LAT2, a lipid raft adaptor protein for AKT signaling, is an early mediator of alkylphospholipid anti-leukemic activity

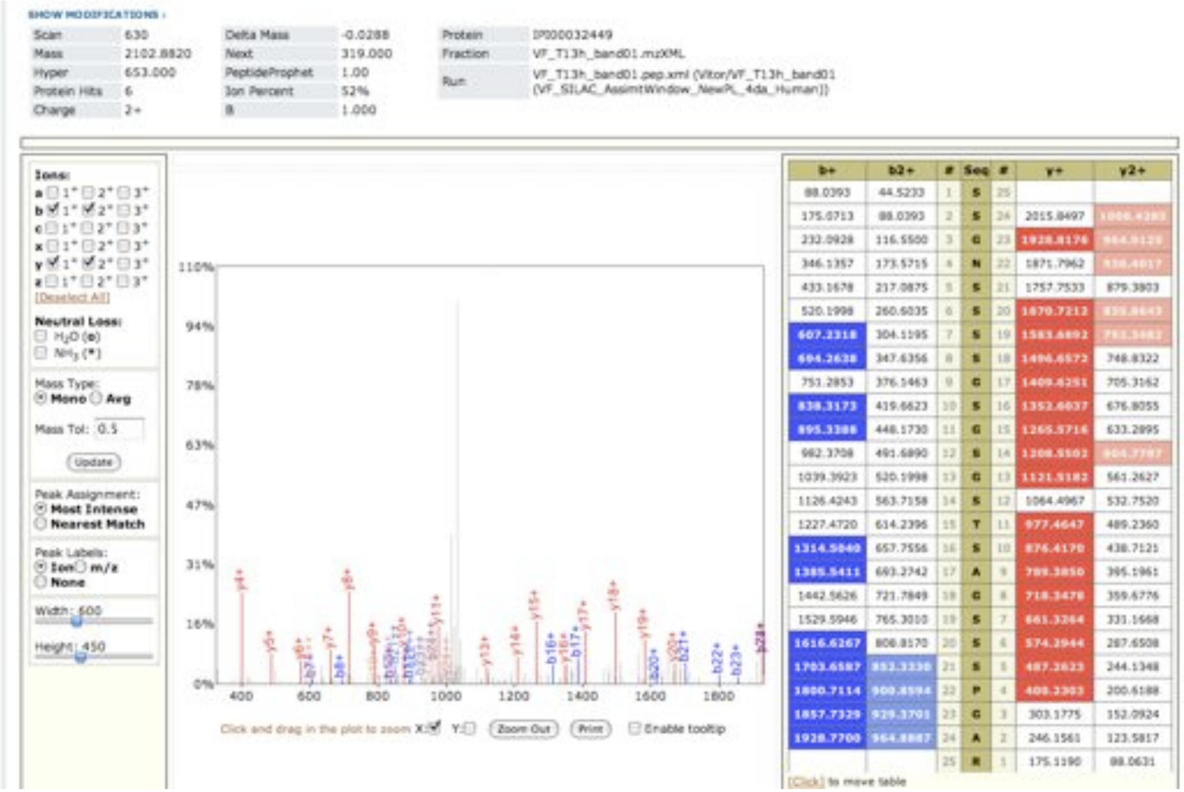
Carolina H. Thomé, Guilherme A. dos Santos, Germano A. Ferreira, Priscila S. Scheucher, Clarice Izumi, Andreia M. Leopoldino, Ana Maria Simão, Pietro Ciancaglini, Kleber T. de Oliveira, Alice Chin, Samir M. Hanash, Roberto P. Falcão, Eduardo M. Rego, Lewis J. Greene, Vitor M. Faça

ANNOTATED SPECTRA FOR SINGLE PEPTIDE HITS – PROTEIN IDENTIFICATION

SPECTRA REPRESENT 317 PEPTIDES OBSERVED WITH PEPTIDE PROPHET SCORE ABOVE 0.8 IN THE IDENTIFICATION OF PROTEINS OF DETERGENT RESISTANT MEMBRANE FRACTIONS.

THE TABLE ON TOP OF EACH ANNOTATED SPECTRUM PRESENT THE PROTEIN (IPI NUMBER), GENE NAME, CHARGE STATE, PEPTIDE PROPHET SCORE AND PEPTIDE SEQUENCE. SPECTRUM FIGURE IS ANNOTATED WITH b AND y IONS MATCHED.

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9810	IPI00796966, IPI00433478, IPI00396582, IPI00746217, IPI00032449, IPI00294834	1	1	ASPH, ASPH, ASPH, ASPH, ASPH, ASPH	630	2+	-0.0288	0.9999	K.SSGNSSSSGSGSGSTSAGSSSPGAR.R



SHOW MODIFICATIONS ›

Scan	630	Delta Mass	-0.0288	Protein	IPI00032449
Mass	2102.8820	Next	319.000	Fraction	VF_T13h_band01.mzXML
Hyper	653.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	6	Ion Percent	52%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	25		
175.0713	88.0393	2	S	24	2015.8497	1008.4285
232.0928	116.5500	3	G	23	1928.8176	964.9125
346.1357	173.5715	4	N	22	1871.7962	936.4017
433.1678	217.0875	5	S	21	1757.7533	879.3803
520.1998	260.6035	6	S	20	1670.7212	835.8643
607.2318	304.1195	7	S	19	1583.6892	792.3482
694.2638	347.6356	8	S	18	1496.6572	748.8322
751.2853	376.1463	9	G	17	1409.6251	705.3162
838.3173	419.6623	10	S	16	1352.6037	676.8055
895.3388	448.1730	11	G	15	1265.5716	633.2895
982.3708	491.6890	12	S	14	1208.5502	604.7787
1039.3923	520.1998	13	G	13	1121.5182	561.2627
1126.4243	563.7158	14	S	12	1064.4967	532.7520
1227.4720	614.2396	15	T	11	977.4647	489.2360
1314.5040	657.7556	16	S	10	876.4170	438.7121
1385.5411	693.2742	17	A	9	789.3850	395.1961
1442.5626	721.7849	18	G	8	718.3478	359.6776
1529.5946	765.3010	19	S	7	661.3264	331.1668
1616.6267	808.8170	20	S	6	574.2944	287.6508
1703.6587	852.3330	21	S	5	487.2623	244.1348
1800.7114	900.8594	22	P	4	400.2303	200.6188
1857.7329	929.3701	23	G	3	303.1775	152.0924
1928.7700	964.8887	24	A	2	246.1561	123.5817
		25	R	1	175.1190	88.0631

[Click] to move table

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9793	IPI00465191, IPI00900318, IPI00900331, IPI00183294, IPI00900325, IPI00646361	1	1	DKFZp686J0330, NUP214, NUP214, NUP214, NUP214, KIAA0023	645	2+	-0.0219	0.9998	R.VGQADDSTKPTNK.A

Peptide Details

SHOW MODIFICATIONS :

Scan	645	Delta Mass	-0.0219	Protein	IPI00183294
Mass	1360.6700	Next	345.000	Fraction	VF_T13h_band01.mzXML
Hyper	570.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	67%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	13		
157.0972	79.0522	2	G	12	1261.6019	631.3046
285.1557	143.0815	3	Q	11	1204.5804	602.7938
356.1928	178.6001	4	A	10	1076.5218	538.7646
471.2198	236.1135	5	D	9	1005.4847	503.2460
586.2467	293.6270	6	D	8	890.4578	445.7325
673.2788	337.1430	7	S	7	775.4308	388.2191
774.3264	387.6669	8	T	6	688.3988	344.7030
902.4214	451.7143	9	K	5	587.3511	294.1792
999.4742	500.2407	10	P	4	459.2562	230.1317
1100.5219	550.7646	11	T	3	362.2034	181.6053
1214.5648	607.7860	12	N	2	261.1557	131.0815
		13	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9514	IPI00856036, IPI00784233, IPI00647635	1	1	GIGYF2, TNRC15, GIGYF2	665	2+	-0.0256	0.9981	K.ALQQQQQQQQQK.L

Peptide Details

Scan	665	Delta Mass	-0.0256	Protein	IPI00647635
Mass	1483.7610	Next	359.000	Fraction	VF_T13h_band01.mzXML
Hyper	488.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
185.1285	93.0679	2	L	11	1412.7241	706.8657
313.1870	157.0972	3	Q	10	1299.6400	650.3236
441.2456	221.1264	4	Q	9	1171.5814	586.2944
569.3042	285.1557	5	Q	8	1043.5228	522.2651
697.3628	349.1850	6	Q	7	915.4643	458.2358
825.4213	413.2143	7	Q	6	787.4057	394.2065
953.4799	477.2436	8	Q	5	659.3471	330.1772
1081.5385	541.2729	9	Q	4	531.2885	266.1479
1209.5971	605.3022	10	Q	3	403.2300	202.1186
1337.6557	669.3315	11	Q	2	275.1714	138.0893
		12	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

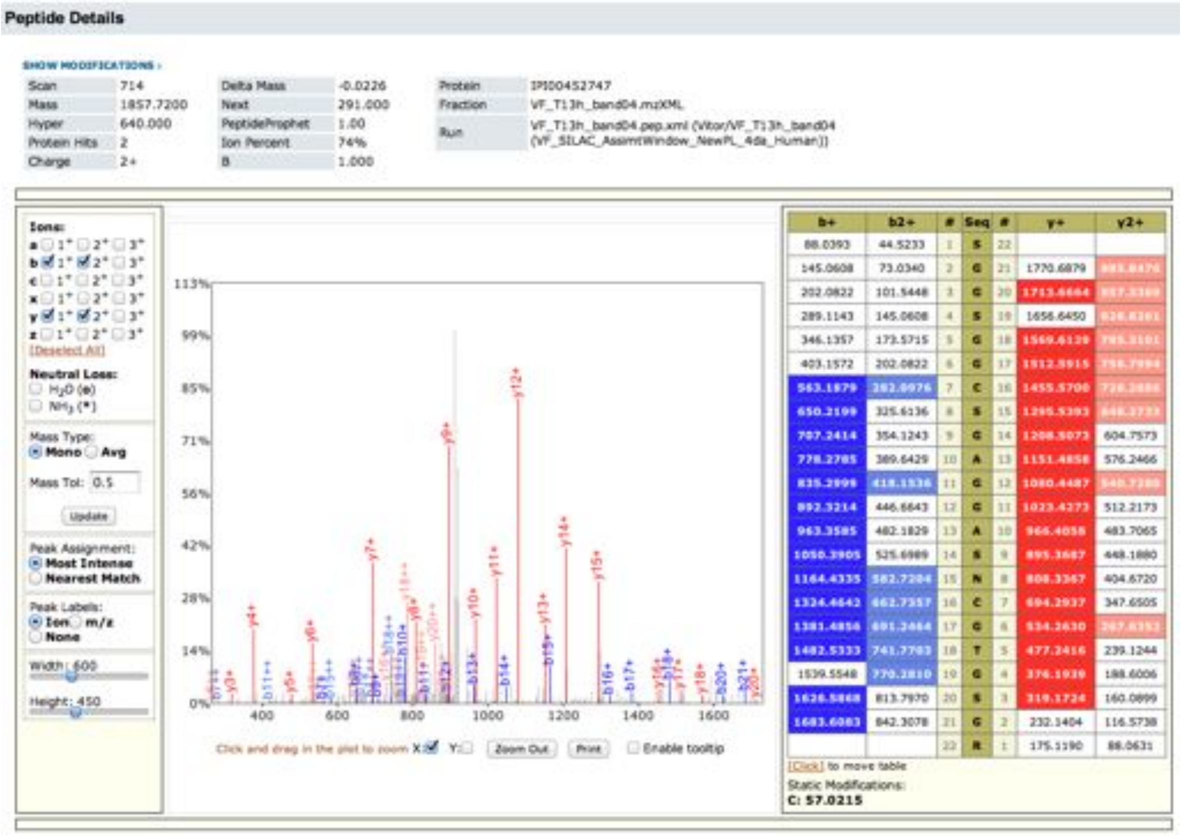
Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600
Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9851	IPI00452747, IPI00472939	1	1	LOC653566, SPCS2	714	2+	-0.0226	1.0000	R.SGGSGGCSGAGGASNCGTGSGR.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	714	Delta Mass	-0.0226	Protein	IPI00452747
Mass	1857.7200	Next	291.000	Fraction	VF_T13h_band04.mzXML
Hyper	640.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	74%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H$_2$O (o)
☐ NH$_3$ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

