

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **TAGAVTPVK**

Found in **Locus_21_Transcript_3/6_Confidence_0.562**, Locus_21_Transcript_3/6_Confidence_0.562

Translated in frame 1 ([nucleic acid sequence](#))

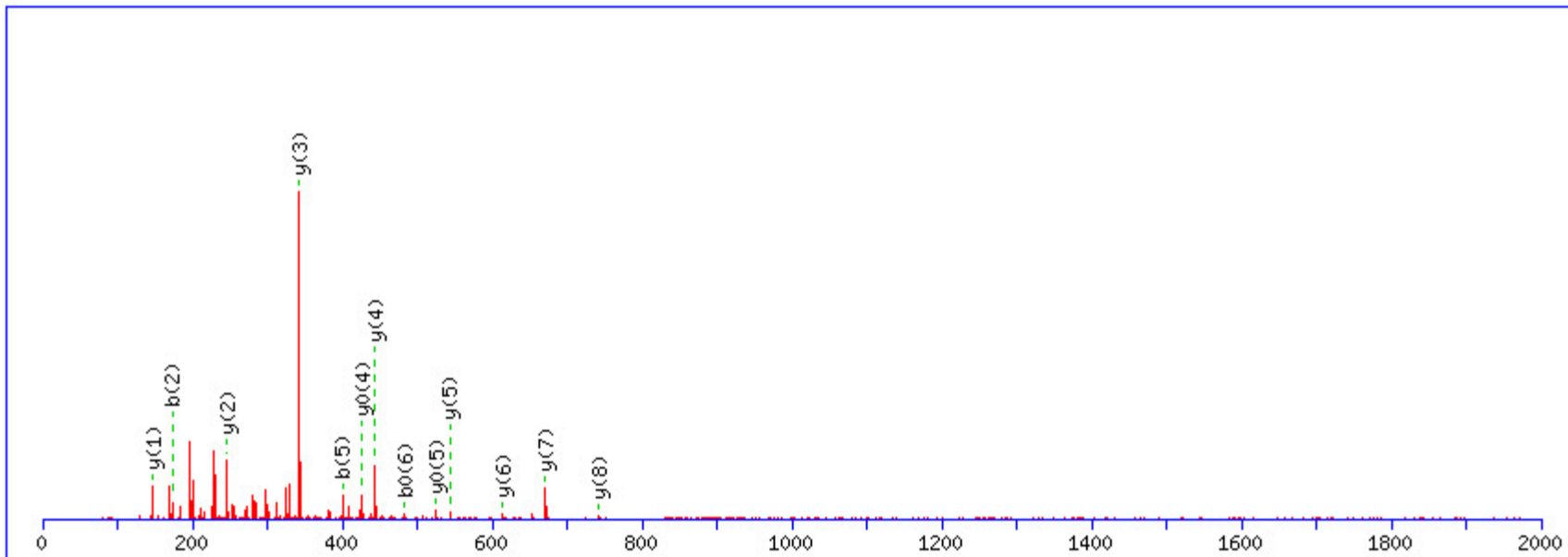
Match to Query 16: 842.385448 from(422.200000,2+) intensity(348.6061) index(2)

Data file VF_040111_3.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



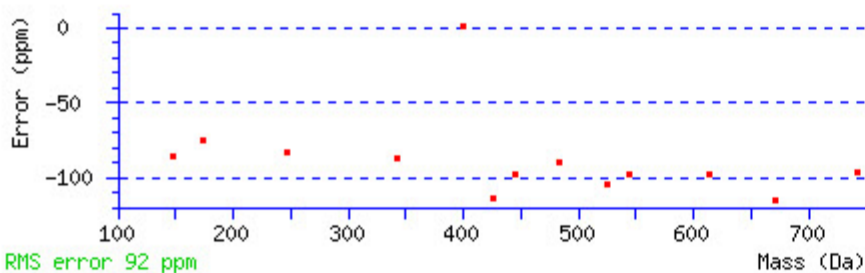
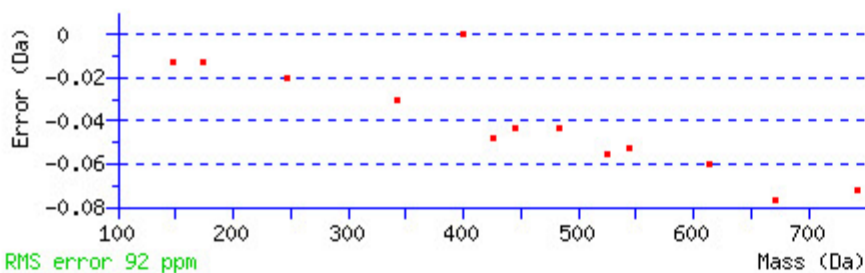
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 842.486176

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 62 Expect: 3.3e-005

Matches : 13/74 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.054955	51.531116	84.044390	42.525833	T							9
2	173.092069	87.049672	155.081504	78.044390	A	742.445767	371.726522	725.419218	363.213247	724.435202	362.721239	8
3	230.113533	115.560404	212.102968	106.555122	G	671.408653	336.207965	654.382104	327.694690	653.398088	327.202682	7
4	301.150647	151.078961	283.140082	142.073679	A	614.387189	307.697233	597.360640	299.183958	596.376624	298.691950	6
5	400.219061	200.613169	382.208496	191.607886	V	543.350075	272.178676	526.323526	263.665401	525.339510	263.173393	5
6	501.266740	251.137008	483.256175	242.131726	T	444.281661	222.644468	427.255112	214.131194	426.271096	213.639186	4
7	598.319504	299.663390	580.308939	290.658108	P	343.233982	172.120629	326.207433	163.607354			3
8	697.387918	349.197597	679.377353	340.192315	V	246.181218	123.594247	229.154669	115.080972			2
9					K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of **TAGAVTPVK**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
61.8	842.486176	-0.100728	TAGAVTPVK
13.1	842.476273	-0.090825	RWGTPVK
10.6	842.413391	-0.027943	DNLGINPT
9.8	842.508621	-0.123173	ATGLGRLR
7.3	841.465744	0.919704	VKANSPNL
6.2	841.527298	0.858150	SVLSLVPK
6.1	841.459244	0.926204	VGRHMOVK
5.9	841.400375	0.985073	QYSGIMK
5.8	842.508621	-0.123173	TQLGRLR
5.8	841.538528	0.846920	VIRIDVK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NSWGTSWGENGYIR**

Found in **Locus_223_Transcript_109/117_Confidence_0.057**, Locus_223_Transcript_109/117_Confidence_0.057

Translated in frame 5 ([nucleic acid sequence](#))

