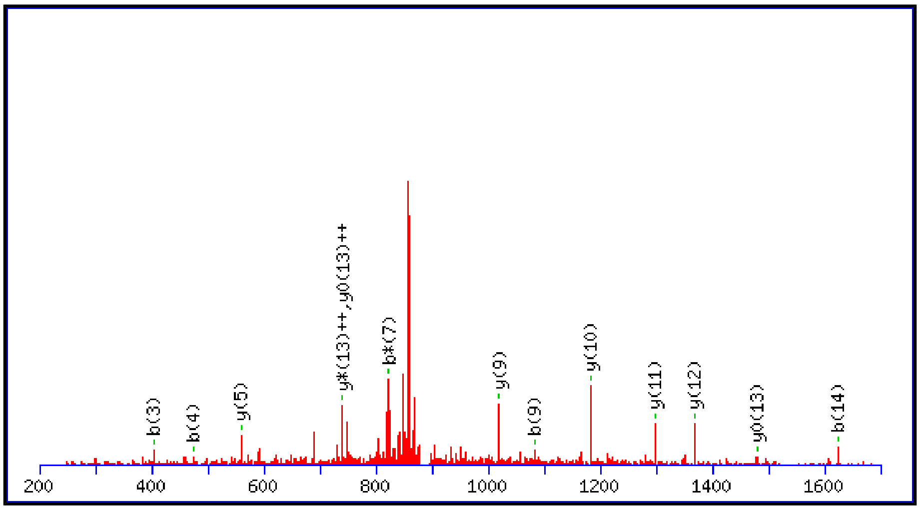
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CIQANYSLMENGKIK**
Found in **C9JF17** in **con_Xuniprot_HUMAN3**, C9JF17_HUMAN Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=2 SV=1

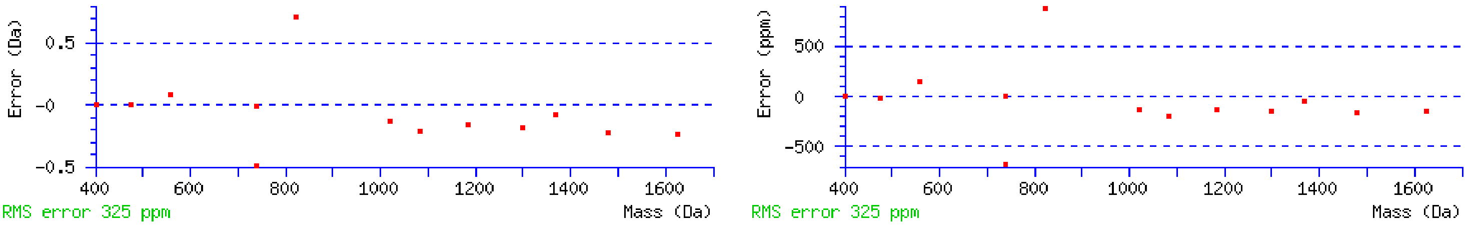
Match to Query 9877: 1769.837868 from(885.926210,2+) intensity(15394.2412) rtinseconds(1188) scans(2754) index(12487)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2391_scans__2754
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1769.8327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.057
Matches : 13/142 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	161.0379	81.0226					**C**							**15**
2	274.1220	137.5646					**I**	1610.8094	805.9084	1593.7829	797.3951	1592.7989	796.9031	**14**
3	***403.1646***	202.0859	386.1380	193.5727			**Q**	1497.7254	749.3663	1480.6988	740.8530	1479.7148	740.3610	**13**
4	***474.2017***	237.6045	457.1751	229.0912			**A**	***1368.6828***	684.8450	1351.6562	676.3318	1350.6722	675.8397	**12**
5	589.2286	295.1180	572.2021	286.6047			**N**	***1297.6457***	649.3265	1280.6191	640.8132	1279.6351	640.3212	**11**
6	752.2920	376.6496	735.2654	368.1363			**Y**	***1182.6187***	591.8130	1165.5922	583.2997	1164.6082	582.8077	**10**
7	839.3240	420.1656	822.2974	411.6524	821.3134	411.1604	**S**	***1019.5554***	510.2813	1002.5288	501.7681	1001.5448	501.2761	**9**
8	952.4081	476.7077	935.3815	468.1944	934.3975	467.7024	**L**	932.5234	466.7653	915.4968	458.2520	914.5128	457.7600	**8**
9	***1083.4485***	542.2279	1066.4220	533.7146	1065.4380	533.2226	**M**	819.4393	410.2233	802.4128	401.7100	801.4287	401.2180	**7**
10	1212.4911	606.7492	1195.4646	598.2359	1194.4806	597.7439	**E**	688.3988	344.7030	671.3723	336.1898	670.3882	335.6978	**6**
11	1326.5341	663.7707	1309.5075	655.2574	1308.5235	654.7654	**N**	***559.3562***	280.1817	542.3297	271.6685			**5**
12	1383.5555	692.2814	1366.5290	683.7681	1365.5450	683.2761	**G**	445.3133	223.1603	428.2867	214.6470			**4**
13	1511.6505	756.3289	1494.6239	747.8156	1493.6399	747.3236	**K**	388.2918	194.6496	371.2653	186.1363			**3**
14	***1624.7346***	812.8709	1607.7080	804.3576	1606.7240	803.8656	**I**	260.1969	130.6021	243.1703	122.0888			**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**



NCBI **BLAST** search of CIQANYSLMENGKIK
(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	1769.8327	0.0051	CIQANYSLMENGKIK
25.6	1769.8327	0.0051	CIQANYSLMENGKIK
24.9	1769.8327	0.0051	CIQANYSLMENGKIK
5.8	1769.8294	0.0084	AVRGFQMVIYDPDNK
5.5	1768.8375	1.0004	AEKSFQMMQVQAEIK
5.3	1769.8328	0.0051	SMLNDKELMWSKEK
3.5	1769.8407	-0.0028	VQFANQSFQELANMK
3.3	1769.8333	0.0046	AQQQDRPLQDWQEK
2.1	1769.8361	0.0017	LQSACKMSMEISKQK
1.9	1768.8335	1.0044	MDMDTQSGQTSLAKKK

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

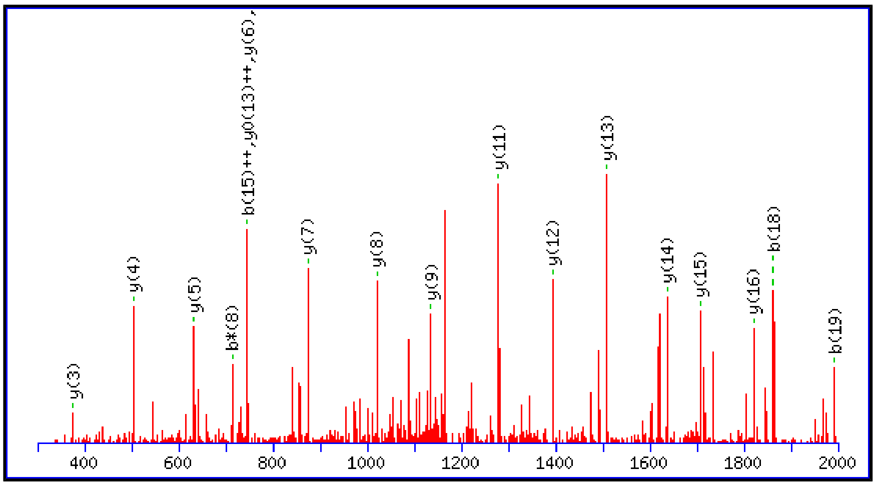
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALAAFNAQNNGSNFQLEEISR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

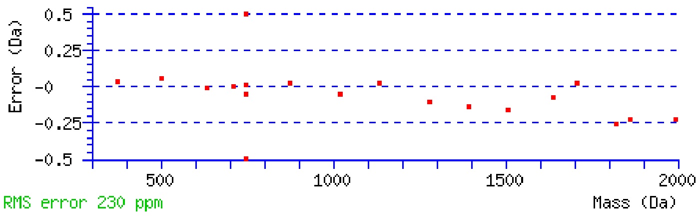
Match to Query 20537: 2365.138288 from(1183.576420,2+) intensity(16121.7236) rtinseconds(1856) scans(4058) index(28908)
Title: 111019_Est_MI_YS_G_15Spectrum3497_scans__4058
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

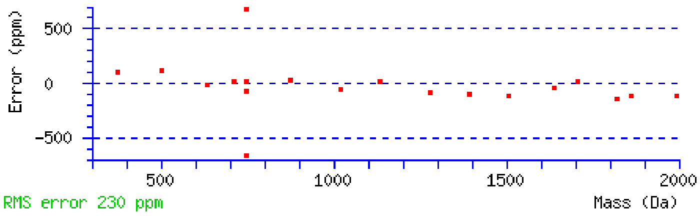
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2365.1298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 135 **Expect:** 7.9e-012
Matches : 19/214 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							22
2	143.0815	72.0444					A	2295.1000	1148.0536	2278.0735	1139.5404	2277.0894	1139.0484	21
3	256.1656	128.5864					L	2224.0629	1112.5351	2207.0364	1104.0218	2206.0523	1103.5298	20
4	327.2027	164.1050					A	2110.9788	1055.9931	2093.9523	1047.4798	2092.9683	1046.9878	19
5	398.2398	199.6235					A	2039.9417	1020.4745	2022.9152	1011.9612	2021.9312	1011.4692	18
6	545.3082	273.1577					F	1968.9046	984.9559	1951.8781	976.4427	1950.8940	975.9507	17
7	659.3511	330.1792	642.3246	321.6659			N	***1821.8362***	911.4217	1804.8096	902.9085	1803.8256	902.4165	16
8	730.3883	365.6978	713.3617	357.1845			A	***1707.7933***	854.4003	1690.7667	845.8870	1689.7827	845.3950	15
9	858.4468	429.7271	841.4203	421.2138			Q	***1636.7562***	818.8817	1619.7296	810.3684	1618.7456	809.8764	14
10	972.4898	486.7485	955.4632	478.2352			N	***1508.6976***	754.8524	1491.6710	746.3392	1490.6870	745.8471	13
11	1087.5167	544.2620	1070.4902	535.7487			N	***1394.6546***	697.8310	1377.6281	689.3177	1376.6441	688.8257	12
12	1144.5382	572.7727	1127.5116	564.2594			G	***1279.6277***	640.3175	1262.6012	631.8042	1261.6171	631.3122	11
13	1231.5702	616.2887	1214.5436	607.7755	1213.5596	607.2835	S	1222.6062	611.8068	1205.5797	603.2935	1204.5957	602.8015	10
14	1345.6131	673.3102	1328.5866	664.7969	1327.6026	664.3049	N	***1135.5742***	568.2907	1118.5477	559.7775	1117.5636	559.2855	9
15	1492.6815	746.8444	1475.6550	738.3311	1474.6710	737.8391	F	***1021.5313***	511.2693	1004.5047	502.7560	1003.5207	502.2640	8
16	1620.7401	810.8737	1603.7136	802.3604	1602.7295	801.8684	Q	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	7
17	1733.8242	867.4157	1716.7976	858.9025	1715.8136	858.4104	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
18	**1862.8668**	931.9370	1845.8402	923.4237	1844.8562	922.9317	E	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
19	**1991.9094**	996.4583	1974.8828	987.9450	1973.8988	987.4530	E	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
20	2104.9934	1053.0003	2087.9669	1044.4871	2086.9829	1043.9951	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2192.0255	1096.5164	2174.9989	1088.0031	2174.0149	1087.5111	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
135.0	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated N11 99.08%
114.5	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated N10 0.87%
100.3	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated N14 0.03%
96.0	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9 0.01%
85.8	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated Q16 0.00%
64.2	2364.1458	0.9925	AALAAFNAQNNGSNFQLEEISR	
60.5	2365.1298	0.0085	AALAAFNAQNNGSNFQLEEISR	Deamidated N7 0.00%
11.4	2365.1372	0.0011	FLEEFEKNLEDTKMNGHLR	
9.0	2365.1397	-0.0014	DSIQQSFSKEAKAQALQAQQR	
8.2	2365.1424	-0.0041	AAWDSQQANPHHLRAHLAADR	

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

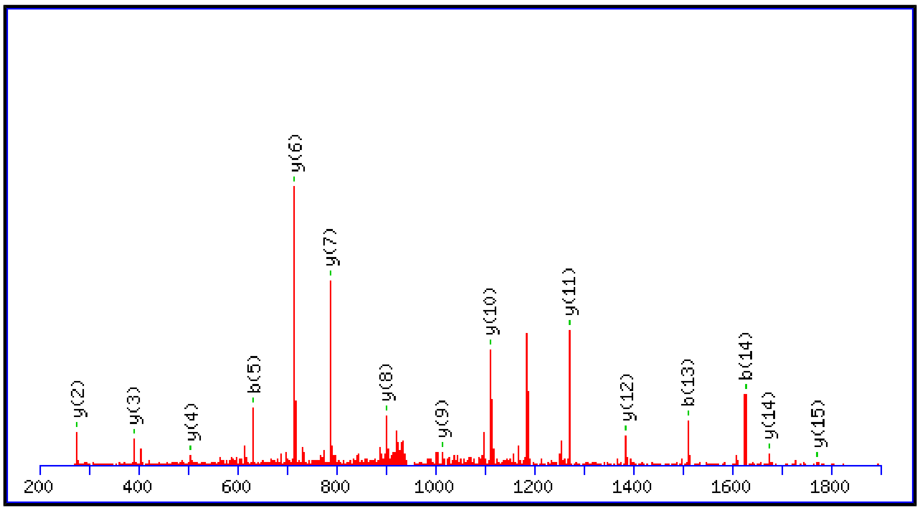
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVCQDCPLLAPLNDTR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

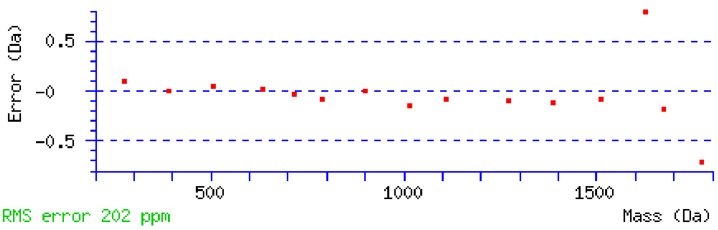
Match to Query 11418: 1900.907868 from(951.461210,2+) intensity(65483.2500) rtinseconds(1462) scans(3571) index(25308)
Title: 111019_Est_MI_YS_G_07Spectrum3026_scans__3571
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

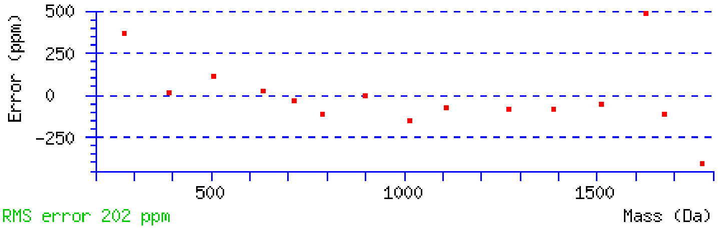
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1900.9023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 116 **Expect:** 5.2e-010
Matches : 15/170 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	228.1707	114.5890	211.1441	106.0757			V	***1773.8146***	887.4109	1756.7881	878.8977	1755.8040	878.4057	15
3	388.2013	194.6043	371.1748	186.0910			C	***1674.7462***	837.8767	1657.7196	829.3635	1656.7356	828.8714	14
4	517.2439	259.1256	500.2173	250.6123			Q	1514.7155	757.8614	1497.6890	749.3481	1496.7050	748.8561	13
5	**632.2708**	316.6391	615.2443	308.1258	614.2603	307.6338	D	***1385.6729***	693.3401	1368.6464	684.8268	1367.6624	684.3348	12
6	792.3015	396.6544	775.2749	388.1411	774.2909	387.6491	C	***1270.6460***	635.8266	1253.6195	627.3134	1252.6354	626.8214	11
7	889.3543	445.1808	872.3277	436.6675	871.3437	436.1755	P	***1110.6154***	555.8113	1093.5888	547.2980	1092.6048	546.8060	10
8	1002.4383	501.7228	985.4118	493.2095	984.4278	492.7175	L	***1013.5626***	507.2849	996.5360	498.7717	995.5520	498.2796	9
9	1115.5224	558.2648	1098.4958	549.7516	1097.5118	549.2595	L	***900.4785***	450.7429	883.4520	442.2296	882.4680	441.7376	8
10	1186.5595	593.7834	1169.5329	585.2701	1168.5489	584.7781	A	***787.3945***	394.2009	770.3679	385.6876	769.3839	385.1956	7
11	1283.6123	642.3098	1266.5857	633.7965	1265.6017	633.3045	P	***716.3573***	358.6823	699.3308	350.1690	698.3468	349.6770	6
12	1396.6963	698.8518	1379.6698	690.3385	1378.6858	689.8465	L	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
13	**1511.7233**	756.3653	1494.6967	747.8520	1493.7127	747.3600	N	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	4
14	**1626.7502**	813.8787	1609.7237	805.3655	1608.7396	804.8735	D	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	3
15	1727.7979	864.4026	1710.7713	855.8893	1709.7873	855.3973	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
116.3	1900.9023	0.0056	KVCQDCPLLAPLNDTR
10.2	1900.9014	0.0065	EEQKQATPKQAEQEEK
8.3	1900.9014	0.0065	EEQEAQKPTAQKQEEK
6.7	1900.9014	0.0065	EEQEAQKPTAQKQEEK
6.4	1900.8989	0.0090	KVTQEWMHVKDQDEK
6.4	1900.8989	0.0090	KVTQEWMHVKDQDEK
5.0	1899.9135	0.9943	VCELQLPDINLVNDQK
4.1	1899.9135	0.9943	VCELQLPDINLVNDQK
3.2	1900.9126	-0.0047	ENEELKQRNGALDQQK
3.2	1900.9126	-0.0047	ENEELKQRNGALDQQK

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

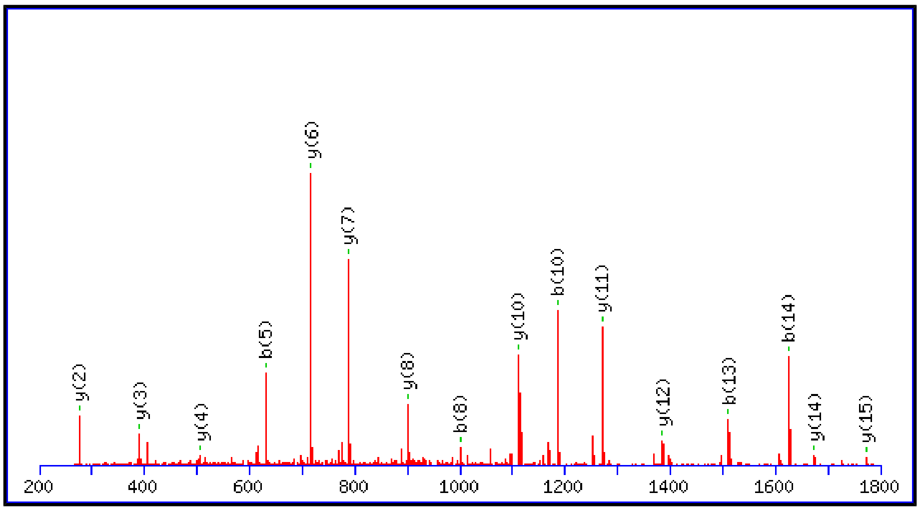
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVCQDCPLLAPLNDTR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

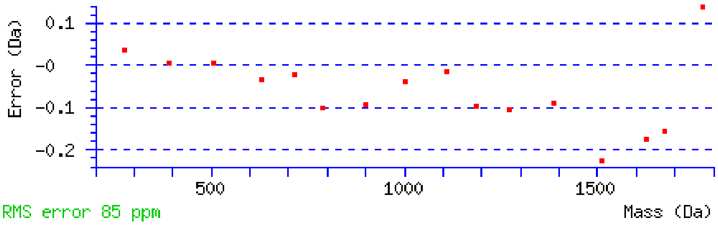
Match to Query 11313: 1899.922568 from(950.968560,2+) intensity(3829381.2500) rtinseconds(1326) scans(3204) index(9423)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum2724_scans__3204
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

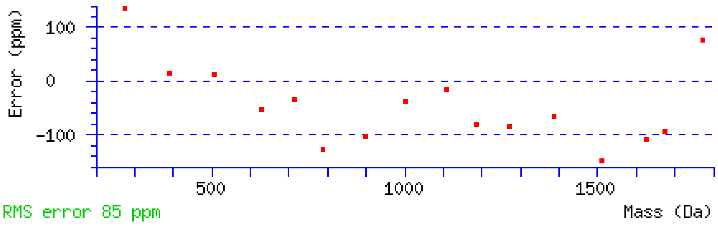
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1899.9183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 116 **Expect:** 5.8e-010
Matches : 16/170 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**16**
2	228.1707	114.5890	211.1441	106.0757			**V**	***1772.8306***	886.9189	1755.8040	878.4057	1754.8200	877.9136	**15**
3	388.2013	194.6043	371.1748	186.0910			**C**	***1673.7622***	837.3847	1656.7356	828.8714	1655.7516	828.3794	**14**
4	516.2599	258.6336	499.2333	250.1203			**Q**	1513.7315	757.3694	1496.7050	748.8561	1495.7210	748.3641	**13**
5	**631.2868**	316.1470	614.2603	307.6338	613.2763	307.1418	**D**	***1385.6729***	693.3401	1368.6464	684.8268	1367.6624	684.3348	**12**
6	791.3175	396.1624	774.2909	387.6491	773.3069	387.1571	**C**	***1270.6460***	635.8266	1253.6195	627.3134	1252.6354	626.8214	**11**
7	888.3702	444.6888	871.3437	436.1755	870.3597	435.6835	**P**	***1110.6154***	555.8113	1093.5888	547.2980	1092.6048	546.8060	**10**
8	**1001.4543**	501.2308	984.4278	492.7175	983.4437	492.2255	**L**	1013.5626	507.2849	996.5360	498.7717	995.5520	498.2796	**9**
9	1114.5384	557.7728	1097.5118	549.2595	1096.5278	548.7675	**L**	***900.4785***	450.7429	883.4520	442.2296	882.4680	441.7376	**8**
10	**1185.5755**	593.2914	1168.5489	584.7781	1167.5649	584.2861	**A**	***787.3945***	394.2009	770.3679	385.6876	769.3839	385.1956	**7**
11	1282.6282	641.8178	1265.6017	633.3045	1264.6177	632.8125	**P**	***716.3573***	358.6823	699.3308	350.1690	698.3468	349.6770	**6**
12	1395.7123	698.3598	1378.6858	689.8465	1377.7017	689.3545	**L**	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	**5**
13	**1510.7392**	755.8733	1493.7127	747.3600	1492.7287	746.8680	**N**	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	**4**
14	**1625.7662**	813.3867	1608.7396	804.8735	1607.7556	804.3815	**D**	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
15	1726.8139	863.9106	1709.7873	855.3973	1708.8033	854.9053	**T**	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
116.0	1899.9183	0.0043	KVCQDCPLLAPLNDTR	Deamidated N13 100.00%
18.6	1899.9183	0.0043	KVCQDCPLLAPLNDTR	Deamidated Q4 0.00%
12.7	1899.9288	-0.0062	MIQKLPEWAADEPVEK	
10.5	1898.9196	1.0029	GYAVDDQFGCREILKK	
9.3	1899.9135	0.0090	VCELQLPDINLVNDQK	
7.9	1899.9149	0.0077	KVTQEWMHVKDQDEK	
5.0	1899.9286	-0.0060	QQDLAGNRQKLEENEK	
4.3	1899.9216	0.0009	QMTLLDMAKGTQKMTR	
4.1	1899.9313	-0.0087	TLNSNDPVQNVVQVLEK	
2.7	1899.9135	0.0090	VCELQLPDINLVNDQK	

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

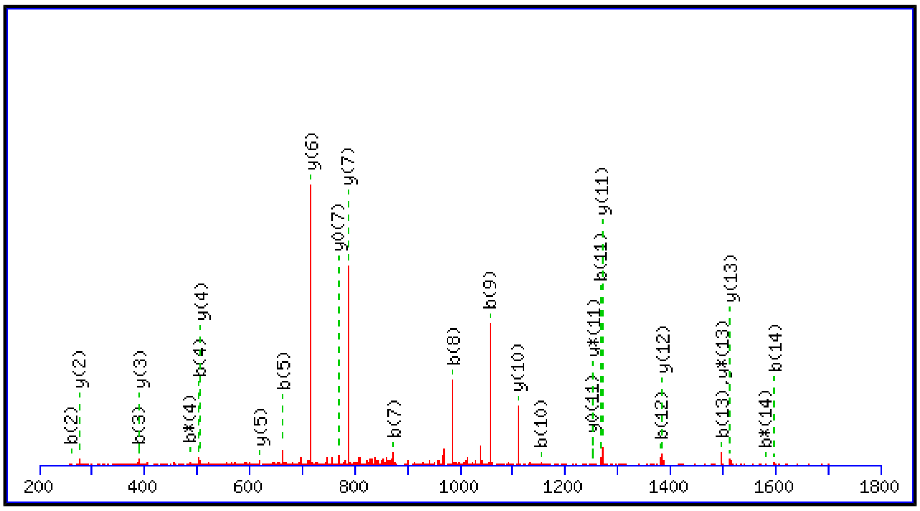
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCQDCPLLAPLNDTR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

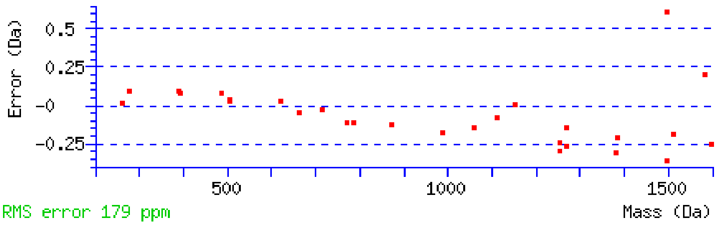
Match to Query 9931: 1771.828648 from(886.921600,2+) intensity(307122.3125) rtinseconds(1645) scans(3858) index(11804)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum3294_scans__3858
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

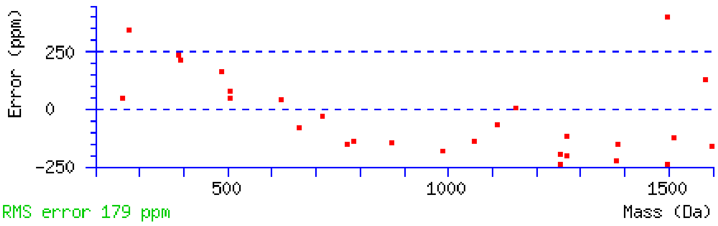
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1771.8233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 89 **Expect:** 2.1e-007
Matches : 28/156 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	100.0757	50.5415					V							15
2	***260.1063***	130.5568					C	1673.7622	837.3847	1656.7356	828.8714	1655.7516	828.3794	14
3	***388.1649***	194.5861	371.1384	186.0728			Q	**1513.7315**	757.3694	1496.7050	748.8561	1495.7210	748.3641	13
4	***503.1919***	252.0996	486.1653	243.5863	485.1813	243.0943	D	**1385.6729**	693.3401	1368.6464	684.8268	1367.6624	684.3348	12
5	***663.2225***	332.1149	646.1960	323.6016	645.2119	323.1096	C	**1270.6460**	635.8266	1253.6195	627.3134	1252.6354	626.8214	11
6	760.2753	380.6413	743.2487	372.1280	742.2647	371.6360	P	**1110.6154**	555.8113	1093.5888	547.2980	1092.6048	546.8060	10
7	***873.3593***	437.1833	856.3328	428.6700	855.3488	428.1780	L	1013.5626	507.2849	996.5360	498.7717	995.5520	498.2796	9
8	***986.4434***	493.7253	969.4169	485.2121	968.4328	484.7201	L	900.4785	450.7429	883.4520	442.2296	882.4680	441.7376	8
9	***1057.4805***	529.2439	1040.4540	520.7306	1039.4700	520.2386	A	**787.3945**	394.2009	770.3679	385.6876	769.3839	385.1956	7
10	***1154.5333***	577.7703	1137.5067	569.2570	1136.5227	568.7650	P	**716.3573**	358.6823	699.3308	350.1690	698.3468	349.6770	6
11	***1267.6173***	634.3123	1250.5908	625.7990	1249.6068	625.3070	L	**619.3046**	310.1559	602.2780	301.6427	601.2940	301.1506	5
12	***1382.6443***	691.8258	1365.6177	683.3125	1364.6337	682.8205	N	**506.2205**	253.6139	489.1940	245.1006	488.2100	244.6086	4
13	***1497.6712***	749.3393	1480.6447	740.8260	1479.6607	740.3340	D	**391.1936**	196.1004	374.1670	187.5872	373.1830	187.0951	3
14	***1598.7189***	799.8631	1581.6924	791.3498	1580.7083	790.8578	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.5	1771.8233	0.0053	VCQDCPLLAPLNDTR	Deamidated N12 100.00%
22.2	1771.8233	0.0053	VCQDCPLLAPLNDTR	Deamidated Q3 0.00%
9.0	1770.8314	0.9972	CKSMEQGMSNLLTLK	
7.7	1771.8264	0.0022	EDWDEPKSADPDKIK	
7.0	1771.8224	0.0063	EQQESLSGRTHELQK	
6.0	1771.8271	0.0015	NAAVMDQGPAGDRTVNR	
4.5	1770.8319	0.9967	GPGMREIGPVSGGGGGGGQK	
4.0	1771.8336	-0.0050	GRNDSGEENVPLDLTR	
3.6	1771.8336	-0.0050	GRNQQQIARPSQEEK	
3.4	1770.8247	1.0040	RFDTVYDQMVQPQK	

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

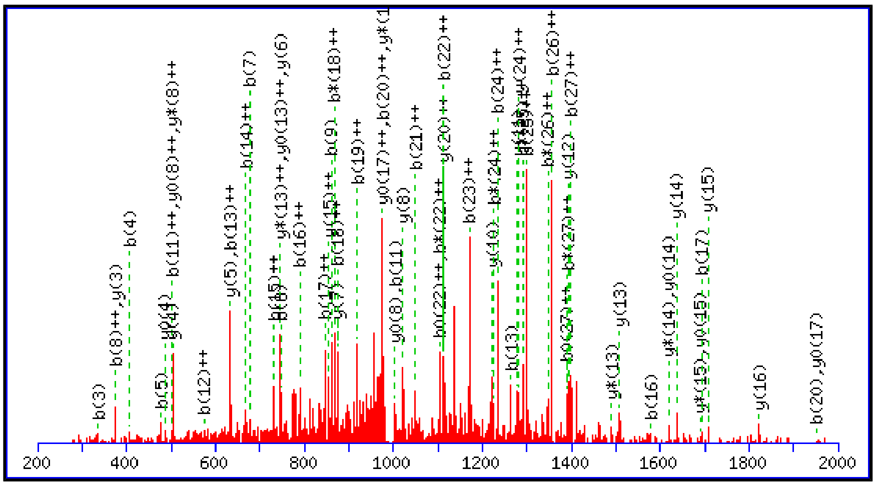
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVHAAKAALAAFNAQNNGSNFQLEEISR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

Match to Query 27064: 2972.510292 from(991.844040,3+) intensity(20918.4844) rtinseconds(1607) scans(3923) index(23226)
Title: 111019_Est_MI_YS_G_04Spectrum3363_scans__3923
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

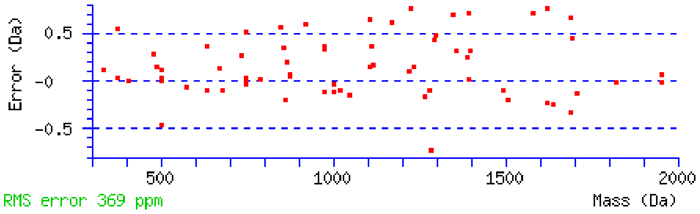
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

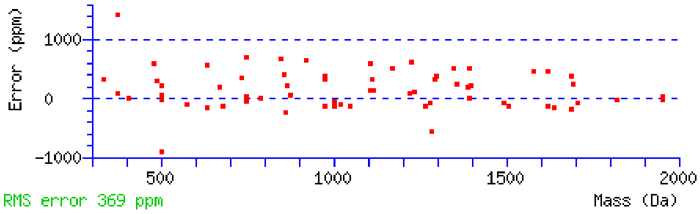


Monoisotopic mass of neutral peptide Mr(calc): 2970.4947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 88 **Expect:** 3.9e-007
Matches : 67/276 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							28
2	199.1441	100.0757					V	2872.4336	1436.7205	2855.4071	1428.2072	2854.4231	1427.7152	27
3	***336.2030***	168.6051					H	2773.3652	1387.1863	2756.3387	1378.6730	2755.3547	1378.1810	26
4	***407.2401***	204.1237					A	2636.3063	1318.6568	2619.2798	1310.1435	2618.2958	1309.6515	25
5	***478.2772***	239.6423					A	2565.2692	1283.1382	2548.2427	1274.6250	2547.2586	1274.1330	24
6	606.3722	303.6897	589.3457	295.1765			K	2494.2321	1247.6197	2477.2055	1239.1064	2476.2215	1238.6144	23
7	***677.4093***	339.2083	660.3828	330.6950			A	2366.1371	1183.5722	2349.1106	1175.0589	2348.1266	1174.5669	22
8	***748.4464***	***374.7269***	731.4199	366.2136			A	2295.1000	1148.0536	2278.0735	1139.5404	2277.0894	1139.0484	21
9	***861.5305***	431.2689	844.5039	422.7556			L	2224.0629	1112.5351	2207.0364	1104.0218	2206.0523	1103.5298	20
10	932.5676	466.7874	915.5411	458.2742			A	2110.9788	1055.9931	2093.9523	1047.4798	2092.9683	1046.9878	19
11	***1003.6047***	***502.3060***	986.5782	493.7927			A	2039.9417	1020.4745	2022.9152	1011.9612	2021.9312	1011.4692	18
12	1150.6731	***575.8402***	1133.6466	567.3269			F	1968.9046	984.9559	1951.8781	976.4427	1950.8940	975.9507	17
13	***1264.7161***	***632.8617***	1247.6895	624.3484			N	**1821.8362**	911.4217	1804.8096	902.9085	1803.8256	902.4165	16
14	1335.7532	***668.3802***	1318.7266	659.8670			A	**1707.7933**	854.4003	1690.7667	845.8870	1689.7827	845.3950	15
15	1463.8118	***732.4095***	1446.7852	723.8962			Q	**1636.7562**	818.8817	1619.7296	810.3684	1618.7456	809.8764	14
16	***1577.8547***	***789.4310***	1560.8281	780.9177			N	**1508.6976**	754.8524	1491.6710	746.3392	1490.6870	745.8471	13
17	***1692.8816***	***846.9445***	1675.8551	838.4312			N	**1394.6546**	697.8310	1377.6281	689.3177	1376.6441	688.8257	12
18	1749.9031	***875.4552***	1732.8765	866.9419			G	**1279.6277**	640.3175	1262.6012	631.8042	1261.6171	631.3122	11
19	1836.9351	***918.9712***	1819.9086	910.4579	1818.9246	909.9659	S	**1222.6062**	611.8068	1205.5797	603.2935	1204.5957	602.8015	10
20	***1950.9780***	***975.9927***	1933.9515	967.4794	1932.9675	966.9874	N	1135.5742	568.2907	1118.5477	559.7775	1117.5636	559.2855	9
21	2098.0465	***1049.5269***	2081.0199	1041.0136	2080.0359	1040.5216	F	**1021.5313**	511.2693	1004.5047	502.7560	1003.5207	502.2640	8
22	2226.1050	***1113.5562***	2209.0785	1105.0429	2208.0945	1104.5509	Q	**874.4629**	437.7351	857.4363	429.2218	856.4523	428.7298	7
23	2339.1891	***1170.0982***	2322.1626	1161.5849	2321.1785	1161.0929	L	**746.4043**	373.7058	729.3777	365.1925	728.3937	364.7005	6

24	2468.2317	***1234.6195***	2451.2051	1226.1062	2450.2211	1225.6142	**E**	**633.3202**	317.1638	616.2937	308.6505	615.3097	308.1585	**5**
25	2597.2743	***1299.1408***	2580.2477	1290.6275	2579.2637	1290.1355	**E**	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	**4**
26	2710.3584	***1355.6828***	2693.3318	1347.1695	2692.3478	1346.6775	**I**	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
27	2797.3904	***1399.1988***	2780.3638	1390.6856	2779.3798	1390.1935	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
28							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.8	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated N17 38.52%
86.7	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated N16 29.97%
85.7	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated Q15 23.64%
80.4	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated N13 6.95%
69.6	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated N20 0.58%
67.3	2970.4947	2.0156	VVHAAKAALAAFNAQNNGSNFQLEEISR	Deamidated Q22 0.34%
14.3	2970.5127	1.9976	YFARSKQQHLLAYYNAIGVLQELDK	
14.3	2970.5127	1.9976	YFARSKQQHLLAYYNAIGVLQELDK	
14.3	2971.4967	1.0136	YFARSKQQHLLAYYNAIGVLQELDK	
13.8	2970.4908	2.0195	DTDNGQRQPLHQSLLKQQPTTTLGHR	

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

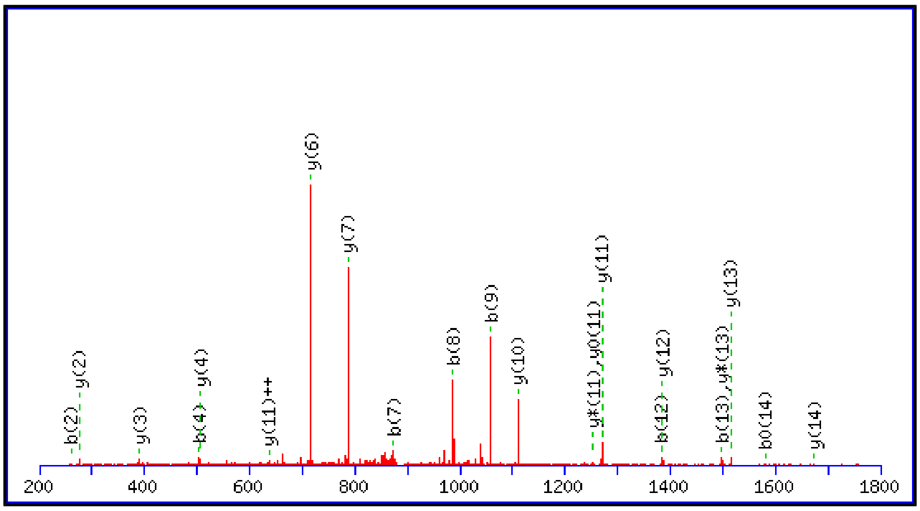
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCQDCPLLAPLNDTR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

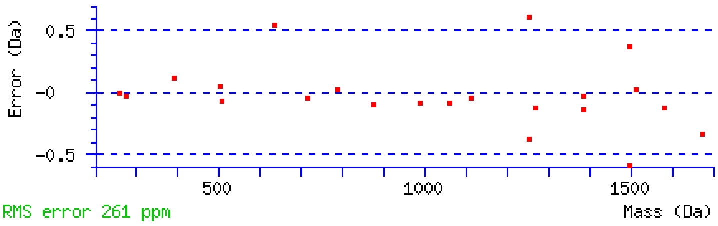
Match to Query 10006: 1772.811488 from(887.413020,2+) intensity(99616.7188) rtinseconds(1695) scans(4155) index(12639)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum3630_scans__4155
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

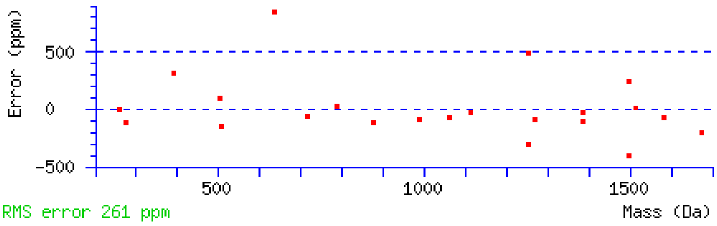
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1772.8073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 71 **Expect:** 1.2e-005
Matches : 22/156 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	100.0757	50.5415					V							15
2	**260.1063**	130.5568					C	***1674.7462***	837.8767	1657.7196	829.3635	1656.7356	828.8714	14
3	389.1489	195.0781	372.1224	186.5648			Q	***1514.7155***	757.8614	1497.6890	749.3481	1496.7050	748.8561	13
4	**504.1759**	252.5916	487.1493	244.0783	486.1653	243.5863	D	***1385.6729***	693.3401	1368.6464	684.8268	1367.6624	684.3348	12
5	664.2065	332.6069	647.1800	324.0936	646.1960	323.6016	C	***1270.6460***	635.8266	1253.6195	627.3134	1252.6354	626.8214	11
6	761.2593	381.1333	744.2327	372.6200	743.2487	372.1280	P	***1110.6154***	555.8113	1093.5888	547.2980	1092.6048	546.8060	10
7	**874.3434**	437.6753	857.3168	429.1620	856.3328	428.6700	L	1013.5626	507.2849	996.5360	498.7717	995.5520	498.2796	9
8	**987.4274**	494.2173	970.4009	485.7041	969.4169	485.2121	L	900.4785	450.7429	883.4520	442.2296	882.4680	441.7376	8
9	**1058.4645**	529.7359	1041.4380	521.2226	1040.4540	520.7306	A	***787.3945***	394.2009	770.3679	385.6876	769.3839	385.1956	7
10	1155.5173	578.2623	1138.4907	569.7490	1137.5067	569.2570	P	***716.3573***	358.6823	699.3308	350.1690	698.3468	349.6770	6
11	1268.6014	634.8043	1251.5748	626.2910	1250.5908	625.7990	L	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
12	**1383.6283**	692.3178	1366.6018	683.8045	1365.6177	683.3125	N	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	4
13	**1498.6552**	749.8313	1481.6287	741.3180	1480.6447	740.8260	D	***391.1936***	196.1004	374.1670	187.5872	373.1830	187.0951	3
14	1599.7029	800.3551	1582.6764	791.8418	1581.6924	791.3498	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
71.3	1772.8073	0.0042	VCQDCPLLAPLNDTR
10.0	1771.8154	0.9961	CKSMEQGMSNLLTLK
7.5	1771.8154	0.9961	CKSMEQGMSNLLTLK
7.3	1772.8177	-0.0062	GRNDSGEENVPLDLTR
3.0	1772.8046	0.0069	SCQQLPATDMRRHR
2.0	1772.8176	-0.0061	GRNQQQIARPSQEEK
1.3	1772.8176	-0.0062	SSEDPNEDIVERNIR
1.3	1771.8047	1.0068	TVAPQGQDMASIAPDNR
1.3	1771.8022	1.0093	RWCDVTGTYMIDAGK
0.4	1771.8151	0.9963	NEYEQLNYAKQLKE

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

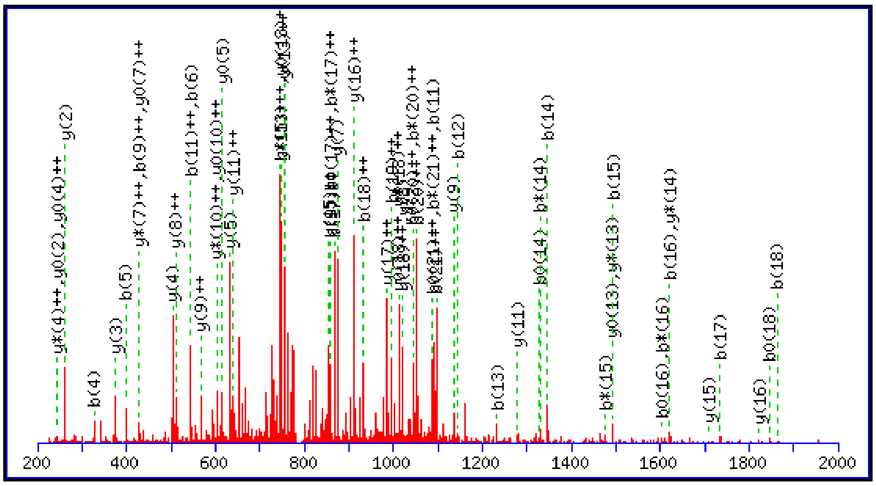
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALAAFNAQNNGSNFQLEEISR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

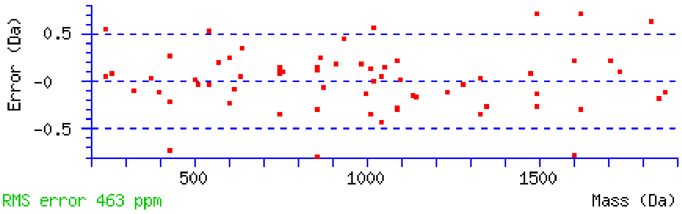
Match to Query 20929: 2366.120322 from(789.714050,3+) intensity(127655.1016) rtinseconds(1748) scans(4435) index(24587)
Title: 111019_Est_MI_YS_G_06Spectrum3858_scans__4435
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

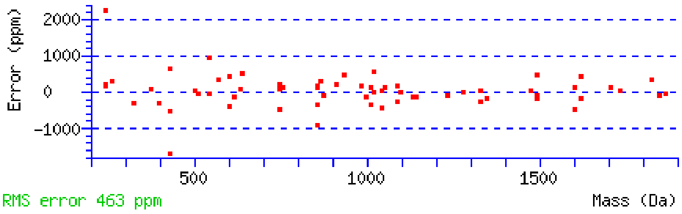
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2366.1138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10     : Deamidated (NQ)
N11     : Deamidated (NQ)
Ions Score: 58  Expect: 0.00035
Matches : 66/214 fragment ions using 103 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							22
2	143.0815	72.0444					A	2296.0840	1148.5457	2279.0575	1140.0324	2278.0735	1139.5404	21
3	256.1656	128.5864					L	2225.0469	1113.0271	2208.0204	1104.5138	2207.0364	1104.0218	20
4	***327.2027***	164.1050					A	2111.9629	1056.4851	2094.9363	1047.9718	2093.9523	1047.4798	19
5	***398.2398***	199.6235					A	2040.9257	1020.9665	2023.8992	1012.4532	2022.9152	1011.9612	18
6	***545.3082***	273.1577					F	1969.8886	985.4480	1952.8621	976.9347	1951.8781	976.4427	17
7	659.3511	330.1792	642.3246	321.6659			N	***1822.8202***	911.9137	1805.7937	903.4005	1804.8096	902.9085	16
8	730.3883	365.6978	713.3617	357.1845			A	***1708.7773***	854.8923	1691.7507	846.3790	1690.7667	845.8870	15
9	***858.4468***	**429.7271**	841.4203	421.2138			Q	1637.7402	819.3737	1620.7136	810.8604	1619.7296	810.3684	14
10	973.4738	487.2405	956.4472	478.7272			N	1509.6816	755.3444	1492.6550	746.8312	1491.6710	746.3392	13
11	***1088.5007***	**544.7540**	1071.4742	536.2407			N	1394.6546	697.8310	1377.6281	689.3177	1376.6441	688.8257	12
12	***1145.5222***	573.2647	1128.4956	564.7515			G	***1279.6277***	640.3175	1262.6012	631.8042	1261.6171	631.3122	11
13	***1232.5542***	616.7807	1215.5277	608.2675	1214.5436	607.7755	S	1222.6062	611.8068	1205.5797	603.2935	1204.5957	602.8015	10
14	***1346.5971***	673.8022	1329.5706	665.2889	1328.5866	664.7969	N	***1135.5742***	568.2907	1118.5477	559.7775	1117.5636	559.2855	9
15	***1493.6655***	**747.3364**	1476.6390	738.8231	1475.6550	738.3311	F	***1021.5313***	511.2693	1004.5047	502.7560	1003.5207	502.2640	8
16	***1621.7241***	811.3657	1604.6976	802.8524	1603.7136	802.3604	Q	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	7
17	***1734.8082***	**867.9077**	1717.7816	859.3945	1716.7976	858.9025	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
18	***1863.8508***	**932.4290**	1846.8242	923.9158	1845.8402	923.4237	E	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
19	1992.8934	**996.9503**	1975.8668	988.4371	1974.8828	987.9450	E	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
20	2105.9774	**1053.4924**	2088.9509	1044.9791	2087.9669	1044.4871	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2193.0095	**1097.0084**	2175.9829	1088.4951	2174.9989	1088.0031	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.3	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, N11 14.58%
57.6	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, N10 12.46%
56.8	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, N11 10.46%
56.0	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N11, N14 8.70%
56.0	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, N14 8.70%
55.8	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, N14 8.27%
55.0	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N11, Q16 6.91%
55.0	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, Q16 6.91%
54.6	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, Q16 6.20%
51.9	2366.1138	0.0065	AALAAFNAQNNGSNFQLEEISR	Deamidated N7, N11 3.38%

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

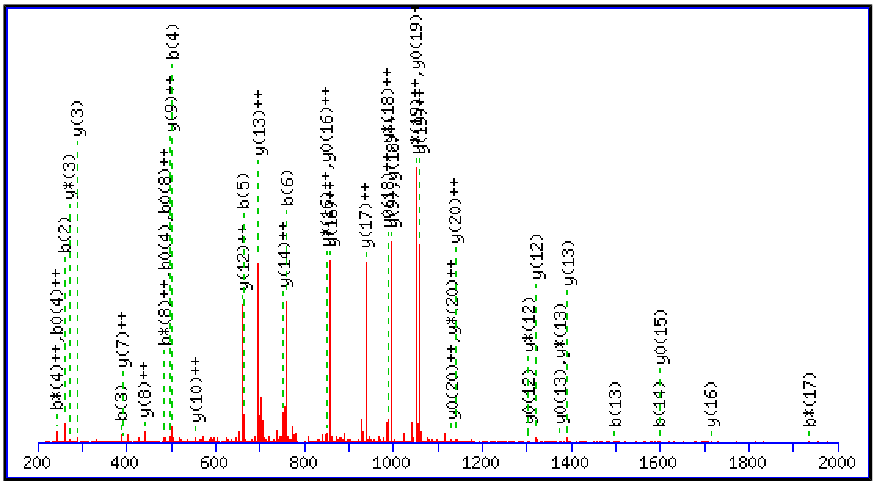
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VCQDCPLLAPLNDTRVVHAAK**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

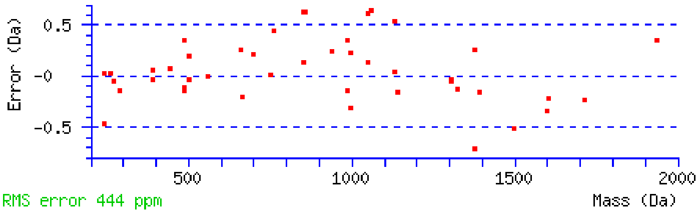
Match to Query 20958: 2377.196382 from(793.406070,3+) intensity(336520.6875) rtinseconds(1474) scans(3638) index(22570)
Title: 111019_Est_MI_YS_G_03Spectrum3166_scans__3638
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

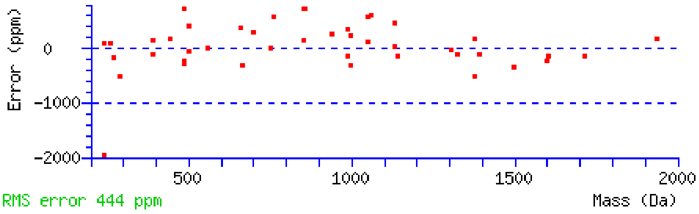
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2377.1882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00085
Matches : 44/216 fragment ions using 83 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							21
2	**260.1063**	130.5568					C	2279.1271	1140.0672	2262.1006	1131.5539	2261.1165	1131.0619	20
3	**388.1649**	194.5861	371.1384	186.0728			Q	2119.0965	1060.0519	2102.0699	1051.5386	2101.0859	1051.0466	19
4	**503.1919**	252.0996	486.1653	243.5863	485.1813	243.0943	D	1991.0379	996.0226	1974.0113	987.5093	1973.0273	987.0173	18
5	**663.2225**	332.1149	646.1960	323.6016	645.2119	323.1096	C	1876.0109	938.5091	1858.9844	929.9958	1858.0004	929.5038	17
6	**760.2753**	380.6413	743.2487	372.1280	742.2647	371.6360	P	**1715.9803**	858.4938	1698.9537	849.9805	1697.9697	849.4885	16
7	873.3593	437.1833	856.3328	428.6700	855.3488	428.1780	L	1618.9275	809.9674	1601.9010	801.4541	1600.9170	800.9621	15
8	986.4434	493.7253	969.4169	485.2121	968.4328	484.7201	L	1505.8435	753.4254	1488.8169	744.9121	1487.8329	744.4201	14
9	1057.4805	529.2439	1040.4540	520.7306	1039.4700	520.2386	A	**1392.7594**	696.8833	1375.7328	688.3701	1374.7488	687.8781	13
10	1154.5333	577.7703	1137.5067	569.2570	1136.5227	568.7650	P	**1321.7223**	661.3648	1304.6957	652.8515	1303.7117	652.3595	12
11	1267.6173	634.3123	1250.5908	625.7990	1249.6068	625.3070	L	1224.6695	612.8384	1207.6430	604.3251	1206.6589	603.8331	11
12	1382.6443	691.8258	1365.6177	683.3125	1364.6337	682.8205	N	1111.5854	556.2964	1094.5589	547.7831	1093.5749	547.2911	10
13	**1497.6712**	749.3393	1480.6447	740.8260	1479.6607	740.3340	D	**996.5585**	498.7829	979.5320	490.2696	978.5479	489.7776	9
14	**1598.7189**	799.8631	1581.6924	791.3498	1580.7083	790.8578	T	881.5316	441.2694	864.5050	432.7561	863.5210	432.2641	8
15	1754.8200	877.9136	1737.7935	869.4004	1736.8095	868.9084	R	780.4839	390.7456	763.4573	382.2323			7
16	1853.8884	927.4479	1836.8619	918.9346	1835.8779	918.4426	V	624.3828	312.6950	607.3562	304.1817			6
17	1952.9568	976.9821	1935.9303	968.4688	1934.9463	967.9768	V	525.3144	263.1608	508.2878	254.6475			5
18	2090.0158	1045.5115	2072.9892	1036.9982	2072.0052	1036.5062	H	426.2459	213.6266	409.2194	205.1133			4
19	2161.0529	1081.0301	2144.0263	1072.5168	2143.0423	1072.0248	A	**289.1870**	145.0972	272.1605	136.5839			3
20	2232.0900	1116.5486	2215.0634	1108.0354	2214.0794	1107.5433	A	218.1499	109.5786	201.1234	101.0653			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.1	2377.1882	0.0081	VCQDCPLLAPLNDTRVVHAAK	Deamidated N12 92.59%
44.1	2377.1882	0.0081	VCQDCPLLAPLNDTRVVHAAK	Deamidated Q3 7.41%
43.8	2376.2042	0.9922	VCQDCPLLAPLNDTRVVHAAK	
9.8	2376.2033	0.9931	DALDQLLTNKRLHPQQAAGQR	
8.6	2376.2033	0.9931	DALDQLLTNKRLHPQQAAGQR	
8.6	2377.1873	0.0091	DALDQLLTNKRLHPQQAAGQR	
8.2	2376.1916	1.0048	MSALVQPCTPESEALTLGSIKK	
7.2	2376.1929	1.0034	HKPQILMMELAHGLQDQNLK	
7.2	2376.1929	1.0034	HKPQILMMELAHGLQDQNLK	
7.1	2376.1916	1.0048	EGEATLVVDIMEALEKMNQIK	

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

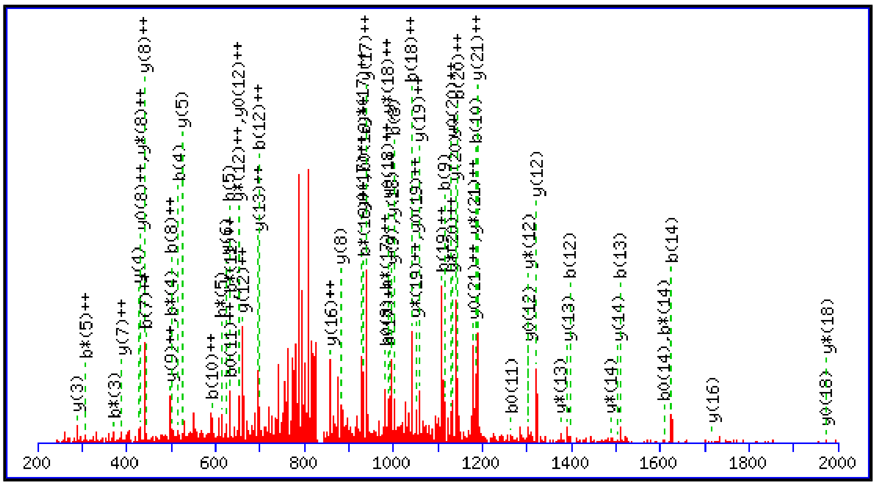
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVCQDCPLLAPLNDTRVVHAAK**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

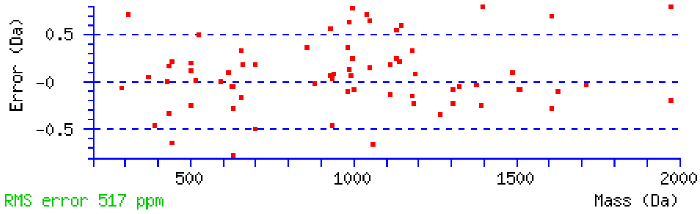
Match to Query 21591: 2505.294552 from(836.105460,3+) intensity(19801.5391) rtinseconds(1194) scans(3014) index(23864)
Title: 111019_Est_MI_YS_G_05Spectrum2583_scans__3014
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

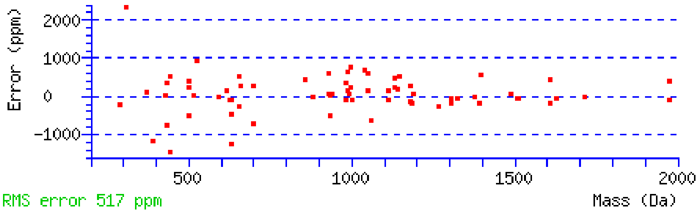
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2505.2832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0012
Matches : 71/230 fragment ions using 150 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							22
2	228.1707	114.5890	211.1441	106.0757			V	2378.1955	1189.6014	2361.1690	1181.0881	2360.1849	1180.5961	21
3	388.2013	194.6043	371.1748	186.0910			C	2279.1271	1140.0672	2262.1006	1131.5539	2261.1165	1131.0619	20
4	**516.2599**	258.6336	499.2333	250.1203			Q	2119.0965	1060.0519	2102.0699	1051.5386	2101.0859	1051.0466	19
5	**631.2868**	316.1470	614.2603	307.6338	613.2763	307.1418	D	1991.0379	996.0226	1974.0113	987.5093	1973.0273	987.0173	18
6	791.3175	396.1624	774.2909	387.6491	773.3069	387.1571	C	1876.0109	938.5091	1858.9844	929.9958	1858.0004	929.5038	17
7	888.3702	***444.6888***	871.3437	436.1755	870.3597	435.6835	P	**1715.9803**	858.4938	1698.9537	849.9805	1697.9697	849.4885	16
8	**1001.4543**	***501.2308***	984.4278	492.7175	983.4437	492.2255	L	1618.9275	809.9674	1601.9010	801.4541	1600.9170	800.9621	15
9	**1114.5384**	557.7728	1097.5118	549.2595	1096.5278	548.7675	L	**1505.8435**	753.4254	1488.8169	744.9121	1487.8329	744.4201	14
10	**1185.5755**	***593.2914***	1168.5489	584.7781	1167.5649	584.2861	A	**1392.7594**	696.8833	1375.7328	688.3701	1374.7488	687.8781	13
11	1282.6282	641.8178	1265.6017	633.3045	1264.6177	632.8125	P	**1321.7223**	661.3648	1304.6957	652.8515	1303.7117	652.3595	12
12	**1395.7123**	***698.3598***	1378.6858	689.8465	1377.7017	689.3545	L	1224.6695	612.8384	1207.6430	604.3251	1206.6589	603.8331	11
13	**1510.7392**	755.8733	1493.7127	747.3600	1492.7287	746.8680	N	1111.5854	556.2964	1094.5589	547.7831	1093.5749	547.2911	10
14	**1625.7662**	813.3867	1608.7396	804.8735	1607.7556	804.3815	D	**996.5585**	498.7829	979.5320	490.2696	978.5479	489.7776	9
15	1726.8139	863.9106	1709.7873	855.3973	1708.8033	854.9053	T	**881.5316**	441.2694	864.5050	432.7561	863.5210	432.2641	8
16	1882.9150	941.9611	1865.8884	933.4479	1864.9044	932.9558	R	780.4839	390.7456	763.4573	382.2323			7
17	1981.9834	***991.4953***	1964.9568	982.9821	1963.9728	982.4901	V	**624.3828**	312.6950	607.3562	304.1817			6
18	2081.0518	***1041.0295***	2064.0253	1032.5163	2063.0412	1032.0243	V	**525.3144**	263.1608	508.2878	254.6475			5
19	2218.1107	***1109.5590***	2201.0842	1101.0457	2200.1002	1100.5537	H	**426.2459**	213.6266	409.2194	205.1133			4
20	2289.1478	***1145.0776***	2272.1213	1136.5643	2271.1373	1136.0723	A	**289.1870**	145.0972	272.1605	136.5839			3
21	2360.1850	***1180.5961***	2343.1584	1172.0828	2342.1744	1171.5908	A	218.1499	109.5786	201.1234	101.0653			2
22							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.5	2505.2832	0.0114	KVCQDCPLLAPLNDTRVVHAAK	Deamidated N13 99.49%
30.0	2504.2992	0.9954	KVCQDCPLLAPLNDTRVVHAAK	
29.6	2505.2832	0.0114	KVCQDCPLLAPLNDTRVVHAAK	Deamidated Q4 0.51%
2.5	2505.2837	0.0109	THVWSPGSRSVAGTGSGSVSHAIIR	

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

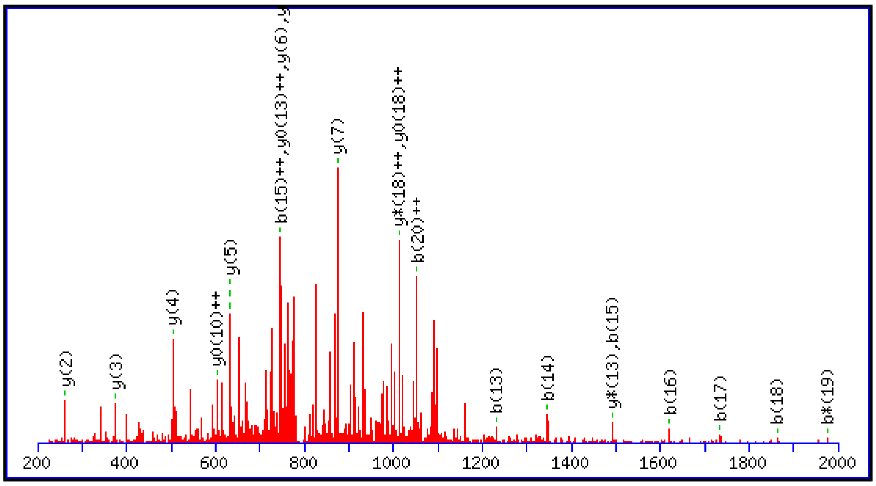
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AALAAFNAQNNGSNFQLEEISR**
Found in **C9JV77** in **con_Xuniprot_HUMAN3**, C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1

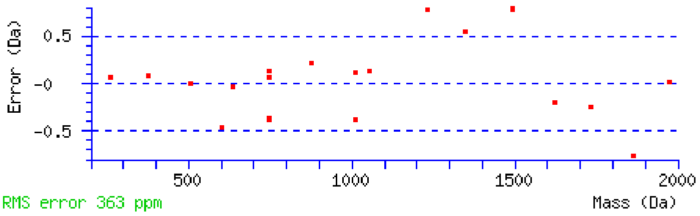
Match to Query 20928: 2366.117772 from(789.713200,3+) intensity(51567.6016) rtinseconds(1763) scans(4477) index(24592)
Title: 111019_Est_MI_YS_G_06Spectrum3894_scans__4477
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

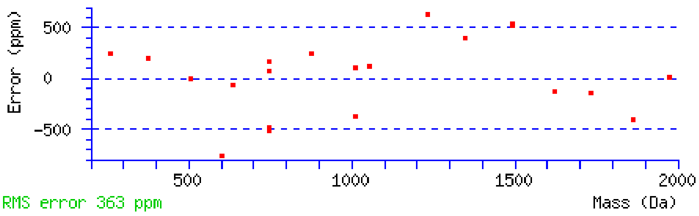
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2366.1138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Q16 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0018
Matches : 21/214 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	72.0444	36.5258					A							22
2	143.0815	72.0444					A	2296.0840	1148.5457	2279.0575	1140.0324	2278.0735	1139.5404	21
3	256.1656	128.5864					L	2225.0469	1113.0271	2208.0204	1104.5138	2207.0364	1104.0218	20
4	327.2027	164.1050					A	2111.9629	1056.4851	2094.9363	1047.9718	2093.9523	1047.4798	19
5	398.2398	199.6235					A	2040.9257	1020.9665	2023.8992	1012.4532	2022.9152	1011.9612	18
6	545.3082	273.1577					F	1969.8886	985.4480	1952.8621	976.9347	1951.8781	976.4427	17
7	659.3511	330.1792	642.3246	321.6659			N	1822.8202	911.9137	1805.7937	903.4005	1804.8096	902.9085	16
8	730.3883	365.6978	713.3617	357.1845			A	1708.7773	854.8923	1691.7507	846.3790	1690.7667	845.8870	15
9	858.4468	429.7271	841.4203	421.2138			Q	1637.7402	819.3737	1620.7136	810.8604	1619.7296	810.3684	14
10	972.4898	486.7485	955.4632	478.2352			N	1509.6816	755.3444	1492.6550	746.8312	1491.6710	746.3392	13
11	1087.5167	544.2620	1070.4902	535.7487			N	1395.6387	698.3230	1378.6121	689.8097	1377.6281	689.3177	12
12	1144.5382	572.7727	1127.5116	564.2594			G	1280.6117	640.8095	1263.5852	632.2962	1262.6012	631.8042	11
13	***1231.5702***	616.2887	1214.5436	607.7755	1213.5596	607.2835	S	1223.5903	612.2988	1206.5637	603.7855	1205.5797	603.2935	10
14	***1345.6131***	673.3102	1328.5866	664.7969	1327.6026	664.3049	N	1136.5582	568.7828	1119.5317	560.2695	1118.5477	559.7775	9
15	***1492.6815***	**746.8444**	1475.6550	738.3311	1474.6710	737.8391	F	1022.5153	511.7613	1005.4888	503.2480	1004.5047	502.7560	8
16	***1621.7241***	811.3657	1604.6976	802.8524	1603.7136	802.3604	Q	***875.4469***	438.2271	858.4203	429.7138	857.4363	429.2218	7
17	***1734.8082***	867.9077	1717.7816	859.3945	1716.7976	858.9025	L	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
18	***1863.8508***	932.4290	1846.8242	923.9158	1845.8402	923.4237	E	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
19	1992.8934	996.9503	1975.8668	988.4371	1974.8828	987.9450	E	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
20	2105.9774	**1053.4924**	2088.9509	1044.9791	2087.9669	1044.4871	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2193.0095	1097.0084	2175.9829	1088.4951	2174.9989	1088.0031	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.3	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N11, Q16 19.46%
51.3	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, Q16 19.46%
51.3	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, Q16 19.46%
51.3	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N7, Q16 19.46%
45.0	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, N11 4.57%
44.2	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N10, N14 3.82%
43.6	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N11, N14 3.30%
41.8	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated N14, Q16 2.16%
39.9	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, N14 1.39%
39.9	2366.1138	0.0040	AALAAFNAQNNGSNFQLEEISR	Deamidated Q9, N11 1.39%

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

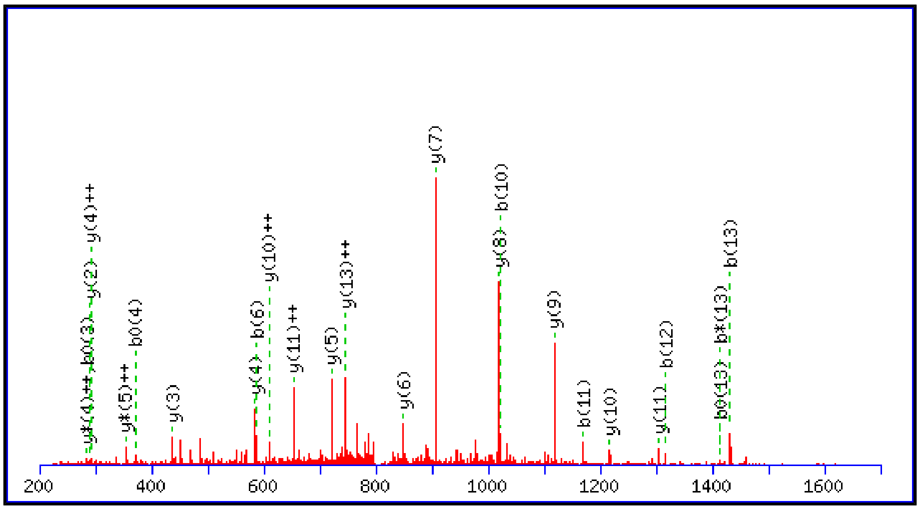
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSVSVVLGQHFFNR**
Found in **D6RAR4** in **con_Xuniprot_HUMAN3**, D6RAR4_HUMAN Hepatocyte growth factor activator OS=Homo sapiens GN=HGFAC PE=2 SV=1

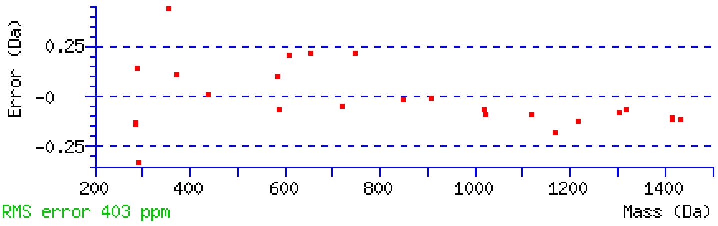
Match to Query 7673: 1604.800368 from(803.407460,2+) intensity(68037.2266) rtinseconds(1707) scans(4384) index(2753)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum3711_scans__4384
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

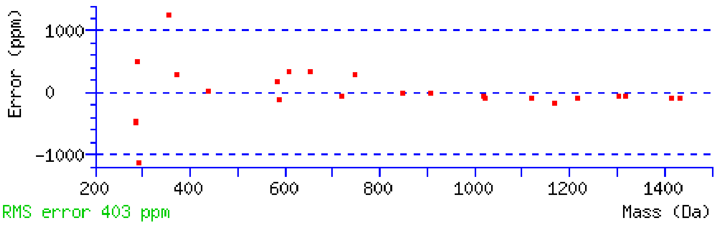
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1604.7947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 67 **Expect:** 5.3e-005
Matches : 25/120 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**14**
2	203.0662	102.0368			185.0557	93.0315	**S**	1490.7750	745.8912	1473.7485	737.3779	1472.7645	736.8859	**13**
3	302.1347	151.5710			284.1241	142.5657	**V**	1403.7430	702.3751	1386.7165	693.8619	1385.7324	693.3699	**12**
4	389.1667	195.0870			371.1561	186.0817	**S**	***1304.6746***	652.8409	1287.6480	644.3277	1286.6640	643.8357	**11**
5	488.2351	244.6212			470.2245	235.6159	**V**	***1217.6426***	609.3249	1200.6160	600.8116			**10**
6	**587.3035**	294.1554			569.2930	285.1501	**V**	***1118.5742***	559.7907	1101.5476	551.2774			**9**
7	700.3876	350.6974			682.3770	341.6921	**L**	***1019.5057***	510.2565	1002.4792	501.7432			**8**
8	757.4090	379.2082			739.3985	370.2029	**G**	***906.4217***	453.7145	889.3951	445.2012			**7**
9	885.4676	443.2374	868.4411	434.7242	867.4571	434.2322	**Q**	***849.4002***	425.2037	832.3737	416.6905			**6**
10	**1022.5265**	511.7669	1005.5000	503.2536	1004.5160	502.7616	**H**	***721.3416***	361.1745	704.3151	352.6612			**5**
11	**1169.5949**	585.3011	1152.5684	576.7878	1151.5844	576.2958	**F**	***584.2827***	292.6450	567.2562	284.1317			**4**
12	**1316.6634**	658.8353	1299.6368	650.3220	1298.6528	649.8300	**F**	***437.2143***	219.1108	420.1878	210.5975			**3**
13	**1431.6903**	716.3488	1414.6638	707.8355	1413.6797	707.3435	**N**	***290.1459***	145.5766	273.1193	137.0633			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.8	1604.7947	0.0056	DSVSVVLGQHFFNR	Deamidated N13 99.96%
32.5	1604.7947	0.0056	DSVSVVLGQHFFNR	Deamidated Q9 0.04%
7.5	1604.8021	-0.0017	WDNGLLSHYMKLK	
4.4	1604.7940	0.0064	RVNNTDEMARLIR	
3.9	1603.7954	1.0049	EPQATGPHGGTSPLQK	
3.2	1604.8046	-0.0042	GPAAGQTFTAVDTALGK	
1.8	1604.8079	-0.0076	SSLGKNLQVPMSESK	
1.7	1604.8046	-0.0042	LGESVTQFVEPDKR	
1.6	1603.8028	0.9976	LGSLNLRWQEVCK	
1.4	1604.8080	-0.0076	LIATMGDTVTTDVPR	

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

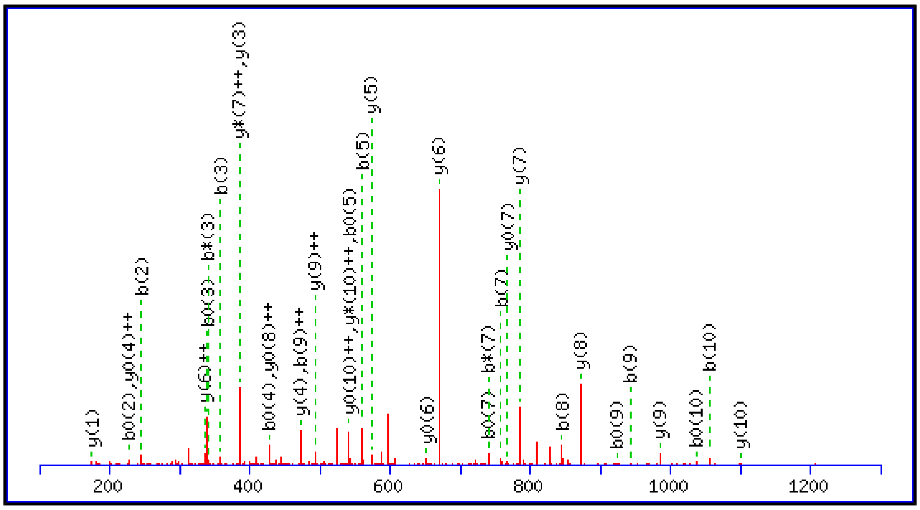
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENISDPTSPLR**
Found in **D6RD17** in **con_Xuniprot_HUMAN3**, D6RD17_HUMAN Immunoglobulin J chain (Fragment) OS=Homo sapiens GN=IGJ PE=2 SV=1

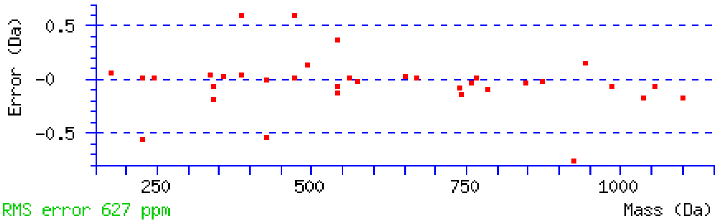
Match to Query 1702: 1228.594768 from(615.304660,2+) intensity(411029.7500) rtinseconds(673) scans(1423) index(1898)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum1172_scans__1423
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

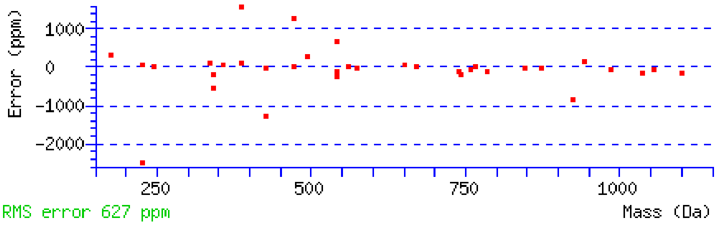
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1228.5935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.00014
Matches : 35/112 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	130.0499	65.5286			112.0393	56.5233	E							11
2	**245.0768**	123.0420	228.0503	114.5288	227.0662	114.0368	N	***1100.5582***	550.7828	1083.5317	542.2695	1082.5477	541.7775	10
3	**358.1609**	179.5841	341.1343	171.0708	340.1503	170.5788	I	***985.5313***	493.2693	968.5047	484.7560	967.5207	484.2640	9
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	S	***872.4472***	436.7272	855.4207	428.2140	854.4367	427.7220	8
5	**560.2198**	280.6136	543.1933	272.1003	542.2093	271.6083	D	***785.4152***	393.2112	768.3886	384.6980	767.4046	384.2060	7
6	657.2726	329.1399	640.2461	320.6267	639.2620	320.1347	P	***670.3883***	335.6978	653.3617	327.1845	652.3777	326.6925	6
7	**758.3203**	379.6638	741.2937	371.1505	740.3097	370.6585	T	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
8	**845.3523**	423.1798	828.3258	414.6665	827.3418	414.1745	S	***472.2878***	236.6475	455.2613	228.1343	454.2772	227.6423	4
9	**942.4051**	471.7062	925.3785	463.1929	924.3945	462.7009	P	***385.2558***	193.1315	368.2292	184.6183			3
10	**1055.4891**	528.2482	1038.4626	519.7349	1037.4786	519.2429	L	288.2030	144.6051	271.1765	136.0919			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ENISDPTSPLR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.9	1228.5935	0.0012	ENISDPTSPLR
20.4	1227.5956	0.9992	QGGDSNQRPLR
14.1	1228.5908	0.0039	QNDAQLDRNR
10.8	1227.5956	0.9992	QGGDSNQRPLR
6.0	1226.5931	2.0016	PKQSVYDAYR
2.5	1228.5935	0.0013	SAEAERQVLEP
1.4	1227.5879	1.0069	LQLNMSFVMK
0.8	1228.5908	0.0039	QRQQQQQQR
0.2	1228.5908	0.0039	RQEQQQQQR
0.2	1228.5908	0.0039	RQEQQQQQR

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

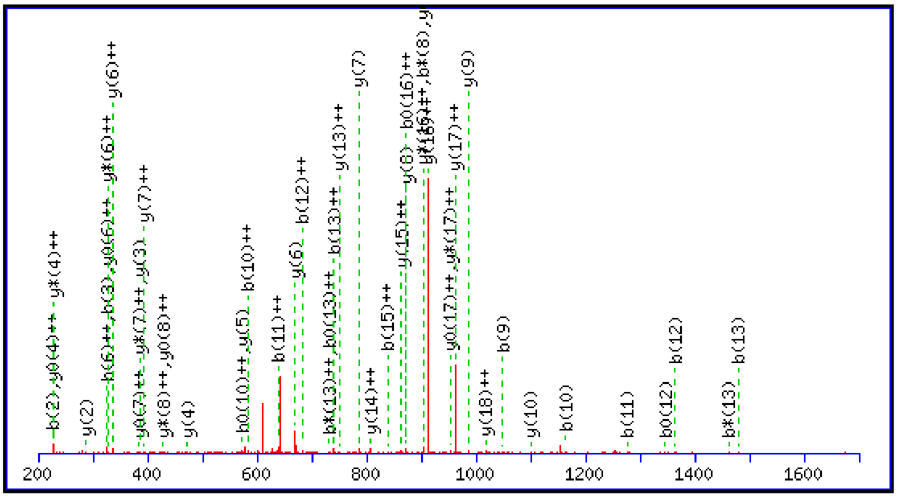
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIVPLNNRENISDPTSPLR**
Found in **D6RD17** in **con_Xuniprot_HUMAN3**, D6RD17_HUMAN Immunoglobulin J chain (Fragment) OS=Homo sapiens GN=IGJ PE=2 SV=1

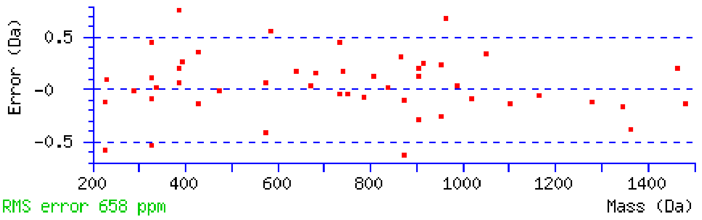
Match to Query 14393: 2148.155352 from(717.059060,3+) intensity(2950954.5000) rtinseconds(1395) scans(3207) index(15098)
Title: 111019_Est_MI_YP_G_04Spectrum2731_scans__3207
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

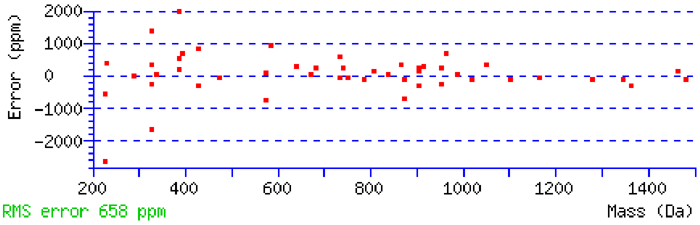
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2148.1538
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.00089
Matches : 49/184 fragment ions using 88 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							19
2	**227.1754**	114.0913					I	2036.0771	1018.5422	2019.0505	1010.0289	2018.0665	1009.5369	18
3	**326.2438**	163.6255					V	1922.9930	962.0002	1905.9665	953.4869	1904.9825	952.9949	17
4	423.2966	212.1519					P	1823.9246	912.4659	1806.8981	903.9527	1805.9141	903.4607	16
5	536.3806	268.6940					L	1726.8719	863.9396	1709.8453	855.4263	1708.8613	854.9343	15
6	650.4236	**325.7154**	633.3970	317.2022			N	1613.7878	807.3975	1596.7612	798.8843	1595.7772	798.3922	14
7	764.4665	382.7369	747.4400	374.2236			N	1499.7449	750.3761	1482.7183	741.8628	1481.7343	741.3708	13
8	920.5676	460.7874	903.5411	452.2742			R	1385.7019	693.3546	1368.6754	684.8413	1367.6914	684.3493	12
9	**1049.6102**	525.3087	1032.5837	516.7955	1031.5996	516.3035	E	1229.6008	615.3040	1212.5743	606.7908	1211.5903	606.2988	11
10	**1164.6371**	**582.8222**	1147.6106	574.3089	1146.6266	573.8169	N	***1100.5582***	550.7828	1083.5317	542.2695	1082.5477	541.7775	10
11	**1277.7212**	**639.3642**	1260.6947	630.8510	1259.7106	630.3590	I	***985.5313***	493.2693	968.5047	484.7560	967.5207	484.2640	9
12	**1364.7532**	**682.8803**	1347.7267	674.3670	1346.7427	673.8750	S	***872.4472***	436.7272	855.4207	428.2140	854.4367	427.7220	8
13	**1479.7802**	**740.3937**	1462.7536	731.8805	1461.7696	731.3884	D	***785.4152***	393.2112	768.3886	384.6980	767.4046	384.2060	7
14	1576.8329	788.9201	1559.8064	780.4068	1558.8224	779.9148	P	***670.3883***	335.6978	653.3617	327.1845	652.3777	326.6925	6
15	1677.8806	**839.4440**	1660.8541	830.9307	1659.8701	830.4387	T	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1764.9127	882.9600	1747.8861	874.4467	1746.9021	873.9547	S	***472.2878***	236.6475	455.2613	228.1343	454.2772	227.6423	4
17	1861.9654	931.4863	1844.9389	922.9731	1843.9549	922.4811	P	***385.2558***	193.1315	368.2292	184.6183			3
18	1975.0495	988.0284	1958.0229	979.5151	1957.0389	979.0231	L	***288.2030***	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.0	2148.1538	0.0015	IIVPLNNRENISDPTSPLR	Deamidated N10 71.08%
45.0	2148.1538	0.0015	IIVPLNNRENISDPTSPLR	Deamidated N6 14.48%
45.0	2148.1538	0.0015	IIVPLNNRENISDPTSPLR	Deamidated N7 14.45%
9.9	2146.1494	2.0060	KPPARPSAAAAAIAVAAAEEER	
8.1	2147.1473	1.0080	LLDHKQEEPASTKAEPLLK	
6.6	2148.1547	0.0006	IMCIHHTRLVIALALQDK	
6.3	2148.1554	-0.0000	IIVGSFMGYLRIFSPHPAK	
5.3	2147.1586	0.9968	EPPQTELALEDASLLLPRR	
4.7	2146.1416	2.0138	LQALRSLSGTPKSMTSLSPR	
4.5	2148.1552	0.0002	ATGPGPRQYLRIIGEDHLR	

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

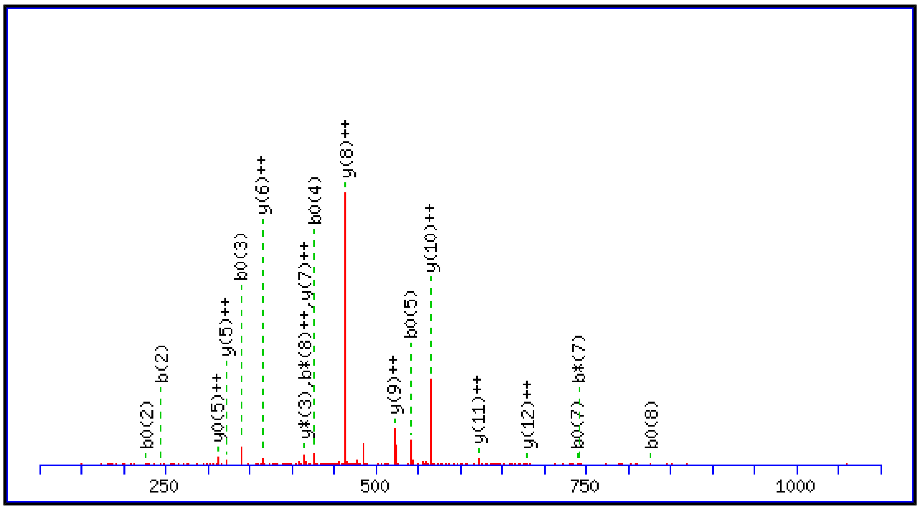
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENISDPTSPLRTR**
Found in **D6RD17** in **con_Xuniprot_HUMAN3**, D6RD17_HUMAN Immunoglobulin J chain (Fragment) OS=Homo sapiens GN=IGJ PE=2 SV=1

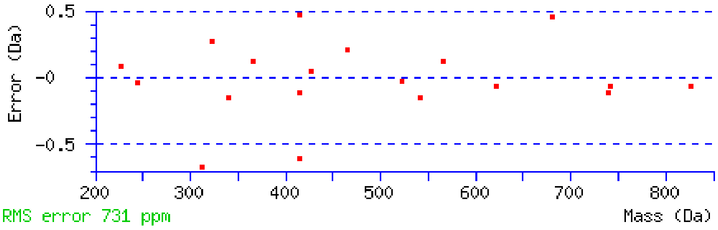
Match to Query 6679: 1485.743382 from(496.255070,3+) intensity(31670.5918) rtinseconds(579) scans(923) index(169)
Title: 111019_Est_ISCardio_NMI_200000g_G_5Spectrum720_scans__923
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

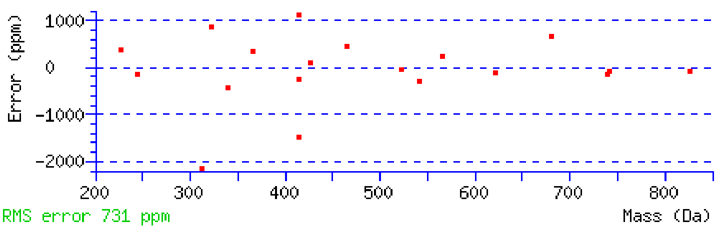
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1485.7423
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Ions Score: 42  Expect: 0.012
Matches : 19/140 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	130.0499	65.5286			112.0393	56.5233	E							13
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	1357.7070	679.3571	1340.6805	670.8439	1339.6965	670.3519	12
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	I	1242.6801	621.8437	1225.6535	613.3304	1224.6695	612.8384	11
4	445.1929	223.1001	428.1664	214.5868	427.1823	214.0948	S	1129.5960	565.3016	1112.5695	556.7884	1111.5854	556.2964	10
5	560.2198	280.6136	543.1933	272.1003	542.2093	271.6083	D	1042.5640	521.7856	1025.5374	513.2724	1024.5534	512.7803	9
6	657.2726	329.1399	640.2461	320.6267	639.2620	320.1347	P	927.5370	464.2722	910.5105	455.7589	909.5265	455.2669	8
7	758.3203	379.6638	741.2937	371.1505	740.3097	370.6585	T	830.4843	415.7458	813.4577	407.2325	812.4737	406.7405	7
8	845.3523	423.1798	828.3258	414.6665	827.3418	414.1745	S	729.4366	365.2219	712.4100	356.7087	711.4260	356.2167	6
9	942.4051	471.7062	925.3785	463.1929	924.3945	462.7009	P	642.4046	321.7059	625.3780	313.1926	624.3940	312.7006	5
10	1055.4891	528.2482	1038.4626	519.7349	1037.4786	519.2429	L	545.3518	273.1795	528.3253	264.6663	527.3412	264.1743	4
11	1211.5903	606.2988	1194.5637	597.7855	1193.5797	597.2935	R	432.2677	216.6375	415.2412	208.1242	414.2572	207.6322	3
12	1312.6379	656.8226	1295.6114	648.3093	1294.6274	647.8173	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
13							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.2	1485.7423	0.0011	ENISDPTSPLRTR
8.5	1483.7381	2.0053	KILGMFTSQQWK
7.6	1485.7423	0.0011	NSLGADDGVAEVLAR
7.1	1485.7365	0.0069	RDLHFAQGQWVK
5.2	1483.7340	2.0093	ELNAEPSQMQIPK
4.8	1485.7423	0.0011	QIANEIPVSSNRR
4.8	1485.7423	0.0011	QLEDAVEQIRER
4.8	1484.7372	1.0062	HPGATTGLFVSAGDR
4.7	1485.7497	-0.0063	AKEEQPLQAMIAR
4.7	1485.7497	-0.0063	AKQEQPLQAMIAR

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

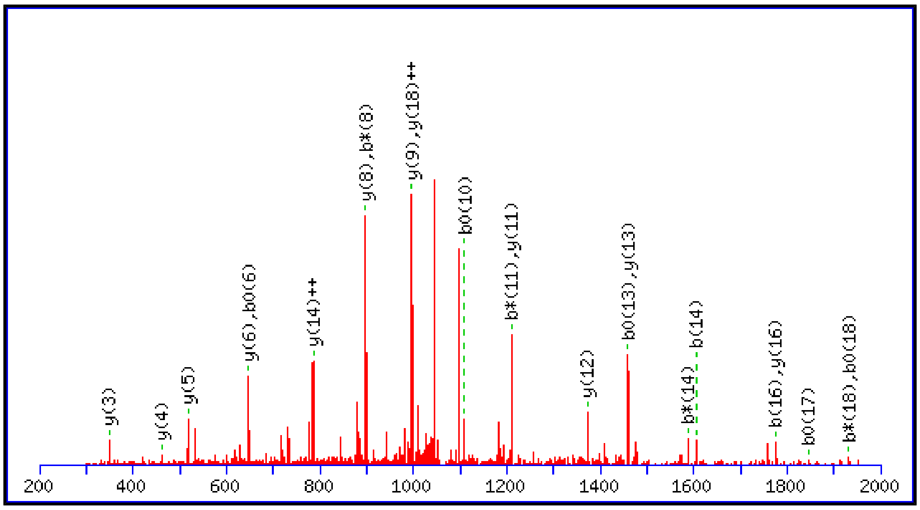
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGYSNISYIVVNHQGISSR**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

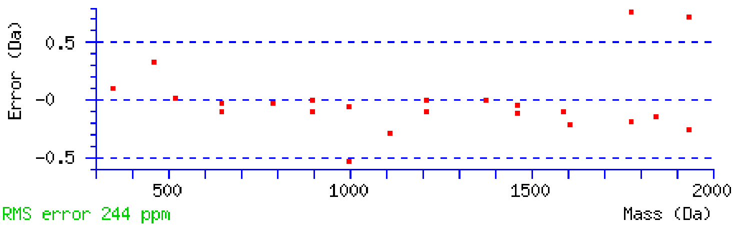
Match to Query 14104: 2123.038908 from(1062.526730,2+) intensity(59457.2383) rtinseconds(1763) scans(4042) index(16790)
Title: 111019_Est_MI_YP_G_06Spectrum3359_scans__4042
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

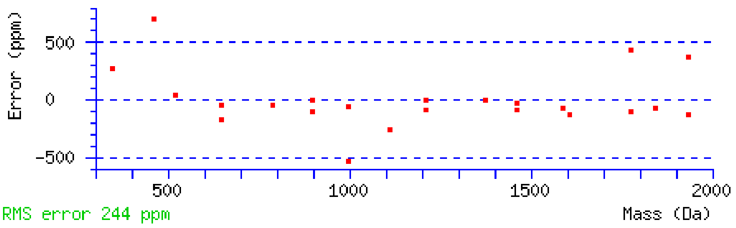
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2123.0283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 98 **Expect:** 4e-008
Matches : 23/206 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	130.0499	65.5286			112.0393	56.5233	E							19
2	187.0713	94.0393			169.0608	85.0340	G	1994.9930	998.0002	1977.9665	989.4869	1976.9825	988.9949	18
3	350.1347	175.5710			332.1241	166.5657	Y	1937.9716	969.4894	1920.9450	960.9761	1919.9610	960.4841	17
4	437.1667	219.0870			419.1561	210.0817	S	***1774.9082***	887.9578	1757.8817	879.4445	1756.8977	878.9525	16
5	552.1936	276.6005	535.1671	268.0872	534.1831	267.5952	N	1687.8762	844.4417	1670.8497	835.9285	1669.8656	835.4365	15
6	665.2777	333.1425	648.2511	324.6292	647.2671	324.1372	I	1572.8493	786.9283	1555.8227	778.4150	1554.8387	777.9230	14
7	752.3097	376.6585	735.2832	368.1452	734.2992	367.6532	S	***1459.7652***	730.3862	1442.7387	721.8730	1441.7546	721.3810	13
8	915.3731	458.1902	898.3465	449.6769	897.3625	449.1849	Y	***1372.7332***	686.8702	1355.7066	678.3570	1354.7226	677.8649	12
9	1028.4571	514.7322	1011.4306	506.2189	1010.4466	505.7269	I	***1209.6698***	605.3386	1192.6433	596.8253	1191.6593	596.3333	11
10	1127.5255	564.2664	1110.4990	555.7531	1109.5150	555.2611	V	1096.5858	548.7965	1079.5592	540.2833	1078.5752	539.7912	10
11	1226.5939	613.8006	1209.5674	605.2873	1208.5834	604.7953	V	***997.5174***	499.2623	980.4908	490.7490	979.5068	490.2570	9
12	1340.6369	670.8221	1323.6103	662.3088	1322.6263	661.8168	N	***898.4490***	449.7281	881.4224	441.2148	880.4384	440.7228	8
13	1477.6958	739.3515	1460.6692	730.8383	1459.6852	730.3462	H	784.4060	392.7067	767.3795	384.1934	766.3955	383.7014	7
14	**1605.7544**	803.3808	1588.7278	794.8675	1587.7438	794.3755	Q	***647.3471***	324.1772	630.3206	315.6639	629.3365	315.1719	6
15	1662.7758	831.8916	1645.7493	823.3783	1644.7653	822.8863	G	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	5
16	**1775.8599**	888.4336	1758.8333	879.9203	1757.8493	879.4283	I	***462.2671***	231.6372	445.2405	223.1239	444.2565	222.6319	4
17	1862.8919	931.9496	1845.8654	923.4363	1844.8814	922.9443	S	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	3
18	1949.9239	975.4656	1932.8974	966.9523	1931.9134	966.4603	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.4	2123.0283	0.0106	EGYSNISYIVVNHQGISSR	Deamidated N5 99.87%
79.8	2122.0443	0.9946	EGYSNISYIVVNHQGISSR	
66.7	2123.0283	0.0106	EGYSNISYIVVNHQGISSR	Deamidated N12 0.07%
66.6	2123.0283	0.0106	EGYSNISYIVVNHQGISSR	Deamidated Q14 0.07%
6.1	2123.0358	0.0032	TDVWSVYIDMTIKHGSQK	
5.4	2123.0416	-0.0027	AISESQVKNMIQDKVSSDK	
5.4	2123.0416	-0.0027	AISESQVKNMIQDKVSSDK	
5.3	2123.0416	-0.0027	AISESQVKNMIQDKVSSDK	
5.1	2121.0313	2.0076	EMKEFYHIQIRDLEDR	
3.8	2123.0415	-0.0026	LTNRTQELESQASKLQMK	

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

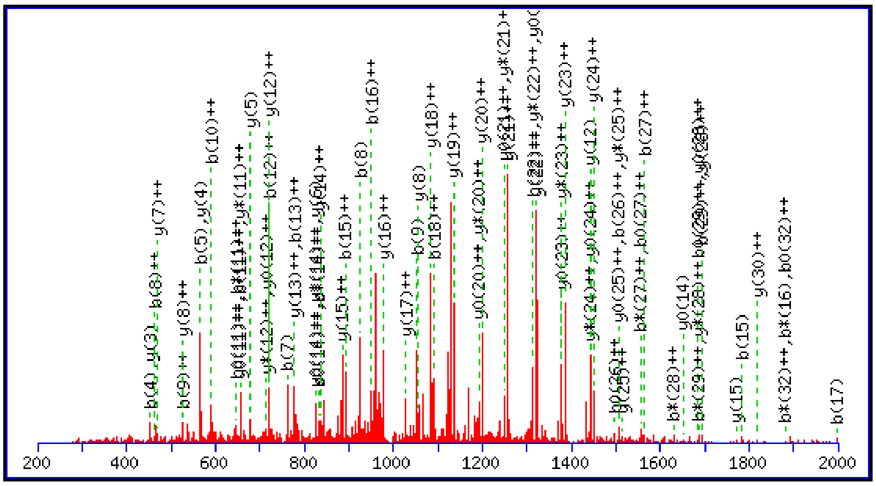
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

Match to Query 28193: 3951.881376 from(988.977620,4+) intensity(27047.4414) rtinseconds(2347) scans(6386) index(17856)
Title: 111019_Est_MI_YP_G_07Spectrum5520_scans__6386
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

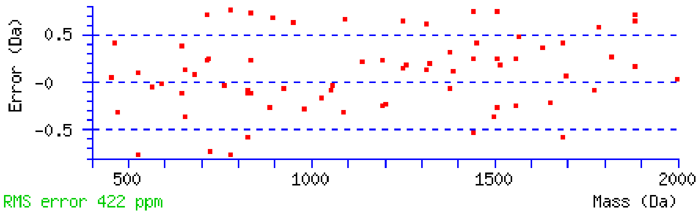
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

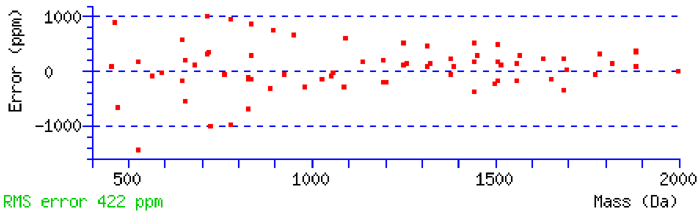


Monoisotopic mass of neutral peptide Mr(calc): 3951.8803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 80 **Expect:** 2.3e-006
Matches : 79/364 fragment ions using 122 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							33
2	187.1077	94.0575			169.0972	85.0522	S	3853.8192	1927.4132	3836.7926	1918.8999	3835.8086	1918.4079	32
3	316.1503	158.5788			298.1397	149.5735	E	3766.7871	1883.8972	3749.7606	1875.3839	3748.7766	1874.8919	31
4	453.2092	227.1082			435.1987	218.1030	H	3637.7445	1819.3759	3620.7180	1810.8626	3619.7340	1810.3706	30
5	566.2933	283.6503			548.2827	274.6450	I	3500.6856	1750.8464	3483.6591	1742.3332	3482.6751	1741.8412	29
6	663.3461	332.1767			645.3355	323.1714	P	3387.6016	1694.3044	3370.5750	1685.7911	3369.5910	1685.2991	28
7	762.4145	381.7109			744.4039	372.7056	V	3290.5488	1645.7780	3273.5222	1637.2648	3272.5382	1636.7728	27
8	925.4778	463.2425			907.4672	454.2373	Y	3191.4804	1596.2438	3174.4538	1587.7306	3173.4698	1587.2385	26
9	1053.5364	527.2718	1036.5098	518.7585	1035.5258	518.2665	Q	3028.4171	1514.7122	3011.3905	1506.1989	3010.4065	1505.7069	25
10	1181.5950	591.3011	1164.5684	582.7878	1163.5844	582.2958	Q	2900.3585	1450.6829	2883.3319	1442.1696	2882.3479	1441.6776	24
11	1310.6375	655.8224	1293.6110	647.3091	1292.6270	646.8171	E	2772.2999	1386.6536	2755.2733	1378.1403	2754.2893	1377.6483	23
12	1439.6801	720.3437	1422.6536	711.8304	1421.6696	711.3384	E	2643.2573	1322.1323	2626.2308	1313.6190	2625.2467	1313.1270	22
13	1553.7231	777.3652	1536.6965	768.8519	1535.7125	768.3599	N	2514.2147	1257.6110	2497.1882	1249.0977	2496.2041	1248.6057	21
14	1681.7816	841.3945	1664.7551	832.8812	1663.7711	832.3892	Q	2400.1718	1200.5895	2383.1452	1192.0763	2382.1612	1191.5842	20
15	1782.8293	891.9183	1765.8028	883.4050	1764.8188	882.9130	T	2272.1132	1136.5602	2255.0867	1128.0470	2254.1026	1127.5550	19
16	1897.8563	949.4318	1880.8297	940.9185	1879.8457	940.4265	D	2171.0655	1086.0364	2154.0390	1077.5231	2153.0550	1077.0311	18
17	1996.9247	998.9660	1979.8981	990.4527	1978.9141	989.9607	V	2056.0386	1028.5229	2039.0120	1020.0097	2038.0280	1019.5176	17
18	2183.0040	1092.0056	2165.9774	1083.4924	2164.9934	1083.0004	W	1956.9702	978.9887	1939.9436	970.4754	1938.9596	969.9834	16
19	2284.0517	1142.5295	2267.0251	1134.0162	2266.0411	1133.5242	T	1770.8909	885.9491	1753.8643	877.4358	1752.8803	876.9438	15
20	2397.1357	1199.0715	2380.1092	1190.5582	2379.1252	1190.0662	L	1669.8432	835.4252	1652.8166	826.9120	1651.8326	826.4199	14
21	2510.2198	1255.6135	2493.1932	1247.1003	2492.2092	1246.6083	L	1556.7591	778.8832	1539.7326	770.3699	1538.7485	769.8779	13
22	2625.2467	1313.1270	2608.2202	1304.6137	2607.2362	1304.1217	N	1443.6750	722.3412	1426.6485	713.8279	1425.6645	713.3359	12
23	2682.2682	1341.6377	2665.2417	1333.1245	2664.2576	1332.6325	G	1328.6481	664.8277	1311.6216	656.3144	1310.6375	655.8224	11

24	2769.3002	1385.1538	2752.2737	1376.6405	2751.2897	1376.1485	**S**	1271.6266	636.3170	1254.6001	627.8037	1253.6161	627.3117	**10**
25	2897.3952	1449.2012	2880.3686	1440.6880	2879.3846	1440.1960	**K**	1184.5946	592.8009	1167.5681	584.2877	1166.5840	583.7957	**9**
26	3012.4221	**1506.7147**	2995.3956	1498.2014	2994.4116	1497.7094	**D**	**1056.4997**	528.7535	1039.4731	520.2402	1038.4891	519.7482	**8**
27	3127.4491	**1564.2282**	3110.4225	1555.7149	3109.4385	1555.2229	**D**	941.4727	471.2400	924.4462	462.7267	923.4621	462.2347	**7**
28	3274.5175	1637.7624	3257.4909	1629.2491	3256.5069	1628.7571	**F**	**826.4458**	413.7265	809.4192	405.2132	808.4352	404.7212	**6**
29	3387.6016	**1694.3044**	3370.5750	1685.7911	3369.5910	1685.2991	**L**	**679.3774**	340.1923	662.3508	331.6790	661.3668	331.1870	**5**
30	3500.6856	1750.8464	3483.6591	1742.3332	3482.6751	1741.8412	**I**	**566.2933**	283.6503	549.2667	275.1370	548.2827	274.6450	**4**
31	3663.7490	1832.3781	3646.7224	1823.8648	3645.7384	1823.3728	**Y**	**453.2092**	227.1082	436.1827	218.5950	435.1987	218.1030	**3**
32	3778.7759	1889.8916	3761.7493	1881.3783	3760.7653	1880.8863	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.1	3951.8803	0.0011	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	Deamidated N22 29.94%
79.1	3951.8803	0.0011	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	Deamidated Q14 23.84%
78.0	3951.8803	0.0011	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	Deamidated N13 18.85%
77.1	3951.8803	0.0011	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	Deamidated Q10 15.21%
76.2	3951.8803	0.0011	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	Deamidated Q9 12.17%
75.7	3950.8963	0.9851	VSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDR	
12.2	3950.8976	0.9838	NELLGTASVNLSNVLKNNGGKMENMQLTLNLQTENK	
9.2	3951.9003	-0.0189	STGFCPPLPHSQADQYVLSWDQQLNLAYVGAVPHR	
9.2	3951.9003	-0.0189	STGFCPPLPHSQADQYVLSWDQQLNLAYVGAVPHR	
8.4	3950.8976	0.9838	NELLGTASVNLSNVLKNNGGKMENMQLTLNLQTENK	

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

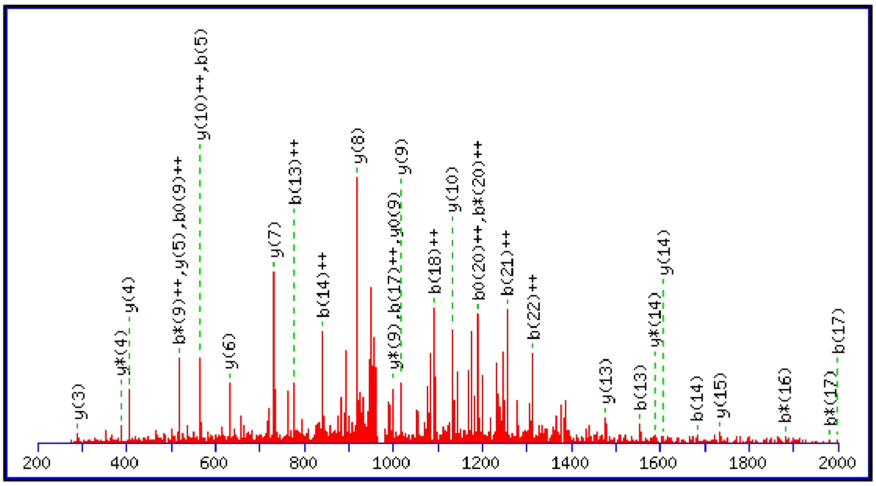
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSEHIPVYQQEENQTDVWTLLNGSK**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

Match to Query 26781: 2914.404132 from(972.475320,3+) intensity(21397.0410) rtinseconds(1919) scans(4997) index(6563)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4390_scans__4997
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

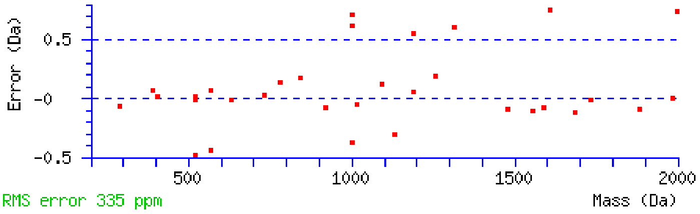
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

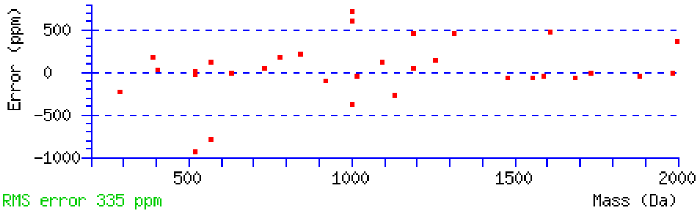


Monoisotopic mass of neutral peptide Mr(calc): 2914.3985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 71 **Expect:** 2e-005
Matches : 32/268 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							25
2	187.1077	94.0575			169.0972	85.0522	S	2816.3373	1408.6723	2799.3108	1400.1590	2798.3268	1399.6670	24
3	316.1503	158.5788			298.1397	149.5735	E	2729.3053	1365.1563	2712.2788	1356.6430	2711.2948	1356.1510	23
4	453.2092	227.1082			435.1987	218.1030	H	2600.2627	1300.6350	2583.2362	1292.1217	2582.2522	1291.6297	22
5	**566.2933**	283.6503			548.2827	274.6450	I	2463.2038	1232.1055	2446.1773	1223.5923	2445.1932	1223.1003	21
6	663.3461	332.1767			645.3355	323.1714	P	2350.1197	1175.5635	2333.0932	1167.0502	2332.1092	1166.5582	20
7	762.4145	381.7109			744.4039	372.7056	V	2253.0670	1127.0371	2236.0404	1118.5239	2235.0564	1118.0318	19
8	925.4778	463.2425			907.4672	454.2373	Y	2153.9986	1077.5029	2136.9720	1068.9896	2135.9880	1068.4976	18
9	1053.5364	527.2718	1036.5098	518.7585	1035.5258	518.2665	Q	1990.9352	995.9713	1973.9087	987.4580	1972.9247	986.9660	17
10	1181.5950	591.3011	1164.5684	582.7878	1163.5844	582.2958	Q	1862.8767	931.9420	1845.8501	923.4287	1844.8661	922.9367	16
11	1310.6375	655.8224	1293.6110	647.3091	1292.6270	646.8171	E	***1734.8181***	867.9127	1717.7915	859.3994	1716.8075	858.9074	15
12	1439.6801	720.3437	1422.6536	711.8304	1421.6696	711.3384	E	***1605.7755***	803.3914	1588.7489	794.8781	1587.7649	794.3861	14
13	**1554.7071**	**777.8572**	1537.6805	769.3439	1536.6965	768.8519	N	***1476.7329***	738.8701	1459.7064	730.3568	1458.7223	729.8648	13
14	**1682.7657**	**841.8865**	1665.7391	833.3732	1664.7551	832.8812	Q	1361.7060	681.3566	1344.6794	672.8433	1343.6954	672.3513	12
15	1783.8133	892.4103	1766.7868	883.8970	1765.8028	883.4050	T	1233.6474	617.3273	1216.6208	608.8141	1215.6368	608.3220	11
16	1898.8403	949.9238	1881.8137	941.4105	1880.8297	940.9185	D	***1132.5997***	566.8035	1115.5732	558.2902	1114.5891	557.7982	10
17	**1997.9087**	**999.4580**	1980.8821	990.9447	1979.8981	990.4527	V	***1017.5728***	509.2900	1000.5462	500.7767	999.5622	500.2847	9
18	2183.9880	**1092.4976**	2166.9615	1083.9844	2165.9774	1083.4924	W	***918.5043***	459.7558	901.4778	451.2425	900.4938	450.7505	8
19	2285.0357	1143.0215	2268.0091	1134.5082	2267.0251	1134.0162	T	***732.4250***	366.7162	715.3985	358.2029	714.4145	357.7109	7
20	2398.1197	1199.5635	2381.0932	1191.0502	2380.1092	1190.5582	L	***631.3774***	316.1923	614.3508	307.6790	613.3668	307.1870	6
21	2511.2038	**1256.1055**	2494.1773	1247.5923	2493.1932	1247.1003	L	***518.2933***	259.6503	501.2667	251.1370	500.2827	250.6450	5
22	2625.2467	**1313.1270**	2608.2202	1304.6137	2607.2362	1304.1217	N	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	4
23	2682.2682	1341.6377	2665.2417	1333.1245	2664.2576	1332.6325	G	***291.1663***	146.0868	274.1397	137.5735	273.1557	137.0815	3

24	2769.3002	1385.1538	2752.2737	1376.6405	2751.2897	1376.1485	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.4	2914.3985	0.0057	VSEHIPVYQQEENQTDVWTLLNGSK	Deamidated N13 62.86%
69.0	2914.3985	0.0057	VSEHIPVYQQEENQTDVWTLLNGSK	Deamidated Q14 36.59%
47.6	2914.3985	0.0057	VSEHIPVYQQEENQTDVWTLLNGSK	Deamidated Q10 0.26%
47.6	2914.3985	0.0057	VSEHIPVYQQEENQTDVWTLLNGSK	Deamidated Q9 0.26%
34.4	2914.3985	0.0057	VSEHIPVYQQEENQTDVWTLLNGSK	Deamidated N22 0.01%
32.0	2913.4145	0.9897	VSEHIPVYQQEENQTDVWTLLNGSK	
5.8	2913.4039	1.0003	SVTDYPQQNPAAQIPARQREIEMNR	
5.8	2913.4039	1.0003	SVTDYPQQNPAAQIPARQREIEMNR	
5.8	2914.3980	0.0061	ELYLSGCVLPEQLSTMQLEGFQDLK	
4.8	2913.4120	0.9922	VGLYTISMNPANIYQFAVGGHDQFVR	

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

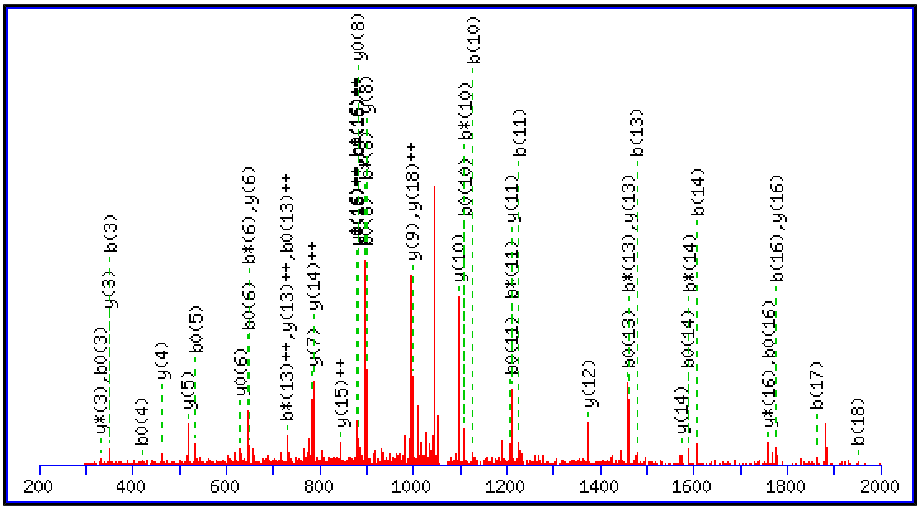
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGYSNISYIVVNHQGISSR**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

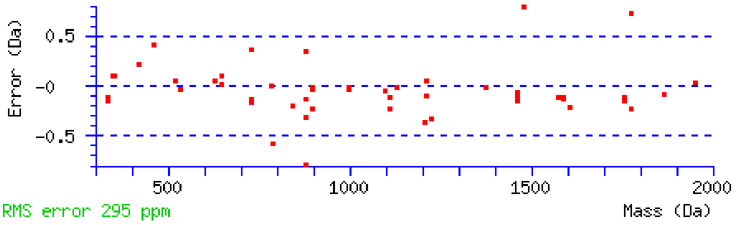
Match to Query 14240: 2124.017728 from(1063.016140,2+) intensity(17187.3340) rtinseconds(1448) scans(3482) index(23196)
Title: 111019_Est_MI_YS_G_04Spectrum2974_scans__3482
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

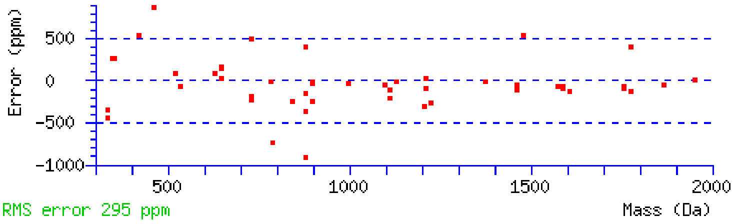
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2124.0123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q14 : Deamidated (NQ)
Ions Score: 69 **Expect:** 3.5e-005
Matches : 51/206 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**19**
2	187.0713	94.0393			169.0608	85.0340	**G**	1995.9770	998.4922	1978.9505	989.9789	1977.9665	989.4869	**18**
3	**350.1347**	175.5710			332.1241	166.5657	**Y**	1938.9556	969.9814	1921.9290	961.4682	1920.9450	960.9761	**17**
4	437.1667	219.0870			419.1561	210.0817	**S**	***1775.8923***	888.4498	1758.8657	879.9365	1757.8817	879.4445	**16**
5	552.1936	276.6005	535.1671	268.0872	534.1831	267.5952	**N**	1688.8602	844.9338	1671.8337	836.4205	1670.8497	835.9285	**15**
6	665.2777	333.1425	648.2511	324.6292	647.2671	324.1372	**I**	***1573.8333***	787.4203	1556.8067	778.9070	1555.8227	778.4150	**14**
7	752.3097	376.6585	735.2832	368.1452	734.2992	367.6532	**S**	***1460.7492***	730.8782	1443.7227	722.3650	1442.7387	721.8730	**13**
8	915.3731	458.1902	898.3465	449.6769	897.3625	449.1849	**Y**	***1373.7172***	687.3622	1356.6906	678.8490	1355.7066	678.3570	**12**
9	1028.4571	514.7322	1011.4306	506.2189	1010.4466	505.7269	**I**	***1210.6539***	605.8306	1193.6273	597.3173	1192.6433	596.8253	**11**
10	**1127.5255**	564.2664	1110.4990	555.7531	1109.5150	555.2611	**V**	***1097.5698***	549.2885	1080.5432	540.7753	1079.5592	540.2833	**10**
11	**1226.5939**	613.8006	1209.5674	605.2873	1208.5834	604.7953	**V**	***998.5014***	499.7543	981.4748	491.2411	980.4908	490.7490	**9**
12	1340.6369	670.8221	1323.6103	662.3088	1322.6263	661.8168	**N**	***899.4330***	450.2201	882.4064	441.7068	881.4224	441.2148	**8**
13	**1477.6958**	739.3515	1460.6692	730.8383	1459.6852	730.3462	**H**	***785.3900***	393.1987	768.3635	384.6854	767.3795	384.1934	**7**
14	**1606.7384**	803.8728	1589.7118	795.3596	1588.7278	794.8675	**Q**	***648.3311***	324.6692	631.3046	316.1559	630.3206	315.6639	**6**
15	1663.7598	832.3836	1646.7333	823.8703	1645.7493	823.3783	**G**	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	**5**
16	**1776.8439**	888.9256	1759.8174	880.4123	1758.8333	879.9203	**I**	***462.2671***	231.6372	445.2405	223.1239	444.2565	222.6319	**4**
17	**1863.8759**	932.4416	1846.8494	923.9283	1845.8654	923.4363	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
18	**1950.9080**	975.9576	1933.8814	967.4443	1932.8974	966.9523	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.5	2124.0123	0.0054	EGYSNISYIVVNHQGISSR	Deamidated N5, Q14 50.26%
68.5	2124.0123	0.0054	EGYSNISYIVVNHQGISSR	Deamidated N5, N12 49.45%
46.2	2124.0123	0.0054	EGYSNISYIVVNHQGISSR	Deamidated N12, Q14 0.29%
8.3	2124.0236	-0.0059	NSFSTIPPGEDSKDVAAPHR	
6.6	2124.0276	-0.0099	AYDKKYETLNSFQNFTR	
1.9	2122.0146	2.0031	MSLADRGNPGNITSRLMEK	

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

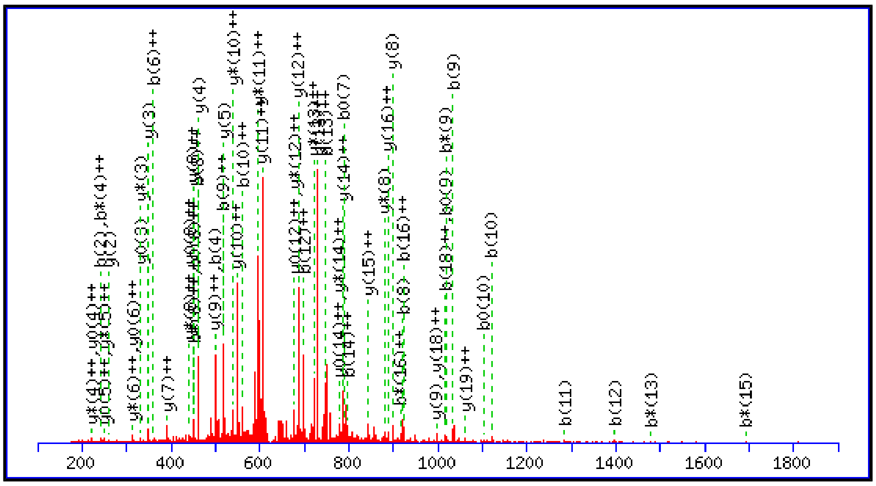
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKKEGYSNISYIVVNHQGISSR**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

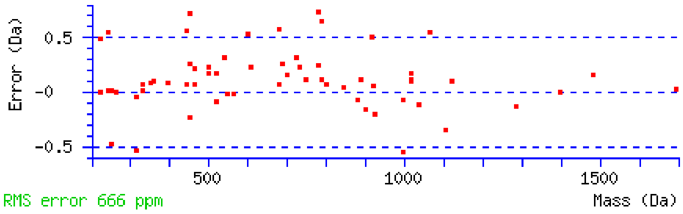
Match to Query 21521: 2492.302936 from(624.083010,4+) intensity(30861.2051) rtinseconds(1023) scans(2544) index(23848)
Title: 111019_Est_MI_YS_G_05Spectrum2164_scans__2544
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

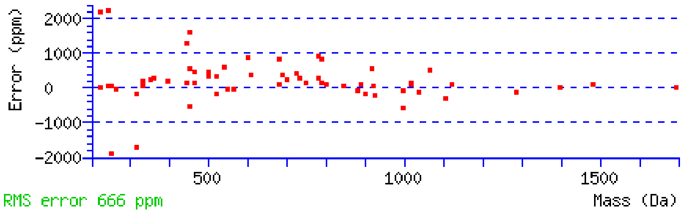
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2492.3023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8      : Deamidated (NQ)
Ions Score: 52  Expect: 0.0011
Matches : 62/242 fragment ions using 113 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							22
2	**242.1863**	121.5968	225.1598	113.0835			K	2380.2255	1190.6164	2363.1990	1182.1031	2362.2150	1181.6111	21
3	370.2813	185.6443	353.2547	177.1310			K	2252.1306	1126.5689	2235.1040	1118.0557	2234.1200	1117.5636	20
4	**499.3239**	250.1656	482.2973	241.6523	481.3133	241.1603	E	2124.0356	1062.5214	2107.0091	1054.0082	2106.0251	1053.5162	19
5	556.3453	278.6763	539.3188	270.1630	538.3348	269.6710	G	1994.9930	998.0002	1977.9665	989.4869	1976.9825	988.9949	18
6	719.4087	**360.2080**	702.3821	351.6947	701.3981	351.2027	Y	1937.9716	969.4894	1920.9450	960.9761	1919.9610	960.4841	17
7	806.4407	403.7240	789.4141	395.2107	788.4301	394.7187	S	1774.9082	887.9578	1757.8817	879.4445	1756.8977	878.9525	16
8	**921.4676**	**461.2374**	904.4411	452.7242	903.4571	452.2322	N	1687.8762	844.4417	1670.8497	835.9285	1669.8656	835.4365	15
9	**1034.5517**	**517.7795**	1017.5251	509.2662	1016.5411	508.7742	I	1572.8493	786.9283	1555.8227	778.4150	1554.8387	777.9230	14
10	**1121.5837**	**561.2955**	1104.5572	552.7822	1103.5731	552.2902	S	1459.7652	730.3862	1442.7387	721.8730	1441.7546	721.3810	13
11	**1284.6470**	642.8272	1267.6205	634.3139	1266.6365	633.8219	Y	1372.7332	686.8702	1355.7066	678.3570	1354.7226	677.8649	12
12	**1397.7311**	**699.3692**	1380.7046	690.8559	1379.7205	690.3639	I	1209.6698	605.3386	1192.6433	596.8253	1191.6593	596.3333	11
13	1496.7995	**748.9034**	1479.7730	740.3901	1478.7890	739.8981	V	1096.5858	548.7965	1079.5592	540.2833	1078.5752	539.7912	10
14	1595.8679	**798.4376**	1578.8414	789.9243	1577.8574	789.4323	V	***997.5174***	499.2623	980.4908	490.7490	979.5068	490.2570	9
15	1709.9109	855.4591	1692.8843	846.9458	1691.9003	846.4538	N	***898.4490***	449.7281	881.4224	441.2148	880.4384	440.7228	8
16	1846.9698	**923.9885**	1829.9432	915.4753	1828.9592	914.9832	H	784.4060	392.7067	767.3795	384.1934	766.3955	383.7014	7
17	1975.0284	988.0178	1958.0018	979.5045	1957.0178	979.0125	Q	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
18	2032.0498	**1016.5285**	2015.0233	1008.0153	2014.0393	1007.5233	G	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	5
19	2145.1339	1073.0706	2128.1073	1064.5573	2127.1233	1064.0653	I	***462.2671***	231.6372	445.2405	223.1239	444.2565	222.6319	4
20	2232.1659	1116.5866	2215.1394	1108.0733	2214.1553	1107.5813	S	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	3
21	2319.1979	1160.1026	2302.1714	1151.5893	2301.1874	1151.0973	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.5	2492.3023	0.0006	LKKEGYSNISYIVVNHQGISSR	Deamidated N8 76.17%
44.8	2492.3023	0.0006	LKKEGYSNISYIVVNHQGISSR	Deamidated N15 12.85%
44.1	2492.3023	0.0006	LKKEGYSNISYIVVNHQGISSR	Deamidated Q17 10.98%
6.0	2491.2998	1.0031	RYETNQLKTYVYIVLDPFTK	
5.6	2492.3122	-0.0093	QASVLDAVLVELTKYNSGSTQIR	
5.3	2491.2932	1.0098	LWAAGTPSPSAPGARQDGALGAGRVK	
4.3	2492.3122	-0.0093	QASVLDAVLVELTKYNSGSTQIR	
3.6	2491.2961	1.0069	TVMVVKVMLTNGGQRIMNVVQR	
3.4	2490.2934	2.0095	MEIKDQTKCAASVGIGSNILLAR	
3.2	2492.3098	-0.0068	FNSTLFGLGLAAMVTLDQGVAVPR	

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

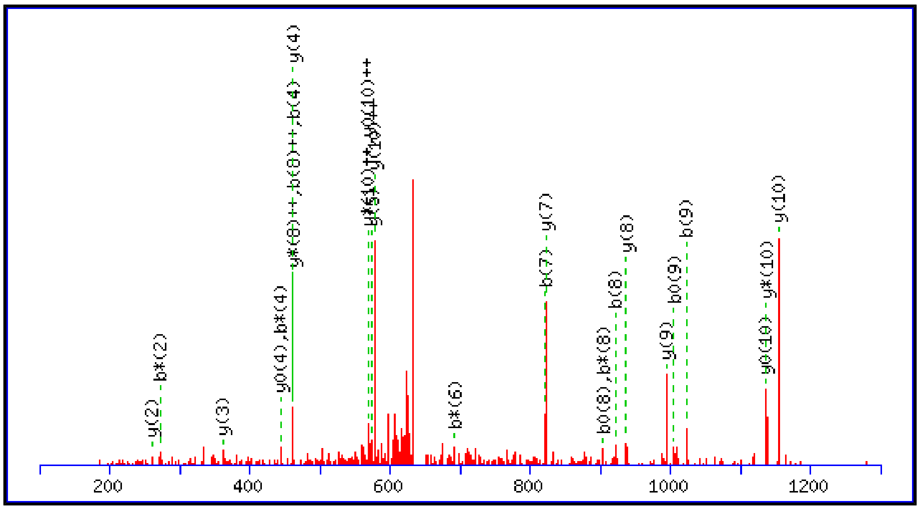
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCGNCSLTTLK**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

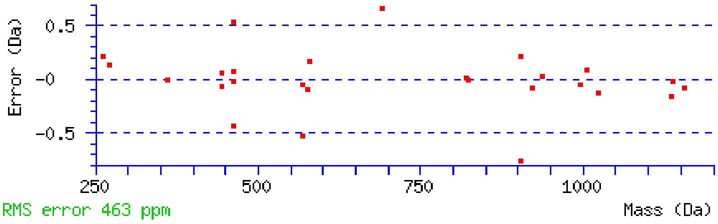
Match to Query 1837: 1281.608868 from(641.811710,2+) intensity(12976.4551) rtinseconds(374) scans(653) index(15573)
Title: 111019_Est_MI_YP_G_05Spectrum529_scans__653
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

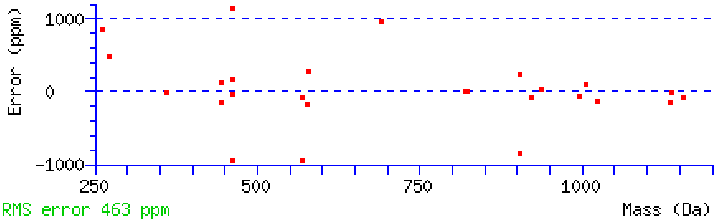
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1281.6057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0016
Matches : 28/106 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							11
2	289.1329	145.0701	272.1063	136.5568			C	***1154.5180***	577.7626	1137.4915	569.2494	1136.5075	568.7574	10
3	346.1544	173.5808	329.1278	165.0675			G	***994.4874***	497.7473	977.4608	489.2341	976.4768	488.7420	9
4	**461.1813**	231.0943	444.1547	222.5810			N	***937.4659***	469.2366	920.4394	460.7233	919.4553	460.2313	8
5	621.2119	311.1096	604.1854	302.5963			C	***822.4390***	411.7231	805.4124	403.2098	804.4284	402.7178	7
6	708.2440	354.6256	691.2174	346.1123	690.2334	345.6203	S	662.4083	331.7078	645.3818	323.1945	644.3978	322.7025	6
7	**821.3280**	411.1677	804.3015	402.6544	803.3175	402.1624	L	***575.3763***	288.1918	558.3497	279.6785	557.3657	279.1865	5
8	**922.3757**	461.6915	905.3492	453.1782	904.3652	452.6862	T	***462.2922***	231.6498	445.2657	223.1365	444.2817	222.6445	4
9	**1023.4234**	512.2153	1006.3968	503.7021	1005.4128	503.2101	T	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	3
10	**1136.5075**	568.7574	1119.4809	560.2441	1118.4969	559.7521	L	***260.1969***	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KCGNCSLTTLK

(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	1281.6057	0.0032	KCGNCSLTTLK
16.4	1281.6135	-0.0047	QCATNQYLRK
13.1	1281.6131	-0.0042	AGDSLMVMIAMK
9.1	1281.6135	-0.0047	QCATNQYLRK
8.1	1281.6070	0.0018	KCHEKACPPR
8.1	1281.6131	-0.0042	AGDSLMVMIAMK
7.4	1281.6088	0.0000	SQEDTEAVFKK
6.7	1281.6122	-0.0033	TQITTMESNLK
6.7	1281.6089	0.0000	QVFSEIEDSTK
6.2	1281.6135	-0.0047	QCATNQYLRK

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

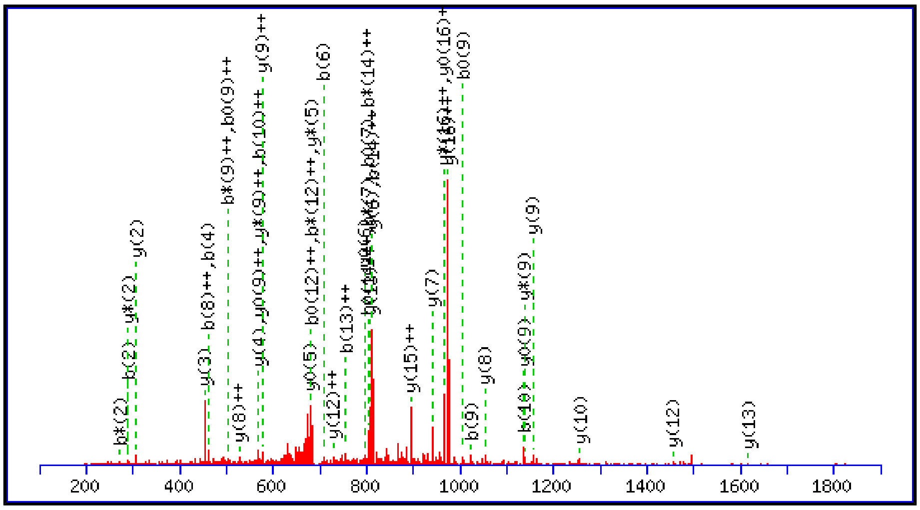
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCGNCSLTTLKDEDFCK**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

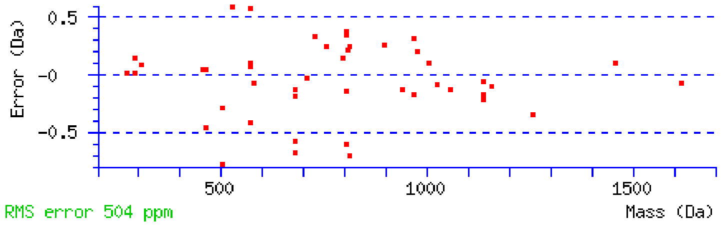
Match to Query 13131: 2075.903172 from(692.975000,3+) intensity(18309.2363) rtinseconds(734) scans(1759) index(23812)
Title: 111019_Est_MI_YS_G_05Spectrum1487_scans__1759
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

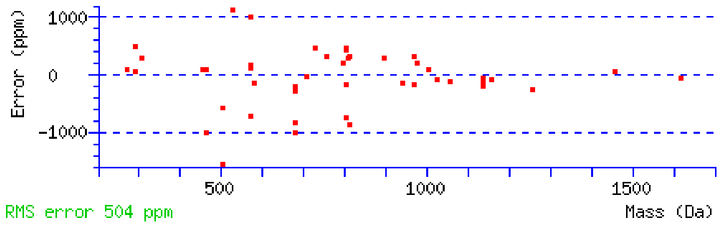
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2075.8962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.0043
Matches : 46/176 fragment ions using 77 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							17
2	**289.1329**	145.0701	272.1063	136.5568			C	1948.8085	974.9079	1931.7820	966.3946	1930.7980	965.9026	16
3	346.1544	173.5808	329.1278	165.0675			G	1788.7779	894.8926	1771.7513	886.3793	1770.7673	885.8873	15
4	**461.1813**	231.0943	444.1547	222.5810			N	1731.7564	866.3818	1714.7299	857.8686	1713.7459	857.3766	14
5	621.2119	311.1096	604.1854	302.5963			C	***1616.7295***	808.8684	1599.7029	800.3551	1598.7189	799.8631	13
6	**708.2440**	354.6256	691.2174	346.1123	690.2334	345.6203	S	***1456.6988***	728.8530	1439.6723	720.3398	1438.6883	719.8478	12
7	821.3280	411.1677	804.3015	402.6544	803.3175	402.1624	L	1369.6668	685.3370	1352.6402	676.8238	1351.6562	676.3318	11
8	922.3757	**461.6915**	905.3492	453.1782	904.3652	452.6862	T	***1256.5827***	628.7950	1239.5562	620.2817	1238.5722	619.7897	10
9	**1023.4234**	512.2153	1006.3968	503.7021	1005.4128	503.2101	T	***1155.5351***	578.2712	1138.5085	569.7579	1137.5245	569.2659	9
10	**1136.5075**	**568.7574**	1119.4809	560.2441	1118.4969	559.7521	L	***1054.4874***	527.7473	1037.4608	519.2341	1036.4768	518.7420	8
11	1264.6024	632.8048	1247.5759	624.2916	1246.5919	623.7996	K	***941.4033***	471.2053	924.3768	462.6920	923.3927	462.2000	7
12	1379.6294	690.3183	1362.6028	681.8050	1361.6188	681.3130	D	***813.3083***	407.1578	796.2818	398.6445	795.2978	398.1525	6
13	1508.6720	**754.8396**	1491.6454	746.3263	1490.6614	745.8343	E	698.2814	349.6443	681.2549	341.1311	680.2708	340.6391	5
14	1623.6989	**812.3531**	1606.6724	803.8398	1605.6883	803.3478	D	***569.2388***	285.1230	552.2123	276.6098	551.2282	276.1178	4
15	1770.7673	885.8873	1753.7408	877.3740	1752.7567	876.8820	F	***454.2119***	227.6096	437.1853	219.0963			3
16	1930.7980	**965.9026**	1913.7714	957.3893	1912.7874	956.8973	C	***307.1435***	154.0754	290.1169	145.5621			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KCGNCSLTTLKDEDFCK
(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	2075.8962	0.0070	KCGNCSLTTLKDEDFCK
4.4	2074.9064	0.9968	MTGGPVMFRQGAGGAWLCF
1.6	2073.9016	2.0015	SNLMGMELDNECSKAKSK
0.8	2075.9119	-0.0087	FPELNGGHSYCRNPGNQK
0.8	2075.9119	-0.0087	FPELNGGHSYCRNPGNQK
0.5	2075.8993	0.0038	QLNPLHSGDIENDMFAEK
0.4	2075.9081	-0.0049	LAKEHNSCYEEYVCFK
0.1	2075.9119	-0.0087	FPELNGGHSYCRNPGNQK
0.1	2075.9119	-0.0087	FPELNGGHSYCRNPGNQK
0.1	2075.9119	-0.0087	FPELNGGHSYCRNPGNQK

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

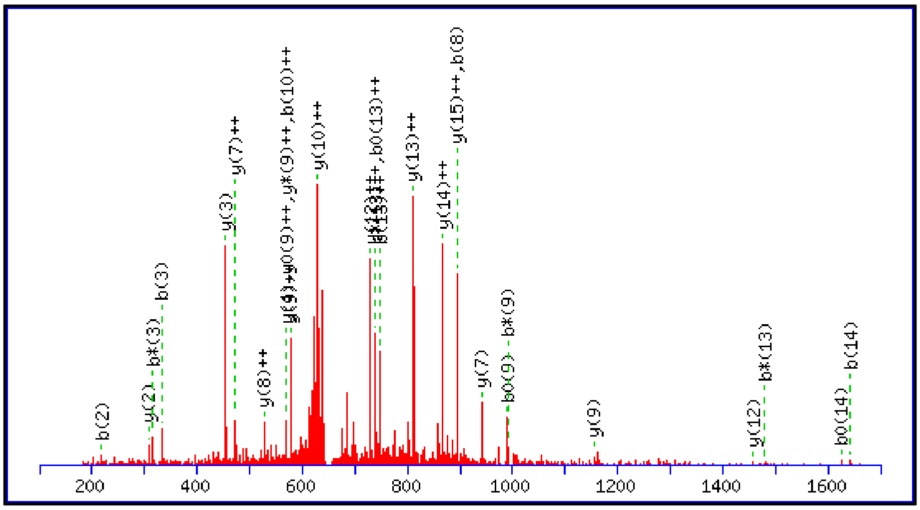
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGNCSLTTLKDEDFCK**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

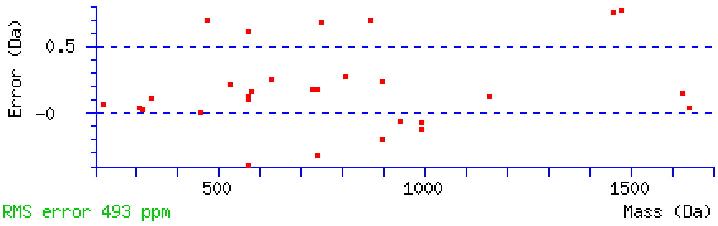
Match to Query 11739: 1947.804402 from(650.275410,3+) intensity(17876.1191) rtinseconds(966) scans(2222) index(25231)
Title: 111019_Est_MI_YS_G_07Spectrum1874_scans__2222
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

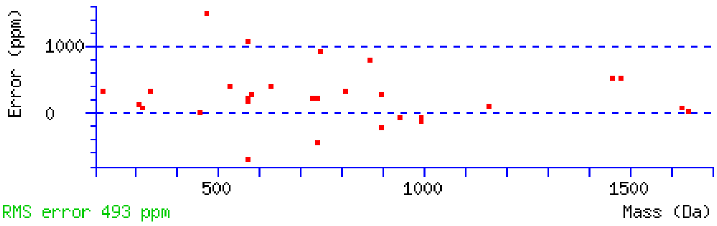
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1947.8013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.0028
Matches : 29/162 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	161.0379	81.0226					C							16
2	**218.0594**	109.5333					G	1788.7779	894.8926	1771.7513	886.3793	1770.7673	885.8873	15
3	**333.0863**	167.0468	316.0598	158.5335			N	1731.7564	866.3818	1714.7299	857.8686	1713.7459	857.3766	14
4	493.1170	247.0621	476.0904	238.5489			C	1616.7295	808.8684	1599.7029	800.3551	1598.7189	799.8631	13
5	580.1490	290.5781	563.1225	282.0649	562.1384	281.5729	S	***1456.6988***	728.8530	1439.6723	720.3398	1438.6883	719.8478	12
6	693.2331	347.1202	676.2065	338.6069	675.2225	338.1149	L	1369.6668	685.3370	1352.6402	676.8238	1351.6562	676.3318	11
7	794.2808	397.6440	777.2542	389.1307	776.2702	388.6387	T	1256.5827	628.7950	1239.5562	620.2817	1238.5722	619.7897	10
8	**895.3284**	448.1679	878.3019	439.6546	877.3179	439.1626	T	***1155.5351***	578.2712	1138.5085	569.7579	1137.5245	569.2659	9
9	1008.4125	504.7099	991.3859	496.1966	990.4019	495.7046	L	1054.4874	527.7473	1037.4608	519.2341	1036.4768	518.7420	8
10	1136.5075	568.7574	1119.4809	560.2441	1118.4969	559.7521	K	***941.4033***	471.2053	924.3768	462.6920	923.3927	462.2000	7
11	1251.5344	626.2708	1234.5079	617.7576	1233.5238	617.2656	D	813.3083	407.1578	796.2818	398.6445	795.2978	398.1525	6
12	1380.5770	690.7921	1363.5504	682.2789	1362.5664	681.7869	E	698.2814	349.6443	681.2549	341.1311	680.2708	340.6391	5
13	1495.6039	748.3056	1478.5774	739.7923	1477.5934	739.3003	D	***569.2388***	285.1230	552.2123	276.6098	551.2282	276.1178	4
14	**1642.6724**	821.8398	1625.6458	813.3265	1624.6618	812.8345	F	***454.2119***	227.6096	437.1853	219.0963			3
15	1802.7030	901.8551	1785.6765	893.3419	1784.6924	892.8499	C	***307.1435***	154.0754	290.1169	145.5621			2
16							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of CGNCSLTTLKDEDFCK
(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	1947.8013	0.0031	CGNCSLTTLKDEDFCK
6.7	1947.8012	0.0032	TMMNQEGSLVEMQFNR
6.7	1947.8012	0.0032	TMMNQEGSLVEMQFNR
3.2	1947.7965	0.0079	EQEMQECTTQIQYLK

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

MATRIX SCIENCE

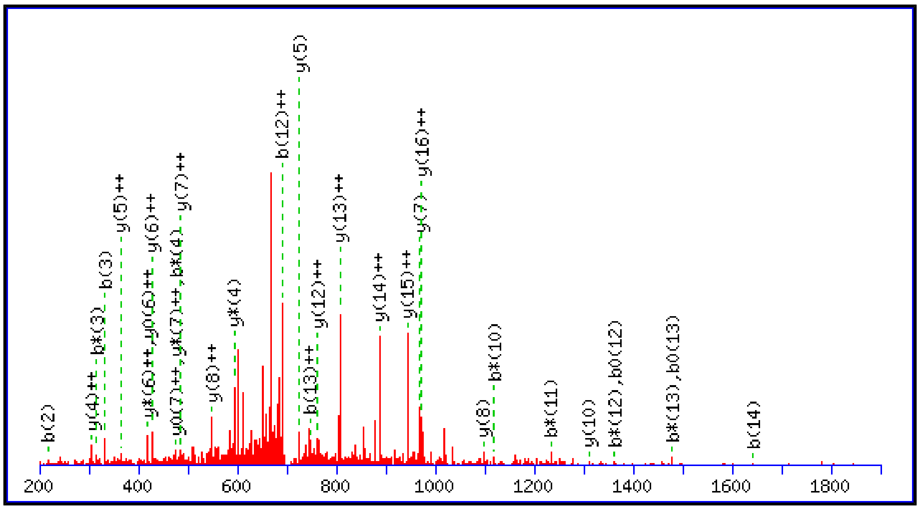
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGNCSLTTLKDEDFCKR**
Found in **D6REX5** in **con_Xuniprot_HUMAN3**, D6REX5_HUMAN Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV=1

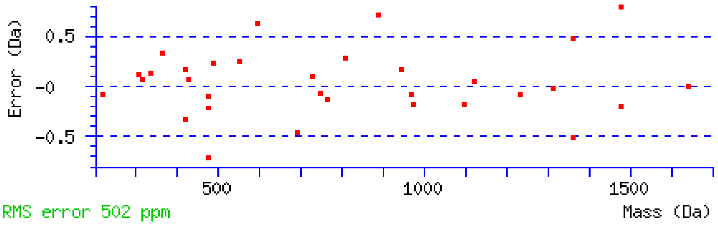
Match to Query 13897: 2103.909732 from(702.310520,3+) intensity(8137.7930) rtinseconds(817) scans(1840) index(23089)
Title: 111019_Est_MI_YS_G_04Spectrum1537_scans__1840
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

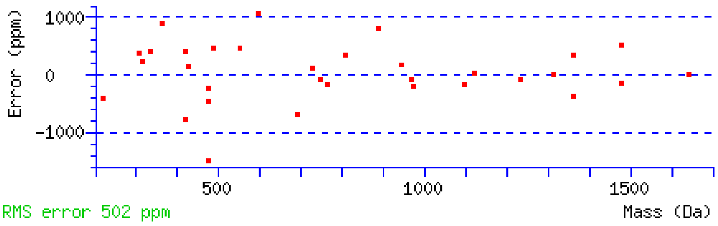
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2103.9024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.0056
Matches : 32/172 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	161.0379	81.0226					**C**							**17**
2	**218.0594**	109.5333					**G**	1944.8790	972.9431	1927.8524	964.4299	1926.8684	963.9379	**16**
3	**333.0863**	167.0468	316.0598	158.5335			**N**	1887.8575	944.4324	1870.8310	935.9191	1869.8470	935.4271	**15**
4	493.1170	247.0621	476.0904	238.5489			**C**	1772.8306	886.9189	1755.8040	878.4057	1754.8200	877.9136	**14**
5	580.1490	290.5781	563.1225	282.0649	562.1384	281.5729	**S**	1612.7999	806.9036	1595.7734	798.3903	1594.7894	797.8983	**13**
6	693.2331	347.1202	676.2065	338.6069	675.2225	338.1149	**L**	1525.7679	763.3876	1508.7414	754.8743	1507.7573	754.3823	**12**
7	794.2808	397.6440	777.2542	389.1307	776.2702	388.6387	**T**	1412.6838	706.8456	1395.6573	698.3323	1394.6733	697.8403	**11**
8	895.3284	448.1679	878.3019	439.6546	877.3179	439.1626	**T**	**1311.6362**	656.3217	1294.6096	647.8084	1293.6256	647.3164	**10**
9	1008.4125	504.7099	991.3859	496.1966	990.4019	495.7046	**L**	1210.5885	605.7979	1193.5619	597.2846	1192.5779	596.7926	**9**
10	1136.5075	568.7574	1119.4809	560.2441	1118.4969	559.7521	**K**	**1097.5044**	549.2558	1080.4779	540.7426	1079.4939	540.2506	**8**
11	1251.5344	626.2708	1234.5079	617.7576	1233.5238	617.2656	**D**	**969.4095**	485.2084	952.3829	476.6951	951.3989	476.2031	**7**
12	1380.5770	690.7921	1363.5504	682.2789	1362.5664	681.7869	**E**	854.3825	427.6949	837.3560	419.1816	836.3719	418.6896	**6**
13	1495.6039	748.3056	1478.5774	739.7923	1477.5934	739.3003	**D**	**725.3399**	363.1736	708.3134	354.6603	707.3294	354.1683	**5**
14	**1642.6724**	821.8398	1625.6458	813.3265	1624.6618	812.8345	**F**	610.3130	305.6601	593.2864	297.1469			**4**
15	1802.7030	901.8551	1785.6765	893.3419	1784.6924	892.8499	**C**	463.2446	232.1259	446.2180	223.6126			**3**
16	1930.7980	965.9026	1913.7714	957.3893	1912.7874	956.8973	**K**	303.2139	152.1106	286.1874	143.5973			**2**
17							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of CGNCSLTTLKDEDFCKR
(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	2103.9024	0.0074	CGNCSLTTLKDEDFCKR

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

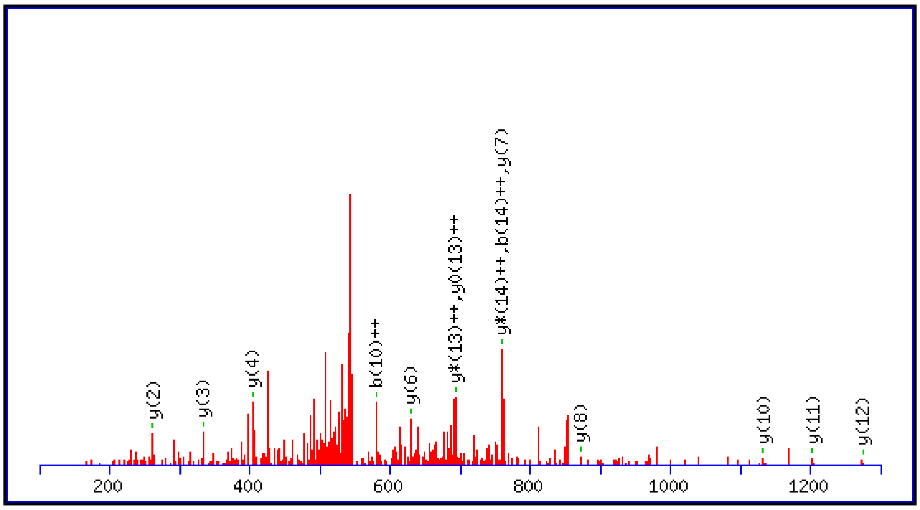
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQEAAMEIQEPAANK**
Found in **E7ER40** in **con_Xuniprot_HUMAN3**, E7ER40_HUMAN PHD finger protein 3 (Fragment) OS=Homo sapiens GN=PHF3 PE=2 SV=1

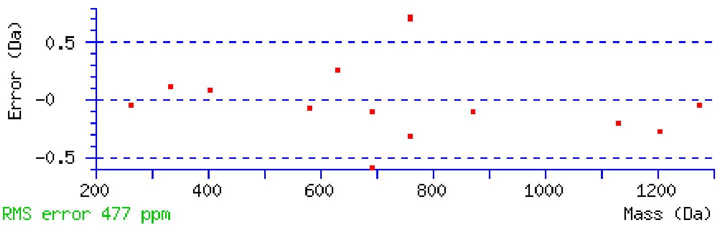
Match to Query 8409: 1661.721132 from(554.914320,3+) intensity(2891.4273) rtinseconds(523) scans(859) index(28331)
Title: 111019_Est_MI_YS_G_13Spectrum686_scans__859
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

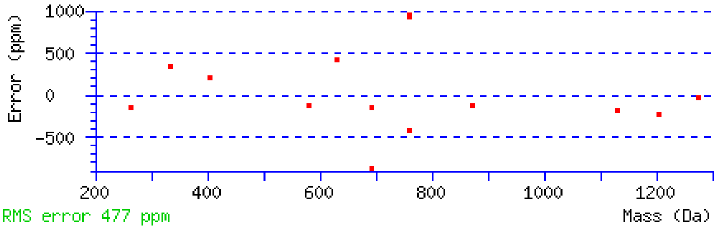
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1660.7137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Deamidated (NQ)
Q9 : Deamidated (NQ)
N14 : Deamidated (NQ)
Ions Score: 48 **Expect:** 0.00095
Matches : 14/156 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	130.0499	65.5286			112.0393	56.5233	E							15
2	259.0925	130.0499	242.0659	121.5366	241.0819	121.0446	Q	1532.6785	766.8429	1515.6519	758.3296	1514.6679	757.8376	14
3	388.1351	194.5712	371.1085	186.0579	370.1245	185.5659	E	1403.6359	702.3216	1386.6093	693.8083	1385.6253	693.3163	13
4	459.1722	230.0897	442.1456	221.5764	441.1616	221.0844	A	***1274.5933***	637.8003	1257.5667	629.2870	1256.5827	628.7950	12
5	530.2093	265.6083	513.1827	257.0950	512.1987	256.6030	A	***1203.5562***	602.2817	1186.5296	593.7685	1185.5456	593.2764	11
6	661.2498	331.1285	644.2232	322.6152	643.2392	322.1232	M	***1132.5191***	566.7632	1115.4925	558.2499	1114.5085	557.7579	10
7	790.2924	395.6498	773.2658	387.1365	772.2818	386.6445	E	1001.4786	501.2429	984.4520	492.7297	983.4680	492.2376	9
8	903.3764	452.1919	886.3499	443.6786	885.3659	443.1866	I	***872.4360***	436.7216	855.4094	428.2084	854.4254	427.7164	8
9	1032.4190	516.7131	1015.3925	508.1999	1014.4085	507.7079	Q	***759.3519***	380.1796	742.3254	371.6663	741.3414	371.1743	7
10	1161.4616	**581.2344**	1144.4351	572.7212	1143.4510	572.2292	E	***630.3093***	315.6583	613.2828	307.1450	612.2988	306.6530	6
11	1258.5144	629.7608	1241.4878	621.2476	1240.5038	620.7555	P	501.2667	251.1370	484.2402	242.6237			5
12	1329.5515	665.2794	1312.5249	656.7661	1311.5409	656.2741	A	***404.2140***	202.6106	387.1874	194.0974			4
13	1400.5886	700.7979	1383.5621	692.2847	1382.5780	691.7927	A	***333.1769***	167.0921	316.1503	158.5788			3
14	1515.6155	**758.3114**	1498.5890	749.7981	1497.6050	749.3061	N	***262.1397***	131.5735	245.1132	123.0602			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EQEAAMEIQEPAANK
(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	1660.7137	1.0074	EQEAAMEIQEPAANK
33.1	1661.7178	0.0034	YKAAFTECCQAADK
5.3	1660.7191	1.0020	YKQSGGWNGTWMTK
2.6	1659.7199	2.0012	GEQFPPGHMTESDTK
2.5	1661.7290	-0.0079	CGDQPRHFAIAMDK
2.3	1661.7243	-0.0031	DRMEYVYEEVANK
1.4	1661.7276	-0.0065	QFSSMESVKNMVNK
1.1	1660.7138	1.0074	DQIAYSATSMDLSDK
1.1	1660.7138	1.0074	NQIAYSATSMDLSDK
0.8	1661.7251	-0.0040	NYWCILSMNGKMK

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

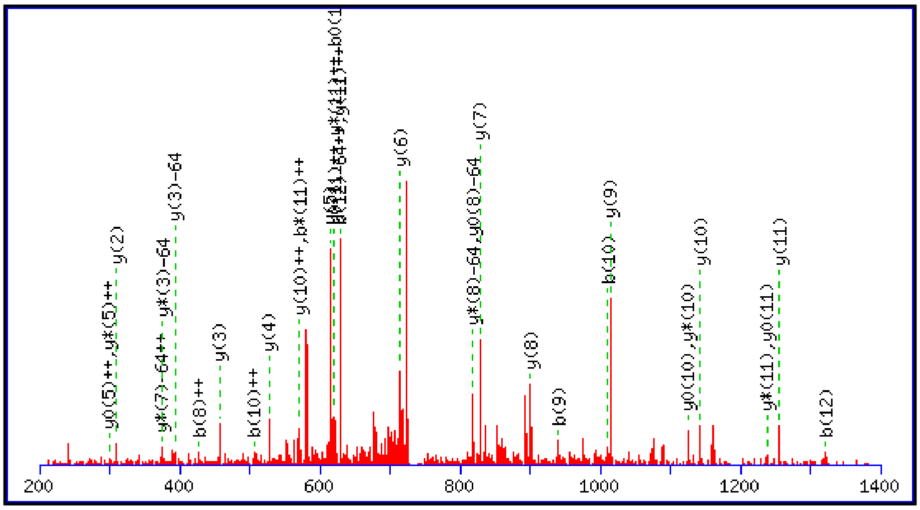
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVIQNANVSAMYK**
Found in **E9PD35** in **con_Xuniprot_HUMAN3**, E9PD35_HUMAN Vascular endothelial growth factor receptor 3 OS=Homo sapiens GN=FLT4 PE=2 SV=1

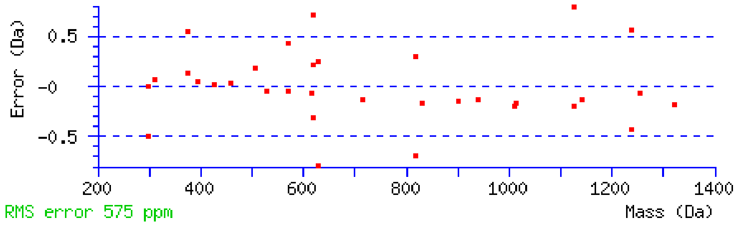
Match to Query 6199: 1466.748588 from(734.381570,2+) intensity(23588.8145) rtinseconds(810) scans(1789) index(10797)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum1498_scans__1789
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

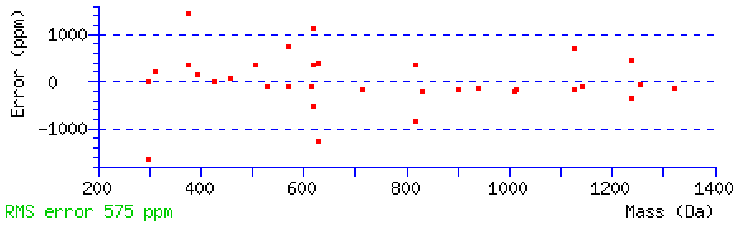
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1466.7439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54 **Expect:** 0.00093
Matches : 33/182 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	114.0913	57.5493					L							13
2	213.1598	107.0835					V	1354.6671	677.8372	1337.6406	669.3239	1336.6566	668.8319	12
3	326.2438	163.6255					I	***1255.5987***	628.3030	1238.5722	619.7897	1237.5882	619.2977	11
4	454.3024	227.6548	437.2758	219.1416			Q	***1142.5147***	571.7610	1125.4881	563.2477	1124.5041	562.7557	10
5	568.3453	284.6763	551.3188	276.1630			N	***1014.4561***	507.7317	997.4295	499.2184	996.4455	498.7264	9
6	639.3824	320.1949	622.3559	311.6816			A	***900.4131***	450.7102	883.3866	442.1969	882.4026	441.7049	8
7	754.4094	377.7083	737.3828	369.1951			N	***829.3760***	415.1917	812.3495	406.6784	811.3655	406.1864	7
8	853.4778	427.2425	836.4512	418.7293			V	***714.3491***	357.6782	697.3225	349.1649	696.3385	348.6729	6
9	**940.5098**	470.7585	923.4833	462.2453	922.4993	461.7533	S	***615.2807***	308.1440	598.2541	299.6307	597.2701	299.1387	5
10	**1011.5469**	506.2771	994.5204	497.7638	993.5364	497.2718	A	***528.2486***	264.6280	511.2221	256.1147			4
11	1158.5823	579.7948	1141.5558	571.2815	1140.5718	570.7895	M	***457.2115***	229.1094	440.1850	220.5961			3
12	**1321.6457**	661.3265	1304.6191	652.8132	1303.6351	652.3212	Y	***310.1761***	155.5917	293.1496	147.0784			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.9	1466.7439	0.0047	LVIQNANVSAMYK	Deamidated N7 99.20%
32.3	1466.7439	0.0047	LVIQNANVSAMYK	Deamidated N5 0.70%
23.9	1466.7439	0.0047	LVIQNANVSAMYK	Deamidated Q4 0.10%
7.8	1464.7381	2.0105	KMTEIQVELETK	
6.5	1464.7428	2.0057	LKQCMQKGQSIK	
6.0	1464.7395	2.0091	YKPNGQIEMKNK	
4.3	1466.7473	0.0013	MSADAMLKALLGSK	
4.2	1464.7395	2.0091	FCKTTNTVEPLR	
3.0	1466.7479	0.0007	FLKSEMPPVQFK	
2.9	1464.7361	2.0125	AFSFTTSLIGHQR	

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

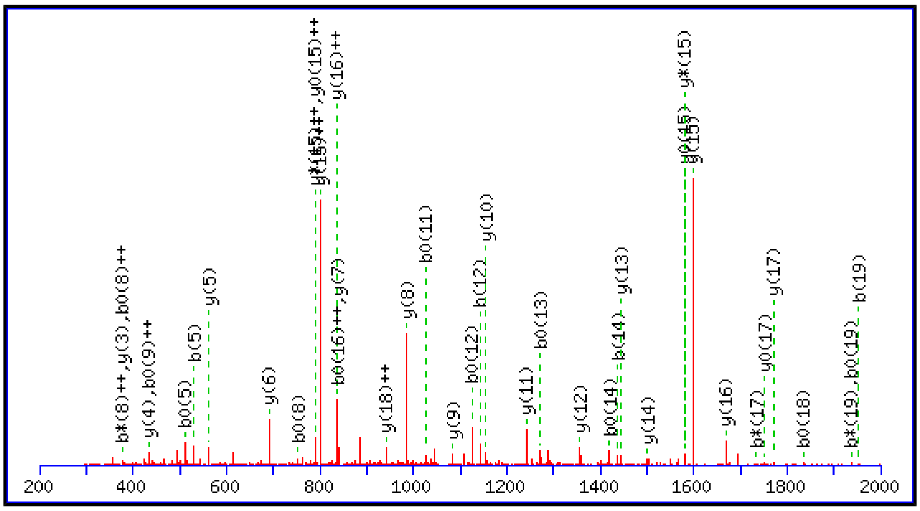
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENLTAPGSDSAVFFEQGTTR**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

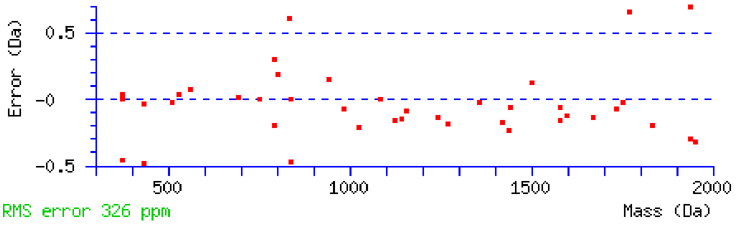
Match to Query 14344: 2126.985308 from(1064.499930,2+) intensity(119924.2266) rtinseconds(1528) scans(3588) index(15116)
Title: 111019_Est_MI_YP_G_04Spectrum3066_scans__3588
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

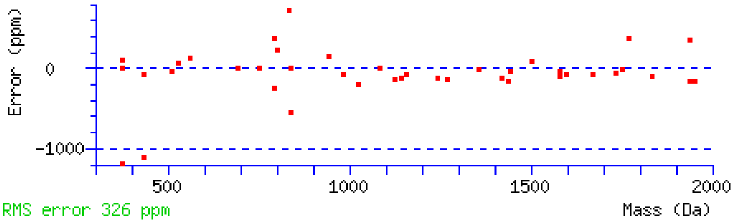
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2126.9756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2     : Deamidated (NQ)
Ions Score: 120  Expect: 2.1e-010
Matches : 41/224 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	130.0499	65.5286			112.0393	56.5233	E							20
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	1998.9403	999.9738	1981.9138	991.4605	1980.9298	990.9685	19
3	358.1609	179.5841	341.1343	171.0708	340.1503	170.5788	L	1883.9134	942.4603	1866.8868	933.9471	1865.9028	933.4550	18
4	459.2086	230.1079	442.1820	221.5946	441.1980	221.1026	T	***1770.8293***	885.9183	1753.8028	877.4050	1752.8188	876.9130	17
5	**530.2457**	265.6265	513.2191	257.1132	512.2351	256.6212	A	***1669.7816***	835.3945	1652.7551	826.8812	1651.7711	826.3892	16
6	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	P	***1598.7445***	799.8759	1581.7180	791.3626	1580.7340	790.8706	15
7	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	G	***1501.6918***	751.3495	1484.6652	742.8362	1483.6812	742.3442	14
8	771.3519	386.1796	754.3254	377.6663	753.3414	377.1743	S	***1444.6703***	722.8388	1427.6438	714.3255	1426.6597	713.8335	13
9	886.3789	443.6931	869.3523	435.1798	868.3683	434.6878	D	***1357.6383***	679.3228	1340.6117	670.8095	1339.6277	670.3175	12
10	973.4109	487.2091	956.3843	478.6958	955.4003	478.2038	S	***1242.6113***	621.8093	1225.5848	613.2960	1224.6008	612.8040	11
11	1044.4480	522.7276	1027.4215	514.2144	1026.4374	513.7224	A	***1155.5793***	578.2933	1138.5528	569.7800	1137.5687	569.2880	10
12	**1143.5164**	572.2619	1126.4899	563.7486	1125.5059	563.2566	V	***1084.5422***	542.7747	1067.5156	534.2615	1066.5316	533.7694	9
13	1290.5848	645.7961	1273.5583	637.2828	1272.5743	636.7908	F	***985.4738***	493.2405	968.4472	484.7273	967.4632	484.2352	8
14	**1437.6533**	719.3303	1420.6267	710.8170	1419.6427	710.3250	F	***838.4054***	419.7063	821.3788	411.1930	820.3948	410.7010	7
15	1566.6958	783.8516	1549.6693	775.3383	1548.6853	774.8463	E	***691.3369***	346.1721	674.3104	337.6588	673.3264	337.1668	6
16	1694.7544	847.8808	1677.7279	839.3676	1676.7439	838.8756	Q	***562.2944***	281.6508	545.2678	273.1375	544.2838	272.6455	5
17	1751.7759	876.3916	1734.7493	867.8783	1733.7653	867.3863	G	***434.2358***	217.6215	417.2092	209.1083	416.2252	208.6162	4
18	1852.8236	926.9154	1835.7970	918.4021	1834.8130	917.9101	T	***377.2143***	189.1108	360.1878	180.5975	359.2037	180.1055	3
19	**1953.8712**	977.4393	1936.8447	968.9260	1935.8607	968.4340	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
119.7	2126.9756	0.0097	ENLTAPGSDSAVFFEQGTTR	Deamidated N2 100.00%
115.2	2125.9916	0.9937	ENLTAPGSDSAVFFEQGTTR	
53.6	2126.9756	0.0097	ENLTAPGSDSAVFFEQGTTR	Deamidated Q16 0.00%
4.0	2124.9884	1.9969	YMNDINNIKNVASTIGPNK	
3.7	2126.9884	-0.0031	AMFQYLDVQEPNKWWR	
3.1	2125.9777	1.0076	NQDTQHGVANGASHPPPLER	
2.4	2124.9806	2.0047	SQKMEIESVLMKQQNLQA	
1.7	2126.9917	-0.0064	EVQYNMGFLFAYSMRQK	
1.1	2126.9902	-0.0049	GQGPELMGGAQTPTKQPEER	
0.4	2125.9725	1.0129	YMNDINNIKNVASTIGPNK	

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

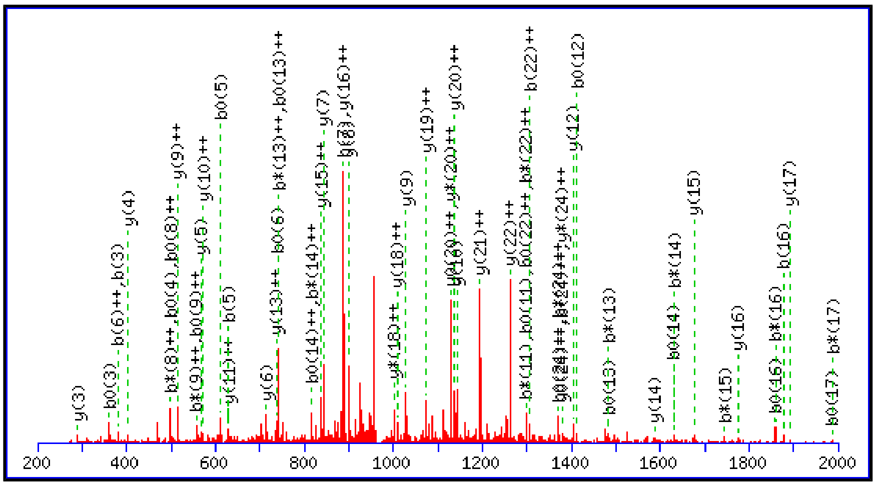
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELHHLQEQNVSNAFLDKGEFYIGSK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

Match to Query 26413: 2903.417052 from(968.812960,3+) intensity(86215.4609) rtinseconds(1606) scans(4095) index(2714)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum3463_scans__4095
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

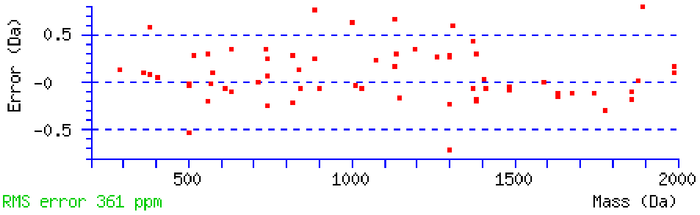
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

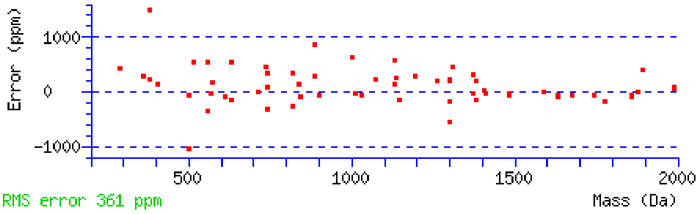


Monoisotopic mass of neutral peptide Mr(calc): 2903.4090
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 101 **Expect:** 2.3e-008
Matches : 64/276 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							25
2	243.1339	122.0706			225.1234	113.0653	L	2775.3737	1388.1905	2758.3471	1379.6772	2757.3631	1379.1852	24
3	**380.1928**	190.6001			362.1823	181.5948	H	2662.2896	1331.6484	2645.2631	1323.1352	2644.2790	1322.6432	23
4	517.2518	259.1295			499.2412	250.1242	H	2525.2307	1263.1190	2508.2041	1254.6057	2507.2201	1254.1137	22
5	**630.3358**	315.6715			612.3253	306.6663	L	2388.1718	1194.5895	2371.1452	1186.0763	2370.1612	1185.5842	21
6	758.3944	379.7008	741.3678	371.1876	740.3838	370.6956	Q	2275.0877	1138.0475	2258.0612	1129.5342	2257.0772	1129.0422	20
7	**887.4370**	444.2221	870.4104	435.7089	869.4264	435.2169	E	2147.0291	1074.0182	2130.0026	1065.5049	2129.0186	1065.0129	19
8	1015.4956	508.2514	998.4690	499.7381	997.4850	499.2461	Q	2017.9865	1009.4969	2000.9600	1000.9836	1999.9760	1000.4916	18
9	1130.5225	565.7649	1113.4960	557.2516	1112.5119	556.7596	N	***1889.9280***	945.4676	1872.9014	936.9543	1871.9174	936.4623	17
10	1229.5909	615.2991	1212.5644	606.7858	1211.5804	606.2938	V	***1774.9010***	887.9542	1757.8745	879.4409	1756.8905	878.9489	16
11	1316.6230	658.8151	1299.5964	650.3018	1298.6124	649.8098	S	***1675.8326***	838.4199	1658.8061	829.9067	1657.8220	829.4147	15
12	1430.6659	715.8366	1413.6393	707.3233	1412.6553	706.8313	N	***1588.8006***	794.9039	1571.7740	786.3907	1570.7900	785.8986	14
13	1501.7030	751.3551	1484.6764	742.8419	1483.6924	742.3499	A	1474.7577	737.8825	1457.7311	729.3692	1456.7471	728.8772	13
14	1648.7714	824.8893	1631.7449	816.3761	1630.7608	815.8841	F	***1403.7205***	702.3639	1386.6940	693.8506	1385.7100	693.3586	12
15	1761.8555	881.4314	1744.8289	872.9181	1743.8449	872.4261	L	1256.6521	628.8297	1239.6256	620.3164	1238.6416	619.8244	11
16	**1876.8824**	938.9448	1859.8559	930.4316	1858.8719	929.9396	D	***1143.5681***	572.2877	1126.5415	563.7744	1125.5575	563.2824	10
17	2004.9774	1002.9923	1987.9508	994.4791	1986.9668	993.9870	K	***1028.5411***	514.7742	1011.5146	506.2609	1010.5306	505.7689	9
18	2061.9988	1031.5031	2044.9723	1022.9898	2043.9883	1022.4978	G	***900.4462***	450.7267	883.4196	442.2134	882.4356	441.7214	8
19	2191.0414	1096.0244	2174.0149	1087.5111	2173.0309	1087.0191	E	***843.4247***	422.2160	826.3981	413.7027	825.4141	413.2107	7
20	2338.1099	1169.5586	2321.0833	1161.0453	2320.0993	1160.5533	F	***714.3821***	357.6947	697.3556	349.1814	696.3715	348.6894	6
21	2501.1732	1251.0902	2484.1466	1242.5770	2483.1626	1242.0849	Y	***567.3137***	284.1605	550.2871	275.6472	549.3031	275.1552	5
22	2614.2572	1307.6323	2597.2307	1299.1190	2596.2467	1298.6270	I	***404.2504***	202.6288	387.2238	194.1155	386.2398	193.6235	4
23	2671.2787	1336.1430	2654.2522	1327.6297	2653.2681	1327.1377	G	***291.1663***	146.0868	274.1397	137.5735	273.1557	137.0815	3

24	2758.3107	1379.6590	2741.2842	1371.1457	2740.3002	1370.6537	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
100.9	2903.4090	0.0081	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated N9 78.98%
91.5	2903.4090	0.0081	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q8 9.13%
90.1	2903.4090	0.0081	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q6 6.69%
89.0	2903.4090	0.0081	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated N12 5.19%
72.4	2902.4249	0.9921	ELHHLQEQNVSNAFLDKGEFYIGSK	
6.6	2903.4117	0.0054	QLQQQNEKEMMEQIRQQTDILEK	
5.9	2903.4247	-0.0076	LNSISDEENLTTIENRLISNEQQLK	
5.7	2901.4001	2.0170	DKAPGMQTLPSHRLMSAFSEVNKPSGV	
5.4	2903.4247	-0.0076	LNSISDEENLTTIENRLISNEQQLK	
5.2	2903.4182	-0.0012	AQAEDLSQDTITMIQQLIDGIDQKGR	

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

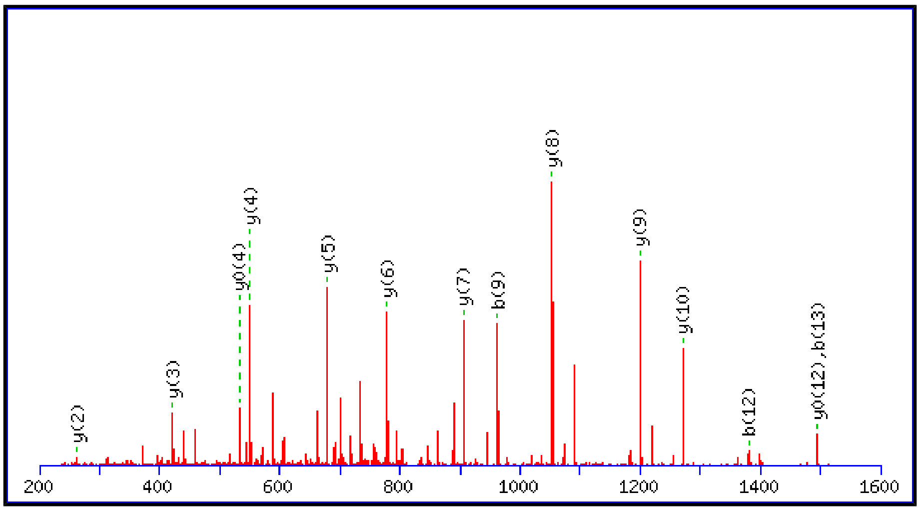
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQAFFQVQECNK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

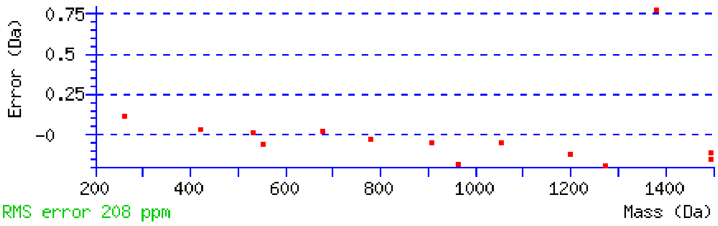
Match to Query 7850: 1639.769268 from(820.891910,2+) intensity(445989.5625) rtinseconds(2030) scans(5160) index(5466)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum4537_scans__5160
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

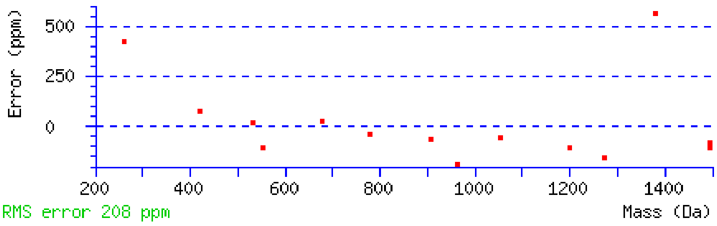
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1639.7664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 94 **Expect:** 7.2e-008
Matches : 14/124 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							14
2	129.0659	65.0366					G	1569.7366	785.3719	1552.7101	776.8587	1551.7260	776.3667	13
3	242.1499	121.5786					L	1512.7151	756.8612	1495.6886	748.3479	1494.7046	747.8559	12
4	370.2085	185.6079	353.1819	177.0946			Q	1399.6311	700.3192	1382.6045	691.8059	1381.6205	691.3139	11
5	441.2456	221.1264	424.2191	212.6132			A	***1271.5725***	636.2899	1254.5460	627.7766	1253.5619	627.2846	10
6	588.3140	294.6607	571.2875	286.1474			F	***1200.5354***	600.7713	1183.5088	592.2581	1182.5248	591.7660	9
7	735.3824	368.1949	718.3559	359.6816			F	***1053.4670***	527.2371	1036.4404	518.7239	1035.4564	518.2318	8
8	863.4410	432.2241	846.4145	423.7109			Q	***906.3986***	453.7029	889.3720	445.1896	888.3880	444.6976	7
9	**962.5094**	481.7584	945.4829	473.2451			V	***778.3400***	389.6736	761.3134	381.1604	760.3294	380.6683	6
10	1090.5680	545.7876	1073.5415	537.2744			Q	***679.2716***	340.1394	662.2450	331.6261	661.2610	331.1341	5
11	1219.6106	610.3089	1202.5841	601.7957	1201.6000	601.3037	E	***551.2130***	276.1101	534.1864	267.5969	533.2024	267.1049	4
12	**1379.6413**	690.3243	1362.6147	681.8110	1361.6307	681.3190	C	***422.1704***	211.5888	405.1438	203.0756			3
13	**1494.6682**	747.8377	1477.6416	739.3245	1476.6576	738.8325	N	***262.1397***	131.5735	245.1132	123.0602			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
93.9	1639.7664	0.0028	AGLQAFFQVQECNK	Deamidated N13 99.96%
60.1	1639.7664	0.0028	AGLQAFFQVQECNK	Deamidated Q10 0.04%
43.6	1639.7664	0.0028	AGLQAFFQVQECNK	Deamidated Q8 0.00%
15.6	1639.7664	0.0028	AGLQAFFQVQECNK	Deamidated Q4 0.00%
5.4	1639.7732	-0.0039	KLIQMSMQQVCDK	
4.9	1639.7664	0.0029	ANSFMWNKGASIADK	
3.6	1639.7736	-0.0044	QPPEQQAPSKQCSR	
3.3	1637.7607	2.0086	NTSALVIVHDTTGMY	
2.9	1639.7763	-0.0070	MASVQQGEKQLFEK	
2.5	1639.7763	-0.0070	MASVQQGEKQLFEK	

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

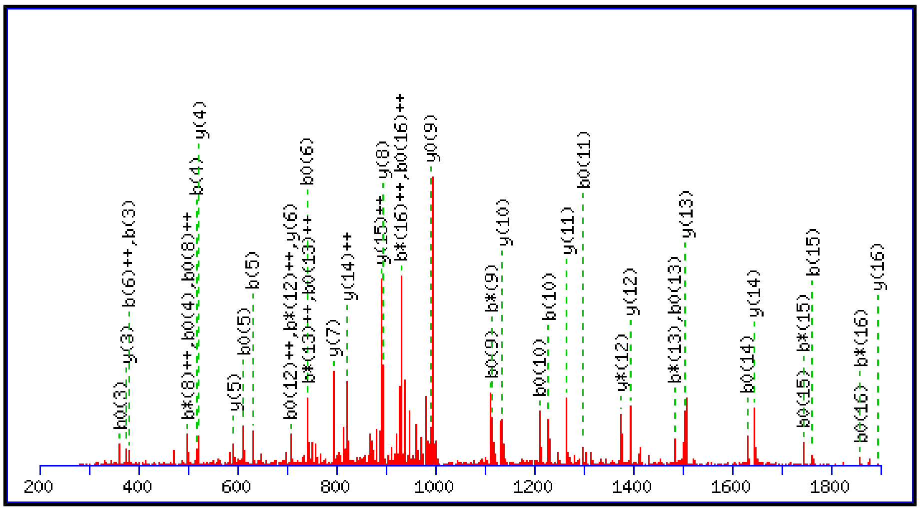
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELHHLQEQNVSNAFLDK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

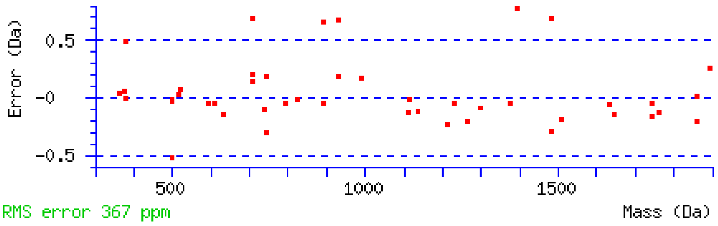
Match to Query 12735: 2021.989048 from(1012.001800,2+) intensity(25765.3047) rtinseconds(972) scans(2335) index(18391)
Title: 111019_Est_MI_YP_G_08Spectrum2041_scans__2335
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

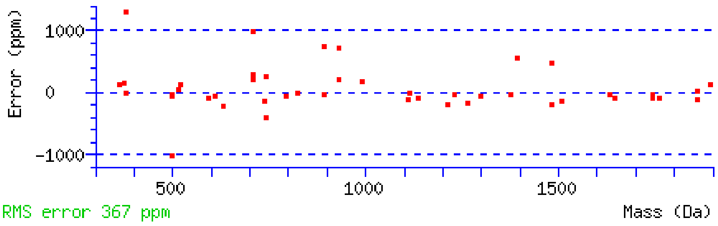
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2021.9806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 93 **Expect:** 1.4e-007
Matches : 45/180 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	130.0499	65.5286			112.0393	56.5233	E							17
2	243.1339	122.0706			225.1234	113.0653	L	***1893.9454***	947.4763	1876.9188	938.9630	1875.9348	938.4710	16
3	**380.1928**	190.6001			362.1823	181.5948	H	1780.8613	890.9343	1763.8347	882.4210	1762.8507	881.9290	15
4	**517.2518**	259.1295			499.2412	250.1242	H	***1643.8024***	822.4048	1626.7758	813.8916	1625.7918	813.3995	14
5	**630.3358**	315.6715			612.3253	306.6663	L	***1506.7435***	753.8754	1489.7169	745.3621	1488.7329	744.8701	13
6	758.3944	379.7008	741.3678	371.1876	740.3838	370.6956	Q	***1393.6594***	697.3333	1376.6329	688.8201	1375.6488	688.3281	12
7	887.4370	444.2221	870.4104	435.7089	869.4264	435.2169	E	***1265.6008***	633.3040	1248.5743	624.7908	1247.5903	624.2988	11
8	1015.4956	508.2514	998.4690	499.7381	997.4850	499.2461	Q	***1136.5582***	568.7828	1119.5317	560.2695	1118.5477	559.7775	10
9	1130.5225	565.7649	1113.4960	557.2516	1112.5119	556.7596	N	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	9
10	**1229.5909**	615.2991	1212.5644	606.7858	1211.5804	606.2938	V	***893.4727***	447.2400	876.4462	438.7267	875.4621	438.2347	8
11	1316.6230	658.8151	1299.5964	650.3018	1298.6124	649.8098	S	***794.4043***	397.7058	777.3777	389.1925	776.3937	388.7005	7
12	1430.6659	715.8366	1413.6393	707.3233	1412.6553	706.8313	N	***707.3723***	354.1898	690.3457	345.6765	689.3617	345.1845	6
13	1501.7030	751.3551	1484.6764	742.8419	1483.6924	742.3499	A	***593.3293***	297.1683	576.3028	288.6550	575.3188	288.1630	5
14	1648.7714	824.8893	1631.7449	816.3761	1630.7608	815.8841	F	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
15	**1761.8555**	881.4314	1744.8289	872.9181	1743.8449	872.4261	L	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
16	1876.8824	938.9448	1859.8559	930.4316	1858.8719	929.9396	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
92.8	2021.9806	0.0084	ELHHLQEQNVSNAFLDK	Deamidated N9 49.30%
92.8	2021.9806	0.0084	ELHHLQEQNVSNAFLDK	Deamidated Q8 49.30%
77.3	2021.9806	0.0084	ELHHLQEQNVSNAFLDK	Deamidated Q6 1.39%
53.0	2021.9806	0.0084	ELHHLQEQNVSNAFLDK	Deamidated N12 0.01%
11.1	2021.9905	-0.0015	QQEQLQLQLLQQQHAGK	
10.9	2021.9905	-0.0015	QQEQLQLQLLQQQHAGK	
9.7	2021.9841	0.0050	LQDVVHMQGGSPLQASPDK	
7.5	2021.9905	-0.0015	QQEQLQLQLLQQQHAGK	
6.4	2021.9905	-0.0015	QQEQLQLQLLQQQHAGK	
5.2	2021.9959	-0.0068	EYSLHSFDRKWGQIQK	

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

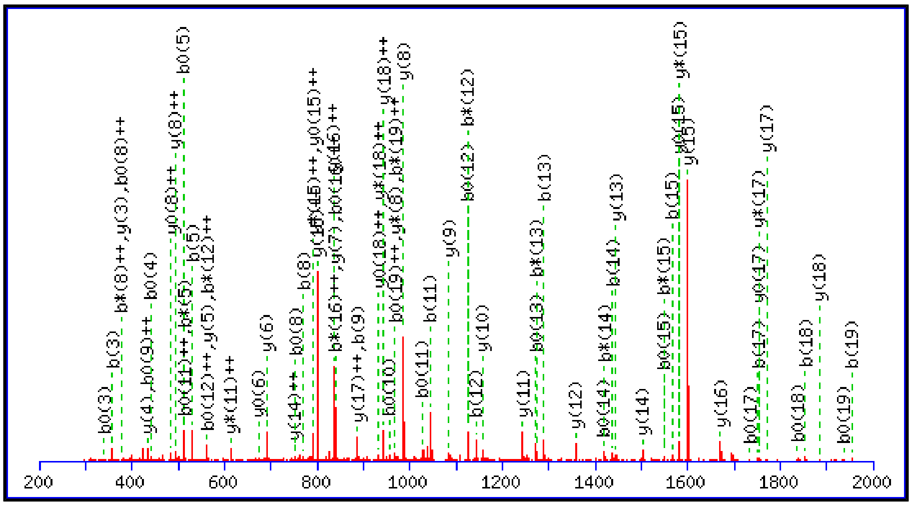
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENLTAPGSDSAVFFEQGTTR**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

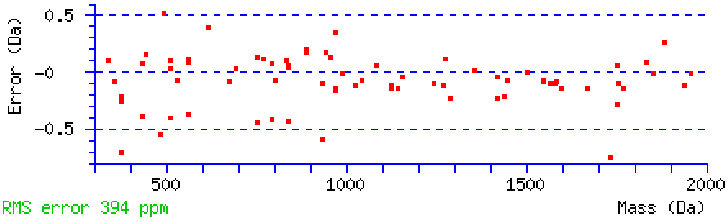
Match to Query 14356: 2127.967828 from(1064.991190,2+) intensity(84965.3203) rtinseconds(1490) scans(3832) index(6428)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum3372_scans__3832
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

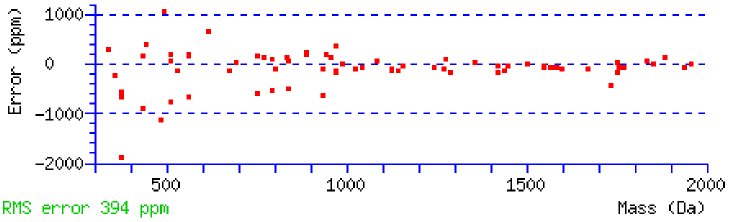
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2127.9597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Q16 : Deamidated (NQ)
Ions Score: 88 **Expect:** 2.5e-007
Matches : 74/224 fragment ions using 135 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							20
2	245.0768	123.0420	228.0503	114.5288	227.0662	114.0368	N	1999.9243	1000.4658	1982.8978	991.9525	1981.9138	991.4605	19
3	**358.1609**	179.5841	341.1343	171.0708	340.1503	170.5788	L	***1884.8974***	942.9523	1867.8709	934.4391	1866.8868	933.9471	18
4	459.2086	230.1079	442.1820	221.5946	441.1980	221.1026	T	***1771.8133***	886.4103	1754.7868	877.8970	1753.8028	877.4050	17
5	**530.2457**	265.6265	513.2191	257.1132	512.2351	256.6212	A	***1670.7657***	835.8865	1653.7391	827.3732	1652.7551	826.8812	16
6	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	P	***1599.7285***	800.3679	1582.7020	791.8546	1581.7180	791.3626	15
7	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	G	***1502.6758***	751.8415	1485.6492	743.3283	1484.6652	742.8362	14
8	**771.3519**	386.1796	754.3254	377.6663	753.3414	377.1743	S	***1445.6543***	723.3308	1428.6278	714.8175	1427.6438	714.3255	13
9	**886.3789**	443.6931	869.3523	435.1798	868.3683	434.6878	D	***1358.6223***	679.8148	1341.5957	671.3015	1340.6117	670.8095	12
10	973.4109	487.2091	956.3843	478.6958	955.4003	478.2038	S	***1243.5953***	622.3013	1226.5688	613.7880	1225.5848	613.2960	11
11	**1044.4480**	522.7276	1027.4215	514.2144	1026.4374	513.7224	A	***1156.5633***	578.7853	1139.5368	570.2720	1138.5528	569.7800	10
12	**1143.5164**	572.2619	1126.4899	563.7486	1125.5059	563.2566	V	***1085.5262***	543.2667	1068.4997	534.7535	1067.5156	534.2615	9
13	**1290.5848**	645.7961	1273.5583	637.2828	1272.5743	636.7908	F	***986.4578***	493.7325	969.4312	485.2193	968.4472	484.7273	8
14	**1437.6533**	719.3303	1420.6267	710.8170	1419.6427	710.3250	F	***839.3894***	420.1983	822.3628	411.6851	821.3788	411.1930	7
15	**1566.6958**	783.8516	1549.6693	775.3383	1548.6853	774.8463	E	***692.3210***	346.6641	675.2944	338.1508	674.3104	337.6588	6
16	1695.7384	848.3729	1678.7119	839.8596	1677.7279	839.3676	Q	***563.2784***	282.1428	546.2518	273.6295	545.2678	273.1375	5
17	**1752.7599**	876.8836	1735.7334	868.3703	1734.7493	867.8783	G	***434.2358***	217.6215	417.2092	209.1083	416.2252	208.6162	4
18	**1853.8076**	927.4074	1836.7810	918.8942	1835.7970	918.4021	T	***377.2143***	189.1108	360.1878	180.5975	359.2037	180.1055	3
19	**1954.8553**	977.9313	1937.8287	969.4180	1936.8447	968.9260	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
88.1	2127.9597	0.0082	ENLTAPGSDSAVFFEQGTTR
6.9	2127.9756	-0.0078	REDQGPPCPSPVGGGDPLHR
1.8	2127.9652	0.0026	AGMQFTMLYRDMHQINR
0.5	2127.9652	0.0026	AGMQFTMLYRDMHQINR

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

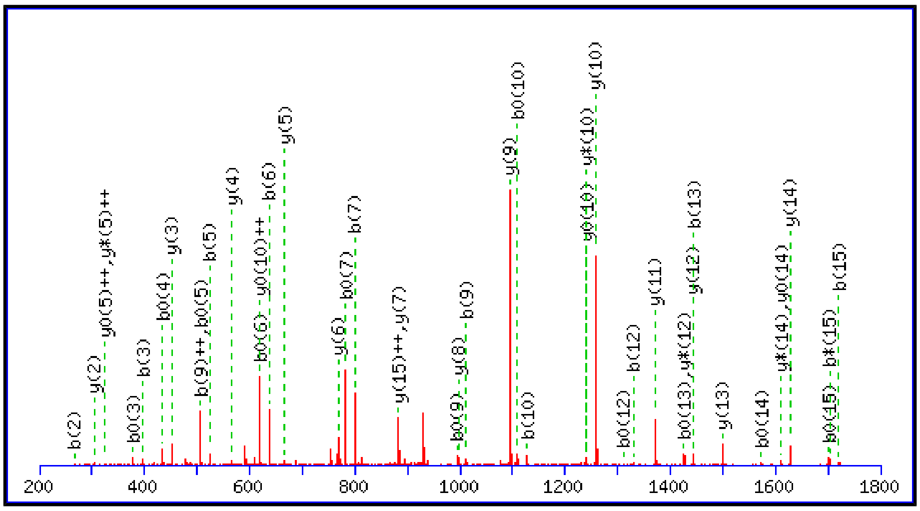
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEGAIYPDNTTDFQR**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

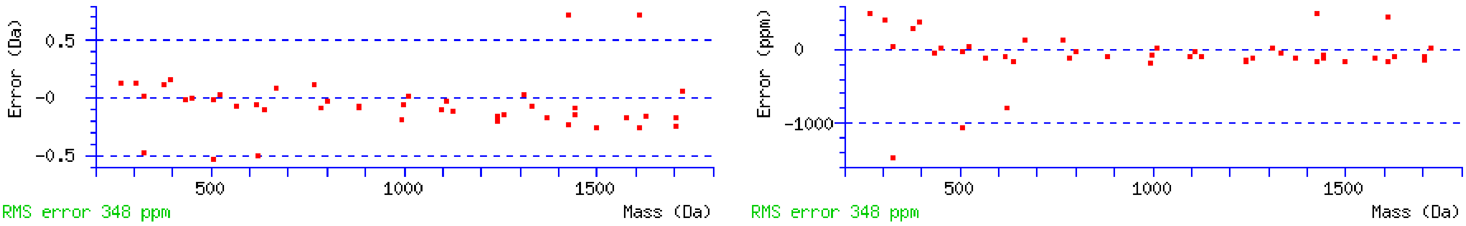
Match to Query 11269: 1893.811308 from(947.912930,2+) intensity(113209.7891) rtinseconds(789) scans(1878) index(4266)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum1635_scans__1878
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1893.8017
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Q15 : Deamidated (NQ)
Ions Score: 82 **Expect:** 4.5e-007
Matches : 45/156 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	130.0499	65.5286			112.0393	56.5233	E							16
2	**267.1088**	134.0580			249.0982	125.0527	H	1765.7664	883.3868	1748.7398	874.8736	1747.7558	874.3815	15
3	**396.1514**	198.5793			378.1408	189.5740	E	***1628.7075***	814.8574	1611.6809	806.3441	1610.6969	805.8521	14
4	453.1728	227.0901			435.1623	218.0848	G	***1499.6649***	750.3361	1482.6383	741.8228	1481.6543	741.3308	13
5	**524.2100**	262.6086			506.1994	253.6033	A	***1442.6434***	721.8253	1425.6169	713.3121	1424.6329	712.8201	12
6	**637.2940**	319.1506			619.2835	310.1454	I	***1371.6063***	686.3068	1354.5798	677.7935	1353.5957	677.3015	11
7	**800.3573**	400.6823			782.3468	391.6770	Y	***1258.5222***	629.7648	1241.4957	621.2515	1240.5117	620.7595	10
8	897.4101	449.2087			879.3995	440.2034	P	***1095.4589***	548.2331	1078.4324	539.7198	1077.4483	539.2278	9
9	**1012.4371**	506.7222			994.4265	497.7169	D	***998.4061***	499.7067	981.3796	491.1934	980.3956	490.7014	8
10	**1127.4640**	564.2356	1110.4374	555.7224	1109.4534	555.2304	N	***883.3792***	442.1932	866.3527	433.6800	865.3686	433.1880	7
11	1228.5117	614.7595	1211.4851	606.2462	1210.5011	605.7542	T	***768.3523***	384.6798	751.3257	376.1665	750.3417	375.6745	6
12	**1329.5594**	665.2833	1312.5328	656.7700	1311.5488	656.2780	T	***667.3046***	334.1559	650.2780	325.6427	649.2940	325.1506	5
13	**1444.5863**	722.7968	1427.5597	714.2835	1426.5757	713.7915	D	***566.2569***	283.6321	549.2304	275.1188	548.2463	274.6268	4
14	1591.6547	796.3310	1574.6282	787.8177	1573.6441	787.3257	F	***451.2300***	226.1186	434.2034	217.6053			3
15	**1720.6973**	860.8523	1703.6708	852.3390	1702.6867	851.8470	Q	***304.1615***	152.5844	287.1350	144.0711			2
16							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.6	1893.8017	0.0096	EHEGAIYPDNTTDFQR
7.5	1892.8107	1.0007	CYKAEMQALFNDMEK
1.4	1893.8122	-0.0009	ELARERENMDTDDER

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

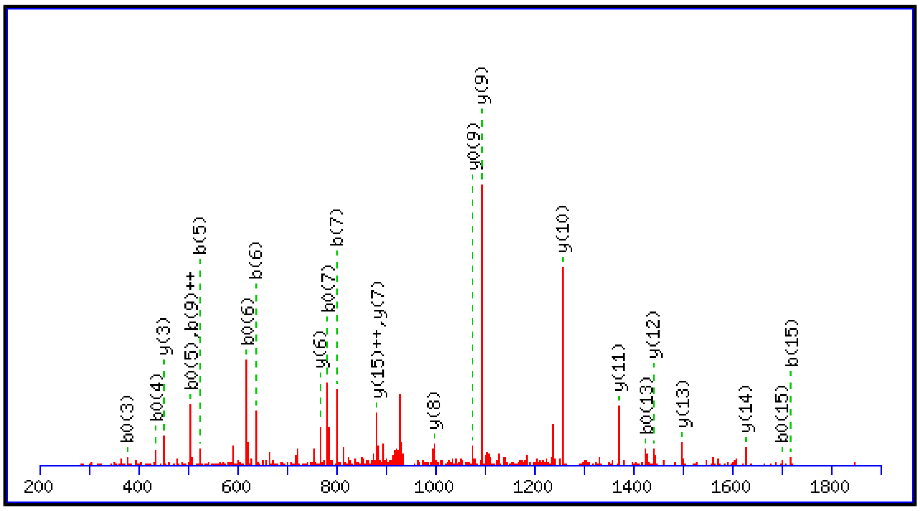
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEGAIYPDNTTDFQR**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

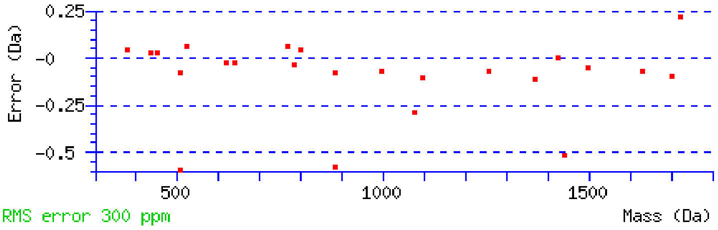
Match to Query 11203: 1892.826368 from(947.420460,2+) intensity(7358.4902) rtinseconds(771) scans(1727) index(3676)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum1452_scans__1727
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

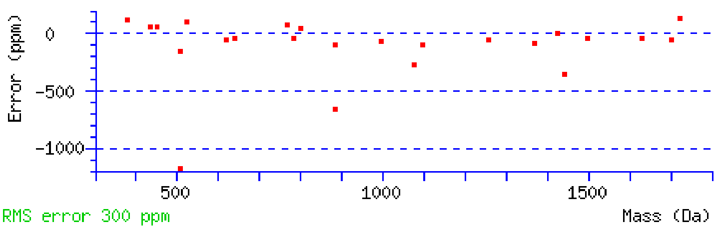
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1892.8177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 77 **Expect:** 1.7e-006
Matches : 24/156 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	130.0499	65.5286			112.0393	56.5233	E							16
2	267.1088	134.0580			249.0982	125.0527	H	1764.7824	882.8948	1747.7558	874.3815	1746.7718	873.8895	15
3	396.1514	198.5793			378.1408	189.5740	E	***1627.7235***	814.3654	1610.6969	805.8521	1609.7129	805.3601	14
4	453.1728	227.0901			435.1623	218.0848	G	***1498.6809***	749.8441	1481.6543	741.3308	1480.6703	740.8388	13
5	**524.2100**	262.6086			506.1994	253.6033	A	***1441.6594***	721.3333	1424.6329	712.8201	1423.6488	712.3281	12
6	**637.2940**	319.1506			619.2835	310.1454	I	***1370.6223***	685.8148	1353.5957	677.3015	1352.6117	676.8095	11
7	**800.3573**	400.6823			782.3468	391.6770	Y	***1257.5382***	629.2728	1240.5117	620.7595	1239.5277	620.2675	10
8	897.4101	449.2087			879.3995	440.2034	P	***1094.4749***	547.7411	1077.4483	539.2278	1076.4643	538.7358	9
9	1012.4371	506.7222			994.4265	497.7169	D	***997.4221***	499.2147	980.3956	490.7014	979.4116	490.2094	8
10	1127.4640	564.2356	1110.4374	555.7224	1109.4534	555.2304	N	***882.3952***	441.7012	865.3686	433.1880	864.3846	432.6959	7
11	1228.5117	614.7595	1211.4851	606.2462	1210.5011	605.7542	T	***767.3682***	384.1878	750.3417	375.6745	749.3577	375.1825	6
12	1329.5594	665.2833	1312.5328	656.7700	1311.5488	656.2780	T	666.3206	333.6639	649.2940	325.1506	648.3100	324.6586	5
13	1444.5863	722.7968	1427.5597	714.2835	1426.5757	713.7915	D	565.2729	283.1401	548.2463	274.6268	547.2623	274.1348	4
14	1591.6547	796.3310	1574.6282	787.8177	1573.6441	787.3257	F	***450.2459***	225.6266	433.2194	217.1133			3
15	**1719.7133**	860.3603	1702.6867	851.8470	1701.7027	851.3550	Q	303.1775	152.0924	286.1510	143.5791			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.3	1892.8177	0.0087	EHEGAIYPDNTTDFQR	Deamidated N10 99.76%
51.1	1892.8177	0.0087	EHEGAIYPDNTTDFQR	Deamidated Q15 0.24%
6.4	1892.8349	-0.0086	HQEVQDELEFITEKM	
2.5	1891.8291	0.9972	SNEQLLPAMDLMDDER	
2.5	1891.8291	0.9972	SNEQLLPAMDLMDDER	

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

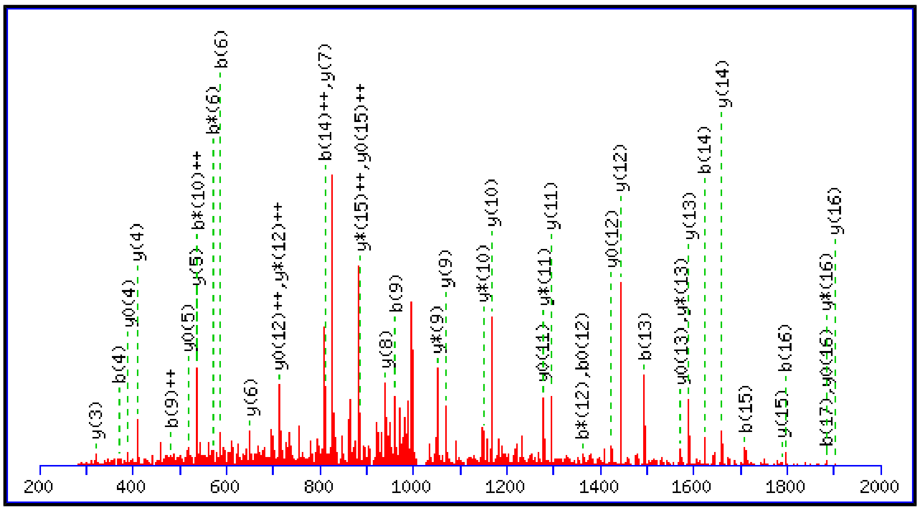
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQAFFQVQECNKSSSK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

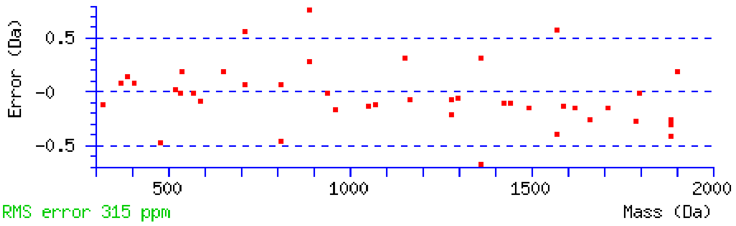
Match to Query 12850: 2028.963888 from(1015.489220,2+) intensity(39348.0586) rtinseconds(1412) scans(3534) index(2640)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum2984_scans__3534
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

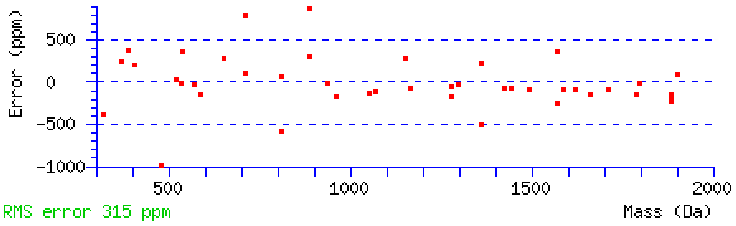
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2028.9575
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 64 **Expect:** 8e-005
Matches : 43/176 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							18
2	129.0659	65.0366					G	1958.9277	979.9675	1941.9011	971.4542	1940.9171	970.9622	17
3	242.1499	121.5786					L	***1901.9062***	951.4567	1884.8796	942.9435	1883.8956	942.4515	16
4	**370.2085**	185.6079	353.1819	177.0946			Q	***1788.8221***	894.9147	1771.7956	886.4014	1770.8116	885.9094	15
5	441.2456	221.1264	424.2191	212.6132			A	***1660.7635***	830.8854	1643.7370	822.3721	1642.7530	821.8801	14
6	**588.3140**	294.6607	571.2875	286.1474			F	***1589.7264***	795.3669	1572.6999	786.8536	1571.7159	786.3616	13
7	735.3824	368.1949	718.3559	359.6816			F	***1442.6580***	721.8326	1425.6315	713.3194	1424.6475	712.8274	12
8	863.4410	432.2241	846.4145	423.7109			Q	***1295.5896***	648.2984	1278.5631	639.7852	1277.5790	639.2932	11
9	**962.5094**	481.7584	945.4829	473.2451			V	***1167.5310***	584.2692	1150.5045	575.7559	1149.5205	575.2639	10
10	1090.5680	545.7876	1073.5415	537.2744			Q	***1068.4626***	534.7349	1051.4361	526.2217	1050.4520	525.7297	9
11	1219.6106	610.3089	1202.5841	601.7957	1201.6000	601.3037	E	***940.4040***	470.7057	923.3775	462.1924	922.3935	461.7004	8
12	1379.6413	690.3243	1362.6147	681.8110	1361.6307	681.3190	C	***811.3614***	406.1844	794.3349	397.6711	793.3509	397.1791	7
13	**1494.6682**	747.8377	1477.6416	739.3245	1476.6576	738.8325	N	***651.3308***	326.1690	634.3042	317.6558	633.3202	317.1638	6
14	**1622.7632**	811.8852	1605.7366	803.3719	1604.7526	802.8799	K	***536.3039***	268.6556	519.2773	260.1423	518.2933	259.6503	5
15	**1709.7952**	855.4012	1692.7686	846.8880	1691.7846	846.3959	S	***408.2089***	204.6081	391.1823	196.0948	390.1983	195.6028	4
16	**1796.8272**	898.9172	1779.8007	890.4040	1778.8166	889.9120	S	***321.1769***	161.0921	304.1503	152.5788	303.1663	152.0868	3
17	**1883.8592**	942.4333	1866.8327	933.9200	1865.8487	933.4280	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.4	2028.9575	0.0064	AGLQAFFQVQECNKSSSK	Deamidated N13 96.03%
50.5	2028.9575	0.0064	AGLQAFFQVQECNKSSSK	Deamidated Q10 3.88%
34.1	2028.9575	0.0064	AGLQAFFQVQECNKSSSK	Deamidated Q8 0.09%
17.6	2028.9575	0.0064	AGLQAFFQVQECNKSSSK	Deamidated Q4 0.00%
3.5	2028.9613	0.0026	AGQGLQNGHEDGPAALAHRK	
3.4	2028.9648	-0.0009	IKAKPRMDQYFNQMEK	
3.4	2028.9648	-0.0009	LKAKPRMDQYFNQMEK	
3.3	2028.9673	-0.0034	HSNLMLEDLDKSQEEIK	
3.0	2028.9680	-0.0041	DLLQEEDFYILDQGGFK	
3.0	2027.9557	1.0082	NKAKPRMDQYFNQMEK	

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

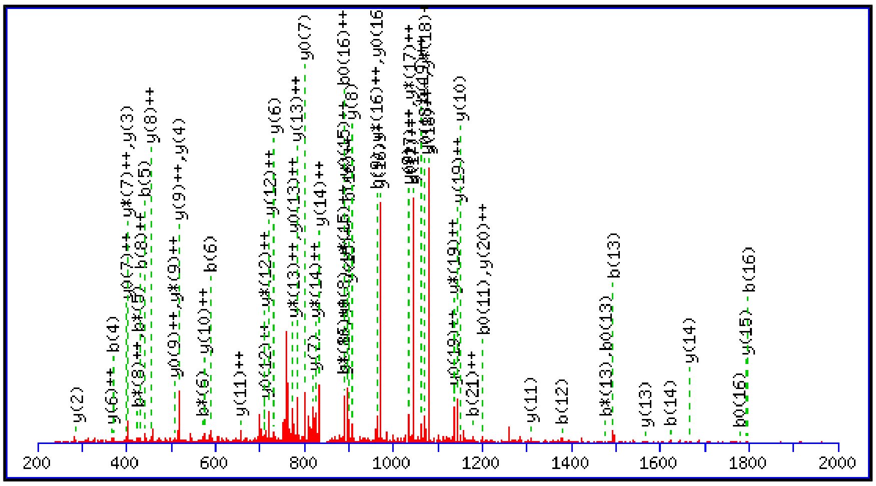
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGLQAFFQVQECNKSSSKDNIR**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

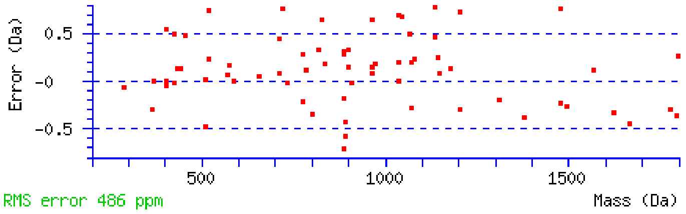
Match to Query 21818: 2527.220292 from(843.414040,3+) intensity(52739.7734) rtinseconds(1394) scans(3204) index(753)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum2745_scans__3204
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

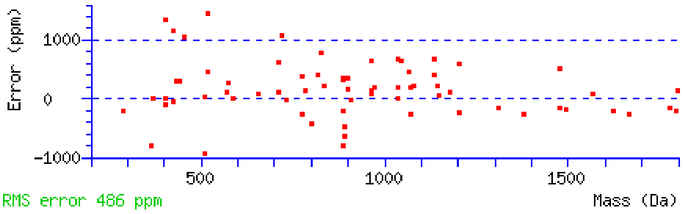
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2527.2125
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00087
Matches : 69/220 fragment ions using 148 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							22
2	129.0659	65.0366					G	2457.1827	1229.0950	2440.1561	1220.5817	2439.1721	1220.0897	21
3	242.1499	121.5786					L	2400.1612	1200.5843	2383.1347	1192.0710	2382.1507	1191.5790	20
4	**370.2085**	185.6079	353.1819	177.0946			Q	2287.0772	1144.0422	2270.0506	1135.5289	2269.0666	1135.0369	19
5	**441.2456**	221.1264	424.2191	212.6132			A	2159.0186	1080.0129	2141.9920	1071.4997	2141.0080	1071.0077	18
6	**588.3140**	294.6607	571.2875	286.1474			F	2087.9815	1044.4944	2070.9549	1035.9811	2069.9709	1035.4891	17
7	735.3824	368.1949	718.3559	359.6816			F	1940.9131	970.9602	1923.8865	962.4469	1922.9025	961.9549	16
8	863.4410	432.2241	846.4145	423.7109			Q	***1793.8447***	897.4260	1776.8181	888.9127	1775.8341	888.4207	15
9	**962.5094**	481.7584	945.4829	473.2451			V	***1665.7861***	833.3967	1648.7595	824.8834	1647.7755	824.3914	14
10	1090.5680	545.7876	1073.5415	537.2744			Q	***1566.7177***	783.8625	1549.6911	775.3492	1548.7071	774.8572	13
11	1219.6106	610.3089	1202.5841	601.7957	1201.6000	601.3037	E	1438.6591	719.8332	1421.6325	711.3199	1420.6485	710.8279	12
12	**1379.6413**	690.3243	1362.6147	681.8110	1361.6307	681.3190	C	***1309.6165***	655.3119	1292.5899	646.7986	1291.6059	646.3066	11
13	**1494.6682**	747.8377	1477.6416	739.3245	1476.6576	738.8325	N	***1149.5858***	575.2966	1132.5593	566.7833	1131.5753	566.2913	10
14	**1622.7632**	811.8852	1605.7366	803.3719	1604.7526	802.8799	K	***1034.5589***	517.7831	1017.5323	509.2698	1016.5483	508.7778	9
15	1709.7952	855.4012	1692.7686	846.8880	1691.7846	846.3959	S	***906.4639***	453.7356	889.4374	445.2223	888.4534	444.7303	8
16	**1796.8272**	898.9172	1779.8007	890.4040	1778.8166	889.9120	S	***819.4319***	410.2196	802.4054	401.7063	801.4213	401.2143	7
17	1883.8592	942.4333	1866.8327	933.9200	1865.8487	933.4280	S	***732.3999***	366.7036	715.3733	358.1903	714.3893	357.6983	6
18	2011.9542	1006.4807	1994.9277	997.9675	1993.9436	997.4755	K	645.3678	323.1876	628.3413	314.6743	627.3573	314.1823	5
19	2126.9811	1063.9942	2109.9546	1055.4809	2108.9706	1054.9889	D	***517.2729***	259.1401	500.2463	250.6268	499.2623	250.1348	4
20	2241.0241	1121.0157	2223.9975	1112.5024	2223.0135	1112.0104	N	***402.2459***	201.6266	385.2194	193.1133			3
21	2354.1081	1177.5577	2337.0816	1169.0444	2336.0976	1168.5524	I	***288.2030***	144.6051	271.1765	136.0919			2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.6	2527.2125	0.0078	AGLQAFFQVQECNKSSSKDNIR	Deamidated N13 54.73%
50.7	2527.2125	0.0078	AGLQAFFQVQECNKSSSKDNIR	Deamidated Q10 22.14%
48.3	2527.2125	0.0078	AGLQAFFQVQECNKSSSKDNIR	Deamidated Q8 12.74%
46.7	2527.2125	0.0078	AGLQAFFQVQECNKSSSKDNIR	Deamidated N20 8.88%
46.1	2526.2285	0.9918	AGLQAFFQVQECNKSSSKDNIR	
39.1	2527.2125	0.0078	AGLQAFFQVQECNKSSSKDNIR	Deamidated Q4 1.51%
4.8	2526.2141	1.0062	NMQAKSPPPMNLGMNNRKPDLR	
3.3	2525.2180	2.0023	GVQSPNQSEMALVTINHIANTER	
3.2	2527.2278	-0.0075	LAFSADEFPKQMQGRSFAGLDGR	
2.5	2525.2115	2.0088	QNEHNCVKLVPRQSMPSLSQR	

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

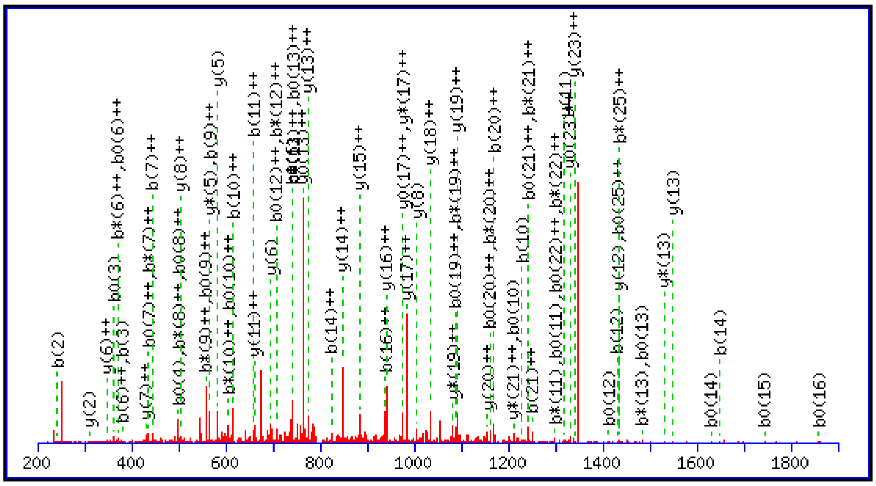
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELHHLQEQNVSNAFLDKGEFYIGSKYK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

Match to Query 27384: 3194.577416 from(799.651630,4+) intensity(44757.7930) rtinseconds(1514) scans(3750) index(14490)
Title: 111019_Est_MI_YP_G_03Spectrum3228_scans__3750
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

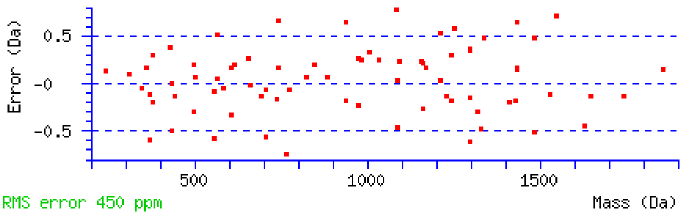
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

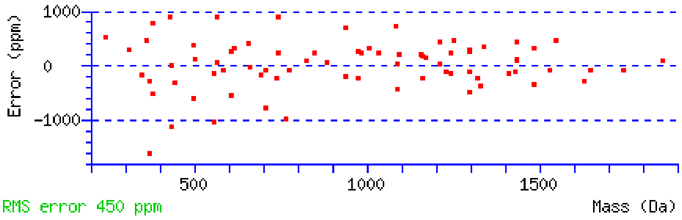


Monoisotopic mass of neutral peptide Mr(calc): 3194.5672
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.0013
Matches : 78/296 fragment ions using 120 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**27**
2	**243.1339**	122.0706			225.1234	113.0653	**L**	3066.5320	1533.7696	3049.5054	1525.2563	3048.5214	1524.7643	**26**
3	**380.1928**	190.6001			362.1823	181.5948	**H**	2953.4479	1477.2276	2936.4214	1468.7143	2935.4373	1468.2223	**25**
4	517.2518	259.1295			499.2412	250.1242	**H**	2816.3890	1408.6981	2799.3624	1400.1849	2798.3784	1399.6928	**24**
5	630.3358	315.6715			612.3253	306.6663	**L**	2679.3301	1340.1687	2662.3035	1331.6554	2661.3195	1331.1634	**23**
6	758.3944	**379.7008**	741.3678	371.1876	740.3838	370.6956	**Q**	2566.2460	1283.6266	2549.2195	1275.1134	2548.2354	1274.6214	**22**
7	887.4370	**444.2221**	870.4104	435.7089	869.4264	435.2169	**E**	2438.1874	1219.5974	2421.1609	1211.0841	2420.1769	1210.5921	**21**
8	1015.4956	508.2514	998.4690	499.7381	997.4850	499.2461	**Q**	2309.1448	1155.0761	2292.1183	1146.5628	2291.1343	1146.0708	**20**
9	1130.5225	**565.7649**	1113.4960	557.2516	1112.5119	556.7596	**N**	2181.0863	1091.0468	2164.0597	1082.5335	2163.0757	1082.0415	**19**
10	**1229.5909**	**615.2991**	1212.5644	606.7858	1211.5804	606.2938	**V**	2066.0593	1033.5333	2049.0328	1025.0200	2048.0488	1024.5280	**18**
11	1316.6230	**658.8151**	1299.5964	650.3018	1298.6124	649.8098	**S**	1966.9909	983.9991	1949.9644	975.4858	1948.9803	974.9938	**17**
12	**1430.6659**	715.8366	1413.6393	707.3233	1412.6553	706.8313	**N**	1879.9589	940.4831	1862.9323	931.9698	1861.9483	931.4778	**16**
13	1501.7030	751.3551	1484.6764	742.8419	1483.6924	742.3499	**A**	1765.9160	883.4616	1748.8894	874.9483	1747.9054	874.4563	**15**
14	**1648.7714**	**824.8893**	1631.7449	816.3761	1630.7608	815.8841	**F**	1694.8788	847.9431	1677.8523	839.4298	1676.8683	838.9378	**14**
15	1761.8555	881.4314	1744.8289	872.9181	1743.8449	872.4261	**L**	**1547.8104**	774.4088	1530.7839	765.8956	1529.7999	765.4036	**13**
16	1876.8824	**938.9448**	1859.8559	930.4316	1858.8719	929.9396	**D**	**1434.7264**	717.8668	1417.6998	709.3535	1416.7158	708.8615	**12**
17	2004.9774	1002.9923	1987.9508	994.4791	1986.9668	993.9870	**K**	**1319.6994**	660.3533	1302.6729	651.8401	1301.6889	651.3481	**11**
18	2061.9988	1031.5031	2044.9723	1022.9898	2043.9883	1022.4978	**G**	1191.6045	596.3059	1174.5779	587.7926	1173.5939	587.3006	**10**
19	2191.0414	1096.0244	2174.0149	1087.5111	2173.0309	1087.0191	**E**	1134.5830	567.7951	1117.5564	559.2819	1116.5724	558.7898	**9**
20	2338.1099	**1169.5586**	2321.0833	1161.0453	2320.0993	1160.5533	**F**	**1005.5404**	503.2738	988.5138	494.7606	987.5298	494.2686	**8**
21	2501.1732	**1251.0902**	2484.1466	1242.5770	2483.1626	1242.0849	**Y**	858.4720	429.7396	841.4454	421.2264	840.4614	420.7343	**7**
22	2614.2572	1307.6323	2597.2307	1299.1190	2596.2467	1298.6270	**I**	**695.4087**	348.2080	678.3821	339.6947	677.3981	339.2027	**6**
23	2671.2787	1336.1430	2654.2522	1327.6297	2653.2681	1327.1377	**G**	**582.3246**	291.6659	565.2980	283.1527	564.3140	282.6606	**5**

24	2758.3107	1379.6590	2741.2842	1371.1457	2740.3002	1370.6537	**S**	525.3031	263.1552	508.2766	254.6419	507.2926	254.1499	**4**
25	2886.4057	1443.7065	2869.3792	1435.1932	2868.3951	1434.7012	**K**	438.2711	219.6392	421.2445	211.1259			**3**
26	3049.4690	1525.2382	3032.4425	1516.7249	3031.4585	1516.2329	**Y**	**310.1761**	155.5917	293.1496	147.0784			**2**
27							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.1	3194.5672	0.0102	ELHHLQEQNVSNAFLDKGEFYIGSKYK	Deamidated N9 38.69%
52.3	3194.5672	0.0102	ELHHLQEQNVSNAFLDKGEFYIGSKYK	Deamidated Q8 32.26%
51.5	3194.5672	0.0102	ELHHLQEQNVSNAFLDKGEFYIGSKYK	Deamidated Q6 26.77%
40.8	3194.5672	0.0102	ELHHLQEQNVSNAFLDKGEFYIGSKYK	Deamidated N12 2.28%
23.3	3193.5832	0.9942	ELHHLQEQNVSNAFLDKGEFYIGSKYK	
9.5	3192.5662	2.0112	VLWTDDLAPQECPHALWLQRKGQESSK	
6.9	3193.5700	1.0074	AQGSLSPPLADEMPTLPEAKIGEPTEGSINK	
5.3	3192.5689	2.0085	TPSSQPLWLTGMPGTSVPYLLNFVQTSPR	
5.1	3192.5714	2.0061	SINYSKIDDFPNELEKLISQIQPEVDR	
5.0	3194.5906	-0.0132	AVTYHNWRHGFNVGQTMFTLLMTGRLK	

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

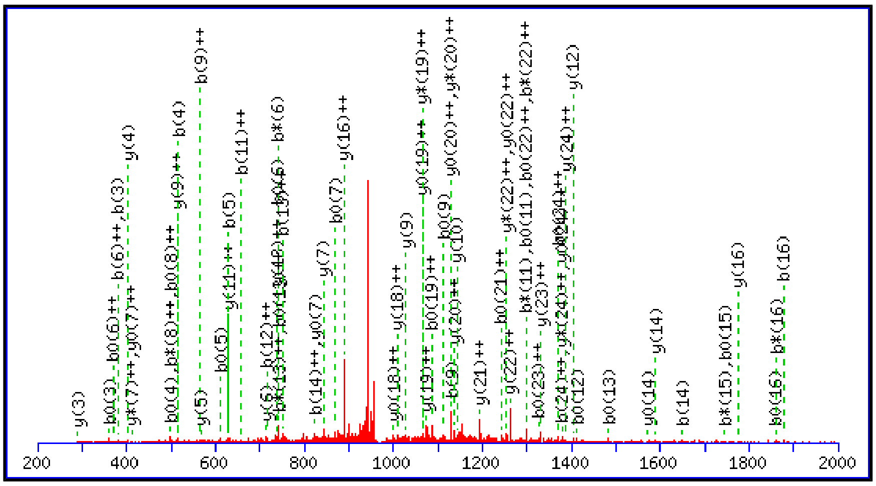
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELHHLQEQNVSNAFLDKGEFYIGSK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

Match to Query 26778: 2905.410732 from(969.477520,3+) intensity(24470.9688) rtinseconds(2289) scans(5724) index(15361)
Title: 111019_Est_MI_YP_G_04Spectrum4942_scans__5724
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

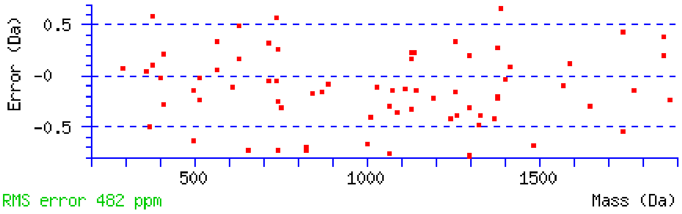
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

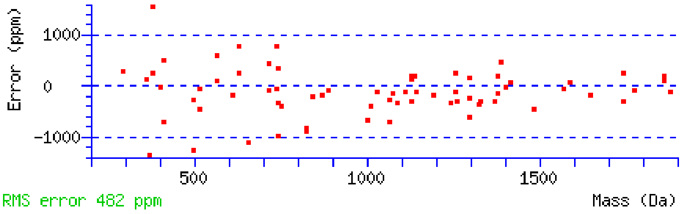


Monoisotopic mass of neutral peptide Mr(calc): 2904.3930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.022
Matches : 73/276 fragment ions using 168 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							25
2	243.1339	122.0706			225.1234	113.0653	L	2776.3577	1388.6825	2759.3311	1380.1692	2758.3471	1379.6772	24
3	**380.1928**	190.6001			362.1823	181.5948	H	2663.2736	1332.1404	2646.2471	1323.6272	2645.2631	1323.1352	23
4	**517.2518**	259.1295			499.2412	250.1242	H	2526.2147	1263.6110	2509.1882	1255.0977	2508.2041	1254.6057	22
5	**630.3358**	315.6715			612.3253	306.6663	L	2389.1558	1195.0815	2372.1292	1186.5683	2371.1452	1186.0763	21
6	758.3944	**379.7008**	741.3678	371.1876	740.3838	370.6956	Q	2276.0717	1138.5395	2259.0452	1130.0262	2258.0612	1129.5342	20
7	887.4370	444.2221	870.4104	435.7089	869.4264	435.2169	E	2148.0132	1074.5102	2130.9866	1065.9969	2130.0026	1065.5049	19
8	1015.4956	508.2514	998.4690	499.7381	997.4850	499.2461	Q	2018.9706	1009.9889	2001.9440	1001.4756	2000.9600	1000.9836	18
9	**1130.5225**	**565.7649**	1113.4960	557.2516	1112.5119	556.7596	N	1890.9120	945.9596	1873.8854	937.4464	1872.9014	936.9543	17
10	1229.5909	615.2991	1212.5644	606.7858	1211.5804	606.2938	V	***1775.8850***	888.4462	1758.8585	879.9329	1757.8745	879.4409	16
11	1316.6230	**658.8151**	1299.5964	650.3018	1298.6124	649.8098	S	1676.8166	838.9120	1659.7901	830.3987	1658.8061	829.9067	15
12	1431.6499	**716.3286**	1414.6233	707.8153	1413.6393	707.3233	N	***1589.7846***	795.3959	1572.7581	786.8827	1571.7740	786.3907	14
13	1502.6870	**751.8471**	1485.6605	743.3339	1484.6764	742.8419	A	1474.7577	737.8825	1457.7311	729.3692	1456.7471	728.8772	13
14	**1649.7554**	**825.3814**	1632.7289	816.8681	1631.7449	816.3761	F	***1403.7205***	702.3639	1386.6940	693.8506	1385.7100	693.3586	12
15	1762.8395	881.9234	1745.8129	873.4101	1744.8289	872.9181	L	1256.6521	628.8297	1239.6256	620.3164	1238.6416	619.8244	11
16	**1877.8664**	939.4369	1860.8399	930.9236	1859.8559	930.4316	D	***1143.5681***	572.2877	1126.5415	563.7744	1125.5575	563.2824	10
17	2005.9614	1003.4843	1988.9348	994.9711	1987.9508	994.4791	K	***1028.5411***	514.7742	1011.5146	506.2609	1010.5306	505.7689	9
18	2062.9829	1031.9951	2045.9563	1023.4818	2044.9723	1022.9898	G	900.4462	450.7267	883.4196	442.2134	882.4356	441.7214	8
19	2192.0255	1096.5164	2174.9989	1088.0031	2174.0149	1087.5111	E	***843.4247***	422.2160	826.3981	413.7027	825.4141	413.2107	7
20	2339.0939	1170.0506	2322.0673	1161.5373	2321.0833	1161.0453	F	***714.3821***	357.6947	697.3556	349.1814	696.3715	348.6894	6
21	2502.1572	1251.5822	2485.1306	1243.0690	2484.1466	1242.5770	Y	***567.3137***	284.1605	550.2871	275.6472	549.3031	275.1552	5
22	2615.2413	1308.1243	2598.2147	1299.6110	2597.2307	1299.1190	I	***404.2504***	202.6288	387.2238	194.1155	386.2398	193.6235	4

23	2672.2627	1336.6350	2655.2362	1328.1217	2654.2522	1327.6297	**G**	***291.1663***	146.0868	274.1397	137.5735	273.1557	137.0815	**3**
24	2759.2948	**1380.1510**	2742.2682	1371.6377	2741.2842	1371.1457	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.0	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated N9, N12 23.60%
41.0	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q8, N12 23.60%
39.4	2903.4090	2.0018	ELHHLQEQNVSNAFLDKGEFYIGSK	
39.3	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q6, N12 15.92%
39.2	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q8, N9 15.66%
38.6	2903.4090	2.0018	ELHHLQEQNVSNAFLDKGEFYIGSK	
38.6	2903.4090	2.0018	ELHHLQEQNVSNAFLDKGEFYIGSK	
37.5	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q6, N9 10.61%
37.5	2904.3930	1.0178	ELHHLQEQNVSNAFLDKGEFYIGSK	Deamidated Q6, Q8 10.61%
31.9	2903.4090	2.0018	ELHHLQEQNVSNAFLDKGEFYIGSK	

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

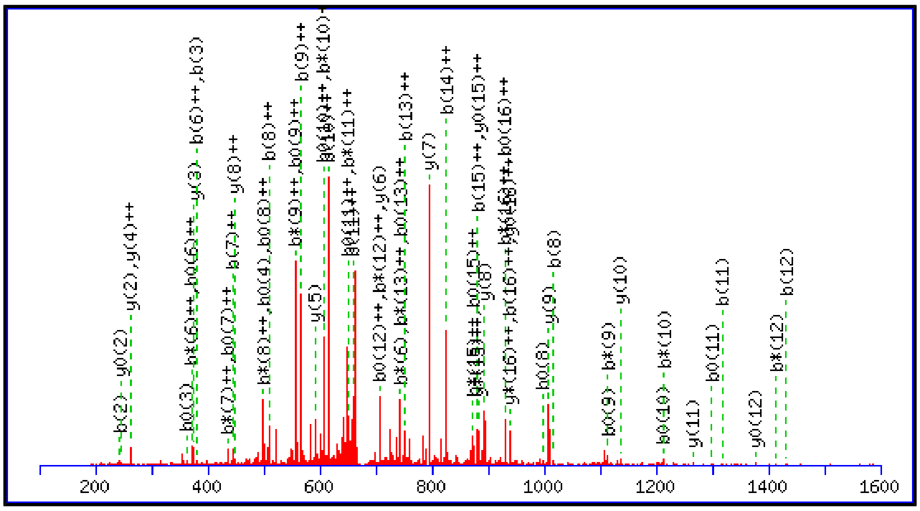
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELHHLQEQNVSNAFLDK**
Found in **E9PFZ2** in **con_Xuniprot_HUMAN3**, E9PFZ2_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=2 SV=1

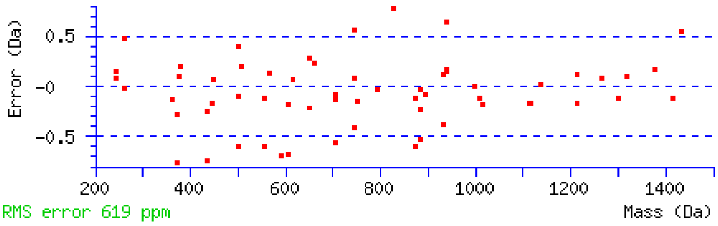
Match to Query 12756: 2022.970422 from(675.330750,3+) intensity(0.0000) rtinseconds(1035) scans(2449) index(1230)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum2097_scans__2449
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

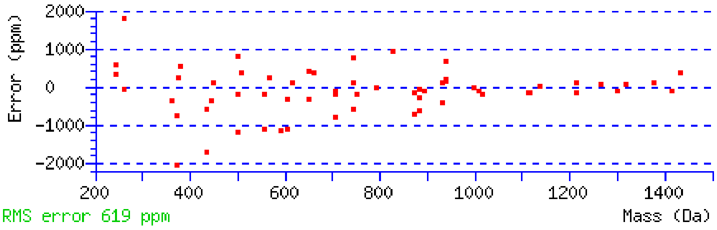
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2022.9646
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.024
Matches : 62/180 fragment ions using 95 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							17
2	**243.1339**	122.0706			225.1234	113.0653	L	1894.9294	947.9683	1877.9028	939.4550	1876.9188	938.9630	16
3	**380.1928**	190.6001			362.1823	181.5948	H	1781.8453	891.4263	1764.8188	882.9130	1763.8347	882.4210	15
4	517.2518	259.1295			499.2412	250.1242	H	1644.7864	822.8968	1627.7598	814.3836	1626.7758	813.8916	14
5	630.3358	315.6715			612.3253	306.6663	L	1507.7275	754.3674	1490.7009	745.8541	1489.7169	745.3621	13
6	759.3784	***380.1928***	742.3519	371.6796	741.3678	371.1876	Q	1394.6434	697.8253	1377.6169	689.3121	1376.6329	688.8201	12
7	888.4210	***444.7141***	871.3945	436.2009	870.4104	435.7089	E	**1265.6008**	633.3040	1248.5743	624.7908	1247.5903	624.2988	11
8	**1016.4796**	***508.7434***	999.4530	500.2302	998.4690	499.7381	Q	**1136.5582**	568.7828	1119.5317	560.2695	1118.5477	559.7775	10
9	1131.5065	***566.2569***	1114.4800	557.7436	1113.4960	557.2516	N	**1008.4997**	504.7535	991.4731	496.2402	990.4891	495.7482	9
10	1230.5749	***615.7911***	1213.5484	607.2778	1212.5644	606.7858	V	**893.4727**	447.2400	876.4462	438.7267	875.4621	438.2347	8
11	**1317.6070**	***659.3071***	1300.5804	650.7938	1299.5964	650.3018	S	**794.4043**	397.7058	777.3777	389.1925	776.3937	388.7005	7
12	**1431.6499**	716.3286	1414.6233	707.8153	1413.6393	707.3233	N	**707.3723**	354.1898	690.3457	345.6765	689.3617	345.1845	6
13	1502.6870	***751.8471***	1485.6605	743.3339	1484.6764	742.8419	A	**593.3293**	297.1683	576.3028	288.6550	575.3188	288.1630	5
14	1649.7554	***825.3814***	1632.7289	816.8681	1631.7449	816.3761	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
15	1762.8395	***881.9234***	1745.8129	873.4101	1744.8289	872.9181	L	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
16	1877.8664	***939.4369***	1860.8399	930.9236	1859.8559	930.4316	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.4	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated Q6, N9 21.97%
39.6	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated Q8, N9 18.62%
39.3	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated Q6, N12 17.25%
38.6	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated Q8, N12 14.62%
38.5	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated N9, N12 14.45%
38.1	2022.9646	0.0058	ELHHLQEQNVSNAFLDK	Deamidated Q6, Q8 13.09%
5.4	2021.9615	1.0089	LLNHIMESYIQGSQKDK	
5.3	2021.9694	1.0010	NGFDFVIDENAPVTERAK	
4.0	2021.9727	0.9977	DQQFLNLMEKLNENIR	
4.0	2021.9727	0.9977	DQQFLNLMEKLNENIR	

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

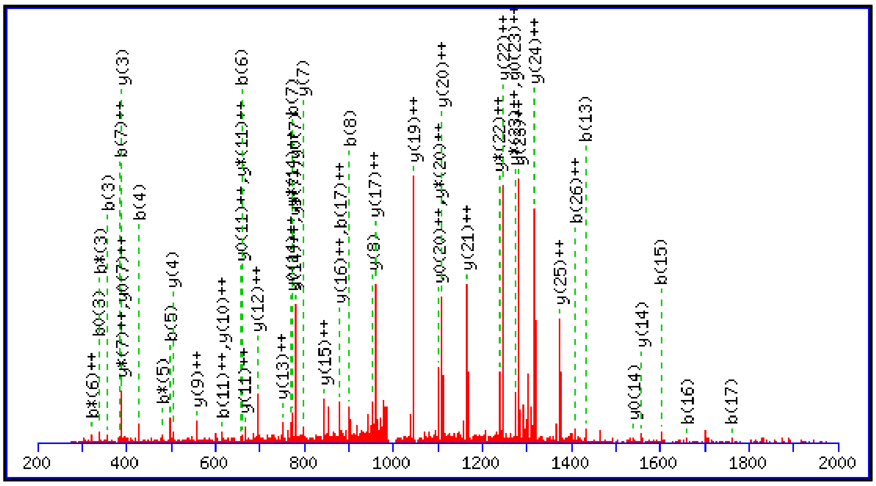
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKLAACLEGNCAEGLGTNYRGHVNITR**
Found in **C9JV37** in **con_Xuniprot_HUMAN3**, C9JV37_HUMAN Thrombin light chain (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 27203: 2989.419672 from(997.480500,3+) intensity(19859.2129) rtinseconds(1230) scans(2834) index(8272)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum2394_scans__2834
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

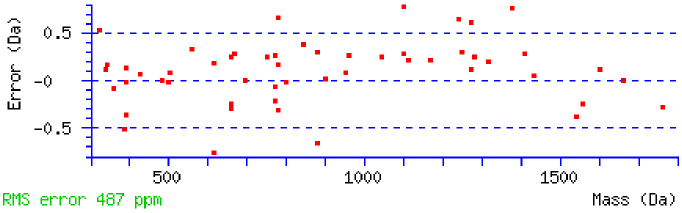
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

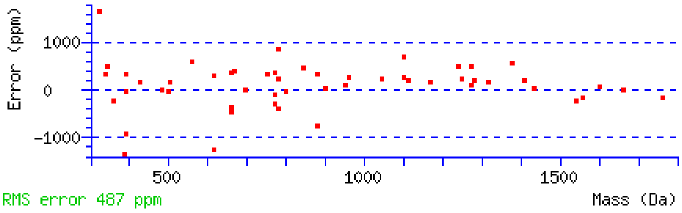


Monoisotopic mass of neutral peptide Mr(calc): 2989.4134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N24 : Deamidated (NQ)
Ions Score: 87 **Expect:** 5.4e-007
Matches : 53/308 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							27
2	244.1292	122.5682	227.1026	114.0550	226.1186	113.5629	K	2875.3938	1438.2005	2858.3672	1429.6873	2857.3832	1429.1952	26
3	**357.2132**	179.1103	340.1867	170.5970	339.2027	170.1050	L	2747.2988	1374.1530	2730.2723	1365.6398	2729.2882	1365.1478	25
4	**428.2504**	214.6288	411.2238	206.1155	410.2398	205.6235	A	2634.2147	1317.6110	2617.1882	1309.0977	2616.2042	1308.6057	24
5	**499.2875**	250.1474	482.2609	241.6341	481.2769	241.1421	A	2563.1776	1282.0925	2546.1511	1273.5792	2545.1671	1273.0872	23
6	**659.3181**	330.1627	642.2916	321.6494	641.3076	321.1574	C	2492.1405	1246.5739	2475.1140	1238.0606	2474.1300	1237.5686	22
7	**772.4022**	**386.7047**	755.3756	378.1915	754.3916	377.6994	L	2332.1099	1166.5586	2315.0833	1158.0453	2314.0993	1157.5533	21
8	**901.4448**	451.2260	884.4182	442.7128	883.4342	442.2207	E	2219.0258	1110.0165	2201.9993	1101.5033	2201.0152	1101.0113	20
9	958.4662	479.7368	941.4397	471.2235	940.4557	470.7315	G	2089.9832	1045.4952	2072.9567	1036.9820	2071.9726	1036.4900	19
10	1072.5092	536.7582	1055.4826	528.2449	1054.4986	527.7529	N	2032.9617	1016.9845	2015.9352	1008.4712	2014.9512	1007.9792	18
11	1232.5398	**616.7735**	1215.5133	608.2603	1214.5293	607.7683	C	1918.9188	959.9630	1901.8923	951.4498	1900.9083	950.9578	17
12	1303.5769	652.2921	1286.5504	643.7788	1285.5664	643.2868	A	1758.8882	879.9477	1741.8616	871.4344	1740.8776	870.9424	16
13	**1432.6195**	716.8134	1415.5930	708.3001	1414.6090	707.8081	E	1687.8511	844.4292	1670.8245	835.9159	1669.8405	835.4239	15
14	1489.6410	745.3241	1472.6144	736.8109	1471.6304	736.3189	G	**1558.8085**	779.9079	1541.7819	771.3946	1540.7979	770.9026	14
15	**1602.7251**	801.8662	1585.6985	793.3529	1584.7145	792.8609	L	1501.7870	751.3971	1484.7605	742.8839	1483.7764	742.3919	13
16	**1659.7465**	830.3769	1642.7200	821.8636	1641.7360	821.3716	G	1388.7029	694.8551	1371.6764	686.3418	1370.6924	685.8498	12
17	**1760.7942**	**880.9007**	1743.7676	872.3875	1742.7836	871.8955	T	1331.6815	666.3444	1314.6549	657.8311	1313.6709	657.3391	11
18	1874.8371	937.9222	1857.8106	929.4089	1856.8266	928.9169	N	1230.6338	615.8205	1213.6072	607.3073	1212.6232	606.8153	10
19	2037.9005	1019.4539	2020.8739	1010.9406	2019.8899	1010.4486	Y	1116.5909	558.7991	1099.5643	550.2858	1098.5803	549.7938	9
20	2194.0016	1097.5044	2176.9750	1088.9911	2175.9910	1088.4991	R	**953.5275**	477.2674	936.5010	468.7541	935.5170	468.2621	8
21	2251.0230	1126.0152	2233.9965	1117.5019	2233.0125	1117.0099	G	**797.4264**	399.2169	780.3999	390.7036	779.4159	390.2116	7
22	2388.0819	1194.5446	2371.0554	1186.0313	2370.0714	1185.5393	H	740.4050	370.7061	723.3784	362.1928	722.3944	361.7008	6
23	2487.1504	1244.0788	2470.1238	1235.5655	2469.1398	1235.0735	V	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5

24	2602.1773	1301.5923	2585.1507	1293.0790	2584.1667	1292.5870	**N**	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	**4**
25	2715.2614	1358.1343	2698.2348	1349.6210	2697.2508	1349.1290	**I**	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	**3**
26	2816.3090	**1408.6582**	2799.2825	1400.1449	2798.2985	1399.6529	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
86.9	2989.4134	0.0063	DKLAACLEGNCAEGLGTNYRGHVNITR	Deamidated N24 97.91%
70.0	2989.4134	0.0063	DKLAACLEGNCAEGLGTNYRGHVNITR	Deamidated N18 2.04%
56.5	2988.4294	0.9903	DKLAACLEGNCAEGLGTNYRGHVNITR	
54.3	2989.4134	0.0063	DKLAACLEGNCAEGLGTNYRGHVNITR	Deamidated N10 0.05%
6.9	2989.4339	-0.0142	TPNMAVVGEPNGIFEQSQSELVEKETR	
4.7	2989.4049	0.0148	LKEGSLGINPSQVSKTGFVFCSDEDMK	
4.5	2988.4108	1.0089	RHNAGSNPTPPASVMGSPPSSLQEAQRGR	
4.5	2988.4108	1.0089	RHNAGSNPTPPASVMGSPPSSLQEAQRGR	
4.3	2987.4267	1.9929	RHNAGSNPTPPASVMGSPPSSLQEAQRGR	
2.9	2987.4083	2.0114	QLNDTLDAIEDGTQKVQNNIFHMWR	

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

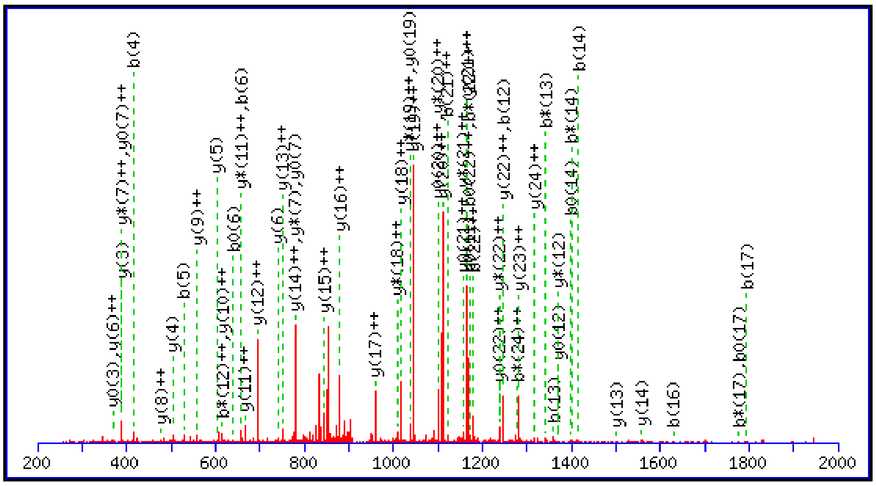
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAACLEGNCAEGLGTNYRGHVNITR**
Found in **C9JV37** in **con_Xuniprot_HUMAN3**, C9JV37_HUMAN Thrombin light chain (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 25462: 2746.298412 from(916.440080,3+) intensity(58875.9648) rtinseconds(1118) scans(2522) index(8252)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum2123_scans__2522
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

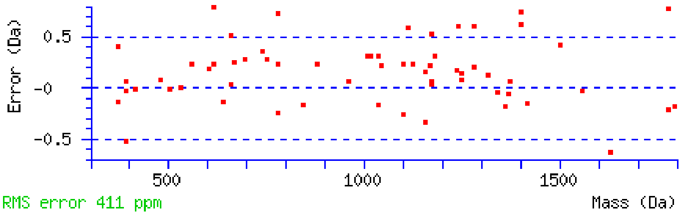
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

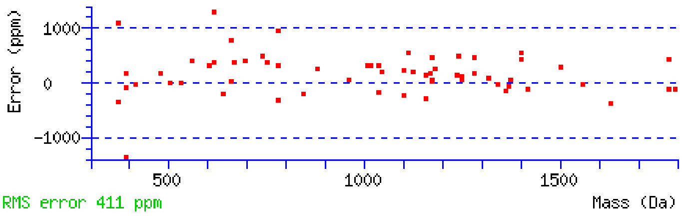


Monoisotopic mass of neutral peptide Mr(calc): 2746.2915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 70 **Expect:** 2.7e-005
Matches : 62/262 fragment ions using 151 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	185.1285	93.0679					A	2634.2147	1317.6110	2617.1882	1309.0977	2616.2042	1308.6057	24
3	256.1656	128.5864					A	2563.1776	1282.0925	2546.1511	1273.5792	2545.1671	1273.0872	23
4	**416.1962**	208.6017					C	2492.1405	1246.5739	2475.1140	1238.0606	2474.1300	1237.5686	22
5	**529.2803**	265.1438					L	2332.1099	1166.5586	2315.0833	1158.0453	2314.0993	1157.5533	21
6	**658.3229**	329.6651			640.3123	320.6598	E	2219.0258	1110.0165	2201.9993	1101.5033	2201.0152	1101.0113	20
7	715.3443	358.1758			697.3338	349.1705	G	2089.9832	1045.4952	2072.9567	1036.9820	2071.9726	1036.4900	19
8	829.3873	415.1973	812.3607	406.6840	811.3767	406.1920	N	2032.9617	1016.9845	2015.9352	1008.4712	2014.9512	1007.9792	18
9	989.4179	495.2126	972.3914	486.6993	971.4073	486.2073	C	1918.9188	959.9630	1901.8923	951.4498	1900.9083	950.9578	17
10	1060.4550	530.7312	1043.4285	522.2179	1042.4445	521.7259	A	1758.8882	879.9477	1741.8616	871.4344	1740.8776	870.9424	16
11	1189.4976	595.2524	1172.4711	586.7392	1171.4871	586.2472	E	1687.8511	844.4292	1670.8245	835.9159	1669.8405	835.4239	15
12	**1246.5191**	623.7632	1229.4925	615.2499	1228.5085	614.7579	G	**1558.8085**	779.9079	1541.7819	771.3946	1540.7979	770.9026	14
13	**1359.6031**	680.3052	1342.5766	671.7919	1341.5926	671.2999	L	**1501.7870**	751.3971	1484.7605	742.8839	1483.7764	742.3919	13
14	**1416.6246**	708.8159	1399.5981	700.3027	1398.6140	699.8107	G	1388.7029	694.8551	1371.6764	686.3418	1370.6924	685.8498	12
15	1517.6723	759.3398	1500.6457	750.8265	1499.6617	750.3345	T	1331.6815	666.3444	1314.6549	657.8311	1313.6709	657.3391	11
16	**1631.7152**	816.3612	1614.6887	807.8480	1613.7047	807.3560	N	1230.6338	615.8205	1213.6072	607.3073	1212.6232	606.8153	10
17	**1794.7785**	897.8929	1777.7520	889.3796	1776.7680	888.8876	Y	1116.5909	558.7991	1099.5643	550.2858	1098.5803	549.7938	9
18	1950.8797	975.9435	1933.8531	967.4302	1932.8691	966.9382	R	953.5275	477.2674	936.5010	468.7541	935.5170	468.2621	8
19	2007.9011	1004.4542	1990.8746	995.9409	1989.8906	995.4489	G	797.4264	399.2169	780.3999	390.7036	779.4159	390.2116	7
20	2144.9600	1072.9837	2127.9335	1064.4704	2126.9495	1063.9784	H	**740.4050**	370.7061	723.3784	362.1928	722.3944	361.7008	6
21	2244.0284	1122.5179	2227.0019	1114.0046	2226.0179	1113.5126	V	**603.3461**	302.1767	586.3195	293.6634	585.3355	293.1714	5
22	2359.0554	1180.0313	2342.0288	1171.5181	2341.0448	1171.0261	N	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	4
23	2472.1395	1236.5734	2455.1129	1228.0601	2454.1289	1227.5681	I	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	3

24	2573.1871	1287.0972	2556.1606	1278.5839	2555.1766	1278.0919	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.7	2746.2915	0.0069	LAACLEGNCAEGLGTNYRGHVNITR	Deamidated N22 93.89%
55.6	2746.2915	0.0069	LAACLEGNCAEGLGTNYRGHVNITR	Deamidated N8 3.68%
53.8	2746.2915	0.0069	LAACLEGNCAEGLGTNYRGHVNITR	Deamidated N16 2.44%
45.2	2745.3075	0.9909	LAACLEGNCAEGLGTNYRGHVNITR	
7.9	2746.2927	0.0057	EKGTNETSGLATSMLTASSSETRASSK	
6.8	2746.2882	0.0103	MNPPFSGPGRFGQIGSEGSGRAENGPK	
5.6	2746.3032	-0.0048	QQNDELTTLADEAQSLKDEIDVLR	
5.6	2746.3032	-0.0048	QQNDELTTLADEAQSLKDEIDVLR	
5.6	2746.3032	-0.0048	QQNDELTTLADEAQSLKDEIDVLR	
5.1	2746.2980	0.0004	TVTINEAESNDSGLPHLHQPRKGNM	

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

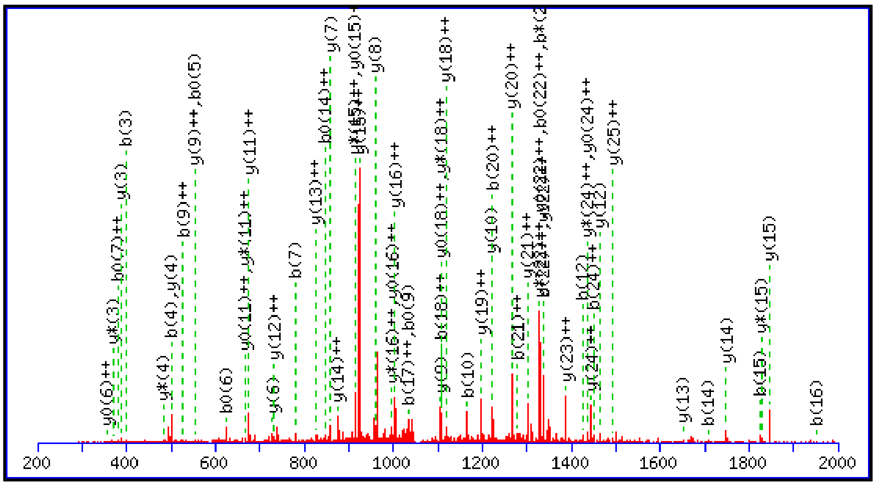
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WVLTAAHCLLYPPWDKNFTENDLLVR**
Found in **E9PIT3** in **con_Xuniprot_HUMAN3**, E9PIT3_HUMAN Thrombin light chain OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 27356: 3172.594392 from(1058.538740,3+) intensity(30926.3691) rtinseconds(2405) scans(6370) index(16235)
Title: 111019_Est_MI_YP_G_05Spectrum5455_scans__6370
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

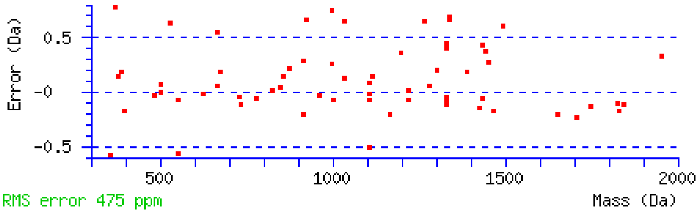
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

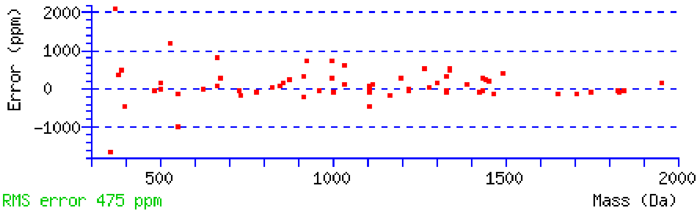


Monoisotopic mass of neutral peptide Mr(calc): 3171.5852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 59 **Expect:** 0.0003
Matches : 65/256 fragment ions using 136 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							26
2	286.1550	143.5811					V	2986.5131	1493.7602	2969.4866	1485.2469	2968.5026	1484.7549	25
3	**399.2391**	200.1232					L	2887.4447	1444.2260	2870.4182	1435.7127	2869.4342	1435.2207	24
4	**500.2867**	250.6470			482.2762	241.6417	T	2774.3607	1387.6840	2757.3341	1379.1707	2756.3501	1378.6787	23
5	571.3239	286.1656			553.3133	277.1603	A	2673.3130	1337.1601	2656.2864	1328.6469	2655.3024	1328.1548	22
6	642.3610	321.6841			624.3504	312.6788	A	2602.2759	1301.6416	2585.2493	1293.1283	2584.2653	1292.6363	21
7	**779.4199**	390.2136			761.4093	381.2083	H	2531.2388	1266.1230	2514.2122	1257.6097	2513.2282	1257.1177	20
8	939.4505	470.2289			921.4400	461.2236	C	2394.1798	1197.5936	2377.1533	1189.0803	2376.1693	1188.5883	19
9	1052.5346	***526.7709***			1034.5240	517.7657	L	2234.1492	1117.5782	2217.1226	1109.0650	2216.1386	1108.5730	18
10	**1165.6187**	583.3130			1147.6081	574.3077	L	2121.0651	1061.0362	2104.0386	1052.5229	2103.0546	1052.0309	17
11	**1328.6820**	664.8446			1310.6714	655.8394	Y	2007.9811	1004.4942	1990.9545	995.9809	1989.9705	995.4889	16
12	**1425.7348**	713.3710			1407.7242	704.3657	P	***1844.9177***	922.9625	1827.8912	914.4492	1826.9072	913.9572	15
13	1522.7875	761.8974			1504.7770	752.8921	P	***1747.8650***	874.4361	1730.8384	865.9229	1729.8544	865.4308	14
14	**1708.8668**	854.9371			1690.8563	845.9318	W	***1650.8122***	825.9097	1633.7857	817.3965	1632.8016	816.9045	13
15	**1823.8938**	912.4505			1805.8832	903.4452	D	***1464.7329***	732.8701	1447.7063	724.3568	1446.7223	723.8648	12
16	**1951.9887**	976.4980	1934.9622	967.9847	1933.9782	967.4927	K	1349.7060	675.3566	1332.6794	666.8433	1331.6954	666.3513	11
17	2067.0157	***1034.0115***	2049.9891	1025.4982	2049.0051	1025.0062	N	***1221.6110***	611.3091	1204.5844	602.7959	1203.6004	602.3039	10
18	2214.0841	***1107.5457***	2197.0575	1099.0324	2196.0735	1098.5404	F	***1106.5840***	553.7957	1089.5575	545.2824	1088.5735	544.7904	9
19	2315.1318	1158.0695	2298.1052	1149.5563	2297.1212	1149.0642	T	***959.5156***	480.2615	942.4891	471.7482	941.5051	471.2562	8
20	2444.1744	***1222.5908***	2427.1478	1214.0775	2426.1638	1213.5855	E	***858.4680***	429.7376	841.4414	421.2243	840.4574	420.7323	7
21	2558.2173	***1279.6123***	2541.1907	1271.0990	2540.2067	1270.6070	N	***729.4254***	365.2163	712.3988	356.7030	711.4148	356.2110	6
22	2673.2442	***1337.1258***	2656.2177	1328.6125	2655.2337	1328.1205	D	615.3824	308.1949	598.3559	299.6816	597.3719	299.1896	5
23	2786.3283	1393.6678	2769.3018	1385.1545	2768.3177	1384.6625	L	***500.3555***	250.6814	483.3289	242.1681			4

24	2899.4124	***1450.2098***	2882.3858	1441.6965	2881.4018	1441.2045	**L**	***387.2714***	194.1394	370.2449	185.6261			**3**
25	2998.4808	1499.7440	2981.4542	1491.2308	2980.4702	1490.7387	**V**	274.1874	137.5973	257.1608	129.0840			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.2	3171.5852	1.0092	WVLTAAHCLLYPPWDKNFTENDLLVR	Deamidated N17 85.08%
51.7	3171.5852	1.0092	WVLTAAHCLLYPPWDKNFTENDLLVR	Deamidated N21 14.92%
38.2	3170.6012	1.9932	WVLTAAHCLLYPPWDKNFTENDLLVR	
9.4	3172.5901	0.0043	SPPLGAPTSHQSAPPPVSPTVPVSSERHAER	
6.5	3171.6061	0.9883	SPPLGAPTSHQSAPPPVSPTVPVSSERHAER	
5.5	3172.5856	0.0088	TVTESRPLSVPVKAMLNISESCRSPEER	
4.6	3171.5917	1.0027	DFLIPIAWYEDRQVPGGYTVINKYQGK	
4.1	3171.6048	0.9896	LLGSNDSPASASQVAGTTDRNQLLFLPIER	
4.1	3171.6048	0.9896	LLGSNDSPASASQVAGTTDRNQLLFLPIER	
4.1	3171.6048	0.9896	LLGSNDSPASASQVAGTTDRNQLLFLPIER	

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

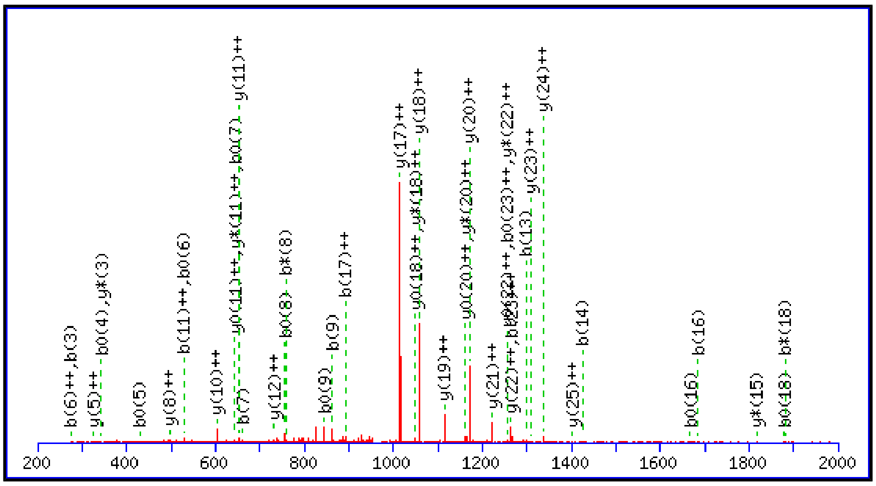
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDRGQQYQGR**
Found in **C9JV37** in **con_Xuniprot_HUMAN3**, C9JV37_HUMAN Thrombin light chain (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 26017: 2888.345502 from(963.789110,3+) intensity(63540.2383) rtinseconds(1167) scans(2747) index(25261)
Title: 111019_Est_MI_YS_G_07Spectrum2322_scans__2747
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

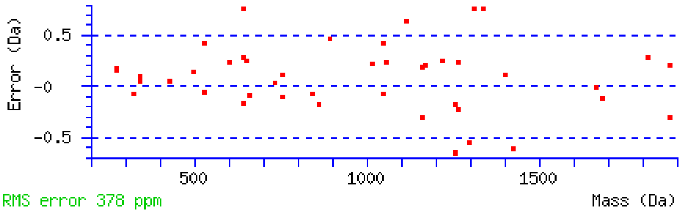
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

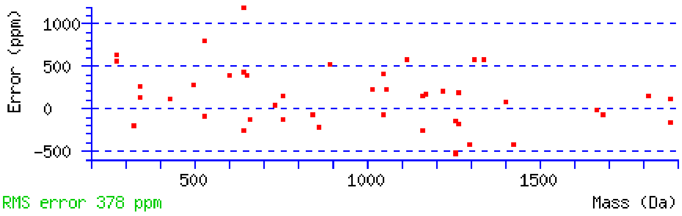


Monoisotopic mass of neutral peptide Mr(calc): 2888.3359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00044
Matches : 45/272 fragment ions using 84 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							26
2	217.0819	109.0446			199.0713	100.0393	E	2802.3111	1401.6592	2785.2846	1393.1459	2784.3006	1392.6539	25
3	**274.1034**	137.5553			256.0928	128.5500	G	2673.2686	1337.1379	2656.2420	1328.6246	2655.2580	1328.1326	24
4	361.1354	181.0713			343.1248	172.0660	S	2616.2471	1308.6272	2599.2205	1300.1139	2598.2365	1299.6219	23
5	448.1674	224.5873			430.1569	215.5821	S	2529.2151	1265.1112	2512.1885	1256.5979	2511.2045	1256.1059	22
6	547.2358	**274.1216**			529.2253	265.1163	V	2442.1830	1221.5952	2425.1565	1213.0819	2424.1725	1212.5899	21
7	**662.2628**	331.6350	645.2362	323.1218	644.2522	322.6297	N	2343.1146	1172.0609	2326.0881	1163.5477	2325.1041	1163.0557	20
8	775.3468	388.1771	758.3203	379.6638	757.3363	379.1718	L	2228.0877	1114.5475	2211.0611	1106.0342	2210.0771	1105.5422	19
9	**862.3789**	431.6931	845.3523	423.1798	844.3683	422.6878	S	2115.0036	1058.0054	2097.9771	1049.4922	2096.9931	1049.0002	18
10	959.4316	480.2195	942.4051	471.7062	941.4211	471.2142	P	2027.9716	1014.4894	2010.9450	1005.9762	2009.9610	1005.4841	17
11	1056.4844	**528.7458**	1039.4578	520.2326	1038.4738	519.7406	P	1930.9188	965.9630	1913.8923	957.4498	1912.9083	956.9578	16
12	1169.5685	585.2879	1152.5419	576.7746	1151.5579	576.2826	L	1833.8661	917.4367	1816.8395	908.9234	1815.8555	908.4314	15
13	**1298.6111**	649.8092	1281.5845	641.2959	1280.6005	640.8039	E	1720.7820	860.8946	1703.7554	852.3814	1702.7714	851.8894	14
14	**1426.6696**	713.8385	1409.6431	705.3252	1408.6591	704.8332	Q	1591.7394	796.3733	1574.7129	787.8601	1573.7288	787.3681	13
15	1586.7003	793.8538	1569.6737	785.3405	1568.6897	784.8485	C	1463.6808	732.3441	1446.6543	723.8308	1445.6703	723.3388	12
16	**1685.7687**	843.3880	1668.7421	834.8747	1667.7581	834.3827	V	1303.6502	652.3287	1286.6236	643.8155	1285.6396	643.3234	11
17	1782.8215	**891.9144**	1765.7949	883.4011	1764.8109	882.9091	P	1204.5818	602.7945	1187.5552	594.2812	1186.5712	593.7892	10
18	1897.8484	949.4278	1880.8219	940.9146	1879.8378	940.4226	D	1107.5290	554.2681	1090.5024	545.7549	1089.5184	545.2629	9
19	2053.9495	1027.4784	2036.9230	1018.9651	2035.9389	1018.4731	R	992.5021	496.7547	975.4755	488.2414			8
20	2110.9710	1055.9891	2093.9444	1047.4759	2092.9604	1046.9838	G	836.4009	418.7041	819.3744	410.1908			7
21	2239.0296	1120.0184	2222.0030	1111.5051	2221.0190	1111.0131	Q	779.3795	390.1934	762.3529	381.6801			6
22	2367.0881	1184.0477	2350.0616	1175.5344	2349.0776	1175.0424	Q	651.3209	326.1641	634.2944	317.6508			5
23	2530.1515	**1265.5794**	2513.1249	1257.0661	2512.1409	1256.5741	Y	523.2623	262.1348	506.2358	253.6215			4

24	2658.2100	1329.6087	2641.1835	1321.0954	2640.1995	1320.6034	**Q**	360.1990	180.6031	343.1724	172.0899			**3**
25	2715.2315	1358.1194	2698.2050	1349.6061	2697.2209	1349.1141	**G**	232.1404	116.5738	215.1139	108.0606			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.4	2888.3359	0.0096	SEGSSVNLSPPLEQCVPDRGQQYQGR	Deamidated N7 34.44%
55.9	2888.3359	0.0096	SEGSSVNLSPPLEQCVPDRGQQYQGR	Deamidated Q14 24.44%
53.4	2888.3359	0.0096	SEGSSVNLSPPLEQCVPDRGQQYQGR	Deamidated Q22 13.74%
53.4	2888.3359	0.0096	SEGSSVNLSPPLEQCVPDRGQQYQGR	Deamidated Q21 13.74%
53.3	2888.3359	0.0096	SEGSSVNLSPPLEQCVPDRGQQYQGR	Deamidated Q24 13.65%
39.8	2887.3519	0.9936	SEGSSVNLSPPLEQCVPDRGQQYQGR	
5.9	2888.3509	-0.0054	ESHTHRDRPSQQQPLRNQNVSSER	
5.5	2886.3310	2.0145	RLDCAAMTNRADFMQQTLEAVSLAR	
4.8	2887.3289	1.0166	LTGAIANVDMESMMVSVDKNNVDFAAK	
4.6	2888.3509	-0.0054	ESHTHRDRPSQQQPLRNQNVSSER	

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

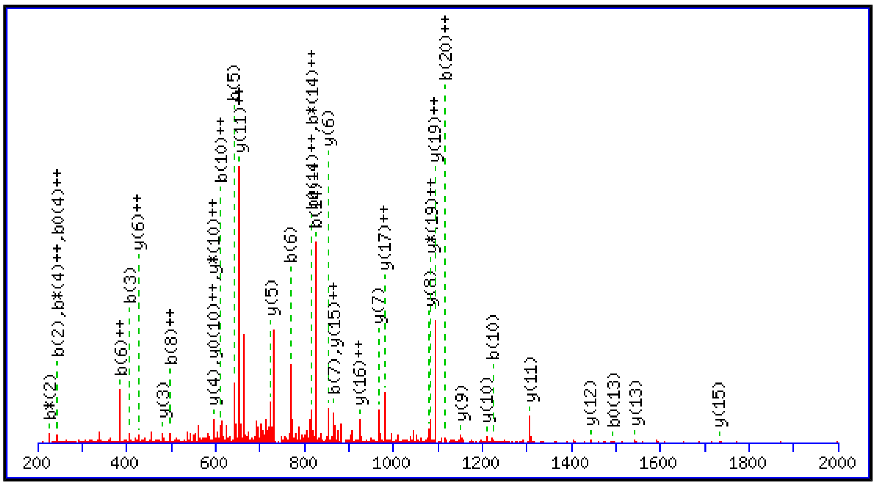
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SRYPHKPEINSTTHPGADLQENFCR**
Found in **C9JV37** in **con_Xuniprot_HUMAN3**, C9JV37_HUMAN Thrombin light chain (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 26787: 2954.379176 from(739.602070,4+) intensity(25717.6152) rtinseconds(797) scans(1664) index(8206)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum1373_scans__1664
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

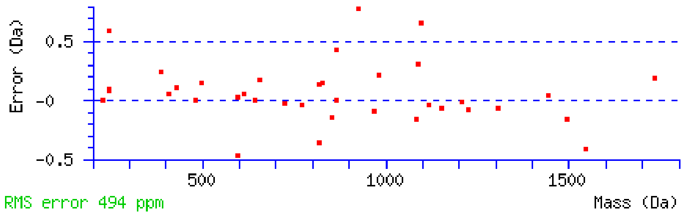
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

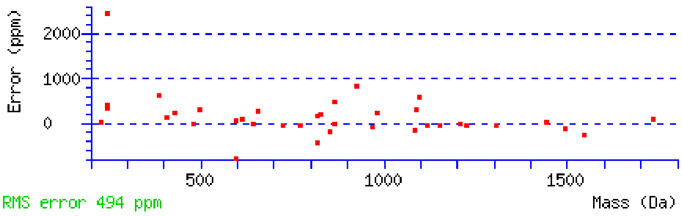


Monoisotopic mass of neutral peptide Mr(calc): 2954.3729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0024
Matches : 38/278 fragment ions using 80 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	***244.1404***	122.5738	227.1139	114.0606	226.1298	113.5686	R	2868.3482	1434.6777	2851.3217	1426.1645	2850.3376	1425.6725	24
3	***407.2037***	204.1055	390.1772	195.5922	389.1932	195.1002	Y	2712.2471	1356.6272	2695.2205	1348.1139	2694.2365	1347.6219	23
4	504.2565	252.6319	487.2300	244.1186	486.2459	243.6266	P	2549.1838	1275.0955	2532.1572	1266.5822	2531.1732	1266.0902	22
5	***641.3154***	321.1613	624.2889	312.6481	623.3049	312.1561	H	2452.1310	1226.5691	2435.1044	1218.0559	2434.1204	1217.5639	21
6	***769.4104***	**385.2088**	752.3838	376.6956	751.3998	376.2035	K	2315.0721	1158.0397	2298.0455	1149.5264	2297.0615	1149.0344	20
7	***866.4631***	433.7352	849.4366	425.2219	848.4526	424.7299	P	2186.9771	1093.9922	2169.9506	1085.4789	2168.9666	1084.9869	19
8	995.5057	**498.2565**	978.4792	489.7432	977.4952	489.2512	E	2089.9244	1045.4658	2072.8978	1036.9525	2071.9138	1036.4605	18
9	1108.5898	554.7985	1091.5633	546.2853	1090.5792	545.7933	I	1960.8818	980.9445	1943.8552	972.4312	1942.8712	971.9392	17
10	***1223.6167***	**612.3120**	1206.5902	603.7987	1205.6062	603.3067	N	1847.7977	924.4025	1830.7712	915.8892	1829.7871	915.3972	16
11	1310.6488	655.8280	1293.6222	647.3148	1292.6382	646.8227	S	***1732.7708***	866.8890	1715.7442	858.3757	1714.7602	857.8837	15
12	1411.6965	706.3519	1394.6699	697.8386	1393.6859	697.3466	T	1645.7387	823.3730	1628.7122	814.8597	1627.7282	814.3677	14
13	1512.7441	756.8757	1495.7176	748.3624	1494.7336	747.8704	T	***1544.6911***	772.8492	1527.6645	764.3359	1526.6805	763.8439	13
14	1649.8030	**825.4052**	1632.7765	816.8919	1631.7925	816.3999	H	***1443.6434***	722.3253	1426.6168	713.8121	1425.6328	713.3200	12
15	1746.8558	873.9315	1729.8293	865.4183	1728.8452	864.9263	P	***1306.5845***	653.7959	1289.5579	645.2826	1288.5739	644.7906	11
16	1803.8773	902.4423	1786.8507	893.9290	1785.8667	893.4370	G	***1209.5317***	605.2695	1192.5051	596.7562	1191.5211	596.2642	10
17	1874.9144	937.9608	1857.8878	929.4476	1856.9038	928.9555	A	***1152.5102***	576.7588	1135.4837	568.2455	1134.4997	567.7535	9
18	1989.9413	995.4743	1972.9148	986.9610	1971.9308	986.4690	D	***1081.4731***	541.2402	1064.4466	532.7269	1063.4626	532.2349	8
19	2103.0254	1052.0163	2085.9988	1043.5031	2085.0148	1043.0111	L	***966.4462***	483.7267	949.4196	475.2135	948.4356	474.7214	7
20	2231.0840	**1116.0456**	2214.0574	1107.5323	2213.0734	1107.0403	Q	***853.3621***	427.1847	836.3356	418.6714	835.3515	418.1794	6
21	2360.1266	1180.5669	2343.1000	1172.0536	2342.1160	1171.5616	E	***725.3035***	363.1554	708.2770	354.6421	707.2930	354.1501	5
22	2474.1695	1237.5884	2457.1429	1229.0751	2456.1589	1228.5831	N	***596.2609***	298.6341	579.2344	290.1208			4
23	2621.2379	1311.1226	2604.2114	1302.6093	2603.2273	1302.1173	F	***482.2180***	241.6126	465.1915	233.0994			3

24	2781.2686	1391.1379	2764.2420	1382.6246	2763.2580	1382.1326	**C**	335.1496	168.0784	318.1231	159.5652			**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.9	2954.3729	0.0063	SRYPHKPEINSTTHPGADLQENFCR	Deamidated N10 85.74%
47.7	2953.3889	0.9903	SRYPHKPEINSTTHPGADLQENFCR	
39.6	2954.3729	0.0063	SRYPHKPEINSTTHPGADLQENFCR	Deamidated Q20 8.04%
38.5	2954.3729	0.0063	SRYPHKPEINSTTHPGADLQENFCR	Deamidated N22 6.23%
4.9	2953.3646	1.0145	FDNMLLIDMLTSASIMNGDATFIAATK	
3.9	2952.3806	1.9985	FDNMLLIDMLTSASIMNGDATFIAATK	
3.3	2952.3806	1.9985	FDNMLLIDMLTSASIMNGDATFIAATK	
2.4	2954.3815	-0.0023	QDGAMKEQGTELLDALDQLAREYQSK	
2.4	2953.3770	1.0021	EPRGPTSPASGGCNGENAPCLTLSLQQR	
2.1	2954.3815	-0.0023	QDGAMKEQGTELLDALDQLAREYQSK	

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

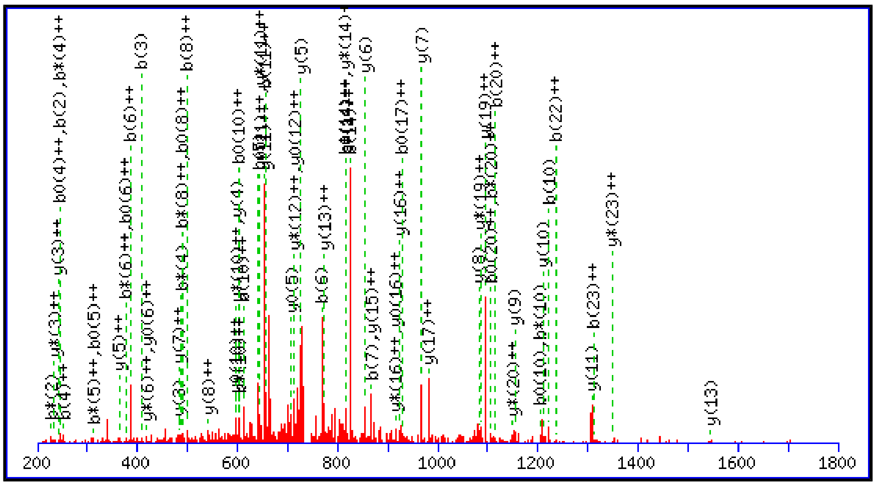
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SRYPHKPEINSTTHPGADLQENFCR**
Found in **C9JV37** in **con_Xuniprot_HUMAN3**, C9JV37_HUMAN Thrombin light chain (Fragment) OS=Homo sapiens GN=F2 PE=2 SV=1

Match to Query 26788: 2954.384936 from(739.603510,4+) intensity(5417.9082) rtinseconds(734) scans(1452) index(8762)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum1172_scans__1452
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

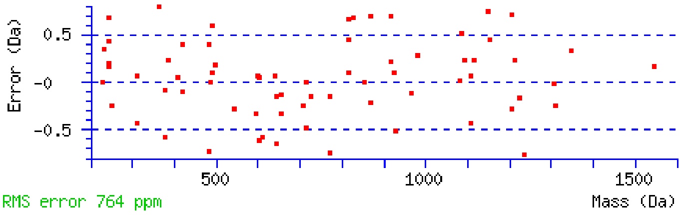
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

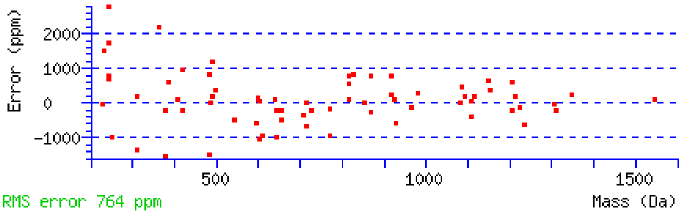


Monoisotopic mass of neutral peptide Mr(calc): 2954.3729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.016
Matches : 70/278 fragment ions using 133 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	***244.1404***	122.5738	227.1139	114.0606	226.1298	113.5686	R	2868.3482	1434.6777	2851.3217	1426.1645	2850.3376	1425.6725	24
3	***407.2037***	204.1055	390.1772	195.5922	389.1932	195.1002	Y	2712.2471	1356.6272	2695.2205	1348.1139	2694.2365	1347.6219	23
4	504.2565	***252.6319***	487.2300	244.1186	486.2459	243.6266	P	2549.1838	1275.0955	2532.1572	1266.5822	2531.1732	1266.0902	22
5	***641.3154***	321.1613	624.2889	312.6481	623.3049	312.1561	H	2452.1310	1226.5691	2435.1044	1218.0559	2434.1204	1217.5639	21
6	***769.4104***	***385.2088***	752.3838	376.6956	751.3998	376.2035	K	2315.0721	1158.0397	2298.0455	1149.5264	2297.0615	1149.0344	20
7	***866.4631***	433.7352	849.4366	425.2219	848.4526	424.7299	P	2186.9771	1093.9922	2169.9506	1085.4789	2168.9666	1084.9869	19
8	995.5057	***498.2565***	978.4792	489.7432	977.4952	489.2512	E	2089.9244	1045.4658	2072.8978	1036.9525	2071.9138	1036.4605	18
9	1108.5898	554.7985	1091.5633	546.2853	1090.5792	545.7933	I	1960.8818	980.9445	1943.8552	972.4312	1942.8712	971.9392	17
10	***1222.6327***	***611.8200***	1205.6062	603.3067	1204.6222	602.8147	N	1847.7977	924.4025	1830.7712	915.8892	1829.7871	915.3972	16
11	1309.6648	***655.3360***	1292.6382	646.8227	1291.6542	646.3307	S	1733.7548	867.3810	1716.7282	858.8678	1715.7442	858.3757	15
12	1410.7124	705.8599	1393.6859	697.3466	1392.7019	696.8546	T	1646.7227	823.8650	1629.6962	815.3517	1628.7122	814.8597	14
13	1511.7601	756.3837	1494.7336	747.8704	1493.7496	747.3784	T	***1545.6751***	773.3412	1528.6485	764.8279	1527.6645	764.3359	13
14	1648.8190	***824.9132***	1631.7925	816.3999	1630.8085	815.9079	H	1444.6274	722.8173	1427.6008	714.3041	1426.6168	713.8121	12
15	1745.8718	873.4395	1728.8452	864.9263	1727.8612	864.4343	P	***1307.5685***	654.2879	1290.5419	645.7746	1289.5579	645.2826	11
16	1802.8933	901.9503	1785.8667	893.4370	1784.8827	892.9450	G	***1210.5157***	605.7615	1193.4892	597.2482	1192.5051	596.7562	10
17	1873.9304	937.4688	1856.9038	928.9555	1855.9198	928.4635	A	***1153.4943***	577.2508	1136.4677	568.7375	1135.4837	568.2455	9
18	1988.9573	994.9823	1971.9308	986.4690	1970.9467	985.9770	D	***1082.4571***	541.7322	1065.4306	533.2189	1064.4466	532.7269	8
19	2102.0414	1051.5243	2085.0148	1043.0111	2084.0308	1042.5190	L	***967.4302***	484.2187	950.4036	475.7055	949.4196	475.2135	7
20	2230.1000	***1115.5536***	2213.0734	1107.0403	2212.0894	1106.5483	Q	***854.3461***	427.6767	837.3196	419.1634	836.3356	418.6714	6
21	2359.1425	1180.0749	2342.1160	1171.5616	2341.1320	1171.0696	E	***726.2876***	363.6474	709.2610	355.1341	708.2770	354.6421	5
22	2474.1695	***1237.5884***	2457.1429	1229.0751	2456.1589	1228.5831	N	***597.2450***	299.1261	580.2184	290.6128			4
23	2621.2379	***1311.1226***	2604.2114	1302.6093	2603.2273	1302.1173	F	***482.2180***	241.6126	465.1915	233.0994			3

24	2781.2686	1391.1379	2764.2420	1382.6246	2763.2580	1382.1326	**C**	335.1496	168.0784	318.1231	159.5652			**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.6	2954.3729	0.0120	SRYPHKPEINSTTHPGADLQENFCR	Deamidated N22 34.77%
41.4	2954.3729	0.0120	SRYPHKPEINSTTHPGADLQENFCR	Deamidated N10 33.51%
41.2	2954.3729	0.0120	SRYPHKPEINSTTHPGADLQENFCR	Deamidated Q20 31.71%
40.6	2953.3889	0.9960	SRYPHKPEINSTTHPGADLQENFCR	
25.4	2952.3806	2.0043	FDNMLLIDMLTSASIMNGDATFIAATK	
16.5	2952.3806	2.0043	FDNMLLIDMLTSASIMNGDATFIAATK	
10.2	2954.3970	-0.0121	DQPLIMGCDRAVSVATLMSDGTVMVTR	
8.6	2954.3970	-0.0121	DQPLIMGCDRAVSVATLMSDGTVMVTR	
6.3	2954.3869	-0.0019	GSVALIIHNVTAEDNGIYQCYFQEGR	
6.0	2952.3667	2.0182	NVLCGNIPPDLFARMTAEEMASDELK	

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

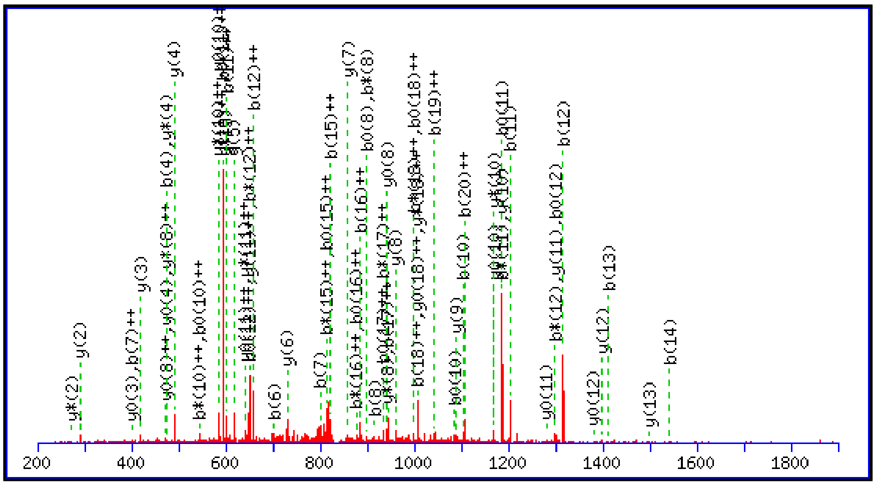
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEEDTKVNSTVIPETQLQAEDR**
Found in **E9PPW2** in **con_Xuniprot_HUMAN3**, E9PPW2_HUMAN Cadherin-related family member 5 (Fragment) OS=Homo sapiens GN=CDHR5 PE=2 SV=1

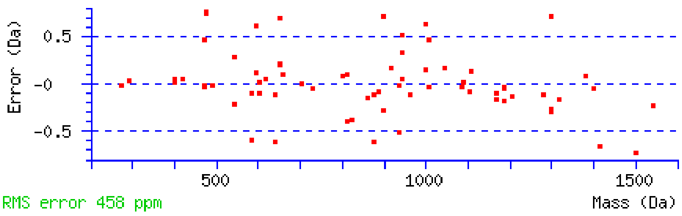
Match to Query 21587: 2501.220852 from(834.747560,3+) intensity(0.0000) rtinseconds(1013) scans(2319) index(10831)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum1952_scans__2319
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

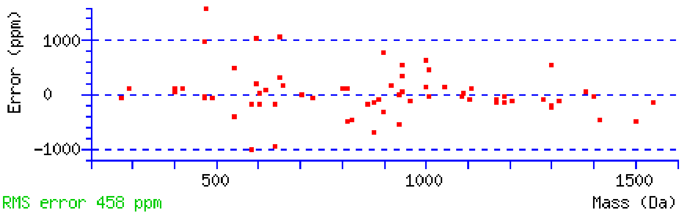
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2501.2133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 49 **Expect:** 0.0037
Matches : 72/238 fragment ions using 132 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							22
2	229.1183	115.0628			211.1077	106.0575	E	2403.1522	1202.0797	2386.1256	1193.5664	2385.1416	1193.0744	21
3	358.1609	179.5841			340.1503	170.5788	E	2274.1096	1137.5584	2257.0830	1129.0452	2256.0990	1128.5531	20
4	***473.1878***	237.0975			455.1773	228.0923	D	2145.0670	1073.0371	2128.0404	1064.5239	2127.0564	1064.0318	19
5	574.2355	287.6214			556.2249	278.6161	T	2030.0400	1015.5237	2013.0135	1007.0104	2012.0295	1006.5184	18
6	***702.3305***	351.6689	685.3039	343.1556	684.3199	342.6636	K	1928.9924	964.9998	1911.9658	956.4865	1910.9818	955.9945	17
7	***801.3989***	**401.2031**	784.3723	392.6898	783.3883	392.1978	V	1800.8974	900.9523	1783.8709	892.4391	1782.8868	891.9471	16
8	***916.4258***	458.7165	899.3993	450.2033	898.4153	449.7113	N	1701.8290	851.4181	1684.8024	842.9049	1683.8184	842.4128	15
9	1003.4578	502.2326	986.4313	493.7193	985.4473	493.2273	S	1586.8020	793.9047	1569.7755	785.3914	1568.7915	784.8994	14
10	***1104.5055***	552.7564	1087.4790	544.2431	1086.4950	543.7511	T	***1499.7700***	750.3886	1482.7435	741.8754	1481.7594	741.3834	13
11	***1203.5739***	**602.2906**	1186.5474	593.7773	1185.5634	593.2853	V	***1398.7223***	699.8648	1381.6958	691.3515	1380.7118	690.8595	12
12	***1316.6580***	**658.8326**	1299.6315	650.3194	1298.6474	649.8274	I	***1299.6539***	650.3306	1282.6274	641.8173	1281.6434	641.3253	11
13	***1413.7108***	707.3590	1396.6842	698.8457	1395.7002	698.3537	P	***1186.5699***	593.7886	1169.5433	585.2753	1168.5593	584.7833	10
14	***1542.7534***	771.8803	1525.7268	763.3670	1524.7428	762.8750	E	***1089.5171***	545.2622	1072.4905	536.7489	1071.5065	536.2569	9
15	1643.8010	**822.4042**	1626.7745	813.8909	1625.7905	813.3989	T	***960.4745***	480.7409	943.4480	472.2276	942.4639	471.7356	8
16	1771.8596	**886.4334**	1754.8331	877.9202	1753.8491	877.4282	Q	***859.4268***	430.2170	842.4003	421.7038	841.4163	421.2118	7
17	1884.9437	**942.9755**	1867.9171	934.4622	1866.9331	933.9702	L	***731.3682***	366.1878	714.3417	357.6745	713.3577	357.1825	6
18	2013.0023	**1007.0048**	1995.9757	998.4915	1994.9917	997.9995	Q	***618.2842***	309.6457	601.2576	301.1325	600.2736	300.6404	5
19	2084.0394	**1042.5233**	2067.0128	1034.0100	2066.0288	1033.5180	A	***490.2256***	245.6164	473.1991	237.1032	472.2150	236.6112	4
20	2213.0820	**1107.0446**	2196.0554	1098.5313	2195.0714	1098.0393	E	***419.1885***	210.0979	402.1619	201.5846	401.1779	201.0926	3
21	2328.1089	1164.5581	2311.0824	1156.0448	2310.0983	1155.5528	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.7	2501.2133	0.0076	VEEDTKVNSTVIPETQLQAEDR	Deamidated N8 99.55%
39.0	2500.2293	0.9916	VEEDTKVNSTVIPETQLQAEDR	
23.5	2501.2133	0.0076	VEEDTKVNSTVIPETQLQAEDR	Deamidated Q16 0.30%
20.4	2501.2133	0.0076	VEEDTKVNSTVIPETQLQAEDR	Deamidated Q18 0.15%
12.5	2501.2121	0.0088	GNIHWHASHMQLILIDQSINR	
10.6	2501.2121	0.0088	GNIHWHASHMQLILIDQSINR	
10.4	2501.2121	0.0088	GNIHWHASHMQLILIDQSINR	
10.1	2500.2281	0.9928	GNIHWHASHMQLILIDQSINR	
9.9	2500.2162	1.0047	QAMRNINPSTANSPKCQELALR	
9.9	2500.2162	1.0047	QAMRNINPSTANSPKCQELALR	

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

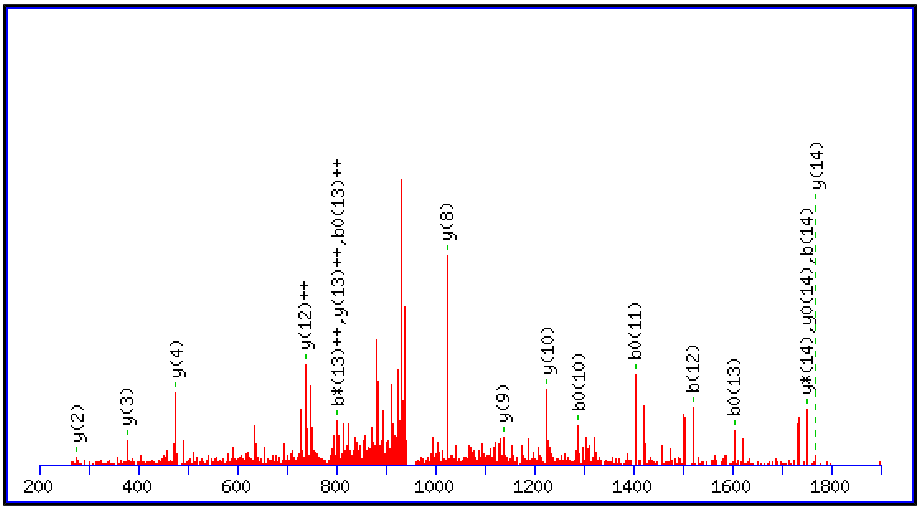
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYESYSDFERNVTEK**
Found in **F5GY80** in **con_Xuniprot_HUMAN3**, F5GY80_HUMAN Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=2 SV=1

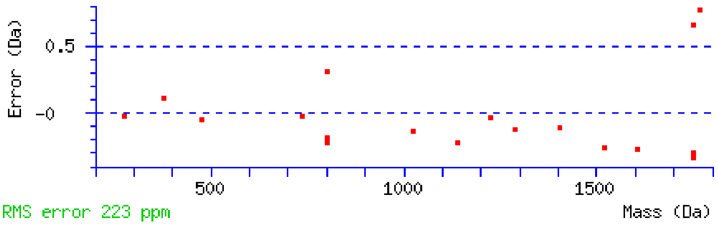
Match to Query 11290: 1895.812908 from(948.913730,2+) intensity(9045.2861) rtinseconds(1222) scans(2881) index(23152)
Title: 111019_Est_MI_YS_G_04Spectrum2446_scans__2881
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

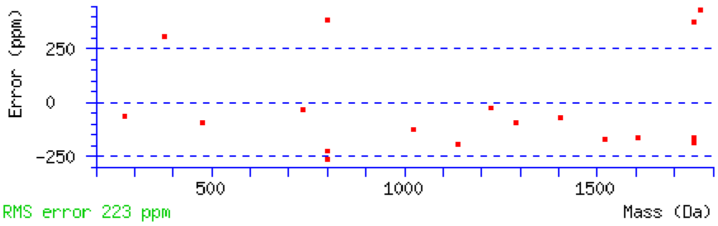
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1895.8061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00013
Matches : 18/148 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	293.1132	147.0602			275.1026	138.0550	Y	***1767.7708***	884.3890	1750.7443	875.8758	1749.7602	875.3838	14
3	422.1558	211.5815			404.1452	202.5763	E	1604.7075	802.8574	1587.6809	794.3441	1586.6969	793.8521	13
4	509.1878	255.0975			491.1773	246.0923	S	1475.6649	738.3361	1458.6383	729.8228	1457.6543	729.3308	12
5	672.2511	336.6292			654.2406	327.6239	Y	1388.6329	694.8201	1371.6063	686.3068	1370.6223	685.8148	11
6	759.2832	380.1452			741.2726	371.1399	S	***1225.5695***	613.2884	1208.5430	604.7751	1207.5590	604.2831	10
7	874.3101	437.6587			856.2996	428.6534	D	***1138.5375***	569.7724	1121.5109	561.2591	1120.5269	560.7671	9
8	1021.3785	511.1929			1003.3680	502.1876	F	***1023.5106***	512.2589	1006.4840	503.7456	1005.5000	503.2536	8
9	1150.4211	575.7142			1132.4106	566.7089	E	876.4421	438.7247	859.4156	430.2114	858.4316	429.7194	7
10	1306.5222	653.7648	1289.4957	645.2515	1288.5117	644.7595	R	747.3995	374.2034	730.3730	365.6901	729.3890	365.1981	6
11	1421.5492	711.2782	1404.5226	702.7650	1403.5386	702.2729	N	591.2984	296.1529	574.2719	287.6396	573.2879	287.1476	5
12	1520.6176	760.8124	1503.5910	752.2992	1502.6070	751.8072	V	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	4
13	1621.6653	811.3363	1604.6387	802.8230	1603.6547	802.3310	T	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	3
14	1750.7079	875.8576	1733.6813	867.3443	1732.6973	866.8523	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EYESYSDFERNVTEK
(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	1895.8061	0.0068	EYESYSDFERNVTEK
9.2	1894.8045	1.0084	SMEGSDGHAMKVAMGMQK
8.5	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
7.9	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
7.9	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
7.9	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
7.4	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
7.3	1895.8054	0.0075	MAQKSQGSDNLQEGQEK
6.8	1894.8124	1.0005	MQHWCKRTLMDDNK
5.7	1895.8142	-0.0013	HTTLNSCQNFAKGCEK

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

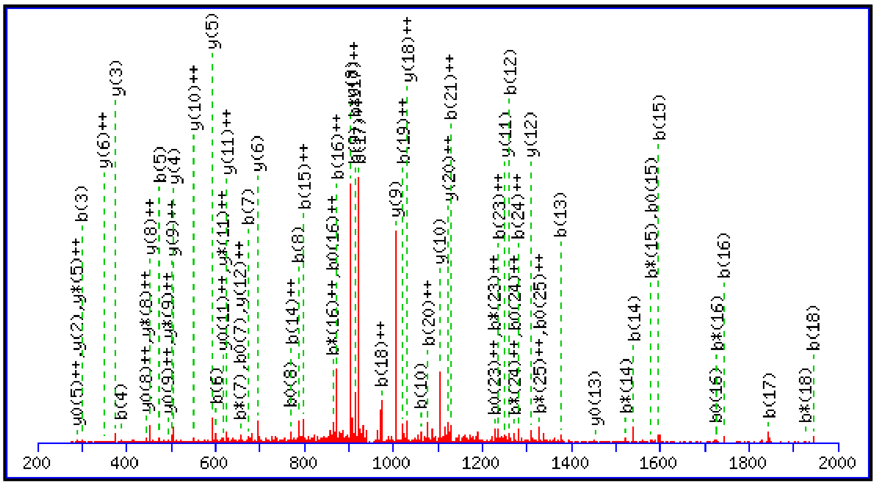
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLSSQALQMSLDYGFVTPLTSMSIR**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 25753: 2846.384502 from(949.802110,3+) intensity(32605.8066) rtinseconds(2535) scans(6602) index(4034)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum5398_scans__6602
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

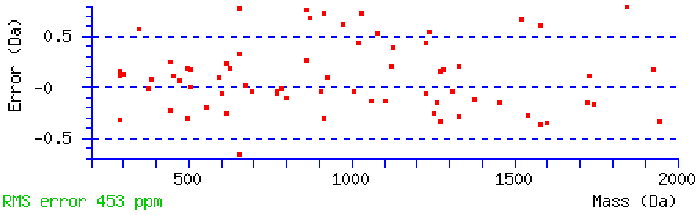
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

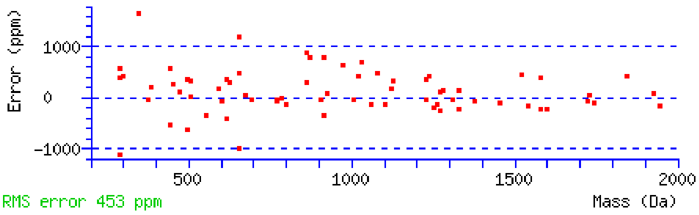


Monoisotopic mass of neutral peptide Mr(calc): 2846.3830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 92 **Expect:** 1.8e-007
Matches : 70/438 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							26
2	187.0713	94.0393	170.0448	85.5260			N	2776.3532	1388.6802	2759.3266	1380.1670	2758.3426	1379.6750	25
3	***300.1554***	150.5813	283.1288	142.0681			L	2661.3263	1331.1668	2644.2997	1322.6535	2643.3157	1322.1615	24
4	***387.1874***	194.0974	370.1609	185.5841	369.1769	185.0921	S	2548.2422	1274.6247	2531.2156	1266.1115	2530.2316	1265.6194	23
5	***474.2195***	237.6134	457.1929	229.1001	456.2089	228.6081	S	2461.2102	1231.1087	2444.1836	1222.5954	2443.1996	1222.1034	22
6	***602.2780***	301.6427	585.2515	293.1294	584.2675	292.6374	Q	2374.1781	1187.5927	2357.1516	1179.0794	2356.1676	1178.5874	21
7	***673.3151***	337.1612	656.2886	328.6479	655.3046	328.1559	A	2246.1196	1123.5634	2229.0930	1115.0501	2228.1090	1114.5581	20
8	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	L	2175.0824	1088.0449	2158.0559	1079.5316	2157.0719	1079.0396	19
9	***914.4578***	457.7325	897.4312	449.2193	896.4472	448.7272	Q	2061.9984	1031.5028	2044.9718	1022.9896	2043.9878	1022.4975	18
10	***1061.4932***	531.2502	1044.4666	522.7370	1043.4826	522.2449	M	1933.9398	967.4735	1916.9133	958.9603	1915.9292	958.4683	17
11	1148.5252	574.7662	1131.4987	566.2530	1130.5147	565.7610	S	1786.9044	893.9558	1769.8779	885.4426	1768.8938	884.9506	16
12	***1261.6093***	631.3083	1244.5827	622.7950	1243.5987	622.3030	L	1699.8724	850.4398	1682.8458	841.9265	1681.8618	841.4345	15
13	***1376.6362***	688.8217	1359.6097	680.3085	1358.6257	679.8165	D	1586.7883	793.8978	1569.7618	785.3845	1568.7777	784.8925	14
14	***1539.6996***	**770.3534**	1522.6730	761.8401	1521.6890	761.3481	Y	1471.7614	736.3843	1454.7348	727.8710	1453.7508	727.3790	13
15	***1596.7210***	**798.8641**	1579.6945	790.3509	1578.7105	789.8589	G	***1308.6980***	654.8527	1291.6715	646.3394	1290.6875	645.8474	12
16	***1743.7894***	**872.3984**	1726.7629	863.8851	1725.7789	863.3931	F	***1251.6766***	626.3419	1234.6500	617.8286	1233.6660	617.3366	11
17	***1842.8578***	**921.9326**	1825.8313	913.4193	1824.8473	912.9273	V	***1104.6082***	552.8077	1087.5816	544.2944	1086.5976	543.8024	10
18	***1943.9055***	**972.4564**	1926.8790	963.9431	1925.8950	963.4511	T	***1005.5397***	503.2735	988.5132	494.7602	987.5292	494.2682	9
19	2040.9583	**1020.9828**	2023.9317	1012.4695	2022.9477	1011.9775	P	***904.4921***	452.7497	887.4655	444.2364	886.4815	443.7444	8
20	2154.0424	**1077.5248**	2137.0158	1069.0115	2136.0318	1068.5195	L	807.4393	404.2233	790.4128	395.7100	789.4287	395.2180	7
21	2255.0900	**1128.0487**	2238.0635	1119.5354	2237.0795	1119.0434	T	***694.3552***	347.6813	677.3287	339.1680	676.3447	338.6760	6

22	2342.1221	1171.5647	2325.0955	1163.0514	2324.1115	1162.5594	**S**	***593.3076***	297.1574	576.2810	288.6441	575.2970	288.1521	**5**
23	2473.1625	**1237.0849**	2456.1360	1228.5716	2455.1520	1228.0796	**M**	***506.2755***	253.6414	489.2490	245.1281	488.2650	244.6361	**4**
24	2560.1946	**1280.6009**	2543.1680	1272.0876	2542.1840	1271.5956	**S**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
25	2673.2786	1337.1430	2656.2521	1328.6297	2655.2681	1328.1377	**I**	***288.2030***	144.6051	271.1765	136.0919			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
91.8	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2, Oxidation M10; 99.50%
68.8	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6, Oxidation M10; 0.50%
48.8	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q9, Oxidation M10; 0.01%
27.1	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2, Oxidation M23; 0.00%
19.6	2845.3929	0.9916	NVAHESAHTGPTIHVDMKFRQPLSR	
12.9	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6, Oxidation M23; 0.00%
7.0	2844.3864	1.9981	GGPQLEAGLRWLIQPEPDLHSCNQK	
6.7	2845.3930	0.9915	LQADPKQGMSLDIGQRLGFHGPGPHSS	
6.3	2846.3830	0.0015	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q9, Oxidation M23; 0.00%
6.1	2845.3772	1.0073	TGATGFGLTMAVKAEKDMLCTGSQSLR	

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

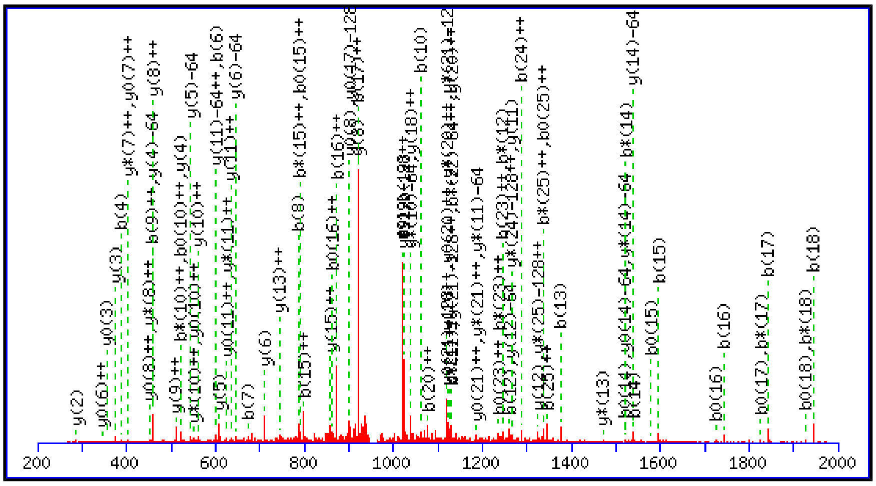
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLSSQALQMSLDYGFVTPLTSMSIR**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 26002: 2862.390132 from(955.137320,3+) intensity(32998.7383) rtinseconds(2370) scans(6144) index(25582)
Title: 111019_Est_MI_YS_G_07Spectrum5282_scans__6144
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

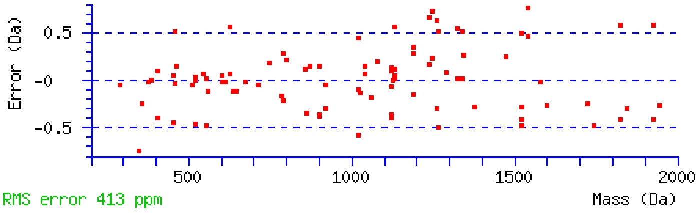
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

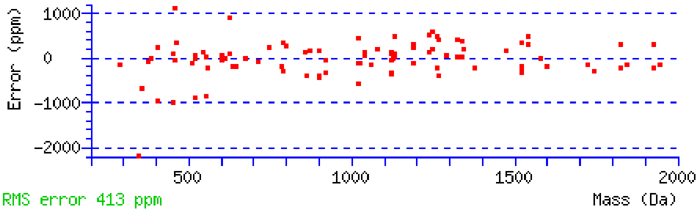


Monoisotopic mass of neutral peptide Mr(calc): 2862.3779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M23 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 81 **Expect:** 2.1e-006
Matches : 95/516 fragment ions using 104 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					**A**							**26**
2	187.0713	94.0393	170.0448	85.5260			**N**	2792.3481	1396.6777	2775.3216	1388.1644	2774.3375	1387.6724	**25**
3	300.1554	150.5813	283.1288	142.0681			**L**	2677.3212	1339.1642	2660.2946	1330.6509	2659.3106	1330.1589	**24**
4	***387.1874***	194.0974	370.1609	185.5841	369.1769	185.0921	**S**	2564.2371	1282.6222	2547.2106	1274.1089	2546.2265	1273.6169	**23**
5	474.2195	237.6134	457.1929	229.1001	456.2089	228.6081	**S**	2477.2051	1239.1062	2460.1785	1230.5929	2459.1945	1230.1009	**22**
6	***602.2780***	301.6427	585.2515	293.1294	584.2675	292.6374	**Q**	2390.1730	1195.5902	2373.1465	1187.0769	2372.1625	1186.5849	**21**
7	***673.3151***	337.1612	656.2886	328.6479	655.3046	328.1559	**A**	2262.1145	1131.5609	2245.0879	1123.0476	2244.1039	1122.5556	**20**
8	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	**L**	2191.0774	1096.0423	2174.0508	1087.5290	2173.0668	1087.0370	**19**
9	914.4578	***457.7325***	897.4312	449.2193	896.4472	448.7272	**Q**	2077.9933	1039.5003	2060.9667	1030.9870	2059.9827	1030.4950	**18**
10	***1061.4932***	531.2502	1044.4666	522.7370	1043.4826	522.2449	**M**	1949.9347	975.4710	1932.9082	966.9577	1931.9241	966.4657	**17**
11	1148.5252	574.7662	1131.4987	566.2530	1130.5147	565.7610	**S**	1802.8993	901.9533	1785.8728	893.4400	1784.8887	892.9480	**16**
12	***1261.6093***	631.3083	1244.5827	622.7950	1243.5987	622.3030	**L**	1715.8673	858.4373	1698.8407	849.9240	1697.8567	849.4320	**15**
13	***1376.6362***	688.8217	1359.6097	680.3085	1358.6257	679.8165	**D**	1602.7832	801.8952	1585.7567	793.3820	1584.7727	792.8900	**14**
14	***1539.6996***	770.3534	1522.6730	761.8401	1521.6890	761.3481	**Y**	1487.7563	744.3818	1470.7297	735.8685	1469.7457	735.3765	**13**
15	***1596.7210***	***798.8641***	1579.6945	790.3509	1578.7105	789.8589	**G**	**1324.6930**	662.8501	1307.6664	654.3368	1306.6824	653.8448	**12**
16	***1743.7894***	***872.3984***	1726.7629	863.8851	1725.7789	863.3931	**F**	**1267.6715**	634.3394	1250.6449	625.8261	1249.6609	625.3341	**11**
17	***1842.8578***	***921.9326***	1825.8313	913.4193	1824.8473	912.9273	**V**	**1120.6031**	560.8052	1103.5765	552.2919	1102.5925	551.7999	**10**
18	***1943.9055***	972.4564	1926.8790	963.9431	1925.8950	963.4511	**T**	**1021.5347**	511.2710	1004.5081	502.7577	1003.5241	502.2657	**9**
19	2040.9583	***1020.9828***	2023.9317	1012.4695	2022.9477	1011.9775	**P**	**920.4870**	460.7471	903.4604	452.2339	902.4764	451.7418	**8**
20	2154.0424	***1077.5248***	2137.0158	1069.0115	2136.0318	1068.5195	**L**	823.4342	412.2207	806.4077	403.7075	805.4237	403.2155	**7**
21	2255.0900	***1128.0487***	2238.0635	1119.5354	2237.0795	1119.0434	**T**	**710.3502**	355.6787	693.3236	347.1654	692.3396	346.6734	**6**

22	2342.1221	1171.5647	2325.0955	1163.0514	2324.1115	1162.5594	**S**	**609.3025**	305.1549	592.2759	296.6416	591.2919	296.1496	**5**
23	2489.1575	***1245.0824***	2472.1309	1236.5691	2471.1469	1236.0771	**M**	**522.2704**	261.6389	505.2439	253.1256	504.2599	252.6336	**4**
24	2576.1895	***1288.5984***	2559.1629	1280.0851	2558.1789	1279.5931	**S**	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
25	2689.2735	***1345.1404***	2672.2470	1336.6271	2671.2630	1336.1351	**I**	**288.2030**	144.6051	271.1765	136.0919			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.2	2862.3779	0.0122	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2 71.14%
74.8	2862.3779	0.0122	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q9 16.52%
73.5	2862.3779	0.0122	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6 12.33%
62.4	2861.3939	0.9962	ANLSSQALQMSLDYGFVTPLTSMSIR	
10.7	2862.3930	-0.0029	AGSEQEEGFEGLPRRVTDLGMVSNLR	
5.4	2860.3701	2.0200	MQLTERWYSNNQKILSLSQNFDK	
5.4	2860.3800	2.0101	DIMQQTTSTVIGQQLRYAQEQLYK	
5.0	2862.3779	0.0122	FNDPNDPCKILVATDAIGMGLNLSIR	
4.9	2861.3939	0.9962	FNDPNDPCKILVATDAIGMGLNLSIR	
4.9	2861.3939	0.9962	FNDPNDPCKILVATDAIGMGLNLSIR	

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

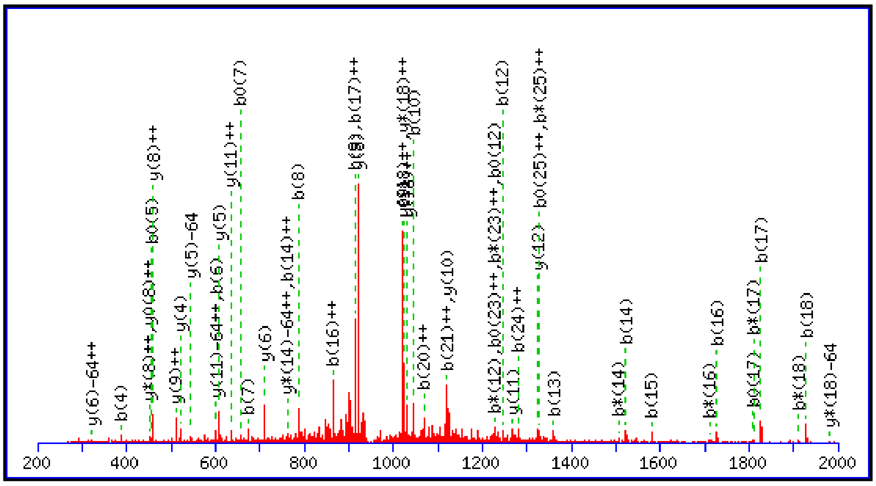
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLSSQALQMSLDYGFVTPLTSMSIR**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 25762: 2846.393412 from(949.805080,3+) intensity(52629.7070) rtinseconds(2488) scans(6352) index(10449)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum5473_scans__6352
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

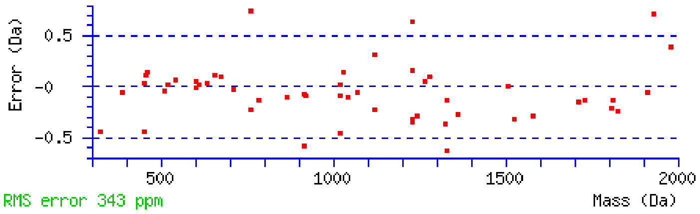
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

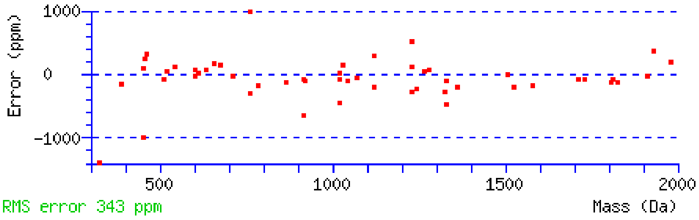


```
Monoisotopic mass of neutral peptide Mr(calc): 2846.3830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2     : Deamidated (NQ)
M23    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 78  Expect: 4.3e-006
Matches : 53/438 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							26
2	187.0713	94.0393	170.0448	85.5260			N	2776.3532	1388.6802	2759.3266	1380.1670	2758.3426	1379.6750	25
3	300.1554	150.5813	283.1288	142.0681			L	2661.3263	1331.1668	2644.2997	1322.6535	2643.3157	1322.1615	24
4	***387.1874***	194.0974	370.1609	185.5841	369.1769	185.0921	S	2548.2422	1274.6247	2531.2156	1266.1115	2530.2316	1265.6194	23
5	474.2195	237.6134	457.1929	229.1001	456.2089	228.6081	S	2461.2102	1231.1087	2444.1836	1222.5954	2443.1996	1222.1034	22
6	***602.2780***	301.6427	585.2515	293.1294	584.2675	292.6374	Q	2374.1781	1187.5927	2357.1516	1179.0794	2356.1676	1178.5874	21
7	***673.3151***	337.1612	656.2886	328.6479	655.3046	328.1559	A	2246.1196	1123.5634	2229.0930	1115.0501	2228.1090	1114.5581	20
8	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	L	2175.0824	1088.0449	2158.0559	1079.5316	2157.0719	1079.0396	19
9	***914.4578***	457.7325	897.4312	449.2193	896.4472	448.7272	Q	2061.9984	1031.5028	2044.9718	1022.9896	2043.9878	1022.4975	18
10	***1045.4983***	523.2528	1028.4717	514.7395	1027.4877	514.2475	M	1933.9398	967.4735	1916.9133	958.9603	1915.9292	958.4683	17
11	1132.5303	566.7688	1115.5038	558.2555	1114.5197	557.7635	S	1802.8993	901.9533	1785.8728	893.4400	1784.8887	892.9480	16
12	***1245.6144***	623.3108	1228.5878	614.7975	1227.6038	614.3055	L	1715.8673	858.4373	1698.8407	849.9240	1697.8567	849.4320	15
13	***1360.6413***	680.8243	1343.6148	672.3110	1342.6307	671.8190	D	1602.7832	801.8952	1585.7567	793.3820	1584.7727	792.8900	14
14	***1523.7046***	**762.3560**	1506.6781	753.8427	1505.6941	753.3507	Y	1487.7563	744.3818	1470.7297	735.8685	1469.7457	735.3765	13
15	***1580.7261***	790.8667	1563.6996	782.3534	1562.7155	781.8614	G	**1324.6930**	662.8501	1307.6664	654.3368	1306.6824	653.8448	12
16	***1727.7945***	**864.4009**	1710.7680	855.8876	1709.7839	855.3956	F	**1267.6715**	634.3394	1250.6449	625.8261	1249.6609	625.3341	11
17	***1826.8629***	**913.9351**	1809.8364	905.4218	1808.8524	904.9298	V	**1120.6031**	560.8052	1103.5765	552.2919	1102.5925	551.7999	10
18	***1927.9106***	964.4589	1910.8841	955.9457	1909.9000	955.4537	T	**1021.5347**	511.2710	1004.5081	502.7577	1003.5241	502.2657	9
19	2024.9634	1012.9853	2007.9368	1004.4720	2006.9528	1003.9800	P	**920.4870**	460.7471	903.4604	452.2339	902.4764	451.7418	8
20	2138.0474	**1069.5274**	2121.0209	1061.0141	2120.0369	1060.5221	L	823.4342	412.2207	806.4077	403.7075	805.4237	403.2155	7
21	2239.0951	**1120.0512**	2222.0686	1111.5379	2221.0845	1111.0459	T	**710.3502**	355.6787	693.3236	347.1654	692.3396	346.6734	6

22	2326.1271	1163.5672	2309.1006	1155.0539	2308.1166	1154.5619	**S**	**609.3025**	305.1549	592.2759	296.6416	591.2919	296.1496	**5**
23	2473.1625	1237.0849	2456.1360	1228.5716	2455.1520	1228.0796	**M**	**522.2704**	261.6389	505.2439	253.1256	504.2599	252.6336	**4**
24	2560.1946	**1280.6009**	2543.1680	1272.0876	2542.1840	1271.5956	**S**	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
25	2673.2786	1337.1430	2656.2521	1328.6297	2655.2681	1328.1377	**I**	288.2030	144.6051	271.1765	136.0919			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.9	2846.3830	0.0104	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2, Oxidation M23; 85.34%
70.0	2846.3830	0.0104	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6, Oxidation M23; 13.81%
57.9	2846.3830	0.0104	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q9, Oxidation M23; 0.85%
37.8	2845.3990	0.9944	ANLSSQALQMSLDYGFVTPLTSMSIR	
16.3	2846.4008	-0.0074	MDSAVQASLSLPATPVGKGTENTFPSPK	
13.9	2846.4008	-0.0074	MDSAVQASLSLPATPVGKGTENTFPSPK	
13.0	2846.3830	0.0104	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2, Oxidation M10; 0.00%
11.9	2844.3739	2.0196	MVTQFKEKNESLQYETSNPTVQLK	
10.6	2844.3820	2.0114	EQTLHTPVMMQTPQLTSTIMREPK	
7.5	2846.3830	0.0104	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6, Oxidation M10; 0.00%

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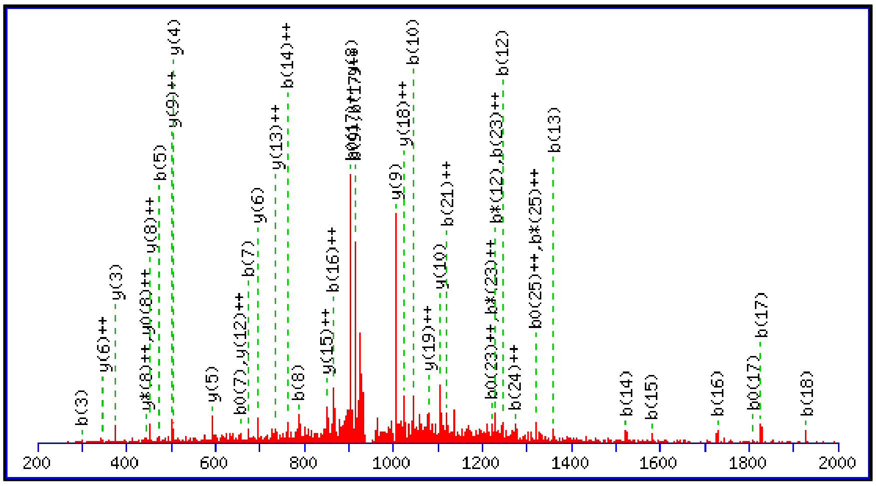
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLSSQALQMSLDYGFVTPLTSMSIR**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 25750: 2830.401042 from(944.474290,3+) intensity(9612.0117) rtinseconds(2681) scans(6962) index(23554)
Title: 111019_Est_MI_YS_G_04Spectrum6052_scans__6962
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

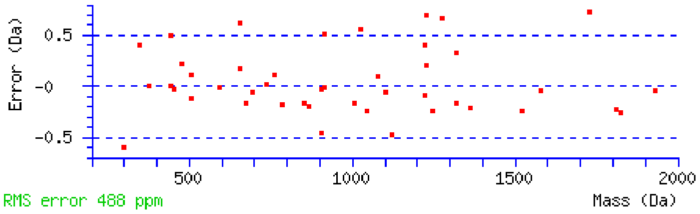
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

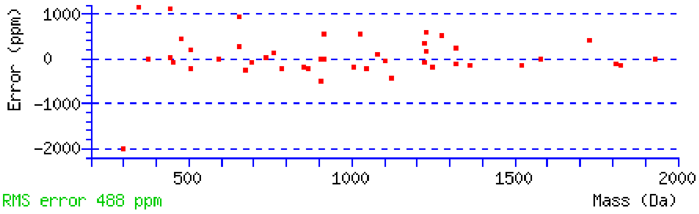


Monoisotopic mass of neutral peptide Mr(calc): 2830.3881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 71 **Expect:** 2.1e-005
Matches : 44/288 fragment ions using 69 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							26
2	187.0713	94.0393	170.0448	85.5260			N	2760.3583	1380.6828	2743.3317	1372.1695	2742.3477	1371.6775	25
3	***300.1554***	150.5813	283.1288	142.0681			L	2645.3313	1323.1693	2628.3048	1314.6560	2627.3208	1314.1640	24
4	387.1874	194.0974	370.1609	185.5841	369.1769	185.0921	S	2532.2473	1266.6273	2515.2207	1258.1140	2514.2367	1257.6220	23
5	***474.2195***	237.6134	457.1929	229.1001	456.2089	228.6081	S	2445.2152	1223.1113	2428.1887	1214.5980	2427.2047	1214.1060	22
6	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	Q	2358.1832	1179.5952	2341.1567	1171.0820	2340.1727	1170.5900	21
7	***673.3151***	337.1612	656.2886	328.6479	655.3046	328.1559	A	2230.1246	1115.5660	2213.0981	1107.0527	2212.1141	1106.5607	20
8	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	L	2159.0875	1080.0474	2142.0610	1071.5341	2141.0770	1071.0421	19
9	***914.4578***	457.7325	897.4312	449.2193	896.4472	448.7272	Q	2046.0035	1023.5054	2028.9769	1014.9921	2027.9929	1014.5001	18
10	***1045.4983***	523.2528	1028.4717	514.7395	1027.4877	514.2475	M	1917.9449	959.4761	1900.9183	950.9628	1899.9343	950.4708	17
11	1132.5303	566.7688	1115.5038	558.2555	1114.5197	557.7635	S	1786.9044	893.9558	1769.8779	885.4426	1768.8938	884.9506	16
12	***1245.6144***	623.3108	1228.5878	614.7975	1227.6038	614.3055	L	1699.8724	850.4398	1682.8458	841.9265	1681.8618	841.4345	15
13	***1360.6413***	680.8243	1343.6148	672.3110	1342.6307	671.8190	D	1586.7883	793.8978	1569.7618	785.3845	1568.7777	784.8925	14
14	***1523.7046***	**762.3560**	1506.6781	753.8427	1505.6941	753.3507	Y	1471.7614	736.3843	1454.7348	727.8710	1453.7508	727.3790	13
15	***1580.7261***	790.8667	1563.6996	782.3534	1562.7155	781.8614	G	1308.6980	654.8527	1291.6715	646.3394	1290.6875	645.8474	12
16	***1727.7945***	**864.4009**	1710.7680	855.8876	1709.7839	855.3956	F	1251.6766	626.3419	1234.6500	617.8286	1233.6660	617.3366	11
17	***1826.8629***	**913.9351**	1809.8364	905.4218	1808.8524	904.9298	V	***1104.6082***	552.8077	1087.5816	544.2944	1086.5976	543.8024	10
18	***1927.9106***	964.4589	1910.8841	955.9457	1909.9000	955.4537	T	***1005.5397***	503.2735	988.5132	494.7602	987.5292	494.2682	9
19	2024.9634	1012.9853	2007.9368	1004.4720	2006.9528	1003.9800	P	***904.4921***	452.7497	887.4655	444.2364	886.4815	443.7444	8
20	2138.0474	1069.5274	2121.0209	1061.0141	2120.0369	1060.5221	L	807.4393	404.2233	790.4128	395.7100	789.4287	395.2180	7
21	2239.0951	**1120.0512**	2222.0686	1111.5379	2221.0845	1111.0459	T	***694.3552***	347.6813	677.3287	339.1680	676.3447	338.6760	6
22	2326.1271	1163.5672	2309.1006	1155.0539	2308.1166	1154.5619	S	***593.3076***	297.1574	576.2810	288.6441	575.2970	288.1521	5

23	2457.1676	**1229.0875**	2440.1411	1220.5742	2439.1571	1220.0822	**M**	***506.2755***	253.6414	489.2490	245.1281	488.2650	244.6361	**4**
24	2544.1997	**1272.6035**	2527.1731	1264.0902	2526.1891	1263.5982	**S**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
25	2657.2837	1329.1455	2640.2572	1320.6322	2639.2732	1320.1402	**I**	288.2030	144.6051	271.1765	136.0919			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.8	2830.3881	0.0130	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated N2 85.56%
62.7	2830.3881	0.0130	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q6 13.31%
52.0	2830.3881	0.0130	ANLSSQALQMSLDYGFVTPLTSMSIR	Deamidated Q9 1.13%
41.6	2829.4041	0.9970	ANLSSQALQMSLDYGFVTPLTSMSIR	
5.8	2829.3902	1.0108	DETQMHFGTMGGLPTPTATLKRAPTR	
3.9	2828.3936	2.0075	EDPAGMEASTMPISALPRTSSDPVLLK	
3.3	2829.3888	1.0122	MVLGMQLSQVSDLLTQEQANLTHQK	
3.2	2830.4018	-0.0008	LTEMADQNTKGLLSEGNVAILQDNVR	
3.2	2830.4018	-0.0008	LTEMADQNTKGLLSEGNVAILQDNVR	
3.2	2828.3936	2.0075	MMQLIIKDVESSDLIGNRDTDYLK	

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

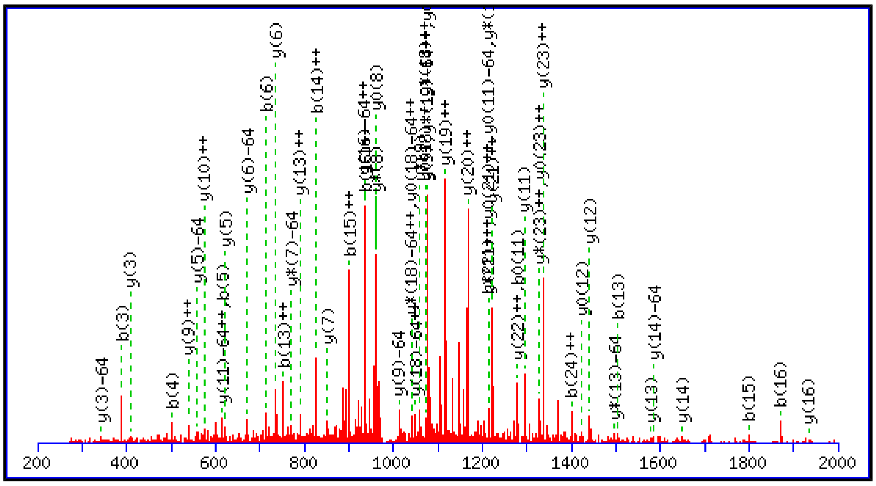
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ICDLLVANNHFAHFFAPQNLTNMNK**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 26784: 2945.402982 from(982.808270,3+) intensity(55012.5664) rtinseconds(1979) scans(5170) index(2908)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum4376_scans__5170
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

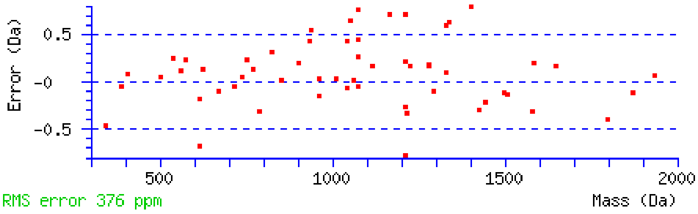
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

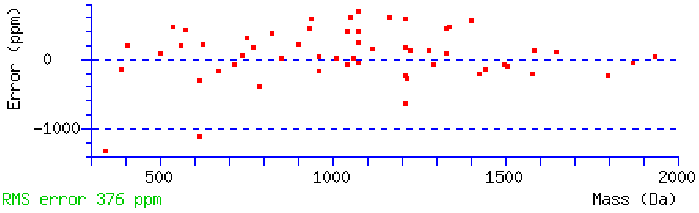


Monoisotopic mass of neutral peptide Mr(calc): 2945.3952
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
M23 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 52 **Expect:** 0.0016
Matches : 58/402 fragment ions using 87 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							25
2	274.1220	137.5646					C	2833.3185	1417.1629	2816.2919	1408.6496	2815.3079	1408.1576	24
3	**389.1489**	195.0781			371.1384	186.0728	D	2673.2878	1337.1476	2656.2613	1328.6343	2655.2773	1328.1423	23
4	**502.2330**	251.6201			484.2224	242.6149	L	2558.2609	1279.6341	2541.2343	1271.1208	2540.2503	1270.6288	22
5	**615.3171**	308.1622			597.3065	299.1569	L	2445.1768	1223.0921	2428.1503	1214.5788	2427.1663	1214.0868	21
6	**714.3855**	357.6964			696.3749	348.6911	V	2332.0928	1166.5500	2315.0662	1158.0367	2314.0822	1157.5447	20
7	785.4226	393.2149			767.4120	384.2096	A	2233.0243	1117.0158	2215.9978	1108.5025	2215.0138	1108.0105	19
8	899.4655	450.2364	882.4390	441.7231	881.4549	441.2311	N	2161.9872	1081.4973	2144.9607	1072.9840	2143.9767	1072.4920	18
9	1013.5084	507.2579	996.4819	498.7446	995.4979	498.2526	N	2047.9443	1024.4758	2030.9178	1015.9625	2029.9337	1015.4705	17
10	1150.5674	575.7873	1133.5408	567.2740	1132.5568	566.7820	H	***1933.9014***	967.4543	1916.8748	958.9411	1915.8908	958.4490	16
11	1297.6358	649.3215	1280.6092	640.8082	1279.6252	640.3162	F	1796.8425	898.9249	1779.8159	890.4116	1778.8319	889.9196	15
12	1368.6729	684.8401	1351.6463	676.3268	1350.6623	675.8348	A	***1649.7741***	825.3907	1632.7475	816.8774	1631.7635	816.3854	14
13	**1505.7318**	**753.3695**	1488.7052	744.8563	1487.7212	744.3643	H	***1578.7369***	789.8721	1561.7104	781.3588	1560.7264	780.8668	13
14	1652.8002	**826.9037**	1635.7737	818.3905	1634.7896	817.8985	F	***1441.6780***	721.3427	1424.6515	712.8294	1423.6675	712.3374	12
15	**1799.8686**	**900.4379**	1782.8421	891.9247	1781.8581	891.4327	F	***1294.6096***	647.8084	1277.5831	639.2952	1276.5990	638.8032	11
16	**1870.9057**	**935.9565**	1853.8792	927.4432	1852.8952	926.9512	A	1147.5412	574.2742	1130.5147	565.7610	1129.5306	565.2690	10
17	1967.9585	984.4829	1950.9320	975.9696	1949.9479	975.4776	P	***1076.5041***	538.7557	1059.4775	530.2424	1058.4935	529.7504	9
18	2096.0171	1048.5122	2078.9905	1039.9989	2078.0065	1039.5069	Q	979.4513	490.2293	962.4248	481.7160	961.4408	481.2240	8
19	2211.0440	1106.0256	2194.0175	1097.5124	2193.0335	1097.0204	N	***851.3927***	426.2000	834.3662	417.6867	833.3822	417.1947	7
20	2324.1281	1162.5677	2307.1015	1154.0544	2306.1175	1153.5624	L	***736.3658***	368.6865	719.3393	360.1733	718.3552	359.6813	6
21	2425.1758	1213.0915	2408.1492	1204.5782	2407.1652	1204.0862	T	***623.2817***	312.1445	606.2552	303.6312	605.2712	303.1392	5

22	2539.2187	1270.1130	2522.1921	1261.5997	2521.2081	1261.1077	**N**	522.2341	261.6207	505.2075	253.1074			**4**
23	2686.2541	1343.6307	2669.2275	1335.1174	2668.2435	1334.6254	**M**	***408.1911***	204.5992	391.1646	196.0859			**3**
24	2800.2970	**1400.6521**	2783.2705	1392.1389	2782.2865	1391.6469	**N**	261.1557	131.0815	244.1292	122.5682			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.1	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N19 62.04%
47.0	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated Q18 19.22%
43.9	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N22 9.33%
40.6	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N9 4.39%
38.4	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N8 2.63%
38.0	2945.3952	0.0077	ICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N24 2.39%
23.3	2944.4112	0.9917	ICDLLVANNHFAHFFAPQNLTNMNK	
8.4	2945.4125	-0.0096	LFVRNQVMSMAMWDGPYVNKGILDK	
8.4	2945.4125	-0.0096	LFVRNQVMSMAMWDGPYVNKGILDK	
3.9	2945.3885	0.0144	ELTDNCVQLFDSTQKSLLISCESKK	

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

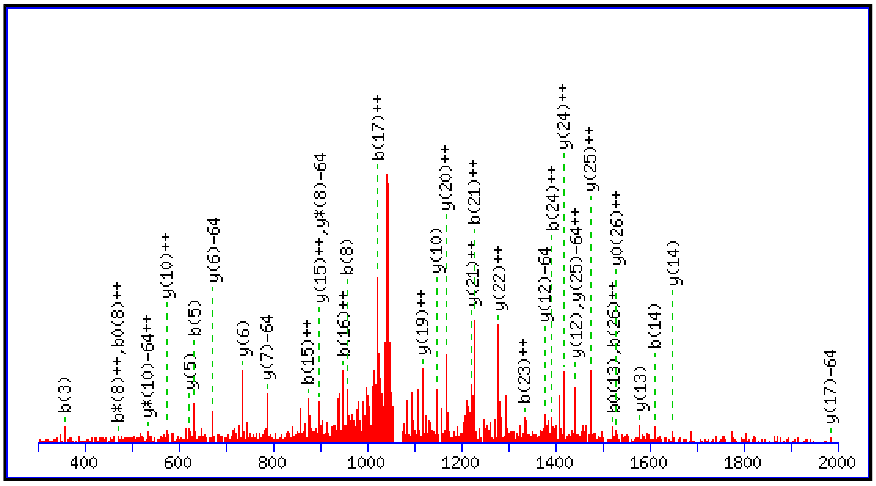
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKICDLLVANNHFAHFFAPQNLTNMNK**
Found in **F5H7E1** in **con_Xuniprot_HUMAN3**, F5H7E1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=2 SV=1

Match to Query 27362: 3188.531022 from(1063.850950,3+) intensity(0.0000) rtinseconds(2075) scans(5445) index(2965)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum4614_scans__5445
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

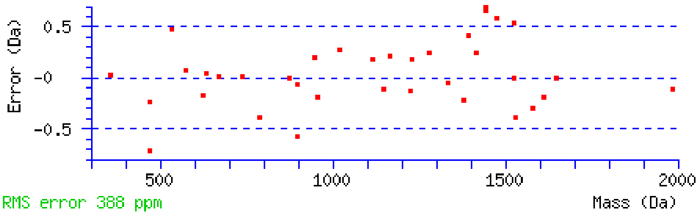
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

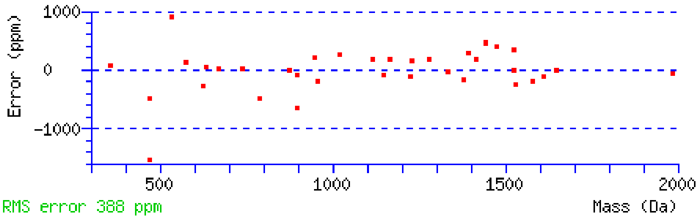


Monoisotopic mass of neutral peptide Mr(calc): 3188.5172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N21 : Deamidated (NQ)
M25 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 52 **Expect:** 0.0018
Matches : 36/454 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	116.0342	58.5207			98.0237	49.5155	D							27
2	244.1292	122.5682	227.1026	114.0550	226.1186	113.5629	K	3074.4975	1537.7524	3057.4710	1529.2391	3056.4869	1528.7471	26
3	**357.2132**	179.1103	340.1867	170.5970	339.2027	170.1050	I	2946.4025	1473.7049	2929.3760	1465.1916	2928.3920	1464.6996	25
4	517.2439	259.1256	500.2173	250.6123	499.2333	250.1203	C	2833.3185	1417.1629	2816.2919	1408.6496	2815.3079	1408.1576	24
5	**632.2708**	316.6391	615.2443	308.1258	614.2603	307.6338	D	2673.2878	1337.1476	2656.2613	1328.6343	2655.2773	1328.1423	23
6	745.3549	373.1811	728.3284	364.6678	727.3443	364.1758	L	2558.2609	1279.6341	2541.2343	1271.1208	2540.2503	1270.6288	22
7	858.4390	429.7231	841.4124	421.2098	840.4284	420.7178	L	2445.1768	1223.0921	2428.1503	1214.5788	2427.1663	1214.0868	21
8	**957.5074**	479.2573	940.4808	470.7441	939.4968	470.2520	V	2332.0928	1166.5500	2315.0662	1158.0367	2314.0822	1157.5447	20
9	1028.5445	514.7759	1011.5179	506.2626	1010.5339	505.7706	A	2233.0243	1117.0158	2215.9978	1108.5025	2215.0138	1108.0105	19
10	1142.5874	571.7973	1125.5609	563.2841	1124.5769	562.7921	N	2161.9872	1081.4973	2144.9607	1072.9840	2143.9767	1072.4920	18
11	1256.6303	628.8188	1239.6038	620.3055	1238.6198	619.8135	N	2047.9443	1024.4758	2030.9178	1015.9625	2029.9337	1015.4705	17
12	1393.6893	697.3483	1376.6627	688.8350	1375.6787	688.3430	H	1933.9014	967.4543	1916.8748	958.9411	1915.8908	958.4490	16
13	1540.7577	770.8825	1523.7311	762.3692	1522.7471	761.8772	F	1796.8425	898.9249	1779.8159	890.4116	1778.8319	889.9196	15
14	**1611.7948**	806.4010	1594.7682	797.8878	1593.7842	797.3957	A	***1649.7741***	825.3907	1632.7475	816.8774	1631.7635	816.3854	14
15	1748.8537	***874.9305***	1731.8272	866.4172	1730.8431	865.9252	H	***1578.7369***	789.8721	1561.7104	781.3588	1560.7264	780.8668	13
16	1895.9221	***948.4647***	1878.8956	939.9514	1877.9115	939.4594	F	***1441.6780***	721.3427	1424.6515	712.8294	1423.6675	712.3374	12
17	2042.9905	***1021.9989***	2025.9640	1013.4856	2024.9800	1012.9936	F	1294.6096	647.8084	1277.5831	639.2952	1276.5990	638.8032	11
18	2114.0276	1057.5175	2097.0011	1049.0042	2096.0171	1048.5122	A	***1147.5412***	574.2742	1130.5147	565.7610	1129.5306	565.2690	10
19	2211.0804	1106.0438	2194.0539	1097.5306	2193.0698	1097.0386	P	1076.5041	538.7557	1059.4775	530.2424	1058.4935	529.7504	9
20	2339.1390	1170.0731	2322.1124	1161.5599	2321.1284	1161.0678	Q	979.4513	490.2293	962.4248	481.7160	961.4408	481.2240	8
21	2454.1659	***1227.5866***	2437.1394	1219.0733	2436.1554	1218.5813	N	851.3927	426.2000	834.3662	417.6867	833.3822	417.1947	7

22	2567.2500	1284.1286	2550.2234	1275.6154	2549.2394	1275.1234	**L**	***736.3658***	368.6865	719.3393	360.1733	718.3552	359.6813	**6**
23	2668.2977	***1334.6525***	2651.2711	1326.1392	2650.2871	1325.6472	**T**	***623.2817***	312.1445	606.2552	303.6312	605.2712	303.1392	**5**
24	2782.3406	***1391.6739***	2765.3140	1383.1607	2764.3300	1382.6687	**N**	522.2341	261.6207	505.2075	253.1074			**4**
25	2929.3760	1465.1916	2912.3494	1456.6784	2911.3654	1456.1864	**M**	408.1911	204.5992	391.1646	196.0859			**3**
26	3043.4189	***1522.2131***	3026.3924	1513.6998	3025.4084	1513.2078	**N**	261.1557	131.0815	244.1292	122.5682			**2**
27							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.5	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N21 43.21%
50.1	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated Q20 30.94%
45.6	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N24 11.03%
43.4	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N11 6.68%
42.1	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N10 4.94%
40.3	3188.5172	0.0139	DKICDLLVANNHFAHFFAPQNLTNMNK	Deamidated N26 3.20%
24.6	3187.5331	0.9979	DKICDLLVANNHFAHFFAPQNLTNMNK	
3.4	3188.5291	0.0019	LDVLSNDLVMNMLKSSFATCVLVSEEDK	
3.0	3187.5246	1.0064	NPFLDFLQKGLMISLSTDDPMQFHFTK	
3.0	3187.5246	1.0064	NPFLDFLQKGLMISLSTDDPMQFHFTK	

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

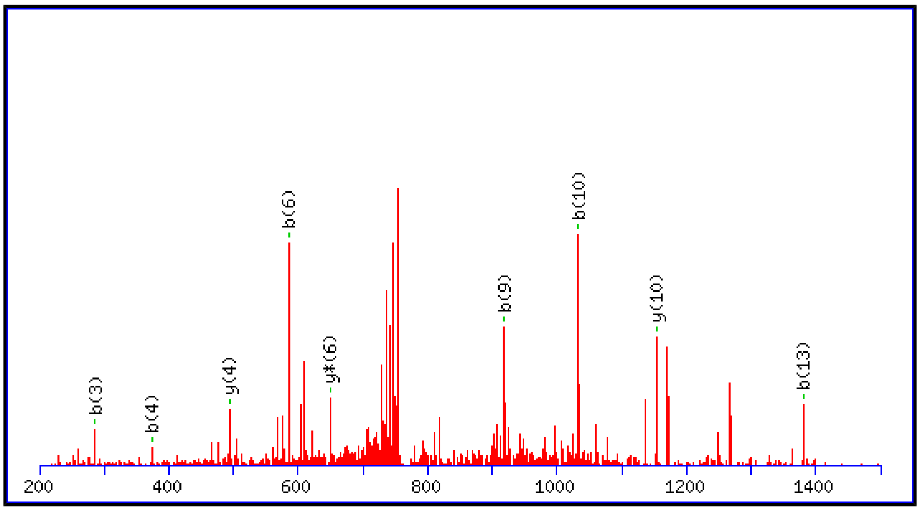
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVSSVLQFGNISFK**
Found in **F8W6L6** in **con_Xuniprot_HUMAN3**, F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1

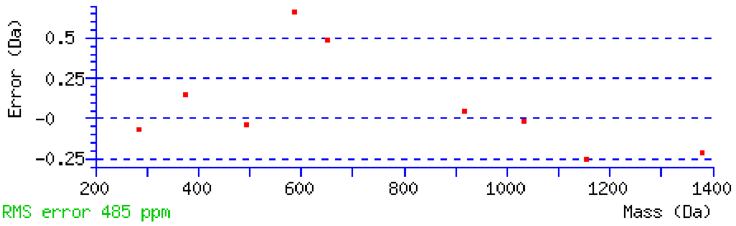
Match to Query 6892: 1525.801928 from(763.908240,2+) intensity(22561.4336) rtinseconds(1593) scans(4113) index(6459)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum3616_scans__4113
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

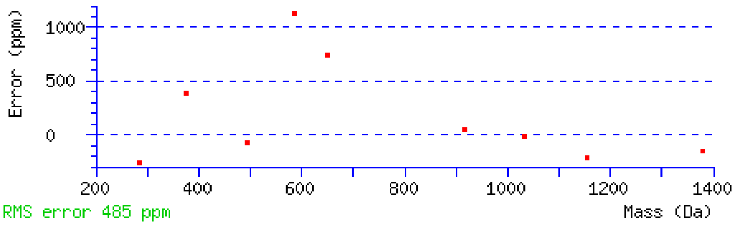
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1525.8028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.011
Matches : 9/136 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	100.0757	50.5415					**V**							**14**
2	199.1441	100.0757					**V**	1427.7417	714.3745	1410.7151	705.8612	1409.7311	705.3692	**13**
3	***286.1761***	143.5917			268.1656	134.5864	**S**	1328.6733	664.8403	1311.6467	656.3270	1310.6627	655.8350	**12**
4	***373.2082***	187.1077			355.1976	178.1024	**S**	1241.6412	621.3243	1224.6147	612.8110	1223.6307	612.3190	**11**
5	472.2766	236.6419			454.2660	227.6366	**V**	**1154.6092**	577.8082	1137.5827	569.2950	1136.5986	568.8030	**10**
6	***585.3606***	293.1840			567.3501	284.1787	**L**	1055.5408	528.2740	1038.5142	519.7608	1037.5302	519.2688	**9**
7	714.4032	357.7053	697.3767	349.1920	696.3927	348.7000	**Q**	942.4567	471.7320	925.4302	463.2187	924.4462	462.7267	**8**
8	861.4716	431.2395	844.4451	422.7262	843.4611	422.2342	**F**	813.4141	407.2107	796.3876	398.6974	795.4036	398.2054	**7**
9	***918.4931***	459.7502	901.4666	451.2369	900.4825	450.7449	**G**	666.3457	333.6765	649.3192	325.1632	648.3352	324.6712	**6**
10	***1033.5201***	517.2637	1016.4935	508.7504	1015.5095	508.2584	**N**	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	**5**
11	1146.6041	573.8057	1129.5776	565.2924	1128.5936	564.8004	**I**	**494.2973**	247.6523	477.2708	239.1390	476.2867	238.6470	**4**
12	1233.6361	617.3217	1216.6096	608.8084	1215.6256	608.3164	**S**	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	**3**
13	***1380.7046***	690.8559	1363.6780	682.3426	1362.6940	681.8506	**F**	294.1812	147.5942	277.1547	139.0810			**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of VVSSVLQFGNISFK
(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	1525.8028	-0.0009	VVSSVLQFGNISFK
10.9	1525.8028	-0.0008	NQYFQLKTELLK
10.9	1525.8028	-0.0008	NQYFQLKTELLK
10.9	1525.8028	-0.0008	NQYFQLKTELLK
8.6	1524.8048	0.9971	TNRIYRIFEQGK
6.4	1525.8035	-0.0015	DLMHRQIRSQIK
6.2	1525.7988	0.0032	IPQDRPTSEELLK
6.1	1524.8049	0.9971	KFDHVNIKGNPEK
4.6	1525.8062	-0.0043	FTLLTVSSGITEMK
4.4	1525.8035	-0.0015	SLRNLMAAHSADLK

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

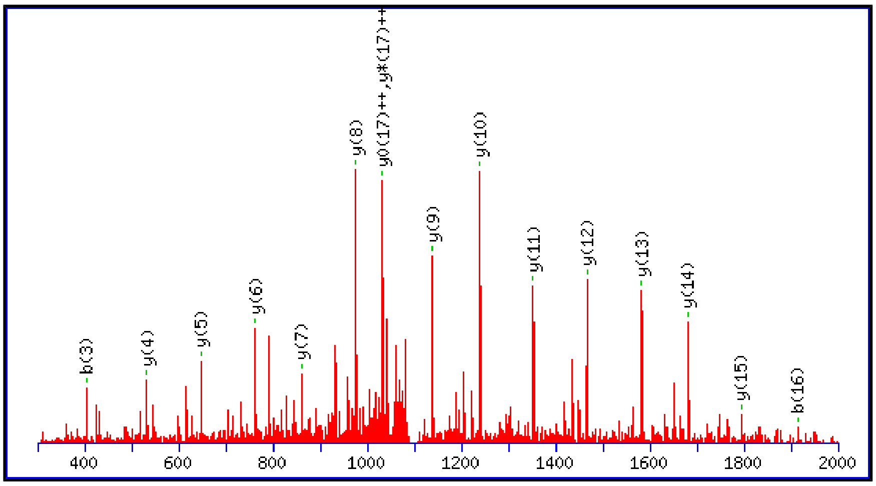
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQCIVDDITYNVNDTFHK**
Found in **F8W7G7** in **con_Xuniprot_HUMAN3**, F8W7G7_HUMAN Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1

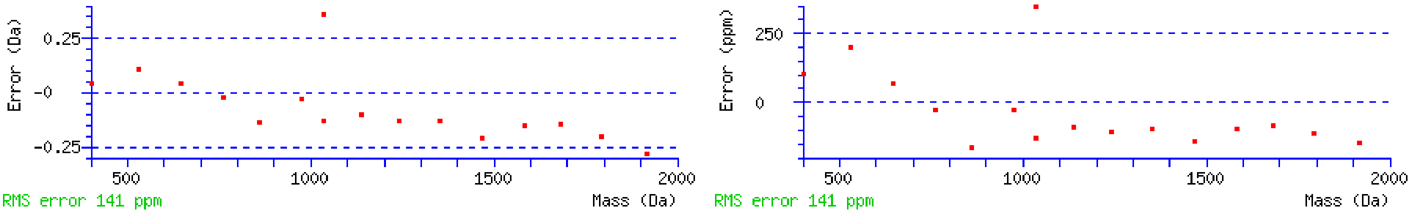
Match to Query 14862: 2196.972488 from(1099.493520,2+) intensity(16723.5469) rtinseconds(1855) scans(4799) index(18690)
Title: 111019_Est_MI_YP_G_08Spectrum4175_scans__4799
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2196.9634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 111 **Expect:** 8.9e-010
Matches : 16/196 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	116.0342	58.5207			98.0237	49.5155	D							18
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	2082.9437	1041.9755	2065.9171	1033.4622	2064.9331	1032.9702	17
3	**404.1234**	202.5654	387.0969	194.0521	386.1129	193.5601	C	1954.8851	977.9462	1937.8586	969.4329	1936.8746	968.9409	16
4	517.2075	259.1074	500.1810	250.5941	499.1969	250.1021	I	***1794.8545***	897.9309	1777.8279	889.4176	1776.8439	888.9256	15
5	616.2759	308.6416	599.2494	300.1283	598.2654	299.6363	V	***1681.7704***	841.3888	1664.7439	832.8756	1663.7598	832.3836	14
6	731.3029	366.1551	714.2763	357.6418	713.2923	357.1498	D	***1582.7020***	791.8546	1565.6754	783.3414	1564.6914	782.8494	13
7	846.3298	423.6685	829.3033	415.1553	828.3192	414.6633	D	***1467.6751***	734.3412	1450.6485	725.8279	1449.6645	725.3359	12
8	959.4139	480.2106	942.3873	471.6973	941.4033	471.2053	I	***1352.6481***	676.8277	1335.6216	668.3144	1334.6375	667.8224	11
9	1060.4616	530.7344	1043.4350	522.2211	1042.4510	521.7291	T	***1239.5640***	620.2857	1222.5375	611.7724	1221.5535	611.2804	10
10	1223.5249	612.2661	1206.4983	603.7528	1205.5143	603.2608	Y	***1138.5164***	569.7618	1121.4898	561.2485	1120.5058	560.7565	9
11	1337.5678	669.2875	1320.5413	660.7743	1319.5572	660.2823	N	***975.4530***	488.2302	958.4265	479.7169	957.4425	479.2249	8
12	1436.6362	718.8217	1419.6097	710.3085	1418.6257	709.8165	V	***861.4101***	431.2087	844.3836	422.6954	843.3995	422.2034	7
13	1551.6632	776.3352	1534.6366	767.8219	1533.6526	767.3299	N	***762.3417***	381.6745	745.3151	373.1612	744.3311	372.6692	6
14	1666.6901	833.8487	1649.6636	825.3354	1648.6795	824.8434	D	***647.3148***	324.1610	630.2882	315.6477	629.3042	315.1557	5
15	1767.7378	884.3725	1750.7112	875.8593	1749.7272	875.3672	T	***532.2878***	266.6475	515.2613	258.1343	514.2772	257.6423	4
16	**1914.8062**	957.9067	1897.7797	949.3935	1896.7956	948.9015	F	431.2401	216.1237	414.2136	207.6104			3
17	2051.8651	1026.4362	2034.8386	1017.9229	2033.8545	1017.4309	H	284.1717	142.5895	267.1452	134.0762			2
18							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
111.0	2196.9634	0.0091	DQCIVDDITYNVNDTFHK	Deamidated N13 99.96%
77.0	2196.9634	0.0091	DQCIVDDITYNVNDTFHK	Deamidated N11 0.04%
22.1	2195.9794	0.9931	DQCIVDDITYNVNDTFHK	
7.2	2194.9735	1.9990	NNSNLWMSSMPGINNVTGAR	
6.4	2194.9735	1.9990	NNSNLWMSSMPGINNVTGAR	
6.4	2194.9735	1.9990	NNSNLWMSSMPGINNVTGAR	
1.7	2196.9634	0.0091	DQCIVDDITYNVNDTFHK	Deamidated Q2 0.00%

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

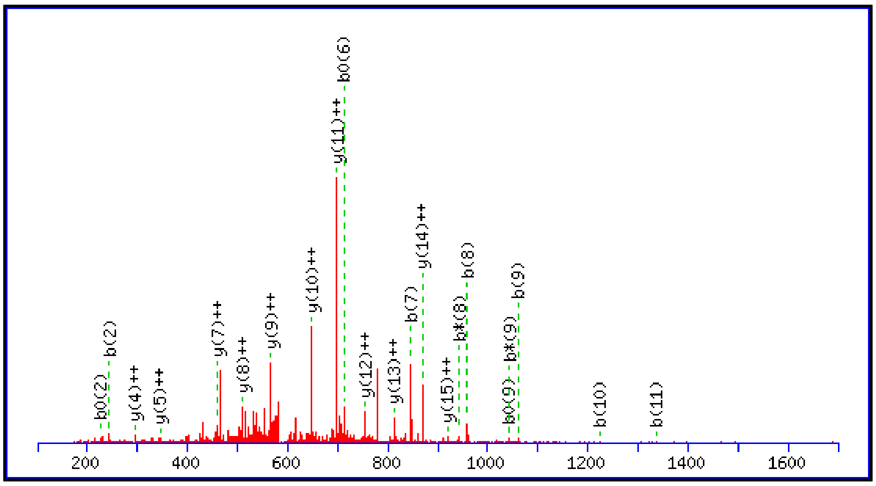
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQCIVDDITYNVNDTFHKR**
Found in **F8W7G7** in **con_Xuniprot_HUMAN3**, F8W7G7_HUMAN Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1

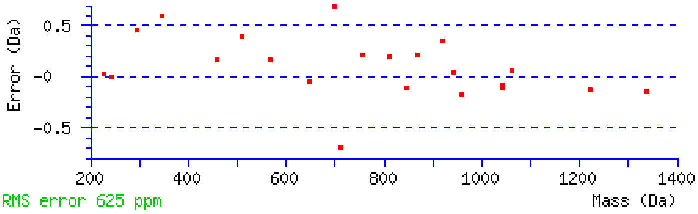
Match to Query 17813: 2353.071496 from(589.275150,4+) intensity(26748.7793) rtinseconds(2051) scans(4876) index(16873)
Title: 111019_Est_MI_YP_G_06Spectrum4037_scans__4876
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

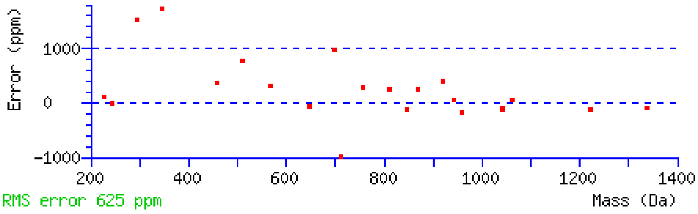
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2353.0645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0013
Matches : 22/206 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	116.0342	58.5207			98.0237	49.5155	D							19
2	**244.0928**	122.5500	227.0662	114.0368	226.0822	113.5448	Q	2239.0448	1120.0260	2222.0183	1111.5128	2221.0342	1111.0208	18
3	404.1234	202.5654	387.0969	194.0521	386.1129	193.5601	C	2110.9862	1055.9968	2093.9597	1047.4835	2092.9757	1046.9915	17
4	517.2075	259.1074	500.1810	250.5941	499.1969	250.1021	I	1950.9556	975.9814	1933.9290	967.4682	1932.9450	966.9761	16
5	616.2759	308.6416	599.2494	300.1283	598.2654	299.6363	V	1837.8715	919.4394	1820.8450	910.9261	1819.8610	910.4341	15
6	731.3029	366.1551	714.2763	357.6418	713.2923	357.1498	D	1738.8031	869.9052	1721.7766	861.3919	1720.7925	860.8999	14
7	**846.3298**	423.6685	829.3033	415.1553	828.3192	414.6633	D	1623.7762	812.3917	1606.7496	803.8784	1605.7656	803.3864	13
8	**959.4139**	480.2106	942.3873	471.6973	941.4033	471.2053	I	1508.7492	754.8782	1491.7227	746.3650	1490.7387	745.8730	12
9	**1060.4616**	530.7344	1043.4350	522.2211	1042.4510	521.7291	T	1395.6652	698.3362	1378.6386	689.8229	1377.6546	689.3309	11
10	**1223.5249**	612.2661	1206.4983	603.7528	1205.5143	603.2608	Y	1294.6175	647.8124	1277.5909	639.2991	1276.6069	638.8071	10
11	**1337.5678**	669.2875	1320.5413	660.7743	1319.5572	660.2823	N	1131.5541	566.2807	1114.5276	557.7674	1113.5436	557.2754	9
12	1436.6362	718.8217	1419.6097	710.3085	1418.6257	709.8165	V	1017.5112	509.2592	1000.4847	500.7460	999.5007	500.2540	8
13	1551.6632	776.3352	1534.6366	767.8219	1533.6526	767.3299	N	918.4428	459.7250	901.4163	451.2118	900.4322	450.7198	7
14	1666.6901	833.8487	1649.6636	825.3354	1648.6795	824.8434	D	803.4159	402.2116	786.3893	393.6983	785.4053	393.2063	6
15	1767.7378	884.3725	1750.7112	875.8593	1749.7272	875.3672	T	688.3889	344.6981	671.3624	336.1848	670.3784	335.6928	5
16	1914.8062	957.9067	1897.7797	949.3935	1896.7956	948.9015	F	587.3412	294.1743	570.3147	285.6610			4
17	2051.8651	1026.4362	2034.8386	1017.9229	2033.8545	1017.4309	H	440.2728	220.6401	423.2463	212.1268			3
18	2179.9601	1090.4837	2162.9335	1081.9704	2161.9495	1081.4784	K	303.2139	152.1106	286.1874	143.5973			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.1	2353.0645	0.0070	DQCIVDDITYNVNDTFHKR	Deamidated N13 92.17%
40.4	2353.0645	0.0070	DQCIVDDITYNVNDTFHKR	Deamidated N11 7.81%
14.8	2353.0645	0.0070	DQCIVDDITYNVNDTFHKR	Deamidated Q2 0.02%
12.5	2352.0724	0.9991	LEGECRSNNATSTASSNLGASAR	
10.5	2353.0719	-0.0004	GIQHVYEDMSSPMDFNVVLR	
5.8	2351.0661	2.0054	ENTTKMELYKVQNEFSMNK	
5.3	2351.0661	2.0054	ENTTKMELYKVQNEFSMNK	
4.8	2351.0706	2.0009	LASKNFPSISDSYNYPNYDR	
4.6	2353.0604	0.0111	QPAPAAPQGQASTSPQGAGEGRASM	
4.6	2353.0604	0.0111	QPAPAAPQGQASTSPQGAGEGRASM	

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

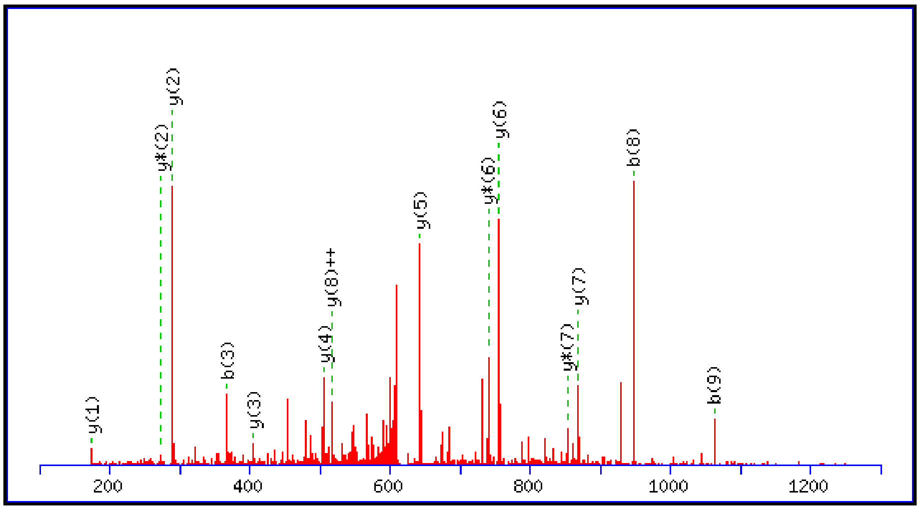
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGYILHTDNR**
Found in **C9JMA2** in **con_Xuniprot_HUMAN3**, C9JMA2_HUMAN Mannan-binding lectin serine protease 1 heavy chain (Fragment) OS=Homo sapiens GN=MASP1 PE=2 SV=1

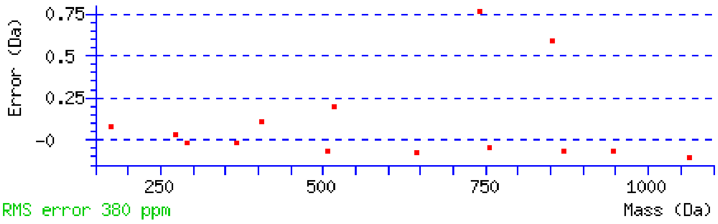
Match to Query 1737: 1235.595548 from(618.805050,2+) intensity(49297.7539) rtinseconds(781) scans(1742) index(2515)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1473_scans__1742
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

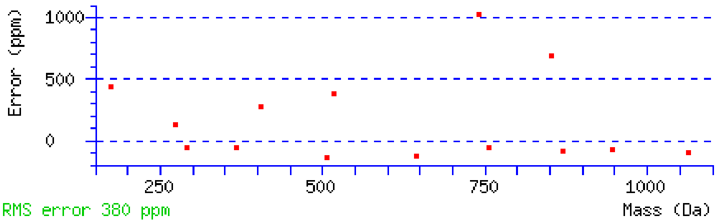
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1235.5935
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 48 **Expect:** 0.0034
Matches : 14/76 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	205.0972	103.0522					G	1089.5324	545.2698	1072.5058	536.7565	1071.5218	536.2645	9
3	**368.1605**	184.5839					Y	1032.5109	516.7591	1015.4843	508.2458	1014.5003	507.7538	8
4	481.2445	241.1259					I	***869.4476***	435.2274	852.4210	426.7141	851.4370	426.2221	7
5	594.3286	297.6679					L	***756.3635***	378.6854	739.3369	370.1721	738.3529	369.6801	6
6	731.3875	366.1974					H	***643.2794***	322.1434	626.2529	313.6301	625.2689	313.1381	5
7	832.4352	416.7212			814.4246	407.7160	T	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	4
8	**947.4621**	474.2347			929.4516	465.2294	D	***405.1728***	203.0901	388.1463	194.5768	387.1623	194.0848	3
9	**1062.4891**	531.7482	1045.4625	523.2349	1044.4785	522.7429	N	***290.1459***	145.5766	273.1193	137.0633			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FGYILHTDNR
(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	1235.5935	0.0021	FGYILHTDNR
12.7	1235.5894	0.0061	GQYRAVSSPDR
7.9	1235.5894	0.0061	ARNLQAQYDR
7.9	1235.5894	0.0061	ARNLQAQYDR
7.9	1235.5894	0.0061	ARNLQAQYDR
7.5	1235.5894	0.0061	VEEHLQPNDR
6.3	1234.5976	0.9980	GNVISCVTNSGK
5.0	1235.5993	-0.0038	GNVTSLSLSSNR
4.7	1235.5928	0.0027	TRTTEMNLNR
4.6	1235.6007	-0.0051	DHGLQAPRADR

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

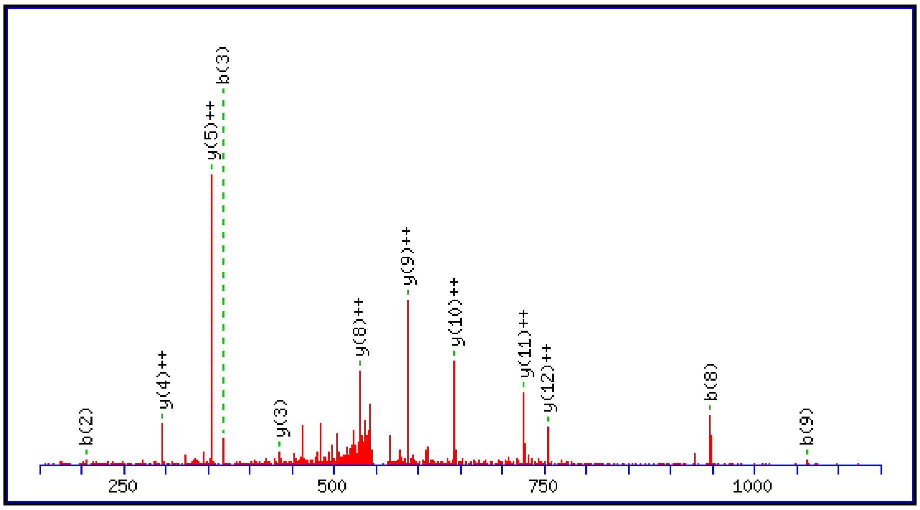
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FGYILHTDNRTCR**
Found in **C9JMA2** in **con_Xuniprot_HUMAN3**, C9JMA2_HUMAN Mannan-binding lectin serine protease 1 heavy chain (Fragment) OS=Homo sapiens GN=MASP1 PE=2 SV=1

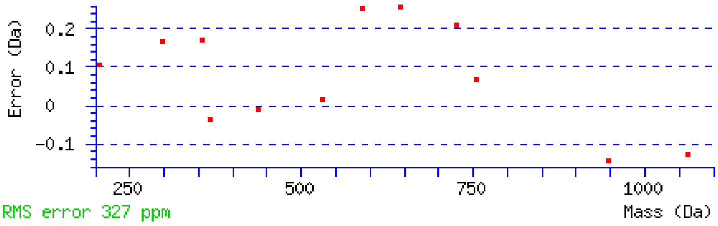
Match to Query 8408: 1652.775522 from(551.932450,3+) intensity(15448.3613) rtinseconds(650) scans(1394) index(1176)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum1179_scans__1394
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

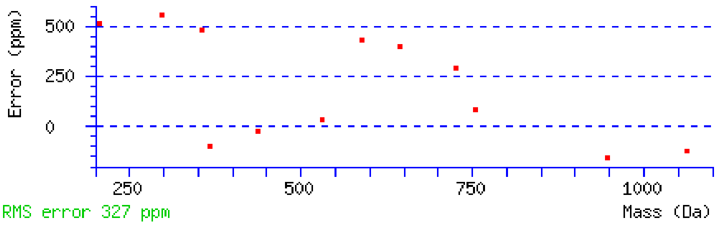
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1150 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1652.7729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.015
Matches : 12/112 fragment ions using 20 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							13
2	**205.0972**	103.0522					G	1506.7118	753.8595	1489.6852	745.3463	1488.7012	744.8542	12
3	**368.1605**	184.5839					Y	1449.6903	725.3488	1432.6638	716.8355	1431.6798	716.3435	11
4	481.2445	241.1259					I	1286.6270	643.8171	1269.6004	635.3039	1268.6164	634.8119	10
5	594.3286	297.6679					L	1173.5429	587.2751	1156.5164	578.7618	1155.5324	578.2698	9
6	731.3875	366.1974					H	1060.4589	530.7331	1043.4323	522.2198	1042.4483	521.7278	8
7	832.4352	416.7212			814.4246	407.7160	T	923.4000	462.2036	906.3734	453.6903	905.3894	453.1983	7
8	**947.4621**	474.2347			929.4516	465.2294	D	822.3523	411.6798	805.3257	403.1665	804.3417	402.6745	6
9	**1062.4891**	531.7482	1045.4625	523.2349	1044.4785	522.7429	N	707.3253	354.1663	690.2988	345.6530	689.3148	345.1610	5
10	1218.5902	609.7987	1201.5637	601.2855	1200.5796	600.7935	R	592.2984	296.6528	575.2718	288.1396	574.2878	287.6476	4
11	1319.6379	660.3226	1302.6113	651.8093	1301.6273	651.3173	T	436.1973	218.6023	419.1707	210.0890	418.1867	209.5970	3
12	1479.6685	740.3379	1462.6420	731.8246	1461.6580	731.3326	C	335.1496	168.0784	318.1231	159.5652			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of FGYILHTDNRTCR
(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	1652.7729	0.0026	FGYILHTDNRTCR
13.2	1652.7835	-0.0080	LEFDSNTPYGVFHK
9.4	1650.7607	2.0149	THLPGAQAAPCPSCGK
8.1	1651.7689	1.0066	TEDDATKTTPNNFAK
6.7	1652.7836	-0.0081	SPMMNNKYKMIHK
6.1	1651.7763	0.9992	QEPCETDSLGLLYK
5.0	1650.7705	2.0050	GSVTANMLCAGLESGGK
4.0	1651.7689	1.0066	DEFSEKKEQAEQGK
3.9	1652.7763	-0.0008	NIMIHHLQGDAMNK
3.6	1651.7763	0.9992	QIKCLEELGDNFGK

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

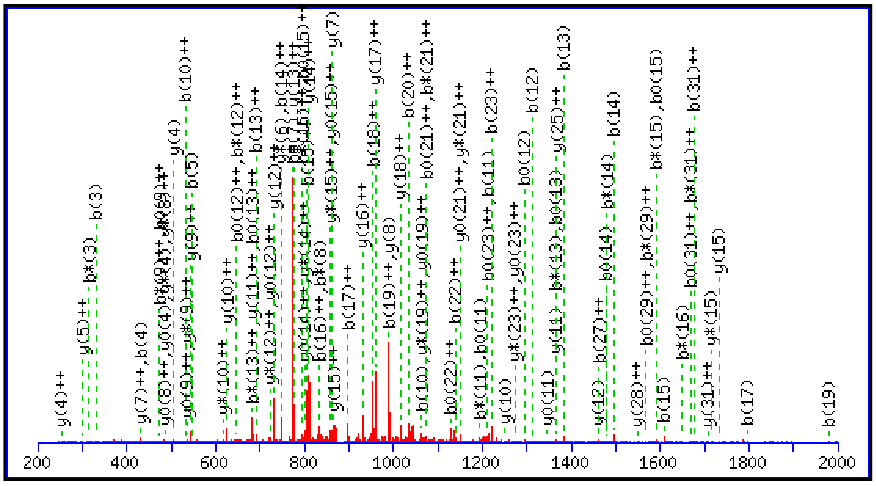
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NCGVNCSGDVFTALIGEIASPNYPKPYPENSR**
Found in **F5H7T4** in **con_Xuniprot_HUMAN3**, F5H7T4_HUMAN Complement C1s subcomponent (Fragment) OS=Homo sapiens GN=C1S PE=2 SV=1

Match to Query 27796: 3526.618896 from(882.662000,4+) intensity(53783.2070) rtinseconds(2541) scans(6619) index(2290)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum5763_scans__6619
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

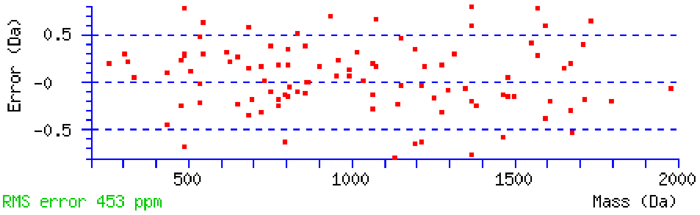
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

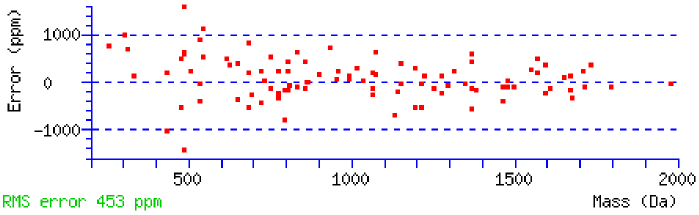


Monoisotopic mass of neutral peptide Mr(calc): 3526.6133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 65 **Expect:** 5.6e-005
Matches : 99/358 fragment ions using 170 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**32**
2	275.0809	138.0441	258.0543	129.5308			**C**	3413.5777	1707.2925	3396.5511	1698.7792	3395.5671	1698.2872	**31**
3	***332.1023***	166.5548	315.0758	158.0415			**G**	3253.5470	1627.2771	3236.5205	1618.7639	3235.5365	1618.2719	**30**
4	***431.1707***	216.0890	414.1442	207.5757			**V**	3196.5256	1598.7664	3179.4990	1590.2531	3178.5150	1589.7611	**29**
5	***546.1977***	273.6025	529.1711	265.0892			**N**	3097.4571	1549.2322	3080.4306	1540.7189	3079.4466	1540.2269	**28**
6	706.2283	353.6178	689.2018	345.1045			**C**	2982.4302	1491.7187	2965.4037	1483.2055	2964.4196	1482.7135	**27**
7	793.2604	397.1338	776.2338	388.6205	775.2498	388.1285	**S**	2822.3996	1411.7034	2805.3730	1403.1901	2804.3890	1402.6981	**26**
8	850.2818	425.6445	833.2553	417.1313	832.2712	416.6393	**G**	2735.3675	1368.1874	2718.3410	1359.6741	2717.3570	1359.1821	**25**
9	965.3088	483.1580	948.2822	474.6447	947.2982	474.1527	**D**	2678.3461	1339.6767	2661.3195	1331.1634	2660.3355	1330.6714	**24**
10	***1064.3772***	**532.6922**	1047.3506	524.1789	1046.3666	523.6869	**V**	2563.3191	1282.1632	2546.2926	1273.6499	2545.3086	1273.1579	**23**
11	***1211.4456***	606.2264	1194.4190	597.7132	1193.4350	597.2211	**F**	2464.2507	1232.6290	2447.2242	1224.1157	2446.2401	1223.6237	**22**
12	***1312.4933***	656.7503	1295.4667	648.2370	1294.4827	647.7450	**T**	2317.1823	1159.0948	2300.1557	1150.5815	2299.1717	1150.0895	**21**
13	***1383.5304***	**692.2688**	1366.5038	683.7556	1365.5198	683.2635	**A**	2216.1346	1108.5709	2199.1081	1100.0577	2198.1240	1099.5657	**20**
14	***1496.6144***	**748.8109**	1479.5879	740.2976	1478.6039	739.8056	**L**	2145.0975	1073.0524	2128.0709	1064.5391	2127.0869	1064.0471	**19**
15	***1609.6985***	**805.3529**	1592.6720	796.8396	1591.6879	796.3476	**I**	2032.0134	1016.5104	2014.9869	1007.9971	2014.0029	1007.5051	**18**
16	1666.7200	**833.8636**	1649.6934	825.3503	1648.7094	824.8583	**G**	1918.9294	959.9683	1901.9028	951.4550	1900.9188	950.9630	**17**
17	***1795.7626***	**898.3849**	1778.7360	889.8716	1777.7520	889.3796	**E**	1861.9079	931.4576	1844.8814	922.9443	1843.8973	922.4523	**16**
18	1908.8466	**954.9270**	1891.8201	946.4137	1890.8361	945.9217	**I**	**1732.8653**	866.9363	1715.8388	858.4230	1714.8547	857.9310	**15**
19	***1979.8837***	**990.4455**	1962.8572	981.9322	1961.8732	981.4402	**A**	1619.7812	810.3943	1602.7547	801.8810	1601.7707	801.3890	**14**
20	2066.9158	**1033.9615**	2049.8892	1025.4482	2048.9052	1024.9562	**S**	1548.7441	774.8757	1531.7176	766.3624	1530.7336	765.8704	**13**
21	2163.9685	1082.4879	2146.9420	1073.9746	2145.9580	1073.4826	**P**	**1461.7121**	731.3597	1444.6856	722.8464	1443.7015	722.3544	**12**
22	2278.0115	**1139.5094**	2260.9849	1130.9961	2260.0009	1130.5041	**N**	**1364.6593**	682.8333	1347.6328	674.3200	1346.6488	673.8280	**11**

23	2441.0748	**1221.0410**	2424.0482	1212.5278	2423.0642	1212.0357	**Y**	**1250.6164**	625.8118	1233.5899	617.2986	1232.6058	616.8066	**10**
24	2538.1276	1269.5674	2521.1010	1261.0541	2520.1170	1260.5621	**P**	1087.5531	544.2802	1070.5265	535.7669	1069.5425	535.2749	**9**
25	2666.2225	1333.6149	2649.1960	1325.1016	2648.2120	1324.6096	**K**	**990.5003**	495.7538	973.4738	487.2405	972.4898	486.7485	**8**
26	2763.2753	1382.1413	2746.2487	1373.6280	2745.2647	1373.1360	**P**	**862.4054**	431.7063	845.3788	423.1930	844.3948	422.7010	**7**
27	2926.3386	**1463.6729**	2909.3121	1455.1597	2908.3280	1454.6677	**Y**	765.3526	383.1799	748.3260	374.6667	747.3420	374.1747	**6**
28	3023.3914	1512.1993	3006.3648	1503.6860	3005.3808	1503.1940	**P**	602.2893	301.6483	585.2627	293.1350	584.2787	292.6430	**5**
29	3152.4340	1576.7206	3135.4074	1568.2073	3134.4234	1567.7153	**E**	**505.2365**	253.1219	488.2100	244.6086	487.2259	244.1166	**4**
30	3266.4769	1633.7421	3249.4503	1625.2288	3248.4663	1624.7368	**N**	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	**3**
31	3353.5089	**1677.2581**	3336.4824	1668.7448	3335.4984	1668.2528	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
32							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.4	3526.6133	0.0056	NCGVNCSGDVFTALIGEIASPNYPKPYPENSR	Deamidated N5 82.59%
55.9	3526.6133	0.0056	NCGVNCSGDVFTALIGEIASPNYPKPYPENSR	Deamidated N1 9.42%
53.5	3526.6133	0.0056	NCGVNCSGDVFTALIGEIASPNYPKPYPENSR	Deamidated N22 5.41%
50.3	3526.6133	0.0056	NCGVNCSGDVFTALIGEIASPNYPKPYPENSR	Deamidated N30 2.58%
45.0	3525.6293	0.9896	NCGVNCSGDVFTALIGEIASPNYPKPYPENSR	
5.9	3526.6245	-0.0056	EITLPTANVSVQVSAPWNTNMQRDEHHYCK	
5.9	3526.6245	-0.0056	EITLPTANVSVQVSAPWNTNMQRDEHHYCK	
5.9	3526.6245	-0.0056	EITLPTANVSVQVSAPWNTNMQRDEHHYCK	
5.9	3526.6245	-0.0056	EITLPTANVSVQVSAPWNTNMQRDEHHYCK	
3.4	3524.6222	1.9967	NGKMLGPTSQPSCPDPDLSLEPGQTGEGMVGPVR	

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

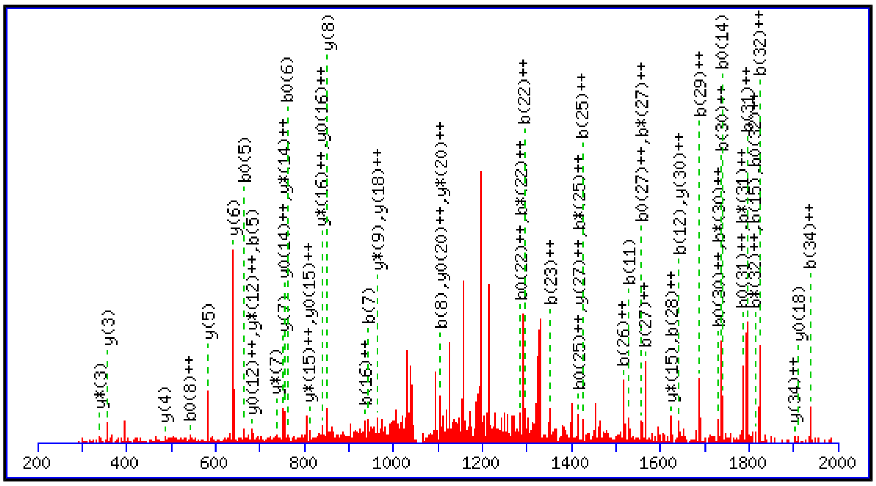
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK**
Found in **F8WCZ6** in **con_Xuniprot_HUMAN3**, F8WCZ6_HUMAN Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=2 SV=1

Match to Query 28983: 4227.757016 from(1057.946530,4+) intensity(18869.6113) rtinseconds(2214) scans(5800) index(19835)
Title: 111019_Est_MI_YP_G_09Spectrum5127_scans__5800
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

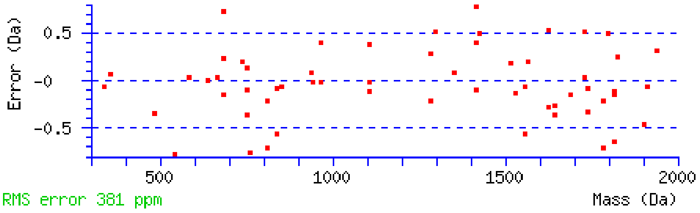
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

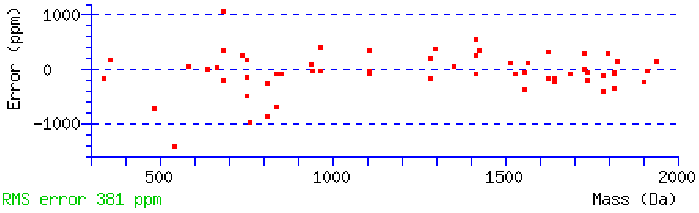


Monoisotopic mass of neutral peptide Mr(calc): 4227.7448
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N23 : Deamidated (NQ)
N28 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.0045
Matches : 59/402 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					**Y**							**37**
2	265.1183	133.0628			247.1077	124.0575	**T**	4065.6888	2033.3480	4048.6623	2024.8348	4047.6783	2024.3428	**36**
3	425.1489	213.0781			407.1384	204.0728	**C**	3964.6411	1982.8242	3947.6146	1974.3109	3946.6306	1973.8189	**35**
4	554.1915	277.5994			536.1810	268.5941	**E**	3804.6105	1902.8089	3787.5839	1894.2956	3786.5999	1893.8036	**34**
5	***683.2341***	342.1207			665.2236	333.1154	**E**	3675.5679	1838.2876	3658.5413	1829.7743	3657.5573	1829.2823	**33**
6	780.2869	390.6471			762.2763	381.6418	**P**	3546.5253	1773.7663	3529.4988	1765.2530	3528.5147	1764.7610	**32**
7	***943.3502***	472.1787			925.3396	463.1735	**Y**	3449.4725	1725.2399	3432.4460	1716.7266	3431.4620	1716.2346	**31**
8	***1106.4135***	553.7104			1088.4030	544.7051	**Y**	3286.4092	1643.7082	3269.3827	1635.1950	3268.3986	1634.7030	**30**
9	1269.4769	635.2421			1251.4663	626.2368	**Y**	3123.3459	1562.1766	3106.3193	1553.6633	3105.3353	1553.1713	**29**
10	1400.5174	700.7623			1382.5068	691.7570	**M**	2960.2826	1480.6449	2943.2560	1472.1316	2942.2720	1471.6396	**28**
11	***1529.5599***	765.2836			1511.5494	756.2783	**E**	2829.2421	1415.1247	2812.2155	1406.6114	2811.2315	1406.1194	**27**
12	***1643.6029***	822.3051	1626.5763	813.7918	1625.5923	813.2998	**N**	2700.1995	1350.6034	2683.1729	1342.0901	2682.1889	1341.5981	**26**
13	1700.6243	850.8158	1683.5978	842.3025	1682.6138	841.8105	**G**	2586.1565	1293.5819	2569.1300	1285.0686	2568.1460	1284.5766	**25**
14	1757.6458	879.3265	1740.6193	870.8133	1739.6352	870.3213	**G**	2529.1351	1265.0712	2512.1085	1256.5579	2511.1245	1256.0659	**24**
15	***1814.6673***	907.8373	1797.6407	899.3240	1796.6567	898.8320	**G**	2472.1136	1236.5604	2455.0871	1228.0472	2454.1031	1227.5552	**23**
16	1871.6887	***936.3480***	1854.6622	927.8347	1853.6782	927.3427	**G**	2415.0922	1208.0497	2398.0656	1199.5364	2397.0816	1199.0444	**22**
17	2000.7313	1000.8693	1983.7048	992.3560	1982.7208	991.8640	**E**	2358.0707	1179.5390	2341.0441	1171.0257	2340.0601	1170.5337	**21**
18	2163.7947	1082.4010	2146.7681	1073.8877	2145.7841	1073.3957	**Y**	2229.0281	1115.0177	2212.0015	1106.5044	2211.0175	1106.0124	**20**
19	2300.8536	1150.9304	2283.8270	1142.4171	2282.8430	1141.9251	**H**	2065.9648	1033.4860	2048.9382	1024.9727	2047.9542	1024.4807	**19**
20	2460.8842	1230.9457	2443.8577	1222.4325	2442.8736	1221.9405	**C**	1928.9059	964.9566	1911.8793	956.4433	1910.8953	955.9513	**18**
21	2531.9213	1266.4643	2514.8948	1257.9510	2513.9108	1257.4590	**A**	1768.8752	884.9412	1751.8487	876.4280	1750.8646	875.9360	**17**
22	2588.9428	***1294.9750***	2571.9162	1286.4618	2570.9322	1285.9698	**G**	1697.8381	849.4227	1680.8115	840.9094	1679.8275	840.4174	**16**

23	2703.9697	***1352.4885***	2686.9432	1343.9752	2685.9592	1343.4832	**N**	1640.8166	820.9120	1623.7901	812.3987	1622.8061	811.9067	**15**
24	2760.9912	1380.9992	2743.9646	1372.4860	2742.9806	1371.9940	**G**	1525.7897	763.3985	1508.7631	754.8852	1507.7791	754.3932	**14**
25	2848.0232	***1424.5153***	2830.9967	1416.0020	2830.0127	1415.5100	**S**	1468.7682	734.8877	1451.7417	726.3745	1450.7577	725.8825	**13**
26	3034.1025	***1517.5549***	3017.0760	1509.0416	3016.0920	1508.5496	**W**	1381.7362	691.3717	1364.7096	682.8585	1363.7256	682.3665	**12**
27	3133.1710	***1567.0891***	3116.1444	1558.5758	3115.1604	1558.0838	**V**	1195.6569	598.3321	1178.6303	589.8188	1177.6463	589.3268	**11**
28	3248.1979	***1624.6026***	3231.1713	1616.0893	3230.1873	1615.5973	**N**	1096.5885	548.7979	1079.5619	540.2846	1078.5779	539.7926	**10**
29	3377.2405	***1689.1239***	3360.2139	1680.6106	3359.2299	1680.1186	**E**	981.5615	491.2844	964.5350	482.7711	963.5510	482.2791	**9**
30	3476.3089	***1738.6581***	3459.2824	1730.1448	3458.2983	1729.6528	**V**	**852.5189**	426.7631	835.4924	418.2498	834.5084	417.7578	**8**
31	3589.3930	***1795.2001***	3572.3664	1786.6868	3571.3824	1786.1948	**L**	**753.4505**	377.2289	736.4240	368.7156	735.4400	368.2236	**7**
32	3646.4144	***1823.7109***	3629.3879	1815.1976	3628.4039	1814.7056	**G**	**640.3665**	320.6869	623.3399	312.1736	622.3559	311.6816	**6**
33	3743.4672	1872.2372	3726.4406	1863.7240	3725.4566	1863.2320	**P**	**583.3450**	292.1761	566.3184	283.6629	565.3344	283.1708	**5**
34	3872.5098	***1936.7585***	3855.4832	1928.2453	3854.4992	1927.7532	**E**	**486.2922**	243.6498	469.2657	235.1365	468.2817	234.6445	**4**
35	3985.5939	1993.3006	3968.5673	1984.7873	3967.5833	1984.2953	**L**	**357.2496**	179.1285	340.2231	170.6152			**3**
36	4082.6466	2041.8269	4065.6201	2033.3137	4064.6361	2032.8217	**P**	244.1656	122.5864	227.1390	114.0731			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.1	4227.7448	0.0122	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	Deamidated N23, N28 41.49%
36.7	4227.7448	0.0122	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	Deamidated N12, N23 37.23%
34.2	4227.7448	0.0122	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	Deamidated N12, N28 21.28%
33.7	4226.7608	0.9962	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	
31.3	4226.7608	0.9962	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	
27.0	4226.7608	0.9962	YTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPK	
0.9	4226.7622	0.9949	MPSLSTAVQNMGMYGNLPCNQPNTYSVTSGMNQLTQQR	
0.9	4226.7622	0.9949	MPSLSTAVQNMGMYGNLPCNQPNTYSVTSGMNQLTQQR	
0.4	4226.7590	0.9980	MSLVMPAMAPNETLSGRGAPGDYEEMMQIECEVMDTR	

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

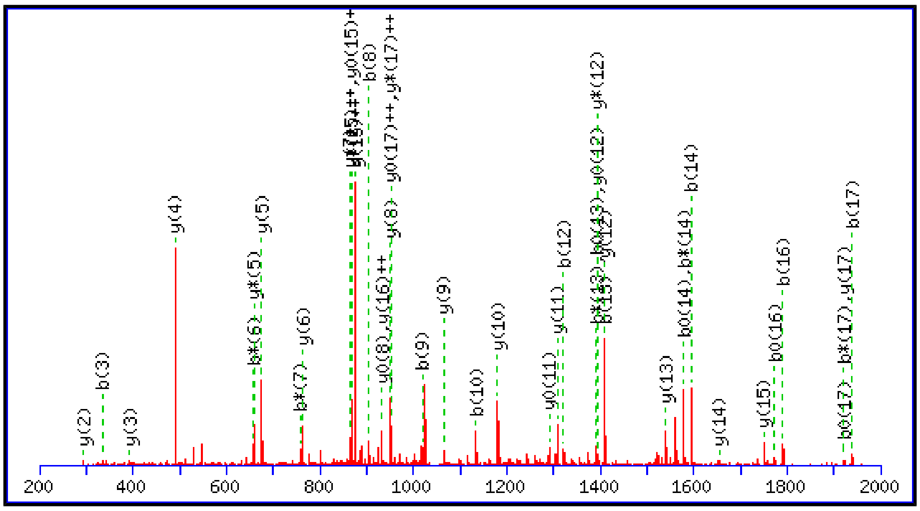
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

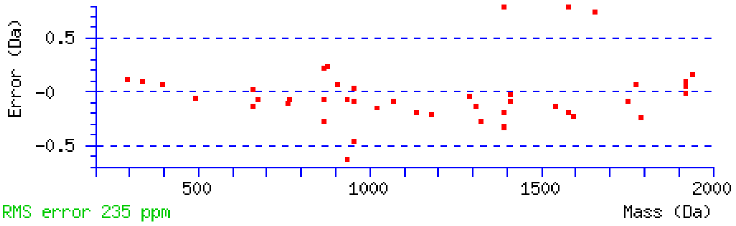
Match to Query 13144: 2083.922268 from(1042.968410,2+) intensity(39014.5586) rtinseconds(1519) scans(3435) index(28127)
Title: 111019_Est_MI_YS_G_12Spectrum3005_scans__3435
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

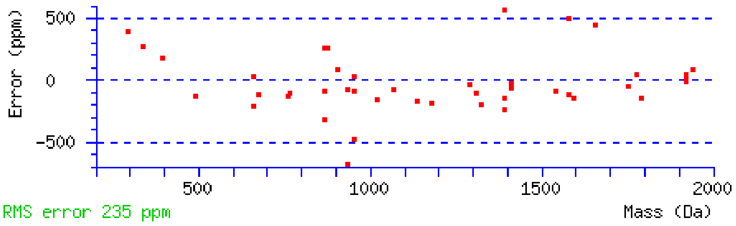
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 91 **Expect:** 9.6e-008
Matches : 44/180 fragment ions using 85 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							18
2	221.0921	111.0497					G	***1921.8563***	961.4318	1904.8297	952.9185	1903.8457	952.4265	17
3	**335.1350**	168.0711	318.1084	159.5579			N	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	16
4	432.1878	216.5975	415.1612	208.0842			P	***1750.7919***	875.8996	1733.7653	867.3863	1732.7813	866.8943	15
5	546.2307	273.6190	529.2041	265.1057			N	***1653.7391***	827.3732	1636.7126	818.8599	1635.7285	818.3679	14
6	675.2733	338.1403	658.2467	329.6270	657.2627	329.1350	E	***1539.6962***	770.3517	1522.6696	761.8385	1521.6856	761.3464	13
7	776.3210	388.6641	759.2944	380.1508	758.3104	379.6588	T	***1410.6536***	705.8304	1393.6270	697.3172	1392.6430	696.8251	12
8	**905.3636**	453.1854	888.3370	444.6721	887.3530	444.1801	Q	***1309.6059***	655.3066	1292.5794	646.7933	1291.5953	646.3013	11
9	**1019.4065**	510.2069	1002.3799	501.6936	1001.3959	501.2016	N	***1180.5633***	590.7853	1163.5368	582.2720	1162.5527	581.7800	10
10	**1134.4334**	567.7203	1117.4069	559.2071	1116.4229	558.7151	N	***1066.5204***	533.7638	1049.4938	525.2506	1048.5098	524.7585	9
11	1221.4655	611.2364	1204.4389	602.7231	1203.4549	602.2311	S	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	**1322.5131**	661.7602	1305.4866	653.2469	1304.5026	652.7549	T	***864.4614***	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	**1409.5452**	705.2762	1392.5186	696.7629	1391.5346	696.2709	S	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	**1595.6245**	798.3159	1578.5979	789.8026	1577.6139	789.3106	W	***676.3817***	338.6945	659.3552	330.1812			5
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	P	***490.3024***	245.6548	473.2758	237.1416			4
16	**1791.7456**	896.3765	1774.7191	887.8632	1773.7351	887.3712	V	***393.2496***	197.1285	376.2231	188.6152			3
17	**1938.8141**	969.9107	1921.7875	961.3974	1920.8035	960.9054	F	***294.1812***	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.8	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 35.20%
90.7	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 34.39%
88.1	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 19.08%
81.9	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 4.59%
81.9	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 4.59%
77.6	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 1.71%
67.1	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 0.15%
67.1	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 0.15%
67.1	2083.9123	0.0100	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 0.15%
53.3	2082.9283	0.9940	YGNPNETQNNSTSWPVFK	

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

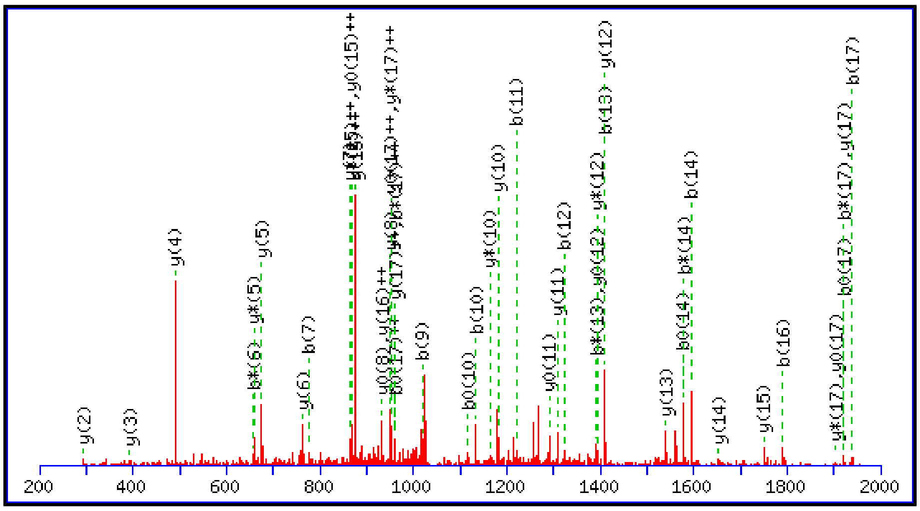
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

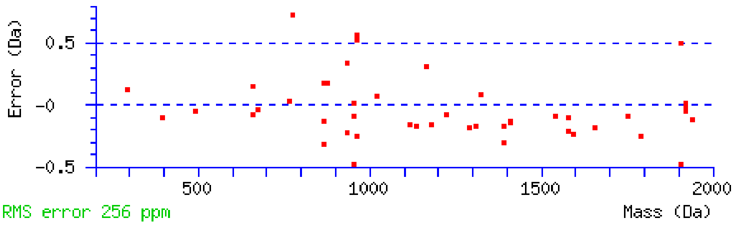
Match to Query 13135: 2083.917868 from(1042.966210,2+) intensity(18234.7734) rtinseconds(1565) scans(3759) index(27432)
Title: 111019_Est_MI_YS_G_10Spectrum3234_scans__3759
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

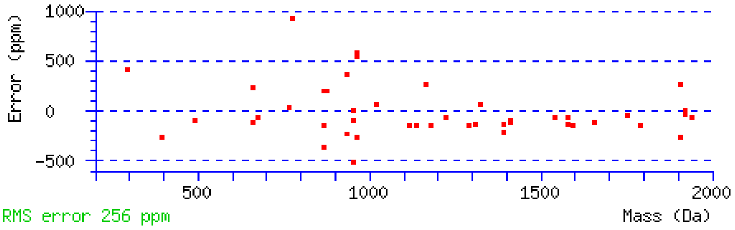
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 78 **Expect:** 1.5e-006
Matches : 47/180 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					**Y**							**18**
2	221.0921	111.0497					**G**	***1921.8563***	961.4318	1904.8297	952.9185	1903.8457	952.4265	**17**
3	335.1350	168.0711	318.1084	159.5579			**N**	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	**16**
4	432.1878	216.5975	415.1612	208.0842			**P**	***1750.7919***	875.8996	1733.7653	867.3863	1732.7813	866.8943	**15**
5	546.2307	273.6190	529.2041	265.1057			**N**	***1653.7391***	827.3732	1636.7126	818.8599	1635.7285	818.3679	**14**
6	675.2733	338.1403	658.2467	329.6270	657.2627	329.1350	**E**	***1539.6962***	770.3517	1522.6696	761.8385	1521.6856	761.3464	**13**
7	**776.3210**	388.6641	759.2944	380.1508	758.3104	379.6588	**T**	***1410.6536***	705.8304	1393.6270	697.3172	1392.6430	696.8251	**12**
8	904.3795	452.6934	887.3530	444.1801	886.3690	443.6881	**Q**	***1309.6059***	655.3066	1292.5794	646.7933	1291.5953	646.3013	**11**
9	**1019.4065**	510.2069	1002.3799	501.6936	1001.3959	501.2016	**N**	***1181.5473***	591.2773	1164.5208	582.7640	1163.5368	582.2720	**10**
10	**1134.4334**	567.7203	1117.4069	559.2071	1116.4229	558.7151	**N**	1066.5204	533.7638	1049.4938	525.2506	1048.5098	524.7585	**9**
11	**1221.4655**	611.2364	1204.4389	602.7231	1203.4549	602.2311	**S**	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	**8**
12	**1322.5131**	661.7602	1305.4866	653.2469	1304.5026	652.7549	**T**	***864.4614***	432.7343	847.4349	424.2211	846.4509	423.7291	**7**
13	**1409.5452**	705.2762	1392.5186	696.7629	1391.5346	696.2709	**S**	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	**6**
14	**1595.6245**	798.3159	1578.5979	789.8026	1577.6139	789.3106	**W**	***676.3817***	338.6945	659.3552	330.1812			**5**
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	**P**	***490.3024***	245.6548	473.2758	237.1416			**4**
16	**1791.7456**	896.3765	1774.7191	887.8632	1773.7351	887.3712	**V**	***393.2496***	197.1285	376.2231	188.6152			**3**
17	**1938.8141**	969.9107	1921.7875	961.3974	1920.8035	960.9054	**F**	***294.1812***	147.5942	277.1547	139.0810			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.4	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 23.96%
78.3	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 23.69%
77.3	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 18.43%
77.1	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 17.81%
76.0	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 13.82%
66.0	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 1.39%
61.0	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 0.44%
61.0	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 0.44%
47.6	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 0.02%
35.3	2083.9123	0.0056	YGNPNETQNNSTSWPVFK	Deamidated N3, N5 0.00%

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

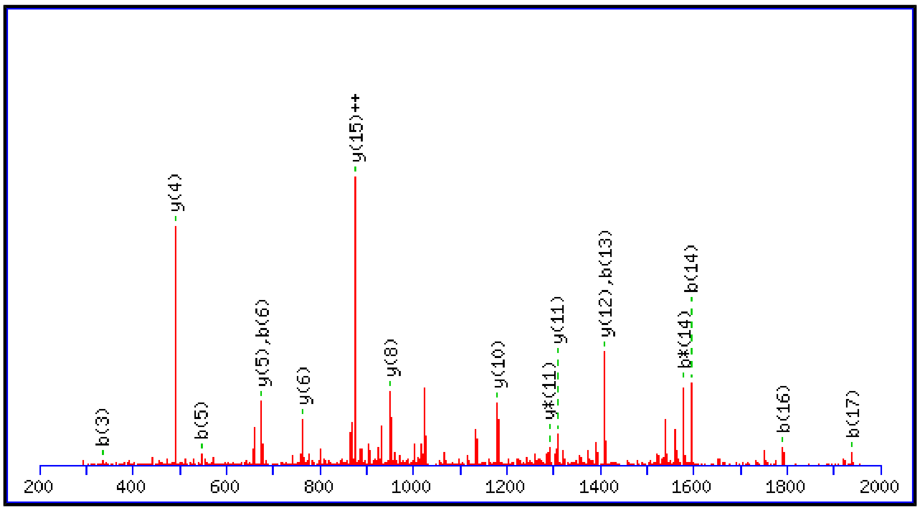
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

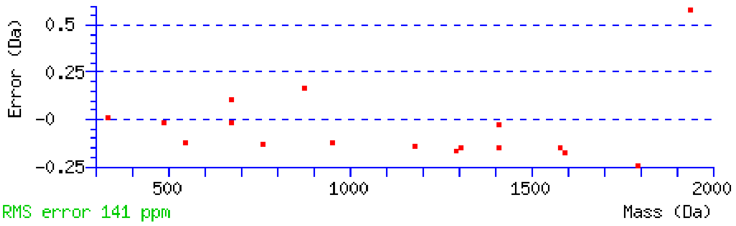
Match to Query 13142: 2083.921688 from(1042.968120,2+) intensity(27549.4844) rtinseconds(1541) scans(3490) index(28129)
Title: 111019_Est_MI_YS_G_12Spectrum3055_scans__3490
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

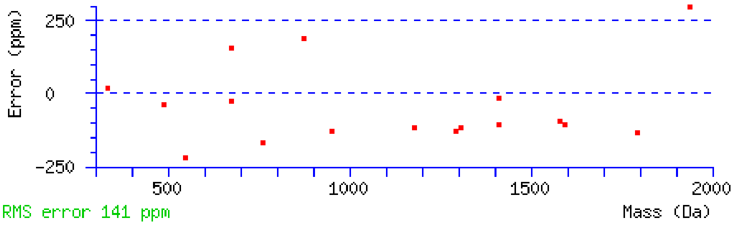
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 75 **Expect:** 3.4e-006
Matches : 17/180 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							18
2	221.0921	111.0497					G	1921.8563	961.4318	1904.8297	952.9185	1903.8457	952.4265	17
3	***335.1350***	168.0711	318.1084	159.5579			N	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	16
4	432.1878	216.5975	415.1612	208.0842			P	1750.7919	875.8996	1733.7653	867.3863	1732.7813	866.8943	15
5	***547.2147***	274.1110	530.1882	265.5977			N	1653.7391	827.3732	1636.7126	818.8599	1635.7285	818.3679	14
6	***676.2573***	338.6323	659.2307	330.1190	658.2467	329.6270	E	1538.7122	769.8597	1521.6856	761.3464	1520.7016	760.8544	13
7	777.3050	389.1561	760.2784	380.6429	759.2944	380.1508	T	***1409.6696***	705.3384	1392.6430	696.8251	1391.6590	696.3331	12
8	905.3636	453.1854	888.3370	444.6721	887.3530	444.1801	Q	***1308.6219***	654.8146	1291.5953	646.3013	1290.6113	645.8093	11
9	1019.4065	510.2069	1002.3799	501.6936	1001.3959	501.2016	N	***1180.5633***	590.7853	1163.5368	582.2720	1162.5527	581.7800	10
10	1134.4334	567.7203	1117.4069	559.2071	1116.4229	558.7151	N	1066.5204	533.7638	1049.4938	525.2506	1048.5098	524.7585	9
11	1221.4655	611.2364	1204.4389	602.7231	1203.4549	602.2311	S	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	1322.5131	661.7602	1305.4866	653.2469	1304.5026	652.7549	T	864.4614	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	***1409.5452***	705.2762	1392.5186	696.7629	1391.5346	696.2709	S	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	***1595.6245***	798.3159	1578.5979	789.8026	1577.6139	789.3106	W	***676.3817***	338.6945	659.3552	330.1812			5
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	P	***490.3024***	245.6548	473.2758	237.1416			4
16	***1791.7456***	896.3765	1774.7191	887.8632	1773.7351	887.3712	V	393.2496	197.1285	376.2231	188.6152			3
17	***1938.8141***	969.9107	1921.7875	961.3974	1920.8035	960.9054	F	294.1812	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.3	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 37.20%
75.3	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 37.20%
68.2	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 7.22%
67.3	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 5.94%
67.3	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 5.84%
62.9	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 2.17%
62.9	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 2.17%
62.7	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 2.06%
51.7	2083.9123	0.0094	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 0.16%
47.8	2082.9283	0.9934	YGNPNETQNNSTSWPVFK	

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

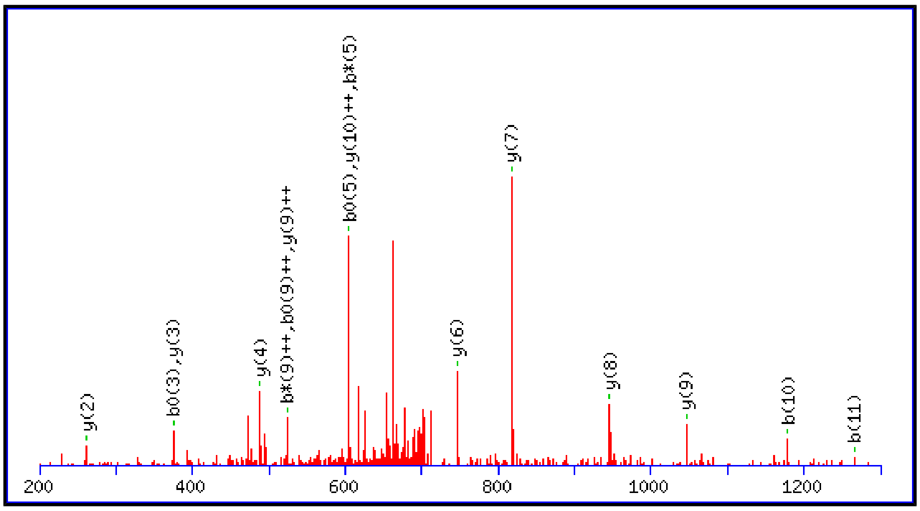
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DNYTKAEEILSR**
Found in **F8WEX7** in **con_Xuniprot_HUMAN3**, F8WEX7_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

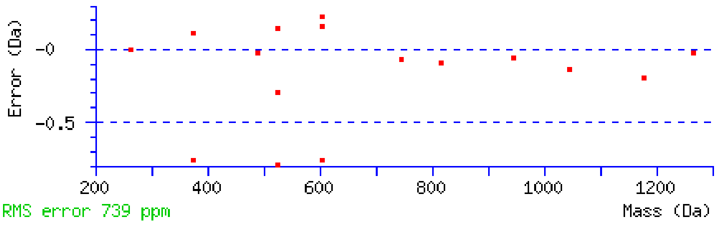
Match to Query 4067: 1438.698008 from(720.356280,2+) intensity(9644.3271) rtinseconds(1198) scans(2339) index(213)
Title: 111019_Est_ISCardio_NMI_200000g_G_5Spectrum1973_scans__2339
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

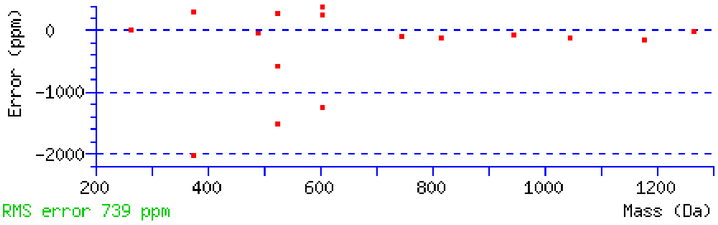
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1438.6939
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 70 **Expect:** 2e-005
Matches : 16/128 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	231.0612	116.0342	214.0346	107.5209	213.0506	107.0289	N	1324.6743	662.8408	1307.6478	654.3275	1306.6638	653.8355	11
3	394.1245	197.5659	377.0979	189.0526	376.1139	188.5606	Y	1209.6474	605.3273	1192.6208	596.8141	1191.6368	596.3220	10
4	495.1722	248.0897	478.1456	239.5764	477.1616	239.0844	T	***1046.5840***	523.7957	1029.5575	515.2824	1028.5735	514.7904	9
5	623.2671	312.1372	606.2406	303.6239	605.2566	303.1319	K	***945.5364***	473.2718	928.5098	464.7585	927.5258	464.2665	8
6	694.3042	347.6558	677.2777	339.1425	676.2937	338.6505	A	***817.4414***	409.2243	800.4149	400.7111	799.4308	400.2191	7
7	823.3468	412.1771	806.3203	403.6638	805.3363	403.1718	E	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
8	952.3894	476.6984	935.3629	468.1851	934.3789	467.6931	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
9	1065.4735	533.2404	1048.4469	524.7271	1047.4629	524.2351	I	***488.3191***	244.6632	471.2926	236.1499	470.3085	235.6579	4
10	**1178.5576**	589.7824	1161.5310	581.2691	1160.5470	580.7771	L	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
11	**1265.5896**	633.2984	1248.5630	624.7852	1247.5790	624.2931	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.9	1438.6939	0.0041	DNYTKAEEILSR
17.8	1438.7020	-0.0040	EASSTKGRMVMSR
14.4	1438.6939	0.0041	NQLHKEPSELNK
12.6	1438.7052	-0.0072	DSTAIQEPSVVHR
12.3	1438.6939	0.0041	NLYSDLKNLDSR
10.9	1438.7014	-0.0033	DIFLSNTMAAIDK
10.6	1438.6914	0.0066	NFCAWQKKLNK
10.1	1438.6915	0.0065	QLFVMQWDLSR
9.6	1438.7014	-0.0034	AQFLDLMETIDK
9.6	1438.7014	-0.0034	SQFLDLMETIDK

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

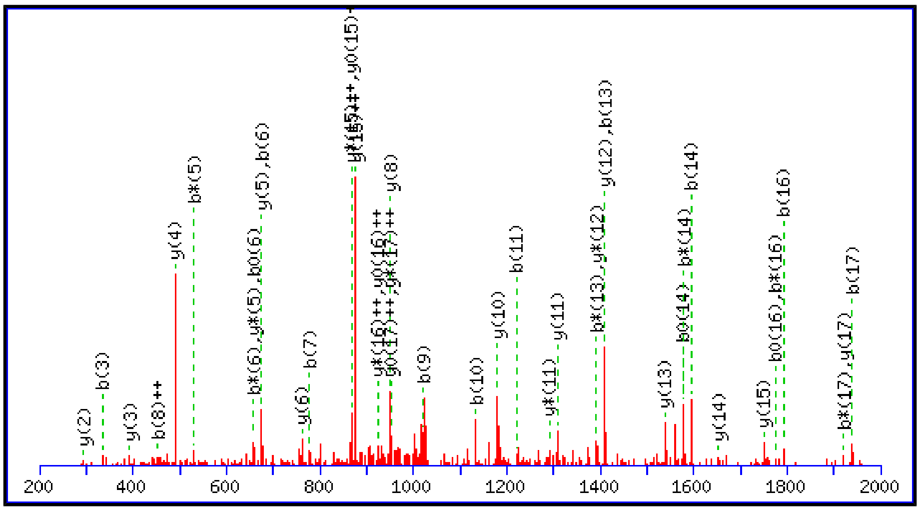
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

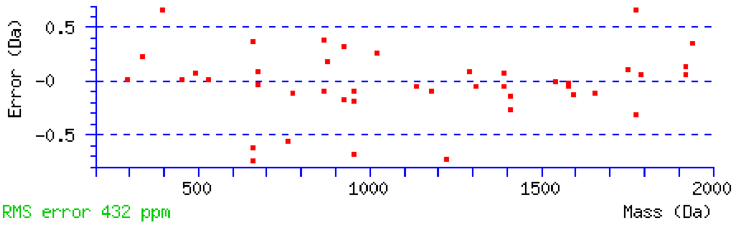
Match to Query 13139: 2083.920728 from(1042.967640,2+) intensity(7130.5996) rtinseconds(1560) scans(3356) index(7616)
Title: 111019_Est_ISCardio_NMI_YP_G_12Spectrum2899_scans__3356
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

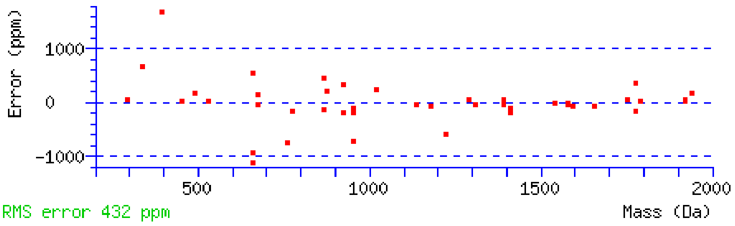
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
N9     : Deamidated (NQ)
Ions Score: 65  Expect: 3.3e-005
Matches : 43/180 fragment ions using 85 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					**Y**							**18**
2	221.0921	111.0497					**G**	***1921.8563***	961.4318	1904.8297	952.9185	1903.8457	952.4265	**17**
3	***335.1350***	168.0711	318.1084	159.5579			**N**	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	**16**
4	432.1878	216.5975	415.1612	208.0842			**P**	***1750.7919***	875.8996	1733.7653	867.3863	1732.7813	866.8943	**15**
5	547.2147	274.1110	530.1882	265.5977			**N**	***1653.7391***	827.3732	1636.7126	818.8599	1635.7285	818.3679	**14**
6	***676.2573***	338.6323	659.2307	330.1190	658.2467	329.6270	**E**	***1538.7122***	769.8597	1521.6856	761.3464	1520.7016	760.8544	**13**
7	***777.3050***	389.1561	760.2784	380.6429	759.2944	380.1508	**T**	***1409.6696***	705.3384	1392.6430	696.8251	1391.6590	696.3331	**12**
8	905.3636	453.1854	888.3370	444.6721	887.3530	444.1801	**Q**	***1308.6219***	654.8146	1291.5953	646.3013	1290.6113	645.8093	**11**
9	***1020.3905***	510.6989	1003.3639	502.1856	1002.3799	501.6936	**N**	***1180.5633***	590.7853	1163.5368	582.2720	1162.5527	581.7800	**10**
10	***1134.4334***	567.7203	1117.4069	559.2071	1116.4229	558.7151	**N**	1065.5364	533.2718	1048.5098	524.7585	1047.5258	524.2665	**9**
11	***1221.4655***	611.2364	1204.4389	602.7231	1203.4549	602.2311	**S**	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	**8**
12	1322.5131	661.7602	1305.4866	653.2469	1304.5026	652.7549	**T**	864.4614	432.7343	847.4349	424.2211	846.4509	423.7291	**7**
13	***1409.5452***	705.2762	1392.5186	696.7629	1391.5346	696.2709	**S**	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	**6**
14	***1595.6245***	798.3159	1578.5979	789.8026	1577.6139	789.3106	**W**	***676.3817***	338.6945	659.3552	330.1812			**5**
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	**P**	***490.3024***	245.6548	473.2758	237.1416			**4**
16	***1791.7456***	896.3765	1774.7191	887.8632	1773.7351	887.3712	**V**	***393.2496***	197.1285	376.2231	188.6152			**3**
17	***1938.8141***	969.9107	1921.7875	961.3974	1920.8035	960.9054	**F**	***294.1812***	147.5942	277.1547	139.0810			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.3	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 47.79%
61.3	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 19.20%
58.6	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 10.24%
56.1	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 5.72%
55.3	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 4.80%
54.3	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 3.84%
54.2	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 3.75%
53.7	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 3.31%
49.6	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 1.30%
33.2	2083.9123	0.0084	YGNPNETQNNSTSWPVFK	Deamidated N3, N5 0.03%

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

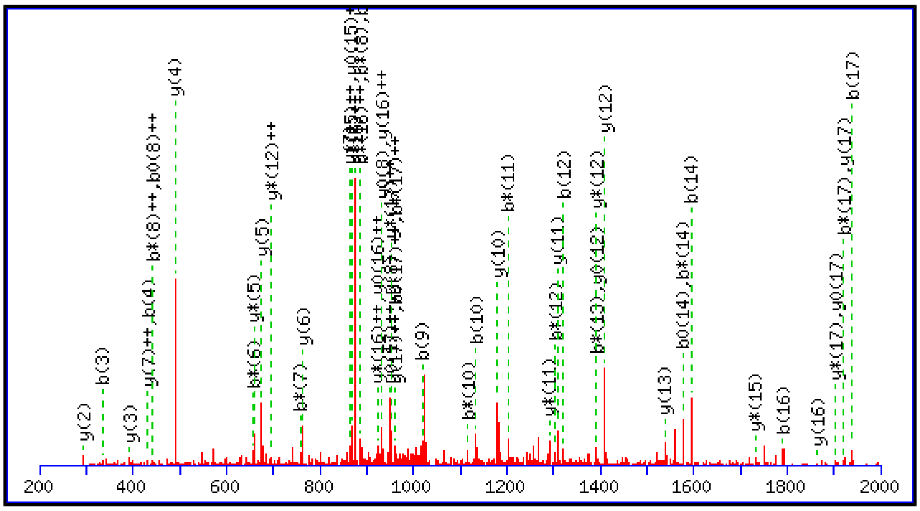
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

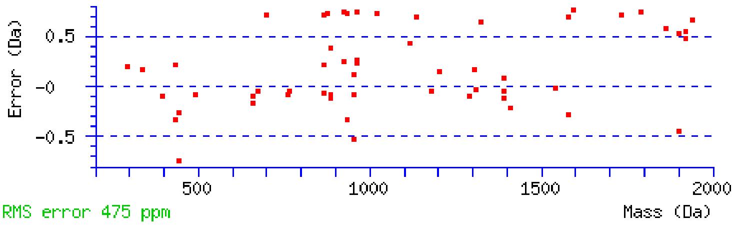
Match to Query 13147: 2083.925168 from(1042.969860,2+) intensity(26204.5996) rtinseconds(1587) scans(3821) index(27439)
Title: 111019_Est_MI_YS_G_10Spectrum3290_scans__3821
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

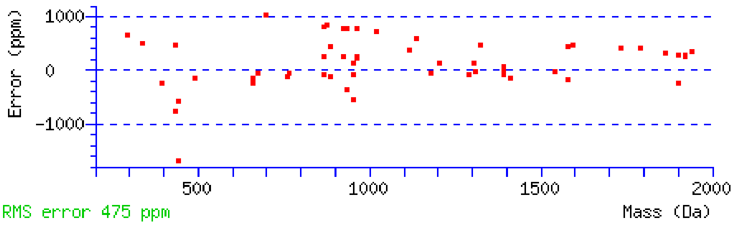
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2082.9283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 62 **Expect:** 8e-005
Matches : 56/180 fragment ions using 104 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							18
2	221.0921	111.0497					G	***1920.8722***	960.9398	1903.8457	952.4265	1902.8617	951.9345	17
3	***335.1350***	168.0711	318.1084	159.5579			N	***1863.8508***	932.4290	1846.8242	923.9158	1845.8402	923.4237	16
4	***432.1878***	216.5975	415.1612	208.0842			P	1749.8079	875.4076	1732.7813	866.8943	1731.7973	866.4023	15
5	546.2307	273.6190	529.2041	265.1057			N	1652.7551	826.8812	1635.7285	818.3679	1634.7445	817.8759	14
6	675.2733	338.1403	658.2467	329.6270	657.2627	329.1350	E	***1538.7122***	769.8597	1521.6856	761.3464	1520.7016	760.8544	13
7	776.3210	388.6641	759.2944	380.1508	758.3104	379.6588	T	***1409.6696***	705.3384	1392.6430	696.8251	1391.6590	696.3331	12
8	904.3795	452.6934	887.3530	444.1801	886.3690	443.6881	Q	***1308.6219***	654.8146	1291.5953	646.3013	1290.6113	645.8093	11
9	***1018.4225***	509.7149	1001.3959	501.2016	1000.4119	500.7096	N	***1180.5633***	590.7853	1163.5368	582.2720	1162.5527	581.7800	10
10	***1133.4494***	567.2283	1116.4229	558.7151	1115.4388	558.2231	N	1066.5204	533.7638	1049.4938	525.2506	1048.5098	524.7585	9
11	1220.4814	610.7444	1203.4549	602.2311	1202.4709	601.7391	S	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	***1321.5291***	661.2682	1304.5026	652.7549	1303.5185	652.2629	T	***864.4614***	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	1408.5611	704.7842	1391.5346	696.2709	1390.5506	695.7789	S	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	***1594.6405***	797.8239	1577.6139	789.3106	1576.6299	788.8186	W	***676.3817***	338.6945	659.3552	330.1812			5
15	1691.6932	846.3502	1674.6667	837.8370	1673.6827	837.3450	P	***490.3024***	245.6548	473.2758	237.1416			4
16	***1790.7616***	895.8845	1773.7351	887.3712	1772.7511	886.8792	V	***393.2496***	197.1285	376.2231	188.6152			3
17	***1937.8300***	969.4187	1920.8035	960.9054	1919.8195	960.4134	F	***294.1812***	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.7	2082.9283	0.9969	YGNPNETQNNSTSWPVFK	Deamidated N10 44.58%
61.7	2082.9283	0.9969	YGNPNETQNNSTSWPVFK	Deamidated N9 44.58%
54.4	2082.9283	0.9969	YGNPNETQNNSTSWPVFK	Deamidated Q8 8.38%
48.9	2082.9283	0.9969	YGNPNETQNNSTSWPVFK	Deamidated N5 2.35%
36.0	2082.9283	0.9969	YGNPNETQNNSTSWPVFK	Deamidated N3 0.12%
3.8	2083.9166	0.0086	FMDPAVNQTCTMFSVAHK	
3.8	2083.9150	0.0102	ESANMKRNSDMQASELQK	
3.5	2083.9191	0.0061	GGYGGGMPANVQMQLVDTKAG	
3.5	2083.9191	0.0061	GGYGGGMPANVQMQLVDTKAG	
3.3	2083.9190	0.0061	SKWNDMLGMNESTAQQVK	

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

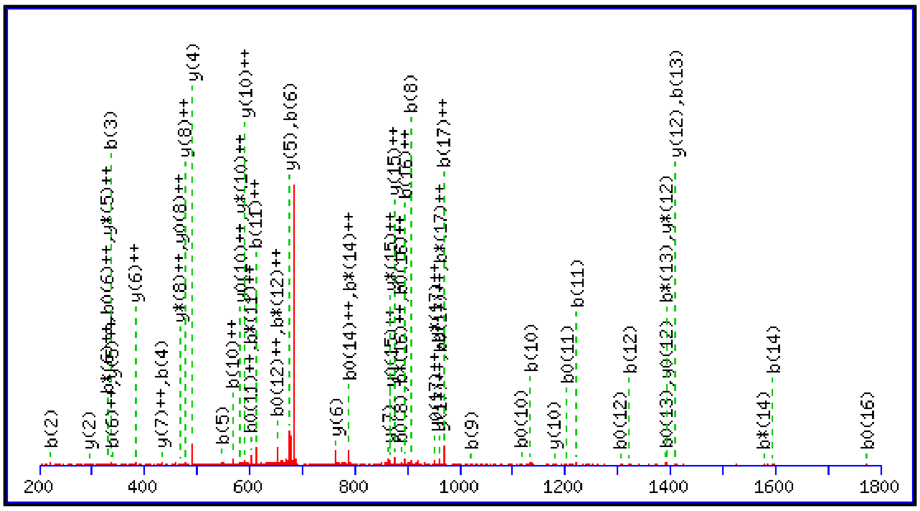
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

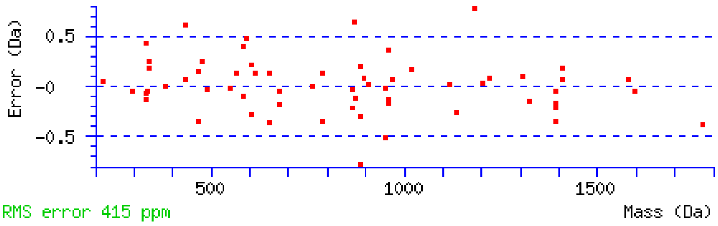
Match to Query 13141: 2083.920822 from(695.647550,3+) intensity(8145.1313) rtinseconds(1529) scans(3460) index(28128)
Title: 111019_Est_MI_YS_G_12Spectrum3028_scans__3460
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

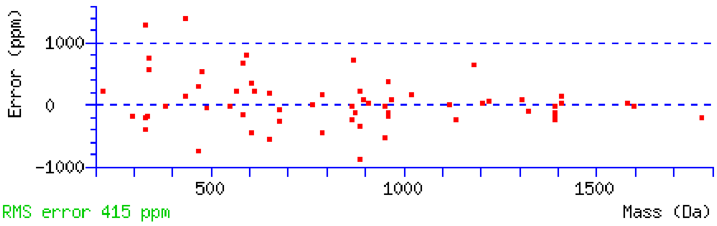
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q8 : Deamidated (NQ)
Ions Score: 56 **Expect:** 0.0003
Matches : 62/180 fragment ions using 94 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							18
2	***221.0921***	111.0497					G	1921.8563	961.4318	1904.8297	952.9185	1903.8457	952.4265	17
3	***335.1350***	168.0711	318.1084	159.5579			N	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	16
4	***432.1878***	216.5975	415.1612	208.0842			P	1750.7919	875.8996	1733.7653	867.3863	1732.7813	866.8943	15
5	***547.2147***	274.1110	530.1882	265.5977			N	1653.7391	827.3732	1636.7126	818.8599	1635.7285	818.3679	14
6	***676.2573***	**338.6323**	659.2307	330.1190	658.2467	329.6270	E	1538.7122	769.8597	1521.6856	761.3464	1520.7016	760.8544	13
7	777.3050	389.1561	760.2784	380.6429	759.2944	380.1508	T	**1409.6696**	705.3384	1392.6430	696.8251	1391.6590	696.3331	12
8	***906.3476***	453.6774	889.3210	445.1641	888.3370	444.6721	Q	1308.6219	654.8146	1291.5953	646.3013	1290.6113	645.8093	11
9	***1020.3905***	510.6989	1003.3639	502.1856	1002.3799	501.6936	N	**1179.5793**	590.2933	1162.5527	581.7800	1161.5687	581.2880	10
10	***1134.4334***	**567.7203**	1117.4069	559.2071	1116.4229	558.7151	N	1065.5364	533.2718	1048.5098	524.7585	1047.5258	524.2665	9
11	***1221.4655***	**611.2364**	1204.4389	602.7231	1203.4549	602.2311	S	951.4934	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	***1322.5131***	661.7602	1305.4866	653.2469	1304.5026	652.7549	T	**864.4614**	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	***1409.5452***	705.2762	1392.5186	696.7629	1391.5346	696.2709	S	**763.4137**	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	***1595.6245***	798.3159	1578.5979	789.8026	1577.6139	789.3106	W	**676.3817**	338.6945	659.3552	330.1812			5
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	P	**490.3024**	245.6548	473.2758	237.1416			4
16	1791.7456	**896.3765**	1774.7191	887.8632	1773.7351	887.3712	V	393.2496	197.1285	376.2231	188.6152			3
17	1938.8141	**969.9107**	1921.7875	961.3974	1920.8035	960.9054	F	**294.1812**	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.7	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 31.35%
54.9	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 26.13%
54.9	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 26.13%
45.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 3.04%
45.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 3.04%
44.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N3, N5 2.39%
44.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 2.38%
43.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 1.89%
43.5	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 1.89%
43.2	2083.9123	0.0085	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 1.76%

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

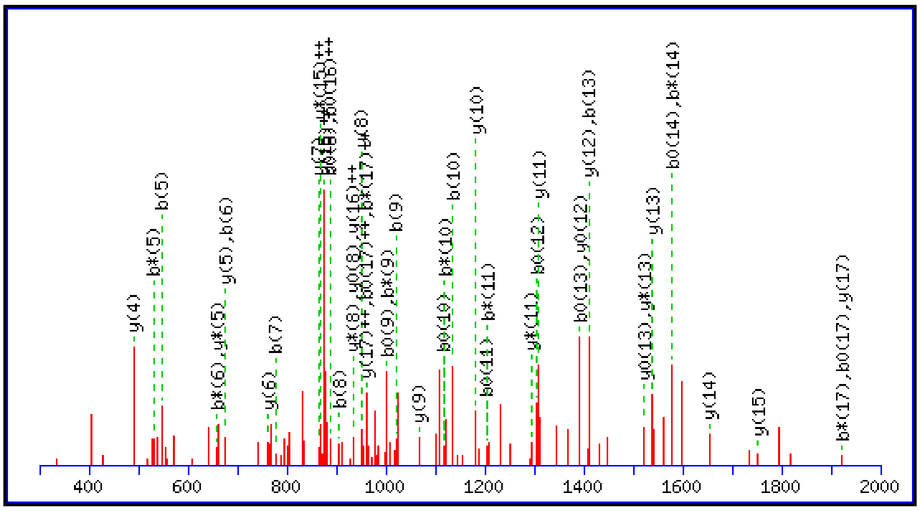
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

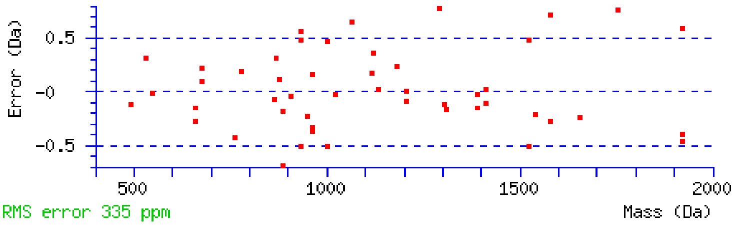
Match to Query 13167: 2084.906748 from(1043.460650,2+) intensity(433.7465) rtinseconds(1539) scans(2966) index(549)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum2514_scans__2966
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

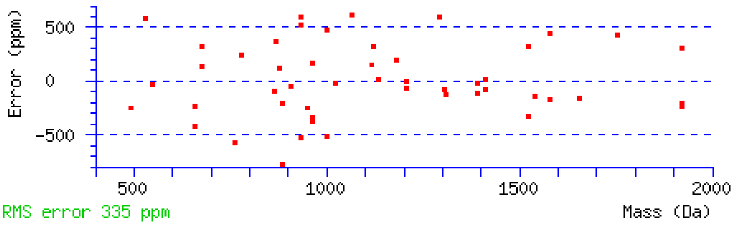
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2084.8963
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
N9 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00032
Matches : 49/180 fragment ions using 101 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							18
2	221.0921	111.0497					G	***1922.8403***	961.9238	1905.8137	953.4105	1904.8297	952.9185	17
3	335.1350	168.0711	318.1084	159.5579			N	1865.8188	933.4130	1848.7923	924.8998	1847.8082	924.4078	16
4	432.1878	216.5975	415.1612	208.0842			P	***1751.7759***	876.3916	1734.7493	867.8783	1733.7653	867.3863	15
5	**547.2147**	274.1110	530.1882	265.5977			N	***1654.7231***	827.8652	1637.6966	819.3519	1636.7126	818.8599	14
6	**676.2573**	338.6323	659.2307	330.1190	658.2467	329.6270	E	***1539.6962***	770.3517	1522.6696	761.8385	1521.6856	761.3464	13
7	**777.3050**	389.1561	760.2784	380.6429	759.2944	380.1508	T	***1410.6536***	705.8304	1393.6270	697.3172	1392.6430	696.8251	12
8	**905.3636**	453.1854	888.3370	444.6721	887.3530	444.1801	Q	***1309.6059***	655.3066	1292.5794	646.7933	1291.5953	646.3013	11
9	**1020.3905**	510.6989	1003.3639	502.1856	1002.3799	501.6936	N	***1181.5473***	591.2773	1164.5208	582.7640	1163.5368	582.2720	10
10	**1135.4174**	568.2124	1118.3909	559.6991	1117.4069	559.2071	N	***1066.5204***	533.7638	1049.4938	525.2506	1048.5098	524.7585	9
11	1222.4495	611.7284	1205.4229	603.2151	1204.4389	602.7231	S	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	1323.4971	662.2522	1306.4706	653.7389	1305.4866	653.2469	T	***864.4614***	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	**1410.5292**	705.7682	1393.5026	697.2550	1392.5186	696.7629	S	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	1596.6085	798.8079	1579.5819	790.2946	1578.5979	789.8026	W	***676.3817***	338.6945	659.3552	330.1812			5
15	1693.6613	847.3343	1676.6347	838.8210	1675.6507	838.3290	P	***490.3024***	245.6548	473.2758	237.1416			4
16	1792.7297	896.8685	1775.7031	888.3552	1774.7191	887.8632	V	393.2496	197.1285	376.2231	188.6152			3
17	1939.7981	970.4027	1922.7715	961.8894	1921.7875	961.3974	F	294.1812	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.6	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N5, N9, N10 58.33%
51.2	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9, N10 26.60%
45.5	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N3, N9, N10 7.26%
44.7	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8, N10 5.97%
36.5	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8, N10 0.91%
35.7	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8, N9 0.75%
28.4	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8, N9 0.14%
24.4	2083.9123	0.9945	YGNPNETQNNSTSWPVFK	
20.7	2084.8963	0.0104	YGNPNETQNNSTSWPVFK	Deamidated N3, N5, N10 0.02%
18.3	2083.9123	0.9945	YGNPNETQNNSTSWPVFK	

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

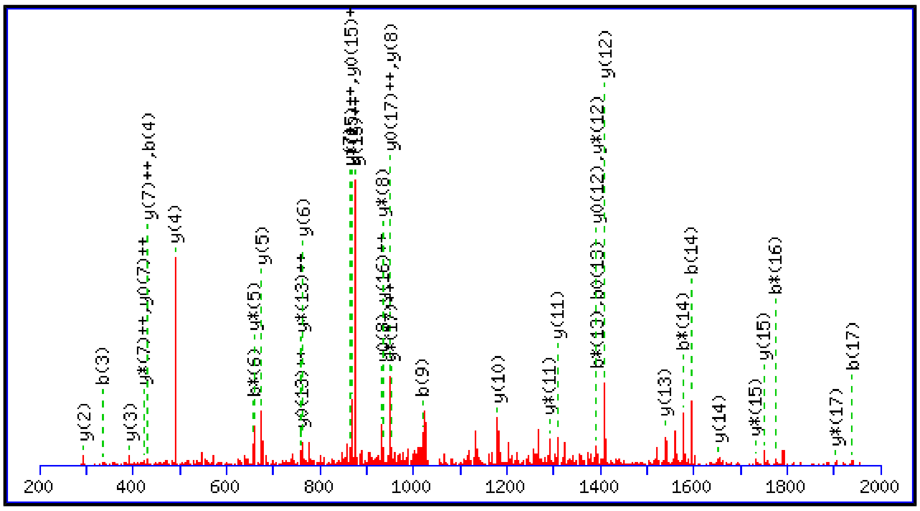
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

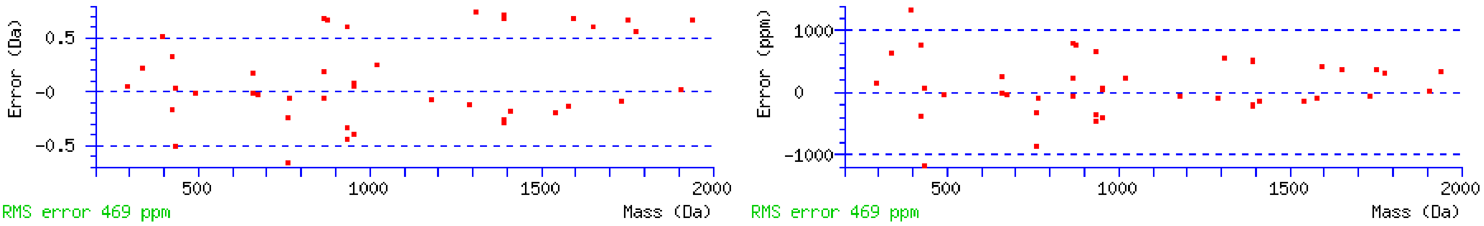
Match to Query 13146: 2083.924188 from(1042.969370,2+) intensity(8984.1543) rtinseconds(1532) scans(3675) index(20287)
Title: 111019_Est_MI_YP_G_10Spectrum3207_scans__3675
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2082.9283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.00077
Matches : 42/180 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.0706	82.5389					**Y**							18
2	221.0921	111.0497					**G**	1920.8722	960.9398	1903.8457	952.4265	1902.8617	951.9345	17
3	**335.1350**	168.0711	318.1084	159.5579			**N**	1863.8508	932.4290	1846.8242	923.9158	1845.8402	923.4237	16
4	**432.1878**	216.5975	415.1612	208.0842			**P**	***1749.8079***	875.4076	1732.7813	866.8943	1731.7973	866.4023	15
5	546.2307	273.6190	529.2041	265.1057			**N**	***1652.7551***	826.8812	1635.7285	818.3679	1634.7445	817.8759	14
6	675.2733	338.1403	658.2467	329.6270	657.2627	329.1350	**E**	***1538.7122***	769.8597	1521.6856	761.3464	1520.7016	760.8544	13
7	776.3210	388.6641	759.2944	380.1508	758.3104	379.6588	**T**	***1409.6696***	705.3384	1392.6430	696.8251	1391.6590	696.3331	12
8	904.3795	452.6934	887.3530	444.1801	886.3690	443.6881	**Q**	***1308.6219***	654.8146	1291.5953	646.3013	1290.6113	645.8093	11
9	**1019.4065**	510.2069	1002.3799	501.6936	1001.3959	501.2016	**N**	***1180.5633***	590.7853	1163.5368	582.2720	1162.5527	581.7800	10
10	1133.4494	567.2283	1116.4229	558.7151	1115.4388	558.2231	**N**	1065.5364	533.2718	1048.5098	524.7585	1047.5258	524.2665	9
11	1220.4814	610.7444	1203.4549	602.2311	1202.4709	601.7391	**S**	***951.4934***	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	1321.5291	661.2682	1304.5026	652.7549	1303.5185	652.2629	**T**	***864.4614***	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	1408.5611	704.7842	1391.5346	696.2709	1390.5506	695.7789	**S**	***763.4137***	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	**1594.6405**	797.8239	1577.6139	789.3106	1576.6299	788.8186	**W**	***676.3817***	338.6945	659.3552	330.1812			5
15	1691.6932	846.3502	1674.6667	837.8370	1673.6827	837.3450	**P**	***490.3024***	245.6548	473.2758	237.1416			4
16	1790.7616	895.8845	1773.7351	887.3712	1772.7511	886.8792	**V**	***393.2496***	197.1285	376.2231	188.6152			3
17	**1937.8300**	969.4187	1920.8035	960.9054	1919.8195	960.4134	**F**	***294.1812***	147.5942	277.1547	139.0810			2
18							**K**	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.7	2082.9283	0.9959	YGNPNETQNNSTSWPVFK	Deamidated N9 49.54%
50.6	2082.9283	0.9959	YGNPNETQNNSTSWPVFK	Deamidated N10 38.73%
42.8	2082.9283	0.9959	YGNPNETQNNSTSWPVFK	Deamidated Q8 6.44%
41.8	2082.9283	0.9959	YGNPNETQNNSTSWPVFK	Deamidated N5 5.14%
26.4	2082.9283	0.9959	YGNPNETQNNSTSWPVFK	Deamidated N3 0.15%
5.9	2083.9341	-0.0099	MQDVQGPRPGSPGDAEDRR	
5.4	2083.9150	0.0092	ESANMKRNSDMQASELQK	
5.3	2083.9150	0.0092	ESANMKRNSDMQASELQK	
3.1	2083.9341	-0.0099	MQDVQGPRPGSPGDAEDRR	
1.7	2083.9190	0.0052	SKWNDMLGMNESTAQQVK	

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

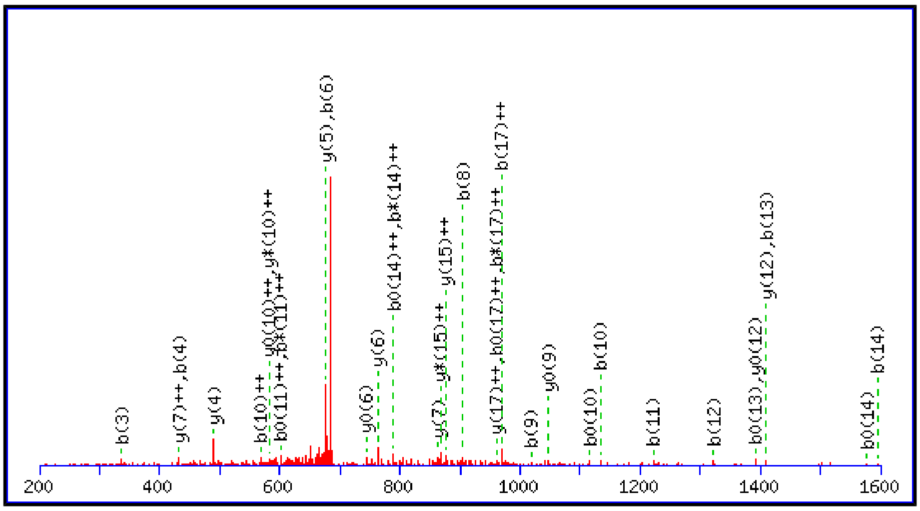
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGNPNETQNNSTSWPVFK**
Found in **F8WF14** in **con_Xuniprot_HUMAN3**, F8WF14_HUMAN Cholinesterase OS=Homo sapiens GN=BCHE PE=2 SV=1

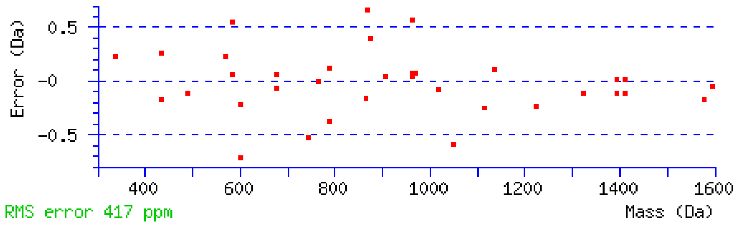
Match to Query 13133: 2083.917462 from(695.646430,3+) intensity(4435.8115) rtinseconds(1508) scans(3406) index(28126)
Title: 111019_Est_MI_YS_G_12Spectrum2979_scans__3406
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

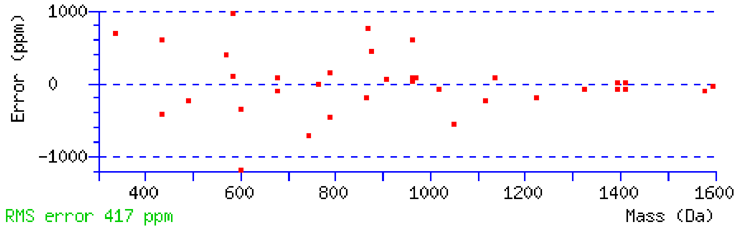
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2083.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N10 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.008
Matches : 35/180 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							18
2	221.0921	111.0497					G	1921.8563	961.4318	1904.8297	952.9185	1903.8457	952.4265	17
3	***336.1190***	168.5631	319.0925	160.0499			N	1864.8348	932.9210	1847.8082	924.4078	1846.8242	923.9158	16
4	***433.1718***	217.0895	416.1452	208.5763			P	1749.8079	875.4076	1732.7813	866.8943	1731.7973	866.4023	15
5	547.2147	274.1110	530.1882	265.5977			N	1652.7551	826.8812	1635.7285	818.3679	1634.7445	817.8759	14
6	***676.2573***	338.6323	659.2307	330.1190	658.2467	329.6270	E	1538.7122	769.8597	1521.6856	761.3464	1520.7016	760.8544	13
7	777.3050	389.1561	760.2784	380.6429	759.2944	380.1508	T	**1409.6696**	705.3384	1392.6430	696.8251	1391.6590	696.3331	12
8	***905.3636***	453.1854	888.3370	444.6721	887.3530	444.1801	Q	1308.6219	654.8146	1291.5953	646.3013	1290.6113	645.8093	11
9	***1019.4065***	510.2069	1002.3799	501.6936	1001.3959	501.2016	N	1180.5633	590.7853	1163.5368	582.2720	1162.5527	581.7800	10
10	***1134.4334***	567.7203	1117.4069	559.2071	1116.4229	558.7151	N	1066.5204	533.7638	1049.4938	525.2506	1048.5098	524.7585	9
11	***1221.4655***	611.2364	1204.4389	602.7231	1203.4549	602.2311	S	951.4934	476.2504	934.4669	467.7371	933.4829	467.2451	8
12	***1322.5131***	661.7602	1305.4866	653.2469	1304.5026	652.7549	T	**864.4614**	432.7343	847.4349	424.2211	846.4509	423.7291	7
13	***1409.5452***	705.2762	1392.5186	696.7629	1391.5346	696.2709	S	**763.4137**	382.2105	746.3872	373.6972	745.4032	373.2052	6
14	***1595.6245***	798.3159	1578.5979	789.8026	1577.6139	789.3106	W	**676.3817**	338.6945	659.3552	330.1812			5
15	1692.6772	846.8423	1675.6507	838.3290	1674.6667	837.8370	P	**490.3024**	245.6548	473.2758	237.1416			4
16	1791.7456	896.3765	1774.7191	887.8632	1773.7351	887.3712	V	393.2496	197.1285	376.2231	188.6152			3
17	1938.8141	969.9107	1921.7875	961.3974	1920.8035	960.9054	F	294.1812	147.5942	277.1547	139.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.1	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N3, N10 43.86%
39.2	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N3, N9 28.45%
33.4	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N5, N10 7.38%
32.5	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N3, N5 6.05%
31.4	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N5, N9 4.69%
29.8	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N3, Q8 3.24%
28.1	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N5, Q8 2.18%
27.0	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated Q8, N10 1.71%
26.3	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated Q8, N9 1.44%
24.7	2083.9123	0.0052	YGNPNETQNNSTSWPVFK	Deamidated N9, N10 1.00%

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

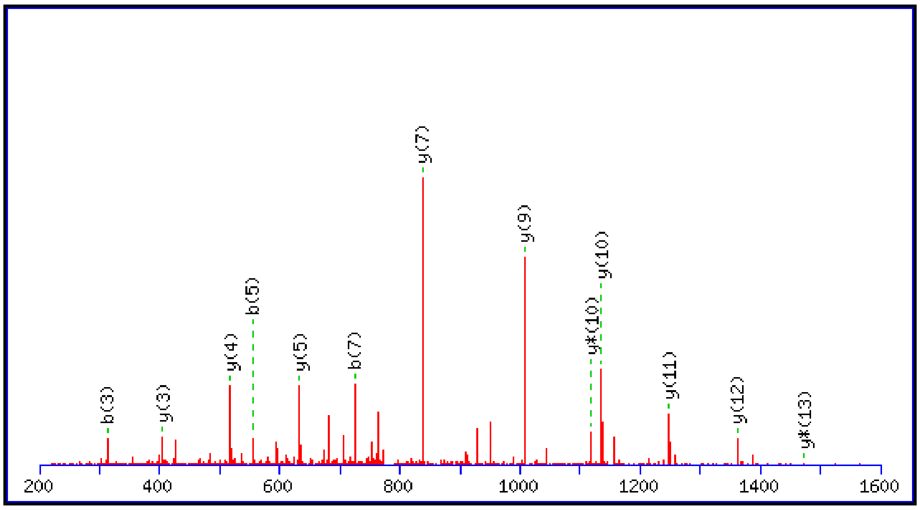
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQLLQGLGFNLTER**
Found in **G3V350** in **con_Xuniprot_HUMAN3**, G3V350_HUMAN Corticosteroid-binding globulin OS=Homo sapiens GN=SERPINA6 PE=3 SV=1

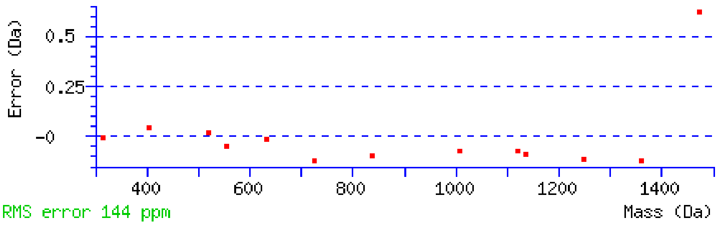
Match to Query 7165: 1559.834908 from(780.924730,2+) intensity(379997.0938) rtinseconds(2144) scans(5559) index(26881)
Title: 111019_Est_MI_YS_G_09Spectrum4848_scans__5559
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

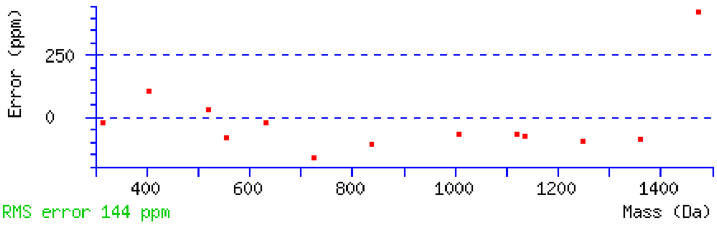
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1559.8307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 81 **Expect:** 1.6e-006
Matches : 13/130 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	72.0444	36.5258					A							14
2	200.1030	100.5551	183.0764	92.0418			Q	1489.8009	745.4041	1472.7744	736.8908	1471.7904	736.3988	13
3	**313.1870**	157.0972	296.1605	148.5839			L	***1361.7423***	681.3748	1344.7158	672.8615	1343.7318	672.3695	12
4	426.2711	213.6392	409.2445	205.1259			L	***1248.6583***	624.8328	1231.6317	616.3195	1230.6477	615.8275	11
5	**554.3297**	277.6685	537.3031	269.1552			Q	***1135.5742***	568.2907	1118.5477	559.7775	1117.5636	559.2855	10
6	611.3511	306.1792	594.3246	297.6659			G	***1007.5156***	504.2615	990.4891	495.7482	989.5051	495.2562	9
7	**724.4352**	362.7212	707.4087	354.2080			L	950.4942	475.7507	933.4676	467.2374	932.4836	466.7454	8
8	781.4567	391.2320	764.4301	382.7187			G	***837.4101***	419.2087	820.3836	410.6954	819.3995	410.2034	7
9	928.5251	464.7662	911.4985	456.2529			F	780.3886	390.6980	763.3621	382.1847	762.3781	381.6927	6
10	1043.5520	522.2796	1026.5255	513.7664			N	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
11	1156.6361	578.8217	1139.6095	570.3084			L	***518.2933***	259.6503	501.2667	251.1370	500.2827	250.6450	4
12	1257.6838	629.3455	1240.6572	620.8322	1239.6732	620.3402	T	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	3
13	1386.7264	693.8668	1369.6998	685.3535	1368.7158	684.8615	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.2	1559.8307	0.0042	AQLLQGLGFNLTER	Deamidated N10 100.00%
27.5	1559.8307	0.0042	AQLLQGLGFNLTER	Deamidated Q5 0.00%
11.8	1559.8307	0.0042	AQLLQGLGFNLTER	Deamidated Q2 0.00%
6.9	1559.8420	-0.0071	SPQLVVQHLSPEAR	
5.0	1559.8280	0.0069	RRAAQAGPTQPGPPR	
4.4	1559.8341	0.0008	RVELAVMLNLTER	
3.3	1558.8315	1.0035	ELKLSKVGQGNTER	
1.5	1559.8280	0.0069	RRAAQAGPTQPGPPR	
0.4	1558.8256	1.0093	WKGTIHIRYEEK	

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

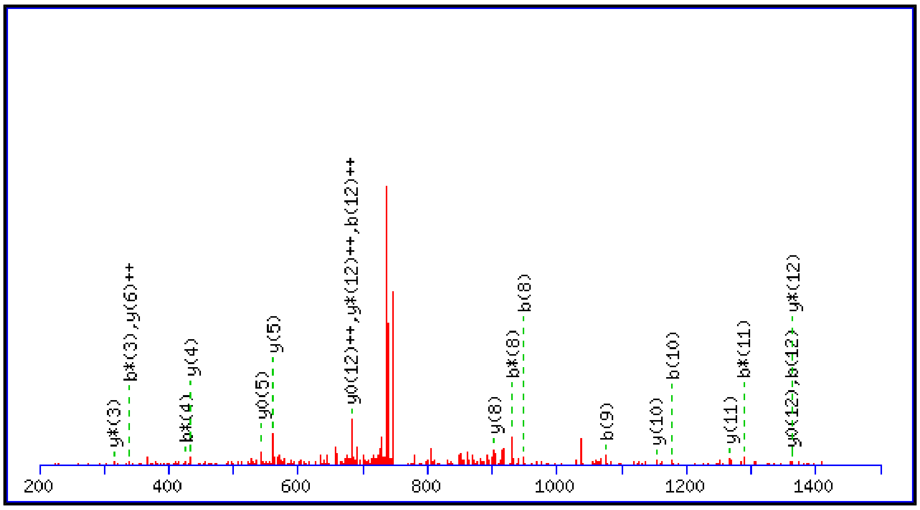
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QINSYVKNKTQGK**
Found in **G3V350** in **con_Xuniprot_HUMAN3**, G3V350_HUMAN Corticosteroid-binding globulin OS=Homo sapiens GN=SERPINA6 PE=3 SV=1

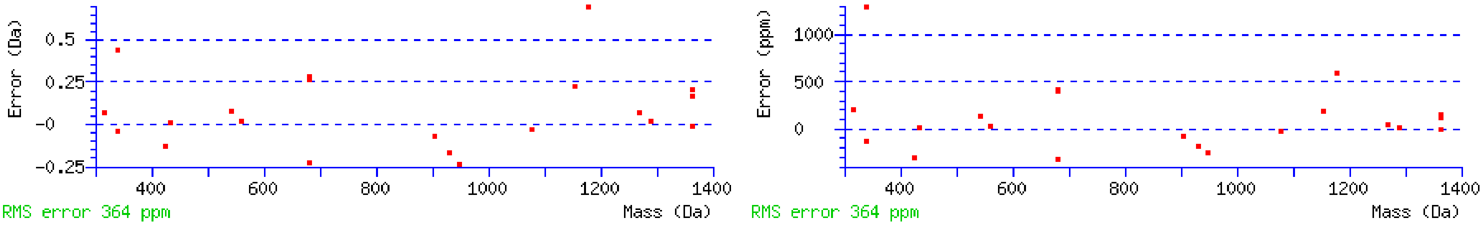
Match to Query 6886: 1507.802828 from(754.908690,2+) intensity(8091.4111) rtinseconds(193) scans(273) index(22453)
Title: 111019_Est_MI_YS_G_03Spectrum197_scans__273
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1507.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.018
Matches : 21/132 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	129.0659	65.0366	112.0393	56.5233			Q							13
2	242.1499	121.5786	225.1234	113.0653			I	1380.7482	690.8777	1363.7216	682.3644	1362.7376	681.8724	12
3	356.1928	178.6001	339.1663	170.0868			N	***1267.6641***	634.3357	1250.6375	625.8224	1249.6535	625.3304	11
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	S	***1153.6212***	577.3142	1136.5946	568.8009	1135.6106	568.3089	10
5	606.2882	303.6477	589.2617	295.1345	588.2776	294.6425	Y	1066.5891	533.7982	1049.5626	525.2849	1048.5786	524.7929	9
6	705.3566	353.1819	688.3301	344.6687	687.3461	344.1767	V	***903.5258***	452.2665	886.4993	443.7533	885.5152	443.2613	8
7	833.4516	417.2294	816.4250	408.7162	815.4410	408.2241	K	804.4574	402.7323	787.4308	394.2191	786.4468	393.7271	7
8	***948.4785***	474.7429	931.4520	466.2296	930.4680	465.7376	N	676.3624	338.6849	659.3359	330.1716	658.3519	329.6796	6
9	***1076.5735***	538.7904	1059.5469	530.2771	1058.5629	529.7851	K	***561.3355***	281.1714	544.3089	272.6581	543.3249	272.1661	5
10	***1177.6212***	589.3142	1160.5946	580.8009	1159.6106	580.3089	T	***433.2405***	217.1239	416.2140	208.6106	415.2300	208.1186	4
11	1305.6797	653.3435	1288.6532	644.8302	1287.6692	644.3382	Q	332.1928	166.6001	315.1663	158.0868			3
12	***1362.7012***	681.8542	1345.6747	673.3410	1344.6906	672.8490	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.9	1507.7994	0.0034	QINSYVKNKTQGK	Deamidated N8 98.03%
21.4	1507.7994	0.0034	QINSYVKNKTQGK	Deamidated N3 1.38%
16.3	1507.7994	0.0034	QINSYVKNKTQGK	Deamidated Q1 0.44%
11.8	1507.7994	0.0034	QINSYVKNKTQGK	Deamidated Q11 0.15%
8.3	1507.8068	-0.0040	DTYLNIMPKGTKK	
7.7	1507.7967	0.0061	GARAGGERPEGRAPK	
7.2	1507.8068	-0.0040	KINDDIKYQLMK	
5.5	1507.8068	-0.0040	KLAKIAFMENTNK	
5.5	1507.8068	-0.0040	KLAKIAFMENTNK	
4.6	1507.8068	-0.0040	KLISGQVLRAEFM	

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

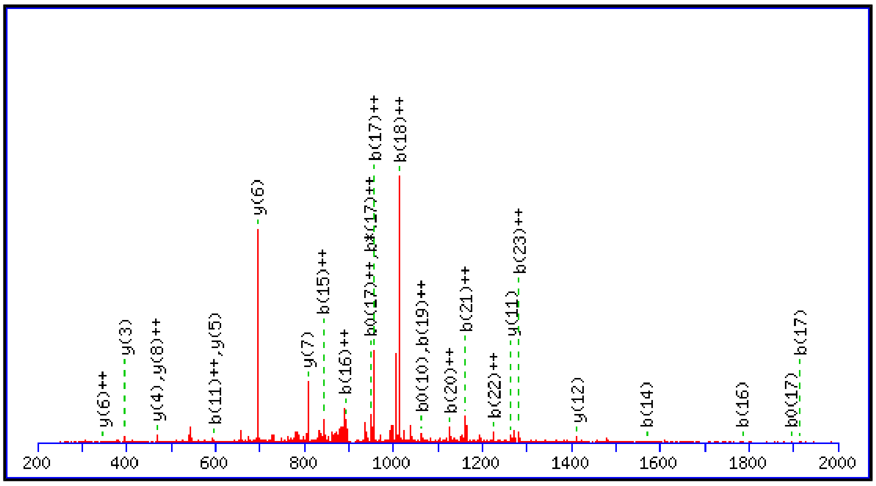
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADTHDEILEGLNFNLTEIPEAQIH**
Found in **G3V387** in **con_Xuniprot_HUMAN3**, G3V387_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=2 SV=1

Match to Query 25402: 2719.308462 from(907.443430,3+) intensity(34716.6563) rtinseconds(2320) scans(6088) index(18857)
Title: 111019_Est_MI_YP_G_08Spectrum5314_scans__6088
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

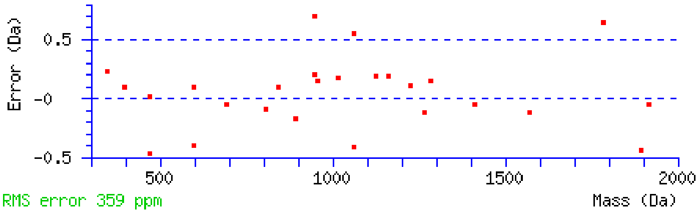
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

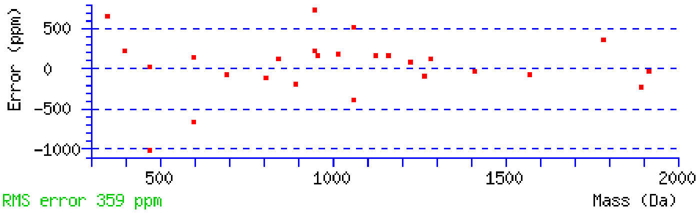