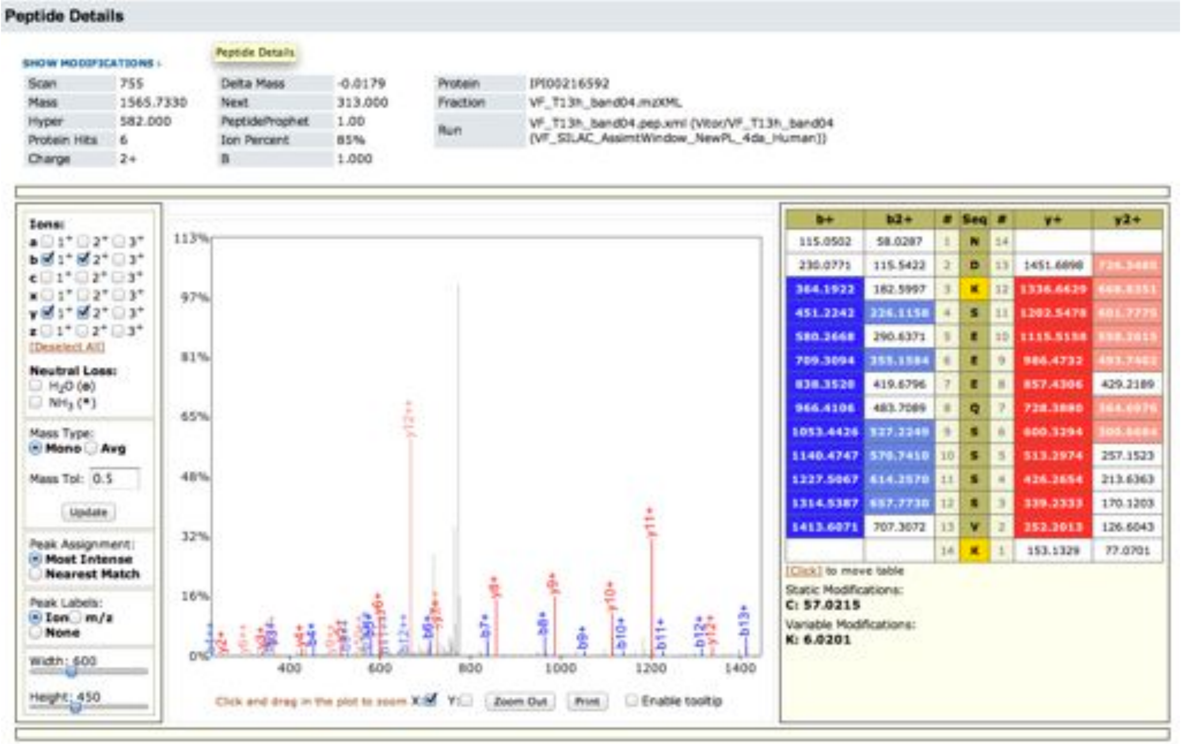
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	22		
145.0608	73.0340	2	G	21	1770.6879	885.8476
202.0822	101.5448	3	G	20	1713.6664	857.3369
289.1143	145.0608	4	S	19	1656.6450	828.8261
346.1357	173.5715	5	G	18	1569.6129	785.3101
403.1572	202.0822	6	G	17	1512.5915	756.7994
563.1879	282.0976	7	C	16	1455.5700	728.2886
650.2199	325.6136	8	S	15	1295.5393	648.2733
707.2414	354.1243	9	G	14	1208.5073	604.7573
778.2785	389.6429	10	A	13	1151.4858	576.2466
835.2999	418.1536	11	G	12	1080.4487	540.7280
892.3214	446.6643	12	G	11	1023.4273	512.2173
963.3585	482.1829	13	A	10	966.4058	483.7065
1050.3905	525.6989	14	S	9	895.3687	448.1880
1164.4335	582.7204	15	N	8	808.3367	404.6720
1324.4642	662.7357	16	C	7	694.2937	347.6505
1381.4856	691.2464	17	G	6	534.2630	267.6352
1482.5333	741.7703	18	T	5	477.2416	239.1244
1539.5548	770.2810	19	G	4	376.1939	188.6006
1626.5868	813.7970	20	S	3	319.1724	160.0899
1683.6083	842.3078	21	G	2	232.1404	116.5738
		22	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9750	IPI00911096, IPI00759822, IPI00759596, IPI00909232, IPI00216592, IPI00477313	1	1	-, HNRNPC, HNRPC, -, HNRPC, HNRPC	755	2+	-0.0179	0.9993	K.NDK'SEEEQSSSSVK'.K



Peptide Details

Scan	755	Delta Mass	-0.0179	Protein	IPI00216592
Mass	1565.7330	Next	313.000	Fraction	VF_T13h_band04.mzXML
Hyper	582.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	14		
230.0771	115.5422	2	D	13	1451.6898	726.3485
364.1922	182.5997	3	K	12	1336.6629	668.8351
451.2242	226.1158	4	S	11	1202.5478	601.7775
580.2668	290.6371	5	E	10	1115.5158	558.2615
709.3094	355.1584	6	E	9	986.4732	493.7402
838.3520	419.6796	7	E	8	857.4306	429.2189
966.4106	483.7089	8	Q	7	728.3880	364.6976
1053.4426	527.2249	9	S	6	600.3294	300.6684
1140.4747	570.7410	10	S	5	513.2974	257.1523
1227.5067	614.2570	11	S	4	426.2654	213.6363
1314.5387	657.7730	12	S	3	339.2333	170.1203
1413.6071	707.3072	13	V	2	252.2013	126.6043
		14	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9810	IPI00030136, IPI00006196, IPI00292771, IPI00872028	1	1	NUMA1, NUMA1, NUMA1, NUMA1	759	2+	-0.0142	0.9999	K.AVQAQGGESQQEAQR.L

Peptide Details

SHOW MODIFICATIONS :

Scan	759	Delta Mass	-0.0142	Protein	IPI00006196
Mass	1586.7520	Next	346.000	Fraction	VF_T13h_band01.mzXML
Hyper	642.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	15		
171.1128	86.0600	2	V	14	1515.7146	758.3609
299.1714	150.0893	3	Q	13	1416.6462	708.8267
370.2085	185.6079	4	A	12	1288.5876	644.7975
498.2671	249.6372	5	Q	11	1217.5505	609.2789
555.2885	278.1479	6	G	10	1089.4919	545.2496
612.3100	306.6586	7	G	9	1032.4705	516.7389
741.3526	371.1799	8	E	8	975.4490	488.2281
828.3846	414.6959	9	S	7	846.4064	423.7068
956.4432	478.7252	10	Q	6	759.3744	380.1908
1084.5018	542.7545	11	Q	5	631.3158	316.1615
1213.5444	607.2758	12	E	4	503.2572	252.1323
1284.5815	642.7944	13	A	3	374.2146	187.6110
1412.6401	706.8237	14	Q	2	303.1775	152.0924
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8545	IPI00026089	1	1	SF3B1	778	2+	-0.0069	0.9914	R.GDTPGHATPGHGGATSSAR.K

Peptide Details

Scan	778	Delta Mass	-0.0069	Protein	IPI00026089
Mass	1733.7950	Next	244.000	Fraction	VF_T13h_band01.mzXML
Hyper	349.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	69%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	19		
173.0557	87.0315	2	D	18	1676.7735	838.8904
274.1034	137.5553	3	T	17	1561.7466	781.3769
371.1561	186.0817	4	P	16	1460.6989	730.8531
428.1776	214.5924	5	G	15	1363.6461	682.3267
565.2365	283.1219	6	H	14	1306.6247	653.8160
636.2736	318.6404	7	A	13	1169.5658	585.2865
737.3213	369.1643	8	T	12	1098.5287	549.7680
834.3741	417.6907	9	P	11	997.4810	499.2441
891.3955	446.2014	10	G	10	900.4282	450.7177
1028.4544	514.7309	11	H	9	843.4068	422.2070
1085.4759	543.2416	12	G	8	706.3478	353.6776
1142.4974	571.7523	13	G	7	649.3264	325.1668
1213.5345	607.2709	14	A	6	592.3049	296.6561
1314.5822	657.7947	15	T	5	521.2678	261.1375
1401.6142	701.3107	16	S	4	420.2201	210.6137
1488.6462	744.8267	17	S	3	333.1881	167.0977
1559.6833	780.3453	18	A	2	246.1561	123.5817
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9801	IPI00017341	1	1	SF3A2	800	2+	-0.0191	0.9999	K.TGSGGVASSSESNR.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	800	Delta Mass	-0.0191	Protein	IPI00017341
Mass	1295.5820	Next	280.000	Fraction	VF_T13h_band02.mzXML
Hyper	510.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	69%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
159.0764	80.0418	2	G	13	1194.5345	597.7709
246.1084	123.5579	3	S	12	1137.5131	569.2603
303.1299	152.0686	4	G	11	1050.4810	525.7442
360.1514	180.5793	5	G	10	993.4596	497.2334
459.2198	230.1135	6	V	9	936.4381	468.7227
530.2569	265.6321	7	A	8	837.3697	419.1885
617.2889	309.1481	8	S	7	766.3326	383.6699
704.3210	352.6641	9	S	6	679.3006	340.1539
791.3530	396.1801	10	S	5	592.2685	296.6379
920.3956	460.7014	11	E	4	505.2365	253.1219
1007.4276	504.2174	12	S	3	376.1939	188.6006
1121.4705	561.2389	13	N	2	289.1619	145.0846
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9062	IPI00796848, IPI00005978	1	1	SFRS2, SFRS2	827	2+	-0.0217	0.9925	R.YGRPPDSHHSR.R

Peptide Details

SHOW MODIFICATIONS ›

Scan	827	Delta Mass	-0.0217	Protein	IPI00005978
Mass	1308.6190	Next	299.000	Fraction	VF_T13h_band03.mzXML
Hyper	399.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	11		
221.0921	111.0497	2	G	10	1145.5559	573.2816
377.1932	189.1002	3	R	9	1088.5344	544.7708
474.2459	237.6266	4	P	8	932.4333	466.7203
571.2987	286.1530	5	P	7	835.3805	418.1939
686.3257	343.6665	6	D	6	738.3278	369.6675
773.3577	387.1825	7	S	5	623.3008	312.1541
910.4166	455.7119	8	H	4	536.2688	268.6380
1047.4755	524.2414	9	H	3	399.2099	200.1086
1134.5075	567.7574	10	S	2	262.1510	131.5791
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9881	IPI00412714, IPI00470498, IPI00470497, IPI00410693	1	1	RP11-102M16.2, RP11-102M16.2, RP11-102M16.2, RP11-102M16.2	851	2+	-0.0151	0.9999	K.SAAQAAAQTNSNAAGK'.Q

Peptide Details

SHOW MODIFICATIONS ›

Scan	851	Delta Mass	-0.0151	Protein	IPI00410693
Mass	1466.7290	Next	306.000	Fraction	VF_T13h_band06.mzXML
Hyper	650.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

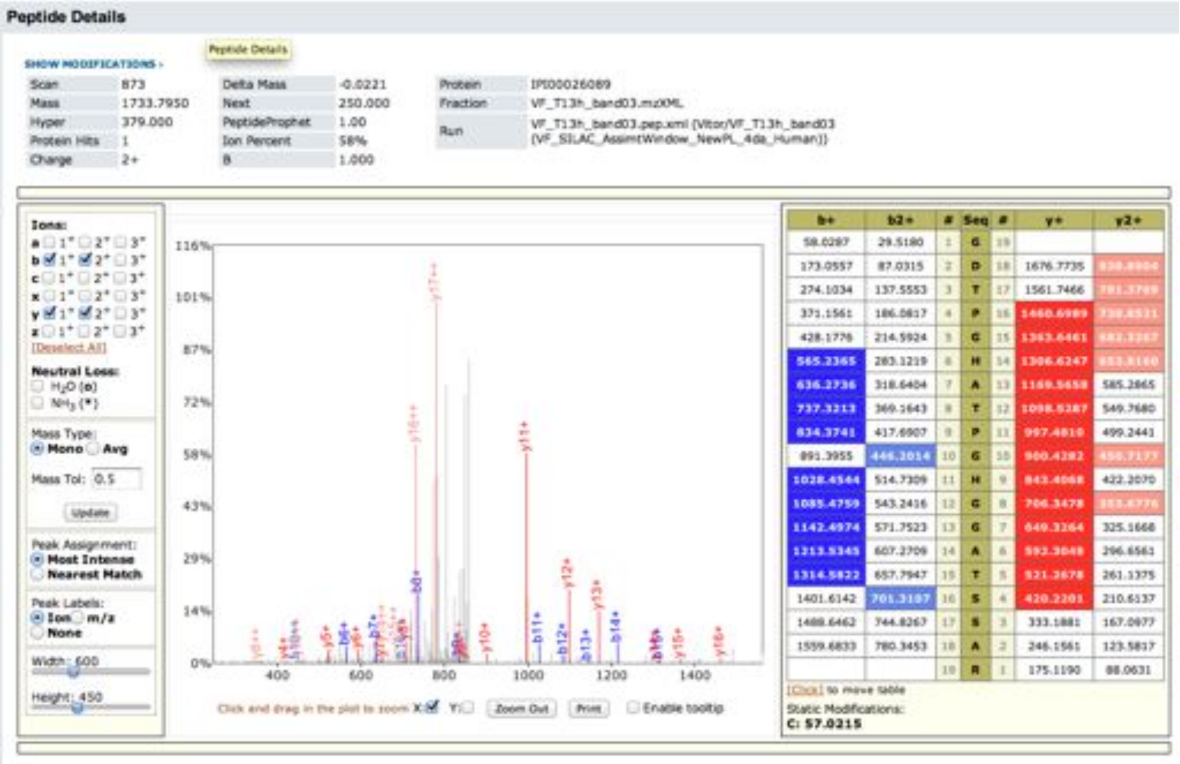
b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	16		
159.0764	80.0418	2	A	15	1379.6969	690.3521
230.1135	115.5604	3	A	14	1308.6598	654.8335
358.1721	179.5897	4	Q	13	1237.6227	619.3150
429.2092	215.1082	5	A	12	1109.5641	555.2857
500.2463	250.6268	6	A	11	1038.5270	519.7671
571.2835	286.1454	7	A	10	967.4898	484.2486
699.3420	350.1747	8	Q	9	896.4527	448.7300
800.3897	400.6985	9	T	8	768.3942	384.7007
914.4326	457.7200	10	N	7	667.3465	334.1769
1001.4647	501.2360	11	S	6	553.3036	277.1554
1115.5076	558.2574	12	N	5	466.2715	233.6394
1186.5447	593.7760	13	A	4	352.2286	176.6179
1257.5818	629.2945	14	A	3	281.1915	141.0994
1314.6033	657.8053	15	G	2	210.1544	105.5808
		16	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9560	IPI00026089	1	1	SF3B1	873	2+	-0.0221	0.9972	R.GDTPGHATPGHGGATSSAR.K