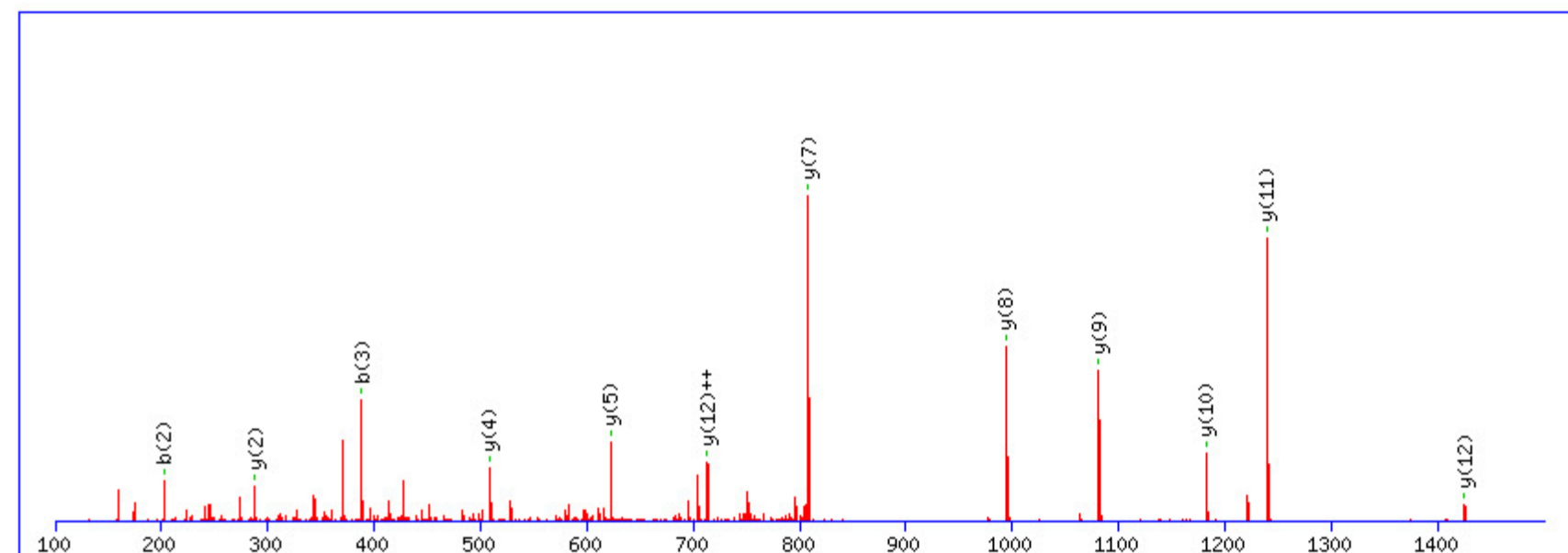
Match to Query 85: 1625.444448 from(813.729500,2+) intensity(3561.7922) index(39)

Data file VF_040111_4.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



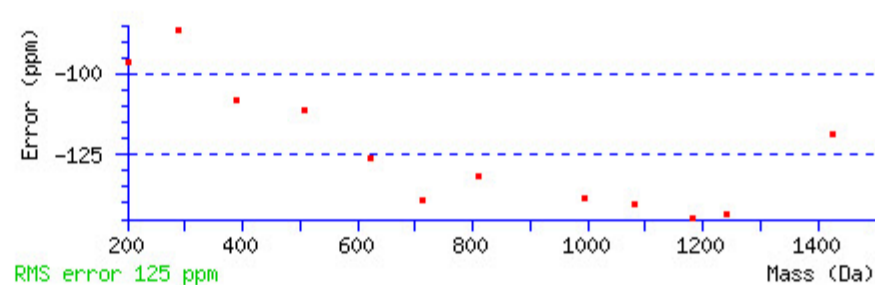
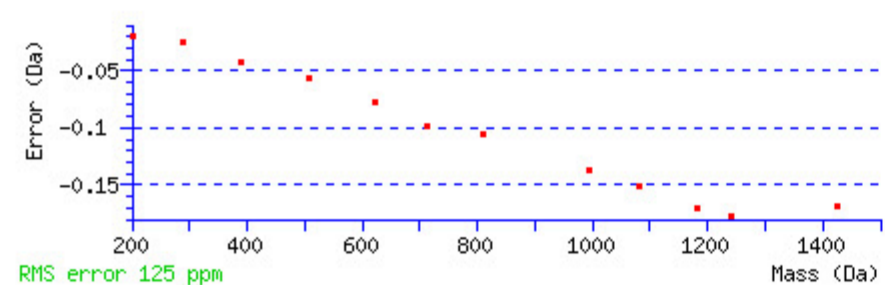
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1625.722260

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 84 Expect: 7.3e-007

Matches : 12/144 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	202.082231	101.544753	185.055682	93.031479	184.071666	92.539471	S	1512.686618	756.846947	1495.660069	748.333673	1494.676053	747.841664	13
3	388.161544	194.584410	371.134995	186.071136	370.150979	185.579128	W	1425.654590	713.330933	1408.628041	704.817658	1407.644025	704.325650	12
4	445.183008	223.095142	428.156459	214.581867	427.172443	214.089859	G	1239.575277	620.291276	1222.548728	611.778002	1221.564712	611.285994	11
5	546.230687	273.618982	529.204138	265.105707	528.220122	264.613699	T	1182.553813	591.780545	1165.527264	583.267270	1164.543248	582.775262	10
6	633.262715	317.134996	616.236166	308.621721	615.252150	308.129713	S	1081.506134	541.256705	1064.479585	532.743431	1063.495569	532.251422	9
7	819.342028	410.174652	802.315479	401.661378	801.331463	401.169370	W	994.474106	497.740691	977.447557	489.227417	976.463541	488.735409	8
8	876.363492	438.685384	859.336943	430.172110	858.352927	429.680102	G	808.394793	404.701034	791.368244	396.187760	790.384228	395.695752	7
9	1005.406085	503.206681	988.379536	494.693406	987.395520	494.201398	E	751.373329	376.190302	734.346780	367.677028	733.362764	367.185020	6
10	1119.449012	560.228144	1102.422463	551.714870	1101.438447	551.222862	N	622.330736	311.669006	605.304187	303.155731			5
11	1176.470476	588.738876	1159.443927	580.225602	1158.459911	579.733593	G	508.287809	254.647542	491.261260	246.134268			4
12	1339.533805	670.270541	1322.507256	661.757266	1321.523240	661.265258	Y	451.266345	226.136810	434.239796	217.623536			3
13	1452.617869	726.812572	1435.591320	718.299298	1434.607304	717.807290	I	288.203016	144.605146	271.176467	136.091871			2
14							R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [NSWGTSWGENGYIR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$	Delta	Sequence
83.5	1625.722260	-0.277812	NSWGTSWGENGYIR
20.5	1624.690628	0.753820	NSWGADWGEGDYIR
19.8	1624.729736	0.714712	SMTGMRSVSVSASPDR
4.3	1624.962433	0.482015	QIVTTPRALTASLVR
3.7	1625.798386	-0.353938	SWNPVDSMAKAPAPR
3.5	1625.863785	-0.419337	IGPQNTRATGWGLGAK
0.9	1624.727203	0.717245	CSLTREGWMNAMR
0.7	1625.709900	-0.265452	LSCPIMSSVNSCEV
0.6	1624.784546	0.659902	WTTTSSGSWGSSILR

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSTVVPYTTLR**

Found in **Locus_258_Transcript_1/1_Confidence_1.000**, Locus_258_Transcript_1/1_Confidence_1.000