```
Monoisotopic mass of neutral peptide Mr(calc): 2719.2977
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14     : Deamidated (NQ)
Ions Score: 37  Expect: 0.049
Matches : 26/240 fragment ions using 52 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							24
2	187.0713	94.0393			169.0608	85.0340	D	2649.2679	1325.1376	2632.2413	1316.6243	2631.2573	1316.1323	23
3	288.1190	144.5631			270.1084	135.5579	T	2534.2409	1267.6241	2517.2144	1259.1108	2516.2304	1258.6188	22
4	425.1779	213.0926			407.1674	204.0873	H	2433.1932	1217.1003	2416.1667	1208.5870	2415.1827	1208.0950	21
5	540.2049	270.6061			522.1943	261.6008	D	2296.1343	1148.5708	2279.1078	1140.0575	2278.1238	1139.5655	20
6	669.2475	335.1274			651.2369	326.1221	E	2181.1074	1091.0573	2164.0808	1082.5441	2163.0968	1082.0521	19
7	782.3315	391.6694			764.3210	382.6641	I	2052.0648	1026.5360	2035.0382	1018.0228	2034.0542	1017.5308	18
8	895.4156	448.2114			877.4050	439.2061	L	1938.9807	969.9940	1921.9542	961.4807	1920.9702	960.9887	17
9	1024.4582	512.7327			1006.4476	503.7274	E	1825.8967	913.4520	1808.8701	904.9387	1807.8861	904.4467	16
10	1081.4796	541.2435			1063.4691	532.2382	G	1696.8541	848.9307	1679.8275	840.4174	1678.8435	839.9254	15
11	1194.5637	***597.7855***			1176.5531	588.7802	L	1639.8326	820.4199	1622.8061	811.9067	1621.8220	811.4147	14
12	1308.6066	654.8070	1291.5801	646.2937	1290.5961	645.8017	N	1526.7486	763.8779	1509.7220	755.3646	1508.7380	754.8726	13
13	1455.6751	728.3412	1438.6485	719.8279	1437.6645	719.3359	F	***1412.7056***	706.8564	1395.6791	698.3432	1394.6951	697.8512	12
14	**1570.7020**	785.8546	1553.6754	777.3414	1552.6914	776.8494	N	***1265.6372***	633.3222	1248.6107	624.8090	1247.6266	624.3170	11
15	1683.7861	***842.3967***	1666.7595	833.8834	1665.7755	833.3914	L	1150.6103	575.8088	1133.5837	567.2955	1132.5997	566.8035	10
16	**1784.8337**	***892.9205***	1767.8072	884.4072	1766.8232	883.9152	T	1037.5262	519.2667	1020.4997	510.7535	1019.5156	510.2615	9
17	**1913.8763**	***957.4418***	1896.8498	948.9285	1895.8658	948.4365	E	936.4785	468.7429	919.4520	460.2296	918.4680	459.7376	8
18	2026.9604	***1013.9838***	2009.9338	1005.4706	2008.9498	1004.9786	I	***807.4359***	404.2216	790.4094	395.7083	789.4254	395.2163	7
19	2124.0132	***1062.5102***	2106.9866	1053.9969	2106.0026	1053.5049	P	***694.3519***	347.6796	677.3253	339.1663	676.3413	338.6743	6
20	2253.0557	***1127.0315***	2236.0292	1118.5182	2235.0452	1118.0262	E	***597.2991***	299.1532	580.2726	290.6399	579.2885	290.1479	5
21	2324.0929	***1162.5501***	2307.0663	1154.0368	2306.0823	1153.5448	A	***468.2565***	234.6319	451.2300	226.1186			4
22	2452.1514	***1226.5794***	2435.1249	1218.0661	2434.1409	1217.5741	Q	***397.2194***	199.1133	380.1928	190.6001			3

23	2565.2355	***1283.1214***	2548.2090	1274.6081	2547.2249	1274.1161	**I**	269.1608	135.0840					**2**
24							**H**	156.0768	78.5420					**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.4	2719.2977	0.0108	ADTHDEILEGLNFNLTEIPEAQIH	Deamidated N14 58.74%
35.5	2719.2977	0.0108	ADTHDEILEGLNFNLTEIPEAQIH	Deamidated N12 38.45%
28.4	2718.3137	0.9948	ADTHDEILEGLNFNLTEIPEAQIH	
24.2	2719.2977	0.0108	ADTHDEILEGLNFNLTEIPEAQIH	Deamidated Q22 2.81%
2.8	2717.2888	2.0197	QHTLNAQEQTLLDSVQSLQMGLVM	
2.4	2718.2959	1.0125	GVDLSGNDFKGGYFPENVKAMTSLR	
1.7	2719.3104	-0.0019	WEILFSEFNINYNNELPMYRK	
1.5	2717.3105	1.9979	VNKLMYLVESPLHSNALDGETLDAS	
1.3	2718.3137	0.9948	NPQKNTPKFLYTVPNGNNPTGNSLT	
1.3	2719.2977	0.0108	NPQKNTPKFLYTVPNGNNPTGNSLT	

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

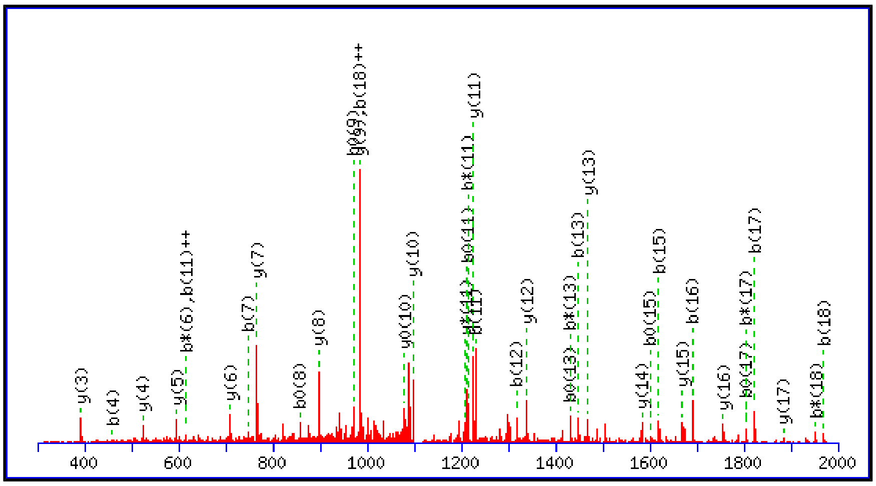
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLNQSSDELQLSMGNAMFVK**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

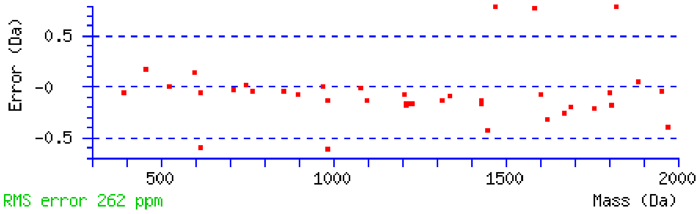
Match to Query 14883: 2213.042368 from(1107.528460,2+) intensity(65689.0234) rtinseconds(2020) scans(4905) index(11918)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum4230_scans__4905
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

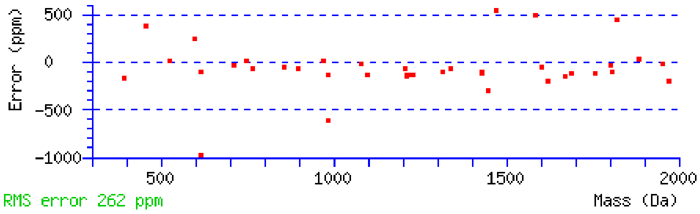
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2213.0344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 107 **Expect:** 4.7e-009
Matches : 39/208 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	102.0550	51.5311			84.0444	42.5258	T							20
2	215.1390	108.0731			197.1285	99.0679	L	2112.9940	1057.0006	2095.9675	1048.4874	2094.9835	1047.9954	19
3	330.1660	165.5866	313.1394	157.0733	312.1554	156.5813	N	1999.9100	1000.4586	1982.8834	991.9453	1981.8994	991.4533	18
4	**458.2245**	229.6159	441.1980	221.1026	440.2140	220.6106	Q	***1884.8830***	942.9451	1867.8565	934.4319	1866.8724	933.9399	17
5	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	S	***1756.8244***	878.9159	1739.7979	870.4026	1738.8139	869.9106	16
6	632.2886	316.6479	615.2620	308.1347	614.2780	307.6427	S	***1669.7924***	835.3998	1652.7659	826.8866	1651.7818	826.3946	15
7	**747.3155**	374.1614	730.2890	365.6481	729.3050	365.1561	D	***1582.7604***	791.8838	1565.7338	783.3706	1564.7498	782.8785	14
8	876.3581	438.6827	859.3316	430.1694	858.3476	429.6774	E	***1467.7334***	734.3704	1450.7069	725.8571	1449.7229	725.3651	13
9	989.4422	495.2247	972.4156	486.7115	971.4316	486.2195	L	***1338.6908***	669.8491	1321.6643	661.3358	1320.6803	660.8438	12
10	1117.5008	559.2540	1100.4742	550.7408	1099.4902	550.2487	Q	***1225.6068***	613.3070	1208.5802	604.7938	1207.5962	604.3017	11
11	**1230.5848**	615.7961	1213.5583	607.2828	1212.5743	606.7908	L	***1097.5482***	549.2777	1080.5217	540.7645	1079.5376	540.2725	10
12	**1317.6169**	659.3121	1300.5903	650.7988	1299.6063	650.3068	S	***984.4641***	492.7357	967.4376	484.2224	966.4536	483.7304	9
13	**1448.6574**	724.8323	1431.6308	716.3190	1430.6468	715.8270	M	***897.4321***	449.2197	880.4056	440.7064			8
14	1505.6788	753.3430	1488.6523	744.8298	1487.6682	744.3378	G	***766.3916***	383.6994	749.3651	375.1862			7
15	**1619.7217**	810.3645	1602.6952	801.8512	1601.7112	801.3592	N	***709.3702***	355.1887	692.3436	346.6754			6
16	**1690.7589**	845.8831	1673.7323	837.3698	1672.7483	836.8778	A	***595.3272***	298.1673	578.3007	289.6540			5
17	**1821.7993**	911.4033	1804.7728	902.8900	1803.7888	902.3980	M	***524.2901***	262.6487	507.2636	254.1354			4
18	**1968.8678**	984.9375	1951.8412	976.4242	1950.8572	975.9322	F	***393.2496***	197.1285	376.2231	188.6152			3
19	2067.9362	1034.4717	2050.9096	1025.9584	2049.9256	1025.4664	V	246.1812	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
106.6	2213.0344	0.0080	TLNQSSDELQLSMGNAMFVK	Deamidated N3 93.32%
94.8	2213.0344	0.0080	TLNQSSDELQLSMGNAMFVK	Deamidated Q4 6.14%
84.2	2213.0344	0.0080	TLNQSSDELQLSMGNAMFVK	Deamidated Q10 0.54%
63.1	2213.0344	0.0080	TLNQSSDELQLSMGNAMFVK	Deamidated N15 0.00%
5.0	2211.0305	2.0119	QFTTNSNNPGTNTGAFVGRAR	
4.6	2211.0305	2.0119	QFTTNSNNPGTNTGAFVGRAR	
3.4	2212.0477	0.9947	MNVGVAHSEVNPNTRVMNSR	
3.4	2212.0477	0.9947	MNVGVAHSEVNPNTRVMNSR	
3.0	2211.0305	2.0119	QFTTNSNNPGTNTGAFVGRAR	
2.2	2212.0477	0.9947	MNVGVAHSEVNPNTRVMNSR	

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

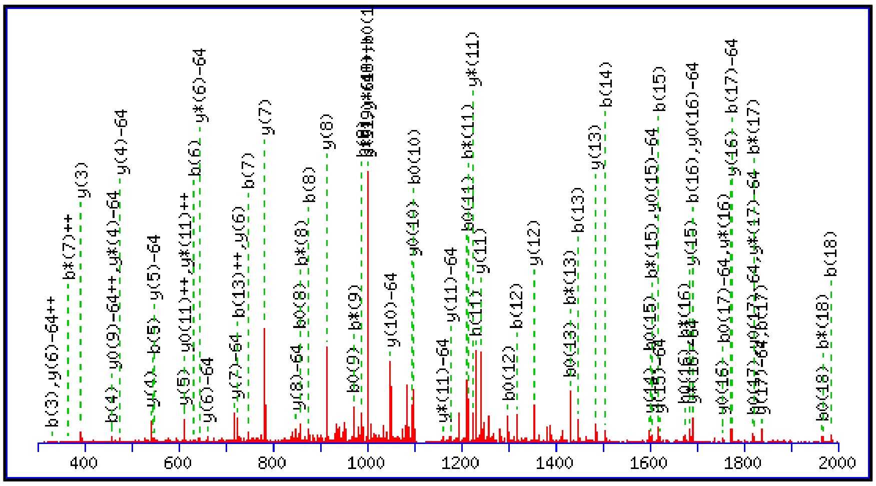
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLNQSSDELQLSMGNAMFVK**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

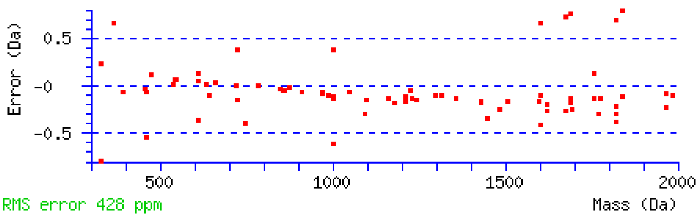
Match to Query 14935: 2229.037368 from(1115.525960,2+) intensity(185032.9844) rtinseconds(1685) scans(3972) index(11818)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum3393_scans__3972
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

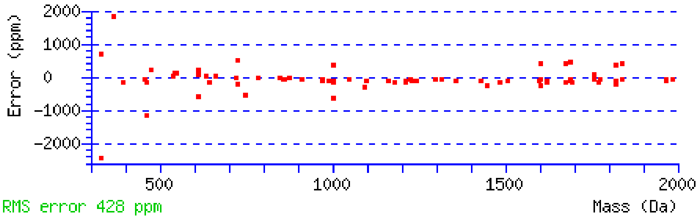
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2229.0293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 87 **Expect:** 3.7e-007
Matches : 78/312 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							20
2	215.1390	108.0731			197.1285	99.0679	L	2128.9889	1064.9981	2111.9624	1056.4848	2110.9784	1055.9928	19
3	***330.1660***	165.5866	313.1394	157.0733	312.1554	156.5813	N	2015.9049	1008.4561	1998.8783	999.9428	1997.8943	999.4508	18
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	Q	1900.8779	950.9426	1883.8514	942.4293	1882.8674	941.9373	17
5	***545.2566***	273.1319	528.2300	264.6186	527.2460	264.1266	S	**1772.8193**	886.9133	1755.7928	878.4000	1754.8088	877.9080	16
6	***632.2886***	316.6479	615.2620	308.1347	614.2780	307.6427	S	**1685.7873**	843.3973	1668.7608	834.8840	1667.7768	834.3920	15
7	***747.3155***	374.1614	730.2890	365.6481	729.3050	365.1561	D	**1598.7553**	799.8813	1581.7287	791.3680	1580.7447	790.8760	14
8	***876.3581***	438.6827	859.3316	430.1694	858.3476	429.6774	E	**1483.7283**	742.3678	1466.7018	733.8545	1465.7178	733.3625	13
9	***989.4422***	495.2247	972.4156	486.7115	971.4316	486.2195	L	**1354.6858**	677.8465	1337.6592	669.3332	1336.6752	668.8412	12
10	1117.5008	559.2540	1100.4742	550.7408	1099.4902	550.2487	Q	**1241.6017**	621.3045	1224.5751	612.7912	1223.5911	612.2992	11
11	***1230.5848***	615.7961	1213.5583	607.2828	1212.5743	606.7908	L	1113.5431	557.2752	1096.5166	548.7619	1095.5325	548.2699	10
12	***1317.6169***	659.3121	1300.5903	650.7988	1299.6063	650.3068	S	**1000.4590**	500.7332	983.4325	492.2199	982.4485	491.7279	9
13	***1448.6574***	724.8323	1431.6308	716.3190	1430.6468	715.8270	M	**913.4270**	457.2171	896.4005	448.7039			8
14	***1505.6788***	753.3430	1488.6523	744.8298	1487.6682	744.3378	G	**782.3865**	391.6969	765.3600	383.1836			7
15	***1619.7217***	810.3645	1602.6952	801.8512	1601.7112	801.3592	N	**725.3651**	363.1862	708.3385	354.6729			6
16	***1690.7589***	845.8831	1673.7323	837.3698	1672.7483	836.8778	A	**611.3221**	306.1647	594.2956	297.6514			5
17	***1837.7943***	919.4008	1820.7677	910.8875	1819.7837	910.3955	M	**540.2850**	270.6462	523.2585	262.1329			4
18	***1984.8627***	992.9350	1967.8361	984.4217	1966.8521	983.9297	F	**393.2496**	197.1285	376.2231	188.6152			3
19	2083.9311	1042.4692	2066.9045	1033.9559	2065.9205	1033.4639	V	246.1812	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.4	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated N3, Oxidation M17; 82.65%
80.0	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated Q4, Oxidation M17; 15.28%
71.3	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated Q10, Oxidation M17; 2.06%
48.3	2228.0453	0.9921	TLNQSSDELQLSMGNAMFVK	
48.2	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated N15, Oxidation M17; 0.01%
38.0	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated N3, Oxidation M13; 0.00%
33.4	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated Q4, Oxidation M13; 0.00%
29.0	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated Q10, Oxidation M13; 0.00%
17.6	2228.0453	0.9921	TLNQSSDELQLSMGNAMFVK	
12.3	2229.0293	0.0081	TLNQSSDELQLSMGNAMFVK	Deamidated N15, Oxidation M13; 0.00%

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

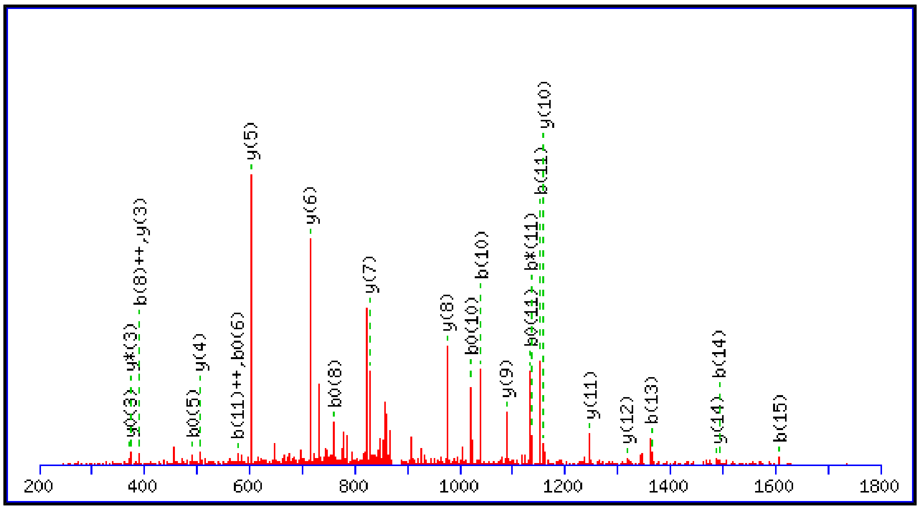
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTGNASALFILPDQDK**
Found in **G3V3A0** in **con_Xuniprot_HUMAN3**, G3V3A0_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

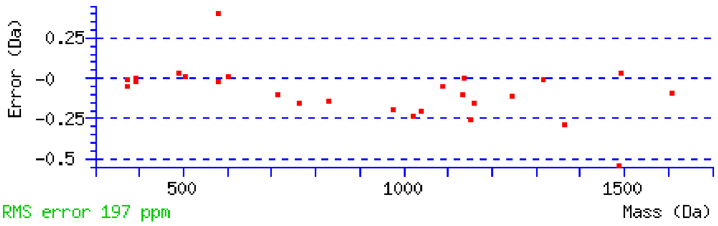
Match to Query 9372: 1752.863648 from(877.439100,2+) intensity(21117.1152) rtinseconds(1865) scans(4455) index(27882)
Title: 111019_Est_MI_YS_G_11Spectrum3886_scans__4455
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

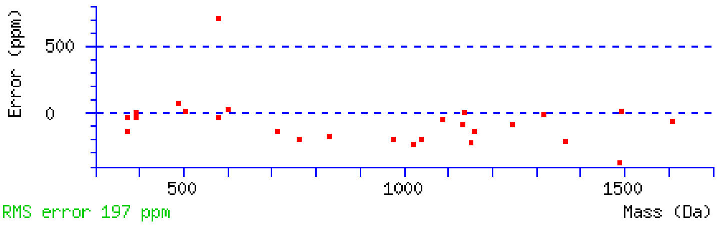
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1752.8570
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 84 **Expect:** 9.6e-007
Matches : 26/170 fragment ions using 43 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					**Y**							**16**
2	265.1183	133.0628			247.1077	124.0575	**T**	1590.8010	795.9041	1573.7744	787.3909	1572.7904	786.8988	**15**
3	322.1397	161.5735			304.1292	152.5682	**G**	***1489.7533***	745.3803	1472.7268	736.8670	1471.7427	736.3750	**14**
4	437.1667	219.0870	420.1401	210.5737	419.1561	210.0817	**N**	1432.7318	716.8696	1415.7053	708.3563	1414.7213	707.8643	**13**
5	508.2038	254.6055	491.1773	246.0923	490.1932	245.6003	**A**	***1317.7049***	659.3561	1300.6783	650.8428	1299.6943	650.3508	**12**
6	595.2358	298.1216	578.2093	289.6083	577.2253	289.1163	**S**	***1246.6678***	623.8375	1229.6412	615.3243	1228.6572	614.8322	**11**
7	666.2729	333.6401	649.2464	325.1268	648.2624	324.6348	**A**	***1159.6358***	580.3215	1142.6092	571.8082	1141.6252	571.3162	**10**
8	779.3570	390.1821	762.3305	381.6689	761.3464	381.1769	**L**	***1088.5986***	544.8030	1071.5721	536.2897	1070.5881	535.7977	**9**
9	926.4254	463.7164	909.3989	455.2031	908.4149	454.7111	**F**	***975.5146***	488.2609	958.4880	479.7477	957.5040	479.2556	**8**
10	**1039.5095**	520.2584	1022.4829	511.7451	1021.4989	511.2531	**I**	***828.4462***	414.7267	811.4196	406.2134	810.4356	405.7214	**7**
11	**1152.5936**	576.8004	1135.5670	568.2871	1134.5830	567.7951	**L**	***715.3621***	358.1847	698.3355	349.6714	697.3515	349.1794	**6**
12	1249.6463	625.3268	1232.6198	616.8135	1231.6358	616.3215	**P**	***602.2780***	301.6427	585.2515	293.1294	584.2675	292.6374	**5**
13	**1364.6733**	682.8403	1347.6467	674.3270	1346.6627	673.8350	**D**	***505.2253***	253.1163	488.1987	244.6030	487.2147	244.1110	**4**
14	**1492.7318**	746.8696	1475.7053	738.3563	1474.7213	737.8643	**Q**	***390.1983***	195.6028	373.1718	187.0895	372.1878	186.5975	**3**
15	**1607.7588**	804.3830	1590.7322	795.8698	1589.7482	795.3777	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
84.0	1752.8570	0.0066	YTGNASALFILPDQDK	Deamidated N4 100.00%
26.9	1752.8570	0.0066	YTGNASALFILPDQDK	Deamidated Q14 0.00%
18.2	1751.8690	0.9947	EFQTSAISRDIDTAAK	
16.4	1752.8577	0.0060	ERVHPKLNQMDQDK	
14.1	1752.8570	0.0066	DPYILEEASFVVQSR	
9.3	1752.8682	-0.0046	NVQFGLAYQEGRLQK	
9.3	1752.8682	-0.0046	NVQFGLAYQEGRLQK	
9.1	1750.8625	2.0012	QLSTGEELYIIDENK	
8.5	1752.8682	-0.0046	FNQLNRSLQDIEFK	
7.1	1751.8619	1.0017	QRADMLEMELKMLK	

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

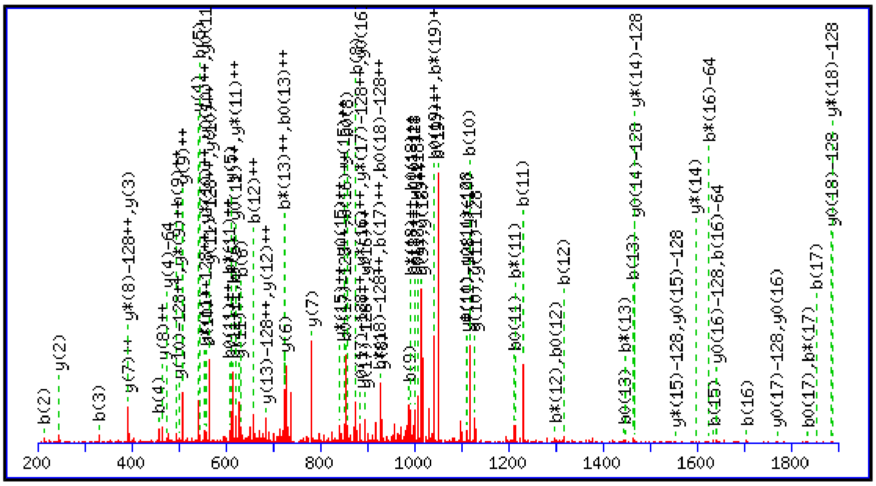
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLNQSSDELQLSMGNAMFVK**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

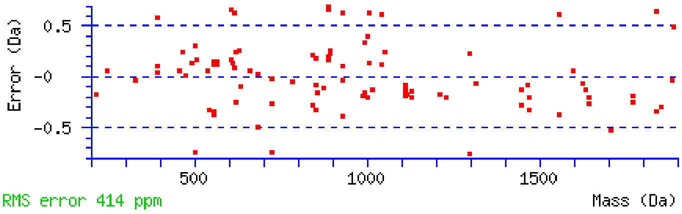
Match to Query 15005: 2245.028652 from(749.350160,3+) intensity(948436.5000) rtinseconds(1342) scans(3214) index(10884)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum2695_scans__3214
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

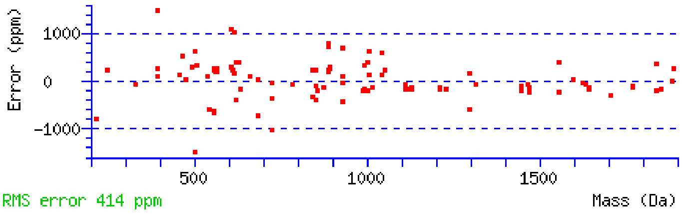
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2245.0242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 74 **Expect:** 7.1e-006
Matches : 100/336 fragment ions using 119 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311			84.0444	42.5258	T							20
2	***215.1390***	108.0731			197.1285	99.0679	L	2144.9838	1072.9956	2127.9573	1064.4823	2126.9733	1063.9903	19
3	***330.1660***	165.5866	313.1394	157.0733	312.1554	156.5813	N	2031.8998	1016.4535	2014.8732	1007.9403	2013.8892	1007.4482	18
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	Q	1916.8728	958.9401	1899.8463	950.4268	1898.8623	949.9348	17
5	***545.2566***	273.1319	528.2300	264.6186	527.2460	264.1266	S	1788.8143	894.9108	1771.7877	886.3975	1770.8037	885.9055	16
6	***632.2886***	316.6479	615.2620	308.1347	614.2780	307.6427	S	1701.7822	851.3948	1684.7557	842.8815	1683.7717	842.3895	15
7	747.3155	374.1614	730.2890	365.6481	729.3050	365.1561	D	1614.7502	807.8787	1597.7237	799.3655	1596.7396	798.8735	14
8	***876.3581***	438.6827	859.3316	430.1694	858.3476	429.6774	E	1499.7233	750.3653	1482.6967	741.8520	1481.7127	741.3600	13
9	***989.4422***	**495.2247**	972.4156	486.7115	971.4316	486.2195	L	1370.6807	685.8440	1353.6541	677.3307	1352.6701	676.8387	12
10	***1117.5008***	**559.2540**	1100.4742	550.7408	1099.4902	550.2487	Q	1257.5966	629.3019	1240.5701	620.7887	1239.5860	620.2967	11
11	***1230.5848***	**615.7961**	1213.5583	607.2828	1212.5743	606.7908	L	**1129.5380**	565.2727	1112.5115	556.7594	1111.5275	556.2674	10
12	***1317.6169***	**659.3121**	1300.5903	650.7988	1299.6063	650.3068	S	**1016.4540**	508.7306	999.4274	500.2173	998.4434	499.7253	9
13	***1464.6523***	732.8298	1447.6257	724.3165	1446.6417	723.8245	M	**929.4219**	465.2146	912.3954	456.7013			8
14	1521.6737	761.3405	1504.6472	752.8272	1503.6632	752.3352	G	**782.3865**	391.6969	765.3600	383.1836			7
15	***1635.7167***	**818.3620**	1618.6901	809.8487	1617.7061	809.3567	N	**725.3651**	363.1862	708.3385	354.6729			6
16	***1706.7538***	**853.8805**	1689.7272	845.3672	1688.7432	844.8752	A	**611.3221**	306.1647	594.2956	297.6514			5
17	***1853.7892***	**927.3982**	1836.7626	918.8849	1835.7786	918.3929	M	**540.2850**	270.6462	523.2585	262.1329			4
18	2000.8576	**1000.9324**	1983.8310	992.4192	1982.8470	991.9271	F	**393.2496**	197.1285	376.2231	188.6152			3
19	2099.9260	**1050.4666**	2082.8994	1041.9534	2081.9154	1041.4614	V	**246.1812**	123.5942	229.1547	115.0810			2
20							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.6	2245.0242	0.0044	TLNQSSDELQLSMGNAMFVK	Deamidated N3 90.75%
63.6	2245.0242	0.0044	TLNQSSDELQLSMGNAMFVK	Deamidated Q4 9.08%
46.0	2245.0242	0.0044	TLNQSSDELQLSMGNAMFVK	Deamidated Q10 0.16%
35.7	2245.0242	0.0044	TLNQSSDELQLSMGNAMFVK	Deamidated N15 0.01%
10.9	2244.0254	1.0032	EPLLSSSENGNGGRETSPADAR	
7.4	2245.0354	-0.0068	RAETLMFSNNAVISMRDEK	
5.6	2245.0359	-0.0073	ENFTTAHNTSGRSAPPSTNVR	
5.6	2245.0359	-0.0073	ENFTTAHNTSGRSAPPSTNVR	
5.0	2245.0190	0.0096	LSEYMVPDFFAFDHWNVK	
4.8	2243.0277	2.0010	RYDGAVQVMATQDGANFTAAR	

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

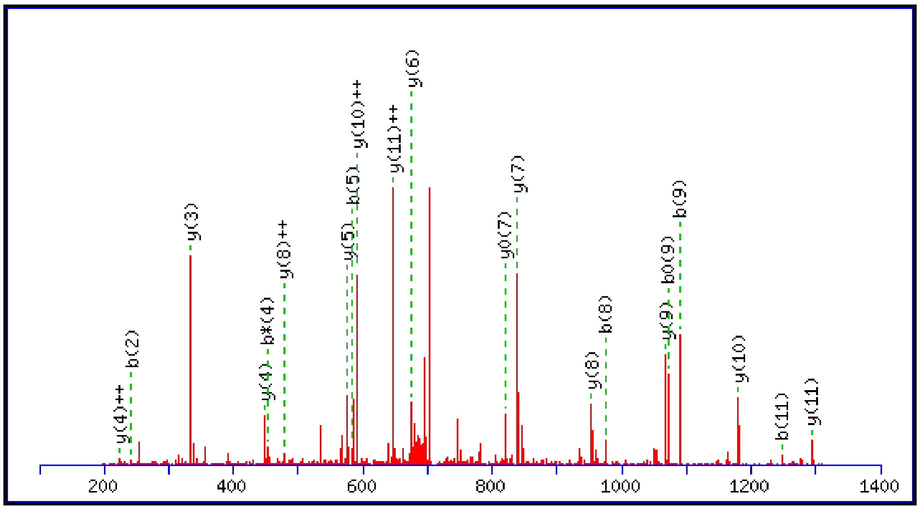
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLINDYVKNGTR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

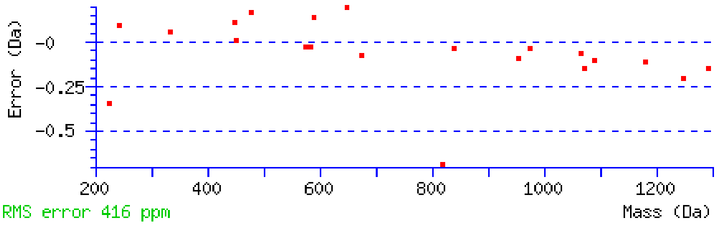
Match to Query 2990: 1420.771428 from(711.392990,2+) intensity(129386.4219) rtinseconds(412) scans(797) index(23026)
Title: 111019_Est_MI_YS_G_04Spectrum633_scans__797
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

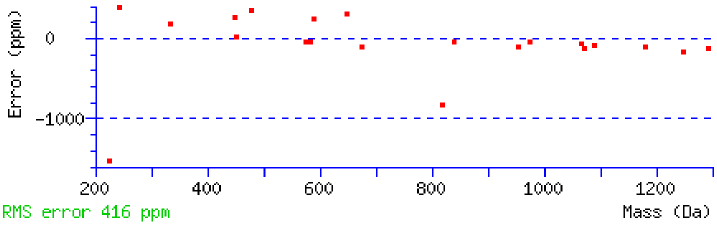
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1420.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 68 **Expect:** 2.5e-005
Matches : 21/122 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							12
2	**242.1863**	121.5968	225.1598	113.0835			L	***1293.6797***	647.3435	1276.6532	638.8302	1275.6692	638.3382	11
3	355.2704	178.1388	338.2438	169.6255			I	***1180.5957***	590.8015	1163.5691	582.2882	1162.5851	581.7962	10
4	469.3133	235.1603	452.2867	226.6470			N	***1067.5116***	534.2594	1050.4851	525.7462	1049.5010	525.2542	9
5	**584.3402**	292.6738	567.3137	284.1605	566.3297	283.6685	D	***953.4687***	477.2380	936.4421	468.7247	935.4581	468.2327	8
6	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	Y	***838.4417***	419.7245	821.4152	411.2112	820.4312	410.7192	7
7	846.4720	423.7396	829.4454	415.2264	828.4614	414.7343	V	***675.3784***	338.1928	658.3519	329.6796	657.3679	329.1876	6
8	**974.5669**	487.7871	957.5404	479.2738	956.5564	478.7818	K	***576.3100***	288.6586	559.2835	280.1454	558.2994	279.6534	5
9	**1089.5939**	545.3006	1072.5673	536.7873	1071.5833	536.2953	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
10	1146.6154	573.8113	1129.5888	565.2980	1128.6048	564.8060	G	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	**1247.6630**	624.3352	1230.6365	615.8219	1229.6525	615.3299	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.9	1420.7674	0.0040	KLINDYVKNGTR	Deamidated N9 99.96%
33.6	1420.7674	0.0040	KLINDYVKNGTR	Deamidated N4 0.04%
16.7	1420.7714	0.0000	KLLLNWVYNTR	
11.8	1420.7786	-0.0072	QLLNKTKGYNSR	
9.9	1420.7786	-0.0072	GANIDLIHLRGDK	
7.7	1420.7782	-0.0067	QIMMLSVLKNTK	
7.7	1420.7782	-0.0067	QIMMLSVLKNTK	
7.7	1420.7714	0.0000	QLSEVYIKWQK	
6.2	1420.7748	-0.0034	KIIMQYQAVAEK	
5.7	1420.7674	0.0040	ELTQRYLALSAR	

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

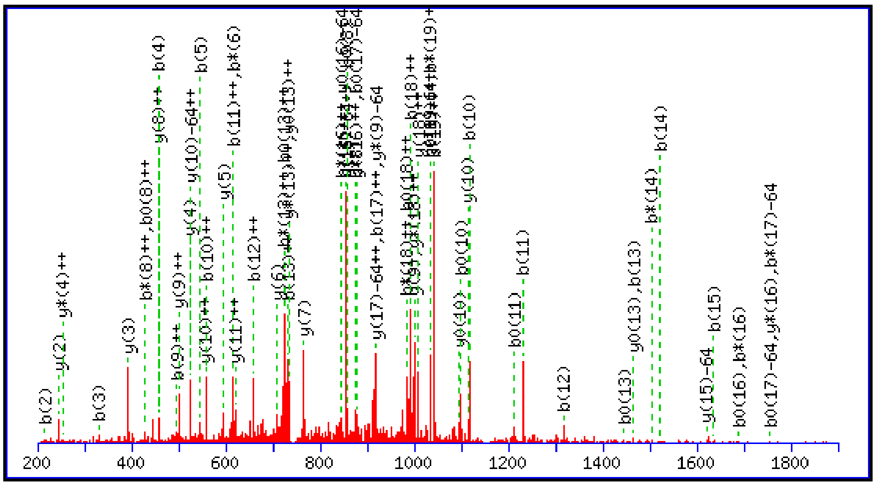
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLNQSSDELQLSMGNAMFVK**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

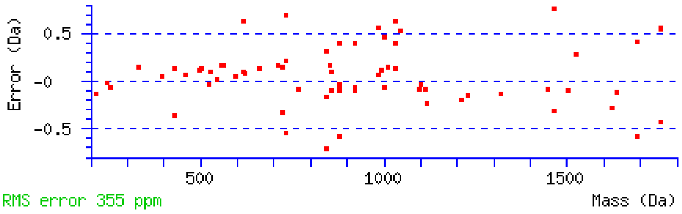
Match to Query 14929: 2229.035892 from(744.019240,3+) intensity(167242.8906) rtinseconds(1584) scans(3962) index(26663)
Title: 111019_Est_MI_YS_G_09Spectrum3433_scans__3962
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

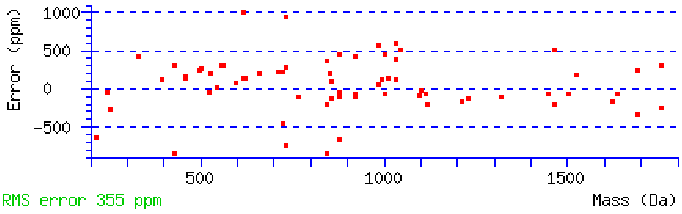
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2229.0293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3     : Deamidated (NQ)
M13    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 68  Expect: 3.4e-005
Matches : 71/320 fragment ions using 96 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**20**
2	***215.1390***	108.0731			197.1285	99.0679	**L**	2128.9889	1064.9981	2111.9624	1056.4848	2110.9784	1055.9928	**19**
3	***330.1660***	165.5866	313.1394	157.0733	312.1554	156.5813	**N**	2015.9049	1008.4561	1998.8783	999.9428	1997.8943	999.4508	**18**
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	**Q**	1900.8779	950.9426	1883.8514	942.4293	1882.8674	941.9373	**17**
5	***545.2566***	273.1319	528.2300	264.6186	527.2460	264.1266	**S**	1772.8193	886.9133	1755.7928	878.4000	1754.8088	877.9080	**16**
6	632.2886	316.6479	615.2620	308.1347	614.2780	307.6427	**S**	1685.7873	843.3973	1668.7608	834.8840	1667.7768	834.3920	**15**
7	747.3155	374.1614	730.2890	365.6481	729.3050	365.1561	**D**	1598.7553	799.8813	1581.7287	791.3680	1580.7447	790.8760	**14**
8	***876.3581***	438.6827	859.3316	430.1694	858.3476	429.6774	**E**	1483.7283	742.3678	1466.7018	733.8545	1465.7178	733.3625	**13**
9	989.4422	***495.2247***	972.4156	486.7115	971.4316	486.2195	**L**	1354.6858	677.8465	1337.6592	669.3332	1336.6752	668.8412	**12**
10	***1117.5008***	***559.2540***	1100.4742	550.7408	1099.4902	550.2487	**Q**	1241.6017	621.3045	1224.5751	612.7912	1223.5911	612.2992	**11**
11	***1230.5848***	***615.7961***	1213.5583	607.2828	1212.5743	606.7908	**L**	**1113.5431**	557.2752	1096.5166	548.7619	1095.5325	548.2699	**10**
12	***1317.6169***	***659.3121***	1300.5903	650.7988	1299.6063	650.3068	**S**	**1000.4590**	500.7332	983.4325	492.2199	982.4485	491.7279	**9**
13	***1464.6523***	***732.8298***	1447.6257	724.3165	1446.6417	723.8245	**M**	913.4270	457.2171	896.4005	448.7039			**8**
14	***1521.6737***	761.3405	1504.6472	752.8272	1503.6632	752.3352	**G**	**766.3916**	383.6994	749.3651	375.1862			**7**
15	***1635.7167***	818.3620	1618.6901	809.8487	1617.7061	809.3567	**N**	**709.3702**	355.1887	692.3436	346.6754			**6**
16	1706.7538	***853.8805***	1689.7272	845.3672	1688.7432	844.8752	**A**	**595.3272**	298.1673	578.3007	289.6540			**5**
17	1837.7943	***919.4008***	1820.7677	910.8875	1819.7837	910.3955	**M**	**524.2901**	262.6487	507.2636	254.1354			**4**
18	1984.8627	***992.9350***	1967.8361	984.4217	1966.8521	983.9297	**F**	**393.2496**	197.1285	376.2231	188.6152			**3**
19	2083.9311	***1042.4692***	2066.9045	1033.9559	2065.9205	1033.4639	**V**	**246.1812**	123.5942	229.1547	115.0810			**2**
20							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.7	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated N3, Oxidation M13; 85.52%
59.9	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated Q4, Oxidation M13; 14.16%
41.3	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated Q10, Oxidation M13; 0.20%
37.3	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated N3, Oxidation M17; 0.08%
31.7	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated Q4, Oxidation M17; 0.02%
30.0	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated N15, Oxidation M13; 0.01%
27.5	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated N15, Oxidation M17; 0.01%
22.2	2229.0293	0.0066	TLNQSSDELQLSMGNAMFVK	Deamidated Q10, Oxidation M17; 0.00%
3.4	2229.0332	0.0027	DDDSMGGSPGVPNAPTTKRAQK	
3.1	2227.0361	1.9998	LMKNRDEVQAMIYDDGASR	

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

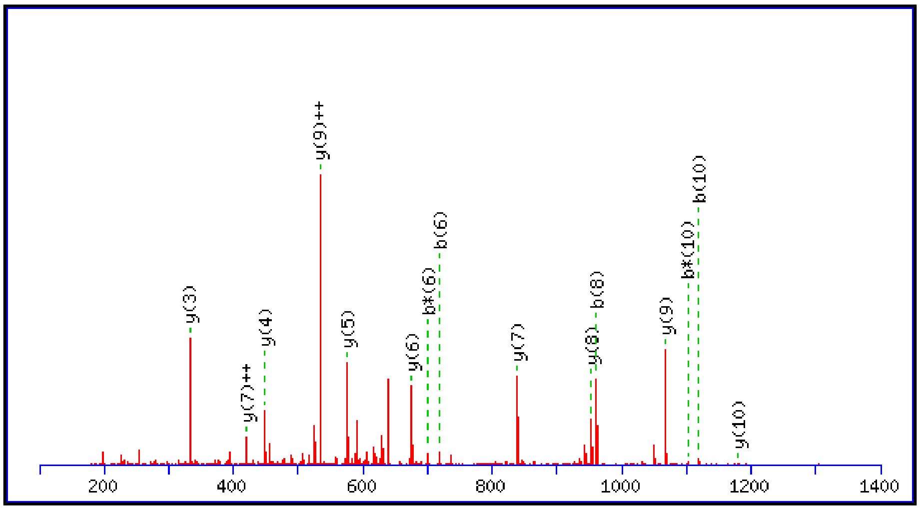
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LINDYVKNGTR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

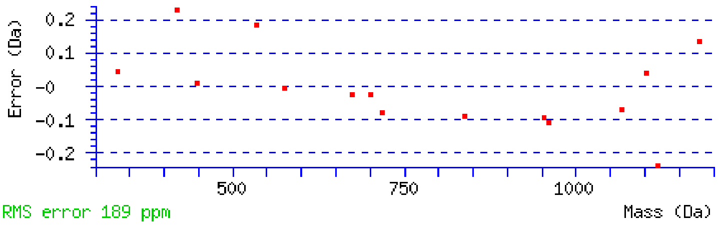
Match to Query 1873: 1292.674468 from(647.344510,2+) intensity(414729.3125) rtinseconds(538) scans(1020) index(9983)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum832_scans__1020
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

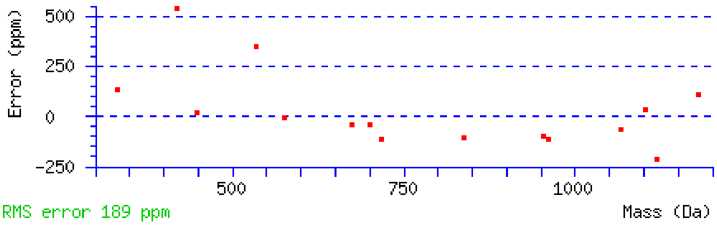
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1292.6724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 65 **Expect:** 6.1e-005
Matches : 15/108 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	114.0913	57.5493					L							11
2	227.1754	114.0913					I	***1180.5957***	590.8015	1163.5691	582.2882	1162.5851	581.7962	10
3	341.2183	171.1128	324.1918	162.5995			N	***1067.5116***	534.2594	1050.4851	525.7462	1049.5010	525.2542	9
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	D	***953.4687***	477.2380	936.4421	468.7247	935.4581	468.2327	8
5	619.3086	310.1579	602.2821	301.6447	601.2980	301.1527	Y	***838.4417***	419.7245	821.4152	411.2112	820.4312	410.7192	7
6	**718.3770**	359.6921	701.3505	351.1789	700.3665	350.6869	V	***675.3784***	338.1928	658.3519	329.6796	657.3678	329.1876	6
7	846.4720	423.7396	829.4454	415.2264	828.4614	414.7343	K	***576.3100***	288.6586	559.2835	280.1454	558.2994	279.6534	5
8	**961.4989**	481.2531	944.4724	472.7398	943.4884	472.2478	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
9	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	G	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
10	**1119.5681**	560.2877	1102.5415	551.7744	1101.5575	551.2824	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LINDYVKNGTR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.3	1292.6724	0.0020	LINDYVKNGTR	Deamidated N8 100.00%
13.4	1292.6724	0.0020	LINDYVKNGTR	Deamidated N3 0.00%
9.1	1292.6733	0.0011	ILNMCQVIFR	
5.1	1292.6720	0.0025	LLQTMDMIISK	
4.5	1292.6765	-0.0020	LLLNWVYNTR	
2.8	1292.6724	0.0020	LLQYRQVQSR	
1.5	1292.6758	-0.0013	TKESQSVQKMK	
1.0	1292.6724	0.0020	ILAESVANSAYR	
0.9	1292.6758	-0.0013	NKNSKLTLSMR	
0.8	1291.6740	1.0004	LLRVMQCLSR	

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

MATRIX SCIENCE

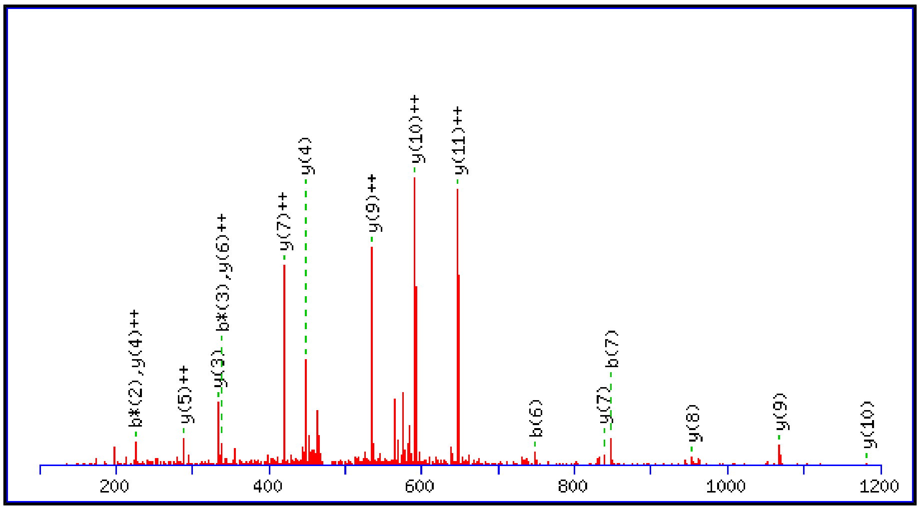
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLINDYVKNGTR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

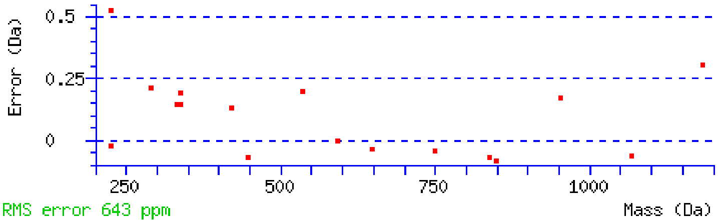
Match to Query 3025: 1421.754132 from(474.925320,3+) intensity(10532.8223) rtinseconds(353) scans(722) index(24326)
Title: 111019_Est_MI_YS_G_06Spectrum610_scans__722
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

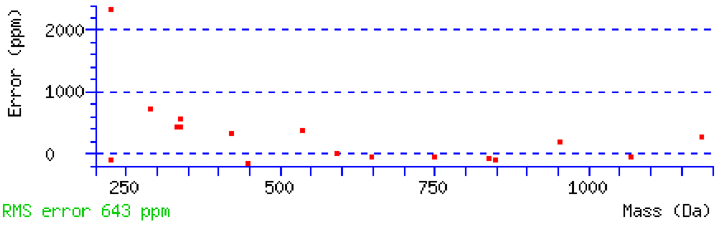
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1421.7514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 65 **Expect:** 5.5e-005
Matches : 17/122 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	129.1022	65.0548	112.0757	56.5415			K							12
2	242.1863	121.5968	225.1598	113.0835			L	1294.6638	647.8355	1277.6372	639.3222	1276.6532	638.8302	11
3	355.2704	178.1388	338.2438	169.6255			I	***1181.5797***	591.2935	1164.5531	582.7802	1163.5691	582.2882	10
4	470.2973	235.6523	453.2708	227.1390			N	***1068.4956***	534.7515	1051.4691	526.2382	1050.4851	525.7462	9
5	585.3243	293.1658	568.2977	284.6525	567.3137	284.1605	D	***953.4687***	477.2380	936.4421	468.7247	935.4581	468.2327	8
6	**748.3876**	374.6974	731.3610	366.1842	730.3770	365.6921	Y	***838.4417***	419.7245	821.4152	411.2112	820.4312	410.7192	7
7	**847.4560**	424.2316	830.4294	415.7184	829.4454	415.2264	V	675.3784	338.1928	658.3519	329.6796	657.3679	329.1876	6
8	975.5510	488.2791	958.5244	479.7658	957.5404	479.2738	K	576.3100	288.6586	559.2835	280.1454	558.2994	279.6534	5
9	1090.5779	545.7926	1073.5514	537.2793	1072.5673	536.7873	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
10	1147.5994	574.3033	1130.5728	565.7900	1129.5888	565.2980	G	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	1248.6470	624.8272	1231.6205	616.3139	1230.6365	615.8219	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.0	1421.7514	0.0027	KLINDYVKNGTR
12.5	1419.7544	1.9997	AMEVVKVGGPVYR
12.5	1419.7544	1.9997	SMEVVKVGGPVYR
9.9	1421.7548	-0.0006	KLSMSSIETASLR
9.9	1421.7588	-0.0047	KIIMQYQAVAEK
9.9	1421.7588	-0.0047	KIIMQYQAVAEK
9.9	1421.7523	0.0018	KILHAGFKMMSK
6.5	1420.7562	0.9979	QIYGGLVGDVSSVK
6.0	1419.7544	1.9997	QIMHQPIPGLIR
5.4	1420.7561	0.9980	KLYQLENEKVR

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

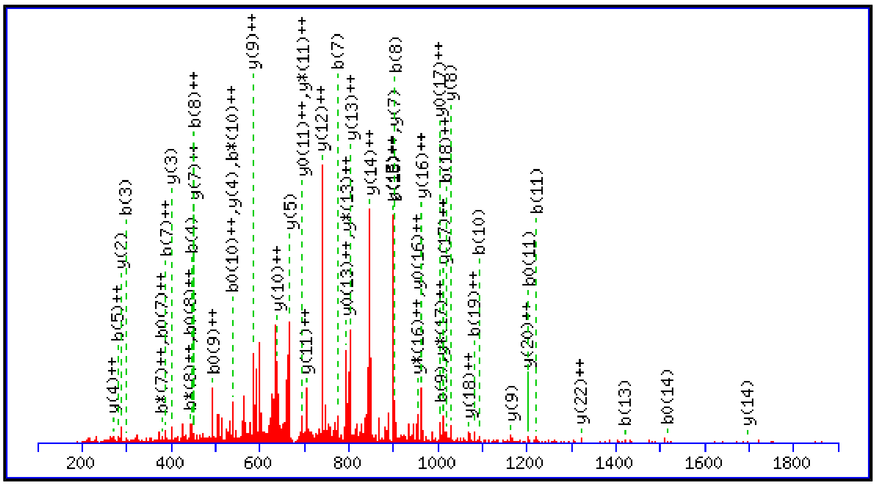
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLKFNLTETSEAEIHQSFQHLLR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

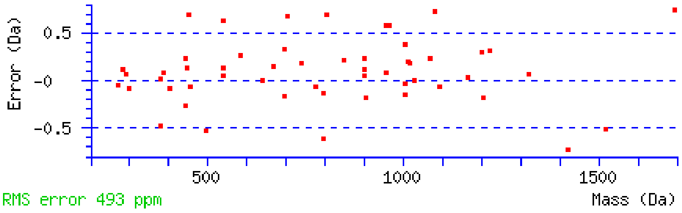
Match to Query 25347: 2698.380856 from(675.602490,4+) intensity(30417.6230) rtinseconds(2133) scans(5220) index(11955)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum4513_scans__5220
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

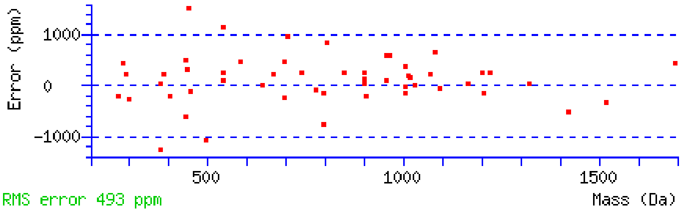
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2698.3714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00036
Matches : 53/236 fragment ions using 108 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							23
2	171.1128	86.0600					L	2642.3573	1321.6823	2625.3307	1313.1690	2624.3467	1312.6770	22
3	**299.2078**	150.1075	282.1812	141.5942			K	2529.2732	1265.1403	2512.2467	1256.6270	2511.2627	1256.1350	21
4	**446.2762**	223.6417	429.2496	215.1285			F	2401.1783	1201.0928	2384.1517	1192.5795	2383.1677	1192.0875	20
5	561.3031	**281.1552**	544.2766	272.6419			N	2254.1099	1127.5586	2237.0833	1119.0453	2236.0993	1118.5533	19
6	674.3872	337.6972	657.3606	329.1840			L	2139.0829	1070.0451	2122.0564	1061.5318	2121.0723	1061.0398	18
7	**775.4349**	**388.2211**	758.4083	379.7078	757.4243	379.2158	T	2025.9988	1013.5031	2008.9723	1004.9898	2007.9883	1004.4978	17
8	**904.4775**	**452.7424**	887.4509	444.2291	886.4669	443.7371	E	1924.9512	962.9792	1907.9246	954.4659	1906.9406	953.9739	16
9	**1005.5251**	503.2662	988.4986	494.7529	987.5146	494.2609	T	1795.9086	898.4579	1778.8820	889.9447	1777.8980	889.4526	15
10	**1092.5572**	546.7822	1075.5306	538.2689	1074.5466	537.7769	S	***1694.8609***	847.9341	1677.8343	839.4208	1676.8503	838.9288	14
11	**1221.5998**	611.3035	1204.5732	602.7902	1203.5892	602.2982	E	1607.8289	804.4181	1590.8023	795.9048	1589.8183	795.4128	13
12	1292.6369	646.8221	1275.6103	638.3088	1274.6263	637.8168	A	1478.7863	739.8968	1461.7597	731.3835	1460.7757	730.8915	12
13	**1421.6795**	711.3434	1404.6529	702.8301	1403.6689	702.3381	E	1407.7492	704.3782	1390.7226	695.8649	1389.7386	695.3729	11
14	1534.7635	767.8854	1517.7370	759.3721	1516.7530	758.8801	I	1278.7066	639.8569	1261.6800	631.3436	1260.6960	630.8516	10
15	1671.8224	836.4149	1654.7959	827.9016	1653.8119	827.4096	H	***1165.6225***	583.3149	1148.5960	574.8016	1147.6119	574.3096	9
16	1799.8810	**900.4441**	1782.8545	891.9309	1781.8705	891.4389	Q	***1028.5636***	514.7854	1011.5370	506.2722	1010.5530	505.7802	8
17	1886.9130	943.9602	1869.8865	935.4469	1868.9025	934.9549	S	***900.5050***	450.7561	883.4785	442.2429	882.4944	441.7509	7
18	2033.9815	**1017.4944**	2016.9549	1008.9811	2015.9709	1008.4891	F	813.4730	407.2401	796.4464	398.7269			6
19	2162.0400	**1081.5237**	2145.0135	1073.0104	2144.0295	1072.5184	Q	***666.4046***	333.7059	649.3780	325.1926			5
20	2299.0990	1150.0531	2282.0724	1141.5398	2281.0884	1141.0478	H	***538.3460***	269.6766	521.3194	261.1634			4
21	2412.1830	1206.5951	2395.1565	1198.0819	2394.1725	1197.5899	L	***401.2871***	201.1472	384.2605	192.6339			3
22	2525.2671	1263.1372	2508.2405	1254.6239	2507.2565	1254.1319	L	***288.2030***	144.6051	271.1765	136.0919			2
23							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.1	2698.3714	0.0094	GLKFNLTETSEAEIHQSFQHLLR	Deamidated N5 41.32%
57.2	2698.3714	0.0094	GLKFNLTETSEAEIHQSFQHLLR	Deamidated Q16 33.20%
56.5	2697.3874	0.9934	GLKFNLTETSEAEIHQSFQHLLR	
56.0	2698.3714	0.0094	GLKFNLTETSEAEIHQSFQHLLR	Deamidated Q19 25.48%
7.3	2697.3874	0.9934	KVEQDLWNHAFKNQITTLQGQAK	
7.3	2697.3874	0.9934	KVEQDLWNHAFKNQITTLQGQAK	
6.4	2698.3714	0.0094	KVEQDLWNHAFKNQITTLQGQAK	
6.4	2698.3714	0.0094	KVEQDLWNHAFKNQITTLQGQAK	
6.3	2696.3802	2.0006	NERELMLISHQKSIEQLQETLR	
6.3	2696.3802	2.0006	NERELMLISHQKSIEQLQETLR	

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

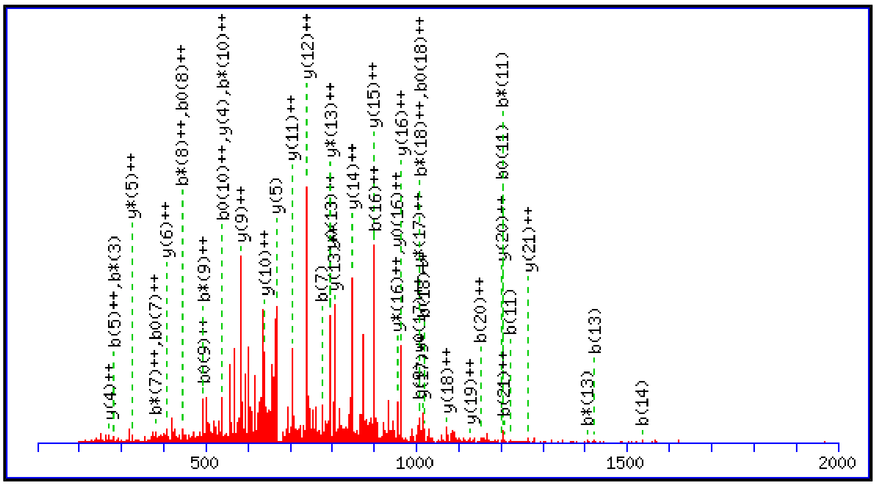
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLKFNLTETSEAEIHQSFQHLLR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

Match to Query 25354: 2699.363016 from(675.848030,4+) intensity(12991.5576) rtinseconds(2788) scans(7393) index(19034)
Title: 111019_Est_MI_YP_G_08Spectrum6469_scans__7393
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

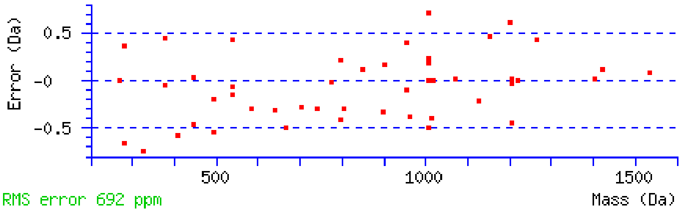
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

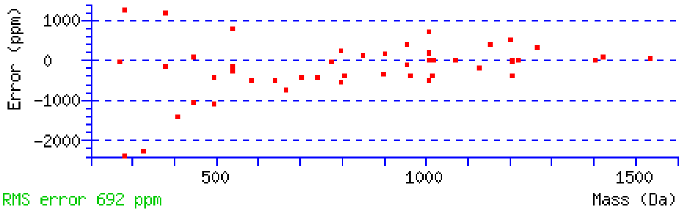


Monoisotopic mass of neutral peptide Mr(calc): 2699.3555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q19 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0011
Matches : 48/236 fragment ions using 114 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							23
2	171.1128	86.0600					L	2643.3413	1322.1743	2626.3148	1313.6610	2625.3307	1313.1690	22
3	299.2078	150.1075	282.1812	141.5942			K	2530.2572	1265.6323	2513.2307	1257.1190	2512.2467	1256.6270	21
4	446.2762	223.6417	429.2496	215.1285			F	2402.1623	1201.5848	2385.1357	1193.0715	2384.1517	1192.5795	20
5	561.3031	**281.1552**	544.2766	272.6419			N	2255.0939	1128.0506	2238.0673	1119.5373	2237.0833	1119.0453	19
6	674.3872	337.6972	657.3606	329.1840			L	2140.0669	1070.5371	2123.0404	1062.0238	2122.0564	1061.5318	18
7	**775.4349**	388.2211	758.4083	379.7078	757.4243	379.2158	T	2026.9829	1013.9951	2009.9563	1005.4818	2008.9723	1004.9898	17
8	904.4775	452.7424	887.4509	444.2291	886.4669	443.7371	E	1925.9352	963.4712	1908.9086	954.9580	1907.9246	954.4659	16
9	**1005.5251**	503.2662	988.4986	494.7529	987.5146	494.2609	T	1796.8926	898.9499	1779.8660	890.4367	1778.8820	889.9447	15
10	1092.5572	546.7822	1075.5306	538.2689	1074.5466	537.7769	S	1695.8449	848.4261	1678.8184	839.9128	1677.8343	839.4208	14
11	**1221.5998**	611.3035	1204.5732	602.7902	1203.5892	602.2982	E	1608.8129	804.9101	1591.7863	796.3968	1590.8023	795.9048	13
12	1292.6369	646.8221	1275.6103	638.3088	1274.6263	637.8168	A	1479.7703	740.3888	1462.7437	731.8755	1461.7597	731.3835	12
13	**1421.6795**	711.3434	1404.6529	702.8301	1403.6689	702.3381	E	1408.7332	704.8702	1391.7066	696.3570	1390.7226	695.8649	11
14	**1534.7635**	767.8854	1517.7370	759.3721	1516.7530	758.8801	I	1279.6906	640.3489	1262.6640	631.8357	1261.6800	631.3436	10
15	1671.8224	836.4149	1654.7959	827.9016	1653.8119	827.4096	H	1166.6065	583.8069	1149.5800	575.2936	1148.5960	574.8016	9
16	1799.8810	**900.4441**	1782.8545	891.9309	1781.8705	891.4389	Q	1029.5476	515.2774	1012.5211	506.7642	1011.5370	506.2722	8
17	1886.9130	943.9602	1869.8865	935.4469	1868.9025	934.9549	S	901.4890	451.2482	884.4625	442.7349	883.4785	442.2429	7
18	2033.9815	**1017.4944**	2016.9549	1008.9811	2015.9709	1008.4891	F	814.4570	407.7321	797.4305	399.2189			6
19	2163.0241	1082.0157	2145.9975	1073.5024	2145.0135	1073.0104	Q	667.3886	334.1979	650.3620	325.6847			5
20	2300.0830	**1150.5451**	2283.0564	1142.0318	2282.0724	1141.5398	H	538.3460	269.6766	521.3194	261.1634			4
21	2413.1670	**1207.0872**	2396.1405	1198.5739	2395.1565	1198.0819	L	401.2871	201.1472	384.2605	192.6339			3
22	2526.2511	1263.6292	2509.2245	1255.1159	2508.2405	1254.6239	L	288.2030	144.6051	271.1765	136.0919			2

23							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.7	2699.3555	0.0076	GLKFNLTETSEAEIHQSFQHLLR	Deamidated N5, Q19 49.98%
53.7	2699.3555	0.0076	GLKFNLTETSEAEIHQSFQHLLR	Deamidated N5, Q16 49.98%
44.1	2698.3714	0.9916	GLKFNLTETSEAEIHQSFQHLLR	
22.9	2698.3714	0.9916	GLKFNLTETSEAEIHQSFQHLLR	
22.9	2698.3714	0.9916	GLKFNLTETSEAEIHQSFQHLLR	
22.2	2699.3555	0.0076	GLKFNLTETSEAEIHQSFQHLLR	Deamidated Q16, Q19 0.03%
7.7	2699.3550	0.0080	NASMKTFGVIDAFLISVEEIQQMK	
7.7	2699.3550	0.0080	NASMKTFGVIDAFLISVEEIQQMK	
6.1	2698.3674	0.9956	QASSQLSRGSATTPRGVLHTFSPSPK	
5.1	2698.3714	0.9916	KVEQDLWNHAFKNQITTLQGQAK	

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

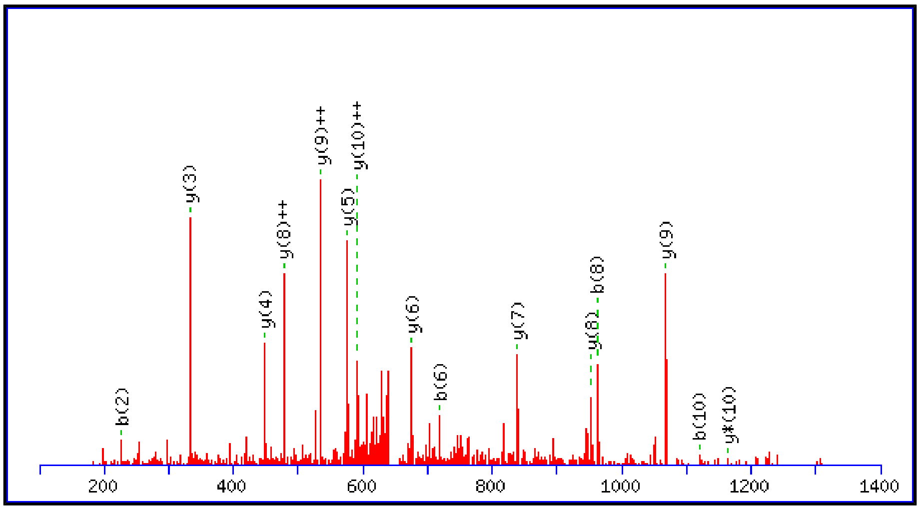
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LINDYVKNGTR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

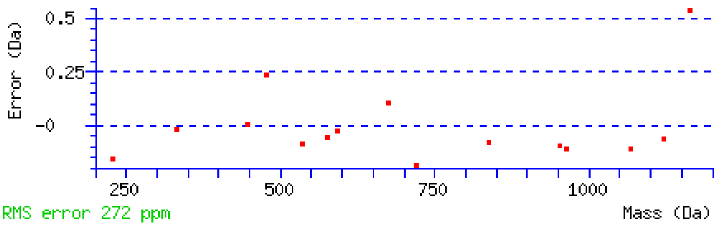
Match to Query 1961: 1293.658828 from(647.836690,2+) intensity(11714.5625) rtinseconds(572) scans(1173) index(10759)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum956_scans__1173
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

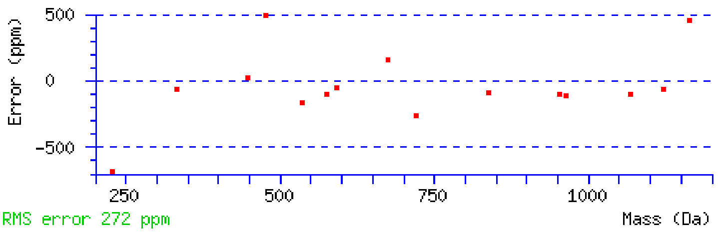
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1293.6564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N8 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0021
Matches : 15/108 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	114.0913	57.5493					L							11
2	**227.1754**	114.0913					I	1181.5797	591.2935	1164.5531	582.7802	1163.5691	582.2882	10
3	342.2023	171.6048	325.1758	163.0915			N	***1068.4956***	534.7515	1051.4691	526.2382	1050.4851	525.7462	9
4	457.2293	229.1183	440.2027	220.6050	439.2187	220.1130	D	***953.4687***	477.2380	936.4421	468.7247	935.4581	468.2327	8
5	620.2926	310.6499	603.2661	302.1367	602.2821	301.6447	Y	***838.4417***	419.7245	821.4152	411.2112	820.4312	410.7192	7
6	**719.3610**	360.1842	702.3345	351.6709	701.3505	351.1789	V	***675.3784***	338.1928	658.3519	329.6796	657.3678	329.1876	6
7	847.4560	424.2316	830.4294	415.7184	829.4454	415.2264	K	***576.3100***	288.6586	559.2835	280.1454	558.2994	279.6534	5
8	**962.4829**	481.7451	945.4564	473.2318	944.4724	472.7398	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
9	1019.5044	510.2558	1002.4779	501.7426	1001.4938	501.2506	G	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
10	**1120.5521**	560.7797	1103.5255	552.2664	1102.5415	551.7744	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
50.1	1293.6564	0.0024	LINDYVKNGTR
7.0	1293.6564	0.0024	LNSYIQGKNEK
6.6	1293.6573	0.0015	ILNMCQVIFR
5.7	1293.6573	0.0015	EPAGKMVMLFR
5.6	1293.6573	0.0015	ILNMCQVIFR
4.3	1292.6580	1.0008	AAMERQLISMK
4.3	1293.6573	0.0015	EPAGKMVMLFR
3.5	1293.6564	0.0024	ILAESVANSAYR
3.4	1293.6639	-0.0050	IISFGISDLQAM
2.9	1293.6605	-0.0016	EPLNLFYIER

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

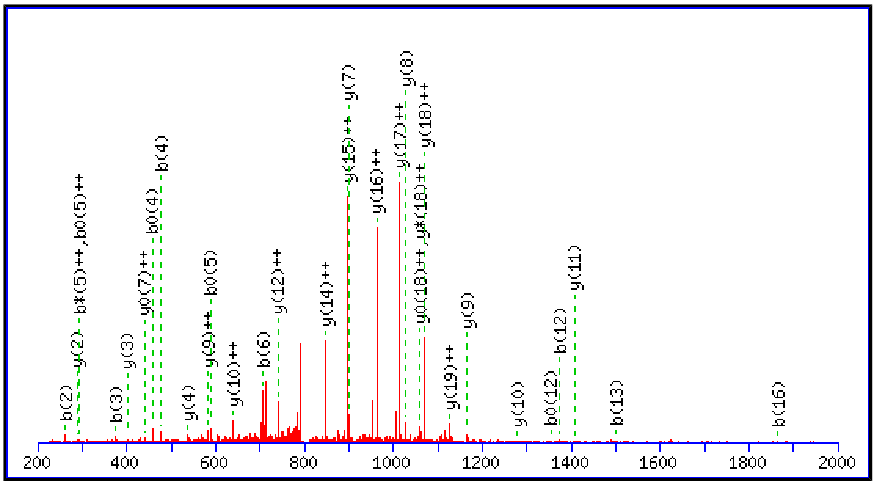
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNLTETSEAEIHQSFQHLLR**
Found in **G3V5I3** in **con_Xuniprot_HUMAN3**, G3V5I3_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=3 SV=1

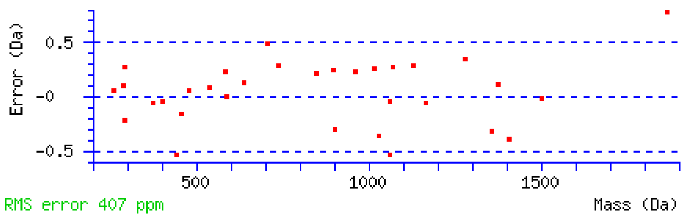
Match to Query 21492: 2400.179952 from(801.067260,3+) intensity(29116.8516) rtinseconds(2293) scans(5566) index(16972)
Title: 111019_Est_MI_YP_G_06Spectrum4624_scans__5566
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

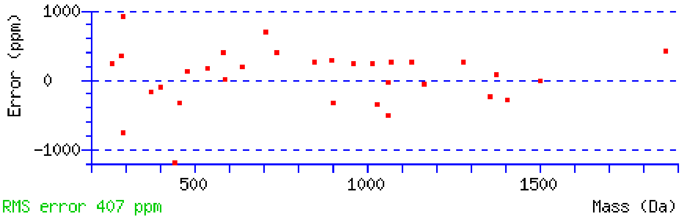
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2400.1710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Ions Score: 47  Expect: 0.0053
Matches : 32/208 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	148.0757	74.5415					F							20
2	**263.1026**	132.0550	246.0761	123.5417			N	2254.1099	1127.5586	2237.0833	1119.0453	2236.0993	1118.5533	19
3	**376.1867**	188.5970	359.1601	180.0837			L	2139.0829	1070.0451	2122.0564	1061.5318	2121.0723	1061.0398	18
4	**477.2344**	239.1208	460.2078	230.6076	459.2238	230.1155	T	2025.9988	1013.5031	2008.9723	1004.9898	2007.9883	1004.4978	17
5	606.2770	303.6421	589.2504	295.1288	588.2664	294.6368	E	1924.9512	962.9792	1907.9246	954.4659	1906.9406	953.9739	16
6	**707.3246**	354.1660	690.2981	345.6527	689.3141	345.1607	T	1795.9086	898.4579	1778.8820	889.9447	1777.8980	889.4526	15
7	794.3567	397.6820	777.3301	389.1687	776.3461	388.6767	S	1694.8609	847.9341	1677.8343	839.4208	1676.8503	838.9288	14
8	923.3993	462.2033	906.3727	453.6900	905.3887	453.1980	E	1607.8289	804.4181	1590.8023	795.9048	1589.8183	795.4128	13
9	994.4364	497.7218	977.4098	489.2086	976.4258	488.7165	A	1478.7863	739.8968	1461.7597	731.3835	1460.7757	730.8915	12
10	1123.4790	562.2431	1106.4524	553.7299	1105.4684	553.2378	E	***1407.7492***	704.3782	1390.7226	695.8649	1389.7386	695.3729	11
11	1236.5630	618.7852	1219.5365	610.2719	1218.5525	609.7799	I	***1278.7066***	639.8569	1261.6800	631.3436	1260.6960	630.8516	10
12	**1373.6220**	687.3146	1356.5954	678.8013	1355.6114	678.3093	H	***1165.6225***	583.3149	1148.5960	574.8016	1147.6119	574.3096	9
13	**1501.6805**	751.3439	1484.6540	742.8306	1483.6700	742.3386	Q	***1028.5636***	514.7854	1011.5370	506.2722	1010.5530	505.7802	8
14	1588.7126	794.8599	1571.6860	786.3466	1570.7020	785.8546	S	***900.5050***	450.7561	883.4785	442.2429	882.4944	441.7509	7
15	1735.7810	868.3941	1718.7544	859.8808	1717.7704	859.3888	F	813.4730	407.2401	796.4464	398.7269			6
16	**1863.8395**	932.4234	1846.8130	923.9101	1845.8290	923.4181	Q	666.4046	333.7059	649.3780	325.1926			5
17	2000.8985	1000.9529	1983.8719	992.4396	1982.8879	991.9476	H	***538.3460***	269.6766	521.3194	261.1634			4
18	2113.9825	1057.4949	2096.9560	1048.9816	2095.9720	1048.4896	L	***401.2871***	201.1472	384.2605	192.6339			3
19	2227.0666	1114.0369	2210.0400	1105.5237	2209.0560	1105.0317	L	***288.2030***	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.1	2400.1710	0.0090	FNLTETSEAEIHQSFQHLLR	Deamidated N2 97.45%
33.8	2399.1870	0.9930	FNLTETSEAEIHQSFQHLLR	
30.3	2400.1710	0.0090	FNLTETSEAEIHQSFQHLLR	Deamidated Q13 2.04%
24.3	2400.1710	0.0090	FNLTETSEAEIHQSFQHLLR	Deamidated Q16 0.51%
22.6	2399.1712	1.0087	MNLVVIPDSLQTTAMPQTLHR	
9.9	2399.1719	1.0081	NFLDLPSFCEEPALKKEFSK	
8.6	2400.1921	-0.0121	AFQEQGGGSKEKEAKPPQEDLK	
8.4	2400.1817	-0.0018	PTMTWLQTLTGLLEQMQVHR	
8.2	2400.1817	-0.0018	PTMTWLQTLTGLLEQMQVHR	
7.7	2400.1759	0.0041	MVDPRWPATFNFYICIVQK	

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

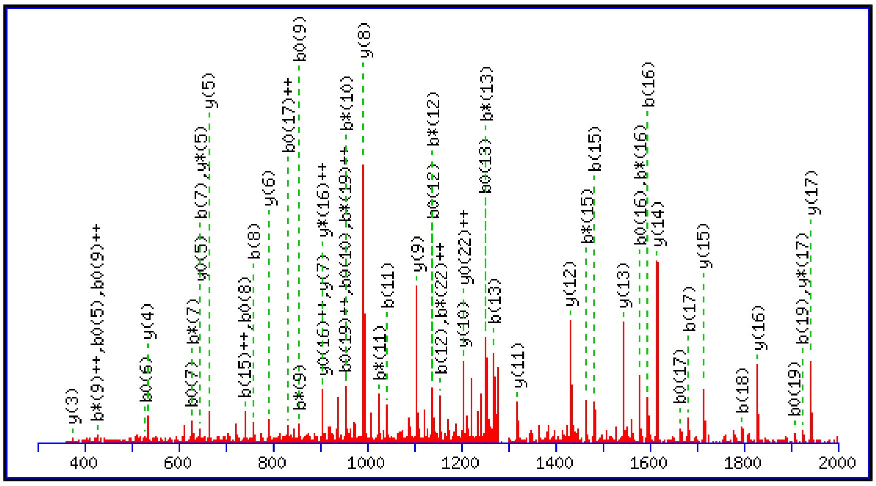
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTGNDTVLNVALLNVISNQECNIK**
Found in **G3XAK1** in **con_Xuniprot_HUMAN3**, G3XAK1_HUMAN Hepatocyte growth factor-like protein alpha chain OS=Homo sapiens GN=MST1 PE=3 SV=1

Match to Query 22180: 2586.307108 from(1294.160830,2+) intensity(18587.8223) rtinseconds(2452) scans(6512) index(4647)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum5557_scans__6512
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

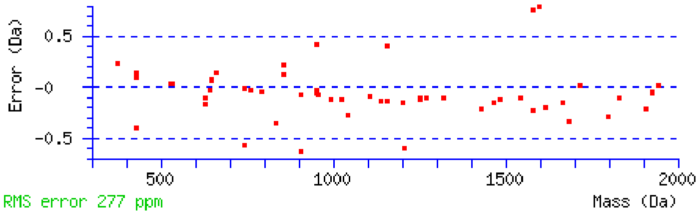
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

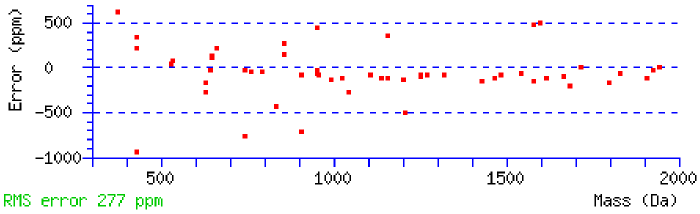


Monoisotopic mass of neutral peptide Mr(calc): 2586.2959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 86 **Expect:** 6.8e-007
Matches : 57/260 fragment ions using 85 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							24
2	159.0764	80.0418			141.0659	71.0366	T	2530.2817	1265.6445	2513.2552	1257.1312	2512.2712	1256.6392	23
3	216.0979	108.5526			198.0873	99.5473	G	2429.2341	1215.1207	2412.2075	1206.6074	2411.2235	1206.1154	22
4	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	N	2372.2126	1186.6099	2355.1861	1178.0967	2354.2020	1177.6047	21
5	446.1518	223.5795	429.1252	215.0662	428.1412	214.5742	D	2257.1857	1129.0965	2240.1591	1120.5832	2239.1751	1120.0912	20
6	547.1994	274.1034	530.1729	265.5901	529.1889	265.0981	T	2142.1587	1071.5830	2125.1322	1063.0697	2124.1481	1062.5777	19
7	**646.2679**	323.6376	629.2413	315.1243	628.2573	314.6323	V	2041.1110	1021.0592	2024.0845	1012.5459	2023.1005	1012.0539	18
8	**759.3519**	380.1796	742.3254	371.6663	741.3414	371.1743	L	***1942.0426***	971.5249	1925.0161	963.0117	1924.0321	962.5197	17
9	873.3949	437.2011	856.3683	428.6878	855.3843	428.1958	N	***1828.9586***	914.9829	1811.9320	906.4696	1810.9480	905.9776	16
10	972.4633	486.7353	955.4367	478.2220	954.4527	477.7300	V	***1714.9156***	857.9615	1697.8891	849.4482	1696.9051	848.9562	15
11	**1043.5004**	522.2538	1026.4738	513.7406	1025.4898	513.2485	A	***1615.8472***	808.4272	1598.8207	799.9140	1597.8367	799.4220	14
12	**1156.5844**	578.7959	1139.5579	570.2826	1138.5739	569.7906	L	***1544.8101***	772.9087	1527.7836	764.3954	1526.7995	763.9034	13
13	**1269.6685**	635.3379	1252.6420	626.8246	1251.6579	626.3326	L	***1431.7260***	716.3667	1414.6995	707.8534	1413.7155	707.3614	12
14	1383.7114	692.3594	1366.6849	683.8461	1365.7009	683.3541	N	***1318.6420***	659.8246	1301.6154	651.3114	1300.6314	650.8193	11
15	**1482.7798**	741.8936	1465.7533	733.3803	1464.7693	732.8883	V	***1204.5990***	602.8032	1187.5725	594.2899	1186.5885	593.7979	10
16	**1595.8639**	798.4356	1578.8374	789.9223	1577.8533	789.4303	I	***1105.5306***	553.2690	1088.5041	544.7557	1087.5201	544.2637	9
17	**1682.8959**	841.9516	1665.8694	833.4383	1664.8854	832.9463	S	***992.4466***	496.7269	975.4200	488.2136	974.4360	487.7216	8
18	**1796.9389**	898.9731	1779.9123	890.4598	1778.9283	889.9678	N	***905.4145***	453.2109	888.3880	444.6976	887.4040	444.2056	7
19	**1924.9974**	963.0024	1907.9709	954.4891	1906.9869	953.9971	Q	***791.3716***	396.1894	774.3451	387.6762	773.3611	387.1842	6
20	2054.0400	1027.5237	2037.0135	1019.0104	2036.0295	1018.5184	E	***663.3130***	332.1602	646.2865	323.6469	645.3025	323.1549	5
21	2214.0707	1107.5390	2197.0441	1099.0257	2196.0601	1098.5337	C	***534.2704***	267.6389	517.2439	259.1256			4
22	2328.1136	1164.5604	2311.0871	1156.0472	2310.1031	1155.5552	N	***374.2398***	187.6235	357.2132	179.1103			3

23	2441.1977	1221.1025	2424.1711	1212.5892	2423.1871	1212.0972	**I**	260.1969	130.6021	243.1703	122.0888			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.7	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated N4 63.98%
83.2	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated N9 35.57%
67.2	2585.3119	0.9952	GTGNDTVLNVALLNVISNQECNIK	
63.3	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated N14 0.37%
56.3	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated N18 0.07%
46.2	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated N22 0.01%
46.1	2586.2959	0.0112	GTGNDTVLNVALLNVISNQECNIK	Deamidated Q19 0.01%
7.2	2584.2941	2.0130	DQADPLDMKNVALLAPKTQLEEK	
7.1	2586.3013	0.0058	HLLQAPVDDAQEILHSRFPMPR	
3.0	2586.3013	0.0058	HLLQAPVDDAQEILHSRFPMPR	

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

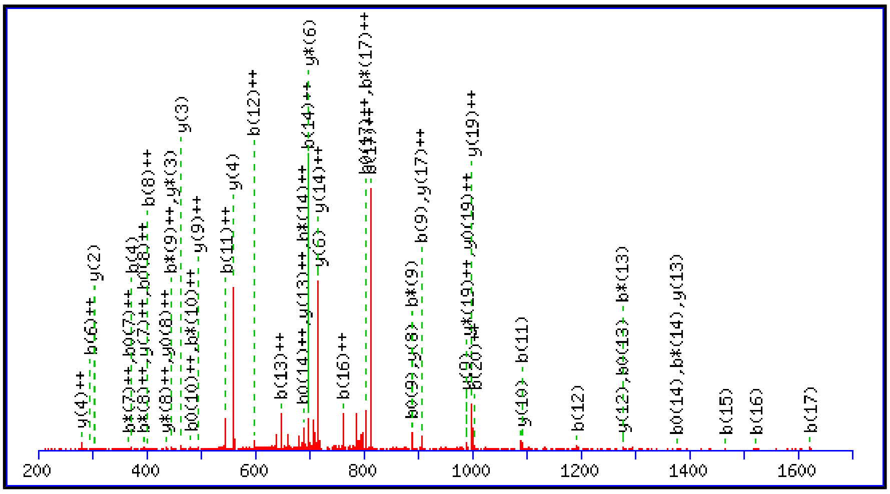
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GKGEGYRGTANTTTAGVPCQR**
Found in **G3XAK1** in **con_Xuniprot_HUMAN3**, G3XAK1_HUMAN Hepatocyte growth factor-like protein alpha chain OS=Homo sapiens GN=MST1 PE=3 SV=1

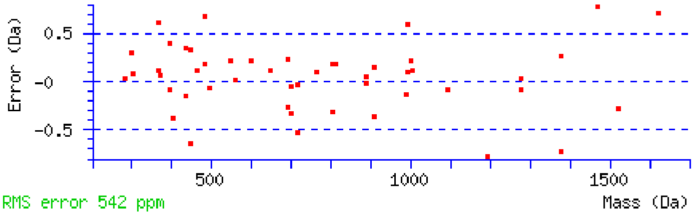
Match to Query 14730: 2181.029142 from(728.016990,3+) intensity(21610.6465) rtinseconds(315) scans(449) index(8178)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum342_scans__449
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

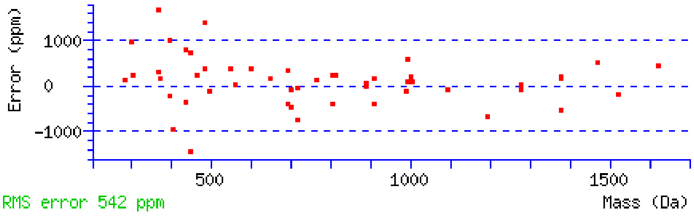
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2181.0233
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00048
Matches : 55/218 fragment ions using 74 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							21
2	186.1237	93.5655	169.0972	85.0522			K	2125.0091	1063.0082	2107.9825	1054.4949	2106.9985	1054.0029	20
3	243.1452	122.0762	226.1186	113.5629			G	1996.9141	998.9607	1979.8876	990.4474	1978.9036	989.9554	19
4	**372.1878**	186.5975	355.1612	178.0842	354.1772	177.5922	E	1939.8927	970.4500	1922.8661	961.9367	1921.8821	961.4447	18
5	429.2092	215.1083	412.1827	206.5950	411.1987	206.1030	G	1810.8501	905.9287	1793.8235	897.4154	1792.8395	896.9234	17
6	592.2726	***296.6399***	575.2460	288.1266	574.2620	287.6346	Y	1753.8286	877.4179	1736.8021	868.9047	1735.8180	868.4127	16
7	748.3737	374.6905	731.3471	366.1772	730.3631	365.6852	R	1590.7653	795.8863	1573.7387	787.3730	1572.7547	786.8810	15
8	805.3951	***403.2012***	788.3686	394.6879	787.3846	394.1959	G	1434.6642	717.8357	1417.6376	709.3224	1416.6536	708.8304	14
9	**906.4428**	453.7250	889.4163	445.2118	888.4322	444.7198	T	***1377.6427***	689.3250	1360.6162	680.8117	1359.6321	680.3197	13
10	977.4799	489.2436	960.4534	480.7303	959.4694	480.2383	A	***1276.5950***	638.8012	1259.5685	630.2879	1258.5845	629.7959	12
11	**1092.5069**	***546.7571***	1075.4803	538.2438	1074.4963	537.7518	N	1205.5579	603.2826	1188.5314	594.7693	1187.5474	594.2773	11
12	**1193.5545**	***597.2809***	1176.5280	588.7676	1175.5440	588.2756	T	***1090.5310***	545.7691	1073.5044	537.2558	1072.5204	536.7638	10
13	1294.6022	***647.8047***	1277.5757	639.2915	1276.5917	638.7995	T	***989.4833***	495.2453	972.4567	486.7320	971.4727	486.2400	9
14	1395.6499	***698.3286***	1378.6234	689.8153	1377.6393	689.3233	T	***888.4356***	444.7214	871.4091	436.2082	870.4250	435.7162	8
15	**1466.6870**	733.8471	1449.6605	725.3339	1448.6765	724.8419	A	787.3879	394.1976	770.3614	385.6843			7
16	**1523.7085**	***762.3579***	1506.6819	753.8446	1505.6979	753.3526	G	***716.3508***	358.6790	699.3243	350.1658			6
17	**1622.7769**	***811.8921***	1605.7503	803.3788	1604.7663	802.8868	V	659.3294	330.1683	642.3028	321.6550			5
18	1719.8297	860.4185	1702.8031	851.9052	1701.8191	851.4132	P	***560.2609***	280.6341	543.2344	272.1208			4
19	1879.8603	940.4338	1862.8338	931.9205	1861.8497	931.4285	C	***463.2082***	232.1077	446.1816	223.5945			3
20	2007.9189	***1004.4631***	1990.8923	995.9498	1989.9083	995.4578	Q	***303.1775***	152.0924	286.1510	143.5791			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
56.9	2181.0233	0.0059	GKGEGYRGTANTTTAGVPCQR	Deamidated N11 96.09%
43.0	2181.0233	0.0059	GKGEGYRGTANTTTAGVPCQR	Deamidated Q20 3.91%
5.3	2180.0206	1.0086	EQLANSQANRVPHSSEAGAGR	
5.2	2181.0233	0.0059	CLQTGTSGRERSTSGEWLR	
5.0	2179.0137	2.0155	IKEGEADSGMALDQEVSCLK	
4.9	2180.0154	1.0137	DSGNNILALEDLLSTSEKTC	
4.9	2180.0154	1.0137	DSGNNILALEDLLSTSEKTC	
4.4	2181.0259	0.0032	TDNDLDLMPSHLGPNGKLDK	
3.9	2180.0320	0.9971	DFAEMSSQLHLTPFTARGR	
3.7	2180.0206	1.0086	EQLANSQANRVPHSSEAGAGR	

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

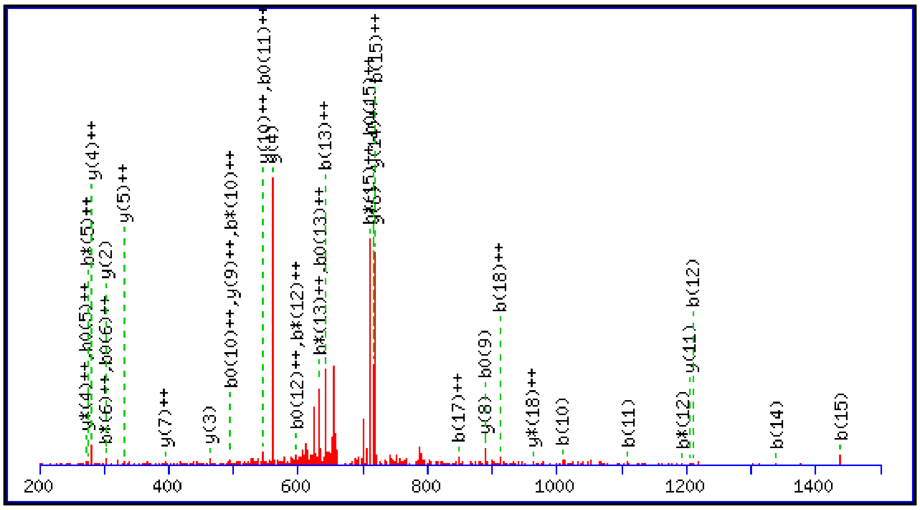
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEGYRGTANTTTAGVPCQR**
Found in **G3XAK1** in **con_Xuniprot_HUMAN3**, G3XAK1_HUMAN Hepatocyte growth factor-like protein alpha chain OS=Homo sapiens GN=MST1 PE=3 SV=1

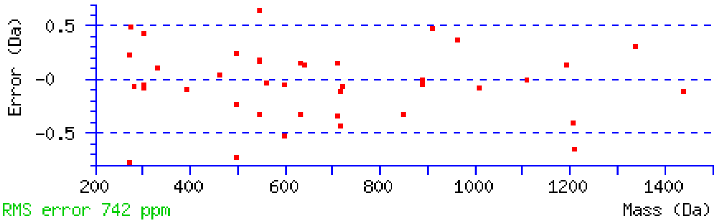
Match to Query 12212: 1995.911262 from(666.311030,3+) intensity(12724.2510) rtinseconds(367) scans(634) index(15572)
Title: 111019_Est_MI_YP_G_05Spectrum512_scans__634
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

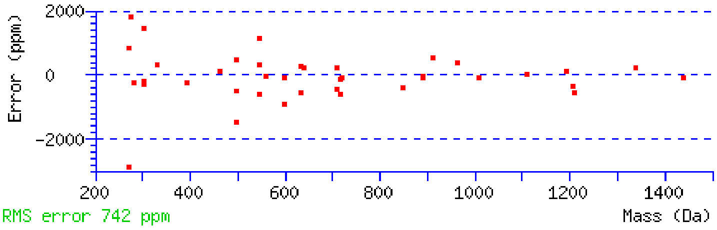
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1995.9069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9      : Deamidated (NQ)
Ions Score: 37  Expect: 0.035
Matches : 40/192 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	58.0287	29.5180					G							19
2	187.0713	94.0393			169.0608	85.0340	E	1939.8927	970.4500	1922.8661	961.9367	1921.8821	961.4447	18
3	244.0928	122.5500			226.0822	113.5448	G	1810.8501	905.9287	1793.8235	897.4154	1792.8395	896.9234	17
4	407.1561	204.0817			389.1456	195.0764	Y	1753.8286	877.4179	1736.8021	868.9047	1735.8180	868.4127	16
5	563.2572	282.1323	546.2307	273.6190	545.2467	273.1270	R	1590.7653	795.8863	1573.7387	787.3730	1572.7547	786.8810	15
6	620.2787	310.6430	603.2522	302.1297	602.2681	301.6377	G	1434.6642	717.8357	1417.6376	709.3224	1416.6536	708.8304	14
7	721.3264	361.1668	704.2998	352.6536	703.3158	352.1615	T	1377.6427	689.3250	1360.6162	680.8117	1359.6321	680.3197	13
8	792.3635	396.6854	775.3369	388.1721	774.3529	387.6801	A	1276.5950	638.8012	1259.5685	630.2879	1258.5845	629.7959	12
9	907.3904	454.1989	890.3639	445.6856	889.3799	445.1936	N	***1205.5579***	603.2826	1188.5314	594.7693	1187.5474	594.2773	11
10	**1008.4381**	504.7227	991.4116	496.2094	990.4276	495.7174	T	1090.5310	545.7691	1073.5044	537.2558	1072.5204	536.7638	10
11	**1109.4858**	555.2465	1092.4592	546.7333	1091.4752	546.2413	T	989.4833	495.2453	972.4567	486.7320	971.4727	486.2400	9
12	**1210.5335**	605.7704	1193.5069	597.2571	1192.5229	596.7651	T	***888.4356***	444.7214	871.4091	436.2082	870.4250	435.7162	8
13	1281.5706	**641.2889**	1264.5440	632.7757	1263.5600	632.2836	A	787.3879	394.1976	770.3614	385.6843			7
14	**1338.5921**	669.7997	1321.5655	661.2864	1320.5815	660.7944	G	***716.3508***	358.6790	699.3243	350.1658			6
15	**1437.6605**	**719.3339**	1420.6339	710.8206	1419.6499	710.3286	V	659.3294	330.1683	642.3028	321.6550			5
16	1534.7132	767.8603	1517.6867	759.3470	1516.7027	758.8550	P	***560.2609***	280.6341	543.2344	272.1208			4
17	1694.7439	**847.8756**	1677.7173	839.3623	1676.7333	838.8703	C	***463.2082***	232.1077	446.1816	223.5945			3
18	1822.8025	**911.9049**	1805.7759	903.3916	1804.7919	902.8996	Q	***303.1775***	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.9	1995.9069	0.0044	GEGYRGTANTTTAGVPCQR	Deamidated N9 99.67%
17.7	1995.9133	-0.0021	GSAIETSDQYQKQEQQR	
16.3	1995.9133	-0.0021	GSAIETSDQYQKQEQQR	
15.5	1995.9043	0.0069	NGQMFEWINCRQGSLR	
15.1	1995.9133	-0.0021	GSAIETSDQYQKQEQQR	
12.8	1995.9043	0.0069	NGQMFEWINCRQGSLR	
12.0	1995.9069	0.0044	GEGYRGTANTTTAGVPCQR	Deamidated Q18 0.33%
11.9	1995.9043	0.0069	NGQMFEWINCRQGSLR	
11.9	1995.9043	0.0069	NGQMFEWINCRQGSLR	
11.4	1995.9133	-0.0021	GSAIETSDQYQKQEQQR	

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

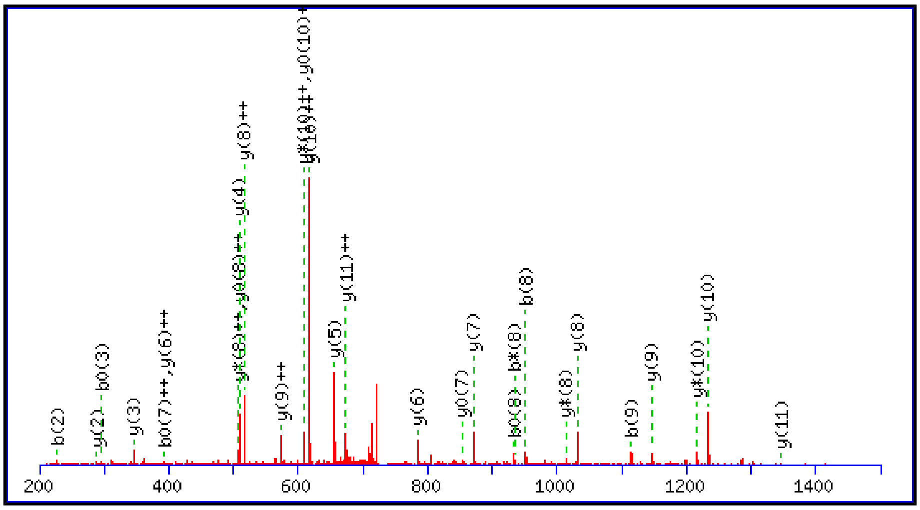
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LISNCSKFYGNR**
Found in **E7ETH0** in **con_Xuniprot_HUMAN3**, E7ETH0_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

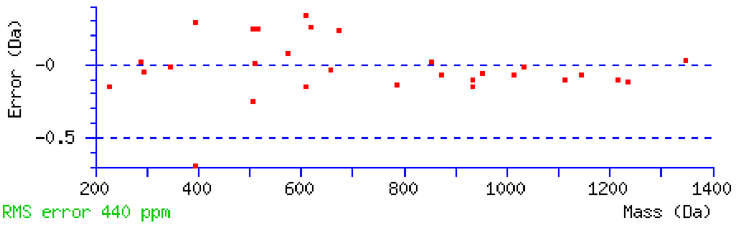
Match to Query 4230: 1458.697448 from(730.356000,2+) intensity(19167.0586) rtinseconds(479) scans(1047) index(24355)
Title: 111019_Est_MI_YS_G_06Spectrum897_scans__1047
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

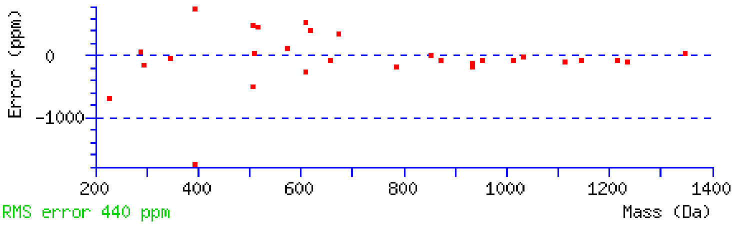
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1458.6925
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 69 **Expect:** 2.1e-005
Matches : 29/110 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	114.0913	57.5493					L							12
2	**227.1754**	114.0913					I	***1346.6158***	673.8115	1329.5892	665.2982	1328.6052	664.8062	11
3	314.2074	157.6074			296.1969	148.6021	S	***1233.5317***	617.2695	1216.5051	608.7562	1215.5211	608.2642	10
4	429.2344	215.1208	412.2078	206.6076	411.2238	206.1155	N	***1146.4997***	573.7535	1129.4731	565.2402	1128.4891	564.7482	9
5	589.2650	295.1362	572.2385	286.6229	571.2545	286.1309	C	***1031.4727***	516.2400	1014.4462	507.7267	1013.4622	507.2347	8
6	676.2971	338.6522	659.2705	330.1389	658.2865	329.6469	S	***871.4421***	436.2247	854.4155	427.7114	853.4315	427.2194	7
7	804.3920	402.6996	787.3655	394.1864	786.3814	393.6944	K	***784.4100***	392.7087	767.3835	384.1954			6
8	**951.4604**	476.2339	934.4339	467.7206	933.4499	467.2286	F	***656.3151***	328.6612	639.2885	320.1479			5
9	**1114.5238**	557.7655	1097.4972	549.2522	1096.5132	548.7602	Y	***509.2467***	255.1270	492.2201	246.6137			4
10	1171.5452	586.2762	1154.5187	577.7630	1153.5347	577.2710	G	***346.1833***	173.5953	329.1568	165.0820			3
11	1285.5881	643.2977	1268.5616	634.7844	1267.5776	634.2924	N	***289.1619***	145.0846	272.1353	136.5713			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.1	1458.6925	0.0049	LISNCSKFYGNR	Deamidated N4 99.99%
27.2	1458.6925	0.0049	LISNCSKFYGNR	Deamidated N11 0.01%
9.5	1458.6950	0.0024	LLQSQGQSPQQSR	
9.5	1458.6950	0.0024	LLQSQGQSPQQSR	
9.1	1458.7024	-0.0050	LQALVNSLCAGQSP	
8.8	1458.7038	-0.0063	LLHDARFCEGNK	
8.0	1458.6950	0.0024	LLQSQGQSPQQSR	
7.3	1457.7007	0.9968	KAYMNTQVVMNK	
6.2	1458.6950	0.0024	LLQSQGQSPQQSR	
6.2	1458.6950	0.0024	LLQSQGQSPQQSR	

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

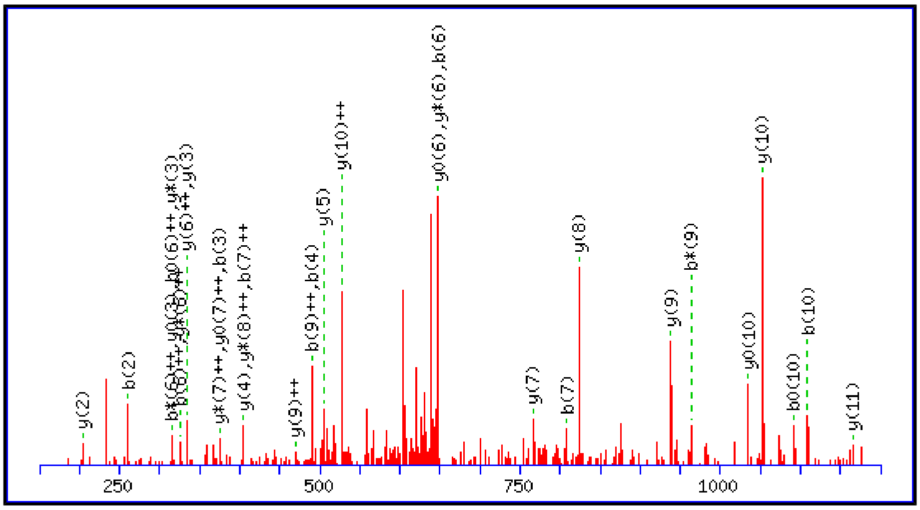
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLNNGTCTAEGK**
Found in **D6R9Z8** in **con_Xuniprot_HUMAN3**, D6R9Z8_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

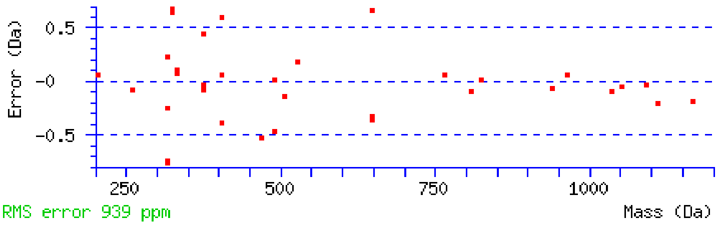
Match to Query 1989: 1311.579728 from(656.797140,2+) intensity(6442.4878) rtinseconds(410) scans(757) index(1836)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum605_scans__757
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

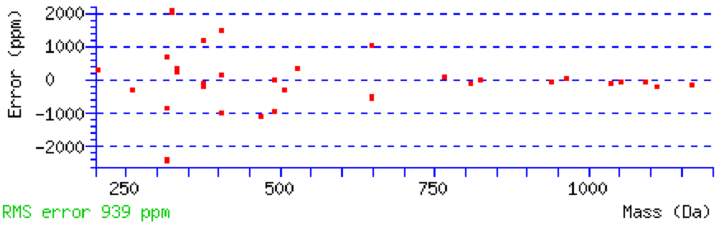
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [150] to [1200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1311.5765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.0001
Matches : 34/114 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	148.0757	74.5415					F							12
2	**261.1598**	131.0835					L	***1165.5154***	583.2613	1148.4888	574.7481	1147.5048	574.2560	11
3	**375.2027**	188.1050	358.1761	179.5917			N	***1052.4313***	526.7193	1035.4048	518.2060	1034.4208	517.7140	10
4	**490.2296**	245.6185	473.2031	237.1052			N	***938.3884***	469.6978	921.3618	461.1846	920.3778	460.6926	9
5	547.2511	274.1292	530.2245	265.6159			G	***823.3614***	412.1844	806.3349	403.6711	805.3509	403.1791	8
6	**648.2988**	**324.6530**	631.2722	316.1397	630.2882	315.6477	T	***766.3400***	383.6736	749.3134	375.1604	748.3294	374.6683	7
7	**808.3294**	**404.6683**	791.3029	396.1551	790.3189	395.6631	C	665.2923	333.1498	648.2658	324.6365	647.2817	324.1445	6
8	909.3771	455.1922	892.3505	446.6789	891.3665	446.1869	T	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5
9	980.4142	**490.7107**	963.3877	482.1975	962.4036	481.7055	A	***404.2140***	202.6106	387.1874	194.0974	386.2034	193.6053	4
10	**1109.4568**	555.2320	1092.4303	546.7188	1091.4462	546.2268	E	***333.1769***	167.0921	316.1503	158.5788	315.1663	158.0868	3
11	1166.4783	583.7428	1149.4517	575.2295	1148.4677	574.7375	G	***204.1343***	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.9	1311.5765	0.0032	FLNNGTCTAEGK	Deamidated N4 94.77%
47.3	1311.5765	0.0032	FLNNGTCTAEGK	Deamidated N3 5.23%
10.8	1310.5738	1.0059	GANNGKQYGSEGK	
9.5	1310.5813	0.9985	QFMNKSLSGPGQ	
8.8	1309.5786	2.0011	QEDGQLNNTYK	
7.7	1310.5772	1.0025	ASTDTSMNRSPK	
5.2	1309.5748	2.0050	QQVPTNLMTFE	
4.7	1310.5813	0.9985	VVCAGYDNGDIK	
3.2	1309.5786	2.0011	QADPNLHEAEGK	
1.3	1311.5765	0.0033	NMREQYDDLK	

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

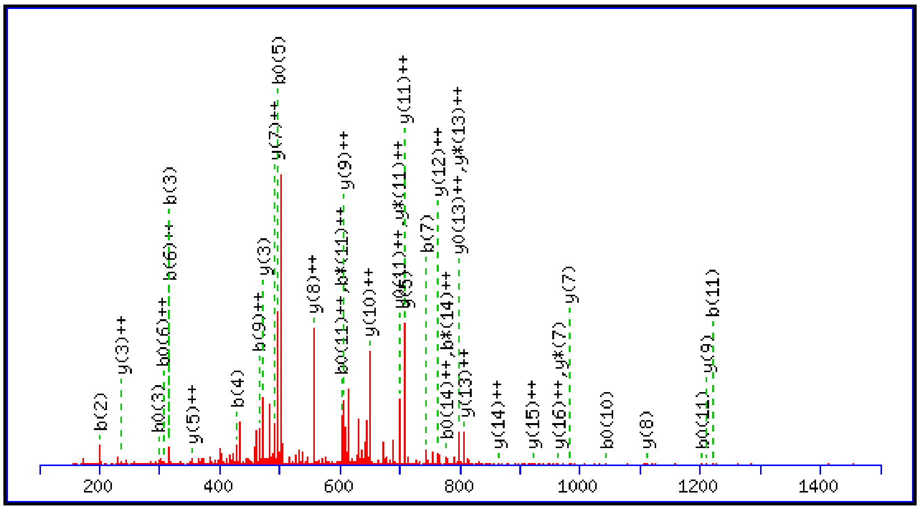
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSDLSINSTECLHVHCR**
Found in **E7ETH0** in **con_Xuniprot_HUMAN3**, E7ETH0_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

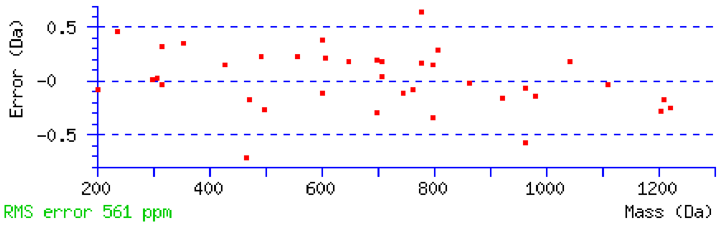
Match to Query 13064: 2040.940376 from(511.242370,4+) intensity(61112.3945) rtinseconds(939) scans(1955) index(724)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum1657_scans__1955
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

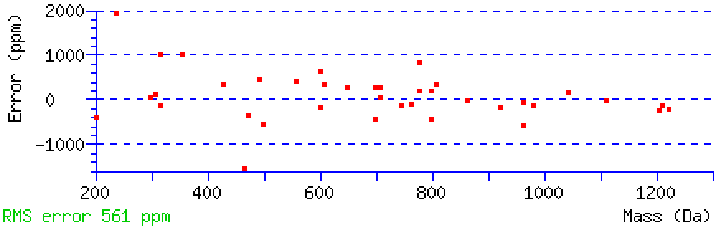
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2040.9357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.0002
Matches : 38/164 fragment ions using 71 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	**201.1234**	101.0653			183.1128	92.0600	S	1928.8589	964.9331	1911.8324	956.4198	1910.8484	955.9278	16
3	**316.1503**	158.5788			298.1397	149.5735	D	1841.8269	921.4171	1824.8003	912.9038	1823.8163	912.4118	15
4	**429.2344**	215.1208			411.2238	206.1155	L	1726.8000	863.9036	1709.7734	855.3903	1708.7894	854.8983	14
5	516.2664	258.6368			498.2558	249.6316	S	1613.7159	807.3616	1596.6893	798.8483	1595.7053	798.3563	13
6	629.3505	315.1789			611.3399	306.1736	I	1526.6839	763.8456	1509.6573	755.3323	1508.6733	754.8403	12
7	**744.3774**	372.6923	727.3509	364.1791	726.3668	363.6871	N	1413.5998	707.3035	1396.5732	698.7903	1395.5892	698.2983	11
8	831.4094	416.2084	814.3829	407.6951	813.3989	407.2031	S	1298.5729	649.7901	1281.5463	641.2768	1280.5623	640.7848	10
9	932.4571	466.7322	915.4306	458.2189	914.4466	457.7269	T	**1211.5408**	606.2740	1194.5143	597.7608	1193.5303	597.2688	9
10	1061.4997	531.2535	1044.4732	522.7402	1043.4891	522.2482	E	**1110.4931**	555.7502	1093.4666	547.2369	1092.4826	546.7449	8
11	**1221.5304**	611.2688	1204.5038	602.7555	1203.5198	602.2635	C	**981.4506**	491.2289	964.4240	482.7156			7
12	1334.6144	667.8108	1317.5879	659.2976	1316.6039	658.8056	L	821.4199	411.2136	804.3934	402.7003			6
13	1471.6733	736.3403	1454.6468	727.8270	1453.6628	727.3350	H	**708.3358**	354.6716	691.3093	346.1583			5
14	1570.7417	785.8745	1553.7152	777.3612	1552.7312	776.8692	V	571.2769	286.1421	554.2504	277.6288			4
15	1707.8007	854.4040	1690.7741	845.8907	1689.7901	845.3987	H	**472.2085**	236.6079	455.1820	228.0946			3
16	1867.8313	934.4193	1850.8048	925.9060	1849.8207	925.4140	C	335.1496	168.0784	318.1231	159.5652			2
17							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
59.7	2040.9357	0.0047	LSDLSINSTECLHVHCR
10.6	2040.9384	0.0020	EATWESVSMMLQLGGTVIG
10.0	2038.9300	2.0104	GVSDMNSTIQVLTADNCAK
6.3	2039.9469	0.9934	ENLATVEGNFASIDERMK
6.2	2040.9310	0.0094	ENLATVEGNFASIDERMK
4.7	2039.9283	1.0121	ETKRALDFTDSQENEEK
4.5	2038.9339	2.0064	SLDTNIMKHMPLNYNSK
4.5	2038.9339	2.0064	SLDTNIMKHMPLNYNSK
4.5	2038.9299	2.0104	QMENGMLVTDSAGKQLQR
4.0	2038.9299	2.0104	QMENGMLVTDSAGKQLQR

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

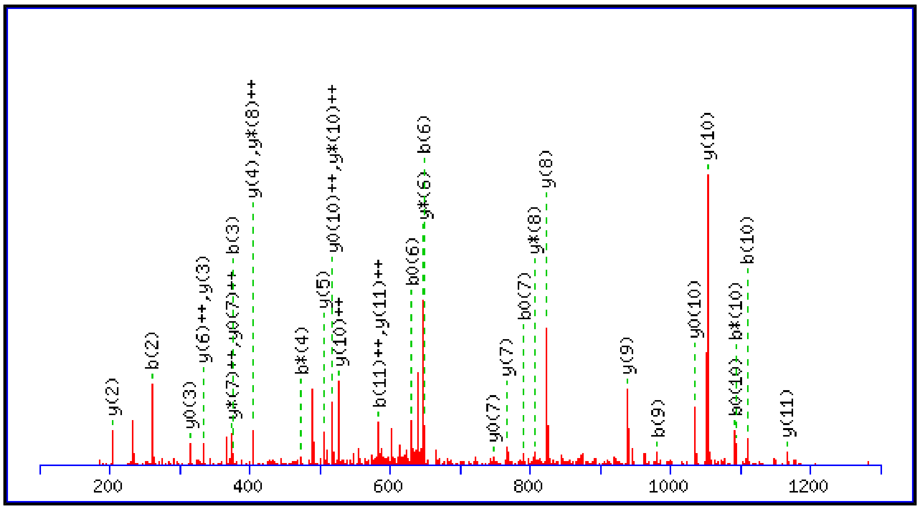
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLNNGTCTAEGK**
Found in **D6R9Z8** in **con_Xuniprot_HUMAN3**, D6R9Z8_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

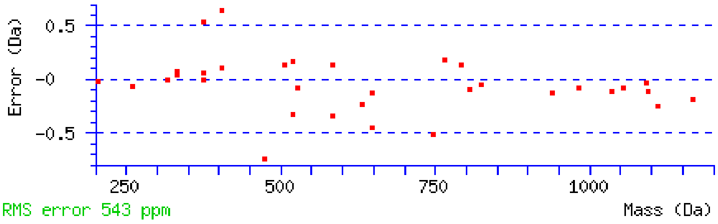
Match to Query 2012: 1312.565368 from(657.289960,2+) intensity(9313.6094) rtinseconds(419) scans(889) index(6135)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum763_scans__889
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

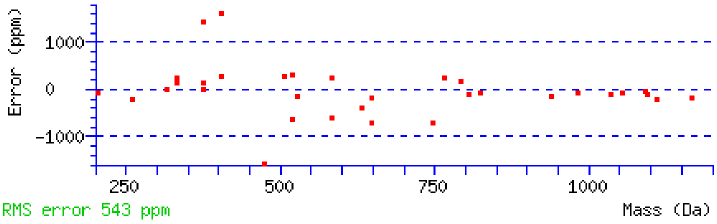
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1312.5605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N4 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00014
Matches : 33/114 fragment ions using 52 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							12
2	**261.1598**	131.0835					L	***1166.4994***	583.7533	1149.4728	575.2401	1148.4888	574.7481	11
3	**376.1867**	188.5970	359.1601	180.0837			N	***1053.4153***	527.2113	1036.3888	518.6980	1035.4048	518.2060	10
4	491.2136	246.1105	474.1871	237.5972			N	***938.3884***	469.6978	921.3618	461.1846	920.3778	460.6926	9
5	548.2351	274.6212	531.2086	266.1079			G	***823.3614***	412.1844	806.3349	403.6711	805.3509	403.1791	8
6	**649.2828**	325.1450	632.2562	316.6318	631.2722	316.1397	T	***766.3400***	383.6736	749.3134	375.1604	748.3294	374.6683	7
7	809.3134	405.1604	792.2869	396.6471	791.3029	396.1551	C	665.2923	333.1498	648.2658	324.6365	647.2817	324.1445	6
8	910.3611	455.6842	893.3346	447.1709	892.3505	446.6789	T	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5
9	**981.3982**	491.2028	964.3717	482.6895	963.3877	482.1975	A	***404.2140***	202.6106	387.1874	194.0974	386.2034	193.6053	4
10	**1110.4408**	555.7240	1093.4143	547.2108	1092.4303	546.7188	E	***333.1769***	167.0921	316.1503	158.5788	315.1663	158.0868	3
11	1167.4623	584.2348	1150.4357	575.7215	1149.4517	575.2295	G	***204.1343***	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.9	1312.5605	0.0049	FLNNGTCTAEGK
10.2	1311.5686	0.9967	MINIESMDTDK
9.2	1312.5717	-0.0063	EMSNANQYISR
9.2	1312.5717	-0.0063	EMSNANQYISR
7.8	1312.5686	-0.0032	MGNGMCSRKQK
6.4	1312.5614	0.0040	MIYCCTGPAPK
6.1	1312.5605	0.0049	NMREQYDDLK
6.0	1310.5595	2.0059	KMGADENQSGMK
5.9	1312.5605	0.0049	NFSCNVNTDIK
5.8	1311.5686	0.9968	MENQMKGLESK

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

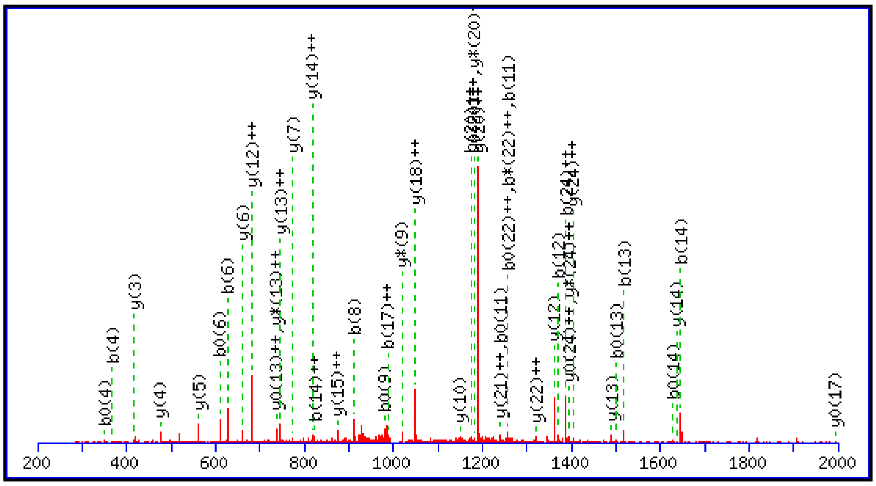
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SIPACVPWSPYLFQPNDTCIVSGWGR**
Found in **E7ETH0** in **con_Xuniprot_HUMAN3**, E7ETH0_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

Match to Query 27252: 3007.411392 from(1003.477740,3+) intensity(72679.7734) rtinseconds(2585) scans(6793) index(24879)
Title: 111019_Est_MI_YS_G_06Spectrum5927_scans__6793
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

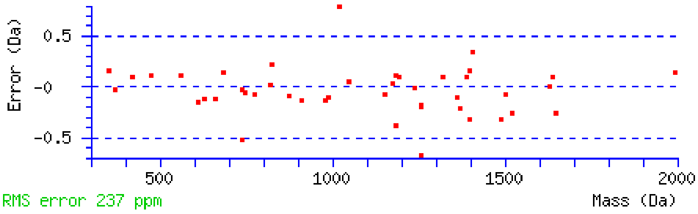
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

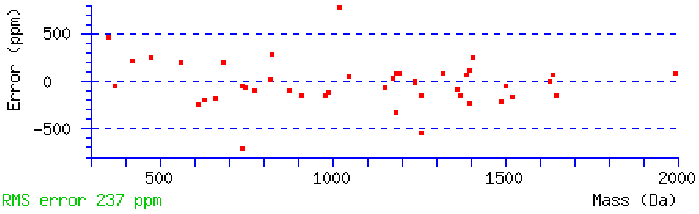


```
Monoisotopic mass of neutral peptide Mr(calc): 3007.3997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16     : Deamidated (NQ)
Ions Score: 55  Expect: 0.00074
Matches : 45/266 fragment ions using 69 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							26
2	201.1234	101.0653			183.1128	92.0600	I	2921.3749	1461.1911	2904.3484	1452.6778	2903.3644	1452.1858	25
3	298.1761	149.5917			280.1656	140.5864	P	2808.2909	1404.6491	2791.2643	1396.1358	2790.2803	1395.6438	24
4	**369.2132**	185.1103			351.2027	176.1050	A	2711.2381	1356.1227	2694.2116	1347.6094	2693.2275	1347.1174	23
5	529.2439	265.1256			511.2333	256.1203	C	2640.2010	1320.6041	2623.1744	1312.0909	2622.1904	1311.5989	22
6	**628.3123**	314.6598			610.3017	305.6545	V	2480.1703	1240.5888	2463.1438	1232.0755	2462.1598	1231.5835	21
7	725.3651	363.1862			707.3545	354.1809	P	2381.1019	1191.0546	2364.0754	1182.5413	2363.0914	1182.0493	20
8	**911.4444**	456.2258			893.4338	447.2205	W	2284.0492	1142.5282	2267.0226	1134.0149	2266.0386	1133.5229	19
9	998.4764	499.7418			980.4658	490.7366	S	2097.9699	1049.4886	2080.9433	1040.9753	2079.9593	1040.4833	18
10	1095.5292	548.2682			1077.5186	539.2629	P	2010.9378	1005.9726	1993.9113	997.4593	1992.9273	996.9673	17
11	**1258.5925**	629.7999			1240.5819	620.7946	Y	1913.8851	957.4462	1896.8585	948.9329	1895.8745	948.4409	16
12	**1371.6766**	686.3419			1353.6660	677.3366	L	1750.8217	875.9145	1733.7952	867.4012	1732.8112	866.9092	15
13	**1518.7450**	759.8761			1500.7344	750.8708	F	***1637.7377***	819.3725	1620.7111	810.8592	1619.7271	810.3672	14
14	**1646.8036**	**823.9054**	1629.7770	815.3921	1628.7930	814.9001	Q	***1490.6693***	745.8383	1473.6427	737.3250	1472.6587	736.8330	13
15	1743.8563	872.4318	1726.8298	863.9185	1725.8458	863.4265	P	***1362.6107***	681.8090	1345.5841	673.2957	1344.6001	672.8037	12
16	1858.8833	929.9453	1841.8567	921.4320	1840.8727	920.9400	N	1265.5579	633.2826	1248.5314	624.7693	1247.5473	624.2773	11
17	1973.9102	**987.4587**	1956.8837	978.9455	1955.8996	978.4535	D	***1150.5310***	575.7691	1133.5044	567.2558	1132.5204	566.7638	10
18	2074.9579	1037.9826	2057.9313	1029.4693	2056.9473	1028.9773	T	1035.5040	518.2557	1018.4775	509.7424	1017.4935	509.2504	9
19	2234.9885	1117.9979	2217.9620	1109.4846	2216.9780	1108.9926	C	934.4563	467.7318	917.4298	459.2185	916.4458	458.7265	8
20	2348.0726	**1174.5399**	2331.0461	1166.0267	2330.0620	1165.5347	I	***774.4257***	387.7165	757.3992	379.2032	756.4151	378.7112	7
21	2447.1410	1224.0741	2430.1145	1215.5609	2429.1305	1215.0689	V	***661.3416***	331.1745	644.3151	322.6612	643.3311	322.1692	6
22	2534.1730	1267.5902	2517.1465	1259.0769	2516.1625	1258.5849	S	***562.2732***	281.6402	545.2467	273.1270	544.2627	272.6350	5
23	2591.1945	1296.1009	2574.1680	1287.5876	2573.1839	1287.0956	G	***475.2412***	238.1242	458.2146	229.6110			4

24	2777.2738	**1389.1405**	2760.2473	1380.6273	2759.2633	1380.1353	**W**	***418.2197***	209.6135	401.1932	201.1002			**3**
25	2834.2953	1417.6513	2817.2687	1409.1380	2816.2847	1408.6460	**G**	232.1404	116.5738	215.1139	108.0606			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.1	3007.3997	0.0117	SIPACVPWSPYLFQPNDTCIVSGWGR	Deamidated N16 74.91%
50.3	3007.3997	0.0117	SIPACVPWSPYLFQPNDTCIVSGWGR	Deamidated Q14 25.09%
40.0	3006.4157	0.9957	SIPACVPWSPYLFQPNDTCIVSGWGR	
14.1	3005.4070	2.0044	SAIEISIAECKGTEQDTCTVHLSGDRK	
8.9	3007.3981	0.0133	QAMNHFVQENGTLRAKPTGNGIYINGR	
8.4	3006.4088	1.0026	SSDKGSPSQSTSVKVMINILDENDNAPR	
8.4	3006.4088	1.0026	SSDKGSPSQSTSVKVMINILDENDNAPR	
8.4	3006.4088	1.0026	SSDKGSPSQSTSVKVMINILDENDNAPR	
4.7	3005.3932	2.0182	SFGRYPSLMENNNMRIQDTLDLVMK	
4.7	3005.3932	2.0182	SFGRYPSLMENNNMRIQDTLDLVMK	

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

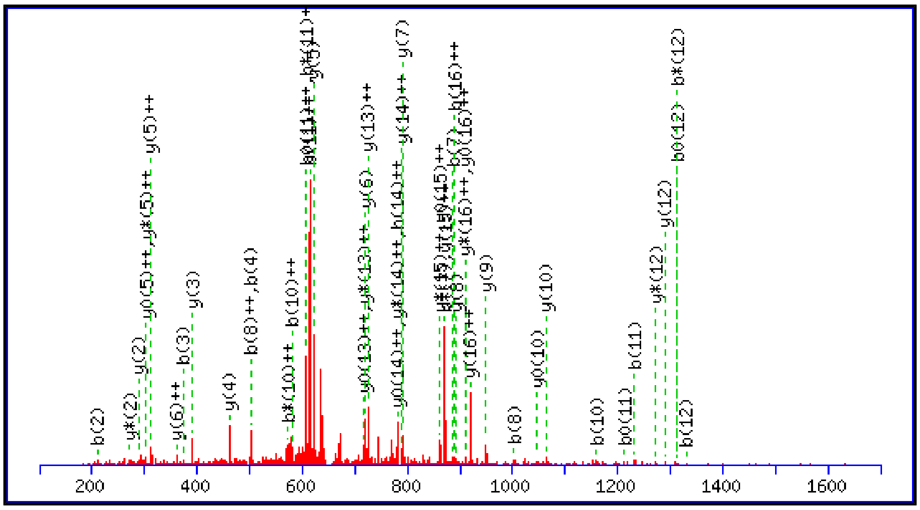
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPYQCPKNGTAVCATNR**
Found in **D6R9Z8** in **con_Xuniprot_HUMAN3**, D6R9Z8_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

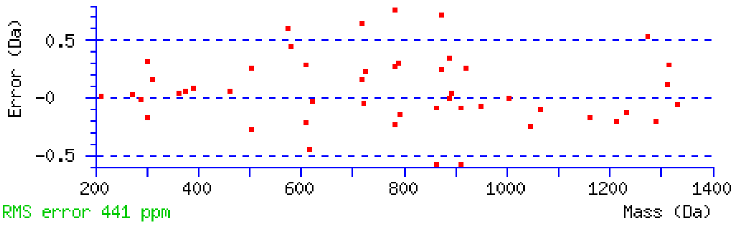
Match to Query 11741: 1949.915232 from(650.979020,3+) intensity(11413.1475) rtinseconds(405) scans(856) index(24338)
Title: 111019_Est_MI_YS_G_06Spectrum729_scans__856
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

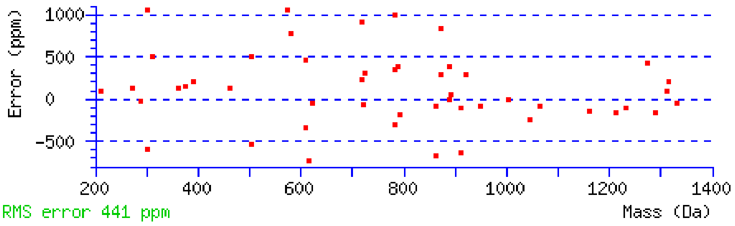
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1949.9088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.015
Matches : 49/164 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**17**
2	**211.1441**	106.0757					**P**	1837.8320	919.4196	1820.8054	910.9064	1819.8214	910.4143	**16**
3	**374.2074**	187.6074					**Y**	1740.7792	870.8932	1723.7527	862.3800	1722.7687	861.8880	**15**
4	**502.2660**	251.6366	485.2395	243.1234			**Q**	1577.7159	789.3616	1560.6893	780.8483	1559.7053	780.3563	**14**
5	662.2967	331.6520	645.2701	323.1387			**C**	1449.6573	725.3323	1432.6308	716.8190	1431.6467	716.3270	**13**
6	759.3494	380.1784	742.3229	371.6651			**P**	***1289.6267***	645.3170	1272.6001	636.8037	1271.6161	636.3117	**12**
7	**887.4444**	444.2258	870.4178	435.7126			**K**	1192.5739	596.7906	1175.5473	588.2773	1174.5633	587.7853	**11**
8	**1002.4713**	**501.7393**	985.4448	493.2260			**N**	***1064.4789***	532.7431	1047.4524	524.2298	1046.4684	523.7378	**10**
9	1059.4928	530.2500	1042.4662	521.7368			**G**	***949.4520***	475.2296	932.4254	466.7164	931.4414	466.2244	**9**
10	**1160.5405**	**580.7739**	1143.5139	572.2606	1142.5299	571.7686	**T**	***892.4305***	446.7189	875.4040	438.2056	874.4200	437.7136	**8**
11	**1231.5776**	**616.2924**	1214.5510	607.7792	1213.5670	607.2871	**A**	***791.3828***	396.1951	774.3563	387.6818	773.3723	387.1898	**7**
12	**1330.6460**	665.8266	1313.6195	657.3134	1312.6354	656.8214	**V**	***720.3457***	360.6765	703.3192	352.1632	702.3352	351.6712	**6**
13	1490.6767	745.8420	1473.6501	737.3287	1472.6661	736.8367	**C**	***621.2773***	311.1423	604.2508	302.6290	603.2668	302.1370	**5**
14	1561.7138	**781.3605**	1544.6872	772.8472	1543.7032	772.3552	**A**	***461.2467***	231.1270	444.2201	222.6137	443.2361	222.1217	**4**
15	1662.7614	831.8844	1645.7349	823.3711	1644.7509	822.8791	**T**	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	**3**
16	1776.8044	**888.9058**	1759.7778	880.3925	1758.7938	879.9005	**N**	***289.1619***	145.0846	272.1353	136.5713			**2**
17							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.8	1949.9088	0.0065	LPYQCPKNGTAVCATNR	Deamidated N8 71.77%
37.7	1949.9088	0.0065	LPYQCPKNGTAVCATNR	Deamidated Q4 27.86%
19.0	1949.9088	0.0065	LPYQCPKNGTAVCATNR	Deamidated N16 0.38%
10.7	1948.9048	1.0105	GSMVNLTSESHENTVSIK	
4.9	1949.9153	-0.0000	SVDESGSLAAYHLCSLNK	
3.1	1948.9086	1.0066	EDEQATIGAVRSASASSDR	
1.8	1948.9061	1.0091	DCGKAFTQNSDLTKHAR	
1.8	1948.9061	1.0091	DCGKAFTQNSDLTKHAR	
1.0	1948.9088	1.0064	MQSSPNGQFVAPSDIQLK	

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

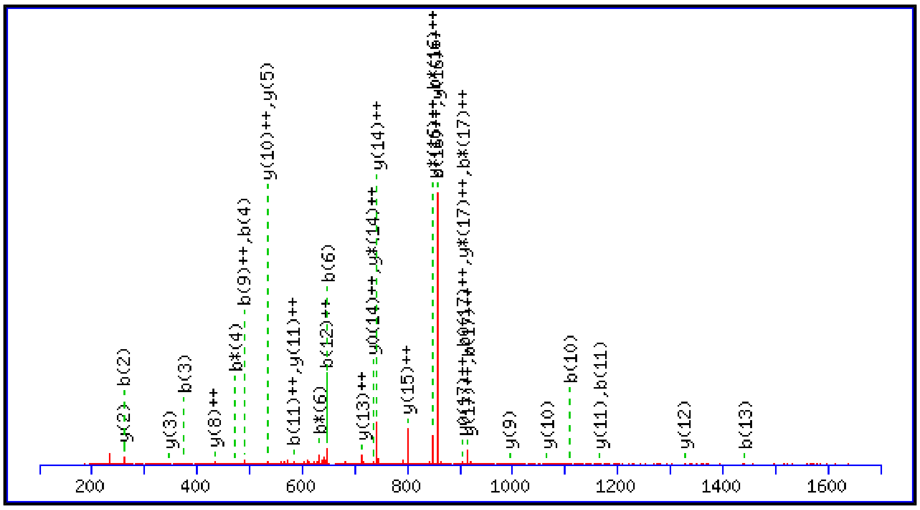
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLNNGTCTAEGKFSVSLK**
Found in **D6R9Z8** in **con_Xuniprot_HUMAN3**, D6R9Z8_HUMAN Complement factor I light chain OS=Homo sapiens GN=CFI PE=2 SV=1

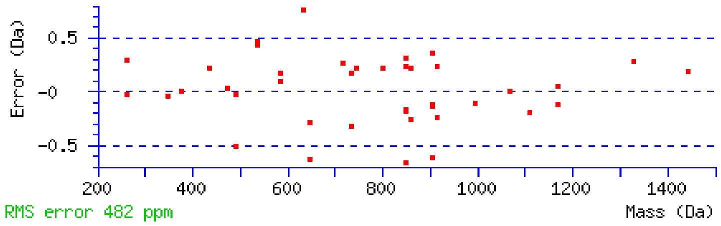
Match to Query 11874: 1972.960932 from(658.660920,3+) intensity(77547.6250) rtinseconds(1304) scans(2913) index(8834)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum2458_scans__2913
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

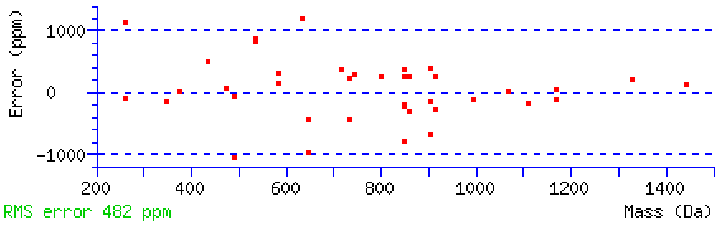
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1972.9564
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.053
Matches : 40/186 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	148.0757	74.5415					F							18
2	**261.1598**	131.0835					L	1826.8953	913.9513	1809.8687	905.4380	1808.8847	904.9460	17
3	**375.2027**	188.1050	358.1761	179.5917			N	1713.8112	857.4093	1696.7847	848.8960	1695.8007	848.4040	16
4	**490.2296**	245.6185	473.2031	237.1052			N	1599.7683	800.3878	1582.7418	791.8745	1581.7577	791.3825	15
5	547.2511	274.1292	530.2245	265.6159			G	1484.7414	742.8743	1467.7148	734.3610	1466.7308	733.8690	14
6	**648.2988**	324.6530	631.2722	316.1397	630.2882	315.6477	T	1427.7199	714.3636	1410.6933	705.8503	1409.7093	705.3583	13
7	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	C	***1326.6722***	663.8397	1309.6457	655.3265	1308.6616	654.8345	12
8	909.3771	455.1922	892.3505	446.6789	891.3665	446.1869	T	***1166.6416***	583.8244	1149.6150	575.3111	1148.6310	574.8191	11
9	980.4142	***490.7107***	963.3877	482.1975	962.4036	481.7055	A	***1065.5939***	533.3006	1048.5673	524.7873	1047.5833	524.2953	10
10	**1109.4568**	555.2320	1092.4303	546.7188	1091.4462	546.2268	E	***994.5568***	497.7820	977.5302	489.2687	976.5462	488.7767	9
11	**1166.4783**	***583.7428***	1149.4517	575.2295	1148.4677	574.7375	G	865.5142	433.2607	848.4876	424.7475	847.5036	424.2554	8
12	1294.5732	***647.7903***	1277.5467	639.2770	1276.5627	638.7850	K	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	7
13	**1441.6416**	721.3245	1424.6151	712.8112	1423.6311	712.3192	F	680.3978	340.7025	663.3712	332.1892	662.3872	331.6972	6
14	1528.6737	764.8405	1511.6471	756.3272	1510.6631	755.8352	S	***533.3293***	267.1683	516.3028	258.6550	515.3188	258.1630	5
15	1627.7421	814.3747	1610.7155	805.8614	1609.7315	805.3694	V	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
16	1714.7741	***857.8907***	1697.7476	849.3774	1696.7635	848.8854	S	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
17	1827.8582	***914.4327***	1810.8316	905.9195	1809.8476	905.4274	L	***260.1969***	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.5	1972.9564	0.0045	FLNNGTCTAEGKFSVSLK	Deamidated N4 50.06%
36.5	1972.9564	0.0045	FLNNGTCTAEGKFSVSLK	Deamidated N3 49.94%
14.6	1970.9594	2.0016	QLYKLMSDMGQASGWIK	
9.5	1971.9645	0.9964	EMTLNKMQKSYQGALTK	
9.0	1972.9564	0.0045	NEYGPVLHMPTSKENLK	
8.9	1972.9630	-0.0020	LLVQVLDVNDNDPEFDK	
8.9	1972.9630	-0.0020	LLVQVLDVNDNDPEFDK	
8.9	1972.9630	-0.0020	LLVQVLDVNDNDPEFDK	
8.6	1972.9602	0.0007	VDFTNHLEDTRRNINK	
8.3	1971.9512	1.0097	HRQAQEPWIGYDMVIK	

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

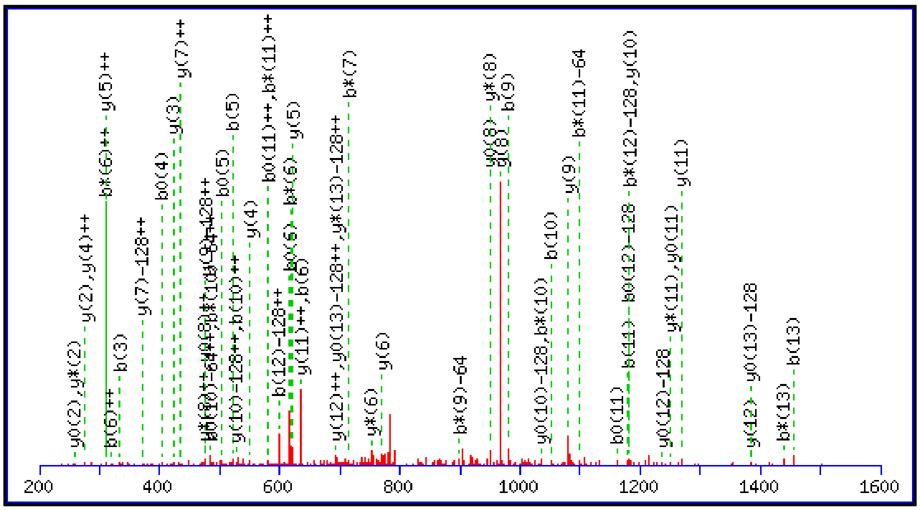
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFNSTLPTMAQMEK**
Found in **E7EPC6** in **con_Xuniprot_HUMAN3**, E7EPC6_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2

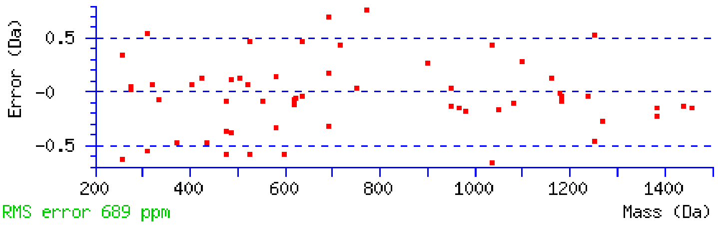
Match to Query 7661: 1600.714648 from(801.364600,2+) intensity(3210.8350) rtinseconds(712) scans(1398) index(11587)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum1175_scans__1398
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

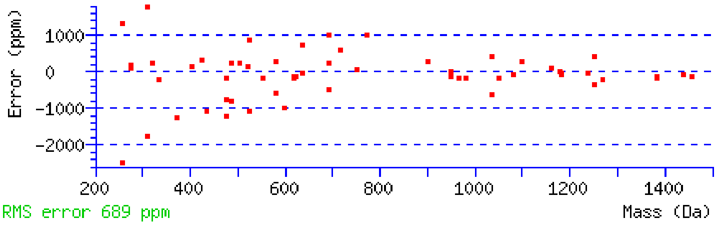
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1600.7113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 36 **Expect:** 0.028
Matches : 59/240 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**14**
2	219.1128	110.0600					**F**	1530.6815	765.8444	1513.6549	757.3311	1512.6709	756.8391	**13**
3	**334.1397**	167.5735	317.1132	159.0602			**N**	***1383.6130***	692.3102	1366.5865	683.7969	1365.6025	683.3049	**12**
4	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	**S**	***1268.5861***	634.7967	1251.5596	626.2834	1250.5755	625.7914	**11**
5	**522.2195**	261.6134	505.1929	253.1001	504.2089	252.6081	**T**	***1181.5541***	591.2807	1164.5275	582.7674	1163.5435	582.2754	**10**
6	**635.3035**	318.1554	618.2770	309.6421	617.2930	309.1501	**L**	***1080.5064***	540.7568	1063.4798	532.2436	1062.4958	531.7516	**9**
7	732.3563	366.6818	715.3297	358.1685	714.3457	357.6765	**P**	***967.4223***	484.2148	950.3958	475.7015	949.4118	475.2095	**8**
8	833.4040	417.2056	816.3774	408.6923	815.3934	408.2003	**T**	870.3696	435.6884	853.3430	427.1751	852.3590	426.6831	**7**
9	**980.4394**	490.7233	963.4128	482.2100	962.4288	481.7180	**M**	***769.3219***	385.1646	752.2953	376.6513	751.3113	376.1593	**6**
10	**1051.4765**	526.2419	1034.4499	517.7286	1033.4659	517.2366	**A**	***622.2865***	311.6469	605.2599	303.1336	604.2759	302.6416	**5**
11	**1179.5351**	590.2712	1162.5085	581.7579	1161.5245	581.2659	**Q**	***551.2494***	276.1283	534.2228	267.6151	533.2388	267.1230	**4**
12	1326.5705	663.7889	1309.5439	655.2756	1308.5599	654.7836	**M**	***423.1908***	212.0990	406.1642	203.5858	405.1802	203.0938	**3**
13	**1455.6130**	728.3102	1438.5865	719.7969	1437.6025	719.3049	**E**	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.7	1600.7113	0.0034	AFNSTLPTMAQMEK	Deamidated N3 99.77%
9.3	1600.7113	0.0034	AFNSTLPTMAQMEK	Deamidated Q11 0.23%
4.1	1600.7191	-0.0045	VNGPMPSFQPQEPR	
2.7	1600.7079	0.0067	IASFSQNCDIYPGK	
2.7	1600.7077	0.0069	QRQPREDGNEEDK	
1.5	1598.7107	2.0040	ACNPQPNGENAISAR	
0.4	1600.7225	-0.0079	MFQIDQATKQCSK	
0.2	1600.7104	0.0042	DVSQSSIYSQTEEK	
0.2	1600.7151	-0.0004	QTSRYSENACEKK	
0.2	1600.7151	-0.0004	QTSRYSENACEKK	

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

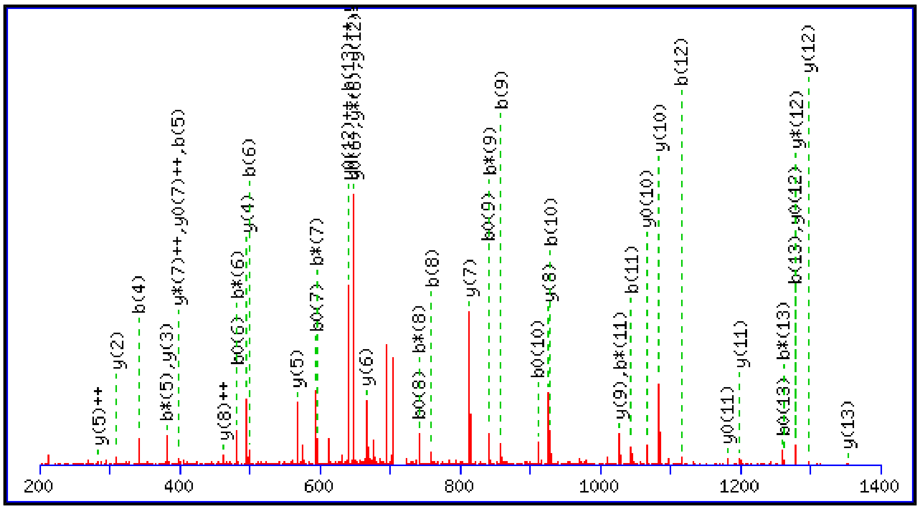
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGPNGTLFVADAYK**
Found in **H0Y512** in **con_Xuniprot_HUMAN3**, H0Y512_HUMAN Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens GN=APMAP PE=4 SV=1

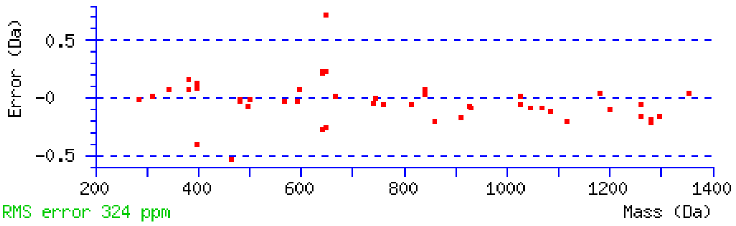
Match to Query 3046: 1423.703028 from(712.858790,2+) intensity(168675.3438) rtinseconds(1282) scans(3108) index(5161)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum2703_scans__3108
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

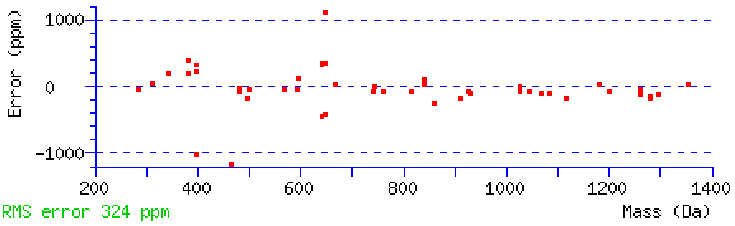
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1423.6983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 100 **Expect:** 2.2e-008
Matches : 48/134 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							14
2	129.0659	65.0366					G	***1353.6685***	677.3379	1336.6420	668.8246	1335.6579	668.3326	13
3	226.1186	113.5629					P	***1296.6470***	648.8272	1279.6205	640.3139	1278.6365	639.8219	12
4	**341.1456**	171.0764	324.1190	162.5631			N	***1199.5943***	600.3008	1182.5677	591.7875	1181.5837	591.2955	11
5	**398.1670**	199.5872	381.1405	191.0739			G	***1084.5673***	542.7873	1067.5408	534.2740	1066.5568	533.7820	10
6	**499.2147**	250.1110	482.1882	241.5977	481.2041	241.1057	T	***1027.5459***	514.2766	1010.5193	505.7633	1009.5353	505.2713	9
7	612.2988	306.6530	595.2722	298.1397	594.2882	297.6477	L	***926.4982***	463.7527	909.4716	455.2395	908.4876	454.7475	8
8	**759.3672**	380.1872	742.3406	371.6740	741.3566	371.1819	F	***813.4141***	407.2107	796.3876	398.6974	795.4036	398.2054	7
9	**858.4356**	429.7214	841.4090	421.2082	840.4250	420.7162	V	***666.3457***	333.6765	649.3192	325.1632	648.3352	324.6712	6
10	**929.4727**	465.2400	912.4462	456.7267	911.4621	456.2347	A	***567.2773***	284.1423	550.2508	275.6290	549.2667	275.1370	5
11	**1044.4997**	522.7535	1027.4731	514.2402	1026.4891	513.7482	D	***496.2402***	248.6237	479.2136	240.1105	478.2296	239.6185	4
12	**1115.5368**	558.2720	1098.5102	549.7587	1097.5262	549.2667	A	***381.2132***	191.1103	364.1867	182.5970			3
13	**1278.6001**	639.8037	1261.5735	631.2904	1260.5895	630.7984	Y	***310.1761***	155.5917	293.1496	147.0784			2
14							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
99.7	1423.6983	0.0047	AGPNGTLFVADAYK
7.9	1423.6977	0.0053	QVLGSSRQTLSTM
7.6	1423.7069	-0.0039	WPGSAGQGAGGRAPR
7.1	1423.6983	0.0047	KPDEIEGWEPPK
5.8	1423.7017	0.0013	QQIQIMDEIYK
4.8	1423.7055	-0.0025	DPGSPRGAEEPGKK
4.2	1423.6958	0.0072	AYLMFDFRAYK
3.0	1421.6998	2.0033	AETETEISTRASK
1.0	1423.7017	0.0013	MPISLLQEYGTR
0.3	1423.7096	-0.0065	HQSLLSTYNFSK

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

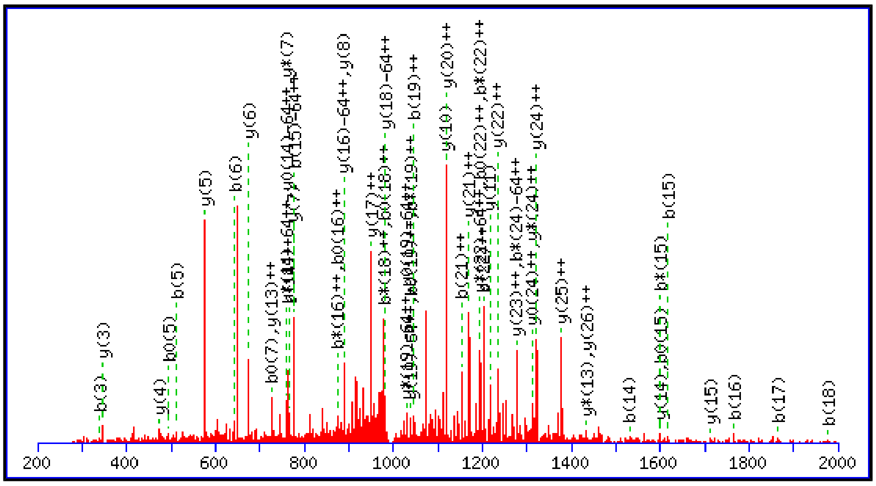
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLLSSETPIEGKNMSFVNDLTVTQDGR**
Found in **H0Y512** in **con_Xuniprot_HUMAN3**, H0Y512_HUMAN Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens GN=APMAP PE=4 SV=1

Match to Query 27083: 2982.491052 from(995.170960,3+) intensity(15082.6826) rtinseconds(1830) scans(4668) index(24632)
Title: 111019_Est_MI_YS_G_06Spectrum4054_scans__4668
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

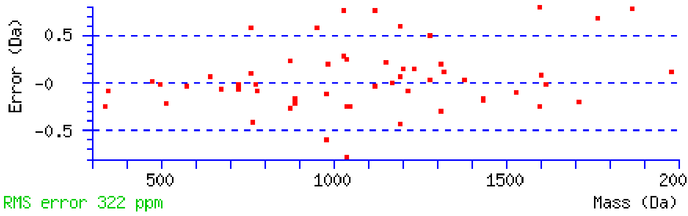
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

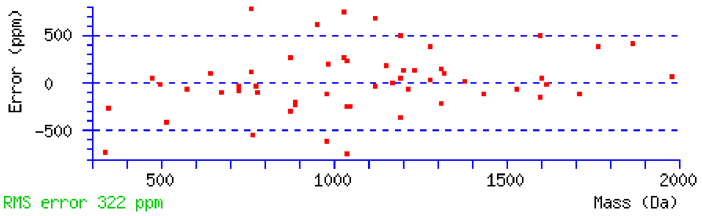


Monoisotopic mass of neutral peptide Mr(calc): 2980.4699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 53 **Expect:** 0.0012
Matches : 57/436 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							27
2	227.1754	114.0913					L	2868.3931	1434.7002	2851.3666	1426.1869	2850.3826	1425.6949	26
3	**340.2595**	170.6334					L	2755.3091	1378.1582	2738.2825	1369.6449	2737.2985	1369.1529	25
4	427.2915	214.1494			409.2809	205.1441	S	2642.2250	1321.6161	2625.1985	1313.1029	2624.2145	1312.6109	24
5	**514.3235**	257.6654			496.3130	248.6601	S	2555.1930	1278.1001	2538.1664	1269.5869	2537.1824	1269.0949	23
6	**643.3661**	322.1867			625.3556	313.1814	E	2468.1610	1234.5841	2451.1344	1226.0708	2450.1504	1225.5788	22
7	744.4138	372.7105			726.4032	363.7053	T	2339.1184	1170.0628	2322.0918	1161.5495	2321.1078	1161.0575	21
8	841.4666	421.2369			823.4560	412.2316	P	2238.0707	1119.5390	2221.0441	1111.0257	2220.0601	1110.5337	20
9	954.5506	477.7790			936.5401	468.7737	I	2141.0179	1071.0126	2123.9914	1062.4993	2123.0074	1062.0073	19
10	1083.5932	542.3002			1065.5827	533.2950	E	2027.9339	1014.4706	2010.9073	1005.9573	2009.9233	1005.4653	18
11	1140.6147	570.8110			1122.6041	561.8057	G	1898.8913	949.9493	1881.8647	941.4360	1880.8807	940.9440	17
12	1268.7096	634.8585	1251.6831	626.3452	1250.6991	625.8532	K	1841.8698	921.4385	1824.8433	912.9253	1823.8592	912.4333	16
13	1383.7366	692.3719	1366.7100	683.8587	1365.7260	683.3666	N	***1713.7748***	857.3911	1696.7483	848.8778	1695.7643	848.3858	15
14	**1530.7720**	**765.8896**	1513.7454	757.3764	1512.7614	756.8843	M	***1598.7479***	799.8776	1581.7213	791.3643	1580.7373	790.8723	14
15	**1617.8040**	809.4056	1600.7775	800.8924	1599.7935	800.4004	S	1451.7125	726.3599	1434.6859	717.8466	1433.7019	717.3546	13
16	**1764.8724**	882.9399	1747.8459	874.4266	1746.8619	873.9346	F	1364.6805	682.8439	1347.6539	674.3306	1346.6699	673.8386	12
17	**1863.9408**	932.4741	1846.9143	923.9608	1845.9303	923.4688	V	***1217.6121***	609.3097	1200.5855	600.7964	1199.6015	600.3044	11
18	**1977.9838**	989.4955	1960.9572	980.9822	1959.9732	980.4902	N	***1118.5436***	559.7755	1101.5171	551.2622	1100.5331	550.7702	10
19	2093.0107	**1047.0090**	2075.9842	1038.4957	2075.0001	1038.0037	D	1004.5007	502.7540	987.4742	494.2407	986.4902	493.7487	9
20	2206.0948	1103.5510	2189.0682	1095.0378	2188.0842	1094.5457	L	***889.4738***	445.2405	872.4472	436.7272	871.4632	436.2352	8
21	2307.1425	**1154.0749**	2290.1159	1145.5616	2289.1319	1145.0696	T	***776.3897***	388.6985	759.3632	380.1852	758.3791	379.6932	7

22	2406.2109	**1203.6091**	2389.1843	1195.0958	2388.2003	1194.6038	**V**	***675.3420***	338.1747	658.3155	329.6614	657.3315	329.1694	**6**
23	2507.2585	1254.1329	2490.2320	1245.6196	2489.2480	1245.1276	**T**	***576.2736***	288.6404	559.2471	280.1272	558.2631	279.6352	**5**
24	2635.3171	1318.1622	2618.2906	1309.6489	2617.3066	1309.1569	**Q**	***475.2259***	238.1166	458.1994	229.6033	457.2154	229.1113	**4**
25	2750.3441	1375.6757	2733.3175	1367.1624	2732.3335	1366.6704	**D**	***347.1674***	174.0873	330.1408	165.5740	329.1568	165.0820	**3**
26	2807.3655	1404.1864	2790.3390	1395.6731	2789.3550	1395.1811	**G**	232.1404	116.5738	215.1139	108.0606			**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.4	2980.4699	2.0211	LLLSSETPIEGKNMSFVNDLTVTQDGR	Deamidated N13 91.39%
42.1	2980.4699	2.0211	LLLSSETPIEGKNMSFVNDLTVTQDGR	Deamidated N18 6.77%
36.4	2980.4699	2.0211	LLLSSETPIEGKNMSFVNDLTVTQDGR	Deamidated Q24 1.84%
5.3	2982.4830	0.0080	KDMLFNQLIEMALLSLGYSHSSAAQAK	
3.6	2980.4925	1.9985	LMYNSSNPVLKNMWPEGKLSITEVTK	
3.1	2980.4925	1.9985	LMYNSSNPVLKNMWPEGKLSITEVTK	
3.1	2980.4925	1.9985	LMYNSSNPVLKNMWPEGKLSITEVTK	
1.8	2982.5008	-0.0097	IPHTPPLETMAIDSAAKYAVLSNEAAEK	
1.1	2981.4765	1.0145	LMYNSSNPVLKNMWPEGKLSITEVTK	
0.9	2982.4929	-0.0018	RQYKLMEPNEIVATSLQAETMIALSK	

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

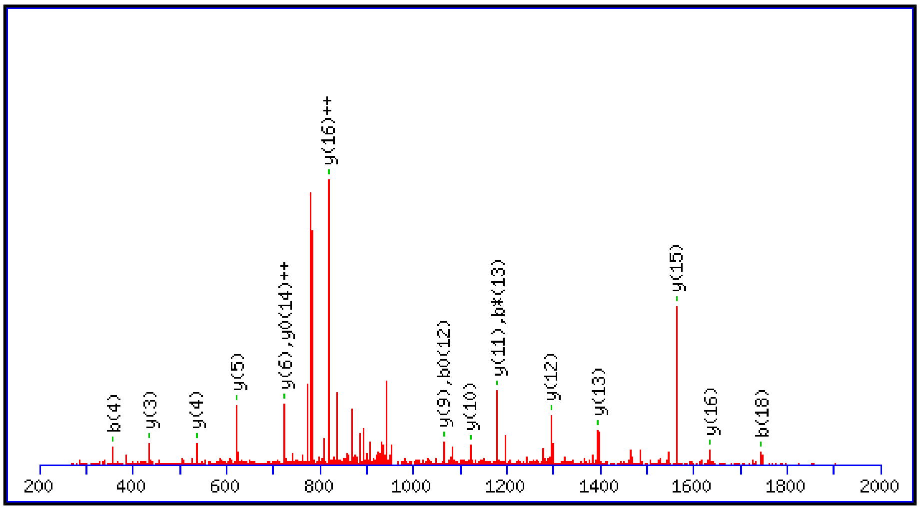
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **SVVAPATDGGLNLTSTFLR**
Found in **F8W7I2** in **con_Xuniprot_HUMAN3**, F8W7I2_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=2 SV=1

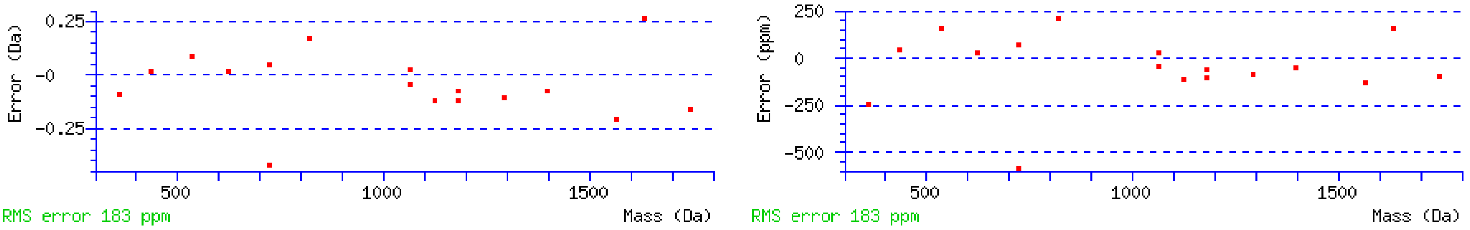
Match to Query 11612: 1919.004988 from(960.509770,2+) intensity(30677.5527) rtinseconds(2074) scans(5480) index(4561)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum4653_scans__5480
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1919.0000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 101 **Expect:** 1.7e-008
Matches : 17/188 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	88.0393	44.5233			70.0287	35.5180	S							19
2	187.1077	94.0575			169.0972	85.0522	V	1832.9753	916.9913	1815.9487	908.4780	1814.9647	907.9860	18
3	286.1761	143.5917			268.1656	134.5864	V	1733.9068	867.4571	1716.8803	858.9438	1715.8963	858.4518	17
4	**357.2132**	179.1103			339.2027	170.1050	A	***1634.8384***	817.9229	1617.8119	809.4096	1616.8279	808.9176	16
5	454.2660	227.6366			436.2554	218.6314	P	***1563.8013***	782.4043	1546.7748	773.8910	1545.7908	773.3990	15
6	525.3031	263.1552			507.2926	254.1499	A	1466.7486	733.8779	1449.7220	725.3646	1448.7380	724.8726	14
7	626.3508	313.6790			608.3402	304.6738	T	***1395.7114***	698.3594	1378.6849	689.8461	1377.7009	689.3541	13
8	741.3777	371.1925			723.3672	362.1872	D	***1294.6638***	647.8355	1277.6372	639.3222	1276.6532	638.8302	12
9	798.3992	399.7032			780.3886	390.6980	G	***1179.6368***	590.3220	1162.6103	581.8088	1161.6263	581.3168	11
10	855.4207	428.2140			837.4101	419.2087	G	***1122.6154***	561.8113	1105.5888	553.2980	1104.6048	552.8060	10
11	968.5047	484.7560			950.4942	475.7507	L	***1065.5939***	533.3006	1048.5673	524.7873	1047.5833	524.2953	9
12	1083.5317	542.2695	1066.5051	533.7562	1065.5211	533.2642	N	952.5098	476.7585	935.4833	468.2453	934.4993	467.7533	8
13	1196.6157	598.8115	1179.5892	590.2982	1178.6052	589.8062	L	837.4829	419.2451	820.4563	410.7318	819.4723	410.2398	7
14	1297.6634	649.3354	1280.6369	640.8221	1279.6529	640.3301	T	***724.3988***	362.7030	707.3723	354.1898	706.3883	353.6978	6
15	1384.6955	692.8514	1367.6689	684.3381	1366.6849	683.8461	S	***623.3511***	312.1792	606.3246	303.6659	605.3406	303.1739	5
16	1485.7431	743.3752	1468.7166	734.8619	1467.7326	734.3699	T	***536.3191***	268.6632	519.2926	260.1499	518.3085	259.6579	4
17	1632.8115	816.9094	1615.7850	808.3961	1614.8010	807.9041	F	***435.2714***	218.1394	418.2449	209.6261			3
18	**1745.8956**	873.4514	1728.8691	864.9382	1727.8850	864.4462	L	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.8	1919.0000	0.0050	SVVAPATDGGLNLTSTFLR
9.2	1918.0094	0.9956	RQANQIGHGEPMIKPLK
5.3	1919.0013	0.0037	ERAIFKVHSDFTAAATR
4.9	1918.0094	0.9956	RQANQIGHGEPMIKPLK
1.8	1918.0094	0.9956	RQANQIGHGEPMIKPLK
1.3	1916.9890	2.0160	LENIQNCLQKLHAAHK
1.3	1916.9890	2.0160	LENIQNCLQKLHAAHK
1.3	1916.9890	2.0160	LENIQNCLQKLHAAHK
0.8	1918.9968	0.0082	KGLLLTNQNLRMTAAQM
0.4	1919.0074	-0.0024	ERFQIIPLVMTDALQK

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

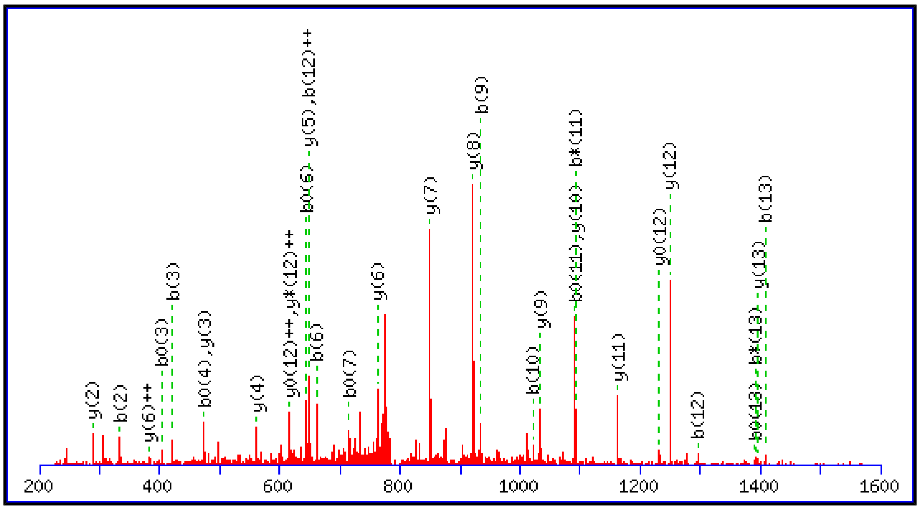
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WFSAGLASNSSWLR**
Found in **F8W7I2** in **con_Xuniprot_HUMAN3**, F8W7I2_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=2 SV=1

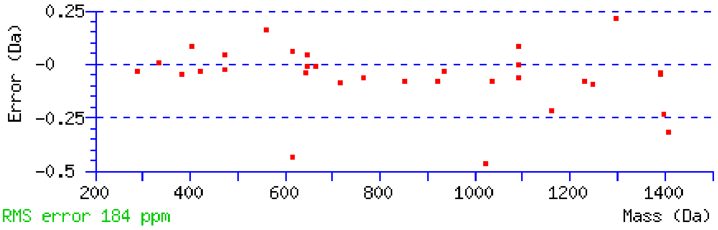
Match to Query 7575: 1581.764228 from(791.889390,2+) intensity(24533.7910) rtinseconds(2175) scans(5368) index(26210)
Title: 111019_Est_MI_YS_G_08Spectrum4649_scans__5368
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

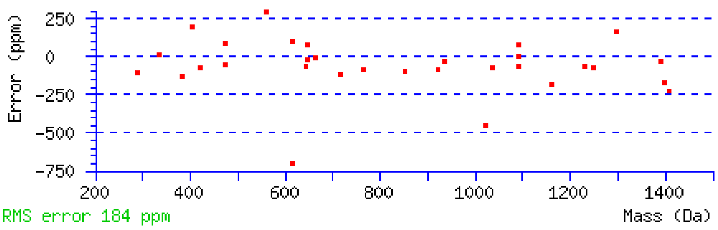
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1581.7576
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 77 **Expect:** 4.2e-006
Matches : 32/130 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	187.0866	94.0469					W							14
2	**334.1550**	167.5811					F	***1396.6856***	698.8464	1379.6590	690.3331	1378.6750	689.8411	13
3	**421.1870**	211.0972			403.1765	202.0919	S	***1249.6171***	625.3122	1232.5906	616.7989	1231.6066	616.3069	12
4	492.2241	246.6157			474.2136	237.6104	A	***1162.5851***	581.7962	1145.5586	573.2829	1144.5745	572.7909	11
5	549.2456	275.1264			531.2350	266.1212	G	***1091.5480***	546.2776	1074.5214	537.7644	1073.5374	537.2724	10
6	**662.3297**	331.6685			644.3191	322.6632	L	***1034.5265***	517.7669	1017.5000	509.2536	1016.5160	508.7616	9
7	733.3668	367.1870			715.3562	358.1817	A	***921.4425***	461.2249	904.4159	452.7116	903.4319	452.2196	8
8	820.3988	410.7030			802.3882	401.6978	S	***850.4054***	425.7063	833.3788	417.1930	832.3948	416.7010	7
9	**935.4258**	468.2165	918.3992	459.7032	917.4152	459.2112	N	***763.3733***	382.1903	746.3468	373.6770	745.3628	373.1850	6
10	**1022.4578**	511.7325	1005.4312	503.2193	1004.4472	502.7272	S	***648.3464***	324.6768	631.3198	316.1636	630.3358	315.6715	5
11	1109.4898	555.2485	1092.4633	546.7353	1091.4792	546.2433	S	***561.3144***	281.1608	544.2878	272.6475	543.3038	272.1555	4
12	**1295.5691**	648.2882	1278.5426	639.7749	1277.5586	639.2829	W	***474.2823***	237.6448	457.2558	229.1315			3
13	**1408.6532**	704.8302	1391.6266	696.3170	1390.6426	695.8250	L	***288.2030***	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
76.8	1581.7576	0.0067	WFSAGLASNSSWLR
8.5	1580.7617	1.0026	DAFSAQMVKNTVNR
7.7	1580.7617	1.0026	DAFSAQMVKNTVNR
5.4	1580.7617	1.0026	DAFSAQMVKNTVNR
3.2	1581.7708	-0.0066	YGLVTNEIAMVQAR
3.0	1581.7610	0.0033	MSVGLFASQRQWGV
2.8	1580.7682	0.9960	VSTSVSAQPSYAVER
2.6	1580.7623	1.0019	FWSQISQGHLSYK
2.4	1579.7624	2.0019	AAMDSRASDAINKSK
2.0	1581.7569	0.0073	MSAKNNEERFVNK

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

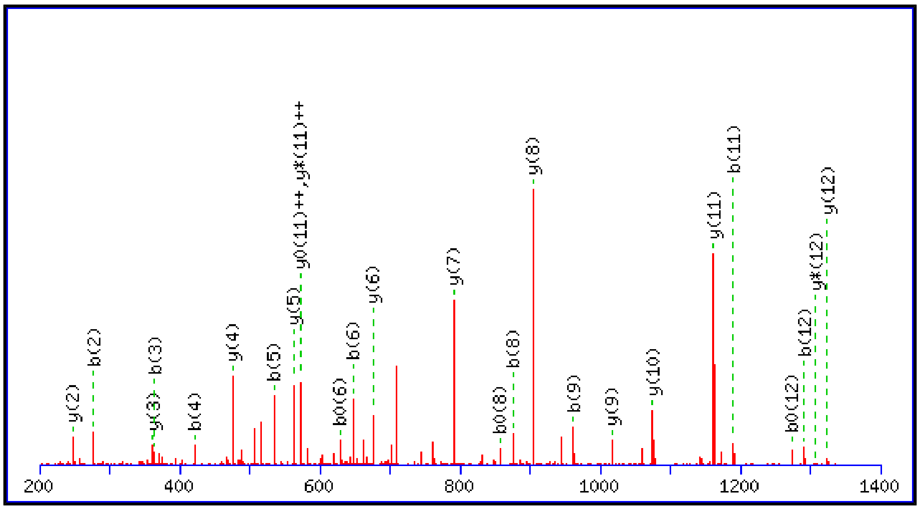
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYSGILNLSDITK**
Found in **E9PBC5** in **con_Xuniprot_HUMAN3**, E9PBC5_HUMAN Plasma kallikrein heavy chain OS=Homo sapiens GN=KLKB1 PE=2 SV=1

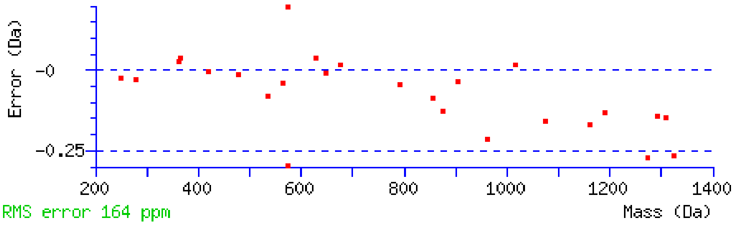
Match to Query 4015: 1436.777328 from(719.395940,2+) intensity(1334619.6250) rtinseconds(1982) scans(5028) index(5445)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum4417_scans__5028
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

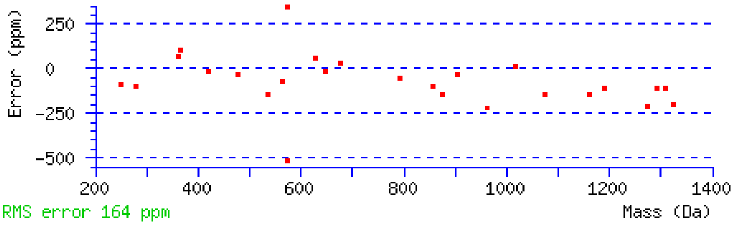
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1436.7762
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 101 **Expect:** 1.3e-008
Matches : 26/126 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	114.0913	57.5493					**I**							**13**
2	**277.1547**	139.0810					**Y**	***1324.6995***	662.8534	1307.6729	654.3401	1306.6889	653.8481	**12**
3	**364.1867**	182.5970			346.1761	173.5917	**S**	***1161.6361***	581.3217	1144.6096	572.8084	1143.6256	572.3164	**11**
4	**421.2082**	211.1077			403.1976	202.1024	**G**	***1074.6041***	537.8057	1057.5776	529.2924	1056.5936	528.8004	**10**
5	**534.2922**	267.6498			516.2817	258.6445	**I**	***1017.5827***	509.2950	1000.5561	500.7817	999.5721	500.2897	**9**
6	**647.3763**	324.1918			629.3657	315.1865	**L**	***904.4986***	452.7529	887.4720	444.2397	886.4880	443.7476	**8**
7	762.4032	381.7053	745.3767	373.1920	744.3927	372.7000	**N**	***791.4145***	396.2109	774.3880	387.6976	773.4040	387.2056	**7**
8	**875.4873**	438.2473	858.4607	429.7340	857.4767	429.2420	**L**	***676.3876***	338.6974	659.3610	330.1842	658.3770	329.6921	**6**
9	**962.5193**	481.7633	945.4928	473.2500	944.5088	472.7580	**S**	***563.3035***	282.1554	546.2770	273.6421	545.2930	273.1501	**5**
10	1077.5463	539.2768	1060.5197	530.7635	1059.5357	530.2715	**D**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
11	**1190.6303**	595.8188	1173.6038	587.3055	1172.6198	586.8135	**I**	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
12	**1291.6780**	646.3426	1274.6515	637.8294	1273.6674	637.3374	**T**	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
13							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.6	1436.7762	0.0011	IYSGILNLSDITK
18.2	1436.7762	0.0011	LYVIQTLEETTK
16.1	1434.7718	2.0055	QKYLAQLLNSVR
15.9	1434.7718	2.0055	KEYLEKIQGAQK
12.8	1434.7718	2.0055	KEEFQELLGKSK
9.2	1434.7718	2.0055	KQEKQFDGIITK
8.5	1434.7718	2.0055	KEYLEKIQGAQK
7.8	1434.7718	2.0055	KQEKQFDGIITK
6.8	1434.7653	2.0121	ENRLMFKILDR
3.4	1436.7776	-0.0003	LSIGEFDVFVRR

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

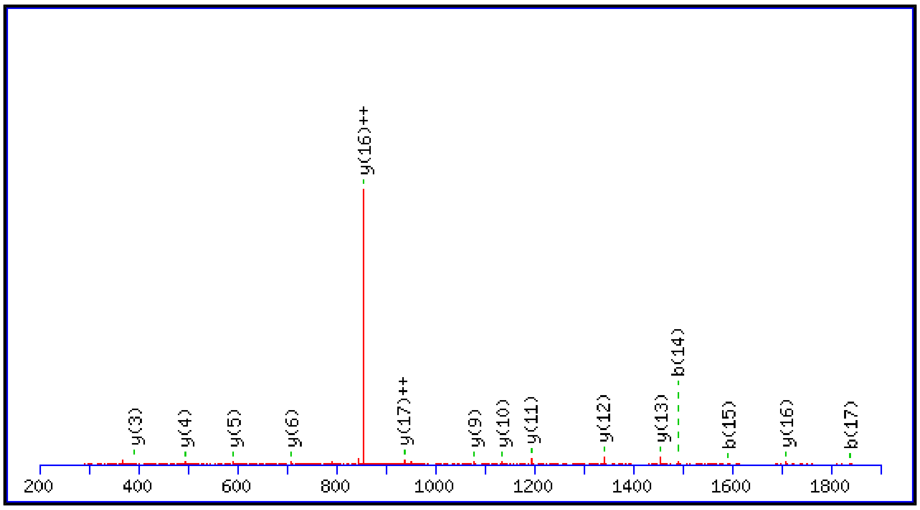
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYPGVDFGGEELNVTFVK**
Found in **E9PBC5** in **con_Xuniprot_HUMAN3**, E9PBC5_HUMAN Plasma kallikrein heavy chain OS=Homo sapiens GN=KLKB1 PE=2 SV=1

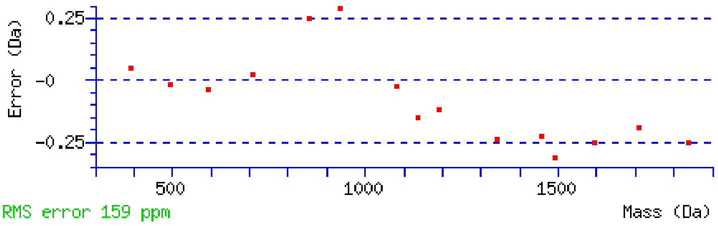
Match to Query 11945: 1983.987048 from(993.000800,2+) intensity(1175188.1250) rtinseconds(2246) scans(5526) index(11992)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum4787_scans__5526
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

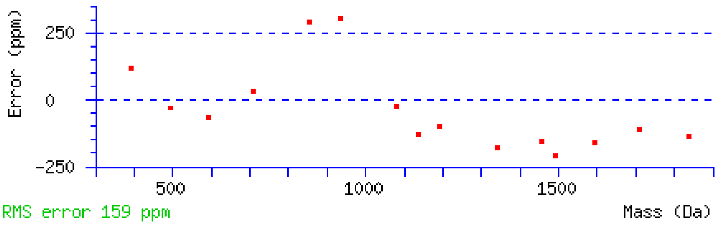
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1983.9830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13    : Deamidated (NQ)
Ions Score: 98  Expect: 3.6e-008
Matches : 15/164 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	114.0913	57.5493					I							18
2	277.1547	139.0810					Y	1871.9062	936.4567	1854.8796	927.9435	1853.8956	927.4514	17
3	374.2074	187.6074					P	***1708.8428***	854.9251	1691.8163	846.4118	1690.8323	845.9198	16
4	431.2289	216.1181					G	1611.7901	806.3987	1594.7635	797.8854	1593.7795	797.3934	15
5	530.2973	265.6523					V	1554.7686	777.8879	1537.7421	769.3747	1536.7581	768.8827	14
6	645.3243	323.1658			627.3137	314.1605	D	***1455.7002***	728.3537	1438.6737	719.8405	1437.6896	719.3485	13
7	792.3927	396.7000			774.3821	387.6947	F	***1340.6733***	670.8403	1323.6467	662.3270	1322.6627	661.8350	12
8	849.4141	425.2107			831.4036	416.2054	G	***1193.6048***	597.3061	1176.5783	588.7928	1175.5943	588.3008	11
9	906.4356	453.7214			888.4250	444.7162	G	***1136.5834***	568.7953	1119.5568	560.2821	1118.5728	559.7900	10
10	1035.4782	518.2427			1017.4676	509.2375	E	***1079.5619***	540.2846	1062.5354	531.7713	1061.5514	531.2793	9
11	1164.5208	582.7640			1146.5102	573.7587	E	950.5193	475.7633	933.4928	467.2500	932.5088	466.7580	8
12	1277.6048	639.3061			1259.5943	630.3008	L	821.4767	411.2420	804.4502	402.7287	803.4662	402.2367	7
13	1392.6318	696.8195	1375.6052	688.3063	1374.6212	687.8143	N	***708.3927***	354.7000	691.3661	346.1867	690.3821	345.6947	6
14	**1491.7002**	746.3537	1474.6737	737.8405	1473.6896	737.3485	V	***593.3657***	297.1865	576.3392	288.6732	575.3552	288.1812	5
15	**1592.7479**	796.8776	1575.7213	788.3643	1574.7373	787.8723	T	***494.2973***	247.6523	477.2708	239.1390	476.2867	238.6470	4
16	1739.8163	870.4118	1722.7897	861.8985	1721.8057	861.4065	F	***393.2496***	197.1285	376.2231	188.6152			3
17	**1838.8847**	919.9460	1821.8582	911.4327	1820.8741	910.9407	V	246.1812	123.5942	229.1547	115.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
98.2	1983.9830	0.0041	IYPGVDFGGEELNVTFVK
13.2	1982.9796	1.0074	SDDITSTKQQSFNLRLK
12.2	1982.9796	1.0074	GKGQLPGSEKQLEEQPQK
12.2	1982.9796	1.0074	GKGQLPGSEKQLEEQPQK
11.5	1982.9796	1.0074	GKGQLPGSEKQLEEQPQK
8.9	1983.9897	-0.0026	FLLTKMEQQQLETVMK
8.9	1983.9897	-0.0026	FLLTKMEQQQLETVMK
8.9	1983.9897	-0.0026	FLLTKMEQQQLETVMK
8.9	1982.9839	1.0032	MSKSSSLMKVEMQLQQK
8.8	1982.9745	1.0126	QHQVLHSARSFAKGCEK

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

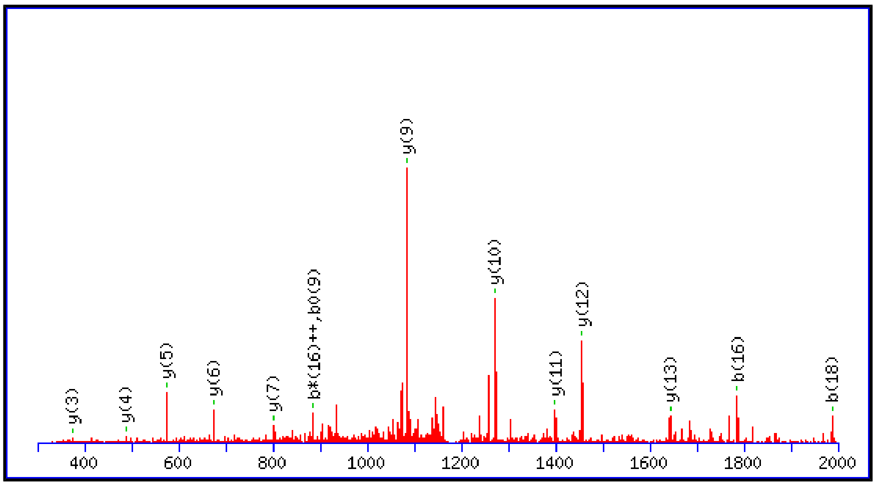
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVGGTNSSWGEWPWQVSLQVK**
Found in **E9PBC5** in **con_Xuniprot_HUMAN3**, E9PBC5_HUMAN Plasma kallikrein heavy chain OS=Homo sapiens GN=KLKB1 PE=2 SV=1

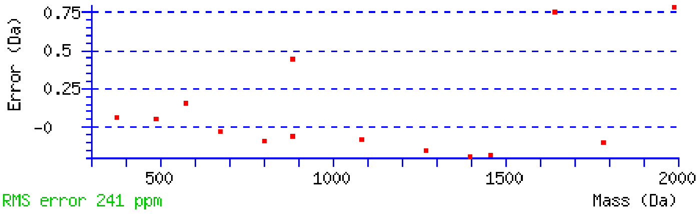
Match to Query 17886: 2358.172568 from(1180.093560,2+) intensity(20610.5195) rtinseconds(2456) scans(6377) index(4011)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum5211_scans__6377
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

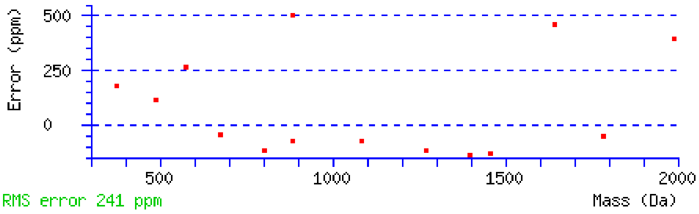
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2358.1645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 75 **Expect:** 8.1e-006
Matches : 14/214 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	114.0913	57.5493					I							21
2	213.1598	107.0835					V	2246.0877	1123.5475	2229.0611	1115.0342	2228.0771	1114.5422	20
3	270.1812	135.5942					G	2147.0192	1074.0133	2129.9927	1065.5000	2129.0087	1065.0080	19
4	327.2027	164.1050					G	2089.9978	1045.5025	2072.9712	1036.9893	2071.9872	1036.4972	18
5	428.2504	214.6288			410.2398	205.6235	T	2032.9763	1016.9918	2015.9498	1008.4785	2014.9658	1007.9865	17
6	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	N	1931.9286	966.4680	1914.9021	957.9547	1913.9181	957.4627	16
7	630.3093	315.6583	613.2828	307.1450	612.2988	306.6530	S	1816.9017	908.9545	1799.8751	900.4412	1798.8911	899.9492	15
8	717.3414	359.1743	700.3148	350.6610	699.3308	350.1690	S	1729.8697	865.4385	1712.8431	856.9252	1711.8591	856.4332	14
9	903.4207	452.2140	886.3941	443.7007	885.4101	443.2087	W	***1642.8376***	821.9225	1625.8111	813.4092	1624.8271	812.9172	13
10	960.4421	480.7247	943.4156	472.2114	942.4316	471.7194	G	***1456.7583***	728.8828	1439.7318	720.3695	1438.7478	719.8775	12
11	1089.4847	545.2460	1072.4582	536.7327	1071.4742	536.2407	E	***1399.7369***	700.3721	1382.7103	691.8588	1381.7263	691.3668	11
12	1275.5640	638.2857	1258.5375	629.7724	1257.5535	629.2804	W	***1270.6943***	635.8508	1253.6677	627.3375	1252.6837	626.8455	10
13	1372.6168	686.8120	1355.5903	678.2988	1354.6062	677.8068	P	***1084.6150***	542.8111	1067.5884	534.2978	1066.6044	533.8058	9
14	1558.6961	779.8517	1541.6696	771.3384	1540.6856	770.8464	W	987.5622	494.2847	970.5356	485.7715	969.5516	485.2795	8
15	1686.7547	843.8810	1669.7281	835.3677	1668.7441	834.8757	Q	***801.4829***	401.2451	784.4563	392.7318	783.4723	392.2398	7
16	**1785.8231**	893.4152	1768.7966	884.9019	1767.8125	884.4099	V	***673.4243***	337.2158	656.3978	328.7025	655.4137	328.2105	6
17	1872.8551	936.9312	1855.8286	928.4179	1854.8446	927.9259	S	***574.3559***	287.6816	557.3293	279.1683	556.3453	278.6763	5
18	**1985.9392**	993.4732	1968.9127	984.9600	1967.9286	984.4680	L	***487.3239***	244.1656	470.2973	235.6523			4
19	2113.9978	1057.5025	2096.9712	1048.9893	2095.9872	1048.4972	Q	***374.2398***	187.6235	357.2132	179.1103			3
20	2213.0662	1107.0367	2196.0396	1098.5235	2195.0556	1098.0315	V	246.1812	123.5942	229.1547	115.0810			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.2	2358.1645	0.0081	IVGGTNSSWGEWPWQVSLQVK	Deamidated N6 100.00%
63.4	2357.1804	0.9921	IVGGTNSSWGEWPWQVSLQVK	
26.7	2358.1645	0.0081	IVGGTNSSWGEWPWQVSLQVK	Deamidated Q15 0.00%
16.9	2357.1658	1.0067	GGEEGGSVQPRAQYARLCPGLR	
4.6	2358.1676	0.0050	QAGSAAPRPPRAQQPQQPSQEK	
4.0	2358.1736	-0.0010	LSEMDNPVLQAAEKLELERR	
3.4	2358.1676	0.0050	QAGSAAPRPPRAQQPQQPSQEK	
3.2	2357.1726	1.0000	LMEEASFDGTFLWKITNVTR	
2.8	2358.1736	-0.0010	GAIEQKQKEMQLELDLAEQR	
1.5	2358.1645	0.0081	IVGGTNSSWGEWPWQVSLQVK	Deamidated Q19 0.00%

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

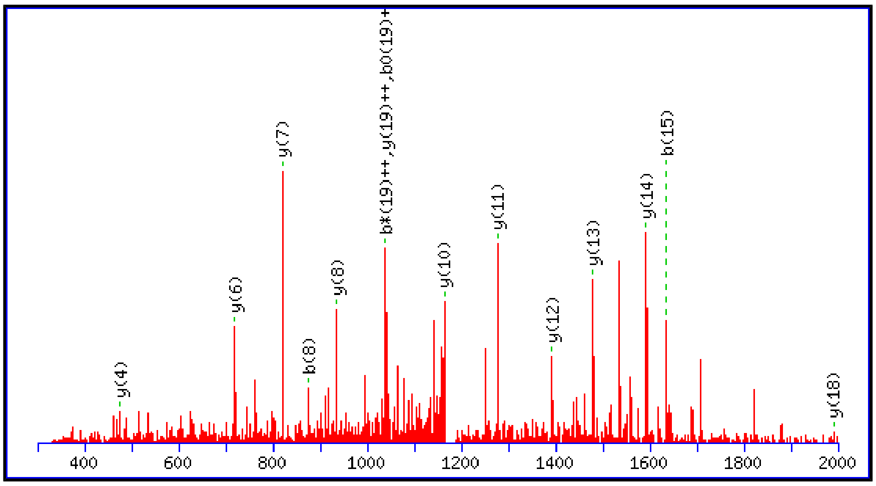
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYSGILNLSDITKDTPFSQIK**
Found in **E9PBC5** in **con_Xuniprot_HUMAN3**, E9PBC5_HUMAN Plasma kallikrein heavy chain OS=Homo sapiens GN=KLKB1 PE=2 SV=1

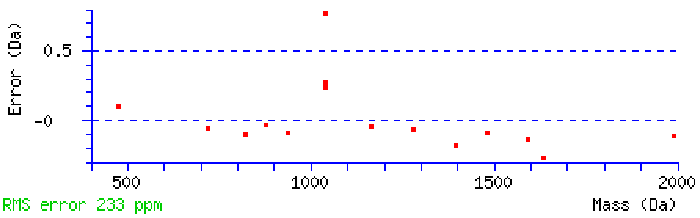
Match to Query 17820: 2353.247468 from(1177.631010,2+) intensity(65463.6328) rtinseconds(2422) scans(6334) index(1557)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum5549_scans__6334
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

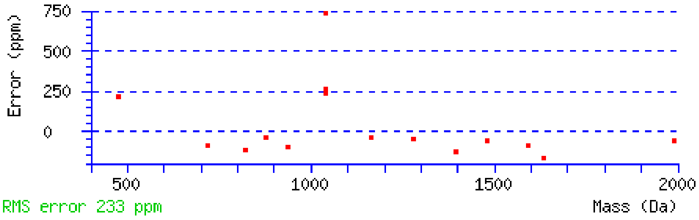
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2353.2417
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 75 **Expect:** 5.6e-006
Matches : 15/218 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	114.0913	57.5493					I							21
2	277.1547	139.0810					Y	2241.1649	1121.0861	2224.1384	1112.5728	2223.1543	1112.0808	20
3	364.1867	182.5970			346.1761	173.5917	S	2078.1016	1039.5544	2061.0750	1031.0412	2060.0910	1030.5491	19
4	421.2082	211.1077			403.1976	202.1024	G	***1991.0696***	996.0384	1974.0430	987.5251	1973.0590	987.0331	18
5	534.2922	267.6498			516.2817	258.6445	I	1934.0481	967.5277	1917.0215	959.0144	1916.0375	958.5224	17
6	647.3763	324.1918			629.3657	315.1865	L	1820.9640	910.9856	1803.9375	902.4724	1802.9535	901.9804	16
7	762.4032	381.7053	745.3767	373.1920	744.3927	372.7000	N	1707.8800	854.4436	1690.8534	845.9303	1689.8694	845.4383	15
8	**875.4873**	438.2473	858.4607	429.7340	857.4767	429.2420	L	***1592.8530***	796.9301	1575.8265	788.4169	1574.8425	787.9249	14
9	962.5193	481.7633	945.4928	473.2500	944.5088	472.7580	S	***1479.7690***	740.3881	1462.7424	731.8748	1461.7584	731.3828	13
10	1077.5463	539.2768	1060.5197	530.7635	1059.5357	530.2715	D	***1392.7369***	696.8721	1375.7104	688.3588	1374.7264	687.8668	12
11	1190.6303	595.8188	1173.6038	587.3055	1172.6198	586.8135	I	***1277.7100***	639.3586	1260.6834	630.8454	1259.6994	630.3533	11
12	1291.6780	646.3426	1274.6515	637.8294	1273.6674	637.3374	T	***1164.6259***	582.8166	1147.5994	574.3033	1146.6154	573.8113	10
13	1419.7730	710.3901	1402.7464	701.8768	1401.7624	701.3848	K	1063.5782	532.2928	1046.5517	523.7795	1045.5677	523.2875	9
14	1534.7999	767.9036	1517.7734	759.3903	1516.7894	758.8983	D	***935.4833***	468.2453	918.4567	459.7320	917.4727	459.2400	8
15	**1635.8476**	818.4274	1618.8210	809.9142	1617.8370	809.4222	T	***820.4563***	410.7318	803.4298	402.2185	802.4458	401.7265	7
16	1732.9004	866.9538	1715.8738	858.4405	1714.8898	857.9485	P	***719.4087***	360.2080	702.3821	351.6947	701.3981	351.2027	6
17	1879.9688	940.4880	1862.9422	931.9748	1861.9582	931.4827	F	622.3559	311.6816	605.3293	303.1683	604.3453	302.6763	5
18	1967.0008	984.0040	1949.9743	975.4908	1948.9902	974.9988	S	***475.2875***	238.1474	458.2609	229.6341	457.2769	229.1421	4
19	2095.0594	1048.0333	2078.0328	1039.5201	2077.0488	1039.0280	Q	388.2554	194.6314	371.2289	186.1181			3
20	2208.1434	1104.5754	2191.1169	1096.0621	2190.1329	1095.5701	I	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
74.7	2353.2417	0.0058	IYSGILNLSDITKDTPFSQIK	Deamidated N7 99.94%
42.5	2353.2417	0.0058	IYSGILNLSDITKDTPFSQIK	Deamidated Q19 0.06%
4.3	2351.2519	1.9956	ILMTELRTLATGYEVDGGKLR	
0.8	2353.2529	-0.0054	QKPQTKLHITFLSTDPIEEK	

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

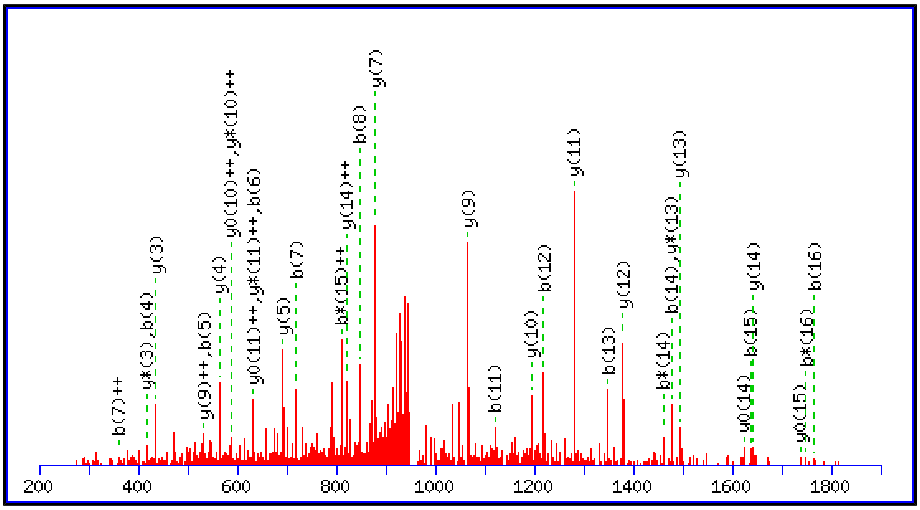
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNFNVSKVSSVEECQK**
Found in **C9IYG8** in **con_Xuniprot_HUMAN3**, C9IYG8_HUMAN Plasma kallikrein heavy chain (Fragment) OS=Homo sapiens GN=KLKB1 PE=2 SV=1

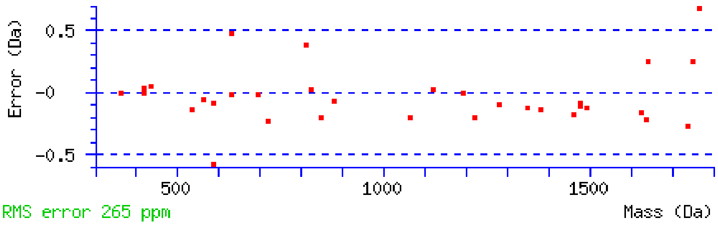
Match to Query 11521: 1910.913668 from(956.464110,2+) intensity(7864.0273) rtinseconds(888) scans(2096) index(24419)
Title: 111019_Est_MI_YS_G_06Spectrum1809_scans__2096
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

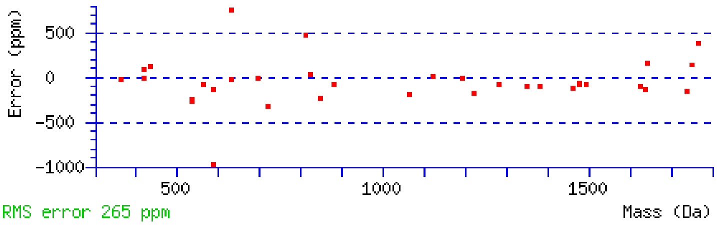
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1910.9044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 72 **Expect:** 1.3e-005
Matches : 35/170 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	58.0287	29.5180					G							17
2	157.0972	79.0522					V	1854.8902	927.9487	1837.8637	919.4355	1836.8796	918.9435	16
3	271.1401	136.0737	254.1135	127.5604			N	1755.8218	878.4145	1738.7952	869.9013	1737.8112	869.4093	15
4	***418.2085***	209.6079	401.1819	201.0946			F	***1641.7789***	821.3931	1624.7523	812.8798	1623.7683	812.3878	14
5	***533.2354***	267.1214	516.2089	258.6081			N	***1494.7104***	747.8589	1477.6839	739.3456	1476.6999	738.8536	13
6	***632.3039***	316.6556	615.2773	308.1423			V	***1379.6835***	690.3454	1362.6570	681.8321	1361.6729	681.3401	12
7	***719.3359***	360.1716	702.3093	351.6583	701.3253	351.1663	S	***1280.6151***	640.8112	1263.5885	632.2979	1262.6045	631.8059	11
8	***847.4308***	424.2191	830.4043	415.7058	829.4203	415.2138	K	***1193.5831***	597.2952	1176.5565	588.7819	1175.5725	588.2899	10
9	946.4993	473.7533	929.4727	465.2400	928.4887	464.7480	V	***1065.4881***	533.2477	1048.4616	524.7344	1047.4775	524.2424	9
10	1033.5313	517.2693	1016.5047	508.7560	1015.5207	508.2640	S	966.4197	483.7135	949.3931	475.2002	948.4091	474.7082	8
11	***1120.5633***	560.7853	1103.5368	552.2720	1102.5527	551.7800	S	***879.3877***	440.1975	862.3611	431.6842	861.3771	431.1922	7
12	***1219.6317***	610.3195	1202.6052	601.8062	1201.6212	601.3142	V	792.3556	396.6815	775.3291	388.1682	774.3451	387.6762	6
13	***1348.6743***	674.8408	1331.6478	666.3275	1330.6638	665.8355	E	***693.2872***	347.1472	676.2607	338.6340	675.2767	338.1420	5
14	***1477.7169***	739.3621	1460.6904	730.8488	1459.7063	730.3568	E	***564.2446***	282.6260	547.2181	274.1127	546.2341	273.6207	4
15	***1637.7476***	819.3774	1620.7210	810.8641	1619.7370	810.3721	C	***435.2020***	218.1047	418.1755	209.5914			3
16	***1765.8061***	883.4067	1748.7796	874.8934	1747.7956	874.4014	Q	275.1714	138.0893	258.1448	129.5761			2
17							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.5	1910.9044	0.0093	GVNFNVSKVSSVEECQK	Deamidated N5 94.40%
60.2	1910.9044	0.0093	GVNFNVSKVSSVEECQK	Deamidated N3 5.60%
31.1	1910.9044	0.0093	GVNFNVSKVSSVEECQK	Deamidated Q16 0.01%
8.8	1910.9084	0.0053	SENSSLLDSIFWMAAPK	
7.4	1910.9203	-0.0067	LSAGQSRFCGERQLMR	
7.3	1909.9091	1.0046	MDSTLAVQQYIQQNIR	
6.9	1909.9091	1.0046	MDSTLAVQQYIQQNIR	
6.9	1909.9091	1.0046	MDSTLAVQQYIQQNIR	
5.7	1909.9091	1.0046	MDSTLAVQQYIQQNIR	
5.7	1909.9091	1.0046	MDSTLAVQQYIQQNIR	

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

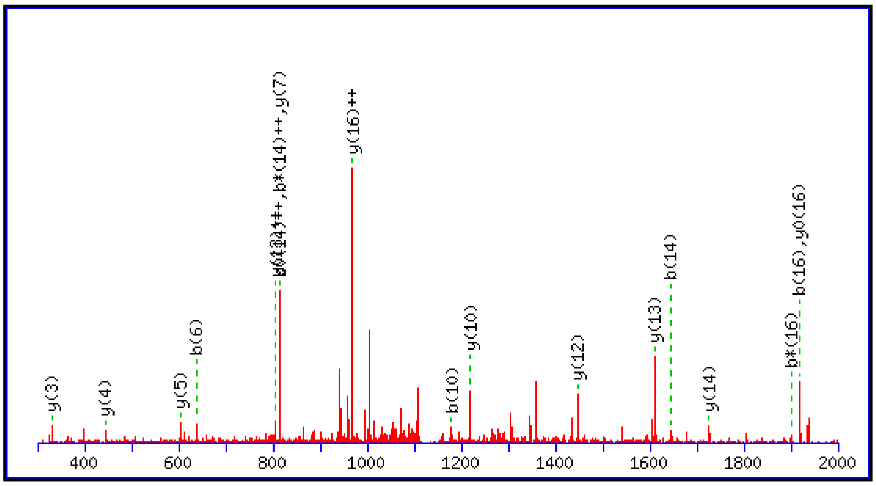
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQAPLNYTEFQKPICLPSK**
Found in **E9PBC5** in **con_Xuniprot_HUMAN3**, E9PBC5_HUMAN Plasma kallikrein heavy chain OS=Homo sapiens GN=KLKB1 PE=2 SV=1

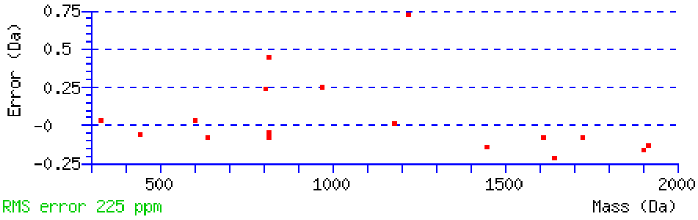
Match to Query 15081: 2247.168268 from(1124.591410,2+) intensity(27035.4980) rtinseconds(1710) scans(4328) index(1321)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum3768_scans__4328
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

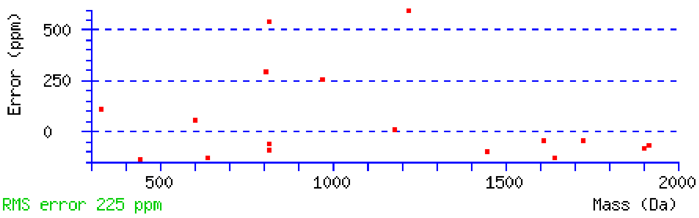
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2247.1609
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6       : Deamidated (NQ)
Ions Score: 67  Expect: 4.9e-005
Matches : 18/198 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	114.0913	57.5493					L							19
2	242.1499	121.5786	225.1234	113.0653			Q	2135.0842	1068.0457	2118.0576	1059.5324	2117.0736	1059.0404	18
3	313.1870	157.0972	296.1605	148.5839			A	2007.0256	1004.0164	1989.9990	995.5032	1989.0150	995.0111	17
4	410.2398	205.6235	393.2132	197.1103			P	1935.9885	968.4979	1918.9619	959.9846	1917.9779	959.4926	16
5	523.3239	262.1656	506.2973	253.6523			L	1838.9357	919.9715	1821.9092	911.4582	1820.9251	910.9662	15
6	**638.3508**	319.6790	621.3243	311.1658			N	***1725.8516***	863.4295	1708.8251	854.9162	1707.8411	854.4242	14
7	801.4141	401.2107	784.3876	392.6974			Y	***1610.8247***	805.9160	1593.7981	797.4027	1592.8141	796.9107	13
8	902.4618	451.7345	885.4353	443.2213	884.4512	442.7293	T	***1447.7614***	724.3843	1430.7348	715.8710	1429.7508	715.3790	12
9	1031.5044	516.2558	1014.4779	507.7426	1013.4938	507.2506	E	1346.7137	673.8605	1329.6871	665.3472	1328.7031	664.8552	11
10	**1178.5728**	589.7900	1161.5463	581.2768	1160.5623	580.7848	F	***1217.6711***	609.3392	1200.6445	600.8259	1199.6605	600.3339	10
11	1306.6314	653.8193	1289.6048	645.3061	1288.6208	644.8141	Q	1070.6027	535.8050	1053.5761	527.2917	1052.5921	526.7997	9
12	1434.7264	717.8668	1417.6998	709.3535	1416.7158	708.8615	K	942.5441	471.7757	925.5176	463.2624	924.5335	462.7704	8
13	1531.7791	766.3932	1514.7526	757.8799	1513.7686	757.3879	P	***814.4491***	407.7282	797.4226	399.2149	796.4386	398.7229	7
14	**1644.8632**	822.9352	1627.8366	814.4220	1626.8526	813.9299	I	717.3964	359.2018	700.3698	350.6885	699.3858	350.1965	6
15	1804.8938	902.9506	1787.8673	894.4373	1786.8833	893.9453	C	***604.3123***	302.6598	587.2858	294.1465	586.3017	293.6545	5
16	**1917.9779**	959.4926	1900.9514	950.9793	1899.9673	950.4873	L	***444.2817***	222.6445	427.2551	214.1312	426.2711	213.6392	4
17	2015.0307	1008.0190	1998.0041	999.5057	1997.0201	999.0137	P	***331.1976***	166.1024	314.1710	157.5892	313.1870	157.0972	3
18	2102.0627	1051.5350	2085.0361	1043.0217	2084.0521	1042.5297	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
19							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.7	2247.1609	0.0074	LQAPLNYTEFQKPICLPSK	Deamidated N6 91.14%
55.0	2247.1609	0.0074	LQAPLNYTEFQKPICLPSK	Deamidated Q11 6.12%
51.5	2247.1609	0.0074	LQAPLNYTEFQKPICLPSK	Deamidated Q2 2.75%
3.0	2246.1735	0.9948	ELKNIKFYAVQLYNYPSR	

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

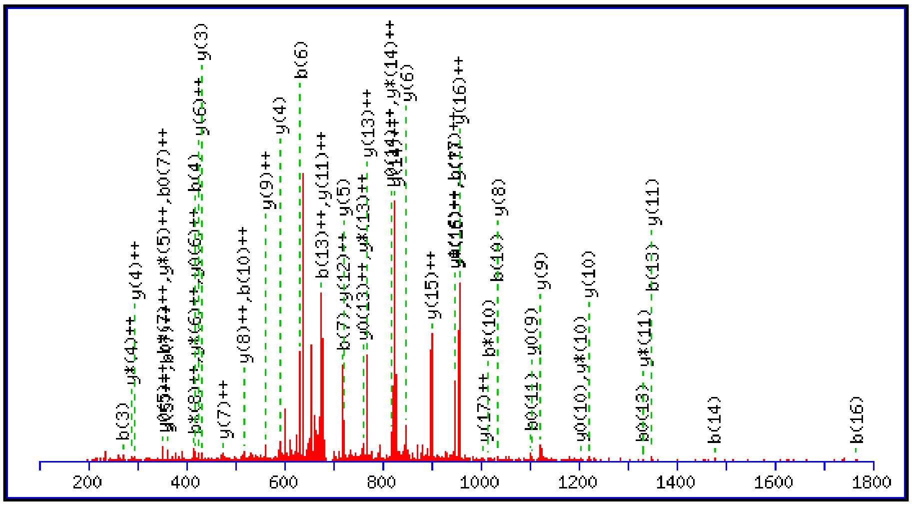
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNFNVSKVSSVEECQKR**
Found in **C9IYG8** in **con_Xuniprot_HUMAN3**, C9IYG8_HUMAN Plasma kallikrein heavy chain (Fragment) OS=Homo sapiens GN=KLKB1 PE=2 SV=1

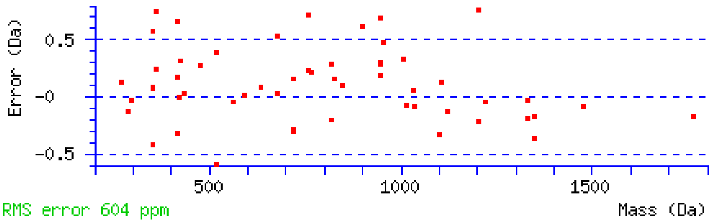
Match to Query 13125: 2067.010392 from(690.010740,3+) intensity(10894.8906) rtinseconds(885) scans(2011) index(23100)
Title: 111019_Est_MI_YS_G_04Spectrum1687_scans__2011
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

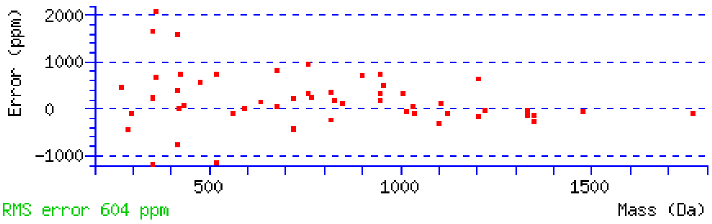
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2067.0055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00046
Matches : 55/180 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**18**
2	157.0972	79.0522					**V**	2010.9913	1005.9993	1993.9648	997.4860	1992.9808	996.9940	**17**
3	**271.1401**	136.0737	254.1135	127.5604			**N**	1911.9229	956.4651	1894.8964	947.9518	1893.9123	947.4598	**16**
4	**418.2085**	209.6079	401.1819	201.0946			**F**	1797.8800	899.4436	1780.8534	890.9304	1779.8694	890.4383	**15**
5	533.2354	267.1214	516.2089	258.6081			**N**	1650.8116	825.9094	1633.7850	817.3961	1632.8010	816.9041	**14**
6	**632.3039**	316.6556	615.2773	308.1423			**V**	1535.7846	768.3959	1518.7581	759.8827	1517.7741	759.3907	**13**
7	**719.3359**	**360.1716**	702.3093	351.6583	701.3253	351.1663	**S**	1436.7162	718.8617	1419.6897	710.3485	1418.7056	709.8565	**12**
8	847.4308	424.2191	830.4043	415.7058	829.4203	415.2138	**K**	**1349.6842**	675.3457	1332.6576	666.8325	1331.6736	666.3404	**11**
9	946.4993	473.7533	929.4727	465.2400	928.4887	464.7480	**V**	**1221.5892**	611.2982	1204.5627	602.7850	1203.5786	602.2930	**10**
10	**1033.5313**	**517.2693**	1016.5047	508.7560	1015.5207	508.2640	**S**	**1122.5208**	561.7640	1105.4942	553.2508	1104.5102	552.7588	**9**
11	1120.5633	560.7853	1103.5368	552.2720	1102.5527	551.7800	**S**	**1035.4888**	518.2480	1018.4622	509.7347	1017.4782	509.2427	**8**
12	1219.6317	610.3195	1202.6052	601.8062	1201.6212	601.3142	**V**	**948.4567**	474.7320	931.4302	466.2187	930.4462	465.7267	**7**
13	**1348.6743**	**674.8408**	1331.6478	666.3275	1330.6638	665.8355	**E**	**849.3883**	425.1978	832.3618	416.6845	831.3778	416.1925	**6**
14	**1477.7169**	739.3621	1460.6904	730.8488	1459.7063	730.3568	**E**	**720.3457**	360.6765	703.3192	352.1632	702.3352	351.6712	**5**
15	1637.7476	819.3774	1620.7210	810.8641	1619.7370	810.3721	**C**	**591.3031**	296.1552	574.2766	287.6419			**4**
16	**1765.8061**	883.4067	1748.7796	874.8934	1747.7956	874.4014	**Q**	**431.2725**	216.1399	414.2459	207.6266			**3**
17	1893.9011	**947.4542**	1876.8746	938.9409	1875.8905	938.4489	**K**	303.2139	152.1106	286.1874	143.5973			**2**
18							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.6	2067.0055	0.0049	GVNFNVSKVSSVEECQKR	Deamidated N5 42.93%
56.8	2067.0055	0.0049	GVNFNVSKVSSVEECQKR	Deamidated Q16 35.95%
54.5	2067.0055	0.0049	GVNFNVSKVSSVEECQKR	Deamidated N3 21.12%
10.7	2066.0069	1.0035	EEHAEQLQSIIRTLFDH	
10.7	2066.0069	1.0035	EEHAEQLQSIIRTLFDH	
4.2	2067.0095	0.0009	ESISQSNYPMVNSVFIPR	
3.9	2067.0008	0.0096	SLEHKTQTPPVEENVTQK	
2.8	2066.0028	1.0076	TALQGDQYRSNIAQQRSK	
2.6	2066.0028	1.0076	TALQGDQYRSNIAQQRSK	
2.1	2066.0028	1.0076	TALQGDQYRSNIAQQRSK	

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

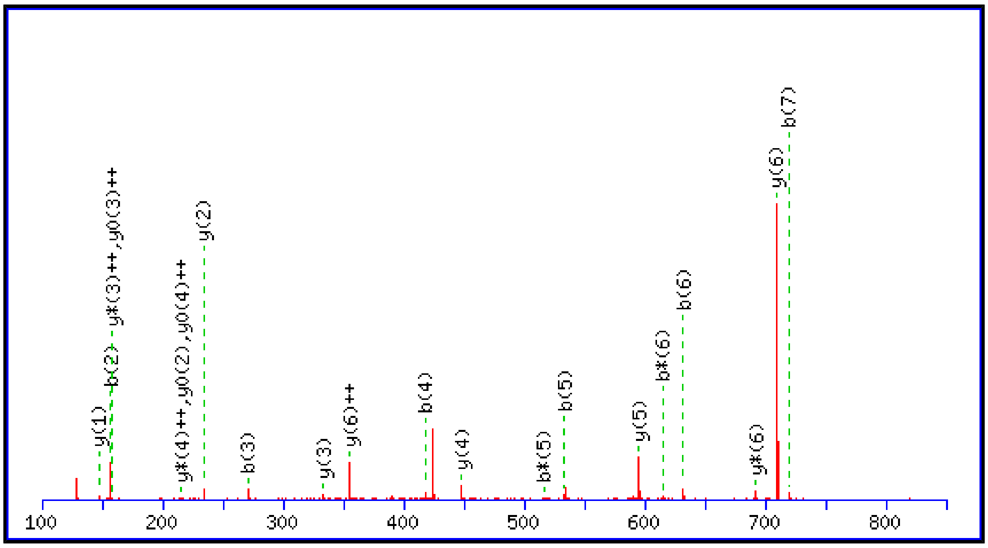
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNFNVSK**
Found in **C9IYG8** in **con_Xuniprot_HUMAN3**, C9IYG8_HUMAN Plasma kallikrein heavy chain (Fragment) OS=Homo sapiens GN=KLKB1 PE=2 SV=1

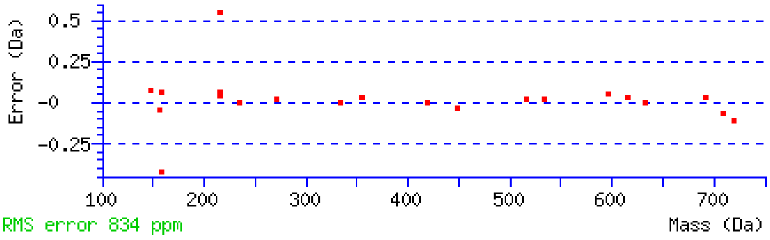
Match to Query 9: 864.435768 from(433.225160,2+) intensity(277389.1875) rtinseconds(469) scans(1065) index(19320)
Title: 111019_Est_MI_YP_G_09Spectrum927_scans__1065
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

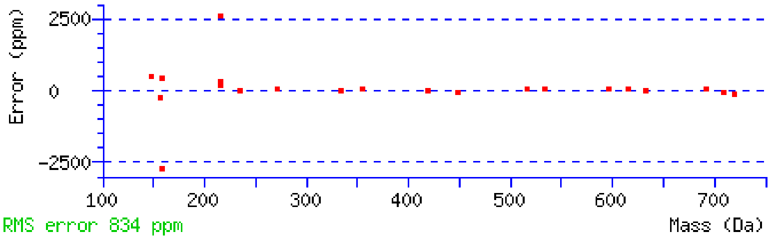
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 864.4341
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.021
Matches : 21/66 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	58.0287	29.5180					G							8
2	***157.0972***	79.0522					V	808.4199	404.7136	791.3934	396.2003	790.4094	395.7083	7
3	***271.1401***	136.0737	254.1135	127.5604			N	**709.3515**	355.1794	692.3250	346.6661	691.3410	346.1741	6
4	***418.2085***	209.6079	401.1819	201.0946			F	**595.3086**	298.1579	578.2821	289.6447	577.2980	289.1527	5
5	***533.2354***	267.1214	516.2089	258.6081			N	**448.2402**	224.6237	431.2136	216.1105	430.2296	215.6184	4
6	***632.3039***	316.6556	615.2773	308.1423			V	**333.2132**	167.1103	316.1867	158.5970	315.2027	158.1050	3
7	***719.3359***	360.1716	702.3093	351.6583	701.3253	351.1663	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
8							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.5	864.4341	0.0016	GVNFNVSK	Deamidated N5 96.03%
25.6	864.4341	0.0016	GVNFNVSK	Deamidated N3 3.97%
13.9	864.4314	0.0043	RNPQHGR	
13.8	864.4388	-0.0031	RNCIFR	
12.1	864.4341	0.0017	KAAEGFDK	
12.1	864.4341	0.0016	QAEFGVSK	
10.6	864.4375	-0.0017	KGMNGTLK	
10.3	864.4341	0.0017	GVYNGINK	
9.3	864.4375	-0.0017	KMKEGEK	
8.2	862.4257	2.0101	RNTTGTGR	

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

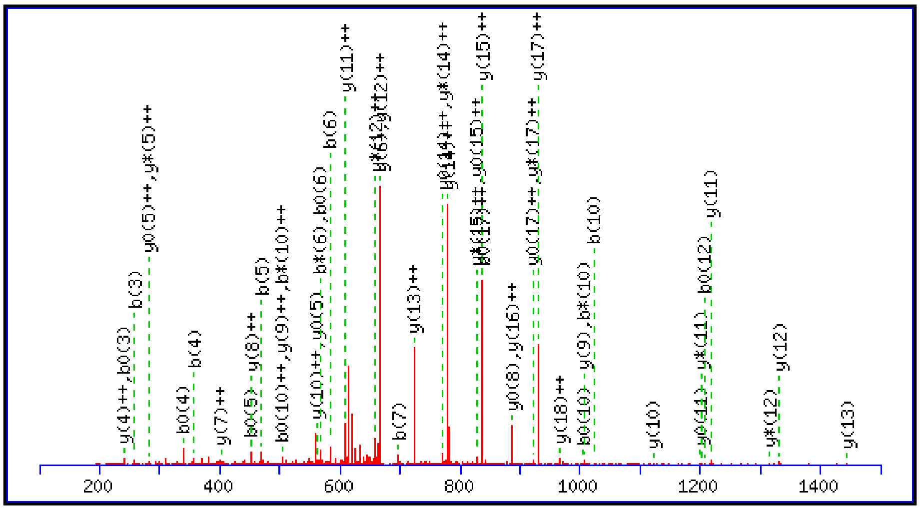
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VASVININPNTTHSTGSCR**
Found in **B4E2S7** in **con_Xuniprot_HUMAN3**, B4E2S7_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1

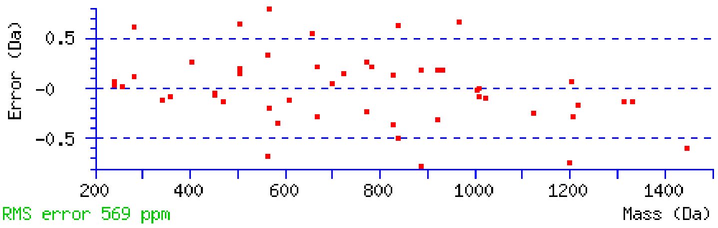
Match to Query 12760: 2027.976822 from(676.999550,3+) intensity(74919.8359) rtinseconds(756) scans(1673) index(25196)
Title: 111019_Est_MI_YS_G_07Spectrum1398_scans__1673
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

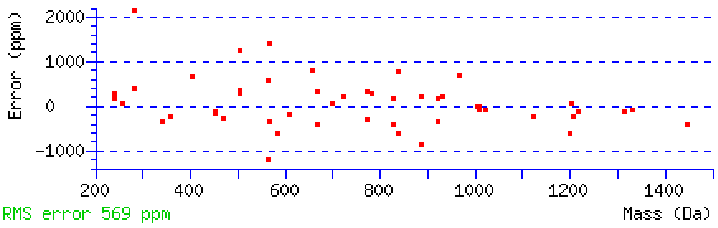
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2027.9695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 74 **Expect:** 9.5e-006
Matches : 50/198 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	100.0757	50.5415					V							19
2	171.1128	86.0600					A	1929.9083	965.4578	1912.8818	956.9445	1911.8978	956.4525	18
3	**258.1448**	129.5761			240.1343	120.5708	S	1858.8712	929.9392	1841.8447	921.4260	1840.8606	920.9340	17
4	**357.2132**	179.1103			339.2027	170.1050	V	1771.8392	886.4232	1754.8126	877.9100	1753.8286	877.4179	16
5	**470.2973**	235.6523			452.2867	226.6470	I	1672.7708	836.8890	1655.7442	828.3757	1654.7602	827.8837	15
6	**584.3402**	292.6738	567.3137	284.1605	566.3297	283.6685	N	1559.6867	780.3470	1542.6601	771.8337	1541.6761	771.3417	14
7	**697.4243**	349.2158	680.3978	340.7025	679.4137	340.2105	I	**1445.6438**	723.3255	1428.6172	714.8122	1427.6332	714.3202	13
8	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	N	**1332.5597**	666.7835	1315.5332	658.2702	1314.5491	657.7782	12
9	908.5200	454.7636	891.4934	446.2504	890.5094	445.7584	P	**1218.5168**	609.7620	1201.4902	601.2488	1200.5062	600.7567	11
10	**1023.5469**	512.2771	1006.5204	503.7638	1005.5364	503.2718	N	**1121.4640**	561.2356	1104.4375	552.7224	1103.4534	552.2304	10
11	1124.5946	562.8009	1107.5681	554.2877	1106.5840	553.7957	T	**1006.4371**	503.7222	989.4105	495.2089	988.4265	494.7169	9
12	1225.6423	613.3248	1208.6157	604.8115	1207.6317	604.3195	T	905.3894	453.1983	888.3628	444.6851	887.3788	444.1931	8
13	1362.7012	681.8542	1345.6747	673.3410	1344.6906	672.8490	H	804.3417	402.6745	787.3152	394.1612	786.3311	393.6692	7
14	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	S	**667.2828**	334.1450	650.2563	325.6318	649.2722	325.1398	6
15	1550.7809	775.8941	1533.7544	767.3808	1532.7703	766.8888	T	580.2508	290.6290	563.2242	282.1157	562.2402	281.6237	5
16	1607.8024	804.4048	1590.7758	795.8916	1589.7918	795.3995	G	479.2031	240.1052	462.1765	231.5919	461.1925	231.0999	4
17	1694.8344	847.9208	1677.8079	839.4076	1676.8238	838.9156	S	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
18	1854.8651	927.9362	1837.8385	919.4229	1836.8545	918.9309	C	335.1496	168.0784	318.1231	159.5652			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.9	2027.9695	0.0074	VASVININPNTTHSTGSCR	Deamidated N10 93.21%
61.1	2027.9695	0.0074	VASVININPNTTHSTGSCR	Deamidated N8 4.91%
56.9	2027.9695	0.0074	VASVININPNTTHSTGSCR	Deamidated N6 1.87%
13.4	2025.9677	2.0091	IASDLTRSQDLMINSSQF	
11.6	2025.9677	2.0091	IASDLTRSQDLMINSSQF	
11.0	2027.9690	0.0078	LRSLLLNSCTGTSCTTMI	
11.0	2027.9690	0.0078	LRSLLLNSCTGTSCTTML	
10.7	2025.9677	2.0091	IASDLTRSQDLMINSSQF	
9.2	2027.9807	-0.0038	RVDNQMSERITVNNAHK	
7.8	2027.9669	0.0099	LIGRHWNEQMLDIACR	

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

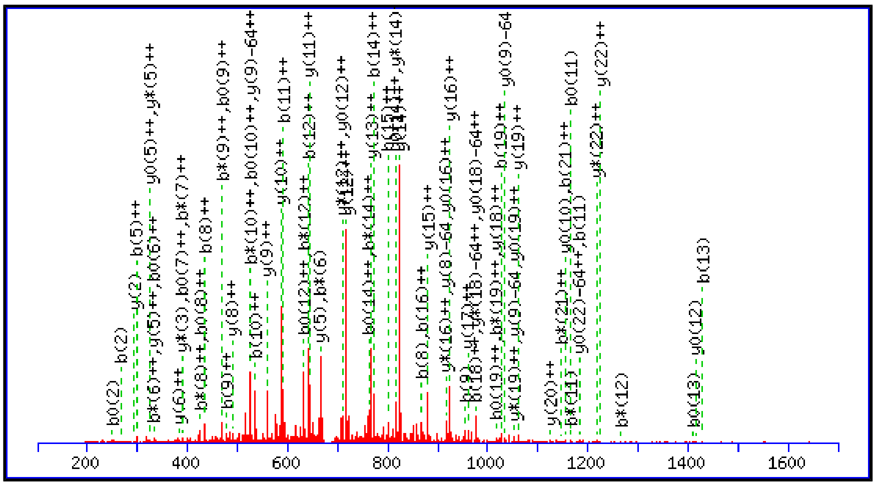
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEAQSNASLDVFLGHTNVEELMK**
Found in **H0YFH3** in **con_Xuniprot_HUMAN3**, H0YFH3_HUMAN Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=2 SV=1

Match to Query 25369: 2714.254416 from(679.570880,4+) intensity(40981.7188) rtinseconds(1595) scans(3978) index(14515)
Title: 111019_Est_MI_YP_G_03Spectrum3433_scans__3978
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

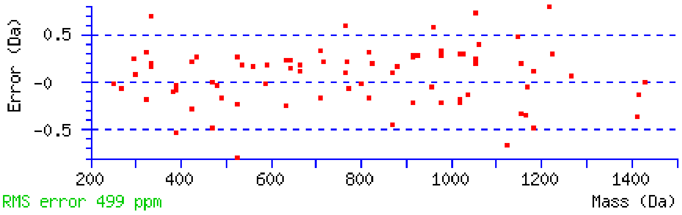
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

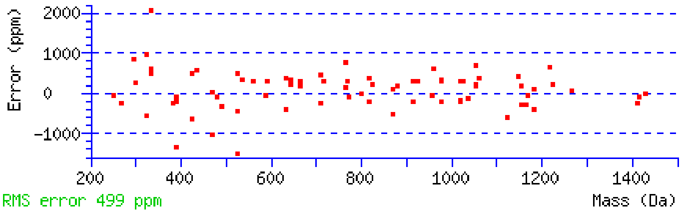


Monoisotopic mass of neutral peptide Mr(calc): 2714.2493
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
M23 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 76 **Expect:** 4.9e-006
Matches : 79/396 fragment ions using 107 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							24
2	**267.1088**	134.0580			249.0982	125.0527	H	2586.2141	1293.6107	2569.1875	1285.0974	2568.2035	1284.6054	23
3	396.1514	198.5793			378.1408	189.5740	E	2449.1551	1225.0812	2432.1286	1216.5679	2431.1446	1216.0759	22
4	467.1885	234.0979			449.1779	225.0926	A	2320.1126	1160.5599	2303.0860	1152.0466	2302.1020	1151.5546	21
5	595.2471	**298.1272**	578.2205	289.6139	577.2365	289.1219	Q	2249.0754	1125.0414	2232.0489	1116.5281	2231.0649	1116.0361	20
6	682.2791	341.6432	665.2525	333.1299	664.2685	332.6379	S	2121.0169	1061.0121	2103.9903	1052.4988	2103.0063	1052.0068	19
7	797.3060	399.1567	780.2795	390.6434	779.2955	390.1514	N	2033.9848	1017.4961	2016.9583	1008.9828	2015.9743	1008.4908	18
8	**868.3432**	**434.6752**	851.3166	426.1619	850.3326	425.6699	A	1918.9579	959.9826	1901.9313	951.4693	1900.9473	950.9773	17
9	**955.3752**	**478.1912**	938.3486	469.6780	937.3646	469.1859	S	1847.9208	924.4640	1830.8942	915.9508	1829.9102	915.4587	16
10	1068.4592	**534.7333**	1051.4327	526.2200	1050.4487	525.7280	L	1760.8887	880.9480	1743.8622	872.4347	1742.8782	871.9427	15
11	**1183.4862**	**592.2467**	1166.4596	583.7335	1165.4756	583.2414	D	1647.8047	824.4060	1630.7781	815.8927	1629.7941	815.4007	14
12	1282.5546	**641.7809**	1265.5281	633.2677	1264.5440	632.7757	V	1532.7777	766.8925	1515.7512	758.3792	1514.7672	757.8872	13
13	**1429.6230**	715.3151	1412.5965	706.8019	1411.6124	706.3099	F	1433.7093	717.3583	1416.6828	708.8450	1415.6988	708.3530	12
14	1542.7071	**771.8572**	1525.6805	763.3439	1524.6965	762.8519	L	1286.6409	643.8241	1269.6144	635.3108	1268.6303	634.8188	11
15	1599.7285	**800.3679**	1582.7020	791.8546	1581.7180	791.3626	G	1173.5569	587.2821	1156.5303	578.7688	1155.5463	578.2768	10
16	1736.7875	**868.8974**	1719.7609	860.3841	1718.7769	859.8921	H	1116.5354	558.7713	1099.5088	550.2581	1098.5248	549.7660	9
17	1837.8351	919.4212	1820.8086	910.9079	1819.8246	910.4159	T	979.4765	490.2419	962.4499	481.7286	961.4659	481.2366	8
18	1951.8781	**976.4427**	1934.8515	967.9294	1933.8675	967.4374	N	878.4288	439.7180	861.4022	431.2048	860.4182	430.7128	7
19	2050.9465	**1025.9769**	2033.9199	1017.4636	2032.9359	1016.9716	V	764.3859	382.6966	747.3593	374.1833	746.3753	373.6913	6
20	2179.9891	1090.4982	2162.9625	1081.9849	2161.9785	1081.4929	E	665.3175	333.1624	648.2909	324.6491	647.3069	324.1571	5
21	2309.0317	**1155.0195**	2292.0051	1146.5062	2291.0211	1146.0142	E	536.2749	268.6411	519.2483	260.1278	518.2643	259.6358	4
22	2422.1157	1211.5615	2405.0892	1203.0482	2404.1052	1202.5562	L	407.2323	204.1198	390.2057	195.6065			3

23	2569.1511	1285.0792	2552.1246	1276.5659	2551.1406	1276.0739	**M**	294.1482	147.5777	277.1217	139.0645			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.3	2714.2493	0.0051	EHEAQSNASLDVFLGHTNVEELMK	Deamidated N7 87.14%
67.8	2714.2493	0.0051	EHEAQSNASLDVFLGHTNVEELMK	Deamidated Q5 12.37%
53.8	2714.2493	0.0051	EHEAQSNASLDVFLGHTNVEELMK	Deamidated N18 0.50%
6.5	2712.2602	1.9942	MEADLSGFNIDAPRWDQRTFLGR	
5.9	2713.2649	0.9895	AVDDGKPQLIDSAMDMLDIGATFMK	
5.9	2714.2489	0.0055	AVDDGKPQLIDSAMDMLDIGATFMK	
5.5	2713.2509	1.0035	YMMDLLNGLSQATCATEQIPARGR	
5.1	2712.2597	1.9947	MDIDAPDVEVQGPDWHLKMPKMK	
5.0	2713.2509	1.0035	YMMDLLNGLSQATCATEQIPARGR	
4.8	2713.2509	1.0035	YMMDLLNGLSQATCATEQIPARGR	

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

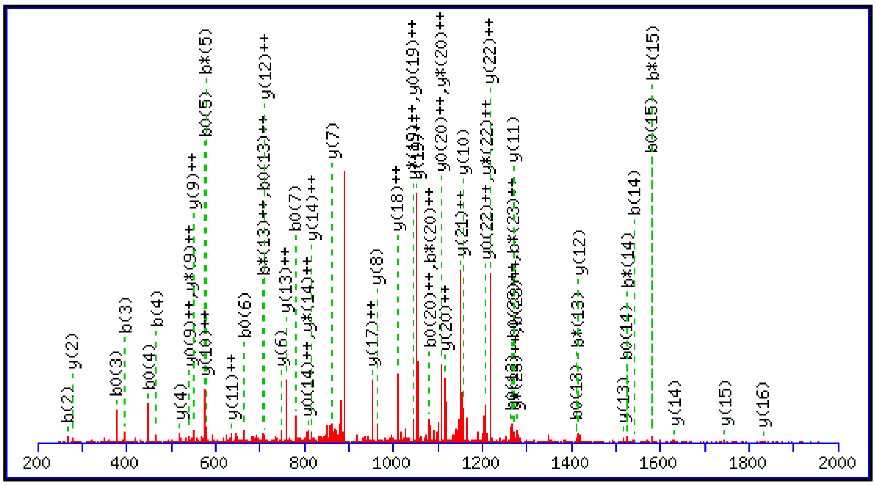
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEAQSNASLDVFLGHTNVEELMK**
Found in **H0YFH3** in **con_Xuniprot_HUMAN3**, H0YFH3_HUMAN Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=2 SV=1

Match to Query 25335: 2698.268172 from(900.430000,3+) intensity(57492.3398) rtinseconds(1991) scans(5078) index(14651)
Title: 111019_Est_MI_YP_G_03Spectrum4412_scans__5078
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

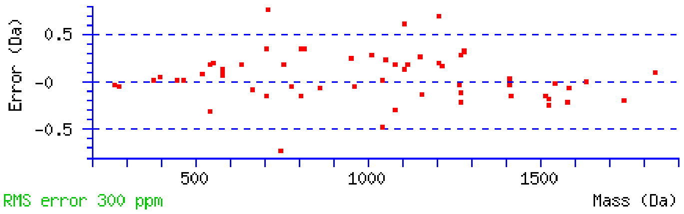
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

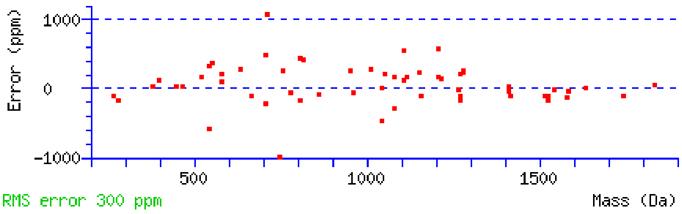


```
Monoisotopic mass of neutral peptide Mr(calc): 2698.2544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7      : Deamidated (NQ)
Ions Score: 76  Expect: 6.4e-006
Matches : 59/262 fragment ions using 103 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							24
2	**267.1088**	134.0580			249.0982	125.0527	H	2570.2191	1285.6132	2553.1926	1277.0999	2552.2086	1276.6079	23
3	**396.1514**	198.5793			378.1408	189.5740	E	2433.1602	1217.0838	2416.1337	1208.5705	2415.1497	1208.0785	22
4	**467.1885**	234.0979			449.1779	225.0926	A	2304.1176	1152.5625	2287.0911	1144.0492	2286.1071	1143.5572	21
5	595.2471	298.1272	578.2205	289.6139	577.2365	289.1219	Q	2233.0805	1117.0439	2216.0540	1108.5306	2215.0700	1108.0386	20
6	682.2791	341.6432	665.2525	333.1299	664.2685	332.6379	S	2105.0219	1053.0146	2087.9954	1044.5013	2087.0114	1044.0093	19
7	797.3060	399.1567	780.2795	390.6434	779.2955	390.1514	N	2017.9899	1009.4986	2000.9634	1000.9853	1999.9794	1000.4933	18
8	868.3432	434.6752	851.3166	426.1619	850.3326	425.6699	A	1902.9630	951.9851	1885.9364	943.4719	1884.9524	942.9798	17
9	955.3752	478.1912	938.3486	469.6780	937.3646	469.1859	S	***1831.9259***	916.4666	1814.8993	907.9533	1813.9153	907.4613	16
10	1068.4592	534.7333	1051.4327	526.2200	1050.4487	525.7280	L	***1744.8938***	872.9506	1727.8673	864.4373	1726.8833	863.9453	15
11	1183.4862	592.2467	1166.4596	583.7335	1165.4756	583.2414	D	***1631.8098***	816.4085	1614.7832	807.8952	1613.7992	807.4032	14
12	1282.5546	641.7809	1265.5281	633.2677	1264.5440	632.7757	V	***1516.7828***	758.8951	1499.7563	750.3818	1498.7723	749.8898	13
13	1429.6230	715.3151	1412.5965	706.8019	1411.6124	706.3099	F	***1417.7144***	709.3608	1400.6879	700.8476	1399.7038	700.3556	12
14	**1542.7071**	771.8572	1525.6805	763.3439	1524.6965	762.8519	L	***1270.6460***	635.8266	1253.6195	627.3134	1252.6354	626.8214	11
15	1599.7285	800.3679	1582.7020	791.8546	1581.7180	791.3626	G	***1157.5619***	579.2846	1140.5354	570.7713	1139.5514	570.2793	10
16	1736.7875	868.8974	1719.7609	860.3841	1718.7769	859.8921	H	1100.5405	550.7739	1083.5139	542.2606	1082.5299	541.7686	9
17	1837.8351	919.4212	1820.8086	910.9079	1819.8246	910.4159	T	***963.4816***	482.2444	946.4550	473.7311	945.4710	473.2391	8
18	1951.8781	976.4427	1934.8515	967.9294	1933.8675	967.4374	N	***862.4339***	431.7206	845.4073	423.2073	844.4233	422.7153	7
19	2050.9465	1025.9769	2033.9199	1017.4636	2032.9359	1016.9716	V	***748.3910***	374.6991	731.3644	366.1858	730.3804	365.6938	6
20	2179.9891	1090.4982	2162.9625	1081.9849	2161.9785	1081.4929	E	649.3225	325.1649	632.2960	316.6516	631.3120	316.1596	5
21	2309.0317	1155.0195	2292.0051	1146.5062	2291.0211	1146.0142	E	***520.2799***	260.6436	503.2534	252.1303	502.2694	251.6383	4
22	2422.1157	1211.5615	2405.0892	1203.0482	2404.1052	1202.5562	L	391.2374	196.1223	374.2108	187.6090			3
23	2553.1562	1277.0817	2536.1297	1268.5685	2535.1456	1268.0765	M	***278.1533***	139.5803	261.1267	131.0670			2

24							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.8	2698.2544	0.0137	EHEAQSNASLDVFLGHTNVEELMK	Deamidated N7 62.04%
73.6	2698.2544	0.0137	EHEAQSNASLDVFLGHTNVEELMK	Deamidated Q5 37.90%
67.4	2697.2704	0.9978	EHEAQSNASLDVFLGHTNVEELMK	
45.0	2698.2544	0.0137	EHEAQSNASLDVFLGHTNVEELMK	Deamidated N18 0.05%
5.1	2696.2541	2.0141	WQYDVWSTDVTVANKMEAGGIPGR	
4.2	2696.2501	2.0181	GFSSDGEQDSTAVPMVSVPAQYPRR	
3.4	2698.2811	-0.0129	FGEKMAFIPQNLFLFQHQEPMK	
3.4	2698.2811	-0.0129	FGEKMAFIPQNLFLFQHQEPMK	
2.0	2698.2632	0.0050	QHQTLYTSHSFTKSCVNCIYPK	
1.9	2698.2771	-0.0089	QGNFMVTAWNDNGKKLVFVINGPM	

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

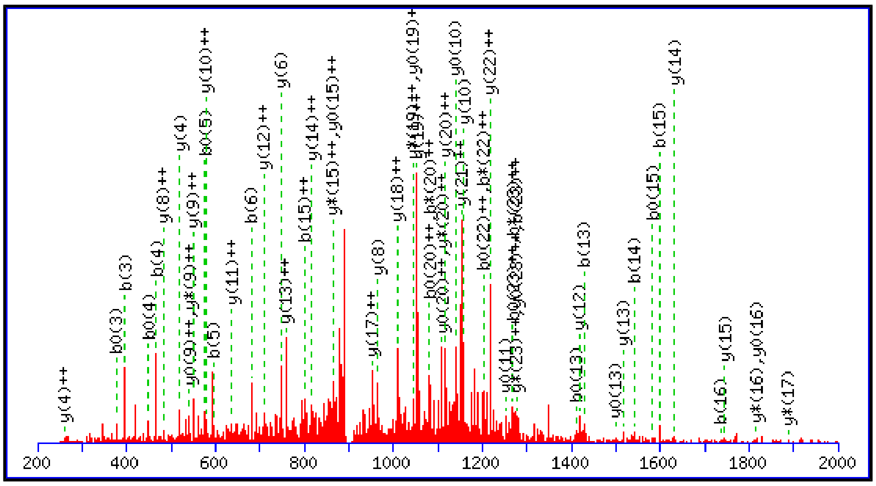
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHEAQSNASLDVFLGHTNVEELMK**
Found in **H0YFH3** in **con_Xuniprot_HUMAN3**, H0YFH3_HUMAN Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=2 SV=1

Match to Query 25352: 2699.237622 from(900.753150,3+) intensity(18860.4766) rtinseconds(2197) scans(5653) index(14699)
Title: 111019_Est_MI_YP_G_03Spectrum4920_scans__5653
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

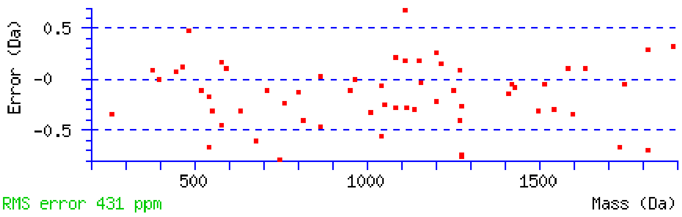
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

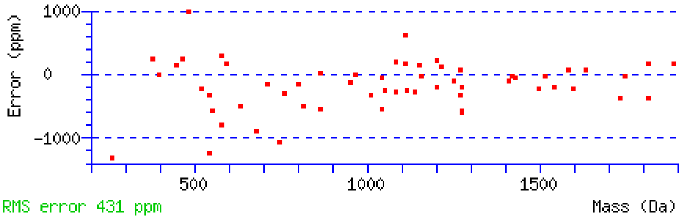


Monoisotopic mass of neutral peptide Mr(calc): 2699.2384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N18 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0057
Matches : 59/262 fragment ions using 142 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							24
2	267.1088	134.0580			249.0982	125.0527	H	2571.2032	1286.1052	2554.1766	1277.5919	2553.1926	1277.0999	23
3	**396.1514**	198.5793			378.1408	189.5740	E	2434.1442	1217.5758	2417.1177	1209.0625	2416.1337	1208.5705	22
4	**467.1885**	234.0979			449.1779	225.0926	A	2305.1017	1153.0545	2288.0751	1144.5412	2287.0911	1144.0492	21
5	**595.2471**	298.1272	578.2205	289.6139	577.2365	289.1219	Q	2234.0645	1117.5359	2217.0380	1109.0226	2216.0540	1108.5306	20
6	**682.2791**	341.6432	665.2525	333.1299	664.2685	332.6379	S	2106.0060	1053.5066	2088.9794	1044.9933	2087.9954	1044.5013	19
7	797.3060	399.1567	780.2795	390.6434	779.2955	390.1514	N	2018.9739	1009.9906	2001.9474	1001.4773	2000.9634	1000.9853	18
8	868.3432	434.6752	851.3166	426.1619	850.3326	425.6699	A	1903.9470	952.4771	1886.9204	943.9639	1885.9364	943.4719	17
9	955.3752	478.1912	938.3486	469.6780	937.3646	469.1859	S	1832.9099	916.9586	1815.8833	908.4453	1814.8993	907.9533	16
10	1068.4592	534.7333	1051.4327	526.2200	1050.4487	525.7280	L	**1745.8779**	873.4426	1728.8513	864.9293	1727.8673	864.4373	15
11	1183.4862	592.2467	1166.4596	583.7335	1165.4756	583.2414	D	**1632.7938**	816.9005	1615.7672	808.3873	1614.7832	807.8952	14
12	1282.5546	641.7809	1265.5281	633.2677	1264.5440	632.7757	V	**1517.7668**	759.3871	1500.7403	750.8738	1499.7563	750.3818	13
13	**1429.6230**	715.3151	1412.5965	706.8019	1411.6124	706.3099	F	**1418.6984**	709.8529	1401.6719	701.3396	1400.6879	700.8476	12
14	**1542.7071**	771.8572	1525.6805	763.3439	1524.6965	762.8519	L	1271.6300	636.3186	1254.6035	627.8054	1253.6195	627.3134	11
15	**1599.7285**	800.3679	1582.7020	791.8546	1581.7180	791.3626	G	**1158.5460**	579.7766	1141.5194	571.2633	1140.5354	570.7713	10
16	**1736.7875**	868.8974	1719.7609	860.3841	1718.7769	859.8921	H	1101.5245	551.2659	1084.4979	542.7526	1083.5139	542.2606	9
17	1837.8351	919.4212	1820.8086	910.9079	1819.8246	910.4159	T	**964.4656**	482.7364	947.4390	474.2232	946.4550	473.7311	8
18	1952.8621	976.9347	1935.8355	968.4214	1934.8515	967.9294	N	863.4179	432.2126	846.3913	423.6993	845.4073	423.2073	7
19	2051.9305	1026.4689	2034.9039	1017.9556	2033.9199	1017.4636	V	**748.3910**	374.6991	731.3644	366.1858	730.3804	365.6938	6
20	2180.9731	1090.9902	2163.9465	1082.4769	2162.9625	1081.9849	E	649.3225	325.1649	632.2960	316.6516	631.3120	316.1596	5
21	2310.0157	1155.5115	2292.9891	1146.9982	2292.0051	1146.5062	E	**520.2799**	260.6436	503.2534	252.1303	502.2694	251.6383	4
22	2423.0997	1212.0535	2406.0732	1203.5402	2405.0892	1203.0482	L	391.2374	196.1223	374.2108	187.6090			3

23	2554.1402	1277.5738	2537.1137	1269.0605	2536.1297	1268.5685	**M**	278.1533	139.5803	261.1267	131.0670			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.2	2699.2384	-0.0008	EHEAQSNASLDVFLGHTNVEELMK	Deamidated N7, N18 66.41%
42.0	2699.2384	-0.0008	EHEAQSNASLDVFLGHTNVEELMK	Deamidated Q5, N18 31.93%
29.1	2699.2384	-0.0008	EHEAQSNASLDVFLGHTNVEELMK	Deamidated Q5, N7 1.66%
8.5	2699.2360	0.0017	RFQQFLDFMFKTNAESLSNMTQ	
8.5	2699.2360	0.0017	RFQQFLDFMFKTNAESLSNMTQ	
1.9	2698.2466	0.9910	NHMSSTSDLLSVVKMEIEDEGFSK	
1.9	2699.2306	0.0070	NHMSSTSDLLSVVKMEIEDEGFSK	
1.9	2699.2254	0.0122	NWNLYPACLREMSRVCTPTTGR	

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

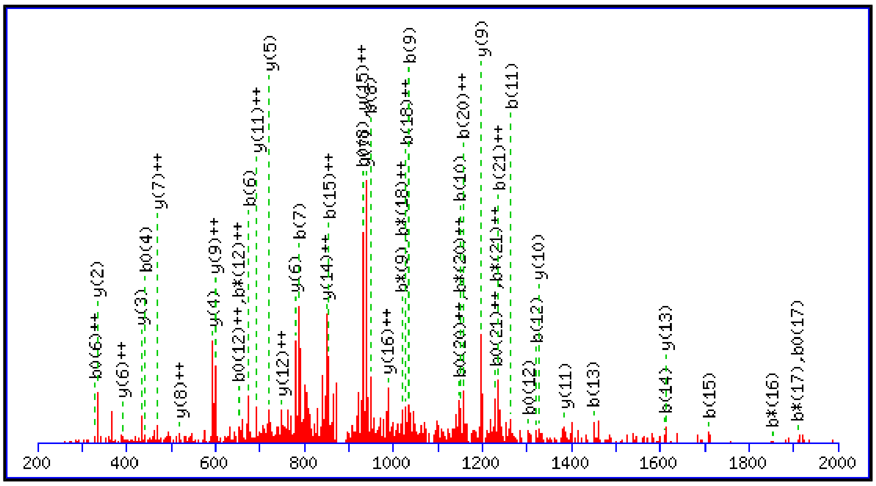
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KENSSEICSNNGECVCGQCVCR**
Found in **H7C4N8** in **con_Xuniprot_HUMAN3**, H7C4N8_HUMAN Integrin beta-1 (Fragment) OS=Homo sapiens GN=ITGB1 PE=4 SV=1

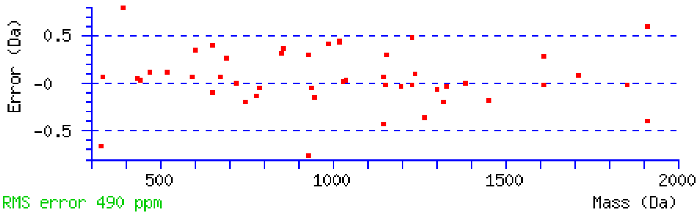
Match to Query 22381: 2647.029252 from(883.350360,3+) intensity(4828.0942) rtinseconds(389) scans(812) index(6125)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum695_scans__812
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

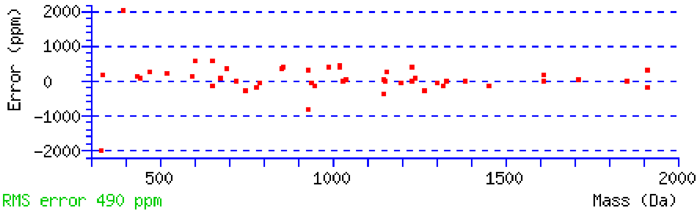
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2647.0189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 55 **Expect:** 3.1e-005
Matches : 48/232 fragment ions using 83 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							22
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	2519.9313	1260.4693	2502.9047	1251.9560	2501.9207	1251.4640	21
3	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	N	2390.8887	1195.9480	2373.8621	1187.4347	2372.8781	1186.9427	20
4	460.2038	230.6055	443.1773	222.0923	442.1932	221.6003	S	2275.8617	1138.4345	2258.8352	1129.9212	2257.8512	1129.4292	19
5	547.2358	274.1216	530.2093	265.6083	529.2253	265.1163	S	2188.8297	1094.9185	2171.8031	1086.4052	2170.8191	1085.9132	18
6	***676.2784***	338.6429	659.2519	330.1296	658.2679	329.6376	E	2101.7977	1051.4025	2084.7711	1042.8892	2083.7871	1042.3972	17
7	***789.3625***	395.1849	772.3359	386.6716	771.3519	386.1796	I	1972.7551	986.8812	1955.7285	978.3679	1954.7445	977.8759	16
8	***949.3931***	475.2002	932.3666	466.6869	931.3826	466.1949	C	1859.6710	930.3391	1842.6445	921.8259	1841.6604	921.3339	15
9	***1036.4252***	518.7162	1019.3986	510.2029	1018.4146	509.7109	S	1699.6404	850.3238	1682.6138	841.8105	1681.6298	841.3185	14
10	***1150.4681***	575.7377	1133.4415	567.2244	1132.4575	566.7324	N	***1612.6083***	806.8078	1595.5818	798.2945	1594.5978	797.8025	13
11	***1264.5110***	632.7591	1247.4845	624.2459	1246.5005	623.7539	N	1498.5654	749.7863	1481.5389	741.2731	1480.5548	740.7811	12
12	***1321.5325***	661.2699	1304.5059	652.7566	1303.5219	652.2646	G	***1384.5225***	692.7649	1367.4959	684.2516	1366.5119	683.7596	11
13	***1450.5751***	725.7912	1433.5485	717.2779	1432.5645	716.7859	E	***1327.5010***	664.2541	1310.4745	655.7409	1309.4904	655.2489	10
14	***1610.6057***	805.8065	1593.5792	797.2932	1592.5952	796.8012	C	***1198.4584***	599.7328	1181.4319	591.2196			9
15	***1709.6741***	**855.3407**	1692.6476	846.8274	1691.6636	846.3354	V	1038.4278	519.7175	1021.4012	511.2042			8
16	1869.7048	935.3560	1852.6782	926.8428	1851.6942	926.3507	C	***939.3594***	470.1833	922.3328	461.6700			7
17	1926.7263	963.8668	1909.6997	955.3535	1908.7157	954.8615	G	***779.3287***	390.1680	762.3022	381.6547			6
18	2054.7848	**1027.8961**	2037.7583	1019.3828	2036.7743	1018.8908	Q	***722.3072***	361.6573	705.2807	353.1440			5
19	2214.8155	1107.9114	2197.7889	1099.3981	2196.8049	1098.9061	C	***594.2487***	297.6280	577.2221	289.1147			4
20	2313.8839	**1157.4456**	2296.8573	1148.9323	2295.8733	1148.4403	V	***434.2180***	217.6126	417.1915	209.0994			3
21	2473.9145	**1237.4609**	2456.8880	1228.9476	2455.9040	1228.4556	C	***335.1496***	168.0784	318.1231	159.5652			2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.1	2647.0189	0.0103	KENSSEICSNNGECVCGQCVCR	Deamidated N3 70.48%
48.8	2647.0189	0.0103	KENSSEICSNNGECVCGQCVCR	Deamidated N10 16.41%
47.8	2647.0189	0.0103	KENSSEICSNNGECVCGQCVCR	Deamidated N11 13.09%
31.2	2646.0349	0.9943	KENSSEICSNNGECVCGQCVCR	
20.1	2647.0189	0.0103	KENSSEICSNNGECVCGQCVCR	Deamidated Q18 0.02%

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

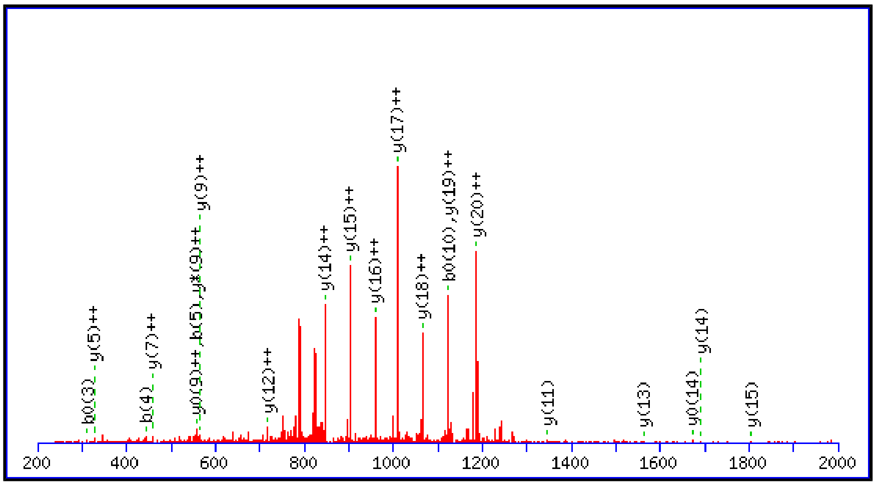
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTQNLTLIEESLTSEFIHDIDR**
Found in **I3L4N7** in **con_Xuniprot_HUMAN3**, I3L4N7_HUMAN Pigment epithelium-derived factor (Fragment) OS=Homo sapiens GN=SERPINF1 PE=2 SV=1

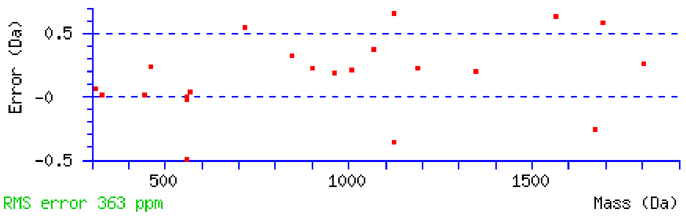
Match to Query 21936: 2573.296692 from(858.772840,3+) intensity(59197.3633) rtinseconds(2756) scans(7375) index(16377)
Title: 111019_Est_MI_YP_G_05Spectrum6349_scans__7375
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

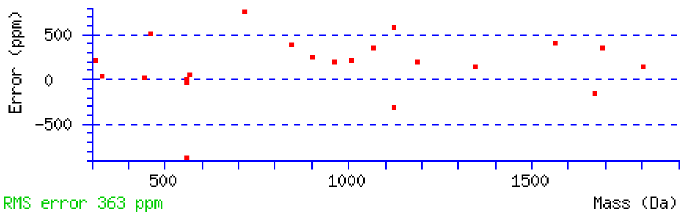
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2573.2861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00038
Matches : 22/244 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	100.0757	50.5415					V							22
2	201.1234	101.0653			183.1128	92.0600	T	2475.2249	1238.1161	2458.1984	1229.6028	2457.2144	1229.1108	21
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	2374.1773	1187.5923	2357.1507	1179.0790	2356.1667	1178.5870	20
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	N	2246.1187	1123.5630	2229.0921	1115.0497	2228.1081	1114.5577	19
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	L	2131.0917	1066.0495	2114.0652	1057.5362	2113.0812	1057.0442	18
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	T	2018.0077	1009.5075	2000.9811	1000.9942	1999.9971	1000.5022	17
7	771.4247	386.2160	754.3981	377.7027	753.4141	377.2107	L	1916.9600	958.9836	1899.9334	950.4704	1898.9494	949.9784	16
8	884.5088	442.7580	867.4822	434.2447	866.4982	433.7527	I	**1803.8759**	902.4416	1786.8494	893.9283	1785.8654	893.4363	15
9	1013.5514	507.2793	996.5248	498.7660	995.5408	498.2740	E	**1690.7919**	845.8996	1673.7653	837.3863	1672.7813	836.8943	14
10	1142.5939	571.8006	1125.5674	563.2873	1124.5834	562.7953	E	**1561.7493**	781.3783	1544.7227	772.8650	1543.7387	772.3730	13
11	1229.6260	615.3166	1212.5994	606.8034	1211.6154	606.3113	S	1432.7067	716.8570	1415.6801	708.3437	1414.6961	707.8517	12
12	1342.7100	671.8587	1325.6835	663.3454	1324.6995	662.8534	L	**1345.6747**	673.3410	1328.6481	664.8277	1327.6641	664.3357	11
13	1443.7577	722.3825	1426.7312	713.8692	1425.7472	713.3772	T	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	10
14	1530.7897	765.8985	1513.7632	757.3852	1512.7792	756.8932	S	1131.5429	566.2751	1114.5164	557.7618	1113.5323	557.2698	9
15	1659.8323	830.4198	1642.8058	821.9065	1641.8218	821.4145	E	1044.5109	522.7591	1027.4843	514.2458	1026.5003	513.7538	8
16	1806.9008	903.9540	1789.8742	895.4407	1788.8902	894.9487	F	915.4683	458.2378	898.4417	449.7245	897.4577	449.2325	7
17	1919.9848	960.4960	1902.9583	951.9828	1901.9743	951.4908	I	768.3999	384.7036	751.3733	376.1903	750.3893	375.6983	6
18	2057.0437	1029.0255	2040.0172	1020.5122	2039.0332	1020.0202	H	655.3158	328.1615	638.2893	319.6483	637.3052	319.1563	5
19	2172.0707	1086.5390	2155.0441	1078.0257	2154.0601	1077.5337	D	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
20	2285.1547	1143.0810	2268.1282	1134.5677	2267.1442	1134.0757	I	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
21	2400.1817	1200.5945	2383.1551	1192.0812	2382.1711	1191.5892	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.4	2573.2861	0.0106	VTQNLTLIEESLTSEFIHDIDR	Deamidated N4 86.51%
50.3	2573.2861	0.0106	VTQNLTLIEESLTSEFIHDIDR	Deamidated Q3 13.49%
47.5	2572.3020	0.9946	VTQNLTLIEESLTSEFIHDIDR	
5.8	2573.3006	-0.0039	AQKENSLQLQKAQLEQLLADMR	
5.8	2573.3006	-0.0039	AQKENSLQLQKAQLEQLLADMR	
5.4	2573.3006	-0.0039	AQKENSLQLQKAQLEQLLADMR	
5.0	2573.3006	-0.0039	AQKENSLQLQKAQLEQLLADMR	
2.5	2571.2978	1.9989	SIRIFVHFINSYMEKPTVAMR	
2.2	2571.2890	2.0077	VKTMEVTSVSIELEKNFSNFPR	
2.0	2571.2830	2.0137	HLSPQGPQLSHLQAQAALPGPHQR	

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

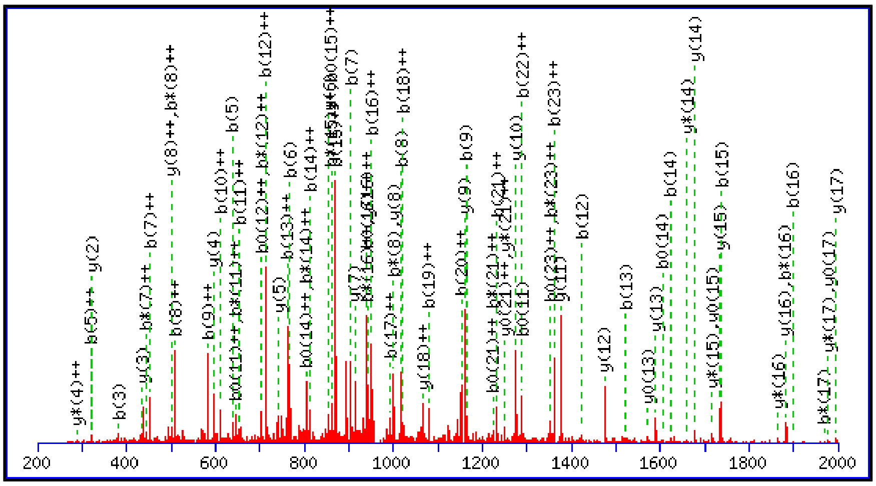
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILRQQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

Match to Query 26121: 2897.382912 from(966.801580,3+) intensity(83093.0703) rtinseconds(1646) scans(4144) index(26690)
Title: 111019_Est_MI_YS_G_09Spectrum3592_scans__4144
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

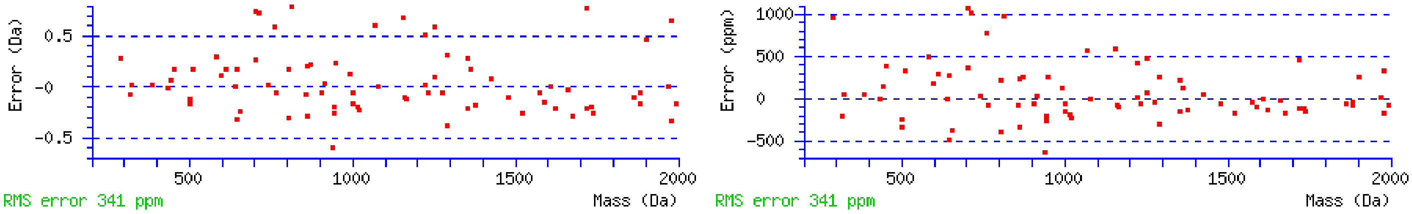
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2897.3701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 90 **Expect:** 2.4e-007
Matches : 79/238 fragment ions using 141 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**I**							**24**
2	227.1754	114.0913					**L**	2785.2933	1393.1503	2768.2668	1384.6370	2767.2828	1384.1450	**23**
3	**383.2765**	192.1419	366.2500	183.6286			**R**	2672.2093	1336.6083	2655.1827	1328.0950	2654.1987	1327.6030	**22**
4	511.3351	256.1712	494.3085	247.6579			**Q**	2516.1082	1258.5577	2499.0816	1250.0444	2498.0976	1249.5524	**21**
5	**639.3937**	***320.2005***	622.3671	311.6872			**Q**	2388.0496	1194.5284	2371.0230	1186.0152	2370.0390	1185.5231	**20**
6	**767.4522**	384.2298	750.4257	375.7165			**Q**	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	**19**
7	**904.5112**	***452.7592***	887.4846	444.2459			**H**	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	**18**
8	**1017.5952**	***509.3013***	1000.5687	500.7880			**L**	**1994.8735**	997.9404	1977.8470	989.4271	1976.8629	988.9351	**17**
9	**1164.6636**	***582.8355***	1147.6371	574.3222			**F**	**1881.7894**	941.3984	1864.7629	932.8851	1863.7789	932.3931	**16**
10	1221.6851	***611.3462***	1204.6586	602.8329			**G**	**1734.7210**	867.8642	1717.6945	859.3509	1716.7105	858.8589	**15**
11	1308.7171	***654.8622***	1291.6906	646.3489	1290.7066	645.8569	**S**	**1677.6996**	839.3534	1660.6730	830.8401	1659.6890	830.3481	**14**
12	**1423.7441**	***712.3757***	1406.7175	703.8624	1405.7335	703.3704	**N**	**1590.6675**	795.8374	1573.6410	787.3241	1572.6570	786.8321	**13**
13	**1522.8125**	***761.9099***	1505.7859	753.3966	1504.8019	752.9046	**V**	**1475.6406**	738.3239	1458.6140	729.8107	1457.6300	729.3187	**12**
14	**1623.8602**	***812.4337***	1606.8336	803.9204	1605.8496	803.4284	**T**	**1376.5722**	688.7897	1359.5456	680.2765	1358.5616	679.7844	**11**
15	**1738.8871**	***869.9472***	1721.8606	861.4339	1720.8765	860.9419	**D**	**1275.5245**	638.2659	1258.4980	629.7526	1257.5139	629.2606	**10**
16	**1898.9178**	***949.9625***	1881.8912	941.4492	1880.9072	940.9572	**C**	**1160.4976**	580.7524	1143.4710	572.2391	1142.4870	571.7471	**9**
17	1985.9498	***993.4785***	1968.9232	984.9653	1967.9392	984.4732	**S**	**1000.4669**	500.7371	983.4404	492.2238	982.4563	491.7318	**8**
18	2042.9713	***1021.9893***	2025.9447	1013.4760	2024.9607	1012.9840	**G**	**913.4349**	457.2211	896.4083	448.7078			**7**
19	2157.0142	***1079.0107***	2139.9876	1070.4975	2139.0036	1070.0054	**N**	**856.4134**	428.7103	839.3869	420.1971			**6**
20	2304.0826	***1152.5449***	2287.0560	1144.0317	2286.0720	1143.5397	**F**	**742.3705**	371.6889	725.3439	363.1756			**5**
21	2464.1132	***1232.5603***	2447.0867	1224.0470	2446.1027	1223.5550	**C**	**595.3021**	298.1547	578.2755	289.6414			**4**
22	2577.1973	***1289.1023***	2560.1708	1280.5890	2559.1867	1280.0970	**L**	**435.2714**	218.1394	418.2449	209.6261			**3**
23	2724.2657	***1362.6365***	2707.2392	1354.1232	2706.2552	1353.6312	**F**	**322.1874**	161.5973	305.1608	153.0840			**2**

24							**R**	175.1190	88.0631	158.0924	79.5498			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.2	2897.3701	0.0128	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated N12 53.17%
84.5	2897.3701	0.0128	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6 14.31%
84.5	2897.3701	0.0128	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4 14.28%
83.6	2897.3701	0.0128	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5 11.55%
81.2	2897.3701	0.0128	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated N19 6.69%
67.5	2896.3861	0.9968	ILRQQQHLFGSNVTDCSGNFCLFR	
8.3	2897.3851	-0.0022	VYELENRLQTETEQLNEIQKLMR	
5.3	2897.3800	0.0029	MNDDATQQLVHRTEVVMNNLSPAWK	
5.3	2897.3800	0.0029	MNDDATQQLVHRTEVVMNNLSPAWK	
4.3	2897.3930	-0.0101	SKSDGTLFALNNIENQIVFNQEERK	

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

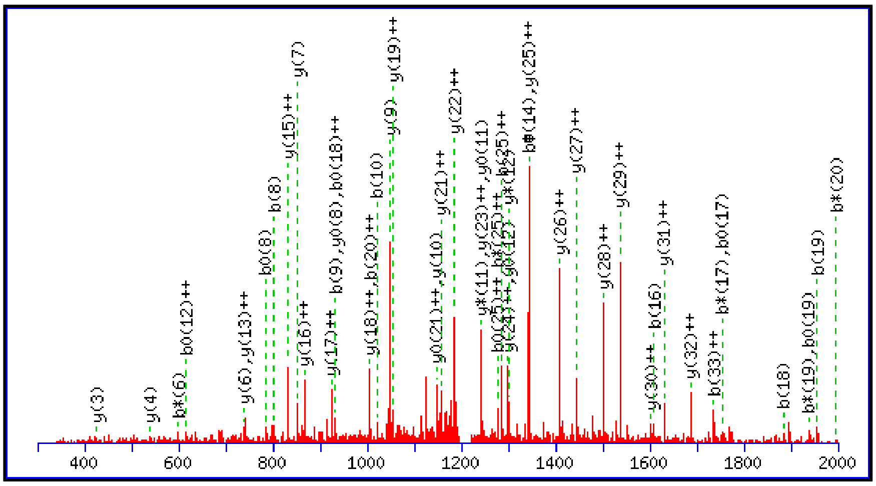
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IMNGEADAMSLDGGFVYIAGKCGLVPVLAENYNK**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

Match to Query 27831: 3616.740852 from(1206.587560,3+) intensity(24875.5430) rtinseconds(2463) scans(6535) index(16259)
Title: 111019_Est_MI_YP_G_05Spectrum5602_scans__6535
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

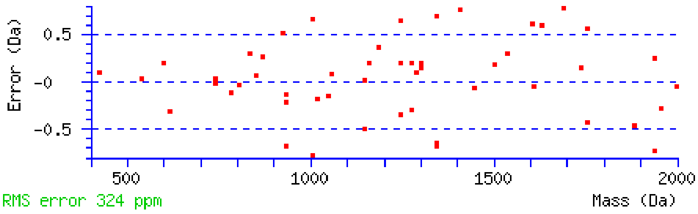
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

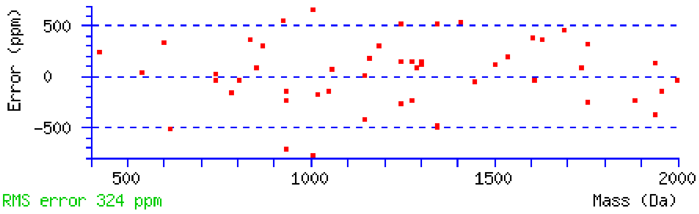


```
Monoisotopic mass of neutral peptide Mr(calc): 3616.7251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N33     : Deamidated (NQ)
Ions Score: 89  Expect: 2.9e-007
Matches : 52/376 fragment ions using 85 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							34
2	245.1318	123.0696					M	3504.6484	1752.8278	3487.6218	1744.3146	3486.6378	1743.8226	33
3	359.1748	180.0910	342.1482	171.5777			N	3373.6079	1687.3076	3356.5814	1678.7943	3355.5973	1678.3023	32
4	416.1962	208.6017	399.1697	200.0885			G	3259.5650	1630.2861	3242.5384	1621.7729	3241.5544	1621.2808	31
5	545.2388	273.1230	528.2123	264.6098	527.2282	264.1178	E	3202.5435	1601.7754	3185.5170	1593.2621	3184.5330	1592.7701	30
6	616.2759	308.6416	599.2494	300.1283	598.2654	299.6363	A	3073.5009	1537.2541	3056.4744	1528.7408	3055.4904	1528.2488	29
7	731.3029	366.1551	714.2763	357.6418	713.2923	357.1498	D	3002.4638	1501.7355	2985.4373	1493.2223	2984.4532	1492.7303	28
8	**802.3400**	401.6736	785.3134	393.1604	784.3294	392.6683	A	2887.4369	1444.2221	2870.4103	1435.7088	2869.4263	1435.2168	27
9	**933.3805**	467.1939	916.3539	458.6806	915.3699	458.1886	M	2816.3998	1408.7035	2799.3732	1400.1902	2798.3892	1399.6982	26
10	**1020.4125**	510.7099	1003.3859	502.1966	1002.4019	501.7046	S	2685.3593	1343.1833	2668.3327	1334.6700	2667.3487	1334.1780	25
11	1133.4966	567.2519	1116.4700	558.7386	1115.4860	558.2466	L	2598.3272	1299.6673	2581.3007	1291.1540	2580.3167	1290.6620	24
12	1248.5235	624.7654	1231.4970	616.2521	1230.5129	615.7601	D	2485.2432	1243.1252	2468.2166	1234.6120	2467.2326	1234.1199	23
13	1305.5450	653.2761	1288.5184	644.7628	1287.5344	644.2708	G	2370.2162	1185.6118	2353.1897	1177.0985	2352.2057	1176.6065	22
14	1362.5664	681.7869	1345.5399	673.2736	1344.5559	672.7816	G	2313.1948	1157.1010	2296.1682	1148.5877	2295.1842	1148.0957	21
15	1509.6348	755.3211	1492.6083	746.8078	1491.6243	746.3158	F	2256.1733	1128.5903	2239.1468	1120.0770	2238.1627	1119.5850	20
16	**1608.7033**	804.8553	1591.6767	796.3420	1590.6927	795.8500	V	2109.1049	1055.0561	2092.0783	1046.5428	2091.0943	1046.0508	19
17	1771.7666	886.3869	1754.7400	877.8737	1753.7560	877.3816	Y	2010.0365	1005.5219	1993.0099	997.0086	1992.0259	996.5166	18
18	**1884.8506**	942.9290	1867.8241	934.4157	1866.8401	933.9237	I	1846.9731	923.9902	1829.9466	915.4769	1828.9626	914.9849	17
19	**1955.8878**	978.4475	1938.8612	969.9342	1937.8772	969.4422	A	1733.8891	867.4482	1716.8625	858.9349	1715.8785	858.4429	16
20	2012.9092	1006.9583	1995.8827	998.4450	1994.8987	997.9530	G	1662.8520	831.9296	1645.8254	823.4163	1644.8414	822.9243	15
21	2141.0042	1071.0057	2123.9776	1062.4925	2122.9936	1062.0005	K	1605.8305	803.4189	1588.8040	794.9056	1587.8199	794.4136	14
22	2301.0348	1151.0211	2284.0083	1142.5078	2283.0243	1142.0158	C	1477.7355	739.3714	1460.7090	730.8581	1459.7250	730.3661	13
23	2358.0563	1179.5318	2341.0298	1171.0185	2340.0457	1170.5265	G	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	12

24	2471.1404	1236.0738	2454.1138	1227.5605	2453.1298	1227.0685	**L**	1260.6834	630.8454	1243.6569	622.3321	1242.6729	621.8401	**11**
25	2570.2088	1285.6080	2553.1822	1277.0948	2552.1982	1276.6027	**V**	**1147.5994**	574.3033	1130.5728	565.7900	1129.5888	565.2980	**10**
26	2667.2615	1334.1344	2650.2350	1325.6211	2649.2510	1325.1291	**P**	**1048.5310**	524.7691	1031.5044	516.2558	1030.5204	515.7638	**9**
27	2766.3300	1383.6686	2749.3034	1375.1553	2748.3194	1374.6633	**V**	951.4782	476.2427	934.4516	467.7295	933.4676	467.2374	**8**
28	2879.4140	1440.2106	2862.3875	1431.6974	2861.4035	1431.2054	**L**	**852.4098**	426.7085	835.3832	418.1953	834.3992	417.7032	**7**
29	2950.4511	1475.7292	2933.4246	1467.2159	2932.4406	1466.7239	**A**	**739.3257**	370.1665	722.2992	361.6532	721.3151	361.1612	**6**
30	3079.4937	1540.2505	3062.4672	1531.7372	3061.4832	1531.2452	**E**	668.2886	334.6479	651.2620	326.1347	650.2780	325.6427	**5**
31	3193.5367	1597.2720	3176.5101	1588.7587	3175.5261	1588.2667	**N**	**539.2460**	270.1266	522.2195	261.6134			**4**
32	3356.6000	1678.8036	3339.5734	1670.2904	3338.5894	1669.7983	**Y**	**425.2031**	213.1052	408.1765	204.5919			**3**
33	3471.6269	1736.3171	3454.6004	1727.8038	3453.6164	1727.3118	**N**	262.1397	131.5735	245.1132	123.0602			**2**
34							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.3	3616.7251	0.0157	IMNGEADAMSLDGGFVYIAGKCGLVPVLAENYNK	Deamidated N33 58.38%
87.8	3616.7251	0.0157	IMNGEADAMSLDGGFVYIAGKCGLVPVLAENYNK	Deamidated N31 41.62%
53.8	3615.7411	0.9997	IMNGEADAMSLDGGFVYIAGKCGLVPVLAENYNK	
47.6	3616.7251	0.0157	IMNGEADAMSLDGGFVYIAGKCGLVPVLAENYNK	Deamidated N3 0.00%
3.6	3616.7290	0.0118	LVCNLSRKVWIYQDSNTGVSHCEEGPQIPTK	
3.6	3615.7501	0.9908	AIGEKEKLYTLEAASNISLLDAGQNQCSVYAEK	
3.6	3615.7501	0.9908	AIGEKEKLYTLEAASNISLLDAGQNQCSVYAEK	
3.6	3615.7501	0.9908	AIGEKEKLYTLEAASNISLLDAGQNQCSVYAEK	
3.6	3615.7501	0.9908	AIGEKEKLYTLEAASNISLLDAGQNQCSVYAEK	
3.3	3616.7290	0.0118	LVCNLSRKVWIYQDSNTGVSHCEEGPQIPTK	

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

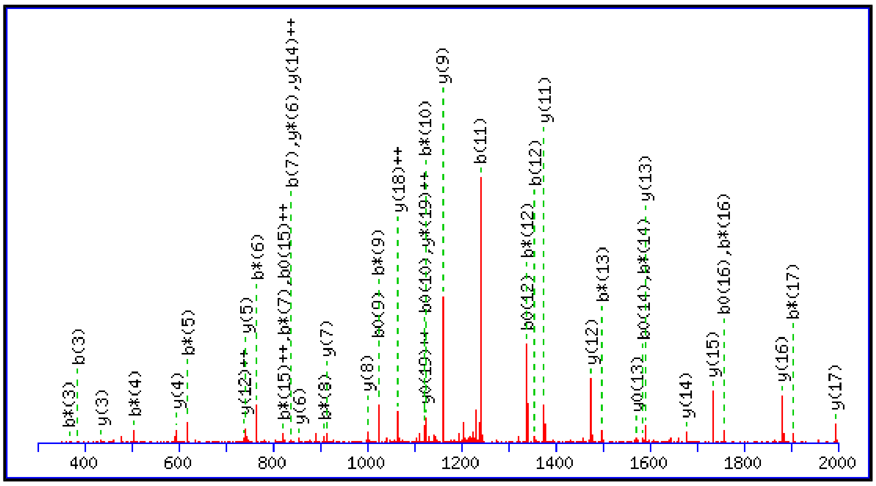
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

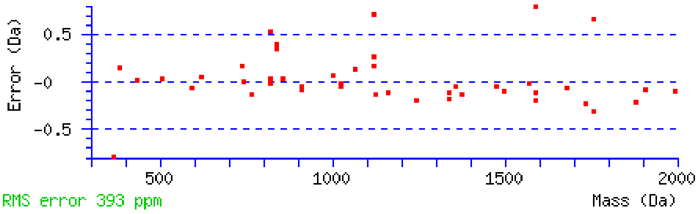
Match to Query 21662: 2515.109248 from(1258.561900,2+) intensity(36848.5430) rtinseconds(1870) scans(4780) index(24658)
Title: 111019_Est_MI_YS_G_06Spectrum4153_scans__4780
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

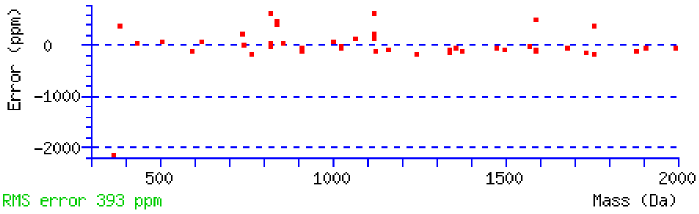
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2515.1009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 85 **Expect:** 3.7e-007
Matches : 45/212 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	129.0659	65.0366	112.0393	56.5233			Q							21
2	257.1244	129.0659	240.0979	120.5526			Q	2388.0496	1194.5284	2371.0230	1186.0152	2370.0390	1185.5231	20
3	**385.1830**	193.0951	368.1565	184.5819			Q	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	19
4	522.2419	261.6246	505.2154	253.1113			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
5	635.3260	318.1666	618.2994	309.6534			L	***1994.8735***	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
6	782.3944	391.7008	765.3679	383.1876			F	***1881.7894***	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
7	**839.4159**	420.2116	822.3893	411.6983			G	***1734.7210***	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
8	926.4479	463.7276	909.4213	455.2143	908.4373	454.7223	S	***1677.6996***	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
9	1041.4748	521.2411	1024.4483	512.7278	1023.4643	512.2358	N	***1590.6675***	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
10	1140.5432	570.7753	1123.5167	562.2620	1122.5327	561.7700	V	***1475.6406***	738.3239	1458.6140	729.8107	1457.6300	729.3187	12
11	**1241.5909**	621.2991	1224.5644	612.7858	1223.5804	612.2938	T	***1376.5722***	688.7897	1359.5456	680.2765	1358.5616	679.7844	11
12	**1356.6179**	678.8126	1339.5913	670.2993	1338.6073	669.8073	D	1275.5245	638.2659	1258.4980	629.7526	1257.5139	629.2606	10
13	1516.6485	758.8279	1499.6220	750.3146	1498.6380	749.8226	C	***1160.4976***	580.7524	1143.4710	572.2391	1142.4870	571.7471	9
14	1603.6805	802.3439	1586.6540	793.8306	1585.6700	793.3386	S	***1000.4669***	500.7371	983.4404	492.2238	982.4563	491.7318	8
15	1660.7020	830.8546	1643.6755	822.3414	1642.6914	821.8494	G	***913.4349***	457.2211	896.4083	448.7078			7
16	1774.7449	887.8761	1757.7184	879.3628	1756.7344	878.8708	N	***856.4134***	428.7103	839.3869	420.1971			6
17	1921.8134	961.4103	1904.7868	952.8970	1903.8028	952.4050	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2081.8440	1041.4256	2064.8175	1032.9124	2063.8334	1032.4204	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2194.9281	1097.9677	2177.9015	1089.4544	2176.9175	1088.9624	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2341.9965	1171.5019	2324.9699	1162.9886	2323.9859	1162.4966	F	322.1874	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.0	2515.1009	0.0083	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9 99.95%
46.9	2515.1009	0.0083	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3 0.02%
46.9	2515.1009	0.0083	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2 0.02%
46.9	2515.1009	0.0083	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1 0.02%
42.7	2515.1009	0.0083	QQQHLFGSNVTDCSGNFCLFR	Deamidated N16 0.01%
40.9	2514.1169	0.9923	QQQHLFGSNVTDCSGNFCLFR	
5.0	2515.1161	-0.0069	NRYSLDYHQHCRQYFPLSM	
1.1	2515.1148	-0.0055	YVLQDARDNDFGSFHIMGGPMK	
0.6	2515.1148	-0.0055	YVLQDARDNDFGSFHIMGGPMK	

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

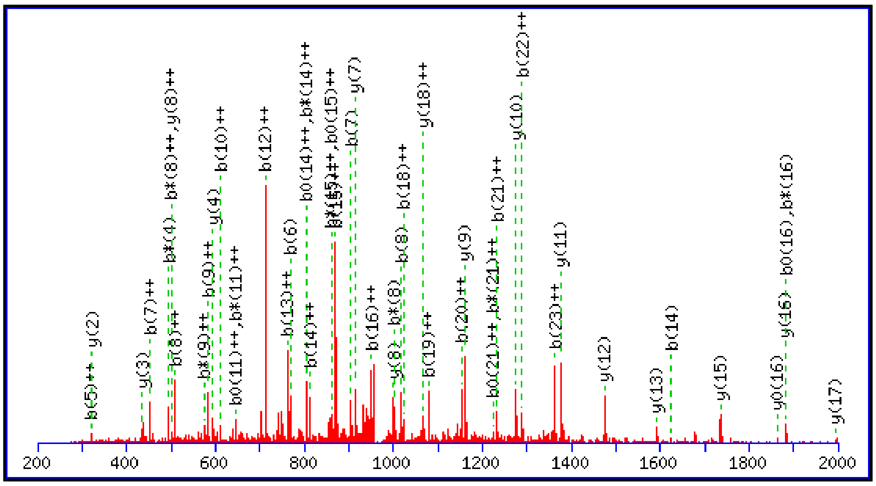
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILRQQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

Match to Query 26149: 2898.365712 from(967.129180,3+) intensity(47065.1914) rtinseconds(1831) scans(4456) index(10201)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum3786_scans__4456
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

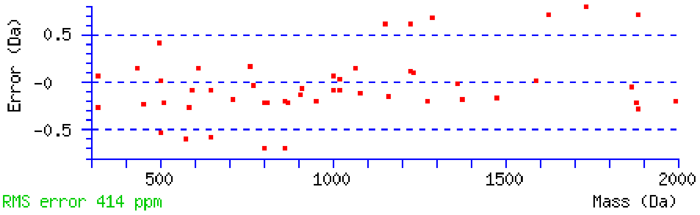
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

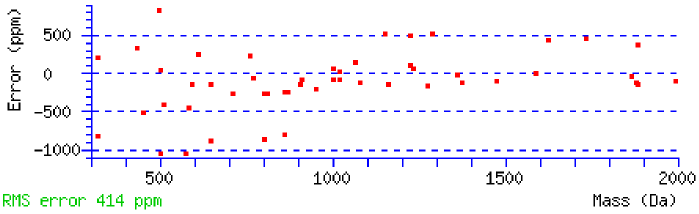


Monoisotopic mass of neutral peptide Mr(calc): 2898.3541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 78 **Expect:** 3.4e-006
Matches : 50/238 fragment ions using 107 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							24
2	227.1754	114.0913					L	2786.2773	1393.6423	2769.2508	1385.1290	2768.2668	1384.6370	23
3	383.2765	192.1419	366.2500	183.6286			R	2673.1933	1337.1003	2656.1667	1328.5870	2655.1827	1328.0950	22
4	512.3191	256.6632	495.2926	248.1499			Q	2517.0922	1259.0497	2500.0656	1250.5364	2499.0816	1250.0444	21
5	640.3777	***320.6925***	623.3511	312.1792			Q	2388.0496	1194.5284	2371.0230	1186.0152	2370.0390	1185.5231	20
6	**768.4363**	384.7218	751.4097	376.2085			Q	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	19
7	**905.4952**	***453.2512***	888.4686	444.7380			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
8	**1018.5792**	***509.7933***	1001.5527	501.2800			L	**1994.8735**	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
9	1165.6477	***583.3275***	1148.6211	574.8142			F	**1881.7894**	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
10	1222.6691	***611.8382***	1205.6426	603.3249			G	**1734.7210**	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
11	1309.7011	655.3542	1292.6746	646.8409	1291.6906	646.3489	S	1677.6996	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
12	1424.7281	***712.8677***	1407.7015	704.3544	1406.7175	703.8624	N	**1590.6675**	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
13	1523.7965	***762.4019***	1506.7700	753.8886	1505.7859	753.3966	V	**1475.6406**	738.3239	1458.6140	729.8107	1457.6300	729.3187	12
14	**1624.8442**	***812.9257***	1607.8176	804.4125	1606.8336	803.9204	T	**1376.5722**	688.7897	1359.5456	680.2765	1358.5616	679.7844	11
15	1739.8711	***870.4392***	1722.8446	861.9259	1721.8606	861.4339	D	**1275.5245**	638.2659	1258.4980	629.7526	1257.5139	629.2606	10
16	1899.9018	***950.4545***	1882.8752	941.9413	1881.8912	941.4492	C	**1160.4976**	580.7524	1143.4710	572.2391	1142.4870	571.7471	9
17	1986.9338	993.9705	1969.9073	985.4573	1968.9232	984.9653	S	**1000.4669**	500.7371	983.4404	492.2238	982.4563	491.7318	8
18	2043.9553	***1022.4813***	2026.9287	1013.9680	2025.9447	1013.4760	G	**913.4349**	457.2211	896.4083	448.7078			7
19	2157.9982	***1079.5027***	2140.9716	1070.9895	2139.9876	1070.4975	N	856.4134	428.7103	839.3869	420.1971			6
20	2305.0666	***1153.0369***	2288.0401	1144.5237	2287.0560	1144.0317	F	742.3705	371.6889	725.3439	363.1756			5
21	2465.0973	***1233.0523***	2448.0707	1224.5390	2447.0867	1224.0470	C	**595.3021**	298.1547	578.2755	289.6414			4
22	2578.1813	***1289.5943***	2561.1548	1281.0810	2560.1708	1280.5890	L	**435.2714**	218.1394	418.2449	209.6261			3

23	2725.2497	***1363.1285***	2708.2232	1354.6152	2707.2392	1354.1232	**F**	**322.1874**	161.5973	305.1608	153.0840			**2**
24							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.4	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, N12 36.70%
77.3	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6, N12 28.49%
77.3	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, N12 28.49%
65.4	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, N19 1.82%
64.4	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, N19 1.45%
63.5	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6, N19 1.17%
60.0	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, Q6 0.53%
59.9	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, Q6 0.52%
59.6	2898.3541	0.0116	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, Q5 0.49%
58.9	2897.3701	0.9956	ILRQQQHLFGSNVTDCSGNFCLFR	

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

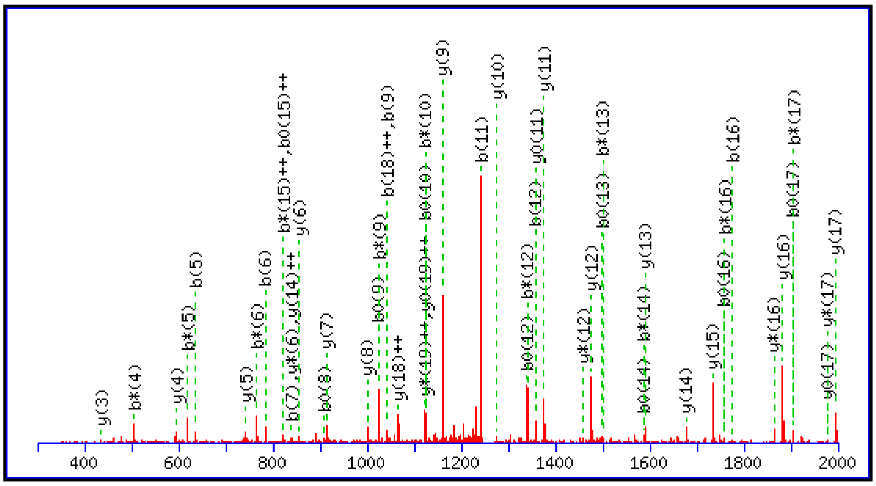
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

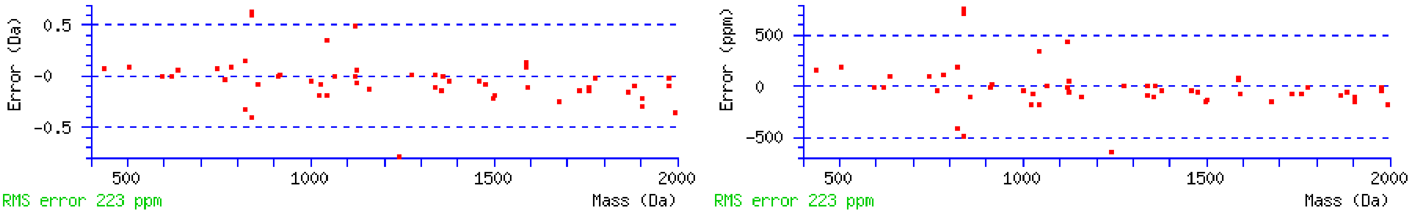
Match to Query 21801: 2516.093588 from(1259.054070,2+) intensity(29714.0586) rtinseconds(1887) scans(4901) index(15977)
Title: 111019_Est_MI_YP_G_05Spectrum4159_scans__4901
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2516.0849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 75 **Expect:** 2.7e-006
Matches : 53/212 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							21
2	257.1244	129.0659	240.0979	120.5526			Q	2389.0336	1195.0204	2372.0070	1186.5072	2371.0230	1186.0152	20
3	386.1670	193.5872	369.1405	185.0739			Q	2260.9750	1130.9911	2243.9485	1122.4779	2242.9645	1121.9859	19
4	523.2259	262.1166	506.1994	253.6033			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
5	**636.3100**	318.6586	619.2835	310.1454			L	***1994.8735***	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
6	**783.3784**	392.1928	766.3519	383.6796			F	***1881.7894***	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
7	**840.3999**	420.7036	823.3733	412.1903			G	***1734.7210***	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
8	927.4319	464.2196	910.4054	455.7063	909.4213	455.2143	S	***1677.6996***	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
9	**1042.4589**	521.7331	1025.4323	513.2198	1024.4483	512.7278	N	***1590.6675***	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
10	1141.5273	571.2673	1124.5007	562.7540	1123.5167	562.2620	V	***1475.6406***	738.3239	1458.6140	729.8107	1457.6300	729.3187	12
11	**1242.5749**	621.7911	1225.5484	613.2778	1224.5644	612.7858	T	***1376.5722***	688.7897	1359.5456	680.2765	1358.5616	679.7844	11
12	**1357.6019**	679.3046	1340.5753	670.7913	1339.5913	670.2993	D	***1275.5245***	638.2659	1258.4980	629.7526	1257.5139	629.2606	10
13	1517.6325	759.3199	1500.6060	750.8066	1499.6220	750.3146	C	***1160.4976***	580.7524	1143.4710	572.2391	1142.4870	571.7471	9
14	1604.6646	802.8359	1587.6380	794.3226	1586.6540	793.8306	S	***1000.4669***	500.7371	983.4404	492.2238	982.4563	491.7318	8
15	1661.6860	831.3467	1644.6595	822.8334	1643.6755	822.3414	G	***913.4349***	457.2211	896.4083	448.7078			7
16	**1775.7290**	888.3681	1758.7024	879.8548	1757.7184	879.3628	N	***856.4134***	428.7103	839.3869	420.1971			6
17	1922.7974	961.9023	1905.7708	953.3890	1904.7868	952.8970	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2082.8280	1041.9176	2065.8015	1033.4044	2064.8175	1032.9124	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2195.9121	1098.4597	2178.8855	1089.9464	2177.9015	1089.4544	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2342.9805	1171.9939	2325.9539	1163.4806	2324.9699	1162.9886	F	322.1874	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N9 32.88%
75.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N9 32.88%
75.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N9 32.88%
56.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N16 0.42%
56.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N16 0.42%
56.2	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N16 0.42%
53.6	2515.1009	0.9927	QQQHLFGSNVTDCSGNFCLFR	
46.7	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9, N16 0.05%
42.5	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, Q3 0.02%
42.5	2516.0849	0.0087	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, Q3 0.02%

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

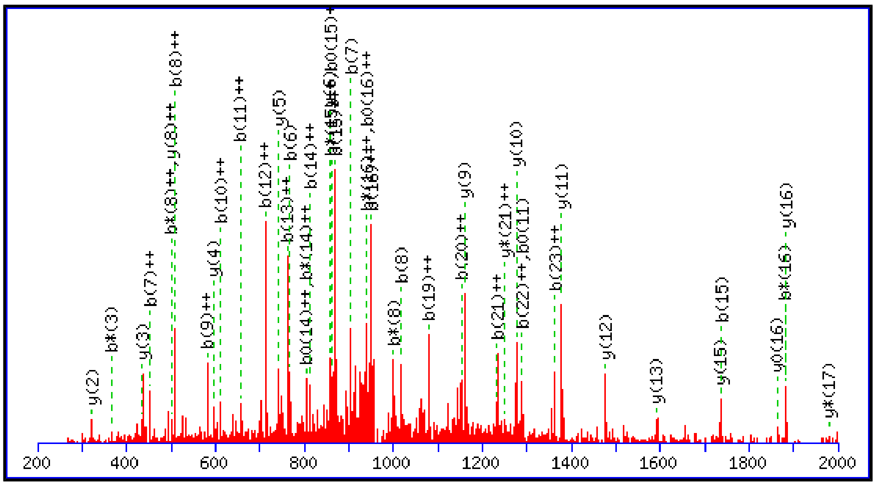
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILRQQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

Match to Query 26144: 2898.351642 from(967.124490,3+) intensity(28517.1113) rtinseconds(1817) scans(4575) index(11040)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum3873_scans__4575
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

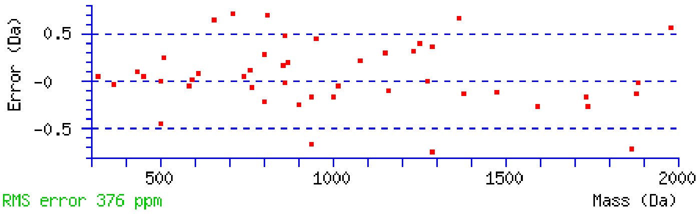
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

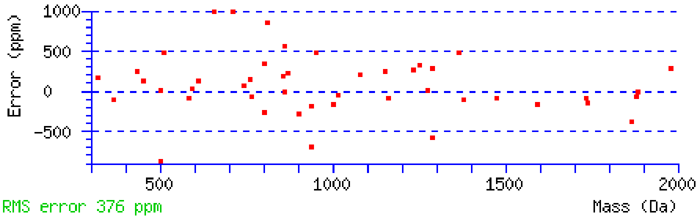


```
Monoisotopic mass of neutral peptide Mr(calc): 2898.3541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12     : Deamidated (NQ)
N19     : Deamidated (NQ)
Ions Score: 69  Expect: 2.7e-005
Matches : 46/238 fragment ions using 90 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							24
2	227.1754	114.0913					L	2786.2773	1393.6423	2769.2508	1385.1290	2768.2668	1384.6370	23
3	383.2765	192.1419	366.2500	183.6286			R	2673.1933	1337.1003	2656.1667	1328.5870	2655.1827	1328.0950	22
4	511.3351	256.1712	494.3085	247.6579			Q	2517.0922	1259.0497	2500.0656	1250.5364	2499.0816	1250.0444	21
5	639.3937	320.2005	622.3671	311.6872			Q	2389.0336	1195.0204	2372.0070	1186.5072	2371.0230	1186.0152	20
6	**767.4522**	384.2298	750.4257	375.7165			Q	2260.9750	1130.9911	2243.9485	1122.4779	2242.9645	1121.9859	19
7	**904.5112**	***452.7592***	887.4846	444.2459			H	2132.9164	1066.9619	2115.8899	1058.4486	2114.9059	1057.9566	18
8	**1017.5952**	***509.3013***	1000.5687	500.7880			L	1995.8575	998.4324	1978.8310	989.9191	1977.8470	989.4271	17
9	1164.6636	***582.8355***	1147.6371	574.3222			F	**1882.7735**	941.8904	1865.7469	933.3771	1864.7629	932.8851	16
10	1221.6851	***611.3462***	1204.6586	602.8329			G	**1735.7050**	868.3562	1718.6785	859.8429	1717.6945	859.3509	15
11	1308.7171	***654.8622***	1291.6906	646.3489	1290.7066	645.8569	S	1678.6836	839.8454	1661.6570	831.3322	1660.6730	830.8401	14
12	1423.7441	***712.3757***	1406.7175	703.8624	1405.7335	703.3704	N	**1591.6516**	796.3294	1574.6250	787.8161	1573.6410	787.3241	13
13	1522.8125	***761.9099***	1505.7859	753.3966	1504.8019	752.9046	V	**1476.6246**	738.8159	1459.5981	730.3027	1458.6140	729.8107	12
14	1623.8602	***812.4337***	1606.8336	803.9204	1605.8496	803.4284	T	**1377.5562**	689.2817	1360.5296	680.7685	1359.5456	680.2765	11
15	**1738.8871**	***869.9472***	1721.8606	861.4339	1720.8765	860.9419	D	**1276.5085**	638.7579	1259.4820	630.2446	1258.4980	629.7526	10
16	1898.9178	***949.9625***	1881.8912	941.4492	1880.9072	940.9572	C	**1161.4816**	581.2444	1144.4550	572.7312	1143.4710	572.2391	9
17	1985.9498	993.4785	1968.9232	984.9653	1967.9392	984.4732	S	1001.4509	501.2291	984.4244	492.7158	983.4404	492.2238	8
18	2042.9713	1021.9893	2025.9447	1013.4760	2024.9607	1012.9840	G	914.4189	457.7131	897.3924	449.1998			7
19	2157.9982	***1079.5027***	2140.9716	1070.9895	2139.9876	1070.4975	N	**857.3974**	429.2024	840.3709	420.6891			6
20	2305.0666	***1153.0369***	2288.0401	1144.5237	2287.0560	1144.0317	F	**742.3705**	371.6889	725.3439	363.1756			5
21	2465.0973	***1233.0523***	2448.0707	1224.5390	2447.0867	1224.0470	C	**595.3021**	298.1547	578.2755	289.6414			4
22	2578.1813	***1289.5943***	2561.1548	1281.0810	2560.1708	1280.5890	L	**435.2714**	218.1394	418.2449	209.6261			3

23	2725.2497	***1363.1285***	2708.2232	1354.6152	2707.2392	1354.1232	**F**	**322.1874**	161.5973	305.1608	153.0840			**2**
24							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.9	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated N12, N19 79.83%
55.4	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6, N19 3.56%
55.1	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, N19 3.39%
55.1	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, N19 3.39%
54.9	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6, N12 3.17%
54.9	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, N12 3.17%
54.9	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, N12 3.17%
40.2	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5, Q6 0.11%
40.2	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, Q6 0.11%
40.2	2898.3541	-0.0025	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4, Q5 0.11%

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

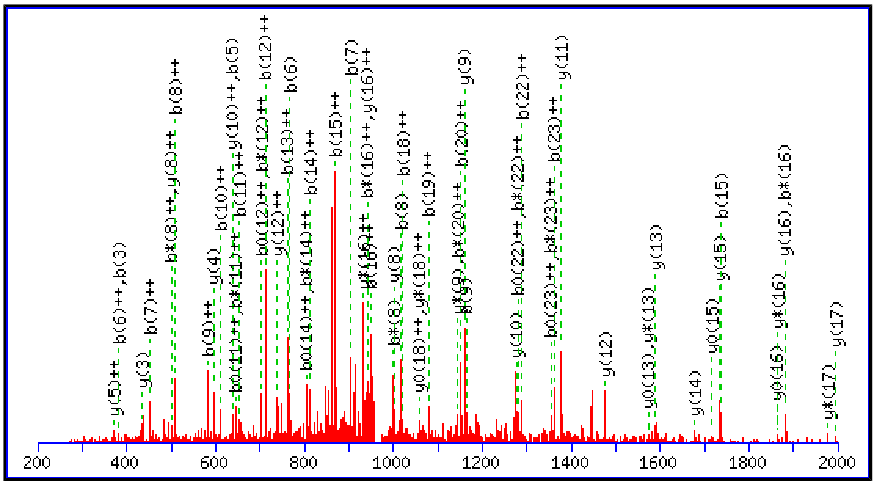
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILRQQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

Match to Query 26119: 2897.382852 from(966.801560,3+) intensity(24861.1074) rtinseconds(1747) scans(4576) index(4447)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3881_scans__4576
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

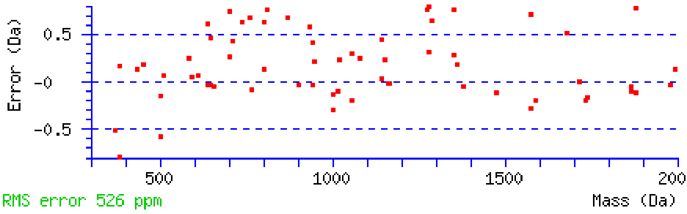
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

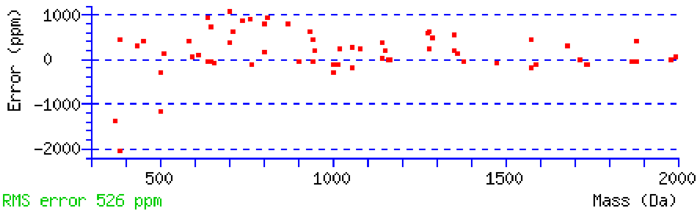


Monoisotopic mass of neutral peptide Mr(calc): 2897.3701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
Ions Score: 66 **Expect:** 5.8e-005
Matches : 65/238 fragment ions using 123 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.0913	57.5493					I							24
2	227.1754	114.0913					L	2785.2933	1393.1503	2768.2668	1384.6370	2767.2828	1384.1450	23
3	**383.2765**	192.1419	366.2500	183.6286			R	2672.2093	1336.6083	2655.1827	1328.0950	2654.1987	1327.6030	22
4	511.3351	256.1712	494.3085	247.6579			Q	2516.1082	1258.5577	2499.0816	1250.0444	2498.0976	1249.5524	21
5	**639.3937**	320.2005	622.3671	311.6872			Q	2388.0496	1194.5284	2371.0230	1186.0152	2370.0390	1185.5231	20
6	**767.4522**	***384.2298***	750.4257	375.7165			Q	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	19
7	**904.5112**	***452.7592***	887.4846	444.2459			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
8	**1017.5952**	***509.3013***	1000.5687	500.7880			L	**1994.8735**	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
9	**1164.6636**	***582.8355***	1147.6371	574.3222			F	**1881.7894**	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
10	1221.6851	***611.3462***	1204.6586	602.8329			G	**1734.7210**	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
11	1308.7171	***654.8622***	1291.6906	646.3489	1290.7066	645.8569	S	**1677.6996**	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
12	1422.7601	***711.8837***	1405.7335	703.3704	1404.7495	702.8784	N	**1590.6675**	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
13	1521.8285	***761.4179***	1504.8019	752.9046	1503.8179	752.4126	V	**1476.6246**	738.8159	1459.5981	730.3027	1458.6140	729.8107	12
14	1622.8762	***811.9417***	1605.8496	803.4284	1604.8656	802.9364	T	**1377.5562**	689.2817	1360.5296	680.7685	1359.5456	680.2765	11
15	**1737.9031**	***869.4552***	1720.8765	860.9419	1719.8925	860.4499	D	**1276.5085**	638.7579	1259.4820	630.2446	1258.4980	629.7526	10
16	1897.9337	***949.4705***	1880.9072	940.9572	1879.9232	940.4652	C	**1161.4816**	581.2444	1144.4550	572.7312	1143.4710	572.2391	9
17	1984.9658	992.9865	1967.9392	984.4732	1966.9552	983.9812	S	**1001.4509**	501.2291	984.4244	492.7158	983.4404	492.2238	8
18	2041.9872	***1021.4973***	2024.9607	1012.9840	2023.9767	1012.4920	G	914.4189	457.7131	897.3924	449.1998			7
19	2157.0142	***1079.0107***	2139.9876	1070.4975	2139.0036	1070.0054	N	857.3974	429.2024	840.3709	420.6891			6
20	2304.0826	***1152.5449***	2287.0560	1144.0317	2286.0720	1143.5397	F	742.3705	371.6889	725.3439	363.1756			5
21	2464.1132	1232.5603	2447.0867	1224.0470	2446.1027	1223.5550	C	**595.3021**	298.1547	578.2755	289.6414			4
22	2577.1973	***1289.1023***	2560.1708	1280.5890	2559.1867	1280.0970	L	**435.2714**	218.1394	418.2449	209.6261			3
23	2724.2657	***1362.6365***	2707.2392	1354.1232	2706.2552	1353.6312	F	322.1874	161.5973	305.1608	153.0840			2

24							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.4	2897.3701	0.0127	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated N19 49.58%
66.0	2897.3701	0.0127	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated N12 45.43%
53.1	2897.3701	0.0127	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q4 2.33%
52.4	2897.3701	0.0127	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q5 1.96%
48.9	2896.3861	0.9967	ILRQQQHLFGSNVTDCSGNFCLFR	
48.0	2897.3701	0.0127	ILRQQQHLFGSNVTDCSGNFCLFR	Deamidated Q6 0.71%
8.8	2897.3825	0.0004	KIPAVGRELAGAGSDGGGGNELPAEATGEAM	
8.4	2897.3800	0.0029	MNDDATQQLVHRTEVVMNNLSPAWK	
8.4	2897.3800	0.0029	MNDDATQQLVHRTEVVMNNLSPAWK	
8.2	2896.3697	1.0132	ADIMFLVDSSGSIGPENFSKMKTFMK	

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

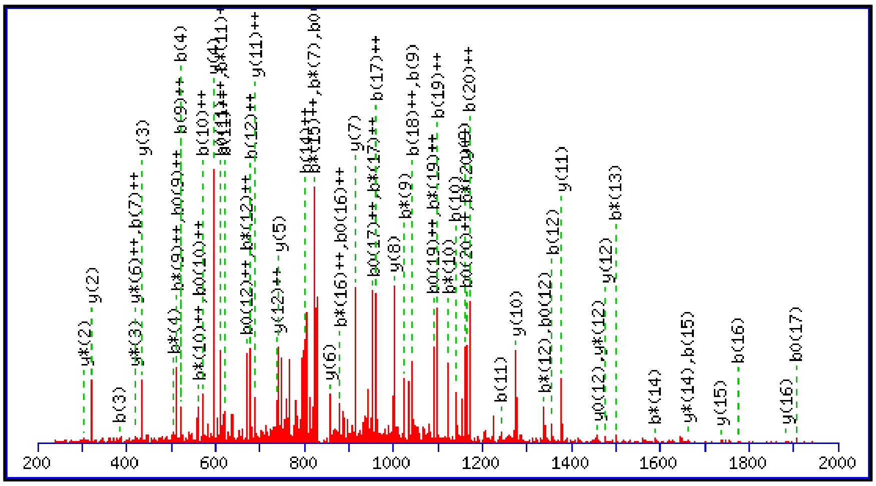
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

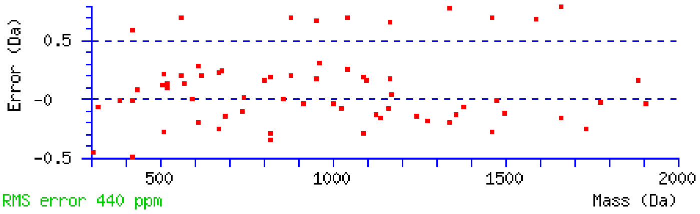
Match to Query 21799: 2516.091552 from(839.704460,3+) intensity(104068.3750) rtinseconds(1982) scans(5052) index(25487)
Title: 111019_Est_MI_YS_G_07Spectrum4314_scans__5052
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

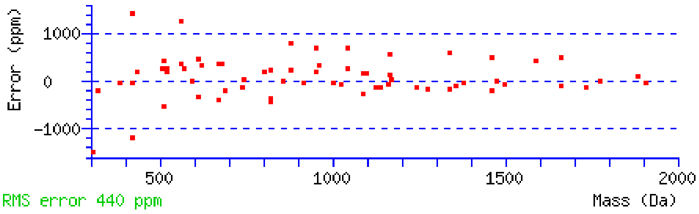
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2516.0849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N16 : Deamidated (NQ)
Ions Score: 60 **Expect:** 7.7e-005
Matches : 66/212 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							21
2	257.1244	129.0659	240.0979	120.5526			Q	2389.0336	1195.0204	2372.0070	1186.5072	2371.0230	1186.0152	20
3	**385.1830**	193.0951	368.1565	184.5819			Q	2260.9750	1130.9911	2243.9485	1122.4779	2242.9645	1121.9859	19
4	**522.2419**	261.6246	505.2154	253.1113			H	2132.9164	1066.9619	2115.8899	1058.4486	2114.9059	1057.9566	18
5	635.3260	318.1666	618.2994	309.6534			L	1995.8575	998.4324	1978.8310	989.9191	1977.8470	989.4271	17
6	782.3944	391.7008	765.3679	383.1876			F	***1882.7735***	941.8904	1865.7469	933.3771	1864.7629	932.8851	16
7	839.4159	**420.2116**	822.3893	411.6983			G	***1735.7050***	868.3562	1718.6785	859.8429	1717.6945	859.3509	15
8	926.4479	463.7276	909.4213	455.2143	908.4373	454.7223	S	1678.6836	839.8454	1661.6570	831.3322	1660.6730	830.8401	14
9	**1041.4748**	**521.2411**	1024.4483	512.7278	1023.4643	512.2358	N	1591.6516	796.3294	1574.6250	787.8161	1573.6410	787.3241	13
10	**1140.5432**	**570.7753**	1123.5167	562.2620	1122.5327	561.7700	V	***1476.6246***	738.8159	1459.5981	730.3027	1458.6140	729.8107	12
11	**1241.5909**	**621.2991**	1224.5644	612.7858	1223.5804	612.2938	T	***1377.5562***	689.2817	1360.5297	680.7685	1359.5456	680.2765	11
12	**1356.6179**	**678.8126**	1339.5913	670.2993	1338.6073	669.8073	D	***1276.5085***	638.7579	1259.4820	630.2446	1258.4980	629.7526	10
13	1516.6485	758.8279	1499.6220	750.3146	1498.6380	749.8226	C	***1161.4816***	581.2444	1144.4550	572.7312	1143.4710	572.2391	9
14	1603.6805	**802.3439**	1586.6540	793.8306	1585.6700	793.3386	S	***1001.4509***	501.2291	984.4244	492.7158	983.4404	492.2238	8
15	**1660.7020**	830.8546	1643.6755	822.3414	1642.6914	821.8494	G	***914.4189***	457.7131	897.3924	449.1998			7
16	**1775.7290**	888.3681	1758.7024	879.8548	1757.7184	879.3628	N	***857.3974***	429.2024	840.3709	420.6891			6
17	1922.7974	**961.9023**	1905.7708	953.3890	1904.7868	952.8970	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2082.8280	**1041.9176**	2065.8015	1033.4044	2064.8175	1032.9124	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2195.9121	**1098.4597**	2178.8855	1089.9464	2177.9015	1089.4544	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2342.9805	**1171.9939**	2325.9539	1163.4806	2324.9699	1162.9886	F	***322.1874***	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.4	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9, N16 37.81%
57.8	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N16 20.64%
57.8	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N16 20.64%
57.8	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N16 20.64%
41.3	2515.1009	0.9906	QQQHLFGSNVTDCSGNFCLFR	
33.9	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N9 0.08%
33.9	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N9 0.08%
33.9	2516.0849	0.0066	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N9 0.08%
32.5	2515.1009	0.9906	QQQHLFGSNVTDCSGNFCLFR	
24.8	2515.1009	0.9906	QQQHLFGSNVTDCSGNFCLFR	

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

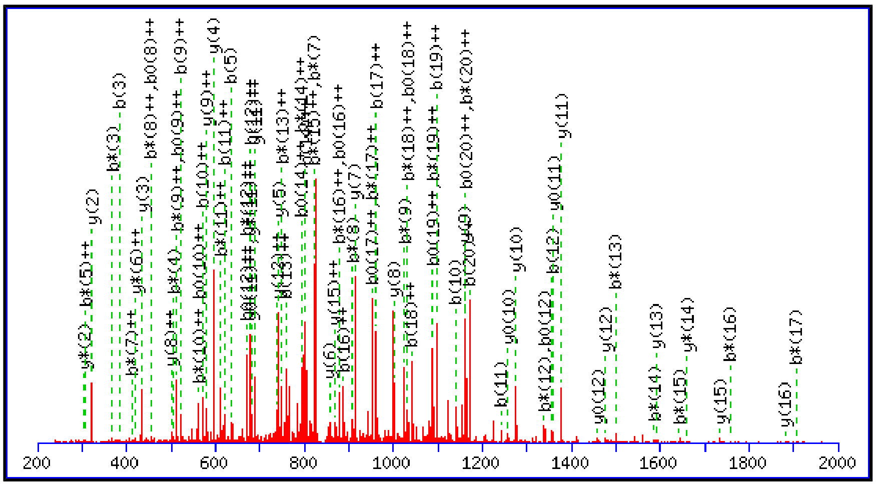
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

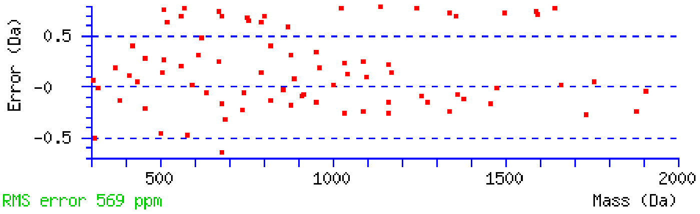
Match to Query 21632: 2515.107822 from(839.376550,3+) intensity(1010477.7500) rtinseconds(1856) scans(4741) index(24647)
Title: 111019_Est_MI_YS_G_06Spectrum4118_scans__4741
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

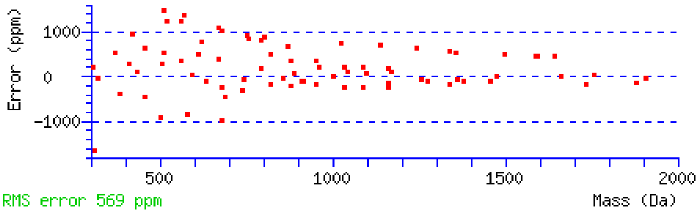
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2515.1009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16     : Deamidated (NQ)
Ions Score: 55  Expect: 0.00036
Matches : 80/212 fragment ions using 154 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							21
2	257.1244	129.0659	240.0979	120.5526			Q	2388.0496	1194.5284	2371.0230	1186.0152	2370.0390	1185.5231	20
3	**385.1830**	193.0951	368.1565	184.5819			Q	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	19
4	522.2419	261.6246	505.2154	253.1113			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
5	**635.3260**	318.1666	618.2994	309.6534			L	1994.8735	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
6	782.3944	391.7008	765.3679	383.1876			F	***1881.7894***	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
7	839.4159	420.2116	822.3893	411.6983			G	***1734.7210***	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
8	926.4479	463.7276	909.4213	455.2143	908.4373	454.7223	S	1677.6996	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
9	1040.4908	**520.7490**	1023.4643	512.2358	1022.4803	511.7438	N	***1590.6675***	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
10	**1139.5592**	**570.2833**	1122.5327	561.7700	1121.5487	561.2780	V	***1476.6246***	738.8159	1459.5981	730.3027	1458.6140	729.8107	12
11	**1240.6069**	**620.8071**	1223.5804	612.2938	1222.5963	611.8018	T	***1377.5562***	689.2817	1360.5297	680.7685	1359.5456	680.2765	11
12	**1355.6339**	**678.3206**	1338.6073	669.8073	1337.6233	669.3153	D	***1276.5085***	638.7579	1259.4820	630.2446	1258.4980	629.7526	10
13	1515.6645	**758.3359**	1498.6380	749.8226	1497.6539	749.3306	C	***1161.4816***	581.2444	1144.4550	572.7312	1143.4710	572.2391	9
14	1602.6965	**801.8519**	1585.6700	793.3386	1584.6860	792.8466	S	***1001.4509***	501.2291	984.4244	492.7158	983.4404	492.2238	8
15	1659.7180	830.3626	1642.6914	821.8494	1641.7074	821.3574	G	***914.4189***	457.7131	897.3924	449.1998			7
16	1774.7449	**887.8761**	1757.7184	879.3628	1756.7344	878.8708	N	***857.3974***	429.2024	840.3709	420.6891			6
17	1921.8134	**961.4103**	1904.7868	952.8970	1903.8028	952.4050	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2081.8440	**1041.4256**	2064.8175	1032.9124	2063.8334	1032.4204	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2194.9281	**1097.9677**	2177.9015	1089.4544	2176.9175	1088.9624	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2341.9965	**1171.5019**	2324.9699	1162.9886	2323.9859	1162.4966	F	***322.1874***	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.0	2515.1009	0.0069	QQQHLFGSNVTDCSGNFCLFR	Deamidated N16 63.49%
50.8	2515.1009	0.0069	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9 23.70%
43.3	2515.1009	0.0069	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3 4.27%
43.3	2515.1009	0.0069	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2 4.27%
43.3	2515.1009	0.0069	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1 4.27%
34.6	2514.1169	0.9909	QQQHLFGSNVTDCSGNFCLFR	
2.0	2514.0978	1.0101	HCNVVKTMQFEPSTAVYDACR	
0.1	2513.0938	2.0141	WATEASAVEQTAESCEVQEMLK	

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

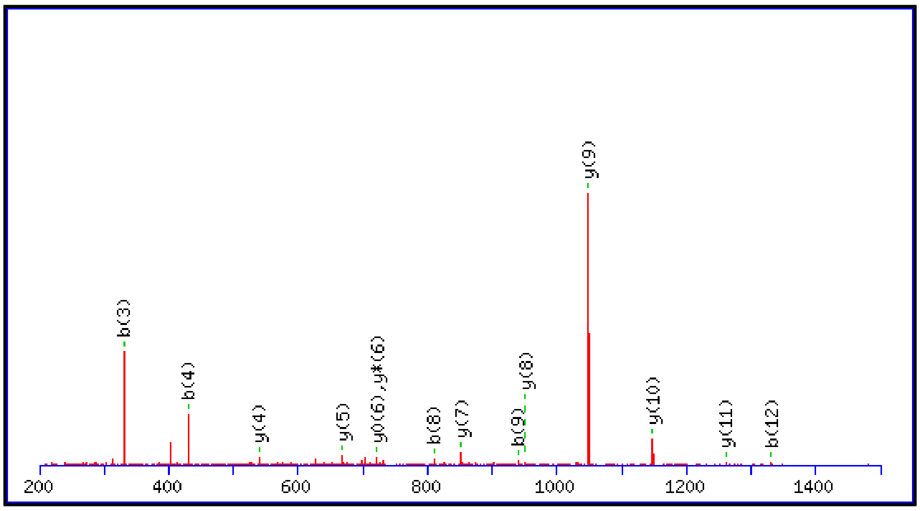
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CGLVPVLAENYNK**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

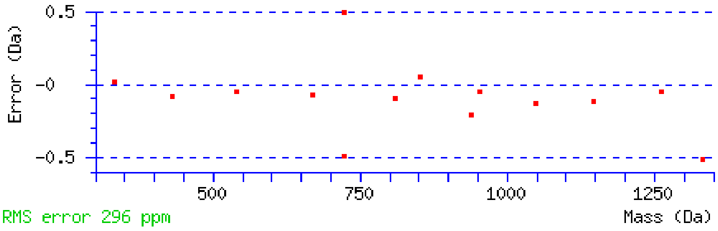
Match to Query 6672: 1476.730868 from(739.372710,2+) intensity(478122.6875) rtinseconds(1447) scans(3566) index(5214)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum3111_scans__3566
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

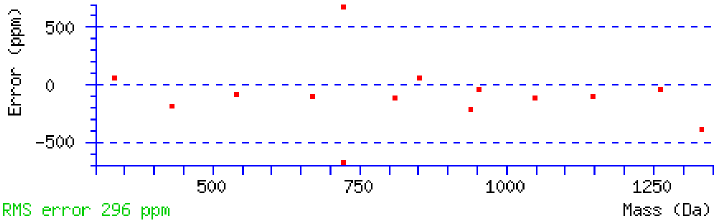
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1476.7282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0074
Matches : 14/102 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	161.0379	81.0226					C							13
2	218.0594	109.5333					G	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	12
3	**331.1435**	166.0754					L	***1260.6834***	630.8454	1243.6569	622.3321	1242.6729	621.8401	11
4	**430.2119**	215.6096					V	***1147.5994***	574.3033	1130.5728	565.7900	1129.5888	565.2980	10
5	527.2646	264.1360					P	***1048.5310***	524.7691	1031.5044	516.2558	1030.5204	515.7638	9
6	626.3330	313.6702					V	***951.4782***	476.2427	934.4516	467.7295	933.4676	467.2374	8
7	739.4171	370.2122					L	***852.4098***	426.7085	835.3832	418.1953	834.3992	417.7032	7
8	**810.4542**	405.7307					A	739.3257	370.1665	722.2992	361.6532	721.3151	361.1612	6
9	**939.4968**	470.2520			921.4863	461.2468	E	***668.2886***	334.6479	651.2620	326.1347	650.2780	325.6427	5
10	1053.5397	527.2735	1036.5132	518.7602	1035.5292	518.2682	N	***539.2460***	270.1266	522.2195	261.6134			4
11	1216.6031	608.8052	1199.5765	600.2919	1198.5925	599.7999	Y	425.2031	213.1052	408.1765	204.5919			3
12	**1331.6300**	666.3186	1314.6035	657.8054	1313.6195	657.3134	N	262.1397	131.5735	245.1132	123.0602			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.9	1476.7282	0.0026	CGLVPVLAENYNK	Deamidated N12 50.00%
44.9	1476.7282	0.0026	CGLVPVLAENYNK	Deamidated N10 50.00%
7.7	1476.7242	0.0067	LMNATSALESNQAK	
7.1	1475.7263	1.0046	TNNDRLEMRGVR	
5.5	1476.7242	0.0067	SGQGAQLRAMIEAK	
5.2	1476.7361	-0.0052	TAQEFGFAEPPRK	
4.9	1475.7256	1.0053	ERAPYQADLVQGK	
4.3	1476.7316	-0.0007	AKEEMMQGIQIAK	
4.3	1476.7316	-0.0007	AKEEMMQGIQIAK	
3.5	1476.7242	0.0067	QSNDKSPMLKVGR	

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

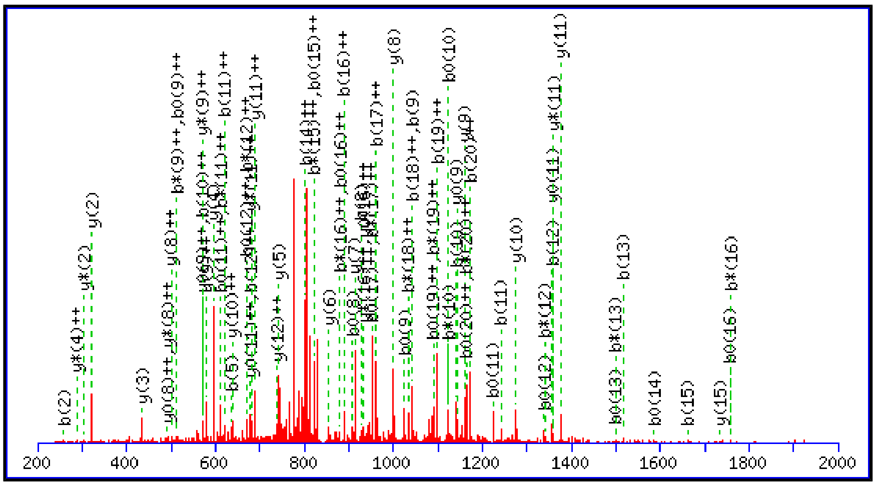
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

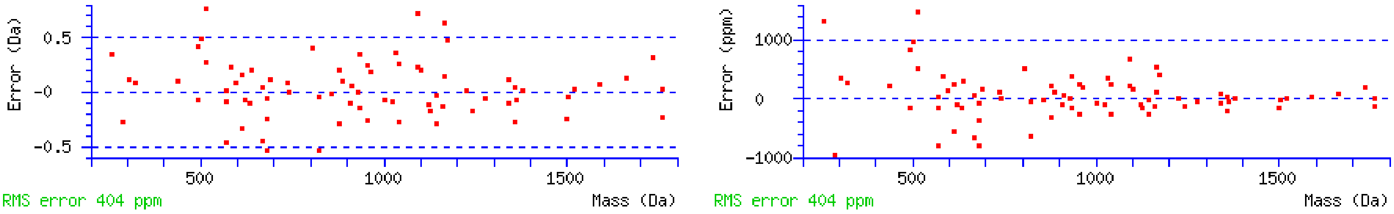
Match to Query 21796: 2516.090112 from(839.703980,3+) intensity(51950.7305) rtinseconds(1872) scans(4731) index(5394)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum4147_scans__4731
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2516.0849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.0045
Matches : 76/212 fragment ions using 144 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							21
2	***258.1084***	129.5579	241.0819	121.0446			Q	2389.0336	1195.0204	2372.0070	1186.5072	2371.0230	1186.0152	20
3	386.1670	193.5872	369.1405	185.0739			Q	2259.9910	1130.4991	2242.9645	1121.9859	2241.9804	1121.4939	19
4	523.2259	262.1166	506.1994	253.6033			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
5	***636.3100***	318.6586	619.2835	310.1454			L	1994.8735	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
6	783.3784	392.1928	766.3519	383.6796			F	1881.7894	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
7	840.3999	420.7036	823.3733	412.1903			G	***1734.7210***	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
8	***927.4319***	464.2196	910.4054	455.7063	909.4213	455.2143	S	1677.6996	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
9	***1042.4589***	521.7331	1025.4323	513.2198	1024.4483	512.7278	N	1590.6675	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
10	***1141.5273***	**571.2673**	1124.5007	562.7540	1123.5167	562.2620	V	1475.6406	738.3239	1458.6140	729.8107	1457.6300	729.3187	12
11	***1242.5749***	**621.7911**	1225.5484	613.2778	1224.5644	612.7858	T	***1376.5722***	688.7897	1359.5456	680.2765	1358.5616	679.7844	11
12	***1357.6019***	**679.3046**	1340.5753	670.7913	1339.5913	670.2993	D	***1275.5245***	638.2659	1258.4980	629.7526	1257.5139	629.2606	10
13	***1517.6325***	759.3199	1500.6060	750.8066	1499.6220	750.3146	C	***1160.4976***	580.7524	1143.4710	572.2391	1142.4870	571.7471	9
14	1604.6646	**802.8359**	1587.6380	794.3226	1586.6540	793.8306	S	***1000.4669***	500.7371	983.4404	492.2238	982.4563	491.7318	8
15	***1661.6860***	831.3467	1644.6595	822.8334	1643.6755	822.3414	G	***913.4349***	457.2211	896.4083	448.7078			7
16	1775.7290	**888.3681**	1758.7024	879.8548	1757.7184	879.3628	N	***856.4134***	428.7103	839.3869	420.1971			6
17	1922.7974	**961.9023**	1905.7708	953.3890	1904.7868	952.8970	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2082.8280	**1041.9176**	2065.8015	1033.4044	2064.8175	1032.9124	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2195.9121	**1098.4597**	2178.8855	1089.9464	2177.9015	1089.4544	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2342.9805	**1171.9939**	2325.9539	1163.4806	2324.9699	1162.9886	F	***322.1874***	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.8	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N9 30.24%
42.8	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N9 30.24%
38.5	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N9 11.47%
37.3	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, Q3 8.60%
37.3	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, Q3 8.60%
37.3	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, Q2 8.60%
28.1	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N16 1.03%
28.1	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N16 1.03%
20.0	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N16 0.16%
12.1	2516.0849	0.0052	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9, N16 0.03%

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

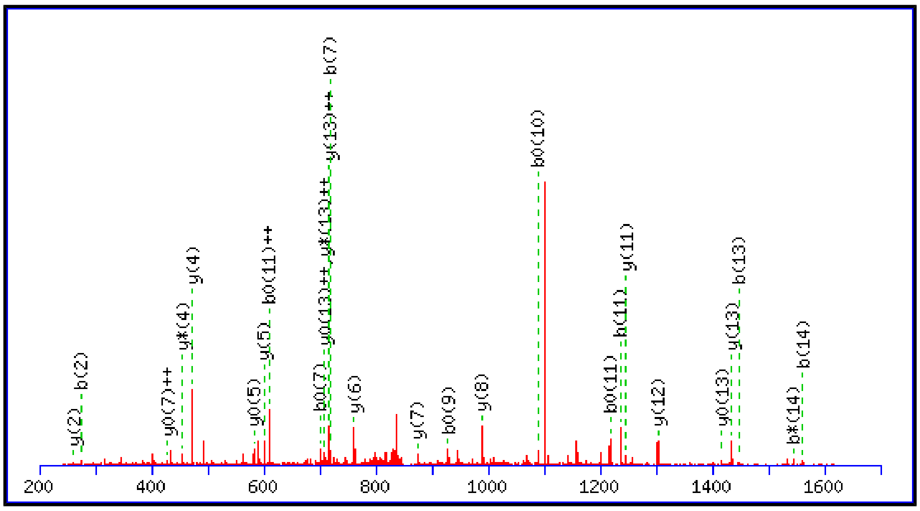
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LCMGSGLNLCEPNNK**
Found in **H7C5E8** in **con_Xuniprot_HUMAN3**, H7C5E8_HUMAN Serotransferrin (Fragment) OS=Homo sapiens GN=TF PE=4 SV=1

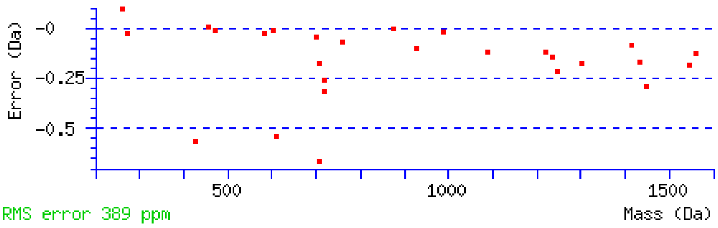
Match to Query 8708: 1707.744188 from(854.879370,2+) intensity(43030.5859) rtinseconds(1261) scans(2810) index(22228)
Title: 111019_Est_MI_YS_G_02Spectrum2373_scans__2810
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

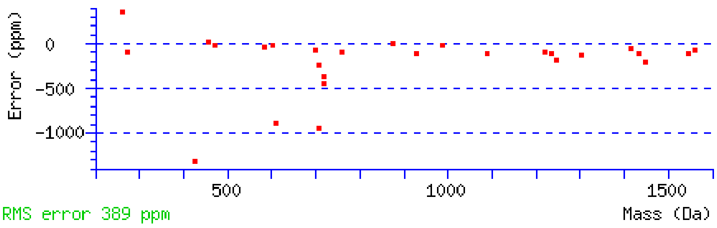
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1706.7426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.0066
Matches : 27/138 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	114.0913	57.5493					L							15
2	**274.1220**	137.5646					C	1594.6658	797.8366	1577.6393	789.3233	1576.6553	788.8313	14
3	405.1625	203.0849					M	***1434.6352***	717.8212	1417.6086	709.3080	1416.6246	708.8159	13
4	462.1839	231.5956					G	***1303.5947***	652.3010	1286.5681	643.7877	1285.5841	643.2957	12
5	549.2160	275.1116			531.2054	266.1063	S	***1246.5732***	623.7903	1229.5467	615.2770	1228.5627	614.7850	11
6	606.2374	303.6224			588.2269	294.6171	G	1159.5412	580.2742	1142.5147	571.7610	1141.5306	571.2690	10
7	**719.3215**	360.1644			701.3109	351.1591	L	1102.5197	551.7635	1085.4932	543.2502	1084.5092	542.7582	9
8	834.3484	417.6779	817.3219	409.1646	816.3379	408.6726	N	***989.4357***	495.2215	972.4091	486.7082	971.4251	486.2162	8
9	947.4325	474.2199	930.4060	465.7066	929.4219	465.2146	L	***874.4087***	437.7080	857.3822	429.1947	856.3982	428.7027	7
10	1107.4632	554.2352	1090.4366	545.7219	1089.4526	545.2299	C	***761.3247***	381.1660	744.2981	372.6527	743.3141	372.1607	6
11	**1236.5057**	618.7565	1219.4792	610.2432	1218.4952	609.7512	E	***601.2940***	301.1506	584.2675	292.6374	583.2834	292.1454	5
12	1333.5585	667.2829	1316.5320	658.7696	1315.5479	658.2776	P	***472.2514***	236.6293	455.2249	228.1161			4
13	**1447.6014**	724.3044	1430.5749	715.7911	1429.5909	715.2991	N	375.1987	188.1030	358.1721	179.5897			3
14	**1561.6444**	781.3258	1544.6178	772.8125	1543.6338	772.3205	N	***261.1557***	131.0815	244.1292	122.5682			2
15							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.1	1706.7426	1.0016	LCMGSGLNLCEPNNK	Deamidated N8 88.37%
30.5	1706.7426	1.0016	LCMGSGLNLCEPNNK	Deamidated N13 7.71%
27.6	1706.7426	1.0016	LCMGSGLNLCEPNNK	Deamidated N14 3.91%
11.6	1706.7343	1.0099	SRNEQEEDEQTSVR	
10.9	1706.7343	1.0099	SRNEQEEDEQTSVR	
10.9	1706.7393	1.0049	VPEFQPMDPTSCAGR	
6.0	1707.7410	0.0032	EYCGVPGDGDEELLR	
5.9	1707.7475	-0.0033	QYDIIKDNEPNNNK	
5.3	1707.7475	-0.0033	QYDIIKDNEPNNNK	
5.3	1707.7370	0.0072	RQNAQSAGEMDEVVR	

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

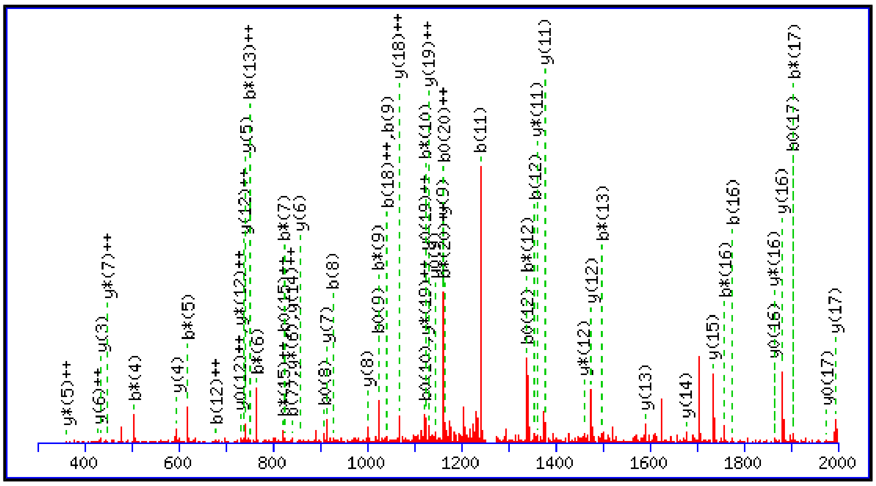
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQQHLFGSNVTDCSGNFCLFR**
Found in **J3KN47** in **con_Xuniprot_HUMAN3**, J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=2 SV=1

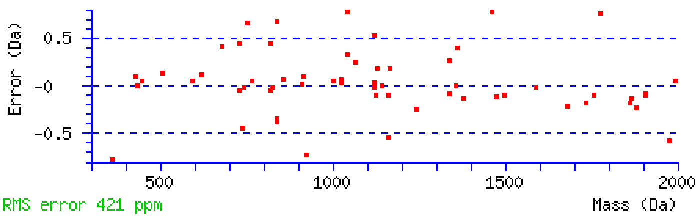
Match to Query 21815: 2517.087668 from(1259.551110,2+) intensity(12182.5811) rtinseconds(1954) scans(4789) index(15257)
Title: 111019_Est_MI_YP_G_04Spectrum4114_scans__4789
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

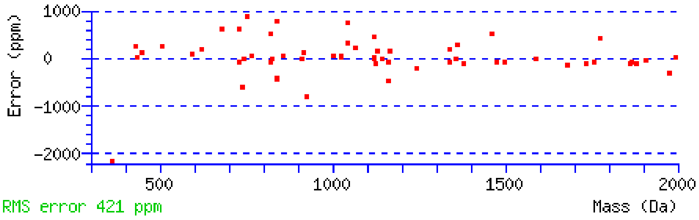
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2516.0849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N16 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.016
Matches : 60/212 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							21
2	257.1244	129.0659	240.0979	120.5526			Q	2389.0336	1195.0204	2372.0070	1186.5072	2371.0230	1186.0152	20
3	386.1670	193.5872	369.1405	185.0739			Q	2260.9750	1130.9911	2243.9485	1122.4779	2242.9645	1121.9859	19
4	523.2259	262.1166	506.1994	253.6033			H	2131.9324	1066.4698	2114.9059	1057.9566	2113.9219	1057.4646	18
5	636.3100	318.6586	619.2835	310.1454			L	***1994.8735***	997.9404	1977.8470	989.4271	1976.8629	988.9351	17
6	783.3784	392.1928	766.3519	383.6796			F	***1881.7894***	941.3984	1864.7629	932.8851	1863.7789	932.3931	16
7	**840.3999**	420.7036	823.3733	412.1903			G	***1734.7210***	867.8642	1717.6945	859.3509	1716.7105	858.8589	15
8	**927.4319**	464.2196	910.4054	455.7063	909.4213	455.2143	S	***1677.6996***	839.3534	1660.6730	830.8401	1659.6890	830.3481	14
9	**1041.4748**	521.2411	1024.4483	512.7278	1023.4643	512.2358	N	***1590.6675***	795.8374	1573.6410	787.3241	1572.6570	786.8321	13
10	1140.5432	570.7753	1123.5167	562.2620	1122.5327	561.7700	V	***1476.6246***	738.8159	1459.5981	730.3027	1458.6140	729.8107	12
11	**1241.5909**	621.2991	1224.5644	612.7858	1223.5804	612.2938	T	***1377.5562***	689.2817	1360.5297	680.7685	1359.5456	680.2765	11
12	**1356.6179**	678.8126	1339.5913	670.2993	1338.6073	669.8073	D	1276.5085	638.7579	1259.4820	630.2446	1258.4980	629.7526	10
13	1516.6485	758.8279	1499.6220	750.3146	1498.6380	749.8226	C	***1161.4816***	581.2444	1144.4550	572.7312	1143.4710	572.2391	9
14	1603.6805	802.3439	1586.6540	793.8306	1585.6700	793.3386	S	***1001.4509***	501.2291	984.4244	492.7158	983.4404	492.2238	8
15	1660.7020	830.8546	1643.6755	822.3414	1642.6914	821.8494	G	***914.4189***	457.7131	897.3924	449.1998			7
16	**1775.7290**	888.3681	1758.7024	879.8548	1757.7184	879.3628	N	***857.3974***	429.2024	840.3709	420.6891			6
17	1922.7974	961.9023	1905.7708	953.3890	1904.7868	952.8970	F	***742.3705***	371.6889	725.3439	363.1756			5
18	2082.8280	1041.9176	2065.8015	1033.4044	2064.8175	1032.9124	C	***595.3021***	298.1547	578.2755	289.6414			4
19	2195.9121	1098.4597	2178.8855	1089.9464	2177.9015	1089.4544	L	***435.2714***	218.1394	418.2449	209.6261			3
20	2342.9805	1171.9939	2325.9539	1163.4806	2324.9699	1162.9886	F	322.1874	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.9	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N16 23.78%
36.9	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N16 23.78%
36.9	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N16 23.78%
36.6	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated N9, N16 22.34%
25.7	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q3, N9 1.82%
25.7	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, N9 1.82%
25.7	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, N9 1.82%
18.2	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q2, Q3 0.33%
18.2	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, Q3 0.33%
16.5	2516.0849	1.0028	QQQHLFGSNVTDCSGNFCLFR	Deamidated Q1, Q2 0.22%

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

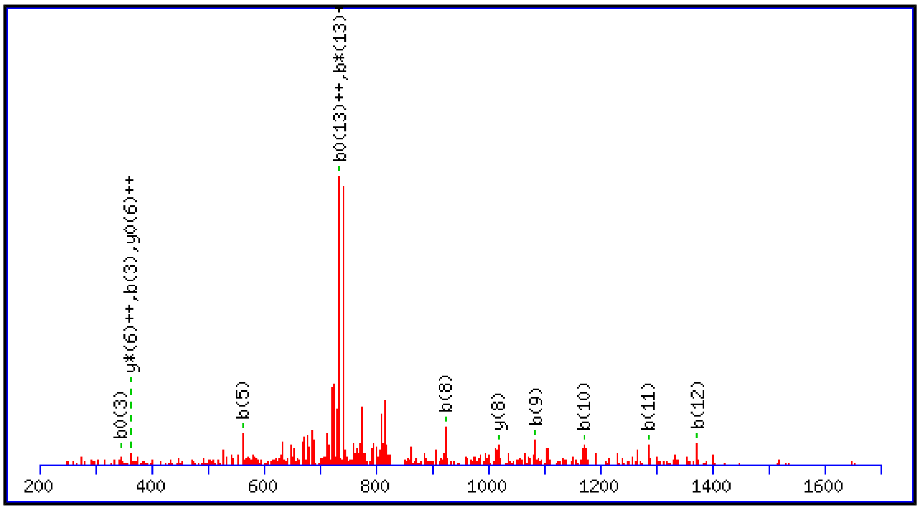
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSCKASCNCSNSIY**
Found in **J3KPA1** in **con_Xuniprot_HUMAN3**, J3KPA1_HUMAN Cysteine-rich secretory protein 3 OS=Homo sapiens GN=CRISP3 PE=2 SV=1

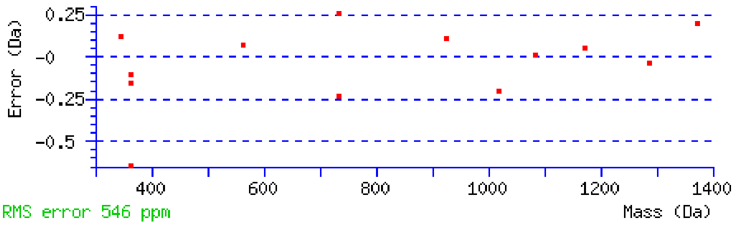
Match to Query 8413: 1665.611608 from(833.813080,2+) intensity(9400.8848) rtinseconds(424) scans(806) index(25954)
Title: 111019_Est_MI_YS_G_08Spectrum669_scans__806
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

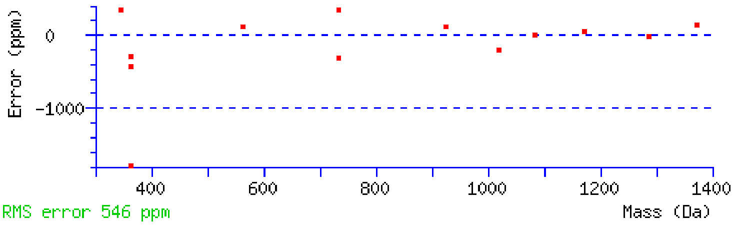
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1665.6069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8     : Deamidated (NQ)
Ions Score: 48  Expect: 5.5e-005
Matches : 13/140 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	203.0662	102.0368			185.0557	93.0315	S	1551.5872	776.2973	1534.5607	767.7840	1533.5767	767.2920	13
3	***363.0969***	182.0521			345.0863	173.0468	C	1464.5552	732.7812	1447.5287	724.2680	1446.5446	723.7760	12
4	491.1919	246.0996	474.1653	237.5863	473.1813	237.0943	K	1304.5246	652.7659	1287.4980	644.2526	1286.5140	643.7606	11
5	***562.2290***	281.6181	545.2024	273.1049	544.2184	272.6128	A	1176.4296	588.7184	1159.4031	580.2052	1158.4190	579.7132	10
6	649.2610	325.1341	632.2345	316.6209	631.2504	316.1289	S	1105.3925	553.1999	1088.3659	544.6866	1087.3819	544.1946	9
7	809.2917	405.1495	792.2651	396.6362	791.2811	396.1442	C	1018.3605	509.6839	1001.3339	501.1706	1000.3499	500.6786	8
8	***924.3186***	462.6629	907.2920	454.1497	906.3080	453.6577	N	858.3298	429.6685	841.3033	421.1553	840.3192	420.6633	7
9	***1084.3492***	542.6783	1067.3227	534.1650	1066.3387	533.6730	C	743.3029	372.1551	726.2763	363.6418	725.2923	363.1498	6
10	***1171.3813***	586.1943	1154.3547	577.6810	1153.3707	577.1890	S	583.2722	292.1397	566.2457	283.6265	565.2617	283.1345	5
11	***1285.4242***	643.2157	1268.3976	634.7025	1267.4136	634.2105	N	496.2402	248.6237	479.2136	240.1105	478.2296	239.6185	4
12	***1372.4562***	686.7318	1355.4297	678.2185	1354.4457	677.7265	S	382.1973	191.6023			364.1867	182.5970	3
13	1485.5403	743.2738	1468.5137	734.7605	1467.5297	734.2685	I	295.1652	148.0863					2
14							Y	182.0812	91.5442					1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.7	1665.6069	0.0047	DSCKASCNCSNSIY	Deamidated N8 99.86%
19.1	1665.6069	0.0047	DSCKASCNCSNSIY	Deamidated N11 0.14%
5.5	1664.6038	1.0078	EQCITTQMCDSKM	

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

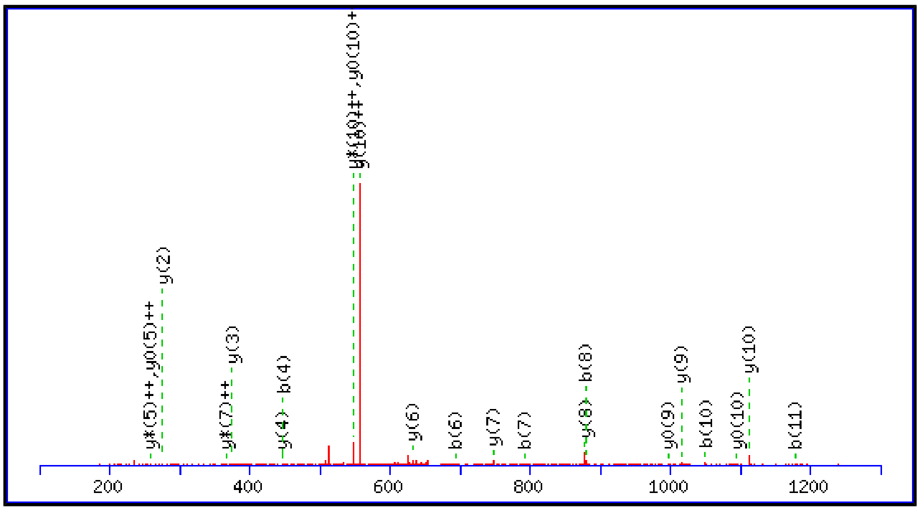
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVPHMNVSAVEK**
Found in **J3KRP0** in **con_Xuniprot_HUMAN3**, J3KRP0_HUMAN Beta-Ala-His dipeptidase OS=Homo sapiens GN=CNDP1 PE=2 SV=1

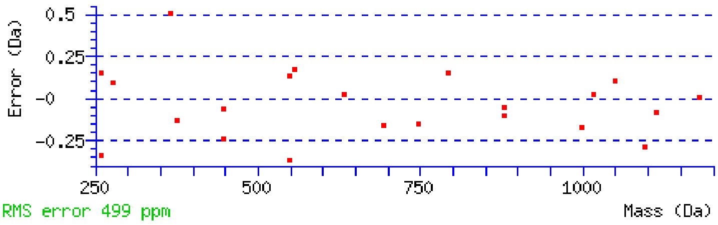
Match to Query 2016: 1323.690268 from(662.852410,2+) intensity(26937.2324) rtinseconds(784) scans(1679) index(12359)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum1443_scans__1679
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

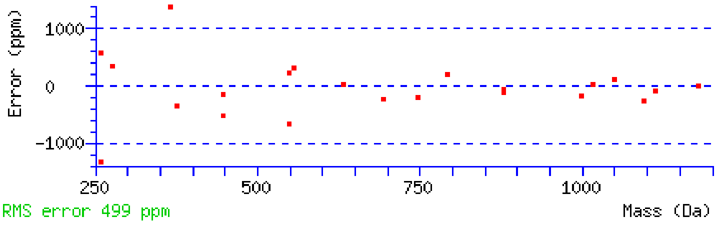
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1323.6857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0051
Matches : 23/106 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	114.0913	57.5493					L							12
2	213.1598	107.0835					V	1211.6089	606.3081	1194.5823	597.7948	1193.5983	597.3028	11
3	310.2125	155.6099					P	***1112.5405***	556.7739	1095.5139	548.2606	1094.5299	547.7686	10
4	***447.2714***	224.1394					H	***1015.4877***	508.2475	998.4612	499.7342	997.4771	499.2422	9
5	578.3119	289.6596					M	***878.4288***	439.7180	861.4022	431.2048	860.4182	430.7128	8
6	***693.3389***	347.1731	676.3123	338.6598			N	***747.3883***	374.1978	730.3618	365.6845	729.3777	365.1925	7
7	***792.4073***	396.7073	775.3807	388.1940			V	***632.3614***	316.6843	615.3348	308.1710	614.3508	307.6790	6
8	***879.4393***	440.2233	862.4128	431.7100	861.4287	431.2180	S	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
9	950.4764	475.7418	933.4499	467.2286	932.4658	466.7366	A	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	***1049.5448***	525.2761	1032.5183	516.7628	1031.5343	516.2708	V	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	***1178.5874***	589.7973	1161.5609	581.2841	1160.5769	580.7921	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LVPHMNVSAVEK
(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	1323.6857	0.0046	LVPHMNVSAVEK
7.1	1322.6904	0.9999	KVQIFDLMDAK
6.8	1321.6846	2.0057	INSKRMMNAIK
4.6	1321.6799	2.0104	MEEKLLQLSSK
4.0	1322.6917	0.9985	FPEHILMHRK
3.7	1321.6886	2.0017	KLMDWKNMIK
3.6	1321.6812	2.0090	NVGLPKEGPHMK
3.5	1321.6812	2.0091	NLMANRPAKYK
3.4	1323.6895	0.0008	VLPGSNGKPNGQR
3.4	1323.6857	0.0046	VITDRLGFKQM

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

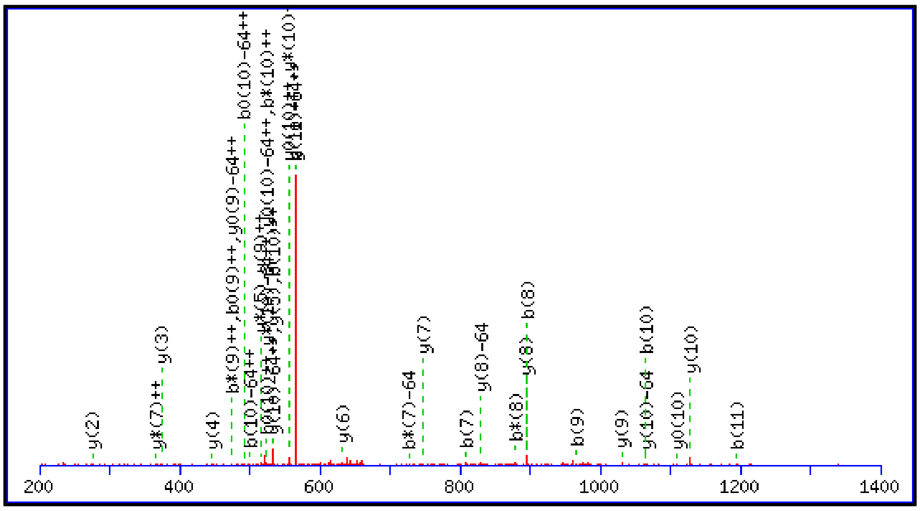
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVPHMNVSAVEK**
Found in **J3KRP0** in **con_Xuniprot_HUMAN3**, J3KRP0_HUMAN Beta-Ala-His dipeptidase OS=Homo sapiens GN=CNDP1 PE=2 SV=1

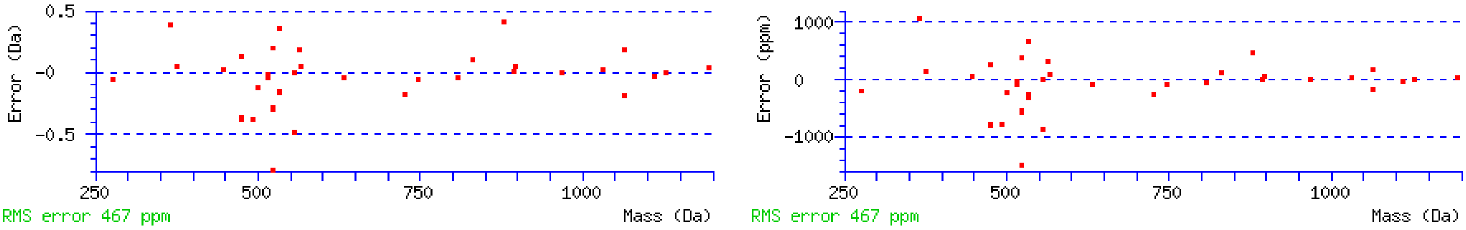
Match to Query 2030: 1339.685168 from(670.849860,2+) intensity(8134.3296) rtinseconds(317) scans(631) index(6112)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum539_scans__631
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1339.6806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.037
Matches : 37/164 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	114.0913	57.5493					L							12
2	213.1598	107.0835					V	1227.6038	614.3055	1210.5773	605.7923	1209.5932	605.3003	11
3	310.2125	155.6099					P	***1128.5354***	564.7713	1111.5088	556.2581	1110.5248	555.7660	10
4	447.2714	224.1394					H	***1031.4826***	516.2449	1014.4561	507.7317	1013.4721	507.2397	9
5	594.3068	297.6571					M	***894.4237***	447.7155	877.3972	439.2022	876.4131	438.7102	8
6	709.3338	355.1705	692.3072	346.6572			N	***747.3883***	374.1978	730.3618	365.6845	729.3777	365.1925	7
7	**808.4022**	404.7047	791.3756	396.1915			V	***632.3614***	316.6843	615.3348	308.1710	614.3508	307.6790	6
8	**895.4342**	448.2207	878.4077	439.7075	877.4236	439.2155	S	***533.2930***	267.1501	516.2664	258.6368	515.2824	258.1448	5
9	**966.4713**	483.7393	949.4448	475.2260	948.4608	474.7340	A	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	**1065.5397**	533.2735	1048.5132	524.7602	1047.5292	524.2682	V	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	**1194.5823**	597.7948	1177.5558	589.2815	1176.5718	588.7895	E	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of LVPHMNVSAVEK
(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	1339.6806	0.0046	LVPHMNVSAVEK
10.0	1338.6788	1.0064	MRIPALNAYMK
7.5	1337.6795	2.0056	SSVQKMMQAGKK
7.3	1337.6728	2.0124	IPSFFTDAERR
7.2	1338.6853	0.9999	FVENGMISVAKK
4.3	1337.6826	2.0025	AYSLEIETREK
4.0	1339.6884	-0.0032	QKYLENYLNR
3.7	1339.6918	-0.0066	IVHPESVVSSMR
3.7	1337.6795	2.0056	MSILGKGSMRDK
3.7	1337.6800	2.0052	RSSNLQSRSFR

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

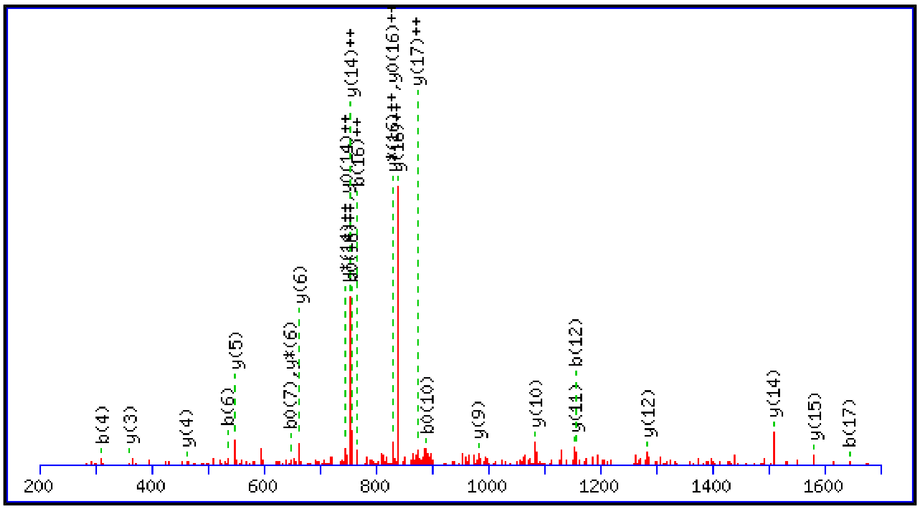
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAPAPQEATATFNSTADR**
Found in **J3QKR4** in **con_Xuniprot_HUMAN3**, J3QKR4_HUMAN Intercellular adhesion molecule 2 OS=Homo sapiens GN=ICAM2 PE=2 SV=1

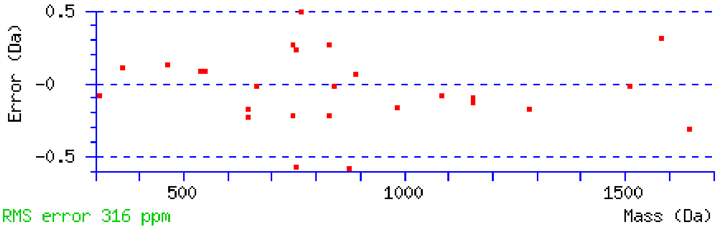
Match to Query 10897: 1818.841468 from(910.428010,2+) intensity(3988.0891) rtinseconds(848) scans(1644) index(28364)
Title: 111019_Est_MI_YS_G_13Spectrum1372_scans__1644
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

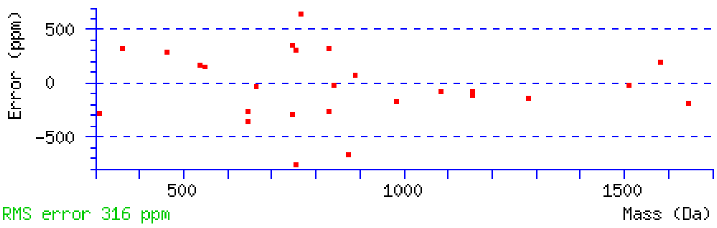
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1818.8384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.014
Matches : 26/180 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	72.0444	36.5258					A							18
2	143.0815	72.0444					A	1748.8086	874.9079	1731.7820	866.3947	1730.7980	865.9026	17
3	240.1343	120.5708					P	1677.7715	839.3894	1660.7449	830.8761	1659.7609	830.3841	16
4	**311.1714**	156.0893					A	***1580.7187***	790.8630	1563.6922	782.3497	1562.7081	781.8577	15
5	408.2241	204.6157					P	***1509.6816***	755.3444	1492.6550	746.8312	1491.6710	746.3392	14
6	**536.2827**	268.6450	519.2562	260.1317			Q	1412.6288	706.8181	1395.6023	698.3048	1394.6183	697.8128	13
7	665.3253	333.1663	648.2988	324.6530	647.3148	324.1610	E	***1284.5703***	642.7888	1267.5437	634.2755	1266.5597	633.7835	12
8	736.3624	368.6849	719.3359	360.1716	718.3519	359.6796	A	***1155.5277***	578.2675	1138.5011	569.7542	1137.5171	569.2622	11
9	837.4101	419.2087	820.3836	410.6954	819.3995	410.2034	T	***1084.4905***	542.7489	1067.4640	534.2356	1066.4800	533.7436	10
10	908.4472	454.7273	891.4207	446.2140	890.4367	445.7220	A	***983.4429***	492.2251	966.4163	483.7118	965.4323	483.2198	9
11	1009.4949	505.2511	992.4684	496.7378	991.4843	496.2458	T	912.4058	456.7065	895.3792	448.1932	894.3952	447.7012	8
12	**1156.5633**	578.7853	1139.5368	570.2720	1138.5528	569.7800	F	811.3581	406.1827	794.3315	397.6694	793.3475	397.1774	7
13	1271.5903	636.2988	1254.5637	627.7855	1253.5797	627.2935	N	***664.2897***	332.6485	647.2631	324.1352	646.2791	323.6432	6
14	1358.6223	679.8148	1341.5957	671.3015	1340.6117	670.8095	S	***549.2627***	275.1350	532.2362	266.6217	531.2522	266.1297	5
15	1459.6700	730.3386	1442.6434	721.8253	1441.6594	721.3333	T	***462.2307***	231.6190	445.2041	223.1057	444.2201	222.6137	4
16	1530.7071	765.8572	1513.6805	757.3439	1512.6965	756.8519	A	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
17	**1645.7340**	823.3707	1628.7075	814.8574	1627.7235	814.3654	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
18							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.2	1818.8384	0.0031	AAPAPQEATATFNSTADR	Deamidated N13 99.99%
2.6	1818.8325	0.0089	RPGPGAAPYYYSDYSR	
1.8	1818.8384	0.0031	AAPAPQEATATFNSTADR	Deamidated Q6 0.01%
0.4	1817.8406	1.0008	YLYGRHMQANPEPPK	
0.2	1817.8440	0.9974	QMGVPEDMPGLLGGFNR	

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

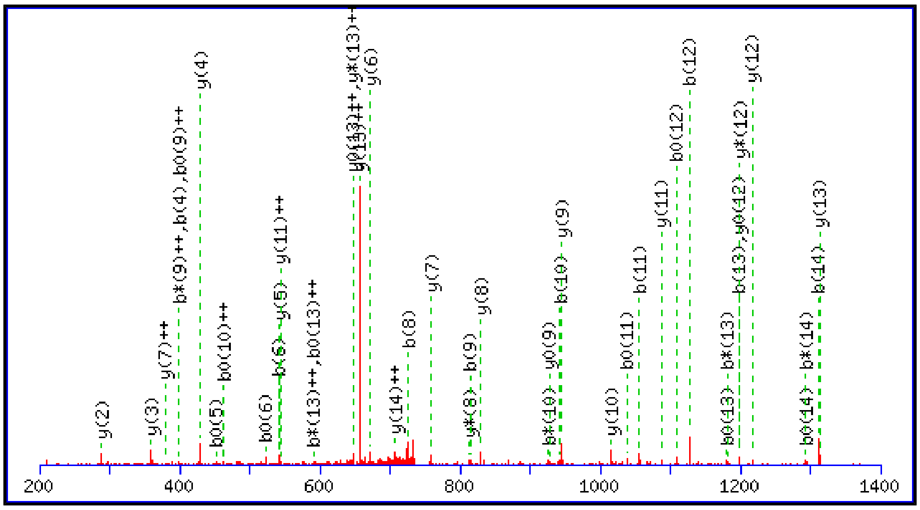
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATPEAANASELAALR**
Found in **K7EKF6** in **con_Xuniprot_HUMAN3**, K7EKF6_HUMAN Angiopoietin-related protein 6 OS=Homo sapiens GN=ANGPTL6 PE=2 SV=1

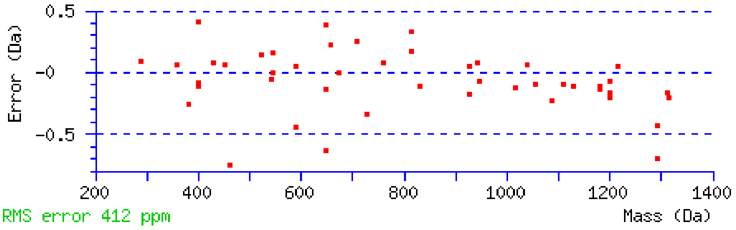
Match to Query 6675: 1484.749768 from(743.382160,2+) intensity(12293.5537) rtinseconds(1218) scans(2517) index(82)
Title: 111019_Est_ISCardio_NMI_200000g_G_3Spectrum2154_scans__2517
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

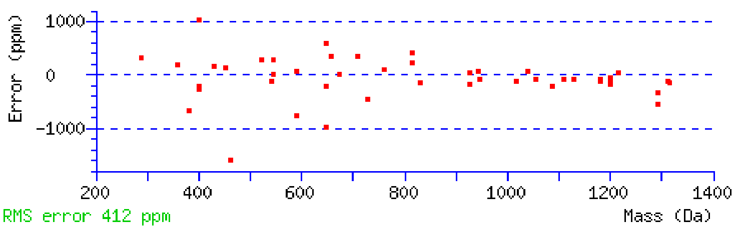
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1400 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1484.7470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 82 **Expect:** 1.1e-006
Matches : 46/144 fragment ions using 72 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**15**
2	173.0921	87.0497			155.0815	78.0444	**T**	1414.7172	707.8623	1397.6907	699.3490	1396.7067	698.8570	**14**
3	270.1448	135.5761			252.1343	126.5708	**P**	***1313.6696***	657.3384	1296.6430	648.8251	1295.6590	648.3331	**13**
4	**399.1874**	200.0974			381.1769	191.0921	**E**	***1216.6168***	608.8120	1199.5903	600.2988	1198.6062	599.8068	**12**
5	470.2245	235.6159			452.2140	226.6106	**A**	***1087.5742***	544.2907	1070.5477	535.7775	1069.5636	535.2855	**11**
6	**541.2617**	271.1345			523.2511	262.1292	**A**	***1016.5371***	508.7722	999.5106	500.2589	998.5265	499.7669	**10**
7	656.2886	328.6479	639.2620	320.1347	638.2780	319.6427	**N**	***945.5000***	473.2536	928.4734	464.7404	927.4894	464.2483	**9**
8	**727.3257**	364.1665	710.2992	355.6532	709.3151	355.1612	**A**	***830.4730***	415.7402	813.4465	407.2269	812.4625	406.7349	**8**
9	**814.3577**	407.6825	797.3312	399.1692	796.3472	398.6772	**S**	***759.4359***	380.2216	742.4094	371.7083	741.4254	371.2163	**7**
10	**943.4003**	472.2038	926.3738	463.6905	925.3898	463.1985	**E**	***672.4039***	336.7056	655.3774	328.1923	654.3933	327.7003	**6**
11	**1056.4844**	528.7458	1039.4578	520.2326	1038.4738	519.7406	**L**	***543.3613***	272.1843	526.3348	263.6710			**5**
12	**1127.5215**	564.2644	1110.4950	555.7511	1109.5109	555.2591	**A**	***430.2772***	215.6423	413.2507	207.1290			**4**
13	**1198.5586**	599.7829	1181.5321	591.2697	1180.5481	590.7777	**A**	***359.2401***	180.1237	342.2136	171.6104			**3**
14	**1311.6427**	656.3250	1294.6161	647.8117	1293.6321	647.3197	**L**	***288.2030***	144.6051	271.1765	136.0919			**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.8	1484.7470	0.0027	ATPEAANASELAALR
13.7	1484.7518	-0.0020	GNEMLRQDPRLR
13.7	1484.7518	-0.0020	GNEMLRQDPRLR
13.7	1484.7480	0.0018	VGMKPMAPTTPSPR
9.8	1484.7471	0.0027	LLAQPDDSEQTLR
8.5	1482.7426	2.0071	IGTGEVPSAPRENR
8.5	1482.7426	2.0071	LGTGEVPSAPRENR
7.9	1484.7518	-0.0020	LACPVGSRAGASSPR
7.7	1484.7480	0.0018	VGMKPMAPTTPSPR
6.8	1483.7518	0.9980	LANDAGNTVLLPER

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

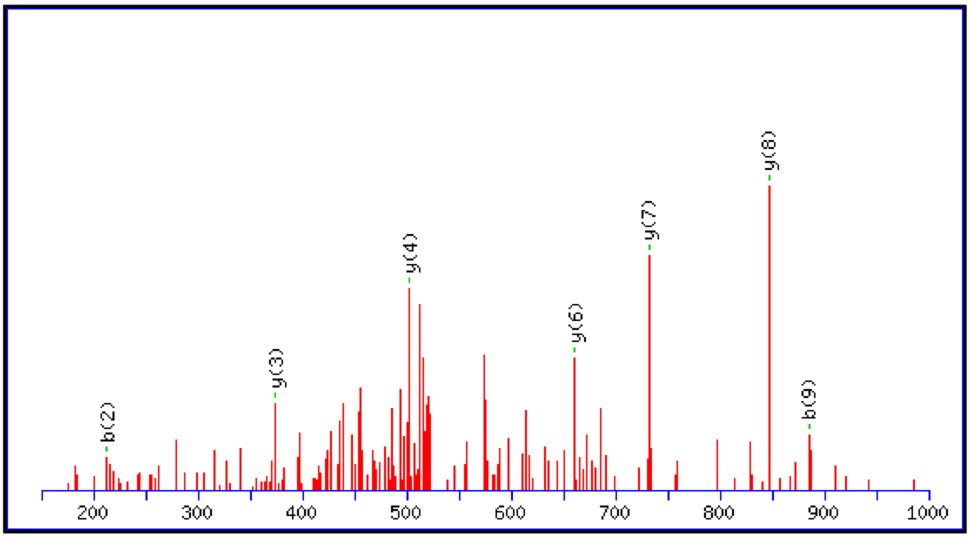
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLNASAEAQR**
Found in **K7EKF6** in **con_Xuniprot_HUMAN3**, K7EKF6_HUMAN Angiopoietin-related protein 6 OS=Homo sapiens GN=ANGPTL6 PE=2 SV=1

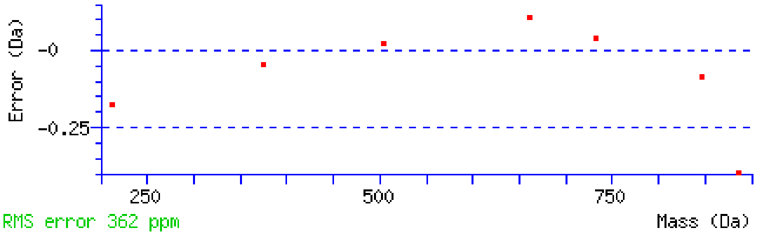
Match to Query 208: 1058.538328 from(530.276440,2+) intensity(1054.8698) rtinseconds(255) scans(402) index(1822)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum306_scans__402
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

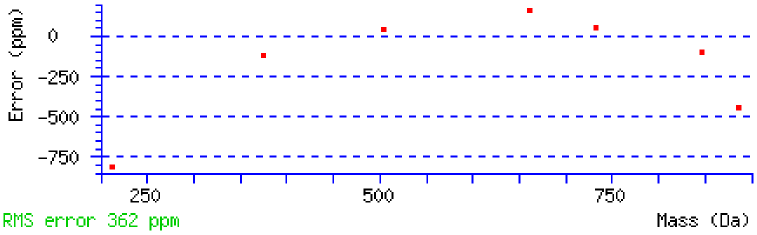
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1058.5356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.032
Matches : 7/90 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	100.0757	50.5415					**V**							**10**
2	**213.1598**	107.0835					**L**	960.4745	480.7409	943.4480	472.2276	942.4639	471.7356	**9**
3	328.1867	164.5970	311.1601	156.0837			**N**	***847.3904***	424.1989	830.3639	415.6856	829.3799	415.1936	**8**
4	399.2238	200.1155	382.1973	191.6023			**A**	***732.3635***	366.6854	715.3369	358.1721	714.3529	357.6801	**7**
5	486.2558	243.6316	469.2293	235.1183	468.2453	234.6263	**S**	***661.3264***	331.1668	644.2998	322.6536	643.3158	322.1615	**6**
6	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	**A**	574.2944	287.6508	557.2678	279.1375	556.2838	278.6455	**5**
7	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	**E**	***503.2572***	252.1323	486.2307	243.6190	485.2467	243.1270	**4**
8	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	**A**	***374.2146***	187.6110	357.1881	179.0977			**3**
9	**885.4312**	443.2193	868.4047	434.7060	867.4207	434.2140	**Q**	303.1775	152.0924	286.1510	143.5791			**2**
10							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
37.7	1058.5356	0.0027	VLNASAEAQR
6.3	1058.5356	0.0027	VIENGEKNR
5.2	1058.5356	0.0027	GEQQIQKAR
4.8	1057.5379	1.0005	FLKFMNSR
4.5	1056.5312	2.0071	GQNPTGEAKR
3.7	1058.5356	0.0027	NQEELLRR
2.9	1056.5274	2.0110	TGKSYLMNK
2.7	1057.5305	1.0078	FPKEGTHSR
2.2	1058.5356	0.0027	QGNASDVVLR
2.2	1058.5430	-0.0047	VLPMQVQSR

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

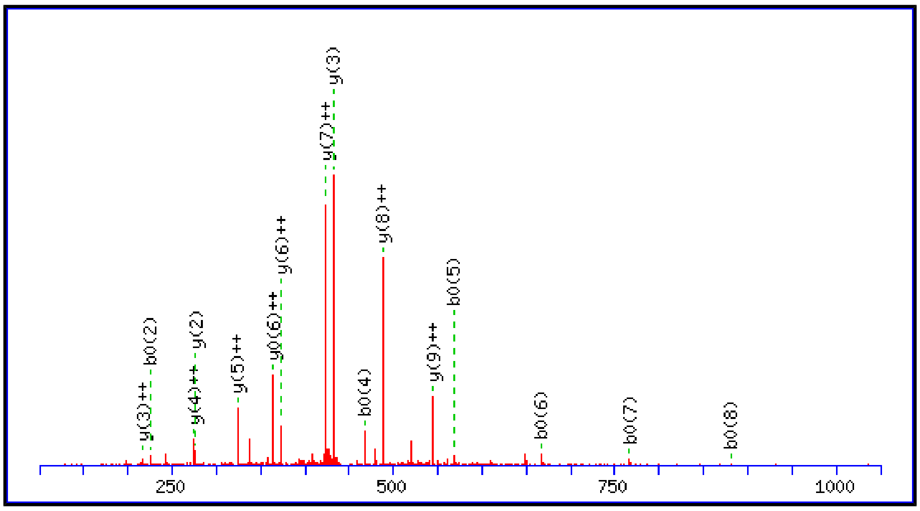
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELLETVVNRTR**
Found in **K7EMC3** in **con_Xuniprot_HUMAN3**, K7EMC3_HUMAN Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=2 SV=1

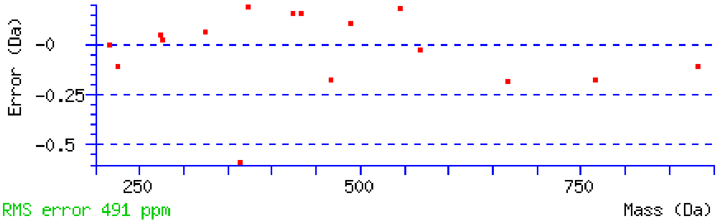
Match to Query 2017: 1329.726852 from(444.249560,3+) intensity(24947.9785) rtinseconds(924) scans(2187) index(24430)
Title: 111019_Est_MI_YS_G_06Spectrum1887_scans__2187
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

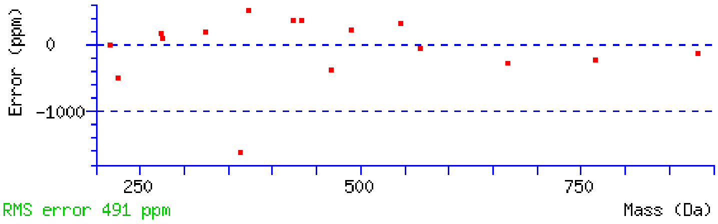
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1329.7252
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.05
Matches : 16/104 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	130.0499	65.5286			112.0393	56.5233	E							11
2	243.1339	122.0706			225.1234	113.0653	L	1201.6899	601.3486	1184.6634	592.8353	1183.6793	592.3433	10
3	356.2180	178.6126			338.2074	169.6074	L	1088.6058	544.8066	1071.5793	536.2933	1070.5953	535.8013	9
4	485.2606	243.1339			467.2500	234.1287	E	975.5218	488.2645	958.4952	479.7513	957.5112	479.2592	8
5	586.3083	293.6578			568.2977	284.6525	T	846.4792	423.7432	829.4526	415.2300	828.4686	414.7380	7
6	685.3767	343.1920			667.3661	334.1867	V	745.4315	373.2194	728.4050	364.7061	727.4209	364.2141	6
7	784.4451	392.7262			766.4345	383.7209	V	646.3631	323.6852	629.3365	315.1719	628.3525	314.6799	5
8	899.4720	450.2397	882.4455	441.7264	881.4615	441.2344	N	547.2947	274.1510	530.2681	265.6377	529.2841	265.1457	4
9	1055.5732	528.2902	1038.5466	519.7769	1037.5626	519.2849	R	**432.2677**	216.6375	415.2412	208.1242	414.2572	207.6322	3
10	1156.6208	578.8141	1139.5943	570.3008	1138.6103	569.8088	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ELLETVVNRTR
(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	1329.7252	0.0016	ELLETVVNRTR
8.9	1328.7300	0.9969	KNLGGITTPAETK
8.3	1327.7208	2.0061	KPEQRLGSREK
7.7	1329.7252	0.0017	LQTAQINAGKKR
7.6	1329.7292	-0.0024	ESWKVKSEIPK
5.2	1329.7252	0.0017	LLESQLQSQKR
5.0	1328.7299	0.9969	LQILNASSDVLR
4.3	1329.7326	-0.0058	ELILAGTMLDVR
4.1	1329.7252	0.0017	DKQNISQLEKK
4.1	1327.7208	2.0061	LQQLEAESRVR

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

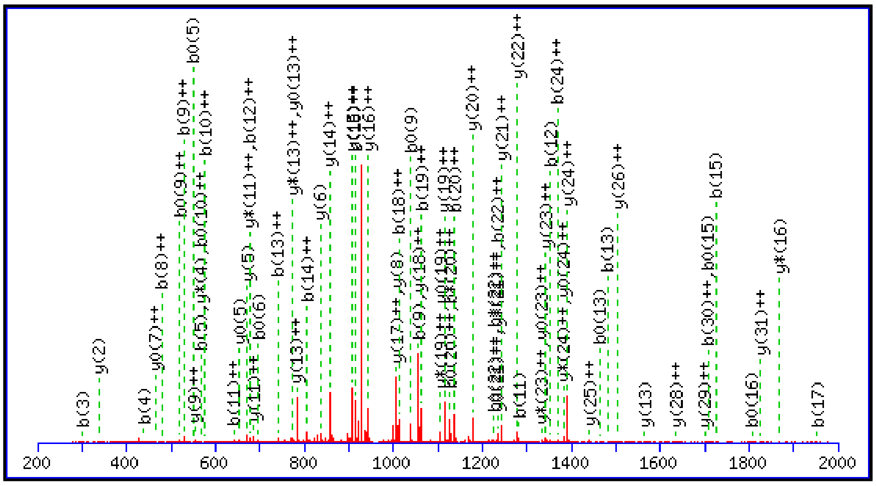
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR**
Found in **M0R009** in **con_Xuniprot_HUMAN3**, M0R009_HUMAN Alpha-1B-glycoprotein (Fragment) OS=Homo sapiens GN=A1BG PE=2 SV=1

Match to Query 28124: 3836.669096 from(960.174550,4+) intensity(1271696.5000) rtinseconds(1871) scans(4945) index(24030)
Title: 111019_Est_MI_YS_G_05Spectrum4276_scans__4945
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

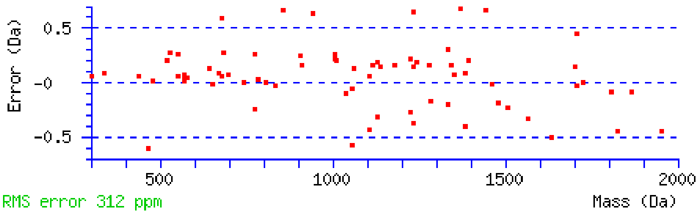
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

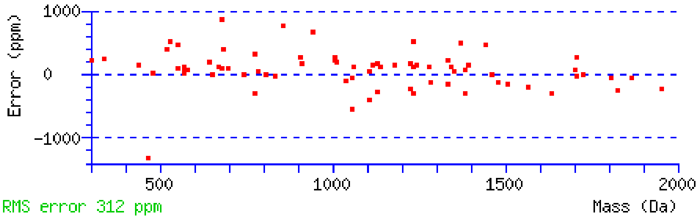


Monoisotopic mass of neutral peptide Mr(calc): 3836.6537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N27 : Deamidated (NQ)
Ions Score: 97 **Expect:** 1.5e-008
Matches : 74/356 fragment ions using 119 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							33
2	187.0713	94.0393			169.0608	85.0340	G	3708.6183	1854.8128	3691.5918	1846.2995	3690.6078	1845.8075	32
3	**302.0983**	151.5528			284.0877	142.5475	D	3651.5969	1826.3021	3634.5703	1817.7888	3633.5863	1817.2968	31
4	**439.1572**	220.0822			421.1466	211.0769	H	3536.5699	1768.7886	3519.5434	1760.2753	3518.5594	1759.7833	30
5	**568.1998**	284.6035			550.1892	275.5982	E	3399.5110	1700.2592	3382.4845	1691.7459	3381.5005	1691.2539	29
6	715.2682	358.1377			697.2576	349.1325	F	3270.4684	1635.7379	3253.4419	1627.2246	3252.4579	1626.7326	28
7	828.3523	414.6798			810.3417	405.6745	L	3123.4000	1562.2036	3106.3735	1553.6904	3105.3895	1553.1984	27
8	957.3949	**479.2011**			939.3843	470.1958	E	3010.3160	1505.6616	2993.2894	1497.1483	2992.3054	1496.6563	26
9	**1056.4633**	**528.7353**			1038.4527	519.7300	V	2881.2734	1441.1403	2864.2468	1432.6270	2863.2628	1432.1350	25
10	1153.5160	**577.2617**			1135.5055	568.2564	P	2782.2050	1391.6061	2765.1784	1383.0928	2764.1944	1382.6008	24
11	**1282.5586**	**641.7829**			1264.5481	632.7777	E	2685.1522	1343.0797	2668.1256	1334.5665	2667.1416	1334.0744	23
12	**1353.5957**	**677.3015**			1335.5852	668.2962	A	2556.1096	1278.5584	2539.0830	1270.0452	2538.0990	1269.5532	22
13	**1481.6543**	**741.3308**	1464.6278	732.8175	1463.6438	732.3255	Q	2485.0725	1243.0399	2468.0459	1234.5266	2467.0619	1234.0346	21
14	1610.6969	**805.8521**	1593.6704	797.3388	1592.6863	796.8468	E	2357.0139	1179.0106	2339.9874	1170.4973	2339.0033	1170.0053	20
15	**1725.7239**	863.3656	1708.6973	854.8523	1707.7133	854.3603	D	2227.9713	1114.4893	2210.9448	1105.9760	2209.9607	1105.4840	19
16	1824.7923	**912.8998**	1807.7657	904.3865	1806.7817	903.8945	V	2112.9444	1056.9758	2095.9178	1048.4625	2094.9338	1047.9705	18
17	**1953.8349**	977.4211	1936.8083	968.9078	1935.8243	968.4158	E	2013.8760	1007.4416	1996.8494	998.9283	1995.8654	998.4363	17
18	2024.8720	**1012.9396**	2007.8454	1004.4263	2006.8614	1003.9343	A	1884.8334	942.9203	1867.8068	934.4070	1866.8228	933.9150	16
19	2125.9197	**1063.4635**	2108.8931	1054.9502	2107.9091	1054.4582	T	1813.7962	907.4018	1796.7697	898.8885	1795.7857	898.3965	15
20	2272.9881	**1136.9977**	2255.9615	1128.4844	2254.9775	1127.9924	F	1712.7486	856.8779	1695.7220	848.3646	1694.7380	847.8726	14
21	2370.0408	1185.5241	2353.0143	1177.0108	2352.0303	1176.5188	P	**1565.6802**	783.3437	1548.6536	774.8304	1547.6696	774.3384	13
22	2469.1092	**1235.0583**	2452.0827	1226.5450	2451.0987	1226.0530	V	1468.6274	734.8173	1451.6008	726.3041	1450.6168	725.8121	12

23	2606.1682	1303.5877	2589.1416	1295.0744	2588.1576	1294.5824	**H**	1369.5590	685.2831	1352.5324	676.7699	1351.5484	676.2778	**11**
24	2734.2267	**1367.6170**	2717.2002	1359.1037	2716.2162	1358.6117	**Q**	1232.5001	616.7537	1215.4735	608.2404	1214.4895	607.7484	**10**
25	2831.2795	1416.1434	2814.2529	1407.6301	2813.2689	1407.1381	**P**	1104.4415	552.7244	1087.4149	544.2111	1086.4309	543.7191	**9**
26	2888.3010	1444.6541	2871.2744	1436.1408	2870.2904	1435.6488	**G**	**1007.3887**	504.1980	990.3622	495.6847	989.3782	495.1927	**8**
27	3003.3279	1502.1676	2986.3014	1493.6543	2985.3173	1493.1623	**N**	950.3673	475.6873	933.3407	467.1740	932.3567	466.6820	**7**
28	3166.3912	1583.6993	3149.3647	1575.1860	3148.3807	1574.6940	**Y**	**835.3403**	418.1738	818.3138	409.6605	817.3298	409.1685	**6**
29	3253.4233	1627.2153	3236.3967	1618.7020	3235.4127	1618.2100	**S**	**672.2770**	336.6421	655.2504	328.1289	654.2664	327.6368	**5**
30	3413.4539	**1707.2306**	3396.4274	1698.7173	3395.4433	1698.2253	**C**	585.2450	293.1261	568.2184	284.6128	567.2344	284.1208	**4**
31	3500.4859	1750.7466	3483.4594	1742.2333	3482.4754	1741.7413	**S**	425.2143	213.1108	408.1878	204.5975	407.2037	204.1055	**3**
32	3663.5493	1832.2783	3646.5227	1823.7650	3645.5387	1823.2730	**Y**	**338.1823**	169.5948	321.1557	161.0815			**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
96.9	3836.6537	0.0154	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated N27 62.67%
93.2	3836.6537	0.0154	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q24 26.49%
89.3	3836.6537	0.0154	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q13 10.84%
78.7	3835.6696	0.9994	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	
6.6	3836.6741	-0.0050	VRNPNSGSRSESPSMFSSTVLLVEYDQEGAGGASSGC	
6.6	3836.6741	-0.0050	VRNPNSGSRSESPSMFSSTVLLVEYDQEGAGGASSGC	
5.8	3834.6526	2.0165	WFTDFNFMGPSTESNQIGSEGSGRAENGPKECGPK	
5.5	3834.6737	1.9954	EDLRTLLRYYNQSEAGSHTLQNMYGCDVGPDGR	
4.8	3836.6835	-0.0144	LQGPLPDESNPNFVGMQCGANWFPQPNYNSSDVR	
4.5	3834.6526	2.0165	WFTDFNFMGPSTESNQIGSEGSGRAENGPKECGPK	

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

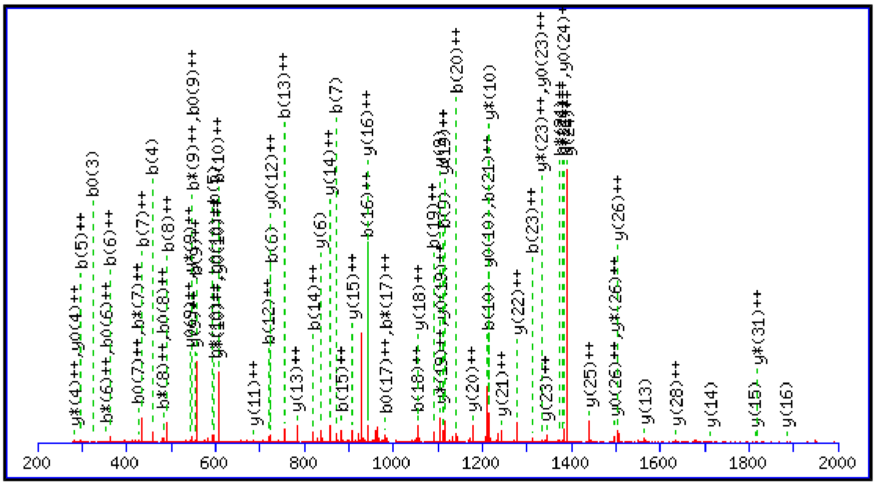
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR**
Found in **M0R009** in **con_Xuniprot_HUMAN3**, M0R009_HUMAN Alpha-1B-glycoprotein (Fragment) OS=Homo sapiens GN=A1BG PE=2 SV=1

Match to Query 28278: 3992.769416 from(999.199630,4+) intensity(87841.7969) rtinseconds(1745) scans(4122) index(8916)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum3528_scans__4122
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

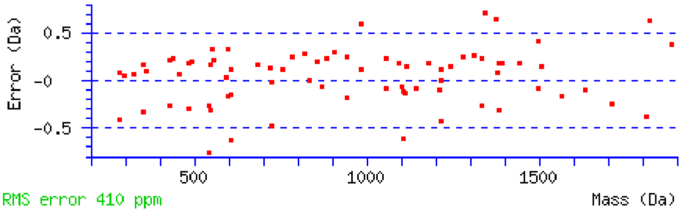
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

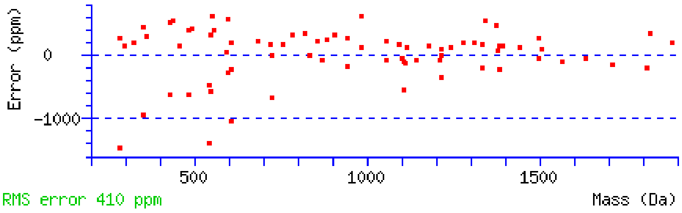


Monoisotopic mass of neutral peptide Mr(calc): 3992.7548
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N28 : Deamidated (NQ)
Ions Score: 80 **Expect:** 9.5e-007
Matches : 77/390 fragment ions using 120 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446			R							34
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	E	3837.6609	1919.3341	3820.6344	1910.8208	3819.6504	1910.3288	33
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	G	3708.6183	1854.8128	3691.5918	1846.2995	3690.6078	1845.8075	32
4	**458.1994**	229.6033	441.1728	221.0901	440.1888	220.5980	D	3651.5969	1826.3021	3634.5703	1817.7888	3633.5863	1817.2968	31
5	**595.2583**	***298.1328***	578.2318	289.6195	577.2477	289.1275	H	3536.5699	1768.7886	3519.5434	1760.2753	3518.5594	1759.7833	30
6	**724.3009**	***362.6541***	707.2743	354.1408	706.2903	353.6488	E	3399.5110	1700.2592	3382.4845	1691.7459	3381.5005	1691.2539	29
7	**871.3693**	***436.1883***	854.3428	427.6750	853.3587	427.1830	F	3270.4684	1635.7379	3253.4419	1627.2246	3252.4579	1626.7326	28
8	984.4534	***492.7303***	967.4268	484.2170	966.4428	483.7250	L	3123.4000	1562.2036	3106.3735	1553.6904	3105.3895	1553.1984	27
9	**1113.4960**	***557.2516***	1096.4694	548.7383	1095.4854	548.2463	E	3010.3160	1505.6616	2993.2894	1497.1483	2992.3054	1496.6563	26
10	**1212.5644**	***606.7858***	1195.5378	598.2726	1194.5538	597.7805	V	2881.2734	1441.1403	2864.2468	1432.6270	2863.2628	1432.1350	25
11	1309.6171	655.3122	1292.5906	646.7989	1291.6066	646.3069	P	2782.2050	1391.6061	2765.1784	1383.0928	2764.1944	1382.6008	24
12	1438.6597	***719.8335***	1421.6332	711.3202	1420.6492	710.8282	E	2685.1522	1343.0797	2668.1256	1334.5665	2667.1416	1334.0744	23
13	1509.6968	***755.3521***	1492.6703	746.8388	1491.6863	746.3468	A	2556.1096	1278.5584	2539.0830	1270.0452	2538.0990	1269.5532	22
14	1637.7554	***819.3814***	1620.7289	810.8681	1619.7449	810.3761	Q	2485.0725	1243.0399	2468.0459	1234.5266	2467.0619	1234.0346	21
15	1766.7980	***883.9026***	1749.7715	875.3894	1748.7875	874.8974	E	2357.0139	1179.0106	2339.9874	1170.4973	2339.0033	1170.0053	20
16	1881.8250	***941.4161***	1864.7984	932.9028	1863.8144	932.4108	D	2227.9713	1114.4893	2210.9448	1105.9760	2209.9607	1105.4840	19
17	1980.8934	990.9503	1963.8668	982.4371	1962.8828	981.9450	V	2112.9444	1056.9758	2095.9178	1048.4625	2094.9338	1047.9705	18
18	2109.9360	***1055.4716***	2092.9094	1046.9583	2091.9254	1046.4663	E	2013.8760	1007.4416	1996.8494	998.9283	1995.8654	998.4363	17
19	2180.9731	***1090.9902***	2163.9465	1082.4769	2162.9625	1081.9849	A	**1884.8334**	942.9203	1867.8068	934.4070	1866.8228	933.9150	16
20	2282.0208	***1141.5140***	2264.9942	1133.0007	2264.0102	1132.5087	T	**1813.7962**	907.4018	1796.7697	898.8885	1795.7857	898.3965	15
21	2429.0892	***1215.0482***	2412.0626	1206.5350	2411.0786	1206.0429	F	**1712.7486**	856.8779	1695.7220	848.3646	1694.7380	847.8726	14
22	2526.1419	1263.5746	2509.1154	1255.0613	2508.1314	1254.5693	P	**1565.6802**	783.3437	1548.6536	774.8304	1547.6696	774.3384	13

23	2625.2104	***1313.1088***	2608.1838	1304.5955	2607.1998	1304.1035	**V**	1468.6274	734.8173	1451.6008	726.3041	1450.6168	725.8121	**12**
24	2762.2693	***1381.6383***	2745.2427	1373.1250	2744.2587	1372.6330	**H**	1369.5590	685.2831	1352.5324	676.7699	1351.5484	676.2778	**11**
25	2890.3278	1445.6676	2873.3013	1437.1543	2872.3173	1436.6623	**Q**	1232.5001	616.7537	1215.4735	608.2404	1214.4895	607.7484	**10**
26	2987.3806	1494.1939	2970.3541	1485.6807	2969.3700	1485.1887	**P**	**1104.4415**	552.7244	1087.4149	544.2111	1086.4309	543.7191	**9**
27	3044.4021	1522.7047	3027.3755	1514.1914	3026.3915	1513.6994	**G**	1007.3887	504.1980	990.3622	495.6847	989.3782	495.1927	**8**
28	3159.4290	1580.2181	3142.4025	1571.7049	3141.4184	1571.2129	**N**	950.3673	475.6873	933.3407	467.1740	932.3567	466.6820	**7**
29	3322.4923	1661.7498	3305.4658	1653.2365	3304.4818	1652.7445	**Y**	**835.3403**	418.1738	818.3138	409.6605	817.3298	409.1685	**6**
30	3409.5244	1705.2658	3392.4978	1696.7525	3391.5138	1696.2605	**S**	672.2770	336.6421	655.2504	328.1289	654.2664	327.6368	**5**
31	3569.5550	1785.2811	3552.5285	1776.7679	3551.5445	1776.2759	**C**	585.2450	293.1261	568.2184	284.6128	567.2344	284.1208	**4**
32	3656.5870	1828.7972	3639.5605	1820.2839	3638.5765	1819.7919	**S**	425.2143	213.1108	408.1878	204.5975	407.2037	204.1055	**3**
33	3819.6504	1910.3288	3802.6238	1901.8156	3801.6398	1901.3235	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.0	3992.7548	0.0147	REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated N28 61.89%
75.6	3992.7548	0.0147	REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q25 22.42%
74.0	3992.7548	0.0147	REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q14 15.69%
73.1	3991.7708	0.9987	REGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	
8.6	3990.7570	2.0124	QGKPRLHTLSGQQMAGYHQQEVLWMTNQRNNCR	
6.2	3992.7740	-0.0046	WEQENLNLDPMLNSQSISGVTGTIMCPLDEVPEQK	
6.2	3992.7605	0.0089	LHREQNGQQNELWNECELAAELNSDYVSNRTLR	
5.8	3992.7740	-0.0046	WEQENLNLDPMLNSQSISGVTGTIMCPLDEVPEQK	
5.7	3992.7740	-0.0046	WEQENLNLDPMLNSQSISGVTGTIMCPLDEVPEQK	
4.8	3992.7740	-0.0046	WEQENLNLDPMLNSQSISGVTGTIMCPLDEVPEQK	

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

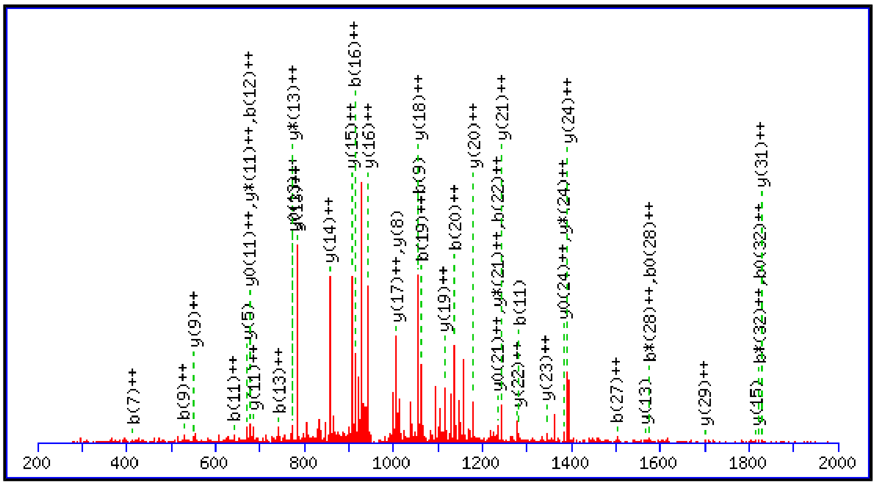
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR**
Found in **M0R009** in **con_Xuniprot_HUMAN3**, M0R009_HUMAN Alpha-1B-glycoprotein (Fragment) OS=Homo sapiens GN=A1BG PE=2 SV=1

Match to Query 28140: 3837.643296 from(960.418100,4+) intensity(25846.1465) rtinseconds(1983) scans(5049) index(2149)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum4375_scans__5049
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

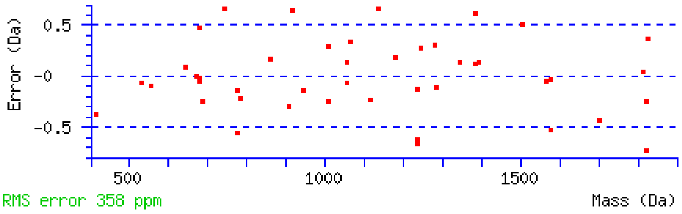
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

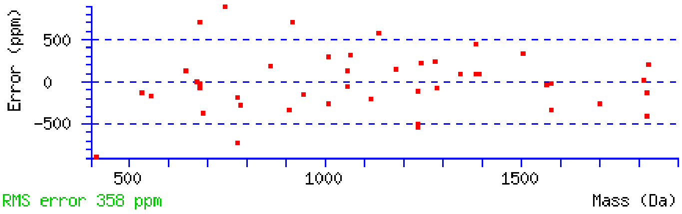


Monoisotopic mass of neutral peptide Mr(calc): 3837.6377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24 : Deamidated (NQ)
N27 : Deamidated (NQ)
Ions Score: 64 **Expect:** 2.3e-005
Matches : 44/356 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	**E**							**33**
2	187.0713	94.0393			169.0608	85.0340	**G**	3709.6024	1855.3048	3692.5758	1846.7915	3691.5918	1846.2995	**32**
3	302.0983	151.5528			284.0877	142.5475	**D**	3652.5809	1826.7941	3635.5544	1818.2808	3634.5703	1817.7888	**31**
4	439.1572	220.0822			421.1466	211.0769	**H**	3537.5540	1769.2806	3520.5274	1760.7673	3519.5434	1760.2753	**30**
5	568.1998	284.6035			550.1892	275.5982	**E**	3400.4950	1700.7512	3383.4685	1692.2379	3382.4845	1691.7459	**29**
6	715.2682	358.1377			697.2576	349.1325	**F**	3271.4525	1636.2299	3254.4259	1627.7166	3253.4419	1627.2246	**28**
7	828.3523	**414.6798**			810.3417	405.6745	**L**	3124.3840	1562.6957	3107.3575	1554.1824	3106.3735	1553.6904	**27**
8	957.3949	479.2011			939.3843	470.1958	**E**	3011.3000	1506.1536	2994.2734	1497.6404	2993.2894	1497.1483	**26**
9	1056.4633	**528.7353**			1038.4527	519.7300	**V**	2882.2574	1441.6323	2865.2308	1433.1191	2864.2468	1432.6270	**25**
10	1153.5160	577.2617			1135.5055	568.2564	**P**	2783.1890	1392.0981	2766.1624	1383.5848	2765.1784	1383.0928	**24**
11	1282.5586	**641.7829**			1264.5481	632.7777	**E**	2686.1362	1343.5717	2669.1097	1335.0585	2668.1256	1334.5665	**23**
12	1353.5957	**677.3015**			1335.5852	668.2962	**A**	2557.0936	1279.0504	2540.0671	1270.5372	2539.0830	1270.0452	**22**
13	1481.6543	**741.3308**	1464.6278	732.8175	1463.6438	732.3255	**Q**	2486.0565	1243.5319	2469.0299	1235.0186	2468.0459	1234.5266	**21**
14	1610.6969	805.8521	1593.6704	797.3388	1592.6863	796.8468	**E**	2357.9979	1179.5026	2340.9714	1170.9893	2339.9874	1170.4973	**20**
15	1725.7239	863.3656	1708.6973	854.8523	1707.7133	854.3603	**D**	2228.9553	1114.9813	2211.9288	1106.4680	2210.9448	1105.9760	**19**
16	1824.7923	**912.8998**	1807.7657	904.3865	1806.7817	903.8945	**V**	2113.9284	1057.4678	2096.9018	1048.9546	2095.9178	1048.4625	**18**
17	1953.8349	977.4211	1936.8083	968.9078	1935.8243	968.4158	**E**	2014.8600	1007.9336	1997.8334	999.4203	1996.8494	998.9283	**17**
18	2024.8720	1012.9396	2007.8454	1004.4263	2006.8614	1003.9343	**A**	1885.8174	943.4123	1868.7908	934.8991	1867.8068	934.4070	**16**
19	2125.9197	**1063.4635**	2108.8931	1054.9502	2107.9091	1054.4582	**T**	**1814.7803**	907.8938	1797.7537	899.3805	1796.7697	898.8885	**15**
20	2272.9881	**1136.9977**	2255.9615	1128.4844	2254.9775	1127.9924	**F**	1713.7326	857.3699	1696.7060	848.8567	1695.7220	848.3646	**14**
21	2370.0408	1185.5241	2353.0143	1177.0108	2352.0303	1176.5188	**P**	**1566.6642**	783.8357	1549.6376	775.3224	1548.6536	774.8304	**13**

22	2469.1092	**1235.0583**	2452.0827	1226.5450	2451.0987	1226.0530	**V**	1469.6114	735.3093	1452.5849	726.7961	1451.6008	726.3041	**12**
23	2606.1682	1303.5877	2589.1416	1295.0744	2588.1576	1294.5824	**H**	1370.5430	685.7751	1353.5164	677.2619	1352.5324	676.7699	**11**
24	2735.2107	1368.1090	2718.1842	1359.5957	2717.2002	1359.1037	**Q**	1233.4841	617.2457	1216.4575	608.7324	1215.4735	608.2404	**10**
25	2832.2635	1416.6354	2815.2370	1408.1221	2814.2529	1407.6301	**P**	1104.4415	552.7244	1087.4149	544.2111	1086.4309	543.7191	**9**
26	2889.2850	1445.1461	2872.2584	1436.6329	2871.2744	1436.1408	**G**	**1007.3887**	504.1980	990.3622	495.6847	989.3782	495.1927	**8**
27	3004.3119	**1502.6596**	2987.2854	1494.1463	2986.3014	1493.6543	**N**	950.3673	475.6873	933.3407	467.1740	932.3567	466.6820	**7**
28	3167.3752	1584.1913	3150.3487	1575.6780	3149.3647	1575.1860	**Y**	835.3403	418.1738	818.3138	409.6605	817.3298	409.1685	**6**
29	3254.4073	1627.7073	3237.3807	1619.1940	3236.3967	1618.7020	**S**	**672.2770**	336.6421	655.2504	328.1289	654.2664	327.6368	**5**
30	3414.4379	1707.7226	3397.4114	1699.2093	3396.4274	1698.7173	**C**	585.2450	293.1261	568.2184	284.6128	567.2344	284.1208	**4**
31	3501.4700	1751.2386	3484.4434	1742.7253	3483.4594	1742.2333	**S**	425.2143	213.1108	408.1878	204.5975	407.2037	204.1055	**3**
32	3664.5333	1832.7703	3647.5067	1824.2570	3646.5227	1823.7650	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.1	3837.6377	0.0056	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q24, N27 75.21%
57.4	3837.6377	0.0056	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q13, N27 15.79%
54.9	3837.6377	0.0056	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	Deamidated Q13, Q24 9.00%
47.2	3836.6537	0.9896	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	
45.6	3836.6537	0.9896	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	
34.8	3836.6537	0.9896	EGDHEFLEVPEAQEDVEATFPVHQPGNYSCSYR	
3.1	3836.6540	0.9893	HLQGMLDMVTLGWYIGSMRLYESMCYEYDDK	
3.1	3836.6540	0.9893	HLQGMLDMVTLGWYIGSMRLYESMCYEYDDK	
1.9	3837.6439	-0.0006	DCVRQTYANSFNMCHGNAICIAHGNPYHMINR	
1.5	3837.6523	-0.0090	DTQQGMYDAVLHVGDFAYNLDQDNARVGDRFMR	