Peptide Details

Scan	873	Delta Mass	-0.0221	Protein	IPI00026089
Mass	1733.7950	Next	250.000	Fraction	VF_T13h_band03.mzXML
Hyper	379.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	58%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	19		
173.0557	87.0315	2	D	18	1676.7735	838.8904
274.1034	137.5553	3	T	17	1561.7466	781.3769
371.1561	186.0817	4	P	16	1460.6989	730.8531
428.1776	214.5924	5	G	15	1363.6461	682.3267
565.2365	283.1219	6	H	14	1306.6247	653.8160
636.2736	318.6404	7	A	13	1169.5658	585.2865
737.3213	369.1643	8	T	12	1098.5287	549.7680
834.3741	417.6907	9	P	11	997.4810	499.2441
891.3955	446.2014	10	G	10	900.4282	450.7177
1028.4544	514.7309	11	H	9	843.4068	422.2070
1085.4759	543.2416	12	G	8	706.3478	353.6776
1142.4974	571.7523	13	G	7	649.3264	325.1668
1213.5345	607.2709	14	A	6	592.3049	296.6561
1314.5822	657.7947	15	T	5	521.2678	261.1375
1401.6142	701.3107	16	S	4	420.2201	210.6137
1488.6462	744.8267	17	S	3	333.1881	167.0977
1559.6833	780.3453	18	A	2	246.1561	123.5817
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9403	IPI00010700, IPI00844237, IPI00893120, IPI00893641, IPI00894143	1	1	BAT2, BAT2, -, -, BAT2	879	2+	-0.0147	0.9974	R.GGGTGGPNHPPAPR.G

Peptide Details

Scan	879	Delta Mass	-0.0147	Protein	IPI00010700
Mass	1271.6240	Next	280.000	Fraction	VF_T13h_band01.mzXML
Hyper	411.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	58%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	14		
115.0502	58.0287	2	G	13	1214.6025	607.8049
172.0717	86.5395	3	G	12	1157.5810	579.2942
273.1193	137.0633	4	T	11	1100.5596	550.7834
330.1408	165.5740	5	G	10	999.5119	500.2596
387.1623	194.0848	6	G	9	942.4904	471.7489
484.2150	242.6112	7	P	8	885.4690	443.2381
598.2580	299.6326	8	N	7	788.4162	394.7117
735.3169	368.1621	9	H	6	674.3733	337.6903
832.3696	416.6885	10	P	5	537.3144	269.1608
929.4224	465.2148	11	P	4	440.2616	220.6344
1000.4595	500.7334	12	A	3	343.2088	172.1081
1097.5123	549.2598	13	P	2	272.1717	136.5895
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9478	IPI00478231	1	1	RHOA	892	2+	-0.0175	0.9966	K.M"KQEPVKPEEGR.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	892	Delta Mass	-0.0175	Protein	IPI00478231
Mass	1443.7260	Next	294.000	Fraction	VF_T13h_band05.mzXML
Hyper	466.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

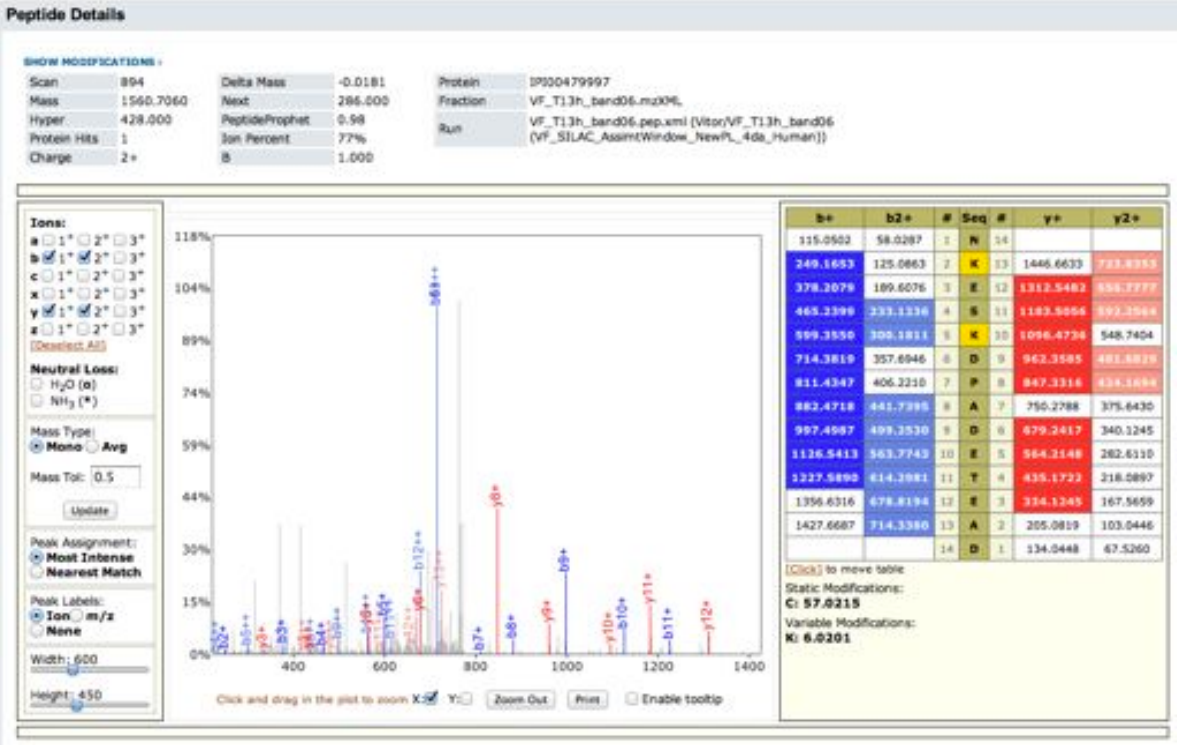
b+	b2+	#	Seq	#	y+	y2+
148.0427	74.5250	1	M	12		
276.1376	138.5724	2	K	11	1296.6906	648.8490
404.1962	202.6017	3	Q	10	1168.5957	584.8015
533.2388	267.1230	4	E	9	1040.5371	520.7722
630.2916	315.6494	5	P	8	911.4945	456.2509
729.3600	365.1836	6	V	7	814.4417	407.7245
857.4549	429.2311	7	K	6	715.3733	358.1903
954.5077	477.7575	8	P	5	587.2784	294.1428
1083.5503	542.2788	9	E	4	490.2256	245.6164
1212.5929	606.8001	10	E	3	361.1830	181.0951
1269.6143	635.3108	11	G	2	232.1404	116.5738
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8167	IPI00479997	1	1	STMN1	894	2+	-0.0181	0.9809	K.NK'ESK'DPADETEAD.-


Peptide Details

SHOW MODIFICATIONS ›

Scan	894	Delta Mass	-0.0181	Protein	IPI00479997
Mass	1560.7060	Next	286.000	Fraction	VF_T13h_band06.mzXML
Hyper	428.000	PeptideProphet	0.98	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	14		
249.1653	125.0863	2	K	13	1446.6633	723.8353
378.2079	189.6076	3	E	12	1312.5482	656.7777
465.2399	233.1236	4	S	11	1183.5056	592.2564
599.3550	300.1811	5	K	10	1096.4736	548.7404
714.3819	357.6946	6	D	9	962.3585	481.6829
811.4347	406.2210	7	P	8	847.3316	424.1694
882.4718	441.7395	8	A	7	750.2788	375.6430
997.4987	499.2530	9	D	6	679.2417	340.1245
1126.5413	563.7743	10	E	5	564.2148	282.6110
1227.5890	614.2981	11	T	4	435.1722	218.0897
1356.6316	678.8194	12	E	3	334.1245	167.5659
1427.6687	714.3380	13	A	2	205.0819	103.0446
		14	D	1	134.0448	67.5260

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9278	IPI00645757, IPI00877802, IPI00552530, IPI00645329, IPI00879702, IPI00877934, IPI00328319, IPI00395865, IPI00646512	1	1	RBBP4, RBBP4, RBBP7, RBBP4, RBBP7, RBBP4, RBBP4, RBBP7, RBBP7	898	2+	-0.0128	0.9968	K.INHEGEVNR.A

Peptide Details

SHOW MODIFICATIONS ›

Scan	898	Delta Mass	-0.0128	Protein	IPI00328319
Mass	1067.5230	Next	320.000	Fraction	VF_T13h_band02.mzXML
Hyper	438.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	9	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	9		
228.1343	114.5708	2	N	8	954.4388	477.7230
365.1932	183.1002	3	H	7	840.3959	420.7016
494.2358	247.6215	4	E	6	703.3369	352.1721
551.2572	276.1323	5	G	5	574.2944	287.6508
680.2998	340.6536	6	E	4	517.2729	259.1401
779.3682	390.1878	7	V	3	388.2303	194.6188
893.4112	447.2092	8	N	2	289.1619	145.0846
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9161	IPI00478231	1	1	RHOA	901	2+	-0.0157	0.9927	K.M"KQEPVKPEEGR.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	901	Delta Mass	-0.0157	Protein	IPI00478231
Mass	1443.7260	Next	291.000	Fraction	VF_T13h_band06.mzXML
Hyper	469.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	64%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

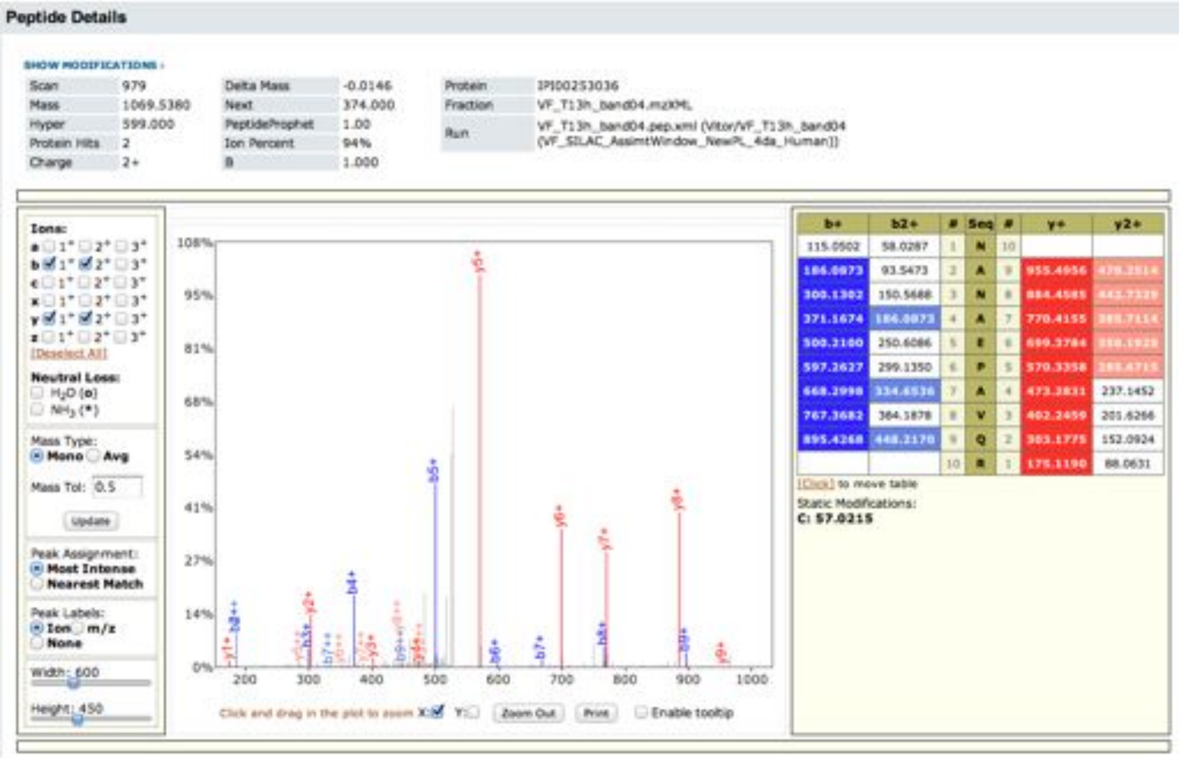
b+	b2+	#	Seq	#	y+	y2+
148.0427	74.5250	1	M	12		
276.1376	138.5724	2	K	11	1296.6906	648.8490
404.1962	202.6017	3	Q	10	1168.5957	584.8015
533.2388	267.1230	4	E	9	1040.5371	520.7722
630.2916	315.6494	5	P	8	911.4945	456.2109
729.3600	365.1836	6	V	7	814.4417	407.7245
857.4549	429.2311	7	K	6	715.3733	358.1903
954.5077	477.7575	8	P	5	587.2784	294.1428
1083.5503	542.2788	9	E	4	490.2256	245.6164
1212.5929	606.8001	10	E	3	361.1830	181.0951
1269.6143	635.3108	11	G	2	232.1404	116.5738
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00642948, IPI00253036	1	1	CD99, CD99	979	2+	-0.0146	0.9998	R.NANAEPAVQR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	979	Delta Mass	-0.0146	Protein	IPI00253036
Mass	1069.5380	Next	374.000	Fraction	VF_T13h_band04.mzXML
Hyper	599.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	2	Ion Percent	94%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	10		
186.0873	93.5473	2	A	9	955.4956	478.2514
300.1302	150.5688	3	N	8	884.4585	442.7329
371.1674	186.0873	4	A	7	770.4155	385.7114
500.2100	250.6086	5	E	6	699.3784	350.1928
597.2627	299.1350	6	P	5	570.3358	285.6715
668.2998	334.6536	7	A	4	473.2831	237.1452
767.3682	384.1878	8	V	3	402.2459	201.6266
895.4268	448.2170	9	Q	2	303.1775	152.0924
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00401264	1	1	TXND4	1016	2+	-0.0199	0.9995	R.VDCDQHSDIAQR.Y