Translated in frame 4 ([nucleic acid sequence](#))

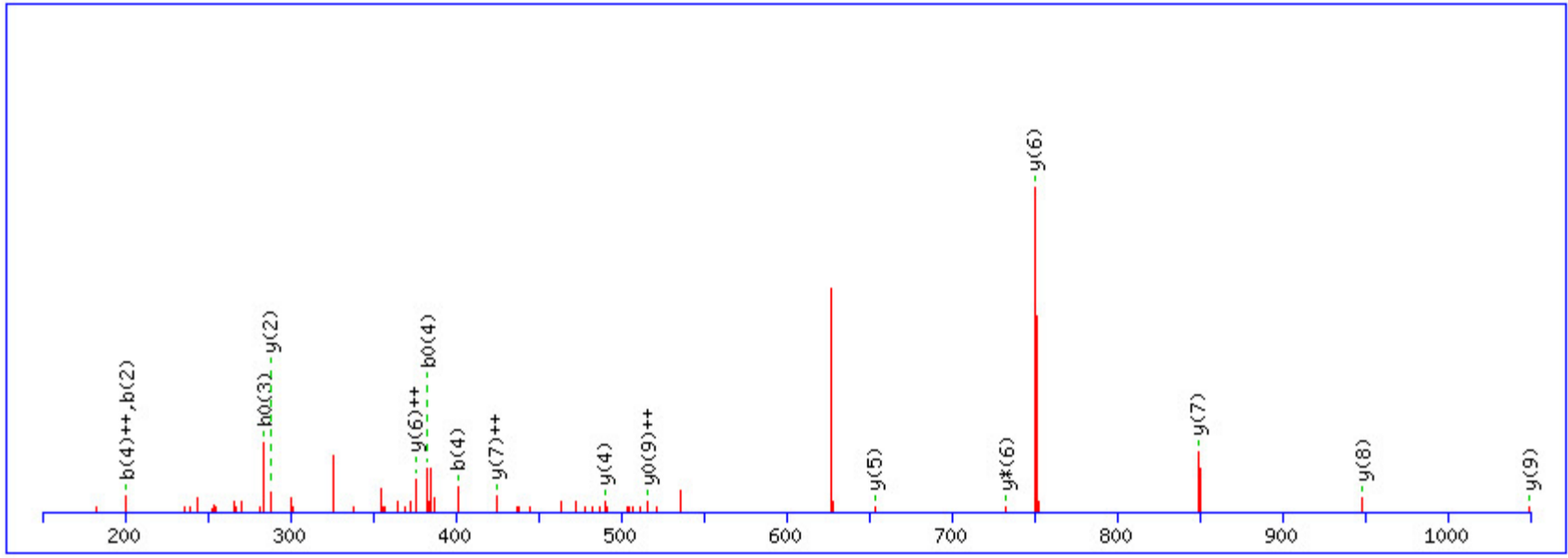
Match to Query 58: 1248.533448 from(625.274000,2+) intensity(222.9741) index(95)

Data file VF_040111_4.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



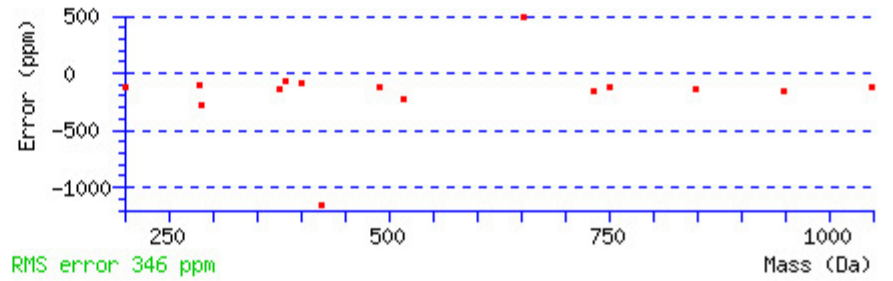
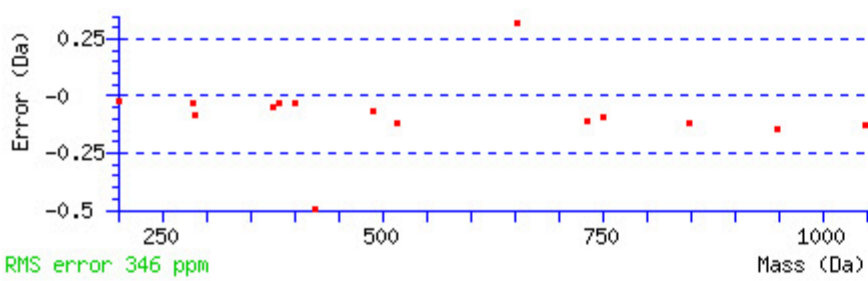
Monoisotopic mass of neutral peptide Mr(calc): 1248.707794

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.016

Matches : 16/94 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.091340	57.549308			L							11
2	201.123368	101.065322	183.112803	92.060039	S	1136.631002	568.819139	1119.604453	560.305865	1118.620437	559.813857	10
3	302.171047	151.589161	284.160482	142.583879	T	1049.598974	525.303125	1032.572425	516.789851	1031.588409	516.297843	9
4	401.239461	201.123369	383.228896	192.118086	V	948.551295	474.779286	931.524746	466.266011	930.540730	465.774003	8
5	500.307875	250.657576	482.297310	241.652293	V	849.482881	425.245078	832.456332	416.731804	831.472316	416.239796	7
6	597.360639	299.183958	579.350074	290.178675	P	750.414467	375.710872	733.387918	367.197597	732.403902	366.705589	6
7	760.423968	380.715622	742.413403	371.710340	Y	653.361703	327.184489	636.335154	318.671215	635.351138	318.179207	5
8	861.471647	431.239462	843.461082	422.234179	T	490.298374	245.652825	473.271825	237.139550	472.287809	236.647542	4
9	962.519326	481.763301	944.508761	472.758019	T	389.250695	195.128985	372.224146	186.615711	371.240130	186.123703	3
10	1075.603390	538.305333	1057.592825	529.300051	L	288.203016	144.605146	271.176467	136.091871			2
11					R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of **LSTVVPYTTLR**

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.6	1248.707794	-0.174346	LSTVVPYTTLR
17.1	1248.635010	-0.101562	STIFSSIETHK
15.2	1248.675446	-0.141998	TVSLVPFPFDK
8.6	1248.624451	-0.091003	NASAGVSKTGMAR
7.1	1248.755386	-0.221938	LEASVLRVLLH
5.4	1248.709122	-0.175674	YHVVVHLLR
2.4	1247.581573	0.951875	SLSLDCPASER
2.2	1248.576828	-0.043380	SSPEDKAVCSR
1.8	1247.585617	0.947831	TFSYQSICTK
1.2	1247.654358	0.879090	ISTSMLTNIPR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **NLCPTSYSYPK**

Found in **Locus_270_Transcript_1/2_Confidence_1.000**, Locus_270_Transcript_1/2_Confidence_1.000

Translated in frame 5 ([nucleic acid sequence](#))