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

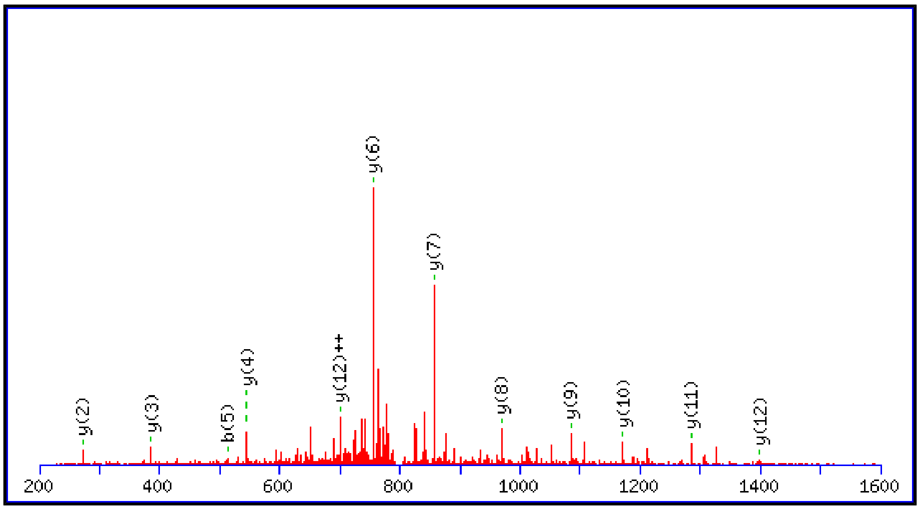
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVINSNITPICLPR**
Found in **O00187** in **con_Xuniprot_HUMAN3**, MASP2_HUMAN Mannan-binding lectin serine protease 2 OS=Homo sapiens GN=MASP2 PE=1 SV=4

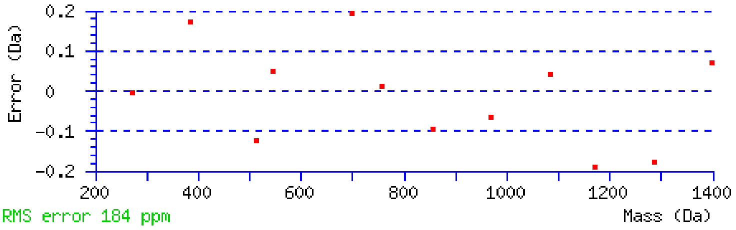
Match to Query 7655: 1595.873008 from(798.943780,2+) intensity(43672.8945) rtinseconds(1621) scans(4222) index(4407)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3582_scans__4222
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

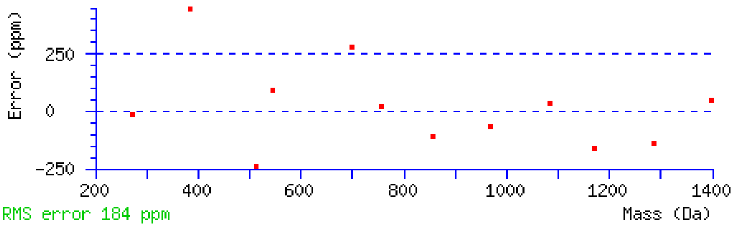
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1595.8705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 85 **Expect:** 3.8e-007
Matches : 12/130 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	100.0757	50.5415					V							14
2	199.1441	100.0757					V	1497.8094	749.4083	1480.7828	740.8951	1479.7988	740.4030	13
3	312.2282	156.6177					I	***1398.7410***	699.8741	1381.7144	691.3608	1380.7304	690.8688	12
4	426.2711	213.6392	409.2445	205.1259			N	***1285.6569***	643.3321	1268.6303	634.8188	1267.6463	634.3268	11
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	S	***1171.6140***	586.3106	1154.5874	577.7973	1153.6034	577.3053	10
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	N	***1084.5819***	542.7946	1067.5554	534.2813	1066.5714	533.7893	9
7	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	I	***969.5550***	485.2811	952.5285	476.7679	951.5444	476.2759	8
8	842.4618	421.7345	825.4353	413.2213	824.4512	412.7293	T	***856.4709***	428.7391	839.4444	420.2258	838.4604	419.7338	7
9	939.5146	470.2609	922.4880	461.7477	921.5040	461.2556	P	***755.4233***	378.2153	738.3967	369.7020			6
10	1052.5986	526.8030	1035.5721	518.2897	1034.5881	517.7977	I	658.3705	329.6889	641.3439	321.1756			5
11	1212.6293	606.8183	1195.6027	598.3050	1194.6187	597.8130	C	***545.2864***	273.1469	528.2599	264.6336			4
12	1325.7134	663.3603	1308.6868	654.8470	1307.7028	654.3550	L	***385.2558***	193.1315	368.2292	184.6183			3
13	1422.7661	711.8867	1405.7396	703.3734	1404.7555	702.8814	P	***272.1717***	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.2	1595.8705	0.0025	VVINSNITPICLPR	Deamidated N6 97.87%
68.6	1595.8705	0.0025	VVINSNITPICLPR	Deamidated N4 2.13%
1.0	1595.8671	0.0059	FNLDHILPTIGSLR	
0.9	1595.8770	-0.0040	AAEVSSLPPSIVLDAK	
0.9	1595.8671	0.0059	SALPEWASPQKLIR	

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

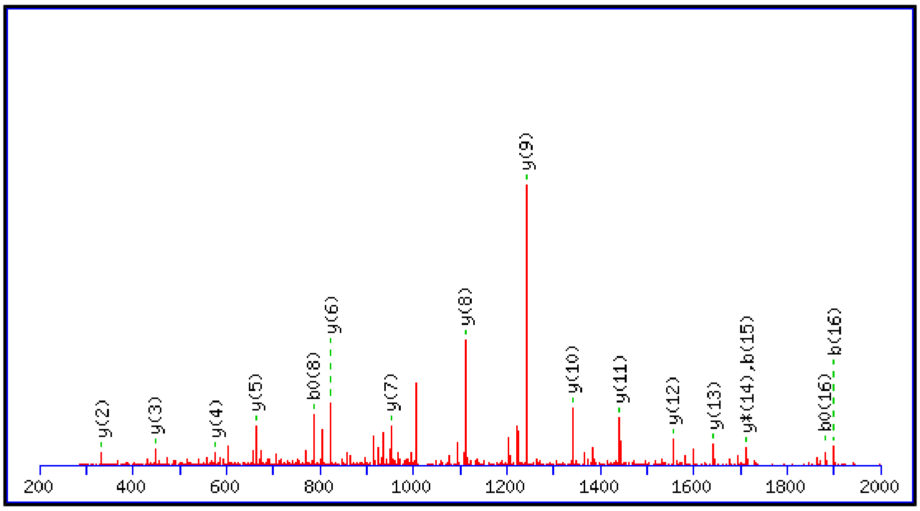
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISNSSDTVECECSENWK**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

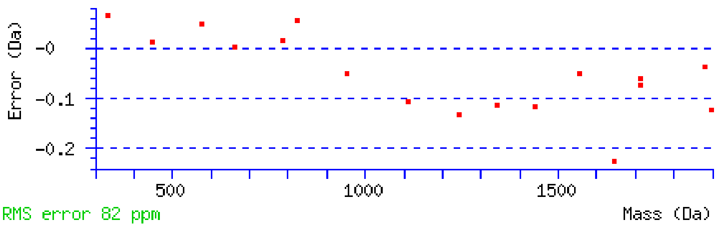
Match to Query 13078: 2044.804908 from(1023.409730,2+) intensity(0.0000) rtinseconds(585) scans(1381) index(19349)
Title: 111019_Est_MI_YP_G_09Spectrum1209_scans__1381
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

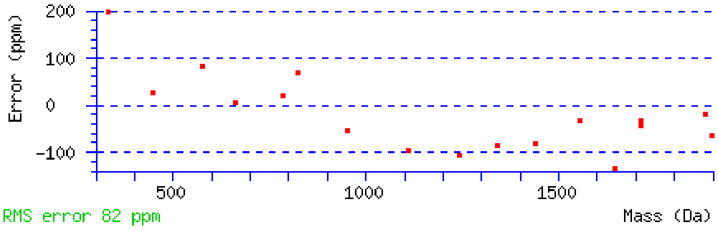
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2044.7990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 121 **Expect:** 1.2e-011
Matches : 17/180 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	114.0913	57.5493					I							17
2	201.1234	101.0653			183.1128	92.0600	S	1932.7222	966.8647	1915.6957	958.3515	1914.7116	957.8595	16
3	316.1503	158.5788	299.1238	150.0655	298.1397	149.5735	N	1845.6902	923.3487	1828.6636	914.8355	1827.6796	914.3434	15
4	403.1823	202.0948	386.1558	193.5815	385.1718	193.0895	S	1730.6632	865.8353	1713.6367	857.3220	1712.6527	856.8300	14
5	490.2144	245.6108	473.1878	237.0975	472.2038	236.6055	S	***1643.6312***	822.3192	1626.6047	813.8060	1625.6206	813.3140	13
6	605.2413	303.1243	588.2148	294.6110	587.2307	294.1190	D	***1556.5992***	778.8032	1539.5726	770.2900	1538.5886	769.7979	12
7	706.2890	353.6481	689.2624	345.1349	688.2784	344.6429	T	***1441.5722***	721.2898	1424.5457	712.7765	1423.5617	712.2845	11
8	805.3574	403.1823	788.3309	394.6691	787.3468	394.1771	V	***1340.5246***	670.7659	1323.4980	662.2526	1322.5140	661.7606	10
9	934.4000	467.7036	917.3734	459.1904	916.3894	458.6984	E	***1241.4561***	621.2317	1224.4296	612.7184	1223.4456	612.2264	9
10	1094.4306	547.7190	1077.4041	539.2057	1076.4201	538.7137	C	***1112.4136***	556.7104	1095.3870	548.1971	1094.4030	547.7051	8
11	1223.4732	612.2403	1206.4467	603.7270	1205.4627	603.2350	E	***952.3829***	476.6951	935.3564	468.1818	934.3723	467.6898	7
12	1383.5039	692.2556	1366.4773	683.7423	1365.4933	683.2503	C	***823.3403***	412.1738	806.3138	403.6605	805.3297	403.1685	6
13	1470.5359	735.7716	1453.5094	727.2583	1452.5253	726.7663	S	***663.3097***	332.1585	646.2831	323.6452	645.2991	323.1532	5
14	1599.5785	800.2929	1582.5520	791.7796	1581.5679	791.2876	E	***576.2776***	288.6425	559.2511	280.1292	558.2671	279.6372	4
15	**1713.6214**	857.3144	1696.5949	848.8011	1695.6109	848.3091	N	***447.2350***	224.1212	430.2085	215.6079			3
16	**1899.7007**	950.3540	1882.6742	941.8407	1881.6902	941.3487	W	***333.1921***	167.0997	316.1656	158.5864			2
17							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
120.6	2044.7990	0.0059	ISNSSDTVECECSENWK	Deamidated N3 100.00%
40.2	2044.7990	0.0059	ISNSSDTVECECSENWK	Deamidated N15 0.00%
0.7	2043.8037	1.0012	QDSNEEDQGGNKPMYAMK	
0.7	2043.8037	1.0012	QDSNEEDQGGNKPMYAMK	

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

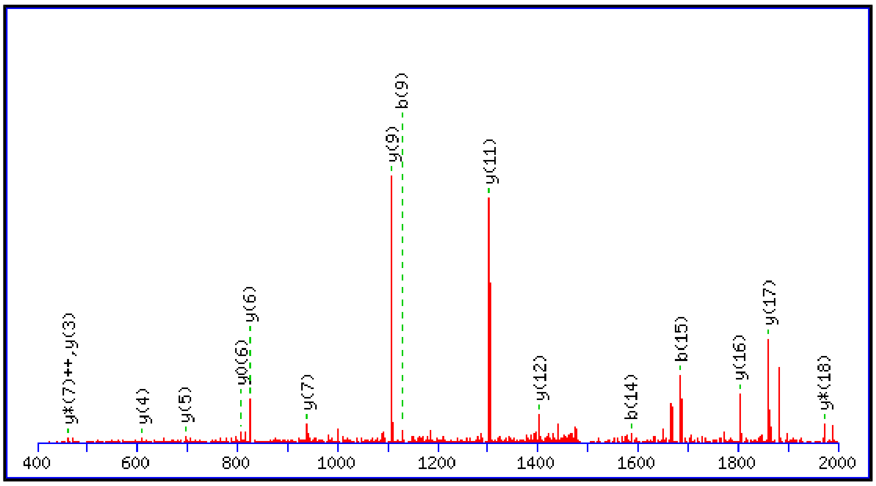
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCSCFSDWQGPGCSVPVPANQSFWTR**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

Match to Query 27089: 2987.243968 from(1494.629260,2+) intensity(9965.8467) rtinseconds(2045) scans(5353) index(19786)
Title: 111019_Est_MI_YP_G_09Spectrum4727_scans__5353
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

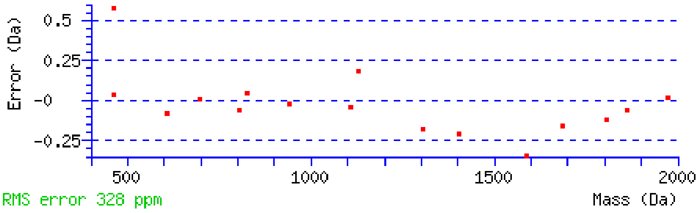
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

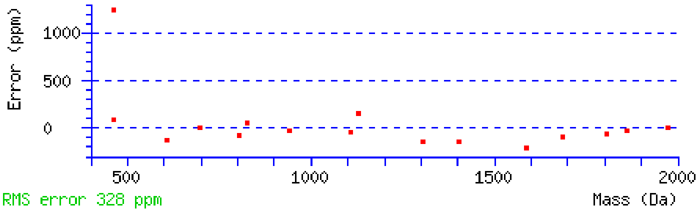


Monoisotopic mass of neutral peptide Mr(calc): 2987.2426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 85 **Expect:** 1.1e-007
Matches : 16/278 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							26
2	218.0594	109.5333					C	2931.2283	1466.1178	2914.2018	1457.6045	2913.2178	1457.1125	25
3	305.0914	153.0493			287.0809	144.0441	S	2771.1977	1386.1025	2754.1711	1377.5892	2753.1871	1377.0972	24
4	465.1221	233.0647			447.1115	224.0594	C	2684.1657	1342.5865	2667.1391	1334.0732	2666.1551	1333.5812	23
5	612.1905	306.5989			594.1799	297.5936	F	2524.1350	1262.5711	2507.1085	1254.0579	2506.1245	1253.5659	22
6	699.2225	350.1149			681.2119	341.1096	S	2377.0666	1189.0369	2360.0401	1180.5237	2359.0560	1180.0317	21
7	814.2495	407.6284			796.2389	398.6231	D	2290.0346	1145.5209	2273.0080	1137.0077	2272.0240	1136.5156	20
8	1000.3288	500.6680			982.3182	491.6627	W	2175.0076	1088.0075	2157.9811	1079.4942	2156.9971	1079.0022	19
9	**1128.3873**	564.6973	1111.3608	556.1840	1110.3768	555.6920	Q	1988.9283	994.9678	1971.9018	986.4545	1970.9178	985.9625	18
10	1185.4088	593.2080	1168.3823	584.6948	1167.3982	584.2028	G	***1860.8697***	930.9385	1843.8432	922.4252	1842.8592	921.9332	17
11	1282.4616	641.7344	1265.4350	633.2211	1264.4510	632.7291	P	***1803.8483***	902.4278	1786.8217	893.9145	1785.8377	893.4225	16
12	1339.4830	670.2452	1322.4565	661.7319	1321.4725	661.2399	G	1706.7955	853.9014	1689.7690	845.3881	1688.7850	844.8961	15
13	1499.5137	750.2605	1482.4871	741.7472	1481.5031	741.2552	C	1649.7741	825.3907	1632.7475	816.8774	1631.7635	816.3854	14
14	**1586.5457**	793.7765	1569.5192	785.2632	1568.5351	784.7712	S	1489.7434	745.3753	1472.7169	736.8621	1471.7328	736.3701	13
15	**1685.6141**	843.3107	1668.5876	834.7974	1667.6036	834.3054	V	***1402.7114***	701.8593	1385.6848	693.3461	1384.7008	692.8540	12
16	1782.6669	891.8371	1765.6403	883.3238	1764.6563	882.8318	P	***1303.6430***	652.3251	1286.6164	643.8118	1285.6324	643.3198	11
17	1881.7353	941.3713	1864.7088	932.8580	1863.7247	932.3660	V	1206.5902	603.7987	1189.5637	595.2855	1188.5796	594.7935	10
18	1978.7881	989.8977	1961.7615	981.3844	1960.7775	980.8924	P	***1107.5218***	554.2645	1090.4952	545.7513	1089.5112	545.2592	9
19	2049.8252	1025.4162	2032.7986	1016.9030	2031.8146	1016.4109	A	1010.4690	505.7381	993.4425	497.2249	992.4585	496.7329	8
20	2164.8521	1082.9297	2147.8256	1074.4164	2146.8416	1073.9244	N	***939.4319***	470.2196	922.4054	461.7063	921.4213	461.2143	7
21	2292.9107	1146.9590	2275.8842	1138.4457	2274.9001	1137.9537	Q	***824.4050***	412.7061	807.3784	404.1928	806.3944	403.7008	6
22	2379.9427	1190.4750	2362.9162	1181.9617	2361.9322	1181.4697	S	***696.3464***	348.6768	679.3198	340.1636	678.3358	339.6715	5
23	2527.0111	1264.0092	2509.9846	1255.4959	2509.0006	1255.0039	F	***609.3144***	305.1608	592.2878	296.6475	591.3038	296.1555	4

24	2713.0905	1357.0489	2696.0639	1348.5356	2695.0799	1348.0436	**W**	*462.2459*	231.6266	445.2194	223.1133	444.2354	222.6213	**3**
25	2814.1381	1407.5727	2797.1116	1399.0594	2796.1276	1398.5674	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.0	2987.2426	0.0014	GCSCFSDWQGPGCSVPVPANQSFWTR	Deamidated N20 99.07%
64.7	2987.2426	0.0014	GCSCFSDWQGPGCSVPVPANQSFWTR	Deamidated Q21 0.93%
17.0	2987.2426	0.0014	GCSCFSDWQGPGCSVPVPANQSFWTR	Deamidated Q9 0.00%

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

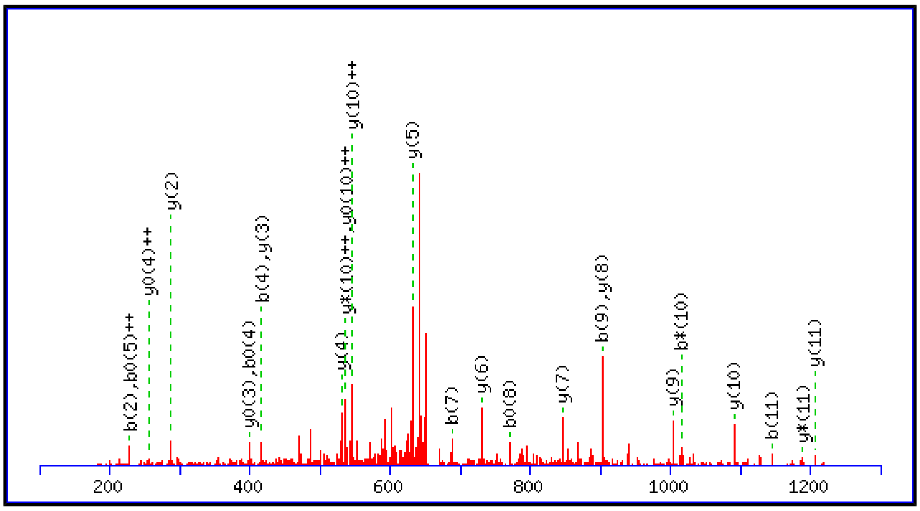
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDSTGNVTNELR**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

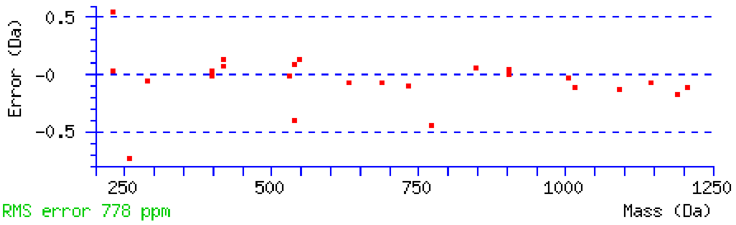
Match to Query 2015: 1318.642328 from(660.328440,2+) intensity(8168.3721) rtinseconds(663) scans(1397) index(1896)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum1149_scans__1397
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

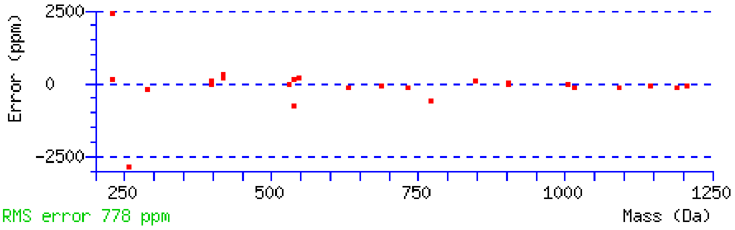
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1318.6365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 79 **Expect:** 2.6e-006
Matches : 25/116 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							12
2	**229.1183**	115.0628			211.1077	106.0575	D	***1206.5597***	603.7835	1189.5331	595.2702	1188.5491	594.7782	11
3	316.1503	158.5788			298.1397	149.5735	S	***1091.5327***	546.2700	1074.5062	537.7567	1073.5222	537.2647	10
4	**417.1980**	209.1026			399.1874	200.0974	T	***1004.5007***	502.7540	987.4742	494.2407	986.4901	493.7487	9
5	474.2195	237.6134			456.2089	228.6081	G	***903.4530***	452.2302	886.4265	443.7169	885.4425	443.2249	8
6	589.2464	295.1268	572.2198	286.6136	571.2358	286.1216	N	***846.4316***	423.7194	829.4050	415.2061	828.4210	414.7141	7
7	**688.3148**	344.6610	671.2883	336.1478	670.3042	335.6558	V	***731.4046***	366.2060	714.3781	357.6927	713.3941	357.2007	6
8	789.3625	395.1849	772.3359	386.6716	771.3519	386.1796	T	***632.3362***	316.6717	615.3097	308.1585	614.3256	307.6665	5
9	**903.4054**	452.2063	886.3789	443.6931	885.3949	443.2011	N	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	4
10	1032.4480	516.7276	1015.4215	508.2144	1014.4374	507.7224	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
11	**1145.5321**	573.2697	1128.5055	564.7564	1127.5215	564.2644	L	***288.2030***	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.2	1318.6365	0.0059	IDSTGNVTNELR	Deamidated N6 99.05%
59.0	1318.6365	0.0059	IDSTGNVTNELR	Deamidated N9 0.95%
23.7	1318.6365	0.0059	TSNLQGSVDQLR	
21.5	1318.6365	0.0059	TSNLQGSVDQLR	
17.5	1318.6365	0.0059	TSNLQGSVDQLR	
12.8	1318.6364	0.0059	LNNTSQKGLEGR	
12.0	1317.6347	1.0076	QSQAICVGGIER	
11.3	1317.6347	1.0076	QSQAICVGGIER	
9.8	1318.6477	-0.0054	GQQQSDTSSLLR	
9.4	1318.6405	0.0019	NLNPVFNETLR	

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

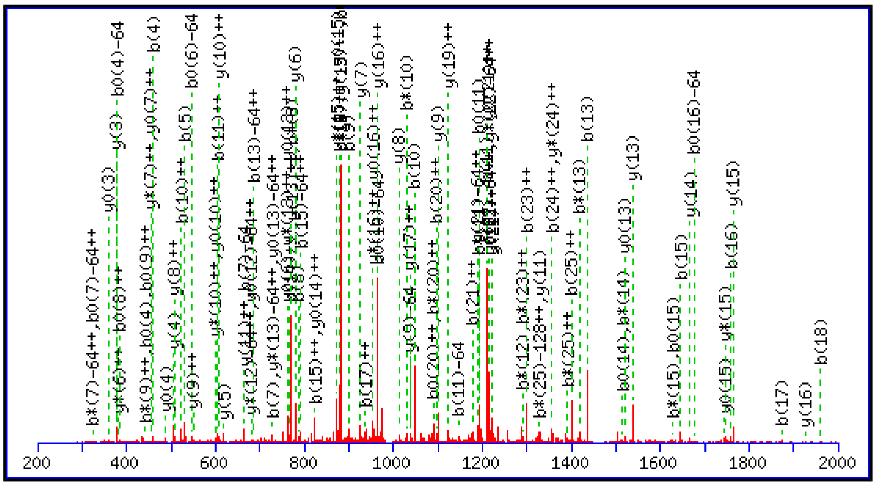
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPSQAPTGNFYPQPLLNSSMCLEDSR**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

Match to Query 27062: 2972.310852 from(991.777560,3+) intensity(18014.0879) rtinseconds(1679) scans(4201) index(5313)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum3673_scans__4201
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

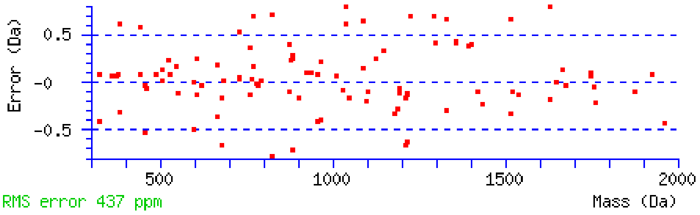
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

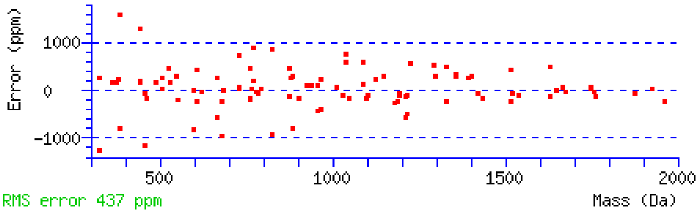


```
Monoisotopic mass of neutral peptide Mr(calc): 2972.2990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N17     : Deamidated (NQ)
M20     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 55  Expect: 0.00031
Matches : 105/542 fragment ions using 171 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							26
2	245.0954	123.0514					P	2826.2709	1413.6391	2809.2444	1405.1258	2808.2604	1404.6338	25
3	332.1275	166.5674			314.1169	157.5621	S	2729.2182	1365.1127	2712.1916	1356.5994	2711.2076	1356.1074	24
4	***460.1860***	230.5967	443.1595	222.0834	442.1755	221.5914	Q	2642.1861	1321.5967	2625.1596	1313.0834	2624.1756	1312.5914	23
5	***531.2232***	266.1152	514.1966	257.6019	513.2126	257.1099	A	2514.1276	1257.5674	2497.1010	1249.0541	2496.1170	1248.5621	22
6	628.2759	314.6416	611.2494	306.1283	610.2654	305.6363	P	2443.0904	1222.0489	2426.0639	1213.5356	2425.0799	1213.0436	21
7	***729.3236***	365.1654	712.2971	356.6522	711.3130	356.1602	T	2346.0377	1173.5225	2329.0111	1165.0092	2328.0271	1164.5172	20
8	***786.3451***	393.6762	769.3185	385.1629	768.3345	384.6709	G	2244.9900	1122.9986	2227.9634	1114.4854	2226.9794	1113.9934	19
9	***900.3880***	450.6976	883.3614	442.1844	882.3774	441.6924	N	2187.9685	1094.4879	2170.9420	1085.9746	2169.9580	1085.4826	18
10	***1047.4564***	***524.2318***	1030.4299	515.7186	1029.4458	515.2266	F	2073.9256	1037.4664	2056.8991	1028.9532	2055.9150	1028.4612	17
11	***1210.5197***	***605.7635***	1193.4932	597.2502	1192.5092	596.7582	Y	***1926.8572***	963.9322	1909.8306	955.4190	1908.8466	954.9270	16
12	1307.5725	654.2899	1290.5460	645.7766	1289.5619	645.2846	P	***1763.7939***	882.4006	1746.7673	873.8873	1745.7833	873.3953	15
13	***1435.6311***	718.3192	1418.6045	709.8059	1417.6205	709.3139	Q	***1666.7411***	833.8742	1649.7145	825.3609	1648.7305	824.8689	14
14	1532.6838	***766.8456***	1515.6573	758.3323	1514.6733	757.8403	P	***1538.6825***	769.8449	1521.6560	761.3316	1520.6720	760.8396	13
15	***1645.7679***	***823.3876***	1628.7414	814.8743	1627.7573	814.3823	L	1441.6298	721.3185	1424.6032	712.8052	1423.6192	712.3132	12
16	***1758.8520***	***879.9296***	1741.8254	871.4163	1740.8414	870.9243	L	***1328.5457***	664.7765	1311.5191	656.2632	1310.5351	655.7712	11
17	***1873.8789***	***937.4431***	1856.8524	928.9298	1855.8683	928.4378	N	***1215.4616***	608.2345	1198.4351	599.7212	1197.4511	599.2292	10
18	***1960.9109***	980.9591	1943.8844	972.4458	1942.9004	971.9538	S	***1100.4347***	550.7210	1083.4081	542.2077	1082.4241	541.7157	9
19	2047.9430	1024.4751	2030.9164	1015.9618	2029.9324	1015.4698	S	***1013.4027***	507.2050	996.3761	498.6917	995.3921	498.1997	8
20	2194.9784	***1097.9928***	2177.9518	1089.4795	2176.9678	1088.9875	M	***926.3706***	463.6890	909.3441	455.1757	908.3601	454.6837	7
21	2355.0090	***1178.0081***	2337.9825	1169.4949	2336.9985	1169.0029	C	***779.3352***	390.1713	762.3087	381.6580	761.3247	381.1660	6
22	2468.0931	1234.5502	2451.0665	1226.0369	2450.0825	1225.5449	L	***619.3046***	310.1559	602.2780	301.6427	601.2940	301.1506	5

23	2597.1357	***1299.0715***	2580.1091	1290.5582	2579.1251	1290.0662	**E**	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	**4**
24	2712.1626	***1356.5849***	2695.1361	1348.0717	2694.1521	1347.5797	**D**	***377.1779***	189.0926	360.1514	180.5793	359.1674	180.0873	**3**
25	2799.1946	***1400.1010***	2782.1681	1391.5877	2781.1841	1391.0957	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.5	2972.2990	0.0118	MPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated N17 45.69%
53.8	2972.2990	0.0118	MPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated N9 30.61%
52.3	2972.2990	0.0118	MPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated Q13 21.92%
45.2	2971.3150	0.9958	MPSQAPTGNFYPQPLLNSSMCLEDSR	
41.4	2972.2990	0.0118	MPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated Q4 1.79%
12.6	2971.3105	1.0004	HSAGNSMLIPSMSVTMETSMIMSNIQR	
4.3	2972.3015	0.0093	MNNGDVDLTSDRYSMVGGNLVINNPDK	
4.0	2972.3015	0.0093	MNNGDVDLTSDRYSMVGGNLVINNPDK	
4.0	2972.3015	0.0093	MNNGDVDLTSDRYSMVGGNLVINNPDK	
3.7	2972.3015	0.0093	MNNGDVDLTSDRYSMVGGNLVINNPDK	

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

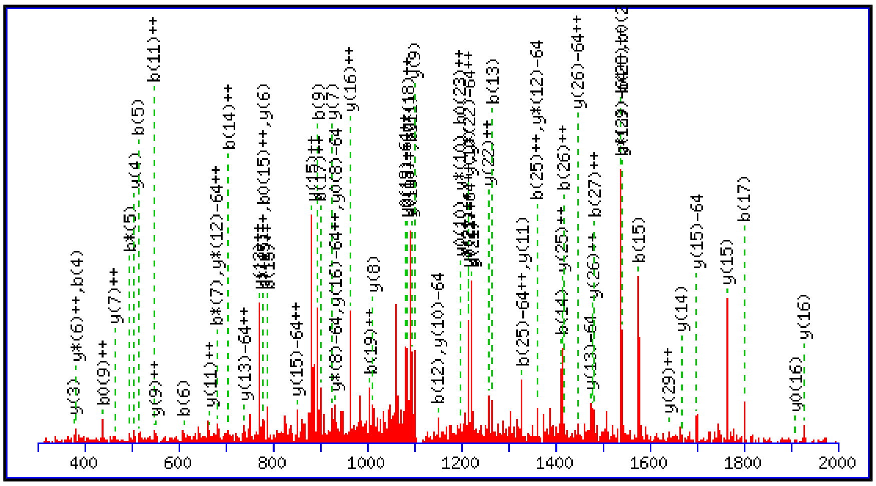
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

Match to Query 27416: 3338.547582 from(1113.856470,3+) intensity(19385.6973) rtinseconds(1788) scans(4497) index(2076)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum3892_scans__4497
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

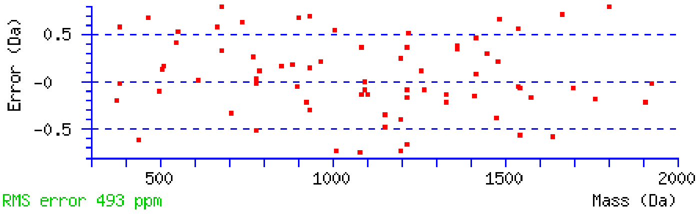
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

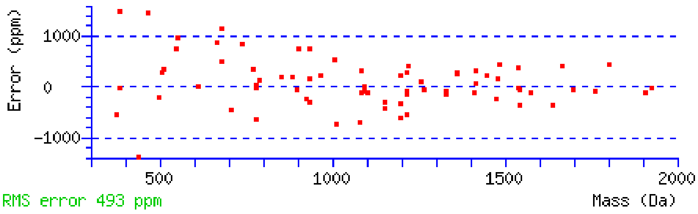


```
Monoisotopic mass of neutral peptide Mr(calc): 3337.5417
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N21     : Deamidated (NQ)
M24     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54  Expect: 0.00078
Matches : 73/502 fragment ions using 119 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	58.0287	29.5180					G							30
2	155.0815	78.0444					P	3281.5275	1641.2674	3264.5010	1632.7541	3263.5170	1632.2621	29
3	254.1499	127.5786					V	3184.4748	1592.7410	3167.4482	1584.2278	3166.4642	1583.7357	28
4	**382.2449**	191.6261	365.2183	183.1128			K	3085.4064	1543.2068	3068.3798	1534.6935	3067.3958	1534.2015	27
5	**513.2854**	257.1463	496.2588	248.6330			M	2957.3114	1479.1593	2940.2849	1470.6461	2939.3008	1470.1541	26
6	**610.3381**	305.6727	593.3116	297.1594			P	2826.2709	1413.6391	2809.2444	1405.1258	2808.2604	1404.6338	25
7	697.3702	349.1887	680.3436	340.6754	679.3596	340.1834	S	2729.2182	1365.1127	2712.1916	1356.5994	2711.2076	1356.1074	24
8	825.4287	413.2180	808.4022	404.7047	807.4182	404.2127	Q	2642.1861	1321.5967	2625.1596	1313.0834	2624.1756	1312.5914	23
9	**896.4659**	448.7366	879.4393	440.2233	878.4553	439.7313	A	2514.1276	1257.5674	2497.1010	1249.0541	2496.1170	1248.5621	22
10	993.5186	497.2629	976.4921	488.7497	975.5080	488.2577	P	2443.0904	1222.0489	2426.0639	1213.5356	2425.0799	1213.0436	21
11	**1094.5663**	**547.7868**	1077.5397	539.2735	1076.5557	538.7815	T	2346.0377	1173.5225	2329.0111	1165.0092	2328.0271	1164.5172	20
12	**1151.5878**	576.2975	1134.5612	567.7842	1133.5772	567.2922	G	2244.9900	1122.9986	2227.9634	1114.4854	2226.9794	1113.9934	19
13	**1265.6307**	633.3190	1248.6041	624.8057	1247.6201	624.3137	N	2187.9685	1094.4879	2170.9420	1085.9746	2169.9580	1085.4826	18
14	**1412.6991**	**706.8532**	1395.6725	698.3399	1394.6885	697.8479	F	2073.9256	1037.4664	2056.8991	1028.9532	2055.9150	1028.4612	17
15	**1575.7624**	**788.3849**	1558.7359	779.8716	1557.7519	779.3796	Y	***1926.8572***	963.9322	1909.8306	955.4190	1908.8466	954.9270	16
16	1672.8152	836.9112	1655.7886	828.3980	1654.8046	827.9060	P	***1763.7939***	882.4006	1746.7673	873.8873	1745.7833	873.3953	15
17	**1800.8738**	**900.9405**	1783.8472	892.4272	1782.8632	891.9352	Q	***1666.7411***	833.8742	1649.7145	825.3609	1648.7305	824.8689	14
18	1897.9265	949.4669	1880.9000	940.9536	1879.9160	940.4616	P	***1538.6825***	769.8449	1521.6560	761.3316	1520.6720	760.8396	13
19	2011.0106	**1006.0089**	1993.9840	997.4957	1993.0000	997.0037	L	1441.6298	721.3185	1424.6032	712.8052	1423.6192	712.3132	12
20	2124.0947	1062.5510	2107.0681	1054.0377	2106.0841	1053.5457	L	***1328.5457***	664.7765	1311.5191	656.2632	1310.5351	655.7712	11
21	2239.1216	1120.0644	2222.0951	1111.5512	2221.1110	1111.0592	N	***1215.4616***	608.2345	1198.4351	599.7212	1197.4511	599.2292	10
22	2326.1536	1163.5805	2309.1271	1155.0672	2308.1431	1154.5752	S	***1100.4347***	550.7210	1083.4081	542.2077	1082.4241	541.7157	9

23	2413.1857	1207.0965	2396.1591	1198.5832	2395.1751	1198.0912	**S**	***1013.4027***	507.2050	996.3761	498.6917	995.3921	498.1997	**8**
24	2560.2211	1280.6142	2543.1945	1272.1009	2542.2105	1271.6089	**M**	***926.3706***	463.6890	909.3441	455.1757	908.3601	454.6837	**7**
25	2720.2517	**1360.6295**	2703.2252	1352.1162	2702.2411	1351.6242	**C**	***779.3352***	390.1713	762.3087	381.6580	761.3247	381.1660	**6**
26	2833.3358	**1417.1715**	2816.3092	1408.6582	2815.3252	1408.1662	**L**	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	**5**
27	2962.3784	**1481.6928**	2945.3518	1473.1795	2944.3678	1472.6875	**E**	***506.2205***	253.6139	489.1940	245.1006	488.2100	244.6086	**4**
28	3077.4053	**1539.2063**	3060.3788	1530.6930	3059.3947	1530.2010	**D**	***377.1779***	189.0926	360.1514	180.5793	359.1674	180.0873	**3**
29	3164.4373	1582.7223	3147.4108	1574.2090	3146.4268	1573.7170	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
30							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.4	3337.5417	1.0059	GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated N21, Oxidation M24; 59.49%
51.3	3337.5417	1.0059	GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated Q17, Oxidation M24; 29.40%
46.0	3337.5417	1.0059	GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated N13, Oxidation M24; 8.72%
40.4	3337.5417	1.0059	GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR	Deamidated Q8, Oxidation M24; 2.39%
39.7	3336.5577	1.9899	GPVKMPSQAPTGNFYPQPLLNSSMCLEDSR	
6.5	3337.5555	0.9921	AQLGTTLVHQFSEQSSINQIDMQLMDESR	
3.5	3338.5587	-0.0111	SASINGVDQLLEVDPMHYTEWLERYMDK	
2.1	3338.5395	0.0081	AQLGTTLVHQFSEQSSINQIDMQLMDESR	
1.0	3336.5497	1.9979	SGMDSDKWLYVQQFNTFTDQTGELPTLSK	
1.0	3337.5554	0.9922	SPSLSYFIQPDLHPAEDFPISIEFTEDDK	

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

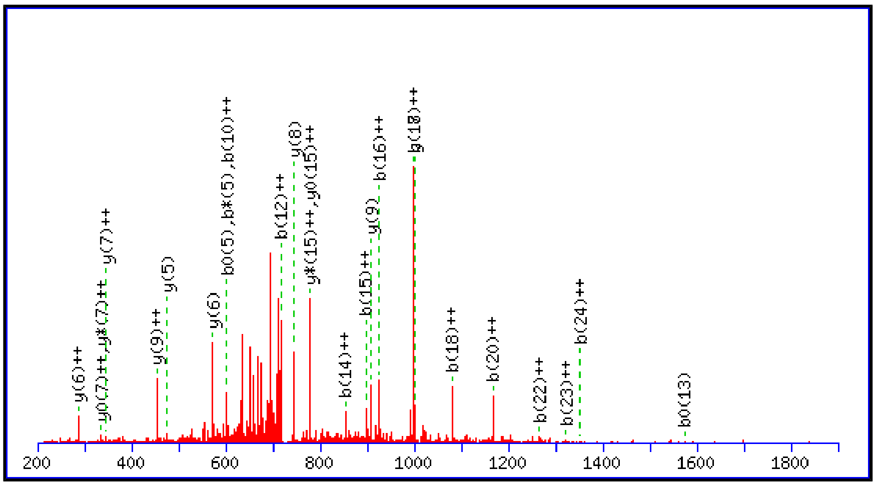
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CENLTTGKHCETCISGFYGDPTNGGK**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

Match to Query 26767: 2904.221616 from(727.062680,4+) intensity(0.0000) rtinseconds(982) scans(2272) index(3712)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum1932_scans__2272
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

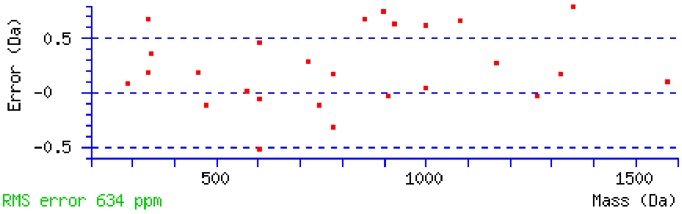
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

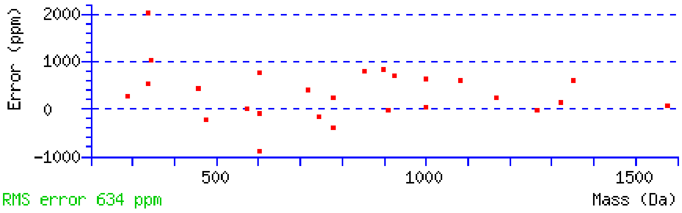


```
Monoisotopic mass of neutral peptide Mr(calc): 2903.2161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3      : Deamidated (NQ)
Ions Score: 49  Expect: 0.00052
Matches : 26/286 fragment ions using 45 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	161.0379	81.0226					**C**							**26**
2	290.0805	145.5439			272.0700	136.5386	**E**	2744.1927	1372.6000	2727.1661	1364.0867	2726.1821	1363.5947	**25**
3	405.1075	203.0574	388.0809	194.5441	387.0969	194.0521	**N**	2615.1501	1308.0787	2598.1235	1299.5654	2597.1395	1299.0734	**24**
4	518.1915	259.5994	501.1650	251.0861	500.1810	250.5941	**L**	2500.1231	1250.5652	2483.0966	1242.0519	2482.1126	1241.5599	**23**
5	619.2392	310.1232	602.2127	301.6100	601.2286	301.1180	**T**	2387.0391	1194.0232	2370.0125	1185.5099	2369.0285	1185.0179	**22**
6	720.2869	360.6471	703.2603	352.1338	702.2763	351.6418	**T**	2285.9914	1143.4993	2268.9648	1134.9861	2267.9808	1134.4941	**21**
7	777.3083	389.1578	760.2818	380.6445	759.2978	380.1525	**G**	2184.9437	1092.9755	2167.9172	1084.4622	2166.9332	1083.9702	**20**
8	905.4033	453.2053	888.3768	444.6920	887.3927	444.2000	**K**	2127.9223	1064.4648	2110.8957	1055.9515	2109.9117	1055.4595	**19**
9	1042.4622	521.7347	1025.4357	513.2215	1024.4517	512.7295	**H**	1999.8273	1000.4173	1982.8007	991.9040	1981.8167	991.4120	**18**
10	1202.4929	***601.7501***	1185.4663	593.2368	1184.4823	592.7448	**C**	1862.7684	931.8878	1845.7418	923.3746	1844.7578	922.8825	**17**
11	1331.5355	666.2714	1314.5089	657.7581	1313.5249	657.2661	**E**	1702.7377	851.8725	1685.7112	843.3592	1684.7272	842.8672	**16**
12	1432.5831	***716.7952***	1415.5566	708.2819	1414.5726	707.7899	**T**	1573.6951	787.3512	1556.6686	778.8379	1555.6846	778.3459	**15**
13	1592.6138	796.8105	1575.5872	788.2973	1574.6032	787.8053	**C**	1472.6475	736.8274	1455.6209	728.3141	1454.6369	727.8221	**14**
14	1705.6979	***853.3526***	1688.6713	844.8393	1687.6873	844.3473	**I**	1312.6168	656.8120	1295.5903	648.2988	1294.6062	647.8068	**13**
15	1792.7299	***896.8686***	1775.7033	888.3553	1774.7193	887.8633	**S**	1199.5327	600.2700	1182.5062	591.7567	1181.5222	591.2647	**12**
16	1849.7513	***925.3793***	1832.7248	916.8660	1831.7408	916.3740	**G**	1112.5007	556.7540	1095.4742	548.2407	1094.4902	547.7487	**11**
17	1996.8198	***998.9135***	1979.7932	990.4002	1978.8092	989.9082	**F**	1055.4793	528.2433	1038.4527	519.7300	1037.4687	519.2380	**10**
18	2159.8831	***1080.4452***	2142.8565	1071.9319	2141.8725	1071.4399	**Y**	**908.4108**	454.7091	891.3843	446.1958	890.4003	445.7038	**9**
19	2216.9046	1108.9559	2199.8780	1100.4426	2198.8940	1099.9506	**G**	**745.3475**	373.1774	728.3210	364.6641	727.3369	364.1721	**8**
20	2331.9315	***1166.4694***	2314.9049	1157.9561	2313.9209	1157.4641	**D**	688.3260	344.6667	671.2995	336.1534	670.3155	335.6614	**7**
21	2428.9843	1214.9958	2411.9577	1206.4825	2410.9737	1205.9905	**P**	**573.2991**	287.1532	556.2726	278.6399	555.2885	278.1479	**6**
22	2530.0319	***1265.5196***	2513.0054	1257.0063	2512.0214	1256.5143	**T**	**476.2463**	238.6268	459.2198	230.1135	458.2358	229.6215	**5**
23	2644.0749	***1322.5411***	2627.0483	1314.0278	2626.0643	1313.5358	**N**	375.1987	188.1030	358.1721	179.5897			**4**

24	2701.0963	***1351.0518***	2684.0698	1342.5385	2683.0858	1342.0465	**G**	261.1557	131.0815	244.1292	122.5682			**3**
25	2758.1178	1379.5625	2741.0912	1371.0493	2740.1072	1370.5573	**G**	204.1343	102.5708	187.1077	94.0575			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.0	2903.2161	1.0056	CENLTTGKHCETCISGFYGDPTNGGK	Deamidated N3 99.99%
8.4	2904.2178	0.0038	FMGEPEAEEGDGGDGQGGAVQPAEAVPMR	
6.6	2904.2178	0.0038	FMGEPEAEEGDGGDGQGGAVQPAEAVPMR	
6.1	2903.2161	1.0056	CENLTTGKHCETCISGFYGDPTNGGK	Deamidated N23 0.01%
2.8	2903.2250	0.9966	QVDGDNSHVEMKLAVDEEENADNNTK	
0.3	2902.2169	2.0047	ELCDPKKAMEEEYNMAVYCFSEK	
0.3	2903.2281	0.9935	RNMGGPPPCMGSGVQPPMNAMNPGYPR	

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

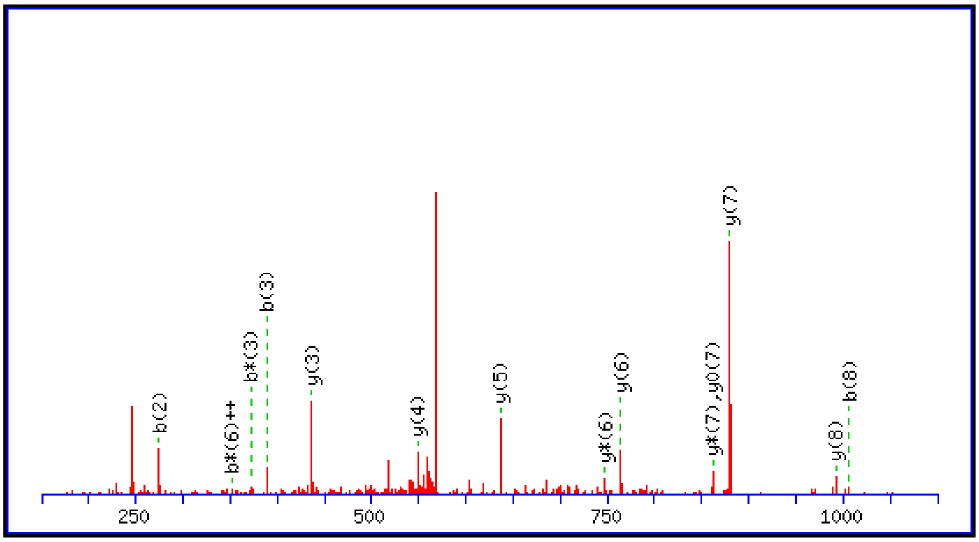
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CINQSICEK**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

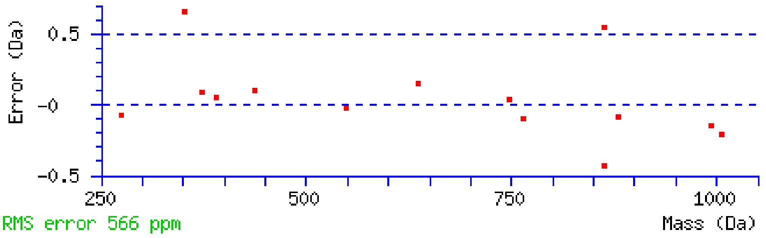
Match to Query 1582: 1151.499408 from(576.756980,2+) intensity(3854.9431) rtinseconds(297) scans(582) index(6108)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum497_scans__582
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

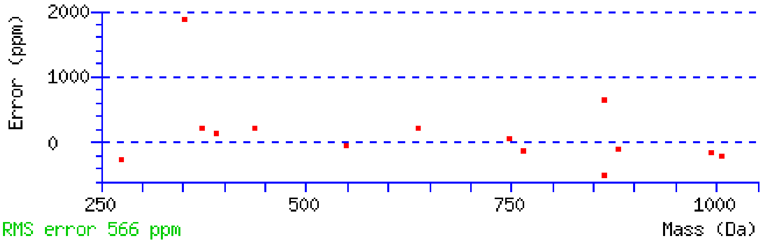
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1151.4951
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 48 **Expect:** 0.0013
Matches : 14/82 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	161.0379	81.0226					C							9
2	**274.1220**	137.5646					I	***992.4717***	496.7395	975.4452	488.2262	974.4612	487.7342	8
3	**389.1489**	195.0781	372.1224	186.5648			N	***879.3877***	440.1975	862.3611	431.6842	861.3771	431.1922	7
4	517.2075	259.1074	500.1810	250.5941			Q	***764.3607***	382.6840	747.3342	374.1707	746.3502	373.6787	6
5	604.2395	302.6234	587.2130	294.1101	586.2290	293.6181	S	***636.3021***	318.6547	619.2756	310.1414	618.2916	309.6494	5
6	717.3236	359.1654	700.2971	350.6522	699.3130	350.1602	I	***549.2701***	275.1387	532.2436	266.6254	531.2595	266.1334	4
7	877.3543	439.1808	860.3277	430.6675	859.3437	430.1755	C	***436.1860***	218.5967	419.1595	210.0834	418.1755	209.5914	3
8	**1006.3968**	503.7021	989.3703	495.1888	988.3863	494.6968	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.6	1151.4951	0.0043	CINQSICEK	Deamidated N3 93.35%
36.2	1151.4951	0.0043	CINQSICEK	Deamidated Q4 6.65%
19.1	1151.4951	0.0044	CNLKQCAQK	
7.5	1150.4924	1.0070	GLTDSECNQK	
6.3	1151.5029	-0.0035	HHNMNELQK	
5.0	1151.5016	-0.0022	ENVSALDMEK	
4.8	1151.5016	-0.0022	LTNGMNNIEK	
4.5	1151.4951	0.0043	CLVSNCGVNK	
3.4	1151.5029	-0.0035	HHNMNELQK	
3.2	1150.4924	1.0070	ENSGTCQVQK	

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

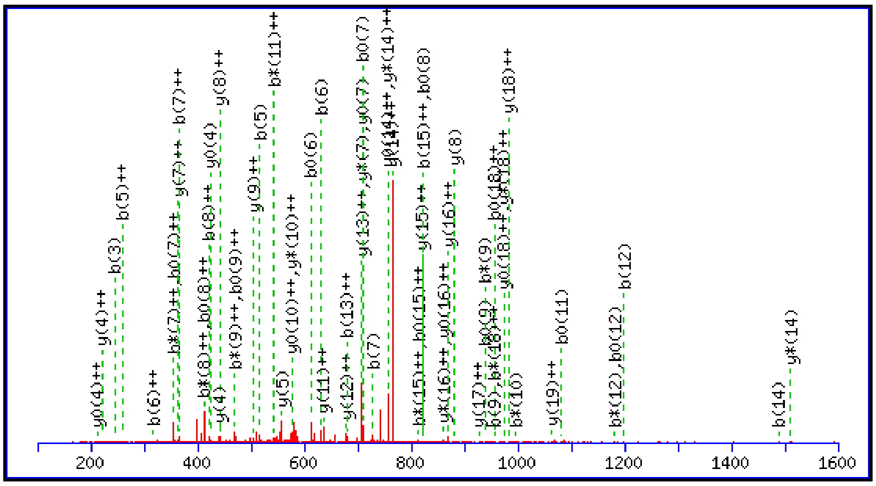
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AATCINPLNGSVCERPANHSAK**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

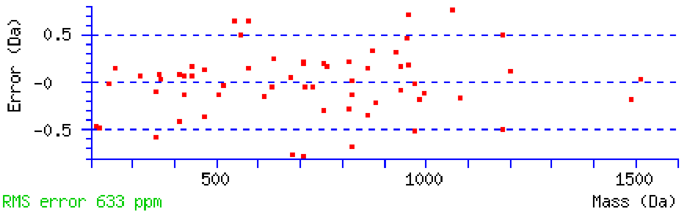
Match to Query 20957: 2368.093016 from(593.030530,4+) intensity(30446.5313) rtinseconds(584) scans(1402) index(17360)
Title: 111019_Est_MI_YP_G_07Spectrum1217_scans__1402
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

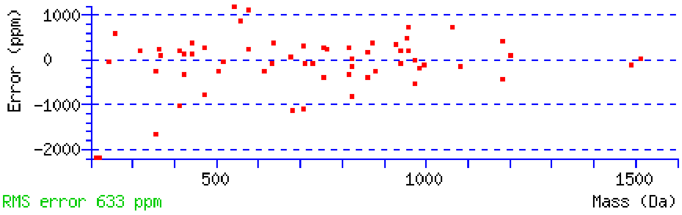
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2368.0899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N18 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0058
Matches : 62/234 fragment ions using 118 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**22**
2	143.0815	72.0444					**A**	2298.0601	1149.5337	2281.0336	1141.0204	2280.0496	1140.5284	**21**
3	**244.1292**	122.5682			226.1186	113.5629	**T**	2227.0230	1114.0152	2209.9965	1105.5019	2209.0125	1105.0099	**20**
4	404.1598	202.5836			386.1493	193.5783	**C**	2125.9753	1063.4913	2108.9488	1054.9780	2107.9648	1054.4860	**19**
5	**517.2439**	**259.1256**			499.2333	250.1203	**I**	1965.9447	983.4760	1948.9182	974.9627	1947.9341	974.4707	**18**
6	**631.2868**	**316.1470**	614.2603	307.6338	613.2763	307.1418	**N**	1852.8606	926.9340	1835.8341	918.4207	1834.8501	917.9287	**17**
7	**728.3396**	**364.6734**	711.3130	356.1602	710.3290	355.6681	**P**	1738.8177	869.9125	1721.7912	861.3992	1720.8071	860.9072	**16**
8	841.4237	**421.2155**	824.3971	412.7022	823.4131	412.2102	**L**	1641.7649	821.3861	1624.7384	812.8728	1623.7544	812.3808	**15**
9	**956.4506**	478.7289	939.4240	470.2157	938.4400	469.7237	**N**	1528.6809	764.8441	1511.6543	756.3308	1510.6703	755.8388	**14**
10	1013.4721	507.2397	996.4455	498.7264	995.4615	498.2344	**G**	1413.6539	707.3306	1396.6274	698.8173	1395.6434	698.3253	**13**
11	1100.5041	550.7557	1083.4775	542.2424	1082.4935	541.7504	**S**	1356.6325	678.8199	1339.6059	670.3066	1338.6219	669.8146	**12**
12	**1199.5725**	600.2899	1182.5460	591.7766	1181.5619	591.2846	**V**	1269.6004	635.3039	1252.5739	626.7906	1251.5899	626.2986	**11**
13	1359.6031	**680.3052**	1342.5766	671.7919	1341.5926	671.2999	**C**	1170.5320	585.7697	1153.5055	577.2564	1152.5215	576.7644	**10**
14	**1488.6457**	744.8265	1471.6192	736.3132	1470.6352	735.8212	**E**	1010.5014	505.7543	993.4748	497.2411	992.4908	496.7490	**9**
15	1644.7469	**822.8771**	1627.7203	814.3638	1626.7363	813.8718	**R**	881.4588	441.2330	864.4322	432.7198	863.4482	432.2278	**8**
16	1741.7996	871.4034	1724.7731	862.8902	1723.7891	862.3982	**P**	725.3577	363.1825	708.3311	354.6692	707.3471	354.1772	**7**
17	1812.8367	906.9220	1795.8102	898.4087	1794.8262	897.9167	**A**	628.3049	314.6561	611.2784	306.1428	610.2944	305.6508	**6**
18	1927.8637	964.4355	1910.8371	955.9222	1909.8531	955.4302	**N**	557.2678	279.1375	540.2413	270.6243	539.2572	270.1323	**5**
19	2064.9226	1032.9649	2047.8960	1024.4517	2046.9120	1023.9596	**H**	442.2409	221.6241	425.2143	213.1108	424.2303	212.6188	**4**
20	2151.9546	1076.4809	2134.9281	1067.9677	2133.9440	1067.4757	**S**	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
21	2222.9917	1111.9995	2205.9652	1103.4862	2204.9812	1102.9942	**A**	218.1499	109.5786	201.1234	101.0653			**2**
22							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.1	2368.0899	0.0031	AATCINPLNGSVCERPANHSAK	Deamidated N9, N18 89.68%
33.3	2368.0899	0.0031	AATCINPLNGSVCERPANHSAK	Deamidated N6, N18 5.97%
31.9	2368.0899	0.0031	AATCINPLNGSVCERPANHSAK	Deamidated N6, N9 4.35%
7.1	2366.0930	2.0001	LGTGAAVGLWGCRNNCMGTITR	
3.0	2367.0776	1.0154	YSEAARSAMIADYMFWLGGGR	
2.9	2367.0835	1.0095	ERKNVNVESSCAVWNSTLIC	
2.8	2368.0940	-0.0010	VHTGERPYECSECGKAFLTK	
2.6	2368.0821	0.0109	LNHMSNKTTSSKNMEMVQQK	
2.6	2368.0821	0.0109	LNHMSNKTTSSKNMEMVQQK	
2.6	2368.0821	0.0109	LNHMSNKTTSSKNMEMVQQK	

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

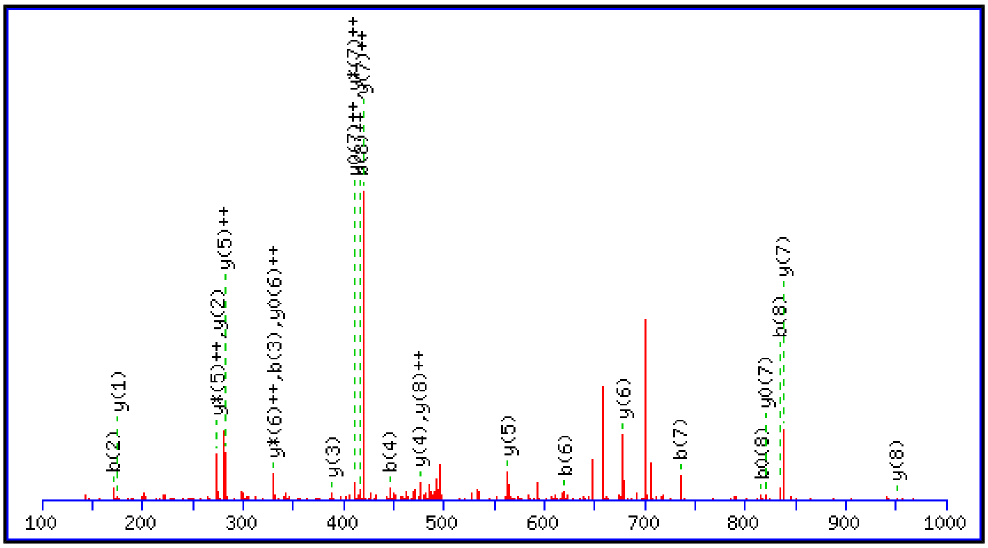
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GICNSSDVR**
Found in **O75882** in **con_Xuniprot_HUMAN3**, ATRN_HUMAN Attractin OS=Homo sapiens GN=ATRN PE=1 SV=2

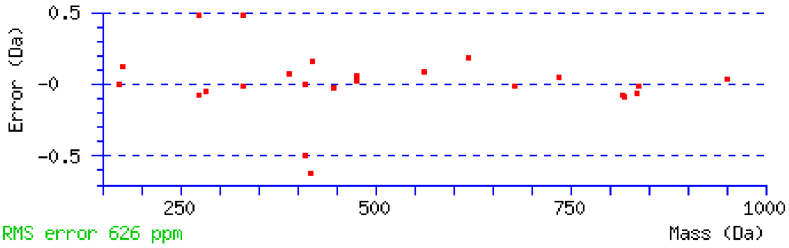
Match to Query 164: 1007.435788 from(504.725170,2+) intensity(8102.9697) rtinseconds(196) scans(383) index(19264)
Title: 111019_Est_MI_YP_G_09Spectrum326_scans__383
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

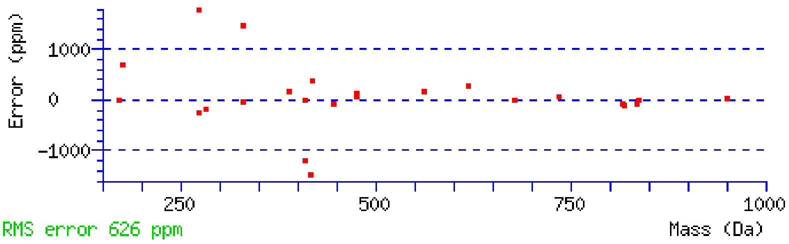
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1007.4342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
Ions Score: 42  Expect: 0.0051
Matches : 25/78 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	58.0287	29.5180					G							9
2	**171.1128**	86.0600					I	***951.4200***	476.2136	934.3935	467.7004	933.4095	467.2084	8
3	**331.1435**	166.0754					C	***838.3360***	419.6716	821.3094	411.1583	820.3254	410.6663	7
4	**446.1704**	223.5888	429.1438	215.0756			N	***678.3053***	339.6563	661.2788	331.1430	660.2947	330.6510	6
5	533.2024	267.1049	516.1759	258.5916	515.1919	258.0996	S	***563.2784***	282.1428	546.2518	273.6295	545.2678	273.1375	5
6	**620.2345**	310.6209	603.2079	302.1076	602.2239	301.6156	S	***476.2463***	238.6268	459.2198	230.1135	458.2358	229.6215	4
7	**735.2614**	368.1343	718.2348	359.6211	717.2508	359.1291	D	***389.2143***	195.1108	372.1878	186.5975	371.2037	186.1055	3
8	**834.3298**	417.6685	817.3033	409.1553	816.3192	408.6633	V	***274.1874***	137.5973	257.1608	129.0840			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GICNSSDVR
(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	1007.4342	0.0016	GICNSSDVR
7.0	1007.4342	0.0016	VACQASSER
4.9	1007.4342	0.0016	AAMSGQGVDR
4.7	1007.4342	0.0016	SSAGGEDMVR
1.5	1006.4291	1.0067	WDAATGACR
1.2	1005.4298	2.0060	CGDKGGGAER
0.5	1007.4342	0.0016	ALMNNSQGR
0.2	1006.4291	1.0067	IGCDYSHR
0.1	1006.4316	1.0042	TQSGAGSDER

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

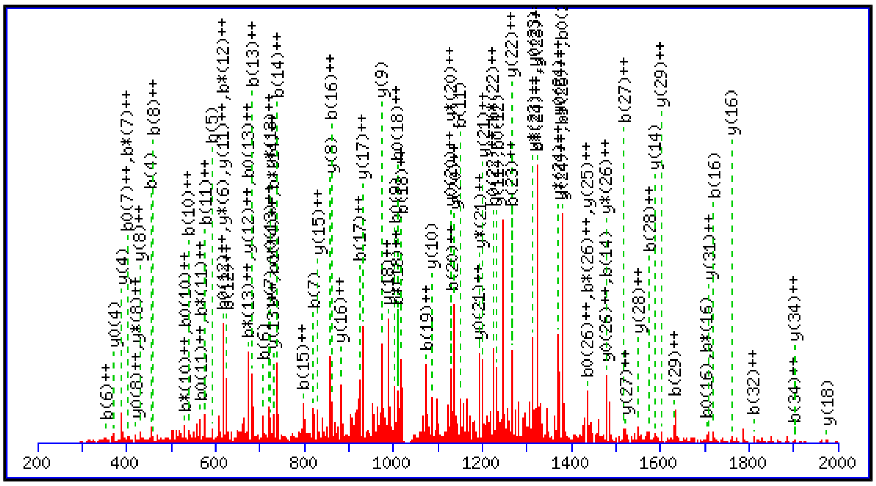
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28443: 4121.065016 from(1031.273530,4+) intensity(57221.5000) rtinseconds(2505) scans(6608) index(19889)
Title: 111019_Est_MI_YP_G_09Spectrum5854_scans__6608
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

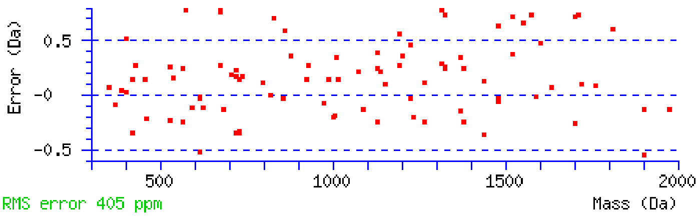
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

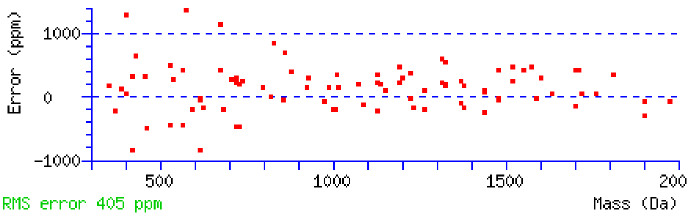


```
Monoisotopic mass of neutral peptide Mr(calc): 4121.0527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6     : Deamidated (NQ)
N29    : Deamidated (NQ)
N33    : Deamidated (NQ)
Ions Score: 130  Expect: 1.7e-011
Matches : 96/414 fragment ions using 119 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					**M**							37
2	231.1162	116.0617					**V**	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	318.1482	159.5777			300.1376	150.5725	**S**	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	**455.2071**	228.1072			437.1966	219.1019	**H**	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	**592.2660**	296.6367			574.2555	287.6314	**H**	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**707.2930**	***354.1501***	690.2664	345.6368	689.2824	345.1448	**N**	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	921.4247	***461.2160***	904.3982	452.7027	903.4141	452.2107	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1022.4724	511.7398	1005.4458	503.2266	1004.4618	502.7346	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	**1150.5310**	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1591.7897	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	**N**	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1720.8323**	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	**E**	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	1848.8909	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	**Q**	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	**W**	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2148.0543	***1074.5308***	2131.0277	1066.0175	2130.0437	1065.5255	**L**	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	**L**	**1975.0131**	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	**T**	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	**T**	**1760.8814**	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2534.2708	***1267.6390***	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2889.4927	1445.2500	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3036.5612	***1518.7842***	3019.5346	1510.2709	3018.5506	1509.7789	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3149.6452	***1575.3262***	3132.6187	1566.8130	3131.6347	1566.3210	**L**	**1086.5062**	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3264.6722	***1632.8397***	3247.6456	1624.3264	3246.6616	1623.8344	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3401.7311	1701.3692	3384.7045	1692.8559	3383.7205	1692.3639	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3617.8057	***1809.4065***	3600.7791	1800.8932	3599.7951	1800.4012	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3732.8326	1866.9200	3715.8061	1858.4067	3714.8221	1857.9147	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3803.8698	***1902.4385***	3786.8432	1893.9252	3785.8592	1893.4332	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3904.9174	1952.9624	3887.8909	1944.4491	3886.9069	1943.9571	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3975.9545	1988.4809	3958.9280	1979.9676	3957.9440	1979.4756	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
130.4	4121.0527	0.0123	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 94.45%
115.6	4121.0527	0.0123	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 3.13%
111.9	4121.0527	0.0123	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 1.34%
110.8	4121.0527	0.0123	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 1.04%
95.9	4121.0527	0.0123	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 0.03%
94.0	4120.0687	0.9963	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
91.3	4120.0687	0.9963	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
89.3	4120.0687	0.9963	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
85.1	4120.0687	0.9963	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
82.8	4120.0687	0.9963	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

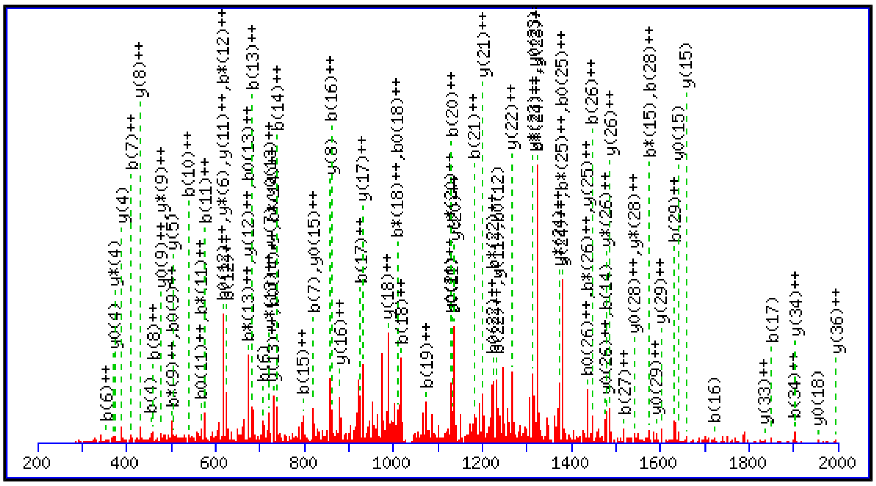
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28479: 4121.069016 from(1031.274530,4+) intensity(134370.2344) rtinseconds(2578) scans(6736) index(25646)
Title: 111019_Est_MI_YS_G_07Spectrum5803_scans__6736
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

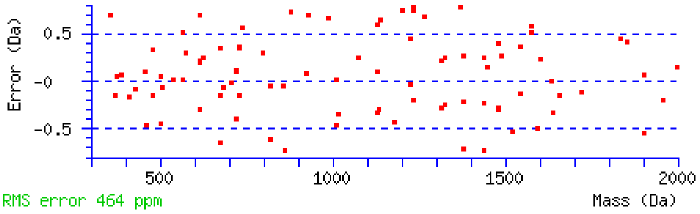
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

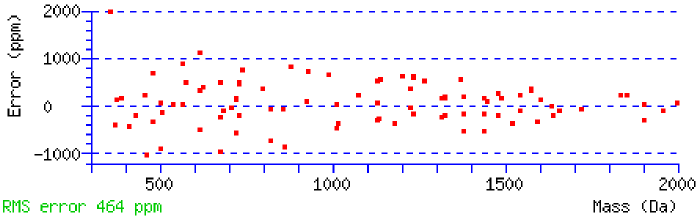


Monoisotopic mass of neutral peptide Mr(calc): 4121.0527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N15 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 123 **Expect:** 8.5e-011
Matches : 94/414 fragment ions using 121 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	318.1482	159.5777			300.1376	150.5725	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	**455.2071**	228.1072			437.1966	219.1019	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	592.2660	296.6367			574.2555	287.6314	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**707.2930**	***354.1501***	690.2664	345.6368	689.2824	345.1448	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	**820.3770**	***410.6922***	803.3505	402.1789	802.3665	401.6869	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	921.4247	***461.2160***	904.3982	452.7027	903.4141	452.2107	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1022.4724	511.7398	1005.4458	503.2266	1004.4618	502.7346	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1150.5310	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1592.7737	***796.8905***	1575.7472	788.3772	1574.7632	787.8852	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1721.8163**	***861.4118***	1704.7898	852.8985	1703.8057	852.4065	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	**1849.8749**	***925.4411***	1832.8483	916.9278	1831.8643	916.4358	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2035.9542	***1018.4807***	2018.9277	1009.9675	2017.9436	1009.4755	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2149.0383	***1075.0228***	2132.0117	1066.5095	2131.0277	1066.0175	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2262.1223	***1131.5648***	2245.0958	1123.0515	2244.1118	1122.5595	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2363.1700	***1182.0886***	2346.1435	1173.5754	2345.1594	1173.0834	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2464.2177	***1232.6125***	2447.1911	1224.0992	2446.2071	1223.6072	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2535.2548	1268.1310	2518.2283	1259.6178	2517.2442	1259.1258	**A**	**1658.8497**	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2663.3498	1332.1785	2646.3232	1323.6652	2645.3392	1323.1732	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2890.4768	***1445.7420***	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3037.5452	***1519.2762***	3020.5186	1510.7629	3019.5346	1510.2709	**F**	**1232.5906**	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3150.6292	***1575.8183***	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3264.6722	***1632.8397***	3247.6456	1624.3264	3246.6616	1623.8344	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3401.7311	1701.3692	3384.7045	1692.8559	3383.7205	1692.3639	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3617.8057	1809.4065	3600.7791	1800.8932	3599.7951	1800.4012	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3732.8326	1866.9200	3715.8061	1858.4067	3714.8221	1857.9147	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3803.8698	***1902.4385***	3786.8432	1893.9252	3785.8592	1893.4332	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3904.9174	1952.9624	3887.8909	1944.4491	3886.9069	1943.9571	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3975.9545	1988.4809	3958.9280	1979.9676	3957.9440	1979.4756	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
123.4	4121.0527	0.0163	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 81.52%
116.1	4121.0527	0.0163	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 15.35%
107.3	4121.0527	0.0163	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 1.99%
104.4	4121.0527	0.0163	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 1.02%
99.6	4120.0687	1.0003	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
91.0	4120.0687	1.0003	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
90.3	4121.0527	0.0163	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 0.04%
87.1	4120.0687	1.0003	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
86.7	4120.0687	1.0003	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
82.6	4120.0687	1.0003	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

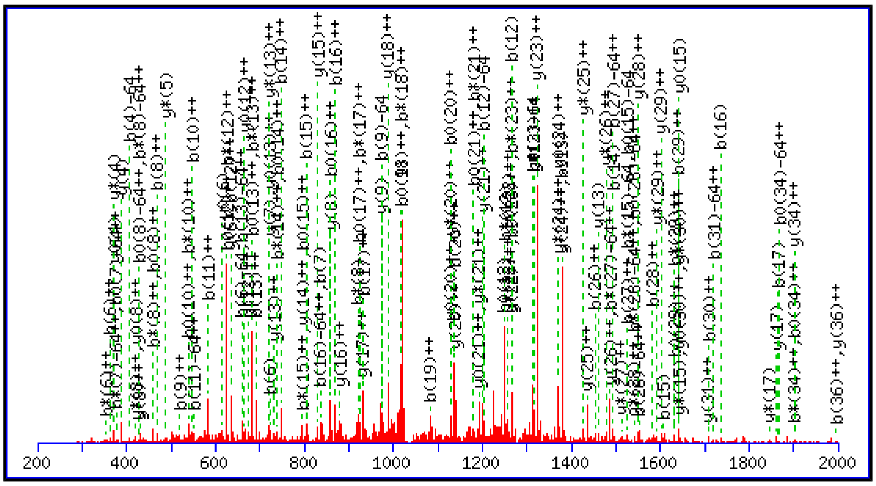
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28817: 4137.065456 from(1035.273640,4+) intensity(69579.8750) rtinseconds(2601) scans(6545) index(26282)
Title: 111019_Est_MI_YS_G_08Spectrum5692_scans__6545
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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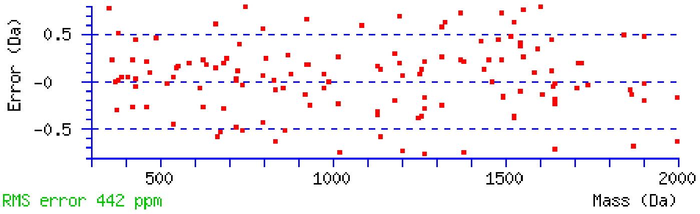
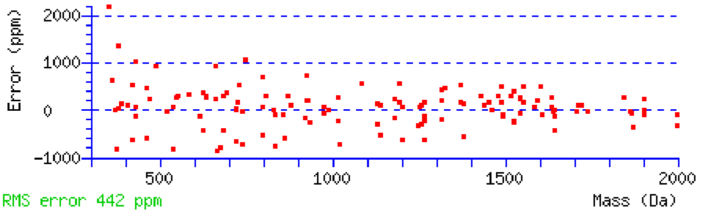
Monoisotopic mass of neutral peptide Mr(calc): 4137.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6     : Deamidated (NQ)
N29    : Deamidated (NQ)
N33    : Deamidated (NQ)
Ions Score: 120  Expect: 2.1e-010
Matches : 135/616 fragment ions using 174 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	334.1431	167.5752			316.1326	158.5699	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	471.2020	236.1047			453.1915	227.0994	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	608.2609	304.6341			590.2504	295.6288	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1038.4673	***519.7373***	1021.4408	511.2240	1020.4567	510.7320	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1166.5259	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	**1607.7846**	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1864.8858**	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2164.0492	***1082.5282***	2147.0226	1074.0149	2146.0386	1073.5229	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	**1460.7016**	730.8544	1443.6750	722.3412	1442.6910	721.8492	**13**
26	2905.4877	***1453.2475***	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3052.5561	***1526.7817***	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3165.6401	***1583.3237***	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3280.6671	***1640.8372***	3263.6405	1632.3239	3262.6565	1631.8319	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3417.7260	***1709.3666***	3400.6994	1700.8534	3399.7154	1700.3614	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3504.7580	1752.8826	3487.7315	1744.3694	3486.7475	1743.8774	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3748.8276	1874.9174	3731.8010	1866.4041	3730.8170	1865.9121	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3819.8647	1910.4360	3802.8381	1901.9227	3801.8541	1901.4307	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3920.9123	1960.9598	3903.8858	1952.4465	3902.9018	1951.9545	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3991.9495	***1996.4784***	3974.9229	1987.9651	3973.9389	1987.4731	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
120.0	4137.0477	0.0178	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 99.88%
88.7	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
85.8	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
85.7	4137.0477	0.0178	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 0.04%
82.2	4137.0477	0.0178	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 0.02%
81.5	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
79.3	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
78.5	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
77.6	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
76.6	4136.0636	1.0018	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28857: 4137.071576 from(1035.275170,4+) intensity(220692.9375) rtinseconds(2414) scans(6158) index(12860)
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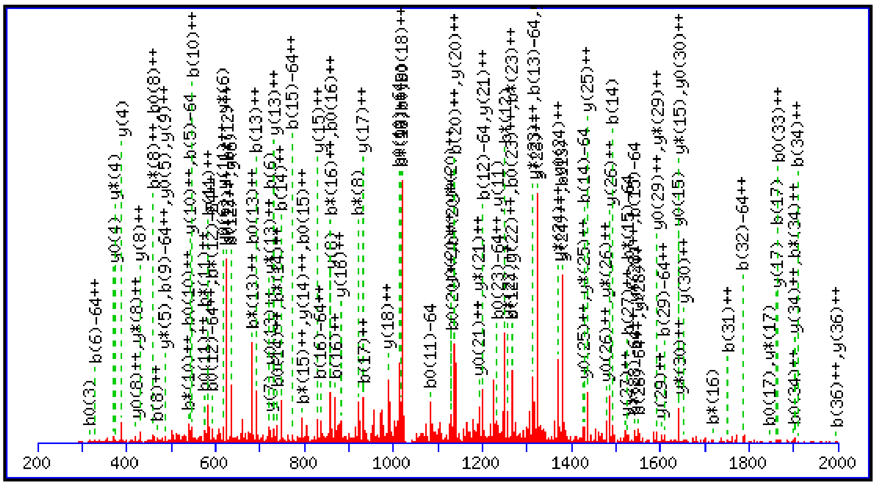
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

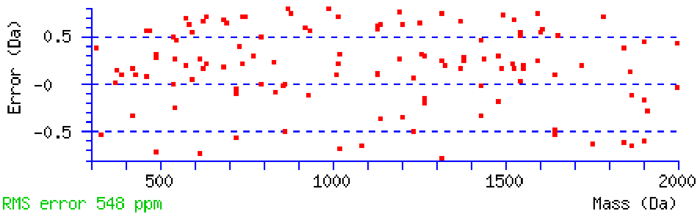
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

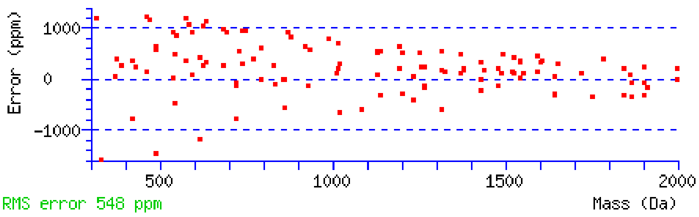


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 119 **Expect:** 2.5e-010
Matches : 129/616 fragment ions using 155 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					**M**							**37**
2	247.1111	124.0592					**V**	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	**36**
3	334.1431	167.5752			316.1326	158.5699	**S**	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	**35**
4	471.2020	236.1047			453.1915	227.0994	**H**	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	**34**
5	608.2609	304.6341			590.2504	295.6288	**H**	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	**33**
6	**722.3039**	361.6556	705.2773	353.1423	704.2933	352.6503	**N**	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	**32**
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	**31**
8	936.4356	**468.7214**	919.4091	460.2082	918.4250	459.7162	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	**30**
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	**29**
10	1094.5048	**547.7560**	1077.4782	539.2427	1076.4942	538.7507	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	**28**
11	1165.5419	**583.2746**	1148.5153	574.7613	1147.5313	574.2693	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	**27**
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	**26**
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	**25**
14	**1492.7577**	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
15	1606.8006	803.9039	1589.7741	795.3907	1588.7900	794.8987	**N**	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	**23**
16	1735.8432	**868.4252**	1718.8166	859.9120	1717.8326	859.4200	**E**	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	**22**
17	**1863.9018**	**932.4545**	1846.8752	923.9413	1845.8912	923.4492	**Q**	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	**21**
18	2049.9811	1025.4942	2032.9545	1016.9809	2031.9705	1016.4889	**W**	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	**20**
19	2163.0652	1082.0362	2146.0386	1073.5229	2145.0546	1073.0309	**L**	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	**19**
20	2276.1492	**1138.5782**	2259.1227	1130.0650	2258.1386	1129.5730	**L**	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	**18**
21	2377.1969	1189.1021	2360.1703	1180.5888	2359.1863	1180.0968	**T**	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	**17**
22	2478.2446	1239.6259	2461.2180	1231.1126	2460.2340	1230.6206	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**

23	2549.2817	1275.1445	2532.2551	1266.6312	2531.2711	1266.1392	A	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	15
24	2677.3766	1339.1920	2660.3501	1330.6787	2659.3661	1330.1867	K	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	14
25	2791.4196	1396.2134	2774.3930	1387.7002	2773.4090	1387.2081	N	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	13
26	2904.5036	1452.7555	2887.4771	1444.2422	2886.4931	1443.7502	L	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	12
27	3051.5721	**1526.2897**	3034.5455	1517.7764	3033.5615	1517.2844	F	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	11
28	3164.6561	1582.8317	3147.6296	1574.3184	3146.6456	1573.8264	L	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	10
29	3279.6831	1640.3452	3262.6565	1631.8319	3261.6725	1631.3399	N	973.4221	487.2147	956.3956	478.7014	955.4116	478.2094	9
30	3416.7420	1708.8746	3399.7154	1700.3614	3398.7314	1699.8693	H	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	8
31	3503.7740	**1752.3906**	3486.7475	1743.8774	3485.7634	1743.3854	S	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	7
32	3632.8166	1816.9119	3615.7900	1808.3987	3614.8060	1807.9067	E	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	6
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	N	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	5
34	3818.8807	**1909.9440**	3801.8541	1901.4307	3800.8701	1900.9387	A	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	4
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
36	3990.9654	**1995.9864**	3973.9389	1987.4731	3972.9549	1986.9811	A	218.1499	109.5786	201.1234	101.0653			2
37							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
119.0	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 84.39%
110.8	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 12.69%
104.3	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 2.87%
83.3	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.02%
76.6	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.00%
75.7	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 0.00%
75.3	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.00%
74.6	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 0.00%
72.5	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 0.00%
72.2	4136.0636	1.0079	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 0.00%

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

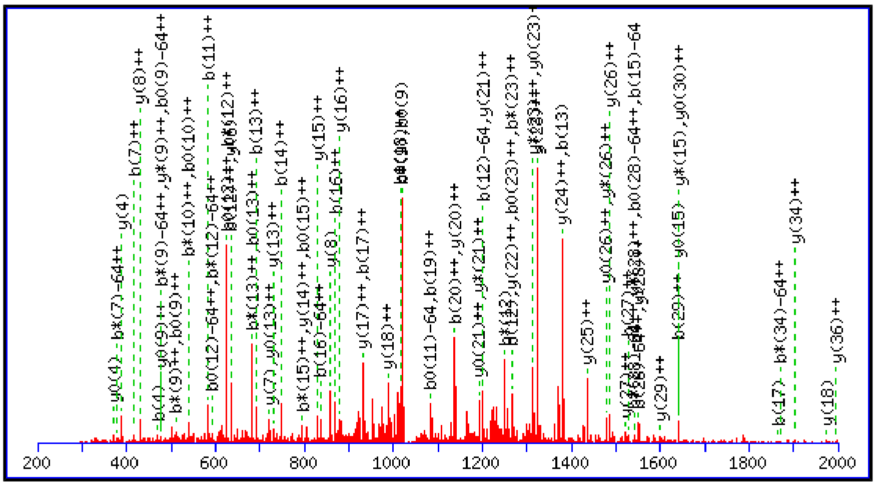
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28870: 4137.072816 from(1035.275480,4+) intensity(477273.9688) rtinseconds(2527) scans(6845) index(24173)
Title: 111019_Est_MI_YS_G_05Spectrum5941_scans__6845
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

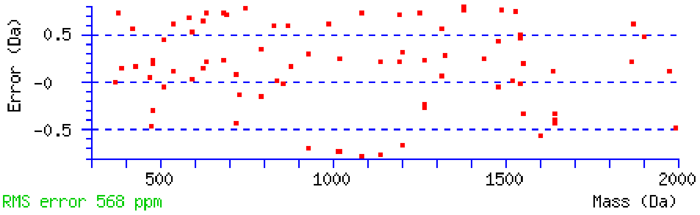
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

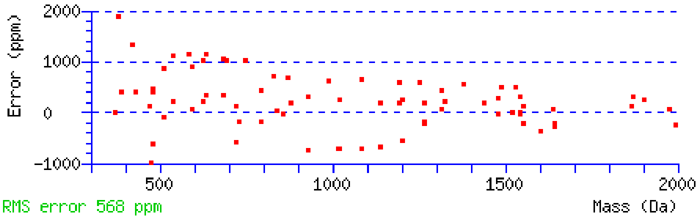


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N25 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 118 **Expect:** 2.9e-010
Matches : 82/616 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					**M**							**37**
2	247.1111	124.0592					**V**	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	**36**
3	334.1431	167.5752			316.1326	158.5699	**S**	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	**35**
4	**471.2020**	236.1047			453.1915	227.0994	**H**	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	**34**
5	608.2609	304.6341			590.2504	295.6288	**H**	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	**33**
6	722.3039	361.6556	705.2773	353.1423	704.2933	352.6503	**N**	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	**32**
7	835.3879	**418.1976**	818.3614	409.6843	817.3774	409.1923	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	**31**
8	936.4356	468.7214	919.4091	460.2082	918.4250	459.7162	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	**30**
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	**29**
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	**28**
11	1165.5419	**583.2746**	1148.5153	574.7613	1147.5313	574.2693	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	**27**
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	**26**
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	**25**
14	1492.7577	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
15	1606.8006	803.9039	1589.7741	795.3907	1588.7900	794.8987	**N**	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	**23**
16	1735.8432	**868.4252**	1718.8166	859.9120	1717.8326	859.4200	**E**	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	**22**
17	**1863.9018**	**932.4545**	1846.8752	923.9413	1845.8912	923.4492	**Q**	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	**21**
18	2049.9811	1025.4942	2032.9545	1016.9809	2031.9705	1016.4889	**W**	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	**20**
19	2163.0652	**1082.0362**	2146.0386	1073.5229	2145.0546	1073.0309	**L**	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	**19**
20	2276.1492	**1138.5782**	2259.1227	1130.0650	2258.1386	1129.5730	**L**	**1975.0131**	988.0102	1957.9865	979.4969	1957.0025	979.0049	**18**
21	2377.1969	1189.1021	2360.1703	1180.5888	2359.1863	1180.0968	**T**	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	**17**
22	2478.2446	1239.6259	2461.2180	1231.1126	2460.2340	1230.6206	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**

23	2549.2817	1275.1445	2532.2551	1266.6312	2531.2711	1266.1392	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2677.3766	1339.1920	2660.3501	1330.6787	2659.3661	1330.1867	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	**1526.7817**	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3279.6831	**1640.3452**	3262.6565	1631.8319	3261.6725	1631.3399	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3416.7420	1708.8746	3399.7154	1700.3614	3398.7314	1699.8693	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3503.7740	1752.3906	3486.7475	1743.8774	3485.7634	1743.3854	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3632.8166	1816.9119	3615.7900	1808.3987	3614.8060	1807.9067	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	1995.9864	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
118.2	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 74.93%
113.2	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 23.42%
100.5	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 1.26%
94.1	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.29%
85.1	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.04%
84.1	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 0.03%
79.7	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.01%
79.7	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 0.01%
70.3	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.00%
70.3	4136.0636	1.0092	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 0.00%

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

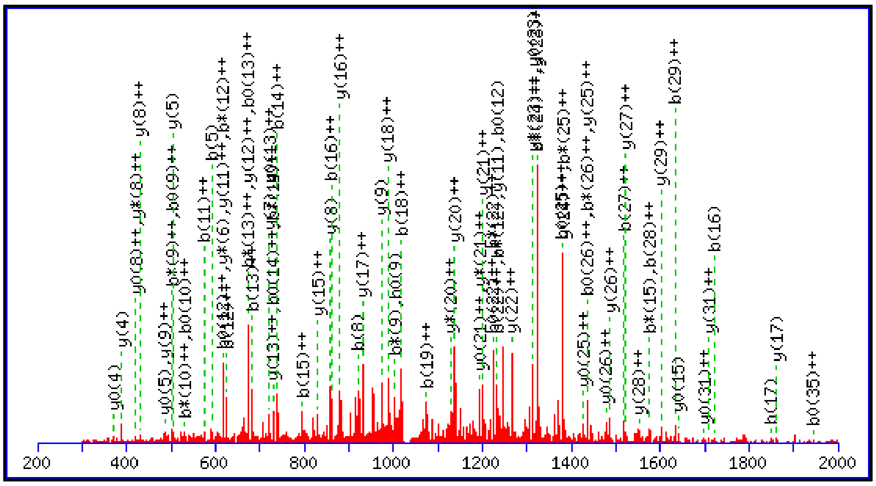
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28595: 4122.050176 from(1031.519820,4+) intensity(34464.0820) rtinseconds(2545) scans(6632) index(4038)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum5425_scans__6632
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

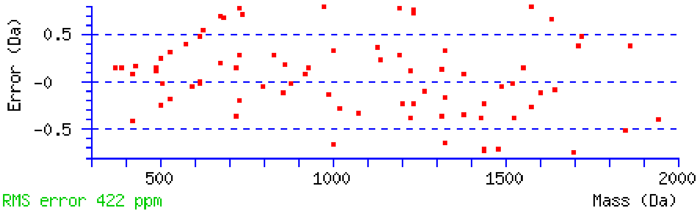
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

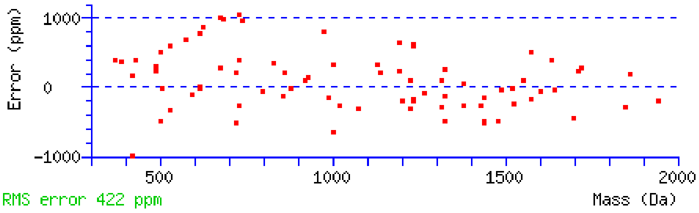


Monoisotopic mass of neutral peptide Mr(calc): 4122.0367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 118 **Expect:** 3.3e-010
Matches : 82/414 fragment ions using 103 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	318.1482	159.5777			300.1376	150.5725	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	455.2071	228.1072			437.1966	219.1019	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	**592.2660**	296.6367			574.2555	287.6314	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3417.7424	1709.3748	3400.7159	1700.8616	3399.7318	1700.3696	31
8	**920.4407**	460.7240	903.4141	452.2107	902.4301	451.7187	T	3304.6583	1652.8328	3287.6318	1644.3195	3286.6478	1643.8275	30
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	T	3203.6107	1602.3090	3186.5841	1593.7957	3185.6001	1593.3037	29
10	1078.5098	539.7586	1061.4833	531.2453	1060.4993	530.7533	G	3102.5630	1551.7851	3085.5364	1543.2719	3084.5524	1542.7799	28
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	A	3045.5415	1523.2744	3028.5150	1514.7611	3027.5310	1514.2691	27
12	1250.5946	**625.8010**	1233.5681	617.2877	1232.5841	616.7957	T	2974.5044	1487.7558	2957.4779	1479.2426	2956.4938	1478.7506	26
13	1363.6787	**682.3430**	1346.6521	673.8297	1345.6681	673.3377	L	2873.4567	1437.2320	2856.4302	1428.7187	2855.4462	1428.2267	25
14	1476.7628	**738.8850**	1459.7362	730.3717	1458.7522	729.8797	I	2760.3727	1380.6900	2743.3461	1372.1767	2742.3621	1371.6847	24
15	1591.7897	**796.3985**	1574.7632	787.8852	1573.7791	787.3932	N	2647.2886	1324.1479	2630.2621	1315.6347	2629.2780	1315.1427	23
16	**1720.8323**	**860.9198**	1703.8057	852.4065	1702.8217	851.9145	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1849.8749**	925.4411	1832.8483	916.9278	1831.8643	916.4358	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2035.9542	**1018.4807**	2018.9277	1009.9675	2017.9436	1009.4755	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2149.0383	**1075.0228**	2132.0117	1066.5095	2131.0277	1066.0175	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2262.1223	1131.5648	2245.0958	1123.0515	2244.1118	1122.5595	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2363.1700	1182.0886	2346.1435	1173.5754	2345.1594	1173.0834	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2464.2177	**1232.6125**	2447.1911	1224.0992	2446.2071	1223.6072	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2535.2548	1268.1310	2518.2283	1259.6178	2517.2442	1259.1258	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2663.3498	1332.1785	2646.3232	1323.6652	2645.3392	1323.1732	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2890.4768	1445.7420	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3037.5452	**1519.2762**	3020.5186	1510.7629	3019.5346	1510.2709	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3150.6292	**1575.8183**	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3265.6562	**1633.3317**	3248.6296	1624.8185	3247.6456	1624.3264	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3402.7151	1701.8612	3385.6885	1693.3479	3384.7045	1692.8559	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3489.7471	1745.3772	3472.7206	1736.8639	3471.7366	1736.3719	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3618.7897	1809.8985	3601.7632	1801.3852	3600.7791	1800.8932	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3733.8167	1867.4120	3716.7901	1858.8987	3715.8061	1858.4067	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3804.8538	1902.9305	3787.8272	1894.4172	3786.8432	1893.9252	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3905.9014	1953.4544	3888.8749	1944.9411	3887.8909	1944.4491	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3976.9386	1988.9729	3959.9120	1980.4596	3958.9280	1979.9676	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
117.9	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 19.71%
116.5	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 14.21%
115.9	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 12.61%
115.9	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 12.61%
114.6	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 9.26%
114.6	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 9.26%
113.4	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 7.04%
113.1	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 6.63%
108.2	4121.0527	0.9974	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
106.7	4122.0367	0.0134	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17, N33 1.50%

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

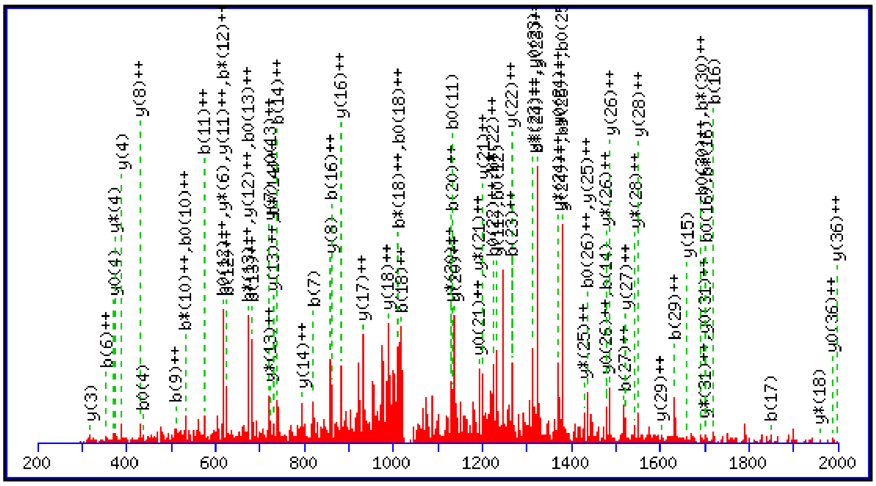
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28597: 4122.054256 from(1031.520840,4+) intensity(25418.1895) rtinseconds(2552) scans(6742) index(18938)
Title: 111019_Est_MI_YP_G_08Spectrum5890_scans__6742
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

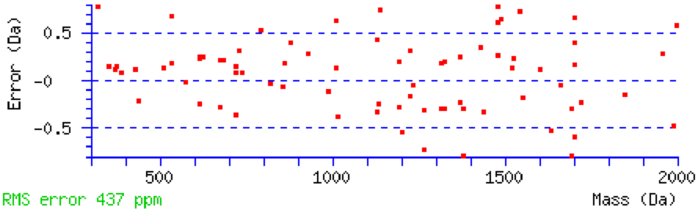
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

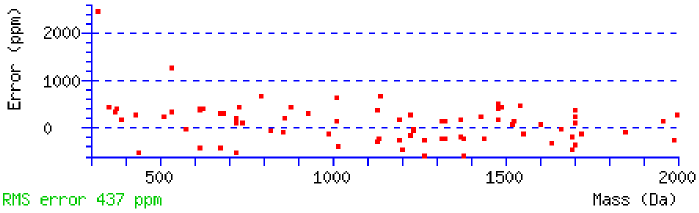


Monoisotopic mass of neutral peptide Mr(calc): 4122.0367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 114 **Expect:** 8.9e-010
Matches : 84/414 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	318.1482	159.5777			300.1376	150.5725	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	455.2071	228.1072			437.1966	219.1019	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	592.2660	296.6367			574.2555	287.6314	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	707.2930	**354.1501**	690.2664	345.6368	689.2824	345.1448	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	921.4247	461.2160	904.3982	452.7027	903.4141	452.2107	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1022.4724	**511.7398**	1005.4458	503.2266	1004.4618	502.7346	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1079.4939	540.2506	1062.4673	531.7373	1061.4833	531.2453	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1150.5310	**575.7691**	1133.5044	567.2558	1132.5204	566.7638	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	1251.5786	**626.2930**	1234.5521	617.7797	1233.5681	617.2877	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	1364.6627	**682.8350**	1347.6362	674.3217	1346.6521	673.8297	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	**1477.7468**	**739.3770**	1460.7202	730.8638	1459.7362	730.3717	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1591.7897	796.3985	1574.7632	787.8852	1573.7791	787.3932	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	**1720.8323**	**860.9198**	1703.8057	852.4065	1702.8217	851.9145	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1849.8749**	925.4411	1832.8483	916.9278	1831.8643	916.4358	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2035.9542	**1018.4807**	2018.9277	1009.9675	2017.9436	1009.4755	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2149.0383	1075.0228	2132.0117	1066.5095	2131.0277	1066.0175	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2262.1223	**1131.5648**	2245.0958	1123.0515	2244.1118	1122.5595	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2363.1700	1182.0886	2346.1435	1173.5754	2345.1594	1173.0834	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2464.2177	1232.6125	2447.1911	1224.0992	2446.2071	1223.6072	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2535.2548	**1268.1310**	2518.2283	1259.6178	2517.2442	1259.1258	**A**	**1659.8337**	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2663.3498	1332.1785	2646.3232	1323.6652	2645.3392	1323.1732	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2890.4768	1445.7420	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3037.5452	**1519.2762**	3020.5186	1510.7629	3019.5346	1510.2709	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3150.6292	1575.8183	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3265.6562	**1633.3317**	3248.6296	1624.8185	3247.6456	1624.3264	**N**	973.4221	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3402.7151	1701.8612	3385.6885	1693.3479	3384.7045	1692.8559	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3489.7471	1745.3772	3472.7206	1736.8639	3471.7366	1736.3719	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3618.7897	1809.8985	3601.7632	1801.3852	3600.7791	1800.8932	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3733.8167	1867.4120	3716.7901	1858.8987	3715.8061	1858.4067	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3804.8538	1902.9305	3787.8272	1894.4172	3786.8432	1893.9252	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3905.9014	1953.4544	3888.8749	1944.9411	3887.8909	1944.4491	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3976.9386	1988.9729	3959.9120	1980.4596	3958.9280	1979.9676	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.6	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 54.51%
112.2	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 39.13%
100.0	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 2.37%
99.6	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 2.16%
97.4	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 1.30%
86.5	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N29 0.11%
85.8	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 0.09%
83.3	4121.0527	1.0015	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
83.3	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 0.05%
83.2	4122.0367	0.0175	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 0.05%

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

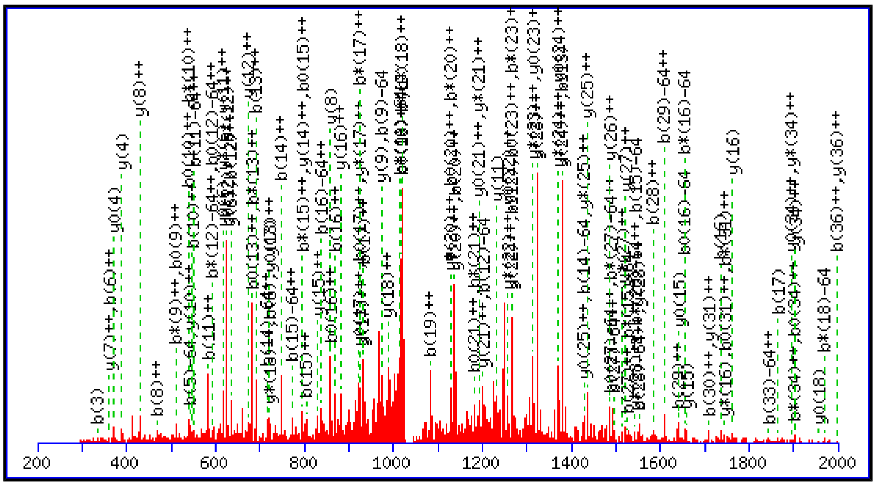
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28928: 4138.043176 from(1035.518070,4+) intensity(0.0000) rtinseconds(2628) scans(6877) index(25666)
Title: 111019_Est_MI_YS_G_07Spectrum5930_scans__6877
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

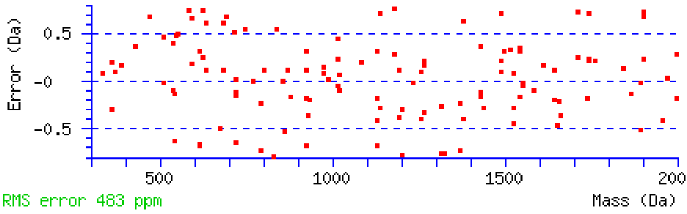
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

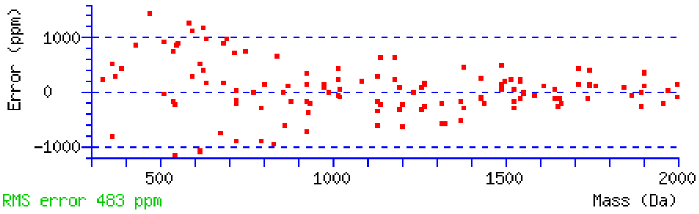


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N15 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 111 **Expect:** 1.9e-009
Matches : 129/616 fragment ions using 172 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	**334.1431**	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	471.2020	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	608.2609	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	**722.3039**	**361.6556**	705.2773	353.1423	704.2933	352.6503	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3417.7424	1709.3748	3400.7159	1700.8616	3399.7318	1700.3696	31
8	936.4356	**468.7214**	919.4091	460.2082	918.4250	459.7162	T	3304.6583	1652.8328	3287.6318	1644.3195	3286.6478	1643.8275	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3203.6107	1602.3090	3186.5841	1593.7957	3185.6001	1593.3037	29
10	1094.5048	**547.7560**	1077.4782	539.2427	1076.4942	538.7507	G	3102.5630	1551.7851	3085.5364	1543.2719	3084.5524	1542.7799	28
11	1165.5419	**583.2746**	1148.5153	574.7613	1147.5313	574.2693	A	3045.5415	1523.2744	3028.5150	1514.7611	3027.5310	1514.2691	27
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	T	2974.5044	1487.7558	2957.4779	1479.2426	2956.4938	1478.7506	26
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	L	2873.4567	1437.2320	2856.4302	1428.7187	2855.4462	1428.2267	25
14	1492.7577	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	I	2760.3727	1380.6900	2743.3461	1372.1767	2742.3621	1371.6847	24
15	1607.7846	**804.3959**	1590.7581	795.8827	1589.7741	795.3907	N	2647.2886	1324.1479	2630.2621	1315.6347	2629.2780	1315.1427	23
16	**1736.8272**	**868.9172**	1719.8007	860.4040	1718.8166	859.9120	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1864.8858**	**932.9465**	1847.8592	924.4333	1846.8752	923.9413	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	20
19	2164.0492	**1082.5282**	2147.0226	1074.0149	2146.0386	1073.5229	L	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	19
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	L	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	1862.9130	931.9602	1845.8865	923.4469	1844.9025	922.9549	17

22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	**1761.8654**	881.4363	1744.8388	872.9230	1743.8548	872.4310	**16**
23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	**1660.8177**	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6750	722.3412	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3053.5401	**1527.2737**	3036.5135	1518.7604	3035.5295	1518.2684	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3166.6242	**1583.8157**	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3281.6511	**1641.3292**	3264.6245	1632.8159	3263.6405	1632.3239	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3418.7100	**1709.8586**	3401.6835	1701.3454	3400.6994	1700.8534	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	1875.4094	3732.7850	1866.8961	3731.8010	1866.4041	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	**1996.9704**	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
110.8	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 24.82%
109.9	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 20.41%
109.4	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 18.15%
106.7	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29, N33 9.61%
104.5	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 5.79%
104.4	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 5.70%
101.8	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 3.13%
101.8	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 3.11%
99.8	4137.0477	0.9955	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
98.9	4138.0317	0.0115	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 1.61%

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

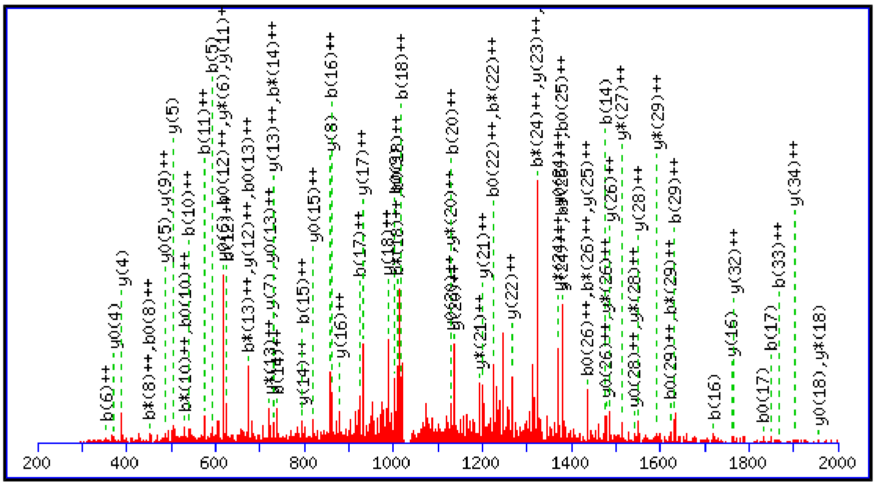
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28556: 4121.084656 from(1031.278440,4+) intensity(0.0000) rtinseconds(2708) scans(7182) index(19936)
Title: 111019_Est_MI_YP_G_09Spectrum6371_scans__7182
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

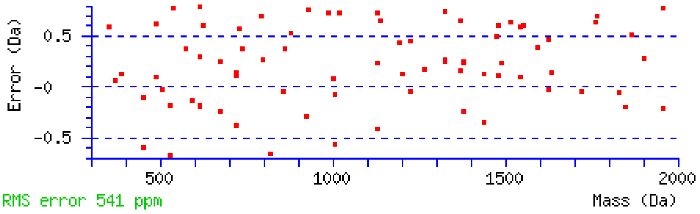
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

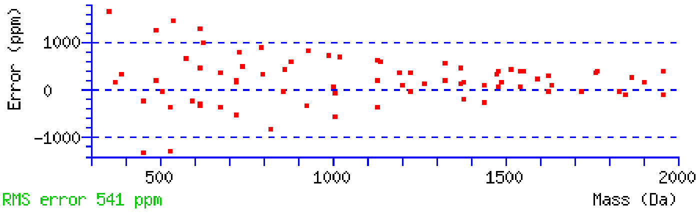


Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 111 **Expect:** 1.4e-009
Matches : 82/414 fragment ions using 87 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	455.2071	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	**592.2660**	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	706.3090	***353.6581***	689.2824	345.1448	688.2984	344.6528	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1078.5098	***539.7586***	1061.4833	531.2453	1060.4993	530.7533	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1149.5470	***575.2771***	1132.5204	566.7638	1131.5364	566.2718	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1250.5946	***625.8010***	1233.5681	617.2877	1232.5841	616.7957	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1363.6787	682.3430	1346.6521	673.8297	1345.6681	673.3377	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1476.7628**	***738.8850***	1459.7362	730.3717	1458.7522	729.8797	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1590.8057	***795.9065***	1573.7791	787.3932	1572.7951	786.9012	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1719.8483**	***860.4278***	1702.8217	851.9145	1701.8377	851.4225	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1848.8909**	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2148.0543	1074.5308	2131.0277	1066.0175	2130.0437	1065.5255	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	T	**1759.8973**	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2534.2708	1267.6390	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2889.4927	1445.2500	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3036.5612	1518.7842	3019.5346	1510.2709	3018.5506	1509.7789	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3149.6452	1575.3262	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3263.6881	***1632.3477***	3246.6616	1623.8344	3245.6776	1623.3424	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3400.7471	1700.8772	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3616.8217	1808.9145	3599.7951	1800.4012	3598.8111	1799.9092	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3731.8486	***1866.4279***	3714.8221	1857.9147	3713.8381	1857.4227	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3802.8857	1901.9465	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
110.8	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 60.07%
104.9	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 15.73%
103.2	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 10.58%
102.7	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 9.28%
96.8	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 2.41%
91.2	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.67%
89.3	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.42%
89.2	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 0.42%
85.1	4119.0847	1.9999	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
81.6	4120.0687	1.0159	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 0.07%

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 24119: 2695.369188 from(1348.691870,2+) intensity(19993.7578) rtinseconds(1783) scans(4535) index(24606)
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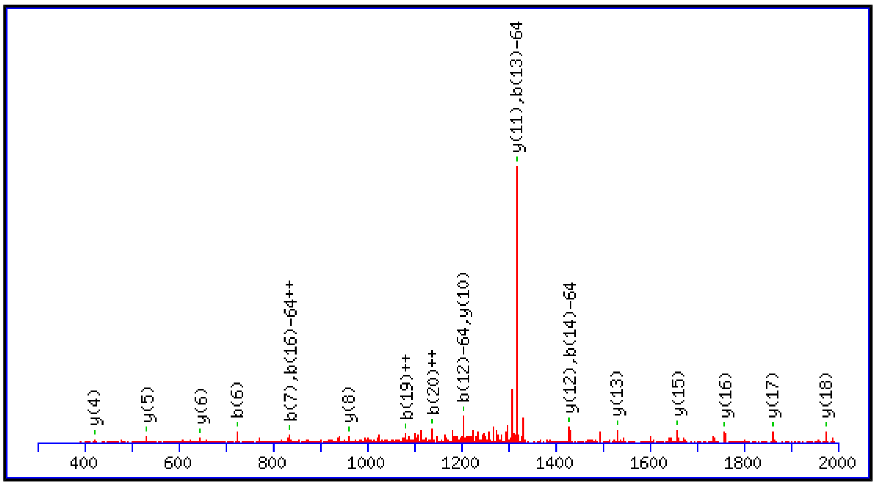
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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Monoisotopic mass of neutral peptide Mr(calc): 2695.3639
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6     : Deamidated (NQ)
Ions Score: 110  Expect: 2.1e-009
Matches : 20/382 fragment ions using 17 most intense peaks    (help)
```
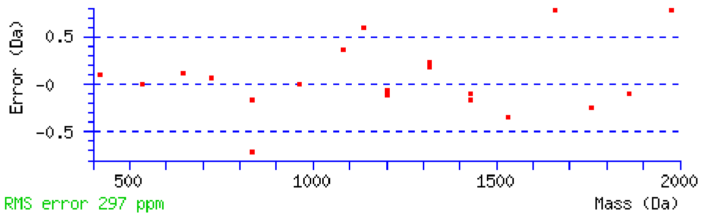
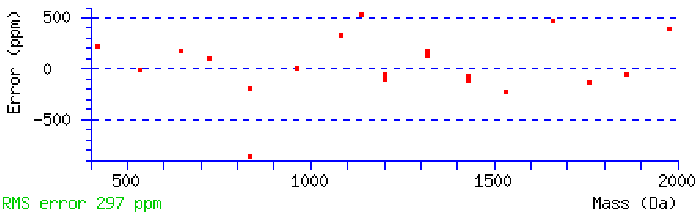

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							24
2	247.1111	124.0592					V	2549.3358	1275.1716	2532.3093	1266.6583	2531.3253	1266.1663	23
3	334.1431	167.5752			316.1326	158.5699	S	2450.2674	1225.6373	2433.2409	1217.1241	2432.2569	1216.6321	22
4	471.2020	236.1047			453.1915	227.0994	H	2363.2354	1182.1213	2346.2088	1173.6081	2345.2248	1173.1160	21
5	608.2609	304.6341			590.2504	295.6288	H	2226.1765	1113.5919	2209.1499	1105.0786	2208.1659	1104.5866	20
6	**723.2879**	362.1476	706.2613	353.6343	705.2773	353.1423	N	2089.1176	1045.0624	2072.0910	1036.5491	2071.1070	1036.0571	19
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	***1974.0906***	987.5489	1957.0641	979.0357	1956.0801	978.5437	18
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	***1861.0066***	931.0069	1843.9800	922.4936	1842.9960	922.0016	17
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	***1759.9589***	880.4831	1742.9323	871.9698	1741.9483	871.4778	16
10	1095.4888	548.2480	1078.4622	539.7347	1077.4782	539.2427	G	***1658.9112***	829.9592	1641.8847	821.4460	1640.9006	820.9540	15
11	1166.5259	583.7666	1149.4993	575.2533	1148.5153	574.7613	A	1601.8897	801.4485	1584.8632	792.9352	1583.8792	792.4432	14
12	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	T	***1530.8526***	765.9299	1513.8261	757.4167	1512.8421	756.9247	13
13	1380.6576	690.8325	1363.6311	682.3192	1362.6471	681.8272	L	***1429.8049***	715.4061	1412.7784	706.8928	1411.7944	706.4008	12
14	1493.7417	747.3745	1476.7151	738.8612	1475.7311	738.3692	I	***1316.7209***	658.8641	1299.6943	650.3508	1298.7103	649.8588	11
15	1607.7846	804.3959	1590.7581	795.8827	1589.7741	795.3907	N	***1203.6368***	602.3220	1186.6103	593.8088	1185.6263	593.3168	10
16	1736.8272	868.9172	1719.8007	860.4040	1718.8166	859.9120	E	1089.5939	545.3006	1072.5673	536.7873	1071.5833	536.2953	9
17	1864.8858	932.9465	1847.8592	924.4333	1846.8752	923.9413	Q	***960.5513***	480.7793	943.5247	472.2660	942.5407	471.7740	8
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	832.4927	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2164.0492	**1082.5282**	2147.0226	1074.0149	2146.0386	1073.5229	L	***646.4134***	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	L	***533.3293***	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	***420.2453***	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	218.1499	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
110.5	2695.3639	0.0053	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6 99.36%
88.5	2695.3639	0.0053	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N15 0.64%
65.4	2695.3639	0.0053	MVSHHNLTTGATLINEQWLLTTAK	Deamidated Q17 0.00%
6.7	2694.3608	1.0084	GTVLWTENALEVLQMTRSLMKEK	
6.7	2694.3608	1.0084	GTVLWTENALEVLQMTRSLMKEK	
5.8	2695.3680	0.0012	VGSLIFHTIGQLLPQQMQAFHSPK	
5.6	2694.3766	0.9926	SDDVNLAIYPDLLFTQPRPGVAHR	
4.8	2694.3646	1.0045	EVQYSNDIMQRGASVGATLLLREK	
4.8	2694.3646	1.0045	EVQYSNDIMQRGASVGATLLLREK	
2.7	2695.3700	-0.0008	VSMIKVIDAQTLLLFAEGDIMEDK	

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

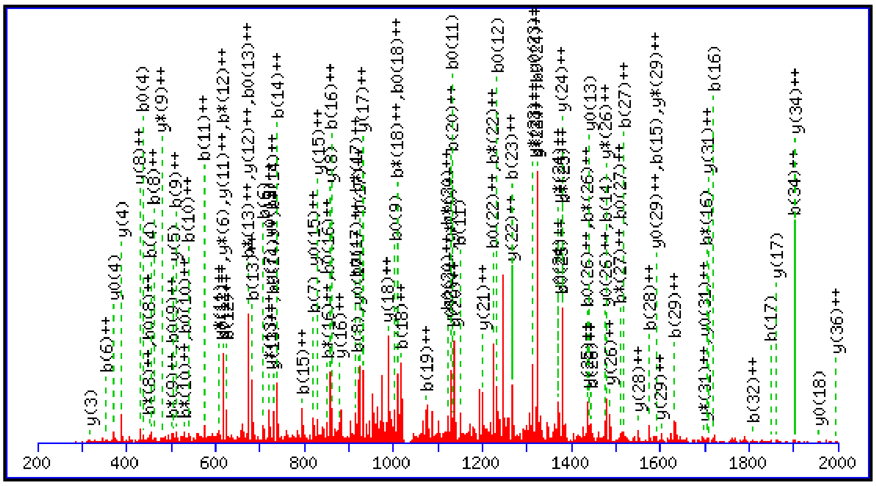
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28554: 4121.083816 from(1031.278230,4+) intensity(59996.1875) rtinseconds(2503) scans(6460) index(23523)
Title: 111019_Est_MI_YS_G_04Spectrum5600_scans__6460
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

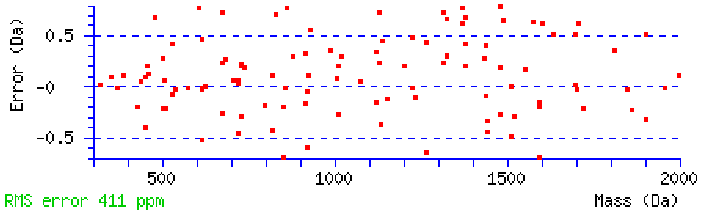
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

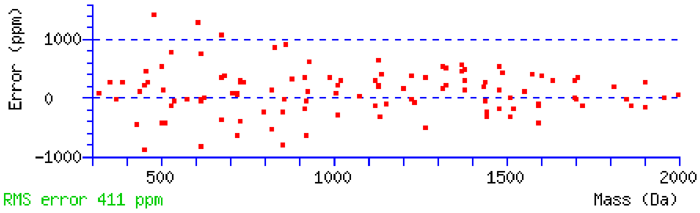


Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 110 **Expect:** 1.7e-009
Matches : 113/414 fragment ions using 173 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	**455.2071**	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	592.2660	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**707.2930**	***354.1501***	690.2664	345.6368	689.2824	345.1448	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	**921.4247**	***461.2160***	904.3982	452.7027	903.4141	452.2107	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1022.4724	***511.7398***	1005.4458	503.2266	1004.4618	502.7346	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1150.5310**	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	**1591.7897**	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	**1720.8323**	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	**1848.8909**	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2148.0543	***1074.5308***	2131.0277	1066.0175	2130.0437	1065.5255	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	T	**1860.9450**	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2534.2708	***1267.6390***	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2889.4927	***1445.2500***	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3036.5612	***1518.7842***	3019.5346	1510.2709	3018.5506	1509.7789	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3149.6452	***1575.3262***	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3263.6881	***1632.3477***	3246.6616	1623.8344	3245.6776	1623.3424	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3400.7471	1700.8772	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3616.8217	***1808.9145***	3599.7951	1800.4012	3598.8111	1799.9092	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3802.8857	***1901.9465***	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
110.2	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 54.43%
108.4	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 36.05%
98.1	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 3.42%
95.2	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 1.75%
95.1	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 1.72%
91.6	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.75%
90.8	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 0.63%
89.0	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.42%
86.9	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.26%
83.4	4120.0687	1.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 0.12%

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

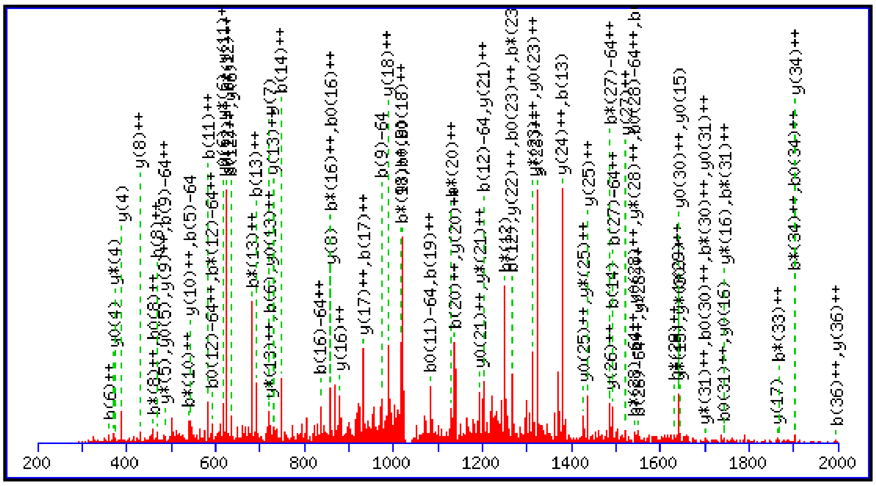
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28706: 4137.057896 from(1035.271750,4+) intensity(5739.0840) rtinseconds(2564) scans(6586) index(5679)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum5816_scans__6586
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

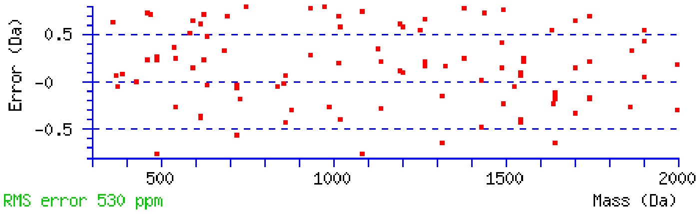
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

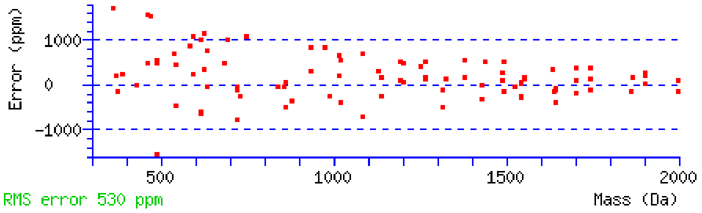


Monoisotopic mass of neutral peptide Mr(calc): 4137.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 110 **Expect:** 2.2e-009
Matches : 101/616 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	334.1431	167.5752			316.1326	158.5699	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	471.2020	236.1047			453.1915	227.0994	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	608.2609	304.6341			590.2504	295.6288	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**722.3039**	**361.6556**	705.2773	353.1423	704.2933	352.6503	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	936.4356	**468.7214**	919.4091	460.2082	918.4250	459.7162	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1165.5419	**583.2746**	1148.5153	574.7613	1147.5313	574.2693	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	**1492.7577**	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1606.8006	803.9039	1589.7741	795.3907	1588.7900	794.8987	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1735.8432	868.4252	1718.8166	859.9120	1717.8326	859.4200	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1863.9018	**932.4545**	1846.8752	923.9413	1845.8912	923.4492	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2049.9811	1025.4942	2032.9545	1016.9809	2031.9705	1016.4889	W	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	20
19	2163.0652	**1082.0362**	2146.0386	1073.5229	2145.0546	1073.0309	L	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	19
20	2276.1492	**1138.5782**	2259.1227	1130.0650	2258.1386	1129.5730	L	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	18
21	2377.1969	1189.1021	2360.1703	1180.5888	2359.1863	1180.0968	T	**1862.9130**	931.9602	1845.8865	923.4469	1844.9025	922.9549	17

22	2478.2446	1239.6259	2461.2180	1231.1126	2460.2340	1230.6206	T	1761.8654	881.4363	1744.8388	872.9230	1743.8548	872.4310	16
23	2549.2817	1275.1445	2532.2551	1266.6312	2531.2711	1266.1392	A	1660.8177	830.9125	1643.7911	822.3992	1642.8071	821.9072	15
24	2677.3766	1339.1920	2660.3501	1330.6787	2659.3661	1330.1867	K	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	14
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	N	1461.6856	731.3464	1444.6591	722.8332	1443.6750	722.3412	13
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	L	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	12
27	3052.5561	1526.7817	3035.5295	1518.2684	3034.5455	1517.7764	F	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	11
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	L	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	10
29	3280.6671	**1640.8372**	3263.6405	1632.3239	3262.6565	1631.8319	N	973.4221	487.2147	956.3956	478.7014	955.4116	478.2094	9
30	3417.7260	1709.3666	3400.6994	1700.8534	3399.7154	1700.3614	H	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	8
31	3504.7580	1752.8826	3487.7315	1744.3694	3486.7475	1743.8774	S	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	7
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	E	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	6
33	3748.8276	1874.9174	3731.8010	1866.4041	3730.8170	1865.9121	N	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	5
34	3819.8647	1910.4360	3802.8381	1901.9227	3801.8541	1901.4307	A	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	4
35	3920.9123	1960.9598	3903.8858	1952.4465	3902.9018	1951.9545	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
36	3991.9495	**1996.4784**	3974.9229	1987.9651	3973.9389	1987.4731	A	218.1499	109.5786	201.1234	101.0653			2
37							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
109.8	4137.0477	0.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 51.65%
109.0	4137.0477	0.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 43.46%
99.0	4137.0477	0.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 4.37%
96.5	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
96.5	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
87.6	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
85.4	4137.0477	0.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 0.19%
84.3	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
83.9	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
77.0	4136.0636	0.9943	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

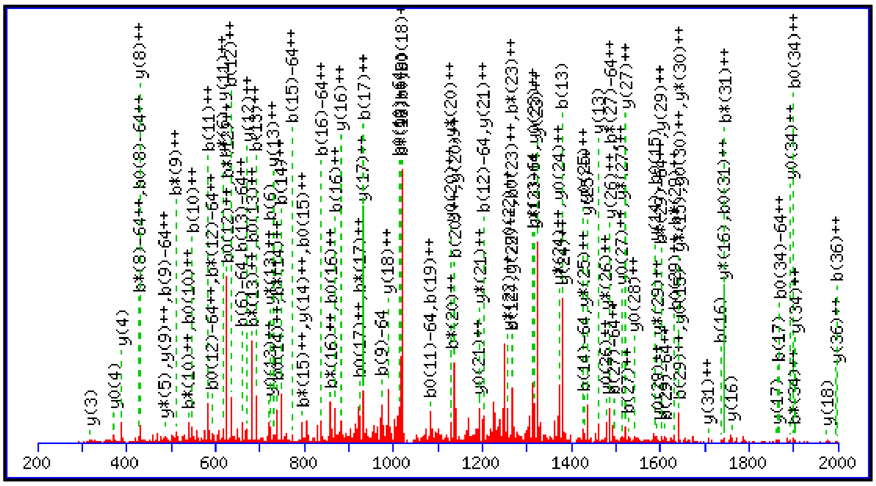
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28827: 4137.066816 from(1035.273980,4+) intensity(90584.1250) rtinseconds(2524) scans(6569) index(4030)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum5371_scans__6569
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

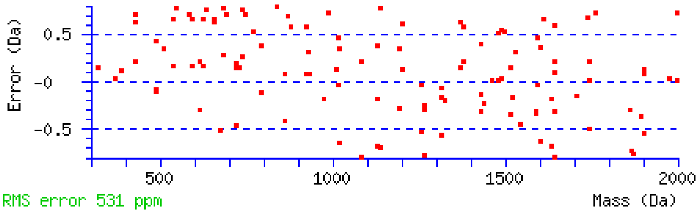
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

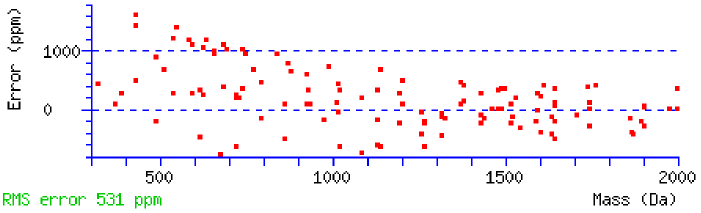


Monoisotopic mass of neutral peptide Mr(calc): 4137.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q17 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 109 **Expect:** 2.5e-009
Matches : 124/616 fragment ions using 155 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	334.1431	167.5752			316.1326	158.5699	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	471.2020	236.1047			453.1915	227.0994	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	608.2609	304.6341			590.2504	295.6288	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**722.3039**	361.6556	705.2773	353.1423	704.2933	352.6503	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	936.4356	468.7214	919.4091	460.2082	918.4250	459.7162	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1094.5048	**547.7560**	1077.4782	539.2427	1076.4942	538.7507	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1165.5419	**583.2746**	1148.5153	574.7613	1147.5313	574.2693	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	1492.7577	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1606.8006	803.9039	1589.7741	795.3907	1588.7900	794.8987	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	**1735.8432**	**868.4252**	1718.8166	859.9120	1717.8326	859.4200	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1864.8858**	**932.9465**	1847.8592	924.4333	1846.8752	923.9413	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2164.0492	**1082.5282**	2147.0226	1074.0149	2146.0386	1073.5229	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	L	**1975.0131**	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	**1760.8814**	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	**1460.7016**	730.8544	1443.6750	722.3412	1442.6910	721.8492	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3053.5401	**1527.2737**	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3166.6242	1583.8157	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3281.6511	**1641.3292**	3264.6245	1632.8159	3263.6405	1632.3239	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3748.8276	1874.9174	3731.8010	1866.4041	3730.8170	1865.9121	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3819.8647	1910.4360	3802.8381	1901.9227	3801.8541	1901.4307	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3920.9123	1960.9598	3903.8858	1952.4465	3902.9018	1951.9545	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3991.9495	**1996.4784**	3974.9229	1987.9651	3973.9389	1987.4731	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
109.1	4137.0477	0.0192	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 78.02%
102.4	4137.0477	0.0192	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 16.76%
96.3	4137.0477	0.0192	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 4.14%
92.3	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
92.2	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
88.9	4137.0477	0.0192	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 0.75%
83.1	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
77.0	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
76.2	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
74.2	4136.0636	1.0032	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

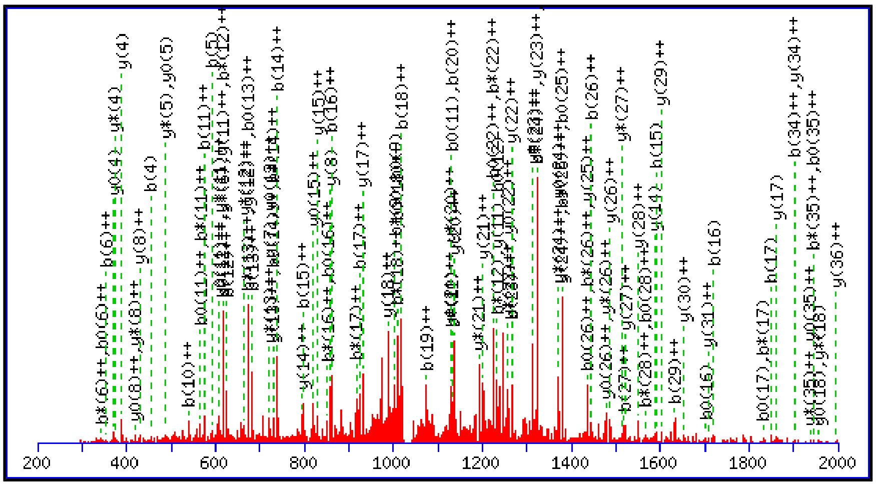
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28629: 4122.088096 from(1031.529300,4+) intensity(0.0000) rtinseconds(2475) scans(6350) index(22344)
Title: 111019_Est_MI_YS_G_02Spectrum5519_scans__6350
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

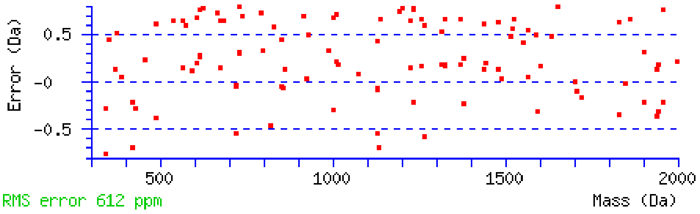
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

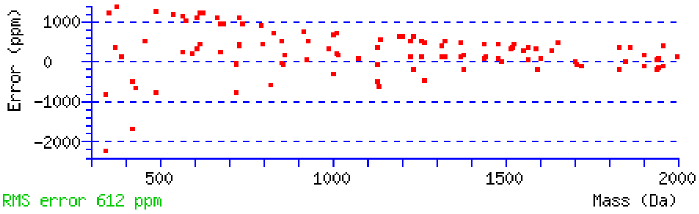


Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 106 **Expect:** 3.9e-009
Matches : 115/414 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					**M**							**37**
2	231.1162	116.0617					**V**	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	**36**
3	318.1482	159.5777			300.1376	150.5725	**S**	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	**35**
4	**455.2071**	228.1072			437.1966	219.1019	**H**	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	**34**
5	**592.2660**	296.6367			574.2555	287.6314	**H**	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	**33**
6	706.3090	**353.6581**	689.2824	345.1448	688.2984	344.6528	**N**	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	**32**
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	**31**
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	**30**
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	**29**
10	1078.5098	**539.7586**	1061.4833	531.2453	1060.4993	530.7533	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	**28**
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	**27**
12	1250.5946	**625.8010**	1233.5681	617.2877	1232.5841	616.7957	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	**26**
13	1363.6787	**682.3430**	1346.6521	673.8297	1345.6681	673.3377	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	**25**
14	1476.7628	**738.8850**	1459.7362	730.3717	1458.7522	729.8797	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
15	**1591.7897**	**796.3985**	1574.7632	787.8852	1573.7791	787.3932	**N**	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	**23**
16	**1720.8323**	**860.9198**	1703.8057	852.4065	1702.8217	851.9145	**E**	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	**22**
17	**1848.8909**	**924.9491**	1831.8643	916.4358	1830.8803	915.9438	**Q**	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	**21**
18	2034.9702	**1017.9887**	2017.9436	1009.4755	2016.9596	1008.9834	**W**	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	**20**
19	2148.0543	**1074.5308**	2131.0277	1066.0175	2130.0437	1065.5255	**L**	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	**19**
20	2261.1383	**1131.0728**	2244.1118	1122.5595	2243.1278	1122.0675	**L**	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	**18**
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	**T**	**1860.9450**	930.9761	1843.9185	922.4629	1842.9345	921.9709	**17**
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	**T**	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	**16**

23	2534.2708	**1267.6390**	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	**1587.8125**	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2889.4927	**1445.2500**	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3036.5612	**1518.7842**	3019.5346	1510.2709	3018.5506	1509.7789	**F**	**1232.5906**	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3149.6452	1575.3262	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3263.6881	**1632.3477**	3246.6616	1623.8344	3245.6776	1623.3424	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3400.7471	1700.8772	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3616.8217	1808.9145	3599.7951	1800.4012	3598.8111	1799.9092	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3802.8857	**1901.9465**	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
106.3	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 77.89%
98.9	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 14.21%
90.7	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 2.11%
89.5	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 1.64%
89.4	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 1.58%
87.7	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 1.06%
87.1	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.93%
83.3	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.39%
78.3	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 0.12%
68.8	4120.0687	2.0194	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 0.01%

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

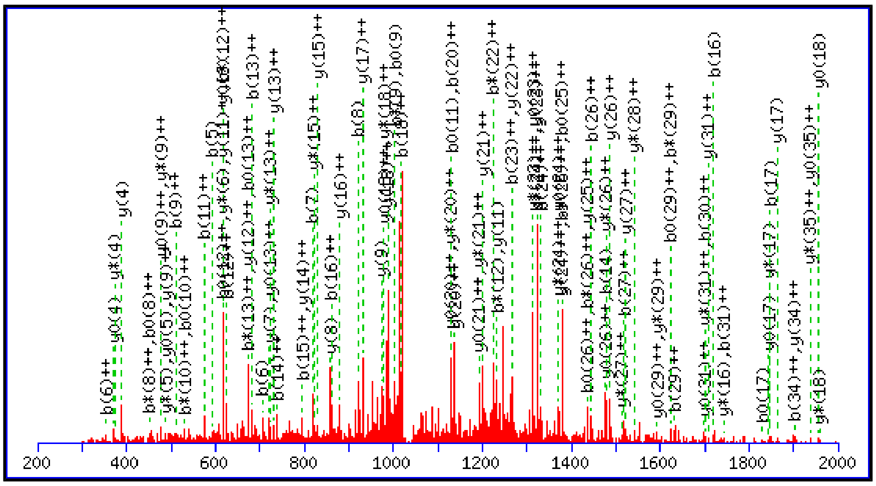
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28382: 4120.079776 from(1031.027220,4+) intensity(0.0000) rtinseconds(2733) scans(7279) index(27026)
Title: 111019_Est_MI_YS_G_09Spectrum6383_scans__7279
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

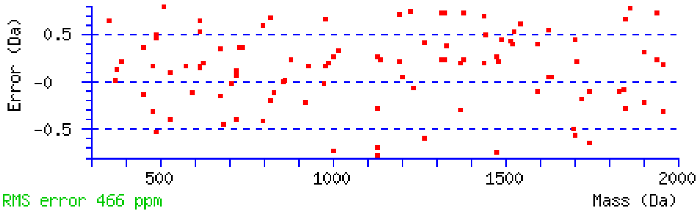
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



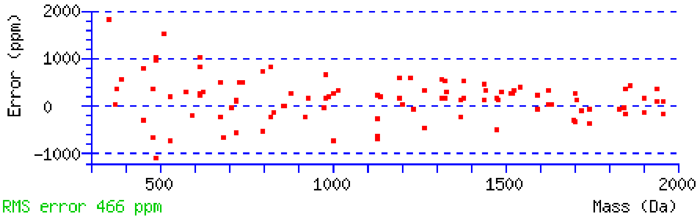
Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 105 **Expect:** 6e-009
Matches : 107/414 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	455.2071	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	**592.2660**	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**706.3090**	***353.6581***	689.2824	345.1448	688.2984	344.6528	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**819.3930**	410.2001	802.3665	401.6869	801.3825	401.1949	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	**920.4407**	460.7240	903.4141	452.2107	902.4301	451.7187	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1021.4884	***511.2478***	1004.4618	502.7346	1003.4778	502.2425	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1078.5098	539.7586	1061.4833	531.2453	1060.4993	530.7533	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1149.5470	***575.2771***	1132.5204	566.7638	1131.5364	566.2718	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1250.5946	***625.8010***	1233.5681	617.2877	1232.5841	616.7957	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1363.6787	***682.3430***	1346.6521	673.8297	1345.6681	673.3377	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1476.7628**	***738.8850***	1459.7362	730.3717	1458.7522	729.8797	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1590.8057	***795.9065***	1573.7791	787.3932	1572.7951	786.9012	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1719.8483**	***860.4278***	1702.8217	851.9145	1701.8377	851.4225	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1847.9069**	924.4571	1830.8803	915.9438	1829.8963	915.4518	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2033.9862	***1017.4967***	2016.9596	1008.9834	2015.9756	1008.4914	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2147.0702	1074.0388	2130.0437	1065.5255	2129.0597	1065.0335	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2260.1543	***1130.5808***	2243.1278	1122.0675	2242.1437	1121.5755	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2361.2020	1181.1046	2344.1754	1172.5914	2343.1914	1172.0993	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2533.2868	***1267.1470***	2516.2602	1258.6337	2515.2762	1258.1417	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2661.3817	***1331.1945***	2644.3552	1322.6812	2643.3712	1322.1892	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2775.4247	1388.2160	2758.3981	1379.7027	2757.4141	1379.2107	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2888.5087	***1444.7580***	2871.4822	1436.2447	2870.4982	1435.7527	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3035.5771	***1518.2922***	3018.5506	1509.7789	3017.5666	1509.2869	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3148.6612	1574.8342	3131.6347	1566.3210	3130.6506	1565.8290	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3263.6881	***1632.3477***	3246.6616	1623.8344	3245.6776	1623.3424	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3400.7471	***1700.8772***	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3487.7791	***1744.3932***	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3616.8217	1808.9145	3599.7951	1800.4012	3598.8111	1799.9092	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3802.8857	***1901.9465***	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**



RMS error 466 ppm



RMS error 466 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.8	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 97.34%
89.0	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 2.57%
69.8	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.03%
69.3	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 0.03%
67.4	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.02%
62.0	4119.0847	0.9951	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
61.3	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.00%
61.1	4119.0847	0.9951	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
59.9	4119.0847	0.9951	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
58.7	4120.0687	0.0111	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 0.00%

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

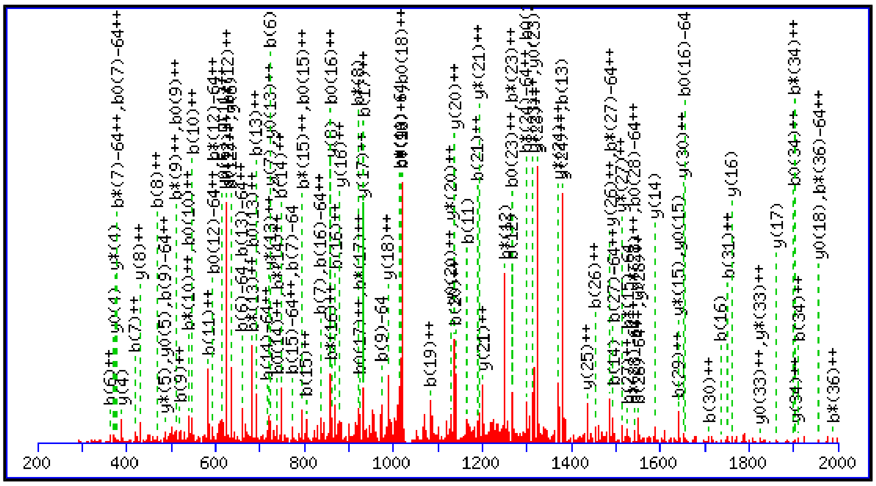
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28858: 4137.071616 from(1035.275180,4+) intensity(640829.3750) rtinseconds(2553) scans(6409) index(26271)
Title: 111019_Est_MI_YS_G_08Spectrum5572_scans__6409
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

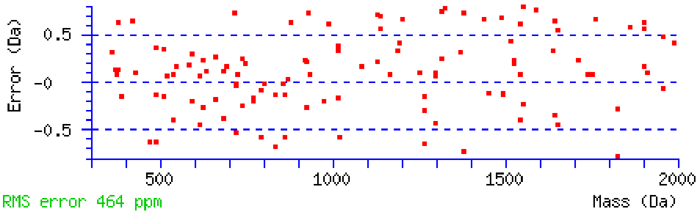
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

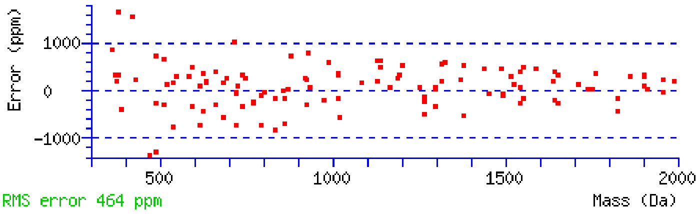


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 104 **Expect:** 7.9e-009
Matches : 119/616 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	471.2020	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	608.2609	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**836.3719**	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1038.4673	***519.7373***	1021.4408	511.2240	1020.4567	510.7320	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1607.7846	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1864.8858	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2164.0492	***1082.5282***	2147.0226	1074.0149	2146.0386	1073.5229	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2378.1809	***1189.5941***	2361.1544	1181.0808	2360.1703	1180.5888	T	**1860.9450**	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	**1759.8973**	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	**1587.8125**	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2905.4877	***1453.2475***	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	***1526.7817***	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3279.6831	***1640.3452***	3262.6565	1631.8319	3261.6725	1631.3399	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3416.7420	***1708.8746***	3399.7154	1700.3614	3398.7314	1699.8693	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3503.7740	***1752.3906***	3486.7475	1743.8774	3485.7634	1743.3854	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3632.8166	1816.9119	3615.7900	1808.3987	3614.8060	1807.9067	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3818.8807	***1909.9440***	3801.8541	1901.4307	3800.8701	1900.9387	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	1995.9864	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.0	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 94.86%
86.8	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 1.84%
86.8	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 1.84%
83.3	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 0.82%
80.3	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15 0.41%
74.5	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 0.11%
70.9	4135.0796	1.9920	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
70.0	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 0.04%
68.2	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 0.03%
63.9	4136.0636	1.0080	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.01%

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

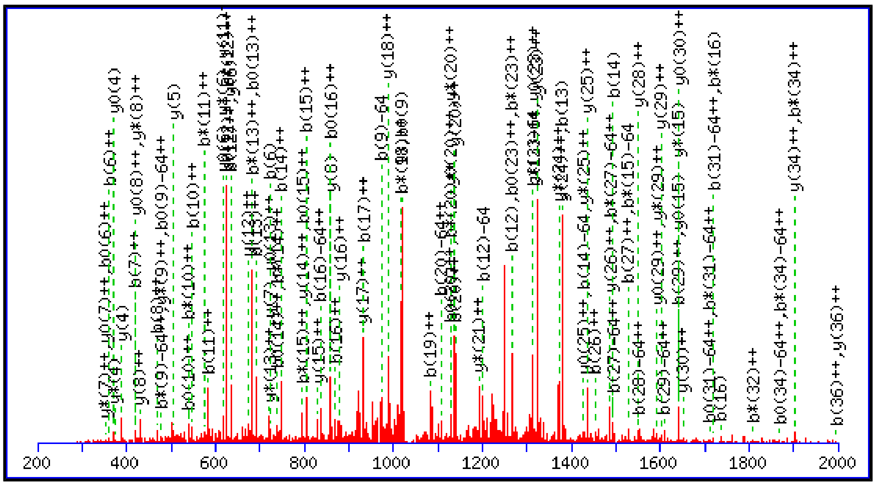
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28849: 4137.070616 from(1035.274930,4+) intensity(60315.5469) rtinseconds(2470) scans(6510) index(18908)
Title: 111019_Est_MI_YP_G_08Spectrum5683_scans__6510
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

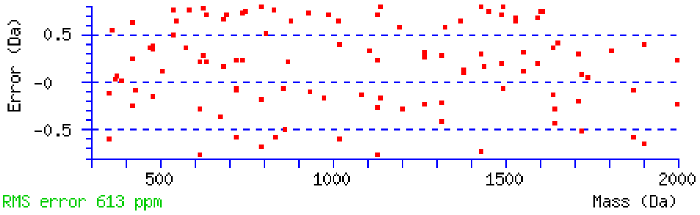
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

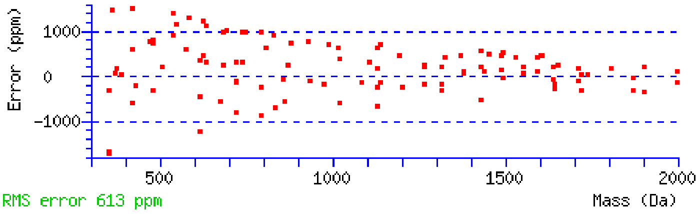


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N15 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 102 **Expect:** 1.4e-008
Matches : 110/616 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0082	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	471.2020	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	608.2609	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**722.3039**	***361.6556***	705.2773	353.1423	704.2933	352.6503	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	835.3879	***418.1976***	818.3614	409.6843	817.3774	409.1923	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	936.4356	***468.7214***	919.4091	460.2082	918.4250	459.7162	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1094.5048	***547.7560***	1077.4782	539.2427	1076.4942	538.7507	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1165.5419	***583.2746***	1148.5153	574.7613	1147.5313	574.2693	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	**1266.5895**	***633.7984***	1249.5630	625.2851	1248.5790	624.7931	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	**1379.6736**	***690.3404***	1362.6471	681.8272	1361.6630	681.3352	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1492.7577**	***746.8825***	1475.7311	738.3692	1474.7471	737.8772	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1607.7846	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2645.3206	1323.1639	2628.2940	1314.6507	2627.3100	1314.1586	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1864.8858	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2164.0492	***1082.5282***	2147.0226	1074.0149	2146.0386	1073.5229	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2905.4877	***1453.2475***	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	***1526.7817***	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3279.6831	***1640.3452***	3262.6565	1631.8319	3261.6725	1631.3399	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3416.7420	1708.8746	3399.7154	1700.3614	3398.7314	1699.8693	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3503.7740	1752.3906	3486.7475	1743.8774	3485.7634	1743.3854	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3632.8166	1816.9119	3615.7900	1808.3987	3614.8060	1807.9067	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	***1995.9864***	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
101.6	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 32.31%
101.4	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 31.43%
98.0	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 14.40%
97.3	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 12.14%
94.2	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 5.91%
90.1	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 2.30%
81.8	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 0.34%
81.6	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 0.32%
81.0	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.28%
77.0	4136.0636	1.0070	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 0.11%

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

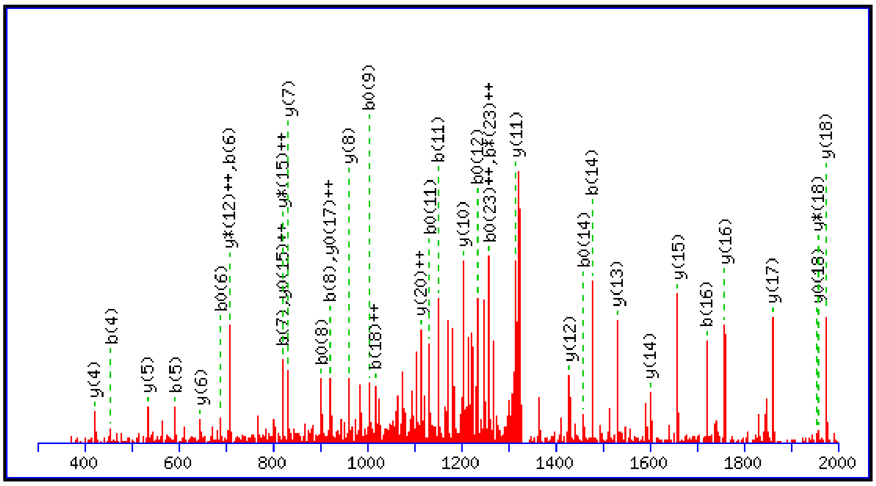
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 22556: 2679.370988 from(1340.692770,2+) intensity(34929.4453) rtinseconds(1848) scans(4672) index(25422)
Title: 111019_Est_MI_YS_G_07Spectrum3983_scans__4672
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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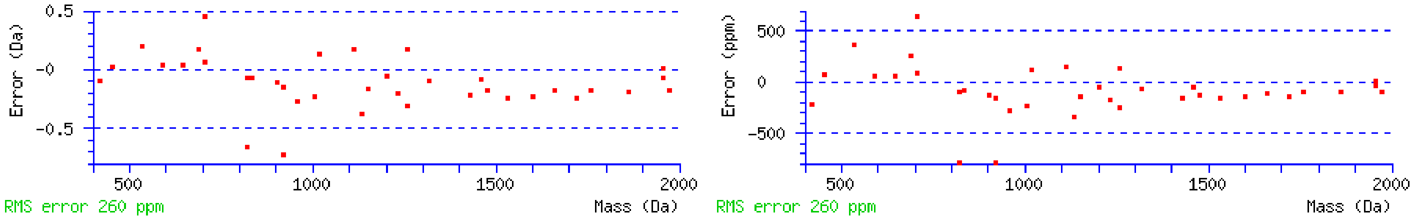
Monoisotopic mass of neutral peptide Mr(calc): 2679.3690
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6      : Deamidated (NQ)
Ions Score: 101  Expect: 1.7e-008
Matches : 38/258 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					**M**							24
2	231.1162	116.0617					**V**	2549.3358	1275.1716	2532.3093	1266.6583	2531.3253	1266.1663	23
3	318.1482	159.5777			300.1376	150.5725	**S**	2450.2674	1225.6373	2433.2409	1217.1241	2432.2569	1216.6321	22
4	**455.2071**	228.1072			437.1966	219.1019	**H**	2363.2354	1182.1213	2346.2088	1173.6081	2345.2248	1173.1160	21
5	**592.2660**	296.6367			574.2555	287.6314	**H**	2226.1765	1113.5919	2209.1499	1105.0786	2208.1659	1104.5866	20
6	**707.2930**	354.1501	690.2664	345.6368	689.2824	345.1448	**N**	2089.1176	1045.0624	2072.0910	1036.5491	2071.1070	1036.0571	19
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	**L**	***1974.0906***	987.5489	1957.0641	979.0357	1956.0801	978.5437	18
8	**921.4247**	461.2160	904.3982	452.7027	903.4141	452.2107	**T**	***1861.0066***	931.0069	1843.9800	922.4936	1842.9960	922.0016	17
9	1022.4724	511.7398	1005.4458	503.2266	1004.4618	502.7346	**T**	***1759.9589***	880.4831	1742.9323	871.9698	1741.9483	871.4778	16
10	1079.4939	540.2506	1062.4673	531.7373	1061.4833	531.2453	**G**	***1658.9112***	829.9592	1641.8847	821.4460	1640.9006	820.9540	15
11	**1150.5310**	575.7691	1133.5044	567.2558	1132.5204	566.7638	**A**	***1601.8897***	801.4485	1584.8632	792.9352	1583.8792	792.4432	14
12	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**T**	***1530.8526***	765.9299	1513.8261	757.4167	1512.8421	756.9247	13
13	1364.6627	682.8350	1347.6362	674.3217	1346.6521	673.8297	**L**	***1429.8049***	715.4061	1412.7784	706.8928	1411.7944	706.4008	12
14	**1477.7468**	739.3770	1460.7202	730.8638	1459.7362	730.3717	**I**	***1316.7209***	658.8641	1299.6943	650.3508	1298.7103	649.8588	11
15	1591.7897	796.3985	1574.7632	787.8852	1573.7791	787.3932	**N**	***1203.6368***	602.3220	1186.6103	593.8088	1185.6262	593.3168	10
16	**1720.8323**	860.9198	1703.8057	852.4065	1702.8217	851.9145	**E**	1089.5939	545.3006	1072.5673	536.7873	1071.5833	536.2953	9
17	1848.8909	924.9491	1831.8643	916.4358	1830.8803	915.9438	**Q**	***960.5513***	480.7793	943.5247	472.2660	942.5407	471.7740	8
18	2034.9702	1017.9887	2017.9436	1009.4755	2016.9596	1008.9834	**W**	***832.4927***	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2148.0543	1074.5308	2131.0277	1066.0175	2130.0437	1065.5255	**L**	***646.4134***	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2261.1383	1131.0728	2244.1118	1122.5595	2243.1278	1122.0675	**L**	***533.3293***	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	**T**	***420.2453***	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
23	2534.2708	1267.6390	2517.2442	1259.1258	2516.2602	1258.6337	**A**	218.1499	109.5786	201.1234	101.0653			2

24							**K**	147.1128	74.0600	130.0863	65.5468			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
101.0	2679.3690	0.0020	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6 100.00%
51.5	2679.3690	0.0020	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N15 0.00%
45.1	2679.3690	0.0020	MVSHHNLTTGATLINEQWLLTTAK	Deamidated Q17 0.00%
4.0	2678.3666	1.0044	MLNMIRQISRPSAAGINLMIGSTR	
1.1	2679.3715	-0.0005	AEQHLKTLPETQRLTAQAATQLTE	
1.1	2679.3715	-0.0005	AEQHLKTLPETQRLTAQAATQLTE	
1.1	2679.3715	-0.0005	AEQHLKTLPETQRLTAQAATQLTQ	
1.1	2679.3715	-0.0005	AEQHLKTLPETQRLTAQAATQLTQ	
0.6	2679.3706	0.0004	KGIGLGFMTAVCVIWFFTPPSAHK	

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

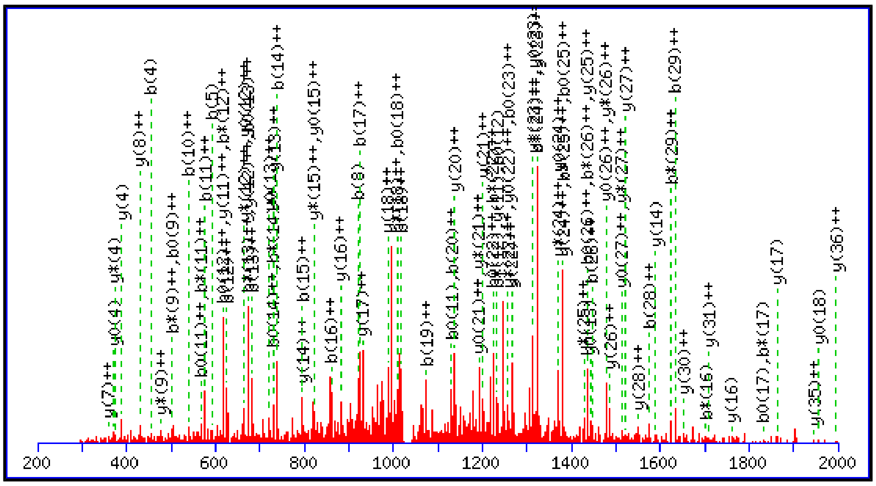
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28608: 4122.076376 from(1031.526370,4+) intensity(0.0000) rtinseconds(2542) scans(6789) index(3219)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum5780_scans__6789
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

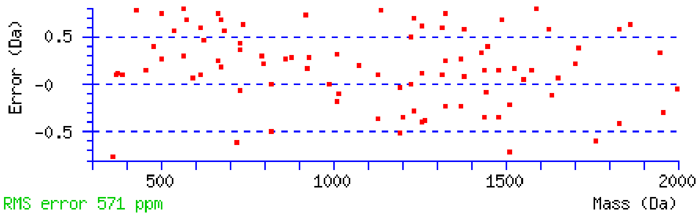
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

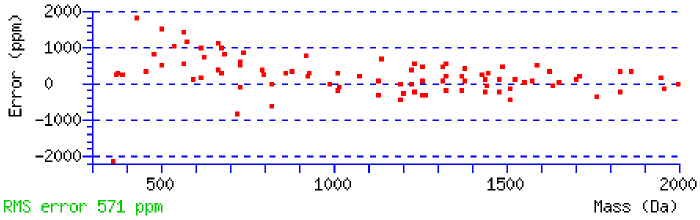


Monoisotopic mass of neutral peptide Mr(calc): 4121.0527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 100 **Expect:** 2e-008
Matches : 95/414 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	318.1482	159.5777			300.1376	150.5725	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	455.2071	228.1072			437.1966	219.1019	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	592.2660	296.6367			574.2555	287.6314	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1078.5098	**539.7586**	1061.4833	531.2453	1060.4993	530.7533	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	1250.5946	**625.8010**	1233.5681	617.2877	1232.5841	616.7957	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	1363.6787	**682.3430**	1346.6521	673.8297	1345.6681	673.3377	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	1476.7628	**738.8850**	1459.7362	730.3717	1458.7522	729.8797	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1590.8057	**795.9065**	1573.7791	787.3932	1572.7951	786.9012	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1719.8483	**860.4278**	1702.8217	851.9145	1701.8377	851.4225	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1848.8909	**924.9491**	1831.8643	916.4358	1830.8803	915.9438	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2034.9702	**1017.9887**	2017.9436	1009.4755	2016.9596	1008.9834	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2148.0543	**1074.5308**	2131.0277	1066.0175	2130.0437	1065.5255	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2261.1383	**1131.0728**	2244.1118	1122.5595	2243.1278	1122.0675	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	T	**1760.8814**	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2534.2708	1267.6390	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2890.4768	**1445.7420**	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3037.5452	1519.2762	3020.5186	1510.7629	3019.5346	1510.2709	**F**	**1232.5906**	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3150.6292	**1575.8183**	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3265.6562	**1633.3317**	3248.6296	1624.8185	3247.6456	1624.3264	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3402.7151	1701.8612	3385.6885	1693.3479	3384.7045	1692.8559	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3489.7471	1745.3772	3472.7206	1736.8639	3471.7366	1736.3719	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3618.7897	1809.8985	3601.7632	1801.3852	3600.7791	1800.8932	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3732.8326	1866.9200	3715.8061	1858.4067	3714.8221	1857.9147	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3803.8698	1902.4385	3786.8432	1893.9252	3785.8592	1893.4332	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3904.9174	1952.9624	3887.8909	1944.4491	3886.9069	1943.9571	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3975.9545	1988.4809	3958.9280	1979.9676	3957.9440	1979.4756	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.5	4121.0527	1.0236	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 58.30%
96.3	4121.0527	1.0236	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 27.97%
92.3	4121.0527	1.0236	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 10.91%
85.8	4121.0527	1.0236	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 2.48%
84.2	4120.0687	2.0076	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
76.5	4120.0687	2.0076	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
71.3	4121.0527	1.0236	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 0.09%
69.3	4120.0687	2.0076	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
65.1	4120.0687	2.0076	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
65.1	4120.0687	2.0076	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

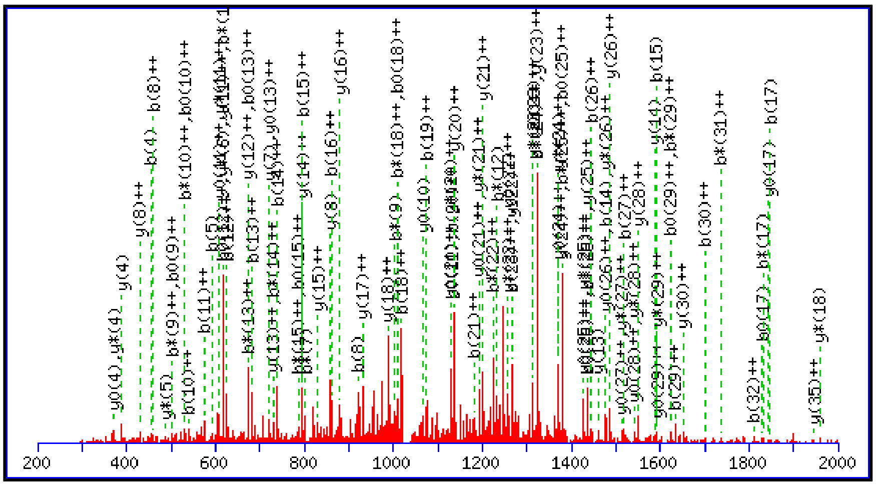
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28525: 4121.076016 from(1031.276280,4+) intensity(395226.6875) rtinseconds(2426) scans(6193) index(12862)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum5442_scans__6193
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

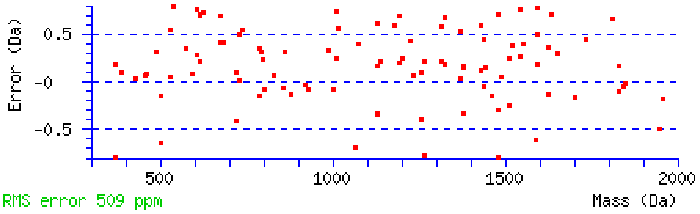
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

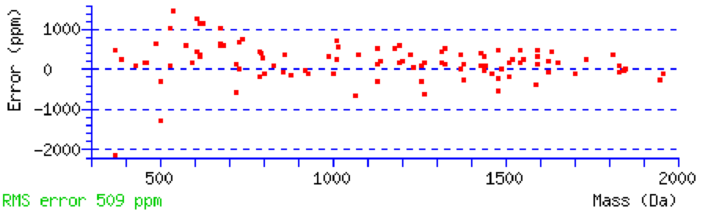


Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 99 **Expect:** 2.4e-008
Matches : 106/414 fragment ions using 153 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	**455.2071**	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	**592.2660**	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	**920.4407**	***460.7240***	903.4141	452.2107	902.4301	451.7187	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1078.5098	***539.7586***	1061.4833	531.2453	1060.4993	530.7533	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1149.5470	***575.2771***	1132.5204	566.7638	1131.5364	566.2718	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1250.5946	***625.8010***	1233.5681	617.2877	1232.5841	616.7957	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1363.6787	***682.3430***	1346.6521	673.8297	1345.6681	673.3377	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1476.7628**	***738.8850***	1459.7362	730.3717	1458.7522	729.8797	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	**1590.8057**	***795.9065***	1573.7791	787.3932	1572.7951	786.9012	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	1719.8483	***860.4278***	1702.8217	851.9145	1701.8377	851.4225	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1847.9069**	924.4571	1830.8803	915.9438	1829.8963	915.4518	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2033.9862	***1017.4967***	2016.9596	1008.9834	2015.9756	1008.4914	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2147.0702	***1074.0388***	2130.0437	1065.5255	2129.0597	1065.0335	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2260.1543	***1130.5808***	2243.1278	1122.0675	2242.1437	1121.5755	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2361.2020	***1181.1046***	2344.1754	1172.5914	2343.1914	1172.0993	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2533.2868	***1267.1470***	2516.2602	1258.6337	2515.2762	1258.1417	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2661.3817	1331.1945	2644.3552	1322.6812	2643.3712	1322.1892	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	**1460.7016**	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2889.4927	***1445.2500***	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3036.5612	***1518.7842***	3019.5346	1510.2709	3018.5506	1509.7789	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3149.6452	1575.3262	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3263.6881	***1632.3477***	3246.6616	1623.8344	3245.6776	1623.3424	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3400.7471	***1700.8772***	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3616.8217	***1808.9145***	3599.7951	1800.4012	3598.8111	1799.9092	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3802.8857	1901.9465	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.6	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 72.33%
94.1	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 25.66%
77.3	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 0.53%
76.6	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 0.46%
75.7	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 0.37%
71.8	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.15%
70.6	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.11%
70.1	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 0.10%
66.8	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.05%
66.7	4120.0687	1.0073	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 0.05%

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

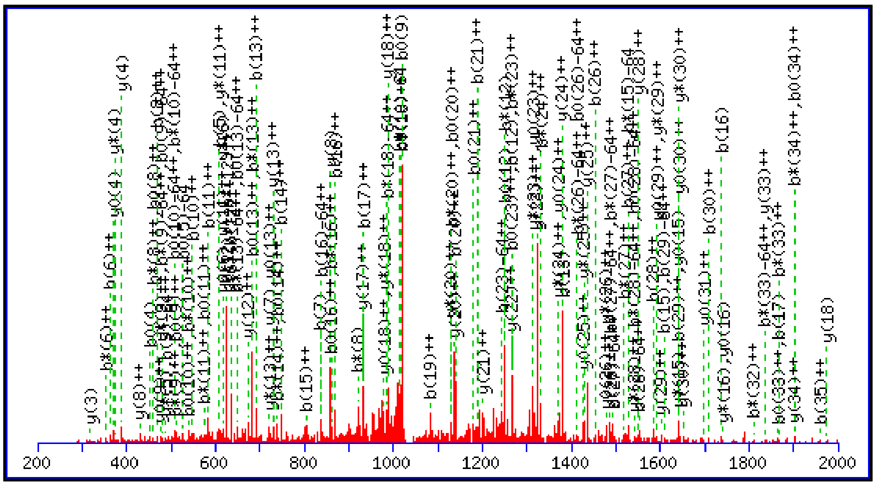
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28841: 4137.068696 from(1035.274450,4+) intensity(10372.8145) rtinseconds(2630) scans(6625) index(26288)
Title: 111019_Est_MI_YS_G_08Spectrum5762_scans__6625
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

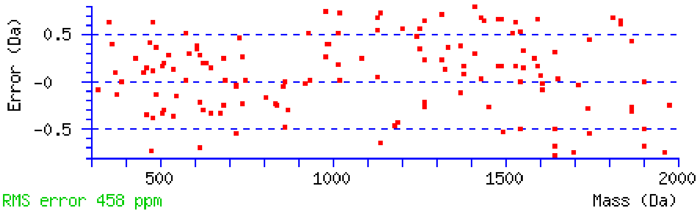
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

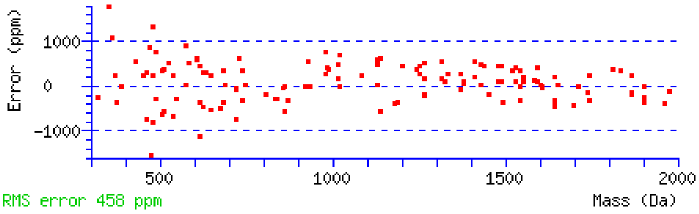


```
Monoisotopic mass of neutral peptide Mr(calc): 4137.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6      : Deamidated (NQ)
N15     : Deamidated (NQ)
N33     : Deamidated (NQ)
Ions Score: 98  Expect: 3.2e-008
Matches : 140/616 fragment ions using 172 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					**M**							**37**
2	247.1111	124.0592					**V**	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	**36**
3	334.1431	167.5752			316.1326	158.5699	**S**	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	**35**
4	471.2020	236.1047			453.1915	227.0994	**H**	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	**34**
5	**608.2609**	304.6341			590.2504	295.6288	**H**	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	**33**
6	723.2879	***362.1476***	706.2613	353.6343	705.2773	353.1423	**N**	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	**32**
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	**31**
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	**30**
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	**29**
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	**28**
11	1166.5259	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	**27**
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	**26**
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	**25**
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
15	**1608.7686**	***804.8880***	1591.7421	796.3747	1590.7581	795.8827	**N**	2645.3206	1323.1639	2628.2940	1314.6507	2627.3100	1314.1586	**23**
16	**1737.8112**	***869.4093***	1720.7847	860.8960	1719.8007	860.4040	**E**	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	**22**
17	**1865.8698**	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	**Q**	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	**21**
18	2051.9491	1026.4782	2034.9226	1017.9649	2033.9386	1017.4729	**W**	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	**20**
19	2165.0332	***1083.0202***	2148.0066	1074.5070	2147.0226	1074.0149	**L**	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	**19**
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	**L**	**1974.0291**	987.5182	1957.0025	979.0049	1956.0185	978.5129	**18**
21	2379.1649	***1190.0861***	2362.1384	1181.5728	2361.1544	1181.0808	**T**	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	**17**

22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	**T**	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	**16**
23	2551.2497	1276.1285	2534.2232	1267.6152	2533.2392	1267.1232	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2679.3447	1340.1760	2662.3181	1331.6627	2661.3341	1331.1707	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2906.4717	***1453.7395***	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3053.5401	***1527.2737***	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3166.6242	***1583.8157***	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3280.6671	***1640.8372***	3263.6405	1632.3239	3262.6565	1631.8319	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3417.7260	***1709.3666***	3400.6994	1700.8534	3399.7154	1700.3614	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3504.7580	1752.8826	3487.7315	1744.3694	3486.7475	1743.8774	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3748.8276	1874.9174	3731.8010	1866.4041	3730.8170	1865.9121	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3819.8647	1910.4360	3802.8381	1901.9227	3801.8541	1901.4307	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3920.9123	***1960.9598***	3903.8858	1952.4465	3902.9018	1951.9545	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3991.9495	1996.4784	3974.9229	1987.9651	3973.9389	1987.4731	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.1	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 91.70%
84.3	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 3.88%
80.1	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 1.47%
79.0	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 1.13%
78.1	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 0.92%
69.7	4136.0636	1.0051	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
69.3	4136.0636	1.0051	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
67.5	4137.0477	0.0210	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17 0.08%
67.3	4136.0636	1.0051	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
67.1	4136.0636	1.0051	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

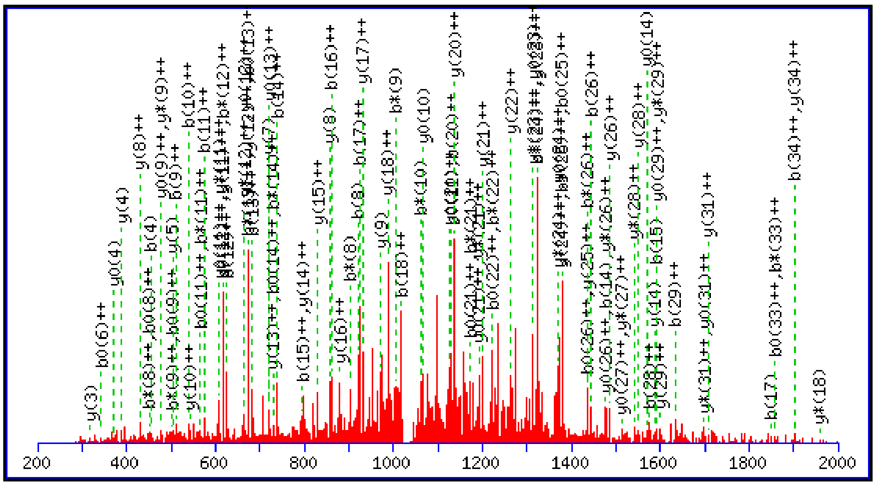
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28576: 4121.092136 from(1031.280310,4+) intensity(65368.3594) rtinseconds(2488) scans(6351) index(10448)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum5472_scans__6351
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

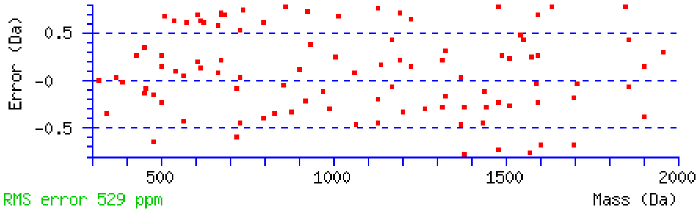
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

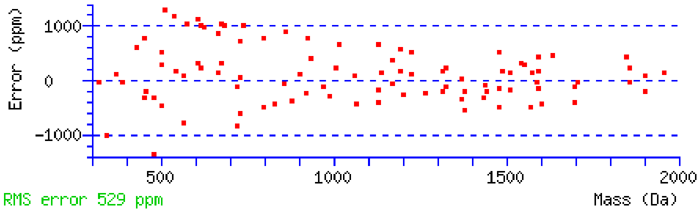


Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 96 **Expect:** 4.3e-008
Matches : 103/414 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	**455.2071**	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	592.2660	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	**920.4407**	460.7240	903.4141	452.2107	902.4301	451.7187	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1021.4884	**511.2478**	1004.4618	502.7346	1003.4778	502.2425	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1078.5098	**539.7586**	1061.4833	531.2453	1060.4993	530.7533	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	1250.5946	**625.8010**	1233.5681	617.2877	1232.5841	616.7957	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	1363.6787	**682.3430**	1346.6521	673.8297	1345.6681	673.3377	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	**1476.7628**	**738.8850**	1459.7362	730.3717	1458.7522	729.8797	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	**1590.8057**	**795.9065**	1573.7791	787.3932	1572.7951	786.9012	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	1719.8483	**860.4278**	1702.8217	851.9145	1701.8377	851.4225	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1847.9069**	**924.4571**	1830.8803	915.9438	1829.8963	915.4518	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2033.9862	**1017.4967**	2016.9596	1008.9834	2015.9756	1008.4914	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2147.0702	1074.0388	2130.0437	1065.5255	2129.0597	1065.0335	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2260.1543	**1130.5808**	2243.1278	1122.0675	2242.1437	1121.5755	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2361.2020	1181.1046	2344.1754	1172.5914	2343.1914	1172.0993	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2533.2868	1267.1470	2516.2602	1258.6337	2515.2762	1258.1417	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2661.3817	1331.1945	2644.3552	1322.6812	2643.3712	1322.1892	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2889.4927	**1445.2500**	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3036.5612	1518.7842	3019.5346	1510.2709	3018.5506	1509.7789	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3149.6452	**1575.3262**	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3264.6722	**1632.8397**	3247.6456	1624.3264	3246.6616	1623.8344	**N**	**972.4381**	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3401.7311	1701.3692	3384.7045	1692.8559	3383.7205	1692.3639	**H**	**857.4112**	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	**S**	**720.3523**	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3617.8057	1809.4065	3600.7791	1800.8932	3599.7951	1800.4012	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	**N**	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3802.8857	**1901.9465**	3785.8592	1893.4332	3784.8752	1892.9412	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
95.8	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 32.46%
94.9	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 26.08%
92.9	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 16.61%
90.0	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 8.48%
87.7	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 4.97%
85.6	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 3.06%
83.8	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 2.01%
82.8	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 1.63%
79.8	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 0.80%
79.7	4120.0687	1.0234	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17 0.78%

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

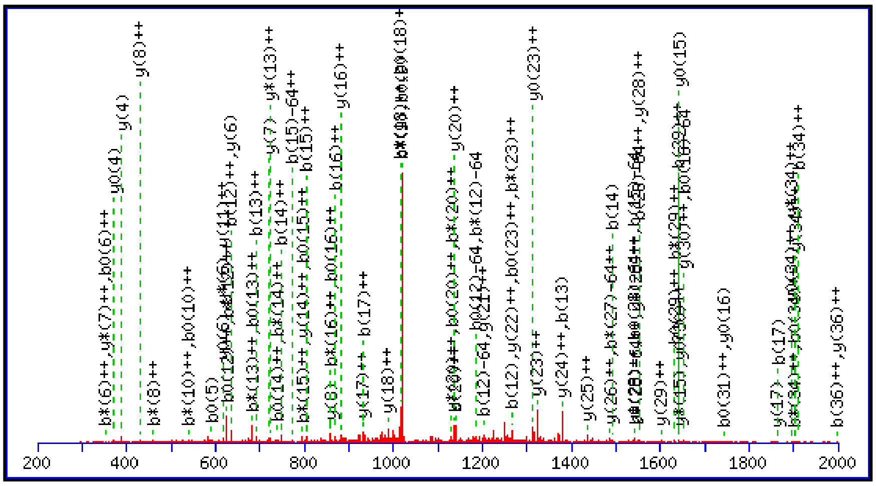
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28929: 4138.043856 from(1035.518240,4+) intensity(15285.0820) rtinseconds(2591) scans(6852) index(18959)
Title: 111019_Est_MI_YP_G_08Spectrum5988_scans__6852
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

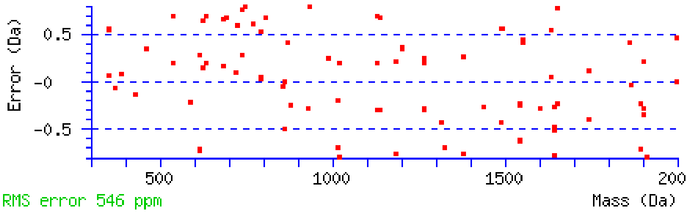
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

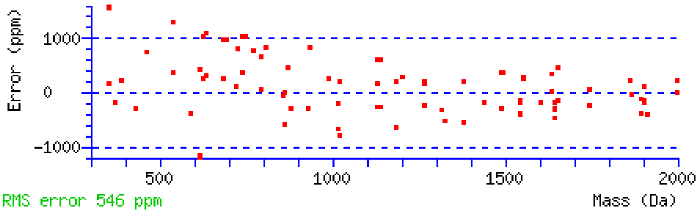


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q17 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 95 **Expect:** 6.7e-008
Matches : 91/616 fragment ions using 104 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					**M**							**37**
2	247.1111	124.0592					**V**	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	**36**
3	334.1431	167.5752			316.1326	158.5699	**S**	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	**35**
4	471.2020	236.1047			453.1915	227.0994	**H**	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	**34**
5	608.2609	304.6341			590.2504	295.6288	**H**	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	**33**
6	722.3039	361.6556	705.2773	353.1423	704.2933	352.6503	**N**	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	**32**
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	**L**	3417.7424	1709.3748	3400.7159	1700.8616	3399.7318	1700.3696	**31**
8	936.4356	468.7214	919.4091	460.2082	918.4250	459.7162	**T**	3304.6583	1652.8328	3287.6318	1644.3195	3286.6478	1643.8275	**30**
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	**T**	3203.6107	1602.3090	3186.5841	1593.7957	3185.6001	1593.3037	**29**
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	**G**	3102.5630	1551.7851	3085.5364	1543.2719	3084.5524	1542.7799	**28**
11	1165.5419	583.2746	1148.5153	574.7613	1147.5313	574.2693	**A**	3045.5415	1523.2744	3028.5150	1514.7611	3027.5310	1514.2691	**27**
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	**T**	2974.5044	1487.7558	2957.4779	1479.2426	2956.4938	1478.7506	**26**
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	**L**	2873.4567	1437.2320	2856.4302	1428.7187	2855.4462	1428.2267	**25**
14	**1492.7577**	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	**I**	2760.3727	1380.6900	2743.3461	1372.1767	2742.3621	1371.6847	**24**
15	1606.8006	**803.9039**	1589.7741	795.3907	1588.7900	794.8987	**N**	2647.2886	1324.1479	2630.2621	1315.6347	2629.2780	1315.1427	**23**
16	1735.8432	**868.4252**	1718.8166	859.9120	1717.8326	859.4200	**E**	2533.2457	1267.1265	2516.2191	1258.6132	2515.2351	1258.1212	**22**
17	**1864.8858**	**932.9465**	1847.8592	924.4333	1846.8752	923.9413	**Q**	2404.2031	1202.6052	2387.1765	1194.0919	2386.1925	1193.5999	**21**
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	**W**	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	**20**
19	2164.0492	1082.5282	2147.0226	1074.0149	2146.0386	1073.5229	**L**	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	**19**
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	**L**	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	**18**
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	**T**	**1862.9130**	931.9602	1845.8865	923.4469	1844.9025	922.9549	**17**

22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	1761.8654	881.4363	1744.8388	872.9230	1743.8548	872.4310	**16**
23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1660.8177	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6751	722.3412	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3053.5401	1527.2737	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3166.6242	1583.8157	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3281.6511	**1641.3292**	3264.6245	1632.8159	3263.6405	1632.3239	**N**	973.4221	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	1875.4094	3732.7850	1866.8961	3731.8010	1866.4041	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	**1910.9280**	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	**1996.9704**	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
95.4	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29, N33 50.40%
91.8	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 21.90%
86.8	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 6.88%
85.8	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 5.48%
84.0	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 3.66%
83.6	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 3.31%
82.0	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 2.28%
82.0	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 2.26%
80.3	4137.0477	0.9962	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
76.6	4138.0317	0.0122	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 0.66%

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

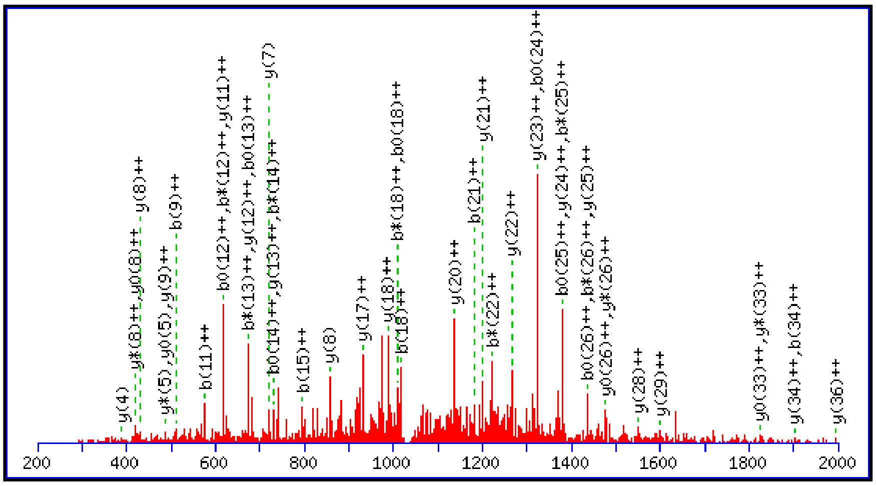
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28587: 4121.102736 from(1031.282960,4+) intensity(0.0000) rtinseconds(2477) scans(6530) index(9785)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum5650_scans__6530
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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Monoisotopic mass of neutral peptide Mr(calc): 4119.0847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N29     : Deamidated (NQ)
Ions Score: 93  Expect: 8.5e-008
Matches : 49/414 fragment ions using 52 most intense peaks    (help)
```
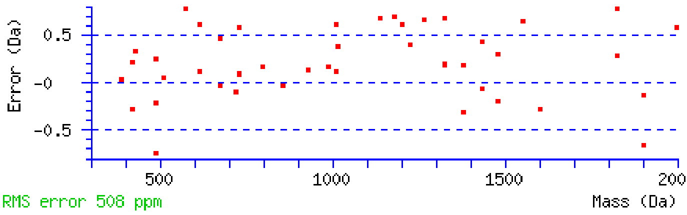
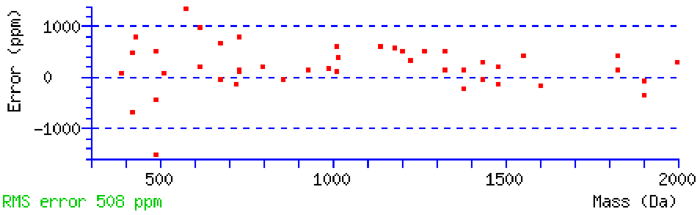

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	36
3	318.1482	159.5777			300.1376	150.5725	S	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	35
4	455.2071	228.1072			437.1966	219.1019	H	3802.9511	1901.9792	3785.9246	1893.4659	3784.9405	1892.9739	34
5	592.2660	296.6367			574.2555	287.6314	H	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1021.4884	**511.2478**	1004.4618	502.7346	1003.4778	502.2425	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1078.5098	539.7586	1061.4833	531.2453	1060.4993	530.7533	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	1250.5946	625.8010	1233.5681	617.2877	1232.5841	616.7957	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	1363.6787	682.3430	1346.6521	673.8297	1345.6681	673.3377	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	1476.7628	738.8850	1459.7362	730.3717	1458.7522	729.8797	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1590.8057	**795.9065**	1573.7791	787.3932	1572.7951	786.9012	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1719.8483	860.4278	1702.8217	851.9145	1701.8377	851.4225	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1847.9069	924.4571	1830.8803	915.9438	1829.8963	915.4518	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2033.9862	**1017.4967**	2016.9596	1008.9834	2015.9756	1008.4914	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2147.0702	1074.0388	2130.0437	1065.5255	2129.0597	1065.0335	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2260.1543	1130.5808	2243.1278	1122.0675	2242.1437	1121.5755	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2361.2020	**1181.1046**	2344.1754	1172.5914	2343.1914	1172.0993	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16
23	2533.2868	1267.1470	2516.2602	1258.6337	2515.2762	1258.1417	A	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	15

24	2661.3817	1331.1945	2644.3552	1322.6812	2643.3712	1322.1892	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2775.4247	1388.2160	2758.3981	1379.7027	2757.4141	1379.2107	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2888.5087	1444.7580	2871.4822	1436.2447	2870.4982	1435.7527	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3035.5771	1518.2922	3018.5506	1509.7789	3017.5666	1509.2869	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3148.6612	1574.8342	3131.6347	1566.3210	3130.6506	1565.8290	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3263.6881	1632.3477	3246.6616	1623.8344	3245.6776	1623.3424	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3400.7471	1700.8772	3383.7205	1692.3639	3382.7365	1691.8719	**H**	**857.4112**	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	**720.3523**	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3616.8217	1808.9145	3599.7951	1800.4012	3598.8111	1799.9092	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3730.8646	1865.9359	3713.8381	1857.4227	3712.8540	1856.9307	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3801.9017	**1901.4545**	3784.8752	1892.9412	3783.8912	1892.4492	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3902.9494	1951.9783	3885.9229	1943.4651	3884.9388	1942.9731	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3973.9865	1987.4969	3956.9600	1978.9836	3955.9759	1978.4916	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
92.6	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29 65.50%
88.9	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33 28.20%
78.0	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17 2.25%
77.8	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25 2.15%
76.9	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15 1.77%
65.2	4119.0847	2.0180	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6 0.12%
12.2	4121.1051	-0.0024	GTRSVFPFGADPSAPNTGTLNWFPFSTAPALPLQVGLYK	
11.5	4120.0997	1.0030	GRQLNISALDLTSSNSLVFLRETLEENMLQDQVQLK	
10.0	4120.0851	1.0176	ITSDQVINSGLIFEDKPKPSKQSLQSYQEALQQQIR	
9.9	4120.0851	1.0176	ITSDQVINSGLIFEDKPKPSKQSLQSYQEALQQQIR	

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

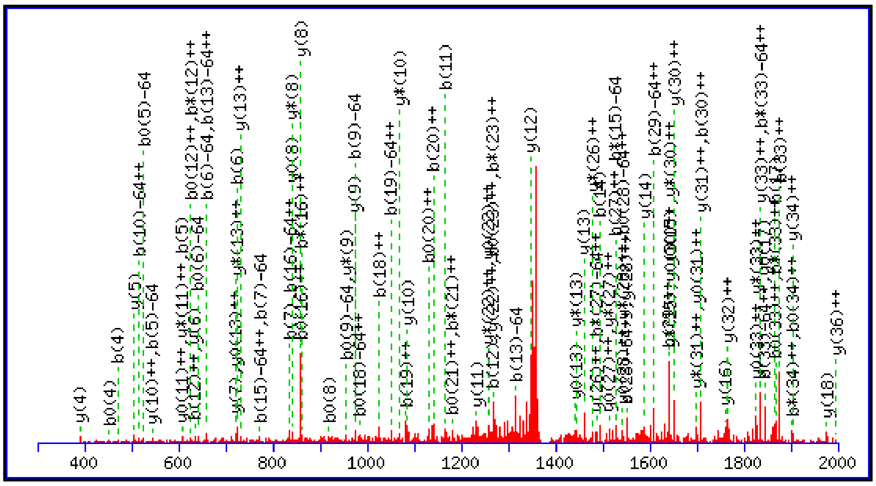
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28930: 4138.048092 from(1380.356640,3+) intensity(60045.7773) rtinseconds(2575) scans(6726) index(25642)
Title: 111019_Est_MI_YS_G_07Spectrum5794_scans__6726
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

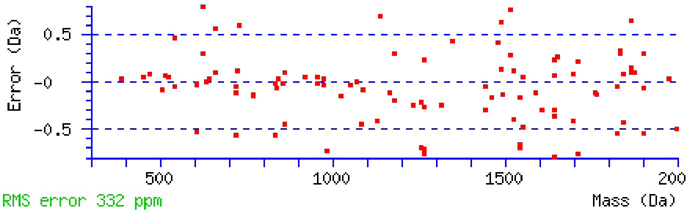
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

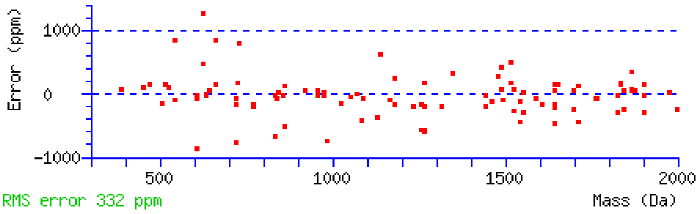


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 92 **Expect:** 1.4e-007
Matches : 102/616 fragment ions using 97 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	334.1431	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	**608.2609**	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	**723.2879**	362.1476	706.2613	353.6343	705.2773	353.1423	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1095.4888	548.2480	1078.4622	539.7347	1077.4782	539.2427	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	**1166.5259**	583.7666	1149.4993	575.2533	1148.5153	574.7613	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1267.5736**	**634.2904**	1250.5470	625.7771	1249.5630	625.2851	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	1380.6576	690.8325	1363.6311	682.3192	1362.6471	681.8272	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	**1493.7417**	747.3745	1476.7151	738.8612	1475.7311	738.3692	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1607.7846	804.3959	1590.7581	795.8827	1589.7741	795.3907	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1736.8272	868.9172	1719.8007	860.4040	1718.8166	859.9120	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1865.8698**	933.4385	1848.8433	924.9253	1847.8592	924.4333	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2051.9491	**1026.4782**	2034.9226	1017.9649	2033.9386	1017.4729	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2165.0332	**1083.0202**	2148.0066	1074.5070	2147.0226	1074.0149	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2278.1172	**1139.5623**	2261.0907	1131.0490	2260.1067	1130.5570	L	***1975.0131***	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2379.1649	1190.0861	2362.1384	1181.5728	2361.1544	1181.0808	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	**T**	***1760.8814***	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2551.2497	1276.1285	2534.2232	1267.6152	2533.2392	1267.1232	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2679.3447	1340.1760	2662.3181	1331.6627	2661.3341	1331.1707	**K**	***1588.7966***	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	***1460.7016***	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	***1346.6587***	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3053.5401	**1527.2737**	3036.5135	1518.7604	3035.5295	1518.2684	**F**	***1233.5746***	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3166.6242	1583.8157	3149.5976	1575.3024	3148.6136	1574.8104	**L**	***1086.5062***	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3281.6511	**1641.3292**	3264.6245	1632.8159	3263.6405	1632.3239	**N**	***973.4221***	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3418.7100	**1709.8586**	3401.6835	1701.3454	3400.6994	1700.8534	**H**	***858.3952***	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	***721.3363***	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	***634.3042***	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	**1875.4094**	3732.7850	1866.8961	3731.8010	1866.4041	**N**	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	1996.9704	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
92.3	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 55.51%
90.8	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 39.39%
88.0	4137.0477	1.0004	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
80.2	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 3.41%
74.6	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 0.94%
65.5	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29, N33 0.12%
65.2	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 0.11%
64.4	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 0.09%
64.3	4138.0317	0.0164	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 0.09%
62.7	4137.0477	1.0004	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28567: 4121.086336 from(1031.278860,4+) intensity(31891.4316) rtinseconds(2519) scans(6618) index(22799)
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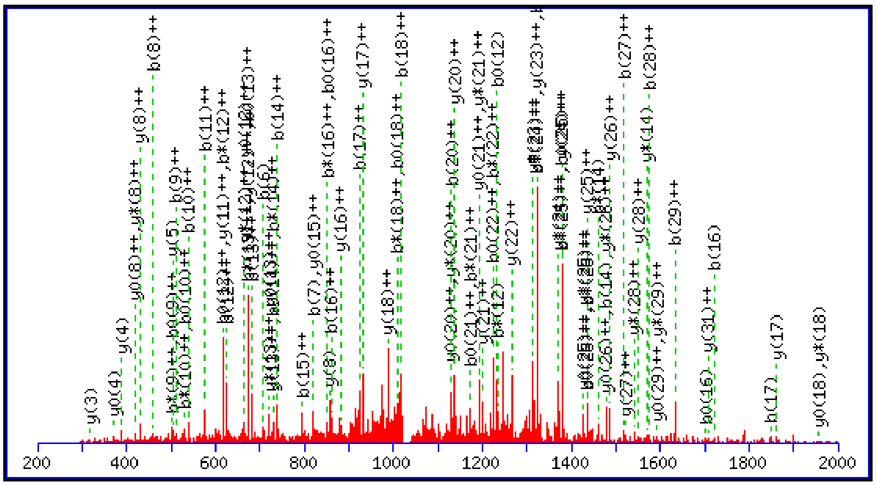
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

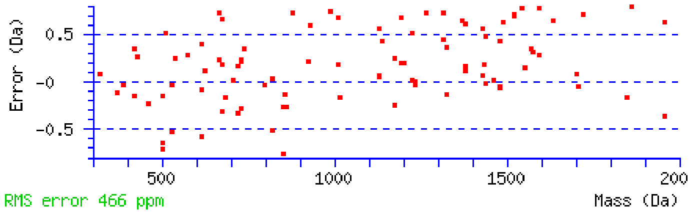
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

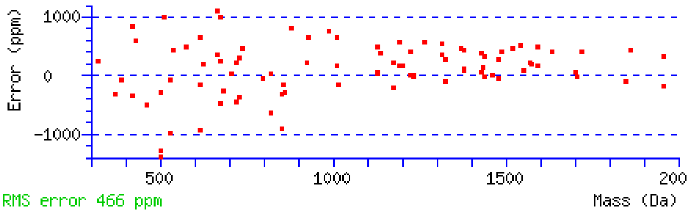


```
Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6     : Deamidated (NQ)
N29    : Deamidated (NQ)
Ions Score: 91  Expect: 1.4e-007
Matches : 95/414 fragment ions using 120 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	455.2071	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	592.2660	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**707.2930**	354.1501	690.2664	345.6368	689.2824	345.1448	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	921.4247	***461.2160***	904.3982	452.7027	903.4141	452.2107	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1022.4724	***511.7398***	1005.4458	503.2266	1004.4618	502.7346	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	1150.5310	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1591.7897	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	**1720.8323**	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	**1848.8909**	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2148.0543	1074.5308	2131.0277	1066.0175	2130.0437	1065.5255	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	T	**1860.9450**	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2534.2708	1267.6390	2517.2442	1259.1258	2516.2602	1258.6337	A	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	15
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	K	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	14
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	N	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	13
26	2889.4927	1445.2500	2872.4662	1436.7367	2871.4822	1436.2447	L	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12
27	3036.5612	***1518.7842***	3019.5346	1510.2709	3018.5506	1509.7789	F	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	11
28	3149.6452	***1575.3262***	3132.6187	1566.8130	3131.6347	1566.3210	L	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	10
29	3264.6722	***1632.8397***	3247.6456	1624.3264	3246.6616	1623.8344	N	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	9
30	3401.7311	1701.3692	3384.7045	1692.8559	3383.7205	1692.3639	H	**857.4112**	429.2092	840.3846	420.6959	839.4006	420.2039	8
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	S	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	7
32	3617.8057	1809.4065	3600.7791	1800.8932	3599.7951	1800.4012	E	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	6
33	3731.8486	1866.4279	3714.8221	1857.9147	3713.8381	1857.4227	N	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	5
34	3802.8857	1901.9465	3785.8592	1893.4332	3784.8752	1892.9412	A	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	4
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	A	218.1499	109.5786	201.1234	101.0653			2
37							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.8	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 27.82%
90.8	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 27.50%
89.0	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 18.29%
87.5	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 13.10%
81.1	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 2.96%
80.4	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 2.54%
79.0	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 1.85%
78.7	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 1.72%
76.7	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 1.07%
74.4	4120.0687	1.0176	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.63%

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

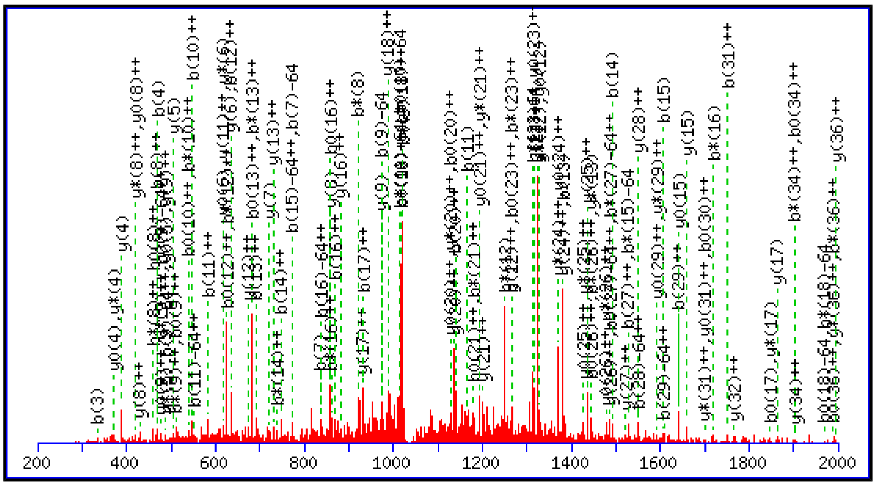
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28926: 4138.030616 from(1035.514930,4+) intensity(16521.1426) rtinseconds(2670) scans(7077) index(19929)
Title: 111019_Est_MI_YP_G_09Spectrum6280_scans__7077
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

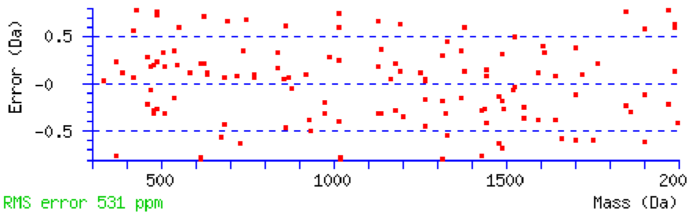
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

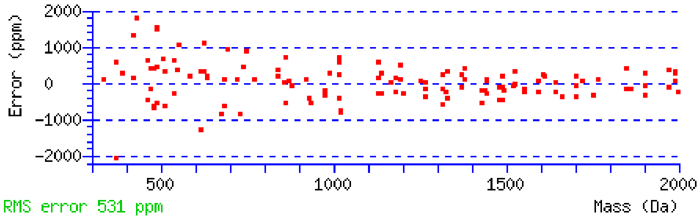


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 90 **Expect:** 2.6e-007
Matches : 130/616 fragment ions using 174 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	**334.1431**	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	608.2609	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	723.2879	362.1476	706.2613	353.6343	705.2773	353.1423	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	937.4196	**469.2135**	920.3931	460.7002	919.4091	460.2082	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1095.4888	**548.2480**	1078.4622	539.7347	1077.4782	539.2427	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	**1166.5259**	**583.7666**	1149.4993	575.2533	1148.5153	574.7613	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1267.5736**	**634.2904**	1250.5470	625.7771	1249.5630	625.2851	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	**1380.6576**	**690.8325**	1363.6311	682.3192	1362.6471	681.8272	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	**1493.7417**	**747.3745**	1476.7151	738.8612	1475.7311	738.3692	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	**1607.7846**	804.3959	1590.7581	795.8827	1589.7741	795.3907	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1736.8272	**868.9172**	1719.8007	860.4040	1718.8166	859.9120	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1864.8858	**932.9465**	1847.8592	924.4333	1846.8752	923.9413	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	20
19	2164.0492	1082.5282	2147.0226	1074.0149	2146.0386	1073.5229	L	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	19
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	L	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	**1862.9130**	931.9602	1845.8865	923.4469	1844.9025	922.9549	17

22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	1761.8654	881.4363	1744.8388	872.9230	1743.8548	872.4310	**16**
23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	**1660.8177**	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6751	722.3412	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3053.5401	**1527.2737**	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3166.6242	1583.8157	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3281.6511	**1641.3292**	3264.6245	1632.8159	3263.6405	1632.3239	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	**1753.3747**	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	1875.4094	3732.7850	1866.8961	3731.8010	1866.4041	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	1996.9704	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
89.7	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 25.36%
89.7	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 25.07%
88.8	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 20.62%
83.6	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 6.24%
83.5	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 6.15%
83.0	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 5.47%
82.2	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 4.54%
81.4	4137.0477	0.9830	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
77.3	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 1.44%
75.1	4138.0317	-0.0010	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17, N33 0.88%

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

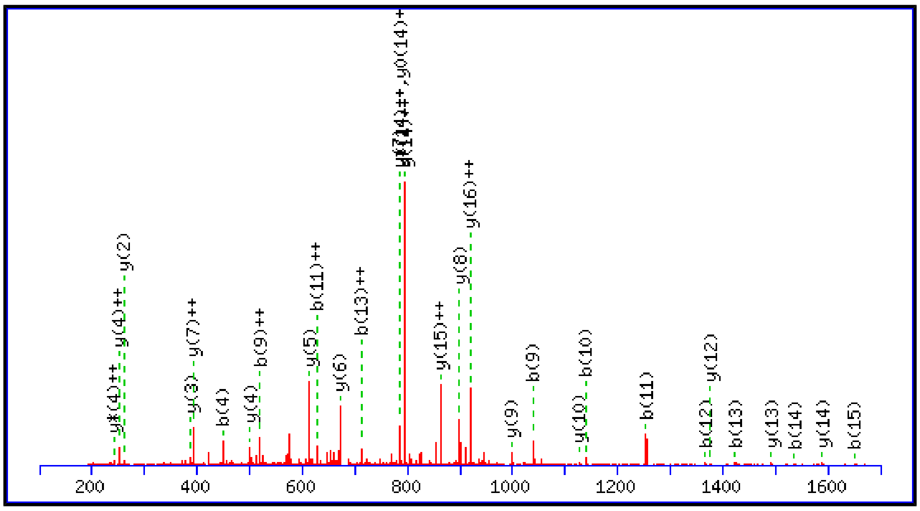
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLHPNYSQVDIGLIKLK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

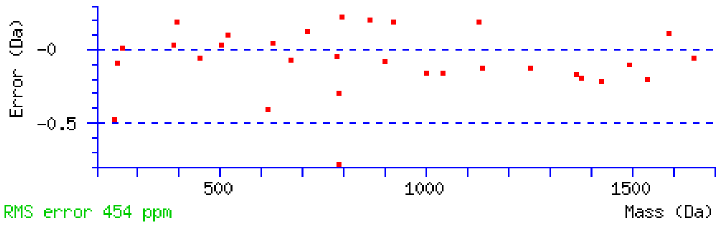
Match to Query 13004: 2036.172732 from(679.731520,3+) intensity(383838.8750) rtinseconds(1690) scans(4256) index(9516)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum3641_scans__4256
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

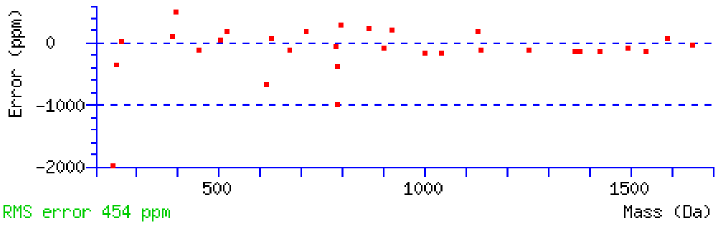
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2036.1670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 88 **Expect:** 4.8e-008
Matches : 31/166 fragment ions using 45 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							18
2	199.1441	100.0757					V	1938.1059	969.5566	1921.0793	961.0433	1920.0953	960.5513	17
3	312.2282	156.6177					L	1839.0375	920.0224	1822.0109	911.5091	1821.0269	911.0171	16
4	**449.2871**	225.1472					H	1725.9534	863.4803	1708.9268	854.9671	1707.9428	854.4751	15
5	546.3398	273.6736					P	***1588.8945***	794.9509	1571.8679	786.4376	1570.8839	785.9456	14
6	661.3668	331.1870	644.3402	322.6738			N	***1491.8417***	746.4245	1474.8152	737.9112	1473.8312	737.4192	13
7	824.4301	412.7187	807.4036	404.2054			Y	***1376.8148***	688.9110	1359.7882	680.3978	1358.8042	679.9057	12
8	911.4621	456.2347	894.4356	447.7214	893.4516	447.2294	S	1213.7514	607.3794	1196.7249	598.8661	1195.7409	598.3741	11
9	**1039.5207**	**520.2640**	1022.4942	511.7507	1021.5102	511.2587	Q	***1126.7194***	563.8633	1109.6929	555.3501	1108.7089	554.8581	10
10	**1138.5891**	569.7982	1121.5626	561.2849	1120.5786	560.7929	V	***998.6608***	499.8341	981.6343	491.3208	980.6503	490.8288	9
11	**1253.6161**	**627.3117**	1236.5895	618.7984	1235.6055	618.3064	D	***899.5924***	450.2999	882.5659	441.7866	881.5819	441.2946	8
12	**1366.7001**	683.8537	1349.6736	675.3404	1348.6896	674.8484	I	***784.5655***	392.7864	767.5389	384.2731			7
13	**1423.7216**	**712.3644**	1406.6951	703.8512	1405.7110	703.3592	G	***671.4814***	336.2443	654.4549	327.7311			6
14	**1536.8057**	768.9065	1519.7791	760.3932	1518.7951	759.9012	L	***614.4600***	307.7336	597.4334	299.2203			5
15	**1649.8897**	825.4485	1632.8632	816.9352	1631.8792	816.4432	I	***501.3759***	251.1916	484.3493	242.6783			4
16	1777.9847	889.4960	1760.9581	880.9827	1759.9741	880.4907	K	***388.2918***	194.6496	371.2653	186.1363			3
17	1891.0688	946.0380	1874.0422	937.5247	1873.0582	937.0327	L	***260.1969***	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.5	2036.1670	0.0057	VVLHPNYSQVDIGLIKLK	Deamidated N6 95.31%
75.4	2036.1670	0.0057	VVLHPNYSQVDIGLIKLK	Deamidated Q9 4.69%
12.6	2036.1703	0.0024	AKEMGLPVGTAAIAPIIAAVK	
4.8	2034.1698	2.0030	IQLQKAIETLNRLQPNR	
2.4	2036.1630	0.0098	QTPSAQLSLIKNGPLTIQK	
1.9	2034.1711	2.0016	HLRHLEILQLSRNHIR	
1.6	2036.1638	0.0089	GMVPIVLVAKLGPQVMAAAR	
1.0	2036.1816	-0.0088	QDSLGQLIAIPRPKMKLK	

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

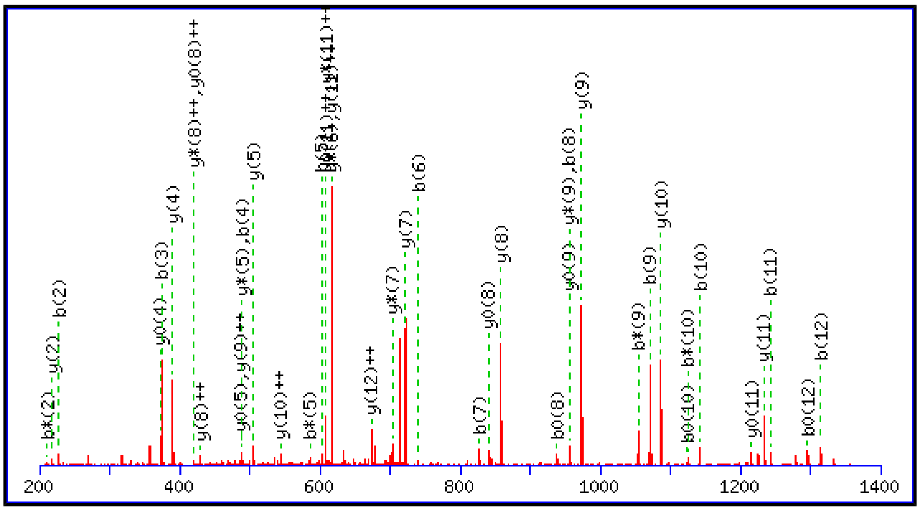
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

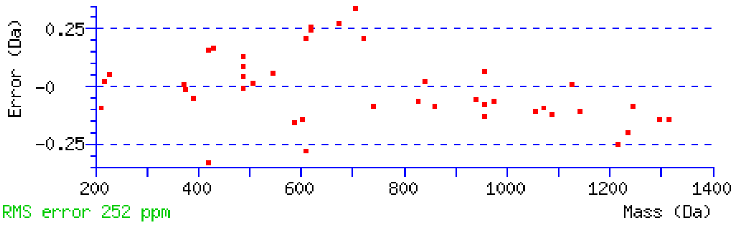
Match to Query 4841: 1459.696948 from(730.855750,2+) intensity(5174931.5000) rtinseconds(669) scans(1585) index(23803)
Title: 111019_Est_MI_YS_G_05Spectrum1333_scans__1585
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

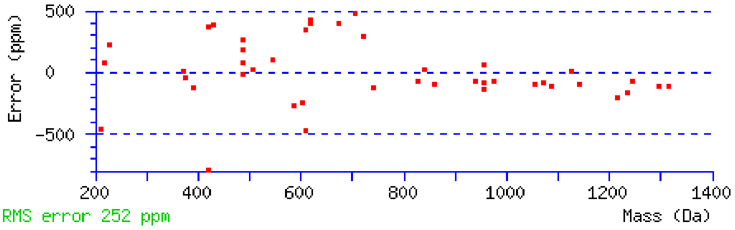
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1459.6943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
N9     : Deamidated (NQ)
Ions Score: 83  Expect: 7.7e-007
Matches : 44/128 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	115.0502	58.0287	98.0237	49.5155			N							13
2	***228.1343***	114.5708	211.1077	106.0575			L	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	12
3	***375.2027***	188.1050	358.1761	179.5917			F	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	11
4	***488.2867***	244.6470	471.2602	236.1337			L	**1086.5062**	543.7567	1069.4796	535.2435	1068.4956	534.7515	10
5	***603.3137***	302.1605	586.2871	293.6472			N	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	9
6	***740.3726***	370.6899	723.3461	362.1767			H	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	8
7	***827.4046***	414.2060	810.3781	405.6927	809.3941	405.2007	S	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	7
8	***956.4472***	478.7272	939.4207	470.2140	938.4367	469.7220	E	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	6
9	***1071.4742***	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	5
10	***1142.5113***	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	4
11	***1243.5590***	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
12	***1314.5961***	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	**218.1499**	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.5	1459.6943	0.0027	NLFLNHSENATAK	Deamidated N5, N9 99.53%
60.2	1459.6943	0.0027	NLFLNHSENATAK	Deamidated N1, N9 0.47%
33.5	1459.6943	0.0027	NLFLNHSENATAK	Deamidated N1, N5 0.00%
21.4	1459.6929	0.0040	VQEQELDEQLVK	
21.2	1459.6929	0.0040	LNQNELELENLK	
16.5	1459.6985	-0.0016	QMLYMKEMRAK	
15.4	1459.6929	0.0040	VEEIENELDEIK	
14.5	1459.6929	0.0040	IEDLENEIEEVK	
14.0	1459.7042	-0.0072	INIQNKDIEAGDK	
13.9	1459.6977	-0.0007	NCTEELDLNPKK	

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

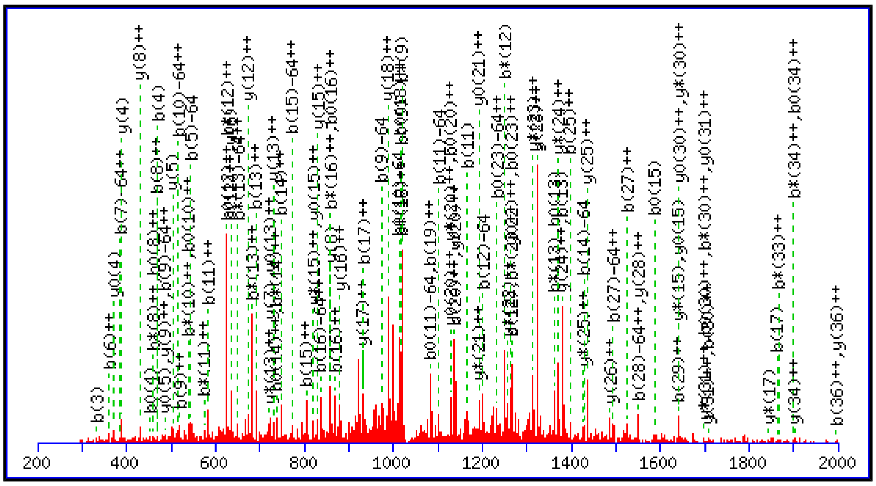
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28920: 4137.099296 from(1035.282100,4+) intensity(0.0000) rtinseconds(2494) scans(6625) index(16272)
Title: 111019_Est_MI_YP_G_05Spectrum5679_scans__6625
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

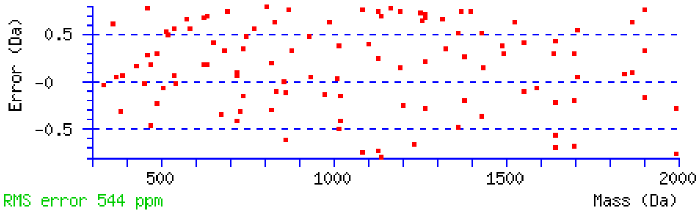
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

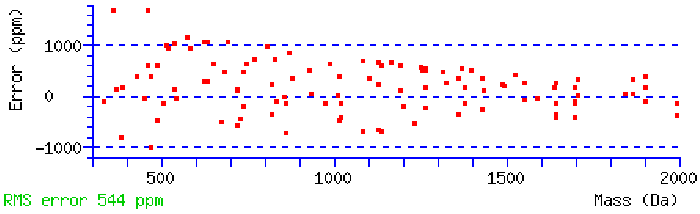


Monoisotopic mass of neutral peptide Mr(calc): 4135.0796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N33 : Deamidated (NQ)
Ions Score: 82 **Expect:** 1.1e-006
Matches : 112/616 fragment ions using 155 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	36
3	**334.1431**	167.5752			316.1326	158.5699	S	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3802.9511	1901.9792	3785.9246	1893.4659	3784.9405	1892.9739	34
5	608.2609	304.6341			590.2504	295.6288	H	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	33
6	722.3039	***361.6556***	705.2773	353.1423	704.2933	352.6503	N	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	936.4356	***468.7214***	919.4091	460.2082	918.4250	459.7162	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1037.4833	***519.2453***	1020.4567	510.7320	1019.4727	510.2400	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1165.5419**	***583.2746***	1148.5153	574.7613	1147.5313	574.2693	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	**1266.5895**	***633.7984***	1249.5630	625.2851	1248.5790	624.7931	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	**1379.6736**	***690.3404***	1362.6471	681.8272	1361.6630	681.3352	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	1492.7577	***746.8825***	1475.7311	738.3692	1474.7471	737.8772	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1606.8006	***803.9039***	1589.7741	795.3907	1588.7900	794.8987	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1735.8432	***868.4252***	1718.8166	859.9120	1717.8326	859.4200	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	**1863.9018**	***932.4545***	1846.8752	923.9413	1845.8912	923.4492	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2049.9811	1025.4942	2032.9545	1016.9809	2031.9705	1016.4889	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2163.0652	***1082.0362***	2146.0386	1073.5229	2145.0546	1073.0309	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2276.1492	***1138.5782***	2259.1227	1130.0650	2258.1386	1129.5730	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2377.1969	1189.1021	2360.1703	1180.5888	2359.1863	1180.0968	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2478.2446	1239.6259	2461.2180	1231.1126	2460.2340	1230.6206	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2549.2817	1275.1445	2532.2551	1266.6312	2531.2711	1266.1392	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2677.3766	1339.1920	2660.3501	1330.6787	2659.3661	1330.1867	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2791.4196	***1396.2134***	2774.3930	1387.7002	2773.4090	1387.2081	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2904.5036	1452.7555	2887.4771	1444.2422	2886.4931	1443.7502	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3051.5721	***1526.2897***	3034.5455	1517.7764	3033.5615	1517.2844	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3164.6561	1582.8317	3147.6296	1574.3184	3146.6456	1573.8264	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3278.6990	***1639.8532***	3261.6725	1631.3399	3260.6885	1630.8479	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3415.7580	***1708.3826***	3398.7314	1699.8693	3397.7474	1699.3773	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3502.7900	1751.8986	3485.7634	1743.3854	3484.7794	1742.8933	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3631.8326	1816.4199	3614.8060	1807.9067	3613.8220	1807.4146	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3746.8595	1873.9334	3729.8330	1865.4201	3728.8490	1864.9281	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3817.8966	1909.4520	3800.8701	1900.9387	3799.8861	1900.4467	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3918.9443	1959.9758	3901.9178	1951.4625	3900.9337	1950.9705	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3989.9814	***1995.4944***	3972.9549	1986.9811	3971.9709	1986.4891	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.6	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33 87.76%
69.8	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25 5.73%
68.9	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29 4.75%
61.3	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15 0.82%
61.2	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6 0.80%
54.0	4135.0796	2.0197	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17 0.15%
14.4	4137.1013	-0.0020	QTKALPSDQIIAAGKIVNTVLQELYVTNNCNLAYPMK	
9.4	4135.1090	1.9903	LAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHK	
9.4	4135.1090	1.9903	LAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHK	
9.0	4137.1033	-0.0040	SAVDLDEKNLVLNDVFMWFFPRPSGPKPRAYQLLR	

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

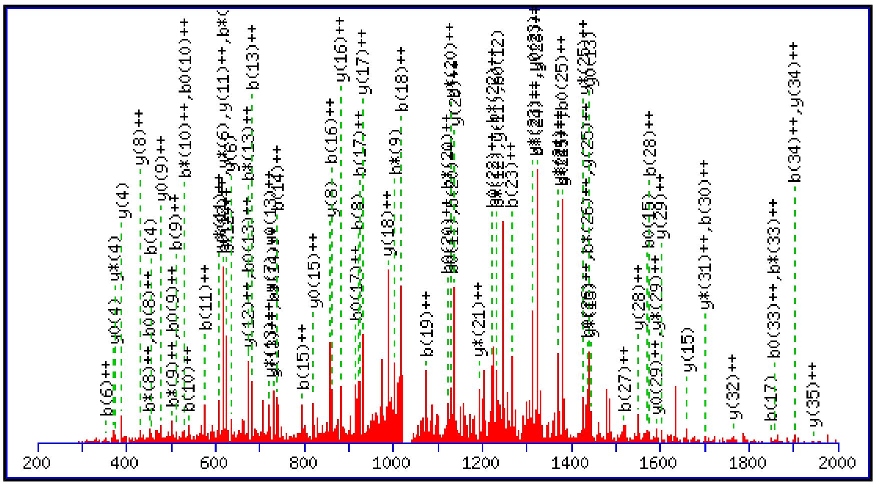
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28583: 4121.097856 from(1031.281740,4+) intensity(0.0000) rtinseconds(2484) scans(6778) index(17900)
Title: 111019_Est_MI_YP_G_07Spectrum5868_scans__6778
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

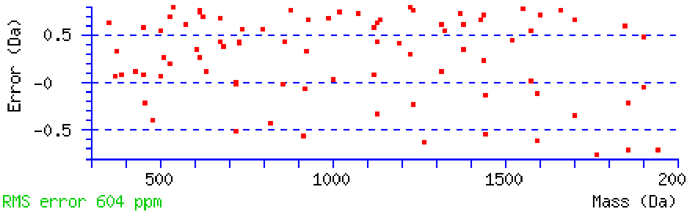
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

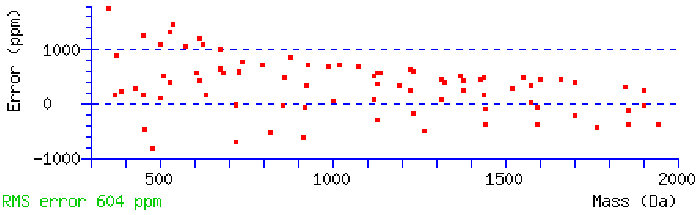


Monoisotopic mass of neutral peptide Mr(calc): 4119.0847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N33 : Deamidated (NQ)
Ions Score: 79 **Expect:** 2.2e-006
Matches : 90/414 fragment ions using 137 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	36
3	318.1482	159.5777			300.1376	150.5725	S	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	35
4	455.2071	228.1072			437.1966	219.1019	H	3802.9511	1901.9792	3785.9246	1893.4659	3784.9405	1892.9739	34
5	592.2660	296.6367			574.2555	287.6314	H	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	33
6	706.3090	***353.6581***	689.2824	345.1448	688.2984	344.6528	N	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1021.4884	***511.2478***	1004.4618	502.7346	1003.4778	502.2425	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1078.5098	***539.7586***	1061.4833	531.2453	1060.4993	530.7533	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	1149.5470	***575.2771***	1132.5204	566.7638	1131.5364	566.2718	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	1250.5946	***625.8010***	1233.5681	617.2877	1232.5841	616.7957	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	1363.6787	***682.3430***	1346.6521	673.8297	1345.6681	673.3377	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	1476.7628	***738.8850***	1459.7362	730.3717	1458.7522	729.8797	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1590.8057	***795.9065***	1573.7791	787.3932	1572.7951	786.9012	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1719.8483	***860.4278***	1702.8217	851.9145	1701.8377	851.4225	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1847.9069	***924.4571***	1830.8803	915.9438	1829.8963	915.4518	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2033.9862	***1017.4967***	2016.9596	1008.9834	2015.9756	1008.4914	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2147.0702	***1074.0388***	2130.0437	1065.5255	2129.0597	1065.0335	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2260.1543	***1130.5808***	2243.1278	1122.0675	2242.1437	1121.5755	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2361.2020	1181.1046	2344.1754	1172.5914	2343.1914	1172.0993	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16
23	2533.2868	***1267.1470***	2516.2602	1258.6337	2515.2762	1258.1417	A	**1658.8497**	829.9285	1641.8231	821.4152	1640.8391	820.9232	15

24	2661.3817	1331.1945	2644.3552	1322.6812	2643.3712	1322.1892	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2775.4247	1388.2160	2758.3981	1379.7027	2757.4141	1379.2107	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2888.5087	1444.7580	2871.4822	1436.2447	2870.4982	1435.7527	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3035.5771	***1518.2922***	3018.5506	1509.7789	3017.5666	1509.2869	**F**	**1232.5906**	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3148.6612	***1574.8342***	3131.6347	1566.3210	3130.6506	1565.8290	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3262.7041	1631.8557	3245.6776	1623.3424	3244.6936	1622.8504	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3399.7630	***1700.3852***	3382.7365	1691.8719	3381.7525	1691.3799	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3486.7951	1743.9012	3469.7685	1735.3879	3468.7845	1734.8959	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3615.8377	1808.4225	3598.8111	1799.9092	3597.8271	1799.4172	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3730.8646	1865.9359	3713.8381	1857.4227	3712.8540	1856.9307	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3801.9017	***1901.4545***	3784.8752	1892.9412	3783.8912	1892.4492	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3902.9494	1951.9783	3885.9229	1943.4651	3884.9388	1942.9731	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3973.9865	1987.4969	3956.9600	1978.9836	3955.9759	1978.4916	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.7	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33 99.80%
51.4	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29 0.18%
39.0	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25 0.01%
37.3	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6 0.01%
17.1	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17 0.00%
16.1	4119.0847	2.0131	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15 0.00%
12.6	4121.1051	-0.0073	GTRSVFPFGADPSAPNTGTLNWFPFSTAPALPLQVGLYK	
10.9	4119.0747	2.0232	AEPVGPSLPSTLSQGSFISTESIKNDLVSASSSLPASTSIR	
9.1	4121.0921	0.0058	CHSSIPAAAGGQVLLALLLLCSTALTGMLFSSVSKQLAAM	
8.2	4121.0939	0.0040	MLGASVATGDVITFLDSHCEANVNWLPPLLDRIARNR	

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

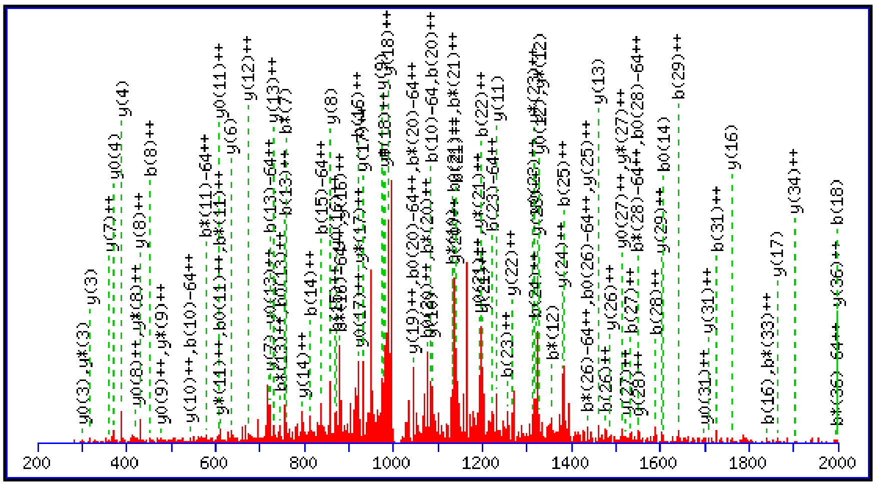
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 29001: 5039.490270 from(1008.905330,5+) intensity(60329.3711) rtinseconds(2527) scans(6847) index(24174)
Title: 111019_Est_MI_YS_G_05Spectrum5943_scans__6847
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

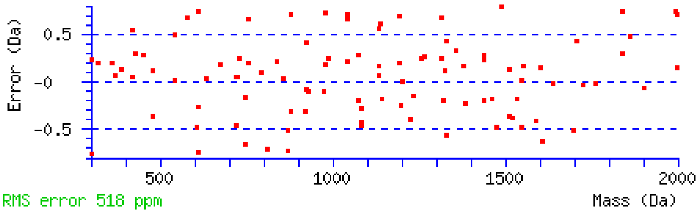
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

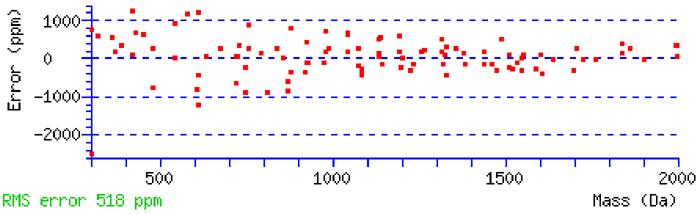


Monoisotopic mass of neutral peptide Mr(calc): 5039.4763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N14 : Deamidated (NQ)
N37 : Deamidated (NQ)
N41 : Deamidated (NQ)
Ions Score: 78 **Expect:** 2.4e-006
Matches : 103/776 fragment ions using 175 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							45
2	145.0608	73.0340			127.0502	64.0287	S	4983.4622	2492.2347	4966.4356	2483.7215	4965.4516	2483.2294	44
3	292.1292	146.5682			274.1186	137.5629	F	4896.4302	2448.7187	4879.4036	2440.2054	4878.4196	2439.7134	43
4	389.1819	195.0946			371.1714	186.0893	P	4749.3617	2375.1845	4732.3352	2366.6712	4731.3512	2366.1792	42
5	575.2613	288.1343			557.2507	279.1290	W	4652.3090	2326.6581	4635.2824	2318.1449	4634.2984	2317.6528	41
6	704.3039	352.6556	687.2773	344.1423	686.2933	343.6503	Q	4466.2297	2233.6185	4449.2031	2225.1052	4448.2191	2224.6132	40
7	775.3410	388.1741	758.3144	379.6608	757.3304	379.1688	A	4337.1871	2169.0972	4320.1605	2160.5839	4319.1765	2160.0919	39
8	903.4359	**452.2216**	886.4094	443.7083	885.4254	443.2163	K	4266.1500	2133.5786	4249.1234	2125.0653	4248.1394	2124.5733	38
9	1050.4713	525.7393	1033.4448	517.2260	1032.4608	516.7340	M	4138.0550	2069.5311	4121.0284	2061.0179	4120.0444	2060.5259	37
10	1149.5397	575.2735	1132.5132	566.7602	1131.5292	566.2682	V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0082	36
11	1236.5718	618.7895	1219.5452	610.2762	1218.5612	609.7842	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
12	1373.6307	687.3190	1356.6041	678.8057	1355.6201	678.3137	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
13	1510.6896	**755.8484**	1493.6630	747.3352	1492.6790	746.8432	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
14	1625.7165	**813.3619**	1608.6900	804.8486	1607.7060	804.3566	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
15	1738.8006	**869.9039**	1721.7741	861.3907	1720.7900	860.8987	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
16	1839.8483	**920.4278**	1822.8217	911.9145	1821.8377	911.4225	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
17	1940.8960	970.9516	1923.8694	962.4383	1922.8854	961.9463	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
18	1997.9174	999.4624	1980.8909	990.9491	1979.9069	990.4571	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
19	2068.9545	1034.9809	2051.9280	1026.4676	2050.9440	1025.9756	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
20	2170.0022	**1085.5047**	2152.9757	1076.9915	2151.9917	1076.4995	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
21	2283.0863	**1142.0468**	2266.0597	1133.5335	2265.0757	1133.0415	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25

22	2396.1703	**1198.5888**	2379.1438	1190.0755	2378.1598	1189.5835	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
23	2510.2133	**1255.6103**	2493.1867	1247.0970	2492.2027	1246.6050	**N**	2645.3206	1323.1639	2628.2940	1314.6507	2627.3100	1314.1586	**23**
24	2639.2559	**1320.1316**	2622.2293	1311.6183	2621.2453	1311.1263	**E**	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	**22**
25	2767.3144	**1384.1609**	2750.2879	1375.6476	2749.3039	1375.1556	**Q**	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	**21**
26	2953.3938	**1477.2005**	2936.3672	1468.6872	2935.3832	1468.1952	**W**	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	**20**
27	3066.4778	**1533.7425**	3049.4513	1525.2293	3048.4673	1524.7373	**L**	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	**19**
28	3179.5619	**1590.2846**	3162.5353	1581.7713	3161.5513	1581.2793	**L**	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	**18**
29	3280.6096	**1640.8084**	3263.5830	1632.2951	3262.5990	1631.8031	**T**	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	**17**
30	3381.6572	1691.3323	3364.6307	1682.8190	3363.6467	1682.3270	**T**	**1760.8814**	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
31	3452.6944	**1726.8508**	3435.6678	1718.3375	3434.6838	1717.8455	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
32	3580.7893	1790.8983	3563.7628	1782.3850	3562.7788	1781.8930	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
33	3694.8322	1847.9198	3677.8057	1839.4065	3676.8217	1838.9145	**N**	**1460.7016**	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
34	3807.9163	1904.4618	3790.8898	1895.9485	3789.9057	1895.4565	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
35	3954.9847	1977.9960	3937.9582	1969.4827	3936.9742	1968.9907	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
36	4068.0688	2034.5380	4051.0422	2026.0248	4050.0582	2025.5328	**L**	**1086.5062**	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
37	4183.0957	2092.0515	4166.0692	2083.5382	4165.0852	2083.0462	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
38	4320.1546	2160.5810	4303.1281	2152.0677	4302.1441	2151.5757	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
39	4407.1867	2204.0970	4390.1601	2195.5837	4389.1761	2195.0917	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
40	4536.2293	2268.6183	4519.2027	2260.1050	4518.2187	2259.6130	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
41	4651.2562	2326.1317	4634.2297	2317.6185	4633.2456	2317.1265	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
42	4722.2933	2361.6503	4705.2668	2353.1370	4704.2828	2352.6450	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
43	4823.3410	2412.1741	4806.3145	2403.6609	4805.3304	2403.1689	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
44	4894.3781	2447.6927	4877.3516	2439.1794	4876.3676	2438.6874	**A**	218.1499	109.5786	201.1234	101.0653			**2**
45							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.3	5039.4763	0.0140	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N14, N37, N41 59.76%
75.3	5038.4923	0.9980	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
71.9	5039.4763	0.0140	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N14, N23, N41 13.75%
71.4	5037.5083	1.9820	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
70.7	5039.4763	0.0140	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N33, N37, N41 10.41%
67.0	5038.4923	0.9980	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
66.3	5037.5083	1.9820	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
64.9	5038.4923	0.9980	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
58.6	5039.4763	0.0140	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q25, N33, N37, N41 0.65%
58.4	5039.4763	0.0140	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N23, Q25, N33, N37 0.62%

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

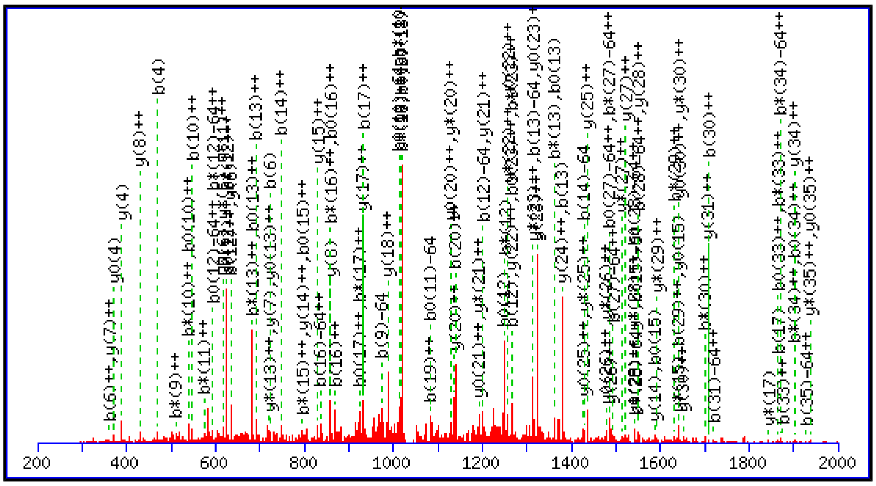
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28867: 4137.072576 from(1035.275420,4+) intensity(40245.8359) rtinseconds(2574) scans(6818) index(26988)
Title: 111019_Est_MI_YS_G_09Spectrum5968_scans__6818
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

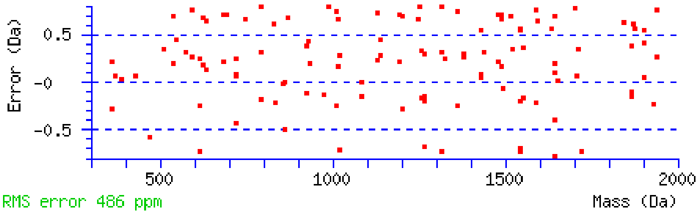
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

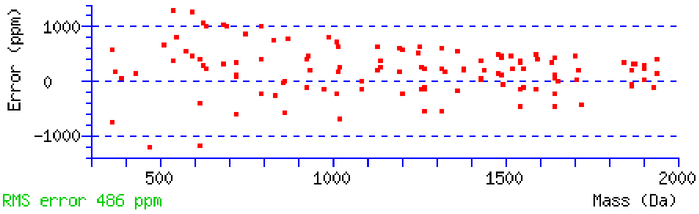


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q17 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 78 **Expect:** 2.9e-006
Matches : 120/616 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					**M**							**37**
2	247.1111	124.0592					**V**	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	**36**
3	334.1431	167.5752			316.1326	158.5699	**S**	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	**35**
4	**471.2020**	236.1047			453.1915	227.0994	**H**	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	**34**
5	608.2609	304.6341			590.2504	295.6288	**H**	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	**33**
6	**722.3039**	**361.6556**	705.2773	353.1423	704.2933	352.6503	**N**	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	**32**
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	**L**	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	**31**
8	936.4356	468.7214	919.4091	460.2082	918.4250	459.7162	**T**	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	**30**
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	**T**	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	**29**
10	1094.5048	**547.7560**	1077.4782	539.2427	1076.4942	538.7507	**G**	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	**28**
11	1165.5419	583.2746	1148.5153	574.7613	1147.5313	574.2693	**A**	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	**27**
12	**1266.5895**	**633.7984**	1249.5630	625.2851	1248.5790	624.7931	**T**	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	**26**
13	**1379.6736**	**690.3404**	1362.6471	681.8272	1361.6630	681.3352	**L**	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	**25**
14	1492.7577	**746.8825**	1475.7311	738.3692	1474.7471	737.8772	**I**	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	**24**
15	1606.8006	803.9039	1589.7741	795.3907	1588.7900	794.8987	**N**	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	**23**
16	1735.8432	**868.4252**	1718.8166	859.9120	1717.8326	859.4200	**E**	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	**22**
17	**1864.8858**	**932.9465**	1847.8592	924.4333	1846.8752	923.9413	**Q**	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	**21**
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	**W**	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	**20**
19	2164.0492	**1082.5282**	2147.0226	1074.0149	2146.0386	1073.5229	**L**	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	**19**
20	2277.1332	**1139.0703**	2260.1067	1130.5570	2259.1227	1130.0650	**L**	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	**18**
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	**T**	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	**17**
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	**T**	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	**16**

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	**1587.8125**	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	1526.7817	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3279.6831	**1640.3452**	3262.6565	1631.8319	3261.6725	1631.3399	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3416.7420	**1708.8746**	3399.7154	1700.3614	3398.7314	1699.8693	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3503.7740	1752.3906	3486.7475	1743.8774	3485.7634	1743.3854	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3632.8166	1816.9119	3615.7900	1808.3987	3614.8060	1807.9067	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3747.8435	**1874.4254**	3730.8170	1865.9121	3729.8330	1865.4201	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	1995.9864	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.2	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 28.83%
76.0	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 17.13%
75.4	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 15.09%
75.4	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 15.03%
72.1	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 7.06%
71.4	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 5.95%
70.4	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 4.81%
64.3	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 1.17%
63.8	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 1.04%
62.5	4136.0636	1.0089	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.78%

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

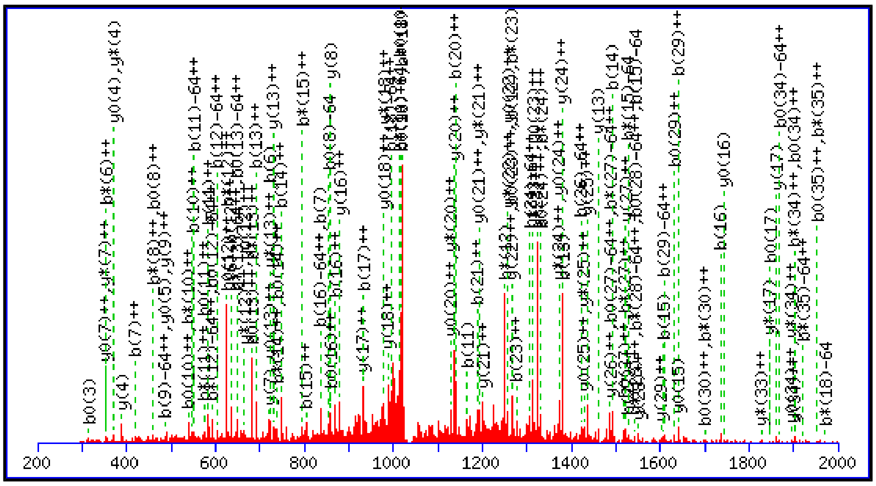
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28931: 4138.051136 from(1035.520060,4+) intensity(10934.0068) rtinseconds(2663) scans(7011) index(24905)
Title: 111019_Est_MI_YS_G_06Spectrum6124_scans__7011
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

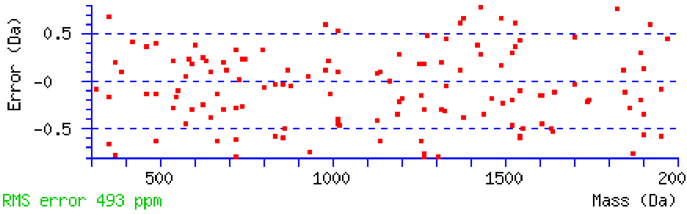
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

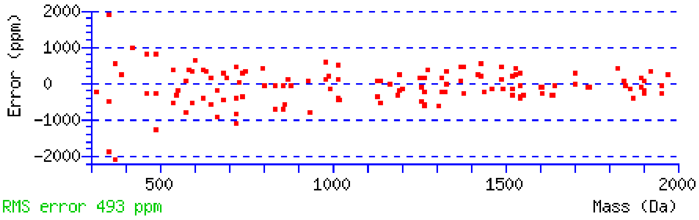


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N25 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 76 **Expect:** 5.1e-006
Matches : 132/616 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	334.1431	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	471.2020	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	608.2609	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	**723.2879**	362.1476	706.2613	353.6343	705.2773	353.1423	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	**836.3719**	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	**1607.7846**	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1865.8698	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2051.9491	1026.4782	2034.9226	1017.9649	2033.9386	1017.4729	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2165.0332	1083.0202	2148.0066	1074.5070	2147.0226	1074.0149	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2379.1649	***1190.0861***	2362.1384	1181.5728	2361.1544	1181.0808	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2551.2497	***1276.1285***	2534.2232	1267.6152	2533.2392	1267.1232	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2679.3447	1340.1760	2662.3181	1331.6627	2661.3341	1331.1707	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2794.3716	1397.6895	2777.3451	1389.1762	2776.3611	1388.6842	**N**	**1460.7016**	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2907.4557	1454.2315	2890.4291	1445.7182	2889.4451	1445.2262	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3054.5241	***1527.7657***	3037.4976	1519.2524	3036.5135	1518.7604	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3167.6082	1584.3077	3150.5816	1575.7944	3149.5976	1575.3024	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3281.6511	***1641.3292***	3264.6245	1632.8159	3263.6405	1632.3239	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	1875.4094	3732.7850	1866.8961	3731.8010	1866.4041	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	1996.9704	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.4	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 22.87%
75.6	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 19.06%
75.6	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 18.98%
74.8	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 15.86%
74.7	4136.0636	1.9875	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
71.2	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17, N33 6.89%
67.9	4137.0477	1.0035	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
66.0	4137.0477	1.0035	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
65.9	4138.0317	0.0195	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 2.04%
65.8	4136.0636	1.9875	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

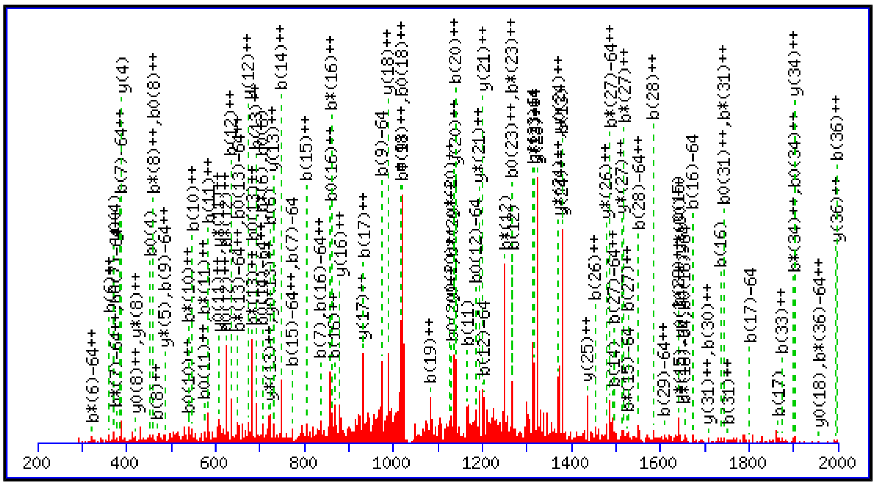
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28946: 4138.076376 from(1035.526370,4+) intensity(0.0000) rtinseconds(2604) scans(6541) index(12110)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum5686_scans__6541
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

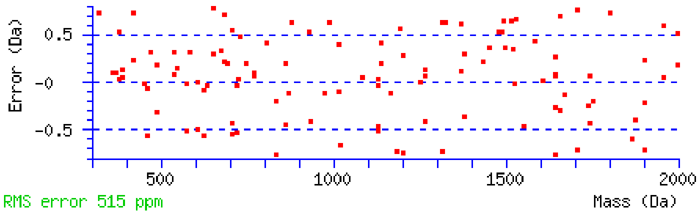
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

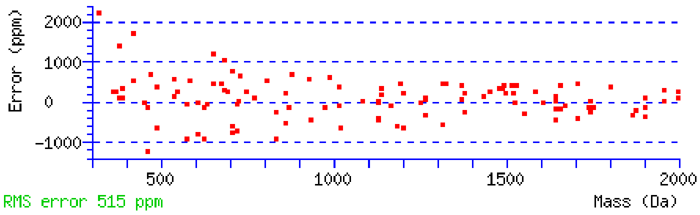


```
Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6     : Deamidated (NQ)
N25    : Deamidated (NQ)
Ions Score: 75  Expect: 6e-006
Matches : 116/616 fragment ions using 175 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	471.2020	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	608.2609	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1607.7846	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	**1864.8858**	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2164.0492	***1082.5282***	2147.0226	1074.0149	2146.0386	1073.5229	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2906.4717	***1453.7395***	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3053.5401	***1527.2737***	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3166.6242	***1583.8157***	3149.5976	1575.3024	3148.6136	1574.8104	**L**	1084.5382	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3280.6671	***1640.8372***	3263.6405	1632.3239	3262.6565	1631.8319	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3417.7260	***1709.3666***	3400.6994	1700.8534	3399.7154	1700.3614	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3504.7580	***1752.8826***	3487.7315	1744.3694	3486.7475	1743.8774	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3747.8435	***1874.4254***	3730.8170	1865.9121	3729.8330	1865.4201	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	***1995.9864***	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.0	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 40.49%
69.8	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 12.40%
68.6	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 9.43%
67.8	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 7.81%
67.8	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 7.77%
67.4	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15 7.12%
65.7	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 4.77%
63.4	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25 2.85%
62.9	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 2.50%
58.8	4136.0636	2.0127	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.98%

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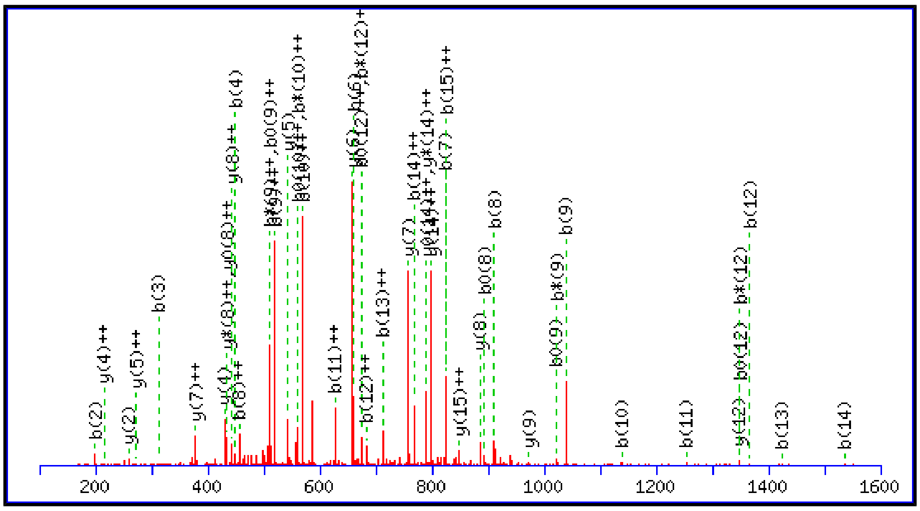
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLHPNYSQVDIGLIK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

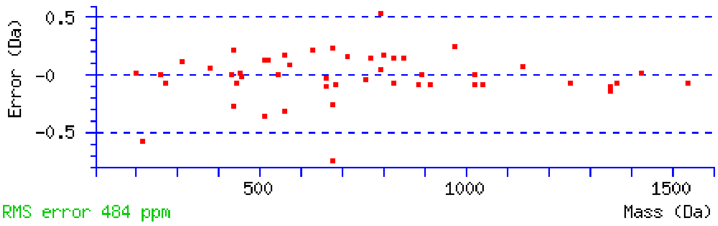
Match to Query 10209: 1794.988002 from(599.336610,3+) intensity(991268.6875) rtinseconds(1743) scans(3673) index(21908)
Title: 111019_Est_MI_YP_G_15Spectrum3167_scans__3673
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

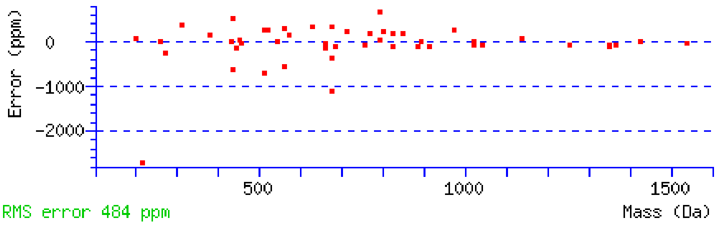
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1794.9880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 73 **Expect:** 4.8e-006
Matches : 50/146 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	100.0757	50.5415					V							16
2	199.1441	100.0757					V	1696.9268	848.9671	1679.9003	840.4538	1678.9163	839.9618	15
3	312.2282	156.6177					L	1597.8584	799.4329	1580.8319	790.9196	1579.8479	790.4276	14
4	449.2871	225.1472					H	1484.7744	742.8908	1467.7478	734.3775	1466.7638	733.8855	13
5	546.3398	273.6736					P	1347.7155	674.3614	1330.6889	665.8481	1329.7049	665.3561	12
6	661.3668	331.1870	644.3402	322.6738			N	1250.6627	625.8350	1233.6361	617.3217	1232.6521	616.8297	11
7	824.4301	412.7187	807.4036	404.2054			Y	1135.6358	568.3215	1118.6092	559.8082	1117.6252	559.3162	10
8	911.4621	456.2347	894.4356	447.7214	893.4516	447.2294	S	972.5724	486.7898	955.5459	478.2766	954.5619	477.7846	9
9	1039.5207	520.2640	1022.4942	511.7507	1021.5102	511.2587	Q	885.5404	443.2738	868.5138	434.7606	867.5298	434.2686	8
10	1138.5891	569.7982	1121.5626	561.2849	1120.5786	560.7929	V	757.4818	379.2445	740.4553	370.7313	739.4713	370.2393	7
11	1253.6161	627.3117	1236.5895	618.7984	1235.6055	618.3064	D	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
12	1366.7001	683.8537	1349.6736	675.3404	1348.6896	674.8484	I	543.3865	272.1969	526.3599	263.6836			5
13	1423.7216	712.3644	1406.6951	703.8512	1405.7110	703.3592	G	430.3024	215.6548	413.2758	207.1416			4
14	1536.8057	768.9065	1519.7791	760.3932	1518.7951	759.9012	L	373.2809	187.1441	356.2544	178.6308			3
15	1649.8897	825.4485	1632.8632	816.9352	1631.8792	816.4432	I	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.5	1794.9880	0.0000	VVLHPNYSQVDIGLIK	Deamidated N6 99.50%
50.5	1794.9880	0.0000	VVLHPNYSQVDIGLIK	Deamidated Q9 0.50%
8.9	1793.9887	0.9993	LDELLGKDHTQVVSLK	
8.5	1792.9795	2.0085	NQLANVPSGKAGKPVGVR	
8.5	1792.9795	2.0085	NQLANVPSGKAGKPVGVR	
6.5	1792.9835	2.0045	QLEQRLWSPLPQGLK	
6.1	1794.9814	0.0066	VNWRSGVEPIVLAPMK	
5.4	1794.9886	-0.0006	LAAGMAKVGAVIKSHNGR	
4.5	1793.9774	1.0106	QLEQSIIPDIPAKDVK	
4.5	1793.9774	1.0106	QLEQSIIPDIPAKDVK	

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

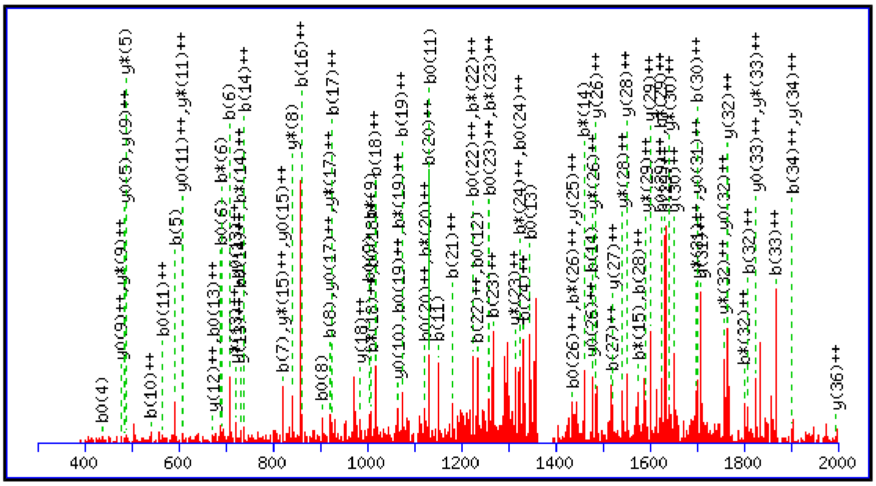
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28628: 4122.088032 from(1375.036620,3+) intensity(0.0000) rtinseconds(2412) scans(6154) index(12859)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum5408_scans__6154
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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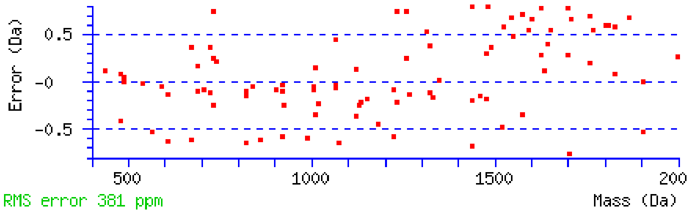
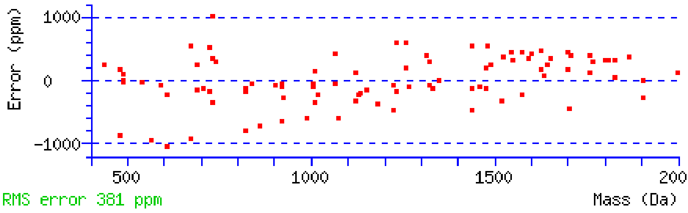
Monoisotopic mass of neutral peptide Mr(calc): 4120.0687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6      : Deamidated (NQ)
Q17     : Deamidated (NQ)
Ions Score: 72  Expect: 9.9e-006
Matches : 96/414 fragment ions using 165 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	318.1482	159.5777			300.1376	150.5725	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	455.2071	228.1072			437.1966	219.1019	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	**592.2660**	296.6367			574.2555	287.6314	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**707.2930**	354.1501	690.2664	345.6368	689.2824	345.1448	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	**921.4247**	461.2160	904.3982	452.7027	903.4141	452.2107	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1022.4724	511.7398	1005.4458	503.2266	1004.4618	502.7346	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1150.5310**	575.7691	1133.5044	567.2558	1132.5204	566.7638	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	1364.6627	682.8350	1347.6362	674.3217	1346.6521	673.8297	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1591.7897	796.3985	1574.7632	787.8852	1573.7791	787.3932	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1720.8323	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1849.8749	***925.4411***	1832.8483	916.9278	1831.8643	916.4358	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2035.9542	***1018.4807***	2018.9277	1009.9675	2017.9436	1009.4755	W	2272.2084	1136.6079	2255.1819	1128.0946	2254.1979	1127.6026	20
19	2149.0383	***1075.0228***	2132.0117	1066.5095	2131.0277	1066.0175	L	2086.1291	1043.5682	2069.1026	1035.0549	2068.1186	1034.5629	19
20	2262.1223	***1131.5648***	2245.0958	1123.0515	2244.1118	1122.5595	L	1973.0451	987.0262	1956.0185	978.5129	1955.0345	978.0209	18
21	2363.1700	***1182.0886***	2346.1435	1173.5754	2345.1594	1173.0834	T	1859.9610	930.4841	1842.9345	921.9709	1841.9504	921.4789	17
22	2464.2177	***1232.6125***	2447.1911	1224.0992	2446.2071	1223.6072	T	1758.9133	879.9603	1741.8868	871.4470	1740.9028	870.9550	16

23	2535.2548	***1268.1310***	2518.2283	1259.6178	2517.2442	1259.1258	**A**	1657.8656	829.4365	1640.8391	820.9232	1639.8551	820.4312	**15**
24	2663.3498	***1332.1785***	2646.3232	1323.6652	2645.3392	1323.1732	**K**	1586.8285	793.9179	1569.8020	785.4046	1568.8180	784.9126	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1458.7336	729.8704	1441.7070	721.3571	1440.7230	720.8651	**13**
26	2890.4768	1445.7420	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3037.5452	***1519.2762***	3020.5186	1510.7629	3019.5346	1510.2709	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3150.6292	***1575.8183***	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1084.5382	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3264.6722	***1632.8397***	3247.6456	1624.3264	3246.6616	1623.8344	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3401.7311	***1701.3692***	3384.7045	1692.8559	3383.7205	1692.3639	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3617.8057	***1809.4065***	3600.7791	1800.8932	3599.7951	1800.4012	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3731.8486	***1866.4279***	3714.8221	1857.9147	3713.8381	1857.4227	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3802.8857	***1901.9465***	3785.8592	1893.4332	3784.8752	1892.9412	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3903.9334	1952.4703	3886.9069	1943.9571	3885.9229	1943.4651	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3974.9705	1987.9889	3957.9440	1979.4756	3956.9600	1978.9836	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.3	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 54.45%
66.9	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15 15.49%
63.9	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 7.85%
63.9	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 7.76%
62.8	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 5.98%
61.1	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 4.06%
59.9	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 3.13%
50.4	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17 0.35%
47.6	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 0.18%
46.6	4120.0687	2.0193	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.15%

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

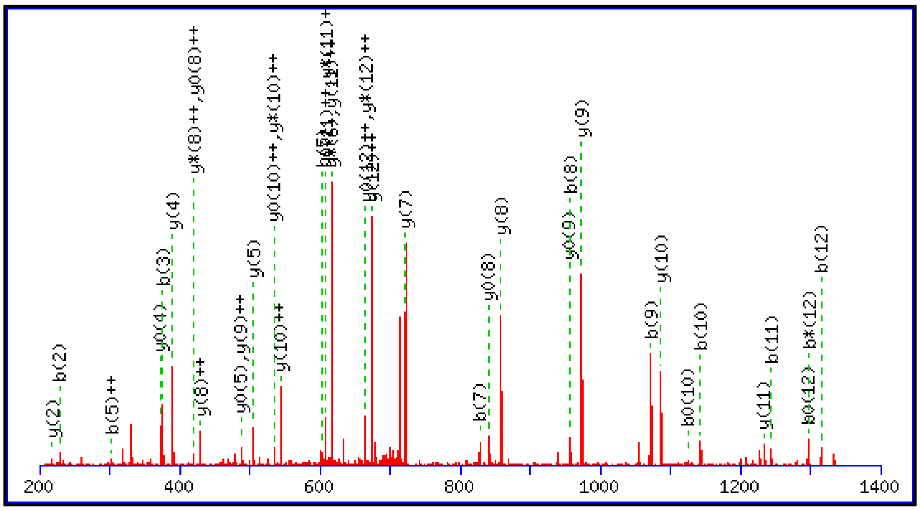
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

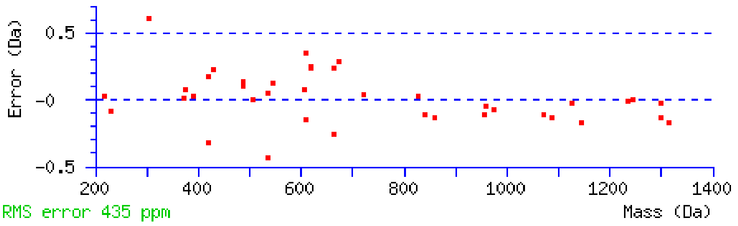
Match to Query 6182: 1460.680948 from(731.347750,2+) intensity(67967.7500) rtinseconds(928) scans(1839) index(28376)
Title: 111019_Est_MI_YS_G_13Spectrum1546_scans__1839
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

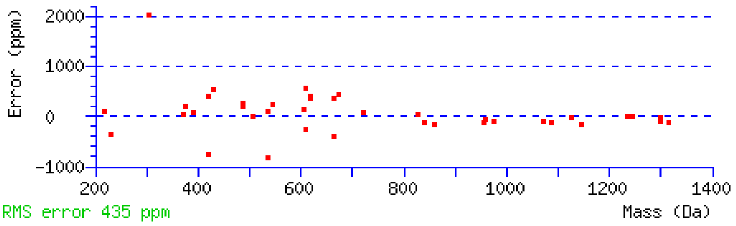
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1460.6783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N5 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 70 **Expect:** 1.4e-005
Matches : 39/128 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	116.0342	58.5207	99.0077	50.0075			**N**							**13**
2	***229.1183***	115.0628	212.0917	106.5495			**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
3	***376.1867***	188.5970	359.1601	180.0837			**F**	***1233.5746***	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
4	489.2708	245.1390	472.2442	236.6257			**L**	***1086.5062***	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
5	***604.2977***	302.6525	587.2712	294.1392			**N**	***973.4221***	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
6	741.3566	371.1819	724.3301	362.6687			**H**	***858.3952***	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
7	***828.3886***	414.6980	811.3621	406.1847	810.3781	405.6927	**S**	***721.3363***	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
8	***957.4312***	479.2193	940.4047	470.7060	939.4207	470.2140	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
9	***1072.4582***	536.7327	1055.4316	528.2195	1054.4476	527.7274	**N**	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
10	***1143.4953***	572.2513	1126.4687	563.7380	1125.4847	563.2460	**A**	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
11	***1244.5430***	622.7751	1227.5164	614.2619	1226.5324	613.7698	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
12	***1315.5801***	658.2937	1298.5535	649.7804	1297.5695	649.2884	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
13							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of NLFLNHSENATAK
(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	1460.6783	0.0027	NLFLNHSENATAK
19.1	1460.6817	-0.0007	NCTEELDLNPKK
16.5	1460.6817	-0.0007	NNMKIIDPDEEK
16.3	1458.6699	2.0111	EVQENIQGDGGRR
16.1	1458.6699	2.0111	EVQENIQGDGGRR
14.5	1458.6699	2.0111	EVQENIQGDGGRR
14.1	1460.6743	0.0066	QVDANVNTNDKDK
13.1	1460.6825	-0.0016	EMLYMKEMRAK
12.8	1460.6743	0.0066	QVDANVNTNDKDK
12.5	1460.6825	-0.0016	QMLYMKEMRAK

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

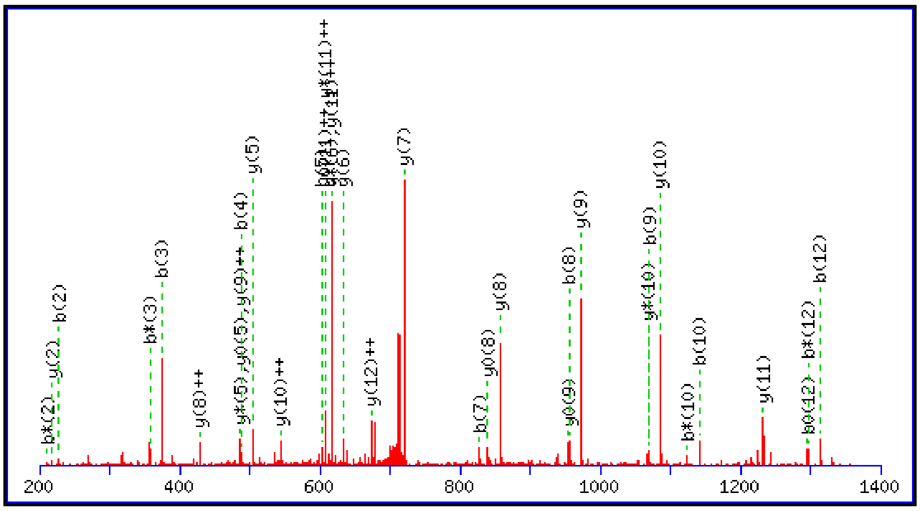
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

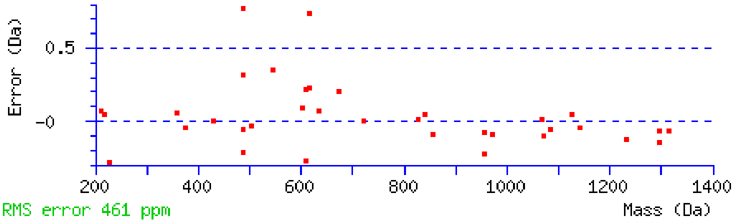
Match to Query 4268: 1458.714108 from(730.364330,2+) intensity(197250.7031) rtinseconds(624) scans(1322) index(2495)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1113_scans__1322
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐

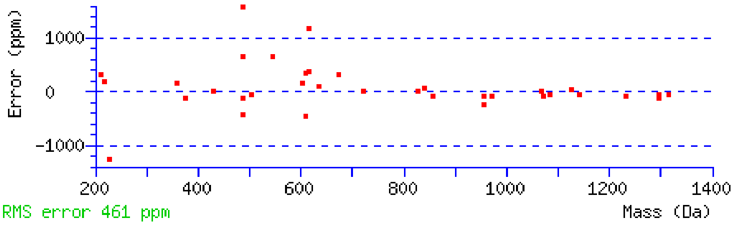


Monoisotopic mass of neutral peptide Mr(calc): 1458.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 70 **Expect:** 1.8e-005
Matches : 35/128 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	***228.1343***	114.5708	211.1077	106.0575			L	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12
3	***375.2027***	188.1050	358.1761	179.5917			F	***1232.5906***	616.7989	1215.5640	608.2857	1214.5800	607.7937	11
4	***488.2867***	244.6470	471.2602	236.1337			L	***1085.5222***	543.2647	1068.4956	534.7515	1067.5116	534.2594	10
5	***603.3137***	302.1605	586.2871	293.6472			N	***972.4381***	486.7227	955.4116	478.2094	954.4275	477.7174	9
6	740.3726	370.6899	723.3461	362.1767			H	***857.4112***	429.2092	840.3846	420.6959	839.4006	420.2039	8
7	***827.4046***	414.2060	810.3781	405.6927	809.3941	405.2007	S	***720.3523***	360.6798	703.3257	352.1665	702.3417	351.6745	7
8	***956.4472***	478.7272	939.4207	470.2140	938.4367	469.7220	E	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	6
9	***1070.4901***	535.7487	1053.4636	527.2354	1052.4796	526.7434	N	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	5
10	***1141.5273***	571.2673	1124.5007	562.7540	1123.5167	562.2620	A	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	4
11	1242.5749	621.7911	1225.5484	613.2778	1224.5644	612.7858	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
12	***1313.6121***	657.3097	1296.5855	648.7964	1295.6015	648.3044	A	***218.1499***	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 461 ppm



RMS error 461 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.3	1458.7103	0.0038	NLFLNHSENATAK	Deamidated N5 99.54%
46.7	1458.7103	0.0038	NLFLNHSENATAK	Deamidated N9 0.44%
34.1	1458.7103	0.0038	NLFLNHSENATAK	Deamidated N1 0.02%
21.0	1458.7089	0.0052	LNQNELELENLK	
20.1	1458.7202	-0.0060	EDLEKPNETQKK	
17.8	1458.7089	0.0052	DAGLLNQLQELDK	
13.1	1458.7202	-0.0060	RVAQQEQELDIK	
13.1	1458.7103	0.0038	SSSGWISHNKLNK	
13.0	1458.7089	0.0052	IEDLENEIEEVK	
12.3	1457.7038	1.0103	EANGLGPQGFPELK	

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

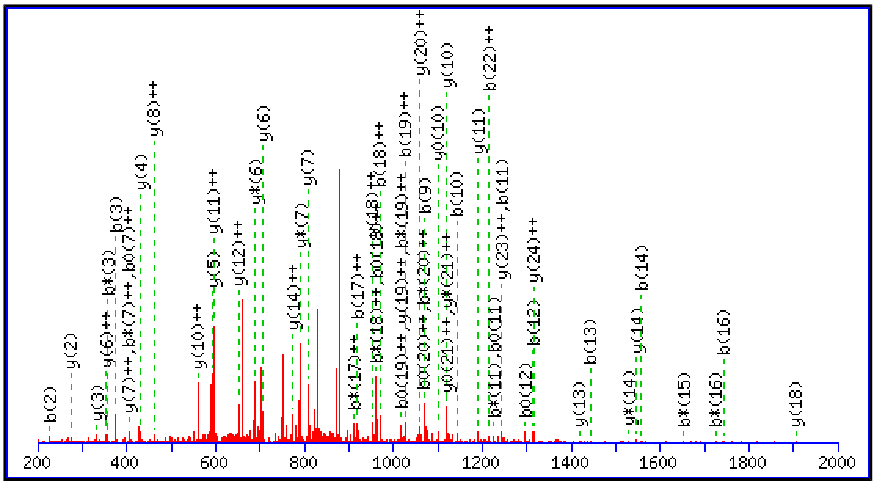
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25843: 2859.509376 from(715.884620,4+) intensity(866449.8125) rtinseconds(1764) scans(4544) index(15913)
Title: 111019_Est_MI_YP_G_05Spectrum3869_scans__4544
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

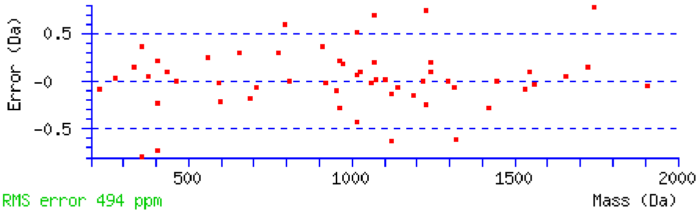
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

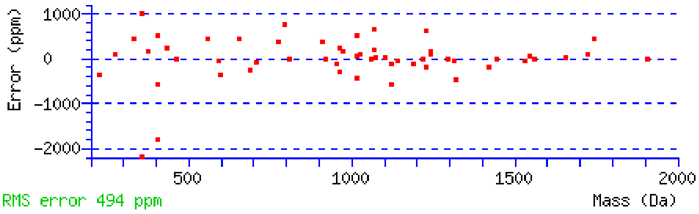


```
Monoisotopic mass of neutral peptide Mr(calc): 2859.5018
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
N9      : Deamidated (NQ)
Ions Score: 66  Expect: 3.5e-005
Matches : 57/276 fragment ions using 98 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							26
2	***228.1343***	114.5708	211.1077	106.0575			L	2746.4662	1373.7367	2729.4396	1365.2235	2728.4556	1364.7314	25
3	***375.2027***	188.1050	358.1761	179.5917			F	2633.3821	1317.1947	2616.3556	1308.6814	2615.3715	1308.1894	24
4	488.2867	244.6470	471.2602	236.1337			L	2486.3137	1243.6605	2469.2871	1235.1472	2468.3031	1234.6552	23
5	603.3137	302.1605	586.2871	293.6472			N	2373.2296	1187.1185	2356.2031	1178.6052	2355.2191	1178.1132	22
6	740.3726	370.6899	723.3461	362.1767			H	2258.2027	1129.6050	2241.1761	1121.0917	2240.1921	1120.5997	21
7	827.4046	414.2060	810.3781	405.6927	809.3941	405.2007	S	2121.1438	1061.0755	2104.1172	1052.5623	2103.1332	1052.0702	20
8	956.4472	478.7272	939.4207	470.2140	938.4367	469.7220	E	2034.1118	1017.5595	2017.0852	1009.0462	2016.1012	1008.5542	19
9	***1071.4742***	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	***1905.0692***	953.0382	1888.0426	944.5249	1887.0586	944.0329	18
10	***1142.5113***	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	1790.0422	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	***1243.5590***	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	1719.0051	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	***1314.5961***	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	1617.9574	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	***1442.6910***	721.8492	1425.6645	713.3359	1424.6805	712.8439	K	***1546.9203***	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	***1557.7180***	779.3626	1540.6914	770.8494	1539.7074	770.3573	D	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	1670.8020	835.9047	1653.7755	827.3914	1652.7915	826.8994	I	1303.7984	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	***1741.8392***	871.4232	1724.8126	862.9099	1723.8286	862.4179	A	***1190.7143***	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	1838.8919	**919.9496**	1821.8654	911.4363	1820.8814	910.9443	P	***1119.6772***	560.3423	1102.6507	551.8290	1101.6667	551.3370	10
18	1939.9396	**970.4734**	1922.9130	961.9602	1921.9290	961.4682	T	1022.6245	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2053.0237	**1027.0155**	2035.9971	1018.5022	2035.0131	1018.0102	L	921.5768	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2154.0713	1077.5393	2137.0448	1069.0260	2136.0608	1068.5340	T	***808.4927***	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2267.1554	1134.0813	2250.1289	1125.5681	2249.1448	1125.0761	L	***707.4450***	354.2262	690.4185	345.7129			6
22	2430.2187	**1215.6130**	2413.1922	1207.0997	2412.2082	1206.6077	Y	***594.3610***	297.6841	577.3344	289.1709			5

23	2529.2871	1265.1472	2512.2606	1256.6339	2511.2766	1256.1419	**V**	***431.2976***	216.1525	414.2711	207.6392			**4**
24	2586.3086	1293.6579	2569.2821	1285.1447	2568.2980	1284.6527	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
25	2714.4036	1357.7054	2697.3770	1349.1922	2696.3930	1348.7001	**K**	***275.2078***	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.8	2859.5018	0.0076	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N5, N9 68.11%
62.1	2859.5018	0.0076	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N9 28.86%
52.3	2859.5018	0.0076	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N5 3.03%
48.9	2858.5178	0.9916	NLFLNHSENATAKDIAPTLTLYVGKK	
42.0	2858.5178	0.9916	NLFLNHSENATAKDIAPTLTLYVGKK	
35.5	2858.5178	0.9916	NLFLNHSENATAKDIAPTLTLYVGKK	
8.3	2858.4973	1.0120	HKPQAPVIVKTEEVINMHTFNDRR	

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

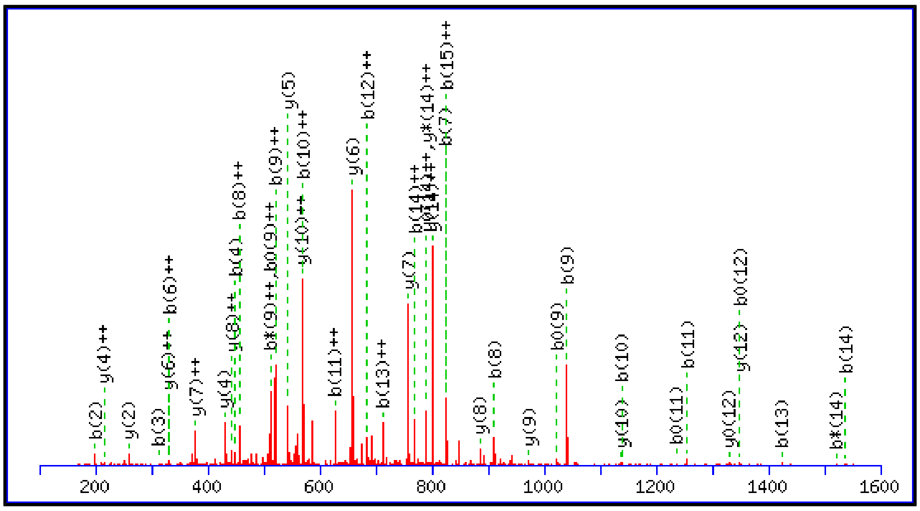
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLHPNYSQVDIGLIK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

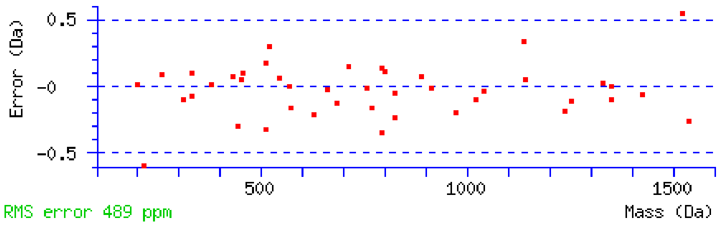
Match to Query 10831: 1795.974312 from(599.665380,3+) intensity(438026.0938) rtinseconds(1659) scans(3951) index(15149)
Title: 111019_Est_MI_YP_G_04Spectrum3388_scans__3951
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

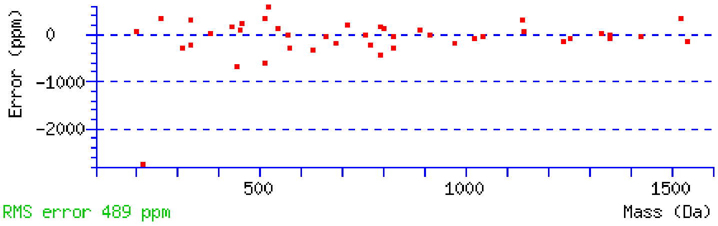
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1795.9720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Q9 : Deamidated (NQ)
Ions Score: 66 **Expect:** 3.6e-005
Matches : 43/146 fragment ions using 69 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					**V**							**16**
2	***199.1441***	100.0757					**V**	1697.9109	849.4591	1680.8843	840.9458	1679.9003	840.4538	**15**
3	***312.2282***	156.6177					**L**	1598.8425	799.9249	1581.8159	791.4116	1580.8319	790.9196	**14**
4	***449.2871***	225.1472					**H**	1485.7584	743.3828	1468.7318	734.8696	1467.7478	734.3775	**13**
5	546.3398	273.6736					**P**	**1348.6995**	674.8534	1331.6729	666.3401	1330.6889	665.8481	**12**
6	661.3668	***331.1870***	644.3402	322.6738			**N**	1251.6467	626.3270	1234.6202	617.8137	1233.6361	617.3217	**11**
7	***824.4301***	412.7187	807.4036	404.2054			**Y**	**1136.6198**	568.8135	1119.5932	560.3002	1118.6092	559.8082	**10**
8	***911.4621***	***456.2347***	894.4356	447.7214	893.4516	447.2294	**S**	**973.5564**	487.2819	956.5299	478.7686	955.5459	478.2766	**9**
9	***1040.5047***	***520.7560***	1023.4782	512.2427	1022.4942	511.7507	**Q**	**886.5244**	443.7658	869.4979	435.2526	868.5138	434.7606	**8**
10	***1139.5732***	***570.2902***	1122.5466	561.7769	1121.5626	561.2849	**V**	**757.4818**	379.2445	740.4553	370.7313	739.4713	370.2393	**7**
11	***1254.6001***	***627.8037***	1237.5735	619.2904	1236.5895	618.7984	**D**	**658.4134**	329.7103	641.3869	321.1971	640.4028	320.7051	**6**
12	1367.6842	***684.3457***	1350.6576	675.8324	1349.6736	675.3404	**I**	**543.3865**	272.1969	526.3599	263.6836			**5**
13	***1424.7056***	***712.8564***	1407.6791	704.3432	1406.6951	703.8512	**G**	**430.3024**	215.6548	413.2758	207.1416			**4**
14	***1537.7897***	***769.3985***	1520.7631	760.8852	1519.7791	760.3932	**L**	373.2809	187.1441	356.2544	178.6308			**3**
15	1650.8738	***825.9405***	1633.8472	817.4272	1632.8632	816.9352	**I**	**260.1969**	130.6021	243.1703	122.0888			**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
65.7	1795.9720	0.0023	VVLHPNYSQVDIGLIK
20.4	1795.9792	-0.0049	SLVENNPRTGNLGALIK
19.6	1795.9792	-0.0049	SLVENNPRTGNLGALIK
16.7	1795.9792	-0.0049	QPDLTSKLRNVSPVNK
12.7	1795.9792	-0.0049	AQQLQKTLDKISSAHK
12.7	1795.9792	-0.0049	AQQLQKTLDKISSAHK
10.1	1795.9767	-0.0024	LLFMRHIQQRVPEK
9.8	1794.9727	1.0016	LDELLGKDHTQVVSLK
9.2	1793.9748	1.9995	SALRQQQQPTVAGGPKK
9.2	1793.9748	1.9995	SALRQQQQPTVAGGPKK

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

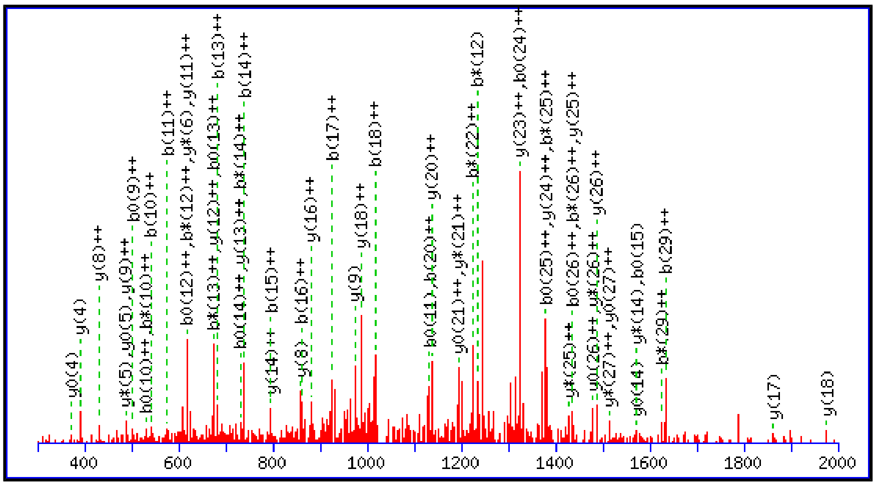
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28596: 4122.051856 from(1031.520240,4+) intensity(57688.2734) rtinseconds(2539) scans(6368) index(26267)
Title: 111019_Est_MI_YS_G_08Spectrum5535_scans__6368
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

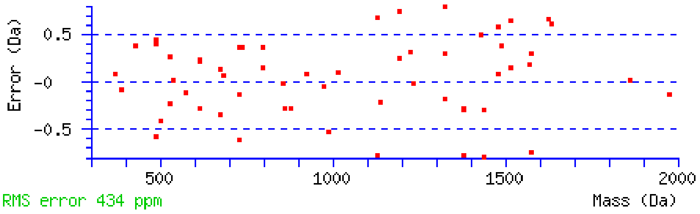
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

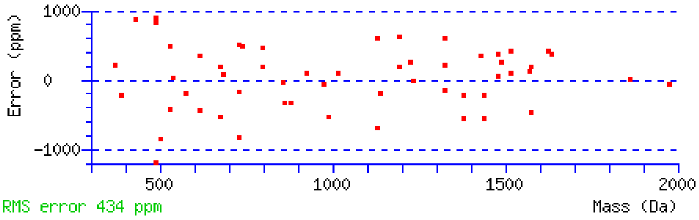


Monoisotopic mass of neutral peptide Mr(calc): 4122.0367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 65 **Expect:** 6e-005
Matches : 61/414 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	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	318.1482	159.5777			300.1376	150.5725	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	455.2071	228.1072			437.1966	219.1019	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	592.2660	296.6367			574.2555	287.6314	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	707.2930	354.1501	690.2664	345.6368	689.2824	345.1448	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	820.3770	410.6922	803.3505	402.1789	802.3665	401.6869	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	921.4247	461.2160	904.3982	452.7027	903.4141	452.2107	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1022.4724	511.7398	1005.4458	503.2266	1004.4618	502.7346	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1150.5310	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	1477.7468	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1591.7897	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1720.8323	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1848.8909	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	W	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	20
19	2148.0543	1074.5308	2131.0277	1066.0175	2130.0437	1065.5255	L	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	19
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	L	**1975.9971**	988.5022	1958.9706	979.9889	1957.9865	979.4969	18
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	T	**1862.9130**	931.9602	1845.8865	923.4469	1844.9025	922.9549	17

22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	**T**	1761.8654	881.4363	1744.8388	872.9230	1743.8548	872.4310	**16**
23	2534.2708	1267.6390	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1660.8177	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
25	2777.3927	1389.2000	2760.3661	1380.6867	2759.3821	1380.1947	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6751	722.3412	**13**
26	2890.4768	1445.7420	2873.4502	1437.2287	2872.4662	1436.7367	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3037.5452	1519.2762	3020.5186	1510.7629	3019.5346	1510.2709	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3150.6292	1575.8183	3133.6027	1567.3050	3132.6187	1566.8130	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3265.6562	***1633.3317***	3248.6296	1624.8185	3247.6456	1624.3264	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3402.7151	1701.8612	3385.6885	1693.3479	3384.7045	1692.8559	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3489.7471	1745.3772	3472.7206	1736.8639	3471.7366	1736.3719	**S**	721.3363	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3618.7897	1809.8985	3601.7632	1801.3852	3600.7791	1800.8932	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3733.8167	1867.4120	3716.7901	1858.8987	3715.8061	1858.4067	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3804.8538	1902.9305	3787.8272	1894.4172	3786.8432	1893.9252	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3905.9014	1953.4544	3888.8749	1944.9411	3887.8909	1944.4491	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3976.9386	1988.9729	3959.9120	1980.4596	3958.9280	1979.9676	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.3	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 24.82%
62.7	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 13.64%
62.2	4121.0527	0.9991	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
62.0	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29, N33 11.58%
62.0	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 11.58%
60.1	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N29, N33 7.51%
59.3	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 6.24%
58.4	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 5.06%
56.6	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25, N33 3.39%
55.8	4122.0367	0.0151	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N29 2.80%

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

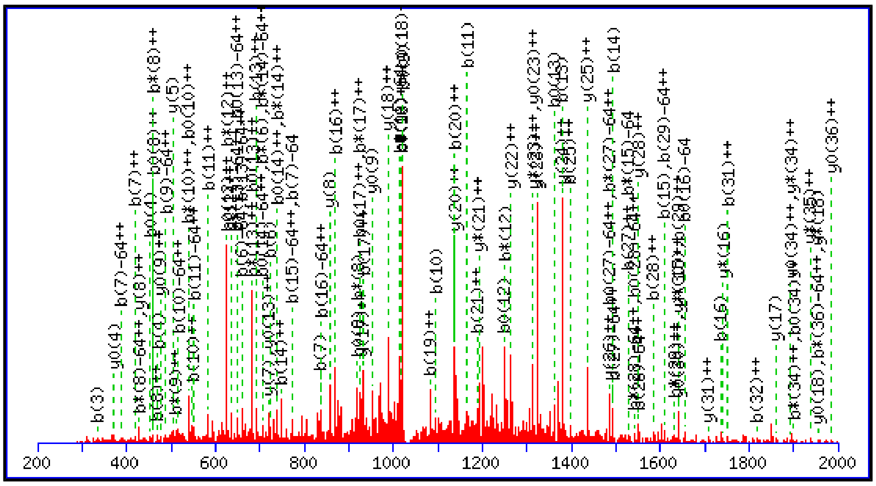
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28922: 4137.102256 from(1035.282840,4+) intensity(0.0000) rtinseconds(2467) scans(6499) index(9782)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum5623_scans__6499
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

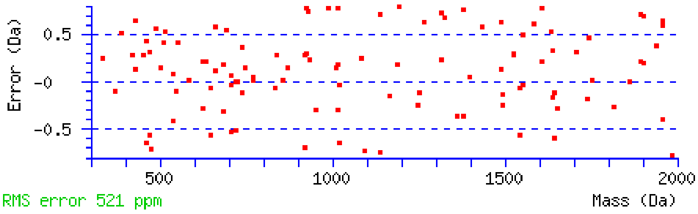
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

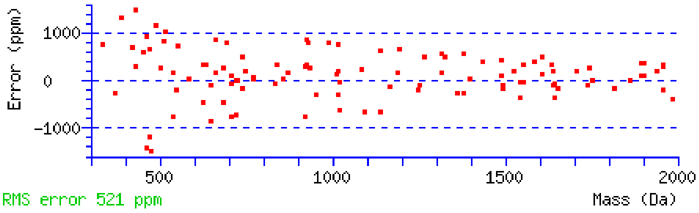


Monoisotopic mass of neutral peptide Mr(calc): 4135.0796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Ions Score: 64 **Expect:** 5.7e-005
Matches : 113/616 fragment ions using 154 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	36
3	**334.1431**	167.5752			316.1326	158.5699	S	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3802.9511	1901.9792	3785.9246	1893.4659	3784.9405	1892.9739	34
5	608.2609	304.6341			590.2504	295.6288	H	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	33
6	**723.2879**	362.1476	706.2613	353.6343	705.2773	353.1423	N	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	32
7	**836.3719**	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3413.8063	1707.4068	3396.7798	1698.8935	3395.7958	1698.4015	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3300.7223	1650.8648	3283.6957	1642.3515	3282.7117	1641.8595	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3199.6746	1600.3409	3182.6481	1591.8277	3181.6640	1591.3357	29
10	**1095.4888**	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3098.6269	1549.8171	3081.6004	1541.3038	3080.6164	1540.8118	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3041.6055	1521.3064	3024.5789	1512.7931	3023.5949	1512.3011	27
12	1267.5736	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2970.5683	1485.7878	2953.5418	1477.2745	2952.5578	1476.7825	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2869.5207	1435.2640	2852.4941	1426.7507	2851.5101	1426.2587	25
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2756.4366	1378.7219	2739.4101	1370.2087	2738.4260	1369.7167	24
15	**1607.7846**	804.3959	1590.7581	795.8827	1589.7741	795.3907	N	2643.3525	1322.1799	2626.3260	1313.6666	2625.3420	1313.1746	23
16	**1736.8272**	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	2529.3096	1265.1584	2512.2831	1256.6452	2511.2990	1256.1532	22
17	1864.8858	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2400.2670	1200.6371	2383.2405	1192.1239	2382.2565	1191.6319	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2272.2084	1136.6079	2255.1819	1128.0946	2254.1979	1127.6026	20
19	2164.0492	***1082.5282***	2147.0226	1074.0149	2146.0386	1073.5229	L	2086.1291	1043.5682	2069.1026	1035.0549	2068.1186	1034.5629	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1973.0451	987.0262	1956.0185	978.5129	1955.0345	978.0209	18
21	2378.1809	***1189.5941***	2361.1544	1181.0808	2360.1703	1180.5888	T	1859.9610	930.4841	1842.9345	921.9709	1841.9504	921.4789	17
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	1758.9133	879.9603	1741.8868	871.4470	1740.9028	870.9550	16

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1657.8656	829.4365	1640.8391	820.9232	1639.8551	820.4312	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1586.8285	793.9179	1569.8020	785.4046	1568.8180	784.9126	**14**
25	2792.4036	***1396.7054***	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1458.7336	729.8704	1441.7070	721.3571	1440.7230	720.8651	**13**
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3052.5561	***1526.7817***	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3165.6401	***1583.3237***	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1084.5382	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3279.6831	***1640.3452***	3262.6565	1631.8319	3261.6725	1631.3399	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3416.7420	1708.8746	3399.7154	1700.3614	3398.7314	1699.8693	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3503.7740	***1752.3906***	3486.7475	1743.8774	3485.7634	1743.3854	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3632.8166	***1816.9119***	3615.7900	1808.3987	3614.8060	1807.9067	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3746.8595	1873.9334	3729.8330	1865.4201	3728.8490	1864.9281	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3817.8966	1909.4520	3800.8701	1900.9387	3799.8861	1900.4467	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3918.9443	1959.9758	3901.9178	1951.4625	3900.9337	1950.9705	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3989.9814	1995.4944	3972.9549	1986.9811	3971.9709	1986.4891	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.4	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6 98.21%
45.7	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15 1.31%
40.8	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29 0.43%
29.1	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25 0.03%
25.2	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17 0.01%
24.0	4135.0796	2.0226	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33 0.01%
11.9	4136.0987	1.0036	REESLNQWLHSIAASVIPLAAEQPTIIGSGTLLDMTQK	
9.3	4135.0855	2.0167	AVEGCVSASQAATEDGQLLRGVGAAATAVTQALNELLQHVK	
9.3	4135.0855	2.0167	AVEGCVSASQAATEDGQLLRGVGAAATAVTQALNELLQHVK	
9.2	4135.1147	1.9876	REESLNQWLHSIAASVIPLAAEQPTIIGSGTLLDMTQK	

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

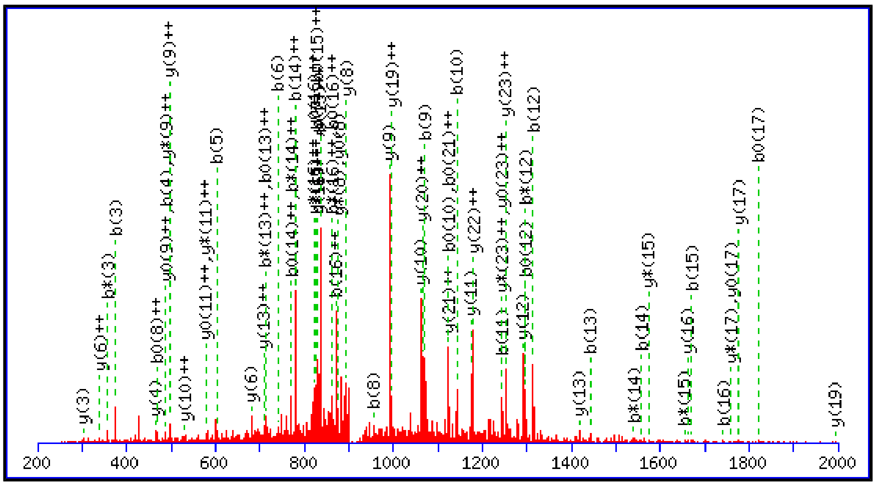
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25456: 2731.420722 from(911.480850,3+) intensity(36380.2070) rtinseconds(1996) scans(5083) index(11107)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum4320_scans__5083
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

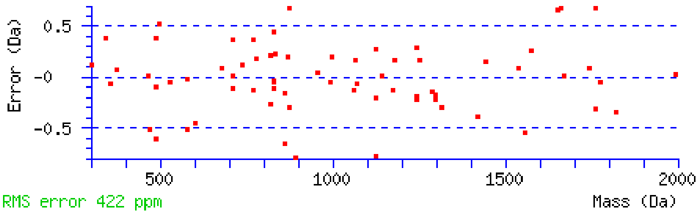
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

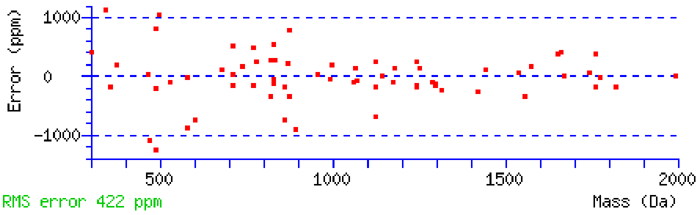


Monoisotopic mass of neutral peptide Mr(calc): 2731.4068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 62 **Expect:** 0.00013
Matches : 70/266 fragment ions using 140 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							25
2	228.1343	114.5708	211.1077	106.0575			L	2618.3712	1309.6892	2601.3447	1301.1760	2600.3606	1300.6840	24
3	***375.2027***	188.1050	358.1761	179.5917			F	2505.2871	1253.1472	2488.2606	1244.6339	2487.2766	1244.1419	23
4	***488.2867***	244.6470	471.2602	236.1337			L	2358.2187	1179.6130	2341.1922	1171.0997	2340.2082	1170.6077	22
5	***603.3137***	302.1605	586.2871	293.6472			N	2245.1347	1123.0710	2228.1081	1114.5577	2227.1241	1114.0657	21
6	***740.3726***	370.6899	723.3461	362.1767			H	2130.1077	1065.5575	2113.0812	1057.0442	2112.0972	1056.5522	20
7	***827.4046***	414.2060	810.3781	405.6927	809.3941	405.2007	S	***1993.0488***	997.0280	1976.0223	988.5148	1975.0383	988.0228	19
8	***956.4472***	478.7272	939.4207	470.2140	938.4367	469.7220	E	1906.0168	953.5120	1888.9902	944.9988	1888.0062	944.5067	18
9	***1071.4742***	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	***1776.9742***	888.9907	1759.9476	880.4775	1758.9636	879.9855	17
10	***1142.5113***	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	***1661.9473***	831.4773	1644.9207	822.9640	1643.9367	822.4720	16
11	***1243.5590***	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	1590.9101	795.9587	1573.8836	787.4454	1572.8996	786.9534	15
12	***1314.5961***	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	1489.8625	745.4349	1472.8359	736.9216	1471.8519	736.4296	14
13	***1442.6910***	721.8492	1425.6645	713.3359	1424.6805	712.8439	K	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
14	***1557.7180***	779.3626	1540.6914	770.8494	1539.7074	770.3573	D	***1290.7304***	645.8688	1273.7038	637.3556	1272.7198	636.8635	12
15	***1670.8020***	835.9047	1653.7755	827.3914	1652.7915	826.8994	I	***1175.7034***	588.3554	1158.6769	579.8421	1157.6929	579.3501	11
16	***1741.8392***	871.4232	1724.8126	862.9099	1723.8286	862.4179	A	***1062.6194***	531.8133	1045.5928	523.3001	1044.6088	522.8080	10
17	1838.8919	919.9496	1821.8654	911.4363	1820.8814	910.9443	P	***991.5823***	496.2948	974.5557	487.7815	973.5717	487.2895	9
18	1939.9396	970.4734	1922.9130	961.9602	1921.9290	961.4682	T	***894.5295***	447.7684	877.5029	439.2551	876.5189	438.7631	8
19	2053.0237	1027.0155	2035.9971	1018.5022	2035.0131	1018.0102	L	793.4818	397.2445	776.4553	388.7313	775.4713	388.2393	7
20	2154.0713	1077.5393	2137.0448	1069.0260	2136.0608	1068.5340	T	***680.3978***	340.7025	663.3712	332.1892	662.3872	331.6972	6
21	2267.1554	1134.0813	2250.1289	1125.5681	2249.1448	1125.0761	L	***579.3501***	290.1787	562.3235	281.6654			5
22	2430.2187	1215.6130	2413.1922	1207.0997	2412.2082	1206.6077	Y	***466.2660***	233.6366	449.2395	225.1234			4

23	2529.2871	1265.1472	2512.2606	1256.6339	2511.2766	1256.1419	**V**	*303.2027*	152.1050	286.1761	143.5917			**3**
24	2586.3086	1293.6579	2569.2821	1285.1447	2568.2980	1284.6527	**G**	204.1343	102.5708	187.1077	94.0575			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.0	2731.4068	0.0139	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N5, N9 72.98%
56.6	2730.4228	0.9979	NLFLNHSENATAKDIAPTLTLYVGK	
56.6	2730.4228	0.9979	NLFLNHSENATAKDIAPTLTLYVGK	
56.6	2731.4068	0.0139	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N1, N9 20.81%
51.3	2731.4068	0.0139	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N1, N5 6.21%
36.4	2730.4228	0.9979	NLFLNHSENATAKDIAPTLTLYVGK	
9.8	2729.4244	1.9963	ELAGIIWAQSQDCIAAALACSKILK	
5.6	2730.4084	1.0123	ELAGIIWAQSQDCIAAALACSKILK	
5.6	2730.4084	1.0123	ELAGIIWAQSQDCIAAALACSKILK	
2.8	2731.4279	-0.0072	DGSLTELQKRLNSIYGELIPELNK	

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

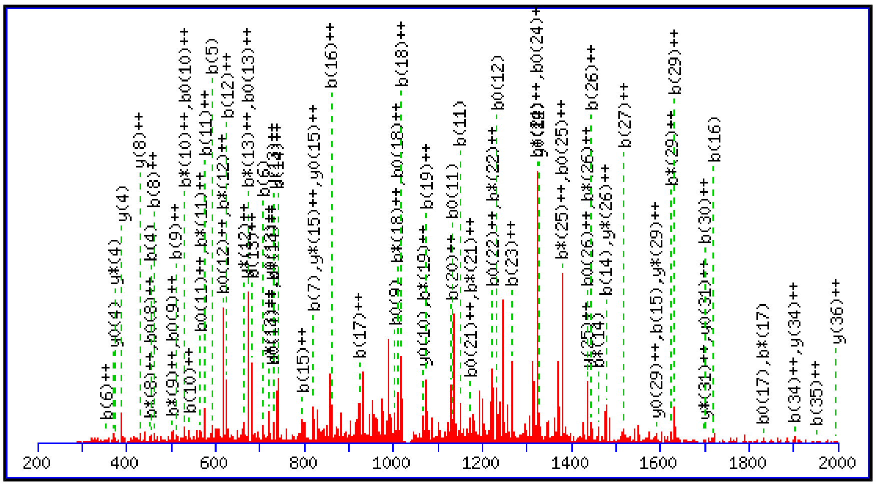
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28578: 4121.094936 from(1031.281010,4+) intensity(0.0000) rtinseconds(2507) scans(6844) index(17910)
Title: 111019_Est_MI_YP_G_07Spectrum5928_scans__6844
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

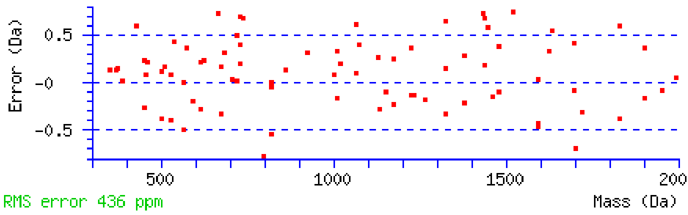
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

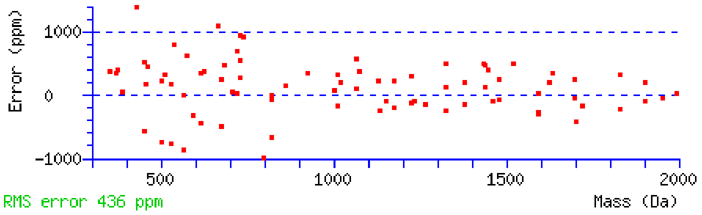


Monoisotopic mass of neutral peptide Mr(calc): 4119.0847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00012
Matches : 83/414 fragment ions using 174 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					**M**							**37**
2	231.1162	116.0617					**V**	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	**36**
3	318.1482	159.5777			300.1376	150.5725	**S**	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	**35**
4	**455.2071**	228.1072			437.1966	219.1019	**H**	3802.9511	1901.9792	3785.9246	1893.4659	3784.9405	1892.9739	**34**
5	**592.2660**	296.6367			574.2555	287.6314	**H**	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	**33**
6	**707.2930**	***354.1501***	690.2664	345.6368	689.2824	345.1448	**N**	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	**32**
7	**820.3770**	410.6922	803.3505	402.1789	802.3665	401.6869	**L**	3413.8063	1707.4068	3396.7798	1698.8935	3395.7958	1698.4015	**31**
8	921.4247	***461.2160***	904.3982	452.7027	903.4141	452.2107	**T**	3300.7223	1650.8648	3283.6957	1642.3515	3282.7117	1641.8595	**30**
9	1022.4724	***511.7398***	1005.4458	503.2266	1004.4618	502.7346	**T**	3199.6746	1600.3409	3182.6481	1591.8277	3181.6640	1591.3357	**29**
10	1079.4939	***540.2506***	1062.4673	531.7373	1061.4833	531.2453	**G**	3098.6269	1549.8171	3081.6004	1541.3038	3080.6164	1540.8118	**28**
11	**1150.5310**	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	**A**	3041.6055	1521.3064	3024.5789	1512.7931	3023.5949	1512.3011	**27**
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	**T**	2970.5683	1485.7878	2953.5418	1477.2745	2952.5578	1476.7825	**26**
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	**L**	2869.5207	1435.2640	2852.4941	1426.7507	2851.5101	1426.2587	**25**
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	**I**	2756.4366	1378.7219	2739.4101	1370.2087	2738.4260	1369.7167	**24**
15	**1591.7897**	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	**N**	2643.3525	1322.1799	2626.3260	1313.6666	2625.3420	1313.1746	**23**
16	**1720.8323**	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	**E**	2529.3096	1265.1584	2512.2831	1256.6452	2511.2990	1256.1532	**22**
17	1848.8909	***924.9491***	1831.8643	916.4358	1830.8803	915.9438	**Q**	2400.2670	1200.6371	2383.2405	1192.1239	2382.2565	1191.6319	**21**
18	2034.9702	***1017.9887***	2017.9436	1009.4755	2016.9596	1008.9834	**W**	2272.2084	1136.6079	2255.1819	1128.0946	2254.1979	1127.6026	**20**
19	2148.0543	***1074.5308***	2131.0277	1066.0175	2130.0437	1065.5255	**L**	2086.1291	1043.5682	2069.1026	1035.0549	2068.1186	1034.5629	**19**
20	2261.1383	***1131.0728***	2244.1118	1122.5595	2243.1278	1122.0675	**L**	1973.0451	987.0262	1956.0185	978.5129	1955.0345	978.0209	**18**
21	2362.1860	1181.5966	2345.1594	1173.0834	2344.1754	1172.5914	**T**	1859.9610	930.4841	1842.9345	921.9709	1841.9504	921.4789	**17**
22	2463.2337	1232.1205	2446.2071	1223.6072	2445.2231	1223.1152	**T**	1758.9133	879.9603	1741.8868	871.4470	1740.9028	870.9550	**16**
23	2534.2708	***1267.6390***	2517.2442	1259.1258	2516.2602	1258.6337	**A**	1657.8656	829.4365	1640.8391	820.9232	1639.8551	820.4312	**15**

24	2662.3658	1331.6865	2645.3392	1323.1732	2644.3552	1322.6812	**K**	1586.8285	793.9179	1569.8020	785.4046	1568.8180	784.9126	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1458.7336	729.8704	1441.7070	721.3571	1440.7230	720.8651	**13**
26	2889.4927	***1445.2500***	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3036.5612	***1518.7842***	3019.5346	1510.2709	3018.5506	1509.7789	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3149.6452	1575.3262	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1084.5382	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3263.6881	***1632.3477***	3246.6616	1623.8344	3245.6776	1623.3424	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3400.7471	***1700.8772***	3383.7205	1692.3639	3382.7365	1691.8719	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3487.7791	1744.3932	3470.7525	1735.8799	3469.7685	1735.3879	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3616.8217	1808.9145	3599.7951	1800.4012	3598.8111	1799.9092	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3730.8646	1865.9359	3713.8381	1857.4227	3712.8540	1856.9307	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3801.9017	***1901.4545***	3784.8752	1892.9412	3783.8912	1892.4492	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3902.9494	***1951.9783***	3885.9229	1943.4651	3884.9388	1942.9731	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3973.9865	1987.4969	3956.9600	1978.9836	3955.9759	1978.4916	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.4	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6 99.15%
36.4	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33 0.32%
36.0	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25 0.29%
34.2	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29 0.19%
26.8	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17 0.03%
23.3	4119.0847	2.0102	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15 0.02%
8.0	4120.0885	1.0064	AAFQIISQVISEATEQVLATTVGKVAGRVCQASQLQGQK	
8.0	4120.0885	1.0064	AAFQIISQVISEATEQVLATTVGKVAGRVCQASQLQGQK	
6.8	4120.0885	1.0064	AAFQIISQVISEATEQVLATTVGKVAGRVCQASQLQGQK	
6.1	4120.0885	1.0064	AAFQIISQVISEATEQVLATTVGKVAGRVCQASQLQGQK	

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

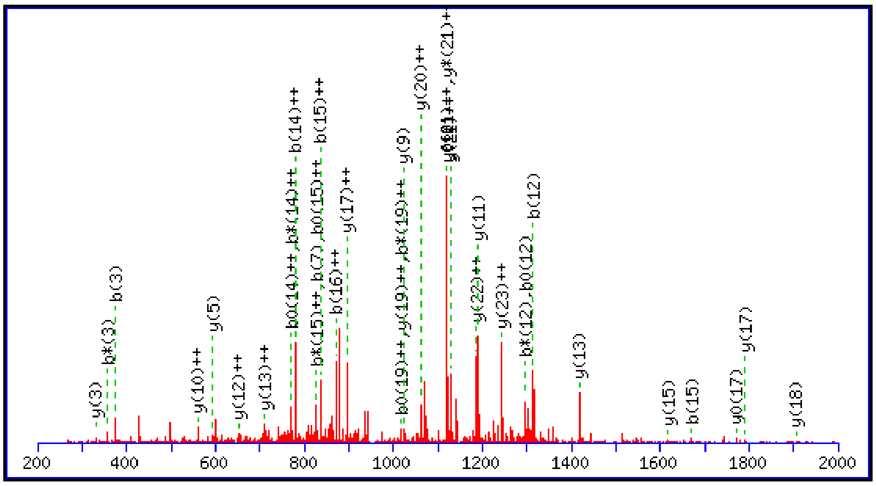
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25971: 2859.519732 from(954.180520,3+) intensity(1235108.3750) rtinseconds(1753) scans(4448) index(24588)
Title: 111019_Est_MI_YS_G_06Spectrum3869_scans__4448
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

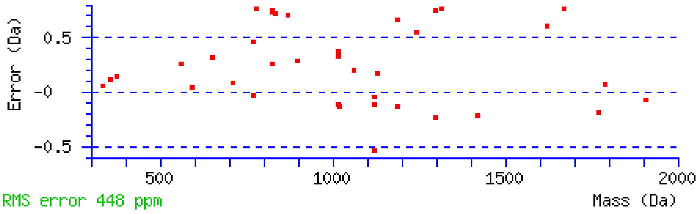
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

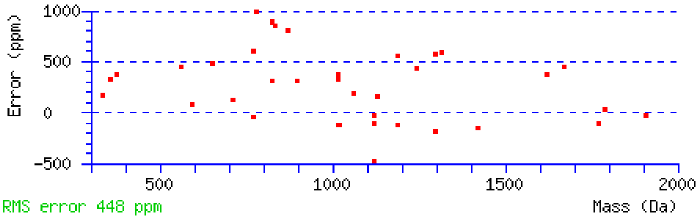


```
Monoisotopic mass of neutral peptide Mr(calc): 2858.5178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9      : Deamidated (NQ)
Ions Score: 59  Expect: 0.00013
Matches : 37/276 fragment ions using 53 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							26
2	228.1343	114.5708	211.1077	106.0575			L	2745.4822	1373.2447	2728.4556	1364.7314	2727.4716	1364.2394	25
3	**375.2027**	188.1050	358.1761	179.5917			F	2632.3981	1316.7027	2615.3715	1308.1894	2614.3875	1307.6974	24
4	488.2867	244.6470	471.2602	236.1337			L	2485.3297	1243.1685	2468.3031	1234.6552	2467.3191	1234.1632	23
5	602.3297	301.6685	585.3031	293.1552			N	2372.2456	1186.6264	2355.2191	1178.1132	2354.2351	1177.6212	22
6	739.3886	370.1979	722.3620	361.6847			H	2258.2027	1129.6050	2241.1761	1121.0917	2240.1921	1120.5997	21
7	**826.4206**	413.7139	809.3941	405.2007	808.4100	404.7087	S	2121.1438	1061.0755	2104.1172	1052.5623	2103.1332	1052.0702	20
8	955.4632	478.2352	938.4367	469.7220	937.4526	469.2300	E	2034.1118	1017.5595	2017.0852	1009.0462	2016.1012	1008.5542	19
9	1070.4901	535.7487	1053.4636	527.2354	1052.4796	526.7434	N	***1905.0692***	953.0382	1888.0426	944.5249	1887.0586	944.0329	18
10	1141.5273	571.2673	1124.5007	562.7540	1123.5167	562.2620	A	***1790.0422***	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	1242.5749	621.7911	1225.5484	613.2778	1224.5644	612.7858	T	1719.0051	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	**1313.6121**	657.3097	1296.5855	648.7964	1295.6015	648.3044	A	***1617.9574***	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	1441.7070	721.3571	1424.6805	712.8439	1423.6965	712.3519	K	1546.9203	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	1556.7340	**778.8706**	1539.7074	770.3573	1538.7234	769.8653	D	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	**1669.8180**	**835.4127**	1652.7915	826.8994	1651.8075	826.4074	I	1303.7984	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	1740.8551	**870.9312**	1723.8286	862.4179	1722.8446	861.9259	A	***1190.7143***	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	1837.9079	919.4576	1820.8814	910.9443	1819.8973	910.4523	P	***1119.6772***	560.3422	1102.6507	551.8290	1101.6667	551.3370	10
18	1938.9556	969.9814	1921.9290	961.4682	1920.9450	960.9761	T	***1022.6245***	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2052.0396	1026.5235	2035.0131	1018.0102	2034.0291	1017.5182	L	921.5768	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2153.0873	1077.0473	2136.0608	1068.5340	2135.0768	1068.0420	T	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2266.1714	1133.5893	2249.1448	1125.0761	2248.1608	1124.5840	L	707.4450	354.2262	690.4185	345.7129			6
22	2429.2347	1215.1210	2412.2082	1206.6077	2411.2242	1206.1157	Y	***594.3610***	297.6841	577.3344	289.1709			5
23	2528.3031	1264.6552	2511.2766	1256.1419	2510.2926	1255.6499	V	431.2976	216.1525	414.2711	207.6392			4

24	2585.3246	1293.1659	2568.2980	1284.6527	2567.3140	1284.1607	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
25	2713.4196	1357.2134	2696.3930	1348.7001	2695.4090	1348.2081	**K**	275.2078	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.4	2858.5178	1.0020	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N9 91.96%
48.6	2858.5178	1.0020	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N5 7.61%
36.1	2858.5178	1.0020	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1 0.43%
3.8	2859.5243	-0.0045	EYLVRVHVPPNIAGTDEPRDITVLR	
0.6	2859.5090	0.0107	HEDVTKQLAEVALHVSNLTNGISAVSK	

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

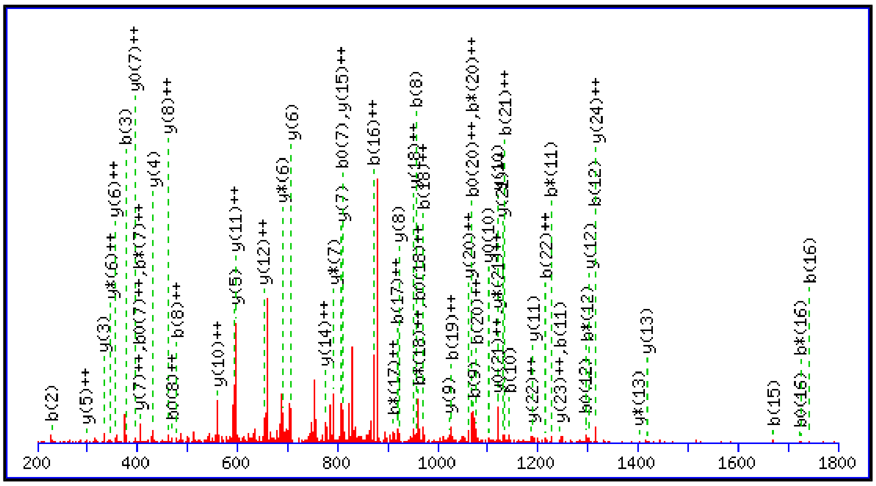
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25834: 2859.508896 from(715.884500,4+) intensity(848562.5625) rtinseconds(1740) scans(4280) index(12659)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum3741_scans__4280
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

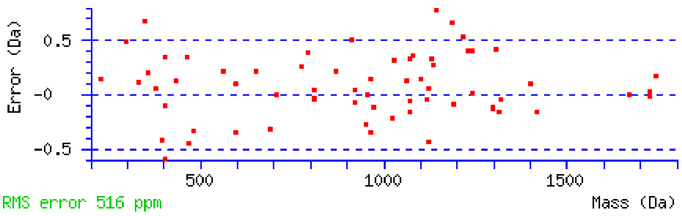
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

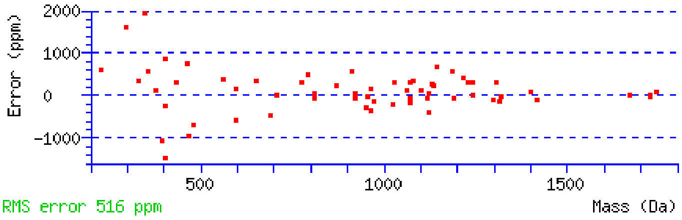


Monoisotopic mass of neutral peptide Mr(calc): 2859.5018
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 59 **Expect:** 0.00017
Matches : 65/276 fragment ions using 141 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			N							26
2	**229.1183**	115.0628	212.0917	106.5495			L	2745.4822	1373.2447	2728.4556	1364.7314	2727.4716	1364.2394	25
3	**376.1867**	188.5970	359.1601	180.0837			F	2632.3981	1316.7027	2615.3715	1308.1894	2614.3875	1307.6974	24
4	489.2708	245.1390	472.2442	236.6257			L	2485.3297	1243.1685	2468.3031	1234.6552	2467.3191	1234.1632	23
5	603.3137	302.1605	586.2871	293.6472			N	2372.2456	1186.6264	2355.2191	1178.1132	2354.2351	1177.6212	22
6	740.3726	370.6899	723.3461	362.1767			H	2258.2027	1129.6050	2241.1761	1121.0917	2240.1921	1120.5997	21
7	827.4046	414.2060	810.3781	405.6927	809.3941	405.2007	S	2121.1438	1061.0755	2104.1172	1052.5623	2103.1332	1052.0702	20
8	**956.4472**	**478.7272**	939.4207	470.2140	938.4367	469.7220	E	2034.1118	1017.5595	2017.0852	1009.0462	2016.1012	1008.5542	19
9	**1071.4742**	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	1905.0692	953.0382	1888.0426	944.5249	1887.0586	944.0329	18
10	**1142.5113**	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	1790.0422	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	**1243.5590**	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	1719.0051	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	**1314.5961**	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	1617.9574	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	1442.6910	721.8492	1425.6645	713.3359	1424.6805	712.8439	K	1546.9203	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	1557.7180	779.3626	1540.6914	770.8494	1539.7074	770.3573	D	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	**1670.8020**	835.9047	1653.7755	827.3914	1652.7915	826.8994	I	***1303.7984***	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	**1741.8392**	**871.4232**	1724.8126	862.9099	1723.8286	862.4179	A	***1190.7143***	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	1838.8919	**919.9496**	1821.8654	911.4363	1820.8814	910.9443	P	***1119.6772***	560.3423	1102.6507	551.8290	1101.6667	551.3370	10
18	1939.9396	**970.4734**	1922.9130	961.9602	1921.9290	961.4682	T	***1022.6245***	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2053.0237	**1027.0155**	2035.9971	1018.5022	2035.0131	1018.0102	L	***921.5768***	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2154.0713	**1077.5393**	2137.0448	1069.0260	2136.0608	1068.5340	T	***808.4927***	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2267.1554	**1134.0813**	2250.1289	1125.5681	2249.1448	1125.0761	L	***707.4450***	354.2262	690.4185	345.7129			6
22	2430.2187	**1215.6130**	2413.1922	1207.0997	2412.2082	1206.6077	Y	***594.3610***	297.6841	577.3344	289.1709			5

23	2529.2871	1265.1472	2512.2606	1256.6339	2511.2766	1256.1419	**V**	***431.2976***	216.1525	414.2711	207.6392			**4**
24	2586.3086	1293.6579	2569.2821	1285.1447	2568.2980	1284.6527	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
25	2714.4036	1357.7054	2697.3770	1349.1922	2696.3930	1348.7001	**K**	275.2078	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.1	2859.5018	0.0071	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N9 52.34%
58.1	2859.5018	0.0071	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N5, N9 41.57%
49.8	2859.5018	0.0071	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N5 6.09%
44.6	2858.5178	0.9911	NLFLNHSENATAKDIAPTLTLYVGKK	
42.3	2858.5178	0.9911	NLFLNHSENATAKDIAPTLTLYVGKK	
26.6	2858.5178	0.9911	NLFLNHSENATAKDIAPTLTLYVGKK	
6.3	2858.4973	1.0116	HKPQAPVIVKTEEVINMHTFNDRR	
4.4	2857.4947	2.0142	ITGVGAVPLPASGNSFDVRPSQGYRRR	
2.3	2858.4940	1.0149	GRSFKQTSLALVHEVHIQLSEWHR	
2.3	2857.4947	2.0142	ITGVGAVPLPASGNSFDVRPSQGYRRR	

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

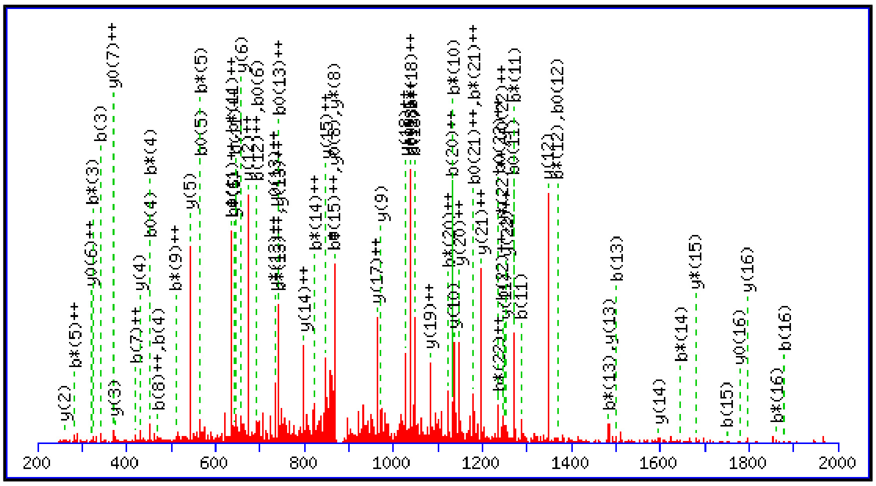
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLVEIEKVVLHPNYSQVDIGLIK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

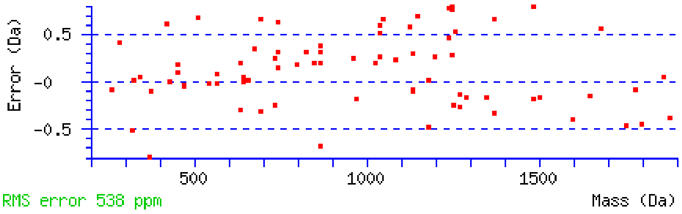
Match to Query 22352: 2634.472242 from(879.164690,3+) intensity(51922.9922) rtinseconds(2127) scans(5498) index(24762)
Title: 111019_Est_MI_YS_G_06Spectrum4782_scans__5498
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

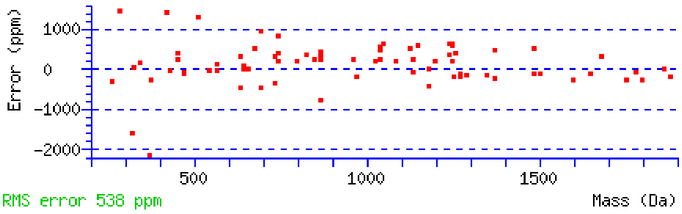
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2634.4632
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 59 **Expect:** 5.3e-005
Matches : 77/248 fragment ions using 158 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							23
2	242.1499	121.5786	225.1234	113.0653			L	2507.4120	1254.2096	2490.3854	1245.6963	2489.4014	1245.2043	22
3	**341.2183**	171.1128	324.1918	162.5995			V	2394.3279	1197.6676	2377.3013	1189.1543	2376.3173	1188.6623	21
4	**470.2609**	235.6341	453.2344	227.1208	452.2504	226.6288	E	2295.2595	1148.1334	2278.2329	1139.6201	2277.2489	1139.1281	20
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	I	2166.2169	1083.6121	2149.1903	1075.0988	2148.2063	1074.6068	19
6	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	E	2053.1328	1027.0700	2036.1063	1018.5568	2035.1223	1018.0648	18
7	840.4825	**420.7449**	823.4560	412.2316	822.4720	411.7396	K	1924.0902	962.5488	1907.0637	954.0355	1906.0797	953.5435	17
8	939.5510	**470.2791**	922.5244	461.7658	921.5404	461.2738	V	***1795.9953***	898.5013	1778.9687	889.9880	1777.9847	889.4960	16
9	**1038.6194**	519.8133	1021.5928	511.3001	1020.6088	510.8080	V	1696.9268	848.9671	1679.9003	840.4538	1678.9163	839.9618	15
10	1151.7034	576.3554	1134.6769	567.8421	1133.6929	567.3501	L	***1597.8584***	799.4329	1580.8319	790.9196	1579.8479	790.4276	14
11	**1288.7623**	**644.8848**	1271.7358	636.3715	1270.7518	635.8795	H	***1484.7744***	742.8908	1467.7478	734.3775	1466.7638	733.8855	13
12	1385.8151	**693.4112**	1368.7886	684.8979	1367.8045	684.4059	P	***1347.7155***	674.3614	1330.6889	665.8481	1329.7049	665.3561	12
13	**1500.8421**	750.9247	1483.8155	742.4114	1482.8315	741.9194	N	***1250.6627***	625.8350	1233.6361	617.3217	1232.6521	616.8297	11
14	1663.9054	832.4563	1646.8788	823.9431	1645.8948	823.4510	Y	***1135.6358***	568.3215	1118.6092	559.8082	1117.6252	559.3162	10
15	**1750.9374**	875.9723	1733.9109	867.4591	1732.9268	866.9671	S	***972.5724***	486.7898	955.5459	478.2766	954.5619	477.7846	9
16	**1878.9960**	940.0016	1861.9694	931.4884	1860.9854	930.9964	Q	885.5404	443.2738	868.5138	434.7606	867.5298	434.2686	8
17	1978.0644	989.5358	1961.0379	981.0226	1960.0538	980.5306	V	757.4818	379.2445	740.4553	370.7313	739.4713	370.2393	7
18	2093.0913	**1047.0493**	2076.0648	1038.5360	2075.0808	1038.0440	D	***658.4134***	329.7103	641.3869	321.1971	640.4028	320.7051	6
19	2206.1754	1103.5913	2189.1489	1095.0781	2188.1648	1094.5861	I	***543.3865***	272.1969	526.3599	263.6836			5
20	2263.1969	**1132.1021**	2246.1703	1123.5888	2245.1863	1123.0968	G	***430.3024***	215.6548	413.2758	207.1416			4
21	2376.2809	1188.6441	2359.2544	1180.1308	2358.2704	1179.6388	L	***373.2809***	187.1441	356.2544	178.6308			3
22	2489.3650	**1245.1861**	2472.3385	1236.6729	2471.3544	1236.1809	I	***260.1969***	130.6021	243.1703	122.0888			2
23							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.1	2634.4632	0.0090	QLVEIEKVVLHPNYSQVDIGLIK	Deamidated N13 53.78%
58.5	2634.4632	0.0090	QLVEIEKVVLHPNYSQVDIGLIK	Deamidated Q16 46.20%
39.3	2633.4792	0.9930	QLVEIEKVVLHPNYSQVDIGLIK	
23.7	2634.4632	0.0090	QLVEIEKVVLHPNYSQVDIGLIK	Deamidated Q1 0.02%

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

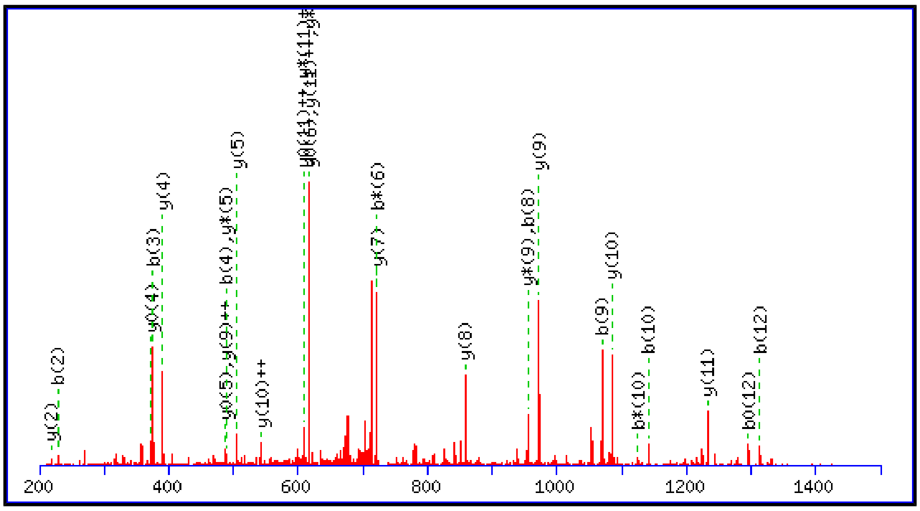
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

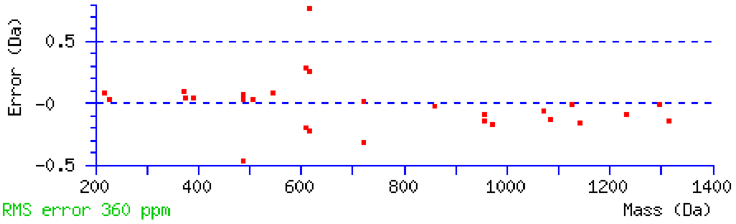
Match to Query 4260: 1458.713448 from(730.364000,2+) intensity(50538.0586) rtinseconds(505) scans(1116) index(6157)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum968_scans__1116
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

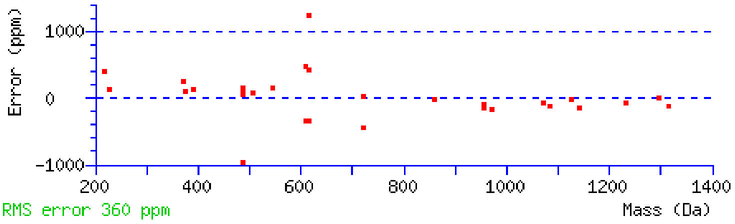
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1458.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00029
Matches : 29/128 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	115.0502	58.0287	98.0237	49.5155			N							13
2	***228.1343***	114.5708	211.1077	106.0575			L	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12
3	***375.2027***	188.1050	358.1761	179.5917			F	***1232.5906***	616.7989	1215.5640	608.2857	1214.5800	607.7937	11
4	***488.2867***	244.6470	471.2602	236.1337			L	***1085.5222***	543.2647	1068.4956	534.7515	1067.5116	534.2594	10
5	602.3297	301.6685	585.3031	293.1552			N	***972.4381***	486.7227	955.4116	478.2094	954.4275	477.7174	9
6	739.3886	370.1979	722.3620	361.6847			H	***858.3952***	429.7012	841.3686	421.1880	840.3846	420.6959	8
7	826.4206	413.7139	809.3941	405.2007	808.4100	404.7087	S	***721.3363***	361.1718	704.3097	352.6585	703.3257	352.1665	7
8	***955.4632***	478.2352	938.4367	469.7220	937.4526	469.2300	E	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	6
9	***1070.4901***	535.7487	1053.4636	527.2354	1052.4796	526.7434	N	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5
10	***1141.5273***	571.2673	1124.5007	562.7540	1123.5167	562.2620	A	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	4
11	1242.5749	621.7911	1225.5484	613.2778	1224.5644	612.7858	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
12	***1313.6121***	657.3097	1296.5855	648.7964	1295.6015	648.3044	A	***218.1499***	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.3	1458.7103	0.0032	NLFLNHSENATAK	Deamidated N9 99.14%
37.4	1458.7103	0.0032	NLFLNHSENATAK	Deamidated N5 0.80%
26.5	1458.7103	0.0032	NLFLNHSENATAK	Deamidated N1 0.07%
23.1	1458.7089	0.0046	LNQNELELENLK	
21.0	1458.7202	-0.0067	INIQNKDIEAGDK	
16.9	1458.7103	0.0032	RIQQALWNGAGNK	
16.6	1458.7201	-0.0067	QARQLENELDLK	
14.4	1458.7103	0.0032	SSSGWISHNKLNK	
14.1	1458.7098	0.0036	SMVQKMIFSLNK	
13.3	1458.7089	0.0045	IEDLENEIEEVK	

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

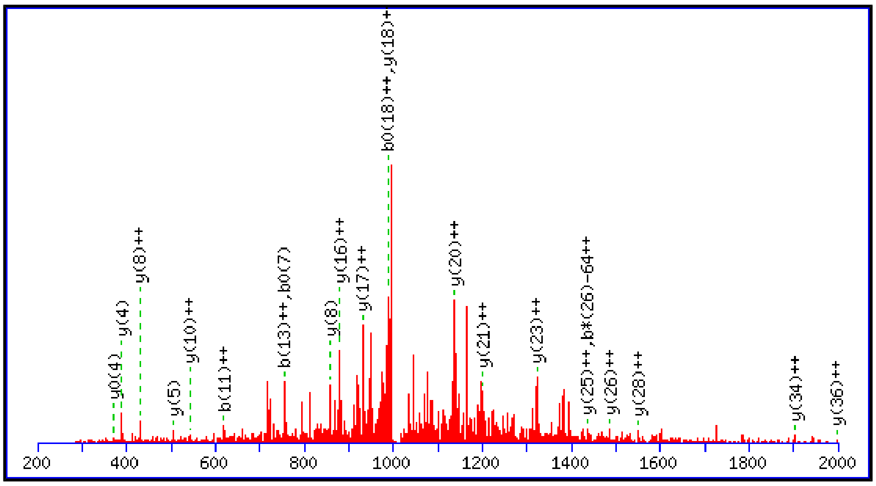
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28999: 5038.502620 from(1008.707800,5+) intensity(42294.6133) rtinseconds(2524) scans(6837) index(24172)
Title: 111019_Est_MI_YS_G_05Spectrum5934_scans__6837
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

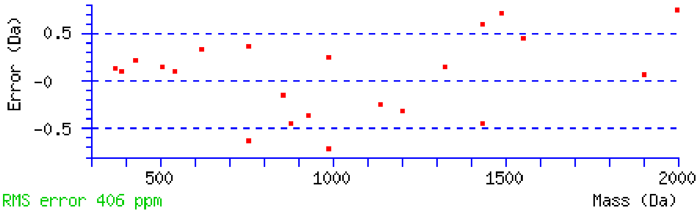
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

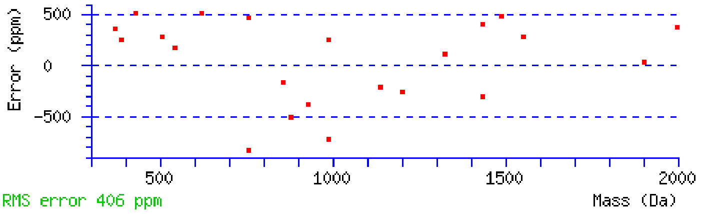


Monoisotopic mass of neutral peptide Mr(calc): 5038.4923
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N33 : Deamidated (NQ)
N37 : Deamidated (NQ)
N41 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00048
Matches : 22/776 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	58.0287	29.5180					G							45
2	145.0608	73.0340			127.0502	64.0287	S	4982.4782	2491.7427	4965.4516	2483.2294	4964.4676	2482.7374	44
3	292.1292	146.5682			274.1186	137.5629	F	4895.4461	2448.2267	4878.4196	2439.7134	4877.4356	2439.2214	43
4	389.1819	195.0946			371.1714	186.0893	P	4748.3777	2374.6925	4731.3512	2366.1792	4730.3672	2365.6872	42
5	575.2613	288.1343			557.2507	279.1290	W	4651.3250	2326.1661	4634.2984	2317.6528	4633.3144	2317.1608	41
6	703.3198	352.1636	686.2933	343.6503	685.3093	343.1583	Q	4465.2456	2233.1265	4448.2191	2224.6132	4447.2351	2224.1212	40
7	774.3570	387.6821	757.3304	379.1688	756.3464	378.6768	A	4337.1871	2169.0972	4320.1605	2160.5839	4319.1765	2160.0919	39
8	902.4519	451.7296	885.4254	443.2163	884.4413	442.7243	K	4266.1500	2133.5786	4249.1234	2125.0653	4248.1394	2124.5733	38
9	1049.4873	525.2473	1032.4608	516.7340	1031.4767	516.2420	M	4138.0550	2069.5311	4121.0284	2061.0179	4120.0444	2060.5259	37
10	1148.5557	574.7815	1131.5292	566.2682	1130.5452	565.7762	V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0082	36
11	1235.5878	618.2975	1218.5612	609.7842	1217.5772	609.2922	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
12	1372.6467	686.8270	1355.6201	678.3137	1354.6361	677.8217	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
13	1509.7056	755.3564	1492.6790	746.8432	1491.6950	746.3511	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
14	1623.7485	812.3779	1606.7220	803.8646	1605.7379	803.3726	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
15	1736.8326	868.9199	1719.8060	860.4066	1718.8220	859.9146	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
16	1837.8802	919.4438	1820.8537	910.9305	1819.8697	910.4385	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
17	1938.9279	969.9676	1921.9014	961.4543	1920.9174	960.9623	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
18	1995.9494	998.4783	1978.9228	989.9651	1977.9388	989.4731	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
19	2066.9865	1033.9969	2049.9600	1025.4836	2048.9759	1024.9916	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
20	2168.0342	1084.5207	2151.0076	1076.0075	2150.0236	1075.5154	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
21	2281.1182	1141.0628	2264.0917	1132.5495	2263.1077	1132.0575	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25

22	2394.2023	1197.6048	2377.1758	1189.0915	2376.1917	1188.5995	**I**	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	**24**
23	2508.2452	1254.6263	2491.2187	1246.1130	2490.2347	1245.6210	**N**	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6507	**23**
24	2637.2878	1319.1476	2620.2613	1310.6343	2619.2773	1310.1423	**E**	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	**22**
25	2765.3464	1383.1768	2748.3199	1374.6636	2747.3358	1374.1716	**Q**	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	**21**
26	2951.4257	1476.2165	2934.3992	1467.7032	2933.4152	1467.2112	**W**	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	**20**
27	3064.5098	1532.7585	3047.4832	1524.2453	3046.4992	1523.7533	**L**	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	**19**
28	3177.5939	1589.3006	3160.5673	1580.7873	3159.5833	1580.2953	**L**	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	**18**
29	3278.6415	1639.8244	3261.6150	1631.3111	3260.6310	1630.8191	**T**	1862.9131	931.9602	1845.8865	923.4469	1844.9025	922.9549	**17**
30	3379.6892	1690.3482	3362.6627	1681.8350	3361.6786	1681.3430	**T**	1761.8654	881.4363	1744.8388	872.9230	1743.8548	872.4310	**16**
31	3450.7263	1725.8668	3433.6998	1717.3535	3432.7158	1716.8615	**A**	1660.8177	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
32	3578.8213	1789.9143	3561.7947	1781.4010	3560.8107	1780.9090	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
33	3693.8482	1847.4278	3676.8217	1838.9145	3675.8377	1838.4225	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6751	722.3412	**13**
34	3806.9323	1903.9698	3789.9057	1895.4565	3788.9217	1894.9645	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
35	3954.0007	1977.5040	3936.9742	1968.9907	3935.9901	1968.4987	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
36	4067.0848	2034.0460	4050.0582	2025.5327	4049.0742	2025.0407	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
37	4182.1117	2091.5595	4165.0852	2083.0462	4164.1012	2082.5542	**N**	973.4221	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
38	4319.1706	2160.0890	4302.1441	2151.5757	4301.1601	2151.0837	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
39	4406.2027	2203.6050	4389.1761	2195.0917	4388.1921	2194.5997	**S**	721.3363	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
40	4535.2452	2268.1263	4518.2187	2259.6130	4517.2347	2259.1210	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
41	4650.2722	2325.6397	4633.2456	2317.1265	4632.2616	2316.6345	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
42	4721.3093	2361.1583	4704.2828	2352.6450	4703.2987	2352.1530	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
43	4822.3570	2411.6821	4805.3304	2403.1689	4804.3464	2402.6768	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
44	4893.3941	2447.2007	4876.3676	2438.6874	4875.3835	2438.1954	**A**	218.1499	109.5786	201.1234	101.0653			**2**
45							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.1	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33, N37, N41 44.52%
54.1	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N37, N41 34.88%
49.9	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N14, N41 13.38%
46.7	5037.5083	0.9943	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
46.0	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q25, N33, N37 5.48%
40.8	5037.5083	0.9943	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
38.3	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N23, Q25, N33 0.93%
30.5	5037.5083	0.9943	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
25.1	5038.4923	0.0103	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N14, N23, Q25 0.04%
23.9	5037.5083	0.9943	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

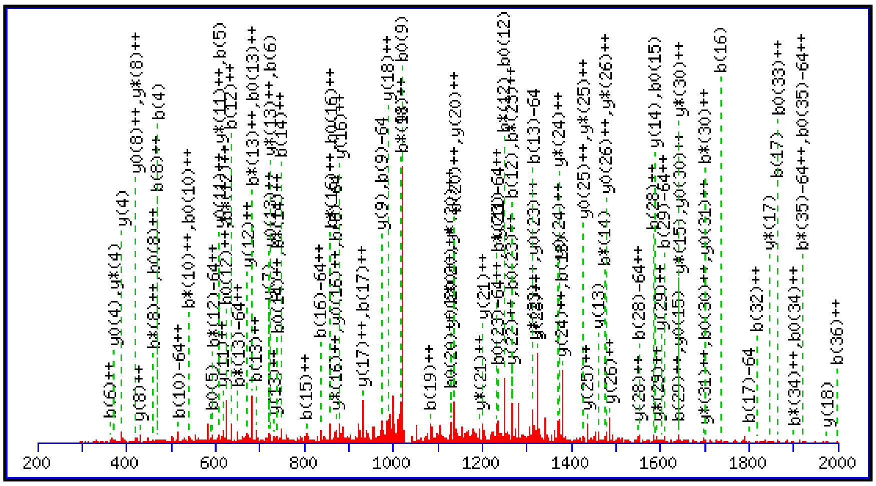
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28881: 4137.075456 from(1035.276140,4+) intensity(23771.8164) rtinseconds(2600) scans(6879) index(19908)
Title: 111019_Est_MI_YP_G_09Spectrum6100_scans__6879
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

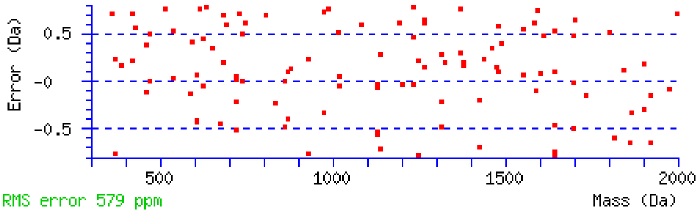
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

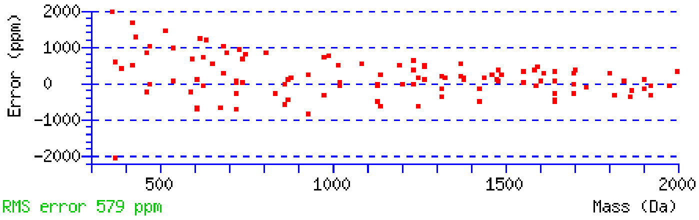


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00063
Matches : 115/616 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	**608.2609**	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**722.3039**	***361.6556***	705.2773	353.1423	704.2933	352.6503	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	936.4356	***468.7214***	919.4091	460.2082	918.4250	459.7162	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	1165.5419	583.2746	1148.5153	574.7613	1147.5313	574.2693	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	**1266.5895**	***633.7984***	1249.5630	625.2851	1248.5790	624.7931	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	**1379.6736**	***690.3404***	1362.6471	681.8272	1361.6630	681.3352	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	1492.7577	***746.8825***	1475.7311	738.3692	1474.7471	737.8772	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1606.8006	***803.9039***	1589.7741	795.3907	1588.7900	794.8987	N	2645.3206	1323.1639	2628.2940	1314.6506	2627.3100	1314.1586	23
16	**1735.8432**	868.4252	1718.8166	859.9120	1717.8326	859.4200	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	**1863.9018**	***932.4545***	1846.8752	923.9413	1845.8912	923.4492	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2049.9811	1025.4942	2032.9545	1016.9809	2031.9705	1016.4889	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2163.0652	***1082.0362***	2146.0386	1073.5229	2145.0546	1073.0309	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2276.1492	***1138.5782***	2259.1227	1130.0650	2258.1386	1129.5730	L	**1975.0131**	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2377.1969	1189.1021	2360.1703	1180.5888	2359.1863	1180.0968	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17
22	2478.2446	1239.6259	2461.2180	1231.1126	2460.2340	1230.6206	T	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	16

23	2549.2817	1275.1445	2532.2551	1266.6312	2531.2711	1266.1392	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2677.3766	1339.1920	2660.3501	1330.6787	2659.3661	1330.1867	**K**	**1588.7966**	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	**1460.7016**	730.8544	1443.6751	722.3412	1442.6910	721.8492	**13**
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	1526.7817	3035.5295	1518.2684	3034.5455	1517.7764	**F**	**1232.5906**	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	***1583.3237***	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3280.6671	***1640.8372***	3263.6405	1632.3239	3262.6565	1631.8319	**N**	**972.4381**	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3417.7260	1709.3666	3400.6994	1700.8534	3399.7154	1700.3614	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3504.7580	1752.8826	3487.7315	1744.3694	3486.7475	1743.8774	**S**	**720.3523**	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3633.8006	***1817.4039***	3616.7741	1808.8907	3615.7900	1808.3987	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	***1995.9864***	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.8	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29 33.67%
52.9	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 21.69%
49.5	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 9.87%
49.1	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 9.11%
48.4	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 7.79%
44.7	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 3.32%
42.3	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 1.88%
42.2	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25 1.86%
42.1	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 1.82%
42.1	4136.0636	1.0118	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 1.81%

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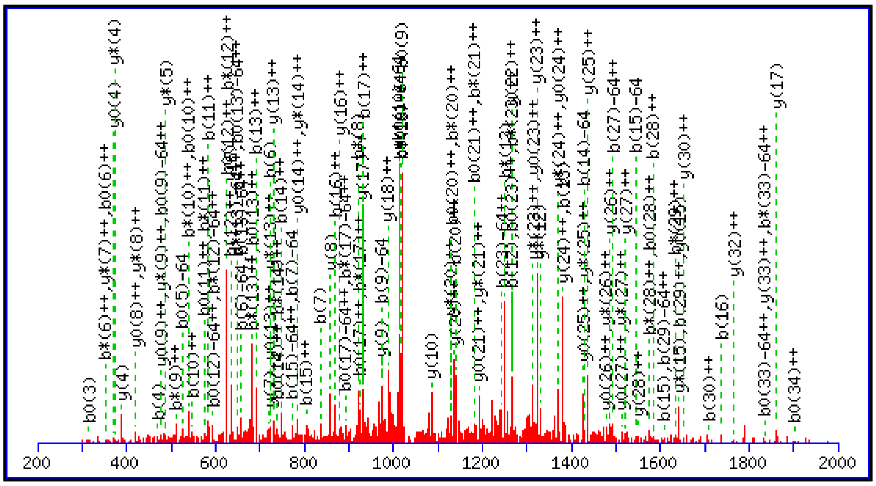
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28932: 4138.051936 from(1035.520260,4+) intensity(0.0000) rtinseconds(3556) scans(8820) index(26400)
Title: 111019_Est_MI_YS_G_08Spectrum7678_scans__8820
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

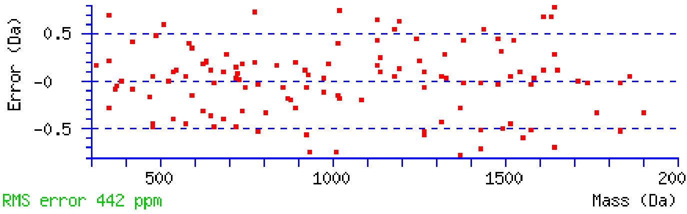
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

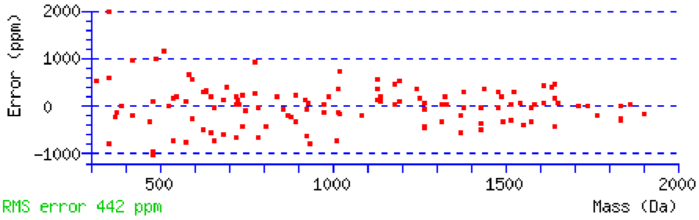


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N15 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.00096
Matches : 122/616 fragment ions using 167 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	334.1431	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	608.2609	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	**723.2879**	362.1476	706.2613	353.6343	705.2773	353.1423	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1166.5259	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	**1608.7686**	***804.8880***	1591.7421	796.3747	1590.7581	795.8827	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	**1737.8112**	***869.4093***	1720.7847	860.8960	1719.8007	860.4040	E	2531.2776	1266.1425	2514.2511	1257.6292	2513.2671	1257.1372	22
17	1865.8698	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	Q	2402.2351	1201.6212	2385.2085	1193.1079	2384.2245	1192.6159	21
18	2051.9491	1026.4782	2034.9226	1017.9649	2033.9386	1017.4729	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2165.0332	1083.0202	2148.0066	1074.5070	2147.0226	1074.0149	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2379.1649	1190.0861	2362.1384	1181.5728	2361.1544	1181.0808	T	**1861.9290**	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2551.2497	1276.1285	2534.2232	1267.6152	2533.2392	1267.1232	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2679.3447	1340.1760	2662.3181	1331.6627	2661.3341	1331.1707	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	1460.7016	730.8544	1443.6750	722.3412	1442.6910	721.8492	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3053.5401	1527.2737	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1233.5746	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3166.6242	***1583.8157***	3149.5976	1575.3024	3148.6136	1574.8104	**L**	**1086.5062**	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3281.6511	***1641.3292***	3264.6245	1632.8159	3263.6405	1632.3239	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3418.7100	***1709.8586***	3401.6835	1701.3454	3400.6994	1700.8534	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	1875.4094	3732.7850	1866.8961	3731.8010	1866.4041	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	1996.9704	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.6	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N29, N33 41.80%
51.8	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N33 27.12%
48.7	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17, N33 13.28%
48.4	4137.0477	1.0043	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
44.2	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25, N29, N33 4.72%
41.0	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N25, N29 2.28%
39.7	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N29, N33 1.70%
38.9	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17, N29 1.39%
38.2	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17, N25, N33 1.19%
38.0	4138.0317	0.0203	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N25, N29, N33 1.13%

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

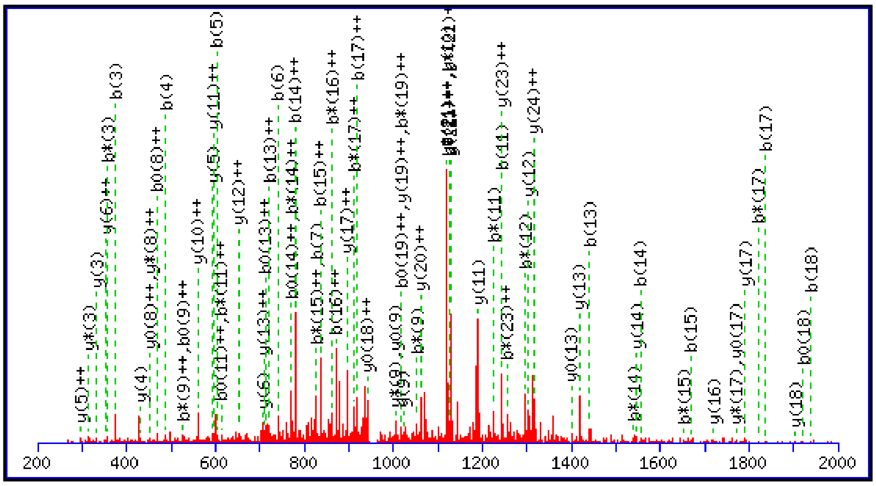
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25970: 2859.519252 from(954.180360,3+) intensity(27577.4766) rtinseconds(1730) scans(4381) index(24575)
Title: 111019_Est_MI_YS_G_06Spectrum3812_scans__4381
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

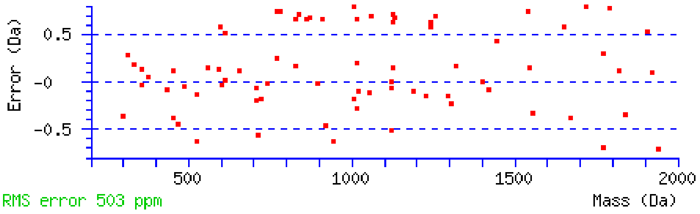
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

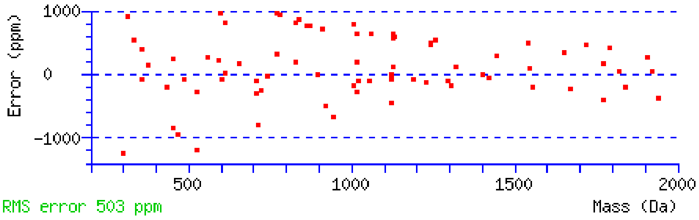


Monoisotopic mass of neutral peptide Mr(calc): 2858.5178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0005
Matches : 77/276 fragment ions using 169 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							26
2	228.1343	114.5708	211.1077	106.0575			L	2745.4822	1373.2447	2728.4556	1364.7314	2727.4716	1364.2394	25
3	***375.2027***	188.1050	358.1761	179.5917			F	2632.3981	1316.7027	2615.3715	1308.1894	2614.3875	1307.6974	24
4	***488.2867***	244.6470	471.2602	236.1337			L	2485.3297	1243.1685	2468.3031	1234.6552	2467.3191	1234.1632	23
5	***603.3137***	302.1605	586.2871	293.6472			N	2372.2456	1186.6264	2355.2191	1178.1132	2354.2351	1177.6212	22
6	***740.3726***	370.6899	723.3461	362.1767			H	2257.2187	1129.1130	2240.1921	1120.5997	2239.2081	1120.1077	21
7	***827.4046***	414.2060	810.3781	405.6927	809.3941	405.2007	S	2120.1598	1060.5835	2103.1332	1052.0702	2102.1492	1051.5782	20
8	956.4472	478.7272	939.4207	470.2140	938.4367	469.7220	E	2033.1277	1017.0675	2016.1012	1008.5542	2015.1172	1008.0622	19
9	1070.4901	535.7487	1053.4636	527.2354	1052.4796	526.7434	N	***1904.0851***	952.5462	1887.0586	944.0329	1886.0746	943.5409	18
10	1141.5273	571.2673	1124.5007	562.7540	1123.5167	562.2620	A	***1790.0422***	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	***1242.5749***	621.7911	1225.5484	613.2778	1224.5644	612.7858	T	***1719.0051***	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	1313.6121	657.3097	1296.5855	648.7964	1295.6015	648.3044	A	1617.9574	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	***1441.7070***	721.3571	1424.6805	712.8439	1423.6965	712.3519	K	***1546.9203***	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	***1556.7340***	778.8706	1539.7074	770.3573	1538.7234	769.8653	D	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	***1669.8180***	835.4127	1652.7915	826.8994	1651.8075	826.4074	I	***1303.7984***	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	1740.8551	870.9312	1723.8286	862.4179	1722.8446	861.9259	A	***1190.7143***	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	***1837.9079***	919.4576	1820.8814	910.9443	1819.8973	910.4523	P	***1119.6772***	560.3422	1102.6507	551.8290	1101.6667	551.3370	10
18	***1938.9556***	969.9814	1921.9290	961.4682	1920.9450	960.9761	T	***1022.6245***	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2052.0396	1026.5235	2035.0131	1018.0102	2034.0291	1017.5182	L	921.5768	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2153.0873	1077.0473	2136.0608	1068.5340	2135.0768	1068.0420	T	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2266.1714	1133.5893	2249.1448	1125.0761	2248.1608	1124.5840	L	***707.4450***	354.2262	690.4185	345.7129			6
22	2429.2347	1215.1210	2412.2082	1206.6077	2411.2242	1206.1157	Y	***594.3610***	297.6841	577.3344	289.1709			5
23	2528.3031	1264.6552	2511.2766	1256.1419	2510.2926	1255.6499	V	***431.2976***	216.1525	414.2711	207.6392			4

24	2585.3246	1293.1659	2568.2980	1284.6527	2567.3140	1284.1607	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
25	2713.4196	1357.2134	2696.3930	1348.7001	2695.4090	1348.2081	**K**	275.2078	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.5	2858.5178	1.0015	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N5 43.60%
52.8	2858.5178	1.0015	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1 37.19%
50.0	2858.5178	1.0015	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N9 19.21%

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

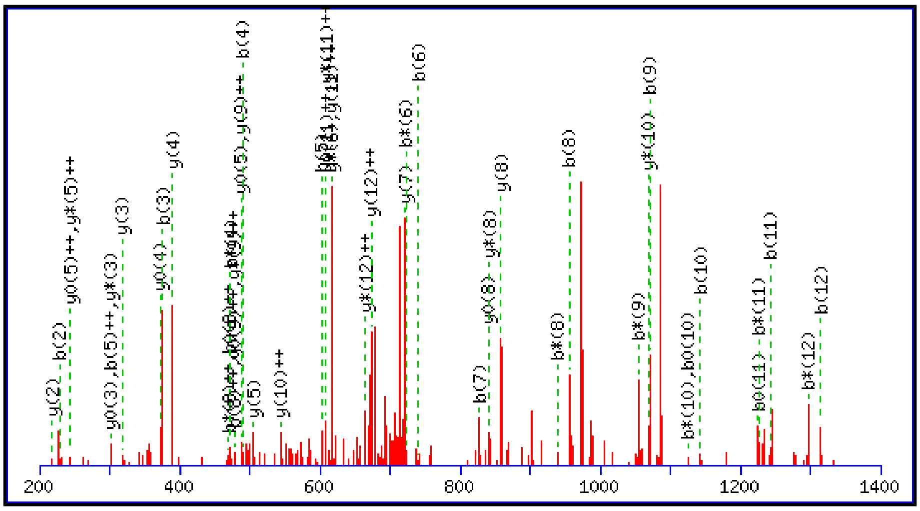
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

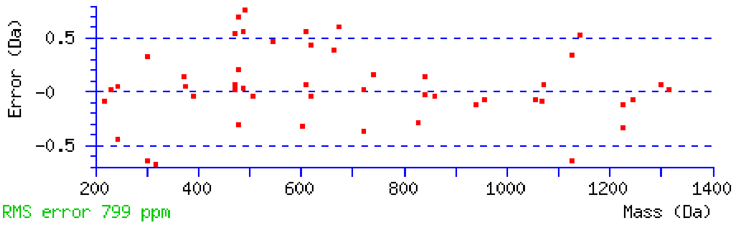
Match to Query 4962: 1459.697248 from(730.855900,2+) intensity(4583.1934) rtinseconds(724) scans(1157) index(501)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum906_scans__1157
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

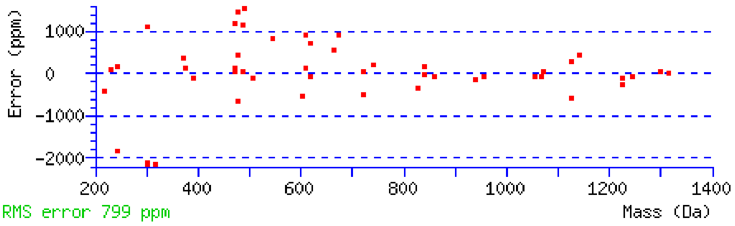
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1459.6943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0013
Matches : 49/128 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			N							13
2	***229.1183***	115.0628	212.0917	106.5495			L	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	12
3	***376.1867***	188.5970	359.1601	180.0837			F	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	11
4	***489.2708***	245.1390	472.2442	236.6257			L	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	10
5	***603.3137***	302.1605	586.2871	293.6472			N	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	9
6	***740.3726***	370.6899	723.3461	362.1767			H	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	8
7	***827.4046***	414.2060	810.3781	405.6927	809.3941	405.2007	S	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	7
8	***956.4472***	478.7272	939.4207	470.2140	938.4367	469.7220	E	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	6
9	***1071.4742***	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	5
10	***1142.5113***	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	4
11	***1243.5590***	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3
12	***1314.5961***	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	**218.1499**	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.1	1459.6943	0.0030	NLFLNHSENATAK	Deamidated N1, N9 64.45%
48.4	1459.6943	0.0030	NLFLNHSENATAK	Deamidated N5, N9 35.25%
27.8	1459.6943	0.0030	NLFLNHSENATAK	Deamidated N1, N5 0.30%
14.9	1459.7042	-0.0069	INIQNKDIEAGDK	
13.5	1459.6929	0.0043	LDENQQQLVQIK	
12.1	1459.7042	-0.0069	EDLEKPNETQKK	
12.0	1459.6903	0.0070	QVDANVNTNDKDK	
11.7	1459.6903	0.0070	VRTDSNNENSVPK	
11.7	1459.6903	0.0070	VRTDSNNENSVPK	
11.0	1459.6977	-0.0004	NCTEELDLNPKK	

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

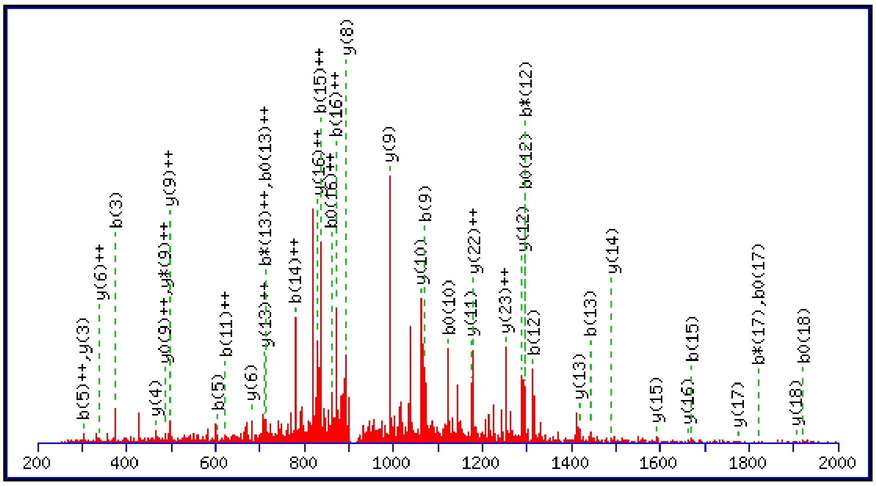
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25452: 2731.414962 from(911.478930,3+) intensity(21250.0000) rtinseconds(1974) scans(4933) index(12750)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4315_scans__4933
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

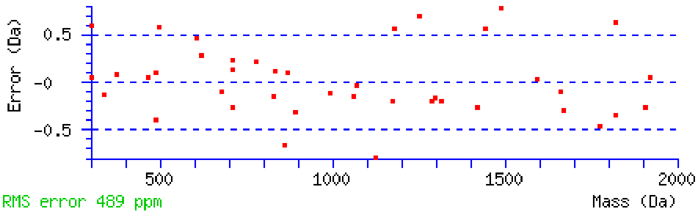
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

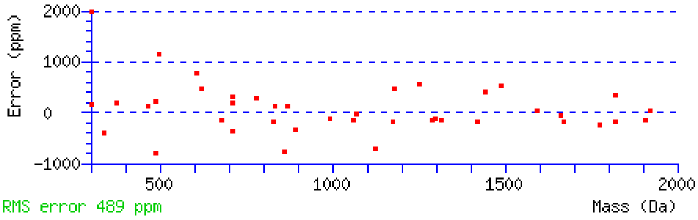


Monoisotopic mass of neutral peptide Mr(calc): 2731.4068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0023
Matches : 42/266 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			**N**							**25**
2	229.1183	115.0628	212.0917	106.5495			**L**	2617.3872	1309.1972	2600.3606	1300.6840	2599.3766	1300.1920	**24**
3	**376.1867**	188.5970	359.1601	180.0837			**F**	2504.3031	1252.6552	2487.2766	1244.1419	2486.2926	1243.6499	**23**
4	489.2708	245.1390	472.2442	236.6257			**L**	2357.2347	1179.1210	2340.2082	1170.6077	2339.2242	1170.1157	**22**
5	**604.2977**	**302.6525**	587.2712	294.1392			**N**	2244.1507	1122.5790	2227.1241	1114.0657	2226.1401	1113.5737	**21**
6	741.3566	371.1819	724.3301	362.6687			**H**	2129.1237	1065.0655	2112.0972	1056.5522	2111.1131	1056.0602	**20**
7	828.3886	414.6980	811.3621	406.1847	810.3781	405.6927	**S**	1992.0648	996.5360	1975.0383	988.0228	1974.0542	987.5308	**19**
8	957.4312	479.2193	940.4047	470.7060	939.4207	470.2140	**E**	***1905.0328***	953.0200	1888.0062	944.5067	1887.0222	944.0147	**18**
9	**1071.4742**	536.2407	1054.4476	527.7274	1053.4636	527.2354	**N**	***1775.9902***	888.4987	1758.9636	879.9855	1757.9796	879.4934	**17**
10	1142.5113	571.7593	1125.4847	563.2460	1124.5007	562.7540	**A**	***1661.9473***	831.4773	1644.9207	822.9640	1643.9367	822.4720	**16**
11	1243.5590	**622.2831**	1226.5324	613.7698	1225.5484	613.2778	**T**	***1590.9101***	795.9587	1573.8836	787.4454	1572.8996	786.9534	**15**
12	**1314.5961**	657.8017	1297.5695	649.2884	1296.5855	648.7964	**A**	***1489.8625***	745.4349	1472.8359	736.9216	1471.8519	736.4296	**14**
13	**1442.6910**	721.8492	1425.6645	713.3359	1424.6805	712.8439	**K**	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	**13**
14	1557.7180	**779.3626**	1540.6914	770.8494	1539.7074	770.3573	**D**	***1290.7304***	645.8688	1273.7038	637.3556	1272.7198	636.8635	**12**
15	**1670.8020**	**835.9047**	1653.7755	827.3914	1652.7915	826.8994	**I**	***1175.7034***	588.3554	1158.6769	579.8421	1157.6929	579.3501	**11**
16	1741.8392	**871.4232**	1724.8126	862.9099	1723.8286	862.4179	**A**	***1062.6194***	531.8133	1045.5928	523.3001	1044.6088	522.8080	**10**
17	1838.8919	919.9496	1821.8654	911.4363	1820.8814	910.9443	**P**	***991.5823***	496.2948	974.5557	487.7815	973.5717	487.2895	**9**
18	1939.9396	970.4734	1922.9130	961.9602	1921.9290	961.4682	**T**	***894.5295***	447.7684	877.5029	439.2551	876.5189	438.7631	**8**
19	2053.0237	1027.0155	2035.9971	1018.5022	2035.0131	1018.0102	**L**	793.4818	397.2445	776.4553	388.7313	775.4713	388.2393	**7**
20	2154.0713	1077.5393	2137.0448	1069.0260	2136.0608	1068.5340	**T**	***680.3978***	340.7025	663.3712	332.1892	662.3872	331.6972	**6**
21	2267.1554	1134.0813	2250.1289	1125.5681	2249.1448	1125.0761	**L**	579.3501	290.1787	562.3235	281.6654			**5**
22	2430.2187	1215.6130	2413.1922	1207.0997	2412.2082	1206.6077	**Y**	***466.2660***	233.6366	449.2395	225.1234			**4**

23	2529.2871	1265.1472	2512.2606	1256.6339	2511.2766	1256.1419	**V**	*303.2027*	152.1050	286.1761	143.5917			**3**
24	2586.3086	1293.6579	2569.2821	1285.1447	2568.2980	1284.6527	**G**	204.1343	102.5708	187.1077	94.0575			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.7	2731.4068	0.0081	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N1, N5 81.69%
46.6	2730.4228	0.9922	NLFLNHSENATAKDIAPTLTLYVGK	
44.2	2730.4228	0.9922	NLFLNHSENATAKDIAPTLTLYVGK	
40.9	2731.4068	0.0081	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N5, N9 10.79%
39.4	2731.4068	0.0081	NLFLNHSENATAKDIAPTLTLYVGK	Deamidated N1, N9 7.52%
32.2	2730.4228	0.9922	NLFLNHSENATAKDIAPTLTLYVGK	
1.2	2730.4044	1.0105	AATATMPASVVGQRPTIAMVTAINSQK	
0.5	2730.4117	1.0032	LAALAKMNIMDRAATPNESMNLLLK	
0.5	2730.4163	0.9987	LLFEVMHQRRSNIAFLLPTNGEK	

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

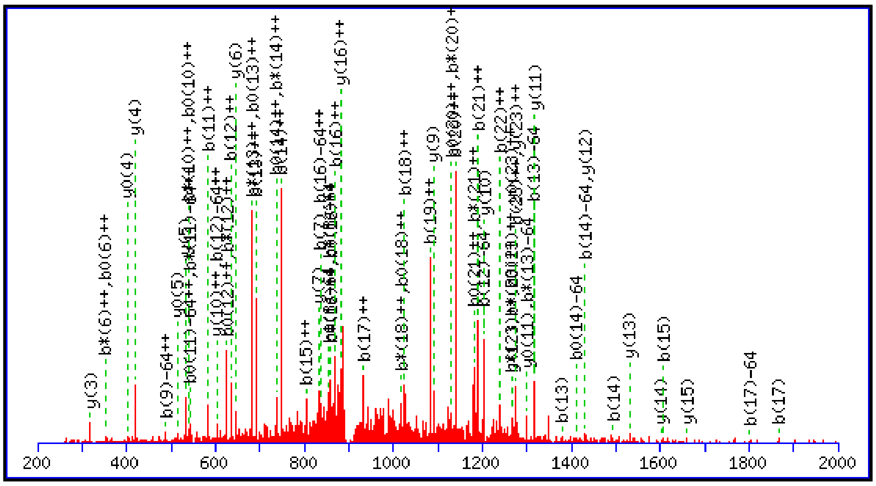
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 25269: 2696.357652 from(899.793160,3+) intensity(11738.8682) rtinseconds(3099) scans(8319) index(9898)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum7249_scans__8319
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

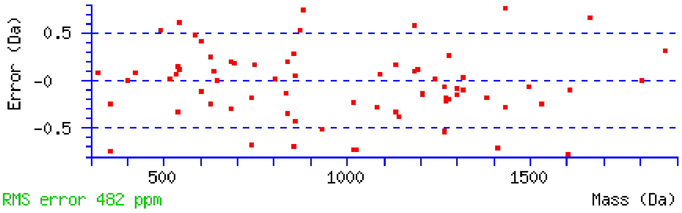
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

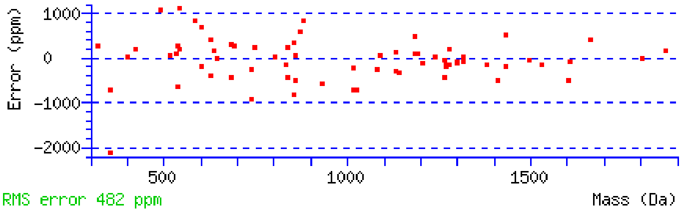


```
Monoisotopic mass of neutral peptide Mr(calc): 2696.3479
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6      : Deamidated (NQ)
Q17     : Deamidated (NQ)
Ions Score: 50  Expect: 0.0029
Matches : 72/382 fragment ions using 121 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0427	74.5250					M							24
2	247.1111	124.0592					V	2550.3198	1275.6636	2533.2933	1267.1503	2532.3093	1266.6583	23
3	334.1431	167.5752			316.1326	158.5699	S	2451.2514	1226.1294	2434.2249	1217.6161	2433.2409	1217.1241	22
4	471.2020	236.1047			453.1915	227.0994	H	2364.2194	1182.6133	2347.1929	1174.1001	2346.2088	1173.6081	21
5	608.2609	304.6341			590.2504	295.6288	H	2227.1605	1114.0839	2210.1339	1105.5706	2209.1499	1105.0786	20
6	723.2879	362.1476	706.2613	353.6343	705.2773	353.1423	N	2090.1016	1045.5544	2073.0750	1037.0412	2072.0910	1036.5491	19
7	**836.3719**	418.6896	819.3454	410.1763	818.3614	409.6843	L	1975.0746	988.0410	1958.0481	979.5277	1957.0641	979.0357	18
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	1861.9906	931.4989	1844.9640	922.9857	1843.9800	922.4936	17
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	1760.9429	880.9751	1743.9163	872.4618	1742.9323	871.9698	16
10	1095.4888	548.2480	1078.4622	539.7347	1077.4782	539.2427	G	**1659.8952**	830.4512	1642.8687	821.9380	1641.8847	821.4460	15
11	1166.5259	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	**1602.8738**	801.9405	1585.8472	793.4272	1584.8632	792.9352	14
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	**1531.8366**	766.4220	1514.8101	757.9087	1513.8261	757.4167	13
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	**1430.7890**	715.8981	1413.7624	707.3848	1412.7784	706.8928	12
14	**1493.7417**	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	**1317.7049**	659.3561	1300.6783	650.8428	1299.6943	650.3508	11
15	**1607.7846**	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	**1204.6208**	602.8141	1187.5943	594.3008	1186.6103	593.8088	10
16	1736.8272	***868.9172***	1719.8007	860.4040	1718.8166	859.9120	E	**1090.5779**	545.7926	1073.5514	537.2793	1072.5673	536.7873	9
17	**1865.8698**	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	Q	961.5353	481.2713	944.5088	472.7580	943.5247	472.2660	8
18	2051.9491	***1026.4782***	2034.9226	1017.9649	2033.9386	1017.4729	W	**832.4927**	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2165.0332	***1083.0202***	2148.0066	1074.5070	2147.0226	1074.0149	L	**646.4134**	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	**533.3293**	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2379.1649	***1190.0861***	2362.1384	1181.5728	2361.1544	1181.0808	T	**420.2453**	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2480.2126	***1240.6099***	2463.1861	1232.0967	2462.2020	1231.6047	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3

23	2551.2497	***1276.1285***	2534.2232	1267.6152	2533.2392	1267.1232	**A**	218.1499	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.5	2696.3479	0.0097	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, Q17 53.32%
48.8	2696.3479	0.0097	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, N15 44.86%
46.1	2695.3639	0.9937	MVSHHNLTTGATLINEQWLLTTAK	
35.5	2695.3639	0.9937	MVSHHNLTTGATLINEQWLLTTAK	
34.9	2696.3479	0.0097	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N15, Q17 1.82%
34.8	2695.3639	0.9937	MVSHHNLTTGATLINEQWLLTTAK	
15.3	2695.3606	0.9971	SDDVNLAIYPDLLFTQPRPGVAHR	
8.6	2695.3680	0.9897	VGSLIFHTIGQLLPQQMQAFHSPK	
7.3	2696.3545	0.0032	FDVVDGEGNRLIDKSFSISILEDK	
7.3	2695.3680	0.9897	VGSLIFHTIGQLLPQQMQAFHSPK	

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

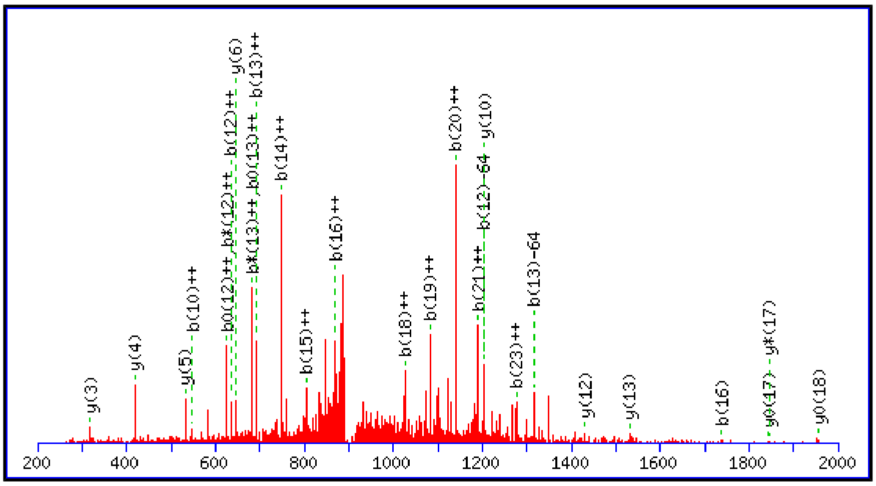
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 25267: 2696.355522 from(899.792450,3+) intensity(12110.0156) rtinseconds(3018) scans(8193) index(24244)
Title: 111019_Est_MI_YS_G_05Spectrum7135_scans__8193
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

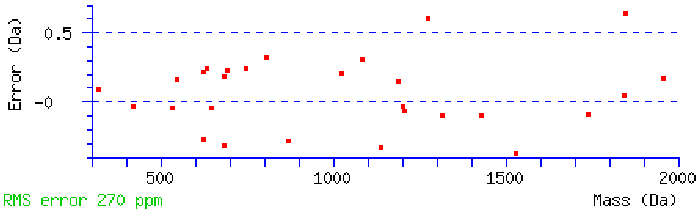
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

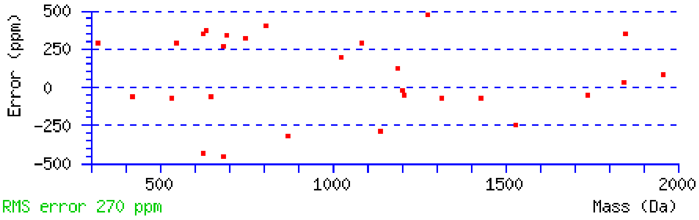


Monoisotopic mass of neutral peptide Mr(calc): 2696.3479
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N15 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0048
Matches : 28/382 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0427	74.5250					M							24
2	247.1111	124.0592					V	2550.3198	1275.6636	2533.2933	1267.1503	2532.3093	1266.6583	23
3	334.1431	167.5752			316.1326	158.5699	S	2451.2514	1226.1294	2434.2249	1217.6161	2433.2409	1217.1241	22
4	471.2020	236.1047			453.1915	227.0994	H	2364.2194	1182.6133	2347.1929	1174.1001	2346.2088	1173.6081	21
5	608.2609	304.6341			590.2504	295.6288	H	2227.1605	1114.0839	2210.1339	1105.5706	2209.1499	1105.0786	20
6	723.2879	362.1476	706.2613	353.6343	705.2773	353.1423	N	2090.1016	1045.5544	2073.0750	1037.0412	2072.0910	1036.5491	19
7	836.3719	418.6896	819.3454	410.1763	818.3614	409.6843	L	1975.0746	988.0410	1958.0481	979.5277	1957.0641	979.0357	18
8	937.4196	469.2135	920.3931	460.7002	919.4091	460.2082	T	1861.9906	931.4989	1844.9640	922.9857	1843.9800	922.4936	17
9	1038.4673	519.7373	1021.4408	511.2240	1020.4567	510.7320	T	1760.9429	880.9751	1743.9163	872.4618	1742.9323	871.9698	16
10	1095.4888	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	1659.8952	830.4512	1642.8687	821.9380	1641.8847	821.4460	15
11	1166.5259	583.7666	1149.4993	575.2533	1148.5153	574.7613	A	1602.8738	801.9405	1585.8472	793.4272	1584.8632	792.9352	14
12	1267.5736	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	**1531.8366**	766.4220	1514.8101	757.9087	1513.8261	757.4167	13
13	1380.6576	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	**1430.7890**	715.8981	1413.7624	707.3848	1412.7784	706.8928	12
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	11
15	1608.7686	***804.8880***	1591.7421	796.3747	1590.7581	795.8827	N	**1204.6208**	602.8141	1187.5943	594.3008	1186.6103	593.8088	10
16	1737.8112	***869.4093***	1720.7847	860.8960	1719.8007	860.4040	E	1089.5939	545.3006	1072.5673	536.7873	1071.5833	536.2953	9
17	1865.8698	933.4385	1848.8433	924.9253	1847.8592	924.4333	Q	960.5513	480.7793	943.5247	472.2660	942.5407	471.7740	8
18	2051.9491	***1026.4782***	2034.9226	1017.9649	2033.9386	1017.4729	W	832.4927	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2165.0332	***1083.0202***	2148.0066	1074.5070	2147.0226	1074.0149	L	**646.4134**	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	**533.3293**	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2379.1649	***1190.0861***	2362.1384	1181.5728	2361.1544	1181.0808	T	**420.2453**	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3

23	2551.2497	***1276.1285***	2534.2232	1267.6152	2533.2392	1267.1232	**A**	218.1499	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.4	2696.3479	0.0076	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, N15 87.44%
37.9	2696.3479	0.0076	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, Q17 9.95%
32.1	2696.3479	0.0076	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N15, Q17 2.62%
30.4	2695.3639	0.9916	MVSHHNLTTGATLINEQWLLTTAK	
27.7	2695.3639	0.9916	MVSHHNLTTGATLINEQWLLTTAK	
27.7	2695.3639	0.9916	MVSHHNLTTGATLINEQWLLTTAK	
13.8	2695.3606	0.9950	SDDVNLAIYPDLLFTQPRPGVAHR	
6.9	2694.3361	2.0194	VYASDSSQTRGFNPVSVRPLDKNR	
6.1	2694.3356	2.0199	EMAINDCSKAIQLNPSYIRAILR	
5.0	2695.3387	1.0168	GLMIYTLDHRNLNLANHLQDQAK	

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

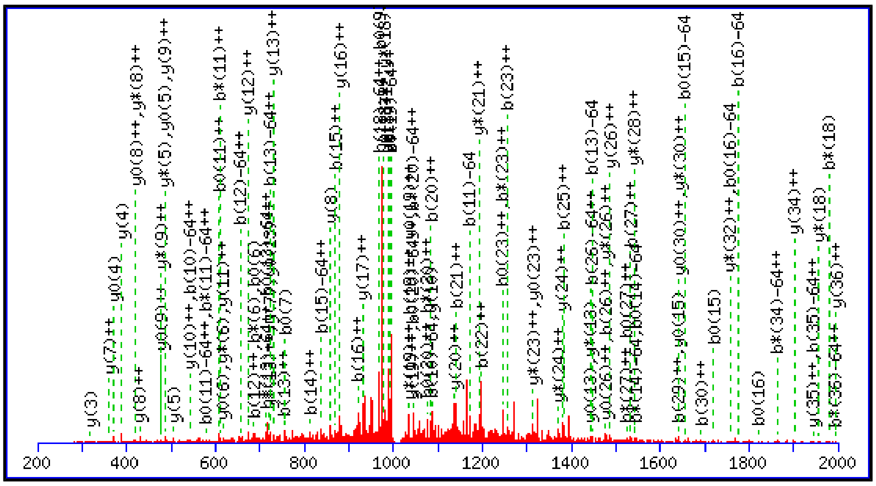
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 29002: 5039.522620 from(1008.911800,5+) intensity(0.0000) rtinseconds(2553) scans(6701) index(24867)
Title: 111019_Est_MI_YS_G_06Spectrum5844_scans__6701
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

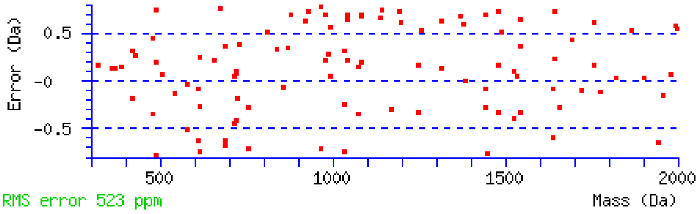
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

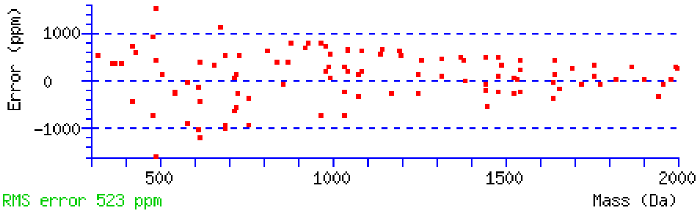


Monoisotopic mass of neutral peptide Mr(calc): 5037.5083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N41 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0024
Matches : 107/776 fragment ions using 173 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							45
2	145.0608	73.0340			127.0502	64.0287	S	4981.4941	2491.2507	4964.4676	2482.7374	4963.4836	2482.2454	44
3	292.1292	146.5682			274.1186	137.5629	F	4894.4621	2447.7347	4877.4356	2439.2214	4876.4516	2438.7294	43
4	389.1819	195.0946			371.1714	186.0893	P	4747.3937	2374.2005	4730.3672	2365.6872	4729.3831	2365.1952	42
5	575.2613	288.1343			557.2507	279.1290	W	4650.3409	2325.6741	4633.3144	2317.1608	4632.3304	2316.6688	41
6	704.3039	352.6556	687.2773	344.1423	686.2933	343.6503	Q	4464.2616	2232.6345	4447.2351	2224.1212	4446.2511	2223.6292	40
7	775.3410	388.1741	758.3144	379.6608	757.3304	379.1688	A	4335.2190	2168.1132	4318.1925	2159.5999	4317.2085	2159.1079	39
8	903.4359	452.2216	886.4094	443.7083	885.4254	443.2163	K	4264.1819	2132.5946	4247.1554	2124.0813	4246.1714	2123.5893	38
9	1050.4713	525.7393	1033.4448	517.2260	1032.4608	516.7340	M	4136.0870	2068.5471	4119.0604	2060.0338	4118.0764	2059.5418	37
10	1149.5397	575.2735	1132.5132	566.7602	1131.5292	566.2682	V	3989.0516	1995.0294	3972.0250	1986.5161	3971.0410	1986.0241	36
11	1236.5718	618.7895	1219.5452	610.2762	1218.5612	609.7842	S	3889.9831	1945.4952	3872.9566	1936.9819	3871.9726	1936.4899	35
12	1373.6307	***687.3190***	1356.6041	678.8057	1355.6201	678.3137	H	3802.9511	1901.9792	3785.9246	1893.4659	3784.9406	1892.9739	34
13	1510.6896	***755.8484***	1493.6630	747.3352	1492.6790	746.8432	H	3665.8922	1833.4497	3648.8657	1824.9365	3647.8816	1824.4445	33
14	1624.7325	***812.8699***	1607.7060	804.3566	1606.7220	803.8646	N	3528.8333	1764.9203	3511.8067	1756.4070	3510.8227	1755.9150	32
15	1737.8166	***869.4119***	1720.7900	860.8987	1719.8060	860.4066	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
16	1838.8643	***919.9358***	1821.8377	911.4225	1820.8537	910.9305	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
17	1939.9119	970.4596	1922.8854	961.9463	1921.9014	961.4543	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
18	1996.9334	998.9703	1979.9069	990.4571	1978.9228	989.9651	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
19	2067.9705	***1034.4889***	2050.9440	1025.9756	2049.9600	1025.4836	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
20	2169.0182	***1085.0127***	2151.9917	1076.4995	2151.0076	1076.0075	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
21	2282.1023	***1141.5548***	2265.0757	1133.0415	2264.0917	1132.5495	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
22	2395.1863	***1198.0968***	2378.1598	1189.5835	2377.1758	1189.0915	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24

23	2509.2293	***1255.1183***	2492.2027	1246.6050	2491.2187	1246.1130	**N**	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	**23**
24	2638.2719	1319.6396	2621.2453	1311.1263	2620.2613	1310.6343	**E**	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	**22**
25	2766.3304	***1383.6689***	2749.3039	1375.1556	2748.3199	1374.6636	**Q**	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	**21**
26	2952.4097	***1476.7085***	2935.3832	1468.1952	2934.3992	1467.7032	**W**	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	**20**
27	3065.4938	***1533.2505***	3048.4673	1524.7373	3047.4832	1524.2453	**L**	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	**19**
28	3178.5779	1589.7926	3161.5513	1581.2793	3160.5673	1580.7873	**L**	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	**18**
29	3279.6255	***1640.3164***	3262.5990	1631.8031	3261.6150	1631.3111	**T**	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	**17**
30	3380.6732	***1690.8403***	3363.6467	1682.3270	3362.6627	1681.8350	**T**	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	**16**
31	3451.7103	1726.3588	3434.6838	1717.8455	3433.6998	1717.3535	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
32	3579.8053	1790.4063	3562.7788	1781.8930	3561.7947	1781.4010	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
33	3693.8482	1847.4278	3676.8217	1838.9145	3675.8377	1838.4225	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
34	3806.9323	1903.9698	3789.9057	1895.4565	3788.9217	1894.9645	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
35	3954.0007	1977.5040	3936.9742	1968.9907	3935.9901	1968.4987	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
36	4067.0848	2034.0460	4050.0582	2025.5328	4049.0742	2025.0407	**L**	**1085.5222**	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
37	4181.1277	2091.0675	4164.1012	2082.5542	4163.1171	2082.0622	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
38	4318.1866	2159.5969	4301.1601	2151.0837	4300.1760	2150.5917	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
39	4405.2186	2203.1130	4388.1921	2194.5997	4387.2081	2194.1077	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
40	4534.2612	2267.6343	4517.2347	2259.1210	4516.2507	2258.6290	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
41	4649.2882	2325.1477	4632.2616	2316.6345	4631.2776	2316.1424	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
42	4720.3253	2360.6663	4703.2987	2352.1530	4702.3147	2351.6610	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
43	4821.3730	2411.1901	4804.3464	2402.6768	4803.3624	2402.1848	**T**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
44	4892.4101	2446.7087	4875.3835	2438.1954	4874.3995	2437.7034	**A**	218.1499	109.5786	201.1234	101.0653			**2**
45							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.3	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N41 89.69%
37.7	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N37, N41 9.86%
20.3	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N33, N37 0.18%
16.0	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q6, N14 0.07%
12.2	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q25, N33 0.03%
12.2	5037.5083	2.0143	GSFPWQAKMVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N14, N23 0.03%
11.6	5039.5186	0.0041	NQLAMDLPTEGKVNQIDLSSGAELLKDVANVNGAAVAWHLPTNQHIK	
9.4	5037.4958	2.0268	LLYGNDAKVLEQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGVK	
9.0	5037.4958	2.0268	LLYGNDAKVLEQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGVK	
9.0	5037.4958	2.0268	LLYGNDAKVLEQPVVVQSVGTDGRVFHFLVFQLNTTDLDCNEGVK	

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

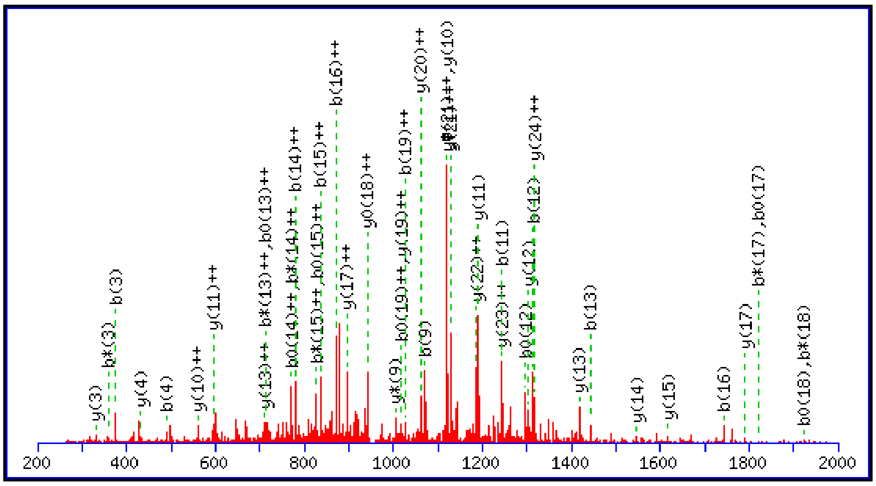
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25892: 2859.512082 from(954.177970,3+) intensity(26360.4766) rtinseconds(1735) scans(4113) index(11836)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum3520_scans__4113
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

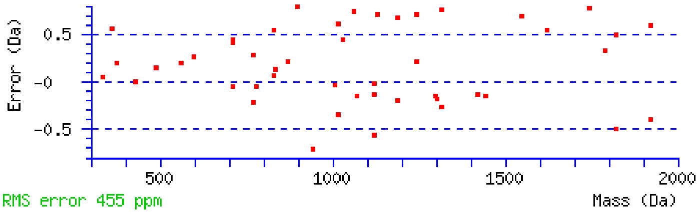
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

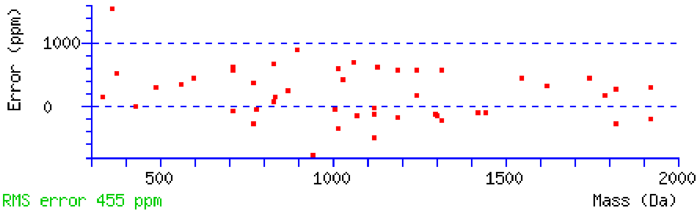


Monoisotopic mass of neutral peptide Mr(calc): 2859.5018
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0027
Matches : 47/276 fragment ions using 86 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	99.0077	50.0075			N							26
2	229.1183	115.0628	212.0917	106.5495			L	2745.4822	1373.2447	2728.4556	1364.7314	2727.4716	1364.2394	25
3	**376.1867**	188.5970	359.1601	180.0837			F	2632.3981	1316.7027	2615.3715	1308.1894	2614.3875	1307.6974	24
4	**489.2708**	245.1390	472.2442	236.6257			L	2485.3297	1243.1685	2468.3031	1234.6552	2467.3191	1234.1632	23
5	604.2977	302.6525	587.2712	294.1392			N	2372.2456	1186.6264	2355.2191	1178.1132	2354.2351	1177.6212	22
6	741.3566	371.1819	724.3301	362.6687			H	2257.2187	1129.1130	2240.1921	1120.5997	2239.2081	1120.1077	21
7	828.3886	414.6980	811.3621	406.1847	810.3781	405.6927	S	2120.1598	1060.5835	2103.1332	1052.0702	2102.1492	1051.5782	20
8	957.4312	479.2193	940.4047	470.7060	939.4207	470.2140	E	2033.1277	1017.0675	2016.1012	1008.5542	2015.1172	1008.0622	19
9	**1071.4742**	536.2407	1054.4476	527.7274	1053.4636	527.2354	N	1904.0851	952.5462	1887.0586	944.0329	1886.0746	943.5409	18
10	1142.5113	571.7593	1125.4847	563.2460	1124.5007	562.7540	A	***1790.0422***	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	**1243.5590**	622.2831	1226.5324	613.7698	1225.5484	613.2778	T	1719.0051	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	**1314.5961**	657.8017	1297.5695	649.2884	1296.5855	648.7964	A	***1617.9574***	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	**1442.6910**	721.8492	1425.6645	713.3359	1424.6805	712.8439	K	***1546.9203***	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	1557.7180	**779.3626**	1540.6914	770.8494	1539.7074	770.3573	D	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	1670.8020	**835.9047**	1653.7755	827.3914	1652.7915	826.8994	I	***1303.7984***	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	**1741.8392**	**871.4232**	1724.8126	862.9099	1723.8286	862.4179	A	***1190.7143***	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	1838.8919	919.9496	1821.8654	911.4363	1820.8814	910.9443	P	***1119.6772***	560.3422	1102.6507	551.8290	1101.6667	551.3370	10
18	1939.9396	970.4734	1922.9130	961.9602	1921.9290	961.4682	T	1022.6245	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2053.0237	**1027.0155**	2035.9971	1018.5022	2035.0131	1018.0102	L	921.5768	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2154.0713	1077.5393	2137.0448	1069.0260	2136.0608	1068.5340	T	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2267.1554	1134.0813	2250.1289	1125.5681	2249.1448	1125.0761	L	707.4450	354.2262	690.4185	345.7129			6
22	2430.2187	1215.6130	2413.1922	1207.0997	2412.2082	1206.6077	Y	594.3610	297.6841	577.3344	289.1709			5

23	2529.2871	1265.1472	2512.2606	1256.6339	2511.2766	1256.1419	**V**	***431.2976***	216.1525	414.2711	207.6392			**4**
24	2586.3086	1293.6579	2569.2821	1285.1447	2568.2980	1284.6527	**G**	***332.2292***	166.6183	315.2027	158.1050			**3**
25	2714.4036	1357.7054	2697.3770	1349.1922	2696.3930	1348.7001	**K**	275.2078	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.9	2859.5018	0.0103	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N5 35.49%
46.9	2859.5018	0.0103	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N1, N9 35.40%
46.0	2859.5018	0.0103	NLFLNHSENATAKDIAPTLTLYVGKK	Deamidated N5, N9 29.11%
35.9	2858.5178	0.9943	NLFLNHSENATAKDIAPTLTLYVGKK	
33.6	2858.5178	0.9943	NLFLNHSENATAKDIAPTLTLYVGKK	
30.1	2858.5178	0.9943	NLFLNHSENATAKDIAPTLTLYVGKK	
3.7	2858.5139	0.9982	EELLNFTLVQLVYLQHAMETKIPK	
3.2	2859.5243	-0.0122	EYLVRVHVPPNIAGTDEPRDITVLR	
1.8	2857.5007	2.0114	DAGTIAGLNVMRIINEPTAAAIAYGLDK	
1.3	2857.4935	2.0186	EELLNFTLVQLVYLQHAMETKIPQ	

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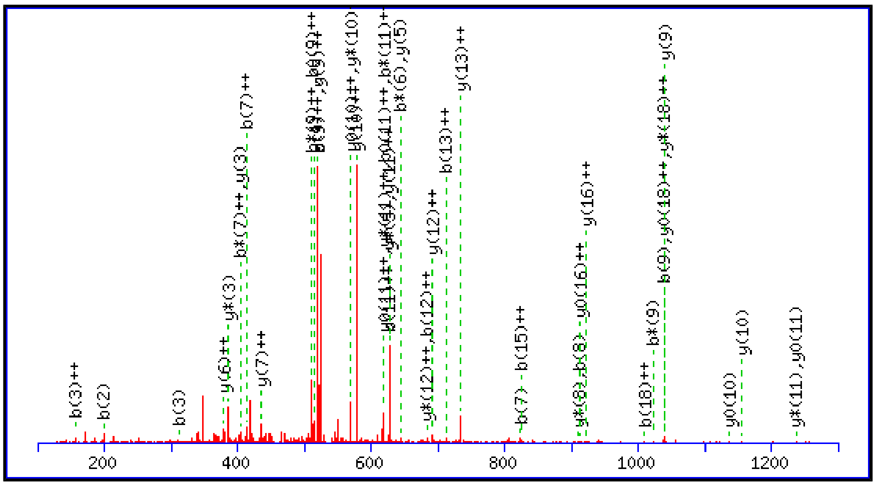
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVLHPNYSQVDIGLIKLKQK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

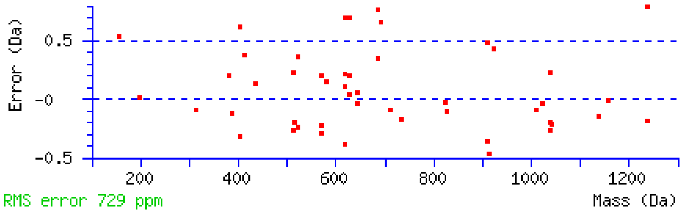
Match to Query 15127: 2292.323420 from(459.471960,5+) intensity(25380.3047) rtinseconds(1419) scans(3652) index(4361)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3104_scans__3652
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

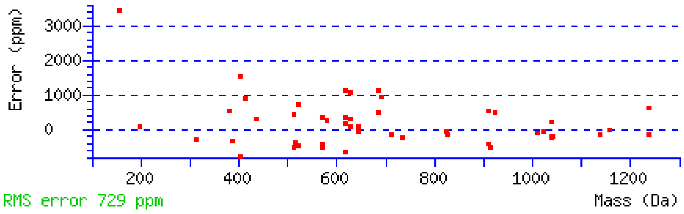
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2292.3205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.00029
Matches : 48/186 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	100.0757	50.5415					**V**							**20**
2	**199.1441**	100.0757					**V**	2194.2594	1097.6333	2177.2329	1089.1201	2176.2489	1088.6281	**19**
3	**312.2282**	***156.6177***					**L**	2095.1910	1048.0991	2078.1645	1039.5859	2077.1804	1039.0939	**18**
4	449.2871	225.1472					**H**	1982.1069	991.5571	1965.0804	983.0438	1964.0964	982.5518	**17**
5	546.3398	273.6736					**P**	1845.0480	923.0277	1828.0215	914.5144	1827.0375	914.0224	**16**
6	661.3668	331.1870	644.3402	322.6738			**N**	1747.9953	874.5013	1730.9687	865.9880	1729.9847	865.4960	**15**
7	**824.4301**	***412.7187***	807.4036	404.2054			**Y**	1632.9683	816.9878	1615.9418	808.4745	1614.9578	807.9825	**14**
8	**911.4621**	456.2347	894.4356	447.7214	893.4516	447.2294	**S**	1469.9050	735.4561	1452.8784	726.9429	1451.8944	726.4509	**13**
9	**1039.5207**	***520.2640***	1022.4942	511.7507	1021.5102	511.2587	**Q**	1382.8730	691.9401	1365.8464	683.4268	1364.8624	682.9348	**12**
10	1138.5891	***569.7982***	1121.5626	561.2849	1120.5786	560.7929	**V**	1254.8144	627.9108	1237.7878	619.3976	1236.8038	618.9055	**11**
11	1253.6161	***627.3117***	1236.5895	618.7984	1235.6055	618.3064	**D**	**1155.7460**	578.3766	1138.7194	569.8633	1137.7354	569.3713	**10**
12	1366.7001	***683.8537***	1349.6736	675.3404	1348.6896	674.8484	**I**	**1040.7190**	520.8632	1023.6925	512.3499			**9**
13	1423.7216	***712.3644***	1406.6951	703.8512	1405.7110	703.3592	**G**	927.6350	464.3211	910.6084	455.8078			**8**
14	1536.8057	768.9065	1519.7791	760.3932	1518.7951	759.9012	**L**	870.6135	435.8104	853.5870	427.2971			**7**
15	1649.8897	***825.4485***	1632.8632	816.9352	1631.8792	816.4432	**I**	757.5294	379.2684	740.5029	370.7551			**6**
16	1777.9847	889.4960	1760.9581	880.9827	1759.9741	880.4907	**K**	**644.4454**	322.7263	627.4188	314.2130			**5**
17	1891.0688	946.0380	1874.0422	937.5247	1873.0582	937.0327	**L**	**516.3504**	258.6788	499.3239	250.1656			**4**
18	2019.1637	***1010.0855***	2002.1372	1001.5722	2001.1532	1001.0802	**K**	**403.2663**	202.1368	386.2398	193.6235			**3**
19	2147.2223	1074.1148	2130.1958	1065.6015	2129.2117	1065.1095	**Q**	275.1714	138.0893	258.1448	129.5761			**2**
20							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.3	2292.3205	0.0029	VVLHPNYSQVDIGLIKLKQK	Deamidated N6 65.41%
43.2	2292.3205	0.0029	VVLHPNYSQVDIGLIKLKQK	Deamidated Q9 31.53%
33.0	2292.3205	0.0029	VVLHPNYSQVDIGLIKLKQK	Deamidated Q19 3.06%
12.1	2291.3213	1.0022	VAITVKQQVAPLQANEVTLLR	
12.1	2291.3213	1.0022	VAITVKQQVAPLQANEVTLLR	
0.8	2291.3187	1.0047	VSMEVAAAKGLPVLKYHLLPR	
0.5	2291.3226	1.0008	RVADQGVWLQRLLELNLLR	

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

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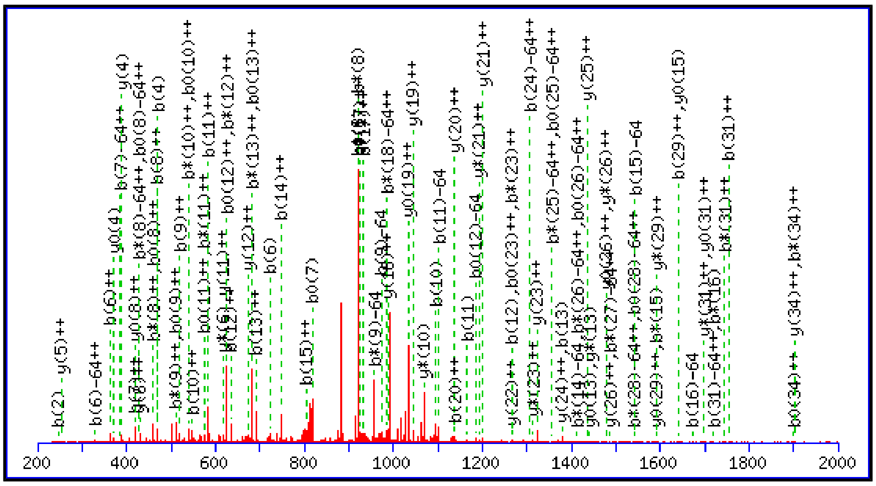
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28754: 4137.061570 from(828.419590,5+) intensity(163084.5469) rtinseconds(2534) scans(6661) index(22805)
Title: 111019_Est_MI_YS_G_03Spectrum5840_scans__6661
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

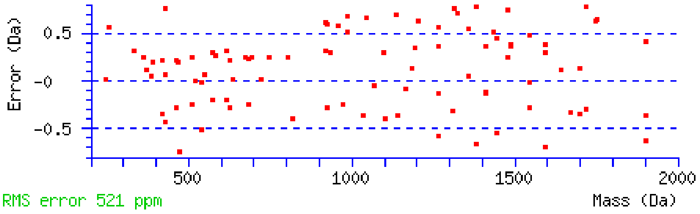
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

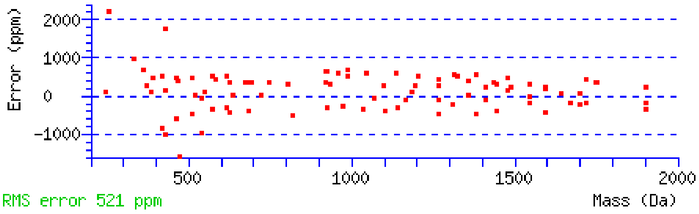


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N29 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.011
Matches : 97/616 fragment ions using 175 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	**247.1111**	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	**471.2020**	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	608.2609	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	836.3719	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1038.4673	***519.7373***	1021.4408	511.2240	1020.4567	510.7320	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	**1095.4888**	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1607.7846	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1736.8272	868.9172	1719.8007	860.4040	1718.8166	859.9120	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1864.8858	***932.9465***	1847.8592	924.4333	1846.8752	923.9413	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2050.9651	1025.9862	2033.9386	1017.4729	2032.9545	1016.9809	W	2273.1925	1137.0999	2256.1659	1128.5866	2255.1819	1128.0946	20
19	2164.0492	1082.5282	2147.0226	1074.0149	2146.0386	1073.5229	L	2087.1131	1044.0602	2070.0866	1035.5469	2069.1026	1035.0549	19
20	2277.1332	***1139.0703***	2260.1067	1130.5570	2259.1227	1130.0650	L	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	18
21	2378.1809	1189.5941	2361.1544	1181.0808	2360.1703	1180.5888	T	1860.9450	930.9761	1843.9185	922.4629	1842.9345	921.9709	17
22	2479.2286	1240.1179	2462.2020	1231.6047	2461.2180	1231.1126	T	1759.8973	880.4523	1742.8708	871.9390	1741.8868	871.4470	16

23	2550.2657	1275.6365	2533.2392	1267.1232	2532.2551	1266.6312	**A**	1658.8497	829.9285	1641.8231	821.4152	1640.8391	820.9232	**15**
24	2678.3607	1339.6840	2661.3341	1331.1707	2660.3501	1330.6787	**K**	1587.8125	794.4099	1570.7860	785.8966	1569.8020	785.4046	**14**
25	2792.4036	1396.7054	2775.3770	1388.1922	2774.3930	1387.7002	**N**	1459.7176	730.3624	1442.6910	721.8492	1441.7070	721.3571	**13**
26	2905.4877	1453.2475	2888.4611	1444.7342	2887.4771	1444.2422	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3052.5561	1526.7817	3035.5295	1518.2684	3034.5455	1517.7764	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3165.6401	1583.3237	3148.6136	1574.8104	3147.6296	1574.3184	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3280.6671	***1640.8372***	3263.6405	1632.3239	3262.6565	1631.8319	**N**	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3417.7260	1709.3666	3400.6994	1700.8534	3399.7154	1700.3614	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3504.7580	***1752.8826***	3487.7315	1744.3694	3486.7475	1743.8774	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3818.8807	1909.9440	3801.8541	1901.4307	3800.8701	1900.9387	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	1995.9864	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.7	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 36.27%
42.7	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 36.27%
40.1	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 20.12%
39.3	4137.0477	0.0139	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
38.8	4137.0477	0.0139	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
36.2	4137.0477	0.0139	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
31.8	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 2.95%
27.9	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15 1.21%
22.9	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N29, N33 0.38%
22.9	4136.0636	0.9979	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N33 0.38%

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

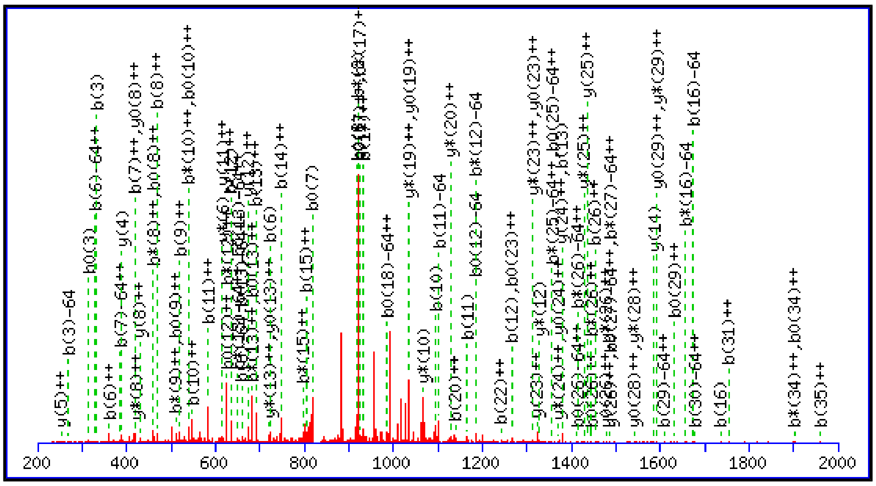
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28711: 4137.058270 from(828.418930,5+) intensity(717329.0000) rtinseconds(2574) scans(6723) index(25641)
Title: 111019_Est_MI_YS_G_07Spectrum5791_scans__6723
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

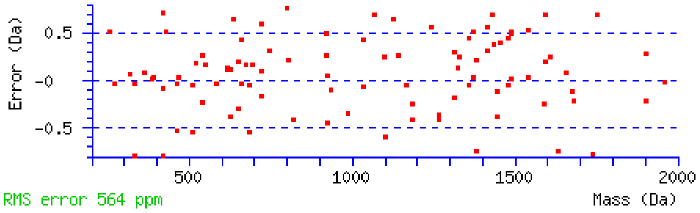
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

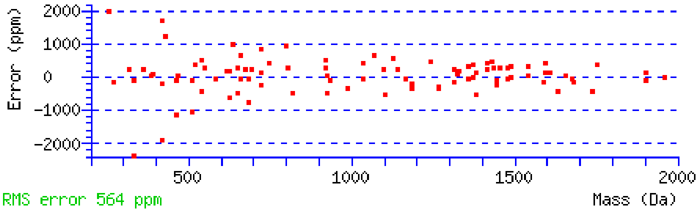


Monoisotopic mass of neutral peptide Mr(calc): 4137.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
N15 : Deamidated (NQ)
Q17 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.012
Matches : 98/616 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	**334.1431**	167.5752			316.1326	158.5699	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	471.2020	236.1047			453.1915	227.0994	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	608.2609	304.6341			590.2504	295.6288	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	836.3719	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3415.7744	1708.3908	3398.7478	1699.8776	3397.7638	1699.3855	31
8	937.4196	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3302.6903	1651.8488	3285.6638	1643.3355	3284.6798	1642.8435	30
9	1038.4673	***519.7373***	1021.4408	511.2240	1020.4567	510.7320	T	3201.6426	1601.3250	3184.6161	1592.8117	3183.6321	1592.3197	29
10	**1095.4888**	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3100.5950	1550.8011	3083.5684	1542.2878	3082.5844	1541.7958	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3043.5735	1522.2904	3026.5469	1513.7771	3025.5629	1513.2851	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2972.5364	1486.7718	2955.5098	1478.2586	2954.5258	1477.7665	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2871.4887	1436.2480	2854.4622	1427.7347	2853.4781	1427.2427	25
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2758.4046	1379.7060	2741.3781	1371.1927	2740.3941	1370.7007	24
15	1608.7686	***804.8880***	1591.7421	796.3747	1590.7581	795.8827	N	2645.3206	1323.1639	2628.2940	1314.6507	2627.3100	1314.1586	23
16	**1737.8112**	869.4093	1720.7847	860.8960	1719.8007	860.4040	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1866.8538	***933.9305***	1849.8273	925.4173	1848.8433	924.9253	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2052.9331	1026.9702	2035.9066	1018.4569	2034.9226	1017.9649	W	2272.2084	1136.6079	2255.1819	1128.0946	2254.1979	1127.6026	20
19	2166.0172	1083.5122	2148.9906	1074.9990	2148.0066	1074.5070	L	2086.1291	1043.5682	2069.1026	1035.0549	2068.1186	1034.5629	19
20	2279.1013	***1140.0543***	2262.0747	1131.5410	2261.0907	1131.0490	L	1973.0451	987.0262	1956.0185	978.5129	1955.0345	978.0209	18
21	2380.1489	1190.5781	2363.1224	1182.0648	2362.1384	1181.5728	T	1859.9610	930.4841	1842.9345	921.9709	1841.9504	921.4789	17

22	2481.1966	***1241.1019***	2464.1701	1232.5887	2463.1861	1232.0967	**T**	1758.9133	879.9603	1741.8868	871.4470	1740.9028	870.9550	**16**
23	2552.2337	1276.6205	2535.2072	1268.1072	2534.2232	1267.6152	**A**	1657.8656	829.4365	1640.8391	820.9232	1639.8551	820.4312	**15**
24	2680.3287	1340.6680	2663.3021	1332.1547	2662.3181	1331.6627	**K**	1586.8285	793.9179	1569.8020	785.4046	1568.8180	784.9126	**14**
25	2794.3716	1397.6895	2777.3451	1389.1762	2776.3611	1388.6842	**N**	1458.7336	729.8704	1441.7070	721.3571	1440.7230	720.8651	**13**
26	2907.4557	***1454.2315***	2890.4291	1445.7182	2889.4451	1445.2262	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3054.5241	1527.7657	3037.4976	1519.2524	3036.5135	1518.7604	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3167.6082	1584.3077	3150.5816	1575.7944	3149.5976	1575.3024	**L**	1084.5382	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3281.6511	1641.3292	3264.6245	1632.8159	3263.6405	1632.3239	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3505.7420	***1753.3747***	3488.7155	1744.8614	3487.7315	1744.3694	**S**	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3748.8276	1874.9174	3731.8010	1866.4041	3730.8170	1865.9121	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3819.8647	1910.4360	3802.8381	1901.9227	3801.8541	1901.4307	**A**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3920.9123	***1960.9598***	3903.8858	1952.4465	3902.9018	1951.9545	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3991.9495	1996.4784	3974.9229	1987.9651	3973.9389	1987.4731	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.6	4137.0477	0.0106	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17 48.55%
40.0	4137.0477	0.0106	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 26.25%
36.8	4137.0477	0.0106	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 12.71%
32.2	4137.0477	0.0106	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 4.39%
32.2	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
32.2	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
32.2	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
32.2	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
31.4	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
23.8	4136.0636	0.9946	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	

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

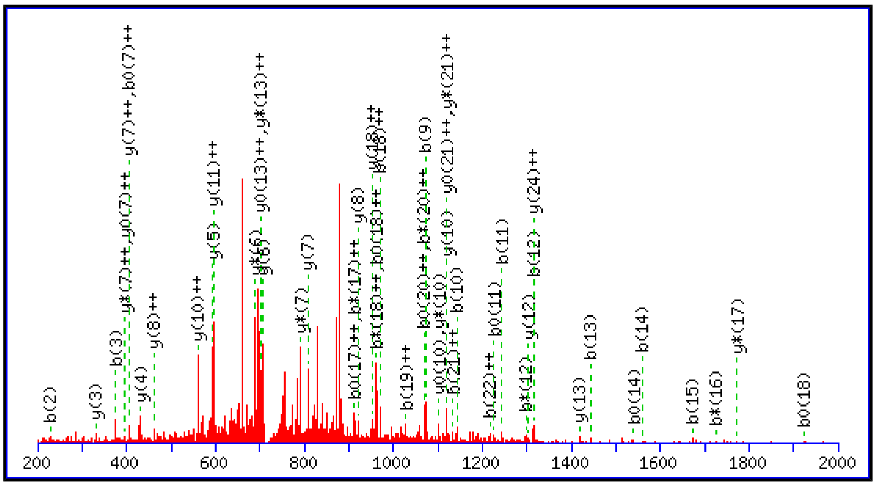
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NLFLNHSENATAKDIAPTLTLYVGKK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25980: 2860.499296 from(716.132100,4+) intensity(19247.6445) rtinseconds(1963) scans(5209) index(24079)
Title: 111019_Est_MI_YS_G_05Spectrum4501_scans__5209
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

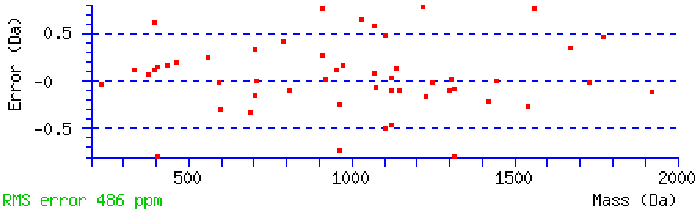
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

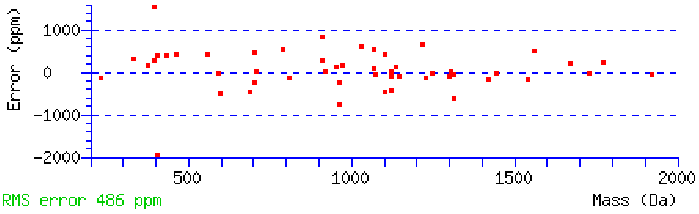


Monoisotopic mass of neutral peptide Mr(calc): 2860.4858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N5 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.0084
Matches : 51/276 fragment ions using 100 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	99.0077	50.0075			**N**							26
2	***229.1183***	115.0628	212.0917	106.5495			**L**	2746.4662	1373.7367	2729.4396	1365.2235	2728.4556	1364.7314	25
3	***376.1867***	188.5970	359.1601	180.0837			**F**	2633.3821	1317.1947	2616.3556	1308.6814	2615.3715	1308.1894	24
4	489.2708	245.1390	472.2442	236.6257			**L**	2486.3137	1243.6605	2469.2871	1235.1472	2468.3031	1234.6552	23
5	604.2977	302.6525	587.2712	294.1392			**N**	2373.2296	1187.1185	2356.2031	1178.6052	2355.2191	1178.1132	22
6	741.3566	371.1819	724.3301	362.6687			**H**	2258.2027	1129.6050	2241.1761	1121.0917	2240.1921	1120.5997	21
7	828.3886	414.6980	811.3621	406.1847	810.3781	405.6927	**S**	2121.1438	1061.0755	2104.1172	1052.5623	2103.1332	1052.0702	20
8	957.4312	479.2193	940.4047	470.7060	939.4207	470.2140	**E**	2034.1118	1017.5595	2017.0852	1009.0462	2016.1012	1008.5542	19
9	***1072.4582***	536.7327	1055.4316	528.2195	1054.4476	527.7274	**N**	1905.0692	953.0382	1888.0426	944.5249	1887.0586	944.0329	18
10	***1143.4953***	572.2513	1126.4687	563.7380	1125.4847	563.2460	**A**	1790.0422	895.5247	1773.0157	887.0115	1772.0316	886.5195	17
11	***1244.5430***	622.7751	1227.5164	614.2619	1226.5324	613.7698	**T**	1719.0051	860.0062	1701.9786	851.4929	1700.9945	851.0009	16
12	***1315.5801***	658.2937	1298.5535	649.7804	1297.5695	649.2884	**A**	1617.9574	809.4823	1600.9309	800.9691	1599.9469	800.4771	15
13	***1443.6751***	722.3412	1426.6485	713.8279	1425.6645	713.3359	**K**	1546.9203	773.9638	1529.8938	765.4505	1528.9097	764.9585	14
14	***1558.7020***	779.8546	1541.6754	771.3414	1540.6914	770.8494	**D**	***1418.8253***	709.9163	1401.7988	701.4030	1400.8148	700.9110	13
15	***1671.7861***	836.3967	1654.7595	827.8834	1653.7755	827.3914	**I**	***1303.7984***	652.4028	1286.7719	643.8896	1285.7878	643.3976	12
16	1742.8232	871.9152	1725.7966	863.4019	1724.8126	862.9099	**A**	1190.7143	595.8608	1173.6878	587.3475	1172.7038	586.8555	11
17	1839.8759	920.4416	1822.8494	911.9283	1821.8654	911.4363	**P**	***1119.6772***	560.3423	1102.6507	551.8290	1101.6667	551.3370	10
18	1940.9236	**970.9654**	1923.8971	962.4522	1922.9130	961.9602	**T**	1022.6245	511.8159	1005.5979	503.3026	1004.6139	502.8106	9
19	2054.0077	**1027.5075**	2036.9811	1018.9942	2035.9971	1018.5022	**L**	***921.5768***	461.2920	904.5502	452.7788	903.5662	452.2867	8
20	2155.0554	1078.0313	2138.0288	1069.5180	2137.0448	1069.0260	**T**	***808.4927***	404.7500	791.4662	396.2367	790.4822	395.7447	7
21	2268.1394	**1134.5733**	2251.1129	1126.0601	2250.1289	1125.5681	**L**	***707.4450***	354.2262	690.4185	345.7129			6
22	2431.2027	**1216.1050**	2414.1762	1207.5917	2413.1922	1207.0997	**Y**	***594.3610***	297.6841	577.3344	289.1709			5

23	2530.2712	1265.6392	2513.2446	1257.1259	2512.2606	1256.6339	**V**	*431.2976*	216.1525	414.2711	207.6392			**4**
24	2587.2926	1294.1500	2570.2661	1285.6367	2569.2821	1285.1447	**G**	*332.2292*	166.6183	315.2027	158.1050			**3**
25	2715.3876	1358.1974	2698.3610	1349.6842	2697.3770	1349.1922	**K**	275.2078	138.1075	258.1812	129.5942			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
42.5	2860.4858	0.0135	NLFLNHSENATAKDIAPTLTLYVGKK
28.0	2859.5018	0.9975	NLFLNHSENATAKDIAPTLTLYVGKK
27.5	2859.5018	0.9975	NLFLNHSENATAKDIAPTLTLYVGKK
27.0	2859.5018	0.9975	NLFLNHSENATAKDIAPTLTLYVGKK
5.2	2859.4874	1.0119	GLPYEKGQVKVPPSVMLNGISDMSAVK
4.2	2858.4973	2.0020	HKPQAPVIVKTEEVINMHTFNDRR
4.2	2859.4874	1.0119	GLPYEKGQVKVPPSVMLNGISDMSAVK
2.2	2859.4814	1.0179	HKPQAPVIVKTEEVINMHTFNDRR
0.5	2858.4787	2.0206	ITGVGAVPLPASGNSFDVRPSQGYRRR

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

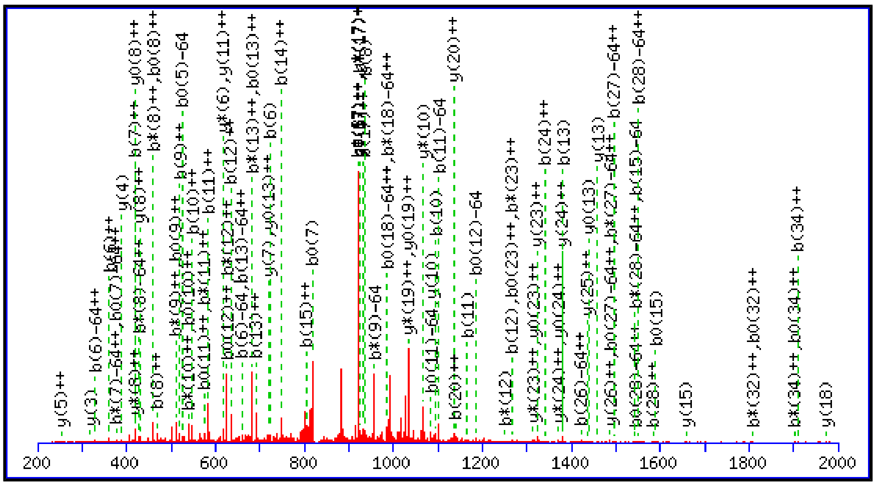
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28888: 4137.076420 from(828.422560,5+) intensity(42867.8242) rtinseconds(2513) scans(6540) index(2282)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum5692_scans__6540
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

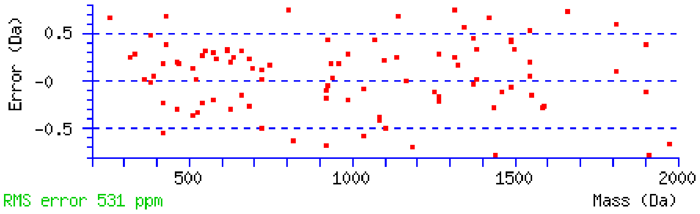
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

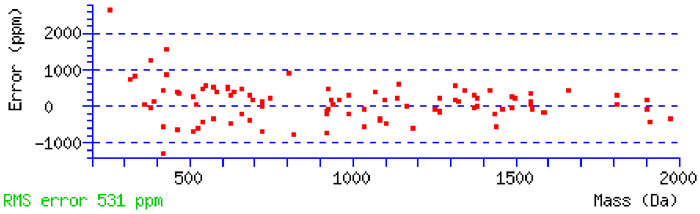


Monoisotopic mass of neutral peptide Mr(calc): 4136.0636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Q17 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.011
Matches : 95/616 fragment ions using 160 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3990.0356	1995.5214	3973.0090	1987.0081	3972.0250	1986.5161	36
3	334.1431	167.5752			316.1326	158.5699	S	3890.9672	1945.9872	3873.9406	1937.4739	3872.9566	1936.9819	35
4	471.2020	236.1047			453.1915	227.0994	H	3803.9351	1902.4712	3786.9086	1893.9579	3785.9246	1893.4659	34
5	608.2609	304.6341			590.2504	295.6288	H	3666.8762	1833.9417	3649.8497	1825.4285	3648.8657	1824.9365	33
6	**723.2879**	***362.1476***	706.2613	353.6343	705.2773	353.1423	N	3529.8173	1765.4123	3512.7908	1756.8990	3511.8067	1756.4070	32
7	836.3719	***418.6896***	819.3454	410.1763	818.3614	409.6843	L	3414.7904	1707.8988	3397.7638	1699.3855	3396.7798	1698.8935	31
8	**937.4196**	***469.2135***	920.3931	460.7002	919.4091	460.2082	T	3301.7063	1651.3568	3284.6798	1642.8435	3283.6957	1642.3515	30
9	1038.4673	***519.7373***	1021.4408	511.2240	1020.4567	510.7320	T	3200.6586	1600.8329	3183.6321	1592.3197	3182.6481	1591.8277	29
10	**1095.4888**	***548.2480***	1078.4622	539.7347	1077.4782	539.2427	G	3099.6109	1550.3091	3082.5844	1541.7958	3081.6004	1541.3038	28
11	**1166.5259**	***583.7666***	1149.4993	575.2533	1148.5153	574.7613	A	3042.5895	1521.7984	3025.5629	1513.2851	3024.5789	1512.7931	27
12	**1267.5736**	***634.2904***	1250.5470	625.7771	1249.5630	625.2851	T	2971.5524	1486.2798	2954.5258	1477.7665	2953.5418	1477.2745	26
13	**1380.6576**	***690.8325***	1363.6311	682.3192	1362.6471	681.8272	L	2870.5047	1435.7560	2853.4781	1427.2427	2852.4941	1426.7507	25
14	1493.7417	***747.3745***	1476.7151	738.8612	1475.7311	738.3692	I	2757.4206	1379.2139	2740.3941	1370.7007	2739.4101	1370.2087	24
15	1607.7846	***804.3959***	1590.7581	795.8827	1589.7741	795.3907	N	2644.3366	1322.6719	2627.3100	1314.1586	2626.3260	1313.6666	23
16	1736.8272	868.9172	1719.8007	860.4040	1718.8166	859.9120	E	2530.2936	1265.6505	2513.2671	1257.1372	2512.2831	1256.6452	22
17	1865.8698	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	Q	2401.2510	1201.1292	2384.2245	1192.6159	2383.2405	1192.1239	21
18	2051.9491	1026.4782	2034.9226	1017.9649	2033.9386	1017.4729	W	2272.2084	1136.6079	2255.1819	1128.0946	2254.1979	1127.6026	20
19	2165.0332	1083.0202	2148.0066	1074.5070	2147.0226	1074.0149	L	2086.1291	1043.5682	2069.1026	1035.0549	2068.1186	1034.5629	19
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	***1973.0451***	987.0262	1956.0185	978.5129	1955.0345	978.0209	18
21	2379.1649	1190.0861	2362.1384	1181.5728	2361.1544	1181.0808	T	1859.9610	930.4841	1842.9345	921.9709	1841.9504	921.4789	17
22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	T	1758.9133	879.9603	1741.8868	871.4470	1740.9028	870.9550	16

23	2551.2497	1276.1285	2534.2232	1267.6152	2533.2392	1267.1232	**A**	***1657.8656***	829.4365	1640.8391	820.9232	1639.8551	820.4312	**15**
24	2679.3447	***1340.1760***	2662.3181	1331.6627	2661.3341	1331.1707	**K**	1586.8285	793.9179	1569.8020	785.4046	1568.8180	784.9126	**14**
25	2793.3876	1397.1974	2776.3611	1388.6842	2775.3770	1388.1922	**N**	***1458.7336***	729.8704	1441.7070	721.3571	1440.7230	720.8651	**13**
26	2906.4717	1453.7395	2889.4451	1445.2262	2888.4611	1444.7342	**L**	1344.6906	672.8490	1327.6641	664.3357	1326.6801	663.8437	**12**
27	3053.5401	1527.2737	3036.5135	1518.7604	3035.5295	1518.2684	**F**	1231.6066	616.3069	1214.5800	607.7937	1213.5960	607.3016	**11**
28	3166.6242	***1583.8157***	3149.5976	1575.3024	3148.6136	1574.8104	**L**	***1084.5382***	542.7727	1067.5116	534.2594	1066.5276	533.7674	**10**
29	3280.6671	1640.8372	3263.6405	1632.3239	3262.6565	1631.8319	**N**	971.4541	486.2307	954.4275	477.7174	953.4435	477.2254	**9**
30	3417.7260	1709.3666	3400.6994	1700.8534	3399.7154	1700.3614	**H**	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	**8**
31	3504.7580	1752.8826	3487.7315	1744.3694	3486.7475	1743.8774	**S**	***720.3523***	360.6798	703.3257	352.1665	702.3417	351.6745	**7**
32	3633.8006	1817.4039	3616.7741	1808.8907	3615.7900	1808.3987	**E**	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	**6**
33	3747.8435	1874.4254	3730.8170	1865.9121	3729.8330	1865.4201	**N**	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	**5**
34	3818.8807	***1909.9440***	3801.8541	1901.4307	3800.8701	1900.9387	**A**	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3919.9283	1960.4678	3902.9018	1951.9545	3901.9178	1951.4625	**T**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3990.9654	1995.9864	3973.9389	1987.4731	3972.9549	1986.9811	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.5	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, Q17 25.36%
42.1	4135.0796	1.9968	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	
41.7	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29 21.39%
41.7	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N33 21.19%
40.8	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15 17.42%
38.6	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N25 10.38%
26.5	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N29 0.65%
26.3	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N29 0.61%
25.1	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, N33 0.47%
24.9	4136.0636	1.0128	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N33 0.44%

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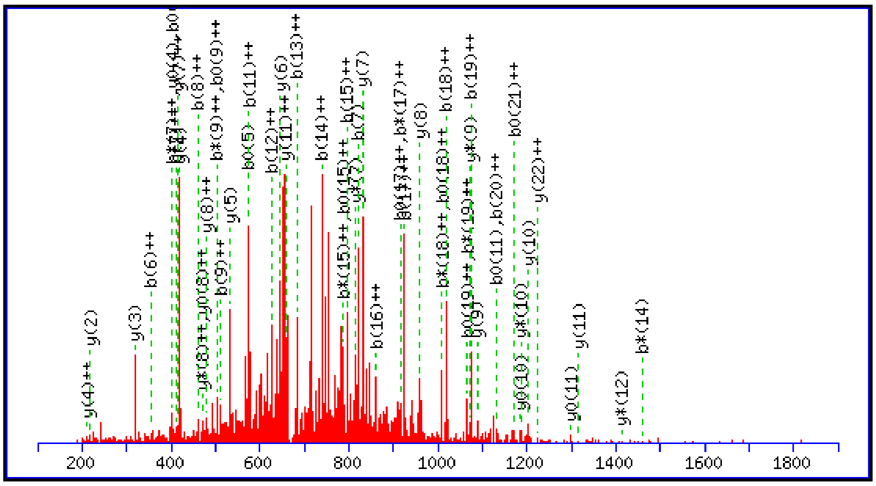
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 23773: 2680.359656 from(671.097190,4+) intensity(17023.2227) rtinseconds(2732) scans(6799) index(17105)
Title: 111019_Est_MI_YP_G_06Spectrum5698_scans__6799
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

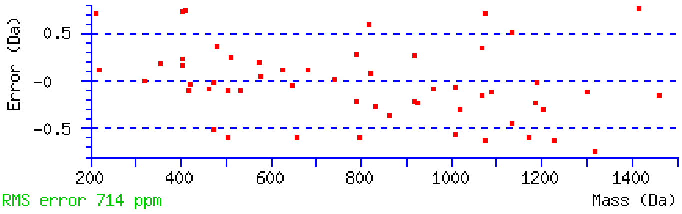
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

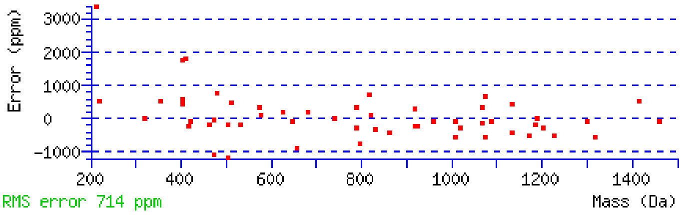


Monoisotopic mass of neutral peptide Mr(calc): 2680.3530
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N15 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.02
Matches : 55/258 fragment ions using 124 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							24
2	231.1162	116.0617					V	2550.3198	1275.6636	2533.2933	1267.1503	2532.3093	1266.6583	23
3	318.1482	159.5777			300.1376	150.5725	S	2451.2514	1226.1294	2434.2249	1217.6161	2433.2409	1217.1241	22
4	455.2071	228.1072			437.1966	219.1019	H	2364.2194	1182.6133	2347.1929	1174.1001	2346.2088	1173.6081	21
5	592.2660	296.6367			574.2555	287.6314	H	2227.1605	1114.0839	2210.1339	1105.5706	2209.1499	1105.0786	20
6	707.2930	***354.1501***	690.2664	345.6368	689.2824	345.1448	N	2090.1016	1045.5544	2073.0750	1037.0412	2072.0910	1036.5491	19
7	820.3770	***410.6922***	803.3505	402.1789	802.3665	401.6869	L	1975.0746	988.0410	1958.0481	979.5277	1957.0641	979.0357	18
8	921.4247	***461.2160***	904.3982	452.7027	903.4141	452.2107	T	1861.9906	931.4989	1844.9640	922.9857	1843.9800	922.4936	17
9	1022.4724	***511.7398***	1005.4458	503.2266	1004.4618	502.7346	T	1760.9429	880.9751	1743.9163	872.4618	1742.9323	871.9698	16
10	1079.4939	540.2506	1062.4673	531.7373	1061.4833	531.2453	G	1659.8952	830.4512	1642.8687	821.9380	1641.8847	821.4460	15
11	1150.5310	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	1602.8738	801.9405	1585.8472	793.4272	1584.8632	792.9352	14
12	1251.5786	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	T	1531.8366	766.4220	1514.8101	757.9087	1513.8261	757.4167	13
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	1430.7890	715.8981	1413.7624	707.3848	1412.7784	706.8928	12
14	1477.7468	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	**1317.7049**	659.3561	1300.6783	650.8428	1299.6943	650.3508	11
15	1592.7737	***796.8905***	1575.7472	788.3772	1574.7632	787.8852	N	**1204.6208**	602.8141	1187.5943	594.3008	1186.6103	593.8088	10
16	1721.8163	***861.4118***	1704.7898	852.8985	1703.8057	852.4065	E	**1089.5939**	545.3006	1072.5673	536.7873	1071.5833	536.2953	9
17	1849.8749	***925.4411***	1832.8483	916.9278	1831.8643	916.4358	Q	**960.5513**	480.7793	943.5247	472.2660	942.5407	471.7740	8
18	2035.9542	***1018.4807***	2018.9277	1009.9675	2017.9436	1009.4755	W	**832.4927**	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2149.0383	***1075.0228***	2132.0117	1066.5095	2131.0277	1066.0175	L	**646.4134**	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2262.1223	***1131.5648***	2245.0958	1123.0515	2244.1118	1122.5595	L	**533.3293**	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2363.1700	1182.0886	2346.1435	1173.5754	2345.1594	1173.0834	T	**420.2453**	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2464.2177	1232.6125	2447.1911	1224.0992	2446.2071	1223.6072	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3