Scan	1016	Delta Mass	-0.0199	Protein	IPI00401264
Mass	1443.6280	Next	415.000	Fraction	VF_T13h_band03.mzXML
Hyper	577.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

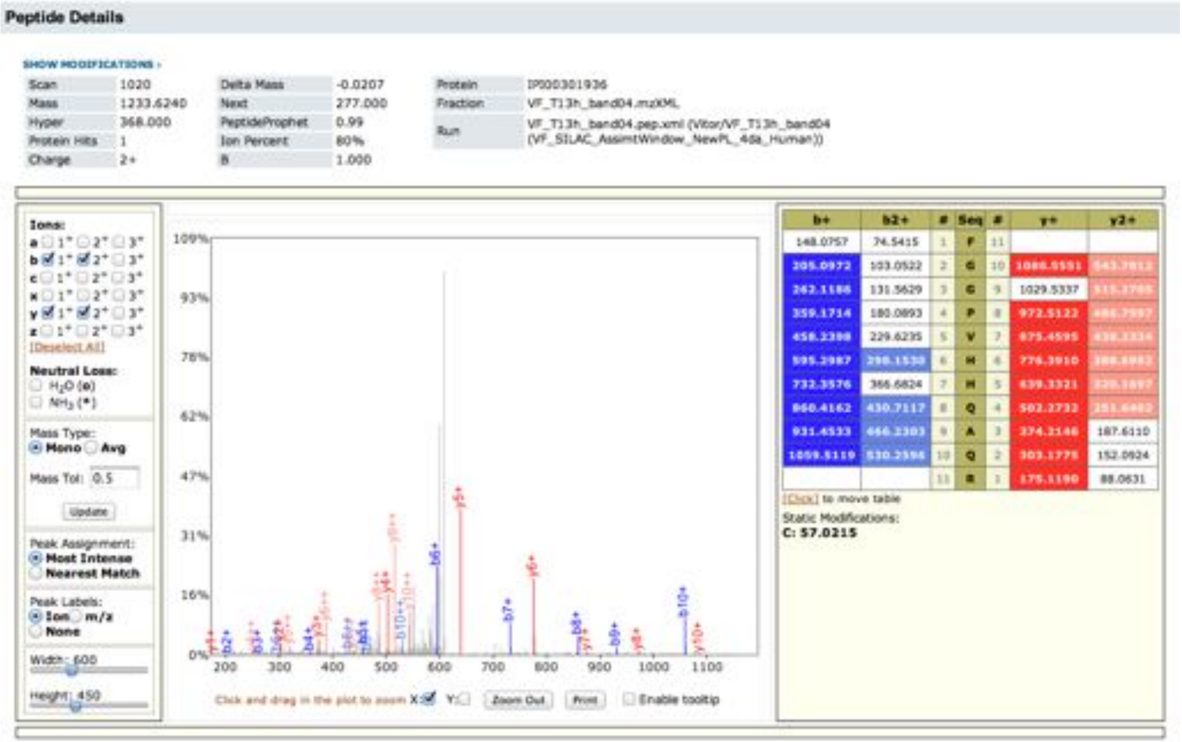
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	12		
215.1026	108.0550	2	D	11	1344.5597	672.7835
375.1333	188.0703	3	C	10	1229.5328	615.2700
490.1603	245.5838	4	D	9	1069.5021	535.2547
618.2188	309.6131	5	Q	8	954.4752	477.7413
755.2777	378.1425	6	H	7	826.4166	413.7119
842.3098	421.6585	7	S	6	689.3577	345.1825
957.3367	479.1720	8	D	5	602.3257	301.6665
1070.4208	535.7140	9	I	4	487.2987	244.1530
1141.4579	571.2326	10	A	3	374.2146	187.6110
1269.5165	635.2619	11	Q	2	303.1775	152.0924
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8452	IPI00301936	1	1	ELAVL1	1020	2+	-0.0207	0.9890	R.FGGPVHHQAQR.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	1020	Delta Mass	-0.0207	Protein	IPI00301936
Mass	1233.6240	Next	277.000	Fraction	VF_T13h_band04.mzXML
Hyper	368.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
205.0972	103.0522	2	G	10	1086.5551	543.7812
262.1186	131.5629	3	G	9	1029.5337	515.2705
359.1714	180.0893	4	P	8	972.5122	486.7597
458.2398	229.6235	5	V	7	875.4595	438.2334
595.2987	298.1530	6	H	6	776.3910	388.6992
732.3576	366.6824	7	H	5	639.3321	320.1697
860.4162	430.7117	8	Q	4	502.2732	251.6402
931.4533	466.2303	9	A	3	374.2146	187.6110
1059.5119	530.2596	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9246	IPI00295889	1	1	SRP19	1023	2+	-0.0158	0.9936	K.TGGADQSLQQGEGSK.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	1023	Delta Mass	-0.0158	Protein	IPI00295889
Mass	1462.6770	Next	203.000	Fraction	VF_T13h_band06.mzXML
Hyper	324.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	15		
159.0764	80.0418	2	G	14	1361.6292	681.3182
216.0979	108.5526	3	G	13	1304.6077	652.8075
287.1350	144.0711	4	A	12	1247.5862	624.2968
402.1619	201.5846	5	D	11	1176.5491	588.7782
530.2205	265.6139	6	Q	10	1061.5222	531.2647
617.2525	309.1299	7	S	9	933.4636	467.2354
730.3366	365.6719	8	L	8	846.4316	423.7194
858.3952	429.7012	9	Q	7	733.3475	367.1774
986.4538	493.7305	10	Q	6	605.2689	303.1481
1043.4752	522.2413	11	G	5	477.2304	239.1188
1172.5178	586.7625	12	E	4	420.2089	210.6081
1229.5393	615.2733	13	G	3	291.1663	146.0868
1316.5713	658.7893	14	S	2	234.1448	117.5761
		15	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9733	IPI00793737, IPI00218214	1	1	NME6, NME6	1034	2+	-0.0077	0.9988	R.NTTHGSDSVVSASR.E

Peptide Details

SHOW MODIFICATIONS ›

Scan	1034	Delta Mass	-0.0077	Protein	IPI00218214
Mass	1417.6666	Next	243.000	Fraction	VF_T13h_band05.mzXML
Hyper	385.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	77%		
Charge	2+	B	0.000		

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	14		
216.0979	108.5526	2	T	13	1303.6237	652.3155
317.1456	159.0764	3	T	12	1202.5760	601.7916
454.2045	227.6059	4	H	11	1101.5283	551.2678
511.2259	256.1166	5	G	10	964.4694	482.7383
598.2580	299.6326	6	S	9	907.4480	454.2276
713.2849	357.1461	7	D	8	820.4159	410.7116
800.3169	400.6621	8	S	7	705.3890	353.1981
899.3853	450.1963	9	V	6	618.3570	309.6821
998.4538	499.7305	10	V	5	519.2885	260.1479
1085.4858	543.2465	11	S	4	420.2201	210.6137
1156.5229	578.7651	12	A	3	333.1881	167.0977
1243.5549	622.2811	13	S	2	262.1510	131.5791
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Mass Tol: 0.5

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8845	IPI00291016	1	1	NDUFV3	1035	2+	-0.0180	0.9903	R.KPEASHSFENR.A

Peptide Details

SHOW MODIFICATIONS ›

Scan	1035	Delta Mass	-0.0180	Protein	IPI00291016
Mass	1301.6230	Next	324.000	Fraction	VF_T13h_band03.mzXML
Hyper	414.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	70%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

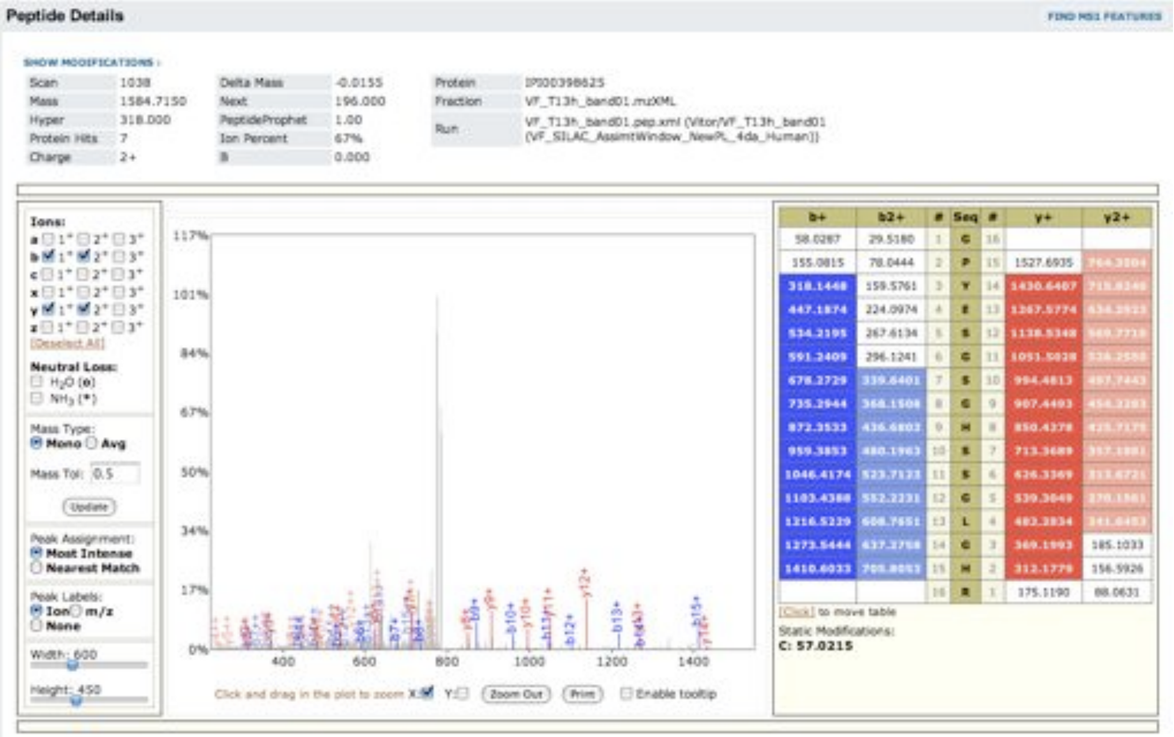
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	11		
226.1550	113.5811	2	P	10	1173.5283	587.2678
355.1976	178.1024	3	E	9	1076.4756	538.7414
426.2347	213.6210	4	A	8	947.4330	474.2201
513.2667	257.1370	5	S	7	876.3959	438.7016
650.3257	325.6665	6	H	6	789.3638	395.1856
737.3577	369.1825	7	S	5	652.3049	326.6561
884.4261	442.7167	8	F	4	565.2729	283.1401
1013.4687	507.2380	9	E	3	418.2045	209.6059
1127.5116	564.2594	10	N	2	289.1619	145.0846
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9056	IPI00787362, IPI00887022, IPI00398625	1	1	LOC730839, LOC730839, HRNR	1038	2+	-0.0155	0.9951	R.GPYESGSGHSSGLGHR.E



Peptide Details

Scan	1038	Delta Mass	-0.0155	Protein	IPI00398625
Mass	1584.7150	Next	196.000	Fraction	VF_T13h_band01.mzXML
Hyper	318.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	67%		
Charge	2+	B	0.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