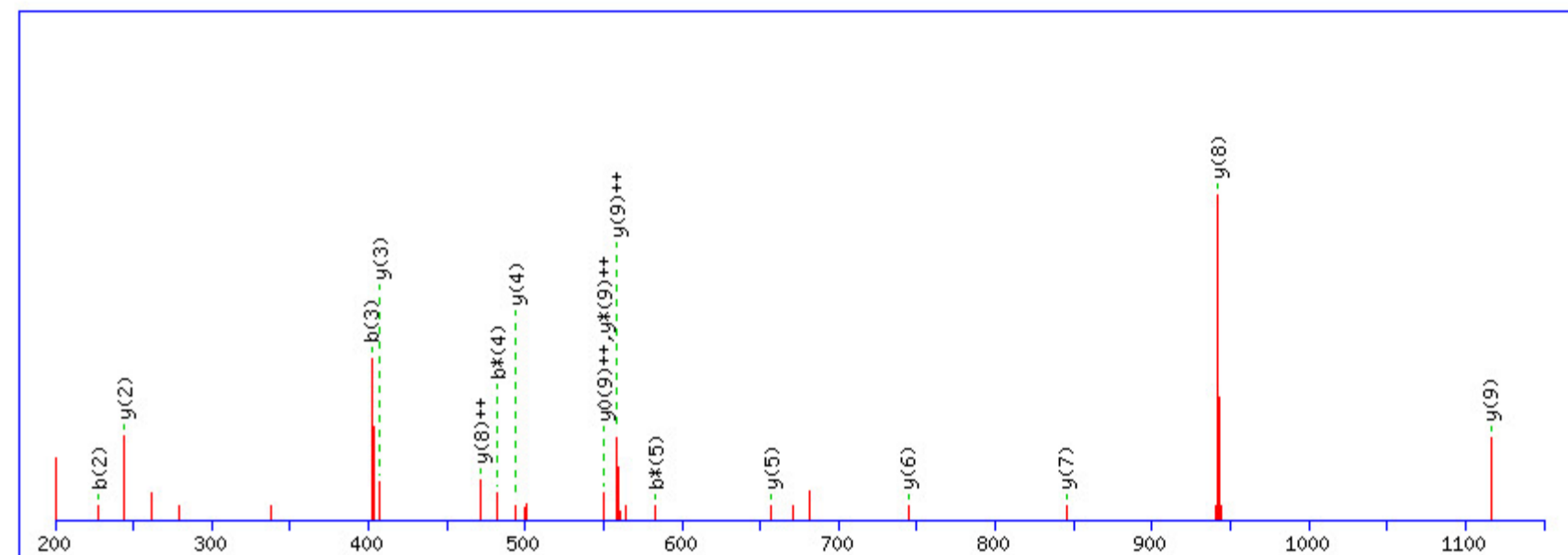
Match to Query 66: 1342.397648 from(672.206100,2+) intensity(315.7793) index(81)

Data file VF_040111_8.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



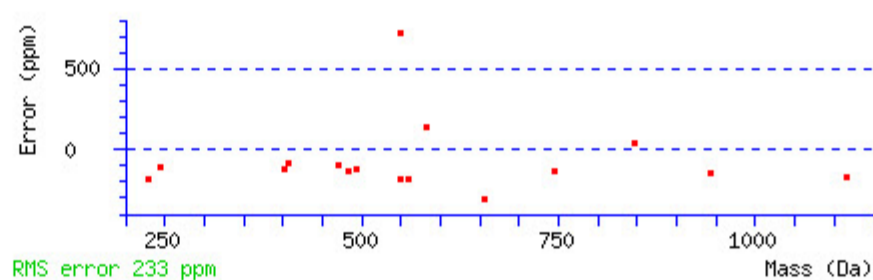
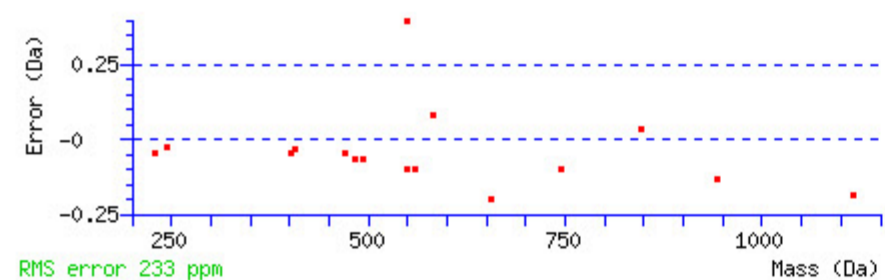
Monoisotopic mass of neutral peptide Mr(calc): 1342.622711

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00012

Matches: 16/106 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.050203	58.028740	98.023654	49.515465			N							11
2	228.134267	114.570771	211.107718	106.057497			L	1229.587088	615.297182	1212.560539	606.783908	1211.576523	606.291900	10
3	402.180566	201.593921	385.154017	193.080647			C	1116.503024	558.755150	1099.476475	550.241875	1098.492459	549.749867	9
4	499.233330	250.120303	482.206781	241.607028			P	942.456725	471.732001	925.430176	463.218726	924.446160	462.726718	8
5	600.281009	300.644143	583.254460	292.130868	582.270444	291.638860	T	845.403961	423.205619	828.377412	414.692344	827.393396	414.200336	7
6	687.313037	344.160157	670.286488	335.646882	669.302472	335.154874	S	744.356282	372.681779	727.329733	364.168504	726.345717	363.676496	6
7	850.376366	425.691821	833.349817	417.178546	832.365801	416.686538	Y	657.324254	329.165765	640.297705	320.652491	639.313689	320.160483	5
8	937.408394	469.207835	920.381845	460.694560	919.397829	460.202552	S	494.260925	247.634100	477.234376	239.120826	476.250360	238.628818	4
9	1100.471723	550.739499	1083.445174	542.226225	1082.461158	541.734217	Y	407.228897	204.118086	390.202348	195.604812			3
10	1197.524487	599.265881	1180.497938	590.752607	1179.513922	590.260599	P	244.165568	122.586422	227.139019	114.073148			2
11							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [NLCPTSYSYPK](#)

(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	1342.622711	-0.225063	NLCPTSYSYPK
9.4	1341.739136	0.658512	IISPIDPTLSLS
9.3	1342.673706	-0.276058	QVCKPSAPPMK
7.7	1341.663666	0.733982	IIQQQEEQRNQ
7.1	1342.572418	-0.174770	ICNQDNWHDK
6.6	1342.764236	-0.366588	NLVLTGKCSIPK
6.5	1341.652435	0.745213	EPLGGESEGSKPR
5.1	1342.585693	-0.188045	SSSTQMIGTCNK
5.0	1342.782028	-0.384380	QTVAVGVKISVDK
4.4	1341.755737	0.641911	LLALVFTWHSR

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **TEQSTPSNIK**

Found in **Locus_326_Transcript_1/1_Confidence_1.000**, Locus_326_Transcript_1/1_Confidence_1.000

Translated in frame 2 ([nucleic acid sequence](#))