23	2535.2548	1268.1310	2518.2283	1259.6178	2517.2442	1259.1258	**A**	**218.1499**	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.0	2680.3530	0.0066	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, N15 53.10%
40.0	2680.3530	0.0066	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N6, Q17 42.96%
36.9	2679.3690	0.9906	MVSHHNLTTGATLINEQWLLTTAK	
29.8	2679.3690	0.9906	MVSHHNLTTGATLINEQWLLTTAK	
29.7	2680.3530	0.0066	MVSHHNLTTGATLINEQWLLTTAK	Deamidated N15, Q17 3.95%
27.2	2679.3690	0.9906	MVSHHNLTTGATLINEQWLLTTAK	
17.0	2678.3446	2.0150	SVSNSLGVSGELAPCGRVSGQLVYSR	
9.6	2679.3676	0.9920	NILKMLFLESDGATEVSAALQGNKK	
7.6	2680.3642	-0.0046	FPASVPMGAQDLISKLLRHNPSER	
6.5	2680.3629	-0.0033	RLISMGLFATVGTQDLKAEELDEK	

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

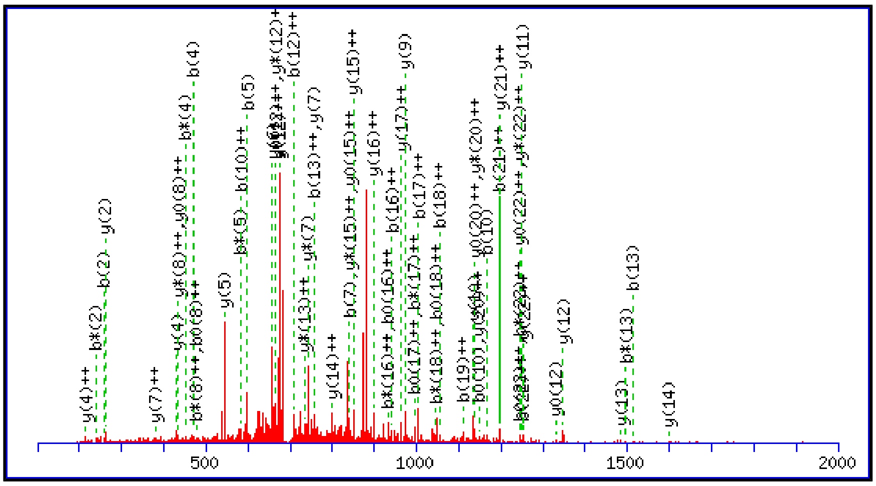
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQLVEIEKVVLHPNYSQVDIGLIK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 25468: 2764.553136 from(692.145560,4+) intensity(34915.6055) rtinseconds(1857) scans(4441) index(8971)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum3806_scans__4441
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

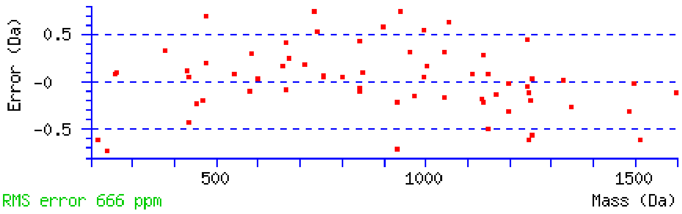
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

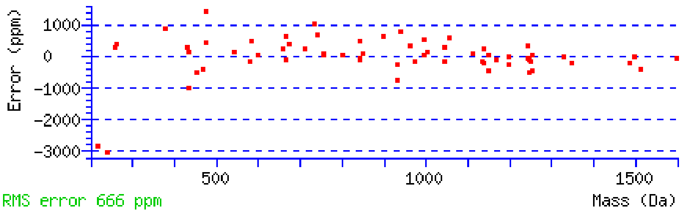


Monoisotopic mass of neutral peptide Mr(calc): 2762.5582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.0027
Matches : 64/258 fragment ions using 143 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							24
2	**257.1608**	129.0840	240.1343	120.5708			Q	2635.4705	1318.2389	2618.4440	1309.7256	2617.4600	1309.2336	23
3	370.2449	185.6261	353.2183	177.1128			L	2507.4120	1254.2096	2490.3854	1245.6963	2489.4014	1245.2043	22
4	**469.3133**	235.1603	452.2867	226.6470			V	2394.3279	1197.6676	2377.3013	1189.1543	2376.3173	1188.6623	21
5	**598.3559**	299.6816	581.3293	291.1683	580.3453	290.6763	E	2295.2595	1148.1334	2278.2329	1139.6201	2277.2489	1139.1281	20
6	711.4400	356.2236	694.4134	347.7103	693.4294	347.2183	I	2166.2169	1083.6121	2149.1903	1075.0988	2148.2063	1074.6068	19
7	**840.4825**	420.7449	823.4560	412.2316	822.4720	411.7396	E	2053.1328	1027.0700	2036.1063	1018.5568	2035.1223	1018.0648	18
8	968.5775	484.7924	951.5510	476.2791	950.5669	475.7871	K	1924.0902	962.5488	1907.0637	954.0355	1906.0797	953.5435	17
9	1067.6459	534.3266	1050.6194	525.8133	1049.6354	525.3213	V	1795.9953	898.5013	1778.9687	889.9880	1777.9847	889.4960	16
10	**1166.7143**	**583.8608**	1149.6878	575.3475	1148.7038	574.8555	V	1696.9268	848.9671	1679.9003	840.4538	1678.9163	839.9618	15
11	1279.7984	640.4028	1262.7719	631.8896	1261.7878	631.3976	L	***1597.8584***	799.4329	1580.8319	790.9196	1579.8479	790.4276	14
12	1416.8573	**708.9323**	1399.8308	700.4190	1398.8467	699.9270	H	***1484.7744***	742.8908	1467.7478	734.3775	1466.7638	733.8855	13
13	**1513.9101**	**757.4587**	1496.8835	748.9454	1495.8995	748.4534	P	***1347.7155***	674.3614	1330.6889	665.8481	1329.7049	665.3561	12
14	1628.9370	814.9721	1611.9105	806.4589	1610.9265	805.9669	N	***1250.6627***	625.8350	1233.6361	617.3217	1232.6521	616.8297	11
15	1792.0003	896.5038	1774.9738	887.9905	1773.9898	887.4985	Y	***1135.6358***	568.3215	1118.6092	559.8082	1117.6252	559.3162	10
16	1879.0324	**940.0198**	1862.0058	931.5066	1861.0218	931.0145	S	***972.5724***	486.7898	955.5459	478.2766	954.5619	477.7846	9
17	2007.0910	**1004.0491**	1990.0644	995.5358	1989.0804	995.0438	Q	885.5404	443.2738	868.5138	434.7606	867.5298	434.2686	8
18	2106.1594	**1053.5833**	2089.1328	1045.0700	2088.1488	1044.5780	V	***757.4818***	379.2445	740.4553	370.7313	739.4713	370.2393	7
19	2221.1863	**1111.0968**	2204.1598	1102.5835	2203.1757	1102.0915	D	***658.4134***	329.7103	641.3869	321.1971	640.4028	320.7051	6
20	2334.2704	1167.6388	2317.2438	1159.1256	2316.2598	1158.6335	I	***543.3865***	272.1969	526.3599	263.6836			5
21	2391.2918	**1196.1496**	2374.2653	1187.6363	2373.2813	1187.1443	G	***430.3024***	215.6548	413.2758	207.1416			4
22	2504.3759	**1252.6916**	2487.3494	1244.1783	2486.3653	1243.6863	L	373.2809	187.1441	356.2544	178.6308			3
23	2617.4600	1309.2336	2600.4334	1300.7203	2599.4494	1300.2283	I	***260.1969***	130.6021	243.1703	122.0888			2

24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.5	2762.5582	1.9950	KQLVEIEKVVLHPNYSQVDIGLIK	Deamidated N14 76.76%
33.5	2762.5582	1.9950	KQLVEIEKVVLHPNYSQVDIGLIK	Deamidated Q17 19.33%
31.1	2763.5422	1.0109	KQLVEIEKVVLHPNYSQVDIGLIK	
29.5	2763.5422	1.0109	KQLVEIEKVVLHPNYSQVDIGLIK	
26.6	2762.5582	1.9950	KQLVEIEKVVLHPNYSQVDIGLIK	Deamidated Q2 3.91%
26.5	2763.5422	1.0109	KQLVEIEKVVLHPNYSQVDIGLIK	

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

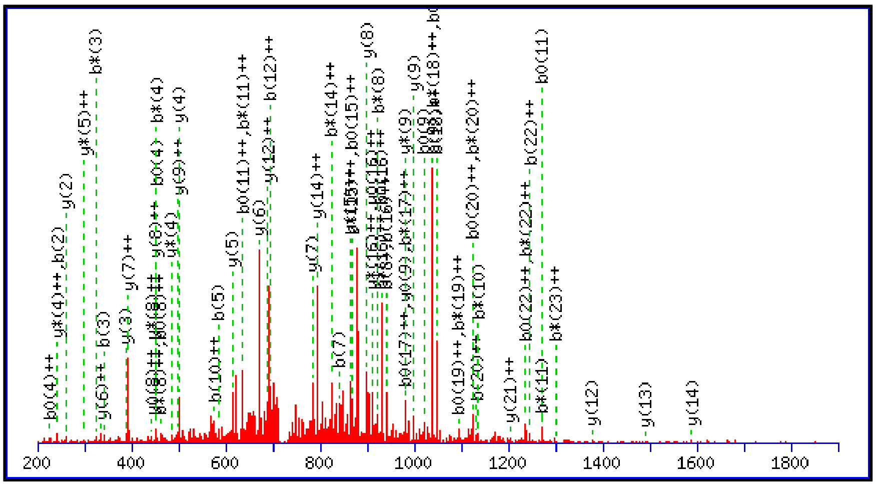
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLVEIEKVVLHPNYSQVDIGLIKLK**
Found in **H3BS21** in **con_Xuniprot_HUMAN3**, H3BS21_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=2 SV=1

Match to Query 26010: 2875.647536 from(719.919160,4+) intensity(22602.9316) rtinseconds(2170) scans(5799) index(24125)
Title: 111019_Est_MI_YS_G_05Spectrum5018_scans__5799
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

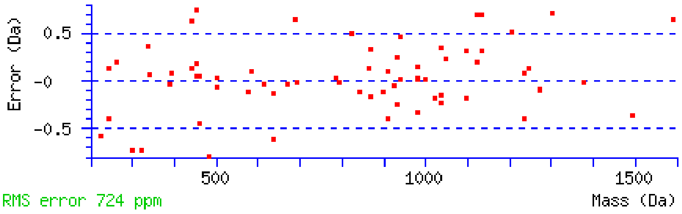
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

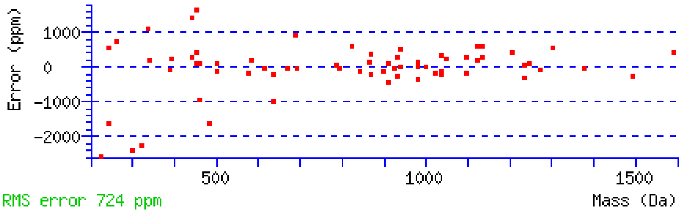


Monoisotopic mass of neutral peptide Mr(calc): 2875.6422
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.0018
Matches : 69/268 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							25
2	***242.1499***	121.5786	225.1234	113.0653			L	2748.5910	1374.7991	2731.5644	1366.2859	2730.5804	1365.7938	24
3	***341.2183***	171.1128	324.1918	162.5995			V	2635.5069	1318.2571	2618.4804	1309.7438	2617.4964	1309.2518	23
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	E	2536.4385	1268.7229	2519.4120	1260.2096	2518.4279	1259.7176	22
5	***583.3450***	292.1761	566.3184	283.6629	565.3344	283.1709	I	2407.3959	1204.2016	2390.3694	1195.6883	2389.3853	1195.1963	21
6	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	E	2294.3118	1147.6596	2277.2853	1139.1463	2276.3013	1138.6543	20
7	***840.4825***	420.7449	823.4560	412.2316	822.4720	411.7396	K	2165.2693	1083.1383	2148.2427	1074.6250	2147.2587	1074.1330	19
8	***939.5510***	470.2791	922.5244	461.7658	921.5404	461.2738	V	2037.1743	1019.0908	2020.1477	1010.5775	2019.1637	1010.0855	18
9	***1038.6194***	519.8133	1021.5928	511.3001	1020.6088	510.8080	V	1938.1059	969.5566	1921.0793	961.0433	1920.0953	960.5513	17
10	1151.7034	**576.3554**	1134.6769	567.8421	1133.6929	567.3501	L	1839.0375	920.0224	1822.0109	911.5091	1821.0269	911.0171	16
11	1288.7623	644.8848	1271.7358	636.3715	1270.7518	635.8795	H	1725.9534	863.4803	1708.9268	854.9671	1707.9428	854.4751	15
12	1385.8151	**693.4112**	1368.7886	684.8979	1367.8045	684.4059	P	***1588.8945***	794.9509	1571.8679	786.4376	1570.8839	785.9456	14
13	1500.8421	750.9247	1483.8155	742.4114	1482.8315	741.9194	N	***1491.8417***	746.4245	1474.8152	737.9112	1473.8312	737.4192	13
14	1663.9054	832.4563	1646.8788	823.9431	1645.8948	823.4510	Y	***1376.8148***	688.9110	1359.7882	680.3978	1358.8042	679.9057	12
15	1750.9374	875.9723	1733.9109	867.4591	1732.9268	866.9671	S	1213.7515	607.3794	1196.7249	598.8661	1195.7409	598.3741	11
16	1878.9960	**940.0016**	1861.9694	931.4884	1860.9854	930.9964	Q	1126.7194	563.8633	1109.6929	555.3501	1108.7089	554.8581	10
17	1978.0644	989.5358	1961.0379	981.0226	1960.0538	980.5306	V	***998.6608***	499.8341	981.6343	491.3208	980.6503	490.8288	9
18	2093.0913	**1047.0493**	2076.0648	1038.5360	2075.0808	1038.0440	D	***899.5924***	450.2999	882.5659	441.7866	881.5819	441.2946	8
19	2206.1754	1103.5913	2189.1489	1095.0781	2188.1648	1094.5861	I	***784.5655***	392.7864	767.5389	384.2731			7
20	2263.1969	**1132.1021**	2246.1703	1123.5888	2245.1863	1123.0968	G	***671.4814***	336.2443	654.4549	327.7311			6
21	2376.2809	1188.6441	2359.2544	1180.1308	2358.2704	1179.6388	L	***614.4600***	307.7336	597.4334	299.2203			5
22	2489.3650	**1245.1861**	2472.3385	1236.6729	2471.3544	1236.1809	I	***501.3759***	251.1916	484.3493	242.6783			4
23	2617.4600	1309.2336	2600.4334	1300.7203	2599.4494	1300.2283	K	***388.2918***	194.6496	371.2653	186.1363			3

24	2730.5440	1365.7757	2713.5175	1357.2624	2712.5335	1356.7704	**L**	***260.1969***	130.6021	243.1703	122.0888			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.8	2875.6422	0.0053	QLVEIEKVVLHPNYSQVDIGLIKLK	Deamidated N13 53.16%
38.2	2875.6422	0.0053	QLVEIEKVVLHPNYSQVDIGLIKLK	Deamidated Q16 46.62%
24.1	2874.6582	0.9893	QLVEIEKVVLHPNYSQVDIGLIKLK	
15.0	2875.6422	0.0053	QLVEIEKVVLHPNYSQVDIGLIKLK	Deamidated Q1 0.23%

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

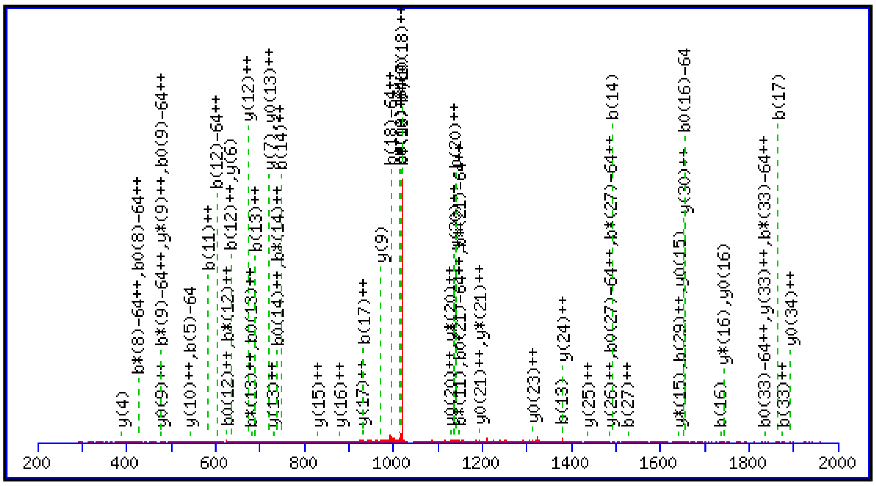
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28927: 4138.039816 from(1035.517230,4+) intensity(28660.0742) rtinseconds(2638) scans(6921) index(11306)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum5959_scans__6921
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

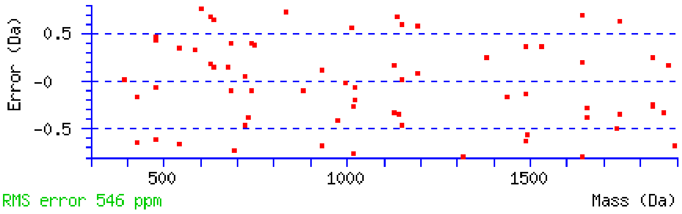
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

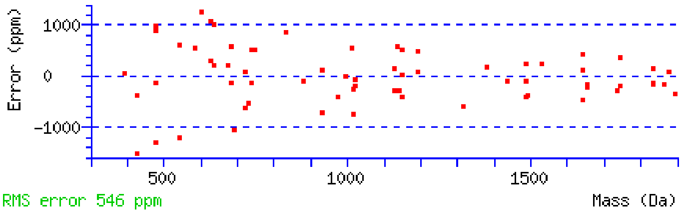


Monoisotopic mass of neutral peptide Mr(calc): 4138.0317
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N15 : Deamidated (NQ)
Q17 : Deamidated (NQ)
N25 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.065
Matches : 68/616 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							37
2	247.1111	124.0592					V	3992.0036	1996.5054	3974.9771	1987.9922	3973.9930	1987.5002	36
3	334.1431	167.5752			316.1326	158.5699	S	3892.9352	1946.9712	3875.9086	1938.4580	3874.9246	1937.9660	35
4	471.2020	236.1047			453.1915	227.0994	H	3805.9032	1903.4552	3788.8766	1894.9419	3787.8926	1894.4499	34
5	608.2609	304.6341			590.2504	295.6288	H	3668.8443	1834.9258	3651.8177	1826.4125	3650.8337	1825.9205	33
6	722.3039	361.6556	705.2773	353.1423	704.2933	352.6503	N	3531.7853	1766.3963	3514.7588	1757.8830	3513.7748	1757.3910	32
7	835.3879	418.1976	818.3614	409.6843	817.3774	409.1923	L	3417.7424	1709.3748	3400.7159	1700.8616	3399.7318	1700.3696	31
8	936.4356	468.7214	919.4091	460.2082	918.4250	459.7162	T	3304.6583	1652.8328	3287.6318	1644.3195	3286.6478	1643.8275	30
9	1037.4833	519.2453	1020.4567	510.7320	1019.4727	510.2400	T	3203.6107	1602.3090	3186.5841	1593.7957	3185.6001	1593.3037	29
10	1094.5048	547.7560	1077.4782	539.2427	1076.4942	538.7507	G	3102.5630	1551.7851	3085.5364	1543.2719	3084.5524	1542.7799	28
11	1165.5419	***583.2746***	1148.5153	574.7613	1147.5313	574.2693	A	3045.5415	1523.2744	3028.5150	1514.7611	3027.5310	1514.2691	27
12	1266.5895	***633.7984***	1249.5630	625.2851	1248.5790	624.7931	T	2974.5044	1487.7558	2957.4779	1479.2426	2956.4938	1478.7506	26
13	**1379.6736**	***690.3404***	1362.6471	681.8272	1361.6630	681.3352	L	2873.4567	1437.2320	2856.4302	1428.7187	2855.4462	1428.2267	25
14	**1492.7577**	***746.8825***	1475.7311	738.3692	1474.7471	737.8772	I	2760.3727	1380.6900	2743.3461	1372.1767	2742.3621	1371.6847	24
15	1607.7846	804.3959	1590.7581	795.8827	1589.7741	795.3907	N	2647.2886	1324.1479	2630.2621	1315.6347	2629.2780	1315.1427	23
16	**1736.8272**	868.9172	1719.8007	860.4040	1718.8166	859.9120	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	**1865.8698**	***933.4385***	1848.8433	924.9253	1847.8592	924.4333	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2051.9491	1026.4782	2034.9226	1017.9649	2033.9386	1017.4729	W	2274.1765	1137.5919	2257.1499	1129.0786	2256.1659	1128.5866	20
19	2165.0332	1083.0202	2148.0066	1074.5070	2147.0226	1074.0149	L	2088.0972	1044.5522	2071.0706	1036.0389	2070.0866	1035.5469	19
20	2278.1172	***1139.5623***	2261.0907	1131.0490	2260.1067	1130.5570	L	1975.0131	988.0102	1957.9865	979.4969	1957.0025	979.0049	18
21	2379.1649	1190.0861	2362.1384	1181.5728	2361.1544	1181.0808	T	1861.9290	931.4682	1844.9025	922.9549	1843.9185	922.4629	17

22	2480.2126	1240.6099	2463.1861	1232.0967	2462.2020	1231.6047	**T**	1760.8814	880.9443	1743.8548	872.4310	1742.8708	871.9390	**16**
23	2551.2497	1276.1285	2534.2232	1267.6152	2533.2392	1267.1232	**A**	1659.8337	830.4205	1642.8071	821.9072	1641.8231	821.4152	**15**
24	2679.3447	1340.1760	2662.3181	1331.6627	2661.3341	1331.1707	**K**	1588.7966	794.9019	1571.7700	786.3886	1570.7860	785.8966	**14**
25	2794.3716	1397.6895	2777.3451	1389.1762	2776.3611	1388.6842	**N**	1460.7016	730.8544	1443.6750	722.3412	1442.6910	721.8492	**13**
26	2907.4557	1454.2315	2890.4291	1445.7182	2889.4451	1445.2262	**L**	1345.6747	673.3410	1328.6481	664.8277	1327.6641	664.3357	**12**
27	3054.5241	***1527.7657***	3037.4976	1519.2524	3036.5135	1518.7604	**F**	1232.5906	616.7989	1215.5640	608.2857	1214.5800	607.7937	**11**
28	3167.6082	1584.3077	3150.5816	1575.7944	3149.5976	1575.3024	**L**	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	**10**
29	3281.6511	***1641.3292***	3264.6245	1632.8159	3263.6405	1632.3239	**N**	**972.4381**	486.7227	955.4116	478.2094	954.4275	477.7174	**9**
30	3418.7100	1709.8586	3401.6835	1701.3454	3400.6994	1700.8534	**H**	858.3952	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3505.7420	1753.3747	3488.7155	1744.8614	3487.7315	1744.3694	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3634.7846	1817.8960	3617.7581	1809.3827	3616.7741	1808.8907	**E**	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3749.8116	***1875.4094***	3732.7850	1866.8961	3731.8010	1866.4041	**N**	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3820.8487	1910.9280	3803.8221	1902.4147	3802.8381	1901.9227	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3921.8964	1961.4518	3904.8698	1952.9385	3903.8858	1952.4465	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3992.9335	1996.9704	3975.9069	1988.4571	3974.9229	1987.9651	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
34.9	4137.0477	0.9922	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
34.4	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
28.3	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
28.3	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
26.9	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
26.5	4137.0477	0.9922	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
26.0	4137.0477	0.9922	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
25.9	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK
25.1	4138.0317	0.0082	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK

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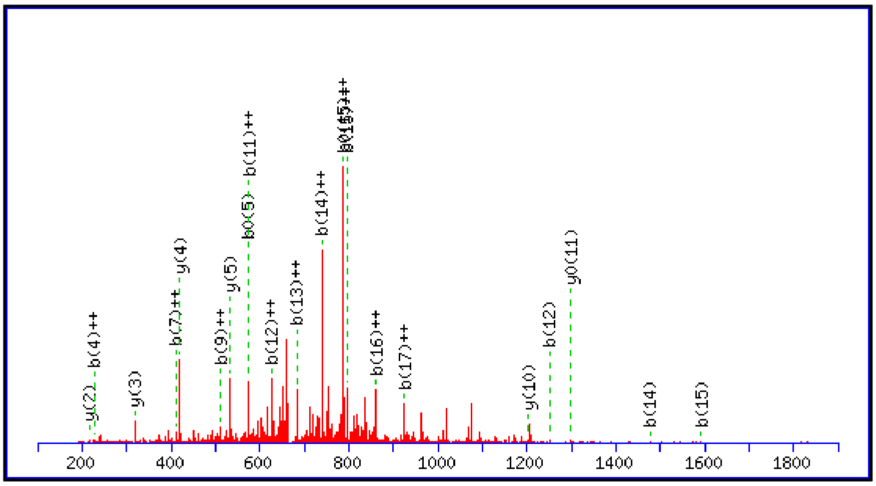
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 23817: 2682.357056 from(671.596540,4+) intensity(11205.3682) rtinseconds(1766) scans(4433) index(25378)
Title: 111019_Est_MI_YS_G_07Spectrum3783_scans__4433
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

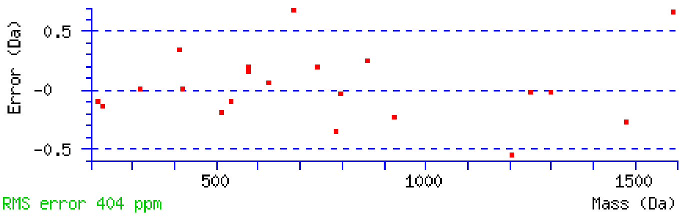
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

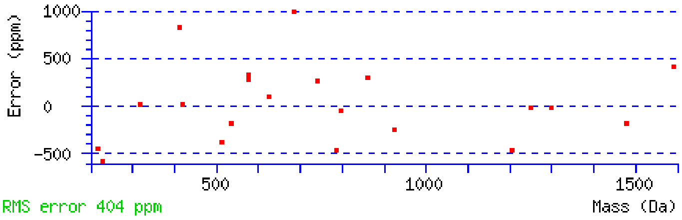


Monoisotopic mass of neutral peptide Mr(calc): 2680.3530
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Q17 : Deamidated (NQ)
Ions Score: 35 **Expect:** 0.075
Matches : 21/258 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.0478	66.5275					M							24
2	231.1162	116.0617					V	2550.3198	1275.6636	2533.2933	1267.1503	2532.3093	1266.6583	23
3	318.1482	159.5777			300.1376	150.5725	S	2451.2514	1226.1294	2434.2249	1217.6161	2433.2409	1217.1241	22
4	455.2071	***228.1072***			437.1966	219.1019	H	2364.2194	1182.6133	2347.1929	1174.1001	2346.2088	1173.6081	21
5	592.2660	296.6367			574.2555	287.6314	H	2227.1605	1114.0839	2210.1339	1105.5706	2209.1499	1105.0786	20
6	707.2930	354.1501	690.2664	345.6368	689.2824	345.1448	N	2090.1016	1045.5544	2073.0750	1037.0412	2072.0910	1036.5491	19
7	820.3770	***410.6922***	803.3505	402.1789	802.3665	401.6869	L	1975.0746	988.0410	1958.0481	979.5277	1957.0641	979.0357	18
8	921.4247	461.2160	904.3982	452.7027	903.4141	452.2107	T	1861.9906	931.4989	1844.9640	922.9857	1843.9800	922.4936	17
9	1022.4724	***511.7398***	1005.4458	503.2266	1004.4618	502.7346	T	1760.9429	880.9751	1743.9163	872.4618	1742.9323	871.9698	16
10	1079.4939	540.2506	1062.4673	531.7373	1061.4833	531.2453	G	1659.8952	830.4512	1642.8687	821.9380	1641.8847	821.4460	15
11	1150.5310	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	A	1602.8738	801.9405	1585.8472	793.4272	1584.8632	792.9352	14
12	**1251.5786**	***626.2930***	1234.5521	617.7797	1233.5681	617.2877	T	1531.8366	766.4220	1514.8101	757.9087	1513.8261	757.4167	13
13	1364.6627	***682.8350***	1347.6362	674.3217	1346.6521	673.8297	L	1430.7890	715.8981	1413.7624	707.3848	1412.7784	706.8928	12
14	**1477.7468**	***739.3770***	1460.7202	730.8638	1459.7362	730.3717	I	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	11
15	**1591.7897**	***796.3985***	1574.7632	787.8852	1573.7791	787.3932	N	***1204.6208***	602.8141	1187.5943	594.3008	1186.6103	593.8088	10
16	1720.8323	***860.9198***	1703.8057	852.4065	1702.8217	851.9145	E	1090.5779	545.7926	1073.5514	537.2793	1072.5673	536.7873	9
17	1849.8749	***925.4411***	1832.8483	916.9278	1831.8643	916.4358	Q	961.5353	481.2713	944.5088	472.7580	943.5247	472.2660	8
18	2035.9542	1018.4807	2018.9277	1009.9675	2017.9436	1009.4755	W	832.4927	416.7500	815.4662	408.2367	814.4822	407.7447	7
19	2149.0383	1075.0228	2132.0117	1066.5095	2131.0277	1066.0175	L	646.4134	323.7103	629.3869	315.1971	628.4028	314.7051	6
20	2262.1223	1131.5648	2245.0958	1123.0515	2244.1118	1122.5595	L	***533.3293***	267.1683	516.3028	258.6550	515.3188	258.1630	5
21	2363.1700	1182.0886	2346.1435	1173.5754	2345.1594	1173.0834	T	***420.2453***	210.6263	403.2187	202.1130	402.2347	201.6210	4
22	2464.2177	1232.6125	2447.1911	1224.0992	2446.2071	1223.6072	T	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	3

23	2535.2548	1268.1310	2518.2283	1259.6178	2517.2442	1259.1258	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of MVSHHNLTTGATLINEQWLLTTAK
(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	2680.3530	2.0040	MVSHHNLTTGATLINEQWLLTTAK
32.6	2680.3530	2.0040	MVSHHNLTTGATLINEQWLLTTAK
16.3	2680.3530	2.0040	MVSHHNLTTGATLINEQWLLTTAK
7.6	2681.3557	1.0014	LGSNGRIMVMHSELLIEPFSPQLP
7.0	2681.3557	1.0014	LGSNGRIMVMHSELLIEPFSPQLP
6.1	2681.3522	1.0049	GPQGPGSVAAGLGRVLLVAGHAGGDQGGEP
5.9	2681.3537	1.0034	GGLTSPNCAHAVAGLWFKRYYSVK
3.9	2680.3456	2.0115	EHVQNNLPRDLLTGEQFIQLRR
3.7	2682.3588	-0.0017	AAAEMVIKGVATNGTYFIHDFRQK
3.7	2681.3602	0.9969	IRYATTEWAYQTNGAWAGGLLLLN

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

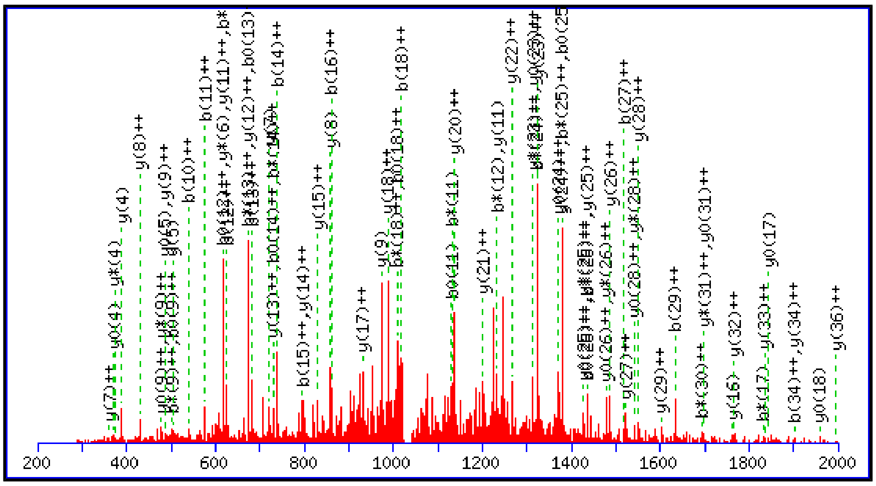
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK**
Found in **J3QR68** in **con_Xuniprot_HUMAN3**, J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1

Match to Query 28645: 4123.067736 from(1031.774210,4+) intensity(45276.7148) rtinseconds(2549) scans(6743) index(9809)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum5839_scans__6743
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

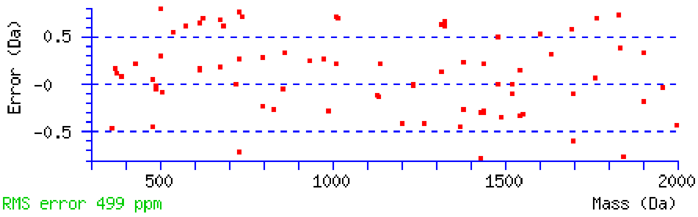
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

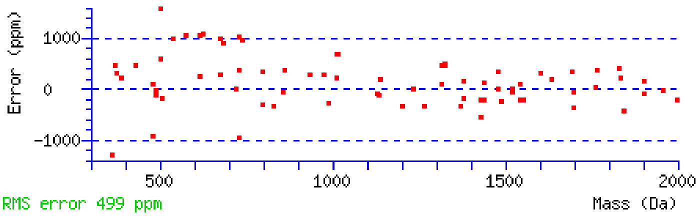


Monoisotopic mass of neutral peptide Mr(calc): 4121.0527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
N29 : Deamidated (NQ)
N33 : Deamidated (NQ)
Ions Score: 142 **Expect:** 1.3e-012
Matches : 81/414 fragment ions using 104 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	132.0478	66.5275					M							37
2	231.1162	116.0617					V	3991.0196	1996.0134	3973.9930	1987.5002	3973.0090	1987.0081	36
3	318.1482	159.5777			300.1376	150.5725	S	3891.9512	1946.4792	3874.9246	1937.9660	3873.9406	1937.4739	35
4	455.2071	228.1072			437.1966	219.1019	H	3804.9191	1902.9632	3787.8926	1894.4499	3786.9086	1893.9579	34
5	592.2660	296.6367			574.2555	287.6314	H	3667.8602	1834.4338	3650.8337	1825.9205	3649.8497	1825.4285	33
6	706.3090	353.6581	689.2824	345.1448	688.2984	344.6528	N	3530.8013	1765.9043	3513.7748	1757.3910	3512.7908	1756.8990	32
7	819.3930	410.2001	802.3665	401.6869	801.3825	401.1949	L	3416.7584	1708.8828	3399.7318	1700.3696	3398.7478	1699.8776	31
8	920.4407	460.7240	903.4141	452.2107	902.4301	451.7187	T	3303.6743	1652.3408	3286.6478	1643.8275	3285.6638	1643.3355	30
9	1021.4884	511.2478	1004.4618	502.7346	1003.4778	502.2425	T	3202.6267	1601.8170	3185.6001	1593.3037	3184.6161	1592.8117	29
10	1078.5098	**539.7586**	1061.4833	531.2453	1060.4993	530.7533	G	3101.5790	1551.2931	3084.5524	1542.7799	3083.5684	1542.2878	28
11	1149.5470	**575.2771**	1132.5204	566.7638	1131.5364	566.2718	A	3044.5575	1522.7824	3027.5310	1514.2691	3026.5469	1513.7771	27
12	1250.5946	**625.8010**	1233.5681	617.2877	1232.5841	616.7957	T	2973.5204	1487.2638	2956.4938	1478.7506	2955.5098	1478.2586	26
13	1363.6787	**682.3430**	1346.6521	673.8297	1345.6681	673.3377	L	2872.4727	1436.7400	2855.4462	1428.2267	2854.4622	1427.7347	25
14	1476.7628	**738.8850**	1459.7362	730.3717	1458.7522	729.8797	I	2759.3887	1380.1980	2742.3621	1371.6847	2741.3781	1371.1927	24
15	1590.8057	**795.9065**	1573.7791	787.3932	1572.7951	786.9012	N	2646.3046	1323.6559	2629.2780	1315.1427	2628.2940	1314.6506	23
16	1719.8483	**860.4278**	1702.8217	851.9145	1701.8377	851.4225	E	2532.2617	1266.6345	2515.2351	1258.1212	2514.2511	1257.6292	22
17	1847.9069	924.4571	1830.8803	915.9438	1829.8963	915.4518	Q	2403.2191	1202.1132	2386.1925	1193.5999	2385.2085	1193.1079	21
18	2033.9862	**1017.4967**	2016.9596	1008.9834	2015.9756	1008.4914	W	2275.1605	1138.0839	2258.1339	1129.5706	2257.1499	1129.0786	20
19	2147.0702	1074.0388	2130.0437	1065.5255	2129.0597	1065.0335	L	2089.0812	1045.0442	2072.0546	1036.5310	2071.0706	1036.0389	19
20	2260.1543	1130.5808	2243.1278	1122.0675	2242.1437	1121.5755	L	1975.9971	988.5022	1958.9706	979.9889	1957.9865	979.4969	18
21	2361.2020	1181.1046	2344.1754	1172.5914	2343.1914	1172.0993	T	1862.9131	931.9602	1845.8865	923.4469	1844.9025	922.9549	17
22	2462.2497	1231.6285	2445.2231	1223.1152	2444.2391	1222.6232	T	**1761.8654**	881.4363	1744.8388	872.9230	1743.8548	872.4310	16

23	2533.2868	1267.1470	2516.2602	1258.6337	2515.2762	1258.1417	**A**	1660.8177	830.9125	1643.7911	822.3992	1642.8071	821.9072	**15**
24	2661.3817	1331.1945	2644.3552	1322.6812	2643.3712	1322.1892	**K**	1589.7806	795.3939	1572.7540	786.8807	1571.7700	786.3886	**14**
25	2776.4087	1388.7080	2759.3821	1380.1947	2758.3981	1379.7027	**N**	1461.6856	731.3464	1444.6591	722.8332	1443.6751	722.3412	**13**
26	2889.4927	1445.2500	2872.4662	1436.7367	2871.4822	1436.2447	**L**	1346.6587	673.8330	1329.6321	665.3197	1328.6481	664.8277	**12**
27	3036.5612	**1518.7842**	3019.5346	1510.2709	3018.5506	1509.7789	**F**	**1233.5746**	617.2909	1216.5481	608.7777	1215.5640	608.2857	**11**
28	3149.6452	1575.3262	3132.6187	1566.8130	3131.6347	1566.3210	**L**	1086.5062	543.7567	1069.4796	535.2435	1068.4956	534.7515	**10**
29	3264.6722	**1632.8397**	3247.6456	1624.3264	3246.6616	1623.8344	**N**	**973.4221**	487.2147	956.3956	478.7014	955.4116	478.2094	**9**
30	3401.7311	1701.3692	3384.7045	1692.8559	3383.7205	1692.3639	**H**	**858.3952**	429.7012	841.3686	421.1880	840.3846	420.6959	**8**
31	3488.7631	1744.8852	3471.7366	1736.3719	3470.7525	1735.8799	**S**	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	**7**
32	3617.8057	1809.4065	3600.7791	1800.8932	3599.7951	1800.4012	**E**	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	**6**
33	3732.8326	1866.9200	3715.8061	1858.4067	3714.8221	1857.9147	**N**	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	**5**
34	3803.8698	**1902.4385**	3786.8432	1893.9252	3785.8592	1893.4332	**A**	**390.2347**	195.6210	373.2082	187.1077	372.2241	186.6157	**4**
35	3904.9174	1952.9624	3887.8909	1944.4491	3886.9069	1943.9571	**T**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
36	3975.9545	1988.4809	3958.9280	1979.9676	3957.9440	1979.4756	**A**	218.1499	109.5786	201.1234	101.0653			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
142.0	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N25, N29, N33 98.23%
124.4	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N29, N33 1.72%
107.7	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated Q17, N25, N29 0.04%
103.9	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, N33 0.02%
68.7	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N6, N15, Q17 0.00%
61.6	4121.0527	2.0150	MVSHHNLTTGATLINEQWLLTTAKNLFLNHSENATAK	Deamidated N15, Q17, N25 0.00%
15.7	4121.0676	2.0002	VMLENFRNLVFLGIDVSKPDLITCLEQGKDPWNMK	
11.1	4122.0549	1.0128	CILFDPLHTKEKSQACLQFLTLLLDESSPMLLCGK	
10.6	4122.0516	1.0162	VMLENFRNLVFLGIDVSKPDLITCLEQGKDPWNMK	
10.5	4122.0549	1.0128	CILFDPLHTKEKSQACLQFLTLLLDESSPMLLCGK	

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

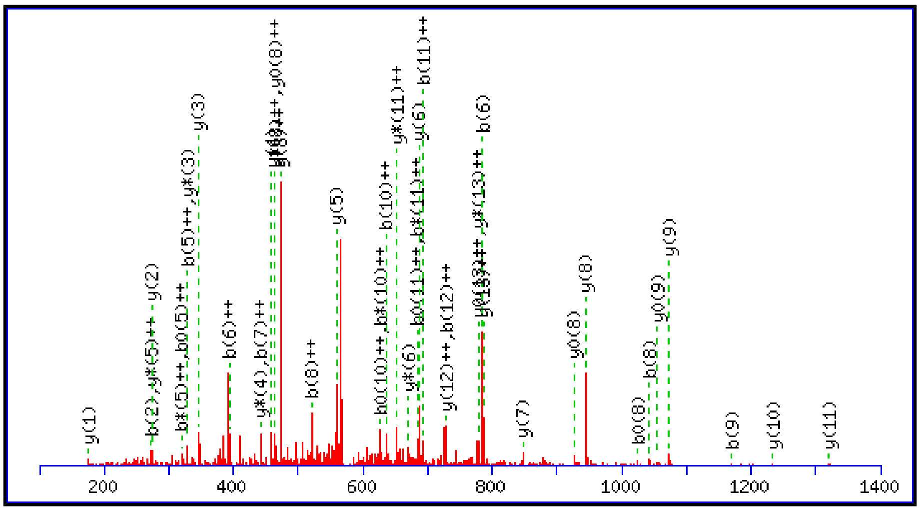
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNHSCEPCQTLAVR**
Found in **P00748** in **con_Xuniprot_HUMAN3**, FA12_HUMAN Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

Match to Query 8782: 1727.787552 from(576.936460,3+) intensity(12174.5117) rtinseconds(314) scans(573) index(22458)
Title: 111019_Est_MI_YS_G_03Spectrum459_scans__573
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1727.7832

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

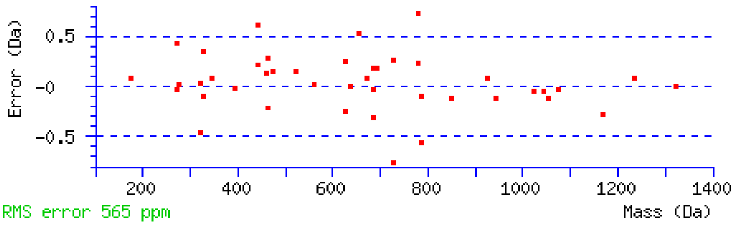
Variable modifications:

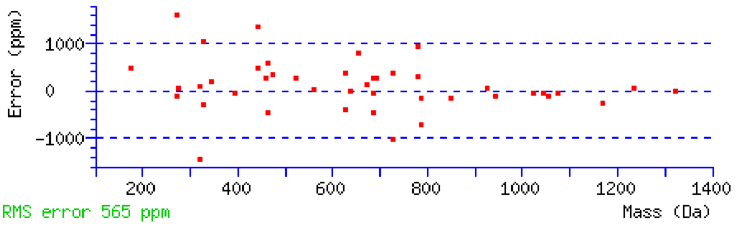
N2 : Deamidated (NQ)

Ions Score: 75 **Expect:** 5e-006

Matches : 44/142 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**							**14**
2	**272.1353**	136.5713	255.1088	128.0580			**N**	1572.6893	786.8483	1555.6628	778.3350	1554.6788	777.8430	**13**
3	409.1942	205.1008	392.1677	196.5875			**H**	1457.6624	729.3348	1440.6358	720.8216	1439.6518	720.3296	**12**
4	496.2263	248.6168	479.1997	240.1035	478.2157	239.6115	**S**	***1320.6035***	660.8054	1303.5769	652.2921	1302.5929	651.8001	**11**
5	656.2569	**328.6321**	639.2304	320.1188	638.2464	319.6268	**C**	***1233.5715***	617.2894	1216.5449	608.7761	1215.5609	608.2841	**10**
6	**785.2995**	**393.1534**	768.2730	384.6401	767.2889	384.1481	**E**	***1073.5408***	537.2740	1056.5143	528.7608	1055.5302	528.2688	**9**
7	882.3523	**441.6798**	865.3257	433.1665	864.3417	432.6745	**P**	***944.4982***	472.7527	927.4717	464.2395	926.4876	463.7475	**8**
8	**1042.3829**	**521.6951**	1025.3564	513.1818	1024.3724	512.6898	**C**	***847.4455***	424.2264	830.4189	415.7131	829.4349	415.2211	**7**
9	**1170.4415**	585.7244	1153.4150	577.2111	1152.4309	576.7191	**Q**	***687.4148***	344.2110	670.3883	335.6978	669.4042	335.2058	**6**
10	1271.4892	**636.2482**	1254.4626	627.7350	1253.4786	627.2429	**T**	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	**5**
11	1384.5732	**692.7903**	1367.5467	684.2770	1366.5627	683.7850	**L**	***458.3085***	229.6579	441.2820	221.1446			**4**
12	1455.6104	**728.3088**	1438.5838	719.7955	1437.5998	719.3035	**A**	***345.2245***	173.1159	328.1979	164.6026			**3**
13	1554.6788	**777.8430**	1537.6522	769.3298	1536.6682	768.8377	**V**	***274.1874***	137.5973	257.1608	129.0840			**2**
14							**R**	***175.1190***	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
74.6	1727.7832	0.0044	RNHSCEPCQTLAVR	Deamidated N2 100.00%
29.9	1727.7832	0.0044	RNHSCEPCQTLAVR	Deamidated Q9 0.00%
11.3	1726.7924	0.9951	GSRGSGWSGPFGHQGPR	
10.8	1727.7896	-0.0021	ELNSANRTYDRNMK	
7.5	1727.7897	-0.0021	GKNETNHVNEKMGPR	
6.3	1726.7832	1.0044	REEELQYTLEDMR	
5.2	1725.7747	2.0128	EPWSGPEWVGESGPGR	
5.0	1726.7832	1.0043	CIAQAQEYQDSTSVK	
4.7	1727.7897	-0.0021	GKNETNHVNEKMGPR	
4.6	1726.7832	1.0044	MQEHQQQVLQAVER	

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

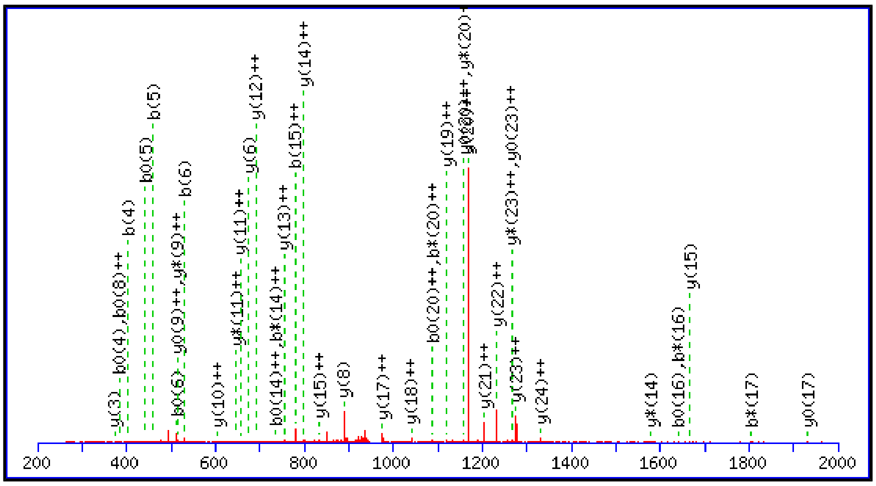
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TTLSGAPCQPWASEATYRNVTAEQAR**
Found in **P00748** in **con_Xuniprot_HUMAN3**, FA12_HUMAN Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

Match to Query 26008: 2865.349032 from(956.123620,3+) intensity(15894.9053) rtinseconds(1367) scans(3265) index(23181)
Title: 111019_Est_MI_YS_G_04Spectrum2783_scans__3265
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

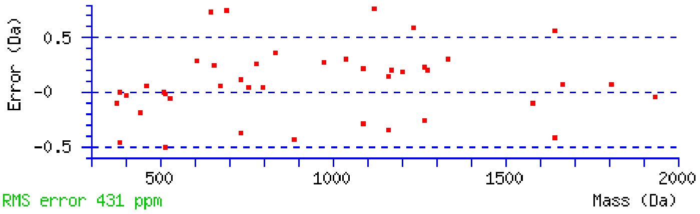
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

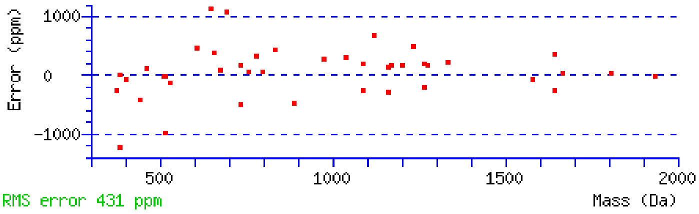


Monoisotopic mass of neutral peptide Mr(calc): 2865.3351
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
Ions Score: 48 **Expect:** 0.0042
Matches : 42/278 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							26
2	203.1026	102.0550			185.0921	93.0497	T	2765.2948	1383.1510	2748.2682	1374.6377	2747.2842	1374.1457	25
3	316.1867	158.5970			298.1761	149.5917	L	2664.2471	1332.6272	2647.2205	1324.1139	2646.2365	1323.6219	24
4	403.2187	202.1130			385.2082	193.1077	S	2551.1630	1276.0852	2534.1365	1267.5719	2533.1525	1267.0799	23
5	460.2402	230.6237			442.2296	221.6185	G	2464.1310	1232.5691	2447.1045	1224.0559	2446.1204	1223.5639	22
6	531.2773	266.1423			513.2667	257.1370	A	2407.1095	1204.0584	2390.0830	1195.5451	2389.0990	1195.0531	21
7	628.3301	314.6687			610.3195	305.6634	P	2336.0724	1168.5398	2319.0459	1160.0266	2318.0619	1159.5346	20
8	788.3607	394.6840			770.3502	385.6787	C	2239.0197	1120.0135	2221.9931	1111.5002	2221.0091	1111.0082	19
9	916.4193	458.7133	899.3927	450.2000	898.4087	449.7080	Q	2078.9890	1039.9981	2061.9625	1031.4849	2060.9784	1030.9929	18
10	1013.4721	507.2397	996.4455	498.7264	995.4615	498.2344	P	1950.9304	975.9689	1933.9039	967.4556	1932.9199	966.9636	17
11	1199.5514	600.2793	1182.5248	591.7660	1181.5408	591.2740	W	1853.8777	927.4425	1836.8511	918.9292	1835.8671	918.4372	16
12	1270.5885	635.7979	1253.5619	627.2846	1252.5779	626.7926	A	**1667.7984**	834.4028	1650.7718	825.8895	1649.7878	825.3975	15
13	1357.6205	679.3139	1340.5940	670.8006	1339.6099	670.3086	S	1596.7612	798.8843	1579.7347	790.3710	1578.7507	789.8790	14
14	1486.6631	743.8352	1469.6366	735.3219	1468.6525	734.8299	E	1509.7292	755.3682	1492.7027	746.8550	1491.7186	746.3630	13
15	1557.7002	779.3537	1540.6737	770.8405	1539.6897	770.3485	A	1380.6866	690.8469	1363.6601	682.3337	1362.6761	681.8417	12
16	1658.7479	829.8776	1641.7214	821.3643	1640.7373	820.8723	T	1309.6495	655.3284	1292.6230	646.8151	1291.6389	646.3231	11
17	1821.8112	911.4093	1804.7847	902.8960	1803.8007	902.4040	Y	1208.6018	604.8046	1191.5753	596.2913	1190.5913	595.7993	10
18	1977.9123	989.4598	1960.8858	980.9465	1959.9018	980.4545	R	1045.5385	523.2729	1028.5119	514.7596	1027.5279	514.2676	9
19	2092.9393	1046.9733	2075.9127	1038.4600	2074.9287	1037.9680	N	**889.4374**	445.2223	872.4108	436.7091	871.4268	436.2170	8
20	2192.0077	1096.5075	2174.9811	1087.9942	2173.9971	1087.5022	V	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	7
21	2293.0554	1147.0313	2276.0288	1138.5181	2275.0448	1138.0260	T	**675.3420**	338.1747	658.3155	329.6614	657.3315	329.1694	6
22	2364.0925	1182.5499	2347.0659	1174.0366	2346.0819	1173.5446	A	574.2944	287.6508	557.2678	279.1375	556.2838	278.6455	5
23	2493.1351	1247.0712	2476.1085	1238.5579	2475.1245	1238.0659	E	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4

24	2621.1937	1311.1005	2604.1671	1302.5872	2603.1831	1302.0952	**Q**	374.2146	187.6110	357.1881	179.0977			**3**
25	2692.2308	1346.6190	2675.2042	1338.1058	2674.2202	1337.6137	**A**	246.1561	123.5817	229.1295	115.0684			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.5	2865.3351	0.0139	TTLSGAPCQPWASEATYRNVTAEQAR	Deamidated N19 78.86%
40.4	2865.3351	0.0139	TTLSGAPCQPWASEATYRNVTAEQAR	Deamidated Q24 15.17%
36.3	2865.3351	0.0139	TTLSGAPCQPWASEATYRNVTAEQAR	Deamidated Q9 5.97%
23.8	2864.3511	0.9979	TTLSGAPCQPWASEATYRNVTAEQAR	
16.6	2863.3521	1.9970	LTSVRFMGDMVSFEEDRINATVWK	
7.9	2863.3521	1.9970	HYNLQVFAPPNMDNSMGTEEITVLK	
7.6	2865.3558	-0.0068	VSSNETEIMKEIMQNGPVQAIMQVR	
6.6	2864.3361	1.0130	HYNLQVFAPPNMDNSMGTEEITVLK	
6.3	2863.3467	2.0024	SQVTLDVEKLCDLEIMPSSEAADGEK	
6.1	2864.3498	0.9993	ASEDKMEQIDQSVDQTGWLRQLIR	

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

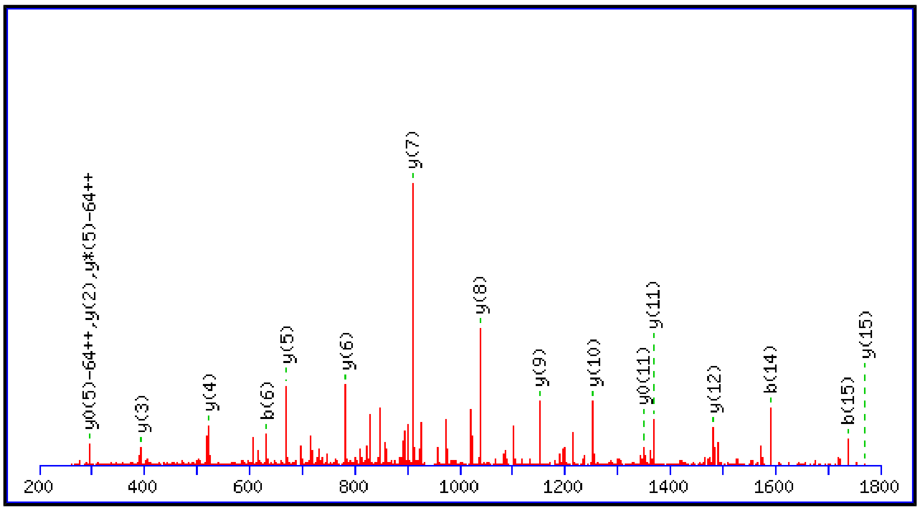
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

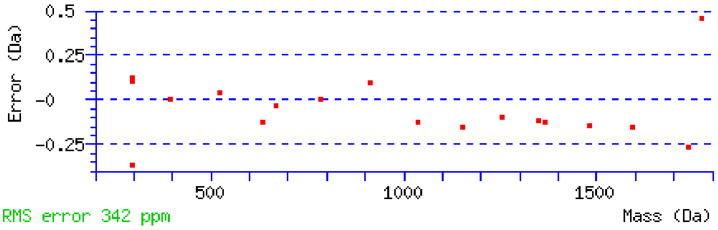
Match to Query 11062: 1882.884128 from(942.449340,2+) intensity(1279338.5000) rtinseconds(2214) scans(5863) index(4587)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum4985_scans__5863
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

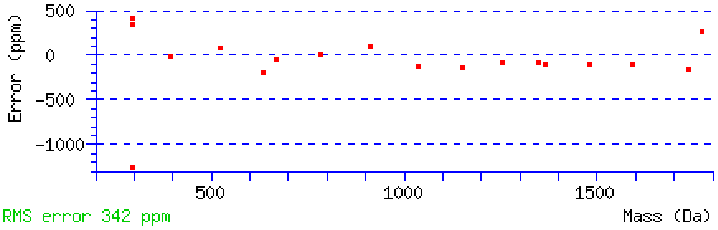
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1882.8805
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
M12    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 131  Expect: 1.7e-011
Matches : 18/246 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	114.0913	57.5493					L							16
2	171.1128	86.0600					G	***1770.8037***	885.9055	1753.7772	877.3922	1752.7931	876.9002	15
3	242.1499	121.5786					A	1713.7822	857.3948	1696.7557	848.8815	1695.7717	848.3895	14
4	402.1806	201.5939					C	1642.7451	821.8762	1625.7186	813.3629	1624.7346	812.8709	13
5	517.2075	259.1074	500.1810	250.5941			N	***1482.7145***	741.8609	1465.6879	733.3476	1464.7039	732.8556	12
6	**632.2345**	316.6209	615.2079	308.1076	614.2239	307.6156	D	***1367.6875***	684.3474	1350.6610	675.8341	1349.6770	675.3421	11
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	T	***1252.6606***	626.8339	1235.6340	618.3207	1234.6500	617.8286	10
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	L	***1151.6129***	576.3101	1134.5864	567.7968	1133.6023	567.3048	9
9	974.4248	487.7160	957.3982	479.2028	956.4142	478.7107	Q	***1038.5288***	519.7681	1021.5023	511.2548	1020.5183	510.7628	8
10	1102.4834	551.7453	1085.4568	543.2320	1084.4728	542.7400	Q	***910.4703***	455.7388	893.4437	447.2255	892.4597	446.7335	7
11	1215.5674	608.2873	1198.5409	599.7741	1197.5569	599.2821	L	***782.4117***	391.7095	765.3851	383.1962	764.4011	382.7042	6
12	1362.6028	681.8050	1345.5763	673.2918	1344.5923	672.7998	M	***669.3276***	335.1675	652.3011	326.6542	651.3171	326.1622	5
13	1491.6454	746.3263	1474.6189	737.8131	1473.6348	737.3211	E	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	**1590.7138**	795.8605	1573.6873	787.3473	1572.7033	786.8553	V	***393.2496***	197.1285	376.2231	188.6152			3
15	**1737.7822**	869.3948	1720.7557	860.8815	1719.7717	860.3895	F	***294.1812***	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
131.1	1882.8805	0.0037	LGACNDTLQQLMEVFK	Deamidated N5 99.99%
87.9	1882.8805	0.0037	LGACNDTLQQLMEVFK	Deamidated Q10 0.00%
87.8	1882.8805	0.0037	LGACNDTLQQLMEVFK	Deamidated Q9 0.00%
21.1	1880.8859	1.9982	DQNDQKLEKLMVQMK	
21.1	1880.8859	1.9982	DQNDQKLEKLMVQMK	
21.1	1880.8859	1.9982	DQNDQKLEKLMVQMK	
12.2	1881.8744	1.0097	KFDEFQKDLNTNEPR	
12.1	1882.8804	0.0037	INQFNLMASEMIALNR	
10.9	1881.8744	1.0097	KFDEFQKDLNTNEPR	
10.9	1882.8917	-0.0075	NILPKQSCYMEAREK	

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

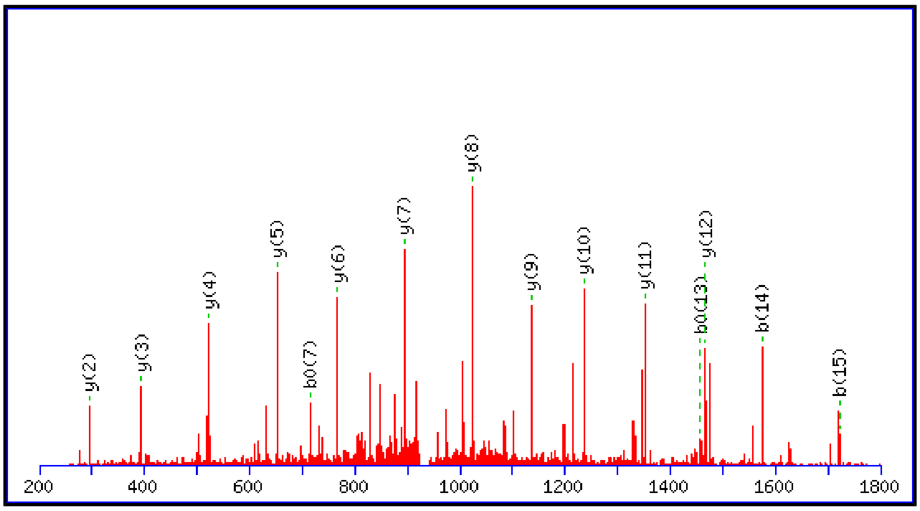
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

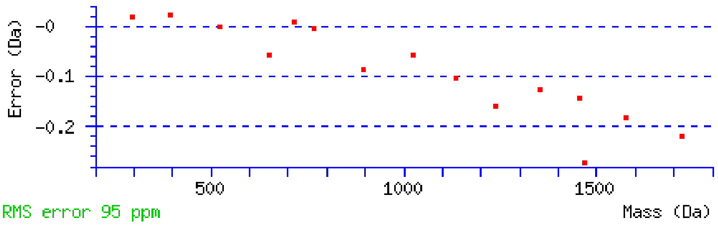
Match to Query 10994: 1866.891948 from(934.453250,2+) intensity(219335.4844) rtinseconds(2601) scans(6813) index(11294)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum5862_scans__6813
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

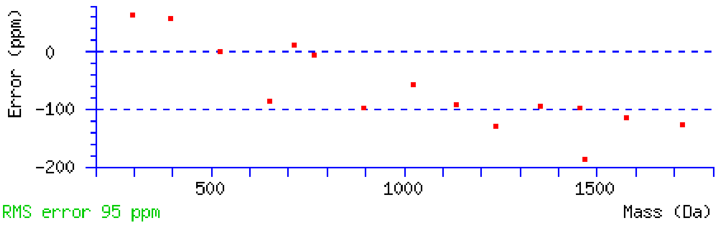
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1866.8856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
Ions Score: 110  Expect: 2.2e-009
Matches : 15/156 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	114.0913	57.5493					L							16
2	171.1128	86.0600					G	1754.8088	877.9080	1737.7822	869.3948	1736.7982	868.9027	15
3	242.1499	121.5786					A	1697.7873	849.3973	1680.7608	840.8840	1679.7768	840.3920	14
4	402.1806	201.5939					C	1626.7502	813.8787	1609.7237	805.3655	1608.7396	804.8735	13
5	517.2075	259.1074	500.1810	250.5941			N	***1466.7196***	733.8634	1449.6930	725.3501	1448.7090	724.8581	12
6	632.2345	316.6209	615.2079	308.1076	614.2239	307.6156	D	***1351.6926***	676.3499	1334.6661	667.8367	1333.6821	667.3447	11
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	T	***1236.6657***	618.8365	1219.6391	610.3232	1218.6551	609.8312	10
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	L	***1135.6180***	568.3126	1118.5914	559.7994	1117.6074	559.3074	9
9	974.4248	487.7160	957.3982	479.2028	956.4142	478.7107	Q	***1022.5339***	511.7706	1005.5074	503.2573	1004.5234	502.7653	8
10	1102.4834	551.7453	1085.4568	543.2320	1084.4728	542.7400	Q	***894.4754***	447.7413	877.4488	439.2280	876.4648	438.7360	7
11	1215.5674	608.2873	1198.5409	599.7741	1197.5569	599.2821	L	***766.4168***	383.7120	749.3902	375.1988	748.4062	374.7067	6
12	1346.6079	673.8076	1329.5814	665.2943	1328.5973	664.8023	M	***653.3327***	327.1700	636.3062	318.6567	635.3221	318.1647	5
13	1475.6505	738.3289	1458.6239	729.8156	1457.6399	729.3236	E	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	1574.7189	787.8631	1557.6924	779.3498	1556.7083	778.8578	V	***393.2496***	197.1285	376.2231	188.6152			3
15	1721.7873	861.3973	1704.7608	852.8840	1703.7768	852.3920	F	***294.1812***	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
110.1	1866.8856	0.0064	LGACNDTLQQLMEVFK	Deamidated N5 99.90%
77.1	1866.8856	0.0064	LGACNDTLQQLMEVFK	Deamidated Q9 0.05%
76.9	1866.8856	0.0064	LGACNDTLQQLMEVFK	Deamidated Q10 0.05%
11.8	1864.8910	2.0009	DQNDQKLEKLMVQMK	
11.8	1864.8910	2.0009	DQNDQKLEKLMVQMK	
11.8	1864.8910	2.0009	DQNDQKLEKLMVQMK	
9.8	1866.8894	0.0025	LDCRSTISRPSGFDEK	
8.3	1866.8934	-0.0015	IGNTMQSLQWYLQER	
5.9	1866.8941	-0.0021	QSWNPFPDFTPQKFK	
5.7	1866.8889	0.0030	TIRPMDMETIEASVMK	

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

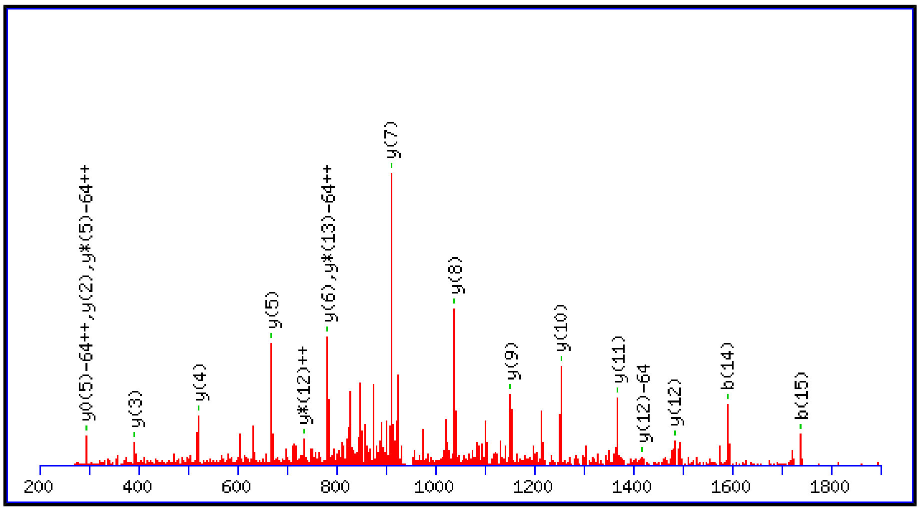
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

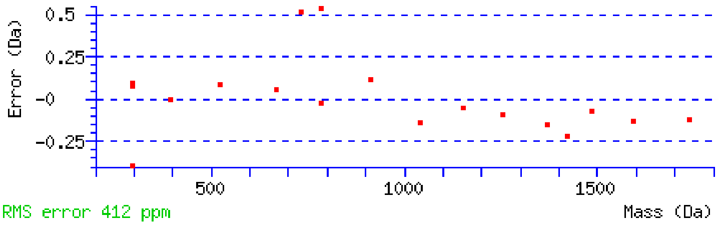
Match to Query 11099: 1883.869588 from(942.942070,2+) intensity(29041.4238) rtinseconds(2311) scans(6132) index(4611)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum5220_scans__6132
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

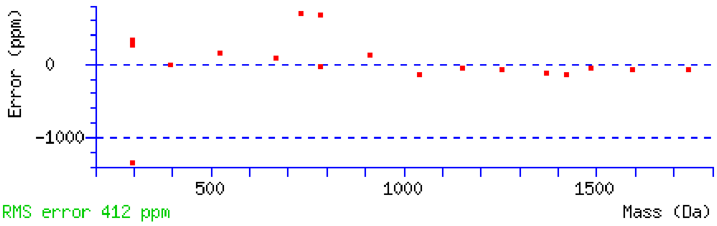
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1883.8645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q10 : Deamidated (NQ)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 109 **Expect:** 2.2e-009
Matches : 18/246 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	114.0913	57.5493					L							16
2	171.1128	86.0600					G	1771.7877	886.3975	1754.7612	877.8842	1753.7772	877.3922	15
3	242.1499	121.5786					A	1714.7663	857.8868	1697.7397	849.3735	1696.7557	848.8815	14
4	402.1806	201.5939					C	1643.7291	822.3682	1626.7026	813.8549	1625.7186	813.3629	13
5	517.2075	259.1074	500.1810	250.5941			N	***1483.6985***	742.3529	1466.6719	733.8396	1465.6879	733.3476	12
6	632.2345	316.6209	615.2079	308.1076	614.2239	307.6156	D	***1368.6715***	684.8394	1351.6450	676.3261	1350.6610	675.8341	11
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	T	***1253.6446***	627.3259	1236.6181	618.8127	1235.6340	618.3207	10
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	L	***1152.5969***	576.8021	1135.5704	568.2888	1134.5864	567.7968	9
9	974.4248	487.7160	957.3982	479.2028	956.4142	478.7107	Q	***1039.5129***	520.2601	1022.4863	511.7468	1021.5023	511.2548	8
10	1103.4674	552.2373	1086.4408	543.7240	1085.4568	543.2320	Q	***911.4543***	456.2308	894.4277	447.7175	893.4437	447.2255	7
11	1216.5514	608.7794	1199.5249	600.2661	1198.5409	599.7741	L	***782.4117***	391.7095	765.3851	383.1962	764.4011	382.7042	6
12	1363.5868	682.2971	1346.5603	673.7838	1345.5763	673.2918	M	***669.3276***	335.1675	652.3011	326.6542	651.3171	326.1622	5
13	1492.6294	746.8184	1475.6029	738.3051	1474.6189	737.8131	E	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	**1591.6978**	796.3526	1574.6713	787.8393	1573.6873	787.3473	V	***393.2496***	197.1285	376.2231	188.6152			3
15	**1738.7663**	869.8868	1721.7397	861.3735	1720.7557	860.8815	F	***294.1812***	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
109.0	1883.8645	0.0051	LGACNDTLQQLMEVFK	Deamidated N5, Q10 95.59%
95.6	1883.8645	0.0051	LGACNDTLQQLMEVFK	Deamidated N5, Q9 4.41%
58.8	1883.8645	0.0051	LGACNDTLQQLMEVFK	Deamidated Q9, Q10 0.00%
24.2	1881.8699	1.9997	DQNDQKLEKLMVQMK	
24.2	1881.8699	1.9997	DQNDQKLEKLMVQMK	
24.2	1881.8699	1.9997	DQNDQKLEKLMVQMK	
10.4	1883.8683	0.0013	SFPEGKSLGSEDSRNMK	
7.8	1882.8665	1.0031	MRAAADTLQGPMQAAYR	
6.9	1881.8535	2.0160	EMMPVWTEMITRGNR	
6.8	1882.8665	1.0031	MRAAADTLQGPMQAAYR	

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

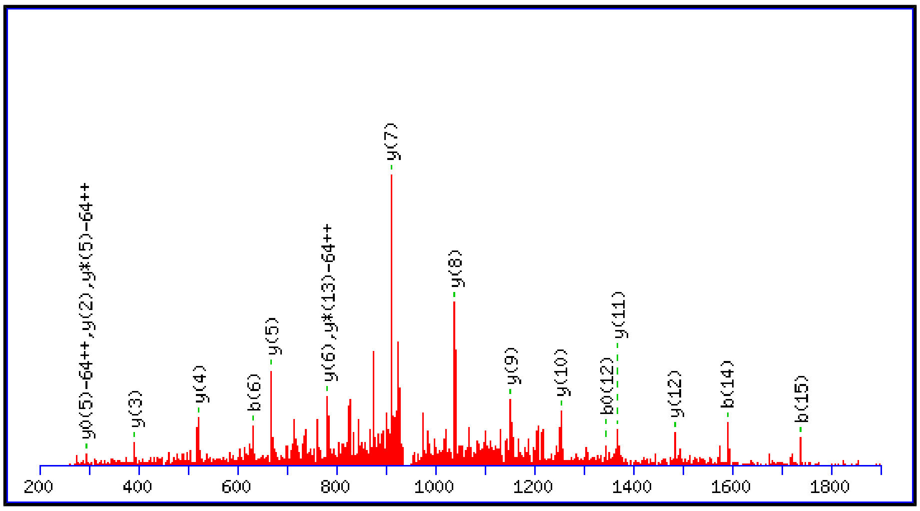
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

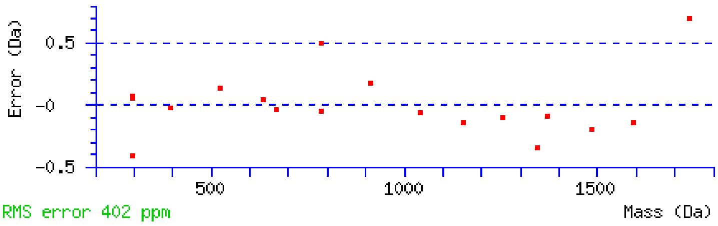
Match to Query 11097: 1883.865048 from(942.939800,2+) intensity(17743.3887) rtinseconds(2234) scans(6067) index(17810)
Title: 111019_Est_MI_YP_G_07Spectrum5236_scans__6067
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

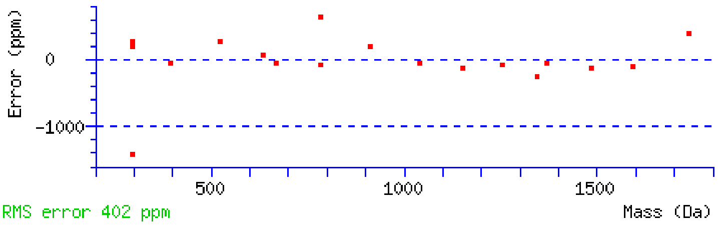
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1883.8645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Q9 : Deamidated (NQ)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 108 **Expect:** 2.5e-009
Matches : 18/246 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	114.0913	57.5493					L							16
2	171.1128	86.0600					G	1771.7877	886.3975	1754.7612	877.8842	1753.7772	877.3922	15
3	242.1499	121.5786					A	1714.7663	857.8868	1697.7397	849.3735	1696.7557	848.8815	14
4	402.1806	201.5939					C	1643.7291	822.3682	1626.7026	813.8549	1625.7186	813.3629	13
5	517.2075	259.1074	500.1810	250.5941			N	***1483.6985***	742.3529	1466.6719	733.8396	1465.6879	733.3476	12
6	**632.2345**	316.6209	615.2079	308.1076	614.2239	307.6156	D	***1368.6715***	684.8394	1351.6450	676.3261	1350.6610	675.8341	11
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	T	***1253.6446***	627.3259	1236.6181	618.8127	1235.6340	618.3207	10
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	L	***1152.5969***	576.8021	1135.5704	568.2888	1134.5864	567.7968	9
9	975.4088	488.2080	958.3822	479.6948	957.3982	479.2028	Q	***1039.5129***	520.2601	1022.4863	511.7468	1021.5023	511.2548	8
10	1103.4674	552.2373	1086.4408	543.7240	1085.4568	543.2320	Q	***910.4703***	455.7388	893.4437	447.2255	892.4597	446.7335	7
11	1216.5514	608.7794	1199.5249	600.2661	1198.5409	599.7741	L	***782.4117***	391.7095	765.3851	383.1962	764.4011	382.7042	6
12	1363.5868	682.2971	1346.5603	673.7838	1345.5763	673.2918	M	***669.3276***	335.1675	652.3011	326.6542	651.3171	326.1622	5
13	1492.6294	746.8184	1475.6029	738.3051	1474.6189	737.8131	E	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	**1591.6978**	796.3526	1574.6713	787.8393	1573.6873	787.3473	V	***393.2496***	197.1285	376.2231	188.6152			3
15	**1738.7663**	869.8868	1721.7397	861.3735	1720.7557	860.8815	F	***294.1812***	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
108.2	1883.8645	0.0006	LGACNDTLQQLMEVFK	Deamidated N5, Q9 95.59%
94.8	1883.8645	0.0006	LGACNDTLQQLMEVFK	Deamidated N5, Q10 4.41%
49.0	1883.8645	0.0006	LGACNDTLQQLMEVFK	Deamidated Q9, Q10 0.00%
34.6	1882.8539	1.0111	DQNDQKLEKLMVQMK	
7.4	1882.8584	1.0066	KFDEFQKDLNTNEPR	
6.7	1883.8683	-0.0033	SFPEGKSLGSEDSRNMK	
4.7	1881.8535	2.0115	EMMPVWTEMITRGNR	
4.4	1883.8584	0.0066	FMDENSLHRNHIDEK	
3.9	1882.8665	0.9985	MRAAADTLQGPMQAAYR	
3.8	1882.8665	0.9985	MRAAADTLQGPMQAAYR	

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

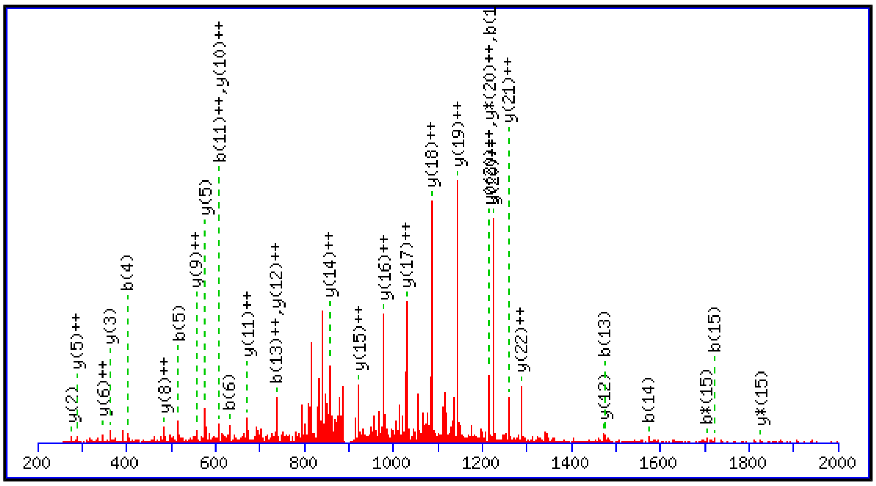
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFKFDTISEK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

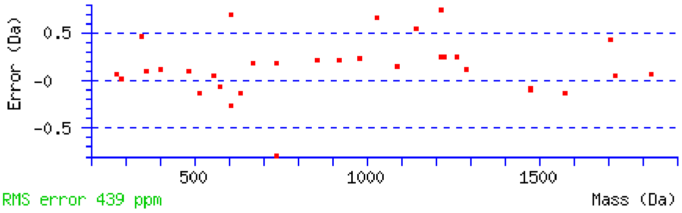
Match to Query 23836: 2687.292582 from(896.771470,3+) intensity(31208.8613) rtinseconds(2672) scans(7259) index(24200)
Title: 111019_Est_MI_YS_G_05Spectrum6313_scans__7259
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

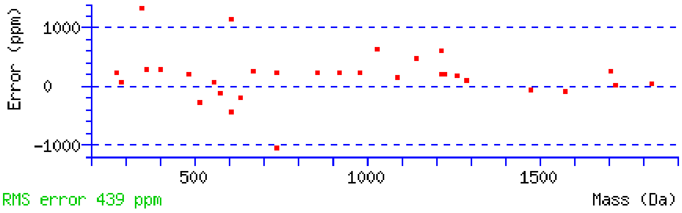
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2687.2822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
Ions Score: 103  Expect: 1.5e-008
Matches : 33/244 fragment ions using 54 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							23
2	171.1128	86.0600					G	2575.2055	1288.1064	2558.1789	1279.5931	2557.1949	1279.1011	22
3	242.1499	121.5786					A	2518.1840	1259.5956	2501.1575	1251.0824	2500.1734	1250.5904	21
4	**402.1806**	201.5939					C	2447.1469	1224.0771	2430.1203	1215.5638	2429.1363	1215.0718	20
5	**517.2075**	259.1074	500.1810	250.5941			N	2287.1162	1144.0618	2270.0897	1135.5485	2269.1057	1135.0565	19
6	**632.2345**	316.6209	615.2079	308.1076	614.2239	307.6156	D	2172.0893	1086.5483	2155.0628	1078.0350	2154.0787	1077.5430	18
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	T	2057.0624	1029.0348	2040.0358	1020.5215	2039.0518	1020.0295	17
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	L	1956.0147	978.5110	1938.9881	969.9977	1938.0041	969.5057	16
9	974.4248	487.7160	957.3982	479.2028	956.4142	478.7107	Q	1842.9306	921.9689	1825.9041	913.4557	1824.9200	912.9637	15
10	1102.4834	551.7453	1085.4568	543.2320	1084.4728	542.7400	Q	1714.8720	857.9397	1697.8455	849.4264	1696.8615	848.9344	14
11	**1215.5674**	608.2873	1198.5409	599.7741	1197.5569	599.2821	L	1586.8135	793.9104	1569.7869	785.3971	1568.8029	784.9051	13
12	1346.6079	673.8076	1329.5814	665.2943	1328.5973	664.8023	M	**1473.7294**	737.3683	1456.7028	728.8551	1455.7188	728.3631	12
13	**1475.6505**	738.3289	1458.6239	729.8156	1457.6399	729.3236	E	1342.6889	671.8481	1325.6624	663.3348	1324.6783	662.8428	11
14	**1574.7189**	787.8631	1557.6924	779.3498	1556.7083	778.8578	V	1213.6463	607.3268	1196.6198	598.8135	1195.6358	598.3215	10
15	**1721.7873**	861.3973	1704.7608	852.8840	1703.7768	852.3920	F	1114.5779	557.7926	1097.5514	549.2793	1096.5673	548.7873	9
16	1849.8823	925.4448	1832.8557	916.9315	1831.8717	916.4395	K	967.5095	484.2584	950.4829	475.7451	949.4989	475.2531	8
17	1996.9507	998.9790	1979.9242	990.4657	1978.9401	989.9737	F	839.4145	420.2109	822.3880	411.6976	821.4040	411.2056	7
18	2111.9776	1056.4925	2094.9511	1047.9792	2093.9671	1047.4872	D	692.3461	346.6767	675.3196	338.1634	674.3355	337.6714	6
19	2213.0253	1107.0163	2195.9988	1098.5030	2195.0148	1098.0110	T	**577.3192**	289.1632	560.2926	280.6499	559.3086	280.1579	5
20	2326.1094	1163.5583	2309.0828	1155.0451	2308.0988	1154.5530	I	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
21	2413.1414	1207.0743	2396.1149	1198.5611	2395.1308	1198.0691	S	**363.1874**	182.0974	346.1609	173.5841	345.1769	173.0921	3
22	2542.1840	1271.5956	2525.1575	1263.0824	2524.1734	1262.5904	E	**276.1554**	138.5813	259.1288	130.0681	258.1448	129.5761	2
23							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
102.6	2687.2822	0.0103	LGACNDTLQQLMEVFKFDTISEK	Deamidated N5 50.30%
100.5	2687.2822	0.0103	LGACNDTLQQLMEVFKFDTISEK	Deamidated Q10 30.66%
98.4	2687.2822	0.0103	LGACNDTLQQLMEVFKFDTISEK	Deamidated Q9 19.04%
85.0	2686.2982	0.9943	LGACNDTLQQLMEVFKFDTISEK	
7.5	2687.2789	0.0137	VPQIHDYLFDPQLNDVCLELTR	
6.1	2686.2756	1.0170	DEQSGGGNVSSTLLKQHLSLEPCTK	
5.1	2686.2756	1.0170	DEQSGGGNVSSTLLKQHLSLEPCTK	
5.0	2687.3007	-0.0081	LQEGMRADPGVLAALCEKTDNDIR	
4.3	2687.2885	0.0040	GQDSEESQEIQLAGRIPTGGSRLQK	
3.0	2687.2813	0.0113	ESIHEEIEFVEGSTININGAEIGAK	

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

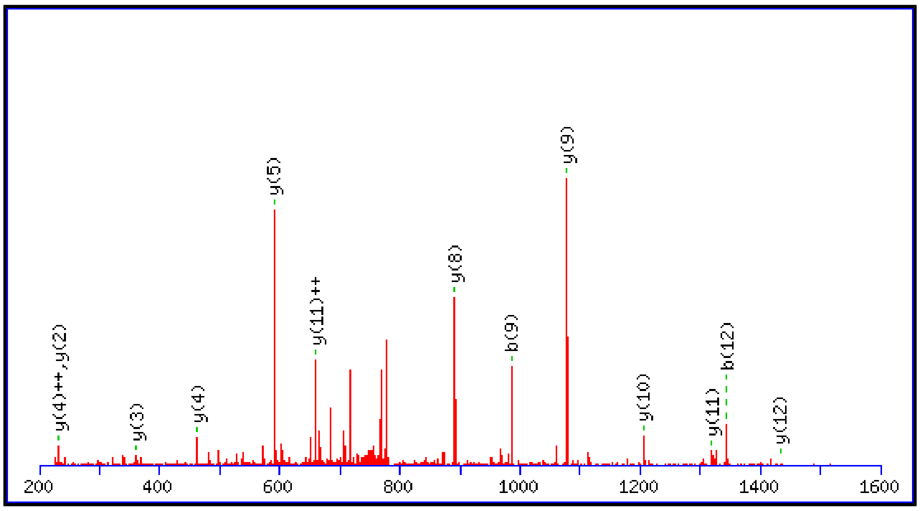
(MATRIX SCIENCE) Mascot Search Results

Peptide View

MS/MS Fragmentation of **AAINKWVSNKTEGR**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

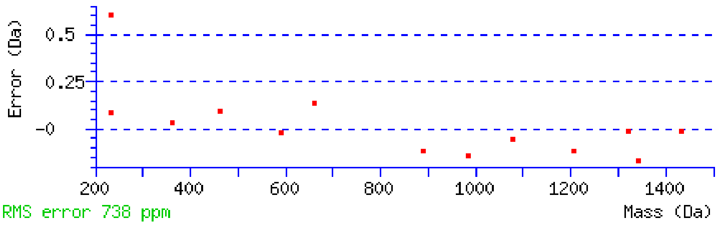
Match to Query 7409: 1573.822368 from(787.918460,2+) intensity(16921.1543) rtinseconds(485) scans(1017) index(22475)
Title: 111019_Est_MI_YS_G_03Spectrum851_scans__1017
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

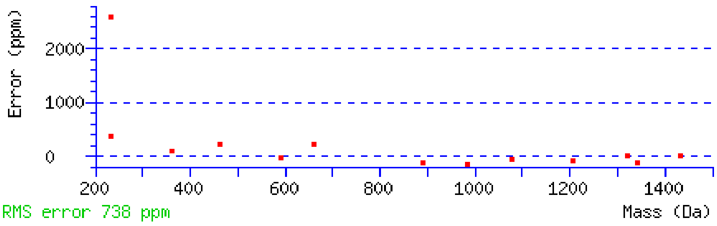
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1573.8212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 94 **Expect:** 8.6e-008
Matches : 13/132 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	72.0444	36.5258					A							14
2	143.0815	72.0444					A	1503.7914	752.3993	1486.7649	743.8861	1485.7809	743.3941	13
3	256.1656	128.5864					I	***1432.7543***	716.8808	1415.7278	708.3675	1414.7437	707.8755	12
4	370.2085	185.6079	353.1819	177.0946			N	***1319.6702***	660.3388	1302.6437	651.8255	1301.6597	651.3335	11
5	498.3035	249.6554	481.2769	241.1421			K	***1205.6273***	603.3173	1188.6008	594.8040	1187.6167	594.3120	10
6	684.3828	342.6950	667.3562	334.1817			W	***1077.5323***	539.2698	1060.5058	530.7565	1059.5218	530.2645	9
7	783.4512	392.2292	766.4246	383.7160			V	***891.4530***	446.2302	874.4265	437.7169	873.4425	437.2249	8
8	870.4832	435.7452	853.4567	427.2320	852.4726	426.7400	S	792.3846	396.6959	775.3581	388.1827	774.3741	387.6907	7
9	**985.5102**	493.2587	968.4836	484.7454	967.4996	484.2534	N	705.3526	353.1799	688.3260	344.6667	687.3420	344.1747	6
10	1113.6051	557.3062	1096.5786	548.7929	1095.5946	548.3009	K	***590.3257***	295.6665	573.2991	287.1532	572.3151	286.6612	5
11	1214.6528	607.8300	1197.6262	599.3168	1196.6422	598.8248	T	***462.2307***	231.6190	445.2041	223.1057	444.2201	222.6137	4
12	**1343.6954**	672.3513	1326.6688	663.8381	1325.6848	663.3461	E	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
13	1400.7169	700.8621	1383.6903	692.3488	1382.7063	691.8568	G	***232.1404***	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
94.1	1573.8212	0.0012	AAINKWVSNKTEGR	Deamidated N9 100.00%
41.3	1573.8212	0.0012	AAINKWVSNKTEGR	Deamidated N4 0.00%
18.6	1573.8246	-0.0022	QNMSKSLTLKNPGR	
18.6	1573.8246	-0.0022	QNMSKSLTLKNPGR	
11.5	1573.8246	-0.0022	AALNQALEMKRQGK	
8.7	1573.8174	0.0050	LAAIEQGTVLNWMK	
5.7	1573.8174	0.0050	LAAIEQGTVLNWMK	
4.2	1572.8181	1.0042	GSSVGVSQVIANPMVK	
3.9	1573.8246	-0.0022	AALNQALEMKRQGK	
1.6	1573.8286	-0.0062	AAIEIFKGLCQPAR	

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

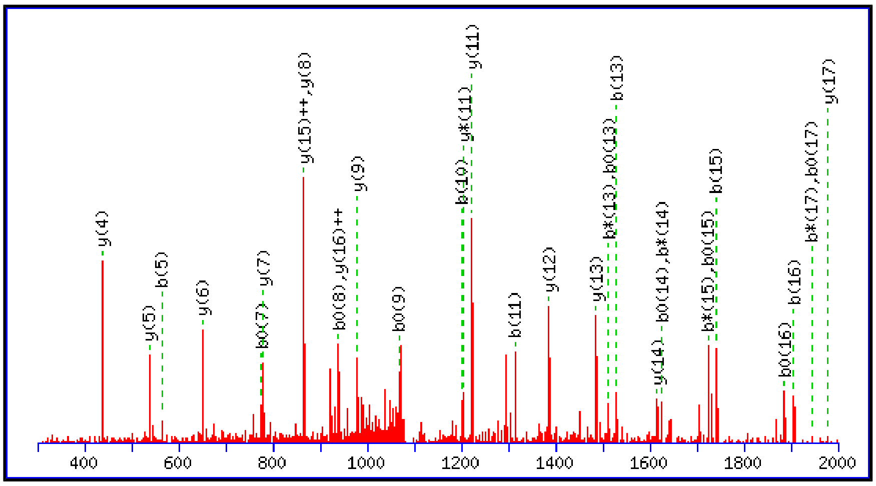
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLTFNETYQDISELVYGAK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

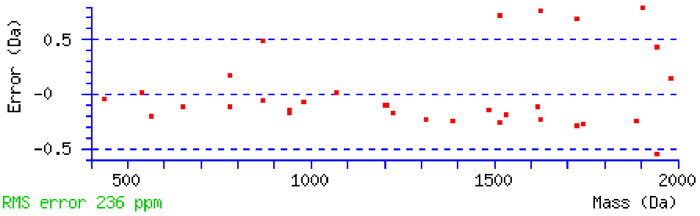
Match to Query 14464: 2178.037508 from(1090.026030,2+) intensity(5959.0059) rtinseconds(2626) scans(6749) index(5714)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum5963_scans__6749
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

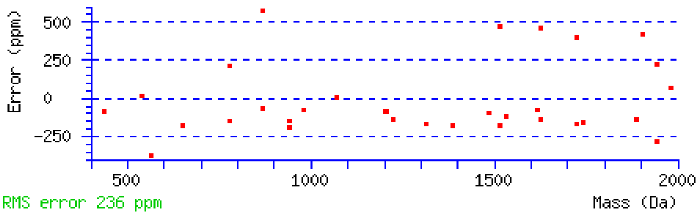
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2178.0368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
Ions Score: 85  Expect: 6.9e-007
Matches : 32/196 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	88.0393	44.5233			70.0287	35.5180	S							19
2	201.1234	101.0653			183.1128	92.0600	L	2092.0121	1046.5097	2074.9855	1037.9964	2074.0015	1037.5044	18
3	302.1710	151.5892			284.1605	142.5839	T	***1978.9280***	989.9677	1961.9015	981.4544	1960.9175	980.9624	17
4	449.2395	225.1234			431.2289	216.1181	F	1877.8804	939.4438	1860.8538	930.9305	1859.8698	930.4385	16
5	**564.2664**	282.6368	547.2399	274.1236	546.2558	273.6316	N	1730.8119	865.9096	1713.7854	857.3963	1712.8014	856.9043	15
6	693.3090	347.1581	676.2824	338.6449	675.2984	338.1529	E	***1615.7850***	808.3961	1598.7584	799.8829	1597.7744	799.3909	14
7	794.3567	397.6820	777.3301	389.1687	776.3461	388.6767	T	***1486.7424***	743.8748	1469.7159	735.3616	1468.7318	734.8696	13
8	957.4200	479.2136	940.3935	470.7004	939.4094	470.2084	Y	***1385.6947***	693.3510	1368.6682	684.8377	1367.6842	684.3457	12
9	1085.4786	543.2429	1068.4520	534.7297	1067.4680	534.2376	Q	***1222.6314***	611.8193	1205.6048	603.3061	1204.6208	602.8141	11
10	**1200.5055**	600.7564	1183.4790	592.2431	1182.4950	591.7511	D	1094.5728	547.7900	1077.5463	539.2768	1076.5623	538.7848	10
11	**1313.5896**	657.2984	1296.5630	648.7852	1295.5790	648.2932	I	***979.5459***	490.2766	962.5193	481.7633	961.5353	481.2713	9
12	1400.6216	700.8144	1383.5951	692.3012	1382.6111	691.8092	S	***866.4618***	433.7345	849.4353	425.2213	848.4512	424.7293	8
13	**1529.6642**	765.3357	1512.6377	756.8225	1511.6536	756.3305	E	***779.4298***	390.2185	762.4032	381.7053	761.4192	381.2132	7
14	1642.7483	821.8778	1625.7217	813.3645	1624.7377	812.8725	L	***650.3872***	325.6972	633.3606	317.1840			6
15	**1741.8167**	871.4120	1724.7901	862.8987	1723.8061	862.4067	V	***537.3031***	269.1552	520.2766	260.6419			5
16	**1904.8800**	952.9436	1887.8535	944.4304	1886.8695	943.9384	Y	***438.2347***	219.6210	421.2082	211.1077			4
17	1961.9015	981.4544	1944.8749	972.9411	1943.8909	972.4491	G	275.1714	138.0893	258.1448	129.5761			3
18	2032.9386	1016.9729	2015.9120	1008.4597	2014.9280	1007.9677	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.4	2178.0368	0.0007	SLTFNETYQDISELVYGAK	Deamidated N5 98.86%
66.0	2178.0368	0.0007	SLTFNETYQDISELVYGAK	Deamidated Q9 1.14%
1.0	2176.0259	2.0116	DVDISNFFCDPSQLLHLR	

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

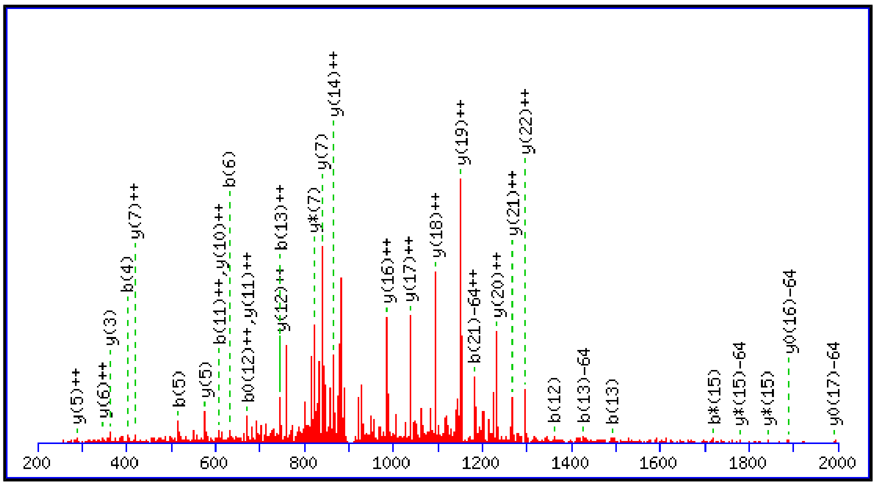
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGACNDTLQQLMEVFKFDTISEK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

Match to Query 25360: 2703.288492 from(902.103440,3+) intensity(59493.2109) rtinseconds(2430) scans(6441) index(16248)
Title: 111019_Est_MI_YP_G_05Spectrum5517_scans__6441
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

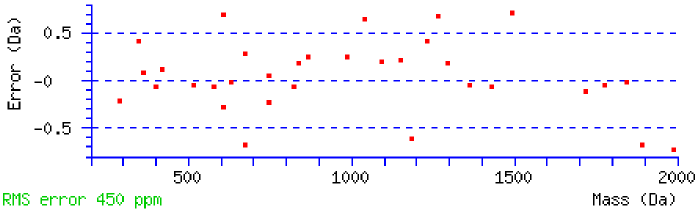
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

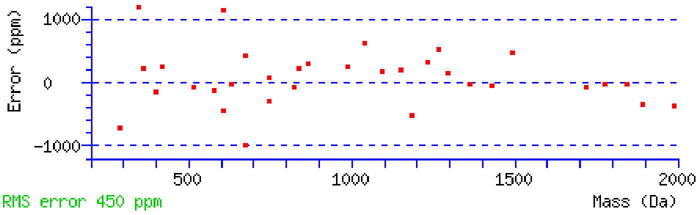


```
Monoisotopic mass of neutral peptide Mr(calc): 2703.2772
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
M12    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 79  Expect: 3.2e-006
Matches : 33/376 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	114.0913	57.5493					**L**							23
2	171.1128	86.0600					**G**	2591.2004	1296.1038	2574.1738	1287.5906	2573.1898	1287.0985	22
3	242.1499	121.5786					**A**	2534.1789	1267.5931	2517.1524	1259.0798	2516.1684	1258.5878	21
4	**402.1806**	201.5939					**C**	2463.1418	1232.0745	2446.1153	1223.5613	2445.1312	1223.0693	20
5	**517.2075**	259.1074	500.1810	250.5941			**N**	2303.1112	1152.0592	2286.0846	1143.5459	2285.1006	1143.0539	19
6	**632.2345**	316.6209	615.2079	308.1076	614.2239	307.6156	**D**	2188.0842	1094.5457	2171.0577	1086.0325	2170.0736	1085.5405	18
7	733.2821	367.1447	716.2556	358.6314	715.2716	358.1394	**T**	2073.0573	1037.0323	2056.0307	1028.5190	2055.0467	1028.0270	17
8	846.3662	423.6867	829.3396	415.1735	828.3556	414.6815	**L**	1972.0096	986.5084	1954.9830	977.9952	1953.9990	977.5032	16
9	974.4248	487.7160	957.3982	479.2028	956.4142	478.7107	**Q**	1858.9255	929.9664	1841.8990	921.4531	1840.9150	920.9611	15
10	1102.4834	551.7453	1085.4568	543.2320	1084.4728	542.7400	**Q**	1730.8670	865.9371	1713.8404	857.4238	1712.8564	856.9318	14
11	1215.5674	608.2873	1198.5409	599.7741	1197.5569	599.2821	**L**	1602.8084	801.9078	1585.7818	793.3946	1584.7978	792.9025	13
12	**1362.6028**	681.8050	1345.5763	673.2918	1344.5923	672.7998	**M**	1489.7243	745.3658	1472.6978	736.8525	1471.7137	736.3605	12
13	**1491.6454**	746.3263	1474.6189	737.8131	1473.6348	737.3211	**E**	1342.6889	671.8481	1325.6624	663.3348	1324.6783	662.8428	11
14	1590.7138	795.8605	1573.6873	787.3473	1572.7033	786.8553	**V**	1213.6463	607.3268	1196.6198	598.8135	1195.6358	598.3215	10
15	1737.7822	869.3948	1720.7557	860.8815	1719.7717	860.3895	**F**	1114.5779	557.7926	1097.5514	549.2793	1096.5673	548.7873	9
16	1865.8772	933.4422	1848.8507	924.9290	1847.8666	924.4370	**K**	967.5095	484.2584	950.4829	475.7451	949.4989	475.2531	8
17	2012.9456	1006.9764	1995.9191	998.4632	1994.9350	997.9712	**F**	**839.4145**	420.2109	822.3880	411.6976	821.4040	411.2056	7
18	2127.9726	1064.4899	2110.9460	1055.9766	2109.9620	1055.4846	**D**	692.3461	346.6767	675.3196	338.1634	674.3355	337.6714	6
19	2229.0202	1115.0138	2211.9937	1106.5005	2211.0097	1106.0085	**T**	**577.3192**	289.1632	560.2926	280.6499	559.3086	280.1579	5
20	2342.1043	1171.5558	2325.0778	1163.0425	2324.0937	1162.5505	**I**	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
21	2429.1363	1215.0718	2412.1098	1206.5585	2411.1258	1206.0665	**S**	**363.1874**	182.0974	346.1609	173.5841	345.1769	173.0921	3
22	2558.1789	1279.5931	2541.1524	1271.0798	2540.1684	1270.5878	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2

23							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.0	2703.2772	0.0113	LGACNDTLQQLMEVFKFDTISEK	Deamidated N5 36.90%
78.3	2703.2772	0.0113	LGACNDTLQQLMEVFKFDTISEK	Deamidated Q10 31.55%
78.3	2703.2772	0.0113	LGACNDTLQQLMEVFKFDTISEK	Deamidated Q9 31.55%
51.1	2702.2932	0.9953	LGACNDTLQQLMEVFKFDTISEK	
8.4	2703.2987	-0.0102	ENDFAQSGQDAVPESPSKLSSKRPK	
7.6	2702.2792	1.0093	MDALFMDLPTGPRGQQAQPQRAEK	
7.3	2701.2905	1.9980	SSSHDPNSQTLDISPSKEPFMLVGK	
5.0	2703.2987	-0.0102	ENDFAQSGQDAVPESPSKLSSKRPK	
5.0	2703.2987	-0.0102	ENDFAQSGQDAVPESPSKLSSKRPK	
4.1	2702.2792	1.0093	MDALFMDLPTGPRGQQAQPQRAEK	

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

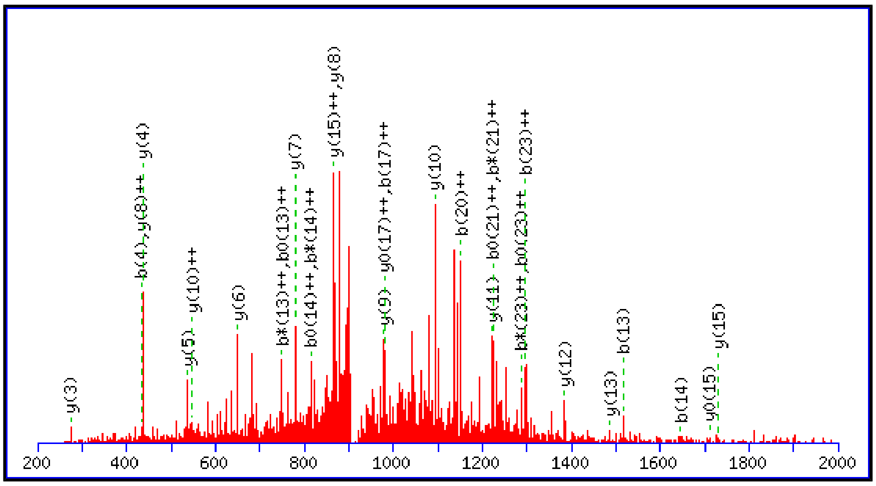
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LFGDKSLTFNETYQDISELVYGAK**
Found in **P01008** in **con_Xuniprot_HUMAN3**, ANT3_HUMAN Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

Match to Query 25458: 2738.339592 from(913.787140,3+) intensity(29754.5840) rtinseconds(2648) scans(6971) index(24901)
Title: 111019_Est_MI_YS_G_06Spectrum6087_scans__6971
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

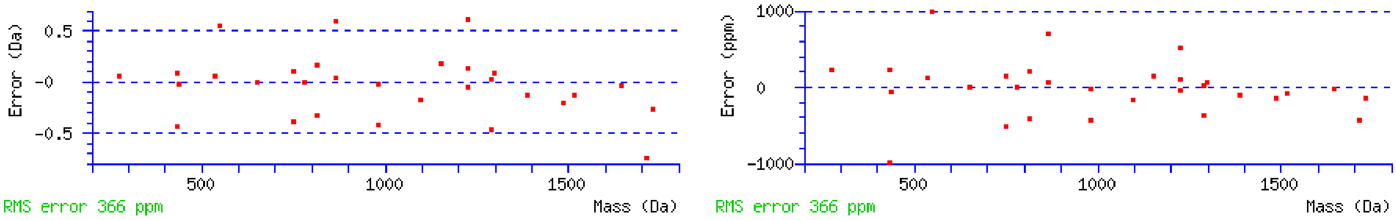
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2738.3327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0019
Matches : 31/250 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							24
2	261.1598	131.0835					F	2626.2559	1313.6316	2609.2294	1305.1183	2608.2453	1304.6263	23
3	318.1812	159.5942					G	2479.1875	1240.0974	2462.1609	1231.5841	2461.1769	1231.0921	22
4	**433.2082**	217.1077			415.1976	208.1024	D	2422.1660	1211.5867	2405.1395	1203.0734	2404.1555	1202.5814	21
5	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	K	2307.1391	1154.0732	2290.1125	1145.5599	2289.1285	1145.0679	20
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	S	2179.0441	1090.0257	2162.0176	1081.5124	2161.0336	1081.0204	19
7	761.4192	381.2132	744.3927	372.7000	743.4087	372.2080	L	2092.0121	1046.5097	2074.9855	1037.9964	2074.0015	1037.5044	18
8	862.4669	431.7371	845.4403	423.2238	844.4563	422.7318	T	1978.9280	989.9677	1961.9015	981.4544	1960.9175	980.9624	17
9	1009.5353	505.2713	992.5088	496.7580	991.5247	496.2660	F	1877.8804	939.4438	1860.8538	930.9305	1859.8698	930.4385	16
10	1124.5623	562.7848	1107.5357	554.2715	1106.5517	553.7795	N	***1730.8119***	865.9096	1713.7854	857.3963	1712.8014	856.9043	15
11	1253.6048	627.3061	1236.5783	618.7928	1235.5943	618.3008	E	1615.7850	808.3961	1598.7584	799.8829	1597.7744	799.3909	14
12	1354.6525	677.8299	1337.6260	669.3166	1336.6420	668.8246	T	***1486.7424***	743.8748	1469.7159	735.3616	1468.7318	734.8696	13
13	**1517.7159**	759.3616	1500.6893	750.8483	1499.7053	750.3563	Y	***1385.6947***	693.3510	1368.6682	684.8377	1367.6842	684.3457	12
14	**1645.7744**	823.3909	1628.7479	814.8776	1627.7639	814.3856	Q	***1222.6314***	611.8193	1205.6048	603.3061	1204.6208	602.8141	11
15	1760.8014	880.9043	1743.7748	872.3911	1742.7908	871.8990	D	***1094.5728***	547.7900	1077.5463	539.2768	1076.5623	538.7848	10
16	1873.8854	937.4464	1856.8589	928.9331	1855.8749	928.4411	I	***979.5459***	490.2766	962.5193	481.7633	961.5353	481.2713	9
17	1960.9175	**980.9624**	1943.8909	972.4491	1942.9069	971.9571	S	***866.4618***	433.7345	849.4353	425.2213	848.4512	424.7293	8
18	2089.9601	1045.4837	2072.9335	1036.9704	2071.9495	1036.4784	E	***779.4298***	390.2185	762.4032	381.7053	761.4192	381.2132	7
19	2203.0441	1102.0257	2186.0176	1093.5124	2185.0336	1093.0204	L	***650.3872***	325.6972	633.3606	317.1840			6
20	2302.1125	**1151.5599**	2285.0860	1143.0466	2284.1020	1142.5546	V	***537.3031***	269.1552	520.2766	260.6419			5
21	2465.1759	1233.0916	2448.1493	1224.5783	2447.1653	1224.0863	Y	***438.2347***	219.6210	421.2082	211.1077			4
22	2522.1973	1261.6023	2505.1708	1253.0890	2504.1868	1252.5970	G	***275.1714***	138.0893	258.1448	129.5761			3
23	2593.2344	**1297.1209**	2576.2079	1288.6076	2575.2239	1288.1156	A	218.1499	109.5786	201.1234	101.0653			2

24							**K**	147.1128	74.0600	130.0863	65.5468			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.2	2738.3327	0.0069	LFGDKSLTFNETYQDISELVYGAK	Deamidated N10 98.93%
36.8	2737.3487	0.9909	LFGDKSLTFNETYQDISELVYGAK	
32.5	2738.3327	0.0069	LFGDKSLTFNETYQDISELVYGAK	Deamidated Q14 1.07%
1.9	2738.3472	-0.0077	NSTKQEILAALEKGCSFLPDPYQK	

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

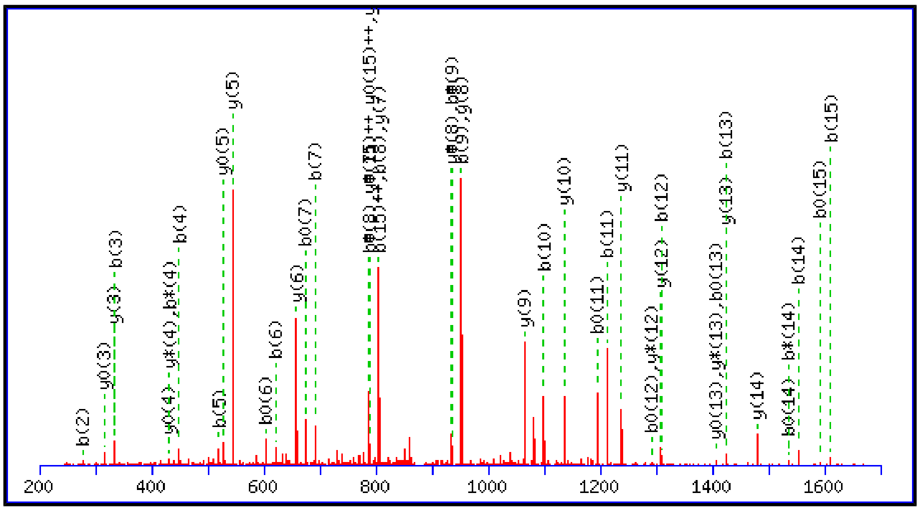
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLGNATAIFFLPDEGK**
Found in **P01009** in **con_Xuniprot_HUMAN3**, A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3

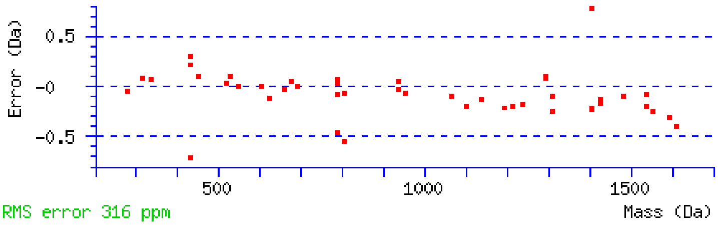
Match to Query 9665: 1755.878848 from(878.946700,2+) intensity(196314.5156) rtinseconds(2372) scans(6296) index(4622)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum5364_scans__6296
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

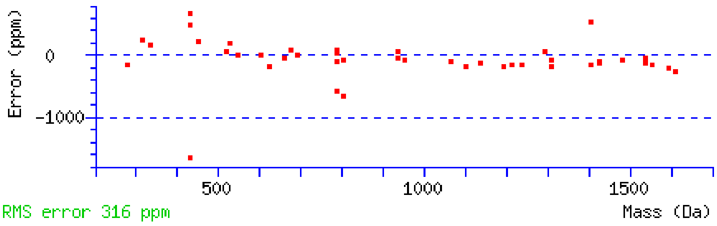
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1755.8719
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 117 **Expect:** 4e-010
Matches : 52/160 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							16
2	***277.1547***	139.0810					L	1593.8159	797.4116	1576.7894	788.8983	1575.8053	788.4063	15
3	***334.1761***	167.5917					G	**1480.7318**	740.8696	1463.7053	732.3563	1462.7213	731.8643	14
4	***449.2031***	225.1052	432.1765	216.5919			N	**1423.7104**	712.3588	1406.6838	703.8456	1405.6998	703.3535	13
5	***520.2402***	260.6237	503.2136	252.1105			A	**1308.6834**	654.8454	1291.6569	646.3321	1290.6729	645.8401	12
6	***621.2879***	311.1476	604.2613	302.6343	603.2773	302.1423	T	**1237.6463**	619.3268	1220.6198	610.8135	1219.6358	610.3215	11
7	***692.3250***	346.6661	675.2984	338.1529	674.3144	337.6608	A	**1136.5986**	568.8030	1119.5721	560.2897	1118.5881	559.7977	10
8	***805.4090***	403.2082	788.3825	394.6949	787.3985	394.2029	I	**1065.5615**	533.2844	1048.5350	524.7711	1047.5510	524.2791	9
9	***952.4775***	476.7424	935.4509	468.2291	934.4669	467.7371	F	**952.4775**	476.7424	935.4509	468.2291	934.4669	467.7371	8
10	***1099.5459***	550.2766	1082.5193	541.7633	1081.5353	541.2713	F	**805.4090**	403.2082	788.3825	394.6949	787.3985	394.2029	7
11	***1212.6299***	606.8186	1195.6034	598.3053	1194.6194	597.8133	L	**658.3406**	329.6740	641.3141	321.1607	640.3301	320.6687	6
12	***1309.6827***	655.3450	1292.6562	646.8317	1291.6721	646.3397	P	**545.2566**	273.1319	528.2300	264.6186	527.2460	264.1266	5
13	***1424.7096***	712.8585	1407.6831	704.3452	1406.6991	703.8532	D	448.2038	224.6055	431.1773	216.0923	430.1932	215.6003	4
14	***1553.7522***	777.3798	1536.7257	768.8665	1535.7417	768.3745	E	**333.1769**	167.0921	316.1503	158.5788	315.1663	158.0868	3
15	***1610.7737***	805.8905	1593.7472	797.3772	1592.7631	796.8852	G	204.1343	102.5708	187.1077	94.0575			2
16							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
117.5	1755.8719	0.0069	YLGNATAIFFLPDEGK
8.4	1755.8791	-0.0003	FGKEGTSLARFNEATK
6.5	1755.8787	0.0002	IEVFNNSMMITLLSK
5.3	1754.8695	1.0094	FKMLQSELAVCREK
4.9	1755.8753	0.0036	MPQKGNLLIYTEFGK
3.7	1753.8669	2.0120	SNCTIEPDAVHIKAAK
3.5	1753.8787	2.0001	TENFKIAFYLSHQR
2.2	1755.8766	0.0022	YRMTSSARFYSLFK
2.0	1754.8812	0.9976	RIGGIRNEGHFAQGDK
1.9	1754.8808	0.9981	VQRVVGVTMGDMYRK

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

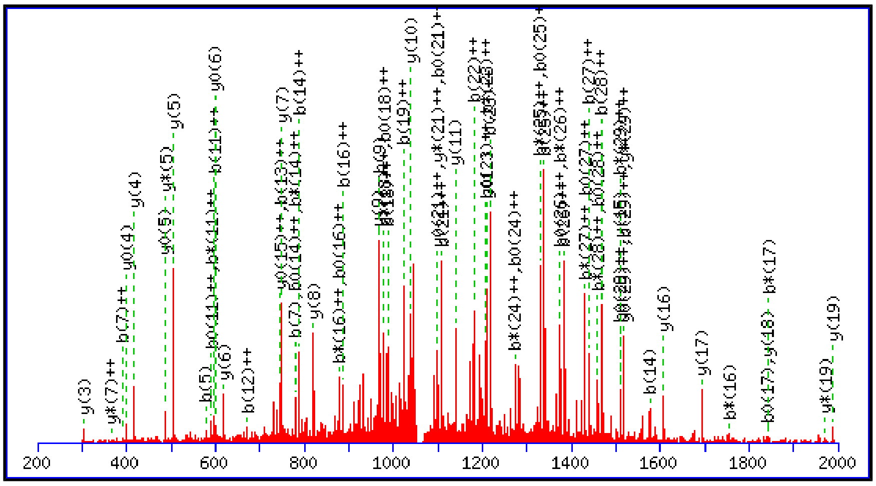
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLAHQSNSTNIFFSPVSIATAFAMLSLGTK**
Found in **G3V387** in **con_Xuniprot_HUMAN3**, G3V387_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=2 SV=1

Match to Query 27358: 3181.620282 from(1061.547370,3+) intensity(21636.8711) rtinseconds(2972) scans(7856) index(8648)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum6854_scans__7856
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

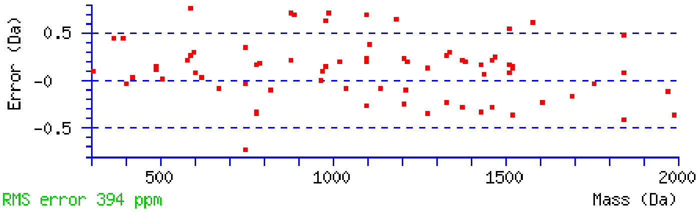
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

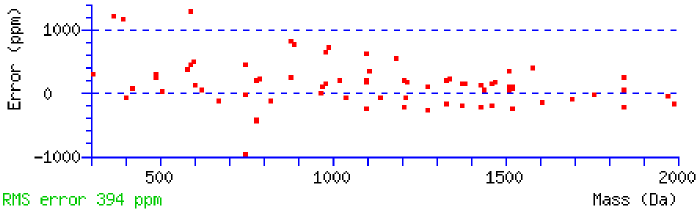


```
Monoisotopic mass of neutral peptide Mr(calc): 3181.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7      : Deamidated (NQ)
Ions Score: 108  Expect: 3.7e-009
Matches : 73/336 fragment ions using 85 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							30
2	242.1499	121.5786	225.1234	113.0653			L	3054.5605	1527.7839	3037.5339	1519.2706	3036.5499	1518.7786	29
3	313.1870	157.0972	296.1605	148.5839			A	2941.4764	1471.2418	2924.4499	1462.7286	2923.4659	1462.2366	28
4	450.2459	225.6266	433.2194	217.1133			H	2870.4393	1435.7233	2853.4128	1427.2100	2852.4287	1426.7180	27
5	**578.3045**	289.6559	561.2780	281.1426			Q	2733.3804	1367.1938	2716.3538	1358.6806	2715.3698	1358.1886	26
6	665.3365	333.1719	648.3100	324.6586	647.3260	324.1666	S	2605.3218	1303.1645	2588.2953	1294.6513	2587.3113	1294.1593	25
7	**780.3635**	***390.6854***	763.3369	382.1721	762.3529	381.6801	N	2518.2898	1259.6485	2501.2632	1251.1353	2500.2792	1250.6433	24
8	867.3955	434.2014	850.3690	425.6881	849.3850	425.1961	S	2403.2628	1202.1351	2386.2363	1193.6218	2385.2523	1193.1298	23
9	**968.4432**	484.7252	951.4167	476.2120	950.4326	475.7200	T	2316.2308	1158.6190	2299.2043	1150.1058	2298.2203	1149.6138	22
10	1082.4861	541.7467	1065.4596	533.2334	1064.4756	532.7414	N	2215.1831	1108.0952	2198.1566	1099.5819	2197.1726	1099.0899	21
11	1195.5702	***598.2887***	1178.5436	589.7755	1177.5596	589.2835	I	2101.1402	1051.0737	2084.1137	1042.5605	2083.1296	1042.0685	20
12	1342.6386	***671.8229***	1325.6121	663.3097	1324.6280	662.8177	F	***1988.0561***	994.5317	1971.0296	986.0184	1970.0456	985.5264	19
13	1489.7070	***745.3571***	1472.6805	736.8439	1471.6965	736.3519	F	***1840.9877***	920.9975	1823.9612	912.4842	1822.9772	911.9922	18
14	**1576.7390**	***788.8732***	1559.7125	780.3599	1558.7285	779.8679	S	***1693.9193***	847.4633	1676.8928	838.9500	1675.9088	838.4580	17
15	1673.7918	837.3995	1656.7653	828.8863	1655.7812	828.3943	P	***1606.8873***	803.9473	1589.8607	795.4340	1588.8767	794.9420	16
16	1772.8602	***886.9338***	1755.8337	878.4205	1754.8497	877.9285	V	***1509.8345***	755.4209	1492.8080	746.9076	1491.8240	746.4156	15
17	1859.8923	930.4498	1842.8657	921.9365	1841.8817	921.4445	S	1410.7661	705.8867	1393.7396	697.3734	1392.7556	696.8814	14
18	1972.9763	***986.9918***	1955.9498	978.4785	1954.9658	977.9865	I	1323.7341	662.3707	1306.7075	653.8574	1305.7235	653.3654	13
19	2044.0134	***1022.5104***	2026.9869	1013.9971	2026.0029	1013.5051	A	***1210.6500***	605.8286	1193.6235	597.3154	1192.6395	596.8234	12
20	2145.0611	1073.0342	2128.0346	1064.5209	2127.0505	1064.0289	T	***1139.6129***	570.3101	1122.5864	561.7968	1121.6023	561.3048	11
21	2216.0982	***1108.5527***	2199.0717	1100.0395	2198.0877	1099.5475	A	***1038.5652***	519.7863	1021.5387	511.2730	1020.5547	510.7810	10
22	2363.1666	***1182.0870***	2346.1401	1173.5737	2345.1561	1173.0817	F	***967.5281***	484.2677	950.5016	475.7544	949.5176	475.2624	9

23	2434.2038	***1217.6055***	2417.1772	1209.0922	2416.1932	1208.6002	**A**	***820.4597***	410.7335	803.4332	402.2202	802.4491	401.7282	**8**
24	2565.2442	1283.1258	2548.2177	1274.6125	2547.2337	1274.1205	**M**	***749.4226***	375.2149	732.3960	366.7017	731.4120	366.2096	**7**
25	2678.3283	***1339.6678***	2661.3018	1331.1545	2660.3177	1330.6625	**L**	***618.3821***	309.6947	601.3556	301.1814	600.3715	300.6894	**6**
26	2765.3603	***1383.1838***	2748.3338	1374.6705	2747.3498	1374.1785	**S**	***505.2980***	253.1527	488.2715	244.6394	487.2875	244.1474	**5**
27	2878.4444	***1439.7258***	2861.4178	1431.2126	2860.4338	1430.7206	**L**	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	**4**
28	2935.4659	***1468.2366***	2918.4393	1459.7233	2917.4553	1459.2313	**G**	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
29	3036.5135	***1518.7604***	3019.4870	1510.2471	3018.5030	1509.7551	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
30							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
107.6	3181.6118	0.0085	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	Deamidated N7 36.07%
107.6	3181.6118	0.0085	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	Deamidated Q5 36.07%
105.9	3181.6118	0.0085	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	Deamidated Q1 24.55%
97.2	3181.6118	0.0085	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	Deamidated N10 3.31%
70.3	3180.6278	0.9925	QLAHQSNSTNIFFSPVSIATAFAMLSLGTK	
18.3	3181.6215	-0.0012	TINKGQNTLNATQDKEDNTELVHLSLSAK	
5.7	3180.6199	1.0004	MEYLIGIQGPDYVLVASDRVAASNIVQMK	
5.6	3180.6060	1.0143	QVPELMHHQLTLNGCAEEKQVEHIIVK	
5.6	3180.6060	1.0143	QVPELMHHQLTLNGCAEEKQVEHIIVK	
2.6	3180.6060	1.0143	QVPELMHHQLTLNGCAEEKQVEHIIVK	

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

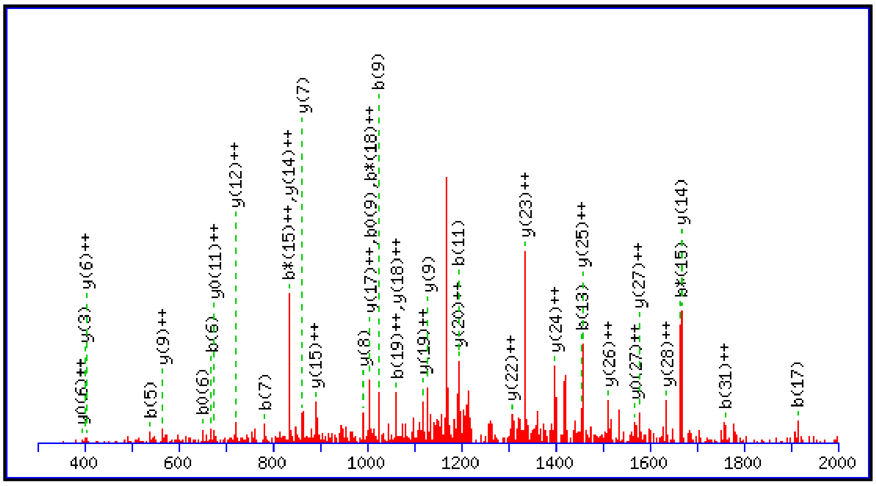
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR**
Found in **G3V2B9** in **con_Xuniprot_HUMAN3**, G3V2B9_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=2 SV=1

Match to Query 27982: 3692.798772 from(1231.940200,3+) intensity(5404.9976) rtinseconds(2718) scans(6633) index(27951)
Title: 111019_Est_MI_YS_G_11Spectrum5817_scans__6633
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

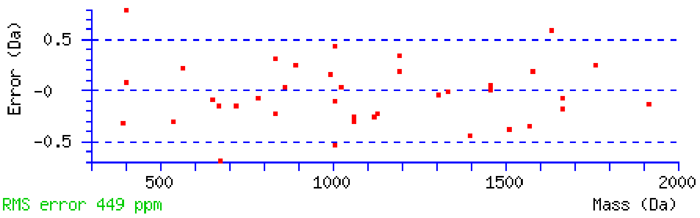
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

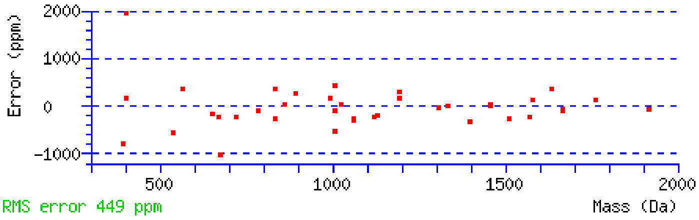


Monoisotopic mass of neutral peptide Mr(calc): 3692.7845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Q22 : Deamidated (NQ)
Ions Score: 103 **Expect:** 1.3e-008
Matches : 38/342 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							32
2	187.0713	94.0393			169.0608	85.0340	D	3622.7548	1811.8810	3605.7282	1803.3677	3604.7442	1802.8757	31
3	288.1190	144.5631			270.1084	135.5579	T	3507.7278	1754.3675	3490.7013	1745.8543	3489.7173	1745.3623	30
4	425.1779	213.0926			407.1674	204.0873	H	3406.6801	1703.8437	3389.6536	1695.3304	3388.6696	1694.8384	29
5	**540.2049**	270.6061			522.1943	261.6008	D	3269.6212	1635.3143	3252.5947	1626.8010	3251.6107	1626.3090	28
6	**669.2475**	335.1274			651.2369	326.1221	E	3154.5943	1577.8008	3137.5677	1569.2875	3136.5837	1568.7955	27
7	**782.3315**	391.6694			764.3210	382.6641	I	3025.5517	1513.2795	3008.5251	1504.7662	3007.5411	1504.2742	26
8	895.4156	448.2114			877.4050	439.2061	L	2912.4676	1456.7375	2895.4411	1448.2242	2894.4571	1447.7322	25
9	**1024.4582**	512.7327			1006.4476	503.7274	E	2799.3836	1400.1954	2782.3570	1391.6821	2781.3730	1391.1901	24
10	1081.4796	541.2435			1063.4691	532.2382	G	2670.3410	1335.6741	2653.3144	1327.1609	2652.3304	1326.6688	23
11	**1194.5637**	597.7855			1176.5531	588.7802	L	2613.3195	1307.1634	2596.2930	1298.6501	2595.3089	1298.1581	22
12	1308.6066	654.8070	1291.5801	646.2937	1290.5961	645.8017	N	2500.2354	1250.6214	2483.2089	1242.1081	2482.2249	1241.6161	21
13	**1455.6751**	728.3412	1438.6485	719.8279	1437.6645	719.3359	F	2386.1925	1193.5999	2369.1660	1185.0866	2368.1820	1184.5946	20
14	1570.7020	785.8546	1553.6754	777.3414	1552.6914	776.8494	N	2239.1241	1120.0657	2222.0976	1111.5524	2221.1135	1111.0604	19
15	1683.7861	842.3967	1666.7595	833.8834	1665.7755	833.3914	L	2124.0972	1062.5522	2107.0706	1054.0389	2106.0866	1053.5469	18
16	1784.8337	892.9205	1767.8072	884.4072	1766.8232	883.9152	T	2011.0131	1006.0102	1993.9866	997.4969	1993.0025	997.0049	17
17	**1913.8763**	957.4418	1896.8498	948.9285	1895.8658	948.4365	E	1909.9654	955.4863	1892.9389	946.9731	1891.9549	946.4811	16
18	2026.9604	1013.9838	2009.9338	1005.4706	2008.9498	1004.9786	I	1780.9228	890.9651	1763.8963	882.4518	1762.9123	881.9598	15
19	2124.0132	1062.5102	2106.9866	1053.9969	2106.0026	1053.5049	P	**1667.8388**	834.4230	1650.8122	825.9097	1649.8282	825.4177	14
20	2253.0557	1127.0315	2236.0292	1118.5182	2235.0452	1118.0262	E	1570.7860	785.8966	1553.7595	777.3834	1552.7754	776.8914	13
21	2324.0929	1162.5501	2307.0663	1154.0368	2306.0823	1153.5448	A	1441.7434	721.3753	1424.7169	712.8621	1423.7328	712.3701	12

22	2453.1355	1227.0714	2436.1089	1218.5581	2435.1249	1218.0661	**Q**	1370.7063	685.8568	1353.6797	677.3435	1352.6957	676.8515	**11**
23	2566.2195	1283.6134	2549.1930	1275.1001	2548.2090	1274.6081	**I**	1241.6637	621.3355	1224.6371	612.8222	1223.6531	612.3302	**10**
24	2703.2784	1352.1429	2686.2519	1343.6296	2685.2679	1343.1376	**H**	**1128.5796**	564.7935	1111.5531	556.2802	1110.5691	555.7882	**9**
25	2832.3210	1416.6642	2815.2945	1408.1509	2814.3105	1407.6589	**E**	**991.5207**	496.2640	974.4942	487.7507	973.5102	487.2587	**8**
26	2889.3425	1445.1749	2872.3159	1436.6616	2871.3319	1436.1696	**G**	**862.4781**	431.7427	845.4516	423.2294	844.4676	422.7374	**7**
27	3036.4109	1518.7091	3019.3844	1510.1958	3018.4003	1509.7038	**F**	805.4567	403.2320	788.4301	394.7187	787.4461	394.2267	**6**
28	3164.4695	1582.7384	3147.4429	1574.2251	3146.4589	1573.7331	**Q**	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	**5**
29	3293.5121	1647.2597	3276.4855	1638.7464	3275.5015	1638.2544	**E**	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	**4**
30	3406.5961	1703.8017	3389.5696	1695.2884	3388.5856	1694.7964	**L**	**401.2871**	201.1472	384.2605	192.6339			**3**
31	3519.6802	1760.3437	3502.6537	1751.8305	3501.6696	1751.3385	**L**	288.2030	144.6051	271.1765	136.0919			**2**
32							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
103.1	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N14, Q22 67.32%
96.3	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N14, Q28 13.94%
95.3	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N12, N14 10.99%
91.0	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N12, Q22 4.09%
89.1	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated Q22, Q28 2.66%
84.8	3692.7845	0.0142	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N12, Q28 1.00%
81.1	3691.8005	0.9982	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	
81.1	3691.8005	0.9982	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	
77.3	3691.8005	0.9982	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	
71.5	3691.8005	0.9982	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	

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

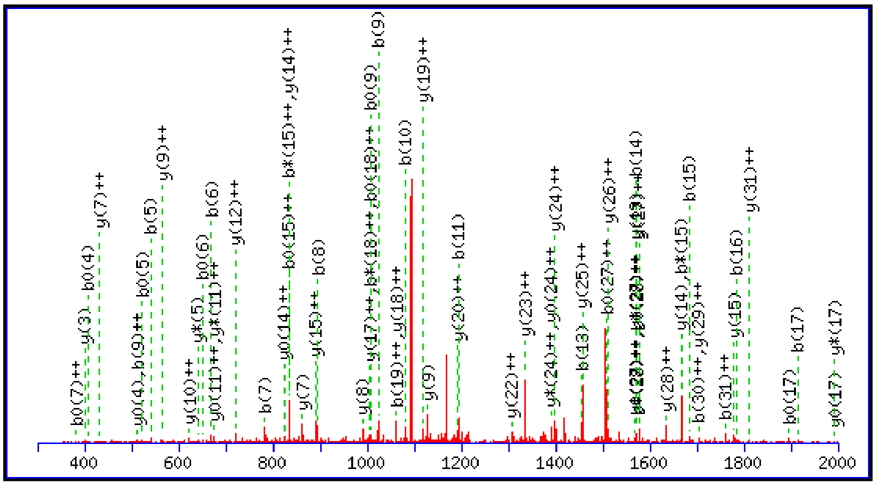
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR**
Found in **G3V2B9** in **con_Xuniprot_HUMAN3**, G3V2B9_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=2 SV=1

Match to Query 27983: 3692.807892 from(1231.943240,3+) intensity(0.0000) rtinseconds(3026) scans(7863) index(1065)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum6910_scans__7863
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

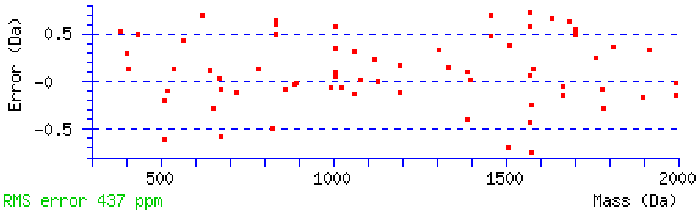
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

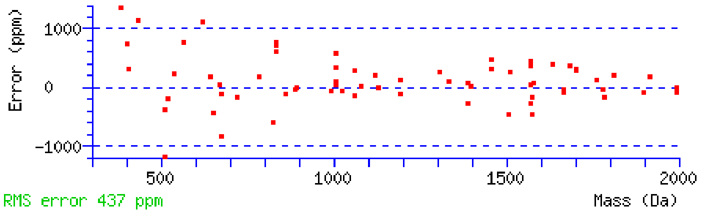


Monoisotopic mass of neutral peptide Mr(calc): 3691.8005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 100 **Expect:** 2.3e-008
Matches : 67/342 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							32
2	187.0713	94.0393			169.0608	85.0340	D	3621.7707	1811.3890	3604.7442	1802.8757	3603.7602	1802.3837	31
3	288.1190	144.5631			270.1084	135.5579	T	3506.7438	1753.8755	3489.7173	1745.3623	3488.7332	1744.8703	30
4	425.1779	213.0926			407.1674	204.0873	H	3405.6961	1703.3517	3388.6696	1694.8384	3387.6856	1694.3464	29
5	**540.2049**	270.6061			522.1943	261.6008	D	3268.6372	1634.8222	3251.6107	1626.3090	3250.6267	1625.8170	28
6	**669.2475**	335.1274			651.2369	326.1221	E	3153.6103	1577.3088	3136.5837	1568.7955	3135.5997	1568.3035	27
7	**782.3315**	391.6694			764.3210	382.6641	I	3024.5677	1512.7875	3007.5411	1504.2742	3006.5571	1503.7822	26
8	**895.4156**	448.2114			877.4050	439.2061	L	2911.4836	1456.2454	2894.4571	1447.7322	2893.4731	1447.2402	25
9	**1024.4582**	**512.7327**			1006.4476	503.7274	E	2798.3996	1399.7034	2781.3730	1391.1901	2780.3890	1390.6981	24
10	**1081.4796**	541.2435			1063.4691	532.2382	G	2669.3570	1335.1821	2652.3304	1326.6688	2651.3464	1326.1768	23
11	**1194.5637**	597.7855			1176.5531	588.7802	L	2612.3355	1306.6714	2595.3089	1298.1581	2594.3249	1297.6661	22
12	1308.6066	654.8070	1291.5801	646.2937	1290.5961	645.8017	N	2499.2514	1250.1294	2482.2249	1241.6161	2481.2409	1241.1241	21
13	**1455.6751**	728.3412	1438.6485	719.8279	1437.6645	719.3359	F	2385.2085	1193.1079	2368.1820	1184.5946	2367.1979	1184.1026	20
14	**1570.7020**	785.8546	1553.6754	777.3414	1552.6914	776.8494	N	2238.1401	1119.5737	2221.1135	1111.0604	2220.1295	1110.5684	19
15	**1683.7861**	842.3967	1666.7595	833.8834	1665.7755	833.3914	L	2123.1131	1062.0602	2106.0866	1053.5469	2105.1026	1053.0549	18
16	**1784.8337**	892.9205	1767.8072	884.4072	1766.8232	883.9152	T	2010.0291	1005.5182	1993.0025	997.0049	1992.0185	996.5129	17
17	**1913.8763**	957.4418	1896.8498	948.9285	1895.8658	948.4365	E	1908.9814	954.9943	1891.9549	946.4811	1890.9708	945.9891	16
18	2026.9604	1013.9838	2009.9338	1005.4706	2008.9498	1004.9786	I	**1779.9388**	890.4730	1762.9123	881.9598	1761.9282	881.4678	15
19	2124.0132	**1062.5102**	2106.9866	1053.9969	2106.0026	1053.5049	P	**1666.8547**	833.9310	1649.8282	825.4177	1648.8442	824.9257	14
20	2253.0557	1127.0315	2236.0292	1118.5182	2235.0452	1118.0262	E	**1569.8020**	785.4046	1552.7754	776.8914	1551.7914	776.3993	13
21	2324.0929	1162.5501	2307.0663	1154.0368	2306.0823	1153.5448	A	1440.7594	720.8833	1423.7328	712.3701	1422.7488	711.8781	12
22	2452.1514	1226.5794	2435.1249	1218.0661	2434.1409	1217.5741	Q	1369.7223	685.3648	1352.6957	676.8515	1351.7117	676.3595	11

23	2565.2355	1283.1214	2548.2090	1274.6081	2547.2249	1274.1161	**I**	1241.6637	621.3355	1224.6371	612.8222	1223.6531	612.3302	**10**
24	2702.2944	1351.6508	2685.2679	1343.1376	2684.2839	1342.6456	**H**	**1128.5796**	564.7935	1111.5531	556.2802	1110.5691	555.7882	**9**
25	2831.3370	1416.1721	2814.3105	1407.6589	2813.3264	1407.1669	**E**	**991.5207**	496.2640	974.4942	487.7507	973.5102	487.2587	**8**
26	2888.3585	1444.6829	2871.3319	1436.1696	2870.3479	1435.6776	**G**	**862.4781**	431.7427	845.4516	423.2294	844.4676	422.7374	**7**
27	3035.4269	1518.2171	3018.4003	1509.7038	3017.4163	1509.2118	**F**	805.4567	403.2320	788.4301	394.7187	787.4461	394.2267	**6**
28	3163.4855	1582.2464	3146.4589	1573.7331	3145.4749	1573.2411	**Q**	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	**5**
29	3292.5281	1646.7677	3275.5015	1638.2544	3274.5175	1637.7624	**E**	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	**4**
30	3405.6121	**1703.3097**	3388.5856	1694.7964	3387.6016	1694.3044	**L**	**401.2871**	201.1472	384.2605	192.6339			**3**
31	3518.6962	**1759.8517**	3501.6696	1751.3385	3500.6856	1750.8464	**L**	288.2030	144.6051	271.1765	136.0919			**2**
32							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
100.4	3691.8005	1.0074	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N14 35.27%
100.4	3691.8005	1.0074	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated N12 35.27%
97.8	3691.8005	1.0074	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated Q22 19.52%
94.9	3691.8005	1.0074	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	Deamidated Q28 9.94%
58.6	3690.8165	1.9914	ADTHDEILEGLNFNLTEIPEAQIHEGFQELLR	
12.5	3690.7923	2.0156	IRMQAQGSLFQGSMIGSFIDIYQQEGTRGLWR	
12.5	3690.7923	2.0156	IRMQAQGSLFQGSMIGSFIDIYQQEGTRGLWR	
12.2	3692.8169	-0.0090	AGSELPEQQVTTKNGPPASPPPPALLQSKSHGQSPR	
9.3	3690.8100	1.9979	RHEALTYVEQLATRQDESLPAMLLQYWAADR	
9.2	3690.7923	2.0156	IRMQAQGSLFQGSMIGSFIDIYQQEGTRGLWR	

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

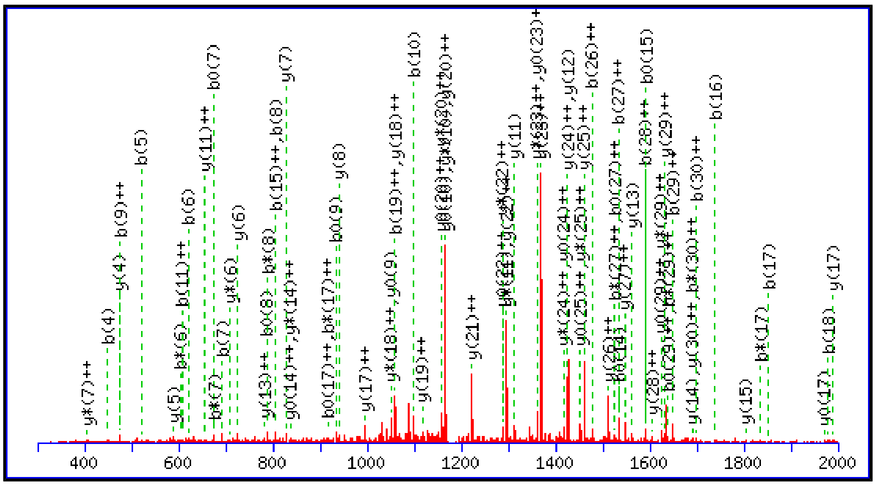
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLGNATAIFFLPDEGKLQHLENELTHDIITK**
Found in **P01009** in **con_Xuniprot_HUMAN3**, A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3

Match to Query 27800: 3540.828012 from(1181.283280,3+) intensity(10833.5225) rtinseconds(2635) scans(6713) index(8118)
Title: 111019_Est_ISCardio_NMI_YS_G_2Spectrum5821_scans__6713
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

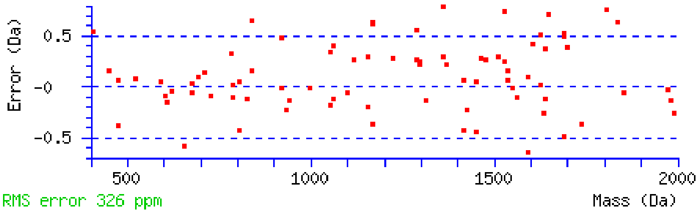
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

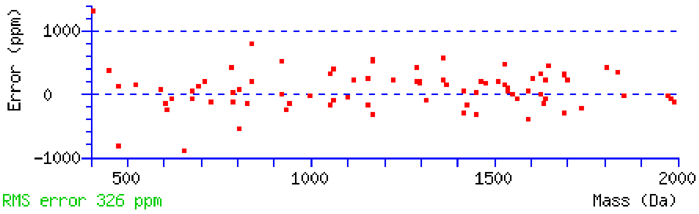


Monoisotopic mass of neutral peptide Mr(calc): 3540.8140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 72 **Expect:** 1.1e-005
Matches : 83/342 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							31
2	277.1547	139.0810					L	3378.7580	1689.8826	3361.7315	1681.3694	3360.7474	1680.8774	30
3	334.1761	167.5917					G	3265.6739	1633.3406	3248.6474	1624.8273	3247.6634	1624.3353	29
4	**449.2031**	225.1052	432.1765	216.5919			N	3208.6525	1604.8299	3191.6259	1596.3166	3190.6419	1595.8246	28
5	**520.2402**	260.6237	503.2136	252.1105			A	3093.6255	1547.3164	3076.5990	1538.8031	3075.6150	1538.3111	27
6	**621.2879**	311.1476	604.2613	302.6343	603.2773	302.1423	T	3022.5884	1511.7978	3005.5619	1503.2846	3004.5779	1502.7926	26
7	**692.3250**	346.6661	675.2984	338.1529	674.3144	337.6608	A	2921.5407	1461.2740	2904.5142	1452.7607	2903.5302	1452.2687	25
8	**805.4090**	403.2082	788.3825	394.6949	787.3985	394.2029	I	2850.5036	1425.7554	2833.4771	1417.2422	2832.4931	1416.7502	24
9	952.4775	**476.7424**	935.4509	468.2291	934.4669	467.7371	F	2737.4196	1369.2134	2720.3930	1360.7001	2719.4090	1360.2081	23
10	**1099.5459**	550.2766	1082.5193	541.7633	1081.5353	541.2713	F	2590.3511	1295.6792	2573.3246	1287.1659	2572.3406	1286.6739	22
11	1212.6299	**606.8186**	1195.6034	598.3053	1194.6194	597.8133	L	2443.2827	1222.1450	2426.2562	1213.6317	2425.2722	1213.1397	21
12	1309.6827	655.3450	1292.6562	646.8317	1291.6721	646.3397	P	2330.1987	1165.6030	2313.1721	1157.0897	2312.1881	1156.5977	20
13	1424.7096	712.8585	1407.6831	704.3452	1406.6991	703.8532	D	2233.1459	1117.0766	2216.1194	1108.5633	2215.1353	1108.0713	19
14	1553.7522	777.3798	1536.7257	768.8665	1535.7417	768.3745	E	2118.1190	1059.5631	2101.0924	1051.0498	2100.1084	1050.5578	18
15	1610.7737	**805.8905**	1593.7472	797.3772	1592.7631	796.8852	G	***1989.0764***	995.0418	1972.0498	986.5285	1971.0658	986.0365	17
16	**1738.8687**	869.9380	1721.8421	861.4247	1720.8581	860.9327	K	1932.0549	966.5311	1915.0284	958.0178	1914.0443	957.5258	16
17	**1851.9527**	926.4800	1834.9262	917.9667	1833.9422	917.4747	L	***1803.9599***	902.4836	1786.9334	893.9703	1785.9494	893.4783	15
18	**1980.0113**	990.5093	1962.9848	981.9960	1962.0007	981.5040	Q	***1690.8759***	845.9416	1673.8493	837.4283	1672.8653	836.9363	14
19	2117.0702	**1059.0387**	2100.0437	1050.5255	2099.0597	1050.0335	H	***1562.8173***	781.9123	1545.7907	773.3990	1544.8067	772.9070	13
20	2230.1543	1115.5808	2213.1277	1107.0675	2212.1437	1106.5755	L	***1425.7584***	713.3828	1408.7318	704.8696	1407.7478	704.3775	12
21	2359.1969	1180.1021	2342.1703	1171.5888	2341.1863	1171.0968	E	***1312.6743***	656.8408	1295.6478	648.3275	1294.6638	647.8355	11
22	2473.2398	1237.1235	2456.2133	1228.6103	2455.2292	1228.1183	N	1183.6317	592.3195	1166.6052	583.8062	1165.6212	583.3142	10
23	2602.2824	1301.6448	2585.2558	1293.1316	2584.2718	1292.6396	E	1069.5888	535.2980	1052.5623	526.7848	1051.5782	526.2928	9

24	2715.3665	1358.1869	2698.3399	1349.6736	2697.3559	1349.1816	**L**	***940.5462***	470.7767	923.5197	462.2635	922.5356	461.7715	**8**
25	2816.4141	1408.7107	2799.3876	1400.1974	2798.4036	1399.7054	**T**	***827.4621***	414.2347	810.4356	405.7214	809.4516	405.2294	**7**
26	2953.4731	**1477.2402**	2936.4465	1468.7269	2935.4625	1468.2349	**H**	***726.4145***	363.7109	709.3879	355.1976	708.4039	354.7056	**6**
27	3068.5000	**1534.7536**	3051.4734	1526.2404	3050.4894	1525.7484	**D**	***589.3556***	295.1814	572.3290	286.6681	571.3450	286.1761	**5**
28	3181.5841	**1591.2957**	3164.5575	1582.7824	3163.5735	1582.2904	**I**	***474.3286***	237.6679	457.3021	229.1547	456.3180	228.6627	**4**
29	3294.6681	**1647.8377**	3277.6416	1639.3244	3276.6576	1638.8324	**I**	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
30	3395.7158	**1698.3615**	3378.6893	1689.8483	3377.7052	1689.3563	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.6	3540.8140	0.0140	YLGNATAIFFLPDEGKLQHLENELTHDIITK	Deamidated N4 84.00%
62.8	3540.8140	0.0140	YLGNATAIFFLPDEGKLQHLENELTHDIITK	Deamidated Q18 11.23%
59.1	3540.8140	0.0140	YLGNATAIFFLPDEGKLQHLENELTHDIITK	Deamidated N22 4.77%
47.5	3539.8300	0.9980	YLGNATAIFFLPDEGKLQHLENELTHDIITK	
10.6	3538.8076	2.0205	NNSLNELMKLKPPANIAQPVATAATDVSNGTVKK	
10.6	3538.8076	2.0205	NNSLNELMKLKPPANIAQPVATAATDVSNGTVKK	
10.6	3538.8076	2.0205	NNSLNELMKLKPPANIAQPVATAATDVSNGTVKK	
4.6	3540.8398	-0.0118	ALWDRGLLNGASQKAEVIMNYHVGETVLSLQK	
3.9	3540.8398	-0.0118	ALWDRGLLNGASQKAEVIMNYHVGETVLSLQK	
3.7	3538.8125	2.0155	MPSLFISGLSDQLIPPVMMKQLYELSPSRTK	

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

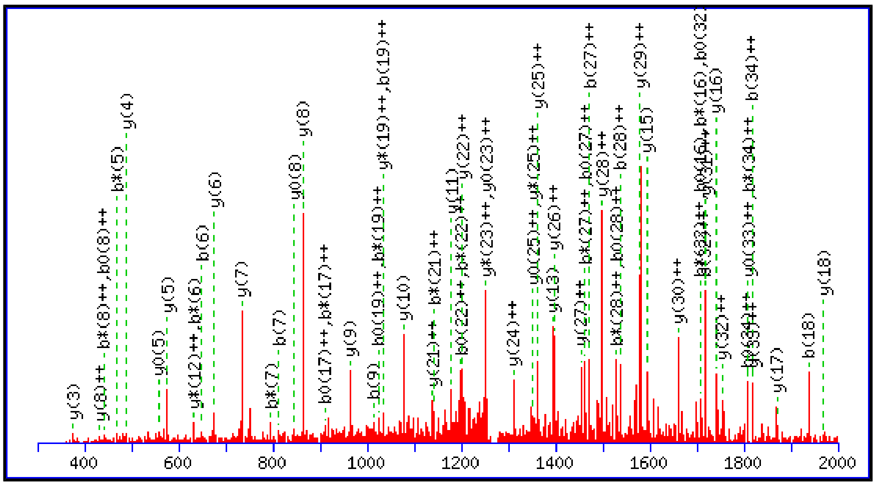
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR**
Found in **P01023** in **con_Xuniprot_HUMAN3**, A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 28089: 3807.746112 from(1270.255980,3+) intensity(0.0000) rtinseconds(3024) scans(8045) index(1695)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum7064_scans__8045
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

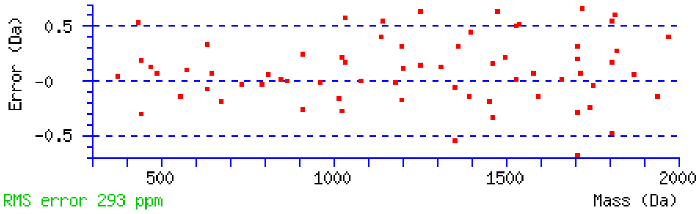
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

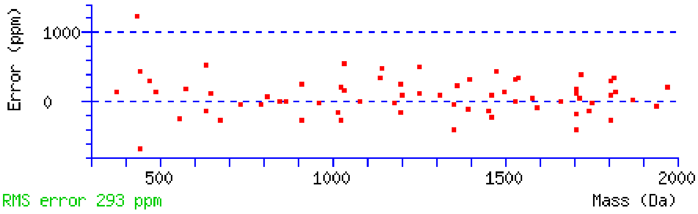


Monoisotopic mass of neutral peptide Mr(calc): 3805.7377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N23 : Deamidated (NQ)
Ions Score: 114 **Expect:** 8e-010
Matches : 67/398 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							35
2	172.0717	86.5395	155.0451	78.0262			N	3749.7235	1875.3654	3732.6970	1866.8521	3731.7130	1866.3601	34
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	3635.6806	1818.3439	3618.6541	1809.8307	3617.6701	1809.3387	33
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	A	3506.6380	1753.8226	3489.6115	1745.3094	3488.6275	1744.8174	32
5	486.1943	243.6008	469.1678	235.0875	468.1837	234.5955	N	3435.6009	1718.3041	3418.5744	1709.7908	3417.5903	1709.2988	31
6	**649.2576**	325.1325	632.2311	316.6192	631.2471	316.1272	Y	3321.5580	1661.2826	3304.5314	1652.7694	3303.5474	1652.2773	30
7	**812.3210**	406.6641	795.2944	398.1508	794.3104	397.6588	Y	3158.4947	1579.7510	3141.4681	1571.2377	3140.4841	1570.7457	29
8	899.3530	450.1801	882.3264	441.6669	881.3424	441.1748	S	2995.4313	1498.2193	2978.4048	1489.7060	2977.4208	1489.2140	28
9	**1014.3799**	507.6936	997.3534	499.1803	996.3694	498.6883	N	2908.3993	1454.7033	2891.3727	1446.1900	2890.3887	1445.6980	27
10	1085.4170	543.2122	1068.3905	534.6989	1067.4065	534.2069	A	2793.3724	1397.1898	2776.3458	1388.6765	2775.3618	1388.1845	26
11	1186.4647	593.7360	1169.4382	585.2227	1168.4542	584.7307	T	2722.3352	1361.6713	2705.3087	1353.1580	2704.3247	1352.6660	25
12	1287.5124	644.2598	1270.4859	635.7466	1269.5018	635.2546	T	2621.2876	1311.1474	2604.2610	1302.6341	2603.2770	1302.1421	24
13	1402.5393	701.7733	1385.5128	693.2600	1384.5288	692.7680	D	2520.2399	1260.6236	2503.2133	1252.1103	2502.2293	1251.6183	23
14	1531.5819	766.2946	1514.5554	757.7813	1513.5714	757.2893	E	2405.2129	1203.1101	2388.1864	1194.5968	2387.2024	1194.1048	22
15	1668.6409	834.8241	1651.6143	826.3108	1650.6303	825.8188	H	2276.1703	1138.5888	2259.1438	1130.0755	2258.1598	1129.5835	21
16	1725.6623	863.3348	1708.6358	854.8215	1707.6517	854.3295	G	2139.1114	1070.0594	2122.0849	1061.5461	2121.1009	1061.0541	20
17	1838.7464	919.8768	1821.7198	911.3636	1820.7358	910.8715	L	2082.0900	1041.5486	2065.0634	1033.0353	2064.0794	1032.5433	19
18	**1937.8148**	969.4110	1920.7882	960.8978	1919.8042	960.4058	V	***1969.0059***	985.0066	1951.9794	976.4933	1950.9953	976.0013	18
19	2065.8734	**1033.4403**	2048.8468	1024.9270	2047.8628	1024.4350	Q	***1869.9375***	935.4724	1852.9109	926.9591	1851.9269	926.4671	17
20	2212.9418	1106.9745	2195.9152	1098.4613	2194.9312	1097.9692	F	***1741.8789***	871.4431	1724.8524	862.9298	1723.8683	862.4378	16
21	2299.9738	1150.4905	2282.9473	1141.9773	2281.9632	1141.4853	S	***1594.8105***	797.9089	1577.7839	789.3956	1576.7999	788.9036	15
22	2413.0579	1207.0326	2396.0313	1198.5193	2395.0473	1198.0273	I	1507.7785	754.3929	1490.7519	745.8796	1489.7679	745.3876	14

23	2528.0848	1264.5460	2511.0583	1256.0328	2510.0743	1255.5408	**N**	***1394.6944***	697.8508	1377.6679	689.3376	1376.6838	688.8456	**13**
24	2629.1325	1315.0699	2612.1059	1306.5566	2611.1219	1306.0646	**T**	1279.6675	640.3374	1262.6409	631.8241	1261.6569	631.3321	**12**
25	2730.1802	1365.5937	2713.1536	1357.0805	2712.1696	1356.5884	**T**	***1178.6198***	589.8135	1161.5932	581.3003	1160.6092	580.8082	**11**
26	2844.2231	1422.6152	2827.1966	1414.1019	2826.2125	1413.6099	**N**	***1077.5721***	539.2897	1060.5456	530.7764	1059.5615	530.2844	**10**
27	2943.2915	**1472.1494**	2926.2650	1463.6361	2925.2810	1463.1441	**V**	***963.5292***	482.2682	946.5026	473.7550	945.5186	473.2629	**9**
28	3074.3320	**1537.6696**	3057.3055	1529.1564	3056.3214	1528.6644	**M**	***864.4608***	432.7340	847.4342	424.2207	846.4502	423.7287	**8**
29	3131.3535	1566.1804	3114.3269	1557.6671	3113.3429	1557.1751	**G**	***733.4203***	367.2138	716.3937	358.7005	715.4097	358.2085	**7**
30	3232.4011	1616.7042	3215.3746	1608.1909	3214.3906	1607.6989	**T**	***676.3988***	338.7030	659.3723	330.1898	658.3883	329.6978	**6**
31	3319.4332	1660.2202	3302.4066	1651.7070	3301.4226	1651.2149	**S**	***575.3511***	288.1792	558.3246	279.6659	557.3406	279.1739	**5**
32	3432.5172	**1716.7623**	3415.4907	1708.2490	3414.5067	1707.7570	**L**	***488.3191***	244.6632	471.2926	236.1499	470.3085	235.6579	**4**
33	3533.5649	1767.2861	3516.5384	1758.7728	3515.5544	1758.2808	**T**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
34	3632.6333	**1816.8203**	3615.6068	1808.3070	3614.6228	1807.8150	**V**	274.1874	137.5973	257.1608	129.0840			**2**
35							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.6	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N23 86.80%
104.5	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N26 10.65%
95.9	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, Q19 1.46%
90.5	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N23 0.43%
90.3	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N23 0.41%
82.4	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2, N23 0.07%
82.4	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N26 0.06%
82.2	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N26 0.06%
74.7	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, Q19 0.01%
74.6	3805.7377	2.0084	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2, N26 0.01%

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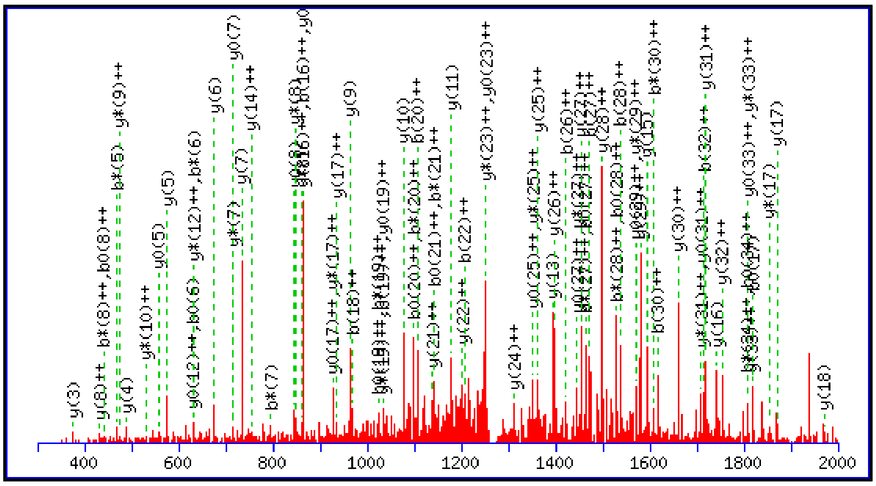
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR**
Found in **P01023** in **con_Xuniprot_HUMAN3**, A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 28077: 3806.741382 from(1269.921070,3+) intensity(13695.8389) rtinseconds(2913) scans(7732) index(1668)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum6783_scans__7732
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

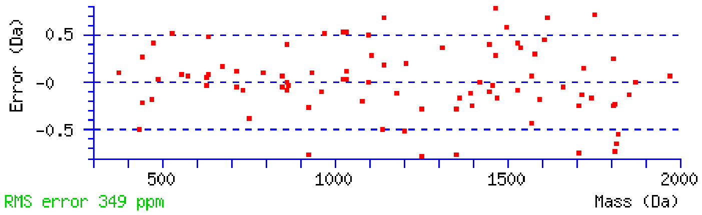
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

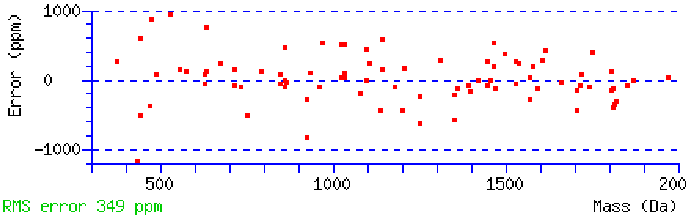


Monoisotopic mass of neutral peptide Mr(calc): 3805.7377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Deamidated (NQ)
N23 : Deamidated (NQ)
Ions Score: 85 **Expect:** 4.8e-007
Matches : 87/398 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							35
2	172.0717	86.5395	155.0451	78.0262			N	3749.7235	1875.3654	3732.6970	1866.8521	3731.7130	1866.3601	34
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	3635.6806	1818.3439	3618.6541	1809.8307	3617.6701	1809.3387	33
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	A	3506.6380	1753.8226	3489.6115	1745.3094	3488.6275	1744.8174	32
5	486.1943	243.6008	469.1678	235.0875	468.1837	234.5955	N	3435.6009	1718.3041	3418.5744	1709.7908	3417.5903	1709.2988	31
6	649.2576	325.1325	632.2311	316.6192	631.2471	316.1272	Y	3321.5580	1661.2826	3304.5314	1652.7694	3303.5474	1652.2773	30
7	812.3210	406.6641	795.2944	398.1508	794.3104	397.6588	Y	3158.4947	1579.7510	3141.4681	1571.2377	3140.4841	1570.7457	29
8	899.3530	450.1801	882.3264	441.6669	881.3424	441.1748	S	2995.4313	1498.2193	2978.4048	1489.7060	2977.4208	1489.2140	28
9	1013.3959	507.2016	996.3694	498.6883	995.3853	498.1963	N	2908.3993	1454.7033	2891.3727	1446.1900	2890.3887	1445.6980	27
10	1084.4330	542.7202	1067.4065	534.2069	1066.4225	533.7149	A	2794.3564	1397.6818	2777.3298	1389.1685	2776.3458	1388.6765	26
11	1185.4807	593.2440	1168.4542	584.7307	1167.4701	584.2387	T	2723.3193	1362.1633	2706.2927	1353.6500	2705.3087	1353.1580	25
12	1286.5284	643.7678	1269.5018	635.2546	1268.5178	634.7625	T	2622.2716	1311.6394	2605.2450	1303.1262	2604.2610	1302.6341	24
13	1401.5553	701.2813	1384.5288	692.7680	1383.5448	692.2760	D	2521.2239	1261.1156	2504.1973	1252.6023	2503.2133	1252.1103	23
14	1530.5979	765.8026	1513.5714	757.2893	1512.5874	756.7973	E	2406.1970	1203.6021	2389.1704	1195.0888	2388.1864	1194.5968	22
15	1667.6568	834.3321	1650.6303	825.8188	1649.6463	825.3268	H	2277.1544	1139.0808	2260.1278	1130.5675	2259.1438	1130.0755	21
16	1724.6783	**862.8428**	1707.6517	854.3295	1706.6677	853.8375	G	2140.0954	1070.5514	2123.0689	1062.0381	2122.0849	1061.5461	20
17	1837.7624	919.3848	1820.7358	910.8715	1819.7518	910.3795	L	2083.0740	1042.0406	2066.0474	1033.5274	2065.0634	1033.0353	19
18	1936.8308	**968.9190**	1919.8042	960.4058	1918.8202	959.9137	V	***1969.9899***	985.4986	1952.9634	976.9853	1951.9794	976.4933	18
19	2065.8734	**1033.4403**	2048.8468	1024.9270	2047.8628	1024.4350	Q	***1870.9215***	935.9644	1853.8950	927.4511	1852.9109	926.9591	17
20	2212.9418	**1106.9745**	2195.9152	1098.4613	2194.9312	1097.9692	F	***1741.8789***	871.4431	1724.8524	862.9298	1723.8683	862.4378	16
21	2299.9738	1150.4905	2282.9473	1141.9773	2281.9632	1141.4853	S	***1594.8105***	797.9089	1577.7839	789.3956	1576.7999	788.9036	15
22	2413.0579	**1207.0326**	2396.0313	1198.5193	2395.0473	1198.0273	I	1507.7785	754.3929	1490.7519	745.8796	1489.7679	745.3876	14

23	2528.0848	1264.5460	2511.0583	1256.0328	2510.0743	1255.5408	**N**	***1394.6944***	697.8508	1377.6679	689.3376	1376.6838	688.8456	**13**
24	2629.1325	1315.0699	2612.1059	1306.5566	2611.1219	1306.0646	**T**	1279.6675	640.3374	1262.6409	631.8241	1261.6569	631.3321	**12**
25	2730.1802	1365.5937	2713.1536	1357.0805	2712.1696	1356.5884	**T**	***1178.6198***	589.8135	1161.5932	581.3003	1160.6092	580.8082	**11**
26	2844.2231	**1422.6152**	2827.1966	1414.1019	2826.2125	1413.6099	**N**	***1077.5721***	539.2897	1060.5456	530.7764	1059.5615	530.2844	**10**
27	2943.2915	**1472.1494**	2926.2650	1463.6361	2925.2810	1463.1441	**V**	***963.5292***	482.2682	946.5026	473.7550	945.5186	473.2629	**9**
28	3074.3320	**1537.6696**	3057.3055	1529.1564	3056.3214	1528.6644	**M**	***864.4608***	432.7340	847.4342	424.2207	846.4502	423.7287	**8**
29	3131.3535	1566.1804	3114.3269	1557.6671	3113.3429	1557.1751	**G**	***733.4203***	367.2138	716.3937	358.7005	715.4097	358.2085	**7**
30	3232.4011	**1616.7042**	3215.3746	1608.1909	3214.3906	1607.6989	**T**	***676.3988***	338.7030	659.3723	330.1898	658.3883	329.6978	**6**
31	3319.4332	1660.2202	3302.4066	1651.7070	3301.4226	1651.2149	**S**	***575.3511***	288.1792	558.3246	279.6659	557.3406	279.1739	**5**
32	3432.5172	**1716.7623**	3415.4907	1708.2490	3414.5067	1707.7570	**L**	***488.3191***	244.6632	471.2926	236.1499	470.3085	235.6579	**4**
33	3533.5649	1767.2861	3516.5384	1758.7728	3515.5544	1758.2808	**T**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
34	3632.6333	1816.8203	3615.6068	1808.3070	3614.6228	1807.8150	**V**	274.1874	137.5973	257.1608	129.0840			**2**
35							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.5	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N23 49.75%
82.5	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N23 25.46%
78.3	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N26 9.46%
75.5	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N26 4.98%
75.2	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N23 4.70%
69.4	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2, N23 1.23%
68.4	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N26 0.98%
68.3	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, Q19 0.96%
67.2	3804.7537	1.9877	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	
64.8	3805.7377	1.0037	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N23, N26 0.43%

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

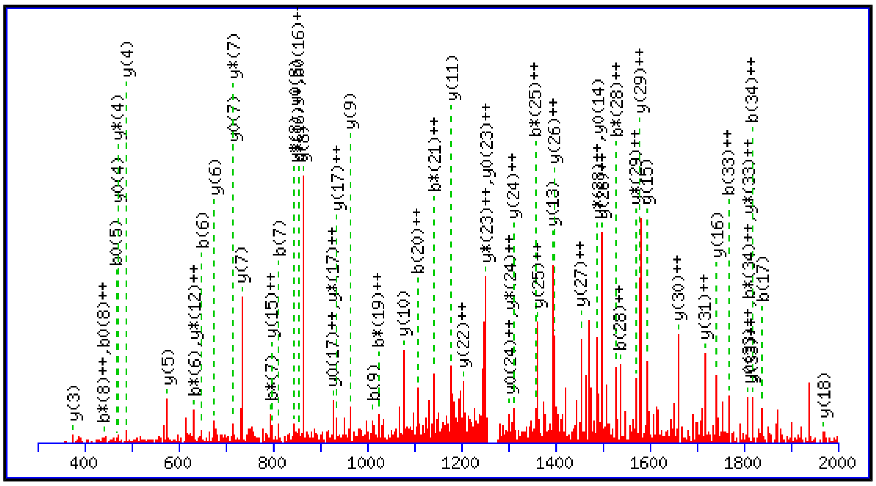
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR**
Found in **P01023** in **con_Xuniprot_HUMAN3**, A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 28080: 3806.763192 from(1269.928340,3+) intensity(0.0000) rtinseconds(3114) scans(8290) index(1726)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum7285_scans__8290
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

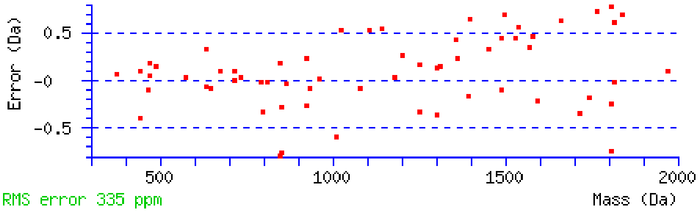
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

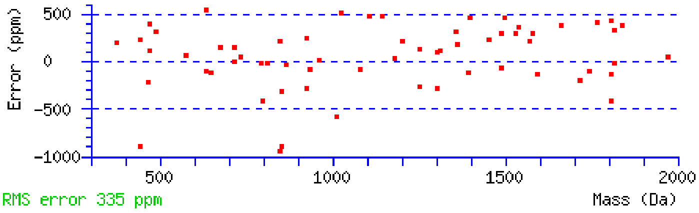


Monoisotopic mass of neutral peptide Mr(calc): 3804.7537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N23 : Deamidated (NQ)
Ions Score: 85 **Expect:** 6.7e-007
Matches : 63/398 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							35
2	172.0717	86.5395	155.0451	78.0262			N	3748.7395	1874.8734	3731.7130	1866.3601	3730.7290	1865.8681	34
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	3634.6966	1817.8519	3617.6701	1809.3387	3616.6860	1808.8467	33
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	A	3505.6540	1753.3306	3488.6275	1744.8174	3487.6434	1744.3254	32
5	486.1943	243.6008	469.1678	235.0875	468.1837	234.5955	N	3434.6169	1717.8121	3417.5903	1709.2988	3416.6063	1708.8068	31
6	**649.2576**	325.1325	632.2311	316.6192	631.2471	316.1272	Y	3320.5740	1660.7906	3303.5474	1652.2773	3302.5634	1651.7853	30
7	**812.3210**	406.6641	795.2944	398.1508	794.3104	397.6588	Y	3157.5106	1579.2590	3140.4841	1570.7457	3139.5001	1570.2537	29
8	899.3530	450.1801	882.3264	441.6669	881.3424	441.1748	S	2994.4473	1497.7273	2977.4208	1489.2140	2976.4367	1488.7220	28
9	**1013.3959**	507.2016	996.3694	498.6883	995.3853	498.1963	N	2907.4153	1454.2113	2890.3887	1445.6980	2889.4047	1445.2060	27
10	1084.4330	542.7202	1067.4065	534.2069	1066.4225	533.7149	A	2793.3724	1397.1898	2776.3458	1388.6765	2775.3618	1388.1845	26
11	1185.4807	593.2440	1168.4542	584.7307	1167.4701	584.2387	T	2722.3352	1361.6713	2705.3087	1353.1580	2704.3247	1352.6660	25
12	1286.5284	643.7678	1269.5018	635.2546	1268.5178	634.7625	T	2621.2876	1311.1474	2604.2610	1302.6341	2603.2770	1302.1421	24
13	1401.5553	701.2813	1384.5288	692.7680	1383.5448	692.2760	D	2520.2399	1260.6236	2503.2133	1252.1103	2502.2293	1251.6183	23
14	1530.5979	765.8026	1513.5714	757.2893	1512.5874	756.7973	E	2405.2129	1203.1101	2388.1864	1194.5968	2387.2024	1194.1048	22
15	1667.6568	834.3321	1650.6303	825.8188	1649.6463	825.3268	H	2276.1703	1138.5888	2259.1438	1130.0755	2258.1598	1129.5835	21
16	1724.6783	862.8428	1707.6517	854.3295	1706.6677	853.8375	G	2139.1114	1070.0594	2122.0849	1061.5461	2121.1009	1061.0541	20
17	**1837.7624**	919.3848	1820.7358	910.8715	1819.7518	910.3795	L	2082.0900	1041.5486	2065.0634	1033.0353	2064.0794	1032.5433	19
18	1936.8308	968.9190	1919.8042	960.4058	1918.8202	959.9137	V	***1969.0059***	985.0066	1951.9794	976.4933	1950.9953	976.0013	18
19	2064.8894	1032.9483	2047.8628	1024.4350	2046.8788	1023.9430	Q	1869.9375	935.4724	1852.9109	926.9591	1851.9269	926.4671	17
20	2211.9578	**1106.4825**	2194.9312	1097.9692	2193.9472	1097.4772	F	***1741.8789***	871.4431	1724.8524	862.9298	1723.8683	862.4378	16
21	2298.9898	1149.9985	2281.9632	1141.4853	2280.9792	1140.9933	S	***1594.8105***	797.9089	1577.7839	789.3956	1576.7999	788.9036	15
22	2412.0739	1206.5406	2395.0473	1198.0273	2394.0633	1197.5353	I	1507.7785	754.3929	1490.7519	745.8796	1489.7679	745.3876	14
23	2527.1008	1264.0540	2510.0743	1255.5408	2509.0902	1255.0488	N	***1394.6944***	697.8508	1377.6679	689.3376	1376.6838	688.8456	13

24	2628.1485	1314.5779	2611.1219	1306.0646	2610.1379	1305.5726	**T**	1279.6675	640.3374	1262.6409	631.8241	1261.6569	631.3321	12
25	2729.1962	1365.1017	2712.1696	1356.5884	2711.1856	1356.0964	**T**	***1178.6198***	589.8135	1161.5932	581.3003	1160.6092	580.8082	11
26	2843.2391	1422.1232	2826.2125	1413.6099	2825.2285	1413.1179	**N**	***1077.5721***	539.2897	1060.5456	530.7764	1059.5615	530.2844	10
27	2942.3075	1471.6574	2925.2810	1463.1441	2924.2969	1462.6521	**V**	***963.5292***	482.2682	946.5026	473.7550	945.5186	473.2629	9
28	3073.3480	**1537.1776**	3056.3214	1528.6644	3055.3374	1528.1723	**M**	***864.4608***	432.7340	847.4342	424.2207	846.4502	423.7287	8
29	3130.3695	1565.6884	3113.3429	1557.1751	3112.3589	1556.6831	**G**	***733.4203***	367.2138	716.3937	358.7005	715.4097	358.2085	7
30	3231.4171	1616.2122	3214.3906	1607.6989	3213.4066	1607.2069	**T**	***676.3988***	338.7030	659.3723	330.1898	658.3883	329.6978	6
31	3318.4492	1659.7282	3301.4226	1651.2149	3300.4386	1650.7229	**S**	***575.3511***	288.1792	558.3246	279.6659	557.3406	279.1739	5
32	3431.5332	1716.2702	3414.5067	1707.7570	3413.5227	1707.2650	**L**	***488.3191***	244.6632	471.2926	236.1499	470.3085	235.6579	4
33	3532.5809	**1766.7941**	3515.5544	1758.2808	3514.5703	1757.7888	**T**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
34	3631.6493	**1816.3283**	3614.6228	1807.8150	3613.6387	1807.3230	**V**	274.1874	137.5973	257.1608	129.0840			2
35							**R**	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.0	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N23 85.41%
76.2	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N26 11.36%
70.0	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19 2.75%
62.4	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9 0.48%
25.1	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5 0.00%
24.5	3804.7537	2.0095	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2 0.00%
12.9	3806.7722	-0.0090	LKPMGAQFLGGLGPPGGGGFSGGGGGGGGGFGGGGGFGGGGGGAGAR	
11.0	3805.7702	0.9929	EDLEYDPYELMETVKVTGPVEAPEGPGGANCALVR	
7.8	3805.7525	1.0107	DGILMTFNTIFAAAPIQMQFEIDQDESARNLMR	
7.7	3805.7525	1.0107	DGILMTFNTIFAAAPIQMQFEIDQDESARNLMR	

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

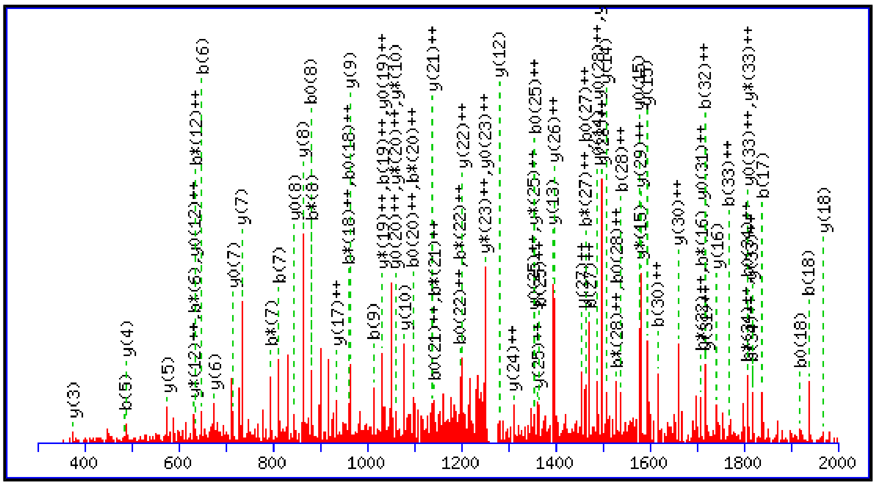
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR**
Found in **P01023** in **con_Xuniprot_HUMAN3**, A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Match to Query 28073: 3805.756512 from(1269.592780,3+) intensity(19010.5195) rtinseconds(3040) scans(8089) index(1700)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum7104_scans__8089
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

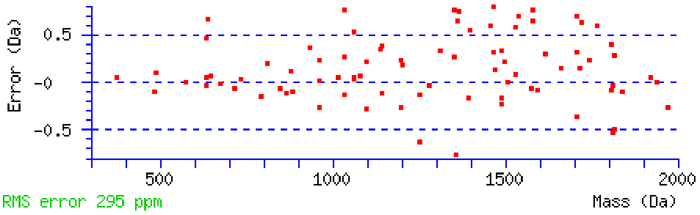
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

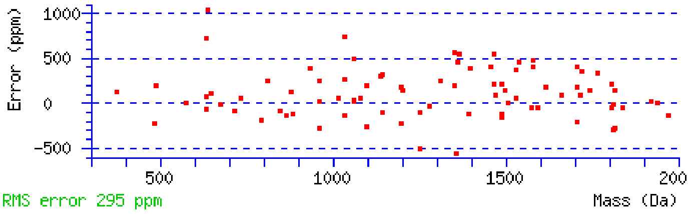


Monoisotopic mass of neutral peptide Mr(calc): 3805.7377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 77 **Expect:** 3.5e-006
Matches : 84/398 fragment ions using 153 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							35
2	172.0717	86.5395	155.0451	78.0262			N	3749.7235	1875.3654	3732.6970	1866.8521	3731.7130	1866.3601	34
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	3635.6806	1818.3439	3618.6541	1809.8307	3617.6701	1809.3387	33
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	A	3506.6380	1753.8226	3489.6115	1745.3094	3488.6275	1744.8174	32
5	**486.1943**	243.6008	469.1678	235.0875	468.1837	234.5955	N	3435.6009	1718.3041	3418.5744	1709.7908	3417.5903	1709.2988	31
6	**649.2576**	325.1325	632.2311	316.6192	631.2471	316.1272	Y	3321.5580	1661.2826	3304.5314	1652.7694	3303.5474	1652.2773	30
7	**812.3210**	406.6641	795.2944	398.1508	794.3104	397.6588	Y	3158.4947	1579.7510	3141.4681	1571.2377	3140.4841	1570.7457	29
8	899.3530	450.1801	882.3264	441.6669	881.3424	441.1748	S	2995.4313	1498.2193	2978.4048	1489.7060	2977.4208	1489.2140	28
9	**1014.3799**	507.6936	997.3534	499.1803	996.3694	498.6883	N	2908.3993	1454.7033	2891.3727	1446.1900	2890.3887	1445.6980	27
10	1085.4170	543.2122	1068.3905	534.6989	1067.4065	534.2069	A	2793.3724	1397.1898	2776.3458	1388.6765	2775.3618	1388.1845	26
11	1186.4647	593.7360	1169.4382	585.2227	1168.4542	584.7307	T	2722.3352	1361.6713	2705.3087	1353.1580	2704.3247	1352.6660	25
12	1287.5124	644.2598	1270.4859	635.7466	1269.5018	635.2546	T	2621.2876	1311.1474	2604.2610	1302.6341	2603.2770	1302.1421	24
13	1402.5393	701.7733	1385.5128	693.2600	1384.5288	692.7680	D	2520.2399	1260.6236	2503.2133	1252.1103	2502.2293	1251.6183	23
14	1531.5819	766.2946	1514.5554	757.7813	1513.5714	757.2893	E	2405.2129	1203.1101	2388.1864	1194.5968	2387.2024	1194.1048	22
15	1668.6409	834.8241	1651.6143	826.3108	1650.6303	825.8188	H	2276.1703	1138.5888	2259.1438	1130.0755	2258.1598	1129.5835	21
16	1725.6623	863.3348	1708.6358	854.8215	1707.6517	854.3295	G	2139.1114	1070.0594	2122.0849	1061.5461	2121.1009	1061.0541	20
17	**1838.7464**	919.8768	1821.7198	911.3636	1820.7358	910.8715	L	2082.0900	1041.5486	2065.0634	1033.0353	2064.0794	1032.5433	19
18	**1937.8148**	969.4110	1920.7882	960.8978	1919.8042	960.4058	V	***1969.0059***	985.0066	1951.9794	976.4933	1950.9953	976.0013	18
19	2065.8734	**1033.4403**	2048.8468	1024.9270	2047.8628	1024.4350	Q	1869.9375	935.4724	1852.9109	926.9591	1851.9269	926.4671	17
20	2212.9418	1106.9745	2195.9152	1098.4613	2194.9312	1097.9692	F	***1741.8789***	871.4431	1724.8524	862.9298	1723.8683	862.4378	16
21	2299.9738	1150.4905	2282.9473	1141.9773	2281.9632	1141.4853	S	***1594.8105***	797.9089	1577.7839	789.3956	1576.7999	788.9036	15
22	2413.0579	1207.0326	2396.0313	1198.5193	2395.0473	1198.0273	I	***1507.7785***	754.3929	1490.7519	745.8796	1489.7679	745.3876	14

23	2527.1008	1264.0540	2510.0743	1255.5408	2509.0902	1255.0488	**N**	***1394.6944***	697.8508	1377.6679	689.3376	1376.6838	688.8456	**13**
24	2628.1485	1314.5779	2611.1219	1306.0646	2610.1379	1305.5726	**T**	***1280.6515***	640.8294	1263.6249	632.3161	1262.6409	631.8241	**12**
25	2729.1962	**1365.1017**	2712.1696	1356.5884	2711.1856	1356.0964	**T**	1179.6038	590.3055	1162.5773	581.7923	1161.5932	581.3003	**11**
26	2844.2231	1422.6152	2827.1966	1414.1019	2826.2125	1413.6099	**N**	***1078.5561***	539.7817	1061.5296	531.2684	1060.5456	530.7764	**10**
27	2943.2915	**1472.1494**	2926.2650	1463.6361	2925.2810	1463.1441	**V**	***963.5292***	482.2682	946.5026	473.7550	945.5186	473.2629	**9**
28	3074.3320	**1537.6696**	3057.3055	1529.1564	3056.3214	1528.6644	**M**	***864.4608***	432.7340	847.4342	424.2207	846.4502	423.7287	**8**
29	3131.3535	1566.1804	3114.3269	1557.6671	3113.3429	1557.1751	**G**	***733.4203***	367.2138	716.3937	358.7005	715.4097	358.2085	**7**
30	3232.4011	**1616.7042**	3215.3746	1608.1909	3214.3906	1607.6989	**T**	***676.3988***	338.7030	659.3723	330.1898	658.3883	329.6978	**6**
31	3319.4332	1660.2202	3302.4066	1651.7070	3301.4226	1651.2149	**S**	***575.3511***	288.1792	558.3246	279.6659	557.3406	279.1739	**5**
32	3432.5172	**1716.7623**	3415.4907	1708.2490	3414.5067	1707.7570	**L**	***488.3191***	244.6632	471.2926	236.1499	470.3085	235.6579	**4**
33	3533.5649	**1767.2861**	3516.5384	1758.7728	3515.5544	1758.2808	**T**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
34	3632.6333	**1816.8203**	3615.6068	1808.3070	3614.6228	1807.8150	**V**	274.1874	137.5973	257.1608	129.0840			**2**
35							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.5	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N26 25.68%
76.7	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, N23 21.60%
75.0	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N26 14.51%
74.3	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N5, N23 12.18%
74.2	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2, N26 11.98%
73.4	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N2, N23 10.06%
63.9	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N26 1.12%
63.7	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N23, N26 1.07%
61.8	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated Q19, N23 0.69%
56.9	3805.7377	0.0188	GNEANYYSNATTDEHGLVQFSINTTNVMGTSLTVR	Deamidated N9, Q19 0.22%

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

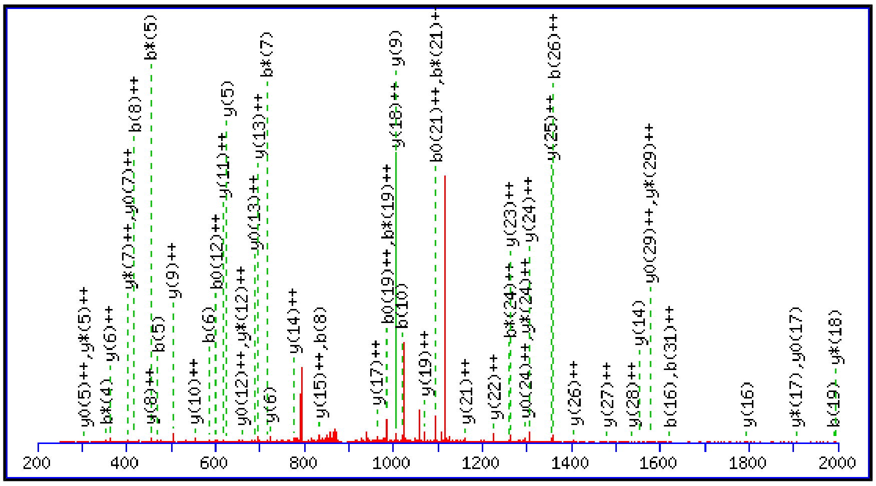
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLGNVNFTVSAEALESQELCGTEVPSVPEHGRK**
Found in **H0YGH6** in **con_Xuniprot_HUMAN3**, H0YGH6_HUMAN Alpha-2-macroglobulin (Fragment) OS=Homo sapiens GN=A2M PE=4 SV=1

Match to Query 27806: 3541.714576 from(886.435920,4+) intensity(25004.4238) rtinseconds(1873) scans(4740) index(14611)
Title: 111019_Est_MI_YP_G_03Spectrum4112_scans__4740
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

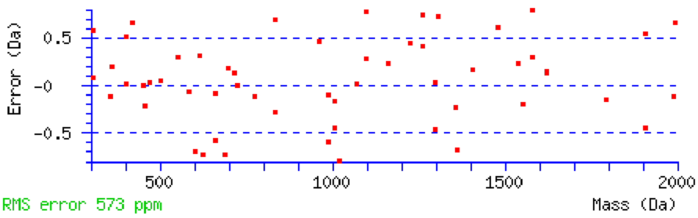
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

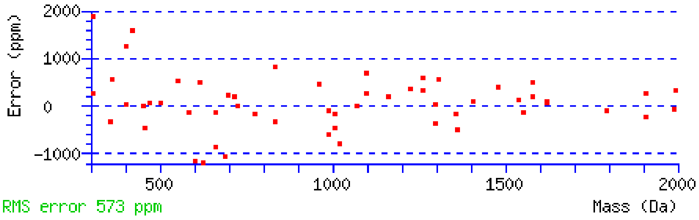


Monoisotopic mass of neutral peptide Mr(calc): 3541.6995
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00046
Matches : 56/370 fragment ions using 144 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							33
2	201.1234	101.0653			183.1128	92.0600	L	3455.6747	1728.3410	3438.6482	1719.8277	3437.6642	1719.3357	32
3	258.1448	129.5761			240.1343	120.5708	G	3342.5907	1671.7990	3325.5641	1663.2857	3324.5801	1662.7937	31
4	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	N	3285.5692	1643.2882	3268.5427	1634.7750	3267.5586	1634.2830	30
5	**471.2562**	236.1317	454.2296	227.6185	453.2456	227.1264	V	3171.5263	1586.2668	3154.4997	1577.7535	3153.5157	1577.2615	29
6	**586.2831**	293.6452	569.2566	285.1319	568.2726	284.6399	N	3072.4579	1536.7326	3055.4313	1528.2193	3054.4473	1527.7273	28
7	733.3515	367.1794	716.3250	358.6661	715.3410	358.1741	F	2957.4309	1479.2191	2940.4044	1470.7058	2939.4204	1470.2138	27
8	**834.3992**	417.7032	817.3727	409.1900	816.3886	408.6980	T	2810.3625	1405.6849	2793.3360	1397.1716	2792.3519	1396.6796	26
9	933.4676	467.2374	916.4411	458.7242	915.4571	458.2322	V	2709.3148	1355.1611	2692.2883	1346.6478	2691.3043	1346.1558	25
10	**1020.4997**	510.7535	1003.4731	502.2402	1002.4891	501.7482	S	2610.2464	1305.6268	2593.2199	1297.1136	2592.2359	1296.6216	24
11	1091.5368	546.2720	1074.5102	537.7587	1073.5262	537.2667	A	2523.2144	1262.1108	2506.1878	1253.5976	2505.2038	1253.1056	23
12	1220.5794	610.7933	1203.5528	602.2800	1202.5688	601.7880	E	2452.1773	1226.5923	2435.1507	1218.0790	2434.1667	1217.5870	22
13	1291.6165	646.3119	1274.5899	637.7986	1273.6059	637.3066	A	2323.1347	1162.0710	2306.1081	1153.5577	2305.1241	1153.0657	21
14	1404.7005	702.8539	1387.6740	694.3406	1386.6900	693.8486	L	2252.0976	1126.5524	2235.0710	1118.0391	2234.0870	1117.5471	20
15	1533.7431	767.3752	1516.7166	758.8619	1515.7326	758.3699	E	2139.0135	1070.0104	2121.9870	1061.4971	2121.0029	1061.0051	19
16	**1620.7752**	810.8912	1603.7486	802.3779	1602.7646	801.8859	S	2009.9709	1005.4891	1992.9444	996.9758	1991.9604	996.4838	18
17	1748.8337	874.9205	1731.8072	866.4072	1730.8232	865.9152	Q	1922.9389	961.9731	1905.9123	953.4598	1904.9283	952.9678	17
18	1877.8763	939.4418	1860.8498	930.9285	1859.8658	930.4365	E	**1794.8803**	897.9438	1777.8538	889.4305	1776.8697	888.9385	16
19	**1990.9604**	995.9838	1973.9338	987.4706	1972.9498	986.9786	L	1665.8377	833.4225	1648.8112	824.9092	1647.8272	824.4172	15
20	2150.9910	1075.9992	2133.9645	1067.4859	2132.9805	1066.9939	C	**1552.7537**	776.8805	1535.7271	768.3672	1534.7431	767.8752	14
21	2208.0125	1104.5099	2190.9860	1095.9966	2190.0019	1095.5046	G	1392.7230	696.8651	1375.6965	688.3519	1374.7124	687.8599	13
22	2309.0602	1155.0337	2292.0336	1146.5205	2291.0496	1146.0284	T	1335.7015	668.3544	1318.6750	659.8411	1317.6910	659.3491	12

23	2438.1028	1219.5550	2421.0762	1211.0418	2420.0922	1210.5497	**E**	1234.6539	617.8306	1217.6273	609.3173	1216.6433	608.8253	**11**
24	2537.1712	1269.0892	2520.1446	1260.5760	2519.1606	1260.0840	**V**	1105.6113	553.3093	1088.5847	544.7960	1087.6007	544.3040	**10**
25	2634.2240	1317.6156	2617.1974	1309.1023	2616.2134	1308.6103	**P**	**1006.5429**	503.7751	989.5163	495.2618	988.5323	494.7698	**9**
26	2721.2560	1361.1316	2704.2294	1352.6184	2703.2454	1352.1263	**S**	909.4901	455.2487	892.4635	446.7354	891.4795	446.2434	**8**
27	2820.3244	1410.6658	2803.2978	1402.1526	2802.3138	1401.6606	**V**	822.4581	411.7327	805.4315	403.2194	804.4475	402.7274	**7**
28	2917.3772	1459.1922	2900.3506	1450.6789	2899.3666	1450.1869	**P**	**723.3896**	362.1985	706.3631	353.6852	705.3791	353.1932	**6**
29	3046.4198	1523.7135	3029.3932	1515.2002	3028.4092	1514.7082	**E**	**626.3369**	313.6721	609.3103	305.1588	608.3263	304.6668	**5**
30	3183.4787	1592.2430	3166.4521	1583.7297	3165.4681	1583.2377	**H**	497.2943	249.1508	480.2677	240.6375			**4**
31	3240.5001	1620.7537	3223.4736	1612.2404	3222.4896	1611.7484	**G**	360.2354	180.6213	343.2088	172.1081			**3**
32	3396.6012	1698.8043	3379.5747	1690.2910	3378.5907	1689.7990	**R**	303.2139	152.1106	286.1874	143.5973			**2**
33							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.3	3541.6995	0.0151	SLGNVNFTVSAEALESQELCGTEVPSVPEHGRK	Deamidated N6 53.54%
56.3	3541.6995	0.0151	SLGNVNFTVSAEALESQELCGTEVPSVPEHGRK	Deamidated N4 41.75%
46.8	3541.6995	0.0151	SLGNVNFTVSAEALESQELCGTEVPSVPEHGRK	Deamidated Q17 4.71%
42.1	3540.7155	0.9991	SLGNVNFTVSAEALESQELCGTEVPSVPEHGRK	
9.0	3539.7202	1.9944	NVGPIRSPALVSQNGGPIAMHDSEASEVFGTEKK	
8.0	3541.7246	-0.0101	CTTPSEDTLNWLASLTFKLTTDVSNQNTKQK	
5.3	3541.7325	-0.0180	YLDNEPVTGTSHDGVRQSEVSGPIFLNTGPLDK	
4.5	3539.6927	2.0218	DPSSCMFFEPLLTISLNRTFPFSLQYICR	
4.3	3539.7202	1.9944	NVGPIRSPALVSQNGGPIAMHDSEASEVFGTEKK	
4.3	3539.7202	1.9944	NVGPIRSPALVSQNGGPIAMHDSEASEVFGTEKK	

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

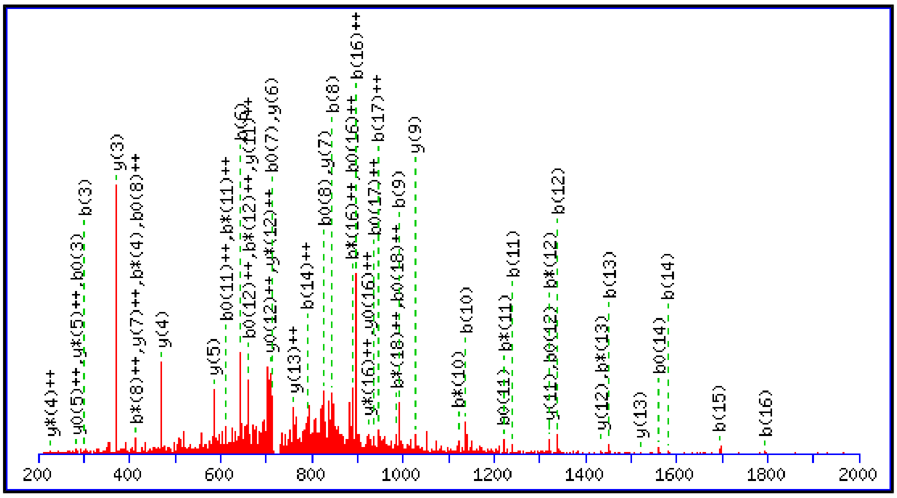
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSNQTLSLFFTVLQDVPVR**
Found in **P01023** in **con_Xuniprot_HUMAN3**, A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

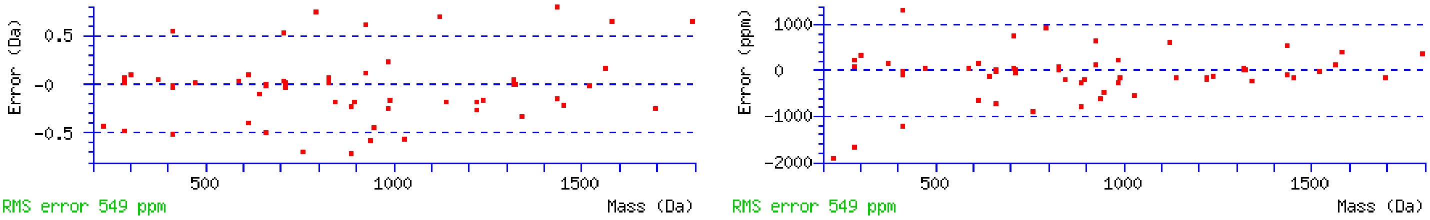
Match to Query 14444: 2163.163332 from(722.061720,3+) intensity(15234.0713) rtinseconds(2886) scans(7578) index(25735)
Title: 111019_Est_MI_YS_G_07Spectrum6555_scans__7578
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2163.1576
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 49 **Expect:** 0.002
Matches : 55/202 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	100.0757	50.5415					**V**							**19**
2	187.1077	94.0575			169.0972	85.0522	**S**	2065.0964	1033.0519	2048.0699	1024.5386	2047.0859	1024.0466	**18**
3	***302.1347***	151.5710	285.1081	143.0577	284.1241	142.5657	**N**	1978.0644	989.5358	1961.0379	981.0226	1960.0538	980.5306	**17**
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	**Q**	1863.0375	932.0224	1846.0109	923.5091	1845.0269	923.0171	**16**
5	531.2409	266.1241	514.2144	257.6108	513.2304	257.1188	**T**	1734.9789	867.9931	1717.9523	859.4798	1716.9683	858.9878	**15**
6	***644.3250***	322.6661	627.2984	314.1529	626.3144	313.6608	**L**	1633.9312	817.4692	1616.9047	808.9560	1615.9206	808.4640	**14**
7	731.3570	366.1821	714.3305	357.6689	713.3464	357.1769	**S**	**1520.8471**	760.9272	1503.8206	752.4139	1502.8366	751.9219	**13**
8	***844.4411***	422.7242	827.4145	414.2109	826.4305	413.7189	**L**	**1433.8151**	717.4112	1416.7886	708.8979	1415.8045	708.4059	**12**
9	***991.5095***	496.2584	974.4829	487.7451	973.4989	487.2531	**F**	**1320.7311**	660.8692	1303.7045	652.3559	1302.7205	651.8639	**11**
10	***1138.5779***	569.7926	1121.5514	561.2793	1120.5673	560.7873	**F**	1173.6626	587.3350	1156.6361	578.8217	1155.6521	578.3297	**10**
11	***1239.6256***	620.3164	1222.5990	611.8032	1221.6150	611.3111	**T**	**1026.5942**	513.8007	1009.5677	505.2875	1008.5837	504.7955	**9**
12	***1338.6940***	669.8506	1321.6674	661.3374	1320.6834	660.8454	**V**	925.5465	463.2769	908.5200	454.7636	907.5360	454.2716	**8**
13	***1451.7781***	726.3927	1434.7515	717.8794	1433.7675	717.3874	**L**	**826.4781**	413.7427	809.4516	405.2294	808.4676	404.7374	**7**
14	***1579.8366***	790.4220	1562.8101	781.9087	1561.8261	781.4167	**Q**	**713.3941**	357.2007	696.3675	348.6874	695.3835	348.1954	**6**
15	***1694.8636***	847.9354	1677.8370	839.4222	1676.8530	838.9301	**D**	**585.3355**	293.1714	568.3089	284.6581	567.3249	284.1661	**5**
16	***1793.9320***	897.4696	1776.9054	888.9564	1775.9214	888.4644	**V**	**470.3085**	235.6579	453.2820	227.1446			**4**
17	1890.9848	945.9960	1873.9582	937.4827	1872.9742	936.9907	**P**	**371.2401**	186.1237	354.2136	177.6104			**3**
18	1990.0532	995.5302	1973.0266	987.0169	1972.0426	986.5249	**V**	274.1874	137.5973	257.1608	129.0840			**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.5	2163.1576	0.0057	VSNQTLSLFFTVLQDVPVR	Deamidated N3 70.55%
44.7	2163.1576	0.0057	VSNQTLSLFFTVLQDVPVR	Deamidated Q4 29.41%
15.6	2163.1576	0.0057	VSNQTLSLFFTVLQDVPVR	Deamidated Q14 0.04%
4.2	2161.1486	2.0147	QLQDILKLMDAVMLQLTR	
3.2	2163.1688	-0.0054	QKLQSQYFPDSVIVKNIR	
1.9	2162.1517	1.0116	ISLRLENITVLDAGLYGCR	
1.6	2163.1688	-0.0054	QKLQSQYFPDSVIVKNIR	
0.2	2163.1688	-0.0054	QKLQSQYFPDSVIVKNIR	
0.2	2163.1688	-0.0054	QKLQSQYFPDSVIVKNIR	

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

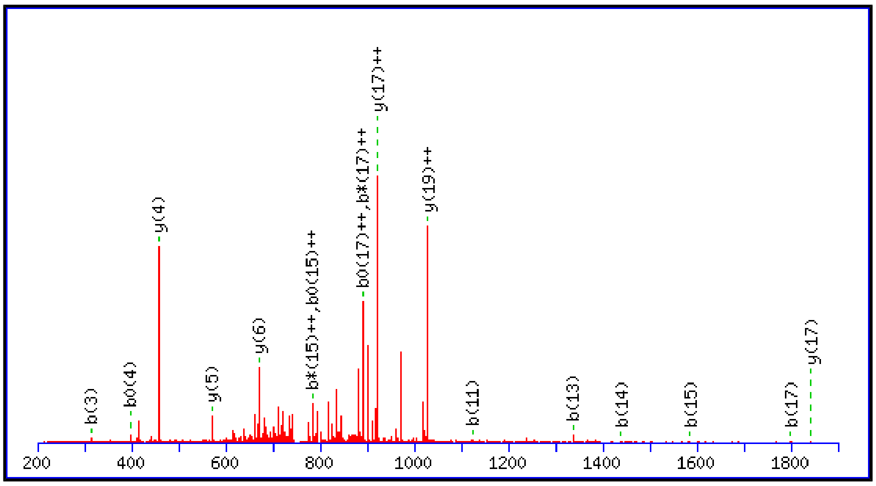
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVLTPATNHMGNVTFTIPANR**
Found in **M0R1Q1** in **con_Xuniprot_HUMAN3**, M0R1Q1_HUMAN Complement C3 (Fragment) OS=Homo sapiens GN=C3 PE=2 SV=1

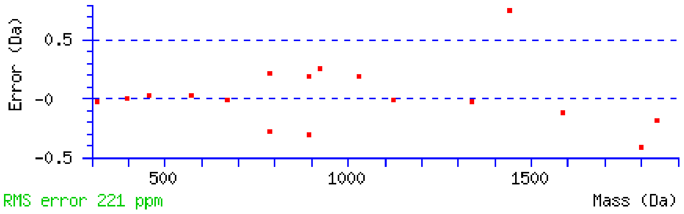
Match to Query 15114: 2255.143182 from(752.721670,3+) intensity(139443.0781) rtinseconds(1576) scans(3728) index(767)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum3218_scans__3728
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

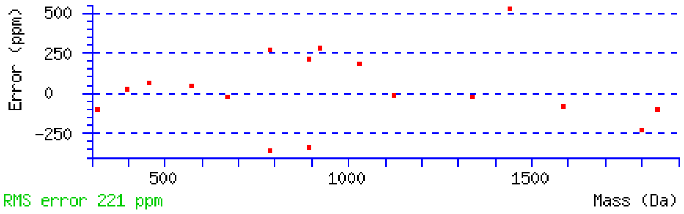
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2255.1369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0054
Matches : 17/216 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	102.0550	51.5311			84.0444	42.5258	**T**							**21**
2	201.1234	101.0653			183.1128	92.0600	**V**	2155.0965	1078.0519	2138.0699	1069.5386	2137.0859	1069.0466	**20**
3	***314.2074***	157.6074			296.1969	148.6021	**L**	2056.0280	1028.5177	2039.0015	1020.0044	2038.0175	1019.5124	**19**
4	415.2551	208.1312			397.2445	199.1259	**T**	1942.9440	971.9756	1925.9174	963.4624	1924.9334	962.9703	**18**
5	512.3079	256.6576			494.2973	247.6523	**P**	***1841.8963***	921.4518	1824.8697	912.9385	1823.8857	912.4465	**17**
6	583.3450	292.1761			565.3344	283.1709	**A**	1744.8435	872.9254	1727.8170	864.4121	1726.8330	863.9201	**16**
7	684.3927	342.7000			666.3821	333.6947	**T**	1673.8064	837.4068	1656.7799	828.8936	1655.7959	828.4016	**15**
8	798.4356	399.7214	781.4090	391.2082	780.4250	390.7162	**N**	1572.7587	786.8830	1555.7322	778.3697	1554.7482	777.8777	**14**
9	935.4945	468.2509	918.4680	459.7376	917.4839	459.2456	**H**	1458.7158	729.8615	1441.6893	721.3483	1440.7052	720.8563	**13**
10	1066.5350	533.7711	1049.5084	525.2579	1048.5244	524.7659	**M**	1321.6569	661.3321	1304.6304	652.8188	1303.6463	652.3268	**12**
11	***1123.5565***	562.2819	1106.5299	553.7686	1105.5459	553.2766	**G**	1190.6164	595.8118	1173.5899	587.2986	1172.6058	586.8066	**11**
12	1238.5834	619.7953	1221.5569	611.2821	1220.5728	610.7901	**N**	1133.5950	567.3011	1116.5684	558.7878	1115.5844	558.2958	**10**
13	***1337.6518***	669.3295	1320.6253	660.8163	1319.6412	660.3243	**V**	1018.5680	509.7876	1001.5415	501.2744	1000.5574	500.7824	**9**
14	***1438.6995***	719.8534	1421.6729	711.3401	1420.6889	710.8481	**T**	919.4996	460.2534	902.4730	451.7402	901.4890	451.2482	**8**
15	***1585.7679***	793.3876	1568.7414	784.8743	1567.7573	784.3823	**F**	818.4519	409.7296	801.4254	401.2163	800.4413	400.7243	**7**
16	1686.8156	843.9114	1669.7890	835.3982	1668.8050	834.9061	**T**	***671.3835***	336.1954	654.3570	327.6821	653.3729	327.1901	**6**
17	***1799.8997***	900.4535	1782.8731	891.9402	1781.8891	891.4482	**I**	***570.3358***	285.6715	553.3093	277.1583			**5**
18	1896.9524	948.9798	1879.9259	940.4666	1878.9418	939.9746	**P**	***457.2518***	229.1295	440.2252	220.6162			**4**
19	1967.9895	984.4984	1950.9630	975.9851	1949.9790	975.4931	**A**	360.1990	180.6031	343.1724	172.0899			**3**
20	2082.0325	1041.5199	2065.0059	1033.0066	2064.0219	1032.5146	**N**	289.1619	145.0846	272.1353	136.5713			**2**
21							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.8	2255.1369	0.0063	TVLTPATNHMGNVTFTIPANR	Deamidated N12 90.87%
36.6	2255.1369	0.0063	TVLTPATNHMGNVTFTIPANR	Deamidated N8 8.72%
23.4	2255.1369	0.0063	TVLTPATNHMGNVTFTIPANR	Deamidated N20 0.41%
13.2	2254.1337	1.0095	SAGAGIRFLGEEKMGTELLLM	
10.0	2255.1369	0.0063	HTFALLDAARGTGECVVVPDK	
7.6	2254.1382	1.0050	WQVGAKFLAYATLANGSQSNK	
6.1	2253.1311	2.0121	LVPSCEEERLLVASGADPSPK	
6.0	2254.1382	1.0050	WQVGAKFLAYATLANGSQSNK	
5.5	2254.1382	1.0050	WQVGAKFLAYATLANGSQSNK	
5.5	2254.1382	1.0050	WQVGAKFLAYATLANGSQSNK	

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

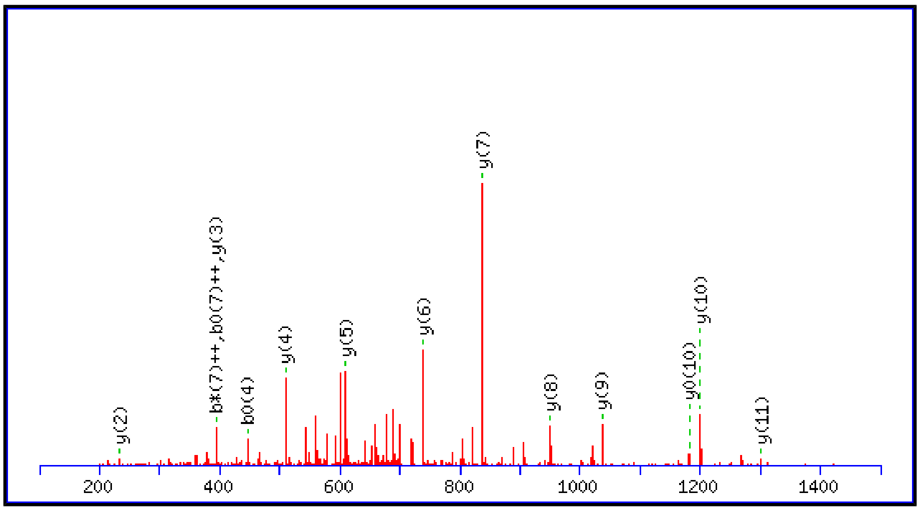
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITYSIVQTNCSK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

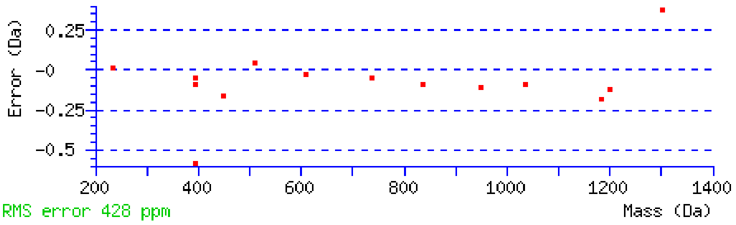
Match to Query 2840: 1413.687948 from(707.851250,2+) intensity(10775.5273) rtinseconds(681) scans(1329) index(28021)
Title: 111019_Est_MI_YS_G_12Spectrum1123_scans__1329
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

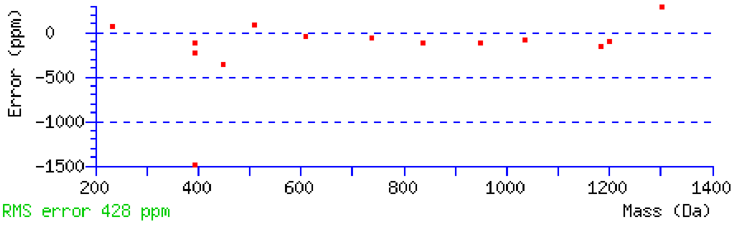
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1413.6810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 105 **Expect:** 4.8e-009
Matches : 14/116 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	114.0913	57.5493					I							12
2	215.1390	108.0731			197.1285	99.0679	T	***1301.6042***	651.3057	1284.5776	642.7925	1283.5936	642.3005	11
3	378.2023	189.6048			360.1918	180.5995	Y	***1200.5565***	600.7819	1183.5300	592.2686	1182.5460	591.7766	10
4	465.2344	233.1208			447.2238	224.1155	S	***1037.4932***	519.2502	1020.4666	510.7370	1019.4826	510.2449	9
5	578.3184	289.6629			560.3079	280.6576	I	***950.4612***	475.7342	933.4346	467.2209	932.4506	466.7289	8
6	677.3869	339.1971			659.3763	330.1918	V	***837.3771***	419.1922	820.3505	410.6789	819.3665	410.1869	7
7	805.4454	403.2264	788.4189	394.7131	787.4349	394.2211	Q	***738.3087***	369.6580	721.2821	361.1447	720.2981	360.6527	6
8	906.4931	453.7502	889.4666	445.2369	888.4825	444.7449	T	***610.2501***	305.6287	593.2236	297.1154	592.2395	296.6234	5
9	1021.5201	511.2637	1004.4935	502.7504	1003.5095	502.2584	N	***509.2024***	255.1048	492.1759	246.5916	491.1919	246.0996	4
10	1181.5507	591.2790	1164.5242	582.7657	1163.5401	582.2737	C	***394.1755***	197.5914	377.1489	189.0781	376.1649	188.5861	3
11	1268.5827	634.7950	1251.5562	626.2817	1250.5722	625.7897	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
105.5	1413.6810	0.0070	ITYSIVQTNCSK	Deamidated N9 99.99%
67.0	1413.6810	0.0070	ITYSIVQTNCSK	Deamidated Q7 0.01%
7.2	1413.6810	0.0070	TMSQEFSKLQSK	
2.1	1413.6843	0.0036	ATSSLMMLDSKSK	
2.0	1412.6877	1.0002	RHQCRVLCQR	
1.6	1413.6922	-0.0043	NHSAVPVLTNMSK	
0.7	1413.6888	-0.0009	LHDVLEEQFER	

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

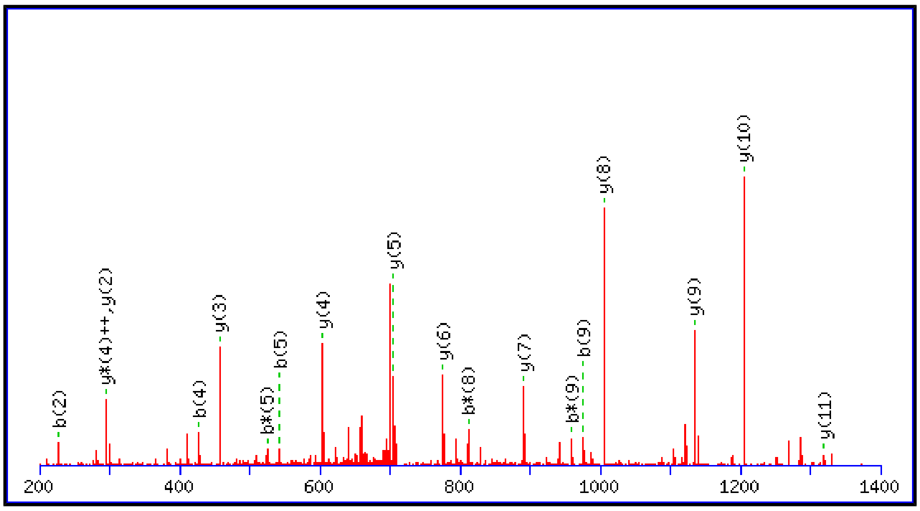
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNAENNATFYFK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

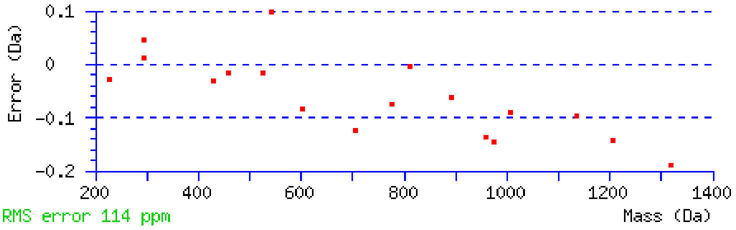
Match to Query 3867: 1431.672548 from(716.843550,2+) intensity(154903.0469) rtinseconds(1468) scans(3721) index(18534)
Title: 111019_Est_MI_YP_G_08Spectrum3237_scans__3721
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

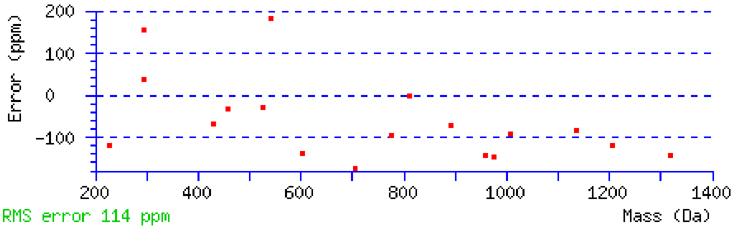
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1431.6670
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 89 **Expect:** 2.2e-007
Matches : 18/116 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	**228.1343**	114.5708	211.1077	106.0575			N	***1319.5903***	660.2988	1302.5637	651.7855	1301.5797	651.2935	11
3	299.1714	150.0893	282.1448	141.5761			A	***1205.5473***	603.2773	1188.5208	594.7640	1187.5368	594.2720	10
4	**428.2140**	214.6106	411.1874	206.0974	410.2034	205.6053	E	***1134.5102***	567.7587	1117.4837	559.2455	1116.4997	558.7535	9
5	**542.2569**	271.6321	525.2304	263.1188	524.2463	262.6268	N	***1005.4676***	503.2375	988.4411	494.7242	987.4571	494.2322	8
6	657.2838	329.1456	640.2573	320.6323	639.2733	320.1403	N	***891.4247***	446.2160	874.3981	437.7027	873.4141	437.2107	7
7	728.3210	364.6641	711.2944	356.1508	710.3104	355.6588	A	***776.3978***	388.7025	759.3712	380.1892	758.3872	379.6972	6
8	829.3686	415.1880	812.3421	406.6747	811.3581	406.1827	T	***705.3606***	353.1840	688.3341	344.6707	687.3501	344.1787	5
9	**976.4371**	488.7222	959.4105	480.2089	958.4265	479.7169	F	***604.3130***	302.6601	587.2864	294.1468			4
10	1139.5004	570.2538	1122.4738	561.7406	1121.4898	561.2485	Y	***457.2445***	229.1259	440.2180	220.6126			3
11	1286.5688	643.7880	1269.5422	635.2748	1268.5582	634.7828	F	***294.1812***	147.5942	277.1547	139.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.5	1431.6670	0.0055	LNAENNATFYFK	Deamidated N6 98.67%
69.8	1431.6670	0.0055	LNAENNATFYFK	Deamidated N5 1.33%
20.6	1431.6670	0.0055	LNAENNATFYFK	Deamidated N2 0.00%
7.6	1431.6729	-0.0003	LLNNEQELQSNK	
4.8	1431.6670	0.0055	NGHFFPEQVLNK	
4.5	1431.6776	-0.0051	GGGGGNGKAAATAAVAAM	
4.4	1431.6729	-0.0003	LLNNEQELQSNK	
4.0	1430.6751	0.9974	MNTEKQLQYFK	
3.4	1431.6776	-0.0051	GRTQCVPTGEQAK	
2.5	1431.6729	-0.0003	LLNNEQELQSNK	

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

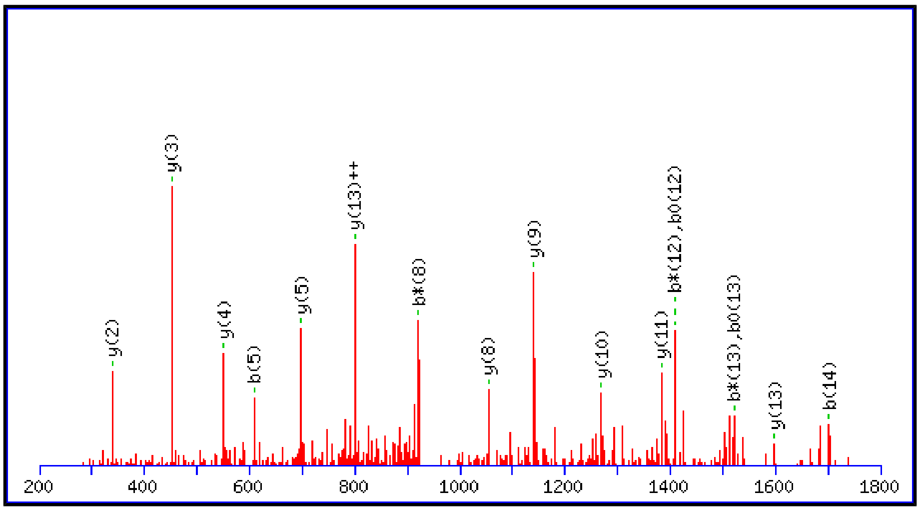
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YNSQNQSNNQFVLYR**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

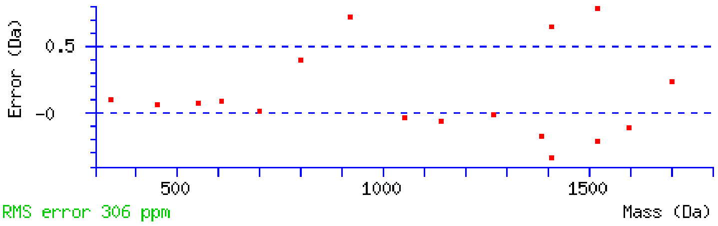
Match to Query 11041: 1874.862128 from(938.438340,2+) intensity(7939.4526) rtinseconds(1032) scans(2209) index(28072)
Title: 111019_Est_MI_YS_G_12Spectrum1910_scans__2209
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

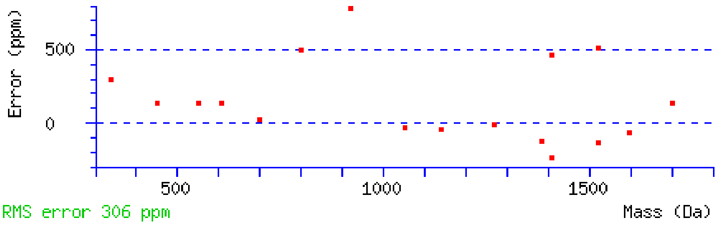
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1874.8547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 84 **Expect:** 6e-007
Matches : 17/146 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	164.0706	82.5389					Y							15
2	278.1135	139.5604	261.0870	131.0471			N	1712.7987	856.9030	1695.7721	848.3897	1694.7881	847.8977	14
3	365.1456	183.0764	348.1190	174.5631	347.1350	174.0711	S	***1598.7558***	799.8815	1581.7292	791.3682	1580.7452	790.8762	13
4	493.2041	247.1057	476.1776	238.5924	475.1936	238.1004	Q	1511.7237	756.3655	1494.6972	747.8522	1493.7132	747.3602	12
5	**608.2311**	304.6192	591.2045	296.1059	590.2205	295.6139	N	***1383.6652***	692.3362	1366.6386	683.8229	1365.6546	683.3309	11
6	736.2897	368.6485	719.2631	360.1352	718.2791	359.6432	Q	***1268.6382***	634.8227	1251.6117	626.3095	1250.6276	625.8175	10
7	823.3217	412.1645	806.2951	403.6512	805.3111	403.1592	S	***1140.5796***	570.7935	1123.5531	562.2802	1122.5691	561.7882	9
8	937.3646	469.1859	920.3381	460.6727	919.3540	460.1807	N	***1053.5476***	527.2774	1036.5211	518.7642			8
9	1051.4075	526.2074	1034.3810	517.6941	1033.3970	517.2021	N	939.5047	470.2560	922.4781	461.7427			7
10	1179.4661	590.2367	1162.4396	581.7234	1161.4556	581.2314	Q	825.4618	413.2345	808.4352	404.7212			6
11	1326.5345	663.7709	1309.5080	655.2576	1308.5240	654.7656	F	***697.4032***	349.2052	680.3766	340.6920			5
12	1425.6029	713.3051	1408.5764	704.7918	1407.5924	704.2998	V	***550.3348***	275.6710	533.3082	267.1577			4
13	1538.6870	769.8471	1521.6605	761.3339	1520.6764	760.8419	L	***451.2663***	226.1368	434.2398	217.6235			3
14	**1701.7503**	851.3788	1684.7238	842.8655	1683.7398	842.3735	Y	***338.1823***	169.5948	321.1557	161.0815			2
15							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
84.1	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated N5 96.88%
66.9	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated Q4 1.87%
61.2	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated Q6 0.50%
60.9	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated N8 0.46%
57.9	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated N9 0.23%
51.2	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated N2 0.05%
46.0	1874.8547	0.0074	YNSQNQSNNQFVLYR	Deamidated Q10 0.02%
4.5	1874.8590	0.0032	QILNEMWLHSCICR	
2.3	1872.8617	2.0004	QQWQWIDGAMYLYR	
1.8	1873.8629	0.9993	FERGLSSFQQSVAMDR	

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

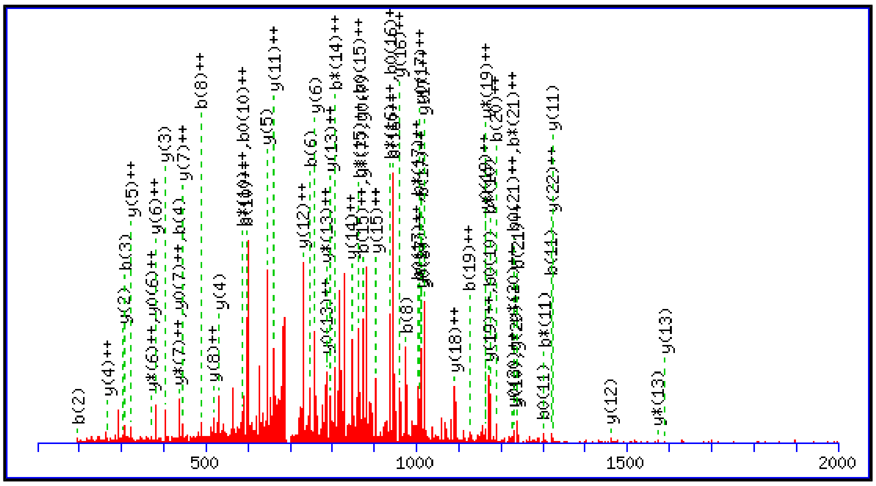
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGIQYFNNNTQHSSLFMLNEVKR**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

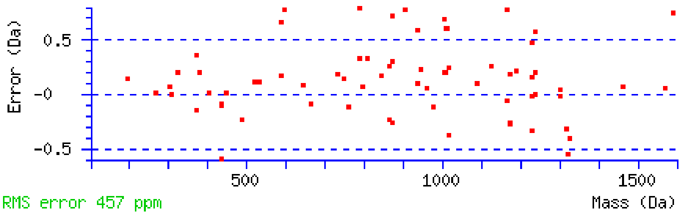
Match to Query 25474: 2777.342256 from(695.342840,4+) intensity(53934.9023) rtinseconds(1376) scans(3250) index(8300)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum2759_scans__3250
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

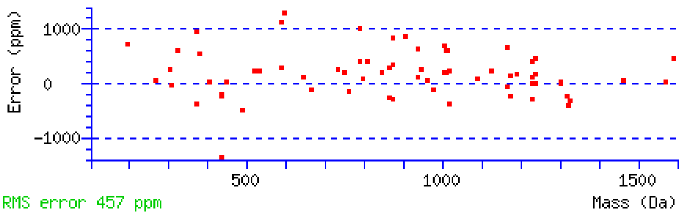
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2777.3344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 72 **Expect:** 1.6e-005
Matches : 70/234 fragment ions using 128 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					H							23
2	**195.0877**	98.0475					G	2641.2827	1321.1450	2624.2562	1312.6317	2623.2722	1312.1397	22
3	**308.1717**	154.5895					I	2584.2613	1292.6343	2567.2347	1284.1210	2566.2507	1283.6290	21
4	**436.2303**	218.6188	419.2037	210.1055			Q	2471.1772	1236.0922	2454.1507	1227.5790	2453.1667	1227.0870	20
5	599.2936	300.1504	582.2671	291.6372			Y	2343.1186	1172.0630	2326.0921	1163.5497	2325.1081	1163.0577	19
6	**746.3620**	373.6847	729.3355	365.1714			F	2180.0553	1090.5313	2163.0288	1082.0180	2162.0447	1081.5260	18
7	860.4050	430.7061	843.3784	422.1928			N	2032.9869	1016.9971	2015.9603	1008.4838	2014.9763	1007.9918	17
8	**975.4319**	**488.2196**	958.4054	479.7063			N	1918.9440	959.9756	1901.9174	951.4623	1900.9334	950.9703	16
9	1089.4748	545.2411	1072.4483	536.7278			N	1803.9170	902.4622	1786.8905	893.9489	1785.9065	893.4569	15
10	1190.5225	**595.7649**	1173.4960	587.2516	1172.5119	586.7596	T	1689.8741	845.4407	1672.8476	836.9274	1671.8635	836.4354	14
11	**1318.5811**	659.7942	1301.5545	651.2809	1300.5705	650.7889	Q	**1588.8264**	794.9168	1571.7999	786.4036	1570.8159	785.9116	13
12	1455.6400	728.3236	1438.6135	719.8104	1437.6294	719.3184	H	**1460.7678**	730.8876	1443.7413	722.3743	1442.7573	721.8823	12
13	1542.6720	771.8397	1525.6455	763.3264	1524.6615	762.8344	S	**1323.7089**	662.3581	1306.6824	653.8448	1305.6984	653.3528	11
14	1629.7041	815.3557	1612.6775	806.8424	1611.6935	806.3504	S	**1236.6769**	618.8421	1219.6504	610.3288	1218.6663	609.8368	10
15	1742.7881	**871.8977**	1725.7616	863.3844	1724.7776	862.8924	L	1149.6449	575.3261	1132.6183	566.8128	1131.6343	566.3208	9
16	1889.8565	**945.4319**	1872.8300	936.9186	1871.8460	936.4266	F	1036.5608	518.7840	1019.5343	510.2708	1018.5502	509.7788	8
17	2020.8970	**1010.9521**	2003.8705	1002.4389	2002.8865	1001.9469	M	889.4924	445.2498	872.4658	436.7366	871.4818	436.2446	7
18	2133.9811	1067.4942	2116.9545	1058.9809	2115.9705	1058.4889	L	**758.4519**	379.7296	741.4254	371.2163	740.4413	370.7243	6
19	2248.0240	**1124.5156**	2230.9975	1116.0024	2230.0134	1115.5104	N	**645.3678**	323.1876	628.3413	314.6743	627.3573	314.1823	5
20	2377.0666	**1189.0369**	2360.0401	1180.5237	2359.0560	1180.0317	E	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	4
21	2476.1350	**1238.5711**	2459.1085	1230.0579	2458.1245	1229.5659	V	**402.2823**	201.6448	385.2558	193.1315			3
22	2604.2300	1302.6186	2587.2034	1294.1054	2586.2194	1293.6133	K	**303.2139**	152.1106	286.1874	143.5973			2
23							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.2	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N8 22.10%
72.2	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N7 22.10%
71.2	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N9 17.56%
71.1	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated Q11 16.88%
69.4	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated Q4 11.63%
68.7	2777.3344	0.0079	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N19 9.74%
57.5	2776.3503	0.9919	HGIQYFNNNTQHSSLFMLNEVKR	
8.5	2777.3501	-0.0078	LKQSLDSSNESIETNNLCVLEARR	
7.0	2776.3409	1.0013	KNNMNRSNTIQSGPEDSLVNSQSLK	
6.4	2776.3319	1.0103	YHMVATAPPFGEGEEQKGWLFPLR	

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

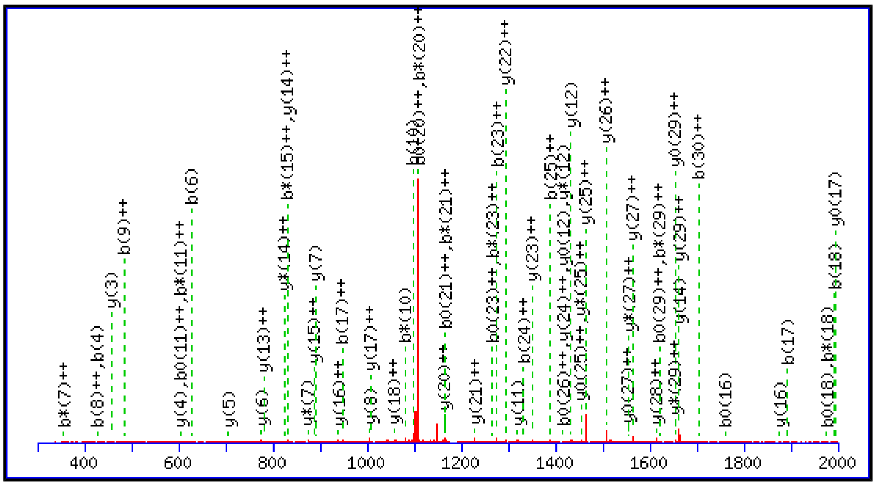
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIPTNSPELEETLTHTITKLNAENNATFYFK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 27827: 3551.746422 from(1184.922750,3+) intensity(73757.4141) rtinseconds(2451) scans(6141) index(9152)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum5303_scans__6141
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

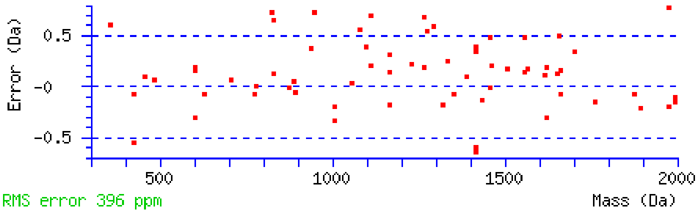
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

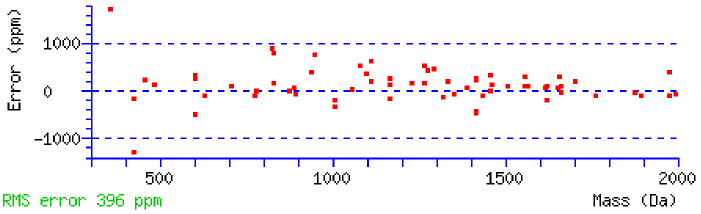


Monoisotopic mass of neutral peptide Mr(calc): 3551.7307
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
Ions Score: 70 **Expect:** 2.6e-005
Matches : 66/344 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**31**
2	229.1183	115.0628			211.1077	106.0575	**I**	3437.7111	1719.3592	3420.6846	1710.8459	3419.7005	1710.3539	**30**
3	326.1710	163.5892			308.1605	154.5839	**P**	3324.6270	1662.8172	3307.6005	1654.3039	3306.6165	1653.8119	**29**
4	**427.2187**	214.1130			409.2082	205.1077	**T**	3227.5743	1614.2908	3210.5477	1605.7775	3209.5637	1605.2855	**28**
5	541.2617	271.1345	524.2351	262.6212	523.2511	262.1292	**N**	3126.5266	1563.7669	3109.5001	1555.2537	3108.5160	1554.7617	**27**
6	**628.2937**	314.6505	611.2671	306.1372	610.2831	305.6452	**S**	3012.4837	1506.7455	2995.4571	1498.2322	2994.4731	1497.7402	**26**
7	725.3464	363.1769	708.3199	354.6636	707.3359	354.1716	**P**	2925.4516	1463.2295	2908.4251	1454.7162	2907.4411	1454.2242	**25**
8	854.3890	**427.6982**	837.3625	419.1849	836.3785	418.6929	**E**	2828.3989	1414.7031	2811.3723	1406.1898	2810.3883	1405.6978	**24**
9	967.4731	**484.2402**	950.4466	475.7269	949.4625	475.2349	**L**	2699.3563	1350.1818	2682.3297	1341.6685	2681.3457	1341.1765	**23**
10	**1096.5157**	548.7615	1079.4891	540.2482	1078.5051	539.7562	**E**	2586.2722	1293.6398	2569.2457	1285.1265	2568.2617	1284.6345	**22**
11	1225.5583	613.2828	1208.5317	604.7695	1207.5477	604.2775	**E**	2457.2296	1229.1185	2440.2031	1220.6052	2439.2191	1220.1132	**21**
12	1326.6060	663.8066	1309.5794	655.2933	1308.5954	654.8013	**T**	2328.1870	1164.5972	2311.1605	1156.0839	2310.1765	1155.5919	**20**
13	1439.6900	720.3487	1422.6635	711.8354	1421.6795	711.3434	**L**	2227.1394	1114.0733	2210.1128	1105.5600	2209.1288	1105.0680	**19**
14	1540.7377	770.8725	1523.7112	762.3592	1522.7271	761.8672	**T**	2114.0553	1057.5313	2097.0287	1049.0180	2096.0447	1048.5260	**18**
15	1677.7966	839.4019	1660.7701	830.8887	1659.7861	830.3967	**H**	2013.0076	1007.0074	1995.9811	998.4942	1994.9971	998.0022	**17**
16	1778.8443	889.9258	1761.8178	881.4125	1760.8337	880.9205	**T**	***1875.9487***	938.4780	1858.9222	929.9647	1857.9381	929.4727	**16**
17	**1891.9284**	**946.4678**	1874.9018	937.9545	1873.9178	937.4625	**I**	1774.9010	887.9542	1757.8745	879.4409	1756.8905	878.9489	**15**
18	**1992.9760**	996.9917	1975.9495	988.4784	1974.9655	987.9864	**T**	***1661.8170***	831.4121	1644.7904	822.8988	1643.8064	822.4068	**14**
19	2121.0710	1061.0391	2104.0445	1052.5259	2103.0604	1052.0339	**K**	1560.7693	780.8883	1543.7427	772.3750	1542.7587	771.8830	**13**
20	2234.1551	1117.5812	2217.1285	1109.0679	2216.1445	1108.5759	**L**	***1432.6743***	716.8408	1415.6478	708.3275	1414.6638	707.8355	**12**
21	2348.1980	1174.6026	2331.1714	1166.0894	2330.1874	1165.5974	**N**	***1319.5903***	660.2988	1302.5637	651.7855	1301.5797	651.2935	**11**
22	2419.2351	1210.1212	2402.2086	1201.6079	2401.2245	1201.1159	**A**	1205.5473	603.2773	1188.5208	594.7640	1187.5368	594.2720	**10**
23	2548.2777	**1274.6425**	2531.2512	1266.1292	2530.2671	1265.6372	**E**	1134.5102	567.7587	1117.4837	559.2455	1116.4997	558.7535	**9**

24	2662.3206	**1331.6640**	2645.2941	1323.1507	2644.3101	1322.6587	**N**	***1005.4676***	503.2374	988.4411	494.7242	987.4571	494.2322	**8**
25	2777.3476	**1389.1774**	2760.3210	1380.6642	2759.3370	1380.1721	**N**	***891.4247***	446.2160	874.3981	437.7027	873.4141	437.2107	**7**
26	2848.3847	1424.6960	2831.3581	1416.1827	2830.3741	1415.6907	**A**	***776.3978***	388.7025	759.3712	380.1892	758.3872	379.6972	**6**
27	2949.4324	1475.2198	2932.4058	1466.7065	2931.4218	1466.2145	**T**	***705.3606***	353.1840	688.3341	344.6707	687.3501	344.1787	**5**
28	3096.5008	1548.7540	3079.4742	1540.2408	3078.4902	1539.7487	**F**	***604.3130***	302.6601	587.2864	294.1468			**4**
29	3259.5641	1630.2857	3242.5376	1621.7724	3241.5535	1621.2804	**Y**	***457.2445***	229.1259	440.2180	220.6126			**3**
30	3406.6325	**1703.8199**	3389.6060	1695.3066	3388.6220	1694.8146	**F**	294.1812	147.5942	277.1547	139.0810			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.0	3551.7307	0.0157	DIPTNSPELEETLTHTITKLNAENNATFYFK	Deamidated N25 66.62%
64.7	3551.7307	0.0157	DIPTNSPELEETLTHTITKLNAENNATFYFK	Deamidated N21 19.80%
63.0	3551.7307	0.0157	DIPTNSPELEETLTHTITKLNAENNATFYFK	Deamidated N24 13.32%
46.0	3551.7307	0.0157	DIPTNSPELEETLTHTITKLNAENNATFYFK	Deamidated N5 0.26%
42.4	3550.7467	0.9997	DIPTNSPELEETLTHTITKLNAENNATFYFK	
11.3	3551.7462	0.0002	RAEAGYITQLACLMLNQLELTEVLDTNWVMG	
9.3	3549.7488	1.9976	YAAAQLSLTQLSSGNPVYEKYYRQVDTGNTGR	
8.8	3550.7328	1.0136	YAAAQLSLTQLSSGNPVYEKYYRQVDTGNTGR	
8.8	3550.7328	1.0136	YAAAQLSLTQLSSGNPVYEKYYRQVDTGNTGR	
7.8	3549.7371	2.0093	HNRFMTELLDSAYPVLSQDGMVELIQSPITK	

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

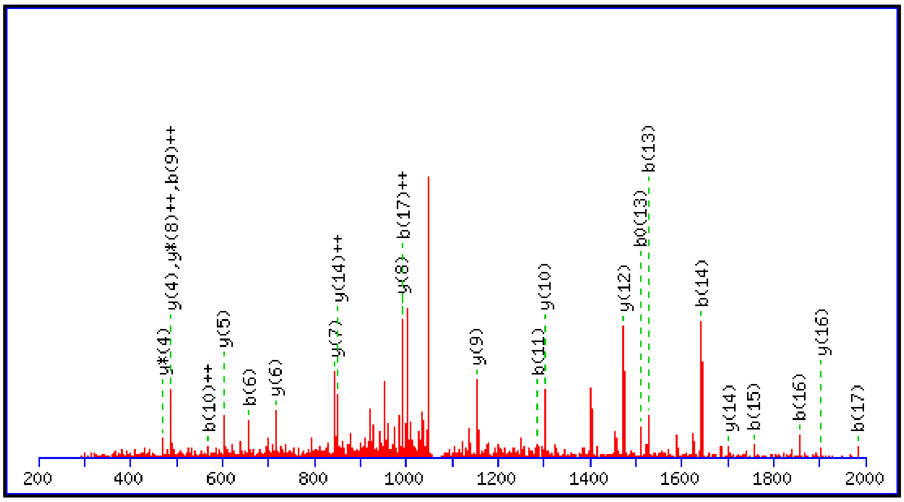
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNAENNATFYFKIDNVKK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

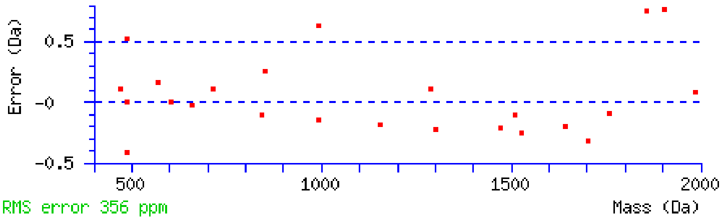
Match to Query 14378: 2129.087008 from(1065.550780,2+) intensity(29417.3184) rtinseconds(1363) scans(3126) index(10097)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum2641_scans__3126
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

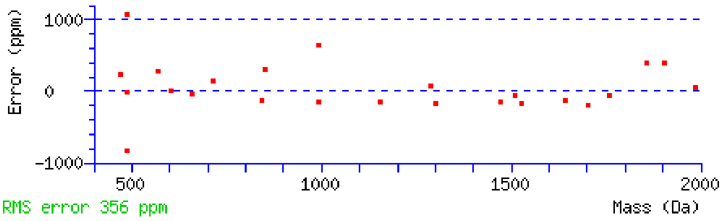
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2129.0793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6      : Deamidated (NQ)
Ions Score: 69  Expect: 2.8e-005
Matches : 24/188 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	114.0913	57.5493					L							18
2	228.1343	114.5708	211.1077	106.0575			N	2017.0025	1009.0049	1999.9760	1000.4916	1998.9920	999.9996	17
3	299.1714	150.0893	282.1448	141.5761			A	***1902.9596***	951.9834	1885.9331	943.4702	1884.9490	942.9782	16
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	E	1831.9225	916.4649	1814.8959	907.9516	1813.9119	907.4596	15
5	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	N	***1702.8799***	851.9436	1685.8533	843.4303	1684.8693	842.9383	14
6	***657.2838***	329.1456	640.2573	320.6323	639.2733	320.1403	N	1588.8370	794.9221	1571.8104	786.4088	1570.8264	785.9168	13
7	728.3210	364.6641	711.2944	356.1508	710.3104	355.6588	A	***1473.8100***	737.4087	1456.7835	728.8954	1455.7995	728.4034	12
8	829.3686	415.1880	812.3421	406.6747	811.3581	406.1827	T	1402.7729	701.8901	1385.7464	693.3768	1384.7623	692.8848	11
9	976.4371	**488.7222**	959.4105	480.2089	958.4265	479.7169	F	***1301.7252***	651.3663	1284.6987	642.8530	1283.7147	642.3610	10
10	1139.5004	**570.2538**	1122.4738	561.7406	1121.4898	561.2485	Y	***1154.6568***	577.8320	1137.6303	569.3188	1136.6463	568.8268	9
11	***1286.5688***	643.7880	1269.5422	635.2748	1268.5582	634.7828	F	***991.5935***	496.3004	974.5669	487.7871	973.5829	487.2951	8
12	1414.6638	707.8355	1397.6372	699.3222	1396.6532	698.8302	K	***844.5251***	422.7662	827.4985	414.2529	826.5145	413.7609	7
13	***1527.7478***	764.3775	1510.7213	755.8643	1509.7373	755.3723	I	***716.4301***	358.7187	699.4036	350.2054	698.4196	349.7134	6
14	***1642.7748***	821.8910	1625.7482	813.3777	1624.7642	812.8857	D	***603.3461***	302.1767	586.3195	293.6634	585.3355	293.1714	5
15	***1756.8177***	878.9125	1739.7911	870.3992	1738.8071	869.9072	N	***488.3191***	244.6632	471.2926	236.1499			4
16	***1855.8861***	928.4467	1838.8596	919.9334	1837.8755	919.4414	V	374.2762	187.6417	357.2496	179.1285			3
17	***1983.9811***	**992.4942**	1966.9545	983.9809	1965.9705	983.4889	K	275.2078	138.1075	258.1812	129.5942			2
18							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.3	2129.0793	0.0077	LNAENNATFYFKIDNVKK	Deamidated N6 44.43%
69.3	2129.0793	0.0077	LNAENNATFYFKIDNVKK	Deamidated N5 44.43%
61.0	2129.0793	0.0077	LNAENNATFYFKIDNVKK	Deamidated N2 6.53%
59.5	2129.0793	0.0077	LNAENNATFYFKIDNVKK	Deamidated N15 4.61%
9.8	2129.0793	0.0077	KVNDIKFYFTANNEANLK	
9.8	2129.0793	0.0077	KVNDIKFYFTANNEANLK	
8.7	2129.0827	0.0043	MDQPALLDVFHSSALVDKK	
8.2	2129.0907	-0.0037	MTPTRLGAMPILCIRPNR	
7.0	2128.0872	0.9998	RNSQRAAEALQSVLDAEIR	
6.8	2128.0872	0.9998	RNSQRAAEALQSVLDAEIR	

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

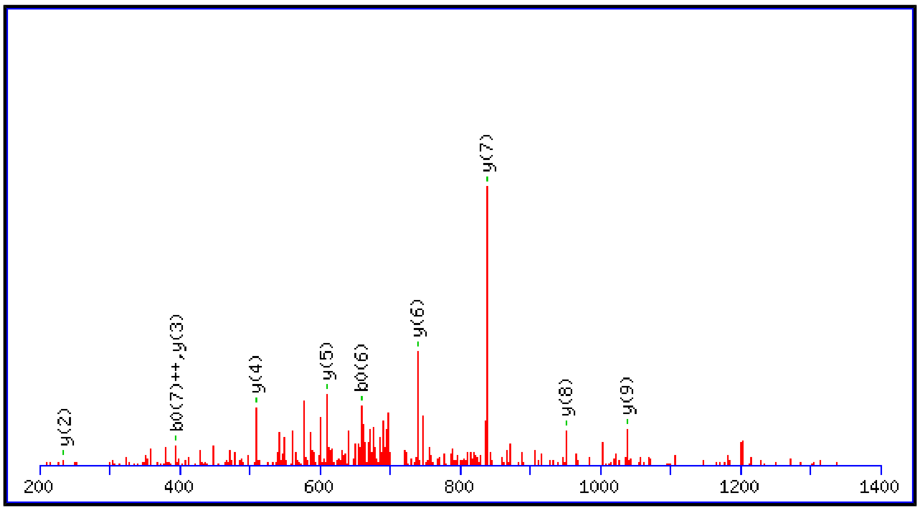
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITYSIVQTNCSK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

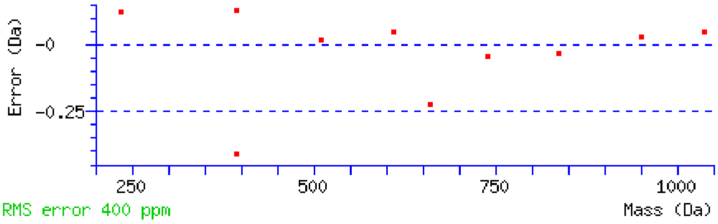
Match to Query 2849: 1414.669588 from(708.342070,2+) intensity(3677.8606) rtinseconds(869) scans(1696) index(28368)
Title: 111019_Est_MI_YS_G_13Spectrum1418_scans__1696
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

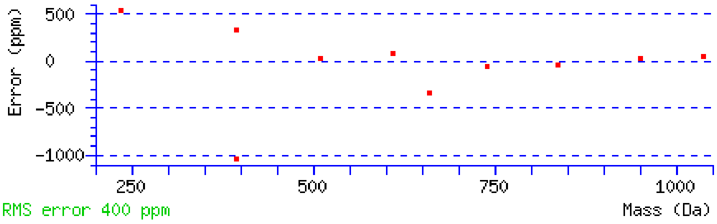
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1414.6650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 63 **Expect:** 7.6e-005
Matches : 10/116 fragment ions using 12 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					**I**							**12**
2	215.1390	108.0731			197.1285	99.0679	**T**	1302.5882	651.7977	1285.5617	643.2845	1284.5776	642.7925	**11**
3	378.2023	189.6048			360.1918	180.5995	**Y**	1201.5405	601.2739	1184.5140	592.7606	1183.5300	592.2686	**10**
4	465.2344	233.1208			447.2238	224.1155	**S**	***1038.4772***	519.7422	1021.4507	511.2290	1020.4666	510.7370	**9**
5	578.3184	289.6629			560.3079	280.6576	**I**	***951.4452***	476.2262	934.4186	467.7130	933.4346	467.2209	**8**
6	677.3869	339.1971			659.3763	330.1918	**V**	***838.3611***	419.6842	821.3346	411.1709	820.3505	410.6789	**7**
7	806.4294	403.7184	789.4029	395.2051	788.4189	394.7131	**Q**	***739.2927***	370.1500	722.2661	361.6367	721.2821	361.1447	**6**
8	907.4771	454.2422	890.4506	445.7289	889.4666	445.2369	**T**	***610.2501***	305.6287	593.2236	297.1154	592.2395	296.6234	**5**
9	1022.5041	511.7557	1005.4775	503.2424	1004.4935	502.7504	**N**	***509.2024***	255.1049	492.1759	246.5916	491.1919	246.0996	**4**
10	1182.5347	591.7710	1165.5082	583.2577	1164.5242	582.7657	**C**	***394.1755***	197.5914	377.1489	189.0781	376.1649	188.5861	**3**
11	1269.5667	635.2870	1252.5402	626.7737	1251.5562	626.2817	**S**	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
12							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ITYSIVQTNCSK
(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	1414.6650	0.0046	ITYSIVQTNCSK
2.5	1414.6762	-0.0066	EEPTMQAVLEPR
1.5	1413.6718	0.9978	RHQCRVLCQR
0.6	1413.6670	1.0026	IGAAEQMHLSNSR

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

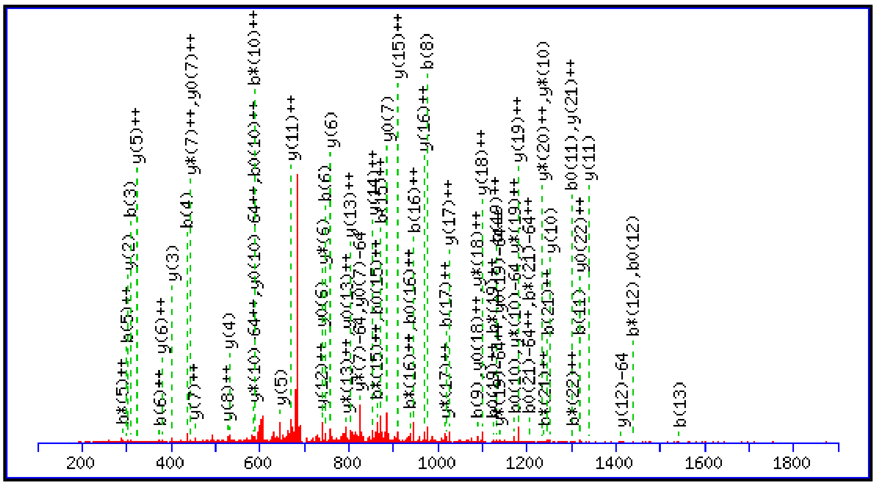
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGIQYFNNNTQHSSLFMLNEVKR**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

Match to Query 25516: 2793.341696 from(699.342700,4+) intensity(65120.5391) rtinseconds(1234) scans(3011) index(15731)
Title: 111019_Est_MI_YP_G_05Spectrum2559_scans__3011
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

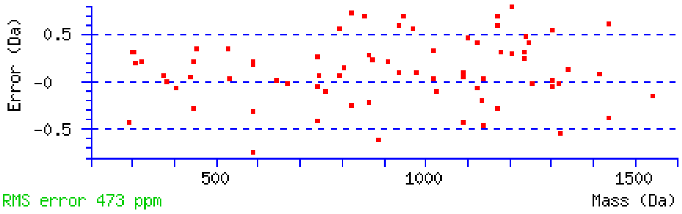
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

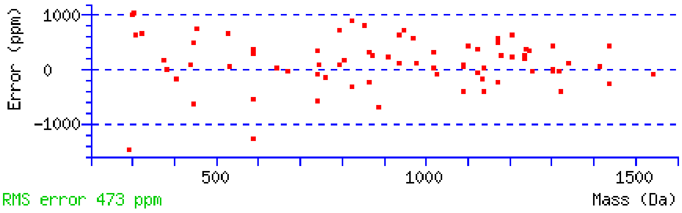


Monoisotopic mass of neutral peptide Mr(calc): 2793.3293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 63 **Expect:** 0.00014
Matches : 74/366 fragment ions using 108 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							23
2	195.0877	98.0475					G	2657.2777	1329.1425	2640.2511	1320.6292	2639.2671	1320.1372	22
3	**308.1717**	154.5895					I	2600.2562	1300.6317	2583.2296	1292.1185	2582.2456	1291.6265	21
4	**436.2303**	218.6188	419.2037	210.1055			Q	2487.1721	1244.0897	2470.1456	1235.5764	2469.1616	1235.0844	20
5	599.2936	**300.1504**	582.2671	291.6372			Y	2359.1136	1180.0604	2342.0870	1171.5471	2341.1030	1171.0551	19
6	**746.3620**	**373.6847**	729.3355	365.1714			F	2196.0502	1098.5288	2179.0237	1090.0155	2178.0397	1089.5235	18
7	860.4050	430.7061	843.3784	422.1928			N	2048.9818	1024.9945	2031.9553	1016.4813	2030.9712	1015.9893	17
8	**975.4319**	488.2196	958.4054	479.7063			N	1934.9389	967.9731	1917.9123	959.4598	1916.9283	958.9678	16
9	**1089.4748**	545.2411	1072.4483	536.7278			N	1819.9119	910.4596	1802.8854	901.9463	1801.9014	901.4543	15
10	1190.5225	595.7649	1173.4960	587.2516	1172.5119	586.7596	T	1705.8690	853.4381	1688.8425	844.9249	1687.8585	844.4329	14
11	**1318.5811**	659.7942	1301.5545	651.2809	1300.5705	650.7889	Q	1604.8213	802.9143	1587.7948	794.4010	1586.8108	793.9090	13
12	1455.6400	728.3236	1438.6135	719.8104	1437.6294	719.3184	H	1476.7628	738.8850	1459.7362	730.3717	1458.7522	729.8797	12
13	**1542.6720**	771.8397	1525.6455	763.3264	1524.6615	762.8344	S	**1339.7038**	670.3556	1322.6773	661.8423	1321.6933	661.3503	11
14	1629.7041	815.3557	1612.6775	806.8424	1611.6935	806.3504	S	**1252.6718**	626.8395	1235.6453	618.3263	1234.6613	617.8343	10
15	1742.7881	**871.8977**	1725.7616	863.3844	1724.7776	862.8924	L	1165.6398	583.3235	1148.6132	574.8103	1147.6292	574.3183	9
16	1889.8565	**945.4319**	1872.8300	936.9186	1871.8460	936.4266	F	1052.5557	526.7815	1035.5292	518.2682	1034.5452	517.7762	8
17	2036.8919	**1018.9496**	2019.8654	1010.4363	2018.8814	1009.9443	M	905.4873	453.2473	888.4608	444.7340	887.4767	444.2420	7
18	2149.9760	1075.4916	2132.9495	1066.9784	2131.9654	1066.4864	L	**758.4519**	379.7296	741.4254	371.2163	740.4413	370.7243	6
19	2264.0189	**1132.5131**	2246.9924	1123.9998	2246.0084	1123.5078	N	**645.3678**	323.1876	628.3413	314.6743	627.3573	314.1823	5
20	2393.0615	1197.0344	2376.0350	1188.5211	2375.0510	1188.0291	E	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	4
21	2492.1299	**1246.5686**	2475.1034	1238.0553	2474.1194	1237.5633	V	**402.2823**	201.6448	385.2558	193.1315			3
22	2620.2249	1310.6161	2603.1983	1302.1028	2602.2143	1301.6108	K	**303.2139**	152.1106	286.1874	143.5973			2

23							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.8	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N8 36.56%
61.7	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated Q11 28.71%
61.7	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N9 28.71%
54.8	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N7 5.82%
37.1	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated Q4 0.10%
36.7	2793.3293	0.0124	HGIQYFNNNTQHSSLFMLNEVKR	Deamidated N19 0.09%
26.1	2792.3453	0.9964	HGIQYFNNNTQHSSLFMLNEVKR	
7.2	2793.3305	0.0112	DTGPEVQSSSELSPSLSSVLDVYNQR	
4.7	2793.3387	0.0030	WLVDMLQIMQLTLMDQRLDDGNK	
4.3	2793.3387	0.0030	WLVDMLQIMQLTLMDQRLDDGNK	

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

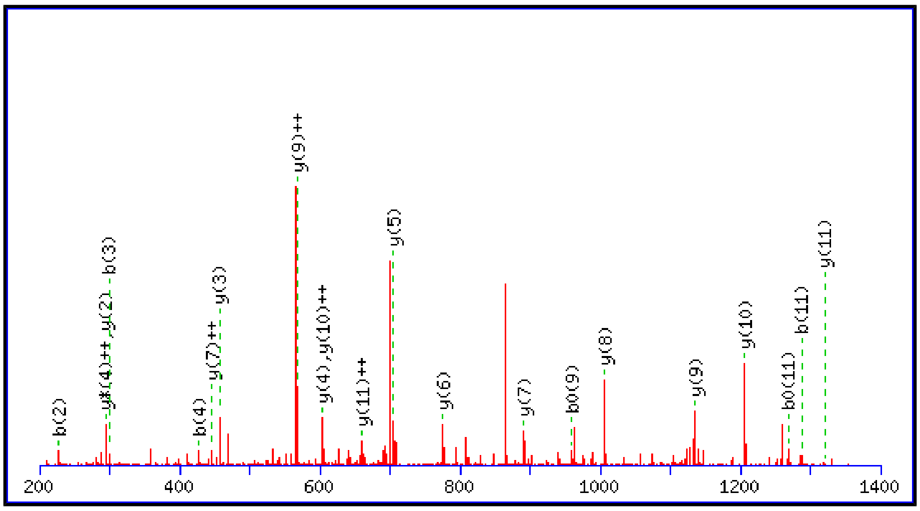
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNAENNATFYFK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

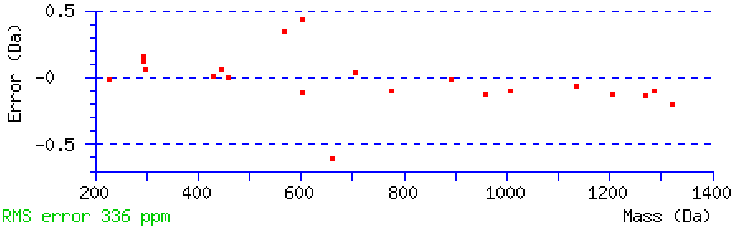
Match to Query 3997: 1432.645828 from(717.330190,2+) intensity(602318.7500) rtinseconds(1353) scans(3403) index(18495)
Title: 111019_Est_MI_YP_G_08Spectrum2957_scans__3403
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐

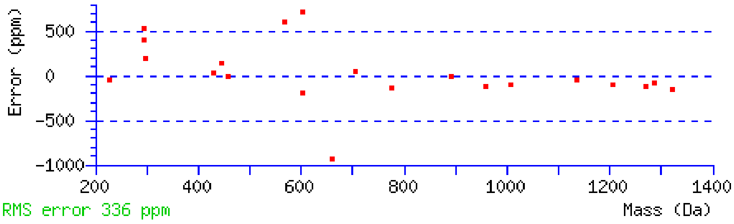


Monoisotopic mass of neutral peptide Mr(calc): 1432.6510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
N6 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.00041
Matches : 21/116 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	**228.1343**	114.5708	211.1077	106.0575			N	***1320.5743***	660.7908	1303.5477	652.2775	1302.5637	651.7855	11
3	**299.1714**	150.0893	282.1448	141.5761			A	***1206.5313***	603.7693	1189.5048	595.2560	1188.5208	594.7640	10
4	**428.2140**	214.6106	411.1874	206.0974	410.2034	205.6053	E	***1135.4942***	568.2508	1118.4677	559.7375	1117.4837	559.2455	9
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	N	***1006.4516***	503.7295	989.4251	495.2162	988.4411	494.7242	8
6	658.2679	329.6376	641.2413	321.1243	640.2573	320.6323	N	***891.4247***	446.2160	874.3981	437.7027	873.4141	437.2107	7
7	729.3050	365.1561	712.2784	356.6429	711.2944	356.1508	A	***776.3978***	388.7025	759.3712	380.1892	758.3872	379.6972	6
8	830.3527	415.6800	813.3261	407.1667	812.3421	406.6747	T	***705.3606***	353.1840	688.3341	344.6707	687.3501	344.1787	5
9	977.4211	489.2142	960.3945	480.7009	959.4105	480.2089	F	***604.3130***	302.6601	587.2864	294.1468			4
10	1140.4844	570.7458	1123.4578	562.2326	1122.4738	561.7406	Y	***457.2445***	229.1259	440.2180	220.6126			3
11	**1287.5528**	644.2800	1270.5263	635.7668	1269.5422	635.2748	F	***294.1812***	147.5942	277.1547	139.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 336 ppm



RMS error 336 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.3	1432.6510	-0.0052	LNAENNATFYFK	Deamidated N5, N6 98.67%
35.2	1432.6510	-0.0052	LNAENNATFYFK	Deamidated N2, N6 1.21%
25.3	1432.6510	-0.0052	LNAENNATFYFK	Deamidated N2, N5 0.12%
6.9	1431.6412	1.0046	QETVMATAASNHR	
4.8	1432.6405	0.0053	NLDQFMDQHRK	
3.8	1432.6513	-0.0054	DFEMIRGMKMK	
3.5	1432.6430	0.0029	DNENSEINQLTR	
3.5	1432.6430	0.0029	NNENSEINQLTR	
3.5	1432.6430	0.0029	NNENSEINQLTR	
2.6	1432.6477	-0.0018	NRNGAANMNLNSR	

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

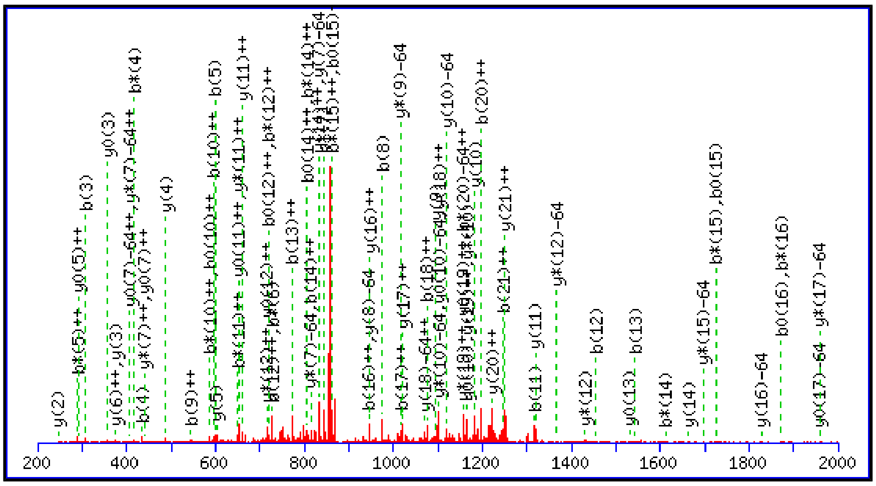
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGIQYFNNNTQHSSLFMLNEVK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

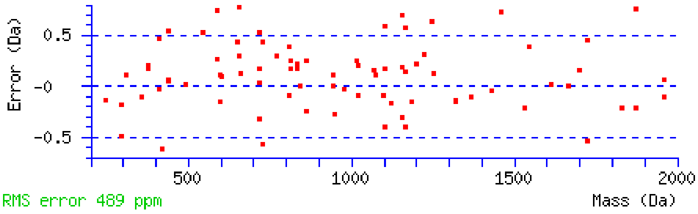
Match to Query 22372: 2637.236292 from(880.086040,3+) intensity(228665.3125) rtinseconds(1523) scans(3741) index(25320)
Title: 111019_Est_MI_YS_G_07Spectrum3175_scans__3741
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

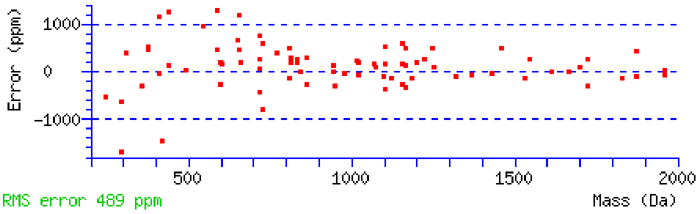
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2637.2282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54 **Expect:** 0.00089
Matches : 82/350 fragment ions using 125 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367					H							22
2	195.0877	98.0475					G	2501.1766	1251.0919	2484.1500	1242.5786	2483.1660	1242.0866	21
3	**308.1717**	154.5895					I	2444.1551	1222.5812	2427.1285	1214.0679	2426.1445	1213.5759	20
4	**436.2303**	218.6188	419.2037	210.1055			Q	2331.0710	1166.0391	2314.0445	1157.5259	2313.0605	1157.0339	19
5	**599.2936**	300.1504	582.2671	291.6372			Y	2203.0124	1102.0099	2185.9859	1093.4966	2185.0019	1093.0046	18
6	746.3620	373.6847	729.3355	365.1714			F	2039.9491	1020.4782	2022.9226	1011.9649	2021.9386	1011.4729	17
7	860.4050	430.7061	843.3784	422.1928			N	1892.8807	946.9440	1875.8542	938.4307	1874.8701	937.9387	16
8	**975.4319**	488.2196	958.4054	479.7063			N	1778.8378	889.9225	1761.8112	881.4093	1760.8272	880.9172	15
9	1089.4748	***545.2411***	1072.4483	536.7278			N	**1663.8108**	832.4091	1646.7843	823.8958	1645.8003	823.4038	14
10	1190.5225	***595.7649***	1173.4960	587.2516	1172.5119	586.7596	T	1549.7679	775.3876	1532.7414	766.8743	1531.7573	766.3823	13
11	**1318.5811**	659.7942	1301.5545	651.2809	1300.5705	650.7889	Q	1448.7202	724.8638	1431.6937	716.3505	1430.7097	715.8585	12
12	**1455.6400**	***728.3236***	1438.6135	719.8104	1437.6294	719.3184	H	**1320.6616**	660.8345	1303.6351	652.3212	1302.6511	651.8292	11
13	**1542.6720**	***771.8397***	1525.6455	763.3264	1524.6615	762.8344	S	**1183.6027**	592.3050	1166.5762	583.7917	1165.5922	583.2997	10
14	1629.7041	***815.3557***	1612.6775	806.8424	1611.6935	806.3504	S	**1096.5707**	548.7890	1079.5442	540.2757	1078.5601	539.7837	9
15	1742.7881	871.8977	1725.7616	863.3844	1724.7776	862.8924	L	1009.5387	505.2730	992.5121	496.7597	991.5281	496.2677	8
16	1889.8565	***945.4319***	1872.8300	936.9186	1871.8460	936.4266	F	896.4546	448.7309	879.4281	440.2177	878.4441	439.7257	7
17	2036.8919	***1018.9496***	2019.8654	1010.4363	2018.8814	1009.9443	M	749.3862	375.1967	732.3597	366.6835	731.3756	366.1915	6
18	2149.9760	***1075.4916***	2132.9495	1066.9784	2131.9654	1066.4864	L	**602.3508**	301.6790	585.3243	293.1658	584.3402	292.6738	5
19	2264.0189	1132.5131	2246.9924	1123.9998	2246.0084	1123.5078	N	**489.2667**	245.1370	472.2402	236.6237	471.2562	236.1317	4
20	2393.0615	***1197.0344***	2376.0350	1188.5211	2375.0510	1188.0291	E	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
21	2492.1299	***1246.5686***	2475.1034	1238.0553	2474.1194	1237.5633	V	**246.1812**	123.5942	229.1547	115.0810			2
22							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.0	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N8 28.14%
53.2	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N9 23.46%
53.1	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N7 23.19%
52.4	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated Q4 19.70%
46.8	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated Q11 5.46%
29.3	2636.2442	0.9921	HGIQYFNNNTQHSSLFMLNEVK	
25.4	2637.2282	0.0081	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N19 0.04%
6.2	2636.2361	1.0002	SLTGTRAPQNNGHQSIHNISSEMR	
3.0	2637.2335	0.0028	VEMLLAANLQSSMAQLPMEELNR	
3.0	2635.2184	2.0179	EEIPDPDVKGSPHLSDSACLGQQR	

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

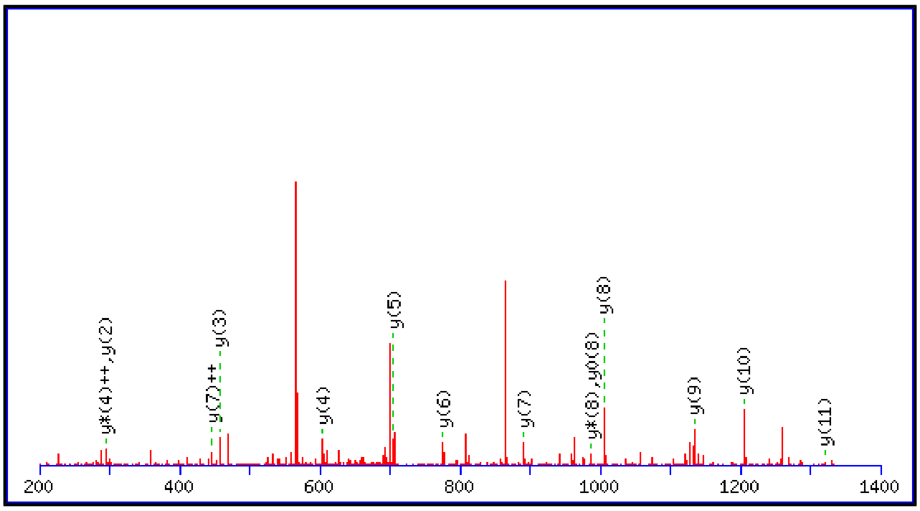
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNAENNATFYFK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

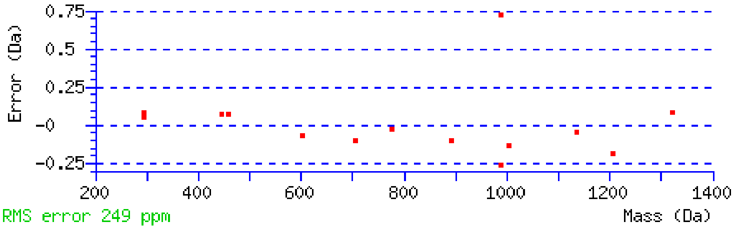
Match to Query 3995: 1432.645548 from(717.330050,2+) intensity(239272.0625) rtinseconds(1513) scans(3623) index(20282)
Title: 111019_Est_MI_YP_G_10Spectrum3159_scans__3623
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐

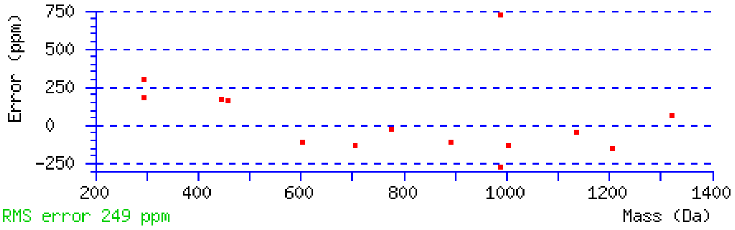


Monoisotopic mass of neutral peptide Mr(calc): 1432.6510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
N6 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.00086
Matches : 14/116 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							12
2	229.1183	115.0628	212.0917	106.5495			N	1320.5743	660.7908	1303.5477	652.2775	1302.5637	651.7855	11
3	300.1554	150.5813	283.1288	142.0681			A	1205.5473	603.2773	1188.5208	594.7640	1187.5368	594.2720	10
4	429.1980	215.1026	412.1714	206.5894	411.1874	206.0974	E	1134.5102	567.7587	1117.4837	559.2455	1116.4997	558.7535	9
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	N	1005.4676	503.2375	988.4411	494.7242	987.4571	494.2322	8
6	658.2679	329.6376	641.2413	321.1243	640.2573	320.6323	N	891.4247	446.2160	874.3981	437.7027	873.4141	437.2107	7
7	729.3050	365.1561	712.2784	356.6429	711.2944	356.1508	A	776.3978	388.7025	759.3712	380.1892	758.3872	379.6972	6
8	830.3527	415.6800	813.3261	407.1667	812.3421	406.6747	T	705.3606	353.1840	688.3341	344.6707	687.3501	344.1787	5
9	977.4211	489.2142	960.3945	480.7009	959.4105	480.2089	F	604.3130	302.6601	587.2864	294.1468			4
10	1140.4844	570.7458	1123.4578	562.2326	1122.4738	561.7406	Y	457.2445	229.1259	440.2180	220.6126			3
11	1287.5528	644.2800	1270.5263	635.7668	1269.5422	635.2748	F	294.1812	147.5942	277.1547	139.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 249 ppm



RMS error 249 ppm

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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.1	1432.6510	-0.0055	LNAENNATFYFK	Deamidated N2, N6 84.68%
41.8	1432.6510	-0.0055	LNAENNATFYFK	Deamidated N5, N6 9.93%
39.1	1432.6510	-0.0055	LNAENNATFYFK	Deamidated N2, N5 5.39%
8.1	1431.6412	1.0043	QETVMATAASNHR	
0.6	1430.6421	2.0034	TPAQAEPDVMPMK	
0.4	1432.6510	-0.0055	EWGPPLKEEDAY	
0.3	1430.6426	2.0030	LLHQEEDNYNR	
0.3	1430.6426	2.0030	LLHQEEDNYNR	

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

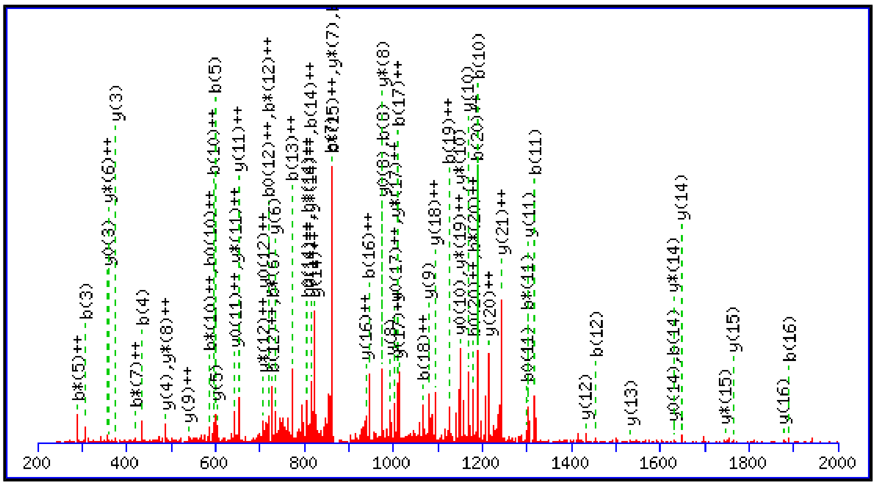
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGIQYFNNNTQHSSLFMLNEVK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

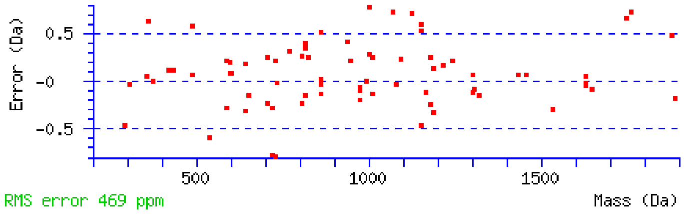
Match to Query 22343: 2621.246412 from(874.756080,3+) intensity(69248.4531) rtinseconds(1616) scans(4047) index(22596)
Title: 111019_Est_MI_YS_G_03Spectrum3530_scans__4047
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

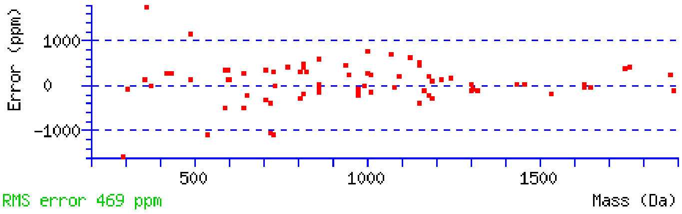
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2621.2332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0024
Matches : 75/224 fragment ions using 140 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					**H**							**22**
2	195.0877	98.0475					**G**	2485.1816	1243.0945	2468.1551	1234.5812	2467.1711	1234.0892	**21**
3	**308.1717**	154.5895					**I**	2428.1602	1214.5837	2411.1336	1206.0704	2410.1496	1205.5784	**20**
4	**436.2303**	218.6188	419.2037	210.1055			**Q**	2315.0761	1158.0417	2298.0496	1149.5284	2297.0655	1149.0364	**19**
5	**599.2936**	300.1504	582.2671	291.6372			**Y**	2187.0175	1094.0124	2169.9910	1085.4991	2169.0070	1085.0071	**18**
6	746.3620	373.6847	729.3355	365.1714			**F**	2023.9542	1012.4807	2006.9277	1003.9675	2005.9436	1003.4755	**17**
7	**860.4050**	430.7061	843.3784	422.1928			**N**	***1876.8858***	938.9465	1859.8592	930.4333	1858.8752	929.9412	**16**
8	**975.4319**	488.2196	958.4054	479.7063			**N**	***1762.8429***	881.9251	1745.8163	873.4118	1744.8323	872.9198	**15**
9	1089.4748	545.2411	1072.4483	536.7278			**N**	***1647.8159***	824.4116	1630.7894	815.8983	1629.8054	815.4063	**14**
10	**1190.5225**	**595.7649**	1173.4960	587.2516	1172.5119	586.7596	**T**	***1533.7730***	767.3901	1516.7464	758.8769	1515.7624	758.3849	**13**
11	**1318.5811**	659.7942	1301.5545	651.2809	1300.5705	650.7889	**Q**	***1432.7253***	716.8663	1415.6988	708.3530	1414.7147	707.8610	**12**
12	**1455.6400**	**728.3236**	1438.6135	719.8104	1437.6294	719.3184	**H**	***1304.6667***	652.8370	1287.6402	644.3237	1286.6562	643.8317	**11**
13	1542.6720	**771.8397**	1525.6455	763.3264	1524.6615	762.8344	**S**	***1167.6078***	584.3075	1150.5813	575.7943	1149.5973	575.3023	**10**
14	**1629.7041**	**815.3557**	1612.6775	806.8424	1611.6935	806.3504	**S**	***1080.5758***	540.7915	1063.5492	532.2783	1062.5652	531.7863	**9**
15	1742.7881	871.8977	1725.7616	863.3844	1724.7776	862.8924	**L**	***993.5438***	497.2755	976.5172	488.7622	975.5332	488.2702	**8**
16	**1889.8565**	**945.4319**	1872.8300	936.9186	1871.8460	936.4266	**F**	880.4597	440.7335	863.4332	432.2202	862.4491	431.7282	**7**
17	2020.8970	**1010.9521**	2003.8705	1002.4389	2002.8865	1001.9469	**M**	***733.3913***	367.1993	716.3647	358.6860	715.3807	358.1940	**6**
18	2133.9811	**1067.4942**	2116.9545	1058.9809	2115.9705	1058.4889	**L**	***602.3508***	301.6790	585.3243	293.1658	584.3402	292.6738	**5**
19	2248.0240	**1124.5156**	2230.9975	1116.0024	2230.0134	1115.5104	**N**	***489.2667***	245.1370	472.2402	236.6237	471.2562	236.1317	**4**
20	2377.0666	**1189.0369**	2360.0401	1180.5237	2359.0560	1180.0317	**E**	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
21	2476.1350	1238.5711	2459.1085	1230.0579	2458.1245	1229.5659	**V**	246.1812	123.5942	229.1547	115.0810			**2**
22							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.2	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N8 37.33%
48.7	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N9 26.43%
46.4	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N7 15.38%
46.4	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated Q11 15.31%
41.8	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated Q4 5.31%
32.8	2620.2492	0.9972	HGIQYFNNNTQHSSLFMLNEVK	
28.2	2621.2332	0.0132	HGIQYFNNNTQHSSLFMLNEVK	Deamidated N19 0.23%
7.6	2621.2490	-0.0026	LKQSLDSSNESIETNNLCVLEAR	
6.5	2619.2270	2.0194	QMLFQMEKSDKVPNLVYMDLR	
6.4	2621.2490	-0.0026	LKQSLDSSNESIETNNLCVLEAR	

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

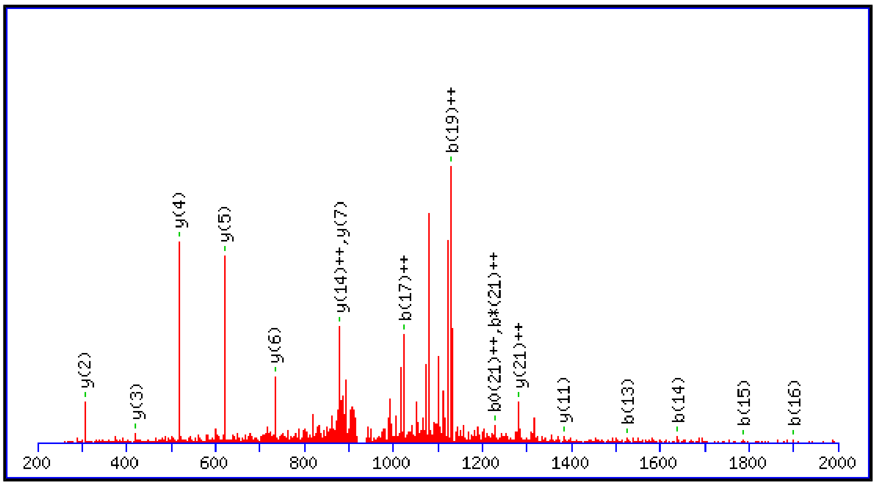
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITYSIVQTNCSKENFLFLTPDCK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

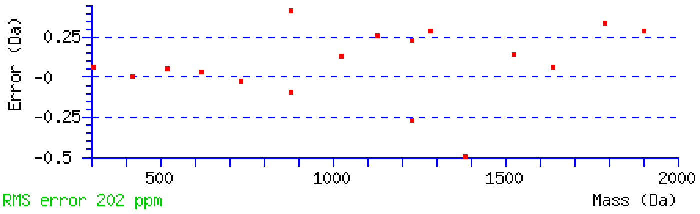
Match to Query 25500: 2778.336252 from(927.119360,3+) intensity(44735.9922) rtinseconds(2199) scans(5301) index(16939)
Title: 111019_Est_MI_YP_G_06Spectrum4396_scans__5301
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

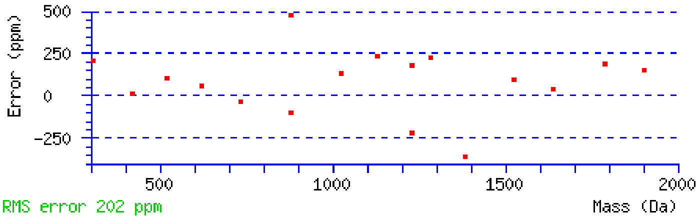
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2778.3244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.003
Matches : 17/246 fragment ions using 18 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.0913	57.5493					I							23
2	215.1390	108.0731			197.1285	99.0679	T	2666.2477	1333.6275	2649.2211	1325.1142	2648.2371	1324.6222	22
3	378.2023	189.6048			360.1918	180.5995	Y	2565.2000	1283.1036	2548.1734	1274.5904	2547.1894	1274.0984	21
4	465.2344	233.1208			447.2238	224.1155	S	2402.1367	1201.5720	2385.1101	1193.0587	2384.1261	1192.5667	20
5	578.3184	289.6629			560.3079	280.6576	I	2315.1046	1158.0560	2298.0781	1149.5427	2297.0941	1149.0507	19
6	677.3869	339.1971			659.3763	330.1918	V	2202.0206	1101.5139	2184.9940	1093.0006	2184.0100	1092.5086	18
7	805.4454	403.2264	788.4189	394.7131	787.4349	394.2211	Q	2102.9522	1051.9797	2085.9256	1043.4664	2084.9416	1042.9744	17
8	906.4931	453.7502	889.4666	445.2369	888.4825	444.7449	T	1974.8936	987.9504	1957.8670	979.4372	1956.8830	978.9451	16
9	1021.5201	511.2637	1004.4935	502.7504	1003.5095	502.2584	N	1873.8459	937.4266	1856.8193	928.9133	1855.8353	928.4213	15
10	1181.5507	591.2790	1164.5242	582.7657	1163.5401	582.2737	C	1758.8190	879.9131	1741.7924	871.3998	1740.8084	870.9078	14
11	1268.5827	634.7950	1251.5562	626.2817	1250.5722	625.7897	S	1598.7883	799.8978	1581.7618	791.3845	1580.7777	790.8925	13
12	1396.6777	698.8425	1379.6511	690.3292	1378.6671	689.8372	K	1511.7563	756.3818	1494.7297	747.8685	1493.7457	747.3765	12
13	***1525.7203***	763.3638	1508.6937	754.8505	1507.7097	754.3585	E	***1383.6613***	692.3343	1366.6348	683.8210	1365.6507	683.3290	11
14	***1639.7632***	820.3852	1622.7367	811.8720	1621.7526	811.3800	N	1254.6187	627.8130	1237.5922	619.2997	1236.6082	618.8077	10
15	***1786.8316***	893.9195	1769.8051	885.4062	1768.8211	884.9142	F	1140.5758	570.7915	1123.5492	562.2783	1122.5652	561.7863	9
16	***1899.9157***	950.4615	1882.8891	941.9482	1881.9051	941.4562	L	993.5074	497.2573	976.4808	488.7441	975.4968	488.2520	8
17	2046.9841	**1023.9957**	2029.9576	1015.4824	2028.9735	1014.9904	F	***880.4233***	440.7153	863.3968	432.2020	862.4128	431.7100	7
18	2160.0682	1080.5377	2143.0416	1072.0244	2142.0576	1071.5324	L	***733.3549***	367.1811	716.3284	358.6678	715.3443	358.1758	6
19	2261.1158	**1131.0616**	2244.0893	1122.5483	2243.1053	1122.0563	T	***620.2708***	310.6391	603.2443	302.1258	602.2603	301.6338	5
20	2358.1686	1179.5879	2341.1421	1171.0747	2340.1580	1170.5827	P	***519.2232***	260.1152	502.1966	251.6019	501.2126	251.1099	4
21	2473.1956	1237.1014	2456.1690	1228.5881	2455.1850	1228.0961	D	***422.1704***	211.5888	405.1438	203.0756	404.1598	202.5836	3
22	2633.2262	1317.1167	2616.1997	1308.6035	2615.2156	1308.1115	C	***307.1435***	154.0754	290.1169	145.5621			2
23							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.6	2778.3244	0.0118	ITYSIVQTNCSKENFLFLTPDCK	Deamidated N9 49.63%
49.6	2778.3244	0.0118	ITYSIVQTNCSKENFLFLTPDCK	Deamidated Q7 49.63%
35.0	2777.3404	0.9958	ITYSIVQTNCSKENFLFLTPDCK	
31.4	2778.3244	0.0118	ITYSIVQTNCSKENFLFLTPDCK	Deamidated N14 0.74%
9.9	2778.3246	0.0116	AVIGILQMICKTCCHIMLSQEEK	
8.6	2777.3355	1.0007	DSDENLTDAEGKVIGLQIFNIDTDR	
6.4	2776.3185	2.0178	LDNATCRSAIDQLAQQQEDEKTLK	
3.8	2776.3378	1.9985	YLGMPSKEESTYQAASVLHNVHGLK	
3.5	2776.3166	2.0196	EEMHYKAVHNTAVLFLQNDPGFAK	
3.4	2778.3317	0.0046	FIEEMMVDQTASIEGKTAGSHVLNR	

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

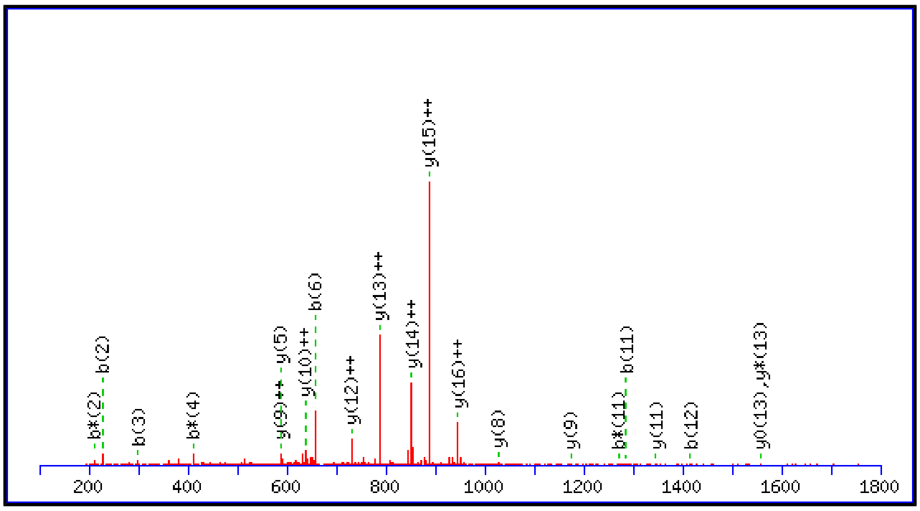
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNAENNATFYFKIDNVK**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

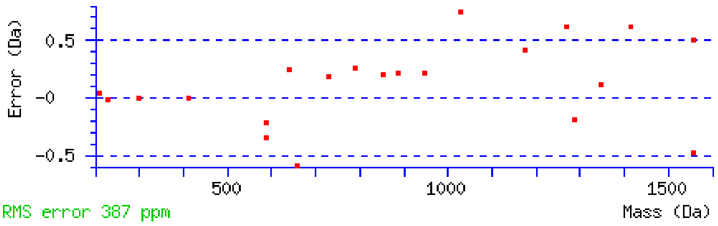
Match to Query 12217: 2000.989722 from(668.003850,3+) intensity(32877.6523) rtinseconds(1576) scans(3820) index(12611)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum3334_scans__3820
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

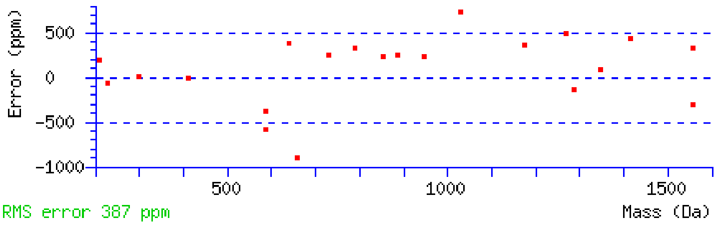
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2000.9843
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0081
Matches : 21/178 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	114.0913	57.5493					L							17
2	***228.1343***	114.5708	211.1077	106.0575			N	1888.9076	944.9574	1871.8810	936.4441	1870.8970	935.9521	16
3	***299.1714***	150.0893	282.1448	141.5761			A	1774.8646	887.9360	1757.8381	879.4227	1756.8541	878.9307	15
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	E	1703.8275	852.4174	1686.8010	843.9041	1685.8170	843.4121	14
5	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	N	1574.7849	787.8961	1557.7584	779.3828	1556.7744	778.8908	13
6	***657.2838***	329.1456	640.2573	320.6323	639.2733	320.1403	N	1460.7420	730.8746	1443.7155	722.3614	1442.7314	721.8694	12
7	728.3210	364.6641	711.2944	356.1508	710.3104	355.6588	A	**1345.7151**	673.3612	1328.6885	664.8479	1327.7045	664.3559	11
8	829.3686	415.1880	812.3421	406.6747	811.3581	406.1827	T	1274.6780	637.8426	1257.6514	629.3293	1256.6674	628.8373	10
9	976.4371	488.7222	959.4105	480.2089	958.4265	479.7169	F	**1173.6303**	587.3188	1156.6037	578.8055	1155.6197	578.3135	9
10	1139.5004	570.2538	1122.4738	561.7406	1121.4898	561.2485	Y	**1026.5619**	513.7846	1009.5353	505.2713	1008.5513	504.7793	8
11	***1286.5688***	643.7880	1269.5422	635.2748	1268.5582	634.7828	F	863.4985	432.2529	846.4720	423.7396	845.4880	423.2476	7
12	***1414.6638***	707.8355	1397.6372	699.3222	1396.6532	698.8302	K	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6
13	1527.7478	764.3775	1510.7213	755.8643	1509.7373	755.3723	I	**588.3352**	294.6712	571.3086	286.1579	570.3246	285.6659	5
14	1642.7748	821.8910	1625.7482	813.3777	1624.7642	812.8857	D	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
15	1756.8177	878.9125	1739.7911	870.3992	1738.8071	869.9072	N	360.2241	180.6157	343.1976	172.1024			3
16	1855.8861	928.4467	1838.8596	919.9334	1837.8755	919.4414	V	246.1812	123.5942	229.1547	115.0810			2
17							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.4	2000.9843	0.0054	LNAENNATFYFKIDNVK	Deamidated N6 43.57%
45.4	2000.9843	0.0054	LNAENNATFYFKIDNVK	Deamidated N5 43.57%
39.5	2000.9843	0.0054	LNAENNATFYFKIDNVK	Deamidated N2 11.43%
30.5	2000.9843	0.0054	LNAENNATFYFKIDNVK	Deamidated N15 1.43%
12.4	2000.9901	-0.0004	INDENQKQKAELLAQEK	
9.8	2000.9989	-0.0092	NNGSLDRPYYMSKSLLK	
8.6	1999.9922	0.9975	EQIEVRAAQSTSPRNANK	
8.6	1999.9922	0.9975	EQIEVRAAQSTSPRNANK	
8.4	1999.9950	0.9948	LQGLQEGLESDDVQVQIK	
8.1	2000.9901	-0.0004	INDENQKQKAELLAQEK	

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

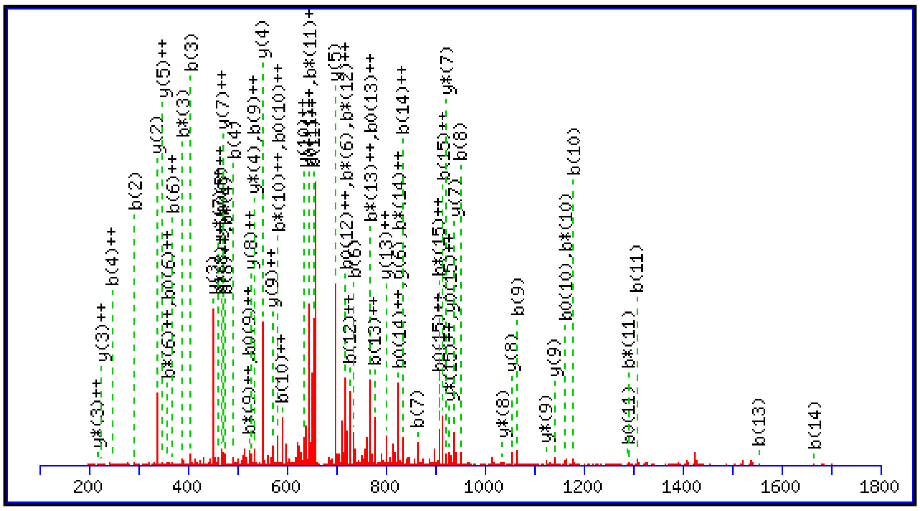
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KYNSQNQSNNQFVLYR**
Found in **P01042** in **con_Xuniprot_HUMAN3**, KNG1_HUMAN Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2

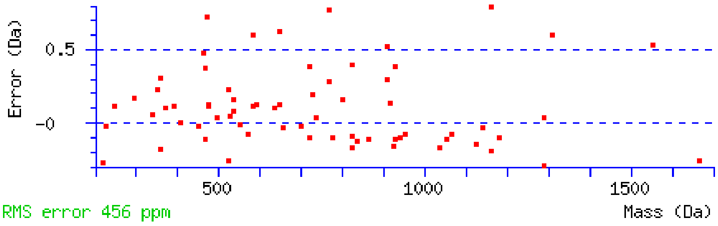
Match to Query 12223: 2002.956342 from(668.659390,3+) intensity(155496.6875) rtinseconds(840) scans(1856) index(9345)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum1564_scans__1856
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

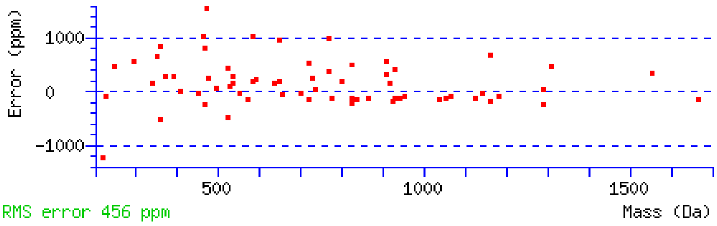
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2002.9497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.027
Matches : 69/158 fragment ions using 147 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	***292.1656***	146.5864	275.1390	138.0731			Y	1875.8620	938.4346	1858.8355	929.9214	1857.8515	929.4294	15
3	***406.2085***	203.6079	389.1819	195.0946			N	1712.7987	856.9030	1695.7721	848.3897	1694.7881	847.8977	14
4	***493.2405***	***247.1239***	476.2140	238.6106	475.2300	238.1186	S	1598.7558	799.8815	1581.7292	791.3682	1580.7452	790.8762	13
5	621.2991	311.1532	604.2726	302.6399	603.2885	302.1479	Q	1511.7237	756.3655	1494.6972	747.8522	1493.7132	747.3602	12
6	***736.3260***	***368.6667***	719.2995	360.1534	718.3155	359.6614	N	1383.6652	692.3362	1366.6386	683.8229	1365.6546	683.3309	11
7	***864.3846***	432.6959	847.3581	424.1827	846.3741	423.6907	Q	1268.6382	634.8227	1251.6117	626.3095	1250.6276	625.8175	10
8	***951.4167***	***476.2120***	934.3901	467.6987	933.4061	467.2067	S	**1140.5796**	570.7935	1123.5531	562.2802	1122.5691	561.7882	9
9	***1065.4596***	***533.2334***	1048.4330	524.7202	1047.4490	524.2281	N	**1053.5476**	527.2774	1036.5211	518.7642			8
10	***1179.5025***	***590.2549***	1162.4760	581.7416	1161.4919	581.2496	N	**939.5047**	470.2560	922.4781	461.7427			7
11	***1307.5611***	***654.2842***	1290.5345	645.7709	1289.5505	645.2789	Q	**825.4618**	413.2345	808.4352	404.7212			6
12	1454.6295	***727.8184***	1437.6029	719.3051	1436.6189	718.8131	F	**697.4032**	349.2052	680.3766	340.6920			5
13	***1553.6979***	***777.3526***	1536.6714	768.8393	1535.6873	768.3473	V	**550.3348**	275.6710	533.3082	267.1577			4
14	***1666.7820***	***833.8946***	1649.7554	825.3814	1648.7714	824.8893	L	**451.2663**	226.1368	434.2398	217.6235			3
15	1829.8453	***915.4263***	1812.8188	906.9130	1811.8347	906.4210	Y	**338.1823**	169.5948	321.1557	161.0815			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.1	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated N6 23.11%
39.1	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated Q5 23.11%
38.7	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated Q7 21.08%
35.1	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated N3 9.27%
35.1	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated N9 9.12%
34.3	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated N10 7.69%
33.7	2002.9497	0.0067	KYNSQNQSNNQFVLYR	Deamidated Q11 6.62%
17.6	2002.9537	0.0026	THFPIVQNHDTFDLYR	
12.4	2002.9537	0.0026	THFPIVQNHDTFDLYR	
8.2	2001.9540	1.0023	MGFEFNIMVVGQSGLGKST	

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

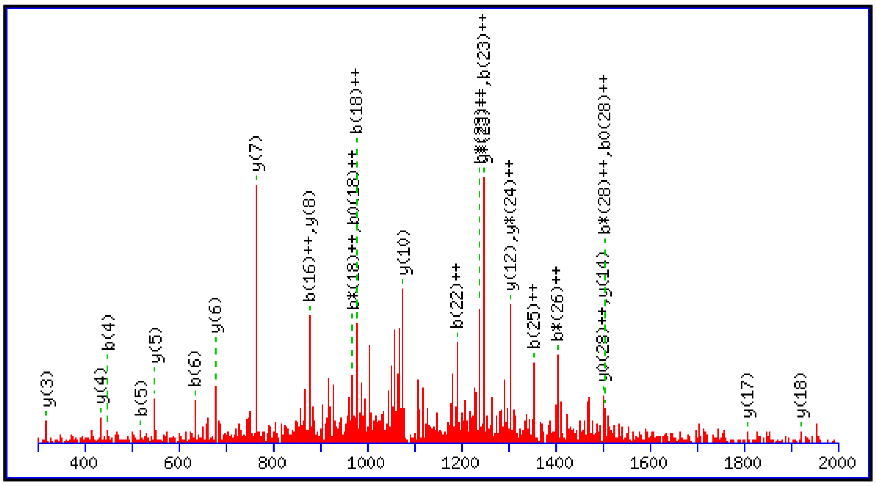
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAGRANLTNFPENGTFVVNIAQLSQDDSGR**
Found in **P01833** in **con_Xuniprot_HUMAN3**, PIGR_HUMAN Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4

Match to Query 27386: 3256.568262 from(1086.530030,3+) intensity(0.0000) rtinseconds(2197) scans(5752) index(19829)
Title: 111019_Est_MI_YP_G_09Spectrum5084_scans__5752
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

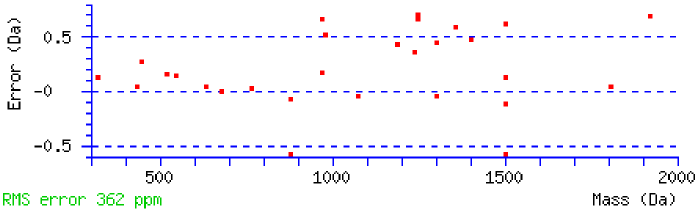
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

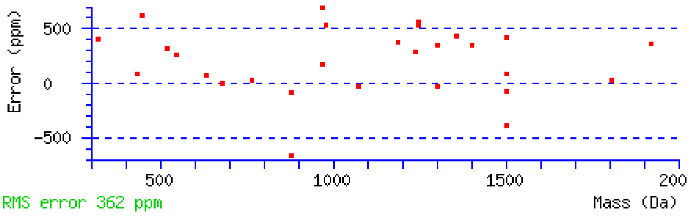


Monoisotopic mass of neutral peptide Mr(calc): 3254.5592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 66 **Expect:** 6.8e-005
Matches : 28/324 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							30
2	235.1077	118.0575					A	3092.5032	1546.7552	3075.4766	1538.2420	3074.4926	1537.7499	29
3	292.1292	146.5682					G	3021.4661	1511.2367	3004.4395	1502.7234	3003.4555	1502.2314	28
4	**448.2303**	224.6188	431.2037	216.1055			R	2964.4446	1482.7259	2947.4181	1474.2127	2946.4340	1473.7207	27
5	**519.2674**	260.1373	502.2409	251.6241			A	2808.3435	1404.6754	2791.3169	1396.1621	2790.3329	1395.6701	26
6	**634.2944**	317.6508	617.2678	309.1375			N	2737.3064	1369.1568	2720.2798	1360.6436	2719.2958	1360.1515	25
7	747.3784	374.1928	730.3519	365.6796			L	2622.2794	1311.6434	2605.2529	1303.1301	2604.2689	1302.6381	24
8	848.4261	424.7167	831.3995	416.2034	830.4155	415.7114	T	2509.1954	1255.1013	2492.1688	1246.5880	2491.1848	1246.0960	23
9	962.4690	481.7381	945.4425	473.2249	944.4585	472.7329	N	2408.1477	1204.5775	2391.1211	1196.0642	2390.1371	1195.5722	22
10	1109.5374	555.2724	1092.5109	546.7591	1091.5269	546.2671	F	2294.1048	1147.5560	2277.0782	1139.0427	2276.0942	1138.5507	21
11	1206.5902	603.7987	1189.5637	595.2855	1188.5796	594.7935	P	2147.0364	1074.0218	2130.0098	1065.5085	2129.0258	1065.0165	20
12	1335.6328	668.3200	1318.6062	659.8068	1317.6222	659.3148	E	2049.9836	1025.4954	2032.9570	1016.9822	2031.9730	1016.4901	19
13	1449.6757	725.3415	1432.6492	716.8282	1431.6652	716.3362	N	***1920.9410***	960.9741	1903.9144	952.4609	1902.9304	951.9689	18
14	1506.6972	753.8522	1489.6706	745.3390	1488.6866	744.8469	G	***1806.8981***	903.9527	1789.8715	895.4394	1788.8875	894.9474	17
15	1607.7449	804.3761	1590.7183	795.8628	1589.7343	795.3708	T	1749.8766	875.4419	1732.8501	866.9287	1731.8660	866.4367	16
16	1754.8133	**877.9103**	1737.7867	869.3970	1736.8027	868.9050	F	1648.8289	824.9181	1631.8024	816.4048	1630.8184	815.9128	15
17	1853.8817	927.4445	1836.8551	918.9312	1835.8711	918.4392	V	***1501.7605***	751.3839	1484.7340	742.8706	1483.7499	742.3786	14
18	1952.9501	**976.9787**	1935.9236	968.4654	1934.9395	967.9734	V	1402.6921	701.8497	1385.6655	693.3364	1384.6815	692.8444	13
19	2066.9930	1034.0002	2049.9665	1025.4869	2048.9825	1024.9949	N	***1303.6237***	652.3155	1286.5971	643.8022	1285.6131	643.3102	12
20	2180.0771	1090.5422	2163.0505	1082.0289	2162.0665	1081.5369	I	1189.5808	595.2940	1172.5542	586.7807	1171.5702	586.2887	11
21	2251.1142	1126.0607	2234.0877	1117.5475	2233.1036	1117.0555	A	***1076.4967***	538.7520	1059.4701	530.2387	1058.4861	529.7467	10
22	2379.1728	**1190.0900**	2362.1462	1181.5768	2361.1622	1181.0847	Q	1005.4596	503.2334	988.4330	494.7202	987.4490	494.2281	9
23	2492.2569	**1246.6321**	2475.2303	1238.1188	2474.2463	1237.6268	L	***877.4010***	439.2041	860.3745	430.6909	859.3904	430.1989	8

24	2579.2889	1290.1481	2562.2623	1281.6348	2561.2783	1281.1428	**S**	***764.3169***	382.6621	747.2904	374.1488	746.3064	373.6568	**7**
25	2707.3475	**1354.1774**	2690.3209	1345.6641	2689.3369	1345.1721	**Q**	***677.2849***	339.1461	660.2584	330.6328	659.2743	330.1408	**6**
26	2822.3744	1411.6908	2805.3479	1403.1776	2804.3638	1402.6856	**D**	***549.2263***	275.1168	532.1998	266.6035	531.2158	266.1115	**5**
27	2937.4013	1469.2043	2920.3748	1460.6910	2919.3908	1460.1990	**D**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
28	3024.4334	1512.7203	3007.4068	1504.2070	3006.4228	1503.7150	**S**	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
29	3081.4548	1541.2311	3064.4283	1532.7178	3063.4443	1532.2258	**G**	232.1404	116.5738	215.1139	108.0606			**2**
30							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.0	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N6 47.08%
63.6	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N9 27.16%
63.3	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N13 25.40%
41.8	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N19 0.18%
41.6	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated Q22 0.17%
22.5	3254.5592	2.0090	YAGRANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated Q25 0.00%
9.4	3254.5765	1.9917	AMDKGDPPLTGETLVVVNVSDINDNPPEFR	
5.4	3254.5594	2.0089	QQNVKSAHRAHCLSMNEELIQGVATMLR	
5.4	3254.5594	2.0089	QQNVKSAHRAHCLSMNEELIQGVATMLR	
5.4	3254.5594	2.0089	QQNVKSAHRAHCLSMNEELIQGVATMLR	

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

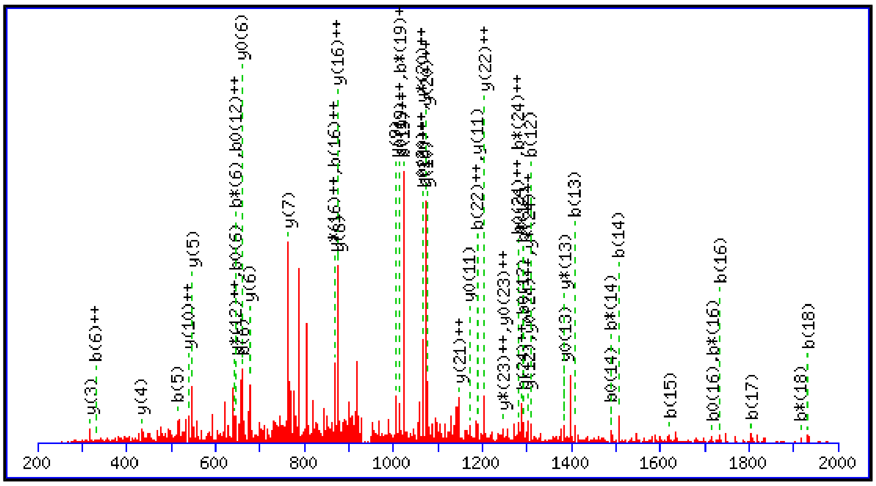
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLTNFPENGTFVVNIAQLSQDDSGR**
Found in **P01833** in **con_Xuniprot_HUMAN3**, PIGR_HUMAN Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4

Match to Query 25608: 2808.331812 from(937.117880,3+) intensity(22292.9648) rtinseconds(2317) scans(6067) index(6616)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum5347_scans__6067
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

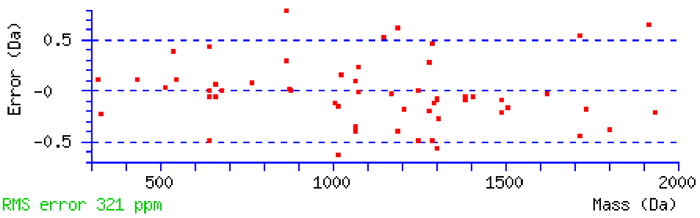
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