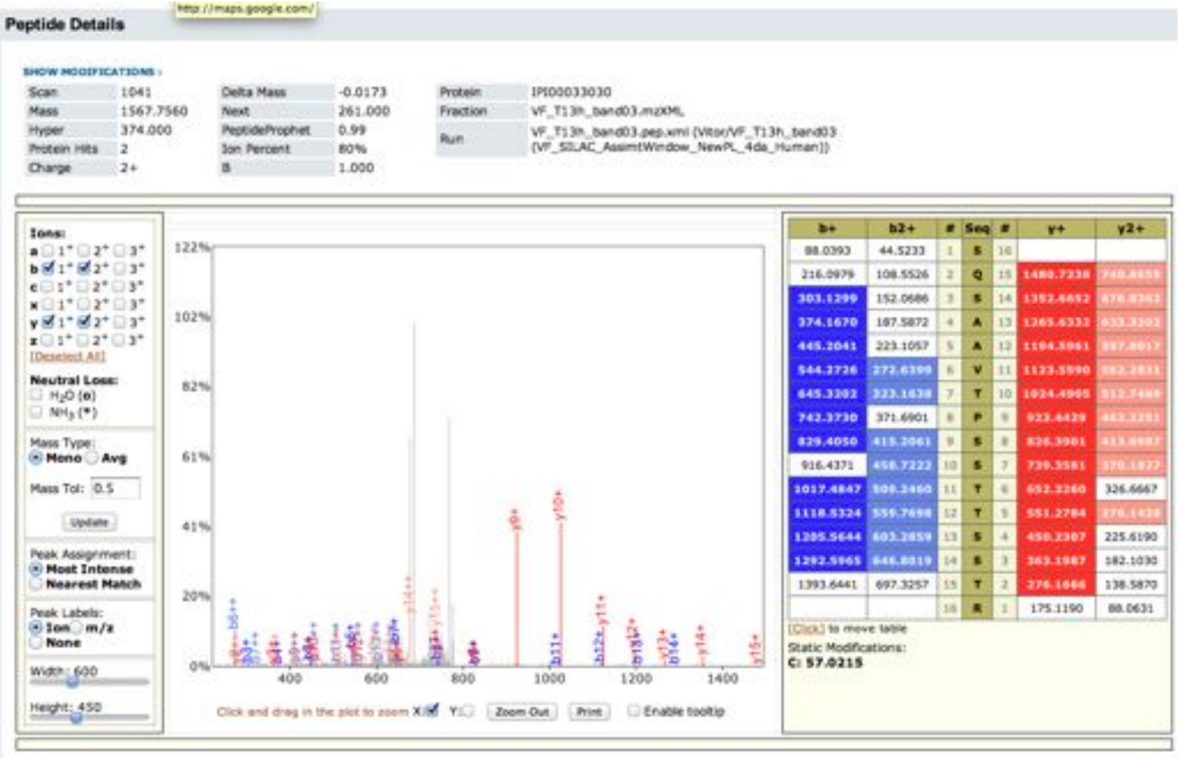
Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	16		
155.0815	78.0444	2	P	15	1527.6935	764.3504
318.1448	159.5761	3	Y	14	1430.6407	715.8240
447.1874	224.0974	4	E	13	1267.5774	634.2923
534.2195	267.6134	5	S	12	1138.5348	569.7710
591.2409	296.1241	6	G	11	1051.5028	526.2550
678.2729	339.6401	7	S	10	994.4813	497.7443
735.2944	368.1508	8	G	9	907.4493	454.2283
872.3533	436.6803	9	H	8	850.4278	425.7175
959.3853	480.1963	10	S	7	713.3689	357.1881
1046.4174	523.7123	11	S	6	626.3369	313.6721
1103.4388	552.2231	12	G	5	539.3049	270.1561
1216.5229	608.7651	13	L	4	482.2834	241.6453
1273.5444	637.2758	14	G	3	369.1993	185.1033
1410.6033	705.8053	15	H	2	312.1779	156.5926
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9289	IPI00470921, IPI00033030	1	1	ADRM1, ADRM1	1041	2+	-0.0173	0.9947	R.SQSAAVTPSSTTSSTR.A



Peptide Details

Scan	1041	Delta Mass	-0.0173	Protein	IPI00033030
Mass	1567.7560	Next	261.000	Fraction	VF_T13h_band03.mzXML
Hyper	374.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

X:☑ Y:☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	16		
216.0979	108.5526	2	Q	15	1480.7238	740.8655
303.1299	152.0686	3	S	14	1352.6652	676.8362
374.1670	187.5872	4	A	13	1265.6332	633.3202
445.2041	223.1057	5	A	12	1194.5961	597.8017
544.2726	272.6399	6	V	11	1123.5590	562.2831
645.3202	323.1638	7	T	10	1024.4905	512.7489
742.3730	371.6901	8	P	9	923.4429	462.2251
829.4050	415.2061	9	S	8	826.3901	413.6987
916.4371	458.7222	10	S	7	739.3581	370.1827
1017.4847	509.2460	11	T	6	652.3260	326.6667
1118.5324	559.7698	12	T	5	551.2784	276.1428
1205.5644	603.2859	13	S	4	450.2307	225.6190
1292.5965	646.8019	14	S	3	363.1987	182.1030
1393.6441	697.3257	15	T	2	276.1666	138.5870
		16	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9838	IPI00216508, IPI00552276, IPI00815770	1	1	SNX3, SNX3, SNX3	1047	2+	-0.0166	0.9995	K.VAGHPLAQNER.C

Peptide Details

SHOW MODIFICATIONS ›

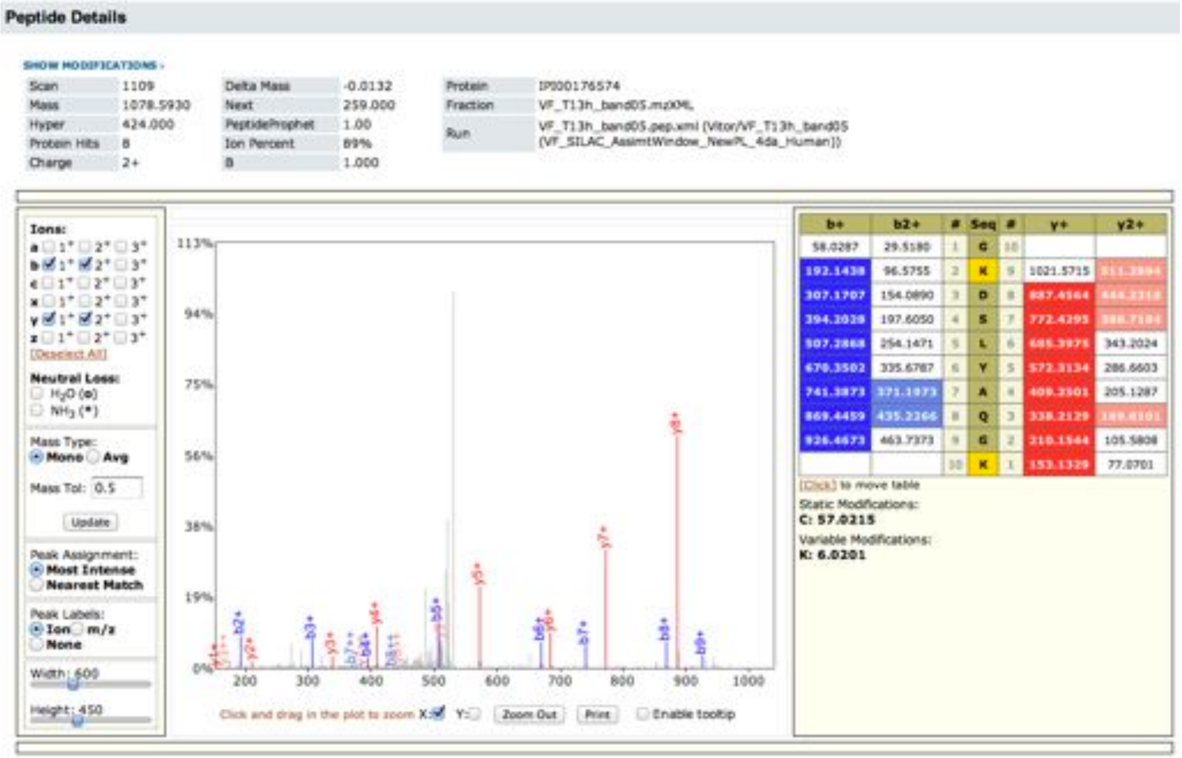
Scan	1047	Delta Mass	-0.0166	Protein	IPI00216508
Mass	1191.6230	Next	307.000	Fraction	VF_T13h_band06.mzXML
Hyper	507.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	95%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
171.1128	86.0600	2	A	10	1092.5545	546.7809
228.1343	114.5708	3	G	9	1021.5174	511.2623
365.1932	183.1002	4	H	8	964.4959	482.7516
462.2459	231.6266	5	P	7	827.4370	414.2221
575.3300	288.1686	6	L	6	730.3842	365.6958
646.3671	323.6872	7	A	5	617.3002	309.1537
774.4257	387.7165	8	Q	4	546.2630	273.6352
888.4686	444.7380	9	N	3	418.2045	209.6059
1017.5112	509.2592	10	E	2	304.1615	152.5844
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9367	IPI00877709, IPI00896410, IPI00786911, IPI00746075, IPI00738898, IPI00176574, IPI00742027, IPI00220344	1	1	-, -, LOC649299, -, hCG_1787519, LOC284230, LOC284230, RPL36A	1109	2+	-0.0132	0.9956	K.GK'DSLYAQGK'.W



Peptide Details

SHOW MODIFICATIONS ›

Scan	1109	Delta Mass	-0.0132	Protein	IPI00176574
Mass	1078.5930	Next	259.000	Fraction	VF_T13h_band05.mzXML
Hyper	424.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	8	Ion Percent	89%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

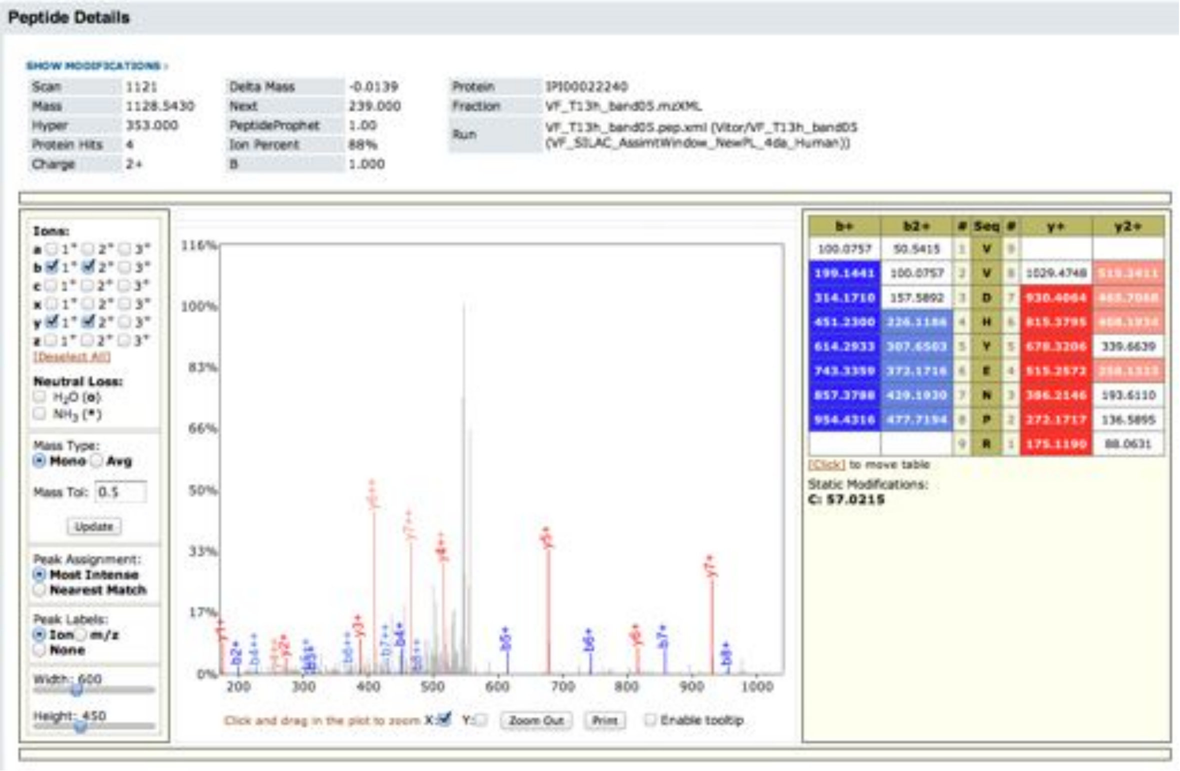
b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	10		
192.1438	96.5755	2	K	9	1021.5715	511.2894
307.1707	154.0890	3	D	8	887.4564	444.2318
394.2028	197.6050	4	S	7	772.4295	386.7184
507.2868	254.1471	5	L	6	685.3975	343.2024
670.3502	335.6787	6	Y	5	572.3134	286.6603
741.3873	371.1973	7	A	4	409.2501	205.1287
869.4459	435.2266	8	Q	3	338.2129	169.6101
926.4673	463.7373	9	G	2	210.1544	105.5808
		10	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9422	IPI00793728, IPI00909212, IPI00848133, IPI00022240	1	1	ISCU, -, ISCU, ISCU	1121	2+	-0.0139	0.9961	K.VVDHYENPR.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	1121	Delta Mass	-0.0139	Protein	IPI00022240
Mass	1128.5430	Next	239.000	Fraction	VF_T13h_band05.mzXML
Hyper	353.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