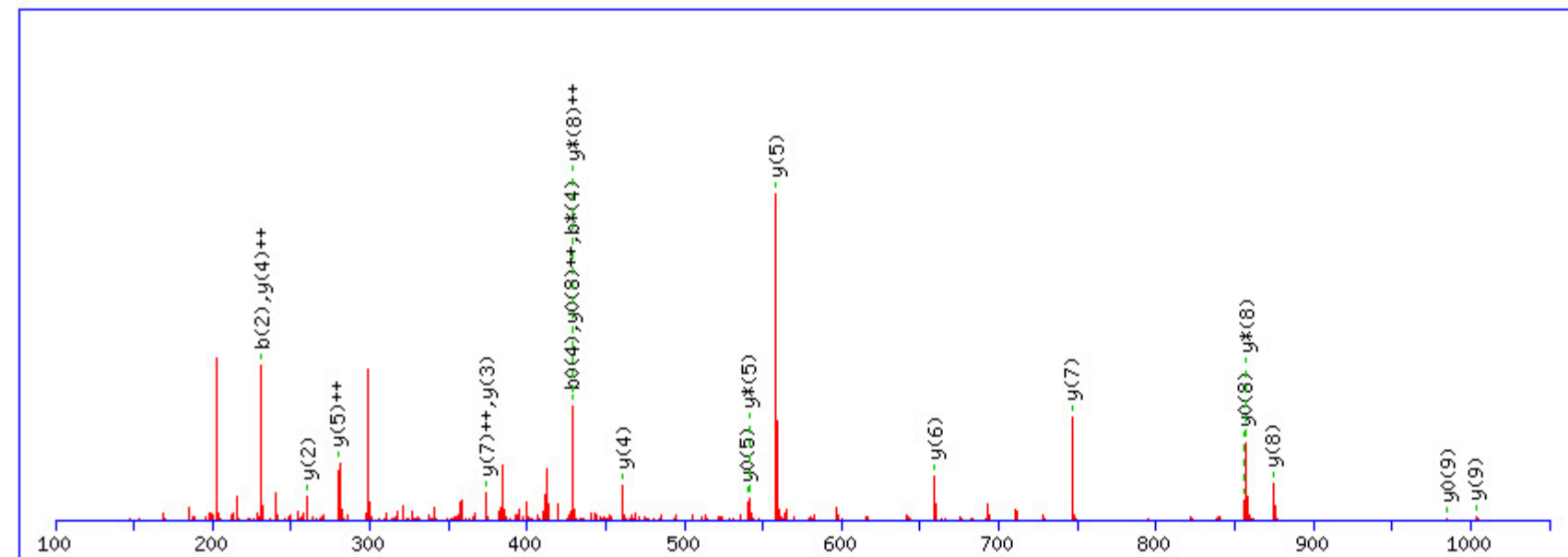
Match to Query 61: 1103.360248 from(552.687400,2+) intensity(272.7057) index(1)

Data file VF_040111_9.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



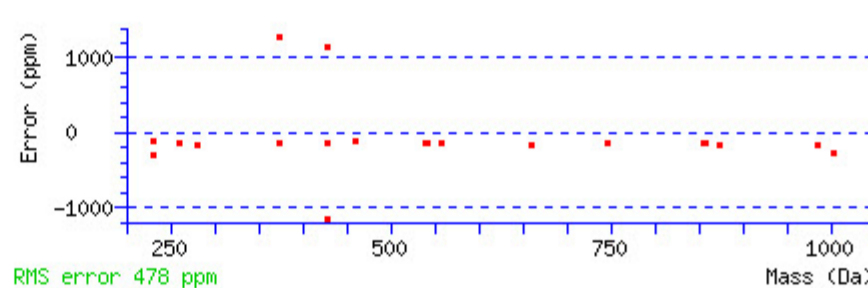
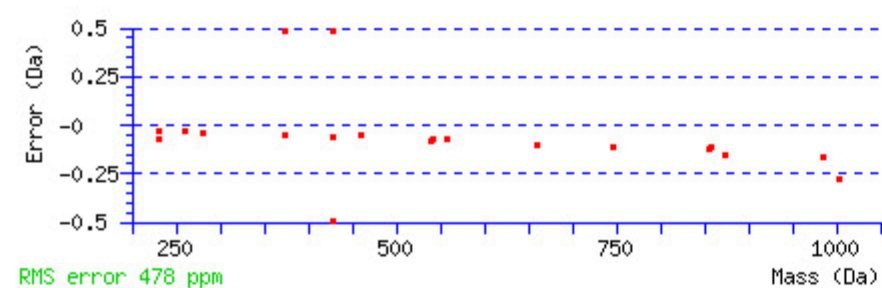
Monoisotopic mass of neutral peptide Mr(calc): 1103.545853

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0032

Matches : 21/98 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	102.054955	51.531116			84.044390	42.525833	T							10
2	231.097548	116.052412			213.086983	107.047130	E	1003.505465	502.256371	986.478916	493.743096	985.494900	493.251088	9
3	359.156126	180.081701	342.129577	171.568427	341.145561	171.076419	Q	874.462872	437.735074	857.436323	429.221800	856.452307	428.729792	8
4	446.188154	223.597715	429.161605	215.084441	428.177589	214.592433	S	746.404294	373.705785	729.377745	365.192511	728.393729	364.700503	7
5	547.235833	274.121555	530.209284	265.608280	529.225268	265.116272	T	659.372266	330.189771	642.345717	321.676497	641.361701	321.184489	6
6	644.288597	322.647937	627.262048	314.134662	626.278032	313.642654	P	558.324587	279.665932	541.298038	271.152657	540.314022	270.660649	5
7	731.320625	366.163951	714.294076	357.650676	713.310060	357.158668	S	461.271823	231.139550	444.245274	222.626275	443.261258	222.134267	4
8	845.363552	423.185414	828.337003	414.672140	827.352987	414.180132	N	374.239795	187.623536	357.213246	179.110261			3
9	958.447616	479.727446	941.421067	471.214172	940.437051	470.722164	I	260.196868	130.602072	243.170319	122.088798			2
10							K	147.112804	74.060040	130.086255	65.546766			1



NCBI BLAST search of [TEQSTPSNIK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.9	1103.545853	-0.185605	TEQSTPSNIK
17.2	1103.484329	-0.124081	TESGGDPNATR
6.9	1103.531937	-0.171689	SQASSPTDRR
6.8	1103.516861	-0.156613	MVQEEEQVL
5.8	1103.626022	-0.265774	TTPLMTILAK
5.3	1102.634613	0.725635	VRTSTLEIGK
4.3	1103.600891	-0.240643	TMTVGKQQVL
4.0	1103.564484	-0.204236	TEITQLPMR
3.8	1103.524734	-0.164486	DDQTQAIWK
3.0	1103.561111	-0.200863	IRSAYPSVDP

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **MPGIDYAR**

Found in **Locus_369_Transcript_1/1_Confidence_1.000**, Locus_369_Transcript_1/1_Confidence_1.000

Translated in frame 1 ([nucleic acid sequence](#))