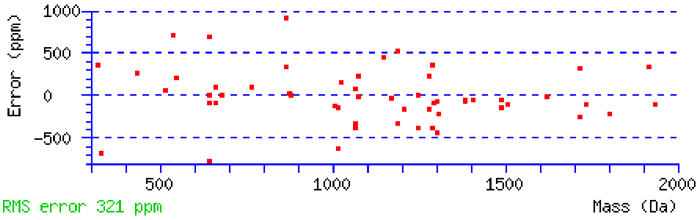


```
Monoisotopic mass of neutral peptide Mr(calc): 2808.3202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
N9     : Deamidated (NQ)
Ions Score: 43  Expect: 0.014
Matches : 56/288 fragment ions using 89 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							26
2	186.0873	93.5473	169.0608	85.0340			N	2738.2904	1369.6488	2721.2638	1361.1356	2720.2798	1360.6436	25
3	299.1714	150.0893	282.1448	141.5761			L	2624.2475	1312.6274	2607.2209	1304.1141	2606.2369	1303.6221	24
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	T	2511.1634	1256.0853	2494.1369	1247.5721	2493.1528	1247.0801	23
5	***515.2460***	258.1266	498.2195	249.6134	497.2354	249.1214	N	2410.1157	1205.5615	2393.0892	1197.0482	2392.1052	1196.5562	22
6	***662.3144***	**331.6608**	645.2879	323.1476	644.3039	322.6556	F	2295.0888	1148.0480	2278.0622	1139.5348	2277.0782	1139.0427	21
7	759.3672	380.1872	742.3406	371.6740	741.3566	371.1819	P	2148.0204	1074.5138	2130.9938	1066.0005	2130.0098	1065.5085	20
8	888.4098	444.7085	871.3832	436.1953	870.3992	435.7032	E	2050.9676	1025.9874	2033.9411	1017.4742	2032.9570	1016.9822	19
9	1003.4367	502.2220	986.4102	493.7087	985.4262	493.2167	N	1921.9250	961.4661	1904.8985	952.9529	1903.9144	952.4609	18
10	1060.4582	530.7327	1043.4316	522.2195	1042.4476	521.7274	G	1806.8981	903.9527	1789.8715	895.4394	1788.8875	894.9474	17
11	1161.5059	581.2566	1144.4793	572.7433	1143.4953	572.2513	T	1749.8766	875.4419	1732.8501	866.9287	1731.8660	866.4367	16
12	***1308.5743***	654.7908	1291.5477	646.2775	1290.5637	645.7855	F	1648.8289	824.9181	1631.8024	816.4048	1630.8184	815.9128	15
13	***1407.6427***	704.3250	1390.6161	695.8117	1389.6321	695.3197	V	1501.7605	751.3839	1484.7340	742.8706	1483.7499	742.3786	14
14	***1506.7111***	753.8592	1489.6846	745.3459	1488.7005	744.8539	V	1402.6921	701.8497	1385.6655	693.3364	1384.6815	692.8444	13
15	***1620.7540***	810.8807	1603.7275	802.3674	1602.7435	801.8754	N	***1303.6237***	652.3155	1286.5971	643.8022	1285.6131	643.3102	12
16	***1733.8381***	**867.4227**	1716.8115	858.9094	1715.8275	858.4174	I	***1189.5808***	595.2940	1172.5542	586.7807	1171.5702	586.2887	11
17	***1804.8752***	902.9412	1787.8487	894.4280	1786.8646	893.9360	A	***1076.4967***	538.7520	1059.4701	530.2387	1058.4861	529.7467	10
18	***1932.9338***	966.9705	1915.9072	958.4573	1914.9232	957.9652	Q	***1005.4596***	503.2334	988.4330	494.7202	987.4490	494.2281	9
19	2046.0178	**1023.5126**	2028.9913	1014.9993	2028.0073	1014.5073	L	***877.4010***	439.2041	860.3745	430.6909	859.3904	430.1989	8
20	2133.0499	**1067.0286**	2116.0233	1058.5153	2115.0393	1058.0233	S	***764.3169***	382.6621	747.2904	374.1488	746.3064	373.6568	7
21	2261.1085	1131.0579	2244.0819	1122.5446	2243.0979	1122.0526	Q	***677.2849***	339.1461	660.2584	330.6328	659.2743	330.1408	6
22	2376.1354	**1188.5713**	2359.1088	1180.0581	2358.1248	1179.5661	D	***549.2263***	275.1168	532.1998	266.6035	531.2158	266.1115	5

23	2491.1623	1246.0848	2474.1358	1237.5715	2473.1518	1237.0795	**D**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
24	2578.1944	**1289.6008**	2561.1678	1281.0875	2560.1838	1280.5955	**S**	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
25	2635.2158	1318.1116	2618.1893	1309.5983	2617.2053	1309.1063	**G**	232.1404	116.5738	215.1139	108.0606			**2**
26							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.5	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N5, N9 42.87%
42.5	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N2, N9 42.87%
34.3	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N2, N5 6.46%
29.0	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N5, N15 1.93%
29.0	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N2, N15 1.93%
28.5	2807.3362	0.9956	ANLTNFPENGTFVVNIAQLSQDDSGR	
26.7	2808.3202	0.0116	ANLTNFPENGTFVVNIAQLSQDDSGR	Deamidated N9, N15 1.13%
25.7	2807.3362	0.9956	ANLTNFPENGTFVVNIAQLSQDDSGR	
22.6	2807.3362	0.9956	ANLTNFPENGTFVVNIAQLSQDDSGR	
22.1	2807.3362	0.9956	ANLTNFPENGTFVVNIAQLSQDDSGR	

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

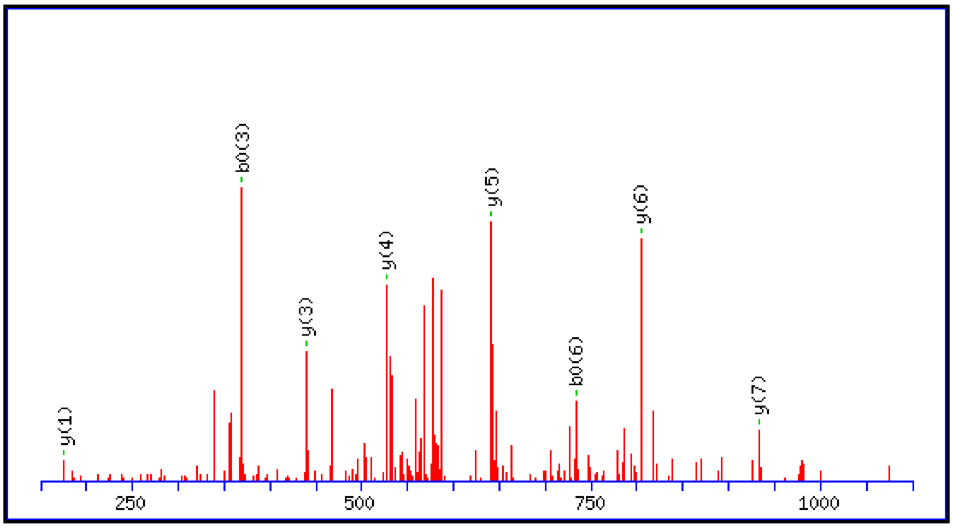
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEQYNSTYR**
Found in **P01857** in **con_Xuniprot_HUMAN3**, IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

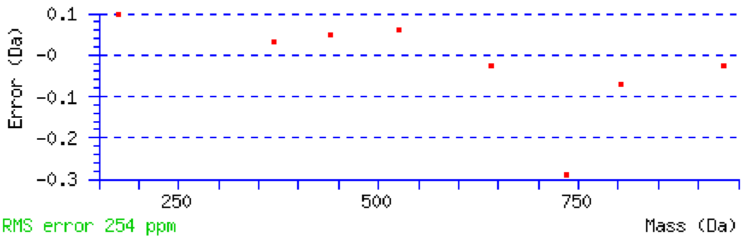
Match to Query 1624: 1189.491228 from(595.752890,2+) intensity(3555.3958) rtinseconds(269) scans(439) index(2454)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum345_scans__439
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

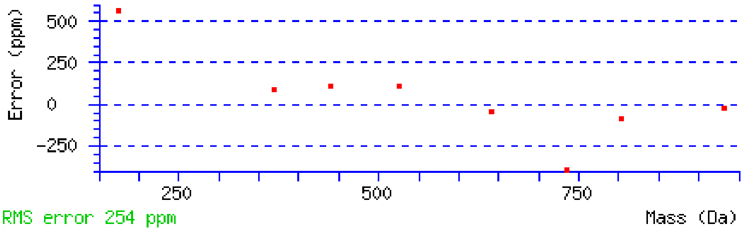
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1189.4887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.0012
Matches : 8/88 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	130.0499	65.5286			112.0393	56.5233	E							9
2	259.0925	130.0499			241.0819	121.0446	E	1061.4534	531.2304	1044.4269	522.7171	1043.4429	522.2251	8
3	387.1510	194.0792	370.1245	185.5659	369.1405	185.0739	Q	***932.4108***	466.7091	915.3843	458.1958	914.4003	457.7038	7
4	550.2144	275.6108	533.1878	267.0975	532.2038	266.6055	Y	***804.3523***	402.6798	787.3257	394.1665	786.3417	393.6745	6
5	665.2413	333.1243	648.2148	324.6110	647.2307	324.1190	N	***641.2889***	321.1481	624.2624	312.6348	623.2784	312.1428	5
6	752.2733	376.6403	735.2468	368.1270	734.2628	367.6350	S	***526.2620***	263.6346	509.2354	255.1214	508.2514	254.6293	4
7	853.3210	427.1641	836.2945	418.6509	835.3105	418.1589	T	***439.2300***	220.1186	422.2034	211.6053	421.2194	211.1133	3
8	1016.3843	508.6958	999.3578	500.1825	998.3738	499.6905	Y	338.1823	169.5948	321.1557	161.0815			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.3	1189.4887	0.0025	EEQYNSTYR	Deamidated N5 99.90%
13.4	1189.4887	0.0025	EEQYNSTYR	Deamidated Q3 0.10%
3.9	1189.4856	0.0056	QPDGCMDPVR	
0.3	1189.4930	-0.0017	ENKCMAMYK	

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

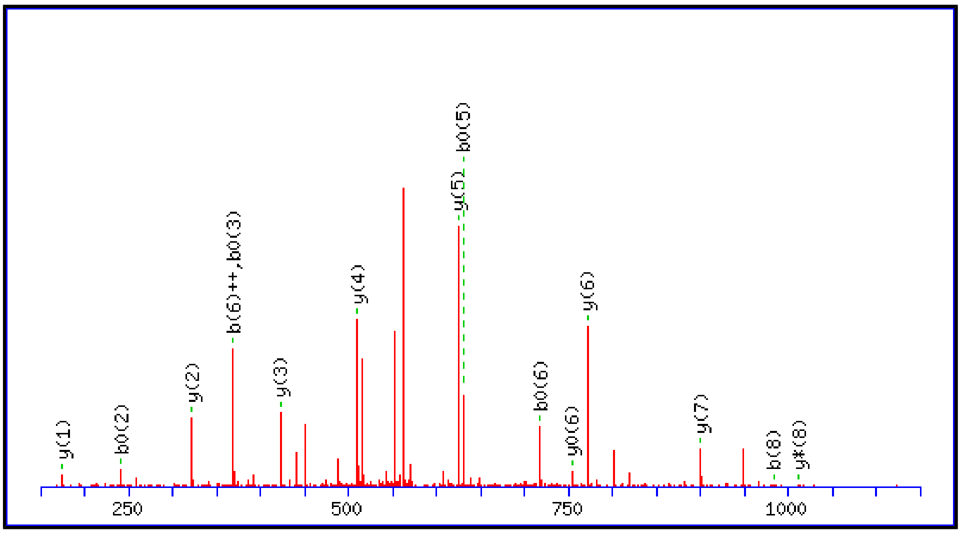
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEQFNSTFR**
Found in **P01859** in **con_Xuniprot_HUMAN3**, IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2

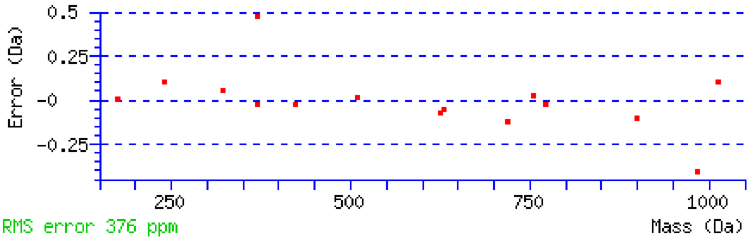
Match to Query 1602: 1157.504308 from(579.759430,2+) intensity(236788.6719) rtinseconds(653) scans(1540) index(23802)
Title: 111019_Est_MI_YS_G_05Spectrum1294_scans__1540
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

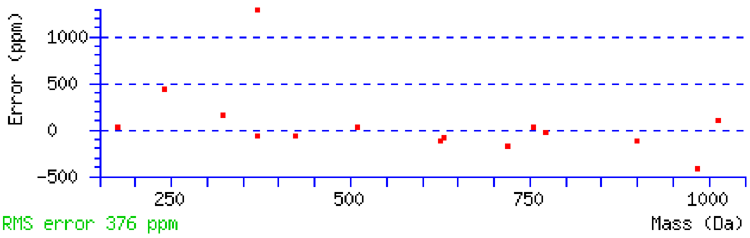
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1157.4989
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 44 **Expect:** 0.0019
Matches : 15/88 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	130.0499	65.5286			112.0393	56.5233	E							9
2	259.0925	130.0499			241.0819	121.0446	E	1029.4636	515.2354	1012.4371	506.7222	1011.4530	506.2302	8
3	387.1510	194.0792	370.1245	185.5659	369.1405	185.0739	Q	***900.4210***	450.7141	883.3945	442.2009	882.4104	441.7089	7
4	534.2195	267.6134	517.1929	259.1001	516.2089	258.6081	F	***772.3624***	386.6849	755.3359	378.1716	754.3519	377.6796	6
5	649.2464	325.1268	632.2198	316.6136	631.2358	316.1216	N	***625.2940***	313.1506	608.2675	304.6374	607.2835	304.1454	5
6	736.2784	368.6429	719.2519	360.1296	718.2679	359.6376	S	***510.2671***	255.6372	493.2405	247.1239	492.2565	246.6319	4
7	837.3261	419.1667	820.2996	410.6534	819.3155	410.1614	T	***423.2350***	212.1212	406.2085	203.6079	405.2245	203.1159	3
8	984.3945	492.7009	967.3680	484.1876	966.3840	483.6956	F	***322.1874***	161.5973	305.1608	153.0840			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.5	1157.4989	0.0054	EEQFNSTFR	Deamidated N5 99.58%
20.7	1157.4989	0.0054	EEQFNSTFR	Deamidated Q3 0.42%
20.1	1156.5039	1.0004	GSLKMGNMMR	
13.1	1156.5039	1.0004	GSLKMGNMMR	
10.7	1157.5061	-0.0018	EEAGPGGAGGGGSR	
10.0	1157.5101	-0.0058	EPNWSSAPDR	
7.6	1157.5023	0.0021	SSREQFMQK	
6.2	1155.4979	2.0064	SSFQVGGGCTR	
5.6	1156.5039	1.0004	GSLKMGNMMR	
5.4	1155.4978	2.0065	NRYPDMSTR	

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

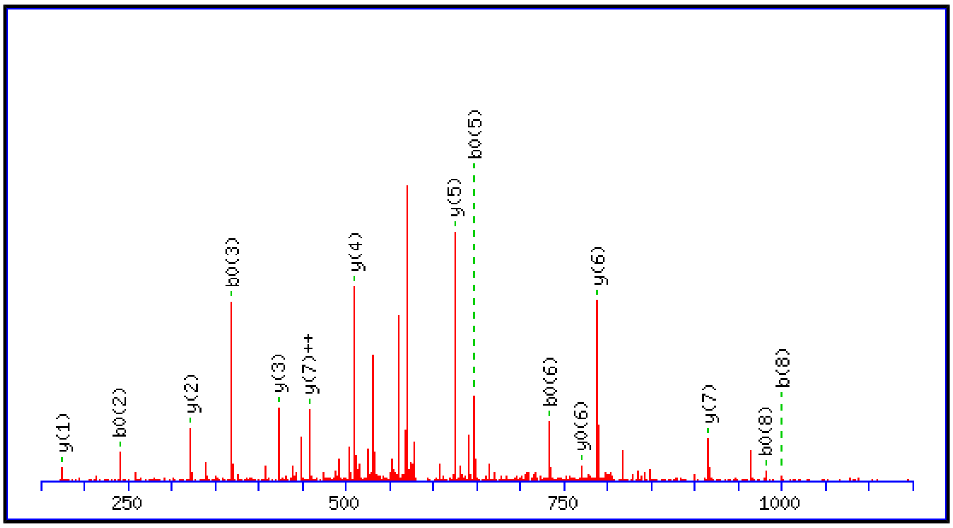
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEQYNSTFR**
Found in **P01860** in **con_Xuniprot_HUMAN3**, IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2

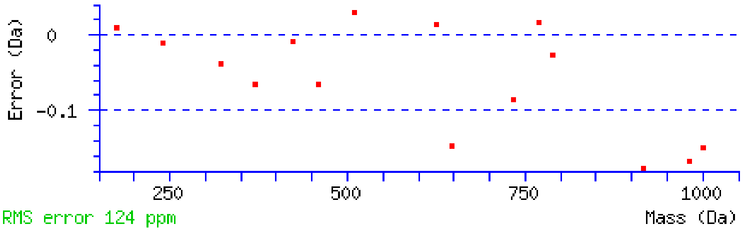
Match to Query 1613: 1173.495288 from(587.754920,2+) intensity(30158.2148) rtinseconds(461) scans(873) index(15589)
Title: 111019_Est_MI_YP_G_05Spectrum718_scans__873
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

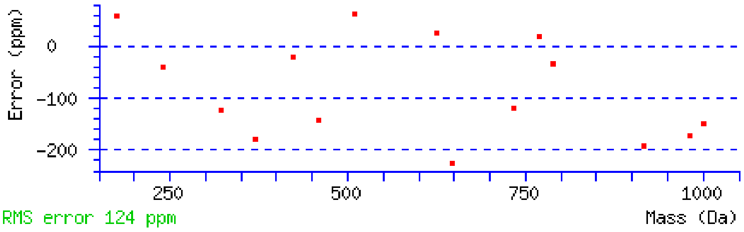
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1173.4938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.0062
Matches : 15/88 fragment ions using 20 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	259.0925	130.0499			241.0819	121.0446	E	1045.4585	523.2329	1028.4320	514.7196	1027.4480	514.2276	8
3	387.1510	194.0792	370.1245	185.5659	369.1405	185.0739	Q	***916.4159***	458.7116	899.3894	450.1983	898.4054	449.7063	7
4	550.2144	275.6108	533.1878	267.0975	532.2038	266.6055	Y	***788.3573***	394.6823	771.3308	386.1690	770.3468	385.6770	6
5	665.2413	333.1243	648.2148	324.6110	647.2307	324.1190	N	***625.2940***	313.1506	608.2675	304.6374	607.2835	304.1454	5
6	752.2733	376.6403	735.2468	368.1270	734.2628	367.6350	S	***510.2671***	255.6372	493.2405	247.1239	492.2565	246.6319	4
7	853.3210	427.1641	836.2945	418.6509	835.3105	418.1589	T	***423.2350***	212.1212	406.2085	203.6079	405.2245	203.1159	3
8	1000.3894	500.6984	983.3629	492.1851	982.3789	491.6931	F	***322.1874***	161.5973	305.1608	153.0840			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.5	1173.4938	0.0015	EEQYNSTFR	Deamidated N5 99.58%
13.8	1173.4938	0.0015	EEQYNSTFR	Deamidated Q3 0.42%
11.6	1173.4938	0.0015	EEQFNSTYR	
7.0	1173.4898	0.0055	EQASTEHQSR	
5.4	1173.4907	0.0046	DNHCMEVIR	
3.8	1173.4906	0.0046	EMYQRQMR	
2.4	1173.4986	-0.0033	QSGQGPCHFR	
2.4	1173.4986	-0.0033	QSGQGPCHFR	

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

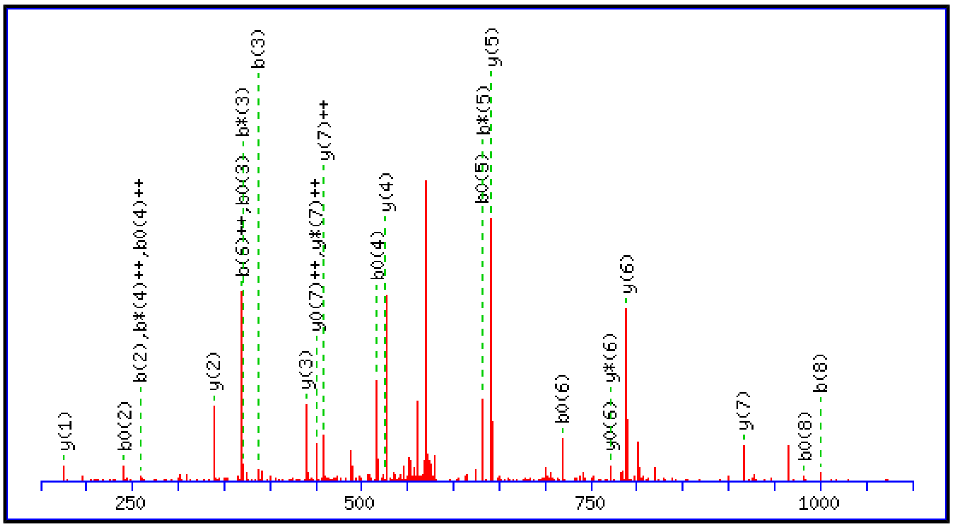
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EEQFNSTYR**
Found in **P01861** in **con_Xuniprot_HUMAN3**, IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1

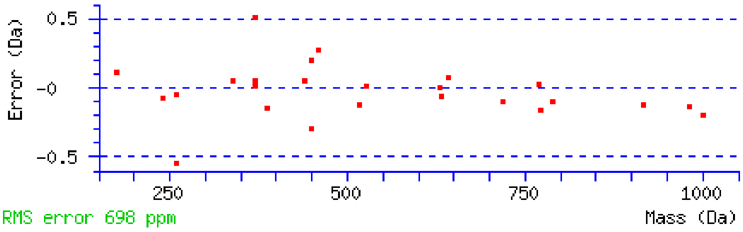
Match to Query 1614: 1173.495308 from(587.754930,2+) intensity(4329.9058) rtinseconds(402) scans(737) index(1834)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum589_scans__737
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

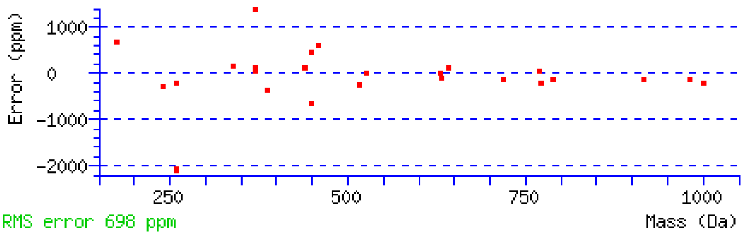
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1100 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1173.4938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.001
Matches : 26/88 fragment ions using 36 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	**259.0925**	130.0499			241.0819	121.0446	E	1045.4585	523.2329	1028.4320	514.7196	1027.4480	514.2276	8
3	**387.1510**	194.0792	370.1245	185.5659	369.1405	185.0739	Q	***916.4159***	458.7116	899.3894	450.1983	898.4054	449.7063	7
4	534.2195	267.6134	517.1929	259.1001	516.2089	258.6081	F	***788.3573***	394.6823	771.3308	386.1690	770.3468	385.6770	6
5	649.2464	325.1268	632.2198	316.6136	631.2358	316.1216	N	***641.2889***	321.1481	624.2624	312.6348	623.2784	312.1428	5
6	736.2784	368.6429	719.2519	360.1296	718.2679	359.6376	S	***526.2620***	263.6346	509.2354	255.1214	508.2514	254.6293	4
7	837.3261	419.1667	820.2996	410.6534	819.3155	410.1614	T	***439.2300***	220.1186	422.2034	211.6053	421.2194	211.1133	3
8	**1000.3894**	500.6984	983.3629	492.1851	982.3789	491.6931	Y	***338.1823***	169.5948	321.1557	161.0815			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.2	1173.4938	0.0015	EEQFNSTYR	Deamidated N5 99.71%
19.9	1173.4938	0.0015	EEQFNSTYR	Deamidated Q3 0.29%
10.9	1172.4945	1.0008	QQQEPAQGQR	
10.9	1172.4945	1.0008	QQQEPAQGQR	
6.5	1173.4938	0.0015	WQDIQNDPR	
5.1	1173.4938	0.0015	EEQYNSTFR	
4.0	1172.4945	1.0008	QQQPQQQQR	
3.2	1172.4945	1.0008	QQQEPAQGQR	
2.8	1172.4954	0.9999	MSGSTPFQMR	
2.1	1171.4928	2.0025	QQQQCPPQR	

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

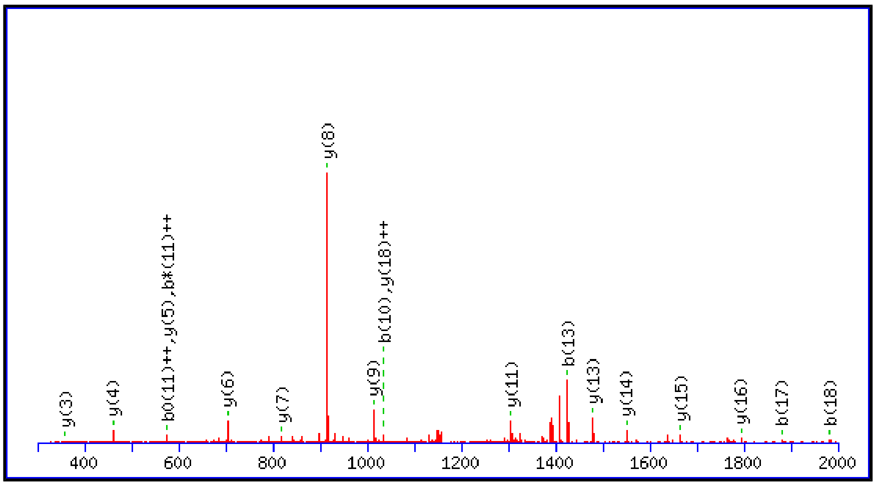
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

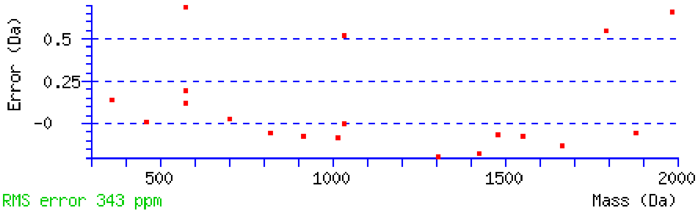
Match to Query 15486: 2339.061968 from(1170.538260,2+) intensity(893289.5625) rtinseconds(1497) scans(3687) index(1992)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum3165_scans__3687
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

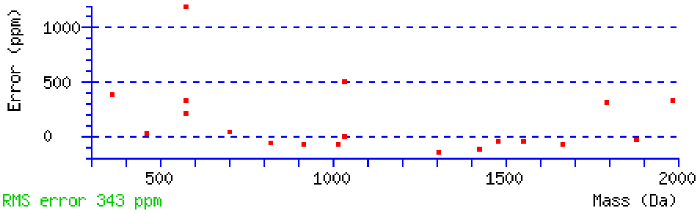
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2339.0522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 122 **Expect:** 9.4e-011
Matches : 19/222 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	58.0287	29.5180					G							21
2	171.1128	86.0600					L	2283.0380	1142.0226	2266.0115	1133.5094	2265.0274	1133.0174	20
3	272.1605	136.5839			254.1499	127.5786	T	2169.9539	1085.4806	2152.9274	1076.9673	2151.9434	1076.4753	19
4	419.2289	210.1181			401.2183	201.1128	F	2068.9063	1034.9568	2051.8797	1026.4435	2050.8957	1025.9515	18
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	Q	1921.8379	961.4226	1904.8113	952.9093	1903.8273	952.4173	17
6	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	Q	***1793.7793***	897.3933	1776.7527	888.8800	1775.7687	888.3880	16
7	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	N	***1665.7207***	833.3640	1648.6941	824.8507	1647.7101	824.3587	15
8	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	A	***1550.6938***	775.8505	1533.6672	767.3372	1532.6832	766.8452	14
9	948.4421	474.7247	931.4156	466.2114	930.4316	465.7194	S	***1479.6566***	740.3320	1462.6301	731.8187	1461.6461	731.3267	13
10	**1035.4742**	518.2407	1018.4476	509.7274	1017.4636	509.2354	S	1392.6246	696.8159	1375.5981	688.3027	1374.6140	687.8107	12
11	1166.5147	583.7610	1149.4881	575.2477	1148.5041	574.7557	M	***1305.5926***	653.2999	1288.5660	644.7867	1287.5820	644.2946	11
12	1326.5453	663.7763	1309.5188	655.2630	1308.5347	654.7710	C	1174.5521	587.7797	1157.5256	579.2664	1156.5415	578.7744	10
13	**1425.6137**	713.3105	1408.5872	704.7972	1407.6031	704.3052	V	***1014.5215***	507.7644	997.4949	499.2511	996.5109	498.7591	9
14	1522.6665	761.8369	1505.6399	753.3236	1504.6559	752.8316	P	***915.4530***	458.2302	898.4265	449.7169	897.4425	449.2249	8
15	1637.6934	819.3503	1620.6669	810.8371	1619.6829	810.3451	D	***818.4003***	409.7038	801.3737	401.1905	800.3897	400.6985	7
16	1765.7520	883.3796	1748.7255	874.8664	1747.7414	874.3744	Q	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	6
17	**1880.7789**	940.8931	1863.7524	932.3798	1862.7684	931.8878	D	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
18	**1981.8266**	991.4169	1964.8001	982.9037	1963.8161	982.4117	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
19	2052.8637	1026.9355	2035.8372	1018.4222	2034.8532	1017.9302	A	***359.2401***	180.1237	342.2136	171.6104			3
20	2165.9478	1083.4775	2148.9213	1074.9643	2147.9372	1074.4723	I	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
122.3	2339.0522	0.0098	GLTFQQNASSMCVPDQDTAIR	Deamidated N7 98.90%
102.7	2339.0522	0.0098	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6 1.08%
85.4	2339.0522	0.0098	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5 0.02%
64.8	2338.0682	0.9938	GLTFQQNASSMCVPDQDTAIR	
51.3	2339.0522	0.0098	GLTFQQNASSMCVPDQDTAIR	Deamidated Q16 0.00%
13.2	2338.0608	1.0012	EQQCGSVNSYRVLDAGDPTSR	
5.7	2338.0576	1.0044	TLFNLDEHQFDPDNLIMNF	
5.4	2337.0648	1.9971	LQQESTFLFHGNKTEDTPDK	
1.2	2339.0627	-0.0007	ENLYGAHESNAEYLQMLINK	
1.2	2339.0627	-0.0007	ENLYGAHESNAEYLQMLINK	

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

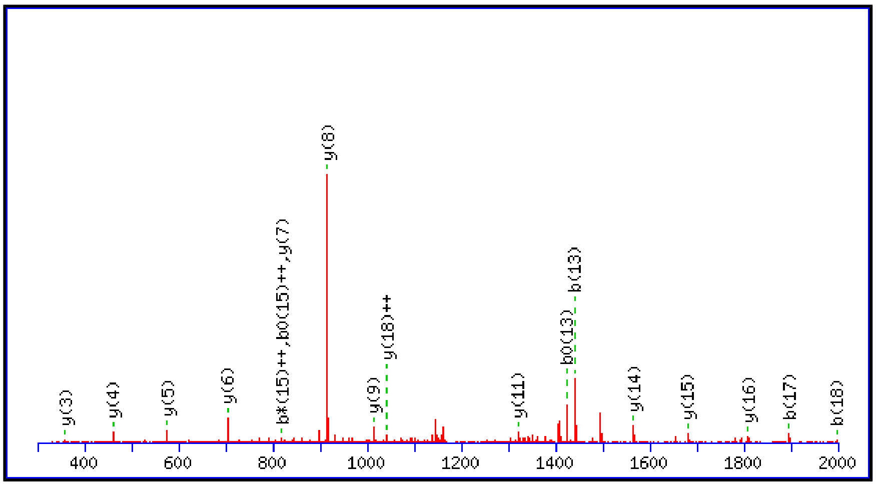
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

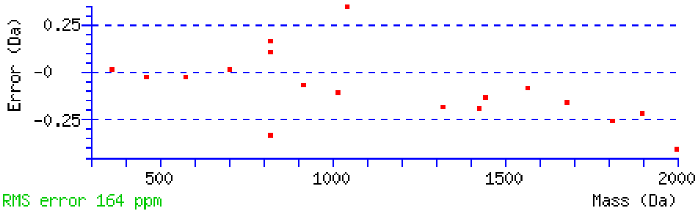
Match to Query 17835: 2355.054988 from(1178.534770,2+) intensity(104471.5625) rtinseconds(1103) scans(2613) index(5118)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum2266_scans__2613
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

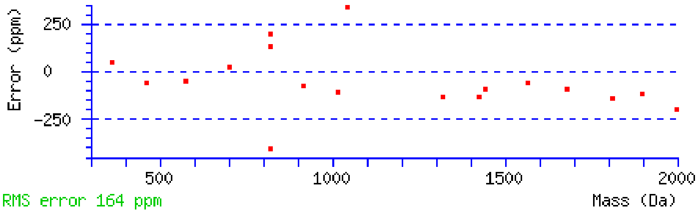
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2355.0471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 103 **Expect:** 7e-009
Matches : 18/342 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	58.0287	29.5180					G							21
2	171.1128	86.0600					L	2299.0329	1150.0201	2282.0064	1141.5068	2281.0224	1141.0148	20
3	272.1605	136.5839			254.1499	127.5786	T	2185.9489	1093.4781	2168.9223	1084.9648	2167.9383	1084.4728	19
4	419.2289	210.1181			401.2183	201.1128	F	2084.9012	1042.9542	2067.8746	1034.4410	2066.8906	1033.9489	18
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	Q	1937.8328	969.4200	1920.8062	960.9067	1919.8222	960.4147	17
6	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	Q	***1809.7742***	905.3907	1792.7476	896.8775	1791.7636	896.3855	16
7	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	N	***1681.7156***	841.3614	1664.6891	832.8482	1663.7050	832.3562	15
8	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	A	***1566.6887***	783.8480	1549.6621	775.3347	1548.6781	774.8427	14
9	948.4421	474.7247	931.4156	466.2114	930.4316	465.7194	S	1495.6516	748.3294	1478.6250	739.8161	1477.6410	739.3241	13
10	1035.4742	518.2407	1018.4476	509.7274	1017.4636	509.2354	S	1408.6195	704.8134	1391.5930	696.3001	1390.6090	695.8081	12
11	1182.5096	591.7584	1165.4830	583.2451	1164.4990	582.7531	M	***1321.5875***	661.2974	1304.5610	652.7841	1303.5769	652.2921	11
12	1342.5402	671.7737	1325.5137	663.2605	1324.5296	662.7685	C	1174.5521	587.7797	1157.5256	579.2664	1156.5415	578.7744	10
13	**1441.6086**	721.3080	1424.5821	712.7947	1423.5981	712.3027	V	***1014.5215***	507.7644	997.4949	499.2511	996.5109	498.7591	9
14	1538.6614	769.8343	1521.6348	761.3211	1520.6508	760.8291	P	***915.4530***	458.2302	898.4265	449.7169	897.4425	449.2249	8
15	1653.6883	827.3478	1636.6618	818.8345	1635.6778	818.3425	D	***818.4003***	409.7038	801.3737	401.1905	800.3897	400.6985	7
16	1781.7469	891.3771	1764.7204	882.8638	1763.7363	882.3718	Q	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	6
17	**1896.7739**	948.8906	1879.7473	940.3773	1878.7633	939.8853	D	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
18	**1997.8215**	999.4144	1980.7950	990.9011	1979.8110	990.4091	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
19	2068.8587	1034.9330	2051.8321	1026.4197	2050.8481	1025.9277	A	***359.2401***	180.1237	342.2136	171.6104			3
20	2181.9427	1091.4750	2164.9162	1082.9617	2163.9321	1082.4697	I	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
102.8	2355.0471	0.0079	GLTFQQNASSMCVPDQDTAIR	Deamidated N7 96.45%
85.5	2355.0471	0.0079	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6 1.78%
85.5	2355.0471	0.0079	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5 1.78%
80.4	2354.0631	0.9919	GLTFQQNASSMCVPDQDTAIR	
52.3	2355.0471	0.0079	GLTFQQNASSMCVPDQDTAIR	Deamidated Q16 0.00%
7.4	2354.0572	0.9978	VAWPCKLDYECPNFDQRR	
7.2	2355.0509	0.0041	ETKTFGGGGGGARSNLNMNAAGNR	
4.3	2355.0583	-0.0033	MSSTNPCSPVSSGPTQYNLRR	
4.1	2355.0509	0.0041	ETKTFGGGGGGARSNLNMNAAGNR	
3.7	2355.0509	0.0041	ETKTFGGGGGGARSNLNMNAAGNR	

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

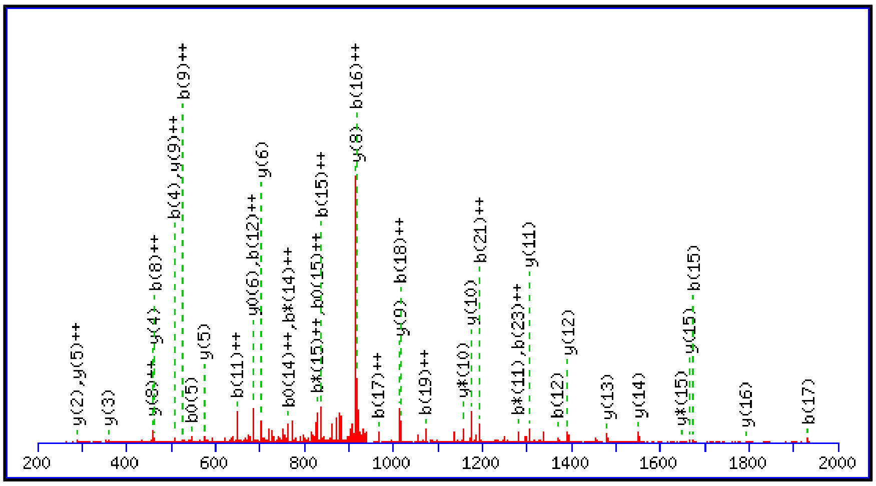
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VDHRGLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 25752: 2846.320632 from(949.780820,3+) intensity(64393.9727) rtinseconds(1214) scans(2898) index(1952)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum2469_scans__2898
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

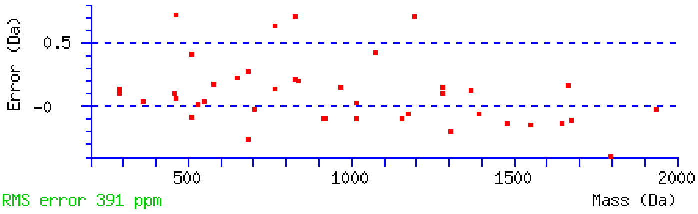
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

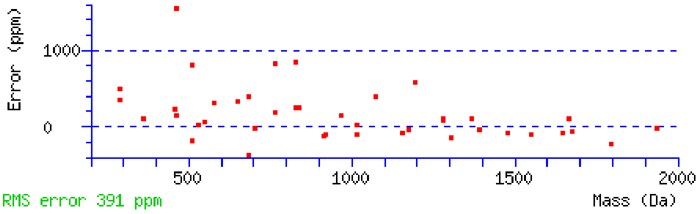


Monoisotopic mass of neutral peptide Mr(calc): 2846.3076
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 96 **Expect:** 5.3e-008
Matches : 41/274 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							25
2	215.1026	108.0550			197.0921	99.0497	D	2748.2464	1374.6269	2731.2199	1366.1136	2730.2359	1365.6216	24
3	352.1615	176.5844			334.1510	167.5791	H	2633.2195	1317.1134	2616.1929	1308.6001	2615.2089	1308.1081	23
4	**508.2627**	254.6350	491.2361	246.1217	490.2521	245.6297	R	2496.1606	1248.5839	2479.1340	1240.0707	2478.1500	1239.5786	22
5	565.2841	283.1457	548.2576	274.6324	547.2736	274.1404	G	2340.0595	1170.5334	2323.0329	1162.0201	2322.0489	1161.5281	21
6	678.3682	339.6877	661.3416	331.1745	660.3576	330.6824	L	2283.0380	1142.0226	2266.0115	1133.5094	2265.0274	1133.0174	20
7	779.4159	390.2116	762.3893	381.6983	761.4053	381.2063	T	2169.9539	1085.4806	2152.9274	1076.9673	2151.9434	1076.4753	19
8	926.4843	***463.7458***	909.4577	455.2325	908.4737	454.7405	F	2068.9063	1034.9568	2051.8797	1026.4435	2050.8957	1025.9515	18
9	1054.5429	***527.7751***	1037.5163	519.2618	1036.5323	518.7698	Q	1921.8379	961.4226	1904.8113	952.9093	1903.8273	952.4173	17
10	1182.6014	591.8044	1165.5749	583.2911	1164.5909	582.7991	Q	***1793.7793***	897.3933	1776.7527	888.8800	1775.7687	888.3880	16
11	1297.6284	***649.3178***	1280.6018	640.8046	1279.6178	640.3125	N	***1665.7207***	833.3640	1648.6941	824.8507	1647.7101	824.3587	15
12	**1368.6655**	***684.8364***	1351.6389	676.3231	1350.6549	675.8311	A	***1550.6938***	775.8505	1533.6672	767.3372	1532.6832	766.8452	14
13	1455.6975	728.3524	1438.6710	719.8391	1437.6870	719.3471	S	***1479.6566***	740.3320	1462.6301	731.8187	1461.6461	731.3267	13
14	1542.7295	771.8684	1525.7030	763.3551	1524.7190	762.8631	S	***1392.6246***	696.8159	1375.5981	688.3027	1374.6140	687.8107	12
15	**1673.7700**	***837.3887***	1656.7435	828.8754	1655.7595	828.3834	M	***1305.5926***	653.2999	1288.5660	644.7867	1287.5820	644.2946	11
16	1833.8007	***917.4040***	1816.7741	908.8907	1815.7901	908.3987	C	***1174.5521***	587.7797	1157.5256	579.2664	1156.5415	578.7744	10
17	**1932.8691**	***966.9382***	1915.8425	958.4249	1914.8585	957.9329	V	***1014.5215***	507.7644	997.4949	499.2511	996.5109	498.7591	9
18	2029.9219	***1015.4646***	2012.8953	1006.9513	2011.9113	1006.4593	P	***915.4530***	458.2302	898.4265	449.7169	897.4425	449.2249	8
19	2144.9488	***1072.9780***	2127.9223	1064.4648	2126.9382	1063.9728	D	818.4003	409.7038	801.3737	401.1905	800.3897	400.6985	7
20	2273.0074	1137.0073	2255.9808	1128.4941	2254.9968	1128.0020	Q	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	6
21	2388.0343	***1194.5208***	2371.0078	1186.0075	2370.0238	1185.5155	D	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
22	2489.0820	1245.0446	2472.0555	1236.5314	2471.0714	1236.0394	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
23	2560.1191	***1280.5632***	2543.0926	1272.0499	2542.1085	1271.5579	A	***359.2401***	180.1237	342.2136	171.6104			3

24	2673.2032	1337.1052	2656.1766	1328.5920	2655.1926	1328.0999	I	*288.2030*	144.6051	271.1765	136.0919			2
25							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
96.0	2846.3076	0.0130	VDHRGLTFQQNASSMCVPDQDTAIR	Deamidated N11 87.46%
84.5	2846.3076	0.0130	VDHRGLTFQQNASSMCVPDQDTAIR	Deamidated Q10 6.25%
84.5	2846.3076	0.0130	VDHRGLTFQQNASSMCVPDQDTAIR	Deamidated Q9 6.25%
67.2	2845.3236	0.9971	VDHRGLTFQQNASSMCVPDQDTAIR	
63.1	2846.3076	0.0130	VDHRGLTFQQNASSMCVPDQDTAIR	Deamidated Q20 0.05%
7.0	2846.3109	0.0097	NQGDFSLSVRTQGISMTCMEGRSLR	
7.0	2846.3109	0.0097	NQGDFSLSVRTQGISMTCMEGRSLR	
5.2	2845.3237	0.9969	TMILNFCSYMQWVPGSDVLVAQNR	
4.1	2846.3078	0.0129	TMILNFCSYMQWVPGSDVLVAQNR	
4.0	2846.3189	0.0017	SQREMEEKYIVSAWYNMGMTLHK	

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

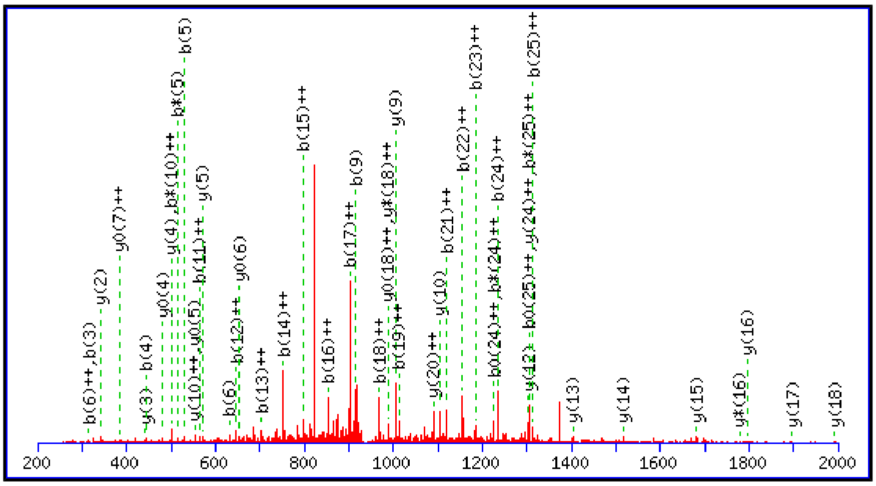
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVDKSTGKPTLYNVSLVMSDTAGTCY**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 25609: 2808.333102 from(937.118310,3+) intensity(39596.9766) rtinseconds(1923) scans(4730) index(859)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum4108_scans__4730
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

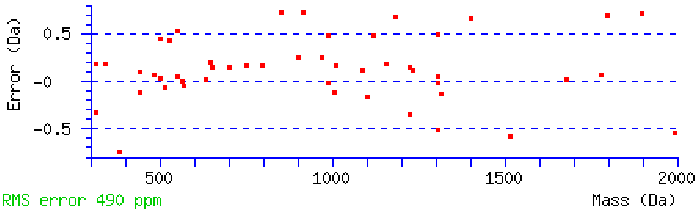
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

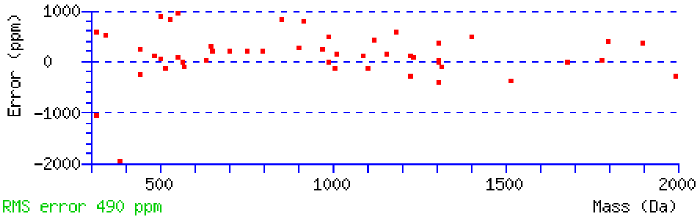


Monoisotopic mass of neutral peptide Mr(calc): 2808.3198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 81 **Expect:** 1.8e-006
Matches : 49/264 fragment ions using 87 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							26
2	201.1234	101.0653			183.1128	92.0600	V	2708.2794	1354.6433	2691.2528	1346.1300	2690.2688	1345.6380	25
3	**316.1503**	158.5788			298.1397	149.5735	D	2609.2109	1305.1091	2592.1844	1296.5958	2591.2004	1296.1038	24
4	**444.2453**	222.6263	427.2187	214.1130	426.2347	213.6210	K	2494.1840	1247.5956	2477.1575	1239.0824	2476.1734	1238.5904	23
5	**531.2773**	266.1423	514.2508	257.6290	513.2667	257.1370	S	2366.0890	1183.5482	2349.0625	1175.0349	2348.0785	1174.5429	22
6	**632.3250**	***316.6661***	615.2984	308.1529	614.3144	307.6608	T	2279.0570	1140.0321	2262.0305	1131.5189	2261.0465	1131.0269	21
7	689.3464	345.1769	672.3199	336.6636	671.3359	336.1716	G	2178.0093	1089.5083	2160.9828	1080.9950	2159.9988	1080.5030	20
8	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	K	2120.9879	1060.9976	2103.9613	1052.4843	2102.9773	1051.9923	19
9	**914.4942**	457.7507	897.4676	449.2375	896.4836	448.7454	P	***1992.8929***	996.9501	1975.8664	988.4368	1974.8823	987.9448	18
10	1015.5419	508.2746	998.5153	499.7613	997.5313	499.2693	T	***1895.8401***	948.4237	1878.8136	939.9104	1877.8296	939.4184	17
11	1128.6259	***564.8166***	1111.5994	556.3033	1110.6154	555.8113	L	***1794.7925***	897.8999	1777.7659	889.3866	1776.7819	888.8946	16
12	1291.6892	***646.3483***	1274.6627	637.8350	1273.6787	637.3430	Y	***1681.7084***	841.3578	1664.6819	832.8446	1663.6978	832.3526	15
13	1406.7162	***703.8617***	1389.6896	695.3485	1388.7056	694.8564	N	***1518.6451***	759.8262	1501.6185	751.3129	1500.6345	750.8209	14
14	1505.7846	***753.3959***	1488.7581	744.8827	1487.7740	744.3907	V	***1403.6181***	702.3127			1385.6076	693.3074	13
15	1592.8166	***796.9120***	1575.7901	788.3987	1574.8061	787.9067	S	***1304.5497***	652.7785			1286.5392	643.7732	12
16	1705.9007	***853.4540***	1688.8741	844.9407	1687.8901	844.4487	L	1217.5177	609.2625			1199.5071	600.2572	11
17	1804.9691	***902.9882***	1787.9426	894.4749	1786.9585	893.9829	V	***1104.4336***	552.7205			1086.4231	543.7152	10
18	1936.0096	***968.5084***	1918.9830	959.9952	1917.9990	959.5032	M	***1005.3652***	503.1862			987.3546	494.1810	9
19	2023.0416	***1012.0244***	2006.0151	1003.5112	2005.0311	1003.0192	S	874.3247	437.6660			856.3142	428.6607	8
20	2138.0686	1069.5379	2121.0420	1061.0246	2120.0580	1060.5326	D	787.2927	394.1500			769.2821	385.1447	7
21	2239.1162	***1120.0618***	2222.0897	1111.5485	2221.1057	1111.0565	T	672.2658	336.6365			654.2552	327.6312	6
22	2310.1534	***1155.5803***	2293.1268	1147.0670	2292.1428	1146.5750	A	***571.2181***	286.1127			553.2075	277.1074	5
23	2367.1748	***1184.0910***	2350.1483	1175.5778	2349.1643	1175.0858	G	***500.1810***	250.5941			482.1704	241.5888	4

24	2468.2225	***1234.6149***	2451.1960	1226.1016	2450.2119	1225.6096	**T**	***443.1595***	222.0834			425.1489	213.0781	**3**
25	2628.2531	***1314.6302***	2611.2266	1306.1169	2610.2426	1305.6249	**C**	***342.1118***	171.5595					**2**
26							**Y**	182.0812	91.5442					**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
81.4	2808.3198	0.0133	TVDKSTGKPTLYNVSLVMSDTAGTCY
55.7	2807.3358	0.9973	TVDKSTGKPTLYNVSLVMSDTAGTCY
6.2	2808.3270	0.0062	NLESARVSMVGQVKQCEGITSPEGSK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
4.0	2806.3177	2.0154	NSTLLVNLAAELNNGNDMLAQRSAEK
2.4	2807.3429	0.9902	NLESARVSMVGQVKQCEGITSPEGSK

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

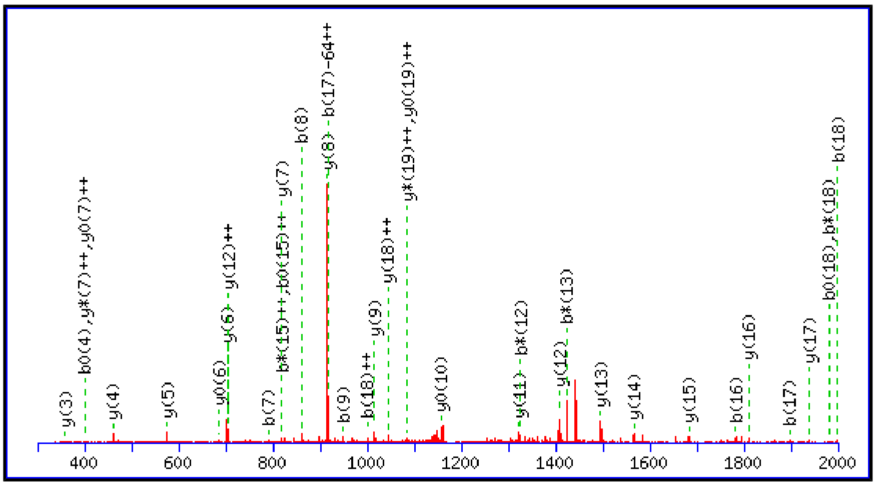
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

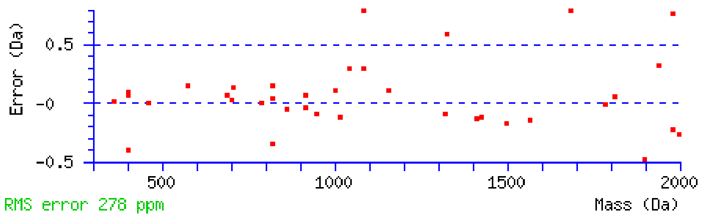
Match to Query 17869: 2356.038748 from(1179.026650,2+) intensity(33681.4531) rtinseconds(1112) scans(2775) index(6293)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum2439_scans__2775
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

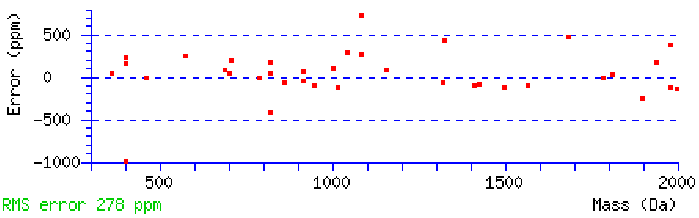
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2356.0311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q16 : Deamidated (NQ)
Ions Score: 77 **Expect:** 2.1e-006
Matches : 37/342 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	58.0287	29.5180					G							21
2	171.1128	86.0600					L	2300.0169	1150.5121	2282.9904	1141.9988	2282.0064	1141.5068	20
3	272.1605	136.5839			254.1499	127.5786	T	2186.9329	1093.9701	2169.9063	1085.4568	2168.9223	1084.9648	19
4	419.2289	210.1181			401.2183	201.1128	F	2085.8852	1043.4462	2068.8586	1034.9330	2067.8746	1034.4410	18
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	Q	***1938.8168***	969.9120	1921.7902	961.3988	1920.8062	960.9067	17
6	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	Q	***1810.7582***	905.8827	1793.7317	897.3695	1792.7476	896.8775	16
7	**790.3730**	395.6901	773.3464	387.1769	772.3624	386.6849	N	***1682.6996***	841.8535	1665.6731	833.3402	1664.6891	832.8482	15
8	**861.4101**	431.2087	844.3836	422.6954	843.3995	422.2034	A	***1567.6727***	784.3400	1550.6461	775.8267	1549.6621	775.3347	14
9	**948.4421**	474.7247	931.4156	466.2114	930.4316	465.7194	S	***1496.6356***	748.8214	1479.6090	740.3081	1478.6250	739.8161	13
10	1035.4742	518.2407	1018.4476	509.7274	1017.4636	509.2354	S	***1409.6035***	705.3054	1392.5770	696.7921	1391.5930	696.3001	12
11	1182.5096	591.7584	1165.4830	583.2451	1164.4990	582.7531	M	***1322.5715***	661.7894	1305.5450	653.2761	1304.5610	652.7841	11
12	1342.5402	671.7737	1325.5137	663.2605	1324.5296	662.7685	C	1175.5361	588.2717	1158.5096	579.7584	1157.5256	579.2664	10
13	1441.6086	721.3080	1424.5821	712.7947	1423.5981	712.3027	V	***1015.5055***	508.2564	998.4789	499.7431	997.4949	499.2511	9
14	1538.6614	769.8343	1521.6348	761.3211	1520.6508	760.8291	P	***916.4371***	458.7222	899.4105	450.2089	898.4265	449.7169	8
15	1653.6883	827.3478	1636.6618	818.8345	1635.6778	818.3425	D	***819.3843***	410.1958	802.3577	401.6825	801.3737	401.1905	7
16	**1782.7309**	891.8691	1765.7044	883.3558	1764.7204	882.8638	Q	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	6
17	**1897.7579**	949.3826	1880.7313	940.8693	1879.7473	940.3773	D	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
18	**1998.8056**	999.9064	1981.7790	991.3931	1980.7950	990.9011	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
19	2069.8427	1035.4250	2052.8161	1026.9117	2051.8321	1026.4197	A	***359.2401***	180.1237	342.2136	171.6104			3
20	2182.9267	1091.9670	2165.9002	1083.4537	2164.9162	1082.9617	I	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.1	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated N7, Q16 53.97%
75.6	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, Q16 38.12%
66.1	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, N7 4.33%
64.7	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q16 3.12%
56.0	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, N7 0.42%
46.6	2356.0311	0.0076	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q6 0.05%
44.8	2355.0471	0.9916	GLTFQQNASSMCVPDQDTAIR	
36.4	2355.0471	0.9916	GLTFQQNASSMCVPDQDTAIR	
36.4	2355.0471	0.9916	GLTFQQNASSMCVPDQDTAIR	
34.1	2355.0471	0.9916	GLTFQQNASSMCVPDQDTAIR	

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

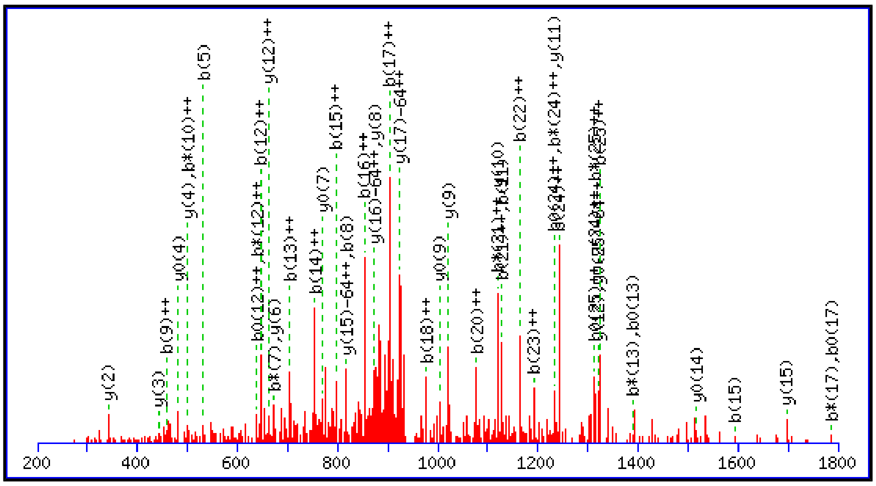
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVDKSTGKPTLYNVSLVMSDTAGTCY**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 25739: 2824.328862 from(942.450230,3+) intensity(2851.9548) rtinseconds(1564) scans(3371) index(102)
Title: 111019_Est_ISCardio_NMI_200000g_G_3Spectrum2915_scans__3371
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

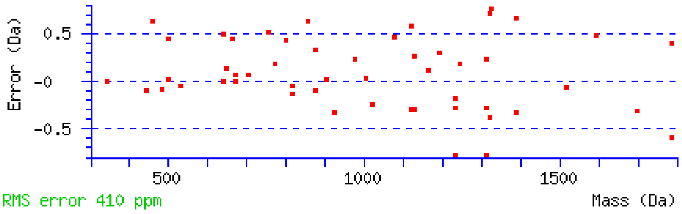
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

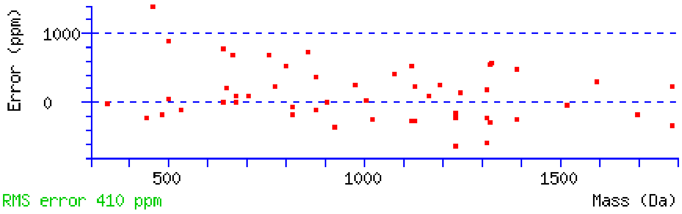


Monoisotopic mass of neutral peptide Mr(calc): 2824.3147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
M18 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 76 **Expect:** 6.2e-006
Matches : 51/404 fragment ions using 74 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311			84.0444	42.5258	T							26
2	201.1234	101.0653			183.1128	92.0600	V	2724.2743	1362.6408	2707.2477	1354.1275	2706.2637	1353.6355	25
3	316.1503	158.5788			298.1397	149.5735	D	2625.2059	1313.1066	2608.1793	1304.5933	2607.1953	1304.1013	24
4	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	K	2510.1789	1255.5931	2493.1524	1247.0798	2492.1684	1246.5878	23
5	**531.2773**	266.1423	514.2508	257.6290	513.2667	257.1370	S	2382.0840	1191.5456	2365.0574	1183.0323	2364.0734	1182.5403	22
6	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	T	2295.0519	1148.0296	2278.0254	1139.5163	2277.0414	1139.0243	21
7	689.3464	345.1769	672.3199	336.6636	671.3359	336.1716	G	2194.0043	1097.5058	2176.9777	1088.9925	2175.9937	1088.5005	20
8	**817.4414**	409.2243	800.4149	400.7111	799.4308	400.2191	K	2136.9828	1068.9950	2119.9562	1060.4818	2118.9722	1059.9897	19
9	914.4942	***457.7507***	897.4676	449.2375	896.4836	448.7454	P	2008.8878	1004.9476	1991.8613	996.4343	1990.8773	995.9423	18
10	1015.5419	508.2746	998.5153	499.7613	997.5313	499.2693	T	1911.8351	956.4212	1894.8085	947.9079	1893.8245	947.4159	17
11	**1128.6259**	564.8166	1111.5994	556.3033	1110.6154	555.8113	L	1810.7874	905.8973	1793.7608	897.3841	1792.7768	896.8920	16
12	1291.6892	***646.3483***	1274.6627	637.8350	1273.6787	637.3430	Y	**1697.7033**	849.3553	1680.6768	840.8420	1679.6928	840.3500	15
13	1406.7162	***703.8617***	1389.6896	695.3485	1388.7056	694.8564	N	1534.6400	767.8236	1517.6134	759.3104	1516.6294	758.8184	14
14	1505.7846	***753.3959***	1488.7581	744.8827	1487.7740	744.3907	V	1419.6130	710.3102			1401.6025	701.3049	13
15	**1592.8166**	***796.9120***	1575.7901	788.3987	1574.8061	787.9067	S	**1320.5446**	660.7760			1302.5341	651.7707	12
16	1705.9007	***853.4540***	1688.8741	844.9407	1687.8901	844.4487	L	**1233.5126**	617.2599			1215.5020	608.2547	11
17	1804.9691	***902.9882***	1787.9426	894.4749	1786.9585	893.9829	V	**1120.4285**	560.7179			1102.4180	551.7126	10
18	1952.0045	***976.5059***	1934.9780	967.9926	1933.9939	967.5006	M	**1021.3601**	511.1837			1003.3496	502.1784	9
19	2039.0365	1020.0219	2022.0100	1011.5086	2021.0260	1011.0166	S	**874.3247**	437.6660			856.3142	428.6607	8
20	2154.0635	***1077.5354***	2137.0369	1069.0221	2136.0529	1068.5301	D	787.2927	394.1500			769.2821	385.1447	7
21	2255.1112	***1128.0592***	2238.0846	1119.5459	2237.1006	1119.0539	T	**672.2658**	336.6365			654.2552	327.6312	6
22	2326.1483	***1163.5778***	2309.1217	1155.0645	2308.1377	1154.5725	A	571.2181	286.1127			553.2075	277.1074	5

23	2383.1697	***1192.0885***	2366.1432	1183.5752	2365.1592	1183.0832	**G**	**500.1810**	250.5941			482.1704	241.5888	**4**
24	2484.2174	***1242.6123***	2467.1909	1234.0991	2466.2069	1233.6071	**T**	**443.1595**	222.0834			425.1489	213.0781	**3**
25	2644.2481	***1322.6277***	2627.2215	1314.1144	2626.2375	1313.6224	**C**	**342.1118**	171.5595					**2**
26							**Y**	182.0812	91.5442					**1**





NCBI **BLAST** search of TVDKSTGKPTLYNVSLVMSDTAGTCY
(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	2824.3147	0.0142	TVDKSTGKPTLYNVSLVMSDTAGTCY
46.2	2823.3307	0.9982	TVDKSTGKPTLYNVSLVMSDTAGTCY
4.0	2823.3167	1.0122	NEDGQVNISIGEMVPSRQAFESMLR
3.6	2823.3167	1.0121	DEDGQVNISIGEMVPSRQAFESMLR
3.5	2824.3200	0.0089	SAAMSFYKFATANNQPVAANGELYMK
3.2	2823.3208	1.0081	MLGSCVSHATFDDDLPGVGNLSEFKK
3.1	2823.3167	1.0122	NEDGQVNISIGEMVPSRQAFESMLR
2.7	2823.3360	0.9929	SAAMSFYKFATANNQPVAANGELYMK
2.3	2824.3214	0.0075	GHFYMYAGSLLLKMGQHGNNVQWR
1.9	2824.3200	0.0089	SAAMSFYKFATANNQPVAANGELYMK

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

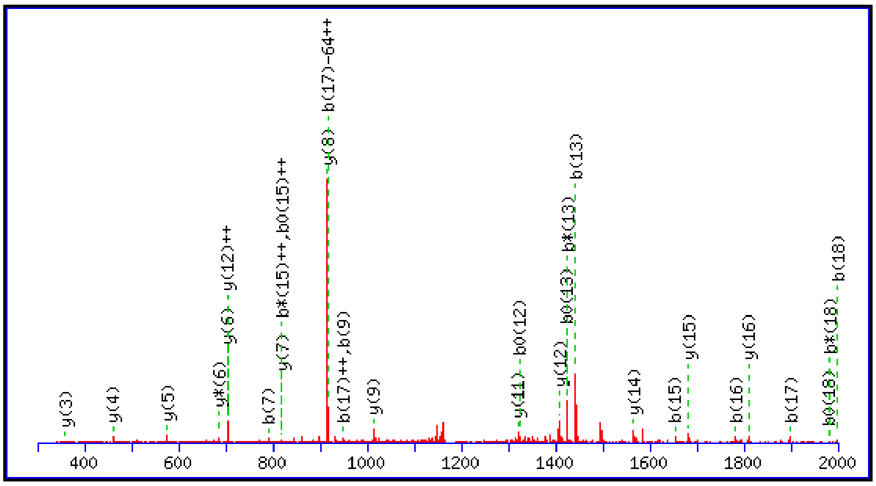
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

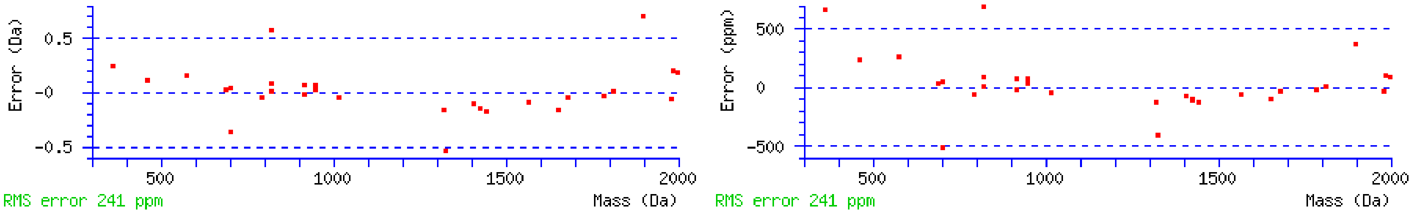
Match to Query 17870: 2356.039868 from(1179.027210,2+) intensity(19703.2813) rtinseconds(1086) scans(2704) index(6284)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum2375_scans__2704
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2356.0311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Deamidated (NQ)
N7 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 73 **Expect:** 5.5e-006
Matches : 30/342 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	58.0287	29.5180					G							21
2	171.1128	86.0600					L	2300.0169	1150.5121	2282.9904	1141.9988	2282.0064	1141.5068	20
3	272.1605	136.5839			254.1499	127.5786	T	2186.9329	1093.9701	2169.9063	1085.4568	2168.9223	1084.9648	19
4	419.2289	210.1181			401.2183	201.1128	F	2085.8852	1043.4462	2068.8587	1034.9330	2067.8746	1034.4410	18
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	Q	1938.8168	969.9120	1921.7902	961.3988	1920.8062	960.9067	17
6	676.3301	338.6687	659.3035	330.1554	658.3195	329.6634	Q	***1810.7582***	905.8827	1793.7317	897.3695	1792.7476	896.8775	16
7	**791.3570**	396.1821	774.3305	387.6689	773.3464	387.1769	N	***1681.7156***	841.3614	1664.6891	832.8482	1663.7050	832.3562	15
8	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	A	***1566.6887***	783.8480	1549.6621	775.3347	1548.6781	774.8427	14
9	**949.4262**	475.2167	932.3996	466.7034	931.4156	466.2114	S	1495.6516	748.3294	1478.6250	739.8161	1477.6410	739.3241	13
10	1036.4582	518.7327	1019.4316	510.2195	1018.4476	509.7274	S	***1408.6195***	704.8134	1391.5930	696.3001	1390.6090	695.8081	12
11	1183.4936	592.2504	1166.4670	583.7372	1165.4830	583.2451	M	***1321.5875***	661.2974	1304.5610	652.7841	1303.5769	652.2921	11
12	1343.5242	672.2658	1326.4977	663.7525	1325.5137	663.2605	C	1174.5521	587.7797	1157.5256	579.2664	1156.5415	578.7744	10
13	**1442.5926**	721.8000	1425.5661	713.2867	1424.5821	712.7947	V	***1014.5215***	507.7644	997.4949	499.2511	996.5109	498.7591	9
14	1539.6454	770.3263	1522.6189	761.8131	1521.6348	761.3211	P	***915.4530***	458.2302	898.4265	449.7169	897.4425	449.2249	8
15	**1654.6724**	827.8398	1637.6458	819.3265	1636.6618	818.8345	D	***818.4003***	409.7038	801.3737	401.1905	800.3897	400.6985	7
16	**1782.7309**	891.8691	1765.7044	883.3558	1764.7204	882.8638	Q	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	6
17	**1897.7579**	949.3826	1880.7313	940.8693	1879.7473	940.3773	D	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
18	**1998.8056**	999.9064	1981.7790	991.3931	1980.7950	990.9011	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
19	2069.8427	1035.4250	2052.8161	1026.9117	2051.8321	1026.4197	A	***359.2401***	180.1237	342.2136	171.6104			3
20	2182.9267	1091.9670	2165.9002	1083.4537	2164.9162	1082.9617	I	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.1	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, N7 84.08%
61.8	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, N7 6.20%
60.7	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated N7, Q16 4.79%
59.7	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, Q16 3.80%
51.5	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q16 0.57%
51.3	2356.0311	0.0087	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q6 0.55%
48.4	2355.0471	0.9927	GLTFQQNASSMCVPDQDTAIR	
39.0	2355.0471	0.9927	GLTFQQNASSMCVPDQDTAIR	
38.1	2355.0471	0.9927	GLTFQQNASSMCVPDQDTAIR	
22.8	2355.0471	0.9927	GLTFQQNASSMCVPDQDTAIR	

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

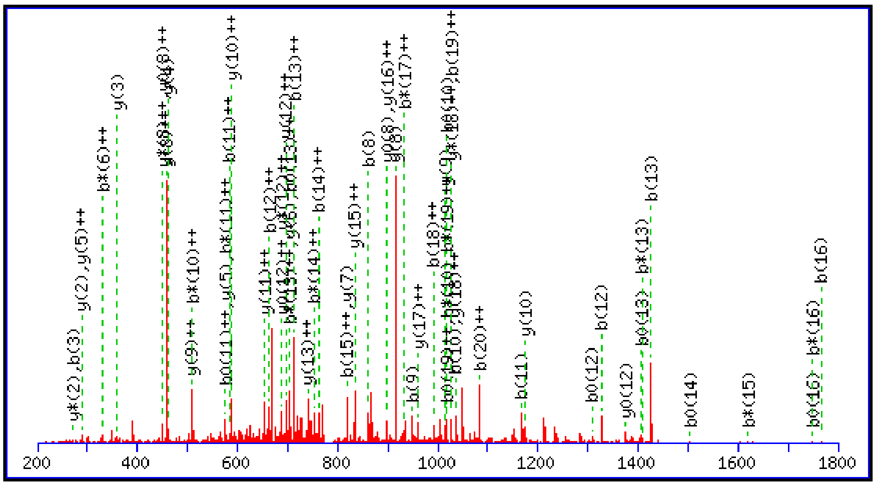
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLTFQQNASSMCVPDQDTAIR**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

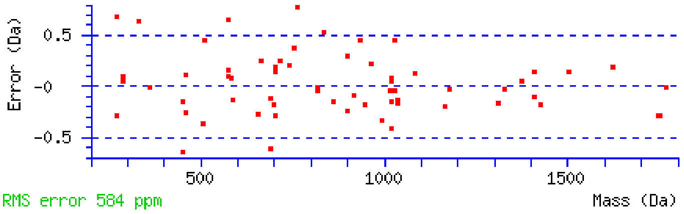
Match to Query 15490: 2340.041922 from(781.021250,3+) intensity(66153.5391) rtinseconds(1574) scans(3900) index(2008)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum3357_scans__3900
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

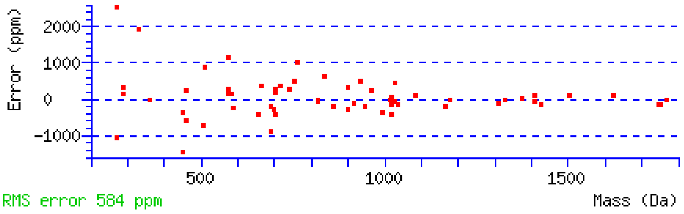
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2340.0362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7     : Deamidated (NQ)
Q16    : Deamidated (NQ)
Ions Score: 46  Expect: 0.0033
Matches : 63/222 fragment ions using 123 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							21
2	171.1128	86.0600					L	2284.0220	1142.5147	2266.9955	1134.0014	2266.0115	1133.5094	20
3	**272.1605**	136.5839			254.1499	127.5786	T	2170.9380	1085.9726	2153.9114	1077.4593	2152.9274	1076.9673	19
4	419.2289	210.1181			401.2183	201.1128	F	2069.8903	1035.4488	2052.8637	1026.9355	2051.8797	1026.4435	18
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	Q	1922.8219	961.9146	1905.7953	953.4013	1904.8113	952.9093	17
6	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	Q	1794.7633	897.8853	1777.7367	889.3720	1776.7527	888.8800	16
7	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	N	1666.7047	833.8560	1649.6782	825.3427	1648.6941	824.8507	15
8	**861.4101**	431.2087	844.3836	422.6954	843.3995	422.2034	A	1551.6778	776.3425	1534.6512	767.8292	1533.6672	767.3372	14
9	**948.4421**	474.7247	931.4156	466.2114	930.4316	465.7194	S	1480.6407	740.8240	1463.6141	732.3107	1462.6301	731.8187	13
10	**1035.4742**	518.2407	1018.4476	509.7274	1017.4636	509.2354	S	1393.6086	697.3080	1376.5821	688.7947	1375.5981	688.3027	12
11	**1166.5147**	***583.7610***	1149.4881	575.2477	1148.5041	574.7557	M	1306.5766	653.7919	1289.5501	645.2787	1288.5660	644.7867	11
12	**1326.5453**	***663.7763***	1309.5188	655.2630	1308.5347	654.7710	C	**1175.5361**	588.2717	1158.5096	579.7584	1157.5256	579.2664	10
13	**1425.6137**	***713.3105***	1408.5872	704.7972	1407.6031	704.3052	V	**1015.5055**	508.2564	998.4789	499.7431	997.4949	499.2511	9
14	1522.6665	***761.8369***	1505.6399	753.3236	1504.6559	752.8316	P	**916.4371**	458.7222	899.4105	450.2089	898.4265	449.7169	8
15	1637.6934	***819.3503***	1620.6669	810.8371	1619.6829	810.3451	D	**819.3843**	410.1958	802.3577	401.6825	801.3737	401.1905	7
16	**1766.7360**	883.8716	1749.7095	875.3584	1748.7255	874.8664	Q	**704.3573**	352.6823	687.3308	344.1690	686.3468	343.6770	6
17	1881.7630	941.3851	1864.7364	932.8718	1863.7524	932.3798	D	**575.3148**	288.1610	558.2882	279.6477	557.3042	279.1557	5
18	1982.8106	***991.9090***	1965.7841	983.3957	1964.8001	982.9037	T	**460.2878**	230.6475	443.2613	222.1343	442.2772	221.6423	4
19	2053.8478	***1027.4275***	2036.8212	1018.9142	2035.8372	1018.4222	A	**359.2401**	180.1237	342.2136	171.6104			3
20	2166.9318	***1083.9695***	2149.9053	1075.4563	2148.9213	1074.9643	I	**288.2030**	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.7	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated N7, Q16 50.74%
39.5	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, Q16 12.12%
39.5	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q16 12.12%
37.8	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated Q6, N7 8.34%
37.8	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, N7 8.34%
37.8	2340.0362	0.0057	GLTFQQNASSMCVPDQDTAIR	Deamidated Q5, Q6 8.34%
7.1	2339.0337	1.0082	ENFNMMNALDQLPKPFSNPK	
3.3	2338.0464	1.9956	DQSPQIVFVEYDAFMQTFR	
3.3	2338.0464	1.9956	DQSPQIVFVEYDAFMQTFR	
2.1	2339.0376	1.0044	EWQDKFVDMNDQAVKSQPR	

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

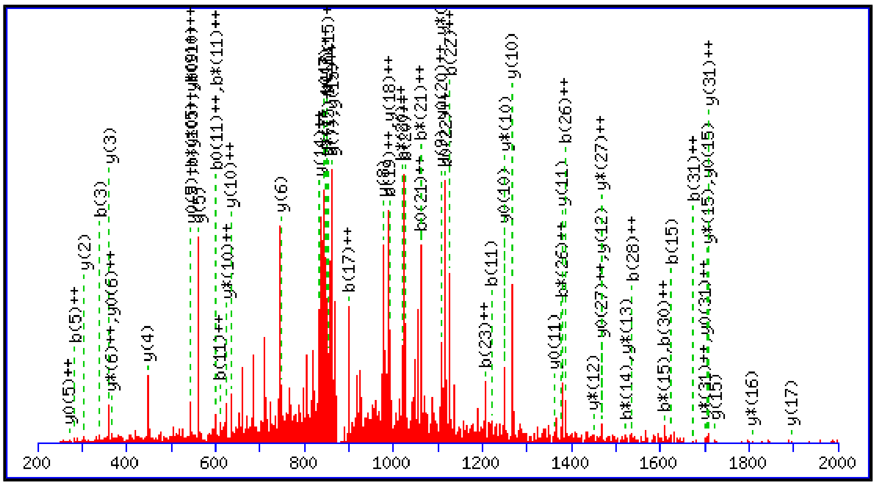
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **THTNISESHPNATFSAVGEASICEDDWNSGER**
Found in **P01871** in **con_Xuniprot_HUMAN3**, IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

Match to Query 27795: 3520.502376 from(881.132870,4+) intensity(0.0000) rtinseconds(2130) scans(5505) index(1483)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum4813_scans__5505
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

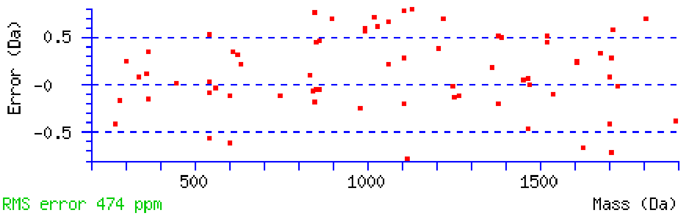
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

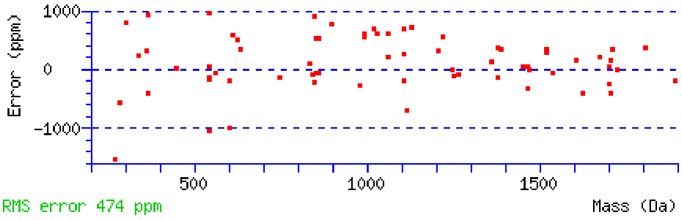


Monoisotopic mass of neutral peptide Mr(calc): 3518.4917
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 35 **Expect:** 0.016
Matches : 70/364 fragment ions using 138 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311			84.0444	42.5258	T							32
2	239.1139	120.0606			221.1033	111.0553	H	3418.4513	1709.7293	3401.4247	1701.2160	3400.4407	1700.7240	31
3	340.1615	170.5844			322.1510	161.5791	T	3281.3924	1641.1998	3264.3658	1632.6865	3263.3818	1632.1945	30
4	454.2045	227.6059	437.1779	219.0926	436.1939	218.6006	N	3180.3447	1590.6760	3163.3181	1582.1627	3162.3341	1581.6707	29
5	567.2885	***284.1479***	550.2620	275.6346	549.2780	275.1426	I	3066.3018	1533.6545	3049.2752	1525.1412	3048.2912	1524.6492	28
6	654.3206	327.6639	637.2940	319.1506	636.3100	318.6586	S	2953.2177	1477.1125	2936.1911	1468.5992	2935.2071	1468.1072	27
7	783.3632	392.1852	766.3366	383.6719	765.3526	383.1799	E	2866.1857	1433.5965	2849.1591	1425.0832	2848.1751	1424.5912	26
8	870.3952	435.7012	853.3686	427.1880	852.3846	426.6959	S	2737.1431	1369.0752	2720.1165	1360.5619	2719.1325	1360.0699	25
9	1007.4541	504.2307	990.4275	495.7174	989.4435	495.2254	H	2650.1111	1325.5592	2633.0845	1317.0459	2632.1005	1316.5539	24
10	1104.5069	552.7571	1087.4803	544.2438	1086.4963	543.7518	P	2513.0521	1257.0297	2496.0256	1248.5164	2495.0416	1248.0244	23
11	1219.5338	***610.2705***	1202.5073	601.7573	1201.5232	601.2653	N	2415.9994	1208.5033	2398.9728	1199.9901	2397.9888	1199.4980	22
12	1290.5709	645.7891	1273.5444	637.2758	1272.5604	636.7838	A	2300.9724	1150.9899	2283.9459	1142.4766	2282.9619	1141.9846	21
13	1391.6186	696.3129	1374.5920	687.7997	1373.6080	687.3077	T	2229.9353	1115.4713	2212.9088	1106.9580	2211.9248	1106.4660	20
14	1538.6870	769.8471	1521.6605	761.3339	1520.6764	760.8419	F	2128.8876	1064.9475	2111.8611	1056.4342	2110.8771	1055.9422	19
15	1625.7190	813.3632	1608.6925	804.8499	1607.7085	804.3579	S	1981.8192	991.4133	1964.7927	982.9000	1963.8087	982.4080	18
16	1696.7562	***848.8817***	1679.7296	840.3684	1678.7456	839.8764	A	***1894.7872***	947.8972	1877.7606	939.3840	1876.7766	938.8920	17
17	1795.8246	***898.4159***	1778.7980	889.9026	1777.8140	889.4106	V	1823.7501	912.3787	1806.7235	903.8654	1805.7395	903.3734	16
18	1852.8460	926.9267	1835.8195	918.4134	1834.8355	917.9214	G	***1724.6817***	862.8445	1707.6551	854.3312	1706.6711	853.8392	15
19	1981.8886	***991.4480***	1964.8621	982.9347	1963.8781	982.4427	E	1667.6602	834.3337	1650.6337	825.8205	1649.6496	825.3285	14
20	2052.9257	***1026.9665***	2035.8992	1018.4532	2034.9152	1017.9612	A	1538.6176	769.8124	1521.5911	761.2992	1520.6070	760.8072	13
21	2139.9578	1070.4825	2122.9312	1061.9692	2121.9472	1061.4772	S	***1467.5805***	734.2939	1450.5539	725.7806	1449.5699	725.2886	12
22	2253.0418	***1127.0246***	2236.0153	1118.5113	2235.0313	1118.0193	I	***1380.5485***	690.7779	1363.5219	682.2646	1362.5379	681.7726	11
23	2413.0725	***1207.0399***	2396.0459	1198.5266	2395.0619	1198.0346	C	***1267.4644***	634.2358	1250.4379	625.7226	1249.4538	625.2306	10

24	2542.1151	1271.5612	2525.0885	1263.0479	2524.1045	1262.5559	**E**	***1107.4338***	554.2205	1090.4072	545.7072	1089.4232	545.2152	**9**
25	2657.1420	1329.0746	2640.1155	1320.5614	2639.1315	1320.0694	**D**	***978.3912***	489.6992	961.3646	481.1859	960.3806	480.6939	**8**
26	2772.1690	***1386.5881***	2755.1424	1378.0748	2754.1584	1377.5828	**D**	***863.3642***	432.1857	846.3377	423.6725	845.3537	423.1805	**7**
27	2958.2483	1479.6278	2941.2217	1471.1145	2940.2377	1470.6225	**W**	***748.3373***	374.6723	731.3107	366.1590	730.3267	365.6670	**6**
28	3072.2912	***1536.6492***	3055.2647	1528.1360	3054.2806	1527.6440	**N**	***562.2580***	281.6326	545.2314	273.1193	544.2474	272.6273	**5**
29	3159.3232	1580.1653	3142.2967	1571.6520	3141.3127	1571.1600	**S**	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	**4**
30	3216.3447	***1608.6760***	3199.3181	1600.1627	3198.3341	1599.6707	**G**	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	**3**
31	3345.3873	***1673.1973***	3328.3607	1664.6840	3327.3767	1664.1920	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
32							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.4	3518.4917	2.0107	THTNISESHPNATFSAVGEASICEDDWNSGER	Deamidated N11 49.97%
35.4	3518.4917	2.0107	THTNISESHPNATFSAVGEASICEDDWNSGER	Deamidated N4 49.97%
6.3	3520.4880	0.0143	RSNGQGGAASSESTDSCASQTELLDFDSADSGRR	
6.1	3520.4880	0.0143	RSNGQGGAASSESTDSCASQTELLDFDSADSGRR	
5.5	3518.4917	2.0107	THTNISESHPNATFSAVGEASICEDDWDSGER	
5.5	3518.4917	2.0107	THTNISESHPNATFSAVGEASICEDDWNSGER	Deamidated N28 0.05%
3.6	3518.4968	2.0055	DGVCTKPMTTCPKSMTYHYHVSTCQPTCR	

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

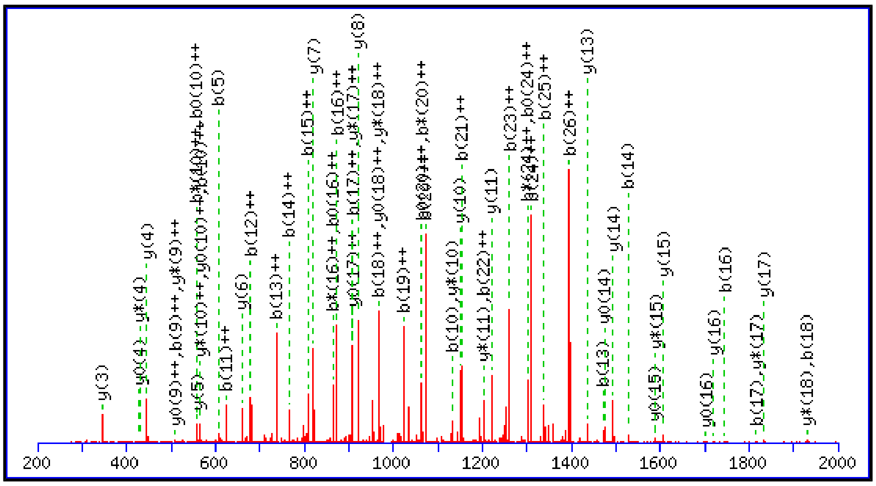
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSLHRPALEDLLLGSEANLTCTLTGLR**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

Match to Query 26995: 2963.587512 from(988.869780,3+) intensity(2124766.7500) rtinseconds(2632) scans(6704) index(8117)
Title: 111019_Est_ISCardio_NMI_YS_G_2Spectrum5812_scans__6704
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

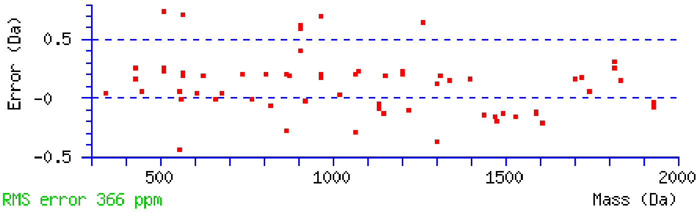
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

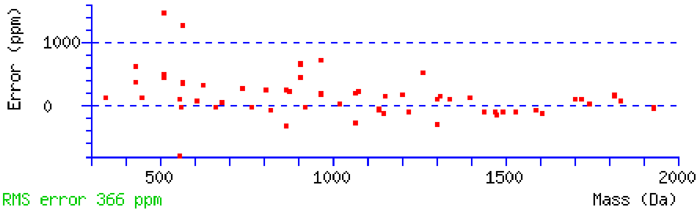


Monoisotopic mass of neutral peptide Mr(calc): 2963.5750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N18 : Deamidated (NQ)
Ions Score: 140 **Expect:** 1.1e-012
Matches : 64/296 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							27
2	201.1234	101.0653			183.1128	92.0600	S	2851.4982	1426.2527	2834.4717	1417.7395	2833.4877	1417.2475	26
3	314.2074	157.6074			296.1969	148.6021	L	2764.4662	1382.7367	2747.4396	1374.2235	2746.4556	1373.7315	25
4	451.2663	226.1368			433.2558	217.1315	H	2651.3821	1326.1947	2634.3556	1317.6814	2633.3716	1317.1894	24
5	**607.3675**	304.1874	590.3409	295.6741	589.3569	295.1821	R	2514.3232	1257.6652	2497.2967	1249.1520	2496.3127	1248.6600	23
6	704.4202	352.7137	687.3937	344.2005	686.4097	343.7085	P	2358.2221	1179.6147	2341.1956	1171.1014	2340.2115	1170.6094	22
7	775.4573	388.2323	758.4308	379.7190	757.4468	379.2270	A	2261.1693	1131.0883	2244.1428	1122.5750	2243.1588	1122.0830	21
8	888.5414	444.7743	871.5148	436.2611	870.5308	435.7691	L	2190.1322	1095.5698	2173.1057	1087.0565	2172.1217	1086.5645	20
9	1017.5840	***509.2956***	1000.5574	500.7824	999.5734	500.2904	E	2077.0482	1039.0277	2060.0216	1030.5144	2059.0376	1030.0224	19
10	**1132.6109**	***566.8091***	1115.5844	558.2958	1114.6004	557.8038	D	1948.0056	974.5064	1930.9790	965.9931	1929.9950	965.5011	18
11	1245.6950	***623.3511***	1228.6684	614.8379	1227.6844	614.3459	L	**1832.9786**	916.9930	1815.9521	908.4797	1814.9681	907.9877	17
12	1358.7791	***679.8932***	1341.7525	671.3799	1340.7685	670.8879	L	**1719.8946**	860.4509	1702.8680	851.9376	1701.8840	851.4456	16
13	**1471.8631**	***736.4352***	1454.8366	727.9219	1453.8526	727.4299	L	**1606.8105**	803.9089	1589.7840	795.3956	1588.7999	794.9036	15
14	**1528.8846**	***764.9459***	1511.8580	756.4327	1510.8740	755.9406	G	**1493.7264**	747.3669	1476.6999	738.8536	1475.7159	738.3616	14
15	1615.9166	***808.4619***	1598.8901	799.9487	1597.9061	799.4567	S	**1436.7050**	718.8561	1419.6784	710.3428	1418.6944	709.8508	13
16	**1744.9592**	***872.9832***	1727.9327	864.4700	1726.9486	863.9780	E	1349.6729	675.3401	1332.6464	666.8268	1331.6624	666.3348	12
17	**1815.9963**	***908.5018***	1798.9698	899.9885	1797.9858	899.4965	A	**1220.6304**	610.8188	1203.6038	602.3055	1202.6198	601.8135	11
18	**1931.0233**	***966.0153***	1913.9967	957.5020	1913.0127	957.0100	N	**1149.5932**	575.3003	1132.5667	566.7870	1131.5827	566.2950	10
19	2044.1073	***1022.5573***	2027.0808	1014.0440	2026.0968	1013.5520	L	1034.5663	517.7868	1017.5397	509.2735	1016.5557	508.7815	9
20	2145.1550	***1073.0811***	2128.1285	1064.5679	2127.1444	1064.0759	T	**921.4822**	461.2448	904.4557	452.7315	903.4717	452.2395	8
21	2305.1857	***1153.0965***	2288.1591	1144.5832	2287.1751	1144.0912	C	**820.4346**	410.7209	803.4080	402.2076	802.4240	401.7156	7
22	2406.2333	***1203.6203***	2389.2068	1195.1070	2388.2228	1194.6150	T	**660.4039**	330.7056	643.3774	322.1923	642.3933	321.7003	6
23	2519.3174	***1260.1623***	2502.2909	1251.6491	2501.3068	1251.1571	L	**559.3562**	280.1817	542.3297	271.6685	541.3457	271.1765	5

24	2620.3651	***1310.6862***	2603.3385	1302.1729	2602.3545	1301.6809	**T**	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	**4**
25	2677.3865	***1339.1969***	2660.3600	1330.6836	2659.3760	1330.1916	**G**	**345.2245**	173.1159	328.1979	164.6026			**3**
26	2790.4706	***1395.7389***	2773.4441	1387.2257	2772.4600	1386.7337	**L**	288.2030	144.6051	271.1765	136.0919			**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
140.4	2963.5750	0.0125	LSLHRPALEDLLLGSEANLTCTLTGLR
119.9	2962.5910	0.9966	LSLHRPALEDLLLGSEANLTCTLTGLR
12.8	2963.5790	0.0085	ELREMIQLPGARPILDPVDFLGLQDK
10.0	2962.5838	1.0038	FNTLRGTNLIKVLDPVIFTQQAICAK
9.7	2962.5838	1.0038	FNTLRGTNLIKVLDPVIFTQQAICAK
8.4	2962.5724	1.0152	GLPPGTQIQIKVQAQGQEGLGAESLSVTR
7.8	2962.5905	0.9970	GSAKSDLAAMGTVLSSIILPLVLMQLMR
7.7	2963.5968	-0.0093	TQLHVNFPPLQTLNLSVGTTGVVSALVR
7.7	2963.5968	-0.0093	TQLHVNFPPLQTLNLSVGTTGVVSALVR
6.9	2962.5724	1.0152	GLPPGTQIQIKVQAQGQEGLGAESLSVTR

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

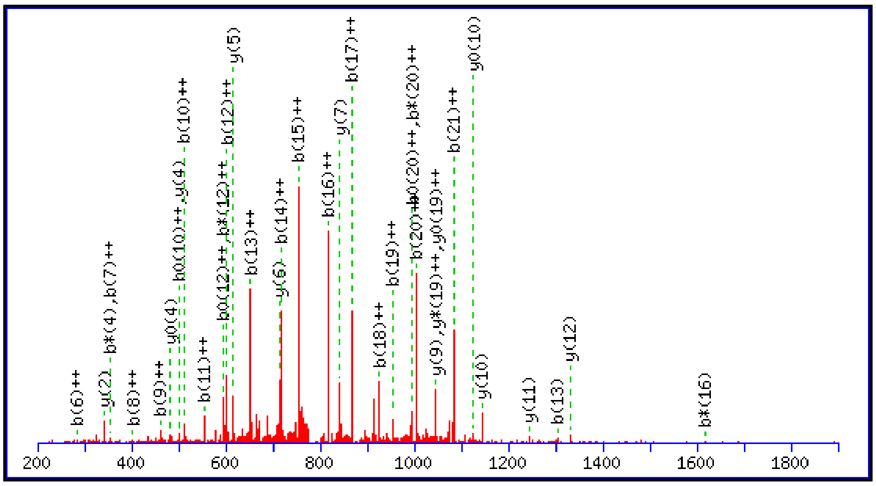
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGKPTHVNVSVVMAEVDGTCY**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

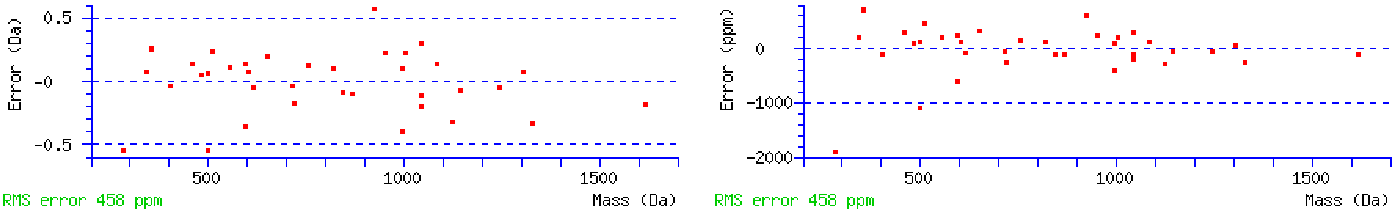
Match to Query 16653: 2347.125822 from(783.382550,3+) intensity(12765.6963) rtinseconds(2201) scans(4813) index(21423)
Title: 111019_Est_MI_YP_G_13Spectrum4222_scans__4813
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2347.1188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 103 **Expect:** 1.3e-008
Matches : 37/206 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							22
2	185.1285	93.0679					A	2235.0420	1118.0247	2218.0155	1109.5114	2217.0315	1109.0194	21
3	242.1499	121.5786					G	2164.0049	1082.5061	2146.9784	1073.9928	2145.9944	1073.5008	20
4	370.2449	185.6261	353.2183	177.1128			K	2106.9835	1053.9954	2089.9569	1045.4821	2088.9729	1044.9901	19
5	467.2976	234.1525	450.2711	225.6392			P	1978.8885	989.9479	1961.8619	981.4346	1960.8779	980.9426	18
6	568.3453	***284.6763***	551.3188	276.1630	550.3348	275.6710	T	1881.8357	941.4215	1864.8092	932.9082	1863.8252	932.4162	17
7	705.4042	***353.2058***	688.3777	344.6925	687.3937	344.2005	H	1780.7881	890.8977	1763.7615	882.3844	1762.7775	881.8924	16
8	804.4727	***402.7400***	787.4461	394.2267	786.4621	393.7347	V	1643.7291	822.3682	1626.7026	813.8549	1625.7186	813.3629	15
9	919.4996	***460.2534***	902.4730	451.7402	901.4890	451.2482	N	1544.6607	772.8340	1527.6342	764.3207	1526.6502	763.8287	14
10	1018.5680	***509.7876***	1001.5415	501.2744	1000.5574	500.7824	V	1429.6338	715.3205			1411.6232	706.3152	13
11	1105.6000	***553.3037***	1088.5735	544.7904	1087.5895	544.2984	S	**1330.5654**	665.7863			1312.5548	656.7810	12
12	1204.6684	***602.8379***	1187.6419	594.3246	1186.6579	593.8326	V	**1243.5333**	622.2703			1225.5228	613.2650	11
13	1303.7369	***652.3721***	1286.7103	643.8588	1285.7263	643.3668	V	**1144.4649**	572.7361			1126.4544	563.7308	10
14	1434.7773	***717.8923***	1417.7508	709.3790	1416.7668	708.8870	M	**1045.3965**	523.2019			1027.3859	514.1966	9
15	1505.8145	***753.4109***	1488.7879	744.8976	1487.8039	744.4056	A	914.3560	457.6817			896.3455	448.6764	8
16	1634.8571	***817.9322***	1617.8305	809.4189	1616.8465	808.9269	E	**843.3189**	422.1631			825.3083	413.1578	7
17	1733.9255	***867.4664***	1716.8989	858.9531	1715.9149	858.4611	V	**714.2763**	357.6418			696.2658	348.6365	6
18	1848.9524	***924.9798***	1831.9259	916.4666	1830.9418	915.9746	D	**615.2079**	308.1076			597.1973	299.1023	5
19	1905.9739	***953.4906***	1888.9473	944.9773	1887.9633	944.4853	G	**500.1810**	250.5941			482.1704	241.5888	4
20	2007.0216	***1004.0144***	1989.9950	995.5011	1989.0110	995.0091	T	443.1595	222.0834			425.1489	213.0781	3
21	2167.0522	***1084.0297***	2150.0257	1075.5165	2149.0416	1075.0245	C	**342.1118**	171.5595					2
22							Y	182.0812	91.5442					1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
102.8	2347.1188	0.0070	LAGKPTHVNVSVVMAEVDGTCY
4.0	2347.1147	0.0111	EEQEMNKCLRANQVLLQNK
3.7	2346.1162	1.0097	SPGQEDVKTTGPAGAMNTLAWSK
3.7	2347.1147	0.0111	EEQEMNKCLRANQVLLQNK
3.0	2346.1162	1.0097	SPGQEDVKTTGPAGAMNTLAWSK
3.0	2345.1144	2.0114	NLYRVGFEGMSDLKCVQDAK
2.8	2346.1243	1.0016	NSRIVSQKDDVHVCIMCLR
2.7	2346.1243	1.0016	NSRIVSQKDDVHVCIMCLR
2.4	2347.1147	0.0111	EEQEMNKCLRANQVLLQNK
1.7	2347.1186	0.0072	LMNRASGTQGASEDNSGGGGKKPK

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

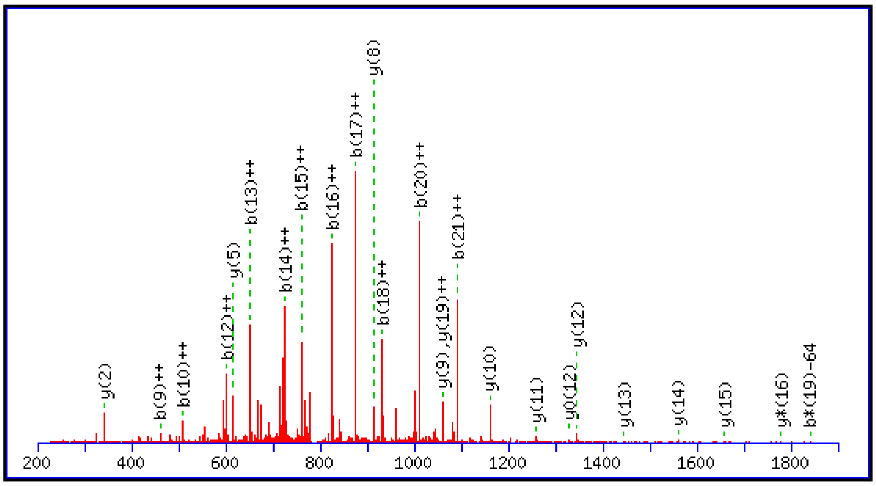
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAGKPTHVNVSVVMAEVDGTCY**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

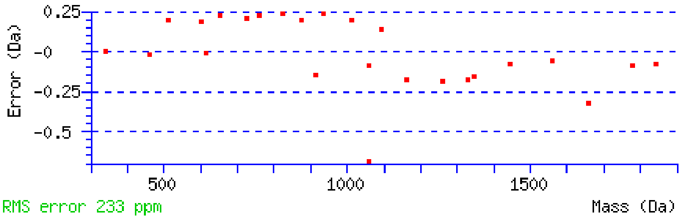
Match to Query 18486: 2363.119872 from(788.713900,3+) intensity(225238.5313) rtinseconds(1335) scans(3128) index(8291)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum2649_scans__3128
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

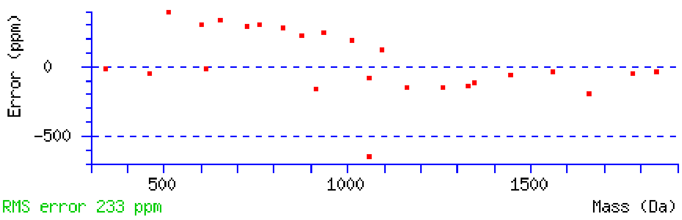
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2363.1138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9     : Deamidated (NQ)
M14    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 97  Expect: 4.8e-008
Matches : 25/322 fragment ions using 33 most intense peaks    (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							22
2	185.1285	93.0679					**A**	2251.0369	1126.0221	2234.0104	1117.5088	2233.0264	1117.0168	21
3	242.1499	121.5786					**G**	2179.9998	1090.5036	2162.9733	1081.9903	2161.9893	1081.4983	20
4	370.2449	185.6261	353.2183	177.1128			**K**	2122.9784	1061.9928	2105.9518	1053.4795	2104.9678	1052.9875	19
5	467.2976	234.1525	450.2711	225.6392			**P**	1994.8834	997.9453	1977.8569	989.4321	1976.8728	988.9401	18
6	568.3453	284.6763	551.3188	276.1630	550.3348	275.6710	**T**	1897.8306	949.4190	1880.8041	940.9057	1879.8201	940.4137	17
7	705.4042	353.2058	688.3777	344.6925	687.3937	344.2005	**H**	1796.7830	898.8951	1779.7564	890.3818	1778.7724	889.8898	16
8	804.4727	402.7400	787.4461	394.2267	786.4621	393.7347	**V**	***1659.7241***	830.3657	1642.6975	821.8524	1641.7135	821.3604	15
9	919.4996	***460.2534***	902.4730	451.7402	901.4890	451.2482	**N**	***1560.6556***	780.8315	1543.6291	772.3182	1542.6451	771.8262	14
10	1018.5680	***509.7876***	1001.5415	501.2744	1000.5574	500.7824	**V**	***1445.6287***	723.3180			1427.6181	714.3127	13
11	1105.6000	553.3037	1088.5735	544.7904	1087.5895	544.2984	**S**	***1346.5603***	673.7838			1328.5497	664.7785	12
12	1204.6684	***602.8379***	1187.6419	594.3246	1186.6579	593.8326	**V**	***1259.5283***	630.2678			1241.5177	621.2625	11
13	1303.7369	***652.3721***	1286.7103	643.8588	1285.7263	643.3668	**V**	***1160.4598***	580.7336			1142.4493	571.7283	10
14	1450.7723	***725.8898***	1433.7457	717.3765	1432.7617	716.8845	**M**	***1061.3914***	531.1994			1043.3809	522.1941	9
15	1521.8094	***761.4083***	1504.7828	752.8951	1503.7988	752.4030	**A**	***914.3560***	457.6817			896.3455	448.6764	8
16	1650.8520	***825.9296***	1633.8254	817.4163	1632.8414	816.9243	**E**	843.3189	422.1631			825.3083	413.1578	7
17	1749.9204	***875.4638***	1732.8938	866.9506	1731.9098	866.4585	**V**	714.2763	357.6418			696.2658	348.6365	6
18	1864.9473	***932.9773***	1847.9208	924.4640	1846.9368	923.9720	**D**	***615.2079***	308.1076			597.1973	299.1023	5
19	1921.9688	961.4880	1904.9422	952.9748	1903.9582	952.4828	**G**	500.1810	250.5941			482.1704	241.5888	4
20	2023.0165	***1012.0119***	2005.9899	1003.4986	2005.0059	1003.0066	**T**	443.1595	222.0834			425.1489	213.0781	3
21	2183.0471	***1092.0272***	2166.0206	1083.5139	2165.0366	1083.0219	**C**	***342.1118***	171.5595					2
22							**Y**	182.0812	91.5442					1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
96.8	2363.1138	0.0061	LAGKPTHVNVSVVMAEVDGTCY
7.7	2363.1236	-0.0037	NLITDICTEQCTLSDQLLPK
7.7	2363.1236	-0.0037	NLITDICTEQCTLSDQLLPK
7.7	2362.1111	1.0088	SPGQEDVKTTGPAGAMNTLAWSK
6.0	2362.1230	0.9969	ELIYNWGKENVVDDQFHEK
6.0	2363.1144	0.0054	HMGGAKVMATTGGTNLRDDIMR
4.1	2363.1313	-0.0114	SKPTSLQSSSTGNANGSDAPSKSR
3.9	2363.1314	-0.0116	SMQQEELTILNIYAPNTGAPR
3.9	2363.1314	-0.0116	SMQQEELTILNIYAPNTGAPR
3.9	2363.1314	-0.0116	SMQQEELTILNIYAPNTGAPR

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

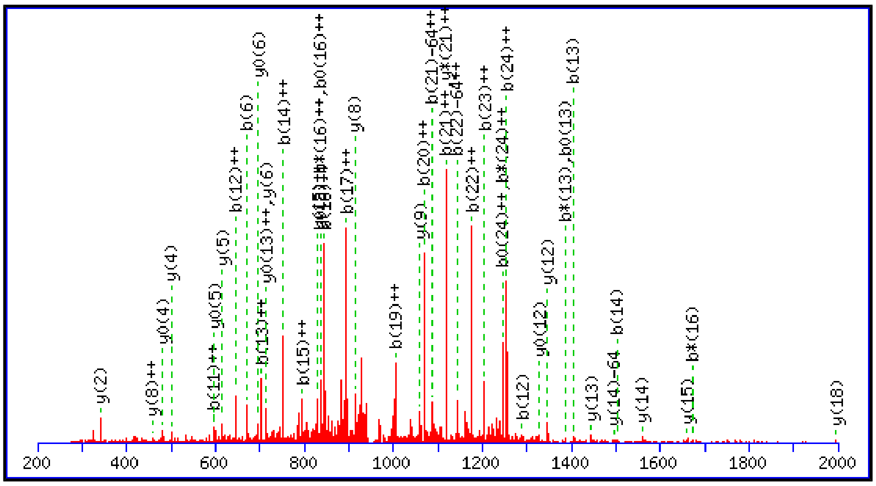
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIDRLAGKPTHVNVSVVMAEVDGTCY**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

Match to Query 25769: 2848.387632 from(950.469820,3+) intensity(48384.0938) rtinseconds(1472) scans(3547) index(23207)
Title: 111019_Est_MI_YS_G_04Spectrum3032_scans__3547
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

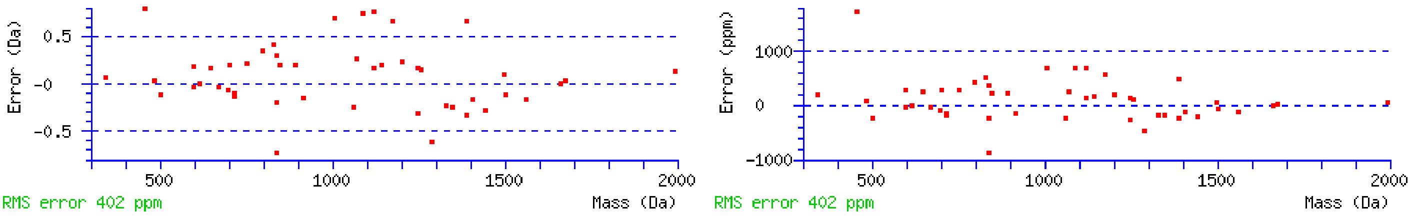
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2848.3735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
M18 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 59 **Expect:** 0.00034
Matches : 47/404 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	102.0550	51.5311			84.0444	42.5258	T							26
2	215.1390	108.0731			197.1285	99.0679	I	2748.3331	1374.6702	2731.3066	1366.1569	2730.3226	1365.6649	25
3	330.1660	165.5866			312.1554	156.5813	D	2635.2491	1318.1282	2618.2225	1309.6149	2617.2385	1309.1229	24
4	486.2671	243.6372	469.2405	235.1239	468.2565	234.6319	R	2520.2221	1260.6147	2503.1956	1252.1014	2502.2116	1251.6094	23
5	599.3511	300.1792	582.3246	291.6659	581.3406	291.1739	L	2364.1210	1182.5641	2347.0945	1174.0509	2346.1104	1173.5589	22
6	**670.3883**	335.6978	653.3617	327.1845	652.3777	326.6925	A	2251.0369	1126.0221	2234.0104	1117.5088	2233.0264	1117.0168	21
7	727.4097	364.2085	710.3832	355.6952	709.3991	355.2032	G	2179.9998	1090.5036	2162.9733	1081.9903	2161.9893	1081.4983	20
8	855.5047	428.2560	838.4781	419.7427	837.4941	419.2507	K	2122.9784	1061.9928	2105.9518	1053.4795	2104.9678	1052.9875	19
9	952.5574	476.7824	935.5309	468.2691	934.5469	467.7771	P	***1994.8834***	997.9453	1977.8569	989.4321	1976.8728	988.9401	18
10	1053.6051	527.3062	1036.5786	518.7929	1035.5946	518.3009	T	1897.8306	949.4190	1880.8041	940.9057	1879.8201	940.4137	17
11	1190.6640	***595.8357***	1173.6375	587.3224	1172.6535	586.8304	H	1796.7830	898.8951	1779.7564	890.3818	1778.7724	889.8898	16
12	**1289.7324**	***645.3699***	1272.7059	636.8566	1271.7219	636.3646	V	***1659.7241***	830.3657	1642.6975	821.8524	1641.7135	821.3604	15
13	**1404.7594**	***702.8833***	1387.7328	694.3701	1386.7488	693.8781	N	***1560.6556***	780.8315	1543.6291	772.3182	1542.6451	771.8262	14
14	**1503.8278**	***752.4175***	1486.8013	743.9043	1485.8172	743.4123	V	***1445.6287***	723.3180			1427.6181	714.3127	13
15	1590.8598	***795.9336***	1573.8333	787.4203	1572.8493	786.9283	S	***1346.5603***	673.7838			1328.5497	664.7785	12
16	1689.9282	***845.4678***	1672.9017	836.9545	1671.9177	836.4625	V	1259.5283	630.2678			1241.5177	621.2625	11
17	1788.9967	***895.0020***	1771.9701	886.4887	1770.9861	885.9967	V	1160.4598	580.7336			1142.4493	571.7283	10
18	1936.0321	968.5197	1919.0055	960.0064	1918.0215	959.5144	M	***1061.3914***	531.1994			1043.3809	522.1941	9
19	2007.0692	***1004.0382***	1990.0426	995.5250	1989.0586	995.0329	A	***914.3560***	457.6817			896.3455	448.6764	8
20	2136.1118	***1068.5595***	2119.0852	1060.0462	2118.1012	1059.5542	E	843.3189	422.1631			825.3083	413.1578	7
21	2235.1802	***1118.0937***	2218.1536	1109.5805	2217.1696	1109.0884	V	***714.2763***	357.6418			696.2658	348.6365	6
22	2350.2071	***1175.6072***	2333.1806	1167.0939	2332.1966	1166.6019	D	***615.2079***	308.1076			597.1973	299.1023	5

23	2407.2286	***1204.1179***	2390.2020	1195.6047	2389.2180	1195.1126	**G**	***500.1810***	250.5941			482.1704	241.5888	**4**
24	2508.2763	***1254.6418***	2491.2497	1246.1285	2490.2657	1245.6365	**T**	443.1595	222.0834			425.1489	213.0781	**3**
25	2668.3069	1334.6571	2651.2804	1326.1438	2650.2964	1325.6518	**C**	***342.1118***	171.5595					**2**
26							**Y**	182.0812	91.5442					**1**



NCBI **BLAST** search of TIDRLAGKPTHVNVSVVMAEVDGTCY
(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	2848.3735	0.0141	TIDRLAGKPTHVNVSVVMAEVDGTCY
33.2	2847.3895	0.9981	TIDRLAGKPTHVNVSVVMAEVDGTCY
7.4	2846.3790	2.0087	SQPQGLVSLMGSPVAESAEQMAEARIK
7.1	2848.3839	0.0038	QDQQDPKSSSATASQPPESLPQPGLQK
4.7	2846.3949	1.9927	KSPMHDTTKFIGQAIVEPALYSPYH
3.8	2847.3742	1.0134	DPSARSNTEMALTLSAVQPCINSEIK
3.1	2846.3922	1.9954	ASCPSRPAGPGPGPGFSHIQLEFVGAPR
2.3	2847.3789	1.0087	LKDVQSMDELKDVYNHFLLYYGR
2.3	2848.3852	0.0024	TYSDSELGHVGSYLQGQRRTITHSR
2.3	2848.3852	0.0024	TYSDSELGHVGSYLQGQRRTITHSR

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

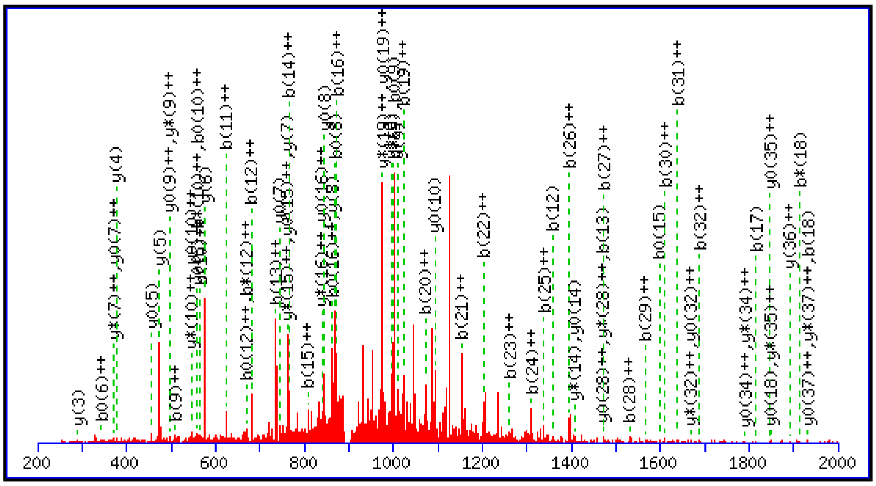
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGK**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

Match to Query 28986: 4485.304170 from(898.068110,5+) intensity(27659.8945) rtinseconds(2866) scans(7493) index(22377)
Title: 111019_Est_MI_YS_G_02Spectrum6519_scans__7493
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

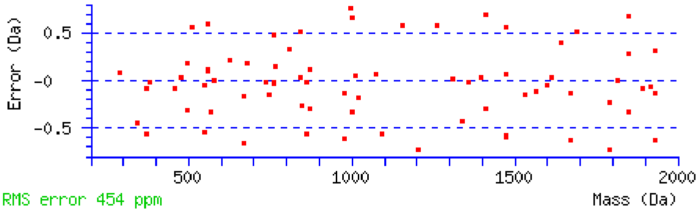
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

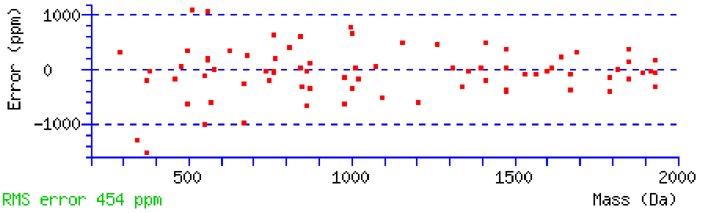


Monoisotopic mass of neutral peptide Mr(calc): 4485.2850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N18 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00017
Matches : 76/478 fragment ions using 160 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							42
2	201.1234	101.0653			183.1128	92.0600	S	4373.2082	2187.1077	4356.1816	2178.5945	4355.1976	2178.1025	41
3	314.2074	157.6074			296.1969	148.6021	L	4286.1762	2143.5917	4269.1496	2135.0784	4268.1656	2134.5864	40
4	451.2663	226.1368			433.2558	217.1315	H	4173.0921	2087.0497	4156.0656	2078.5364	4155.0815	2078.0444	39
5	607.3675	304.1874	590.3409	295.6741	589.3569	295.1821	R	4036.0332	2018.5202	4019.0066	2010.0070	4018.0226	2009.5150	38
6	704.4202	352.7137	687.3937	344.2005	686.4097	343.7085	P	3879.9321	1940.4697	3862.9055	1931.9564	3861.9215	1931.4644	37
7	775.4573	388.2323	758.4308	379.7190	757.4468	379.2270	A	3782.8793	1891.9433	3765.8528	1883.4300	3764.8688	1882.9380	36
8	888.5414	444.7743	871.5148	436.2611	870.5308	435.7691	L	3711.8422	1856.4247	3694.8157	1847.9115	3693.8316	1847.4195	35
9	1017.5840	***509.2956***	1000.5574	500.7824	999.5734	500.2904	E	3598.7581	1799.8827	3581.7316	1791.3694	3580.7476	1790.8774	34
10	1132.6109	***566.8091***	1115.5844	558.2958	1114.6004	557.8038	D	3469.7155	1735.3614	3452.6890	1726.8481	3451.7050	1726.3561	33
11	1245.6950	***623.3511***	1228.6684	614.8379	1227.6844	614.3459	L	3354.6886	1677.8479	3337.6621	1669.3347	3336.6780	1668.8427	32
12	1358.7791	***679.8932***	1341.7525	671.3799	1340.7685	670.8879	L	3241.6045	1621.3059	3224.5780	1612.7926	3223.5940	1612.3006	31
13	1471.8631	***736.4352***	1454.8366	727.9219	1453.8526	727.4299	L	3128.5205	1564.7639	3111.4939	1556.2506	3110.5099	1555.7586	30
14	1528.8846	***764.9459***	1511.8580	756.4327	1510.8740	755.9406	G	3015.4364	1508.2218	2998.4099	1499.7086	2997.4258	1499.2166	29
15	1615.9166	***808.4619***	1598.8901	799.9487	1597.9061	799.4567	S	2958.4149	1479.7111	2941.3884	1471.1978	2940.4044	1470.7058	28
16	1744.9592	***872.9832***	1727.9327	864.4700	1726.9486	863.9780	E	2871.3829	1436.1951	2854.3564	1427.6818	2853.3724	1427.1898	27
17	1815.9963	908.5018	1798.9698	899.9885	1797.9858	899.4965	A	2742.3403	1371.6738	2725.3138	1363.1605	2724.3298	1362.6685	26
18	1931.0233	966.0153	1913.9967	957.5020	1913.0127	957.0100	N	2671.3032	1336.1552	2654.2767	1327.6420	2653.2926	1327.1500	25
19	2044.1073	***1022.5573***	2027.0808	1014.0440	2026.0968	1013.5520	L	2556.2763	1278.6418	2539.2497	1270.1285	2538.2657	1269.6365	24
20	2145.1550	***1073.0811***	2128.1285	1064.5679	2127.1444	1064.0759	T	2443.1922	1222.0997	2426.1657	1213.5865	2425.1816	1213.0945	23
21	2305.1857	***1153.0965***	2288.1591	1144.5832	2287.1751	1144.0912	C	2342.1445	1171.5759	2325.1180	1163.0626	2324.1340	1162.5706	22
22	2406.2333	***1203.6203***	2389.2068	1195.1070	2388.2228	1194.6150	T	2182.1139	1091.5606	2165.0873	1083.0473	2164.1033	1082.5553	21
23	2519.3174	***1260.1623***	2502.2909	1251.6491	2501.3068	1251.1571	L	2081.0662	1041.0367	2064.0396	1032.5235	2063.0556	1032.0315	20

24	2620.3651	***1310.6862***	2603.3385	1302.1729	2602.3545	1301.6809	**T**	1967.9821	984.4947	1950.9556	975.9814	1949.9716	975.4894	**19**
25	2677.3865	***1339.1969***	2660.3600	1330.6836	2659.3760	1330.1916	**G**	1866.9345	933.9709	1849.9079	925.4576	1848.9239	924.9656	**18**
26	2790.4706	***1395.7389***	2773.4441	1387.2257	2772.4600	1386.7337	**L**	1809.9130	905.4601	1792.8864	896.9469	1791.9024	896.4549	**17**
27	2946.5717	***1473.7895***	2929.5452	1465.2762	2928.5612	1464.7842	**R**	1696.8289	848.9181	1679.8024	840.4048	1678.8184	839.9128	**16**
28	3061.5987	***1531.3030***	3044.5721	1522.7897	3043.5881	1522.2977	**D**	1540.7278	770.8675	1523.7013	762.3543	1522.7172	761.8623	**15**
29	3132.6358	***1566.8215***	3115.6092	1558.3083	3114.6252	1557.8162	**A**	1425.7009	713.3541	1408.6743	704.8408	1407.6903	704.3488	**14**
30	3219.6678	***1610.3375***	3202.6413	1601.8243	3201.6572	1601.3323	**S**	1354.6638	677.8355	1337.6372	669.3222	1336.6532	668.8302	**13**
31	3276.6893	***1638.8483***	3259.6627	1630.3350	3258.6787	1629.8430	**G**	1267.6317	634.3195	1250.6052	625.8062	1249.6212	625.3142	**12**
32	3375.7577	***1688.3825***	3358.7311	1679.8692	3357.7471	1679.3772	**V**	1210.6103	605.8088	1193.5837	597.2955	1192.5997	596.8035	**11**
33	3476.8054	1738.9063	3459.7788	1730.3930	3458.7948	1729.9010	**T**	1111.5419	556.2746	1094.5153	547.7613	1093.5313	547.2693	**10**
34	3623.8738	1812.4405	3606.8472	1803.9273	3605.8632	1803.4352	**F**	**1010.4942**	505.7507	993.4676	497.2374	992.4836	496.7454	**9**
35	3724.9215	1862.9644	3707.8949	1854.4511	3706.9109	1853.9591	**T**	**863.4258**	432.2165	846.3992	423.7032	845.4152	423.2112	**8**
36	3911.0008	1956.0040	3893.9742	1947.4907	3892.9902	1946.9987	**W**	**762.3781**	381.6927	745.3515	373.1794	744.3675	372.6874	**7**
37	4012.0484	2006.5279	3995.0219	1998.0146	3994.0379	1997.5226	**T**	**576.2988**	288.6530	559.2722	280.1397	558.2882	279.6477	**6**
38	4109.1012	2055.0542	4092.0747	2046.5410	4091.0906	2046.0490	**P**	**475.2511**	238.1292	458.2245	229.6159	457.2405	229.1239	**5**
39	4196.1332	2098.5703	4179.1067	2090.0570	4178.1227	2089.5650	**S**	**378.1983**	189.6028	361.1718	181.0895	360.1878	180.5975	**4**
40	4283.1653	2142.0863	4266.1387	2133.5730	4265.1547	2133.0810	**S**	**291.1663**	146.0868	274.1397	137.5735	273.1557	137.0815	**3**
41	4340.1867	2170.5970	4323.1602	2162.0837	4322.1762	2161.5917	**G**	204.1343	102.5708	187.1077	94.0575			**2**
42							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGK
(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	4485.2850	0.0192	LSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGK
44.5	4484.3010	1.0032	LSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGK
7.0	4483.2953	2.0089	ALALVRNPINSPIPQSTPVVPVFKPCNAMQEQVKLCSSIY
6.9	4484.2793	1.0248	ALALVRNPINSPIPQSTPVVPVFKPCNAMQEQVKLCSSIY
6.5	4484.3095	0.9947	GANVNRTTANNDHTVLSLACAGGHLAVVELLLAHGADPTHRLK
6.5	4484.3095	0.9947	GANVNRTTANNDHTVLSLACAGGHLAVVELLLAHGADPTHRLK
5.6	4484.3095	0.9947	GANVNRTTANNDHTVLSLACAGGHLAVVELLLAHGADPTHRLK
5.2	4484.3095	0.9947	GANVNRTTANNDHTVLSLACAGGHLAVVELLLAHGADPTHRLK
5.1	4483.2780	2.0261	VPMLTWSTCAFTIQAIENLLGDEGKPLFGALQNRQHNGLK
4.7	4485.2910	0.0132	TEKKPPPPPPPTAIEEEEDMSGLDVGLLVSLTTMIRPDQLK

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

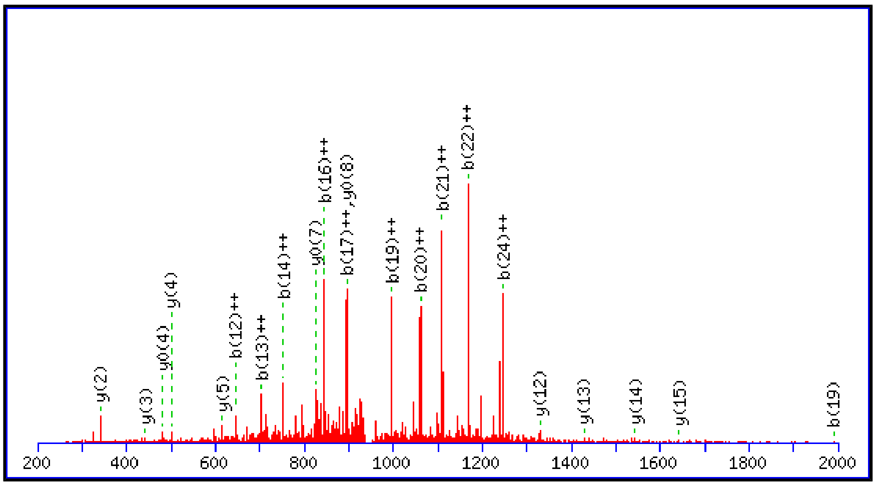
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIDRLAGKPTHVNVSVVMAEVDGTCY**
Found in **P01876** in **con_Xuniprot_HUMAN3**, IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

Match to Query 25751: 2832.387102 from(945.136310,3+) intensity(46664.5313) rtinseconds(1787) scans(4427) index(23282)
Title: 111019_Est_MI_YS_G_04Spectrum3811_scans__4427
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

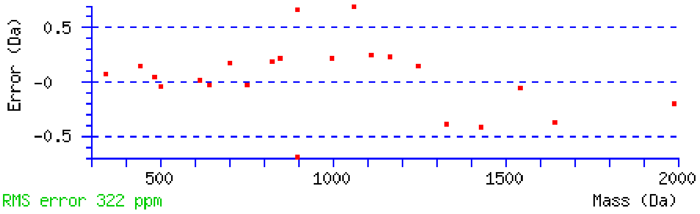
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

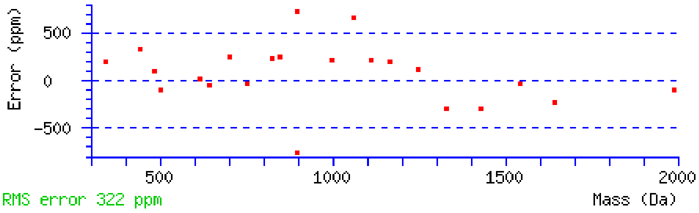


Monoisotopic mass of neutral peptide Mr(calc): 2832.3786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00047
Matches : 22/264 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							26
2	215.1390	108.0731			197.1285	99.0679	I	2732.3382	1366.6727	2715.3117	1358.1595	2714.3277	1357.6675	25
3	330.1660	165.5866			312.1554	156.5813	D	2619.2542	1310.1307	2602.2276	1301.6174	2601.2436	1301.1254	24
4	486.2671	243.6372	469.2405	235.1239	468.2565	234.6319	R	2504.2272	1252.6172	2487.2007	1244.1040	2486.2166	1243.6120	23
5	599.3511	300.1792	582.3246	291.6659	581.3406	291.1739	L	2348.1261	1174.5667	2331.0995	1166.0534	2330.1155	1165.5614	22
6	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	A	2235.0420	1118.0247	2218.0155	1109.5114	2217.0315	1109.0194	21
7	727.4097	364.2085	710.3832	355.6952	709.3991	355.2032	G	2164.0049	1082.5061	2146.9784	1073.9928	2145.9944	1073.5008	20
8	855.5047	428.2560	838.4781	419.7427	837.4941	419.2507	K	2106.9835	1053.9954	2089.9569	1045.4821	2088.9729	1044.9901	19
9	952.5574	476.7824	935.5309	468.2691	934.5469	467.7771	P	1978.8885	989.9479	1961.8619	981.4346	1960.8779	980.9426	18
10	1053.6051	527.3062	1036.5786	518.7929	1035.5946	518.3009	T	1881.8357	941.4215	1864.8092	932.9082	1863.8252	932.4162	17
11	1190.6640	595.8357	1173.6375	587.3224	1172.6535	586.8304	H	1780.7880	890.8977	1763.7615	882.3844	1762.7775	881.8924	16
12	1289.7324	***645.3699***	1272.7059	636.8566	1271.7219	636.3646	V	***1643.7291***	822.3682	1626.7026	813.8549	1625.7186	813.3629	15
13	1404.7594	***702.8833***	1387.7328	694.3701	1386.7488	693.8781	N	***1544.6607***	772.8340	1527.6342	764.3207	1526.6502	763.8287	14
14	1503.8278	***752.4175***	1486.8013	743.9043	1485.8172	743.4123	V	***1429.6338***	715.3205			1411.6232	706.3152	13
15	1590.8598	795.9336	1573.8333	787.4203	1572.8493	786.9283	S	***1330.5654***	665.7863			1312.5548	656.7810	12
16	1689.9282	***845.4678***	1672.9017	836.9545	1671.9177	836.4625	V	1243.5333	622.2703			1225.5228	613.2650	11
17	1788.9967	***895.0020***	1771.9701	886.4887	1770.9861	885.9967	V	1144.4649	572.7361			1126.4544	563.7308	10
18	1920.0371	960.5222	1903.0106	952.0089	1902.0266	951.5169	M	1045.3965	523.2019			1027.3859	514.1966	9
19	1991.0743	***996.0408***	1974.0477	987.5275	1973.0637	987.0355	A	914.3560	457.6817			896.3455	448.6764	8
20	2120.1169	***1060.5621***	2103.0903	1052.0488	2102.1063	1051.5568	E	843.3189	422.1631			825.3083	413.1578	7
21	2219.1853	***1110.0963***	2202.1587	1101.5830	2201.1747	1101.0910	V	714.2763	357.6418			696.2658	348.6365	6
22	2334.2122	***1167.6097***	2317.1857	1159.0965	2316.2016	1158.6045	D	***615.2079***	308.1076			597.1973	299.1023	5
23	2391.2337	1196.1205	2374.2071	1187.6072	2373.2231	1187.1152	G	***500.1810***	250.5941			482.1704	241.5888	4

24	2492.2814	***1246.6443***	2475.2548	1238.1310	2474.2708	1237.6390	**T**	***443.1595***	222.0834			425.1489	213.0781	**3**
25	2652.3120	1326.6596	2635.2855	1318.1464	2634.3014	1317.6544	**C**	***342.1118***	171.5595					**2**
26							**Y**	182.0812	91.5442					**1**





NCBI **BLAST** search of TIDRLAGKPTHVNVSVVMAEVDGTCY
(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	2832.3786	0.0085	TIDRLAGKPTHVNVSVVMAEVDGTCY
44.8	2831.3946	0.9925	TIDRLAGKPTHVNVSVVMAEVDGTCY
8.8	2832.3963	-0.0092	QVNSALKQKMEGGIEEFKPPESNQK
8.8	2832.3963	-0.0092	QVNSALKQKMEGGIEEFKPPESNQK
4.0	2832.3963	-0.0092	QVNSALKQKMEGGIEEFKPPESNQK
3.7	2830.3742	2.0129	LRNLNLLVDSAHRTFQICSDAPSAM
3.0	2830.3840	2.0031	SQPQGLVSLMGSPVAESAEQMAEARIK
3.0	2830.3840	2.0031	SQPQGLVSLMGSPVAESAEQMAEARIK
2.9	2832.3963	-0.0092	QVNSALKQKMEGGIEEFKPPESNQK
2.9	2832.3963	-0.0092	QVNSALKQKMEGGIEEFKPPESNQK

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

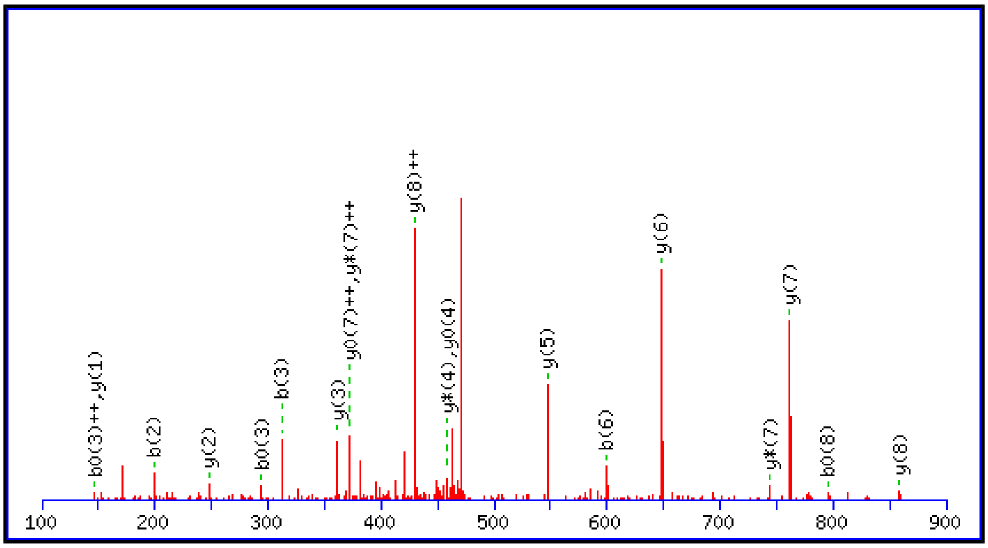
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TPLTANITK**
Found in **P01877** in **con_Xuniprot_HUMAN3**, IGHA2_HUMAN Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3

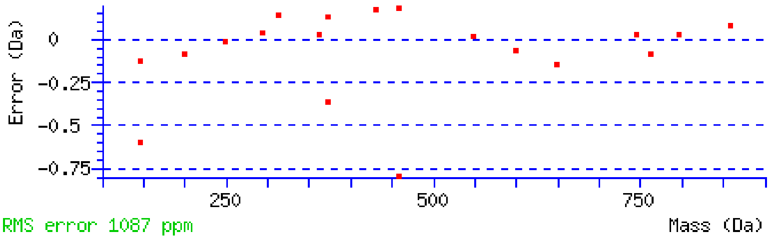
Match to Query 90: 958.534888 from(480.274720,2+) intensity(4797.5962) rtinseconds(584) scans(1092) index(11575)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum908_scans__1092
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

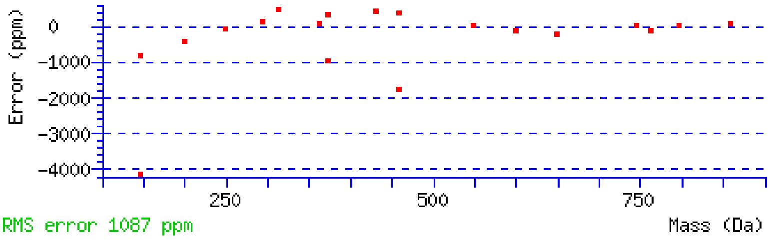
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 958.5335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00017
Matches : 19/84 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	102.0550	51.5311			84.0444	42.5258	T							9
2	**199.1077**	100.0575			181.0972	91.0522	P	***858.4931***	429.7502	841.4666	421.2369	840.4825	420.7449	8
3	**312.1918**	156.5995			294.1812	147.5942	L	***761.4403***	381.2238	744.4138	372.7105	743.4298	372.2185	7
4	413.2395	207.1234			395.2289	198.1181	T	***648.3563***	324.6818	631.3297	316.1685	630.3457	315.6765	6
5	484.2766	242.6419			466.2660	233.6366	A	***547.3086***	274.1579	530.2821	265.6447	529.2980	265.1527	5
6	**599.3035**	300.1554	582.2770	291.6421	581.2930	291.1501	N	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
7	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	I	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	3
8	813.4353	407.2213	796.4087	398.7080	795.4247	398.2160	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
9							K	***147.1128***	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.8	958.5335	0.0014	TPLTANITK
12.7	958.5349	0.0000	TFIGKTHR
8.5	958.5335	0.0014	TPTTALLDK
8.4	958.5335	0.0014	SLNSVPLTK
8.0	958.5335	0.0014	TINATLPTK
7.5	956.5291	2.0058	VVEISAPSR
6.0	958.5335	0.0014	EEVLQLTK
5.8	956.5291	2.0058	VKAQTAPNK
5.8	956.5291	2.0058	VKAQTAPNK
5.2	957.5317	1.0032	VPTLLRQM

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

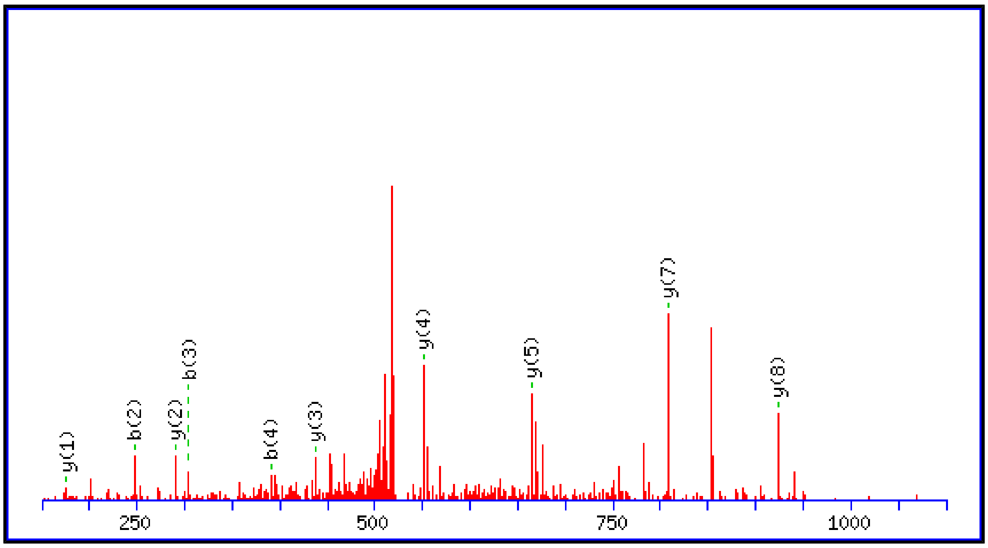
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDGSLNFNR**
Found in **P02671** in **con_Xuniprot_HUMAN3**, FIBA_HUMAN Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

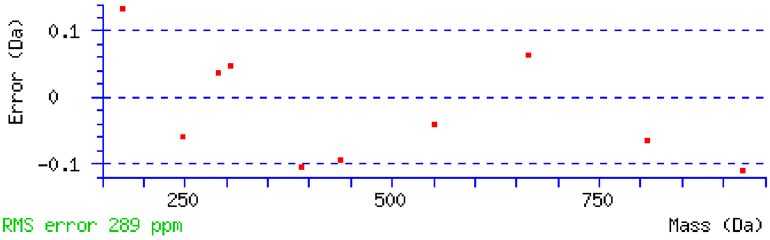
Match to Query 207: 1053.457028 from(527.735790,2+) intensity(5731.5474) rtinseconds(792) scans(1417) index(28810)
Title: 111019_Est_MI_YS_G_15Spectrum1157_scans__1417
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

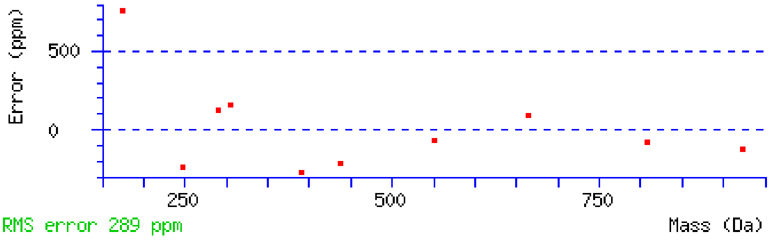
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1053.4549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.0034
Matches : 10/74 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	132.0478	66.5275					M							9
2	**247.0747**	124.0410			229.0641	115.0357	D	***923.4217***	462.2145	906.3952	453.7012	905.4112	453.2092	8
3	**304.0962**	152.5517			286.0856	143.5464	G	***808.3948***	404.7010	791.3682	396.1878	790.3842	395.6958	7
4	**391.1282**	196.0677			373.1176	187.0625	S	751.3733	376.1903	734.3468	367.6770	733.3628	367.1850	6
5	504.2123	252.6098			486.2017	243.6045	L	***664.3413***	332.6743	647.3148	324.1610			5
6	618.2552	309.6312	601.2286	301.1180	600.2446	300.6259	N	***551.2572***	276.1323	534.2307	267.6190			4
7	765.3236	383.1654	748.2971	374.6522	747.3130	374.1602	F	***437.2143***	219.1108	420.1878	210.5975			3
8	880.3505	440.6789	863.3240	432.1656	862.3400	431.6736	N	***290.1459***	145.5766	273.1193	137.0633			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.7	1053.4549	0.0021	MDGSLNFNR	Deamidated N8 99.25%
21.4	1053.4549	0.0021	MDGSLNFNR	Deamidated N6 0.75%
6.5	1052.4523	1.0048	EAREYNDR	
5.8	1053.4614	-0.0044	EYSQLEQR	
5.7	1053.4549	0.0021	FNEITCNR	
5.1	1053.4549	0.0021	NMDKFQDR	
4.8	1053.4549	0.0021	QNMLNDFR	
4.8	1053.4549	0.0021	QNMLNDFR	
4.7	1053.4614	-0.0044	LSQEEYER	
4.2	1053.4588	-0.0017	NHQEQQDR	

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

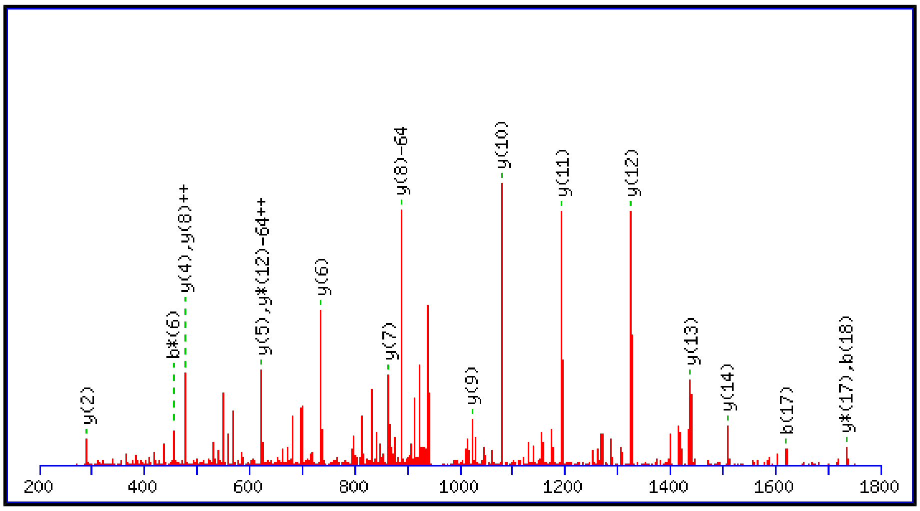
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

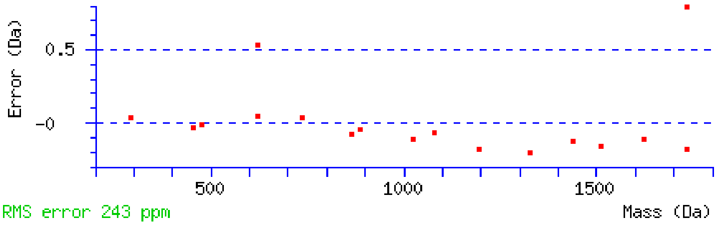
Match to Query 11494: 1908.838568 from(955.426560,2+) intensity(338346.1563) rtinseconds(1251) scans(3000) index(1961)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum2556_scans__3000
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

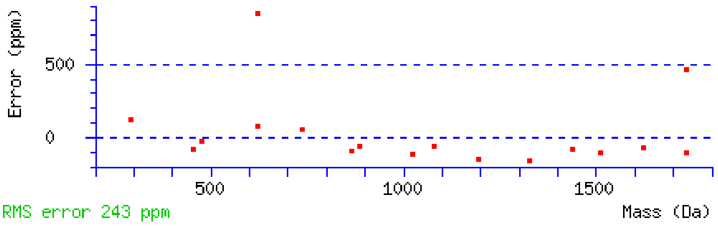
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1908.8306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N18 : Deamidated (NQ)
Ions Score: 113 **Expect:** 5e-010
Matches : 18/310 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	58.0287	29.5180					G							19
2	159.0764	80.0418			141.0659	71.0366	T	1852.8164	926.9118	1835.7898	918.3986	1834.8058	917.9066	18
3	230.1135	115.5604			212.1030	106.5551	A	1751.7687	876.3880	1734.7422	867.8747	1733.7581	867.3827	17
4	287.1350	144.0711			269.1244	135.0659	G	1680.7316	840.8694	1663.7050	832.3562	1662.7210	831.8642	16
5	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	N	1623.7101	812.3587	1606.6836	803.8454	1605.6996	803.3534	15
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	A	***1509.6672***	755.3372	1492.6407	746.8240	1491.6566	746.3320	14
7	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	L	***1438.6301***	719.8187	1421.6035	711.3054	1420.6195	710.8134	13
8	716.3396	358.6734	699.3130	350.1602	698.3290	349.6681	M	***1325.5460***	663.2767	1308.5195	654.7634	1307.5355	654.2714	12
9	831.3665	416.1869	814.3400	407.6736	813.3560	407.1816	D	***1194.5055***	597.7564	1177.4790	589.2431	1176.4950	588.7511	11
10	888.3880	444.6976	871.3614	436.1844	870.3774	435.6924	G	***1079.4786***	540.2429	1062.4521	531.7297	1061.4680	531.2377	10
11	959.4251	480.2162	942.3986	471.7029	941.4145	471.2109	A	***1022.4571***	511.7322	1005.4306	503.2189	1004.4466	502.7269	9
12	1046.4571	523.7322	1029.4306	515.2189	1028.4466	514.7269	S	951.4200	476.2136	934.3935	467.7004	933.4095	467.2084	8
13	1174.5157	587.7615	1157.4892	579.2482	1156.5051	578.7562	Q	***864.3880***	432.6976	847.3614	424.1844	846.3774	423.6924	7
14	1287.5998	644.3035	1270.5732	635.7903	1269.5892	635.2982	L	***736.3294***	368.6683	719.3029	360.1551	718.3189	359.6631	6
15	1434.6352	717.8212	1417.6086	709.3080	1416.6246	708.8159	M	***623.2454***	312.1263	606.2188	303.6130	605.2348	303.1210	5
16	1491.6566	746.3320	1474.6301	737.8187	1473.6461	737.3267	G	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	4
17	**1620.6992**	810.8533	1603.6727	802.3400	1602.6887	801.8480	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
18	**1735.7262**	868.3667	1718.6996	859.8535	1717.7156	859.3614	N	***290.1459***	145.5766	273.1193	137.0633			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
113.1	1908.8306	0.0080	GTAGNALMDGASQLMGENR	Deamidated N18, Oxidation M15; 100.00%
45.8	1908.8306	0.0080	GTAGNALMDGASQLMGENR	Deamidated Q13, Oxidation M15; 0.00%
20.6	1908.8306	0.0080	GTAGNALMDGASQLMGENR	Deamidated N18, Oxidation M8; 0.00%
10.3	1908.8306	0.0080	GTAGNALMDGASQLMGENR	Deamidated N5, Oxidation M15; 0.00%
9.5	1908.8306	0.0080	GTAGNALMDGASQLMGENR	Deamidated Q13, Oxidation M8; 0.00%

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

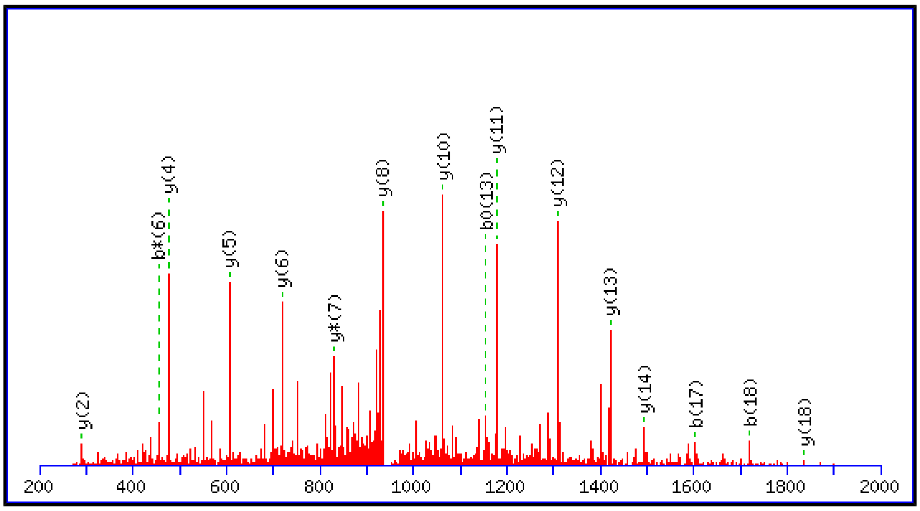
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

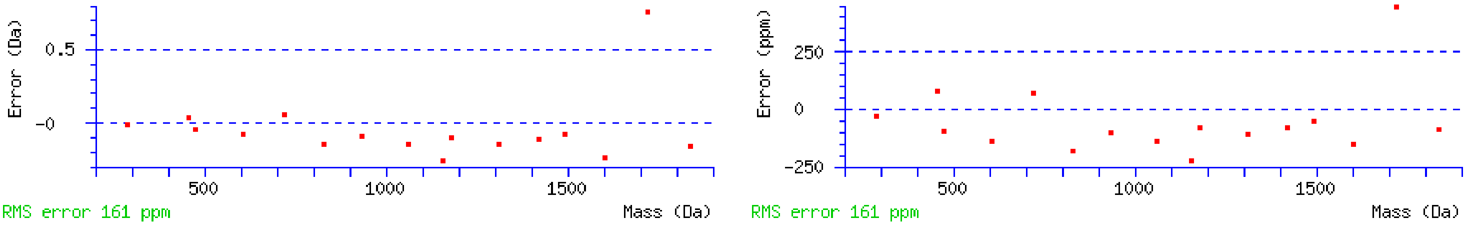
Match to Query 11219: 1892.837848 from(947.426200,2+) intensity(28318.0117) rtinseconds(1780) scans(4667) index(4460)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3956_scans__4667
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1892.8356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N18 : Deamidated (NQ)
Ions Score: 113 **Expect:** 5.9e-010
Matches : 17/202 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	58.0287	29.5180					G							19
2	159.0764	80.0418			141.0659	71.0366	T	***1836.8215***	918.9144	1819.7949	910.4011	1818.8109	909.9091	18
3	230.1135	115.5604			212.1030	106.5551	A	1735.7738	868.3905	1718.7472	859.8773	1717.7632	859.3853	17
4	287.1350	144.0711			269.1244	135.0659	G	1664.7367	832.8720	1647.7101	824.3587	1646.7261	823.8667	16
5	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	N	1607.7152	804.3612	1590.6887	795.8480	1589.7047	795.3560	15
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	A	***1493.6723***	747.3398	1476.6457	738.8265	1475.6617	738.3345	14
7	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	L	***1422.6352***	711.8212	1405.6086	703.3080	1404.6246	702.8159	13
8	716.3396	358.6734	699.3130	350.1602	698.3290	349.6681	M	***1309.5511***	655.2792	1292.5246	646.7659	1291.5405	646.2739	12
9	**831.3665**	416.1869	814.3400	407.6736	813.3560	407.1816	D	***1178.5106***	589.7590	1161.4841	581.2457	1160.5001	580.7537	11
10	888.3880	444.6976	871.3614	436.1844	870.3774	435.6924	G	***1063.4837***	532.2455	1046.4571	523.7322	1045.4731	523.2402	10
11	959.4251	480.2162	942.3986	471.7029	941.4145	471.2109	A	1006.4622	503.7347	989.4357	495.2215	988.4517	494.7295	9
12	1046.4571	523.7322	1029.4306	515.2189	1028.4466	514.7269	S	***935.4251***	468.2162	918.3986	459.7029	917.4145	459.2109	8
13	1174.5157	587.7615	1157.4892	579.2482	1156.5051	578.7562	Q	848.3931	424.7002	831.3665	416.1869	830.3825	415.6949	7
14	1287.5998	644.3035	1270.5732	635.7903	1269.5892	635.2982	L	***720.3345***	360.6709	703.3080	352.1576	702.3239	351.6656	6
15	1418.6403	709.8238	1401.6137	701.3105	1400.6297	700.8185	M	***607.2504***	304.1289	590.2239	295.6156	589.2399	295.1236	5
16	1475.6617	738.3345	1458.6352	729.8212	1457.6512	729.3292	G	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	4
17	**1604.7043**	802.8558	1587.6778	794.3425	1586.6938	793.8505	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
18	**1719.7313**	860.3693	1702.7047	851.8560	1701.7207	851.3640	N	***290.1459***	145.5766	273.1193	137.0633			2
19							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
112.8	1892.8356	0.0022	GTAGNALMDGASQLMGENR	Deamidated N18 100.00%
42.3	1892.8356	0.0022	GTAGNALMDGASQLMGENR	Deamidated Q13 0.00%
7.5	1892.8460	-0.0081	ENKQASTSNTRAQGQNR	
5.0	1892.8356	0.0022	GTAGNALMDGASQLMGENR	Deamidated N5 0.00%
3.9	1892.8460	-0.0081	ENKQASTSNTRAQGQNR	
3.9	1892.8460	-0.0081	ENKQASTSNTRAQGQNR	
1.3	1892.8460	-0.0081	ENKQASTSNTRAQGQNR	

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

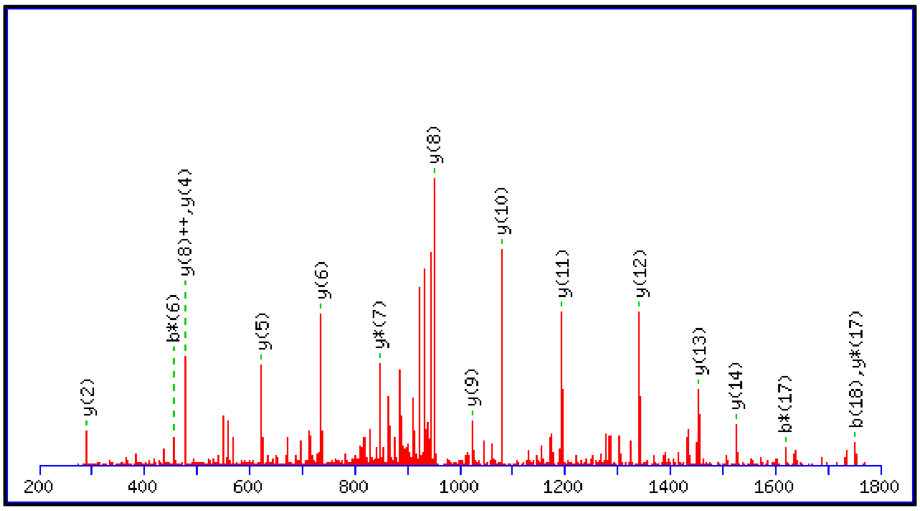
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

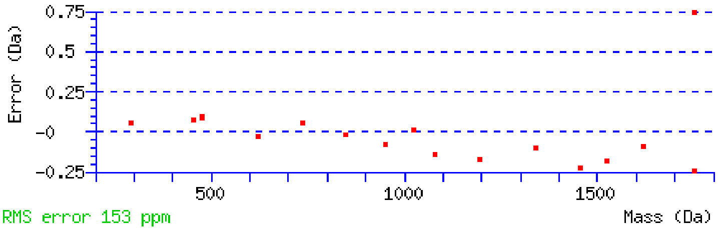
Match to Query 11695: 1924.832728 from(963.423640,2+) intensity(230297.8750) rtinseconds(944) scans(2139) index(9372)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum1806_scans__2139
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

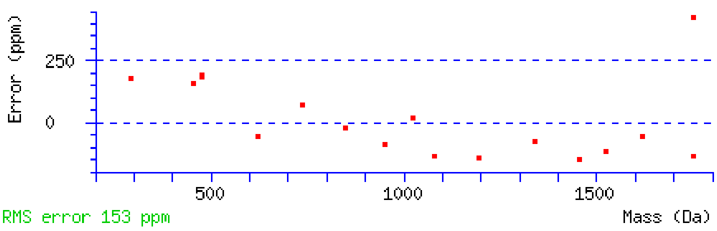
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1924.8255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M15    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N18    : Deamidated (NQ)
Ions Score: 113  Expect: 4.3e-010
Matches : 18/352 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	58.0287	29.5180					G							19
2	159.0764	80.0418			141.0659	71.0366	T	1868.8113	934.9093	1851.7848	926.3960	1850.8007	925.9040	18
3	230.1135	115.5604			212.1030	106.5551	A	1767.7636	884.3855	1750.7371	875.8722	1749.7531	875.3802	17
4	287.1350	144.0711			269.1244	135.0659	G	1696.7265	848.8669	1679.7000	840.3536	1678.7159	839.8616	16
5	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	N	1639.7050	820.3562	1622.6785	811.8429	1621.6945	811.3509	15
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	A	***1525.6621***	763.3347	1508.6356	754.8214	1507.6516	754.3294	14
7	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	L	***1454.6250***	727.8161	1437.5985	719.3029	1436.6144	718.8109	13
8	732.3345	366.6709	715.3080	358.1576	714.3239	357.6656	M	***1341.5409***	671.2741	1324.5144	662.7608	1323.5304	662.2688	12
9	**847.3614**	424.1844	830.3349	415.6711	829.3509	415.1791	D	***1194.5055***	597.7564	1177.4790	589.2431	1176.4950	588.7511	11
10	904.3829	452.6951	887.3564	444.1818	886.3723	443.6898	G	***1079.4786***	540.2429	1062.4521	531.7297	1061.4680	531.2377	10
11	975.4200	488.2136	958.3935	479.7004	957.4095	479.2084	A	***1022.4571***	511.7322	1005.4306	503.2189	1004.4466	502.7269	9
12	1062.4521	531.7297	1045.4255	523.2164	1044.4415	522.7244	S	***951.4200***	476.2136	934.3935	467.7004	933.4095	467.2084	8
13	1190.5106	595.7590	1173.4841	587.2457	1172.5001	586.7537	Q	864.3880	432.6976	847.3614	424.1844	846.3774	423.6924	7
14	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	L	***736.3294***	368.6683	719.3029	360.1551	718.3189	359.6631	6
15	1450.6301	725.8187	1433.6035	717.3054	1432.6195	716.8134	M	***623.2454***	312.1263	606.2188	303.6130	605.2348	303.1210	5
16	1507.6516	754.3294	1490.6250	745.8161	1489.6410	745.3241	G	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	4
17	1636.6942	818.8507	1619.6676	810.3374	1618.6836	809.8454	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
18	**1751.7211**	876.3642	1734.6945	867.8509	1733.7105	867.3589	N	***290.1459***	145.5766	273.1193	137.0633			2
19							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
112.7	1924.8255	0.0073	GTAGNALMDGASQLMGENR	Deamidated N18 100.00%
45.5	1924.8255	0.0073	GTAGNALMDGASQLMGENR	Deamidated Q13 0.00%
11.5	1924.8255	0.0073	GTAGNALMDGASQLMGENR	Deamidated N5 0.00%
7.3	1924.8360	-0.0033	ALANVFDDLEVMGNENR	
5.3	1924.8393	-0.0066	MQIEMENKGENSDLIR	
3.9	1924.8393	-0.0066	MQIEMENKGENSDLIR	
3.4	1924.8407	-0.0080	AWMAVDGAVGSAPNSSSMR	

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

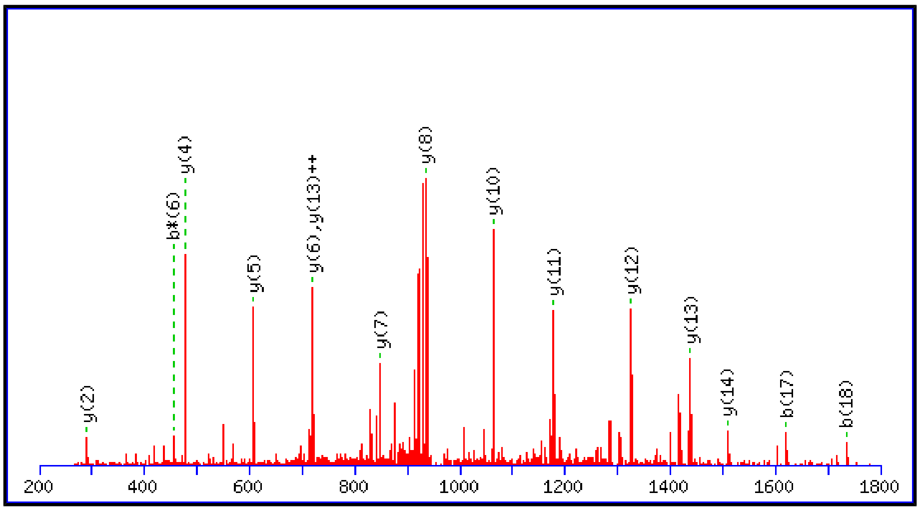
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

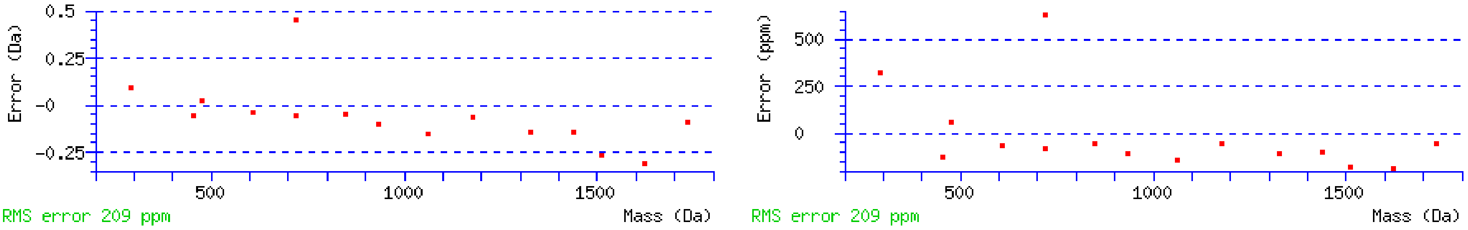
Match to Query 11499: 1908.838848 from(955.426700,2+) intensity(175680.4531) rtinseconds(1331) scans(3219) index(14466)
Title: 111019_Est_MI_YP_G_03Spectrum2751_scans__3219
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1908.8306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N18 : Deamidated (NQ)
Ions Score: 100 **Expect:** 9.4e-009
Matches : 15/310 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	58.0287	29.5180					**G**							**19**
2	159.0764	80.0418			141.0659	71.0366	**T**	1852.8164	926.9118	1835.7898	918.3986	1834.8058	917.9066	**18**
3	230.1135	115.5604			212.1030	106.5551	**A**	1751.7687	876.3880	1734.7422	867.8747	1733.7581	867.3827	**17**
4	287.1350	144.0711			269.1244	135.0659	**G**	1680.7316	840.8694	1663.7050	832.3562	1662.7210	831.8642	**16**
5	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	**N**	1623.7101	812.3587	1606.6836	803.8454	1605.6996	803.3534	**15**
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	**A**	***1509.6672***	755.3372	1492.6407	746.8240	1491.6566	746.3320	**14**
7	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	**L**	***1438.6301***	719.8187	1421.6035	711.3054	1420.6195	710.8134	**13**
8	732.3345	366.6709	715.3080	358.1576	714.3239	357.6656	**M**	***1325.5460***	663.2767	1308.5195	654.7634	1307.5355	654.2714	**12**
9	847.3614	424.1844	830.3349	415.6711	829.3509	415.1791	**D**	***1178.5106***	589.7590	1161.4841	581.2457	1160.5001	580.7537	**11**
10	904.3829	452.6951	887.3564	444.1818	886.3723	443.6898	**G**	***1063.4837***	532.2455	1046.4571	523.7322	1045.4731	523.2402	**10**
11	975.4200	488.2136	958.3935	479.7004	957.4095	479.2084	**A**	1006.4622	503.7347	989.4357	495.2215	988.4517	494.7295	**9**
12	1062.4521	531.7297	1045.4255	523.2164	1044.4415	522.7244	**S**	***935.4251***	468.2162	918.3986	459.7029	917.4145	459.2109	**8**
13	1190.5106	595.7590	1173.4841	587.2457	1172.5001	586.7537	**Q**	***848.3931***	424.7002	831.3665	416.1869	830.3825	415.6949	**7**
14	1303.5947	652.3010	1286.5681	643.7877	1285.5841	643.2957	**L**	***720.3345***	360.6709	703.3080	352.1576	702.3239	351.6656	**6**
15	1434.6352	717.8212	1417.6086	709.3080	1416.6246	708.8159	**M**	***607.2504***	304.1289	590.2239	295.6156	589.2399	295.1236	**5**
16	1491.6566	746.3320	1474.6301	737.8187	1473.6461	737.3267	**G**	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	**4**
17	**1620.6992**	810.8533	1603.6727	802.3400	1602.6887	801.8480	**E**	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	**3**
18	**1735.7262**	868.3667	1718.6996	859.8535	1717.7156	859.3614	**N**	***290.1459***	145.5766	273.1193	137.0633			**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
100.4	1908.8306	0.0083	GTAGNALMDGASQLMGENR	Deamidated N18, Oxidation M8; 100.00%
40.5	1908.8306	0.0083	GTAGNALMDGASQLMGENR	Deamidated Q13, Oxidation M8; 0.00%
26.9	1908.8306	0.0083	GTAGNALMDGASQLMGENR	Deamidated N18, Oxidation M15; 0.00%
14.7	1908.8306	0.0083	GTAGNALMDGASQLMGENR	Deamidated Q13, Oxidation M15; 0.00%
6.8	1908.8306	0.0083	GTAGNALMDGASQLMGENR	Deamidated N5, Oxidation M8; 0.00%
6.2	1908.8411	-0.0022	ALANVFDDLEVMGNENR	
1.5	1908.8411	-0.0023	GKQSETMNLGSAPDWTGI	

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

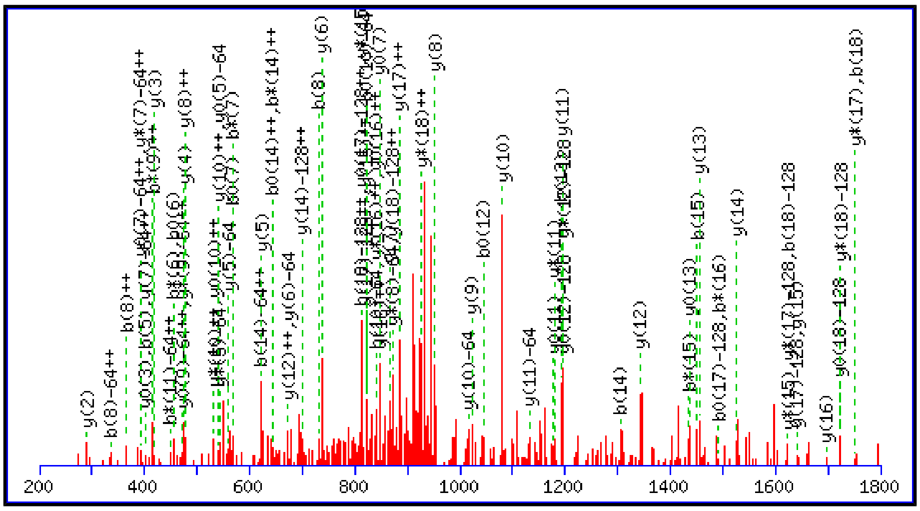
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

Match to Query 11732: 1925.812588 from(963.913570,2+) intensity(3139.1653) rtinseconds(1087) scans(2174) index(7575)
Title: 111019_Est_ISCardio_NMI_YP_G_12Spectrum1843_scans__2174
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

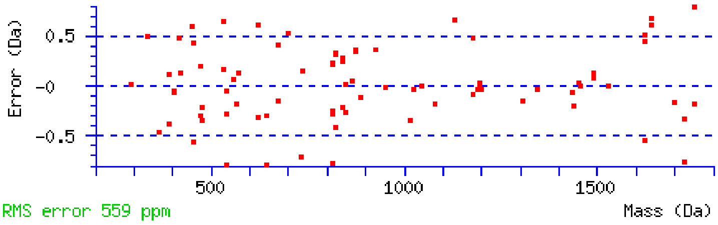
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

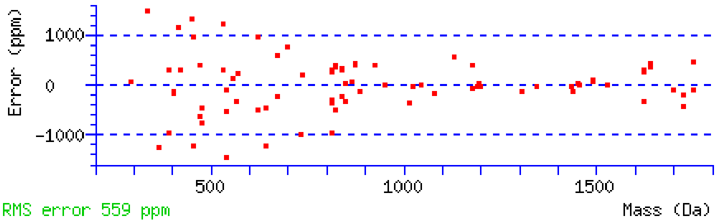


Monoisotopic mass of neutral peptide Mr(calc): 1925.8095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q13 : Deamidated (NQ)
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N18 : Deamidated (NQ)
Ions Score: 62 **Expect:** 3.2e-005
Matches : 86/352 fragment ions using 146 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							19
2	159.0764	80.0418			141.0659	71.0366	T	1869.7953	935.4013	1852.7688	926.8880	1851.7848	926.3960	18
3	230.1135	115.5604			212.1030	106.5551	A	1768.7476	884.8775	1751.7211	876.3642	1750.7371	875.8722	17
4	287.1350	144.0711			269.1244	135.0659	G	***1697.7105***	849.3589	1680.6840	840.8456	1679.7000	840.3536	16
5	**401.1779**	201.0926	384.1514	192.5793	383.1674	192.0873	N	***1640.6891***	820.8482	1623.6625	812.3349	1622.6785	811.8429	15
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	A	***1526.6461***	763.8267	1509.6196	755.3134	1508.6356	754.8214	14
7	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	L	***1455.6090***	728.3081	1438.5825	719.7949	1437.5985	719.3029	13
8	**732.3345**	366.6709	715.3080	358.1576	714.3239	357.6656	M	***1342.5250***	671.7661	1325.4984	663.2528	1324.5144	662.7608	12
9	**847.3614**	424.1844	830.3349	415.6711	829.3509	415.1791	D	***1195.4896***	598.2484	1178.4630	589.7351	1177.4790	589.2431	11
10	904.3829	452.6951	887.3564	444.1818	886.3723	443.6898	G	***1080.4626***	540.7349	1063.4361	532.2217	1062.4521	531.7297	10
11	975.4200	488.2136	958.3935	479.7004	957.4095	479.2084	A	***1023.4412***	512.2242	1006.4146	503.7109	1005.4306	503.2189	9
12	1062.4521	531.7297	1045.4255	523.2164	1044.4415	522.7244	S	***952.4040***	476.7057	935.3775	468.1924	934.3935	467.7004	8
13	**1191.4946**	596.2510	1174.4681	587.7377	1173.4841	587.2457	Q	***865.3720***	433.1896	848.3455	424.6764	847.3614	424.1844	7
14	**1304.5787**	652.7930	1287.5522	644.2797	1286.5681	643.7877	L	***736.3294***	368.6683	719.3029	360.1551	718.3189	359.6631	6
15	**1451.6141**	726.3107	1434.5876	717.7974	1433.6035	717.3054	M	***623.2454***	312.1263	606.2188	303.6130	605.2348	303.1210	5
16	1508.6356	754.8214	1491.6090	746.3082	1490.6250	745.8161	G	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	4
17	1637.6782	819.3427	1620.6516	810.8294	1619.6676	810.3374	E	***419.1885***	210.0979	402.1619	201.5846	401.1779	201.0926	3
18	**1752.7051**	876.8562	1735.6786	868.3429	1734.6945	867.8509	N	***290.1459***	145.5766	273.1193	137.0633			2

19							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.2	1925.8095	0.0031	GTAGNALMDGASQLMGENR	Deamidated Q13, N18 100.00%
11.3	1925.8095	0.0031	GTAGNALMDGASQLMGENR	Deamidated N5, N18 0.00%

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

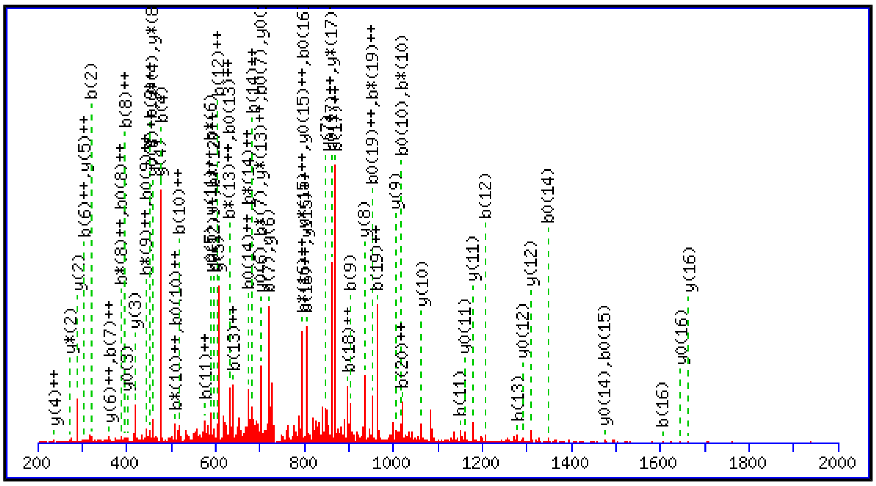
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YRGTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

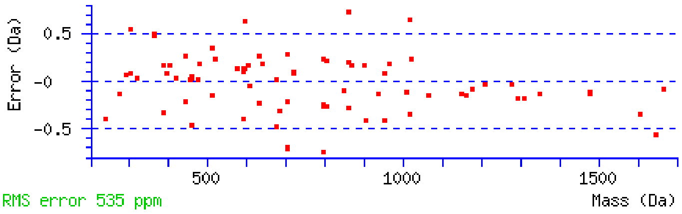
Match to Query 14868: 2212.004622 from(738.342150,3+) intensity(109300.4766) rtinseconds(1577) scans(4010) index(2699)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum3389_scans__4010
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

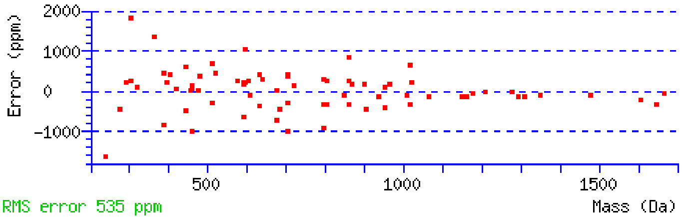
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2212.0001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 62 **Expect:** 0.00012
Matches : 82/228 fragment ions using 129 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							21
2	**320.1717**	160.5895	303.1452	152.0762			R	2049.9440	1025.4757	2032.9175	1016.9624	2031.9335	1016.4704	20
3	377.1932	189.1002	360.1666	180.5870			G	1893.8429	947.4251	1876.8164	938.9118	1875.8324	938.4198	19
4	**478.2409**	239.6241	461.2143	231.1108	460.2303	230.6188	T	1836.8215	918.9144	1819.7949	910.4011	1818.8109	909.9091	18
5	549.2780	275.1426	532.2514	266.6294	531.2674	266.1373	A	1735.7738	868.3905	1718.7472	859.8773	1717.7632	859.3853	17
6	606.2994	***303.6534***	589.2729	295.1401	588.2889	294.6481	G	**1664.7367**	832.8720	1647.7101	824.3587	1646.7261	823.8667	16
7	**720.3424**	***360.6748***	703.3158	352.1615	702.3318	351.6695	N	1607.7152	804.3612	1590.6887	795.8480	1589.7047	795.3560	15
8	791.3795	***396.1934***	774.3529	387.6801	773.3689	387.1881	A	1493.6723	747.3398	1476.6457	738.8265	1475.6617	738.3345	14
9	**904.4635**	***452.7354***	887.4370	444.2221	886.4530	443.7301	L	1422.6352	711.8212	1405.6086	703.3080	1404.6246	702.8159	13
10	1035.5040	***518.2557***	1018.4775	509.7424	1017.4935	509.2504	M	**1309.5511**	655.2792	1292.5246	646.7659	1291.5405	646.2739	12
11	**1150.5310**	***575.7691***	1133.5044	567.2558	1132.5204	566.7638	D	**1178.5106**	589.7590	1161.4841	581.2457	1160.5001	580.7537	11
12	**1207.5524**	***604.2799***	1190.5259	595.7666	1189.5419	595.2746	G	**1063.4837**	532.2455	1046.4571	523.7322	1045.4731	523.2402	10
13	**1278.5895**	***639.7984***	1261.5630	631.2851	1260.5790	630.7931	A	**1006.4622**	503.7347	989.4357	495.2215	988.4517	494.7295	9
14	1365.6216	***683.3144***	1348.5950	674.8012	1347.6110	674.3091	S	**935.4251**	468.2162	918.3986	459.7029	917.4145	459.2109	8
15	1493.6802	747.3437	1476.6536	738.8304	1475.6696	738.3384	Q	**848.3931**	424.7002	831.3665	416.1869	830.3825	415.6949	7
16	**1606.7642**	***803.8857***	1589.7377	795.3725	1588.7537	794.8805	L	**720.3345**	360.6709	703.3080	352.1576	702.3239	351.6656	6
17	1737.8047	***869.4060***	1720.7782	860.8927	1719.7941	860.4007	M	**607.2504**	304.1289	590.2239	295.6156	589.2399	295.1236	5
18	1794.8262	***897.9167***	1777.7996	889.4034	1776.8156	888.9114	G	**476.2100**	238.6086	459.1834	230.0953	458.1994	229.6033	4
19	1923.8688	***962.4380***	1906.8422	953.9247	1905.8582	953.4327	E	**419.1885**	210.0979	402.1619	201.5846	401.1779	201.0926	3
20	2038.8957	***1019.9515***	2021.8692	1011.4382	2020.8851	1010.9462	N	**290.1459**	145.5766	273.1193	137.0633			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.6	2212.0001	0.0046	YRGTAGNALMDGASQLMGENR	Deamidated N20 58.08%
60.2	2212.0001	0.0046	YRGTAGNALMDGASQLMGENR	Deamidated Q15 41.78%
35.5	2212.0001	0.0046	YRGTAGNALMDGASQLMGENR	Deamidated N7 0.14%
14.2	2210.9945	1.0101	VKSMQMFHMPITSAMQGDR	
13.3	2212.0140	-0.0094	TFNLMPNLDDVVRDSMGQK	
12.9	2210.9945	1.0101	VKSMQMFHMPITSAMQGDR	
11.4	2212.0140	-0.0094	VMDVFQVAIEEGCRSQAEK	
9.9	2210.9945	1.0101	VKSMQMFHMPITSAMQGDR	
8.9	2212.0140	-0.0094	TFNLMPNLDDVVRDSMGQK	
8.0	2210.9945	1.0101	VKSMQMFHMPITSAMQGDR	

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

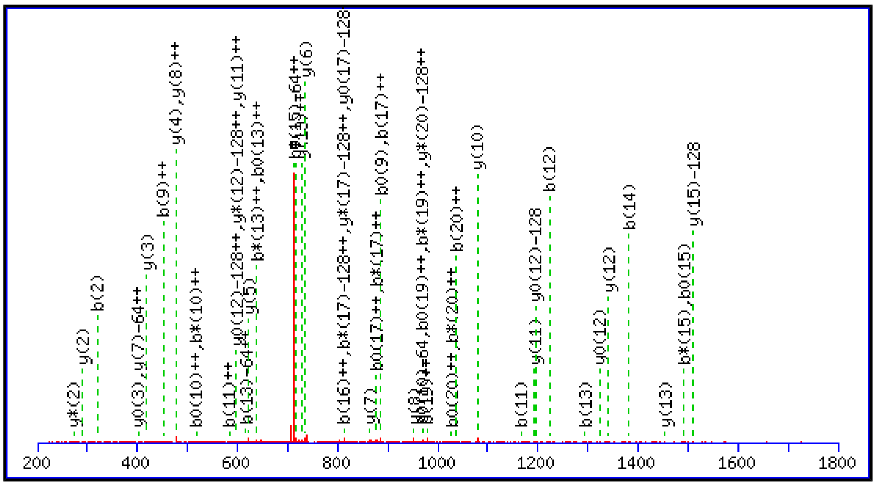
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YRGTAGNALMDGASQLMGENR**
Found in **D6REL8** in **con_Xuniprot_HUMAN3**, D6REL8_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=2 SV=1

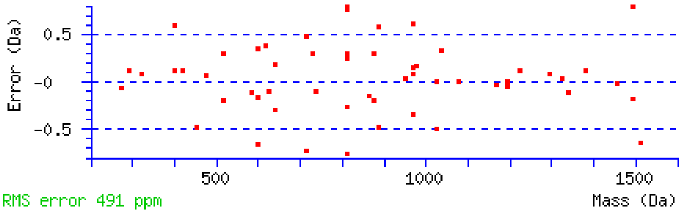
Match to Query 14996: 2243.994402 from(749.005410,3+) intensity(273908.9063) rtinseconds(767) scans(1704) index(2513)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1441_scans__1704
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

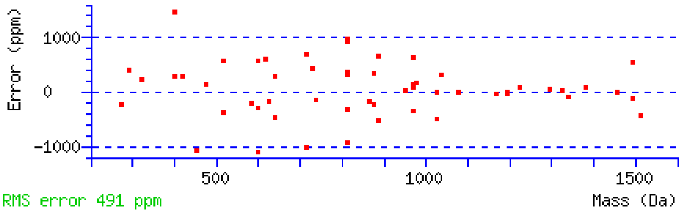
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2243.9899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N20 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00022
Matches : 57/390 fragment ions using 58 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							21
2	**320.1717**	160.5895	303.1452	152.0762			R	2081.9339	1041.4706	2064.9073	1032.9573	2063.9233	1032.4653	20
3	377.1932	189.1002	360.1666	180.5870			G	1925.8328	963.4200	1908.8062	954.9067	1907.8222	954.4147	19
4	478.2409	239.6241	461.2143	231.1108	460.2303	230.6188	T	1868.8113	934.9093	1851.7848	926.3960	1850.8007	925.9040	18
5	549.2780	275.1426	532.2514	266.6294	531.2674	266.1373	A	1767.7636	884.3855	1750.7371	875.8722	1749.7531	875.3802	17
6	606.2994	303.6534	589.2729	295.1401	588.2889	294.6481	G	1696.7265	848.8669	1679.7000	840.3536	1678.7159	839.8616	16
7	720.3424	360.6748	703.3158	352.1615	702.3318	351.6695	N	1639.7050	820.3562	1622.6785	811.8429	1621.6945	811.3509	15
8	791.3795	396.1934	774.3529	387.6801	773.3689	387.1881	A	1525.6621	763.3347	1508.6356	754.8214	1507.6516	754.3294	14
9	904.4635	**452.7354**	887.4370	444.2221	886.4530	443.7301	L	***1454.6250***	727.8161	1437.5985	719.3029	1436.6144	718.8109	13
10	1051.4989	526.2531	1034.4724	517.7398	1033.4884	517.2478	M	***1341.5409***	671.2741	1324.5144	662.7608	1323.5304	662.2688	12
11	**1166.5259**	**583.7666**	1149.4993	575.2533	1148.5153	574.7613	D	***1194.5055***	597.7564	1177.4790	589.2431	1176.4950	588.7511	11
12	**1223.5473**	612.2773	1206.5208	603.7640	1205.5368	603.2720	G	***1079.4786***	540.2429	1062.4521	531.7297	1061.4680	531.2377	10
13	**1294.5845**	647.7959	1277.5579	639.2826	1276.5739	638.7906	A	1022.4571	511.7322	1005.4306	503.2189	1004.4466	502.7269	9
14	**1381.6165**	691.3119	1364.5899	682.7986	1363.6059	682.3066	S	***951.4200***	476.2136	934.3935	467.7004	933.4095	467.2084	8
15	1509.6751	755.3412	1492.6485	746.8279	1491.6645	746.3359	Q	***864.3880***	432.6976	847.3614	424.1844	846.3774	423.6924	7
16	1622.7591	**811.8832**	1605.7326	803.3699	1604.7486	802.8779	L	***736.3294***	368.6683	719.3029	360.1551	718.3189	359.6631	6
17	1769.7945	**885.4009**	1752.7680	876.8876	1751.7840	876.3956	M	***623.2454***	312.1263	606.2188	303.6130	605.2348	303.1210	5
18	1826.8160	913.9116	1809.7894	905.3984	1808.8054	904.9064	G	***476.2100***	238.6086	459.1834	230.0953	458.1994	229.6033	4
19	1955.8586	**978.4329**	1938.8320	969.9197	1937.8480	969.4277	E	***419.1885***	210.0979	402.1619	201.5846	401.1779	201.0926	3
20	2070.8855	**1035.9464**	2053.8590	1027.4331	2052.8750	1026.9411	N	***290.1459***	145.5766	273.1193	137.0633			2
21							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.0	2243.9899	0.0045	YRGTAGNALMDGASQLMGENR	Deamidated N20 97.24%
42.4	2243.9899	0.0045	YRGTAGNALMDGASQLMGENR	Deamidated Q15 2.71%
25.5	2243.9899	0.0045	YRGTAGNALMDGASQLMGENR	Deamidated N7 0.06%
6.1	2242.9987	0.9957	HACYGVSVLNSYNELMVDR	
5.7	2242.9915	1.0029	DFMLMADDVKGFQEFYQK	
5.5	2244.0038	-0.0094	GPMPSPPPNQSSIQVKMSGNR	
5.5	2244.0005	-0.0061	SDQLQQAVQSQGFINYCQK	
5.5	2244.0005	-0.0061	SDQLQQAVQSQGFINYCQK	
5.5	2244.0005	-0.0061	SDQLQQAVQSQGFINYCQK	
5.4	2244.0045	-0.0101	DPDAYKFIFSNAGQLGDPCK	

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

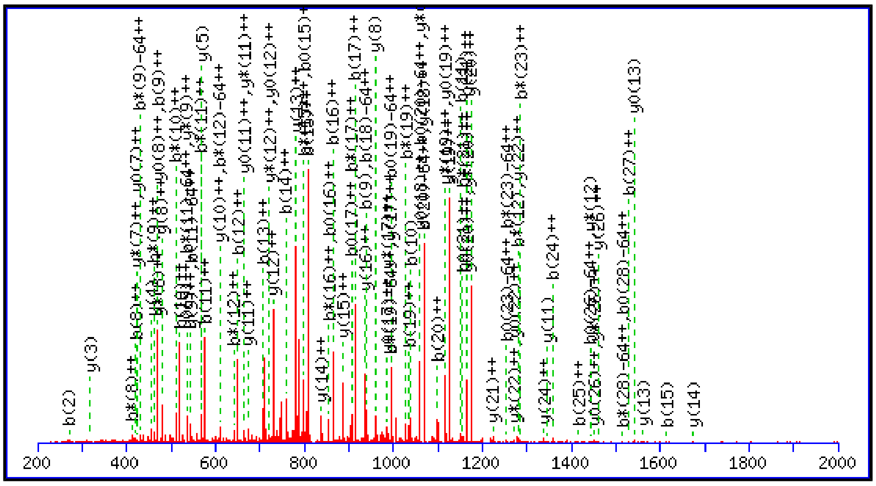
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNPPMGGNVVIFDTVITNQEEPYQNHSGR**
Found in **P02745** in **con_Xuniprot_HUMAN3**, C1QA_HUMAN Complement C1q subcomponent subunit A OS=Homo sapiens GN=C1QA PE=1 SV=2

Match to Query 27412: 3285.552296 from(822.395350,4+) intensity(78405.9766) rtinseconds(1329) scans(3286) index(1254)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum2842_scans__3286
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

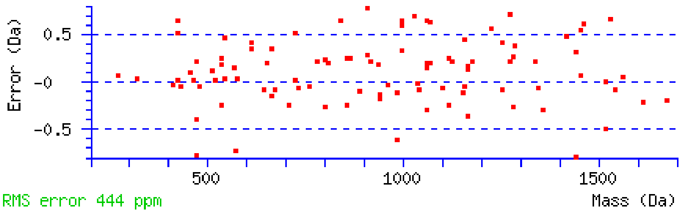
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

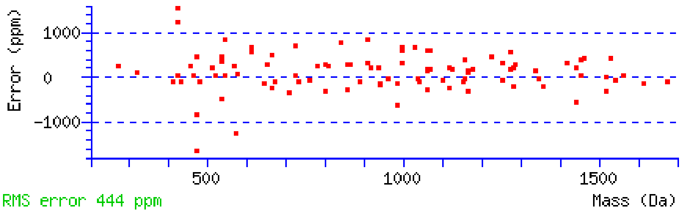


Monoisotopic mass of neutral peptide Mr(calc): 3285.5473
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N25 : Deamidated (NQ)
Ions Score: 80 **Expect:** 2.7e-006
Matches : 100/460 fragment ions using 152 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**							**29**
2	**271.1513**	136.0793	254.1248	127.5660			**N**	3130.4535	1565.7304	3113.4269	1557.2171	3112.4429	1556.7251	**28**
3	368.2041	184.6057	351.1775	176.0924			**P**	3016.4105	1508.7089	2999.3840	1500.1956	2998.4000	1499.7036	**27**
4	465.2568	233.1321	448.2303	224.6188			**P**	2919.3578	1460.1825	2902.3312	1451.6692	2901.3472	1451.1772	**26**
5	612.2922	306.6498	595.2657	298.1365			**M**	2822.3050	1411.6561	2805.2785	1403.1429	2804.2944	1402.6509	**25**
6	669.3137	335.1605	652.2872	326.6472			**G**	2675.2696	1338.1384	2658.2431	1329.6252	2657.2590	1329.1332	**24**
7	726.3352	363.6712	709.3086	355.1579			**G**	2618.2481	1309.6277	2601.2216	1301.1144	2600.2376	1300.6224	**23**
8	840.3781	***420.6927***	823.3515	412.1794			**N**	2561.2267	1281.1170	2544.2001	1272.6037	2543.2161	1272.1117	**22**
9	**939.4465**	***470.2269***	922.4200	461.7136			**V**	2447.1837	1224.0955	2430.1572	1215.5822	2429.1732	1215.0902	**21**
10	**1038.5149**	***519.7611***	1021.4884	511.2478			**V**	2348.1153	1174.5613	2331.0888	1166.0480	2330.1048	1165.5560	**20**
11	**1151.5990**	***576.3031***	1134.5724	567.7899			**I**	2249.0469	1125.0271	2232.0204	1116.5138	2231.0364	1116.0218	**19**
12	1298.6674	***649.8373***	1281.6409	641.3241			**F**	2135.9629	1068.4851	2118.9363	1059.9718	2117.9523	1059.4798	**18**
13	1413.6943	***707.3508***	1396.6678	698.8375	1395.6838	698.3455	**D**	1988.8944	994.9509	1971.8679	986.4376	1970.8839	985.9456	**17**
14	1514.7420	***757.8747***	1497.7155	749.3614	1496.7315	748.8694	**T**	1873.8675	937.4374	1856.8409	928.9241	1855.8569	928.4321	**16**
15	**1613.8104**	***807.4089***	1596.7839	798.8956	1595.7999	798.4036	**V**	1772.8198	886.9135	1755.7933	878.4003	1754.8093	877.9083	**15**
16	1726.8945	***863.9509***	1709.8680	855.4376	1708.8839	854.9456	**I**	**1673.7514**	837.3793	1656.7249	828.8661	1655.7408	828.3741	**14**
17	1827.9422	***914.4747***	1810.9156	905.9615	1809.9316	905.4694	**T**	**1560.6673**	780.8373	1543.6408	772.3240	1542.6568	771.8320	**13**
18	1941.9851	971.4962	1924.9586	962.9829	1923.9745	962.4909	**N**	1459.6197	730.3135	1442.5931	721.8002	1441.6091	721.3082	**12**
19	2070.0437	***1035.5255***	2053.0171	1027.0122	2052.0331	1026.5202	**Q**	**1345.5767**	673.2920	1328.5502	664.7787	1327.5662	664.2867	**11**
20	2199.0863	***1100.0468***	2182.0597	1091.5335	2181.0757	1091.0415	**E**	1217.5182	609.2627	1200.4916	600.7494	1199.5076	600.2574	**10**
21	2328.1289	***1164.5681***	2311.1023	1156.0548	2310.1183	1155.5628	**E**	1088.4756	544.7414	1071.4490	536.2281	1070.4650	535.7361	**9**

22	2425.1816	1213.0945	2408.1551	1204.5812	2407.1711	1204.0892	**P**	**959.4330**	480.2201	942.4064	471.7068	941.4224	471.2148	**8**
23	2588.2450	1294.6261	2571.2184	1286.1128	2570.2344	1285.6208	**Y**	862.3802	431.6937	845.3537	423.1805	844.3696	422.6885	**7**
24	2716.3035	***1358.6554***	2699.2770	1350.1421	2698.2930	1349.6501	**Q**	699.3169	350.1621	682.2903	341.6488	681.3063	341.1568	**6**
25	2831.3305	***1416.1689***	2814.3039	1407.6556	2813.3199	1407.1636	**N**	**571.2583**	286.1328	554.2317	277.6195	553.2477	277.1275	**5**
26	2968.3894	1484.6983	2951.3629	1476.1851	2950.3788	1475.6931	**H**	**456.2314**	228.6193	439.2048	220.1060	438.2208	219.6140	**4**
27	3055.4214	***1528.2144***	3038.3949	1519.7011	3037.4109	1519.2091	**S**	**319.1724**	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
28	3112.4429	1556.7251	3095.4163	1548.2118	3094.4323	1547.7198	**G**	232.1404	116.5738	215.1139	108.0606			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.7	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N25 31.14%
79.7	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q24 31.14%
77.9	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q19 20.20%
77.1	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N18 16.92%
60.8	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N8 0.39%
57.9	3285.5473	0.0050	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N2 0.21%
56.4	3284.5633	0.9890	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	
9.8	3284.5475	1.0048	YSSQLAQMQCMITNVEAQLAEIRADLER	
9.2	3284.5475	1.0048	YSSQLAQMQCMITNVEAQLAEIRADLER	
6.5	3284.5475	1.0048	YSSQLAQMQCMITNVEAQLAEIRADLER	

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

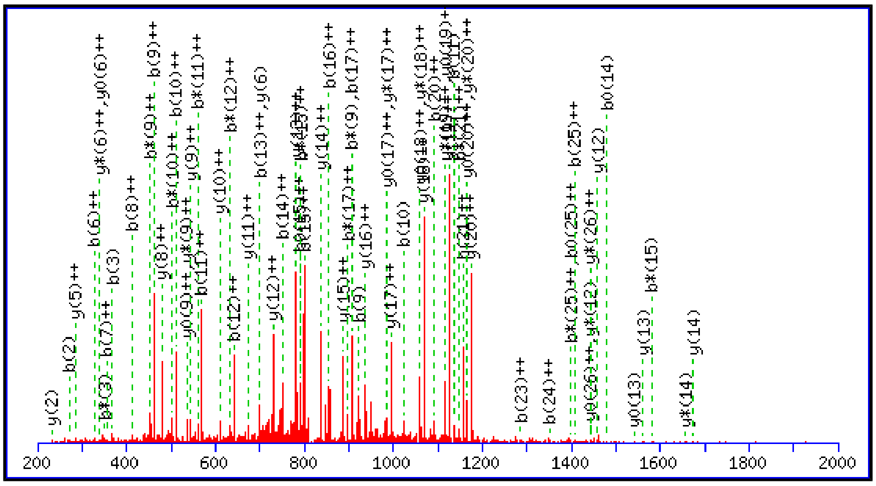
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **RNPPMGGNVVIFDTVITNQEEPYQNHSGR**
Found in **P02745** in **con_Xuniprot_HUMAN3**, C1QA_HUMAN Complement C1q subcomponent subunit A OS=Homo sapiens GN=C1QA PE=1 SV=2

Match to Query 27401: 3269.561936 from(818.397760,4+) intensity(73956.1406) rtinseconds(1743) scans(4212) index(801)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum3648_scans__4212
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

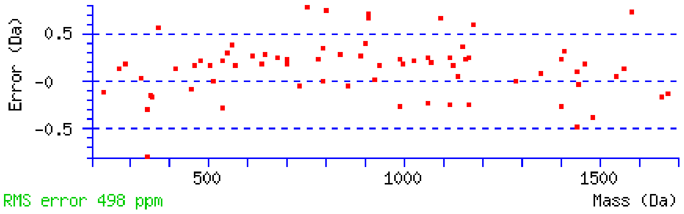
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

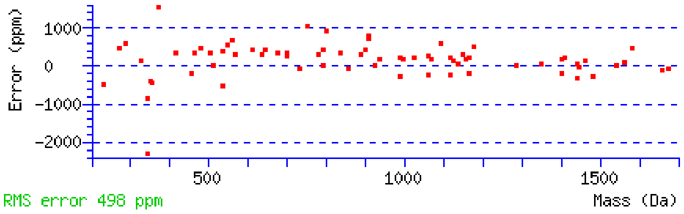


Monoisotopic mass of neutral peptide Mr(calc): 3269.5524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
Ions Score: 72 **Expect:** 1.8e-005
Matches : 72/308 fragment ions using 147 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							29
2	**271.1513**	136.0793	254.1248	127.5660			N	3114.4585	1557.7329	3097.4320	1549.2196	3096.4480	1548.7276	28
3	**368.2041**	184.6057	351.1775	176.0924			P	3000.4156	1500.7114	2983.3891	1492.1982	2982.4050	1491.7062	27
4	465.2568	233.1321	448.2303	224.6188			P	2903.3629	1452.1851	2886.3363	1443.6718	2885.3523	1443.1798	26
5	596.2973	298.6523	579.2708	290.1390			M	2806.3101	1403.6587	2789.2835	1395.1454	2788.2995	1394.6534	25
6	653.3188	***327.1630***	636.2922	318.6498			G	2675.2696	1338.1384	2658.2431	1329.6252	2657.2590	1329.1332	24
7	710.3403	***355.6738***	693.3137	347.1605			G	2618.2481	1309.6277	2601.2216	1301.1144	2600.2376	1300.6224	23
8	824.3832	***412.6952***	807.3566	404.1820			N	2561.2267	1281.1170	2544.2001	1272.6037	2543.2161	1272.1117	22
9	**923.4516**	***462.2294***	906.4250	453.7162			V	2447.1837	1224.0955	2430.1572	1215.5822	2429.1732	1215.0902	21
10	**1022.5200**	***511.7636***	1005.4935	503.2504			V	2348.1153	1174.5613	2331.0888	1166.0480	2330.1048	1165.5560	20
11	**1135.6041**	***568.3057***	1118.5775	559.7924			I	2249.0469	1125.0271	2232.0204	1116.5138	2231.0364	1116.0218	19
12	1282.6725	***641.8399***	1265.6459	633.3266			F	2135.9629	1068.4851	2118.9363	1059.9718	2117.9523	1059.4798	18
13	1397.6994	***699.3534***	1380.6729	690.8401	1379.6889	690.3481	D	1988.8944	994.9509	1971.8679	986.4376	1970.8839	985.9456	17
14	1498.7471	***749.8772***	1481.7206	741.3639	1480.7365	740.8719	T	1873.8675	937.4374	1856.8409	928.9241	1855.8569	928.4321	16
15	1597.8155	***799.4114***	1580.7890	790.8981	1579.8050	790.4061	V	1772.8198	886.9135	1755.7933	878.4003	1754.8093	877.9083	15
16	1710.8996	***855.9534***	1693.8730	847.4402	1692.8890	846.9481	I	**1673.7514**	837.3793	1656.7249	828.8661	1655.7408	828.3741	14
17	1811.9473	***906.4773***	1794.9207	897.9640	1793.9367	897.4720	T	**1560.6673**	780.8373	1543.6408	772.3240	1542.6568	771.8320	13
18	1925.9902	963.4987	1908.9636	954.9855	1907.9796	954.4935	N	**1459.6197**	730.3135	1442.5931	721.8002	1441.6091	721.3082	12
19	2054.0488	1027.5280	2037.0222	1019.0147	2036.0382	1018.5227	Q	1345.5767	673.2920	1328.5502	664.7787	1327.5662	664.2867	11
20	2183.0914	***1092.0493***	2166.0648	1083.5360	2165.0808	1083.0440	E	1217.5182	609.2627	1200.4916	600.7494	1199.5076	600.2574	10
21	2312.1340	***1156.5706***	2295.1074	1148.0573	2294.1234	1147.5653	E	1088.4756	544.7414	1071.4490	536.2281	1070.4650	535.7361	9
22	2409.1867	1205.0970	2392.1602	1196.5837	2391.1762	1196.0917	P	959.4330	480.2201	942.4064	471.7068	941.4224	471.2148	8

23	2572.2501	***1286.6287***	2555.2235	1278.1154	2554.2395	1277.6234	**Y**	862.3802	431.6937	845.3537	423.1805	844.3696	422.6885	**7**
24	2700.3086	***1350.6580***	2683.2821	1342.1447	2682.2981	1341.6527	**Q**	**699.3169**	350.1621	682.2903	341.6488	681.3063	341.1568	**6**
25	2815.3356	***1408.1714***	2798.3090	1399.6581	2797.3250	1399.1661	**N**	571.2583	286.1328	554.2317	277.6195	553.2477	277.1275	**5**
26	2952.3945	1476.7009	2935.3679	1468.1876	2934.3839	1467.6956	**H**	456.2314	228.6193	439.2048	220.1060	438.2208	219.6140	**4**
27	3039.4265	1520.2169	3022.4000	1511.7036	3021.4159	1511.2116	**S**	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
28	3096.4480	1548.7276	3079.4214	1540.2144	3078.4374	1539.7223	**G**	**232.1404**	116.5738	215.1139	108.0606			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.6	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N25 40.53%
71.6	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q24 40.53%
63.6	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q19 6.50%
63.6	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N18 6.50%
60.6	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N8 3.25%
59.8	3269.5524	0.0096	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N2 2.68%
49.6	3268.5684	0.9936	RNPPMGGNVVIFDTVITNQEEPYQNHSGR	
13.3	3267.5589	2.0031	FLYMSVTMGAMMFLLLGHRPNGYNSLGAK	
13.3	3267.5589	2.0031	FLYMSVTMGAMMFLLLGHRPNGYNSLGAK	
12.4	3269.5577	0.0042	LAIAQELLGLNGRTMMDQMESEDTVTSKR	

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

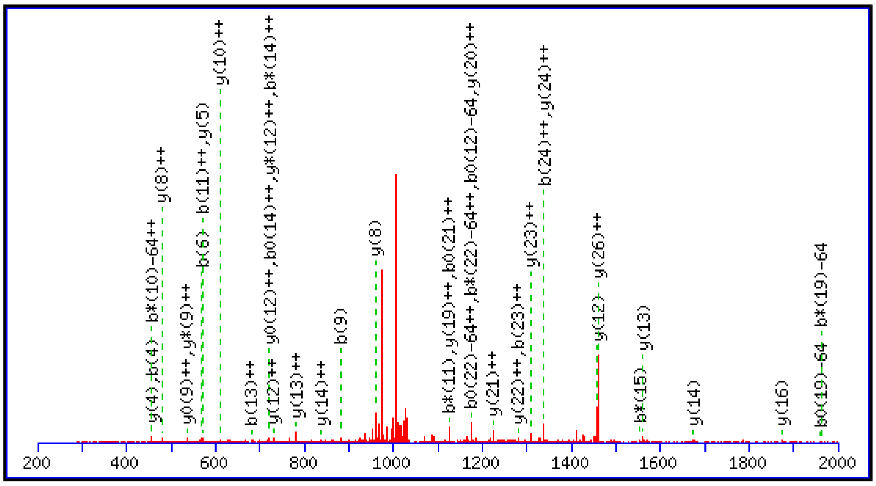
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPPMGGNVVIFDTVITNQEEPYQNHSGR**
Found in **P02745** in **con_Xuniprot_HUMAN3**, C1QA_HUMAN Complement C1q subcomponent subunit A OS=Homo sapiens GN=C1QA PE=1 SV=2

Match to Query 27330: 3129.460782 from(1044.160870,3+) intensity(53258.8281) rtinseconds(1761) scans(4422) index(2069)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum3824_scans__4422
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

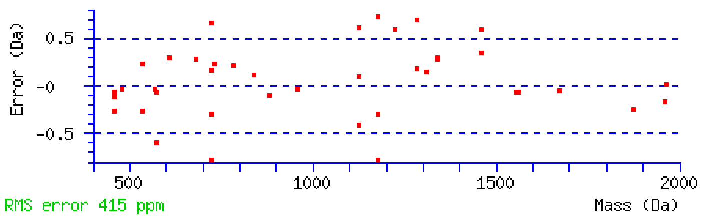
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

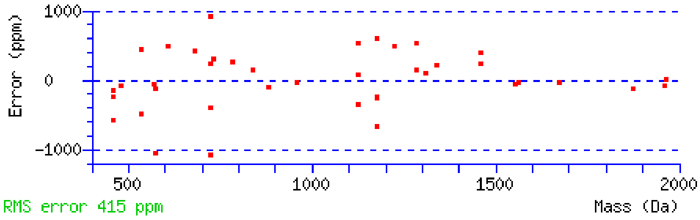


Monoisotopic mass of neutral peptide Mr(calc): 3129.4462
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N24 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0017
Matches : 41/444 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	115.0502	58.0287	98.0237	49.5155			N							28
2	212.1030	106.5551	195.0764	98.0418			P	3016.4105	1508.7089	2999.3840	1500.1956	2998.4000	1499.7036	27
3	309.1557	155.0815	292.1292	146.5682			P	2919.3578	1460.1825	2902.3312	1451.6692	2901.3472	1451.1772	26
4	**456.1911**	228.5992	439.1646	220.0859			M	2822.3050	1411.6561	2805.2785	1403.1429	2804.2944	1402.6509	25
5	513.2126	257.1099	496.1860	248.5967			G	2675.2696	1338.1384	2658.2431	1329.6252	2657.2590	1329.1332	24
6	**570.2341**	285.6207	553.2075	277.1074			G	2618.2481	1309.6277	2601.2216	1301.1144	2600.2376	1300.6224	23
7	684.2770	342.6421	667.2504	334.1289			N	2561.2267	1281.1170	2544.2001	1272.6037	2543.2161	1272.1117	22
8	783.3454	392.1763	766.3189	383.6631			V	2447.1837	1224.0955	2430.1572	1215.5822	2429.1732	1215.0902	21
9	**882.4138**	441.7105	865.3873	433.1973			V	2348.1153	1174.5613	2331.0888	1166.0480	2330.1048	1165.5560	20
10	995.4979	498.2526	978.4713	489.7393			I	2249.0469	1125.0271	2232.0204	1116.5138	2231.0364	1116.0218	19
11	1142.5663	**571.7868**	1125.5397	563.2735			F	2135.9629	1068.4851	2118.9363	1059.9718	2117.9523	1059.4798	18
12	1257.5932	629.3003	1240.5667	620.7870	1239.5827	620.2950	D	1988.8944	994.9509	1971.8679	986.4376	1970.8839	985.9456	17
13	1358.6409	**679.8241**	1341.6144	671.3108	1340.6303	670.8188	T	**1873.8675**	937.4374	1856.8409	928.9241	1855.8569	928.4321	16
14	1457.7093	729.3583	1440.6828	720.8450	1439.6988	720.3530	V	1772.8198	886.9135	1755.7933	878.4003	1754.8093	877.9083	15
15	1570.7934	785.9003	1553.7668	777.3871	1552.7828	776.8951	I	**1673.7514**	837.3793	1656.7249	828.8661	1655.7408	828.3741	14
16	1671.8411	836.4242	1654.8145	827.9109	1653.8305	827.4189	T	**1560.6673**	780.8373	1543.6408	772.3240	1542.6568	771.8320	13
17	1785.8840	893.4456	1768.8574	884.9324	1767.8734	884.4404	N	**1459.6197**	730.3135	1442.5931	721.8002	1441.6091	721.3082	12
18	1913.9426	957.4749	1896.9160	948.9617	1895.9320	948.4696	Q	1345.5767	673.2920	1328.5502	664.7787	1327.5662	664.2867	11
19	2042.9852	1021.9962	2025.9586	1013.4829	2024.9746	1012.9909	E	1217.5182	609.2627	1200.4916	600.7494	1199.5076	600.2574	10
20	2172.0278	1086.5175	2155.0012	1078.0042	2154.0172	1077.5122	E	1088.4756	544.7414	1071.4490	536.2281	1070.4650	535.7361	9
21	2269.0805	1135.0439	2252.0540	1126.5306	2251.0700	1126.0386	P	**959.4330**	480.2201	942.4064	471.7068	941.4224	471.2148	8

22	2432.1439	1216.5756	2415.1173	1208.0623	2414.1333	1207.5703	**Y**	862.3802	431.6937	845.3537	423.1805	844.3696	422.6885	**7**
23	2560.2024	**1280.6049**	2543.1759	1272.0916	2542.1919	1271.5996	**Q**	699.3169	350.1621	682.2903	341.6488	681.3063	341.1568	**6**
24	2675.2294	**1338.1183**	2658.2028	1329.6051	2657.2188	1329.1130	**N**	**571.2583**	286.1328	554.2317	277.6195	553.2477	277.1275	**5**
25	2812.2883	1406.6478	2795.2617	1398.1345	2794.2777	1397.6425	**H**	**456.2314**	228.6193	439.2048	220.1060	438.2208	219.6140	**4**
26	2899.3203	1450.1638	2882.2938	1441.6505	2881.3098	1441.1585	**S**	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
27	2956.3418	1478.6745	2939.3152	1470.1613	2938.3312	1469.6692	**G**	232.1404	116.5738	215.1139	108.0606			**2**
28							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.9	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N24 27.64%
50.9	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q23 27.64%
50.5	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N17 25.21%
49.0	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated Q18 17.68%
36.4	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N7 0.98%
35.8	3129.4462	0.0146	NPPMGGNVVIFDTVITNQEEPYQNHSGR	Deamidated N1 0.85%
33.4	3128.4622	0.9986	NPPMGGNVVIFDTVITNQEEPYQNHSGR	
5.1	3127.4694	1.9914	NAGTDIEDRIHHVTNQSGTWTSSKLETK	
4.6	3127.4511	2.0096	QYLEKMLDESSGAAAGGQSHSMVMETLLK	
3.5	3129.4608	0.0000	MNFLRGVMGGQSAGPQHTEAETVRGAADPK	

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

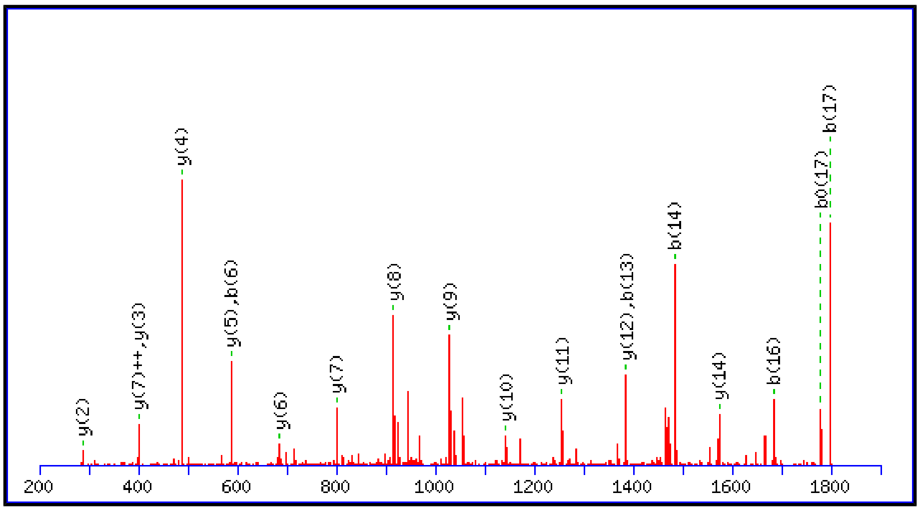
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVNITSENLIDDVVSLIR**
Found in **P02748** in **con_Xuniprot_HUMAN3**, CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

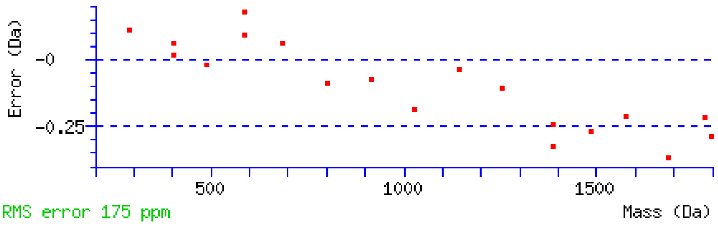
Match to Query 11794: 1971.057528 from(986.536040,2+) intensity(935934.3125) rtinseconds(2936) scans(7609) index(1048)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum6684_scans__7609
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

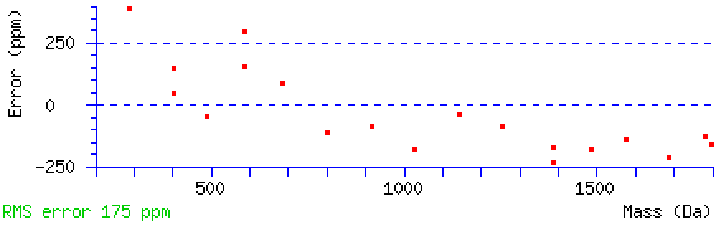
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1971.0524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 130 **Expect:** 1.7e-011
Matches : 19/186 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							18
2	171.1128	86.0600					V	1901.0226	951.0149	1883.9960	942.5017	1883.0120	942.0097	17
3	286.1397	143.5735	269.1132	135.0602			N	1801.9542	901.4807	1784.9276	892.9675	1783.9436	892.4754	16
4	399.2238	200.1155	382.1973	191.6023			I	1686.9272	843.9673	1669.9007	835.4540	1668.9167	834.9620	15
5	500.2715	250.6394	483.2449	242.1261	482.2609	241.6341	T	**1573.8432**	787.4252	1556.8166	778.9120	1555.8326	778.4199	14
6	**587.3035**	294.1554	570.2770	285.6421	569.2930	285.1501	S	1472.7955	736.9014	1455.7689	728.3881	1454.7849	727.8961	13
7	716.3461	358.6767	699.3196	350.1634	698.3355	349.6714	E	**1385.7635**	693.3854	1368.7369	684.8721	1367.7529	684.3801	12
8	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	N	**1256.7209**	628.8641	1239.6943	620.3508	1238.7103	619.8588	11
9	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	L	**1142.6780**	571.8426	1125.6514	563.3293	1124.6674	562.8373	10
10	1056.5572	528.7822	1039.5306	520.2689	1038.5466	519.7769	I	**1029.5939**	515.3006	1012.5673	506.7873	1011.5833	506.2953	9
11	1171.5841	586.2957	1154.5576	577.7824	1153.5735	577.2904	D	**916.5098**	458.7585	899.4833	450.2453	898.4993	449.7533	8
12	1286.6111	643.8092	1269.5845	635.2959	1268.6005	634.8039	D	**801.4829**	401.2451	784.4563	392.7318	783.4723	392.2398	7
13	**1385.6795**	693.3434	1368.6529	684.8301	1367.6689	684.3381	V	**686.4559**	343.7316	669.4294	335.2183	668.4454	334.7263	6
14	**1484.7479**	742.8776	1467.7213	734.3643	1466.7373	733.8723	V	**587.3875**	294.1974	570.3610	285.6841	569.3770	285.1921	5
15	1571.7799	786.3936	1554.7534	777.8803	1553.7693	777.3883	S	**488.3191**	244.6632	471.2926	236.1499	470.3085	235.6579	4
16	**1684.8640**	842.9356	1667.8374	834.4223	1666.8534	833.9303	L	**401.2871**	201.1472	384.2605	192.6339			3
17	**1797.9480**	899.4777	1780.9215	890.9644	1779.9375	890.4724	I	**288.2030**	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
129.9	1971.0524	0.0051	AVNITSENLIDDVVSLIR	Deamidated N3 100.00%
78.5	1971.0524	0.0051	AVNITSENLIDDVVSLIR	Deamidated N8 0.00%
23.8	1970.0486	1.0089	RAVDPFDVEWVAARALR	
21.2	1970.0506	1.0069	LLPMNDQIRELQTIIR	
12.4	1970.0506	1.0069	LLPMNDQIRELQTIIR	
12.1	1970.0506	1.0069	LLPMNDQIRELQTIIR	
12.0	1971.0637	-0.0061	SSSSPLVVVSVKSPNQSLR	
12.0	1971.0637	-0.0061	SSSSPLVVVSVKSPNQSLR	
9.8	1970.0545	1.0031	IAANVARSSEQNLQVTLR	
9.6	1970.0480	1.0096	NMLVEVRGEGVQAGSRLR	

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

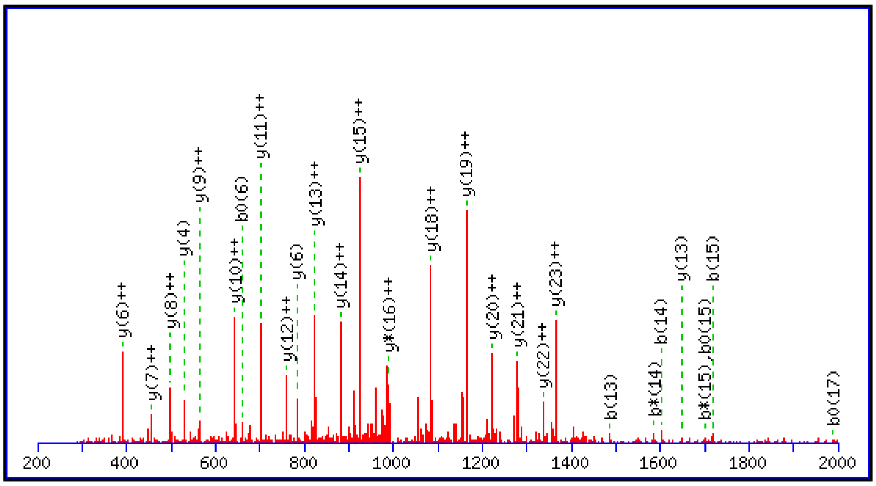
Mascot Search Results

Peptide View

MS/MS Fragmentation of **CNGDNDCGDFSDEDDCESEPRPPCR**
Found in **P02748** in **con_Xuniprot_HUMAN3**, CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

Match to Query 27245: 3003.033762 from(1002.018530,3+) intensity(12545.1436) rtinseconds(635) scans(1221) index(14042)
Title: 111019_Est_MI_YP_G_02Spectrum1000_scans__1221
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

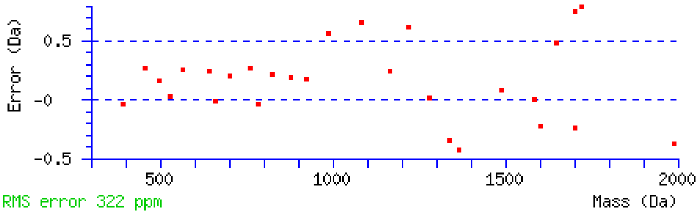
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

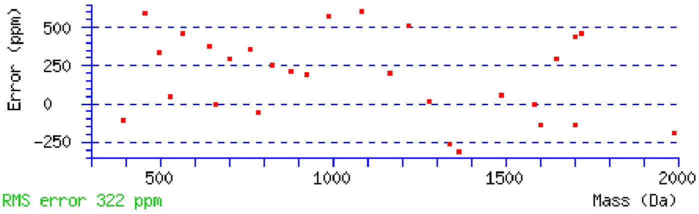


Monoisotopic mass of neutral peptide Mr(calc): 3003.0284
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 100 **Expect:** 9.4e-011
Matches : 28/268 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							25
2	275.0809	138.0441	258.0543	129.5308			N	2844.0050	1422.5061	2826.9785	1413.9929	2825.9944	1413.5009	24
3	332.1023	166.5548	315.0758	158.0415			G	2729.9621	1365.4847	2712.9355	1356.9714	2711.9515	1356.4794	23
4	447.1293	224.0683	430.1027	215.5550	429.1187	215.0630	D	2672.9406	1336.9739	2655.9141	1328.4607	2654.9301	1327.9687	22
5	562.1562	281.5817	545.1297	273.0685	544.1456	272.5765	N	2557.9137	1279.4605	2540.8871	1270.9472	2539.9031	1270.4552	21
6	677.1831	339.0952	660.1566	330.5819	659.1726	330.0899	D	2442.8867	1221.9470	2425.8602	1213.4337	2424.8762	1212.9417	20
7	837.2138	419.1105	820.1872	410.5973	819.2032	410.1053	C	2327.8598	1164.4335	2310.8332	1155.9203	2309.8492	1155.4282	19
8	894.2353	447.6213	877.2087	439.1080	876.2247	438.6160	G	2167.8291	1084.4182	2150.8026	1075.9049	2149.8186	1075.4129	18
9	1009.2622	505.1347	992.2357	496.6215	991.2516	496.1295	D	2110.8077	1055.9075	2093.7811	1047.3942	2092.7971	1046.9022	17
10	1156.3306	578.6689	1139.3041	570.1557	1138.3201	569.6637	F	1995.7807	998.3940	1978.7542	989.8807	1977.7702	989.3887	16
11	1243.3626	622.1850	1226.3361	613.6717	1225.3521	613.1797	S	1848.7123	924.8598	1831.6858	916.3465	1830.7018	915.8545	15
12	1358.3896	679.6984	1341.3630	671.1852	1340.3790	670.6931	D	1761.6803	881.3438	1744.6537	872.8305	1743.6697	872.3385	14
13	**1487.4322**	744.2197	1470.4056	735.7065	1469.4216	735.2144	E	**1646.6533**	823.8303	1629.6268	815.3170	1628.6428	814.8250	13
14	**1602.4591**	801.7332	1585.4326	793.2199	1584.4486	792.7279	D	1517.6108	759.3090	1500.5842	750.7957	1499.6002	750.3037	12
15	**1717.4861**	859.2467	1700.4595	850.7334	1699.4755	850.2414	D	1402.5838	701.7955	1385.5573	693.2823	1384.5732	692.7903	11
16	1877.5167	939.2620	1860.4902	930.7487	1859.5061	930.2567	C	1287.5569	644.2821	1270.5303	635.7688	1269.5463	635.2768	10
17	2006.5593	1003.7833	1989.5328	995.2700	1988.5487	994.7780	E	1127.5262	564.2667	1110.4997	555.7535	1109.5157	555.2615	9
18	2093.5913	1047.2993	2076.5648	1038.7860	2075.5808	1038.2940	S	998.4836	499.7455	981.4571	491.2322	980.4731	490.7402	8
19	2222.6339	1111.8206	2205.6074	1103.3073	2204.6234	1102.8153	E	911.4516	456.2294	894.4250	447.7162	893.4410	447.2242	7
20	2319.6867	1160.3470	2302.6601	1151.8337	2301.6761	1151.3417	P	**782.4090**	391.7081	765.3825	383.1949			6
21	2475.7878	1238.3975	2458.7613	1229.8843	2457.7772	1229.3923	R	685.3562	343.1818	668.3297	334.6685			5
22	2572.8406	1286.9239	2555.8140	1278.4106	2554.8300	1277.9186	P	**529.2551**	265.1312	512.2286	256.6179			4
23	2669.8933	1335.4503	2652.8668	1326.9370	2651.8828	1326.4450	P	432.2024	216.6048	415.1758	208.0915			3

24	2829.9240	1415.4656	2812.8974	1406.9524	2811.9134	1406.4603	**C**	335.1496	168.0784	318.1231	159.5652			**2**
25							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
100.3	3003.0284	0.0054	CNGDNDCGDFSDEDDCESEPRPPCR	Deamidated N5 62.56%
98.0	3003.0284	0.0054	CNGDNDCGDFSDEDDCESEPRPPCR	Deamidated N2 37.44%
81.4	3002.0444	0.9894	CNGDNDCGDFSDEDDCESEPRPPCR	

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

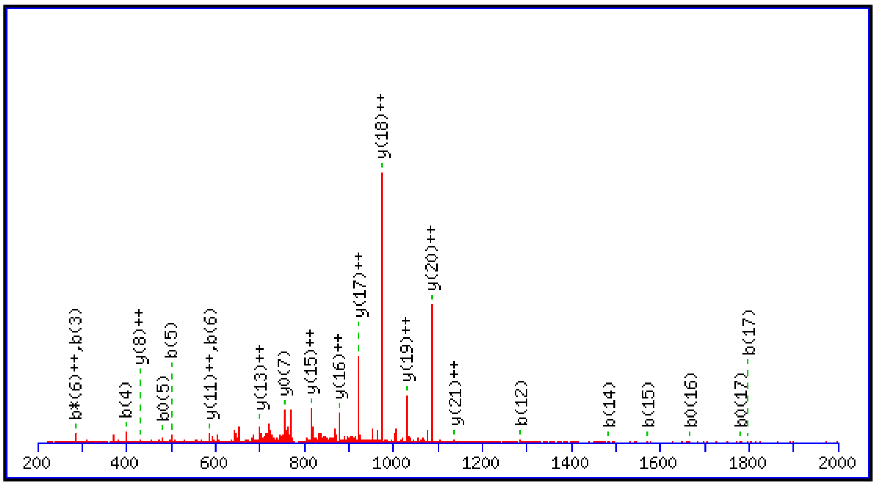
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVNITSENLIDDVVSLIRGGTR**
Found in **P02748** in **con_Xuniprot_HUMAN3**, CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2

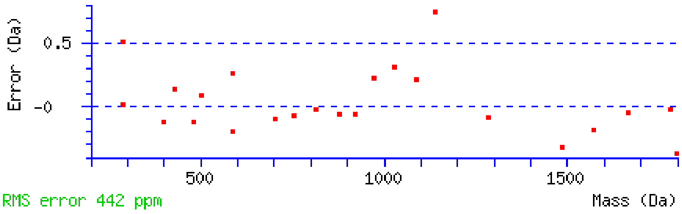
Match to Query 15494: 2342.251122 from(781.757650,3+) intensity(23989.6855) rtinseconds(2924) scans(7937) index(24229)
Title: 111019_Est_MI_YS_G_05Spectrum6910_scans__7937
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

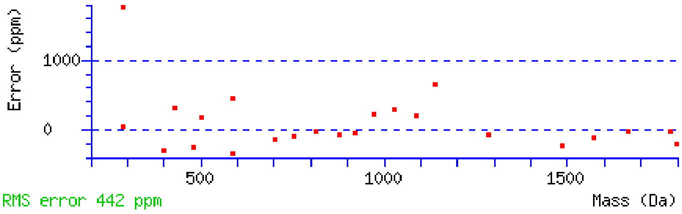
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.2441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3      : Deamidated (NQ)
Ions Score: 46  Expect: 0.0037
Matches : 23/238 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	72.0444	36.5258					A							22
2	171.1128	86.0600					V	2272.2143	1136.6108	2255.1878	1128.0975	2254.2038	1127.6055	21
3	***286.1397***	143.5735	269.1132	135.0602			N	2173.1459	1087.0766	2156.1194	1078.5633	2155.1353	1078.0713	20
4	***399.2238***	200.1155	382.1973	191.6023			I	2058.1190	1029.5631	2041.0924	1021.0498	2040.1084	1020.5578	19
5	***500.2715***	250.6394	483.2449	242.1261	482.2609	241.6341	T	1945.0349	973.0211	1928.0083	964.5078	1927.0243	964.0158	18
6	***587.3035***	294.1554	570.2770	285.6421	569.2930	285.1501	S	1843.9872	922.4972	1826.9607	913.9840	1825.9767	913.4920	17
7	716.3461	358.6767	699.3196	350.1634	698.3355	349.6714	E	1756.9552	878.9812	1739.9286	870.4680	1738.9446	869.9759	16
8	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	N	1627.9126	814.4599	1610.8860	805.9467	1609.9020	805.4547	15
9	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	L	1513.8697	757.4385	1496.8431	748.9252	1495.8591	748.4332	14
10	1056.5572	528.7822	1039.5306	520.2689	1038.5466	519.7769	I	1400.7856	700.8964	1383.7591	692.3832	1382.7750	691.8912	13
11	1171.5841	586.2957	1154.5576	577.7824	1153.5735	577.2904	D	1287.7015	644.3544	1270.6750	635.8411	1269.6910	635.3491	12
12	***1286.6111***	643.8092	1269.5845	635.2959	1268.6005	634.8039	D	1172.6746	586.8409	1155.6480	578.3277	1154.6640	577.8357	11
13	1385.6795	693.3434	1368.6529	684.8301	1367.6689	684.3381	V	1057.6477	529.3275	1040.6211	520.8142	1039.6371	520.3222	10
14	***1484.7479***	742.8776	1467.7213	734.3643	1466.7373	733.8723	V	958.5792	479.7933	941.5527	471.2800	940.5687	470.7880	9
15	***1571.7799***	786.3936	1554.7534	777.8803	1553.7693	777.3883	S	859.5108	430.2591	842.4843	421.7458	841.5003	421.2538	8
16	1684.8640	842.9356	1667.8374	834.4223	1666.8534	833.9303	L	772.4788	386.7430	755.4522	378.2298	754.4682	377.7378	7
17	***1797.9480***	899.4777	1780.9215	890.9644	1779.9375	890.4724	I	659.3947	330.2010	642.3682	321.6877	641.3842	321.1957	6
18	1954.0491	977.5282	1937.0226	969.0149	1936.0386	968.5229	R	546.3107	273.6590	529.2841	265.1457	528.3001	264.6537	5
19	2011.0706	1006.0389	1994.0441	997.5257	1993.0600	997.0337	G	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	4
20	2068.0921	1034.5497	2051.0655	1026.0364	2050.0815	1025.5444	G	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
21	2169.1398	1085.0735	2152.1132	1076.5602	2151.1292	1076.0682	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.5	2342.2441	0.0070	AVNITSENLIDDVVSLIRGGTR	Deamidated N3 86.67%
38.3	2342.2441	0.0070	AVNITSENLIDDVVSLIRGGTR	Deamidated N8 13.33%
7.7	2340.2325	2.0186	AIVLFNPDSKGLSNPAEVEALR	
7.1	2341.2376	1.0135	QLQQLQQLRDSGEKVVEIVK	
6.2	2341.2376	1.0135	QLQQLQQLRDSGEKVVEIVK	
6.2	2341.2376	1.0135	QLQQLQQLRDSGEKVVEIVK	
5.9	2342.2481	0.0030	AVDLTKPYQNQQLSIRVPLR	
5.8	2341.2376	1.0135	QLQQLQQLRDSGEKVVEIVK	
5.0	2340.2536	1.9975	QLQQLQQLRDSGEKVVEIVK	
5.0	2340.2536	1.9975	QLQQLQQLRDSGEKVVEIVK	

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

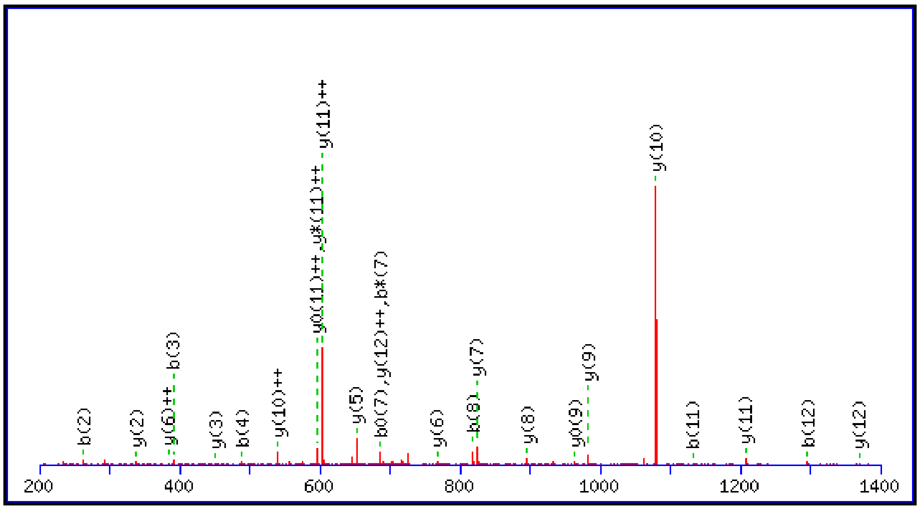
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYKPSAGNNSLYR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

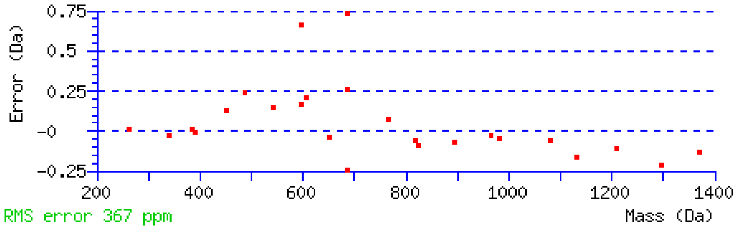
Match to Query 6284: 1468.735208 from(735.374880,2+) intensity(94156.0234) rtinseconds(506) scans(1013) index(26430)
Title: 111019_Est_MI_YS_G_09Spectrum843_scans__1013
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

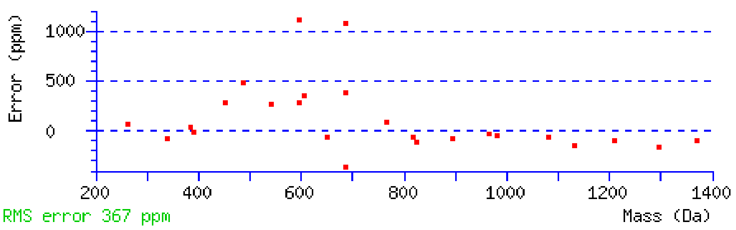
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.7310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 76 **Expect:** 5.7e-006
Matches : 25/126 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	100.0757	50.5415					V							13
2	**263.1390**	132.0731					Y	***1370.6699***	685.8386	1353.6434	677.3253	1352.6593	676.8333	12
3	**391.2340**	196.1206	374.2074	187.6074			K	***1207.6066***	604.3069	1190.5800	595.7937	1189.5960	595.3016	11
4	**488.2867**	244.6470	471.2602	236.1337			P	***1079.5116***	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
5	575.3188	288.1630	558.2922	279.6498	557.3082	279.1577	S	***982.4588***	491.7331	965.4323	483.2198	964.4483	482.7278	9
6	646.3559	323.6816	629.3293	315.1683	628.3453	314.6763	A	***895.4268***	448.2170	878.4003	439.7038	877.4163	439.2118	8
7	703.3774	352.1923	686.3508	343.6790	685.3668	343.1870	G	***824.3897***	412.6985	807.3632	404.1852	806.3791	403.6932	7
8	**818.4043**	409.7058	801.3777	401.1925	800.3937	400.7005	N	***767.3682***	384.1878	750.3417	375.6745	749.3577	375.1825	6
9	932.4472	466.7272	915.4207	458.2140	914.4367	457.7220	N	***652.3413***	326.6743	635.3148	318.1610	634.3307	317.6690	5
10	1019.4793	510.2433	1002.4527	501.7300	1001.4687	501.2380	S	538.2984	269.6528	521.2718	261.1396	520.2878	260.6475	4
11	**1132.5633**	566.7853	1115.5368	558.2720	1114.5527	557.7800	L	***451.2663***	226.1368	434.2398	217.6235			3
12	**1295.6266**	648.3170	1278.6001	639.8037	1277.6161	639.3117	Y	***338.1823***	169.5948	321.1557	161.0815			2
13							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.7	1468.7310	0.0042	VYKPSAGNNSLYR	Deamidated N8 62.72%
73.5	1468.7310	0.0042	VYKPSAGNNSLYR	Deamidated N9 37.28%
14.3	1468.7378	-0.0026	VKSLMASLTNMSR	
13.3	1468.7422	-0.0070	NKFPKLHNEDAR	
12.1	1467.7252	1.0100	MEQNKTAATRYR	
11.7	1467.7245	1.0107	AYQKQPTIFQNK	
11.6	1467.7245	1.0107	AYQKQPTIFQNK	
10.2	1468.7409	-0.0057	VHQQLEKTLQDK	
9.6	1468.7310	0.0042	VARNKFYAEQDK	
8.6	1467.7279	1.0073	MNQLTQELFSLK	

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

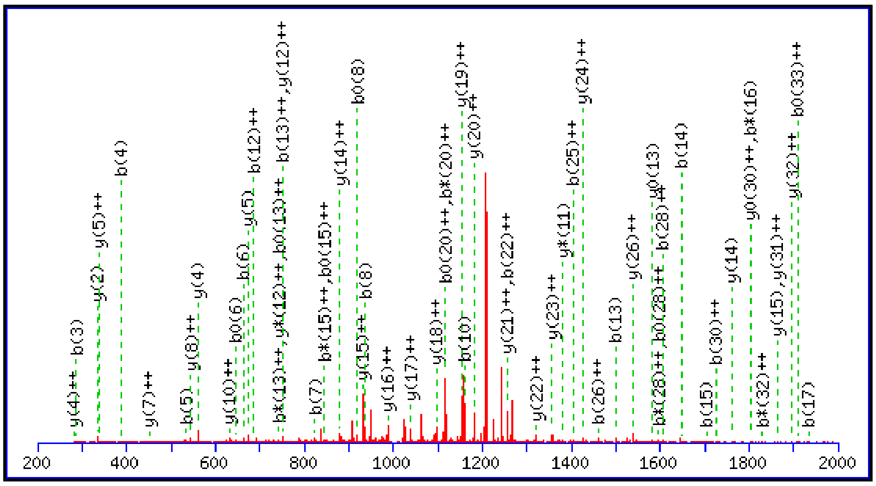
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28303: 4008.770856 from(1003.199990,4+) intensity(86767.2891) rtinseconds(1969) scans(4945) index(23368)
Title: 111019_Est_MI_YS_G_04Spectrum4264_scans__4945
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

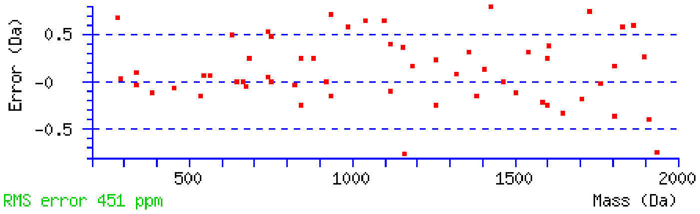
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

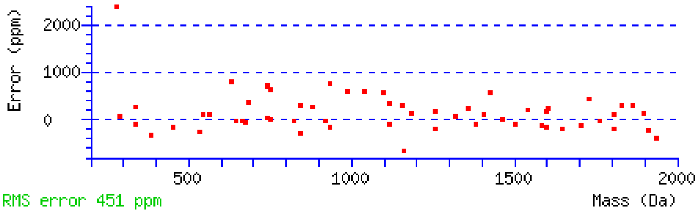


Monoisotopic mass of neutral peptide Mr(calc): 4008.7540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 73 **Expect:** 5.1e-006
Matches : 60/374 fragment ions using 137 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3894.7343	1947.8708	3877.7077	1939.3575	3876.7237	1938.8655	33
3	**288.1190**	144.5631			270.1084	135.5579	A	3793.6866	1897.3469	3776.6600	1888.8337	3775.6760	1888.3417	32
4	**387.1874**	194.0974			369.1769	185.0921	V	3722.6495	1861.8284	3705.6229	1853.3151	3704.6389	1852.8231	31
5	**534.2558**	267.6316			516.2453	258.6263	F	3623.5811	1812.2942	3606.5545	1803.7809	3605.5705	1803.2889	30
6	**663.2984**	332.1529			645.2879	323.1476	E	3476.5126	1738.7600	3459.4861	1730.2467	3458.5021	1729.7547	29
7	**823.3291**	412.1682			805.3185	403.1629	C	3347.4701	1674.2387	3330.4435	1665.7254	3329.4595	1665.2334	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3187.4394	1594.2233	3170.4129	1585.7101	3169.4288	1585.2181	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3074.3553	1537.6813	3057.3288	1529.1680	3056.3448	1528.6760	26
10	**1161.5245**	581.2659	1144.4979	572.7526	1143.5139	572.2606	Q	2977.3026	1489.1549	2960.2760	1480.6417	2959.2920	1480.1496	25
11	1298.5834	649.7953	1281.5569	641.2821	1280.5728	640.7901	H	2849.2440	1425.1256	2832.2175	1416.6124	2831.2334	1416.1204	24
12	1369.6205	**685.3139**	1352.5940	676.8006	1351.6099	676.3086	A	2712.1851	1356.5962	2695.1585	1348.0829	2694.1745	1347.5909	23
13	**1500.6610**	**750.8341**	1483.6345	742.3209	1482.6504	741.8289	M	2641.1480	1321.0776	2624.1214	1312.5644	2623.1374	1312.0723	22
14	**1647.7294**	824.3683	1630.7029	815.8551	1629.7188	815.3631	F	2510.1075	1255.5574	2493.0809	1247.0441	2492.0969	1246.5521	21
15	**1704.7509**	852.8791	1687.7243	844.3658	1686.7403	843.8738	G	2363.0391	1182.0232	2346.0125	1173.5099	2345.0285	1173.0179	20
16	1819.7778	910.3925	1802.7513	901.8793	1801.7673	901.3873	N	2306.0176	1153.5124	2288.9911	1144.9992	2288.0070	1144.5072	19
17	**1934.8048**	967.9060	1917.7782	959.3927	1916.7942	958.9007	D	2190.9907	1095.9990	2173.9641	1087.4857	2172.9801	1086.9937	18
18	2035.8524	1018.4299	2018.8259	1009.9166	2017.8419	1009.4246	T	2075.9637	1038.4855	2058.9372	1029.9722	2057.9532	1029.4802	17
19	2148.9365	1074.9719	2131.9100	1066.4586	2130.9259	1065.9666	I	1974.9160	987.9617	1957.8895	979.4484	1956.9055	978.9564	16
20	2249.9842	1125.4957	2232.9576	1116.9825	2231.9736	1116.4904	T	**1861.8320**	931.4196	1844.8054	922.9064	1843.8214	922.4143	15
21	2410.0148	1205.5111	2392.9883	1196.9978	2392.0043	1196.5058	C	**1760.7843**	880.8958	1743.7578	872.3825	1742.7737	871.8905	14
22	2511.0625	**1256.0349**	2494.0360	1247.5216	2493.0519	1247.0296	T	1600.7537	800.8805	1583.7271	792.3672	1582.7431	791.8752	13

23	2612.1102	1306.5587	2595.0836	1298.0455	2594.0996	1297.5535	**T**	1499.7060	750.3566	1482.6794	741.8434	1481.6954	741.3513	**12**
24	2749.1691	1375.0882	2732.1426	1366.5749	2731.1585	1366.0829	**H**	1398.6583	699.8328	1381.6317	691.3195	1380.6477	690.8275	**11**
25	2806.1906	**1403.5989**	2789.1640	1395.0856	2788.1800	1394.5936	**G**	1261.5994	631.3033	1244.5728	622.7901	1243.5888	622.2980	**10**
26	2921.2175	**1461.1124**	2904.1910	1452.5991	2903.2069	1452.1071	**N**	1204.5779	602.7926	1187.5514	594.2793	1186.5674	593.7873	**9**
27	3107.2968	1554.1520	3090.2703	1545.6388	3089.2863	1545.1468	**W**	1089.5510	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3208.3445	**1604.6759**	3191.3180	1596.1626	3190.3339	1595.6706	**T**	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3336.4395	1668.7234	3319.4129	1660.2101	3318.4289	1659.7181	**K**	802.4240	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3449.5235	**1725.2654**	3432.4970	1716.7521	3431.5130	1716.2601	**L**	**674.3290**	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3546.5763	1773.7918	3529.5497	1765.2785	3528.5657	1764.7865	**P**	**561.2450**	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3675.6189	1838.3131	3658.5923	1829.7998	3657.6083	1829.3078	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3835.6495	1918.3284	3818.6230	1909.8151	3817.6390	1909.3231	**C**	**335.1496**	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.9	4008.7540	0.0169	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16, N26 99.60%
48.9	4008.7540	0.0169	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N26 0.40%
48.6	4007.7699	1.0009	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
25.1	4007.7699	1.0009	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
21.1	4008.7540	0.0169	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N16 0.00%
11.7	4007.7699	1.0009	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
8.9	4007.7711	0.9998	AVEMTDQLMVPTLGSQEGAFENVRMNYSGDQGQTIR	
6.3	4008.7551	0.0158	AVEMTDQLMVPTLGSQEGAFENVRMNYSGDQGQTIR	
4.7	4006.7717	1.9991	NLHSHYHEAPMTRKHYQVTGYGINGTGDSNDFWR	
4.2	4007.7711	0.9998	AVEMTDQLMVPTLGSQEGAFENVRMNYSGDQGQTIR	

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

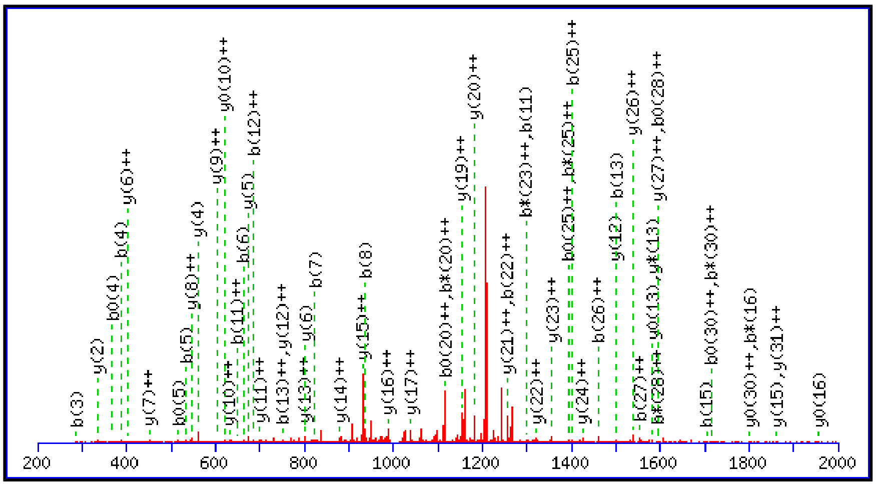
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28313: 4008.776376 from(1003.201370,4+) intensity(64177.7578) rtinseconds(1912) scans(4889) index(22693)
Title: 111019_Est_MI_YS_G_03Spectrum4276_scans__4889
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

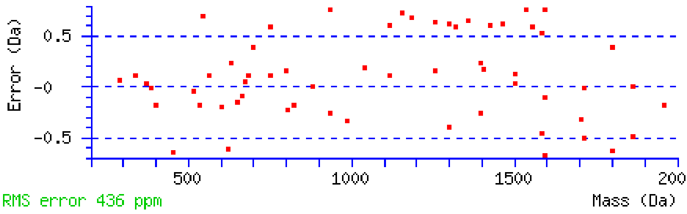
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

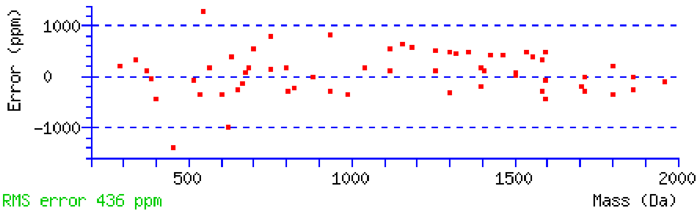


Monoisotopic mass of neutral peptide Mr(calc): 4007.7699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N26 : Deamidated (NQ)
Ions Score: 67 **Expect:** 2e-005
Matches : 60/374 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3893.7503	1947.3788	3876.7237	1938.8655	3875.7397	1938.3735	33
3	**288.1190**	144.5631			270.1084	135.5579	A	3792.7026	1896.8549	3775.6760	1888.3417	3774.6920	1887.8496	32
4	**387.1874**	194.0974			369.1769	185.0921	V	3721.6655	1861.3364	3704.6389	1852.8231	3703.6549	1852.3311	31
5	**534.2558**	267.6316			516.2453	258.6263	F	3622.5970	1811.8022	3605.5705	1803.2889	3604.5865	1802.7969	30
6	**663.2984**	332.1529			645.2879	323.1476	E	3475.5286	1738.2680	3458.5021	1729.7547	3457.5181	1729.2627	29
7	**823.3291**	412.1682			805.3185	403.1629	C	3346.4860	1673.7467	3329.4595	1665.2334	3328.4755	1664.7414	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3186.4554	1593.7313	3169.4288	1585.2181	3168.4448	1584.7261	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3073.3713	1537.1893	3056.3448	1528.6760	3055.3608	1528.1840	26
10	1161.5245	581.2659	1144.4979	572.7526	1143.5139	572.2606	Q	2976.3186	1488.6629	2959.2920	1480.1496	2958.3080	1479.6576	25
11	**1298.5834**	**649.7953**	1281.5569	641.2821	1280.5728	640.7901	H	2848.2600	1424.6336	2831.2334	1416.1204	2830.2494	1415.6283	24
12	1369.6205	**685.3139**	1352.5940	676.8006	1351.6099	676.3086	A	2711.2011	1356.1042	2694.1745	1347.5909	2693.1905	1347.0989	23
13	**1500.6610**	**750.8341**	1483.6345	742.3209	1482.6504	741.8289	M	2640.1640	1320.5856	2623.1374	1312.0723	2622.1534	1311.5803	22
14	1647.7294	824.3683	1630.7029	815.8551	1629.7188	815.3631	F	2509.1235	1255.0654	2492.0969	1246.5521	2491.1129	1246.0601	21
15	**1704.7509**	852.8791	1687.7243	844.3658	1686.7403	843.8738	G	2362.0551	1181.5312	2345.0285	1173.0179	2344.0445	1172.5259	20
16	1818.7938	909.9005	1801.7673	901.3873	1800.7832	900.8953	N	2305.0336	1153.0204	2288.0070	1144.5072	2287.0230	1144.0152	19
17	1933.8207	967.4140	1916.7942	958.9007	1915.8102	958.4087	D	2190.9907	1095.9990	2173.9641	1087.4857	2172.9801	1086.9937	18
18	2034.8684	1017.9379	2017.8419	1009.4246	2016.8579	1008.9326	T	2075.9637	1038.4855	2058.9372	1029.9722	2057.9532	1029.4802	17
19	2147.9525	1074.4799	2130.9259	1065.9666	2129.9419	1065.4746	I	1974.9160	987.9617	1957.8895	979.4484	1956.9055	978.9564	16
20	2249.0002	1125.0037	2231.9736	1116.4904	2230.9896	1115.9984	T	**1861.8320**	931.4196	1844.8054	922.9064	1843.8214	922.4143	15
21	2409.0308	1205.0190	2392.0043	1196.5058	2391.0203	1196.0138	C	1760.7843	880.8958	1743.7578	872.3825	1742.7737	871.8905	14
22	2510.0785	**1255.5429**	2493.0519	1247.0296	2492.0679	1246.5376	T	1600.7537	800.8805	1583.7271	792.3672	1582.7431	791.8752	13
23	2611.1262	1306.0667	2594.0996	1297.5535	2593.1156	1297.0614	T	**1499.7060**	750.3566	1482.6794	741.8434	1481.6954	741.3513	12

24	2748.1851	1374.5962	2731.1585	1366.0829	2730.1745	1365.5909	**H**	1398.6583	699.8328	1381.6317	691.3195	1380.6477	690.8275	**11**
25	2805.2066	**1403.1069**	2788.1800	1394.5936	2787.1960	1394.1016	**G**	1261.5994	631.3033	1244.5728	622.7901	1243.5888	622.2980	**10**
26	2920.2335	**1460.6204**	2903.2069	1452.1071	2902.2229	1451.6151	**N**	1204.5779	602.7926	1187.5514	594.2793	1186.5674	593.7873	**9**
27	3106.3128	**1553.6600**	3089.2863	1545.1468	3088.3022	1544.6548	**W**	1089.5510	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3207.3605	1604.1839	3190.3339	1595.6706	3189.3499	1595.1786	**T**	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3335.4554	1668.2314	3318.4289	1659.7181	3317.4449	1659.2261	**K**	**802.4240**	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3448.5395	1724.7734	3431.5130	1716.2601	3430.5289	1715.7681	**L**	**674.3290**	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3545.5923	1773.2998	3528.5657	1764.7865	3527.5817	1764.2945	**P**	**561.2450**	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3674.6349	1837.8211	3657.6083	1829.3078	3656.6243	1828.8158	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3834.6655	1917.8364	3817.6390	1909.3231	3816.6550	1908.8311	**C**	**335.1496**	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.1	4007.7699	1.0064	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N26 97.86%
50.5	4007.7699	1.0064	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16 2.13%
26.8	4007.7699	1.0064	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10 0.01%
19.4	4006.7859	1.9904	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
9.3	4006.7740	2.0024	YYAVPDGEKQMYIPNQCMQGVPPPIYNYVHGDTK	
6.8	4006.7749	2.0015	DTNDDPDEDHLTSYDIQLSIQESIEASKTALCPER	
6.8	4006.7749	2.0015	DTNDDPDEDHLTSYDIQLSIQESIEASKTALCPER	
6.6	4006.7738	2.0026	SFHVQHSPKQFQLHQDVTGQSQGQNMEVQYMQSK	
5.6	4007.7578	1.0186	SFHVQHSPKQFQLHQDVTGQSQGQNMEVQYMQSK	
5.5	4006.7699	2.0064	QFQSFCCSLSELFMSSFQSYGAPRGDKEELTPQK	

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

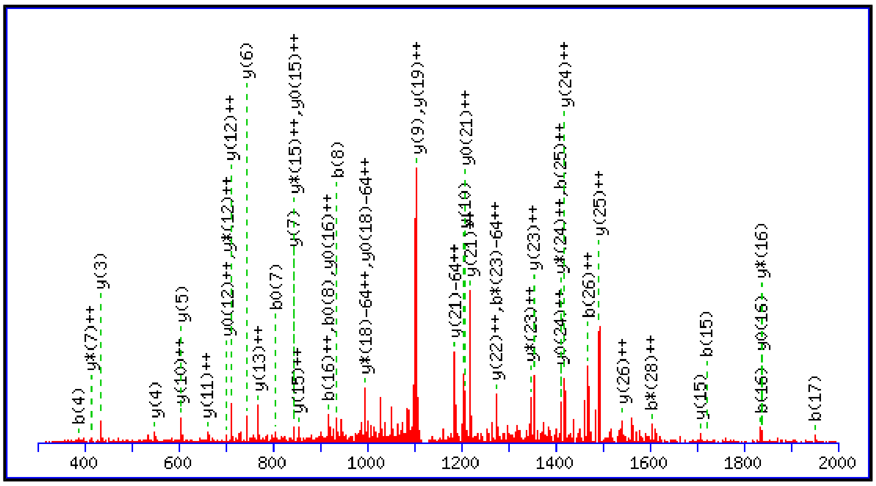
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTK**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 27557: 3369.441792 from(1124.154540,3+) intensity(20308.2070) rtinseconds(1641) scans(4128) index(26686)
Title: 111019_Est_MI_YS_G_09Spectrum3579_scans__4128
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

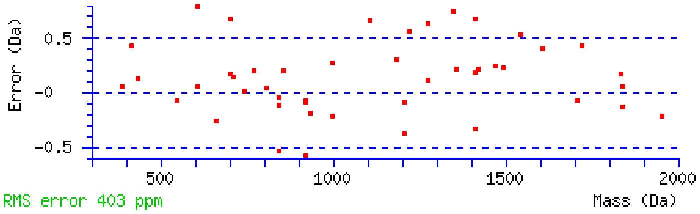
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

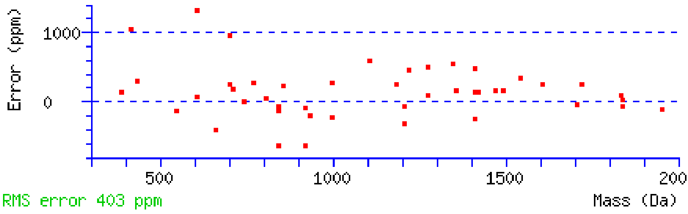


```
Monoisotopic mass of neutral peptide Mr(calc): 3369.4377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N16     : Deamidated (NQ)
N26     : Deamidated (NQ)
Ions Score: 67  Expect: 1.2e-005
Matches : 47/484 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	116.0342	58.5207			98.0237	49.5155	**D**							**29**
2	217.0819	109.0446			199.0713	100.0393	**T**	3255.4180	1628.2126	3238.3915	1619.6994	3237.4074	1619.2074	**28**
3	288.1190	144.5631			270.1084	135.5579	**A**	3154.3703	1577.6888	3137.3438	1569.1755	3136.3598	1568.6835	**27**
4	**387.1874**	194.0974			369.1769	185.0921	**V**	3083.3332	1542.1702	3066.3067	1533.6570	3065.3226	1533.1650	**26**
5	534.2558	267.6316			516.2453	258.6263	**F**	2984.2648	1492.6360	2967.2382	1484.1228	2966.2542	1483.6308	**25**
6	663.2984	332.1529			645.2879	323.1476	**E**	2837.1964	1419.1018	2820.1698	1410.5886	2819.1858	1410.0965	**24**
7	823.3291	412.1682			805.3185	403.1629	**C**	2708.1538	1354.5805	2691.1272	1346.0673	2690.1432	1345.5752	**23**
8	**936.4131**	468.7102			918.4026	459.7049	**L**	2548.1231	1274.5652	2531.0966	1266.0519	2530.1126	1265.5599	**22**
9	1033.4659	517.2366			1015.4553	508.2313	**P**	2435.0391	1218.0232	2418.0125	1209.5099	2417.0285	1209.0179	**21**
10	1161.5245	581.2659	1144.4979	572.7526	1143.5139	572.2606	**Q**	2337.9863	1169.4968	2320.9598	1160.9835	2319.9757	1160.4915	**20**
11	1298.5834	649.7953	1281.5569	641.2821	1280.5728	640.7901	**H**	2209.9277	1105.4675	2192.9012	1096.9542	2191.9172	1096.4622	**19**
12	1369.6205	685.3139	1352.5940	676.8006	1351.6099	676.3086	**A**	2072.8688	1036.9380	2055.8423	1028.4248	2054.8583	1027.9328	**18**
13	1516.6559	758.8316	1499.6294	750.3183	1498.6453	749.8263	**M**	2001.8317	1001.4195	1984.8052	992.9062	1983.8211	992.4142	**17**
14	1663.7243	832.3658	1646.6978	823.8525	1645.7138	823.3605	**F**	1854.7963	927.9018	1837.7698	919.3885	1836.7857	918.8965	**16**
15	**1720.7458**	860.8765	1703.7192	852.3633	1702.7352	851.8713	**G**	***1707.7279***	854.3676	1690.7013	845.8543	1689.7173	845.3623	**15**
16	**1835.7727**	918.3900	1818.7462	909.8767	1817.7622	909.3847	**N**	1650.7064	825.8569	1633.6799	817.3436	1632.6959	816.8516	**14**
17	**1950.7997**	975.9035	1933.7731	967.3902	1932.7891	966.8982	**D**	1535.6795	768.3434	1518.6529	759.8301	1517.6689	759.3381	**13**
18	2051.8474	1026.4273	2034.8208	1017.9140	2033.8368	1017.4220	**T**	1420.6525	710.8299	1403.6260	702.3166	1402.6420	701.8246	**12**
19	2164.9314	1082.9693	2147.9049	1074.4561	2146.9209	1073.9641	**I**	1319.6049	660.3061	1302.5783	651.7928	1301.5943	651.3008	**11**
20	2265.9791	1133.4932	2248.9526	1124.9799	2247.9685	1124.4879	**T**	***1206.5208***	603.7640	1189.4943	595.2508	1188.5102	594.7588	**10**
21	2426.0097	1213.5085	2408.9832	1204.9952	2407.9992	1204.5032	**C**	***1105.4731***	553.2402	1088.4466	544.7269	1087.4626	544.2349	**9**
22	2527.0574	1264.0324	2510.0309	1255.5191	2509.0469	1255.0271	**T**	945.4425	473.2249	928.4159	464.7116	927.4319	464.2196	**8**

23	2628.1051	1314.5562	2611.0786	1306.0429	2610.0945	1305.5509	**T**	***844.3948***	422.7010	827.3682	414.1878	826.3842	413.6958	**7**
24	2765.1640	1383.0856	2748.1375	1374.5724	2747.1535	1374.0804	**H**	***743.3471***	372.1772	726.3206	363.6639	725.3365	363.1719	**6**
25	2822.1855	1411.5964	2805.1589	1403.0831	2804.1749	1402.5911	**G**	***606.2882***	303.6477	589.2617	295.1345	588.2776	294.6425	**5**
26	2937.2124	1469.1099	2920.1859	1460.5966	2919.2019	1460.1046	**N**	***549.2667***	275.1370	532.2402	266.6237	531.2562	266.1317	**4**
27	3123.2917	1562.1495	3106.2652	1553.6362	3105.2812	1553.1442	**W**	***434.2398***	217.6235	417.2132	209.1103	416.2292	208.6183	**3**
28	3224.3394	1612.6733	3207.3129	1604.1601	3206.3289	1603.6681	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.9	3369.4377	0.0041	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated N16, N26 68.03%
63.5	3369.4377	0.0041	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated Q10, N26 30.81%
49.4	3368.4537	0.9881	DTAVFECLPQHAMFGNDTITCTTHGNWTK	
49.3	3369.4377	0.0041	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated Q10, N16 1.16%
36.7	3368.4537	0.9881	DTAVFECLPQHAMFGNDTITCTTHGNWTK	
29.2	3368.4537	0.9881	DTAVFECLPQHAMFGNDTITCTTHGNWTK	
1.4	3369.4298	0.0120	DCEYMGLSATTNTGPWGTGLCQMTGLNFLR	
0.9	3369.4451	-0.0033	MAYNMTFFPNLMGHYDQSIAAVEMEGTQTG	
0.8	3369.4429	-0.0011	TSDMTSPRSGMPSSSTTNGSLTSSTAGLTSMCR	

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

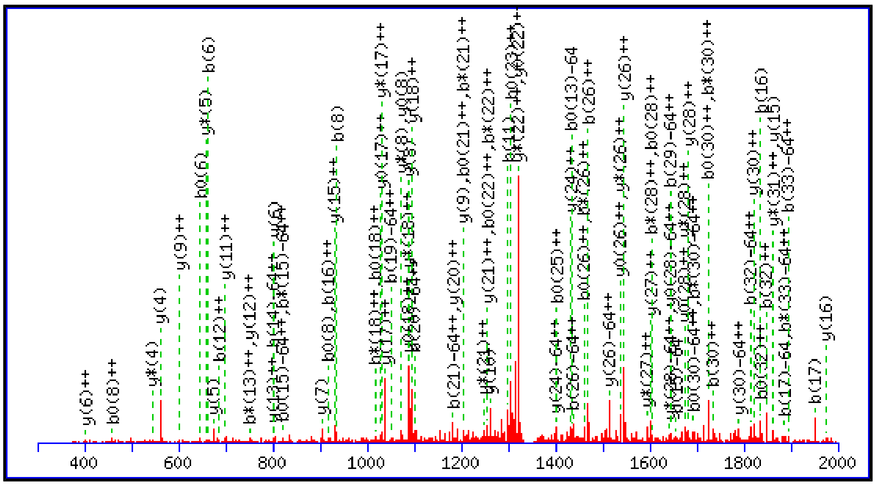
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28339: 4025.759082 from(1342.926970,3+) intensity(27981.1387) rtinseconds(1836) scans(4469) index(10204)
Title: 111019_Est_ISCardio_NMI_YS_G_6Spectrum3798_scans__4469
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

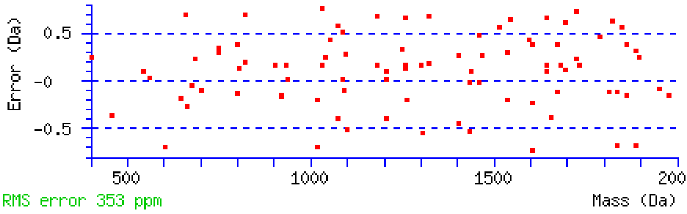
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

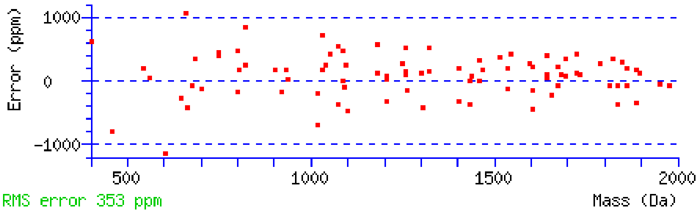


Monoisotopic mass of neutral peptide Mr(calc): 4024.7489
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N16 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 62 **Expect:** 5.4e-005
Matches : 91/572 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3910.7292	1955.8682	3893.7026	1947.3550	3892.7186	1946.8629	33
3	288.1190	144.5631			270.1084	135.5579	A	3809.6815	1905.3444	3792.6550	1896.8311	3791.6709	1896.3391	32
4	387.1874	194.0974			369.1769	185.0921	V	3738.6444	1869.8258	3721.6178	1861.3126	3720.6338	1860.8206	31
5	534.2558	267.6316			516.2453	258.6263	F	3639.5760	1820.2916	3622.5494	1811.7784	3621.5654	1811.2863	30
6	**663.2984**	332.1529			645.2879	323.1476	E	3492.5076	1746.7574	3475.4810	1738.2441	3474.4970	1737.7521	29
7	823.3291	412.1682			805.3185	403.1629	C	3363.4650	1682.2361	3346.4384	1673.7228	3345.4544	1673.2308	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3203.4343	1602.2208	3186.4078	1593.7075	3185.4238	1593.2155	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3090.3503	1545.6788	3073.3237	1537.1655	3072.3397	1536.6735	26
10	1161.5245	581.2659	1144.4979	572.7526	1143.5139	572.2606	Q	2993.2975	1497.1524	2976.2709	1488.6391	2975.2869	1488.1471	25
11	**1298.5834**	649.7953	1281.5569	641.2821	1280.5728	640.7901	H	2865.2389	1433.1231	2848.2124	1424.6098	2847.2283	1424.1178	24
12	1369.6205	**685.3139**	1352.5940	676.8006	1351.6099	676.3086	A	2728.1800	1364.5936	2711.1535	1356.0804	2710.1694	1355.5884	23
13	1516.6559	758.8316	1499.6294	750.3183	1498.6453	749.8263	M	2657.1429	1329.0751	2640.1163	1320.5618	2639.1323	1320.0698	22
14	1663.7243	832.3658	1646.6978	823.8525	1645.7138	823.3605	F	2510.1075	1255.5574	2493.0809	1247.0441	2492.0969	1246.5521	21
15	1720.7458	860.8765	1703.7192	852.3633	1702.7352	851.8713	G	2363.0391	1182.0232	2346.0125	1173.5099	2345.0285	1173.0179	20
16	**1835.7727**	**918.3900**	1818.7462	909.8767	1817.7622	909.3847	N	2306.0176	1153.5124	2288.9911	1144.9992	2288.0070	1144.5072	19
17	**1950.7997**	975.9035	1933.7731	967.3902	1932.7891	966.8982	D	2190.9907	1095.9990	2173.9641	1087.4857	2172.9801	1086.9937	18
18	2051.8474	1026.4273	2034.8208	1017.9140	2033.8368	1017.4220	T	2075.9637	1038.4855	2058.9372	1029.9722	2057.9532	1029.4802	17
19	2164.9314	1082.9693	2147.9049	1074.4561	2146.9209	1073.9641	I	***1974.9160***	987.9617	1957.8895	979.4484	1956.9055	978.9564	16
20	2265.9791	1133.4932	2248.9526	1124.9799	2247.9685	1124.4879	T	***1861.8320***	931.4196	1844.8054	922.9064	1843.8214	922.4143	15
21	2426.0097	1213.5085	2408.9832	1204.9952	2407.9992	1204.5032	C	1760.7843	880.8958	1743.7578	872.3825	1742.7737	871.8905	14
22	2527.0574	1264.0324	2510.0309	1255.5191	2509.0469	1255.0271	T	1600.7537	800.8805	1583.7271	792.3672	1582.7431	791.8752	13

23	2628.1051	1314.5562	2611.0786	1306.0429	2610.0945	1305.5509	**T**	1499.7060	750.3566	1482.6794	741.8434	1481.6954	741.3513	**12**
24	2765.1640	1383.0856	2748.1375	1374.5724	2747.1535	1374.0804	**H**	1398.6583	699.8328	1381.6317	691.3195	1380.6477	690.8275	**11**
25	2822.1855	1411.5964	2805.1589	1403.0831	2804.1749	1402.5911	**G**	***1261.5994***	631.3033	1244.5728	622.7901	1243.5888	622.2980	**10**
26	2937.2124	**1469.1099**	2920.1859	1460.5966	2919.2019	1460.1046	**N**	***1204.5779***	602.7926	1187.5514	594.2793	1186.5674	593.7873	**9**
27	3123.2917	1562.1495	3106.2652	1553.6362	3105.2812	1553.1442	**W**	***1089.5510***	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3224.3394	1612.6733	3207.3129	1604.1601	3206.3289	1603.6681	**T**	***903.4717***	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3352.4344	1676.7208	3335.4078	1668.2076	3334.4238	1667.7155	**K**	***802.4240***	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3465.5184	**1733.2629**	3448.4919	1724.7496	3447.5079	1724.2576	**L**	***674.3290***	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3562.5712	1781.7892	3545.5447	1773.2760	3544.5606	1772.7840	**P**	***561.2450***	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3691.6138	**1846.3105**	3674.5873	1837.7973	3673.6032	1837.3053	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3851.6445	1926.3259	3834.6179	1917.8126	3833.6339	1917.3206	**C**	335.1496	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.9	4024.7489	1.0102	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16, N26 64.45%
58.6	4024.7489	1.0102	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N26 30.15%
51.1	4024.7489	1.0102	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N16 5.40%
42.9	4023.7649	1.9942	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
31.1	4023.7649	1.9942	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
27.8	4023.7649	1.9942	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
4.2	4025.7598	-0.0007	QILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELK	
4.0	4025.7598	-0.0007	QILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELK	
3.7	4024.7756	0.9835	KSPPSYDDDEAPVEMETGENGESSHHSGQLPKSLPQK	
3.7	4024.7756	0.9835	KSPPSYDDDEAPVEMETGENGESSHHSGQLPKSLPQK	

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

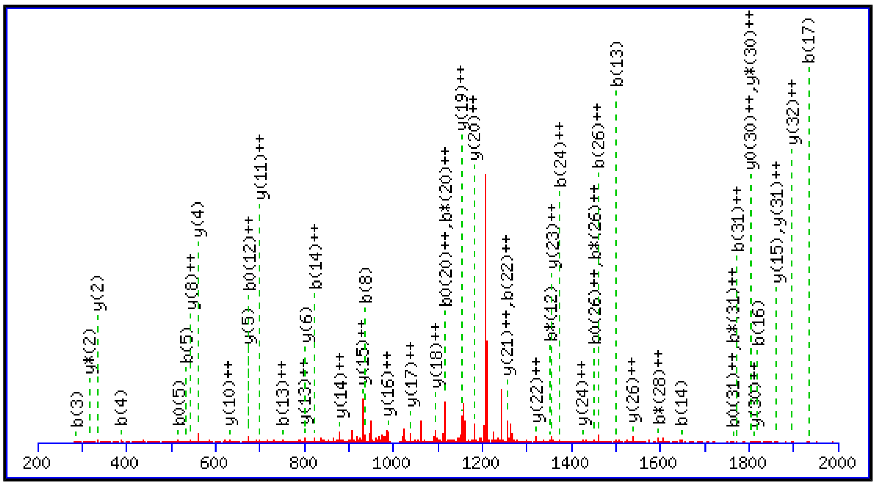
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28304: 4008.771536 from(1003.200160,4+) intensity(15442.9561) rtinseconds(1962) scans(5205) index(24077)
Title: 111019_Est_MI_YS_G_05Spectrum4497_scans__5205
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

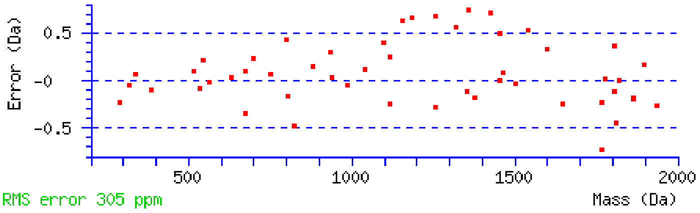
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

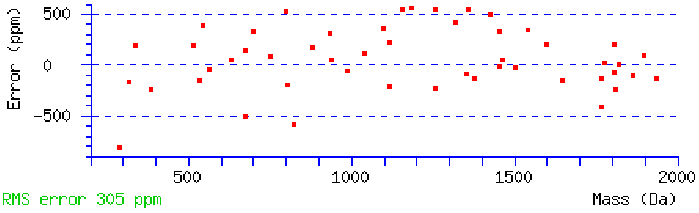


Monoisotopic mass of neutral peptide Mr(calc): 4008.7540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 61 **Expect:** 8.2e-005
Matches : 51/374 fragment ions using 137 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3894.7343	1947.8708	3877.7077	1939.3575	3876.7237	1938.8655	33
3	**288.1190**	144.5631			270.1084	135.5579	A	3793.6866	1897.3469	3776.6600	1888.8337	3775.6760	1888.3417	32
4	**387.1874**	194.0974			369.1769	185.0921	V	3722.6495	1861.8284	3705.6229	1853.3151	3704.6389	1852.8231	31
5	**534.2558**	267.6316			516.2453	258.6263	F	3623.5811	1812.2942	3606.5545	1803.7809	3605.5705	1803.2889	30
6	663.2984	332.1529			645.2879	323.1476	E	3476.5126	1738.7600	3459.4861	1730.2467	3458.5021	1729.7547	29
7	823.3291	412.1682			805.3185	403.1629	C	3347.4701	1674.2387	3330.4435	1665.7254	3329.4595	1665.2334	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3187.4394	1594.2233	3170.4129	1585.7101	3169.4288	1585.2181	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3074.3553	1537.6813	3057.3288	1529.1680	3056.3448	1528.6760	26
10	1162.5085	581.7579	1145.4820	573.2446	1144.4979	572.7526	Q	2977.3026	1489.1549	2960.2760	1480.6417	2959.2920	1480.1496	25
11	1299.5674	650.2873	1282.5409	641.7741	1281.5569	641.2821	H	2848.2600	1424.6336	2831.2334	1416.1204	2830.2494	1415.6283	24
12	1370.6045	685.8059	1353.5780	677.2926	1352.5940	676.8006	A	2711.2011	1356.1042	2694.1745	1347.5909	2693.1905	1347.0989	23
13	**1501.6450**	**751.3261**	1484.6185	742.8129	1483.6345	742.3209	M	2640.1640	1320.5856	2623.1374	1312.0723	2622.1534	1311.5803	22
14	**1648.7134**	**824.8604**	1631.6869	816.3471	1630.7029	815.8551	F	2509.1235	1255.0654	2492.0969	1246.5521	2491.1129	1246.0601	21
15	1705.7349	853.3711	1688.7083	844.8578	1687.7243	844.3658	G	2362.0551	1181.5312	2345.0285	1173.0179	2344.0445	1172.5259	20
16	**1819.7778**	910.3925	1802.7513	901.8793	1801.7673	901.3873	N	2305.0336	1153.0204	2288.0070	1144.5072	2287.0230	1144.0152	19
17	**1934.8048**	967.9060	1917.7782	959.3927	1916.7942	958.9007	D	2190.9907	1095.9990	2173.9641	1087.4857	2172.9801	1086.9937	18
18	2035.8524	1018.4299	2018.8259	1009.9166	2017.8419	1009.4246	T	2075.9637	1038.4855	2058.9372	1029.9722	2057.9532	1029.4802	17
19	2148.9365	1074.9719	2131.9100	1066.4586	2130.9259	1065.9666	I	1974.9160	987.9617	1957.8895	979.4484	1956.9055	978.9564	16
20	2249.9842	1125.4957	2232.9576	1116.9825	2231.9736	1116.4904	T	**1861.8320**	931.4196	1844.8054	922.9064	1843.8214	922.4143	15
21	2410.0148	1205.5111	2392.9883	1196.9978	2392.0043	1196.5058	C	1760.7843	880.8958	1743.7578	872.3825	1742.7737	871.8905	14
22	2511.0625	**1256.0349**	2494.0360	1247.5216	2493.0519	1247.0296	T	1600.7537	800.8805	1583.7271	792.3672	1582.7431	791.8752	13

23	2612.1102	1306.5587	2595.0836	1298.0455	2594.0996	1297.5535	**T**	1499.7060	750.3566	1482.6794	741.8434	1481.6954	741.3513	**12**
24	2749.1691	**1375.0882**	2732.1426	1366.5749	2731.1585	1366.0829	**H**	1398.6583	699.8328	1381.6317	691.3195	1380.6477	690.8275	**11**
25	2806.1906	1403.5989	2789.1640	1395.0856	2788.1800	1394.5936	**G**	1261.5994	631.3033	1244.5728	622.7901	1243.5888	622.2980	**10**
26	2921.2175	**1461.1124**	2904.1910	1452.5991	2903.2069	1452.1071	**N**	1204.5779	602.7926	1187.5514	594.2793	1186.5674	593.7873	**9**
27	3107.2968	1554.1520	3090.2703	1545.6388	3089.2863	1545.1468	**W**	1089.5510	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3208.3445	1604.6759	3191.3180	1596.1626	3190.3339	1595.6706	**T**	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3336.4395	1668.7234	3319.4129	1660.2101	3318.4289	1659.7181	**K**	**802.4240**	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3449.5235	1725.2654	3432.4970	1716.7521	3431.5130	1716.2601	**L**	**674.3290**	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3546.5763	**1773.7918**	3529.5497	1765.2785	3528.5657	1764.7865	**P**	**561.2450**	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3675.6189	1838.3131	3658.5923	1829.7998	3657.6083	1829.3078	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3835.6495	1918.3284	3818.6230	1909.8151	3817.6390	1909.3231	**C**	**335.1496**	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.0	4008.7540	0.0176	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N26 53.31%
59.9	4008.7540	0.0176	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16, N26 42.05%
50.4	4008.7540	0.0176	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N16 4.64%
47.1	4007.7699	1.0016	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
42.1	4007.7699	1.0016	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
19.2	4007.7699	1.0016	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
9.0	4008.7869	-0.0153	ITYFYINMGNQCAALNQERPSHAPNVYRMWNSK	
9.0	4008.7869	-0.0153	ITYFYINMGNQCAALNQERPSHAPNVYRMWNSK	
8.7	4008.7869	-0.0153	ITYFYINMGNQCAALNQERPSHAPNVYRMWNSK	
7.2	4008.7771	-0.0055	GATMSNQMKMAEIVCIEQGEAVVTGLFQISMNGGAER	

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

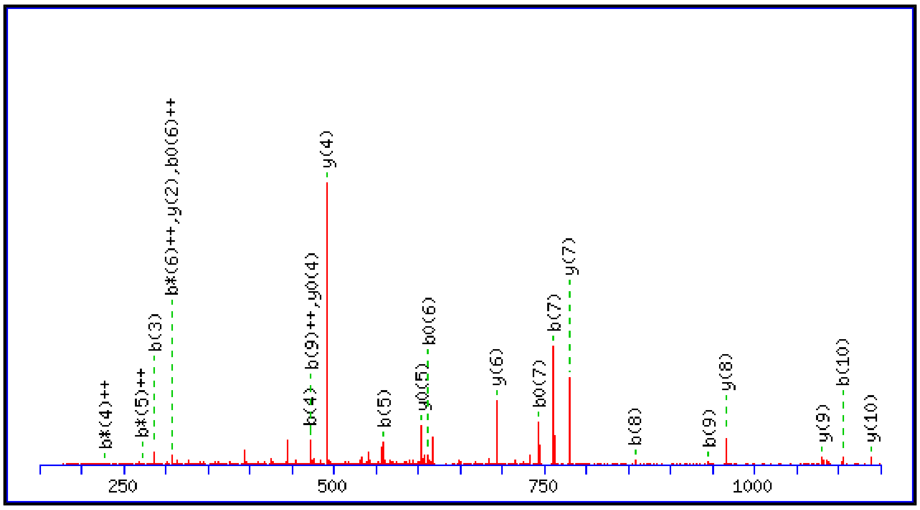
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNWSAMPSCK**
Found in **J3KS17** in **con_Xuniprot_HUMAN3**, J3KS17_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=4 SV=1

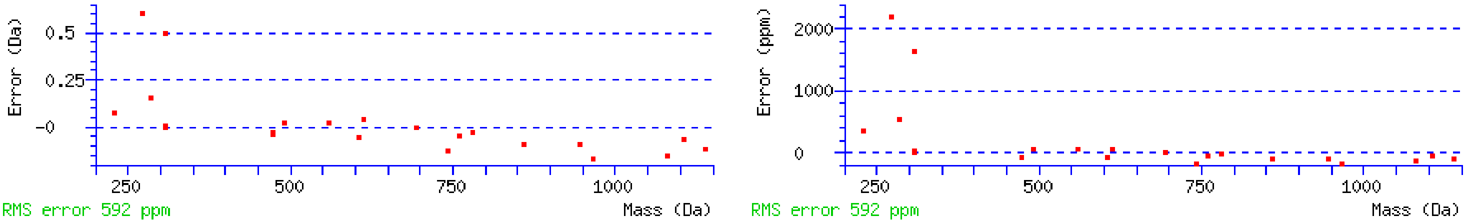
Match to Query 1743: 1250.544788 from(626.279670,2+) intensity(315795.1563) rtinseconds(994) scans(2288) index(23118)
Title: 111019_Est_MI_YS_G_04Spectrum1930_scans__2288
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1250.5424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 59 **Expect:** 9.9e-005
Matches : 23/104 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	114.0913	57.5493					**L**							**11**
2	171.1128	86.0600					**G**	***1138.4656***	569.7364	1121.4390	561.2232	1120.4550	560.7312	**10**
3	***286.1397***	143.5735	269.1132	135.0602			**N**	***1081.4441***	541.2257	1064.4176	532.7124	1063.4336	532.2204	**9**
4	***472.2191***	236.6132	455.1925	228.0999			**W**	***966.4172***	483.7122	949.3906	475.1990	948.4066	474.7069	**8**
5	***559.2511***	280.1292	542.2245	271.6159	541.2405	271.1239	**S**	***780.3379***	390.6726	763.3113	382.1593	762.3273	381.6673	**7**
6	630.2882	315.6477	613.2617	307.1345	612.2776	306.6425	**A**	***693.3058***	347.1566	676.2793	338.6433	675.2953	338.1513	**6**
7	***761.3287***	381.1680	744.3021	372.6547	743.3181	372.1627	**M**	622.2687	311.6380	605.2422	303.1247	604.2582	302.6327	**5**
8	***858.3815***	429.6944	841.3549	421.1811	840.3709	420.6891	**P**	***491.2282***	246.1178	474.2017	237.6045	473.2177	237.1125	**4**
9	***945.4135***	473.2104	928.3869	464.6971	927.4029	464.2051	**S**	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	**3**
10	***1105.4441***	553.2257	1088.4176	544.7124	1087.4336	544.2204	**C**	***307.1435***	154.0754	290.1169	145.5621			**2**
11							**K**	147.1128	74.0600	130.0863	65.5468			**1**



NCBI **BLAST** search of LGNWSAMPSCK

(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	1250.5424	0.0024	LGNWSAMPSCK
1.5	1250.5449	-0.0001	LDGITDDTNCK
0.3	1250.5449	-0.0001	CNTDDTIGDLK

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

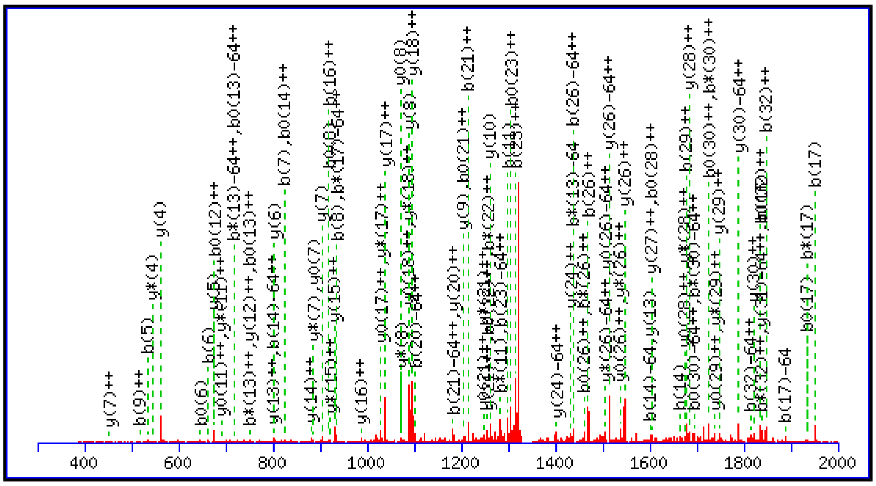
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28350: 4027.759842 from(1343.593890,3+) intensity(22425.1543) rtinseconds(1815) scans(4620) index(26765)
Title: 111019_Est_MI_YS_G_09Spectrum4018_scans__4620
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

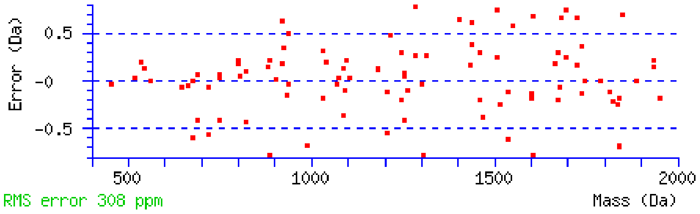
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

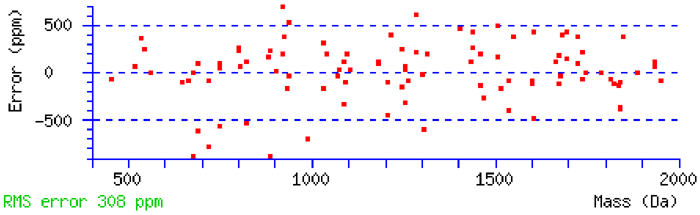


Monoisotopic mass of neutral peptide Mr(calc): 4025.7329
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Deamidated (NQ)
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N16 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00017
Matches : 99/572 fragment ions using 166 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3911.7132	1956.3602	3894.6867	1947.8470	3893.7026	1947.3550	33
3	288.1190	144.5631			270.1084	135.5579	A	3810.6655	1905.8364	3793.6390	1897.3231	3792.6550	1896.8311	32
4	387.1874	194.0974			369.1769	185.0921	V	3739.6284	1870.3178	3722.6019	1861.8046	3721.6178	1861.3126	31
5	**534.2558**	267.6316			516.2453	258.6263	F	3640.5600	1820.7836	3623.5334	1812.2704	3622.5494	1811.7784	30
6	**663.2984**	332.1529			645.2879	323.1476	E	3493.4916	1747.2494	3476.4650	1738.7362	3475.4810	1738.2441	29
7	**823.3291**	412.1682			805.3185	403.1629	C	3364.4490	1682.7281	3347.4224	1674.2149	3346.4384	1673.7228	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3204.4183	1602.7128	3187.3918	1594.1995	3186.4078	1593.7075	27
9	1033.4659	**517.2366**			1015.4553	508.2313	P	3091.3343	1546.1708	3074.3077	1537.6575	3073.3237	1537.1655	26
10	1162.5085	581.7579	1145.4820	573.2446	1144.4979	572.7526	Q	2994.2815	1497.6444	2977.2550	1489.1311	2976.2709	1488.6391	25
11	**1299.5674**	650.2873	1282.5409	641.7741	1281.5569	641.2821	H	2865.2389	1433.1231	2848.2124	1424.6098	2847.2283	1424.1178	24
12	1370.6045	685.8059	1353.5780	677.2926	1352.5940	676.8006	A	2728.1800	1364.5936	2711.1535	1356.0804	2710.1694	1355.5884	23
13	1517.6399	759.3236	1500.6134	750.8103	1499.6294	750.3183	M	2657.1429	1329.0751	2640.1163	1320.5618	2639.1323	1320.0698	22
14	**1664.7083**	832.8578	1647.6818	824.3445	1646.6978	823.8525	F	2510.1075	1255.5574	2493.0809	1247.0441	2492.0969	1246.5521	21
15	1721.7298	861.3685	1704.7033	852.8553	1703.7192	852.3633	G	2363.0391	1182.0232	2346.0125	1173.5099	2345.0285	1173.0179	20
16	**1836.7568**	**918.8820**	1819.7302	910.3687	1818.7462	909.8767	N	2306.0176	1153.5124	2288.9911	1144.9992	2288.0070	1144.5072	19
17	**1951.7837**	976.3955	1934.7571	967.8822	1933.7731	967.3902	D	2190.9907	1095.9990	2173.9641	1087.4857	2172.9801	1086.9937	18
18	2052.8314	1026.9193	2035.8048	1018.4061	2034.8208	1017.9140	T	2075.9637	1038.4855	2058.9372	1029.9722	2057.9532	1029.4802	17
19	2165.9154	1083.4614	2148.8889	1074.9481	2147.9049	1074.4561	I	1974.9160	987.9617	1957.8895	979.4484	1956.9055	978.9564	16
20	2266.9631	1133.9852	2249.9366	1125.4719	2248.9526	1124.9799	T	1861.8320	931.4196	1844.8054	922.9064	1843.8214	922.4143	15
21	2426.9938	**1214.0005**	2409.9672	1205.4872	2408.9832	1204.9952	C	1760.7843	880.8958	1743.7578	872.3825	1742.7737	871.8905	14

22	2528.0414	1264.5244	2511.0149	1256.0111	2510.0309	1255.5191	**T**	***1600.7537***	800.8805	1583.7271	792.3672	1582.7431	791.8752	**13**
23	2629.0891	**1315.0482**	2612.0626	1306.5349	2611.0786	1306.0429	**T**	1499.7060	750.3566	1482.6794	741.8434	1481.6954	741.3513	**12**
24	2766.1480	1383.5777	2749.1215	1375.0644	2748.1375	1374.5724	**H**	1398.6583	699.8328	1381.6317	691.3195	1380.6477	690.8275	**11**
25	2823.1695	1412.0884	2806.1429	1403.5751	2805.1589	1403.0831	**G**	***1261.5994***	631.3033	1244.5728	622.7901	1243.5888	622.2980	**10**
26	2938.1964	**1469.6019**	2921.1699	1461.0886	2920.1859	1460.5966	**N**	***1204.5779***	602.7926	1187.5514	594.2793	1186.5674	593.7873	**9**
27	3124.2758	1562.6415	3107.2492	1554.1282	3106.2652	1553.6362	**W**	***1089.5510***	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3225.3234	1613.1654	3208.2969	1604.6521	3207.3129	1604.1601	**T**	***903.4717***	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3353.4184	**1677.2128**	3336.3918	1668.6996	3335.4078	1668.2076	**K**	***802.4240***	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3466.5025	1733.7549	3449.4759	1725.2416	3448.4919	1724.7496	**L**	***674.3290***	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3563.5552	1782.2813	3546.5287	1773.7680	3545.5447	1773.2760	**P**	***561.2450***	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3692.5978	**1846.8025**	3675.5713	1838.2893	3674.5873	1837.7973	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3852.6285	1926.8179	3835.6019	1918.3046	3834.6179	1917.8126	**C**	335.1496	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
56.7	4025.7329	2.0270	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR
2.5	4026.7735	0.9863	SRDEENDEDVRNGLFSYHGQLDDGMCLLTPVSIDK
1.9	4027.7665	-0.0067	SCFHIICLVGTISLACNDMTPEQMATNVNCSSPER
1.3	4026.7575	1.0024	TMPPPNMGMPAMPTMPPMQHQIPRQFIQVHAMQR
1.3	4026.7575	1.0024	TMPPPNMGMPAMPTMPPMQHQIPRQFIQVHAMQR
1.3	4026.7575	1.0024	TMPPPNMGMPAMPTMPPMQHQIPRQFIQVHAMQR
1.0	4025.7625	1.9973	MERVNDASCGPSGCYTYQVSRHSTEMLHNLNQQR
1.0	4025.7625	1.9973	MERVNDASCGPSGCYTYQVSRHSTEMLHNLNQQR
0.7	4026.7498	1.0100	NNCYQFFDESKNWYESQASCMSQNASLLKVYSK
0.7	4025.7735	1.9864	TMPPPNMGMPAMPTMPPMQHQIPRQFIQVHAMQR

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

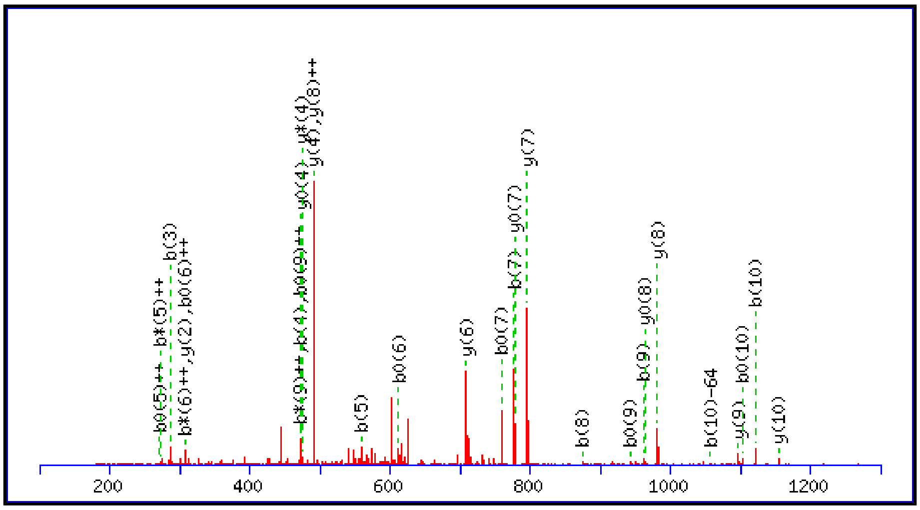
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNWSAMPSCK**
Found in **J3KS17** in **con_Xuniprot_HUMAN3**, J3KS17_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=4 SV=1

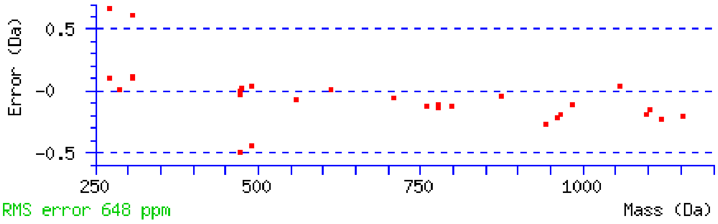
Match to Query 1776: 1266.540328 from(634.277440,2+) intensity(53583.2227) rtinseconds(510) scans(1039) index(5001)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum901_scans__1039
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

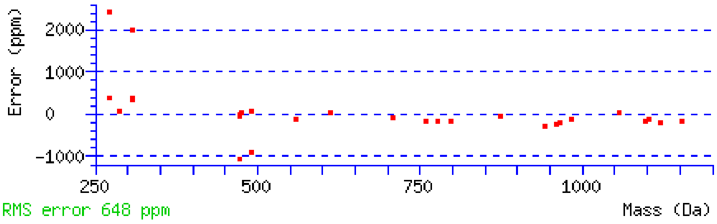
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1266.5373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3     : Deamidated (NQ)
M7     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54  Expect: 0.00022
Matches : 30/164 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	114.0913	57.5493					L							11
2	171.1128	86.0600					G	***1154.4605***	577.7339	1137.4340	569.2206	1136.4499	568.7286	10
3	***286.1397***	143.5735	269.1132	135.0602			N	***1097.4390***	549.2232	1080.4125	540.7099	1079.4285	540.2179	9
4	***472.2191***	236.6132	455.1925	228.0999			W	***982.4121***	491.7097	965.3856	483.1964	964.4015	482.7044	8
5	***559.2511***	280.1292	542.2245	271.6159	541.2405	271.1239	S	***796.3328***	398.6700	779.3062	390.1568	778.3222	389.6647	7
6	630.2882	315.6477	613.2617	307.1345	612.2776	306.6425	A	***709.3008***	355.1540	692.2742	346.6407	691.2902	346.1487	6
7	***777.3236***	389.1654	760.2971	380.6522	759.3130	380.1602	M	638.2636	319.6355	621.2371	311.1222	620.2531	310.6302	5
8	***874.3764***	437.6918	857.3498	429.1785	856.3658	428.6865	P	***491.2282***	246.1178	474.2017	237.6045	473.2177	237.1125	4
9	***961.4084***	481.2078	944.3818	472.6946	943.3978	472.2026	S	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
10	***1121.4390***	561.2232	1104.4125	552.7099	1103.4285	552.2179	C	***307.1435***	154.0754	290.1169	145.5621			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGNWSAMPSCK
(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	1266.5373	0.0031	LGNWSAMPSCK
10.3	1266.5373	0.0030	LFTEMHSDCK
0.7	1266.5397	0.0006	KNEENEKSCK
0.1	1265.5420	0.9983	YGEALMLHDAM

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

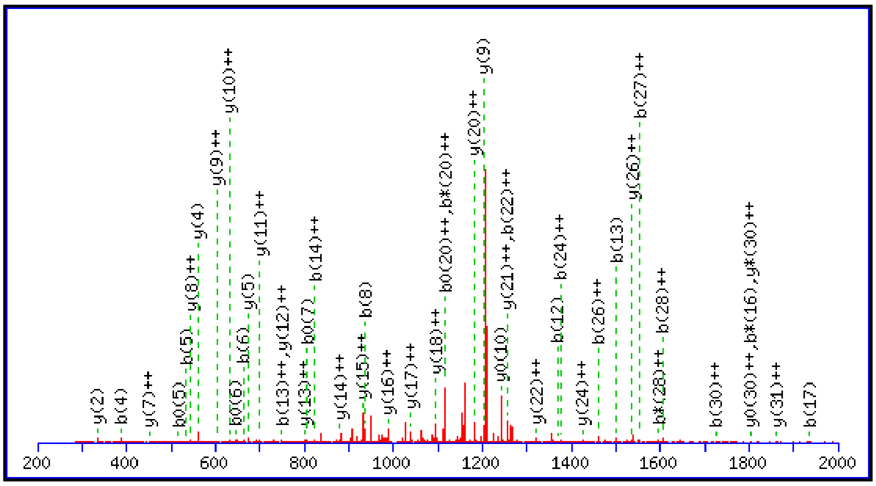
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28315: 4008.781136 from(1003.202560,4+) intensity(55459.2969) rtinseconds(1970) scans(5058) index(26836)
Title: 111019_Est_MI_YS_G_09Spectrum4402_scans__5058
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

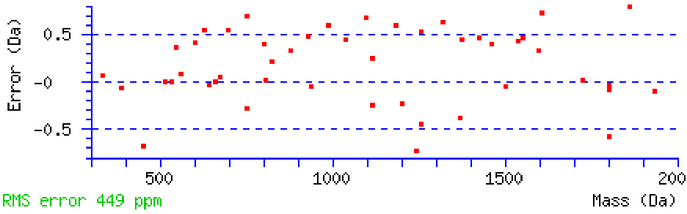
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

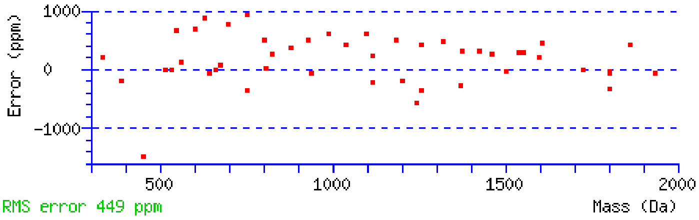


Monoisotopic mass of neutral peptide Mr(calc): 4007.7699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.00049
Matches : 47/374 fragment ions using 120 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3893.7503	1947.3788	3876.7237	1938.8655	3875.7397	1938.3735	33
3	288.1190	144.5631			270.1084	135.5579	A	3792.7026	1896.8549	3775.6760	1888.3417	3774.6920	1887.8496	32
4	387.1874	194.0974			369.1769	185.0921	V	3721.6655	1861.3364	3704.6389	1852.8231	3703.6549	1852.3311	31
5	534.2558	267.6316			516.2453	258.6263	F	3622.5970	1811.8022	3605.5705	1803.2889	3604.5865	1802.7969	30
6	663.2984	332.1529			645.2879	323.1476	E	3475.5286	1738.2680	3458.5021	1729.7547	3457.5181	1729.2627	29
7	823.3291	412.1682			805.3185	403.1629	C	3346.4860	1673.7467	3329.4595	1665.2334	3328.4755	1664.7414	28
8	936.4131	468.7102			918.4026	459.7049	L	3186.4554	1593.7313	3169.4288	1585.2181	3168.4448	1584.7261	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3073.3713	1537.1893	3056.3448	1528.6760	3055.3608	1528.1840	26
10	1161.5245	581.2659	1144.4979	572.7526	1143.5139	572.2606	Q	2976.3186	1488.6629	2959.2920	1480.1496	2958.3080	1479.6576	25
11	1298.5834	649.7953	1281.5569	641.2821	1280.5728	640.7901	H	2848.2600	1424.6336	2831.2334	1416.1204	2830.2494	1415.6283	24
12	1369.6205	685.3139	1352.5940	676.8006	1351.6099	676.3086	A	2711.2011	1356.1042	2694.1745	1347.5909	2693.1905	1347.0989	23
13	1500.6610	750.8341	1483.6345	742.3209	1482.6504	741.8289	M	2640.1640	1320.5856	2623.1374	1312.0723	2622.1534	1311.5803	22
14	1647.7294	824.3683	1630.7029	815.8551	1629.7188	815.3631	F	2509.1235	1255.0654	2492.0969	1246.5521	2491.1129	1246.0601	21
15	1704.7509	852.8791	1687.7243	844.3658	1686.7403	843.8738	G	2362.0551	1181.5312	2345.0285	1173.0179	2344.0445	1172.5259	20
16	1819.7778	910.3925	1802.7513	901.8793	1801.7673	901.3873	N	2305.0336	1153.0204	2288.0070	1144.5072	2287.0230	1144.0152	19
17	1934.8048	967.9060	1917.7782	959.3927	1916.7942	958.9007	D	2190.0067	1095.5070	2172.9801	1086.9937	2171.9961	1086.5017	18
18	2035.8524	1018.4299	2018.8259	1009.9166	2017.8419	1009.4246	T	2074.9797	1037.9935	2057.9532	1029.4802	2056.9691	1028.9882	17
19	2148.9365	1074.9719	2131.9100	1066.4586	2130.9259	1065.9666	I	1973.9320	987.4697	1956.9055	978.9564	1955.9215	978.4644	16
20	2249.9842	1125.4957	2232.9576	1116.9825	2231.9736	1116.4904	T	1860.8480	930.9276	1843.8214	922.4143	1842.8374	921.9223	15
21	2410.0148	1205.5111	2392.9883	1196.9978	2392.0043	1196.5058	C	1759.8003	880.4038	1742.7737	871.8905	1741.7897	871.3985	14
22	2511.0625	1256.0349	2494.0360	1247.5216	2493.0519	1247.0296	T	1599.7696	800.3885	1582.7431	791.8752	1581.7591	791.3832	13
23	2612.1102	1306.5587	2595.0836	1298.0455	2594.0996	1297.5535	T	1498.7220	749.8646	1481.6954	741.3513	1480.7114	740.8593	12

24	2749.1691	**1375.0882**	2732.1426	1366.5749	2731.1585	1366.0829	**H**	1397.6743	699.3408	1380.6477	690.8275	1379.6637	690.3355	**11**
25	2806.1906	1403.5989	2789.1640	1395.0856	2788.1800	1394.5936	**G**	1260.6154	630.8113	1243.5888	622.2980	1242.6048	621.8060	**10**
26	2920.2335	**1460.6204**	2903.2069	1452.1071	2902.2229	1451.6151	**N**	1203.5939	602.3006	1186.5674	593.7873	1185.5833	593.2953	**9**
27	3106.3128	**1553.6600**	3089.2863	1545.1468	3088.3022	1544.6548	**W**	1089.5510	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3207.3605	**1604.1839**	3190.3339	1595.6706	3189.3499	1595.1786	**T**	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3335.4554	1668.2314	3318.4289	1659.7181	3317.4449	1659.2261	**K**	802.4240	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3448.5395	**1724.7734**	3431.5130	1716.2601	3430.5289	1715.7681	**L**	674.3290	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3545.5923	1773.2998	3528.5657	1764.7865	3527.5817	1764.2945	**P**	561.2450	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3674.6349	1837.8211	3657.6083	1829.3078	3656.6243	1828.8158	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3834.6655	1917.8364	3817.6390	1909.3231	3816.6550	1908.8311	**C**	335.1496	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.5	4007.7699	1.0112	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16 53.39%
52.4	4007.7699	1.0112	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N26 41.06%
43.7	4007.7699	1.0112	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10 5.55%
22.8	4006.7859	1.9952	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	
4.4	4008.7957	-0.0145	EQQRPPPRPQQQQQQQQWSNLGRQVAERSSGGR	

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

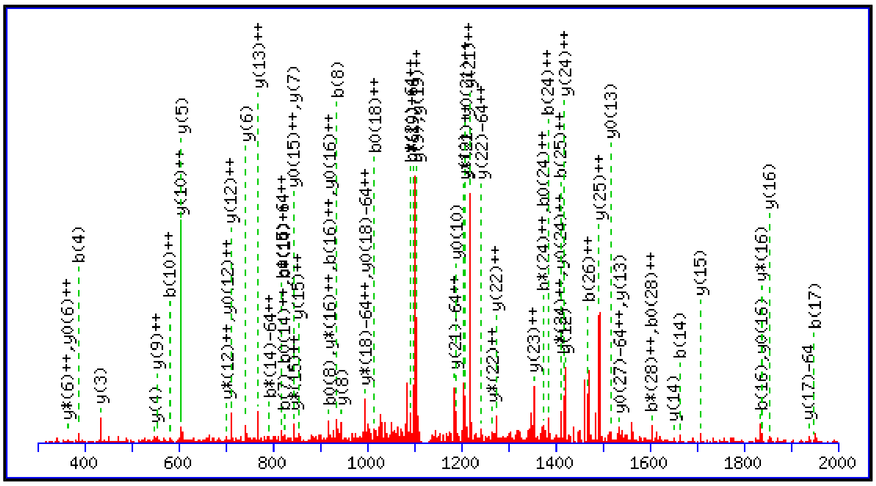
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTK**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 27558: 3369.470502 from(1124.164110,3+) intensity(8820.1172) rtinseconds(1637) scans(4117) index(26683)
Title: 111019_Est_MI_YS_G_09Spectrum3569_scans__4117
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

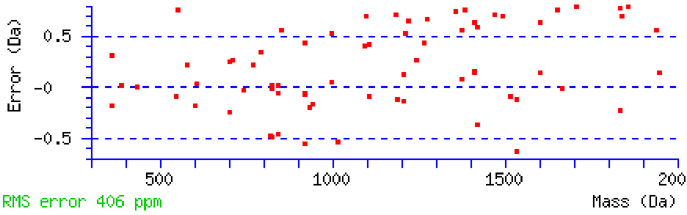
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

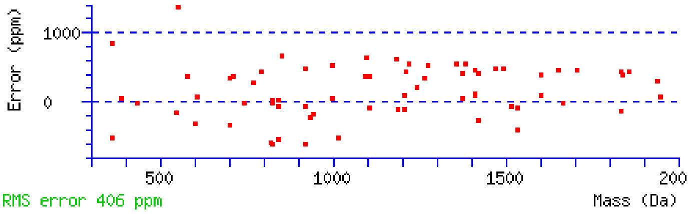


Monoisotopic mass of neutral peptide Mr(calc): 3368.4537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N26 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0024
Matches : 70/484 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							29
2	217.0819	109.0446			199.0713	100.0393	T	3254.4340	1627.7206	3237.4074	1619.2074	3236.4234	1618.7153	28
3	288.1190	144.5631			270.1084	135.5579	A	3153.3863	1577.1968	3136.3598	1568.6835	3135.3757	1568.1915	27
4	**387.1874**	194.0974			369.1769	185.0921	V	3082.3492	1541.6782	3065.3226	1533.1650	3064.3386	1532.6730	26
5	534.2558	267.6316			516.2453	258.6263	F	2983.2808	1492.1440	2966.2542	1483.6308	2965.2702	1483.1387	25
6	663.2984	332.1529			645.2879	323.1476	E	2836.2124	1418.6098	2819.1858	1410.0965	2818.2018	1409.6045	24
7	**823.3291**	412.1682			805.3185	403.1629	C	2707.1698	1354.0885	2690.1432	1345.5752	2689.1592	1345.0832	23
8	**936.4131**	468.7102			918.4026	459.7049	L	2547.1391	1274.0732	2530.1126	1265.5599	2529.1286	1265.0679	22
9	1033.4659	517.2366			1015.4553	508.2313	P	2434.0551	1217.5312	2417.0285	1209.0179	2416.0445	1208.5259	21
10	1161.5245	**581.2659**	1144.4979	572.7526	1143.5139	572.2606	Q	2337.0023	1169.0048	2319.9757	1160.4915	2318.9917	1159.9995	20
11	1298.5834	649.7953	1281.5569	641.2821	1280.5728	640.7901	H	2208.9437	1104.9755	2191.9172	1096.4622	2190.9332	1095.9702	19
12	1369.6205	685.3139	1352.5940	676.8006	1351.6099	676.3086	A	2071.8848	1036.4460	2054.8583	1027.9328	2053.8742	1027.4408	18
13	1516.6559	758.8316	1499.6294	750.3183	1498.6453	749.8263	M	2000.8477	1000.9275	1983.8211	992.4142	1982.8371	991.9222	17
14	**1663.7243**	832.3658	1646.6978	823.8525	1645.7138	823.3605	F	***1853.8123***	927.4098	1836.7857	918.8965	1835.8017	918.4045	16
15	1720.7458	860.8765	1703.7192	852.3633	1702.7352	851.8713	G	***1706.7439***	853.8756	1689.7173	845.3623	1688.7333	844.8703	15
16	**1834.7887**	**917.8980**	1817.7622	909.3847	1816.7782	908.8927	N	***1649.7224***	825.3648	1632.6959	816.8516	1631.7118	816.3596	14
17	**1949.8157**	975.4115	1932.7891	966.8982	1931.8051	966.4062	D	***1535.6795***	768.3434	1518.6529	759.8301	1517.6689	759.3381	13
18	2050.8633	1025.9353	2033.8368	1017.4220	2032.8528	1016.9300	T	***1420.6525***	710.8299	1403.6260	702.3166	1402.6420	701.8246	12
19	2163.9474	1082.4773	2146.9209	1073.9641	2145.9368	1073.4721	I	1319.6049	660.3061	1302.5783	651.7928	1301.5943	651.3008	11
20	2264.9951	1133.0012	2247.9685	1124.4879	2246.9845	1123.9959	T	***1206.5208***	603.7640	1189.4943	595.2508	1188.5102	594.7588	10
21	2425.0257	1213.0165	2407.9992	1204.5032	2407.0152	1204.0112	C	***1105.4731***	553.2402	1088.4466	544.7269	1087.4626	544.2349	9
22	2526.0734	1263.5403	2509.0469	1255.0271	2508.0628	1254.5351	T	***945.4425***	473.2249	928.4159	464.7116	927.4319	464.2196	8

23	2627.1211	1314.0642	2610.0945	1305.5509	2609.1105	1305.0589	**T**	***844.3948***	422.7010	827.3682	414.1878	826.3842	413.6958	**7**
24	2764.1800	**1382.5936**	2747.1535	1374.0804	2746.1694	1373.5884	**H**	***743.3471***	372.1772	726.3206	363.6639	725.3365	363.1719	**6**
25	2821.2015	**1411.1044**	2804.1749	1402.5911	2803.1909	1402.0991	**G**	***606.2882***	303.6477	589.2617	295.1345	588.2776	294.6425	**5**
26	2936.2284	**1468.6178**	2919.2019	1460.1046	2918.2178	1459.6126	**N**	***549.2667***	275.1370	532.2402	266.6237	531.2562	266.1317	**4**
27	3122.3077	1561.6575	3105.2812	1553.1442	3104.2972	1552.6522	**W**	***434.2398***	217.6235	417.2132	209.1103	416.2292	208.6183	**3**
28	3223.3554	1612.1813	3206.3289	1603.6681	3205.3448	1603.1761	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.2	3368.4537	1.0168	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated N26 99.40%
21.8	3368.4537	1.0168	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated N16 0.46%
16.7	3368.4537	1.0168	DTAVFECLPQHAMFGNDTITCTTHGNWTK	Deamidated Q10 0.14%
2.2	3367.4697	2.0008	DTAVFECLPQHAMFGNDTITCTTHGNWTK	
1.7	3368.4589	1.0116	TSDMTSPRSGMPSSSTTNGSLTSSTAGLTSMCR	
1.0	3367.4478	2.0227	GPMSGHCNCPLQRYPNEEVMNGDKQFIR	
1.0	3367.4478	2.0227	GPMSGHCNCPLQRYPNEEVMNGDKQFIR	
0.8	3368.4589	1.0116	TSDMTSPRSGMPSSSTTNGSLTSSTAGLTSMCR	
0.7	3367.4478	2.0227	GPMSGHCNCPLQRYPNEEVMNGDKQFIR	

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

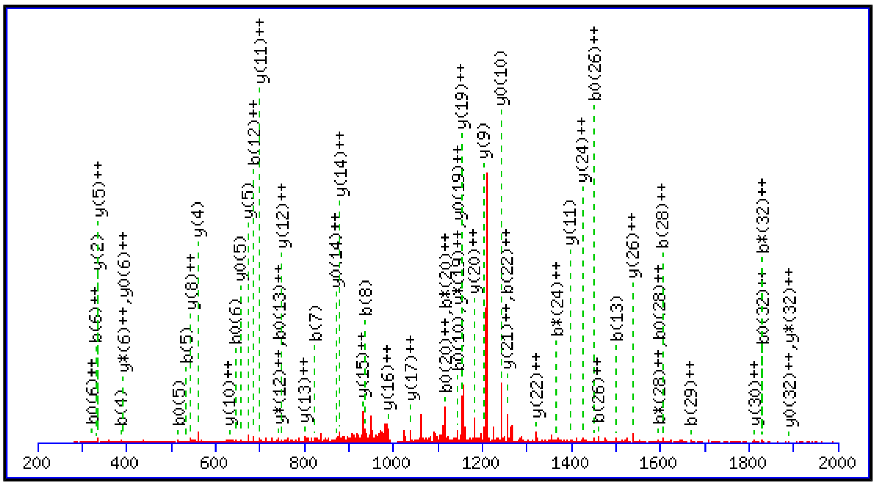
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR**
Found in **J3QLI0** in **con_Xuniprot_HUMAN3**, J3QLI0_HUMAN Beta-2-glycoprotein 1 (Fragment) OS=Homo sapiens GN=APOH PE=2 SV=1

Match to Query 28289: 4008.755776 from(1003.196220,4+) intensity(16854.0879) rtinseconds(1951) scans(5083) index(16006)
Title: 111019_Est_MI_YP_G_05Spectrum4316_scans__5083
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

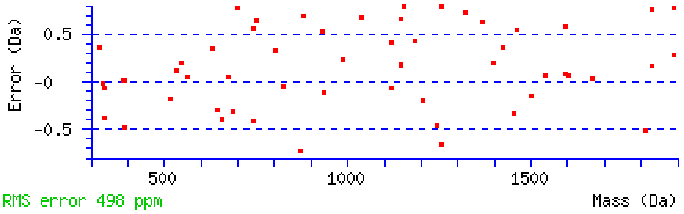
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

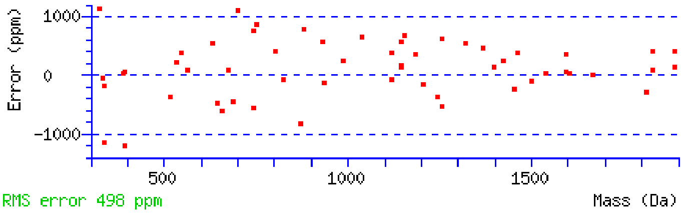


```
Monoisotopic mass of neutral peptide Mr(calc): 4008.7540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Deamidated (NQ)
N16     : Deamidated (NQ)
Ions Score: 41  Expect: 0.0061
Matches : 56/374 fragment ions using 154 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							34
2	217.0819	109.0446			199.0713	100.0393	T	3894.7343	1947.8708	3877.7077	1939.3575	3876.7237	1938.8655	33
3	288.1190	144.5631			270.1084	135.5579	A	3793.6866	1897.3469	3776.6600	1888.8337	3775.6760	1888.3417	32
4	**387.1874**	194.0974			369.1769	185.0921	V	3722.6495	1861.8284	3705.6229	1853.3151	3704.6389	1852.8231	31
5	**534.2558**	267.6316			516.2453	258.6263	F	3623.5811	1812.2942	3606.5545	1803.7809	3605.5705	1803.2889	30
6	663.2984	**332.1529**			645.2879	323.1476	E	3476.5126	1738.7600	3459.4861	1730.2467	3458.5021	1729.7547	29
7	**823.3291**	412.1682			805.3185	403.1629	C	3347.4701	1674.2387	3330.4435	1665.7254	3329.4595	1665.2334	28
8	**936.4131**	468.7102			918.4026	459.7049	L	3187.4394	1594.2233	3170.4129	1585.7101	3169.4288	1585.2181	27
9	1033.4659	517.2366			1015.4553	508.2313	P	3074.3553	1537.6813	3057.3288	1529.1680	3056.3448	1528.6760	26
10	1162.5085	581.7579	1145.4820	573.2446	1144.4979	572.7526	Q	2977.3026	1489.1549	2960.2760	1480.6417	2959.2920	1480.1496	25
11	1299.5674	650.2873	1282.5409	641.7741	1281.5569	641.2821	H	2848.2600	1424.6336	2831.2334	1416.1204	2830.2494	1415.6283	24
12	1370.6045	**685.8059**	1353.5780	677.2926	1352.5940	676.8006	A	2711.2011	1356.1042	2694.1745	1347.5909	2693.1905	1347.0989	23
13	**1501.6450**	751.3261	1484.6185	742.8129	1483.6345	742.3209	M	2640.1640	1320.5856	2623.1374	1312.0723	2622.1534	1311.5803	22
14	1648.7134	824.8604	1631.6869	816.3471	1630.7029	815.8551	F	2509.1235	1255.0654	2492.0969	1246.5521	2491.1129	1246.0601	21
15	1705.7349	853.3711	1688.7083	844.8578	1687.7243	844.3658	G	2362.0551	1181.5312	2345.0285	1173.0179	2344.0445	1172.5259	20
16	1820.7618	910.8846	1803.7353	902.3713	1802.7513	901.8793	N	2305.0336	1153.0204	2288.0070	1144.5072	2287.0230	1144.0152	19
17	1935.7888	968.3980	1918.7622	959.8848	1917.7782	959.3927	D	2190.0067	1095.5070	2172.9801	1086.9937	2171.9961	1086.5017	18
18	2036.8365	1018.9219	2019.8099	1010.4086	2018.8259	1009.9166	T	2074.9797	1037.9935	2057.9532	1029.4802	2056.9691	1028.9882	17
19	2149.9205	1075.4639	2132.8940	1066.9506	2131.9100	1066.4586	I	1973.9320	987.4697	1956.9055	978.9564	1955.9215	978.4644	16
20	2250.9682	1125.9877	2233.9417	1117.4745	2232.9576	1116.9825	T	1860.8480	930.9276	1843.8214	922.4143	1842.8374	921.9223	15
21	2410.9988	1206.0031	2393.9723	1197.4898	2392.9883	1196.9978	C	1759.8003	880.4038	1742.7737	871.8905	1741.7897	871.3985	14
22	2512.0465	**1256.5269**	2495.0200	1248.0136	2494.0360	1247.5216	T	1599.7696	800.3885	1582.7431	791.8752	1581.7591	791.3832	13

23	2613.0942	1307.0507	2596.0677	1298.5375	2595.0836	1298.0455	**T**	1498.7220	749.8646	1481.6954	741.3513	1480.7114	740.8593	**12**
24	2750.1531	1375.5802	2733.1266	1367.0669	2732.1426	1366.5749	**H**	**1397.6743**	699.3408	1380.6477	690.8275	1379.6637	690.3355	**11**
25	2807.1746	1404.0909	2790.1480	1395.5777	2789.1640	1395.0856	**G**	1260.6154	630.8113	1243.5888	622.2980	1242.6048	621.8060	**10**
26	2921.2175	**1461.1124**	2904.1910	1452.5991	2903.2069	1452.1071	**N**	**1203.5939**	602.3006	1186.5674	593.7873	1185.5833	593.2953	**9**
27	3107.2968	1554.1520	3090.2703	1545.6388	3089.2863	1545.1468	**W**	1089.5510	545.2791	1072.5244	536.7659	1071.5404	536.2738	**8**
28	3208.3445	**1604.6759**	3191.3180	1596.1626	3190.3339	1595.6706	**T**	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	**7**
29	3336.4395	**1668.7234**	3319.4129	1660.2101	3318.4289	1659.7181	**K**	802.4240	401.7156	785.3974	393.2024	784.4134	392.7103	**6**
30	3449.5235	1725.2654	3432.4970	1716.7521	3431.5130	1716.2601	**L**	**674.3290**	337.6681	657.3025	329.1549	656.3185	328.6629	**5**
31	3546.5763	1773.7918	3529.5497	1765.2785	3528.5657	1764.7865	**P**	**561.2450**	281.1261	544.2184	272.6128	543.2344	272.1208	**4**
32	3675.6189	1838.3131	3658.5923	1829.7998	3657.6083	1829.3078	**E**	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	**3**
33	3835.6495	1918.3284	3818.6230	1909.8151	3817.6390	1909.3231	**C**	**335.1496**	168.0784	318.1231	159.5652			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.5	4008.7540	0.0018	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N16 53.12%
40.2	4008.7540	0.0018	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated N16, N26 39.56%
39.8	4007.7699	0.9858	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
32.9	4008.7540	0.0018	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	Deamidated Q10, N26 7.32%
27.3	4007.7699	0.9858	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
16.4	4007.7699	0.9858	DTAVFECLPQHAMFGNDTITCTTHGNWTKLPECR	
6.3	4007.7589	0.9969	DTNDDPDEDHLTSYDIQLSIQESIEASKTALCPER	
5.5	4007.7711	0.9847	AVEMTDQLMVPTLGSQEGAFENVRMNYSGDQGQTIR	
4.8	4006.7684	1.9874	TNEGNAMSQSLVLYGASKENSEGFHESKMTNTEGVNK	
2.9	4008.7752	-0.0195	SCFNFLDELSPGLLEMVMVNYDGEAGCWKISPIGC	

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

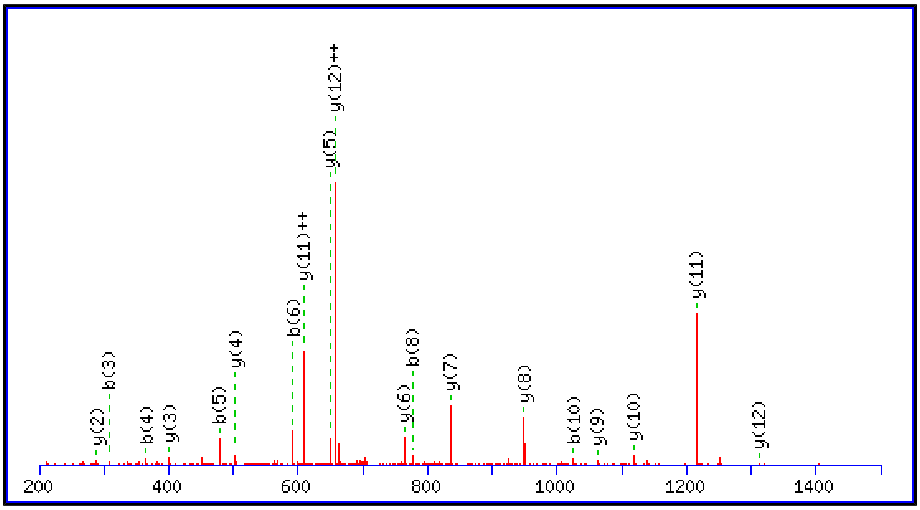
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPPGLLANFTLLR**
Found in **P02750** in **con_Xuniprot_HUMAN3**, A2GL_HUMAN Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2

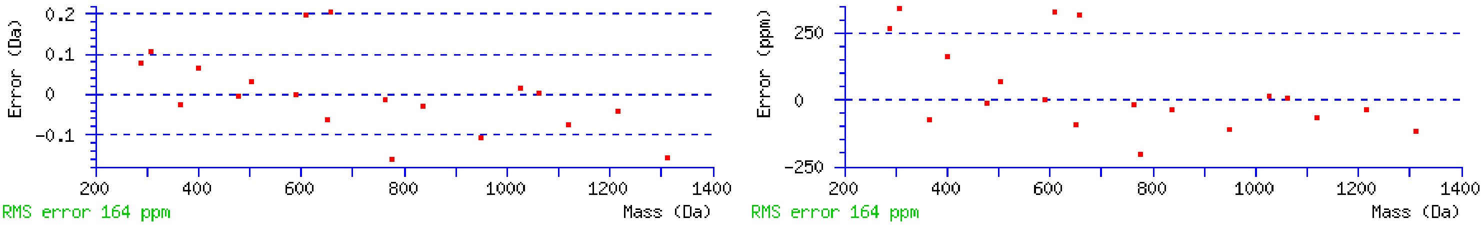
Match to Query 3177: 1424.842628 from(713.428590,2+) intensity(493325.7500) rtinseconds(2602) scans(6801) index(25654)
Title: 111019_Est_MI_YS_G_07Spectrum5862_scans__6801
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1424.8391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 107 **Expect:** 7e-010
Matches : 19/106 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							13
2	211.1441	106.0757					P	*1312.7623*	656.8848	1295.7358	648.3715	1294.7518	647.8795	12
3	**308.1969**	154.6021					P	*1215.7096*	608.3584	1198.6830	599.8452	1197.6990	599.3531	11
4	**365.2183**	183.1128					G	*1118.6568*	559.8320	1101.6303	551.3188	1100.6463	550.8268	10
5	**478.3024**	239.6548					L	*1061.6354*	531.3213	1044.6088	522.8080	1043.6248	522.3160	9
6	**591.3865**	296.1969					L	*948.5513*	474.7793	931.5247	466.2660	930.5407	465.7740	8
7	662.4236	331.7154					A	*835.4672*	418.2373	818.4407	409.7240	817.4567	409.2320	7
8	**777.4505**	389.2289	760.4240	380.7156			N	*764.4301*	382.7187	747.4036	374.2054	746.4196	373.7134	6
9	924.5189	462.7631	907.4924	454.2498			F	*649.4032*	325.2052	632.3766	316.6919	631.3926	316.1999	5
10	**1025.5666**	513.2869	1008.5401	504.7737	1007.5560	504.2817	T	*502.3348*	251.6710	485.3082	243.1577	484.3242	242.6657	4
11	1138.6507	569.8290	1121.6241	561.3157	1120.6401	560.8237	L	*401.2871*	201.1472	384.2605	192.6339			3
12	1251.7347	626.3710	1234.7082	617.8577	1233.7242	617.3657	L	*288.2030*	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
107.4	1424.8391	0.0035	LPPGLLANFTLLR
4.1	1423.8333	1.0093	LLMLHGQKLKSR
3.3	1423.8439	0.9988	IPIGWQIELVKK
2.7	1424.8398	0.0028	LMRNATVVRPLR
2.7	1424.8398	0.0028	NRVATMPVRLLR
1.5	1424.8391	0.0035	LVPPELIVSHPPK
1.4	1424.8405	0.0022	LVKPWPFRNIR
0.3	1423.8412	1.0015	IPRHLKQTYIR
0.3	1424.8463	-0.0037	LLLAQRNLQSIR

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

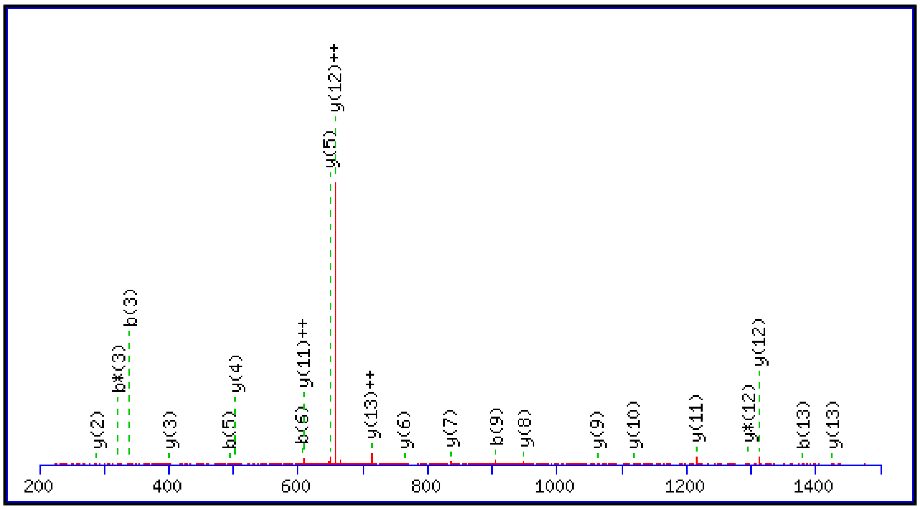
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLPPGLLANFTLLR**
Found in **P02750** in **con_Xuniprot_HUMAN3**, A2GL_HUMAN Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2

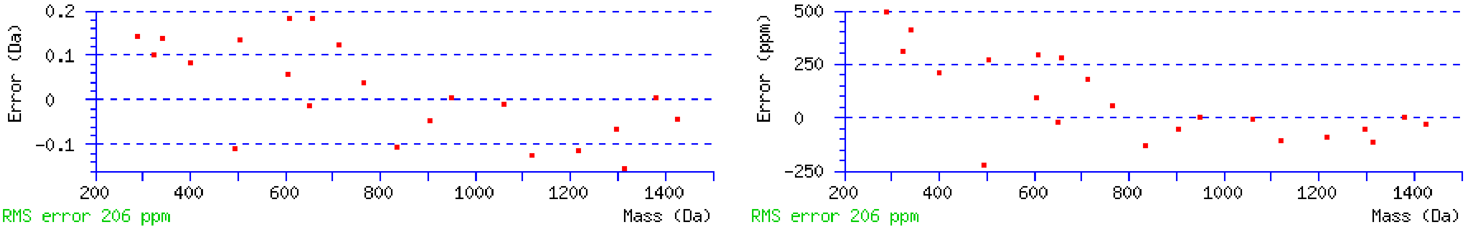
Match to Query 7064: 1552.937468 from(777.476010,2+) intensity(2003475.7500) rtinseconds(2266) scans(5827) index(8564)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum5067_scans__5827
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1552.9341
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 95 **Expect:** 7.3e-009
Matches : 22/130 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	129.1022	65.0548	112.0757	56.5415			K							14
2	242.1863	121.5968	225.1598	113.0835			L	***1425.8464***	713.4268	1408.8199	704.9136	1407.8358	704.4216	13
3	**339.2391**	170.1232	322.2125	161.6099			P	***1312.7623***	656.8848	1295.7358	648.3715	1294.7518	647.8795	12
4	436.2918	218.6496	419.2653	210.1363			P	***1215.7096***	608.3584	1198.6830	599.8452	1197.6990	599.3531	11
5	**493.3133**	247.1603	476.2867	238.6470			G	***1118.6568***	559.8320	1101.6303	551.3188	1100.6463	550.8268	10
6	**606.3974**	303.7023	589.3708	295.1890			L	***1061.6354***	531.3213	1044.6088	522.8080	1043.6248	522.3160	9
7	719.4814	360.2443	702.4549	351.7311			L	***948.5513***	474.7793	931.5247	466.2660	930.5407	465.7740	8
8	790.5185	395.7629	773.4920	387.2496			A	***835.4672***	418.2373	818.4407	409.7240	817.4567	409.2320	7
9	**905.5455**	453.2764	888.5189	444.7631			N	***764.4301***	382.7187	747.4036	374.2054	746.4196	373.7134	6
10	1052.6139	526.8106	1035.5873	518.2973			F	***649.4032***	325.2052	632.3766	316.6919	631.3926	316.1999	5
11	1153.6616	577.3344	1136.6350	568.8212	1135.6510	568.3291	T	***502.3348***	251.6710	485.3082	243.1577	484.3242	242.6657	4
12	1266.7456	633.8765	1249.7191	625.3632	1248.7351	624.8712	L	***401.2871***	201.1472	384.2605	192.6339			3
13	**1379.8297**	690.4185	1362.8032	681.9052	1361.8191	681.4132	L	***288.2030***	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.8	1552.9341	0.0034	KLPPGLLANFTLLR
7.0	1552.9413	-0.0038	IQNNKLILNKLSR
5.7	1552.9413	-0.0038	KLLLAQRNLQSIR
5.7	1552.9301	0.0074	KLNVLVASRETPVK
3.8	1552.9300	0.0074	EIVLKAQILAGGRGK
3.5	1552.9413	-0.0038	KLLLAQRNLQSIR
3.5	1552.9413	-0.0038	KLLLAQRNLQSIR
3.5	1552.9301	0.0074	QLVTGKGTVVVSLPR
3.5	1552.9300	0.0074	LQKINAGQRGIILK
3.5	1552.9300	0.0074	LQKINAGQRGIILK

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

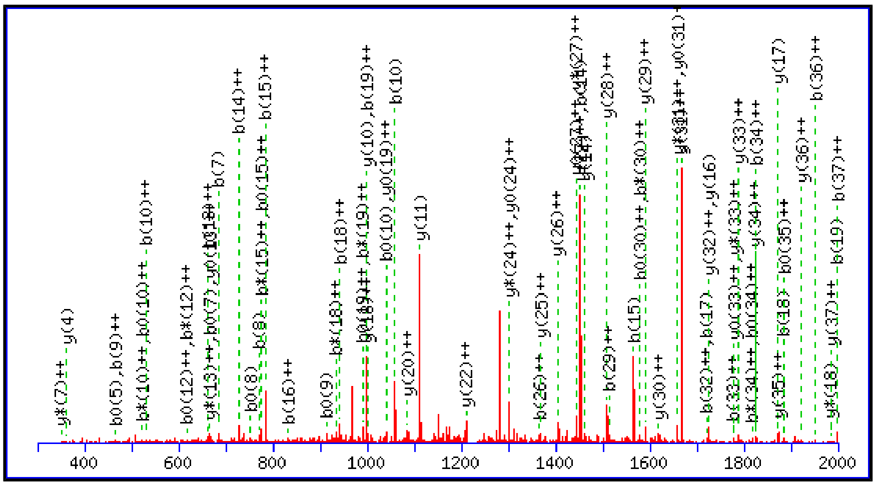
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK**
Found in **P02750** in **con_Xuniprot_HUMAN3**, A2GL_HUMAN Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2

Match to Query 28995: 4899.437576 from(1225.866670,4+) intensity(23810.3164) rtinseconds(2933) scans(7721) index(14844)
Title: 111019_Est_MI_YP_G_03Spectrum6744_scans__7721
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

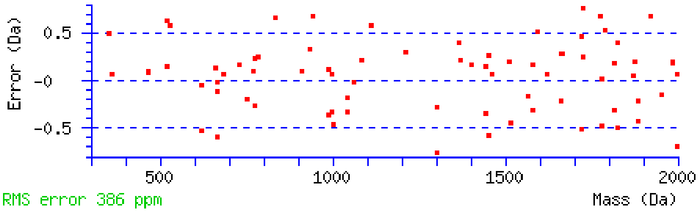
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

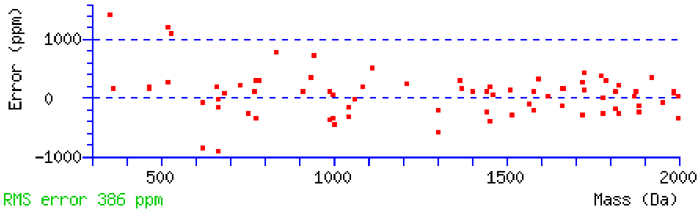


Monoisotopic mass of neutral peptide Mr(calc): 4899.4178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N32 : Deamidated (NQ)
Ions Score: 65 **Expect:** 4.6e-005
Matches : 77/520 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							46
2	203.0662	102.0368			185.0557	93.0315	D	4813.3930	2407.2002	4796.3665	2398.6869	4795.3825	2398.1949	45
3	340.1252	170.5662			322.1146	161.5609	H	4698.3661	2349.6867	4681.3395	2341.1734	4680.3555	2340.6814	44
4	397.1466	199.0769			379.1361	190.0717	G	4561.3072	2281.1572	4544.2806	2272.6440	4543.2966	2272.1519	43
5	484.1787	242.5930			466.1681	233.5877	S	4504.2857	2252.6465	4487.2592	2244.1332	4486.2752	2243.6412	42
6	571.2107	286.1090			553.2001	277.1037	S	4417.2537	2209.1305	4400.2271	2200.6172	4399.2431	2200.1252	41
7	**684.2947**	342.6510			666.2842	333.6457	I	4330.2217	2165.6145	4313.1951	2157.1012	4312.2111	2156.6092	40
8	**771.3268**	386.1670			753.3162	377.1617	S	4217.1376	2109.0724	4200.1110	2100.5592	4199.1270	2100.0672	39
9	931.3574	***466.1823***			913.3469	457.1771	C	4130.1056	2065.5564	4113.0790	2057.0431	4112.0950	2056.5511	38
10	**1059.4160**	***530.2116***	1042.3894	521.6984	1041.4054	521.2064	Q	3970.0749	1985.5411	3953.0484	1977.0278	3952.0644	1976.5358	37
11	1156.4688	578.7380	1139.4422	570.2247	1138.4582	569.7327	P	3842.0163	1921.5118	3824.9898	1912.9985	3824.0058	1912.5065	36
12	1253.5215	627.2644	1236.4950	618.7511	1235.5110	618.2591	P	3744.9636	1872.9854	3727.9370	1864.4722	3726.9530	1863.9801	35
13	1324.5586	***662.7830***	1307.5321	654.2697	1306.5481	653.7777	A	3647.9108	1824.4590	3630.8843	1815.9458	3629.9002	1815.4538	34
14	**1453.6012**	***727.3043***	1436.5747	718.7910	1435.5907	718.2990	E	3576.8737	1788.9405	3559.8472	1780.4272	3558.8631	1779.9352	33
15	**1566.6853**	***783.8463***	1549.6587	775.3330	1548.6747	774.8410	I	3447.8311	1724.4192	3430.8046	1715.9059	3429.8205	1715.4139	32
16	1663.7381	***832.3727***	1646.7115	823.8594	1645.7275	823.3674	P	3334.7470	1667.8772	3317.7205	1659.3639	3316.7365	1658.8719	31
17	**1720.7595**	860.8834	1703.7330	852.3701	1702.7490	851.8781	G	3237.6943	1619.3508	3220.6677	1610.8375	3219.6837	1610.3455	30
18	**1883.8229**	***942.4151***	1866.7963	933.9018	1865.8123	933.4098	Y	3180.6728	1590.8400	3163.6463	1582.3268	3162.6622	1581.8348	29
19	**1996.9069**	***998.9571***	1979.8804	990.4438	1978.8964	989.9518	L	3017.6095	1509.3084	3000.5829	1500.7951	2999.5989	1500.3031	28
20	2093.9597	1047.4835	2076.9331	1038.9702	2075.9491	1038.4782	P	2904.5254	1452.7663	2887.4989	1444.2531	2886.5149	1443.7611	27
21	2164.9968	1083.0020	2147.9702	1074.4888	2146.9862	1073.9968	A	2807.4727	1404.2400	2790.4461	1395.7267	2789.4621	1395.2347	26
22	2280.0237	1140.5155	2262.9972	1132.0022	2262.0132	1131.5102	D	2736.4355	1368.7214	2719.4090	1360.2081	2718.4250	1359.7161	25
23	2381.0714	1191.0393	2364.0449	1182.5261	2363.0609	1182.0341	T	2621.4086	1311.2079	2604.3821	1302.6947	2603.3980	1302.2027	24

24	2480.1398	1240.5736	2463.1133	1232.0603	2462.1293	1231.5683	**V**	2520.3609	1260.6841	2503.3344	1252.1708	2502.3504	1251.6788	**23**
25	2617.1987	1309.1030	2600.1722	1300.5897	2599.1882	1300.0977	**H**	2421.2925	1211.1499	2404.2660	1202.6366	2403.2819	1202.1446	**22**
26	2730.2828	***1365.6450***	2713.2563	1357.1318	2712.2722	1356.6398	**L**	2284.2336	1142.6204	2267.2070	1134.1072	2266.2230	1133.6152	**21**
27	2801.3199	1401.1636	2784.2934	1392.6503	2783.3094	1392.1583	**A**	2171.1495	1086.0784	2154.1230	1077.5651	2153.1390	1077.0731	**20**
28	2900.3883	1450.6978	2883.3618	1442.1845	2882.3778	1441.6925	**V**	2100.1124	1050.5598	2083.0859	1042.0466	2082.1019	1041.5546	**19**
29	3029.4309	***1515.2191***	3012.4044	1506.7058	3011.4204	1506.2138	**E**	2001.0440	1001.0256	1984.0175	992.5124	1983.0334	992.0204	**18**
30	3176.4993	1588.7533	3159.4728	1580.2400	3158.4888	1579.7480	**F**	**1872.0014**	936.5043	1854.9749	927.9911	1853.9908	927.4991	**17**
31	3323.5678	1662.2875	3306.5412	1653.7742	3305.5572	1653.2822	**F**	**1724.9330**	862.9701	1707.9064	854.4569	1706.9224	853.9649	**16**
32	3438.5947	***1719.8010***	3421.5682	1711.2877	3420.5841	1710.7957	**N**	1577.8646	789.4359	1560.8380	780.9227	1559.8540	780.4306	**15**
33	3551.6788	***1776.3430***	3534.6522	1767.8297	3533.6682	1767.3377	**L**	**1462.8376**	731.9225	1445.8111	723.4092	1444.8271	722.9172	**14**
34	3652.7264	***1826.8669***	3635.6999	1818.3536	3634.7159	1817.8616	**T**	1349.7536	675.3804	1332.7270	666.8672	1331.7430	666.3751	**13**
35	3789.7854	1895.3963	3772.7588	1886.8830	3771.7748	1886.3910	**H**	1248.7059	624.8566	1231.6793	616.3433	1230.6953	615.8513	**12**
36	3902.8694	***1951.9383***	3885.8429	1943.4251	3884.8589	1942.9331	**L**	**1111.6470**	556.3271	1094.6204	547.8139	1093.6364	547.3218	**11**
37	3999.9222	***2000.4647***	3982.8956	1991.9515	3981.9116	1991.4594	**P**	**998.5629**	499.7851	981.5364	491.2718	980.5524	490.7798	**10**
38	4070.9593	2035.9833	4053.9327	2027.4700	4052.9487	2026.9780	**A**	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	**9**
39	4185.0022	2093.0048	4167.9757	2084.4915	4166.9917	2083.9995	**N**	830.4730	415.7402	813.4465	407.2269	812.4625	406.7349	**8**
40	4298.0863	2149.5468	4281.0597	2141.0335	4280.0757	2140.5415	**L**	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	**7**
41	4411.1704	2206.0888	4394.1438	2197.5755	4393.1598	2197.0835	**L**	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	**6**
42	4539.2289	2270.1181	4522.2024	2261.6048	4521.2184	2261.1128	**Q**	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	**5**
43	4596.2504	2298.6288	4579.2238	2290.1156	4578.2398	2289.6236	**G**	**362.2034**	181.6053	345.1769	173.0921	344.1928	172.6001	**4**
44	4667.2875	2334.1474	4650.2610	2325.6341	4649.2769	2325.1421	**A**	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
45	4754.3195	2377.6634	4737.2930	2369.1501	4736.3090	2368.6581	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
46							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.5	4899.4178	0.0198	SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK	Deamidated N32 84.71%
54.9	4899.4178	0.0198	SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK	Deamidated Q42 7.50%
54.9	4899.4178	0.0198	SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK	Deamidated N39 7.50%
40.8	4899.4178	0.0198	SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK	Deamidated Q10 0.29%
40.7	4898.4338	1.0038	SDHGSSISCQPPAEIPGYLPADTVHLAVEFFNLTHLPANLLQGASK	
19.4	4899.4355	0.0020	ENSTKVVFLITDGYSNGGDPRPIAASLRDSGVEIFTFGIWQGNIR	
16.5	4898.4515	0.9861	ENSTKVVFLITDGYSNGGDPRPIAASLRDSGVEIFTFGIWQGNIR	
15.2	4898.4319	1.0057	VGAGLELEMVEMESEPMWFAVTHDPTLSETLALLEPKNVLGKLAS	
14.9	4898.4515	0.9861	ENSTKVVFLITDGYSNGGDPRPIAASLRDSGVEIFTFGIWQGNIR	
14.4	4899.4355	0.0020	ENSTKVVFLITDGYSNGGDPRPIAASLRDSGVEIFTFGIWQGNIR	

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

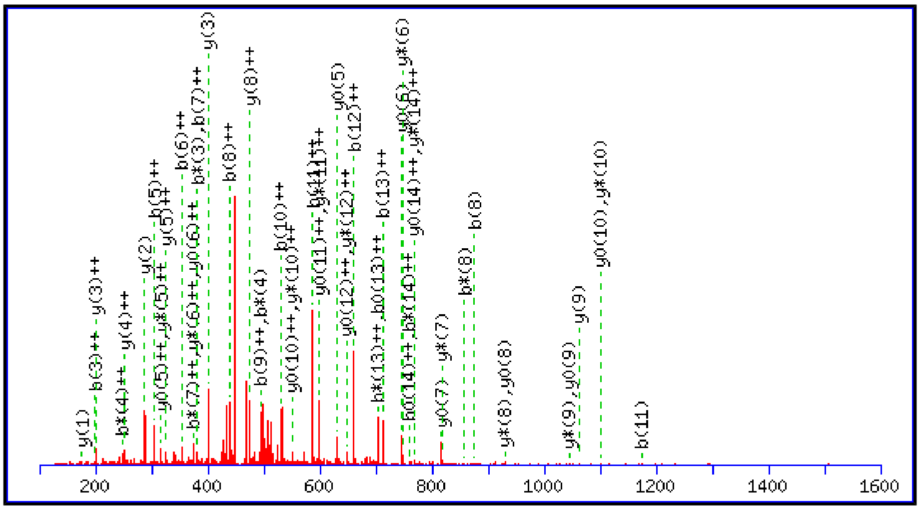
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LRKLPPGLLANFTLLR**
Found in **P02750** in **con_Xuniprot_HUMAN3**, A2GL_HUMAN Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2

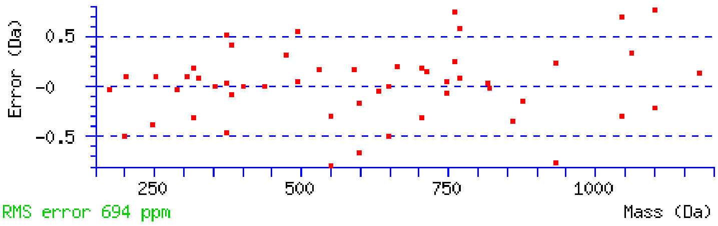
Match to Query 10899: 1822.126056 from(456.538790,4+) intensity(14124.9121) rtinseconds(2051) scans(5086) index(22319)
Title: 111019_Est_MI_YS_G_02Spectrum4402_scans__5086
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

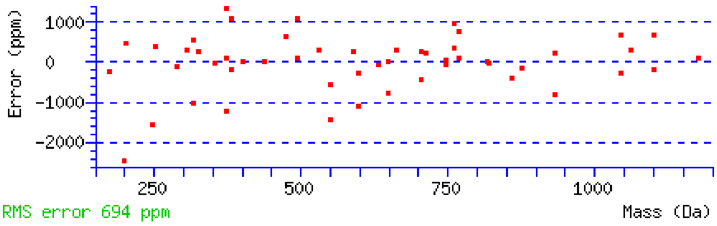
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1822.1192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 52 **Expect:** 3.1e-005
Matches : 53/148 fragment ions using 79 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							16
2	270.1925	135.5999	253.1659	127.0866			R	1710.0425	855.5249	1693.0159	847.0116	1692.0319	846.5196	15
3	398.2874	***199.6473***	381.2609	191.1341			K	1553.9414	777.4743	1536.9148	768.9611	1535.9308	768.4690	14
4	511.3715	256.1894	494.3449	247.6761			L	1425.8464	713.4268	1408.8199	704.9136	1407.8358	704.4216	13
5	608.4242	***304.7158***	591.3977	296.2025			P	1312.7624	656.8848	1295.7358	648.3715	1294.7518	647.8795	12
6	705.4770	***353.2421***	688.4505	344.7289			P	1215.7096	608.3584	1198.6830	599.8452	1197.6990	599.3531	11
7	762.4985	***381.7529***	745.4719	373.2396			G	1118.6568	559.8320	1101.6303	551.3188	1100.6463	550.8268	10
8	875.5825	***438.2949***	858.5560	429.7816			L	**1061.6354**	531.3213	1044.6088	522.8080	1043.6248	522.3160	9
9	988.6666	***494.8369***	971.6400	486.3237			L	948.5513	474.7793	931.5247	466.2660	930.5407	465.7740	8
10	1059.7037	***530.3555***	1042.6772	521.8422			A	835.4672	418.2373	818.4407	409.7240	817.4567	409.2320	7
11	1174.7307	***587.8690***	1157.7041	579.3557			N	764.4301	382.7187	747.4036	374.2054	746.4196	373.7134	6
12	1321.7991	***661.4032***	1304.7725	652.8899			F	649.4032	325.2052	632.3766	316.6919	631.3926	316.1999	5
13	1422.8467	***711.9270***	1405.8202	703.4137	1404.8362	702.9217	T	502.3348	251.6710	485.3082	243.1577	484.3242	242.6657	4
14	1535.9308	***768.4690***	1518.9043	759.9558	1517.9202	759.4638	L	**401.2871**	201.1472	384.2605	192.6339			3
15	1649.0149	825.0111	1631.9883	816.4978	1631.0043	816.0058	L	**288.2030**	144.6051	271.1765	136.0919			2
16							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence
52.0	1822.1192	0.0068	LRKLPPGLLANFTLLR

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

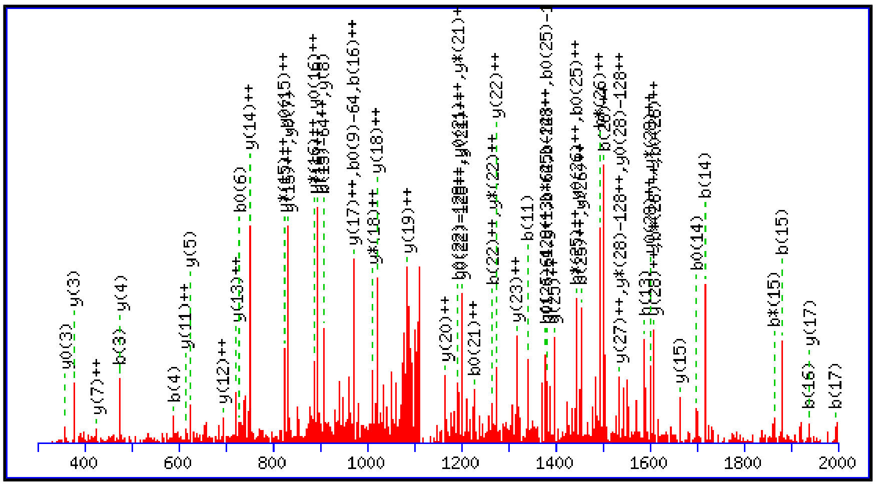
{MATRIX} *{SCIENCE}* Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27609: 3379.331112 from(1127.450980,3+) intensity(9821.7988) rtinseconds(2377) scans(6310) index(4625)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum5377_scans__6310
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

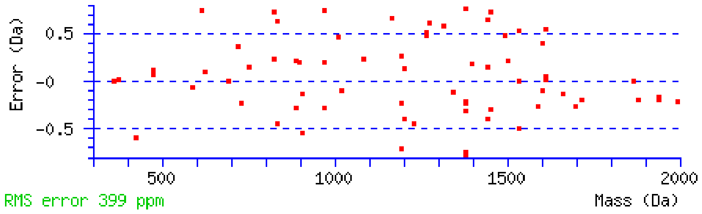
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

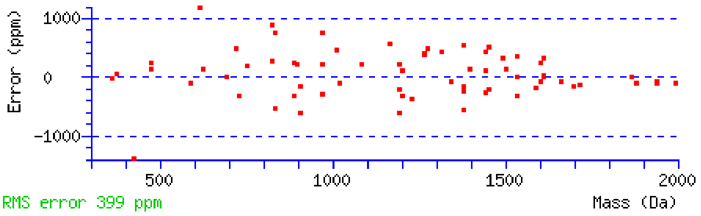


```
Monoisotopic mass of neutral peptide Mr(calc): 3379.3203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M19     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 133  Expect: 5.4e-013
Matches : 70/552 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	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3217.2642	1609.1357	3200.2377	1600.6225	3199.2536	1600.1305	28
3	**474.2023**	237.6048					Y	3070.1958	1535.6015	3053.1692	1527.0883	3052.1852	1526.5962	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2907.1325	1454.0699	2890.1059	1445.5566	2889.1219	1445.0646	26
5	646.2508	323.6290	629.2242	315.1157			G	2792.1055	1396.5564	2775.0790	1388.0431	2774.0950	1387.5511	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2735.0841	1368.0457	2718.0575	1359.5324	2717.0735	1359.0404	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2634.0364	1317.5218	2617.0098	1309.0086	2616.0258	1308.5165	23
8	981.3659	491.1866	964.3393	482.6733	963.3553	482.1813	M	2547.0043	1274.0058	2529.9778	1265.4925	2528.9938	1265.0005	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	1212.4336	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	**1341.4762**	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1442.5239	721.7656	1425.4973	713.2523	1424.5133	712.7603	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	**1938.8109**	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1717.6509**	859.3291	1700.6243	850.8158	1699.6403	850.3238	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1880.7142**	940.8607	1863.6877	932.3475	1862.7037	931.8555	Y	**1663.6839**	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1937.7357**	**969.3715**	1920.7091	960.8582	1919.7251	960.3662	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	**1994.7571**	997.8822	1977.7306	989.3689	1976.7466	988.8769	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2154.7878	1077.8975	2137.7612	1069.3843	2136.7772	1068.8923	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2301.8232	1151.4152	2284.7966	1142.9020	2283.8126	1142.4100	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2358.8447	1179.9260	2341.8181	1171.4127	2340.8341	1170.9207	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2472.8876	1236.9474	2455.8610	1228.4342	2454.8770	1227.9421	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2529.9090	**1265.4582**	2512.8825	1256.9449	2511.8985	1256.4529	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2643.9520	1322.4796	2626.9254	1313.9664	2625.9414	1313.4743	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2757.9949	**1379.5011**	2740.9684	1370.9878	2739.9843	1370.4958	**N**	737.3828	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2905.0633	**1453.0353**	2888.0368	1444.5220	2887.0528	1444.0300	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	3004.1317	**1502.5695**	2987.1052	1494.0562	2986.1212	1493.5642	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3105.1794	1553.0933	3088.1529	1544.5801	3087.1688	1544.0881	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3234.2220	1617.6146	3217.1955	1609.1014	3216.2114	1608.6094	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
133.5	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4 70.29%
129.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14 25.58%
127.0	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
120.9	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21 3.84%
113.0	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
111.3	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
109.5	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
109.5	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
106.6	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N24 0.14%
106.6	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23 0.14%

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

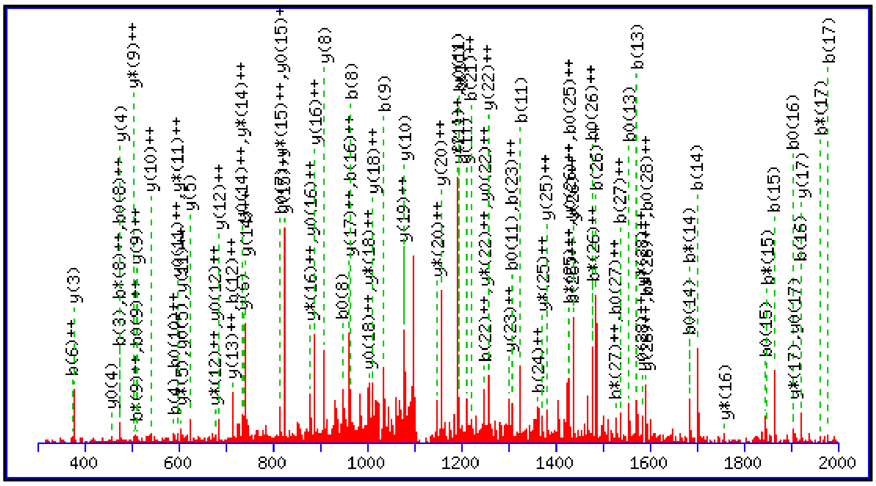
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27497: 3347.338362 from(1116.786730,3+) intensity(25581.5449) rtinseconds(1973) scans(4930) index(12749)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4312_scans__4930
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

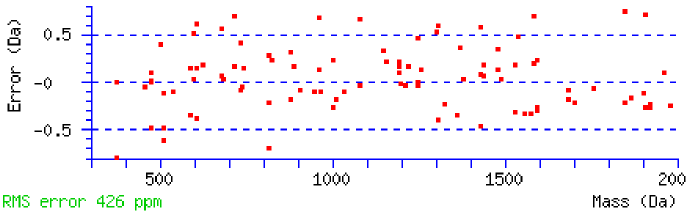
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

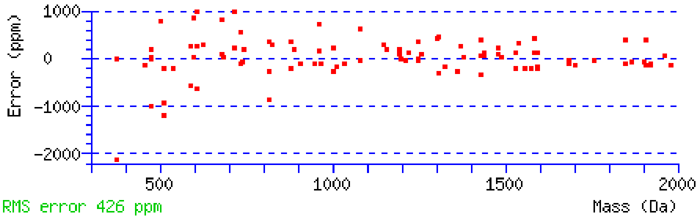


Monoisotopic mass of neutral peptide Mr(calc): 3347.3304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 116 **Expect:** 3e-011
Matches : 98/318 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3185.2744	1593.1408	3168.2478	1584.6275	3167.2638	1584.1355	28
3	**474.2023**	237.6048					Y	3038.2060	1519.6066	3021.1794	1511.0933	3020.1954	1510.6013	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2875.1426	1438.0750	2858.1161	1429.5617	2857.1321	1429.0697	26
5	646.2508	323.6290	629.2242	315.1157			G	2760.1157	1380.5615	2743.0891	1372.0482	2742.1051	1371.5562	25
6	747.2984	***374.1529***	730.2719	365.6396	729.2879	365.1476	T	2703.0942	1352.0507	2686.0677	1343.5375	2685.0837	1343.0455	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2602.0465	1301.5269	2585.0200	1293.0136	2584.0360	1292.5216	23
8	**965.3709**	483.1891	948.3444	474.6758	947.3604	474.1838	M	2515.0145	1258.0109	2497.9880	1249.4976	2497.0040	1249.0056	22
9	**1036.4081**	518.7077	1019.3815	510.1944	1018.3975	509.7024	A	2383.9740	1192.4907	2366.9475	1183.9774	2365.9635	1183.4854	21
10	**1196.4387**	598.7230	1179.4122	590.2097	1178.4281	589.7177	C	2312.9369	1156.9721	2295.9104	1148.4588	2294.9264	1147.9668	20
11	**1325.4813**	663.2443	1308.4548	654.7310	1307.4707	654.2390	E	2152.9063	1076.9568	2135.8797	1068.4435	2134.8957	1067.9515	19
12	1426.5290	***713.7681***	1409.5024	705.2549	1408.5184	704.7628	T	2023.8637	1012.4355	2006.8371	1003.9222	2005.8531	1003.4302	18
13	**1573.5974**	787.3023	1556.5708	778.7891	1555.5868	778.2971	F	**1922.8160**	961.9116	1905.7894	953.3984	1904.8054	952.9064	17
14	**1701.6560**	851.3316	1684.6294	842.8184	1683.6454	842.3263	Q	1775.7476	888.3774	1758.7210	879.8642	1757.7370	879.3721	16
15	**1864.7193**	932.8633	1847.6928	924.3500	1846.7087	923.8580	Y	1647.6890	824.3481	1630.6625	815.8349	1629.6784	815.3429	15
16	**1921.7408**	***961.3740***	1904.7142	952.8607	1903.7302	952.3687	G	1484.6257	742.8165	1467.5991	734.3032	1466.6151	733.8112	14
17	**1978.7622**	989.8848	1961.7357	981.3715	1960.7517	980.8795	G	1427.6042	714.3057	1410.5777	705.7925	1409.5936	705.3005	13
18	2138.7929	1069.9001	2121.7663	1061.3868	2120.7823	1060.8948	C	1370.5827	685.7950	1353.5562	677.2817	1352.5722	676.7897	12
19	2269.8334	1135.4203	2252.8068	1126.9070	2251.8228	1126.4150	M	**1210.5521**	605.7797	1193.5255	597.2664	1192.5415	596.7744	11
20	2326.8548	1163.9311	2309.8283	1155.4178	2308.8443	1154.9258	G	**1079.5116**	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2440.8978	***1220.9525***	2423.8712	1212.4392	2422.8872	1211.9472	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2497.9192	***1249.4632***	2480.8927	1240.9500	2479.9087	1240.4580	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8
23	2611.9621	***1306.4847***	2594.9356	1297.9714	2593.9516	1297.4794	N	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	7

24	2726.0051	***1363.5062***	2708.9785	1354.9929	2707.9945	1354.5009	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2873.0735	***1437.0404***	2856.0469	1428.5271	2855.0629	1428.0351	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2972.1419	***1486.5746***	2955.1154	1478.0613	2954.1313	1477.5693	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3073.1896	***1537.0984***	3056.1630	1528.5852	3055.1790	1528.0931	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3202.2322	1601.6197	3185.2056	1593.1065	3184.2216	1592.6144	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
116.5	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4 73.94%
111.1	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14 21.52%
103.4	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
103.2	3346.3464	0.9919	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
101.4	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
101.4	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
101.3	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21 2.25%
99.7	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
99.4	3347.3304	0.0079	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23 1.45%
98.0	3346.3464	0.9919	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

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

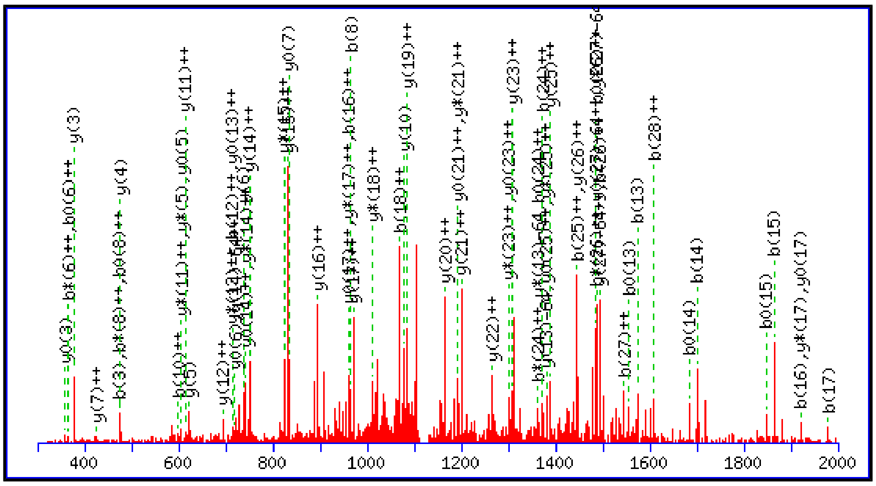
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27518: 3363.339252 from(1122.120360,3+) intensity(0.0000) rtinseconds(1779) scans(4665) index(4459)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3954_scans__4665
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

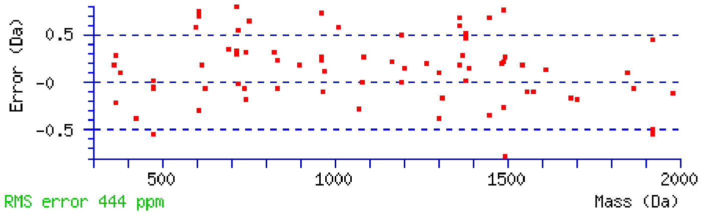
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

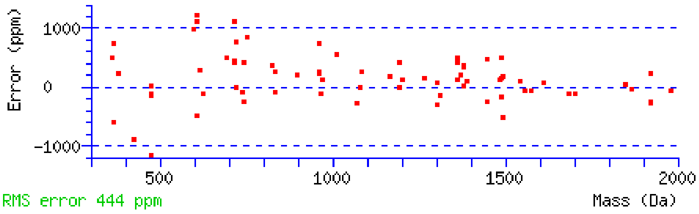


```
Monoisotopic mass of neutral peptide Mr(calc): 3363.3253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4     : Deamidated (NQ)
M19    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 100  Expect: 1.5e-009
Matches : 74/486 fragment ions using 68 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3201.2693	1601.1383	3184.2427	1592.6250	3183.2587	1592.1330	28
3	**474.2023**	237.6048					Y	3054.2009	1527.6041	3037.1743	1519.0908	3036.1903	1518.5988	27
4	589.2293	295.1183	572.2027	286.6050			N	2891.1375	1446.0724	2874.1110	1437.5591	2873.1270	1437.0671	26
5	646.2508	323.6290	629.2242	315.1157			G	2776.1106	1388.5589	2759.0841	1380.0457	2758.1000	1379.5537	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2719.0891	1360.0482	2702.0626	1351.5349	2701.0786	1351.0429	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2618.0415	1309.5244	2601.0149	1301.0111	2600.0309	1300.5191	23
8	**965.3709**	483.1891	948.3444	474.6758	947.3604	474.1838	M	2531.0094	1266.0084	2513.9829	1257.4951	2512.9989	1257.0031	22
9	1036.4081	518.7077	1019.3815	510.1944	1018.3975	509.7024	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	1196.4387	***598.7230***	1179.4122	590.2097	1178.4281	589.7177	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	1325.4813	663.2443	1308.4548	654.7310	1307.4707	654.2390	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1426.5290	***713.7681***	1409.5024	705.2549	1408.5184	704.7628	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1573.5974**	787.3023	1556.5708	778.7891	1555.5868	778.2971	F	1938.8109	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1701.6560**	851.3316	1684.6294	842.8184	1683.6454	842.3263	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1864.7193**	932.8633	1847.6928	924.3500	1846.7087	923.8580	Y	1663.6839	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1921.7408**	***961.3740***	1904.7142	952.8607	1903.7302	952.3687	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	**1978.7622**	989.8848	1961.7357	981.3715	1960.7517	980.8795	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2138.7929	***1069.9001***	2121.7663	1061.3868	2120.7823	1060.8948	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2285.8283	1143.4178	2268.8017	1134.9045	2267.8177	1134.4125	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2342.8497	1171.9285	2325.8232	1163.4152	2324.8392	1162.9232	G	**1079.5116**	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2456.8927	1228.9500	2439.8661	1220.4367	2438.8821	1219.9447	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2513.9141	1257.4607	2496.8876	1248.9474	2495.9036	1248.4554	G	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2627.9571	1314.4822	2610.9305	1305.9689	2609.9465	1305.4769	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2742.0000	***1371.5036***	2724.9734	1362.9904	2723.9894	1362.4983	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2889.0684	***1445.0378***	2872.0419	1436.5246	2871.0578	1436.0326	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2988.1368	***1494.5720***	2971.1103	1486.0588	2970.1263	1485.5668	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3089.1845	***1545.0959***	3072.1579	1536.5826	3071.1739	1536.0906	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3218.2271	***1609.6172***	3201.2005	1601.1039	3200.2165	1600.6119	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.7	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M19; 49.30%
97.8	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14, Oxidation M19; 31.83%
93.8	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, Oxidation M19; 12.70%
87.8	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
87.2	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N24, Oxidation M19; 2.77%
87.2	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23, Oxidation M19; 2.77%
82.3	3362.3413	0.9979	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
78.8	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M8; 0.40%
75.2	3362.3413	0.9979	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
71.6	3363.3253	0.0139	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

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

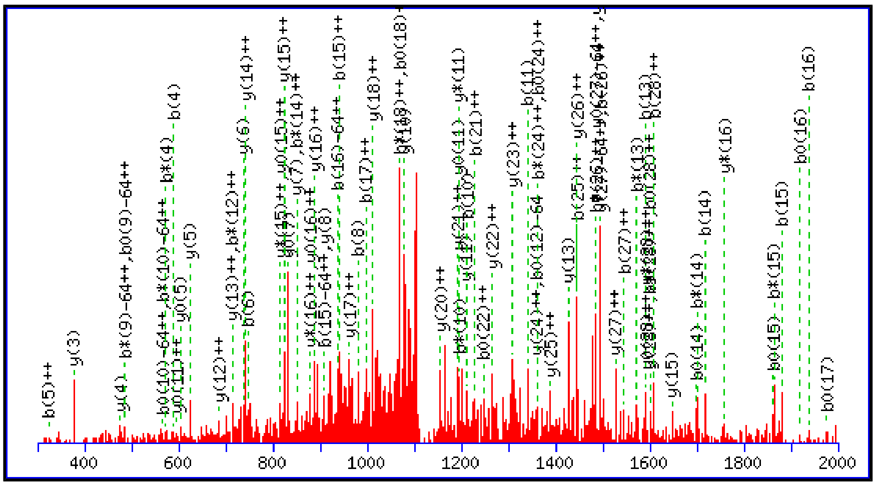
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27530: 3364.327122 from(1122.449650,3+) intensity(9716.8701) rtinseconds(2989) scans(7919) index(4813)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum6799_scans__7919
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

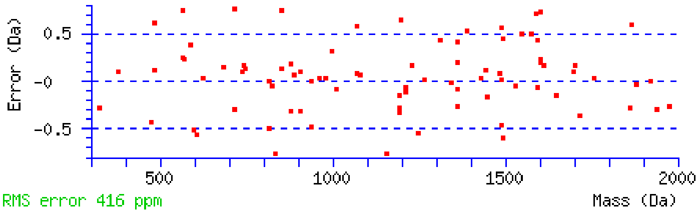
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

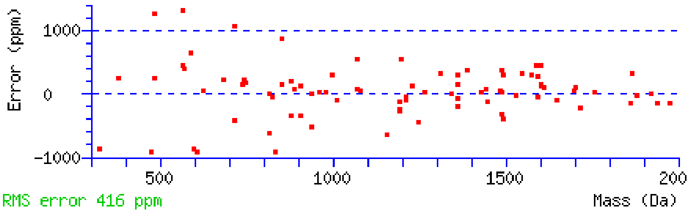


Monoisotopic mass of neutral peptide Mr(calc): 3363.3253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 77 **Expect:** 1.9e-007
Matches : 85/486 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					**Y**							**29**
2	311.1390	156.0731					**F**	3201.2693	1601.1383	3184.2427	1592.6250	3183.2587	1592.1330	**28**
3	474.2023	237.6048					**Y**	3054.2009	1527.6041	3037.1743	1519.0908	3036.1903	1518.5988	**27**
4	**589.2293**	295.1183	572.2027	286.6050			**N**	2891.1375	1446.0724	2874.1110	1437.5591	2873.1270	1437.0671	**26**
5	646.2508	**323.6290**	629.2242	315.1157			**G**	2776.1106	1388.5589	2759.0841	1380.0457	2758.1000	1379.5537	**25**
6	**747.2984**	374.1529	730.2719	365.6396	729.2879	365.1476	**T**	2719.0891	1360.0482	2702.0626	1351.5349	2701.0786	1351.0429	**24**
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	**S**	2618.0415	1309.5244	2601.0149	1301.0111	2600.0309	1300.5191	**23**
8	**981.3659**	491.1866	964.3393	482.6733	963.3553	482.1813	**M**	2531.0094	1266.0084	2513.9829	1257.4951	2512.9989	1257.0031	**22**
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	**A**	2383.9740	1192.4907	2366.9475	1183.9774	2365.9635	1183.4854	**21**
10	**1212.4336**	606.7205	1195.4071	598.2072	1194.4231	597.7152	**C**	2312.9369	1156.9721	2295.9104	1148.4588	2294.9264	1147.9668	**20**
11	**1341.4762**	671.2417	1324.4497	662.7285	1323.4657	662.2365	**E**	2152.9063	1076.9568	2135.8797	1068.4435	2134.8957	1067.9515	**19**
12	1442.5239	721.7656	1425.4973	713.2523	1424.5133	712.7603	**T**	2023.8637	1012.4355	2006.8371	1003.9222	2005.8531	1003.4302	**18**
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	**F**	1922.8160	961.9116	1905.7894	953.3984	1904.8054	952.9064	**17**
14	**1717.6509**	859.3291	1700.6243	850.8158	1699.6403	850.3238	**Q**	1775.7476	888.3774	1758.7210	879.8642	1757.7370	879.3721	**16**
15	**1880.7142**	**940.8607**	1863.6877	932.3475	1862.7037	931.8555	**Y**	***1647.6890***	824.3481	1630.6625	815.8349	1629.6784	815.3429	**15**
16	**1937.7357**	969.3715	1920.7091	960.8582	1919.7251	960.3662	**G**	1484.6257	742.8165	1467.5991	734.3032	1466.6151	733.8112	**14**
17	1994.7571	**997.8822**	1977.7306	989.3689	1976.7466	988.8769	**G**	***1427.6042***	714.3057	1410.5777	705.7925	1409.5936	705.3005	**13**
18	2154.7878	1077.8975	2137.7612	1069.3843	2136.7772	1068.8923	**C**	1370.5827	685.7950	1353.5562	677.2817	1352.5722	676.7897	**12**
19	2285.8283	1143.4178	2268.8017	1134.9045	2267.8177	1134.4125	**M**	***1210.5521***	605.7797	1193.5255	597.2664	1192.5415	596.7744	**11**
20	2342.8497	1171.9285	2325.8232	1163.4152	2324.8392	1162.9232	**G**	***1079.5116***	540.2594	1062.4851	531.7462	1061.5010	531.2542	**10**
21	2456.8927	**1228.9500**	2439.8661	1220.4367	2438.8821	1219.9447	**N**	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	**9**
22	2513.9141	1257.4607	2496.8876	1248.9474	2495.9036	1248.4554	**G**	***908.4472***	454.7272	891.4207	446.2140	890.4367	445.7220	**8**

23	2627.9571	1314.4822	2610.9305	1305.9689	2609.9465	1305.4769	**N**	***851.4258***	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2742.0000	1371.5036	2724.9734	1362.9904	2723.9894	1362.4983	**N**	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2889.0684	**1445.0378**	2872.0419	1436.5246	2871.0578	1436.0326	**F**	***623.3399***	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2988.1368	**1494.5720**	2971.1103	1486.0588	2970.1263	1485.5668	**V**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3089.1845	**1545.0959**	3072.1579	1536.5826	3071.1739	1536.0906	**T**	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3218.2271	**1609.6172**	3201.2005	1601.1039	3200.2165	1600.6119	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.6	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M8; 91.54%
66.2	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
63.4	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14, Oxidation M8; 4.36%
59.6	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
59.6	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
56.1	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N24, Oxidation M8; 0.82%
56.1	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23, Oxidation M8; 0.82%
56.1	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, Oxidation M8; 0.82%
53.5	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, Oxidation M19; 0.45%
52.8	3363.3253	1.0018	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

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

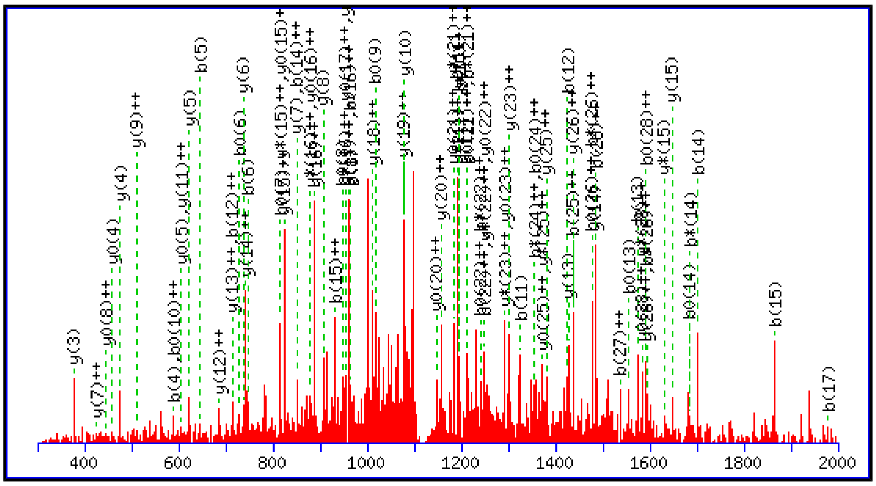
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27501: 3348.298962 from(1117.106930,3+) intensity(0.0000) rtinseconds(2002) scans(5008) index(12763)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4382_scans__5008
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

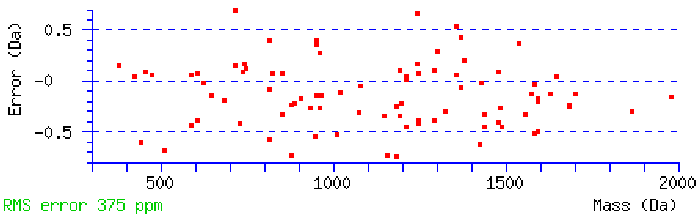
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

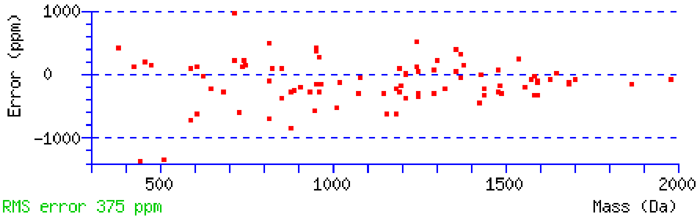


Monoisotopic mass of neutral peptide Mr(calc): 3348.3144
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Q14 : Deamidated (NQ)
Ions Score: 73 **Expect:** 2e-007
Matches : 89/318 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3186.2584	1593.6328	3169.2318	1585.1196	3168.2478	1584.6275	28
3	474.2023	237.6048					Y	3039.1900	1520.0986	3022.1634	1511.5854	3021.1794	1511.0933	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2876.1266	1438.5670	2859.1001	1430.0537	2858.1161	1429.5617	26
5	**646.2508**	323.6290	629.2242	315.1157			G	2761.0997	1381.0535	2744.0732	1372.5402	2743.0891	1372.0482	25
6	**747.2984**	374.1529	730.2719	365.6396	729.2879	365.1476	T	2704.0782	1352.5428	2687.0517	1344.0295	2686.0677	1343.5375	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2603.0306	1302.0189	2586.0040	1293.5056	2585.0200	1293.0136	23
8	**965.3709**	483.1891	948.3444	474.6758	947.3604	474.1838	M	2515.9985	1258.5029	2498.9720	1249.9896	2497.9880	1249.4976	22
9	1036.4081	518.7077	1019.3815	510.1944	1018.3975	509.7024	A	2384.9580	1192.9827	2367.9315	1184.4694	2366.9475	1183.9774	21
10	**1196.4387**	598.7230	1179.4122	590.2097	1178.4281	589.7177	C	2313.9209	1157.4641	2296.8944	1148.9508	2295.9104	1148.4588	20
11	**1325.4813**	663.2443	1308.4548	654.7310	1307.4707	654.2390	E	2153.8903	1077.4488	2136.8637	1068.9355	2135.8797	1068.4435	19
12	**1426.5290**	**713.7681**	1409.5024	705.2549	1408.5184	704.7628	T	2024.8477	1012.9275	2007.8211	1004.4142	2006.8371	1003.9222	18
13	**1573.5974**	787.3023	1556.5708	778.7891	1555.5868	778.2971	F	1923.8000	962.4036	1906.7735	953.8904	1905.7894	953.3984	17
14	**1702.6400**	**851.8236**	1685.6134	843.3104	1684.6294	842.8184	Q	1776.7316	888.8694	1759.7050	880.3562	1758.7210	879.8642	16
15	**1865.7033**	**933.3553**	1848.6768	924.8420	1847.6928	924.3500	Y	***1647.6890***	824.3481	1630.6625	815.8349	1629.6784	815.3429	15
16	1922.7248	**961.8660**	1905.6982	953.3528	1904.7142	952.8607	G	***1484.6257***	742.8165	1467.5991	734.3032	1466.6151	733.8112	14
17	**1979.7462**	990.3768	1962.7197	981.8635	1961.7357	981.3715	G	***1427.6042***	714.3057	1410.5777	705.7925	1409.5936	705.3005	13
18	2139.7769	1070.3921	2122.7503	1061.8788	2121.7663	1061.3868	C	1370.5827	685.7950	1353.5562	677.2817	1352.5722	676.7897	12
19	2270.8174	1135.9123	2253.7908	1127.3991	2252.8068	1126.9070	M	***1210.5521***	605.7797	1193.5255	597.2664	1192.5415	596.7744	11
20	2327.8388	1164.4231	2310.8123	1155.9098	2309.8283	1155.4178	G	***1079.5116***	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2441.8818	1221.4445	2424.8552	1212.9312	2423.8712	1212.4392	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2498.9032	**1249.9553**	2481.8767	1241.4420	2480.8927	1240.9500	G	***908.4472***	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2612.9462	1306.9767	2595.9196	1298.4634	2594.9356	1297.9714	**N**	***851.4258***	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2726.9891	1363.9982	2709.9625	1355.4849	2708.9785	1354.9929	**N**	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2874.0575	**1437.5324**	2857.0310	1429.0191	2856.0469	1428.5271	**F**	***623.3399***	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2973.1259	**1487.0666**	2956.0994	1478.5533	2955.1154	1478.0613	**V**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3074.1736	**1537.5904**	3057.1470	1529.0772	3056.1630	1528.5852	**T**	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3203.2162	1602.1117	3186.1896	1593.5985	3185.2056	1593.1065	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.2	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Q14 95.68%
61.4	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
60.6	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
60.6	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
56.5	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, N21 2.04%
53.8	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, N23 1.10%
53.8	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, N24 1.10%
39.7	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
38.1	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14, N21 0.03%
34.7	3348.3144	-0.0155	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, N23 0.01%

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

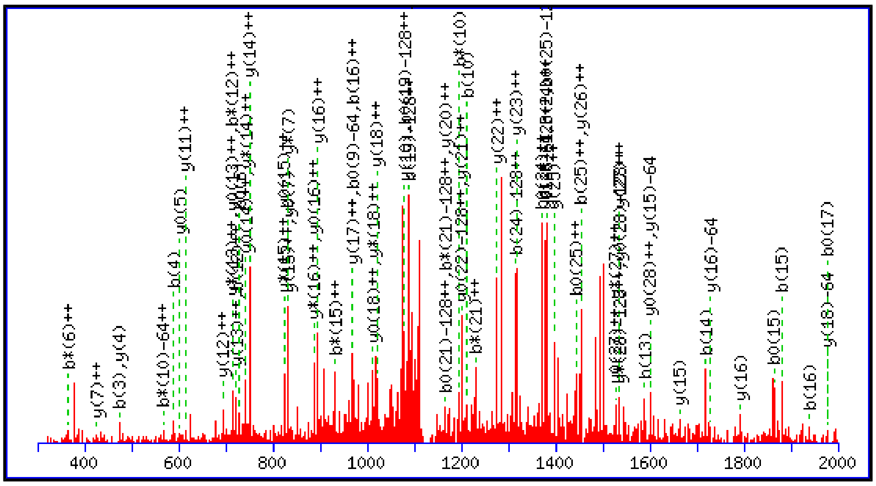
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTVR**
Found in **S4R471** in **con_Xuniprot_HUMAN3**, S4R471_HUMAN Protein AMBP (Fragment) OS=Homo sapiens GN=AMBP PE=4 SV=1

Match to Query 27688: 3380.310462 from(1127.777430,3+) intensity(15255.6231) rtinseconds(1981) scans(5351) index(17729)
Title: 111019_Est_MI_YP_G_07Spectrum4595_scans__5351
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

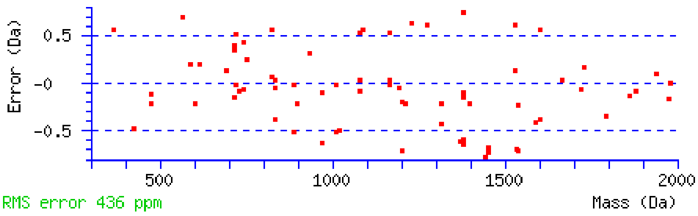
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

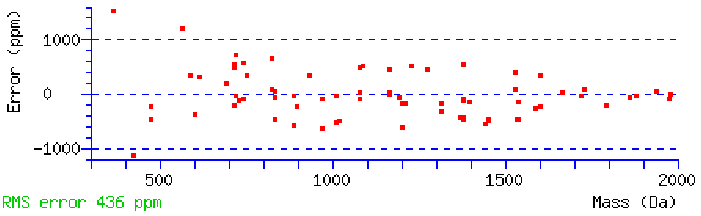


```
Monoisotopic mass of neutral peptide Mr(calc): 3380.3043
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q14     : Deamidated (NQ)
M19     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N21     : Deamidated (NQ)
N24     : Deamidated (NQ)
Ions Score: 71  Expect: 4.6e-007
Matches : 76/550 fragment ions using 102 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3218.2482	1609.6277	3201.2217	1601.1145	3200.2377	1600.6225	28
3	**474.2023**	237.6048					Y	3071.1798	1536.0935	3054.1533	1527.5803	3053.1692	1527.0883	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2908.1165	1454.5619	2891.0899	1446.0486	2890.1059	1445.5566	26
5	646.2508	323.6290	629.2242	315.1157			G	2793.0895	1397.0484	2776.0630	1388.5351	2775.0790	1388.0431	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2736.0681	1368.5377	2719.0415	1360.0244	2718.0575	1359.5324	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2635.0204	1318.0138	2617.9938	1309.5006	2617.0098	1309.0086	23
8	981.3659	491.1866	964.3393	482.6733	963.3553	482.1813	M	2547.9884	1274.4978	2530.9618	1265.9845	2529.9778	1265.4925	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2400.9530	1200.9801	2383.9264	1192.4668	2382.9424	1191.9748	21
10	**1212.4336**	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2329.9158	1165.4616	2312.8893	1156.9483	2311.9053	1156.4563	20
11	1341.4762	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2169.8852	1085.4462	2152.8587	1076.9330	2151.8746	1076.4410	19
12	1442.5239	**721.7656**	1425.4973	713.2523	1424.5133	712.7603	T	2040.8426	1020.9249	2023.8161	1012.4117	2022.8320	1011.9197	18
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	1939.7949	970.4011	1922.7684	961.8878	1921.7844	961.3958	17
14	**1718.6349**	859.8211	1701.6084	851.3078	1700.6243	850.8158	Q	**1792.7265**	896.8669	1775.7000	888.3536	1774.7159	887.8616	16
15	**1881.6982**	941.3528	1864.6717	932.8395	1863.6877	932.3475	Y	**1663.6839**	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1938.7197**	**969.8635**	1921.6931	961.3502	1920.7091	960.8582	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	1995.7412	998.3742	1978.7146	989.8609	1977.7306	989.3689	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2155.7718	1078.3895	2138.7453	1069.8763	2137.7612	1069.3843	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2302.8072	1151.9072	2285.7807	1143.3940	2284.7966	1142.9020	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2359.8287	1180.4180	2342.8021	1171.9047	2341.8181	1171.4127	G	**1079.5116**	540.2594	1062.4851	531.7462	1061.5010	531.2542	10

21	2474.8556	1237.9314	2457.8291	1229.4182	2456.8451	1228.9262	**N**	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	**9**
22	2531.8771	1266.4422	2514.8505	1257.9289	2513.8665	1257.4369	**G**	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	**8**
23	2645.9200	1323.4636	2628.8935	1314.9504	2627.9094	1314.4584	**N**	850.4417	425.7245	833.4152	417.2112	832.4312	416.7192	**7**
24	2760.9470	**1380.9771**	2743.9204	1372.4638	2742.9364	1371.9718	**N**	736.3988	368.7030	719.3723	360.1898	718.3883	359.6978	**6**
25	2908.0154	**1454.5113**	2890.9888	1445.9980	2890.0048	1445.5060	**F**	621.3719	311.1896	604.3453	302.6763	603.3613	302.1843	**5**
26	3007.0838	1504.0455	2990.0572	1495.5323	2989.0732	1495.0402	**V**	**474.3035**	237.6554	457.2769	229.1421	456.2929	228.6501	**4**
27	3108.1315	1554.5694	3091.1049	1546.0561	3090.1209	1545.5641	**T**	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
28	3207.1999	1604.1036	3190.1733	1595.5903	3189.1893	1595.0983	**V**	274.1874	137.5973	257.1608	129.0840			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.8	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14, N21, N24 34.73%
70.8	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14, N21, N23 34.73%
69.6	3379.3203	0.9902	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
69.6	3379.3203	0.9902	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
68.4	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
68.3	3379.3203	0.9902	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
67.1	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
67.1	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
67.1	3380.3043	0.0062	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
66.5	3379.3203	0.9902	YFYNGTSMACETFQYGGCMGNGNNFVTEK	

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

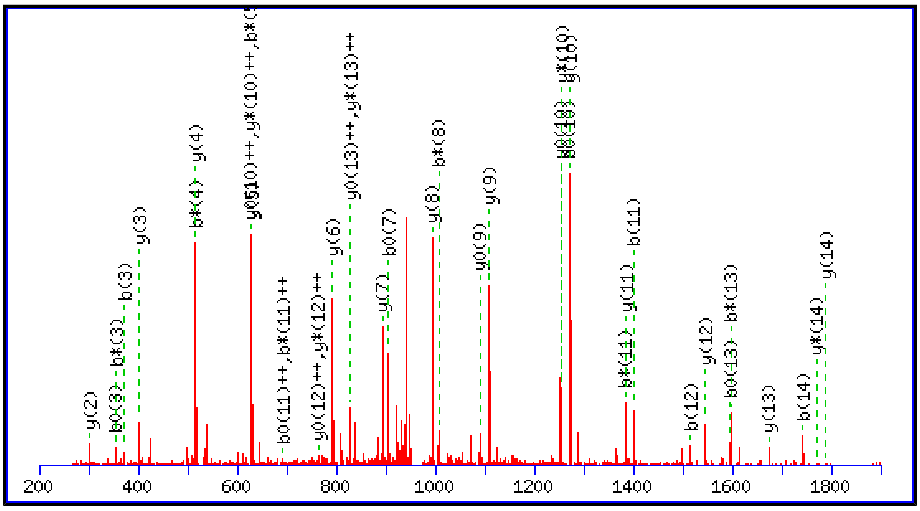
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

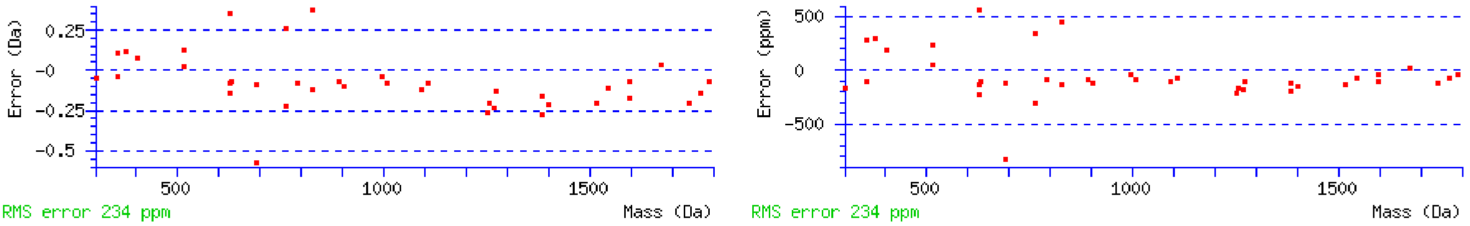
Match to Query 11591: 1915.881788 from(958.948170,2+) intensity(53074.4570) rtinseconds(1364) scans(3214) index(27375)
Title: 111019_Est_MI_YS_G_10Spectrum2759_scans__3214
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1915.8734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 99 **Expect:** 2e-008
Matches : 39/154 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	129.0659	65.0366	112.0393	56.5233			Q							15
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	D	***1788.8221***	894.9147	1771.7956	886.4014	1770.8116	885.9094	14
3	**372.1514**	186.5793	355.1248	178.0661	354.1408	177.5740	Q	***1673.7952***	837.4012	1656.7686	828.8880	1655.7846	828.3959	13
4	532.1820	266.5947	515.1555	258.0814	514.1715	257.5894	C	***1545.7366***	773.3719	1528.7101	764.8587	1527.7260	764.3667	12
5	645.2661	323.1367	628.2395	314.6234	627.2555	314.1314	I	***1385.7060***	693.3566	1368.6794	684.8433	1367.6954	684.3513	11
6	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	Y	***1272.6219***	636.8146	1255.5953	628.3013	1254.6113	627.8093	10
7	923.3564	462.1818	906.3298	453.6685	905.3458	453.1765	N	***1109.5586***	555.2829	1092.5320	546.7696	1091.5480	546.2776	9
8	1024.4040	512.7057	1007.3775	504.1924	1006.3935	503.7004	T	***994.5316***	497.7694	977.5051	489.2562	976.5211	488.7642	8
9	1125.4517	563.2295	1108.4252	554.7162	1107.4412	554.2242	T	***893.4839***	447.2456	876.4574	438.7323	875.4734	438.2403	7
10	1288.5150	644.7612	1271.4885	636.2479	1270.5045	635.7559	Y	***792.4363***	396.7218	775.4097	388.2085			6
11	**1401.5991**	701.3032	1384.5726	692.7899	1383.5885	692.2979	L	***629.3729***	315.1901	612.3464	306.6768			5
12	**1515.6420**	758.3247	1498.6155	749.8114	1497.6315	749.3194	N	***516.2889***	258.6481	499.2623	250.1348			4
13	1614.7105	807.8589	1597.6839	799.3456	1596.6999	798.8536	V	***402.2459***	201.6266	385.2194	193.1133			3
14	**1742.7690**	871.8882	1725.7425	863.3749	1724.7585	862.8829	Q	***303.1775***	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.4	1915.8734	0.0084	QDQCIYNTTYLNVQR	Deamidated N7 98.68%
80.6	1915.8734	0.0084	QDQCIYNTTYLNVQR	Deamidated N12 1.30%
58.8	1915.8734	0.0084	QDQCIYNTTYLNVQR	Deamidated Q3 0.01%
58.1	1915.8734	0.0084	QDQCIYNTTYLNVQR	Deamidated Q14 0.01%
37.5	1915.8734	0.0084	QDQCIYNTTYLNVQR	Deamidated Q1 0.00%
7.1	1915.8880	-0.0062	MHDRSGMEQGLAANVVGK	
5.9	1914.8820	0.9998	EQQQGSSPAGHGAGPPVPGR	
5.9	1914.8820	0.9998	EQQQGSSPAGHGAGPPVPGR	
5.3	1915.8813	0.0005	FVVPNSNYSVSGHQSHR	
5.1	1914.8806	1.0012	EEQEEQENRPKLINR	

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

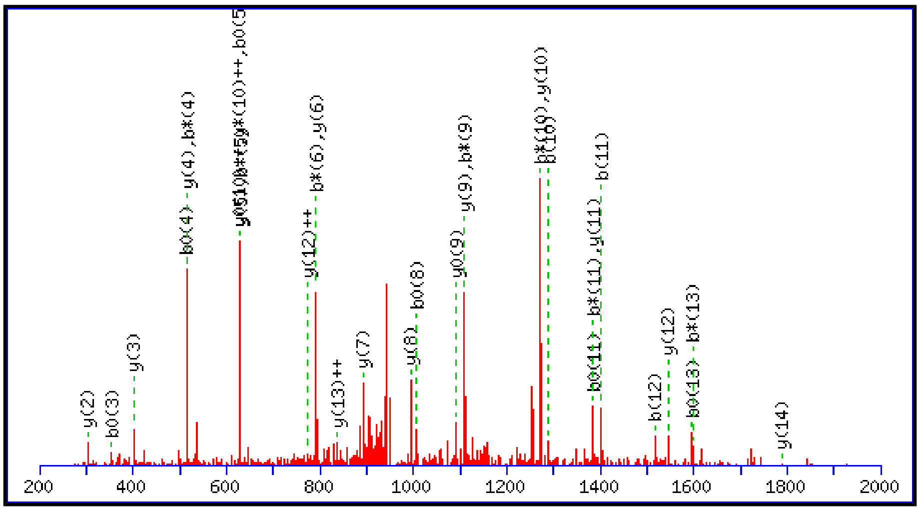
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

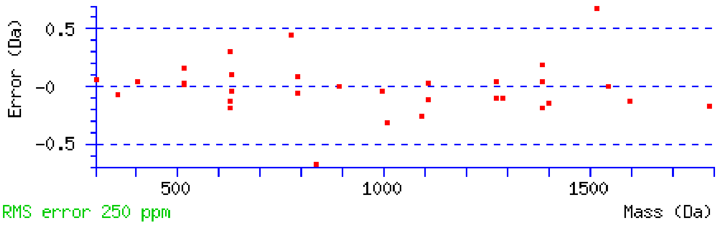
Match to Query 11605: 1916.855348 from(959.434950,2+) intensity(4687.6553) rtinseconds(1317) scans(3111) index(20237)
Title: 111019_Est_MI_YP_G_10Spectrum2708_scans__3111
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

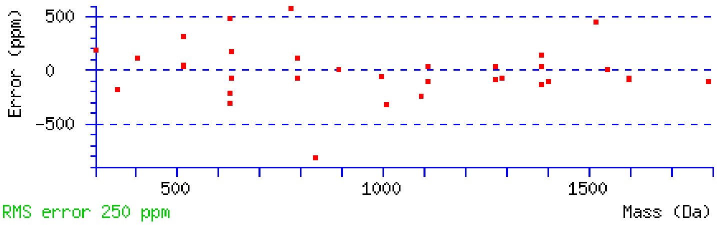
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1916.8574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 72 **Expect:** 7.6e-006
Matches : 33/154 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	129.0659	65.0366	112.0393	56.5233			**Q**							**15**
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	**D**	***1789.8061***	895.4067	1772.7796	886.8934	1771.7956	886.4014	**14**
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	**Q**	1674.7792	837.8932	1657.7527	829.3800	1656.7686	828.8880	**13**
4	533.1660	267.0867	516.1395	258.5734	515.1555	258.0814	**C**	***1545.7366***	773.3719	1528.7101	764.8587	1527.7260	764.3667	**12**
5	646.2501	323.6287	629.2236	315.1154	628.2395	314.6234	**I**	***1385.7060***	693.3566	1368.6794	684.8433	1367.6954	684.3513	**11**
6	809.3134	405.1604	792.2869	396.6471	791.3029	396.1551	**Y**	***1272.6219***	636.8146	1255.5953	628.3013	1254.6113	627.8093	**10**
7	924.3404	462.6738	907.3138	454.1606	906.3298	453.6685	**N**	***1109.5586***	555.2829	1092.5320	546.7696	1091.5480	546.2776	**9**
8	1025.3881	513.1977	1008.3615	504.6844	1007.3775	504.1924	**T**	***994.5316***	497.7694	977.5051	489.2562	976.5211	488.7642	**8**
9	1126.4357	563.7215	1109.4092	555.2082	1108.4252	554.7162	**T**	***893.4839***	447.2456	876.4574	438.7323	875.4734	438.2403	**7**
10	**1289.4991**	645.2532	1272.4725	636.7399	1271.4885	636.2479	**Y**	***792.4363***	396.7218	775.4097	388.2085			**6**
11	**1402.5831**	701.7952	1385.5566	693.2819	1384.5726	692.7899	**L**	***629.3729***	315.1901	612.3464	306.6768			**5**
12	**1516.6261**	758.8167	1499.5995	750.3034	1498.6155	749.8114	**N**	***516.2889***	258.6481	499.2623	250.1348			**4**
13	1615.6945	808.3509	1598.6679	799.8376	1597.6839	799.3456	**V**	***402.2459***	201.6266	385.2194	193.1133			**3**
14	1743.7530	872.3802	1726.7265	863.8669	1725.7425	863.3749	**Q**	***303.1775***	152.0924	286.1510	143.5791			**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.9	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q3, N7 75.33%
65.2	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q1, N7 16.18%
61.3	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q3, N12 6.62%
51.3	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q1, Q3 0.66%
51.3	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q1, N12 0.66%
48.1	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q3, Q14 0.32%
45.5	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated N7, N12 0.17%
39.3	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated Q1, Q14 0.04%
33.7	1916.8574	-0.0021	QDQCIYNTTYLNVQR	Deamidated N7, Q14 0.01%
9.2	1916.8588	-0.0035	GDNDLLTGHYVCGFHGR	

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

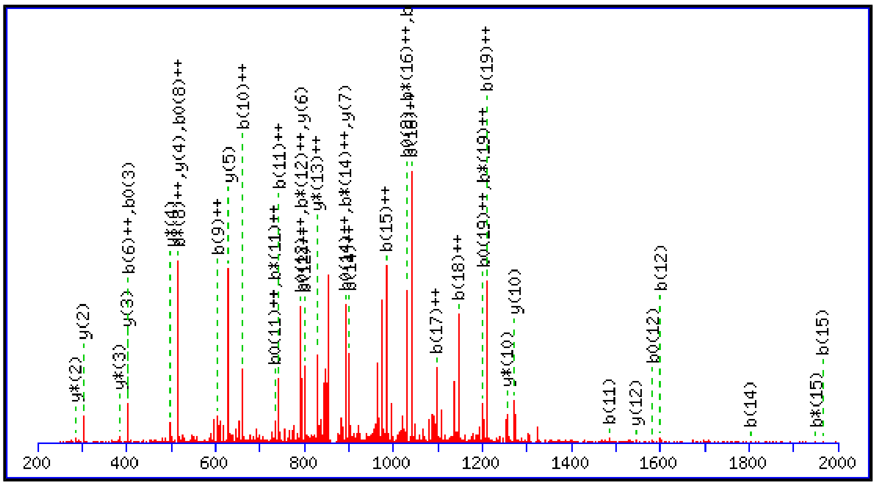
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYQTRQDQCIYNTTYLNVQR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

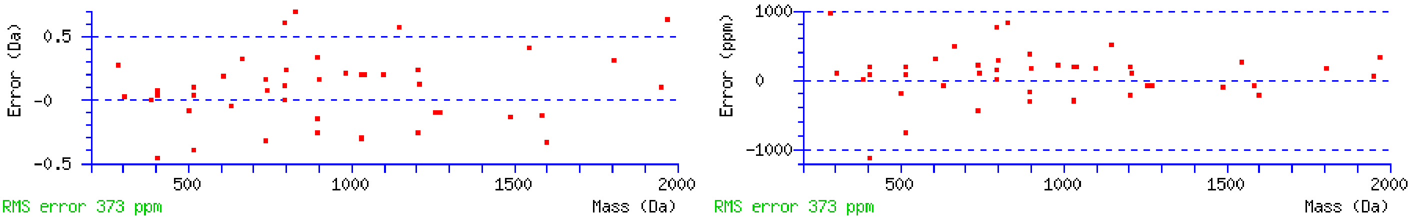
Match to Query 22190: 2593.194042 from(865.405290,3+) intensity(90556.7109) rtinseconds(1218) scans(2834) index(12498)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2462_scans__2834
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2593.1867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 62 **Expect:** 0.00012
Matches : 44/212 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							20
2	293.1132	147.0602			275.1026	138.0550	Y	2465.1514	1233.0793	2448.1249	1224.5661	2447.1408	1224.0741	19
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	2302.0881	1151.5477	2285.0615	1143.0344	2284.0775	1142.5424	18
4	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	T	2174.0295	1087.5184	2157.0029	1079.0051	2156.0189	1078.5131	17
5	678.3206	339.6639	661.2940	331.1506	660.3100	330.6586	R	2072.9818	1036.9945	2055.9553	1028.4813	2054.9713	1027.9893	16
6	806.3791	***403.6932***	789.3526	395.1799	788.3686	394.6879	Q	1916.8807	958.9440	1899.8542	950.4307	1898.8701	949.9387	15
7	921.4061	461.2067	904.3795	452.6934	903.3955	452.2014	D	1788.8221	894.9147	1771.7956	886.4014	1770.8116	885.9094	14
8	1049.4647	525.2360	1032.4381	516.7227	1031.4541	516.2307	Q	1673.7952	837.4012	1656.7686	828.8880	1655.7846	828.3959	13
9	1209.4953	***605.2513***	1192.4688	596.7380	1191.4847	596.2460	C	***1545.7366***	773.3719	1528.7101	764.8587	1527.7260	764.3667	12
10	1322.5794	***661.7933***	1305.5528	653.2801	1304.5688	652.7880	I	1385.7060	693.3566	1368.6794	684.8433	1367.6954	684.3513	11
11	**1485.6427**	***743.3250***	1468.6162	734.8117	1467.6321	734.3197	Y	***1272.6219***	636.8146	1255.5953	628.3013	1254.6113	627.8093	10
12	**1600.6697**	***800.8385***	1583.6431	792.3252	1582.6591	791.8332	N	1109.5586	555.2829	1092.5320	546.7696	1091.5480	546.2776	9
13	1701.7173	851.3623	1684.6908	842.8490	1683.7068	842.3570	T	994.5316	497.7694	977.5051	489.2562	976.5211	488.7642	8
14	**1802.7650**	***901.8861***	1785.7385	893.3729	1784.7544	892.8809	T	***893.4839***	447.2456	876.4574	438.7323	875.4734	438.2403	7
15	**1965.8283**	***983.4178***	1948.8018	974.9045	1947.8178	974.4125	Y	***792.4363***	396.7218	775.4097	388.2085			6
16	2078.9124	***1039.9598***	2061.8859	1031.4466	2060.9018	1030.9546	L	***629.3729***	315.1901	612.3464	306.6768			5
17	2192.9553	***1096.9813***	2175.9288	1088.4680	2174.9448	1087.9760	N	***516.2889***	258.6481	499.2623	250.1348			4
18	2292.0237	***1146.5155***	2274.9972	1138.0022	2274.0132	1137.5102	V	***402.2459***	201.6266	385.2194	193.1133			3
19	2420.0823	***1210.5448***	2403.0558	1202.0315	2402.0718	1201.5395	Q	***303.1775***	152.0924	286.1510	143.5791			2
20							R	175.1190	88.0631	158.0924	79.5498			1



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.0	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated N12 75.85%
56.2	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated Q8 19.63%
46.3	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated Q6 2.02%
45.0	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated Q3 1.51%
42.0	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated N17 0.74%
39.8	2592.2027	0.9914	EYQTRQDQCIYNTTYLNVQR	
37.0	2593.1867	0.0074	EYQTRQDQCIYNTTYLNVQR	Deamidated Q19 0.24%
8.8	2593.1822	0.0119	LNLGRLPGMTQGNLTQSMQNMPR	
7.7	2592.2012	0.9929	SRNGTSPNLESNVNINSGTETGTSR	
6.0	2593.1853	0.0087	NIWSPGTNGQISLLDNTVGRMAET	

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

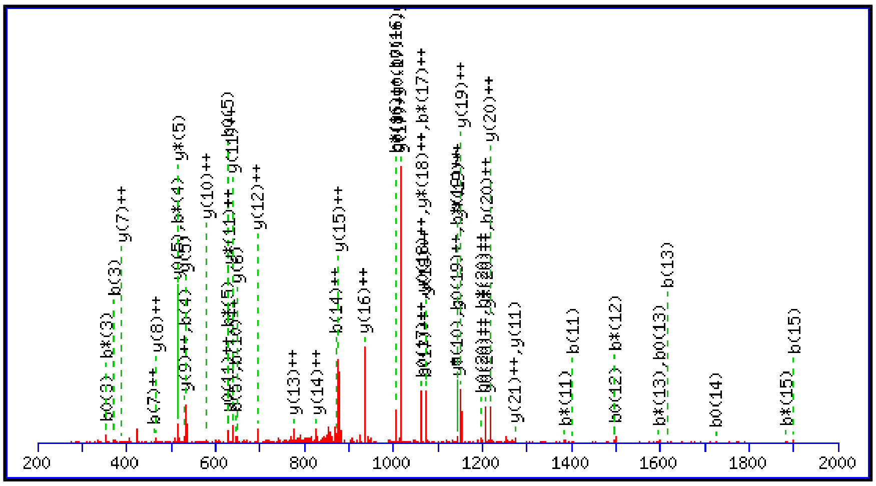
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQRENGTISR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

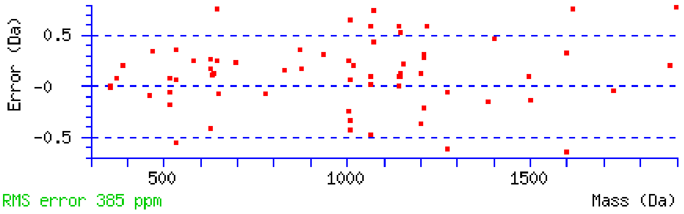
Match to Query 22476: 2674.236492 from(892.419440,3+) intensity(9456.8760) rtinseconds(1414) scans(3307) index(20715)
Title: 111019_Est_MI_YP_G_11Spectrum2895_scans__3307
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

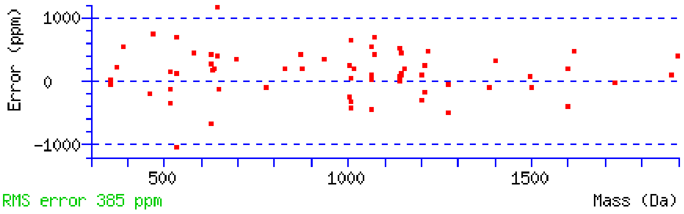
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2674.2293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00056
Matches : 65/248 fragment ions using 124 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	D	2547.1780	1274.0926	2530.1515	1265.5794	2529.1674	1265.0874	21
3	**372.1514**	186.5793	355.1248	178.0661	354.1408	177.5740	Q	2432.1511	1216.5792	2415.1245	1208.0659	2414.1405	1207.5739	20
4	**532.1820**	266.5947	515.1555	258.0814	514.1715	257.5894	C	2304.0925	1152.5499	2287.0659	1144.0366	2286.0819	1143.5446	19
5	**645.2661**	323.1367	628.2395	314.6234	627.2555	314.1314	I	2144.0618	1072.5346	2127.0353	1064.0213	2126.0513	1063.5293	18
6	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	Y	2030.9778	1015.9925	2013.9512	1007.4793	2012.9672	1006.9872	17
7	923.3564	**462.1818**	906.3298	453.6685	905.3458	453.1765	N	1867.9144	934.4609	1850.8879	925.9476	1849.9039	925.4556	16
8	1024.4040	512.7057	1007.3775	504.1924	1006.3935	503.7004	T	1752.8875	876.9474	1735.8610	868.4341	1734.8769	867.9421	15
9	1125.4517	563.2295	1108.4252	554.7162	1107.4412	554.2242	T	1651.8398	826.4236	1634.8133	817.9103	1633.8293	817.4183	14
10	1288.5150	**644.7612**	1271.4885	636.2479	1270.5045	635.7559	Y	1550.7921	775.8997	1533.7656	767.3864	1532.7816	766.8944	13
11	**1401.5991**	701.3032	1384.5726	692.7899	1383.5885	692.2979	L	1387.7288	694.3680	1370.7023	685.8548	1369.7183	685.3628	12
12	1515.6420	758.3247	1498.6155	749.8114	1497.6315	749.3194	N	1274.6448	637.8260	1257.6182	629.3127	1256.6342	628.8207	11
13	**1614.7105**	807.8589	1597.6839	799.3456	1596.6999	798.8536	V	1160.6018	580.8046	1143.5753	572.2913	1142.5913	571.7993	10
14	1742.7690	**871.8882**	1725.7425	863.3749	1724.7585	862.8829	Q	1061.5334	531.2703	1044.5069	522.7571	1043.5228	522.2651	9
15	**1898.8701**	949.9387	1881.8436	941.4254	1880.8596	940.9334	R	933.4748	467.2411	916.4483	458.7278	915.4643	458.2358	8
16	2027.9127	1014.4600	2010.8862	1005.9467	2009.9022	1005.4547	E	777.3737	389.1905	760.3472	380.6772	759.3632	380.1852	7
17	2142.9397	**1071.9735**	2125.9131	1063.4602	2124.9291	1062.9682	N	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
18	2199.9611	1100.4842	2182.9346	1091.9709	2181.9506	1091.4789	G	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
19	2301.0088	1151.0080	2283.9823	1142.4948	2282.9983	1142.0028	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
20	2414.0929	**1207.5501**	2397.0663	1199.0368	2396.0823	1198.5448	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2501.1249	1251.0661	2484.0984	1242.5528	2483.1143	1242.0608	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
55.5	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N17 45.13%
51.9	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, N17 19.84%
47.9	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated Q14, N17 7.88%
47.4	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, Q14 7.04%
46.7	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N17 6.00%
44.9	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated Q1, N17 3.96%
44.1	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, Q14 3.31%
42.2	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N12 2.13%
39.2	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, Q14 1.08%
37.6	2674.2293	0.0072	QDQCIYNTTYLNVQRENGTISR	Deamidated Q1, Q14 0.73%

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

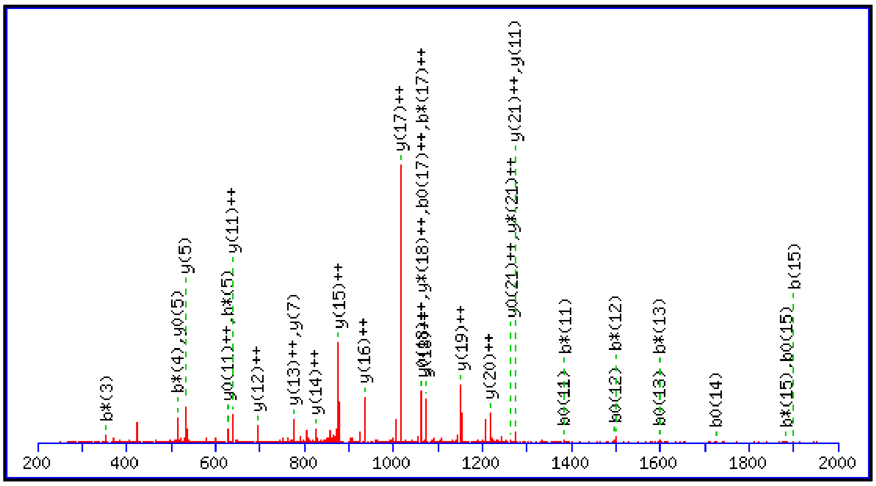
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQRENGTISR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

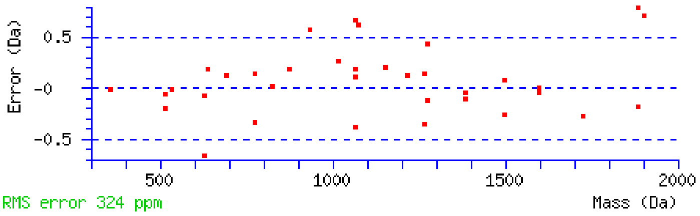
Match to Query 22478: 2674.239372 from(892.420400,3+) intensity(66870.8984) rtinseconds(1364) scans(3326) index(26584)
Title: 111019_Est_MI_YS_G_09Spectrum2871_scans__3326
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

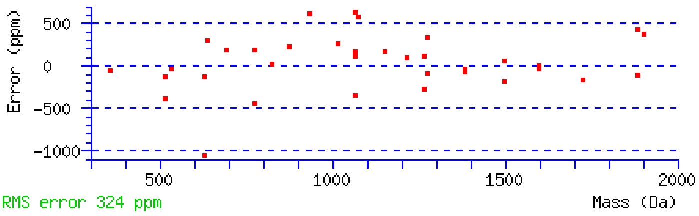
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2674.2293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0009
Matches : 35/248 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	129.0659	65.0366	112.0393	56.5233			Q							22
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	D	2547.1780	1274.0926	2530.1515	1265.5794	2529.1674	1265.0874	21
3	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	Q	2432.1511	1216.5792	2415.1245	1208.0659	2414.1405	1207.5739	20
4	532.1820	266.5947	515.1555	258.0814	514.1715	257.5894	C	2304.0925	1152.5499	2287.0659	1144.0366	2286.0819	1143.5446	19
5	645.2661	323.1367	628.2395	314.6234	627.2555	314.1314	I	2144.0618	1072.5346	2127.0353	1064.0213	2126.0513	1063.5293	18
6	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	Y	2030.9778	1015.9925	2013.9512	1007.4793	2012.9672	1006.9872	17
7	923.3564	462.1818	906.3298	453.6685	905.3458	453.1765	N	1867.9144	934.4609	1850.8879	925.9476	1849.9039	925.4556	16
8	1024.4040	512.7057	1007.3775	504.1924	1006.3935	503.7004	T	1752.8875	876.9474	1735.8610	868.4341	1734.8769	867.9421	15
9	1125.4517	563.2295	1108.4252	554.7162	1107.4412	554.2242	T	1651.8398	826.4236	1634.8133	817.9103	1633.8293	817.4183	14
10	1288.5150	644.7612	1271.4885	636.2479	1270.5045	635.7559	Y	1550.7921	775.8997	1533.7656	767.3864	1532.7816	766.8944	13
11	1401.5991	701.3032	1384.5726	692.7899	1383.5885	692.2979	L	1387.7288	694.3680	1370.7023	685.8548	1369.7183	685.3628	12
12	1516.6261	758.8167	1499.5995	750.3034	1498.6155	749.8114	N	**1274.6448**	637.8260	1257.6182	629.3127	1256.6342	628.8207	11
13	1615.6945	808.3509	1598.6679	799.8376	1597.6839	799.3456	V	1159.6178	580.3125	1142.5913	571.7993	1141.6072	571.3073	10
14	1743.7530	872.3802	1726.7265	863.8669	1725.7425	863.3749	Q	1060.5494	530.7783	1043.5228	522.2651	1042.5388	521.7731	9
15	1899.8542	950.4307	1882.8276	941.9174	1881.8436	941.4254	R	932.4908	466.7490	915.4643	458.2358	914.4803	457.7438	8
16	2028.8968	1014.9520	2011.8702	1006.4387	2010.8862	1005.9467	E	**776.3897**	388.6985	759.3632	380.1852	758.3791	379.6932	7
17	2142.9397	1071.9735	2125.9131	1063.4602	2124.9291	1062.9682	N	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
18	2199.9611	1100.4842	2182.9346	1091.9709	2181.9506	1091.4789	G	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	5
19	2301.0088	1151.0080	2283.9823	1142.4948	2282.9983	1142.0028	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
20	2414.0929	1207.5501	2397.0663	1199.0368	2396.0823	1198.5448	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2501.1249	1251.0661	2484.0984	1242.5528	2483.1143	1242.0608	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.6	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N12 41.55%
53.5	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, Q14 41.26%
42.5	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N17 3.23%
42.4	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, Q14 3.18%
42.4	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated Q14, N17 3.17%
41.9	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, N17 2.85%
38.6	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, Q14 1.34%
38.6	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N12 1.34%
35.0	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N17 0.58%
32.2	2674.2293	0.0101	QDQCIYNTTYLNVQRENGTISR	Deamidated Q1, Q14 0.30%

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

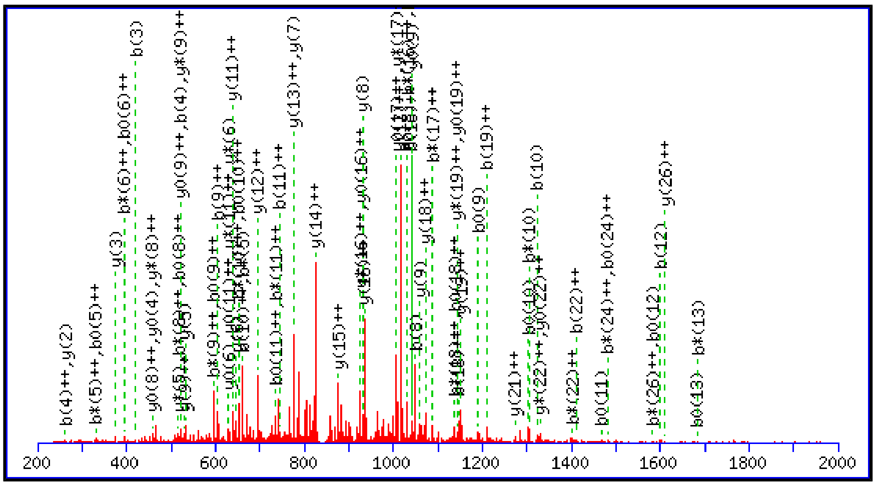
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EYQTRQDQCIYNTTYLNVQRENGTISR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

Match to Query 27506: 3351.550856 from(838.894990,4+) intensity(110283.2031) rtinseconds(1343) scans(3264) index(26573)
Title: 111019_Est_MI_YS_G_09Spectrum2819_scans__3264
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

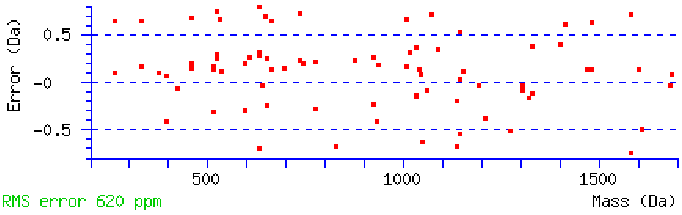
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

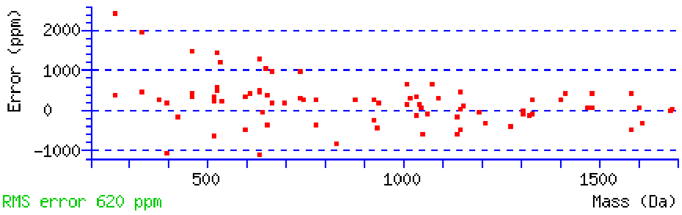


Monoisotopic mass of neutral peptide Mr(calc): 3351.5426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 44 **Expect:** 0.0093
Matches : 81/306 fragment ions using 118 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							27
2	293.1132	147.0602			275.1026	138.0550	Y	3223.5073	1612.2573	3206.4807	1603.7440	3205.4967	1603.2520	26
3	**421.1718**	211.0895	404.1452	202.5763	403.1612	202.0842	Q	3060.4440	1530.7256	3043.4174	1522.2123	3042.4334	1521.7203	25
4	**522.2195**	**261.6134**	505.1929	253.1001	504.2089	252.6081	T	2932.3854	1466.6963	2915.3588	1458.1831	2914.3748	1457.6910	24
5	678.3206	339.6639	661.2940	331.1506	660.3100	330.6586	R	2831.3377	1416.1725	2814.3111	1407.6592	2813.3271	1407.1672	23
6	806.3791	403.6932	789.3526	395.1799	788.3686	394.6879	Q	2675.2366	1338.1219	2658.2100	1329.6087	2657.2260	1329.1166	22
7	921.4061	461.2067	904.3795	452.6934	903.3955	452.2014	D	2547.1780	1274.0926	2530.1515	1265.5794	2529.1674	1265.0874	21
8	**1049.4647**	525.2360	1032.4381	516.7227	1031.4541	516.2307	Q	2432.1511	1216.5792	2415.1245	1208.0659	2414.1405	1207.5739	20
9	1209.4953	**605.2513**	1192.4688	596.7380	1191.4847	596.2460	C	2304.0925	1152.5499	2287.0659	1144.0366	2286.0819	1143.5446	19
10	**1322.5794**	**661.7933**	1305.5528	653.2801	1304.5688	652.7880	I	2144.0618	1072.5346	2127.0353	1064.0213	2126.0513	1063.5293	18
11	1485.6427	**743.3250**	1468.6162	734.8117	1467.6321	734.3197	Y	2030.9778	1015.9925	2013.9512	1007.4793	2012.9672	1006.9872	17
12	**1600.6697**	800.8385	1583.6431	792.3252	1582.6591	791.8332	N	1867.9144	934.4609	1850.8879	925.9476	1849.9039	925.4556	16
13	1701.7173	851.3623	1684.6908	842.8490	1683.7068	842.3570	T	1752.8875	876.9474	1735.8610	868.4341	1734.8769	867.9421	15
14	1802.7650	901.8861	1785.7385	893.3729	1784.7544	892.8809	T	1651.8398	826.4236	1634.8133	817.9103	1633.8293	817.4183	14
15	1965.8283	983.4178	1948.8018	974.9045	1947.8178	974.4125	Y	1550.7921	775.8997	1533.7656	767.3864	1532.7816	766.8944	13
16	2078.9124	**1039.9598**	2061.8859	1031.4466	2060.9018	1030.9546	L	1387.7288	694.3680	1370.7023	685.8548	1369.7183	685.3628	12
17	2193.9393	1097.4733	2176.9128	1088.9600	2175.9288	1088.4680	N	1274.6448	637.8260	1257.6182	629.3127	1256.6342	628.8207	11
18	2293.0078	**1147.0075**	2275.9812	1138.4942	2274.9972	1138.0022	V	1159.6178	580.3125	1142.5913	571.7993	1141.6072	571.3073	10
19	2421.0663	**1211.0368**	2404.0398	1202.5235	2403.0558	1202.0315	Q	***1060.5494***	530.7783	1043.5228	522.2651	1042.5388	521.7731	9
20	2577.1674	1289.0874	2560.1409	1280.5741	2559.1569	1280.0821	R	***932.4908***	466.7490	915.4643	458.2358	914.4803	457.7438	8
21	2706.2100	1353.6087	2689.1835	1345.0954	2688.1995	1344.6034	E	***776.3897***	388.6985	759.3632	380.1852	758.3791	379.6932	7
22	2820.2530	**1410.6301**	2803.2264	1402.1168	2802.2424	1401.6248	N	***647.3471***	324.1772	630.3206	315.6639	629.3365	315.1719	6

23	2877.2744	1439.1409	2860.2479	1430.6276	2859.2639	1430.1356	**G**	***533.3042***	267.1557	516.2776	258.6425	515.2936	258.1504	**5**
24	2978.3221	1489.6647	2961.2956	1481.1514	2960.3115	1480.6594	**T**	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	**4**
25	3091.4062	1546.2067	3074.3796	1537.6935	3073.3956	1537.2014	**I**	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
26	3178.4382	1589.7227	3161.4117	1581.2095	3160.4276	1580.7175	**S**	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.7	3351.5426	0.0083	EYQTRQDQCIYNTTYLNVQRENGTISR	Deamidated N12, N17 65.66%
42.3	3350.5585	0.9923	EYQTRQDQCIYNTTYLNVQRENGTISR	
37.0	3351.5426	0.0083	EYQTRQDQCIYNTTYLNVQRENGTISR	Deamidated Q19, N22 14.01%
36.8	3350.5585	0.9923	EYQTRQDQCIYNTTYLNVQRENGTISR	
34.1	3350.5585	0.9923	EYQTRQDQCIYNTTYLNVQRENGTISR	
33.2	3351.5426	0.0083	EYQTRQDQCIYNTTYLNVQRENGTISR	Deamidated N17, Q19 5.77%
32.8	3351.5426	0.0083	EYQTRQDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N22 5.26%
32.6	3350.5585	0.9923	EYQTRQDQCIYNTTYLNVQRENGTISR	
31.3	3351.5426	0.0083	EYQTRQDQCIYNTTYLNVQRENGTISR	Deamidated Q8, N12 3.76%
21.9	3350.5585	0.9923	EYQTRQDQCIYNTTYLNVQRENGTISR	

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

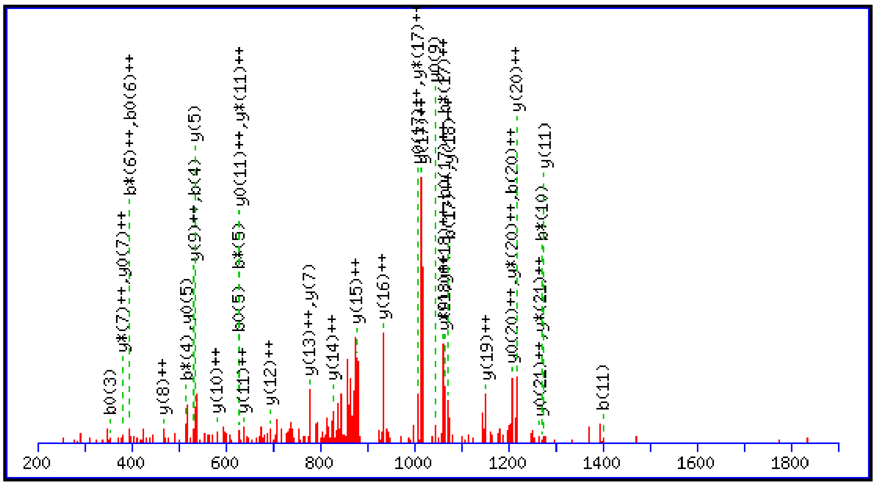
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQRENGTISR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

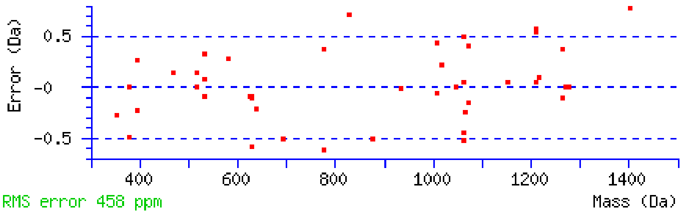
Match to Query 22474: 2674.230792 from(892.417540,3+) intensity(781.5458) rtinseconds(1415) scans(2745) index(21592)
Title: 111019_Est_MI_YP_G_14Spectrum2329_scans__2745
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

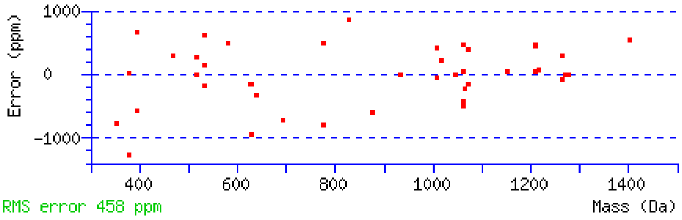
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2674.2293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Deamidated (NQ)
N17 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.015
Matches : 44/248 fragment ions using 83 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	D	2547.1780	1274.0926	2530.1515	1265.5794	2529.1674	1265.0874	21
3	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	Q	2432.1511	1216.5792	2415.1245	1208.0659	2414.1405	1207.5739	20
4	532.1820	266.5947	515.1555	258.0814	514.1715	257.5894	C	2304.0925	1152.5499	2287.0659	1144.0366	2286.0819	1143.5446	19
5	645.2661	323.1367	628.2395	314.6234	627.2555	314.1314	I	2144.0618	1072.5346	2127.0353	1064.0213	2126.0513	1063.5293	18
6	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	Y	2030.9778	1015.9925	2013.9512	1007.4793	2012.9672	1006.9872	17
7	922.3723	461.6898	905.3458	453.1765	904.3618	452.6845	N	1867.9144	934.4609	1850.8879	925.9476	1849.9039	925.4556	16
8	1023.4200	512.2136	1006.3935	503.7004	1005.4095	503.2084	T	1753.8715	877.4394	1736.8450	868.9261	1735.8610	868.4341	15
9	1124.4677	562.7375	1107.4412	554.2242	1106.4571	553.7322	T	1652.8238	826.9156	1635.7973	818.4023	1634.8133	817.9103	14
10	1287.5310	644.2692	1270.5045	635.7559	1269.5205	635.2639	Y	1551.7762	776.3917	1534.7496	767.8784	1533.7656	767.3864	13
11	1400.6151	700.8112	1383.5885	692.2979	1382.6045	691.8059	L	1388.7128	694.8601	1371.6863	686.3468	1370.7023	685.8548	12
12	1514.6580	757.8326	1497.6315	749.3194	1496.6475	748.8274	N	**1275.6288**	638.3180	1258.6022	629.8047	1257.6182	629.3127	11
13	1613.7264	807.3669	1596.6999	798.8536	1595.7159	798.3616	V	1161.5858	581.2966	1144.5593	572.7833	1143.5753	572.2913	10
14	1742.7690	871.8882	1725.7425	863.3749	1724.7585	862.8829	Q	**1062.5174**	531.7624	1045.4909	523.2491	1044.5069	522.7571	9
15	1898.8701	949.9387	1881.8436	941.4254	1880.8596	940.9334	R	933.4748	467.2411	916.4483	458.7278	915.4643	458.2358	8
16	2027.9127	1014.4600	2010.8862	1005.9467	2009.9022	1005.4547	E	**777.3737**	389.1905	760.3472	380.6772	759.3632	380.1852	7
17	2142.9397	1071.9735	2125.9131	1063.4602	2124.9291	1062.9682	N	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
18	2199.9611	1100.4842	2182.9346	1091.9709	2181.9506	1091.4789	G	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	5
19	2301.0088	1151.0080	2283.9823	1142.4948	2282.9983	1142.0028	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
20	2414.0929	1207.5501	2397.0663	1199.0368	2396.0823	1198.5448	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2501.1249	1251.0661	2484.0984	1242.5528	2483.1143	1242.0608	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.9	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated Q14, N17 70.10%
34.1	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, N17 14.75%
34.1	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated N12, Q14 14.75%
10.7	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N17 0.07%
10.7	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, Q14 0.07%
9.4	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated N7, N12 0.05%
7.0	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N17 0.03%
7.0	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, Q14 0.03%
7.0	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3, N12 0.03%
7.0	2674.2293	0.0015	QDQCIYNTTYLNVQRENGTISR	Deamidated Q1, N17 0.03%

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

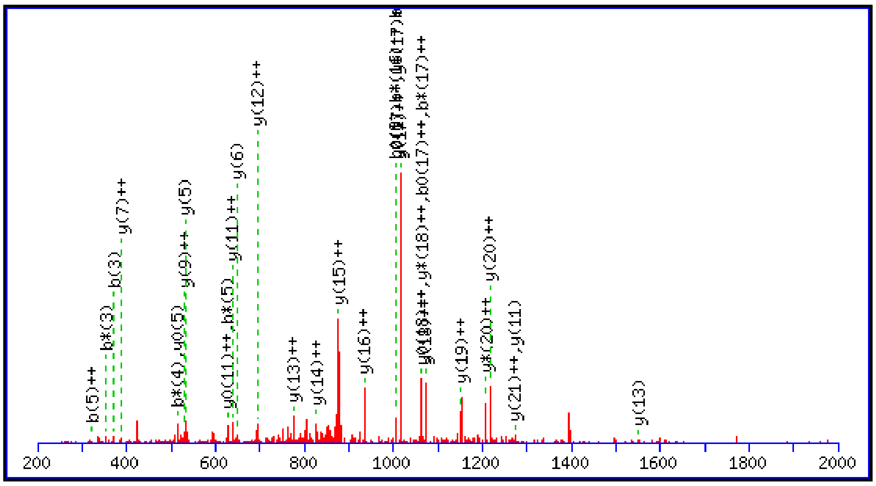
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDQCIYNTTYLNVQRENGTISR**
Found in **P02763** in **con_Xuniprot_HUMAN3**, A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1

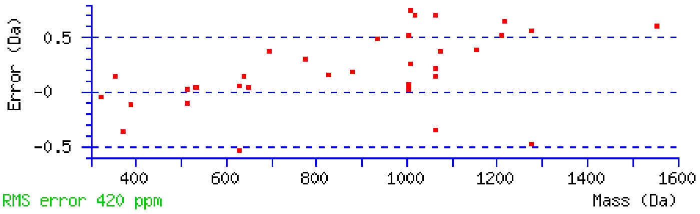
Match to Query 22479: 2674.243182 from(892.421670,3+) intensity(3724.8096) rtinseconds(1391) scans(3251) index(20711)
Title: 111019_Est_MI_YP_G_11Spectrum2845_scans__3251
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

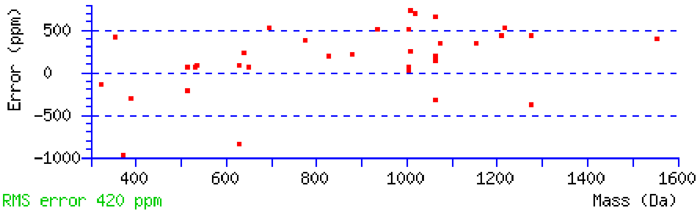
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2673.2453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.033
Matches : 34/248 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	129.0659	65.0366	112.0393	56.5233			Q							22
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	D	2546.1940	1273.6006	2529.1674	1265.0874	2528.1834	1264.5954	21
3	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	Q	2431.1671	1216.0872	2414.1405	1207.5739	2413.1565	1207.0819	20
4	532.1820	266.5947	515.1555	258.0814	514.1715	257.5894	C	2303.1085	1152.0579	2286.0819	1143.5446	2285.0979	1143.0526	19
5	645.2661	323.1367	628.2395	314.6234	627.2555	314.1314	I	2143.0778	1072.0425	2126.0513	1063.5293	2125.0673	1063.0373	18
6	808.3294	404.6683	791.3029	396.1551	790.3189	395.6631	Y	2029.9938	1015.5005	2012.9672	1006.9872	2011.9832	1006.4952	17
7	922.3723	461.6898	905.3458	453.1765	904.3618	452.6845	N	1866.9304	933.9689	1849.9039	925.4556	1848.9199	924.9636	16
8	1023.4200	512.2136	1006.3935	503.7004	1005.4095	503.2084	T	1752.8875	876.9474	1735.8610	868.4341	1734.8769	867.9421	15
9	1124.4677	562.7375	1107.4412	554.2242	1106.4571	553.7322	T	1651.8398	826.4236	1634.8133	817.9103	1633.8293	817.4183	14
10	1287.5310	644.2692	1270.5045	635.7559	1269.5205	635.2639	Y	**1550.7921**	775.8997	1533.7656	767.3864	1532.7816	766.8944	13
11	1400.6151	700.8112	1383.5885	692.2979	1382.6045	691.8059	L	1387.7288	694.3680	1370.7023	685.8548	1369.7183	685.3628	12
12	1514.6580	757.8326	1497.6315	749.3194	1496.6475	748.8274	N	**1274.6448**	637.8260	1257.6182	629.3127	1256.6342	628.8207	11
13	1613.7264	807.3669	1596.6999	798.8536	1595.7159	798.3616	V	1160.6018	580.8046	1143.5753	572.2913	1142.5913	571.7993	10
14	1741.7850	871.3961	1724.7585	862.8829	1723.7744	862.3909	Q	1061.5334	531.2703	1044.5069	522.7571	1043.5228	522.2651	9
15	1897.8861	949.4467	1880.8596	940.9334	1879.8756	940.4414	R	933.4748	467.2411	916.4483	458.7278	915.4643	458.2358	8
16	2026.9287	1013.9680	2009.9022	1005.4547	2008.9182	1004.9627	E	777.3737	389.1905	760.3472	380.6772	759.3632	380.1852	7
17	2141.9557	1071.4815	2124.9291	1062.9682	2123.9451	1062.4762	N	**648.3311**	324.6692	631.3046	316.1559	630.3206	315.6639	6
18	2198.9771	1099.9922	2181.9506	1091.4789	2180.9666	1090.9869	G	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	5
19	2300.0248	1150.5160	2282.9983	1142.0028	2282.0142	1141.5108	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
20	2413.1089	1207.0581	2396.0823	1198.5448	2395.0983	1198.0528	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2500.1409	1250.5741	2483.1143	1242.0608	2482.1303	1241.5688	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.0	2673.2453	0.9979	QDQCIYNTTYLNVQRENGTISR	Deamidated N17 40.04%
36.6	2673.2453	0.9979	QDQCIYNTTYLNVQRENGTISR	Deamidated Q14 28.68%
36.6	2673.2453	0.9979	QDQCIYNTTYLNVQRENGTISR	Deamidated N12 28.68%
25.9	2673.2453	0.9979	QDQCIYNTTYLNVQRENGTISR	Deamidated N7 2.46%
12.8	2673.2453	0.9979	QDQCIYNTTYLNVQRENGTISR	Deamidated Q3 0.12%
11.0	2674.2367	0.0065	FPQEQSCASSIESCPSHPEKKIK	
8.9	2674.2367	0.0065	FPQEQSCASSIESCPSHPEKKIK	
7.5	2673.2340	1.0092	INGSIPAGPKQEPCAQHNGSEPASPK	
5.9	2673.2300	1.0132	MNNGGKAEKENTPSEANLQEEEVR	
5.5	2674.2340	0.0091	ESAQATGSPHTSPTHGGGRPMPMPVR	

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

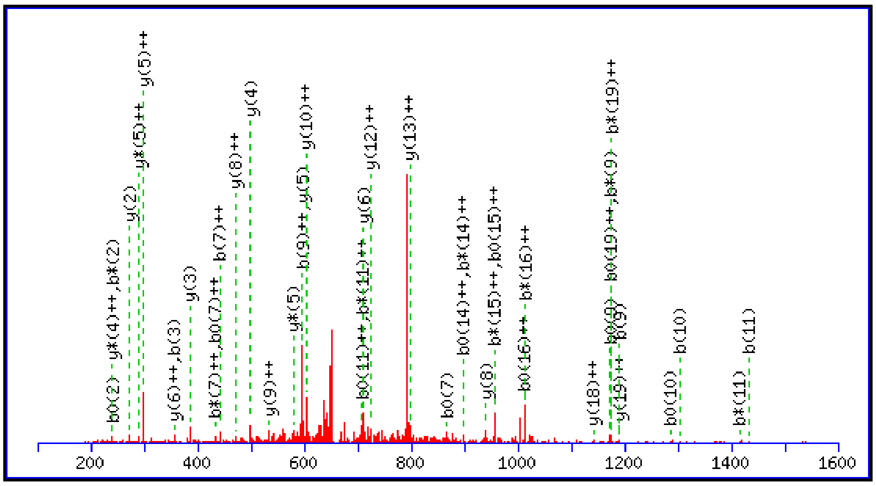
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEPERNECFLQHKDDNPNLPR**
Found in **H7C013** in **con_Xuniprot_HUMAN3**, H7C013_HUMAN Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=2 SV=1

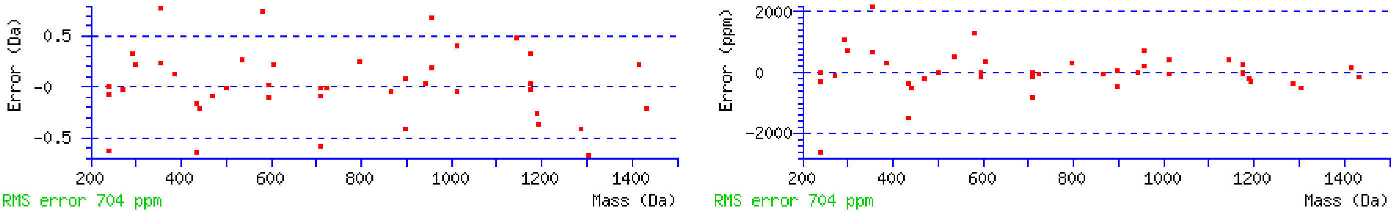
Match to Query 22357: 2636.203256 from(660.058090,4+) intensity(4326.5254) rtinseconds(566) scans(990) index(13057)
Title: 111019_Est_ISCardio_NMI_YS_G_10Spectrum769_scans__990
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2636.2037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0033
Matches : 43/226 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			**Q**							**21**
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	**E**	2509.1525	1255.0799	2492.1259	1246.5666	2491.1419	1246.0746	**20**
3	**355.1612**	178.0842	338.1347	169.5710	337.1506	169.0790	**P**	2380.1099	1190.5586	2363.0833	1182.0453	2362.0993	1181.5533	**19**
4	484.2038	242.6055	467.1773	234.0923	466.1932	233.6003	**E**	2283.0571	1142.0322	2266.0306	1133.5189	2265.0465	1133.0269	**18**
5	640.3049	320.6561	623.2784	312.1428	622.2944	311.6508	**R**	2154.0145	1077.5109	2136.9880	1068.9976	2136.0039	1068.5056	**17**
6	755.3319	378.1696	738.3053	369.6563	737.3213	369.1643	**N**	1997.9134	999.4603	1980.8869	990.9471	1979.9028	990.4551	**16**
7	884.3745	442.6909	867.3479	434.1776	866.3639	433.6856	**E**	1882.8865	941.9469	1865.8599	933.4336	1864.8759	932.9416	**15**
8	1044.4051	522.7062	1027.3786	514.1929	1026.3945	513.7009	**C**	1753.8439	877.4256	1736.8173	868.9123	1735.8333	868.4203	**14**
9	**1191.4735**	596.2404	1174.4470	587.7271	1173.4629	587.2351	**F**	1593.8132	797.4102	1576.7867	788.8970	1575.8027	788.4050	**13**
10	**1304.5576**	652.7824	1287.5310	644.2692	1286.5470	643.7771	**L**	1446.7448	723.8760	1429.7183	715.3628	1428.7342	714.8708	**12**
11	**1432.6162**	716.8117	1415.5896	708.2984	1414.6056	707.8064	**Q**	1333.6607	667.3340	1316.6342	658.8207	1315.6502	658.3287	**11**
12	1569.6751	785.3412	1552.6485	776.8279	1551.6645	776.3359	**H**	1205.6022	603.3047	1188.5756	594.7914	1187.5916	594.2994	**10**
13	1697.7700	849.3887	1680.7435	840.8754	1679.7595	840.3834	**K**	1068.5432	534.7753	1051.5167	526.2620	1050.5327	525.7700	**9**
14	1812.7970	906.9021	1795.7704	898.3889	1794.7864	897.8968	**D**	***940.4483***	470.7278	923.4217	462.2145	922.4377	461.7225	**8**
15	1927.8239	964.4156	1910.7974	955.9023	1909.8134	955.4103	**D**	825.4213	413.2143	808.3948	404.7010	807.4108	404.2090	**7**
16	2041.8668	1021.4371	2024.8403	1012.9238	2023.8563	1012.4318	**N**	***710.3944***	355.7008	693.3678	347.1876			**6**
17	2138.9196	1069.9634	2121.8931	1061.4502	2120.9090	1060.9582	**P**	***596.3515***	298.6794	579.3249	290.1661			**5**
18	2252.9625	1126.9849	2235.9360	1118.4716	2234.9520	1117.9796	**N**	***499.2987***	250.1530	482.2722	241.6397			**4**
19	2366.0466	1183.5269	2349.0201	1175.0137	2348.0360	1174.5217	**L**	***385.2558***	193.1315	368.2292	184.6183			**3**
20	2463.0994	1232.0533	2446.0728	1223.5400	2445.0888	1223.0480	**P**	***272.1717***	136.5895	255.1452	128.0762			**2**
21							**R**	175.1190	88.0631	158.0924	79.5498			**1**



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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.2	2636.2037	-0.0005	QEPERNECFLQHKDDNPNLPR	Deamidated N6 42.60%
46.0	2636.2037	-0.0005	QEPERNECFLQHKDDNPNLPR	Deamidated Q11 31.87%
43.5	2636.2037	-0.0005	QEPERNECFLQHKDDNPNLPR	Deamidated Q1 18.25%
38.7	2636.2037	-0.0005	QEPERNECFLQHKDDNPNLPR	Deamidated N16 5.98%
32.1	2636.2037	-0.0005	QEPERNECFLQHKDDNPNLPR	Deamidated N18 1.30%
12.8	2636.1999	0.0034	NLMYNGMADEVNNKIQFPPPGNR	
12.1	2636.2123	-0.0090	VDGIPNDSSDSEMEDKTTANLAALK	
7.8	2636.1919	0.0114	QEQIDLECRSSTSPCGTSKSPNR	
5.2	2636.2098	-0.0065	LKGMVNLGEMNNKPPPGSDASGGYGK	
5.1	2636.2064	-0.0032	KRAGGANSNVFSMFEQTQIQEFK	

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

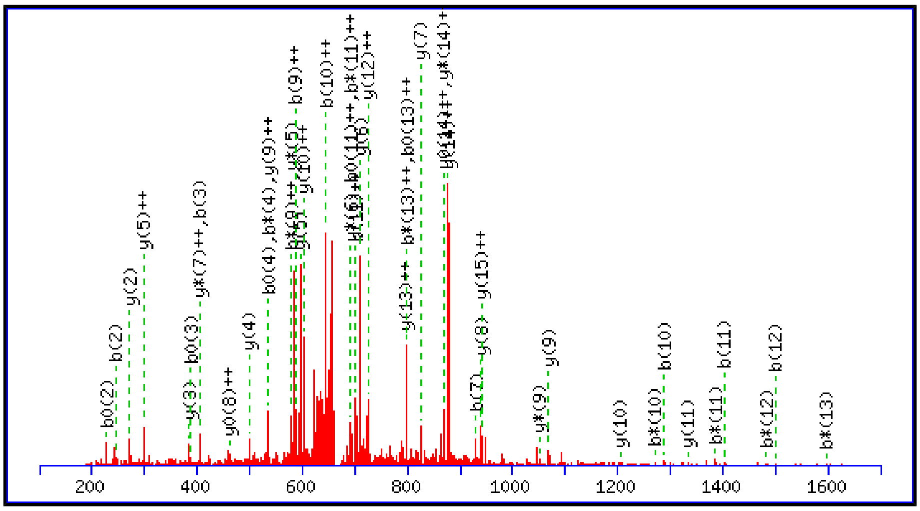
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NECFLQHKDDNPNLPR**
Found in **H7C013** in **con_Xuniprot_HUMAN3**, H7C013_HUMAN Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=2 SV=1

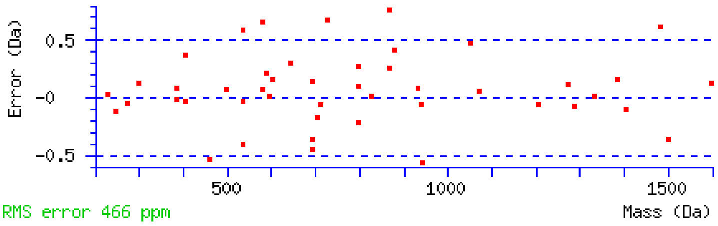
Match to Query 12214: 1996.911942 from(666.644590,3+) intensity(13401.8525) rtinseconds(746) scans(1554) index(13333)
Title: 111019_Est_ISCardio_NMI_YS_G_12Spectrum1310_scans__1554
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

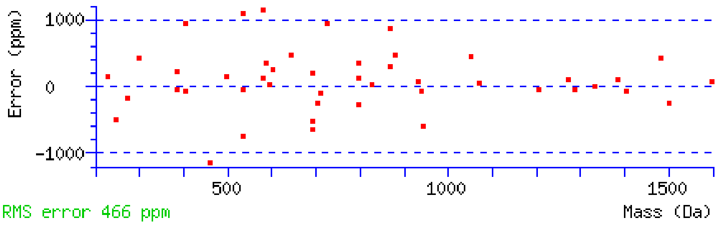
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1996.9061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1      : Deamidated (NQ)
Ions Score: 40  Expect: 0.017
Matches : 46/166 fragment ions using 98 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			N							16
2	**245.0768**	123.0420	228.0503	114.5288	227.0662	114.0368	E	1882.8865	941.9469	1865.8599	933.4336	1864.8759	932.9416	15
3	**405.1075**	203.0574	388.0809	194.5441	387.0969	194.0521	C	1753.8439	877.4256	1736.8173	868.9123	1735.8333	868.4203	14
4	552.1759	276.5916	535.1493	268.0783	534.1653	267.5863	F	1593.8132	797.4102	1576.7867	788.8970	1575.8026	788.4050	13
5	665.2599	333.1336	648.2334	324.6203	647.2494	324.1283	L	1446.7448	723.8760	1429.7183	715.3628	1428.7342	714.8708	12
6	793.3185	397.1629	776.2920	388.6496	775.3080	388.1576	Q	***1333.6607***	667.3340	1316.6342	658.8207	1315.6502	658.3287	11
7	**930.3774**	465.6924	913.3509	457.1791	912.3669	456.6871	H	***1205.6022***	603.3047	1188.5756	594.7914	1187.5916	594.2994	10
8	1058.4724	529.7398	1041.4458	521.2266	1040.4618	520.7346	K	***1068.5432***	534.7753	1051.5167	526.2620	1050.5327	525.7700	9
9	1173.4993	587.2533	1156.4728	578.7400	1155.4888	578.2480	D	***940.4483***	470.7278	923.4217	462.2145	922.4377	461.7225	8
10	**1288.5263**	644.7668	1271.4997	636.2535	1270.5157	635.7615	D	***825.4213***	413.2143	808.3948	404.7010	807.4108	404.2090	7
11	**1402.5692**	701.7882	1385.5427	693.2750	1384.5586	692.7830	N	***710.3944***	355.7008	693.3678	347.1876			6
12	**1499.6220**	750.3146	1482.5954	741.8013	1481.6114	741.3093	P	***596.3515***	298.6794	579.3249	290.1661			5
13	1613.6649	807.3361	1596.6383	798.8228	1595.6543	798.3308	N	***499.2987***	250.1530	482.2722	241.6397			4
14	1726.7490	863.8781	1709.7224	855.3648	1708.7384	854.8728	L	***385.2558***	193.1315	368.2292	184.6183			3
15	1823.8017	912.4045	1806.7752	903.8912	1805.7912	903.3992	P	***272.1717***	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.0	1996.9061	0.0058	NECFLQHKDDNPNLPR	Deamidated N1 87.35%
31.3	1996.9061	0.0058	NECFLQHKDDNPNLPR	Deamidated Q6 11.70%
19.5	1996.9061	0.0058	NECFLQHKDDNPNLPR	Deamidated N11 0.77%
12.8	1996.9061	0.0058	NECFLQHKDDNPNLPR	Deamidated N13 0.17%
3.8	1994.9098	2.0022	TAGFCGNPSFHLYWPNK	

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

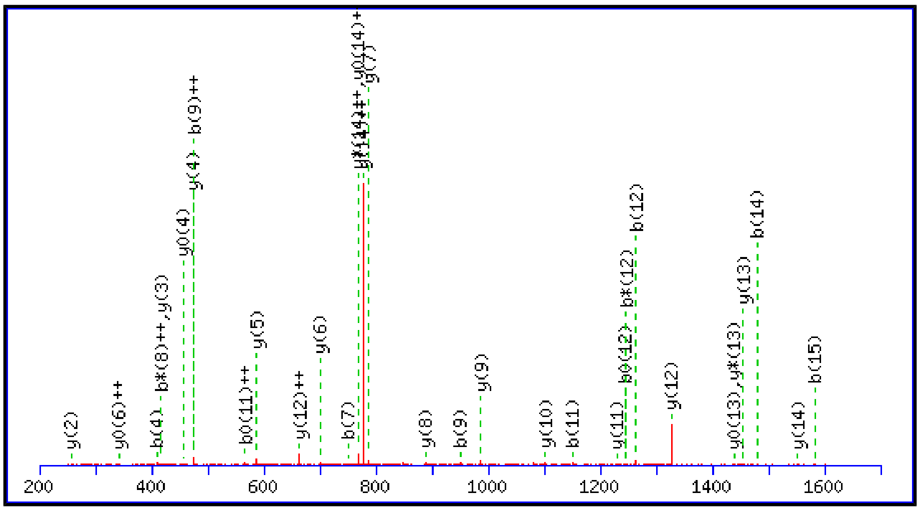
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPQPQNVTSLLGCTH**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

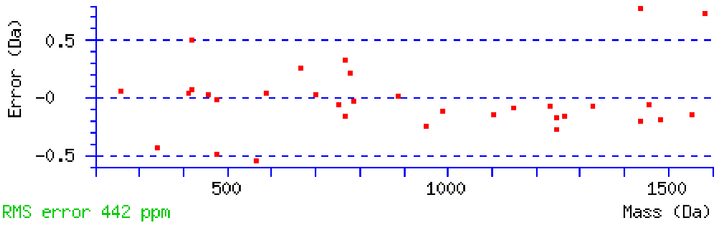
Match to Query 8841: 1735.857968 from(868.936260,2+) intensity(7247075.0000) rtinseconds(1820) scans(4627) index(22651)
Title: 111019_Est_MI_YS_G_03Spectrum4043_scans__4627
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

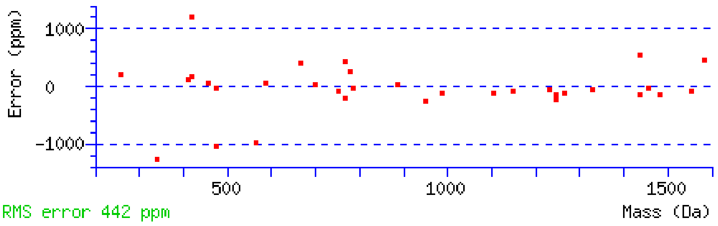
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1735.8563
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 104 **Expect:** 9.1e-009
Matches : 33/138 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					**A**							**16**
2	185.1285	93.0679					**L**	1665.8265	833.4169	1648.7999	824.9036	1647.8159	824.4116	**15**
3	282.1812	141.5942					**P**	***1552.7424***	776.8748	1535.7159	768.3616	1534.7319	767.8696	**14**
4	**410.2398**	205.6235	393.2132	197.1103			**Q**	***1455.6897***	728.3485	1438.6631	719.8352	1437.6791	719.3432	**13**
5	507.2926	254.1499	490.2660	245.6366			**P**	***1327.6311***	664.3192	1310.6045	655.8059	1309.6205	655.3139	**12**
6	635.3511	318.1792	618.3246	309.6659			**Q**	***1230.5783***	615.7928	1213.5518	607.2795	1212.5677	606.7875	**11**
7	**750.3781**	375.6927	733.3515	367.1794			**N**	***1102.5197***	551.7635	1085.4932	543.2502	1084.5092	542.7582	**10**
8	849.4465	425.2269	832.4199	416.7136			**V**	***987.4928***	494.2500			969.4822	485.2448	**9**
9	**950.4942**	475.7507	933.4676	467.2375	932.4836	466.7454	**T**	***888.4244***	444.7158			870.4138	435.7105	**8**
10	1037.5262	519.2667	1020.4997	510.7535	1019.5156	510.2615	**S**	***787.3767***	394.1920			769.3661	385.1867	**7**
11	**1150.6103**	575.8088	1133.5837	567.2955	1132.5997	566.8035	**L**	***700.3447***	350.6760			682.3341	341.6707	**6**
12	**1263.6943**	632.3508	1246.6678	623.8375	1245.6838	623.3455	**L**	***587.2606***	294.1339			569.2500	285.1287	**5**
13	1320.7158	660.8615	1303.6892	652.3483	1302.7052	651.8563	**G**	***474.1765***	237.5919			456.1660	228.5866	**4**
14	**1480.7464**	740.8769	1463.7199	732.3636	1462.7359	731.8716	**C**	***417.1551***	209.0812			399.1445	200.0759	**3**
15	**1581.7941**	791.4007	1564.7676	782.8874	1563.7836	782.3954	**T**	***257.1244***	129.0659			239.1139	120.0606	**2**
16							**H**	156.0768	78.5420					**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.3	1735.8563	0.0016	ALPQPQNVTSLLGCTH	Deamidated N7 96.69%
89.7	1735.8563	0.0016	ALPQPQNVTSLLGCTH	Deamidated Q6 3.31%
61.5	1735.8563	0.0016	ALPQPQNVTSLLGCTH	Deamidated Q4 0.01%
7.6	1735.8602	-0.0022	DSPRHALTSPSLGGQGR	
7.6	1735.8601	-0.0022	NSPRHALTSPSLGGQGR	
6.1	1735.8549	0.0030	ILLMDNNKLNSLDSK	
3.5	1733.8505	2.0074	VEDNEALITKMELGR	
3.3	1733.8559	2.0020	TCWDADPLKRPTFK	
3.2	1733.8544	2.0036	SGGNSSSSLGDIVPSSRK	
3.1	1733.8552	2.0028	NKNMKPEERANIMK	

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

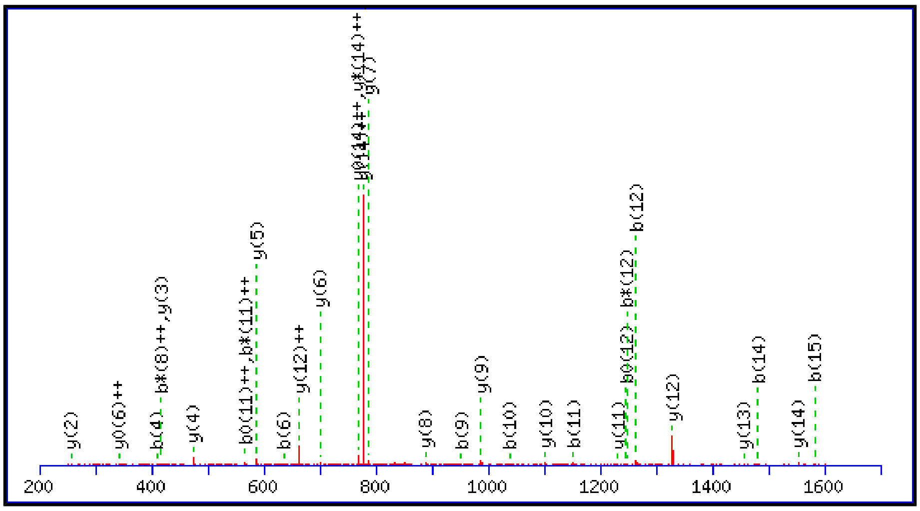
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPQPQNVTSLLGCTH**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

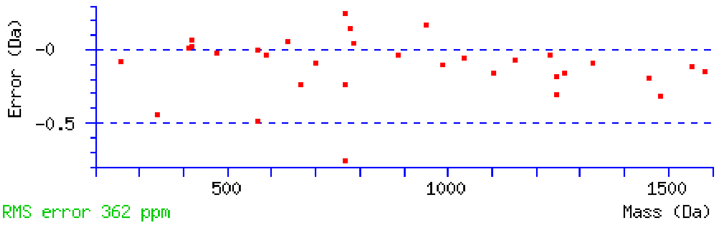
Match to Query 9263: 1736.842348 from(869.428450,2+) intensity(2626051.0000) rtinseconds(1883) scans(4676) index(12720)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4088_scans__4676
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

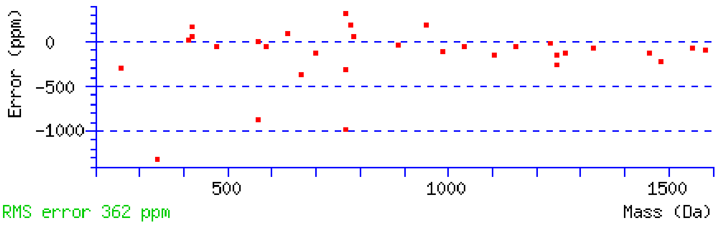
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1736.8403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Deamidated (NQ)
N7     : Deamidated (NQ)
Ions Score: 87  Expect: 4.4e-007
Matches : 32/138 fragment ions using 56 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							16
2	185.1285	93.0679					L	1666.8105	833.9089	1649.7840	825.3956	1648.7999	824.9036	15
3	282.1812	141.5942					P	***1553.7264***	777.3669	1536.6999	768.8536	1535.7159	768.3616	14
4	**410.2398**	205.6235	393.2132	197.1103			Q	***1456.6737***	728.8405	1439.6471	720.3272	1438.6631	719.8352	13
5	507.2926	254.1499	490.2660	245.6366			P	***1328.6151***	664.8112	1311.5885	656.2979	1310.6045	655.8059	12
6	**636.3352**	318.6712	619.3086	310.1579			Q	***1231.5623***	616.2848	1214.5358	607.7715	1213.5518	607.2795	11
7	751.3621	376.1847	734.3355	367.6714			N	***1102.5197***	551.7635	1085.4932	543.2502	1084.5092	542.7582	10
8	850.4305	425.7189	833.4040	417.2056			V	***987.4928***	494.2500			969.4822	485.2448	9
9	**951.4782**	476.2427	934.4516	467.7295	933.4676	467.2375	T	***888.4244***	444.7158			870.4138	435.7105	8
10	**1038.5102**	519.7587	1021.4837	511.2455	1020.4997	510.7535	S	***787.3767***	394.1920			769.3661	385.1867	7
11	**1151.5943**	576.3008	1134.5677	567.7875	1133.5837	567.2955	L	***700.3447***	350.6760			682.3341	341.6707	6
12	**1264.6783**	632.8428	1247.6518	624.3295	1246.6678	623.8375	L	***587.2606***	294.1339			569.2500	285.1287	5
13	1321.6998	661.3535	1304.6733	652.8403	1303.6892	652.3483	G	***474.1765***	237.5919			456.1660	228.5866	4
14	**1481.7305**	741.3689	1464.7039	732.8556	1463.7199	732.3636	C	***417.1551***	209.0812			399.1445	200.0759	3
15	**1582.7781**	791.8927	1565.7516	783.3794	1564.7676	782.8874	T	***257.1244***	129.0659			239.1139	120.0606	2
16							H	156.0768	78.5420					1





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.1	1736.8403	0.0020	ALPQPQNVTSLLGCTH	Deamidated Q6, N7 70.04%
83.2	1736.8403	0.0020	ALPQPQNVTSLLGCTH	Deamidated Q4, N7 28.53%
70.2	1736.8403	0.0020	ALPQPQNVTSLLGCTH	Deamidated Q4, Q6 1.42%
6.9	1735.8386	1.0038	SPQPCSLLGTKFNCK	
6.1	1736.8477	-0.0054	MGPNCSISLIPIYQK	
5.7	1735.8307	1.0117	KMCDEIIEQVACIK	
3.4	1734.8359	2.0065	YQDLLDVMNPKNNR	
3.0	1736.8403	0.0020	QDCSQLVERINVFK	
3.0	1735.8450	0.9973	FIKDCIVQLNNNVR	
2.9	1736.8457	-0.0033	GKALMYRLHHYSDF	

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

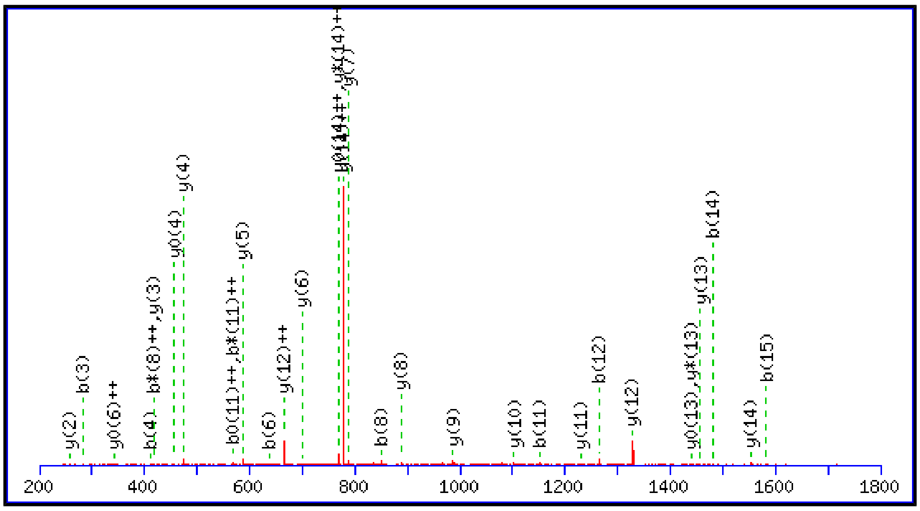
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPQPQNVTSLLGCTH**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

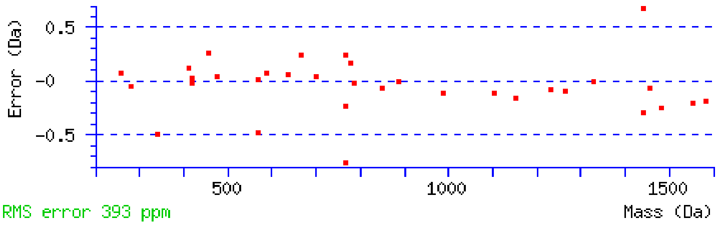
Match to Query 9322: 1736.844948 from(869.429750,2+) intensity(1026361.3750) rtinseconds(1878) scans(4804) index(1399)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum4190_scans__4804
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

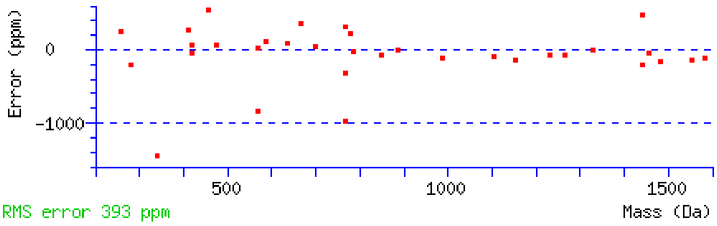
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1736.8403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 86 **Expect:** 6.4e-007
Matches : 33/138 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	72.0444	36.5258					**A**							**16**
2	185.1285	93.0679					**L**	1666.8105	833.9089	1649.7840	825.3956	1648.7999	824.9036	**15**
3	**282.1812**	141.5942					**P**	***1553.7264***	777.3669	1536.6999	768.8536	1535.7159	768.3616	**14**
4	**411.2238**	206.1155	394.1973	197.6023			**Q**	***1456.6737***	728.8405	1439.6471	720.3272	1438.6631	719.8352	**13**
5	508.2766	254.6419	491.2500	246.1287			**P**	***1327.6311***	664.3192	1310.6045	655.8059	1309.6205	655.3139	**12**
6	**636.3352**	318.6712	619.3086	310.1579			**Q**	***1230.5783***	615.7928	1213.5518	607.2795	1212.5677	606.7875	**11**
7	751.3621	376.1847	734.3355	367.6714			**N**	***1102.5197***	551.7635	1085.4932	543.2502	1084.5092	542.7582	**10**
8	**850.4305**	425.7189	833.4040	417.2056			**V**	***987.4928***	494.2500			969.4822	485.2448	**9**
9	951.4782	476.2427	934.4516	467.7295	933.4676	467.2375	**T**	***888.4244***	444.7158			870.4138	435.7105	**8**
10	1038.5102	519.7587	1021.4837	511.2455	1020.4997	510.7535	**S**	***787.3767***	394.1920			769.3661	385.1867	**7**
11	**1151.5943**	576.3008	1134.5677	567.7875	1133.5837	567.2955	**L**	***700.3447***	350.6760			682.3341	341.6707	**6**
12	**1264.6783**	632.8428	1247.6518	624.3295	1246.6678	623.8375	**L**	***587.2606***	294.1339			569.2500	285.1287	**5**
13	1321.6998	661.3535	1304.6733	652.8403	1303.6892	652.3483	**G**	***474.1765***	237.5919			456.1660	228.5866	**4**
14	**1481.7305**	741.3689	1464.7039	732.8556	1463.7199	732.3636	**C**	***417.1551***	209.0812			399.1445	200.0759	**3**
15	**1582.7781**	791.8927	1565.7516	783.3794	1564.7676	782.8874	**T**	***257.1244***	129.0659			239.1139	120.0606	**2**
16							**H**	156.0768	78.5420					**1**





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

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.7	1736.8403	0.0046	ALPQPQNVTSLLGCTH	Deamidated Q4, N7 83.32%
77.8	1736.8403	0.0046	ALPQPQNVTSLLGCTH	Deamidated Q6, N7 13.57%
71.4	1736.8403	0.0046	ALPQPQNVTSLLGCTH	Deamidated Q4, Q6 3.11%
5.4	1736.8482	-0.0032	NAEEFTLRFGVDRPS	
5.3	1736.8477	-0.0028	MGPNCSISLIPIYQK	
4.2	1735.8386	1.0064	SPQPCSLLGTKFNCK	
3.8	1735.8464	0.9985	AIWGTKCSKWAESGR	
3.8	1736.8369	0.0080	ANQPLGAPPPQPQTYR	
3.5	1734.8464	1.9985	YEEALDILQWGQLR	
3.2	1734.8384	2.0065	SGGNSSSSLGDIVPSSRK	

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

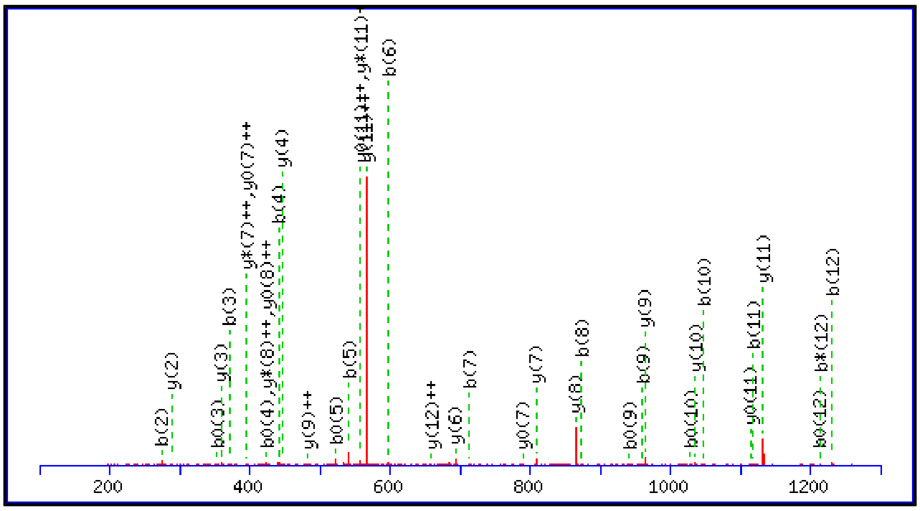
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SWPAVGNCSSALR**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

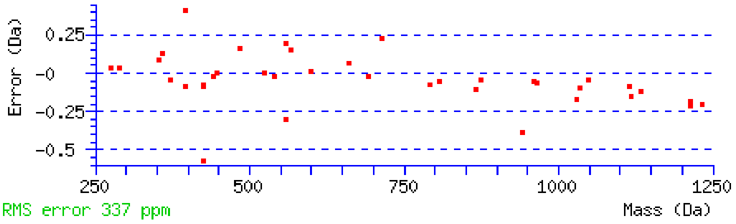
Match to Query 2463: 1404.646728 from(703.330640,2+) intensity(7324408.5000) rtinseconds(1073) scans(2478) index(10855)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum2085_scans__2478
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

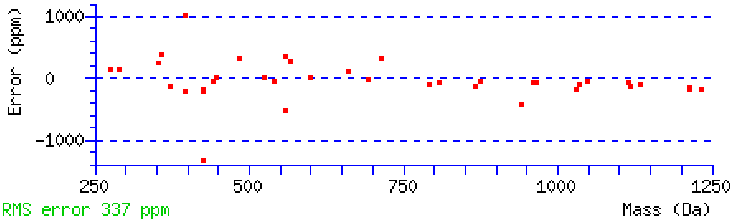
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1404.6456
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 85 **Expect:** 4.4e-007
Matches : 38/126 fragment ions using 55 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	***274.1186***	137.5629			256.1081	128.5577	W	1318.6208	659.8141	1301.5943	651.3008	1300.6103	650.8088	12
3	***371.1714***	186.0893			353.1608	177.0840	P	**1132.5415**	566.7744	1115.5150	558.2611	1114.5310	557.7691	11
4	***442.2085***	221.6079			424.1979	212.6026	A	**1035.4888**	518.2480	1018.4622	509.7347	1017.4782	509.2427	10
5	***541.2769***	271.1421			523.2663	262.1368	V	**964.4517**	482.7295	947.4251	474.2162	946.4411	473.7242	9
6	***598.2984***	299.6528			580.2878	290.6475	G	**865.3832**	433.1953	848.3567	424.6820	847.3727	424.1900	8
7	***713.3253***	357.1663	696.2988	348.6530	695.3148	348.1610	N	**808.3618**	404.6845	791.3352	396.1713	790.3512	395.6792	7
8	***873.3560***	437.1816	856.3294	428.6683	855.3454	428.1763	C	**693.3348**	347.1711	676.3083	338.6578	675.3243	338.1658	6
9	***960.3880***	480.6976	943.3614	472.1844	942.3774	471.6924	S	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
10	***1047.4200***	524.2136	1030.3935	515.7004	1029.4095	515.2084	S	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	4
11	***1118.4571***	559.7322	1101.4306	551.2189	1100.4466	550.7269	A	**359.2401**	180.1237	342.2136	171.6104			3
12	***1231.5412***	616.2742	1214.5147	607.7610	1213.5306	607.2690	L	**288.2030**	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SWPAVGNCSSALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
85.0	1404.6456	0.0011	SWPAVGNCSSALR
13.3	1403.6470	0.9998	WQYSGQLHEVR
11.5	1403.6503	0.9964	CLDLSFLNHER
11.4	1404.6534	-0.0067	DASPHAAYFDRR
10.5	1403.6398	1.0069	RDAPVCCDRQK
9.7	1402.6333	2.0134	VTAGNLHCQMVR
9.7	1404.6416	0.0052	NGAQSCGGLERVR
9.3	1404.6456	0.0011	GCALQYQHATVR
7.7	1404.6496	-0.0029	GVMDWDWLEVR
7.4	1404.6490	-0.0022	MAAVEACGGSPVTR

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE

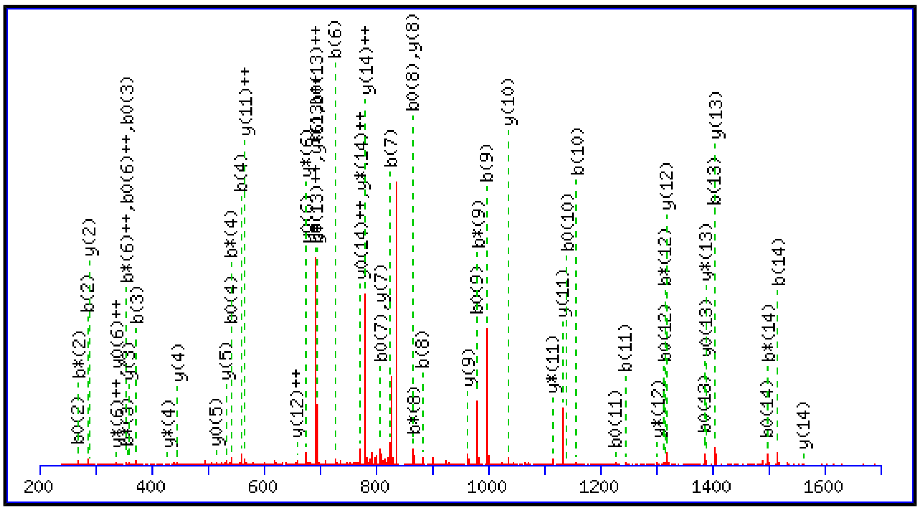
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ERSWPAVGNCSSALR**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

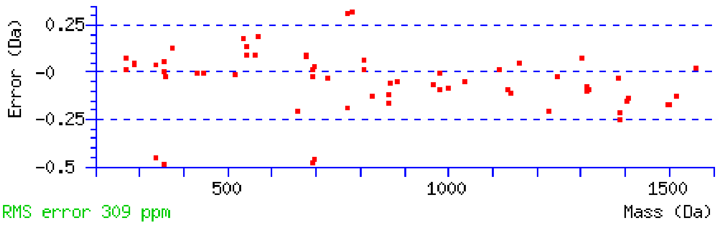
Match to Query 8690: 1689.795928 from(845.905240,2+) intensity(43656.9023) rtinseconds(724) scans(1678) index(24391)
Title: 111019_Est_MI_YS_G_06Spectrum1445_scans__1678
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

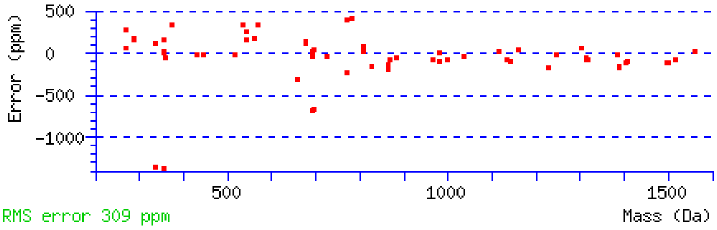
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1689.7893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 79 **Expect:** 2.1e-006
Matches : 63/160 fragment ions using 99 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	**286.1510**	143.5791	269.1244	135.0659	268.1404	134.5738	R	***1561.7540***	781.3806	1544.7274	772.8674	1543.7434	772.3753	14
3	**373.1830**	187.0951	356.1565	178.5819	355.1724	178.0899	S	***1405.6529***	703.3301	1388.6263	694.8168	1387.6423	694.3248	13
4	**559.2623**	280.1348	542.2358	271.6215	541.2518	271.1295	W	***1318.6208***	659.8141	1301.5943	651.3008	1300.6103	650.8088	12
5	656.3151	328.6612	639.2885	320.1479	638.3045	319.6559	P	***1132.5415***	566.7744	1115.5150	558.2611	1114.5310	557.7691	11
6	**727.3522**	364.1797	710.3257	355.6665	709.3416	355.1745	A	***1035.4888***	518.2480	1018.4622	509.7347	1017.4782	509.2427	10
7	**826.4206**	413.7139	809.3941	405.2007	808.4100	404.7087	V	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	9
8	**883.4421**	442.2247	866.4155	433.7114	865.4315	433.2194	G	***865.3832***	433.1953	848.3567	424.6820	847.3727	424.1900	8
9	**998.4690**	499.7381	981.4425	491.2249	980.4585	490.7329	N	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	7
10	**1158.4997**	579.7535	1141.4731	571.2402	1140.4891	570.7482	C	***693.3348***	347.1711	676.3083	338.6578	675.3243	338.1658	6
11	**1245.5317**	623.2695	1228.5051	614.7562	1227.5211	614.2642	S	***533.3042***	267.1557	516.2776	258.6425	515.2936	258.1504	5
12	1332.5637	666.7855	1315.5372	658.2722	1314.5532	657.7802	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
13	**1403.6008**	702.3041	1386.5743	693.7908	1385.5903	693.2988	A	***359.2401***	180.1237	342.2136	171.6104			3
14	**1516.6849**	758.8461	1499.6584	750.3328	1498.6743	749.8408	L	***288.2030***	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ERSWPAVGNCSSALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
79.5	1689.7893	0.0067	ERSWPAVGNCSSALR
12.7	1689.7958	0.0001	VQGSAISHYADSVQAR
5.6	1689.8039	-0.0080	GSVGRVSQCNLCPTR
5.1	1688.7927	1.0032	TVSSEDVAEMHNILK
4.9	1689.8032	-0.0072	SESFMQKYEQKIR
4.1	1687.7909	2.0050	MLASTLNYAQSAVMR
3.4	1687.7909	2.0050	MLASTLNYAQSAVMR
2.4	1689.7992	-0.0033	CVIEGNLGSDKDQVR
2.4	1689.7992	-0.0033	CVIEGNLGSDKDQVR
2.2	1688.7853	1.0107	SSEPSEELQELRER

Mascot: http://www.matrixscience.com/

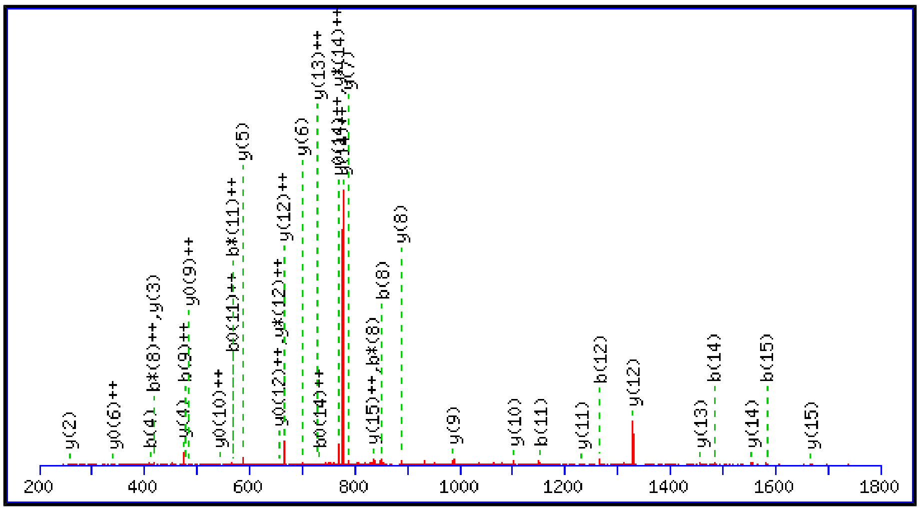
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALPQPQNVTSLLGCTH**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

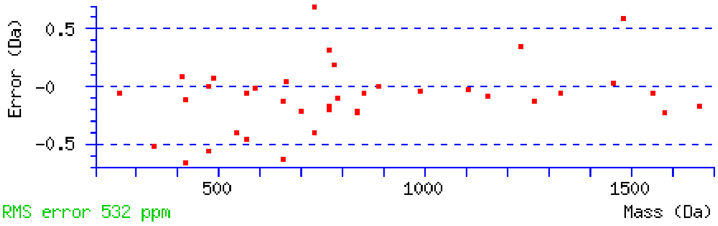
Match to Query 9357: 1737.825528 from(869.920040,2+) intensity(26586.1719) rtinseconds(1952) scans(4872) index(12741)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4260_scans__4872
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

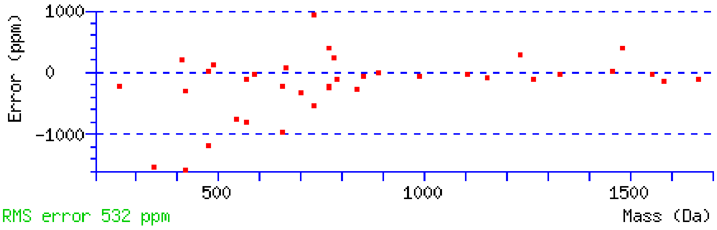
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1737.8243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
Q6 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 71 **Expect:** 1.8e-005
Matches : 38/138 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							16
2	185.1285	93.0679					L	***1667.7945***	834.4009	1650.7680	825.8876	1649.7840	825.3956	15
3	282.1812	141.5942					P	***1554.7105***	777.8589	1537.6839	769.3456	1536.6999	768.8536	14
4	**411.2238**	206.1155	394.1973	197.6023			Q	***1457.6577***	729.3325	1440.6311	720.8192	1439.6471	720.3272	13
5	508.2766	254.6419	491.2500	246.1287			P	***1328.6151***	664.8112	1311.5885	656.2979	1310.6045	655.8059	12
6	637.3192	319.1632	620.2926	310.6499			Q	***1231.5623***	616.2848	1214.5358	607.7715	1213.5518	607.2795	11
7	752.3461	376.6767	735.3196	368.1634			N	***1102.5197***	551.7635	1085.4932	543.2502	1084.5092	542.7582	10
8	**851.4145**	426.2109	834.3880	417.6976			V	***987.4928***	494.2500			969.4822	485.2448	9
9	952.4622	476.7347	935.4357	468.2215	934.4516	467.7295	T	***888.4244***	444.7158			870.4138	435.7105	8
10	1039.4942	520.2508	1022.4677	511.7375	1021.4837	511.2455	S	***787.3767***	394.1920			769.3661	385.1867	7
11	**1152.5783**	576.7928	1135.5517	568.2795	1134.5677	567.7875	L	***700.3447***	350.6760			682.3341	341.6707	6
12	**1265.6624**	633.3348	1248.6358	624.8215	1247.6518	624.3295	L	***587.2606***	294.1339			569.2500	285.1287	5
13	1322.6838	661.8456	1305.6573	653.3323	1304.6733	652.8403	G	***474.1765***	237.5919			456.1660	228.5866	4
14	**1482.7145**	741.8609	1465.6879	733.3476	1464.7039	732.8556	C	***417.1551***	209.0812			399.1445	200.0759	3
15	**1583.7622**	792.3847	1566.7356	783.8714	1565.7516	783.3794	T	***257.1244***	129.0659			239.1139	120.0606	2
16							H	156.0768	78.5420					1





NCBI **BLAST** search of ALPQPQNVTSLLGCTH
(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	1737.8243	0.0012	ALPQPQNVTSLLGCTH
3.3	1737.8277	-0.0021	MQMLKLDKENAIDR
3.3	1737.8277	-0.0021	MQMLKLDKENALDR
3.0	1737.8209	0.0046	ANQPLGAPPPQPQTYR
2.9	1737.8317	-0.0062	AILIVQDSPCFQSMK
2.8	1737.8317	-0.0062	MGPNCSISLIPIYQK
2.2	1737.8282	-0.0027	APDGPTGPTAEEDLGRR
2.1	1736.8192	1.0064	GQVYSELKYHPEMR
2.1	1737.8243	0.0012	ALEEFAEMKEREEK
0.6	1735.8212	2.0043	YVRRYMQEGQPHR

Mascot: http://www.matrixscience.com/

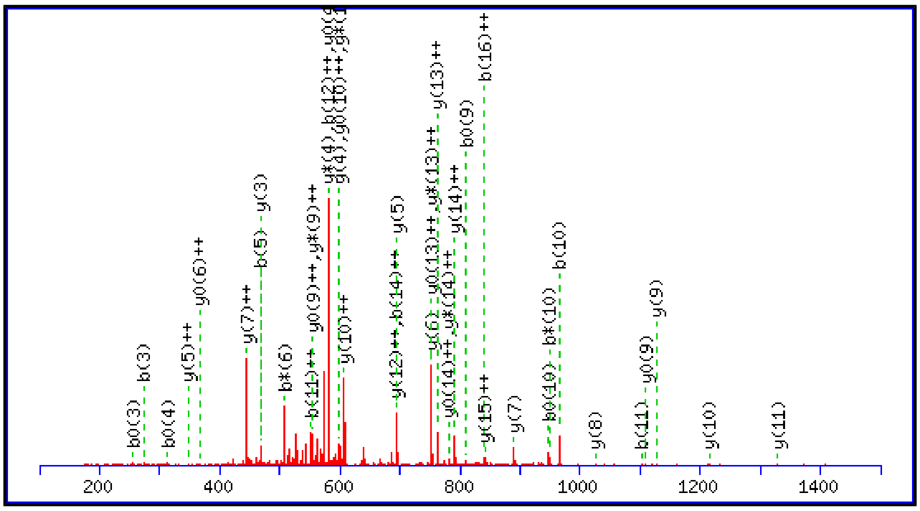
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGTGHGNSTHHGPEYMR**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

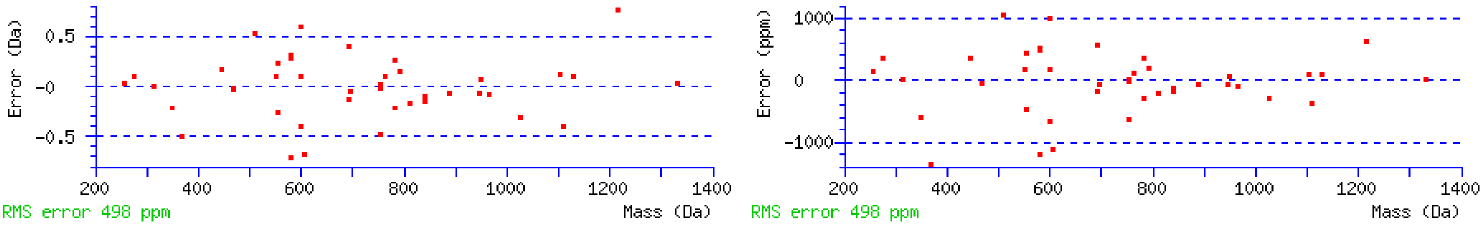
Match to Query 10960: 1852.759782 from(618.593870,3+) intensity(14343.3838) rtinseconds(167) scans(198) index(23014)
Title: 111019_Est_MI_YS_G_04Spectrum133_scans__198
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1852.7547
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 57 **Expect:** 6.5e-005
Matches : 42/182 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			N							17
2	173.0557	87.0315	156.0291	78.5182			G	1738.7350	869.8712	1721.7085	861.3579	1720.7245	860.8659	16
3	**274.1034**	137.5553	257.0768	129.0420	256.0928	128.5500	T	1681.7136	841.3604	1664.6870	832.8472	1663.7030	832.3551	15
4	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	G	1580.6659	790.8366	1563.6394	782.3233	1562.6553	781.8313	14
5	**468.1837**	234.5955	451.1572	226.0822	450.1732	225.5902	H	1523.6444	762.3259	1506.6179	753.8126	1505.6339	753.3206	13
6	525.2052	263.1062	508.1787	254.5930	507.1946	254.1010	G	1386.5855	693.7964	1369.5590	685.2831	1368.5750	684.7911	12
7	640.2321	320.6197	623.2056	312.1064	622.2216	311.6144	N	***1329.5641***	665.2857	1312.5375	656.7724	1311.5535	656.2804	11
8	727.2642	364.1357	710.2376	355.6225	709.2536	355.1304	S	***1214.5371***	607.7722	1197.5106	599.2589	1196.5266	598.7669	10
9	828.3119	414.6596	811.2853	406.1463	810.3013	405.6543	T	***1127.5051***	564.2562	1110.4785	555.7429	1109.4945	555.2509	9
10	**965.3708**	483.1890	948.3442	474.6757	947.3602	474.1837	H	***1026.4574***	513.7323	1009.4309	505.2191	1008.4468	504.7271	8
11	**1102.4297**	**551.7185**	1085.4031	543.2052	1084.4191	542.7132	H	***889.3985***	445.2029	872.3720	436.6896	871.3879	436.1976	7
12	1159.4511	**580.2292**	1142.4246	571.7159	1141.4406	571.2239	G	***752.3396***	376.6734	735.3130	368.1602	734.3290	367.6681	6
13	1256.5039	628.7556	1239.4774	620.2423	1238.4933	619.7503	P	***695.3181***	348.1627	678.2916	339.6494	677.3076	339.1574	5
14	1385.5465	**693.2769**	1368.5199	684.7636	1367.5359	684.2716	E	***598.2654***	299.6363	581.2388	291.1230	580.2548	290.6310	4
15	1548.6098	774.8086	1531.5833	766.2953	1530.5993	765.8033	Y	***469.2228***	235.1150	452.1962	226.6017			3
16	1679.6503	**840.3288**	1662.6238	831.8155	1661.6397	831.3235	M	306.1594	153.5834	289.1329	145.0701			2
17							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of NGTGHGNSTHHGPEYMR
(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	1852.7547	0.0051	NGTGHGNSTHHGPEYMR
5.3	1852.7608	-0.0010	QYKDMMSEGGPPGAEPQ
4.7	1850.7597	2.0001	CSTCGKCFSQSSSLNK
0.8	1850.7485	2.0113	EGVMNTGVCTYMGADSK
0.4	1850.7597	2.0001	CSTCGKCFSQSSSLNK

Mascot: http://www.matrixscience.com/

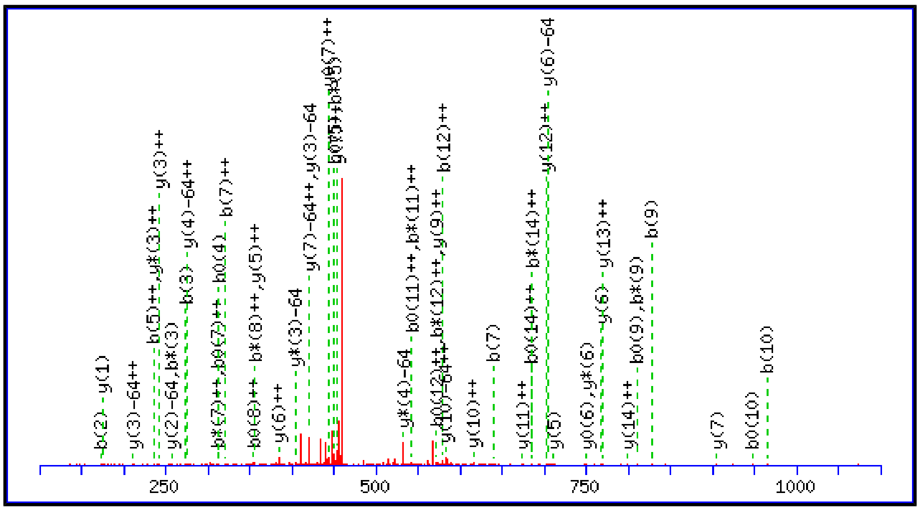
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NGTGHGNSTHHGPEYMR**
Found in **P02790** in **con_Xuniprot_HUMAN3**, HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

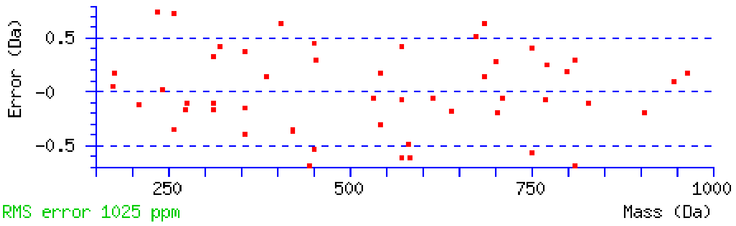
Match to Query 11004: 1868.753136 from(468.195560,4+) intensity(10256.5479) rtinseconds(152) scans(132) index(10731)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum71_scans__132
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

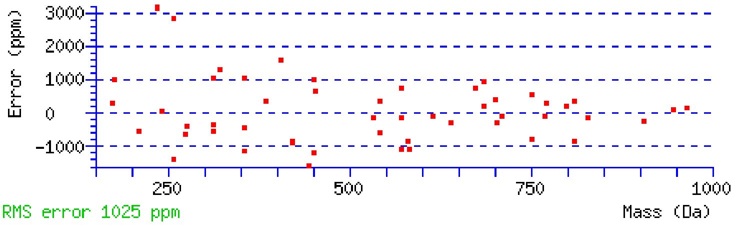
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1868.7496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N7 : Deamidated (NQ)
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 41 **Expect:** 0.0015
Matches : 52/274 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	116.0342	58.5207	99.0077	50.0075			N							17
2	**173.0557**	87.0315	156.0291	78.5182			G	1754.7300	877.8686	1737.7034	869.3553	1736.7194	868.8633	16
3	**274.1034**	137.5553	257.0768	129.0420	256.0928	128.5500	T	1697.7085	849.3579	1680.6819	840.8446	1679.6979	840.3526	15
4	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	G	1596.6608	798.8340	1579.6343	790.3208	1578.6503	789.8288	14
5	468.1837	234.5955	451.1572	226.0822	450.1732	225.5902	H	1539.6394	770.3233	1522.6128	761.8100	1521.6288	761.3180	13
6	525.2052	263.1062	508.1787	254.5930	507.1946	254.1010	G	1402.5804	701.7939	1385.5539	693.2806	1384.5699	692.7886	12
7	**640.2321**	320.6197	623.2056	312.1064	622.2216	311.6144	N	1345.5590	673.2831	1328.5324	664.7699	1327.5484	664.2778	11
8	727.2642	364.1357	710.2376	355.6225	709.2536	355.1304	S	1230.5320	615.7697	1213.5055	607.2564	1212.5215	606.7644	10
9	**828.3119**	414.6596	811.2853	406.1463	810.3013	405.6543	T	1143.5000	572.2536	1126.4735	563.7404	1125.4894	563.2484	9
10	**965.3708**	483.1890	948.3442	474.6757	947.3602	474.1837	H	1042.4523	521.7298	1025.4258	513.2165	1024.4418	512.7245	8
11	1102.4297	551.7185	1085.4031	543.2052	1084.4191	542.7132	H	**905.3934**	453.2003	888.3669	444.6871	887.3828	444.1951	7
12	1159.4511	580.2292	1142.4246	571.7159	1141.4406	571.2239	G	**768.3345**	384.6709	751.3080	376.1576	750.3239	375.6656	6
13	1256.5039	628.7556	1239.4774	620.2423	1238.4933	619.7503	P	**711.3130**	356.1602	694.2865	347.6469	693.3025	347.1549	5
14	1385.5465	693.2769	1368.5199	684.7636	1367.5359	684.2716	E	614.2603	307.6338	597.2337	299.1205	596.2497	298.6285	4
15	1548.6098	774.8086	1531.5833	766.2953	1530.5993	765.8033	Y	485.2177	243.1125	468.1911	234.5992			3
16	1695.6452	848.3263	1678.6187	839.8130	1677.6347	839.3210	M	322.1544	161.5808	305.1278	153.0675			2
17							R	**175.1190**	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NGTGHGNSTHHGPEYMR
(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	1868.7496	0.0035	NGTGHGNSTHHGPEYMR
9.3	1867.7440	1.0091	TCPTNYMWNNHICR
9.3	1867.7440	1.0091	TCPTNYMWNNHICR
9.3	1867.7440	1.0091	TCPTNYMWNNHICR
4.4	1866.7551	1.9980	HGHDAAPSSGQQGCSVDR
3.0	1868.7444	0.0087	IMEWGGMPQDQESTNK
3.0	1868.7444	0.0087	IMEWGGMPQDQESTNK
3.0	1867.7440	1.0091	CFQCHEGETHYLCK
3.0	1868.7505	0.0026	CRPYGHFGPSCTDCR
3.0	1866.7481	2.0050	CQESGQPMSCTCGPLR

Mascot: http://www.matrixscience.com/

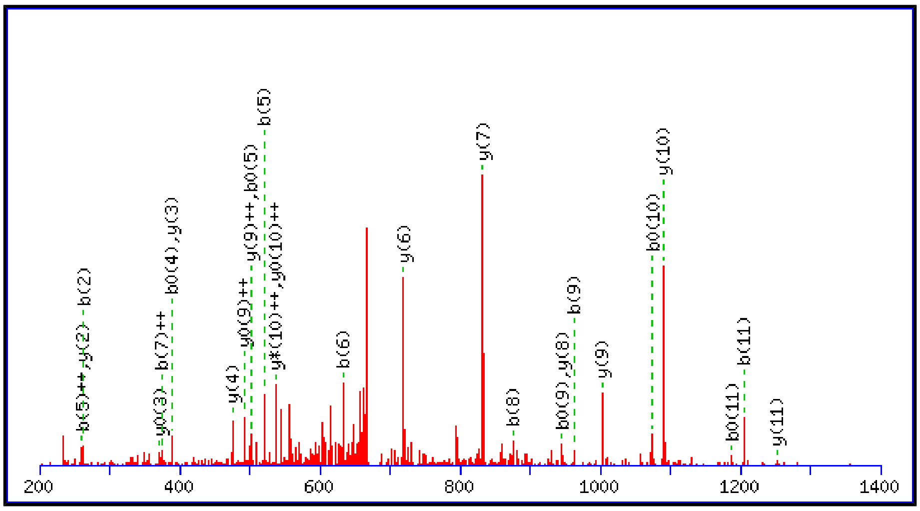
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYSGILNQSEIK**
Found in **E9PGP2** in **con_Xuniprot_HUMAN3**, E9PGP2_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=2 SV=1

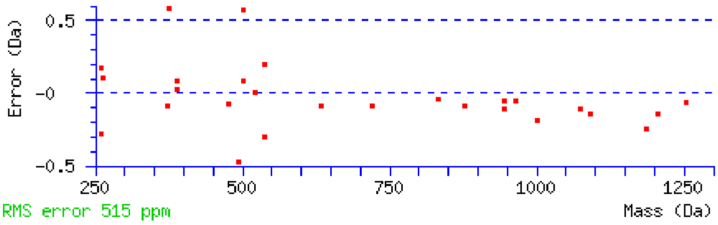
Match to Query 2140: 1350.708488 from(676.361520,2+) intensity(9060.8760) rtinseconds(1167) scans(2645) index(7394)
Title: 111019_Est_ISCardio_NMI_YP_G_11Spectrum2297_scans__2645
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

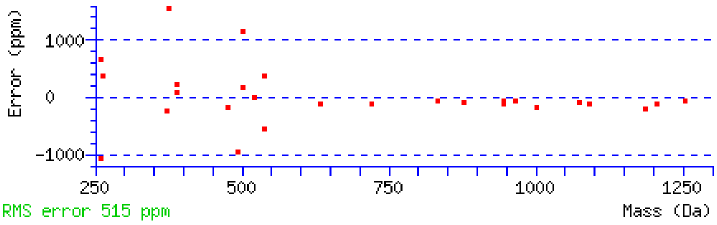
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1350.7031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 66 **Expect:** 4.6e-005
Matches : 27/112 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	100.0757	50.5415					V							12
2	**263.1390**	132.0731					Y	***1252.6420***	626.8246	1235.6154	618.3113	1234.6314	617.8193	11
3	350.1710	175.5892			332.1605	166.5839	S	***1089.5786***	545.2930	1072.5521	536.7797	1071.5681	536.2877	10
4	407.1925	204.0999			389.1819	195.0946	G	***1002.5466***	501.7769	985.5201	493.2637	984.5360	492.7717	9
5	**520.2766**	260.6419			502.2660	251.6366	I	***945.5251***	473.2662	928.4986	464.7529	927.5146	464.2609	8
6	**633.3606**	317.1840			615.3501	308.1787	L	***832.4411***	416.7242	815.4145	408.2109	814.4305	407.7189	7
7	748.3876	374.6974	731.3610	366.1842	730.3770	365.6921	N	***719.3570***	360.1821	702.3305	351.6689	701.3464	351.1769	6
8	**876.4462**	438.7267	859.4196	430.2134	858.4356	429.7214	Q	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
9	**963.4782**	482.2427	946.4516	473.7295	945.4676	473.2374	S	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	4
10	1092.5208	546.7640	1075.4942	538.2508	1074.5102	537.7587	E	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	**1205.6048**	603.3061	1188.5783	594.7928	1187.5943	594.3008	I	***260.1969***	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VYSGILNQSEIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.2	1350.7031	0.0054	VYSGILNQSEIK	Deamidated N7 50.23%
66.1	1350.7031	0.0054	VYSGILNQSEIK	Deamidated Q8 49.77%
9.7	1350.7031	0.0054	YQKAGDVSLELK	
8.4	1350.7031	0.0054	VYEGAKSIEEVK	
7.3	1349.7078	1.0007	ELYLAKEEDLK	
5.5	1350.7030	0.0054	KELFSNKDQLK	
5.5	1350.7031	0.0054	SFEELIQEKTK	
5.3	1350.7143	-0.0058	KGFNQISTSQIK	
5.1	1350.7031	0.0054	SLFSLDGKNELK	
4.6	1350.7031	0.0054	SEKLSSFPSLQK	

Mascot: http://www.matrixscience.com/

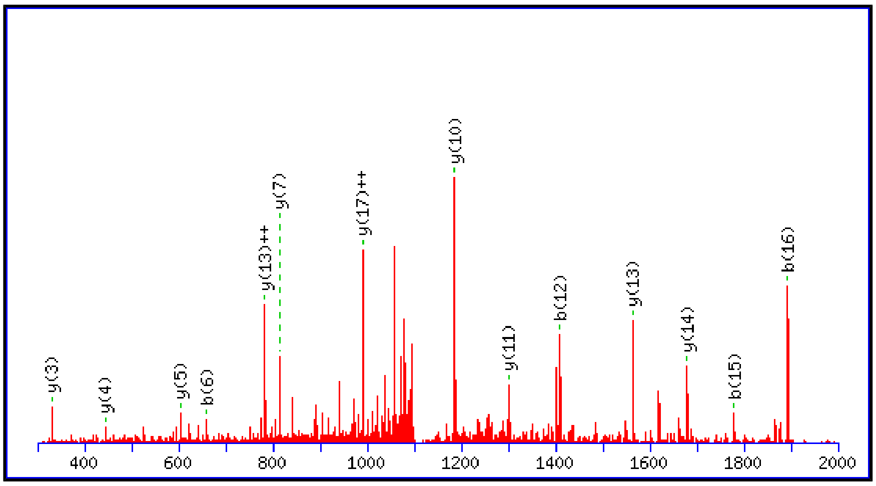
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LETTVNYTDSQRPICLPSK**
Found in **E9PGP2** in **con_Xuniprot_HUMAN3**, E9PGP2_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=2 SV=1

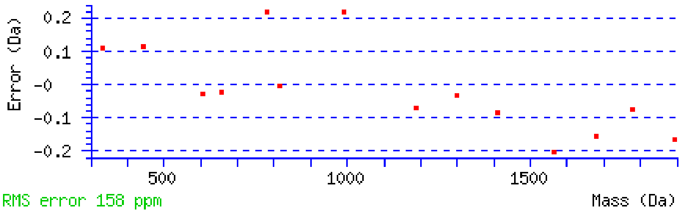
Match to Query 14904: 2222.094788 from(1112.054670,2+) intensity(19839.8242) rtinseconds(1031) scans(2435) index(2567)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum2064_scans__2435
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

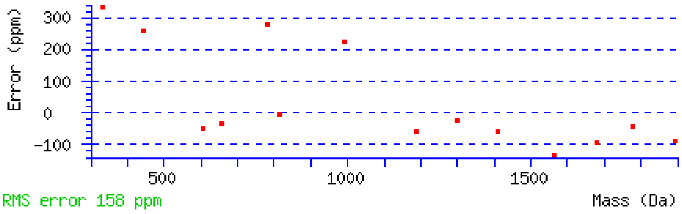
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2222.0889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00043
Matches : 14/202 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	114.0913	57.5493					L							19
2	243.1339	122.0706			225.1234	113.0653	E	2110.0121	1055.5097	2092.9856	1046.9964	2092.0015	1046.5044	18
3	344.1816	172.5944			326.1710	163.5892	T	1980.9695	990.9884	1963.9430	982.4751	1962.9590	981.9831	17
4	445.2293	223.1183			427.2187	214.1130	T	1879.9218	940.4646	1862.8953	931.9513	1861.9113	931.4593	16
5	544.2977	272.6525			526.2871	263.6472	V	1778.8742	889.9407	1761.8476	881.4274	1760.8636	880.9354	15
6	**659.3246**	330.1660	642.2981	321.6527	641.3141	321.1607	N	***1679.8057***	840.4065	1662.7792	831.8932	1661.7952	831.4012	14
7	822.3880	411.6976	805.3614	403.1844	804.3774	402.6923	Y	***1564.7788***	782.8930	1547.7523	774.3798	1546.7682	773.8878	13
8	923.4357	462.2215	906.4091	453.7082	905.4251	453.2162	T	1401.7155	701.3614	1384.6889	692.8481	1383.7049	692.3561	12
9	1038.4626	519.7349	1021.4361	511.2217	1020.4520	510.7297	D	***1300.6678***	650.8375	1283.6412	642.3243	1282.6572	641.8323	11
10	1125.4946	563.2510	1108.4681	554.7377	1107.4841	554.2457	S	***1185.6409***	593.3241	1168.6143	584.8108	1167.6303	584.3188	10
11	1253.5532	627.2802	1236.5267	618.7670	1235.5426	618.2750	Q	1098.6088	549.8081	1081.5823	541.2948	1080.5983	540.8028	9
12	**1409.6543**	705.3308	1392.6278	696.8175	1391.6438	696.3255	R	970.5502	485.7788	953.5237	477.2655	952.5397	476.7735	8
13	1506.7071	753.8572	1489.6805	745.3439	1488.6965	744.8519	P	***814.4491***	407.7282	797.4226	399.2149	796.4386	398.7229	7
14	1619.7911	810.3992	1602.7646	801.8859	1601.7806	801.3939	I	717.3964	359.2018	700.3698	350.6885	699.3858	350.1965	6
15	**1779.8218**	890.4145	1762.7952	881.9013	1761.8112	881.4093	C	***604.3123***	302.6598	587.2858	294.1465	586.3017	293.6545	5
16	**1892.9059**	946.9566	1875.8793	938.4433	1874.8953	937.9513	L	***444.2817***	222.6445	427.2551	214.1312	426.2711	213.6392	4
17	1989.9586	995.4829	1972.9321	986.9697	1971.9481	986.4777	P	***331.1976***	166.1024	314.1710	157.5892	313.1870	157.0972	3
18	2076.9906	1038.9990	2059.9641	1030.4857	2058.9801	1029.9937	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
19							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LETTVNYTDSQRPICLPSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
58.2	2222.0889	0.0059	LETTVNYTDSQRPICLPSK	Deamidated N6 86.54%
50.1	2222.0889	0.0059	LETTVNYTDSQRPICLPSK	Deamidated Q11 13.46%
9.2	2220.0845	2.0103	QTVLQSISDAFEQPMPTRR	
8.8	2222.0954	-0.0006	LAEETLHSDPLEQQSIVSPK	
7.6	2221.0949	0.9998	FLMRVEQDENELAWLRR	
6.1	2222.0936	0.0012	LEPCCQAITYLGRDTLRR	
1.6	2222.0967	-0.0019	LDNDKARWEPVTSSPQLHK	
0.9	2222.0981	-0.0033	HIHHNEHLFNIGNAAGQAIK	
0.9	2220.0804	2.0144	SIQNTLKNKTRPSENMDSR	

Mascot: http://www.matrixscience.com/

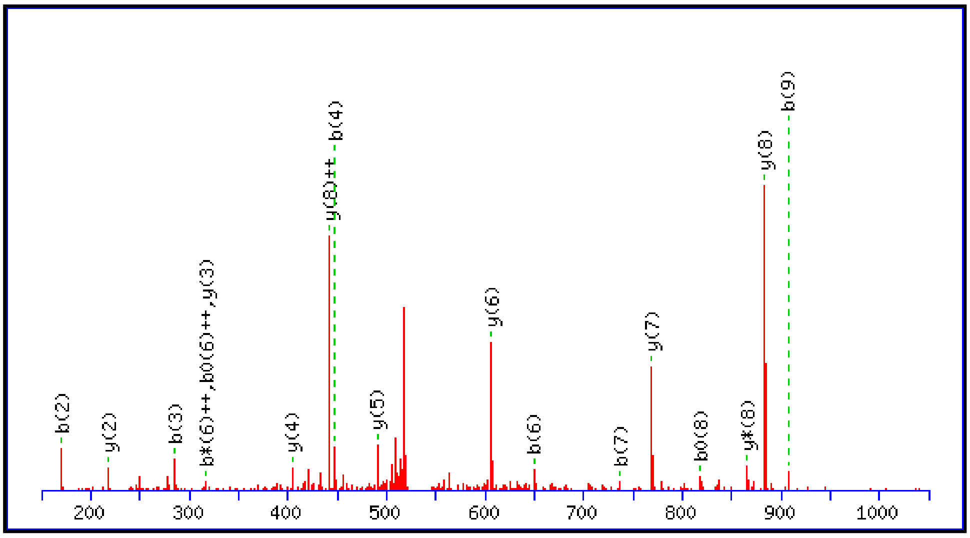
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GINYNSSVAK**
Found in **D6RB32** in **con_Xuniprot_HUMAN3**, D6RB32_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=2 SV=1

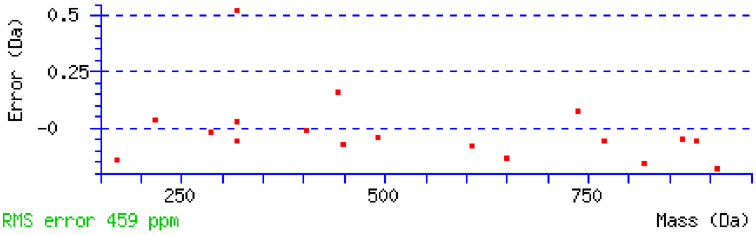
Match to Query 203: 1052.516348 from(527.265450,2+) intensity(10074.6318) rtinseconds(418) scans(791) index(26411)
Title: 111019_Est_MI_YS_G_09Spectrum652_scans__791
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

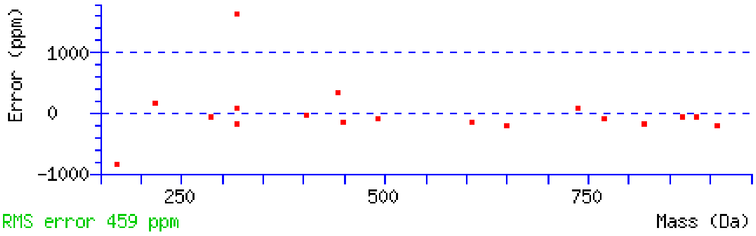
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1050 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1052.5138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.00059
Matches : 18/88 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	58.0287	29.5180					**G**							**10**
2	***171.1128***	86.0600					**I**	996.4997	498.7535	979.4731	490.2402	978.4891	489.7482	**9**
3	***285.1557***	143.0815	268.1292	134.5682			**N**	***883.4156***	442.2114	866.3890	433.6982	865.4050	433.2061	**8**
4	***448.2191***	224.6132	431.1925	216.0999			**Y**	***769.3727***	385.1900	752.3461	376.6767	751.3621	376.1847	**7**
5	563.2460	282.1266	546.2195	273.6134			**N**	***606.3093***	303.6583	589.2828	295.1450	588.2988	294.6530	**6**
6	***650.2780***	325.6427	633.2515	317.1294	632.2675	316.6374	**S**	***491.2824***	246.1448	474.2558	237.6316	473.2718	237.1395	**5**
7	***737.3101***	369.1587	720.2835	360.6454	719.2995	360.1534	**S**	***404.2504***	202.6288	387.2238	194.1155	386.2398	193.6235	**4**
8	836.3785	418.6929	819.3519	410.1796	818.3679	409.6876	**V**	***317.2183***	159.1128	300.1918	150.5995			**3**
9	***907.4156***	454.2114	890.3890	445.6982	889.4050	445.2061	**A**	***218.1499***	109.5786	201.1234	101.0653			**2**
10							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GINYNSSVAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.6	1052.5138	0.0025	GINYNSSVAK	Deamidated N5 99.83%
25.9	1052.5138	0.0025	GINYNSSVAK	Deamidated N3 0.17%
7.0	1051.5120	1.0043	WMLSQSKR	
3.9	1052.5172	-0.0008	MDKKSTAEK	
2.3	1052.5138	0.0025	AVSSNYNIGK	
1.9	1052.5147	0.0017	WGKMMEKK	
1.5	1052.5138	0.0025	AVSSNYNIGK	
1.0	1051.5121	1.0043	GNVMVDFRV	
0.3	1051.5161	1.0003	MLYTPYHK	
0.3	1052.5138	0.0025	GLDNGYSISK	

Mascot: http://www.matrixscience.com/

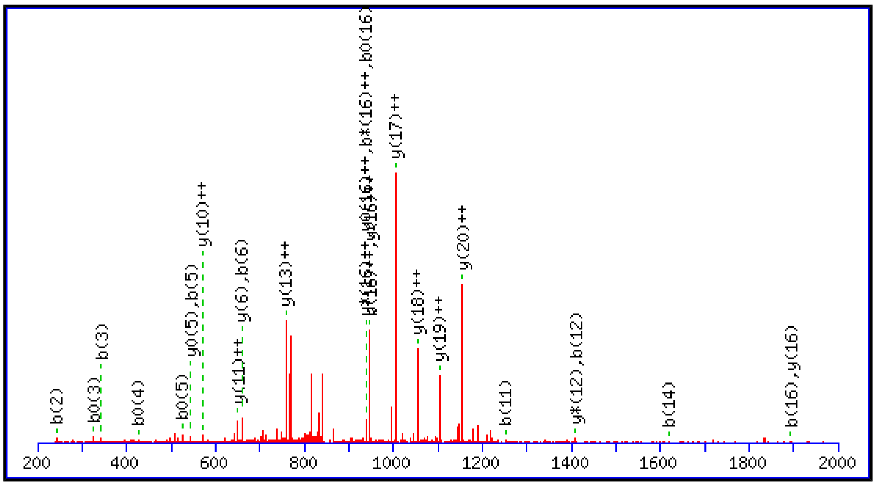
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LETTVNYTDSQRPICLPSKGDR**
Found in **E9PGP2** in **con_Xuniprot_HUMAN3**, E9PGP2_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=2 SV=1

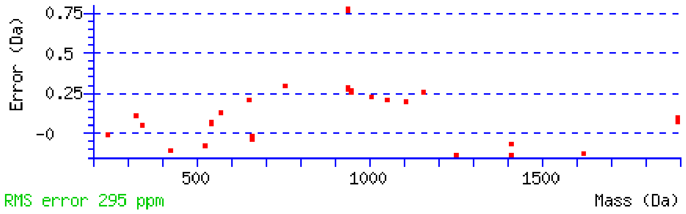
Match to Query 21927: 2550.243162 from(851.088330,3+) intensity(39617.5742) rtinseconds(916) scans(2034) index(14426)
Title: 111019_Est_MI_YP_G_03Spectrum1705_scans__2034
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

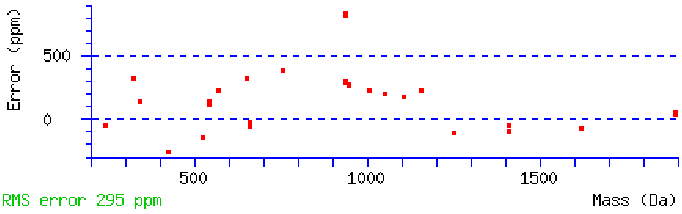
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2550.2384
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0079
Matches : 28/238 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							22
2	***243.1339***	122.0706			225.1234	113.0653	E	2438.1616	1219.5845	2421.1351	1211.0712	2420.1511	1210.5792	21
3	***344.1816***	172.5944			326.1710	163.5892	T	2309.1190	1155.0632	2292.0925	1146.5499	2291.1085	1146.0579	20
4	445.2293	223.1183			427.2187	214.1130	T	2208.0714	1104.5393	2191.0448	1096.0260	2190.0608	1095.5340	19
5	***544.2977***	272.6525			526.2871	263.6472	V	2107.0237	1054.0155	2089.9971	1045.5022	2089.0131	1045.0102	18
6	***659.3246***	330.1660	642.2981	321.6527	641.3141	321.1607	N	2007.9553	1004.4813	1990.9287	995.9680	1989.9447	995.4760	17
7	822.3880	411.6976	805.3614	403.1844	804.3774	402.6923	Y	1892.9283	946.9678	1875.9018	938.4545	1874.9178	937.9625	16
8	923.4357	462.2215	906.4091	453.7082	905.4251	453.2162	T	1729.8650	865.4361	1712.8384	856.9229	1711.8544	856.4309	15
9	1038.4626	519.7349	1021.4361	511.2217	1020.4520	510.7297	D	1628.8173	814.9123	1611.7908	806.3990	1610.8067	805.9070	14
10	1125.4946	563.2510	1108.4681	554.7377	1107.4841	554.2457	S	1513.7904	757.3988	1496.7638	748.8855	1495.7798	748.3935	13
11	***1253.5532***	627.2802	1236.5267	618.7670	1235.5426	618.2750	Q	1426.7583	713.8828	1409.7318	705.3695	1408.7478	704.8775	12
12	***1409.6543***	705.3308	1392.6278	696.8175	1391.6438	696.3255	R	1298.6998	649.8535	1281.6732	641.3402	1280.6892	640.8482	11
13	1506.7071	753.8572	1489.6805	745.3439	1488.6965	744.8519	P	1142.5987	571.8030	1125.5721	563.2897	1124.5881	562.7977	10
14	***1619.7911***	810.3992	1602.7646	801.8859	1601.7806	801.3939	I	1045.5459	523.2766	1028.5193	514.7633	1027.5353	514.2713	9
15	1779.8218	890.4145	1762.7952	881.9013	1761.8112	881.4093	C	932.4618	466.7346	915.4353	458.2213	914.4513	457.7293	8
16	***1892.9059***	946.9566	1875.8793	938.4433	1874.8953	937.9513	L	772.4312	386.7192	755.4046	378.2060	754.4206	377.7139	7
17	1989.9586	995.4829	1972.9321	986.9697	1971.9481	986.4777	P	659.3471	330.1772	642.3206	321.6639	641.3365	321.1719	6
18	2076.9906	1038.9990	2059.9641	1030.4857	2058.9801	1029.9937	S	562.2943	281.6508	545.2678	273.1375	544.2838	272.6455	5
19	2205.0856	1103.0464	2188.0591	1094.5332	2187.0750	1094.0412	K	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	4
20	2262.1071	1131.5572	2245.0805	1123.0439	2244.0965	1122.5519	G	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
21	2377.1340	1189.0706	2360.1075	1180.5574	2359.1235	1180.0654	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
22							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LETTVNYTDSQRPICLPSKGDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.6	2550.2384	0.0048	LETTVNYTDSQRPICLPSKGDR	Deamidated N6 74.25%
41.0	2550.2384	0.0048	LETTVNYTDSQRPICLPSKGDR	Deamidated Q11 25.75%
5.5	2549.2525	0.9906	QLATASWDTFLMLWNFKPHAR	
5.0	2548.2422	2.0009	FQTYLLPMYGYVKVFFNICK	
3.3	2548.2492	1.9939	GMTEHTKNLLRAFYELSQTHR	
2.5	2549.2361	1.0070	LDALLNMHKSMDTALVMDIVMR	
1.4	2550.2359	0.0072	MTFHHSMTFKQIVLVGQETQR	
1.2	2550.2310	0.0122	RSDSPAADSDASSLHEQPQQIAIK	
1.2	2549.2510	0.9922	QNLSRSWHDVQVSSAYVKTSEK	
1.2	2550.2424	0.0008	LQGEIDIELTPFMSQHQHALNK	

Mascot: http://www.matrixscience.com/

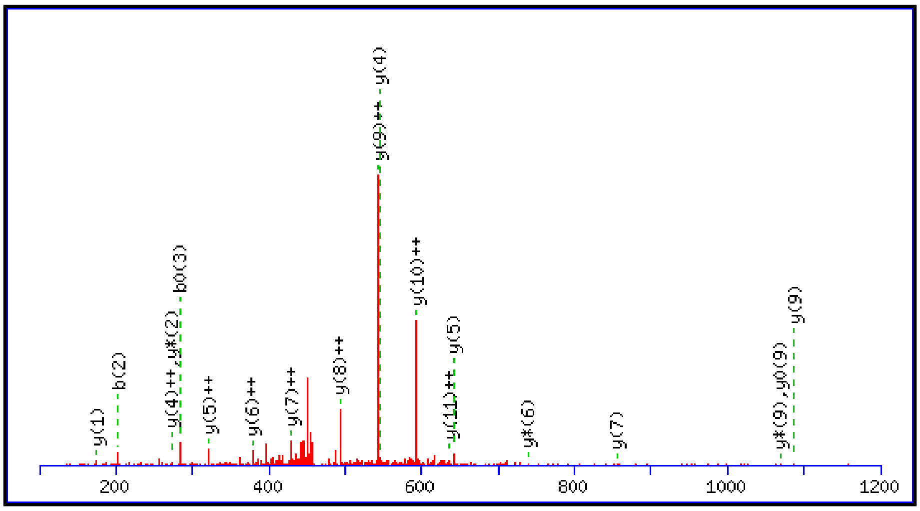
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSVTETLPRVNR**
Found in **D6RB32** in **con_Xuniprot_HUMAN3**, D6RB32_HUMAN Coagulation factor XI OS=Homo sapiens GN=F11 PE=2 SV=1

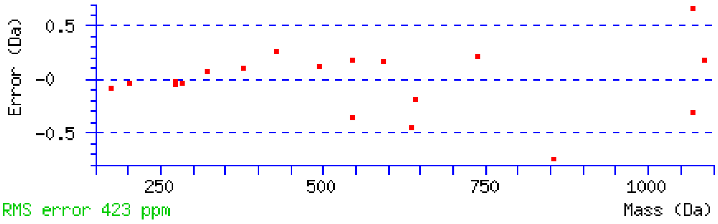
Match to Query 2397: 1386.714402 from(463.245410,3+) intensity(6614.6401) rtinseconds(690) scans(1460) index(25986)
Title: 111019_Est_MI_YS_G_08Spectrum1246_scans__1460
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

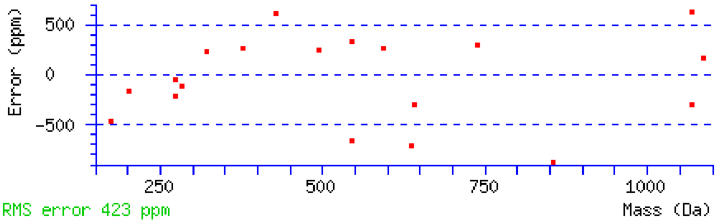
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1386.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.046
Matches : 19/104 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	203.0662	102.0368			185.0557	93.0315	S	1272.6906	636.8490	1255.6641	628.3357	1254.6801	627.8437	11
3	302.1347	151.5710			284.1241	142.5657	V	1185.6586	593.3329	1168.6321	584.8197	1167.6480	584.3277	10
4	403.1823	202.0948			385.1718	193.0895	T	**1086.5902**	543.7987	1069.5637	535.2855	1068.5796	534.7935	9
5	532.2249	266.6161			514.2144	257.6108	E	985.5425	493.2749	968.5160	484.7616	967.5320	484.2696	8
6	633.2726	317.1399			615.2620	308.1347	T	**856.4999**	428.7536	839.4734	420.2403	838.4894	419.7483	7
7	746.3567	373.6820			728.3461	364.6767	L	755.4522	378.2298	738.4257	369.7165			6
8	843.4094	422.2084			825.3989	413.2031	P	**642.3682**	321.6877	625.3416	313.1745			5
9	999.5106	500.2589	982.4840	491.7456	981.5000	491.2536	R	**545.3154**	273.1613	528.2889	264.6481			4
10	1098.5790	549.7931	1081.5524	541.2798	1080.5684	540.7878	V	389.2143	195.1108	372.1878	186.5975			3
11	1213.6059	607.3066	1196.5794	598.7933	1195.5953	598.3013	N	290.1459	145.5766	273.1193	137.0633			2
12							R	**175.1190**	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DSVTETLPRVNR
(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	1386.7103	0.0041	DSVTETLPRVNR
10.5	1384.7094	2.0050	TVQVVSKMFAMK
9.8	1386.7105	0.0039	MTFFVTQLAITV
9.1	1386.7177	-0.0033	VMAALDQIIEQR
8.2	1386.7177	-0.0033	VMAALDQIIEQR
7.7	1385.7052	1.0092	GTAAGPPVEERFR
6.8	1386.7143	0.0001	HYGQGVISQVIGK
6.8	1386.7103	0.0041	DVSLDSVLVNNGR
6.3	1384.7133	2.0011	AEVQHIVMGTRK
6.2	1386.7103	0.0041	ETEALNPASATRK

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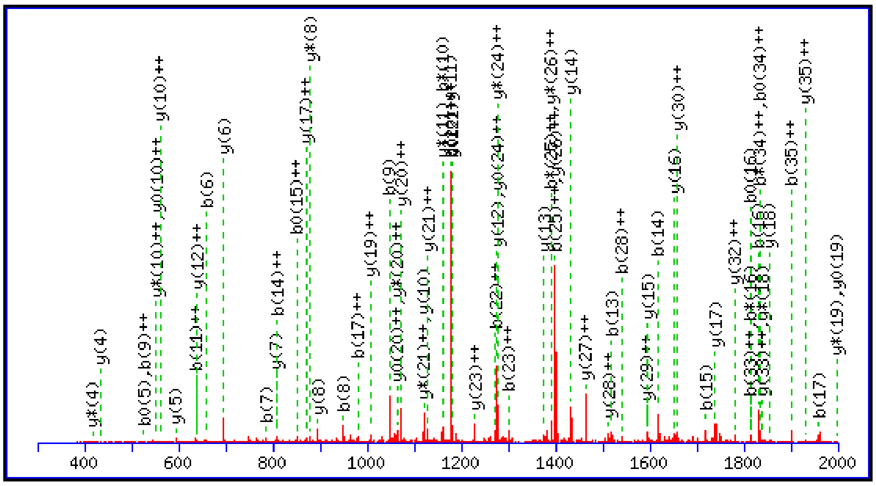
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28231: 3972.817632 from(1325.279820,3+) intensity(20894.2852) rtinseconds(1594) scans(4001) index(24541)
Title: 111019_Est_MI_YS_G_06Spectrum3469_scans__4001
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

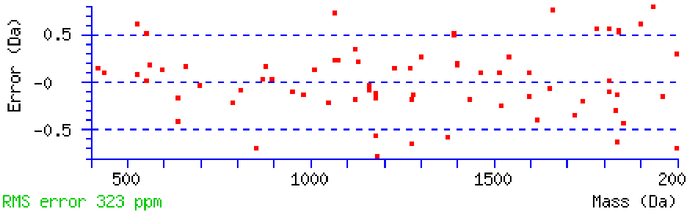
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

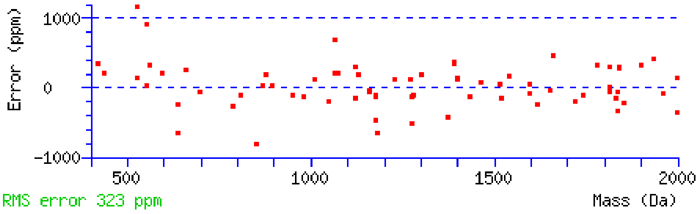


Monoisotopic mass of neutral peptide Mr(calc): 3972.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
N35 : Deamidated (NQ)
Ions Score: 108 **Expect:** 2.6e-009
Matches : 73/404 fragment ions using 118 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**L**							**36**
2	201.1234	101.0653			183.1128	92.0600	**S**	3860.7226	1930.8649	3843.6960	1922.3516	3842.7120	1921.8596	**35**
3	300.1918	150.5995			282.1812	141.5942	**V**	3773.6905	1887.3489	3756.6640	1878.8356	3755.6800	1878.3436	**34**
4	415.2187	208.1130			397.2082	199.1077	**D**	3674.6221	1837.8147	3657.5956	1829.3014	3656.6116	1828.8094	**33**
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	**K**	3559.5952	1780.3012	3542.5686	1771.7879	3541.5846	1771.2959	**32**
6	**658.3406**	329.6740	641.3141	321.1607	640.3301	320.6687	**D**	3431.5002	1716.2537	3414.4737	1707.7405	3413.4896	1707.2485	**31**
7	**786.3992**	393.7032	769.3727	385.1900	768.3886	384.6980	**Q**	3316.4733	1658.7403	3299.4467	1650.2270	3298.4627	1649.7350	**30**
8	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	**Y**	3188.4147	1594.7110	3171.3881	1586.1977	3170.4041	1585.7057	**29**
9	**1048.5310**	**524.7691**	1031.5044	516.2558	1030.5204	515.7638	**V**	3025.3514	1513.1793	3008.3248	1504.6660	3007.3408	1504.1740	**28**
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	**E**	2926.2829	1463.6451	2909.2564	1455.1318	2908.2724	1454.6398	**27**
11	1274.6263	**637.8168**	1257.5998	629.3035	1256.6157	628.8115	**P**	2797.2404	1399.1238	2780.2138	1390.6105	2779.2298	1390.1185	**26**
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	**E**	2700.1876	1350.5974	2683.1610	1342.0842	2682.1770	1341.5921	**25**
13	**1518.6958**	759.8516	1501.6693	751.3383	1500.6853	750.8463	**N**	2571.1450	1286.0761	2554.1184	1277.5629	2553.1344	1277.0709	**24**
14	**1617.7643**	**809.3858**	1600.7377	800.8725	1599.7537	800.3805	**V**	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	**23**
15	**1718.8119**	859.9096	1701.7854	851.3963	1700.8014	850.9043	**T**	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	**22**
16	**1831.8960**	916.4516	1814.8695	907.9384	1813.8854	907.4464	**I**	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	**21**
17	**1959.9546**	**980.4809**	1942.9280	971.9677	1941.9440	971.4756	**Q**	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	**20**
18	2119.9852	1060.4963	2102.9587	1051.9830	2101.9747	1051.4910	**C**	2014.8593	1007.9333	1997.8328	999.4200	1996.8488	998.9280	**19**
19	2235.0122	1118.0097	2217.9856	1109.4964	2217.0016	1109.0044	**D**	***1854.8287***	927.9180	1837.8021	919.4047	1836.8181	918.9127	**18**
20	2322.0442	1161.5257	2305.0177	1153.0125	2304.0336	1152.5205	**S**	***1739.8017***	870.4045	1722.7752	861.8912	1721.7912	861.3992	**17**
21	2379.0657	1190.0365	2362.0391	1181.5232	2361.0551	1181.0312	**G**	***1652.7697***	826.8885	1635.7431	818.3752	1634.7591	817.8832	**16**
22	2542.1290	**1271.5681**	2525.1024	1263.0549	2524.1184	1262.5629	**Y**	***1595.7482***	798.3778	1578.7217	789.8645	1577.7377	789.3725	**15**

23	2599.1505	**1300.0789**	2582.1239	1291.5656	2581.1399	1291.0736	**G**	***1432.6849***	716.8461	1415.6584	708.3328	1414.6743	707.8408	**14**
24	2698.2189	1349.6131	2681.1923	1341.0998	2680.2083	1340.6078	**V**	***1375.6634***	688.3354	1358.6369	679.8221	1357.6529	679.3301	**13**
25	2797.2873	**1399.1473**	2780.2607	1390.6340	2779.2767	1390.1420	**V**	***1276.5950***	638.8012	1259.5685	630.2879	1258.5845	629.7959	**12**
26	2854.3087	1427.6580	2837.2822	1419.1447	2836.2982	1418.6527	**G**	***1177.5266***	589.2669	1160.5001	580.7537	1159.5160	580.2617	**11**
27	2951.3615	1476.1844	2934.3350	1467.6711	2933.3509	1467.1791	**P**	***1120.5051***	560.7562	1103.4786	552.2429	1102.4946	551.7509	**10**
28	3079.4201	**1540.2137**	3062.3935	1531.7004	3061.4095	1531.2084	**Q**	1023.4524	512.2298	1006.4258	503.7166	1005.4418	503.2245	**9**
29	3166.4521	1583.7297	3149.4256	1575.2164	3148.4416	1574.7244	**S**	***895.3938***	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3279.5362	1640.2717	3262.5096	1631.7585	3261.5256	1631.2664	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3380.5839	1690.7956	3363.5573	1682.2823	3362.5733	1681.7903	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3540.6145	1770.8109	3523.5880	1762.2976	3522.6039	1761.8056	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3627.6465	**1814.3269**	3610.6200	1805.8136	3609.6360	1805.3216	**S**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3684.6680	1842.8376	3667.6415	1834.3244	3666.6574	1833.8324	**G**	347.1674	174.0873	330.1408	165.5740			**3**
35	3799.6949	**1900.3511**	3782.6684	1891.8378	3781.6844	1891.3458	**N**	290.1459	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
107.9	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, N35 54.57%
104.3	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N35 23.99%
103.8	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, N35 21.28%
80.8	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q28, N35 0.11%
72.6	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17 0.02%
72.5	3971.8154	1.0023	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
71.9	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28 0.01%
69.5	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, Q28 0.01%
68.8	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28 0.01%
64.3	3972.7994	0.0183	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17 0.00%

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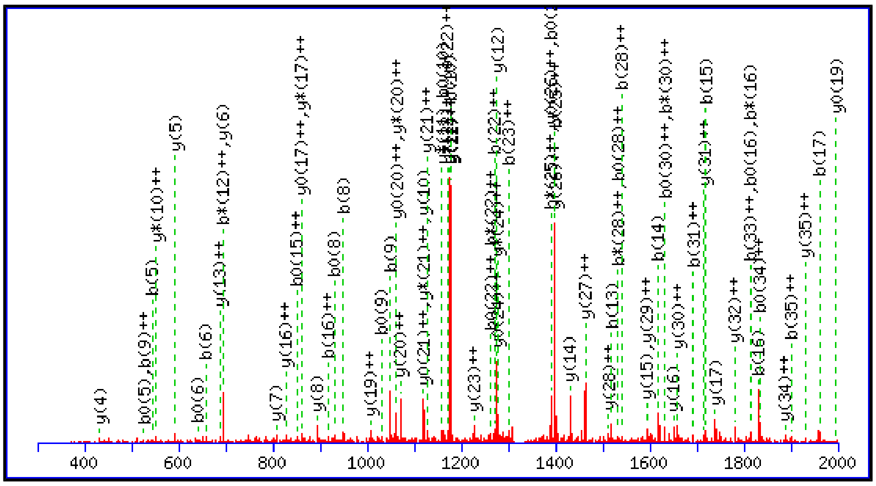
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28232: 3972.818262 from(1325.280030,3+) intensity(0.0000) rtinseconds(1648) scans(4093) index(25352)
Title: 111019_Est_MI_YS_G_07Spectrum3483_scans__4093
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

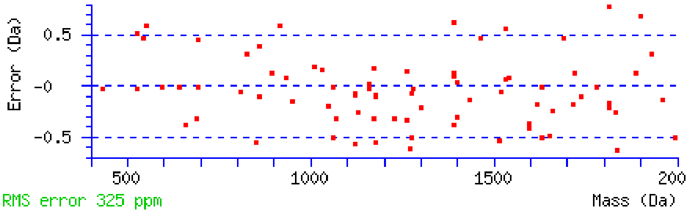
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

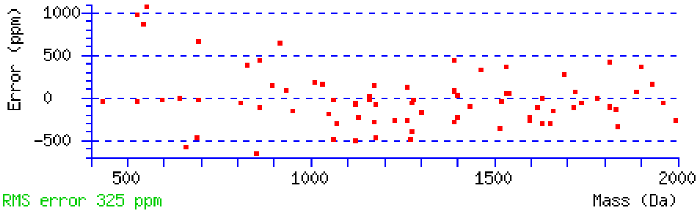


Monoisotopic mass of neutral peptide Mr(calc): 3972.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Q17 : Deamidated (NQ)
Ions Score: 102 **Expect:** 1.1e-008
Matches : 80/404 fragment ions using 119 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**36**
2	201.1234	101.0653			183.1128	92.0600	**S**	3860.7226	1930.8649	3843.6960	1922.3516	3842.7120	1921.8596	**35**
3	300.1918	150.5995			282.1812	141.5942	**V**	3773.6905	1887.3489	3756.6640	1878.8356	3755.6800	1878.3436	**34**
4	415.2187	208.1130			397.2082	199.1077	**D**	3674.6221	1837.8147	3657.5956	1829.3014	3656.6116	1828.8094	**33**
5	**543.3137**	272.1605	526.2871	263.6472	525.3031	263.1552	**K**	3559.5952	1780.3012	3542.5686	1771.7879	3541.5846	1771.2959	**32**
6	**658.3406**	329.6740	641.3141	321.1607	640.3301	320.6687	**D**	3431.5002	1716.2537	3414.4737	1707.7405	3413.4896	1707.2485	**31**
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	**Q**	3316.4733	1658.7403	3299.4467	1650.2270	3298.4627	1649.7350	**30**
8	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	**Y**	3188.4147	1594.7110	3171.3881	1586.1977	3170.4041	1585.7057	**29**
9	**1048.5310**	**524.7691**	1031.5044	516.2558	1030.5204	515.7638	**V**	3025.3514	1513.1793	3008.3248	1504.6660	3007.3408	1504.1740	**28**
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	**E**	2926.2829	1463.6451	2909.2564	1455.1318	2908.2724	1454.6398	**27**
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	**P**	2797.2404	1399.1238	2780.2138	1390.6105	2779.2298	1390.1185	**26**
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	**E**	2700.1876	1350.5974	2683.1610	1342.0842	2682.1770	1341.5921	**25**
13	**1518.6958**	759.8516	1501.6693	751.3383	1500.6853	750.8463	**N**	2571.1450	1286.0761	2554.1184	1277.5629	2553.1344	1277.0709	**24**
14	**1617.7643**	809.3858	1600.7377	800.8725	1599.7537	800.3805	**V**	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	**23**
15	**1718.8119**	859.9096	1701.7854	851.3963	1700.8014	850.9043	**T**	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	**22**
16	**1831.8960**	**916.4516**	1814.8695	907.9384	1813.8854	907.4464	**I**	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	**21**
17	**1960.9386**	980.9729	1943.9120	972.4597	1942.9280	971.9677	**Q**	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	**20**
18	2120.9692	1060.9883	2103.9427	1052.4750	2102.9587	1051.9830	**C**	2013.8753	1007.4413	1996.8488	998.9280	1995.8647	998.4360	**19**
19	2235.9962	1118.5017	2218.9696	1109.9885	2217.9856	1109.4964	**D**	1853.8447	927.4260	1836.8181	918.9127	1835.8341	918.4207	**18**
20	2323.0282	1162.0177	2306.0017	1153.5045	2305.0177	1153.0125	**S**	***1738.8177***	869.9125	1721.7912	861.3992	1720.8071	860.9072	**17**
21	2380.0497	1190.5285	2363.0231	1182.0152	2362.0391	1181.5232	**G**	***1651.7857***	826.3965	1634.7591	817.8832	1633.7751	817.3912	**16**
22	2543.1130	**1272.0601**	2526.0865	1263.5469	2525.1024	1263.0549	**Y**	***1594.7642***	797.8857	1577.7377	789.3725	1576.7537	788.8805	**15**

23	2600.1345	**1300.5709**	2583.1079	1292.0576	2582.1239	1291.5656	**G**	***1431.7009***	716.3541	1414.6743	707.8408	1413.6903	707.3488	**14**
24	2699.2029	1350.1051	2682.1763	1341.5918	2681.1923	1341.0998	**V**	1374.6794	687.8434	1357.6529	679.3301	1356.6689	678.8381	**13**
25	2798.2713	**1399.6393**	2781.2448	1391.1260	2780.2607	1390.6340	**V**	***1275.6110***	638.3091	1258.5845	629.7959	1257.6004	629.3039	**12**
26	2855.2928	1428.1500	2838.2662	1419.6367	2837.2822	1419.1447	**G**	***1176.5426***	588.7749	1159.5160	580.2617	1158.5320	579.7697	**11**
27	2952.3455	1476.6764	2935.3190	1468.1631	2934.3350	1467.6711	**P**	***1119.5211***	560.2642	1102.4946	551.7509	1101.5106	551.2589	**10**
28	3080.4041	**1540.7057**	3063.3776	1532.1924	3062.3935	1531.7004	**Q**	1022.4684	511.7378	1005.4418	503.2245	1004.4578	502.7325	**9**
29	3167.4361	1584.2217	3150.4096	1575.7084	3149.4256	1575.2164	**S**	***894.4098***	447.7085	877.3832	439.1953	876.3992	438.7033	**8**
30	3280.5202	1640.7637	3263.4936	1632.2505	3262.5096	1631.7585	**I**	***807.3778***	404.1925	790.3512	395.6792	789.3672	395.1872	**7**
31	3381.5679	**1691.2876**	3364.5413	1682.7743	3363.5573	1682.2823	**T**	***694.2937***	347.6505	677.2671	339.1372	676.2831	338.6452	**6**
32	3541.5985	1771.3029	3524.5720	1762.7896	3523.5880	1762.2976	**C**	***593.2460***	297.1266	576.2195	288.6134	575.2355	288.1214	**5**
33	3628.6306	**1814.8189**	3611.6040	1806.3056	3610.6200	1805.8136	**S**	***433.2154***	217.1113	416.1888	208.5980	415.2048	208.1060	**4**
34	3685.6520	1843.3296	3668.6255	1834.8164	3667.6415	1834.3244	**G**	346.1833	173.5953	329.1568	165.0820			**3**
35	3799.6949	**1900.3511**	3782.6684	1891.8378	3781.6844	1891.3458	**N**	289.1619	145.0846	272.1353	136.5713			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
101.8	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17 61.62%
95.3	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28 14.08%
94.6	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28 11.77%
93.2	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17 8.64%
87.7	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N13 2.44%
87.3	3971.8154	1.0029	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
85.3	3971.8154	1.0029	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
81.4	3972.7994	0.0189	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, Q28 0.57%
78.4	3971.8154	1.0029	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
78.3	3971.8154	1.0029	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	

Mascot: http://www.matrixscience.com/

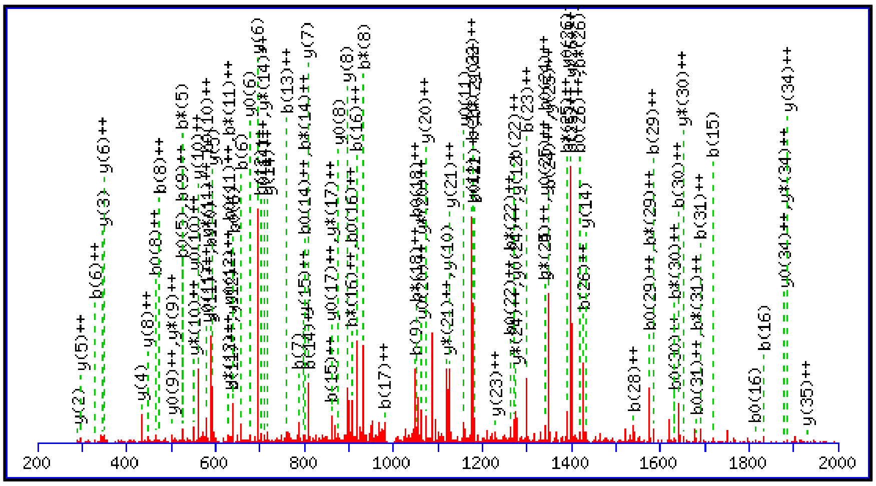
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28225: 3972.814016 from(994.210780,4+) intensity(62808.0781) rtinseconds(1576) scans(3918) index(5270)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum3420_scans__3918
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

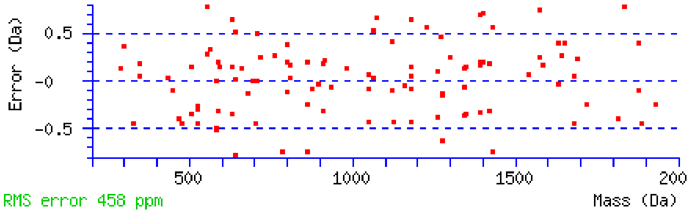
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

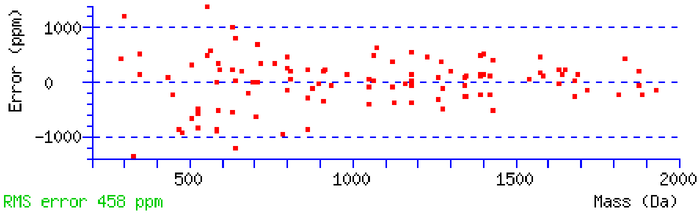


Monoisotopic mass of neutral peptide Mr(calc): 3972.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Deamidated (NQ)
N35 : Deamidated (NQ)
Ions Score: 88 **Expect:** 2.7e-007
Matches : 111/404 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**36**
2	201.1234	101.0653			183.1128	92.0600	**S**	3860.7226	1930.8649	3843.6960	1922.3516	3842.7120	1921.8596	**35**
3	300.1918	150.5995			282.1812	141.5942	**V**	3773.6905	1887.3489	3756.6640	1878.8356	3755.6800	1878.3436	**34**
4	415.2187	208.1130			397.2082	199.1077	**D**	3674.6221	1837.8147	3657.5956	1829.3014	3656.6116	1828.8094	**33**
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	**K**	3559.5952	1780.3012	3542.5686	1771.7879	3541.5846	1771.2959	**32**
6	**658.3406**	***329.6740***	641.3141	321.1607	640.3301	320.6687	**D**	3431.5002	1716.2537	3414.4737	1707.7405	3413.4896	1707.2485	**31**
7	**787.3832**	394.1953	770.3567	385.6820	769.3727	385.1900	**Q**	3316.4733	1658.7403	3299.4467	1650.2270	3298.4627	1649.7350	**30**
8	950.4466	***475.7269***	933.4200	467.2136	932.4360	466.7216	**Y**	3187.4307	1594.2190	3170.4041	1585.7057	3169.4201	1585.2137	**29**
9	**1049.5150**	***525.2611***	1032.4884	516.7478	1031.5044	516.2558	**V**	3024.3673	1512.6873	3007.3408	1504.1740	3006.3568	1503.6820	**28**
10	**1178.5576**	***589.7824***	1161.5310	581.2691	1160.5470	580.7771	**E**	2925.2989	1463.1531	2908.2724	1454.6398	2907.2884	1454.1478	**27**
11	1275.6103	***638.3088***	1258.5838	629.7955	1257.5998	629.3035	**P**	2796.2563	1398.6318	2779.2298	1390.1185	2778.2458	1389.6265	**26**
12	1404.6529	***702.8301***	1387.6264	694.3168	1386.6424	693.8248	**E**	2699.2036	1350.1054	2682.1770	1341.5921	2681.1930	1341.1001	**25**
13	1518.6958	***759.8516***	1501.6693	751.3383	1500.6853	750.8463	**N**	2570.1610	1285.5841	2553.1344	1277.0709	2552.1504	1276.5788	**24**
14	1617.7643	***809.3858***	1600.7377	800.8725	1599.7537	800.3805	**V**	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	**23**
15	**1718.8119**	***859.9096***	1701.7854	851.3963	1700.8014	850.9043	**T**	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	**22**
16	**1831.8960**	***916.4516***	1814.8695	907.9384	1813.8854	907.4464	**I**	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	**21**
17	1959.9546	***980.4809***	1942.9280	971.9677	1941.9440	971.4756	**Q**	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	**20**
18	2119.9852	1060.4963	2102.9587	1051.9830	2101.9747	1051.4910	**C**	2014.8593	1007.9333	1997.8328	999.4200	1996.8488	998.9280	**19**
19	2235.0122	1118.0097	2217.9856	1109.4964	2217.0016	1109.0044	**D**	1854.8287	927.9180	1837.8021	919.4047	1836.8181	918.9127	**18**
20	2322.0442	1161.5257	2305.0177	1153.0125	2304.0336	1152.5205	**S**	1739.8017	870.4045	1722.7752	861.8912	1721.7912	861.3992	**17**
21	2379.0657	1190.0365	2362.0391	1181.5232	2361.0551	1181.0312	**G**	1652.7697	826.8885	1635.7431	818.3752	1634.7591	817.8832	**16**
22	2542.1290	***1271.5681***	2525.1024	1263.0549	2524.1184	1262.5629	**Y**	1595.7482	798.3778	1578.7217	789.8645	1577.7377	789.3725	**15**

23	2599.1505	***1300.0789***	2582.1239	1291.5656	2581.1399	1291.0736	**G**	**1432.6849**	716.8461	1415.6584	708.3328	1414.6743	707.8408	**14**
24	2698.2189	***1349.6131***	2681.1923	1341.0998	2680.2083	1340.6078	**V**	1375.6634	688.3354	1358.6369	679.8221	1357.6529	679.3301	**13**
25	2797.2873	***1399.1473***	2780.2607	1390.6340	2779.2767	1390.1420	**V**	**1276.5950**	638.8012	1259.5685	630.2879	1258.5845	629.7959	**12**
26	2854.3087	***1427.6580***	2837.2822	1419.1447	2836.2982	1418.6527	**G**	**1177.5266**	589.2669	1160.5001	580.7537	1159.5160	580.2617	**11**
27	2951.3615	1476.1844	2934.3350	1467.6711	2933.3509	1467.1791	**P**	**1120.5051**	560.7562	1103.4786	552.2429	1102.4946	551.7509	**10**
28	3079.4201	***1540.2137***	3062.3935	1531.7004	3061.4095	1531.2084	**Q**	1023.4524	512.2298	1006.4258	503.7166	1005.4418	503.2245	**9**
29	3166.4521	***1583.7297***	3149.4256	1575.2164	3148.4416	1574.7244	**S**	**895.3938**	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3279.5362	***1640.2717***	3262.5096	1631.7585	3261.5256	1631.2664	**I**	**808.3618**	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3380.5839	***1690.7956***	3363.5573	1682.2823	3362.5733	1681.7903	**T**	**695.2777**	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3540.6145	1770.8109	3523.5880	1762.2976	3522.6039	1761.8056	**C**	**594.2300**	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3627.6465	1814.3269	3610.6200	1805.8136	3609.6360	1805.3216	**S**	**434.1994**	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3684.6680	1842.8376	3667.6415	1834.3244	3666.6574	1833.8324	**G**	**347.1674**	174.0873	330.1408	165.5740			**3**
35	3799.6949	1900.3511	3782.6684	1891.8378	3781.6844	1891.3458	**N**	**290.1459**	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.6	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N35 59.68%
84.4	3971.8154	0.9987	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
82.5	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, N35 18.27%
78.4	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q28, N35 7.21%
77.5	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, N35 5.81%
74.3	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17 2.75%
74.3	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17 2.75%
72.0	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28 1.65%
68.8	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N13 0.79%
67.7	3972.7994	0.0147	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28 0.61%

Mascot: http://www.matrixscience.com/

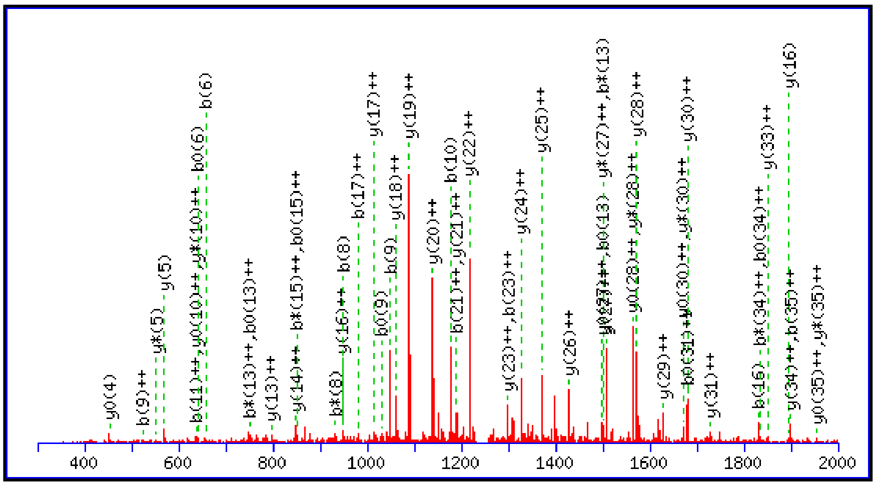
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28997: 4973.322976 from(1244.338020,4+) intensity(18160.8047) rtinseconds(1940) scans(4968) index(26820)
Title: 111019_Est_MI_YS_G_09Spectrum4322_scans__4968
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

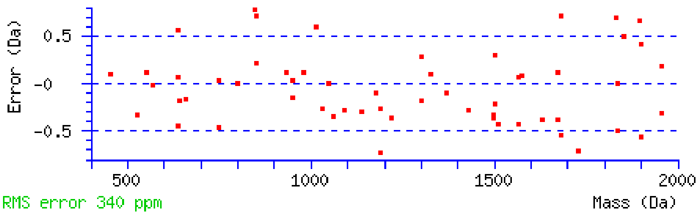
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