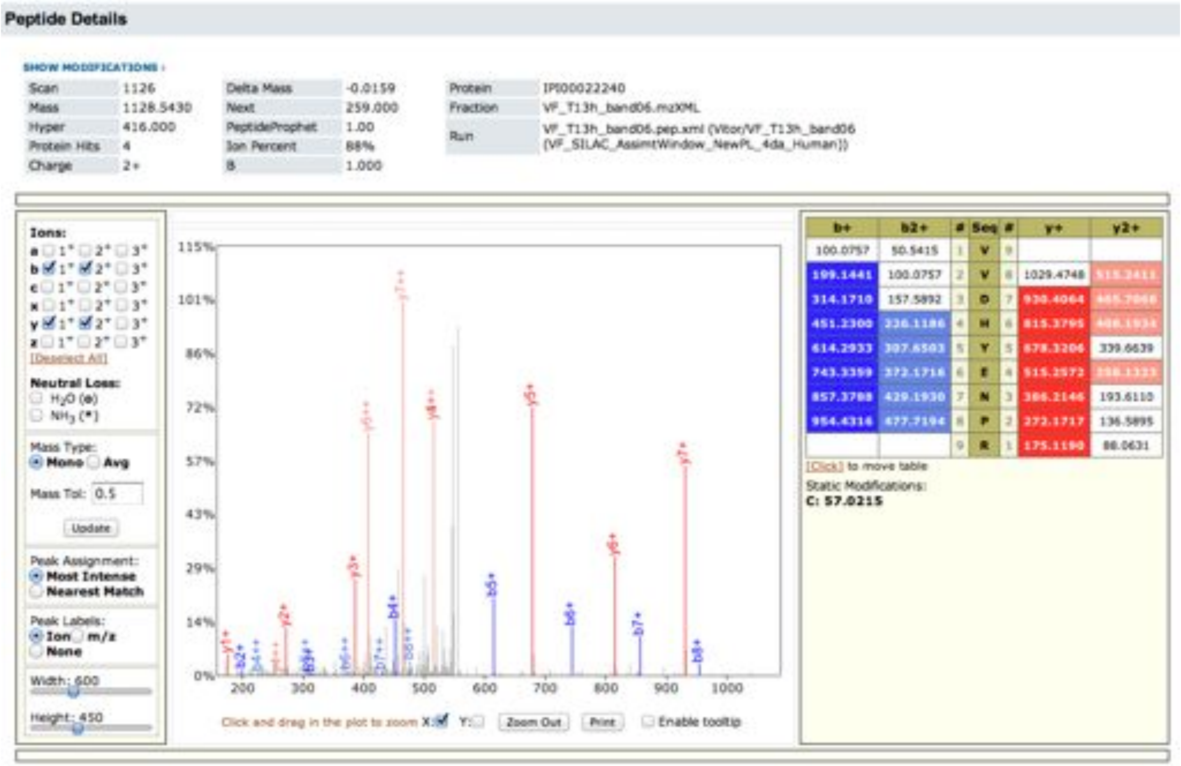
Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	9		
199.1441	100.0757	2	V	8	1029.4748	515.2411
314.1710	157.5892	3	D	7	930.4064	465.7068
451.2300	226.1186	4	H	6	815.3795	408.1934
614.2933	307.6503	5	Y	5	678.3206	339.6639
743.3359	372.1716	6	E	4	515.2572	258.1323
857.3788	429.1930	7	N	3	386.2146	193.6110
954.4316	477.7194	8	P	2	272.1717	136.5895
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9723	IPI00793728, IPI00909212, IPI00848133, IPI00022240	1	1	ISCU, -, ISCU, ISCU	1126	2+	-0.0159	0.9984	K.VVDHYENPR.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	1126	Delta Mass	-0.0159	Protein	IPI00022240
Mass	1128.5430	Next	259.000	Fraction	VF_T13h_band06.mzXML
Hyper	416.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	88%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	9		
199.1441	100.0757	2	V	8	1029.4748	515.2411
314.1710	157.5892	3	D	7	930.4064	465.7068
451.2300	226.1186	4	H	6	815.3795	408.1934
614.2933	307.6503	5	Y	5	678.3206	339.6639
743.3359	372.1716	6	E	4	515.2572	258.1323
857.3788	429.1930	7	N	3	386.2146	193.6110
954.4316	477.7194	8	P	2	272.1717	136.5895
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8719	IPI00639797, IPI00336094, IPI00017726	1	1	HSD17B10, HSD17B10, HADH2	1171	2+	-0.0174	0.9931	R.LVAGEM"GQNEPDQGGQR.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	1171	Delta Mass	-0.0174	Protein	IPI00017726
Mass	1801.8130	Next	227.000	Fraction	VF_T13h_band02.mzXML
Hyper	340.000	PeptideProphet	0.99	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	56%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	17		
213.1598	107.0835	2	V	16	1688.7293	844.8683
284.1969	142.6021	3	A	15	1589.6609	795.3341
341.2183	171.1128	4	G	14	1518.6237	759.8155
470.2609	235.6341	5	E	13	1461.6023	731.3048
617.2963	309.1518	6	M	12	1332.5597	666.7835
674.3178	337.6625	7	G	11	1185.5243	593.2658
802.3764	401.6918	8	Q	10	1128.5028	564.7551
916.4193	458.7133	9	N	9	1000.4443	500.7258
1045.4619	523.2346	10	E	8	886.4013	443.7043
1142.5146	571.7610	11	P	7	757.3587	379.1830
1257.5416	629.2744	12	D	6	660.3060	330.6566
1385.6002	693.3037	13	Q	5	545.2790	273.1432
1442.6216	721.8144	14	G	4	417.2205	209.1139
1499.6431	750.3252	15	G	3	360.1990	180.6031
1627.7017	814.3545	16	Q	2	303.1775	152.0924
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9765	IPI00012535	1	1	DNAJA1	1177	2+	+0.9795	0.9997	R.HYNGEAYEDDEHHPR.G


Peptide Details

SHOW MODIFICATIONS ›

Scan	1177	Delta Mass	+0.9795	Protein	IPI00012535
Mass	1868.7580	Next	348.000	Fraction	VF_T13h_band02.mzXML
Hyper	667.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	93%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	15		
301.1295	151.0684	2	Y	14	1731.6904	866.3533
415.1724	208.0899	3	N	13	1566.6360	783.8217
472.1939	236.6006	4	G	12	1454.5931	727.8002
601.2365	301.1219	5	E	11	1397.5716	699.2895
672.2736	336.6404	6	A	10	1268.5291	634.7683
835.3369	418.1721	7	Y	9	1197.4919	599.2496
964.3795	482.6934	8	E	8	1034.4286	517.7179
1079.4065	540.2069	9	D	7	905.3860	453.1966
1194.4334	597.7203	10	D	6	790.3591	395.6832
1323.4760	662.2416	11	E	5	675.3321	338.1697
1460.5349	730.7711	12	H	4	546.2895	273.6484
1597.5938	799.3006	13	H	3	409.2306	205.1190
1694.6466	847.8269	14	P	2	272.1717	136.5895
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9693	IPI00910417, IPI00909437, IPI00790569, IPI00062151, IPI00470528, IPI00550032	1	1	RPL15, -, RPL15, LOC136321, RPL15, LOC653232	1219	2+	-0.0127	0.9992	K.GATYGKPVHHGVNQLK.F

Peptide Details

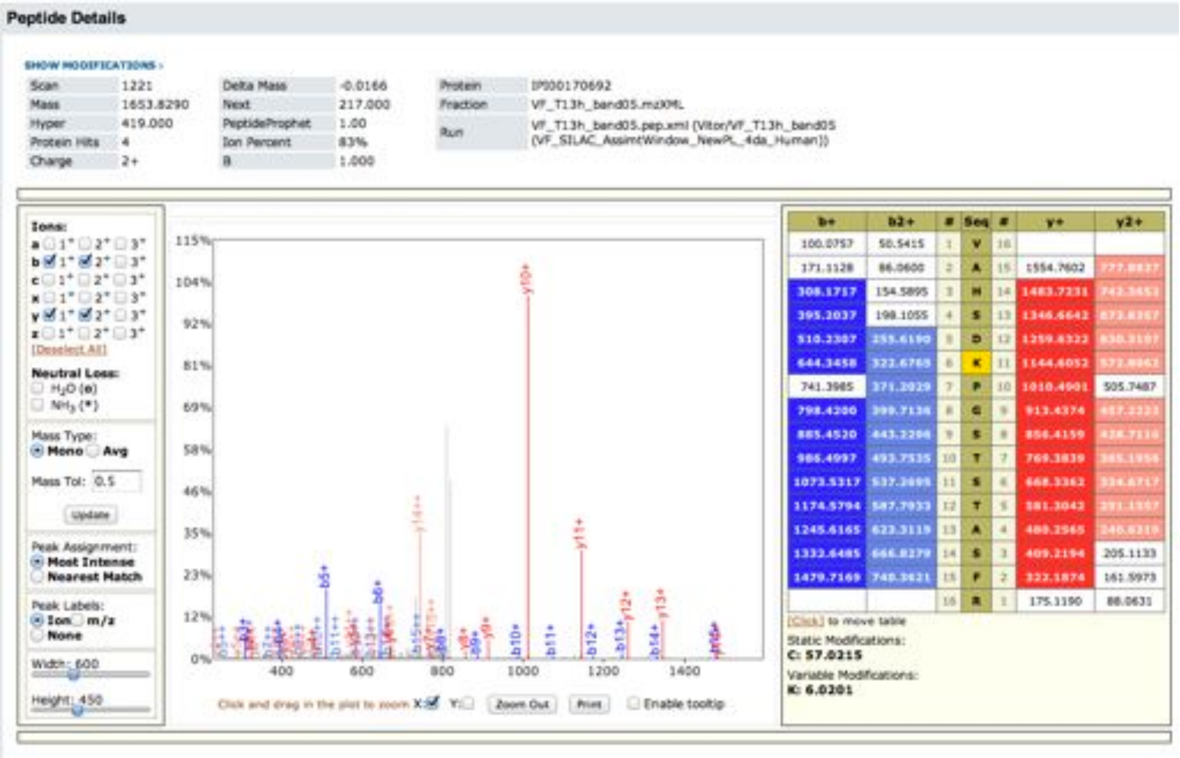
Scan	1219	Delta Mass	-0.0127	Protein	IPI00062151
Mass	1705.9130	Next	237.000	Fraction	VF_T13h_band01.mzXML
Hyper	407.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	80%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	16		
129.0659	65.0366	2	A	15	1648.8918	824.9495
230.1135	115.5604	3	T	14	1577.8547	789.4310
393.1769	197.0921	4	Y	13	1476.8070	738.9071
450.1983	225.6028	5	G	12	1313.7437	657.3755
578.2933	289.6503	6	K	11	1256.7222	628.8647
675.3461	338.1767	7	P	10	1128.6273	564.8173
774.4145	387.7109	8	V	9	1031.5745	516.2909
911.4734	456.2403	9	H	8	932.5061	466.7567
1048.5323	524.7698	10	H	7	795.4472	398.2272
1105.5538	553.2805	11	G	6	658.3883	329.6979
1204.6222	602.8147	12	V	5	601.3668	301.1870
1318.6651	659.8362	13	N	4	502.2984	251.6528
1446.7237	723.8655	14	Q	3	388.2554	194.6314
1559.8077	780.4075	15	L	2	260.1969	130.6021
		16	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9852	IPI00640416, IPI00170692, IPI00871804, IPI00374657	1	1	VAPA, VAPA, VAPA, VAPA	1221	2+	-0.0166	0.9998	K.VAHSDK'PGSTSTASFR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	1221	Delta Mass	-0.0166	Protein	IPI00170692
Mass	1653.8290	Next	217.000	Fraction	VF_T13h_band05.mzXML
Hyper	419.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