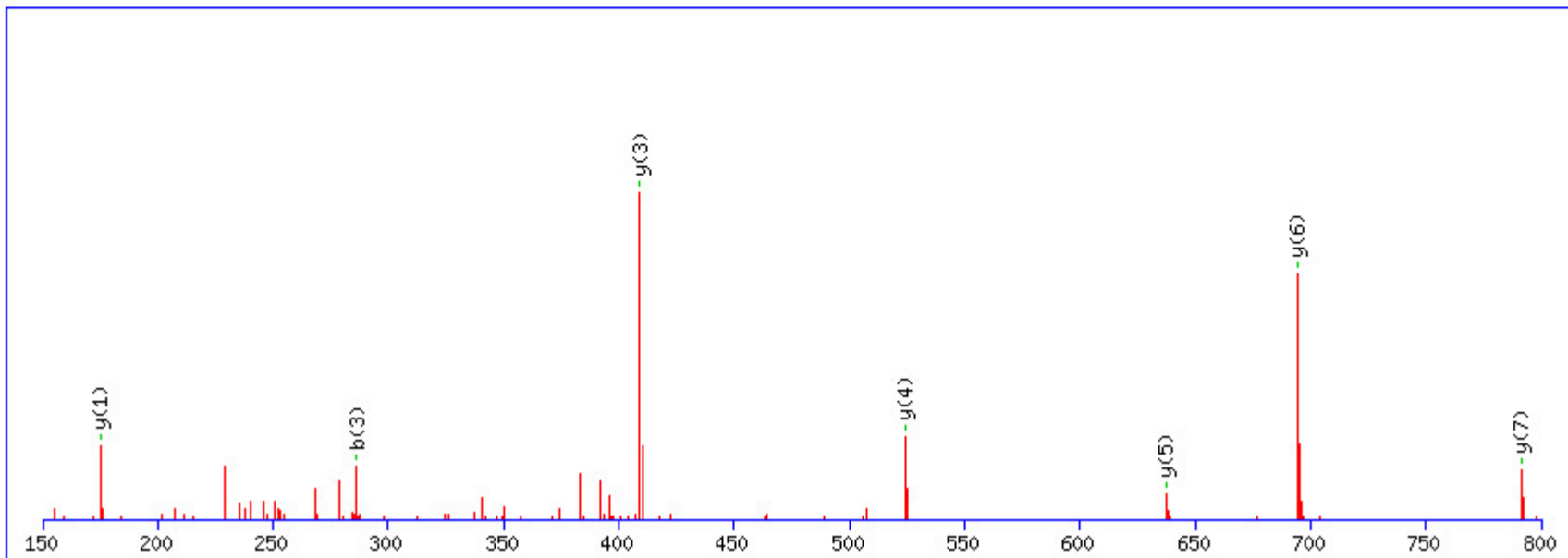
Match to Query 38: 921.292448 from(461.653500,2+) intensity(375.8312) index(21)

Data file VF_040111_11.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



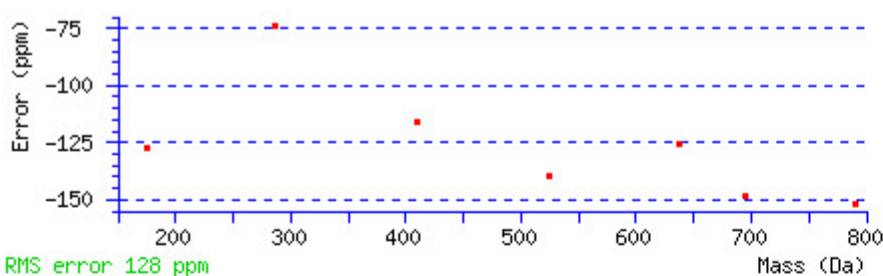
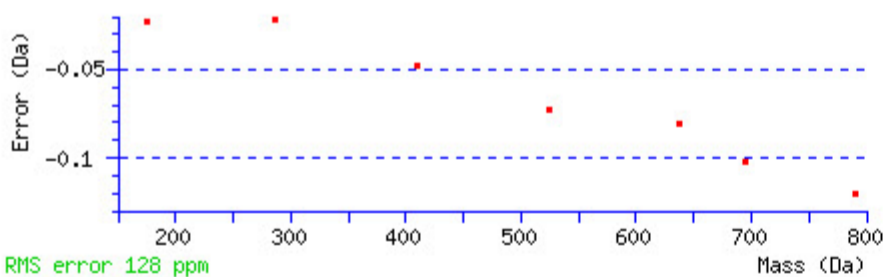
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 921.437820

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 60 Expect: 0.00026

Matches : 7/56 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.047761	66.527518			M							8
2	229.100525	115.053900			P	791.404630	396.205953	774.378081	387.692679	773.394065	387.200671	7
3	286.121989	143.564632			G	694.351866	347.679571	677.325317	339.166296	676.341301	338.674288	6
4	399.206053	200.106664			I	637.330402	319.168839	620.303853	310.655565	619.319837	310.163557	5
5	514.232996	257.620136	496.222431	248.614854	D	524.246338	262.626807	507.219789	254.113532	506.235773	253.621524	4
6	677.296325	339.151801	659.285760	330.146518	Y	409.219395	205.113335	392.192846	196.600061			3
7	748.333439	374.670358	730.322874	365.665075	A	246.156066	123.581671	229.129517	115.068396			2
8					R	175.118952	88.063114	158.092403	79.549839			1



NCBI BLAST search of [MPGIDYAR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	$M_r(\text{calc})$:	Delta	Sequence
59.8	921.437820	-0.145372	MPGIDYAR
20.2	921.466827	-0.174379	LDGPIHDR
15.2	921.434464	-0.142016	LDGEWFR
14.7	920.482803	0.809645	RAGSFVER
14.7	920.471573	0.820875	INGDFSIR
14.4	921.411346	-0.118898	DLAVDMDK
14.3	921.420074	-0.127626	PMVWMSR
14.2	920.471573	0.820875	EPTKGFSR
13.0	921.452911	-0.160463	GQRGDHPR
13.0	921.478043	-0.185595	RLEDHPR

MASCOT Mascot Search Results

Peptide View

MS/MS Fragmentation of **GFDQIAAIK**

Found in **Locus_52_Transcript_1/5_Confidence_0.154**, Locus_52_Transcript_1/5_Confidence_0.154

Translated in frame 5 ([nucleic acid sequence](#))