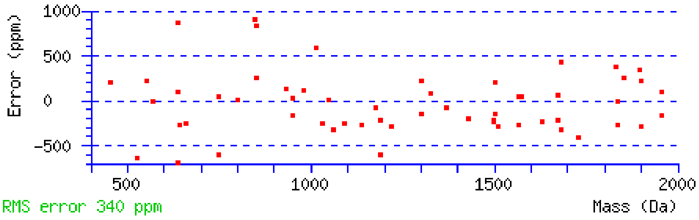


Monoisotopic mass of neutral peptide Mr(calc): 4973.3012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q28 : Deamidated (NQ)
N35 : Deamidated (NQ)
Ions Score: 87 **Expect:** 3e-007
Matches : 57/500 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							44
2	201.1234	101.0653			183.1128	92.0600	S	4861.2244	2431.1158	4844.1978	2422.6026	4843.2138	2422.1105	43
3	300.1918	150.5995			282.1812	141.5942	V	4774.1923	2387.5998	4757.1658	2379.0865	4756.1818	2378.5945	42
4	415.2187	208.1130			397.2082	199.1077	D	4675.1239	2338.0656	4658.0974	2329.5523	4657.1134	2329.0603	41
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	K	4560.0970	2280.5521	4543.0704	2272.0389	4542.0864	2271.5469	40
6	**658.3406**	329.6740	641.3141	321.1607	640.3301	320.6687	D	4432.0020	2216.5047	4414.9755	2207.9914	4413.9915	2207.4994	39
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	Q	4316.9751	2158.9912	4299.9485	2150.4779	4298.9645	2149.9859	38
8	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	Y	4188.9165	2094.9619	4171.8900	2086.4486	4170.9059	2085.9566	37
9	**1048.5310**	**524.7691**	1031.5044	516.2558	1030.5204	515.7638	V	4025.8532	2013.4302	4008.8266	2004.9170	4007.8426	2004.4249	36
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	E	3926.7848	1963.8960	3909.7582	1955.3827	3908.7742	1954.8907	35
11	1274.6263	**637.8168**	1257.5998	629.3035	1256.6157	628.8115	P	3797.7422	1899.3747	3780.7156	1890.8614	3779.7316	1890.3694	34
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	3700.6894	1850.8483	3683.6629	1842.3351	3682.6788	1841.8431	33
13	1517.7118	759.3596	1500.6853	750.8463	1499.7013	750.3543	N	3571.6468	1786.3270	3554.6203	1777.8138	3553.6362	1777.3218	32
14	1616.7802	808.8938	1599.7537	800.3805	1598.7697	799.8885	V	3457.6039	1729.3056	3440.5773	1720.7923	3439.5933	1720.3003	31
15	1717.8279	859.4176	1700.8014	850.9043	1699.8174	850.4123	T	3358.5355	1679.7714	3341.5089	1671.2581	3340.5249	1670.7661	30
16	**1830.9120**	915.9596	1813.8854	907.4464	1812.9014	906.9543	I	3257.4878	1629.2475	3240.4612	1620.7343	3239.4772	1620.2423	29
17	1958.9706	**979.9889**	1941.9440	971.4756	1940.9600	970.9836	Q	3144.4037	1572.7055	3127.3772	1564.1922	3126.3932	1563.7002	28
18	2119.0012	1060.0042	2101.9747	1051.4910	2100.9906	1050.9990	C	3016.3452	1508.6762	2999.3186	1500.1629	2998.3346	1499.6709	27
19	2234.0282	1117.5177	2217.0016	1109.0044	2216.0176	1108.5124	D	2856.3145	1428.6609	2839.2880	1420.1476	2838.3039	1419.6556	26
20	2321.0602	1161.0337	2304.0336	1152.5205	2303.0496	1152.0284	S	2741.2876	1371.1474	2724.2610	1362.6341	2723.2770	1362.1421	25
21	2378.0816	**1189.5445**	2361.0551	1181.0312	2360.0711	1180.5392	G	2654.2555	1327.6314	2637.2290	1319.1181	2636.2450	1318.6261	24
22	2541.1450	1271.0761	2524.1184	1262.5629	2523.1344	1262.0708	Y	2597.2341	1299.1207	2580.2075	1290.6074	2579.2235	1290.1154	23

23	2598.1664	**1299.5869**	2581.1399	1291.0736	2580.1559	1290.5816	**G**	2434.1707	1217.5890	2417.1442	1209.0757	2416.1602	1208.5837	**22**
24	2697.2349	1349.1211	2680.2083	1340.6078	2679.2243	1340.1158	**V**	2377.1493	1189.0783	2360.1227	1180.5650	2359.1387	1180.0730	**21**
25	2796.3033	1398.6553	2779.2767	1390.1420	2778.2927	1389.6500	**V**	2278.0809	1139.5441	2261.0543	1131.0308	2260.0703	1130.5388	**20**
26	2853.3247	1427.1660	2836.2982	1418.6527	2835.3142	1418.1607	**G**	2179.0124	1090.0099	2161.9859	1081.4966	2161.0019	1081.0046	**19**
27	2950.3775	1475.6924	2933.3509	1467.1791	2932.3669	1466.6871	**P**	2121.9910	1061.4991	2104.9644	1052.9859	2103.9804	1052.4938	**18**
28	3079.4201	1540.2137	3062.3935	1531.7004	3061.4095	1531.2084	**Q**	2024.9382	1012.9727	2007.9117	1004.4595	2006.9277	1003.9675	**17**
29	3166.4521	1583.7297	3149.4256	1575.2164	3148.4416	1574.7244	**S**	1895.8956	948.4515	1878.8691	939.9382	1877.8851	939.4462	**16**
30	3279.5362	1640.2717	3262.5096	1631.7585	3261.5256	1631.2664	**I**	1808.8636	904.9354	1791.8370	896.4222	1790.8530	895.9302	**15**
31	3380.5839	1690.7956	3363.5573	1682.2823	3362.5733	1681.7903	**T**	1695.7795	848.3934	1678.7530	839.8801	1677.7690	839.3881	**14**
32	3540.6145	1770.8109	3523.5880	1762.2976	3522.6039	1761.8056	**C**	1594.7319	797.8696	1577.7053	789.3563	1576.7213	788.8643	**13**
33	3627.6465	1814.3269	3610.6200	1805.8136	3609.6360	1805.3216	**S**	1434.7012	717.8542	1417.6747	709.3410	1416.6906	708.8490	**12**
34	3684.6680	1842.8376	3667.6415	1834.3244	3666.6574	1833.8324	**G**	1347.6692	674.3382	1330.6426	665.8250	1329.6586	665.3329	**11**
35	3799.6949	**1900.3511**	3782.6684	1891.8378	3781.6844	1891.3458	**N**	1290.6477	645.8275	1273.6212	637.3142	1272.6371	636.8222	**10**
36	3955.7961	1978.4017	3938.7695	1969.8884	3937.7855	1969.3964	**R**	1175.6208	588.3140	1158.5942	579.8007	1157.6102	579.3087	**9**
37	4056.8437	2028.9255	4039.8172	2020.4122	4038.8332	2019.9202	**T**	1019.5197	510.2635	1002.4931	501.7502	1001.5091	501.2582	**8**
38	4242.9230	2121.9652	4225.8965	2113.4519	4224.9125	2112.9599	**W**	918.4720	459.7396	901.4454	451.2264	900.4614	450.7343	**7**
39	4405.9864	2203.4968	4388.9598	2194.9836	4387.9758	2194.4915	**Y**	732.3927	366.7000	715.3661	358.1867	714.3821	357.6947	**6**
40	4503.0391	2252.0232	4486.0126	2243.5099	4485.0286	2243.0179	**P**	569.3293	285.1683	552.3028	276.6550	551.3188	276.1630	**5**
41	4632.0817	2316.5445	4615.0552	2308.0312	4614.0712	2307.5392	**E**	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	**4**
42	4731.1501	2366.0787	4714.1236	2357.5654	4713.1396	2357.0734	**V**	343.2340	172.1206	326.2074	163.6074			**3**
43	4828.2029	2414.6051	4811.1764	2406.0918	4810.1923	2405.5998	**P**	244.1656	122.5864	227.1390	114.0731			**2**
44							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.4	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated Q28, N35 94.47%
71.4	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated Q17, N35 2.41%
68.8	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated Q17, Q28 1.33%
67.4	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated N13, N35 0.96%
64.8	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated N13, Q28 0.53%
60.6	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated N13, Q17 0.20%
57.8	4972.3172	1.0058	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	
55.7	4973.3012	0.0218	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	Deamidated Q7, N35 0.06%
51.9	4972.3172	1.0058	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	
50.6	4972.3172	1.0058	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNRTWYPEVPK	

Mascot: http://www.matrixscience.com/

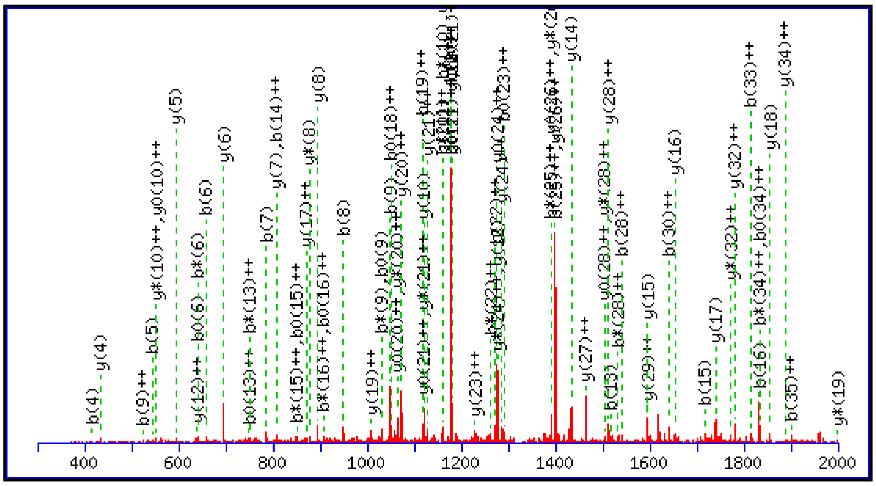
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28228: 3972.815832 from(1325.279220,3+) intensity(12761.7080) rtinseconds(1604) scans(3995) index(5284)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum3489_scans__3995
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

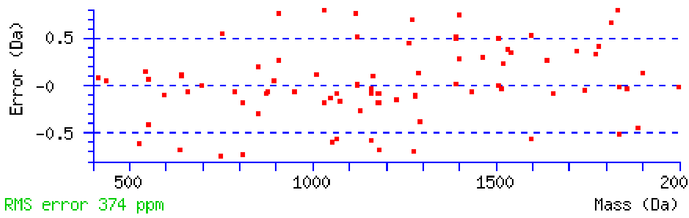
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

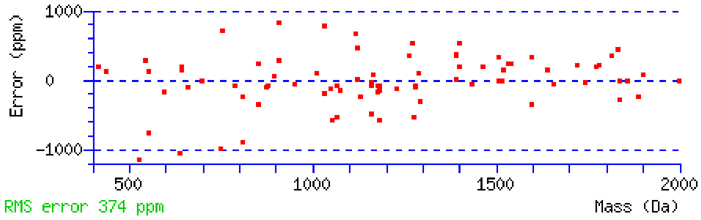


Monoisotopic mass of neutral peptide Mr(calc): 3972.7994
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q28 : Deamidated (NQ)
N35 : Deamidated (NQ)
Ions Score: 80 **Expect:** 1.5e-006
Matches : 84/404 fragment ions using 133 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3860.7226	1930.8649	3843.6960	1922.3516	3842.7120	1921.8596	35
3	300.1918	150.5995			282.1812	141.5942	V	3773.6905	1887.3489	3756.6640	1878.8356	3755.6800	1878.3436	34
4	**415.2187**	208.1130			397.2082	199.1077	D	3674.6221	1837.8147	3657.5956	1829.3014	3656.6116	1828.8094	33
5	**543.3137**	272.1605	526.2871	263.6472	525.3031	263.1552	K	3559.5952	1780.3012	3542.5686	1771.7879	3541.5846	1771.2959	32
6	**658.3406**	329.6740	641.3141	321.1607	640.3301	320.6687	D	3431.5002	1716.2537	3414.4737	1707.7405	3413.4896	1707.2485	31
7	**786.3992**	393.7032	769.3727	385.1900	768.3886	384.6980	Q	3316.4733	1658.7403	3299.4467	1650.2270	3298.4627	1649.7350	30
8	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3188.4147	1594.7110	3171.3881	1586.1977	3170.4041	1585.7057	29
9	**1048.5310**	**524.7691**	1031.5044	516.2558	1030.5204	515.7638	V	3025.3514	1513.1793	3008.3248	1504.6660	3007.3408	1504.1740	28
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	E	2926.2829	1463.6451	2909.2564	1455.1318	2908.2724	1454.6398	27
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	P	2797.2404	1399.1238	2780.2138	1390.6105	2779.2298	1390.1185	26
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	2700.1876	1350.5974	2683.1610	1342.0842	2682.1770	1341.5921	25
13	**1517.7118**	759.3596	1500.6853	750.8463	1499.7013	750.3543	N	2571.1450	1286.0761	2554.1184	1277.5629	2553.1344	1277.0709	24
14	1616.7802	**808.8938**	1599.7537	800.3805	1598.7697	799.8885	V	2457.1021	1229.0547	2440.0755	1220.5414	2439.0915	1220.0494	23
15	**1717.8279**	859.4176	1700.8014	850.9043	1699.8174	850.4123	T	2358.0337	1179.5205	2341.0071	1171.0072	2340.0231	1170.5152	22
16	**1830.9120**	915.9596	1813.8854	907.4464	1812.9014	906.9543	I	2256.9860	1128.9966	2239.9594	1120.4834	2238.9754	1119.9913	21
17	1958.9706	979.9889	1941.9440	971.4756	1940.9600	970.9836	Q	2143.9019	1072.4546	2126.8754	1063.9413	2125.8913	1063.4493	20
18	2119.0012	1060.0042	2101.9747	1051.4910	2100.9906	1050.9990	C	2015.8433	1008.4253	1998.8168	999.9120	1997.8328	999.4200	19
19	2234.0282	**1117.5177**	2217.0016	1109.0044	2216.0176	1108.5124	D	***1855.8127***	928.4100	1838.7861	919.8967	1837.8021	919.4047	18
20	2321.0602	**1161.0337**	2304.0336	1152.5205	2303.0496	1152.0284	S	***1740.7857***	870.8965	1723.7592	862.3832	1722.7752	861.8912	17
21	2378.0816	1189.5445	2361.0551	1181.0312	2360.0711	1180.5392	G	***1653.7537***	827.3805	1636.7272	818.8672	1635.7431	818.3752	16
22	2541.1450	**1271.0761**	2524.1184	1262.5629	2523.1344	1262.0708	Y	***1596.7322***	798.8698	1579.7057	790.3565	1578.7217	789.8645	15

23	2598.1664	1299.5869	2581.1399	1291.0736	2580.1559	1290.5816	**G**	***1433.6689***	717.3381	1416.6424	708.8248	1415.6584	708.3328	**14**
24	2697.2349	1349.1211	2680.2083	1340.6078	2679.2243	1340.1158	**V**	1376.6475	688.8274	1359.6209	680.3141	1358.6369	679.8221	**13**
25	2796.3033	**1398.6553**	2779.2767	1390.1420	2778.2927	1389.6500	**V**	***1277.5790***	639.2932	1260.5525	630.7799	1259.5685	630.2879	**12**
26	2853.3247	1427.1660	2836.2982	1418.6527	2835.3142	1418.1607	**G**	***1178.5106***	589.7590	1161.4841	581.2457	1160.5001	580.7537	**11**
27	2950.3775	1475.6924	2933.3509	1467.1791	2932.3669	1466.6871	**P**	***1121.4892***	561.2482	1104.4626	552.7349	1103.4786	552.2429	**10**
28	3079.4201	**1540.2137**	3062.3935	1531.7004	3061.4095	1531.2084	**Q**	1024.4364	512.7218	1007.4099	504.2086	1006.4258	503.7166	**9**
29	3166.4521	1583.7297	3149.4256	1575.2164	3148.4416	1574.7244	**S**	***895.3938***	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3279.5362	**1640.2717**	3262.5096	1631.7585	3261.5256	1631.2664	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3380.5839	1690.7956	3363.5573	1682.2823	3362.5733	1681.7903	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3540.6145	1770.8109	3523.5880	1762.2976	3522.6039	1761.8056	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3627.6465	**1814.3269**	3610.6200	1805.8136	3609.6360	1805.3216	**S**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3684.6680	1842.8376	3667.6415	1834.3244	3666.6574	1833.8324	**G**	347.1674	174.0873	330.1408	165.5740			**3**
35	3799.6949	**1900.3511**	3782.6684	1891.8378	3781.6844	1891.3458	**N**	290.1459	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.1	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q28, N35 52.29%
76.6	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, N35 23.20%
74.2	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, N35 13.44%
73.0	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N35 10.20%
63.3	3971.8154	1.0005	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
57.5	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28 0.28%
56.4	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, Q28 0.22%
55.8	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28 0.19%
52.3	3971.8154	1.0005	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
51.1	3972.7994	0.0165	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17 0.07%

Mascot: http://www.matrixscience.com/

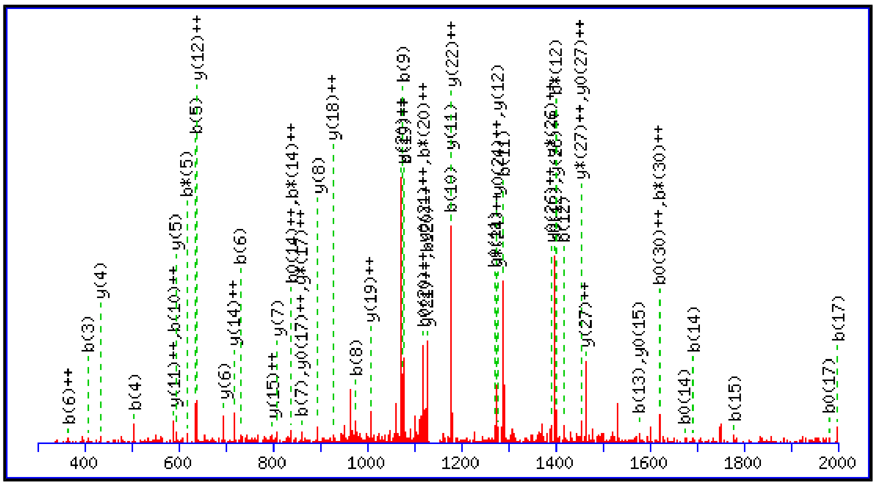
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 27716: 3430.503822 from(1144.508550,3+) intensity(6541.9609) rtinseconds(1740) scans(4263) index(7090)
Title: 111019_Est_ISCardio_NMI_YP_G_10Spectrum3708_scans__4263
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

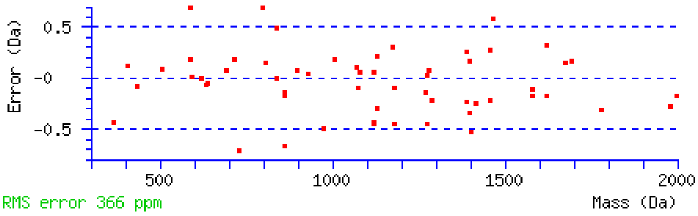
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

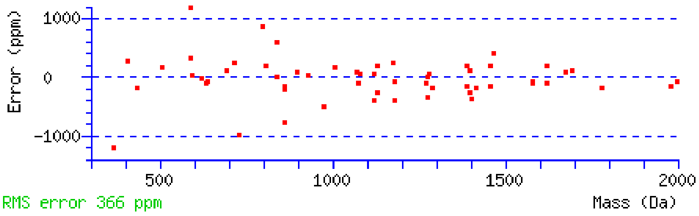


Monoisotopic mass of neutral peptide Mr(calc): 3430.4929
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
N30 : Deamidated (NQ)
Ions Score: 78 **Expect:** 1.8e-006
Matches : 58/352 fragment ions using 85 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							31
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	3316.4733	1658.7403	3299.4467	1650.2270	3298.4627	1649.7350	30
3	***407.1561***	204.0817	390.1296	195.5684	389.1456	195.0764	Y	3188.4147	1594.7110	3171.3881	1586.1977	3170.4041	1585.7057	29
4	***506.2245***	253.6159	489.1980	245.1026	488.2140	244.6106	V	3025.3514	1513.1793	3008.3248	1504.6660	3007.3408	1504.1740	28
5	***635.2671***	318.1372	618.2406	309.6239	617.2566	309.1319	E	2926.2829	1463.6451	2909.2564	1455.1318	2908.2724	1454.6398	27
6	***732.3199***	**366.6636**	715.2933	358.1503	714.3093	357.6583	P	2797.2404	1399.1238	2780.2138	1390.6105	2779.2298	1390.1185	26
7	***861.3625***	431.1849	844.3359	422.6716	843.3519	422.1796	E	2700.1876	1350.5974	2683.1610	1342.0842	2682.1770	1341.5921	25
8	***976.3894***	488.6984	959.3629	480.1851	958.3789	479.6931	N	2571.1450	1286.0761	2554.1184	1277.5629	2553.1344	1277.0709	24
9	***1075.4578***	538.2326	1058.4313	529.7193	1057.4473	529.2273	V	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	23
10	***1176.5055***	**588.7564**	1159.4790	580.2431	1158.4950	579.7511	T	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	22
11	***1289.5896***	645.2984	1272.5630	636.7852	1271.5790	636.2932	I	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	21
12	***1417.6482***	709.3277	1400.6216	700.8144	1399.6376	700.3224	Q	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	20
13	***1577.6788***	789.3430	1560.6523	780.8298	1559.6683	780.3378	C	2014.8593	1007.9333	1997.8328	999.4200	1996.8488	998.9280	19
14	***1692.7058***	846.8565	1675.6792	838.3432	1674.6952	837.8512	D	1854.8287	927.9180	1837.8021	919.4047	1836.8181	918.9127	18
15	***1779.7378***	890.3725	1762.7112	881.8593	1761.7272	881.3672	S	1739.8017	870.4045	1722.7752	861.8912	1721.7912	861.3992	17
16	1836.7593	918.8833	1819.7327	910.3700	1818.7487	909.8780	G	1652.7697	826.8885	1635.7431	818.3752	1634.7591	817.8832	16
17	***1999.8226***	1000.4149	1982.7960	991.9017	1981.8120	991.4096	Y	1595.7482	798.3778	1578.7217	789.8645	1577.7377	789.3725	15
18	2056.8440	1028.9257	2039.8175	1020.4124	2038.8335	1019.9204	G	1432.6849	716.8461	1415.6584	708.3328	1414.6743	707.8408	14
19	2155.9125	**1078.4599**	2138.8859	1069.9466	2137.9019	1069.4546	V	1375.6634	688.3354	1358.6369	679.8221	1357.6529	679.3301	13
20	2254.9809	**1127.9941**	2237.9544	1119.4808	2236.9703	1118.9888	V	***1276.5950***	638.8012	1259.5685	630.2879	1258.5845	629.7959	12
21	2312.0023	1156.5048	2294.9758	1147.9915	2293.9918	1147.4995	G	***1177.5266***	589.2669	1160.5001	580.7537	1159.5160	580.2617	11
22	2409.0551	1205.0312	2392.0286	1196.5179	2391.0445	1196.0259	P	1120.5051	560.7562	1103.4786	552.2429	1102.4946	551.7509	10

23	2537.1137	1269.0605	2520.0871	1260.5472	2519.1031	1260.0552	**Q**	1023.4524	512.2298	1006.4258	503.7166	1005.4418	503.2245	**9**
24	2624.1457	1312.5765	2607.1192	1304.0632	2606.1351	1303.5712	**S**	***895.3938***	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
25	2737.2298	1369.1185	2720.2032	1360.6052	2719.2192	1360.1132	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
26	2838.2774	1419.6424	2821.2509	1411.1291	2820.2669	1410.6371	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
27	2998.3081	1499.6577	2981.2815	1491.1444	2980.2975	1490.6524	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
28	3085.3401	1543.1737	3068.3136	1534.6604	3067.3296	1534.1684	**S**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
29	3142.3616	1571.6844	3125.3350	1563.1712	3124.3510	1562.6792	**G**	347.1674	174.0873	330.1408	165.5740			**3**
30	3257.3885	1629.1979	3240.3620	1620.6846	3239.3780	1620.1926	**N**	290.1459	145.5766	273.1193	137.0633			**2**
31							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.7	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N8, N30 96.14%
61.7	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q12, N30 2.40%
57.0	3429.5089	0.9949	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
55.6	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N8, Q23 0.59%
53.9	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q2, N30 0.40%
52.8	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q23, N30 0.31%
49.9	3429.5089	0.9949	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
48.5	3430.4929	0.0109	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q12, Q23 0.12%
41.7	3429.5089	0.9949	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
39.9	3429.5089	0.9949	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	

Mascot: http://www.matrixscience.com/

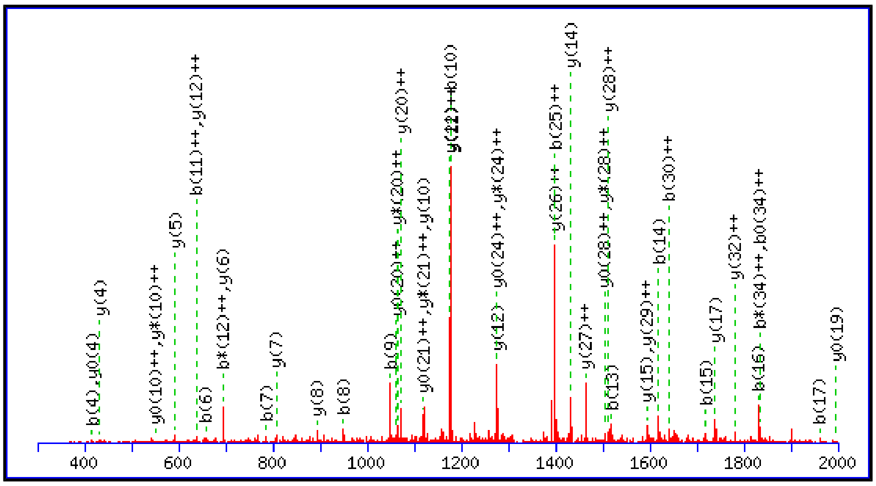
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28253: 3973.836762 from(1325.619530,3+) intensity(17220.0371) rtinseconds(1664) scans(4158) index(3816)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum3414_scans__4158
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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Monoisotopic mass of neutral peptide Mr(calc): 3971.8154
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13     : Deamidated (NQ)
Ions Score: 75  Expect: 5.3e-006
Matches : 48/404 fragment ions using 68 most intense peaks   (help)
```
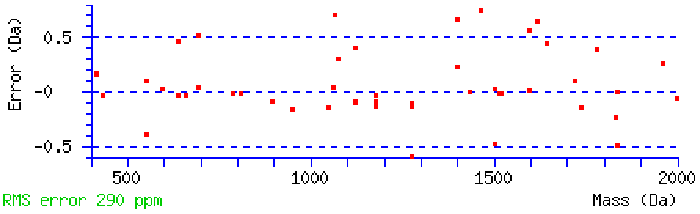
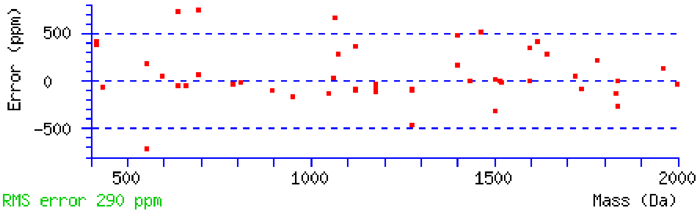

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3859.7385	1930.3729	3842.7120	1921.8596	3841.7280	1921.3676	35
3	300.1918	150.5995			282.1812	141.5942	V	3772.7065	1886.8569	3755.6800	1878.3436	3754.6959	1877.8516	34
4	***415.2187***	208.1130			397.2082	199.1077	D	3673.6381	1837.3227	3656.6116	1828.8094	3655.6275	1828.3174	33
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	K	3558.6112	1779.8092	3541.5846	1771.2959	3540.6006	1770.8039	32
6	***658.3406***	329.6740	641.3141	321.1607	640.3301	320.6687	D	3430.5162	1715.7617	3413.4896	1707.2485	3412.5056	1706.7565	31
7	***786.3992***	393.7032	769.3727	385.1900	768.3886	384.6980	Q	3315.4893	1658.2483	3298.4627	1649.7350	3297.4787	1649.2430	30
8	***949.4625***	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3187.4307	1594.2190	3170.4041	1585.7057	3169.4201	1585.2137	29
9	***1048.5310***	524.7691	1031.5044	516.2558	1030.5204	515.7638	V	3024.3673	1512.6873	3007.3408	1504.1740	3006.3568	1503.6820	28
10	***1177.5735***	589.2904	1160.5470	580.7771	1159.5630	580.2851	E	2925.2989	1463.1531	2908.2724	1454.6398	2907.2884	1454.1478	27
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	P	2796.2563	1398.6318	2779.2298	1390.1185	2778.2458	1389.6265	26
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	2699.2036	1350.1054	2682.1770	1341.5921	2681.1930	1341.1001	25
13	***1518.6958***	759.8516	1501.6693	751.3383	1500.6853	750.8463	N	2570.1610	1285.5841	2553.1344	1277.0709	2552.1504	1276.5788	24
14	***1617.7643***	809.3858	1600.7377	800.8725	1599.7537	800.3805	V	2455.1340	1228.0707	2438.1075	1219.5574	2437.1235	1219.0654	23
15	***1718.8119***	859.9096	1701.7854	851.3963	1700.8014	850.9043	T	2356.0656	1178.5364	2339.0391	1170.0232	2338.0551	1169.5312	22
16	***1831.8960***	916.4516	1814.8695	907.9384	1813.8854	907.4464	I	2255.0179	1128.0126	2237.9914	1119.4993	2237.0074	1119.0073	21
17	***1959.9546***	980.4809	1942.9280	971.9677	1941.9440	971.4756	Q	2141.9339	1071.4706	2124.9073	1062.9573	2123.9233	1062.4653	20
18	2119.9852	1060.4963	2102.9587	1051.9830	2101.9747	1051.4910	C	2013.8753	1007.4413	1996.8488	998.9280	1995.8647	998.4360	19
19	2235.0122	1118.0097	2217.9856	1109.4964	2217.0016	1109.0044	D	1853.8447	927.4260	1836.8181	918.9127	1835.8341	918.4207	18
20	2322.0442	1161.5257	2305.0177	1153.0125	2304.0336	1152.5205	S	***1738.8177***	869.9125	1721.7912	861.3992	1720.8071	860.9072	17
21	2379.0657	1190.0365	2362.0391	1181.5232	2361.0551	1181.0312	G	1651.7857	826.3965	1634.7591	817.8832	1633.7751	817.3912	16
22	2542.1290	1271.5681	2525.1024	1263.0549	2524.1184	1262.5629	Y	***1594.7642***	797.8857	1577.7377	789.3725	1576.7537	788.8805	15
23	2599.1505	1300.0789	2582.1239	1291.5656	2581.1399	1291.0736	G	***1431.7009***	716.3541	1414.6743	707.8408	1413.6903	707.3488	14

24	2698.2189	1349.6131	2681.1923	1341.0998	2680.2083	1340.6078	**V**	1374.6794	687.8434	1357.6529	679.3301	1356.6689	678.8381	**13**
25	2797.2873	1399.1473	2780.2607	1390.6340	2779.2767	1390.1420	**V**	***1275.6110***	638.3091	1258.5845	629.7959	1257.6004	629.3039	**12**
26	2854.3087	1427.6580	2837.2822	1419.1447	2836.2982	1418.6527	**G**	***1176.5426***	588.7749	1159.5160	580.2617	1158.5320	579.7697	**11**
27	2951.3615	1476.1844	2934.3350	1467.6711	2933.3509	1467.1791	**P**	***1119.5211***	560.2642	1102.4946	551.7509	1101.5106	551.2589	**10**
28	3079.4201	1540.2137	3062.3935	1531.7004	3061.4095	1531.2084	**Q**	1022.4684	511.7378	1005.4418	503.2245	1004.4578	502.7325	**9**
29	3166.4521	1583.7297	3149.4256	1575.2164	3148.4416	1574.7244	**S**	***894.4098***	447.7085	877.3832	439.1953	876.3992	438.7033	**8**
30	3279.5362	1640.2717	3262.5096	1631.7585	3261.5256	1631.2664	**I**	***807.3778***	404.1925	790.3512	395.6792	789.3672	395.1872	**7**
31	3380.5839	1690.7956	3363.5573	1682.2823	3362.5733	1681.7903	**T**	***694.2937***	347.6505	677.2671	339.1372	676.2831	338.6452	**6**
32	3540.6145	1770.8109	3523.5880	1762.2976	3522.6039	1761.8056	**C**	***593.2460***	297.1266	576.2195	288.6134	575.2355	288.1214	**5**
33	3627.6465	1814.3269	3610.6200	1805.8136	3609.6360	1805.3216	**S**	***433.2154***	217.1113	416.1888	208.5980	415.2048	208.1060	**4**
34	3684.6680	1842.8376	3667.6415	1834.3244	3666.6574	1833.8324	**G**	346.1833	173.5953	329.1568	165.0820			**3**
35	3798.7109	1899.8591	3781.6844	1891.3458	3780.7004	1890.8538	**N**	289.1619	145.0846	272.1353	136.5713			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.2	3971.8154	2.0214	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13 85.29%
64.4	3971.8154	2.0214	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7 7.21%
63.5	3971.8154	2.0214	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17 5.79%
57.6	3971.8154	2.0214	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q28 1.49%
49.4	3971.8154	2.0214	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N35 0.23%
6.2	3973.8437	-0.0069	VETPEGEVMSPRQQKWMHSLPNDWIMENPVLHR	
3.9	3971.8451	1.9917	YTAGTPYKVPPTQSNTAPPPYSPSPNPYQTAMYPIR	
3.4	3972.8420	0.9948	NGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAFQ	
3.3	3973.8475	-0.0108	TYWQFLSGVTPLNEGVADYIPFNHEHITANFTQY	
2.8	3973.8475	-0.0108	TYWQFLSGVTPLNEGVADYIPFNHEHITANFTQY	

Mascot: http://www.matrixscience.com/

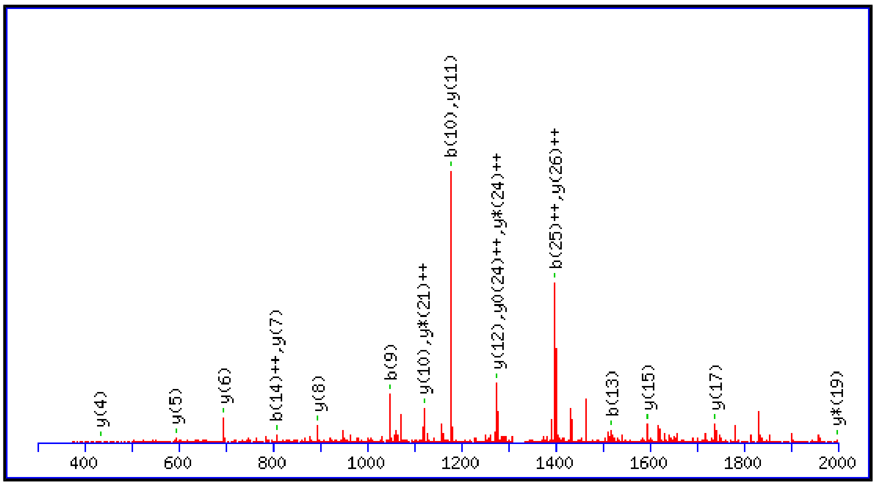
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28249: 3972.835092 from(1325.285640,3+) intensity(0.0000) rtinseconds(1608) scans(4098) index(15844)
Title: 111019_Est_MI_YP_G_05Spectrum3491_scans__4098
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

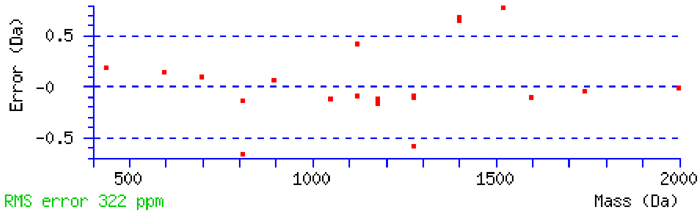
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

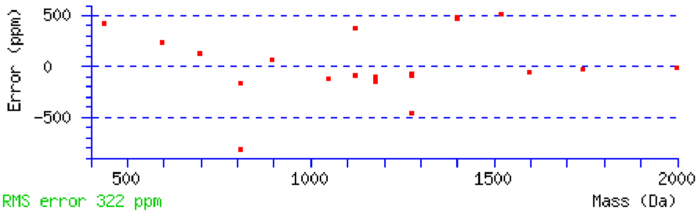


Monoisotopic mass of neutral peptide Mr(calc): 3971.8154
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N35 : Deamidated (NQ)
Ions Score: 69 **Expect:** 2.1e-005
Matches : 20/404 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3859.7385	1930.3729	3842.7120	1921.8596	3841.7280	1921.3676	35
3	300.1918	150.5995			282.1812	141.5942	V	3772.7065	1886.8569	3755.6800	1878.3436	3754.6959	1877.8516	34
4	415.2187	208.1130			397.2082	199.1077	D	3673.6381	1837.3227	3656.6116	1828.8094	3655.6275	1828.3174	33
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	K	3558.6112	1779.8092	3541.5846	1771.2959	3540.6006	1770.8039	32
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	D	3430.5162	1715.7617	3413.4896	1707.2485	3412.5056	1706.7565	31
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	Q	3315.4893	1658.2483	3298.4627	1649.7350	3297.4787	1649.2430	30
8	949.4625	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3187.4307	1594.2190	3170.4041	1585.7057	3169.4201	1585.2137	29
9	**1048.5310**	524.7691	1031.5044	516.2558	1030.5204	515.7638	V	3024.3673	1512.6873	3007.3408	1504.1740	3006.3568	1503.6820	28
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	E	2925.2989	1463.1531	2908.2724	1454.6398	2907.2884	1454.1478	27
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	P	2796.2563	1398.6318	2779.2298	1390.1185	2778.2458	1389.6265	26
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	2699.2036	1350.1054	2682.1770	1341.5921	2681.1930	1341.1001	25
13	**1517.7118**	759.3596	1500.6853	750.8463	1499.7013	750.3543	N	2570.1610	1285.5841	2553.1344	1277.0709	2552.1504	1276.5788	24
14	1616.7802	**808.8938**	1599.7537	800.3805	1598.7697	799.8885	V	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	23
15	1717.8279	859.4176	1700.8014	850.9043	1699.8174	850.4123	T	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	22
16	1830.9120	915.9596	1813.8854	907.4464	1812.9014	906.9543	I	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	21
17	1958.9706	979.9889	1941.9440	971.4756	1940.9600	970.9836	Q	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	20
18	2119.0012	1060.0042	2101.9747	1051.4910	2100.9906	1050.9990	C	2014.8593	1007.9333	1997.8328	999.4200	1996.8488	998.9280	19
19	2234.0282	1117.5177	2217.0016	1109.0044	2216.0176	1108.5124	D	1854.8287	927.9180	1837.8021	919.4047	1836.8181	918.9127	18
20	2321.0602	1161.0337	2304.0336	1152.5205	2303.0496	1152.0284	S	***1739.8017***	870.4045	1722.7752	861.8912	1721.7912	861.3992	17
21	2378.0816	1189.5445	2361.0551	1181.0312	2360.0711	1180.5392	G	1652.7697	826.8885	1635.7431	818.3752	1634.7591	817.8832	16
22	2541.1450	1271.0761	2524.1184	1262.5629	2523.1344	1262.0708	Y	***1595.7482***	798.3778	1578.7217	789.8645	1577.7377	789.3725	15
23	2598.1664	1299.5869	2581.1399	1291.0736	2580.1559	1290.5816	G	1432.6849	716.8461	1415.6584	708.3328	1414.6743	707.8408	14

24	2697.2349	1349.1211	2680.2083	1340.6078	2679.2243	1340.1158	**V**	1375.6634	688.3354	1358.6369	679.8221	1357.6529	679.3301	**13**
25	2796.3033	**1398.6553**	2779.2767	1390.1420	2778.2927	1389.6500	**V**	***1276.5950***	638.8012	1259.5685	630.2879	1258.5845	629.7959	**12**
26	2853.3247	1427.1660	2836.2982	1418.6527	2835.3142	1418.1607	**G**	***1177.5266***	589.2669	1160.5001	580.7537	1159.5160	580.2617	**11**
27	2950.3775	1475.6924	2933.3509	1467.1791	2932.3669	1466.6871	**P**	***1120.5051***	560.7562	1103.4786	552.2429	1102.4946	551.7509	**10**
28	3078.4361	1539.7217	3061.4095	1531.2084	3060.4255	1530.7164	**Q**	1023.4524	512.2298	1006.4258	503.7166	1005.4418	503.2245	**9**
29	3165.4681	1583.2377	3148.4416	1574.7244	3147.4575	1574.2324	**S**	***895.3938***	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3278.5522	1639.7797	3261.5256	1631.2664	3260.5416	1630.7744	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3379.5998	1690.3036	3362.5733	1681.7903	3361.5893	1681.2983	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3539.6305	1770.3189	3522.6039	1761.8056	3521.6199	1761.3136	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3626.6625	1813.8349	3609.6360	1805.3216	3608.6520	1804.8296	**S**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3683.6840	1842.3456	3666.6574	1833.8324	3665.6734	1833.3403	**G**	347.1674	174.0873	330.1408	165.5740			**3**
35	3798.7109	1899.8591	3781.6844	1891.3458	3780.7004	1890.8538	**N**	290.1459	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.3	3971.8154	1.0197	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N35 99.57%
44.6	3971.8154	1.0197	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q28 0.34%
36.3	3971.8154	1.0197	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13 0.05%
34.6	3971.8154	1.0197	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17 0.03%
14.8	3970.8313	2.0037	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
14.5	3971.8154	1.0197	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7 0.00%
9.9	3970.8282	2.0069	LGSDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYK	
9.9	3970.8282	2.0069	LGSDDFFYVGGSPSTADLPGSPVSNNFMGCLKEVVYK	
9.3	3972.8420	-0.0069	NGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAFQ	
7.6	3970.8126	2.0225	YQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDR	

Mascot: http://www.matrixscience.com/

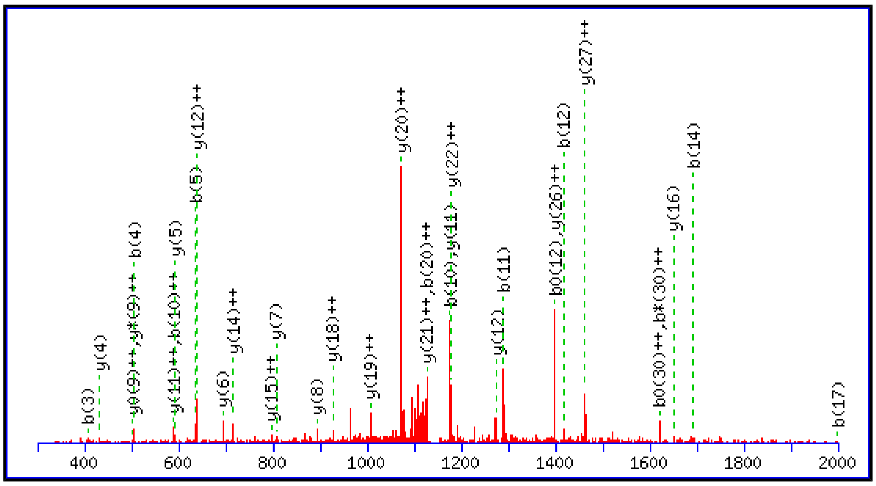
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 27715: 3429.515622 from(1144.179150,3+) intensity(17205.7773) rtinseconds(1655) scans(4134) index(3812)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum3394_scans__4134
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

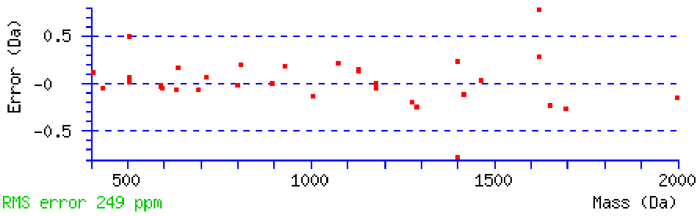
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

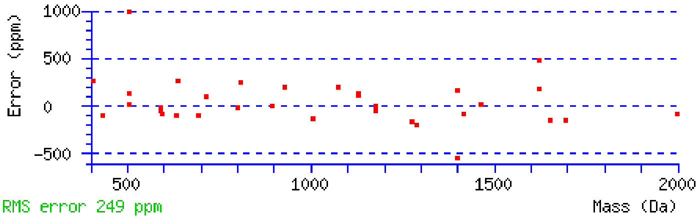


Monoisotopic mass of neutral peptide Mr(calc): 3429.5089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 66 **Expect:** 2.9e-005
Matches : 34/352 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**31**
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	**Q**	3315.4893	1658.2483	3298.4627	1649.7350	3297.4787	1649.2430	**30**
3	**407.1561**	204.0817	390.1296	195.5684	389.1456	195.0764	**Y**	3187.4307	1594.2190	3170.4041	1585.7057	3169.4201	1585.2137	**29**
4	**506.2245**	253.6159	489.1980	245.1026	488.2140	244.6106	**V**	3024.3673	1512.6873	3007.3408	1504.1740	3006.3568	1503.6820	**28**
5	**635.2671**	318.1372	618.2406	309.6239	617.2566	309.1319	**E**	2925.2989	1463.1531	2908.2724	1454.6398	2907.2884	1454.1478	**27**
6	732.3199	366.6636	715.2933	358.1503	714.3093	357.6583	**P**	2796.2563	1398.6318	2779.2298	1390.1185	2778.2458	1389.6265	**26**
7	861.3625	431.1849	844.3359	422.6716	843.3519	422.1796	**E**	2699.2036	1350.1054	2682.1770	1341.5921	2681.1930	1341.1001	**25**
8	976.3894	488.6984	959.3629	480.1851	958.3789	479.6931	**N**	2570.1610	1285.5841	2553.1344	1277.0709	2552.1504	1276.5788	**24**
9	1075.4578	538.2326	1058.4313	529.7193	1057.4473	529.2273	**V**	2455.1340	1228.0707	2438.1075	1219.5574	2437.1235	1219.0654	**23**
10	**1176.5055**	588.7564	1159.4790	580.2431	1158.4950	579.7511	**T**	2356.0656	1178.5364	2339.0391	1170.0232	2338.0551	1169.5312	**22**
11	**1289.5896**	645.2984	1272.5630	636.7852	1271.5790	636.2932	**I**	2255.0179	1128.0126	2237.9914	1119.4993	2237.0074	1119.0073	**21**
12	**1417.6482**	709.3277	1400.6216	700.8144	1399.6376	700.3224	**Q**	2141.9339	1071.4706	2124.9073	1062.9573	2123.9233	1062.4653	**20**
13	1577.6788	789.3430	1560.6523	780.8298	1559.6683	780.3378	**C**	2013.8753	1007.4413	1996.8488	998.9280	1995.8647	998.4360	**19**
14	**1692.7058**	846.8565	1675.6792	838.3432	1674.6952	837.8512	**D**	1853.8447	927.4260	1836.8181	918.9127	1835.8341	918.4207	**18**
15	1779.7378	890.3725	1762.7112	881.8593	1761.7272	881.3672	**S**	1738.8177	869.9125	1721.7912	861.3992	1720.8071	860.9072	**17**
16	1836.7593	918.8833	1819.7327	910.3700	1818.7487	909.8780	**G**	***1651.7857***	826.3965	1634.7591	817.8832	1633.7751	817.3912	**16**
17	**1999.8226**	1000.4149	1982.7960	991.9017	1981.8120	991.4096	**Y**	1594.7642	797.8857	1577.7377	789.3725	1576.7537	788.8805	**15**
18	2056.8440	1028.9257	2039.8175	1020.4124	2038.8335	1019.9204	**G**	1431.7009	716.3541	1414.6743	707.8408	1413.6903	707.3488	**14**
19	2155.9125	1078.4599	2138.8859	1069.9466	2137.9019	1069.4546	**V**	1374.6794	687.8434	1357.6529	679.3301	1356.6689	678.8381	**13**
20	2254.9809	1127.9941	2237.9543	1119.4808	2236.9703	1118.9888	**V**	***1275.6110***	638.3091	1258.5845	629.7959	1257.6004	629.3039	**12**
21	2312.0023	1156.5048	2294.9758	1147.9915	2293.9918	1147.4995	**G**	***1176.5426***	588.7749	1159.5160	580.2617	1158.5320	579.7697	**11**
22	2409.0551	1205.0312	2392.0286	1196.5179	2391.0445	1196.0259	**P**	1119.5211	560.2642	1102.4946	551.7509	1101.5106	551.2589	**10**
23	2537.1137	1269.0605	2520.0871	1260.5472	2519.1031	1260.0552	**Q**	1022.4684	511.7378	1005.4418	503.2245	1004.4578	502.7325	**9**

24	2624.1457	1312.5765	2607.1192	1304.0632	2606.1351	1303.5712	**S**	***894.4098***	447.7085	877.3832	439.1953	876.3992	438.7033	**8**
25	2737.2298	1369.1185	2720.2032	1360.6052	2719.2192	1360.1132	**I**	***807.3778***	404.1925	790.3512	395.6792	789.3672	395.1872	**7**
26	2838.2774	1419.6424	2821.2509	1411.1291	2820.2669	1410.6371	**T**	***694.2937***	347.6505	677.2671	339.1372	676.2831	338.6452	**6**
27	2998.3081	1499.6577	2981.2815	1491.1444	2980.2975	1490.6524	**C**	***593.2460***	297.1266	576.2195	288.6134	575.2355	288.1214	**5**
28	3085.3401	1543.1737	3068.3136	1534.6604	3067.3296	1534.1684	**S**	***433.2154***	217.1113	416.1888	208.5980	415.2048	208.1060	**4**
29	3142.3616	1571.6844	3125.3350	1563.1712	3124.3510	1562.6792	**G**	346.1833	173.5953	329.1568	165.0820			**3**
30	3256.4045	1628.7059	3239.3780	1620.1926	3238.3940	1619.7006	**N**	289.1619	145.0846	272.1353	136.5713			**2**
31							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
66.0	3429.5089	0.0067	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N8 48.18%
64.2	3429.5089	0.0067	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q12 31.90%
60.9	3429.5089	0.0067	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q2 14.96%
59.2	3428.5249	0.9907	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
55.8	3429.5089	0.0067	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q23 4.63%
44.3	3429.5089	0.0067	DQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N30 0.33%
15.0	3427.4982	2.0174	TGGTWTSWTFSWVPGMKMTSNCQMQTSGLK	
15.0	3427.4982	2.0174	TGGTWTSWTFSWVPGMKMTSNCQMQTSGLK	
14.5	3427.4982	2.0174	TGGTWTSWTFSWVPGMKMTSNCQMQTSGLK	
10.8	3427.4982	2.0174	TGGTWTSWTFSWVPGMKMTSNCQMQTSGLK	

Mascot: http://www.matrixscience.com/

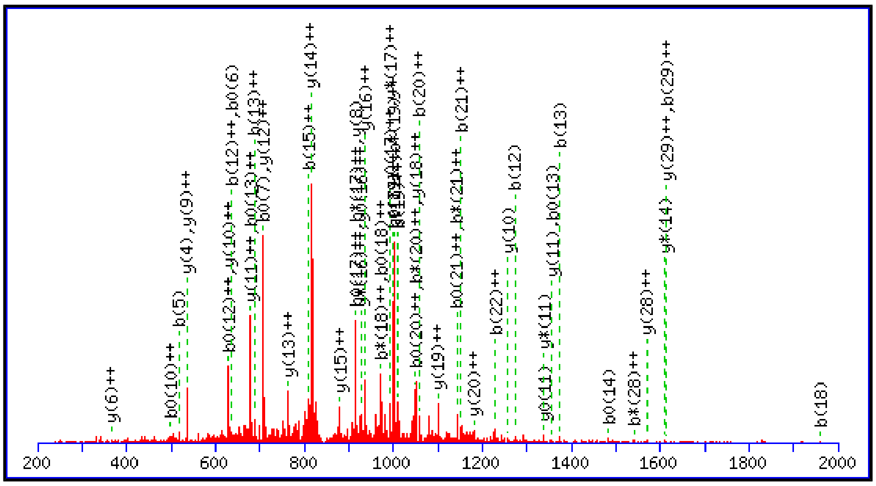
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSLLGHASISCTVENETIGVWRPSPPTCEK**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 27566: 3372.628736 from(844.164460,4+) intensity(24365.2656) rtinseconds(2224) scans(5373) index(16950)
Title: 111019_Est_MI_YP_G_06Spectrum4458_scans__5373
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

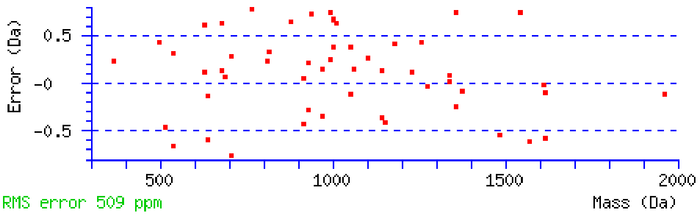
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

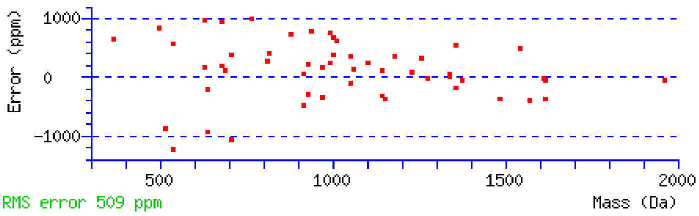


Monoisotopic mass of neutral peptide Mr(calc): 3372.6119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 62 **Expect:** 0.00018
Matches : 56/316 fragment ions using 99 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							30
2	235.1077	118.0575			217.0972	109.0522	S	3226.5507	1613.7790	3209.5242	1605.2657	3208.5402	1604.7737	29
3	348.1918	174.5995			330.1812	165.5942	L	3139.5187	1570.2630	3122.4921	1561.7497	3121.5081	1561.2577	28
4	461.2758	231.1416			443.2653	222.1363	L	3026.4346	1513.7210	3009.4081	1505.2077	3008.4241	1504.7157	27
5	**518.2973**	259.6523			500.2867	250.6470	G	2913.3506	1457.1789	2896.3240	1448.6656	2895.3400	1448.1736	26
6	655.3562	328.1817			637.3457	319.1765	H	2856.3291	1428.6682	2839.3026	1420.1549	2838.3185	1419.6629	25
7	726.3933	363.7003			708.3828	354.6950	A	2719.2702	1360.1387	2702.2436	1351.6255	2701.2596	1351.1335	24
8	813.4254	407.2163			795.4148	398.2110	S	2648.2331	1324.6202	2631.2065	1316.1069	2630.2225	1315.6149	23
9	926.5094	463.7584			908.4989	454.7531	I	2561.2011	1281.1042	2544.1745	1272.5909	2543.1905	1272.0989	22
10	1013.5415	507.2744			995.5309	498.2691	S	2448.1170	1224.5621	2431.0904	1216.0489	2430.1064	1215.5568	21
11	1173.5721	587.2897			1155.5615	578.2844	C	2361.0850	1181.0461	2344.0584	1172.5328	2343.0744	1172.0408	20
12	**1274.6198**	**637.8135**			1256.6092	628.8082	T	2201.0543	1101.0308	2184.0278	1092.5175	2183.0437	1092.0255	19
13	**1373.6882**	**687.3477**			1355.6776	678.3425	V	2100.0066	1050.5070	2082.9801	1041.9937	2081.9961	1041.5017	18
14	1502.7308	751.8690			1484.7202	742.8638	E	2000.9382	1000.9727	1983.9117	992.4595	1982.9277	991.9675	17
15	1617.7577	**809.3825**	1600.7312	800.8692	1599.7472	800.3772	N	1871.8956	936.4515	1854.8691	927.9382	1853.8851	927.4462	16
16	1746.8003	873.9038	1729.7738	865.3905	1728.7898	864.8985	E	1756.8687	878.9380	1739.8421	870.4247	1738.8581	869.9327	15
17	1847.8480	924.4276	1830.8215	915.9144	1829.8374	915.4224	T	1627.8261	814.4167	1610.7995	805.9034	1609.8155	805.4114	14
18	**1960.9321**	980.9697	1943.9055	972.4564	1942.9215	971.9644	I	1526.7784	763.8928	1509.7519	755.3796	1508.7678	754.8876	13
19	2017.9535	**1009.4804**	2000.9270	1000.9671	1999.9430	1000.4751	G	1413.6943	707.3508	1396.6678	698.8375	1395.6838	698.3455	12
20	2117.0219	**1059.0146**	2099.9954	1050.5013	2099.0114	1050.0093	V	**1356.6729**	678.8401	1339.6463	670.3268	1338.6623	669.8348	11
21	2303.1013	**1152.0543**	2286.0747	1143.5410	2285.0907	1143.0490	W	**1257.6045**	629.3059	1240.5779	620.7926	1239.5939	620.3006	10
22	2459.2024	**1230.1048**	2442.1758	1221.5915	2441.1918	1221.0995	R	1071.5252	536.2662	1054.4986	527.7529	1053.5146	527.2609	9
23	2556.2551	1278.6312	2539.2286	1270.1179	2538.2446	1269.6259	P	**915.4240**	458.2157	898.3975	449.7024	897.4135	449.2104	8

24	2643.2872	1322.1472	2626.2606	1313.6339	2625.2766	1313.1419	**S**	818.3713	409.6893	801.3447	401.1760	800.3607	400.6840	**7**
25	2740.3399	1370.6736	2723.3134	1362.1603	2722.3294	1361.6683	**P**	731.3393	366.1733	714.3127	357.6600	713.3287	357.1680	**6**
26	2837.3927	1419.2000	2820.3661	1410.6867	2819.3821	1410.1947	**P**	634.2865	317.6469	617.2599	309.1336	616.2759	308.6416	**5**
27	2938.4404	1469.7238	2921.4138	1461.2105	2920.4298	1460.7185	**T**	**537.2337**	269.1205	520.2072	260.6072	519.2232	260.1152	**4**
28	3098.4710	1549.7391	3081.4445	1541.2259	3080.4605	1540.7339	**C**	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	**3**
29	3227.5136	**1614.2604**	3210.4871	1605.7472	3209.5030	1605.2552	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
30							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of FSLLGHASISCTVENETIGVWRPSPPTCEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.9	3372.6119	0.0169	FSLLGHASISCTVENETIGVWRPSPPTCEK
46.5	3371.6279	1.0009	FSLLGHASISCTVENETIGVWRPSPPTCEK
11.4	3371.6256	1.0031	FVDYKTSAATSNQGGKVTSGVNSTLPVPSAEEK
9.2	3371.6103	1.0184	QQSTLNEGLPKATASSEDKQPSLPEESVSPSK
8.9	3372.6383	-0.0096	SGWAIDPFGHSPTMAYLLNRAGLSHMLIQR
7.5	3370.6263	2.0024	QQSTLNEGLPKATASSEDKQPSLPEESVSPSK
7.5	3370.6263	2.0024	QQSTLNEGLPKATASSEDKQPSLPEESVSPSK
7.5	3370.6263	2.0024	QQSTLNEGLPKATASSEDKQPSLPEESVSPSK
7.2	3372.6370	-0.0082	INDFSKENTIDYVLMIGMAGRYYATTITR
7.2	3372.6370	-0.0082	INDFSKENTIDYVLMIGMAGRYYATTITR

Mascot: http://www.matrixscience.com/

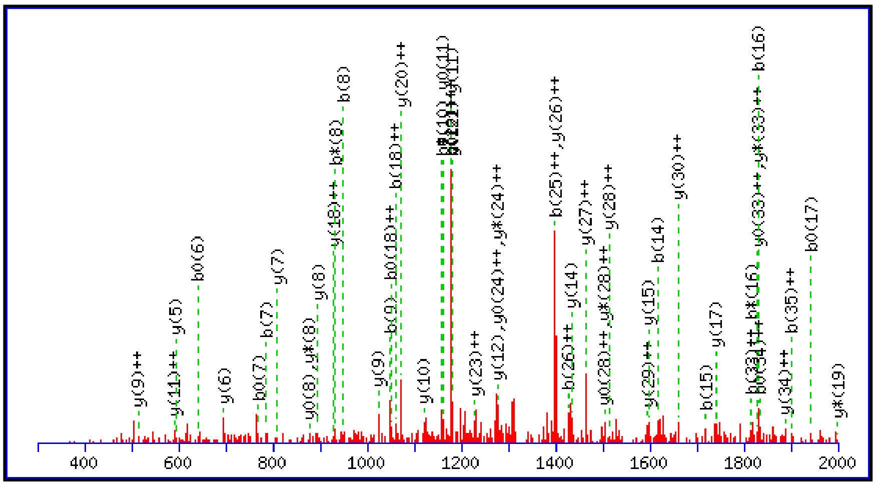
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28257: 3974.799462 from(1325.940430,3+) intensity(0.0000) rtinseconds(2066) scans(5258) index(5477)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum4624_scans__5258
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

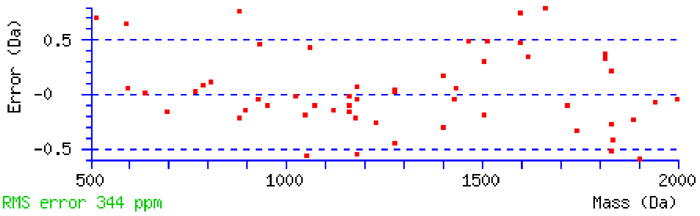
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

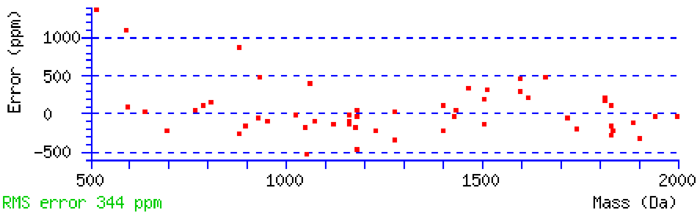


Monoisotopic mass of neutral peptide Mr(calc): 3973.7834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Q28 : Deamidated (NQ)
N35 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.012
Matches : 55/404 fragment ions using 147 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3861.7066	1931.3569	3844.6800	1922.8437	3843.6960	1922.3516	35
3	300.1918	150.5995			282.1812	141.5942	V	3774.6745	1887.8409	3757.6480	1879.3276	3756.6640	1878.8356	34
4	415.2187	208.1130			397.2082	199.1077	D	3675.6061	1838.3067	3658.5796	1829.7934	3657.5956	1829.3014	33
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	K	3560.5792	1780.7932	3543.5526	1772.2800	3542.5686	1771.7879	32
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	D	3432.4842	1716.7458	3415.4577	1708.2325	3414.4737	1707.7405	31
7	**786.3992**	393.7032	769.3727	385.1900	768.3886	384.6980	Q	3317.4573	1659.2323	3300.4307	1650.7190	3299.4467	1650.2270	30
8	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	Y	3189.3987	1595.2030	3172.3722	1586.6897	3171.3881	1586.1977	29
9	**1048.5310**	524.7691	1031.5044	516.2558	1030.5204	515.7638	V	3026.3354	1513.6713	3009.3088	1505.1581	3008.3248	1504.6660	28
10	**1177.5735**	589.2904	1160.5470	580.7771	1159.5630	580.2851	E	2927.2670	1464.1371	2910.2404	1455.6238	2909.2564	1455.1318	27
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	P	2798.2244	1399.6158	2781.1978	1391.1025	2780.2138	1390.6105	26
12	1403.6689	702.3381	1386.6424	693.8248	1385.6583	693.3328	E	2701.1716	1351.0894	2684.1451	1342.5762	2683.1610	1342.0842	25
13	1518.6958	759.8516	1501.6693	751.3383	1500.6853	750.8463	N	2572.1290	1286.5681	2555.1025	1278.0549	2554.1184	1277.5629	24
14	**1617.7643**	809.3858	1600.7377	800.8725	1599.7537	800.3805	V	2457.1021	1229.0547	2440.0755	1220.5414	2439.0915	1220.0494	23
15	**1718.8119**	859.9096	1701.7854	851.3963	1700.8014	850.9043	T	2358.0337	1179.5205	2341.0071	1171.0072	2340.0231	1170.5152	22
16	**1831.8960**	916.4516	1814.8695	907.9384	1813.8854	907.4464	I	2256.9860	1128.9966	2239.9594	1120.4834	2238.9754	1119.9913	21
17	1959.9546	980.4809	1942.9280	971.9677	1941.9440	971.4756	Q	2143.9019	1072.4546	2126.8754	1063.9413	2125.8913	1063.4493	20
18	2119.9852	**1060.4963**	2102.9587	1051.9830	2101.9747	1051.4910	C	2015.8433	1008.4253	1998.8168	999.9120	1997.8328	999.4200	19
19	2235.0122	1118.0097	2217.9856	1109.4964	2217.0016	1109.0044	D	1855.8127	928.4100	1838.7861	919.8967	1837.8021	919.4047	18
20	2322.0442	1161.5257	2305.0177	1153.0125	2304.0336	1152.5205	S	***1740.7857***	870.8965	1723.7592	862.3832	1722.7752	861.8912	17
21	2379.0657	1190.0365	2362.0391	1181.5232	2361.0551	1181.0312	G	1653.7537	827.3805	1636.7272	818.8672	1635.7431	818.3752	16
22	2542.1290	1271.5681	2525.1024	1263.0549	2524.1184	1262.5629	Y	***1596.7322***	798.8698	1579.7057	790.3565	1578.7217	789.8645	15

23	2599.1505	1300.0789	2582.1239	1291.5656	2581.1399	1291.0736	**G**	***1433.6689***	717.3381	1416.6424	708.8248	1415.6584	708.3328	**14**
24	2698.2189	1349.6131	2681.1923	1341.0998	2680.2083	1340.6078	**V**	1376.6475	688.8274	1359.6209	680.3141	1358.6369	679.8221	**13**
25	2797.2873	**1399.1473**	2780.2607	1390.6340	2779.2767	1390.1420	**V**	***1277.5790***	639.2932	1260.5525	630.7799	1259.5685	630.2879	**12**
26	2854.3087	**1427.6580**	2837.2822	1419.1447	2836.2982	1418.6527	**G**	***1178.5106***	589.7590	1161.4841	581.2457	1160.5001	580.7537	**11**
27	2951.3615	1476.1844	2934.3350	1467.6711	2933.3509	1467.1791	**P**	***1121.4892***	561.2482	1104.4626	552.7349	1103.4786	552.2429	**10**
28	3080.4041	1540.7057	3063.3776	1532.1924	3062.3935	1531.7004	**Q**	***1024.4364***	512.7218	1007.4099	504.2086	1006.4258	503.7166	**9**
29	3167.4361	1584.2217	3150.4096	1575.7084	3149.4256	1575.2164	**S**	***895.3938***	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3280.5202	1640.7637	3263.4936	1632.2505	3262.5096	1631.7585	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3381.5679	1691.2876	3364.5413	1682.7743	3363.5573	1682.2823	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3541.5985	1771.3029	3524.5720	1762.7896	3523.5880	1762.2976	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3628.6306	**1814.8189**	3611.6040	1806.3056	3610.6200	1805.8136	**S**	434.1994	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3685.6520	1843.3296	3668.6255	1834.8164	3667.6415	1834.3244	**G**	347.1674	174.0873	330.1408	165.5740			**3**
35	3800.6790	**1900.8431**	3783.6524	1892.3298	3782.6684	1891.8378	**N**	290.1459	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.3	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28, N35 49.67%
38.8	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, Q28, N35 35.49%
30.3	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17, N35 4.92%
28.7	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17, N35 3.45%
28.3	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28, N35 3.16%
26.6	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N13, N35 2.12%
22.8	3972.7994	2.0001	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
20.1	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17, Q28 0.48%
19.4	3972.7994	2.0001	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
17.8	3973.7834	1.0161	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17, Q28 0.28%

Mascot: http://www.matrixscience.com/

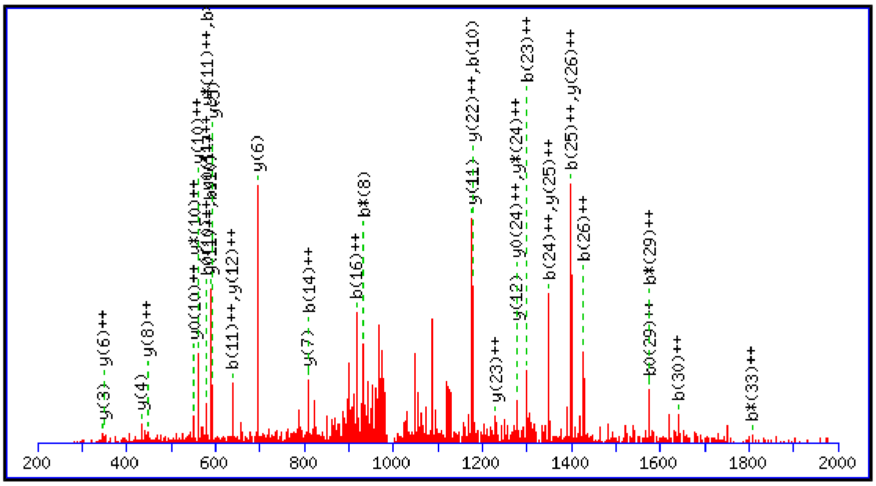
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR**
Found in **P04003** in **con_Xuniprot_HUMAN3**, C4BPA_HUMAN C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

Match to Query 28256: 3974.797656 from(994.706690,4+) intensity(22500.8281) rtinseconds(1597) scans(4076) index(18595)
Title: 111019_Est_MI_YP_G_08Spectrum3542_scans__4076
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

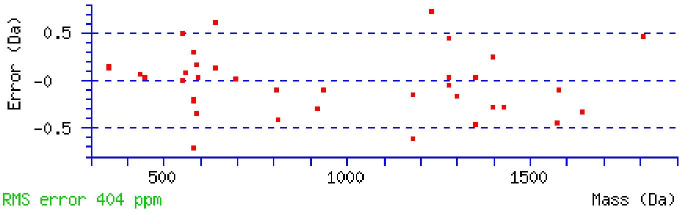
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

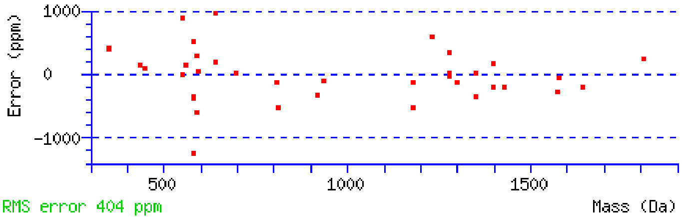


```
Monoisotopic mass of neutral peptide Mr(calc): 3973.7834
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Deamidated (NQ)
N13     : Deamidated (NQ)
N35     : Deamidated (NQ)
Ions Score: 40  Expect: 0.013
Matches : 38/404 fragment ions using 51 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							36
2	201.1234	101.0653			183.1128	92.0600	S	3861.7066	1931.3569	3844.6800	1922.8437	3843.6960	1922.3516	35
3	300.1918	150.5995			282.1812	141.5942	V	3774.6745	1887.8409	3757.6480	1879.3276	3756.6640	1878.8356	34
4	415.2187	208.1130			397.2082	199.1077	D	3675.6061	1838.3067	3658.5796	1829.7934	3657.5956	1829.3014	33
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	K	3560.5792	1780.7932	3543.5526	1772.2800	3542.5686	1771.7879	32
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	D	3432.4842	1716.7458	3415.4577	1708.2325	3414.4737	1707.7405	31
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	Q	3317.4573	1659.2323	3300.4307	1650.7190	3299.4467	1650.2270	30
8	950.4466	475.7269	933.4200	467.2136	932.4360	466.7216	Y	3188.4147	1594.7110	3171.3881	1586.1977	3170.4041	1585.7057	29
9	1049.5150	525.2611	1032.4884	516.7478	1031.5044	516.2558	V	3025.3514	1513.1793	3008.3248	1504.6660	3007.3408	1504.1740	28
10	1178.5576	***589.7824***	1161.5310	581.2691	1160.5470	580.7771	E	2926.2829	1463.6451	2909.2564	1455.1318	2908.2724	1454.6398	27
11	1275.6103	***638.3088***	1258.5838	629.7955	1257.5998	629.3035	P	2797.2404	1399.1238	2780.2138	1390.6105	2779.2298	1390.1185	26
12	1404.6529	702.8301	1387.6264	694.3168	1386.6424	693.8248	E	2700.1876	1350.5974	2683.1610	1342.0842	2682.1770	1341.5921	25
13	1519.6799	760.3436	1502.6533	751.8303	1501.6693	751.3383	N	2571.1450	1286.0761	2554.1184	1277.5629	2553.1344	1277.0709	24
14	1618.7483	***809.8778***	1601.7217	801.3645	1600.7377	800.8725	V	2456.1181	1228.5627	2439.0915	1220.0494	2438.1075	1219.5574	23
15	1719.7960	860.4016	1702.7694	851.8883	1701.7854	851.3963	T	2357.0496	1179.0285	2340.0231	1170.5152	2339.0391	1170.0232	22
16	1832.8800	***916.9436***	1815.8535	908.4304	1814.8695	907.9384	I	2256.0020	1128.5046	2238.9754	1119.9913	2237.9914	1119.4993	21
17	1960.9386	980.9729	1943.9120	972.4597	1942.9280	971.9677	Q	2142.9179	1071.9626	2125.8913	1063.4493	2124.9073	1062.9573	20
18	2120.9692	1060.9883	2103.9427	1052.4750	2102.9587	1051.9830	C	2014.8593	1007.9333	1997.8328	999.4200	1996.8488	998.9280	19
19	2235.9962	1118.5017	2218.9696	1109.9885	2217.9856	1109.4964	D	1854.8287	927.9180	1837.8021	919.4047	1836.8181	918.9127	18
20	2323.0282	1162.0177	2306.0017	1153.5045	2305.0177	1153.0125	S	1739.8017	870.4045	1722.7752	861.8912	1721.7912	861.3992	17
21	2380.0497	1190.5285	2363.0231	1182.0152	2362.0391	1181.5232	G	1652.7697	826.8885	1635.7431	818.3752	1634.7591	817.8832	16
22	2543.1130	1272.0601	2526.0865	1263.5469	2525.1024	1263.0549	Y	1595.7482	798.3778	1578.7217	789.8645	1577.7377	789.3725	15

23	2600.1345	***1300.5709***	2583.1079	1292.0576	2582.1239	1291.5656	**G**	1432.6849	716.8461	1415.6584	708.3328	1414.6743	707.8408	**14**
24	2699.2029	***1350.1051***	2682.1763	1341.5918	2681.1923	1341.0998	**V**	1375.6634	688.3354	1358.6369	679.8221	1357.6529	679.3301	**13**
25	2798.2713	***1399.6393***	2781.2448	1391.1260	2780.2607	1390.6340	**V**	***1276.5950***	638.8012	1259.5685	630.2879	1258.5845	629.7959	**12**
26	2855.2928	***1428.1500***	2838.2662	1419.6367	2837.2822	1419.1447	**G**	***1177.5266***	589.2669	1160.5001	580.7537	1159.5160	580.2617	**11**
27	2952.3455	1476.6764	2935.3190	1468.1631	2934.3350	1467.6711	**P**	1120.5051	560.7562	1103.4786	552.2429	1102.4946	551.7509	**10**
28	3080.4041	1540.7057	3063.3776	1532.1924	3062.3935	1531.7004	**Q**	1023.4524	512.2298	1006.4258	503.7166	1005.4418	503.2245	**9**
29	3167.4361	1584.2217	3150.4096	1575.7084	3149.4256	1575.2164	**S**	895.3938	448.2005	878.3673	439.6873	877.3832	439.1953	**8**
30	3280.5202	***1640.7637***	3263.4936	1632.2505	3262.5096	1631.7585	**I**	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	**7**
31	3381.5679	1691.2876	3364.5413	1682.7743	3363.5573	1682.2823	**T**	***695.2777***	348.1425	678.2512	339.6292	677.2671	339.1372	**6**
32	3541.5985	1771.3029	3524.5720	1762.7896	3523.5880	1762.2976	**C**	***594.2300***	297.6187	577.2035	289.1054	576.2195	288.6134	**5**
33	3628.6306	1814.8189	3611.6040	1806.3056	3610.6200	1805.8136	**S**	***434.1994***	217.6033	417.1728	209.0901	416.1888	208.5980	**4**
34	3685.6520	1843.3296	3668.6255	1834.8164	3667.6415	1834.3244	**G**	***347.1674***	174.0873	330.1408	165.5740			**3**
35	3800.6790	1900.8431	3783.6524	1892.3298	3782.6684	1891.8378	**N**	290.1459	145.5766	273.1193	137.0633			**2**
36							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.8	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, N13, N35 35.33%
38.1	3972.7994	1.9983	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
36.8	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q17, N35 17.87%
35.0	3972.7994	1.9983	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
34.7	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q7, Q28, N35 11.12%
33.7	3972.7994	1.9983	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
32.2	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated Q17, Q28, N35 6.22%
32.2	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q28, N35 6.22%
31.8	3972.7994	1.9983	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	
31.7	3973.7834	1.0143	LSVDKDQYVEPENVTIQCDSGYGVVGPQSITCSGNR	Deamidated N13, Q17, N35 5.56%

Mascot: http://www.matrixscience.com/

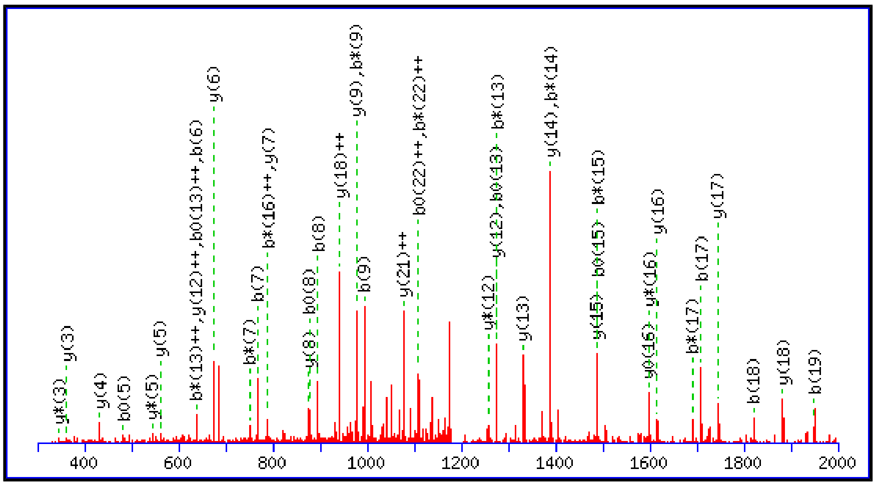
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNATVHEQVGGPSLTSDLQAQSK**
Found in **F5GX75** in **con_Xuniprot_HUMAN3**, F5GX75_HUMAN Vitronectin (Fragment) OS=Homo sapiens GN=VTN PE=2 SV=2

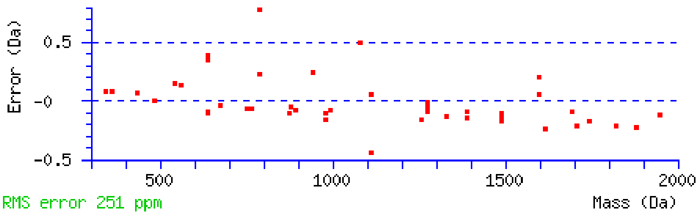
Match to Query 21427: 2381.156948 from(1191.585750,2+) intensity(41018.5938) rtinseconds(892) scans(2040) index(15671)
Title: 111019_Est_MI_YP_G_05Spectrum1728_scans__2040
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

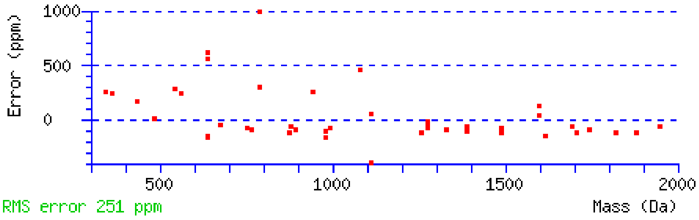
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2381.1459
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Ions Score: 107  Expect: 5.9e-009
Matches : 44/256 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	115.0502	58.0287	98.0237	49.5155			**N**							**23**
2	230.0771	115.5422	213.0506	107.0289			**N**	2268.1102	1134.5588	2251.0837	1126.0455	2250.0997	1125.5535	**22**
3	301.1143	151.0608	284.0877	142.5475			**A**	2153.0833	1077.0453	2136.0568	1068.5320	2135.0727	1068.0400	**21**
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	**T**	2082.0462	1041.5267	2065.0196	1033.0135	2064.0356	1032.5215	**20**
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	**V**	1980.9985	991.0029	1963.9720	982.4896	1962.9879	981.9976	**19**
6	**638.2893**	319.6483	621.2627	311.1350	620.2787	310.6430	**H**	***1881.9301***	941.4687	1864.9035	932.9554	1863.9195	932.4634	**18**
7	**767.3319**	384.1696	750.3053	375.6563	749.3213	375.1643	**E**	***1744.8712***	872.9392	1727.8446	864.4260	1726.8606	863.9339	**17**
8	**895.3904**	448.1989	878.3639	439.6856	877.3799	439.1936	**Q**	***1615.8286***	808.4179	1598.8020	799.9047	1597.8180	799.4127	**16**
9	**994.4589**	497.7331	977.4323	489.2198	976.4483	488.7278	**V**	***1487.7700***	744.3886	1470.7435	735.8754	1469.7594	735.3834	**15**
10	1051.4803	526.2438	1034.4538	517.7305	1033.4697	517.2385	**G**	***1388.7016***	694.8544	1371.6751	686.3412	1370.6910	685.8492	**14**
11	1108.5018	554.7545	1091.4752	546.2413	1090.4912	545.7492	**G**	***1331.6801***	666.3437	1314.6536	657.8304	1313.6696	657.3384	**13**
12	1205.5545	603.2809	1188.5280	594.7676	1187.5440	594.2756	**P**	***1274.6587***	637.8330	1257.6321	629.3197	1256.6481	628.8277	**12**
13	1292.5866	646.7969	1275.5600	638.2836	1274.5760	637.7916	**S**	1177.6059	589.3066	1160.5794	580.7933	1159.5953	580.3013	**11**
14	1405.6706	703.3390	1388.6441	694.8257	1387.6601	694.3337	**L**	1090.5739	545.7906	1073.5473	537.2773	1072.5633	536.7853	**10**
15	1506.7183	753.8628	1489.6918	745.3495	1488.7077	744.8575	**T**	***977.4898***	489.2485	960.4633	480.7353	959.4793	480.2433	**9**
16	1593.7503	797.3788	1576.7238	788.8655	1575.7398	788.3735	**S**	***876.4421***	438.7247	859.4156	430.2114	858.4316	429.7194	**8**
17	**1708.7773**	854.8923	1691.7507	846.3790	1690.7667	845.8870	**D**	***789.4101***	395.2087	772.3836	386.6954	771.3995	386.2034	**7**
18	**1821.8613**	911.4343	1804.8348	902.9210	1803.8508	902.4290	**L**	***674.3832***	337.6952	657.3566	329.1819	656.3726	328.6899	**6**
19	**1949.9199**	975.4636	1932.8934	966.9503	1931.9094	966.4583	**Q**	***561.2991***	281.1532	544.2726	272.6399	543.2885	272.1479	**5**
20	2020.9570	1010.9822	2003.9305	1002.4689	2002.9465	1001.9769	**A**	***433.2405***	217.1239	416.2140	208.6106	415.2300	208.1186	**4**
21	2149.0156	1075.0114	2131.9891	1066.4982	2131.0051	1066.0062	**Q**	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	**3**
22	2236.0476	1118.5275	2219.0211	1110.0142	2218.0371	1109.5222	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
23							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of NNATVHEQVGGPSLTSDLQAQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
106.8	2381.1459	0.0111	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2 49.58%
106.8	2381.1459	0.0111	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1 49.58%
89.1	2381.1459	0.0111	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8 0.83%
73.2	2380.1619	0.9951	NNATVHEQVGGPSLTSDLQAQSK	
39.4	2381.1459	0.0111	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q19 0.00%
34.0	2381.1459	0.0111	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q21 0.00%
14.7	2380.1501	1.0068	CEQQMAKVQKLEESLLATEK	
5.6	2380.1501	1.0068	CEQQMAKVQKLEESLLATEK	
5.6	2380.1501	1.0068	CEQQMAKVQKLEESLLATEK	
0.4	2379.1423	2.0146	LLNRMSSDDRHLGSSCGSFIK	

Mascot: http://www.matrixscience.com/

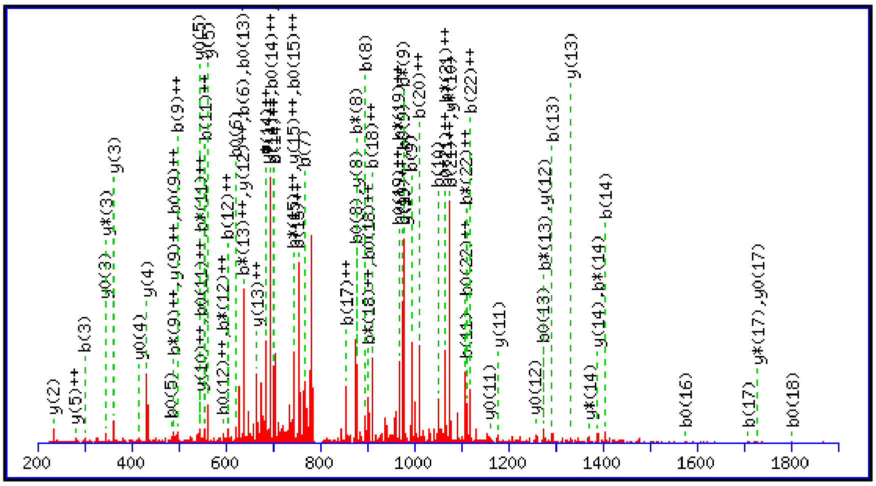
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNATVHEQVGGPSLTSDLQAQSK**
Found in **F5GX75** in **con_Xuniprot_HUMAN3**, F5GX75_HUMAN Vitronectin (Fragment) OS=Homo sapiens GN=VTN PE=2 SV=2

Match to Query 21457: 2382.133812 from(795.051880,3+) intensity(18164.0273) rtinseconds(910) scans(2262) index(19413)
Title: 111019_Est_MI_YP_G_09Spectrum1991_scans__2262
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

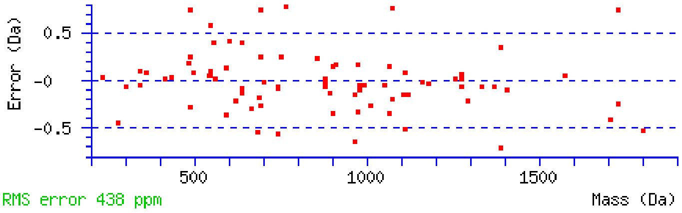
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

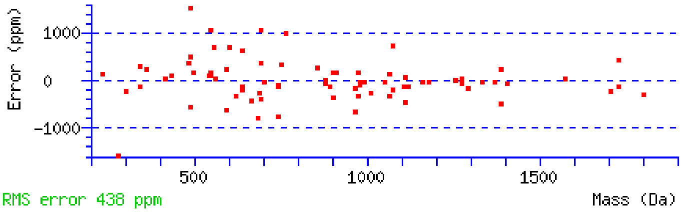


```
Monoisotopic mass of neutral peptide Mr(calc): 2382.1299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Q19     : Deamidated (NQ)
Ions Score: 62  Expect: 0.00014
Matches : 81/256 fragment ions using 123 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							23
2	230.0771	115.5422	213.0506	107.0289			N	2269.0943	1135.0508	2252.0677	1126.5375	2251.0837	1126.0455	22
3	**301.1143**	151.0608	284.0877	142.5475			A	2154.0673	1077.5373	2137.0408	1069.0240	2136.0568	1068.5320	21
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	T	2083.0302	1042.0187	2066.0037	1033.5055	2065.0196	1033.0135	20
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	V	1981.9825	991.4949	1964.9560	982.9816	1963.9720	982.4896	19
6	**638.2893**	319.6483	621.2627	311.1350	620.2787	310.6430	H	1882.9141	941.9607	1865.8876	933.4474	1864.9035	932.9554	18
7	**767.3319**	384.1696	750.3053	375.6563	749.3213	375.1643	E	1745.8552	873.4312	1728.8287	864.9180	1727.8446	864.4260	17
8	**895.3904**	448.1989	878.3639	439.6856	877.3799	439.1936	Q	1616.8126	808.9099	1599.7861	800.3967	1598.8020	799.9047	16
9	**994.4589**	**497.7331**	977.4323	489.2198	976.4483	488.7278	V	1488.7540	744.8807	1471.7275	736.3674	1470.7435	735.8754	15
10	**1051.4803**	526.2438	1034.4538	517.7305	1033.4697	517.2385	G	**1389.6856**	695.3464	1372.6591	686.8332	1371.6751	686.3412	14
11	**1108.5018**	**554.7545**	1091.4752	546.2413	1090.4912	545.7492	G	**1332.6642**	666.8357	1315.6376	658.3224	1314.6536	657.8304	13
12	1205.5545	**603.2809**	1188.5280	594.7676	1187.5440	594.2756	P	**1275.6427**	638.3250	1258.6161	629.8117	1257.6321	629.3197	12
13	**1292.5866**	646.7969	1275.5600	638.2836	1274.5760	637.7916	S	**1178.5899**	589.7986	1161.5634	581.2853	1160.5794	580.7933	11
14	**1405.6706**	**703.3390**	1388.6441	694.8257	1387.6601	694.3337	L	1091.5579	546.2826	1074.5313	537.7693	1073.5473	537.2773	10
15	1506.7183	**753.8628**	1489.6918	745.3495	1488.7077	744.8575	T	**978.4738**	489.7406	961.4473	481.2273	960.4633	480.7353	9
16	1593.7503	797.3788	1576.7238	788.8655	1575.7398	788.3735	S	**877.4262**	439.2167	860.3996	430.7034	859.4156	430.2114	8
17	**1708.7773**	**854.8923**	1691.7507	846.3790	1690.7667	845.8870	D	790.3941	395.7007	773.3676	387.1874	772.3836	386.6954	7
18	1821.8613	**911.4343**	1804.8348	902.9210	1803.8508	902.4290	L	675.3672	338.1872	658.3406	329.6740	657.3566	329.1819	6
19	1950.9039	**975.9556**	1933.8774	967.4423	1932.8934	966.9503	Q	**562.2831**	281.6452	545.2566	273.1319	544.2726	272.6399	5
20	2021.9411	**1011.4742**	2004.9145	1002.9609	2003.9305	1002.4689	A	**433.2405**	217.1239	416.2140	208.6106	415.2300	208.1186	4
21	2149.9996	**1075.5035**	2132.9731	1066.9902	2131.9891	1066.4982	Q	**362.2034**	181.6053	345.1769	173.0921	344.1928	172.6001	3
22	2237.0317	**1119.0195**	2220.0051	1110.5062	2219.0211	1110.0142	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2

23							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of NNATVHEQVGGPSLTSDLQAQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.4	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q19 25.75%
62.4	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q19 25.75%
61.0	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q21 18.40%
61.0	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q21 18.40%
54.7	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q8 4.39%
54.7	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q8 4.39%
48.6	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q19 1.08%
48.6	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, N2 1.07%
47.3	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q21 0.79%
18.6	2382.1299	0.0039	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q19, Q21 0.00%

Mascot: http://www.matrixscience.com/

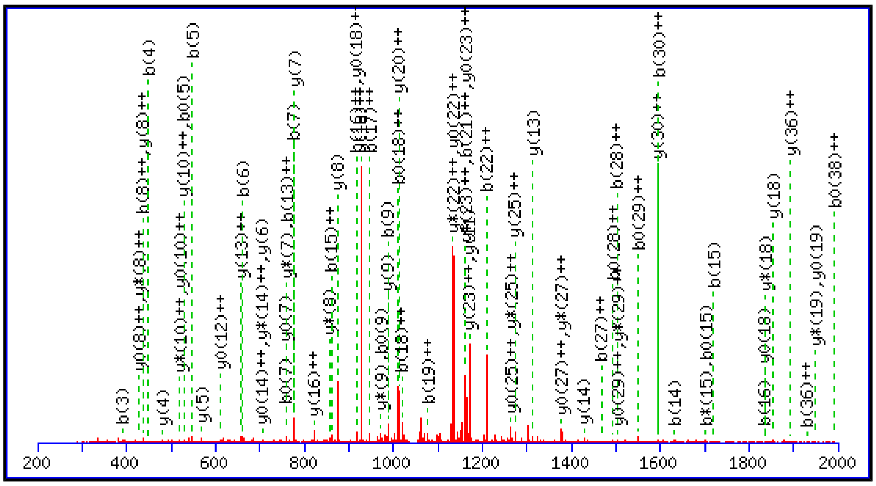
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEDGVLDPDYPRNISDGFDGIPDNVDAALALPAHSYSGR**
Found in **P04004** in **con_Xuniprot_HUMAN3**, VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 28978: 4175.954096 from(1044.995800,4+) intensity(117478.6016) rtinseconds(2348) scans(6148) index(9758)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum5315_scans__6148
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

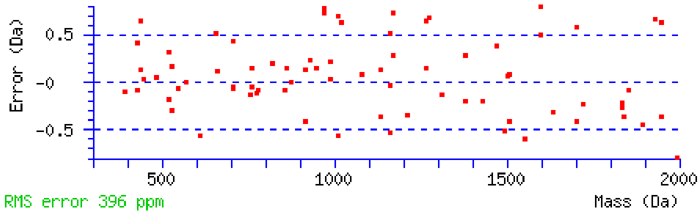
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

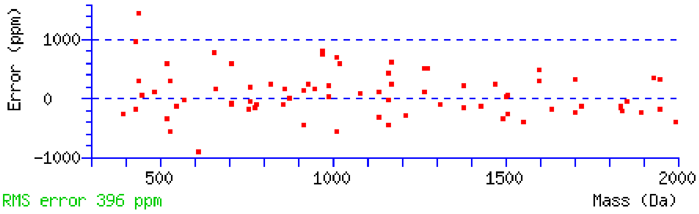


Monoisotopic mass of neutral peptide Mr(calc): 4175.9348
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00015
Matches : 77/428 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**39**
2	277.1183	139.0628			259.1077	130.0575	**E**	4029.8737	2015.4405	4012.8472	2006.9272	4011.8631	2006.4352	**38**
3	***392.1452***	196.5763			374.1347	187.5710	**D**	3900.8311	1950.9192	3883.8046	1942.4059	3882.8206	1941.9139	**37**
4	***449.1667***	225.0870			431.1561	216.0817	**G**	3785.8042	1893.4057	3768.7776	1884.8925	3767.7936	1884.4004	**36**
5	***548.2351***	274.6212			530.2245	265.6159	**V**	3728.7827	1864.8950	3711.7562	1856.3817	3710.7721	1855.8897	**35**
6	***661.3192***	331.1632			643.3086	322.1579	**L**	3629.7143	1815.3608	3612.6877	1806.8475	3611.7037	1806.3555	**34**
7	***776.3461***	388.6767			758.3355	379.6714	**D**	3516.6302	1758.8188	3499.6037	1750.3055	3498.6197	1749.8135	**33**
8	873.3989	***437.2031***			855.3883	428.1978	**P**	3401.6033	1701.3053	3384.5767	1692.7920	3383.5927	1692.3000	**32**
9	***988.4258***	494.7165			970.4153	485.7113	**D**	3304.5505	1652.7789	3287.5240	1644.2656	3286.5400	1643.7736	**31**
10	1151.4891	576.2482			1133.4786	567.2429	**Y**	3189.5236	1595.2654	3172.4970	1586.7522	3171.5130	1586.2601	**30**
11	1248.5419	624.7746			1230.5313	615.7693	**P**	3026.4603	1513.7338	3009.4337	1505.2205	3008.4497	1504.7285	**29**
12	1404.6430	702.8251	1387.6165	694.3119	1386.6325	693.8199	**R**	2929.4075	1465.2074	2912.3809	1456.6941	2911.3969	1456.2021	**28**
13	1519.6700	***760.3386***	1502.6434	751.8253	1501.6594	751.3333	**N**	2773.3064	1387.1568	2756.2798	1378.6436	2755.2958	1378.1515	**27**
14	***1632.7540***	816.8807	1615.7275	808.3674	1614.7435	807.8754	**I**	2658.2794	1329.6434	2641.2529	1321.1301	2640.2689	1320.6381	**26**
15	***1719.7861***	***860.3967***	1702.7595	851.8834	1701.7755	851.3914	**S**	2545.1954	1273.1013	2528.1688	1264.5880	2527.1848	1264.0960	**25**
16	***1834.8130***	***917.9101***	1817.7865	909.3969	1816.8024	908.9049	**D**	2458.1633	1229.5853	2441.1368	1221.0720	2440.1528	1220.5800	**24**
17	1891.8345	***946.4209***	1874.8079	937.9076	1873.8239	937.4156	**G**	2343.1364	1172.0718	2326.1099	1163.5586	2325.1258	1163.0666	**23**
18	2038.9029	***1019.9551***	2021.8763	1011.4418	2020.8923	1010.9498	**F**	2286.1149	1143.5611	2269.0884	1135.0478	2268.1044	1134.5558	**22**
19	2153.9298	***1077.4685***	2136.9033	1068.9553	2135.9193	1068.4633	**D**	2139.0465	1070.0269	2122.0200	1061.5136	2121.0360	1061.0216	**21**
20	2210.9513	1105.9793	2193.9247	1097.4660	2192.9407	1096.9740	**G**	2024.0196	1012.5134	2006.9930	1004.0002	2006.0090	1003.5081	**20**
21	2324.0353	***1162.5213***	2307.0088	1154.0080	2306.0248	1153.5160	**I**	1966.9981	984.0027	1949.9716	975.4894	1948.9876	974.9974	**19**
22	2421.0881	***1211.0477***	2404.0616	1202.5344	2403.0775	1202.0424	**P**	***1853.9141***	927.4607	1836.8875	918.9474	1835.9035	918.4554	**18**
23	2536.1151	1268.5612	2519.0885	1260.0479	2518.1045	1259.5559	**D**	1756.8613	878.9343	1739.8347	870.4210	1738.8507	869.9290	**17**

24	2650.1580	1325.5826	2633.1314	1317.0694	2632.1474	1316.5773	**N**	1641.8343	821.4208	1624.8078	812.9075	1623.8238	812.4155	**16**
25	2749.2264	1375.1168	2732.1998	1366.6036	2731.2158	1366.1116	**V**	1527.7914	764.3993	1510.7649	755.8861	1509.7809	755.3941	**15**
26	2864.2533	1432.6303	2847.2268	1424.1170	2846.2428	1423.6250	**D**	***1428.7230***	714.8651	1411.6965	706.3519	1410.7124	705.8599	**14**
27	2935.2905	***1468.1489***	2918.2639	1459.6356	2917.2799	1459.1436	**A**	***1313.6961***	657.3517	1296.6695	648.8384	1295.6855	648.3464	**13**
28	3006.3276	***1503.6674***	2989.3010	1495.1541	2988.3170	1494.6621	**A**	1242.6589	621.8331	1225.6324	613.3198	1224.6484	612.8278	**12**
29	3119.4116	1560.2095	3102.3851	1551.6962	3101.4011	1551.2042	**L**	***1171.6218***	586.3146	1154.5953	577.8013	1153.6113	577.3093	**11**
30	3190.4487	***1595.7280***	3173.4222	1587.2147	3172.4382	1586.7227	**A**	1058.5378	529.7725	1041.5112	521.2592	1040.5272	520.7672	**10**
31	3303.5328	1652.2700	3286.5063	1643.7568	3285.5222	1643.2648	**L**	***987.5007***	494.2540	970.4741	485.7407	969.4901	485.2487	**9**
32	3400.5856	1700.7964	3383.5590	1692.2832	3382.5750	1691.7911	**P**	***874.4166***	437.7119	857.3900	429.1987	856.4060	428.7067	**8**
33	3471.6227	1736.3150	3454.5961	1727.8017	3453.6121	1727.3097	**A**	***777.3638***	389.1856	760.3373	380.6723	759.3533	380.1803	**7**
34	3608.6816	1804.8444	3591.6551	1796.3312	3590.6710	1795.8392	**H**	***706.3267***	353.6670	689.3002	345.1537	688.3161	344.6617	**6**
35	3695.7136	1848.3605	3678.6871	1839.8472	3677.7031	1839.3552	**S**	***569.2678***	285.1375	552.2413	276.6243	551.2572	276.1323	**5**
36	3858.7770	***1929.8921***	3841.7504	1921.3788	3840.7664	1920.8868	**Y**	***482.2358***	241.6215	465.2092	233.1083	464.2252	232.6162	**4**
37	3945.8090	1973.4081	3928.7824	1964.8949	3927.7984	1964.4028	**S**	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
38	4002.8304	2001.9189	3985.8039	1993.4056	3984.8199	1992.9136	**G**	232.1404	116.5738	215.1139	108.0606			**2**
39							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of FEDGVLDPDYPRNISDGFDGIPDNVDAALALPAHSYSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.1	4175.9348	0.0193	FEDGVLDPDYPRNISDGFDGIPDNVDAALALPAHSYSGR	Deamidated N13 52.36%
60.7	4175.9348	0.0193	FEDGVLDPDYPRNISDGFDGIPDNVDAALALPAHSYSGR	Deamidated N24 47.64%
49.8	4174.9508	1.0033	FEDGVLDPDYPRNISDGFDGIPDNVDAALALPAHSYSGR	
11.0	4174.9699	0.9842	LIALMEDSDSNQDVTESQKSKPLKNPKPNDIASDSSNR	
10.9	4175.9574	-0.0033	LSDLNHWQVGAMTVNQGYLHYDFEYIKNFKSLGER	
10.9	4175.9574	-0.0033	LSDLNHWQVGAMTVNQGYLHYDFEYIKNFKSLGER	
10.9	4175.9574	-0.0033	LSDLNHWQVGAMTVNQGYLHYDFEYIKNFKSLGER	
10.9	4175.9574	-0.0033	LSDLNHWQVGAMTVNQGYLHYDFEYIKNFKSLGER	
9.3	4174.9699	0.9842	LIALMEDSDSNQDVTESQKSKPLKNPKPNDIASDSSNR	
8.7	4174.9699	0.9842	LIALMEDSDSNQDVTESQKSKPLKNPKPNDIASDSSNR	

Mascot: http://www.matrixscience.com/

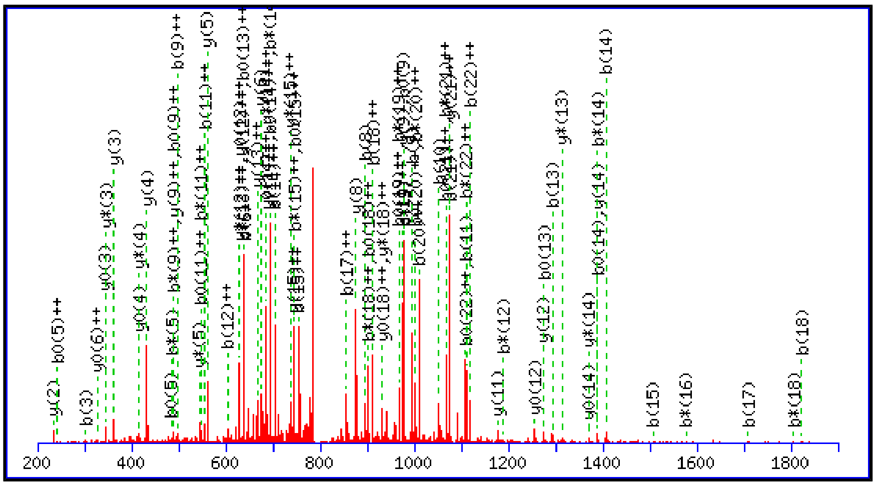
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNATVHEQVGGPSLTSDLQAQSK**
Found in **F5GX75** in **con_Xuniprot_HUMAN3**, F5GX75_HUMAN Vitronectin (Fragment) OS=Homo sapiens GN=VTN PE=2 SV=2

Match to Query 21460: 2382.136542 from(795.052790,3+) intensity(280292.8438) rtinseconds(890) scans(2148) index(4280)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum1870_scans__2148
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

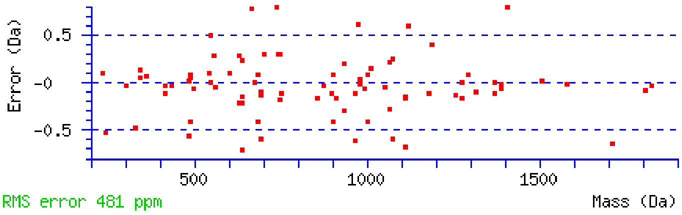
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

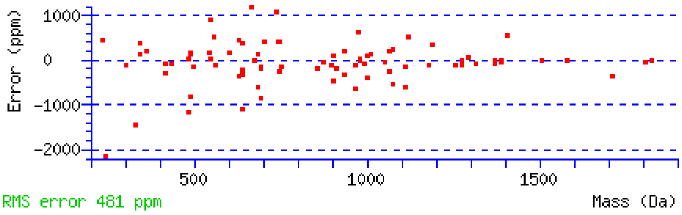


Monoisotopic mass of neutral peptide Mr(calc): 2382.1299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
N2 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.00026
Matches : 86/256 fragment ions using 137 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	99.0077	50.0075			N							23
2	231.0612	116.0342	214.0346	107.5209			N	2268.1102	1134.5588	2251.0837	1126.0455	2250.0997	1125.5535	22
3	***302.0983***	151.5528	285.0717	143.0395			A	2153.0833	1077.0453	2136.0568	1068.5320	2135.0727	1068.0400	21
4	403.1460	202.0766	386.1194	193.5633	385.1354	193.0713	T	2082.0462	1041.5267	2065.0196	1033.0135	2064.0356	1032.5215	20
5	502.2144	251.6108	485.1878	243.0975	484.2038	242.6055	V	1980.9985	991.0029	1963.9720	982.4896	1962.9879	981.9976	19
6	***639.2733***	320.1403	622.2467	311.6270	621.2627	311.1350	H	1881.9301	941.4687	1864.9035	932.9554	1863.9195	932.4634	18
7	768.3159	384.6616	751.2893	376.1483	750.3053	375.6563	E	1744.8712	872.9392	1727.8446	864.4260	1726.8606	863.9339	17
8	***896.3745***	448.6909	879.3479	440.1776	878.3639	439.6856	Q	1615.8286	808.4179	1598.8020	799.9047	1597.8180	799.4127	16
9	***995.4429***	***498.2251***	978.4163	489.7118	977.4323	489.2198	V	1487.7700	744.3886	1470.7435	735.8754	1469.7594	735.3834	15
10	***1052.4643***	526.7358	1035.4378	518.2225	1034.4538	517.7305	G	**1388.7016**	694.8544	1371.6751	686.3412	1370.6910	685.8492	14
11	***1109.4858***	***555.2465***	1092.4592	546.7333	1091.4752	546.2413	G	1331.6801	666.3437	1314.6536	657.8304	1313.6696	657.3384	13
12	1206.5386	***603.7729***	1189.5120	595.2596	1188.5280	594.7676	P	**1274.6587**	637.8330	1257.6321	629.3197	1256.6481	628.8277	12
13	***1293.5706***	647.2889	1276.5440	638.7757	1275.5600	638.2836	S	**1177.6059**	589.3066	1160.5794	580.7933	1159.5953	580.3013	11
14	***1406.6546***	***703.8310***	1389.6281	695.3177	1388.6441	694.8257	L	1090.5739	545.7906	1073.5473	537.2773	1072.5633	536.7853	10
15	***1507.7023***	***754.3548***	1490.6758	745.8415	1489.6918	745.3495	T	**977.4898**	489.2485	960.4633	480.7353	959.4793	480.2433	9
16	1594.7344	797.8708	1577.7078	789.3575	1576.7238	788.8655	S	**876.4421**	438.7247	859.4156	430.2114	858.4316	429.7194	8
17	***1709.7613***	***855.3843***	1692.7348	846.8710	1691.7507	846.3790	D	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
18	***1822.8454***	***911.9263***	1805.8188	903.4130	1804.8348	902.9210	L	**674.3832**	337.6952	657.3566	329.1819	656.3726	328.6899	6
19	1950.9039	***975.9556***	1933.8774	967.4423	1932.8934	966.9503	Q	**561.2991**	281.1532	544.2726	272.6399	543.2885	272.1479	5
20	2021.9411	***1011.4742***	2004.9145	1002.9609	2003.9305	1002.4689	A	**433.2405**	217.1239	416.2140	208.6106	415.2300	208.1186	4
21	2149.9996	***1075.5035***	2132.9731	1066.9902	2131.9891	1066.4982	Q	**362.2034**	181.6053	345.1769	173.0921	344.1928	172.6001	3
22	2237.0317	***1119.0195***	2220.0051	1110.5062	2219.0211	1110.0142	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2

23							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NNATVHEQVGGPSLTSDLQAQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.8	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, N2 79.15%
49.2	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q8 6.86%
49.2	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q8 6.86%
42.5	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q19 1.47%
42.5	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q19 1.47%
42.0	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q19 1.30%
40.8	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q21 1.00%
40.8	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q21 1.00%
40.3	2382.1299	0.0066	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q21 0.88%
7.9	2382.1478	-0.0113	NVSLIAQFTDDVFKQLTGQSAP	

Mascot: http://www.matrixscience.com/

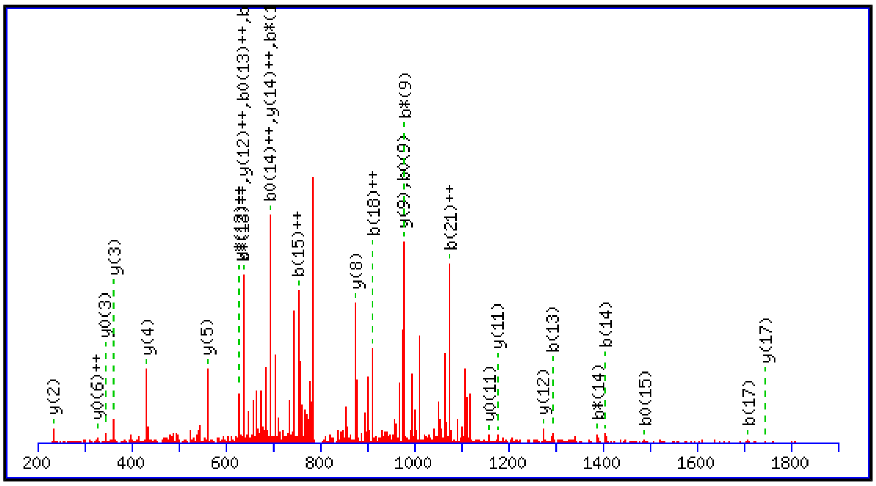
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNATVHEQVGGPSLTSDLQAQSK**
Found in **F5GX75** in **con_Xuniprot_HUMAN3**, F5GX75_HUMAN Vitronectin (Fragment) OS=Homo sapiens GN=VTN PE=2 SV=2

Match to Query 21454: 2382.132582 from(795.051470,3+) intensity(53558.9688) rtinseconds(788) scans(1827) index(18345)
Title: 111019_Est_MI_YP_G_08Spectrum1602_scans__1827
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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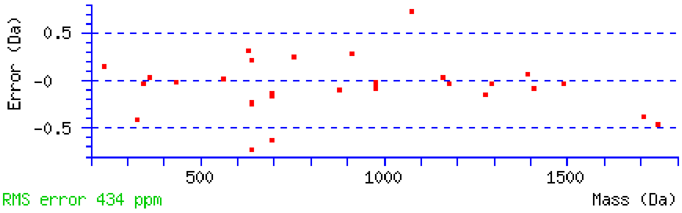
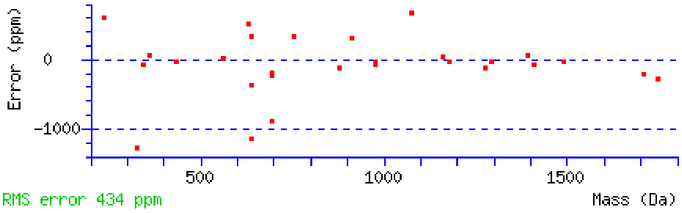
Monoisotopic mass of neutral peptide Mr(calc): 2382.1299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2      : Deamidated (NQ)
Q8      : Deamidated (NQ)
Ions Score: 59  Expect: 0.00029
Matches : 30/256 fragment ions using 32 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							23
2	230.0771	115.5422	213.0506	107.0289			N	2269.0943	1135.0508	2252.0677	1126.5375	2251.0837	1126.0455	22
3	301.1143	151.0608	284.0877	142.5475			A	2154.0673	1077.5373	2137.0408	1069.0240	2136.0568	1068.5320	21
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	T	2083.0302	1042.0187	2066.0037	1033.5055	2065.0196	1033.0135	20
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	V	1981.9825	991.4949	1964.9560	982.9816	1963.9720	982.4896	19
6	**638.2893**	319.6483	621.2627	311.1350	620.2787	310.6430	H	1882.9141	941.9607	1865.8876	933.4474	1864.9035	932.9554	18
7	767.3319	384.1696	750.3053	375.6563	749.3213	375.1643	E	***1745.8552***	873.4312	1728.8287	864.9180	1727.8446	864.4260	17
8	896.3745	448.6909	879.3479	440.1776	878.3639	439.6856	Q	1616.8126	808.9099	1599.7861	800.3967	1598.8020	799.9047	16
9	995.4429	498.2251	978.4163	489.7118	977.4323	489.2198	V	1487.7700	744.3886	1470.7435	735.8754	1469.7594	735.3834	15
10	1052.4643	526.7358	1035.4378	518.2225	1034.4538	517.7305	G	1388.7016	694.8544	1371.6751	686.3412	1370.6910	685.8492	14
11	1109.4858	555.2465	1092.4592	546.7333	1091.4752	546.2413	G	1331.6801	666.3437	1314.6536	657.8304	1313.6696	657.3384	13
12	1206.5386	603.7729	1189.5120	595.2596	1188.5280	594.7676	P	***1274.6587***	637.8330	1257.6321	629.3197	1256.6481	628.8277	12
13	**1293.5706**	647.2889	1276.5440	638.7757	1275.5600	638.2836	S	***1177.6059***	589.3066	1160.5794	580.7933	1159.5953	580.3013	11
14	**1406.6546**	703.8310	1389.6281	695.3177	1388.6441	694.8257	L	1090.5739	545.7906	1073.5473	537.2773	1072.5633	536.7853	10
15	1507.7023	**754.3548**	1490.6758	745.8415	1489.6918	745.3495	T	***977.4898***	489.2485	960.4633	480.7353	959.4793	480.2433	9
16	1594.7344	797.8708	1577.7078	789.3575	1576.7238	788.8655	S	***876.4421***	438.7247	859.4156	430.2114	858.4316	429.7194	8
17	**1709.7613**	855.3843	1692.7348	846.8710	1691.7507	846.3790	D	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
18	1822.8454	**911.9263**	1805.8188	903.4130	1804.8348	902.9210	L	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
19	1950.9039	975.9556	1933.8774	967.4423	1932.8934	966.9503	Q	***561.2991***	281.1532	544.2726	272.6399	543.2885	272.1479	5
20	2021.9411	1011.4742	2004.9145	1002.9609	2003.9305	1002.4689	A	***433.2405***	217.1239	416.2140	208.6106	415.2300	208.1186	4
21	2149.9996	**1075.5035**	2132.9731	1066.9902	2131.9891	1066.4982	Q	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	3
22	2237.0317	1119.0195	2220.0051	1110.5062	2219.0211	1110.0142	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2

23							K	147.1128	74.0600	130.0863	65.5468		1





NCBI **BLAST** search of NNATVHEQVGGPSLTSDLQAQSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.5	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q8 30.84%
59.5	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q8 30.84%
59.5	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, N2 30.84%
47.3	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q19 1.87%
46.0	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated Q8, Q21 1.40%
46.0	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q19 1.39%
46.0	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q19 1.39%
43.1	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N2, Q21 0.71%
43.1	2382.1299	0.0027	NNATVHEQVGGPSLTSDLQAQSK	Deamidated N1, Q21 0.71%
7.0	2380.1308	2.0018	FYGRFAESENGQVERHQVAR	

Mascot: http://www.matrixscience.com/

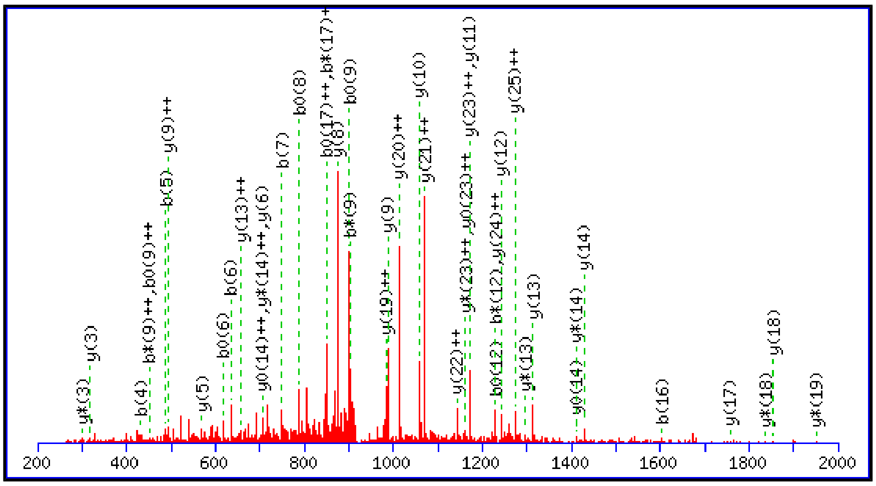
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NISDGFDGIPDNVDAALALPAHSYSGR**
Found in **P04004** in **con_Xuniprot_HUMAN3**, VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 25469: 2772.296082 from(925.105970,3+) intensity(9836.7295) rtinseconds(2194) scans(5644) index(3940)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum4611_scans__5644
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

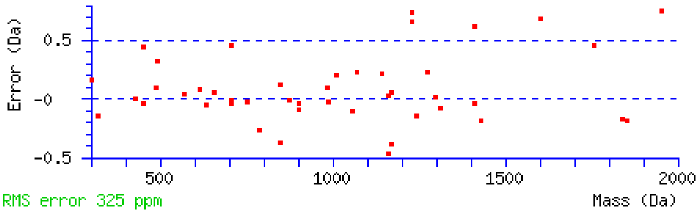
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

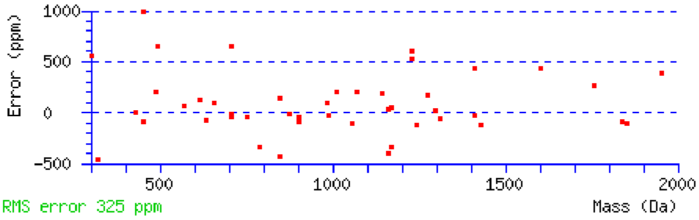


```
Monoisotopic mass of neutral peptide Mr(calc): 2772.2991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1      : Deamidated (NQ)
Ions Score: 47  Expect: 0.0041
Matches : 46/304 fragment ions using 115 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	99.0077	50.0075			N							27
2	229.1183	115.0628	212.0917	106.5495			I	2658.2794	1329.6434	2641.2529	1321.1301	2640.2689	1320.6381	26
3	316.1503	158.5788	299.1238	150.0655	298.1397	149.5735	S	2545.1954	1273.1013	2528.1688	1264.5880	2527.1848	1264.0960	25
4	**431.1773**	216.0923	414.1507	207.5790	413.1667	207.0870	D	2458.1633	1229.5853	2441.1368	1221.0720	2440.1528	1220.5800	24
5	**488.1987**	244.6030	471.1722	236.0897	470.1882	235.5977	G	2343.1364	1172.0718	2326.1099	1163.5586	2325.1258	1163.0666	23
6	**635.2671**	318.1372	618.2406	309.6239	617.2566	309.1319	F	2286.1149	1143.5611	2269.0884	1135.0478	2268.1044	1134.5558	22
7	**750.2941**	375.6507	733.2675	367.1374	732.2835	366.6454	D	2139.0465	1070.0269	2122.0200	1061.5136	2121.0360	1061.0216	21
8	807.3155	404.1614	790.2890	395.6481	789.3050	395.1561	G	2024.0196	1012.5134	2006.9930	1004.0002	2006.0090	1003.5081	20
9	920.3996	460.7034	903.3731	452.1902	902.3890	451.6982	I	1966.9981	984.0027	1949.9716	975.4894	1948.9876	974.9974	19
10	1017.4524	509.2298	1000.4258	500.7165	999.4418	500.2245	P	***1853.9141***	927.4607	1836.8875	918.9474	1835.9035	918.4554	18
11	1132.4793	566.7433	1115.4528	558.2300	1114.4687	557.7380	D	***1756.8613***	878.9343	1739.8347	870.4210	1738.8507	869.9290	17
12	1246.5222	623.7648	1229.4957	615.2515	1228.5117	614.7595	N	1641.8343	821.4208	1624.8078	812.9075	1623.8238	812.4155	16
13	1345.5907	673.2990	1328.5641	664.7857	1327.5801	664.2937	V	1527.7914	764.3993	1510.7649	755.8861	1509.7809	755.3941	15
14	1460.6176	730.8124	1443.5910	722.2992	1442.6070	721.8072	D	***1428.7230***	714.8651	1411.6965	706.3519	1410.7124	705.8599	14
15	1531.6547	766.3310	1514.6282	757.8177	1513.6441	757.3257	A	***1313.6961***	657.3517	1296.6695	648.8384	1295.6855	648.3464	13
16	**1602.6918**	801.8495	1585.6653	793.3363	1584.6813	792.8443	A	***1242.6589***	621.8331	1225.6324	613.3198	1224.6484	612.8278	12
17	1715.7759	858.3916	1698.7493	849.8783	1697.7653	849.3863	L	***1171.6218***	586.3146	1154.5953	577.8013	1153.6113	577.3093	11
18	1786.8130	893.9101	1769.7865	885.3969	1768.8024	884.9049	A	***1058.5378***	529.7725	1041.5112	521.2592	1040.5272	520.7672	10
19	1899.8971	950.4522	1882.8705	941.9389	1881.8865	941.4469	L	***987.5007***	494.2540	970.4741	485.7407	969.4901	485.2487	9
20	1996.9498	998.9786	1979.9233	990.4653	1978.9393	989.9733	P	***874.4166***	437.7119	857.3900	429.1987	856.4060	428.7067	8
21	2067.9869	1034.4971	2050.9604	1025.9838	2049.9764	1025.4918	A	777.3638	389.1856	760.3373	380.6723	759.3533	380.1803	7
22	2205.0459	1103.0266	2188.0193	1094.5133	2187.0353	1094.0213	H	***706.3267***	353.6670	689.3002	345.1537	688.3161	344.6617	6
23	2292.0779	1146.5426	2275.0513	1138.0293	2274.0673	1137.5373	S	***569.2678***	285.1375	552.2413	276.6243	551.2572	276.1323	5

24	2455.1412	1228.0742	2438.1147	1219.5610	2437.1306	1219.0690	**Y**	482.2358	241.6215	465.2092	233.1083	464.2252	232.6162	**4**
25	2542.1732	1271.5903	2525.1467	1263.0770	2524.1627	1262.5850	**S**	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
26	2599.1947	1300.1010	2582.1682	1291.5877	2581.1841	1291.0957	**G**	232.1404	116.5738	215.1139	108.0606			**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of NISDGFDGIPDNVDAALALPAHSYSGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.4	2772.2991	-0.0030	NISDGFDGIPDNVDAALALPAHSYSGR	Deamidated N1 66.25%
44.5	2772.2991	-0.0030	NISDGFDGIPDNVDAALALPAHSYSGR	Deamidated N12 33.75%
4.4	2770.3005	1.9956	NEAALLQSTLEQNHKSEENKSNER	
4.4	2770.3005	1.9956	NEAALLQSTLEQNHKSEENKSNER	
4.4	2770.3005	1.9956	NEAALLQSTLEQNHKSEENKSNER	
4.4	2770.3005	1.9956	NEAALLQSTLEQNHKSEENKSNER	
4.4	2771.2845	1.0116	NEAALLQSTLEQNHKSEENKSNER	
4.3	2772.2881	0.0080	AGIMTSTNRMPPAPPKDQIDLGNNSM	
4.3	2772.2881	0.0080	MSNNGLDIQDKPPAPPMRNTSTMIGA	
4.3	2772.2881	0.0080	MSNNGLDIQDKPPAPPMRNTSTMIGA	

Mascot: http://www.matrixscience.com/

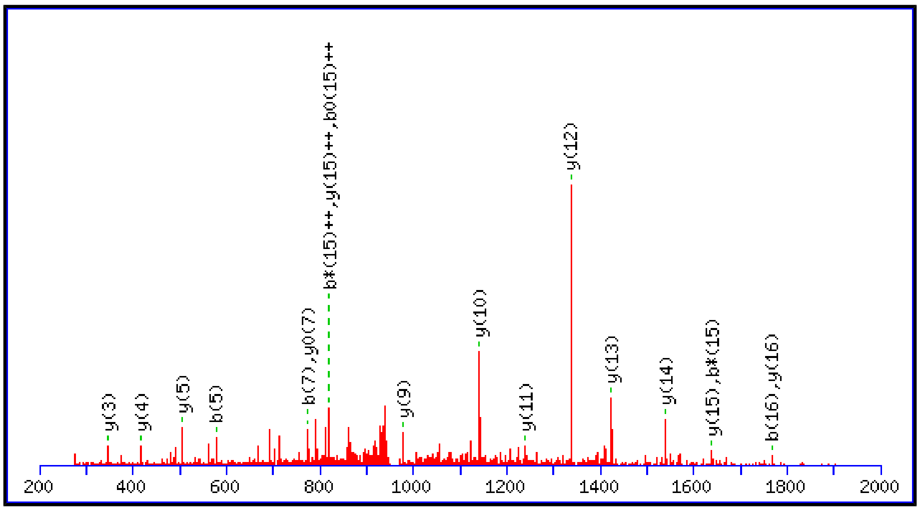
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FEVDSPVYNATWSASLK**
Found in **P04114** in **con_Xuniprot_HUMAN3**, APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2

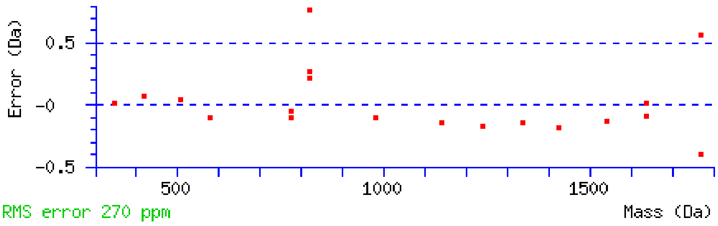
Match to Query 11534: 1913.911148 from(957.962850,2+) intensity(57838.4414) rtinseconds(1911) scans(4792) index(8470)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum4134_scans__4792
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

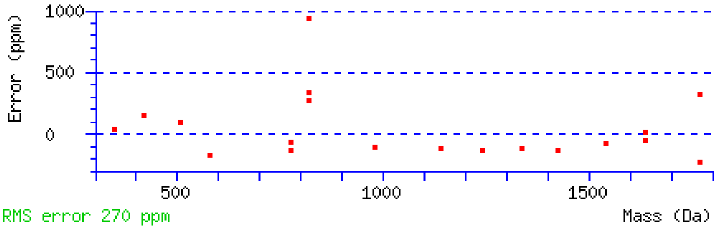
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1913.9047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 102 **Expect:** 1.3e-008
Matches : 19/170 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	148.0757	74.5415					F							17
2	277.1183	139.0628			259.1077	130.0575	E	***1767.8436***	884.4254	1750.8170	875.9121	1749.8330	875.4201	16
3	376.1867	188.5970			358.1761	179.5917	V	***1638.8010***	819.9041	1621.7744	811.3909	1620.7904	810.8988	15
4	491.2136	246.1105			473.2031	237.1052	D	***1539.7326***	770.3699	1522.7060	761.8566	1521.7220	761.3646	14
5	**578.2457**	289.6265			560.2351	280.6212	S	***1424.7056***	712.8564	1407.6791	704.3432	1406.6951	703.8512	13
6	675.2984	338.1529			657.2879	329.1476	P	***1337.6736***	669.3404	1320.6470	660.8272	1319.6630	660.3352	12
7	**774.3668**	387.6871			756.3563	378.6818	V	***1240.6208***	620.8141	1223.5943	612.3008	1222.6103	611.8088	11
8	937.4302	469.2187			919.4196	460.2134	Y	***1141.5524***	571.2798	1124.5259	562.7666	1123.5419	562.2746	10
9	1052.4571	526.7322	1035.4306	518.2189	1034.4466	517.7269	N	***978.4891***	489.7482	961.4625	481.2349	960.4785	480.7429	9
10	1123.4942	562.2508	1106.4677	553.7375	1105.4837	553.2455	A	863.4621	432.2347	846.4356	423.7214	845.4516	423.2294	8
11	1224.5419	612.7746	1207.5154	604.2613	1206.5313	603.7693	T	792.4250	396.7162	775.3985	388.2029	774.4145	387.7109	7
12	1410.6212	705.8143	1393.5947	697.3010	1392.6107	696.8090	W	691.3774	346.1923	674.3508	337.6790	673.3668	337.1870	6
13	1497.6533	749.3303	1480.6267	740.8170	1479.6427	740.3250	S	***505.2980***	253.1527	488.2715	244.6394	487.2875	244.1474	5
14	1568.6904	784.8488	1551.6638	776.3355	1550.6798	775.8435	A	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	4
15	1655.7224	828.3648	1638.6958	819.8516	1637.7118	819.3596	S	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
16	**1768.8065**	884.9069	1751.7799	876.3936	1750.7959	875.9016	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FEVDSPVYNATWSASLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
102.5	1913.9047	0.0065	FEVDSPVYNATWSASLK
8.3	1913.9022	0.0090	IVMDFLGFNWNWINK
8.1	1912.9023	1.0089	CEECGKALIQFSTLTR
6.5	1913.9087	0.0024	GSPNAVMEHRQMTSPKK
6.2	1913.9153	-0.0041	NQISNAAVHMAVATEQTK
6.2	1913.9153	-0.0041	NQISNAAVHMAVATEQTK
6.2	1913.9153	-0.0041	NQISNAAVHMAVATEQTK
6.1	1913.9022	0.0090	IVMDFLGFNWNWINK
5.8	1912.9023	1.0089	MNECTHLIVQEPKGQK
5.8	1913.9087	0.0024	GSPNAVMEHRQMTSPKK

Mascot: http://www.matrixscience.com/

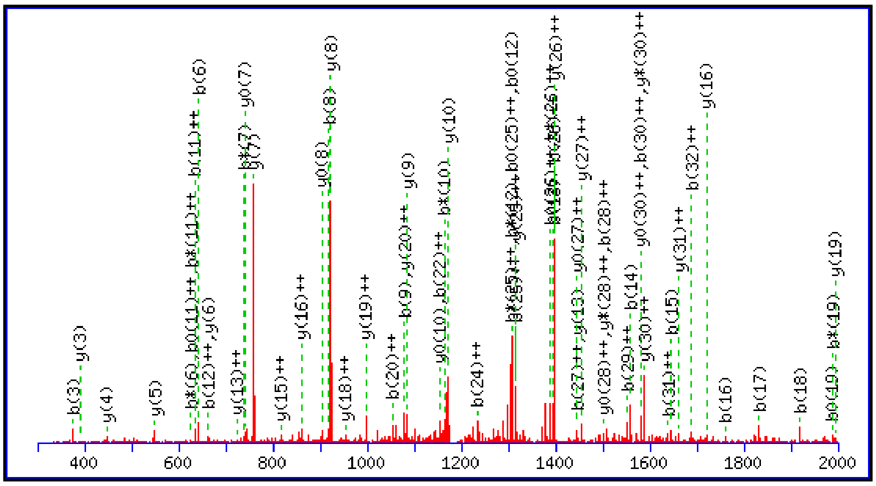
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR**
Found in **P04114** in **con_Xuniprot_HUMAN3**, APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2

Match to Query 27814: 3550.558392 from(1184.526740,3+) intensity(166897.3750) rtinseconds(1957) scans(5190) index(24072)
Title: 111019_Est_MI_YS_G_05Spectrum4484_scans__5190
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

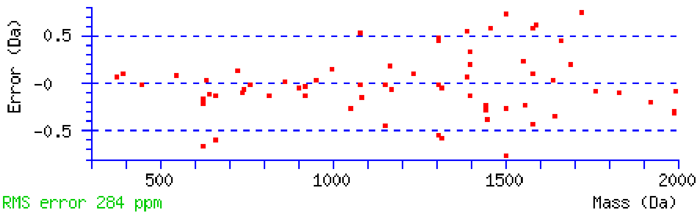
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

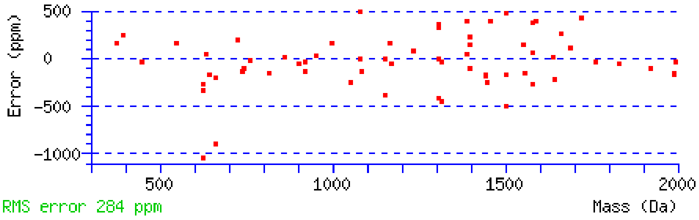


Monoisotopic mass of neutral peptide Mr(calc): 3550.5471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
Ions Score: 78 **Expect:** 1.2e-006
Matches : 66/364 fragment ions using 102 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							33
2	228.1343	114.5708	211.1077	106.0575			V	3423.4958	1712.2515	3406.4692	1703.7383	3405.4852	1703.2462	32
3	**375.2027**	188.1050	358.1761	179.5917			F	3324.4274	1662.7173	3307.4008	1654.2040	3306.4168	1653.7120	31
4	472.2554	236.6314	455.2289	228.1181			P	3177.3589	1589.1831	3160.3324	1580.6698	3159.3484	1580.1778	30
5	529.2769	265.1421	512.2504	256.6288			G	3080.3062	1540.6567	3063.2796	1532.1435	3062.2956	1531.6514	29
6	**642.3610**	321.6841	625.3344	313.1709			L	3023.2847	1512.1460	3006.2582	1503.6327	3005.2742	1503.1407	28
7	756.4039	378.7056	739.3774	370.1923			N	2910.2007	1455.6040	2893.1741	1447.0907	2892.1901	1446.5987	27
8	**919.4672**	460.2373	902.4407	451.7240			Y	2796.1577	1398.5825	2779.1312	1390.0692	2778.1472	1389.5772	26
9	**1079.4979**	540.2526	1062.4713	531.7393			C	2633.0944	1317.0508	2616.0678	1308.5376	2615.0838	1308.0456	25
10	1180.5456	590.7764	1163.5190	582.2631	1162.5350	581.7711	T	2473.0637	1237.0355	2456.0372	1228.5222	2455.0532	1228.0302	24
11	1267.5776	***634.2924***	1250.5510	625.7792	1249.5670	625.2871	S	2372.0161	1186.5117	2354.9895	1177.9984	2354.0055	1177.5064	23
12	1324.5991	***662.8032***	1307.5725	654.2899	1306.5885	653.7979	G	2284.9840	1142.9957	2267.9575	1134.4824	2266.9735	1133.9904	22
13	**1395.6362**	698.3217	1378.6096	689.8084	1377.6256	689.3164	A	2227.9626	1114.4849	2210.9360	1105.9717	2209.9520	1105.4796	21
14	**1558.6995**	779.8534	1541.6729	771.3401	1540.6889	770.8481	Y	2156.9255	1078.9664	2139.8989	1070.4531	2138.9149	1069.9611	20
15	**1645.7315**	823.3694	1628.7050	814.8561	1627.7210	814.3641	S	**1993.8621**	997.4347	1976.8356	988.9214	1975.8516	988.4294	19
16	**1760.7585**	880.8829	1743.7319	872.3696	1742.7479	871.8776	N	1906.8301	953.9187	1889.8036	945.4054	1888.8195	944.9134	18
17	**1831.7956**	916.4014	1814.7690	907.8882	1813.7850	907.3961	A	1791.8032	896.4052	1774.7766	887.8919	1773.7926	887.3999	17
18	**1918.8276**	959.9174	1901.8011	951.4042	1900.8170	950.9122	S	**1720.7661**	860.8867	1703.7395	852.3734	1702.7555	851.8814	16
19	2005.8596	1003.4335	1988.8331	994.9202	1987.8491	994.4282	S	1633.7340	817.3706	1616.7075	808.8574	1615.7235	808.3654	15
20	2106.9073	***1053.9573***	2089.8808	1045.4440	2088.8967	1044.9520	T	1546.7020	773.8546	1529.6754	765.3414	1528.6914	764.8494	14
21	2221.9343	1111.4708	2204.9077	1102.9575	2203.9237	1102.4655	D	**1445.6543**	723.3308	1428.6278	714.8175	1427.6438	714.3255	13
22	2308.9663	***1154.9868***	2291.9397	1146.4735	2290.9557	1145.9815	S	1330.6274	665.8173	1313.6008	657.3041	1312.6168	656.8120	12
23	2380.0034	1190.5053	2362.9768	1181.9921	2361.9928	1181.5001	A	1243.5953	622.3013	1226.5688	613.7880	1225.5848	613.2960	11

24	2467.0354	***1234.0214***	2450.0089	1225.5081	2449.0249	1225.0161	**S**	**1172.5582**	586.7828	1155.5317	578.2695	1154.5477	577.7775	**10**
25	2630.0988	***1315.5530***	2613.0722	1307.0397	2612.0882	1306.5477	**Y**	**1085.5262**	543.2667	1068.4997	534.7535	1067.5156	534.2615	**9**
26	2793.1621	***1397.0847***	2776.1355	1388.5714	2775.1515	1388.0794	**Y**	**922.4629**	461.7351	905.4363	453.2218	904.4523	452.7298	**8**
27	2890.2148	***1445.6111***	2873.1883	1437.0978	2872.2043	1436.6058	**P**	**759.3995**	380.2034	742.3730	371.6901	741.3890	371.1981	**7**
28	3003.2989	***1502.1531***	2986.2724	1493.6398	2985.2883	1493.1478	**L**	**662.3468**	331.6770	645.3202	323.1638	644.3362	322.6717	**6**
29	3104.3466	***1552.6769***	3087.3200	1544.1637	3086.3360	1543.6717	**T**	**549.2627**	275.1350	532.2362	266.6217	531.2522	266.1297	**5**
30	3161.3681	***1581.1877***	3144.3415	1572.6744	3143.3575	1572.1824	**G**	**448.2150**	224.6112	431.1885	216.0979	430.2045	215.6059	**4**
31	3276.3950	***1638.7011***	3259.3684	1630.1879	3258.3844	1629.6959	**D**	**391.1936**	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
32	3377.4427	***1689.2250***	3360.4161	1680.7117	3359.4321	1680.2197	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.4	3550.5471	0.0113	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated N16 49.67%
78.3	3550.5471	0.0113	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated N7 48.43%
64.3	3550.5471	0.0113	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated Q1 1.90%
56.5	3549.5631	0.9953	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	
7.0	3550.5408	0.0176	QEPQLCGMGTEQGCWIPVSSDKGSCPQVMER	
3.7	3548.5640	1.9944	CLPLSCTVESAPQQAEDCPVGTDNTCLVNRR	
2.2	3549.5480	1.0104	CLPLSCTVESAPQQAEDCPVGTDNTCLVNRR	
1.6	3550.5690	-0.0106	FSGYMQNDAHEFLSQCLDQLKEDMEKLNK	
1.5	3548.5520	2.0064	MAEYEKQEETMEDIPNPMPEELHGTILNID	
1.5	3548.5520	2.0064	MAEYEKQEETMEDIPNPMPEELHGTILNIN	

Mascot: http://www.matrixscience.com/

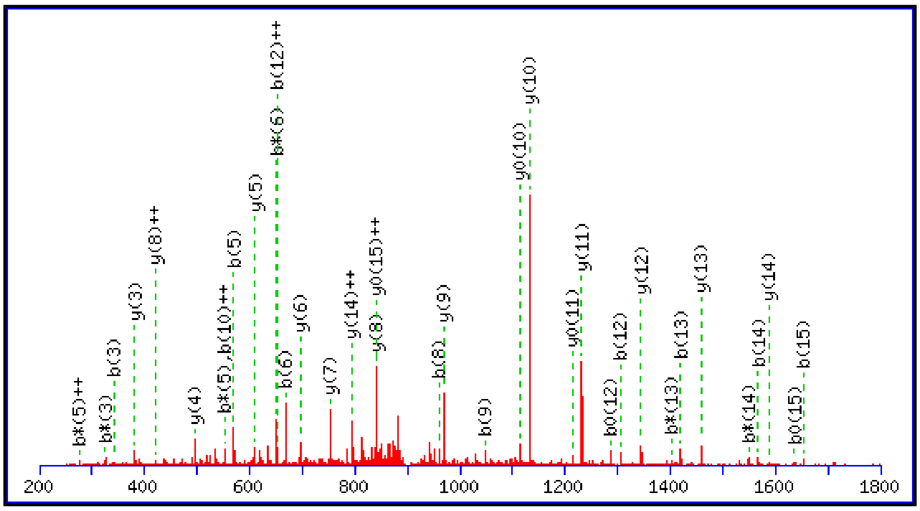
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNQNLVYESGSLNFSK**
Found in **P04114** in **con_Xuniprot_HUMAN3**, APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2

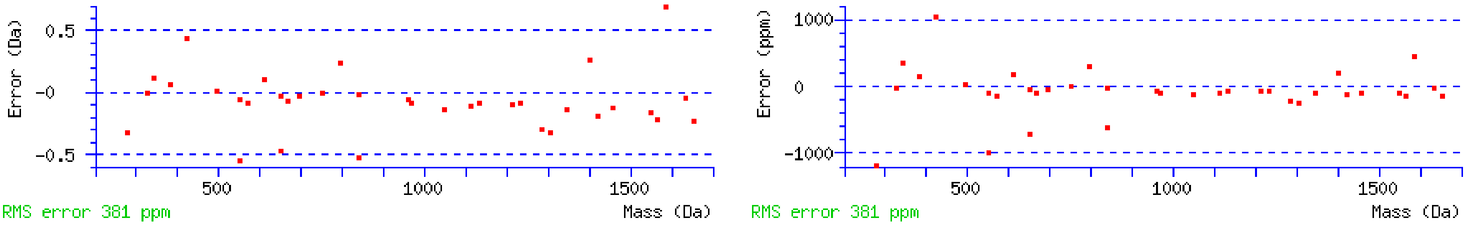
Match to Query 10888: 1798.879088 from(900.446820,2+) intensity(38580.1797) rtinseconds(1411) scans(3219) index(11741)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum2746_scans__3219
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1798.8737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 76 **Expect:** 5.1e-006
Matches : 36/162 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	100.0757	50.5415					**V**							**16**
2	214.1186	107.5629	197.0921	99.0497			**N**	1700.8126	850.9099	1683.7861	842.3967	1682.8020	841.9047	**15**
3	**342.1772**	171.5922	325.1506	163.0790			**Q**	***1586.7697***	793.8885	1569.7431	785.3752	1568.7591	784.8832	**14**
4	456.2201	228.6137	439.1936	220.1004			**N**	***1458.7111***	729.8592	1441.6846	721.3459	1440.7005	720.8539	**13**
5	**569.3042**	285.1557	552.2776	276.6425			**L**	***1344.6682***	672.8377	1327.6416	664.3245	1326.6576	663.8324	**12**
6	**668.3726**	334.6899	651.3461	326.1767			**V**	***1231.5841***	616.2957	1214.5576	607.7824	1213.5735	607.2904	**11**
7	831.4359	416.2216	814.4094	407.7083			**Y**	***1132.5157***	566.7615	1115.4891	558.2482	1114.5051	557.7562	**10**
8	**960.4785**	480.7429	943.4520	472.2296	942.4680	471.7376	**E**	***969.4524***	485.2298	952.4258	476.7165	951.4418	476.2245	**9**
9	**1047.5106**	524.2589	1030.4840	515.7456	1029.5000	515.2536	**S**	***840.4098***	420.7085	823.3832	412.1953	822.3992	411.7032	**8**
10	1104.5320	552.7696	1087.5055	544.2564	1086.5214	543.7644	**G**	***753.3777***	377.1925	736.3512	368.6792	735.3672	368.1872	**7**
11	1191.5640	596.2857	1174.5375	587.7724	1173.5535	587.2804	**S**	***696.3563***	348.6818	679.3297	340.1685	678.3457	339.6765	**6**
12	**1304.6481**	652.8277	1287.6216	644.3144	1286.6375	643.8224	**L**	***609.3243***	305.1658	592.2977	296.6525	591.3137	296.1605	**5**
13	**1419.6750**	710.3412	1402.6485	701.8279	1401.6645	701.3359	**N**	***496.2402***	248.6237	479.2136	240.1105	478.2296	239.6185	**4**
14	**1566.7435**	783.8754	1549.7169	775.3621	1548.7329	774.8701	**F**	***381.2132***	191.1103	364.1867	182.5970	363.2027	182.1050	**3**
15	**1653.7755**	827.3914	1636.7489	818.8781	1635.7649	818.3861	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**



NCBI **BLAST** search of VNQNLVYESGSLNFSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
76.5	1798.8737	0.0054	VNQNLVYESGSLNFSK	Deamidated N13 100.00%
8.7	1798.8737	0.0054	VNQNLVYESGSLNFSK	Deamidated N4 0.00%
6.6	1798.8737	0.0054	VNQNLVYESGSLNFSK	Deamidated Q3 0.00%
6.5	1798.8737	0.0054	VNQNLVYESGSLNFSK	Deamidated N2 0.00%
5.6	1796.8765	2.0026	SGENAANIASELARHTR	
5.3	1796.8765	2.0026	SGENAANIASELARHTR	
1.9	1798.8737	0.0054	LVEHNLSSITHYQQK	
1.9	1798.8737	0.0054	YYKIANNPTTDKENK	
1.1	1797.8758	1.0033	GRLGERLENYDDPHK	

Mascot: http://www.matrixscience.com/

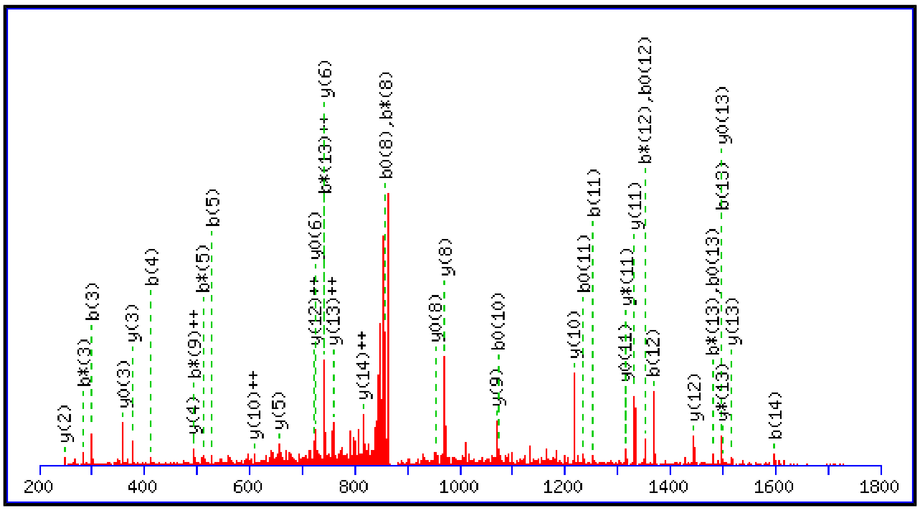
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NNALDFVTKSYNETK**
Found in **P04114** in **con_Xuniprot_HUMAN3**, APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2

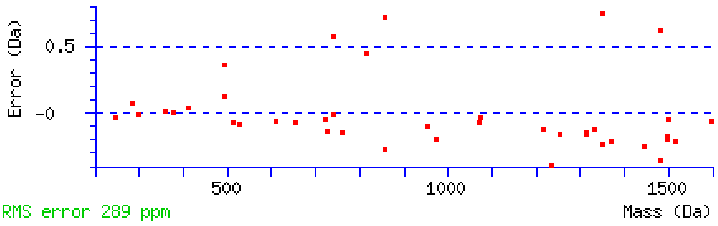
Match to Query 9362: 1743.835248 from(872.924900,2+) intensity(37395.5039) rtinseconds(1433) scans(3491) index(25304)
Title: 111019_Est_MI_YS_G_07Spectrum2960_scans__3491
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

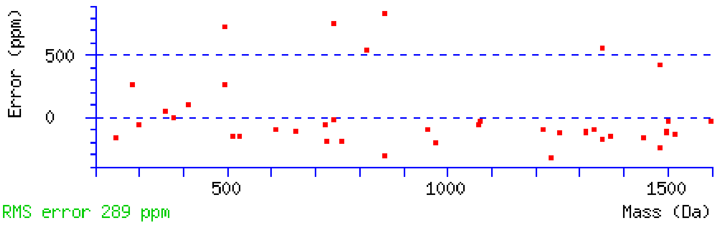
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1743.8315
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.00086
Matches : 41/158 fragment ions using 90 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	229.0931	115.0502	212.0666	106.5369			N	1630.7959	815.9016	1613.7693	807.3883	1612.7853	806.8963	14
3	**300.1302**	150.5688	283.1037	142.0555			A	***1516.7530***	758.8801	1499.7264	750.3668	1498.7424	749.8748	13
4	**413.2143**	207.1108	396.1878	198.5975			L	***1445.7159***	723.3616	1428.6893	714.8483	1427.7053	714.3563	12
5	**528.2413**	264.6243	511.2147	256.1110	510.2307	255.6190	D	***1332.6318***	666.8195	1315.6052	658.3063	1314.6212	657.8143	11
6	675.3097	338.1585	658.2831	329.6452	657.2991	329.1532	F	***1217.6048***	609.3061	1200.5783	600.7928	1199.5943	600.3008	10
7	774.3781	387.6927	757.3515	379.1794	756.3675	378.6874	V	***1070.5364***	535.7719	1053.5099	527.2586	1052.5259	526.7666	9
8	875.4258	438.2165	858.3992	429.7032	857.4152	429.2112	T	***971.4680***	486.2376	954.4415	477.7244	953.4575	477.2324	8
9	1003.5207	502.2640	986.4942	493.7507	985.5102	493.2587	K	870.4203	435.7138	853.3938	427.2005	852.4098	426.7085	7
10	1090.5527	545.7800	1073.5262	537.2667	1072.5422	536.7747	S	***742.3254***	371.6663	725.2988	363.1531	724.3148	362.6610	6
11	**1253.6161**	627.3117	1236.5895	618.7984	1235.6055	618.3064	Y	***655.2933***	328.1503	638.2668	319.6370	637.2828	319.1450	5
12	**1368.6430**	684.8251	1351.6165	676.3119	1350.6325	675.8199	N	***492.2300***	246.6186	475.2035	238.1054	474.2195	237.6134	4
13	**1497.6856**	749.3464	1480.6591	740.8332	1479.6750	740.3412	E	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	3
14	**1598.7333**	799.8703	1581.7067	791.3570	1580.7227	790.8650	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NNALDFVTKSYNETK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.2	1743.8315	0.0037	NNALDFVTKSYNETK	Deamidated N12 99.98%
12.9	1743.8315	0.0037	NNALDFVTKSYNETK	Deamidated N2 0.01%
12.3	1743.8315	0.0037	NNALDFVTKSYNETK	Deamidated N1 0.01%
4.0	1743.8290	0.0063	HKLIQLMWNDWNK	
3.8	1743.8275	0.0077	DQGPDKENSGAIEASVK	
2.5	1743.8315	0.0037	HQEVQDELEFITEK	
1.1	1743.8349	0.0003	NSPVEGAPLSGQDMTLK	
0.6	1742.8369	0.9983	DMELSHLRSRQQDK	
0.6	1742.8369	0.9983	DMELSHLRSRQQDK	
0.6	1743.8289	0.0064	QNGAGPLSGQPPNQDHK	

Mascot: http://www.matrixscience.com/

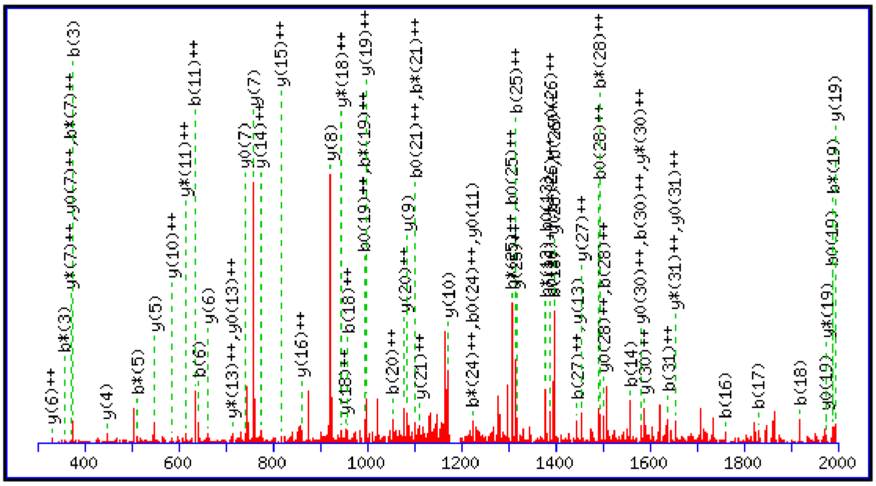
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR**
Found in **P04114** in **con_Xuniprot_HUMAN3**, APOB_HUMAN Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2

Match to Query 27828: 3552.547272 from(1185.189700,3+) intensity(0.0000) rtinseconds(1947) scans(5163) index(24068)
Title: 111019_Est_MI_YS_G_05Spectrum4462_scans__5163
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

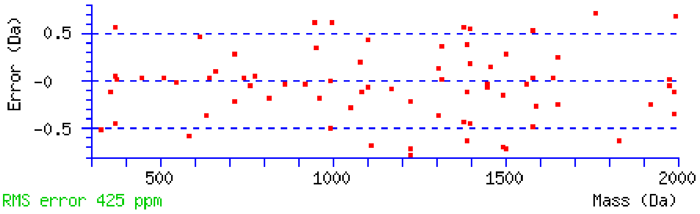
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

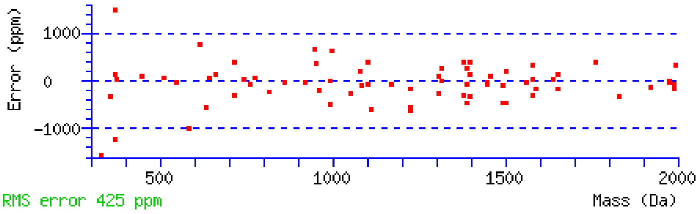


Monoisotopic mass of neutral peptide Mr(calc): 3550.5471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.0084
Matches : 73/364 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							33
2	228.1343	114.5708	211.1077	106.0575			V	3423.4958	1712.2515	3406.4692	1703.7383	3405.4852	1703.2462	32
3	**375.2027**	188.1050	358.1761	179.5917			F	3324.4274	1662.7173	3307.4008	1654.2040	3306.4168	1653.7120	31
4	472.2554	236.6314	455.2289	228.1181			P	3177.3589	1589.1831	3160.3324	1580.6698	3159.3484	1580.1778	30
5	529.2769	265.1421	512.2504	256.6288			G	3080.3062	1540.6567	3063.2796	1532.1435	3062.2956	1531.6514	29
6	**642.3610**	321.6841	625.3344	313.1709			L	3023.2847	1512.1460	3006.2582	1503.6327	3005.2742	1503.1407	28
7	757.3879	379.1976	740.3614	370.6843			N	2910.2007	1455.6040	2893.1741	1447.0907	2892.1901	1446.5987	27
8	920.4512	460.7293	903.4247	452.2160			Y	2795.1737	1398.0905	2778.1472	1389.5772	2777.1631	1389.0852	26
9	1080.4819	540.7446	1063.4553	532.2313			C	2632.1104	1316.5588	2615.0838	1308.0456	2614.0998	1307.5535	25
10	1181.5296	591.2684	1164.5030	582.7552	1163.5190	582.2631	T	2472.0797	1236.5435	2455.0532	1228.0302	2454.0692	1227.5382	24
11	1268.5616	***634.7844***	1251.5351	626.2712	1250.5510	625.7792	S	2371.0321	1186.0197	2354.0055	1177.5064	2353.0215	1177.0144	23
12	1325.5831	663.2952	1308.5565	654.7819	1307.5725	654.2899	G	2284.0000	1142.5037	2266.9735	1133.9904	2265.9895	1133.4984	22
13	**1396.6202**	698.8137	1379.5936	690.3005	1378.6096	689.8084	A	2226.9786	1113.9929	2209.9520	1105.4796	2208.9680	1104.9876	21
14	**1559.6835**	780.3454	1542.6570	771.8321	1541.6729	771.3401	Y	2155.9414	1078.4744	2138.9149	1069.9611	2137.9309	1069.4691	20
15	1646.7155	823.8614	1629.6890	815.3481	1628.7050	814.8561	S	**1992.8781**	996.9427	1975.8516	988.4294	1974.8676	987.9374	19
16	**1760.7585**	880.8829	1743.7319	872.3696	1742.7479	871.8776	N	1905.8461	953.4267	1888.8195	944.9134	1887.8355	944.4214	18
17	**1831.7956**	916.4014	1814.7690	907.8882	1813.7850	907.3961	A	1791.8032	896.4052	1774.7766	887.8919	1773.7926	887.3999	17
18	**1918.8276**	***959.9174***	1901.8011	951.4042	1900.8170	950.9122	S	1720.7661	860.8867	1703.7395	852.3734	1702.7555	851.8814	16
19	2005.8596	1003.4335	1988.8331	994.9202	1987.8491	994.4282	S	1633.7340	817.3706	1616.7075	808.8574	1615.7235	808.3654	15
20	2106.9073	***1053.9573***	2089.8808	1045.4440	2088.8967	1044.9520	T	1546.7020	773.8546	1529.6754	765.3414	1528.6914	764.8494	14
21	2221.9343	1111.4708	2204.9077	1102.9575	2203.9237	1102.4655	D	**1445.6543**	723.3308	1428.6278	714.8175	1427.6438	714.3255	13
22	2308.9663	1154.9868	2291.9397	1146.4735	2290.9557	1145.9815	S	1330.6274	665.8173	1313.6008	657.3041	1312.6168	656.8120	12
23	2380.0034	1190.5053	2362.9768	1181.9921	2361.9928	1181.5001	A	1243.5953	622.3013	1226.5688	613.7880	1225.5848	613.2960	11

24	2467.0354	1234.0214	2450.0089	1225.5081	2449.0249	1225.0161	**S**	**1172.5582**	586.7828	1155.5317	578.2695	1154.5477	577.7775	**10**
25	2630.0988	***1315.5530***	2613.0722	1307.0397	2612.0882	1306.5477	**Y**	**1085.5262**	543.2667	1068.4997	534.7535	1067.5156	534.2615	**9**
26	2793.1621	***1397.0847***	2776.1355	1388.5714	2775.1515	1388.0794	**Y**	**922.4629**	461.7351	905.4363	453.2218	904.4523	452.7298	**8**
27	2890.2148	***1445.6111***	2873.1883	1437.0978	2872.2043	1436.6058	**P**	**759.3995**	380.2034	742.3730	371.6901	741.3890	371.1981	**7**
28	3003.2989	***1502.1531***	2986.2724	1493.6398	2985.2883	1493.1478	**L**	**662.3468**	331.6770	645.3202	323.1638	644.3362	322.6717	**6**
29	3104.3466	1552.6769	3087.3200	1544.1637	3086.3360	1543.6717	**T**	**549.2627**	275.1350	532.2362	266.6217	531.2522	266.1297	**5**
30	3161.3681	***1581.1877***	3144.3415	1572.6744	3143.3575	1572.1824	**G**	**448.2150**	224.6112	431.1885	216.0979	430.2045	215.6059	**4**
31	3276.3950	***1638.7011***	3259.3684	1630.1879	3258.3844	1629.6959	**D**	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	**3**
32	3377.4427	1689.2250	3360.4161	1680.7117	3359.4321	1680.2197	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.5	3550.5471	2.0002	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated N7 40.56%
38.6	3550.5471	2.0002	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated N16 33.12%
37.6	3550.5471	2.0002	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	Deamidated Q1 26.31%
32.3	3551.5311	1.0162	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	
29.1	3551.5311	1.0162	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	
27.4	3551.5311	1.0162	QVFPGLNYCTSGAYSNASSTDSASYYPLTGDTR	
4.5	3550.5524	1.9948	DLQICQTILDPLNDMMDTVSEEDQNPDALAK	
4.5	3550.5524	1.9948	DLQICQTILDPLNDMMDTVSEEDQNPDALAK	
4.3	3551.5365	1.0108	ALADPNQDEESVTDMMDNLPDLITQCIQLDK	
4.3	3550.5524	1.9948	ALADPNQDEESVTDMMDNLPDLITQCIQLDK	

Mascot: http://www.matrixscience.com/

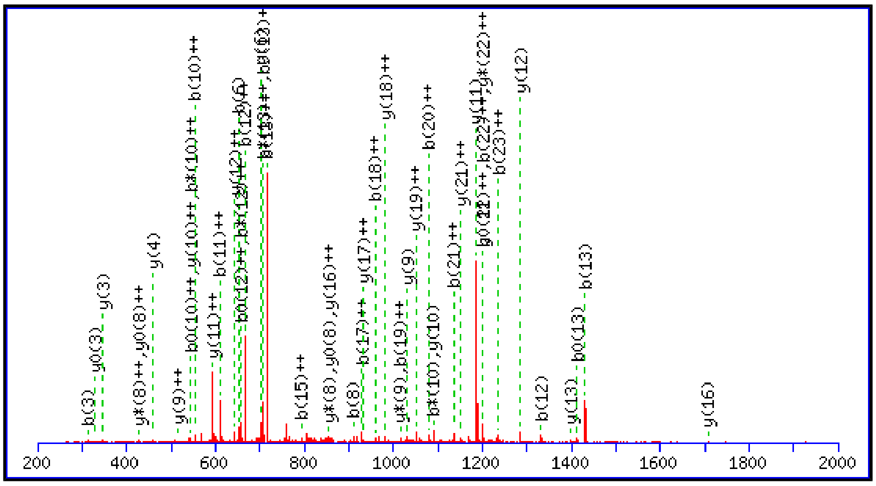
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AELSNHTRPVILVPGCLGNQLEAK**
Found in **P04180** in **con_Xuniprot_HUMAN3**, LCAT_HUMAN Phosphatidylcholine-sterol acyltransferase OS=Homo sapiens GN=LCAT PE=1 SV=1

Match to Query 22317: 2616.375582 from(873.132470,3+) intensity(179783.5469) rtinseconds(1540) scans(3807) index(3783)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum3128_scans__3807
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

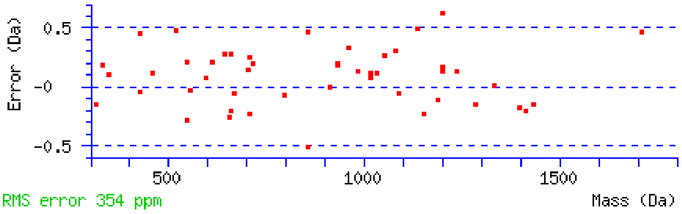
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

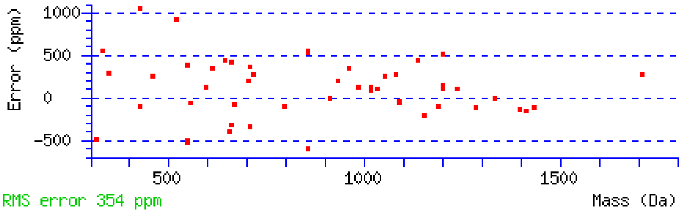


Monoisotopic mass of neutral peptide Mr(calc): 2616.3693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 67 **Expect:** 3.5e-005
Matches : 52/262 fragment ions using 89 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							24
2	201.0870	101.0471			183.0764	92.0418	E	2546.3395	1273.6734	2529.3130	1265.1601	2528.3290	1264.6681	23
3	**314.1710**	157.5892			296.1605	148.5839	L	2417.2969	1209.1521	2400.2704	1200.6388	2399.2864	1200.1468	22
4	401.2031	201.1052			383.1925	192.0999	S	2304.2129	1152.6101	2287.1863	1144.0968	2286.2023	1143.6048	21
5	516.2300	258.6186	499.2035	250.1054	498.2195	249.6134	N	2217.1808	1109.0941	2200.1543	1100.5808	2199.1703	1100.0888	20
6	**653.2889**	327.1481	636.2624	318.6348	635.2784	318.1428	H	2102.1539	1051.5806	2085.1274	1043.0673	2084.1433	1042.5753	19
7	754.3366	377.6719	737.3101	369.1587	736.3260	368.6667	T	1965.0950	983.0511	1948.0684	974.5379	1947.0844	974.0459	18
8	**910.4377**	455.7225	893.4112	447.2092	892.4272	446.7172	R	1864.0473	932.5273	1847.0208	924.0140	1846.0368	923.5220	17
9	1007.4905	504.2489	990.4639	495.7356	989.4799	495.2436	P	**1707.9462**	854.4767	1690.9197	845.9635	1689.9356	845.4715	16
10	1106.5589	***553.7831***	1089.5323	545.2698	1088.5483	544.7778	V	1610.8934	805.9504	1593.8669	797.4371	1592.8829	796.9451	15
11	1219.6430	***610.3251***	1202.6164	601.8118	1201.6324	601.3198	I	1511.8250	756.4162	1494.7985	747.9029	1493.8145	747.4109	14
12	**1332.7270**	***666.8672***	1315.7005	658.3539	1314.7165	657.8619	L	**1398.7410**	699.8741	1381.7144	691.3608	1380.7304	690.8688	13
13	**1431.7954**	***716.4014***	1414.7689	707.8881	1413.7849	707.3961	V	**1285.6569**	643.3321	1268.6304	634.8188	1267.6463	634.3268	12
14	1528.8482	764.9277	1511.8217	756.4145	1510.8376	755.9225	P	**1186.5885**	593.7979	1169.5619	585.2846	1168.5779	584.7926	11
15	1585.8697	***793.4385***	1568.8431	784.9252	1567.8591	784.4332	G	**1089.5357**	545.2715	1072.5092	536.7582	1071.5252	536.2662	10
16	1745.9003	873.4538	1728.8738	864.9405	1727.8898	864.4485	C	**1032.5143**	516.7608	1015.4877	508.2475	1014.5037	507.7555	9
17	1858.9844	***929.9958***	1841.9578	921.4826	1840.9738	920.9905	L	872.4836	436.7454	855.4571	428.2322	854.4730	427.7402	8
18	1916.0058	***958.5066***	1898.9793	949.9933	1897.9953	949.5013	G	759.3995	380.2034	742.3730	371.6901	741.3890	371.1981	7
19	2030.0488	***1015.5280***	2013.0222	1007.0147	2012.0382	1006.5227	N	**702.3781**	351.6927	685.3515	343.1794	684.3675	342.6874	6
20	2158.1073	***1079.5573***	2141.0808	1071.0440	2140.0968	1070.5520	Q	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
21	2271.1914	***1136.0993***	2254.1649	1127.5861	2253.1808	1127.0941	L	**460.2766**	230.6419	443.2500	222.1287	442.2660	221.6366	4
22	2400.2340	***1200.6206***	2383.2075	1192.1074	2382.2234	1191.6154	E	**347.1925**	174.0999	330.1660	165.5866	329.1819	165.0946	3

23	2471.2711	***1236.1392***	2454.2446	1227.6259	2453.2606	1227.1339	**A**	218.1499	109.5786	201.1234	101.0653			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of AELSNHTRPVILVPGCLGNQLEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
67.0	2616.3693	0.0062	AELSNHTRPVILVPGCLGNQLEAK	Deamidated N5 94.40%
51.7	2616.3693	0.0062	AELSNHTRPVILVPGCLGNQLEAK	Deamidated Q20 2.80%
51.7	2616.3693	0.0062	AELSNHTRPVILVPGCLGNQLEAK	Deamidated N19 2.80%
41.9	2615.3853	0.9903	AELSNHTRPVILVPGCLGNQLEAK	
11.1	2614.3642	2.0114	ELPVNAQNYVRFIEDELQIPVK	
9.6	2616.3880	-0.0124	MIWEQNTGIIVMITNLVEKGRR	
8.4	2616.3628	0.0128	SPATMRPMLAPKTAVAAAPPSVAGHR	
6.2	2616.3812	-0.0056	VVAPNAYYTRPVYPNNIAIAPRR	
5.8	2615.3653	1.0102	VNGIREEALQTAQALSDQTVKTLK	
4.8	2616.3772	-0.0016	SVAAEGALLPQTPPSPRNLIPHGHR	

Mascot: http://www.matrixscience.com/

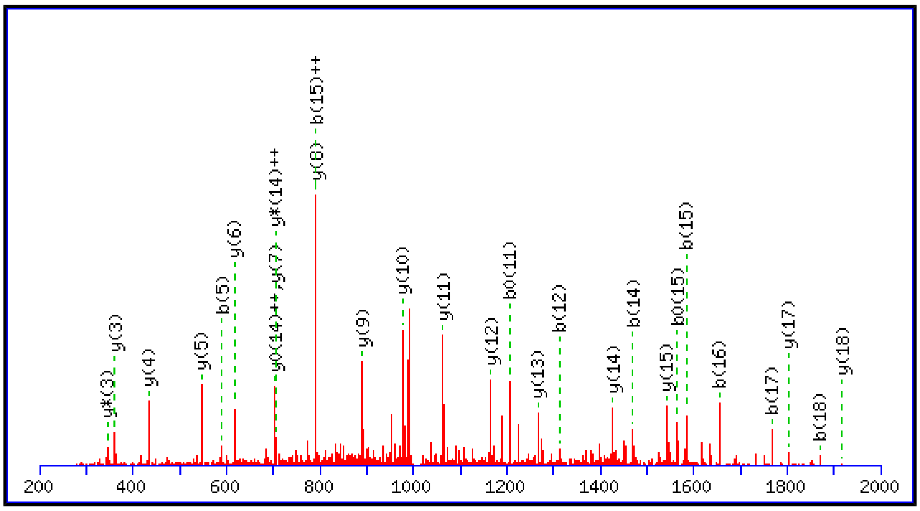
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIDFNCTTSSVSSALANTK**
Found in **P04196** in **con_Xuniprot_HUMAN3**, HRG_HUMAN Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1

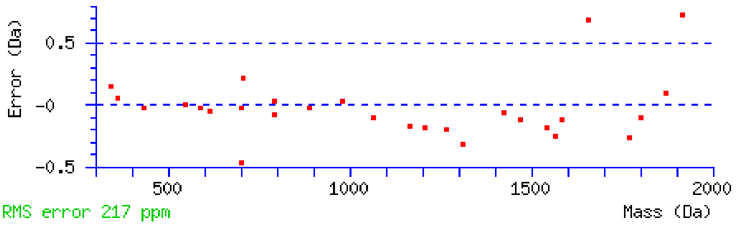
Match to Query 12292: 2014.954708 from(1008.484630,2+) intensity(25883.1406) rtinseconds(3079) scans(7899) index(5950)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum6988_scans__7899
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

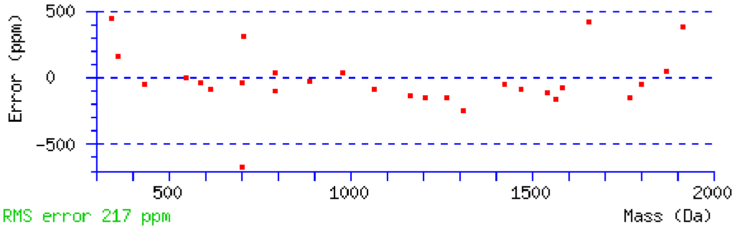
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2014.9517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 142 **Expect:** 1.3e-012
Matches : 28/202 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							19
2	213.1598	107.0835					I	***1916.8906***	958.9489	1899.8641	950.4357	1898.8800	949.9437	18
3	328.1867	164.5970			310.1761	155.5917	D	***1803.8065***	902.4069	1786.7800	893.8936	1785.7960	893.4016	17
4	475.2551	238.1312			457.2445	229.1259	F	1688.7796	844.8934	1671.7530	836.3802	1670.7690	835.8882	16
5	**590.2821**	295.6447	573.2555	287.1314	572.2715	286.6394	N	***1541.7112***	771.3592	1524.6846	762.8460	1523.7006	762.3539	15
6	750.3127	375.6600	733.2862	367.1467	732.3021	366.6547	C	***1426.6842***	713.8458	1409.6577	705.3325	1408.6737	704.8405	14
7	851.3604	426.1838	834.3338	417.6706	833.3498	417.1785	T	***1266.6536***	633.8304	1249.6270	625.3172	1248.6430	624.8251	13
8	952.4081	476.7077	935.3815	468.1944	934.3975	467.7024	T	***1165.6059***	583.3066	1148.5794	574.7933	1147.5953	574.3013	12
9	1039.4401	520.2237	1022.4135	511.7104	1021.4295	511.2184	S	***1064.5582***	532.7828	1047.5317	524.2695	1046.5477	523.7775	11
10	1126.4721	563.7397	1109.4456	555.2264	1108.4616	554.7344	S	***977.5262***	489.2667	960.4997	480.7535	959.5156	480.2615	10
11	1225.5405	613.2739	1208.5140	604.7606	1207.5300	604.2686	V	***890.4942***	445.7507	873.4676	437.2374	872.4836	436.7454	9
12	**1312.5726**	656.7899	1295.5460	648.2766	1294.5620	647.7846	S	***791.4258***	396.2165	774.3992	387.7032	773.4152	387.2112	8
13	1399.6046	700.3059	1382.5780	691.7927	1381.5940	691.3006	S	***704.3937***	352.7005	687.3672	344.1872	686.3832	343.6952	7
14	**1470.6417**	735.8245	1453.6152	727.3112	1452.6311	726.8192	A	***617.3617***	309.1845	600.3352	300.6712	599.3511	300.1792	6
15	**1583.7258**	792.3665	1566.6992	783.8532	1565.7152	783.3612	L	***546.3246***	273.6659	529.2980	265.1527	528.3140	264.6606	5
16	**1654.7629**	827.8851	1637.7363	819.3718	1636.7523	818.8798	A	***433.2405***	217.1239	416.2140	208.6106	415.2300	208.1186	4
17	**1768.8058**	884.9065	1751.7793	876.3933	1750.7952	875.9013	N	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	3
18	**1869.8535**	935.4304	1852.8269	926.9171	1851.8429	926.4251	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
19							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VIDFNCTTSSVSSALANTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
142.4	2014.9517	0.0030	VIDFNCTTSSVSSALANTK	Deamidated N5 100.00%
78.9	2014.9517	0.0030	VIDFNCTTSSVSSALANTK	Deamidated N17 0.00%
6.8	2014.9531	0.0016	MNTSRFADHHDLLTETK	
6.5	2013.9425	1.0122	TQNMNNPLKLHNRNATK	
5.0	2012.9473	2.0074	MVPESGSVSTSGFSAGRNVK	
4.3	2013.9425	1.0122	TQNMNNPLKLHNRNATK	
3.2	2014.9452	0.0095	YRDSMAIQELMASGTNTK	
2.4	2014.9537	0.0010	VWQGSKYEFGQPRQFR	
1.2	2014.9492	0.0055	GAVYAENCILAAFSICQK	
1.0	2014.9492	0.0055	GAVYAENCILAAFSICQK	

Mascot: http://www.matrixscience.com/

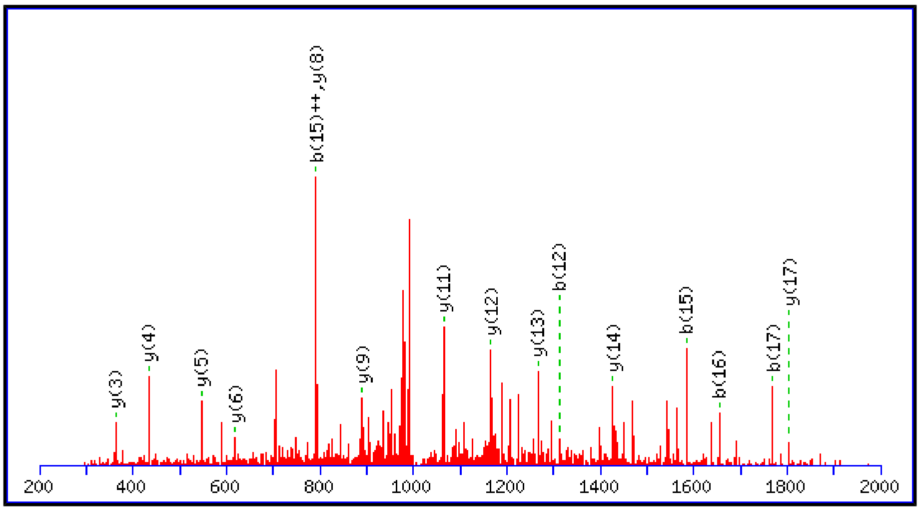
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VIDFNCTTSSVSSALANTK**
Found in **P04196** in **con_Xuniprot_HUMAN3**, HRG_HUMAN Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1

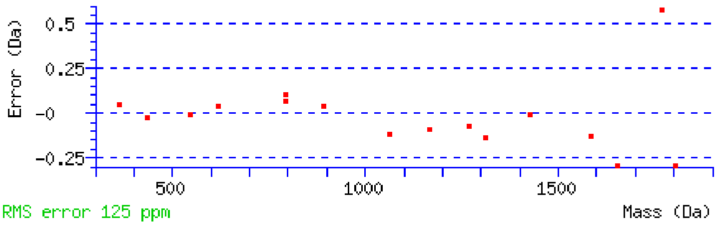
Match to Query 12496: 2015.942608 from(1008.978580,2+) intensity(48878.3750) rtinseconds(1676) scans(4377) index(4426)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum3714_scans__4377
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

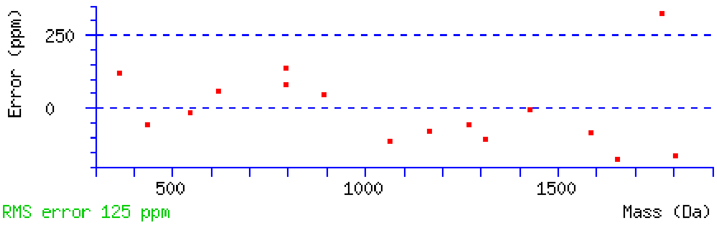
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2015.9357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
N17    : Deamidated (NQ)
Ions Score: 105  Expect: 5.7e-009
Matches : 16/202 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	100.0757	50.5415					V							19
2	213.1598	107.0835					I	1917.8746	959.4409	1900.8481	950.9277	1899.8641	950.4357	18
3	328.1867	164.5970			310.1761	155.5917	D	***1804.7906***	902.8989	1787.7640	894.3856	1786.7800	893.8936	17
4	475.2551	238.1312			457.2445	229.1259	F	1689.7636	845.3854	1672.7371	836.8722	1671.7530	836.3802	16
5	590.2821	295.6447	573.2555	287.1314	572.2715	286.6394	N	1542.6952	771.8512	1525.6686	763.3380	1524.6846	762.8460	15
6	750.3127	375.6600	733.2862	367.1467	732.3021	366.6547	C	***1427.6683***	714.3378	1410.6417	705.8245	1409.6577	705.3325	14
7	851.3604	426.1838	834.3338	417.6706	833.3498	417.1785	T	***1267.6376***	634.3224	1250.6111	625.8092	1249.6270	625.3172	13
8	952.4081	476.7077	935.3815	468.1944	934.3975	467.7024	T	***1166.5899***	583.7986	1149.5634	575.2853	1148.5794	574.7933	12
9	1039.4401	520.2237	1022.4135	511.7104	1021.4295	511.2184	S	***1065.5422***	533.2748	1048.5157	524.7615	1047.5317	524.2695	11
10	1126.4721	563.7397	1109.4456	555.2264	1108.4616	554.7344	S	978.5102	489.7587	961.4837	481.2455	960.4997	480.7535	10
11	1225.5405	613.2739	1208.5140	604.7606	1207.5300	604.2686	V	***891.4782***	446.2427	874.4516	437.7295	873.4676	437.2374	9
12	**1312.5726**	656.7899	1295.5460	648.2766	1294.5620	647.7846	S	***792.4098***	396.7085	775.3832	388.1953	774.3992	387.7032	8
13	1399.6046	700.3059	1382.5780	691.7927	1381.5940	691.3006	S	705.3777	353.1925	688.3512	344.6792	687.3672	344.1872	7
14	1470.6417	735.8245	1453.6152	727.3112	1452.6311	726.8192	A	***618.3457***	309.6765	601.3192	301.1632	600.3352	300.6712	6
15	**1583.7258**	792.3665	1566.6992	783.8532	1565.7152	783.3612	L	***547.3086***	274.1579	530.2821	265.6447	529.2980	265.1527	5
16	**1654.7629**	827.8851	1637.7363	819.3718	1636.7523	818.8798	A	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	4
17	**1769.7898**	885.3985	1752.7633	876.8853	1751.7793	876.3933	N	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	3
18	1870.8375	935.9224	1853.8110	927.4091	1852.8269	926.9171	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
19							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VIDFNCTTSSVSSALANTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
105.4	2015.9357	0.0069	VIDFNCTTSSVSSALANTK
4.8	2015.9371	0.0055	MNTSRFADHHDLLTETK
4.4	2015.9411	0.0015	DPWSMYQLQYVSRSEK
2.4	2014.9452	0.9974	YRDSMAIQELMASGTNTK
2.4	2014.9492	0.9934	GAVYAENCILAAFSICQK
1.8	2014.9371	1.0055	GQVFNTIDENSDFVSLTK
0.7	2013.9360	2.0066	LETEMQSYRCRLNAAR

Mascot: http://www.matrixscience.com/

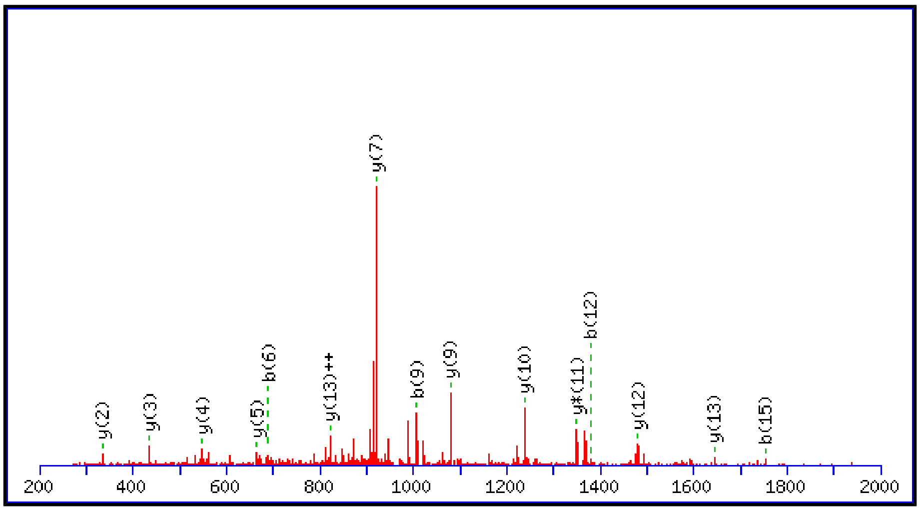
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQVYLQCGTPCNLTCR**
Found in **P04275** in **con_Xuniprot_HUMAN3**, VWF_HUMAN von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

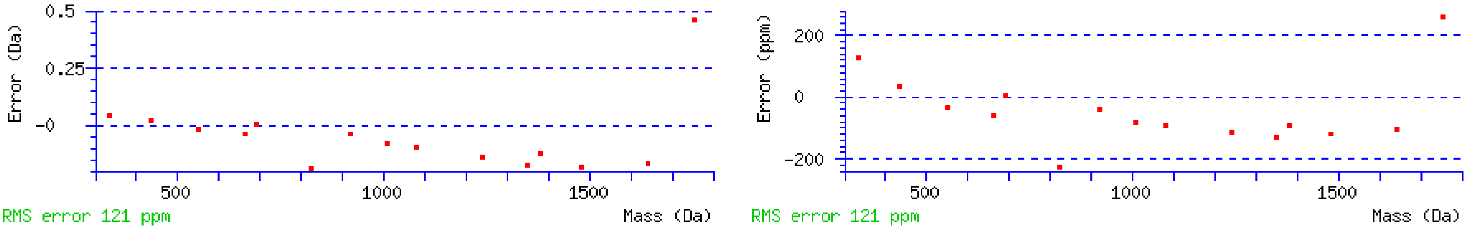
Match to Query 11736: 1926.845928 from(964.430240,2+) intensity(12668.8857) rtinseconds(1004) scans(2173) index(27780)
Title: 111019_Est_MI_YS_G_11Spectrum1853_scans__2173
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1926.8387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 73 **Expect:** 4.5e-006
Matches : 15/158 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	58.0287	29.5180					G							16
2	186.0873	93.5473	169.0608	85.0340			Q	1870.8245	935.9159	1853.7979	927.4026	1852.8139	926.9106	15
3	285.1557	143.0815	268.1292	134.5682			V	1742.7659	871.8866	1725.7393	863.3733	1724.7553	862.8813	14
4	448.2191	224.6132	431.1925	216.0999			Y	***1643.6975***	822.3524	1626.6709	813.8391	1625.6869	813.3471	13
5	561.3031	281.1552	544.2766	272.6419			L	***1480.6341***	740.8207	1463.6076	732.3074	1462.6236	731.8154	12
6	**689.3617**	345.1845	672.3352	336.6712			Q	1367.5501	684.2787	1350.5235	675.7654	1349.5395	675.2734	11
7	849.3924	425.1998	832.3658	416.6865			C	***1239.4915***	620.2494	1222.4649	611.7361	1221.4809	611.2441	10
8	906.4138	453.7105	889.3873	445.1973			G	***1079.4608***	540.2341	1062.4343	531.7208	1061.4503	531.2288	9
9	**1007.4615**	504.2344	990.4349	495.7211	989.4509	495.2291	T	1022.4394	511.7233	1005.4128	503.2101	1004.4288	502.7180	8
10	1104.5143	552.7608	1087.4877	544.2475	1086.5037	543.7555	P	***921.3917***	461.1995	904.3652	452.6862	903.3811	452.1942	7
11	1264.5449	632.7761	1247.5184	624.2628	1246.5343	623.7708	C	824.3389	412.6731	807.3124	404.1598	806.3284	403.6678	6
12	**1379.5719**	690.2896	1362.5453	681.7763	1361.5613	681.2843	N	***664.3083***	332.6578	647.2817	324.1445	646.2977	323.6525	5
13	1492.6559	746.8316	1475.6294	738.3183	1474.6454	737.8263	L	***549.2813***	275.1443	532.2548	266.6310	531.2708	266.1390	4
14	1593.7036	797.3554	1576.6770	788.8422	1575.6930	788.3502	T	***436.1973***	218.6023	419.1707	210.0890	418.1867	209.5970	3
15	**1753.7342**	877.3708	1736.7077	868.8575	1735.7237	868.3655	C	***335.1496***	168.0784	318.1231	159.5652			2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of GQVYLQCGTPCNLTCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.2	1926.8387	0.0073	GQVYLQCGTPCNLTCR	Deamidated N12 100.00%
20.5	1926.8387	0.0073	GQVYLQCGTPCNLTCR	Deamidated Q6 0.00%
10.1	1925.8369	1.0091	MHINKCAMCQSIFDR	
9.7	1926.8387	0.0073	GQVYLQCGTPCNLTCR	Deamidated Q2 0.00%
8.1	1926.8451	0.0008	AKMEEAFNQSQNLCQK	
0.5	1926.8451	0.0008	AKMEEAFNQSQNLCQK	
0.5	1926.8451	0.0008	AKMEEAFNQSQNLCQK	

Mascot: http://www.matrixscience.com/

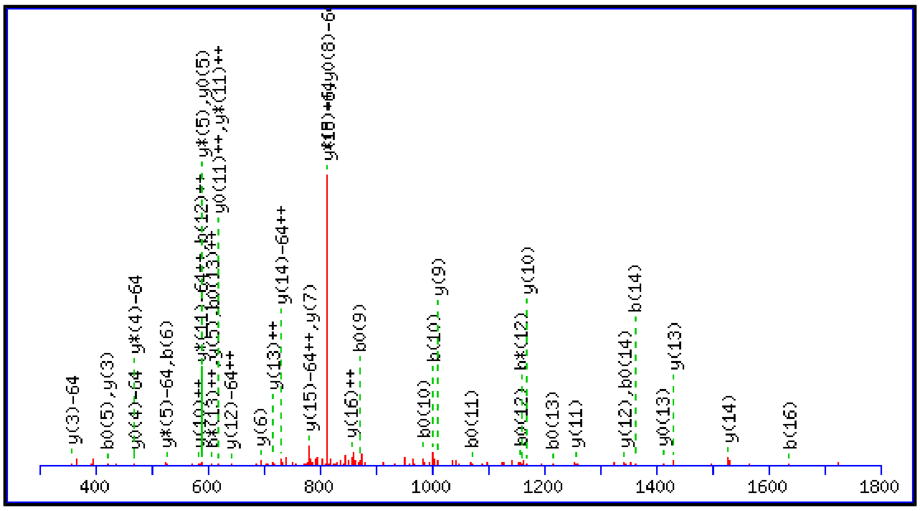
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASPPSSSCNISSGEMQK**
Found in **P04275** in **con_Xuniprot_HUMAN3**, VWF_HUMAN von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

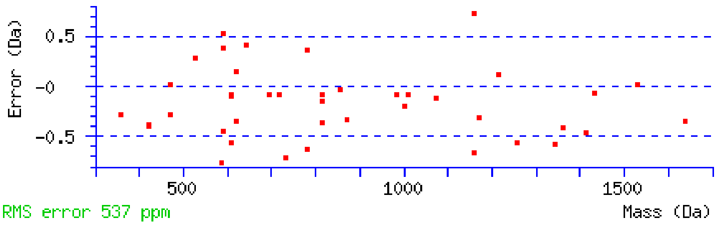
Match to Query 10184: 1782.746448 from(892.380500,2+) intensity(1824.0968) rtinseconds(290) scans(391) index(27719)
Title: 111019_Est_MI_YS_G_11Spectrum281_scans__391
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

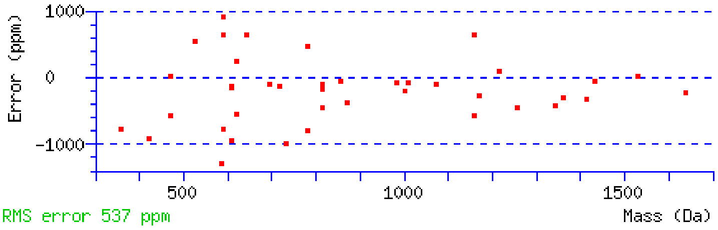
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1782.7400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 43 **Expect:** 0.0022
Matches : 44/262 fragment ions using 84 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					**A**							**17**
2	159.0764	80.0418			141.0659	71.0366	**S**	1712.7102	856.8587	1695.6836	848.3455	1694.6996	847.8535	**16**
3	256.1292	128.5682			238.1186	119.5629	**P**	1625.6782	813.3427	1608.6516	804.8294	1607.6676	804.3374	**15**
4	353.1819	177.0946			335.1714	168.0893	**P**	***1528.6254***	764.8163	1511.5989	756.3031	1510.6148	755.8111	**14**
5	440.2140	220.6106			422.2034	211.6053	**S**	***1431.5726***	716.2900	1414.5461	707.7767	1413.5621	707.2847	**13**
6	**527.2460**	264.1266			509.2354	255.1214	**S**	***1344.5406***	672.7739	1327.5141	664.2607	1326.5300	663.7687	**12**
7	614.2780	307.6427			596.2675	298.6374	**S**	***1257.5086***	629.2579	1240.4820	620.7447	1239.4980	620.2526	**11**
8	774.3087	387.6580			756.2981	378.6527	**C**	***1170.4766***	585.7419	1153.4500	577.2286	1152.4660	576.7366	**10**
9	889.3356	445.1714	872.3091	436.6582	871.3251	436.1662	**N**	***1010.4459***	505.7266	993.4194	497.2133	992.4353	496.7213	**9**
10	**1002.4197**	501.7135	985.3931	493.2002	984.4091	492.7082	**I**	895.4190	448.2131	878.3924	439.6998	877.4084	439.2078	**8**
11	1089.4517	545.2295	1072.4252	536.7162	1071.4411	536.2242	**S**	***782.3349***	391.6711	765.3083	383.1578	764.3243	382.6658	**7**
12	1176.4837	588.7455	1159.4572	580.2322	1158.4732	579.7402	**S**	***695.3029***	348.1551	678.2763	339.6418	677.2923	339.1498	**6**
13	1233.5052	617.2562	1216.4787	608.7430	1215.4946	608.2510	**G**	***608.2708***	304.6391	591.2443	296.1258	590.2603	295.6338	**5**
14	**1362.5478**	681.7775	1345.5213	673.2643	1344.5372	672.7723	**E**	551.2494	276.1283	534.2228	267.6151	533.2388	267.1230	**4**
15	1509.5832	755.2952	1492.5567	746.7820	1491.5726	746.2900	**M**	***422.2068***	211.6070	405.1802	203.0938			**3**
16	**1637.6418**	819.3245	1620.6152	810.8113	1619.6312	810.3192	**Q**	275.1714	138.0893	258.1448	129.5761			**2**
17							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ASPPSSSCNISSGEMQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.2	1782.7400	0.0064	ASPPSSSCNISSGEMQK	Deamidated N9 99.26%
21.9	1782.7400	0.0064	ASPPSSSCNISSGEMQK	Deamidated Q16 0.74%
3.6	1782.7449	0.0015	NSGFFMEMMSMKPAK	
0.1	1782.7518	-0.0054	ASPEYEENMHRYQK	

Mascot: http://www.matrixscience.com/

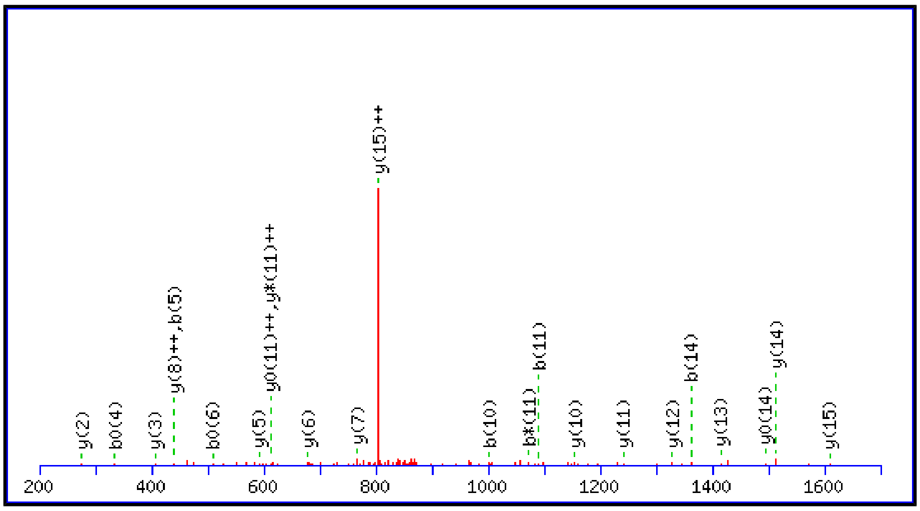
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASPPSSSCNISSGEMQK**
Found in **P04275** in **con_Xuniprot_HUMAN3**, VWF_HUMAN von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

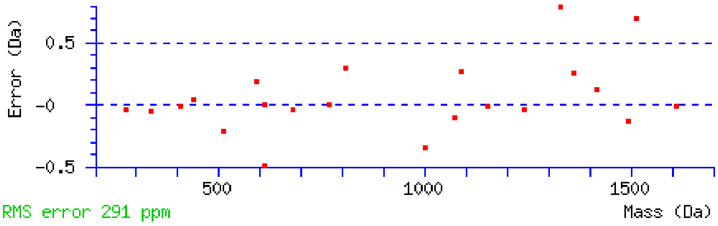
Match to Query 9871: 1766.749228 from(884.381890,2+) intensity(1502.4076) rtinseconds(355) scans(545) index(28002)
Title: 111019_Est_MI_YS_G_12Spectrum431_scans__545
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

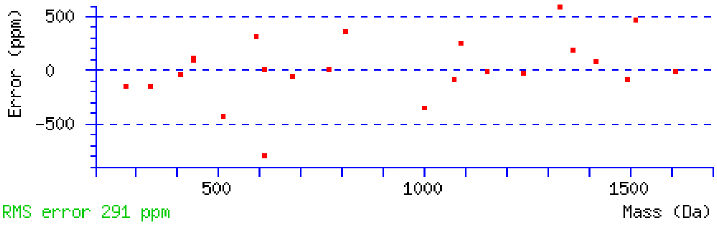
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1766.7451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 43 **Expect:** 0.0029
Matches : 23/168 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	72.0444	36.5258					A							17
2	159.0764	80.0418			141.0659	71.0366	S	1696.7153	848.8613	1679.6887	840.3480	1678.7047	839.8560	16
3	256.1292	128.5682			238.1186	119.5629	P	***1609.6832***	805.3453	1592.6567	796.8320	1591.6727	796.3400	15
4	353.1819	177.0946			335.1714	168.0893	P	***1512.6305***	756.8189	1495.6039	748.3056	1494.6199	747.8136	14
5	**440.2140**	220.6106			422.2034	211.6053	S	***1415.5777***	708.2925	1398.5512	699.7792	1397.5672	699.2872	13
6	527.2460	264.1266			509.2354	255.1214	S	***1328.5457***	664.7765	1311.5191	656.2632	1310.5351	655.7712	12
7	614.2780	307.6427			596.2675	298.6374	S	***1241.5137***	621.2605	1224.4871	612.7472	1223.5031	612.2552	11
8	774.3087	387.6580			756.2981	378.6527	C	***1154.4816***	577.7445	1137.4551	569.2312	1136.4711	568.7392	10
9	889.3356	445.1714	872.3091	436.6582	871.3251	436.1662	N	994.4510	497.7291	977.4244	489.2159	976.4404	488.7238	9
10	**1002.4197**	501.7135	985.3931	493.2002	984.4091	492.7082	I	879.4240	440.2157	862.3975	431.7024	861.4135	431.2104	8
11	**1089.4517**	545.2295	1072.4252	536.7162	1071.4411	536.2242	S	***766.3400***	383.6736	749.3134	375.1604	748.3294	374.6683	7
12	1176.4837	588.7455	1159.4572	580.2322	1158.4732	579.7402	S	***679.3080***	340.1576	662.2814	331.6443	661.2974	331.1523	6
13	1233.5052	617.2562	1216.4787	608.7430	1215.4946	608.2510	G	***592.2759***	296.6416	575.2494	288.1283	574.2654	287.6363	5
14	**1362.5478**	681.7775	1345.5213	673.2643	1344.5372	672.7723	E	535.2545	268.1309	518.2279	259.6176	517.2439	259.1256	4
15	1493.5883	747.2978	1476.5617	738.7845	1475.5777	738.2925	M	***406.2119***	203.6096	389.1853	195.0963			3
16	1621.6469	811.3271	1604.6203	802.8138	1603.6363	802.3218	Q	***275.1714***	138.0893	258.1448	129.5761			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ASPPSSSCNISSGEMQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
43.0	1766.7451	0.0041	ASPPSSSCNISSGEMQK	Deamidated N9 99.64%
18.6	1766.7451	0.0041	ASPPSSSCNISSGEMQK	Deamidated Q16 0.36%
3.3	1764.7438	2.0054	ESWGQESNAGNQTVVR	
3.0	1764.7447	2.0045	RMEEFDKMVDYNR	
2.8	1765.7433	1.0059	MGELYRGAMTSSMER	
2.5	1766.7442	0.0050	RESETESPNSLESNTS	
2.5	1766.7442	0.0050	RESETESPNSLESNTS	
2.5	1766.7464	0.0028	RGIQMCSEENGGAWR	
2.5	1766.7464	0.0028	RGIQMCSEENGGAWR	
1.9	1765.7453	1.0039	RECWPAQWGPYCR	

Mascot: http://www.matrixscience.com/

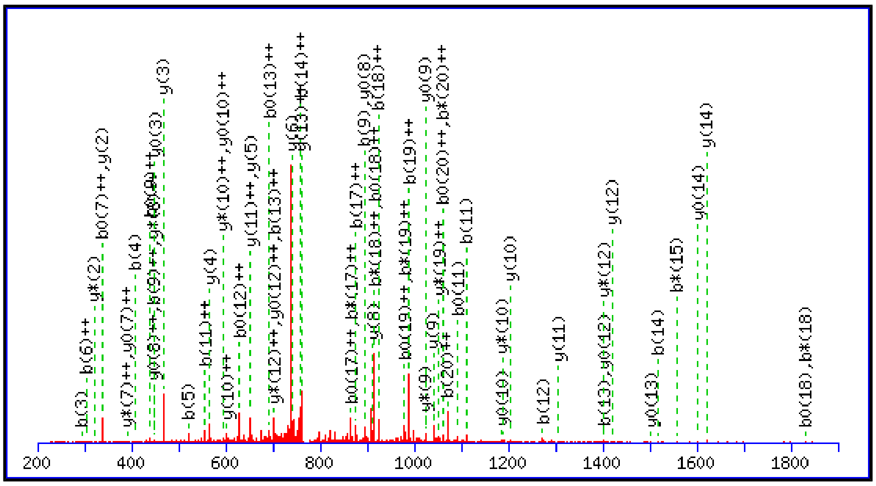
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **HGVIISSTVDTYENGSSVEYR**
Found in **P05160** in **con_Xuniprot_HUMAN3**, F13B_HUMAN Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3

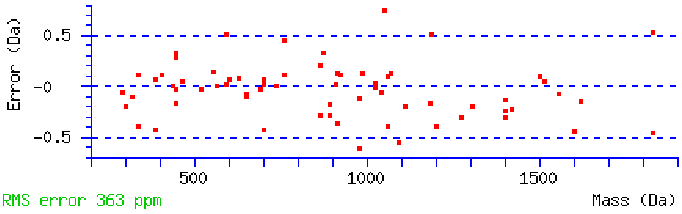
Match to Query 15147: 2313.073362 from(772.031730,3+) intensity(25915.6582) rtinseconds(1157) scans(2720) index(25259)
Title: 111019_Est_MI_YS_G_07Spectrum2299_scans__2720
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

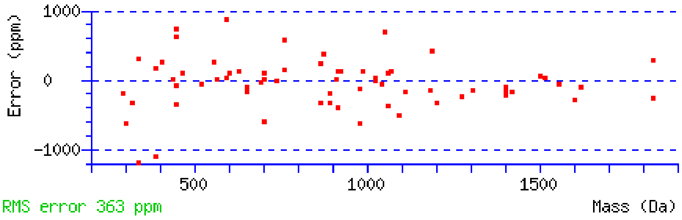
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2313.0761
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0048
Matches : 67/200 fragment ions using 105 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367					H							21
2	195.0877	98.0475					G	2177.0244	1089.0159	2159.9979	1080.5026	2159.0139	1080.0106	20
3	***294.1561***	147.5817					V	2120.0030	1060.5051	2102.9764	1051.9919	2101.9924	1051.4998	19
4	***407.2401***	204.1237					I	2020.9346	1010.9709	2003.9080	1002.4576	2002.9240	1001.9656	18
5	***520.3242***	260.6657					I	1907.8505	954.4289	1890.8240	945.9156	1889.8399	945.4236	17
6	607.3562	***304.1817***			589.3457	295.1765	S	1794.7664	897.8869	1777.7399	889.3736	1776.7559	888.8816	16
7	694.3882	347.6978			676.3777	338.6925	S	1707.7344	854.3708	1690.7079	845.8576	1689.7239	845.3656	15
8	795.4359	398.2216			777.4254	389.2163	T	***1620.7024***	810.8548	1603.6758	802.3416	1602.6918	801.8495	14
9	***894.5043***	***447.7558***			876.4938	438.7505	V	1519.6547	760.3310	1502.6282	751.8177	1501.6441	751.3257	13
10	1009.5313	505.2693			991.5207	496.2640	D	***1420.5863***	710.7968	1403.5597	702.2835	1402.5757	701.7915	12
11	***1110.5790***	***555.7931***			1092.5684	546.7878	T	***1305.5594***	653.2833	1288.5328	644.7700	1287.5488	644.2780	11
12	***1273.6423***	637.3248			1255.6317	628.3195	Y	***1204.5117***	602.7595	1187.4851	594.2462	1186.5011	593.7542	10
13	***1402.6849***	***701.8461***			1384.6743	692.8408	E	***1041.4483***	521.2278	1024.4218	512.7145	1023.4378	512.2225	9
14	***1517.7118***	***759.3596***	1500.6853	750.8463	1499.7013	750.3543	N	***912.4058***	456.7065	895.3792	448.1932	894.3952	447.7012	8
15	1574.7333	787.8703	1557.7067	779.3570	1556.7227	778.8650	G	797.3788	399.1930	780.3523	390.6798	779.3682	390.1878	7
16	1661.7653	831.3863	1644.7388	822.8730	1643.7548	822.3810	S	***740.3573***	370.6823	723.3308	362.1690	722.3468	361.6770	6
17	1748.7974	***874.9023***	1731.7708	866.3890	1730.7868	865.8970	S	***653.3253***	327.1663	636.2988	318.6530	635.3148	318.1610	5
18	1847.8658	***924.4365***	1830.8392	915.9232	1829.8552	915.4312	V	***566.2933***	283.6503	549.2667	275.1370	548.2827	274.6450	4
19	1976.9084	***988.9578***	1959.8818	980.4445	1958.8978	979.9525	E	***467.2249***	234.1161	450.1983	225.6028	449.2143	225.1108	3
20	2139.9717	***1070.4895***	2122.9451	1061.9762	2121.9611	1061.4842	Y	***338.1823***	169.5948	321.1557	161.0815			2
21							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of HGVIISSTVDTYENGSSVEYR
(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	2313.0761	-0.0027	HGVIISSTVDTYENGSSVEYR
4.3	2312.0702	1.0031	HLMKNNPGQAQQTGLATNTER
3.9	2312.0702	1.0031	HLMKNNPGQAQQTGLATNTER
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.6	2312.0637	1.0096	DSRMHQNQICEGNGIAPLVR
3.5	2312.0685	1.0049	NYHHLDNMYGFVVQEGFVK

Mascot: http://www.matrixscience.com/

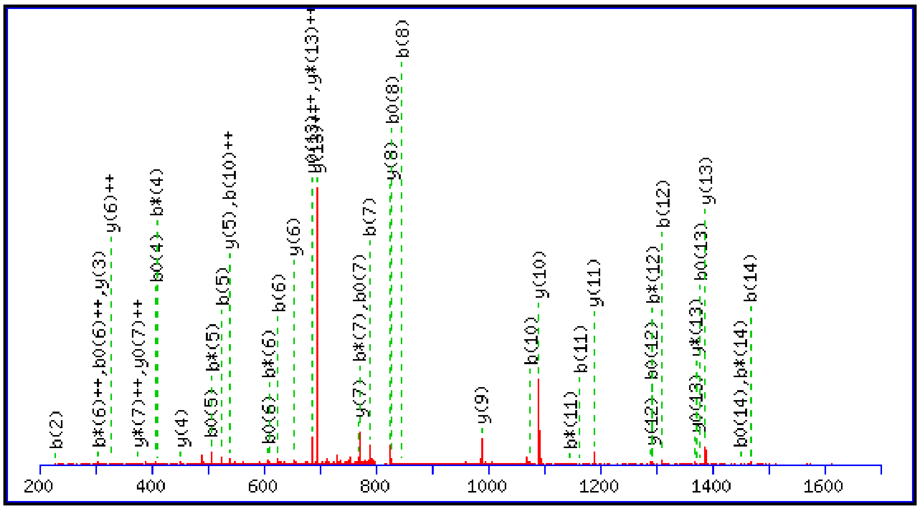
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNPTVTYGNDSFSAK**
Found in **E7ESS4** in **con_Xuniprot_HUMAN3**, E7ESS4_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=2 SV=1

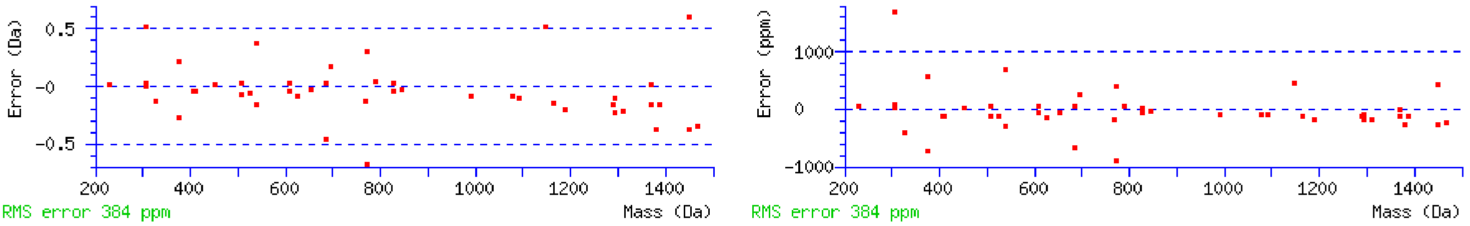
Match to Query 7689: 1613.764428 from(807.889490,2+) intensity(44953.8711) rtinseconds(1058) scans(2473) index(26516)
Title: 111019_Est_MI_YS_G_09Spectrum2121_scans__2473
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1613.7573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0008
Matches : 46/156 fragment ions using 93 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**15**
2	**228.1343**	114.5708	211.1077	106.0575			**N**	1501.6805	751.3439	1484.6540	742.8306	1483.6700	742.3386	**14**
3	325.1870	163.0972	308.1605	154.5839			**P**	***1387.6376***	694.3224	1370.6111	685.8092	1369.6270	685.3172	**13**
4	426.2347	213.6210	409.2082	205.1077	408.2241	204.6157	**T**	***1290.5848***	645.7961	1273.5583	637.2828	1272.5743	636.7908	**12**
5	**525.3031**	263.1552	508.2766	254.6419	507.2926	254.1499	**V**	***1189.5372***	595.2722	1172.5106	586.7589	1171.5266	586.2669	**11**
6	**626.3508**	313.6790	609.3243	305.1658	608.3402	304.6738	**T**	***1090.4687***	545.7380	1073.4422	537.2247	1072.4582	536.7327	**10**
7	**789.4141**	395.2107	772.3876	386.6974	771.4036	386.2054	**Y**	***989.4211***	495.2142	972.3945	486.7009	971.4105	486.2089	**9**
8	**846.4356**	423.7214	829.4090	415.2082	828.4250	414.7162	**G**	***826.3577***	413.6825	809.3312	405.1692	808.3472	404.6772	**8**
9	961.4625	481.2349	944.4360	472.7216	943.4520	472.2296	**N**	***769.3363***	385.1718	752.3097	376.6585	751.3257	376.1665	**7**
10	**1076.4895**	538.7484	1059.4629	530.2351	1058.4789	529.7431	**D**	***654.3093***	327.6583	637.2828	319.1450	636.2988	318.6530	**6**
11	**1163.5215**	582.2644	1146.4950	573.7511	1145.5109	573.2591	**S**	***539.2824***	270.1448	522.2558	261.6316	521.2718	261.1395	**5**
12	**1310.5899**	655.7986	1293.5634	647.2853	1292.5794	646.7933	**F**	***452.2504***	226.6288	435.2238	218.1155	434.2398	217.6235	**4**
13	1397.6220	699.3146	1380.5954	690.8013	1379.6114	690.3093	**S**	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
14	**1468.6591**	734.8332	1451.6325	726.3199	1450.6485	725.8279	**A**	218.1499	109.5786	201.1234	101.0653			**2**
15							**K**	147.1128	74.0600	130.0863	65.5468			**1**



NCBI **BLAST** search of LNPTVTYGNDSFSAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
53.7	1613.7573	0.0071	LNPTVTYGNDSFSAK	Deamidated N9 99.97%
18.8	1613.7573	0.0071	LNPTVTYGNDSFSAK	Deamidated N2 0.03%
7.5	1613.7694	-0.0050	LVNFPMDGHACPLK	
6.0	1612.7562	1.0082	NYPATFWVNPQFK	
5.3	1612.7654	0.9990	LLNYETIIMNESR	
2.9	1613.7719	-0.0074	HQQNSPMLKLNSAK	
2.9	1613.7719	-0.0074	HQQNSPMLKLNSAK	
2.9	1613.7719	-0.0074	HQQNSPMLKLNSAK	
2.9	1613.7719	-0.0074	HQQNSPMLKLNSAK	
2.9	1613.7579	0.0065	RHDRENEEMIASK	

Mascot: http://www.matrixscience.com/

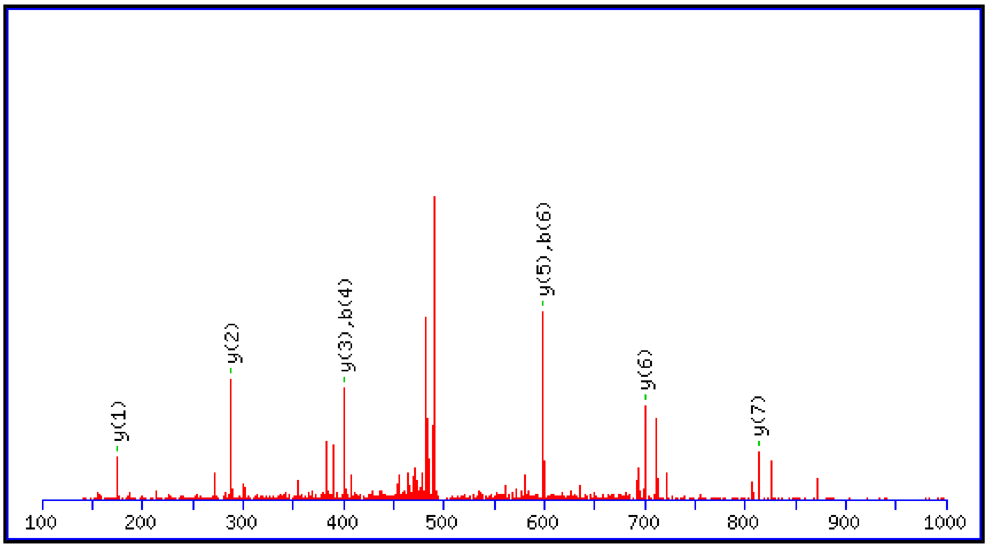
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANLTVVLLR**
Found in **K7EKL8** in **con_Xuniprot_HUMAN3**, K7EKL8_HUMAN Intercellular adhesion molecule 1 (Fragment) OS=Homo sapiens GN=ICAM1 PE=2 SV=1

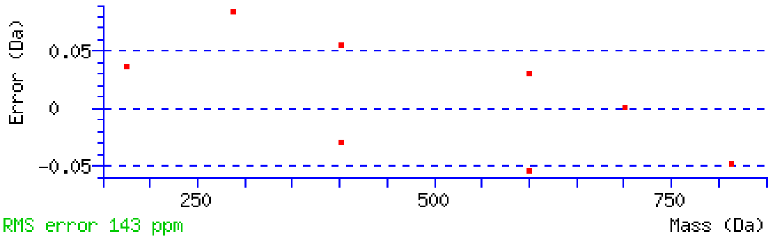
Match to Query 155: 998.615468 from(500.315010,2+) intensity(31896.3340) rtinseconds(1625) scans(4020) index(10963)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum3388_scans__4020
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

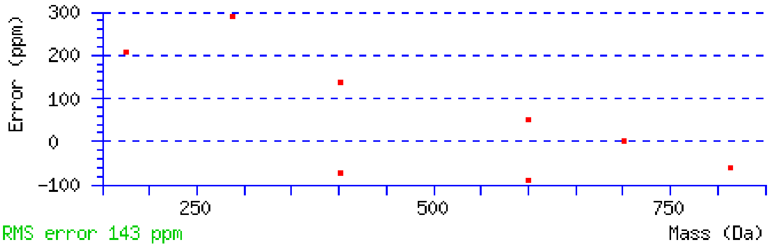
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 998.6124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N2 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.0003
Matches : 8/78 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							9
2	187.0713	94.0393	170.0448	85.5260			N	928.5826	464.7949	911.5560	456.2817	910.5720	455.7897	8
3	300.1554	150.5813	283.1288	142.0681			L	813.5557	407.2815	796.5291	398.7682	795.5451	398.2762	7
4	401.2031	201.1052	384.1765	192.5919	383.1925	192.0999	T	700.4716	350.7394	683.4450	342.2262	682.4610	341.7341	6
5	500.2715	250.6394	483.2449	242.1261	482.2609	241.6341	V	599.4239	300.2156	582.3974	291.7023			5
6	599.3399	300.1736	582.3134	291.6603	581.3293	291.1683	V	500.3555	250.6814	483.3289	242.1681			4
7	712.4240	356.7156	695.3974	348.2023	694.4134	347.7103	L	401.2871	201.1472	384.2605	192.6339			3
8	825.5080	413.2577	808.4815	404.7444	807.4975	404.2524	L	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ANLTVVLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
53.5	998.6124	0.0031	ANLTVVLLR
32.9	998.6124	0.0031	SSLLPITLR
23.4	998.6124	0.0031	KEEVLILR
23.3	996.6080	2.0075	RLETPILR
22.7	997.6073	1.0082	QLGIWLLR
15.5	998.6124	0.0031	DQLIKILR
13.6	998.6124	0.0031	ALIEATLLR
13.6	998.6124	0.0031	EKILDIIR
13.6	998.6124	0.0031	EKLVEILR
13.6	998.6124	0.0031	IDLKELLR

Mascot: http://www.matrixscience.com/

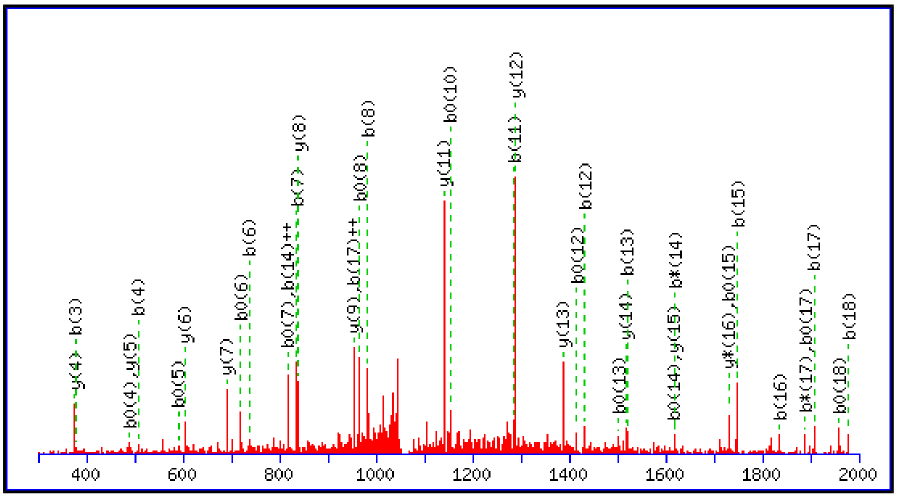
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLYETEVFSTDFSNISAAK**
Found in **P05543** in **con_Xuniprot_HUMAN3**, THBG_HUMAN Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2

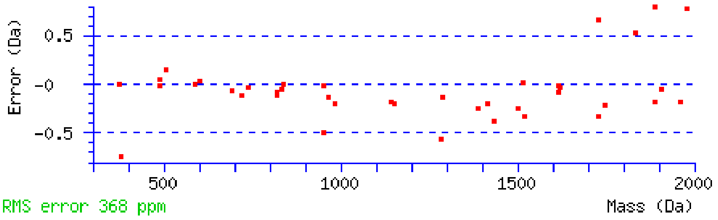
Match to Query 13913: 2123.004928 from(1062.509740,2+) intensity(11014.7676) rtinseconds(2042) scans(5122) index(12778)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4485_scans__5122
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

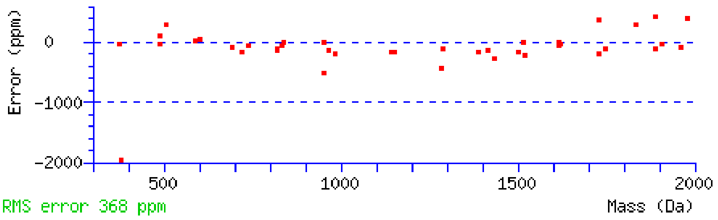
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2122.9946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14 : Deamidated (NQ)
Ions Score: 96 **Expect:** 6.1e-008
Matches : 40/184 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	102.0550	51.5311			84.0444	42.5258	T							19
2	215.1390	108.0731			197.1285	99.0679	L	2022.9542	1011.9808	2005.9277	1003.4675	2004.9437	1002.9755	18
3	***378.2023***	189.6048			360.1918	180.5995	Y	1909.8702	955.4387	1892.8436	946.9255	1891.8596	946.4334	17
4	***507.2449***	254.1261			489.2344	245.1208	E	1746.8069	873.9071	1729.7803	865.3938	1728.7963	864.9018	16
5	608.2926	304.6499			590.2821	295.6447	T	***1617.7643***	809.3858	1600.7377	800.8725	1599.7537	800.3805	15
6	***737.3352***	369.1712			719.3246	360.1660	E	***1516.7166***	758.8619	1499.6900	750.3487	1498.7060	749.8566	14
7	***836.4036***	418.7055			818.3931	409.7002	V	***1387.6740***	694.3406	1370.6474	685.8274	1369.6634	685.3353	13
8	***983.4720***	492.2397			965.4615	483.2344	F	***1288.6056***	644.8064	1271.5790	636.2932	1270.5950	635.8011	12
9	1070.5041	535.7557			1052.4935	526.7504	S	***1141.5372***	571.2722	1124.5106	562.7589	1123.5266	562.2669	11
10	1171.5517	586.2795			1153.5412	577.2742	T	1054.5051	527.7562	1037.4786	519.2429	1036.4946	518.7509	10
11	***1286.5787***	643.7930			1268.5681	634.7877	D	***953.4575***	477.2324	936.4309	468.7191	935.4469	468.2271	9
12	***1433.6471***	717.3272			1415.6365	708.3219	F	***838.4305***	419.7189	821.4040	411.2056	820.4199	410.7136	8
13	***1520.6791***	760.8432			1502.6686	751.8379	S	***691.3621***	346.1847	674.3355	337.6714	673.3515	337.1794	7
14	1635.7061	818.3567	1618.6795	809.8434	1617.6955	809.3514	N	***604.3301***	302.6687	587.3035	294.1554	586.3195	293.6634	6
15	***1748.7901***	874.8987	1731.7636	866.3854	1730.7796	865.8934	I	***489.3031***	245.1552	472.2766	236.6419	471.2926	236.1499	5
16	***1835.8222***	918.4147	1818.7956	909.9014	1817.8116	909.4094	S	***376.2191***	188.6132	359.1925	180.0999	358.2085	179.6079	4
17	***1906.8593***	953.9333	1889.8327	945.4200	1888.8487	944.9280	A	289.1870	145.0972	272.1605	136.5839			3
18	***1977.8964***	989.4518	1960.8698	980.9386	1959.8858	980.4466	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of TLYETEVFSTDFSNISAAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
95.9	2122.9946	0.0103	TLYETEVFSTDFSNISAAK
49.4	2122.0106	0.9943	TLYETEVFSTDFSNISAAK
4.1	2122.0040	1.0009	IMNEHLYKQAWEADKTK
2.9	2122.9986	0.0063	LVMENREGLNMNLSSNSAK

Mascot: http://www.matrixscience.com/

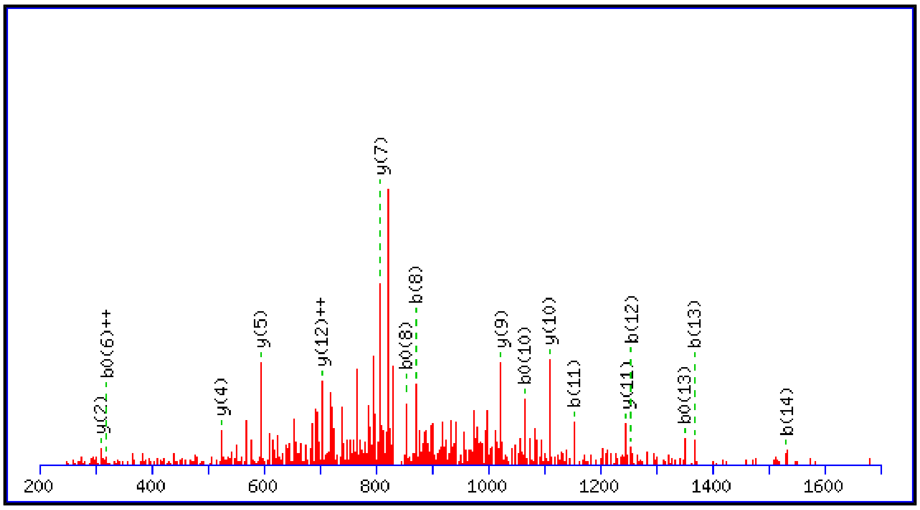
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTACHSSQPNATLYK**
Found in **P05543** in **con_Xuniprot_HUMAN3**, THBG_HUMAN Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2

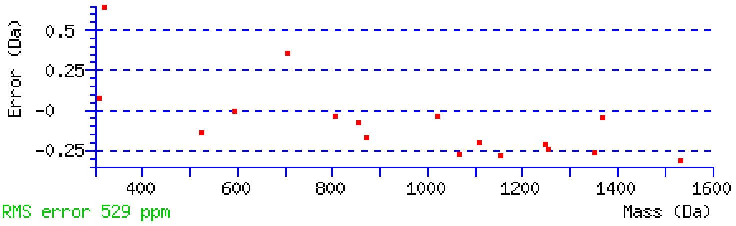
Match to Query 8441: 1676.786308 from(839.400430,2+) intensity(5980.4795) rtinseconds(345) scans(584) index(9262)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum468_scans__584
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

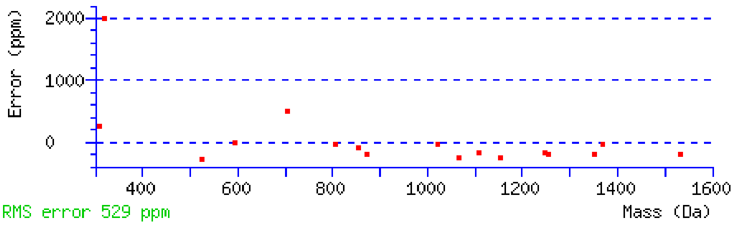
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1676.7828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.018
Matches : 17/146 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							15
2	201.1234	101.0653			183.1128	92.0600	T	1578.7217	789.8645	1561.6951	781.3512	1560.7111	780.8592	14
3	272.1605	136.5839			254.1499	127.5786	A	1477.6740	739.3406	1460.6475	730.8274	1459.6634	730.3354	13
4	432.1911	216.5992			414.1806	207.5939	C	1406.6369	703.8221	1389.6103	695.3088	1388.6263	694.8168	12
5	569.2500	285.1287			551.2395	276.1234	H	***1246.6062***	623.8068	1229.5797	615.2935	1228.5957	614.8015	11
6	656.2821	328.6447			638.2715	319.6394	S	***1109.5473***	555.2773	1092.5208	546.7640	1091.5368	546.2720	10
7	743.3141	372.1607			725.3035	363.1554	S	***1022.5153***	511.7613	1005.4888	503.2480	1004.5047	502.7560	9
8	***871.3727***	436.1900	854.3461	427.6767	853.3621	427.1847	Q	935.4833	468.2453	918.4567	459.7320	917.4727	459.2400	8
9	968.4254	484.7164	951.3989	476.2031	950.4149	475.7111	P	***807.4247***	404.2160	790.3981	395.7027	789.4141	395.2107	7
10	1083.4524	542.2298	1066.4258	533.7166	1065.4418	533.2245	N	710.3719	355.6896	693.3454	347.1763	692.3614	346.6843	6
11	***1154.4895***	577.7484	1137.4630	569.2351	1136.4789	568.7431	A	***595.3450***	298.1761	578.3184	289.6629	577.3344	289.1709	5
12	***1255.5372***	628.2722	1238.5106	619.7590	1237.5266	619.2669	T	***524.3079***	262.6576	507.2813	254.1443	506.2973	253.6523	4
13	***1368.6212***	684.8143	1351.5947	676.3010	1350.6107	675.8090	L	423.2602	212.1337	406.2336	203.6205			3
14	***1531.6846***	766.3459	1514.6580	757.8326	1513.6740	757.3406	Y	***310.1761***	155.5917	293.1496	147.0784			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VTACHSSQPNATLYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
40.2	1676.7828	0.0035	VTACHSSQPNATLYK	Deamidated N10 93.46%
28.7	1676.7828	0.0035	VTACHSSQPNATLYK	Deamidated Q8 6.54%
3.2	1676.7893	-0.0030	GPFDGEQGGSNQKLLK	
1.4	1676.7893	-0.0030	DQINPDARNDLLYK	
1.2	1676.7868	-0.0005	EYKDAFMKANPGYK	
1.0	1675.7763	1.0100	YGEKIETKCQQYK	

Mascot: http://www.matrixscience.com/

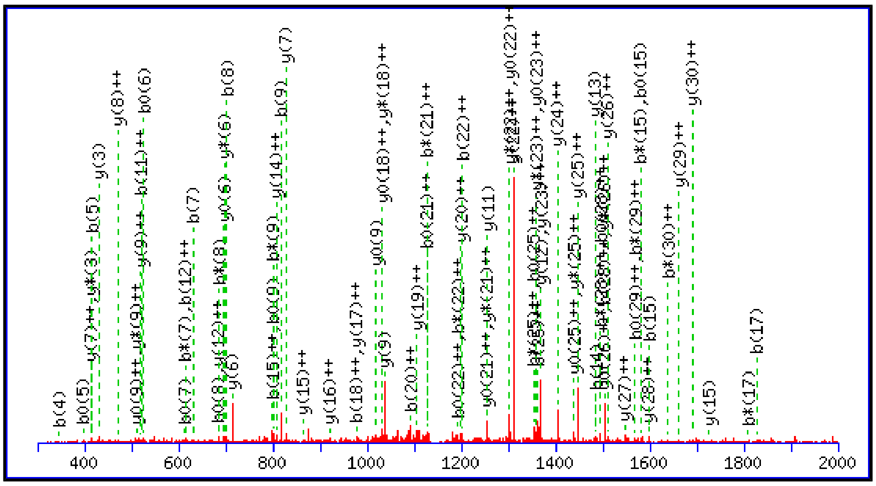
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27729: 3436.652022 from(1146.557950,3+) intensity(27008.2930) rtinseconds(1937) scans(4914) index(11083)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum4171_scans__4914
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

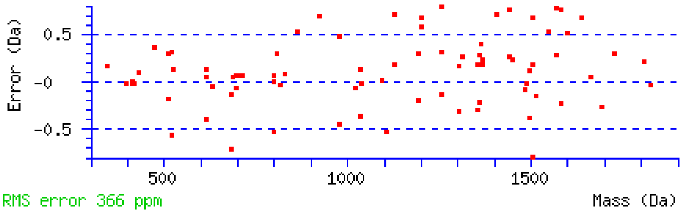
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

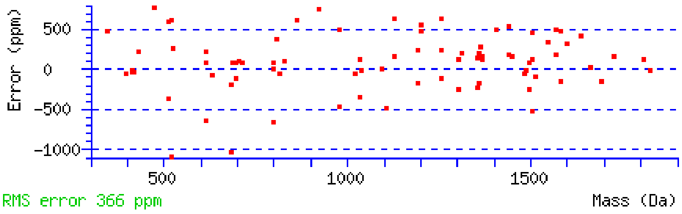


Monoisotopic mass of neutral peptide Mr(calc): 3436.6357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
Ions Score: 73 **Expect:** 1.3e-005
Matches : 83/340 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							31
2	115.0502	58.0287					G	3380.6216	1690.8144	3363.5950	1682.3012	3362.6110	1681.8091	30
3	244.0928	122.5500			226.0822	113.5448	E	3323.6001	1662.3037	3306.5736	1653.7904	3305.5896	1653.2984	29
4	**345.1405**	173.0739			327.1299	164.0686	T	3194.5575	1597.7824	3177.5310	1589.2691	3176.5470	1588.7771	28
5	**416.1776**	208.5924			398.1670	199.5872	A	3093.5098	1547.2586	3076.4833	1538.7453	3075.4993	1538.2533	27
6	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	Q	3022.4727	1511.7400	3005.4462	1503.2267	3004.4622	1502.7347	26
7	**631.2682**	316.1377	614.2416	307.6245	613.2576	307.1325	S	2894.4142	1447.7107	2877.3876	1439.1974	2876.4036	1438.7054	25
8	**702.3053**	351.6563	685.2788	343.1430	684.2947	342.6510	A	2807.3821	1404.1947	2790.3556	1395.6814	2789.3716	1395.1894	24
9	**817.3323**	409.1698	800.3057	400.6565	799.3217	400.1645	D	2736.3450	1368.6761	2719.3185	1360.1629	2718.3344	1359.6709	23
10	914.3850	457.6961	897.3585	449.1829	896.3745	448.6909	P	2621.3181	1311.1627	2604.2915	1302.6494	2603.3075	1302.1574	22
11	1042.4436	**521.7254**	1025.4170	513.2122	1024.4330	512.7202	Q	2524.2653	1262.6363	2507.2388	1254.1230	2506.2547	1253.6310	21
12	1228.5229	**614.7651**	1211.4964	606.2518	1210.5123	605.7598	W	2396.2067	1198.6070	2379.1802	1190.0937	2378.1962	1189.6017	20
13	1357.5655	679.2864	1340.5390	670.7731	1339.5549	670.2811	E	2210.1274	1105.5673	2193.1009	1097.0541	2192.1168	1096.5621	19
14	**1485.6241**	743.3157	1468.5975	734.8024	1467.6135	734.3104	Q	2081.0848	1041.0460	2064.0583	1032.5328	2063.0743	1032.0408	18
15	**1598.7081**	**799.8577**	1581.6816	791.3444	1580.6976	790.8524	L	1953.0262	977.0168	1935.9997	968.5035	1935.0157	968.0115	17
16	1712.7511	856.8792	1695.7245	848.3659	1694.7405	847.8739	N	1839.9422	920.4747	1822.9156	911.9615	1821.9316	911.4694	16
17	**1826.7940**	913.9006	1809.7674	905.3874	1808.7834	904.8954	N	**1725.8993**	863.4533	1708.8727	854.9400	1707.8887	854.4480	15
18	1954.8890	**977.9481**	1937.8624	969.4348	1936.8784	968.9428	K	1611.8563	806.4318	1594.8298	797.9185	1593.8458	797.4265	14
19	2069.9159	1035.4616	2052.8894	1026.9483	2051.9053	1026.4563	N	**1483.7614**	742.3843	1466.7348	733.8710	1465.7508	733.3790	13
20	2183.0000	**1092.0036**	2165.9734	1083.4903	2164.9894	1082.9983	L	**1368.7344**	684.8708	1351.7079	676.3576	1350.7239	675.8656	12
21	2270.0320	1135.5196	2253.0054	1127.0064	2252.0214	1126.5144	S	**1255.6504**	628.3288	1238.6238	619.8155	1237.6398	619.3235	11
22	2401.0725	**1201.0399**	2384.0459	1192.5266	2383.0619	1192.0346	M	1168.6183	584.8128	1151.5918	576.2995	1150.6078	575.8075	10
23	2498.1252	1249.5663	2481.0987	1241.0530	2480.1147	1240.5610	P	**1037.5778**	519.2926	1020.5513	510.7793	1019.5673	510.2873	9

24	2611.2093	1306.1083	2594.1828	1297.5950	2593.1987	1297.1030	L	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	8
25	2724.2934	**1362.6503**	2707.2668	1354.1370	2706.2828	1353.6450	L	**827.4410**	414.2241	810.4145	405.7109	809.4305	405.2189	7
26	2821.3461	1411.1767	2804.3196	1402.6634	2803.3356	1402.1714	P	**714.3570**	357.6821	697.3304	349.1688	696.3464	348.6768	6
27	2892.3833	1446.6953	2875.3567	1438.1820	2874.3727	1437.6900	A	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	5
28	3007.4102	**1504.2087**	2990.3836	1495.6955	2989.3996	1495.2035	D	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	4
29	3154.4786	1577.7429	3137.4521	1569.2297	3136.4680	1568.7377	F	**431.2401**	216.1237	414.2136	207.6104			3
30	3291.5375	1646.2724	3274.5110	1637.7591	3273.5270	1637.2671	H	284.1717	142.5895	267.1452	134.0762			2
31							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.9	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N19 45.29%
72.8	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17 45.08%
66.0	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16 9.38%
50.0	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14 0.23%
39.5	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11 0.02%
33.4	3436.6357	0.0163	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q6 0.01%
25.5	3435.6517	1.0003	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
5.8	3436.6555	-0.0034	KISEQLVELAAENQLIPSPMDPPELGNNESR	
4.2	3435.6546	0.9974	IMKLVNVTSESTLQTNMPMVYEITFCRGR	
4.2	3435.6546	0.9974	IMKLVNVTSESTLQTNMPMVYEITFCRGR	

Mascot: http://www.matrixscience.com/

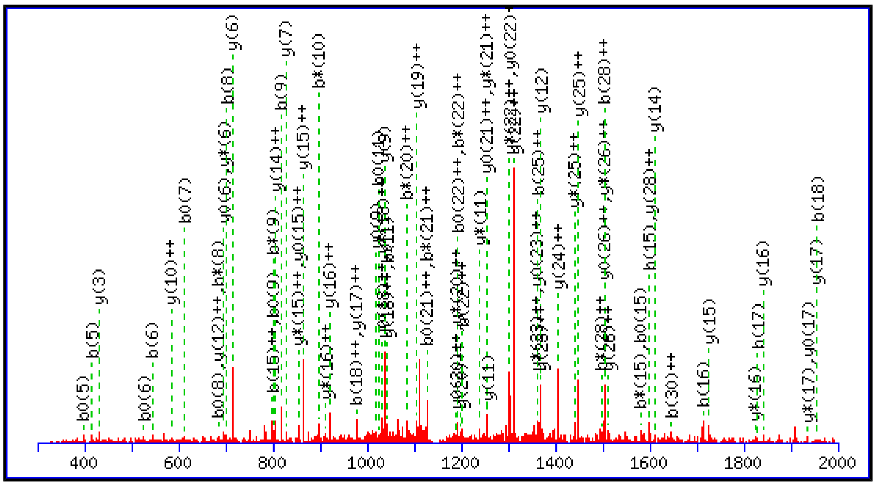
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27743: 3437.636622 from(1146.886150,3+) intensity(31734.4746) rtinseconds(2028) scans(4926) index(9034)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum4230_scans__4926
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

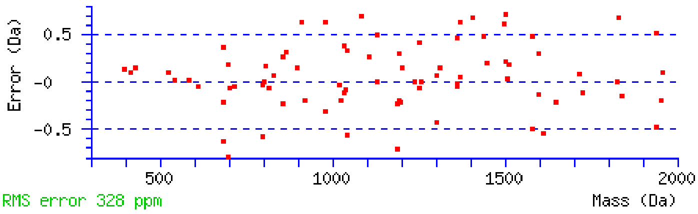
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

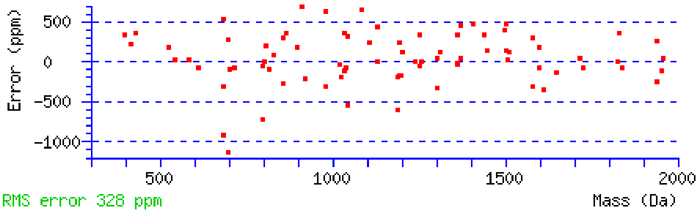


Monoisotopic mass of neutral peptide Mr(calc): 3437.6197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N16 : Deamidated (NQ)
N19 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0019
Matches : 80/340 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**31**
2	115.0502	58.0287					**G**	3381.6056	1691.3064	3364.5790	1682.7932	3363.5950	1682.3012	**30**
3	244.0928	122.5500			226.0822	113.5448	**E**	3324.5841	1662.7957	3307.5576	1654.2824	3306.5736	1653.7904	**29**
4	345.1405	173.0739			327.1299	164.0686	**T**	3195.5415	1598.2744	3178.5150	1589.7611	3177.5310	1589.2691	**28**
5	**416.1776**	208.5924			398.1670	199.5872	**A**	3094.4939	1547.7506	3077.4673	1539.2373	3076.4833	1538.7453	**27**
6	**544.2362**	272.6217	527.2096	264.1084	526.2256	263.6164	**Q**	3023.4567	1512.2320	3006.4302	1503.7187	3005.4462	1503.2267	**26**
7	631.2682	316.1377	614.2416	307.6245	613.2576	307.1325	**S**	2895.3982	1448.2027	2878.3716	1439.6894	2877.3876	1439.1974	**25**
8	**702.3053**	351.6563	685.2788	343.1430	684.2947	342.6510	**A**	2808.3661	1404.6867	2791.3396	1396.1734	2790.3556	1395.6814	**24**
9	**817.3323**	409.1698	800.3057	400.6565	799.3217	400.1645	**D**	2737.3290	1369.1682	2720.3025	1360.6549	2719.3185	1360.1629	**23**
10	914.3850	457.6961	897.3585	449.1829	896.3745	448.6909	**P**	2622.3021	1311.6547	2605.2755	1303.1414	2604.2915	1302.6494	**22**
11	**1042.4436**	521.7254	1025.4170	513.2122	1024.4330	512.7202	**Q**	2525.2493	1263.1283	2508.2228	1254.6150	2507.2388	1254.1230	**21**
12	1228.5229	614.7651	1211.4964	606.2518	1210.5123	605.7598	**W**	2397.1907	1199.0990	2380.1642	1190.5857	2379.1802	1190.0937	**20**
13	1357.5655	679.2864	1340.5390	670.7731	1339.5549	670.2811	**E**	2211.1114	1106.0594	2194.0849	1097.5461	2193.1009	1097.0541	**19**
14	1485.6241	743.3157	1468.5975	734.8024	1467.6135	734.3104	**Q**	2082.0688	1041.5381	2065.0423	1033.0248	2064.0583	1032.5328	**18**
15	**1598.7081**	**799.8577**	1581.6816	791.3444	1580.6976	790.8524	**L**	***1954.0103***	977.5088	1936.9837	968.9955	1935.9997	968.5035	**17**
16	**1713.7351**	857.3712	1696.7085	848.8579	1695.7245	848.3659	**N**	***1840.9262***	920.9667	1823.8996	912.4535	1822.9156	911.9615	**16**
17	**1827.7780**	914.3926	1810.7515	905.8794	1809.7674	905.3874	**N**	***1725.8993***	863.4533	1708.8727	854.9400	1707.8887	854.4480	**15**
18	**1955.8730**	**978.4401**	1938.8464	969.9269	1937.8624	969.4348	**K**	***1611.8563***	806.4318	1594.8298	797.9185	1593.8458	797.4265	**14**
19	2070.8999	1035.9536	2053.8734	1027.4403	2052.8894	1026.9483	**N**	1483.7614	742.3843	1466.7348	733.8710	1465.7508	733.3790	**13**
20	2183.9840	1092.4956	2166.9574	1083.9824	2165.9734	1083.4903	**L**	***1368.7344***	684.8708	1351.7079	676.3576	1350.7239	675.8656	**12**
21	2271.0160	1136.0116	2253.9895	1127.4984	2253.0054	1127.0064	**S**	***1255.6504***	628.3288	1238.6238	619.8155	1237.6398	619.3235	**11**
22	2402.0565	**1201.5319**	2385.0299	1193.0186	2384.0459	1192.5266	**M**	1168.6183	584.8128	1151.5918	576.2995	1150.6078	575.8075	**10**

23	2499.1093	1250.0583	2482.0827	1241.5450	2481.0987	1241.0530	**P**	***1037.5778***	519.2926	1020.5513	510.7793	1019.5673	510.2873	**9**
24	2612.1933	1306.6003	2595.1668	1298.0870	2594.1828	1297.5950	**L**	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	**8**
25	2725.2774	**1363.1423**	2708.2508	1354.6291	2707.2668	1354.1370	**L**	***827.4410***	414.2241	810.4145	405.7109	809.4305	405.2189	**7**
26	2822.3302	1411.6687	2805.3036	1403.1554	2804.3196	1402.6634	**P**	***714.3570***	357.6821	697.3304	349.1688	696.3464	348.6768	**6**
27	2893.3673	1447.1873	2876.3407	1438.6740	2875.3567	1438.1820	**A**	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	**5**
28	3008.3942	**1504.7007**	2991.3677	1496.1875	2990.3836	1495.6955	**D**	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	**4**
29	3155.4626	1578.2349	3138.4361	1569.7217	3137.4521	1569.2297	**F**	***431.2401***	216.1237	414.2136	207.6104			**3**
30	3292.5215	**1646.7644**	3275.4950	1638.2511	3274.5110	1637.7591	**H**	284.1717	142.5895	267.1452	134.0762			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.4	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N19 22.08%
50.8	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N17 19.41%
50.8	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17, N19 19.19%
48.0	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N19 10.14%
47.4	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N17 8.96%
44.5	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N17 4.59%
44.5	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N19 4.54%
40.5	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q6, N19 1.80%
40.5	3437.6197	0.0169	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q6, N17 1.80%
39.9	3436.6357	1.0009	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	

Mascot: http://www.matrixscience.com/

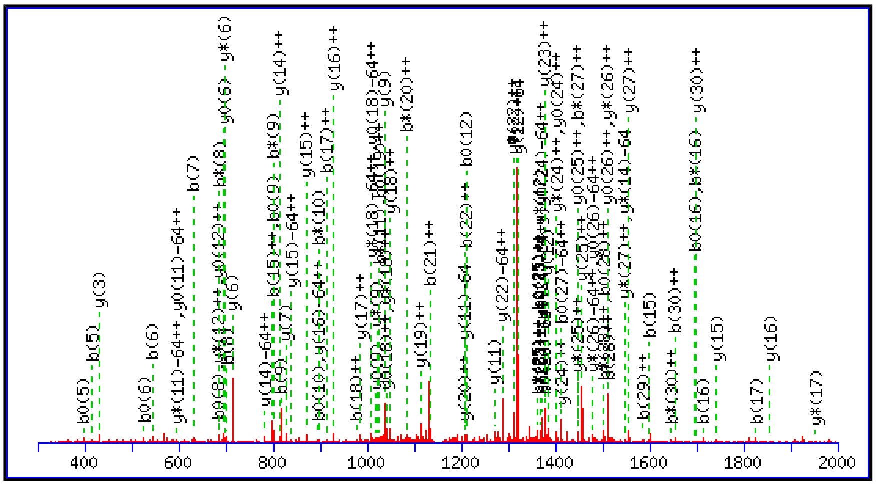
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27765: 3452.646462 from(1151.889430,3+) intensity(57500.5234) rtinseconds(1707) scans(4198) index(23251)
Title: 111019_Est_MI_YS_G_04Spectrum3606_scans__4198
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

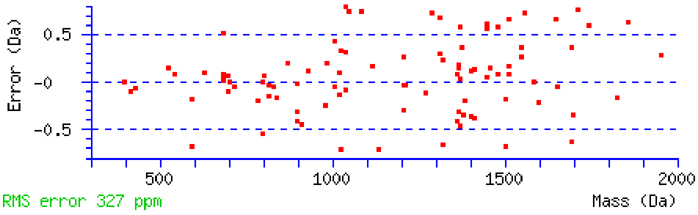
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

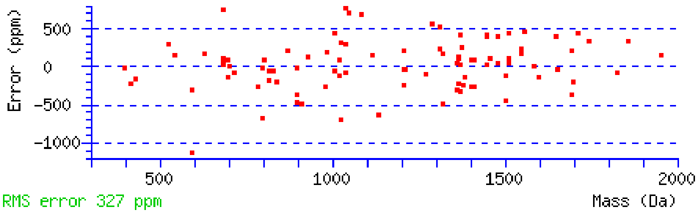


Monoisotopic mass of neutral peptide Mr(calc): 3452.6306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48 **Expect:** 0.0038
Matches : 96/520 fragment ions using 170 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							31
2	115.0502	58.0287					G	3396.6165	1698.8119	3379.5899	1690.2986	3378.6059	1689.8066	30
3	244.0928	122.5500			226.0822	113.5448	E	3339.5950	1670.3012	3322.5685	1661.7879	3321.5845	1661.2959	29
4	345.1405	173.0739			327.1299	164.0686	T	3210.5524	1605.7799	3193.5259	1597.2666	3192.5419	1596.7746	28
5	**416.1776**	208.5924			398.1670	199.5872	A	3109.5048	1555.2560	3092.4782	1546.7427	3091.4942	1546.2507	27
6	**544.2362**	272.6217	527.2096	264.1084	526.2256	263.6164	Q	3038.4676	1519.7375	3021.4411	1511.2242	3020.4571	1510.7322	26
7	**631.2682**	316.1377	614.2416	307.6245	613.2576	307.1325	S	2910.4091	1455.7082	2893.3825	1447.1949	2892.3985	1446.7029	25
8	**702.3053**	351.6563	685.2788	343.1430	684.2947	342.6510	A	2823.3770	1412.1922	2806.3505	1403.6789	2805.3665	1403.1869	24
9	**817.3323**	409.1698	800.3057	400.6565	799.3217	400.1645	D	2752.3399	1376.6736	2735.3134	1368.1603	2734.3294	1367.6683	23
10	914.3850	457.6961	897.3585	449.1829	896.3745	448.6909	P	2637.3130	1319.1601	2620.2864	1310.6469	2619.3024	1310.1548	22
11	1042.4436	521.7254	1025.4170	513.2122	1024.4330	512.7202	Q	2540.2602	1270.6337	2523.2337	1262.1205	2522.2497	1261.6285	21
12	1228.5229	614.7651	1211.4964	606.2518	1210.5123	605.7598	W	2412.2016	1206.6045	2395.1751	1198.0912	2394.1911	1197.5992	20
13	1357.5655	679.2864	1340.5390	670.7731	1339.5549	670.2811	E	2226.1223	1113.5648	2209.0958	1105.0515	2208.1118	1104.5595	19
14	1485.6241	743.3157	1468.5975	734.8024	1467.6135	734.3104	Q	2097.0797	1049.0435	2080.0532	1040.5302	2079.0692	1040.0382	18
15	**1598.7081**	***799.8577***	1581.6816	791.3444	1580.6976	790.8524	L	1969.0212	985.0142	1951.9946	976.5009	1951.0106	976.0089	17
16	**1712.7511**	856.8792	1695.7245	848.3659	1694.7405	847.8739	N	**1855.9371**	928.4722	1838.9105	919.9589	1837.9265	919.4669	16
17	**1826.7940**	***913.9006***	1809.7674	905.3874	1808.7834	904.8954	N	**1741.8942**	871.4507	1724.8676	862.9374	1723.8836	862.4454	15
18	1954.8890	***977.9481***	1937.8624	969.4348	1936.8784	968.9428	K	1627.8512	814.4293	1610.8247	805.9160	1609.8407	805.4240	14
19	2069.9159	1035.4616	2052.8894	1026.9483	2051.9053	1026.4563	N	1499.7563	750.3818	1482.7297	741.8685	1481.7457	741.3765	13
20	2183.0000	1092.0036	2165.9734	1083.4903	2164.9894	1082.9983	L	**1384.7293**	692.8683	1367.7028	684.3550	1366.7188	683.8630	12
21	2270.0320	***1135.5196***	2253.0054	1127.0064	2252.0214	1126.5144	S	**1271.6453**	636.3263	1254.6187	627.8130	1253.6347	627.3210	11
22	2417.0674	***1209.0373***	2400.0408	1200.5241	2399.0568	1200.0321	M	1184.6132	592.8103	1167.5867	584.2970	1166.6027	583.8050	10

23	2514.1202	1257.5637	2497.0936	1249.0504	2496.1096	1248.5584	**P**	**1037.5778**	519.2926	1020.5513	510.7793	1019.5673	510.2873	**9**
24	2627.2042	1314.1057	2610.1777	1305.5925	2609.1937	1305.1005	**L**	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	**8**
25	2740.2883	***1370.6478***	2723.2617	1362.1345	2722.2777	1361.6425	**L**	**827.4410**	414.2241	810.4145	405.7109	809.4305	405.2189	**7**
26	2837.3411	1419.1742	2820.3145	1410.6609	2819.3305	1410.1689	**P**	**714.3570**	357.6821	697.3304	349.1688	696.3464	348.6768	**6**
27	2908.3782	1454.6927	2891.3516	1446.1794	2890.3676	1445.6874	**A**	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	**5**
28	3023.4051	***1512.2062***	3006.3786	1503.6929	3005.3945	1503.2009	**D**	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	**4**
29	3170.4735	***1585.7404***	3153.4470	1577.2271	3152.4630	1576.7351	**F**	**431.2401**	216.1237	414.2136	207.6104			**3**
30	3307.5324	***1654.2699***	3290.5059	1645.7566	3289.5219	1645.2646	**H**	284.1717	142.5895	267.1452	134.0762			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.1	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N19 29.07%
47.4	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16 24.46%
47.4	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17 24.46%
45.9	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14 17.23%
40.2	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11 4.65%
33.6	3451.6466	0.9998	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
24.8	3452.6306	0.0158	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q6 0.14%
8.8	3452.6439	0.0026	QAEMECRLESLQAELGGILGQIQQLQTAYR	
7.1	3450.6460	2.0005	NDCEELVPKLGEQLLEEAEQGGAQLLGEPER	
7.1	3450.6460	2.0005	NDCEELVPKLGEQLLEEAEQGGAQLLGEPER	

Mascot: http://www.matrixscience.com/

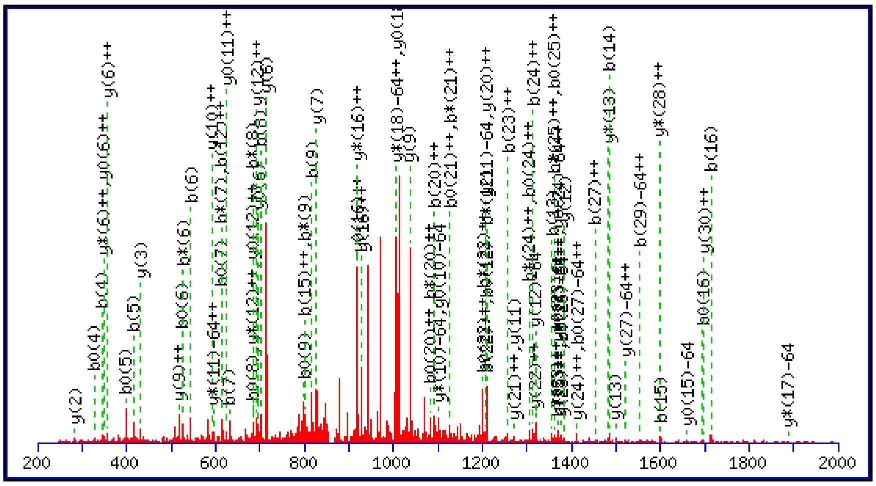
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27773: 3453.630016 from(864.414780,4+) intensity(60341.8516) rtinseconds(1686) scans(4244) index(9515)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum3631_scans__4244
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

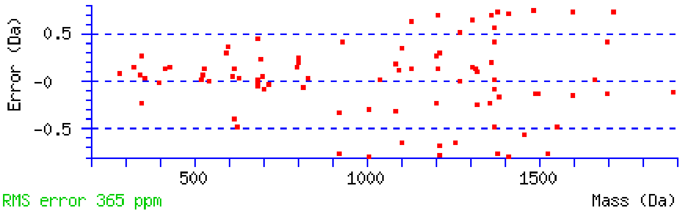
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

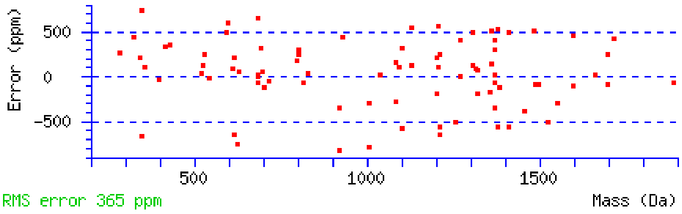


Monoisotopic mass of neutral peptide Mr(calc): 3453.6147
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Deamidated (NQ)
N19 : Deamidated (NQ)
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 **Expect:** 0.0042
Matches : 87/520 fragment ions using 139 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							31
2	115.0502	58.0287					G	3397.6005	1699.3039	3380.5740	1690.7906	3379.5899	1690.2986	30
3	244.0928	122.5500			226.0822	113.5448	E	3340.5790	1670.7932	3323.5525	1662.2799	3322.5685	1661.7879	29
4	***345.1405***	173.0739			327.1299	164.0686	T	3211.5365	1606.2719	3194.5099	1597.7586	3193.5259	1597.2666	28
5	***416.1776***	208.5924			398.1670	199.5872	A	3110.4888	1555.7480	3093.4622	1547.2348	3092.4782	1546.7427	27
6	***544.2362***	272.6217	527.2096	264.1084	526.2256	263.6164	Q	3039.4517	1520.2295	3022.4251	1511.7162	3021.4411	1511.2242	26
7	***631.2682***	316.1377	614.2416	307.6245	613.2576	307.1325	S	2911.3931	1456.2002	2894.3665	1447.6869	2893.3825	1447.1949	25
8	***702.3053***	351.6563	685.2788	343.1430	684.2947	342.6510	A	2824.3611	1412.6842	2807.3345	1404.1709	2806.3505	1403.6789	24
9	***817.3323***	409.1698	800.3057	400.6565	799.3217	400.1645	D	2753.3239	1377.1656	2736.2974	1368.6523	2735.3134	1368.1603	23
10	914.3850	457.6961	897.3585	449.1829	896.3745	448.6909	P	2638.2970	1319.6521	2621.2705	1311.1389	2620.2864	1310.6469	22
11	1042.4436	521.7254	1025.4170	513.2122	1024.4330	512.7202	Q	2541.2442	1271.1258	2524.2177	1262.6125	2523.2337	1262.1205	21
12	1228.5229	***614.7651***	1211.4964	606.2518	1210.5123	605.7598	W	2413.1857	1207.0965	2396.1591	1198.5832	2395.1751	1198.0912	20
13	***1357.5655***	679.2864	1340.5390	670.7731	1339.5549	670.2811	E	2227.1063	1114.0568	2210.0798	1105.5435	2209.0958	1105.0515	19
14	***1486.6081***	743.8077	1469.5815	735.2944	1468.5975	734.8024	Q	2098.0638	1049.5355	2081.0372	1041.0222	2080.0532	1040.5302	18
15	***1599.6922***	***800.3497***	1582.6656	791.8364	1581.6816	791.3444	L	1969.0212	985.0142	1951.9946	976.5009	1951.0106	976.0089	17
16	***1713.7351***	857.3712	1696.7085	848.8579	1695.7245	848.3659	N	1855.9371	928.4722	1838.9105	919.9589	1837.9265	919.4669	16
17	1827.7780	914.3926	1810.7515	905.8794	1809.7674	905.3874	N	1741.8942	871.4507	1724.8676	862.9374	1723.8836	862.4454	15
18	1955.8730	978.4401	1938.8464	969.9269	1937.8624	969.4348	K	1627.8512	814.4293	1610.8247	805.9160	1609.8407	805.4240	14
19	2070.8999	1035.9536	2053.8734	1027.4403	2052.8894	1026.9483	N	***1499.7563***	750.3818	1482.7297	741.8685	1481.7457	741.3765	13
20	2183.9840	***1092.4956***	2166.9574	1083.9824	2165.9734	1083.4903	L	***1384.7293***	692.8683	1367.7028	684.3550	1366.7188	683.8630	12
21	2271.0160	1136.0116	2253.9895	1127.4984	2253.0054	1127.0064	S	***1271.6453***	636.3263	1254.6187	627.8130	1253.6347	627.3210	11
22	2418.0514	***1209.5293***	2401.0249	1201.0161	2400.0408	1200.5241	M	1184.6132	592.8103	1167.5867	584.2970	1166.6027	583.8050	10

23	2515.1042	***1258.0557***	2498.0776	1249.5425	2497.0936	1249.0504	P	***1037.5778***	519.2926	1020.5513	510.7793	1019.5673	510.2873	9
24	2628.1882	***1314.5978***	2611.1617	1306.0845	2610.1777	1305.5925	L	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	8
25	2741.2723	***1371.1398***	2724.2458	1362.6265	2723.2617	1362.1345	L	***827.4410***	414.2241	810.4145	405.7109	809.4305	405.2189	7
26	2838.3251	1419.6662	2821.2985	1411.1529	2820.3145	1410.6609	P	***714.3570***	357.6821	697.3304	349.1688	696.3464	348.6768	6
27	2909.3622	***1455.1847***	2892.3356	1446.6715	2891.3516	1446.1794	A	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	5
28	3024.3891	1512.6982	3007.3626	1504.1849	3006.3786	1503.6929	D	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	4
29	3171.4575	1586.2324	3154.4310	1577.7191	3153.4470	1577.2271	F	***431.2401***	216.1237	414.2136	207.6104			3
30	3308.5165	1654.7619	3291.4899	1646.2486	3290.5059	1645.7566	H	***284.1717***	142.5895	267.1452	134.0762			2
31							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.4	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N19 18.58%
47.1	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N19 17.54%
46.5	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17, N19 15.38%
45.3	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N17 11.48%
45.0	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N17 10.84%
44.7	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N16 10.05%
41.7	3452.6306	0.9994	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
40.5	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N19 3.79%
37.7	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N17 2.02%
37.2	3453.6147	0.0154	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N16 1.79%

Mascot: http://www.matrixscience.com/

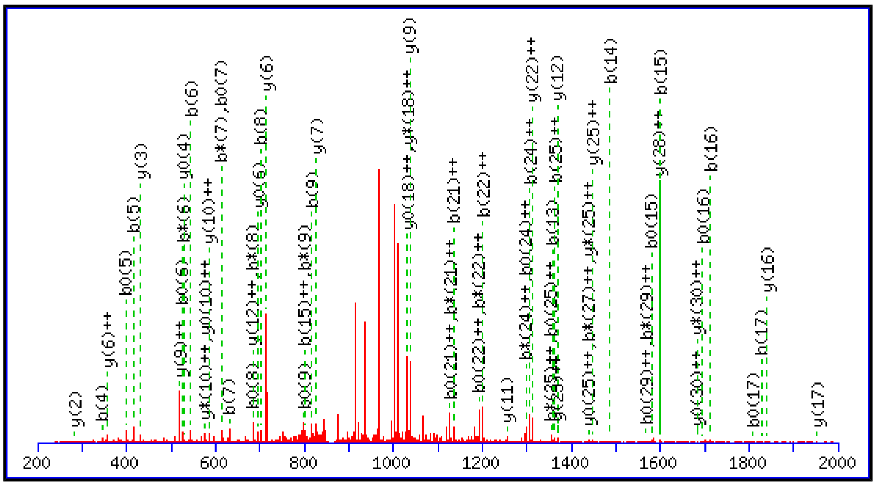
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27736: 3437.631296 from(860.415100,4+) intensity(113996.0703) rtinseconds(1997) scans(5024) index(23381)
Title: 111019_Est_MI_YS_G_04Spectrum4332_scans__5024
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

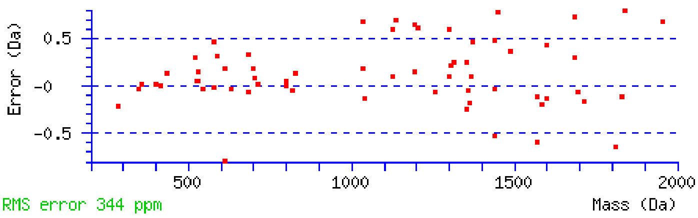
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

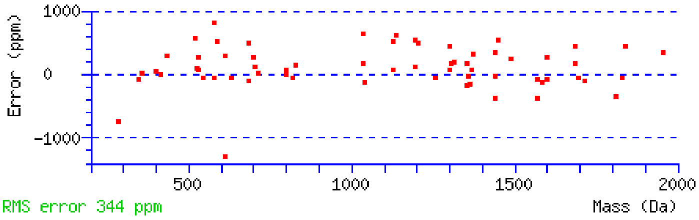


Monoisotopic mass of neutral peptide Mr(calc): 3437.6197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Deamidated (NQ)
N19 : Deamidated (NQ)
Ions Score: 47 **Expect:** 0.0049
Matches : 66/340 fragment ions using 126 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							31
2	115.0502	58.0287					G	3381.6056	1691.3064	3364.5790	1682.7932	3363.5950	1682.3012	30
3	244.0928	122.5500			226.0822	113.5448	E	3324.5841	1662.7957	3307.5576	1654.2824	3306.5736	1653.7904	29
4	***345.1405***	173.0739			327.1299	164.0686	T	3195.5415	1598.2744	3178.5150	1589.7611	3177.5310	1589.2691	28
5	***416.1776***	208.5924			398.1670	199.5872	A	3094.4939	1547.7506	3077.4673	1539.2373	3076.4833	1538.7453	27
6	***544.2362***	272.6217	527.2096	264.1084	526.2256	263.6164	Q	3023.4567	1512.2320	3006.4302	1503.7187	3005.4462	1503.2267	26
7	***631.2682***	316.1377	614.2416	307.6245	613.2576	307.1325	S	2895.3982	1448.2027	2878.3716	1439.6894	2877.3876	1439.1974	25
8	***702.3053***	351.6563	685.2788	343.1430	684.2947	342.6510	A	2808.3661	1404.6867	2791.3396	1396.1734	2790.3556	1395.6814	24
9	***817.3323***	409.1698	800.3057	400.6565	799.3217	400.1645	D	2737.3290	1369.1682	2720.3025	1360.6549	2719.3185	1360.1629	23
10	914.3850	457.6961	897.3585	449.1829	896.3745	448.6909	P	2622.3021	1311.6547	2605.2755	1303.1414	2604.2915	1302.6494	22
11	1043.4276	522.2174	1026.4011	513.7042	1025.4170	513.2122	Q	2525.2493	1263.1283	2508.2228	1254.6150	2507.2388	1254.1230	21
12	1229.5069	615.2571	1212.4804	606.7438	1211.4964	606.2518	W	2396.2067	1198.6070	2379.1802	1190.0937	2378.1962	1189.6017	20
13	***1358.5495***	679.7784	1341.5230	671.2651	1340.5390	670.7731	E	2210.1274	1105.5673	2193.1009	1097.0541	2192.1168	1096.5621	19
14	***1486.6081***	743.8077	1469.5815	735.2944	1468.5975	734.8024	Q	2081.0848	1041.0460	2064.0583	1032.5328	2063.0743	1032.0408	18
15	***1599.6922***	**800.3497**	1582.6656	791.8364	1581.6816	791.3444	L	***1953.0262***	977.0168	1935.9997	968.5035	1935.0157	968.0115	17
16	***1713.7351***	857.3712	1696.7085	848.8579	1695.7245	848.3659	N	***1839.9422***	920.4747	1822.9156	911.9615	1821.9316	911.4694	16
17	***1827.7780***	914.3926	1810.7515	905.8794	1809.7674	905.3874	N	1725.8993	863.4533	1708.8727	854.9400	1707.8887	854.4480	15
18	1955.8730	978.4401	1938.8464	969.9269	1937.8624	969.4348	K	1611.8563	806.4318	1594.8298	797.9185	1593.8458	797.4265	14
19	2070.8999	1035.9536	2053.8734	1027.4403	2052.8894	1026.9483	N	1483.7614	742.3843	1466.7348	733.8710	1465.7508	733.3790	13
20	2183.9840	1092.4956	2166.9574	1083.9824	2165.9734	1083.4903	L	***1368.7344***	684.8708	1351.7079	676.3576	1350.7239	675.8656	12
21	2271.0160	**1136.0116**	2253.9895	1127.4984	2253.0054	1127.0064	S	***1255.6504***	628.3288	1238.6238	619.8155	1237.6398	619.3235	11
22	2402.0565	**1201.5319**	2385.0299	1193.0186	2384.0459	1192.5266	M	1168.6183	584.8128	1151.5918	576.2995	1150.6078	575.8075	10

23	2499.1093	1250.0583	2482.0827	1241.5450	2481.0987	1241.0530	**P**	***1037.5778***	519.2926	1020.5513	510.7793	1019.5673	510.2873	**9**
24	2612.1933	**1306.6003**	2595.1668	1298.0870	2594.1828	1297.5950	**L**	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	**8**
25	2725.2774	**1363.1423**	2708.2508	1354.6291	2707.2668	1354.1370	**L**	***827.4410***	414.2241	810.4145	405.7109	809.4305	405.2189	**7**
26	2822.3302	1411.6687	2805.3036	1403.1554	2804.3196	1402.6634	**P**	***714.3570***	357.6821	697.3304	349.1688	696.3464	348.6768	**6**
27	2893.3673	1447.1873	2876.3407	1438.6740	2875.3567	1438.1820	**A**	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	**5**
28	3008.3942	1504.7007	2991.3677	1496.1875	2990.3836	1495.6955	**D**	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	**4**
29	3155.4626	1578.2349	3138.4361	1569.7217	3137.4521	1569.2297	**F**	***431.2401***	216.1237	414.2136	207.6104			**3**
30	3292.5215	1646.7644	3275.4950	1638.2511	3274.5110	1637.7591	**H**	***284.1717***	142.5895	267.1452	134.0762			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.1	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N19 31.55%
44.2	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N19 16.40%
43.4	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N19 13.68%
41.5	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N17 8.67%
39.2	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N17 5.18%
39.2	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17, N19 5.18%
38.2	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N17 4.12%
37.2	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N16 3.27%
35.5	3437.6197	0.0116	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N16 2.20%
35.2	3436.6357	0.9956	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	

Mascot: http://www.matrixscience.com/

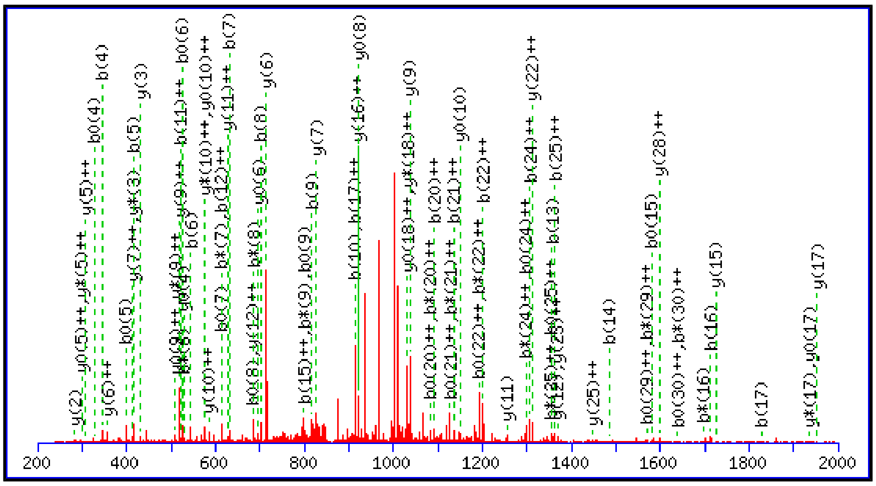
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27734: 3437.628256 from(860.414340,4+) intensity(78495.5156) rtinseconds(1935) scans(4953) index(22699)
Title: 111019_Est_MI_YS_G_03Spectrum4332_scans__4953
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

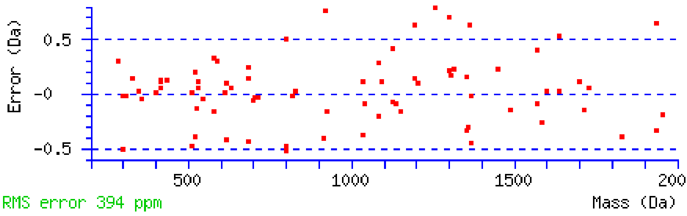
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

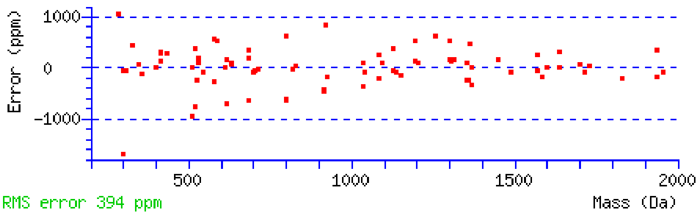


Monoisotopic mass of neutral peptide Mr(calc): 3437.6197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Deamidated (NQ)
N19 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0057
Matches : 82/340 fragment ions using 180 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							31
2	115.0502	58.0287					G	3381.6056	1691.3064	3364.5790	1682.7932	3363.5950	1682.3012	30
3	244.0928	122.5500			226.0822	113.5448	E	3324.5841	1662.7957	3307.5576	1654.2824	3306.5736	1653.7904	29
4	***345.1405***	173.0739			327.1299	164.0686	T	3195.5415	1598.2744	3178.5150	1589.7611	3177.5310	1589.2691	28
5	***416.1776***	208.5924			398.1670	199.5872	A	3094.4939	1547.7506	3077.4673	1539.2373	3076.4833	1538.7453	27
6	***544.2362***	272.6217	527.2096	264.1084	526.2256	263.6164	Q	3023.4567	1512.2320	3006.4302	1503.7187	3005.4462	1503.2267	26
7	***631.2682***	316.1377	614.2416	307.6245	613.2576	307.1325	S	2895.3982	1448.2027	2878.3716	1439.6894	2877.3876	1439.1974	25
8	***702.3053***	351.6563	685.2788	343.1430	684.2947	342.6510	A	2808.3661	1404.6867	2791.3396	1396.1734	2790.3556	1395.6814	24
9	***817.3323***	409.1698	800.3057	400.6565	799.3217	400.1645	D	2737.3290	1369.1682	2720.3025	1360.6549	2719.3185	1360.1629	23
10	***914.3850***	457.6961	897.3585	449.1829	896.3745	448.6909	P	2622.3021	1311.6547	2605.2755	1303.1414	2604.2915	1302.6494	22
11	1042.4436	**521.7254**	1025.4170	513.2122	1024.4330	512.7202	Q	2525.2493	1263.1283	2508.2228	1254.6150	2507.2388	1254.1230	21
12	1228.5229	**614.7651**	1211.4964	606.2518	1210.5123	605.7598	W	2397.1907	1199.0990	2380.1642	1190.5857	2379.1802	1190.0937	20
13	***1357.5655***	679.2864	1340.5390	670.7731	1339.5549	670.2811	E	2211.1114	1106.0594	2194.0849	1097.5461	2193.1009	1097.0541	19
14	***1486.6081***	743.8077	1469.5815	735.2944	1468.5975	734.8024	Q	2082.0688	1041.5381	2065.0423	1033.0248	2064.0583	1032.5328	18
15	1599.6922	**800.3497**	1582.6656	791.8364	1581.6816	791.3444	L	**1953.0262**	977.0168	1935.9997	968.5035	1935.0157	968.0115	17
16	***1713.7351***	857.3712	1696.7085	848.8579	1695.7245	848.3659	N	1839.9422	920.4747	1822.9156	911.9615	1821.9316	911.4694	16
17	***1827.7780***	**914.3926**	1810.7515	905.8794	1809.7674	905.3874	N	**1725.8993**	863.4533	1708.8727	854.9400	1707.8887	854.4480	15
18	1955.8730	978.4401	1938.8464	969.9269	1937.8624	969.4348	K	1611.8563	806.4318	1594.8298	797.9185	1593.8458	797.4265	14
19	2070.8999	1035.9536	2053.8734	1027.4403	2052.8894	1026.9483	N	1483.7614	742.3843	1466.7348	733.8710	1465.7508	733.3790	13
20	2183.9840	**1092.4956**	2166.9574	1083.9824	2165.9734	1083.4903	L	**1368.7344**	684.8708	1351.7079	676.3576	1350.7239	675.8656	12
21	2271.0160	**1136.0116**	2253.9895	1127.4984	2253.0054	1127.0064	S	**1255.6504**	628.3288	1238.6238	619.8155	1237.6398	619.3235	11
22	2402.0565	**1201.5319**	2385.0299	1193.0186	2384.0459	1192.5266	M	1168.6183	584.8128	1151.5918	576.2995	1150.6078	575.8075	10

23	2499.1093	1250.0583	2482.0827	1241.5450	2481.0987	1241.0530	**P**	**1037.5778**	519.2926	1020.5513	510.7793	1019.5673	510.2873	**9**
24	2612.1933	**1306.6003**	2595.1668	1298.0870	2594.1828	1297.5950	**L**	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	**8**
25	2725.2774	**1363.1423**	2708.2508	1354.6291	2707.2668	1354.1370	**L**	**827.4410**	414.2241	810.4145	405.7109	809.4305	405.2189	**7**
26	2822.3302	1411.6687	2805.3036	1403.1554	2804.3196	1402.6634	**P**	**714.3570**	357.6821	697.3304	349.1688	696.3464	348.6768	**6**
27	2893.3673	1447.1873	2876.3407	1438.6740	2875.3567	1438.1820	**A**	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	**5**
28	3008.3942	1504.7007	2991.3677	1496.1875	2990.3836	1495.6955	**D**	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	**4**
29	3155.4626	1578.2349	3138.4361	1569.7217	3137.4521	1569.2297	**F**	**431.2401**	216.1237	414.2136	207.6104			**3**
30	3292.5215	1646.7644	3275.4950	1638.2511	3274.5110	1637.7591	**H**	**284.1717**	142.5895	267.1452	134.0762			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
46.3	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N19 14.62%
46.2	3436.6357	0.9925	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
46.0	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N19 13.70%
45.8	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N19 13.03%
45.4	3436.6357	0.9925	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
45.3	3436.6357	0.9925	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
44.3	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17, N19 9.16%
42.6	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N17 6.28%
42.2	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N17 5.69%
41.7	3437.6197	0.0085	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N17 5.10%

Mascot: http://www.matrixscience.com/

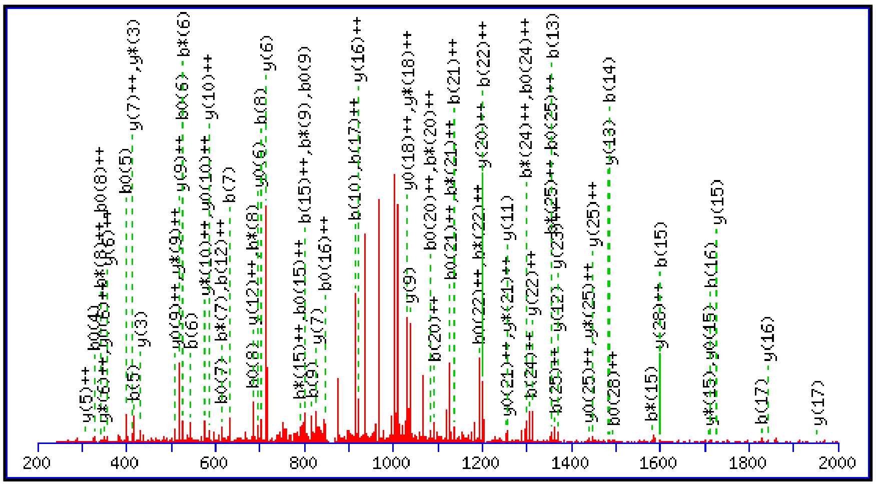
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGETAQSADPQWEQLNNKNLSMPLLPADFHK**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Match to Query 27738: 3437.632536 from(860.415410,4+) intensity(186124.4844) rtinseconds(2032) scans(4935) index(9036)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum4238_scans__4935
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

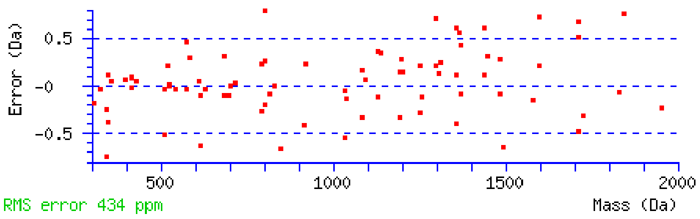
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

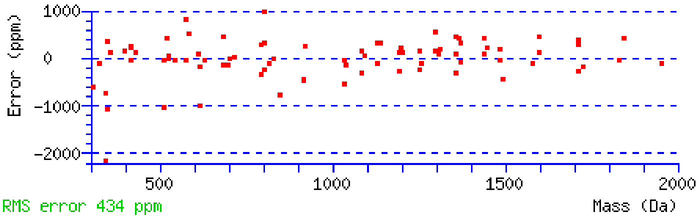


Monoisotopic mass of neutral peptide Mr(calc): 3437.6197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
N19 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0079
Matches : 84/340 fragment ions using 162 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					**G**							**31**
2	115.0502	58.0287					**G**	3381.6056	1691.3064	3364.5790	1682.7932	3363.5950	1682.3012	**30**
3	244.0928	122.5500			226.0822	113.5448	**E**	3324.5841	1662.7957	3307.5576	1654.2824	3306.5736	1653.7904	**29**
4	345.1405	173.0739			327.1299	164.0686	**T**	3195.5415	1598.2744	3178.5150	1589.7611	3177.5310	1589.2691	**28**
5	***416.1776***	208.5924			398.1670	199.5872	**A**	3094.4939	1547.7506	3077.4673	1539.2373	3076.4833	1538.7453	**27**
6	***544.2362***	272.6217	527.2096	264.1084	526.2256	263.6164	**Q**	3023.4567	1512.2320	3006.4302	1503.7187	3005.4462	1503.2267	**26**
7	***631.2682***	316.1377	614.2416	307.6245	613.2576	307.1325	**S**	2895.3982	1448.2027	2878.3716	1439.6894	2877.3876	1439.1974	**25**
8	***702.3053***	351.6563	685.2788	343.1430	684.2947	342.6510	**A**	2808.3661	1404.6867	2791.3396	1396.1734	2790.3556	1395.6814	**24**
9	***817.3323***	409.1698	800.3057	400.6565	799.3217	400.1645	**D**	2737.3290	1369.1682	2720.3025	1360.6549	2719.3185	1360.1629	**23**
10	***914.3850***	457.6961	897.3585	449.1829	896.3745	448.6909	**P**	2622.3021	1311.6547	2605.2755	1303.1414	2604.2915	1302.6494	**22**
11	1042.4436	521.7254	1025.4170	513.2122	1024.4330	512.7202	**Q**	2525.2493	1263.1283	2508.2228	1254.6150	2507.2388	1254.1230	**21**
12	1228.5229	**614.7651**	1211.4964	606.2518	1210.5123	605.7598	**W**	2397.1907	1199.0990	2380.1642	1190.5857	2379.1802	1190.0937	**20**
13	***1357.5655***	679.2864	1340.5390	670.7731	1339.5549	670.2811	**E**	2211.1114	1106.0594	2194.0849	1097.5461	2193.1009	1097.0541	**19**
14	***1485.6241***	743.3157	1468.5975	734.8024	1467.6135	734.3104	**Q**	2082.0688	1041.5381	2065.0423	1033.0248	2064.0583	1032.5328	**18**
15	***1598.7081***	**799.8577**	1581.6816	791.3444	1580.6976	790.8524	**L**	***1954.0103***	977.5088	1936.9837	968.9955	1935.9997	968.5035	**17**
16	***1712.7511***	856.8792	1695.7245	848.3659	1694.7405	847.8739	**N**	***1840.9262***	920.9667	1823.8996	912.4535	1822.9156	911.9615	**16**
17	***1827.7780***	**914.3926**	1810.7515	905.8794	1809.7674	905.3874	**N**	***1726.8833***	863.9453	1709.8567	855.4320	1708.8727	854.9400	**15**
18	1955.8730	978.4401	1938.8464	969.9269	1937.8624	969.4348	**K**	1611.8563	806.4318	1594.8298	797.9185	1593.8458	797.4265	**14**
19	2070.8999	1035.9536	2053.8734	1027.4403	2052.8894	1026.9483	**N**	***1483.7614***	742.3843	1466.7348	733.8710	1465.7508	733.3790	**13**
20	2183.9840	**1092.4956**	2166.9574	1083.9824	2165.9734	1083.4903	**L**	***1368.7344***	684.8708	1351.7079	676.3576	1350.7239	675.8656	**12**
21	2271.0160	**1136.0116**	2253.9895	1127.4984	2253.0054	1127.0064	**S**	***1255.6504***	628.3288	1238.6238	619.8155	1237.6398	619.3235	**11**
22	2402.0565	**1201.5319**	2385.0299	1193.0186	2384.0459	1192.5266	**M**	1168.6183	584.8128	1151.5918	576.2995	1150.6078	575.8075	**10**

23	2499.1093	1250.0583	2482.0827	1241.5450	2481.0987	1241.0530	**P**	***1037.5778***	519.2926	1020.5513	510.7793	1019.5673	510.2873	**9**
24	2612.1933	**1306.6003**	2595.1668	1298.0870	2594.1828	1297.5950	**L**	940.5251	470.7662	923.4985	462.2529	922.5145	461.7609	**8**
25	2725.2774	**1363.1423**	2708.2508	1354.6291	2707.2668	1354.1370	**L**	***827.4410***	414.2241	810.4145	405.7109	809.4305	405.2189	**7**
26	2822.3302	1411.6687	2805.3036	1403.1554	2804.3196	1402.6634	**P**	***714.3570***	357.6821	697.3304	349.1688	696.3464	348.6768	**6**
27	2893.3673	1447.1873	2876.3407	1438.6740	2875.3567	1438.1820	**A**	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	**5**
28	3008.3942	1504.7007	2991.3677	1496.1875	2990.3836	1495.6955	**D**	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	**4**
29	3155.4626	1578.2349	3138.4361	1569.7217	3137.4521	1569.2297	**F**	***431.2401***	216.1237	414.2136	207.6104			**3**
30	3292.5215	1646.7644	3275.4950	1638.2511	3274.5110	1637.7591	**H**	284.1717	142.5895	267.1452	134.0762			**2**
31							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GGETAQSADPQWEQLNNKNLSMPLLPADFHK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.0	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N17, N19 30.20%
43.9	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N19 23.61%
42.4	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N19 16.87%
40.2	3436.6357	0.9968	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
38.5	3436.6357	0.9968	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
38.3	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q11, N19 6.49%
37.9	3436.6357	0.9968	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	
37.6	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated N16, N17 5.51%
34.4	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N17 2.69%
33.1	3437.6197	0.0128	GGETAQSADPQWEQLNNKNLSMPLLPADFHK	Deamidated Q14, N16 1.99%

Mascot: http://www.matrixscience.com/

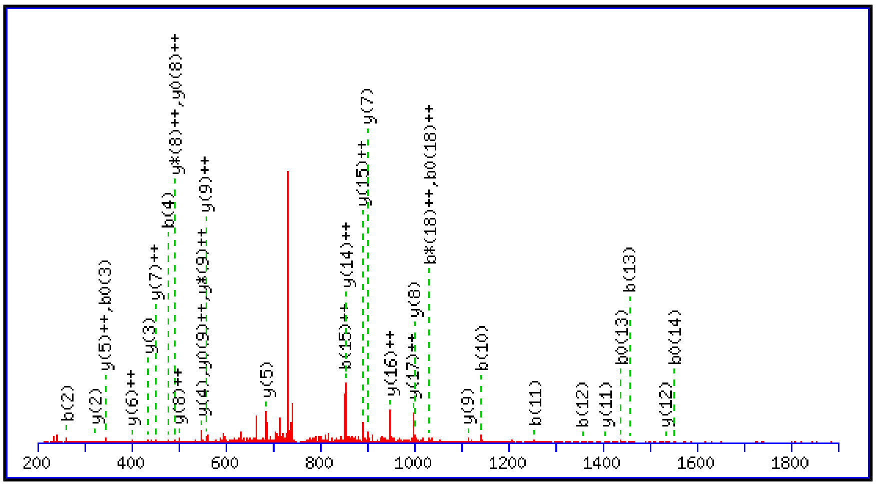
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFVNASSKYEITTIHNLFR**
Found in **P05546** in **con_Xuniprot_HUMAN3**, HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

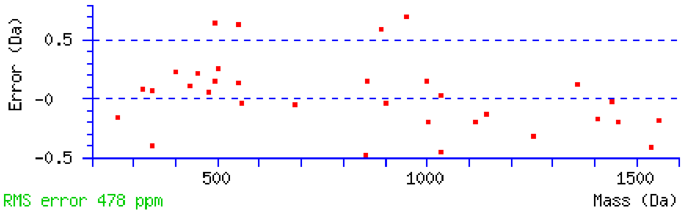
Match to Query 15112: 2255.126952 from(752.716260,3+) intensity(47865.0586) rtinseconds(2127) scans(5502) index(22734)
Title: 111019_Est_MI_YS_G_03Spectrum4821_scans__5502
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

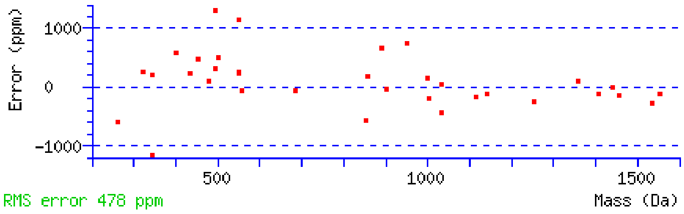
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2255.1222
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.033
Matches : 34/198 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	116.0342	58.5207			98.0237	49.5155	**D**							**19**
2	**263.1026**	132.0550			245.0921	123.0497	**F**	2141.1026	1071.0549	2124.0760	1062.5417	2123.0920	1062.0496	**18**
3	362.1710	181.5892			344.1605	172.5839	**V**	1994.0342	997.5207	1977.0076	989.0074	1976.0236	988.5154	**17**
4	**477.1980**	239.1026	460.1714	230.5894	459.1874	230.0974	**N**	1894.9658	947.9865	1877.9392	939.4732	1876.9552	938.9812	**16**
5	548.2351	274.6212	531.2086	266.1079	530.2245	265.6159	**A**	1779.9388	890.4730	1762.9123	881.9598	1761.9282	881.4678	**15**
6	635.2671	318.1372	618.2406	309.6239	617.2566	309.1319	**S**	1708.9017	854.9545	1691.8751	846.4412	1690.8911	845.9492	**14**
7	722.2992	361.6532	705.2726	353.1399	704.2886	352.6479	**S**	1621.8697	811.4385	1604.8431	802.9252	1603.8591	802.4332	**13**
8	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	**K**	***1534.8376***	767.9225	1517.8111	759.4092	1516.8271	758.9172	**12**
9	1013.4575	507.2324	996.4309	498.7191	995.4469	498.2271	**Y**	***1406.7427***	703.8750	1389.7161	695.3617	1388.7321	694.8697	**11**
10	**1142.5000**	571.7537	1125.4735	563.2404	1124.4895	562.7484	**E**	1243.6793	622.3433	1226.6528	613.8300	1225.6688	613.3380	**10**
11	**1255.5841**	628.2957	1238.5576	619.7824	1237.5735	619.2904	**I**	***1114.6368***	557.8220	1097.6102	549.3087	1096.6262	548.8167	**9**
12	**1356.6318**	678.8195	1339.6052	670.3063	1338.6212	669.8142	**T**	***1001.5527***	501.2800	984.5261	492.7667	983.5421	492.2747	**8**
13	**1457.6795**	729.3434	1440.6529	720.8301	1439.6689	720.3381	**T**	***900.5050***	450.7561	883.4785	442.2429	882.4944	441.7509	**7**
14	1570.7635	785.8854	1553.7370	777.3721	1552.7530	776.8801	**I**	799.4573	400.2323	782.4308	391.7190			**6**
15	1707.8224	854.4149	1690.7959	845.9016	1689.8119	845.4096	**H**	***686.3733***	343.6903	669.3467	335.1770			**5**
16	1821.8654	911.4363	1804.8388	902.9230	1803.8548	902.4310	**N**	***549.3144***	275.1608	532.2878	266.6475			**4**
17	1934.9494	967.9784	1917.9229	959.4651	1916.9389	958.9731	**L**	***435.2714***	218.1394	418.2449	209.6261			**3**
18	2082.0178	1041.5126	2064.9913	1032.9993	2064.0073	1032.5073	**F**	***322.1874***	161.5973	305.1608	153.0840			**2**
19							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DFVNASSKYEITTIHNLFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.2	2255.1222	0.0047	DFVNASSKYEITTIHNLFR	Deamidated N4 98.51%
21.0	2255.1222	0.0047	DFVNASSKYEITTIHNLFR	Deamidated N16 1.49%
11.5	2253.1310	1.9959	QETEKNHCDIAIEELILAK	
6.3	2255.1330	-0.0060	TLRDMAIICFAVFTEPNLK	
5.4	2253.1138	2.0132	LTEQLTQAFSALRHGDSHNK	
3.7	2253.1133	2.0137	TQIHIMPDTPEIMLARQNK	
3.7	2253.1133	2.0137	TQIHIMPDTPEIMLARQNK	
2.7	2255.1369	-0.0099	HTFALLDAARGTGECVVVPDK	
2.1	2254.1151	1.0119	MRELKQNQELEGLPQPGLAT	
1.4	2254.1328	0.9941	TAPPVTNNSEIQASEVLVAADK	

Mascot: http://www.matrixscience.com/

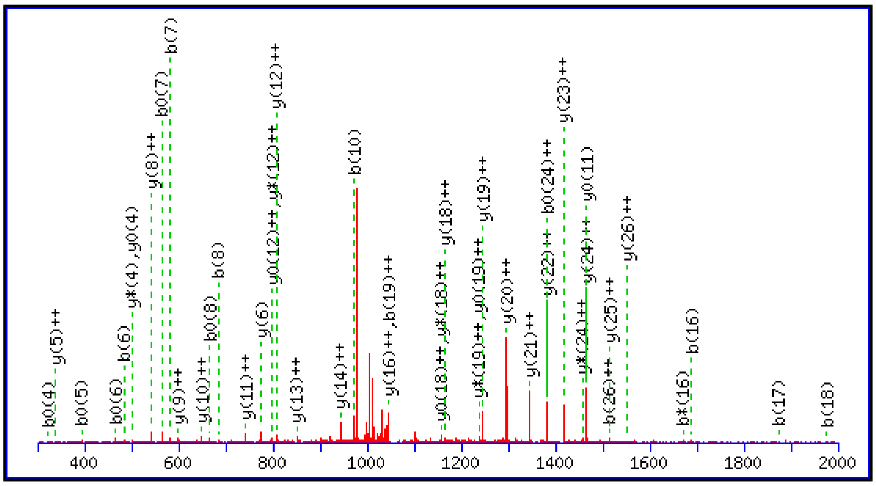
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AATPAAVTCQLSNWSEWTDCFPCQDKK**
Found in **P07357** in **con_Xuniprot_HUMAN3**, CO8A_HUMAN Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

Match to Query 27337: 3171.375672 from(1058.132500,3+) intensity(12581.0137) rtinseconds(2152) scans(5568) index(24769)
Title: 111019_Est_MI_YS_G_06Spectrum4844_scans__5568
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

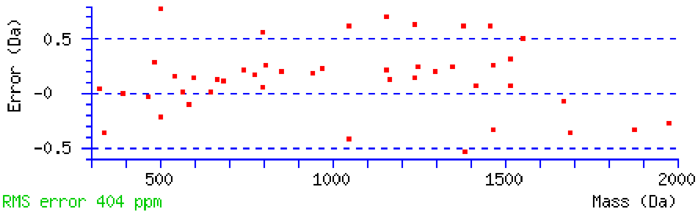
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

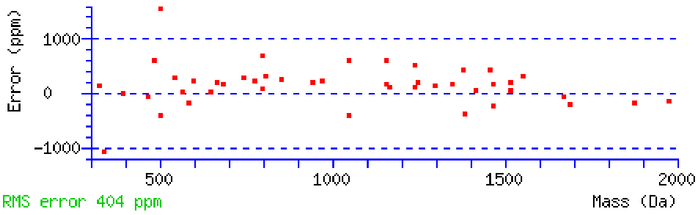


Monoisotopic mass of neutral peptide Mr(calc): 3171.3736
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 80 **Expect:** 7.2e-007
Matches : 45/286 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							27
2	143.0815	72.0444					A	3101.3438	1551.1755	3084.3172	1542.6622	3083.3332	1542.1702	26
3	244.1292	122.5682			226.1186	113.5629	T	3030.3067	1515.6570	3013.2801	1507.1437	3012.2961	1506.6517	25
4	341.1819	171.0946			323.1714	162.0893	P	2929.2590	1465.1331	2912.2324	1456.6199	2911.2484	1456.1278	24
5	412.2191	206.6132			394.2085	197.6079	A	2832.2062	1416.6067	2815.1797	1408.0935	2814.1957	1407.6015	23
6	**483.2562**	242.1317			465.2456	233.1264	A	2761.1691	1381.0882	2744.1426	1372.5749	2743.1585	1372.0829	22
7	**582.3246**	291.6659			564.3140	282.6606	V	2690.1320	1345.5696	2673.1054	1337.0564	2672.1214	1336.5643	21
8	**683.3723**	342.1898			665.3617	333.1845	T	2591.0636	1296.0354	2574.0370	1287.5222	2573.0530	1287.0301	20
9	843.4029	422.2051			825.3924	413.1998	C	2490.0159	1245.5116	2472.9893	1236.9983	2472.0053	1236.5063	19
10	**971.4615**	486.2344	954.4349	477.7211	953.4509	477.2291	Q	2329.9852	1165.4963	2312.9587	1156.9830	2311.9747	1156.4910	18
11	1084.5456	542.7764	1067.5190	534.2631	1066.5350	533.7711	L	2201.9267	1101.4670	2184.9001	1092.9537	2183.9161	1092.4617	17
12	1171.5776	586.2924	1154.5510	577.7792	1153.5670	577.2871	S	2088.8426	1044.9249	2071.8161	1036.4117	2070.8320	1035.9197	16
13	1286.6045	643.8059	1269.5780	635.2926	1268.5940	634.8006	N	2001.8106	1001.4089	1984.7840	992.8957	1983.8000	992.4036	15
14	1472.6838	736.8456	1455.6573	728.3323	1454.6733	727.8403	W	1886.7836	943.8955	1869.7571	935.3822	1868.7731	934.8902	14
15	1559.7159	780.3616	1542.6893	771.8483	1541.7053	771.3563	S	1700.7043	850.8558	1683.6778	842.3425	1682.6938	841.8505	13
16	**1688.7585**	844.8829	1671.7319	836.3696	1670.7479	835.8776	E	1613.6723	807.3398	1596.6457	798.8265	1595.6617	798.3345	12
17	**1874.8378**	937.9225	1857.8112	929.4093	1856.8272	928.9172	W	1484.6297	742.8185	1467.6031	734.3052	1466.6191	733.8132	11
18	**1975.8855**	988.4464	1958.8589	979.9331	1957.8749	979.4411	T	1298.5504	649.7788	1281.5238	641.2656	1280.5398	640.7735	10
19	2090.9124	1045.9598	2073.8858	1037.4466	2072.9018	1036.9546	D	1197.5027	599.2550	1180.4762	590.7417	1179.4921	590.2497	9
20	2250.9430	1125.9752	2233.9165	1117.4619	2232.9325	1116.9699	C	1082.4758	541.7415	1065.4492	533.2282	1064.4652	532.7362	8
21	2398.0115	1199.5094	2380.9849	1190.9961	2380.0009	1190.5041	F	922.4451	461.7262	905.4186	453.2129	904.4345	452.7209	7
22	2495.0642	1248.0358	2478.0377	1239.5225	2477.0537	1239.0305	P	775.3767	388.1920	758.3502	379.6787	757.3661	379.1867	6
23	2655.0949	1328.0511	2638.0683	1319.5378	2637.0843	1319.0458	C	678.3239	339.6656	661.2974	331.1523	660.3134	330.6603	5

24	2783.1535	1392.0804	2766.1269	1383.5671	2765.1429	1383.0751	**Q**	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	**4**
25	2898.1804	1449.5938	2881.1538	1441.0806	2880.1698	1440.5886	**D**	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	**3**
26	3026.2754	1513.6413	3009.2488	1505.1280	3008.2648	1504.6360	**K**	275.2078	138.1075	258.1812	129.5942			**2**
27							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of AATPAAVTCQLSNWSEWTDCFPCQDKK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
80.1	3171.3736	0.0021	AATPAAVTCQLSNWSEWTDCFPCQDKK	Deamidated N13 83.36%
70.1	3171.3736	0.0021	AATPAAVTCQLSNWSEWTDCFPCQDKK	Deamidated Q10 8.37%
70.0	3171.3736	0.0021	AATPAAVTCQLSNWSEWTDCFPCQDKK	Deamidated Q24 8.26%
0.1	3171.3657	0.0100	MEINNRNMYDVNVTCPELCVPPSSWK	
0.0	3171.3657	0.0100	MEINNRNMYDVNVTCPELCVPPSSWK	
0.0	3171.3657	0.0100	MEINNRNMYDVNVTCPELCVPPSSWK	

Mascot: http://www.matrixscience.com/

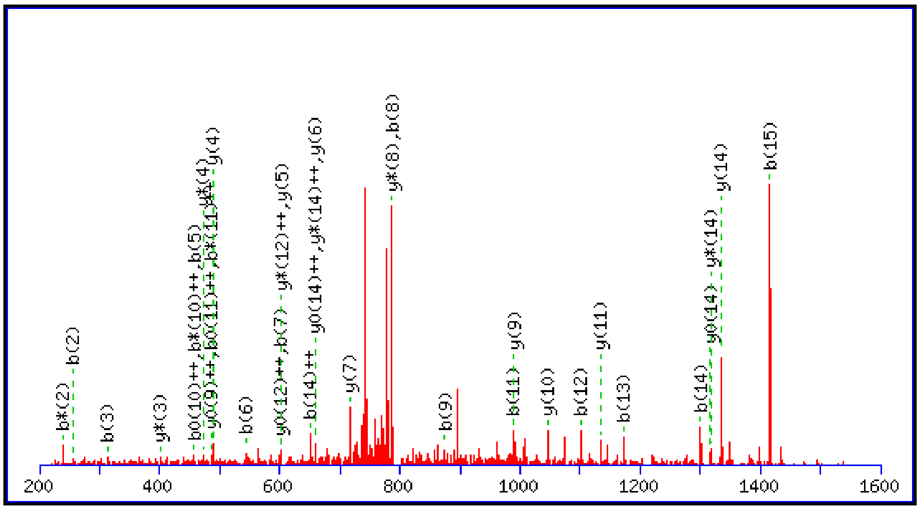
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VRGGSSGWSGGLAQNR**
Found in **P07357** in **con_Xuniprot_HUMAN3**, CO8A_HUMAN Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

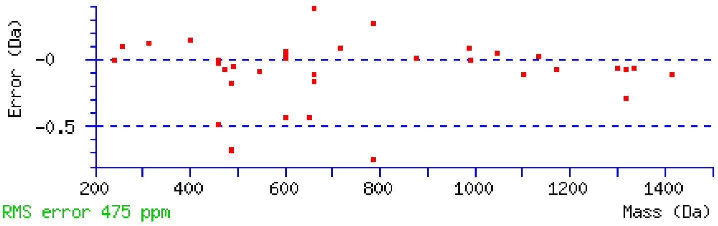
Match to Query 7598: 1588.774548 from(795.394550,2+) intensity(19271.7539) rtinseconds(406) scans(858) index(24339)
Title: 111019_Est_MI_YS_G_06Spectrum731_scans__858
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

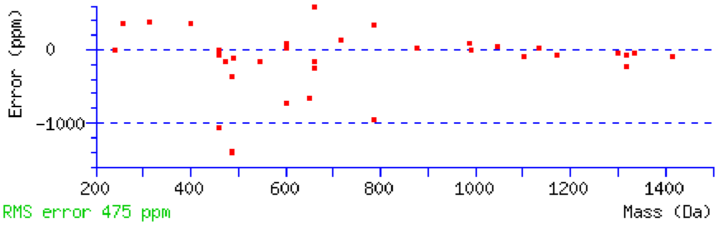
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1588.7706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 74 **Expect:** 9.4e-006
Matches : 36/156 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					**V**							**16**
2	***256.1768***	128.5920	239.1503	120.0788			**R**	1490.7095	745.8584	1473.6829	737.3451	1472.6989	736.8531	**15**
3	***313.1983***	157.1028	296.1717	148.5895			**G**	**1334.6084**	667.8078	1317.5818	659.2945	1316.5978	658.8025	**14**
4	370.2197	185.6135	353.1932	177.1002			**G**	1277.5869	639.2971	1260.5604	630.7838	1259.5763	630.2918	**13**
5	***457.2518***	229.1295	440.2252	220.6162	439.2412	220.1242	**S**	1220.5654	610.7864	1203.5389	602.2731	1202.5549	601.7811	**12**
6	***544.2838***	272.6455	527.2572	264.1323	526.2732	263.6402	**S**	**1133.5334**	567.2703	1116.5069	558.7571	1115.5228	558.2651	**11**
7	***601.3052***	301.1563	584.2787	292.6430	583.2947	292.1510	**G**	**1046.5014**	523.7543	1029.4748	515.2411	1028.4908	514.7490	**10**
8	***787.3846***	394.1959	770.3580	385.6826	769.3740	385.1906	**W**	**989.4799**	495.2436	972.4534	486.7303	971.4694	486.2383	**9**
9	***874.4166***	437.7119	857.3900	429.1987	856.4060	428.7067	**S**	803.4006	402.2039	786.3741	393.6907	785.3900	393.1987	**8**
10	931.4381	466.2227	914.4115	457.7094	913.4275	457.2174	**G**	**716.3686**	358.6879	699.3420	350.1747			**7**
11	***988.4595***	494.7334	971.4330	486.2201	970.4490	485.7281	**G**	**659.3471**	330.1772	642.3206	321.6639			**6**
12	***1101.5436***	551.2754	1084.5170	542.7622	1083.5330	542.2701	**L**	**602.3257**	301.6665	585.2991	293.1532			**5**
13	***1172.5807***	586.7940	1155.5541	578.2807	1154.5701	577.7887	**A**	**489.2416**	245.1244	472.2150	236.6112			**4**
14	***1300.6393***	650.8233	1283.6127	642.3100	1282.6287	641.8180	**Q**	418.2045	209.6059	401.1779	201.0926			**3**
15	***1415.6662***	708.3367	1398.6397	699.8235	1397.6557	699.3315	**N**	290.1459	145.5766	273.1193	137.0633			**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VRGGSSGWSGGLAQNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.9	1588.7706	0.0039	VRGGSSGWSGGLAQNR	Deamidated N15 50.75%
73.8	1588.7706	0.0039	VRGGSSGWSGGLAQNR	Deamidated Q14 49.25%
8.3	1588.7805	-0.0059	DRQKLVSSQEQDR	
6.4	1588.7746	-0.0001	WRQQWSGPGTTKR	
4.3	1588.7780	-0.0034	RMLEAPYQNQPSR	
4.1	1588.7766	-0.0021	IMEDIEENKVNVR	
4.1	1588.7766	-0.0021	IMEDIEENKVNVR	
3.3	1588.7766	-0.0021	LEQDLQQMQAKVR	
2.5	1588.7746	-0.0001	ASIDGFDRYFRSR	
1.6	1588.7733	0.0013	ELYELPIGQEENR	

Mascot: http://www.matrixscience.com/

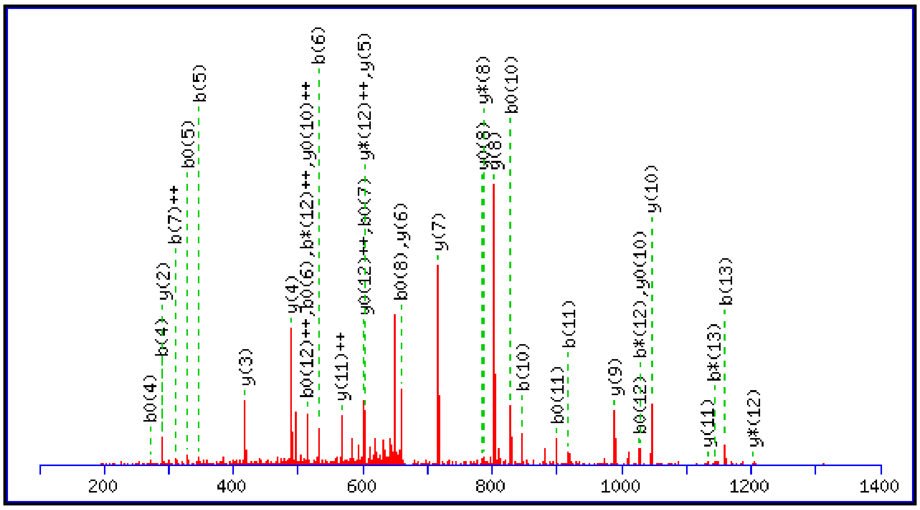
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGSSGWSGGLAQNR**
Found in **P07357** in **con_Xuniprot_HUMAN3**, CO8A_HUMAN Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

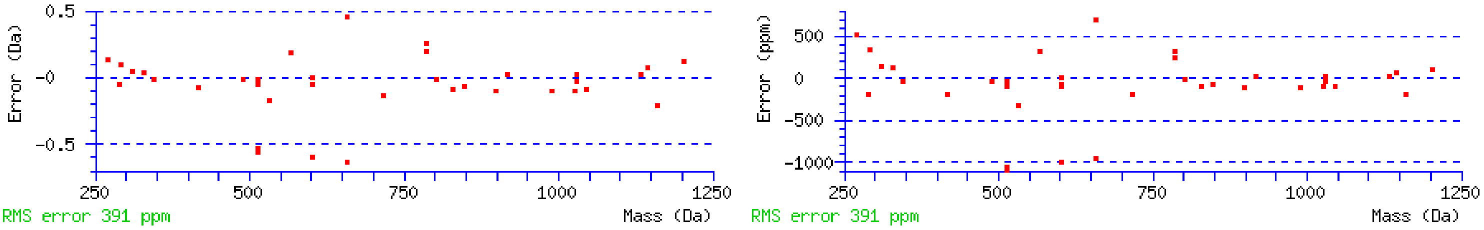
Match to Query 2029: 1333.607748 from(667.811150,2+) intensity(14344.3994) rtinseconds(568) scans(1150) index(1871)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum945_scans__1150
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1333.6011
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13    : Deamidated (NQ)
Ions Score: 65  Expect: 4.4e-005
Matches : 37/116 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					**G**							**14**
2	115.0502	58.0287					**G**	1277.5869	639.2971	1260.5604	630.7838	1259.5763	630.2918	**13**
3	202.0822	101.5448			184.0717	92.5395	**S**	1220.5654	610.7864	1203.5389	602.2731	1202.5549	601.7811	**12**
4	**289.1143**	145.0608			271.1037	136.0555	**S**	***1133.5334***	567.2703	1116.5069	558.7571	1115.5228	558.2651	**11**
5	**346.1357**	173.5715			328.1252	164.5662	**G**	***1046.5014***	523.7543	1029.4748	515.2411	1028.4908	514.7490	**10**
6	**532.2150**	266.6112			514.2045	257.6059	**W**	***989.4799***	495.2436	972.4534	486.7303	971.4694	486.2383	**9**
7	619.2471	310.1272			601.2365	301.1219	**S**	***803.4006***	402.2039	786.3741	393.6907	785.3900	393.1987	**8**
8	676.2685	338.6379			658.2580	329.6326	**G**	***716.3686***	358.6879	699.3420	350.1747			**7**
9	733.2900	367.1486			715.2794	358.1434	**G**	***659.3471***	330.1772	642.3206	321.6639			**6**
10	**846.3741**	423.6907			828.3635	414.6854	**L**	***602.3257***	301.6665	585.2991	293.1532			**5**
11	**917.4112**	459.2092			899.4006	450.2039	**A**	***489.2416***	245.1244	472.2150	236.6112			**4**
12	1045.4697	523.2385	1028.4432	514.7252	1027.4592	514.2332	**Q**	***418.2045***	209.6059	401.1779	201.0926			**3**
13	**1160.4967**	580.7520	1143.4701	572.2387	1142.4861	571.7467	**N**	***290.1459***	145.5766	273.1193	137.0633			**2**
14							**R**	175.1190	88.0631	158.0924	79.5498			**1**



NCBI **BLAST** search of GGSSGWSGGLAQNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.6	1333.6011	0.0067	GGSSGWSGGLAQNR	Deamidated N13 65.43%
61.8	1333.6011	0.0067	GGSSGWSGGLAQNR	Deamidated Q12 34.57%
10.1	1333.6109	-0.0032	QAQPSSKTASGNR	
9.1	1332.6058	1.0019	NNLYPNSSPGNR	
9.1	1332.6058	1.0019	NNLYPNSSPGNR	
8.9	1333.6085	-0.0007	LCELSAQGWNR	
8.9	1332.6092	0.9986	AEQMASVQNAQR	
8.7	1332.6058	1.0019	NNLYPNSSPGNR	
8.5	1332.6092	0.9986	AEQMASVQNAQR	
8.5	1332.6092	0.9986	AEQMASVQNAQR	

Mascot: http://www.matrixscience.com/

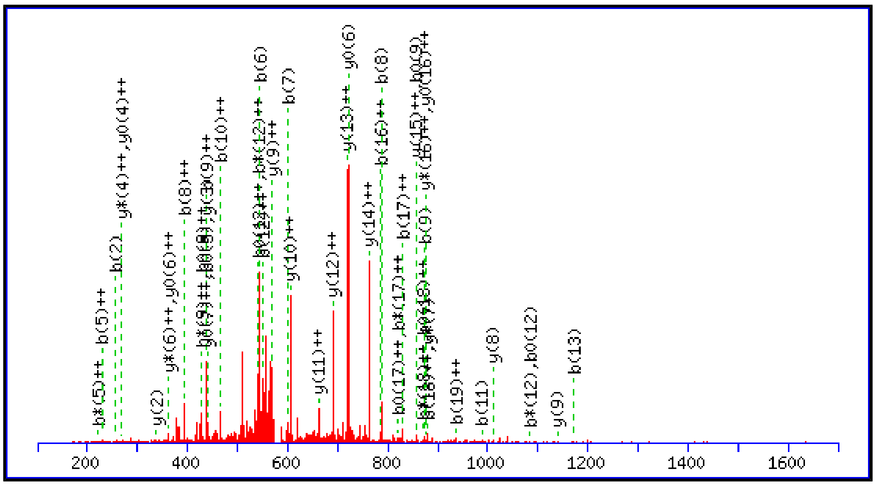
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VRGGSSGWSGGLAQNRSTITYR**
Found in **P07357** in **con_Xuniprot_HUMAN3**, CO8A_HUMAN Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

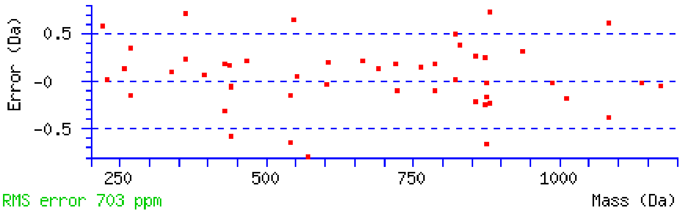
Match to Query 15146: 2310.154456 from(578.545890,4+) intensity(7498.9004) rtinseconds(818) scans(1887) index(22498)
Title: 111019_Est_MI_YS_G_03Spectrum1615_scans__1887
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

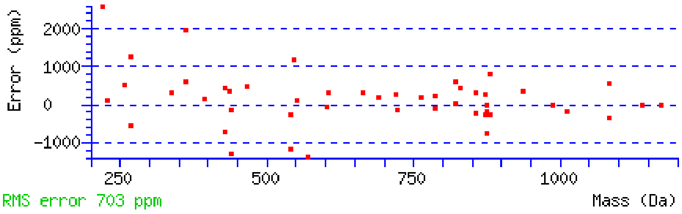
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2310.1465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15     : Deamidated (NQ)
Ions Score: 38  Expect: 0.041
Matches : 49/238 fragment ions using 93 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							**22**
2	***256.1768***	128.5920	239.1503	120.0788			**R**	2212.0854	1106.5463	2195.0588	1098.0330	2194.0748	1097.5410	**21**
3	313.1983	157.1028	296.1717	148.5895			**G**	2055.9843	1028.4958	2038.9577	1019.9825	2037.9737	1019.4905	**20**
4	370.2197	185.6135	353.1932	177.1002			**G**	1998.9628	999.9850	1981.9362	991.4718	1980.9522	990.9798	**19**
5	457.2518	***229.1295***	440.2252	220.6162	439.2412	220.1242	**S**	1941.9413	971.4743	1924.9148	962.9610	1923.9308	962.4690	**18**
6	***544.2838***	272.6455	527.2572	264.1323	526.2732	263.6402	**S**	1854.9093	927.9583	1837.8828	919.4450	1836.8987	918.9530	**17**
7	***601.3052***	301.1563	584.2787	292.6430	583.2947	292.1510	**G**	1767.8773	884.4423	1750.8507	875.9290	1749.8667	875.4370	**16**
8	***787.3846***	***394.1959***	770.3580	385.6826	769.3740	385.1906	**W**	1710.8558	855.9315	1693.8293	847.4183	1692.8452	846.9263	**15**
9	***874.4166***	***437.7119***	857.3900	429.1987	856.4060	428.7067	**S**	1524.7765	762.8919	1507.7499	754.3786	1506.7659	753.8866	**14**
10	931.4381	***466.2227***	914.4115	457.7094	913.4275	457.2174	**G**	1437.7445	719.3759	1420.7179	710.8626	1419.7339	710.3706	**13**
11	***988.4595***	494.7334	971.4330	486.2201	970.4490	485.7281	**G**	1380.7230	690.8651	1363.6965	682.3519	1362.7124	681.8599	**12**
12	1101.5436	***551.2754***	1084.5170	542.7622	1083.5330	542.2701	**L**	1323.7015	662.3544	1306.6750	653.8411	1305.6910	653.3491	**11**
13	***1172.5807***	586.7940	1155.5541	578.2807	1154.5701	577.7887	**A**	1210.6175	605.8124	1193.5909	597.2991	1192.6069	596.8071	**10**
14	1300.6393	650.8233	1283.6127	642.3100	1282.6287	641.8180	**Q**	**1139.5804**	570.2938	1122.5538	561.7805	1121.5698	561.2885	**9**
15	1415.6662	708.3367	1398.6397	699.8235	1397.6557	699.3315	**N**	**1011.5218**	506.2645	994.4952	497.7513	993.5112	497.2592	**8**
16	1571.7673	***786.3873***	1554.7408	777.8740	1553.7568	777.3820	**R**	896.4948	448.7511	879.4683	440.2378	878.4843	439.7458	**7**
17	1658.7994	***829.9033***	1641.7728	821.3900	1640.7888	820.8980	**S**	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	**6**
18	1759.8470	***880.4272***	1742.8205	871.9139	1741.8365	871.4219	**T**	653.3617	327.1845	636.3352	318.6712	635.3511	318.1792	**5**
19	1872.9311	***936.9692***	1855.9046	928.4559	1854.9205	927.9639	**I**	552.3140	276.6607	535.2875	268.1474	534.3035	267.6554	**4**
20	1973.9788	987.4930	1956.9522	978.9798	1955.9682	978.4877	**T**	**439.2300**	220.1186	422.2034	211.6053	421.2194	211.1133	**3**
21	2137.0421	1069.0247	2120.0156	1060.5114	2119.0315	1060.0194	**Y**	**338.1823**	169.5948	321.1557	161.0815			**2**
22							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of VRGGSSGWSGGLAQNRSTITYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.0	2310.1465	0.0080	VRGGSSGWSGGLAQNRSTITYR	Deamidated N15 63.42%
35.7	2310.1465	0.0080	VRGGSSGWSGGLAQNRSTITYR	Deamidated Q14 36.58%
24.9	2309.1625	0.9920	VRGGSSGWSGGLAQNRSTITYR	
10.1	2309.1427	1.0118	VFQWTASTATITKEKQDQPK	
8.5	2308.1587	1.9958	VFQWTASTATITKEKQDQPK	
7.7	2308.1528	2.0016	LMTRHMAQPSERIQTSIHR	
7.3	2308.1587	1.9958	VFQWTASTATITKEKQDQPK	
6.2	2310.1644	-0.0100	QDIYRKAISPQFDPSELFR	
5.1	2308.1434	2.0110	FLKNEDQVDQLLQTKSSLDS	
5.1	2308.1434	2.0110	FLKNEDQVDQLLQTKSSLDS	

Mascot: http://www.matrixscience.com/

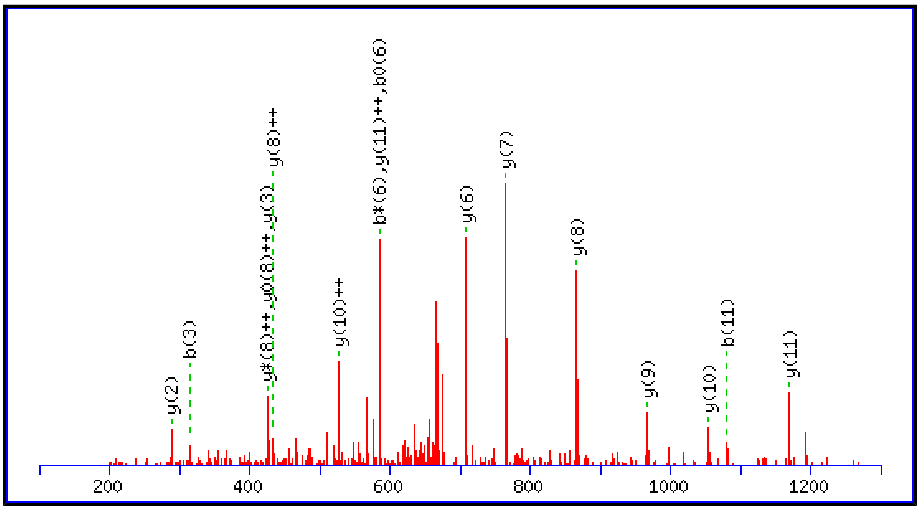
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVNSTTGPGEHLR**
Found in **P07996** in **con_Xuniprot_HUMAN3**, TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2

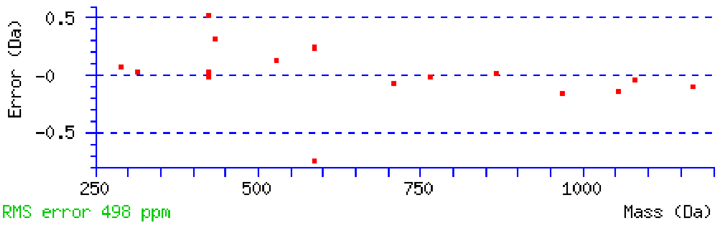
Match to Query 2378: 1366.686608 from(684.350580,2+) intensity(7093.3613) rtinseconds(285) scans(434) index(15566)
Title: 111019_Est_MI_YP_G_05Spectrum340_scans__434
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

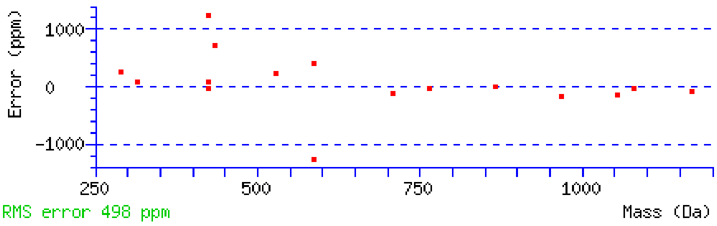
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1366.6841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.00019
Matches : 17/128 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	100.0757	50.5415					V							13
2	199.1441	100.0757					V	1268.6230	634.8151	1251.5964	626.3018	1250.6124	625.8098	12
3	**314.1710**	157.5892	297.1445	149.0759			N	***1169.5545***	585.2809	1152.5280	576.7676	1151.5440	576.2756	11
4	401.2031	201.1052	384.1765	192.5919	383.1925	192.0999	S	***1054.5276***	527.7674	1037.5011	519.2542	1036.5170	518.7622	10
5	502.2508	251.6290	485.2242	243.1157	484.2402	242.6237	T	***967.4956***	484.2514	950.4690	475.7381	949.4850	475.2461	9
6	603.2984	302.1529	586.2719	293.6396	585.2879	293.1476	T	***866.4479***	433.7276	849.4213	425.2143	848.4373	424.7223	8
7	660.3199	330.6636	643.2933	322.1503	642.3093	321.6583	G	***765.4002***	383.2037	748.3737	374.6905	747.3896	374.1985	7
8	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	P	***708.3787***	354.6930	691.3522	346.1797	690.3682	345.6877	6
9	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	G	611.3260	306.1666	594.2994	297.6534	593.3154	297.1613	5
10	943.4367	472.2220	926.4102	463.7087	925.4262	463.2167	E	554.3045	277.6559	537.2780	269.1426	536.2940	268.6506	4
11	**1080.4956**	540.7515	1063.4691	532.2382	1062.4851	531.7462	H	***425.2619***	213.1346	408.2354	204.6213			3
12	1193.5797	597.2935	1176.5531	588.7802	1175.5691	588.2882	L	***288.2030***	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of VVNSTTGPGEHLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
60.2	1366.6841	0.0025	VVNSTTGPGEHLR
11.1	1366.6841	0.0026	TPNNRPDAPKEK
7.9	1366.6915	-0.0049	TPGVYCSTLLRT
4.8	1364.6765	2.0101	GDIIEGFFWPGK
4.0	1366.6841	0.0026	TPNNRPDAPKEK
2.0	1365.6888	0.9978	VVSQSTDPSKYR
0.8	1364.6837	2.0029	RWEEVQSYIR
0.8	1365.6888	0.9978	TGEQYSVLGKER
0.4	1366.6841	0.0025	VDVGRYTDVSTR
0.3	1364.6792	2.0074	MIDLLQSLCTR

Mascot: http://www.matrixscience.com/

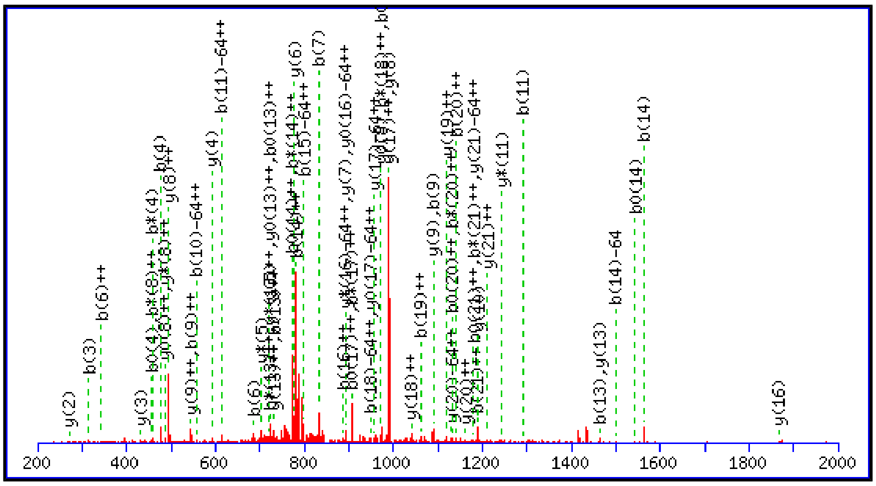
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KVSCPIMPCSNATVPDGECCPR**
Found in **P07996** in **con_Xuniprot_HUMAN3**, TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2

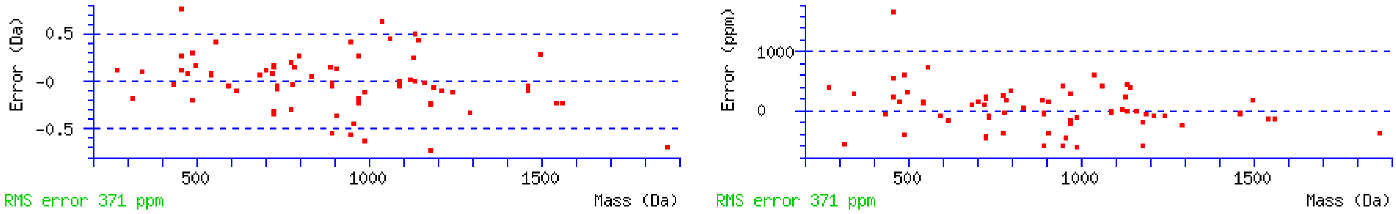
Match to Query 21931: 2551.074642 from(851.365490,3+) intensity(4140.8208) rtinseconds(650) scans(1420) index(3661)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum1185_scans__1420
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2551.0634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N11 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.0069
Matches : 69/366 fragment ions using 144 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							22
2	228.1707	114.5890	211.1441	106.0757			V	2423.9757	1212.4915	2406.9491	1203.9782	2405.9651	1203.4862	21
3	**315.2027**	158.1050	298.1761	149.5917	297.1921	149.0997	S	2324.9073	1162.9573	2307.8807	1154.4440	2306.8967	1153.9520	20
4	**475.2333**	238.1203	458.2068	229.6070	457.2228	229.1150	C	2237.8752	1119.4413	2220.8487	1110.9280	2219.8647	1110.4360	19
5	572.2861	286.6467	555.2595	278.1334	554.2755	277.6414	P	2077.8446	1039.4259	2060.8180	1030.9127	2059.8340	1030.4207	18
6	**685.3702**	**343.1887**	668.3436	334.6754	667.3596	334.1834	I	1980.7918	990.8996	1963.7653	982.3863	1962.7813	981.8943	17
7	**832.4056**	416.7064	815.3790	408.1931	814.3950	407.7011	M	***1867.7078***	934.3575	1850.6812	925.8442	1849.6972	925.3522	16
8	929.4583	465.2328	912.4318	456.7195	911.4478	456.2275	P	1720.6724	860.8398	1703.6458	852.3265	1702.6618	851.8345	15
9	**1089.4890**	**545.2481**	1072.4624	536.7348	1071.4784	536.2428	C	1623.6196	812.3134	1606.5931	803.8002	1605.6090	803.3082	14
10	1176.5210	588.7641	1159.4945	580.2509	1158.5104	579.7589	S	***1463.5890***	732.2981	1446.5624	723.7848	1445.5784	723.2928	13
11	**1291.5479**	646.2776	1274.5214	637.7643	1273.5374	637.2723	N	1376.5569	688.7821	1359.5304	680.2688	1358.5464	679.7768	12
12	1362.5851	681.7962	1345.5585	673.2829	1344.5745	672.7909	A	1261.5300	631.2686	1244.5034	622.7554	1243.5194	622.2633	11
13	**1463.6327**	**732.3200**	1446.6062	723.8067	1445.6222	723.3147	T	***1190.4929***	595.7501	1173.4663	587.2368	1172.4823	586.7448	10
14	**1562.7011**	**781.8542**	1545.6746	773.3409	1544.6906	772.8489	V	***1089.4452***	545.2262	1072.4186	536.7130	1071.4346	536.2210	9
15	1659.7539	830.3806	1642.7274	821.8673	1641.7433	821.3753	P	***990.3768***	495.6920	973.3502	487.1788	972.3662	486.6867	8
16	1774.7809	**887.8941**	1757.7543	879.3808	1756.7703	878.8888	D	***893.3240***	447.1656	876.2975	438.6524	875.3134	438.1604	7
17	1831.8023	916.4048	1814.7758	907.8915	1813.7918	907.3995	G	***778.2971***	389.6522	761.2705	381.1389	760.2865	380.6469	6
18	1960.8449	980.9261	1943.8184	972.4128	1942.8343	971.9208	E	***721.2756***	361.1414	704.2491	352.6282	703.2650	352.1362	5
19	2120.8756	**1060.9414**	2103.8490	1052.4281	2102.8650	1051.9361	C	***592.2330***	296.6201	575.2065	288.1069			4
20	2280.9062	**1140.9567**	2263.8797	1132.4435	2262.8956	1131.9515	C	***432.2024***	216.6048	415.1758	208.0915			3
21	2377.9590	**1189.4831**	2360.9324	1180.9699	2359.9484	1180.4778	P	***272.1717***	136.5895	255.1452	128.0762			2
22							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of KVSCPIMPCSNATVPDGECCPR
(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	2551.0634	0.0113	KVSCPIMPCSNATVPDGECCPR
28.4	2550.0794	0.9953	KVSCPIMPCSNATVPDGECCPR
2.8	2551.0782	-0.0036	WAGDQSHQPSLCAGPTARSNESHG
2.7	2549.0648	2.0099	KENYTATLEDFMTSNMEMFAK
1.9	2551.0690	0.0056	GCEETVEGELDDDIDKPDVMNR
1.7	2551.0793	-0.0047	ASSNPNATSSSSQDPESLQDRGEGK
1.7	2551.0793	-0.0047	ASSNPNATSSSSQDPESLQDRGEGK
1.7	2551.0793	-0.0047	ASSNPNATSSSSQDPESLQDRGEGK
1.7	2551.0793	-0.0047	ASSNPNATSSSSQDPESLQDRGEGK
0.1	2551.0730	0.0016	SLFQEQEEPEPGMEEAGEMEQK

Mascot: http://www.matrixscience.com/

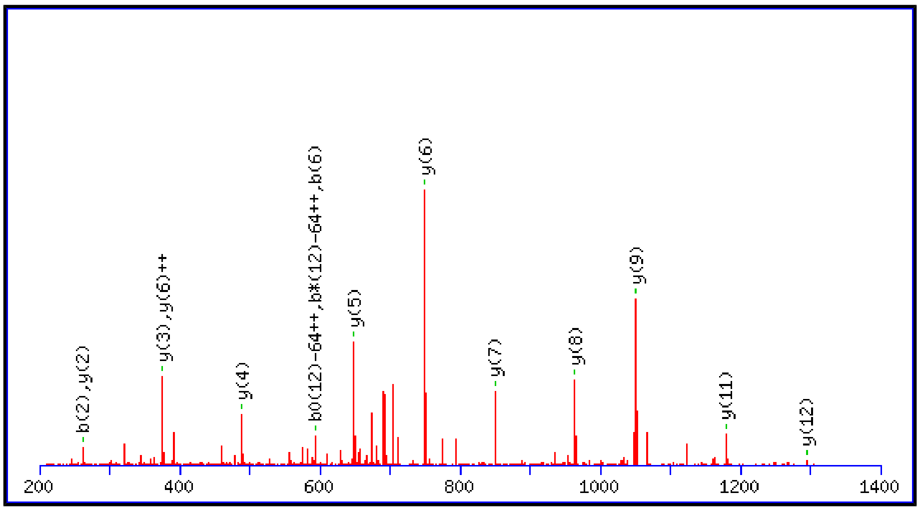
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDGASNVTCINSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

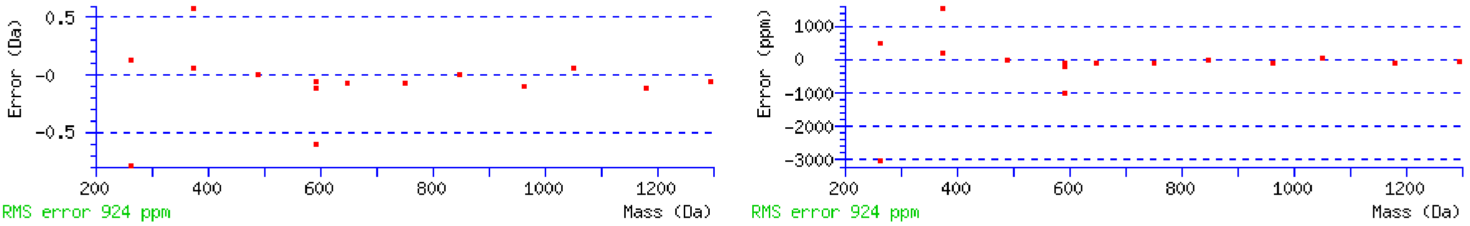
Match to Query 4075: 1440.597408 from(721.305980,2+) intensity(964745.7500) rtinseconds(320) scans(678) index(19284)
Title: 111019_Est_MI_YP_G_09Spectrum586_scans__678
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1440.5973
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N6 : Deamidated (NQ)
Ions Score: 113 **Expect:** 2.2e-010
Matches : 15/190 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							13
2	**263.0696**	132.0384			245.0591	123.0332	D	***1294.5692***	647.7882	1277.5427	639.2750	1276.5586	638.7830	12
3	320.0911	160.5492			302.0805	151.5439	G	***1179.5423***	590.2748	1162.5157	581.7615	1161.5317	581.2695	11
4	391.1282	196.0677			373.1176	187.0625	A	1122.5208	561.7640	1105.4942	553.2508	1104.5102	552.7588	10
5	478.1602	239.5838			460.1497	230.5785	S	***1051.4837***	526.2455	1034.4571	517.7322	1033.4731	517.2402	9
6	**593.1872**	297.0972	576.1606	288.5839	575.1766	288.0919	N	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	8
7	692.2556	346.6314	675.2290	338.1182	674.2450	337.6261	V	***849.4247***	425.2160	832.3982	416.7027	831.4141	416.2107	7
8	793.3033	397.1553	776.2767	388.6420	775.2927	388.1500	T	***750.3563***	375.6818	733.3298	367.1685	732.3457	366.6765	6
9	953.3339	477.1706	936.3074	468.6573	935.3233	468.1653	C	***649.3086***	325.1579	632.2821	316.6447	631.2981	316.1527	5
10	1066.4180	533.7126	1049.3914	525.1994	1048.4074	524.7073	I	***489.2780***	245.1426	472.2514	236.6293	471.2674	236.1373	4
11	1180.4609	590.7341	1163.4344	582.2208	1162.4503	581.7288	N	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	3
12	1267.4929	634.2501	1250.4664	625.7368	1249.4824	625.2448	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of MDGASNVTCINSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
112.8	1440.5973	0.0001	MDGASNVTCINSR	Deamidated N6 99.99%
73.2	1440.5973	0.0001	MDGASNVTCINSR	Deamidated N11 0.01%
14.3	1439.5987	0.9987	DGDNVMTWNSRK	
9.9	1439.5987	0.9987	WTNATNNMNLSR	
8.8	1439.5987	0.9987	WTNATNNMNLSR	
7.5	1439.5947	1.0027	TKSCNGGSGGGDGTGK	
5.3	1438.5956	2.0019	QEDSMAEMEQLK	
3.7	1438.5848	2.0126	YQEQGGEASPQSR	

Mascot: http://www.matrixscience.com/

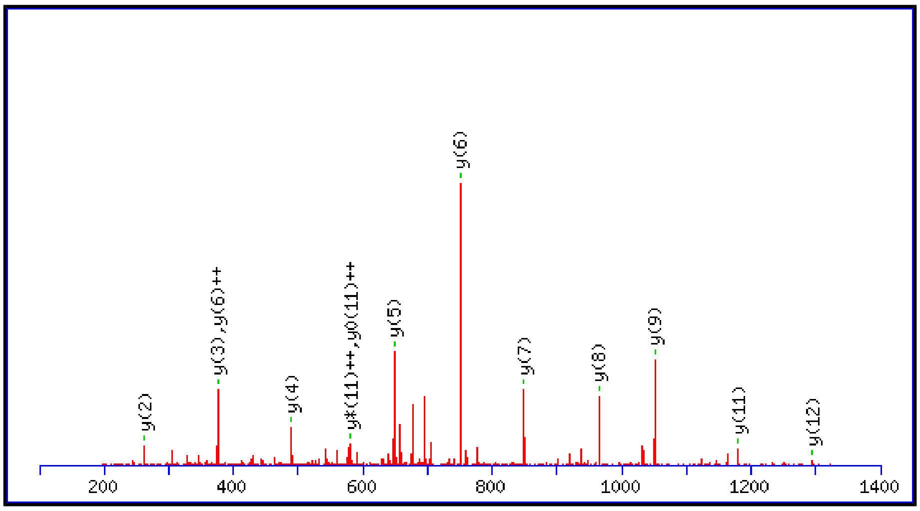
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDGASNVTCINSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

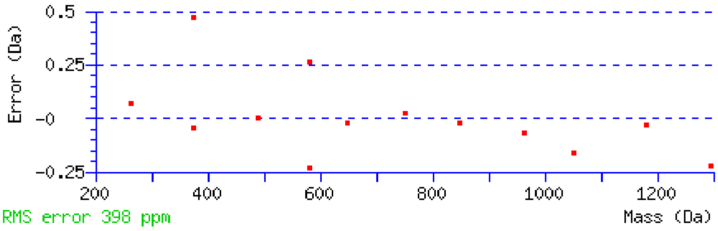
Match to Query 3058: 1424.603388 from(713.308970,2+) intensity(342887.8125) rtinseconds(535) scans(1030) index(12300)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum864_scans__1030
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

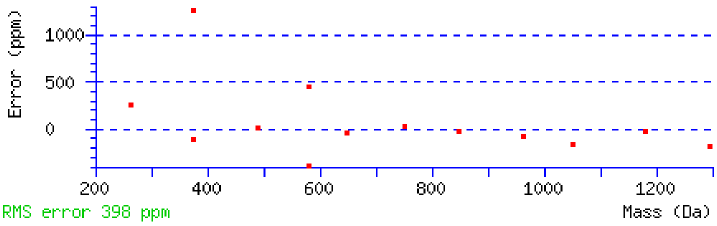
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1424.6024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 106 **Expect:** 1.4e-009
Matches : 13/130 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	132.0478	66.5275					M							13
2	247.0747	124.0410			229.0641	115.0357	D	***1294.5692***	647.7882	1277.5427	639.2750	1276.5586	638.7830	12
3	304.0962	152.5517			286.0856	143.5464	G	***1179.5423***	590.2748	1162.5157	581.7615	1161.5317	581.2695	11
4	375.1333	188.0703			357.1227	179.0650	A	1122.5208	561.7640	1105.4942	553.2508	1104.5102	552.7588	10
5	462.1653	231.5863			444.1547	222.5810	S	***1051.4837***	526.2455	1034.4571	517.7322	1033.4731	517.2402	9
6	577.1923	289.0998	560.1657	280.5865	559.1817	280.0945	N	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	8
7	676.2607	338.6340	659.2341	330.1207	658.2501	329.6287	V	***849.4247***	425.2160	832.3982	416.7027	831.4141	416.2107	7
8	777.3083	389.1578	760.2818	380.6445	759.2978	380.1525	T	***750.3563***	375.6818	733.3298	367.1685	732.3457	366.6765	6
9	937.3390	469.1731	920.3124	460.6599	919.3284	460.1679	C	***649.3086***	325.1579	632.2821	316.6447	631.2981	316.1527	5
10	1050.4231	525.7152	1033.3965	517.2019	1032.4125	516.7099	I	***489.2780***	245.1426	472.2514	236.6293	471.2674	236.1373	4
11	1164.4660	582.7366	1147.4394	574.2234	1146.4554	573.7313	N	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	3
12	1251.4980	626.2526	1234.4715	617.7394	1233.4874	617.2474	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MDGASNVTCINSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
106.1	1424.6024	0.0010	MDGASNVTCINSR	Deamidated N6 99.96%
72.4	1424.6024	0.0010	MDGASNVTCINSR	Deamidated N11 0.04%
8.8	1423.6071	0.9963	VCNSAGCAEKQAK	
5.8	1423.6063	0.9971	DQENSVQSSNSTK	
5.5	1423.6063	0.9971	AESSSDEAVADTSR	
4.0	1423.5997	1.0036	MEGGGKPNSSSNSR	
4.0	1423.6037	0.9996	WTNATNNMNLSR	
4.0	1423.6063	0.9971	DQENSVQSSNSTK	
3.3	1422.5998	2.0036	NKQESSEQQVDK	
2.7	1424.6056	-0.0022	SSSDSWEPTSAGSK	

Mascot: http://www.matrixscience.com/

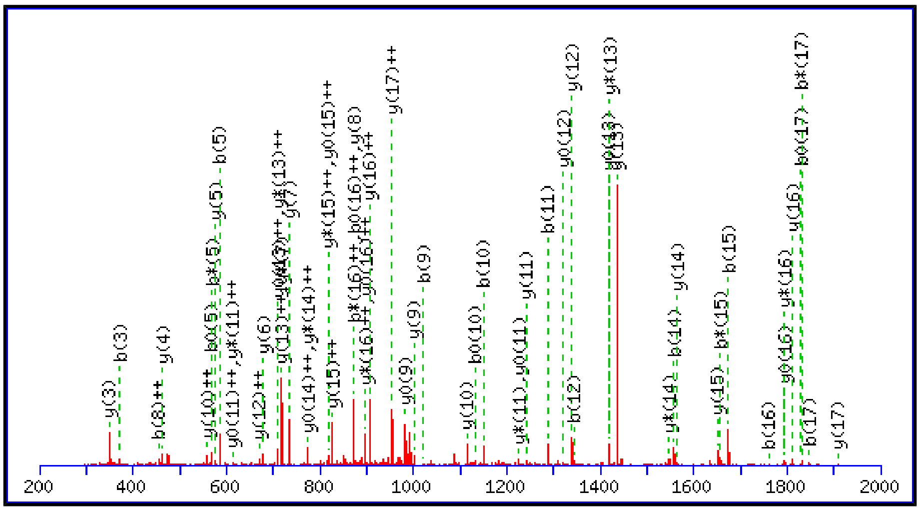
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPCSQPPQIEHGTINSSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

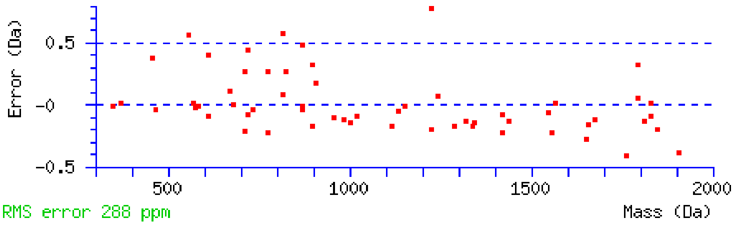
Match to Query 12567: 2020.970348 from(1011.492450,2+) intensity(54633.2422) rtinseconds(504) scans(1114) index(24361)
Title: 111019_Est_MI_YS_G_06Spectrum954_scans__1114
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

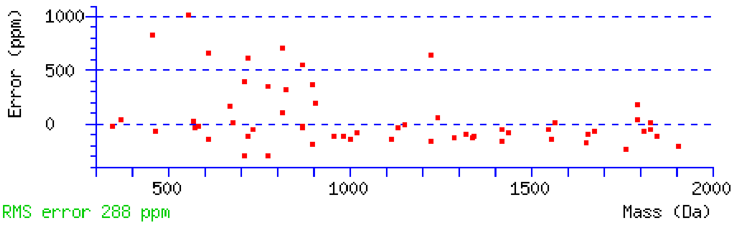
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2020.9636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 99 **Expect:** 3.1e-008
Matches : 60/188 fragment ions using 97 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							18
2	211.1441	106.0757					P	***1908.8869***	954.9471	1891.8603	946.4338	1890.8763	945.9418	17
3	**371.1748**	186.0910					C	***1811.8341***	906.4207	1794.8075	897.9074	1793.8235	897.4154	16
4	458.2068	229.6070			440.1962	220.6017	S	***1651.8034***	826.4054	1634.7769	817.8921	1633.7929	817.4001	15
5	**586.2654**	293.6363	569.2388	285.1230	568.2548	284.6310	Q	***1564.7714***	782.8893	1547.7449	774.3761	1546.7608	773.8841	14
6	683.3181	342.1627	666.2916	333.6494	665.3076	333.1574	P	***1436.7128***	718.8601	1419.6863	710.3468	1418.7023	709.8548	13
7	780.3709	390.6891	763.3443	382.1758	762.3603	381.6838	P	***1339.6601***	670.3337	1322.6335	661.8204	1321.6495	661.3284	12
8	908.4295	454.7184	891.4029	446.2051	890.4189	445.7131	Q	***1242.6073***	621.8073	1225.5808	613.2940	1224.5967	612.8020	11
9	**1021.5135**	511.2604	1004.4870	502.7471	1003.5030	502.2551	I	***1114.5487***	557.7780	1097.5222	549.2647	1096.5382	548.7727	10
10	**1150.5561**	575.7817	1133.5296	567.2684	1132.5456	566.7764	E	***1001.4647***	501.2360	984.4381	492.7227	983.4541	492.2307	9
11	**1287.6150**	644.3112	1270.5885	635.7979	1269.6045	635.3059	H	***872.4221***	436.7147	855.3955	428.2014	854.4115	427.7094	8
12	**1344.6365**	672.8219	1327.6099	664.3086	1326.6259	663.8166	G	***735.3632***	368.1852	718.3366	359.6719	717.3526	359.1799	7
13	1445.6842	723.3457	1428.6576	714.8325	1427.6736	714.3404	T	***678.3417***	339.6745	661.3151	331.1612	660.3311	330.6692	6
14	**1558.7682**	779.8878	1541.7417	771.3745	1540.7577	770.8825	I	***577.2940***	289.1506	560.2675	280.6374	559.2835	280.1454	5
15	**1673.7952**	837.4012	1656.7686	828.8880	1655.7846	828.3959	N	***464.2100***	232.6086	447.1834	224.0953	446.1994	223.6033	4
16	**1760.8272**	880.9172	1743.8007	872.4040	1742.8166	871.9120	S	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	3
17	**1847.8592**	924.4333	1830.8327	915.9200	1829.8487	915.4280	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
18							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IPCSQPPQIEHGTINSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.0	2020.9636	0.0067	IPCSQPPQIEHGTINSSR	Deamidated N15 100.00%
47.4	2020.9636	0.0067	IPCSQPPQIEHGTINSSR	Deamidated Q8 0.00%
30.7	2020.9636	0.0067	IPCSQPPQIEHGTINSSR	Deamidated Q5 0.00%
2.7	2019.9572	1.0132	IAVEQGTAVDMATYVTGSAH	
2.6	2020.9710	-0.0007	GLYRSEMHLLSVPECSK	
2.5	2019.9605	1.0098	QLLVEVERMECATPSDK	
2.4	2019.9709	0.9995	SVNRQVSEVDISQLSSNR	
1.8	2019.9684	1.0019	DTSCVNPPTVQNAYIVSR	
0.3	2019.9670	1.0033	AIIKVGDTEDNMDNILDK	

Mascot: http://www.matrixscience.com/

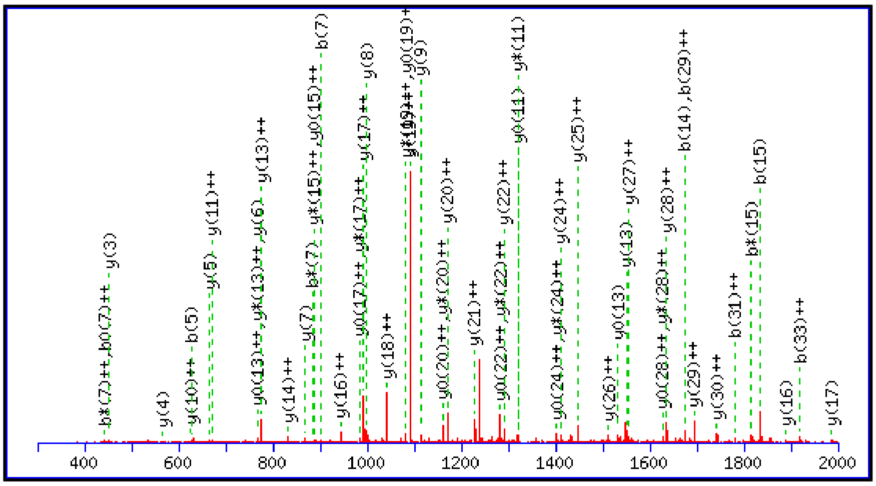
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28329: 4010.815872 from(1337.945900,3+) intensity(21858.7637) rtinseconds(2018) scans(5054) index(12770)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4423_scans__5054
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

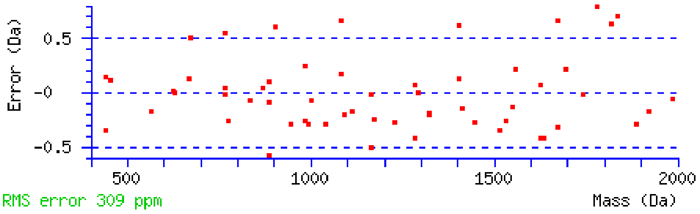
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

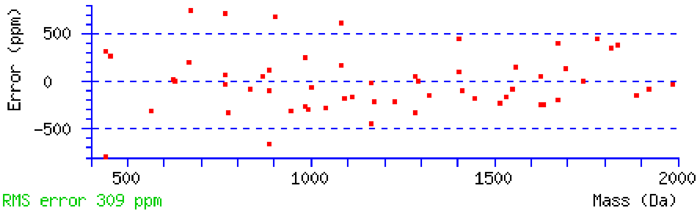


```
Monoisotopic mass of neutral peptide Mr(calc): 4010.8059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N23     : Deamidated (NQ)
N26     : Deamidated (NQ)
Ions Score: 98  Expect: 2.6e-008
Matches : 58/376 fragment ions using 101 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3825.7339	1913.3706	3808.7074	1904.8573	3807.7234	1904.3653	33
3	399.1663	200.0868			381.1557	191.0815	P	3710.7070	1855.8571	3693.6804	1847.3439	3692.6964	1846.8518	32
4	528.2089	264.6081			510.1983	255.6028	E	3613.6542	1807.3308	3596.6277	1798.8175	3595.6437	1798.3255	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3484.6116	1742.8095	3467.5851	1734.2962	3466.6011	1733.8042	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3385.5432	1693.2752	3368.5167	1684.7620	3367.5327	1684.2700	29
7	**901.3509**	451.1791	884.3243	442.6658	883.3403	442.1738	C	3271.5003	1636.2538	3254.4737	1627.7405	3253.4897	1627.2485	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3111.4696	1556.2385	3094.4431	1547.7252	3093.4591	1547.2332	27
9	1119.4234	560.2153	1102.3968	551.7021	1101.4128	551.2101	M	3024.4376	1512.7224	3007.4111	1504.2092	3006.4270	1503.7172	26
10	1190.4605	595.7339	1173.4340	587.2206	1172.4499	586.7286	A	2893.3971	1447.2022	2876.3706	1438.6889	2875.3866	1438.1969	25
11	1318.5191	659.7632	1301.4925	651.2499	1300.5085	650.7579	Q	2822.3600	1411.6836	2805.3335	1403.1704	2804.3494	1402.6784	24
12	1431.6031	716.3052	1414.5766	707.7919	1413.5926	707.2999	I	2694.3014	1347.6544	2677.2749	1339.1411	2676.2909	1338.6491	23
13	1559.6617	780.3345	1542.6352	771.8212	1541.6512	771.3292	Q	2581.2174	1291.1123	2564.1908	1282.5990	2563.2068	1282.1070	22
14	**1672.7458**	836.8765	1655.7192	828.3633	1654.7352	827.8713	L	2453.1588	1227.0830	2436.1322	1218.5698	2435.1482	1218.0778	21
15	**1832.7764**	916.8919	1815.7499	908.3786	1814.7659	907.8866	C	2340.0747	1170.5410	2323.0482	1162.0277	2322.0642	1161.5357	20
16	1929.8292	965.4182	1912.8027	956.9050	1911.8186	956.4130	P	2180.0441	1090.5257	2163.0175	1082.0124	2162.0335	1081.5204	19
17	2026.8820	1013.9446	2009.8554	1005.4313	2008.8714	1004.9393	P	2082.9913	1041.9993	2065.9648	1033.4860	2064.9808	1032.9940	18
18	2123.9347	1062.4710	2106.9082	1053.9577	2105.9242	1053.4657	P	***1985.9386***	993.4729	1968.9120	984.9596	1967.9280	984.4676	17
19	2220.9875	1110.9974	2203.9609	1102.4841	2202.9769	1101.9921	P	***1888.8858***	944.9465	1871.8592	936.4333	1870.8752	935.9413	16
20	2349.0461	1175.0267	2332.0195	1166.5134	2331.0355	1166.0214	Q	1791.8330	896.4202	1774.8065	887.9069	1773.8225	887.4149	15
21	2462.1301	1231.5687	2445.1036	1223.0554	2444.1196	1222.5634	I	1663.7744	832.3909	1646.7479	823.8776	1645.7639	823.3856	14
22	2559.1829	1280.0951	2542.1564	1271.5818	2541.1723	1271.0898	P	***1550.6904***	775.8488	1533.6638	767.3356	1532.6798	766.8435	13

23	2674.2098	1337.6086	2657.1833	1329.0953	2656.1993	1328.6033	**N**	1453.6376	727.3224	1436.6111	718.8092	1435.6271	718.3172	**12**
24	2761.2419	1381.1246	2744.2153	1372.6113	2743.2313	1372.1193	**S**	1338.6107	669.8090	1321.5841	661.2957	1320.6001	660.8037	**11**
25	2898.3008	1449.6540	2881.2742	1441.1408	2880.2902	1440.6487	**H**	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**10**
26	3013.3277	1507.1675	2996.3012	1498.6542	2995.3172	1498.1622	**N**	***1114.5197***	557.7635	1097.4932	549.2502	1096.5092	548.7582	**9**
27	3144.3682	1572.6877	3127.3417	1564.1745	3126.3576	1563.6825	**M**	***999.4928***	500.2500	982.4662	491.7368	981.4822	491.2448	**8**
28	3245.4159	1623.2116	3228.3893	1614.6983	3227.4053	1614.2063	**T**	***868.4523***	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3346.4636	1673.7354	3329.4370	1665.2221	3328.4530	1664.7301	**T**	***767.4046***	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3447.5112	1724.2593	3430.4847	1715.7460	3429.5007	1715.2540	**T**	***666.3570***	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3560.5953	1780.8013	3543.5688	1772.2880	3542.5847	1771.7960	**L**	***565.3093***	283.1583	548.2827	274.6450			**4**
32	3674.6382	1837.8228	3657.6117	1829.3095	3656.6277	1828.8175	**N**	***452.2252***	226.6162	435.1987	218.1030			**3**
33	3837.7016	1919.3544	3820.6750	1910.8411	3819.6910	1910.3491	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.7	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26 81.96%
89.2	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32 11.74%
83.4	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, N32 3.06%
82.6	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23 2.58%
81.8	4009.8219	0.9939	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
71.6	4009.8219	0.9939	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
69.2	4009.8219	0.9939	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
68.5	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20 0.10%
66.5	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11 0.06%
64.6	4010.8059	0.0099	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Q13 0.04%

Mascot: http://www.matrixscience.com/

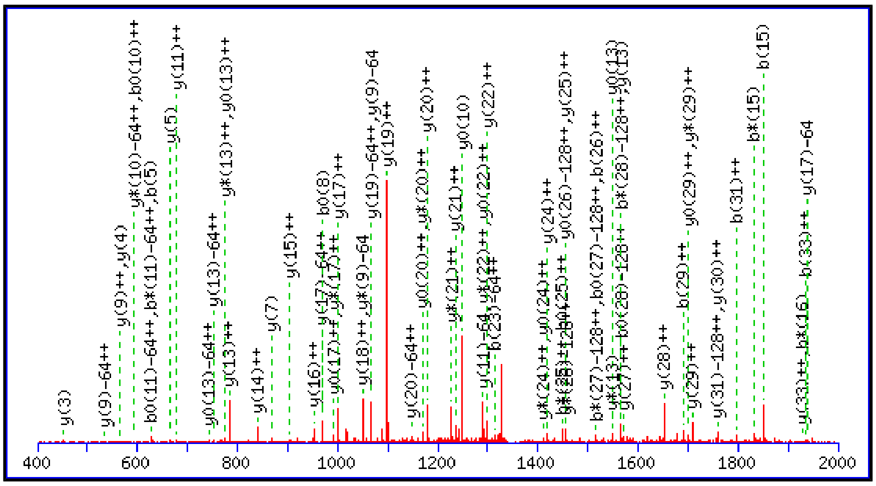
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28360: 4043.810652 from(1348.944160,3+) intensity(21335.4180) rtinseconds(1948) scans(4577) index(16843)
Title: 111019_Est_MI_YP_G_06Spectrum3797_scans__4577
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

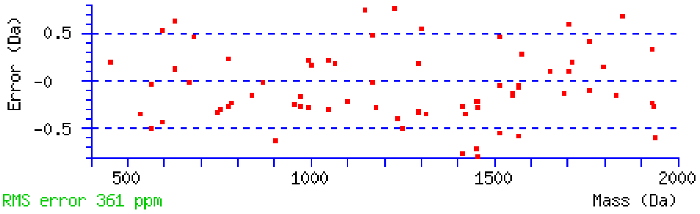
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

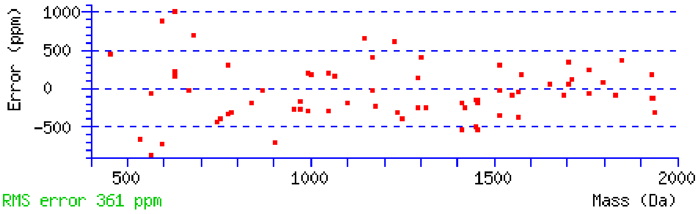


Monoisotopic mass of neutral peptide Mr(calc): 4042.7958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N23 : Deamidated (NQ)
N26 : Deamidated (NQ)
M27 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 97 **Expect:** 2.2e-008
Matches : 73/682 fragment ions using 96 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3857.7238	1929.3655	3840.6972	1920.8522	3839.7132	1920.3602	33
3	399.1663	200.0868			381.1557	191.0815	P	3742.6968	1871.8520	3725.6703	1863.3388	3724.6863	1862.8468	32
4	528.2089	264.6081			510.1983	255.6028	E	3645.6441	1823.3257	3628.6175	1814.8124	3627.6335	1814.3204	31
5	627.2773	314.1423			609.2667	305.1370	V	3516.6015	1758.8044	3499.5749	1750.2911	3498.5909	1749.7991	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3417.5330	1709.2702	3400.5065	1700.7569	3399.5225	1700.2649	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3303.4901	1652.2487	3286.4636	1643.7354	3285.4796	1643.2434	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3143.4595	1572.2334	3126.4329	1563.7201	3125.4489	1563.2281	27
9	1135.4183	568.2128	1118.3918	559.6995	1117.4077	559.2075	M	3056.4274	1528.7174	3039.4009	1520.2041	3038.4169	1519.7121	26
10	1206.4554	603.7313	1189.4289	595.2181	1188.4449	594.7261	A	2909.3920	1455.1997	2892.3655	1446.6864	2891.3815	1446.1944	25
11	1334.5140	667.7606	1317.4875	659.2474	1316.5034	658.7554	Q	2838.3549	1419.6811	2821.3284	1411.1678	2820.3444	1410.6758	24
12	1447.5981	724.3027	1430.5715	715.7894	1429.5875	715.2974	I	2710.2964	1355.6518	2693.2698	1347.1385	2692.2858	1346.6465	23
13	1575.6566	788.3320	1558.6301	779.8187	1557.6461	779.3267	Q	2597.2123	1299.1098	2580.1857	1290.5965	2579.2017	1290.1045	22
14	1688.7407	844.8740	1671.7142	836.3607	1670.7301	835.8687	L	2469.1537	1235.0805	2452.1272	1226.5672	2451.1431	1226.0752	21
15	1848.7714	924.8893	1831.7448	916.3760	1830.7608	915.8840	C	2356.0696	1178.5385	2339.0431	1170.0252	2338.0591	1169.5332	20
16	1945.8241	973.4157	1928.7976	964.9024	1927.8136	964.4104	P	2196.0390	1098.5231	2179.0124	1090.0099	2178.0284	1089.5179	19
17	2042.8769	1021.9421	2025.8503	1013.4288	2024.8663	1012.9368	P	2098.9862	1049.9968	2081.9597	1041.4835	2080.9757	1040.9915	18
18	2139.9296	1070.4685	2122.9031	1061.9552	2121.9191	1061.4632	P	2001.9335	1001.4704	1984.9069	992.9571	1983.9229	992.4651	17
19	2236.9824	1118.9948	2219.9559	1110.4816	2218.9718	1109.9896	P	1904.8807	952.9440	1887.8542	944.4307	1886.8701	943.9387	16
20	2365.0410	1183.0241	2348.0144	1174.5109	2347.0304	1174.0188	Q	1807.8279	904.4176	1790.8014	895.9043	1789.8174	895.4123	15
21	2478.1251	1239.5662	2461.0985	1231.0529	2460.1145	1230.5609	I	1679.7694	840.3883	1662.7428	831.8750	1661.7588	831.3830	14

22	2575.1778	1288.0925	2558.1513	1279.5793	2557.1673	1279.0873	**P**	**1566.6853**	783.8463	1549.6587	775.3330	1548.6747	774.8410	**13**
23	2690.2048	1345.6060	2673.1782	1337.0927	2672.1942	1336.6007	**N**	1469.6325	735.3199	1452.6060	726.8066	1451.6220	726.3146	**12**
24	2777.2368	1389.1220	2760.2102	1380.6088	2759.2262	1380.1167	**S**	1354.6056	677.8064	1337.5790	669.2932	1336.5950	668.8012	**11**
25	2914.2957	1457.6515	2897.2691	1449.1382	2896.2851	1448.6462	**H**	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	**10**
26	3029.3226	**1515.1650**	3012.2961	1506.6517	3011.3121	1506.1597	**N**	1130.5147	565.7610	1113.4881	557.2477	1112.5041	556.7557	**9**
27	3176.3580	1588.6827	3159.3315	1580.1694	3158.3475	1579.6774	**M**	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	**8**
28	3277.4057	1639.2065	3260.3792	1630.6932	3259.3952	1630.2012	**T**	**868.4523**	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3378.4534	**1689.7303**	3361.4269	1681.2171	3360.4428	1680.7251	**T**	767.4046	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3479.5011	1740.2542	3462.4745	1731.7409	3461.4905	1731.2489	**T**	**666.3570**	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3592.5851	**1796.7962**	3575.5586	1788.2829	3574.5746	1787.7909	**L**	**565.3093**	283.1583	548.2827	274.6450			**4**
32	3706.6281	1853.8177	3689.6015	1845.3044	3688.6175	1844.8124	**N**	**452.2252**	226.6162	435.1987	218.1030			**3**
33	3869.6914	**1935.3493**	3852.6648	1926.8361	3851.6808	1926.3441	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
97.0	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26 90.65%
85.8	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23 6.91%
80.7	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20 2.14%
72.3	4041.8118	1.9989	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
67.5	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Q13 0.10%
67.1	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11 0.09%
64.3	4041.8118	1.9989	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
62.9	4042.7958	1.0149	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32 0.04%
62.0	4041.8118	1.9989	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
55.4	4041.8118	1.9989	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	

Mascot: http://www.matrixscience.com/

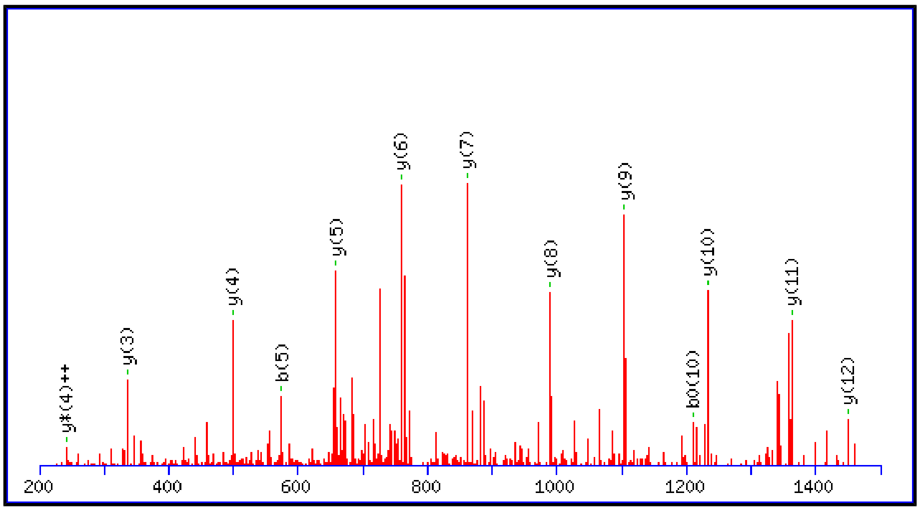
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISEENETTCYMGK**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

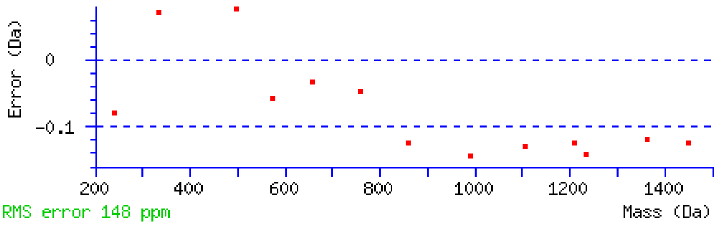
Match to Query 7227: 1561.630188 from(781.822370,2+) intensity(35270.2813) rtinseconds(592) scans(1022) index(28338)
Title: 111019_Est_MI_YS_G_13Spectrum822_scans__1022
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

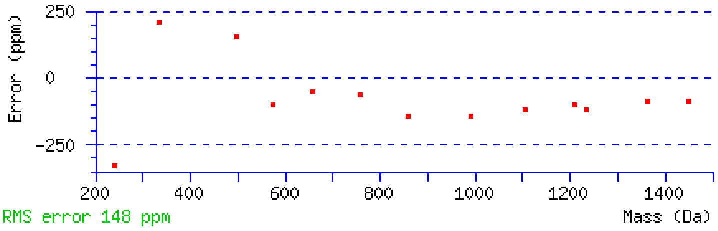
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1561.6276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 95 **Expect:** 8.7e-009
Matches : 13/124 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	201.1234	101.0653			183.1128	92.0600	S	***1449.5508***	725.2791	1432.5243	716.7658	1431.5403	716.2738	12
3	330.1660	165.5866			312.1554	156.5813	E	***1362.5188***	681.7630	1345.4923	673.2498	1344.5082	672.7578	11
4	459.2086	230.1079			441.1980	221.1026	E	***1233.4762***	617.2417	1216.4497	608.7285	1215.4657	608.2365	10
5	574.2355	287.6214	557.2089	279.1081	556.2249	278.6161	N	***1104.4336***	552.7205	1087.4071	544.2072	1086.4231	543.7152	9
6	703.2781	352.1427	686.2515	343.6294	685.2675	343.1374	E	***989.4067***	495.2070	972.3801	486.6937	971.3961	486.2017	8
7	804.3258	402.6665	787.2992	394.1532	786.3152	393.6612	T	***860.3641***	430.6857	843.3375	422.1724	842.3535	421.6804	7
8	905.3734	453.1904	888.3469	444.6771	887.3629	444.1851	T	***759.3164***	380.1618	742.2899	371.6486	741.3058	371.1566	6
9	1065.4041	533.2057	1048.3775	524.6924	1047.3935	524.2004	C	***658.2687***	329.6380	641.2422	321.1247			5
10	1228.4674	614.7374	1211.4409	606.2241	1210.4569	605.7321	Y	***498.2381***	249.6227	481.2115	241.1094			4
11	1359.5079	680.2576	1342.4814	671.7443	1341.4973	671.2523	M	***335.1748***	168.0910	318.1482	159.5777			3
12	1416.5294	708.7683	1399.5028	700.2551	1398.5188	699.7630	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ISEENETTCYMGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
94.6	1561.6276	0.0026	ISEENETTCYMGK
2.9	1561.6379	-0.0078	QQAQGEPASESGENK
2.8	1561.6379	-0.0078	QQAQGEPASESGENK

Mascot: http://www.matrixscience.com/

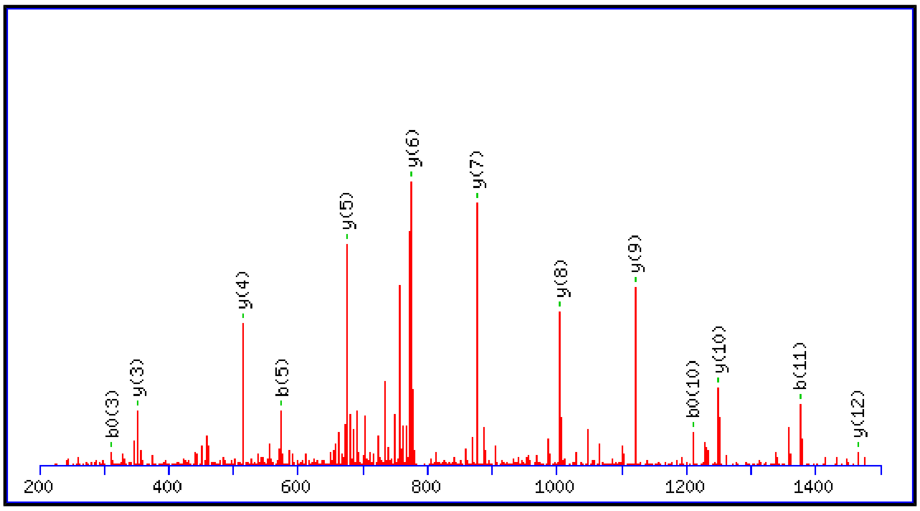
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISEENETTCYMGK**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

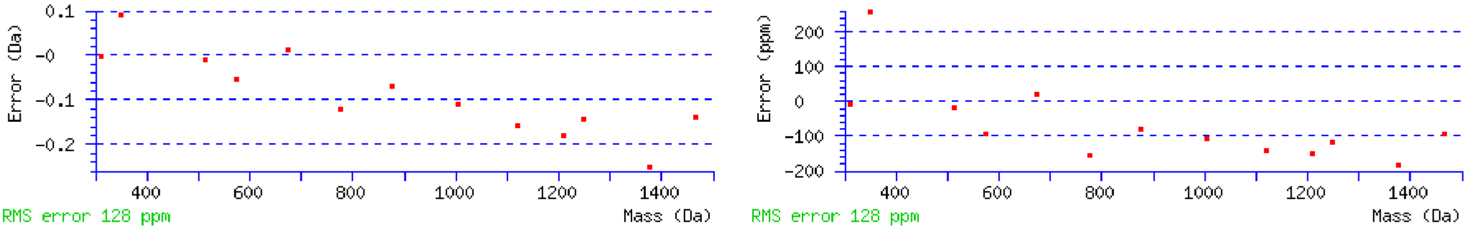
Match to Query 7479: 1577.625948 from(789.820250,2+) intensity(93876.5156) rtinseconds(657) scans(1122) index(16633)
Title: 111019_Est_MI_YP_G_06Spectrum917_scans__1122
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1577.6225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 94 **Expect:** 6e-009
Matches : 13/190 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	114.0913	57.5493					I							13
2	201.1234	101.0653			183.1128	92.0600	S	***1465.5458***	733.2765	1448.5192	724.7632	1447.5352	724.2712	12
3	330.1660	165.5866			312.1554	156.5813	E	1378.5137	689.7605	1361.4872	681.2472	1360.5032	680.7552	11
4	459.2086	230.1079			441.1980	221.1026	E	***1249.4711***	625.2392	1232.4446	616.7259	1231.4606	616.2339	10
5	**574.2355**	287.6214	557.2089	279.1081	556.2249	278.6161	N	***1120.4285***	560.7179	1103.4020	552.2046	1102.4180	551.7126	9
6	703.2781	352.1427	686.2515	343.6294	685.2675	343.1374	E	***1005.4016***	503.2044	988.3750	494.6912	987.3910	494.1992	8
7	804.3258	402.6665	787.2992	394.1532	786.3152	393.6612	T	***876.3590***	438.6831	859.3325	430.1699	858.3484	429.6779	7
8	905.3734	453.1904	888.3469	444.6771	887.3629	444.1851	T	***775.3113***	388.1593	758.2848	379.6460	757.3008	379.1540	6
9	1065.4041	533.2057	1048.3775	524.6924	1047.3935	524.2004	C	***674.2636***	337.6355	657.2371	329.1222			5
10	1228.4674	614.7374	1211.4409	606.2241	1210.4569	605.7321	Y	***514.2330***	257.6201	497.2064	249.1069			4
11	**1375.5028**	688.2551	1358.4763	679.7418	1357.4923	679.2498	M	***351.1697***	176.0885	334.1431	167.5752			3
12	1432.5243	716.7658	1415.4977	708.2525	1414.5137	707.7605	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of ISEENETTCYMGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.7	1577.6225	0.0034	ISEENETTCYMGK

Mascot: http://www.matrixscience.com/

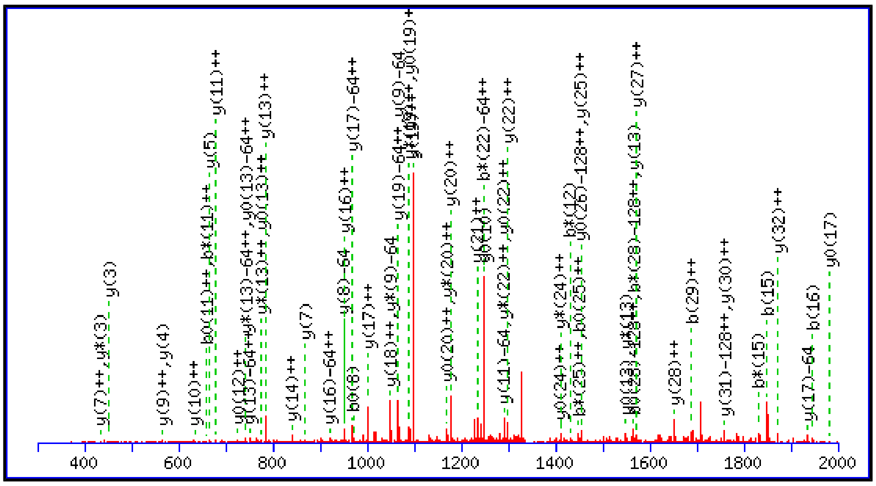
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28361: 4043.837172 from(1348.953000,3+) intensity(0.0000) rtinseconds(1686) scans(4222) index(3821)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum3465_scans__4222
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

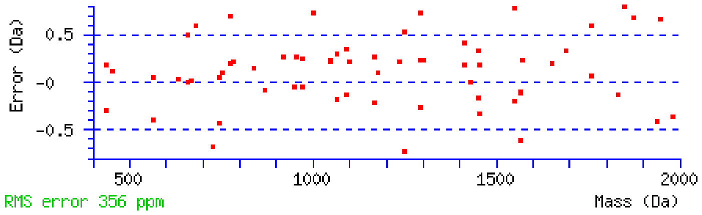
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

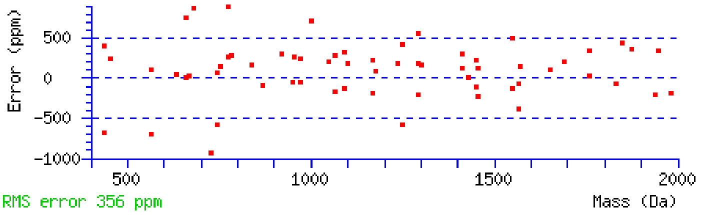


```
Monoisotopic mass of neutral peptide Mr(calc): 4041.8118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N26    : Deamidated (NQ)
M27    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 86  Expect: 3.5e-007
Matches : 65/682 fragment ions using 83 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3856.7397	1928.8735	3839.7132	1920.3602	3838.7292	1919.8682	33
3	399.1663	200.0868			381.1557	191.0815	P	3741.7128	1871.3600	3724.6863	1862.8468	3723.7022	1862.3548	32
4	528.2089	264.6081			510.1983	255.6028	E	3644.6600	1822.8337	3627.6335	1814.3204	3626.6495	1813.8284	31
5	627.2773	314.1423			609.2667	305.1370	V	3515.6174	1758.3124	3498.5909	1749.7991	3497.6069	1749.3071	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3416.5490	1708.7782	3399.5225	1700.2649	3398.5385	1699.7729	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3302.5061	1651.7567	3285.4796	1643.2434	3284.4955	1642.7514	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3142.4755	1571.7414	3125.4489	1563.2281	3124.4649	1562.7361	27
9	1135.4183	568.2128	1118.3918	559.6995	1117.4077	559.2075	M	3055.4434	1528.2254	3038.4169	1519.7121	3037.4329	1519.2201	26
10	1206.4554	603.7313	1189.4289	595.2181	1188.4449	594.7261	A	2908.4080	1454.7077	2891.3815	1446.1944	2890.3975	1445.7024	25
11	1334.5140	667.7606	1317.4875	659.2474	1316.5034	658.7554	Q	2837.3709	1419.1891	2820.3444	1410.6758	2819.3603	1410.1838	24
12	1447.5981	724.3027	1430.5715	715.7894	1429.5875	715.2974	I	2709.3123	1355.1598	2692.2858	1346.6465	2691.3018	1346.1545	23
13	1575.6566	788.3320	1558.6301	779.8187	1557.6461	779.3267	Q	2596.2283	1298.6178	2579.2017	1290.1045	2578.2177	1289.6125	22
14	1688.7407	844.8740	1671.7142	836.3607	1670.7301	835.8687	L	2468.1697	1234.5885	2451.1431	1226.0752	2450.1591	1225.5832	21
15	1848.7714	924.8893	1831.7448	916.3760	1830.7608	915.8840	C	2355.0856	1178.0465	2338.0591	1169.5332	2337.0751	1169.0412	20
16	1945.8241	973.4157	1928.7976	964.9024	1927.8136	964.4104	P	2195.0550	1098.0311	2178.0284	1089.5179	2177.0444	1089.0258	19
17	2042.8769	1021.9421	2025.8503	1013.4288	2024.8663	1012.9368	P	2098.0022	1049.5047	2080.9757	1040.9915	2079.9917	1040.4995	18
18	2139.9296	1070.4685	2122.9031	1061.9552	2121.9191	1061.4632	P	2000.9495	1000.9784	1983.9229	992.4651	1982.9389	991.9731	17
19	2236.9824	1118.9948	2219.9559	1110.4816	2218.9718	1109.9896	P	1903.8967	952.4520	1886.8701	943.9387	1885.8861	943.4467	16
20	2365.0410	1183.0241	2348.0144	1174.5109	2347.0304	1174.0188	Q	1806.8439	903.9256	1789.8174	895.4123	1788.8334	894.9203	15
21	2478.1251	1239.5662	2461.0985	1231.0529	2460.1145	1230.5609	I	1678.7853	839.8963	1661.7588	831.3830	1660.7748	830.8910	14
22	2575.1778	1288.0925	2558.1513	1279.5793	2557.1673	1279.0873	P	**1565.7013**	783.3543	1548.6747	774.8410	1547.6907	774.3490	13

23	2689.2207	1345.1140	2672.1942	1336.6007	2671.2102	1336.1087	**N**	1468.6485	734.8279	1451.6220	726.3146	1450.6380	725.8226	**12**
24	2776.2528	1388.6300	2759.2262	1380.1167	2758.2422	1379.6247	**S**	1354.6056	677.8064	1337.5790	669.2932	1336.5950	668.8012	**11**
25	2913.3117	1457.1595	2896.2851	1448.6462	2895.3011	1448.1542	**H**	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	**10**
26	3028.3386	1514.6730	3011.3121	1506.1597	3010.3281	1505.6677	**N**	1130.5147	565.7610	1113.4881	557.2477	1112.5041	556.7557	**9**
27	3175.3740	1588.1907	3158.3475	1579.6774	3157.3635	1579.1854	**M**	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	**8**
28	3276.4217	1638.7145	3259.3952	1630.2012	3258.4111	1629.7092	**T**	**868.4523**	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3377.4694	1689.2383	3360.4428	1680.7251	3359.4588	1680.2330	**T**	767.4046	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3478.5171	1739.7622	3461.4905	1731.2489	3460.5065	1730.7569	**T**	**666.3570**	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3591.6011	1796.3042	3574.5746	1787.7909	3573.5906	1787.2989	**L**	**565.3093**	283.1583	548.2827	274.6450			**4**
32	3705.6441	1853.3257	3688.6175	1844.8124	3687.6335	1844.3204	**N**	**452.2252**	226.6162	435.1987	218.1030			**3**
33	3868.7074	1934.8573	3851.6808	1926.3441	3850.6968	1925.8520	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.9	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26 34.05%
85.9	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11 34.05%
84.5	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6 24.44%
76.3	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23 3.71%
73.4	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20 1.91%
73.2	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13 1.83%
47.0	4041.8118	2.0254	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N32 0.00%
10.3	4042.8380	0.9992	LVLQWAAMYGDLLQEDDVSMAFLEEFYVSVSDDAR	
9.6	4043.8250	0.0122	TMEQKLSSVLSHLASHNSSSNGVFTESNDSSSTARSSR	
9.1	4041.8443	1.9928	MIPGVVDTGLFINMAERVYFGMQDGSVNMREKPFC	

Mascot: http://www.matrixscience.com/

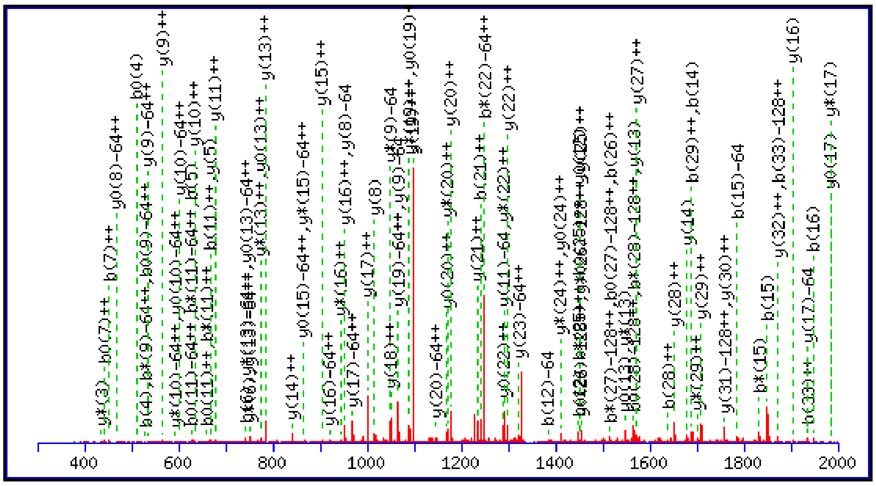
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28357: 4042.802472 from(1348.608100,3+) intensity(7677.0967) rtinseconds(1565) scans(4036) index(6450)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum3547_scans__4036
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

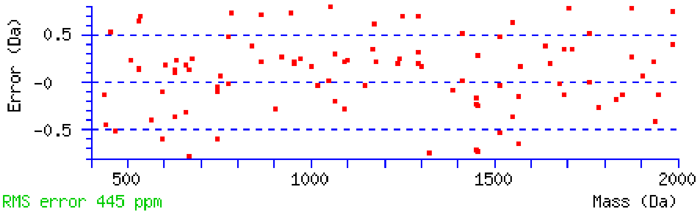
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

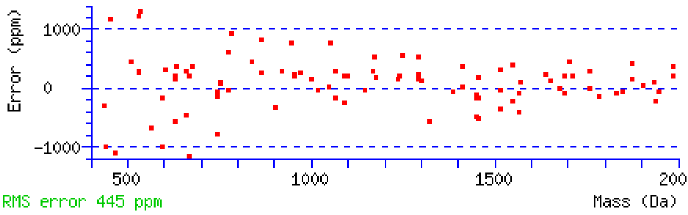


Monoisotopic mass of neutral peptide Mr(calc): 4042.7958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M27 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N32 : Deamidated (NQ)
Ions Score: 85 **Expect:** 3.1e-007
Matches : 99/682 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3857.7238	1929.3655	3840.6972	1920.8522	3839.7132	1920.3602	33
3	399.1663	200.0868			381.1557	191.0815	P	3742.6968	1871.8520	3725.6703	1863.3388	3724.6863	1862.8468	32
4	**528.2089**	264.6081			510.1983	255.6028	E	3645.6441	1823.3257	3628.6175	1814.8124	3627.6335	1814.3204	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3516.6015	1758.8044	3499.5749	1750.2911	3498.5909	1749.7991	30
6	**742.3042**	371.6558	725.2777	363.1425	724.2937	362.6505	N	3417.5330	1709.2702	3400.5065	1700.7569	3399.5225	1700.2649	29
7	902.3349	**451.6711**	885.3083	443.1578	884.3243	442.6658	C	3302.5061	1651.7567	3285.4796	1643.2434	3284.4955	1642.7514	28
8	989.3669	495.1871	972.3404	486.6738	971.3564	486.1818	S	3142.4755	1571.7414	3125.4489	1563.2281	3124.4649	1562.7361	27
9	1136.4023	568.7048	1119.3758	560.1915	1118.3918	559.6995	M	3055.4434	1528.2254	3038.4169	1519.7121	3037.4329	1519.2201	26
10	1207.4394	604.2234	1190.4129	595.7101	1189.4289	595.2181	A	2908.4080	1454.7077	2891.3815	1446.1944	2890.3975	1445.7024	25
11	1335.4980	**668.2526**	1318.4715	659.7394	1317.4874	659.2474	Q	2837.3709	1419.1891	2820.3444	1410.6758	2819.3603	1410.1838	24
12	**1448.5821**	724.7947	1431.5555	716.2814	1430.5715	715.7894	I	2709.3123	1355.1598	2692.2858	1346.6465	2691.3018	1346.1545	23
13	1576.6407	788.8240	1559.6141	780.3107	1558.6301	779.8187	Q	2596.2283	1298.6178	2579.2017	1290.1045	2578.2177	1289.6125	22
14	**1689.7247**	845.3660	1672.6982	836.8527	1671.7142	836.3607	L	2468.1697	1234.5885	2451.1431	1226.0752	2450.1591	1225.5832	21
15	**1849.7554**	925.3813	1832.7288	916.8680	1831.7448	916.3760	C	2355.0856	1178.0465	2338.0591	1169.5332	2337.0751	1169.0412	20
16	**1946.8081**	973.9077	1929.7816	965.3944	1928.7976	964.9024	P	2195.0550	1098.0311	2178.0284	1089.5179	2177.0444	1089.0258	19
17	2043.8609	1022.4341	2026.8343	1013.9208	2025.8503	1013.4288	P	2098.0022	1049.5047	2080.9757	1040.9915	2079.9917	1040.4995	18
18	2140.9137	1070.9605	2123.8871	1062.4472	2122.9031	1061.9552	P	2000.9495	1000.9784	1983.9229	992.4651	1982.9389	991.9731	17
19	2237.9664	1119.4869	2220.9399	1110.9736	2219.9559	1110.4816	P	**1903.8967**	952.4520	1886.8701	943.9387	1885.8861	943.4467	16
20	2366.0250	1183.5161	2348.9985	1175.0029	2348.0144	1174.5109	Q	1806.8439	903.9256	1789.8174	895.4123	1788.8334	894.9203	15
21	2479.1091	**1240.0582**	2462.0825	1231.5449	2461.0985	1231.0529	I	**1678.7853**	839.8963	1661.7588	831.3830	1660.7748	830.8910	14

22	2576.1618	1288.5846	2559.1353	1280.0713	2558.1513	1279.5793	**P**	**1565.7013**	783.3543	1548.6747	774.8410	1547.6907	774.3490	**13**
23	2690.2048	1345.6060	2673.1782	1337.0927	2672.1942	1336.6007	**N**	1468.6485	734.8279	1451.6220	726.3146	1450.6380	725.8226	**12**
24	2777.2368	1389.1220	2760.2102	1380.6088	2759.2262	1380.1167	**S**	1354.6056	677.8064	1337.5790	669.2932	1336.5950	668.8012	**11**
25	2914.2957	1457.6515	2897.2691	1449.1382	2896.2851	1448.6462	**H**	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	**10**
26	3028.3386	**1514.6730**	3011.3121	1506.1597	3010.3281	1505.6677	**N**	1130.5147	565.7610	1113.4881	557.2477	1112.5041	556.7557	**9**
27	3175.3740	1588.1907	3158.3475	1579.6774	3157.3635	1579.1854	**M**	**1016.4717**	508.7395	999.4452	500.2262	998.4612	499.7342	**8**
28	3276.4217	**1638.7145**	3259.3952	1630.2012	3258.4111	1629.7092	**T**	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	**7**
29	3377.4694	**1689.2383**	3360.4428	1680.7251	3359.4588	1680.2330	**T**	768.3886	384.6980	751.3621	376.1847	750.3781	375.6927	**6**
30	3478.5171	1739.7622	3461.4905	1731.2489	3460.5065	1730.7569	**T**	**667.3410**	334.1741	650.3144	325.6608	649.3304	325.1688	**5**
31	3591.6011	1796.3042	3574.5746	1787.7909	3573.5906	1787.2989	**L**	566.2933	283.6503	549.2667	275.1370			**4**
32	3706.6281	1853.8177	3689.6015	1845.3044	3688.6175	1844.8124	**N**	453.2092	227.1082	436.1827	218.5950			**3**
33	3869.6914	**1935.3493**	3852.6648	1926.8361	3851.6808	1926.3441	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.3	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32 29.71%
85.3	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23 29.37%
84.6	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26 25.52%
78.6	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Q13 6.40%
77.9	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20 5.44%
73.4	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11 1.92%
69.2	4042.7958	0.0067	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, N32 0.73%
63.7	4041.8118	0.9907	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
61.4	4041.8118	0.9907	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
59.6	4041.8118	0.9907	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	

Mascot: http://www.matrixscience.com/

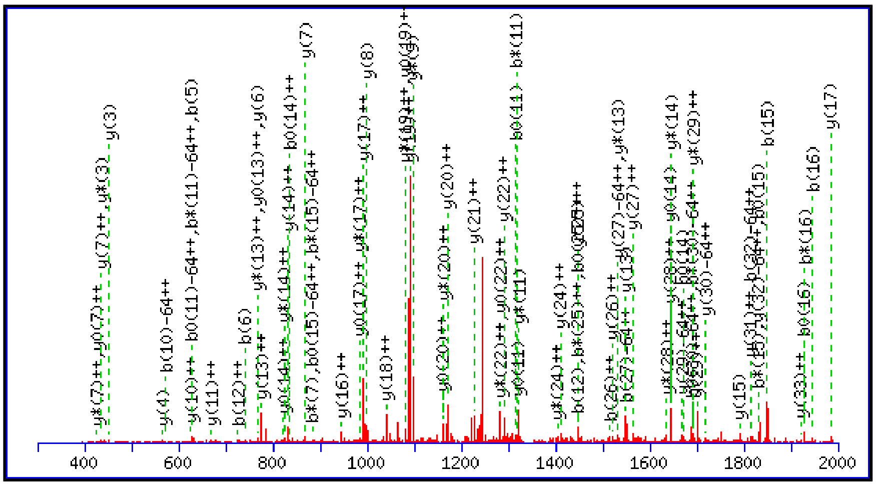
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28343: 4026.823722 from(1343.281850,3+) intensity(19949.1875) rtinseconds(1790) scans(4648) index(6527)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4086_scans__4648
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

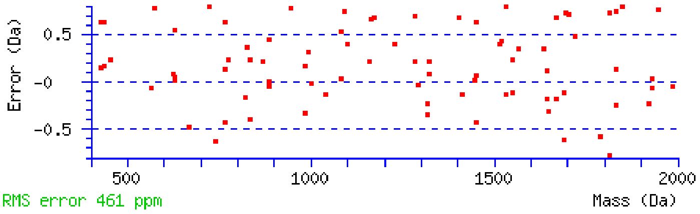
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

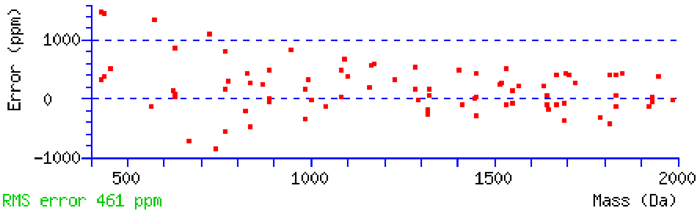


Monoisotopic mass of neutral peptide Mr(calc): 4025.8168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N26 : Deamidated (NQ)
Ions Score: 82 **Expect:** 8.1e-007
Matches : 83/574 fragment ions using 144 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3840.7448	1920.8761	3823.7183	1912.3628	3822.7343	1911.8708	33
3	399.1663	200.0868			381.1557	191.0815	P	3725.7179	1863.3626	3708.6913	1854.8493	3707.7073	1854.3573	32
4	528.2089	264.6081			510.1983	255.6028	E	3628.6651	1814.8362	3611.6386	1806.3229	3610.6546	1805.8309	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3499.6225	1750.3149	3482.5960	1741.8016	3481.6120	1741.3096	30
6	**741.3202**	371.1638	724.2937	362.6505	723.3097	362.1585	N	3400.5541	1700.7807	3383.5276	1692.2674	3382.5436	1691.7754	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3286.5112	1643.7592	3269.4846	1635.2460	3268.5006	1634.7540	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3126.4805	1563.7439	3109.4540	1555.2306	3108.4700	1554.7386	27
9	1135.4183	568.2128	1118.3918	559.6995	1117.4077	559.2075	M	3039.4485	1520.2279	3022.4220	1511.7146	3021.4379	1511.2226	26
10	1206.4554	603.7313	1189.4289	595.2181	1188.4449	594.7261	A	2892.4131	1446.7102	2875.3866	1438.1969	2874.4025	1437.7049	25
11	1334.5140	667.7606	1317.4875	659.2474	1316.5034	658.7554	Q	2821.3760	1411.1916	2804.3494	1402.6784	2803.3654	1402.1864	24
12	**1447.5981**	724.3027	1430.5715	715.7894	1429.5875	715.2974	I	2693.3174	1347.1623	2676.2909	1338.6491	2675.3069	1338.1571	23
13	1575.6566	788.3320	1558.6301	779.8187	1557.6461	779.3267	Q	2580.2334	1290.6203	2563.2068	1282.1070	2562.2228	1281.6150	22
14	1688.7407	844.8740	1671.7142	836.3607	1670.7301	835.8687	L	2452.1748	1226.5910	2435.1482	1218.0778	2434.1642	1217.5857	21
15	**1848.7714**	924.8893	1831.7448	916.3760	1830.7608	915.8840	C	2339.0907	1170.0490	2322.0642	1161.5357	2321.0801	1161.0437	20
16	**1945.8241**	973.4157	1928.7976	964.9024	1927.8136	964.4104	P	2179.0601	1090.0337	2162.0335	1081.5204	2161.0495	1081.0284	19
17	2042.8769	1021.9421	2025.8503	1013.4288	2024.8663	1012.9368	P	2082.0073	1041.5073	2064.9808	1032.9940	2063.9967	1032.5020	18
18	2139.9296	1070.4685	2122.9031	1061.9552	2121.9191	1061.4632	P	**1984.9545**	992.9809	1967.9280	984.4676	1966.9440	983.9756	17
19	2236.9824	1118.9948	2219.9559	1110.4816	2218.9718	1109.9896	P	1887.9018	944.4545	1870.8752	935.9413	1869.8912	935.4492	16
20	2365.0410	1183.0241	2348.0144	1174.5109	2347.0304	1174.0188	Q	**1790.8490**	895.9281	1773.8225	887.4149	1772.8384	886.9229	15
21	2478.1251	1239.5662	2461.0985	1231.0529	2460.1145	1230.5609	I	1662.7904	831.8989	1645.7639	823.3856	1644.7799	822.8936	14
22	2575.1778	1288.0925	2558.1513	1279.5793	2557.1673	1279.0873	P	**1549.7064**	775.3568	1532.6798	766.8435	1531.6958	766.3515	13

23	2689.2207	1345.1140	2672.1942	1336.6007	2671.2102	1336.1087	**N**	1452.6536	726.8304	1435.6271	718.3172	1434.6430	717.8252	**12**
24	2776.2528	1388.6300	2759.2262	1380.1167	2758.2422	1379.6247	**S**	1338.6107	669.8090	1321.5841	661.2957	1320.6001	660.8037	**11**
25	2913.3117	1457.1595	2896.2851	1448.6462	2895.3011	1448.1542	**H**	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**10**
26	3028.3386	1514.6730	3011.3121	1506.1597	3010.3281	1505.6677	**N**	1114.5197	557.7635	1097.4932	549.2502	1096.5092	548.7582	**9**
27	3159.3791	1580.1932	3142.3526	1571.6799	3141.3685	1571.1879	**M**	**999.4928**	500.2500	982.4662	491.7368	981.4822	491.2448	**8**
28	3260.4268	1630.7170	3243.4002	1622.2038	3242.4162	1621.7118	**T**	**868.4523**	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3361.4745	1681.2409	3344.4479	1672.7276	3343.4639	1672.2356	**T**	**767.4046**	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3462.5221	1731.7647	3445.4956	1723.2514	3444.5116	1722.7594	**T**	666.3570	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3575.6062	1788.3067	3558.5797	1779.7935	3557.5956	1779.3015	**L**	**565.3093**	283.1583	548.2827	274.6450			**4**
32	3689.6491	1845.3282	3672.6226	1836.8149	3671.6386	1836.3229	**N**	**452.2252**	226.6162	435.1987	218.1030			**3**
33	3852.7125	1926.8599	3835.6859	1918.3466	3834.7019	1917.8546	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
82.2	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, Oxidation M9; 29.74%
82.1	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N32, Oxidation M9; 29.26%
81.0	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, Oxidation M9; 22.82%
80.0	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, Oxidation M9; 17.88%
60.1	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Oxidation M9; 0.18%
58.2	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Oxidation M9; 0.12%
42.4	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Oxidation M9; 0.00%
33.3	4024.8328	1.9909	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
25.8	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, Oxidation M27; 0.00%
23.5	4025.8168	1.0069	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, Oxidation M27; 0.00%

Mascot: http://www.matrixscience.com/

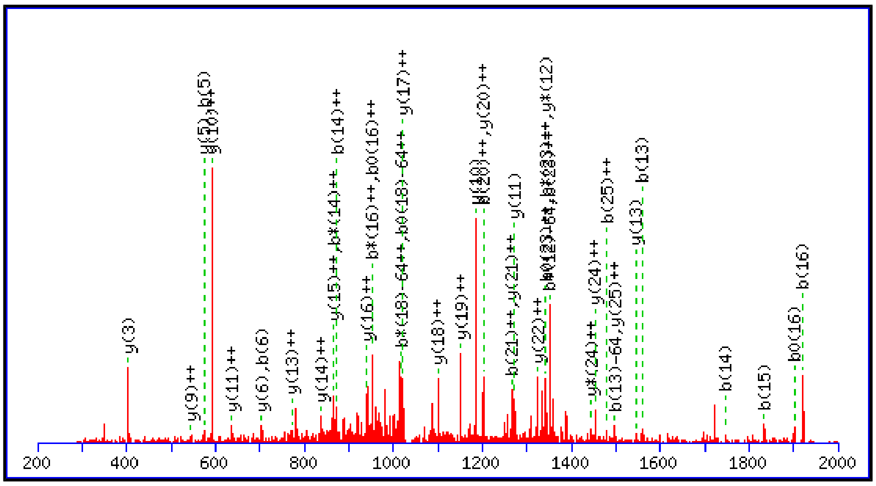
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISEENETTCYMGKWSSPPQCEGLPCK**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27317: 3104.296152 from(1035.772660,3+) intensity(30452.9336) rtinseconds(992) scans(2327) index(2557)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1970_scans__2327
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

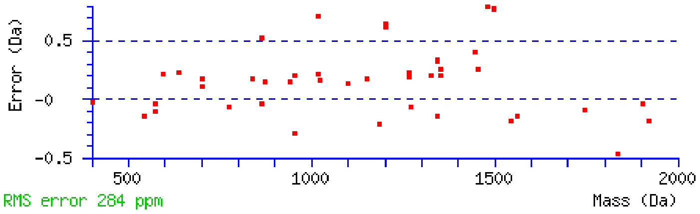
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

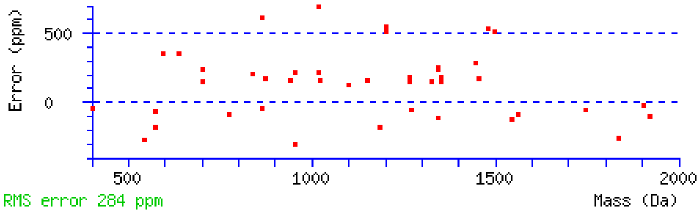


```
Monoisotopic mass of neutral peptide Mr(calc): 3104.2871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
M11    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 77  Expect: 8.3e-007
Matches : 44/430 fragment ions using 70 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							26
2	201.1234	101.0653			183.1128	92.0600	S	2992.2104	1496.6088	2975.1838	1488.0956	2974.1998	1487.6035	25
3	330.1660	165.5866			312.1554	156.5813	E	2905.1783	1453.0928	2888.1518	1444.5795	2887.1678	1444.0875	24
4	459.2086	230.1079			441.1980	221.1026	E	2776.1358	1388.5715	2759.1092	1380.0582	2758.1252	1379.5662	23
5	**574.2355**	287.6214	557.2089	279.1081	556.2249	278.6161	N	2647.0932	1324.0502	2630.0666	1315.5369	2629.0826	1315.0449	22
6	**703.2781**	352.1427	686.2515	343.6294	685.2675	343.1374	E	2532.0662	1266.5367	2515.0397	1258.0235	2514.0557	1257.5315	21
7	804.3258	402.6665	787.2992	394.1532	786.3152	393.6612	T	2403.0236	1202.0155	2385.9971	1193.5022	2385.0131	1193.0102	20
8	905.3734	453.1904	888.3469	444.6771	887.3629	444.1851	T	2301.9759	1151.4916	2284.9494	1142.9783	2283.9654	1142.4863	19
9	1065.4041	533.2057	1048.3775	524.6924	1047.3935	524.2004	C	2200.9283	1100.9678	2183.9017	1092.4545	2182.9177	1091.9625	18
10	1228.4674	614.7374	1211.4409	606.2241	1210.4569	605.7321	Y	2040.8976	1020.9524	2023.8711	1012.4392	2022.8871	1011.9472	17
11	1375.5028	688.2551	1358.4763	679.7418	1357.4923	679.2498	M	1877.8343	939.4208	1860.8077	930.9075	1859.8237	930.4155	16
12	1432.5243	716.7658	1415.4977	708.2525	1414.5137	707.7605	G	1730.7989	865.9031	1713.7723	857.3898	1712.7883	856.8978	15
13	**1560.6193**	780.8133	1543.5927	772.3000	1542.6087	771.8080	K	1673.7774	837.3924	1656.7509	828.8791	1655.7669	828.3871	14
14	**1746.6986**	**873.8529**	1729.6720	865.3396	1728.6880	864.8476	W	**1545.6825**	773.3449	1528.6559	764.8316	1527.6719	764.3396	13
15	**1833.7306**	917.3689	1816.7040	908.8557	1815.7200	908.3637	S	1359.6031	680.3052	1342.5766	671.7919	1341.5926	671.2999	12
16	**1920.7626**	960.8849	1903.7361	952.3717	1902.7521	951.8797	S	**1272.5711**	636.7892	1255.5446	628.2759	1254.5606	627.7839	11
17	2017.8154	1009.4113	2000.7888	1000.8981	1999.8048	1000.4060	P	**1185.5391**	593.2732	1168.5125	584.7599	1167.5285	584.2679	10
18	2114.8681	1057.9377	2097.8416	1049.4244	2096.8576	1048.9324	P	1088.4863	544.7468	1071.4598	536.2335	1070.4758	535.7415	9
19	2242.9267	1121.9670	2225.9002	1113.4537	2224.9162	1112.9617	Q	991.4336	496.2204	974.4070	487.7071	973.4230	487.2151	8
20	2402.9574	**1201.9823**	2385.9308	1193.4691	2384.9468	1192.9770	C	863.3750	432.1911	846.3484	423.6779	845.3644	423.1858	7
21	2532.0000	**1266.5036**	2514.9734	1257.9903	2513.9894	1257.4983	E	**703.3443**	352.1758	686.3178	343.6625	685.3338	343.1705	6
22	2589.0214	1295.0144	2571.9949	1286.5011	2571.0109	1286.0091	G	**574.3017**	287.6545	557.2752	279.1412			5

23	2702.1055	**1351.5564**	2685.0789	1343.0431	2684.0949	1342.5511	**L**	517.2803	259.1438	500.2537	250.6305			**4**
24	2799.1583	1400.0828	2782.1317	1391.5695	2781.1477	1391.0775	**P**	**404.1962**	202.6017	387.1697	194.0885			**3**
25	2959.1889	**1480.0981**	2942.1624	1471.5848	2941.1783	1471.0928	**C**	307.1435	154.0754	290.1169	145.5621			**2**
26							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ISEENETTCYMGKWSSPPQCEGLPCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.0	3104.2871	0.0090	ISEENETTCYMGKWSSPPQCEGLPCK	Deamidated N5 95.82%
63.4	3104.2871	0.0090	ISEENETTCYMGKWSSPPQCEGLPCK	Deamidated Q19 4.18%
56.2	3103.3031	0.9930	ISEENETTCYMGKWSSPPQCEGLPCK	
8.8	3104.3103	-0.0141	AQCCPSAALIDYTYMTGLQHWSGDWR	
3.5	3104.2936	0.0025	NSMHVDMADEAYSIGPAPSQQSYLSMEK	
0.3	3104.3060	-0.0099	QEYTWQQGYSDEVDNIWRDDWDVR	
0.3	3104.3060	-0.0099	QEYTWQQGYSDEVDNIWRDDWDVR	
0.3	3104.3060	-0.0099	QEYTWQQGYSDEVDNIWRDDWDVR	

Mascot: http://www.matrixscience.com/

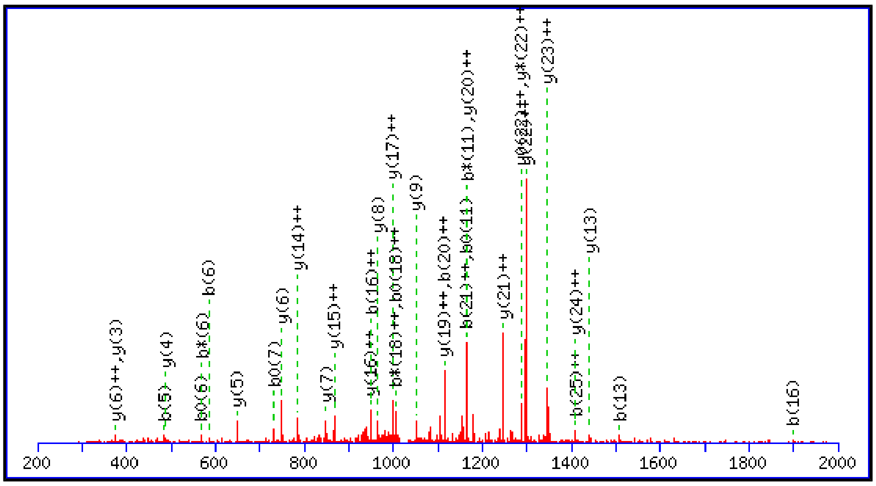
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYKMDGASNVTCINSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27299: 3076.324182 from(1026.448670,3+) intensity(14095.3291) rtinseconds(1039) scans(2410) index(25241)
Title: 111019_Est_MI_YS_G_07Spectrum2032_scans__2410
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

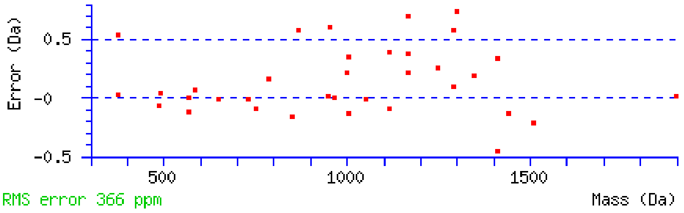
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

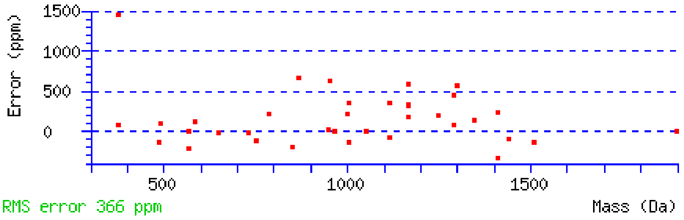


Monoisotopic mass of neutral peptide Mr(calc): 3076.3212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N20 : Deamidated (NQ)
Ions Score: 73 **Expect:** 3.1e-006
Matches : 36/456 fragment ions using 51 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							27
2	129.0659	65.0366					G	3006.2914	1503.6493	2989.2649	1495.1361	2988.2808	1494.6441	26
3	258.1084	129.5579			240.0979	120.5526	E	2949.2699	1475.1386	2932.2434	1466.6253	2931.2594	1466.1333	25
4	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	Q	2820.2273	1410.6173	2803.2008	1402.1040	2802.2168	1401.6120	24
5	**485.2354**	243.1214	468.2089	234.6081	467.2249	234.1161	V	2692.1688	1346.5880	2675.1422	1338.0747	2674.1582	1337.5827	23
6	**586.2831**	293.6452	569.2566	285.1319	568.2726	284.6399	T	2593.1004	1297.0538	2576.0738	1288.5405	2575.0898	1288.0485	22
7	749.3464	375.1769	732.3199	366.6636	731.3359	366.1716	Y	2492.0527	1246.5300	2475.0261	1238.0167	2474.0421	1237.5247	21
8	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	T	2328.9893	1164.9983	2311.9628	1156.4850	2310.9788	1155.9930	20
9	1010.4248	505.7160	993.3982	497.2028	992.4142	496.7107	C	2227.9417	1114.4745	2210.9151	1105.9612	2209.9311	1105.4692	19
10	1081.4619	541.2346	1064.4353	532.7213	1063.4513	532.2293	A	2067.9110	1034.4591	2050.8845	1025.9459	2049.9005	1025.4539	18
11	1182.5096	591.7584	1165.4830	583.2451	1164.4990	582.7531	T	1996.8739	998.9406	1979.8474	990.4273	1978.8633	989.9353	17
12	1345.5729	673.2901	1328.5463	664.7768	1327.5623	664.2848	Y	1895.8262	948.4168	1878.7997	939.9035	1877.8157	939.4115	16
13	**1508.6362**	754.8218	1491.6097	746.3085	1490.6257	745.8165	Y	1732.7629	866.8851	1715.7363	858.3718	1714.7523	857.8798	15
14	1636.7312	818.8692	1619.7046	810.3560	1618.7206	809.8640	K	1569.6996	785.3534	1552.6730	776.8401	1551.6890	776.3481	14
15	1783.7666	892.3869	1766.7400	883.8737	1765.7560	883.3817	M	***1441.6046***	721.3059	1424.5781	712.7927	1423.5940	712.3007	13
16	**1898.7935**	**949.9004**	1881.7670	941.3871	1880.7830	940.8951	D	1294.5692	647.7882	1277.5427	639.2750	1276.5586	638.7830	12
17	1955.8150	978.4111	1938.7884	969.8979	1937.8044	969.4059	G	1179.5423	590.2748	1162.5157	581.7615	1161.5317	581.2695	11
18	2026.8521	1013.9297	2009.8256	1005.4164	2008.8415	1004.9244	A	1122.5208	561.7640	1105.4942	553.2508	1104.5102	552.7588	10
19	2113.8841	1057.4457	2096.8576	1048.9324	2095.8736	1048.4404	S	***1051.4837***	526.2455	1034.4571	517.7322	1033.4731	517.2402	9
20	2228.9111	**1114.9592**	2211.8845	1106.4459	2210.9005	1105.9539	N	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	8
21	2327.9795	**1164.4934**	2310.9529	1155.9801	2309.9689	1155.4881	V	***849.4247***	425.2160	832.3982	416.7027	831.4141	416.2107	7
22	2429.0272	1215.0172	2412.0006	1206.5040	2411.0166	1206.0119	T	***750.3563***	375.6818	733.3297	367.1685	732.3457	366.6765	6

23	2589.0578	1295.0325	2572.0313	1286.5193	2571.0473	1286.0273	**C**	***649.3086***	325.1579	632.2821	316.6447	631.2981	316.1527	**5**
24	2702.1419	1351.5746	2685.1153	1343.0613	2684.1313	1342.5693	**I**	***489.2780***	245.1426	472.2514	236.6293	471.2674	236.1373	**4**
25	2816.1848	**1408.5960**	2799.1583	1400.0828	2798.1742	1399.5908	**N**	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	**3**
26	2903.2168	1452.1121	2886.1903	1443.5988	2885.2063	1443.1068	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of AGEQVTYTCATYYKMDGASNVTCINSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.4	3076.3212	0.0030	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated N20 99.01%
53.3	3076.3212	0.0030	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated N25 0.97%
35.7	3076.3212	0.0030	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated Q4 0.02%
3.6	3076.3187	0.0054	FMPEVSDAGQAYKCFCPQGQIPMGADR	

Mascot: http://www.matrixscience.com/

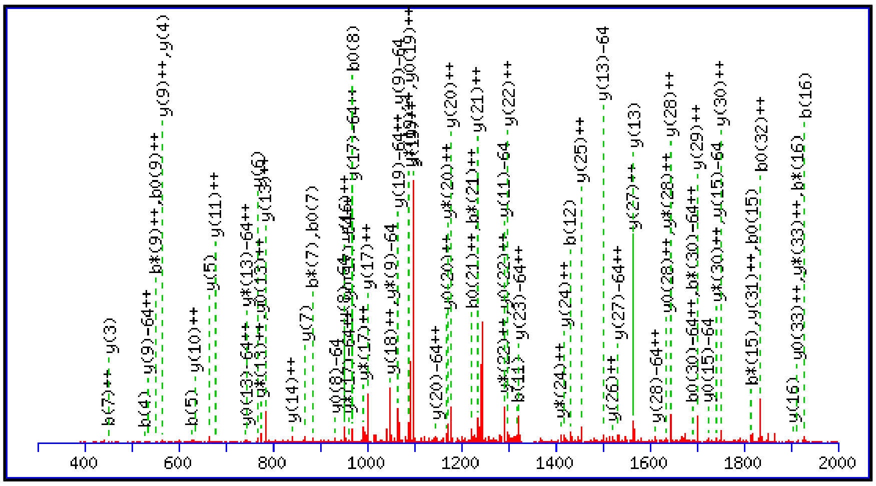
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28344: 4026.823932 from(1343.281920,3+) intensity(15620.7725) rtinseconds(1816) scans(4721) index(6536)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4149_scans__4721
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

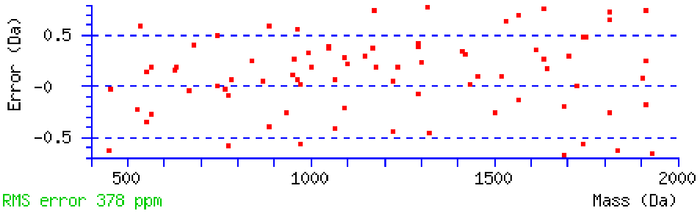
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

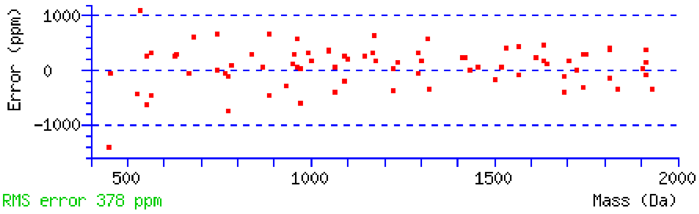


Monoisotopic mass of neutral peptide Mr(calc): 4025.8168
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N26 : Deamidated (NQ)
M27 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 73 **Expect:** 6.9e-006
Matches : 80/574 fragment ions using 147 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3840.7448	1920.8761	3823.7183	1912.3628	3822.7343	1911.8708	33
3	399.1663	200.0868			381.1557	191.0815	P	3725.7179	1863.3626	3708.6913	1854.8493	3707.7073	1854.3573	32
4	**528.2089**	264.6081			510.1983	255.6028	E	3628.6651	1814.8362	3611.6386	1806.3229	3610.6546	1805.8309	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3499.6225	1750.3149	3482.5960	1741.8016	3481.6120	1741.3096	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3400.5541	1700.7807	3383.5276	1692.2674	3382.5436	1691.7754	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3286.5112	1643.7592	3269.4846	1635.2460	3268.5006	1634.7540	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3126.4805	1563.7439	3109.4540	1555.2306	3108.4700	1554.7386	27
9	1119.4234	560.2153	1102.3968	551.7021	1101.4128	551.2101	M	3039.4485	1520.2279	3022.4220	1511.7146	3021.4379	1511.2226	26
10	1190.4605	595.7339	1173.4340	587.2206	1172.4499	586.7286	A	2908.4080	1454.7077	2891.3815	1446.1944	2890.3975	1445.7024	25
11	**1318.5191**	659.7632	1301.4925	651.2499	1300.5085	650.7579	Q	2837.3709	1419.1891	2820.3444	1410.6758	2819.3603	1410.1838	24
12	**1431.6031**	716.3052	1414.5766	707.7919	1413.5926	707.2999	I	2709.3123	1355.1598	2692.2858	1346.6465	2691.3018	1346.1545	23
13	1559.6617	780.3345	1542.6352	771.8212	1541.6512	771.3292	Q	2596.2283	1298.6178	2579.2017	1290.1045	2578.2177	1289.6125	22
14	1672.7458	836.8765	1655.7192	828.3633	1654.7352	827.8713	L	2468.1697	1234.5885	2451.1431	1226.0752	2450.1591	1225.5832	21
15	1832.7764	916.8919	1815.7499	908.3786	1814.7659	907.8866	C	2355.0856	1178.0465	2338.0591	1169.5332	2337.0751	1169.0412	20
16	**1929.8292**	965.4182	1912.8027	956.9050	1911.8186	956.4130	P	2195.0550	1098.0311	2178.0284	1089.5179	2177.0444	1089.0258	19
17	2026.8820	1013.9446	2009.8554	1005.4313	2008.8714	1004.9393	P	2098.0022	1049.5047	2080.9757	1040.9915	2079.9917	1040.4995	18
18	2123.9347	1062.4710	2106.9082	1053.9577	2105.9242	1053.4657	P	2000.9495	1000.9784	1983.9229	992.4651	1982.9389	991.9731	17
19	2220.9875	1110.9974	2203.9609	1102.4841	2202.9769	1101.9921	P	**1903.8967**	952.4520	1886.8701	943.9387	1885.8861	943.4467	16
20	2349.0461	1175.0267	2332.0195	1166.5134	2331.0355	1166.0214	Q	1806.8439	903.9256	1789.8174	895.4123	1788.8334	894.9203	15
21	2462.1301	1231.5687	2445.1036	1223.0554	2444.1196	1222.5634	I	1678.7853	839.8963	1661.7588	831.3830	1660.7748	830.8910	14
22	2559.1829	1280.0951	2542.1564	1271.5818	2541.1723	1271.0898	P	**1565.7013**	783.3543	1548.6747	774.8410	1547.6907	774.3490	13

23	2673.2258	1337.1166	2656.1993	1328.6033	2655.2153	1328.1113	**N**	1468.6485	734.8279	1451.6220	726.3146	1450.6380	725.8226	**12**
24	2760.2579	1380.6326	2743.2313	1372.1193	2742.2473	1371.6273	**S**	1354.6056	677.8064	1337.5790	669.2932	1336.5950	668.8012	**11**
25	2897.3168	1449.1620	2880.2902	1440.6487	2879.3062	1440.1567	**H**	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	**10**
26	3012.3437	1506.6755	2995.3172	1498.1622	2994.3331	1497.6702	**N**	1130.5147	565.7610	1113.4881	557.2477	1112.5041	556.7557	**9**
27	3159.3791	1580.1932	3142.3526	1571.6799	3141.3685	1571.1879	**M**	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	**8**
28	3260.4268	1630.7170	3243.4002	1622.2038	3242.4162	1621.7118	**T**	**868.4523**	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3361.4745	1681.2409	3344.4479	1672.7276	3343.4639	1672.2356	**T**	**767.4046**	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3462.5221	1731.7647	3445.4956	1723.2514	3444.5116	1722.7594	**T**	**666.3570**	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3575.6062	1788.3067	3558.5797	1779.7935	3557.5956	1779.3015	**L**	**565.3093**	283.1583	548.2827	274.6450			**4**
32	3689.6491	1845.3282	3672.6226	1836.8149	3671.6386	1836.3229	**N**	**452.2252**	226.6162	435.1987	218.1030			**3**
33	3852.7125	1926.8599	3835.6859	1918.3466	3834.7019	1917.8546	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.9	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, Oxidation M27; 53.78%
70.9	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N32, Oxidation M27; 33.93%
63.6	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, Oxidation M27; 6.45%
61.6	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, Oxidation M27; 4.07%
55.8	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Oxidation M27; 1.05%
53.9	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Oxidation M27; 0.69%
40.2	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Oxidation M27; 0.03%
26.8	4024.8328	1.9911	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
15.2	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N32, Oxidation M9; 0.00%
15.0	4025.8168	1.0071	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, Oxidation M9; 0.00%

Mascot: http://www.matrixscience.com/

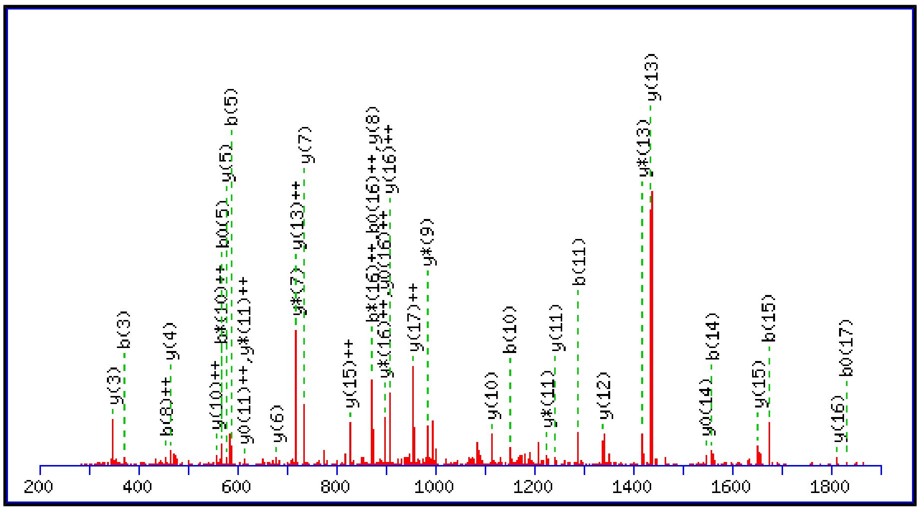
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPCSQPPQIEHGTINSSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

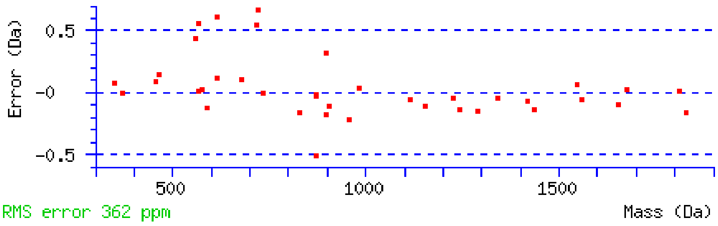
Match to Query 12588: 2021.950548 from(1011.982550,2+) intensity(68493.7969) rtinseconds(618) scans(1308) index(2493)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1101_scans__1308
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

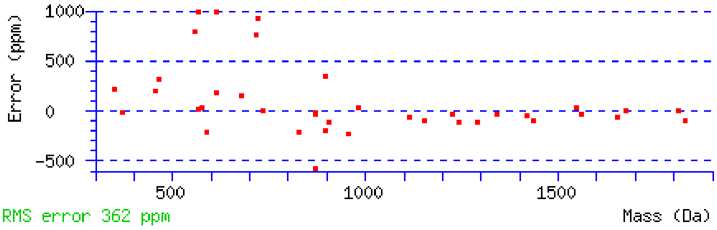
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2021.9476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Deamidated (NQ)
N15 : Deamidated (NQ)
Ions Score: 73 **Expect:** 1.2e-005
Matches : 38/188 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	114.0913	57.5493					**I**							**18**
2	211.1441	106.0757					**P**	1909.8709	955.4391	1892.8443	946.9258	1891.8603	946.4338	**17**
3	**371.1748**	186.0910					**C**	***1812.8181***	906.9127	1795.7916	898.3994	1794.8075	897.9074	**16**
4	458.2068	229.6070			440.1962	220.6017	**S**	***1652.7875***	826.8974	1635.7609	818.3841	1634.7769	817.8921	**15**
5	**587.2494**	294.1283	570.2228	285.6151	569.2388	285.1230	**Q**	1565.7554	783.3814	1548.7289	774.8681	1547.7449	774.3761	**14**
6	684.3021	342.6547	667.2756	334.1414	666.2916	333.6494	**P**	***1436.7128***	718.8601	1419.6863	710.3468	1418.7023	709.8548	**13**
7	781.3549	391.1811	764.3284	382.6678	763.3443	382.1758	**P**	***1339.6601***	670.3337	1322.6335	661.8204	1321.6495	661.3284	**12**
8	909.4135	455.2104	892.3869	446.6971	891.4029	446.2051	**Q**	***1242.6073***	621.8073	1225.5808	613.2940	1224.5967	612.8020	**11**
9	1022.4975	511.7524	1005.4710	503.2391	1004.4870	502.7471	**I**	***1114.5487***	557.7780	1097.5222	549.2647	1096.5382	548.7727	**10**
10	**1151.5401**	576.2737	1134.5136	567.7604	1133.5296	567.2684	**E**	1001.4647	501.2360	984.4381	492.7227	983.4541	492.2307	**9**
11	**1288.5991**	644.8032	1271.5725	636.2899	1270.5885	635.7979	**H**	***872.4221***	436.7147	855.3955	428.2014	854.4115	427.7094	**8**
12	1345.6205	673.3139	1328.5940	664.8006	1327.6099	664.3086	**G**	***735.3632***	368.1852	718.3366	359.6719	717.3526	359.1799	**7**
13	1446.6682	723.8377	1429.6416	715.3245	1428.6576	714.8325	**T**	***678.3417***	339.6745	661.3151	331.1612	660.3311	330.6692	**6**
14	**1559.7523**	780.3798	1542.7257	771.8665	1541.7417	771.3745	**I**	***577.2940***	289.1506	560.2675	280.6374	559.2835	280.1454	**5**
15	**1674.7792**	837.8932	1657.7527	829.3800	1656.7686	828.8880	**N**	***464.2100***	232.6086	447.1834	224.0953	446.1994	223.6033	**4**
16	1761.8112	881.4093	1744.7847	872.8960	1743.8007	872.4040	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
17	1848.8433	924.9253	1831.8167	916.4120	1830.8327	915.9200	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
18							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IPCSQPPQIEHGTINSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.7	2021.9476	0.0029	IPCSQPPQIEHGTINSSR	Deamidated Q5, N15 92.14%
62.0	2021.9476	0.0029	IPCSQPPQIEHGTINSSR	Deamidated Q8, N15 7.86%
25.3	2021.9476	0.0029	IPCSQPPQIEHGTINSSR	Deamidated Q5, Q8 0.00%
5.3	2020.9445	1.0060	QLLVEVERMECATPSDK	
0.2	2021.9550	-0.0045	KGYAEALVEPTMMKTGHSG	
0.0	2021.9582	-0.0077	YVQPPTTPEFGGNPSTTTK	

Mascot: http://www.matrixscience.com/

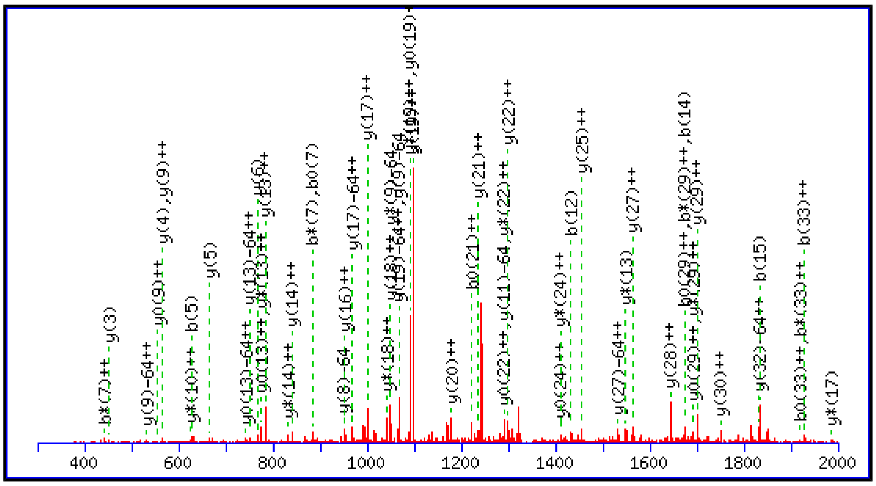
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28351: 4027.818012 from(1343.613280,3+) intensity(0.0000) rtinseconds(1829) scans(4756) index(6538)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4181_scans__4756
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

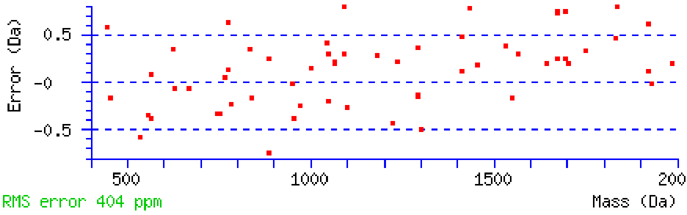
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

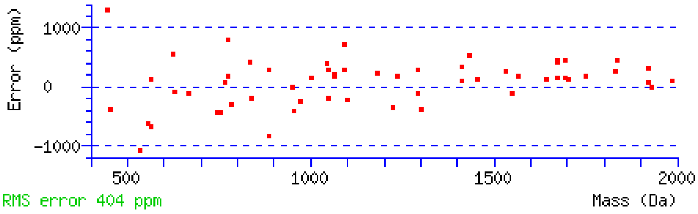


```
Monoisotopic mass of neutral peptide Mr(calc): 4026.8009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N23    : Deamidated (NQ)
N26    : Deamidated (NQ)
M27    : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 72  Expect: 8.7e-006
Matches : 59/574 fragment ions using 85 most intense peaks    (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3841.7288	1921.3681	3824.7023	1912.8548	3823.7183	1912.3628	33
3	399.1663	200.0868			381.1557	191.0815	P	3726.7019	1863.8546	3709.6754	1855.3413	3708.6913	1854.8493	32
4	528.2089	264.6081			510.1983	255.6028	E	3629.6491	1815.3282	3612.6226	1806.8149	3611.6386	1806.3229	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3500.6065	1750.8069	3483.5800	1742.2936	3482.5960	1741.8016	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3401.5381	1701.2727	3384.5116	1692.7594	3383.5276	1692.2674	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3287.4952	1644.2512	3270.4687	1635.7380	3269.4846	1635.2460	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3127.4646	1564.2359	3110.4380	1555.7226	3109.4540	1555.2306	27
9	1119.4234	560.2153	1102.3968	551.7021	1101.4128	551.2101	M	3040.4325	1520.7199	3023.4060	1512.2066	3022.4220	1511.7146	26
10	1190.4605	595.7339	1173.4340	587.2206	1172.4499	586.7286	A	2909.3920	1455.1997	2892.3655	1446.6864	2891.3815	1446.1944	25
11	1318.5191	659.7632	1301.4925	651.2499	1300.5085	650.7579	Q	2838.3549	1419.6811	2821.3284	1411.1678	2820.3444	1410.6758	24
12	**1431.6031**	716.3052	1414.5766	707.7919	1413.5926	707.2999	I	2710.2964	1355.6518	2693.2698	1347.1385	2692.2858	1346.6465	23
13	1559.6617	780.3345	1542.6352	771.8212	1541.6512	771.3292	Q	2597.2123	1299.1098	2580.1857	1290.5965	2579.2017	1290.1045	22
14	**1672.7458**	836.8765	1655.7192	828.3633	1654.7352	827.8713	L	2469.1537	1235.0805	2452.1272	1226.5672	2451.1431	1226.0752	21
15	**1832.7764**	916.8919	1815.7499	908.3786	1814.7659	907.8866	C	2356.0696	1178.5385	2339.0431	1170.0252	2338.0591	1169.5332	20
16	1929.8292	965.4182	1912.8027	956.9050	1911.8186	956.4130	P	2196.0390	1098.5231	2179.0124	1090.0099	2178.0284	1089.5179	19
17	2026.8820	1013.9446	2009.8554	1005.4313	2008.8714	1004.9393	P	2098.9862	1049.9968	2081.9597	1041.4835	2080.9757	1040.9915	18
18	2123.9347	1062.4710	2106.9082	1053.9577	2105.9242	1053.4657	P	2001.9335	1001.4704	1984.9069	992.9571	1983.9229	992.4651	17
19	2220.9875	1110.9974	2203.9609	1102.4841	2202.9769	1101.9921	P	1904.8807	952.9440	1887.8542	944.4307	1886.8701	943.9387	16
20	2349.0461	1175.0267	2332.0195	1166.5134	2331.0355	1166.0214	Q	1807.8279	904.4176	1790.8014	895.9043	1789.8174	895.4123	15
21	2462.1301	1231.5687	2445.1036	1223.0554	2444.1196	1222.5634	I	1679.7694	840.3883	1662.7428	831.8750	1661.7588	831.3830	14
22	2559.1829	1280.0951	2542.1564	1271.5818	2541.1723	1271.0898	P	1566.6853	783.8463	1549.6587	775.3330	1548.6747	774.8410	13

23	2674.2098	1337.6086	2657.1833	1329.0953	2656.1993	1328.6033	N	1469.6325	735.3199	1452.6060	726.8066	1451.6220	726.3146	12
24	2761.2419	1381.1246	2744.2153	1372.6113	2743.2313	1372.1193	S	1354.6056	677.8064	1337.5790	669.2932	1336.5950	668.8012	11
25	2898.3008	1449.6540	2881.2742	1441.1408	2880.2902	1440.6487	H	1267.5736	634.2904	1250.5470	625.7771	1249.5630	625.2851	10
26	3013.3277	1507.1675	2996.3012	1498.6542	2995.3172	1498.1622	N	1130.5147	565.7610	1113.4881	557.2477	1112.5041	556.7557	9
27	3160.3631	1580.6852	3143.3366	1572.1719	3142.3526	1571.6799	M	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	8
28	3261.4108	1631.2090	3244.3843	1622.6958	3243.4002	1622.2038	T	868.4523	434.7298	851.4258	426.2165	850.4417	425.7245	7
29	3362.4585	1681.7329	3345.4319	1673.2196	3344.4479	1672.7276	T	**767.4046**	384.2060	750.3781	375.6927	749.3941	375.2007	6
30	3463.5062	1732.2567	3446.4796	1723.7434	3445.4956	1723.2514	T	**666.3570**	333.6821	649.3304	325.1688	648.3464	324.6768	5
31	3576.5902	1788.7988	3559.5637	1780.2855	3558.5797	1779.7935	L	**565.3093**	283.1583	548.2827	274.6450			4
32	3690.6332	1845.8202	3673.6066	1837.3069	3672.6226	1836.8149	N	**452.2252**	226.6162	435.1987	218.1030			3
33	3853.6965	1927.3519	3836.6699	1918.8386	3835.6859	1918.3466	Y	338.1823	169.5948	321.1557	161.0815			2
34							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
71.8	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26, Oxidation M27; 72.22%
66.8	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23, Oxidation M27; 23.05%
56.5	4025.8168	2.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
54.6	4025.8168	2.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
54.0	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20, Oxidation M27; 1.21%
51.9	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, N32, Oxidation M9; 0.75%
46.3	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32, Oxidation M9; 0.20%
46.2	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26, Oxidation M9; 0.20%
43.0	4025.8168	2.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
42.3	4026.8009	1.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32, Oxidation M27; 0.08%

Mascot: http://www.matrixscience.com/

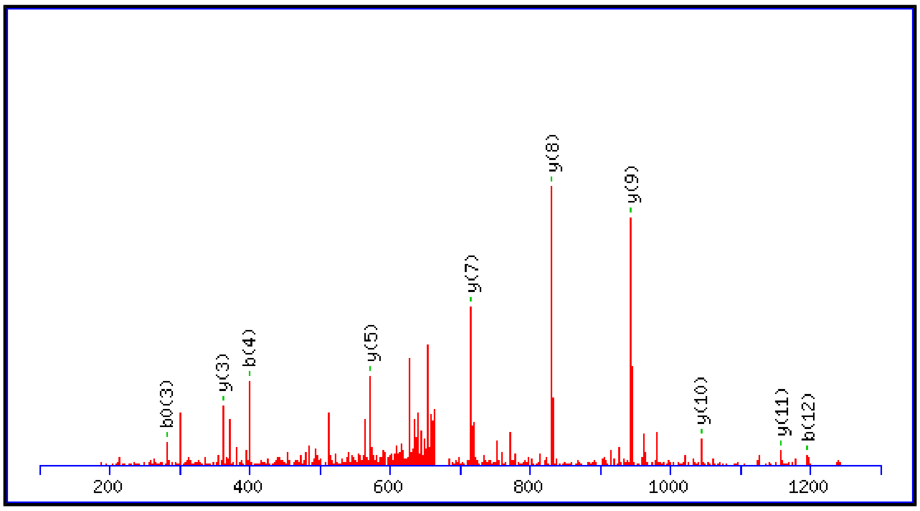
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPDVINGSPISQK**
Found in **F8WDX4** in **con_Xuniprot_HUMAN3**, F8WDX4_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=2 SV=1