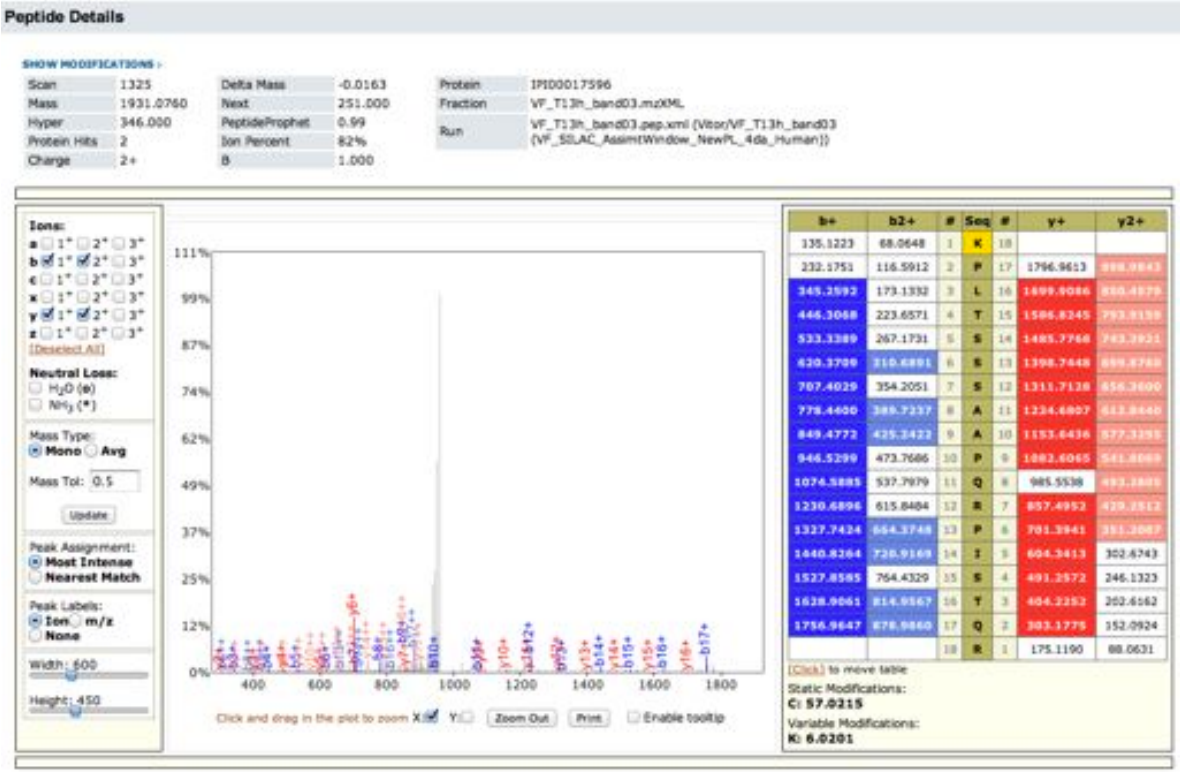
b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	16		
171.1128	86.0600	2	A	15	1554.7602	777.8837
308.1717	154.5895	3	H	14	1483.7231	742.3651
395.2037	198.1055	4	S	13	1346.6642	673.8357
510.2307	255.6190	5	D	12	1259.6322	630.3197
644.3458	322.6765	6	K	11	1144.6052	572.8062
741.3985	371.2029	7	P	10	1010.4901	505.7487
798.4200	399.7136	8	G	9	913.4374	457.2223
885.4520	443.2206	9	S	8	856.4159	428.7116
986.4997	493.7535	10	T	7	769.3839	385.1956
1073.5317	537.2695	11	S	6	668.3362	334.6717
1174.5794	587.7933	12	T	5	581.3042	291.1557
1245.6165	623.3119	13	A	4	480.2565	240.6319
1332.6485	666.8279	14	S	3	409.2194	205.1133
1479.7169	740.3621	15	F	2	322.1874	161.5973
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8429	IPI00910350, IPI00017596	1	1	-, MAPRE1	1325	2+	-0.0163	0.9858	K.K'PLTSSSAAPQRPISTQR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	1325	Delta Mass	-0.0163	Protein	IPI00017596
Mass	1931.0760	Next	251.000	Fraction	VF_T13h_band03.mzXML
Hyper	346.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
135.1223	68.0648	1	K	18		
232.1751	116.5912	2	P	17	1796.9613	898.9843
345.2592	173.1332	3	L	16	1699.9086	850.4579
446.3068	223.6571	4	T	15	1586.8245	793.9159
533.3389	267.1731	5	S	14	1485.7768	743.3921
620.3709	310.6891	6	S	13	1398.7448	699.8760
707.4029	354.2051	7	S	12	1311.7128	656.3600
778.4400	389.7237	8	A	11	1234.6807	617.8440
849.4772	425.2422	9	A	10	1153.6436	577.3255
946.5299	473.7686	10	P	9	1082.6065	541.8069
1074.5885	537.7979	11	Q	8	985.5538	493.2805
1230.6896	615.8484	12	R	7	857.4952	429.2512
1327.7424	664.3748	13	P	6	701.3941	351.2007
1440.8264	720.9169	14	I	5	604.3413	302.6743
1527.8585	764.4329	15	S	4	491.2572	246.1323
1628.9061	814.9567	16	T	3	404.2252	202.6162
1756.9647	878.9860	17	Q	2	303.1775	152.0924
		18	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9361	IPI00173589, IPI00454907, IPI00888051, IPI00419919, IPI00796934, IPI00644657, IPI00052885, IPI00792336, IPI00792866	1	1	LOC284064, LOC283412, LOC283412, RPL29, RPL29, -, LOC729611, LOC729611, LOC729611	1357	2+	-0.0133	0.9948	K.AQAAAPASVPAQAPK.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	1357	Delta Mass	-0.0133	Protein	IPI00052885
Mass	1377.7480	Next	229.000	Fraction	VF_T13h_band06.mzXML
Hyper	353.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	9	Ion Percent	64%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

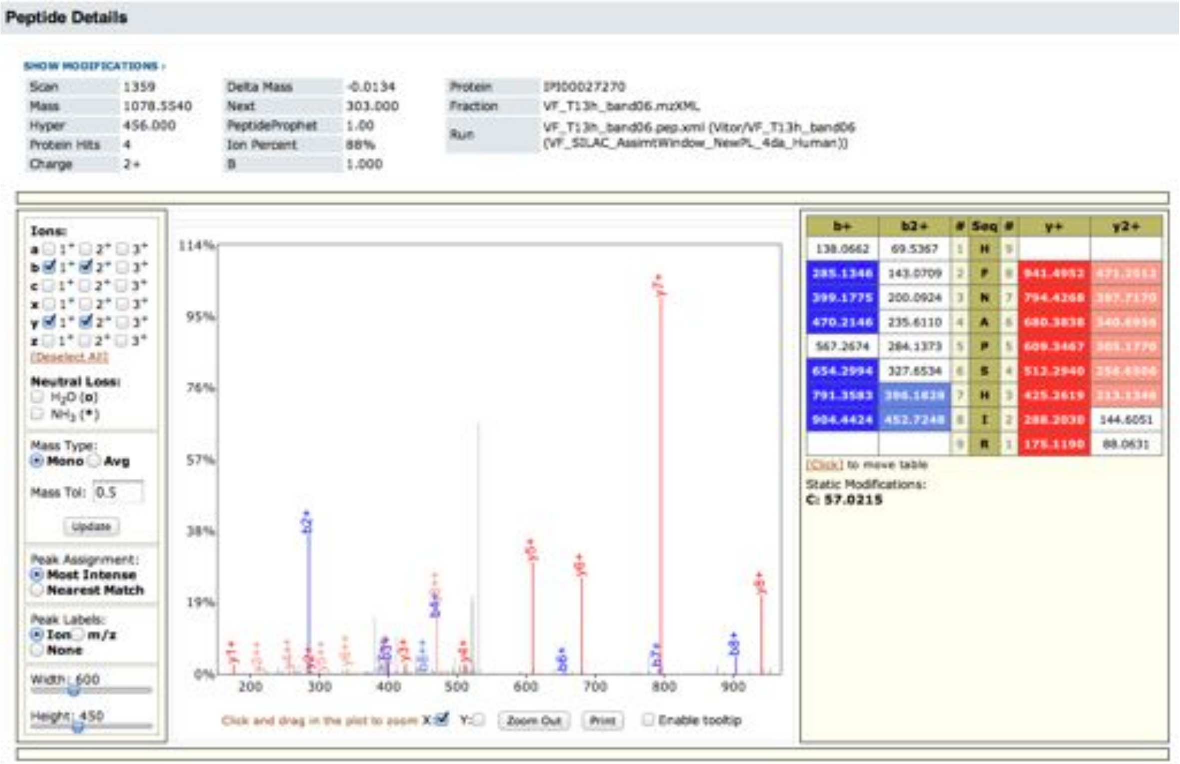
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	15		
200.1030	100.5551	2	Q	14	1306.7114	653.8593
271.1401	136.0737	3	A	13	1178.6528	589.8300
342.1772	171.5922	4	A	12	1107.6157	554.3115
413.2143	207.1108	5	A	11	1036.5786	518.7929
510.2671	255.6372	6	P	10	965.5415	483.2744
581.3042	291.1557	7	A	9	868.4887	434.7480
668.3362	334.6717	8	S	8	797.4516	399.2294
767.4046	384.2060	9	V	7	710.4196	355.7134
864.4574	432.7323	10	P	6	611.3511	306.1793
935.4945	468.2509	11	A	5	514.2984	257.6529
1063.5531	532.2803	12	Q	4	443.2613	222.1343
1134.5902	567.7987	13	A	3	315.2027	158.1050
1231.6430	616.3251	14	P	2	244.1656	122.5864
		15	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9723	IPI00792420, IPI00789514, IPI00027270, IPI00433834	1	1	RPL26, RPL26, RPL26, RPL26	1359	2+	-0.0134	0.9984	R.HFNAPSHIR.R



Peptide Details

SHOW MODIFICATIONS ›

Scan	1359	Delta Mass	-0.0134	Protein	IPI00027270
Mass	1078.5540	Next	303.000	Fraction	VF_T13h_band06.mzXML
Hyper	456.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

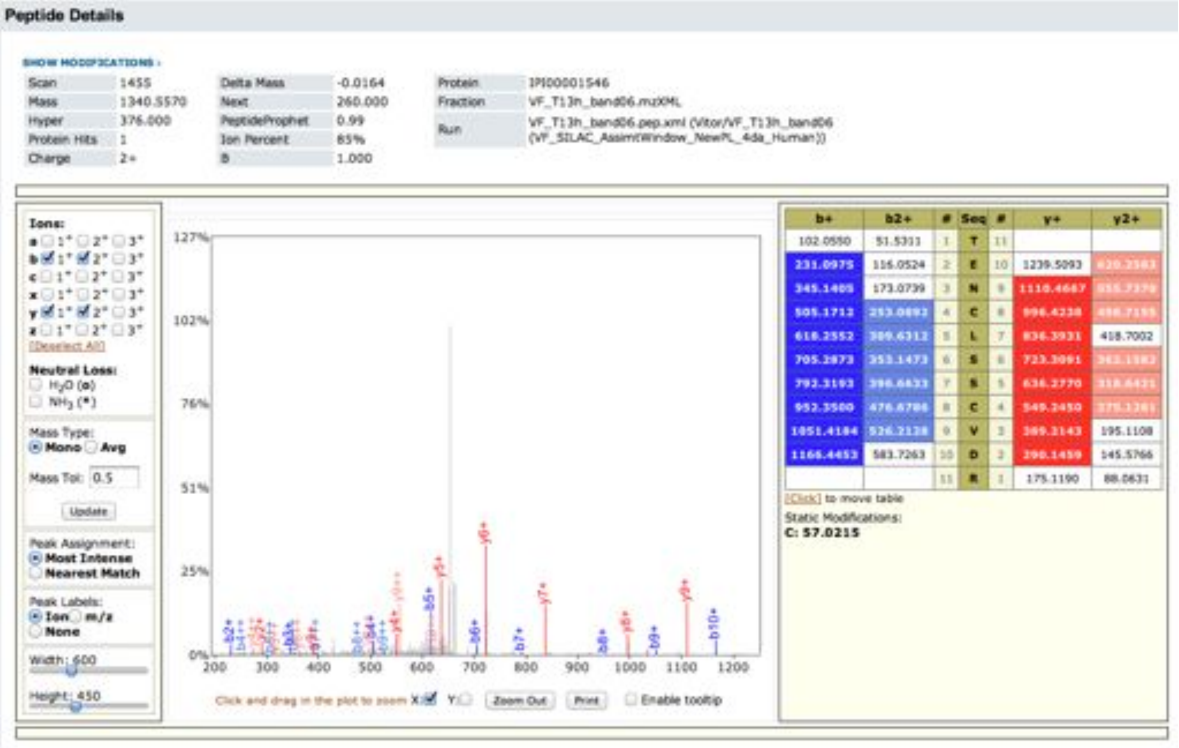
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	9		
285.1346	143.0709	2	F	8	941.4952	471.2512
399.1775	200.0924	3	N	7	794.4268	397.7170
470.2146	235.6110	4	A	6	680.3838	340.6956
567.2674	284.1373	5	P	5	609.3467	305.1770
654.2994	327.6534	6	S	4	512.2940	256.6506
791.3583	396.1828	7	H	3	425.2619	213.1346
904.4424	452.7248	8	I	2	288.2030	144.6051
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9265	IPI00001546	1	1	TIMM8B	1455	2+	-0.0164	0.9938	R.TENCLSSCVDR.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	1455	Delta Mass	-0.0164	Protein	IPI00001546
Mass	1340.5570	Next	260.000	Fraction	VF_T13h_band06.mzXML
Hyper	376.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
231.0975	116.0524	2	E	10	1239.5093	620.2583
345.1405	173.0739	3	N	9	1110.4667	555.7370
505.1712	253.0892	4	C	8	996.4238	498.7155
618.2552	309.6312	5	L	7	836.3931	418.7002
705.2873	353.1473	6	S	6	723.3091	362.1582
792.3193	396.6633	7	S	5	636.2770	318.6421
952.3500	476.6786	8	C	4	549.2450	275.1261
1051.4184	526.2128	9	V	3	389.2143	195.1108
1166.4453	583.7263	10	D	2	290.1459	145.5766
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9759	IPI00479514, IPI00470535	1	1	CACNA2D1, CACNA2D1	1482	2+	-0.0191	0.9996	R.KTPNNPSCNADLINR.V

Peptide Details

SHOW MODIFICATIONS ›

Scan	1482	Delta Mass	-0.0191	Protein	IPI00470535
Mass	1713.8340	Next	245.000	Fraction	VF_T13h_band01.mzXML
Hyper	441.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