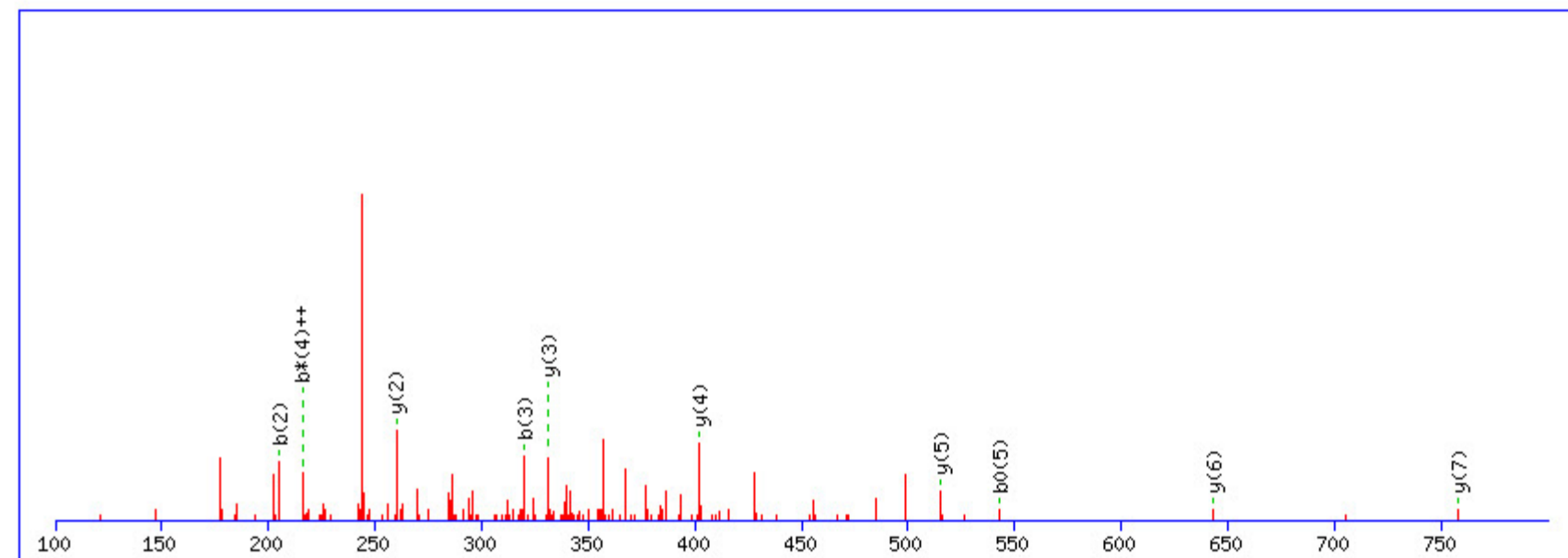
Match to Query 43: 961.374648 from(481.694600,2+) intensity(159.5801) index(105)

Data file VF_040111_9.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



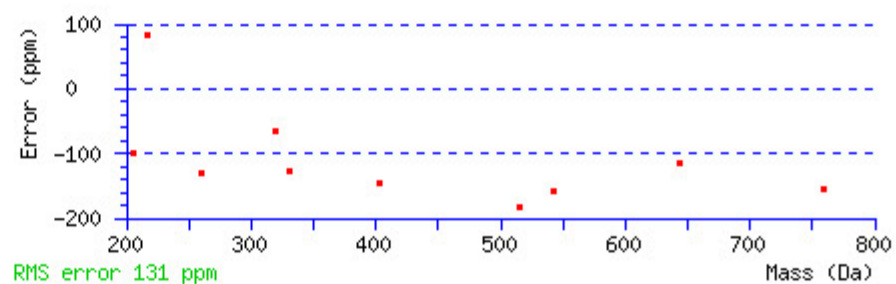
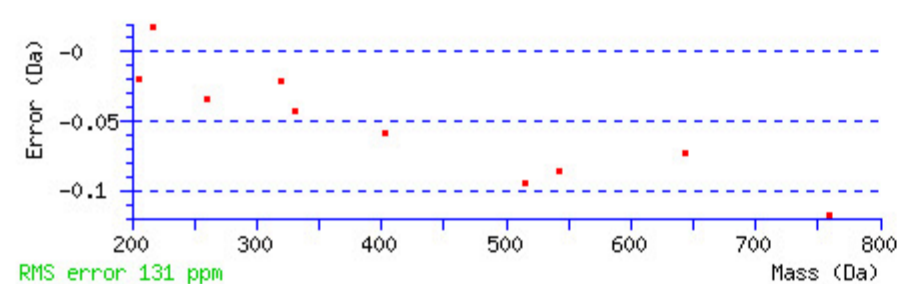
Monoisotopic mass of neutral peptide Mr(calc): 961.523270

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0028

Matches : 10/74 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	58.028740	29.518008					G							9
2	205.097154	103.052215					F	905.509095	453.258186	888.482546	444.744911	887.498530	444.252903	8
3	320.124097	160.565687			302.113532	151.560404	D	758.440681	379.723979	741.414132	371.210704	740.430116	370.718696	7
4	448.182675	224.594976	431.156126	216.081701	430.172110	215.589693	Q	643.413738	322.210507	626.387189	313.697232			6
5	561.266739	281.137008	544.240190	272.623733	543.256174	272.131725	I	515.355160	258.181218	498.328611	249.667943			5
6	632.303853	316.655565	615.277304	308.142290	614.293288	307.650282	A	402.271096	201.639186	385.244547	193.125911			4
7	703.340967	352.174122	686.314418	343.660847	685.330402	343.168839	A	331.233982	166.120629	314.207433	157.607354			3
8	816.425031	408.716154	799.398482	400.202879	798.414466	399.710871	I	260.196868	130.602072	243.170319	122.088798			2
9							K	147.112804	74.060040	130.086255	65.546765			1



NCBI BLAST search of [GFDQIAAIK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	961.523270	-0.148622	GFDQIAAIK
12.8	960.528030	0.846618	SVLFSPSPK
11.3	961.544388	-0.169740	AATSAITSLK
7.9	961.526642	-0.151994	NTLMQVIK
6.1	961.534500	-0.159852	SRFGASPIK
5.9	960.408310	0.966338	DAGPSACNR
5.5	960.473877	0.900771	GWASLMSLP
5.5	961.453873	-0.079225	MGGVESASPK
4.5	961.526642	-0.151994	SMQGLVALK
4.5	960.439972	0.934676	DEEADAAIK

MASCOT Search Results

Peptide View

MS/MS Fragmentation of **GGKTDPGVTINLCGQIPTS**

Found in **Locus_8322_Transcript_1/1_Confidence_1.000**, Locus_8322_Transcript_1/1_Confidence_1.000

Translated in frame 6 ([nucleic acid sequence](#))