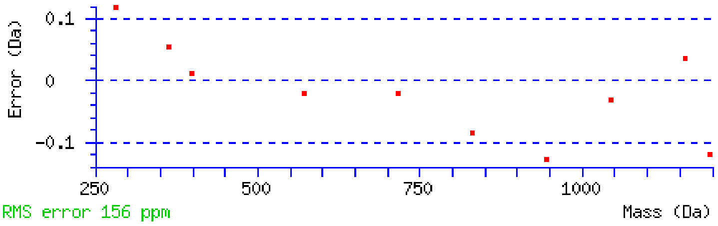
Match to Query 2031: 1341.682188 from(671.848370,2+) intensity(11115.4336) rtinseconds(692) scans(1476) index(1905)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum1218_scans__1476
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

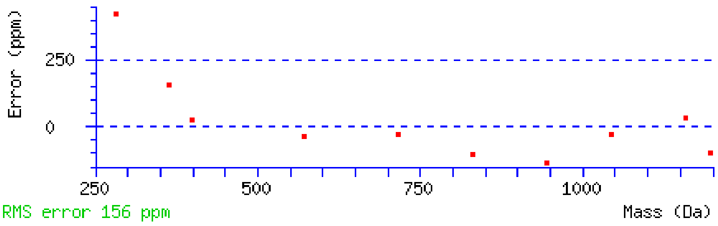
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1341.6776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 70 **Expect:** 1.7e-005
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	88.0393	44.5233			70.0287	35.5180	S							13
2	185.0921	93.0497			167.0815	84.0444	P	1255.6529	628.3301	1238.6263	619.8168	1237.6423	619.3248	12
3	300.1190	150.5631			282.1084	141.5579	D	***1158.6001***	579.8037	1141.5735	571.2904	1140.5895	570.7984	11
4	**399.1874**	200.0974			381.1769	191.0921	V	***1043.5732***	522.2902	1026.5466	513.7769	1025.5626	513.2849	10
5	512.2715	256.6394			494.2609	247.6341	I	***944.5047***	472.7560	927.4782	464.2427	926.4942	463.7507	9
6	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	N	***831.4207***	416.2140	814.3941	407.7007	813.4101	407.2087	8
7	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	G	***716.3937***	358.7005	699.3672	350.1872	698.3832	349.6952	7
8	771.3519	386.1796	754.3254	377.6663	753.3414	377.1743	S	659.3723	330.1898	642.3457	321.6765	641.3617	321.1845	6
9	868.4047	434.7060	851.3781	426.1927	850.3941	425.7007	P	***572.3402***	286.6738	555.3137	278.1605	554.3297	277.6685	5
10	981.4888	491.2480	964.4622	482.7347	963.4782	482.2427	I	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
11	1068.5208	534.7640	1051.4942	526.2508	1050.5102	525.7587	S	***362.2034***	181.6053	345.1769	173.0921	344.1928	172.6001	3
12	**1196.5794**	598.7933	1179.5528	590.2800	1178.5688	589.7880	Q	275.1714	138.0893	258.1448	129.5761			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SPDVINGSPISQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
70.4	1341.6776	0.0046	SPDVINGSPISQK	Deamidated N6 100.00%
23.0	1341.6776	0.0046	SPDVINGSPISQK	Deamidated Q12 0.00%
14.4	1341.6776	0.0046	TAIIIDDETHSK	
4.2	1341.6823	-0.0001	RVVETMHQSQK	
3.1	1341.6776	0.0046	LANQEDVSGALPK	
2.5	1341.6816	0.0006	GLVEGSFQYTLK	

Mascot: http://www.matrixscience.com/

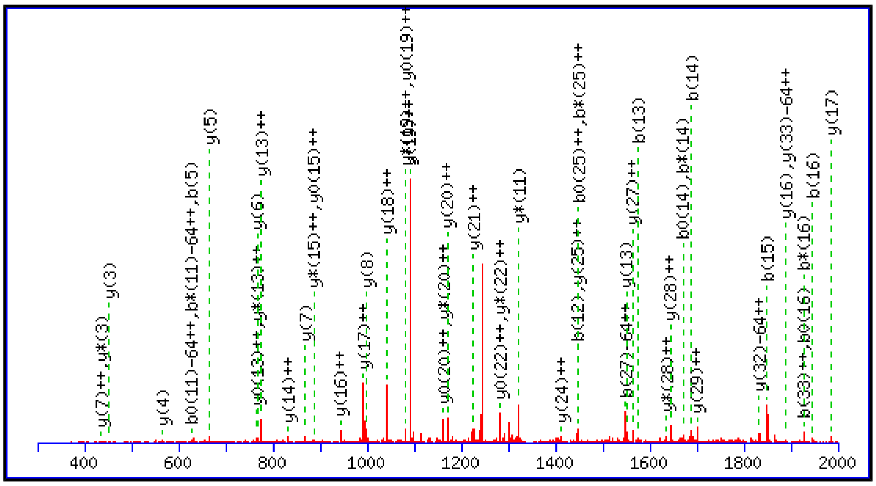
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28341: 4026.786402 from(1343.269410,3+) intensity(0.0000) rtinseconds(1852) scans(4825) index(19694)
Title: 111019_Est_MI_YP_G_09Spectrum4256_scans__4825
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

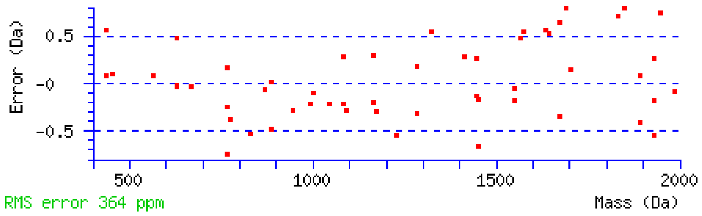
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

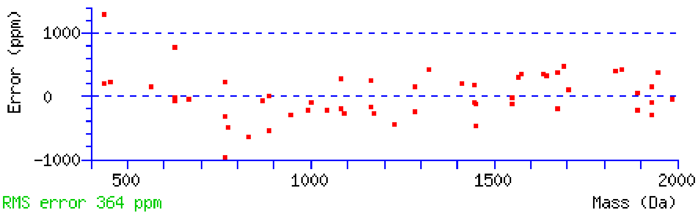


Monoisotopic mass of neutral peptide Mr(calc): 4026.8009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N23 : Deamidated (NQ)
N26 : Deamidated (NQ)
Ions Score: 70 **Expect:** 1.1e-005
Matches : 54/574 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3841.7288	1921.3681	3824.7023	1912.8548	3823.7183	1912.3628	33
3	399.1663	200.0868			381.1557	191.0815	P	3726.7019	1863.8546	3709.6754	1855.3413	3708.6913	1854.8493	32
4	528.2089	264.6081			510.1983	255.6028	E	3629.6491	1815.3282	3612.6226	1806.8149	3611.6386	1806.3229	31
5	**627.2773**	314.1423			609.2667	305.1370	V	3500.6065	1750.8069	3483.5800	1742.2936	3482.5960	1741.8016	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3401.5381	1701.2727	3384.5116	1692.7594	3383.5276	1692.2674	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3287.4952	1644.2512	3270.4687	1635.7380	3269.4846	1635.2460	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3127.4646	1564.2359	3110.4380	1555.7226	3109.4540	1555.2306	27
9	1135.4183	568.2128	1118.3918	559.6995	1117.4077	559.2075	M	3040.4325	1520.7199	3023.4060	1512.2066	3022.4220	1511.7146	26
10	1206.4554	603.7313	1189.4289	595.2181	1188.4449	594.7261	A	2893.3971	1447.2022	2876.3706	1438.6889	2875.3866	1438.1969	25
11	1334.5140	667.7606	1317.4875	659.2474	1316.5034	658.7554	Q	2822.3600	1411.6836	2805.3335	1403.1704	2804.3494	1402.6784	24
12	**1447.5981**	724.3027	1430.5715	715.7894	1429.5875	715.2974	I	2694.3014	1347.6544	2677.2749	1339.1411	2676.2909	1338.6491	23
13	**1575.6566**	788.3320	1558.6301	779.8187	1557.6461	779.3267	Q	2581.2174	1291.1123	2564.1908	1282.5990	2563.2068	1282.1070	22
14	**1688.7407**	844.8740	1671.7142	836.3607	1670.7301	835.8687	L	2453.1588	1227.0830	2436.1322	1218.5698	2435.1482	1218.0778	21
15	**1848.7714**	924.8893	1831.7448	916.3760	1830.7608	915.8840	C	2340.0747	1170.5410	2323.0482	1162.0277	2322.0642	1161.5357	20
16	**1945.8241**	973.4157	1928.7976	964.9024	1927.8136	964.4104	P	2180.0441	1090.5257	2163.0175	1082.0124	2162.0335	1081.5204	19
17	2042.8769	1021.9421	2025.8503	1013.4288	2024.8663	1012.9368	P	2082.9913	1041.9993	2065.9648	1033.4860	2064.9808	1032.9940	18
18	2139.9296	1070.4685	2122.9031	1061.9552	2121.9191	1061.4632	P	***1985.9386***	993.4729	1968.9120	984.9596	1967.9280	984.4676	17
19	2236.9824	1118.9948	2219.9559	1110.4816	2218.9718	1109.9896	P	***1888.8858***	944.9465	1871.8592	936.4333	1870.8752	935.9413	16
20	2365.0410	1183.0241	2348.0144	1174.5109	2347.0304	1174.0188	Q	1791.8330	896.4202	1774.8065	887.9069	1773.8225	887.4149	15
21	2478.1251	1239.5662	2461.0985	1231.0529	2460.1145	1230.5609	I	1663.7744	832.3909	1646.7479	823.8776	1645.7639	823.3856	14
22	2575.1778	1288.0925	2558.1513	1279.5793	2557.1673	1279.0873	P	***1550.6904***	775.8488	1533.6638	767.3356	1532.6798	766.8435	13

23	2690.2048	1345.6060	2673.1782	1337.0927	2672.1942	1336.6007	**N**	1453.6376	727.3224	1436.6111	718.8092	1435.6271	718.3172	**12**
24	2777.2368	1389.1220	2760.2102	1380.6088	2759.2262	1380.1167	**S**	1338.6107	669.8090	1321.5841	661.2957	1320.6001	660.8037	**11**
25	2914.2957	1457.6515	2897.2691	1449.1382	2896.2851	1448.6462	**H**	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**10**
26	3029.3226	1515.1650	3012.2961	1506.6517	3011.3121	1506.1597	**N**	1114.5197	557.7635	1097.4932	549.2502	1096.5092	548.7582	**9**
27	3160.3631	1580.6852	3143.3366	1572.1719	3142.3526	1571.6799	**M**	***999.4928***	500.2500	982.4662	491.7368	981.4822	491.2448	**8**
28	3261.4108	1631.2090	3244.3843	1622.6958	3243.4002	1622.2038	**T**	***868.4523***	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3362.4585	1681.7329	3345.4319	1673.2196	3344.4479	1672.7276	**T**	***767.4046***	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3463.5062	1732.2567	3446.4796	1723.7434	3445.4956	1723.2514	**T**	***666.3570***	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3576.5902	1788.7988	3559.5637	1780.2855	3558.5797	1779.7935	**L**	***565.3093***	283.1583	548.2827	274.6450			**4**
32	3690.6332	1845.8202	3673.6066	1837.3069	3672.6226	1836.8149	**N**	***452.2252***	226.6162	435.1987	218.1030			**3**
33	3853.6965	1927.3519	3836.6699	1918.8386	3835.6859	1918.3466	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.8	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26, Oxidation M9; 33.54%
69.8	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, N32, Oxidation M9; 32.86%
68.6	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23, Oxidation M9; 25.10%
62.8	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20, Oxidation M9; 6.62%
54.5	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Q13, Oxidation M9; 0.99%
53.5	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32, Oxidation M9; 0.78%
45.3	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11, Oxidation M9; 0.12%
10.4	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26, Oxidation M27; 0.00%
9.8	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20, Oxidation M27; 0.00%
9.5	4026.8009	-0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23, Oxidation M27; 0.00%

Mascot: http://www.matrixscience.com/

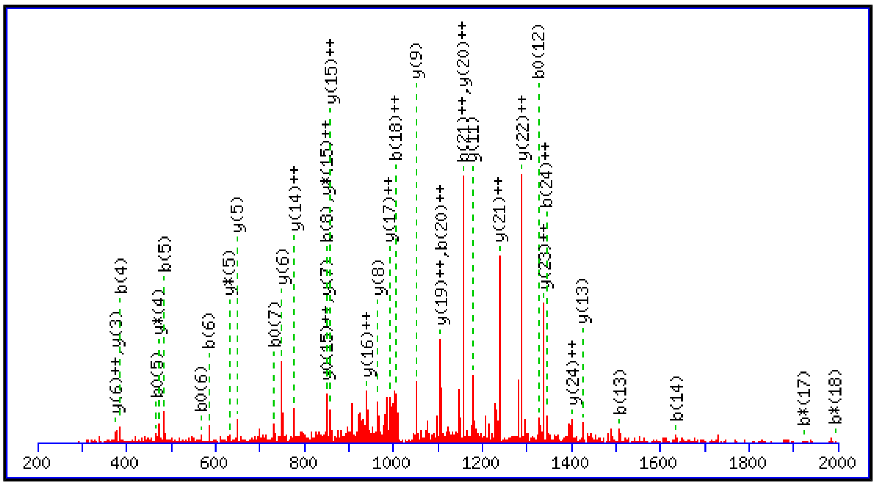
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGEQVTYTCATYYKMDGASNVTCINSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27293: 3060.335022 from(1021.118950,3+) intensity(20258.6289) rtinseconds(1322) scans(3219) index(22543)
Title: 111019_Est_MI_YS_G_03Spectrum2790_scans__3219
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

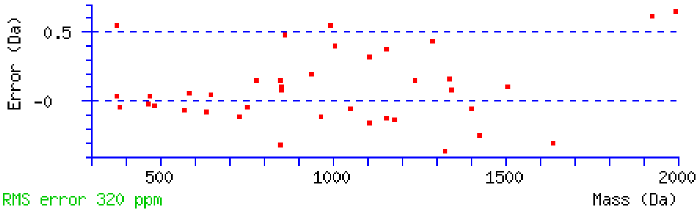
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

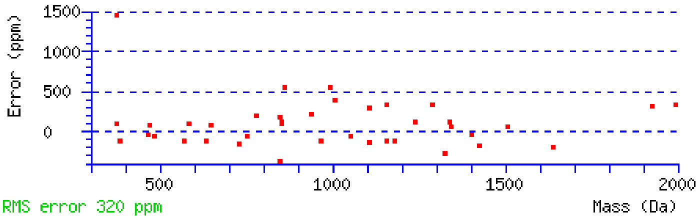


Monoisotopic mass of neutral peptide Mr(calc): 3060.3263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 62 **Expect:** 6.2e-005
Matches : 39/300 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							27
2	129.0659	65.0366					G	2990.2965	1495.6519	2973.2699	1487.1386	2972.2859	1486.6466	26
3	258.1084	129.5579			240.0979	120.5526	E	2933.2750	1467.1412	2916.2485	1458.6279	2915.2645	1458.1359	25
4	**386.1670**	193.5872	369.1405	185.0739	368.1565	184.5819	Q	2804.2324	1402.6199	2787.2059	1394.1066	2786.2219	1393.6146	24
5	**485.2354**	243.1214	468.2089	234.6081	467.2249	234.1161	V	2676.1739	1338.5906	2659.1473	1330.0773	2658.1633	1329.5853	23
6	**586.2831**	293.6452	569.2566	285.1319	568.2726	284.6399	T	2577.1054	1289.0564	2560.0789	1280.5431	2559.0949	1280.0511	22
7	749.3464	375.1769	732.3199	366.6636	731.3359	366.1716	Y	2476.0578	1238.5325	2459.0312	1230.0192	2458.0472	1229.5272	21
8	**850.3941**	425.7007	833.3676	417.1874	832.3836	416.6954	T	2312.9944	1157.0009	2295.9679	1148.4876	2294.9839	1147.9956	20
9	1010.4248	505.7160	993.3982	497.2028	992.4142	496.7107	C	2211.9468	1106.4770	2194.9202	1097.9637	2193.9362	1097.4717	19
10	1081.4619	541.2346	1064.4353	532.7213	1063.4513	532.2293	A	2051.9161	1026.4617	2034.8896	1017.9484	2033.9055	1017.4564	18
11	1182.5096	591.7584	1165.4830	583.2451	1164.4990	582.7531	T	1980.8790	990.9431	1963.8524	982.4299	1962.8684	981.9379	17
12	1345.5729	673.2901	1328.5463	664.7768	1327.5623	664.2848	Y	1879.8313	940.4193	1862.8048	931.9060	1861.8207	931.4140	16
13	**1508.6362**	754.8218	1491.6097	746.3085	1490.6257	745.8165	Y	1716.7680	858.8876	1699.7414	850.3744	1698.7574	849.8823	15
14	**1636.7312**	818.8692	1619.7046	810.3560	1618.7206	809.8640	K	1553.7047	777.3560	1536.6781	768.8427	1535.6941	768.3507	14
15	1767.7717	884.3895	1750.7451	875.8762	1749.7611	875.3842	M	***1425.6097***	713.3085	1408.5831	704.7952	1407.5991	704.3032	13
16	1882.7986	941.9029	1865.7721	933.3897	1864.7881	932.8977	D	1294.5692	647.7882	1277.5427	639.2750	1276.5586	638.7830	12
17	1939.8201	970.4137	1922.7935	961.9004	1921.8095	961.4084	G	***1179.5423***	590.2748	1162.5157	581.7615	1161.5317	581.2695	11
18	2010.8572	**1005.9322**	1993.8306	997.4190	1992.8466	996.9270	A	1122.5208	561.7640	1105.4942	553.2508	1104.5102	552.7588	10
19	2097.8892	1049.4482	2080.8627	1040.9350	2079.8787	1040.4430	S	***1051.4837***	526.2455	1034.4571	517.7322	1033.4731	517.2402	9
20	2212.9162	**1106.9617**	2195.8896	1098.4484	2194.9056	1097.9564	N	***964.4517***	482.7295	947.4251	474.2162	946.4411	473.7242	8
21	2311.9846	**1156.4959**	2294.9580	1147.9827	2293.9740	1147.4906	V	***849.4247***	425.2160	832.3982	416.7027	831.4141	416.2107	7
22	2413.0323	1207.0198	2396.0057	1198.5065	2395.0217	1198.0145	T	***750.3563***	375.6818	733.3297	367.1685	732.3457	366.6765	6
23	2573.0629	1287.0351	2556.0364	1278.5218	2555.0523	1278.0298	C	***649.3086***	325.1579	632.2821	316.6447	631.2981	316.1527	5

24	2686.1470	**1343.5771**	2669.1204	1335.0638	2668.1364	1334.5718	**I**	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	**4**
25	2800.1899	1400.5986	2783.1633	1392.0853	2782.1793	1391.5933	**N**	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	**3**
26	2887.2219	1444.1146	2870.1954	1435.6013	2869.2114	1435.1093	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
27							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of AGEQVTYTCATYYKMDGASNVTCINSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.7	3060.3263	0.0087	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated N20 76.33%
56.6	3060.3263	0.0087	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated N25 23.64%
30.6	3059.3423	0.9927	AGEQVTYTCATYYKMDGASNVTCINSR	
28.1	3060.3263	0.0087	AGEQVTYTCATYYKMDGASNVTCINSR	Deamidated Q4 0.03%
5.5	3060.3353	-0.0003	QMANSYSINSSSNQQLTNDEDALVGLNK	
3.0	3060.3492	-0.0142	MESQEPTESSQNGKQYIISEELISEGK	
0.4	3060.3310	0.0040	MLKEGHHSMVQGAAEMSVNQLYNHCR	
0.3	3060.3310	0.0040	MLKEGHHSMVQGAAEMSVNQLYNHCR	

Mascot: http://www.matrixscience.com/

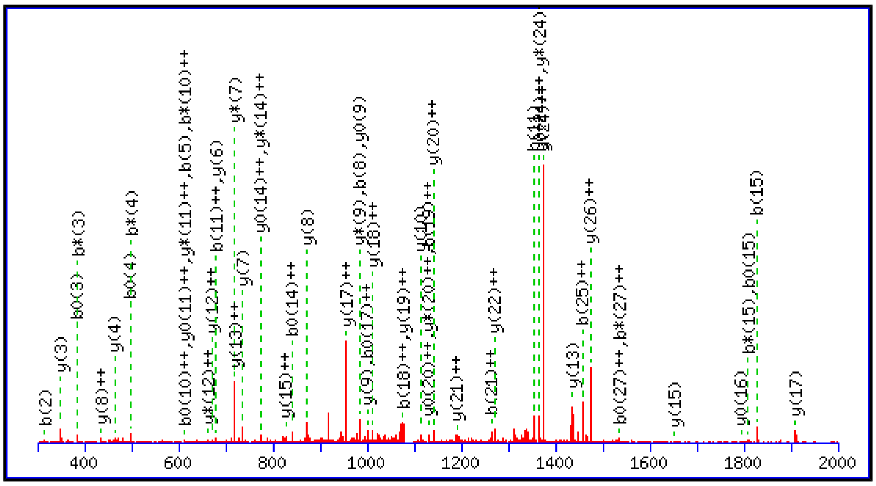
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WQSIPLCVEKIPCSQPPQIEHGTINSSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27388: 3261.598242 from(1088.206690,3+) intensity(35745.0547) rtinseconds(1535) scans(3711) index(8325)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum3164_scans__3711
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

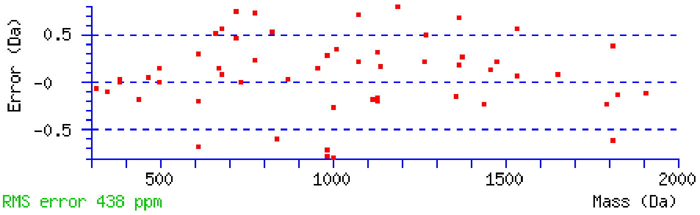
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

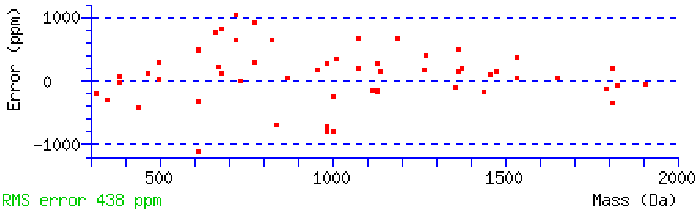


Monoisotopic mass of neutral peptide Mr(calc): 3261.5910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00046
Matches : 57/316 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							28
2	**315.1452**	158.0762	298.1186	149.5629			Q	3076.5190	1538.7632	3059.4925	1530.2499	3058.5085	1529.7579	27
3	402.1772	201.5922	385.1506	193.0790	384.1666	192.5870	S	2948.4605	1474.7339	2931.4339	1466.2206	2930.4499	1465.7286	26
4	515.2613	258.1343	498.2347	249.6210	497.2507	249.1290	I	2861.4284	1431.2179	2844.4019	1422.7046	2843.4179	1422.2126	25
5	**612.3140**	306.6606	595.2875	298.1474	594.3035	297.6554	P	2748.3444	1374.6758	2731.3178	1366.1625	2730.3338	1365.6705	24
6	725.3981	363.2027	708.3715	354.6894	707.3875	354.1974	L	2651.2916	1326.1494	2634.2650	1317.6362	2633.2810	1317.1442	23
7	885.4287	443.2180	868.4022	434.7047	867.4182	434.2127	C	2538.2075	1269.6074	2521.1810	1261.0941	2520.1970	1260.6021	22
8	**984.4972**	492.7522	967.4706	484.2389	966.4866	483.7469	V	2378.1769	1189.5921	2361.1503	1181.0788	2360.1663	1180.5868	21
9	1113.5397	557.2735	1096.5132	548.7602	1095.5292	548.2682	E	2279.1085	1140.0579	2262.0819	1131.5446	2261.0979	1131.0526	20
10	1241.6347	621.3210	1224.6082	612.8077	1223.6241	612.3157	K	2150.0659	1075.5366	2133.0393	1067.0233	2132.0553	1066.5313	19
11	**1354.7188**	**677.8630**	1337.6922	669.3497	1336.7082	668.8577	I	2021.9709	1011.4891	2004.9444	1002.9758	2003.9604	1002.4838	18
12	1451.7715	726.3894	1434.7450	717.8761	1433.7610	717.3841	P	***1908.8869***	954.9471	1891.8603	946.4338	1890.8763	945.9418	17
13	1611.8022	806.4047	1594.7756	797.8915	1593.7916	797.3994	C	1811.8341	906.4207	1794.8075	897.9074	1793.8235	897.4154	16
14	1698.8342	849.9207	1681.8077	841.4075	1680.8236	840.9155	S	***1651.8034***	826.4054	1634.7769	817.8921	1633.7929	817.4001	15
15	**1826.8928**	913.9500	1809.8662	905.4368	1808.8822	904.9448	Q	1564.7714	782.8893	1547.7449	774.3761	1546.7608	773.8841	14
16	1923.9456	962.4764	1906.9190	953.9631	1905.9350	953.4711	P	***1436.7128***	718.8601	1419.6863	710.3468	1418.7023	709.8548	13
17	2020.9983	1011.0028	2003.9718	1002.4895	2002.9878	1001.9975	P	1339.6601	670.3337	1322.6335	661.8204	1321.6495	661.3284	12
18	2149.0569	**1075.0321**	2132.0303	1066.5188	2131.0463	1066.0268	Q	1242.6073	621.8073	1225.5808	613.2940	1224.5967	612.8020	11
19	2262.1410	**1131.5741**	2245.1144	1123.0608	2244.1304	1122.5688	I	***1114.5487***	557.7780	1097.5222	549.2647	1096.5382	548.7727	10
20	2391.1836	1196.0954	2374.1570	1187.5821	2373.1730	1187.0901	E	***1001.4647***	501.2360	984.4381	492.7227	983.4541	492.2307	9
21	2528.2425	**1264.6249**	2511.2159	1256.1116	2510.2319	1255.6196	H	***872.4221***	436.7147	855.3955	428.2014	854.4115	427.7094	8
22	2585.2639	1293.1356	2568.2374	1284.6223	2567.2534	1284.1303	G	***735.3632***	368.1852	718.3366	359.6719	717.3526	359.1799	7
23	2686.3116	1343.6594	2669.2851	1335.1462	2668.3010	1334.6542	T	***678.3417***	339.6745	661.3151	331.1612	660.3311	330.6692	6

24	2799.3957	1400.2015	2782.3691	1391.6882	2781.3851	1391.1962	**I**	577.2940	289.1506	560.2675	280.6374	559.2835	280.1454	**5**
25	2914.4226	**1457.7149**	2897.3961	1449.2017	2896.4120	1448.7097	**N**	***464.2100***	232.6086	447.1834	224.0953	446.1994	223.6033	**4**
26	3001.4546	1501.2310	2984.4281	1492.7177	2983.4441	1492.2257	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
27	3088.4867	1544.7470	3071.4601	1536.2337	3070.4761	1535.7417	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
28							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WQSIPLCVEKIPCSQPPQIEHGTINSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.6	3261.5910	0.0072	WQSIPLCVEKIPCSQPPQIEHGTINSSR	Deamidated N25 91.91%
45.0	3261.5910	0.0072	WQSIPLCVEKIPCSQPPQIEHGTINSSR	Deamidated Q18 5.10%
42.7	3261.5910	0.0072	WQSIPLCVEKIPCSQPPQIEHGTINSSR	Deamidated Q15 2.95%
24.2	3261.5910	0.0072	WQSIPLCVEKIPCSQPPQIEHGTINSSR	Deamidated Q2 0.04%
23.0	3260.6070	0.9912	WQSIPLCVEKIPCSQPPQIEHGTINSSR	
4.4	3260.5967	1.0015	QAIHWMHVDVPVAQPKDLAMLCICDAVK	
4.2	3261.6034	-0.0052	KEGEAELLDQSKQLTTVNEVLAMNNGGETK	
3.7	3260.5936	1.0047	VKSAENIIQFRTSDEDTTVSDLLAQYTSK	
3.7	3260.5936	1.0047	VKSAENIIQFRTSDEDTTVSDLLAQYTSK	
3.6	3261.6056	-0.0073	FIIENNQFLLESMIDPNEWNLWLPRK	

Mascot: http://www.matrixscience.com/

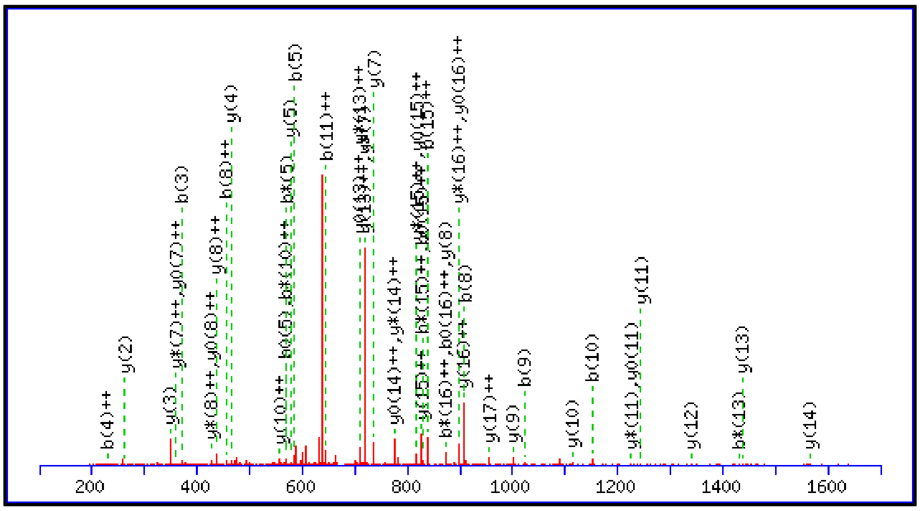
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IPCSQPPQIEHGTINSSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

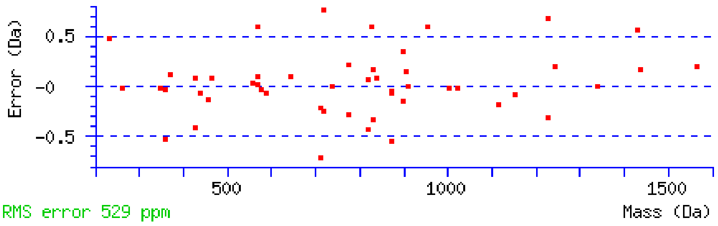
Match to Query 12586: 2021.948802 from(674.990210,3+) intensity(459632.1875) rtinseconds(645) scans(1379) index(2498)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1161_scans__1379
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

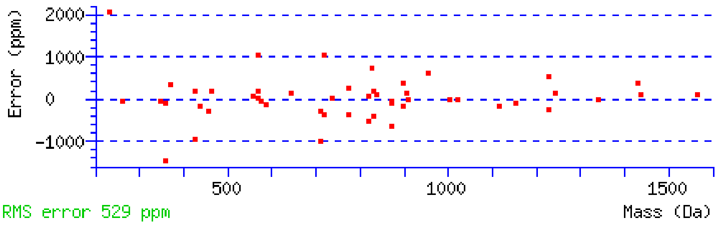
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2021.9476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Deamidated (NQ)
N15 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0013
Matches : 50/188 fragment ions using 98 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							**18**
2	211.1441	106.0757					**P**	1909.8709	955.4391	1892.8443	946.9258	1891.8603	946.4338	**17**
3	**371.1748**	186.0910					**C**	1812.8181	906.9127	1795.7916	898.3994	1794.8075	897.9074	**16**
4	458.2068	**229.6070**			440.1962	220.6017	**S**	1652.7875	826.8974	1635.7609	818.3841	1634.7769	817.8921	**15**
5	**586.2654**	293.6363	569.2388	285.1230	568.2548	284.6310	**Q**	***1565.7554***	783.3814	1548.7289	774.8681	1547.7449	774.3761	**14**
6	683.3181	342.1627	666.2916	333.6494	665.3076	333.1574	**P**	***1437.6968***	719.3521	1420.6703	710.8388	1419.6863	710.3468	**13**
7	780.3709	390.6891	763.3443	382.1758	762.3603	381.6838	**P**	***1340.6441***	670.8257	1323.6175	662.3124	1322.6335	661.8204	**12**
8	**909.4135**	**455.2104**	892.3869	446.6971	891.4029	446.2051	**Q**	***1243.5913***	622.2993	1226.5648	613.7860	1225.5808	613.2940	**11**
9	**1022.4975**	511.7524	1005.4710	503.2391	1004.4870	502.7471	**I**	***1114.5487***	557.7780	1097.5222	549.2647	1096.5382	548.7727	**10**
10	**1151.5401**	576.2737	1134.5136	567.7604	1133.5296	567.2684	**E**	***1001.4647***	501.2360	984.4381	492.7227	983.4541	492.2307	**9**
11	1288.5991	**644.8032**	1271.5725	636.2899	1270.5885	635.7979	**H**	***872.4221***	436.7147	855.3955	428.2014	854.4115	427.7094	**8**
12	1345.6205	673.3139	1328.5940	664.8006	1327.6099	664.3086	**G**	***735.3632***	368.1852	718.3366	359.6719	717.3526	359.1799	**7**
13	1446.6682	723.8377	1429.6416	715.3245	1428.6576	714.8325	**T**	678.3417	339.6745	661.3151	331.1612	660.3311	330.6692	**6**
14	1559.7523	780.3798	1542.7257	771.8665	1541.7417	771.3745	**I**	***577.2940***	289.1506	560.2675	280.6374	559.2835	280.1454	**5**
15	1674.7792	**837.8932**	1657.7527	829.3800	1656.7686	828.8880	**N**	***464.2100***	232.6086	447.1834	224.0953	446.1994	223.6033	**4**
16	1761.8112	881.4093	1744.7847	872.8960	1743.8007	872.4040	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
17	1848.8433	924.9253	1831.8167	916.4120	1830.8327	915.9200	**S**	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
18							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IPCSQPPQIEHGTINSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.4	2021.9476	0.0012	IPCSQPPQIEHGTINSSR	Deamidated Q8, N15 88.00%
43.6	2021.9476	0.0012	IPCSQPPQIEHGTINSSR	Deamidated Q5, N15 11.73%
27.3	2021.9476	0.0012	IPCSQPPQIEHGTINSSR	Deamidated Q5, Q8 0.27%
7.8	2021.9516	-0.0028	EENSAIIIQSWYRMHK	
7.5	2021.9584	-0.0096	MCPAMNLGLVGQQKLATR	
3.4	2021.9438	0.0050	ADASHFIEATDMVLLMNK	
2.9	2019.9473	2.0015	VYDNYSGNLFVDRRVGM	
2.9	2020.9537	0.9951	QGNHIRYSCRYDDPLK	
2.4	2020.9445	1.0043	QLLVEVERMECATPSDK	
2.3	2020.9510	0.9978	QLEEAMNTQLELSEQLK	

Mascot: http://www.matrixscience.com/

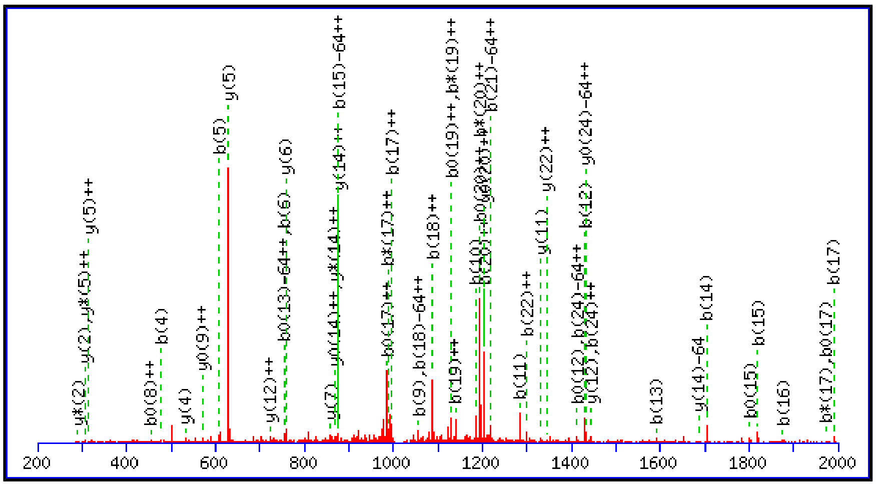
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYEMFGDEEVMCLNGNWTEPPQCK**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27288: 3034.221132 from(1012.414320,3+) intensity(38303.7031) rtinseconds(2038) scans(5253) index(26858)
Title: 111019_Est_MI_YS_G_09Spectrum4575_scans__5253
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

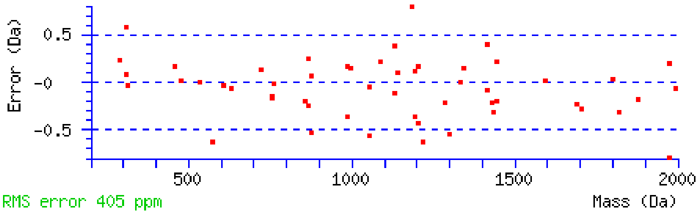
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

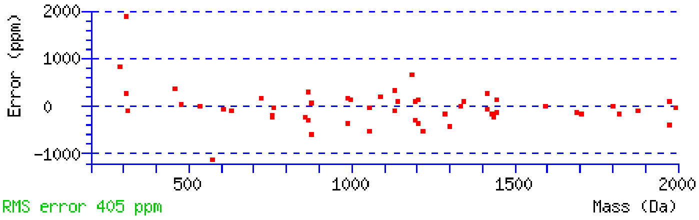


Monoisotopic mass of neutral peptide Mr(calc): 3034.2129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N17 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.00049
Matches : 53/388 fragment ions using 107 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	185.0921	93.0497			167.0815	84.0444	P	2948.1882	1474.5977	2931.1616	1466.0845	2930.1776	1465.5924	24
3	348.1554	174.5813			330.1448	165.5761	Y	2851.1354	1426.0713	2834.1089	1417.5581	2833.1249	1417.0661	23
4	***477.1980***	239.1026			459.1874	230.0974	E	2688.0721	1344.5397	2671.0455	1336.0264	2670.0615	1335.5344	22
5	***608.2385***	304.6229			590.2279	295.6176	M	2559.0295	1280.0184	2542.0029	1271.5051	2541.0189	1271.0131	21
6	***755.3069***	378.1571			737.2963	369.1518	F	2427.9890	1214.4981	2410.9625	1205.9849	2409.9784	1205.4929	20
7	812.3284	406.6678			794.3178	397.6625	G	2280.9206	1140.9639	2263.8940	1132.4507	2262.9100	1131.9587	19
8	927.3553	464.1813			909.3447	455.1760	D	2223.8991	1112.4532	2206.8726	1103.9399	2205.8886	1103.4479	18
9	***1056.3979***	528.7026			1038.3873	519.6973	E	2108.8722	1054.9397	2091.8456	1046.4265	2090.8616	1045.9345	17
10	***1185.4405***	593.2239			1167.4299	584.2186	E	1979.8296	990.4184	1962.8030	981.9052	1961.8190	981.4132	16
11	***1284.5089***	642.7581			1266.4983	633.7528	V	1850.7870	925.8971	1833.7605	917.3839	1832.7764	916.8919	15
12	***1431.5443***	716.2758			1413.5337	707.2705	M	1751.7186	876.3629	1734.6920	867.8497	1733.7080	867.3577	14
13	***1591.5749***	796.2911			1573.5644	787.2858	C	1604.6832	802.8452	1587.6566	794.3320	1586.6726	793.8400	13
14	***1704.6590***	852.8331			1686.6484	843.8279	L	***1444.6525***	722.8299	1427.6260	714.3166	1426.6420	713.8246	12
15	***1818.7019***	909.8546	1801.6754	901.3413	1800.6914	900.8493	N	***1331.5685***	666.2879	1314.5419	657.7746	1313.5579	657.2826	11
16	***1875.7234***	938.3653	1858.6969	929.8521	1857.7128	929.3601	G	1217.5256	609.2664	1200.4990	600.7531	1199.5150	600.2611	10
17	***1990.7503***	**995.8788**	1973.7238	987.3655	1972.7398	986.8735	N	1160.5041	580.7557	1143.4775	572.2424	1142.4935	571.7504	9
18	2176.8297	**1088.9185**	2159.8031	1080.4052	2158.8191	1079.9132	W	1045.4771	523.2422	1028.4506	514.7289	1027.4666	514.2369	8
19	2277.8773	**1139.4423**	2260.8508	1130.9290	2259.8668	1130.4370	T	***859.3978***	430.2026	842.3713	421.6893	841.3873	421.1973	7
20	2406.9199	**1203.9636**	2389.8934	1195.4503	2388.9094	1194.9583	E	***758.3502***	379.6787	741.3236	371.1654	740.3396	370.6734	6
21	2503.9727	1252.4900	2486.9461	1243.9767	2485.9621	1243.4847	P	***629.3076***	315.1574	612.2810	306.6441			5
22	2601.0255	**1301.0164**	2583.9989	1292.5031	2583.0149	1292.0111	P	***532.2548***	266.6310	515.2282	258.1178			4

23	2729.0840	1365.0457	2712.0575	1356.5324	2711.0735	1356.0404	**Q**	435.2020	218.1047	418.1755	209.5914			**3**
24	2889.1147	**1445.0610**	2872.0881	1436.5477	2871.1041	1436.0557	**C**	***307.1435***	154.0754	290.1169	145.5621			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SPYEMFGDEEVMCLNGNWTEPPQCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.3	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N17, Oxidation M12; 59.31%
43.7	3033.2289	0.9922	SPYEMFGDEEVMCLNGNWTEPPQCK	
41.6	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated Q23, Oxidation M12; 25.48%
38.8	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N15, Oxidation M12; 13.40%
27.1	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N17, Oxidation M5; 0.89%
26.1	3033.2289	0.9922	SPYEMFGDEEVMCLNGNWTEPPQCK	
24.5	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated Q23, Oxidation M5; 0.49%
23.9	3034.2129	0.0082	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N15, Oxidation M5; 0.43%
8.2	3033.2152	1.0060	AALTHHPAAMSNGNMNTMGHMMEMMGSR	
7.6	3033.2152	1.0060	AALTHHPAAMSNGNMNTMGHMMEMMGSR	

Mascot: http://www.matrixscience.com/

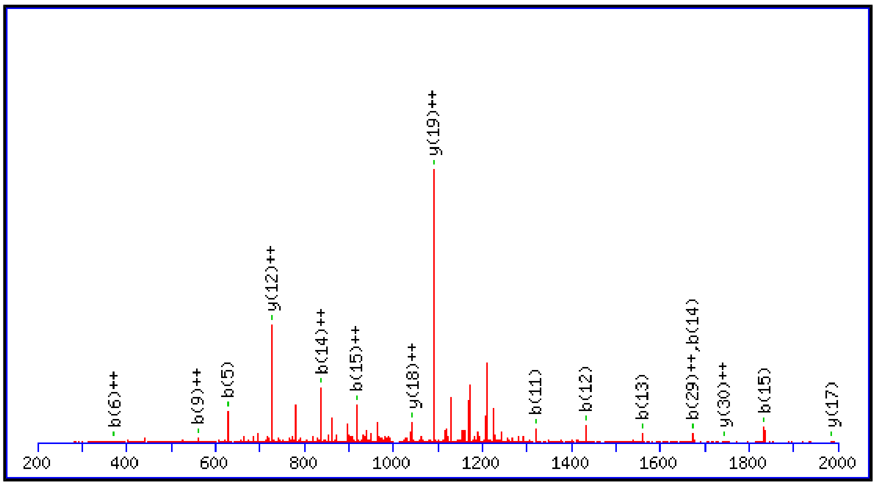
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28332: 4010.823096 from(1003.713050,4+) intensity(52049.0156) rtinseconds(2024) scans(5069) index(12773)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4436_scans__5069
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

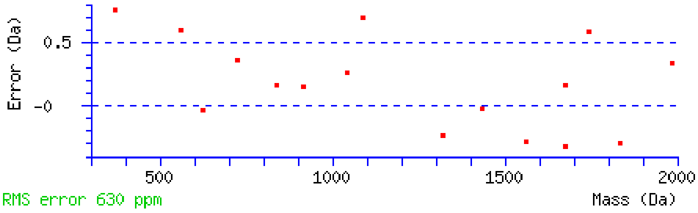
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

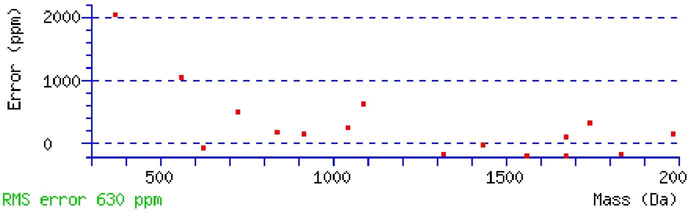


```
Monoisotopic mass of neutral peptide Mr(calc): 4010.8059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6      : Deamidated (NQ)
N32     : Deamidated (NQ)
Ions Score: 43  Expect: 0.0085
Matches : 16/376 fragment ions using 18 most intense peaks    (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3825.7339	1913.3706	3808.7074	1904.8573	3807.7234	1904.3653	33
3	399.1663	200.0868			381.1557	191.0815	P	3710.7070	1855.8571	3693.6804	1847.3439	3692.6964	1846.8518	32
4	528.2089	264.6081			510.1983	255.6028	E	3613.6542	1807.3308	3596.6277	1798.8175	3595.6437	1798.3255	31
5	***627.2773***	314.1423			609.2667	305.1370	V	3484.6116	1742.8095	3467.5851	1734.2962	3466.6011	1733.8042	30
6	742.3042	***371.6558***	725.2777	363.1425	724.2937	362.6505	N	3385.5432	1693.2752	3368.5167	1684.7620	3367.5327	1684.2700	29
7	902.3349	451.6711	885.3083	443.1578	884.3243	442.6658	C	3270.5163	1635.7618	3253.4897	1627.2485	3252.5057	1626.7565	28
8	989.3669	495.1871	972.3404	486.6738	971.3564	486.1818	S	3110.4856	1555.7465	3093.4591	1547.2332	3092.4751	1546.7412	27
9	1120.4074	***560.7073***	1103.3809	552.1941	1102.3968	551.7021	M	3023.4536	1512.2304	3006.4270	1503.7172	3005.4430	1503.2252	26
10	1191.4445	596.2259	1174.4180	587.7126	1173.4340	587.2206	A	2892.4131	1446.7102	2875.3866	1438.1969	2874.4025	1437.7049	25
11	***1319.5031***	660.2552	1302.4766	651.7419	1301.4925	651.2499	Q	2821.3760	1411.1916	2804.3494	1402.6784	2803.3654	1402.1864	24
12	***1432.5872***	716.7972	1415.5606	708.2839	1414.5766	707.7919	I	2693.3174	1347.1623	2676.2909	1338.6491	2675.3069	1338.1571	23
13	***1560.6457***	780.8265	1543.6192	772.3132	1542.6352	771.8212	Q	2580.2334	1290.6203	2563.2068	1282.1070	2562.2228	1281.6150	22
14	***1673.7298***	***837.3685***	1656.7033	828.8553	1655.7192	828.3633	L	2452.1748	1226.5910	2435.1482	1218.0778	2434.1642	1217.5857	21
15	***1833.7605***	***917.3839***	1816.7339	908.8706	1815.7499	908.3786	C	2339.0907	1170.0490	2322.0642	1161.5357	2321.0801	1161.0437	20
16	1930.8132	965.9102	1913.7867	957.3970	1912.8027	956.9050	P	2179.0601	1090.0337	2162.0335	1081.5204	2161.0495	1081.0284	19
17	2027.8660	1014.4366	2010.8394	1005.9234	2009.8554	1005.4313	P	2082.0073	1041.5073	2064.9808	1032.9940	2063.9967	1032.5020	18
18	2124.9187	1062.9630	2107.8922	1054.4497	2106.9082	1053.9577	P	1984.9545	992.9809	1967.9280	984.4676	1966.9440	983.9756	17
19	2221.9715	1111.4894	2204.9450	1102.9761	2203.9609	1102.4841	P	1887.9018	944.4545	1870.8752	935.9413	1869.8912	935.4492	16
20	2350.0301	1175.5187	2333.0035	1167.0054	2332.0195	1166.5134	Q	1790.8490	895.9281	1773.8225	887.4149	1772.8384	886.9229	15
21	2463.1142	1232.0607	2446.0876	1223.5474	2445.1036	1223.0554	I	1662.7904	831.8989	1645.7639	823.3856	1644.7799	822.8936	14
22	2560.1669	1280.5871	2543.1404	1272.0738	2542.1564	1271.5818	P	1549.7064	775.3568	1532.6798	766.8435	1531.6958	766.3515	13

23	2674.2098	1337.6086	2657.1833	1329.0953	2656.1993	1328.6033	**N**	1452.6536	726.8304	1435.6271	718.3172	1434.6430	717.8252	**12**
24	2761.2419	1381.1246	2744.2153	1372.6113	2743.2313	1372.1193	**S**	1338.6107	669.8090	1321.5841	661.2957	1320.6001	660.8037	**11**
25	2898.3008	1449.6540	2881.2742	1441.1408	2880.2902	1440.6487	**H**	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**10**
26	3012.3437	1506.6755	2995.3172	1498.1622	2994.3331	1497.6702	**N**	1114.5197	557.7635	1097.4932	549.2502	1096.5092	548.7582	**9**
27	3143.3842	1572.1957	3126.3576	1563.6825	3125.3736	1563.1905	**M**	1000.4768	500.7420	983.4503	492.2288	982.4662	491.7368	**8**
28	3244.4319	1622.7196	3227.4053	1614.2063	3226.4213	1613.7143	**T**	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	**7**
29	3345.4796	***1673.2434***	3328.4530	1664.7301	3327.4690	1664.2381	**T**	768.3886	384.6980	751.3621	376.1847	750.3781	375.6927	**6**
30	3446.5272	1723.7673	3429.5007	1715.2540	3428.5167	1714.7620	**T**	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	**5**
31	3559.6113	1780.3093	3542.5847	1771.7960	3541.6007	1771.3040	**L**	566.2933	283.6503	549.2667	275.1370			**4**
32	3674.6382	1837.8228	3657.6117	1829.3095	3656.6277	1828.8175	**N**	453.2092	227.1082	436.1827	218.5950			**3**
33	3837.7016	1919.3544	3820.6750	1910.8411	3819.6910	1910.3491	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.6	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32 89.82%
30.3	4009.8219	1.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
26.9	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26, N32 2.40%
24.4	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11 1.34%
23.9	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26 1.20%
23.9	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23 1.20%
20.0	4009.8219	1.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
19.0	4010.8059	0.0172	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20 0.39%
18.0	4009.8219	1.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
18.0	4009.8219	1.0012	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	

Mascot: http://www.matrixscience.com/

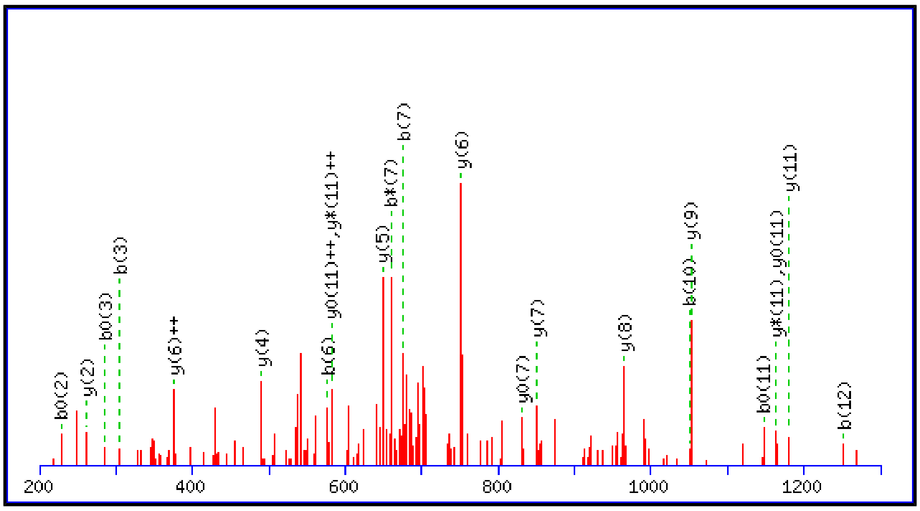
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MDGASNVTCINSR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

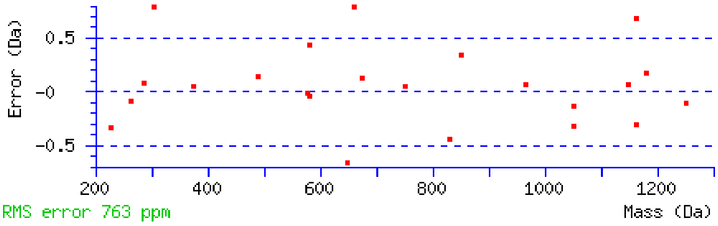
Match to Query 3196: 1425.587808 from(713.801180,2+) intensity(1074.9924) rtinseconds(483) scans(624) index(480)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum437_scans__624
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

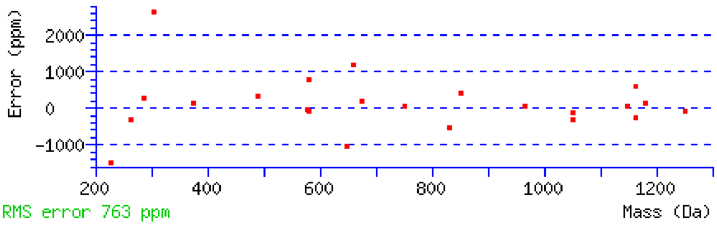
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1425.5864
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
N11 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.0048
Matches : 23/130 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	132.0478	66.5275					M							13
2	247.0747	124.0410			229.0641	115.0357	D	1295.5532	648.2802	1278.5267	639.7670	1277.5427	639.2750	12
3	***304.0962***	152.5517			286.0856	143.5464	G	***1180.5263***	590.7668	1163.4997	582.2535	1162.5157	581.7615	11
4	375.1333	188.0703			357.1227	179.0650	A	1123.5048	562.2560	1106.4783	553.7428	1105.4942	553.2508	10
5	462.1653	231.5863			444.1547	222.5810	S	***1052.4677***	526.7375	1035.4412	518.2242	1034.4571	517.7322	9
6	***577.1923***	289.0998	560.1657	280.5865	559.1817	280.0945	N	***965.4357***	483.2215	948.4091	474.7082	947.4251	474.2162	8
7	***676.2607***	338.6340	659.2341	330.1207	658.2501	329.6287	V	***850.4087***	425.7080	833.3822	417.1947	832.3982	416.7027	7
8	777.3083	389.1578	760.2818	380.6445	759.2978	380.1525	T	***751.3403***	376.1738	734.3138	367.6605	733.3298	367.1685	6
9	937.3390	469.1731	920.3124	460.6599	919.3284	460.1679	C	***650.2926***	325.6500	633.2661	317.1367	632.2821	316.6447	5
10	***1050.4231***	525.7152	1033.3965	517.2019	1032.4125	516.7099	I	***490.2620***	245.6346	473.2354	237.1214	472.2514	236.6293	4
11	1165.4500	583.2286	1148.4235	574.7154	1147.4394	574.2234	N	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
12	***1252.4820***	626.7447	1235.4555	618.2314	1234.4715	617.7394	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MDGASNVTCINSR
(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	1425.5864	0.0014	MDGASNVTCINSR
7.1	1425.5864	0.0014	MVVQNSADAGDMR
7.0	1425.5864	0.0014	MVVQNSADAGDMR
6.2	1424.5903	0.9975	DQENSVQSSNSTK
5.2	1424.5903	0.9975	DQENSVQSSNSTK
5.2	1424.5903	0.9975	DQENSVQSSNSTK
3.4	1424.5903	0.9975	DQENSVQSSNSTK
3.4	1424.5903	0.9975	DQENSVQSSNSTK
3.0	1425.5830	0.0048	ENTNTATPFCNR
3.0	1425.5830	0.0048	QNTNTATPFCNR

Mascot: http://www.matrixscience.com/

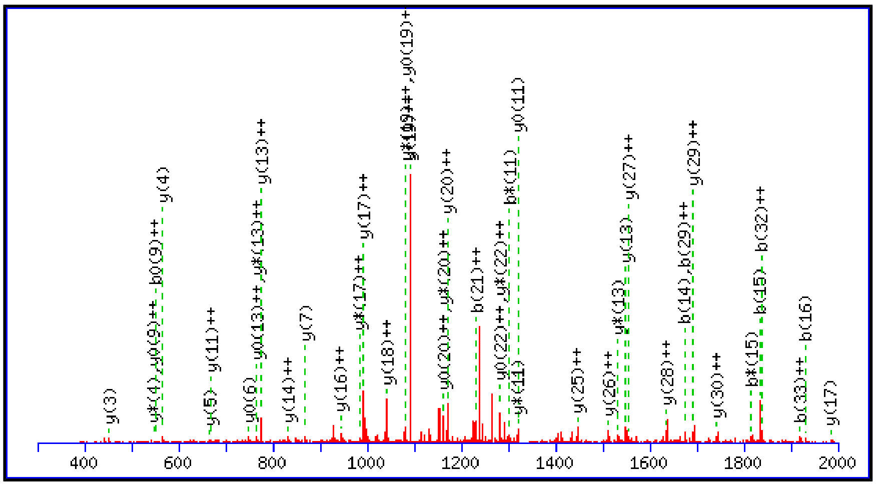
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28336: 4011.839502 from(1338.287110,3+) intensity(0.0000) rtinseconds(2032) scans(5317) index(19779)
Title: 111019_Est_MI_YP_G_09Spectrum4694_scans__5317
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

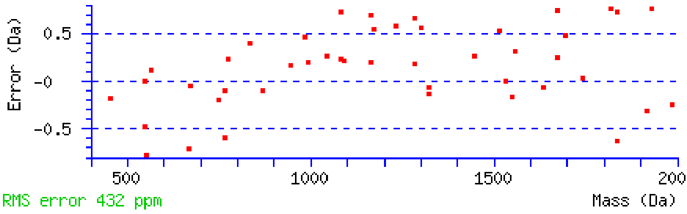
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

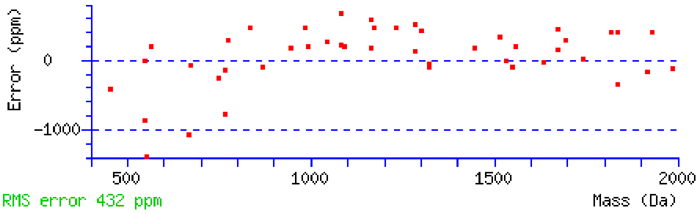


Monoisotopic mass of neutral peptide Mr(calc): 4009.8219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N26 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.033
Matches : 45/376 fragment ions using 97 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3824.7499	1912.8786	3807.7234	1904.3653	3806.7394	1903.8733	33
3	399.1663	200.0868			381.1557	191.0815	P	3709.7230	1855.3651	3692.6964	1846.8518	3691.7124	1846.3598	32
4	528.2089	264.6081			510.1983	255.6028	E	3612.6702	1806.8387	3595.6437	1798.3255	3594.6596	1797.8335	31
5	627.2773	314.1423			609.2667	305.1370	V	3483.6276	1742.3174	3466.6011	1733.8042	3465.6171	1733.3122	30
6	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	N	3384.5592	1692.7832	3367.5327	1684.2700	3366.5486	1683.7780	29
7	901.3509	451.1791	884.3243	442.6658	883.3403	442.1738	C	3270.5163	1635.7618	3253.4897	1627.2485	3252.5057	1626.7565	28
8	988.3829	494.6951	971.3564	486.1818	970.3723	485.6898	S	3110.4856	1555.7465	3093.4591	1547.2332	3092.4751	1546.7412	27
9	1119.4234	560.2153	1102.3968	551.7021	1101.4128	551.2101	M	3023.4536	1512.2304	3006.4270	1503.7172	3005.4430	1503.2252	26
10	1190.4605	595.7339	1173.4340	587.2206	1172.4499	586.7286	A	2892.4131	1446.7102	2875.3866	1438.1969	2874.4025	1437.7049	25
11	1318.5191	659.7632	1301.4925	651.2499	1300.5085	650.7579	Q	2821.3760	1411.1916	2804.3494	1402.6784	2803.3654	1402.1864	24
12	1431.6031	716.3052	1414.5766	707.7919	1413.5926	707.2999	I	2693.3174	1347.1623	2676.2909	1338.6491	2675.3069	1338.1571	23
13	1559.6617	780.3345	1542.6352	771.8212	1541.6512	771.3292	Q	2580.2334	1290.6203	2563.2068	1282.1070	2562.2228	1281.6150	22
14	1672.7458	836.8765	1655.7192	828.3633	1654.7352	827.8713	L	2452.1748	1226.5910	2435.1482	1218.0778	2434.1642	1217.5857	21
15	1832.7764	916.8919	1815.7499	908.3786	1814.7659	907.8866	C	2339.0907	1170.0490	2322.0642	1161.5357	2321.0801	1161.0437	20
16	1929.8292	965.4182	1912.8027	956.9050	1911.8186	956.4130	P	2179.0601	1090.0337	2162.0335	1081.5204	2161.0495	1081.0284	19
17	2026.8820	1013.9446	2009.8554	1005.4313	2008.8714	1004.9393	P	2082.0073	1041.5073	2064.9808	1032.9940	2063.9967	1032.5020	18
18	2123.9347	1062.4710	2106.9082	1053.9577	2105.9242	1053.4657	P	**1984.9545**	992.9809	1967.9280	984.4676	1966.9440	983.9756	17
19	2220.9875	1110.9974	2203.9609	1102.4841	2202.9769	1101.9921	P	1887.9018	944.4545	1870.8752	935.9413	1869.8912	935.4492	16
20	2349.0461	1175.0267	2332.0195	1166.5134	2331.0355	1166.0214	Q	1790.8490	895.9281	1773.8225	887.4149	1772.8384	886.9229	15
21	2462.1301	**1231.5687**	2445.1036	1223.0554	2444.1196	1222.5634	I	1662.7904	831.8989	1645.7639	823.3856	1644.7799	822.8936	14
22	2559.1829	1280.0951	2542.1564	1271.5818	2541.1723	1271.0898	P	**1549.7064**	775.3568	1532.6798	766.8435	1531.6958	766.3515	13
23	2673.2258	1337.1166	2656.1993	1328.6033	2655.2153	1328.1113	N	1452.6536	726.8304	1435.6271	718.3172	1434.6430	717.8252	12

24	2760.2579	1380.6326	2743.2313	1372.1193	2742.2473	1371.6273	**S**	1338.6107	669.8090	1321.5841	661.2957	1320.6001	660.8037	**11**
25	2897.3168	1449.1620	2880.2902	1440.6487	2879.3062	1440.1567	**H**	1251.5786	626.2930	1234.5521	617.7797	1233.5681	617.2877	**10**
26	3012.3437	1506.6755	2995.3172	1498.1622	2994.3331	1497.6702	**N**	1114.5197	557.7635	1097.4932	549.2502	1096.5092	548.7582	**9**
27	3143.3842	1572.1957	3126.3576	1563.6825	3125.3736	1563.1905	**M**	999.4928	500.2500	982.4662	491.7368	981.4822	491.2448	**8**
28	3244.4319	1622.7196	3227.4053	1614.2063	3226.4213	1613.7143	**T**	**868.4523**	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3345.4796	**1673.2434**	3328.4530	1664.7301	3327.4690	1664.2381	**T**	767.4046	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3446.5272	1723.7673	3429.5007	1715.2540	3428.5167	1714.7620	**T**	**666.3570**	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3559.6113	1780.3093	3542.5847	1771.7960	3541.6007	1771.3040	**L**	**565.3093**	283.1583	548.2827	274.6450			**4**
32	3673.6542	**1837.3307**	3656.6277	1828.8175	3655.6437	1828.3255	**N**	**452.2252**	226.6162	435.1987	218.1030			**3**
33	3836.7176	**1918.8624**	3819.6910	1910.3491	3818.7070	1909.8571	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.4	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N26 32.39%
37.3	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23 32.17%
34.4	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N32 16.50%
31.9	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11 9.17%
30.0	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20 5.93%
26.2	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6 2.45%
23.7	4009.8219	2.0176	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13 1.39%
9.7	4011.8532	-0.0137	FTVDTISAGQGDVMVFVEDPEGNKEEAQVTPDSDKNK	
6.7	4009.8139	2.0256	SASNGIMGTSSNGLNGQNGIMGQNGMMGPQPIVSYPSSNR	
5.3	4010.8269	1.0126	LYELDLTNQTLDDAVQWTSTWSSPLGCNASFSPHR	

Mascot: http://www.matrixscience.com/

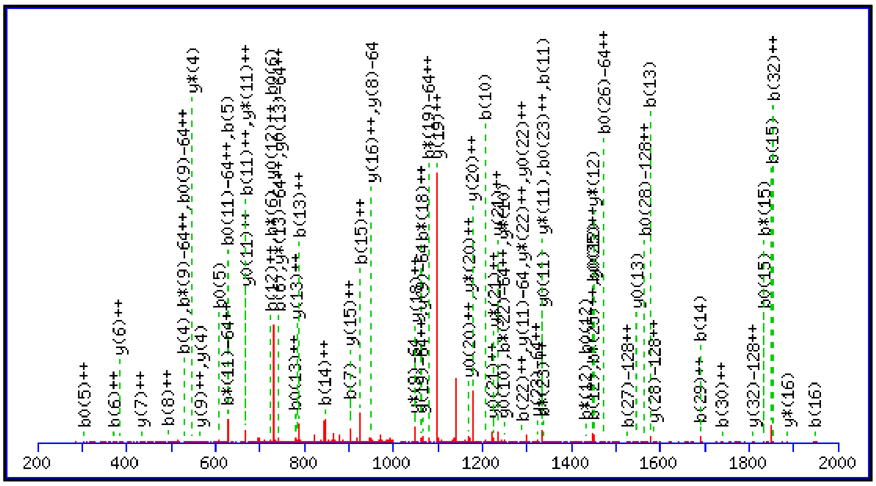
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 28359: 4042.810256 from(1011.709840,4+) intensity(30689.8672) rtinseconds(1571) scans(4053) index(6452)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum3562_scans__4053
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

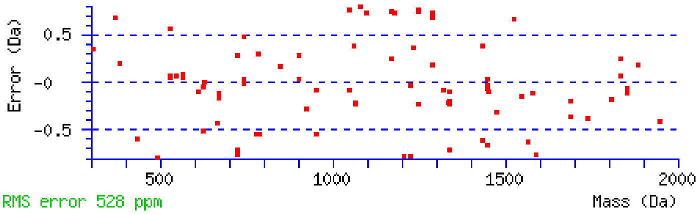
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

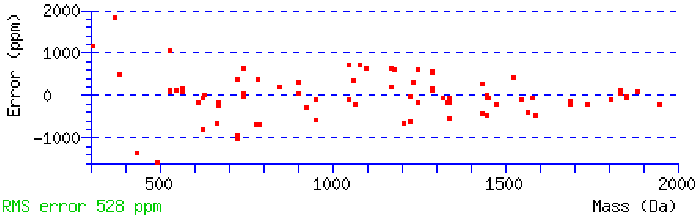


Monoisotopic mass of neutral peptide Mr(calc): 4042.7958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q11 : Deamidated (NQ)
M27 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.033
Matches : 84/682 fragment ions using 132 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469					W							34
2	302.1135	151.5604			284.1030	142.5551	D	3857.7238	1929.3655	3840.6972	1920.8522	3839.7132	1920.3602	33
3	399.1663	200.0868			381.1557	191.0815	P	3742.6968	1871.8520	3725.6703	1863.3388	3724.6863	1862.8468	32
4	***528.2089***	264.6081			510.1983	255.6028	E	3645.6441	1823.3257	3628.6175	1814.8124	3627.6335	1814.3204	31
5	***627.2773***	314.1423			609.2667	305.1370	V	3516.6015	1758.8044	3499.5749	1750.2911	3498.5909	1749.7991	30
6	***742.3042***	***371.6558***	725.2777	363.1425	724.2937	362.6505	N	3417.5330	1709.2702	3400.5065	1700.7569	3399.5225	1700.2649	29
7	***902.3349***	451.6711	885.3083	443.1578	884.3243	442.6658	C	3302.5061	1651.7567	3285.4796	1643.2434	3284.4955	1642.7514	28
8	989.3669	***495.1871***	972.3404	486.6738	971.3564	486.1818	S	3142.4755	1571.7414	3125.4489	1563.2281	3124.4649	1562.7361	27
9	1136.4023	568.7048	1119.3758	560.1915	1118.3918	559.6995	M	3055.4434	1528.2254	3038.4169	1519.7121	3037.4329	1519.2201	26
10	***1207.4394***	604.2234	1190.4129	595.7101	1189.4289	595.2181	A	2908.4080	1454.7077	2891.3815	1446.1944	2890.3975	1445.7024	25
11	***1336.4820***	***668.7447***	1319.4555	660.2314	1318.4715	659.7394	Q	2837.3709	1419.1891	2820.3444	1410.6758	2819.3603	1410.1838	24
12	***1449.5661***	***725.2867***	1432.5395	716.7734	1431.5555	716.2814	I	2708.3283	1354.6678	2691.3018	1346.1545	2690.3178	1345.6625	23
13	***1577.6247***	***789.3160***	1560.5981	780.8027	1559.6141	780.3107	Q	2595.2443	1298.1258	2578.2177	1289.6125	2577.2337	1289.1205	22
14	***1690.7087***	***845.8580***	1673.6822	837.3447	1672.6982	836.8527	L	2467.1857	1234.0965	2450.1591	1225.5832	2449.1751	1225.0912	21
15	***1850.7394***	***925.8733***	1833.7128	917.3601	1832.7288	916.8680	C	2354.1016	1177.5544	2337.0751	1169.0412	2336.0910	1168.5492	20
16	***1947.7922***	974.3997	1930.7656	965.8864	1929.7816	965.3944	P	2194.0710	1097.5391	2177.0444	1089.0258	2176.0604	1088.5338	19
17	2044.8449	1022.9261	2027.8184	1014.4128	2026.8343	1013.9208	P	2097.0182	1049.0127	2079.9917	1040.4995	2079.0076	1040.0075	18
18	2141.8977	1071.4525	2124.8711	1062.9392	2123.8871	1062.4472	P	1999.9654	1000.4864	1982.9389	991.9731	1981.9549	991.4811	17
19	2238.9504	1119.9789	2221.9239	1111.4656	2220.9399	1110.9736	P	1902.9127	951.9600	1885.8861	943.4467	1884.9021	942.9547	16
20	2367.0090	1184.0081	2349.9825	1175.4949	2348.9985	1175.0029	Q	1805.8599	903.4336	1788.8334	894.9203	1787.8493	894.4283	15
21	2480.0931	1240.5502	2463.0665	1232.0369	2462.0825	1231.5449	I	1677.8013	839.4043	1660.7748	830.8910	1659.7908	830.3990	14

22	2577.1458	***1289.0766***	2560.1193	1280.5633	2559.1353	1280.0713	**P**	1564.7173	782.8623	1547.6907	774.3490	1546.7067	773.8570	**13**
23	2691.1888	1346.0980	2674.1622	1337.5848	2673.1782	1337.0927	**N**	1467.6645	734.3359	1450.6380	725.8226	1449.6539	725.3306	**12**
24	2778.2208	1389.6140	2761.1943	1381.1008	2760.2102	1380.6088	**S**	1353.6216	677.3144	1336.5950	668.8012	1335.6110	668.3091	**11**
25	2915.2797	1458.1435	2898.2532	1449.6302	2897.2692	1449.1382	**H**	1266.5895	633.7984	1249.5630	625.2851	1248.5790	624.7931	**10**
26	3029.3226	1515.1650	3012.2961	1506.6517	3011.3121	1506.1597	**N**	1129.5306	565.2690	1112.5041	556.7557	1111.5201	556.2637	**9**
27	3176.3580	1588.6827	3159.3315	1580.1694	3158.3475	1579.6774	**M**	1015.4877	508.2475	998.4612	499.7342	997.4771	499.2422	**8**
28	3277.4057	1639.2065	3260.3792	1630.6932	3259.3952	1630.2012	**T**	868.4523	434.7298	851.4258	426.2165	850.4417	425.7245	**7**
29	3378.4534	***1689.7303***	3361.4269	1681.2171	3360.4428	1680.7251	**T**	767.4046	384.2060	750.3781	375.6927	749.3941	375.2007	**6**
30	3479.5011	***1740.2542***	3462.4745	1731.7409	3461.4905	1731.2489	**T**	666.3570	333.6821	649.3304	325.1688	648.3464	324.6768	**5**
31	3592.5851	1796.7962	3575.5586	1788.2829	3574.5746	1787.7909	**L**	565.3093	283.1583	548.2827	274.6450			**4**
32	3706.6281	***1853.8177***	3689.6015	1845.3044	3688.6175	1844.8124	**N**	452.2252	226.6162	435.1987	218.1030			**3**
33	3869.6914	1935.3493	3852.6648	1926.8361	3851.6808	1926.3441	**Y**	338.1823	169.5948	321.1557	161.0815			**2**
34							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
35.2	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, Q11 48.34%
33.0	4041.8118	0.9985	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
31.2	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q11, Q13 19.16%
29.2	4041.8118	0.9985	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
29.0	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N6, N32 11.41%
25.5	4041.8118	0.9985	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	
25.4	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q13, Q20 5.00%
21.7	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated Q20, N23 2.13%
20.2	4042.7958	0.0145	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	Deamidated N23, N26 1.53%
18.6	4041.8118	0.9985	WDPEVNCSMAQIQLCPPPPQIPNSHNMTTTLNYR	

Mascot: http://www.matrixscience.com/

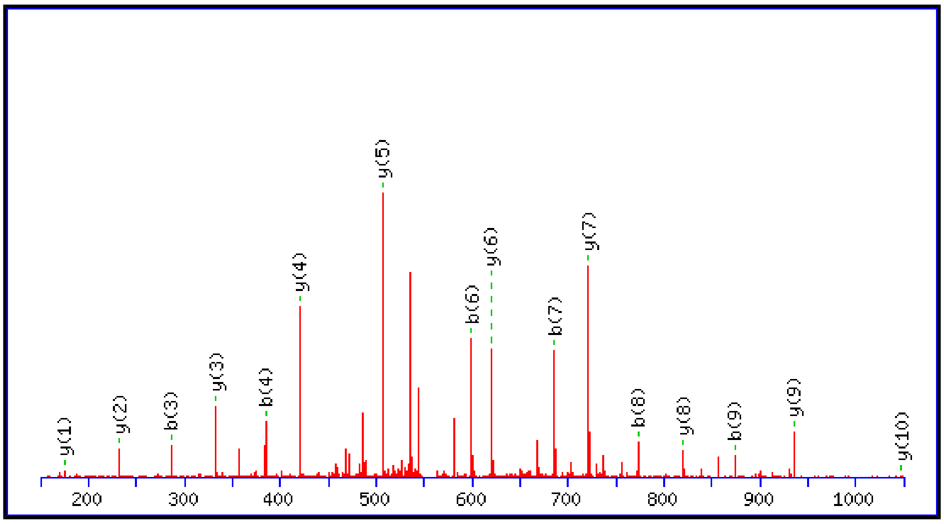
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLNVTLSSTGR**
Found in **F5GXS0** in **con_Xuniprot_HUMAN3**, F5GXS0_HUMAN Complement C4-B OS=Homo sapiens GN=C4B_2 PE=2 SV=1

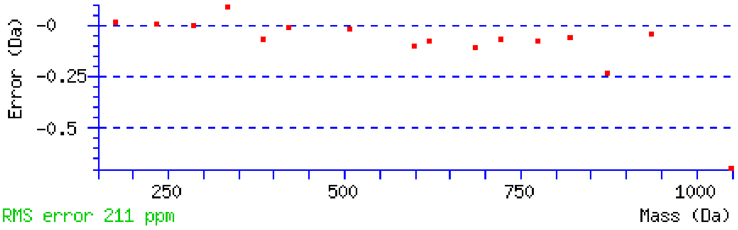
Match to Query 747: 1104.580008 from(553.297280,2+) intensity(92521.2891) rtinseconds(765) scans(1670) index(10787)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum1396_scans__1670
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

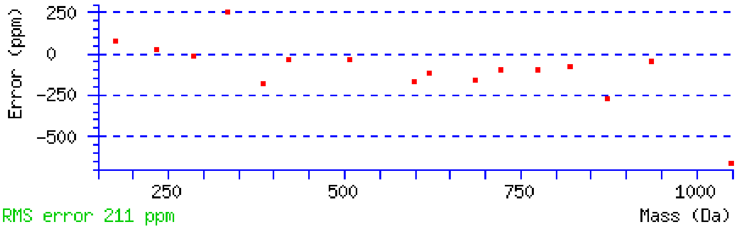
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1104.5775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 115 **Expect:** 7.3e-010
Matches : 16/104 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							11
2	171.1128	86.0600					L	***1048.5633***	524.7853	1031.5368	516.2720	1030.5528	515.7800	10
3	**286.1397**	143.5735	269.1132	135.0602			N	***935.4793***	468.2433	918.4527	459.7300	917.4687	459.2380	9
4	**385.2082**	193.1077	368.1816	184.5944			V	***820.4523***	410.7298	803.4258	402.2165	802.4417	401.7245	8
5	486.2558	243.6316	469.2293	235.1183	468.2453	234.6263	T	***721.3839***	361.1956	704.3573	352.6823	703.3733	352.1903	7
6	**599.3399**	300.1736	582.3134	291.6603	581.3293	291.1683	L	***620.3362***	310.6717	603.3097	302.1585	602.3257	301.6665	6
7	**686.3719**	343.6896	669.3454	335.1763	668.3614	334.6843	S	***507.2522***	254.1297	490.2256	245.6164	489.2416	245.1244	5
8	**773.4040**	387.2056	756.3774	378.6923	755.3934	378.2003	S	***420.2201***	210.6137	403.1936	202.1004	402.2096	201.6084	4
9	**874.4516**	437.7295	857.4251	429.2162	856.4411	428.7242	T	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
10	931.4731	466.2402	914.4466	457.7269	913.4625	457.2349	G	***232.1404***	116.5738	215.1139	108.0606			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GLNVTLSSTGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
115.0	1104.5775	0.0025	GLNVTLSSTGR
14.1	1104.5750	0.0050	SMGLPLQFGR
10.9	1103.5724	1.0077	FVHTSKTER
10.6	1104.5788	0.0012	QHQILHSSR
10.6	1104.5788	0.0012	QHQLLHSSR
10.0	1104.5775	0.0025	GTSSLTVNLGR
8.9	1103.5757	1.0043	QTKVIDMGGR
7.2	1103.5822	0.9978	QLNTLLSTGR
6.9	1104.5775	0.0025	GLDIESTSKR
5.4	1103.5757	1.0043	NAVARACLTK

Mascot: http://www.matrixscience.com/

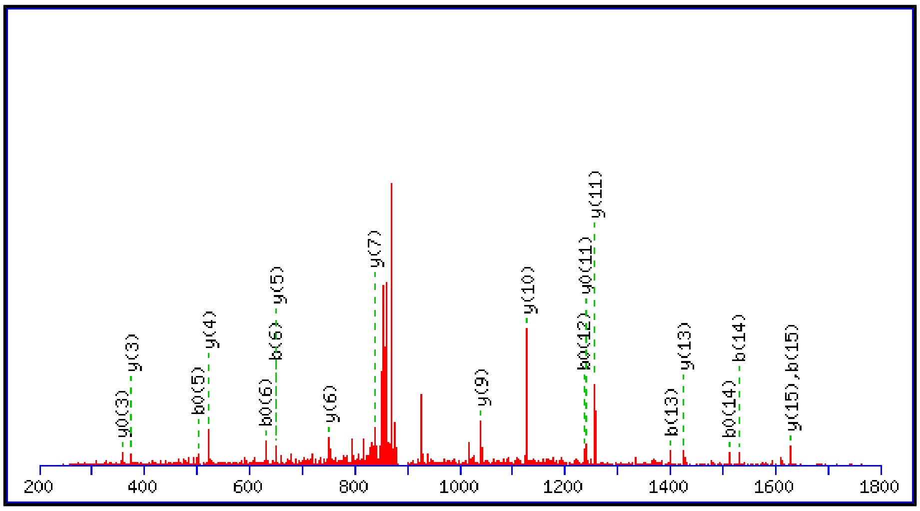
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSDGLESNSSTQFEVK**
Found in **F5GXS0** in **con_Xuniprot_HUMAN3**, F5GXS0_HUMAN Complement C4-B OS=Homo sapiens GN=C4B_2 PE=2 SV=1

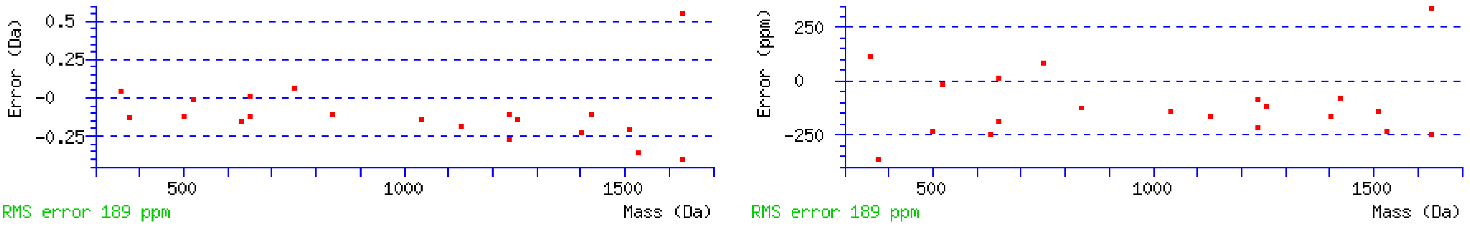
Match to Query 10011: 1774.797888 from(888.406220,2+) intensity(25752.5645) rtinseconds(1176) scans(2598) index(736)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum2219_scans__2598
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1774.7897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 74 **Expect:** 5.8e-006
Matches : 20/160 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	148.0757	74.5415					F							16
2	235.1077	118.0575			217.0972	109.0522	S	***1628.7286***	814.8679	1611.7021	806.3547	1610.7180	805.8627	15
3	350.1347	175.5710			332.1241	166.5657	D	1541.6966	771.3519	1524.6700	762.8387	1523.6860	762.3466	14
4	407.1561	204.0817			389.1456	195.0764	G	***1426.6696***	713.8385	1409.6431	705.3252	1408.6591	704.8332	13
5	520.2402	260.6237			502.2296	251.6185	L	1369.6482	685.3277	1352.6216	676.8144	1351.6376	676.3224	12
6	**649.2828**	325.1450			631.2722	316.1397	E	***1256.5641***	628.7857	1239.5376	620.2724	1238.5535	619.7804	11
7	736.3148	368.6610			718.3042	359.6558	S	***1127.5215***	564.2644	1110.4950	555.7511	1109.5109	555.2591	10
8	851.3418	426.1745	834.3152	417.6612	833.3312	417.1692	N	***1040.4895***	520.7484	1023.4629	512.2351	1022.4789	511.7431	9
9	938.3738	469.6905	921.3472	461.1773	920.3632	460.6852	S	925.4625	463.2349	908.4360	454.7216	907.4520	454.2296	8
10	1025.4058	513.2065	1008.3793	504.6933	1007.3952	504.2013	S	***838.4305***	419.7189	821.4040	411.2056	820.4199	410.7136	7
11	1126.4535	563.7304	1109.4269	555.2171	1108.4429	554.7251	T	***751.3985***	376.2029	734.3719	367.6896	733.3879	367.1976	6
12	1254.5121	627.7597	1237.4855	619.2464	1236.5015	618.7544	Q	***650.3508***	325.6790	633.3243	317.1658	632.3402	316.6738	5
13	**1401.5805**	701.2939	1384.5539	692.7806	1383.5699	692.2886	F	***522.2922***	261.6498	505.2657	253.1365	504.2817	252.6445	4
14	**1530.6231**	765.8152	1513.5965	757.3019	1512.6125	756.8099	E	***375.2238***	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	**1629.6915**	815.3494	1612.6649	806.8361	1611.6809	806.3441	V	246.1812	123.5942	229.1547	115.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of FSDGLESNSSTQFEVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.8	1774.7897	0.0082	FSDGLESNSSTQFEVK	Deamidated N8 99.97%
38.2	1774.7897	0.0082	FSDGLESNSSTQFEVK	Deamidated Q12 0.03%
6.0	1772.7848	2.0131	KVMEYMAQEEEELK	
5.9	1773.7887	1.0092	DQTRPPCGQSRCPSK	
5.4	1773.7913	1.0066	TGSAAMEQLMTDLFSR	
3.9	1774.8043	-0.0064	QEDQQLDIQVMAEAR	
3.4	1774.7940	0.0039	LMKMEESTGVQFCAK	
3.4	1774.7940	0.0039	LMKMEESTGVQFCAK	
3.0	1774.8057	-0.0078	NCFPTATNTNHKNGAK	
2.7	1773.7887	1.0092	DQTRPPCGQSRCPSK	

Mascot: http://www.matrixscience.com/

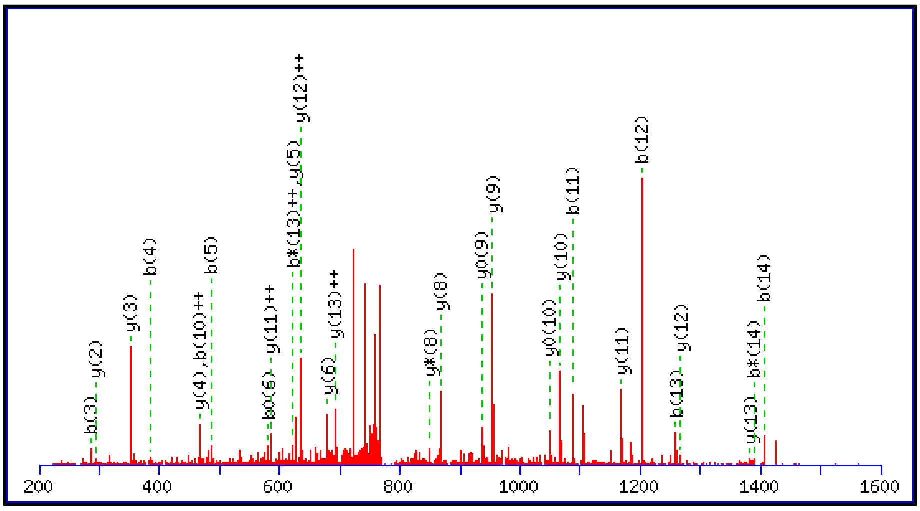
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLNVTLSSTGRNGFK**
Found in **F5GXS0** in **con_Xuniprot_HUMAN3**, F5GXS0_HUMAN Complement C4-B OS=Homo sapiens GN=C4B_2 PE=2 SV=1

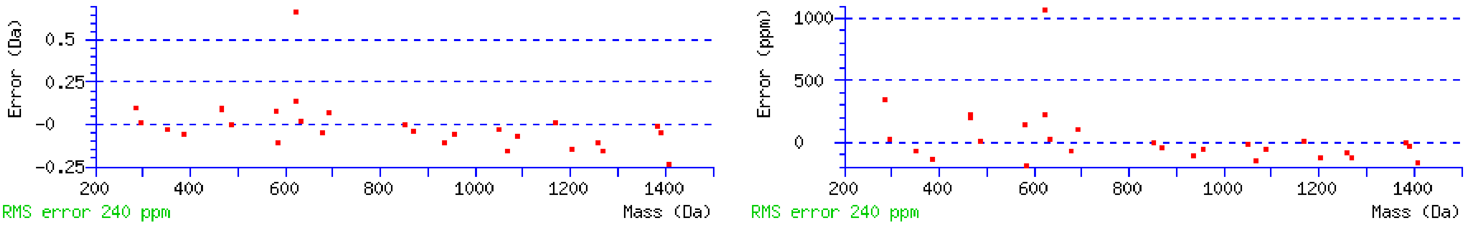
Match to Query 7008: 1551.794748 from(776.904650,2+) intensity(60743.7969) rtinseconds(1027) scans(2423) index(2565)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum2054_scans__2423
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1551.7893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 70 **Expect:** 2.3e-005
Matches : 28/144 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	58.0287	29.5180					G							15
2	171.1128	86.0600					L	1495.7751	748.3912	1478.7486	739.8779	1477.7645	739.3859	14
3	**286.1397**	143.5735	269.1132	135.0602			N	***1382.6910***	691.8492	1365.6645	683.3359	1364.6805	682.8439	13
4	**385.2082**	193.1077	368.1816	184.5944			V	***1267.6641***	634.3357	1250.6375	625.8224	1249.6535	625.3304	12
5	**486.2558**	243.6316	469.2293	235.1183	468.2453	234.6263	T	***1168.5957***	584.8015	1151.5691	576.2882	1150.5851	575.7962	11
6	599.3399	300.1736	582.3134	291.6603	581.3293	291.1683	L	***1067.5480***	534.2776	1050.5215	525.7644	1049.5374	525.2724	10
7	686.3719	343.6896	669.3454	335.1763	668.3614	334.6843	S	***954.4639***	477.7356	937.4374	469.2223	936.4534	468.7303	9
8	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	S	***867.4319***	434.2196	850.4054	425.7063	849.4213	425.2143	8
9	874.4516	437.7295	857.4251	429.2162	856.4411	428.7242	T	780.3999	390.7036	763.3733	382.1903	762.3893	381.6983	7
10	931.4731	466.2402	914.4466	457.7269	913.4625	457.2349	G	***679.3522***	340.1797	662.3257	331.6665			6
11	**1087.5742**	544.2907	1070.5477	535.7775	1069.5636	535.2855	R	***622.3307***	311.6690	605.3042	303.1557			5
12	**1202.6012**	601.8042	1185.5746	593.2909	1184.5906	592.7989	N	***466.2296***	233.6185	449.2031	225.1052			4
13	**1259.6226**	630.3149	1242.5961	621.8017	1241.6121	621.3097	G	***351.2027***	176.1050	334.1761	167.5917			3
14	**1406.6910**	703.8492	1389.6645	695.3359	1388.6805	694.8439	F	***294.1812***	147.5942	277.1547	139.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of GLNVTLSSTGRNGFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
69.8	1551.7893	0.0055	GLNVTLSSTGRNGFK
5.2	1551.7893	0.0055	QRETAVTSEQKFK
5.0	1551.7926	0.0021	NRITLMSQSSTGKK
2.1	1550.7861	1.0086	LLEESEKSSTGLMK
2.0	1551.7966	-0.0019	LNEKLSIDMAQFK
1.9	1551.8005	-0.0057	AEREEKPKHTEAK
1.9	1551.7901	0.0046	REAFCQLLQLMK
0.6	1551.7980	-0.0033	ARSFCKTHASLFK

Mascot: http://www.matrixscience.com/

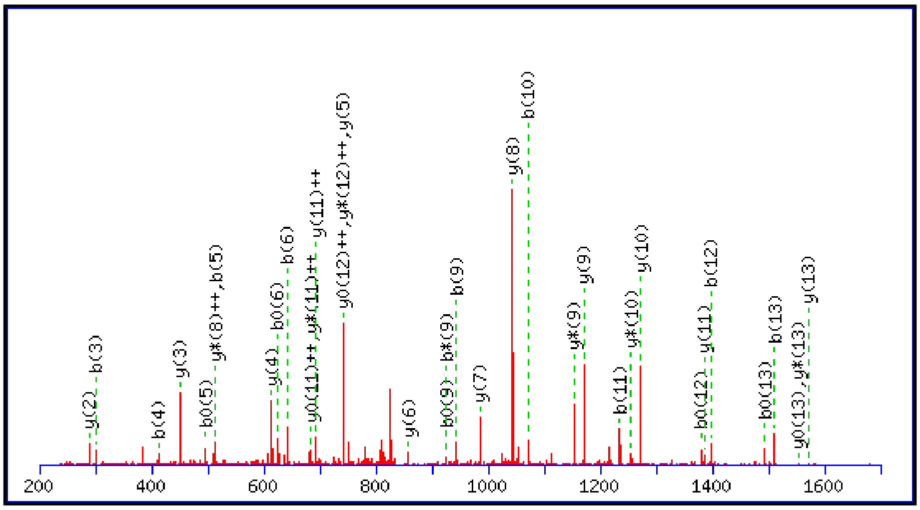
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LANLTQGEDQYYLR**
Found in **H0YAS8** in **con_Xuniprot_HUMAN3**, H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1

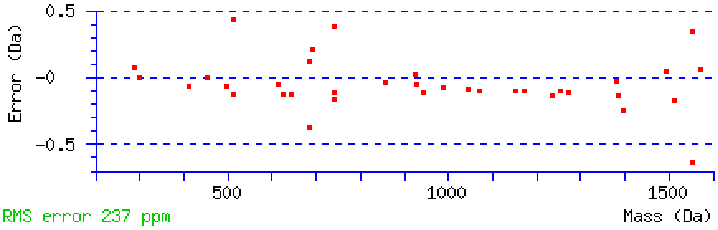
Match to Query 8590: 1683.817568 from(842.916060,2+) intensity(430116.6875) rtinseconds(1379) scans(3367) index(26593)
Title: 111019_Est_MI_YS_G_09Spectrum2906_scans__3367
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

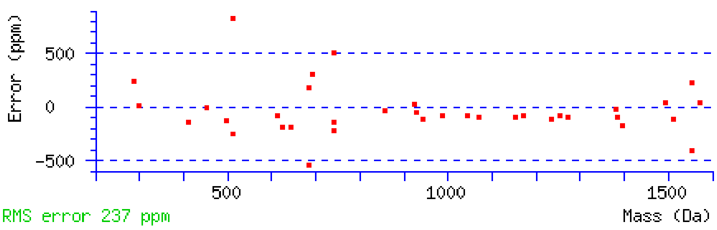
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1683.8104
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 89 **Expect:** 2.7e-007
Matches : 36/134 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	114.0913	57.5493					L							14
2	185.1285	93.0679					A	***1571.7336***	786.3705	1554.7071	777.8572	1553.7231	777.3652	13
3	**300.1554**	150.5813	283.1288	142.0681			N	1500.6965	750.8519	1483.6700	742.3386	1482.6860	741.8466	12
4	**413.2395**	207.1234	396.2129	198.6101			L	***1385.6696***	693.3384	1368.6430	684.8252	1367.6590	684.3331	11
5	**514.2871**	257.6472	497.2606	249.1339	496.2766	248.6419	T	***1272.5855***	636.7964	1255.5590	628.2831	1254.5749	627.7911	10
6	**642.3457**	321.6765	625.3192	313.1632	624.3352	312.6712	Q	***1171.5378***	586.2726	1154.5113	577.7593	1153.5273	577.2673	9
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	G	***1043.4793***	522.2433	1026.4527	513.7300	1025.4687	513.2380	8
8	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	E	***986.4578***	493.7325	969.4312	485.2193	968.4472	484.7272	7
9	**943.4367**	472.2220	926.4102	463.7087	925.4262	463.2167	D	***857.4152***	429.2112	840.3886	420.6980	839.4046	420.2060	6
10	**1071.4953**	536.2513	1054.4687	527.7380	1053.4847	527.2460	Q	***742.3883***	371.6978	725.3617	363.1845			5
11	**1234.5586**	617.7830	1217.5321	609.2697	1216.5481	608.7777	Y	***614.3297***	307.6685	597.3031	299.1552			4
12	**1397.6220**	699.3146	1380.5954	690.8013	1379.6114	690.3093	Y	***451.2663***	226.1368	434.2398	217.6235			3
13	**1510.7060**	755.8566	1493.6795	747.3434	1492.6955	746.8514	L	***288.2030***	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LANLTQGEDQYYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.7	1683.8104	0.0072	LANLTQGEDQYYLR	Deamidated N3 97.41%
72.8	1683.8104	0.0072	LANLTQGEDQYYLR	Deamidated Q6 2.50%
58.0	1683.8104	0.0072	LANLTQGEDQYYLR	Deamidated Q10 0.08%
6.9	1683.8104	0.0071	DVSPPSTWSVDQPIR	
6.7	1683.8216	-0.0041	HAPGSEQTVTYEPLR	
6.6	1683.8178	-0.0002	IGEDVDLFDMKQFK	
6.6	1683.8178	-0.0002	LGEDVDLFDMKQFK	
5.3	1683.8113	0.0063	ETPGFQLLGMYCLR	
3.0	1683.8185	-0.0009	MRDAGDPSPPNKMLR	
3.0	1681.8159	2.0017	TANDTSTEAYNLLLR	

Mascot: http://www.matrixscience.com/

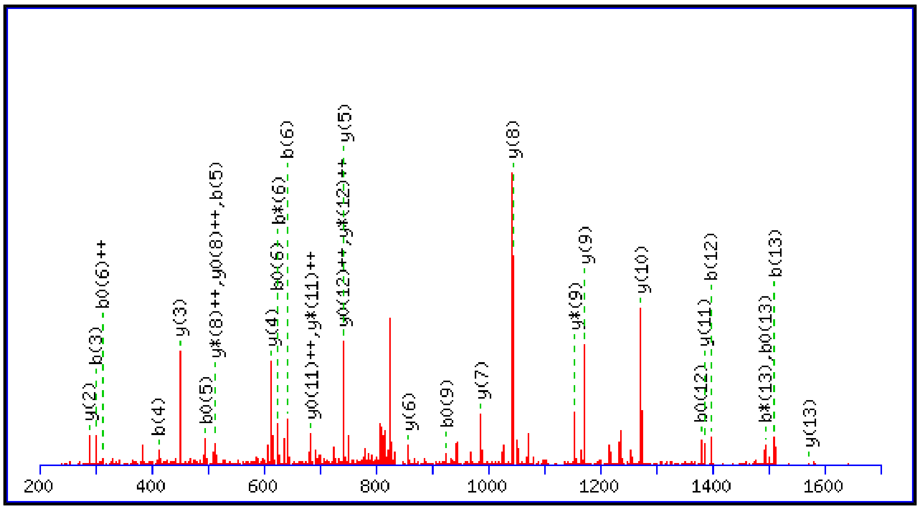
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LANLTQGEDQYYLR**
Found in **H0YAS8** in **con_Xuniprot_HUMAN3**, H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1

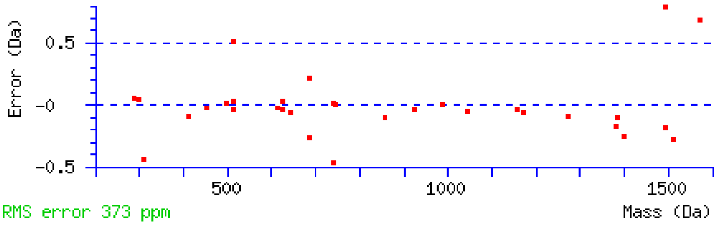
Match to Query 8611: 1684.793888 from(843.404220,2+) intensity(33906.6406) rtinseconds(1418) scans(3375) index(20265)
Title: 111019_Est_MI_YP_G_10Spectrum2941_scans__3375
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

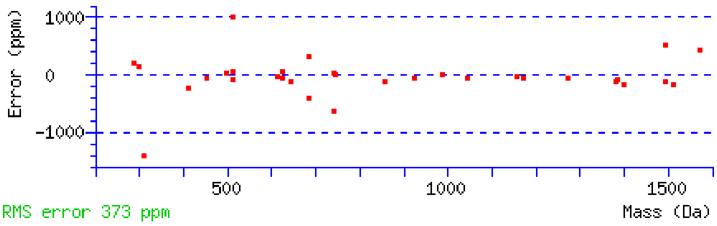
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1684.7944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Q10 : Deamidated (NQ)
Ions Score: 79 **Expect:** 2e-006
Matches : 32/134 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	114.0913	57.5493					L							14
2	185.1285	93.0679					A	***1572.7176***	786.8625	1555.6911	778.3492	1554.7071	777.8572	13
3	**300.1554**	150.5813	283.1288	142.0681			N	1501.6805	751.3439	1484.6540	742.8306	1483.6700	742.3386	12
4	**413.2395**	207.1234	396.2129	198.6101			L	***1386.6536***	693.8304	1369.6270	685.3172	1368.6430	684.8252	11
5	**514.2871**	257.6472	497.2606	249.1339	496.2766	248.6419	T	***1273.5695***	637.2884	1256.5430	628.7751	1255.5590	628.2831	10
6	**642.3457**	321.6765	625.3192	313.1632	624.3352	312.6712	Q	***1172.5218***	586.7646	1155.4953	578.2513	1154.5113	577.7593	9
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	G	***1044.4633***	522.7353	1027.4367	514.2220	1026.4527	513.7300	8
8	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	E	***987.4418***	494.2245	970.4153	485.7113	969.4312	485.2193	7
9	943.4367	472.2220	926.4102	463.7087	925.4262	463.2167	D	***858.3992***	429.7032	841.3727	421.1900	840.3886	420.6980	6
10	1072.4793	536.7433	1055.4528	528.2300	1054.4687	527.7380	Q	***743.3723***	372.1898	726.3457	363.6765			5
11	1235.5426	618.2750	1218.5161	609.7617	1217.5321	609.2697	Y	***614.3297***	307.6685	597.3031	299.1552			4
12	**1398.6060**	699.8066	1381.5794	691.2933	1380.5954	690.8013	Y	***451.2663***	226.1368	434.2398	217.6235			3
13	**1511.6900**	756.3487	1494.6635	747.8354	1493.6795	747.3434	L	***288.2030***	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LANLTQGEDQYYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
79.5	1684.7944	-0.0005	LANLTQGEDQYYLR	Deamidated N3, Q10 68.61%
75.9	1684.7944	-0.0005	LANLTQGEDQYYLR	Deamidated N3, Q6 30.23%
61.8	1684.7944	-0.0005	LANLTQGEDQYYLR	Deamidated Q6, Q10 1.17%
9.1	1683.7965	0.9974	TLVWNASVNGHTGGNR	
6.7	1684.7978	-0.0039	LGQLETNMETLYTR	
4.2	1684.7917	0.0021	GQHQVSPHLGQPGADR	
3.5	1684.8025	-0.0086	MRDAGDPSPPNKMLR	
2.8	1684.8018	-0.0079	IGEDVDLFDMKQFK	
2.8	1684.8018	-0.0079	LGEDVDLFDMKQFK	
2.4	1684.7912	0.0027	KCKPQMNYDKLSR	

Mascot: http://www.matrixscience.com/

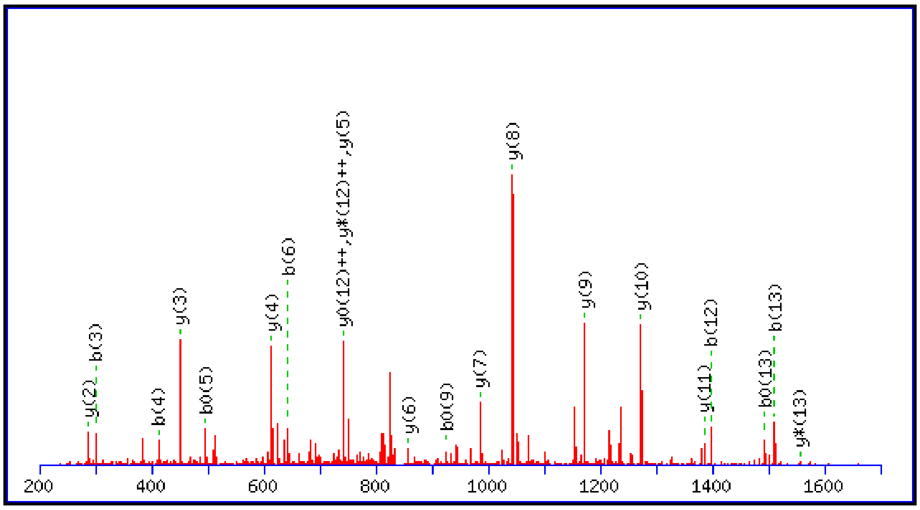
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LANLTQGEDQYYLR**
Found in **H0YAS8** in **con_Xuniprot_HUMAN3**, H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1

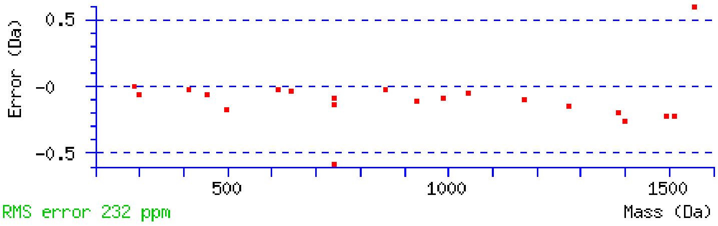
Match to Query 8615: 1684.795828 from(843.405190,2+) intensity(83411.5313) rtinseconds(1465) scans(3483) index(27408)
Title: 111019_Est_MI_YS_G_10Spectrum2992_scans__3483
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

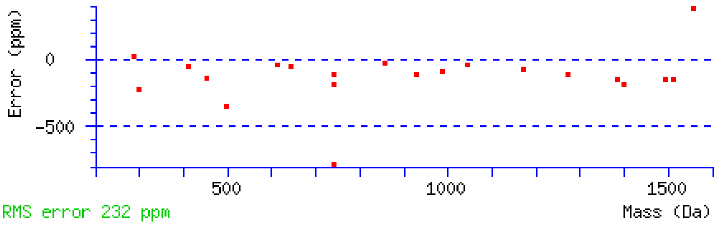
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1684.7944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Q6 : Deamidated (NQ)
Ions Score: 74 **Expect:** 7.8e-006
Matches : 21/134 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	185.1285	93.0679					A	1572.7176	786.8625	1555.6911	778.3492	1554.7071	777.8572	13
3	**300.1554**	150.5813	283.1288	142.0681			N	1501.6805	751.3439	1484.6540	742.8306	1483.6700	742.3386	12
4	**413.2395**	207.1234	396.2129	198.6101			L	***1386.6536***	693.8304	1369.6270	685.3172	1368.6430	684.8252	11
5	514.2871	257.6472	497.2606	249.1339	496.2766	248.6419	T	***1273.5695***	637.2884	1256.5430	628.7751	1255.5590	628.2831	10
6	**643.3297**	322.1685	626.3032	313.6552	625.3192	313.1632	Q	***1172.5218***	586.7646	1155.4953	578.2513	1154.5113	577.7593	9
7	700.3512	350.6792	683.3246	342.1660	682.3406	341.6740	G	***1043.4793***	522.2433	1026.4527	513.7300	1025.4687	513.2380	8
8	829.3938	415.2005	812.3672	406.6873	811.3832	406.1953	E	***986.4578***	493.7325	969.4312	485.2193	968.4472	484.7272	7
9	944.4207	472.7140	927.3942	464.2007	926.4102	463.7087	D	***857.4152***	429.2112	840.3886	420.6980	839.4046	420.2060	6
10	1072.4793	536.7433	1055.4528	528.2300	1054.4687	527.7380	Q	***742.3883***	371.6978	725.3617	363.1845			5
11	1235.5426	618.2750	1218.5161	609.7617	1217.5321	609.2697	Y	***614.3297***	307.6685	597.3031	299.1552			4
12	**1398.6060**	699.8066	1381.5794	691.2933	1380.5954	690.8013	Y	***451.2663***	226.1368	434.2398	217.6235			3
13	**1511.6900**	756.3487	1494.6635	747.8354	1493.6795	747.3434	L	***288.2030***	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LANLTQGEDQYYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
73.8	1684.7944	0.0014	LANLTQGEDQYYLR	Deamidated N3, Q6 95.84%
59.0	1684.7944	0.0014	LANLTQGEDQYYLR	Deamidated N3, Q10 3.18%
53.8	1684.7944	0.0014	LANLTQGEDQYYLR	Deamidated Q6, Q10 0.97%
5.8	1684.8025	-0.0066	MRDAGDPSPPNKMLR	
5.5	1684.7978	-0.0019	LGQLETNMETLYTR	
3.3	1684.7912	0.0046	KCKPQMNYDKLSR	
3.1	1684.7953	0.0005	ETPGFQLLGMYCLR	
2.9	1683.7965	0.9993	TLVWNASVNGHTGGNR	

Mascot: http://www.matrixscience.com/

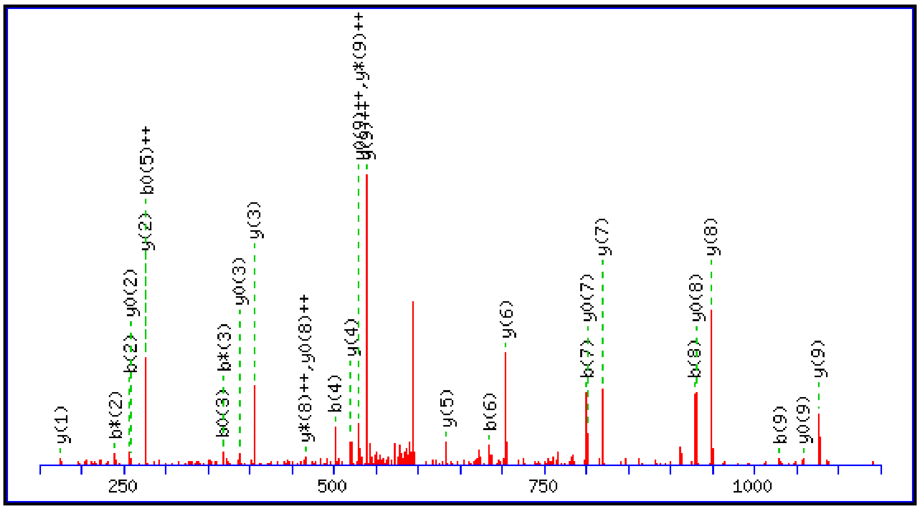
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KKEDALNETR**
Found in **E5RGB0** in **con_Xuniprot_HUMAN3**, E5RGB0_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=2 SV=1

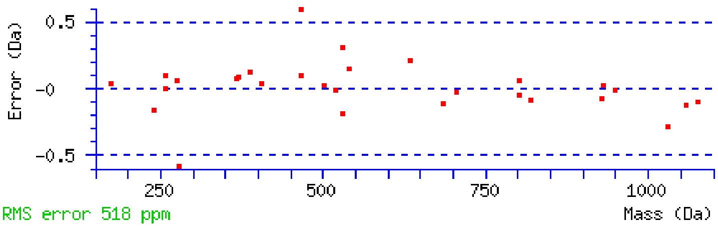
Match to Query 1679: 1203.611708 from(602.813130,2+) intensity(10490.8281) rtinseconds(158) scans(133) index(15561)
Title: 111019_Est_MI_YP_G_05Spectrum70_scans__133
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

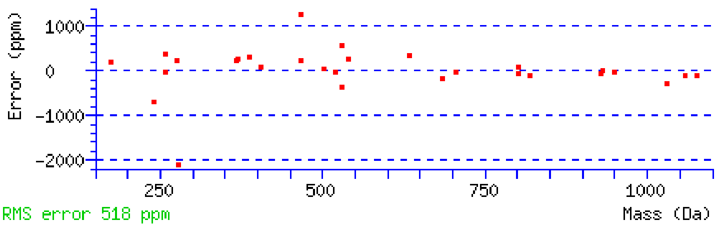
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1203.6095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 73 **Expect:** 1.4e-005
Matches : 29/102 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	129.1022	65.0548	112.0757	56.5415			K							10
2	**257.1972**	129.1022	240.1707	120.5890			K	***1076.5218***	538.7646	1059.4953	530.2513	1058.5113	529.7593	9
3	386.2398	193.6235	369.2132	185.1103	368.2292	184.6183	E	***948.4269***	474.7171	931.4003	466.2038	930.4163	465.7118	8
4	**501.2667**	251.1370	484.2402	242.6237	483.2562	242.1317	D	***819.3843***	410.1958	802.3577	401.6825	801.3737	401.1905	7
5	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	A	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	6
6	**685.3879**	343.1976	668.3614	334.6843	667.3774	334.1923	L	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
7	**800.4149**	400.7111	783.3883	392.1978	782.4043	391.7058	N	***520.2362***	260.6217	503.2096	252.1084	502.2256	251.6164	4
8	**929.4575**	465.2324	912.4309	456.7191	911.4469	456.2271	E	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	3
9	**1030.5051**	515.7562	1013.4786	507.2429	1012.4946	506.7509	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KKEDALNETR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.8	1203.6095	0.0022	KKEDALNETR
38.8	1203.6135	-0.0018	KKQNLQWEK
28.7	1203.6169	-0.0052	QKEDLELAMK
21.3	1202.6143	0.9974	RVQVSQVQEK
20.5	1203.6135	-0.0018	KKENQIEWK
14.6	1203.6095	0.0022	VGTGKQNELTR
14.4	1202.6044	1.0073	FAGQLQGQPTR
14.4	1203.6095	0.0022	SELNSRLEEK
14.0	1203.6095	0.0022	SSQSKGPKEEK
11.3	1202.6044	1.0073	FAGQLQGQPTR

Mascot: http://www.matrixscience.com/

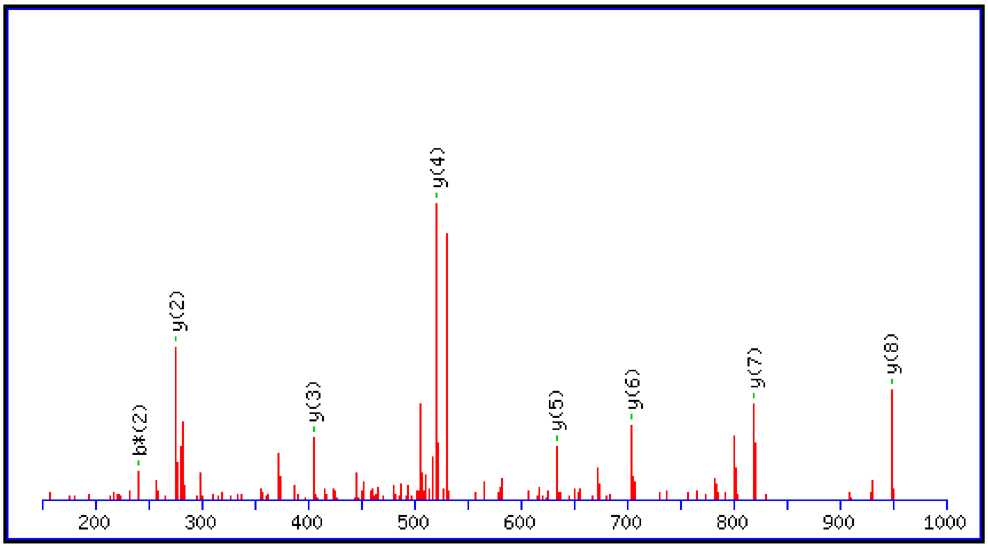
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDALNETR**
Found in **E5RGB0** in **con_Xuniprot_HUMAN3**, E5RGB0_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=2 SV=1

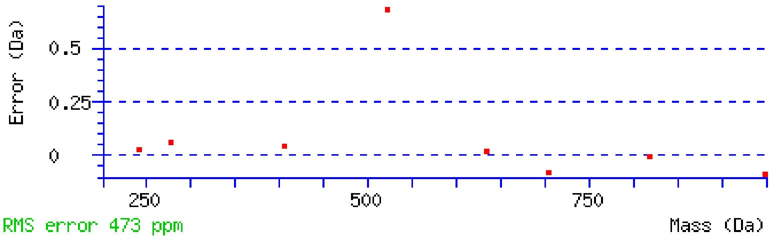
Match to Query 213: 1075.517288 from(538.765920,2+) intensity(2928.1667) rtinseconds(183) scans(234) index(25940)
Title: 111019_Est_MI_YS_G_08Spectrum160_scans__234
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

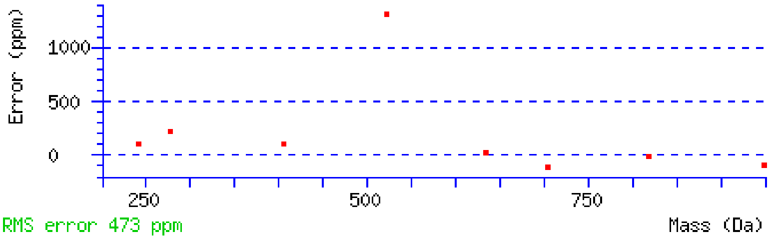
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1075.5145
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 69 **Expect:** 2.4e-005
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	129.1022	65.0548	112.0757	56.5415			K							9
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	***948.4269***	474.7171	931.4003	466.2038	930.4163	465.7118	8
3	373.1718	187.0895	356.1452	178.5763	355.1612	178.0842	D	***819.3843***	410.1958	802.3577	401.6825	801.3737	401.1905	7
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	A	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	6
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	L	***633.3202***	317.1638	616.2937	308.6505	615.3097	308.1585	5
6	672.3199	336.6636	655.2933	328.1503	654.3093	327.6583	N	***520.2362***	260.6217	503.2096	252.1084	502.2256	251.6164	4
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	E	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	3
8	902.4102	451.7087	885.3836	443.1954	884.3996	442.7034	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KEDALNETR
(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	1075.5145	0.0028	KEDALNETR
33.9	1075.5145	0.0027	KADELDETR
21.2	1075.5185	-0.0013	KQNLQWEK
21.1	1075.5145	0.0028	KQREEEEK
21.0	1075.5186	-0.0013	KQWQEVEK
20.7	1075.5186	-0.0013	KELWQDEK
20.3	1075.5145	0.0028	KDGKQNEEK
20.2	1075.5185	-0.0013	KWEIQNEK
19.1	1075.5146	0.0027	ISGEGQTQQK
14.5	1075.5145	0.0028	EKEREQEK

Mascot: http://www.matrixscience.com/

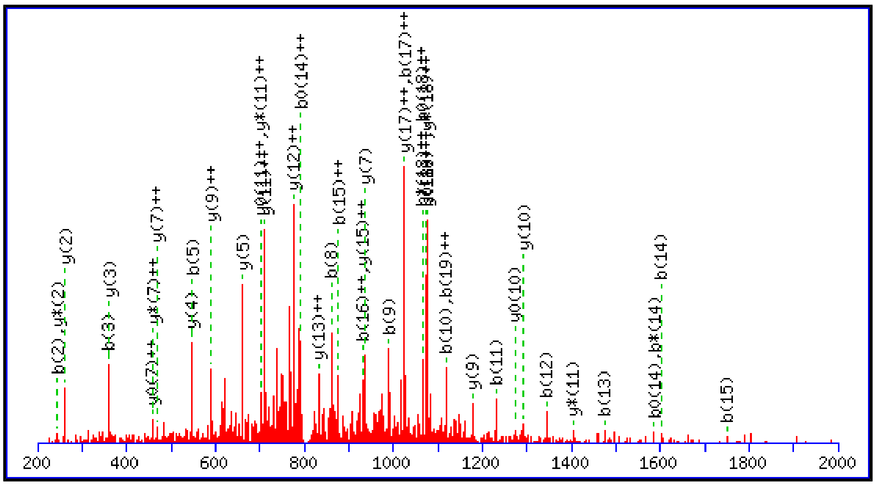
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLNTSSLLEQLNEQFNWVSR**
Found in **H0YAS8** in **con_Xuniprot_HUMAN3**, H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1

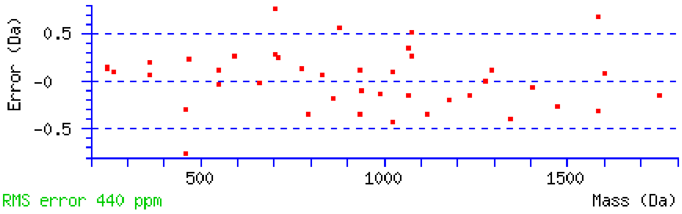
Match to Query 21498: 2409.169992 from(804.063940,3+) intensity(27012.7285) rtinseconds(2760) scans(7112) index(1010)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum6240_scans__7112
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

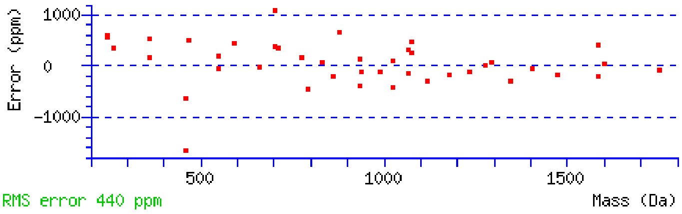
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2409.1634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 56 **Expect:** 0.00069
Matches : 44/216 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	132.0478	66.5275					M							20
2	***245.1318***	123.0696					L	2279.1303	1140.0688	2262.1037	1131.5555	2261.1197	1131.0635	19
3	***360.1588***	180.5830	343.1322	172.0697			N	2166.0462	1083.5267	2149.0196	1075.0135	2148.0356	1074.5214	18
4	461.2064	231.1069	444.1799	222.5936	443.1959	222.1016	T	2051.0192	1026.0133	2033.9927	1017.5000	2033.0087	1017.0080	17
5	***548.2385***	274.6229	531.2119	266.1096	530.2279	265.6176	S	1949.9716	975.4894	1932.9450	966.9761	1931.9610	966.4841	16
6	635.2705	318.1389	618.2440	309.6256	617.2599	309.1336	S	1862.9395	931.9734	1845.9130	923.4601	1844.9290	922.9681	15
7	748.3546	374.6809	731.3280	366.1676	730.3440	365.6756	L	1775.9075	888.4574	1758.8810	879.9441	1757.8969	879.4521	14
8	***861.4386***	431.2230	844.4121	422.7097	843.4281	422.2177	L	1662.8234	831.9154	1645.7969	823.4021	1644.8129	822.9101	13
9	***990.4812***	495.7443	973.4547	487.2310	972.4707	486.7390	E	1549.7394	775.3733	1532.7128	766.8601	1531.7288	766.3680	12
10	***1118.5398***	559.7735	1101.5133	551.2603	1100.5292	550.7683	Q	1420.6968	710.8520	1403.6702	702.3388	1402.6862	701.8467	11
11	***1231.6239***	616.3156	1214.5973	607.8023	1213.6133	607.3103	L	***1292.6382***	646.8227	1275.6117	638.3095	1274.6276	637.8175	10
12	***1345.6668***	673.3370	1328.6402	664.8238	1327.6562	664.3318	N	***1179.5541***	590.2807	1162.5276	581.7674	1161.5436	581.2754	9
13	***1474.7094***	737.8583	1457.6828	729.3451	1456.6988	728.8530	E	1065.5112	533.2592	1048.4847	524.7460	1047.5007	524.2540	8
14	***1602.7680***	801.8876	1585.7414	793.3743	1584.7574	792.8823	Q	***936.4686***	468.7380	919.4421	460.2247	918.4581	459.7327	7
15	***1749.8364***	**875.4218**	1732.8098	866.9086	1731.8258	866.4165	F	808.4100	404.7087	791.3835	396.1954	790.3995	395.7034	6
16	1863.8793	**932.4433**	1846.8528	923.9300	1845.8687	923.4380	N	***661.3416***	331.1745	644.3151	322.6612	643.3311	322.1692	5
17	2049.9586	**1025.4829**	2032.9321	1016.9697	2031.9481	1016.4777	W	***547.2987***	274.1530	530.2722	265.6397	529.2881	265.1477	4
18	2149.0270	**1075.0172**	2132.0005	1066.5039	2131.0165	1066.0119	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
19	2236.0591	**1118.5332**	2219.0325	1110.0199	2218.0485	1109.5279	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
20							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of MLNTSSLLEQLNEQFNWVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
56.0	2409.1634	0.0066	MLNTSSLLEQLNEQFNWVSR	Deamidated N3 92.22%
41.6	2409.1634	0.0066	MLNTSSLLEQLNEQFNWVSR	Deamidated Q10 3.37%
39.7	2409.1634	0.0066	MLNTSSLLEQLNEQFNWVSR	Deamidated N12 2.14%
37.7	2409.1634	0.0066	MLNTSSLLEQLNEQFNWVSR	Deamidated Q14 1.35%
36.0	2409.1634	0.0066	MLNTSSLLEQLNEQFNWVSR	Deamidated N16 0.92%
9.5	2407.1689	2.0011	NAEFEREQLITGSVESPCTLK	
7.4	2407.1550	2.0150	VCAQYLAEAEQAKAQAEERSR	
5.3	2408.1675	1.0025	ENVACMRAVSGINNTITVLTAR	
4.9	2407.1714	1.9986	NELESQSSNSLTKNTLQNRLK	
4.9	2407.1714	1.9986	NELESQSSNSLTKNTLQNRLK	

Mascot: http://www.matrixscience.com/

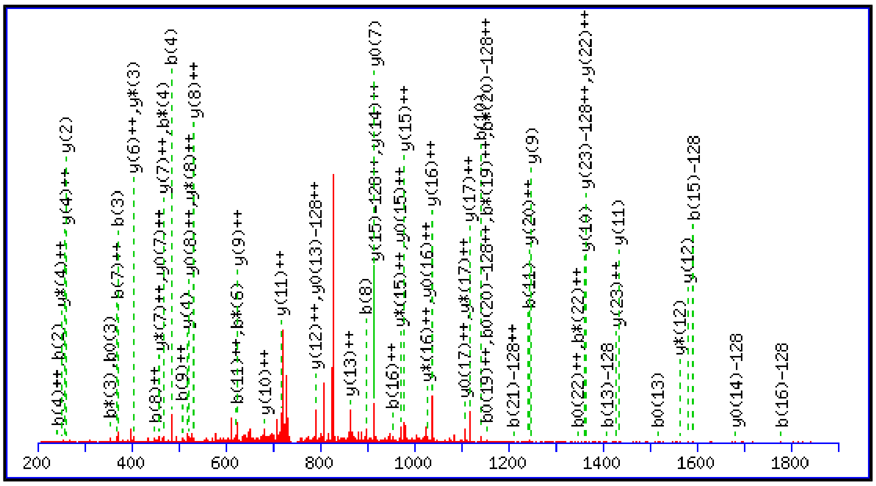
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LKELPGVCNETMMALWEECKPCLK**
Found in **E5RGB0** in **con_Xuniprot_HUMAN3**, E5RGB0_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=2 SV=1

Match to Query 27058: 2968.356376 from(743.096370,4+) intensity(12222.9014) rtinseconds(1442) scans(3582) index(24497)
Title: 111019_Est_MI_YS_G_06Spectrum3103_scans__3582
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

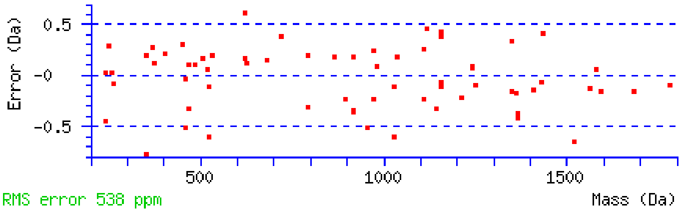
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

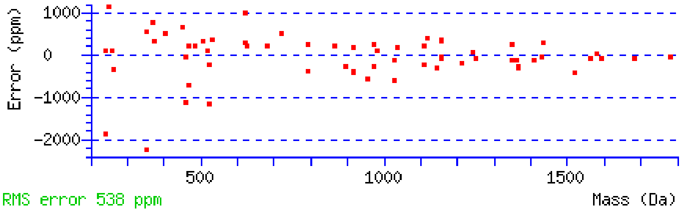


Monoisotopic mass of neutral peptide Mr(calc): 2968.3512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 54 **Expect:** 0.00068
Matches : 67/402 fragment ions using 138 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							24
2	**242.1863**	121.5968	225.1598	113.0835			K	2856.2745	1428.6409	2839.2479	1420.1276	2838.2639	1419.6356	23
3	**371.2289**	186.1181	354.2023	177.6048	353.2183	177.1128	E	2728.1795	1364.5934	2711.1530	1356.0801	2710.1690	1355.5881	22
4	**484.3130**	**242.6601**	467.2864	234.1468	466.3024	233.6548	L	2599.1369	1300.0721	2582.1104	1291.5588	2581.1264	1291.0668	21
5	581.3657	291.1865	564.3392	282.6732	563.3552	282.1812	P	2486.0529	1243.5301	2469.0263	1235.0168	2468.0423	1234.5248	20
6	638.3872	319.6972	621.3606	311.1840	620.3766	310.6919	G	2389.0001	1195.0037	2371.9736	1186.4904	2370.9895	1185.9984	19
7	737.4556	**369.2314**	720.4291	360.7182	719.4450	360.2262	V	2331.9786	1166.4930	2314.9521	1157.9797	2313.9681	1157.4877	18
8	**897.4863**	**449.2468**	880.4597	440.7335	879.4757	440.2415	C	2232.9102	1116.9588	2215.8837	1108.4455	2214.8997	1107.9535	17
9	1012.5132	**506.7602**	995.4866	498.2470	994.5026	497.7550	N	2072.8796	1036.9434	2055.8530	1028.4302	2054.8690	1027.9381	16
10	**1141.5558**	571.2815	1124.5292	562.7683	1123.5452	562.2762	E	1957.8526	979.4300	1940.8261	970.9167	1939.8421	970.4247	15
11	**1242.6035**	**621.8054**	1225.5769	613.2921	1224.5929	612.8001	T	1828.8100	914.9087	1811.7835	906.3954	1810.7995	905.9034	14
12	1389.6389	695.3231	1372.6123	686.8098	1371.6283	686.3178	M	1727.7624	864.3848	1710.7358	855.8715	1709.7518	855.3795	13
13	1536.6743	768.8408	1519.6477	760.3275	1518.6637	759.8355	M	**1580.7270**	790.8671	1563.7004	782.3538	1562.7164	781.8618	12
14	1607.7114	804.3593	1590.6848	795.8461	1589.7008	795.3540	A	**1433.6916**	717.3494	1416.6650	708.8361	1415.6810	708.3441	11
15	1720.7954	860.9014	1703.7689	852.3881	1702.7849	851.8961	L	**1362.6545**	681.8309	1345.6279	673.3176	1344.6439	672.8256	10
16	1906.8748	**953.9410**	1889.8482	945.4277	1888.8642	944.9357	W	**1249.5704**	625.2888	1232.5438	616.7756	1231.5598	616.2836	9
17	2035.9173	1018.4623	2018.8908	1009.9490	2017.9068	1009.4570	E	1063.4911	532.2492	1046.4645	523.7359	1045.4805	523.2439	8
18	2164.9599	1082.9836	2147.9334	1074.4703	2146.9494	1073.9783	E	934.4485	467.7279	917.4219	459.2146	916.4379	458.7226	7
19	2324.9906	1162.9989	2307.9640	1154.4857	2306.9800	1153.9937	C	805.4059	403.2066	788.3793	394.6933			6
20	2453.0856	1227.0464	2436.0590	1218.5331	2435.0750	1218.0411	K	645.3752	323.1913	628.3487	314.6780			5
21	2550.1383	1275.5728	2533.1118	1267.0595	2532.1278	1266.5675	P	**517.2803**	259.1438	500.2537	250.6305			4
22	2710.1690	1355.5881	2693.1424	1347.0748	2692.1584	1346.5828	C	420.2275	210.6174	403.2010	202.1041			3

23	2823.2530	1412.1302	2806.2265	1403.6169	2805.2425	1403.1249	**L**	**260.1969**	130.6021	243.1703	122.0888			**2**
24							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LKELPGVCNETMMALWEECKPCLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
54.3	2968.3512	0.0051	LKELPGVCNETMMALWEECKPCLK
49.7	2967.3672	0.9891	LKELPGVCNETMMALWEECKPCLK
8.8	2967.3610	0.9954	IWDFVHLADYTMGRESPTGVSDGWGR
4.7	2968.3591	-0.0028	MNFASVFAVLFNGCTGIMAGANMSGELK
4.0	2966.3421	2.0143	LLQETMYMTVSIIDRFMQNNCVPK
3.6	2968.3695	-0.0131	VMSELRQSMETFNNSAERGFEAYLK
1.5	2967.3556	1.0008	EQVMGSEPGPAFPTQPQKTQSDPQEPR
1.3	2966.3484	2.0079	AGINQNMDAVTEELQAKTGSLEEMTQR
1.3	2966.3484	2.0079	AGINQNMDAVTEELQAKTGSLEEMTQR
1.3	2966.3484	2.0079	AGINQNMDAVTEELQAKTGSLEEMTQR

Mascot: http://www.matrixscience.com/

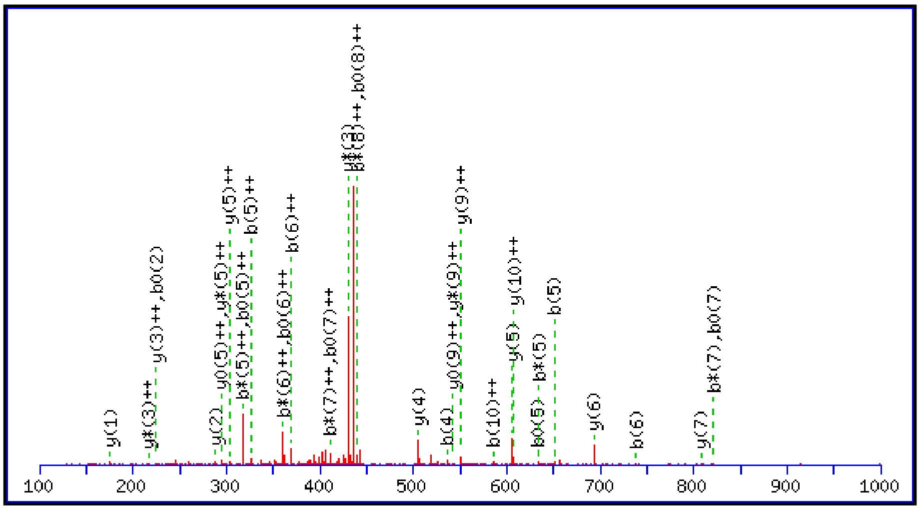
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EIRHNSTGCLR**
Found in **E7ETB4** in **con_Xuniprot_HUMAN3**, E7ETB4_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=2 SV=1

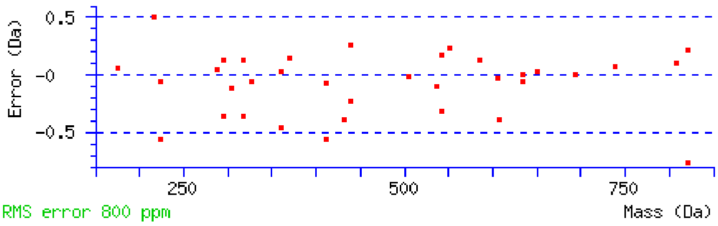
Match to Query 2035: 1342.642932 from(448.554920,3+) intensity(4826.1958) rtinseconds(144) scans(216) index(24317)
Title: 111019_Est_MI_YS_G_06Spectrum168_scans__216
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

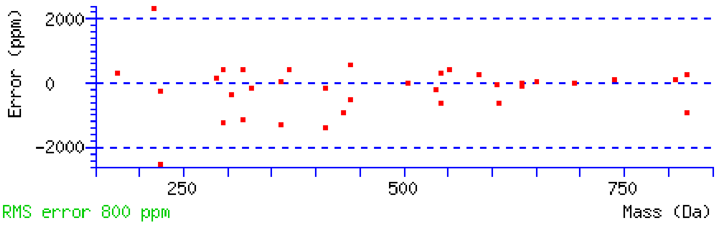
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1342.6412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.022
Matches : 35/108 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	130.0499	65.5286			112.0393	56.5233	E							11
2	243.1339	122.0706			225.1234	113.0653	I	1214.6059	607.8066	1197.5793	599.2933	1196.5953	598.8013	10
3	399.2350	200.1212	382.2085	191.6079	381.2245	191.1159	R	1101.5218	551.2645	1084.4953	542.7513	1083.5112	542.2593	9
4	**536.2940**	268.6506	519.2674	260.1373	518.2834	259.6453	H	945.4207	473.2140	928.3941	464.7007	927.4101	464.2087	8
5	**651.3209**	**326.1641**	634.2944	317.6508	633.3103	317.1588	N	***808.3618***	404.6845	791.3352	396.1713	790.3512	395.6792	7
6	**738.3529**	**369.6801**	721.3264	361.1668	720.3424	360.6748	S	***693.3348***	347.1711	676.3083	338.6578	675.3243	338.1658	6
7	839.4006	420.2039	822.3741	411.6907	821.3900	411.1987	T	***606.3028***	303.6550	589.2763	295.1418	588.2922	294.6498	5
8	896.4221	448.7147	879.3955	440.2014	878.4115	439.7094	G	***505.2551***	253.1312	488.2286	244.6179			4
9	1056.4527	528.7300	1039.4262	520.2167	1038.4422	519.7247	C	448.2337	224.6205	431.2071	216.1072			3
10	1169.5368	**585.2720**	1152.5102	576.7588	1151.5262	576.2667	L	***288.2030***	144.6051	271.1765	136.0919			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EIRHNSTGCLR

(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	1342.6412	0.0018	EIRHNSTGCLR
8.5	1342.6452	-0.0023	SRQGGFVYLCR
6.9	1342.6452	-0.0023	ERGSNLAFMFR
5.6	1341.6412	1.0017	NFKTLSDSSTNK
5.2	1341.6353	1.0076	DLSIFNGFWSR
5.0	1342.6477	-0.0048	GSAAPAPTTAGTGQR
4.5	1340.6320	2.0109	FQSSSQSRKQR
4.2	1341.6353	1.0076	NIDYLNFTWR
3.7	1342.6405	0.0025	DSNLSFEEFKK
3.6	1341.6347	1.0083	LLCPEENGSPAR

Mascot: http://www.matrixscience.com/

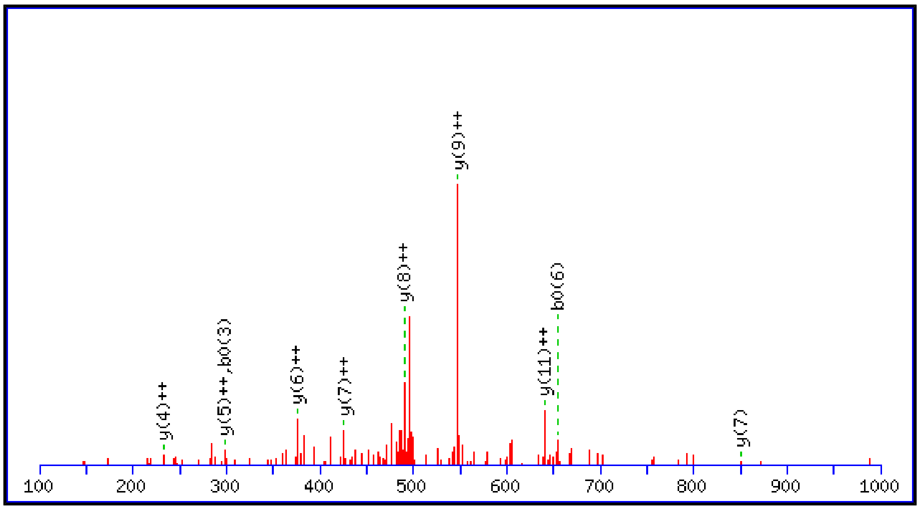
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDALNETRESETK**
Found in **E5RGB0** in **con_Xuniprot_HUMAN3**, E5RGB0_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=2 SV=1

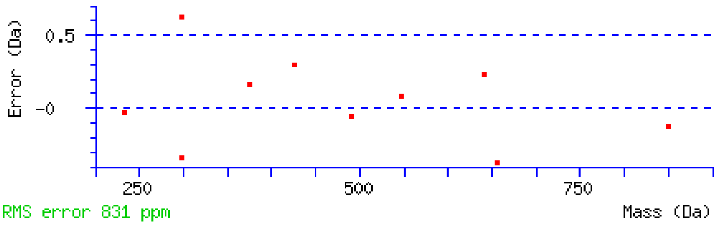
Match to Query 6891: 1521.680922 from(508.234250,3+) intensity(765.4598) rtinseconds(277) scans(319) index(39)
Title: 111019_Est_ISCardio_NMI_200000g_G_3Spectrum212_scans__319
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

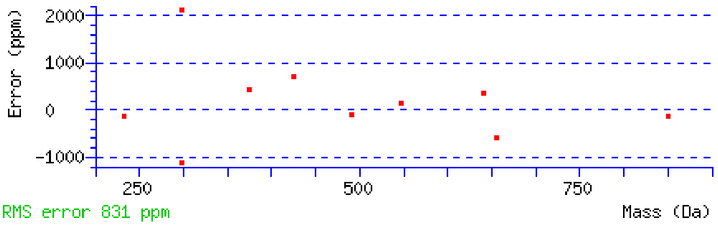
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1521.6794
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.029
Matches : 10/134 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	130.0499	65.5286			112.0393	56.5233	E							13
2	245.0768	123.0420			227.0662	114.0368	D	1393.6441	697.3257	1376.6176	688.8124	1375.6336	688.3204	12
3	316.1139	158.5606			298.1034	149.5553	A	1278.6172	639.8122	1261.5907	631.2990	1260.6066	630.8070	11
4	429.1980	215.1026			411.1874	206.0974	L	1207.5801	604.2937	1190.5535	595.7804	1189.5695	595.2884	10
5	544.2249	272.6161	527.1984	264.1028	526.2144	263.6108	N	1094.4960	547.7516	1077.4695	539.2384	1076.4855	538.7464	9
6	673.2675	337.1374	656.2410	328.6241	655.2570	328.1321	E	979.4691	490.2382	962.4425	481.7249	961.4585	481.2329	8
7	774.3152	387.6612	757.2887	379.1480	756.3046	378.6560	T	850.4265	425.7169	833.3999	417.2036	832.4159	416.7116	7
8	930.4163	465.7118	913.3898	457.1985	912.4058	456.7065	R	749.3788	375.1930	732.3523	366.6798	731.3682	366.1878	6
9	1059.4589	530.2331	1042.4324	521.7198	1041.4483	521.2278	E	593.2777	297.1425	576.2511	288.6292	575.2671	288.1372	5
10	1146.4909	573.7491	1129.4644	565.2358	1128.4804	564.7438	S	464.2351	232.6212	447.2086	224.1079	446.2245	223.6159	4
11	1275.5335	638.2704	1258.5070	629.7571	1257.5230	629.2651	E	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
12	1376.5812	688.7942	1359.5547	680.2810	1358.5706	679.7890	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EDALNETRESETK
(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	1521.6794	0.0015	EDALNETRESETK
8.7	1519.6759	2.0050	NTLPGVGPCESSMR
8.0	1519.6765	2.0044	CHKNSYYQYKK
7.9	1520.6851	0.9958	IKEGNLTCGPGEVM
7.8	1521.6769	0.0040	KDMTFLHEGNDSK
6.5	1520.6776	1.0033	GPAEDMSSKLNQAR
4.7	1521.6803	0.0006	MDQLMQLPGQTSR
4.0	1519.6766	2.0043	FDGGLDNMSVFFR
3.8	1521.6738	0.0071	NLLSCCKNQCPK
3.8	1521.6738	0.0071	NLLSCCKNQCPK

Mascot: http://www.matrixscience.com/

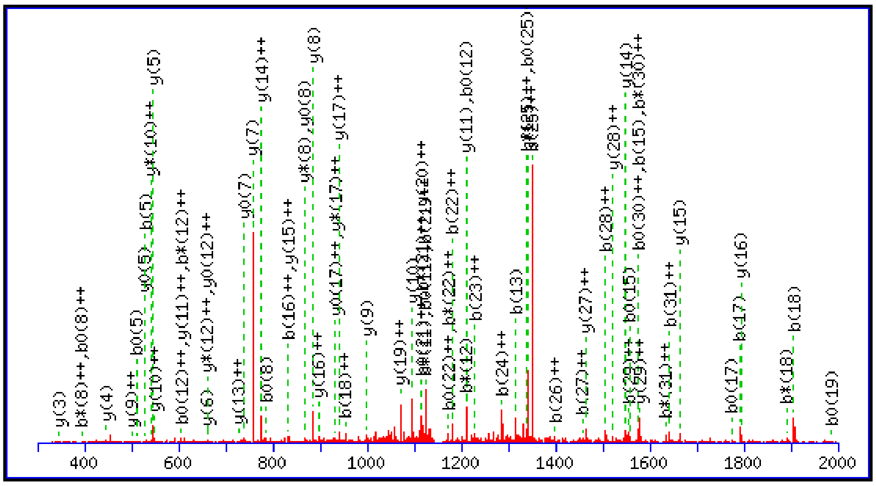
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR**
Found in **P12259** in **con_Xuniprot_HUMAN3**, FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

Match to Query 27779: 3454.615962 from(1152.545930,3+) intensity(13982.8486) rtinseconds(1739) scans(4659) index(17614)
Title: 111019_Est_MI_YP_G_07Spectrum3999_scans__4659
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

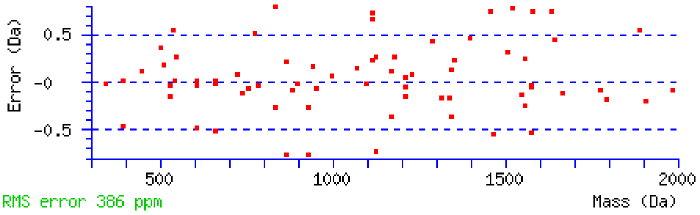
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

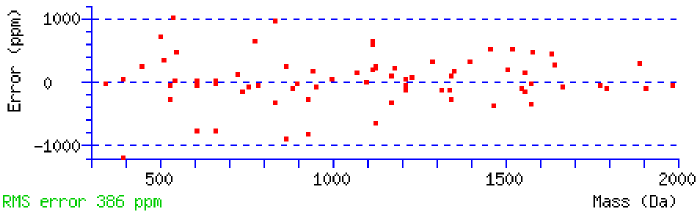


Monoisotopic mass of neutral peptide Mr(calc): 3454.6012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 64 **Expect:** 9.1e-005
Matches : 75/364 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							32
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	3341.5656	1671.2864	3324.5390	1662.7731	3323.5550	1662.2811	31
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	V	3254.5335	1627.7704	3237.5070	1619.2571	3236.5230	1618.7651	30
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	L	3155.4651	1578.2362	3138.4386	1569.7229	3137.4546	1569.2309	29
5	**529.2617**	265.1345	512.2351	256.6212	511.2511	256.1292	N	3042.3811	1521.6942	3025.3545	1513.1809	3024.3705	1512.6889	28
6	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	S	2927.3541	1464.1807	2910.3276	1455.6674	2909.3436	1455.1754	27
7	703.3257	352.1665	686.2992	343.6532	685.3151	343.1612	S	2840.3221	1420.6647	2823.2955	1412.1514	2822.3115	1411.6594	26
8	804.3734	402.6903	787.3468	394.1771	786.3628	393.6850	T	2753.2901	1377.1487	2736.2635	1368.6354	2735.2795	1368.1434	25
9	875.4105	438.2089	858.3840	429.6956	857.3999	429.2036	A	2652.2424	1326.6248	2635.2158	1318.1116	2634.2318	1317.6195	24
10	1004.4531	502.7302	987.4265	494.2169	986.4425	493.7249	E	2581.2053	1291.1063	2564.1787	1282.5930	2563.1947	1282.1010	23
11	1141.5120	571.2596	1124.4855	562.7464	1123.5014	562.2544	H	2452.1627	1226.5850	2435.1361	1218.0717	2434.1521	1217.5797	22
12	1228.5440	614.7757	1211.5175	606.2624	1210.5335	605.7704	S	2315.1038	1158.0555	2298.0772	1149.5422	2297.0932	1149.0502	21
13	**1315.5761**	658.2917	1298.5495	649.7784	1297.5655	649.2864	S	2228.0717	1114.5395	2211.0452	1106.0262	2210.0612	1105.5342	20
14	1412.6288	706.8181	1395.6023	698.3048	1394.6183	697.8128	P	2141.0397	1071.0235	2124.0132	1062.5102	2123.0291	1062.0182	19
15	**1575.6922**	788.3497	1558.6656	779.8364	1557.6816	779.3444	Y	2043.9869	1022.4971	2026.9604	1013.9838	2025.9764	1013.4918	18
16	1662.7242	**831.8657**	1645.6976	823.3525	1644.7136	822.8604	S	1880.9236	940.9654	1863.8971	932.4522	1862.9130	931.9602	17
17	**1791.7668**	896.3870	1774.7402	887.8738	1773.7562	887.3817	E	***1793.8916***	897.4494	1776.8650	888.9362	1775.8810	888.4441	16
18	**1906.7937**	**953.9005**	1889.7672	945.3872	1888.7832	944.8952	D	***1664.8490***	832.9281	1647.8224	824.4149	1646.8384	823.9229	15
19	2003.8465	1002.4269	1986.8199	993.9136	1985.8359	993.4216	P	***1549.8220***	775.4147	1532.7955	766.9014	1531.8115	766.4094	14
20	2116.9305	1058.9689	2099.9040	1050.4556	2098.9200	1049.9636	I	1452.7693	726.8883	1435.7427	718.3750	1434.7587	717.8830	13
21	2245.9731	**1123.4902**	2228.9466	1114.9769	2227.9626	1114.4849	E	***1339.6852***	670.3462	1322.6587	661.8330	1321.6747	661.3410	12
22	2361.0001	**1181.0037**	2343.9735	1172.4904	2342.9895	1171.9984	D	***1210.6426***	605.8250	1193.6161	597.3117	1192.6321	596.8197	11
23	2458.0528	**1229.5301**	2441.0263	1221.0168	2440.0423	1220.5248	P	***1095.6157***	548.3115	1078.5891	539.7982	1077.6051	539.3062	10

24	2571.1369	**1286.0721**	2554.1104	1277.5588	2553.1263	1277.0668	**L**	***998.5629***	499.7851	981.5364	491.2718	980.5524	490.7798	**9**
25	2699.1955	**1350.1014**	2682.1689	1341.5881	2681.1849	1341.0961	**Q**	***885.4789***	443.2431	868.4523	434.7298	867.4683	434.2378	**8**
26	2796.2483	**1398.6278**	2779.2217	1390.1145	2778.2377	1389.6225	**P**	***757.4203***	379.2138	740.3937	370.7005	739.4097	370.2085	**7**
27	2911.2752	**1456.1412**	2894.2486	1447.6280	2893.2646	1447.1360	**D**	***660.3675***	330.6874	643.3410	322.1741	642.3570	321.6821	**6**
28	3010.3436	**1505.6754**	2993.3171	1497.1622	2992.3330	1496.6702	**V**	***545.3406***	273.1739	528.3140	264.6606	527.3300	264.1686	**5**
29	3111.3913	**1556.1993**	3094.3647	1547.6860	3093.3807	1547.1940	**T**	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	**4**
30	3168.4128	1584.7100	3151.3862	1576.1967	3150.4022	1575.7047	**G**	***345.2245***	173.1159	328.1979	164.6026			**3**
31	3281.4968	**1641.2520**	3264.4703	1632.7388	3263.4863	1632.2468	**I**	288.2030	144.6051	271.1765	136.0919			**2**
32							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
63.9	3454.6012	0.0148	NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR	Deamidated N5 81.80%
56.9	3454.6012	0.0148	NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR	Deamidated N1 16.47%
47.1	3454.6012	0.0148	NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR	Deamidated Q25 1.72%
39.1	3453.6172	0.9988	NSVLNSSTAEHSSPYSEDPIEDPLQPDVTGIR	
9.7	3453.6101	1.0058	IIKGYMKQGNLHNMALQSQNGDAMQILASDK	
7.9	3453.6101	1.0058	IIKGYMKQGNLHNMALQSQNGDAMQILASDK	
7.5	3454.5987	0.0172	AGGLGINLTAADTVIFYDSDWNPTVDQQAMDR	
7.5	3454.5987	0.0172	AGGLGINLTAADTVIFYDSDWNPTVDQQAMDR	
7.5	3454.5987	0.0172	AGGLGINLTAADTVIFYDSDWNPTVDQQAMDR	
6.3	3452.6261	1.9898	IIKGYMKQGNLHNMALQSQNGDAMQILASDK	

Mascot: http://www.matrixscience.com/

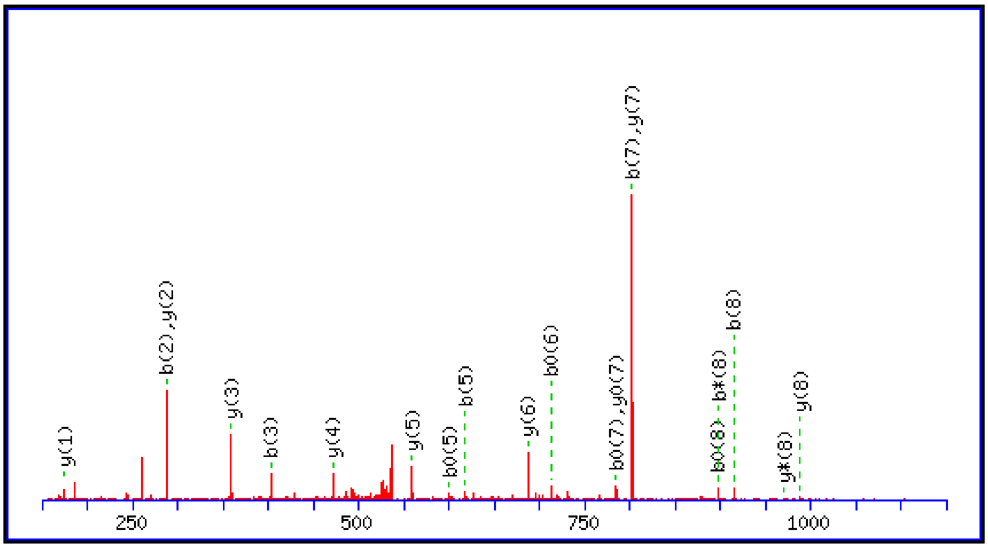
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TWNQSIALR**
Found in **P12259** in **con_Xuniprot_HUMAN3**, FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

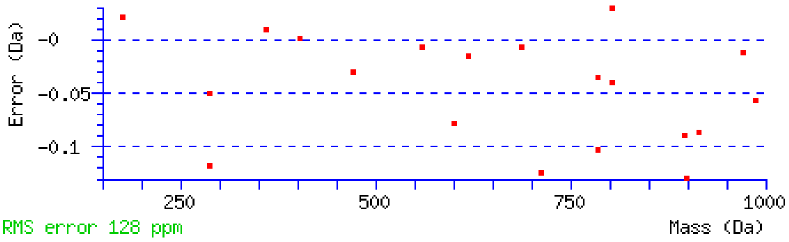
Match to Query 217: 1088.565228 from(545.289890,2+) intensity(24401.3145) rtinseconds(1076) scans(2326) index(11660)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum1993_scans__2326
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

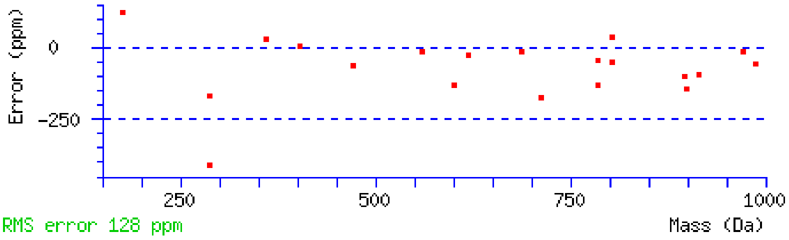
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1088.5614
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00017
Matches : 20/84 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	**288.1343**	144.5708			270.1237	135.5655	W	***988.5211***	494.7642	971.4945	486.2509	970.5105	485.7589	8
3	**403.1612**	202.0842	386.1347	193.5710	385.1506	193.0790	N	***802.4417***	401.7245	785.4152	393.2112	784.4312	392.7192	7
4	531.2198	266.1135	514.1932	257.6003	513.2092	257.1083	Q	***687.4148***	344.2110	670.3883	335.6978	669.4042	335.2058	6
5	**618.2518**	309.6295	601.2253	301.1163	600.2413	300.6243	S	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	5
6	731.3359	366.1716	714.3093	357.6583	713.3253	357.1663	I	***472.3242***	236.6657	455.2976	228.1525			4
7	**802.3730**	401.6901	785.3464	393.1769	784.3624	392.6849	A	***359.2401***	180.1237	342.2136	171.6104			3
8	**915.4571**	458.2322	898.4305	449.7189	897.4465	449.2269	L	***288.2030***	144.6051	271.1765	136.0919			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TWNQSIALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.3	1088.5614	0.0038	TWNQSIALR	Deamidated N3 63.10%
59.0	1088.5614	0.0038	TWNQSIALR	Deamidated Q4 36.90%
22.0	1088.5648	0.0004	DMKPAKDLR	
17.0	1088.5686	-0.0034	SAESRRVQR	
14.0	1088.5648	0.0004	EGKLMQLDR	
14.0	1088.5686	-0.0034	QRGESSRIR	
13.6	1088.5655	-0.0002	WEFQLPLR	
13.4	1088.5648	0.0004	SEAILQCLR	
13.1	1088.5648	0.0004	EMTLQQALR	
11.7	1088.5648	0.0004	NQEVKIAMR	

Mascot: http://www.matrixscience.com/

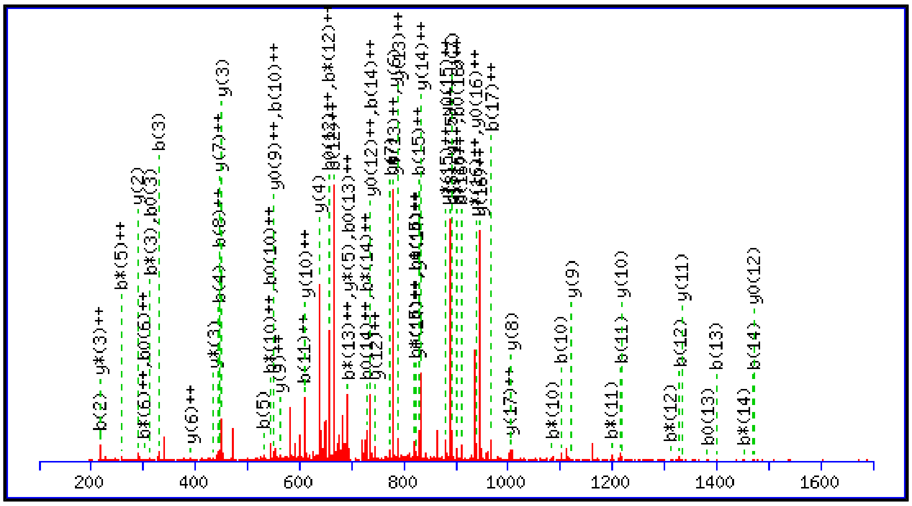
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNINSSRDPDNIAAWYLR**
Found in **P12259** in **con_Xuniprot_HUMAN3**, FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

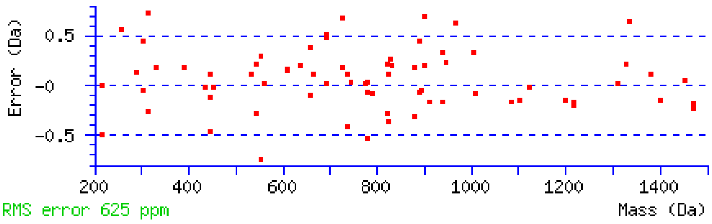
Match to Query 13899: 2106.017202 from(703.013010,3+) intensity(251547.2969) rtinseconds(1619) scans(4068) index(24549)
Title: 111019_Est_MI_YS_G_06Spectrum3529_scans__4068
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

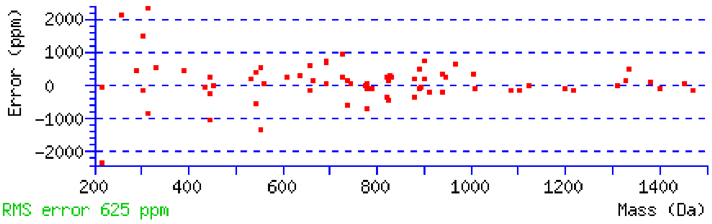
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2106.0130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0019
Matches : 74/186 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							18
2	***216.0979***	108.5526	199.0713	100.0393	198.0873	99.5473	N	2005.9726	1003.4900	1988.9461	994.9767	1987.9621	994.4847	17
3	***329.1819***	165.0946	312.1554	156.5813	311.1714	156.0893	I	1891.9297	946.4685	1874.9032	937.9552	1873.9191	937.4632	16
4	***444.2089***	222.6081	427.1823	214.0948	426.1983	213.6028	N	1778.8456	889.9265	1761.8191	881.4132	1760.8351	880.9212	15
5	***531.2409***	266.1241	514.2144	257.6108	513.2304	257.1188	S	1663.8187	832.4130	1646.7921	823.8997	1645.8081	823.4077	14
6	618.2729	309.6401	601.2464	301.1268	600.2624	300.6348	S	1576.7867	788.8970	1559.7601	780.3837	1558.7761	779.8917	13
7	***774.3741***	387.6907	757.3475	379.1774	756.3635	378.6854	R	1489.7546	745.3810	1472.7281	736.8677	1471.7441	736.3757	12
8	***889.4010***	***445.2041***	872.3745	436.6909	871.3904	436.1989	D	**1333.6535**	667.3304	1316.6270	658.8171	1315.6430	658.3251	11
9	986.4538	493.7305	969.4272	485.2172	968.4432	484.7252	P	**1218.6266**	609.8169	1201.6000	601.3037	1200.6160	600.8116	10
10	***1101.4807***	***551.2440***	1084.4542	542.7307	1083.4701	542.2387	D	**1121.5738**	561.2905	1104.5473	552.7773	1103.5633	552.2853	9
11	***1215.5236***	***608.2655***	1198.4971	599.7522	1197.5131	599.2602	N	**1006.5469**	503.7771	989.5203	495.2638			8
12	***1328.6077***	***664.8075***	1311.5811	656.2942	1310.5971	655.8022	I	**892.5040**	446.7556	875.4774	438.2423			7
13	***1399.6448***	700.3260	1382.6183	691.8128	1381.6342	691.3208	A	**779.4199**	390.2136	762.3933	381.7003			6
14	***1470.6819***	***735.8446***	1453.6554	727.3313	1452.6714	726.8393	A	708.3828	354.6950	691.3562	346.1817			5
15	1656.7612	***828.8843***	1639.7347	820.3710	1638.7507	819.8790	W	**637.3457**	319.1765	620.3191	310.6632			4
16	1819.8246	***910.4159***	1802.7980	901.9026	1801.8140	901.4106	Y	**451.2663**	226.1368	434.2398	217.6235			3
17	1932.9086	***966.9580***	1915.8821	958.4447	1914.8981	957.9527	L	**288.2030**	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TNINSSRDPDNIAAWYLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.5	2106.0130	0.0042	TNINSSRDPDNIAAWYLR	Deamidated N4 46.20%
49.7	2106.0130	0.0042	TNINSSRDPDNIAAWYLR	Deamidated N2 30.59%
48.5	2106.0130	0.0042	TNINSSRDPDNIAAWYLR	Deamidated N11 23.21%
27.4	2106.0269	-0.0097	VNDTTPNNFPLLYEEALR	
25.9	2106.0269	-0.0097	VNDTTPNNFPLLYEEALR	
18.3	2106.0269	-0.0097	VNDTTPNNFPLLYEEALR	
16.4	2106.0076	0.0096	TIIDKRLQDEDASSTQQR	
12.1	2105.0236	0.9936	TIIDKRLQDEDASSTQQR	
10.1	2105.0236	0.9936	TIIDKRLQDEDASSTQQR	
9.0	2106.0262	-0.0090	MSLNELEILRNSAVSQER	

Mascot: http://www.matrixscience.com/

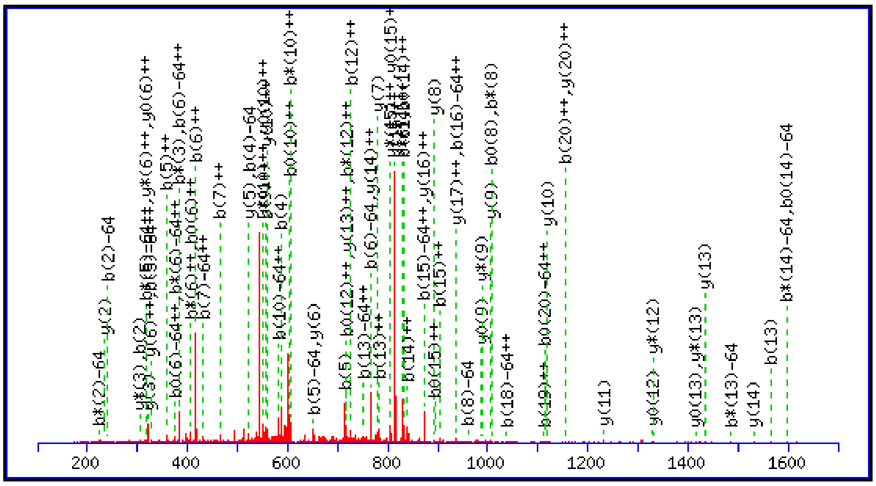
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **MRPWKDPPSDLLLLKQSNSSK**
Found in **P12259** in **con_Xuniprot_HUMAN3**, FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

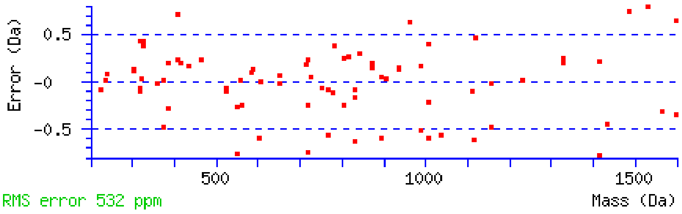
Match to Query 21514: 2456.278536 from(615.076910,4+) intensity(11709.9590) rtinseconds(1070) scans(2570) index(24441)
Title: 111019_Est_MI_YS_G_06Spectrum2219_scans__2570
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

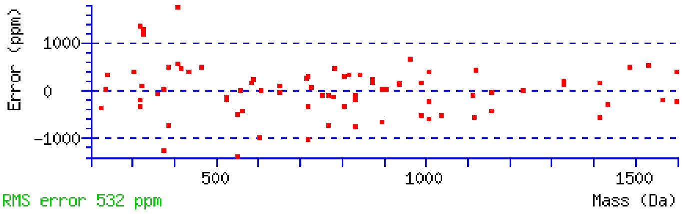
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2456.2733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N18    : Deamidated (NQ)
Ions Score: 42  Expect: 0.013
Matches : 80/334 fragment ions using 134 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0427	74.5250					M							21
2	**304.1438**	152.5755	287.1172	144.0623			R	2310.2452	1155.6262	2293.2187	1147.1130	2292.2347	1146.6210	20
3	401.1966	201.1019	384.1700	192.5886			P	2154.1441	1077.5757	2137.1176	1069.0624	2136.1335	1068.5704	19
4	**587.2759**	294.1416	570.2493	285.6283			W	2057.0913	1029.0493	2040.0648	1020.5360	2039.0808	1020.0440	18
5	**715.3708**	**358.1891**	698.3443	349.6758			K	1871.0120	936.0097	1853.9855	927.4964	1853.0015	927.0044	17
6	**830.3978**	**415.7025**	813.3712	407.1892	812.3872	406.6972	D	1742.9171	871.9622	1725.8905	863.4489	1724.9065	862.9569	16
7	927.4505	**464.2289**	910.4240	455.7156	909.4400	455.2236	P	1627.8901	814.4487	1610.8636	805.9354	1609.8796	805.4434	15
8	1024.5033	512.7553	1007.4767	504.2420	1006.4927	503.7500	P	***1530.8374***	765.9223	1513.8108	757.4090	1512.8268	756.9170	14
9	1111.5353	**556.2713**	1094.5088	547.7580	1093.5248	547.2660	S	***1433.7846***	717.3959	1416.7580	708.8827	1415.7740	708.3907	13
10	1226.5623	613.7848	1209.5357	605.2715	1208.5517	604.7795	D	1346.7526	673.8799	1329.7260	665.3666	1328.7420	664.8746	12
11	1339.6463	670.3268	1322.6198	661.8135	1321.6358	661.3215	L	***1231.7256***	616.3665	1214.6991	607.8532	1213.7151	607.3612	11
12	1452.7304	**726.8688**	1435.7038	718.3556	1434.7198	717.8636	L	***1118.6416***	559.8244	1101.6150	551.3111	1100.6310	550.8191	10
13	**1565.8145**	**783.4109**	1548.7879	774.8976	1547.8039	774.4056	L	***1005.5575***	503.2824	988.5310	494.7691	987.5469	494.2771	9
14	1678.8985	**839.9529**	1661.8720	831.4396	1660.8880	830.9476	L	***892.4734***	446.7404	875.4469	438.2271	874.4629	437.7351	8
15	1806.9935	**904.0004**	1789.9669	895.4871	1788.9829	894.9951	K	***779.3894***	390.1983	762.3628	381.6850	761.3788	381.1930	7
16	1935.0521	968.0297	1918.0255	959.5164	1917.0415	959.0244	Q	***651.2944***	326.1508	634.2679	317.6376	633.2838	317.1456	6
17	2022.0841	1011.5457	2005.0575	1003.0324	2004.0735	1002.5404	S	***523.2358***	262.1216	506.2093	253.6083	505.2253	253.1163	5
18	2137.1110	1069.0592	2120.0845	1060.5459	2119.1005	1060.0539	N	436.2038	218.6055	419.1773	210.0923	418.1932	209.6003	4
19	2224.1431	**1112.5752**	2207.1165	1104.0619	2206.1325	1103.5699	S	***321.1769***	161.0921	304.1503	152.5788	303.1663	152.0868	3
20	2311.1751	**1156.0912**	2294.1485	1147.5779	2293.1645	1147.0859	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
21							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of MRPWKDPPSDLLLLKQSNSSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
42.4	2456.2733	0.0052	MRPWKDPPSDLLLLKQSNSSK	Deamidated N18 57.03%
41.1	2456.2733	0.0052	MRPWKDPPSDLLLLKQSNSSK	Deamidated Q16 42.97%
10.1	2456.2897	-0.0111	KNLETQKEIAEDELVAAEALLK	
6.5	2455.2853	0.9933	DMERLTSLRAGIEGPLLASDVGR	
6.0	2456.2702	0.0084	MQVMNLNVPMRPGILVQRQSK	
5.6	2455.2861	0.9924	MQVMNLNVPMRPGILVQRQSK	
5.6	2455.2861	0.9924	MQVMNLNVPMRPGILVQRQSK	
4.3	2454.2676	2.0110	VADEQGALEPTEMLQLLAVTGLR	
4.2	2456.2832	-0.0047	LQMVELTDAQPQVRQLLVTQK	
3.5	2456.2832	-0.0047	LQMVELTDAQPQVRQLLVTQK	

Mascot: http://www.matrixscience.com/

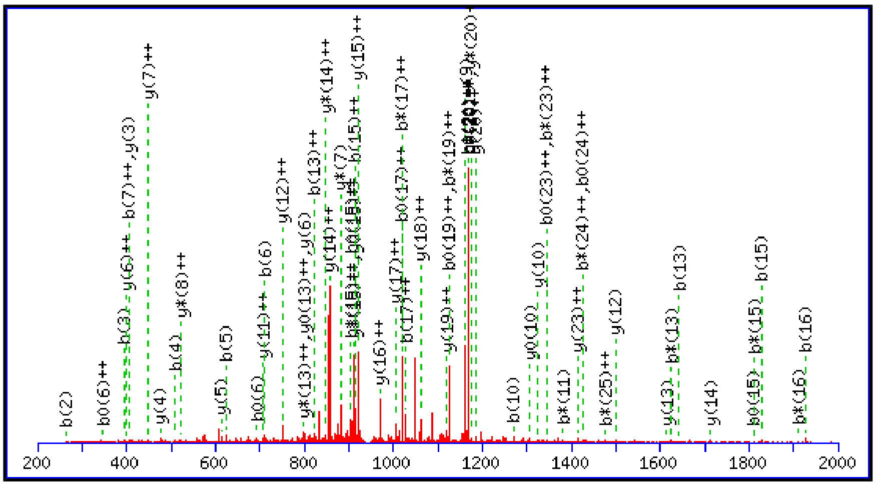
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYEDDSPEWFKEDNAVQPNSSYTYVWHATER**
Found in **P12259** in **con_Xuniprot_HUMAN3**, FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

Match to Query 28064: 3764.631616 from(942.165180,4+) intensity(29439.2773) rtinseconds(1810) scans(4771) index(24001)
Title: 111019_Est_MI_YS_G_05Spectrum4128_scans__4771
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

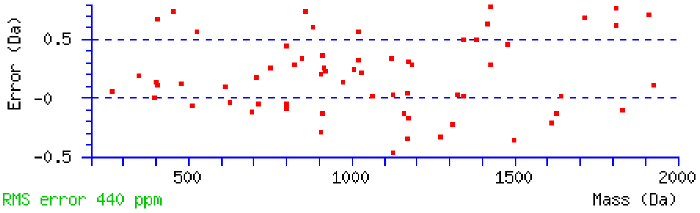
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

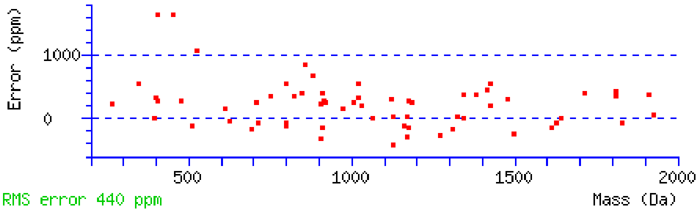


Monoisotopic mass of neutral peptide Mr(calc): 3764.6179
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.0046
Matches : 64/338 fragment ions using 154 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							31
2	***265.1183***	133.0628			247.1077	124.0575	Y	3664.5775	1832.7924	3647.5510	1824.2791	3646.5670	1823.7871	30
3	***394.1609***	197.5841			376.1503	188.5788	E	3501.5142	1751.2607	3484.4877	1742.7475	3483.5036	1742.2555	29
4	***509.1878***	255.0975			491.1773	246.0923	D	3372.4716	1686.7394	3355.4451	1678.2262	3354.4610	1677.7342	28
5	***624.2148***	312.6110			606.2042	303.6057	D	3257.4447	1629.2260	3240.4181	1620.7127	3239.4341	1620.2207	27
6	***711.2468***	356.1270			693.2362	347.1218	S	3142.4177	1571.7125	3125.3912	1563.1992	3124.4072	1562.7072	26
7	808.2996	404.6534			790.2890	395.6481	P	3055.3857	1528.1965	3038.3591	1519.6832	3037.3751	1519.1912	25
8	937.3421	469.1747			919.3316	460.1694	E	2958.3329	1479.6701	2941.3064	1471.1568	2940.3224	1470.6648	24
9	1123.4215	562.2144			1105.4109	553.2091	W	2829.2903	1415.1488	2812.2638	1406.6355	2811.2798	1406.1435	23
10	***1270.4899***	635.7486			1252.4793	626.7433	F	2643.2110	1322.1091	2626.1845	1313.5959	2625.2005	1313.1039	22
11	1398.5848	699.7961	1381.5583	691.2828	1380.5743	690.7908	K	2496.1426	1248.5749	2479.1161	1240.0617	2478.1320	1239.5697	21
12	1527.6274	764.3174	1510.6009	755.8041	1509.6169	755.3121	E	2368.0476	1184.5275	2351.0211	1176.0142	2350.0371	1175.5222	20
13	***1642.6544***	821.8308	1625.6278	813.3176	1624.6438	812.8255	D	2239.0051	1120.0062	2221.9785	1111.4929	2220.9945	1111.0009	19
14	1756.6973	878.8523	1739.6708	870.3390	1738.6867	869.8470	N	2123.9781	1062.4927	2106.9516	1053.9794	2105.9675	1053.4874	18
15	***1827.7344***	914.3708	1810.7079	905.8576	1809.7239	905.3656	A	2009.9352	1005.4712	1992.9086	996.9580	1991.9246	996.4659	17
16	***1926.8028***	963.9051	1909.7763	955.3918	1908.7923	954.8998	V	1938.8981	969.9527	1921.8715	961.4394	1920.8875	960.9474	16
17	2054.8614	1027.9343	2037.8349	1019.4211	2036.8508	1018.9291	Q	1839.8297	920.4185	1822.8031	911.9052	1821.8191	911.4132	15
18	2151.9142	1076.4607	2134.8876	1067.9474	2133.9036	1067.4554	P	***1711.7711***	856.3892	1694.7445	847.8759	1693.7605	847.3839	14
19	2266.9411	1133.9742	2249.9146	1125.4609	2248.9305	1124.9689	N	***1614.7183***	807.8628	1597.6918	799.3495	1596.7077	798.8575	13
20	2353.9731	1177.4902	2336.9466	1168.9769	2335.9626	1168.4849	S	***1499.6914***	750.3493	1482.6648	741.8360	1481.6808	741.3440	12
21	2441.0052	1221.0062	2423.9786	1212.4929	2422.9946	1212.0009	S	1412.6593	706.8333	1395.6328	698.3200	1394.6488	697.8280	11
22	2604.0685	1302.5379	2587.0419	1294.0246	2586.0579	1293.5326	Y	***1325.6273***	663.3173	1308.6008	654.8040	1307.6167	654.3120	10
23	2705.1162	1353.0617	2688.0896	1344.5485	2687.1056	1344.0564	T	***1162.5640***	581.7856	1145.5374	573.2724	1144.5534	572.7803	9

24	2868.1795	1434.5934	2851.1530	1426.0801	2850.1689	1425.5881	**Y**	1061.5163	531.2618	1044.4898	522.7485	1043.5057	522.2565	**8**
25	2967.2479	1484.1276	2950.2214	1475.6143	2949.2374	1475.1223	**V**	898.4530	449.7301	881.4264	441.2169	880.4424	440.7248	**7**
26	3153.3272	1577.1673	3136.3007	1568.6540	3135.3167	1568.1620	**W**	***799.3846***	400.1959	782.3580	391.6826	781.3740	391.1906	**6**
27	3290.3861	1645.6967	3273.3596	1637.1834	3272.3756	1636.6914	**H**	***613.3053***	307.1563	596.2787	298.6430	595.2947	298.1510	**5**
28	3361.4233	1681.2153	3344.3967	1672.7020	3343.4127	1672.2100	**A**	***476.2463***	238.6268	459.2198	230.1135	458.2358	229.6215	**4**
29	3462.4709	1731.7391	3445.4444	1723.2258	3444.4604	1722.7338	**T**	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	**3**
30	3591.5135	1796.2604	3574.4870	1787.7471	3573.5030	1787.2551	**E**	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
31							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TYEDDSPEWFKEDNAVQPNSSYTYVWHATER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.3	3764.6179	0.0137	TYEDDSPEWFKEDNAVQPNSSYTYVWHATER	Deamidated N19 49.82%
38.7	3764.6179	0.0137	TYEDDSPEWFKEDNAVQPNSSYTYVWHATER	Deamidated Q17 27.25%
37.9	3764.6179	0.0137	TYEDDSPEWFKEDNAVQPNSSYTYVWHATER	Deamidated N14 22.93%
32.3	3763.6339	0.9977	TYEDDSPEWFKEDNAVQPNSSYTYVWHATER	
10.2	3764.6467	-0.0151	AFLEDGGPFPVMSNSPDTLEYNMQLCLCGLSDR	
10.0	3764.6157	0.0160	SEGEQQLKPNNSNAPNEDQEEEIQQSEQHTPAR	
8.5	3764.6157	0.0160	SEGEQQLKPNNSNAPNEDQEEEIQQSEQHTPAR	
7.8	3763.6317	1.0000	SEGEQQLKPNNSNAPNEDQEEEIQQSEQHTPAR	
7.8	3763.6317	1.0000	SEGEQQLKPNNSNAPNEDQEEEIQQSEQHTPAR	
5.6	3762.6349	1.9967	GRMDNEHVSAVLTWGGGGSTMDCFTQYIVGNETR	

Mascot: http://www.matrixscience.com/

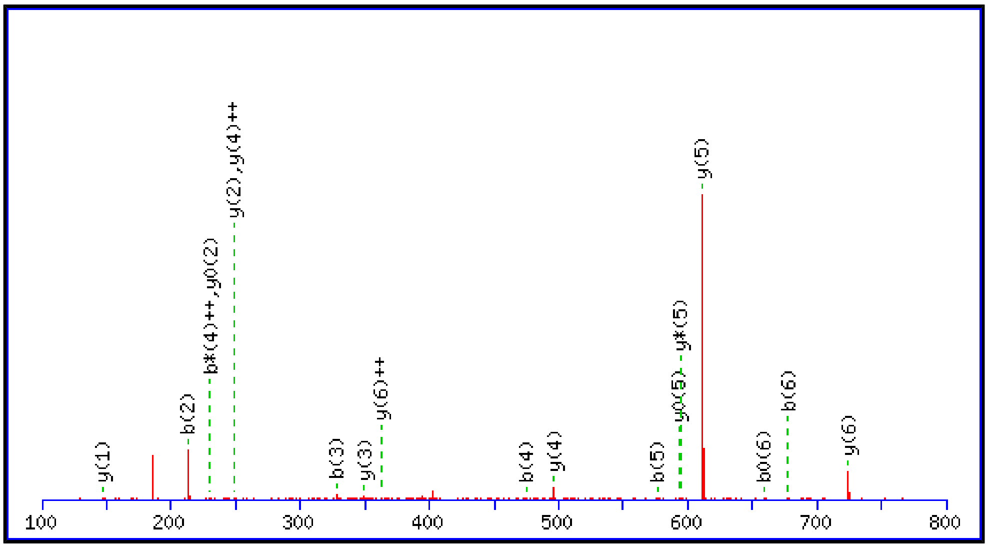
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VLNFTTK**
Found in **P13671** in **con_Xuniprot_HUMAN3**, CO6_HUMAN Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3

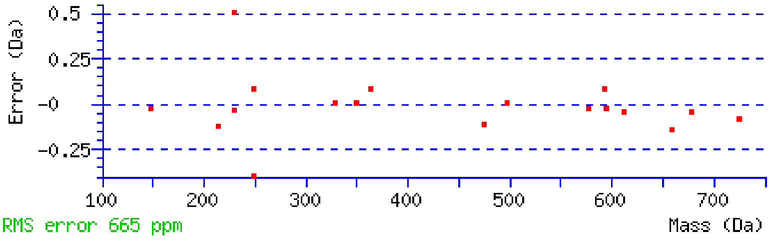
Match to Query 1: 822.449668 from(412.232110,2+) intensity(88312.2813) rtinseconds(613) scans(1300) index(5013)
Title: 111019_Est_ISCardio_NMI_YP_G_8Spectrum1120_scans__1300
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

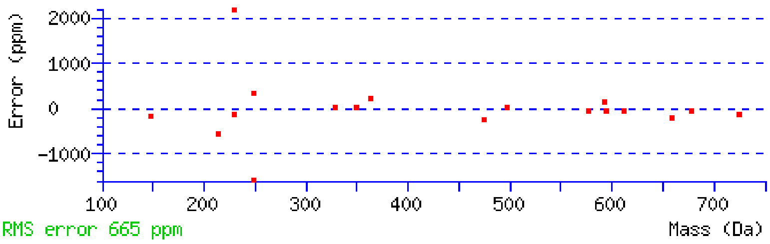
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 822.4487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 37 **Expect:** 0.024
Matches : 18/58 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	100.0757	50.5415					V							7
2	**213.1598**	107.0835					L	***724.3876***	362.6974	707.3610	354.1842	706.3770	353.6921	6
3	**328.1867**	164.5970	311.1601	156.0837			N	***611.3035***	306.1554	594.2770	297.6421	593.2930	297.1501	5
4	**475.2551**	238.1312	458.2286	229.6179			F	***496.2766***	248.6419	479.2500	240.1287	478.2660	239.6366	4
5	**576.3028**	288.6550	559.2762	280.1418	558.2922	279.6498	T	***349.2082***	175.1077	332.1816	166.5944	331.1976	166.1024	3
6	**677.3505**	339.1789	660.3239	330.6656	659.3399	330.1736	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
7							K	***147.1128***	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VLNFTTK
(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	822.4487	0.0010	VLNFTTK
13.1	822.4487	0.0009	VITDTFK
4.5	820.4416	2.0081	PAARGGHR

Mascot: http://www.matrixscience.com/

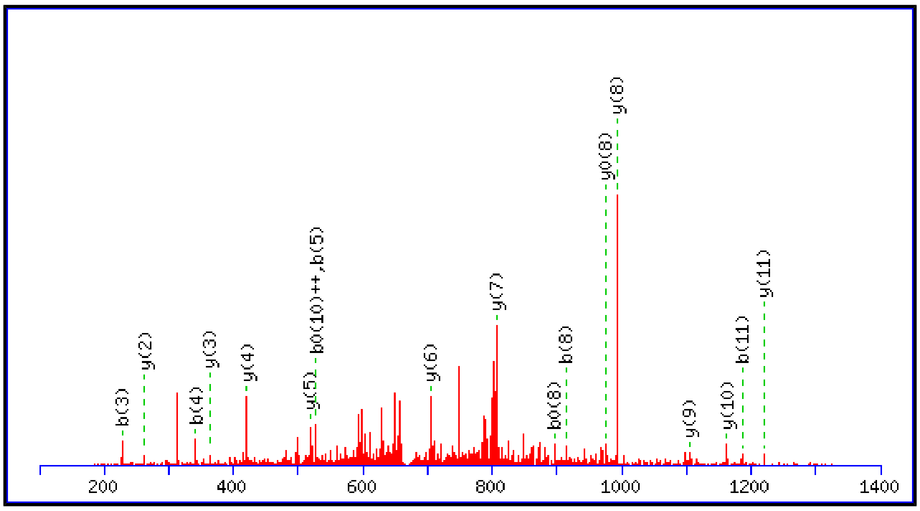
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGIWTWVGTNK**
Found in **P14151** in **con_Xuniprot_HUMAN3**, LYAM1_HUMAN L-selectin OS=Homo sapiens GN=SELL PE=1 SV=2

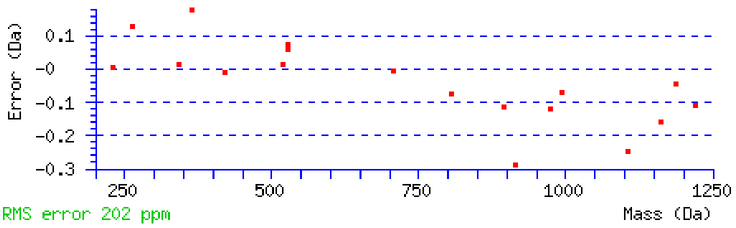
Match to Query 2018: 1331.691368 from(666.852960,2+) intensity(32922.0000) rtinseconds(1967) scans(5047) index(26832)
Title: 111019_Est_MI_YS_G_09Spectrum4392_scans__5047
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

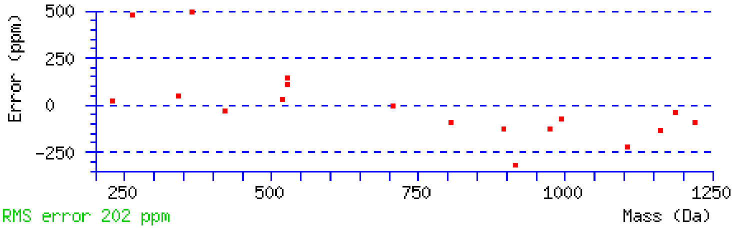
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1331.6874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 69 **Expect:** 3.5e-005
Matches : 18/98 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	114.0913	57.5493					I							12
2	171.1128	86.0600					G	***1219.6106***	610.3089	1202.5841	601.7957	1201.6000	601.3037	11
3	**228.1343**	114.5708					G	***1162.5891***	581.7982	1145.5626	573.2849	1144.5786	572.7929	10
4	**341.2183**	171.1128					I	***1105.5677***	553.2875	1088.5411	544.7742	1087.5571	544.2822	9
5	**527.2976**	264.1525					W	***992.4836***	496.7454	975.4571	488.2322	974.4730	487.7402	8
6	628.3453	314.6763			610.3348	305.6710	T	***806.4043***	403.7058	789.3777	395.1925	788.3937	394.7005	7
7	814.4246	407.7160			796.4141	398.7107	W	***705.3566***	353.1819	688.3301	344.6687	687.3461	344.1767	6
8	**913.4931**	457.2502			895.4825	448.2449	V	***519.2773***	260.1423	502.2508	251.6290	501.2667	251.1370	5
9	970.5145	485.7609			952.5040	476.7556	G	***420.2089***	210.6081	403.1823	202.0948	402.1983	201.6028	4
10	1071.5622	536.2847			1053.5516	527.2795	T	***363.1874***	182.0974	346.1609	173.5841	345.1769	173.0921	3
11	**1186.5891**	593.7982	1169.5626	585.2849	1168.5786	584.7929	N	***262.1397***	131.5735	245.1132	123.0602			2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of IGGIWTWVGTNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
68.6	1331.6874	0.0040	IGGIWTWVGTNK
11.9	1329.6889	2.0025	KPQTLGGTQGTGGK
9.1	1331.6932	-0.0019	NLLITADNSKDK
8.5	1331.6906	0.0008	AVQRSSQRGTDK
7.5	1331.6932	-0.0018	LNISADKENSIK
6.7	1330.6888	1.0026	MGGLGPRRAGTSR
5.8	1329.6889	2.0025	KPQTLGGTQGTGGK
5.2	1329.6902	2.0012	QPHARDPVAPSR
5.1	1331.6932	-0.0019	VKDVGSNIKDEK
4.8	1331.6867	0.0046	LLANVQCLGTSR

Mascot: http://www.matrixscience.com/

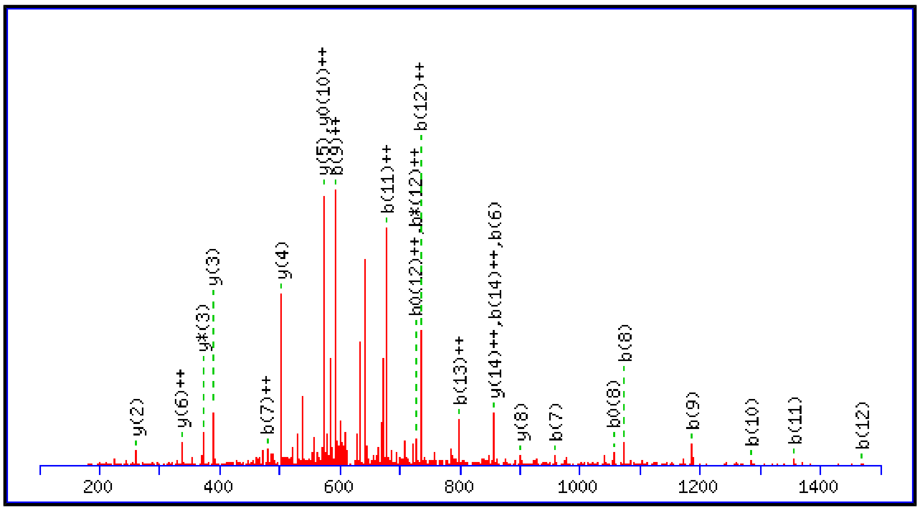
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FCRDNYTDLVAIQNK**
Found in **P14151** in **con_Xuniprot_HUMAN3**, LYAM1_HUMAN L-selectin OS=Homo sapiens GN=SELL PE=1 SV=2

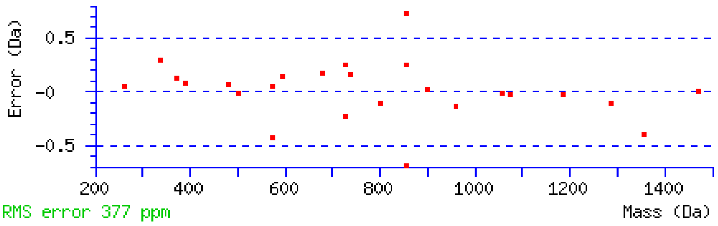
Match to Query 10970: 1856.878902 from(619.966910,3+) intensity(33575.8125) rtinseconds(1211) scans(2814) index(12496)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2444_scans__2814
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

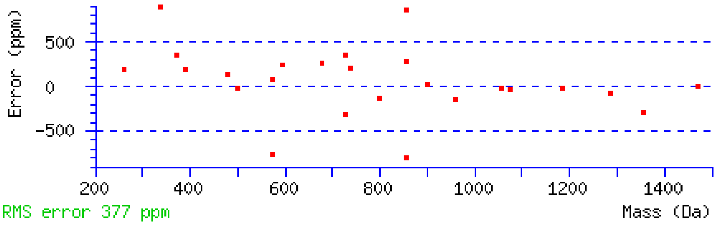
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1856.8727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
Ions Score: 50  Expect: 0.0023
Matches : 25/144 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	148.0757	74.5415					F							15
2	308.1063	154.5568					C	1710.8116	855.9094	1693.7850	847.3961	1692.8010	846.9041	14
3	464.2074	232.6074	447.1809	224.0941			R	1550.7809	775.8941	1533.7544	767.3808	1532.7703	766.8888	13
4	579.2344	290.1208	562.2078	281.6076	561.2238	281.1156	D	1394.6798	697.8435	1377.6533	689.3303	1376.6692	688.8383	12
5	694.2613	347.6343	677.2348	339.1210	676.2508	338.6290	N	1279.6529	640.3301	1262.6263	631.8168	1261.6423	631.3248	11
6	***857.3247***	429.1660	840.2981	420.6527	839.3141	420.1607	Y	1164.6259	582.8166	1147.5994	574.3033	1146.6154	573.8113	10
7	***958.3723***	**479.6898**	941.3458	471.1765	940.3618	470.6845	T	1001.5626	501.2849	984.5360	492.7717	983.5520	492.2796	9
8	***1073.3993***	537.2033	1056.3727	528.6900	1055.3887	528.1980	D	**900.5149**	450.7611	883.4884	442.2478	882.5043	441.7558	8
9	***1186.4834***	**593.7453**	1169.4568	585.2320	1168.4728	584.7400	L	785.4880	393.2476	768.4614	384.7343			7
10	***1285.5518***	643.2795	1268.5252	634.7662	1267.5412	634.2742	V	672.4039	336.7056	655.3774	328.1923			6
11	***1356.5889***	**678.7981**	1339.5623	670.2848	1338.5783	669.7928	A	**573.3355**	287.1714	556.3089	278.6581			5
12	***1469.6729***	**735.3401**	1452.6464	726.8268	1451.6624	726.3348	I	**502.2984**	251.6528	485.2718	243.1395			4
13	1597.7315	**799.3694**	1580.7050	790.8561	1579.7210	790.3641	Q	**389.2143**	195.1108	372.1878	186.5975			3
14	1711.7744	**856.3909**	1694.7479	847.8776	1693.7639	847.3856	N	**261.1557**	131.0815	244.1292	122.5682			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FCRDNYTDLVAIQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.6	1856.8727	0.0062	FCRDNYTDLVAIQNK	Deamidated N5 99.51%
23.5	1856.8727	0.0062	FCRDNYTDLVAIQNK	Deamidated Q13 0.25%
23.4	1856.8727	0.0062	FCRDNYTDLVAIQNK	Deamidated N14 0.24%
19.7	1855.8734	1.0055	NEVCAPASQPSVVQGANK	
17.0	1855.8734	1.0055	NEVCAPASQPSVVQGANK	
14.5	1855.8734	1.0055	NEVCAPASQPSVVQGANK	
9.7	1855.8774	1.0015	NVLCGYVSEFEGLQNK	
8.7	1856.8805	-0.0016	GWAGNEGLNEELQVWR	
7.5	1856.8832	-0.0043	LNKYQEPDVVNFDFK	
6.7	1855.8799	0.9990	GDAQISVTLVNHSEQEK	

Mascot: http://www.matrixscience.com/

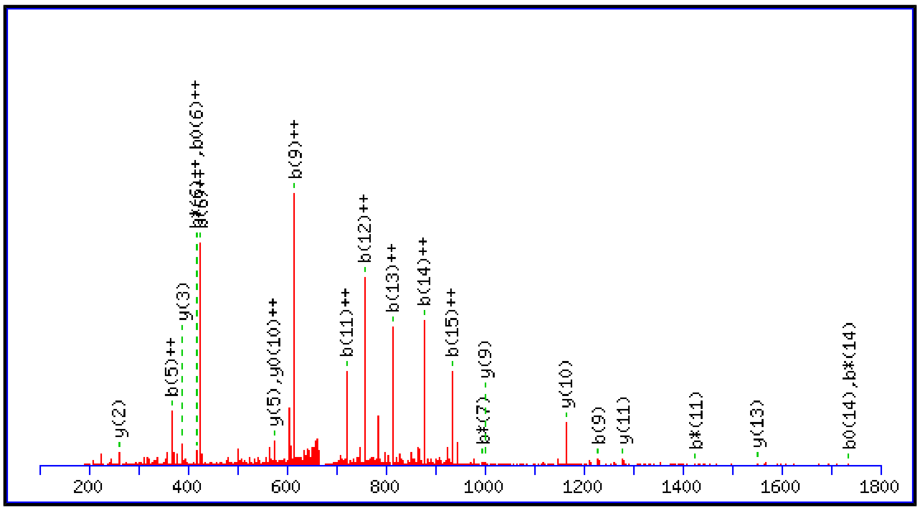
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RFCRDNYTDLVAIQNK**
Found in **P14151** in **con_Xuniprot_HUMAN3**, LYAM1_HUMAN L-selectin OS=Homo sapiens GN=SELL PE=1 SV=2

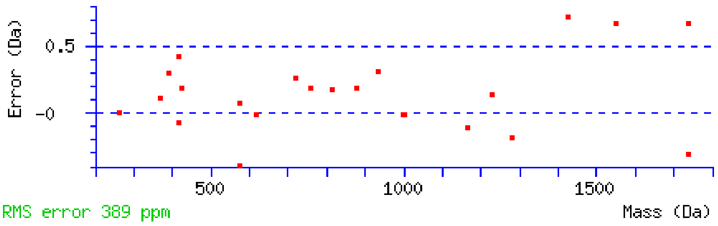
Match to Query 12263: 2012.978892 from(672.000240,3+) intensity(29095.2637) rtinseconds(901) scans(2128) index(24425)
Title: 111019_Est_MI_YS_G_06Spectrum1836_scans__2128
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

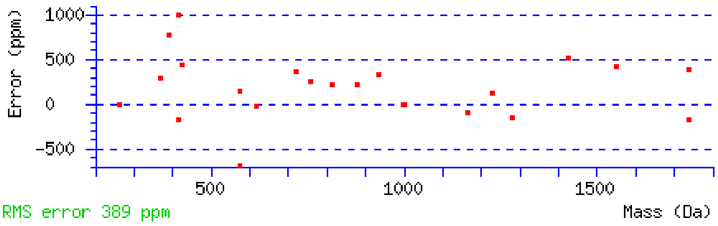
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2012.9738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.0091
Matches : 23/158 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	157.1084	79.0578	140.0818	70.5446			R							16
2	304.1768	152.5920	287.1503	144.0788			F	1857.8800	929.4436	1840.8534	920.9304	1839.8694	920.4383	15
3	464.2075	232.6074	447.1809	224.0941			C	1710.8116	855.9094	1693.7850	847.3961	1692.8010	846.9041	14
4	620.3086	310.6579	603.2820	302.1446			R	***1550.7809***	775.8941	1533.7544	767.3808	1532.7703	766.8888	13
5	735.3355	***368.1714***	718.3090	359.6581	717.3249	359.1661	D	1394.6798	697.8435	1377.6533	689.3303	1376.6692	688.8383	12
6	850.3624	***425.6849***	833.3359	417.1716	832.3519	416.6796	N	***1279.6529***	640.3301	1262.6263	631.8168	1261.6423	631.3248	11
7	1013.4258	507.2165	996.3992	498.7033	995.4152	498.2112	Y	***1164.6259***	582.8166	1147.5994	574.3033	1146.6154	573.8113	10
8	1114.4735	557.7404	1097.4469	549.2271	1096.4629	548.7351	T	***1001.5626***	501.2849	984.5360	492.7717	983.5520	492.2796	9
9	1229.5004	***615.2538***	1212.4738	606.7406	1211.4898	606.2486	D	900.5149	450.7611	883.4884	442.2478	882.5043	441.7558	8
10	1342.5845	671.7959	1325.5579	663.2826	1324.5739	662.7906	L	785.4880	393.2476	768.4614	384.7343			7
11	1441.6529	***721.3301***	1424.6263	712.8168	1423.6423	712.3248	V	672.4039	336.7056	655.3774	328.1923			6
12	1512.6900	***756.8486***	1495.6634	748.3354	1494.6794	747.8434	A	***573.3355***	287.1714	556.3089	278.6581			5
13	1625.7741	***813.3907***	1608.7475	804.8774	1607.7635	804.3854	I	502.2984	251.6528	485.2718	243.1395			4
14	1753.8326	***877.4200***	1736.8061	868.9067	1735.8221	868.4147	Q	***389.2143***	195.1108	372.1878	186.5975			3
15	1867.8756	***934.4414***	1850.8490	925.9281	1849.8650	925.4361	N	***261.1557***	131.0815	244.1292	122.5682			2
16							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of RFCRDNYTDLVAIQNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.5	2012.9738	0.0051	RFCRDNYTDLVAIQNK	Deamidated N6 88.84%
33.3	2012.9738	0.0051	RFCRDNYTDLVAIQNK	Deamidated Q14 6.69%
31.5	2012.9738	0.0051	RFCRDNYTDLVAIQNK	Deamidated N15 4.46%
9.7	2010.9745	2.0044	EETHQKLIANIVDNEQK	
9.7	2010.9745	2.0044	EETHQKLIANIVDNEQK	
8.4	2012.9850	-0.0061	YPKEGTHIMRHSNLASR	
7.0	2012.9877	-0.0088	ANNNSIMSFFKTLVSPNK	
7.0	2012.9877	-0.0088	ANNNSIMSFFKTLVSPNK	
7.0	2012.9877	-0.0088	ANNNSIMSFFKTLVSPNK	
6.7	2012.9799	-0.0010	YPSQVSTAVTPMATATLMK	

Mascot: http://www.matrixscience.com/

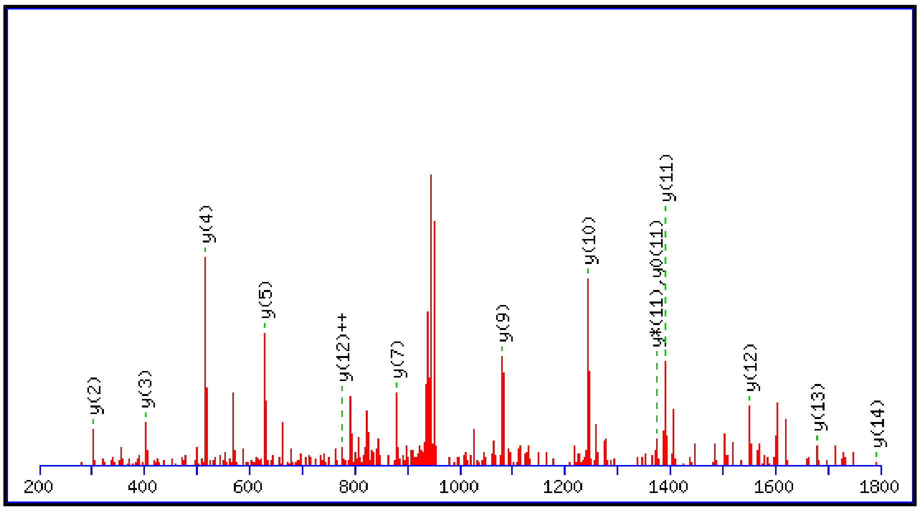
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNQCFYNSSYLNVQR**
Found in **P19652** in **con_Xuniprot_HUMAN3**, A1AG2_HUMAN Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2

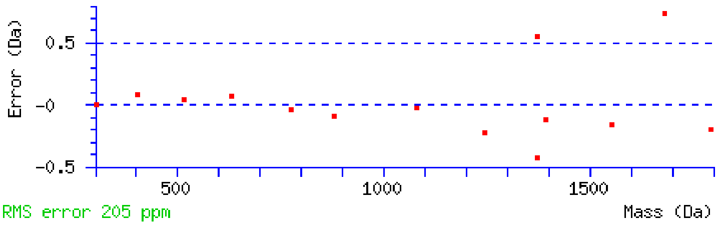
Match to Query 11625: 1920.850288 from(961.432420,2+) intensity(5708.4731) rtinseconds(1344) scans(2580) index(21587)
Title: 111019_Est_MI_YP_G_14Spectrum2180_scans__2580
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

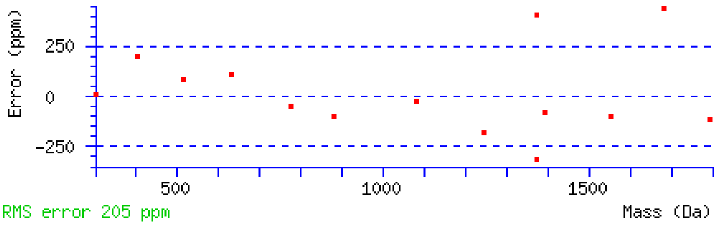
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1920.8424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 92 **Expect:** 7.7e-008
Matches : 14/142 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	129.0659	65.0366	112.0393	56.5233			Q							15
2	243.1088	122.0580	226.0822	113.5448			N	***1793.7912***	897.3992	1776.7646	888.8859	1775.7806	888.3939	14
3	371.1674	186.0873	354.1408	177.5740			Q	***1679.7482***	840.3778	1662.7217	831.8645	1661.7377	831.3725	13
4	531.1980	266.1026	514.1715	257.5894			C	***1551.6897***	776.3485	1534.6631	767.8352	1533.6791	767.3432	12
5	678.2664	339.6368	661.2399	331.1236			F	***1391.6590***	696.3331	1374.6325	687.8199	1373.6484	687.3279	11
6	841.3298	421.1685	824.3032	412.6552			Y	***1244.5906***	622.7989	1227.5640	614.2857	1226.5800	613.7937	10
7	956.3567	478.6820	939.3301	470.1687			N	***1081.5273***	541.2673	1064.5007	532.7540	1063.5167	532.2620	9
8	1043.3887	522.1980	1026.3622	513.6847	1025.3782	513.1927	S	966.5003	483.7538	949.4738	475.2405	948.4898	474.7485	8
9	1130.4208	565.7140	1113.3942	557.2007	1112.4102	556.7087	S	***879.4683***	440.2378	862.4417	431.7245	861.4577	431.2325	7
10	1293.4841	647.2457	1276.4575	638.7324	1275.4735	638.2404	Y	792.4363	396.7218	775.4097	388.2085			6
11	1406.5681	703.7877	1389.5416	695.2744	1388.5576	694.7824	L	***629.3729***	315.1901	612.3464	306.6768			5
12	1520.6111	760.8092	1503.5845	752.2959	1502.6005	751.8039	N	***516.2889***	258.6481	499.2623	250.1348			4
13	1619.6795	810.3434	1602.6529	801.8301	1601.6689	801.3381	V	***402.2459***	201.6266	385.2194	193.1133			3
14	1747.7381	874.3727	1730.7115	865.8594	1729.7275	865.3674	Q	***303.1775***	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QNQCFYNSSYLNVQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
92.0	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated N7 99.99%
49.6	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated N12 0.01%
46.6	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated Q3 0.00%
34.5	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated N2 0.00%
34.5	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated Q1 0.00%
28.9	1920.8424	0.0078	QNQCFYNSSYLNVQR	Deamidated Q14 0.00%
9.3	1920.8450	0.0053	QRETEDNTGDFPIDER	
3.6	1919.8506	0.9997	CLQKMGSGLNSFYDQR	
3.0	1918.8439	2.0064	TSDQPSSTQPNNRPRSM	
2.1	1920.8564	-0.0061	PYEVNAGYDFTNMVRK	

Mascot: http://www.matrixscience.com/

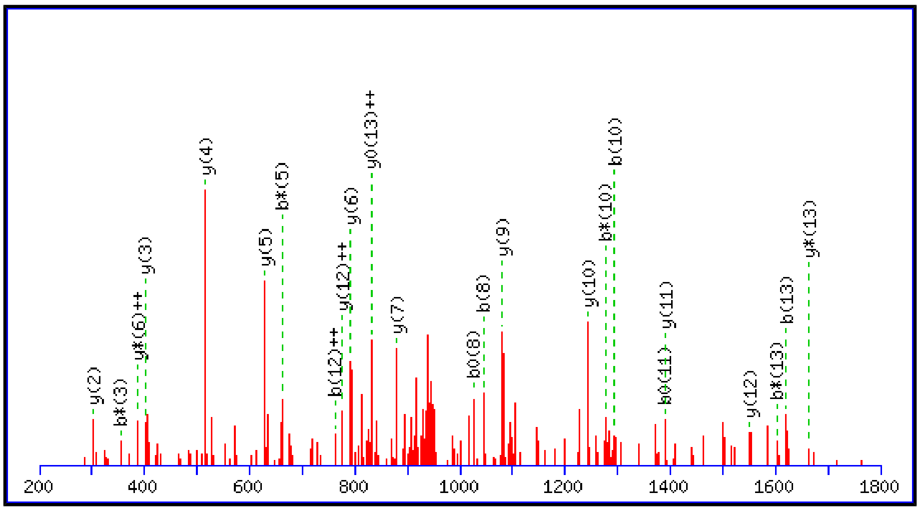
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNQCFYNSSYLNVQR**
Found in **P19652** in **con_Xuniprot_HUMAN3**, A1AG2_HUMAN Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2

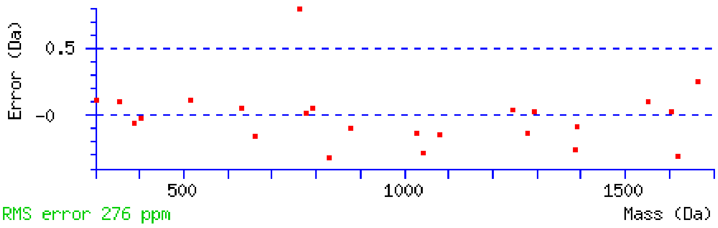
Match to Query 11634: 1921.825528 from(961.920040,2+) intensity(649.6456) rtinseconds(1430) scans(2625) index(7837)
Title: 111019_Est_ISCardio_NMI_YP_G_14Spectrum2190_scans__2625
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

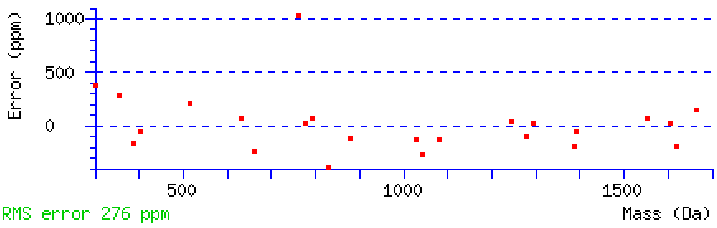
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1921.8264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Deamidated (NQ)
N7 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.008
Matches : 24/142 fragment ions using 58 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			**Q**							**15**
2	243.1088	122.0580	226.0822	113.5448			**N**	1794.7752	897.8912	1777.7486	889.3780	1776.7646	888.8859	**14**
3	372.1514	186.5793	355.1248	178.0661			**Q**	1680.7322	840.8698	1663.7057	832.3565	1662.7217	831.8645	**13**
4	532.1820	266.5947	515.1555	258.0814			**C**	***1551.6897***	776.3485	1534.6631	767.8352	1533.6791	767.3432	**12**
5	679.2504	340.1289	662.2239	331.6156			**F**	***1391.6590***	696.3331	1374.6325	687.8199	1373.6484	687.3279	**11**
6	842.3138	421.6605	825.2872	413.1472			**Y**	***1244.5906***	622.7989	1227.5640	614.2857	1226.5800	613.7937	**10**
7	957.3407	479.1740	940.3142	470.6607			**N**	***1081.5273***	541.2673	1064.5007	532.7540	1063.5167	532.2620	**9**
8	**1044.3727**	522.6900	1027.3462	514.1767	1026.3622	513.6847	**S**	966.5003	483.7538	949.4738	475.2405	948.4898	474.7485	**8**
9	1131.4048	566.2060	1114.3782	557.6927	1113.3942	557.2007	**S**	***879.4683***	440.2378	862.4417	431.7245	861.4577	431.2325	**7**
10	**1294.4681**	647.7377	1277.4415	639.2244	1276.4575	638.7324	**Y**	***792.4363***	396.7218	775.4097	388.2085			**6**
11	1407.5522	704.2797	1390.5256	695.7664	1389.5416	695.2744	**L**	***629.3729***	315.1901	612.3464	306.6768			**5**
12	1521.5951	761.3012	1504.5685	752.7879	1503.5845	752.2959	**N**	***516.2889***	258.6481	499.2623	250.1348			**4**
13	**1620.6635**	810.8354	1603.6370	802.3221	1602.6529	801.8301	**V**	***402.2459***	201.6266	385.2194	193.1133			**3**
14	1748.7221	874.8647	1731.6955	866.3514	1730.7115	865.8594	**Q**	***303.1775***	152.0924	286.1510	143.5791			**2**
15							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of QNQCFYNSSYLNVQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
39.8	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q3, N7 39.99%
38.5	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated N2, N7 29.64%
38.5	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q1, N7 29.64%
15.4	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q3, N12 0.15%
14.9	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated N2, N12 0.13%
14.9	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q1, N12 0.13%
10.3	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q3, Q14 0.04%
9.9	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated N7, N12 0.04%
9.8	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated N2, Q14 0.04%
9.8	1921.8264	-0.0009	QNQCFYNSSYLNVQR	Deamidated Q1, Q14 0.04%

Mascot: http://www.matrixscience.com/

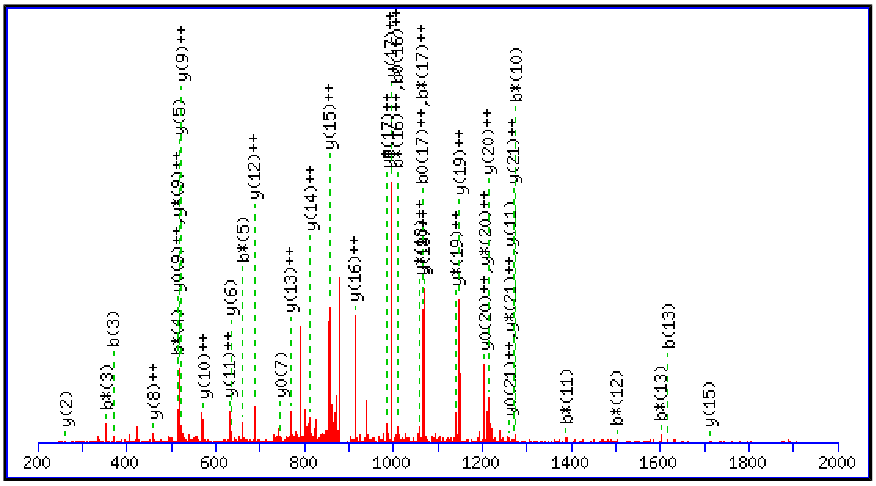
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QNQCFYNSSYLNVQRENGTVSR**
Found in **P19652** in **con_Xuniprot_HUMAN3**, A1AG2_HUMAN Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2

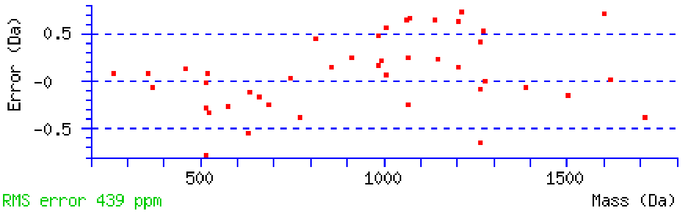
Match to Query 22384: 2665.189002 from(889.403610,3+) intensity(16984.2383) rtinseconds(1265) scans(3046) index(26553)
Title: 111019_Est_MI_YS_G_09Spectrum2623_scans__3046
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

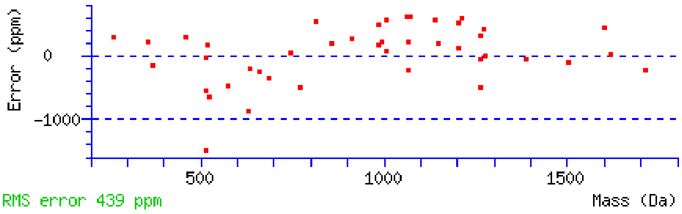
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2665.1827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Deamidated (NQ)
N17     : Deamidated (NQ)
Ions Score: 36  Expect: 0.033
Matches : 43/236 fragment ions using 116 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	243.1088	122.0580	226.0822	113.5448			N	2538.1314	1269.5693	2521.1048	1261.0561	2520.1208	1260.5641	21
3	371.1674	186.0873	354.1408	177.5740			Q	2424.0885	1212.5479	2407.0619	1204.0346	2406.0779	1203.5426	20
4	531.1980	266.1026	514.1715	257.5894			C	2296.0299	1148.5186	2279.0033	1140.0053	2278.0193	1139.5133	19
5	678.2664	339.6368	661.2399	331.1236			F	2135.9992	1068.5033	2118.9727	1059.9900	2117.9887	1059.4980	18
6	841.3298	421.1685	824.3032	412.6552			Y	1988.9308	994.9690	1971.9043	986.4558	1970.9203	985.9638	17
7	955.3727	478.1900	938.3461	469.6767			N	1825.8675	913.4374	1808.8409	904.9241	1807.8569	904.4321	16
8	1042.4047	521.7060	1025.3782	513.1927	1024.3941	512.7007	S	**1711.8246**	856.4159	1694.7980	847.9026	1693.8140	847.4106	15
9	1129.4367	565.2220	1112.4102	556.7087	1111.4262	556.2167	S	1624.7925	812.8999	1607.7660	804.3866	1606.7820	803.8946	14
10	1292.5001	646.7537	1275.4735	638.2404	1274.4895	637.7484	Y	1537.7605	769.3839	1520.7340	760.8706	1519.7499	760.3786	13
11	1405.5841	703.2957	1388.5576	694.7824	1387.5736	694.2904	L	1374.6972	687.8522	1357.6706	679.3390	1356.6866	678.8469	12
12	1519.6271	760.3172	1502.6005	751.8039	1501.6165	751.3119	N	**1261.6131**	631.3102	1244.5866	622.7969	1243.6026	622.3049	11
13	1618.6955	809.8514	1601.6689	801.3381	1600.6849	800.8461	V	1147.5702	574.2887	1130.5436	565.7755	1129.5596	565.2835	10
14	1747.7381	874.3727	1730.7115	865.8594	1729.7275	865.3674	Q	1048.5018	524.7545	1031.4752	516.2413	1030.4912	515.7492	9
15	1903.8392	952.4232	1886.8126	943.9100	1885.8286	943.4179	R	919.4592	460.2332	902.4326	451.7200	901.4486	451.2279	8
16	2032.8818	1016.9445	2015.8552	1008.4312	2014.8712	1007.9392	E	763.3581	382.1827	746.3315	373.6694	745.3475	373.1774	7
17	2147.9087	1074.4580	2130.8822	1065.9447	2129.8981	1065.4527	N	**634.3155**	317.6614	617.2889	309.1481	616.3049	308.6561	6
18	2204.9302	1102.9687	2187.9036	1094.4554	2186.9196	1093.9634	G	**519.2885**	260.1479	502.2620	251.6346	501.2780	251.1426	5
19	2305.9779	1153.4926	2288.9513	1144.9793	2287.9673	1144.4873	T	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
20	2405.0463	1203.0268	2388.0197	1194.5135	2387.0357	1194.0215	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
21	2492.0783	1246.5428	2475.0517	1238.0295	2474.0677	1237.5375	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of QNQCFYNSSYLNVQRENGTVSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
36.5	2665.1827	0.0063	QNQCFYNSSYLNVQRENGTVSR	Deamidated Q14, N17 59.64%
32.6	2665.1827	0.0063	QNQCFYNSSYLNVQRENGTVSR	Deamidated N7, N12 24.13%
29.6	2665.1827	0.0063	QNQCFYNSSYLNVQRENGTVSR	Deamidated N12, Q14 12.35%
22.9	2664.1987	0.9903	QNQCFYNSSYLNVQRENGTVSR	
22.9	2664.1987	0.9903	QNQCFYNSSYLNVQRENGTVSR	
22.8	2665.1827	0.0063	QNQCFYNSSYLNVQRENGTVSR	Deamidated Q1, N17 2.57%
21.9	2664.1987	0.9903	QNQCFYNSSYLNVQRENGTVSR	
18.2	2665.1827	0.0063	QNQCFYNSSYLNVQRENGTVSR	Deamidated Q3, N7 0.89%
16.9	2664.1987	0.9903	QNQCFYNSSYLNVQRENGTVSR	
4.0	2665.1959	-0.0069	EGAGVDMKAQGMAQSQGEALPNTRGK	

Mascot: http://www.matrixscience.com/

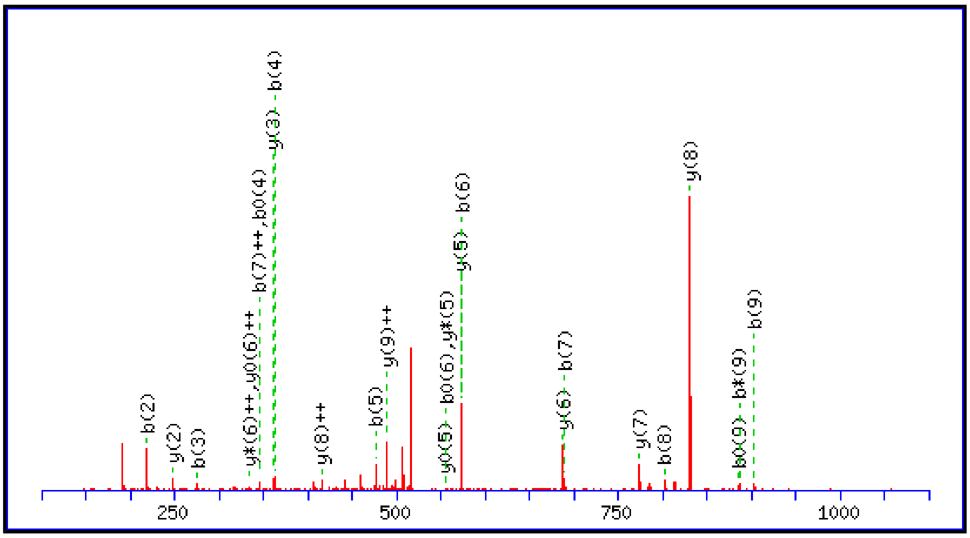
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFGSNPNLTK**
Found in **P22792** in **con_Xuniprot_HUMAN3**, CPN2_HUMAN Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

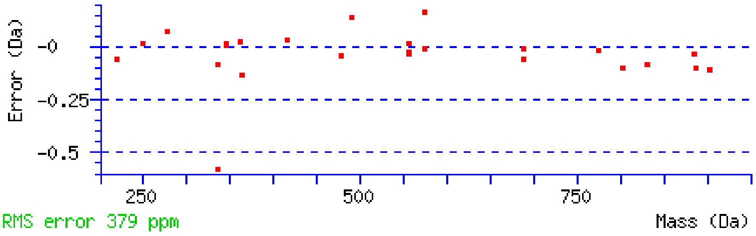
Match to Query 191: 1048.519708 from(525.267130,2+) intensity(72408.2422) rtinseconds(455) scans(869) index(6864)
Title: 111019_Est_ISCardio_NMI_YP_G_10Spectrum710_scans__869
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

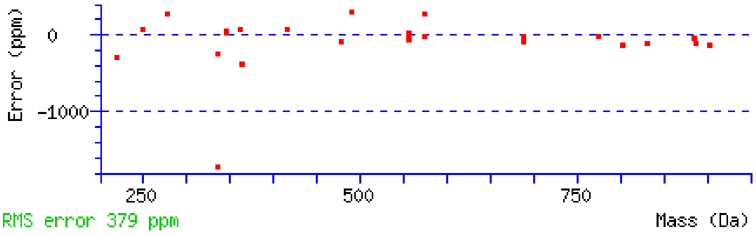
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1048.5189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 63 **Expect:** 0.0001
Matches : 25/92 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	72.0444	36.5258					A							10
2	***219.1128***	110.0600					F	978.4891	489.7482	961.4625	481.2349	960.4785	480.7429	9
3	***276.1343***	138.5708					G	**831.4207**	416.2140	814.3941	407.7007	813.4101	407.2087	8
4	***363.1663***	182.0868			345.1557	173.0815	S	**774.3992**	387.7032	757.3727	379.1900	756.3886	378.6980	7
5	***477.2092***	239.1082	460.1827	230.5950	459.1987	230.1030	N	**687.3672**	344.1872	670.3406	335.6740	669.3566	335.1819	6
6	***574.2620***	287.6346	557.2354	279.1214	556.2514	278.6293	P	**573.3243**	287.1658	556.2977	278.6525	555.3137	278.1605	5
7	***689.2889***	345.1481	672.2624	336.6348	671.2784	336.1428	N	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
8	***802.3730***	401.6901	785.3464	393.1769	784.3624	392.6849	L	**361.2445**	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	***903.4207***	452.2140	886.3941	443.7007	885.4101	443.2087	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AFGSNPNLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
63.3	1048.5189	0.0008	AFGSNPNLTK	Deamidated N7 99.81%
36.1	1048.5189	0.0008	AFGSNPNLTK	Deamidated N5 0.19%
24.5	1048.5223	-0.0026	SCLVISNEK	
11.2	1048.5148	0.0049	EASRNKSEK	
11.2	1048.5148	0.0049	QASRNKSEK	
9.8	1048.5149	0.0048	TSRNNDTLK	
8.8	1048.5149	0.0048	LTGTSNNSAGK	
8.6	1048.5149	0.0048	TSRNNDTLK	
8.3	1048.5223	-0.0026	MAASQVLGEK	
7.6	1048.5149	0.0048	RETEGKDSK	

Mascot: http://www.matrixscience.com/

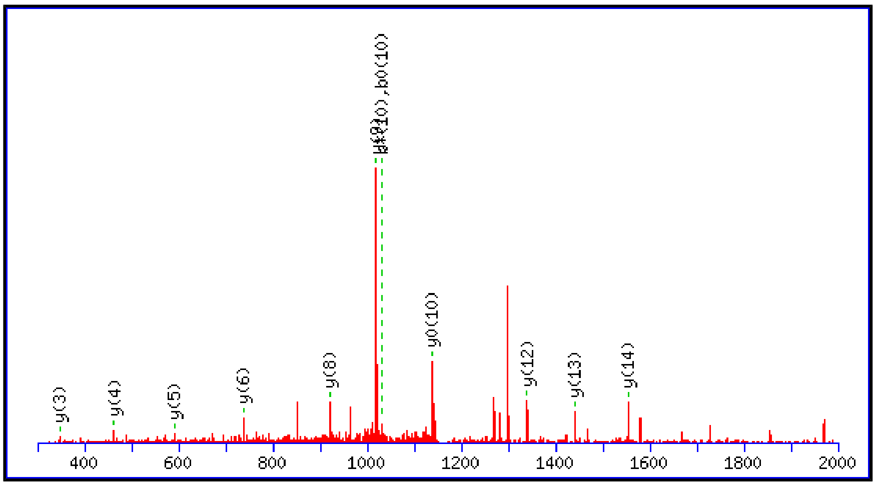
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYLGSNNLTALHPALFQNLSK**
Found in **P22792** in **con_Xuniprot_HUMAN3**, CPN2_HUMAN Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

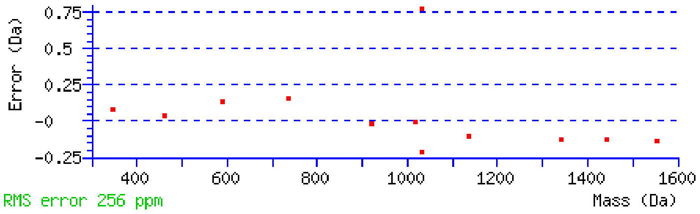
Match to Query 15444: 2315.236668 from(1158.625610,2+) intensity(0.0000) rtinseconds(2124) scans(5548) index(6592)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4880_scans__5548
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

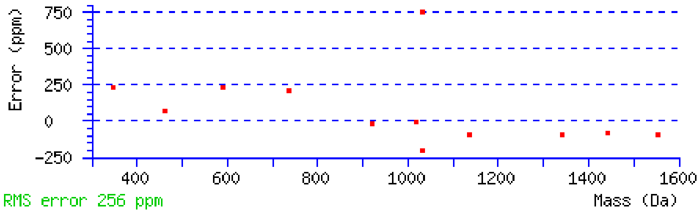
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2314.2321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N18 : Deamidated (NQ)
Ions Score: 54 **Expect:** 0.00054
Matches : 12/220 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	114.0913	57.5493					**L**							**21**
2	277.1547	139.0810					**Y**	2202.1553	1101.5813	2185.1288	1093.0680	2184.1448	1092.5760	**20**
3	390.2387	195.6230					**L**	2039.0920	1020.0496	2022.0655	1011.5364	2021.0815	1011.0444	**19**
4	447.2602	224.1337					**G**	1926.0080	963.5076	1908.9814	954.9943	1907.9974	954.5023	**18**
5	534.2922	267.6498			516.2817	258.6445	**S**	1868.9865	934.9969	1851.9599	926.4836	1850.9759	925.9916	**17**
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	**N**	1781.9545	891.4809	1764.9279	882.9676	1763.9439	882.4756	**16**
7	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	**N**	1667.9115	834.4594	1650.8850	825.9461	1649.9010	825.4541	**15**
8	875.4621	438.2347	858.4356	429.7214	857.4516	429.2294	**L**	***1553.8686***	777.4379	1536.8421	768.9247	1535.8580	768.4327	**14**
9	976.5098	488.7585	959.4833	480.2453	958.4993	479.7533	**T**	***1440.7845***	720.8959	1423.7580	712.3826	1422.7740	711.8906	**13**
10	1047.5469	524.2771	1030.5204	515.7638	1029.5364	515.2718	**A**	***1339.7369***	670.3721	1322.7103	661.8588	1321.7263	661.3668	**12**
11	1160.6310	580.8191	1143.6045	572.3059	1142.6204	571.8139	**L**	1268.6997	634.8535	1251.6732	626.3402	1250.6892	625.8482	**11**
12	1297.6899	649.3486	1280.6634	640.8353	1279.6793	640.3433	**H**	1155.6157	578.3115	1138.5891	569.7982	1137.6051	569.3062	**10**
13	1394.7427	697.8750	1377.7161	689.3617	1376.7321	688.8697	**P**	***1018.5568***	509.7820	1001.5302	501.2688	1000.5462	500.7767	**9**
14	1465.7798	733.3935	1448.7532	724.8803	1447.7692	724.3883	**A**	***921.5040***	461.2556	904.4775	452.7424	903.4934	452.2504	**8**
15	1578.8639	789.9356	1561.8373	781.4223	1560.8533	780.9303	**L**	850.4669	425.7371	833.4403	417.2238	832.4563	416.7318	**7**
16	1725.9323	863.4698	1708.9057	854.9565	1707.9217	854.4645	**F**	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
17	1853.9908	927.4991	1836.9643	918.9858	1835.9803	918.4938	**Q**	***590.3144***	295.6608	573.2879	287.1476	572.3039	286.6556	**5**
18	1969.0178	985.0125	1951.9912	976.4993	1951.0072	976.0073	**N**	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	**4**
19	2082.1019	1041.5546	2065.0753	1033.0413	2064.0913	1032.5493	**L**	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	**3**
20	2169.1339	1085.0706	2152.1073	1076.5573	2151.1233	1076.0653	**S**	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
21							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LYLGSNNLTALHPALFQNLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.4	2314.2321	1.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N18 94.60%
42.0	2314.2321	1.0046	LYLGSNNLTALHPALFQNLSK	Deamidated Q17 5.39%
8.4	2314.2321	1.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N7 0.00%
8.4	2314.2321	1.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N6 0.00%

Mascot: http://www.matrixscience.com/

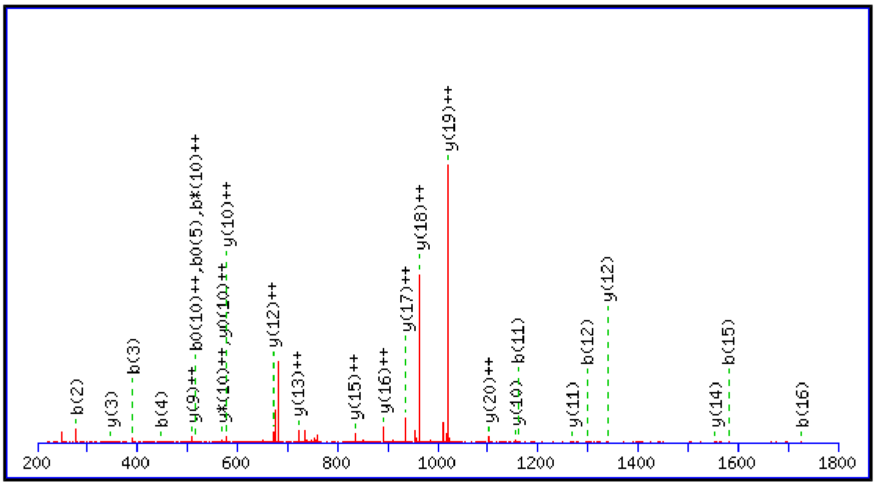
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYLGSNNLTALHPALFQNLSK**
Found in **P22792** in **con_Xuniprot_HUMAN3**, CPN2_HUMAN Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3

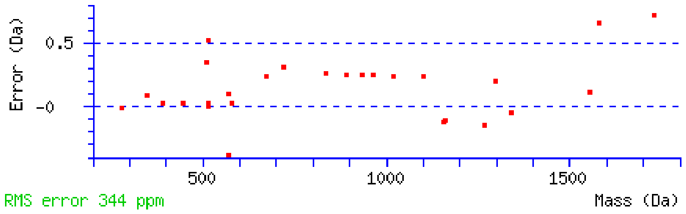
Match to Query 15442: 2315.220732 from(772.747520,3+) intensity(257583.1094) rtinseconds(2134) scans(5575) index(6594)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4904_scans__5575
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

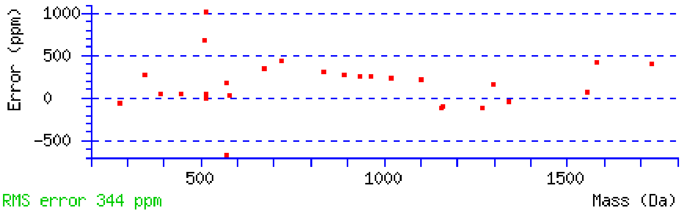
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1800] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2315.2161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7     : Deamidated (NQ)
N18    : Deamidated (NQ)
Ions Score: 53  Expect: 0.001
Matches : 27/220 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	114.0913	57.5493					L							21
2	***277.1547***	139.0810					Y	2203.1394	1102.0733	2186.1128	1093.5600	2185.1288	1093.0680	20
3	***390.2387***	195.6230					L	2040.0760	1020.5417	2023.0495	1012.0284	2022.0655	1011.5364	19
4	***447.2602***	224.1337					G	1926.9920	963.9996	1909.9654	955.4863	1908.9814	954.9943	18
5	534.2922	267.6498			516.2817	258.6445	S	1869.9705	935.4889	1852.9440	926.9756	1851.9599	926.4836	17
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	N	1782.9385	891.9729	1765.9119	883.4596	1764.9279	882.9676	16
7	763.3621	382.1847	746.3355	373.6714	745.3515	373.1794	N	1668.8955	834.9514	1651.8690	826.4381	1650.8850	825.9461	15
8	876.4462	438.7267	859.4196	430.2134	858.4356	429.7214	L	***1553.8686***	777.4379	1536.8421	768.9247	1535.8580	768.4327	14
9	977.4938	489.2506	960.4673	480.7373	959.4833	480.2453	T	1440.7845	720.8959	1423.7580	712.3826	1422.7740	711.8906	13
10	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	A	***1339.7369***	670.3721	1322.7103	661.8588	1321.7263	661.3668	12
11	***1161.6150***	581.3111	1144.5885	572.7979	1143.6045	572.3059	L	***1268.6997***	634.8535	1251.6732	626.3402	1250.6892	625.8482	11
12	***1298.6739***	649.8406	1281.6474	641.3273	1280.6634	640.8353	H	***1155.6157***	578.3115	1138.5891	569.7982	1137.6051	569.3062	10
13	1395.7267	698.3670	1378.7001	689.8537	1377.7161	689.3617	P	1018.5568	509.7820	1001.5302	501.2688	1000.5462	500.7767	9
14	1466.7638	733.8855	1449.7373	725.3723	1448.7532	724.8803	A	921.5040	461.2556	904.4775	452.7424	903.4934	452.2504	8
15	***1579.8479***	790.4276	1562.8213	781.9143	1561.8373	781.4223	L	850.4669	425.7371	833.4403	417.2238	832.4563	416.7318	7
16	***1726.9163***	863.9618	1709.8897	855.4485	1708.9057	854.9565	F	737.3828	369.1951	720.3563	360.6818	719.3723	360.1898	6
17	1854.9749	927.9911	1837.9483	919.4778	1836.9643	918.9858	Q	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	5
18	1970.0018	985.5045	1952.9753	976.9913	1951.9912	976.4993	N	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
19	2083.0859	1042.0466	2066.0593	1033.5333	2065.0753	1033.0413	L	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
20	2170.1179	1085.5626	2153.0913	1077.0493	2152.1073	1076.5573	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
21							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LYLGSNNLTALHPALFQNLSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.8	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N7, N18 24.11%
52.8	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N7, Q17 24.11%
52.8	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N6, N18 24.11%
52.8	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N6, Q17 24.11%
44.4	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated Q17, N18 3.48%
28.4	2315.2161	0.0046	LYLGSNNLTALHPALFQNLSK	Deamidated N6, N7 0.09%
6.7	2314.2216	0.9991	GPSHIPTLRSGIVMEVPPGNTR	
6.4	2315.2154	0.0053	EMLQRAARSPSIALQLITGNK	
5.9	2314.2251	0.9956	LAGLPMIPLLQMQNVSIWMK	
4.9	2314.2090	1.0118	LDLKVLVMNNQLEALTQDQK	

Mascot: http://www.matrixscience.com/

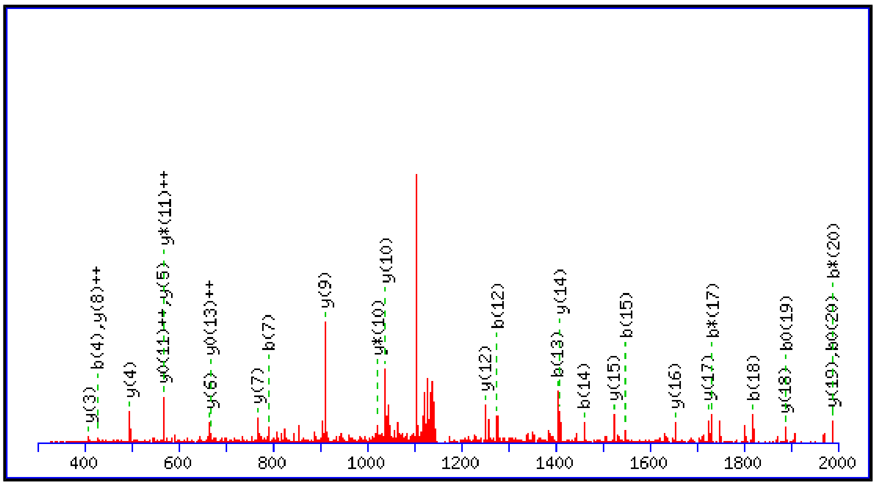
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTQVYAENGTVLQGSTVASVYK**
Found in **F5H4W9** in **con_Xuniprot_HUMAN3**, F5H4W9_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=2 SV=1

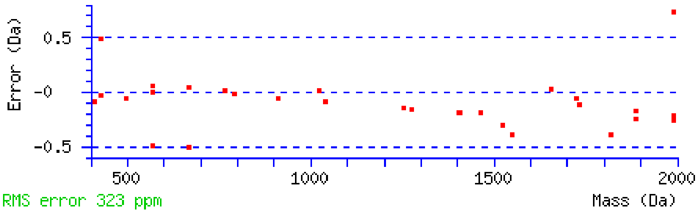
Match to Query 15361: 2314.178848 from(1158.096700,2+) intensity(17772.5078) rtinseconds(1408) scans(3617) index(23902)
Title: 111019_Est_MI_YS_G_05Spectrum3117_scans__3617
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

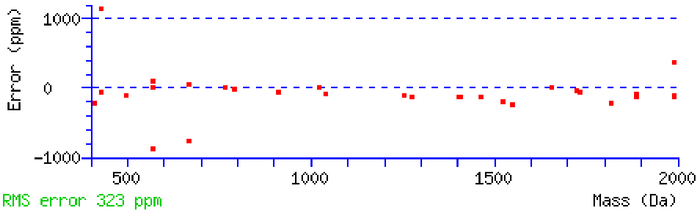
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2314.1693
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 124 **Expect:** 1e-010
Matches : 30/240 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	100.0757	50.5415					V							22
2	201.1234	101.0653			183.1128	92.0600	T	2216.1081	1108.5577	2199.0816	1100.0444	2198.0976	1099.5524	21
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	2115.0604	1058.0339	2098.0339	1049.5206	2097.0499	1049.0286	20
4	**428.2504**	214.6288	411.2238	206.1155	410.2398	205.6235	V	***1987.0019***	994.0046	1969.9753	985.4913	1968.9913	984.9993	19
5	591.3137	296.1605	574.2871	287.6472	573.3031	287.1552	Y	***1887.9335***	944.4704	1870.9069	935.9571	1869.9229	935.4651	18
6	662.3508	331.6790	645.3243	323.1658	644.3402	322.6738	A	***1724.8701***	862.9387	1707.8436	854.4254	1706.8596	853.9334	17
7	**791.3934**	396.2003	774.3668	387.6871	773.3828	387.1951	E	***1653.8330***	827.4201	1636.8065	818.9069	1635.8224	818.4149	16
8	906.4203	453.7138	889.3938	445.2005	888.4098	444.7085	N	***1524.7904***	762.8988	1507.7639	754.3856	1506.7799	753.8936	15
9	963.4418	482.2245	946.4153	473.7113	945.4312	473.2193	G	***1409.7635***	705.3854	1392.7369	696.8721	1391.7529	696.3801	14
10	1064.4895	532.7484	1047.4629	524.2351	1046.4789	523.7431	T	1352.7420	676.8746	1335.7155	668.3614	1334.7314	667.8694	13
11	1163.5579	582.2826	1146.5313	573.7693	1145.5473	573.2773	V	***1251.6943***	626.3508	1234.6678	617.8375	1233.6838	617.3455	12
12	**1276.6420**	638.8246	1259.6154	630.3113	1258.6314	629.8193	L	1152.6259	576.8166	1135.5994	568.3033	1134.6154	567.8113	11
13	**1404.7005**	702.8539	1387.6740	694.3406	1386.6900	693.8486	Q	***1039.5419***	520.2746	1022.5153	511.7613	1021.5313	511.2693	10
14	**1461.7220**	731.3646	1444.6955	722.8514	1443.7114	722.3594	G	***911.4833***	456.2453	894.4567	447.7320	893.4727	447.2400	9
15	**1548.7540**	774.8807	1531.7275	766.3674	1530.7435	765.8754	S	854.4618	427.7345	837.4353	419.2213	836.4512	418.7293	8
16	1649.8017	825.4045	1632.7752	816.8912	1631.7911	816.3992	T	***767.4298***	384.2185	750.4032	375.7053	749.4192	375.2132	7
17	1748.8701	874.9387	1731.8436	866.4254	1730.8596	865.9334	V	***666.3821***	333.6947	649.3556	325.1814	648.3715	324.6894	6
18	**1819.9072**	910.4573	1802.8807	901.9440	1801.8967	901.4520	A	***567.3137***	284.1605	550.2871	275.6472	549.3031	275.1552	5
19	1906.9393	953.9733	1889.9127	945.4600	1888.9287	944.9680	S	***496.2766***	248.6419	479.2500	240.1287	478.2660	239.6366	4
20	2006.0077	1003.5075	1988.9811	994.9942	1987.9971	994.5022	V	***409.2445***	205.1259	392.2180	196.6126			3
21	2169.0710	1085.0391	2152.0445	1076.5259	2151.0604	1076.0339	Y	310.1761	155.5917	293.1496	147.0784			2
22							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VTQVYAENGTVLQGSTVASVYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
123.8	2314.1693	0.0096	VTQVYAENGTVLQGSTVASVYK	Deamidated N8 99.99%
81.1	2314.1693	0.0096	VTQVYAENGTVLQGSTVASVYK	Deamidated Q13 0.01%
76.1	2314.1693	0.0096	VTQVYAENGTVLQGSTVASVYK	Deamidated Q3 0.00%
73.4	2313.1853	0.9936	VTQVYAENGTVLQGSTVASVYK	
3.7	2312.1794	1.9994	HRDSLDLSQSLMASPSAAAVLK	

Mascot: http://www.matrixscience.com/

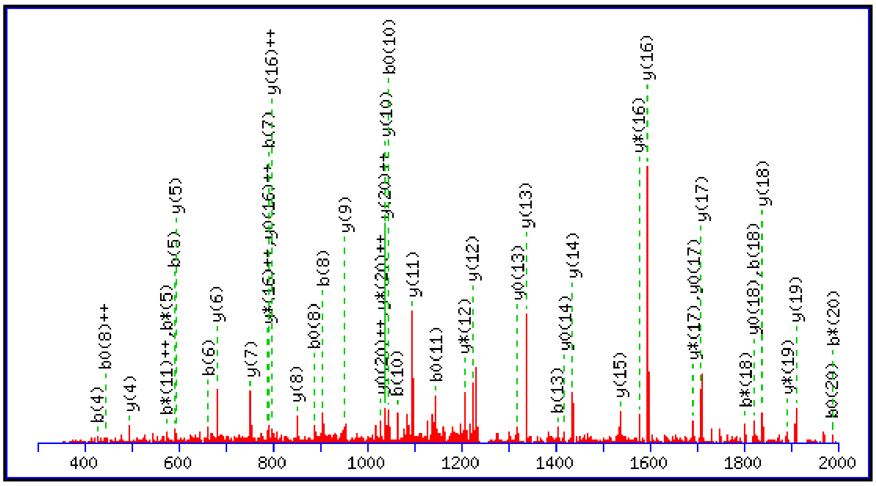
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTQVYAENGTVLQGSTVASVYKGK**
Found in **F5H4W9** in **con_Xuniprot_HUMAN3**, F5H4W9_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=2 SV=1

Match to Query 21583: 2499.298168 from(1250.656360,2+) intensity(28029.2520) rtinseconds(1616) scans(3612) index(16769)
Title: 111019_Est_MI_YP_G_06Spectrum3011_scans__3612
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

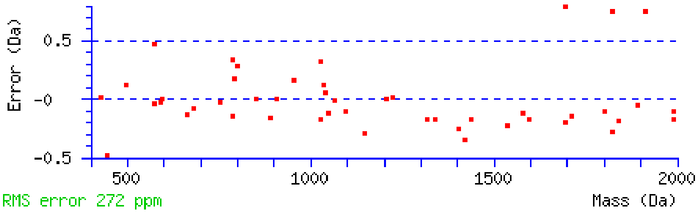
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

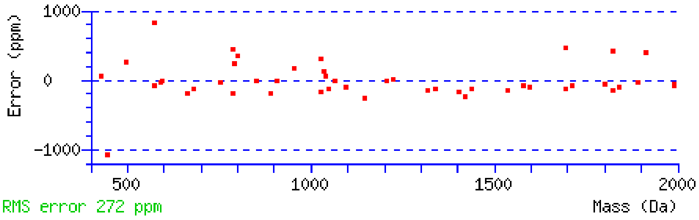


Monoisotopic mass of neutral peptide Mr(calc): 2499.2857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 106 **Expect:** 4.5e-009
Matches : 47/260 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					**V**							24
2	201.1234	101.0653			183.1128	92.0600	**T**	2401.2245	1201.1159	2384.1980	1192.6026	2383.2140	1192.1106	23
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	**Q**	2300.1769	1150.5921	2283.1503	1142.0788	2282.1663	1141.5868	22
4	**428.2504**	214.6288	411.2238	206.1155	410.2398	205.6235	**V**	2172.1183	1086.5628	2155.0917	1078.0495	2154.1077	1077.5575	21
5	**591.3137**	296.1605	574.2871	287.6472	573.3031	287.1552	**Y**	2073.0499	1037.0286	2056.0233	1028.5153	2055.0393	1028.0233	20
6	**662.3508**	331.6790	645.3243	323.1658	644.3402	322.6738	**A**	***1909.9866***	955.4969	1892.9600	946.9836	1891.9760	946.4916	19
7	**791.3934**	396.2003	774.3668	387.6871	773.3828	387.1951	**E**	***1838.9494***	919.9784	1821.9229	911.4651	1820.9389	910.9731	18
8	**906.4203**	453.7138	889.3938	445.2005	888.4098	444.7085	**N**	***1709.9068***	855.4571	1692.8803	846.9438	1691.8963	846.4518	17
9	963.4418	482.2245	946.4153	473.7113	945.4312	473.2193	**G**	***1594.8799***	797.9436	1577.8534	789.4303	1576.8693	788.9383	16
10	**1064.4895**	532.7484	1047.4629	524.2351	1046.4789	523.7431	**T**	***1537.8584***	769.4329	1520.8319	760.9196	1519.8479	760.4276	15
11	1163.5579	582.2826	1146.5313	573.7693	1145.5473	573.2773	**V**	***1436.8108***	718.9090	1419.7842	710.3957	1418.8002	709.9037	14
12	1276.6420	638.8246	1259.6154	630.3113	1258.6314	629.8193	**L**	***1337.7423***	669.3748	1320.7158	660.8615	1319.7318	660.3695	13
13	**1404.7005**	702.8539	1387.6740	694.3406	1386.6900	693.8486	**Q**	***1224.6583***	612.8328	1207.6317	604.3195	1206.6477	603.8275	12
14	1461.7220	731.3646	1444.6955	722.8514	1443.7114	722.3594	**G**	***1096.5997***	548.8035	1079.5732	540.2902	1078.5891	539.7982	11
15	1548.7540	774.8807	1531.7275	766.3674	1530.7435	765.8754	**S**	***1039.5782***	520.2928	1022.5517	511.7795	1021.5677	511.2875	10
16	1649.8017	825.4045	1632.7752	816.8912	1631.7911	816.3992	**T**	***952.5462***	476.7767	935.5197	468.2635	934.5356	467.7715	9
17	1748.8701	874.9387	1731.8436	866.4254	1730.8596	865.9334	**V**	***851.4985***	426.2529	834.4720	417.7396	833.4880	417.2476	8
18	**1819.9072**	910.4573	1802.8807	901.9440	1801.8967	901.4520	**A**	***752.4301***	376.7187	735.4036	368.2054	734.4196	367.7134	7
19	1906.9393	953.9733	1889.9127	945.4600	1888.9287	944.9680	**S**	***681.3930***	341.2001	664.3665	332.6869	663.3824	332.1949	6
20	2006.0077	1003.5075	1988.9811	994.9942	1987.9971	994.5022	**V**	***594.3610***	297.6841	577.3344	289.1709			5
21	2169.0710	1085.0391	2152.0445	1076.5259	2151.0604	1076.0339	**Y**	***495.2926***	248.1499	478.2660	239.6366			4
22	2297.1660	1149.0866	2280.1394	1140.5733	2279.1554	1140.0813	**K**	332.2292	166.6183	315.2027	158.1050			3
23	2354.1874	1177.5974	2337.1609	1169.0841	2336.1769	1168.5921	**G**	204.1343	102.5708	187.1077	94.0575			2

24							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VTQVYAENGTVLQGSTVASVYKGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
106.3	2499.2857	0.0125	VTQVYAENGTVLQGSTVASVYKGK	Deamidated N8 96.72%
91.5	2499.2857	0.0125	VTQVYAENGTVLQGSTVASVYKGK	Deamidated Q13 3.20%
75.3	2499.2857	0.0125	VTQVYAENGTVLQGSTVASVYKGK	Deamidated Q3 0.08%
72.8	2498.3017	0.9965	VTQVYAENGTVLQGSTVASVYKGK	
0.4	2499.2870	0.0112	VQWGPPGRLAQFQKTNVTSEVR	

Mascot: http://www.matrixscience.com/

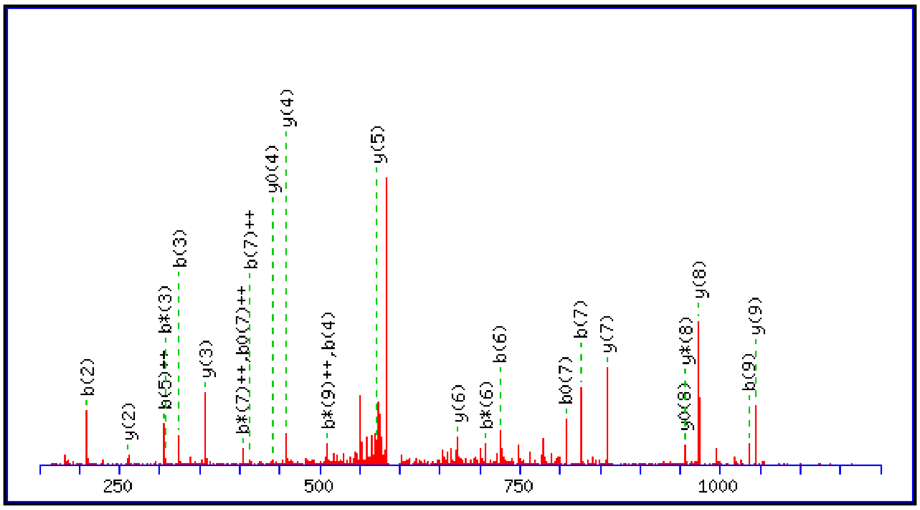
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HANWTLTPLK**
Found in **F5H4W9** in **con_Xuniprot_HUMAN3**, F5H4W9_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=2 SV=1

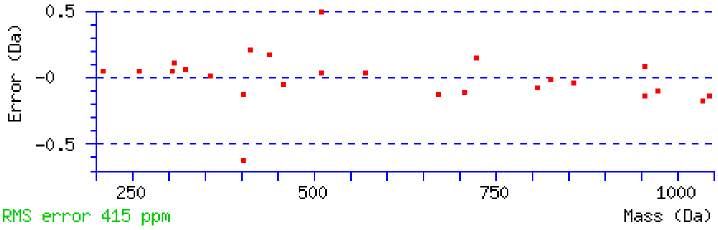
Match to Query 1619: 1180.627228 from(591.320890,2+) intensity(120399.2031) rtinseconds(1023) scans(2410) index(15705)
Title: 111019_Est_MI_YP_G_05Spectrum2041_scans__2410
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

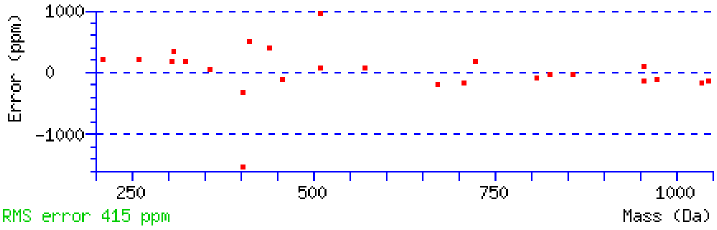
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1180.6240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 40 **Expect:** 0.013
Matches : 25/90 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	138.0662	69.5367					H							10
2	**209.1033**	105.0553					A	***1044.5724***	522.7899	1027.5459	514.2766	1026.5619	513.7846	9
3	**324.1302**	162.5688	307.1037	154.0555			N	***973.5353***	487.2713	956.5088	478.7580	955.5247	478.2660	8
4	**510.2096**	255.6084	493.1830	247.0951			W	***858.5084***	429.7578	841.4818	421.2445	840.4978	420.7525	7
5	611.2572	306.1323	594.2307	297.6190	593.2467	297.1270	T	***672.4291***	336.7182	655.4025	328.2049	654.4185	327.7129	6
6	**724.3413**	362.6743	707.3148	354.1610	706.3307	353.6690	L	***571.3814***	286.1943	554.3548	277.6811	553.3708	277.1890	5
7	**825.3890**	413.1981	808.3624	404.6849	807.3784	404.1928	T	***458.2973***	229.6523	441.2708	221.1390	440.2867	220.6470	4
8	922.4417	461.7245	905.4152	453.2112	904.4312	452.7192	P	***357.2496***	179.1285	340.2231	170.6152			3
9	**1035.5258**	518.2665	1018.4993	509.7533	1017.5152	509.2613	L	***260.1969***	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of HANWTLTPLK
(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	1180.6240	0.0032	HANWTLTPLK
2.3	1180.6274	-0.0002	GSGPPGCLVLPK

Mascot: http://www.matrixscience.com/

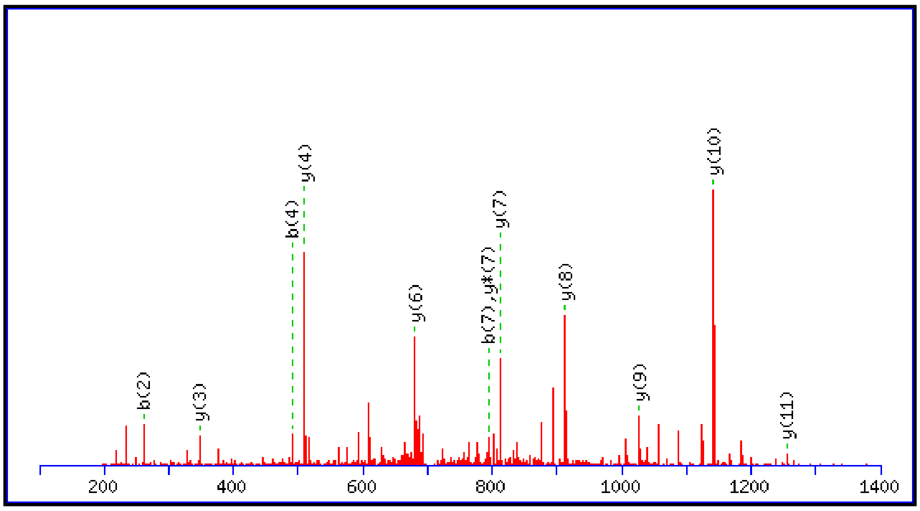
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FLNDTMAVYEAK**
Found in **P29622** in **con_Xuniprot_HUMAN3**, KAIN_HUMAN Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3

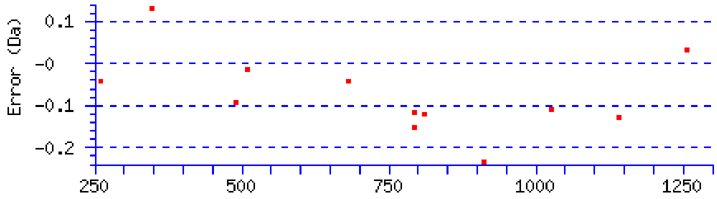
Match to Query 2410: 1401.652948 from(701.833750,2+) intensity(68505.5391) rtinseconds(1371) scans(3249) index(12559)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2834_scans__3249
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐

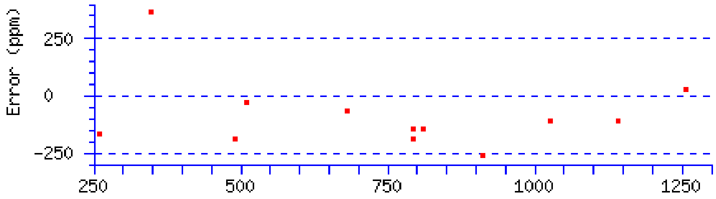


Monoisotopic mass of neutral peptide Mr(calc): 1401.6486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
Ions Score: 78 **Expect:** 2.4e-006
Matches : 12/118 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							12
2	**261.1598**	131.0835					L	***1255.5875***	628.2974	1238.5609	619.7841	1237.5769	619.2921	11
3	376.1867	188.5970	359.1601	180.0837			N	***1142.5034***	571.7553	1125.4769	563.2421	1124.4929	562.7501	10
4	**491.2136**	246.1105	474.1871	237.5972	473.2031	237.1052	D	***1027.4765***	514.2419	1010.4499	505.7286	1009.4659	505.2366	9
5	592.2613	296.6343	575.2348	288.1210	574.2508	287.6290	T	***912.4495***	456.7284	895.4230	448.2151	894.4390	447.7231	8
6	723.3018	362.1545	706.2753	353.6413	705.2912	353.1493	M	***811.4019***	406.2046	794.3753	397.6913	793.3913	397.1993	7
7	**794.3389**	397.6731	777.3124	389.1598	776.3284	388.6678	A	***680.3614***	340.6843	663.3348	332.1710	662.3508	331.6790	6
8	893.4073	447.2073	876.3808	438.6940	875.3968	438.2020	V	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
9	1056.4707	528.7390	1039.4441	520.2257	1038.4601	519.7337	Y	***510.2558***	255.6316	493.2293	247.1183	492.2453	246.6263	4
10	1185.5133	593.2603	1168.4867	584.7470	1167.5027	584.2550	E	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
11	1256.5504	628.7788	1239.5238	620.2655	1238.5398	619.7735	A	218.1499	109.5786	201.1234	101.0653			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 176 ppm



RMS error 176 ppm

NCBI **BLAST** search of FLNDTMAVYEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
77.6	1401.6486	0.0044	FLNDTMAVYEAK
15.4	1401.6558	-0.0029	MLNGTHGPSSEKK
15.3	1400.6532	0.9998	STHNASVGGESDIK
10.3	1400.6428	1.0102	NVTEMAMNPHIK
8.2	1400.6502	1.0028	YVSCGMMEALLK
7.7	1400.6428	1.0102	NVTEMAMNPHIK
6.6	1400.6493	1.0036	MQYTSAVTENIK
5.8	1401.6486	0.0044	MEDEFAKELYK
5.7	1400.6428	1.0102	NVTEMAMNPHIK
3.7	1400.6428	1.0102	IHPNMAMETVNK

Mascot: http://www.matrixscience.com/

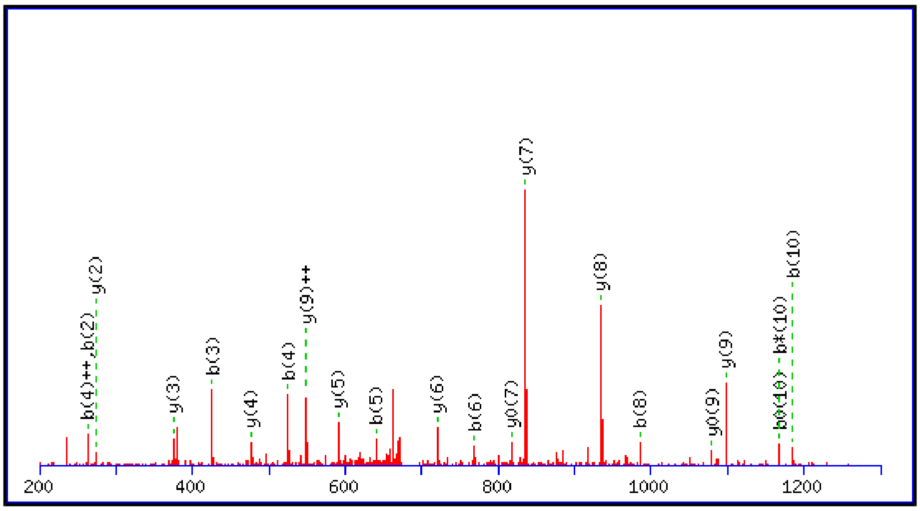
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DFYVDENTTVR**
Found in **P29622** in **con_Xuniprot_HUMAN3**, KAIN_HUMAN Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3

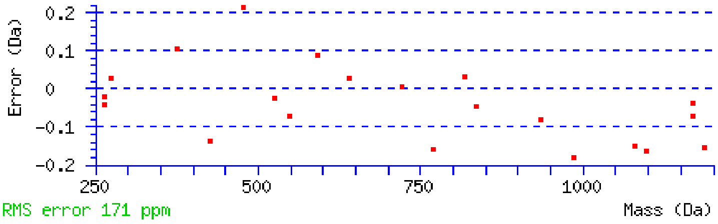
Match to Query 2374: 1358.602648 from(680.308600,2+) intensity(12927.8008) rtinseconds(955) scans(2046) index(27775)
Title: 111019_Est_MI_YS_G_11Spectrum1741_scans__2046
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

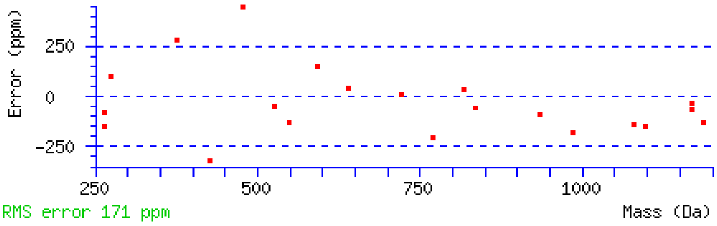
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1358.5990
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00025
Matches : 21/104 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	116.0342	58.5207			98.0237	49.5155	D							11
2	***263.1026***	132.0550			245.0921	123.0497	F	1244.5794	622.7933	1227.5528	614.2800	1226.5688	613.7880	10
3	***426.1660***	213.5866			408.1554	204.5813	Y	***1097.5109***	549.2591	1080.4844	540.7458	1079.5004	540.2538	9
4	***525.2344***	263.1208			507.2238	254.1155	V	***934.4476***	467.7274	917.4211	459.2142	916.4371	458.7222	8
5	***640.2613***	320.6343			622.2508	311.6290	D	***835.3792***	418.1932	818.3527	409.6800	817.3686	409.1880	7
6	***769.3039***	385.1556			751.2933	376.1503	E	***720.3523***	360.6798	703.3257	352.1665	702.3417	351.6745	6
7	884.3309	442.6691	867.3043	434.1558	866.3203	433.6638	N	***591.3097***	296.1585	574.2831	287.6452	573.2991	287.1532	5
8	***985.3785***	493.1929	968.3520	484.6796	967.3680	484.1876	T	***476.2827***	238.6450	459.2562	230.1317	458.2722	229.6397	4
9	1086.4262	543.7167	1069.3997	535.2035	1068.4156	534.7115	T	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	***1185.4946***	593.2510	1168.4681	584.7377	1167.4841	584.2457	V	***274.1874***	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DFYVDENTTVR
(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	1358.5990	0.0036	DFYVDENTTVR
10.9	1356.5941	2.0086	MNELEAFNMLK
6.9	1356.5941	2.0086	MNELEAFNMLK
5.4	1357.6006	1.0020	MLDMSFKDAER
4.9	1358.6062	-0.0036	LSAHVDDSGSQSR
4.7	1358.5993	0.0034	VMCVSMGSTTVR
4.0	1358.5959	0.0068	QLFSKGEMCSR
3.6	1358.6071	-0.0044	MYMRQTESTGR
3.5	1356.5980	2.0047	DFEVSMNTRNK
3.3	1358.5990	0.0037	FNEEAYKESDK

Mascot: http://www.matrixscience.com/

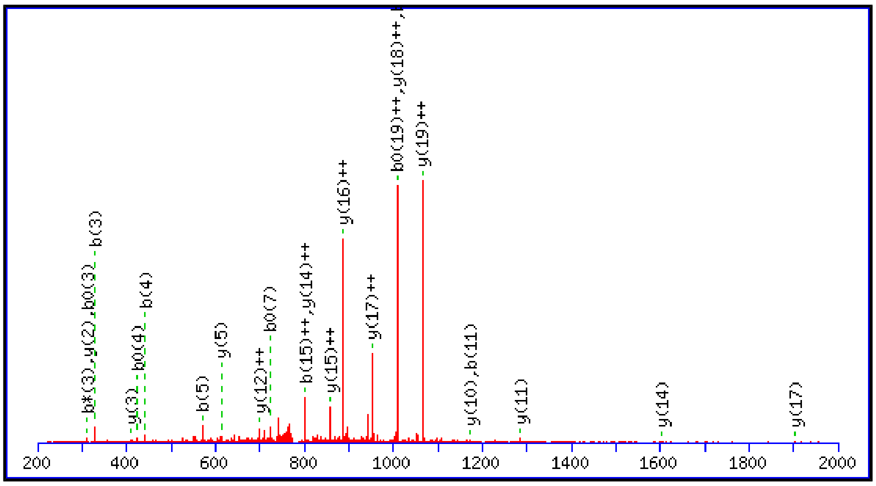
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQILEGLGFNLTELSESDVHR**
Found in **P29622** in **con_Xuniprot_HUMAN3**, KAIN_HUMAN Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3

Match to Query 15496: 2344.163532 from(782.395120,3+) intensity(18527.3359) rtinseconds(2314) scans(6073) index(19855)
Title: 111019_Est_MI_YP_G_09Spectrum5373_scans__6073
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2344.1546

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

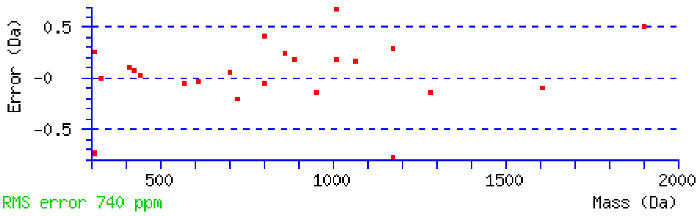
Variable modifications:

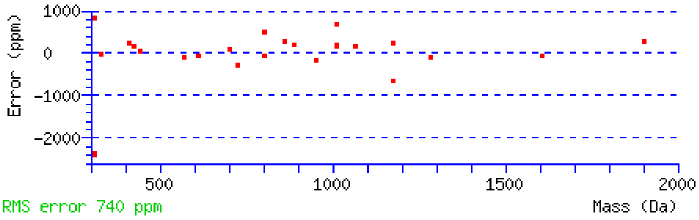
N10 : Deamidated (NQ)

Ions Score: 50 **Expect:** 0.0029

Matches : 25/232 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	88.0393	44.5233			70.0287	35.5180	S							21
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	2258.1299	1129.5686	2241.1034	1121.0553	2240.1194	1120.5633	20
3	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	I	2130.0713	1065.5393	2113.0448	1057.0260	2112.0608	1056.5340	19
4	**442.2660**	221.6366	425.2395	213.1234	424.2554	212.6314	L	2016.9873	1008.9973	1999.9607	1000.4840	1998.9767	999.9920	18
5	**571.3086**	286.1579	554.2821	277.6447	553.2980	277.1527	E	***1903.9032***	952.4552	1886.8767	943.9420	1885.8926	943.4500	17
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	G	1774.8606	887.9339	1757.8341	879.4207	1756.8501	878.9287	16
7	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	L	1717.8392	859.4232	1700.8126	850.9099	1699.8286	850.4179	15
8	798.4356	399.7214	781.4090	391.2082	780.4250	390.7162	G	***1604.7551***	802.8812	1587.7285	794.3679	1586.7445	793.8759	14
9	945.5040	473.2556	928.4775	464.7424	927.4934	464.2504	F	1547.7336	774.3705	1530.7071	765.8572	1529.7231	765.3652	13
10	1060.5310	530.7691	1043.5044	522.2558	1042.5204	521.7638	N	1400.6652	700.8362	1383.6387	692.3230	1382.6546	691.8310	12
11	**1173.6150**	587.3111	1156.5885	578.7979	1155.6045	578.3059	L	***1285.6383***	643.3228	1268.6117	634.8095	1267.6277	634.3175	11
12	1274.6627	637.8350	1257.6361	629.3217	1256.6521	628.8297	T	***1172.5542***	586.7807	1155.5277	578.2675	1154.5436	577.7755	10
13	1403.7053	702.3563	1386.6787	693.8430	1385.6947	693.3510	E	1071.5065	536.2569	1054.4800	527.7436	1053.4960	527.2516	9
14	1516.7894	758.8983	1499.7628	750.3850	1498.7788	749.8930	L	942.4639	471.7356	925.4374	463.2223	924.4534	462.7303	8
15	1603.8214	802.4143	1586.7948	793.9011	1585.8108	793.4090	S	829.3799	415.1936	812.3533	406.6803	811.3693	406.1883	7
16	1732.8640	866.9356	1715.8374	858.4224	1714.8534	857.9303	E	742.3478	371.6776	725.3213	363.1643	724.3373	362.6723	6
17	1819.8960	910.4516	1802.8695	901.9384	1801.8854	901.4464	S	***613.3052***	307.1563	596.2787	298.6430	595.2947	298.1510	5
18	1934.9229	967.9651	1917.8964	959.4518	1916.9124	958.9598	D	526.2732	263.6402	509.2467	255.1270	508.2627	254.6350	4
19	2033.9914	1017.4993	2016.9648	1008.9860	2015.9808	1008.4940	V	***411.2463***	206.1268	394.2197	197.6135			3
20	2171.0503	1086.0288	2154.0237	1077.5155	2153.0397	1077.0235	H	***312.1779***	156.5926	295.1513	148.0793			2
21							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SQILEGLGFNLTELSESDVHR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.5	2344.1546	0.0089	SQILEGLGFNLTELSESDVHR	Deamidated N10 98.41%
39.7	2343.1706	0.9929	SQILEGLGFNLTELSESDVHR	
31.6	2344.1546	0.0089	SQILEGLGFNLTELSESDVHR	Deamidated Q2 1.59%
15.4	2343.1594	1.0042	GSAIIELFHSSIAEVENEELR	
13.0	2342.1650	1.9985	MYFIQHGVVSVLTKGNKEMK	
7.1	2342.1650	1.9985	VLLMLVDGIDPNFKMEHQNK	
7.1	2342.1650	1.9985	VLLMLVDGIDPNFKMEHQNK	
7.1	2342.1650	1.9985	VLLMLVDGIDPNFKMEHQNK	
7.1	2344.1645	-0.0010	ITLLENNDQRLAVLEEETNK	
7.1	2344.1645	-0.0010	ITLLENNDQRLAVLEEETNK	

Mascot: http://www.matrixscience.com/

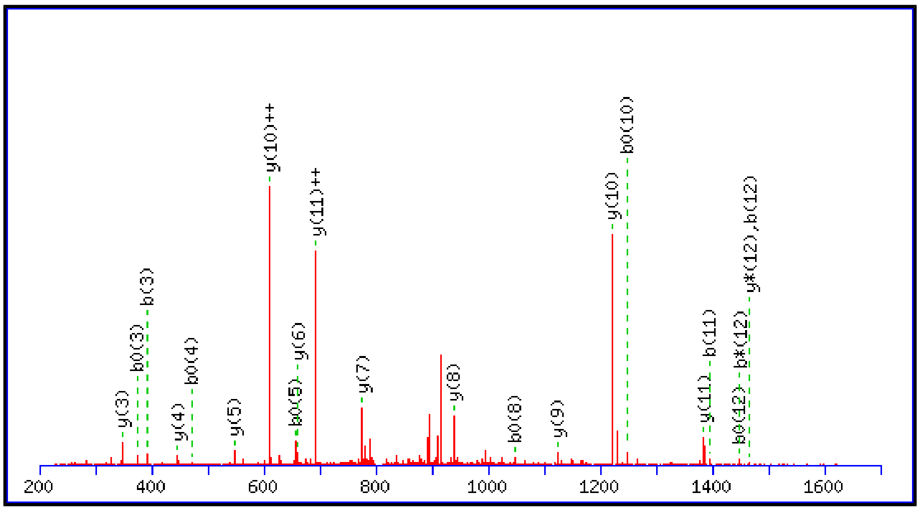
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EVYPWYNLTVEAK**
Found in **P33151** in **con_Xuniprot_HUMAN3**, CADH5_HUMAN Cadherin-5 OS=Homo sapiens GN=CDH5 PE=1 SV=5

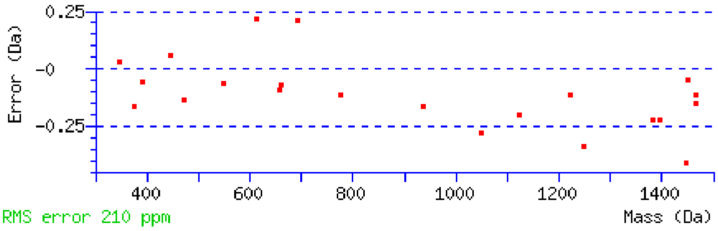
Match to Query 7676: 1611.787828 from(806.901190,2+) intensity(363477.8438) rtinseconds(1973) scans(4973) index(8493)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum4297_scans__4973
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

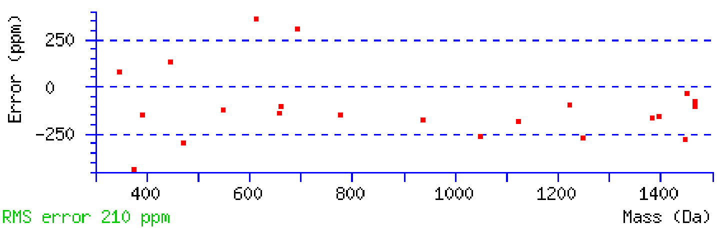
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1700] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1611.7820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7      : Deamidated (NQ)
Ions Score: 49  Expect: 0.0026
Matches : 22/128 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	229.1183	115.0628			211.1077	106.0575	V	1483.7468	742.3770	1466.7202	733.8637	1465.7362	733.3717	12
3	**392.1816**	196.5944			374.1710	187.5892	Y	***1384.6783***	692.8428	1367.6518	684.3295	1366.6678	683.8375	11
4	489.2344	245.1208			471.2238	236.1155	P	***1221.6150***	611.3111	1204.5885	602.7979	1203.6045	602.3059	10
5	675.3137	338.1605			657.3031	329.1552	W	***1124.5623***	562.7848	1107.5357	554.2715	1106.5517	553.7795	9
6	838.3770	419.6921			820.3665	410.6869	Y	***938.4829***	469.7451	921.4564	461.2318	920.4724	460.7398	8
7	953.4040	477.2056	936.3774	468.6923	935.3934	468.2003	N	***775.4196***	388.2134	758.3931	379.7002	757.4090	379.2082	7
8	1066.4880	533.7477	1049.4615	525.2344	1048.4775	524.7424	L	***660.3927***	330.7000	643.3661	322.1867	642.3821	321.6947	6
9	1167.5357	584.2715	1150.5092	575.7582	1149.5251	575.2662	T	***547.3086***	274.1579	530.2821	265.6447	529.2980	265.1527	5
10	1266.6041	633.8057	1249.5776	625.2924	1248.5936	624.8004	V	***446.2609***	223.6341	429.2344	215.1208	428.2504	214.6288	4
11	**1395.6467**	698.3270	1378.6202	689.8137	1377.6361	689.3217	E	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
12	**1466.6838**	733.8456	1449.6573	725.3323	1448.6733	724.8403	A	218.1499	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of EVYPWYNLTVEAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
49.1	1611.7820	0.0058	EVYPWYNLTVEAK
11.3	1611.7960	-0.0082	LNTMSKTSLGQSMSK
6.3	1611.7926	-0.0048	DLYETCKARISQK
6.2	1611.7814	0.0065	GGLMNYQEKTVKNK
5.5	1611.7899	-0.0021	EVMHNRLNRGQNK
3.0	1610.7900	0.9978	VHAESLQQVVQSQR
2.9	1609.7803	2.0075	LMEREQDMKLSAK
2.8	1610.7835	1.0044	LNHDQLAAVQAQMR
2.5	1610.7900	0.9978	VHAESLQQVVQSQR
2.3	1611.7814	0.0064	TDLKTFMGKAQNQK

Mascot: http://www.matrixscience.com/

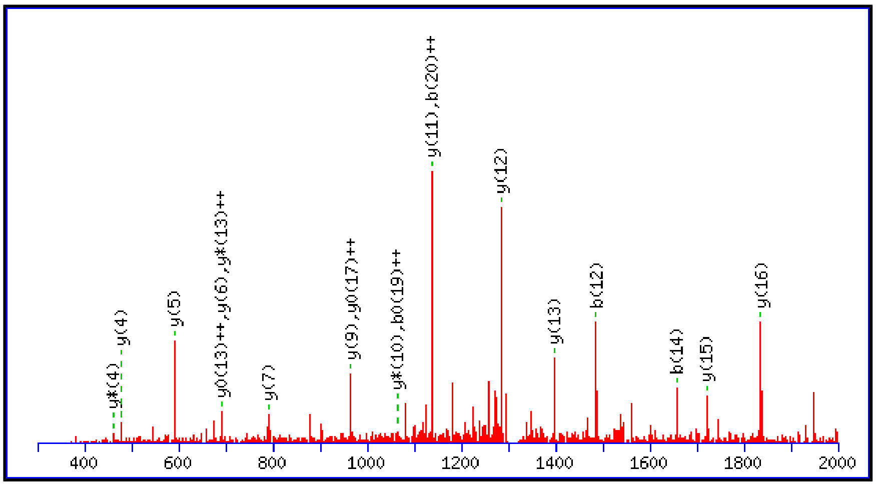
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYLQGLIDCYLFGNSSTVLEDSK**
Found in **P35542** in **con_Xuniprot_HUMAN3**, SAA4_HUMAN Serum amyloid A-4 protein OS=Homo sapiens GN=SAA4 PE=1 SV=2

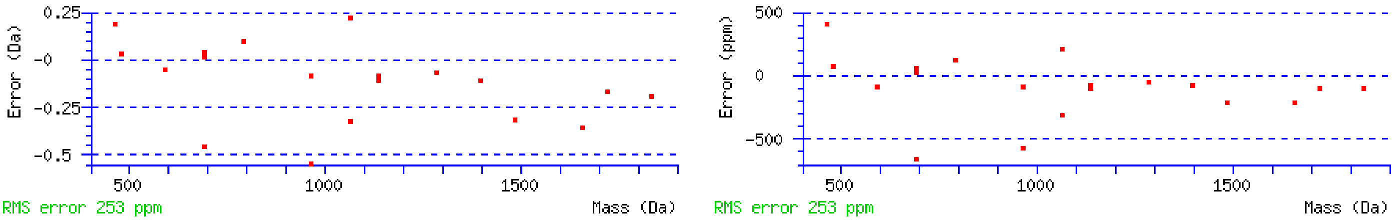
Match to Query 22346: 2623.267548 from(1312.641050,2+) intensity(26509.6289) rtinseconds(2803) scans(7353) index(14824)
Title: 111019_Est_MI_YP_G_03Spectrum6422_scans__7353
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2621.2571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N14     : Deamidated (NQ)
Ions Score: 78  Expect: 4.4e-006
Matches : 19/242 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	100.0757	50.5415					V							23
2	263.1390	132.0731					Y	2523.1959	1262.1016	2506.1694	1253.5883	2505.1854	1253.0963	22
3	376.2231	188.6152					L	2360.1326	1180.5699	2343.1061	1172.0567	2342.1221	1171.5647	21
4	504.2817	252.6445	487.2551	244.1312			Q	2247.0486	1124.0279	2230.0220	1115.5146	2229.0380	1115.0226	20
5	561.3031	281.1552	544.2766	272.6419			G	2118.9900	1059.9986	2101.9634	1051.4854	2100.9794	1050.9933	19
6	674.3872	337.6972	657.3606	329.1840			L	2061.9685	1031.4879	2044.9420	1022.9746	2043.9579	1022.4826	18
7	787.4713	394.2393	770.4447	385.7260			I	1948.8845	974.9459	1931.8579	966.4326	1930.8739	965.9406	17
8	902.4982	451.7527	885.4716	443.2395	884.4876	442.7475	D	***1835.8004***	918.4038	1818.7738	909.8906	1817.7898	909.3985	16
9	1062.5288	531.7681	1045.5023	523.2548	1044.5183	522.7628	C	***1720.7734***	860.8904	1703.7469	852.3771	1702.7629	851.8851	15
10	1225.5922	613.2997	1208.5656	604.7865	1207.5816	604.2944	Y	1560.7428	780.8750	1543.7162	772.3618	1542.7322	771.8698	14
11	1338.6762	669.8418	1321.6497	661.3285	1320.6657	660.8365	L	***1397.6795***	699.3434	1380.6529	690.8301	1379.6689	690.3381	13
12	**1485.7447**	743.3760	1468.7181	734.8627	1467.7341	734.3707	F	***1284.5954***	642.8013	1267.5689	634.2881	1266.5848	633.7961	12
13	1542.7661	771.8867	1525.7396	763.3734	1524.7556	762.8814	G	***1137.5270***	569.2671	1120.5004	560.7539	1119.5164	560.2618	11
14	**1657.7931**	829.4002	1640.7665	820.8869	1639.7825	820.3949	N	1080.5055	540.7564	1063.4790	532.2431	1062.4950	531.7511	10
15	1744.8251	872.9162	1727.7985	864.4029	1726.8145	863.9109	S	***965.4786***	483.2429	948.4520	474.7297	947.4680	474.2376	9
16	1831.8571	916.4322	1814.8306	907.9189	1813.8466	907.4269	S	878.4466	439.7269	861.4200	431.2136	860.4360	430.7216	8
17	1932.9048	966.9560	1915.8782	958.4428	1914.8942	957.9508	T	***791.4145***	396.2109	774.3880	387.6976	773.4040	387.2056	7
18	2031.9732	1016.4902	2014.9467	1007.9770	2013.9626	1007.4850	V	***690.3668***	345.6871	673.3403	337.1738	672.3563	336.6818	6
19	2145.0573	1073.0323	2128.0307	1064.5190	2127.0467	1064.0270	L	***591.2984***	296.1529	574.2719	287.6396	573.2879	287.1476	5
20	2274.0999	1137.5536	2257.0733	1129.0403	2256.0893	1128.5483	E	***478.2144***	239.6108	461.1878	231.0975	460.2038	230.6055	4
21	2389.1268	1195.0670	2372.1003	1186.5538	2371.1162	1186.0618	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
22	2476.1588	1238.5831	2459.1323	1230.0698	2458.1483	1229.5778	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
23							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of VYLQGLIDCYLFGNSSTVLEDSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
77.7	2621.2571	2.0105	VYLQGLIDCYLFGNSSTVLEDSK	Deamidated N14 100.00%
23.3	2621.2571	2.0105	VYLQGLIDCYLFGNSSTVLEDSK	Deamidated Q4 0.00%
0.7	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.7	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.1	2623.2621	0.0054	NKAIMESLSKGGNIMEQNFEPIR	
0.0	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.0	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.0	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.0	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	
0.0	2621.2708	1.9968	LEETNVTVQQQLVATQREFQEK	

Mascot: http://www.matrixscience.com/

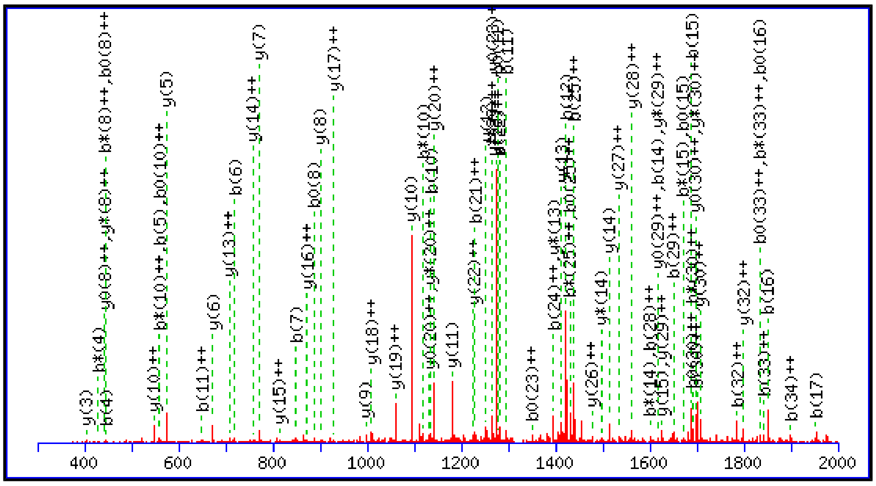
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR**
Found in **P35858** in **con_Xuniprot_HUMAN3**, ALS_HUMAN Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

Match to Query 28202: 3969.795912 from(1324.272580,3+) intensity(16562.0469) rtinseconds(2140) scans(5601) index(19813)
Title: 111019_Est_MI_YP_G_09Spectrum4946_scans__5601
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

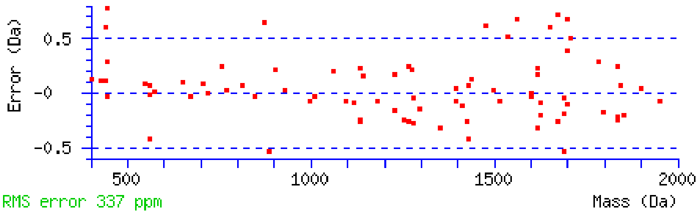
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

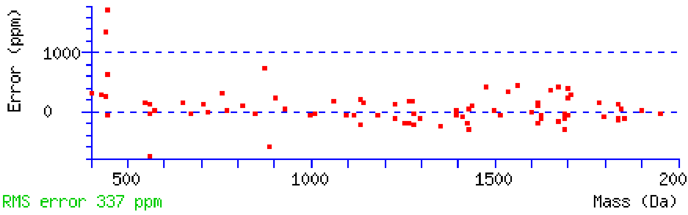


Monoisotopic mass of neutral peptide Mr(calc): 3969.7860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N20 : Deamidated (NQ)
Ions Score: 92 **Expect:** 1e-007
Matches : 82/388 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							35
2	247.1441	124.0757					V	3823.7248	1912.3660	3806.6983	1903.8528	3805.7142	1903.3608	34
3	375.2027	188.1050	358.1761	179.5917			Q	3724.6564	1862.8318	3707.6298	1854.3186	3706.6458	1853.8266	33
4	**446.2398**	223.6235	429.2132	215.1103			A	3596.5978	1798.8025	3579.5713	1790.2893	3578.5873	1789.7973	32
5	**559.3239**	280.1656	542.2973	271.6523			I	3525.5607	1763.2840	3508.5342	1754.7707	3507.5501	1754.2787	31
6	**719.3545**	360.1809	702.3280	351.6676			C	3412.4766	1706.7420	3395.4501	1698.2287	3394.4661	1697.7367	30
7	**848.3971**	424.7022	831.3706	416.1889	830.3865	415.6969	E	3252.4460	1626.7266	3235.4194	1618.2134	3234.4354	1617.7213	29
8	905.4186	453.2129	888.3920	444.6996	887.4080	444.2076	G	3123.4034	1562.2053	3106.3768	1553.6921	3105.3928	1553.2001	28
9	1020.4455	510.7264	1003.4190	502.2131	1002.4349	501.7211	D	3066.3819	1533.6946	3049.3554	1525.1813	3048.3714	1524.6893	27
10	**1135.4725**	568.2399	1118.4459	559.7266	1117.4619	559.2346	D	2951.3550	1476.1811	2934.3284	1467.6679	2933.3444	1467.1758	26
11	**1295.5031**	**648.2552**	1278.4766	639.7419	1277.4925	639.2499	C	2836.3280	1418.6677	2819.3015	1410.1544	2818.3175	1409.6624	25
12	**1423.5617**	712.2845	1406.5351	703.7712	1405.5511	703.2792	Q	2676.2974	1338.6523	2659.2708	1330.1391	2658.2868	1329.6471	24
13	1520.6144	760.8109	1503.5879	752.2976	1502.6039	751.8056	P	2548.2388	1274.6230	2531.2123	1266.1098	2530.2283	1265.6178	23
14	**1617.6672**	809.3372	1600.6407	800.8240	1599.6566	800.3320	P	2451.1861	1226.0967	2434.1595	1217.5834	2433.1755	1217.0914	22
15	**1688.7043**	844.8558	1671.6778	836.3425	1670.6938	835.8505	A	2354.1333	1177.5703	2337.1067	1169.0570	2336.1227	1168.5650	21
16	**1851.7677**	926.3875	1834.7411	917.8742	1833.7571	917.3822	Y	2283.0962	1142.0517	2266.0696	1133.5385	2265.0856	1133.0464	20
17	**1952.8153**	976.9113	1935.7888	968.3980	1934.8048	967.9060	T	2120.0328	1060.5201	2103.0063	1052.0068	2102.0223	1051.5148	19
18	2115.8787	1058.4430	2098.8521	1049.9297	2097.8681	1049.4377	Y	2018.9852	1009.9962	2001.9586	1001.4829	2000.9746	1000.9909	18
19	2229.9216	1115.4644	2212.8950	1106.9512	2211.9110	1106.4591	N	1855.9218	928.4646	1838.8953	919.9513	1837.9113	919.4593	17
20	2344.9485	1172.9779	2327.9220	1164.4646	2326.9380	1163.9726	N	1741.8789	871.4431	1724.8524	862.9298	1723.8683	862.4378	16
21	2458.0326	**1229.5199**	2441.0060	1221.0067	2440.0220	1220.5147	I	***1626.8520***	813.9296	1609.8254	805.4163	1608.8414	804.9243	15
22	2559.0803	**1280.0438**	2542.0537	1271.5305	2541.0697	1271.0385	T	***1513.7679***	757.3876	1496.7414	748.8743	1495.7573	748.3823	14

23	2719.1109	1360.0591	2702.0844	1351.5458	2701.1004	1351.0538	**C**	***1412.7202***	706.8638	1395.6937	698.3505	1394.7097	697.8585	**13**
24	2790.1480	**1395.5777**	2773.1215	1387.0644	2772.1375	1386.5724	**A**	***1252.6896***	626.8484	1235.6630	618.3352	1234.6790	617.8431	**12**
25	2877.1801	**1439.0937**	2860.1535	1430.5804	2859.1695	1430.0884	**S**	***1181.6525***	591.3299	1164.6259	582.8166	1163.6419	582.3246	**11**
26	2974.2328	1487.6201	2957.2063	1479.1068	2956.2223	1478.6148	**P**	***1094.6204***	547.8139	1077.5939	539.3006	1076.6099	538.8086	**10**
27	3071.2856	1536.1464	3054.2590	1527.6332	3053.2750	1527.1412	**P**	***997.5677***	499.2875	980.5411	490.7742	979.5571	490.2822	**9**
28	3200.3282	**1600.6677**	3183.3016	1592.1545	3182.3176	1591.6624	**E**	***900.5149***	450.7611	883.4884	442.2478	882.5043	441.7558	**8**
29	3299.3966	**1650.2019**	3282.3700	1641.6887	3281.3860	1641.1967	**V**	***771.4723***	386.2398	754.4458	377.7265	753.4617	377.2345	**7**
30	3398.4650	**1699.7361**	3381.4385	1691.2229	3380.4544	1690.7309	**V**	***672.4039***	336.7056	655.3774	328.1923	654.3933	327.7003	**6**
31	3455.4865	1728.2469	3438.4599	1719.7336	3437.4759	1719.2416	**G**	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	**5**
32	3568.5705	**1784.7889**	3551.5440	1776.2756	3550.5600	1775.7836	**L**	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	**4**
33	3683.5975	**1842.3024**	3666.5709	1833.7891	3665.5869	1833.2971	**D**	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	**3**
34	3796.6815	**1898.8444**	3779.6550	1890.3311	3778.6710	1889.8391	**L**	288.2030	144.6051	271.1765	136.0919			**2**
35							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
91.6	3969.7860	0.0100	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated N20 78.37%
84.5	3969.7860	0.0100	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated N19 15.39%
80.6	3969.7860	0.0100	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q12 6.24%
66.0	3968.8019	0.9940	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	
49.9	3969.7860	0.0100	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q3 0.01%
8.6	3968.7833	1.0126	EPDKFTSSSQVFQQRSGMYNPEAPFNDTQIISMR	
6.5	3968.7833	1.0126	EPDKFTSSSQVFQQRSGMYNPEAPFNDTQIISMR	
3.5	3969.7989	-0.0030	LMGSLTNFDNNESSDAELNYTLPKFSDPQTYTLNK	
2.7	3967.8046	1.9913	ASSVFWQQMEFVDSLHGQPKMPEWLSTHPSHGNR	
2.7	3967.8046	1.9913	ASSVFWQQMEFVDSLHGQPKMPEWLSTHPSHGNR	

Mascot: http://www.matrixscience.com/

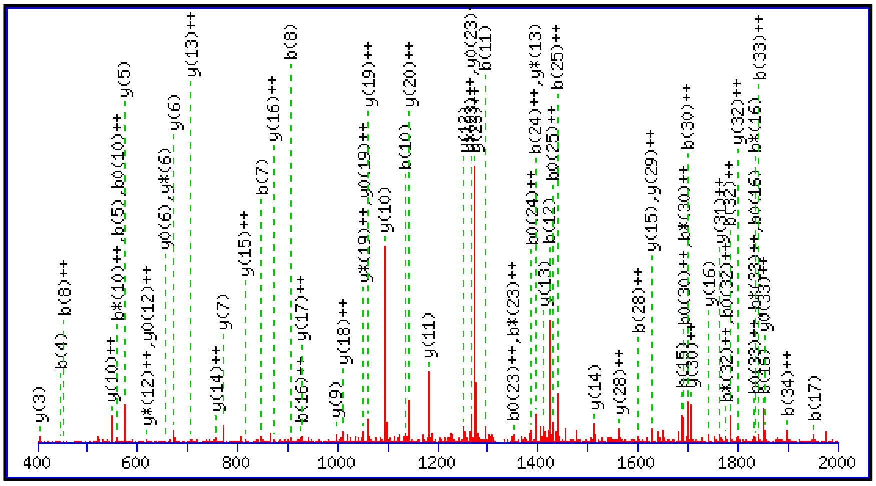
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR**
Found in **P35858** in **con_Xuniprot_HUMAN3**, ALS_HUMAN Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1

Match to Query 28204: 3970.782432 from(1324.601420,3+) intensity(20419.4355) rtinseconds(2162) scans(5447) index(12813)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4775_scans__5447
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

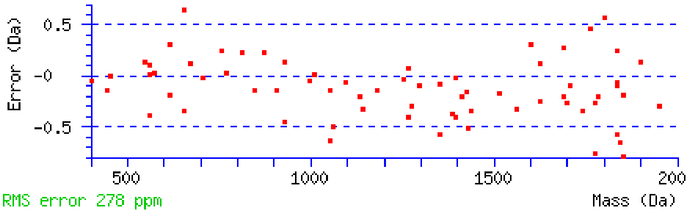
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

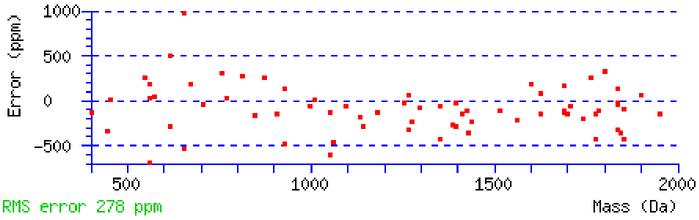


```
Monoisotopic mass of neutral peptide Mr(calc): 3970.7700
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19     : Deamidated (NQ)
N20     : Deamidated (NQ)
Ions Score: 84  Expect: 5.6e-007
Matches : 70/388 fragment ions using 112 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**35**
2	247.1441	124.0757					**V**	3824.7088	1912.8580	3807.6823	1904.3448	3806.6983	1903.8528	**34**
3	375.2027	188.1050	358.1761	179.5917			**Q**	3725.6404	1863.3238	3708.6139	1854.8106	3707.6298	1854.3186	**33**
4	**446.2398**	223.6235	429.2132	215.1103			**A**	3597.5818	1799.2946	3580.5553	1790.7813	3579.5713	1790.2893	**32**
5	**559.3239**	280.1656	542.2973	271.6523			**I**	3526.5447	1763.7760	3509.5182	1755.2627	3508.5342	1754.7707	**31**
6	719.3545	360.1809	702.3280	351.6676			**C**	3413.4607	1707.2340	3396.4341	1698.7207	3395.4501	1698.2287	**30**
7	**848.3971**	424.7022	831.3706	416.1889	830.3865	415.6969	**E**	3253.4300	1627.2186	3236.4035	1618.7054	3235.4194	1618.2134	**29**
8	**905.4186**	**453.2129**	888.3920	444.6996	887.4080	444.2076	**G**	3124.3874	1562.6973	3107.3609	1554.1841	3106.3768	1553.6921	**28**
9	1020.4455	510.7264	1003.4190	502.2131	1002.4349	501.7211	**D**	3067.3659	1534.1866	3050.3394	1525.6733	3049.3554	1525.1813	**27**
10	**1135.4725**	568.2399	1118.4459	559.7266	1117.4619	559.2346	**D**	2952.3390	1476.6731	2935.3125	1468.1599	2934.3284	1467.6679	**26**
11	**1295.5031**	648.2552	1278.4766	639.7419	1277.4925	639.2499	**C**	2837.3121	1419.1597	2820.2855	1410.6464	2819.3015	1410.1544	**25**
12	**1423.5617**	712.2845	1406.5351	703.7712	1405.5511	703.2792	**Q**	2677.2814	1339.1443	2660.2549	1330.6311	2659.2708	1330.1391	**24**
13	1520.6144	760.8109	1503.5879	752.2976	1502.6039	751.8056	**P**	2549.2228	1275.1151	2532.1963	1266.6018	2531.2123	1266.1098	**23**
14	1617.6672	809.3372	1600.6407	800.8240	1599.6566	800.3320	**P**	2452.1701	1226.5887	2435.1435	1218.0754	2434.1595	1217.5834	**22**
15	**1688.7043**	844.8558	1671.6778	836.3425	1670.6938	835.8505	**A**	2355.1173	1178.0623	2338.0908	1169.5490	2337.1067	1169.0570	**21**
16	**1851.7677**	**926.3875**	1834.7411	917.8742	1833.7571	917.3822	**Y**	2284.0802	1142.5437	2267.0536	1134.0305	2266.0696	1133.5385	**20**
17	**1952.8153**	976.9113	1935.7888	968.3980	1934.8048	967.9060	**T**	2121.0169	1061.0121	2103.9903	1052.4988	2103.0063	1052.0068	**19**
18	2115.8787	1058.4430	2098.8521	1049.9297	2097.8681	1049.4377	**Y**	2019.9692	1010.4882	2002.9426	1001.9750	2001.9586	1001.4829	**18**
19	2230.9056	1115.9564	2213.8791	1107.4432	2212.8950	1106.9512	**N**	1856.9059	928.9566	1839.8793	920.4433	1838.8953	919.9513	**17**
20	2345.9325	1173.4699	2328.9060	1164.9566	2327.9220	1164.4646	**N**	***1741.8789***	871.4431	1724.8524	862.9298	1723.8683	862.4378	**16**
21	2459.0166	1230.0119	2441.9901	1221.4987	2441.0060	1221.0067	**I**	***1626.8520***	813.9296	1609.8254	805.4163	1608.8414	804.9243	**15**

22	2560.0643	1280.5358	2543.0377	1272.0225	2542.0537	1271.5305	**T**	***1513.7679***	757.3876	1496.7414	748.8743	1495.7573	748.3823	**14**
23	2720.0949	1360.5511	2703.0684	1352.0378	2702.0844	1351.5458	**C**	***1412.7202***	706.8638	1395.6937	698.3505	1394.7097	697.8585	**13**
24	2791.1320	**1396.0697**	2774.1055	1387.5564	2773.1215	1387.0644	**A**	***1252.6896***	626.8484	1235.6630	618.3352	1234.6790	617.8431	**12**
25	2878.1641	**1439.5857**	2861.1375	1431.0724	2860.1535	1430.5804	**S**	***1181.6525***	591.3299	1164.6259	582.8166	1163.6419	582.3246	**11**
26	2975.2168	1488.1121	2958.1903	1479.5988	2957.2063	1479.1068	**P**	***1094.6204***	547.8139	1077.5939	539.3006	1076.6099	538.8086	**10**
27	3072.2696	1536.6384	3055.2431	1528.1252	3054.2590	1527.6332	**P**	***997.5677***	499.2875	980.5411	490.7742	979.5571	490.2822	**9**
28	3201.3122	**1601.1597**	3184.2856	1592.6465	3183.3016	1592.1545	**E**	900.5149	450.7611	883.4884	442.2478	882.5043	441.7558	**8**
29	3300.3806	1650.6939	3283.3541	1642.1807	3282.3700	1641.6887	**V**	***771.4723***	386.2398	754.4458	377.7265	753.4617	377.2345	**7**
30	3399.4490	**1700.2282**	3382.4225	1691.7149	3381.4385	1691.2229	**V**	***672.4039***	336.7056	655.3774	328.1923	654.3933	327.7003	**6**
31	3456.4705	1728.7389	3439.4439	1720.2256	3438.4599	1719.7336	**G**	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	**5**
32	3569.5546	**1785.2809**	3552.5280	1776.7676	3551.5440	1776.2756	**L**	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	**4**
33	3684.5815	**1842.7944**	3667.5549	1834.2811	3666.5709	1833.7891	**D**	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	**3**
34	3797.6656	**1899.3364**	3780.6390	1890.8231	3779.6550	1890.3311	**L**	288.2030	144.6051	271.1765	136.0919			**2**
35							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.7	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated N19, N20 52.76%
80.1	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q12, N20 23.03%
80.1	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q12, N19 23.03%
71.0	3969.7860	0.9965	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	
70.2	3969.7860	0.9965	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	
66.0	3969.7860	0.9965	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	
64.1	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q3, N20 0.58%
64.1	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q3, N19 0.58%
48.4	3969.7860	0.9965	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	
47.9	3970.7700	0.0125	FVQAICEGDDCQPPAYTYNNITCASPPEVVGLDLR	Deamidated Q3, Q12 0.01%

Mascot: http://www.matrixscience.com/

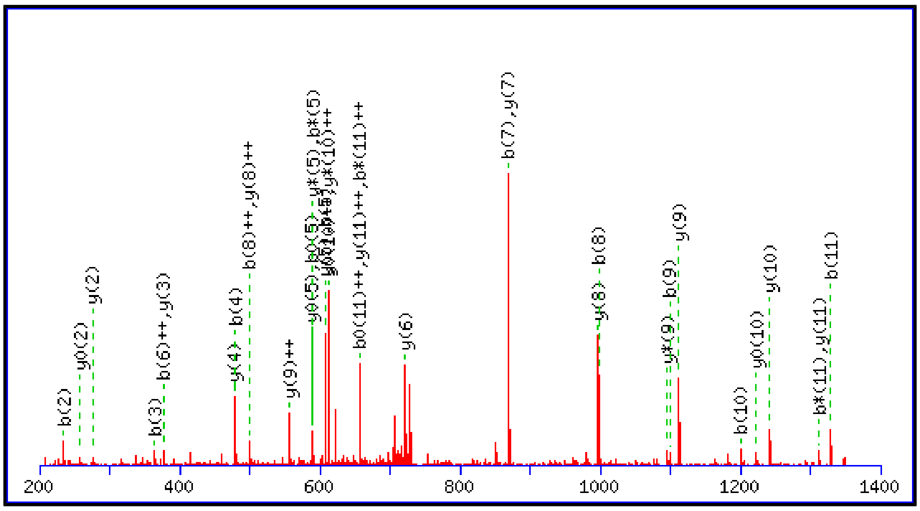
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YAEDKFNETTEK**
Found in **P43652** in **con_Xuniprot_HUMAN3**, AFAM_HUMAN Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

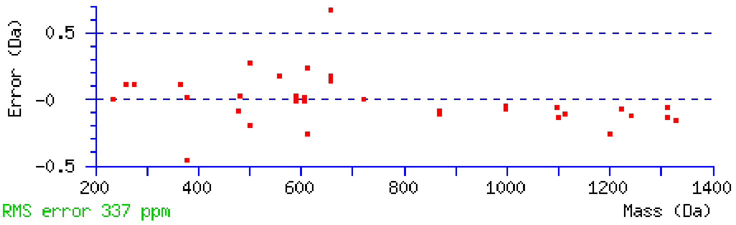
Match to Query 6653: 1474.650668 from(738.332610,2+) intensity(38833.9063) rtinseconds(332) scans(586) index(25157)
Title: 111019_Est_MI_YS_G_07Spectrum454_scans__586
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

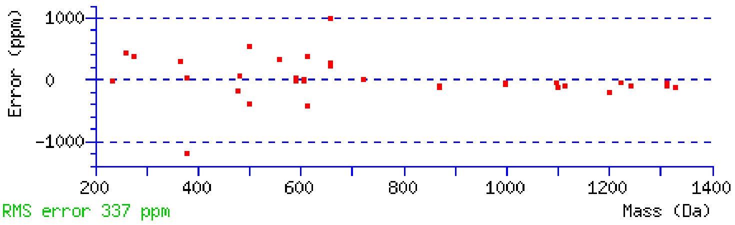
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1474.6463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 88 **Expect:** 1.3e-007
Matches : 36/118 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	164.0706	82.5389					Y							12
2	**235.1077**	118.0575					A	**1312.5903**	656.7988	1295.5638	648.2855	1294.5798	647.7935	11
3	**364.1503**	182.5788			346.1397	173.5735	E	**1241.5532**	621.2802	1224.5267	612.7670	1223.5426	612.2750	10
4	**479.1773**	240.0923			461.1667	231.0870	D	**1112.5106**	556.7589	1095.4841	548.2457	1094.5000	547.7537	9
5	**607.2722**	304.1397	590.2457	295.6265	589.2617	295.1345	K	**997.4837**	499.2455	980.4571	490.7322	979.4731	490.2402	8
6	754.3406	377.6740	737.3141	369.1607	736.3301	368.6687	F	**869.3887**	435.1980	852.3622	426.6847	851.3781	426.1927	7
7	**869.3676**	435.1874	852.3410	426.6742	851.3570	426.1821	N	**722.3203**	361.6638	705.2937	353.1505	704.3097	352.6585	6
8	**998.4102**	499.7087	981.3836	491.1954	980.3996	490.7034	E	**607.2933**	304.1503	590.2668	295.6370	589.2828	295.1450	5
9	**1099.4578**	550.2326	1082.4313	541.7193	1081.4473	541.2273	T	**478.2508**	239.6290	461.2242	231.1157	460.2402	230.6237	4
10	**1200.5055**	600.7564	1183.4790	592.2431	1182.4950	591.7511	T	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	3
11	**1329.5481**	665.2777	1312.5216	656.7644	1311.5376	656.2724	E	**276.1554**	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of YAEDKFNETTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
87.8	1474.6463	0.0043	YAEDKFNETTEK
8.5	1472.6379	2.0128	SGESNTHQDIEEK
4.4	1474.6511	-0.0004	MGGSFRGAFSNSEK
4.0	1474.6544	-0.0037	MQSNYGKQMKAR
4.0	1473.6526	0.9980	SMMSRACWAKSK
3.9	1474.6497	0.0010	VNATPQQMPQTEK
3.3	1474.6544	-0.0037	MQSNYGKQMKAR
3.2	1474.6576	-0.0069	TQNKEESYDFSK
2.5	1474.6544	-0.0037	MQSNYGKQMKAR
1.4	1474.6470	0.0036	QQDGQSAGPAMETR

Mascot: http://www.matrixscience.com/

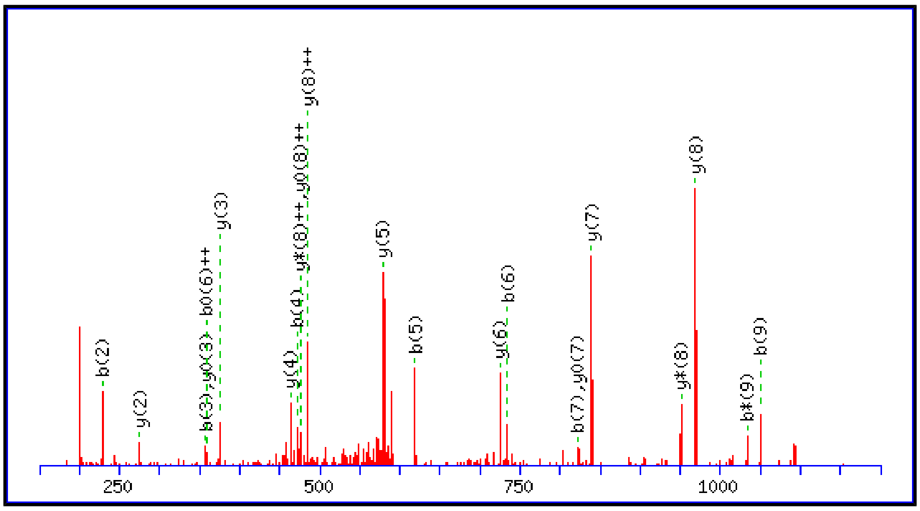
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DIENFNSTQK**
Found in **P43652** in **con_Xuniprot_HUMAN3**, AFAM_HUMAN Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

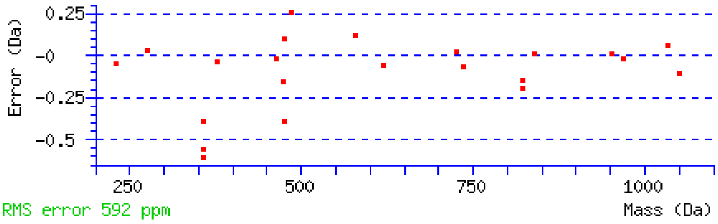
Match to Query 1640: 1195.537608 from(598.776080,2+) intensity(6700.7188) rtinseconds(513) scans(957) index(7320)
Title: 111019_Est_ISCardio_NMI_YP_G_11Spectrum792_scans__957
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

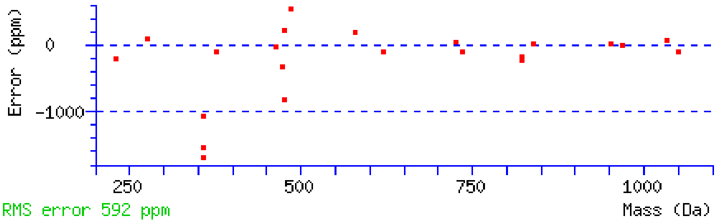
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1200 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1195.5357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 57 **Expect:** 0.00019
Matches : 22/98 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	***229.1183***	115.0628			211.1077	106.0575	I	1081.5160	541.2617	1064.4895	532.7484	1063.5055	532.2564	9
3	***358.1609***	179.5841			340.1503	170.5788	E	***968.4320***	484.7196	951.4054	476.2063	950.4214	475.7143	8
4	***472.2038***	236.6055	455.1773	228.0923	454.1932	227.6003	N	***839.3894***	420.1983	822.3628	411.6851	821.3788	411.1930	7
5	***619.2722***	310.1397	602.2457	301.6265	601.2617	301.1345	F	***725.3464***	363.1769	708.3199	354.6636	707.3359	354.1716	6
6	***734.2992***	367.6532	717.2726	359.1399	716.2886	358.6479	N	***578.2780***	289.6427	561.2515	281.1294	560.2675	280.6374	5
7	***821.3312***	411.1692	804.3046	402.6560	803.3206	402.1639	S	***463.2511***	232.1292	446.2245	223.6159	445.2405	223.1239	4
8	922.3789	461.6931	905.3523	453.1798	904.3683	452.6878	T	***376.2191***	188.6132	359.1925	180.0999	358.2085	179.6079	3
9	***1050.4374***	525.7224	1033.4109	517.2091	1032.4269	516.7171	Q	***275.1714***	138.0893	258.1448	129.5761			2
10							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of DIENFNSTQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.3	1195.5357	0.0019	DIENFNSTQK	Deamidated N6 99.67%
30.3	1195.5357	0.0019	DIENFNSTQK	Deamidated N4 0.20%
28.5	1195.5357	0.0019	DIENFNSTQK	Deamidated Q9 0.13%
8.2	1195.5365	0.0011	NIKFMNHMK	
7.3	1194.5339	1.0037	LNQDFLECR	
6.6	1194.5339	1.0037	LNQDFLECR	
4.5	1194.5299	1.0077	NCTSDSVREK	
3.5	1195.5357	0.0019	INAYEQSDVR	
2.3	1195.5356	0.0020	EAEKQGYNEK	
1.9	1195.5391	-0.0015	VMKTGGENTDK	

Mascot: http://www.matrixscience.com/

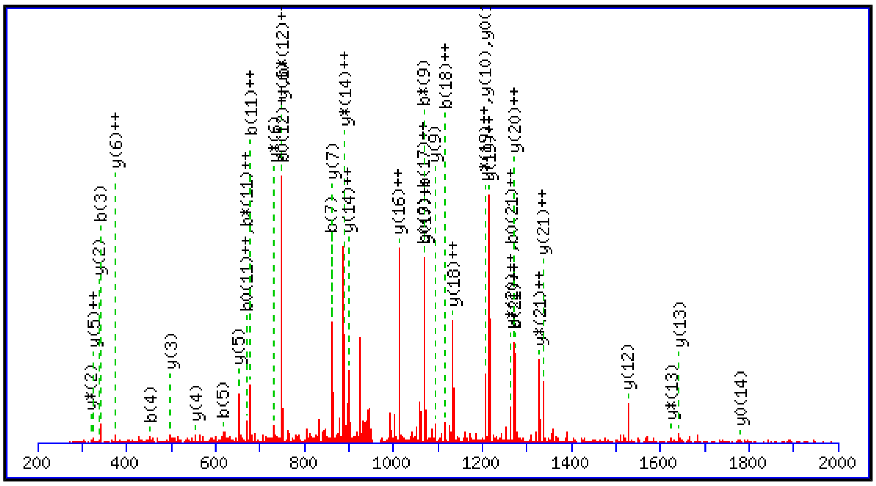
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVQIYKDLLRNCCNTENPPGCYR**
Found in **P43652** in **con_Xuniprot_HUMAN3**, AFAM_HUMAN Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

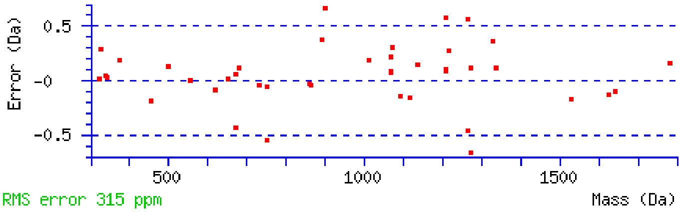
Match to Query 26015: 2883.359832 from(962.127220,3+) intensity(130010.4141) rtinseconds(1442) scans(3552) index(22565)
Title: 111019_Est_MI_YS_G_03Spectrum3088_scans__3552
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

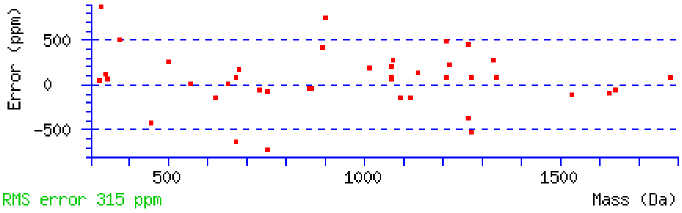
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2883.3466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0016
Matches : 43/234 fragment ions using 86 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							23
2	213.1598	107.0835					V	2771.2698	1386.1385	2754.2433	1377.6253	2753.2593	1377.1333	22
3	**341.2183**	171.1128	324.1918	162.5995			Q	2672.2014	1336.6043	2655.1749	1328.0911	2654.1908	1327.5991	21
4	**454.3024**	227.6548	437.2758	219.1416			I	2544.1428	1272.5751	2527.1163	1264.0618	2526.1323	1263.5698	20
5	**617.3657**	309.1865	600.3392	300.6732			Y	2431.0588	1216.0330	2414.0322	1207.5197	2413.0482	1207.0277	19
6	745.4607	373.2340	728.4341	364.7207			K	2267.9954	1134.5014	2250.9689	1125.9881	2249.9849	1125.4961	18
7	**860.4876**	430.7475	843.4611	422.2342	842.4771	421.7422	D	2139.9005	1070.4539	2122.8739	1061.9406	2121.8899	1061.4486	17
8	973.5717	487.2895	956.5451	478.7762	955.5611	478.2842	L	2024.8735	1012.9404	2007.8470	1004.4271	2006.8630	1003.9351	16
9	1086.6558	543.8315	1069.6292	535.3182	1068.6452	534.8262	L	1911.7895	956.3984	1894.7629	947.8851	1893.7789	947.3931	15
10	1242.7569	621.8821	1225.7303	613.3688	1224.7463	612.8768	R	1798.7054	899.8563	1781.6789	891.3431	1780.6948	890.8511	14
11	1357.7838	**679.3955**	1340.7573	670.8823	1339.7732	670.3903	N	***1642.6043***	821.8058	1625.5777	813.2925	1624.5937	812.8005	13
12	1517.8145	759.4109	1500.7879	750.8976	1499.8039	750.4056	C	***1527.5773***	764.2923	1510.5508	755.7790	1509.5668	755.2870	12
13	1677.8451	839.4262	1660.8186	830.9129	1659.8345	830.4209	C	1367.5467	684.2770	1350.5201	675.7637	1349.5361	675.2717	11
14	1791.8880	896.4477	1774.8615	887.9344	1773.8775	887.4424	N	***1207.5160***	604.2617	1190.4895	595.7484	1189.5055	595.2564	10
15	1892.9357	946.9715	1875.9092	938.4582	1874.9252	937.9662	T	***1093.4731***	547.2402	1076.4466	538.7269	1075.4626	538.2349	9
16	2021.9783	1011.4928	2004.9518	1002.9795	2003.9677	1002.4875	E	992.4254	496.7164	975.3989	488.2031	974.4149	487.7111	8
17	2136.0212	**1068.5143**	2118.9947	1060.0010	2118.0107	1059.5090	N	***863.3828***	432.1951	846.3563	423.6818			7
18	2233.0740	**1117.0406**	2216.0475	1108.5274	2215.0634	1108.0354	P	***749.3399***	375.1736	732.3134	366.6603			6
19	2330.1268	1165.5670	2313.1002	1157.0537	2312.1162	1156.5617	P	***652.2872***	326.6472	635.2606	318.1339			5
20	2387.1482	1194.0778	2370.1217	1185.5645	2369.1377	1185.0725	G	***555.2344***	278.1208	538.2078	269.6076			4
21	2547.1789	**1274.0931**	2530.1523	1265.5798	2529.1683	1265.0878	C	***498.2129***	249.6101	481.1864	241.0968			3
22	2710.2422	1355.6247	2693.2157	1347.1115	2692.2316	1346.6195	Y	***338.1823***	169.5948	321.1557	161.0815			2
23							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IVQIYKDLLRNCCNTENPPGCYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.9	2883.3466	0.0133	IVQIYKDLLRNCCNTENPPGCYR	Deamidated N11 68.03%
45.9	2883.3466	0.0133	IVQIYKDLLRNCCNTENPPGCYR	Deamidated N14 16.97%
45.1	2883.3466	0.0133	IVQIYKDLLRNCCNTENPPGCYR	Deamidated N17 13.99%
40.5	2882.3626	0.9973	IVQIYKDLLRNCCNTENPPGCYR	
33.6	2883.3466	0.0133	IVQIYKDLLRNCCNTENPPGCYR	Deamidated Q3 1.01%
7.7	2882.3603	0.9995	ARVVDQPIYIISQCGSSTRSEEQQK	
4.7	2883.3670	-0.0072	VSISLTVGENDTGLCYNSKMKYFEK	
4.3	2882.3465	1.0134	MDPQNQHGSGSSLVVIQQPSLDSRQR	
4.0	2883.3605	-0.0006	FQEESMACLEKGALEQFAKGMPPLR	
4.0	2882.3465	1.0134	MDPQNQHGSGSSLVVIQQPSLDSRQR	

Mascot: http://www.matrixscience.com/

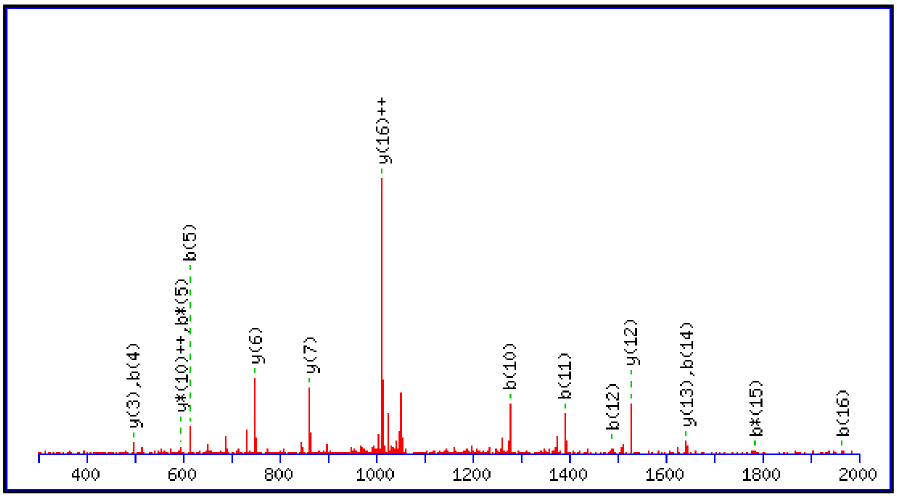
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DLLRNCCNTENPPGCYR**
Found in **P43652** in **con_Xuniprot_HUMAN3**, AFAM_HUMAN Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

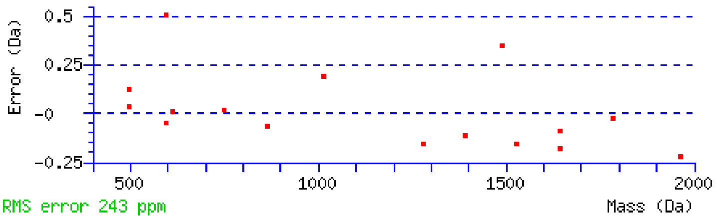
Match to Query 14386: 2138.901268 from(1070.457910,2+) intensity(16322.9268) rtinseconds(765) scans(1533) index(11593)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum1295_scans__1533
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

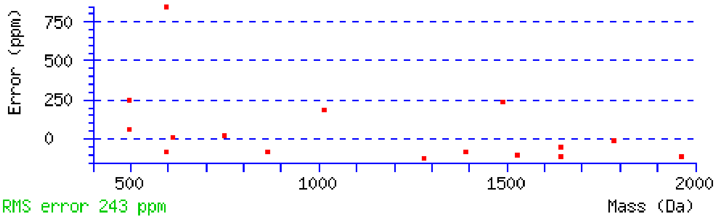
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2138.8932
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 44 **Expect:** 0.0018
Matches : 16/172 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	116.0342	58.5207			98.0237	49.5155	D							17
2	229.1183	115.0628			211.1077	106.0575	L	2024.8735	1012.9404	2007.8470	1004.4271	2006.8630	1003.9351	16
3	342.2023	171.6048			324.1918	162.5995	L	1911.7895	956.3984	1894.7629	947.8851	1893.7789	947.3931	15
4	***498.3035***	249.6554	481.2769	241.1421	480.2929	240.6501	R	1798.7054	899.8563	1781.6789	891.3431	1780.6948	890.8511	14
5	***613.3304***	307.1688	596.3039	298.6556	595.3198	298.1636	N	**1642.6043**	821.8058	1625.5777	813.2925	1624.5937	812.8005	13
6	773.3611	387.1842	756.3345	378.6709	755.3505	378.1789	C	**1527.5773**	764.2923	1510.5508	755.7790	1509.5668	755.2870	12
7	933.3917	467.1995	916.3652	458.6862	915.3811	458.1942	C	1367.5467	684.2770	1350.5201	675.7637	1349.5361	675.2717	11
8	1047.4346	524.2210	1030.4081	515.7077	1029.4241	515.2157	N	1207.5160	604.2617	1190.4895	595.7484	1189.5055	595.2564	10
9	1148.4823	574.7448	1131.4558	566.2315	1130.4717	565.7395	T	1093.4731	547.2402	1076.4466	538.7269	1075.4626	538.2349	9
10	***1277.5249***	639.2661	1260.4983	630.7528	1259.5143	630.2608	E	992.4254	496.7164	975.3989	488.2031	974.4149	487.7111	8
11	***1391.5678***	696.2876	1374.5413	687.7743	1373.5573	687.2823	N	**863.3828**	432.1951	846.3563	423.6818			7
12	***1488.6206***	744.8139	1471.5940	736.3007	1470.6100	735.8087	P	**749.3399**	375.1736	732.3134	366.6603			6
13	1585.6734	793.3403	1568.6468	784.8270	1567.6628	784.3350	P	652.2872	326.6472	635.2606	318.1339			5
14	***1642.6948***	821.8510	1625.6683	813.3378	1624.6843	812.8458	G	555.2344	278.1208	538.2078	269.6076			4
15	1802.7255	901.8664	1785.6989	893.3531	1784.7149	892.8611	C	**498.2129**	249.6101	481.1864	241.0968			3
16	***1965.7888***	983.3980	1948.7622	974.8848	1947.7782	974.3928	Y	338.1823	169.5948	321.1557	161.0815			2
17							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of DLLRNCCNTENPPGCYR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
44.4	2138.8932	0.0081	DLLRNCCNTENPPGCYR	Deamidated N5 96.22%
30.1	2138.8932	0.0081	DLLRNCCNTENPPGCYR	Deamidated N8 3.57%
17.8	2138.8932	0.0081	DLLRNCCNTENPPGCYR	Deamidated N11 0.21%
3.5	2138.9071	-0.0058	QQAMHLCFENLMEGIER	
3.1	2138.9071	-0.0058	QQAMHLCFENLMEGIER	
0.5	2138.8957	0.0056	NSQISNENDCNLQSCSLR	
0.5	2138.8957	0.0056	NSQISNENDCNLQSCSLR	

Mascot: http://www.matrixscience.com/

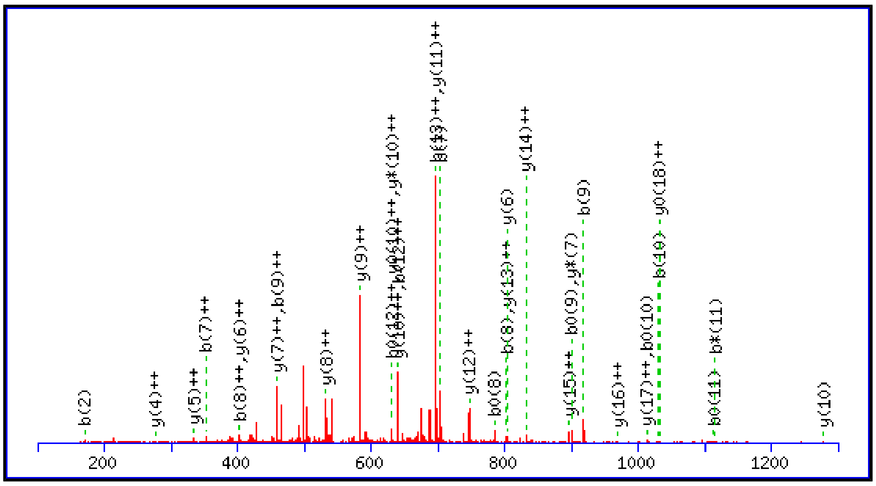
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGSFEGLVNLTFIHLQHNR**
Found in **P51884** in **con_Xuniprot_HUMAN3**, LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

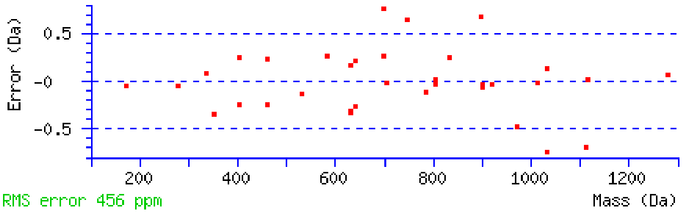
Match to Query 14856: 2195.159776 from(549.797220,4+) intensity(11262.4043) rtinseconds(2331) scans(6035) index(14734)
Title: 111019_Est_MI_YP_G_03Spectrum5260_scans__6035
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

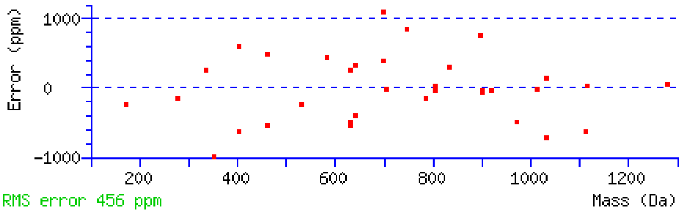
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2195.1487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 104 **Expect:** 6.9e-009
Matches : 36/180 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					**L**							19
2	**171.1128**	86.0600					**G**	2083.0719	1042.0396	2066.0454	1033.5263	2065.0614	1033.0343	18
3	258.1448	129.5761			240.1343	120.5708	**S**	2026.0505	1013.5289	2009.0239	1005.0156	2008.0399	1004.5236	17
4	405.2132	203.1103			387.2027	194.1050	**F**	1939.0185	970.0129	1921.9919	961.4996	1921.0079	961.0076	16
5	534.2558	267.6316			516.2453	258.6263	**E**	1791.9500	896.4787	1774.9235	887.9654	1773.9395	887.4734	15
6	591.2773	296.1423			573.2667	287.1370	**G**	1662.9075	831.9574	1645.8809	823.4441	1644.8969	822.9521	14
7	**704.3614**	**352.6843**			686.3508	343.6790	**L**	1605.8860	803.4466	1588.8594	794.9334	1587.8754	794.4413	13
8	**803.4298**	**402.2185**			785.4192	393.2132	**V**	1492.8019	746.9046	1475.7754	738.3913	1474.7914	737.8993	12
9	**918.4567**	**459.7320**	901.4302	451.2187	900.4462	450.7267	**N**	1393.7335	697.3704	1376.7070	688.8571	1375.7229	688.3651	11
10	**1031.5408**	516.2740	1014.5142	507.7608	1013.5302	507.2687	**L**	1278.7066	639.8569	1261.6800	631.3436	1260.6960	630.8516	10
11	1132.5885	566.7979	1115.5619	558.2846	1114.5779	557.7926	**T**	1165.6225	583.3149	1148.5960	574.8016	1147.6119	574.3096	9
12	1279.6569	**640.3321**	1262.6303	631.8188	1261.6463	631.3268	**F**	1064.5748	532.7910	1047.5483	524.2778			8
13	1392.7409	**696.8741**	1375.7144	688.3608	1374.7304	687.8688	**I**	917.5064	459.2568	900.4799	450.7436			7
14	1529.7999	765.4036	1512.7733	756.8903	1511.7893	756.3983	**H**	804.4223	402.7148	787.3958	394.2015			6
15	1642.8839	821.9456	1625.8574	813.4323	1624.8734	812.9403	**L**	667.3634	334.1854	650.3369	325.6721			5
16	1770.9425	885.9749	1753.9160	877.4616	1752.9319	876.9696	**Q**	554.2794	277.6433	537.2528	269.1300			4
17	1908.0014	954.5043	1890.9749	945.9911	1889.9908	945.4991	**H**	426.2208	213.6140	409.1942	205.1008			3
18	2022.0443	1011.5258	2005.0178	1003.0125	2004.0338	1002.5205	**N**	289.1619	145.0846	272.1353	136.5713			2
19							**R**	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LGSFEGLVNLTFIHLQHNR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
104.0	2195.1487	0.0110	LGSFEGLVNLTFIHLQHNR	Deamidated N9 58.77%
99.5	2195.1487	0.0110	LGSFEGLVNLTFIHLQHNR	Deamidated N18 20.85%
99.4	2195.1487	0.0110	LGSFEGLVNLTFIHLQHNR	Deamidated Q16 20.38%
70.9	2194.1647	0.9951	LGSFEGLVNLTFIHLQHNR	
12.6	2195.1507	0.0091	MAAEQASLAELKLHEAELLK	
11.7	2195.1660	-0.0062	MTVADSPESLFRLATFAKIV	
9.0	2194.1602	0.9996	LPEKNRQMLQLLMNHLAK	
8.9	2193.1555	2.0043	RFDLIRDLHFAAIEANHR	
8.3	2195.1620	-0.0022	ILVIREIQEAIAVANASTMH	
8.3	2195.1620	-0.0022	ILVIREIQEAIAVANASTMH	

Mascot: http://www.matrixscience.com/

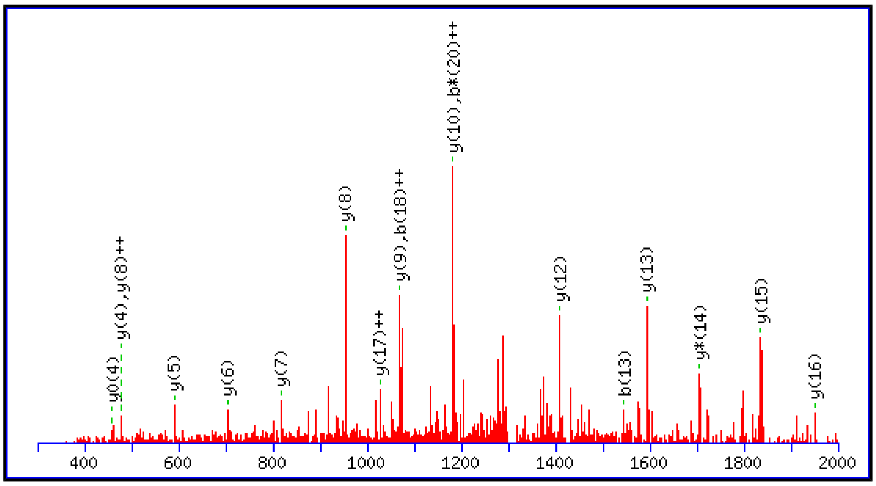
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFENVTDLQWLILDHNLLENSK**
Found in **P51884** in **con_Xuniprot_HUMAN3**, LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

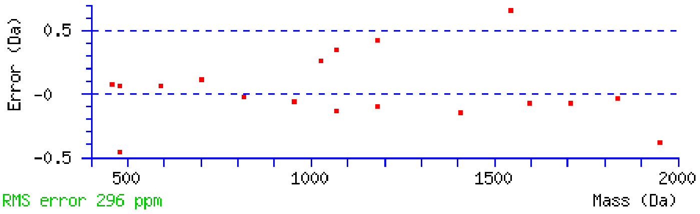
Match to Query 22296: 2612.314888 from(1307.164720,2+) intensity(28115.1191) rtinseconds(2539) scans(6513) index(12886)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum5729_scans__6513
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

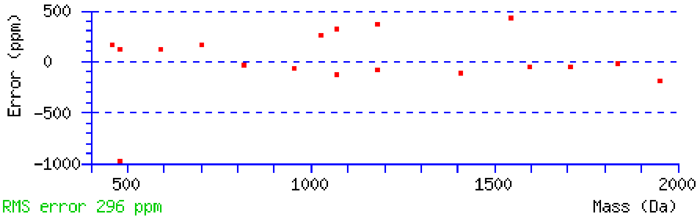
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2612.3122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
Ions Score: 88  Expect: 3.4e-007
Matches : 18/240 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							22
2	219.1128	110.0600					F	2542.2824	1271.6448	2525.2558	1263.1316	2524.2718	1262.6396	21
3	348.1554	174.5813			330.1448	165.5761	E	2395.2140	1198.1106	2378.1874	1189.5974	2377.2034	1189.1053	20
4	463.1823	232.0948	446.1558	223.5815	445.1718	223.0895	N	2266.1714	1133.5893	2249.1448	1125.0761	2248.1608	1124.5840	19
5	562.2508	281.6290	545.2242	273.1157	544.2402	272.6237	V	2151.1444	1076.0759	2134.1179	1067.5626	2133.1339	1067.0706	18
6	663.2984	332.1529	646.2719	323.6396	645.2879	323.1476	T	2052.0760	1026.5417	2035.0495	1018.0284	2034.0655	1017.5364	17
7	778.3254	389.6663	761.2988	381.1531	760.3148	380.6610	D	***1951.0284***	976.0178	1934.0018	967.5045	1933.0178	967.0125	16
8	891.4094	446.2084	874.3829	437.6951	873.3989	437.2031	L	***1836.0014***	918.5043	1818.9749	909.9911	1817.9908	909.4991	15
9	1019.4680	510.2376	1002.4415	501.7244	1001.4575	501.2324	Q	1722.9173	861.9623	1705.8908	853.4490	1704.9068	852.9570	14
10	1205.5473	603.2773	1188.5208	594.7640	1187.5368	594.2720	W	***1594.8588***	797.9330	1577.8322	789.4197	1576.8482	788.9277	13
11	1318.6314	659.8193	1301.6048	651.3061	1300.6208	650.8141	L	***1408.7795***	704.8934	1391.7529	696.3801	1390.7689	695.8881	12
12	1431.7155	716.3614	1414.6889	707.8481	1413.7049	707.3561	I	1295.6954	648.3513	1278.6688	639.8381	1277.6848	639.3461	11
13	1544.7995	772.9034	1527.7730	764.3901	1526.7890	763.8981	L	***1182.6113***	591.8093	1165.5848	583.2960	1164.6008	582.8040	10
14	1659.8265	830.4169	1642.7999	821.9036	1641.8159	821.4116	D	***1069.5273***	535.2673	1052.5007	526.7540	1051.5167	526.2620	9
15	1796.8854	898.9463	1779.8588	890.4331	1778.8748	889.9410	H	***954.5003***	477.7538	937.4738	469.2405	936.4898	468.7485	8
16	1910.9283	955.9678	1893.9018	947.4545	1892.9177	946.9625	N	***817.4414***	409.2243	800.4149	400.7111	799.4308	400.2191	7
17	2024.0124	1012.5098	2006.9858	1003.9965	2006.0018	1003.5045	L	***703.3985***	352.2029	686.3719	343.6896	685.3879	343.1976	6
18	2137.0964	1069.0519	2120.0699	1060.5386	2119.0859	1060.0466	L	***590.3144***	295.6608	573.2879	287.1476	572.3039	286.6556	5
19	2266.1390	1133.5732	2249.1125	1125.0599	2248.1285	1124.5679	E	***477.2304***	239.1188	460.2038	230.6055	459.2198	230.1135	4
20	2380.1820	1190.5946	2363.1554	1182.0813	2362.1714	1181.5893	N	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	3
21	2467.2140	1234.1106	2450.1874	1225.5974	2449.2034	1225.1053	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
22							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AFENVTDLQWLILDHNLLENSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
88.3	2612.3122	0.0027	AFENVTDLQWLILDHNLLENSK	Deamidated N4 99.78%
61.4	2612.3122	0.0027	AFENVTDLQWLILDHNLLENSK	Deamidated Q9 0.20%
49.5	2612.3122	0.0027	AFENVTDLQWLILDHNLLENSK	Deamidated N16 0.01%
25.1	2612.3122	0.0027	AFENVTDLQWLILDHNLLENSK	Deamidated N20 0.00%
3.7	2611.3243	0.9906	YQALGHLLEQYIYELLEKVCK	
3.1	2610.2959	2.0190	RPPLQPSQRLNDDMKEILNSEK	
1.9	2612.3056	0.0092	YLVTWNIQRPNRKSLFASECK	

Mascot: http://www.matrixscience.com/

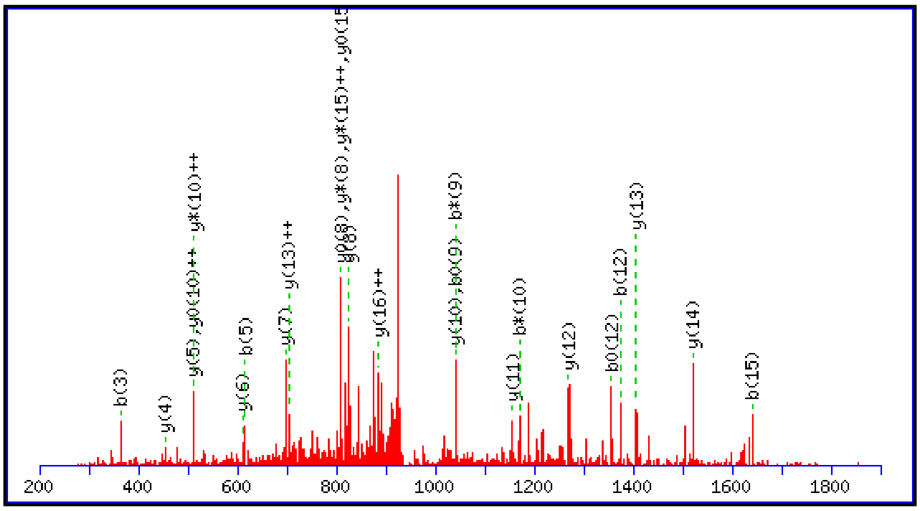
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LHINHNNLTESVGPLPK**
Found in **P51884** in **con_Xuniprot_HUMAN3**, LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

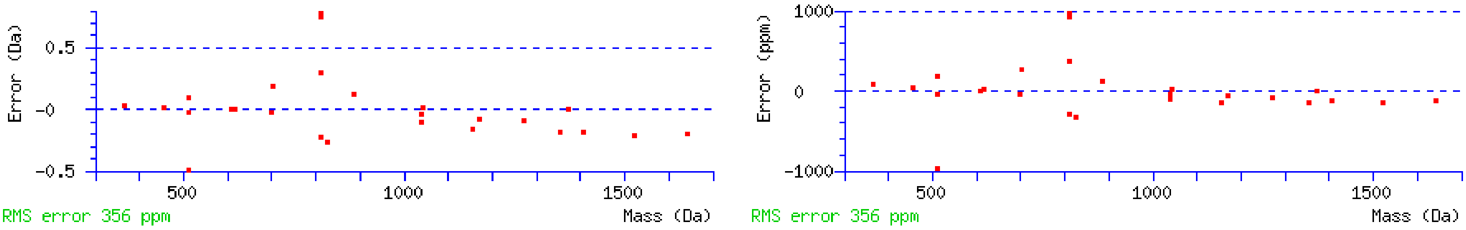
Match to Query 11095: 1882.996668 from(942.505610,2+) intensity(22605.3535) rtinseconds(1011) scans(2233) index(8239)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum1870_scans__2233
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1882.9901
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 73 **Expect:** 9e-006
Matches : 26/158 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	114.0913	57.5493					L							17
2	251.1503	126.0788					H	1770.9133	885.9603	1753.8868	877.4470	1752.9028	876.9550	16
3	**364.2343**	182.6208					I	1633.8544	817.4308	1616.8279	808.9176	1615.8438	808.4256	15
4	478.2772	239.6423	461.2507	231.1290			N	***1520.7703***	760.8888	1503.7438	752.3755	1502.7598	751.8835	14
5	**615.3362**	308.1717	598.3096	299.6584			H	***1406.7274***	703.8673	1389.7009	695.3541	1388.7169	694.8621	13
6	729.3791	365.1932	712.3525	356.6799			N	***1269.6685***	635.3379	1252.6420	626.8246	1251.6579	626.3326	12
7	844.4060	422.7067	827.3795	414.1934			N	***1155.6256***	578.3164	1138.5990	569.8032	1137.6150	569.3111	11
8	957.4901	479.2487	940.4635	470.7354			L	***1040.5986***	520.8030	1023.5721	512.2897	1022.5881	511.7977	10
9	1058.5378	529.7725	1041.5112	521.2592	1040.5272	520.7672	T	927.5146	464.2609	910.4880	455.7477	909.5040	455.2556	9
10	1187.5804	594.2938	1170.5538	585.7805	1169.5698	585.2885	E	***826.4669***	413.7371	809.4403	405.2238	808.4563	404.7318	8
11	1274.6124	637.8098	1257.5858	629.2966	1256.6018	628.8046	S	***697.4243***	349.2158	680.3978	340.7025	679.4137	340.2105	7
12	**1373.6808**	687.3440	1356.6543	678.8308	1355.6702	678.3388	V	***610.3923***	305.6998	593.3657	297.1865			6
13	1430.7023	715.8548	1413.6757	707.3415	1412.6917	706.8495	G	***511.3239***	256.1656	494.2973	247.6523			5
14	1527.7550	764.3812	1510.7285	755.8679	1509.7445	755.3759	P	***454.3024***	227.6548	437.2758	219.1416			4
15	**1640.8391**	820.9232	1623.8125	812.4099	1622.8285	811.9179	L	357.2496	179.1285	340.2231	170.6152			3
16	1737.8919	869.4496	1720.8653	860.9363	1719.8813	860.4443	P	244.1656	122.5864	227.1390	114.0731			2
17							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of LHINHNNLTESVGPLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
72.9	1882.9901	0.0066	LHINHNNLTESVGPLPK	Deamidated N7 95.44%
59.7	1882.9901	0.0066	LHINHNNLTESVGPLPK	Deamidated N6 4.53%
38.9	1882.9901	0.0066	LHINHNNLTESVGPLPK	Deamidated N4 0.04%
3.6	1881.9982	0.9985	NKGPVSIKVQVPNMQDK	
0.3	1881.9870	1.0097	DIKLENLMLDKDGHIK	
0.3	1881.9870	1.0097	DLKLENLMLDKDGHIK	

Mascot: http://www.matrixscience.com/

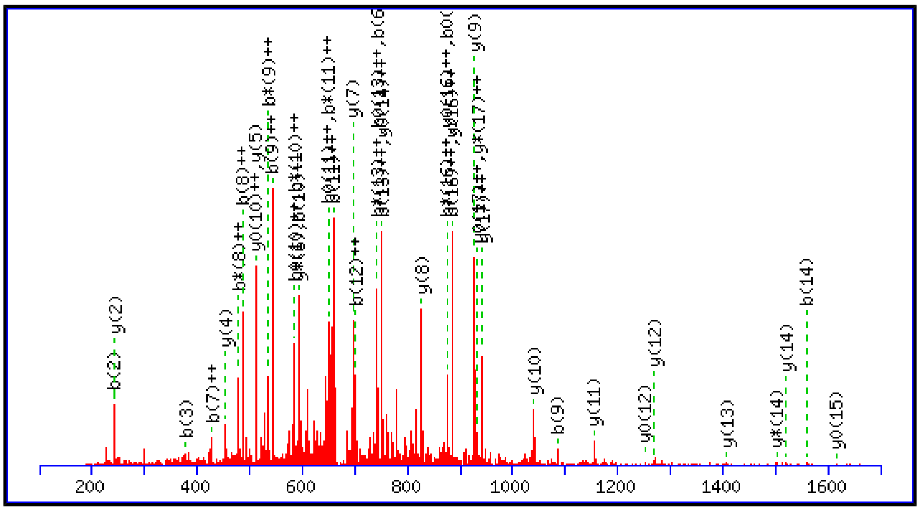
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLHINHNNLTESVGPLPK**
Found in **P51884** in **con_Xuniprot_HUMAN3**, LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

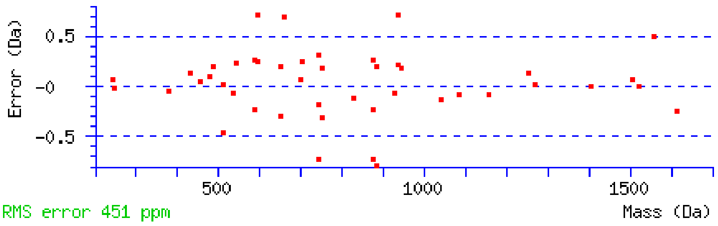
Match to Query 12255: 2011.092822 from(671.371550,3+) intensity(25432.5391) rtinseconds(866) scans(1850) index(8219)
Title: 111019_Est_ISCardio_NMI_YS_G_3Spectrum1533_scans__1850
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

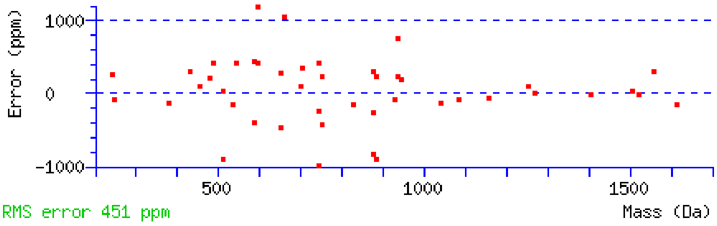
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2011.0850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 62 **Expect:** 8.3e-005
Matches : 46/174 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	129.1022	65.0548	112.0757	56.5415			**K**							**18**
2	**242.1863**	121.5968	225.1598	113.0835			**L**	1883.9974	942.5023	1866.9708	933.9891	1865.9868	933.4970	**17**
3	**379.2452**	190.1262	362.2187	181.6130			**H**	1770.9133	885.9603	1753.8868	877.4470	1752.9028	876.9550	**16**
4	492.3293	246.6683	475.3027	238.1550			**I**	1633.8544	817.4308	1616.8279	808.9176	1615.8438	808.4256	**15**
5	606.3722	303.6897	589.3457	295.1765			**N**	***1520.7703***	760.8888	1503.7438	752.3755	1502.7598	751.8835	**14**
6	**743.4311**	372.2192	726.4046	363.7059			**H**	***1406.7274***	703.8673	1389.7009	695.3541	1388.7169	694.8621	**13**
7	857.4740	***429.2407***	840.4475	420.7274			**N**	***1269.6685***	635.3379	1252.6420	626.8246	1251.6579	626.3326	**12**
8	972.5010	***486.7541***	955.4744	478.2409			**N**	***1155.6256***	578.3164	1138.5990	569.8032	1137.6150	569.3111	**11**
9	**1085.5851**	***543.2962***	1068.5585	534.7829			**L**	***1040.5986***	520.8030	1023.5721	512.2897	1022.5881	511.7977	**10**
10	1186.6327	***593.8200***	1169.6062	585.3067	1168.6222	584.8147	**T**	***927.5146***	464.2609	910.4880	455.7477	909.5040	455.2556	**9**
11	1315.6753	***658.3413***	1298.6488	649.8280	1297.6648	649.3360	**E**	***826.4669***	413.7371	809.4403	405.2238	808.4563	404.7318	**8**
12	1402.7074	***701.8573***	1385.6808	693.3440	1384.6968	692.8520	**S**	***697.4243***	349.2158	680.3978	340.7025	679.4137	340.2105	**7**
13	1501.7758	***751.3915***	1484.7492	742.8782	1483.7652	742.3862	**V**	610.3923	305.6998	593.3657	297.1865			**6**
14	**1558.7972**	779.9023	1541.7707	771.3890	1540.7867	770.8970	**G**	***511.3239***	256.1656	494.2973	247.6523			**5**
15	1655.8500	828.4286	1638.8234	819.9154	1637.8394	819.4234	**P**	***454.3024***	227.6548	437.2758	219.1416			**4**
16	1768.9341	***884.9707***	1751.9075	876.4574	1750.9235	875.9654	**L**	357.2496	179.1285	340.2231	170.6152			**3**
17	1865.9868	***933.4970***	1848.9603	924.9838	1847.9763	924.4918	**P**	***244.1656***	122.5864	227.1390	114.0731			**2**
18							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of KLHINHNNLTESVGPLPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.3	2011.0850	0.0078	KLHINHNNLTESVGPLPK	Deamidated N8 68.20%
58.5	2011.0850	0.0078	KLHINHNNLTESVGPLPK	Deamidated N7 28.36%
49.3	2011.0850	0.0078	KLHINHNNLTESVGPLPK	Deamidated N5 3.44%
7.5	2011.0963	-0.0034	QLRIEALRFTASAAAHEK	
3.2	2011.1024	-0.0096	VTGVTTQGVKSLLTSMYVK	
2.3	2011.0884	0.0044	PSLMGLGDIISQQLVERR	
2.2	2011.0850	0.0078	HLKQQQYRAENQILLK	
2.1	2011.0850	0.0078	EAKDVWNQIALARAVLGR	
1.8	2011.0837	0.0091	ENVALKVESAQQPKQVLK	
1.8	2011.0837	0.0091	ENVALKVESAQQPKQVLK	

Mascot: http://www.matrixscience.com/

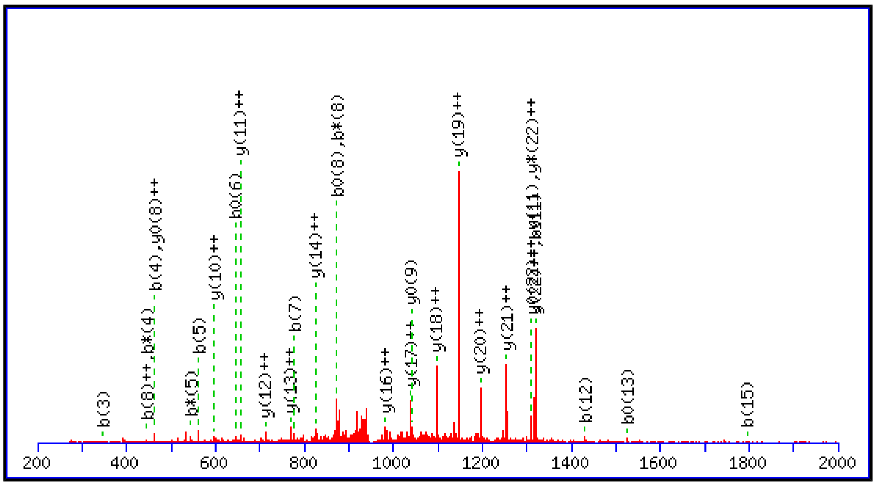
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFENVTDLQWLILDHNLLENSKIK**
Found in **P51884** in **con_Xuniprot_HUMAN3**, LUM_HUMAN Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

Match to Query 25778: 2853.501972 from(952.174600,3+) intensity(29710.4375) rtinseconds(2485) scans(6723) index(24166)
Title: 111019_Est_MI_YS_G_05Spectrum5835_scans__6723
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

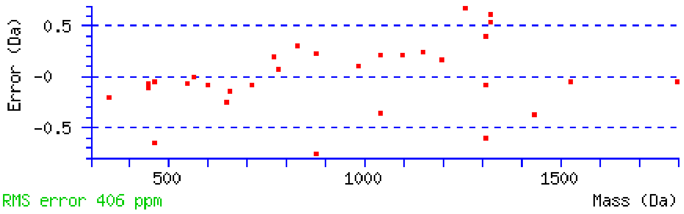
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

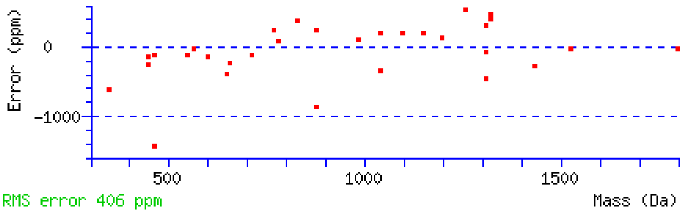


Monoisotopic mass of neutral peptide Mr(calc): 2853.4912
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 56 **Expect:** 0.00035
Matches : 31/260 fragment ions using 53 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							24
2	219.1128	110.0600					F	2783.4614	1392.2343	2766.4349	1383.7211	2765.4509	1383.2291	23
3	**348.1554**	174.5813			330.1448	165.5761	E	2636.3930	1318.7001	2619.3665	1310.1869	2618.3824	1309.6949	22
4	**463.1823**	232.0948	446.1558	223.5815	445.1718	223.0895	N	2507.3504	1254.1788	2490.3239	1245.6656	2489.3398	1245.1736	21
5	**562.2508**	281.6290	545.2242	273.1157	544.2402	272.6237	V	2392.3235	1196.6654	2375.2969	1188.1521	2374.3129	1187.6601	20
6	663.2984	332.1529	646.2719	323.6396	645.2879	323.1476	T	2293.2551	1147.1312	2276.2285	1138.6179	2275.2445	1138.1259	19
7	**778.3254**	389.6663	761.2988	381.1531	760.3148	380.6610	D	2192.2074	1096.6073	2175.1808	1088.0941	2174.1968	1087.6020	18
8	891.4094	446.2084	874.3829	437.6951	873.3989	437.2031	L	2077.1804	1039.0939	2060.1539	1030.5806	2059.1699	1030.0886	17
9	1019.4680	510.2376	1002.4415	501.7244	1001.4575	501.2324	Q	1964.0964	982.5518	1947.0698	974.0385	1946.0858	973.5465	16
10	1205.5473	603.2773	1188.5208	594.7640	1187.5368	594.2720	W	1836.0378	918.5225	1819.0112	910.0093	1818.0272	909.5173	15
11	**1318.6314**	659.8193	1301.6048	651.3061	1300.6208	650.8141	L	1649.9585	825.4829	1632.9319	816.9696	1631.9479	816.4776	14
12	**1431.7155**	716.3614	1414.6889	707.8481	1413.7049	707.3561	I	1536.8744	768.9408	1519.8479	760.4276	1518.8639	759.9356	13
13	1544.7995	772.9034	1527.7730	764.3901	1526.7890	763.8981	L	1423.7904	712.3988	1406.7638	703.8855	1405.7798	703.3935	12
14	1659.8265	830.4169	1642.7999	821.9036	1641.8159	821.4116	D	1310.7063	655.8568	1293.6797	647.3435	1292.6957	646.8515	11
15	**1796.8854**	898.9463	1779.8588	890.4331	1778.8748	889.9410	H	1195.6793	598.3433	1178.6528	589.8300	1177.6688	589.3380	10
16	1910.9283	955.9678	1893.9018	947.4545	1892.9177	946.9625	N	1058.6204	529.8139	1041.5939	521.3006	1040.6099	520.8086	9
17	2024.0124	1012.5098	2006.9858	1003.9965	2006.0018	1003.5045	L	944.5775	472.7924	927.5510	464.2791	926.5669	463.7871	8
18	2137.0964	1069.0519	2120.0699	1060.5386	2119.0859	1060.0466	L	831.4934	416.2504	814.4669	407.7371	813.4829	407.2451	7
19	2266.1390	1133.5732	2249.1125	1125.0599	2248.1285	1124.5679	E	718.4094	359.7083	701.3828	351.1951	700.3988	350.7030	6
20	2380.1820	1190.5946	2363.1554	1182.0813	2362.1714	1181.5893	N	589.3668	295.1870	572.3402	286.6738	571.3562	286.1817	5
21	2467.2140	1234.1106	2450.1874	1225.5974	2449.2034	1225.1053	S	475.3239	238.1656	458.2973	229.6523	457.3133	229.1603	4
22	2595.3089	1298.1581	2578.2824	1289.6448	2577.2984	1289.1528	K	388.2918	194.6496	371.2653	186.1363			3
23	2708.3930	1354.7001	2691.3665	1346.1869	2690.3824	1345.6949	I	260.1969	130.6021	243.1703	122.0888			2

24							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AFENVTDLQWLILDHNLLENSKIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
56.1	2853.4912	0.0108	AFENVTDLQWLILDHNLLENSKIK	Deamidated N4 66.98%
52.0	2853.4912	0.0108	AFENVTDLQWLILDHNLLENSKIK	Deamidated Q9 26.00%
43.3	2853.4912	0.0108	AFENVTDLQWLILDHNLLENSKIK	Deamidated N16 3.52%
43.3	2853.4912	0.0108	AFENVTDLQWLILDHNLLENSKIK	Deamidated N20 3.50%
33.3	2852.5072	0.9948	AFENVTDLQWLILDHNLLENSKIK	
9.8	2853.5124	-0.0104	IRYTTDPQLNNIIYSTVKGVTLSQK	
7.2	2851.4823	2.0196	GSSAGNIMPTTYISVTPKIGMGKPAITK	
7.1	2851.4868	2.0151	WQLLTGSLASTSPSLLSGQGPWAPLQR	
6.7	2853.5124	-0.0104	IRYTTDPQLNNIIYSTVKGVTLSQK	
6.7	2853.5124	-0.0104	IRYTTDPQLNNIIYSTVKGVTLSQK	

Mascot: http://www.matrixscience.com/

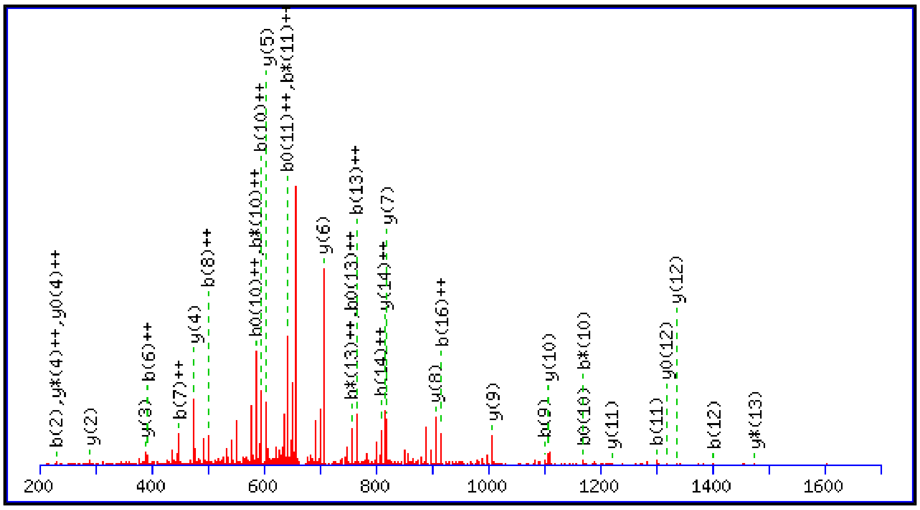
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NDFHRNLTTSLTESVDR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

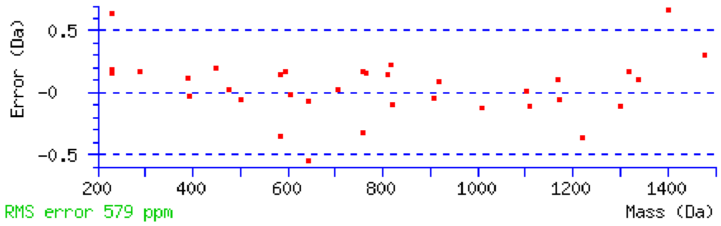
Match to Query 12245: 2004.958362 from(669.326730,3+) intensity(82866.1094) rtinseconds(1077) scans(2520) index(1941)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum2137_scans__2520
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

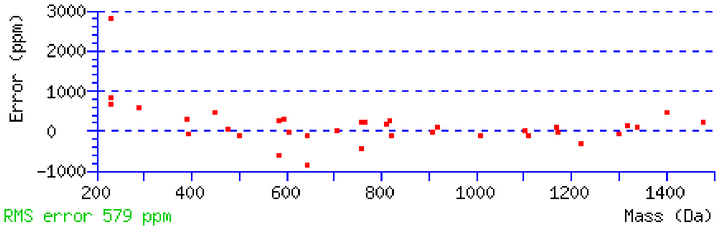
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2004.9501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 81 **Expect:** 1.9e-006
Matches : 35/188 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	115.0502	58.0287	98.0237	49.5155			**N**							**17**
2	**230.0771**	115.5422	213.0506	107.0289	212.0666	106.5369	**D**	1891.9144	946.4609	1874.8879	937.9476	1873.9039	937.4556	**16**
3	377.1456	189.0764	360.1190	180.5631	359.1350	180.0711	**F**	1776.8875	888.9474	1759.8610	880.4341	1758.8769	879.9421	**15**
4	514.2045	257.6059	497.1779	249.0926	496.1939	248.6006	**H**	1629.8191	815.4132	1612.7925	806.8999	1611.8085	806.4079	**14**
5	670.3056	335.6564	653.2790	327.1432	652.2950	326.6511	**R**	1492.7602	746.8837	1475.7336	738.3705	1474.7496	737.8784	**13**
6	785.3325	**393.1699**	768.3060	384.6566	767.3220	384.1646	**N**	***1336.6591***	668.8332	1319.6325	660.3199	1318.6485	659.8279	**12**
7	898.4166	**449.7119**	881.3900	441.1987	880.4060	440.7067	**L**	***1221.6321***	611.3197	1204.6056	602.8064	1203.6216	602.3144	**11**
8	999.4643	**500.2358**	982.4377	491.7225	981.4537	491.2305	**T**	***1108.5481***	554.7777	1091.5215	546.2644	1090.5375	545.7724	**10**
9	**1100.5119**	550.7596	1083.4854	542.2463	1082.5014	541.7543	**T**	***1007.5004***	504.2538	990.4738	495.7406	989.4898	495.2485	**9**
10	1187.5440	**594.2756**	1170.5174	585.7624	1169.5334	585.2703	**S**	***906.4527***	453.7300	889.4262	445.2167	888.4421	444.7247	**8**
11	**1300.6280**	650.8177	1283.6015	642.3044	1282.6175	641.8124	**L**	***819.4207***	410.2140	802.3941	401.7007	801.4101	401.2087	**7**
12	**1401.6757**	701.3415	1384.6492	692.8282	1383.6652	692.3362	**T**	***706.3366***	353.6719	689.3101	345.1587	688.3260	344.6667	**6**
13	1530.7183	**765.8628**	1513.6918	757.3495	1512.7077	756.8575	**E**	***605.2889***	303.1481	588.2624	294.6348	587.2784	294.1428	**5**
14	1617.7503	**809.3788**	1600.7238	800.8655	1599.7398	800.3735	**S**	***476.2463***	238.6268	459.2198	230.1135	458.2358	229.6215	**4**
15	1716.8188	858.9130	1699.7922	850.3997	1698.8082	849.9077	**V**	***389.2143***	195.1108	372.1878	186.5975	371.2037	186.1055	**3**
16	1831.8457	**916.4265**	1814.8191	907.9132	1813.8351	907.4212	**D**	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
17							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of NDFHRNLTTSLTESVDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.0	2004.9501	0.0083	NDFHRNLTTSLTESVDR	Deamidated N6 95.29%
67.9	2004.9501	0.0083	NDFHRNLTTSLTESVDR	Deamidated N1 4.71%
12.4	2003.9595	0.9988	EPMGNEQRARAPPPPSDR	
9.4	2003.9590	0.9993	IGGNAMMKLTHLAMQQAR	
9.4	2003.9590	0.9993	IGGNAMMKLTHLAMQQAR	
8.4	2004.9505	0.0079	LAPGLKLGMYKMMMDSR	
8.2	2003.9470	1.0114	DSLSMSSFQSVKSISNSGK	
8.1	2003.9622	0.9961	MQQATLPSFPAPNLSQTR	
7.5	2004.9541	0.0043	KYYPRQTNLDSYVDSR	
7.0	2003.9469	1.0114	NNKDSHSLTTNIMEILR	

Mascot: http://www.matrixscience.com/

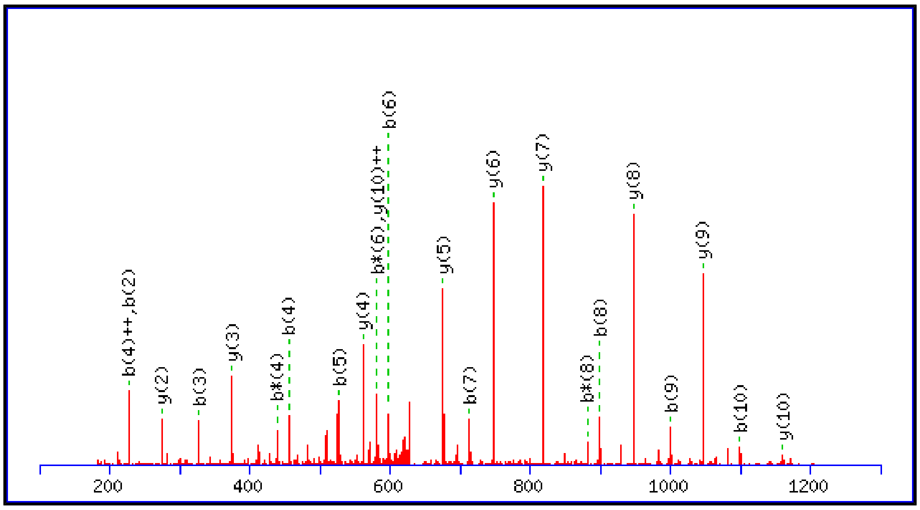
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNVEAANWTVR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

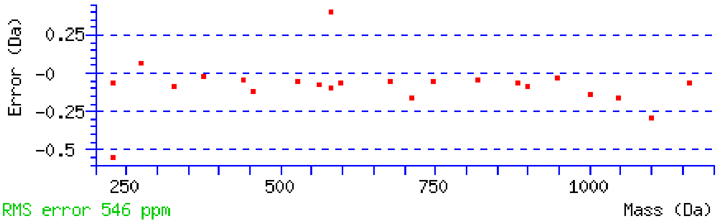
Match to Query 1825: 1272.651068 from(637.332810,2+) intensity(79093.5547) rtinseconds(1340) scans(3173) index(20245)
Title: 111019_Est_MI_YP_G_10Spectrum2763_scans__3173
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

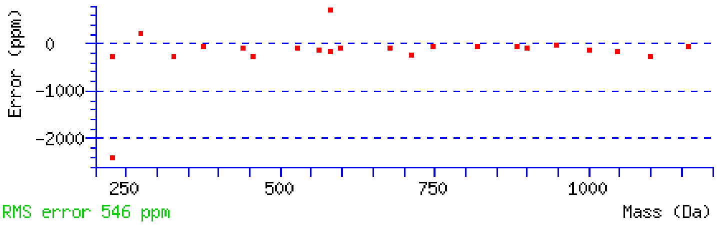
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1272.6462
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 75 **Expect:** 5.9e-006
Matches : 23/108 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	***228.1343***	114.5708	211.1077	106.0575			N	***1160.5695***	580.7884	1143.5429	572.2751	1142.5589	571.7831	10
3	***327.2027***	164.1050	310.1761	155.5917			V	***1046.5265***	523.7669	1029.5000	515.2536	1028.5160	514.7616	9
4	***456.2453***	228.6263	439.2187	220.1130	438.2347	219.6210	E	***947.4581***	474.2327	930.4316	465.7194	929.4476	465.2274	8
5	***527.2824***	264.1448	510.2558	255.6316	509.2718	255.1395	A	***818.4155***	409.7114	801.3890	401.1981	800.4050	400.7061	7
6	***598.3195***	299.6634	581.2930	291.1501	580.3089	290.6581	A	***747.3784***	374.1928	730.3519	365.6796	729.3679	365.1876	6
7	***713.3464***	357.1769	696.3199	348.6636	695.3359	348.1716	N	***676.3413***	338.6743	659.3148	330.1610	658.3307	329.6690	5
8	***899.4258***	450.2165	882.3992	441.7032	881.4152	441.2112	W	***561.3144***	281.1608	544.2878	272.6475	543.3038	272.1555	4
9	***1000.4734***	500.7404	983.4469	492.2271	982.4629	491.7351	T	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	***1099.5419***	550.2746	1082.5153	541.7613	1081.5313	541.2693	V	***274.1874***	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LNVEAANWTVR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.2	1272.6462	0.0048	LNVEAANWTVR	Deamidated N7 100.00%
20.7	1272.6462	0.0048	LNVEAANWTVR	Deamidated N2 0.00%
19.2	1272.6574	-0.0064	NNKVAWNLASR	
12.2	1272.6536	-0.0026	GLGMTLSYLFR	
12.2	1272.6575	-0.0064	LINPNHTHAVR	
8.3	1272.6561	-0.0051	QVLDGKEEVEK	
8.3	1272.6561	-0.0051	QVQVEGLSGNIK	
5.0	1272.6463	0.0048	PEVWVSSNTVR	
3.5	1272.6462	0.0048	GPSLTAPFAEAGR	
3.5	1272.6496	0.0015	IGDLGAVQAAAMR	

Mascot: http://www.matrixscience.com/

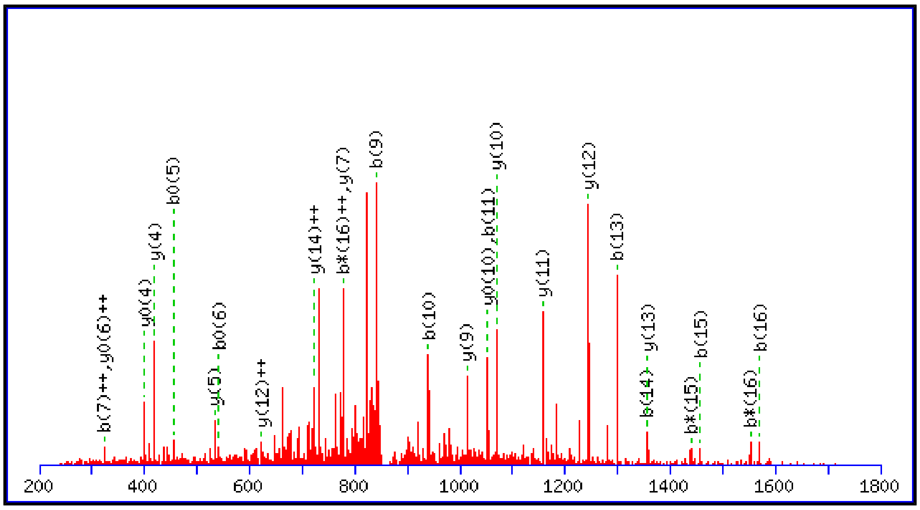
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGTSLSSGHVLMNGTLK**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

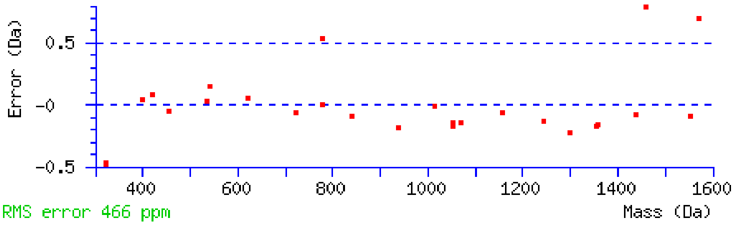
Match to Query 8715: 1714.898948 from(858.456750,2+) intensity(37311.8594) rtinseconds(1203) scans(2851) index(9403)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum2422_scans__2851
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

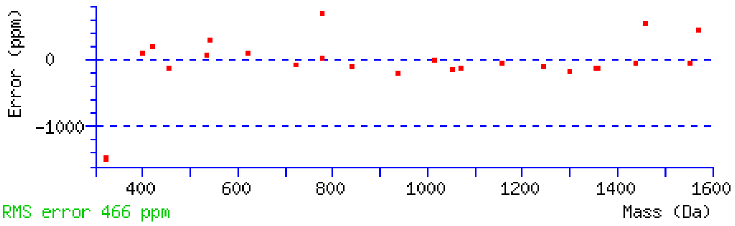
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1714.8924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 74 **Expect:** 9.7e-006
Matches : 26/160 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	114.0913	57.5493					**L**							**17**
2	171.1128	86.0600					**G**	1602.8156	801.9114	1585.7890	793.3982	1584.8050	792.9061	**16**
3	272.1605	136.5839			254.1499	127.5786	**T**	1545.7941	773.4007	1528.7676	764.8874	1527.7836	764.3954	**15**
4	359.1925	180.0999			341.1819	171.0946	**S**	1444.7464	722.8769	1427.7199	714.3636	1426.7359	713.8716	**14**
5	472.2766	236.6419			454.2660	227.6366	**L**	***1357.7144***	679.3608	1340.6879	670.8476	1339.7038	670.3556	**13**
6	559.3086	280.1579			541.2980	271.1527	**S**	***1244.6303***	622.8188	1227.6038	614.3055	1226.6198	613.8135	**12**
7	646.3406	323.6740			628.3301	314.6687	**S**	***1157.5983***	579.3028	1140.5718	570.7895	1139.5878	570.2975	**11**
8	703.3621	352.1847			685.3515	343.1794	**G**	***1070.5663***	535.7868	1053.5397	527.2735	1052.5557	526.7815	**10**
9	***840.4210***	420.7141			822.4104	411.7089	**H**	***1013.5448***	507.2761	996.5183	498.7628	995.5343	498.2708	**9**
10	***939.4894***	470.2483			921.4789	461.2431	**V**	876.4859	438.7466	859.4594	430.2333	858.4754	429.7413	**8**
11	***1052.5735***	526.7904			1034.5629	517.7851	**L**	***777.4175***	389.2124	760.3910	380.6991	759.4069	380.2071	**7**
12	1183.6140	592.3106			1165.6034	583.3053	**M**	664.3334	332.6704	647.3069	324.1571	646.3229	323.6651	**6**
13	***1298.6409***	649.8241	1281.6144	641.3108	1280.6303	640.8188	**N**	***533.2930***	267.1501	516.2664	258.6368	515.2824	258.1448	**5**
14	***1355.6624***	678.3348	1338.6358	669.8216	1337.6518	669.3295	**G**	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	**4**
15	***1456.7101***	728.8587	1439.6835	720.3454	1438.6995	719.8534	**T**	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
16	***1569.7941***	785.4007	1552.7676	776.8874	1551.7836	776.3954	**L**	260.1969	130.6021	243.1703	122.0888			**2**
17							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LGTSLSSGHVLMNGTLK
(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	1714.8924	0.0066	LGTSLSSGHVLMNGTLK
6.3	1714.9035	-0.0046	MAQLAEKARALEQEK
6.2	1713.8971	1.0019	KETIELQIPEKMQGA
5.4	1714.8923	0.0066	ECKNLQVQIDVLQK
4.0	1713.8906	1.0084	SPGRLSDMLLICPQK
3.0	1714.8988	0.0001	LQQKVDELNKEIQK
2.9	1714.8988	0.0001	LQQKVDELNKEIQK
2.9	1714.8988	0.0001	LQQKVDELNKEIQK
2.9	1714.8932	0.0057	HVSCGMMEALLKVIK
2.5	1714.8989	0.0001	GGTNGILVLDEELSGLK

Mascot: http://www.matrixscience.com/

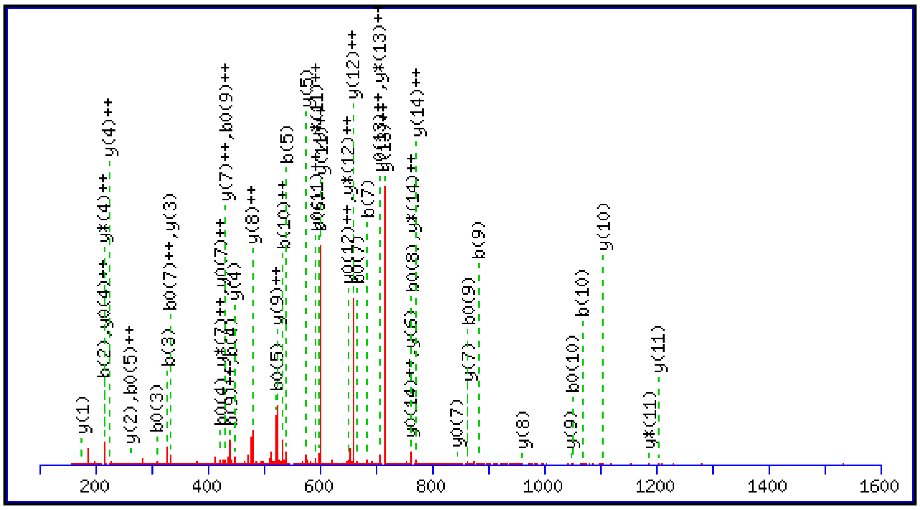
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLLLVGSPTWKNASR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

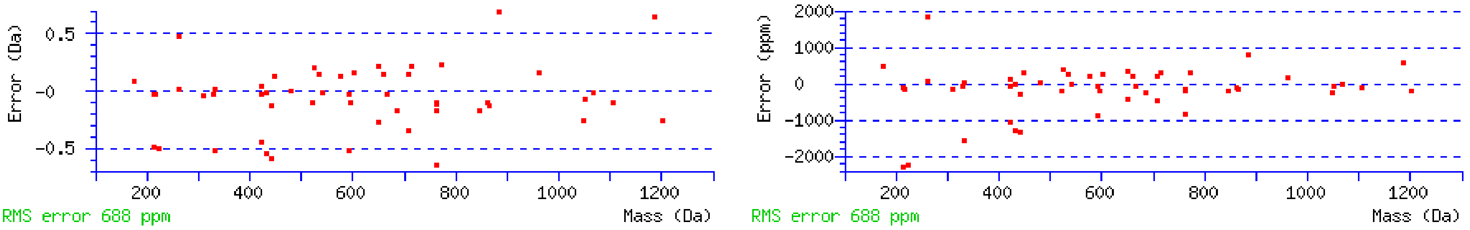
Match to Query 8397: 1642.908102 from(548.643310,3+) intensity(107643.9219) rtinseconds(1420) scans(3219) index(8859)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum2728_scans__3219
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1642.9042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 68 **Expect:** 2.4e-005
Matches : 53/146 fragment ions using 77 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							15
2	**215.1390**	108.0731			197.1285	99.0679	L	1542.8639	771.9356	1525.8373	763.4223	1524.8533	762.9303	14
3	**328.2231**	164.6152			310.2125	155.6099	L	1429.7798	715.3935	1412.7532	706.8803	1411.7692	706.3883	13
4	**441.3071**	221.1572			423.2966	212.1519	L	1316.6957	658.8515	1299.6692	650.3382	1298.6852	649.8462	12
5	**540.3756**	270.6914			522.3650	261.6861	V	***1203.6117***	602.3095	1186.5851	593.7962	1185.6011	593.3042	11
6	**597.3970**	299.2022			579.3865	290.1969	G	***1104.5432***	552.7753	1087.5167	544.2620	1086.5327	543.7700	10
7	**684.4291**	342.7182			666.4185	333.7129	S	***1047.5218***	524.2645	1030.4952	515.7513	1029.5112	515.2592	9
8	781.4818	391.2445			763.4713	382.2393	P	***960.4898***	480.7485	943.4632	472.2352	942.4792	471.7432	8
9	**882.5295**	441.7684			864.5189	432.7631	T	***863.4370***	432.2221	846.4104	423.7089	845.4264	423.2169	7
10	**1068.6088**	534.8080			1050.5982	525.8028	W	***762.3893***	381.6983	745.3628	373.1850	744.3787	372.6930	6
11	1196.7038	598.8555	1179.6772	590.3422	1178.6932	589.8502	K	***576.3100***	288.6586	559.2835	280.1454	558.2994	279.6534	5
12	1311.7307	656.3690	1294.7042	647.8557	1293.7202	647.3637	N	***448.2150***	224.6112	431.1885	216.0979	430.2045	215.6059	4
13	1382.7678	691.8876	1365.7413	683.3743	1364.7573	682.8823	A	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
14	1469.7999	735.4036	1452.7733	726.8903	1451.7893	726.3983	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	***175.1190***	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of TLLLVGSPTWKNASR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
67.9	1642.9042	0.0039	TLLLVGSPTWKNASR
12.7	1642.9155	-0.0074	WQVGAQTVLALSKSR
9.9	1641.9049	1.0032	VDELIAKLVNNRTR
9.2	1641.9090	0.9991	DVLLELVEHHLTPK
8.8	1642.9141	-0.0060	ITLLELKEQQTLGR
8.7	1641.9090	0.9991	TLAQFPNTLLGNPKK
6.8	1640.9072	2.0009	VVKLEEVLFHLCR
6.1	1642.9141	-0.0060	VIDNLVSNLEASIKK
5.2	1642.9155	-0.0074	IVEKWASDLRLTGR
5.0	1642.9128	-0.0047	GASLVKNQHIRQHR

Mascot: http://www.matrixscience.com/

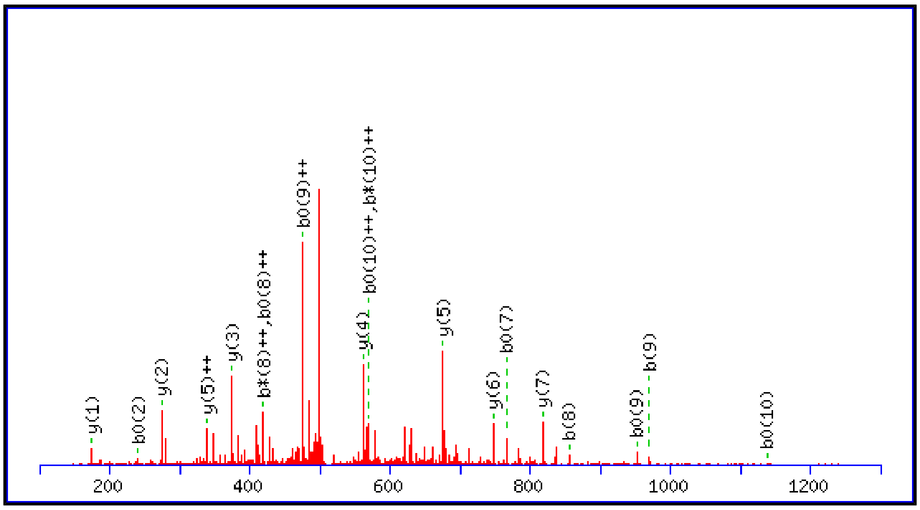
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EKLNVEAANWTVR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

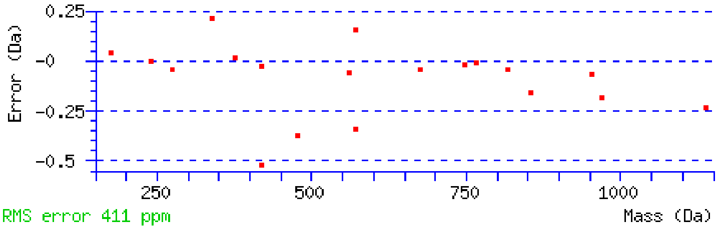
Match to Query 6907: 1529.786592 from(510.936140,3+) intensity(29084.5020) rtinseconds(1048) scans(2483) index(2570)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum2105_scans__2483
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

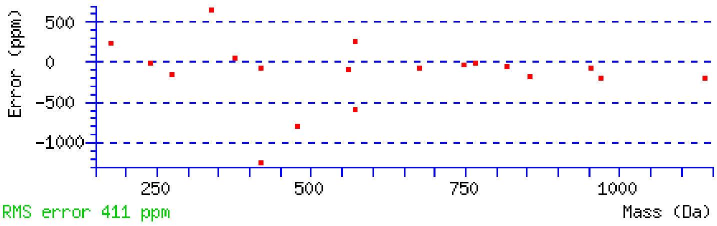
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1300] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1529.7838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 49 **Expect:** 0.0029
Matches : 19/138 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	130.0499	65.5286			112.0393	56.5233	E							13
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	K	1401.7485	701.3779	1384.7219	692.8646	1383.7379	692.3726	12
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	L	1273.6535	637.3304	1256.6270	628.8171	1255.6430	628.3251	11
4	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	N	1160.5695	580.7884	1143.5429	572.2751	1142.5589	571.7831	10
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	V	1046.5265	523.7669	1029.5000	515.2536	1028.5160	514.7616	9
6	713.3828	357.1951	696.3563	348.6818	695.3723	348.1898	E	947.4581	474.2327	930.4316	465.7194	929.4476	465.2274	8
7	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	A	***818.4155***	409.7114	801.3890	401.1981	800.4050	400.7061	7
8	**855.4571**	428.2322	838.4305	419.7189	837.4465	419.2269	A	***747.3784***	374.1928	730.3519	365.6796	729.3678	365.1876	6
9	**970.4840**	485.7456	953.4575	477.2324	952.4734	476.7404	N	***676.3413***	338.6743	659.3148	330.1610	658.3307	329.6690	5
10	1156.5633	578.7853	1139.5368	570.2720	1138.5527	569.7800	W	***561.3144***	281.1608	544.2878	272.6475	543.3038	272.1555	4
11	1257.6110	629.3091	1240.5844	620.7959	1239.6004	620.3039	T	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
12	1356.6794	678.8433	1339.6529	670.3301	1338.6688	669.8381	V	***274.1874***	137.5973	257.1608	129.0840			2
13							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EKLNVEAANWTVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.0	1529.7838	0.0028	EKLNVEAANWTVR	Deamidated N9 99.78%
22.4	1529.7838	0.0028	EKLNVEAANWTVR	Deamidated N4 0.22%
20.0	1527.7762	2.0104	MNGHVGKLDRMVR	
17.7	1528.7820	1.0046	NVSLLWAAPGQAMR	
10.2	1529.7838	0.0028	IERFNPPSNVTVR	
7.8	1528.7773	1.0093	EDFTSLSLVLYSR	
6.2	1528.7780	1.0086	INMASDSRHTLLR	
6.2	1528.7780	1.0086	LNMASDSRHTLLR	
5.7	1527.7728	2.0138	ARSNMSRYLQFR	
5.0	1527.7827	2.0039	ISSGRMNLIQHVR	

Mascot: http://www.matrixscience.com/

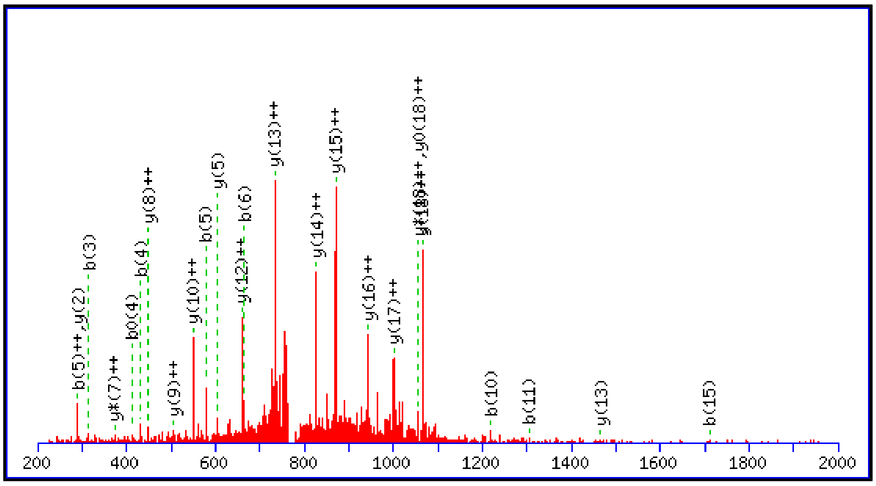
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GEEDFSWFGYSLHGVTVDNR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

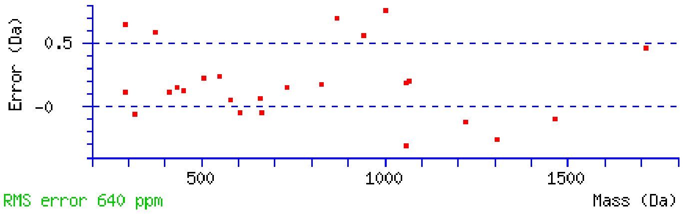
Match to Query 15425: 2315.018862 from(772.680230,3+) intensity(20896.7305) rtinseconds(2249) scans(5576) index(26220)
Title: 111019_Est_MI_YS_G_08Spectrum4836_scans__5576
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

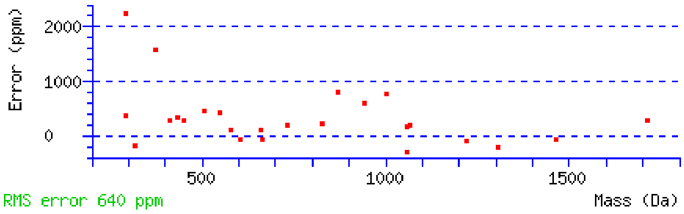
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2315.0131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N19 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0029
Matches : 25/186 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							20
2	187.0713	94.0393			169.0608	85.0340	E	2258.9989	1130.0031	2241.9724	1121.4898	2240.9883	1120.9978	19
3	**316.1139**	158.5606			298.1034	149.5553	E	2129.9563	1065.4818	2112.9298	1056.9685	2111.9457	1056.4765	18
4	**431.1409**	216.0741			413.1303	207.0688	D	2000.9137	1000.9605	1983.8872	992.4472	1982.9032	991.9552	17
5	**578.2093**	289.6083			560.1987	280.6030	F	1885.8868	943.4470	1868.8602	934.9338	1867.8762	934.4417	16
6	**665.2413**	333.1243			647.2307	324.1190	S	1738.8184	869.9128	1721.7918	861.3995	1720.8078	860.9075	15
7	851.3206	426.1640			833.3101	417.1587	W	1651.7863	826.3968	1634.7598	817.8835	1633.7758	817.3915	14
8	998.3890	499.6982			980.3785	490.6929	F	**1465.7070**	733.3571	1448.6805	724.8439	1447.6965	724.3519	13
9	1055.4105	528.2089			1037.3999	519.2036	G	1318.6386	659.8229	1301.6121	651.3097	1300.6280	650.8177	12
10	**1218.4738**	609.7406			1200.4633	600.7353	Y	1261.6171	631.3122	1244.5906	622.7989	1243.6066	622.3069	11
11	**1305.5059**	653.2566			1287.4953	644.2513	S	1098.5538	549.7805	1081.5273	541.2673	1080.5432	540.7753	10
12	1418.5899	709.7986			1400.5794	700.7933	L	1011.5218	506.2645	994.4952	497.7513	993.5112	497.2592	9
13	1555.6488	778.3281			1537.6383	769.3228	H	898.4377	449.7225	881.4112	441.2092	880.4272	440.7172	8
14	1612.6703	806.8388			1594.6597	797.8335	G	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	7
15	**1711.7387**	856.3730			1693.7281	847.3677	V	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	6
16	1812.7864	906.8968			1794.7758	897.8916	T	**605.2889**	303.1481	588.2624	294.6348	587.2784	294.1428	5
17	1911.8548	956.4310			1893.8442	947.4258	V	504.2413	252.6243	487.2147	244.1110	486.2307	243.6190	4
18	2026.8817	1013.9445			2008.8712	1004.9392	D	405.1728	203.0901	388.1463	194.5768	387.1623	194.0848	3
19	2141.9087	1071.4580	2124.8821	1062.9447	2123.8981	1062.4527	N	**290.1459**	145.5766	273.1193	137.0633			2
20							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GEEDFSWFGYSLHGVTVDNR
(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	2315.0131	0.0058	GEEDFSWFGYSLHGVTVDNR
1.8	2314.0127	1.0062	QEEVSMSSQMGCQALNQLLK
0.3	2313.0067	2.0122	VSQDMGVEGQSIEPSGSFSAQR

Mascot: http://www.matrixscience.com/

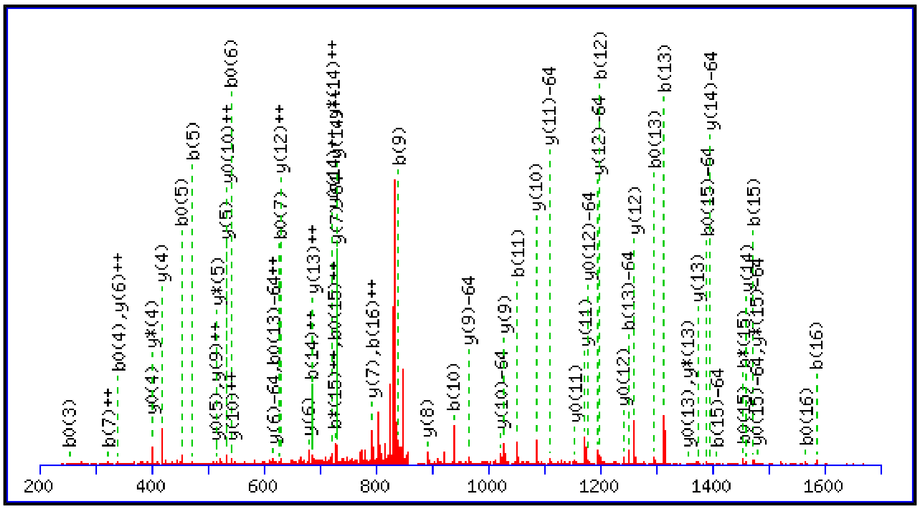
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGTSLSSGHVLMNGTLK**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

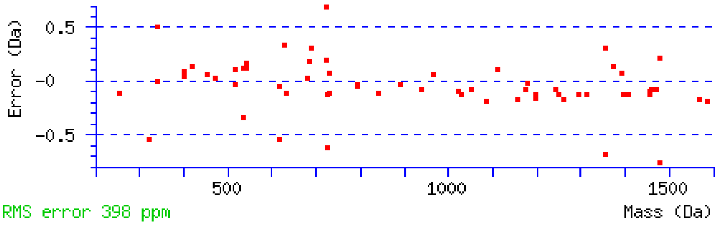
Match to Query 8787: 1730.895348 from(866.454950,2+) intensity(33774.7813) rtinseconds(871) scans(2130) index(23829)
Title: 111019_Est_MI_YS_G_05Spectrum1808_scans__2130
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

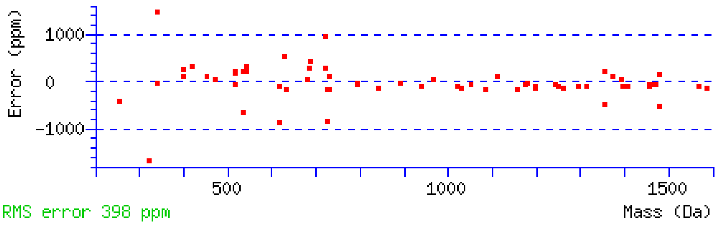
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1730.8873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N13 : Deamidated (NQ)
Ions Score: 45 **Expect:** 0.007
Matches : 64/254 fragment ions using 129 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	171.1128	86.0600					G	1618.8105	809.9089	1601.7840	801.3956	1600.7999	800.9036	16
3	272.1605	136.5839			254.1499	127.5786	T	1561.7890	781.3982	1544.7625	772.8849	1543.7785	772.3929	15
4	359.1925	180.0999			341.1819	171.0946	S	***1460.7414***	730.8743	1443.7148	722.3610	1442.7308	721.8690	14
5	**472.2766**	236.6419			454.2660	227.6366	L	***1373.7093***	687.3583	1356.6828	678.8450	1355.6988	678.3530	13
6	559.3086	280.1579			541.2980	271.1527	S	***1260.6253***	630.8163	1243.5987	622.3030	1242.6147	621.8110	12
7	646.3406	323.6740			628.3301	314.6687	S	***1173.5932***	587.3003	1156.5667	578.7870	1155.5827	578.2950	11
8	703.3621	352.1847			685.3515	343.1794	G	***1086.5612***	543.7842	1069.5347	535.2710	1068.5506	534.7790	10
9	**840.4210**	420.7141			822.4104	411.7089	H	***1029.5397***	515.2735	1012.5132	506.7602	1011.5292	506.2682	9
10	**939.4894**	470.2483			921.4789	461.2431	V	***892.4808***	446.7441	875.4543	438.2308	874.4703	437.7388	8
11	**1052.5735**	526.7904			1034.5629	517.7851	L	***793.4124***	397.2098	776.3859	388.6966	775.4019	388.2046	7
12	**1199.6089**	600.3081			1181.5983	591.3028	M	***680.3284***	340.6678	663.3018	332.1545	662.3178	331.6625	6
13	**1314.6358**	657.8216	1297.6093	649.3083	1296.6253	648.8163	N	***533.2930***	267.1501	516.2664	258.6368	515.2824	258.1448	5
14	1371.6573	686.3323	1354.6307	677.8190	1353.6467	677.3270	G	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	4
15	**1472.7050**	736.8561	1455.6784	728.3428	1454.6944	727.8508	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
16	**1585.7890**	793.3982	1568.7625	784.8849	1567.7785	784.3929	L	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LGTSLSSGHVLMNGTLK
(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	1730.8873	0.0081	LGTSLSSGHVLMNGTLK
10.9	1730.8873	0.0081	LTGNMLVHGSSLSTGLK
3.2	1730.8913	0.0041	MEKYYNLIKESGLK
3.0	1730.8888	0.0066	FNVNMNLFVVFKMK
3.0	1730.8888	0.0066	FNVNMNLFVVFKMK
3.0	1730.8888	0.0066	FNVNMNLFVVFKMK
1.1	1728.8869	2.0085	QFGGMLLAYSGVQSKK
0.6	1730.8913	0.0040	YNGVIVGDPNLMPVVK

Mascot: http://www.matrixscience.com/

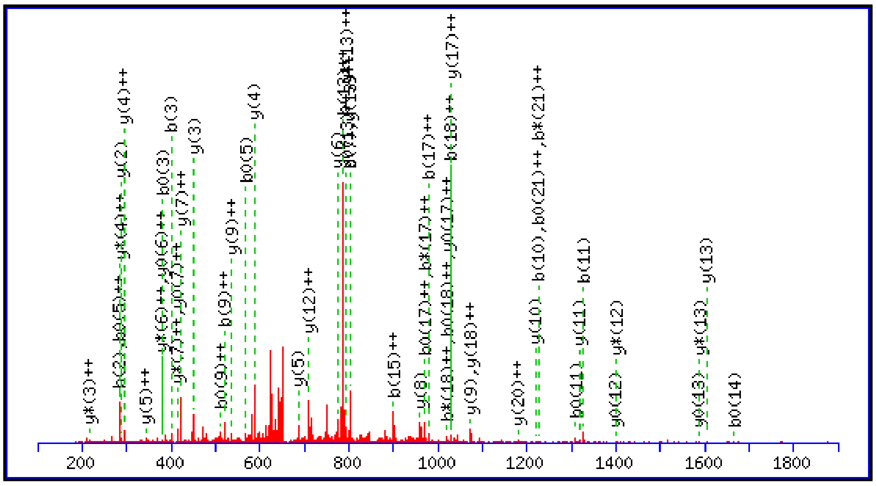
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **FHDVSESTHWTPFLNASVHYIR**
Found in **P80108** in **con_Xuniprot_HUMAN3**, PHLD_HUMAN Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

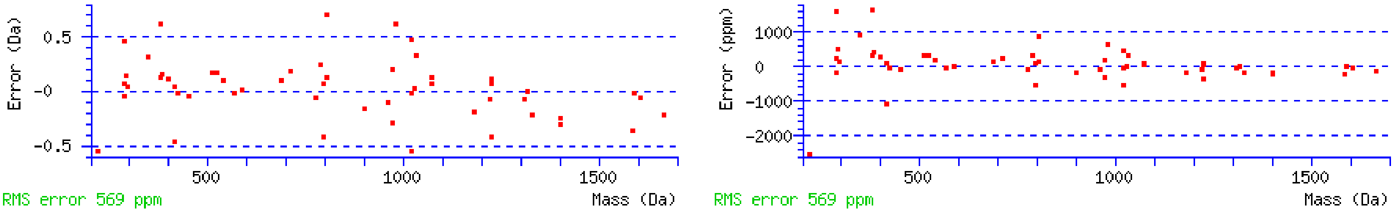
Match to Query 22379: 2643.257016 from(661.821530,4+) intensity(18459.5449) rtinseconds(1688) scans(4268) index(1314)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum3714_scans__4268
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2643.2506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.029
Matches : 54/210 fragment ions using 108 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**22**
2	**285.1346**	143.0709					**H**	2497.1895	1249.0984	2480.1629	1240.5851	2479.1789	1240.0931	**21**
3	**400.1615**	200.5844			382.1510	191.5791	**D**	2360.1306	1180.5689	2343.1040	1172.0557	2342.1200	1171.5636	**20**
4	499.2300	250.1186			481.2194	241.1133	**V**	2245.1036	1123.0555	2228.0771	1114.5422	2227.0931	1114.0502	**19**
5	586.2620	293.6346			568.2514	284.6293	**S**	2146.0352	1073.5213	2129.0087	1065.0080	2128.0247	1064.5160	**18**
6	715.3046	358.1559			697.2940	349.1506	**E**	2059.0032	1030.0052	2041.9767	1021.4920	2040.9926	1021.0000	**17**
7	**802.3366**	401.6719			784.3260	392.6667	**S**	1929.9606	965.4839	1912.9341	956.9707	1911.9500	956.4787	**16**
8	903.3843	452.1958			885.3737	443.1905	**T**	1842.9286	921.9679	1825.9020	913.4547	1824.9180	912.9626	**15**
9	1040.4432	**520.7252**			1022.4326	511.7200	**H**	1741.8809	871.4441	1724.8544	862.9308	1723.8703	862.4388	**14**
10	**1226.5225**	613.7649			1208.5119	604.7596	**W**	***1604.8220***	802.9146	1587.7954	794.4014	1586.8114	793.9094	**13**
11	**1327.5702**	664.2887			1309.5596	655.2835	**T**	1418.7427	709.8750	1401.7161	701.3617	1400.7321	700.8697	**12**
12	1424.6230	712.8151			1406.6124	703.8098	**P**	***1317.6950***	659.3511	1300.6684	650.8379	1299.6844	650.3459	**11**
13	1571.6914	**786.3493**			1553.6808	777.3440	**F**	***1220.6422***	610.8248	1203.6157	602.3115	1202.6317	601.8195	**10**
14	1684.7754	842.8914			1666.7649	833.8861	**L**	***1073.5738***	537.2905	1056.5473	528.7773	1055.5633	528.2853	**9**
15	1799.8024	**900.4048**	1782.7758	891.8916	1781.7918	891.3995	**N**	***960.4898***	480.7485	943.4632	472.2352	942.4792	471.7432	**8**
16	1870.8395	935.9234	1853.8129	927.4101	1852.8289	926.9181	**A**	845.4628	423.2350	828.4363	414.7218	827.4522	414.2298	**7**
17	1957.8715	**979.4394**	1940.8450	970.9261	1939.8610	970.4341	**S**	***774.4257***	387.7165	757.3992	379.2032	756.4151	378.7112	**6**
18	2056.9399	**1028.9736**	2039.9134	1020.4603	2038.9294	1019.9683	**V**	***687.3937***	344.2005	670.3671	335.6872			**5**
19	2193.9988	1097.5031	2176.9723	1088.9898	2175.9883	1088.4978	**H**	***588.3253***	294.6663	571.2987	286.1530			**4**
20	2357.0622	1179.0347	2340.0356	1170.5214	2339.0516	1170.0294	**Y**	***451.2663***	226.1368	434.2398	217.6235			**3**
21	2470.1462	1235.5768	2453.1197	1227.0635	2452.1357	1226.5715	**I**	***288.2030***	144.6051	271.1765	136.0919			**2**
22							**R**	175.1190	88.0631	158.0924	79.5498			**1**



NCBI **BLAST** search of FHDVSESTHWTPFLNASVHYIR
(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	2643.2506	0.0064	FHDVSESTHWTPFLNASVHYIR
27.3	2642.2666	0.9904	FHDVSESTHWTPFLNASVHYIR
9.2	2643.2565	0.0005	IHEFESRLGPQQFLDEQQVANR
8.8	2643.2565	0.0005	IHEFESRLGPQQFLDEQQVANR
8.2	2643.2565	0.0005	IHEFESRLGPQQFLDEQQVANR
5.1	2643.2565	0.0005	NAVQQEDLFQQPGLRSEFEHIR
5.1	2643.2565	0.0005	NAVQQEDLFQQPGLRSEFEHIR
4.4	2643.2565	0.0005	NAVQQEDLFQQPGLRSEFEHIR
4.4	2643.2565	0.0005	NAVQQEDLFQQPGLRSEFEHIR
4.4	2643.2565	0.0005	NAVQQEDLFQQPGLRSEFEHIR

Mascot: http://www.matrixscience.com/

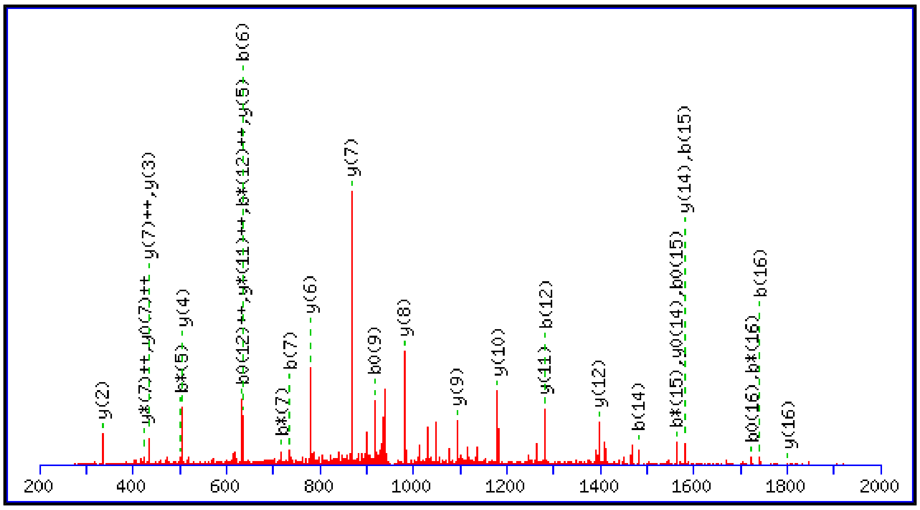
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGYNANTSILSFQAVCR**
Found in **Q02985** in **con_Xuniprot_HUMAN3**, FHR3_HUMAN Complement factor H-related protein 3 OS=Homo sapiens GN=CFHR3 PE=1 SV=2

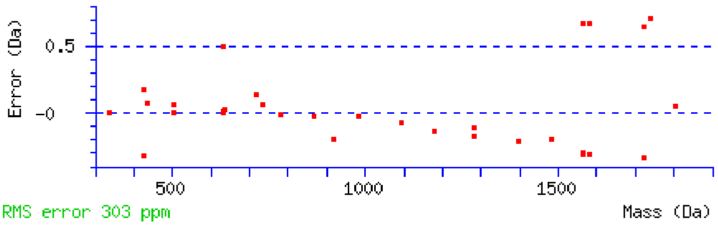
Match to Query 11543: 1913.936968 from(957.975760,2+) intensity(34843.8984) rtinseconds(1861) scans(4892) index(4497)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum4145_scans__4892
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

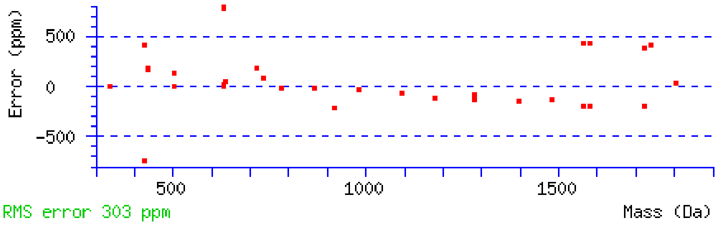
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1913.9305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 114 **Expect:** 9.4e-010
Matches : 33/162 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	171.1128	86.0600					G	***1801.8538***	901.4305	1784.8272	892.9172	1783.8432	892.4252	16
3	334.1761	167.5917					Y	1744.8323	872.9198	1727.8057	864.4065	1726.8217	863.9145	15
4	448.2191	224.6132	431.1925	216.0999			N	***1581.7690***	791.3881	1564.7424	782.8748	1563.7584	782.3828	14
5	519.2562	260.1317	502.2296	251.6185			A	1467.7260	734.3667	1450.6995	725.8534	1449.7155	725.3614	13
6	**634.2831**	317.6452	617.2566	309.1319			N	***1396.6889***	698.8481	1379.6624	690.3348	1378.6784	689.8428	12
7	**735.3308**	368.1690	718.3042	359.6558	717.3202	359.1638	T	***1281.6620***	641.3346	1264.6354	632.8214	1263.6514	632.3293	11
8	822.3628	411.6851	805.3363	403.1718	804.3523	402.6798	S	***1180.6143***	590.8108	1163.5878	582.2975	1162.6037	581.8055	10
9	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	I	***1093.5823***	547.2948	1076.5557	538.7815	1075.5717	538.2895	9
10	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	L	***980.4982***	490.7527	963.4717	482.2395	962.4876	481.7475	8
11	1135.5630	568.2851	1118.5364	559.7719	1117.5524	559.2798	S	***867.4141***	434.2107	850.3876	425.6974	849.4036	425.2054	7
12	**1282.6314**	641.8193	1265.6048	633.3061	1264.6208	632.8141	F	***780.3821***	390.6947	763.3556	382.1814			6
13	1410.6900	705.8486	1393.6634	697.3353	1392.6794	696.8433	Q	***633.3137***	317.1605	616.2872	308.6472			5
14	**1481.7271**	741.3672	1464.7005	732.8539	1463.7165	732.3619	A	***505.2551***	253.1312	488.2286	244.6179			4
15	**1580.7955**	790.9014	1563.7690	782.3881	1562.7849	781.8961	V	***434.2180***	217.6126	417.1915	209.0994			3
16	**1740.8261**	870.9167	1723.7996	862.4034	1722.8156	861.9114	C	***335.1496***	168.0784	318.1231	159.5652			2
17							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LGYNANTSILSFQAVCR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
114.3	1913.9305	0.0064	LGYNANTSILSFQAVCR	Deamidated N6 65.52%
111.2	1913.9305	0.0064	LGYNANTSILSFQAVCR	Deamidated N4 32.16%
99.8	1913.9305	0.0064	LGYNANTSILSFQAVCR	Deamidated Q13 2.31%
9.1	1913.9305	0.0064	DKGFAPNHLNVEKMALD	
9.1	1913.9305	0.0065	DKGFAPNHLNVEKMALN	
5.5	1913.9305	0.0065	DKGFAPNHLNVEKMALN	
4.2	1912.9425	0.9945	HNNGSAASGALLMRQLEK	
3.0	1913.9404	-0.0035	IACKSPPPESVDTPTSTK	
2.0	1913.9378	-0.0008	LPARLPSTSTSGSTSHCR	
1.4	1913.9418	-0.0048	MRFLGGFPGSSKQVSSGR	

Mascot: http://www.matrixscience.com/

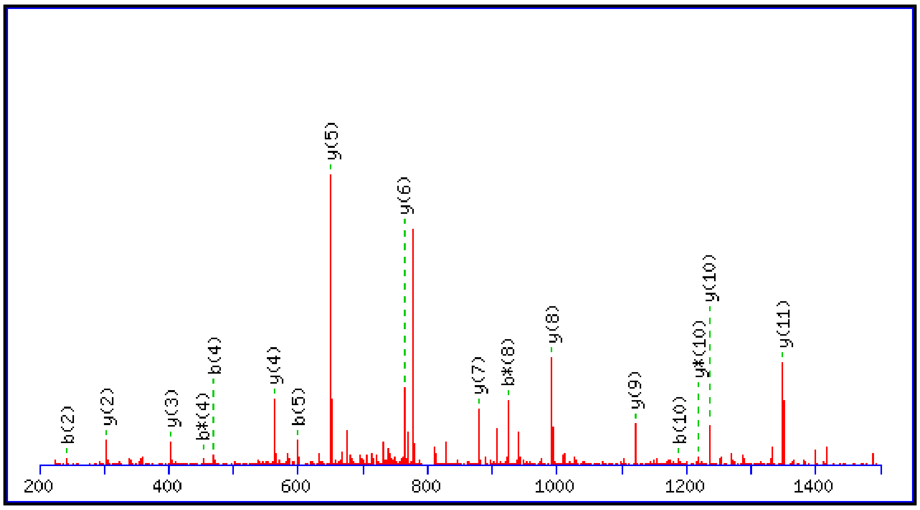
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQNNENNISCVER**
Found in **B1AKG0** in **con_Xuniprot_HUMAN3**, B1AKG0_HUMAN Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=2 SV=1

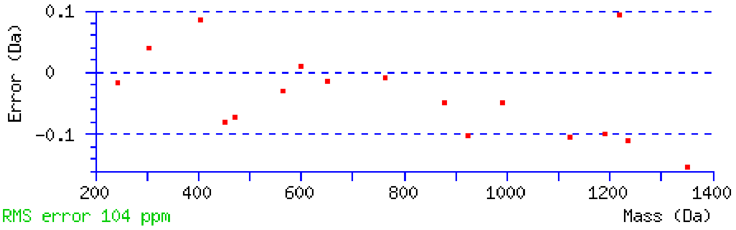
Match to Query 7619: 1589.713948 from(795.864250,2+) intensity(108922.0703) rtinseconds(416) scans(882) index(6134)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum757_scans__882
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

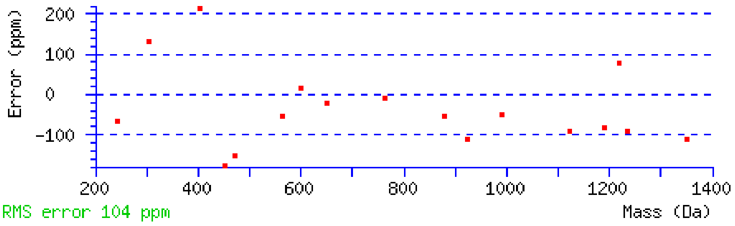
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1589.7103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 79 **Expect:** 1.3e-006
Matches : 17/132 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							13
2	**242.1499**	121.5786	225.1234	113.0653			Q	1477.6336	739.3204	1460.6070	730.8072	1459.6230	730.3152	12
3	356.1928	178.6001	339.1663	170.0868			N	***1349.5750***	675.2911	1332.5485	666.7779	1331.5645	666.2859	11
4	**470.2358**	235.6215	453.2092	227.1082			N	***1235.5321***	618.2697	1218.5055	609.7564	1217.5215	609.2644	10
5	**599.2784**	300.1428	582.2518	291.6295	581.2678	291.1375	E	***1121.4892***	561.2482	1104.4626	552.7349	1103.4786	552.2429	9
6	713.3213	357.1643	696.2947	348.6510	695.3107	348.1590	N	***992.4466***	496.7269	975.4200	488.2136	974.4360	487.7216	8
7	828.3482	414.6778	811.3217	406.1645	810.3377	405.6725	N	***878.4036***	439.7055	861.3771	431.1922	860.3931	430.7002	7
8	941.4323	471.2198	924.4058	462.7065	923.4217	462.2145	I	***763.3767***	382.1920	746.3502	373.6787	745.3661	373.1867	6
9	1028.4643	514.7358	1011.4378	506.2225	1010.4538	505.7305	S	***650.2926***	325.6500	633.2661	317.1367	632.2821	316.6447	5
10	**1188.4950**	594.7511	1171.4684	586.2379	1170.4844	585.7458	C	***563.2606***	282.1339	546.2341	273.6207	545.2500	273.1287	4
11	1287.5634	644.2853	1270.5368	635.7721	1269.5528	635.2801	V	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1416.6060	708.8066	1399.5794	700.2934	1398.5954	699.8013	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LQNNENNISCVER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
78.8	1589.7103	0.0036	LQNNENNISCVER	Deamidated N7 96.38%
64.5	1589.7103	0.0036	LQNNENNISCVER	Deamidated N6 3.56%
45.8	1589.7103	0.0036	LQNNENNISCVER	Deamidated N4 0.05%
34.8	1589.7103	0.0036	LQNNENNISCVER	Deamidated N3 0.00%
23.6	1589.7103	0.0036	LQNNENNISCVER	Deamidated Q2 0.00%
1.7	1589.7216	-0.0076	GQPMGKNRTSNNQR	
0.5	1589.7182	-0.0043	TSSTWHNTSQRER	

Mascot: http://www.matrixscience.com/

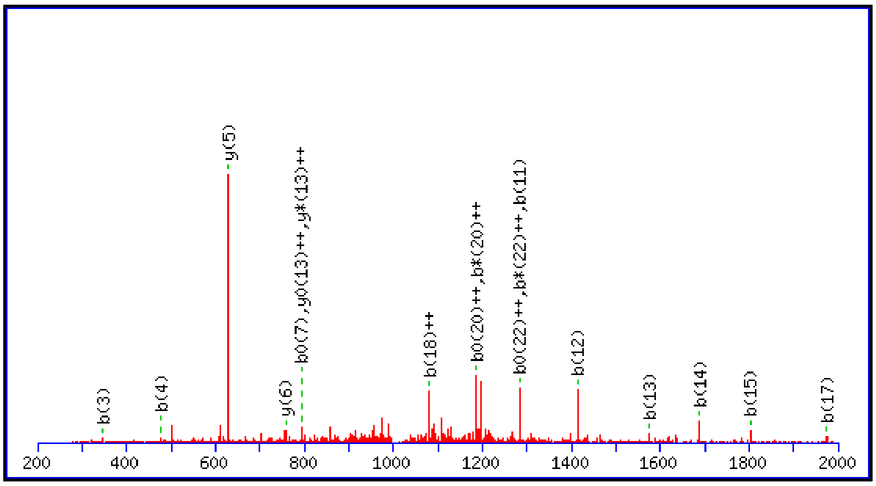
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYEMFGDEEVMCLNGNWTEPPQCK**
Found in **P08603** in **con_Xuniprot_HUMAN3**, CFAH_HUMAN Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4

Match to Query 27260: 3018.225702 from(1007.082510,3+) intensity(26975.1504) rtinseconds(2171) scans(5473) index(12816)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum4799_scans__5473
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

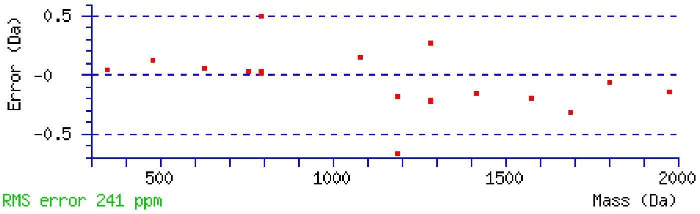
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

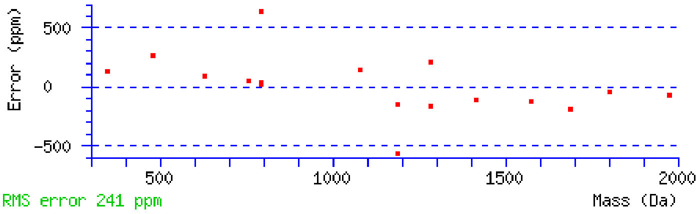


Monoisotopic mass of neutral peptide Mr(calc): 3018.2180
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.00053
Matches : 18/250 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	185.0921	93.0497			167.0815	84.0444	P	2932.1933	1466.6003	2915.1667	1458.0870	2914.1827	1457.5950	24
3	***348.1554***	174.5813			330.1448	165.5761	Y	2835.1405	1418.0739	2818.1140	1409.5606	2817.1299	1409.0686	23
4	***477.1980***	239.1026			459.1874	230.0974	E	2672.0772	1336.5422	2655.0506	1328.0290	2654.0666	1327.5369	22
5	608.2385	304.6229			590.2279	295.6176	M	2543.0346	1272.0209	2526.0080	1263.5077	2525.0240	1263.0156	21
6	755.3069	378.1571			737.2963	369.1518	F	2411.9941	1206.5007	2394.9675	1197.9874	2393.9835	1197.4954	20
7	812.3284	406.6678			794.3178	397.6625	G	2264.9257	1132.9665	2247.8991	1124.4532	2246.9151	1123.9612	19
8	927.3553	464.1813			909.3447	455.1760	D	2207.9042	1104.4557	2190.8777	1095.9425	2189.8937	1095.4505	18
9	1056.3979	528.7026			1038.3873	519.6973	E	2092.8773	1046.9423	2075.8507	1038.4290	2074.8667	1037.9370	17
10	1185.4405	593.2239			1167.4299	584.2186	E	1963.8347	982.4210	1946.8081	973.9077	1945.8241	973.4157	16
11	***1284.5089***	642.7581			1266.4983	633.7528	V	1834.7921	917.8997	1817.7655	909.3864	1816.7815	908.8944	15
12	***1415.5494***	708.2783			1397.5388	699.2730	M	1735.7237	868.3655	1718.6971	859.8522	1717.7131	859.3602	14
13	***1575.5800***	788.2937			1557.5695	779.2884	C	1604.6832	802.8452	1587.6566	794.3320	1586.6726	793.8400	13
14	***1688.6641***	844.8357			1670.6535	835.8304	L	1444.6525	722.8299	1427.6260	714.3166	1426.6420	713.8246	12
15	***1802.7070***	901.8571	1785.6805	893.3439	1784.6965	892.8519	N	1331.5685	666.2879	1314.5419	657.7746	1313.5579	657.2826	11
16	1859.7285	930.3679	1842.7019	921.8546	1841.7179	921.3626	G	1217.5256	609.2664	1200.4990	600.7531	1199.5150	600.2611	10
17	***1974.7554***	987.8814	1957.7289	979.3681	1956.7449	978.8761	N	1160.5041	580.7557	1143.4775	572.2424	1142.4935	571.7504	9
18	2160.8347	1080.9210	2143.8082	1072.4077	2142.8242	1071.9157	W	1045.4771	523.2422	1028.4506	514.7289	1027.4666	514.2369	8
19	2261.8824	1131.4448	2244.8559	1122.9316	2243.8719	1122.4396	T	859.3978	430.2026	842.3713	421.6893	841.3873	421.1973	7
20	2390.9250	1195.9661	2373.8985	1187.4529	2372.9144	1186.9609	E	**758.3502**	379.6787	741.3236	371.1654	740.3396	370.6734	6
21	2487.9778	1244.4925	2470.9512	1235.9793	2469.9672	1235.4872	P	**629.3076**	315.1574	612.2810	306.6441			5
22	2585.0305	1293.0189	2568.0040	1284.5056	2567.0200	1284.0136	P	532.2548	266.6310	515.2282	258.1178			4
23	2713.0891	1357.0482	2696.0626	1348.5349	2695.0786	1348.0429	Q	435.2020	218.1047	418.1755	209.5914			3

24	2873.1198	1437.0635	2856.0932	1428.5502	2855.1092	1428.0582	**C**	307.1435	154.0754	290.1169	145.5621			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of SPYEMFGDEEVMCLNGNWTEPPQCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.6	3018.2180	0.0077	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N17 88.79%
36.0	3018.2180	0.0077	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated N15 9.89%
34.7	3017.2340	0.9917	SPYEMFGDEEVMCLNGNWTEPPQCK	
27.3	3018.2180	0.0077	SPYEMFGDEEVMCLNGNWTEPPQCK	Deamidated Q23 1.31%

Mascot: http://www.matrixscience.com/

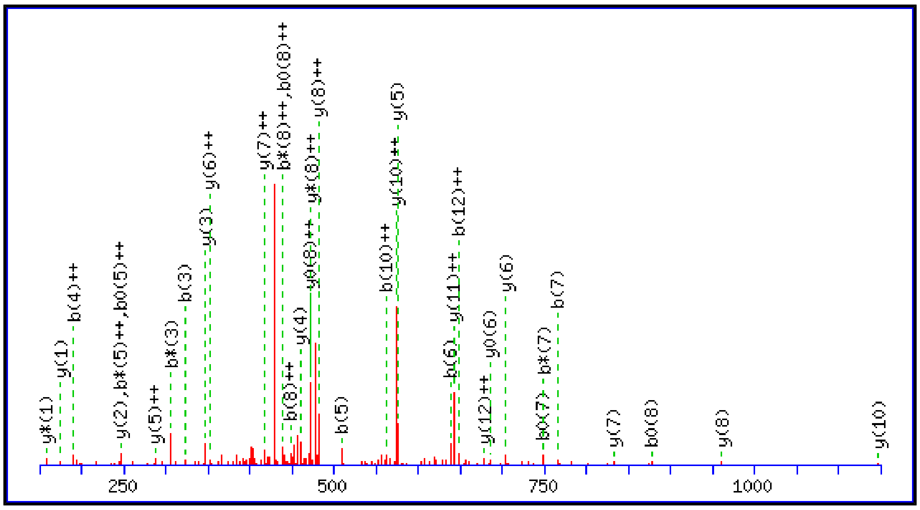
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NAHGEEKENLTAR**
Found in **Q06033** in **con_Xuniprot_HUMAN3**, ITIH3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

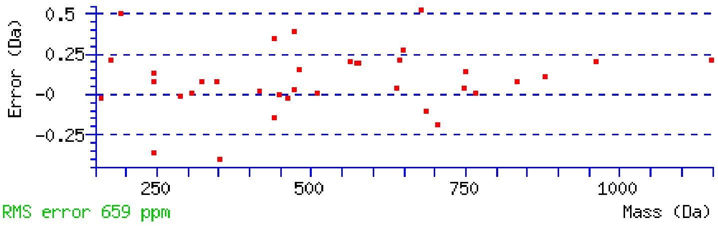
Match to Query 6207: 1468.692762 from(490.571530,3+) intensity(3675.6692) rtinseconds(114) scans(204) index(19262)
Title: 111019_Est_MI_YP_G_09Spectrum167_scans__204
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

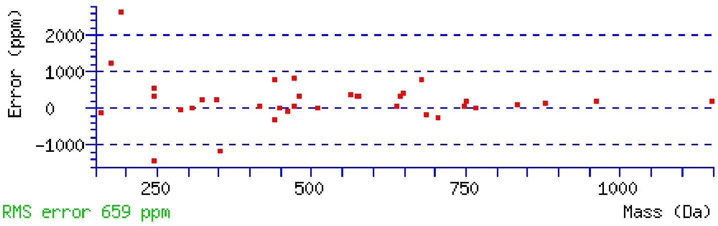
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1468.6906
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 51 **Expect:** 0.0013
Matches : 36/132 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	115.0502	58.0287	98.0237	49.5155			N							13
2	186.0873	93.5473	169.0608	85.0340			A	1355.6550	678.3311	1338.6284	669.8179	1337.6444	669.3258	12
3	**323.1462**	162.0768	306.1197	153.5635			H	1284.6179	642.8126	1267.5913	634.2993	1266.6073	633.8073	11
4	380.1677	**190.5875**	363.1411	182.0742			G	***1147.5590***	574.2831	1130.5324	565.7698	1129.5484	565.2778	10
5	**509.2103**	255.1088	492.1837	246.5955	491.1997	246.1035	E	1090.5375	545.7724	1073.5109	537.2591	1072.5269	536.7671	9
6	**638.2529**	319.6301	621.2263	311.1168	620.2423	310.6248	E	***961.4949***	481.2511	944.4684	472.7378	943.4843	472.2458	8
7	**766.3478**	383.6776	749.3213	375.1643	748.3373	374.6723	K	***832.4523***	416.7298	815.4258	408.2165	814.4417	407.7245	7
8	895.3904	**448.1989**	878.3639	439.6856	877.3799	439.1936	E	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	6
9	1010.4174	505.7123	993.3908	497.1991	992.4068	496.7070	N	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
10	1123.5014	**562.2544**	1106.4749	553.7411	1105.4909	553.2491	L	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
11	1224.5491	612.7782	1207.5226	604.2649	1206.5386	603.7729	T	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
12	1295.5862	**648.2968**	1278.5597	639.7835	1277.5757	639.2915	A	***246.1561***	123.5817	229.1295	115.0684			2
13							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of NAHGEEKENLTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.2	1468.6906	0.0022	NAHGEEKENLTAR	Deamidated N9 99.83%
23.5	1468.6906	0.0022	NAHGEEKENLTAR	Deamidated N1 0.17%
7.7	1466.6790	2.0138	GNFIPYANEERR	
7.6	1468.6901	0.0026	QISIMQETRSMK	
6.7	1467.6841	1.0086	YTDLNSNDVTGLR	
6.6	1467.6841	1.0086	YTDLNSNDVTGLR	
6.4	1468.6980	-0.0053	NLEPLVHDETMR	
6.4	1467.6850	1.0077	VMNFTIDGMGNLR	
6.2	1466.6862	2.0065	HGQQGGQEGDSIVR	
5.6	1466.6857	2.0070	MATLRDGMAGTSPK	

Mascot: http://www.matrixscience.com/

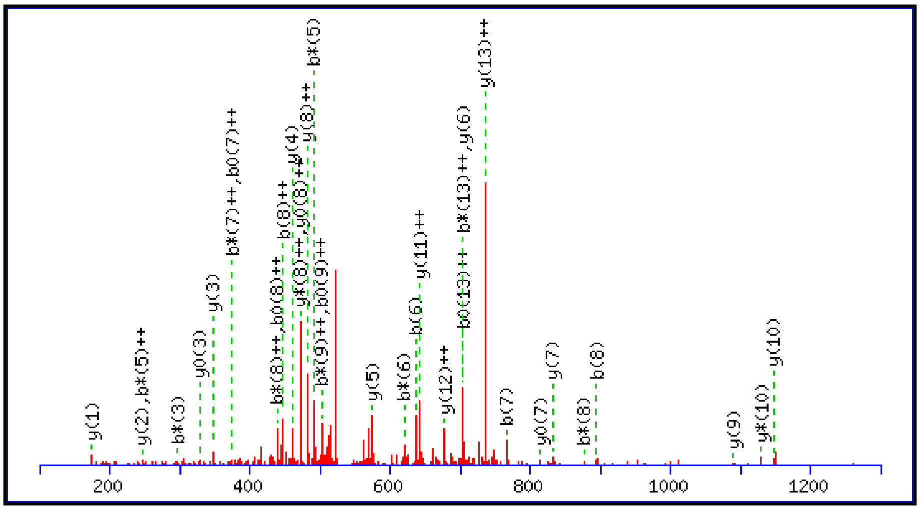
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KNAHGEEKENLTAR**
Found in **Q06033** in **con_Xuniprot_HUMAN3**, ITIH3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

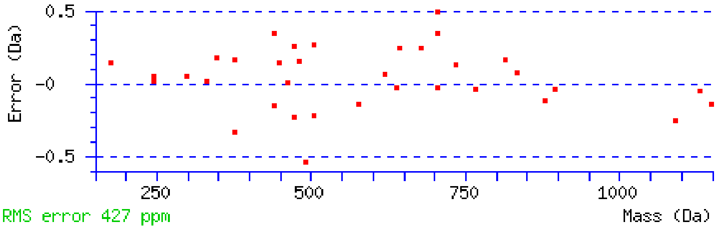
Match to Query 7660: 1596.789612 from(533.270480,3+) intensity(6347.7988) rtinseconds(56) scans(89) index(17320)
Title: 111019_Est_MI_YP_G_07Spectrum67_scans__89
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

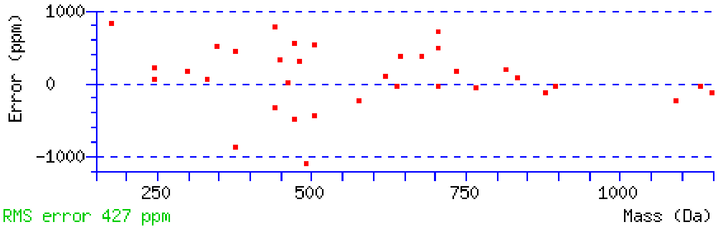
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1596.7855
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 50 **Expect:** 0.0023
Matches : 35/142 fragment ions using 59 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							14
2	243.1452	122.0762	226.1186	113.5629			N	1469.6979	735.3526	1452.6714	726.8393	1451.6873	726.3473	13
3	314.1823	157.5948	297.1557	149.0815			A	1355.6550	678.3311	1338.6284	669.8179	1337.6444	669.3258	12
4	451.2412	226.1242	434.2146	217.6110			H	1284.6179	642.8126	1267.5913	634.2993	1266.6073	633.8073	11
5	508.2627	254.6350	491.2361	246.1217			G	***1147.5590***	574.2831	1130.5324	565.7698	1129.5484	565.2778	10
6	**637.3052**	319.1563	620.2787	310.6430	619.2947	310.1510	E	***1090.5375***	545.7724	1073.5109	537.2591	1072.5269	536.7671	9
7	**766.3478**	383.6776	749.3213	375.1643	748.3373	374.6723	E	961.4949	481.2511	944.4684	472.7378	943.4843	472.2458	8
8	**894.4428**	447.7250	877.4163	439.2118	876.4322	438.7198	K	***832.4523***	416.7298	815.4258	408.2165	814.4417	407.7245	7
9	1023.4854	512.2463	1006.4588	503.7331	1005.4748	503.2411	E	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	6
10	1138.5123	569.7598	1121.4858	561.2465	1120.5018	560.7545	N	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	5
11	1251.5964	626.3018	1234.5699	617.7886	1233.5858	617.2966	L	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
12	1352.6441	676.8257	1335.6175	668.3124	1334.6335	667.8204	T	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
13	1423.6812	712.3442	1406.6546	703.8310	1405.6706	703.3390	A	***246.1561***	123.5817	229.1295	115.0684			2
14							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KNAHGEEKENLTAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
49.6	1596.7855	0.0041	KNAHGEEKENLTAR	Deamidated N10 99.44%
27.1	1596.7855	0.0041	KNAHGEEKENLTAR	Deamidated N2 0.56%
8.0	1596.7817	0.0079	LMSLQEAYSAKEAR	
5.7	1595.7845	1.0051	ASPQHHLFGVYPSR	
5.7	1596.7896	0.0000	TAWPSGPSAPEAVTAR	
5.3	1596.7929	-0.0033	KSKPNMNYDKLSR	
5.3	1596.7929	-0.0033	KSKPNMNYDKLSR	
4.9	1595.7831	1.0065	FAENLKAGDEFVEK	
3.8	1596.7856	0.0040	ESPRSGAPSPGEASLR	
3.8	1596.7943	-0.0047	QVRHVGGEFKMHR	

Mascot: http://www.matrixscience.com/

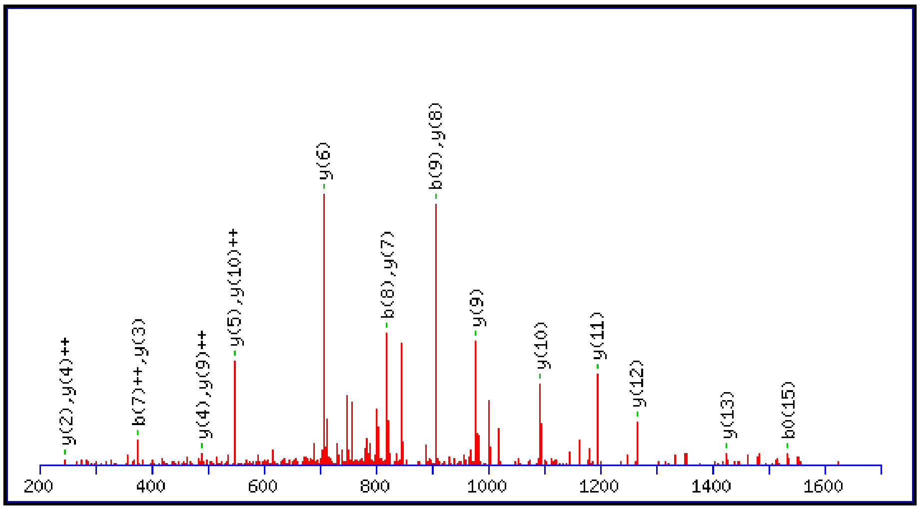
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTSCATNASICGDEAR**
Found in **Q07954** in **con_Xuniprot_HUMAN3**, LRP1_HUMAN Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2

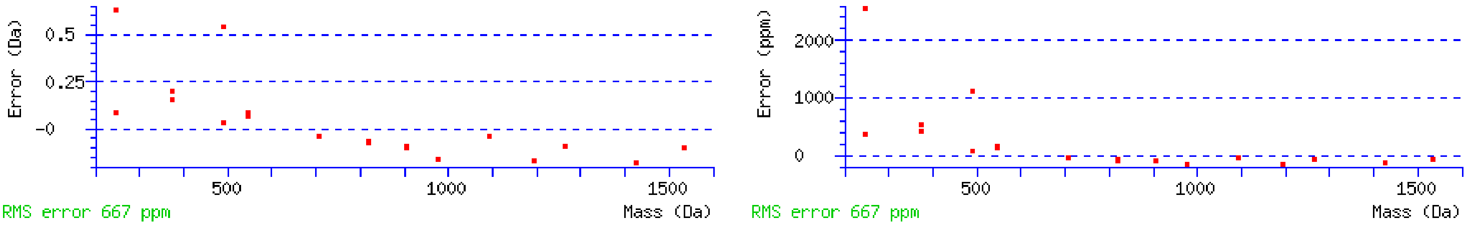
Match to Query 8772: 1725.732768 from(863.873660,2+) intensity(14809.2334) rtinseconds(406) scans(463) index(472)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum302_scans__463
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1725.7298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 127 **Expect:** 1.1e-011
Matches : 19/162 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	114.0913	57.5493					L							16
2	215.1390	108.0731			197.1285	99.0679	T	1613.6530	807.3301	1596.6265	798.8169	1595.6424	798.3249	15
3	302.1710	151.5892			284.1605	142.5839	S	1512.6053	756.8063	1495.5788	748.2930	1494.5948	747.8010	14
4	462.2017	231.6045			444.1911	222.5992	C	***1425.5733***	713.2903	1408.5468	704.7770	1407.5627	704.2850	13
5	533.2388	267.1230			515.2282	258.1178	A	***1265.5427***	633.2750	1248.5161	624.7617	1247.5321	624.2697	12
6	634.2865	317.6469			616.2759	308.6416	T	***1194.5055***	597.7564	1177.4790	589.2431	1176.4950	588.7511	11
7	749.3134	375.1604	732.2869	366.6471	731.3029	366.1551	N	***1093.4579***	547.2326	1076.4313	538.7193	1075.4473	538.2273	10
8	**820.3505**	410.6789	803.3240	402.1656	802.3400	401.6736	A	***978.4309***	489.7191	961.4044	481.2058	960.4204	480.7138	9
9	**907.3826**	454.1949	890.3560	445.6817	889.3720	445.1896	S	***907.3938***	454.2005	890.3673	445.6873	889.3832	445.1953	8
10	1020.4666	510.7370	1003.4401	502.2237	1002.4561	501.7317	I	***820.3618***	410.6845	803.3352	402.1713	802.3512	401.6792	7
11	1180.4973	590.7523	1163.4707	582.2390	1162.4867	581.7470	C	***707.2777***	354.1425	690.2512	345.6292	689.2671	345.1372	6
12	1237.5188	619.2630	1220.4922	610.7497	1219.5082	610.2577	G	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	5
13	1352.5457	676.7765	1335.5191	668.2632	1334.5351	667.7712	D	***490.2256***	245.6164	473.1991	237.1032	472.2150	236.6112	4
14	1481.5883	741.2978	1464.5617	732.7845	1463.5777	732.2925	E	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
15	1552.6254	776.8163	1535.5989	768.3031	1534.6148	767.8111	A	***246.1561***	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of LTSCATNASICGDEAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
127.1	1725.7298	0.0030	LTSCATNASICGDEAR
12.6	1725.7298	0.0030	INMNGINNSSGMVDAR
11.5	1725.7298	0.0030	INMNGINNSSGMVDAR
6.3	1725.7298	0.0030	INMNGINNSSGMVDAR
5.0	1725.7298	0.0030	INMNGINNSSGMVDAR
1.7	1725.7369	-0.0042	SQDNSVNFSNSWPLK
0.3	1723.7280	2.0047	LEDACIEMDDGAIQK
0.3	1724.7345	0.9983	CNNAAISSMQEELNK
0.3	1724.7345	0.9983	CNNAAISSMQEELNK
0.1	1725.7298	0.0030	INMNGINNSSGMVDAR

Mascot: http://www.matrixscience.com/

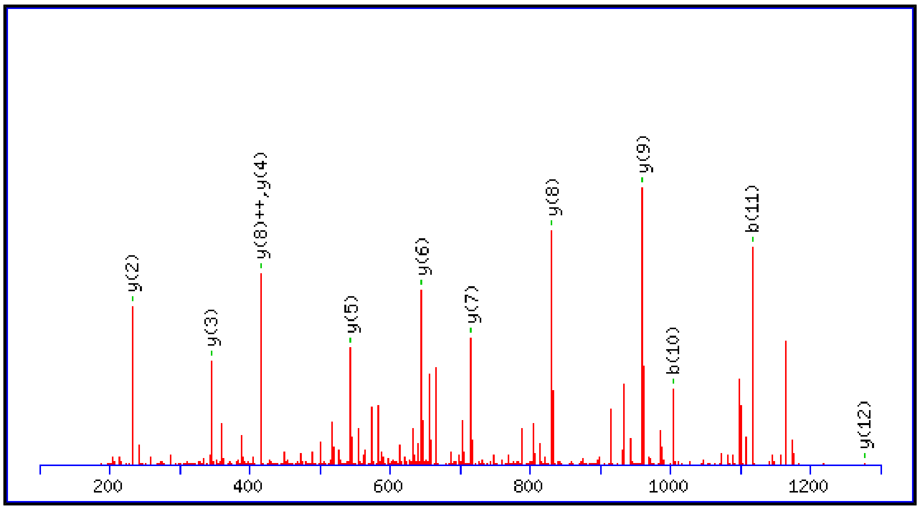
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGFENATQALGR**
Found in **K7EJD3** in **con_Xuniprot_HUMAN3**, K7EJD3_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=2 SV=1

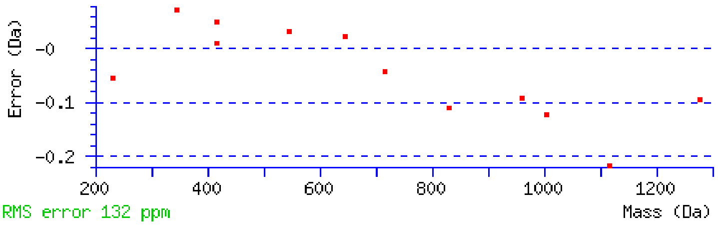
Match to Query 2040: 1347.677868 from(674.846210,2+) intensity(277199.8438) rtinseconds(1423) scans(2703) index(536)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum2280_scans__2703
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

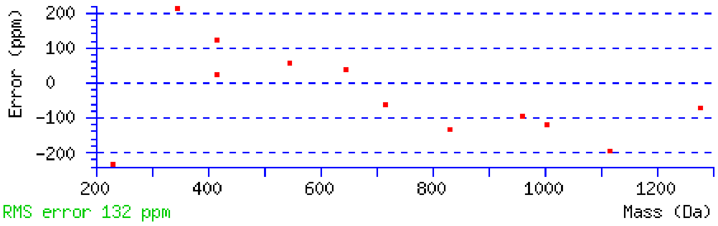
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1347.6783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 98 **Expect:** 3.9e-008
Matches : 12/116 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							13
2	185.1285	93.0679					L	***1277.6484***	639.3279	1260.6219	630.8146	1259.6379	630.3226	12
3	242.1499	121.5786					G	1164.5644	582.7858	1147.5378	574.2726	1146.5538	573.7805	11
4	389.2183	195.1128					F	1107.5429	554.2751	1090.5164	545.7618	1089.5323	545.2698	10
5	518.2609	259.6341			500.2504	250.6288	E	***960.4745***	480.7409	943.4480	472.2276	942.4639	471.7356	9
6	633.2879	317.1476	616.2613	308.6343	615.2773	308.1423	N	***831.4319***	416.2196	814.4054	407.7063	813.4213	407.2143	8
7	704.3250	352.6661	687.2984	344.1529	686.3144	343.6608	A	***716.4050***	358.7061	699.3784	350.1928	698.3944	349.7008	7
8	805.3727	403.1900	788.3461	394.6767	787.3621	394.1847	T	***645.3679***	323.1876	628.3413	314.6743	627.3573	314.1823	6
9	933.4312	467.2193	916.4047	458.7060	915.4207	458.2140	Q	***544.3202***	272.6637	527.2936	264.1504			5
10	**1004.4684**	502.7378	987.4418	494.2245	986.4578	493.7325	A	***416.2616***	208.6344	399.2350	200.1212			4
11	**1117.5524**	559.2798	1100.5259	550.7666	1099.5419	550.2746	L	***345.2245***	173.1159	328.1979	164.6026			3
12	1174.5739	587.7906	1157.5473	579.2773	1156.5633	578.7853	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALGFENATQALGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.0	1347.6783	-0.0004	ALGFENATQALGR	Deamidated N6 99.90%
67.9	1347.6783	-0.0004	ALGFENATQALGR	Deamidated Q9 0.10%
13.6	1347.6783	-0.0004	GLFQQAADQNKK	
12.7	1347.6751	0.0028	KEMEMRQLQR	
9.5	1347.6790	-0.0011	MTRGTGGTAQRGR	
9.0	1345.6725	2.0054	EKEKQELEEGK	
8.3	1347.6816	-0.0038	EMIRAVDELTR	
6.0	1347.6751	0.0028	RMGADLCKQLR	
5.6	1345.6725	2.0054	KEEKQQEANLK	
4.3	1346.6765	1.0014	ITNVCNKVWGR	

Mascot: http://www.matrixscience.com/

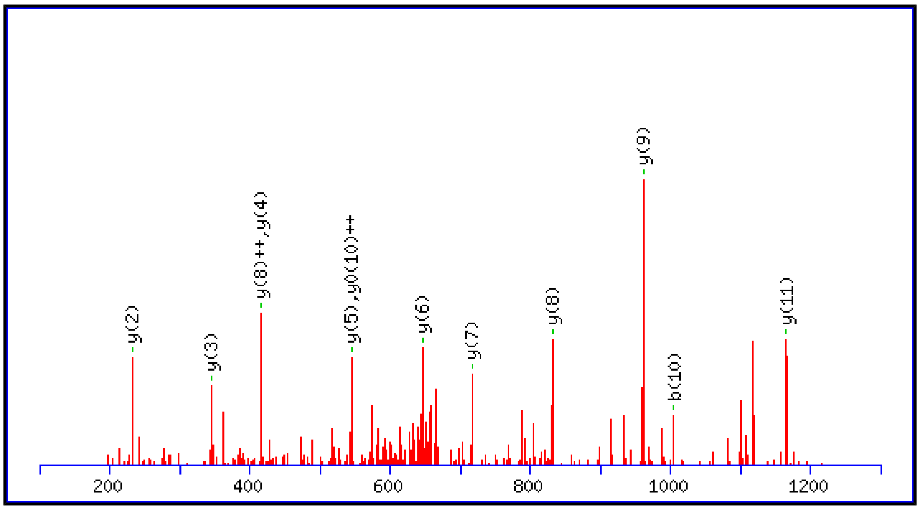
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGFENATQALGR**
Found in **K7EJD3** in **con_Xuniprot_HUMAN3**, K7EJD3_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=2 SV=1

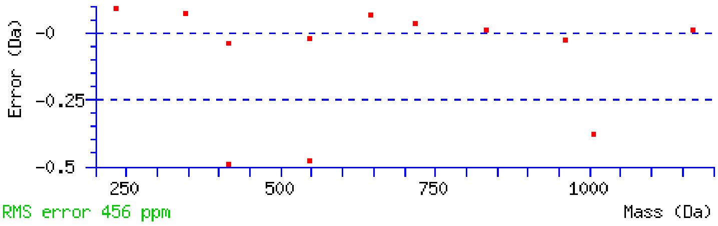
Match to Query 2125: 1348.667288 from(675.340920,2+) intensity(4077.7703) rtinseconds(1464) scans(2332) index(597)
Title: 111019_Est_ISCardio_NMI_200000g_G_8Spectrum1832_scans__2332
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

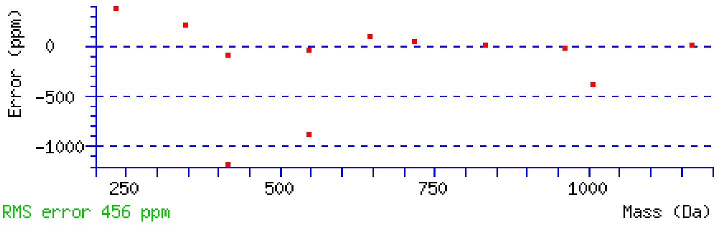
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1348.6623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Q9 : Deamidated (NQ)
Ions Score: 85 **Expect:** 8.9e-007
Matches : 12/116 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	72.0444	36.5258					A							13
2	185.1285	93.0679					L	1278.6325	639.8199	1261.6059	631.3066	1260.6219	630.8146	12
3	242.1499	121.5786					G	***1165.5484***	583.2778	1148.5218	574.7646	1147.5378	574.2726	11
4	389.2183	195.1128					F	1108.5269	554.7671	1091.5004	546.2538	1090.5164	545.7618	10
5	518.2609	259.6341			500.2504	250.6288	E	***961.4585***	481.2329	944.4320	472.7196	943.4480	472.2276	9
6	633.2879	317.1476	616.2613	308.6343	615.2773	308.1423	N	***832.4159***	416.7116	815.3894	408.1983	814.4054	407.7063	8
7	704.3250	352.6661	687.2984	344.1529	686.3144	343.6608	A	***717.3890***	359.1981	700.3624	350.6849	699.3784	350.1928	7
8	805.3727	403.1900	788.3461	394.6767	787.3621	394.1847	T	***646.3519***	323.6796	629.3253	315.1663	628.3413	314.6743	6
9	934.4153	467.7113	917.3887	459.1980	916.4047	458.7060	Q	***545.3042***	273.1557	528.2776	264.6425			5
10	1005.4524	503.2298	988.4258	494.7165	987.4418	494.2245	A	***416.2616***	208.6344	399.2350	200.1212			4
11	1118.5364	559.7719	1101.5099	551.2586	1100.5259	550.7666	L	***345.2245***	173.1159	328.1979	164.6026			3
12	1175.5579	588.2826	1158.5313	579.7693	1157.5473	579.2773	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALGFENATQALGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
84.7	1348.6623	0.0050	ALGFENATQALGR
13.4	1348.6623	0.0050	GLFQQAADQNKK
13.4	1348.6623	0.0050	GLFQQAADQNKK
12.8	1348.6735	-0.0062	NDLRDTFAALGR
10.4	1348.6623	0.0050	GLFQQAADQNKK
10.4	1348.6623	0.0050	GLFQQAADQNKK
5.7	1347.6670	1.0003	ADAIFQEGIQQK
5.7	1347.6670	1.0003	ADAIFQEGIQQK
5.2	1347.6605	1.0068	ITNVCNKVWGR
4.9	1347.6670	1.0003	NQLISFQNGTPK

Mascot: http://www.matrixscience.com/

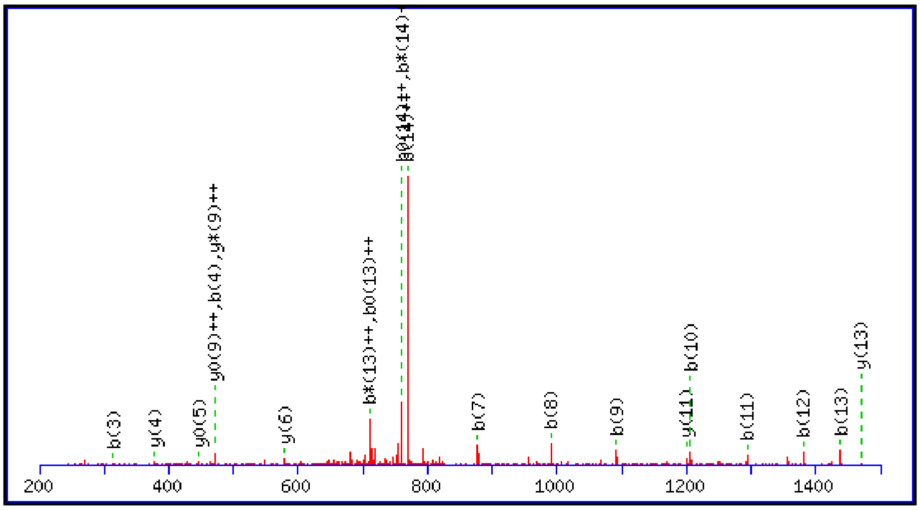
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TVIRPFYLTNSSGVD**
Found in **Q08380** in **con_Xuniprot_HUMAN3**, LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

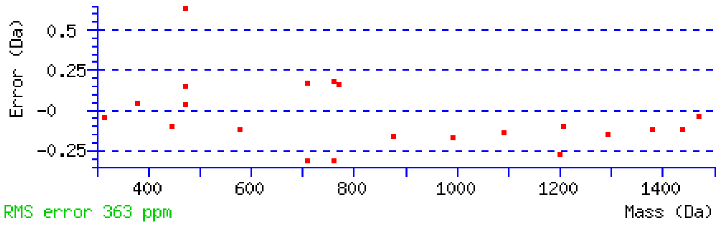
Match to Query 8418: 1668.840248 from(835.427400,2+) intensity(23981.0137) rtinseconds(1600) scans(2629) index(600)
Title: 111019_Est_ISCardio_NMI_200000g_G_8Spectrum2094_scans__2629
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

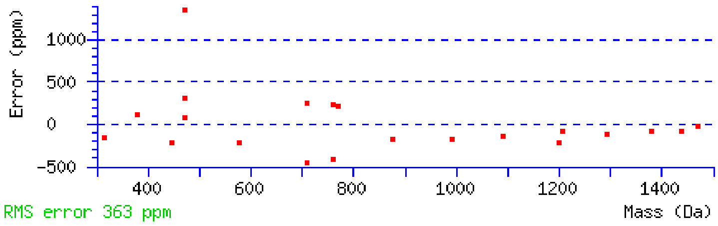
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1668.8359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00016
Matches : 21/152 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	102.0550	51.5311			84.0444	42.5258	T							15
2	201.1234	101.0653			183.1128	92.0600	V	1568.7955	784.9014	1551.7690	776.3881	1550.7849	775.8961	14
3	***314.2074***	157.6074			296.1969	148.6021	I	**1469.7271**	735.3672	1452.7005	726.8539	1451.7165	726.3619	13
4	***470.3085***	235.6579	453.2820	227.1446	452.2980	226.6526	R	1356.6430	678.8251	1339.6165	670.3119	1338.6325	669.8199	12
5	567.3613	284.1843	550.3348	275.6710	549.3507	275.1790	P	**1200.5419**	600.7746	1183.5154	592.2613	1182.5313	591.7693	11
6	714.4297	357.7185	697.4032	349.2052	696.4192	348.7132	F	1103.4891	552.2482	1086.4626	543.7349	1085.4786	543.2429	10
7	***877.4931***	439.2502	860.4665	430.7369	859.4825	430.2449	Y	956.4207	478.7140	939.3942	470.2007	938.4102	469.7087	9
8	***990.5771***	495.7922	973.5506	487.2789	972.5665	486.7869	L	793.3574	397.1823	776.3309	388.6691	775.3468	388.1771	8
9	***1091.6248***	546.3160	1074.5982	537.8028	1073.6142	537.3108	T	680.2733	340.6403	663.2468	332.1270	662.2628	331.6350	7
10	***1206.6517***	603.8295	1189.6252	595.3162	1188.6412	594.8242	N	**579.2257**	290.1165	562.1991	281.6032	561.2151	281.1112	6
11	***1293.6838***	647.3455	1276.6572	638.8322	1275.6732	638.3402	S	464.1987	232.6030			446.1882	223.5977	5
12	***1380.7158***	690.8615	1363.6892	682.3483	1362.7052	681.8563	S	**377.1667**	189.0870			359.1561	180.0817	4
13	***1437.7373***	719.3723	1420.7107	710.8590	1419.7267	710.3670	G	290.1347	145.5710			272.1241	136.5657	3
14	1536.8057	768.9065	1519.7791	760.3932	1518.7951	759.9012	V	233.1132	117.0602			215.1026	108.0550	2
15							D	134.0448	67.5260			116.0342	58.5207	1





NCBI **BLAST** search of TVIRPFYLTNSSGVD
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
61.3	1668.8359	0.0043	TVIRPFYLTNSSGVD
5.4	1667.8301	1.0102	LAELLTQQHGLQCR
4.8	1667.8339	1.0064	AKNQSQKQHGNASIR
4.3	1667.8339	1.0064	AKNQSQKQHGNASIR
4.3	1667.8339	1.0064	AKNQSQKQHGNASIR
4.0	1667.8301	1.0101	QATSIKDVGAPMVSQH
1.4	1667.8452	0.9951	GRQPNSATSGRAGVGPR
1.4	1667.8452	0.9951	GRQPNSATSGRAGVGPR
1.0	1668.8332	0.0071	YASLSNHQRVHTEK
0.5	1668.8372	0.0030	NFSAASALNFPFARR

Mascot: http://www.matrixscience.com/

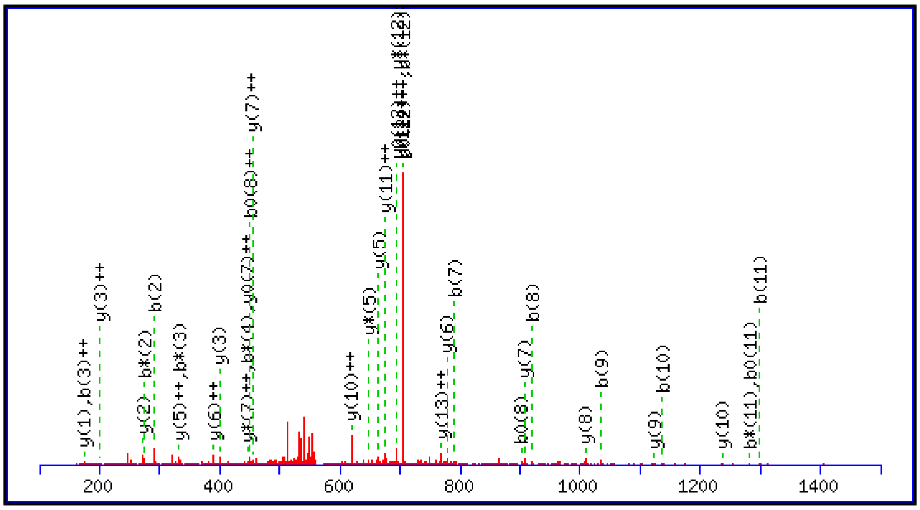
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YKGLNLTEDTYKPR**
Found in **Q08380** in **con_Xuniprot_HUMAN3**, LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

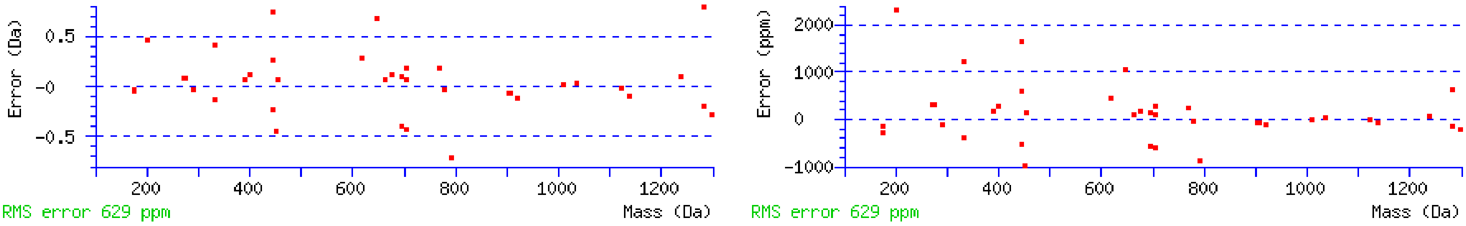
Match to Query 8707: 1697.867322 from(566.963050,3+) intensity(23558.4063) rtinseconds(737) scans(1814) index(17376)
Title: 111019_Est_MI_YP_G_07Spectrum1579_scans__1814
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1697.8624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5      : Deamidated (NQ)
Ions Score: 46  Expect: 0.0051
Matches : 38/134 fragment ions using 61 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							14
2	**292.1656**	146.5864	275.1390	138.0731			K	1535.8064	768.4068	1518.7799	759.8936	1517.7958	759.4016	13
3	349.1870	175.0972	332.1605	166.5839			G	1407.7114	704.3594	1390.6849	695.8461	1389.7009	695.3541	12
4	462.2711	231.6392	445.2445	223.1259			L	1350.6900	675.8486	1333.6634	667.3354	1332.6794	666.8433	11
5	577.2980	289.1527	560.2715	280.6394			N	***1237.6059***	619.3066	1220.5794	610.7933	1219.5953	610.3013	10
6	690.3821	345.6947	673.3556	337.1814			L	***1122.5790***	561.7931	1105.5524	553.2798	1104.5684	552.7878	9
7	**791.4298**	396.2185	774.4032	387.7053	773.4192	387.2132	T	***1009.4949***	505.2511	992.4684	496.7378	991.4843	496.2458	8
8	**920.4724**	460.7398	903.4458	452.2266	902.4618	451.7345	E	***908.4472***	454.7272	891.4207	446.2140	890.4367	445.7220	7
9	**1035.4993**	518.2533	1018.4728	509.7400	1017.4888	509.2480	D	***779.4046***	390.2060	762.3781	381.6927	761.3941	381.2007	6
10	**1136.5470**	568.7771	1119.5204	560.2639	1118.5364	559.7719	T	***664.3777***	332.6925	647.3511	324.1792	646.3671	323.6872	5
11	**1299.6103**	650.3088	1282.5838	641.7955	1281.5998	641.3035	Y	563.3300	282.1686	546.3035	273.6554			4
12	1427.7053	714.3563	1410.6787	705.8430	1409.6947	705.3510	K	***400.2667***	200.6370	383.2401	192.1237			3
13	1524.7581	762.8827	1507.7315	754.3694	1506.7475	753.8774	P	***272.1717***	136.5895	255.1452	128.0762			2
14							R	***175.1190***	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of YKGLNLTEDTYKPR
(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	1697.8624	0.0049	YKGLNLTEDTYKPR
6.9	1696.8631	1.0042	AEAKLHDEESVVTAAK
5.8	1697.8737	-0.0063	YQRDEIATVYLTAR
4.8	1697.8658	0.0015	EPVGEGEALLGMDLLR
3.9	1695.8614	2.0060	YKSQMLQLQQKQR
3.9	1695.8614	2.0060	YKSQMLQLQQKQR
3.9	1695.8614	2.0060	YKSQMLQLQQKQR
3.8	1696.8640	1.0033	YKGLMDCAKQVLQK
3.7	1697.8737	-0.0064	GGGPVFPAPVVGSGGATSGK
3.0	1696.8566	1.0107	KYQLSVSKECGGVSR

Mascot: http://www.matrixscience.com/

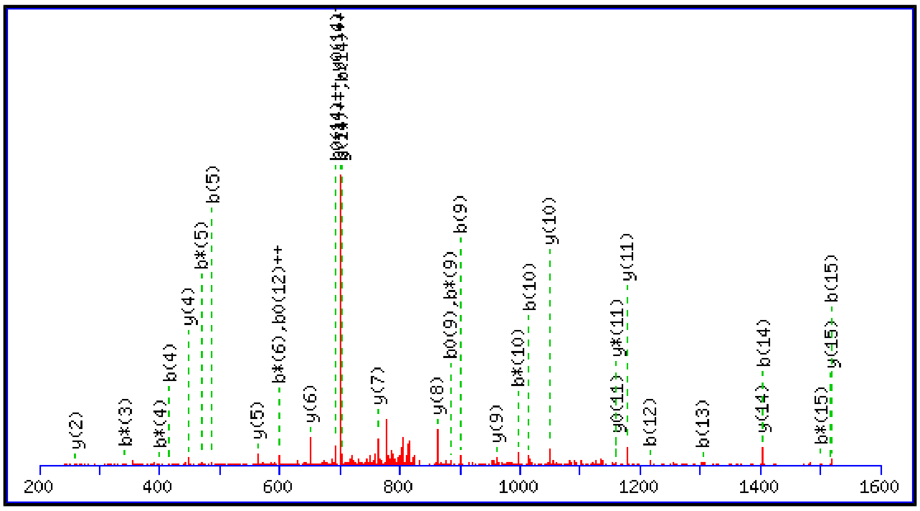
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FNPGAESVVLSNSTLK**
Found in **Q13201** in **con_Xuniprot_HUMAN3**, MMRN1_HUMAN Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3

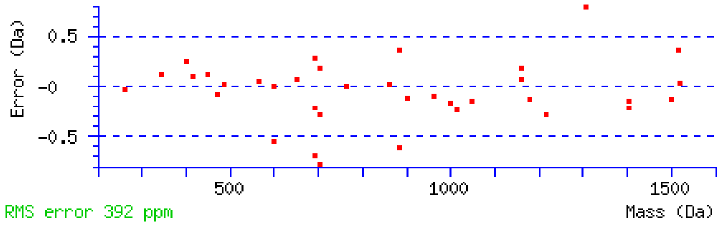
Match to Query 8411: 1662.849808 from(832.432180,2+) intensity(8042.7842) rtinseconds(1498) scans(3520) index(20725)
Title: 111019_Est_MI_YP_G_11Spectrum3088_scans__3520
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

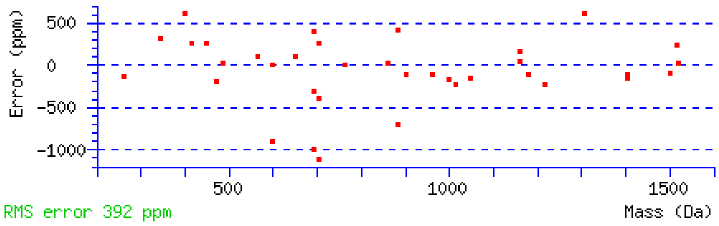
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1662.8465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 68 **Expect:** 3.9e-005
Matches : 36/164 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							16
2	262.1186	131.5629	245.0921	123.0497			N	***1516.7853***	758.8963	1499.7588	750.3830	1498.7748	749.8910	15
3	359.1714	180.0893	342.1448	171.5761			P	***1402.7424***	701.8748	1385.7159	693.3616	1384.7318	692.8696	14
4	***416.1928***	208.6001	399.1663	200.0868			G	1305.6896	653.3485	1288.6631	644.8352	1287.6791	644.3432	13
5	***487.2300***	244.1186	470.2034	235.6053			A	1248.6682	624.8377	1231.6416	616.3245	1230.6576	615.8324	12
6	616.2726	308.6399	599.2460	300.1266	598.2620	299.6346	E	***1177.6311***	589.3192	1160.6045	580.8059	1159.6205	580.3139	11
7	***703.3046***	352.1559	686.2780	343.6427	685.2940	343.1506	S	***1048.5885***	524.7979	1031.5619	516.2846	1030.5779	515.7926	10
8	802.3730	401.6901	785.3464	393.1769	784.3624	392.6849	V	***961.5564***	481.2819	944.5299	472.7686	943.5459	472.2766	9
9	***901.4414***	451.2243	884.4149	442.7111	883.4308	442.2191	V	***862.4880***	431.7477	845.4615	423.2344	844.4775	422.7424	8
10	***1014.5255***	507.7664	997.4989	499.2531	996.5149	498.7611	L	***763.4196***	382.2134	746.3931	373.7002	745.4090	373.2082	7
11	1101.5575	551.2824	1084.5310	542.7691	1083.5469	542.2771	S	***650.3355***	325.6714	633.3090	317.1581	632.3250	316.6661	6
12	***1216.5844***	608.7959	1199.5579	600.2826	1198.5739	599.7906	N	***563.3035***	282.1554	546.2770	273.6421	545.2930	273.1501	5
13	***1303.6165***	652.3119	1286.5899	643.7986	1285.6059	643.3066	S	***448.2766***	224.6419	431.2500	216.1287	430.2660	215.6366	4
14	***1404.6642***	702.8357	1387.6376	694.3224	1386.6536	693.8304	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
15	***1517.7482***	759.3777	1500.7217	750.8645	1499.7376	750.3725	L	***260.1969***	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FNPGAESVVLSNSTLK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.1	1662.8465	0.0034	FNPGAESVVLSNSTLK	Deamidated N12 100.00%
20.1	1662.8465	0.0034	FNPGAESVVLSNSTLK	Deamidated N2 0.00%
16.4	1662.8433	0.0065	ALDNLARQMIMKDK	
13.2	1662.8478	0.0020	FNHAIYSQAQSRLK	
12.2	1662.8478	0.0020	FNHAIYSQAQSRLK	
10.3	1662.8478	0.0020	FNHAIYSQAQSRLK	
9.9	1662.8507	-0.0009	LMMAQLPTLEKMNK	
9.7	1662.8465	0.0034	FDKATLQVEGADELK	
8.5	1662.8577	-0.0078	VAARDNKLQQIYDK	
8.5	1662.8577	-0.0078	VAARDNKLQQIYDK	

Mascot: http://www.matrixscience.com/

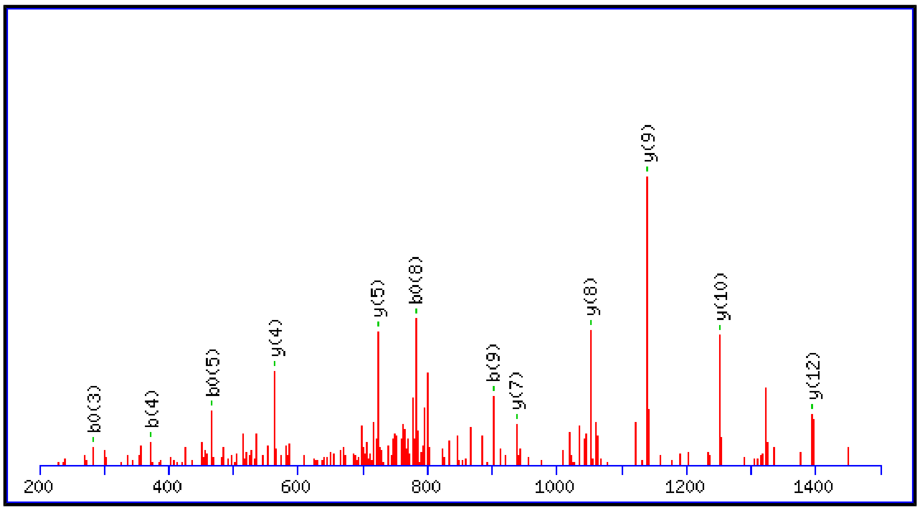
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQAALSNLTCCIDR**
Found in **E7EPG1** in **con_Xuniprot_HUMAN3**, E7EPG1_HUMAN Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=2 SV=1

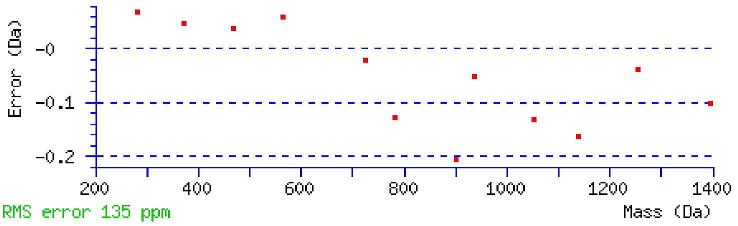
Match to Query 7719: 1622.743388 from(812.378970,2+) intensity(2622.8303) rtinseconds(1307) scans(2437) index(524)
Title: 111019_Est_ISCardio_NMI_200000g_G_7Spectrum2041_scans__2437
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

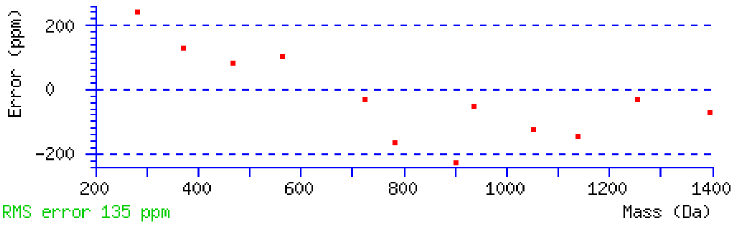
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1622.7392
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.0001
Matches : 12/152 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	102.0550	51.5311			84.0444	42.5258	**T**							14
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	**Q**	1522.6988	761.8531	1505.6723	753.3398	1504.6883	752.8478	13
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	**A**	***1394.6403***	697.8238	1377.6137	689.3105	1376.6297	688.8185	12
4	**372.1878**	186.5975	355.1612	178.0842	354.1772	177.5922	**A**	1323.6031	662.3052	1306.5766	653.7919	1305.5926	653.2999	11
5	485.2718	243.1396	468.2453	234.6263	467.2613	234.1343	**L**	***1252.5660***	626.7867	1235.5395	618.2734	1234.5555	617.7814	10
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	**S**	***1139.4820***	570.2446	1122.4554	561.7313	1121.4714	561.2393	9
7	687.3308	344.1690	670.3042	335.6558	669.3202	335.1638	**N**	***1052.4499***	526.7286	1035.4234	518.2153	1034.4394	517.7233	8
8	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	**L**	***937.4230***	469.2151	920.3965	460.7019	919.4124	460.2099	7
9	**901.4625**	451.2349	884.4360	442.7216	883.4520	442.2296	**T**	824.3389	412.6731	807.3124	404.1598	806.3284	403.6678	6
10	1061.4932	531.2502	1044.4666	522.7370	1043.4826	522.2449	**C**	***723.2913***	362.1493	706.2647	353.6360	705.2807	353.1440	5
11	1221.5238	611.2656	1204.4973	602.7523	1203.5133	602.2603	**C**	***563.2606***	282.1339	546.2341	273.6207	545.2500	273.1287	4
12	1334.6079	667.8076	1317.5814	659.2943	1316.5973	658.8023	**I**	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	1449.6348	725.3211	1432.6083	716.8078	1431.6243	716.3158	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
14							**R**	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TQAALSNLTCCIDR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
61.4	1622.7392	0.0042	TQAALSNLTCCIDR	Deamidated N7 100.00%
11.0	1622.7392	0.0042	TQAALSNLTCCIDR	Deamidated Q2 0.00%
2.5	1622.7392	0.0042	ERVAQQEAMKEMR	

Mascot: http://www.matrixscience.com/

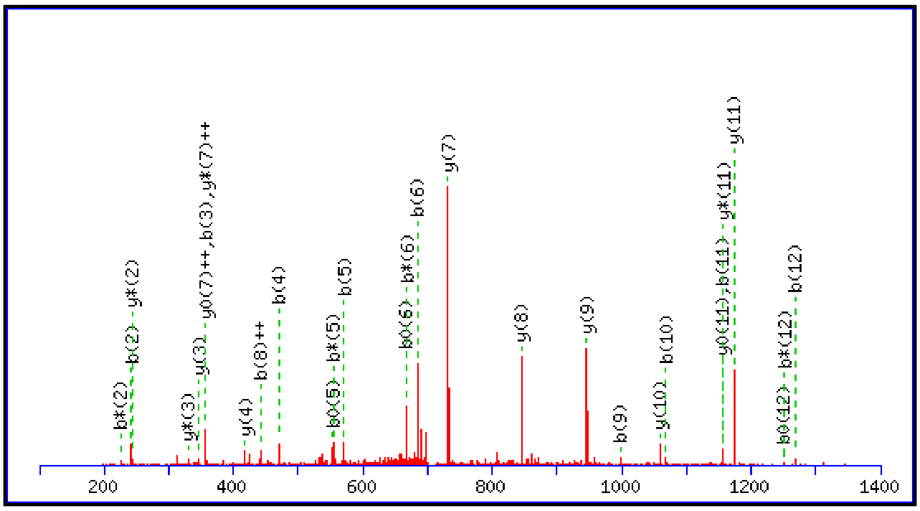
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LQNLTLPTNASIK**
Found in **Q13201** in **con_Xuniprot_HUMAN3**, MMRN1_HUMAN Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3

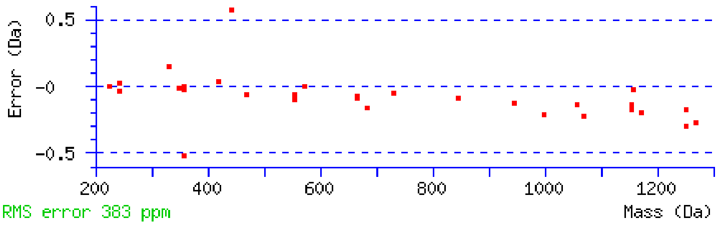
Match to Query 2845: 1413.776848 from(707.895700,2+) intensity(24701.0742) rtinseconds(1359) scans(3120) index(13194)
Title: 111019_Est_ISCardio_NMI_YS_G_11Spectrum2718_scans__3120
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

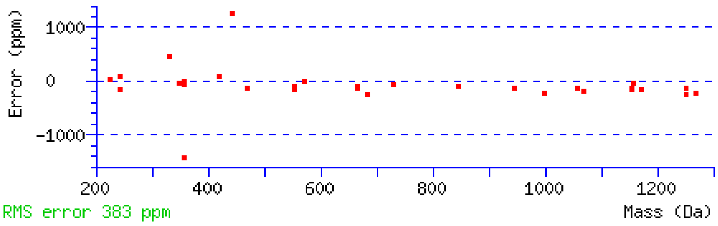
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1413.7715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N3 : Deamidated (NQ)
N9 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00014
Matches : 30/130 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	114.0913	57.5493					L							13
2	***242.1499***	121.5786	225.1234	113.0653			Q	1301.6947	651.3510	1284.6682	642.8377	1283.6842	642.3457	12
3	***357.1769***	179.0921	340.1503	170.5788			N	**1173.6361**	587.3217	1156.6096	578.8084	1155.6256	578.3164	11
4	***470.2609***	235.6341	453.2344	227.1208			L	**1058.6092**	529.8082	1041.5827	521.2950	1040.5986	520.8030	10
5	***571.3086***	286.1579	554.2821	277.6447	553.2980	277.1527	T	**945.5251**	473.2662	928.4986	464.7529	927.5146	464.2609	9
6	***684.3927***	342.7000	667.3661	334.1867	666.3821	333.6947	L	**844.4775**	422.7424	827.4509	414.2291	826.4669	413.7371	8
7	781.4454	391.2264	764.4189	382.7131	763.4349	382.2211	P	**731.3934**	366.2003	714.3668	357.6871	713.3828	357.1951	7
8	882.4931	441.7502	865.4666	433.2369	864.4825	432.7449	T	634.3406	317.6740	617.3141	309.1607	616.3301	308.6687	6
9	***997.5201***	499.2637	980.4935	490.7504	979.5095	490.2584	N	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
10	***1068.5572***	534.7822	1051.5306	526.2689	1050.5466	525.7769	A	**418.2660**	209.6366	401.2395	201.1234	400.2554	200.6314	4
11	***1155.5892***	578.2982	1138.5626	569.7850	1137.5786	569.2930	S	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	***1268.6733***	634.8403	1251.6467	626.3270	1250.6627	625.8350	I	260.1969	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LQNLTLPTNASIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.5	1413.7715	0.0054	LQNLTLPTNASIK	Deamidated N3, N9 73.04%
56.2	1413.7715	0.0054	LQNLTLPTNASIK	Deamidated Q2, N9 26.95%
22.1	1413.7715	0.0054	LQNLTLPTNASIK	Deamidated Q2, N3 0.01%
20.5	1413.7827	-0.0059	AGNSLKLIIQNKD	
20.5	1413.7827	-0.0058	AGNSLKLIIQNKN	
16.9	1413.7715	0.0054	LKDLQGELEQIK	
16.9	1413.7715	0.0054	LKDLQGELEQIK	
14.6	1413.7827	-0.0058	AGNSLKLIIQNKN	
14.5	1413.7827	-0.0059	AGNSLKLIIQNKD	
14.5	1413.7827	-0.0058	AGNSLKLIIQNKN	

Mascot: http://www.matrixscience.com/

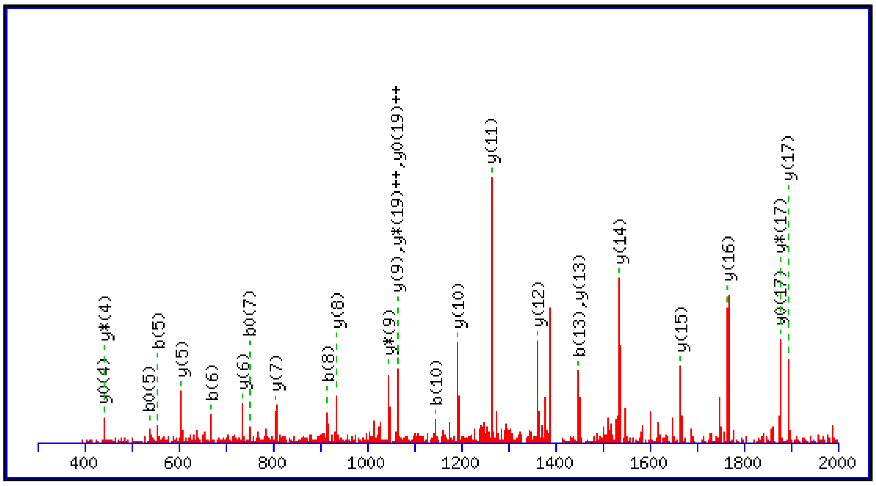
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPTQNITFQTESSVAEQEAEFQSPK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

Match to Query 25679: 2809.341508 from(1405.678030,2+) intensity(30516.6270) rtinseconds(1778) scans(4630) index(19664)
Title: 111019_Est_MI_YP_G_09Spectrum4087_scans__4630
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

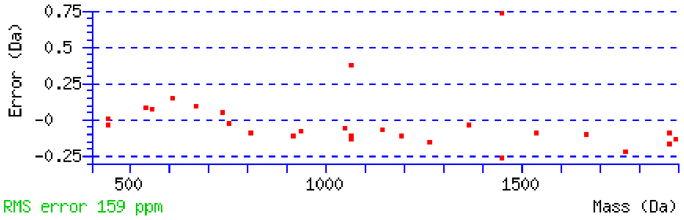
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

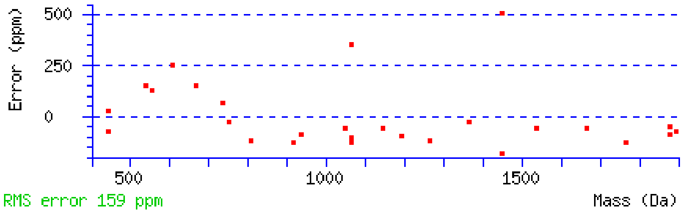


Monoisotopic mass of neutral peptide Mr(calc): 2809.3294
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 94 **Expect:** 1e-007
Matches : 27/274 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							25
2	211.1441	106.0757					P	2697.2526	1349.1299	2680.2261	1340.6167	2679.2420	1340.1247	24
3	312.1918	156.5995			294.1812	147.5942	T	2600.1999	1300.6036	2583.1733	1292.0903	2582.1893	1291.5983	23
4	440.2504	220.6288	423.2238	212.1155	422.2398	211.6235	Q	2499.1522	1250.0797	2482.1256	1241.5664	2481.1416	1241.0744	22
5	**555.2773**	278.1423	538.2508	269.6290	537.2667	269.1370	N	2371.0936	1186.0504	2354.0670	1177.5372	2353.0830	1177.0452	21
6	**668.3614**	334.6843	651.3348	326.1710	650.3508	325.6790	I	2256.0667	1128.5370	2239.0401	1120.0237	2238.0561	1119.5317	20
7	769.4090	385.2082	752.3825	376.6949	751.3985	376.2029	T	2142.9826	1071.9949	2125.9560	1063.4817	2124.9720	1062.9896	19
8	**916.4775**	458.7424	899.4509	450.2291	898.4669	449.7371	F	2041.9349	1021.4711	2024.9084	1012.9578	2023.9243	1012.4658	18
9	1044.5360	522.7717	1027.5095	514.2584	1026.5255	513.7664	Q	***1894.8665***	947.9369	1877.8399	939.4236	1876.8559	938.9316	17
10	**1145.5837**	573.2955	1128.5572	564.7822	1127.5732	564.2902	T	***1766.8079***	883.9076	1749.7814	875.3943	1748.7974	874.9023	16
11	1274.6263	637.8168	1257.5998	629.3035	1256.6157	628.8115	E	***1665.7602***	833.3838	1648.7337	824.8705	1647.7497	824.3785	15
12	1361.6583	681.3328	1344.6318	672.8195	1343.6478	672.3275	S	***1536.7176***	768.8625	1519.6911	760.3492	1518.7071	759.8572	14
13	**1448.6904**	724.8488	1431.6638	716.3355	1430.6798	715.8435	S	***1449.6856***	725.3464	1432.6591	716.8332	1431.6751	716.3412	13
14	1547.7588	774.3830	1530.7322	765.8698	1529.7482	765.3777	V	***1362.6536***	681.8304	1345.6270	673.3172	1344.6430	672.8251	12
15	1618.7959	809.9016	1601.7693	801.3883	1600.7853	800.8963	A	***1263.5852***	632.2962	1246.5586	623.7830	1245.5746	623.2909	11
16	1747.8385	874.4229	1730.8119	865.9096	1729.8279	865.4176	E	***1192.5481***	596.7777	1175.5215	588.2644	1174.5375	587.7724	10
17	1875.8971	938.4522	1858.8705	929.9389	1857.8865	929.4469	Q	***1063.5055***	532.2564	1046.4789	523.7431	1045.4949	523.2511	9
18	2004.9397	1002.9735	1987.9131	994.4602	1986.9291	993.9682	E	***935.4469***	468.2271	918.4203	459.7138	917.4363	459.2218	8
19	2075.9768	1038.4920	2058.9502	1029.9788	2057.9662	1029.4867	A	***806.4043***	403.7058	789.3777	395.1925	788.3937	394.7005	7
20	2205.0194	1103.0133	2187.9928	1094.5000	2187.0088	1094.0080	E	***735.3672***	368.1872	718.3406	359.6740	717.3566	359.1819	6
21	2352.0878	1176.5475	2335.0612	1168.0343	2334.0772	1167.5422	F	***606.3246***	303.6659	589.2980	295.1527	588.3140	294.6606	5
22	2480.1464	1240.5768	2463.1198	1232.0635	2462.1358	1231.5715	Q	459.2562	230.1317	442.2296	221.6185	441.2456	221.1264	4

23	2567.1784	1284.0928	2550.1518	1275.5796	2549.1678	1275.0875	**S**	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	**3**
24	2664.2312	1332.6192	2647.2046	1324.1059	2646.2206	1323.6139	**P**	244.1656	122.5864	227.1390	114.0731			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LPTQNITFQTESSVAEQEAEFQSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
93.8	2809.3294	0.0121	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated N5 49.81%
93.8	2809.3294	0.0121	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q4 49.81%
74.8	2808.3454	0.9961	LPTQNITFQTESSVAEQEAEFQSPK	
72.6	2809.3294	0.0121	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q9 0.37%
40.6	2809.3294	0.0121	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q17 0.00%
25.6	2809.3294	0.0121	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q22 0.00%
5.2	2808.3514	0.9901	RRSEAPPHIFAVANNAFQDMLHNR	
4.8	2808.3514	0.9901	RRSEAPPHIFAVANNAFQDMLHNR	
4.8	2808.3514	0.9901	RRSEAPPHIFAVANNAFQDMLHNR	
4.8	2808.3514	0.9901	RRSEAPPHIFAVANNAFQDMLHNR	

Mascot: http://www.matrixscience.com/

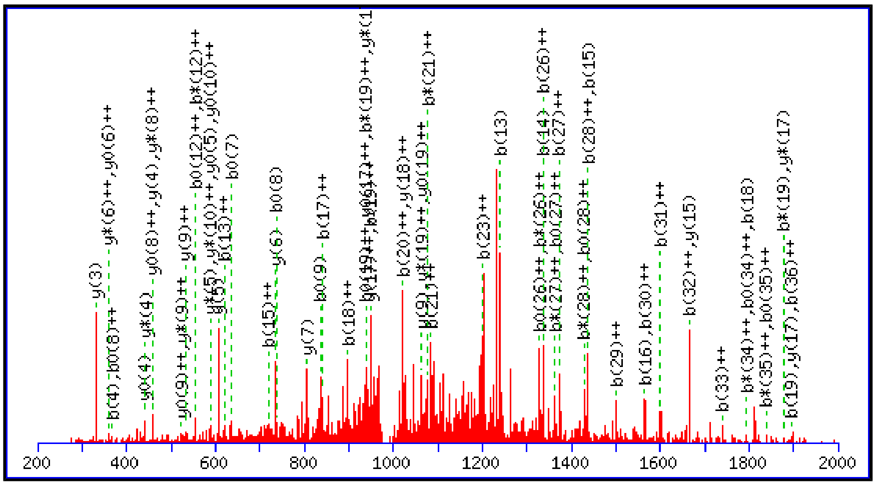
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

Match to Query 28173: 3934.947016 from(984.744030,4+) intensity(18123.5273) rtinseconds(2130) scans(5279) index(15297)
Title: 111019_Est_MI_YP_G_04Spectrum4545_scans__5279
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

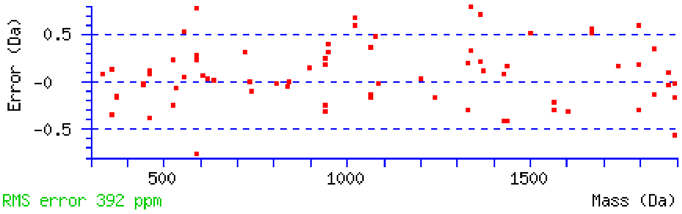
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

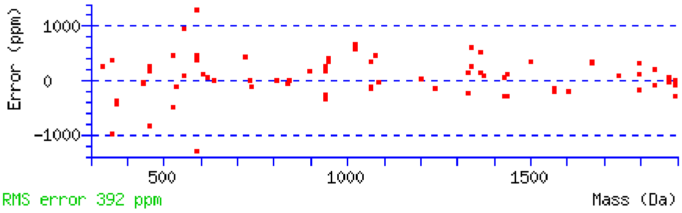


```
Monoisotopic mass of neutral peptide Mr(calc): 3934.9324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17     : Deamidated (NQ)
Ions Score: 86  Expect: 5.7e-007
Matches : 72/402 fragment ions using 86 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							37
2	155.0815	78.0444					P	3878.9182	1939.9627	3861.8917	1931.4495	3860.9076	1930.9575	36
3	270.1084	135.5579			252.0979	126.5526	D	3781.8654	1891.4364	3764.8389	1882.9231	3763.8549	1882.4311	35
4	**369.1769**	185.0921			351.1663	176.0868	V	3666.8385	1833.9229	3649.8119	1825.4096	3648.8279	1824.9176	34
5	482.2609	241.6341			464.2504	232.6288	L	3567.7701	1784.3887	3550.7435	1775.8754	3549.7595	1775.3834	33
6	583.3086	292.1579			565.2980	283.1527	T	3454.6860	1727.8466	3437.6595	1719.3334	3436.6755	1718.8414	32
7	654.3457	327.6765			636.3352	318.6712	A	3353.6383	1677.3228	3336.6118	1668.8095	3335.6278	1668.3175	31
8	755.3934	378.2003			737.3828	369.1951	T	3282.6012	1641.8043	3265.5747	1633.2910	3264.5907	1632.7990	30
9	854.4618	427.7345			836.4512	418.7293	V	3181.5535	1591.2804	3164.5270	1582.7671	3163.5430	1582.2751	29
10	941.4938	471.2506			923.4833	462.2453	S	3082.4851	1541.7462	3065.4586	1533.2329	3064.4746	1532.7409	28
11	998.5153	499.7613			980.5047	490.7560	G	2995.4531	1498.2302	2978.4266	1489.7169	2977.4425	1489.2249	27
12	1126.6103	563.8088	1109.5837	555.2955	1108.5997	554.8035	K	2938.4316	1469.7195	2921.4051	1461.2062	2920.4211	1460.7142	26
13	**1239.6943**	***620.3508***	1222.6678	611.8375	1221.6838	611.3455	L	2810.3367	1405.6720	2793.3101	1397.1587	2792.3261	1396.6667	25
14	**1336.7471**	668.8772	1319.7205	660.3639	1318.7365	659.8719	P	2697.2526	1349.1299	2680.2261	1340.6167	2679.2420	1340.1247	24
15	**1437.7948**	***719.4010***	1420.7682	710.8877	1419.7842	710.3957	T	2600.1999	1300.6036	2583.1733	1292.0903	2582.1893	1291.5983	23
16	**1565.8534**	783.4303	1548.8268	774.9170	1547.8428	774.4250	Q	2499.1522	1250.0797	2482.1256	1241.5664	2481.1416	1241.0744	22
17	1680.8803	***840.9438***	1663.8537	832.4305	1662.8697	831.9385	N	2371.0936	1186.0504	2354.0670	1177.5372	2353.0830	1177.0452	21
18	**1793.9644**	***897.4858***	1776.9378	888.9725	1775.9538	888.4805	I	2256.0667	1128.5370	2239.0401	1120.0237	2238.0561	1119.5317	20
19	**1895.0120**	***948.0097***	1877.9855	939.4964	1877.0015	939.0044	T	2142.9826	1071.9949	2125.9560	1063.4817	2124.9720	1062.9896	19
20	2042.0805	***1021.5439***	2025.0539	1013.0306	2024.0699	1012.5386	F	2041.9349	1021.4711	2024.9084	1012.9578	2023.9243	1012.4658	18
21	2170.1390	***1085.5732***	2153.1125	1077.0599	2152.1285	1076.5679	Q	**1894.8665**	947.9369	1877.8399	939.4236	1876.8559	938.9316	17
22	2271.1867	1136.0970	2254.1602	1127.5837	2253.1761	1127.0917	T	1766.8079	883.9076	1749.7814	875.3943	1748.7974	874.9023	16

23	2400.2293	***1200.6183***	2383.2028	1192.1050	2382.2187	1191.6130	**E**	**1665.7602**	833.3838	1648.7337	824.8705	1647.7497	824.3785	**15**
24	2487.2613	1244.1343	2470.2348	1235.6210	2469.2508	1235.1290	**S**	1536.7176	768.8625	1519.6911	760.3492	1518.7071	759.8572	**14**
25	2574.2934	1287.6503	2557.2668	1279.1370	2556.2828	1278.6450	**S**	1449.6856	725.3464	1432.6591	716.8332	1431.6751	716.3412	**13**
26	2673.3618	***1337.1845***	2656.3352	1328.6712	2655.3512	1328.1792	**V**	1362.6536	681.8304	1345.6270	673.3172	1344.6430	672.8251	**12**
27	2744.3989	***1372.7031***	2727.3723	1364.1898	2726.3883	1363.6978	**A**	1263.5852	632.2962	1246.5586	623.7830	1245.5746	623.2909	**11**
28	2873.4415	***1437.2244***	2856.4149	1428.7111	2855.4309	1428.2191	**E**	1192.5481	596.7777	1175.5215	588.2644	1174.5375	587.7724	**10**
29	3001.5001	***1501.2537***	2984.4735	1492.7404	2983.4895	1492.2484	**Q**	**1063.5055**	532.2564	1046.4789	523.7431	1045.4949	523.2511	**9**
30	3130.5426	***1565.7750***	3113.5161	1557.2617	3112.5321	1556.7697	**E**	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	**8**
31	3201.5798	***1601.2935***	3184.5532	1592.7802	3183.5692	1592.2882	**A**	**806.4043**	403.7058	789.3777	395.1925	788.3937	394.7005	**7**
32	3330.6224	***1665.8148***	3313.5958	1657.3015	3312.6118	1656.8095	**E**	**735.3672**	368.1872	718.3406	359.6740	717.3566	359.1819	**6**
33	3477.6908	***1739.3490***	3460.6642	1730.8357	3459.6802	1730.3437	**F**	**606.3246**	303.6659	589.2980	295.1527	588.3140	294.6606	**5**
34	3605.7493	1803.3783	3588.7228	1794.8650	3587.7388	1794.3730	**Q**	**459.2562**	230.1317	442.2296	221.6185	441.2456	221.1264	**4**
35	3692.7814	1846.8943	3675.7548	1838.3811	3674.7708	1837.8890	**S**	**331.1976**	166.1024	314.1710	157.5892	313.1870	157.0972	**3**
36	3789.8341	***1895.4207***	3772.8076	1886.9074	3771.8236	1886.4154	**P**	244.1656	122.5864	227.1390	114.0731			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.7	3934.9324	0.0146	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated N17 47.23%
85.7	3934.9324	0.0146	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q16 47.23%
75.7	3934.9324	0.0146	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q21 4.75%
67.0	3934.9324	0.0146	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q29 0.63%
62.8	3933.9484	0.9986	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	
61.0	3934.9324	0.0146	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q34 0.16%
17.8	3932.9236	2.0234	AVHHMSSPAIPSASPNPLSSPHLYHKQHNGMKLSMK	
12.4	3932.9236	2.0234	AVHHMSSPAIPSASPNPLSSPHLYHKQHNGMKLSMK	
10.9	3932.9474	1.9996	ILDYMQTVIQSHGQLSINLANLHMTMDVLFALDR	
10.8	3932.9474	1.9996	ILDYMQTVIQSHGQLSINLANLHMTMDVLFALDR	

Mascot: http://www.matrixscience.com/

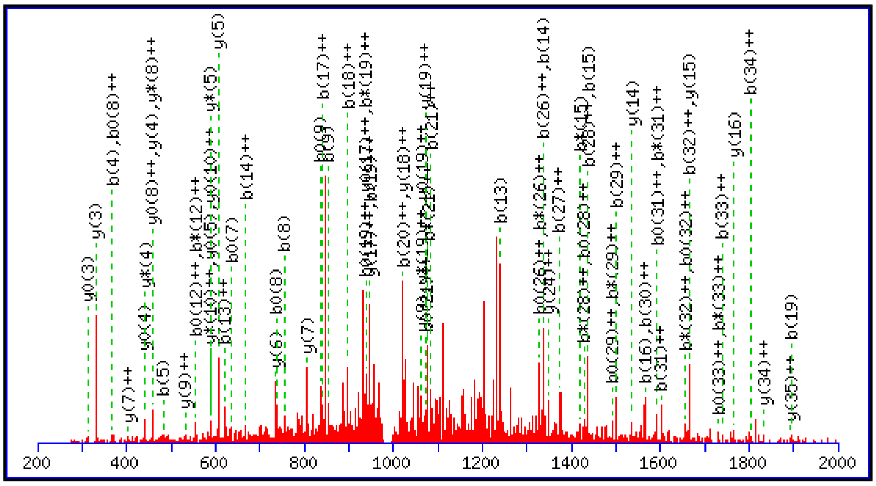
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

Match to Query 28191: 3937.921856 from(985.487740,4+) intensity(24666.3457) rtinseconds(2253) scans(5622) index(15348)
Title: 111019_Est_MI_YP_G_04Spectrum4850_scans__5622
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

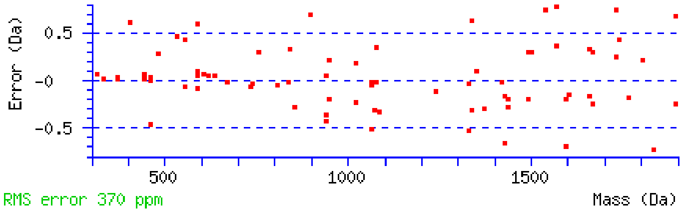
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

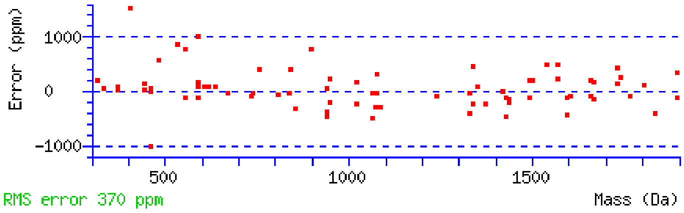


```
Monoisotopic mass of neutral peptide Mr(calc): 3935.9164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N17     : Deamidated (NQ)
Q21     : Deamidated (NQ)
Ions Score: 69  Expect: 2.6e-005
Matches : 77/402 fragment ions using 121 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							37
2	155.0815	78.0444					P	3879.9022	1940.4547	3862.8757	1931.9415	3861.8917	1931.4495	36
3	270.1084	135.5579			252.0979	126.5526	D	3782.8495	1891.9284	3765.8229	1883.4151	3764.8389	1882.9231	35
4	***369.1769***	185.0921			351.1663	176.0868	V	3667.8225	1834.4149	3650.7960	1825.9016	3649.8119	1825.4096	34
5	***482.2609***	241.6341			464.2504	232.6288	L	3568.7541	1784.8807	3551.7276	1776.3674	3550.7435	1775.8754	33
6	583.3086	292.1579			565.2980	283.1527	T	3455.6700	1728.3387	3438.6435	1719.8254	3437.6595	1719.3334	32
7	654.3457	327.6765			636.3352	318.6712	A	3354.6224	1677.8148	3337.5958	1669.3015	3336.6118	1668.8095	31
8	***755.3934***	378.2003			737.3828	369.1951	T	3283.5852	1642.2963	3266.5587	1633.7830	3265.5747	1633.2910	30
9	***854.4618***	427.7345			836.4512	418.7293	V	3182.5376	1591.7724	3165.5110	1583.2591	3164.5270	1582.7671	29
10	941.4938	471.2506			923.4833	462.2453	S	3083.4691	1542.2382	3066.4426	1533.7249	3065.4586	1533.2329	28
11	998.5153	499.7613			980.5047	490.7560	G	2996.4371	1498.7222	2979.4106	1490.2089	2978.4266	1489.7169	27
12	1126.6103	563.8088	1109.5837	555.2955	1108.5997	554.8035	K	2939.4157	1470.2115	2922.3891	1461.6982	2921.4051	1461.2062	26
13	***1239.6943***	***620.3508***	1222.6678	611.8375	1221.6838	611.3455	L	2811.3207	1406.1640	2794.2941	1397.6507	2793.3101	1397.1587	25
14	***1336.7471***	***668.8772***	1319.7205	660.3639	1318.7365	659.8719	P	2698.2366	1349.6220	2681.2101	1341.1087	2680.2261	1340.6167	24
15	***1437.7948***	719.4010	1420.7682	710.8877	1419.7842	710.3957	T	2601.1839	1301.0956	2584.1573	1292.5823	2583.1733	1292.0903	23
16	***1565.8534***	783.4303	1548.8268	774.9170	1547.8428	774.4250	Q	2500.1362	1250.5717	2483.1096	1242.0585	2482.1256	1241.5664	22
17	1680.8803	***840.9438***	1663.8537	832.4305	1662.8697	831.9385	N	2372.0776	1186.5424	2355.0511	1178.0292	2354.0670	1177.5372	21
18	1793.9644	***897.4858***	1776.9378	888.9725	1775.9538	888.4805	I	2257.0507	1129.0290	2240.0241	1120.5157	2239.0401	1120.0237	20
19	***1895.0120***	***948.0097***	1877.9855	939.4964	1877.0015	939.0044	T	2143.9666	1072.4869	2126.9401	1063.9737	2125.9560	1063.4817	19
20	2042.0805	***1021.5439***	2025.0539	1013.0306	2024.0699	1012.5386	F	2042.9189	1021.9631	2025.8924	1013.4498	2024.9084	1012.9578	18
21	2171.1230	***1086.0652***	2154.0965	1077.5519	2153.1125	1077.0599	Q	1895.8505	948.4289	1878.8240	939.9156	1877.8399	939.4236	17

22	2272.1707	1136.5890	2255.1442	1128.0757	2254.1602	1127.5837	**T**	**1766.8079**	883.9076	1749.7814	875.3943	1748.7974	874.9023	**16**
23	2401.2133	1201.1103	2384.1868	1192.5970	2383.2028	1192.1050	**E**	**1665.7602**	833.3838	1648.7337	824.8705	1647.7497	824.3785	**15**
24	2488.2453	1244.6263	2471.2188	1236.1130	2470.2348	1235.6210	**S**	**1536.7176**	768.8625	1519.6911	760.3492	1518.7071	759.8572	**14**
25	2575.2774	1288.1423	2558.2508	1279.6290	2557.2668	1279.1370	**S**	1449.6856	725.3464	1432.6591	716.8332	1431.6751	716.3412	**13**
26	2674.3458	***1337.6765***	2657.3192	1329.1633	2656.3352	1328.6712	**V**	1362.6536	681.8304	1345.6270	673.3172	1344.6430	672.8251	**12**
27	2745.3829	***1373.1951***	2728.3564	1364.6818	2727.3723	1364.1898	**A**	1263.5852	632.2962	1246.5586	623.7830	1245.5746	623.2909	**11**
28	2874.4255	***1437.7164***	2857.3989	1429.2031	2856.4149	1428.7111	**E**	1192.5481	596.7777	1175.5215	588.2644	1174.5375	587.7724	**10**
29	3002.4841	***1501.7457***	2985.4575	1493.2324	2984.4735	1492.7404	**Q**	**1063.5055**	532.2564	1046.4789	523.7431	1045.4949	523.2511	**9**
30	3131.5267	***1566.2670***	3114.5001	1557.7537	3113.5161	1557.2617	**E**	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	**8**
31	3202.5638	***1601.7855***	3185.5372	1593.2723	3184.5532	1592.7802	**A**	**806.4043**	403.7058	789.3777	395.1925	788.3937	394.7005	**7**
32	3331.6064	***1666.3068***	3314.5798	1657.7935	3313.5958	1657.3015	**E**	**735.3672**	368.1872	718.3406	359.6740	717.3566	359.1819	**6**
33	3478.6748	***1739.8410***	3461.6482	1731.3278	3460.6642	1730.8357	**F**	**606.3246**	303.6659	589.2980	295.1527	588.3140	294.6606	**5**
34	3606.7334	***1803.8703***	3589.7068	1795.3570	3588.7228	1794.8650	**Q**	**459.2562**	230.1317	442.2296	221.6185	441.2456	221.1264	**4**
35	3693.7654	1847.3863	3676.7388	1838.8731	3675.7548	1838.3811	**S**	**331.1976**	166.1024	314.1710	157.5892	313.1870	157.0972	**3**
36	3790.8182	1895.9127	3773.7916	1887.3994	3772.8076	1886.9074	**P**	244.1656	122.5864	227.1390	114.0731			**2**
37							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
69.4	3935.9164	2.0055	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated N17, Q21 29.78%
69.4	3935.9164	2.0055	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q16, Q21 29.78%
67.6	3936.9004	1.0215	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	
66.5	3935.9164	2.0055	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q16, N17 15.45%
63.1	3936.9004	1.0215	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	
63.0	3936.9004	1.0215	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	
62.9	3935.9164	2.0055	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated N17, Q29 6.67%
62.9	3935.9164	2.0055	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q16, Q29 6.67%
59.5	3936.9004	1.0215	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	
59.3	3936.9004	1.0215	GPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPK	

Mascot: http://www.matrixscience.com/

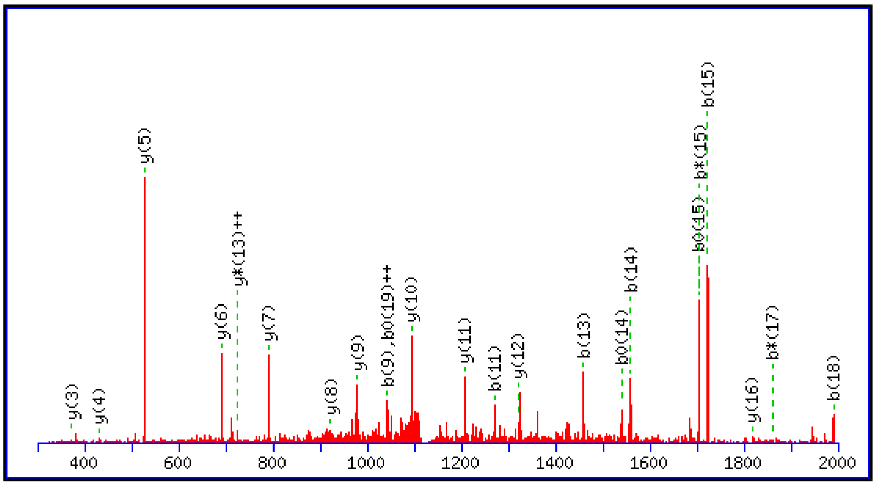
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFITNFSMIIDGMTYPGIIK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

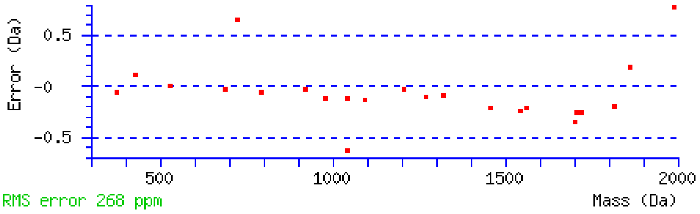
Match to Query 15083: 2248.123528 from(1125.069040,2+) intensity(32334.7051) rtinseconds(2800) scans(7498) index(16392)
Title: 111019_Est_MI_YP_G_05Spectrum6461_scans__7498
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

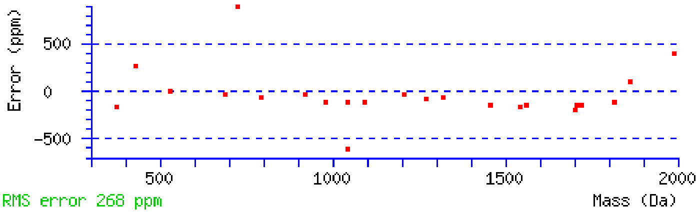
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2248.1160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5     : Deamidated (NQ)
M8     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57  Expect: 0.00051
Matches : 23/316 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	72.0444	36.5258					A							20
2	219.1128	110.0600					F	2178.0861	1089.5467	2161.0596	1081.0334	2160.0756	1080.5414	19
3	332.1969	166.6021					I	2031.0177	1016.0125	2013.9912	1007.4992	2013.0072	1007.0072	18
4	433.2445	217.1259			415.2340	208.1206	T	1917.9337	959.4705	1900.9071	950.9572	1899.9231	950.4652	17
5	548.2715	274.6394	531.2449	266.1261	530.2609	265.6341	N	***1816.8860***	908.9466	1799.8594	900.4333	1798.8754	899.9413	16
6	695.3399	348.1736	678.3134	339.6603	677.3293	339.1683	F	1701.8590	851.4332	1684.8325	842.9199	1683.8485	842.4279	15
7	782.3719	391.6896	765.3454	383.1763	764.3614	382.6843	S	1554.7906	777.8989	1537.7641	769.3857	1536.7801	768.8937	14
8	929.4073	465.2073	912.3808	456.6940	911.3968	456.2020	M	1467.7586	734.3829	1450.7320	725.8697	1449.7480	725.3776	13
9	**1042.4914**	521.7493	1025.4648	513.2361	1024.4808	512.7441	I	***1320.7232***	660.8652	1303.6966	652.3520	1302.7126	651.8599	12
10	1155.5755	578.2914	1138.5489	569.7781	1137.5649	569.2861	I	***1207.6391***	604.3232	1190.6126	595.8099	1189.6286	595.3179	11
11	**1270.6024**	635.8048	1253.5759	627.2916	1252.5918	626.7996	D	***1094.5551***	547.7812	1077.5285	539.2679	1076.5445	538.7759	10
12	1327.6239	664.3156	1310.5973	655.8023	1309.6133	655.3103	G	***979.5281***	490.2677	962.5016	481.7544	961.5176	481.2624	9
13	**1458.6644**	729.8358	1441.6378	721.3225	1440.6538	720.8305	M	***922.5067***	461.7570	905.4801	453.2437	904.4961	452.7517	8
14	**1559.7120**	780.3597	1542.6855	771.8464	1541.7015	771.3544	T	***791.4662***	396.2367	774.4396	387.7234	773.4556	387.2314	7
15	**1722.7754**	861.8913	1705.7488	853.3780	1704.7648	852.8860	Y	***690.4185***	345.7129	673.3919	337.1996			6
16	1819.8281	910.4177	1802.8016	901.9044	1801.8176	901.4124	P	***527.3552***	264.1812	510.3286	255.6679			5
17	1876.8496	938.9284	1859.8230	930.4152	1858.8390	929.9231	G	***430.3024***	215.6548	413.2758	207.1416			4
18	**1989.9337**	995.4705	1972.9071	986.9572	1971.9231	986.4652	I	***373.2809***	187.1441	356.2544	178.6308			3
19	2103.0177	1052.0125	2085.9912	1043.4992	2085.0072	1043.0072	I	260.1969	130.6021	243.1703	122.0888			2
20							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of AFITNFSMIIDGMTYPGIIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.3	2248.1160	0.0076	AFITNFSMIIDGMTYPGIIK	Oxidation M8 100.00%
13.8	2248.1160	0.0076	AFITNFSMIIDGMTYPGIIK	Oxidation M13 0.00%
5.6	2248.1310	-0.0075	MLINQHTLLFGGDTNPVHPK	
5.0	2248.1310	-0.0075	MLINQHTLLFGGDTNPVHPK	
3.6	2247.1093	1.0142	YTMLSALAKVEDVSVDTSYR	
3.1	2247.1153	1.0082	MHHLNKTHSGLIHMFSIGR	
1.1	2248.1158	0.0078	KLMDDPVQTLIEGHQHDKK	
0.6	2246.1154	2.0082	KAWEANKFLTPGLTHTMER	
0.5	2248.1158	0.0078	KLMDDPVQTLIEGHQHDKK	
0.4	2247.1279	0.9956	VGTLIMCLHDVSDFLLEAAK	

Mascot: http://www.matrixscience.com/

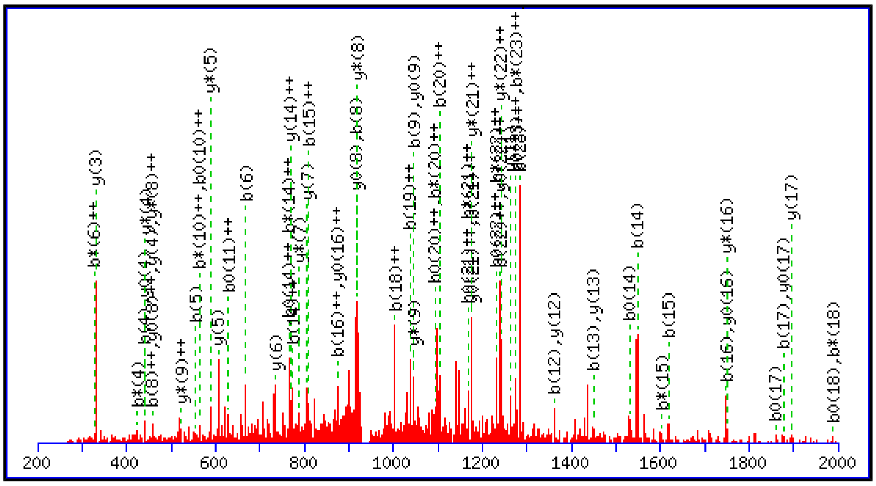
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LPTQNITFQTESSVAEQEAEFQSPK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

Match to Query 25706: 2811.320892 from(938.114240,3+) intensity(18923.9219) rtinseconds(1786) scans(4639) index(6525)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4078_scans__4639
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

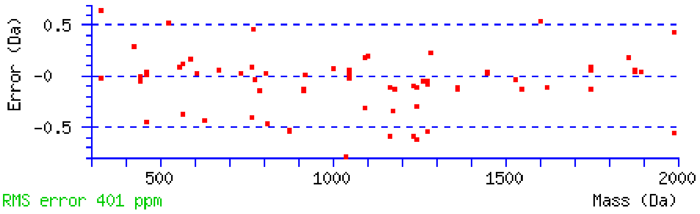
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

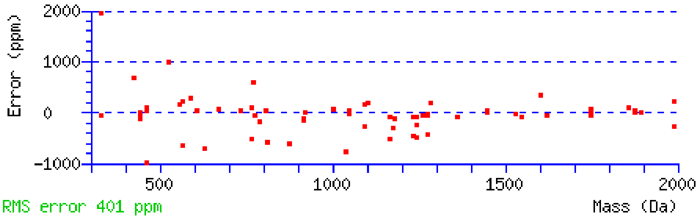


Monoisotopic mass of neutral peptide Mr(calc): 2810.3134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Deamidated (NQ)
N5 : Deamidated (NQ)
Ions Score: 46 **Expect:** 0.0059
Matches : 71/274 fragment ions using 140 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	211.1441	106.0757					P	2698.2366	1349.6220	2681.2101	1341.1087	2680.2261	1340.6167	24
3	312.1918	156.5995			294.1812	147.5942	T	2601.1839	1301.0956	2584.1573	1292.5823	2583.1733	1292.0903	23
4	***441.2344***	221.1208	424.2078	212.6076	423.2238	212.1155	Q	2500.1362	1250.5717	2483.1096	1242.0585	2482.1256	1241.5664	22
5	***556.2613***	278.6343	539.2348	270.1210	538.2508	269.6290	N	2371.0936	1186.0504	2354.0670	1177.5372	2353.0830	1177.0452	21
6	***669.3454***	335.1763	652.3188	326.6631	651.3348	326.1710	I	2256.0667	1128.5370	2239.0401	1120.0237	2238.0561	1119.5317	20
7	770.3931	385.7002	753.3665	377.1869	752.3825	376.6949	T	2142.9826	1071.9949	2125.9560	1063.4817	2124.9720	1062.9896	19
8	***917.4615***	***459.2344***	900.4349	450.7211	899.4509	450.2291	F	2041.9349	1021.4711	2024.9084	1012.9578	2023.9243	1012.4658	18
9	***1045.5201***	523.2637	1028.4935	514.7504	1027.5095	514.2584	Q	**1894.8665**	947.9369	1877.8399	939.4236	1876.8559	938.9316	17
10	1146.5677	573.7875	1129.5412	565.2742	1128.5572	564.7822	T	1766.8079	883.9076	1749.7814	875.3943	1748.7974	874.9023	16
11	***1275.6103***	638.3088	1258.5838	629.7955	1257.5998	629.3035	E	1665.7602	833.3838	1648.7337	824.8705	1647.7497	824.3785	15
12	***1362.6424***	681.8248	1345.6158	673.3115	1344.6318	672.8195	S	1536.7176	768.8625	1519.6911	760.3492	1518.7071	759.8572	14
13	***1449.6744***	725.3408	1432.6478	716.8276	1431.6638	716.3355	S	**1449.6856**	725.3464	1432.6591	716.8332	1431.6751	716.3412	13
14	***1548.7428***	***774.8750***	1531.7162	766.3618	1530.7322	765.8698	V	**1362.6536**	681.8304	1345.6270	673.3172	1344.6430	672.8251	12
15	***1619.7799***	***810.3936***	1602.7534	801.8803	1601.7693	801.3883	A	**1263.5852**	632.2962	1246.5586	623.7830	1245.5746	623.2909	11
16	***1748.8225***	***874.9149***	1731.7960	866.4016	1730.8119	865.9096	E	1192.5481	596.7777	1175.5215	588.2644	1174.5375	587.7724	10
17	***1876.8811***	938.9442	1859.8545	930.4309	1858.8705	929.9389	Q	1063.5055	532.2564	1046.4789	523.7431	1045.4949	523.2511	9
18	2005.9237	***1003.4655***	1988.8971	994.9522	1987.9131	994.4602	E	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	8
19	2076.9608	***1038.9840***	2059.9342	1030.4708	2058.9502	1029.9788	A	**806.4043**	403.7058	789.3777	395.1925	788.3937	394.7005	7
20	2206.0034	***1103.5053***	2188.9768	1094.9921	2187.9928	1094.5000	E	**735.3672**	368.1872	718.3406	359.6740	717.3566	359.1819	6
21	2353.0718	***1177.0395***	2336.0452	1168.5263	2335.0612	1168.0343	F	**606.3246**	303.6659	589.2980	295.1527	588.3140	294.6606	5

22	2481.1304	***1241.0688***	2464.1038	1232.5556	2463.1198	1232.0635	**Q**	**459.2562**	230.1317	442.2296	221.6185	441.2456	221.1264	**4**
23	2568.1624	***1284.5848***	2551.1359	1276.0716	2550.1518	1275.5796	**S**	**331.1976**	166.1024	314.1710	157.5892	313.1870	157.0972	**3**
24	2665.2152	1333.1112	2648.1886	1324.5979	2647.2046	1324.1059	**P**	244.1656	122.5864	227.1390	114.0731			**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LPTQNITFQTESSVAEQEAEFQSPK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
45.7	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q4, N5 17.35%
45.4	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated N5, Q17 15.89%
45.3	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q4, Q17 15.86%
44.7	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q4, Q22 13.62%
44.0	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated N5, Q22 11.78%
43.8	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated N5, Q9 11.05%
43.8	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q4, Q9 11.05%
36.2	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q9, Q17 1.92%
35.0	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q9, Q22 1.47%
14.9	2810.3134	1.0075	LPTQNITFQTESSVAEQEAEFQSPK	Deamidated Q17, Q22 0.01%

Mascot: http://www.matrixscience.com/

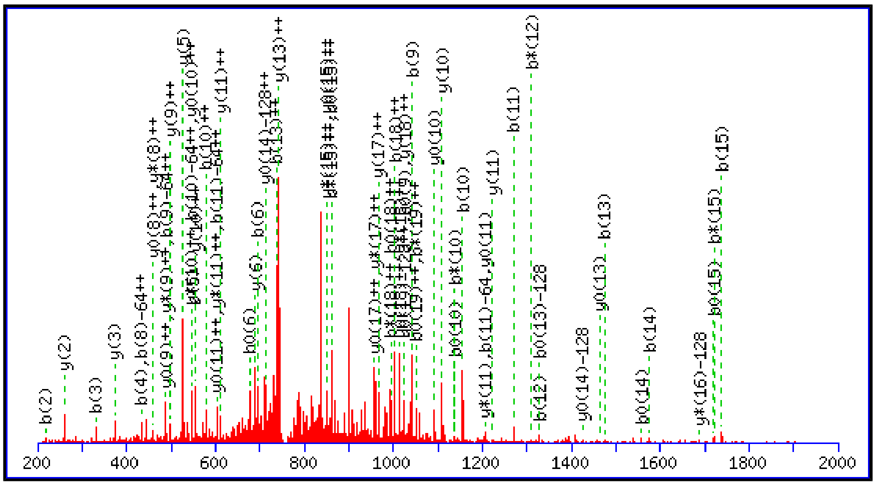
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AFITNFSMIIDGMTYPGIIK**
Found in **B7ZKJ8** in **con_Xuniprot_HUMAN3**, B7ZKJ8_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1

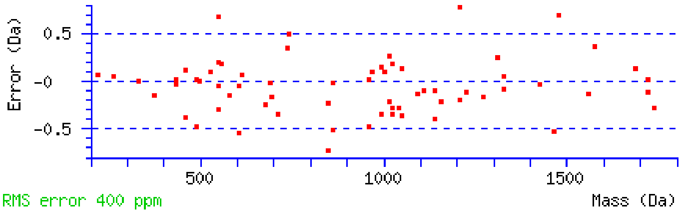
Match to Query 15116: 2264.118312 from(755.713380,3+) intensity(19407.0332) rtinseconds(2556) scans(6673) index(25634)
Title: 111019_Est_MI_YS_G_07Spectrum5747_scans__6673
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

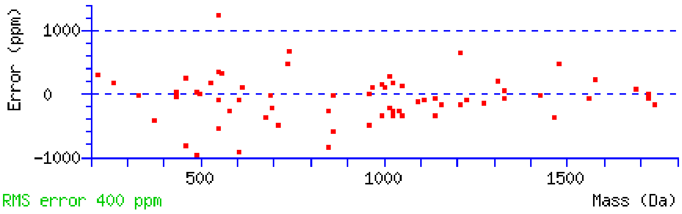
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2264.1109
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 **Expect:** 0.018
Matches : 69/346 fragment ions using 117 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**20**
2	***219.1128***	110.0600					**F**	2194.0810	1097.5442	2177.0545	1089.0309	2176.0705	1088.5389	**19**
3	***332.1969***	166.6021					**I**	2047.0126	1024.0100	2029.9861	1015.4967	2029.0021	1015.0047	**18**
4	***433.2445***	217.1259			415.2340	208.1206	**T**	1933.9286	967.4679	1916.9020	958.9546	1915.9180	958.4626	**17**
5	***548.2715***	274.6394	531.2449	266.1261	530.2609	265.6341	**N**	1832.8809	916.9441	1815.8543	908.4308	1814.8703	907.9388	**16**
6	***695.3399***	348.1736	678.3134	339.6603	677.3293	339.1683	**F**	1717.8539	859.4306	1700.8274	850.9173	1699.8434	850.4253	**15**
7	782.3719	391.6896	765.3454	383.1763	764.3614	382.6843	**S**	1570.7855	785.8964	1553.7590	777.3831	1552.7750	776.8911	**14**
8	929.4073	465.2073	912.3808	456.6940	911.3968	456.2020	**M**	1483.7535	742.3804	1466.7270	733.8671	1465.7429	733.3751	**13**
9	***1042.4914***	521.7493	1025.4648	513.2361	1024.4808	512.7441	**I**	1336.7181	668.8627	1319.6916	660.3494	1318.7075	659.8574	**12**
10	***1155.5755***	578.2914	1138.5489	569.7781	1137.5649	569.2861	**I**	**1223.6340**	612.3207	1206.6075	603.8074	1205.6235	603.3154	**11**
11	***1270.6024***	635.8048	1253.5759	627.2916	1252.5918	626.7996	**D**	**1110.5500**	555.7786	1093.5234	547.2654	1092.5394	546.7733	**10**
12	***1327.6239***	664.3156	1310.5973	655.8023	1309.6133	655.3103	**G**	995.5230	498.2652	978.4965	489.7519	977.5125	489.2599	**9**
13	***1474.6593***	737.8333	1457.6327	729.3200	1456.6487	728.8280	**M**	938.5016	469.7544	921.4750	461.2411	920.4910	460.7491	**8**
14	***1575.7069***	788.3571	1558.6804	779.8438	1557.6964	779.3518	**T**	791.4662	396.2367	774.4396	387.7234	773.4556	387.2314	**7**
15	***1738.7703***	869.8888	1721.7437	861.3755	1720.7597	860.8835	**Y**	**690.4185**	345.7129	673.3919	337.1996			**6**
16	1835.8230	918.4152	1818.7965	909.9019	1817.8125	909.4099	**P**	**527.3552**	264.1812	510.3286	255.6679			**5**
17	1892.8445	946.9259	1875.8180	938.4126	1874.8339	937.9206	**G**	430.3024	215.6548	413.2758	207.1416			**4**
18	2005.9286	1003.4679	1988.9020	994.9546	1987.9180	994.4626	**I**	**373.2809**	187.1441	356.2544	178.6308			**3**
19	2119.0126	1060.0100	2101.9861	1051.4967	2101.0021	1051.0047	**I**	**260.1969**	130.6021	243.1703	122.0888			**2**
20							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of AFITNFSMIIDGMTYPGIIK
(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	2264.1109	0.0074	AFITNFSMIIDGMTYPGIIK
4.5	2263.1188	0.9995	EKTVVTMSMTPTAAAEGSSPLR
3.4	2263.1253	0.9930	NITSCIVTSDLPLSASLTQNK
3.2	2263.1228	0.9955	FVIMCTEPDVGQLSVAQQLK
2.3	2262.1024	2.0159	VKDGKWDEMEILLETPGMR
1.1	2262.1058	2.0125	ILVMHIPDSISLMTTSDAMR
1.0	2263.1120	1.0063	QEIEDRLNTWVVFNEKNK
1.0	2263.1120	1.0063	QEIEDRLNTWVVFNEKNK
1.0	2263.1120	1.0063	QEIEDRLNTWVVFNEKNK
1.0	2263.1120	1.0063	QEIEDRLNTWVVFNEKNK

Mascot: http://www.matrixscience.com/

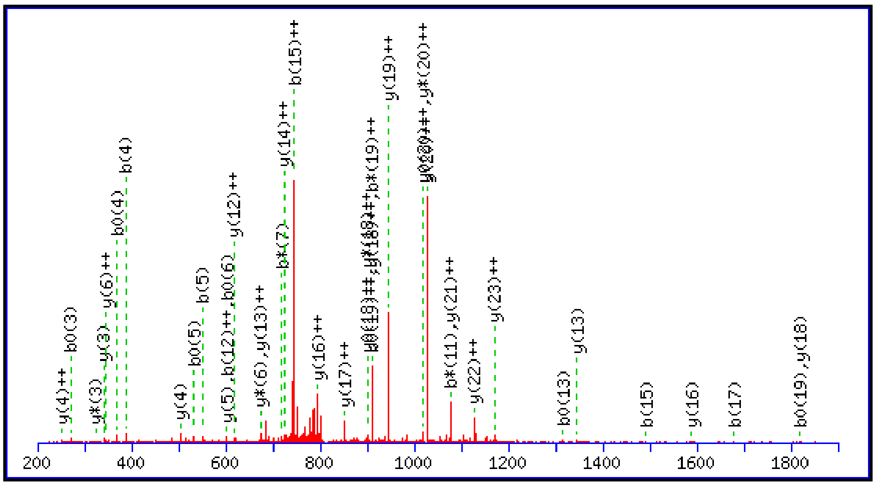
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSTVYANNGSVLQGTSVASVYHGK**
Found in **Q15166** in **con_Xuniprot_HUMAN3**, PON3_HUMAN Serum paraoxonase/lactonase 3 OS=Homo sapiens GN=PON3 PE=1 SV=3

Match to Query 21505: 2438.214192 from(813.745340,3+) intensity(49160.6328) rtinseconds(1308) scans(3166) index(26562)
Title: 111019_Est_MI_YS_G_09Spectrum2731_scans__3166
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

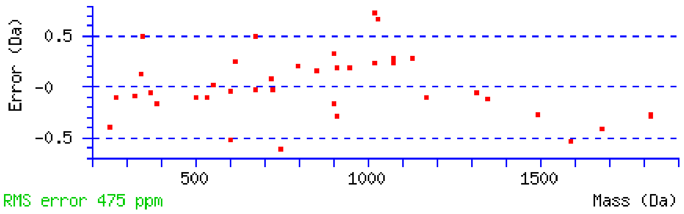
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

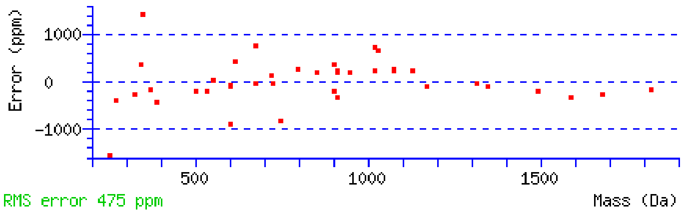


Monoisotopic mass of neutral peptide Mr(calc): 2438.2078
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 65 **Expect:** 9.1e-005
Matches : 41/252 fragment ions using 66 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							24
2	187.1077	94.0575			169.0972	85.0522	S	2340.1466	1170.5770	2323.1201	1162.0637	2322.1361	1161.5717	23
3	288.1554	144.5813			270.1448	135.5761	T	2253.1146	1127.0609	2236.0881	1118.5477	2235.1040	1118.0557	22
4	**387.2238**	194.1155			369.2132	185.1103	V	2152.0669	1076.5371	2135.0404	1068.0238	2134.0564	1067.5318	21
5	**550.2871**	275.6472			532.2766	266.6419	Y	2052.9985	1027.0029	2035.9720	1018.4896	2034.9879	1017.9976	20
6	621.3243	311.1658			603.3137	302.1605	A	1889.9352	945.4712	1872.9086	936.9580	1871.9246	936.4659	19
7	735.3672	368.1872	718.3406	359.6740	717.3566	359.1819	N	**1818.8981**	909.9527	1801.8715	901.4394	1800.8875	900.9474	18
8	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	N	1704.8551	852.9312	1687.8286	844.4179	1686.8446	843.9259	17
9	907.4156	454.2114	890.3890	445.6982	889.4050	445.2061	G	**1589.8282**	795.4177	1572.8016	786.9045	1571.8176	786.4125	16
10	994.4476	497.7274	977.4211	489.2142	976.4371	488.7222	S	1532.8067	766.9070	1515.7802	758.3937	1514.7962	757.9017	15
11	1093.5160	547.2617	1076.4895	538.7484	1075.5055	538.2564	V	1445.7747	723.3910	1428.7482	714.8777	1427.7641	714.3857	14
12	1206.6001	603.8037	1189.5735	595.2904	1188.5895	594.7984	L	**1346.7063**	673.8568	1329.6797	665.3435	1328.6957	664.8515	13
13	1334.6587	667.8330	1317.6321	659.3197	1316.6481	658.8277	Q	1233.6222	617.3148	1216.5957	608.8015	1215.6117	608.3095	12
14	1391.6801	696.3437	1374.6536	687.8304	1373.6696	687.3384	G	1105.5637	553.2855	1088.5371	544.7722	1087.5531	544.2802	11
15	**1492.7278**	746.8675	1475.7013	738.3543	1474.7172	737.8623	T	1048.5422	524.7747	1031.5156	516.2615	1030.5316	515.7694	10
16	1579.7598	790.3836	1562.7333	781.8703	1561.7493	781.3783	S	947.4945	474.2509	930.4680	465.7376	929.4839	465.2456	9
17	**1678.8283**	839.9178	1661.8017	831.4045	1660.8177	830.9125	V	860.4625	430.7349	843.4359	422.2216	842.4519	421.7296	8
18	1749.8654	875.4363	1732.8388	866.9230	1731.8548	866.4310	A	761.3941	381.2007	744.3675	372.6874	743.3835	372.1954	7
19	1836.8974	918.9523	1819.8709	910.4391	1818.8868	909.9471	S	690.3570	345.6821	673.3304	337.1688	672.3464	336.6768	6
20	1935.9658	968.4865	1918.9393	959.9733	1917.9552	959.4813	V	**603.3249**	302.1661	586.2984	293.6528			5
21	2099.0291	1050.0182	2082.0026	1041.5049	2081.0186	1041.0129	Y	**504.2565**	252.6319	487.2300	244.1186			4
22	2236.0881	1118.5477	2219.0615	1110.0344	2218.0775	1109.5424	H	**341.1932**	171.1002	324.1666	162.5870			3
23	2293.1095	1147.0584	2276.0830	1138.5451	2275.0990	1138.0531	G	204.1343	102.5708	187.1077	94.0575			2

24							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of VSTVYANNGSVLQGTSVASVYHGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.8	2438.2078	0.0064	VSTVYANNGSVLQGTSVASVYHGK	Deamidated N8 33.33%
64.8	2438.2078	0.0064	VSTVYANNGSVLQGTSVASVYHGK	Deamidated N7 33.33%
64.8	2438.2078	0.0064	VSTVYANNGSVLQGTSVASVYHGK	Deamidated Q13 33.33%
14.4	2438.2151	-0.0009	LNPEMLQIAQDTGKLNVAYFR	
6.2	2438.2151	-0.0009	LNPEMLQIAQDTGKLNVAYFR	
6.2	2438.2151	-0.0009	LNPEMLQIAQDTGKLNVAYFR	
6.2	2438.2086	0.0056	FQLCVLGQNAQTMAYNITPLR	
4.4	2438.2138	0.0004	KWFCNGRGNTSGSHIVNHLVR	
4.3	2438.2151	-0.0009	LNPEMLQIAQDTGKLNVAYFR	
4.3	2438.2151	-0.0009	LNPEMLQIAQDTGKLNVAYFR	

Mascot: http://www.matrixscience.com/

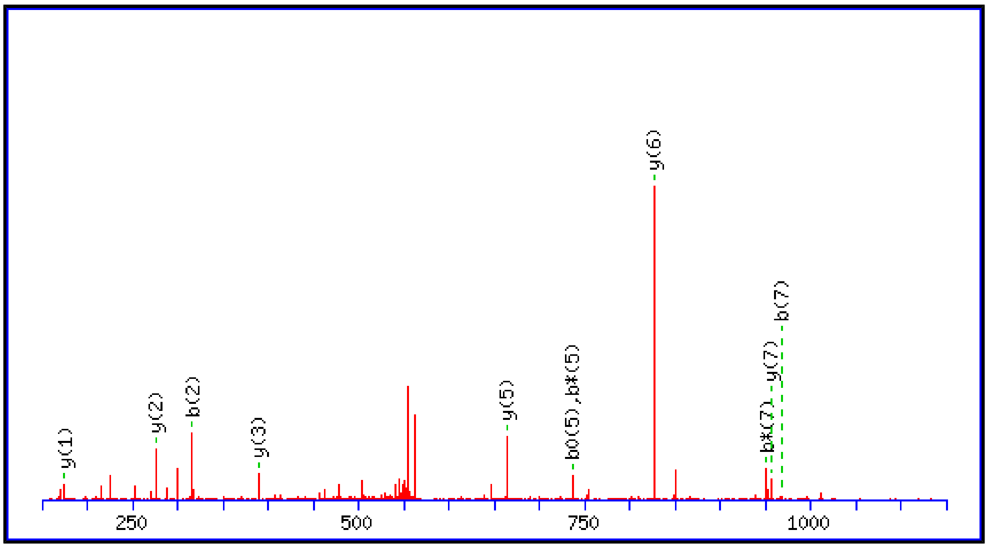
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WEYCNLTR**
Found in **P08519** in **con_Xuniprot_HUMAN3**, APOA_HUMAN Apolipoprotein(a) OS=Homo sapiens GN=LPA PE=1 SV=1

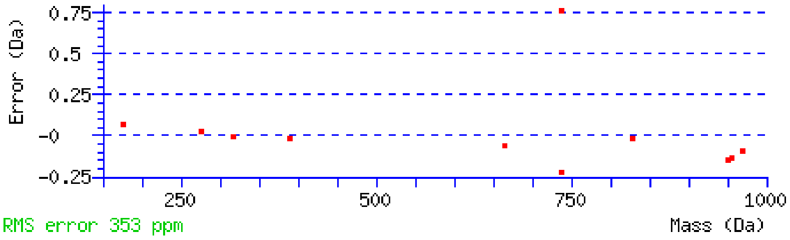
Match to Query 1536: 1141.488348 from(571.751450,2+) intensity(48562.1445) rtinseconds(1067) scans(2302) index(11658)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum1972_scans__2302
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

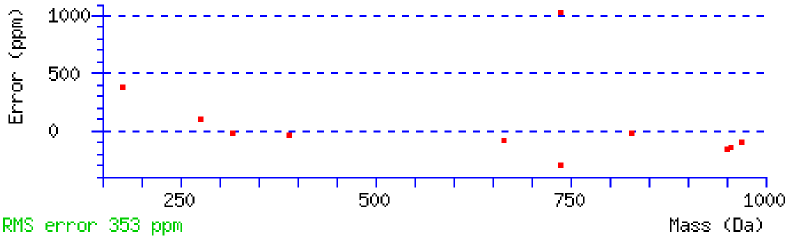
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1141.4862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.0034
Matches : 11/72 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	187.0866	94.0469					W							8
2	**316.1292**	158.5682			298.1186	149.5629	E	***956.4142***	478.7107	939.3877	470.1975	938.4036	469.7055	7
3	479.1925	240.0999			461.1819	231.0946	Y	***827.3716***	414.1894	810.3451	405.6762	809.3611	405.1842	6
4	639.2232	320.1152			621.2126	311.1099	C	***664.3083***	332.6578	647.2817	324.1445	646.2977	323.6525	5
5	754.2501	377.6287	737.2236	369.1154	736.2395	368.6234	N	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
6	867.3342	434.1707	850.3076	425.6574	849.3236	425.1654	L	***389.2507***	195.1290	372.2241	186.6157	371.2401	186.1237	3
7	**968.3818**	484.6946	951.3553	476.1813	950.3713	475.6893	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of WEYCNLTR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
41.5	1141.4862	0.0021	WEYCNLTR
13.8	1141.4896	-0.0013	DAIECFMTR
3.2	1141.4896	-0.0013	MSGSTPFQMR
2.8	1141.4862	0.0021	DSLGWMFNR
2.3	1139.4838	2.0045	AIEMEMQQK
1.9	1140.4903	0.9980	QMSLMNETR
0.3	1140.4845	1.0039	CHYMFNLR

Mascot: http://www.matrixscience.com/

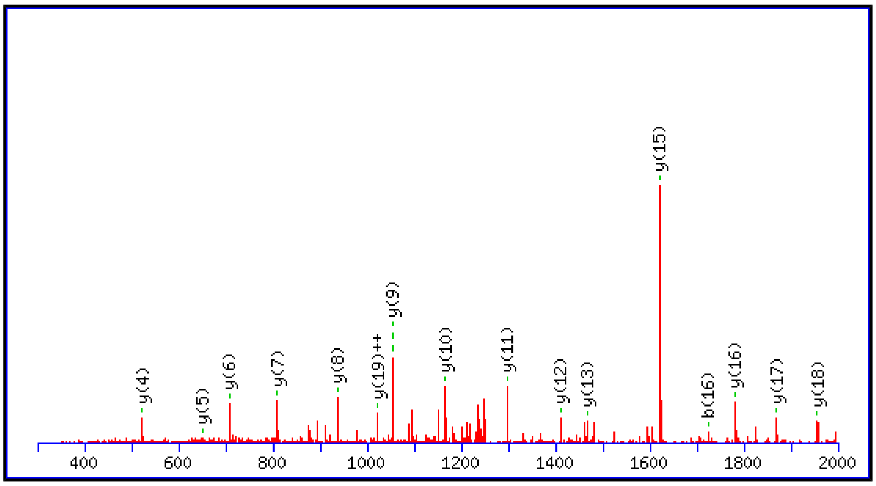
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TELFSSSCPGGIMLNETGQGYQR**
Found in **O95445** in **con_Xuniprot_HUMAN3**, APOM_HUMAN Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

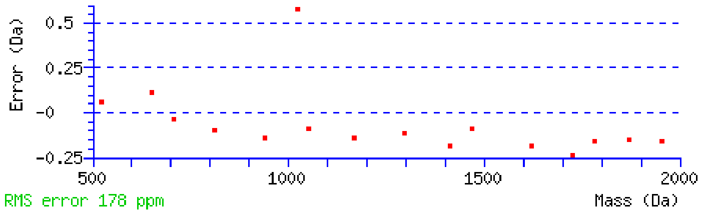
Match to Query 21827: 2532.132008 from(1267.073280,2+) intensity(55107.6602) rtinseconds(1702) scans(4021) index(11825)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum3437_scans__4021
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

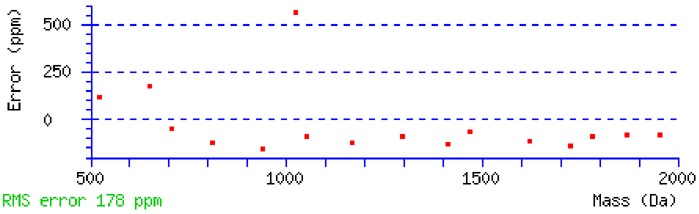
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2532.1261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
Ions Score: 127 **Expect:** 2.7e-011
Matches : 16/224 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	102.0550	51.5311			84.0444	42.5258	T							23
2	231.0975	116.0524			213.0870	107.0471	E	2432.0857	1216.5465	2415.0591	1208.0332	2414.0751	1207.5412	22
3	344.1816	172.5944			326.1710	163.5892	L	2303.0431	1152.0252	2286.0165	1143.5119	2285.0325	1143.0199	21
4	491.2500	246.1287			473.2395	237.1234	F	2189.9590	1095.4832	2172.9325	1086.9699	2171.9485	1086.4779	20
5	578.2821	289.6447			560.2715	280.6394	S	2042.8906	1021.9489	2025.8641	1013.4357	2024.8801	1012.9437	19
6	665.3141	333.1607			647.3035	324.1554	S	***1955.8586***	978.4329	1938.8320	969.9197	1937.8480	969.4277	18
7	752.3461	376.6767			734.3355	367.6714	S	***1868.8266***	934.9169	1851.8000	926.4036	1850.8160	925.9116	17
8	912.3768	456.6920			894.3662	447.6867	C	***1781.7945***	891.4009	1764.7680	882.8876	1763.7840	882.3956	16
9	1009.4295	505.2184			991.4190	496.2131	P	***1621.7639***	811.3856	1604.7373	802.8723	1603.7533	802.3803	15
10	1066.4510	533.7291			1048.4404	524.7238	G	1524.7111	762.8592	1507.6846	754.3459	1506.7006	753.8539	14
11	1123.4725	562.2399			1105.4619	553.2346	G	***1467.6897***	734.3485	1450.6631	725.8352	1449.6791	725.3432	13
12	1236.5565	618.7819			1218.5459	609.7766	I	***1410.6682***	705.8377	1393.6416	697.3245	1392.6576	696.8325	12
13	1367.5970	684.3021			1349.5864	675.2969	M	***1297.5841***	649.2957	1280.5576	640.7824	1279.5736	640.2904	11
14	1480.6811	740.8442			1462.6705	731.8389	L	***1166.5436***	583.7755	1149.5171	575.2622	1148.5331	574.7702	10
15	1595.7080	798.3576	1578.6815	789.8444	1577.6974	789.3524	N	***1053.4596***	527.2334	1036.4330	518.7202	1035.4490	518.2281	9
16	1724.7506	862.8789	1707.7241	854.3657	1706.7400	853.8737	E	***938.4326***	469.7200	921.4061	461.2067	920.4221	460.7147	8
17	1825.7983	913.4028	1808.7717	904.8895	1807.7877	904.3975	T	***809.3900***	405.1987	792.3635	396.6854	791.3795	396.1934	7
18	1882.8197	941.9135	1865.7932	933.4002	1864.8092	932.9082	G	***708.3424***	354.6748	691.3158	346.1615			6
19	2010.8783	1005.9428	1993.8518	997.4295	1992.8678	996.9375	Q	***651.3209***	326.1641	634.2944	317.6508			5
20	2067.8998	1034.4535	2050.8732	1025.9403	2049.8892	1025.4482	G	***523.2623***	262.1348	506.2358	253.6215			4
21	2230.9631	1115.9852	2213.9366	1107.4719	2212.9525	1106.9799	Y	466.2409	233.6241	449.2143	225.1108			3
22	2359.0217	1180.0145	2341.9951	1171.5012	2341.0111	1171.0092	Q	303.1775	152.0924	286.1510	143.5791			2
23							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TELFSSSCPGGIMLNETGQGYQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
127.1	2532.1261	0.0059	TELFSSSCPGGIMLNETGQGYQR	Deamidated N15 99.98%
89.8	2532.1261	0.0059	TELFSSSCPGGIMLNETGQGYQR	Deamidated Q19 0.02%
75.8	2532.1261	0.0059	TELFSSSCPGGIMLNETGQGYQR	Deamidated Q22 0.00%
3.4	2532.1334	-0.0014	GMDTYIEIARMLCNIAESWNK	
2.5	2530.1169	2.0151	LGKADETKDEQFEQCVQNFNK	
2.5	2530.1169	2.0151	LGKADETKDEQFEQCVQNFNK	

Mascot: http://www.matrixscience.com/

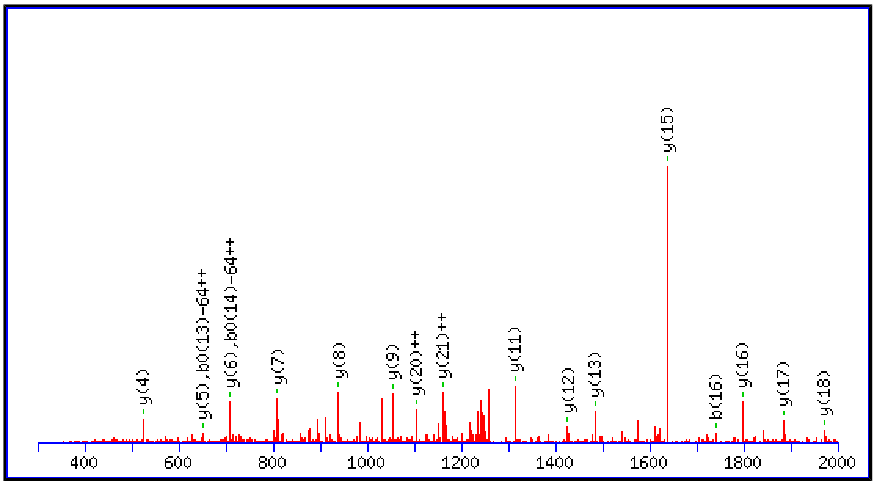
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TELFSSSCPGGIMLNETGQGYQR**
Found in **O95445** in **con_Xuniprot_HUMAN3**, APOM_HUMAN Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

Match to Query 21917: 2548.131548 from(1275.073050,2+) intensity(25419.6875) rtinseconds(1533) scans(3716) index(23213)
Title: 111019_Est_MI_YS_G_04Spectrum3183_scans__3716
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

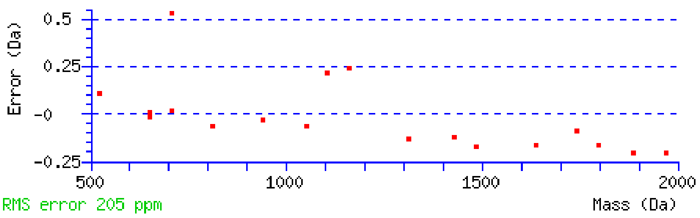
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

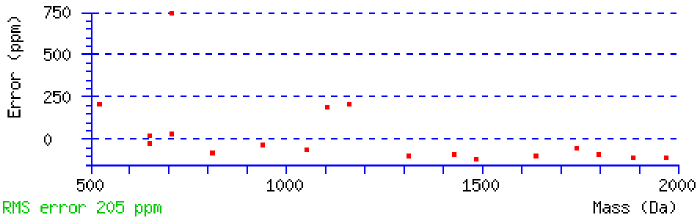


Monoisotopic mass of neutral peptide Mr(calc): 2548.1210
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N15 : Deamidated (NQ)
Ions Score: 120 **Expect:** 1.2e-010
Matches : 18/352 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	102.0550	51.5311			84.0444	42.5258	T							23
2	231.0975	116.0524			213.0870	107.0471	E	2448.0806	1224.5439	2431.0541	1216.0307	2430.0700	1215.5387	22
3	344.1816	172.5944			326.1710	163.5892	L	2319.0380	1160.0226	2302.0115	1151.5094	2301.0274	1151.0174	21
4	491.2500	246.1287			473.2395	237.1234	F	2205.9539	1103.4806	2188.9274	1094.9673	2187.9434	1094.4753	20
5	578.2821	289.6447			560.2715	280.6394	S	2058.8855	1029.9464	2041.8590	1021.4331	2040.8750	1020.9411	19
6	665.3141	333.1607			647.3035	324.1554	S	***1971.8535***	986.4304	1954.8270	977.9171	1953.8429	977.4251	18
7	752.3461	376.6767			734.3355	367.6714	S	***1884.8215***	942.9144	1867.7949	934.4011	1866.8109	933.9091	17
8	912.3768	456.6920			894.3662	447.6867	C	***1797.7894***	899.3984	1780.7629	890.8851	1779.7789	890.3931	16
9	1009.4295	505.2184			991.4190	496.2131	P	***1637.7588***	819.3830	1620.7323	810.8698	1619.7482	810.3778	15
10	1066.4510	533.7291			1048.4404	524.7238	G	1540.7060	770.8567	1523.6795	762.3434	1522.6955	761.8514	14
11	1123.4725	562.2399			1105.4619	553.2346	G	***1483.6846***	742.3459	1466.6580	733.8326	1465.6740	733.3406	13
12	1236.5565	618.7819			1218.5459	609.7766	I	***1426.6631***	713.8352	1409.6366	705.3219	1408.6525	704.8299	12
13	1383.5919	692.2996			1365.5813	683.2943	M	***1313.5790***	657.2932	1296.5525	648.7799	1295.5685	648.2879	11
14	1496.6760	748.8416			1478.6654	739.8363	L	1166.5436	583.7755	1149.5171	575.2622	1148.5331	574.7702	10
15	1611.7029	806.3551	1594.6764	797.8418	1593.6924	797.3498	N	***1053.4596***	527.2334	1036.4330	518.7202	1035.4490	518.2281	9
16	1740.7455	870.8764	1723.7190	862.3631	1722.7349	861.8711	E	***938.4326***	469.7200	921.4061	461.2067	920.4221	460.7147	8
17	1841.7932	921.4002	1824.7666	912.8870	1823.7826	912.3950	T	***809.3900***	405.1987	792.3635	396.6854	791.3795	396.1934	7
18	1898.8147	949.9110	1881.7881	941.3977	1880.8041	940.9057	G	***708.3424***	354.6748	691.3158	346.1615			6
19	2026.8732	1013.9403	2009.8467	1005.4270	2008.8627	1004.9350	Q	***651.3209***	326.1641	634.2944	317.6508			5
20	2083.8947	1042.4510	2066.8682	1033.9377	2065.8841	1033.4457	G	***523.2623***	262.1348	506.2358	253.6215			4
21	2246.9580	1123.9827	2229.9315	1115.4694	2228.9475	1114.9774	Y	466.2409	233.6241	449.2143	225.1108			3
22	2375.0166	1188.0119	2357.9901	1179.4987	2357.0060	1179.0067	Q	303.1775	152.0924	286.1510	143.5791			2

23							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TELFSSSCPGGIMLNETGQGYQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
119.8	2548.1210	0.0105	TELFSSSCPGGIMLNETGQGYQR	Deamidated N15 99.98%
80.8	2548.1210	0.0105	TELFSSSCPGGIMLNETGQGYQR	Deamidated Q19 0.01%
77.8	2548.1210	0.0105	TELFSSSCPGGIMLNETGQGYQR	Deamidated Q22 0.01%
32.8	2547.1370	0.9946	TELFSSSCPGGIMLNETGQGYQR	
2.0	2548.1283	0.0032	GMDTYIEIARMLCNIAESWNK	
1.3	2548.1235	0.0081	NTVCPEQSEALAGGSAGDGAQAAGVTK	
1.2	2548.1371	-0.0056	FFNIQGHAFGIMPEMMAMQKR	
1.2	2548.1371	-0.0056	FFNIQGHAFGIMPEMMAMQKR	

Mascot: http://www.matrixscience.com/

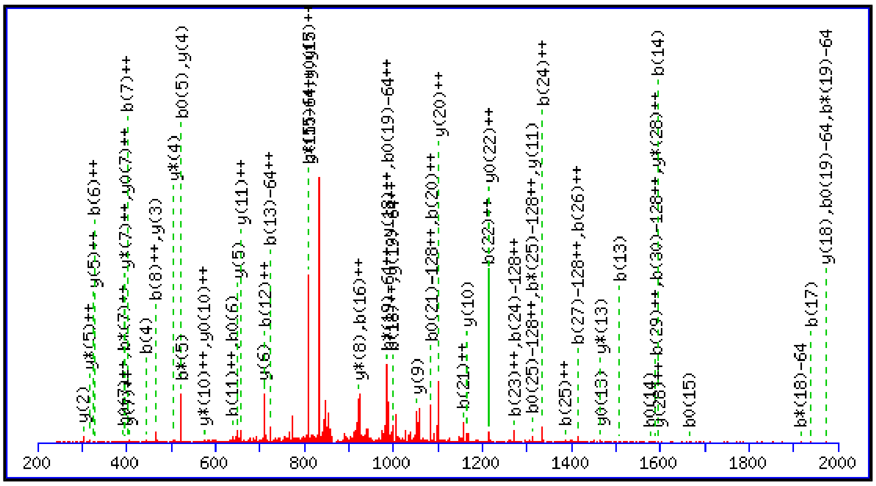
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEGRPDMKTELFSSSCPGGIMLNETGQGYQR**
Found in **O95445** in **con_Xuniprot_HUMAN3**, APOM_HUMAN Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2

Match to Query 27786: 3478.554176 from(870.645820,4+) intensity(23090.9902) rtinseconds(1232) scans(3123) index(23868)
Title: 111019_Est_MI_YS_G_05Spectrum2679_scans__3123
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

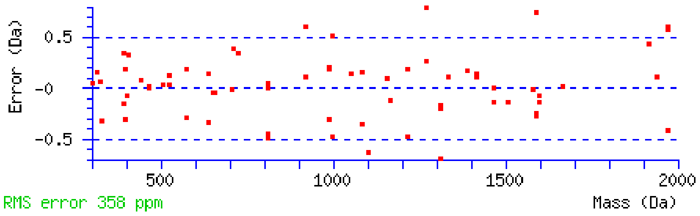
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

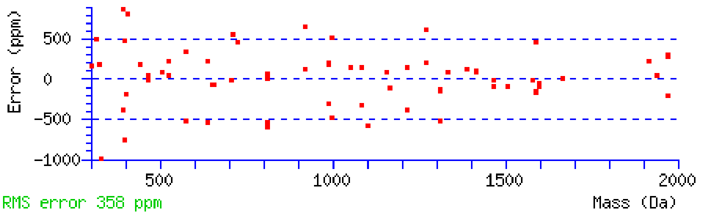


Monoisotopic mass of neutral peptide Mr(calc): 3478.5439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M21 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N23 : Deamidated (NQ)
Ions Score: 58 **Expect:** 0.00024
Matches : 69/606 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**31**
2	231.0975	116.0524			213.0870	107.0471	**E**	3378.5035	1689.7554	3361.4770	1681.2421	3360.4930	1680.7501	**30**
3	288.1190	144.5631			270.1084	135.5579	**G**	3249.4609	1625.2341	3232.4344	1616.7208	3231.4504	1616.2288	**29**
4	**444.2201**	222.6137	427.1936	214.1004	426.2096	213.6084	**R**	3192.4395	1596.7234	3175.4129	1588.2101	3174.4289	1587.7181	**28**
5	541.2729	271.1401	524.2463	262.6268	523.2623	262.1348	**P**	3036.3384	1518.6728	3019.3118	1510.1595	3018.3278	1509.6675	**27**
6	656.2998	***328.6536***	639.2733	320.1403	638.2893	319.6483	**D**	2939.2856	1470.1464	2922.2590	1461.6332	2921.2750	1461.1411	**26**
7	803.3352	***402.1713***	786.3087	393.6580	785.3247	393.1660	**M**	2824.2586	1412.6330	2807.2321	1404.1197	2806.2481	1403.6277	**25**
8	931.4302	***466.2187***	914.4036	457.7055	913.4196	457.2135	**K**	2677.2232	1339.1153	2660.1967	1330.6020	2659.2127	1330.1100	**24**
9	1032.4779	516.7426	1015.4513	508.2293	1014.4673	507.7373	**T**	2549.1283	1275.0678	2532.1017	1266.5545	2531.1177	1266.0625	**23**
10	1161.5205	581.2639	1144.4939	572.7506	1143.5099	572.2586	**E**	2448.0806	1224.5439	2431.0541	1216.0307	2430.0700	1215.5387	**22**
11	1274.6045	***637.8059***	1257.5780	629.2926	1256.5940	628.8006	**L**	2319.0380	1160.0226	2302.0115	1151.5094	2301.0274	1151.0174	**21**
12	1421.6729	***711.3401***	1404.6464	702.8268	1403.6624	702.3348	**F**	2205.9539	1103.4806	2188.9274	1094.9673	2187.9434	1094.4753	**20**
13	**1508.7050**	754.8561	1491.6784	746.3428	1490.6944	745.8508	**S**	2058.8855	1029.9464	2041.8590	1021.4331	2040.8750	1020.9411	**19**
14	**1595.7370**	798.3721	1578.7105	789.8589	1577.7264	789.3669	**S**	**1971.8535**	986.4304	1954.8270	977.9171	1953.8429	977.4251	**18**
15	1682.7690	841.8882	1665.7425	833.3749	1664.7585	832.8829	**S**	1884.8215	942.9144	1867.7949	934.4011	1866.8109	933.9091	**17**
16	1842.7997	***921.9035***	1825.7731	913.3902	1824.7891	912.8982	**C**	1797.7894	899.3984	1780.7629	890.8851	1779.7789	890.3931	**16**
17	**1939.8524**	970.4299	1922.8259	961.9166	1921.8419	961.4246	**P**	1637.7588	819.3830	1620.7323	810.8698	1619.7482	810.3778	**15**
18	1996.8739	***998.9406***	1979.8474	990.4273	1978.8633	989.9353	**G**	1540.7060	770.8567	1523.6795	762.3434	1522.6955	761.8514	**14**
19	2053.8954	1027.4513	2036.8688	1018.9380	2035.8848	1018.4460	**G**	1483.6846	742.3459	1466.6580	733.8326	1465.6740	733.3406	**13**
20	2166.9794	***1083.9934***	2149.9529	1075.4801	2148.9689	1074.9881	**I**	1426.6631	713.8352	1409.6366	705.3219	1408.6525	704.8299	**12**
21	2314.0148	***1157.5111***	2296.9883	1148.9978	2296.0043	1148.5058	**M**	**1313.5790**	657.2932	1296.5525	648.7799	1295.5685	648.2879	**11**
22	2427.0989	***1214.0531***	2410.0723	1205.5398	2409.0883	1205.0478	**L**	**1166.5436**	583.7755	1149.5171	575.2622	1148.5331	574.7702	**10**

23	2542.1258	***1271.5666***	2525.0993	1263.0533	2524.1153	1262.5613	**N**	**1053.4596**	527.2334	1036.4330	518.7202	1035.4490	518.2281	**9**
24	2671.1684	***1336.0879***	2654.1419	1327.5746	2653.1579	1327.0826	**E**	938.4326	469.7200	921.4061	461.2067	920.4221	460.7147	**8**
25	2772.2161	***1386.6117***	2755.1896	1378.0984	2754.2055	1377.6064	**T**	**809.3900**	405.1987	792.3635	396.6854	791.3795	396.1934	**7**
26	2829.2376	***1415.1224***	2812.2110	1406.6092	2811.2270	1406.1171	**G**	**708.3424**	354.6748	691.3158	346.1615			**6**
27	2957.2962	1479.1517	2940.2696	1470.6384	2939.2856	1470.1464	**Q**	**651.3209**	326.1641	634.2944	317.6508			**5**
28	3014.3176	1507.6624	2997.2911	1499.1492	2996.3071	1498.6572	**G**	**523.2623**	262.1348	506.2358	253.6215			**4**
29	3177.3809	***1589.1941***	3160.3544	1580.6808	3159.3704	1580.1888	**Y**	**466.2409**	233.6241	449.2143	225.1108			**3**
30	3305.4395	1653.2234	3288.4130	1644.7101	3287.4290	1644.2181	**Q**	**303.1775**	152.0924	286.1510	143.5791			**2**
31							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of TEGRPDMKTELFSSSCPGGIMLNETGQGYQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
57.6	3478.5439	0.0103	TEGRPDMKTELFSSSCPGGIMLNETGQGYQR	Deamidated N23 40.28%
56.3	3478.5439	0.0103	TEGRPDMKTELFSSSCPGGIMLNETGQGYQR	Deamidated Q27 30.00%
56.3	3478.5439	0.0103	TEGRPDMKTELFSSSCPGGIMLNETGQGYQR	Deamidated Q30 29.72%
54.4	3477.5599	0.9943	TEGRPDMKTELFSSSCPGGIMLNETGQGYQR	
7.3	3476.5421	2.0120	GMQESEEKNYSAPSIKCASTLDVFTNCPPAK	
4.0	3476.5421	2.0120	GMQESEEKNYSAPSIKCASTLDVFTNCPPAK	
3.6	3476.5421	2.0120	GMQESEEKNYSAPSIKCASTLDVFTNCPPAK	
2.7	3478.5657	-0.0115	DYQILCGNQAPGFLTDIHTGKPLDVDECGSR	
2.7	3478.5657	-0.0115	NYQILCGNQAPGFLTDIHTGKPLDVDECGSR	
2.6	3477.5673	0.9869	YHSCDVMQKTQKACEIGQLHEPQTLGMLR	

Mascot: http://www.matrixscience.com/

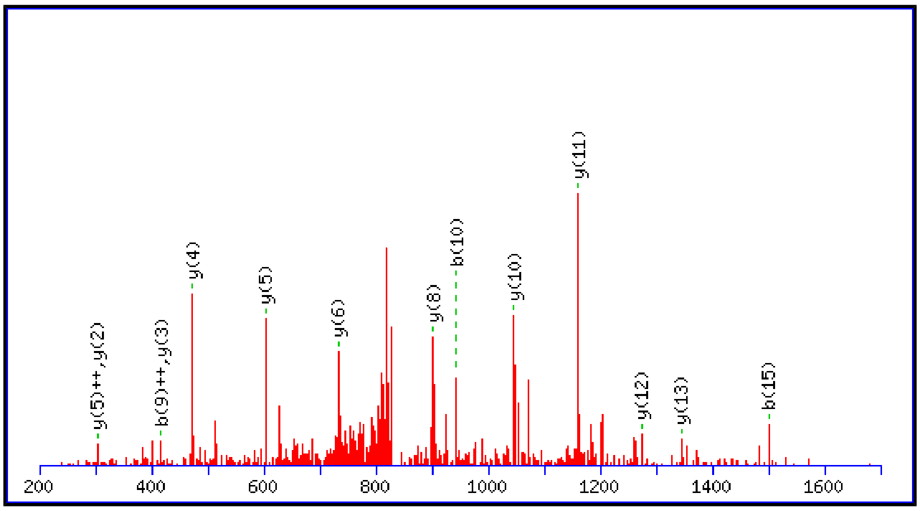
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEAINGSGLQMGLQR**
Found in **P09172** in **con_Xuniprot_HUMAN3**, DOPO_HUMAN Dopamine beta-hydroxylase OS=Homo sapiens GN=DBH PE=1 SV=3

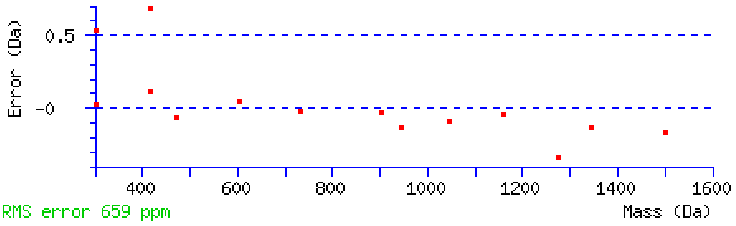
Match to Query 8437: 1673.845548 from(837.930050,2+) intensity(7584.5684) rtinseconds(1676) scans(3689) index(28455)
Title: 111019_Est_MI_YS_G_13Spectrum3206_scans__3689
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

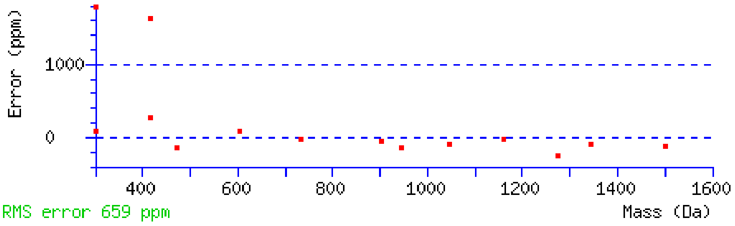
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1673.8406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 98 **Expect:** 4.1e-008
Matches : 14/154 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**16**
2	201.1234	101.0653			183.1128	92.0600	**L**	1587.8159	794.4116	1570.7894	785.8983	1569.8054	785.4063	**15**
3	330.1660	165.5866			312.1554	156.5813	**E**	1474.7319	737.8696	1457.7053	729.3563	1456.7213	728.8643	**14**
4	401.2031	201.1052			383.1925	192.0999	**A**	***1345.6893***	673.3483	1328.6627	664.8350	1327.6787	664.3430	**13**
5	514.2871	257.6472			496.2766	248.6419	**I**	***1274.6521***	637.8297	1257.6256	629.3164	1256.6416	628.8244	**12**
6	629.3141	315.1607	612.2875	306.6474	611.3035	306.1554	**N**	***1161.5681***	581.2877	1144.5415	572.7744	1143.5575	572.2824	**11**
7	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	**G**	***1046.5411***	523.7742	1029.5146	515.2609	1028.5306	514.7689	**10**
8	773.3676	387.1874	756.3410	378.6742	755.3570	378.1821	**S**	989.5197	495.2635	972.4931	486.7502	971.5091	486.2582	**9**
9	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	**G**	***902.4876***	451.7475	885.4611	443.2342			**8**
10	**943.4731**	472.2402	926.4466	463.7269	925.4625	463.2349	**L**	845.4662	423.2367	828.4396	414.7235			**7**
11	1071.5317	536.2695	1054.5051	527.7562	1053.5211	527.2642	**Q**	***732.3821***	366.6947	715.3556	358.1814			**6**
12	1202.5722	601.7897	1185.5456	593.2764	1184.5616	592.7844	**M**	***604.3235***	302.6654	587.2970	294.1521			**5**
13	1259.5936	630.3005	1242.5671	621.7872	1241.5831	621.2952	**G**	***473.2831***	237.1452	456.2565	228.6319			**4**
14	1372.6777	686.8425	1355.6511	678.3292	1354.6671	677.8372	**L**	***416.2616***	208.6344	399.2350	200.1212			**3**
15	**1500.7363**	750.8718	1483.7097	742.3585	1482.7257	741.8665	**Q**	***303.1775***	152.0924	286.1510	143.5791			**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SLEAINGSGLQMGLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
98.1	1673.8406	0.0049	SLEAINGSGLQMGLQR	Deamidated N6 99.99%
59.6	1673.8406	0.0049	SLEAINGSGLQMGLQR	Deamidated Q11 0.01%
39.6	1673.8406	0.0049	SLEAINGSGLQMGLQR	Deamidated Q15 0.00%
7.4	1673.8413	0.0042	DFNIKLSDFGFSKR	
6.9	1673.8481	-0.0025	LQLIAMDLPMVSGDR	
6.1	1673.8472	-0.0016	DVDAEREKITQEIK	
5.7	1673.8373	0.0083	SASNTAAEFGEPLPKR	
5.5	1671.8362	2.0093	KATLGPTGEGEPRGMR	
5.3	1673.8519	-0.0063	EVTGSIQLCRDAGIR	
5.1	1673.8447	0.0009	MVFIPSGPVEAQVQR	

Mascot: http://www.matrixscience.com/

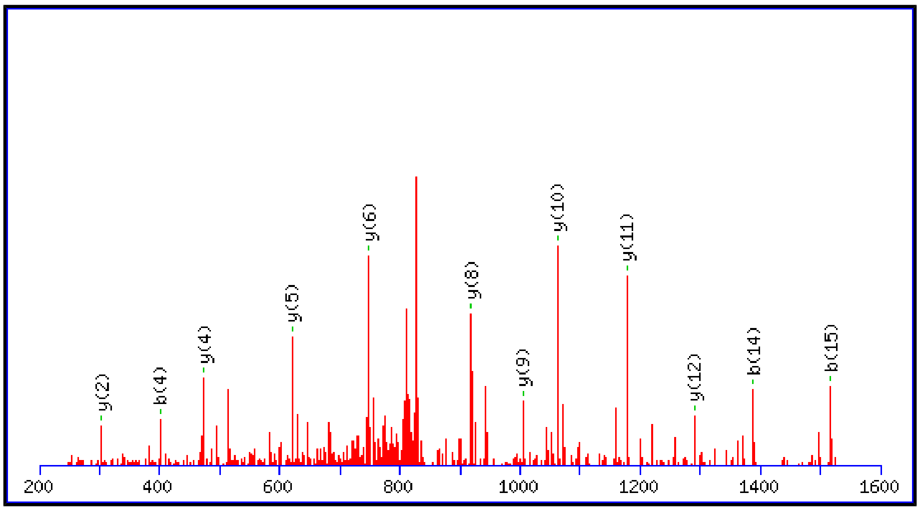
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLEAINGSGLQMGLQR**
Found in **P09172** in **con_Xuniprot_HUMAN3**, DOPO_HUMAN Dopamine beta-hydroxylase OS=Homo sapiens GN=DBH PE=1 SV=3

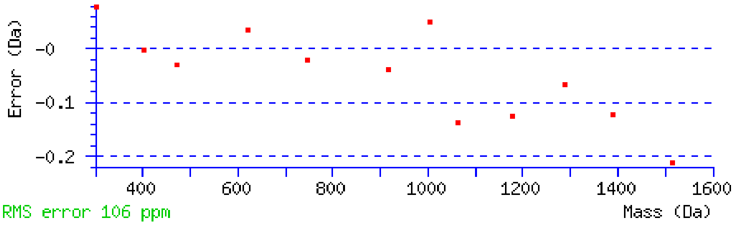
Match to Query 8703: 1689.842068 from(845.928310,2+) intensity(7863.5850) rtinseconds(1252) scans(2582) index(7593)
Title: 111019_Est_ISCardio_NMI_YP_G_12Spectrum2212_scans__2582
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

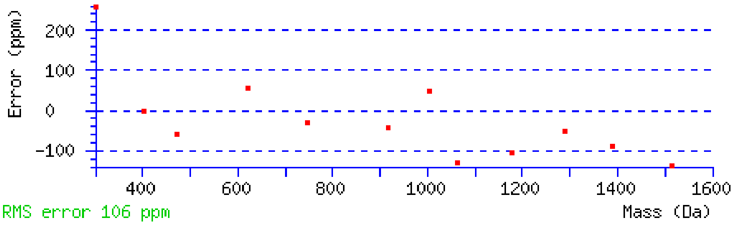
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1689.8356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 91 **Expect:** 1.9e-007
Matches : 12/236 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**16**
2	201.1234	101.0653			183.1128	92.0600	**L**	1603.8108	802.4091	1586.7843	793.8958	1585.8003	793.4038	**15**
3	330.1660	165.5866			312.1554	156.5813	**E**	1490.7268	745.8670	1473.7002	737.3537	1472.7162	736.8617	**14**
4	**401.2031**	201.1052			383.1925	192.0999	**A**	1361.6842	681.3457	1344.6576	672.8325	1343.6736	672.3404	**13**
5	514.2871	257.6472			496.2766	248.6419	**I**	***1290.6471***	645.8272	1273.6205	637.3139	1272.6365	636.8219	**12**
6	629.3141	315.1607	612.2875	306.6474	611.3035	306.1554	**N**	***1177.5630***	589.2851	1160.5364	580.7719	1159.5524	580.2799	**11**
7	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	**G**	***1062.5361***	531.7717	1045.5095	523.2584	1044.5255	522.7664	**10**
8	773.3676	387.1874	756.3410	378.6742	755.3570	378.1821	**S**	***1005.5146***	503.2609	988.4880	494.7477	987.5040	494.2557	**9**
9	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	**G**	***918.4826***	459.7449	901.4560	451.2316			**8**
10	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	**L**	861.4611	431.2342	844.4346	422.7209			**7**
11	1071.5317	536.2695	1054.5051	527.7562	1053.5211	527.2642	**Q**	***748.3770***	374.6922	731.3505	366.1789			**6**
12	1218.5671	609.7872	1201.5405	601.2739	1200.5565	600.7819	**M**	***620.3185***	310.6629	603.2919	302.1496			**5**
13	1275.5885	638.2979	1258.5620	629.7846	1257.5780	629.2926	**G**	***473.2831***	237.1452	456.2565	228.6319			**4**
14	**1388.6726**	694.8399	1371.6461	686.3267	1370.6620	685.8347	**L**	416.2616	208.6344	399.2350	200.1212			**3**
15	**1516.7312**	758.8692	1499.7046	750.3560	1498.7206	749.8639	**Q**	***303.1775***	152.0924	286.1510	143.5791			**2**
16							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SLEAINGSGLQMGLQR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
91.3	1689.8356	0.0065	SLEAINGSGLQMGLQR	Deamidated N6 99.99%
50.6	1689.8356	0.0065	SLEAINGSGLQMGLQR	Deamidated Q11 0.01%
37.3	1689.8356	0.0065	SLEAINGSGLQMGLQR	Deamidated Q15 0.00%
10.3	1689.8396	0.0025	AQALMEQYVAALPER	
10.3	1689.8396	0.0025	AQALMEQYVAALPER	
9.2	1688.8318	1.0103	CGWGPFGRSERKPR	
9.1	1689.8355	0.0065	RQLETDELSLAMQR	
6.5	1689.8434	-0.0013	TLQGPSVHNLHNSKR	
5.1	1689.8355	0.0065	NQRIQELIDEMRK	
4.6	1687.8318	2.0102	GDKGNPGWPGAPGVPGPK	

Mascot: http://www.matrixscience.com/

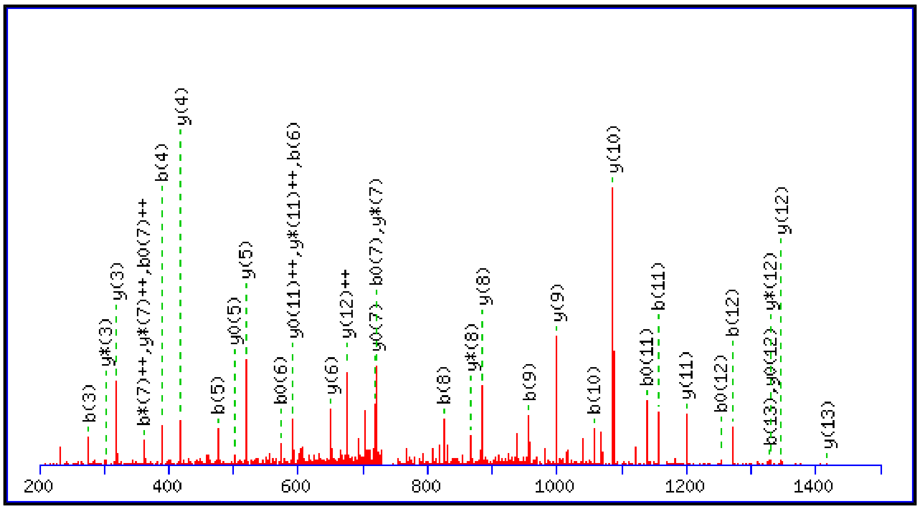
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFISNFSMTVDGK**
Found in **P19823** in **con_Xuniprot_HUMAN3**, ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

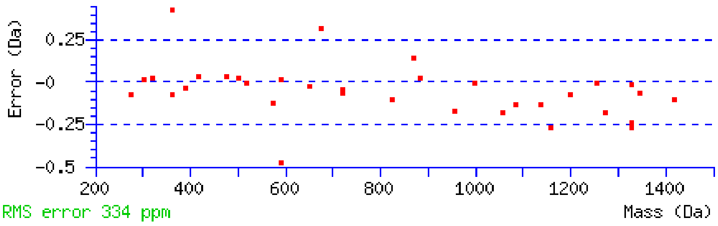
Match to Query 6477: 1473.685488 from(737.850020,2+) intensity(209025.8438) rtinseconds(1778) scans(4524) index(1355)
Title: 111019_Est_ISCardio_NMI_YP_G_3Spectrum3942_scans__4524
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

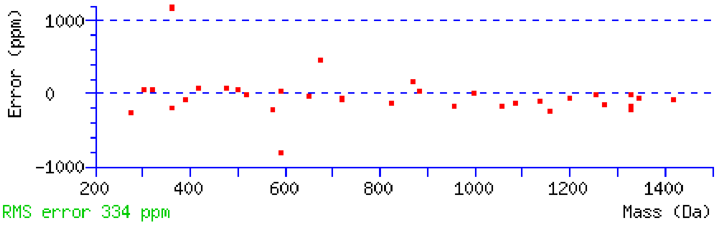
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1473.6810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 100 **Expect:** 1.3e-008
Matches : 37/134 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	58.0287	29.5180					G							14
2	129.0659	65.0366					A	***1417.6668***	709.3370	1400.6402	700.8238	1399.6562	700.3318	13
3	***276.1343***	138.5708					F	***1346.6297***	673.8185	1329.6031	665.3052	1328.6191	664.8132	12
4	***389.2183***	195.1128					I	***1199.5613***	600.2843	1182.5347	591.7710	1181.5507	591.2790	11
5	***476.2504***	238.6288			458.2398	229.6235	S	***1086.4772***	543.7422	1069.4507	535.2290	1068.4666	534.7370	10
6	***591.2773***	296.1423	574.2508	287.6290	573.2667	287.1370	N	***999.4452***	500.2262	982.4186	491.7130	981.4346	491.2209	9
7	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	F	***884.4182***	442.7128	867.3917	434.1995	866.4077	433.7075	8
8	***825.3777***	413.1925	808.3512	404.6792	807.3672	404.1872	S	737.3498	369.1785	720.3233	360.6653	719.3393	360.1733	7
9	***956.4182***	478.7128	939.3917	470.1995	938.4077	469.7075	M	***650.3178***	325.6625	633.2912	317.1493	632.3072	316.6573	6
10	***1057.4659***	529.2366	1040.4394	520.7233	1039.4553	520.2313	T	***519.2773***	260.1423	502.2508	251.6290	501.2667	251.1370	5
11	***1156.5343***	578.7708	1139.5078	570.2575	1138.5238	569.7655	V	***418.2296***	209.6185	401.2031	201.1052	400.2191	200.6132	4
12	***1271.5613***	636.2843	1254.5347	627.7710	1253.5507	627.2790	D	***319.1612***	160.0842	302.1347	151.5710	301.1506	151.0790	3
13	***1328.5827***	664.7950	1311.5562	656.2817	1310.5722	655.7897	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GAFISNFSMTVDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
100.1	1473.6810	0.0045	GAFISNFSMTVDGK
11.8	1473.6823	0.0032	HYGPGWVSMANAGK
5.2	1472.6752	1.0103	CDICATHLNQLK
4.8	1473.6922	-0.0067	GNGNFTLHPMLEK
4.8	1473.6922	-0.0067	GNGNFTLHPMLEK
4.8	1473.6843	0.0012	CNNEAILSPMPVK
4.4	1471.6790	2.0065	NSADYSSESKKQK
4.2	1473.6922	-0.0067	ELMPHLTFNGNGK
4.0	1473.6834	0.0021	NKEGPQVSENLQK
3.9	1473.6922	-0.0067	ELMPHLTFNGNGK

Mascot: http://www.matrixscience.com/

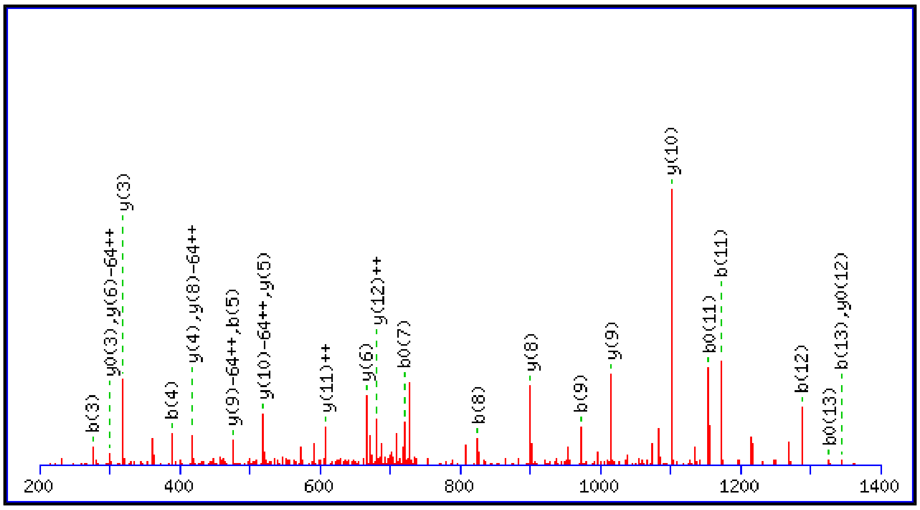
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFISNFSMTVDGK**
Found in **P19823** in **con_Xuniprot_HUMAN3**, ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

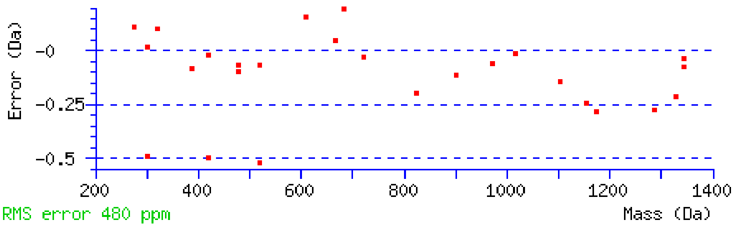
Match to Query 6724: 1489.678748 from(745.846650,2+) intensity(25581.0605) rtinseconds(1598) scans(2798) index(13830)
Title: 111019_Est_MI_200000g_G_08Spectrum2282_scans__2798
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

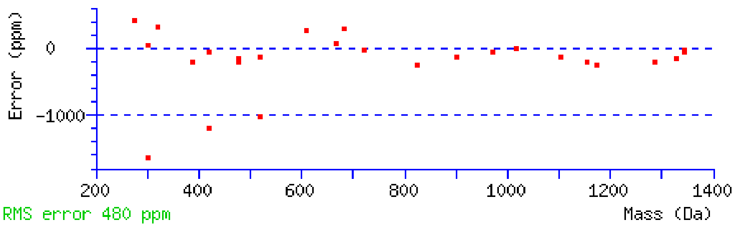
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1489.6759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 83 **Expect:** 5.6e-007
Matches : 26/212 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	58.0287	29.5180					G							14
2	129.0659	65.0366					A	1433.6617	717.3345	1416.6352	708.8212	1415.6511	708.3292	13
3	***276.1343***	138.5708					F	1362.6246	681.8159	1345.5980	673.3027	1344.6140	672.8107	12
4	***389.2183***	195.1128					I	1215.5562	608.2817	1198.5296	599.7685	1197.5456	599.2764	11
5	***476.2504***	238.6288			458.2398	229.6235	S	***1102.4721***	551.7397	1085.4456	543.2264	1084.4616	542.7344	10
6	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	N	***1015.4401***	508.2237	998.4135	499.7104	997.4295	499.2184	9
7	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	F	***900.4131***	450.7102	883.3866	442.1969	882.4026	441.7049	8
8	***825.3777***	413.1925	808.3512	404.6792	807.3672	404.1872	S	753.3447	377.1760	736.3182	368.6627	735.3342	368.1707	7
9	***972.4131***	486.7102	955.3866	478.1969	954.4026	477.7049	M	***666.3127***	333.6600	649.2862	325.1467	648.3021	324.6547	6
10	1073.4608	537.2340	1056.4343	528.7208	1055.4503	528.2288	T	***519.2773***	260.1423	502.2508	251.6290	501.2667	251.1370	5
11	***1172.5292***	586.7683	1155.5027	578.2550	1154.5187	577.7630	V	***418.2296***	209.6185	401.2031	201.1052	400.2191	200.6132	4
12	***1287.5562***	644.2817	1270.5296	635.7685	1269.5456	635.2764	D	***319.1612***	160.0842	302.1347	151.5710	301.1506	151.0790	3
13	***1344.5776***	672.7925	1327.5511	664.2792	1326.5671	663.7872	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of GAFISNFSMTVDGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
83.0	1489.6759	0.0028	GAFISNFSMTVDGK
12.1	1489.6718	0.0069	QEAEQAIQCLNGK
11.1	1489.6718	0.0069	QEAEQAIQCLNGK
8.4	1489.6718	0.0069	QEAEQAIQCLNGK
8.4	1489.6759	0.0028	QMTTFDEFTLTR
6.8	1489.6772	0.0015	HYGPGWVSMANAGK
6.7	1488.6732	1.0055	YGQIQGNPEEPEK
6.7	1489.6718	0.0069	QEAEQAIQCLNGK
5.6	1489.6718	0.0069	QEAEQAIQCLNGK
3.0	1489.6792	-0.0005	CNNEAILSPMPVK

Mascot: http://www.matrixscience.com/

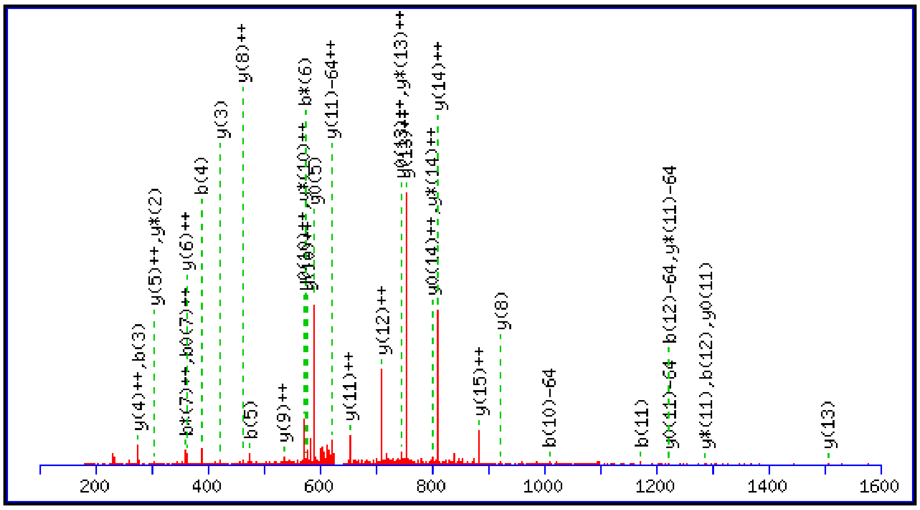
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GAFISNFSMTVDGKTFR**
Found in **P19823** in **con_Xuniprot_HUMAN3**, ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

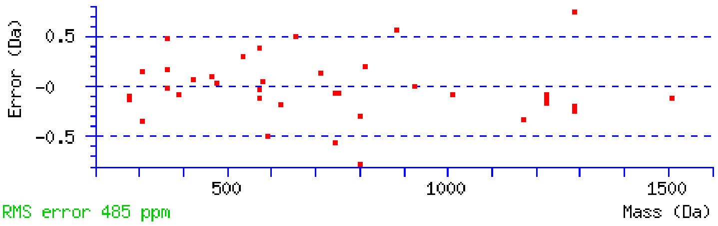
Match to Query 11275: 1893.895542 from(632.305790,3+) intensity(31405.6621) rtinseconds(1679) scans(3940) index(8898)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum3367_scans__3940
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

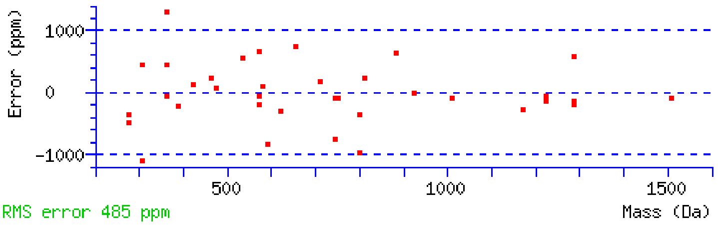
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1893.8931
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 64 **Expect:** 7.8e-005
Matches : 37/266 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	58.0287	29.5180					G							17
2	129.0659	65.0366					A	1837.8789	919.4431	1820.8524	910.9298	1819.8683	910.4378	16
3	**276.1343**	138.5708					F	1766.8418	883.9245	1749.8153	875.4113	1748.8312	874.9193	15
4	**389.2183**	195.1128					I	1619.7734	810.3903	1602.7468	801.8771	1601.7628	801.3850	14
5	**476.2504**	238.6288			458.2398	229.6235	S	**1506.6893**	753.8483	1489.6628	745.3350	1488.6788	744.8430	13
6	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	N	1419.6573	710.3323	1402.6307	701.8190	1401.6467	701.3270	12
7	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	F	1304.6304	652.8188	1287.6038	644.3055	1286.6198	643.8135	11
8	825.3777	413.1925	808.3512	404.6792	807.3672	404.1872	S	1157.5619	579.2846	1140.5354	570.7713	1139.5514	570.2793	10
9	972.4131	486.7102	955.3866	478.1969	954.4026	477.7049	M	1070.5299	535.7686	1053.5034	527.2553	1052.5193	526.7633	9
10	1073.4608	537.2340	1056.4343	528.7208	1055.4503	528.2288	T	**923.4945**	462.2509	906.4680	453.7376	905.4839	453.2456	8
11	**1172.5292**	586.7683	1155.5027	578.2550	1154.5187	577.7630	V	822.4468	411.7271	805.4203	403.2138	804.4363	402.7218	7
12	**1287.5562**	644.2817	1270.5296	635.7685	1269.5456	635.2764	D	723.3784	362.1928	706.3519	353.6796	705.3679	353.1876	6
13	1344.5776	672.7925	1327.5511	664.2792	1326.5671	663.7872	G	608.3515	304.6794	591.3249	296.1661	590.3409	295.6741	5
14	1472.6726	736.8399	1455.6461	728.3267	1454.6620	727.8347	K	551.3300	276.1686	534.3035	267.6554	533.3194	267.1634	4
15	1573.7203	787.3638	1556.6937	778.8505	1555.7097	778.3585	T	**423.2350**	212.1212	406.2085	203.6079	405.2245	203.1159	3
16	1720.7887	860.8980	1703.7622	852.3847	1702.7781	851.8927	F	322.1874	161.5973	305.1608	153.0840			2
17							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GAFISNFSMTVDGKTFR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
64.4	1893.8931	0.0024	GAFISNFSMTVDGKTFR
13.9	1893.8859	0.0096	DCLCAKCTLIAERQR
10.5	1893.8951	0.0004	ELTMNDMLTQVQVLEK
9.8	1893.9037	-0.0081	MKLISNGGDSAVEMDRR
8.6	1893.8899	0.0056	MMVNNYRPLQPLMNR
8.1	1892.8859	1.0096	LSGSHAMEMSQLLSELK
7.6	1893.8924	0.0031	ASCVNAMEGKKLAQDVR
6.9	1893.8989	-0.0034	KQMVSAQETINQQITR
5.2	1892.8851	1.0104	GQSTVGTEVTSQVDNLQK
5.2	1892.8972	0.9984	GKSDLPCSSMNLAQIQK

Mascot: http://www.matrixscience.com/

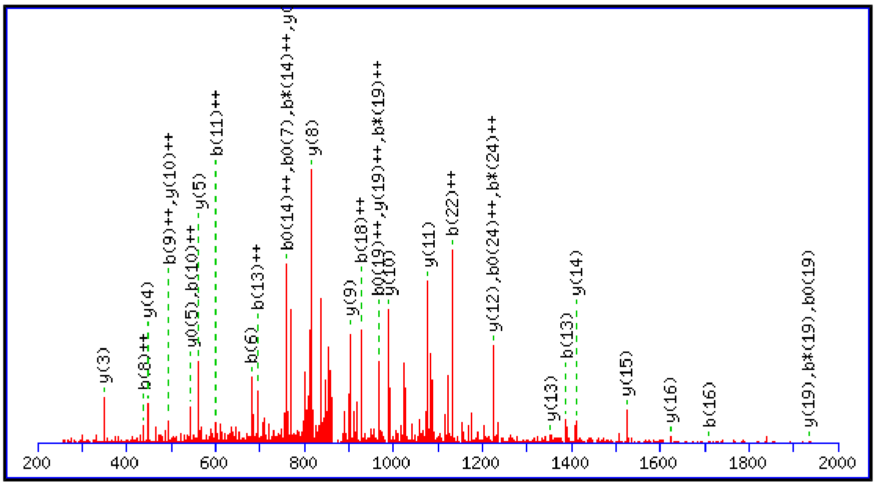
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGHCPDPVLVNGEFSSSGPVNVSDK**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

Match to Query 22237: 2611.229682 from(871.417170,3+) intensity(46794.3828) rtinseconds(1191) scans(2996) index(6320)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum2639_scans__2996
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

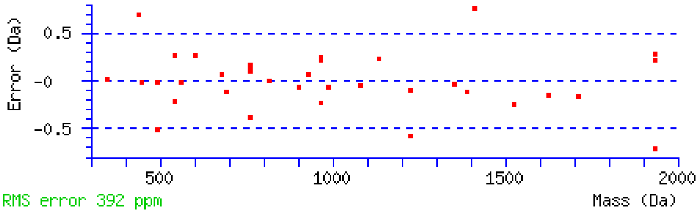
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

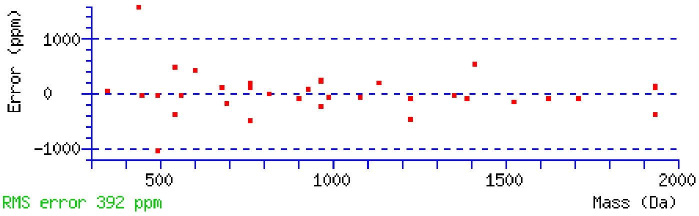


Monoisotopic mass of neutral peptide Mr(calc): 2611.2225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N21 : Deamidated (NQ)
Ions Score: 109 **Expect:** 2.8e-009
Matches : 36/256 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	171.1128	86.0600					G	2499.1456	1250.0765	2482.1191	1241.5632	2481.1351	1241.0712	24
3	308.1717	154.5895					H	2442.1242	1221.5657	2425.0976	1213.0525	2424.1136	1212.5604	23
4	468.2024	234.6048					C	2305.0653	1153.0363	2288.0387	1144.5230	2287.0547	1144.0310	22
5	565.2551	283.1312					P	2145.0346	1073.0209	2128.0081	1064.5077	2127.0241	1064.0157	21
6	**680.2821**	340.6447			662.2715	331.6394	D	2047.9819	1024.4946	2030.9553	1015.9813	2029.9713	1015.4893	20
7	777.3348	389.1711			759.3243	380.1658	P	***1932.9549***	966.9811	1915.9284	958.4678	1914.9443	957.9758	19
8	876.4033	**438.7053**			858.3927	429.7000	V	1835.9021	918.4547	1818.8756	909.9414	1817.8916	909.4494	18
9	989.4873	**495.2473**			971.4767	486.2420	L	1736.8337	868.9205	1719.8072	860.4072	1718.8232	859.9152	17
10	1088.5557	**544.7815**			1070.5452	535.7762	V	***1623.7497***	812.3785	1606.7231	803.8652	1605.7391	803.3732	16
11	1202.5987	**601.8030**	1185.5721	593.2897	1184.5881	592.7977	N	***1524.6813***	762.8443	1507.6547	754.3310	1506.6707	753.8390	15
12	1259.6201	630.3137	1242.5936	621.8004	1241.6096	621.3084	G	***1410.6383***	705.8228	1393.6118	697.3095	1392.6278	696.8175	14
13	**1388.6627**	**694.8350**	1371.6362	686.3217	1370.6521	685.8297	E	***1353.6169***	677.3121	1336.5903	668.7988	1335.6063	668.3068	13
14	1535.7311	768.3692	1518.7046	759.8559	1517.7206	759.3639	F	***1224.5743***	612.7908	1207.5477	604.2775	1206.5637	603.7855	12
15	1622.7632	811.8852	1605.7366	803.3719	1604.7526	802.8799	S	***1077.5059***	539.2566	1060.4793	530.7433	1059.4953	530.2513	11
16	**1709.7952**	855.4012	1692.7686	846.8880	1691.7846	846.3959	S	***990.4738***	495.7406	973.4473	487.2273	972.4633	486.7353	10
17	1796.8272	898.9172	1779.8007	890.4040	1778.8166	889.9120	S	***903.4418***	452.2245	886.4153	443.7113	885.4312	443.2193	9
18	1853.8487	**927.4280**	1836.8221	918.9147	1835.8381	918.4227	G	***816.4098***	408.7085	799.3832	400.1953	798.3992	399.7032	8
19	1950.9014	975.9544	1933.8749	967.4411	1932.8909	966.9491	P	***759.3883***	380.1978	742.3618	371.6845	741.3777	371.1925	7
20	2049.9699	1025.4886	2032.9433	1016.9753	2031.9593	1016.4833	V	662.3355	331.6714	645.3090	323.1581	644.3250	322.6661	6
21	2164.9968	1083.0020	2147.9702	1074.4888	2146.9862	1073.9968	N	***563.2671***	282.1372	546.2406	273.6239	545.2566	273.1319	5
22	2264.0652	**1132.5362**	2247.0387	1124.0230	2246.0546	1123.5310	V	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6184	4
23	2351.0972	1176.0523	2334.0707	1167.5390	2333.0867	1167.0470	S	***349.1718***	175.0895	332.1452	166.5763	331.1612	166.0842	3

24	2466.1242	1233.5657	2449.0976	1225.0525	2448.1136	1224.5604	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LGHCPDPVLVNGEFSSSGPVNVSDK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
109.3	2611.2225	0.0072	LGHCPDPVLVNGEFSSSGPVNVSDK	Deamidated N21 100.00%
60.4	2611.2225	0.0072	LGHCPDPVLVNGEFSSSGPVNVSDK	Deamidated N11 0.00%
38.6	2610.2384	0.9912	LGHCPDPVLVNGEFSSSGPVNVSDK	
4.4	2609.2212	2.0085	KTNATNNMNLSRSSSDNNTNTLGR	
1.1	2611.2297	0.0000	SVTIGRNSSQGSVDVSMGHSSFISR	
0.3	2611.2258	0.0039	MQVTMSLSSLVGTTQNFSEEHLR	
0.3	2611.2258	0.0039	MQVTMSLSSLVGTTQNFSEEHLR	

Mascot: http://www.matrixscience.com/

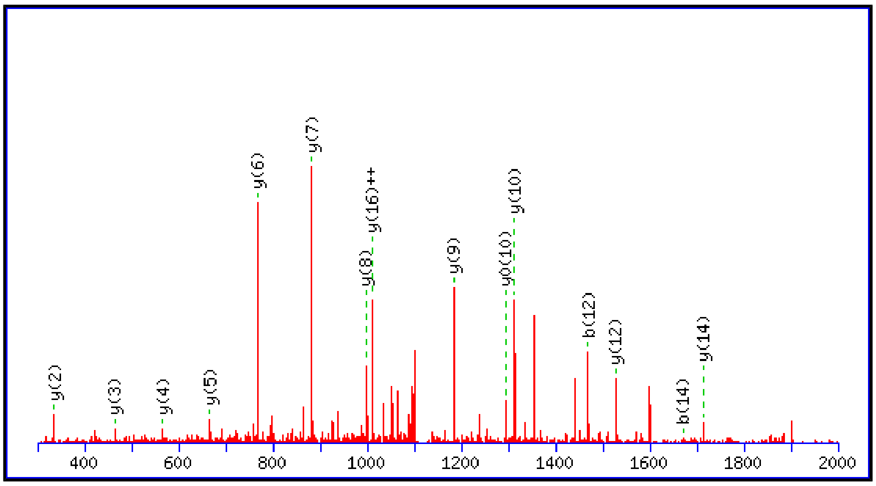
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLFCNASKEWDNTTTECR**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

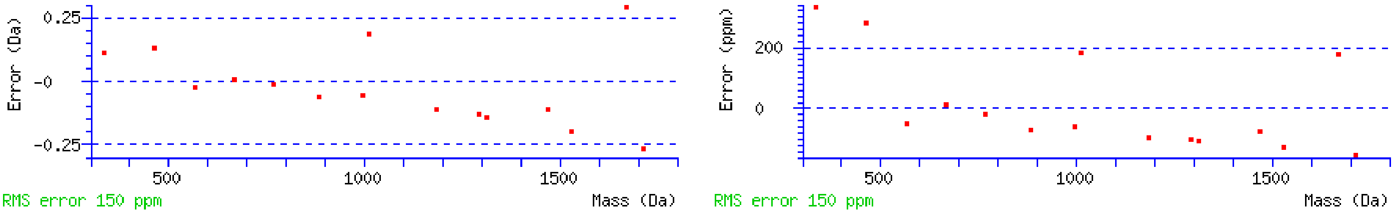
Match to Query 14986: 2233.936948 from(1117.975750,2+) intensity(22622.4277) rtinseconds(1475) scans(3513) index(27412)
Title: 111019_Est_MI_YS_G_10Spectrum3020_scans__3513
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2233.9256
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
N12 : Deamidated (NQ)
Ions Score: 93 **Expect:** 1.9e-008
Matches : 15/192 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	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	L	2133.8852	1067.4462	2116.8586	1058.9330	2115.8746	1058.4410	17
3	362.2074	181.6074			344.1969	172.6021	F	2020.8011	1010.9042	2003.7746	1002.3909	2002.7906	1001.8989	16
4	522.2381	261.6227			504.2275	252.6174	C	1873.7327	937.3700	1856.7062	928.8567	1855.7222	928.3647	15
5	637.2650	319.1362	620.2385	310.6229	619.2545	310.1309	N	***1713.7021***	857.3547	1696.6755	848.8414	1695.6915	848.3494	14
6	708.3021	354.6547	691.2756	346.1414	690.2916	345.6494	A	1598.6751	799.8412	1581.6486	791.3279	1580.6646	790.8359	13
7	795.3342	398.1707	778.3076	389.6574	777.3236	389.1654	S	***1527.6380***	764.3226	1510.6115	755.8094	1509.6274	755.3174	12
8	923.4291	462.2182	906.4026	453.7049	905.4186	453.2129	K	1440.6060	720.8066	1423.5794	712.2934	1422.5954	711.8013	11
9	1052.4717	526.7395	1035.4452	518.2262	1034.4612	517.7342	E	***1312.5110***	656.7591	1295.4845	648.2459	1294.5005	647.7539	10
10	1238.5510	619.7792	1221.5245	611.2659	1220.5405	610.7739	W	***1183.4684***	592.2379	1166.4419	583.7246	1165.4579	583.2326	9
11	1353.5780	677.2926	1336.5514	668.7794	1335.5674	668.2873	D	***997.3891***	499.1982	980.3626	490.6849	979.3786	490.1929	8
12	**1468.6049**	734.8061	1451.5784	726.2928	1450.5944	725.8008	N	***882.3622***	441.6847	865.3356	433.1715	864.3516	432.6794	7
13	1569.6526	785.3299	1552.6261	776.8167	1551.6420	776.3247	T	***767.3352***	384.1713	750.3087	375.6580	749.3247	375.1660	6
14	**1670.7003**	835.8538	1653.6737	827.3405	1652.6897	826.8485	T	***666.2876***	333.6474	649.2610	325.1341	648.2770	324.6421	5
15	1771.7480	886.3776	1754.7214	877.8643	1753.7374	877.3723	T	***565.2399***	283.1236	548.2133	274.6103	547.2293	274.1183	4
16	1900.7906	950.8989	1883.7640	942.3856	1882.7800	941.8936	E	***464.1922***	232.5997	447.1656	224.0865	446.1816	223.5945	3
17	2060.8212	1030.9142	2043.7947	1022.4010	2042.8106	1021.9090	C	***335.1496***	168.0784	318.1231	159.5652			2
18							R	175.1190	88.0631	158.0924	79.5498			1



NCBI **BLAST** search of TLFCNASKEWDNTTTECR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
93.1	2233.9256	0.0114	TLFCNASKEWDNTTTECR
84.1	2232.9416	0.9954	TLFCNASKEWDNTTTECR
29.1	2232.9416	0.9954	TLFCNASKEWDNTTTECR

Mascot: http://www.matrixscience.com/

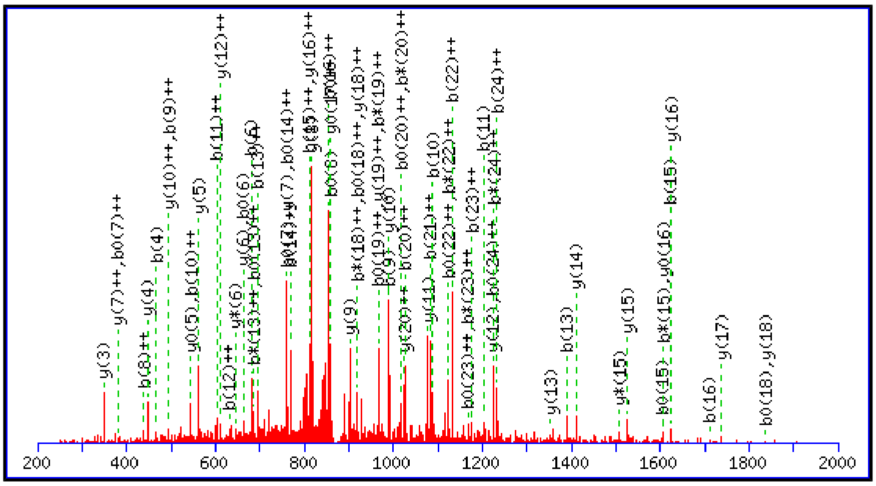
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGHCPDPVLVNGEFSSSGPVNVSDK**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

Match to Query 22292: 2612.219352 from(871.747060,3+) intensity(69056.0781) rtinseconds(1744) scans(3986) index(16786)
Title: 111019_Est_MI_YP_G_06Spectrum3315_scans__3986
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

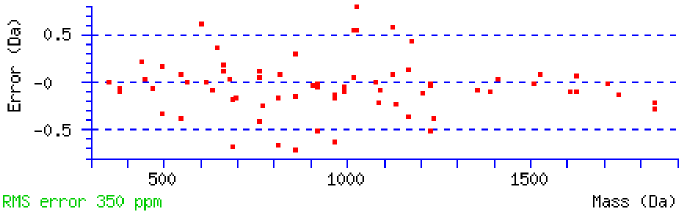
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

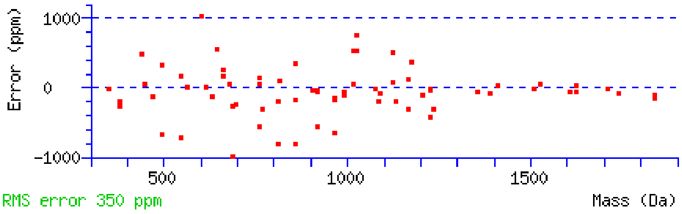


```
Monoisotopic mass of neutral peptide Mr(calc): 2612.2065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N11     : Deamidated (NQ)
N21     : Deamidated (NQ)
Ions Score: 85  Expect: 6.5e-007
Matches : 72/256 fragment ions using 111 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	171.1128	86.0600					G	2500.1297	1250.5685	2483.1031	1242.0552	2482.1191	1241.5632	24
3	308.1717	154.5895					H	2443.1082	1222.0577	2426.0816	1213.5445	2425.0976	1213.0525	23
4	**468.2024**	234.6048					C	2306.0493	1153.5283	2289.0227	1145.0150	2288.0387	1144.5230	22
5	565.2551	283.1312					P	2146.0186	1073.5130	2128.9921	1064.9997	2128.0081	1064.5077	21
6	**680.2821**	340.6447			662.2715	331.6394	D	2048.9659	1024.9866	2031.9393	1016.4733	2030.9553	1015.9813	20
7	777.3348	389.1711			759.3243	380.1658	P	1933.9389	967.4731	1916.9124	958.9598	1915.9284	958.4678	19
8	876.4033	**438.7053**			858.3927	429.7000	V	***1836.8862***	918.9467	1819.8596	910.4334	1818.8756	909.9414	18
9	**989.4873**	**495.2473**			971.4767	486.2420	L	***1737.8177***	869.4125	1720.7912	860.8992	1719.8072	860.4072	17
10	**1088.5557**	**544.7815**			1070.5452	535.7762	V	***1624.7337***	812.8705	1607.7071	804.3572	1606.7231	803.8652	16
11	**1203.5827**	**602.2950**	1186.5561	593.7817	1185.5721	593.2897	N	***1525.6653***	763.3363	1508.6387	754.8230	1507.6547	754.3310	15
12	1260.6041	**630.8057**	1243.5776	622.2924	1242.5936	621.8004	G	***1410.6383***	705.8228	1393.6118	697.3095	1392.6278	696.8175	14
13	**1389.6467**	**695.3270**	1372.6202	686.8137	1371.6362	686.3217	E	***1353.6169***	677.3121	1336.5903	668.7988	1335.6063	668.3068	13
14	1536.7151	**768.8612**	1519.6886	760.3479	1518.7046	759.8559	F	***1224.5743***	612.7908	1207.5477	604.2775	1206.5637	603.7855	12
15	**1623.7472**	**812.3772**	1606.7206	803.8639	1605.7366	803.3719	S	***1077.5059***	539.2566	1060.4793	530.7433	1059.4953	530.2513	11
16	**1710.7792**	**855.8932**	1693.7526	847.3800	1692.7686	846.8880	S	***990.4738***	495.7406	973.4473	487.2273	972.4633	486.7353	10
17	1797.8112	899.4093	1780.7847	890.8960	1779.8007	890.4040	S	***903.4418***	452.2245	886.4153	443.7113	885.4312	443.2193	9
18	1854.8327	927.9200	1837.8061	919.4067	1836.8221	918.9147	G	***816.4098***	408.7085	799.3832	400.1953	798.3992	399.7032	8
19	1951.8855	976.4464	1934.8589	967.9331	1933.8749	967.4411	P	***759.3883***	380.1978	742.3618	371.6845	741.3777	371.1925	7
20	2050.9539	**1025.9806**	2033.9273	1017.4673	2032.9433	1016.9753	V	***662.3355***	331.6714	645.3090	323.1581	644.3250	322.6661	6
21	2165.9808	**1083.4940**	2148.9543	1074.9808	2147.9702	1074.4888	N	***563.2671***	282.1372	546.2406	273.6239	545.2566	273.1319	5
22	2265.0492	**1133.0283**	2248.0227	1124.5150	2247.0387	1124.0230	V	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6184	4

23	2352.0813	**1176.5443**	2335.0547	1168.0310	2334.0707	1167.5390	**S**	***349.1718***	175.0895	332.1452	166.5763	331.1612	166.0842	**3**
24	2467.1082	**1234.0577**	2450.0816	1225.5445	2449.0976	1225.0525	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LGHCPDPVLVNGEFSSSGPVNVSDK
 (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	2612.2065	0.0129	LGHCPDPVLVNGEFSSSGPVNVSDK
66.0	2611.2225	0.9969	LGHCPDPVLVNGEFSSSGPVNVSDK
49.6	2611.2225	0.9969	LGHCPDPVLVNGEFSSSGPVNVSDK
7.0	2611.2249	0.9945	RPDVVENQPDAASQLNVDASGNLAK
5.8	2612.2137	0.0057	SVTIGRNSSQGSVDVSMGHSSFISR
4.6	2611.2249	0.9945	RPDVVENQPDAASQLNVDASGNLAK
4.5	2611.2146	1.0048	LVSTSGSSAQASMIDMFAKSTDSFK
4.5	2611.2112	1.0082	LAEAFAKAGEDGVQNGWMGVESISK
4.0	2610.2007	2.0187	QLIFSSIPETQIQDRCQNVSDK
3.6	2611.2072	1.0122	LTPGPPSASTAPTPSAGCSEEGAAAEAK

Mascot: http://www.matrixscience.com/

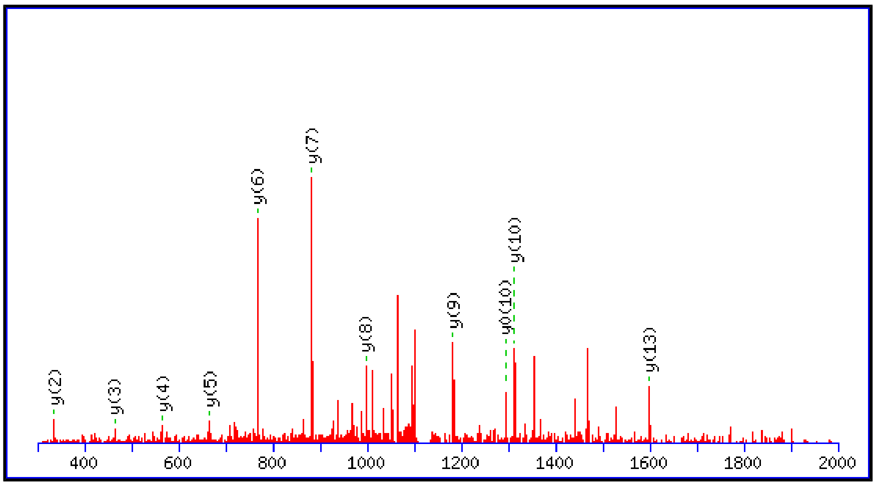
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TLFCNASKEWDNTTTECR**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

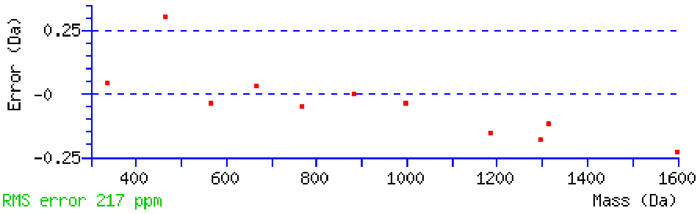
Match to Query 14989: 2233.939348 from(1117.976950,2+) intensity(11150.5088) rtinseconds(1410) scans(3370) index(7021)
Title: 111019_Est_ISCardio_NMI_YP_G_10Spectrum2920_scans__3370
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

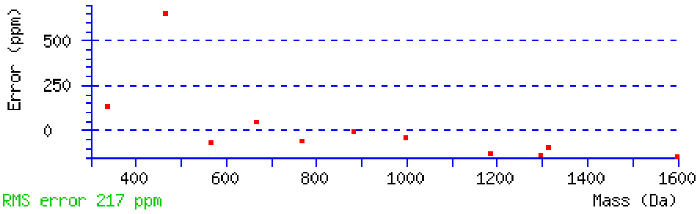
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2232.9416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12 : Deamidated (NQ)
Ions Score: 68 **Expect:** 5.5e-006
Matches : 11/192 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	102.0550	51.5311			84.0444	42.5258	T							18
2	215.1390	108.0731			197.1285	99.0679	L	2132.9012	1066.9542	2115.8746	1058.4410	2114.8906	1057.9489	17
3	362.2074	181.6074			344.1969	172.6021	F	2019.8171	1010.4122	2002.7906	1001.8989	2001.8066	1001.4069	16
4	522.2381	261.6227			504.2275	252.6174	C	1872.7487	936.8780	1855.7222	928.3647	1854.7381	927.8727	15
5	636.2810	318.6441	619.2545	310.1309	618.2704	309.6389	N	1712.7181	856.8627	1695.6915	848.3494	1694.7075	847.8574	14
6	707.3181	354.1627	690.2916	345.6494	689.3076	345.1574	A	***1598.6751***	799.8412	1581.6486	791.3279	1580.6646	790.8359	13
7	794.3502	397.6787	777.3236	389.1654	776.3396	388.6734	S	1527.6380	764.3226	1510.6115	755.8094	1509.6274	755.3174	12
8	922.4451	461.7262	905.4186	453.2129	904.4345	452.7209	K	1440.6060	720.8066	1423.5794	712.2934	1422.5954	711.8013	11
9	1051.4877	526.2475	1034.4612	517.7342	1033.4771	517.2422	E	***1312.5110***	656.7591	1295.4845	648.2459	1294.5005	647.7539	10
10	1237.5670	619.2871	1220.5405	610.7739	1219.5565	610.2819	W	***1183.4684***	592.2379	1166.4419	583.7246	1165.4579	583.2326	9
11	1352.5940	676.8006	1335.5674	668.2873	1334.5834	667.7953	D	***997.3891***	499.1982	980.3626	490.6849	979.3786	490.1929	8
12	1467.6209	734.3141	1450.5944	725.8008	1449.6103	725.3088	N	***882.3622***	441.6847	865.3356	433.1715	864.3516	432.6794	7
13	1568.6686	784.8379	1551.6420	776.3247	1550.6580	775.8326	T	***767.3352***	384.1713	750.3087	375.6580	749.3247	375.1660	6
14	1669.7163	835.3618	1652.6897	826.8485	1651.7057	826.3565	T	***666.2876***	333.6474	649.2610	325.1341	648.2770	324.6421	5
15	1770.7639	885.8856	1753.7374	877.3723	1752.7534	876.8803	T	***565.2399***	283.1236	548.2133	274.6103	547.2293	274.1183	4
16	1899.8065	950.4069	1882.7800	941.8936	1881.7960	941.4016	E	***464.1922***	232.5997	447.1656	224.0865	446.1816	223.5945	3
17	2059.8372	1030.4222	2042.8106	1021.9090	2041.8266	1021.4169	C	***335.1496***	168.0784	318.1231	159.5652			2
18							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of TLFCNASKEWDNTTTECR
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
68.2	2232.9416	0.9978	TLFCNASKEWDNTTTECR	Deamidated N12 100.00%
18.0	2232.9416	0.9978	TLFCNASKEWDNTTTECR	Deamidated N5 0.00%

Mascot: http://www.matrixscience.com/

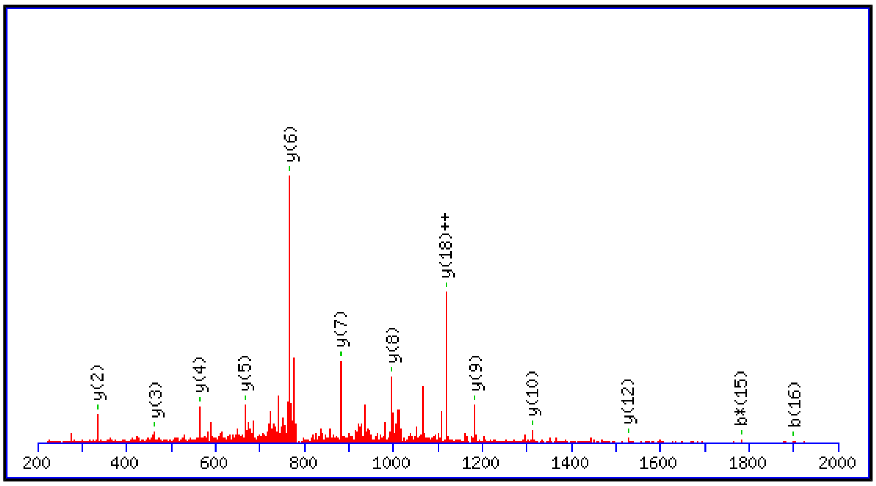
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTLFCNASKEWDNTTTECR**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

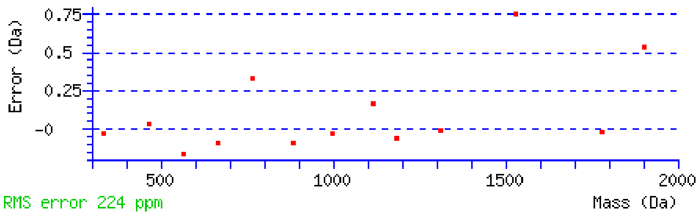
Match to Query 17891: 2362.028682 from(788.350170,3+) intensity(28577.5078) rtinseconds(1020) scans(2404) index(2563)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum2037_scans__2404
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

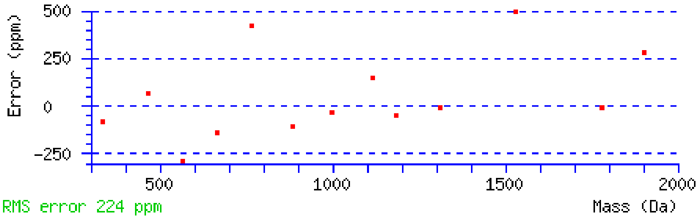
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 2362.0205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6     : Deamidated (NQ)
N13    : Deamidated (NQ)
Ions Score: 65  Expect: 3.1e-005
Matches : 13/210 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							19
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	2234.9329	1117.9701	2217.9063	1109.4568	2216.9223	1108.9648	18
3	343.2340	172.1206	326.2074	163.6074	325.2234	163.1153	L	2133.8852	1067.4462	2116.8586	1058.9330	2115.8746	1058.4410	17
4	490.3024	245.6548	473.2758	237.1416	472.2918	236.6496	F	2020.8011	1010.9042	2003.7746	1002.3909	2002.7906	1001.8989	16
5	650.3330	325.6702	633.3065	317.1569	632.3225	316.6649	C	1873.7327	937.3700	1856.7062	928.8567	1855.7222	928.3647	15
6	765.3600	383.1836	748.3334	374.6704	747.3494	374.1783	N	1713.7021	857.3547	1696.6755	848.8414	1695.6915	848.3494	14
7	836.3971	418.7022	819.3706	410.1889	818.3865	409.6969	A	1598.6751	799.8412	1581.6486	791.3279	1580.6646	790.8359	13
8	923.4291	462.2182	906.4026	453.7049	905.4186	453.2129	S	***1527.6380***	764.3226	1510.6115	755.8094	1509.6274	755.3174	12
9	1051.5241	526.2657	1034.4975	517.7524	1033.5135	517.2604	K	1440.6060	720.8066	1423.5794	712.2934	1422.5954	711.8013	11
10	1180.5667	590.7870	1163.5401	582.2737	1162.5561	581.7817	E	***1312.5110***	656.7591	1295.4845	648.2459	1294.5005	647.7539	10
11	1366.6460	683.8266	1349.6194	675.3134	1348.6354	674.8214	W	***1183.4684***	592.2379	1166.4419	583.7246	1165.4579	583.2326	9
12	1481.6729	741.3401	1464.6464	732.8268	1463.6624	732.3348	D	***997.3891***	499.1982	980.3626	490.6849	979.3786	490.1929	8
13	1596.6999	798.8536	1579.6733	790.3403	1578.6893	789.8483	N	***882.3622***	441.6847	865.3356	433.1715	864.3516	432.6794	7
14	1697.7476	849.3774	1680.7210	840.8641	1679.7370	840.3721	T	***767.3352***	384.1713	750.3087	375.6580	749.3247	375.1660	6
15	1798.7952	899.9013	1781.7687	891.3880	1780.7847	890.8960	T	***666.2876***	333.6474	649.2610	325.1341	648.2770	324.6421	5
16	1899.8429	950.4251	1882.8164	941.9118	1881.8324	941.4198	T	***565.2399***	283.1236	548.2133	274.6103	547.2293	274.1183	4
17	2028.8855	1014.9464	2011.8590	1006.4331	2010.8750	1005.9411	E	***464.1922***	232.5997	447.1656	224.0865	446.1816	223.5945	3
18	2188.9162	1094.9617	2171.8896	1086.4484	2170.9056	1085.9564	C	***335.1496***	168.0784	318.1231	159.5652			2
19							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KTLFCNASKEWDNTTTECR
(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	2362.0205	0.0081	KTLFCNASKEWDNTTTECR
64.8	2361.0365	0.9922	KTLFCNASKEWDNTTTECR
19.0	2361.0365	0.9922	KTLFCNASKEWDNTTTECR

Mascot: http://www.matrixscience.com/

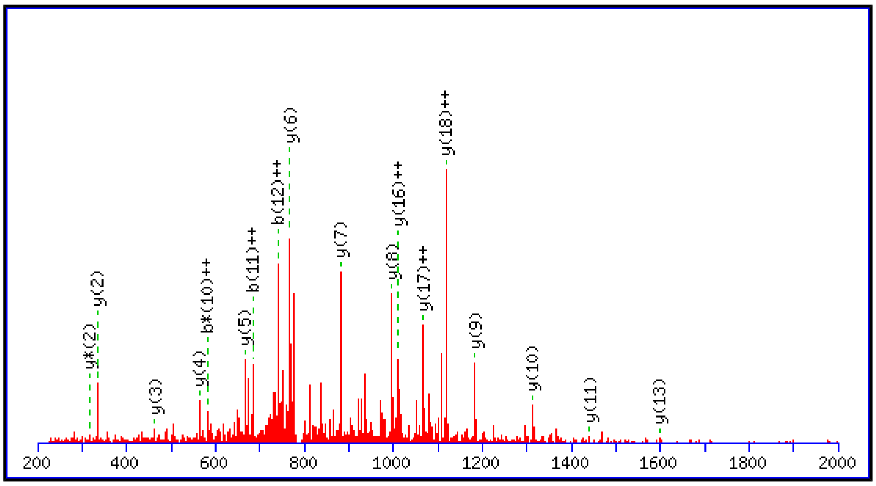
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTLFCNASKEWDNTTTECR**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

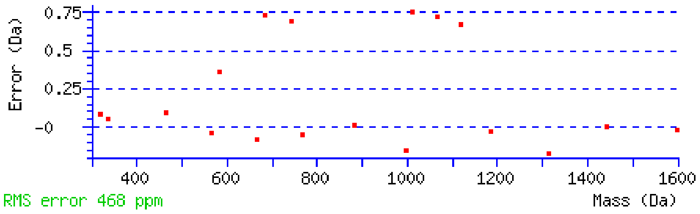
Match to Query 17895: 2362.033932 from(788.351920,3+) intensity(77596.1953) rtinseconds(1171) scans(2785) index(26539)
Title: 111019_Est_MI_YS_G_09Spectrum2396_scans__2785
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

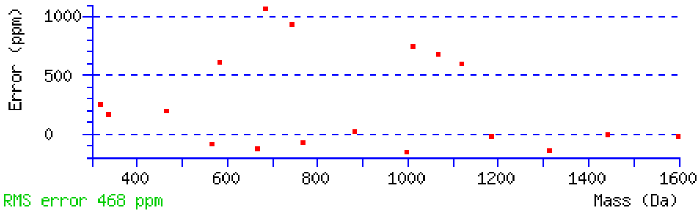
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2361.0365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N13 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.00062
Matches : 18/210 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							19
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	2233.9489	1117.4781	2216.9223	1108.9648	2215.9383	1108.4728	18
3	343.2340	172.1206	326.2074	163.6074	325.2234	163.1153	L	2132.9012	1066.9542	2115.8746	1058.4410	2114.8906	1057.9489	17
4	490.3024	245.6548	473.2758	237.1416	472.2918	236.6496	F	2019.8171	1010.4122	2002.7906	1001.8989	2001.8066	1001.4069	16
5	650.3330	325.6702	633.3065	317.1569	632.3225	316.6649	C	1872.7487	936.8780	1855.7222	928.3647	1854.7381	927.8727	15
6	764.3760	382.6916	747.3494	374.1783	746.3654	373.6863	N	1712.7181	856.8627	1695.6915	848.3494	1694.7075	847.8574	14
7	835.4131	418.2102	818.3865	409.6969	817.4025	409.2049	A	***1598.6751***	799.8412	1581.6486	791.3279	1580.6646	790.8359	13
8	922.4451	461.7262	905.4186	453.2129	904.4345	452.7209	S	1527.6380	764.3226	1510.6115	755.8094	1509.6274	755.3174	12
9	1050.5401	525.7737	1033.5135	517.2604	1032.5295	516.7684	K	***1440.6060***	720.8066	1423.5794	712.2934	1422.5954	711.8013	11
10	1179.5827	590.2950	1162.5561	581.7817	1161.5721	581.2897	E	***1312.5110***	656.7591	1295.4845	648.2459	1294.5005	647.7539	10
11	1365.6620	683.3346	1348.6354	674.8214	1347.6514	674.3293	W	***1183.4684***	592.2379	1166.4419	583.7246	1165.4579	583.2326	9
12	1480.6889	740.8481	1463.6624	732.3348	1462.6784	731.8428	D	***997.3891***	499.1982	980.3626	490.6849	979.3786	490.1929	8
13	1595.7159	798.3616	1578.6893	789.8483	1577.7053	789.3563	N	***882.3622***	441.6847	865.3356	433.1715	864.3516	432.6794	7
14	1696.7635	848.8854	1679.7370	840.3721	1678.7530	839.8801	T	***767.3352***	384.1713	750.3087	375.6580	749.3247	375.1660	6
15	1797.8112	899.4093	1780.7847	890.8960	1779.8007	890.4040	T	***666.2876***	333.6474	649.2610	325.1341	648.2770	324.6421	5
16	1898.8589	949.9331	1881.8324	941.4198	1880.8483	940.9278	T	***565.2399***	283.1236	548.2133	274.6103	547.2293	274.1183	4
17	2027.9015	1014.4544	2010.8750	1005.9411	2009.8909	1005.4491	E	***464.1922***	232.5997	447.1656	224.0865	446.1816	223.5945	3
18	2187.9321	1094.4697	2170.9056	1085.9564	2169.9216	1085.4644	C	***335.1496***	168.0784	318.1231	159.5652			2
19							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of KTLFCNASKEWDNTTTECR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
51.9	2361.0365	0.9974	KTLFCNASKEWDNTTTECR	Deamidated N13 99.83%
24.2	2361.0365	0.9974	KTLFCNASKEWDNTTTECR	Deamidated N6 0.17%
0.7	2362.0457	-0.0118	EWVPESAPVLEQDPTTRNMM	

Mascot: http://www.matrixscience.com/

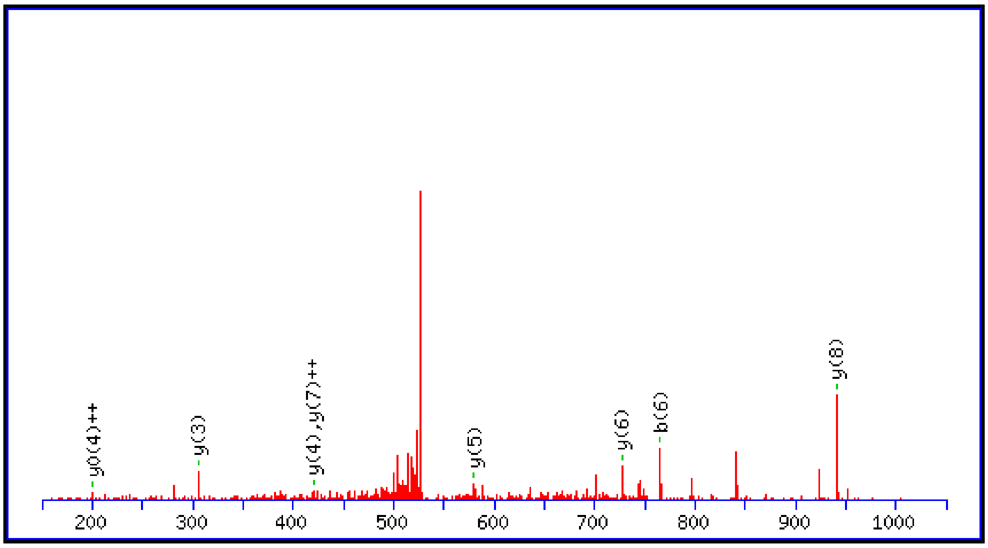
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KTLFCNASK**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

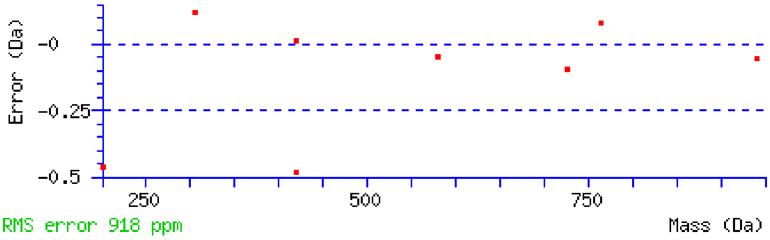
Match to Query 209: 1068.528128 from(535.271340,2+) intensity(9511.8828) rtinseconds(348) scans(588) index(15570)
Title: 111019_Est_MI_YP_G_05Spectrum471_scans__588
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

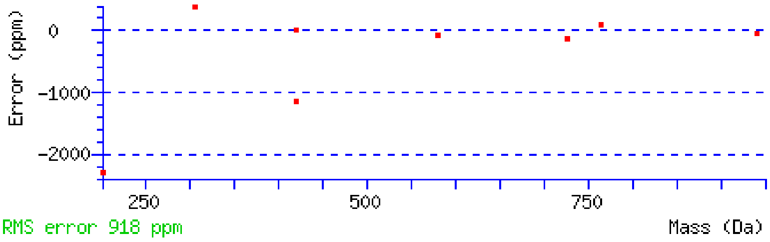
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1068.5274
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.015
Matches : 8/92 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			K							9
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	***941.4397***	471.2235	924.4131	462.7102	923.4291	462.2182	8
3	343.2340	172.1206	326.2074	163.6074	325.2234	163.1153	L	840.3920	420.6996	823.3655	412.1864	822.3815	411.6944	7
4	490.3024	245.6548	473.2758	237.1416	472.2918	236.6496	F	***727.3080***	364.1576	710.2814	355.6443	709.2974	355.1523	6
5	650.3330	325.6702	633.3065	317.1569	632.3225	316.6649	C	***580.2395***	290.6234	563.2130	282.1101	562.2290	281.6181	5
6	765.3600	383.1836	748.3334	374.6704	747.3494	374.1783	N	***420.2089***	210.6081	403.1823	202.0948	402.1983	201.6028	4
7	836.3971	418.7022	819.3706	410.1889	818.3865	409.6969	A	***305.1819***	153.0946	288.1554	144.5813	287.1714	144.0893	3
8	923.4291	462.2182	906.4026	453.7049	905.4186	453.2129	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
9							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KTLFCNASK
(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	1068.5274	0.0008	KTLFCNASK
3.4	1066.5229	2.0052	ARNMAVDYK
1.1	1066.5229	2.0052	LNLMQNYR
0.4	1067.5247	1.0034	YSLRQDGTK
0.3	1066.5230	2.0051	LFQVCSGTR

Mascot: http://www.matrixscience.com/

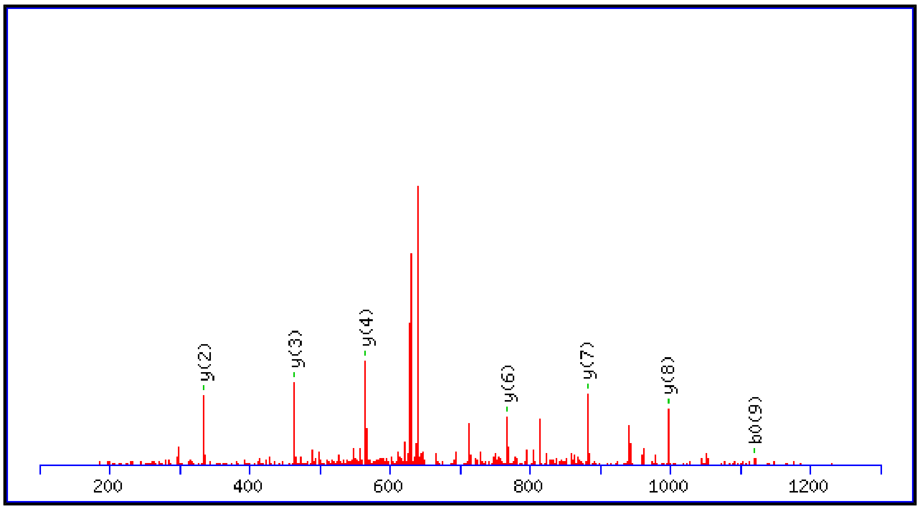
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EWDNTTTECR**
Found in **E7EQT9** in **con_Xuniprot_HUMAN3**, E7EQT9_HUMAN C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=2 SV=1

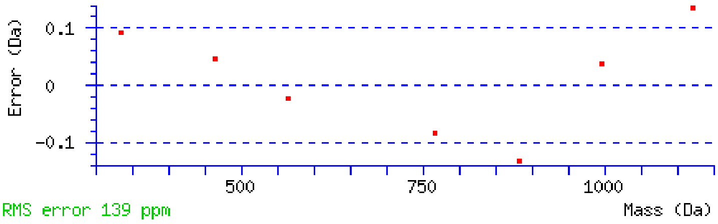
Match to Query 1963: 1311.507468 from(656.761010,2+) intensity(8613.1387) rtinseconds(350) scans(688) index(3643)
Title: 111019_Est_ISCardio_NMI_YP_G_6Spectrum571_scans__688
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

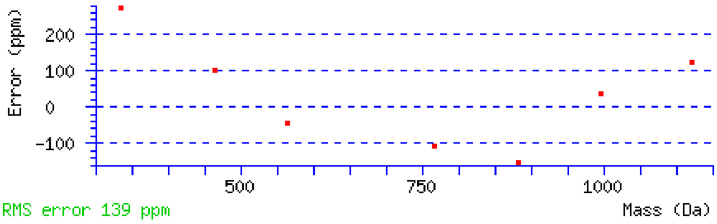
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1311.5037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
Ions Score: 36 **Expect:** 0.0035
Matches : 7/98 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	130.0499	65.5286			112.0393	56.5233	E							10
2	316.1292	158.5682			298.1186	149.5629	W	1183.4684	592.2379	1166.4419	583.7246	1165.4579	583.2326	9
3	431.1561	216.0817			413.1456	207.0764	D	***997.3891***	499.1982	980.3626	490.6849	979.3786	490.1929	8
4	546.1831	273.5952	529.1565	265.0819	528.1725	264.5899	N	***882.3622***	441.6847	865.3356	433.1715	864.3516	432.6794	7
5	647.2307	324.1190	630.2042	315.6057	629.2202	315.1137	T	***767.3352***	384.1713	750.3087	375.6580	749.3247	375.1660	6
6	748.2784	374.6429	731.2519	366.1296	730.2679	365.6376	T	666.2876	333.6474	649.2610	325.1341	648.2770	324.6421	5
7	849.3261	425.1667	832.2996	416.6534	831.3155	416.1614	T	***565.2399***	283.1236	548.2133	274.6103	547.2293	274.1183	4
8	978.3687	489.6880	961.3421	481.1747	960.3581	480.6827	E	***464.1922***	232.5997	447.1656	224.0865	446.1816	223.5945	3
9	1138.3993	569.7033	1121.3728	561.1900	1120.3888	560.6980	C	***335.1496***	168.0784	318.1231	159.5652			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of EWDNTTTECR
(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	1311.5037	0.0037	EWDNTTTECR
3.7	1311.5037	0.0037	AQSPNNTSCDAF

Mascot: http://www.matrixscience.com/

MATRIX SCIENCE

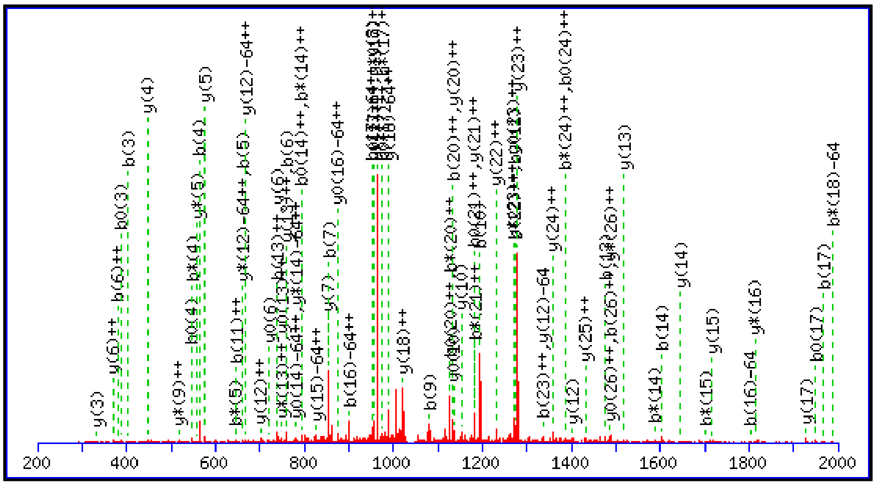
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQFCPPPPQIPNAQNMTTTVNYQDGEK**
Found in **Q5VYL6** in **con_Xuniprot_HUMAN3**, Q5VYL6_HUMAN Complement factor H-related protein 5 OS=Homo sapiens GN=CFHR5 PE=2 SV=1

Match to Query 27323: 3120.383832 from(1041.135220,3+) intensity(9938.5928) rtinseconds(1226) scans(2742) index(15081)
Title: 111019_Est_MI_YP_G_04Spectrum2319_scans__2742
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

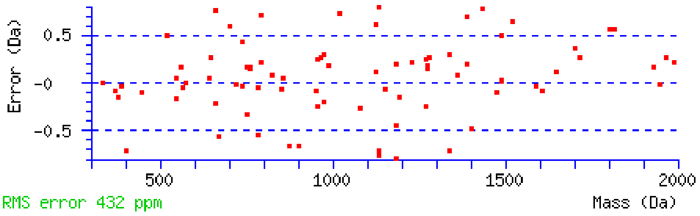
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

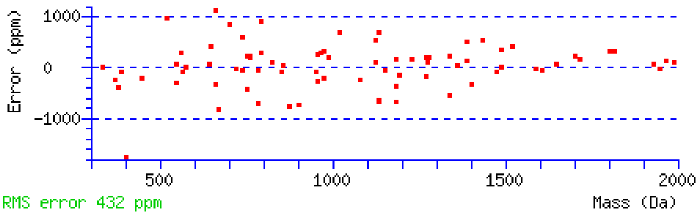


Monoisotopic mass of neutral peptide Mr(calc): 3120.3805
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N15 : Deamidated (NQ)
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 50 **Expect:** 0.0011
Matches : 83/464 fragment ions using 153 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							27
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	2992.3452	1496.6762	2975.3186	1488.1629	2974.3346	1487.6709	26
3	**405.1769**	203.0921	388.1503	194.5788	387.1663	194.0868	F	2864.2866	1432.6469	2847.2600	1424.1337	2846.2760	1423.6416	25
4	**565.2075**	283.1074	548.1810	274.5941	547.1969	274.1021	C	2717.2182	1359.1127	2700.1916	1350.5994	2699.2076	1350.1074	24
5	**662.2603**	331.6338	645.2337	323.1205	644.2497	322.6285	P	2557.1875	1279.0974	2540.1610	1270.5841	2539.1769	1270.0921	23
6	**759.3130**	**380.1602**	742.2865	371.6469	741.3025	371.1549	P	2460.1347	1230.5710	2443.1082	1222.0577	2442.1242	1221.5657	22
7	**856.3658**	428.6865	839.3393	420.1733	838.3552	419.6813	P	2363.0820	1182.0446	2346.0554	1173.5314	2345.0714	1173.0393	21
8	953.4186	477.2129	936.3920	468.6996	935.4080	468.2076	P	2266.0292	1133.5182	2249.0027	1125.0050	2248.0187	1124.5130	20
9	**1081.4771**	541.2422	1064.4506	532.7289	1063.4666	532.2369	Q	2168.9765	1084.9919	2151.9499	1076.4786	2150.9659	1075.9866	19
10	**1194.5612**	597.7842	1177.5347	589.2710	1176.5506	588.7790	I	2040.9179	1020.9626	2023.8913	1012.4493	2022.9073	1011.9573	18
11	1291.6140	**646.3106**	1274.5874	637.7973	1273.6034	637.3053	P	***1927.8338***	964.4205	1910.8073	955.9073	1909.8232	955.4153	17
12	1405.6569	703.3321	1388.6304	694.8188	1387.6463	694.3268	N	1830.7811	915.8942	1813.7545	907.3809	1812.7705	906.8889	16
13	**1476.6940**	**738.8506**	1459.6675	730.3374	1458.6834	729.8454	A	***1716.7381***	858.8727	1699.7116	850.3594	1698.7276	849.8674	15
14	**1604.7526**	802.8799	1587.7260	794.3667	1586.7420	793.8747	Q	***1645.7010***	823.3541	1628.6745	814.8409	1627.6904	814.3489	14
15	1719.7795	860.3934	1702.7530	851.8801	1701.7690	851.3881	N	***1517.6424***	759.3249	1500.6159	750.8116	1499.6319	750.3196	13
16	1866.8149	933.9111	1849.7884	925.3978	1848.8044	924.9058	M	***1402.6155***	701.8114	1385.5889	693.2981	1384.6049	692.8061	12
17	**1967.8626**	984.4349	1950.8361	975.9217	1949.8520	975.4297	T	1255.5801	628.2937	1238.5535	619.7804	1237.5695	619.2884	11
18	2068.9103	1034.9588	2051.8837	1026.4455	2050.8997	1025.9535	T	***1154.5324***	577.7698	1137.5059	569.2566	1136.5218	568.7646	10
19	2169.9580	1085.4826	2152.9314	1076.9693	2151.9474	1076.4773	T	1053.4847	527.2460	1036.4582	518.7327	1035.4742	518.2407	9
20	2269.0264	**1135.0168**	2251.9998	1126.5036	2251.0158	1126.0115	V	***952.4371***	476.7222	935.4105	468.2089	934.4265	467.7169	8
21	2383.0693	1192.0383	2366.0428	1183.5250	2365.0587	1183.0330	N	***853.3686***	427.1880	836.3421	418.6747	835.3581	418.1827	7

22	2546.1326	**1273.5700**	2529.1061	1265.0567	2528.1221	1264.5647	**Y**	***739.3257***	370.1665	722.2992	361.6532	721.3151	361.1612	**6**
23	2674.1912	**1337.5992**	2657.1647	1329.0860	2656.1807	1328.5940	**Q**	***576.2624***	288.6348	559.2358	280.1216	558.2518	279.6295	**5**
24	2789.2182	1395.1127	2772.1916	1386.5994	2771.2076	1386.1074	**D**	***448.2038***	224.6055	431.1773	216.0923	430.1932	215.6003	**4**
25	2846.2396	1423.6235	2829.2131	1415.1102	2828.2291	1414.6182	**G**	***333.1769***	167.0921	316.1503	158.5788	315.1663	158.0868	**3**
26	2975.2822	**1488.1447**	2958.2557	1479.6315	2957.2717	1479.1395	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
27							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of EQFCPPPPQIPNAQNMTTTVNYQDGEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
50.2	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated N15 56.92%
47.8	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated Q14 32.60%
37.5	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated N12 3.08%
36.8	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated N21 2.61%
35.6	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated Q9 1.99%
34.5	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated Q2 1.52%
33.7	3120.3805	0.0034	EQFCPPPPQIPNAQNMTTTVNYQDGEK	Deamidated Q23 1.27%
2.7	3118.3716	2.0123	LMSANASDLPLSIECFMNDVDVSGTMNR	
2.3	3120.3830	0.0009	QGVNVSANQDDELDHETFLMQIDQETK	
2.3	3120.3830	0.0009	QGVNVSANQDDELDHETFLMQIDQETK	

Mascot: http://www.matrixscience.com/

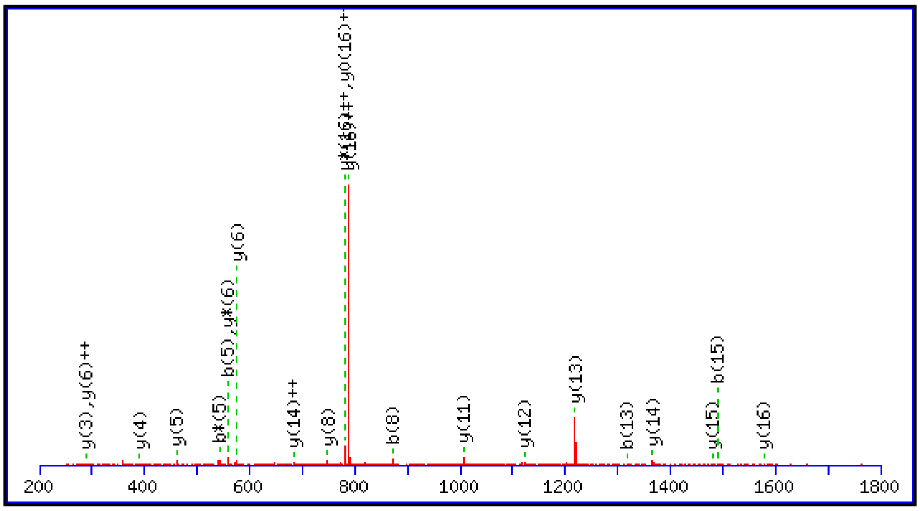
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLPNFPNTSATANATGGR**
Found in **Q6UXB8** in **con_Xuniprot_HUMAN3**, PI16_HUMAN Peptidase inhibitor 16 OS=Homo sapiens GN=PI16 PE=1 SV=1

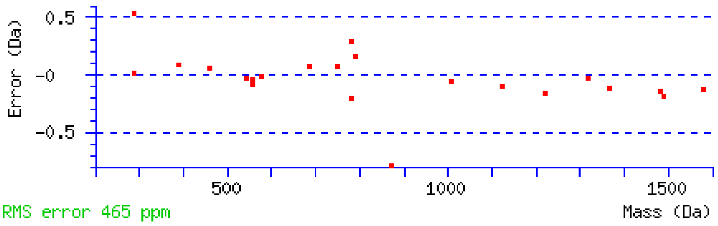
Match to Query 10055: 1776.832788 from(889.423670,2+) intensity(57619.4766) rtinseconds(1074) scans(2384) index(13172)
Title: 111019_Est_ISCardio_NMI_YS_G_11Spectrum2059_scans__2384
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

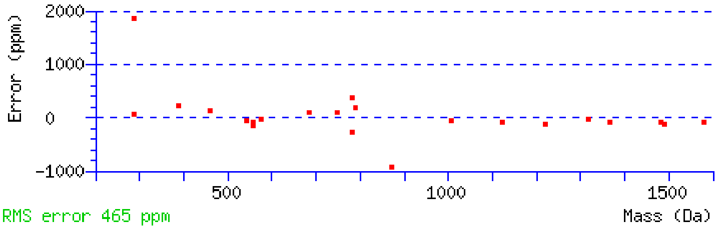
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1776.8278
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
N13 : Deamidated (NQ)
Ions Score: 85 **Expect:** 6.1e-007
Matches : 22/192 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	88.0393	44.5233			70.0287	35.5180	S							18
2	201.1234	101.0653			183.1128	92.0600	L	1690.8031	845.9052	1673.7766	837.3919	1672.7925	836.8999	17
3	298.1761	149.5917			280.1656	140.5864	P	***1577.7190***	789.3632	1560.6925	780.8499	1559.7085	780.3579	16
4	412.2191	206.6132	395.1925	198.0999	394.2085	197.6079	N	***1480.6663***	740.8368	1463.6397	732.3235	1462.6557	731.8315	15
5	**559.2875**	280.1474	542.2609	271.6341	541.2769	271.1421	F	***1366.6234***	683.8153	1349.5968	675.3020	1348.6128	674.8100	14
6	656.3402	328.6738	639.3137	320.1605	638.3297	319.6685	P	***1219.5549***	610.2811	1202.5284	601.7678	1201.5444	601.2758	13
7	771.3672	386.1872	754.3406	377.6740	753.3566	377.1819	N	***1122.5022***	561.7547	1105.4756	553.2414	1104.4916	552.7494	12
8	**872.4149**	436.7111	855.3883	428.1978	854.4043	427.7058	T	***1007.4752***	504.2413	990.4487	495.7280	989.4647	495.2360	11
9	959.4469	480.2271	942.4203	471.7138	941.4363	471.2218	S	906.4276	453.7174	889.4010	445.2041	888.4170	444.7121	10
10	1030.4840	515.7456	1013.4575	507.2324	1012.4734	506.7404	A	819.3955	410.2014	802.3690	401.6881	801.3850	401.1961	9
11	1131.5317	566.2695	1114.5051	557.7562	1113.5211	557.2642	T	***748.3584***	374.6828	731.3319	366.1696	730.3478	365.6776	8
12	1202.5688	601.7880	1185.5422	593.2748	1184.5582	592.7828	A	647.3107	324.1590	630.2842	315.6457	629.3002	315.1537	7
13	**1317.5957**	659.3015	1300.5692	650.7882	1299.5852	650.2962	N	***576.2736***	288.6404	559.2471	280.1272	558.2631	279.6352	6
14	1388.6329	694.8201	1371.6063	686.3068	1370.6223	685.8148	A	***461.2467***	231.1270	444.2201	222.6137	443.2361	222.1217	5
15	**1489.6805**	745.3439	1472.6540	736.8306	1471.6700	736.3386	T	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	4
16	1546.7020	773.8546	1529.6754	765.3414	1528.6914	764.8494	G	***289.1619***	145.0846	272.1353	136.5713			3
17	1603.7235	802.3654	1586.6969	793.8521	1585.7129	793.3601	G	232.1404	116.5738	215.1139	108.0606			2
18							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of SLPNFPNTSATANATGGR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
85.1	1776.8278	0.0050	SLPNFPNTSATANATGGR	Deamidated N7, N13 99.99%
46.7	1776.8278	0.0050	SLPNFPNTSATANATGGR	Deamidated N4, N13 0.01%
15.2	1776.8278	0.0050	SLPNFPNTSATANATGGR	Deamidated N4, N7 0.00%
9.3	1776.8377	-0.0049	QASQKQPSVTGSKEGDK	
8.2	1776.8240	0.0088	QLVQKSYSTDFMTNV	
4.5	1775.8261	1.0067	KSHCFDRGSLQDIDV	
4.3	1776.8274	0.0054	AMHLSQLDMILDQTK	
3.2	1776.8326	0.0002	LSNSKQHHPGLQCDR	
3.2	1776.8326	0.0002	LSNSKQHHPGLQCDR	
3.0	1776.8325	0.0003	EAPLRHSESAEMHAGR	

Mascot: http://www.matrixscience.com/

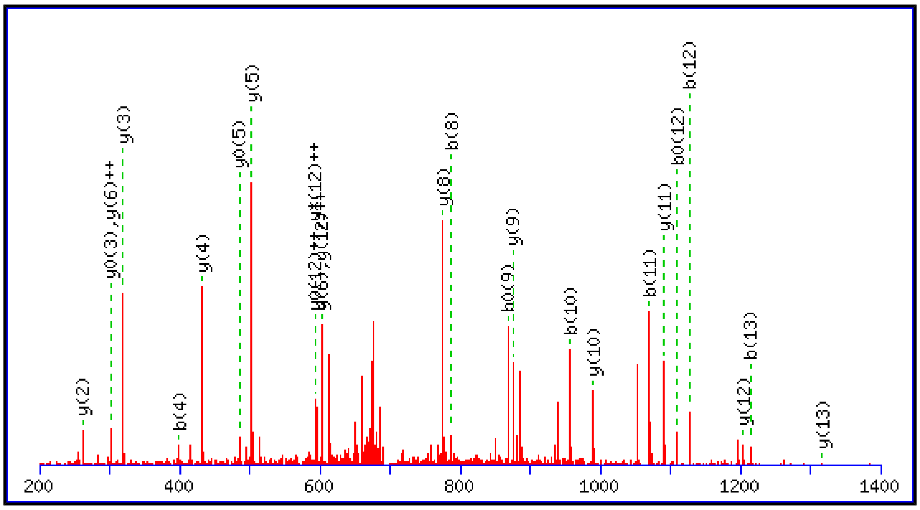
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLTNVSSVALGSR**
Found in **Q7Z7M0** in **con_Xuniprot_HUMAN3**, MEGF8_HUMAN Multiple epidermal growth factor-like domains protein 8 OS=Homo sapiens GN=MEGF8 PE=1 SV=2

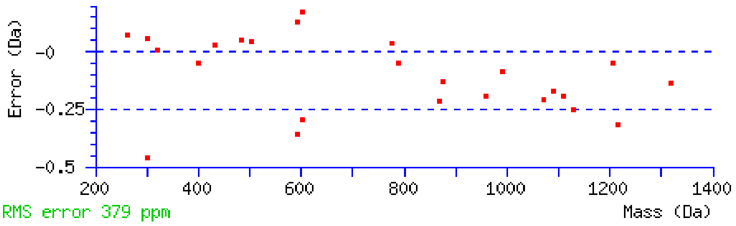
Match to Query 2398: 1387.770848 from(694.892700,2+) intensity(33726.1875) rtinseconds(1537) scans(3912) index(18570)
Title: 111019_Est_MI_YP_G_08Spectrum3402_scans__3912
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

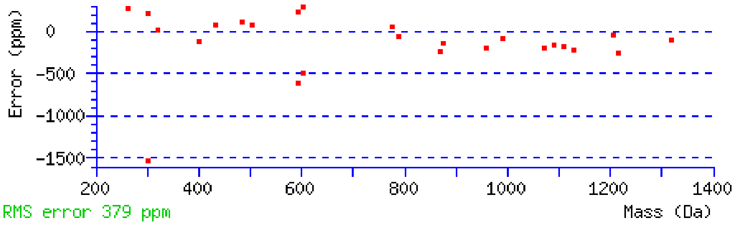
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1387.7671
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 120 **Expect:** 1.6e-010
Matches : 25/140 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							14
2	185.1285	93.0679					L	***1317.7373***	659.3723	1300.7107	650.8590	1299.7267	650.3670	13
3	298.2125	149.6099					L	***1204.6532***	602.8302	1187.6266	594.3170	1186.6426	593.8250	12
4	**399.2602**	200.1337			381.2496	191.1285	T	***1091.5691***	546.2882	1074.5426	537.7749	1073.5586	537.2829	11
5	514.2871	257.6472	497.2606	249.1339	496.2766	248.6419	N	***990.5214***	495.7644	973.4949	487.2511	972.5109	486.7591	10
6	613.3556	307.1814	596.3290	298.6681	595.3450	298.1761	V	***875.4945***	438.2509	858.4680	429.7376	857.4839	429.2456	9
7	700.3876	350.6974	683.3610	342.1842	682.3770	341.6921	S	***776.4261***	388.7167	759.3995	380.2034	758.4155	379.7114	8
8	**787.4196**	394.2134	770.3931	385.7002	769.4090	385.2082	S	689.3941	345.2007	672.3675	336.6874	671.3835	336.1954	7
9	886.4880	443.7476	869.4615	435.2344	868.4775	434.7424	V	***602.3620***	301.6847	585.3355	293.1714	584.3515	292.6794	6
10	**957.5251**	479.2662	940.4986	470.7529	939.5146	470.2609	A	***503.2936***	252.1504	486.2671	243.6372	485.2831	243.1452	5
11	**1070.6092**	535.8082	1053.5827	527.2950	1052.5986	526.8030	L	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	4
12	**1127.6307**	564.3190	1110.6041	555.8057	1109.6201	555.3137	G	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
13	**1214.6627**	607.8350	1197.6361	599.3217	1196.6521	598.8297	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALLTNVSSVALGSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
120.0	1387.7671	0.0038	ALLTNVSSVALGSR
12.3	1387.7671	0.0038	SSSVAALLGSVIER
7.1	1386.7718	0.9990	KAPSSLTTPGSTLK
7.0	1387.7684	0.0025	ALLNNSGPRYKR
6.5	1385.7626	2.0082	IERLATRNIGDK
4.2	1386.7653	1.0056	LRQSLVMLQGNK
4.0	1386.7732	0.9977	AGPAAVPLAHGLASR
3.7	1386.7718	0.9990	PSLVNASISSSVVK
3.5	1386.7619	1.0089	LFDGPQLLARTR
1.5	1387.7724	-0.0016	SHLPYRIALYR

Mascot: http://www.matrixscience.com/

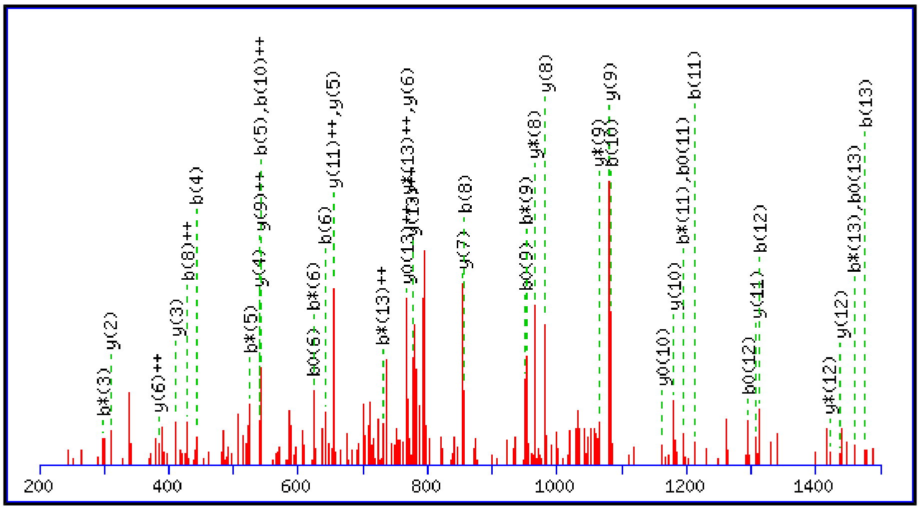
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANEQVVQSLNQTYK**
Found in **E9PBS6** in **con_Xuniprot_HUMAN3**, E9PBS6_HUMAN Probable G-protein-coupled receptor 116 OS=Homo sapiens GN=GPR116 PE=2 SV=1

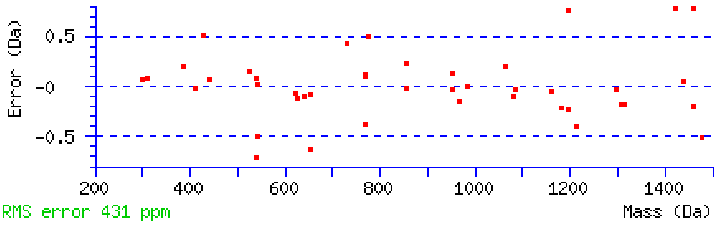
Match to Query 7716: 1621.799208 from(811.906880,2+) intensity(2184.0955) rtinseconds(981) scans(1597) index(7811)
Title: 111019_Est_ISCardio_NMI_YP_G_14Spectrum1271_scans__1597
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

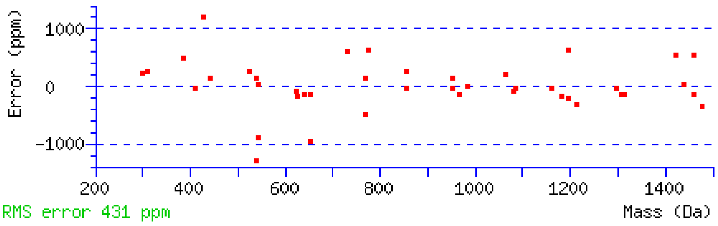
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1500 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1621.7947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10     : Deamidated (NQ)
Ions Score: 60  Expect: 0.00023
Matches : 43/146 fragment ions using 77 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**14**
2	186.0873	93.5473	169.0608	85.0340			**N**	1551.7649	776.3861	1534.7384	767.8728	1533.7544	767.3808	**13**
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	**E**	***1437.7220***	719.3646	1420.6955	710.8514	1419.7114	710.3594	**12**
4	**443.1885**	222.0979	426.1619	213.5846	425.1779	213.0926	**Q**	***1308.6794***	654.8433	1291.6529	646.3301	1290.6688	645.8381	**11**
5	**542.2569**	271.6321	525.2304	263.1188	524.2463	262.6268	**V**	***1180.6208***	590.8141	1163.5943	582.3008	1162.6103	581.8088	**10**
6	**641.3253**	321.1663	624.2988	312.6530	623.3148	312.1610	**V**	***1081.5524***	541.2798	1064.5259	532.7666	1063.5419	532.2746	**9**
7	769.3839	385.1956	752.3573	376.6823	751.3733	376.1903	**Q**	***982.4840***	491.7456	965.4575	483.2324	964.4734	482.7404	**8**
8	**856.4159**	428.7116	839.3894	420.1983	838.4054	419.7063	**S**	***854.4254***	427.7164	837.3989	419.2031	836.4149	418.7111	**7**
9	969.5000	485.2536	952.4734	476.7404	951.4894	476.2483	**L**	***767.3934***	384.2003	750.3668	375.6871	749.3828	375.1951	**6**
10	**1084.5269**	542.7671	1067.5004	534.2538	1066.5164	533.7618	**N**	***654.3093***	327.6583	637.2828	319.1450	636.2988	318.6530	**5**
11	**1212.5855**	606.7964	1195.5590	598.2831	1194.5749	597.7911	**Q**	***539.2824***	270.1448	522.2558	261.6316	521.2718	261.1396	**4**
12	**1313.6332**	657.3202	1296.6066	648.8070	1295.6226	648.3149	**T**	***411.2238***	206.1155	394.1973	197.6023	393.2132	197.1103	**3**
13	**1476.6965**	738.8519	1459.6700	730.3386	1458.6860	729.8466	**Y**	***310.1761***	155.5917	293.1496	147.0784			**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ANEQVVQSLNQTYK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.4	1621.7947	0.0045	ANEQVVQSLNQTYK	Deamidated N10 62.78%
58.1	1621.7947	0.0045	ANEQVVQSLNQTYK	Deamidated Q11 36.97%
36.3	1621.7947	0.0045	ANEQVVQSLNQTYK	Deamidated Q7 0.24%
20.5	1621.7947	0.0045	ANEQVVQSLNQTYK	Deamidated Q4 0.01%
13.8	1621.7947	0.0045	ANEQVVQSLNQTYK	Deamidated N2 0.00%
5.6	1620.7995	0.9998	ALEEQKEGLAENYK	
2.5	1621.7916	0.0076	VLDTLRDAMMSQAR	
2.4	1621.8022	-0.0029	EDVPMFTSLKPQSK	
2.2	1621.7995	-0.0002	AAGEVNPIGGKQHMGR	
2.2	1621.7995	-0.0003	AMPQDQVTQSPKHR	

Mascot: http://www.matrixscience.com/

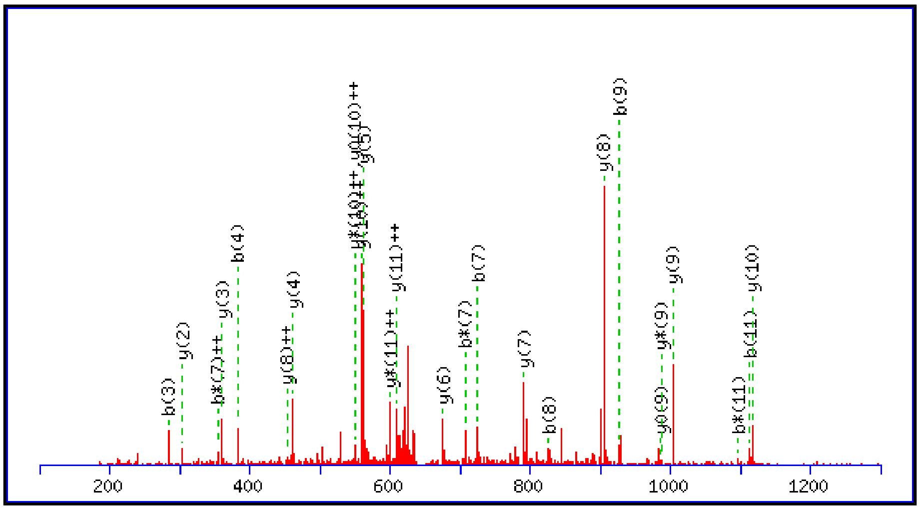
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVLVNNITTGER**
Found in **C9JYM4** in **con_Xuniprot_HUMAN3**, C9JYM4_HUMAN Golgi membrane protein 1 (Fragment) OS=Homo sapiens GN=GOLM1 PE=2 SV=1

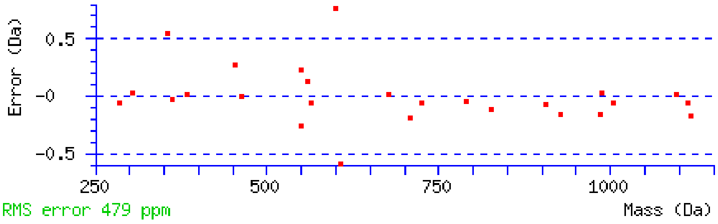
Match to Query 1839: 1286.688688 from(644.351620,2+) intensity(20036.6523) rtinseconds(914) scans(2090) index(26492)
Title: 111019_Est_MI_YS_G_09Spectrum1787_scans__2090
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

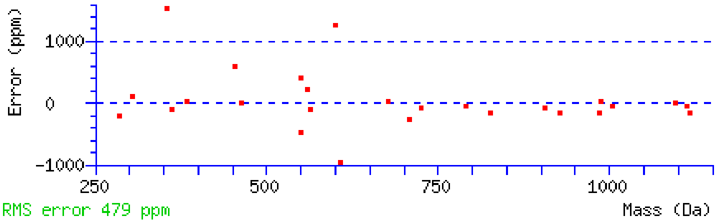
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1286.6830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0012
Matches : 26/108 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	72.0444	36.5258					A							12
2	171.1128	86.0600					V	1216.6532	608.8302	1199.6266	600.3170	1198.6426	599.8250	11
3	**284.1969**	142.6021					L	***1117.5848***	559.2960	1100.5582	550.7828	1099.5742	550.2907	10
4	**383.2653**	192.1363					V	***1004.5007***	502.7540	987.4742	494.2407	986.4902	493.7487	9
5	497.3082	249.1577	480.2817	240.6445			N	***905.4323***	453.2198	888.4058	444.7065	887.4217	444.2145	8
6	612.3352	306.6712	595.3086	298.1579			N	***791.3894***	396.1983	774.3628	387.6851	773.3788	387.1930	7
7	**725.4192**	363.2132	708.3927	354.7000			I	***676.3624***	338.6849	659.3359	330.1716	658.3519	329.6796	6
8	**826.4669**	413.7371	809.4403	405.2238	808.4563	404.7318	T	***563.2784***	282.1428	546.2518	273.6295	545.2678	273.1375	5
9	**927.5146**	464.2609	910.4880	455.7477	909.5040	455.2556	T	***462.2307***	231.6190	445.2041	223.1057	444.2201	222.6137	4
10	984.5360	492.7717	967.5095	484.2584	966.5255	483.7664	G	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
11	**1113.5786**	557.2930	1096.5521	548.7797	1095.5681	548.2877	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of AVLVNNITTGER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.4	1286.6830	0.0057	AVLVNNITTGER	Deamidated N6 92.89%
41.2	1286.6830	0.0057	AVLVNNITTGER	Deamidated N5 7.11%
5.3	1286.6843	0.0043	RPQWRSTSLR	
3.0	1286.6871	0.0016	LGGVNVWVTDVK	
0.4	1285.6851	1.0036	GARGGNLVTGTQR	

Mascot: http://www.matrixscience.com/

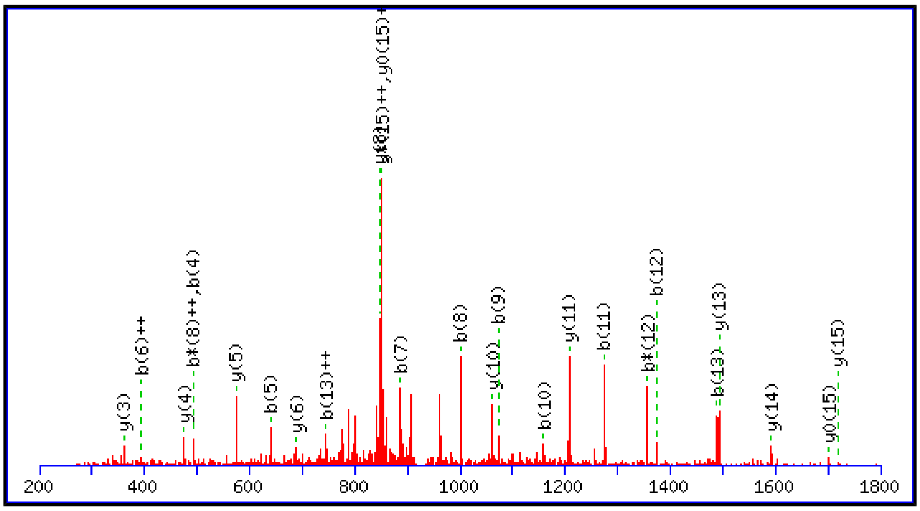
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQVHFFVNASDVDNVK**
Found in **Q96IY4** in **con_Xuniprot_HUMAN3**, CBPB2_HUMAN Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

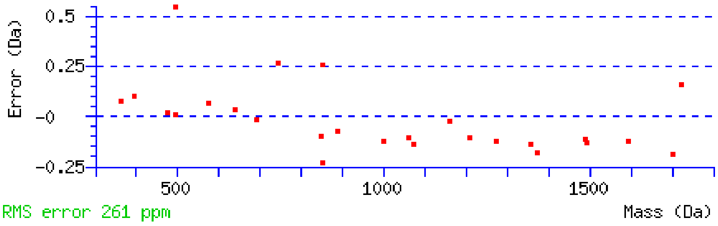
Match to Query 10953: 1846.928428 from(924.471490,2+) intensity(39045.0430) rtinseconds(987) scans(2418) index(4296)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum2093_scans__2418
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

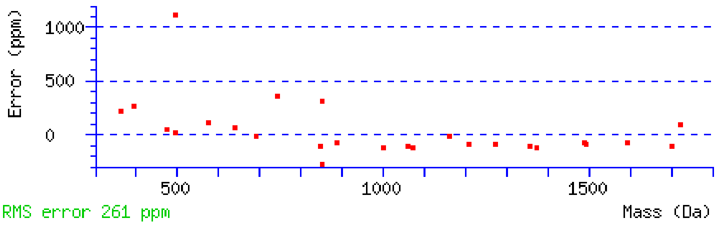
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1846.9214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N8 : Deamidated (NQ)
Ions Score: 100 **Expect:** 2.5e-008
Matches : 28/156 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							**16**
2	257.1608	129.0840	240.1343	120.5708			**Q**	***1719.8337***	860.4205	1702.8071	851.9072	1701.8231	851.4152	**15**
3	356.2292	178.6183	339.2027	170.1050			**V**	***1591.7751***	796.3912	1574.7485	787.8779	1573.7645	787.3859	**14**
4	***493.2881***	247.1477	476.2616	238.6344			**H**	***1492.7067***	746.8570	1475.6801	738.3437	1474.6961	737.8517	**13**
5	***640.3566***	320.6819	623.3300	312.1686			**F**	1355.6478	678.3275	1338.6212	669.8142	1337.6372	669.3222	**12**
6	787.4250	**394.2161**	770.3984	385.7028			**F**	***1208.5794***	604.7933	1191.5528	596.2800	1190.5688	595.7880	**11**
7	***886.4934***	443.7503	869.4668	435.2371			**V**	***1061.5109***	531.2591	1044.4844	522.7458	1043.5004	522.2538	**10**
8	***1001.5203***	501.2638	984.4938	492.7505			**N**	962.4425	481.7249	945.4160	473.2116	944.4320	472.7196	**9**
9	***1072.5574***	536.7824	1055.5309	528.2691			**A**	***847.4156***	424.2114	830.3890	415.6982	829.4050	415.2061	**8**
10	***1159.5895***	580.2984	1142.5629	571.7851	1141.5789	571.2931	**S**	776.3785	388.6929	759.3519	380.1796	758.3679	379.6876	**7**
11	***1274.6164***	637.8118	1257.5899	629.2986	1256.6058	628.8066	**D**	***689.3464***	345.1769	672.3199	336.6636	671.3359	336.1716	**6**
12	***1373.6848***	687.3461	1356.6583	678.8328	1355.6743	678.3408	**V**	***574.3195***	287.6634	557.2930	279.1501	556.3089	278.6581	**5**
13	***1488.7118***	**744.8595**	1471.6852	736.3462	1470.7012	735.8542	**D**	***475.2511***	238.1292	458.2245	229.6159	457.2405	229.1239	**4**
14	1602.7547	801.8810	1585.7281	793.3677	1584.7441	792.8757	**N**	***360.2241***	180.6157	343.1976	172.1024			**3**
15	***1701.8231***	**851.4152**	1684.7966	842.9019	1683.8125	842.4099	**V**	246.1812	123.5942	229.1547	115.0810			**2**
16							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of KQVHFFVNASDVDNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
100.3	1846.9214	0.0071	KQVHFFVNASDVDNVK	Deamidated N8 100.00%
43.3	1846.9214	0.0071	KQVHFFVNASDVDNVK	Deamidated Q2 0.00%
39.5	1846.9214	0.0071	KQVHFFVNASDVDNVK	Deamidated N14 0.00%
10.8	1846.9254	0.0031	FVLDYFFEEKQNLR	
9.8	1846.9346	-0.0061	QMIEQLQNSKAVIQSK	
9.8	1846.9346	-0.0061	QMIEQLQNSKAVIQSK	
9.8	1846.9346	-0.0061	QMIEQLQNSKAVIQSK	
9.8	1846.9346	-0.0061	QMIEQLQNSKAVIQSK	
8.6	1846.9254	0.0031	FIVDYFFEEKQNLR	
6.9	1845.9319	0.9965	QDNNTRIEAVKSLVQK	

Mascot: http://www.matrixscience.com/

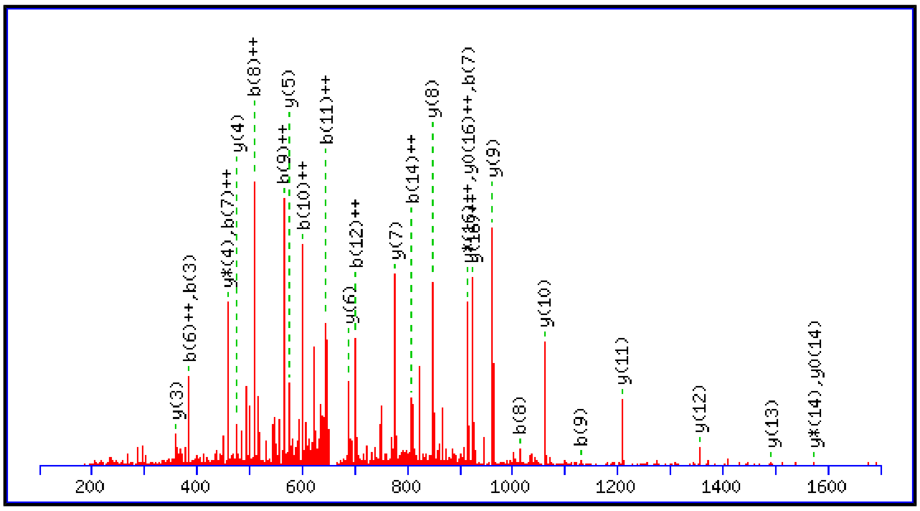
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KKQVHFFVNASDVDNVK**
Found in **Q96IY4** in **con_Xuniprot_HUMAN3**, CBPB2_HUMAN Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

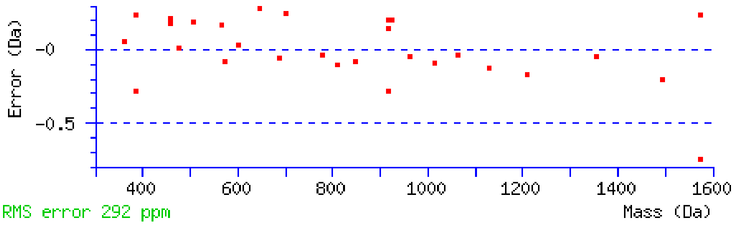
Match to Query 11890: 1975.023432 from(659.348420,3+) intensity(30812.8301) rtinseconds(803) scans(1802) index(2522)
Title: 111019_Est_ISCardio_NMI_YP_G_5Spectrum1523_scans__1802
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

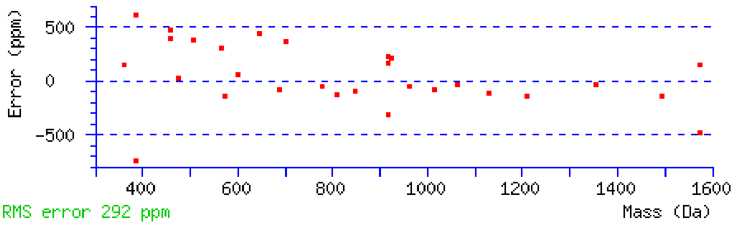
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1975.0163
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 66 **Expect:** 6.1e-005
Matches : 30/166 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	129.1022	65.0548	112.0757	56.5415			K							17
2	257.1972	129.1022	240.1707	120.5890			K	1847.9286	924.4680	1830.9021	915.9547	1829.9181	915.4627	16
3	**385.2558**	193.1315	368.2292	184.6183			Q	1719.8337	860.4205	1702.8071	851.9072	1701.8231	851.4152	15
4	484.3242	242.6657	467.2976	234.1525			V	1591.7751	796.3912	1574.7485	787.8779	1573.7645	787.3859	14
5	621.3831	311.1952	604.3566	302.6819			H	***1492.7067***	746.8570	1475.6801	738.3437	1474.6961	737.8517	13
6	768.4515	**384.7294**	751.4250	376.2161			F	***1355.6478***	678.3275	1338.6212	669.8142	1337.6372	669.3222	12
7	**915.5199**	**458.2636**	898.4934	449.7503			F	***1208.5794***	604.7933	1191.5528	596.2800	1190.5688	595.7880	11
8	**1014.5883**	**507.7978**	997.5618	499.2845			V	***1061.5109***	531.2591	1044.4844	522.7458	1043.5004	522.2538	10
9	**1129.6153**	**565.3113**	1112.5887	556.7980			N	***962.4425***	481.7249	945.4160	473.2116	944.4320	472.7196	9
10	1200.6524	**600.8298**	1183.6259	592.3166			A	***847.4156***	424.2114	830.3890	415.6982	829.4050	415.2061	8
11	1287.6844	**644.3459**	1270.6579	635.8326	1269.6739	635.3406	S	***776.3785***	388.6929	759.3519	380.1796	758.3679	379.6876	7
12	1402.7114	**701.8593**	1385.6848	693.3461	1384.7008	692.8540	D	***689.3464***	345.1769	672.3199	336.6636	671.3359	336.1716	6
13	1501.7798	751.3935	1484.7532	742.8803	1483.7692	742.3883	V	***574.3195***	287.6634	557.2930	279.1501	556.3089	278.6581	5
14	1616.8067	**808.9070**	1599.7802	800.3937	1598.7962	799.9017	D	***475.2511***	238.1292	458.2245	229.6159	457.2405	229.1239	4
15	1730.8497	865.9285	1713.8231	857.4152	1712.8391	856.9232	N	***360.2241***	180.6157	343.1976	172.1024			3
16	1829.9181	**915.4627**	1812.8915	906.9494	1811.9075	906.4574	V	246.1812	123.5942	229.1547	115.0810			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of KKQVHFFVNASDVDNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
65.8	1975.0163	0.0071	KKQVHFFVNASDVDNVK	Deamidated N9 99.52%
40.2	1975.0163	0.0071	KKQVHFFVNASDVDNVK	Deamidated Q3 0.27%
39.1	1975.0163	0.0071	KKQVHFFVNASDVDNVK	Deamidated N15 0.21%
4.5	1974.0170	1.0064	FNENLRDAVQLNVIATR	
2.1	1973.0265	1.9970	SARIMSFHEAASIIERR	
0.8	1974.0105	1.0129	LFTIPRQGMAQADGINAR	
0.6	1975.0309	-0.0075	QVAEQFLNMRGGLGLSGAK	
0.5	1975.0309	-0.0075	AGSLGLGGRMNLFQEAVQK	
0.2	1975.0316	-0.0082	FIFNVQPWIKGTSGQPR	
0.1	1974.0244	0.9990	IWNRLMVVSDEKENIK	

Mascot: http://www.matrixscience.com/

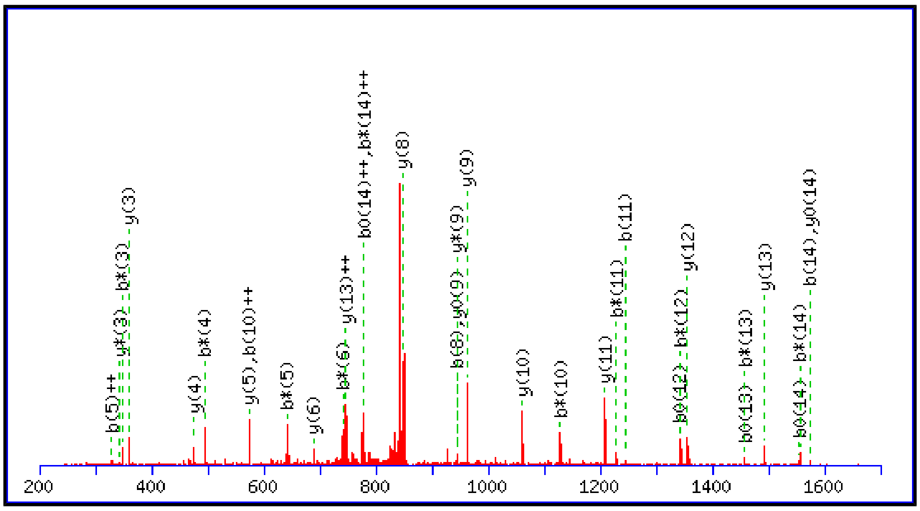
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVHFFVNASDVDNVK**
Found in **Q96IY4** in **con_Xuniprot_HUMAN3**, CBPB2_HUMAN Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

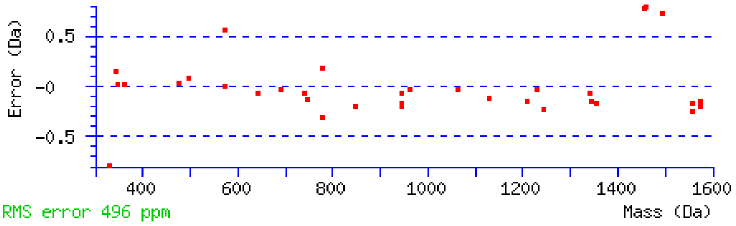
Match to Query 8723: 1718.831408 from(860.422980,2+) intensity(27278.6230) rtinseconds(1372) scans(3251) index(12560)
Title: 111019_Est_ISCardio_NMI_YS_G_9Spectrum2836_scans__3251
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

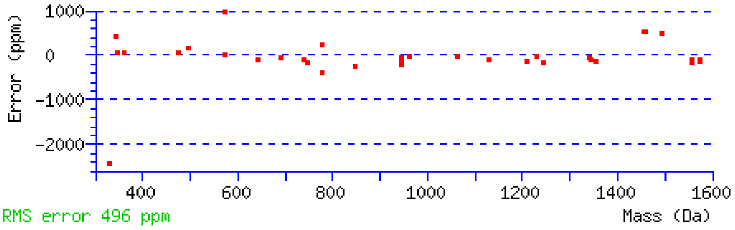
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1718.8264
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N7 : Deamidated (NQ)
Ions Score: 60 **Expect:** 0.00025
Matches : 34/146 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	129.0659	65.0366	112.0393	56.5233			Q							15
2	228.1343	114.5708	211.1077	106.0575			V	1591.7751	796.3912	1574.7485	787.8779	1573.7645	787.3859	14
3	365.1932	183.1002	348.1666	174.5870			H	***1492.7067***	746.8570	1475.6801	738.3437	1474.6961	737.8517	13
4	512.2616	256.6344	495.2350	248.1212			F	***1355.6478***	678.3275	1338.6212	669.8142	1337.6372	669.3222	12
5	659.3300	330.1686	642.3035	321.6554			F	***1208.5794***	604.7933	1191.5528	596.2800	1190.5688	595.7880	11
6	758.3984	379.7028	741.3719	371.1896			V	***1061.5109***	531.2591	1044.4844	522.7458	1043.5004	522.2538	10
7	873.4254	437.2163	856.3988	428.7030			N	***962.4425***	481.7249	945.4160	473.2116	944.4320	472.7196	9
8	**944.4625**	472.7349	927.4359	464.2216			A	***847.4156***	424.2114	830.3890	415.6982	829.4050	415.2061	8
9	1031.4945	516.2509	1014.4680	507.7376	1013.4839	507.2456	S	776.3785	388.6929	759.3519	380.1796	758.3679	379.6876	7
10	1146.5215	573.7644	1129.4949	565.2511	1128.5109	564.7591	D	***689.3464***	345.1769	672.3199	336.6636	671.3359	336.1716	6
11	**1245.5899**	623.2986	1228.5633	614.7853	1227.5793	614.2933	V	***574.3195***	287.6634	557.2930	279.1501	556.3089	278.6581	5
12	1360.6168	680.8120	1343.5903	672.2988	1342.6062	671.8068	D	***475.2511***	238.1292	458.2245	229.6159	457.2405	229.1239	4
13	1474.6597	737.8335	1457.6332	729.3202	1456.6492	728.8282	N	***360.2241***	180.6157	343.1976	172.1024			3
14	**1573.7281**	787.3677	1556.7016	778.8544	1555.7176	778.3624	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QVHFFVNASDVDNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
59.7	1718.8264	0.0050	QVHFFVNASDVDNVK	Deamidated N7 99.68%
34.1	1718.8264	0.0050	QVHFFVNASDVDNVK	Deamidated N13 0.28%
26.4	1718.8264	0.0050	QVHFFVNASDVDNVK	Deamidated Q1 0.05%
9.0	1718.8336	-0.0022	AGVGEVGGGPAPEPGQGRQ	
4.7	1717.8305	1.0009	LSQMIEQADIRGDNK	
3.9	1718.8396	-0.0082	VANAEEKLMDDLLNK	
3.3	1717.8312	1.0002	VDPWSFTETPSLPSR	
1.8	1718.8264	0.0050	VNDVDSANVFFHVQK	
1.3	1718.8284	0.0030	MVEVQLDENLSPTVK	

Mascot: http://www.matrixscience.com/

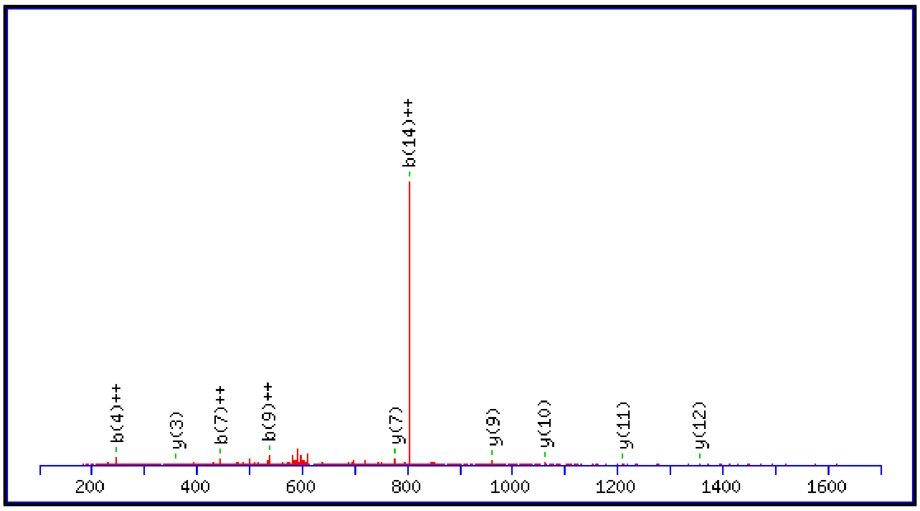
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQVHFFVNASDVDNVK**
Found in **Q96IY4** in **con_Xuniprot_HUMAN3**, CBPB2_HUMAN Carboxypeptidase B2 OS=Homo sapiens GN=CPB2 PE=1 SV=2

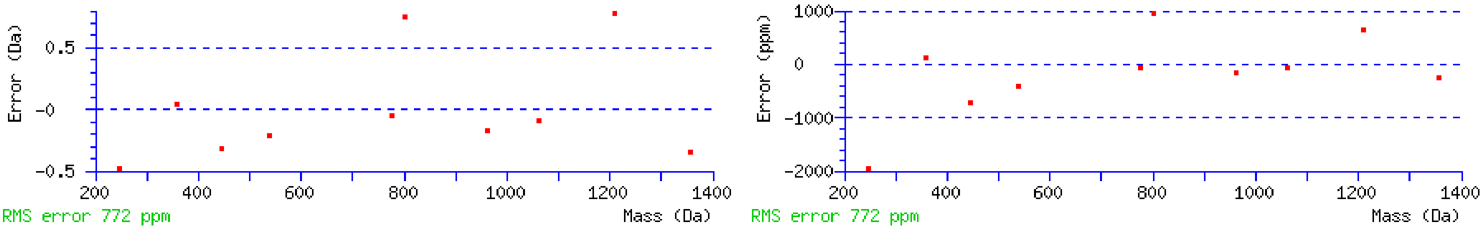
Match to Query 10957: 1849.911972 from(617.644600,3+) intensity(31361.2129) rtinseconds(1059) scans(2642) index(23857)
Title: 111019_Est_MI_YS_G_05Spectrum2252_scans__2642
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

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 ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1847.9054
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Deamidated (NQ)
N8 : Deamidated (NQ)
Ions Score: 38 **Expect:** 0.042
Matches : 10/156 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	129.1022	65.0548	112.0757	56.5415			K							16
2	258.1448	129.5761	241.1183	121.0628			Q	1720.8177	860.9125	1703.7911	852.3992	1702.8071	851.9072	15
3	357.2132	179.1103	340.1867	170.5970			V	1591.7751	796.3912	1574.7485	787.8779	1573.7645	787.3859	14
4	494.2722	**247.6397**	477.2456	239.1264			H	1492.7067	746.8570	1475.6801	738.3437	1474.6961	737.8517	13
5	641.3406	321.1739	624.3140	312.6607			F	***1355.6478***	678.3275	1338.6212	669.8142	1337.6372	669.3222	12
6	788.4090	394.7081	771.3824	386.1949			F	***1208.5794***	604.7933	1191.5528	596.2800	1190.5688	595.7880	11
7	887.4774	**444.2423**	870.4509	435.7291			V	***1061.5109***	531.2591	1044.4844	522.7458	1043.5004	522.2538	10
8	1002.5043	501.7558	985.4778	493.2425			N	***962.4425***	481.7249	945.4160	473.2116	944.4320	472.7196	9
9	1073.5415	**537.2744**	1056.5149	528.7611			A	847.4156	424.2114	830.3890	415.6982	829.4050	415.2061	8
10	1160.5735	580.7904	1143.5469	572.2771	1142.5629	571.7851	S	***776.3785***	388.6929	759.3519	380.1796	758.3679	379.6876	7
11	1275.6004	638.3039	1258.5739	629.7906	1257.5899	629.2986	D	689.3464	345.1769	672.3199	336.6636	671.3359	336.1716	6
12	1374.6688	687.8381	1357.6423	679.3248	1356.6583	678.8328	V	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	5
13	1489.6958	745.3515	1472.6692	736.8383	1471.6852	736.3462	D	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
14	1603.7387	**802.3730**	1586.7122	793.8597	1585.7281	793.3677	N	***360.2241***	180.6157	343.1976	172.1024			3
15	1702.8071	851.9072	1685.7806	843.3939	1684.7966	842.9019	V	246.1812	123.5942	229.1547	115.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of KQVHFFVNASDVDNVK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
37.9	1847.9054	2.0066	KQVHFFVNASDVDNVK	Deamidated Q2, N8 59.07%
35.2	1847.9054	2.0066	KQVHFFVNASDVDNVK	Deamidated N8, N14 31.50%
30.0	1847.9054	2.0066	KQVHFFVNASDVDNVK	Deamidated Q2, N14 9.43%
8.0	1849.9026	0.0094	VMLTNGGQRIMNVVQR	
6.9	1847.9113	2.0007	NQVTATKADGGTQVIDTK	
6.9	1847.9113	2.0007	NQVTATKADGGTQVIDTK	
6.6	1849.9066	0.0053	VMPICLPSKDYAEVGR	
6.6	1849.9066	0.0054	VMPICLPSKNYAEVGR	
6.3	1848.9006	1.0114	NQFWVQVRAESLNVR	
5.6	1849.9057	0.0062	DAAEADRTLFVGNLETK	

Mascot: http://www.matrixscience.com/

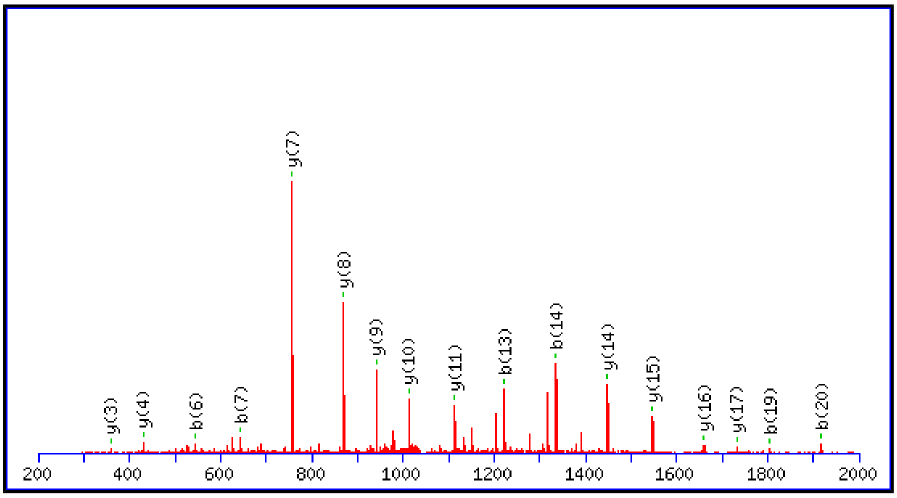
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFGVAIVGNYTAALPTEAALR**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

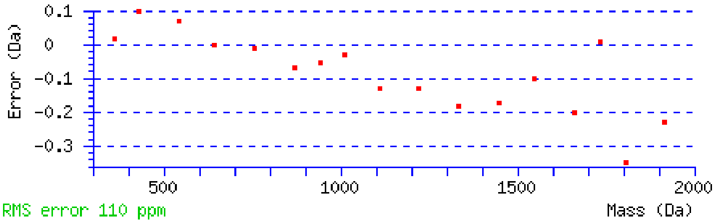
Match to Query 13413: 2091.108668 from(1046.561610,2+) intensity(43503.0352) rtinseconds(2292) scans(6159) index(24140)
Title: 111019_Est_MI_YS_G_05Spectrum5338_scans__6159
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

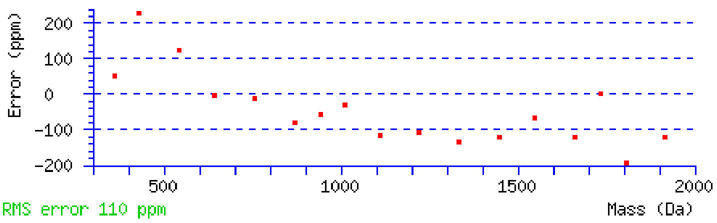
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2091.1000
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N9 : Deamidated (NQ)
Ions Score: 111 **Expect:** 1.6e-009
Matches : 17/196 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	58.0287	29.5180					G							21
2	205.0972	103.0522					F	2035.0859	1018.0466	2018.0593	1009.5333	2017.0753	1009.0413	20
3	262.1186	131.5629					G	1888.0175	944.5124	1870.9909	935.9991	1870.0069	935.5071	19
4	361.1870	181.0972					V	1830.9960	916.0016	1813.9694	907.4884	1812.9854	906.9964	18
5	432.2241	216.6157					A	***1731.9276***	866.4674	1714.9010	857.9542	1713.9170	857.4621	17
6	**545.3082**	273.1577					I	***1660.8905***	830.9489	1643.8639	822.4356	1642.8799	821.9436	16
7	**644.3766**	322.6920					V	***1547.8064***	774.4068	1530.7799	765.8936	1529.7958	765.4016	15
8	701.3981	351.2027					G	***1448.7380***	724.8726	1431.7114	716.3594	1430.7274	715.8673	14
9	816.4250	408.7162	799.3985	400.2029			N	1391.7165	696.3619	1374.6900	687.8486	1373.7060	687.3566	13
10	979.4884	490.2478	962.4618	481.7345			Y	1276.6896	638.8484	1259.6630	630.3352	1258.6790	629.8431	12
11	1080.5360	540.7717	1063.5095	532.2584	1062.5255	531.7664	T	***1113.6263***	557.3168	1096.5997	548.8035	1095.6157	548.3115	11
12	1151.5732	576.2902	1134.5466	567.7769	1133.5626	567.2849	A	***1012.5786***	506.7929	995.5520	498.2796	994.5680	497.7876	10
13	**1222.6103**	611.8088	1205.5837	603.2955	1204.5997	602.8035	A	***941.5415***	471.2744	924.5149	462.7611	923.5309	462.2691	9
14	**1335.6943**	668.3508	1318.6678	659.8375	1317.6838	659.3455	L	***870.5043***	435.7558	853.4778	427.2425	852.4938	426.7505	8
15	1432.7471	716.8772	1415.7205	708.3639	1414.7365	707.8719	P	***757.4203***	379.2138	740.3937	370.7005	739.4097	370.2085	7
16	1533.7948	767.4010	1516.7682	758.8878	1515.7842	758.3957	T	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
17	1662.8374	831.9223	1645.8108	823.4090	1644.8268	822.9170	E	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
18	1733.8745	867.4409	1716.8479	858.9276	1715.8639	858.4356	A	***430.2772***	215.6423	413.2507	207.1290			4
19	**1804.9116**	902.9594	1787.8850	894.4462	1786.9010	893.9542	A	***359.2401***	180.1237	342.2136	171.6104			3
20	**1917.9957**	959.5015	1900.9691	950.9882	1899.9851	950.4962	L	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GFGVAIVGNYTAALPTEAALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
110.9	2091.1000	0.0086	GFGVAIVGNYTAALPTEAALR
17.4	2091.1000	0.0087	EWEEYVQIRTLVEKIR
13.3	2091.1142	-0.0055	VQIVGEMMSVMKNVVAIVK
11.3	2091.1001	0.0086	GAVAVFVTPIGDGEYEAKIR
9.4	2091.1187	-0.0100	GFQHTGIYSVMIQKVILR
7.2	2091.1142	-0.0055	VQIVGEMMSVMKNVVAIVK
6.7	2091.1142	-0.0055	VQIVGEMMSVMKNVVAIVK
5.7	2091.1142	-0.0055	VQIVGEMMSVMKNVVAIVK
5.7	2091.1142	-0.0055	VQIVGEMMSVMKNVVAIVK
5.0	2090.1021	1.0066	NTLLNGAAIFFPNRQTRR

Mascot: http://www.matrixscience.com/

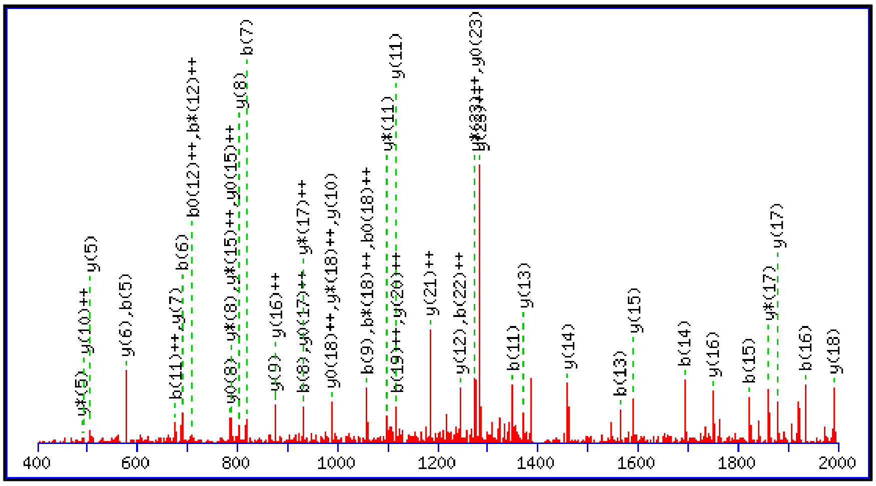
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25599: 2807.406828 from(1404.710690,2+) intensity(0.0000) rtinseconds(1928) scans(4950) index(9635)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum4248_scans__4950
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

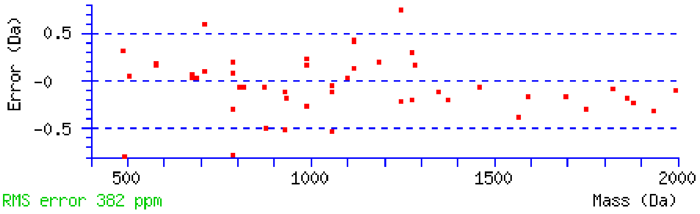
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

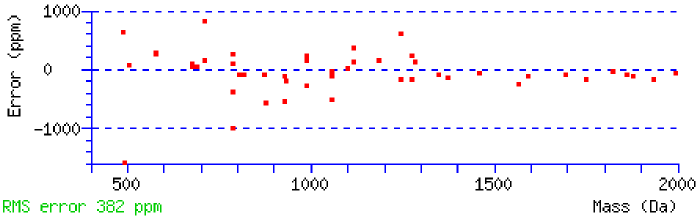


Monoisotopic mass of neutral peptide Mr(calc): 2807.3946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N22 : Deamidated (NQ)
Ions Score: 88 **Expect:** 4.6e-007
Matches : 49/272 fragment ions using 64 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2695.3178	1348.1625	2678.2913	1339.6493	2677.3073	1339.1573	24
3	340.1867	170.5970			322.1761	161.5917	P	2566.2752	1283.6412	2549.2487	1275.1280	2548.2647	1274.6360	23
4	439.2551	220.1312			421.2445	211.1259	V	2469.2225	1235.1149	2452.1959	1226.6016	2451.2119	1226.1096	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2370.1540	1185.5807	2353.1275	1177.0674	2352.1435	1176.5754	21
6	**689.3981**	345.2027			671.3875	336.1974	L	2233.0951	1117.0512	2216.0686	1108.5379	2215.0846	1108.0459	20
7	**817.4567**	409.2320	800.4301	400.7187	799.4461	400.2267	Q	2120.0111	1060.5092	2102.9845	1051.9959	2102.0005	1051.5039	19
8	**930.5407**	465.7740	913.5142	457.2607	912.5302	456.7687	L	***1991.9525***	996.4799	1974.9259	987.9666	1973.9419	987.4746	18
9	**1058.5993**	529.8033	1041.5728	521.2900	1040.5887	520.7980	Q	***1878.8684***	939.9379	1861.8419	931.4246	1860.8579	930.9326	17
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	C	***1750.8098***	875.9086	1733.7833	867.3953	1732.7993	866.9033	16
11	**1349.6704**	675.3389	1332.6439	666.8256	1331.6599	666.3336	M	***1590.7792***	795.8932	1573.7527	787.3800	1572.7686	786.8880	15
12	1436.7025	718.8549	1419.6759	710.3416	1418.6919	709.8496	S	***1459.7387***	730.3730	1442.7122	721.8597	1441.7282	721.3677	14
13	**1564.7610**	782.8842	1547.7345	774.3709	1546.7505	773.8789	Q	***1372.7067***	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
14	**1693.8036**	847.4055	1676.7771	838.8922	1675.7931	838.4002	E	***1244.6481***	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	**1821.8622**	911.4347	1804.8357	902.9215	1803.8517	902.4295	Q	***1115.6055***	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	**1934.9463**	967.9768	1917.9197	959.4635	1916.9357	958.9715	L	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2005.9834	1003.4953	1988.9568	994.9821	1987.9728	994.4901	A	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2134.0420	1067.5246	2117.0154	1059.0114	2116.0314	1058.5193	Q	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2233.1104	1117.0588	2216.0838	1108.5456	2215.0998	1108.0535	V	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2304.1475	1152.5774	2287.1210	1144.0641	2286.1369	1143.5721	A	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2375.1846	1188.0959	2358.1581	1179.5827	2357.1741	1179.0907	A	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5
22	2490.2116	1245.6094	2473.1850	1237.0961	2472.2010	1236.6041	N	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4

23	2561.2487	1281.1280	2544.2221	1272.6147	2543.2381	1272.1227	**A**	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2662.2964	1331.6518	2645.2698	1323.1385	2644.2858	1322.6465	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
87.8	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated N22 98.34%
70.0	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18 1.65%
46.4	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15 0.01%
42.9	2806.4106	0.9963	LEPVHLQLQCMSQEQLAQVAANATK	
38.4	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13 0.00%
29.0	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9 0.00%
25.3	2807.3946	0.0123	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7 0.00%
11.2	2807.4044	0.0024	EIPSDMKGINVATSLRSALTMELNGK	
8.9	2807.4044	0.0024	EIPSDMKGINVATSLRSALTMELNGK	
8.2	2807.4164	-0.0095	KGQLVYGQLMEPVNRENFTQTLPK	

Mascot: http://www.matrixscience.com/

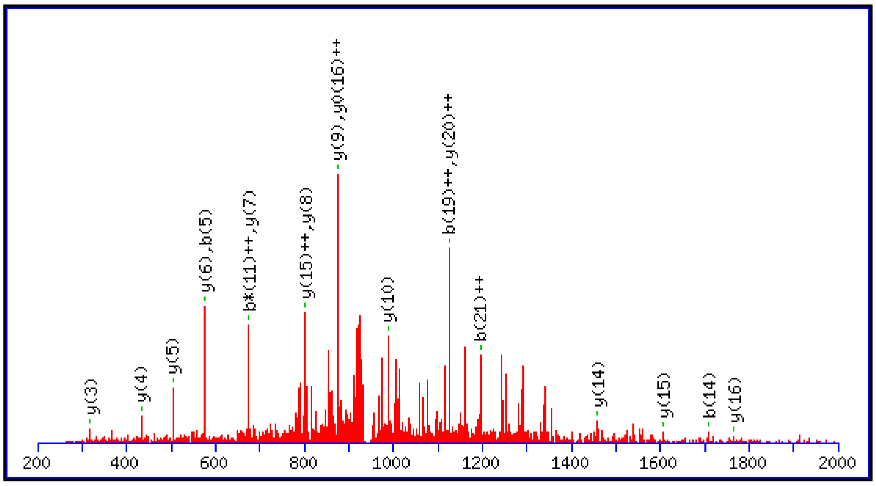
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25709: 2823.387462 from(942.136430,3+) intensity(10599.6465) rtinseconds(1688) scans(3981) index(11820)
Title: 111019_Est_ISCardio_NMI_YS_G_8Spectrum3402_scans__3981
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

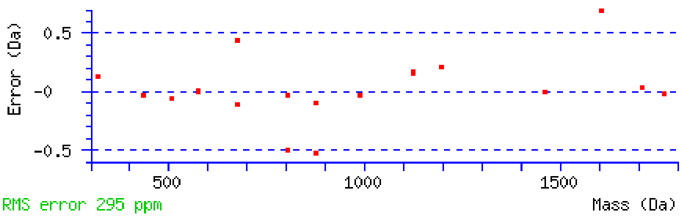
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

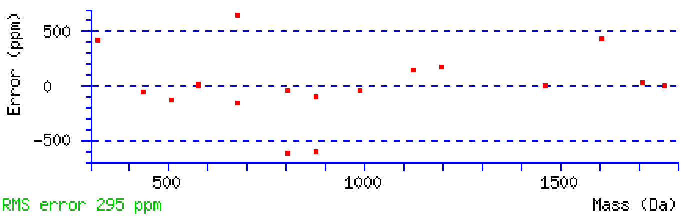


Monoisotopic mass of neutral peptide Mr(calc): 2823.3895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N22 : Deamidated (NQ)
Ions Score: 81 **Expect:** 2e-006
Matches : 19/416 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	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2711.3127	1356.1600	2694.2862	1347.6467	2693.3022	1347.1547	24
3	340.1867	170.5970			322.1761	161.5917	P	2582.2701	1291.6387	2565.2436	1283.1254	2564.2596	1282.6334	23
4	439.2551	220.1312			421.2445	211.1259	V	2485.2174	1243.1123	2468.1908	1234.5991	2467.2068	1234.1070	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2386.1490	1193.5781	2369.1224	1185.0648	2368.1384	1184.5728	21
6	689.3981	345.2027			671.3875	336.1974	L	2249.0900	1125.0487	2232.0635	1116.5354	2231.0795	1116.0434	20
7	817.4567	409.2320	800.4301	400.7187	799.4461	400.2267	Q	2136.0060	1068.5066	2118.9794	1059.9934	2117.9954	1059.5013	19
8	930.5407	465.7740	913.5142	457.2607	912.5302	456.7687	L	2007.9474	1004.4773	1990.9209	995.9641	1989.9368	995.4721	18
9	1058.5993	529.8033	1041.5728	521.2900	1040.5887	520.7980	Q	1894.8633	947.9353	1877.8368	939.4220	1876.8528	938.9300	17
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	C	***1766.8048***	883.9060	1749.7782	875.3927	1748.7942	874.9007	16
11	1365.6654	683.3363	1348.6388	674.8230	1347.6548	674.3310	M	***1606.7741***	803.8907	1589.7476	795.3774	1588.7636	794.8854	15
12	1452.6974	726.8523	1435.6708	718.3391	1434.6868	717.8470	S	***1459.7387***	730.3730	1442.7122	721.8597	1441.7282	721.3677	14
13	1580.7560	790.8816	1563.7294	782.3683	1562.7454	781.8763	Q	1372.7067	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
14	**1709.7986**	855.4029	1692.7720	846.8896	1691.7880	846.3976	E	1244.6481	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	1837.8571	919.4322	1820.8306	910.9189	1819.8466	910.4269	Q	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	1950.9412	975.9742	1933.9146	967.4610	1932.9306	966.9690	L	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2021.9783	1011.4928	2004.9518	1002.9795	2003.9677	1002.4875	A	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2150.0369	1075.5221	2133.0103	1067.0088	2132.0263	1066.5168	Q	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2249.1053	**1125.0563**	2232.0788	1116.5430	2231.0947	1116.0510	V	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2320.1424	1160.5748	2303.1159	1152.0616	2302.1319	1151.5696	A	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2391.1795	**1196.0934**	2374.1530	1187.5801	2373.1690	1187.0881	A	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2506.2065	1253.6069	2489.1799	1245.0936	2488.1959	1244.6016	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2577.2436	1289.1254	2560.2170	1280.6122	2559.2330	1280.1201	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2678.2913	1339.6493	2661.2647	1331.1360	2660.2807	1330.6440	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.4	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated N22 98.33%
59.9	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15 0.70%
59.3	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18 0.60%
56.8	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13 0.34%
42.7	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9 0.01%
39.4	2823.3895	-0.0020	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7 0.01%
5.3	2823.3821	0.0054	LLDQTQNVHTVLLGNDSNQGLGNMNK	
5.3	2823.3821	0.0054	LLDQTQNVHTVLLGNDSNQGLGNMNK	
5.2	2823.3861	0.0013	IEPAPLAQFAPQRSTTELSSHQPTSM	
2.6	2822.3794	1.0080	GRQEKTTAPSGGSAPPEQALPQESATAR	

Mascot: http://www.matrixscience.com/

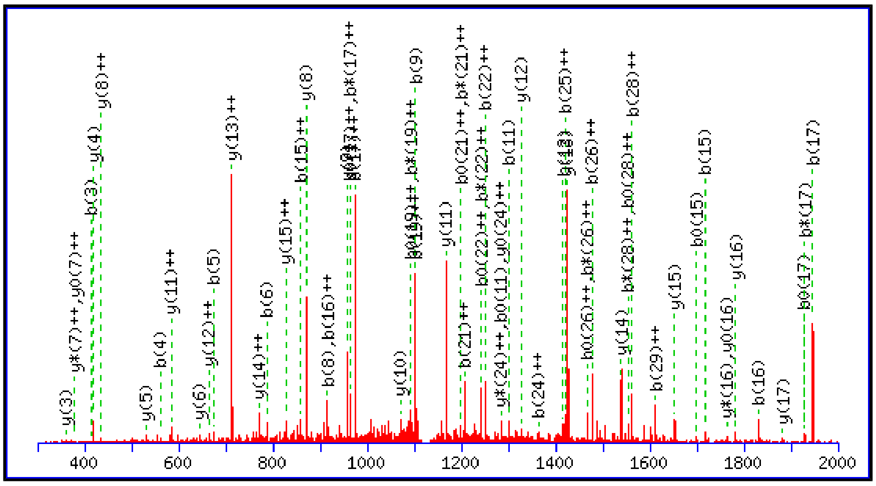
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LYHFLLGAWSLNATELDPCPLSPELLGLTK**
Found in **M0QYW3** in **con_Xuniprot_HUMAN3**, M0QYW3_HUMAN N-acetylmuramoyl-L-alanine amidase (Fragment) OS=Homo sapiens GN=PGLYRP2 PE=2 SV=1

Match to Query 27548: 3368.743092 from(1123.921640,3+) intensity(18209.6191) rtinseconds(2753) scans(7060) index(14251)
Title: 111019_Est_MI_YP_G_02Spectrum6182_scans__7060
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

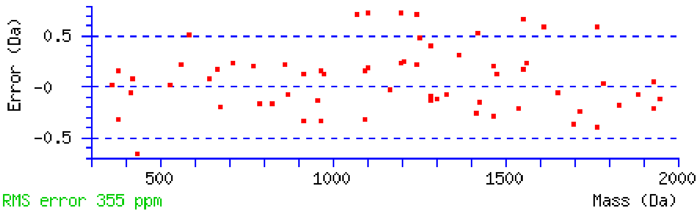
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

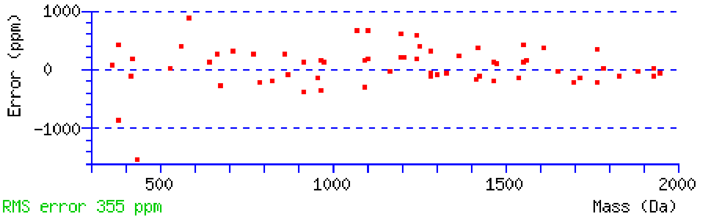


```
Monoisotopic mass of neutral peptide Mr(calc): 3368.7366
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N12     : Deamidated (NQ)
Ions Score: 73  Expect: 9.3e-006
Matches : 64/306 fragment ions using 119 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							30
2	277.1547	139.0810					Y	3256.6599	1628.8336	3239.6333	1620.3203	3238.6493	1619.8283	29
3	***414.2136***	207.6104					H	3093.5965	1547.3019	3076.5700	1538.7886	3075.5860	1538.2966	28
4	***561.2820***	281.1446					F	2956.5376	1478.7725	2939.5111	1470.2592	2938.5271	1469.7672	27
5	***674.3661***	337.6867					L	2809.4692	1405.2382	2792.4427	1396.7250	2791.4586	1396.2330	26
6	***787.4501***	394.2287					L	2696.3851	1348.6962	2679.3586	1340.1829	2678.3746	1339.6909	25
7	844.4716	422.7394					G	2583.3011	1292.1542	2566.2745	1283.6409	2565.2905	1283.1489	24
8	***915.5087***	458.2580					A	2526.2796	1263.6434	2509.2531	1255.1302	2508.2691	1254.6382	23
9	***1101.5880***	551.2976					W	2455.2425	1228.1249	2438.2160	1219.6116	2437.2319	1219.1196	22
10	1188.6200	594.8137			1170.6095	585.8084	S	2269.1632	1135.0852	2252.1366	1126.5720	2251.1526	1126.0800	21
11	***1301.7041***	651.3557			1283.6935	642.3504	L	2182.1312	1091.5692	2165.1046	1083.0559	2164.1206	1082.5639	20
12	***1416.7310***	708.8692	1399.7045	700.3559	1398.7205	699.8639	N	2069.0471	1035.0272	2052.0206	1026.5139	2051.0365	1026.0219	19
13	1487.7682	744.3877	1470.7416	735.8744	1469.7576	735.3824	A	1954.0202	977.5137	1936.9936	969.0004	1936.0096	968.5084	18
14	1588.8158	794.9116	1571.7893	786.3983	1570.8053	785.9063	T	***1882.9830***	941.9952	1865.9565	933.4819	1864.9725	932.9899	17
15	***1717.8584***	**859.4329**	1700.8319	850.9196	1699.8479	850.4276	E	***1781.9354***	891.4713	1764.9088	882.9580	1763.9248	882.4660	16
16	***1830.9425***	**915.9749**	1813.9160	907.4616	1812.9319	906.9696	L	***1652.8928***	826.9500	1635.8662	818.4367	1634.8822	817.9447	15
17	***1945.9694***	**973.4884**	1928.9429	964.9751	1927.9589	964.4831	D	***1539.8087***	770.4080	1522.7822	761.8947	1521.7981	761.4027	14
18	2043.0222	1022.0147	2025.9957	1013.5015	2025.0116	1013.0095	P	***1424.7818***	712.8945	1407.7552	704.3812	1406.7712	703.8892	13
19	2203.0529	**1102.0301**	2186.0263	1093.5168	2185.0423	1093.0248	C	***1327.7290***	664.3681	1310.7025	655.8549	1309.7184	655.3629	12
20	2300.1056	1150.5564	2283.0791	1142.0432	2282.0951	1141.5512	P	***1167.6984***	584.3528	1150.6718	575.8395	1149.6878	575.3475	11
21	2413.1897	**1207.0985**	2396.1631	1198.5852	2395.1791	1198.0932	L	***1070.6456***	535.8264	1053.6190	527.3132	1052.6350	526.8211	10
22	2500.2217	**1250.6145**	2483.1952	1242.1012	2482.2111	1241.6092	S	***957.5615***	479.2844	940.5350	470.7711	939.5510	470.2791	9

23	2597.2745	1299.1409	2580.2479	1290.6276	2579.2639	1290.1356	**P**	***870.5295***	435.7684	853.5029	427.2551	852.5189	426.7631	**8**
24	2726.3171	**1363.6622**	2709.2905	1355.1489	2708.3065	1354.6569	**E**	773.4767	387.2420	756.4502	378.7287	755.4662	378.2367	**7**
25	2839.4011	**1420.2042**	2822.3746	1411.6909	2821.3906	1411.1989	**L**	***644.4341***	322.7207	627.4076	314.2074	626.4236	313.7154	**6**
26	2952.4852	**1476.7462**	2935.4586	1468.2330	2934.4746	1467.7410	**L**	***531.3501***	266.1787	514.3235	257.6654	513.3395	257.1734	**5**
27	3009.5067	1505.2570	2992.4801	1496.7437	2991.4961	1496.2517	**G**	***418.2660***	209.6366	401.2395	201.1234	400.2554	200.6314	**4**
28	3122.5907	**1561.7990**	3105.5642	1553.2857	3104.5802	1552.7937	**L**	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
29	3223.6384	**1612.3228**	3206.6119	1603.8096	3205.6278	1603.3176	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
30							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LYHFLLGAWSLNATELDPCPLSPELLGLTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
72.6	3368.7366	0.0065	LYHFLLGAWSLNATELDPCPLSPELLGLTK
52.3	3367.7526	0.9905	LYHFLLGAWSLNATELDPCPLSPELLGLTK
14.0	3368.7472	-0.0041	DLMQVLATFCTEINVNFRASTEVVLLNKK
7.7	3367.7302	1.0129	KPIALIAVSEKGSMNLMLQVNMTSGHSSAPPK
5.7	3366.7223	2.0208	THTYFNPLWYSQLKFLAVKQMHSLIER
5.2	3366.7349	2.0082	ILGTTVKLMELKPNTCYCLSVRAANTAGVGK
5.1	3367.7372	1.0059	QRQDDLDTLGLGLQGGIPNGYLVLDLSVQGGR
4.7	3367.7372	1.0059	QRQDDLDTLGLGLQGGIPNGYLVLDLSVQGGR
4.7	3366.7307	2.0124	IRQLAERSFEGLGQLEVLTLDHNQLQEVK
4.2	3367.7374	1.0057	DMNPLATKIVGTKPEVSFYPQGQLISYVVR

Mascot: http://www.matrixscience.com/

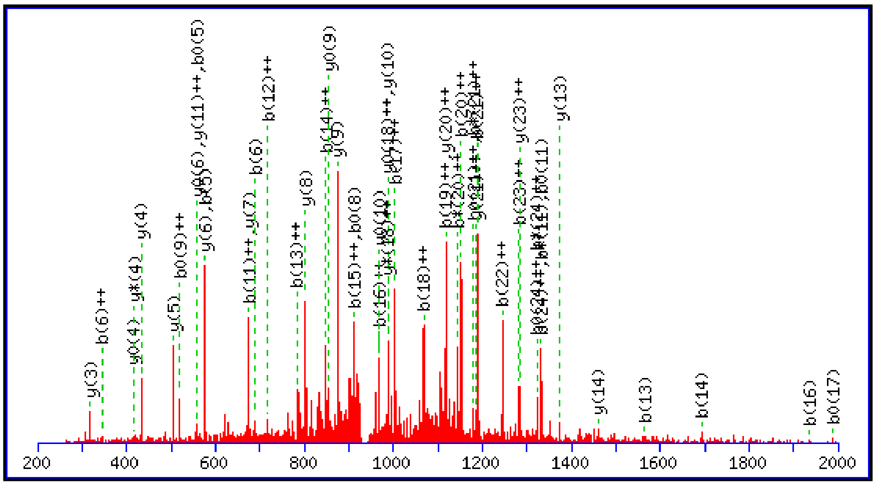
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25612: 2808.387462 from(937.136430,3+) intensity(36048.7891) rtinseconds(2054) scans(5254) index(2164)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum4558_scans__5254
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

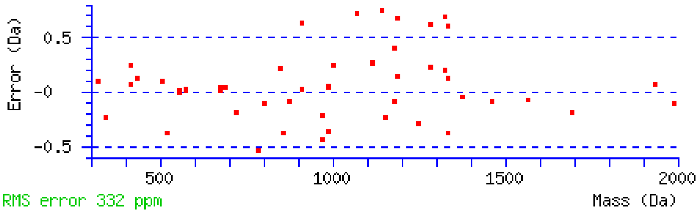
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

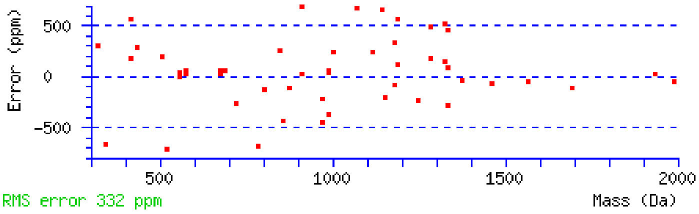


```
Monoisotopic mass of neutral peptide Mr(calc): 2808.3786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Deamidated (NQ)
N22     : Deamidated (NQ)
Ions Score: 64  Expect: 9.6e-005
Matches : 52/272 fragment ions using 107 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2696.3018	1348.6546	2679.2753	1340.1413	2678.2913	1339.6493	24
3	340.1867	170.5970			322.1761	161.5917	P	2567.2592	1284.1333	2550.2327	1275.6200	2549.2487	1275.1280	23
4	439.2551	220.1312			421.2445	211.1259	V	2470.2065	1235.6069	2453.1799	1227.0936	2452.1959	1226.6016	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2371.1381	1186.0727	2354.1115	1177.5594	2353.1275	1177.0674	21
6	**689.3981**	***345.2027***			671.3875	336.1974	L	2234.0791	1117.5432	2217.0526	1109.0299	2216.0686	1108.5379	20
7	817.4567	409.2320	800.4301	400.7187	799.4461	400.2267	Q	2120.9951	1061.0012	2103.9685	1052.4879	2102.9845	1051.9959	19
8	930.5407	465.7740	913.5142	457.2607	912.5302	456.7687	L	1992.9365	996.9719	1975.9100	988.4586	1974.9259	987.9666	18
9	1058.5993	529.8033	1041.5728	521.2900	1040.5887	520.7980	Q	1879.8524	940.4299	1862.8259	931.9166	1861.8419	931.4246	17
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	C	1751.7939	876.4006	1734.7673	867.8873	1733.7833	867.3953	16
11	1349.6704	***675.3389***	1332.6439	666.8256	1331.6599	666.3336	M	1591.7632	796.3852	1574.7367	787.8720	1573.7527	787.3800	15
12	1436.7025	***718.8549***	1419.6759	710.3416	1418.6919	709.8496	S	**1460.7227**	730.8650	1443.6962	722.3517	1442.7122	721.8597	14
13	**1565.7451**	***783.3762***	1548.7185	774.8629	1547.7345	774.3709	Q	**1373.6907**	687.3490	1356.6642	678.8357	1355.6801	678.3437	13
14	**1694.7877**	***847.8975***	1677.7611	839.3842	1676.7771	838.8922	E	1244.6481	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	1822.8462	***911.9268***	1805.8197	903.4135	1804.8357	902.9215	Q	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	**1935.9303**	***968.4688***	1918.9037	959.9555	1917.9197	959.4635	L	**987.5469**	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2006.9674	***1003.9873***	1989.9409	995.4741	1988.9568	994.9821	A	**874.4629**	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2135.0260	***1068.0166***	2117.9994	1059.5034	2117.0154	1059.0114	Q	**803.4258**	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2234.0944	***1117.5508***	2217.0679	1109.0376	2216.0838	1108.5456	V	**675.3672**	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2305.1315	***1153.0694***	2288.1050	1144.5561	2287.1210	1144.0641	A	**576.2988**	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2376.1686	***1188.5880***	2359.1421	1180.0747	2358.1581	1179.5827	A	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2491.1956	***1246.1014***	2474.1690	1237.5882	2473.1850	1237.0961	**N**	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2562.2327	***1281.6200***	2545.2061	1273.1067	2544.2221	1272.6147	**A**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2663.2804	***1332.1438***	2646.2538	1323.6305	2645.2698	1323.1385	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
64.4	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 13.49%
64.4	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 13.49%
63.5	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 11.02%
63.5	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, N22 11.02%
63.3	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 10.52%
63.3	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 10.52%
62.4	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q18 8.59%
62.4	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q18 8.59%
59.9	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q15 4.78%
55.2	2808.3786	0.0089	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 1.61%

Mascot: http://www.matrixscience.com/

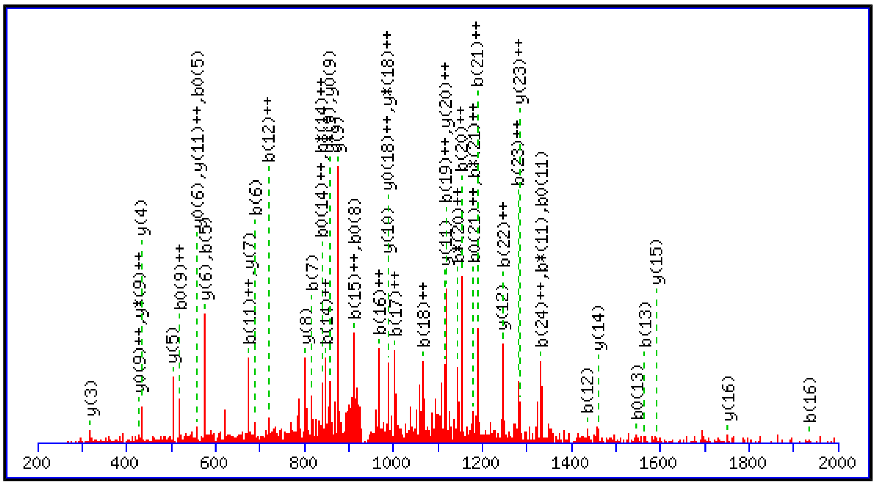
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25614: 2808.391992 from(937.137940,3+) intensity(40898.8477) rtinseconds(2030) scans(5185) index(2160)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum4496_scans__5185
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

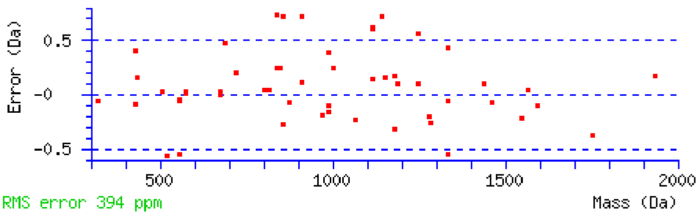
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

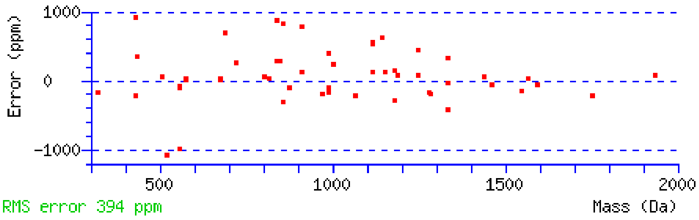


Monoisotopic mass of neutral peptide Mr(calc): 2808.3786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 63 **Expect:** 0.00014
Matches : 53/272 fragment ions using 89 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2696.3018	1348.6546	2679.2753	1340.1413	2678.2913	1339.6493	24
3	340.1867	170.5970			322.1761	161.5917	P	2567.2592	1284.1333	2550.2327	1275.6200	2549.2487	1275.1280	23
4	439.2551	220.1312			421.2445	211.1259	V	2470.2065	1235.6069	2453.1799	1227.0936	2452.1959	1226.6016	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2371.1381	1186.0727	2354.1115	1177.5594	2353.1275	1177.0674	21
6	**689.3981**	345.2027			671.3875	336.1974	L	2234.0791	1117.5432	2217.0526	1109.0299	2216.0686	1108.5379	20
7	**817.4567**	409.2320	800.4301	400.7187	799.4461	400.2267	Q	2120.9951	1061.0012	2103.9685	1052.4879	2102.9845	1051.9959	19
8	930.5407	465.7740	913.5142	457.2607	912.5302	456.7687	L	1992.9365	996.9719	1975.9100	988.4586	1974.9259	987.9666	18
9	1058.5993	529.8033	1041.5728	521.2900	1040.5887	520.7980	Q	1879.8524	940.4299	1862.8259	931.9166	1861.8419	931.4246	17
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	C	***1751.7939***	876.4006	1734.7673	867.8873	1733.7833	867.3953	16
11	1349.6704	***675.3389***	1332.6439	666.8256	1331.6599	666.3336	M	***1591.7632***	796.3852	1574.7367	787.8720	1573.7527	787.3800	15
12	**1436.7025**	***718.8549***	1419.6759	710.3416	1418.6919	709.8496	S	***1460.7227***	730.8650	1443.6962	722.3517	1442.7122	721.8597	14
13	**1564.7610**	782.8842	1547.7345	774.3709	1546.7505	773.8789	Q	1373.6907	687.3490	1356.6642	678.8357	1355.6801	678.3437	13
14	1693.8036	***847.4055***	1676.7771	838.8922	1675.7931	838.4002	E	***1245.6321***	623.3197	1228.6056	614.8064	1227.6216	614.3144	12
15	1822.8462	***911.9268***	1805.8197	903.4135	1804.8357	902.9215	Q	***1116.5895***	558.7984	1099.5630	550.2851	1098.5790	549.7931	11
16	**1935.9303**	***968.4688***	1918.9037	959.9555	1917.9197	959.4635	L	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2006.9674	***1003.9873***	1989.9409	995.4741	1988.9568	994.9821	A	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2135.0260	***1068.0166***	2117.9994	1059.5034	2117.0154	1059.0114	Q	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2234.0944	***1117.5508***	2217.0679	1109.0376	2216.0838	1108.5456	V	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2305.1315	***1153.0694***	2288.1050	1144.5561	2287.1210	1144.0641	A	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2376.1686	***1188.5880***	2359.1421	1180.0747	2358.1581	1179.5827	A	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2491.1956	***1246.1014***	2474.1690	1237.5882	2473.1850	1237.0961	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2562.2327	***1281.6200***	2545.2061	1273.1067	2544.2221	1272.6147	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2663.2804	***1332.1438***	2646.2538	1323.6305	2645.2698	1323.1385	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
62.7	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 14.71%
62.2	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, N22 13.08%
61.0	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 9.83%
60.7	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 9.24%
59.5	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q18 7.11%
59.4	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 6.87%
58.3	2807.3946	0.9974	LEPVHLQLQCMSQEQLAQVAANATK	
58.3	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q18 5.34%
58.0	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 5.01%
58.0	2808.3786	0.0134	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 5.00%

Mascot: http://www.matrixscience.com/

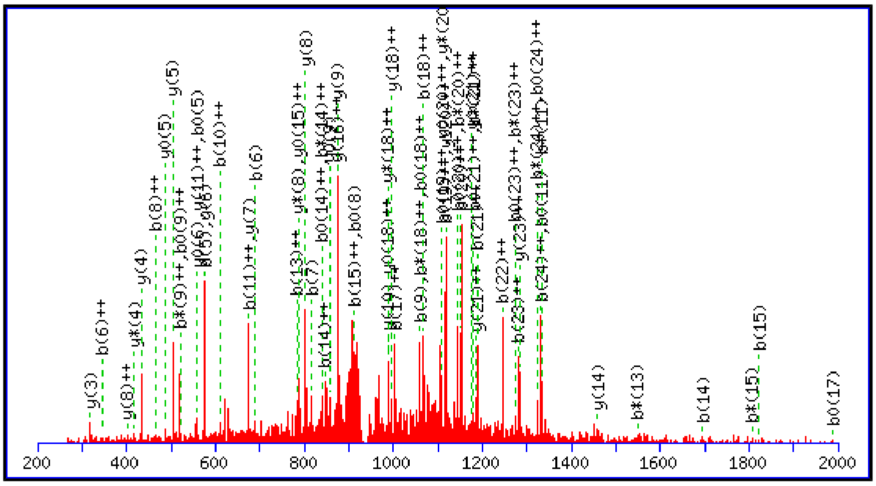
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25613: 2808.388002 from(937.136610,3+) intensity(44950.2148) rtinseconds(2137) scans(5238) index(9070)
Title: 111019_Est_ISCardio_NMI_YS_G_4Spectrum4505_scans__5238
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

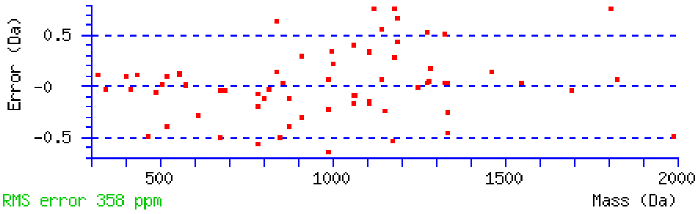
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

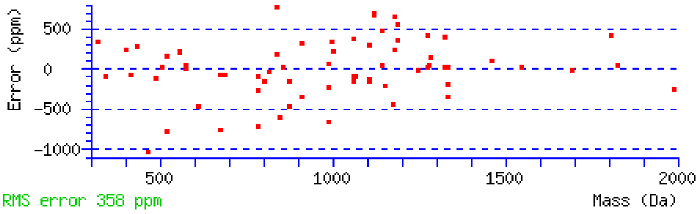


Monoisotopic mass of neutral peptide Mr(calc): 2808.3786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 53 **Expect:** 0.0014
Matches : 71/272 fragment ions using 156 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2696.3018	1348.6546	2679.2753	1340.1413	2678.2913	1339.6493	24
3	340.1867	170.5970			322.1761	161.5917	P	2567.2592	1284.1333	2550.2327	1275.6200	2549.2487	1275.1280	23
4	439.2551	220.1312			421.2445	211.1259	V	2470.2065	1235.6069	2453.1799	1227.0936	2452.1959	1226.6016	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2371.1381	1186.0727	2354.1115	1177.5594	2353.1275	1177.0674	21
6	**689.3981**	***345.2027***			671.3875	336.1974	L	2234.0791	1117.5432	2217.0526	1109.0299	2216.0686	1108.5379	20
7	**817.4567**	409.2320	800.4301	400.7187	799.4461	400.2267	Q	2120.9951	1061.0012	2103.9685	1052.4879	2102.9845	1051.9959	19
8	930.5407	***465.7740***	913.5142	457.2607	912.5302	456.7687	L	1992.9365	996.9719	1975.9100	988.4586	1974.9259	987.9666	18
9	**1059.5833**	530.2953	1042.5568	521.7820	1041.5728	521.2900	Q	1879.8524	940.4299	1862.8259	931.9166	1861.8419	931.4246	17
10	1219.6140	***610.3106***	1202.5874	601.7973	1201.6034	601.3053	C	1750.8098	875.9086	1733.7833	867.3953	1732.7993	866.9033	16
11	1350.6545	***675.8309***	1333.6279	667.3176	1332.6439	666.8256	M	1590.7792	795.8932	1573.7527	787.3800	1572.7686	786.8880	15
12	1437.6865	719.3469	1420.6599	710.8336	1419.6759	710.3416	S	**1459.7387**	730.3730	1442.7122	721.8597	1441.7282	721.3677	14
13	1565.7451	***783.3762***	1548.7185	774.8629	1547.7345	774.3709	Q	1372.7067	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
14	**1694.7877**	***847.8975***	1677.7611	839.3842	1676.7771	838.8922	E	1244.6481	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	**1822.8462**	***911.9268***	1805.8197	903.4135	1804.8357	902.9215	Q	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	1935.9303	968.4688	1918.9037	959.9555	1917.9197	959.4635	L	**987.5469**	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2006.9674	***1003.9873***	1989.9409	995.4741	1988.9568	994.9821	A	**874.4629**	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2135.0260	***1068.0166***	2117.9994	1059.5034	2117.0154	1059.0114	Q	**803.4258**	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2234.0944	***1117.5508***	2217.0679	1109.0376	2216.0838	1108.5456	V	**675.3672**	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2305.1315	***1153.0694***	2288.1050	1144.5561	2287.1210	1144.0641	A	**576.2988**	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2376.1686	***1188.5880***	2359.1421	1180.0747	2358.1581	1179.5827	A	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2491.1956	***1246.1014***	2474.1690	1237.5882	2473.1850	1237.0961	**N**	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2562.2327	***1281.6200***	2545.2061	1273.1067	2544.2221	1272.6147	**A**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2663.2804	***1332.1438***	2646.2538	1323.6305	2645.2698	1323.1385	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
52.7	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 26.71%
51.5	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q18 20.31%
48.6	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 10.27%
48.6	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 10.27%
48.0	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 9.11%
48.0	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 9.09%
46.9	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 7.02%
41.2	2807.3946	0.9934	LEPVHLQLQCMSQEQLAQVAANATK	
40.7	2807.3946	0.9934	LEPVHLQLQCMSQEQLAQVAANATK	
38.9	2808.3786	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q18 1.10%

Mascot: http://www.matrixscience.com/

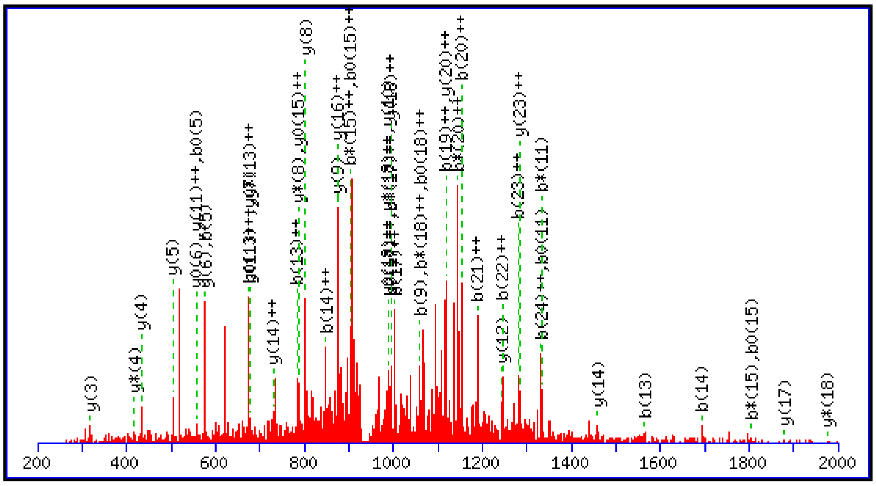
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25611: 2808.380112 from(937.133980,3+) intensity(47824.6680) rtinseconds(2016) scans(5204) index(9662)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum4475_scans__5204
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

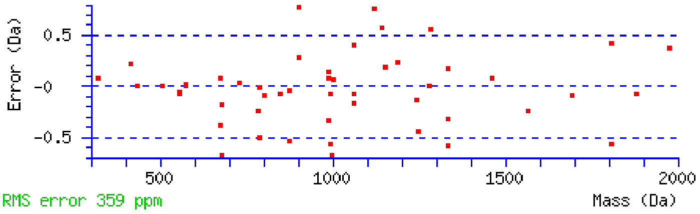
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

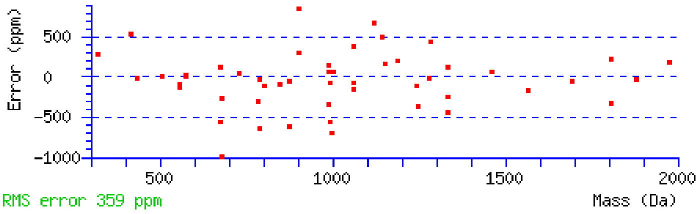


```
Monoisotopic mass of neutral peptide Mr(calc): 2808.3786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Deamidated (NQ)
N22    : Deamidated (NQ)
Ions Score: 47  Expect: 0.0049
Matches : 52/272 fragment ions using 88 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2696.3018	1348.6546	2679.2753	1340.1413	2678.2913	1339.6493	24
3	340.1867	170.5970			322.1761	161.5917	P	2567.2592	1284.1333	2550.2327	1275.6200	2549.2487	1275.1280	23
4	439.2551	220.1312			421.2445	211.1259	V	2470.2065	1235.6069	2453.1799	1227.0936	2452.1959	1226.6016	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2371.1381	1186.0727	2354.1115	1177.5594	2353.1275	1177.0674	21
6	689.3981	345.2027			671.3875	336.1974	L	2234.0791	1117.5432	2217.0526	1109.0299	2216.0686	1108.5379	20
7	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	Q	2120.9951	1061.0012	2103.9685	1052.4879	2102.9845	1051.9959	19
8	931.5247	466.2660	914.4982	457.7527	913.5142	457.2607	L	1991.9525	996.4799	1974.9259	987.9666	1973.9419	987.4746	18
9	**1059.5833**	530.2953	1042.5568	521.7820	1041.5728	521.2900	Q	***1878.8684***	939.9379	1861.8419	931.4246	1860.8579	930.9326	17
10	1219.6140	610.3106	1202.5874	601.7973	1201.6034	601.3053	C	1750.8098	875.9086	1733.7833	867.3953	1732.7993	866.9033	16
11	1350.6545	***675.8309***	1333.6279	667.3176	1332.6439	666.8256	M	1590.7792	795.8932	1573.7527	787.3800	1572.7686	786.8880	15
12	1437.6865	719.3469	1420.6599	710.8336	1419.6759	710.3416	S	***1459.7387***	730.3730	1442.7122	721.8597	1441.7282	721.3677	14
13	**1565.7451**	***783.3762***	1548.7185	774.8629	1547.7345	774.3709	Q	1372.7067	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
14	**1694.7877**	***847.8975***	1677.7611	839.3842	1676.7771	838.8922	E	***1244.6481***	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	1822.8462	911.9268	1805.8197	903.4135	1804.8357	902.9215	Q	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	1935.9303	968.4688	1918.9037	959.9555	1917.9197	959.4635	L	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2006.9674	***1003.9873***	1989.9409	995.4741	1988.9568	994.9821	A	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2135.0260	1068.0166	2117.9994	1059.5034	2117.0154	1059.0114	Q	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2234.0944	***1117.5508***	2217.0679	1109.0376	2216.0838	1108.5456	V	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2305.1315	***1153.0694***	2288.1050	1144.5561	2287.1210	1144.0641	A	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2376.1686	***1188.5880***	2359.1421	1180.0747	2358.1581	1179.5827	A	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2491.1956	***1246.1014***	2474.1690	1237.5882	2473.1850	1237.0961	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2562.2327	***1281.6200***	2545.2061	1273.1067	2544.2221	1272.6147	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2663.2804	***1332.1438***	2646.2538	1323.6305	2645.2698	1323.1385	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
47.4	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, N22 48.83%
41.1	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q18 11.26%
40.8	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 10.63%
39.9	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 8.60%
35.8	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 3.36%
35.8	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q18 3.34%
35.8	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 3.32%
35.7	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 3.26%
32.4	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 1.53%
31.3	2808.3786	0.0015	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q15 1.18%

Mascot: http://www.matrixscience.com/

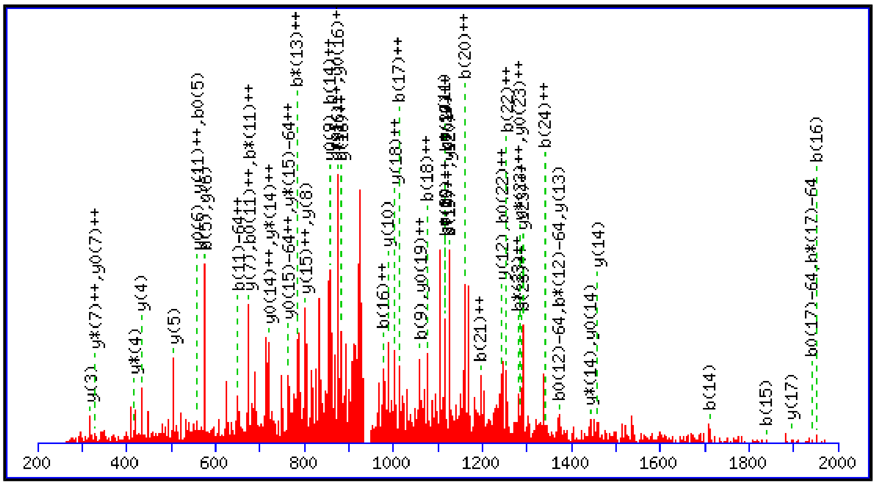
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25743: 2824.377912 from(942.466580,3+) intensity(27197.3047) rtinseconds(1795) scans(4564) index(9571)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum3910_scans__4564
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

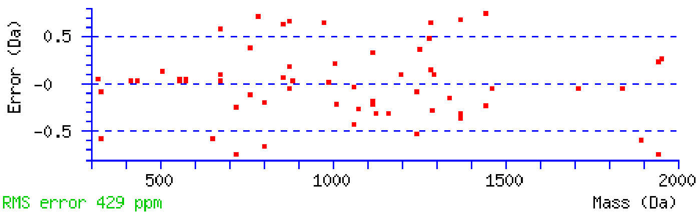
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

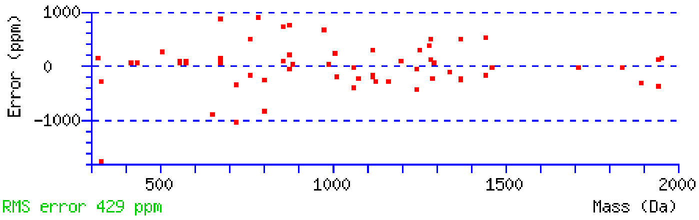


Monoisotopic mass of neutral peptide Mr(calc): 2824.3735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Deamidated (NQ)
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N22 : Deamidated (NQ)
Ions Score: 41 **Expect:** 0.022
Matches : 65/416 fragment ions using 137 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							25
2	243.1339	122.0706			225.1234	113.0653	E	2712.2967	1356.6520	2695.2702	1348.1387	2694.2862	1347.6467	24
3	340.1867	170.5970			322.1761	161.5917	P	2583.2542	1292.1307	2566.2276	1283.6174	2565.2436	1283.1254	23
4	439.2551	220.1312			421.2445	211.1259	V	2486.2014	1243.6043	2469.1748	1235.0911	2468.1908	1234.5991	22
5	**576.3140**	288.6606			558.3035	279.6554	H	2387.1330	1194.0701	2370.1064	1185.5569	2369.1224	1185.0648	21
6	689.3981	345.2027			671.3875	336.1974	L	2250.0741	1125.5407	2233.0475	1117.0274	2232.0635	1116.5354	20
7	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	Q	2136.9900	1068.9986	2119.9635	1060.4854	2118.9794	1059.9934	19
8	931.5247	466.2660	914.4982	457.7527	913.5142	457.2607	L	2007.9474	1004.4773	1990.9209	995.9641	1989.9368	995.4721	18
9	**1059.5833**	530.2953	1042.5568	521.7820	1041.5728	521.2900	Q	***1894.8633***	947.9353	1877.8368	939.4220	1876.8528	938.9300	17
10	1219.6140	610.3106	1202.5874	601.7973	1201.6034	601.3053	C	1766.8048	883.9060	1749.7782	875.3927	1748.7942	874.9007	16
11	1366.6494	683.8283	1349.6228	675.3150	1348.6388	674.8230	M	1606.7741	803.8907	1589.7476	795.3774	1588.7636	794.8854	15
12	1453.6814	727.3443	1436.6549	718.8311	1435.6708	718.3391	S	***1459.7387***	730.3730	1442.7122	721.8597	1441.7282	721.3677	14
13	1581.7400	791.3736	1564.7134	782.8604	1563.7294	782.3683	Q	***1372.7067***	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
14	**1710.7826**	**855.8949**	1693.7560	847.3816	1692.7720	846.8896	E	***1244.6481***	622.8277	1227.6216	614.3144	1226.6375	613.8224	12
15	**1838.8411**	919.9242	1821.8146	911.4109	1820.8306	910.9189	Q	***1115.6055***	558.3064	1098.5790	549.7931	1097.5950	549.3011	11
16	**1951.9252**	**976.4662**	1934.8987	967.9530	1933.9146	967.4610	L	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	10
17	2022.9623	**1011.9848**	2005.9358	1003.4715	2004.9518	1002.9795	A	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	9
18	2151.0209	**1076.0141**	2133.9944	1067.5008	2133.0103	1067.0088	Q	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	8
19	2250.0893	**1125.5483**	2233.0628	1117.0350	2232.0788	1116.5430	V	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	7
20	2321.1264	**1161.0669**	2304.0999	1152.5536	2303.1159	1152.0616	A	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	6
21	2392.1635	**1196.5854**	2375.1370	1188.0721	2374.1530	1187.5801	A	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	5

22	2507.1905	**1254.0989**	2490.1639	1245.5856	2489.1799	1245.0936	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2578.2276	**1289.6174**	2561.2011	1281.1042	2560.2170	1280.6122	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2679.2753	**1340.1413**	2662.2487	1331.6280	2661.2647	1331.1360	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.0	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, N22 45.05%
37.5	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 20.36%
36.3	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 15.55%
32.9	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 7.11%
29.5	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 3.21%
28.4	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 2.50%
25.2	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, Q18 1.20%
24.6	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 1.05%
22.7	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q13 0.67%
22.6	2824.3735	0.0044	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q15 0.66%

Mascot: http://www.matrixscience.com/

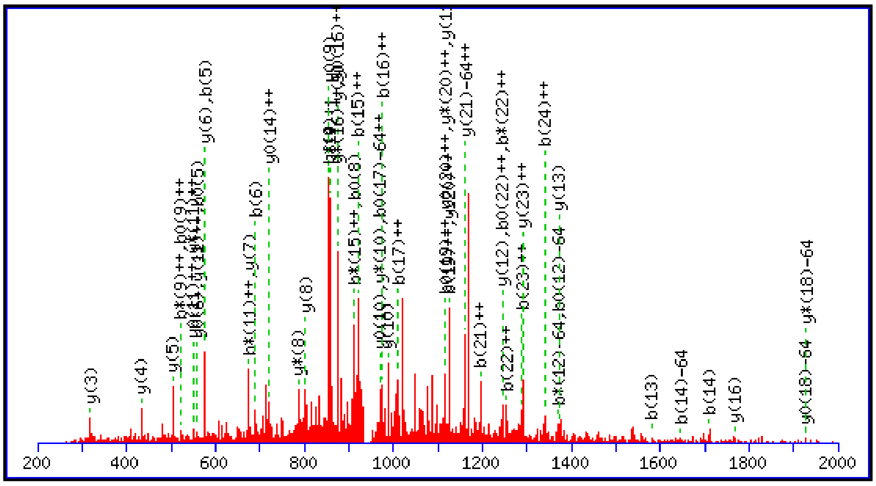
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25744: 2824.382922 from(942.468250,3+) intensity(38684.0469) rtinseconds(1782) scans(4528) index(9564)
Title: 111019_Est_ISCardio_NMI_YS_G_5Spectrum3878_scans__4528
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

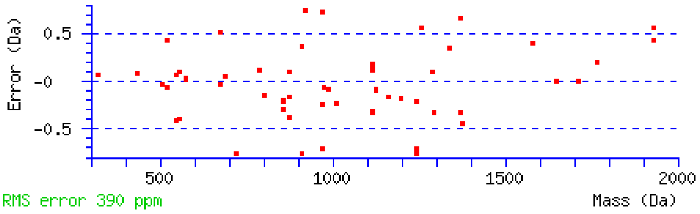
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

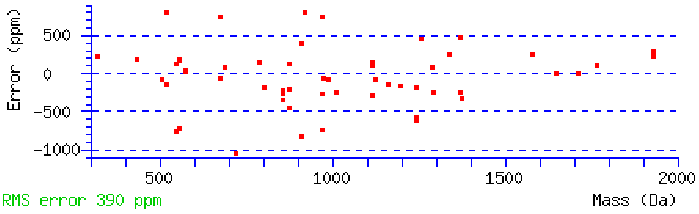


Monoisotopic mass of neutral peptide Mr(calc): 2824.3735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q15 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 39 **Expect:** 0.038
Matches : 58/416 fragment ions using 103 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**L**							**25**
2	243.1339	122.0706			225.1234	113.0653	**E**	2712.2967	1356.6520	2695.2702	1348.1387	2694.2862	1347.6467	**24**
3	340.1867	170.5970			322.1761	161.5917	**P**	2583.2542	1292.1307	2566.2276	1283.6174	2565.2436	1283.1254	**23**
4	439.2551	220.1312			421.2445	211.1259	**V**	2486.2014	1243.6043	2469.1748	1235.0911	2468.1908	1234.5991	**22**
5	**576.3140**	288.6606			558.3035	279.6554	**H**	2387.1330	1194.0701	2370.1064	1185.5569	2369.1224	1185.0648	**21**
6	**689.3981**	345.2027			671.3875	336.1974	**L**	2250.0741	1125.5407	2233.0475	1117.0274	2232.0635	1116.5354	**20**
7	817.4567	409.2320	800.4301	400.7187	799.4461	400.2267	**Q**	2136.9900	1068.9986	2119.9635	1060.4854	2118.9794	1059.9934	**19**
8	930.5407	465.7740	913.5142	457.2607	912.5302	456.7687	**L**	2008.9314	1004.9693	1991.9049	996.4561	1990.9209	995.9641	**18**
9	1058.5993	529.8033	1041.5728	521.2900	1040.5887	520.7980	**Q**	1895.8474	948.4273	1878.8208	939.9140	1877.8368	939.4220	**17**
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	**C**	***1767.7888***	884.3980	1750.7622	875.8848	1749.7782	875.3927	**16**
11	1365.6654	683.3363	1348.6388	674.8230	1347.6548	674.3310	**M**	1607.7581	804.3827	1590.7316	795.8694	1589.7476	795.3774	**15**
12	1452.6974	726.8523	1435.6708	718.3391	1434.6868	717.8470	**S**	1460.7227	730.8650	1443.6962	722.3517	1442.7122	721.8597	**14**
13	**1580.7560**	790.8816	1563.7294	782.3683	1562.7454	781.8763	**Q**	***1373.6907***	687.3490	1356.6642	678.8357	1355.6801	678.3437	**13**
14	**1709.7986**	**855.4029**	1692.7720	846.8896	1691.7880	846.3976	**E**	***1245.6321***	623.3197	1228.6056	614.8064	1227.6216	614.3144	**12**
15	1838.8411	**919.9242**	1821.8146	911.4109	1820.8306	910.9189	**Q**	***1116.5895***	558.7984	1099.5630	550.2851	1098.5790	549.7931	**11**
16	1951.9252	**976.4662**	1934.8987	967.9530	1933.9146	967.4610	**L**	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	**10**
17	2022.9623	**1011.9848**	2005.9358	1003.4715	2004.9518	1002.9795	**A**	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	**9**
18	2151.0209	1076.0141	2133.9944	1067.5008	2133.0103	1067.0088	**Q**	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	**8**
19	2250.0893	**1125.5483**	2233.0628	1117.0350	2232.0788	1116.5430	**V**	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	**7**
20	2321.1264	1161.0669	2304.0999	1152.5536	2303.1159	1152.0616	**A**	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	**6**
21	2392.1635	**1196.5854**	2375.1370	1188.0721	2374.1530	1187.5801	**A**	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	**5**

22	2507.1905	**1254.0989**	2490.1639	1245.5856	2489.1799	1245.0936	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2578.2276	**1289.6174**	2561.2011	1281.1042	2560.2170	1280.6122	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2679.2753	**1340.1413**	2662.2487	1331.6280	2661.2647	1331.1360	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
38.6	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, N22 28.11%
34.9	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, N22 11.99%
34.5	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, N22 11.01%
34.3	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q9, Q18 10.52%
33.5	2823.3895	0.9934	LEPVHLQLQCMSQEQLAQVAANATK	
33.0	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q7, N22 7.89%
32.7	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q15, Q18 7.34%
30.4	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q13, Q18 4.23%
29.7	2824.3735	0.0094	LEPVHLQLQCMSQEQLAQVAANATK	Deamidated Q18, N22 3.67%
28.5	2823.3895	0.9934	LEPVHLQLQCMSQEQLAQVAANATK	

Mascot: http://www.matrixscience.com/

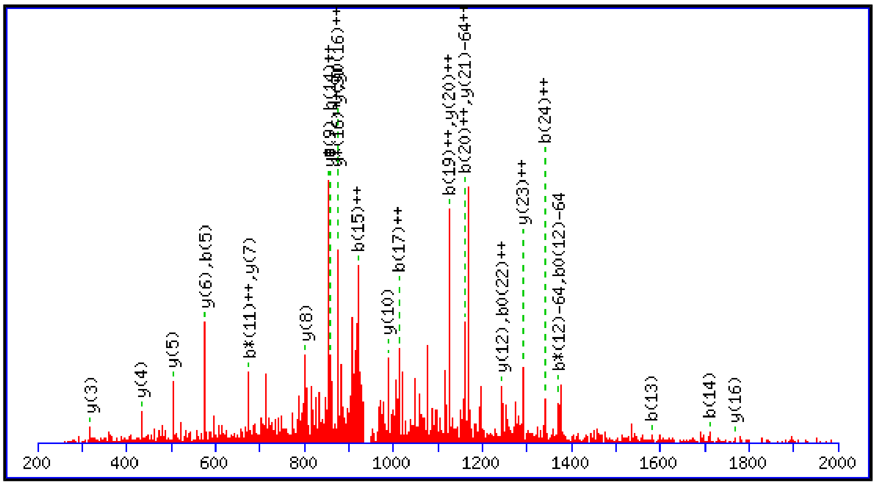
{MATRIX}{SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPVHLQLQCMSQEQLAQVAANATK**
Found in **Q96PD5** in **con_Xuniprot_HUMAN3**, PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYRP2 PE=1 SV=1

Match to Query 25742: 2824.376982 from(942.466270,3+) intensity(24475.5840) rtinseconds(1834) scans(4628) index(2097)
Title: 111019_Est_ISCardio_NMI_YP_G_4Spectrum4008_scans__4628
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

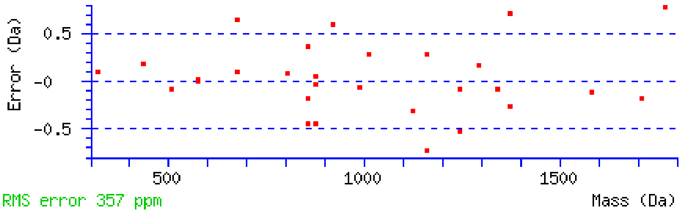
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

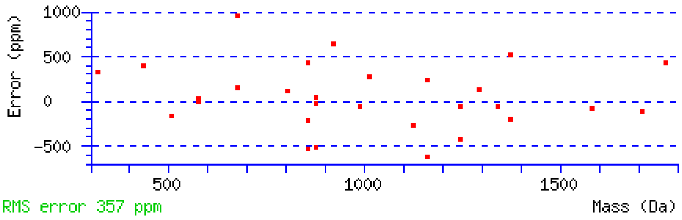


Monoisotopic mass of neutral peptide Mr(calc): 2824.3735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q13 : Deamidated (NQ)
N22 : Deamidated (NQ)
Ions Score: 35 **Expect:** 0.076
Matches : 30/416 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	114.0913	57.5493					**L**							**25**
2	243.1339	122.0706			225.1234	113.0653	**E**	2712.2967	1356.6520	2695.2702	1348.1387	2694.2862	1347.6467	**24**
3	340.1867	170.5970			322.1761	161.5917	**P**	2583.2542	1292.1307	2566.2276	1283.6174	2565.2436	1283.1254	**23**
4	439.2551	220.1312			421.2445	211.1259	**V**	2486.2014	1243.6043	2469.1748	1235.0911	2468.1908	1234.5991	**22**
5	**576.3140**	288.6606			558.3035	279.6554	**H**	2387.1330	1194.0701	2370.1064	1185.5569	2369.1224	1185.0648	**21**
6	689.3981	345.2027			671.3875	336.1974	**L**	2250.0741	1125.5407	2233.0475	1117.0274	2232.0635	1116.5354	**20**
7	817.4567	409.2320	800.4301	400.7187	799.4461	400.2267	**Q**	2136.9900	1068.9986	2119.9635	1060.4854	2118.9794	1059.9934	**19**
8	930.5407	465.7740	913.5142	457.2607	912.5302	456.7687	**L**	2008.9314	1004.9693	1991.9049	996.4561	1990.9209	995.9641	**18**
9	1058.5993	529.8033	1041.5728	521.2900	1040.5887	520.7980	**Q**	1895.8474	948.4273	1878.8208	939.9140	1877.8368	939.4220	**17**
10	1218.6300	609.8186	1201.6034	601.3053	1200.6194	600.8133	**C**	***1767.7888***	884.3980	1750.7622	875.8848	1749.7782	875.3927	**16**
11	1365.6654	683.3363	1348.6388	674.8230	1347.6548	674.3310	**M**	1607.7581	804.3827	1590.7316	795.8694	1589.7476	795.3774	**15**
12	1452.6974	726.8523	1435.6708	718.3391	1434.6868	717.8470	**S**	1460.7227	730.8650	1443.6962	722.3517	1442.7122	721.8597	**14**
13	**1581.7400**	791.3736	1564.7134	782.8604	1563.7294	782.3683	**Q**	1373.6907	687.3490	1356.6642	678.8357	1355.6801	678.3437	**13**
14	**1710.7826**	**855.8949**	1693.7560	847.3816	1692.7720	846.8896	**E**	***1244.6481***	622.8277	1227.6216	614.3144	1226.6375	613.8224	**12**
15	1838.8411	**919.9242**	1821.8146	911.4109	1820.8306	910.9189	**Q**	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	**11**
16	1951.9252	976.4662	1934.8987	967.9530	1933.9146	967.4610	**L**	***987.5469***	494.2771	970.5204	485.7638	969.5364	485.2718	**10**
17	2022.9623	**1011.9848**	2005.9358	1003.4715	2004.9518	1002.9795	**A**	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	**9**
18	2151.0209	1076.0141	2133.9944	1067.5008	2133.0103	1067.0088	**Q**	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	**8**
19	2250.0893	**1125.5483**	2233.0628	1117.0350	2232.0788	1116.5430	**V**	***675.3672***	338.1872	658.3406	329.6740	657.3566	329.1819	**7**
20	2321.1264	**1161.0669**	2304.0999	1152.5536	2303.1159	1152.0616	**A**	***576.2988***	288.6530	559.2722	280.1397	558.2882	279.6477	**6**
21	2392.1635	1196.5854	2375.1370	1188.0721	2374.1530	1187.5801	**A**	***505.2617***	253.1345	488.2351	244.6212	487.2511	244.1292	**5**

22	2507.1905	1254.0989	2490.1639	1245.5856	2489.1799	1245.0936	**N**	***434.2245***	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
23	2578.2276	1289.6174	2561.2011	1281.1042	2560.2170	1280.6122	**A**	***319.1976***	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
24	2679.2753	**1340.1413**	2662.2487	1331.6280	2661.2647	1331.1360	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
25							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of LEPVHLQLQCMSQEQLAQVAANATK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
35.5	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
33.1	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
29.3	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
27.5	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
25.9	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
20.7	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
20.6	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
19.3	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
18.1	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK
16.6	2824.3735	0.0035	LEPVHLQLQCMSQEQLAQVAANATK

Mascot: http://www.matrixscience.com/

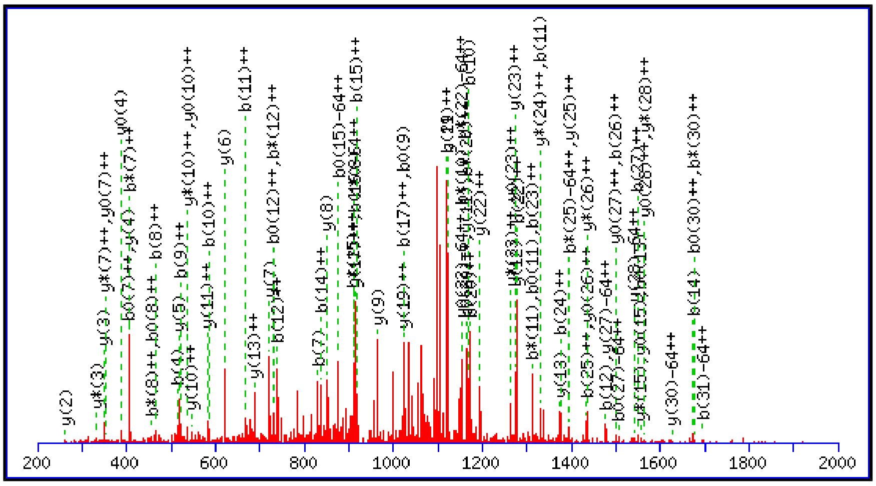
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR**
Found in **Q9NZP8** in **con_Xuniprot_HUMAN3**, C1RL_HUMAN Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

Match to Query 28052: 3715.748736 from(929.944460,4+) intensity(21039.8418) rtinseconds(999) scans(2383) index(24438)
Title: 111019_Est_MI_YS_G_06Spectrum2055_scans__2383
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

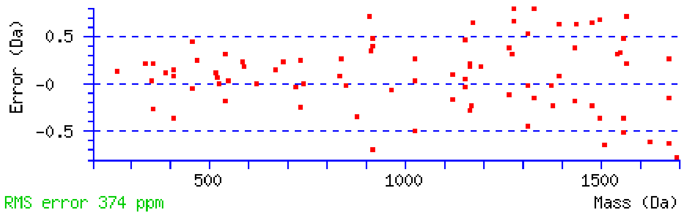
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

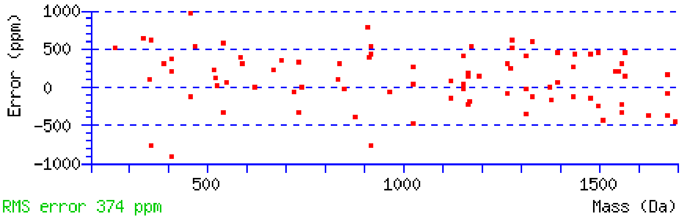


Monoisotopic mass of neutral peptide Mr(calc): 3715.7353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N25 : Deamidated (NQ)
Ions Score: 81 **Expect:** 1.7e-006
Matches : 85/572 fragment ions using 112 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							33
2	272.1353	136.5713	255.1088	128.0580	254.1248	127.5660	R	3601.7156	1801.3614	3584.6890	1792.8482	3583.7050	1792.3561	32
3	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	Q	3445.6145	1723.3109	3428.5879	1714.7976	3427.6039	1714.3056	31
4	**515.2209**	258.1141	498.1943	249.6008	497.2103	249.1088	D	3317.5559	1659.2816	3300.5293	1650.7683	3299.5453	1650.2763	30
5	572.2423	286.6248	555.2158	278.1115	554.2318	277.6195	G	3202.5289	1601.7681	3185.5024	1593.2548	3184.5184	1592.7628	29
6	701.2849	351.1461	684.2584	342.6328	683.2743	342.1408	E	3145.5075	1573.2574	3128.4809	1564.7441	3127.4969	1564.2521	28
7	**830.3275**	415.6674	813.3010	407.1541	812.3169	406.6621	E	3016.4649	1508.7361	2999.4383	1500.2228	2998.4543	1499.7308	27
8	929.3959	***465.2016***	912.3694	456.6883	911.3854	456.1963	V	2887.4223	1444.2148	2870.3957	1435.7015	2869.4117	1435.2095	26
9	1042.4800	***521.7436***	1025.4534	513.2304	1024.4694	512.7383	L	2788.3539	1394.6806	2771.3273	1386.1673	2770.3433	1385.6753	25
10	**1170.5386**	***585.7729***	1153.5120	577.2596	1152.5280	576.7676	Q	2675.2698	1338.1385	2658.2433	1329.6253	2657.2593	1329.1333	24
11	**1330.5692**	***665.7882***	1313.5427	657.2750	1312.5586	656.7830	C	2547.2112	1274.1093	2530.1847	1265.5960	2529.2007	1265.1040	23
12	**1477.6046**	***739.3059***	1460.5781	730.7927	1459.5940	730.3007	M	2387.1806	1194.0939	2370.1540	1185.5807	2369.1700	1185.0887	22
13	1574.6574	787.8323	1557.6308	779.3190	1556.6468	778.8270	P	2240.1452	1120.5762	2223.1186	1112.0630	2222.1346	1111.5710	21
14	**1673.7258**	***837.3665***	1656.6992	828.8533	1655.7152	828.3612	V	2143.0924	1072.0499	2126.0659	1063.5366	2125.0819	1063.0446	20
15	1833.7564	***917.3819***	1816.7299	908.8686	1815.7459	908.3766	C	2044.0240	1022.5156	2026.9975	1014.0024	2026.0135	1013.5104	19
16	1890.7779	945.8926	1873.7513	937.3793	1872.7673	936.8873	G	1883.9934	942.5003	1866.9668	933.9870	1865.9828	933.4950	18
17	2046.8790	***1023.9431***	2029.8525	1015.4299	2028.8684	1014.9379	R	1826.9719	913.9896	1809.9454	905.4763	1808.9613	904.9843	17
18	2143.9318	1072.4695	2126.9052	1063.9562	2125.9212	1063.4642	P	1670.8708	835.9390	1653.8442	827.4258	1652.8602	826.9338	16
19	2243.0002	***1122.0037***	2225.9736	1113.4905	2224.9896	1112.9984	V	1573.8180	787.4127	1556.7915	778.8994	1555.8075	778.4074	15
20	2344.0479	***1172.5276***	2327.0213	1164.0143	2326.0373	1163.5223	T	1474.7496	737.8784	1457.7231	729.3652	1456.7390	728.8732	14
21	2441.1006	1221.0540	2424.0741	1212.5407	2423.0901	1212.0487	P	***1373.7019***	687.3546	1356.6754	678.8413	1355.6914	678.3493	13

22	2554.1847	***1277.5960***	2537.1581	1269.0827	2536.1741	1268.5907	**I**	***1276.6492***	638.8282	1259.6226	630.3149	1258.6386	629.8229	**12**
23	2625.2218	***1313.1145***	2608.1953	1304.6013	2607.2112	1304.1093	**A**	***1163.5651***	582.2862	1146.5386	573.7729	1145.5545	573.2809	**11**
24	2753.2804	***1377.1438***	2736.2538	1368.6306	2735.2698	1368.1385	**Q**	1092.5280	546.7676	1075.5014	538.2544	1074.5174	537.7624	**10**
25	2868.3073	***1434.6573***	2851.2808	1426.1440	2850.2968	1425.6520	**N**	***964.4694***	482.7383	947.4429	474.2251	946.4588	473.7331	**9**
26	2996.3659	***1498.6866***	2979.3394	1490.1733	2978.3553	1489.6813	**Q**	***849.4425***	425.2249	832.4159	416.7116	831.4319	416.2196	**8**
27	3097.4136	***1549.2104***	3080.3870	1540.6972	3079.4030	1540.2051	**T**	***721.3839***	361.1956	704.3573	352.6823	703.3733	352.1903	**7**
28	3198.4613	1599.7343	3181.4347	1591.2210	3180.4507	1590.7290	**T**	***620.3362***	310.6717	603.3097	302.1585	602.3257	301.6665	**6**
29	3311.5453	1656.2763	3294.5188	1647.7630	3293.5348	1647.2710	**L**	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	**5**
30	3368.5668	1684.7870	3351.5402	1676.2738	3350.5562	1675.7818	**G**	***406.2045***	203.6059	389.1779	195.0926	388.1939	194.6006	**4**
31	3455.5988	1728.3030	3438.5723	1719.7898	3437.5883	1719.2978	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
32	3542.6308	1771.8191	3525.6043	1763.3058	3524.6203	1762.8138	**S**	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
81.0	3715.7353	0.0135	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated N25 47.92%
78.7	3715.7353	0.0135	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q26 27.89%
78.0	3715.7353	0.0135	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q24 23.69%
60.5	3714.7513	0.9975	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	
59.4	3715.7353	0.0135	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q3 0.33%
56.7	3715.7353	0.0135	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q10 0.17%
6.9	3715.7451	0.0036	TGLTANFGSNQLDSSGEVLQGCSPNSPVFLLFQVK	
6.1	3714.7611	0.9876	VQFLLFVPSNPSCGQLVEGSSDLQNSGFNATLGTK	
4.6	3715.7451	0.0036	VQFLLFVPSNPSCGQLVEGSSDLQNSGFNATLGTK	
4.6	3714.7611	0.9876	TGLTANFGSNQLDSSGEVLQGCSPNSPVFLLFQVK	

Mascot: http://www.matrixscience.com/

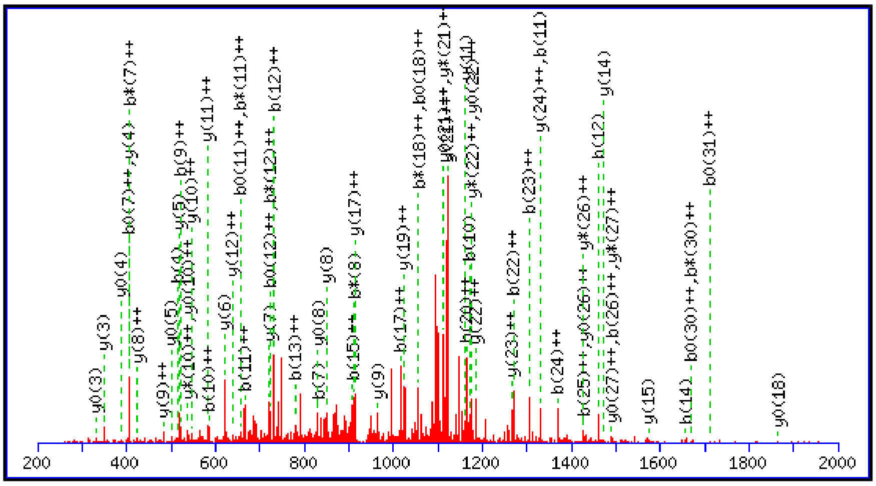
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR**
Found in **Q9NZP8** in **con_Xuniprot_HUMAN3**, C1RL_HUMAN Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2

Match to Query 28003: 3699.752296 from(925.945350,4+) intensity(19184.2441) rtinseconds(1392) scans(3445) index(24486)
Title: 111019_Est_MI_YS_G_06Spectrum2983_scans__3445
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

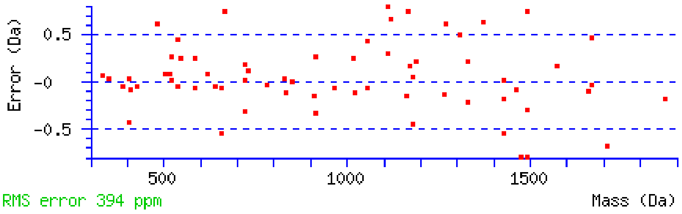
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

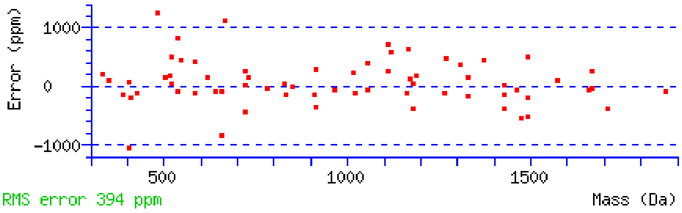


Monoisotopic mass of neutral peptide Mr(calc): 3699.7403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N25 : Deamidated (NQ)
Ions Score: 55 **Expect:** 0.00076
Matches : 67/380 fragment ions using 128 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**33**
2	272.1353	136.5713	255.1088	128.0580	254.1248	127.5660	**R**	3585.7207	1793.3640	3568.6941	1784.8507	3567.7101	1784.3587	**32**
3	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	**Q**	3429.6196	1715.3134	3412.5930	1706.8001	3411.6090	1706.3081	**31**
4	**515.2209**	258.1141	498.1943	249.6008	497.2103	249.1088	**D**	3301.5610	1651.2841	3284.5344	1642.7709	3283.5504	1642.2788	**30**
5	572.2423	286.6248	555.2158	278.1115	554.2318	277.6195	**G**	3186.5340	1593.7707	3169.5075	1585.2574	3168.5235	1584.7654	**29**
6	701.2849	351.1461	684.2584	342.6328	683.2743	342.1408	**E**	3129.5126	1565.2599	3112.4860	1556.7466	3111.5020	1556.2546	**28**
7	**830.3275**	415.6674	813.3010	407.1541	812.3169	406.6621	**E**	3000.4700	1500.7386	2983.4434	1492.2254	2982.4594	1491.7333	**27**
8	929.3959	465.2016	912.3694	456.6883	911.3854	456.1963	**V**	2871.4274	1436.2173	2854.4008	1427.7041	2853.4168	1427.2120	**26**
9	1042.4800	***521.7436***	1025.4534	513.2304	1024.4694	512.7383	**L**	2772.3590	1386.6831	2755.3324	1378.1698	2754.3484	1377.6778	**25**
10	**1170.5386**	***585.7729***	1153.5120	577.2596	1152.5280	576.7676	**Q**	2659.2749	1330.1411	2642.2484	1321.6278	2641.2643	1321.1358	**24**
11	**1330.5692**	***665.7882***	1313.5427	657.2750	1312.5586	656.7830	**C**	2531.2163	1266.1118	2514.1898	1257.5985	2513.2058	1257.1065	**23**
12	**1461.6097**	***731.3085***	1444.5831	722.7952	1443.5991	722.3032	**M**	2371.1857	1186.0965	2354.1591	1177.5832	2353.1751	1177.0912	**22**
13	1558.6625	***779.8349***	1541.6359	771.3216	1540.6519	770.8296	**P**	2240.1452	1120.5762	2223.1186	1112.0630	2222.1346	1111.5710	**21**
14	**1657.7309**	829.3691	1640.7043	820.8558	1639.7203	820.3638	**V**	2143.0924	1072.0499	2126.0659	1063.5366	2125.0819	1063.0446	**20**
15	1817.7615	***909.3844***	1800.7350	900.8711	1799.7510	900.3791	**C**	2044.0240	1022.5156	2026.9975	1014.0024	2026.0135	1013.5104	**19**
16	1874.7830	937.8951	1857.7564	929.3819	1856.7724	928.8898	**G**	1883.9934	942.5003	1866.9668	933.9870	1865.9828	933.4950	**18**
17	2030.8841	***1015.9457***	2013.8575	1007.4324	2012.8735	1006.9404	**R**	1826.9719	913.9896	1809.9454	905.4763	1808.9613	904.9843	**17**
18	2127.9369	1064.4721	2110.9103	1055.9588	2109.9263	1055.4668	**P**	1670.8708	835.9390	1653.8442	827.4258	1652.8602	826.9338	**16**
19	2227.0053	1114.0063	2209.9787	1105.4930	2208.9947	1105.0010	**V**	***1573.8180***	787.4127	1556.7915	778.8994	1555.8075	778.4074	**15**
20	2328.0529	***1164.5301***	2311.0264	1156.0168	2310.0424	1155.5248	**T**	***1474.7496***	737.8784	1457.7231	729.3652	1456.7390	728.8732	**14**
21	2425.1057	1213.0565	2408.0792	1204.5432	2407.0951	1204.0512	**P**	1373.7019	687.3546	1356.6754	678.8413	1355.6914	678.3493	**13**
22	2538.1898	***1269.5985***	2521.1632	1261.0853	2520.1792	1260.5932	**I**	1276.6492	638.8282	1259.6226	630.3149	1258.6386	629.8229	**12**

23	2609.2269	***1305.1171***	2592.2003	1296.6038	2591.2163	1296.1118	**A**	***1163.5651***	582.2862	1146.5386	573.7729	1145.5545	573.2809	**11**
24	2737.2855	***1369.1464***	2720.2589	1360.6331	2719.2749	1360.1411	**Q**	1092.5280	546.7676	1075.5014	538.2544	1074.5174	537.7624	**10**
25	2852.3124	***1426.6598***	2835.2859	1418.1466	2834.3018	1417.6546	**N**	***964.4694***	482.7383	947.4429	474.2251	946.4588	473.7331	**9**
26	2980.3710	***1490.6891***	2963.3444	1482.1759	2962.3604	1481.6839	**Q**	***849.4425***	425.2249	832.4159	416.7116	831.4319	416.2196	**8**
27	3081.4187	1541.2130	3064.3921	1532.6997	3063.4081	1532.2077	**T**	***721.3839***	361.1956	704.3573	352.6823	703.3733	352.1903	**7**
28	3182.4663	1591.7368	3165.4398	1583.2235	3164.4558	1582.7315	**T**	***620.3362***	310.6717	603.3097	302.1585	602.3257	301.6665	**6**
29	3295.5504	1648.2788	3278.5239	1639.7656	3277.5398	1639.2736	**L**	***519.2885***	260.1479	502.2620	251.6346	501.2780	251.1426	**5**
30	3352.5719	1676.7896	3335.5453	1668.2763	3334.5613	1667.7843	**G**	***406.2045***	203.6059	389.1779	195.0926	388.1939	194.6006	**4**
31	3439.6039	1720.3056	3422.5774	1711.7923	3421.5933	1711.3003	**S**	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	**3**
32	3526.6359	1763.8216	3509.6094	1755.3083	3508.6254	1754.8163	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
33							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
54.7	3699.7403	0.0120	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated N25 45.87%
52.2	3699.7403	0.0120	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q26 25.56%
51.1	3699.7403	0.0120	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q24 19.93%
46.4	3699.7403	0.0120	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q10 6.78%
42.7	3698.7563	0.9960	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	
40.8	3699.7403	0.0120	DRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSR	Deamidated Q3 1.85%
7.8	3699.7522	0.0001	LETPIPQLSGLDHWQVGAQAVSHSGACHGQSMKR	
5.9	3699.7547	-0.0024	HSSVVQGDVSEEVNIHFNSSSGGGGSSAERIAIGAMK	
4.0	3699.7668	-0.0145	NLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQR	
4.0	3699.7668	-0.0145	NLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQR	

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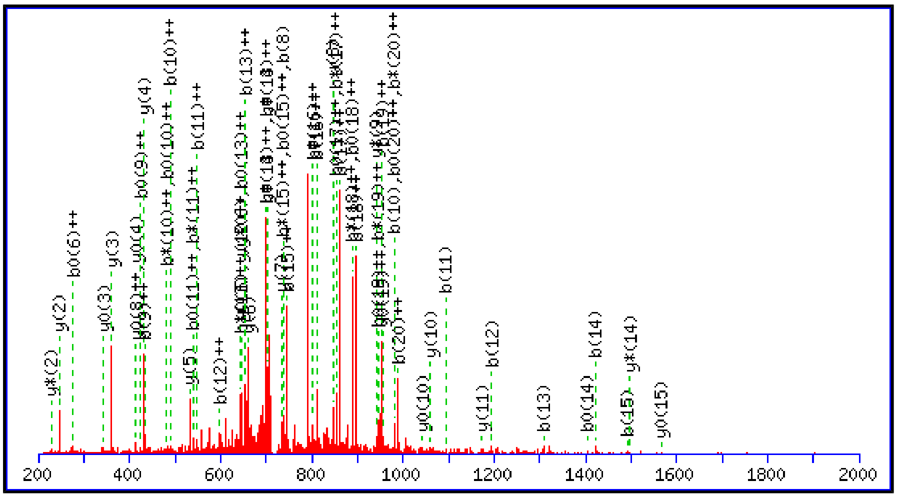
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SHAASDAPENLTLLAETADAR**
Found in **Q9ULI3** in **con_Xuniprot_HUMAN3**, HEG1_HUMAN Protein HEG homolog 1 OS=Homo sapiens GN=HEG1 PE=1 SV=3

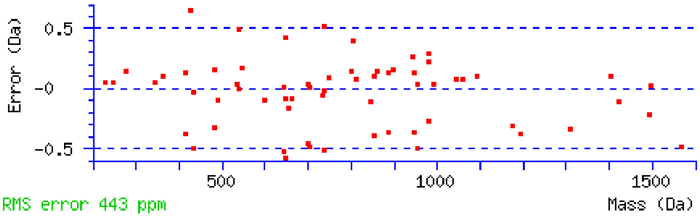
Match to Query 14426: 2153.030622 from(718.684150,3+) intensity(40453.0156) rtinseconds(1719) scans(4134) index(26133)
Title: 111019_Est_MI_YS_G_08Spectrum3563_scans__4134
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

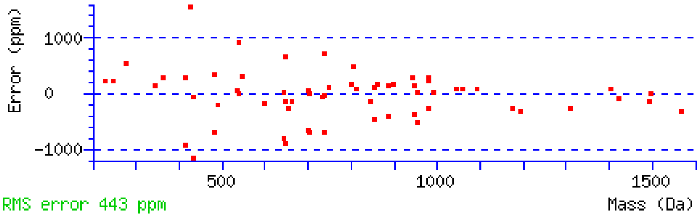
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 2153.0236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 35 **Expect:** 0.078
Matches : 64/218 fragment ions using 125 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**21**
2	225.0982	113.0527			207.0877	104.0475	**H**	2066.9989	1034.0031	2049.9724	1025.4898	2048.9883	1024.9978	**20**
3	296.1353	148.5713			278.1248	139.5660	**A**	1929.9400	965.4736	1912.9134	956.9604	1911.9294	956.4684	**19**
4	367.1724	184.0899			349.1619	175.0846	**A**	1858.9029	929.9551	1841.8763	921.4418	1840.8923	920.9498	**18**
5	454.2045	227.6059			436.1939	218.6006	**S**	1787.8658	894.4365	1770.8392	885.9232	1769.8552	885.4312	**17**
6	569.2314	285.1193			551.2208	276.1141	**D**	1700.8337	850.9205	1683.8072	842.4072	1682.8232	841.9152	**16**
7	640.2685	320.6379			622.2580	311.6326	**A**	1585.8068	793.4070	1568.7802	784.8938	1567.7962	784.4018	**15**
8	**737.3213**	369.1643			719.3107	360.1590	**P**	1514.7697	757.8885	1497.7431	749.3752	1496.7591	748.8832	**14**
9	866.3639	***433.6856***			848.3533	424.6803	**E**	1417.7169	709.3621	1400.6904	700.8488	1399.7064	700.3568	**13**
10	**981.3908**	***491.1991***	964.3643	482.6858	963.3803	482.1938	**N**	1288.6743	644.8408	1271.6478	636.3275	1270.6638	635.8355	**12**
11	**1094.4749**	***547.7411***	1077.4483	539.2278	1076.4643	538.7358	**L**	**1173.6474**	587.3273	1156.6208	578.8141	1155.6368	578.3220	**11**
12	**1195.5226**	***598.2649***	1178.4960	589.7516	1177.5120	589.2596	**T**	**1060.5633**	530.7853	1043.5368	522.2720	1042.5528	521.7800	**10**
13	**1308.6066**	***654.8070***	1291.5801	646.2937	1290.5961	645.8017	**L**	959.5156	480.2615	942.4891	471.7482	941.5051	471.2562	**9**
14	**1421.6907**	711.3490	1404.6642	702.8357	1403.6801	702.3437	**L**	**846.4316**	423.7194	829.4050	415.2062	828.4210	414.7141	**8**
15	**1492.7278**	***746.8675***	1475.7013	738.3543	1474.7172	737.8623	**A**	**733.3475**	367.1774	716.3210	358.6641	715.3369	358.1721	**7**
16	1621.7704	***811.3888***	1604.7439	802.8756	1603.7598	802.3836	**E**	**662.3104**	331.6588	645.2838	323.1456	644.2998	322.6536	**6**
17	1722.8181	***861.9127***	1705.7915	853.3994	1704.8075	852.9074	**T**	**533.2678**	267.1375	516.2413	258.6243	515.2572	258.1323	**5**
18	1793.8552	***897.4312***	1776.8287	888.9180	1775.8446	888.4260	**A**	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	**4**
19	1908.8821	***954.9447***	1891.8556	946.4314	1890.8716	945.9394	**D**	**361.1830**	181.0951	344.1565	172.5819	343.1724	172.0899	**3**
20	1979.9193	***990.4633***	1962.8927	981.9500	1961.9087	981.4580	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
21							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of SHAASDAPENLTLLAETADAR
(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	2153.0236	0.0070	SHAASDAPENLTLLAETADAR
13.7	2151.0232	2.0074	IFPARSNGNEDLEYLADAR
10.3	2151.0232	2.0074	FVQLKNNSDKDQSLGNWR
10.3	2151.0232	2.0074	FVQLKNNSDKDQSLGNWR
7.8	2151.0232	2.0074	IFPARSNGNEDLEYLADAR
6.8	2151.0154	2.0153	EIQSVYIREGMGQLVAANDG
5.5	2152.0219	1.0087	QMDPTDFVNSSETRLAVSR
5.3	2151.0187	2.0119	ETENRKIMGQCEALITEK
5.1	2153.0231	0.0075	SQKMEIESVLMKQQNLQT
4.7	2153.0211	0.0095	SDPMVVLYTQSRASQEWR

Mascot: http://www.matrixscience.com/

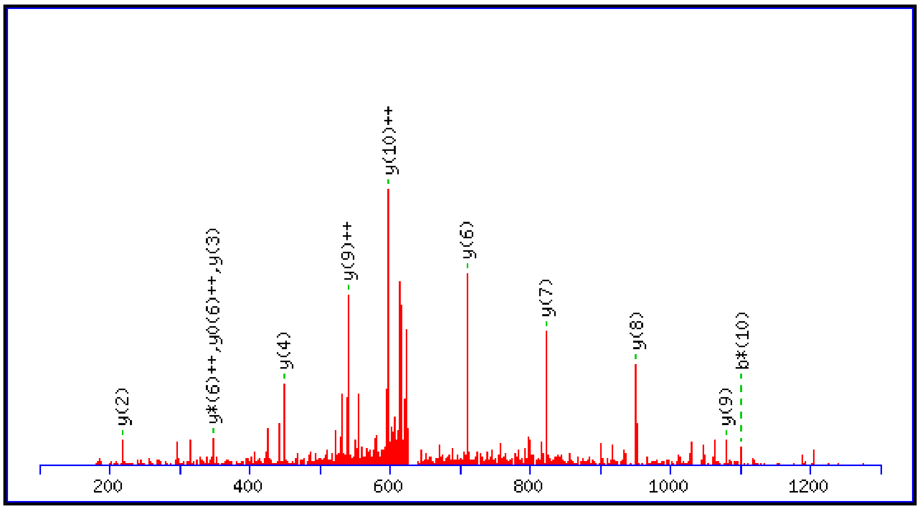
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ANQQLNFTEAK**
Found in **Q9Y5Y7** in **con_Xuniprot_HUMAN3**, LYVE1_HUMAN Lymphatic vessel endothelial hyaluronic acid receptor 1 OS=Homo sapiens GN=LYVE1 PE=1 SV=2

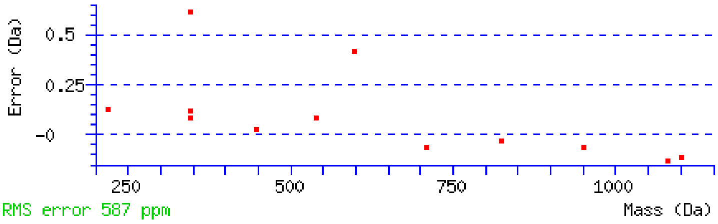
Match to Query 1765: 1263.611808 from(632.813180,2+) intensity(14774.6035) rtinseconds(580) scans(1342) index(23789)
Title: 111019_Est_MI_YS_G_05Spectrum1122_scans__1342
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

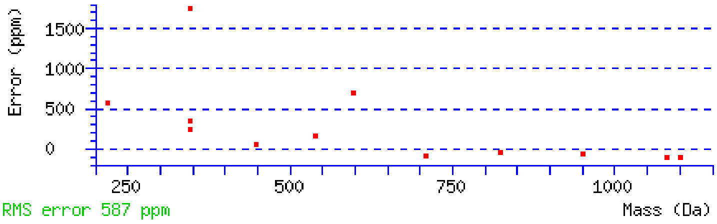
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1300 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1263.6095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
Ions Score: 61 **Expect:** 0.00017
Matches : 12/100 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							11
2	186.0873	93.5473	169.0608	85.0340			N	1193.5797	597.2935	1176.5531	588.7802	1175.5691	588.2882	10
3	314.1459	157.5766	297.1193	149.0633			Q	***1079.5368***	540.2720	1062.5102	531.7587	1061.5262	531.2667	9
4	442.2045	221.6059	425.1779	213.0926			Q	***951.4782***	476.2427	934.4516	467.7295	933.4676	467.2374	8
5	555.2885	278.1479	538.2620	269.6346			L	***823.4196***	412.2134	806.3931	403.7002	805.4090	403.2082	7
6	670.3155	335.6614	653.2889	327.1481			N	***710.3355***	355.6714	693.3090	347.1581	692.3250	346.6661	6
7	817.3839	409.1956	800.3573	400.6823			F	595.3086	298.1579	578.2821	289.6447	577.2980	289.1527	5
8	918.4316	459.7194	901.4050	451.2061	900.4210	450.7141	T	***448.2402***	224.6237	431.2136	216.1105	430.2296	215.6185	4
9	1047.4742	524.2407	1030.4476	515.7274	1029.4636	515.2354	E	***347.1925***	174.0999	330.1660	165.5866	329.1819	165.0946	3
10	1118.5113	559.7593	1101.4847	551.2460	1100.5007	550.7540	A	***218.1499***	109.5786	201.1234	101.0653			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ANQQLNFTEAK

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
60.5	1263.6095	0.0023	ANQQLNFTEAK	Deamidated N6 99.85%
31.0	1263.6095	0.0023	ANQQLNFTEAK	Deamidated Q4 0.11%
25.8	1263.6095	0.0023	ANQQLNFTEAK	Deamidated Q3 0.03%
17.0	1263.6095	0.0023	ANQQLNFTEAK	Deamidated N2 0.00%
4.8	1263.6095	0.0023	EPTNIYVASDR	
3.6	1263.6129	-0.0010	KLDEEMREAK	
3.5	1263.6064	0.0055	ADPDRLMRMK	
2.2	1262.6102	1.0016	RNPDSVSSVSSK	
1.0	1262.6077	1.0041	VNYHMLTNVR	

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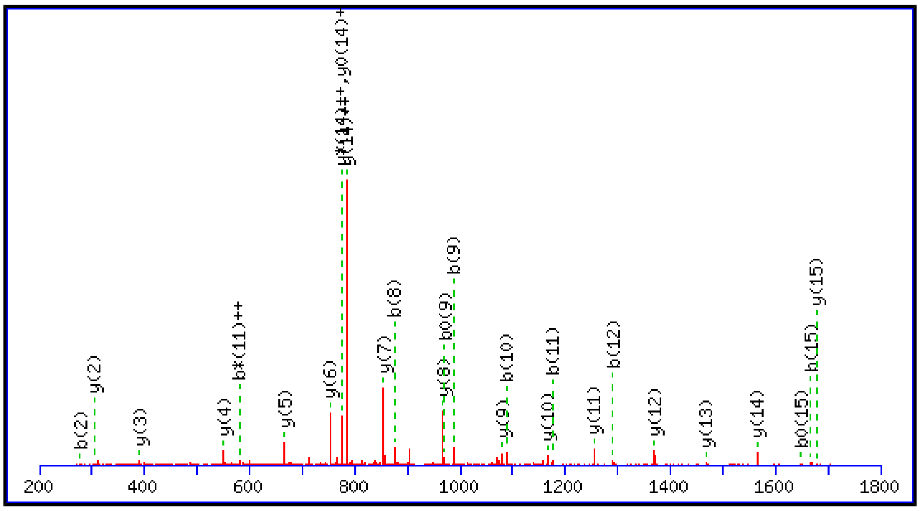
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLPVNSSLLTSDCSER**
Found in **Q9Y6R7** in **con_Xuniprot_HUMAN3**, FCGBP_HUMAN IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

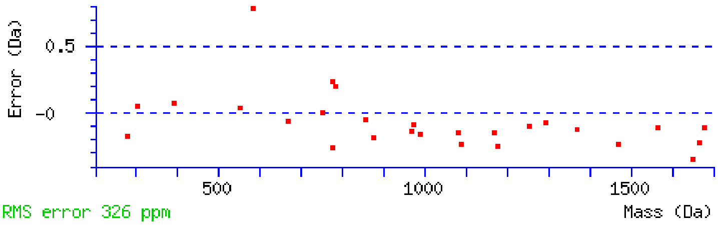
Match to Query 10927: 1840.857388 from(921.435970,2+) intensity(65188.9609) rtinseconds(1532) scans(3290) index(99)
Title: 111019_Est_ISCardio_NMI_200000g_G_3Spectrum2842_scans__3290
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

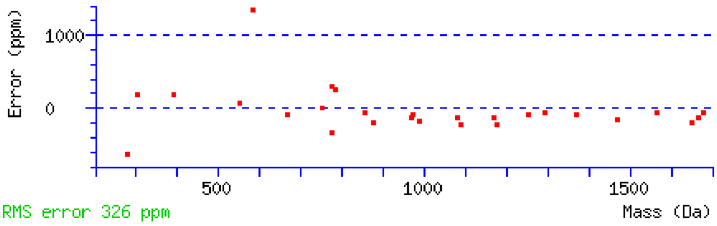
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1840.8513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N5 : Deamidated (NQ)
Ions Score: 106 **Expect:** 5.3e-009
Matches : 27/160 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	164.0706	82.5389					Y							16
2	**277.1547**	139.0810					L	***1678.7952***	839.9013	1661.7687	831.3880	1660.7847	830.8960	15
3	374.2074	187.6074					P	***1565.7112***	783.3592	1548.6846	774.8460	1547.7006	774.3539	14
4	473.2758	237.1416					V	***1468.6584***	734.8328	1451.6319	726.3196	1450.6478	725.8276	13
5	588.3028	294.6550	571.2762	286.1418			N	***1369.5900***	685.2986	1352.5635	676.7854	1351.5794	676.2934	12
6	675.3348	338.1710	658.3083	329.6578	657.3243	329.1658	S	***1254.5631***	627.7852	1237.5365	619.2719	1236.5525	618.7799	11
7	762.3668	381.6871	745.3403	373.1738	744.3563	372.6818	S	***1167.5310***	584.2692	1150.5045	575.7559	1149.5205	575.2639	10
8	**875.4509**	438.2291	858.4244	429.7158	857.4403	429.2238	L	***1080.4990***	540.7531	1063.4725	532.2399	1062.4884	531.7479	9
9	**988.5350**	494.7711	971.5084	486.2579	970.5244	485.7658	L	***967.4149***	484.2111	950.3884	475.6978	949.4044	475.2058	8
10	**1089.5827**	545.2950	1072.5561	536.7817	1071.5721	536.2897	T	***854.3309***	427.6691	837.3043	419.1558	836.3203	418.6638	7
11	**1176.6147**	588.8110	1159.5881	580.2977	1158.6041	579.8057	S	***753.2832***	377.1452	736.2566	368.6320	735.2726	368.1400	6
12	**1291.6416**	646.3245	1274.6151	637.8112	1273.6311	637.3192	D	***666.2512***	333.6292	649.2246	325.1159	648.2406	324.6239	5
13	1451.6723	726.3398	1434.6457	717.8265	1433.6617	717.3345	C	***551.2242***	276.1157	534.1977	267.6025	533.2137	267.1105	4
14	1538.7043	769.8558	1521.6778	761.3425	1520.6937	760.8505	S	***391.1936***	196.1004	374.1670	187.5871	373.1830	187.0951	3
15	**1667.7469**	834.3771	1650.7203	825.8638	1649.7363	825.3718	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
16							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of YLPVNSSLLTSDCSER
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
105.6	1840.8513	0.0061	YLPVNSSLLTSDCSER
11.1	1840.8625	-0.0051	VLMIDNRHDKNPLSNG
10.0	1840.8486	0.0088	GMSHSPSVALRGNENER
10.0	1840.8486	0.0088	GMSHSPSVALRGNENER
9.0	1840.8488	0.0086	VLWSPQAAMREMYDK
7.9	1840.8488	0.0086	VLWSPQAAMREMYDK
3.3	1840.8513	0.0061	LGPQLPSCQPQVEQTR
2.4	1840.8631	-0.0057	YFYKVHQLEQEQAR
2.3	1839.8607	0.9966	NGLCRNLVCTDLFTR
1.9	1840.8521	0.0053	ALKAMEMTWNNMEKK

Mascot: http://www.matrixscience.com/

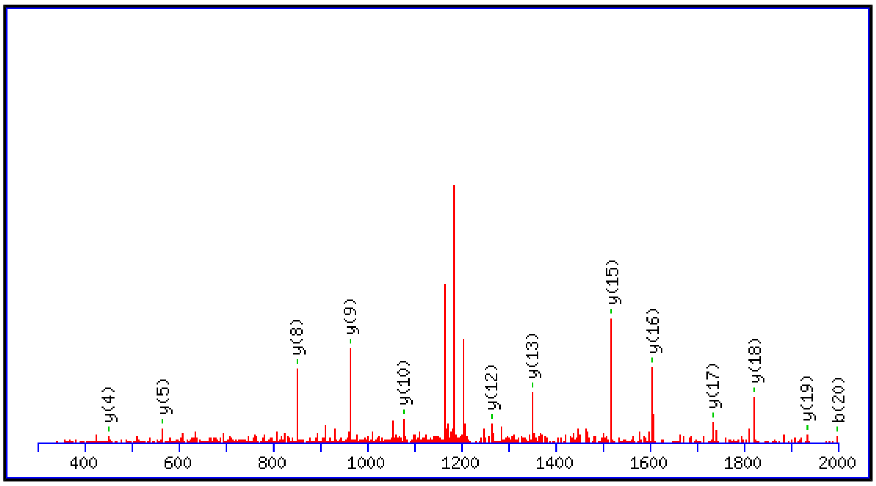
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLISSLSESPASVSILSQADNTSK**
Found in **Q9Y6R7** in **con_Xuniprot_HUMAN3**, FCGBP_HUMAN IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

Match to Query 21512: 2447.271848 from(1224.643200,2+) intensity(15055.8242) rtinseconds(1998) scans(5210) index(6582)
Title: 111019_Est_ISCardio_NMI_YP_G_9Spectrum4581_scans__5210
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

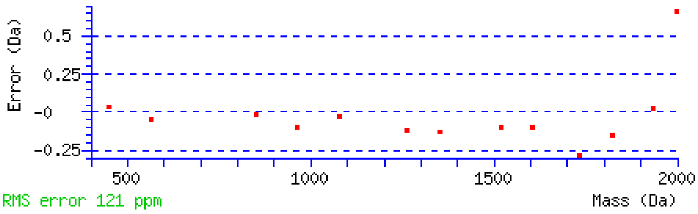
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

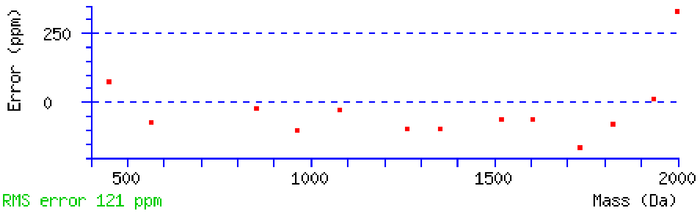


Monoisotopic mass of neutral peptide Mr(calc): 2447.2642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N21 : Deamidated (NQ)
Ions Score: 91 **Expect:** 1.9e-007
Matches : 13/234 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							24
2	227.1754	114.0913					L	2335.1875	1168.0974	2318.1609	1159.5841	2317.1769	1159.0921	23
3	340.2595	170.6334					I	2222.1034	1111.5554	2205.0769	1103.0421	2204.0929	1102.5501	22
4	427.2915	214.1494			409.2809	205.1441	S	2109.0194	1055.0133	2091.9928	1046.5000	2091.0088	1046.0080	21
5	514.3235	257.6654			496.3130	248.6601	S	2021.9873	1011.4973	2004.9608	1002.9840	2003.9768	1002.4920	20
6	627.4076	314.2074			609.3970	305.2021	L	***1934.9553***	967.9813	1917.9288	959.4680	1916.9447	958.9760	19
7	714.4396	357.7234			696.4291	348.7182	S	***1821.8712***	911.4393	1804.8447	902.9260	1803.8607	902.4340	18
8	843.4822	422.2447			825.4716	413.2395	E	***1734.8392***	867.9232	1717.8127	859.4100	1716.8286	858.9180	17
9	930.5142	465.7608			912.5037	456.7555	S	***1605.7966***	803.4019	1588.7701	794.8887	1587.7861	794.3967	16
10	1027.5670	514.2871			1009.5564	505.2819	P	***1518.7646***	759.8859	1501.7380	751.3727	1500.7540	750.8807	15
11	1098.6041	549.8057			1080.5935	540.8004	A	1421.7118	711.3596	1404.6853	702.8463	1403.7013	702.3543	14
12	1185.6361	593.3217			1167.6256	584.3164	S	***1350.6747***	675.8410	1333.6482	667.3277	1332.6641	666.8357	13
13	1284.7046	642.8559			1266.6940	633.8506	V	***1263.6427***	632.3250	1246.6161	623.8117	1245.6321	623.3197	12
14	1371.7366	686.3719			1353.7260	677.3666	S	1164.5743	582.7908	1147.5477	574.2775	1146.5637	573.7855	11
15	1484.8206	742.9140			1466.8101	733.9087	I	***1077.5422***	539.2748	1060.5157	530.7615	1059.5317	530.2695	10
16	1597.9047	799.4560			1579.8941	790.4507	L	***964.4582***	482.7327	947.4316	474.2195	946.4476	473.7274	9
17	1684.9367	842.9720			1666.9262	833.9667	S	***851.3741***	426.1907	834.3476	417.6774	833.3636	417.1854	8
18	1812.9953	907.0013	1795.9688	898.4880	1794.9848	897.9960	Q	764.3421	382.6747	747.3155	374.1614	746.3315	373.6694	7
19	1884.0324	942.5199	1867.0059	934.0066	1866.0219	933.5146	A	636.2835	318.6454	619.2570	310.1321	618.2729	309.6401	6
20	1999.0594	1000.0333	1982.0328	991.5201	1981.0488	991.0280	D	***565.2464***	283.1268	548.2198	274.6136	547.2358	274.1216	5
21	2114.0863	1057.5468	2097.0598	1049.0335	2096.0758	1048.5415	N	***450.2195***	225.6134	433.1929	217.1001	432.2089	216.6081	4
22	2215.1340	1108.0706	2198.1074	1099.5574	2197.1234	1099.0654	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
23	2302.1660	1151.5867	2285.1395	1143.0734	2284.1555	1142.5814	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2

24							K	147.1128	74.0600	130.0863	65.5468		1





NCBI **BLAST** search of LLISSLSESPASVSILSQADNTSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
90.6	2447.2642	0.0076	LLISSLSESPASVSILSQADNTSK	Deamidated N21 99.87%
61.6	2447.2642	0.0076	LLISSLSESPASVSILSQADNTSK	Deamidated Q18 0.13%
20.0	2446.2802	0.9916	LLISSLSESPASVSILSQADNTSK	
4.1	2447.2703	0.0016	QRAHVIVMAATNRPNSIDPALR	
4.0	2447.2617	0.0101	RWKLINEALEETETVLIDMK	
0.2	2447.2703	0.0016	QRAHVIVMAATNRPNSIDPALR	
0.2	2447.2703	0.0016	QRAHVIVMAATNRPNSIDPALR	
0.0	2447.2804	-0.0085	LVWLKEVLQNELLTMSQVMR	

Mascot: http://www.matrixscience.com/

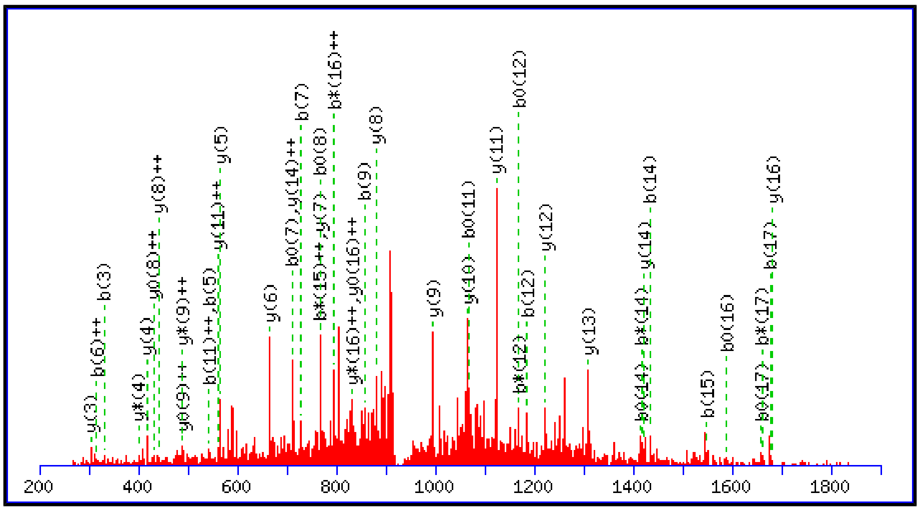
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLCVLSVGANLTTFDGAR**
Found in **Q9Y6R7** in **con_Xuniprot_HUMAN3**, FCGBP_HUMAN IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3

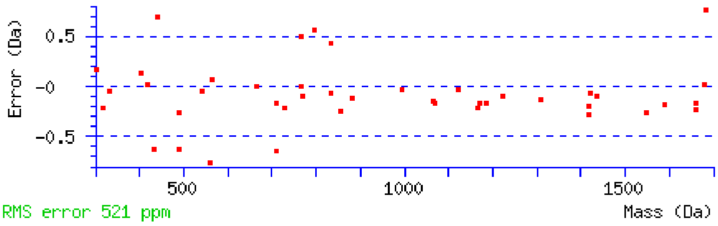
Match to Query 10958: 1850.924268 from(926.469410,2+) intensity(33367.8008) rtinseconds(2232) scans(5627) index(921)
Title: 111019_Est_ISCardio_NMI_YP_G_2Spectrum4914_scans__5627
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

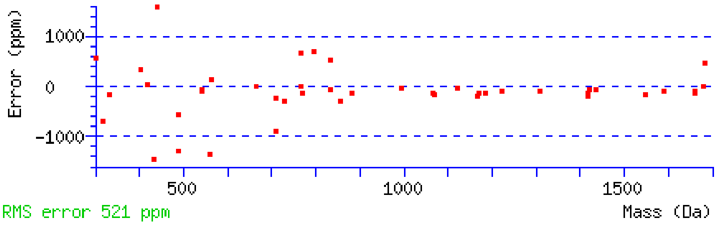
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



Monoisotopic mass of neutral peptide Mr(calc): 1850.9197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N10 : Deamidated (NQ)
Ions Score: 52 **Expect:** 0.0018
Matches : 44/170 fragment ions using 112 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**18**
2	171.1128	86.0600					**L**	1794.9055	897.9564	1777.8789	889.4431	1776.8949	888.9511	**17**
3	**331.1435**	166.0754					**C**	***1681.8214***	841.4143	1664.7949	832.9011	1663.8108	832.4091	**16**
4	430.2119	215.6096					**V**	1521.7907	761.3990	1504.7642	752.8857	1503.7802	752.3937	**15**
5	**543.2959**	272.1516					**L**	***1422.7223***	711.8648	1405.6958	703.3515	1404.7118	702.8595	**14**
6	630.3280	315.6676			612.3174	306.6623	**S**	***1309.6383***	655.3228	1292.6117	646.8095	1291.6277	646.3175	**13**
7	**729.3964**	365.2018			711.3858	356.1965	**V**	***1222.6062***	611.8068	1205.5797	603.2935	1204.5957	602.8015	**12**
8	786.4178	393.7126			768.4073	384.7073	**G**	***1123.5378***	562.2726	1106.5113	553.7593	1105.5273	553.2673	**11**
9	**857.4550**	429.2311			839.4444	420.2258	**A**	***1066.5164***	533.7618	1049.4898	525.2485	1048.5058	524.7565	**10**
10	972.4819	486.7446	955.4553	478.2313	954.4713	477.7393	**N**	***995.4793***	498.2433	978.4527	489.7300	977.4687	489.2380	**9**
11	1085.5660	543.2866	1068.5394	534.7733	1067.5554	534.2813	**L**	***880.4523***	440.7298	863.4258	432.2165	862.4417	431.7245	**8**
12	**1186.6136**	593.8105	1169.5871	585.2972	1168.6031	584.8052	**T**	***767.3682***	384.1878	750.3417	375.6745	749.3577	375.1825	**7**
13	1287.6613	644.3343	1270.6348	635.8210	1269.6508	635.3290	**T**	***666.3206***	333.6639	649.2940	325.1506	648.3100	324.6586	**6**
14	**1434.7297**	717.8685	1417.7032	709.3552	1416.7192	708.8632	**F**	***565.2729***	283.1401	548.2463	274.6268	547.2623	274.1348	**5**
15	**1549.7567**	775.3820	1532.7301	766.8687	1531.7461	766.3767	**D**	***418.2045***	209.6059	401.1779	201.0926	400.1939	200.6006	**4**
16	1606.7781	803.8927	1589.7516	795.3794	1588.7676	794.8874	**G**	***303.1775***	152.0924	286.1510	143.5791			**3**
17	**1677.8153**	839.4113	1660.7887	830.8980	1659.8047	830.4060	**A**	246.1561	123.5817	229.1295	115.0684			**2**
18							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of GLCVLSVGANLTTFDGAR
(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	1850.9197	0.0046	GLCVLSVGANLTTFDGAR
1.9	1848.9217	2.0025	EIQTRPITDETFDKR

Mascot: http://www.matrixscience.com/

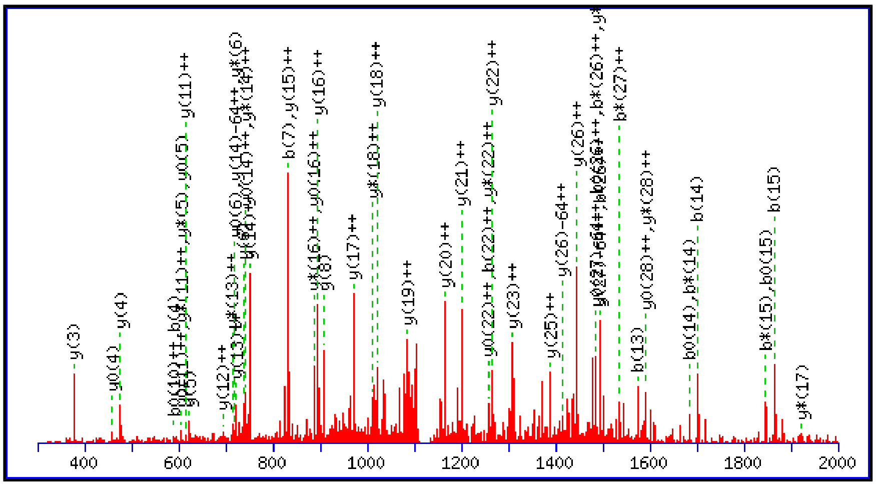
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27524: 3363.355122 from(1122.125650,3+) intensity(9446.5313) rtinseconds(1780) scans(4468) index(11024)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum3783_scans__4468
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

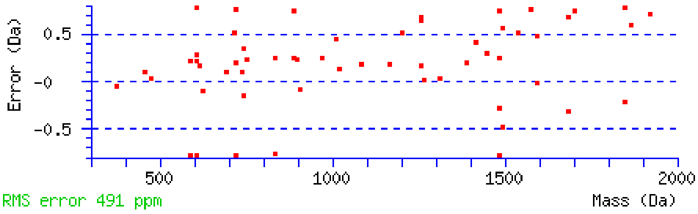
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

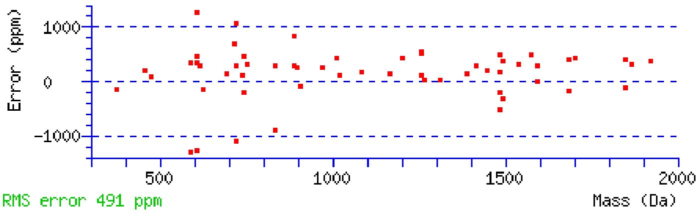


Monoisotopic mass of neutral peptide Mr(calc): 3362.3413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 87 **Expect:** 4.8e-008
Matches : 58/486 fragment 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	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3200.2853	1600.6463	3183.2587	1592.1330	3182.2747	1591.6410	28
3	474.2023	237.6048					Y	3053.2169	1527.1121	3036.1903	1518.5988	3035.2063	1518.1068	27
4	**588.2453**	294.6263	571.2187	286.1130			N	2890.1535	1445.5804	2873.1270	1437.0671	2872.1430	1436.5751	26
5	645.2667	323.1370	628.2402	314.6237			G	2776.1106	1388.5589	2759.0841	1380.0457	2758.1000	1379.5537	25
6	746.3144	373.6608	729.2879	365.1476	728.3039	364.6556	T	2719.0891	1360.0482	2702.0626	1351.5349	2701.0786	1351.0429	24
7	**833.3464**	417.1769	816.3199	408.6636	815.3359	408.1716	S	2618.0415	1309.5244	2601.0149	1301.0111	2600.0309	1300.5191	23
8	964.3869	482.6971	947.3604	474.1838	946.3764	473.6918	M	2531.0094	1266.0084	2513.9829	1257.4951	2512.9989	1257.0031	22
9	1035.4240	518.2157	1018.3975	509.7024	1017.4135	509.2104	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	1195.4547	598.2310	1178.4281	589.7177	1177.4441	589.2257	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	1324.4973	662.7523	1307.4707	654.2390	1306.4867	653.7470	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1425.5450	713.2761	1408.5184	704.7628	1407.5344	704.2708	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1572.6134**	786.8103	1555.5868	778.2971	1554.6028	777.8050	F	1938.8109	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1700.6720**	850.8396	1683.6454	842.3263	1682.6614	841.8343	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1863.7353**	932.3713	1846.7087	923.8580	1845.7247	923.3660	Y	1663.6839	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	1920.7568	960.8820	1903.7302	952.3687	1902.7462	951.8767	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	1977.7782	989.3927	1960.7517	980.8795	1959.7677	980.3875	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2137.8089	1069.4081	2120.7823	1060.8948	2119.7983	1060.4028	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2284.8443	1142.9258	2267.8177	1134.4125	2266.8337	1133.9205	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2341.8657	1171.4365	2324.8392	1162.9232	2323.8552	1162.4312	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2455.9087	1228.4580	2438.8821	1219.9447	2437.8981	1219.4527	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2512.9301	1256.9687	2495.9036	1248.4554	2494.9196	1247.9634	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8
23	2626.9730	1313.9902	2609.9465	1305.4769	2608.9625	1304.9849	N	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	7

24	2741.0160	1371.0116	2723.9894	1362.4983	2723.0054	1362.0063	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2888.0844	1444.5458	2871.0578	1436.0326	2870.0738	1435.5405	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2987.1528	1494.0800	2970.1263	1485.5668	2969.1422	1485.0748	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3088.2005	1544.6039	3071.1739	1536.0906	3070.1899	1535.5986	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3217.2431	1609.1252	3200.2165	1600.6119	3199.2325	1600.1199	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence
86.6	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTEK
73.6	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR
69.1	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR
64.6	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR
64.4	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR
54.5	3361.3573	1.9978	YFYNGTSMACETFQYGGCMGNGNNFVTVR
54.5	3361.3573	1.9978	YFYNGTSMACETFQYGGCMGNGNNFVTVR
54.5	3361.3573	1.9978	YFYNGTSMACETFQYGGCMGNGNNFVTVR
47.2	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR
45.8	3362.3413	1.0138	YFYNGTSMACETFQYGGCMGNGNNFVTVR

Mascot: http://www.matrixscience.com/

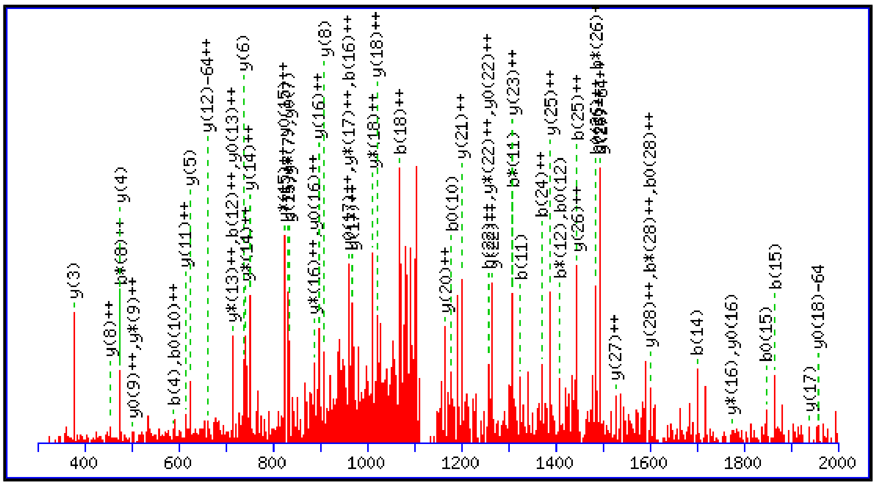
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27514: 3363.334872 from(1122.118900,3+) intensity(0.0000) rtinseconds(3021) scans(7999) index(4828)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum6867_scans__7999
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

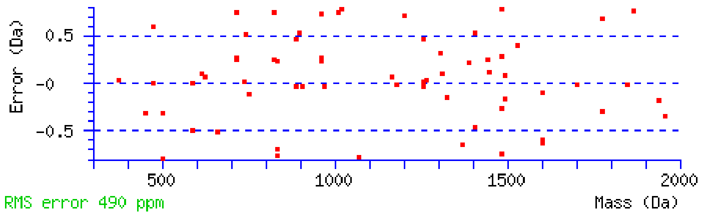
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

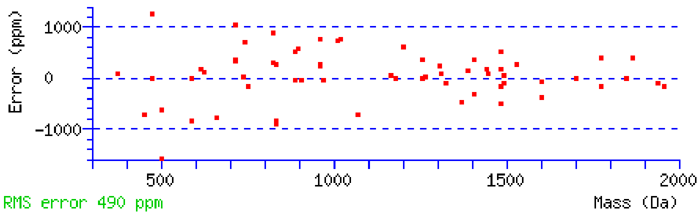


Monoisotopic mass of neutral peptide Mr(calc): 3363.3253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 75 **Expect:** 3.5e-007
Matches : 67/486 fragment ions using 85 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3201.2693	1601.1383	3184.2427	1592.6250	3183.2587	1592.1330	28
3	474.2023	237.6048					Y	3054.2009	1527.6041	3037.1743	1519.0908	3036.1903	1518.5988	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2891.1375	1446.0724	2874.1110	1437.5591	2873.1270	1437.0671	26
5	646.2508	323.6290	629.2242	315.1157			G	2776.1106	1388.5589	2759.0841	1380.0457	2758.1000	1379.5537	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2719.0891	1360.0482	2702.0626	1351.5349	2701.0786	1351.0429	24
7	**834.3305**	417.6689	817.3039	409.1556	816.3199	408.6636	S	2618.0415	1309.5244	2601.0149	1301.0111	2600.0309	1300.5191	23
8	965.3709	483.1891	948.3444	474.6758	947.3604	474.1838	M	2531.0094	1266.0084	2513.9829	1257.4951	2512.9989	1257.0031	22
9	1036.4081	518.7077	1019.3815	510.1944	1018.3975	509.7024	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	1196.4387	598.7230	1179.4122	590.2097	1178.4281	589.7177	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	**1325.4813**	663.2443	1308.4548	654.7310	1307.4707	654.2390	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1426.5290	***713.7681***	1409.5024	705.2549	1408.5184	704.7628	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	1573.5974	787.3023	1556.5708	778.7891	1555.5868	778.2971	F	**1938.8109**	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1701.6560**	851.3316	1684.6294	842.8184	1683.6454	842.3263	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1864.7193**	932.8633	1847.6928	924.3500	1846.7087	923.8580	Y	1663.6839	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	1921.7408	***961.3740***	1904.7142	952.8607	1903.7302	952.3687	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	1978.7622	989.8848	1961.7357	981.3715	1960.7517	980.8795	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2138.7929	***1069.9001***	2121.7663	1061.3868	2120.7823	1060.8948	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2285.8283	1143.4178	2268.8017	1134.9045	2267.8177	1134.4125	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2342.8497	1171.9285	2325.8232	1163.4152	2324.8392	1162.9232	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2456.8927	1228.9500	2439.8661	1220.4367	2438.8821	1219.9447	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2513.9141	***1257.4607***	2496.8876	1248.9474	2495.9036	1248.4554	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2627.9571	1314.4822	2610.9305	1305.9689	2609.9465	1305.4769	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2742.0000	***1371.5036***	2724.9734	1362.9904	2723.9894	1362.4983	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2889.0684	***1445.0378***	2872.0419	1436.5246	2871.0578	1436.0326	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2988.1368	***1494.5720***	2971.1103	1486.0588	2970.1263	1485.5668	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3089.1845	1545.0959	3072.1579	1536.5826	3071.1739	1536.0906	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3218.2271	1609.6172	3201.2005	1601.1039	3200.2165	1600.6119	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
75.4	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M19; 38.49%
74.3	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, Oxidation M19; 30.15%
70.4	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14, Oxidation M19; 12.12%
68.6	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
68.5	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
67.1	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M8; 5.69%
65.5	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
64.8	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
64.0	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
63.9	3363.3253	0.0095	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23, Oxidation M19; 2.72%

Mascot: http://www.matrixscience.com/

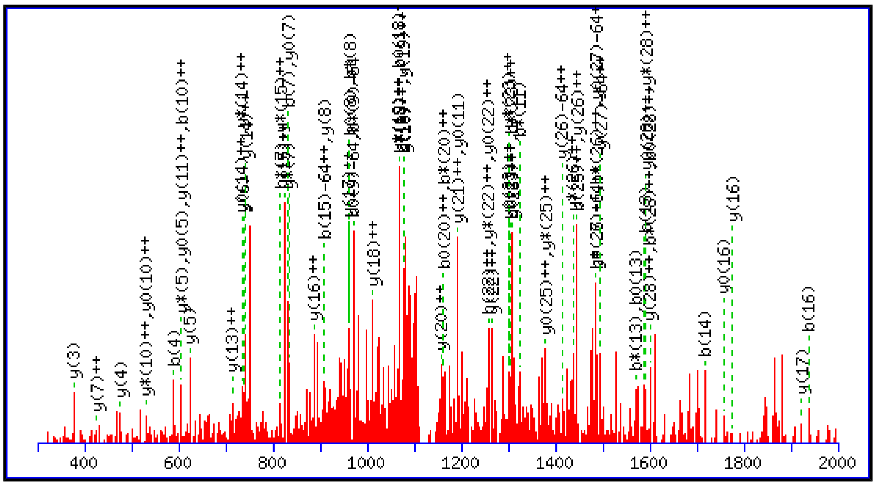
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27537: 3364.360812 from(1122.460880,3+) intensity(3124.8772) rtinseconds(3089) scans(8171) index(4861)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum7018_scans__8171
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

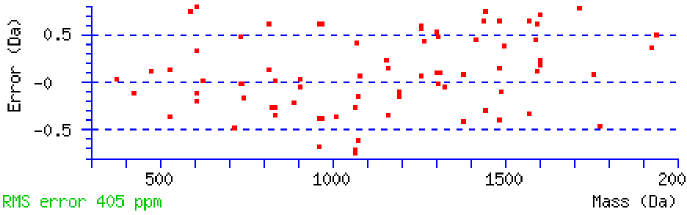
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [300] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

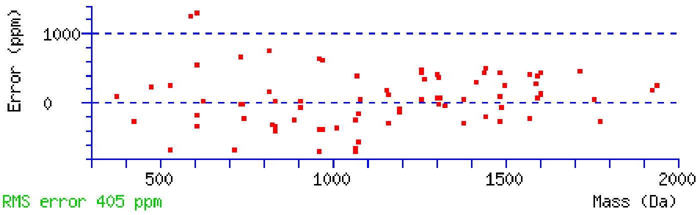


```
Monoisotopic mass of neutral peptide Mr(calc): 3362.3413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 48  Expect: 0.00038
Matches : 77/486 fragment ions using 136 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3200.2853	1600.6463	3183.2587	1592.1330	3182.2747	1591.6410	28
3	474.2023	237.6048					Y	3053.2169	1527.1121	3036.1903	1518.5988	3035.2063	1518.1068	27
4	**588.2453**	294.6263	571.2187	286.1130			N	2890.1535	1445.5804	2873.1270	1437.0671	2872.1430	1436.5751	26
5	645.2667	323.1370	628.2402	314.6237			G	2776.1106	1388.5589	2759.0841	1380.0457	2758.1000	1379.5537	25
6	746.3144	373.6608	729.2879	365.1476	728.3039	364.6556	T	2719.0891	1360.0482	2702.0626	1351.5349	2701.0786	1351.0429	24
7	**833.3464**	417.1769	816.3199	408.6636	815.3359	408.1716	S	2618.0415	1309.5244	2601.0149	1301.0111	2600.0309	1300.5191	23
8	980.3818	490.6946	963.3553	482.1813	962.3713	481.6893	M	2531.0094	1266.0084	2513.9829	1257.4951	2512.9989	1257.0031	22
9	1051.4190	526.2131	1034.3924	517.6998	1033.4084	517.2078	A	2383.9740	1192.4907	2366.9475	1183.9774	2365.9635	1183.4854	21
10	1211.4496	606.2284	1194.4231	597.7152	1193.4390	597.2232	C	2312.9369	1156.9721	2295.9104	1148.4588	2294.9264	1147.9668	20
11	1340.4922	670.7497	1323.4657	662.2365	1322.4816	661.7445	E	2152.9063	1076.9568	2135.8797	1068.4435	2134.8957	1067.9515	19
12	1441.5399	721.2736	1424.5133	712.7603	1423.5293	712.2683	T	2023.8637	1012.4355	2006.8371	1003.9222	2005.8531	1003.4302	18
13	**1588.6083**	794.8078	1571.5817	786.2945	1570.5977	785.8025	F	***1922.8160***	961.9116	1905.7894	953.3984	1904.8054	952.9064	17
14	**1716.6669**	858.8371	1699.6403	850.3238	1698.6563	849.8318	Q	***1775.7476***	888.3774	1758.7210	879.8642	1757.7370	879.3721	16
15	1879.7302	940.3687	1862.7037	931.8555	1861.7196	931.3635	Y	1647.6890	824.3481	1630.6625	815.8349	1629.6784	815.3429	15
16	**1936.7517**	968.8795	1919.7251	960.3662	1918.7411	959.8742	G	1484.6257	742.8165	1467.5991	734.3032	1466.6151	733.8112	14
17	1993.7731	997.3902	1976.7466	988.8769	1975.7626	988.3849	G	1427.6042	714.3057	1410.5777	705.7925	1409.5936	705.3005	13
18	2153.8038	1077.4055	2136.7772	1068.8923	2135.7932	1068.4002	C	1370.5827	685.7950	1353.5562	677.2817	1352.5722	676.7897	12
19	2284.8443	1142.9258	2267.8177	1134.4125	2266.8337	1133.9205	M	1210.5521	605.7797	1193.5255	597.2664	1192.5415	596.7744	11
20	2341.8657	1171.4365	2324.8392	1162.9232	2323.8552	1162.4312	G	***1079.5116***	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2455.9087	1228.4580	2438.8821	1219.9447	2437.8981	1219.4527	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2512.9301	1256.9687	2495.9036	1248.4554	2494.9196	1247.9634	G	***908.4472***	454.7272	891.4207	446.2140	890.4367	445.7220	8
23	2626.9730	1313.9902	2609.9465	1305.4769	2608.9625	1304.9849	N	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	7

24	2741.0160	1371.0116	2723.9894	1362.4983	2723.0054	1362.0063	**N**	***737.3828***	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2888.0844	1444.5458	2871.0578	1436.0326	2870.0738	1435.5405	**F**	***623.3399***	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2987.1528	1494.0800	2970.1263	1485.5668	2969.1422	1485.0748	**V**	***476.2715***	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3088.2005	1544.6039	3071.1739	1536.0906	3070.1899	1535.5986	**T**	***377.2031***	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3217.2431	1609.1252	3200.2165	1600.6119	3199.2325	1600.1199	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
48.0	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Oxidation M8 95.44%
42.8	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
41.3	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
39.7	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
34.8	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Oxidation M19 4.56%
34.5	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
34.5	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
22.6	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
22.3	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
20.9	3362.3413	2.0195	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

Mascot: http://www.matrixscience.com/

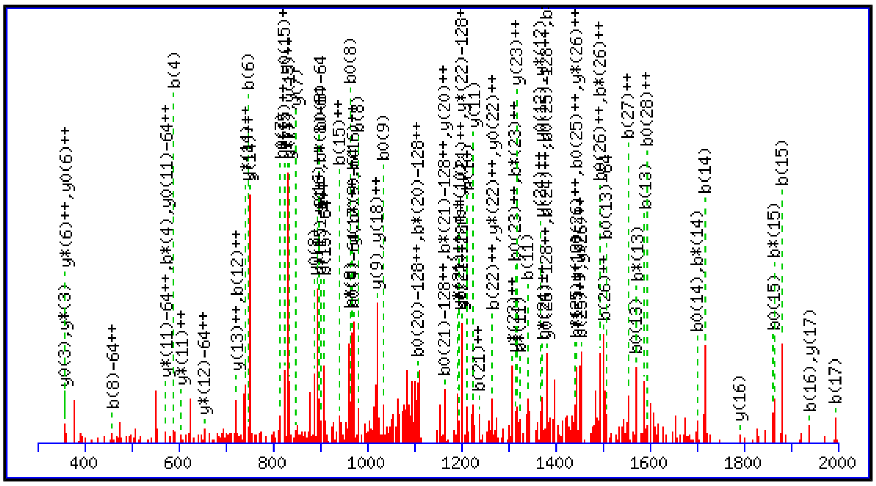
Mascot Search Results

Peptide View

MS/MS Fragmentation of YFYNGTSMACETFQYGGCMGNGNNFVTVR
Found in S4R471 in con_Xuniprot_HUMAN3, S4R471_HUMAN Protein AMBP (Fragment) OS=Homo sapiens GN=AMBP PE=4 SV=1

Match to Query 27660: 3379.342482 from(1127.454770,3+) intensity(2847.7961) rtinseconds(1732) scans(3645) index(21902)
Title: 111019_Est_MI_YP_G_15Spectrum3142_scans__3645
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

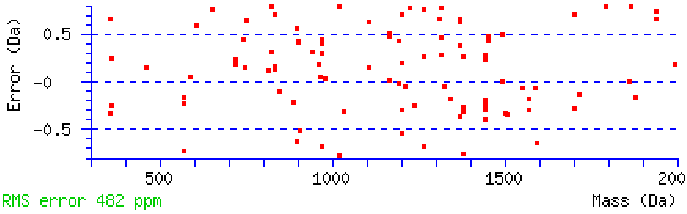
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

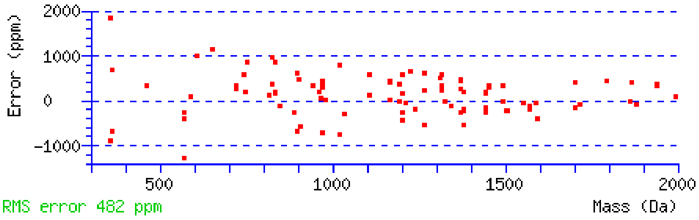


Monoisotopic mass of neutral peptide Mr(calc): 3378.3363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N21 : Deamidated (NQ)
Ions Score: 42 **Expect:** 0.00098
Matches : 98/550 fragment ions using 162 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3216.2802	1608.6437	3199.2536	1600.1305	3198.2696	1599.6384	28
3	474.2023	237.6048					Y	3069.2118	1535.1095	3052.1852	1526.5963	3051.2012	1526.1042	27
4	***589.2293***	295.1183	572.2027	286.6050			N	2906.1484	1453.5779	2889.1219	1445.0646	2888.1379	1444.5726	26
5	646.2508	323.6290	629.2242	315.1157			G	2791.1215	1396.0644	2774.0950	1387.5511	2773.1109	1387.0591	25
6	***747.2984***	374.1529	730.2719	365.6396	729.2879	365.1476	T	2734.1000	1367.5537	2717.0735	1359.0404	2716.0895	1358.5484	24
7	***834.3305***	417.6689	817.3039	409.1556	816.3199	408.6636	S	2633.0524	1317.0298	2616.0258	1308.5165	2615.0418	1308.0245	23
8	***981.3659***	491.1866	964.3393	482.6733	963.3553	482.1813	M	2546.0203	1273.5138	2528.9938	1265.0005	2528.0098	1264.5085	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2398.9849	1199.9961	2381.9584	1191.4828	2380.9744	1190.9908	21
10	***1212.4336***	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2327.9478	1164.4775	2310.9213	1155.9643	2309.9373	1155.4723	20
11	***1341.4762***	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2167.9172	1084.4622	2150.8906	1075.9489	2149.9066	1075.4569	19
12	***1442.5239***	***721.7656***	1425.4973	713.2523	1424.5133	712.7603	T	2038.8746	1019.9409	2021.8480	1011.4277	2020.8640	1010.9356	18
13	***1589.5923***	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	**1937.8269**	969.4171	1920.8003	960.9038	1919.8163	960.4118	17
14	***1717.6509***	859.3291	1700.6243	850.8158	1699.6403	850.3238	Q	**1790.7585**	895.8829	1773.7319	887.3696	1772.7479	886.8776	16
15	***1880.7142***	***940.8607***	1863.6877	932.3475	1862.7037	931.8555	Y	1662.6999	831.8536	1645.6734	823.3403	1644.6893	822.8483	15
16	***1937.7357***	***969.3715***	1920.7091	960.8582	1919.7251	960.3662	G	1499.6366	750.3219	1482.6100	741.8087	1481.6260	741.3166	14
17	***1994.7571***	997.8822	1977.7306	989.3689	1976.7466	988.8769	G	**1442.6151**	721.8112	1425.5886	713.2979	1424.6045	712.8059	13
18	2154.7878	1077.8975	2137.7612	1069.3843	2136.7772	1068.8923	C	1385.5936	693.3005	1368.5671	684.7872	1367.5831	684.2952	12
19	2301.8232	1151.4152	2284.7966	1142.9020	2283.8126	1142.4100	M	**1225.5630**	613.2851	1208.5364	604.7719	1207.5524	604.2799	11
20	2358.8447	1179.9260	2341.8181	1171.4127	2340.8341	1170.9207	G	1078.5276	539.7674	1061.5010	531.2542	1060.5170	530.7622	10
21	2473.8716	***1237.4394***	2456.8451	1228.9262	2455.8610	1228.4342	N	**1021.5061**	511.2567	1004.4796	502.7434	1003.4956	502.2514	9

22	2530.8931	***1265.9502***	2513.8665	1257.4369	2512.8825	1256.9449	**G**	906.4792	453.7432	889.4526	445.2300	888.4686	444.7380	**8**
23	2644.9360	1322.9716	2627.9094	1314.4584	2626.9254	1313.9664	**N**	**849.4577**	425.2325	832.4312	416.7192	831.4472	416.2272	**7**
24	2758.9789	***1379.9931***	2741.9524	1371.4798	2740.9684	1370.9878	**N**	735.4148	368.2110	718.3883	359.6978	717.4042	359.2058	**6**
25	2906.0473	***1453.5273***	2889.0208	1445.0140	2888.0368	1444.5220	**F**	621.3719	311.1896	604.3453	302.6763	603.3613	302.1843	**5**
26	3005.1157	***1503.0615***	2988.0892	1494.5482	2987.1052	1494.0562	**V**	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	**4**
27	3106.1634	***1553.5854***	3089.1369	1545.0721	3088.1529	1544.5801	**T**	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
28	3205.2318	1603.1196	3188.2053	1594.6063	3187.2213	1594.1143	**V**	274.1874	137.5973	257.1608	129.0840			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
41.8	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, N21 20.11%
41.4	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated Q14, N21 18.26%
40.7	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, N24 15.87%
40.7	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, N23 15.87%
39.9	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated Q14, N24 12.96%
39.9	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated Q14, N23 12.96%
39.7	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
32.5	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14 2.40%
26.6	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N23, N24 0.62%
26.1	3378.3363	1.0062	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N21, N24 0.54%

Mascot: http://www.matrixscience.com/

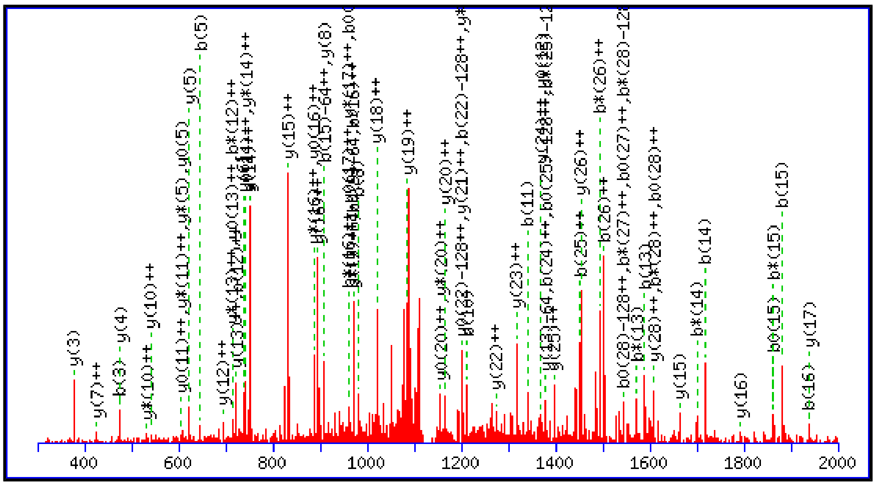
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27608: 3379.331022 from(1127.450950,3+) intensity(10924.8106) rtinseconds(1693) scans(4528) index(17594)
Title: 111019_Est_MI_YP_G_07Spectrum3887_scans__4528
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

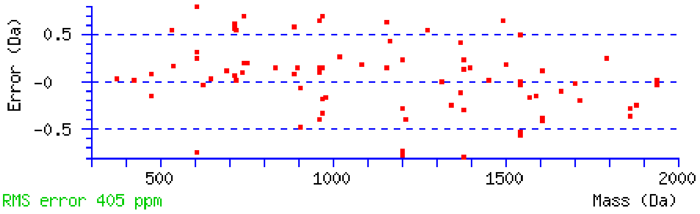
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

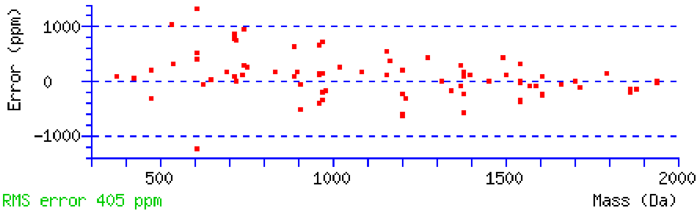


```
Monoisotopic mass of neutral peptide Mr(calc): 3379.3203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M19     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 131  Expect: 9.7e-013
Matches : 80/552 fragment ions using 68 most intense peaks     (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3217.2642	1609.1357	3200.2377	1600.6225	3199.2536	1600.1305	28
3	**474.2023**	237.6048					Y	3070.1958	1535.6015	3053.1692	1527.0883	3052.1852	1526.5962	27
4	589.2293	295.1183	572.2027	286.6050			N	2907.1325	1454.0699	2890.1059	1445.5566	2889.1219	1445.0646	26
5	**646.2508**	323.6290	629.2242	315.1157			G	2792.1055	1396.5564	2775.0790	1388.0431	2774.0950	1387.5511	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2735.0841	1368.0457	2718.0575	1359.5324	2717.0735	1359.0404	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2634.0364	1317.5218	2617.0098	1309.0086	2616.0258	1308.5165	23
8	**981.3659**	491.1866	964.3393	482.6733	963.3553	482.1813	M	2547.0043	1274.0058	2529.9778	1265.4925	2528.9938	1265.0005	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	**1212.4336**	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	**1341.4762**	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1442.5239	**721.7656**	1425.4973	713.2523	1424.5133	712.7603	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	**1938.8109**	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1717.6509**	859.3291	1700.6243	850.8158	1699.6403	850.3238	Q	**1791.7425**	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1880.7142**	940.8607	1863.6877	932.3475	1862.7037	931.8555	Y	**1663.6839**	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1937.7357**	**969.3715**	1920.7091	960.8582	1919.7251	960.3662	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	1994.7571	997.8822	1977.7306	989.3689	1976.7466	988.8769	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2154.7878	1077.8975	2137.7612	1069.3843	2136.7772	1068.8923	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2301.8232	1151.4152	2284.7966	1142.9020	2283.8126	1142.4100	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2358.8447	1179.9260	2341.8181	1171.4127	2340.8341	1170.9207	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2472.8876	1236.9474	2455.8610	1228.4342	2454.8770	1227.9421	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2529.9090	1265.4582	2512.8825	1256.9449	2511.8985	1256.4529	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2643.9520	1322.4796	2626.9254	1313.9664	2625.9414	1313.4743	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2757.9949	**1379.5011**	2740.9684	1370.9878	2739.9843	1370.4958	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2905.0633	**1453.0353**	2888.0368	1444.5220	2887.0528	1444.0300	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	3004.1317	**1502.5695**	2987.1052	1494.0562	2986.1212	1493.5642	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3105.1794	1553.0933	3088.1529	1544.5801	3087.1688	1544.0881	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3234.2220	1617.6146	3217.1955	1609.1014	3216.2114	1608.6094	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of [YFYNGTSMACETFQYGGCMGNGNNFVTEK]()
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways]()

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
130.9	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4 46.94%
128.8	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14 28.68%
124.5	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N24 10.68%
122.6	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23 6.85%
122.6	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21 6.85%
122.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
122.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
118.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
118.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
118.1	3379.3203	0.0108	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

Mascot: http://www.matrixscience.com/

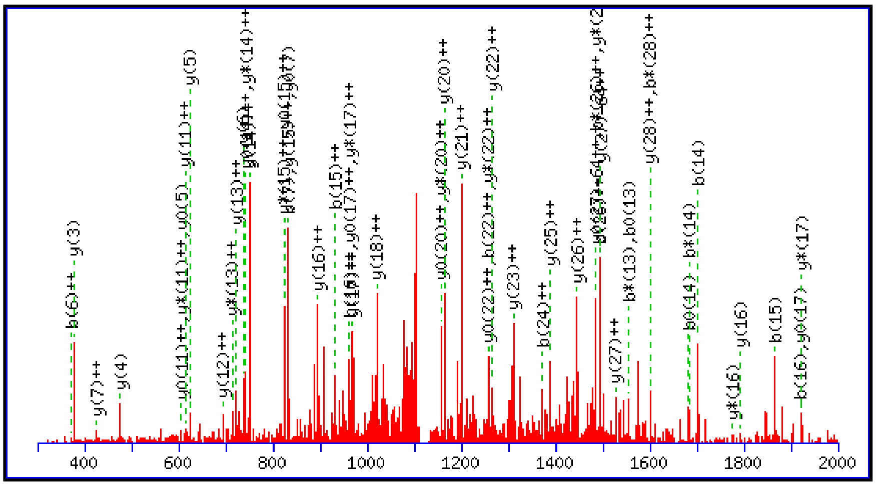
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27516: 3363.336522 from(1122.119450,3+) intensity(23263.3320) rtinseconds(1787) scans(4490) index(11031)
Title: 111019_Est_ISCardio_NMI_YS_G_7Spectrum3801_scans__4490
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

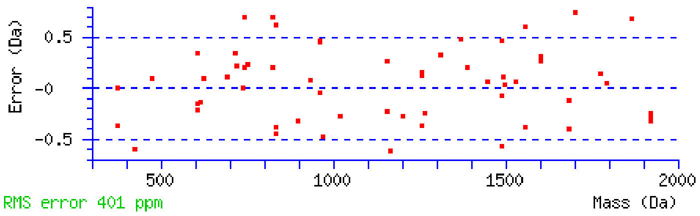
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

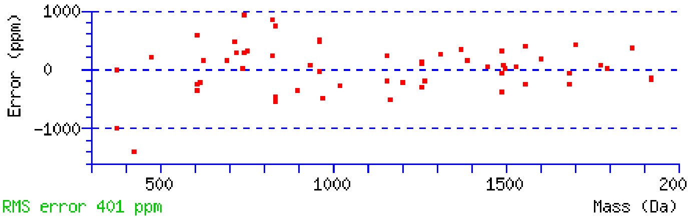


```
Monoisotopic mass of neutral peptide Mr(calc): 3363.3253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Deamidated (NQ)
M19     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 122  Expect: 9e-012
Matches : 59/486 fragment ions using 68 most intense peaks    (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3201.2693	1601.1383	3184.2427	1592.6250	3183.2587	1592.1330	28
3	474.2023	237.6048					Y	3054.2009	1527.6041	3037.1743	1519.0908	3036.1903	1518.5988	27
4	588.2453	294.6263	571.2187	286.1130			N	2891.1375	1446.0724	2874.1110	1437.5591	2873.1270	1437.0671	26
5	645.2667	323.1370	628.2402	314.6237			G	2777.0946	1389.0509	2760.0681	1380.5377	2759.0841	1380.0457	25
6	746.3144	**373.6608**	729.2879	365.1476	728.3039	364.6556	T	2720.0732	1360.5402	2703.0466	1352.0269	2702.0626	1351.5349	24
7	**833.3464**	417.1769	816.3199	408.6636	815.3359	408.1716	S	2619.0255	1310.0164	2601.9989	1301.5031	2601.0149	1301.0111	23
8	964.3869	482.6971	947.3604	474.1838	946.3764	473.6918	M	2531.9934	1266.5004	2514.9669	1257.9871	2513.9829	1257.4951	22
9	1035.4240	518.2157	1018.3975	509.7024	1017.4135	509.2104	A	2400.9530	1200.9801	2383.9264	1192.4668	2382.9424	1191.9748	21
10	1195.4547	598.2310	1178.4281	589.7177	1177.4441	589.2257	C	2329.9158	1165.4616	2312.8893	1156.9483	2311.9053	1156.4563	20
11	1324.4973	662.7523	1307.4707	654.2390	1306.4867	653.7470	E	2169.8852	1085.4462	2152.8586	1076.9330	2151.8746	1076.4410	19
12	1425.5450	713.2761	1408.5184	704.7628	1407.5344	704.2708	T	2040.8426	1020.9249	2023.8161	1012.4117	2022.8320	1011.9197	18
13	1572.6134	786.8103	1555.5868	778.2971	1554.6028	777.8050	F	1939.7949	970.4011	1922.7684	961.8878	1921.7844	961.3958	17
14	**1701.6560**	851.3316	1684.6294	842.8184	1683.6454	842.3263	Q	**1792.7265**	896.8669	1775.7000	888.3536	1774.7159	887.8616	16
15	**1864.7193**	**932.8633**	1847.6928	924.3500	1846.7087	923.8580	Y	1663.6839	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1921.7408**	**961.3740**	1904.7142	952.8607	1903.7302	952.3687	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	1978.7622	989.8848	1961.7357	981.3715	1960.7517	980.8795	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2138.7929	1069.9001	2121.7663	1061.3868	2120.7823	1060.8948	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2285.8283	1143.4178	2268.8017	1134.9045	2267.8177	1134.4125	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2342.8497	1171.9285	2325.8232	1163.4152	2324.8392	1162.9232	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2456.8927	1228.9500	2439.8661	1220.4367	2438.8821	1219.9447	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2513.9141	**1257.4607**	2496.8876	1248.9474	2495.9036	1248.4554	G	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2627.9571	1314.4822	2610.9305	1305.9689	2609.9465	1305.4769	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2742.0000	**1371.5036**	2724.9734	1362.9904	2723.9894	1362.4984	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2889.0684	1445.0378	2872.0419	1436.5246	2871.0578	1436.0326	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	2988.1368	**1494.5720**	2971.1103	1486.0588	2970.1263	1485.5668	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3089.1845	1545.0959	3072.1579	1536.5826	3071.1739	1536.0906	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3218.2271	1609.6172	3201.2005	1601.1039	3200.2165	1600.6119	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
121.9	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14, Oxidation M19; 43.76%
119.8	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4, Oxidation M19; 27.35%
116.1	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N24, Oxidation M19; 11.51%
115.6	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N21, Oxidation M19; 10.30%
113.6	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N23, Oxidation M19; 6.59%
104.0	3362.3413	0.9952	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
102.1	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
96.7	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
96.4	3362.3413	0.9952	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
96.3	3363.3253	0.0112	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

Mascot: http://www.matrixscience.com/

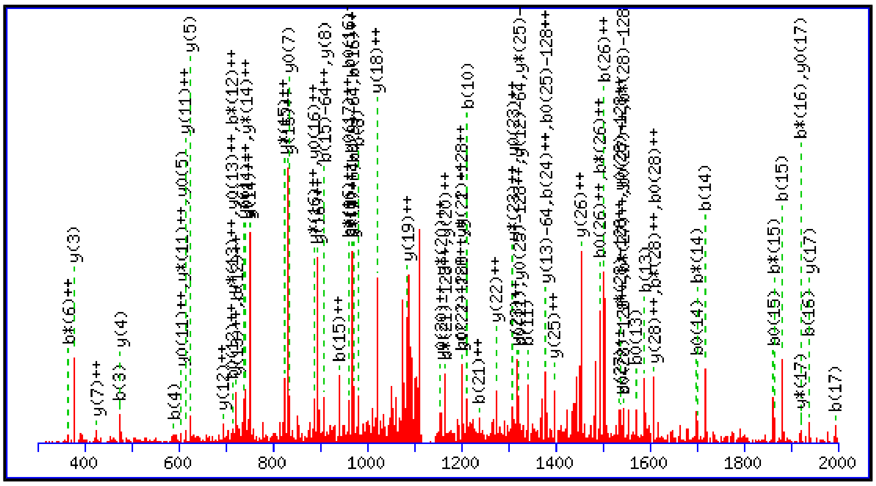
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTEK**
Found in **P02760** in **con_Xuniprot_HUMAN3**, AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

Match to Query 27594: 3379.328652 from(1127.450160,3+) intensity(24610.3223) rtinseconds(1902) scans(5005) index(4515)
Title: 111019_Est_ISCardio_NMI_YP_G_7Spectrum4242_scans__5005
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

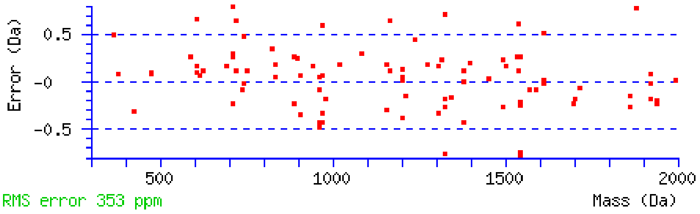
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

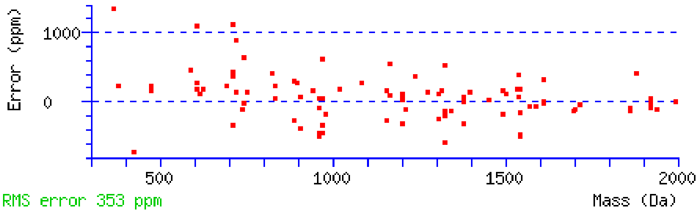


Monoisotopic mass of neutral peptide Mr(calc): 3379.3203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4 : Deamidated (NQ)
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 105 **Expect:** 3.1e-010
Matches : 94/552 fragment ions using 102 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3217.2642	1609.1357	3200.2377	1600.6225	3199.2536	1600.1305	28
3	**474.2023**	237.6048					Y	3070.1958	1535.6015	3053.1692	1527.0883	3052.1852	1526.5962	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2907.1325	1454.0699	2890.1059	1445.5566	2889.1219	1445.0646	26
5	646.2508	323.6290	629.2242	315.1157			G	2792.1055	1396.5564	2775.0790	1388.0431	2774.0950	1387.5511	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2735.0841	1368.0457	2718.0575	1359.5324	2717.0735	1359.0404	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2634.0364	1317.5218	2617.0098	1309.0086	2616.0258	1308.5165	23
8	**981.3659**	491.1866	964.3393	482.6733	963.3553	482.1813	M	2547.0043	1274.0058	2529.9778	1265.4925	2528.9938	1265.0005	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	**1212.4336**	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	**1341.4762**	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1442.5239	**721.7656**	1425.4973	713.2523	1424.5133	712.7603	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	**1938.8109**	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1717.6509**	859.3291	1700.6243	850.8158	1699.6403	850.3238	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1880.7142**	**940.8607**	1863.6877	932.3475	1862.7037	931.8555	Y	1663.6839	832.3456	1646.6574	823.8323	1645.6734	823.3403	15
16	**1937.7357**	**969.3715**	1920.7091	960.8582	1919.7251	960.3662	G	1500.6206	750.8139	1483.5940	742.3007	1482.6100	741.8087	14
17	**1994.7571**	997.8822	1977.7306	989.3689	1976.7466	988.8769	G	1443.5991	722.3032	1426.5726	713.7899	1425.5886	713.2979	13
18	2154.7878	1077.8975	2137.7612	1069.3843	2136.7772	1068.8923	C	1386.5777	693.7925	1369.5511	685.2792	1368.5671	684.7872	12
19	2301.8232	1151.4152	2284.7966	1142.9020	2283.8126	1142.4100	M	1226.5470	613.7771	1209.5205	605.2639	1208.5364	604.7719	11
20	2358.8447	1179.9260	2341.8181	1171.4127	2340.8341	1170.9207	G	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	10
21	2472.8876	**1236.9474**	2455.8610	1228.4342	2454.8770	1227.9421	N	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	9
22	2529.9090	1265.4582	2512.8825	1256.9449	2511.8985	1256.4529	G	**908.4472**	454.7272	891.4207	446.2140	890.4367	445.7220	8

23	2643.9520	1322.4796	2626.9254	1313.9664	2625.9414	1313.4743	**N**	851.4258	426.2165	834.3992	417.7032	833.4152	417.2112	**7**
24	2757.9949	**1379.5011**	2740.9684	1370.9878	2739.9843	1370.4958	**N**	**737.3828**	369.1951	720.3563	360.6818	719.3723	360.1898	**6**
25	2905.0633	1453.0353	2888.0368	1444.5220	2887.0528	1444.0300	**F**	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	**5**
26	3004.1317	**1502.5695**	2987.1052	1494.0562	2986.1212	1493.5642	**V**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
27	3105.1794	1553.0933	3088.1529	1544.5801	3087.1688	1544.0881	**T**	**377.2031**	189.1052	360.1765	180.5919	359.1925	180.0999	**3**
28	3234.2220	1617.6146	3217.1955	1609.1014	3216.2114	1608.6094	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
29							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
105.3	3379.3203	0.0084	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated N4 47.54%
103.9	3379.3203	0.0084	YFYNGTSMACETFQYGGCMGNGNNFVTEK	Deamidated Q14 34.92%
101.9	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
101.9	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
101.9	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
97.4	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
97.4	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
97.4	3378.3363	0.9924	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
97.2	3379.3203	0.0084	YFYNGTSMACETFQYGGCMGNGNNFVTVR	
97.2	3379.3203	0.0084	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

Mascot: http://www.matrixscience.com/

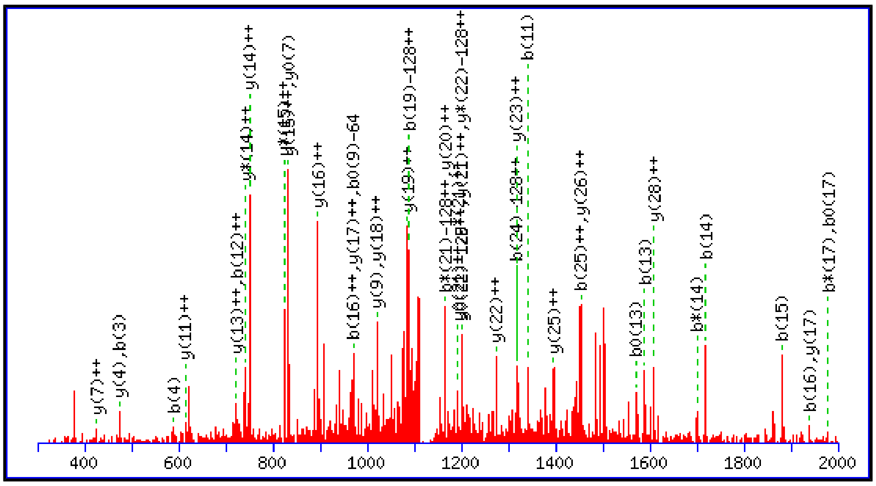
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **YFYNGTSMACETFQYGGCMGNGNNFVTVR**
Found in **S4R471** in **con_Xuniprot_HUMAN3**, S4R471_HUMAN Protein AMBP (Fragment) OS=Homo sapiens GN=AMBP PE=4 SV=1

Match to Query 27689: 3380.317482 from(1127.779770,3+) intensity(9494.3203) rtinseconds(1725) scans(4620) index(17606)
Title: 111019_Est_MI_YP_G_07Spectrum3966_scans__4620
Data file C:\\mascot\\20140703_Tmgf_1D\\CSV_UseAnalysis\\MasterCSV\\All_Glyco\\mgf\\ptm\\UC18ERLIC_PTM_35D.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



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Monoisotopic mass of neutral peptide Mr(calc): 3379.3203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N4      : Deamidated (NQ)
M8      : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Q14     : Deamidated (NQ)
M19     : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
N24     : Deamidated (NQ)
Ions Score: 100  Expect: 8.4e-010
Matches : 44/550 fragment ions using 51 most intense peaks   (help)
```
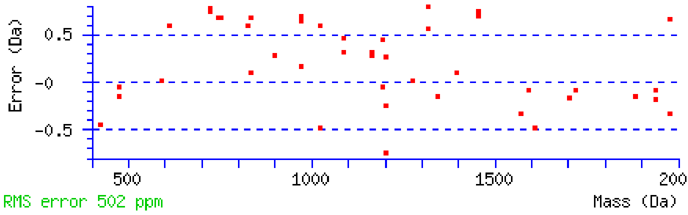
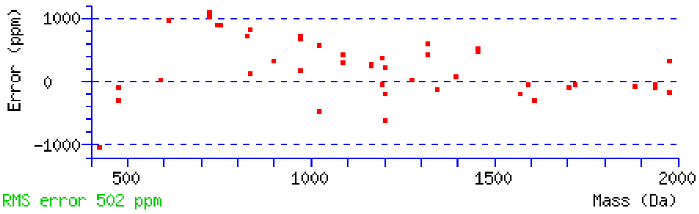

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							29
2	311.1390	156.0731					F	3217.2642	1609.1357	3200.2377	1600.6225	3199.2536	1600.1305	28
3	**474.2023**	237.6048					Y	3070.1958	1535.6015	3053.1692	1527.0883	3052.1852	1526.5963	27
4	**589.2293**	295.1183	572.2027	286.6050			N	2907.1325	1454.0699	2890.1059	1445.5566	2889.1219	1445.0646	26
5	646.2508	323.6290	629.2242	315.1157			G	2792.1055	1396.5564	2775.0790	1388.0431	2774.0950	1387.5511	25
6	747.2984	374.1529	730.2719	365.6396	729.2879	365.1476	T	2735.0841	1368.0457	2718.0575	1359.5324	2717.0735	1359.0404	24
7	834.3305	417.6689	817.3039	409.1556	816.3199	408.6636	S	2634.0364	1317.5218	2617.0098	1309.0086	2616.0258	1308.5165	23
8	981.3659	491.1866	964.3393	482.6733	963.3553	482.1813	M	2547.0043	1274.0058	2529.9778	1265.4925	2528.9938	1265.0005	22
9	1052.4030	526.7051	1035.3764	518.1919	1034.3924	517.6998	A	2399.9689	1200.4881	2382.9424	1191.9748	2381.9584	1191.4828	21
10	1212.4336	606.7205	1195.4071	598.2072	1194.4231	597.7152	C	2328.9318	1164.9696	2311.9053	1156.4563	2310.9213	1155.9643	20
11	**1341.4762**	671.2417	1324.4497	662.7285	1323.4657	662.2365	E	2168.9012	1084.9542	2151.8746	1076.4410	2150.8906	1075.9489	19
12	1442.5239	**721.7656**	1425.4973	713.2523	1424.5133	712.7603	T	2039.8586	1020.4329	2022.8320	1011.9197	2021.8480	1011.4277	18
13	**1589.5923**	795.2998	1572.5658	786.7865	1571.5817	786.2945	F	**1938.8109**	969.9091	1921.7844	961.3958	1920.8003	960.9038	17
14	**1718.6349**	859.8211	1701.6084	851.3078	1700.6243	850.8158	Q	1791.7425	896.3749	1774.7159	887.8616	1773.7319	887.3696	16
15	**1881.6982**	941.3528	1864.6717	932.8395	1863.6877	932.3475	Y	1662.6999	831.8536	1645.6734	823.3403	1644.6893	822.8483	15
16	**1938.7197**	**969.8635**	1921.6931	961.3502	1920.7091	960.8582	G	1499.6366	750.3219	1482.6100	741.8087	1481.6260	741.3166	14
17	1995.7412	998.3742	1978.7146	989.8609	1977.7306	989.3689	G	1442.6151	721.8112	1425.5886	713.2979	1424.6045	712.8059	13
18	2155.7718	1078.3895	2138.7453	1069.8763	2137.7612	1069.3843	C	1385.5936	693.3005	1368.5671	684.7872	1367.5831	684.2952	12
19	2302.8072	1151.9072	2285.7807	1143.3940	2284.7966	1142.9020	M	1225.5630	613.2851	1208.5364	604.7719	1207.5524	604.2799	11
20	2359.8287	1180.4180	2342.8021	1171.9047	2341.8181	1171.4127	G	1078.5276	539.7674	1061.5010	531.2542	1060.5170	530.7622	10
21	2473.8716	1237.4394	2456.8451	1228.9262	2455.8610	1228.4342	N	**1021.5061**	511.2567	1004.4796	502.7434	1003.4956	502.2514	9

22	2530.8931	1265.9502	2513.8665	1257.4369	2512.8825	1256.9449	**G**	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	**8**
23	2644.9360	1322.9716	2627.9094	1314.4584	2626.9254	1313.9664	**N**	850.4417	425.7245	833.4152	417.2112	832.4312	416.7192	**7**
24	2759.9629	1380.4851	2742.9364	1371.9718	2741.9524	1371.4798	**N**	736.3988	368.7030	719.3723	360.1898	718.3883	359.6978	**6**
25	2907.0313	**1454.0193**	2890.0048	1445.5060	2889.0208	1445.0140	**F**	621.3719	311.1896	604.3453	302.6763	603.3613	302.1843	**5**
26	3006.0998	1503.5535	2989.0732	1495.0402	2988.0892	1494.5482	**V**	**474.3035**	237.6554	457.2769	229.1421	456.2929	228.6501	**4**
27	3107.1474	1554.0774	3090.1209	1545.5641	3089.1369	1545.0721	**T**	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	**3**
28	3206.2159	1603.6116	3189.1893	1595.0983	3188.2053	1594.6063	**V**	274.1874	137.5973	257.1608	129.0840			**2**
29							**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of YFYNGTSMACETFQYGGCMGNGNNFVTVR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc)	Delta	Sequence	Site Analysis
99.6	3379.3203	0.9972	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14, N24 28.78%
99.6	3379.3203	0.9972	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14, N23 28.78%
99.6	3379.3203	0.9972	YFYNGTSMACETFQYGGCMGNGNNFVTVR	Deamidated N4, Q14, N21 28.78%
98.5	3379.3203	0.9972	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
97.4	3380.3043	0.0132	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
92.7	3380.3043	0.0132	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
92.7	3380.3043	0.0132	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
90.5	3380.3043	0.0132	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
89.9	3379.3203	0.9972	YFYNGTSMACETFQYGGCMGNGNNFVTEK	
89.0	3380.3043	0.0132	YFYNGTSMACETFQYGGCMGNGNNFVTVR	

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