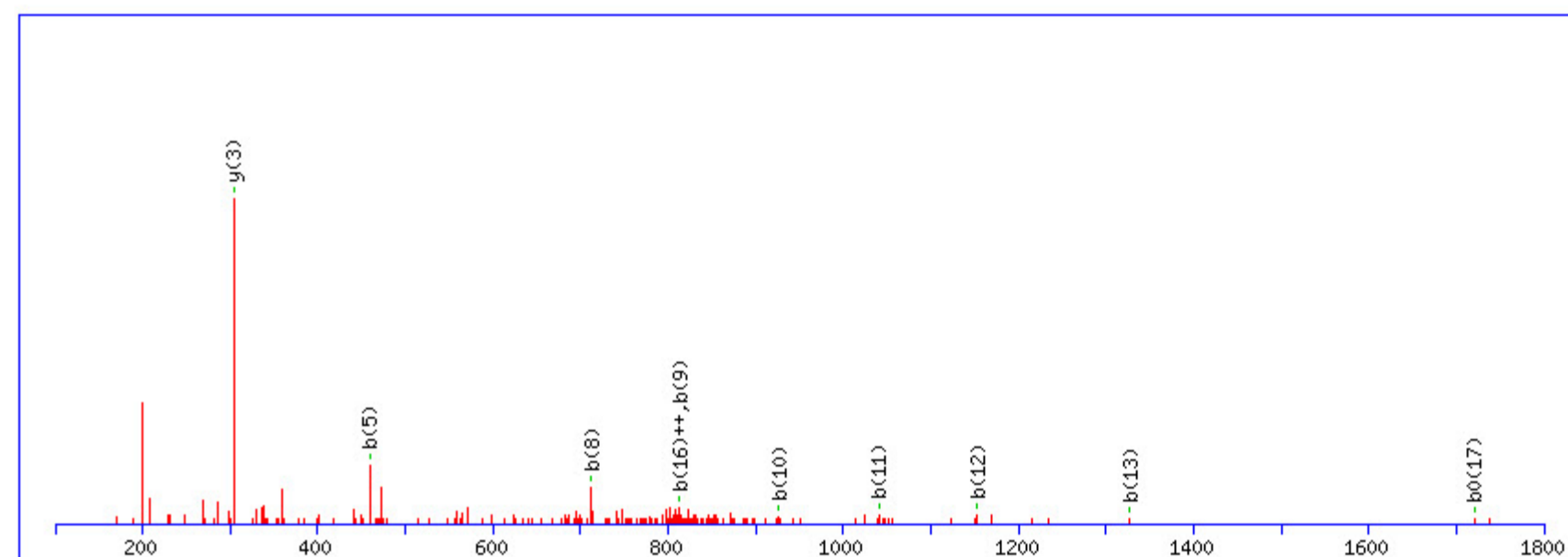
Match to Query 128: 2040.673648 from(1021.344100,2+) intensity(650.1049) index(102)

Data file VF_040111_10.pkl

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from to Da

Label all possible matches Label matches used for scoring



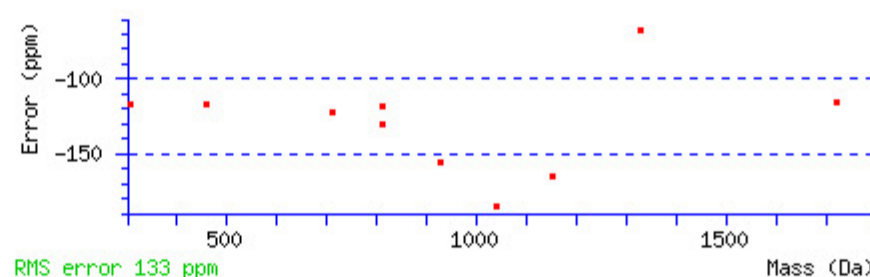
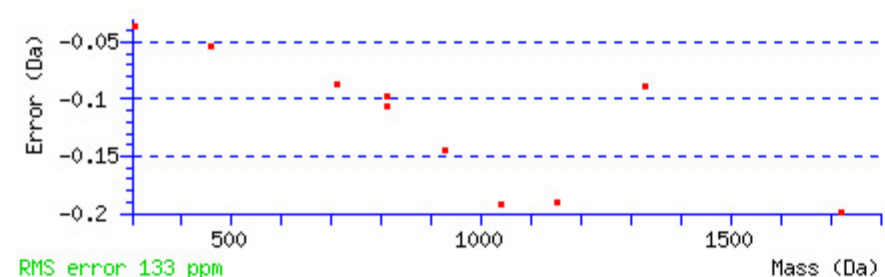
Monoisotopic mass of neutral peptide Mr(calc): 2041.051407

Fixed modifications: Propionamide (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.00037

Matches : 10/208 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	58.028740	29.518008					G							20
2	115.050204	58.028740					G	1985.037206	993.022241	1968.010657	984.508967	1967.026641	984.016958	19
3	243.145167	122.076222	226.118618	113.562947			K	1928.015742	964.511509	1910.989193	955.998234	1910.005177	955.506226	18
4	344.192846	172.600061	327.166297	164.086787	326.182281	163.594779	T	1799.920779	900.464027	1782.894230	891.950753	1781.910214	891.458745	17
5	459.219789	230.113533	442.193240	221.600258	441.209224	221.108250	D	1698.873100	849.940188	1681.846551	841.426913	1680.862535	840.934905	16
6	556.272553	278.639915	539.246004	270.126640	538.261988	269.634632	P	1583.846157	792.426716	1566.819608	783.913442	1565.835592	783.421434	15
7	613.294017	307.150647	596.267468	298.637372	595.283452	298.145364	G	1486.793393	743.900334	1469.766844	735.387060	1468.782828	734.895052	14
8	712.362431	356.684854	695.335882	348.171579	694.351866	347.679571	V	1429.771929	715.389602	1412.745380	706.876328	1411.761364	706.384320	13
9	813.410110	407.208693	796.383561	398.695419	795.399545	398.203411	T	1330.703515	665.855395	1313.676966	657.342121	1312.692950	656.850113	12
10	926.494174	463.750725	909.467625	455.237451	908.483609	454.745443	I	1229.655836	615.331556	1212.629287	606.818281	1211.645271	606.326273	11
11	1040.537101	520.772189	1023.510552	512.258914	1022.526536	511.766906	N	1116.571772	558.789524	1099.545223	550.276249	1098.561207	549.784241	10
12	1153.621165	577.314221	1136.594616	568.800946	1135.610600	568.308938	L	1002.528845	501.768060	985.502296	493.254786	984.518280	492.762778	9
13	1327.667464	664.337370	1310.640915	655.824096	1309.656899	655.332088	C	889.444781	445.226028	872.418232	436.712754	871.434216	436.220746	8
14	1384.688928	692.848102	1367.662379	684.334828	1366.678363	683.842820	G	715.398482	358.202879	698.371933	349.689604	697.387917	349.197596	7
15	1512.747506	756.877391	1495.720957	748.364117	1494.736941	747.872108	Q	658.377018	329.692147	641.350469	321.178872	640.366453	320.686864	6
16	1625.831570	813.419423	1608.805021	804.906148	1607.821005	804.414140	I	530.318440	265.662858			512.307875	256.657576	5
17	1738.915634	869.961455	1721.889085	861.448180	1720.905069	860.956172	I	417.234376	209.120826			399.223811	200.115544	4
18	1835.968398	918.487837	1818.941849	909.974562	1817.957833	909.482554	P	304.150312	152.578794			286.139747	143.573512	3
19	1937.016077	969.011676	1919.989528	960.498402	1919.005512	960.006394	T	207.097548	104.052412			189.086983	95.047130	2
20							S	106.049869	53.528573			88.039304	44.523290	1



NCBI BLAST search of [GGKTDPGVTINLCGQIPTS](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	2041.051407	-0.377759	GGKTDPGVTINLCGQIPTS
5.7	2039.980682	0.692966	AVSDGKGPSIQGATAANGMHR
2.7	2040.819153	-0.145505	ECSPHSTNHKSSNQDQG
1.1	2040.893433	-0.219785	CFQVGHWTYECKNER