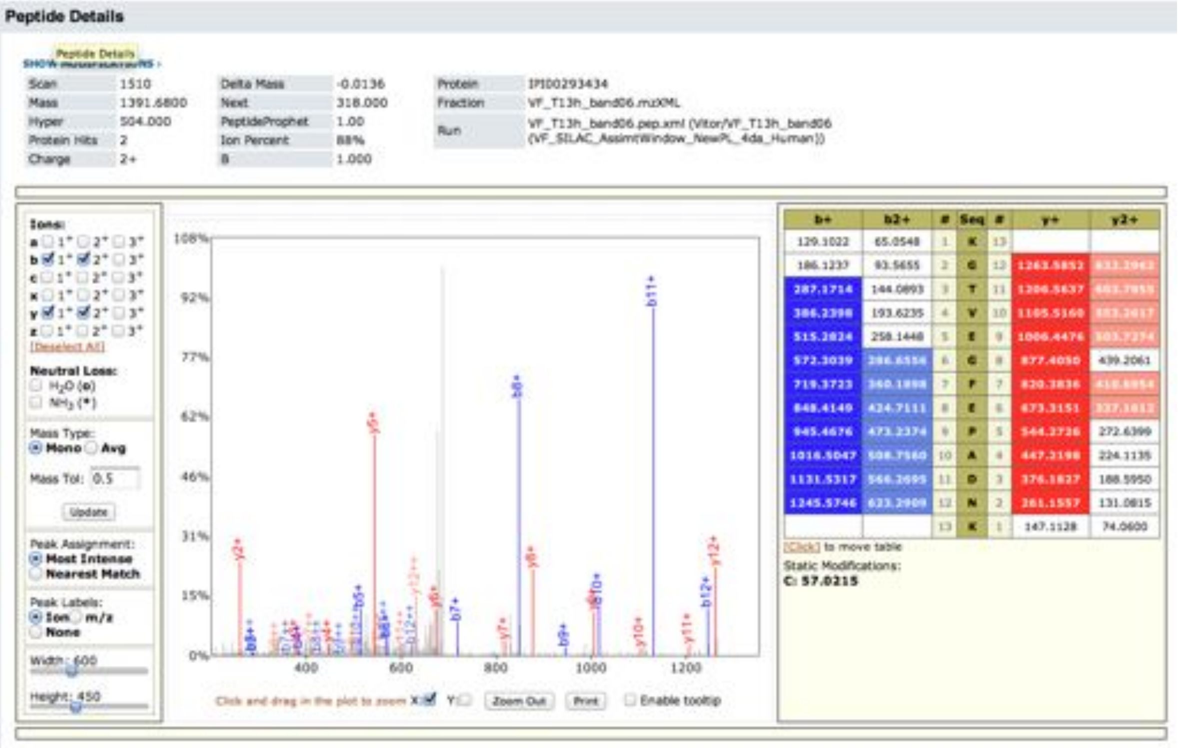
Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	15		
230.1499	115.5786	2	T	14	1585.7388	793.3730
327.2027	164.1050	3	P	13	1484.6911	742.8492
441.2456	221.1264	4	N	12	1387.6383	694.3228
555.2885	278.1479	5	N	11	1273.5954	637.3013
652.3413	326.6743	6	P	10	1159.5525	580.2799
739.3733	370.1903	7	S	9	1062.4997	531.7535
899.4040	450.2056	8	C	8	975.4677	488.2375
1013.4469	507.2271	9	N	7	815.4370	408.2221
1084.4841	542.7457	10	A	6	701.3941	351.2007
1199.5110	600.2591	11	D	5	630.3570	315.6821
1312.5951	656.8012	12	L	4	515.3300	258.1686
1425.6791	713.3432	13	I	3	402.2459	201.6266
1539.7221	770.3647	14	N	2	289.1619	145.0846
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9817	IPI00790432, IPI00293434	1	1	SRP14, SRP14	1510	2+	-0.0136	0.9993	K.KGTVEGFEPADNK.C


Peptide Details

Peptide Details
SHOW MODIFICATIONS ›

Scan	1510	Delta Mass	-0.0136	Protein	IPI00293434
Mass	1391.6800	Next	318.000	Fraction	VF_T13h_band06.mzXML
Hyper	504.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	13		
186.1237	93.5655	2	G	12	1263.5852	632.2962
287.1714	144.0893	3	T	11	1206.5637	603.7855
386.2398	193.6235	4	V	10	1105.5160	553.2617
515.2824	258.1448	5	E	9	1006.4476	503.7274
572.3039	286.6556	6	G	8	877.4050	439.2061
719.3723	360.1898	7	F	7	820.3836	410.6954
848.4149	424.7111	8	E	6	673.3151	337.1612
945.4676	473.2374	9	P	5	544.2726	272.6399
1016.5047	508.7560	10	A	4	447.2198	224.1135
1131.5317	566.2695	11	D	3	376.1827	188.5950
1245.5746	623.2909	12	N	2	261.1557	131.0815
		13	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8038	IPI00793189, IPI00015602	1	1	TOMM70A, TOMM70A	1517	2+	-0.0122	0.9873	R.LRPESALAQAQK'.C

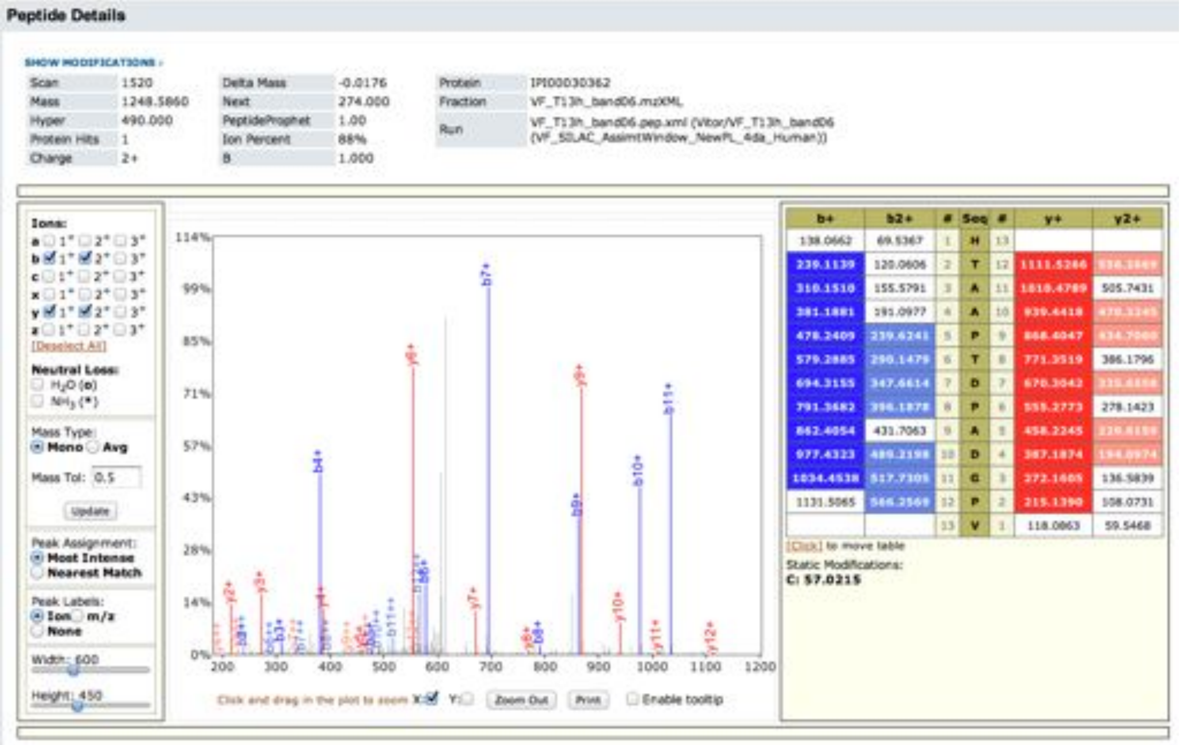
Scan	1517	Delta Mass	-0.0122	Protein	IPI00015602
Mass	1317.7580	Next	229.000	Fraction	VF_T13h_band01.mzXML
Hyper	328.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	12		
270.1925	135.5999	2	R	11	1204.6740	602.8406
367.2452	184.1262	3	P	10	1048.5728	524.7981
496.2878	248.6475	4	E	9	951.5201	476.2637
583.3198	292.1636	5	S	8	822.4775	411.7424
654.3570	327.6821	6	A	7	735.4455	368.2264
767.4410	384.2241	7	L	6	664.4084	332.7078
838.4781	419.7427	8	A	5	551.3243	276.1656
966.5367	483.7720	9	Q	4	480.2872	240.6472
1037.5738	519.2905	10	A	3	352.2286	176.6179
1165.6324	583.3198	11	Q	2	281.1915	141.0994
		12	K	1	153.1329	77.0701

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9849	IPI00030362	1	1	PLP2	1520	2+	-0.0176	0.9996	R.HTAAPTDPADGPV.-



Peptide Details

SHOW MODIFICATIONS ›

Scan	1520	Delta Mass	-0.0176	Protein	IPI00030362
Mass	1248.5860	Next	274.000	Fraction	VF_T13h_band06.mzXML
Hyper	490.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	88%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	13		
239.1139	120.0606	2	T	12	1111.5286	[illegible]
310.1510	155.5791	3	A	11	1010.4789	505.7431
381.1881	191.0977	4	A	10	939.4418	470.2245
478.2409	239.6241	5	P	9	868.4047	434.7060
579.2885	290.1479	6	T	8	771.3519	386.1796
694.3155	347.6614	7	D	7	670.3042	335.6558
791.3682	396.1878	8	P	6	555.2773	278.1423
862.4054	431.7063	9	A	5	458.2245	229.6159
977.4323	489.2198	10	D	4	387.1874	194.0974
1034.4538	517.7305	11	G	3	272.1605	136.5839
1131.5065	566.2569	12	P	2	215.1390	108.0731
		13	V	1	118.0863	59.5468

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00788938, IPI00795075, IPI00910754, IPI00908791, IPI00148061, IPI00217966, IPI00554498, IPI00607708, IPI00219217	1	1	LDHB, LDHA, LDHA, -, LDHAL6A, LDHA, LDHC, LDHA, LDHB	1527	2+	-0.0157	0.9998	R.VIGSGCNLDSAR.F

Peptide Details

Scan	1527	Delta Mass	-0.0157	Protein	IPI00148061
Mass	1248.6000	Next	272.000	Fraction	VF_T13h_band04.mzXML
Hyper	491.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	9	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

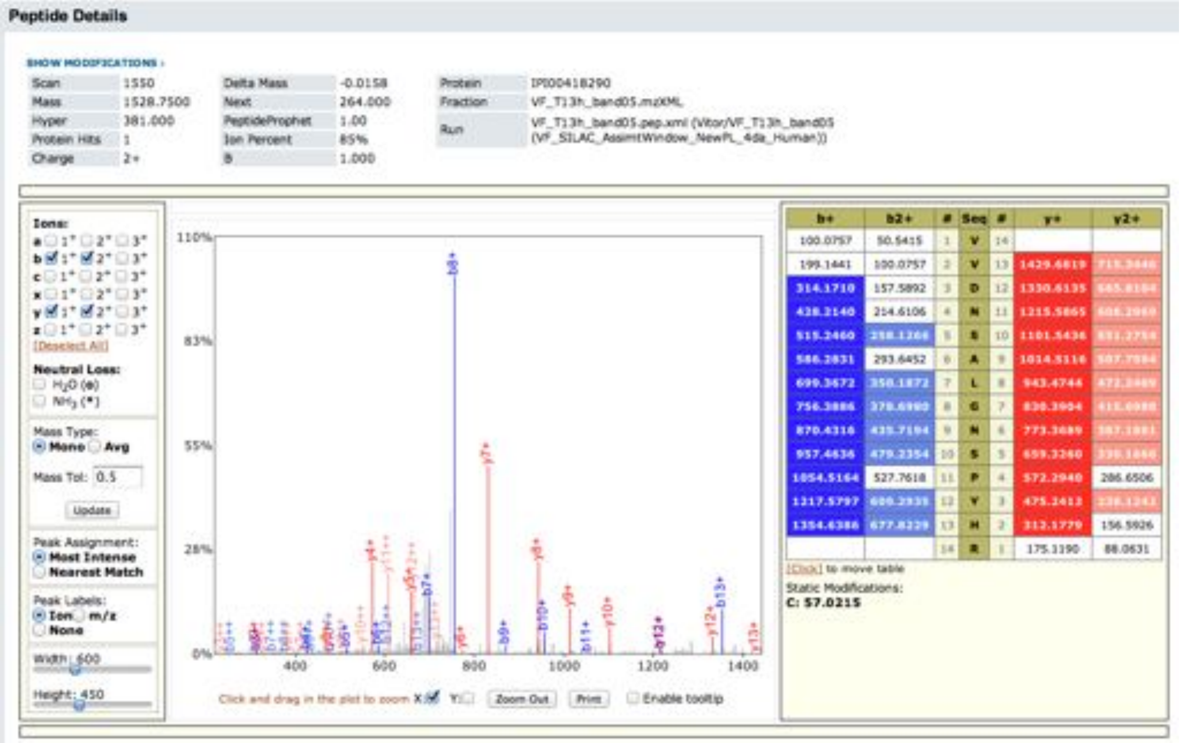
Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	12		
213.1598	107.0835	2	I	11	1149.5317	575.2695
270.1812	135.5942	3	G	10	1036.4477	518.7275
357.2132	179.1103	4	S	9	979.4262	490.2167
414.2347	207.6210	5	G	8	892.3942	446.7007
574.2654	287.6363	6	C	7	835.3727	418.1900
688.3083	344.6578	7	N	6	675.3420	338.1747
801.3924	401.1998	8	L	5	561.2991	281.1532
916.4193	458.7133	9	D	4	448.2150	224.6112
1003.4514	502.2293	10	S	3	333.1881	167.0977
1074.4885	537.7479	11	A	2	246.1561	123.5817
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9524	IPI00418290	1	1	MRPL14	1550	2+	-0.0158	0.9970	R.VVDNSALGNSPYHR.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	1550	Delta Mass	-0.0158	Protein	IPI00418290
Mass	1528.7500	Next	264.000	Fraction	VF_T13h_band05.mzXML
Hyper	381.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

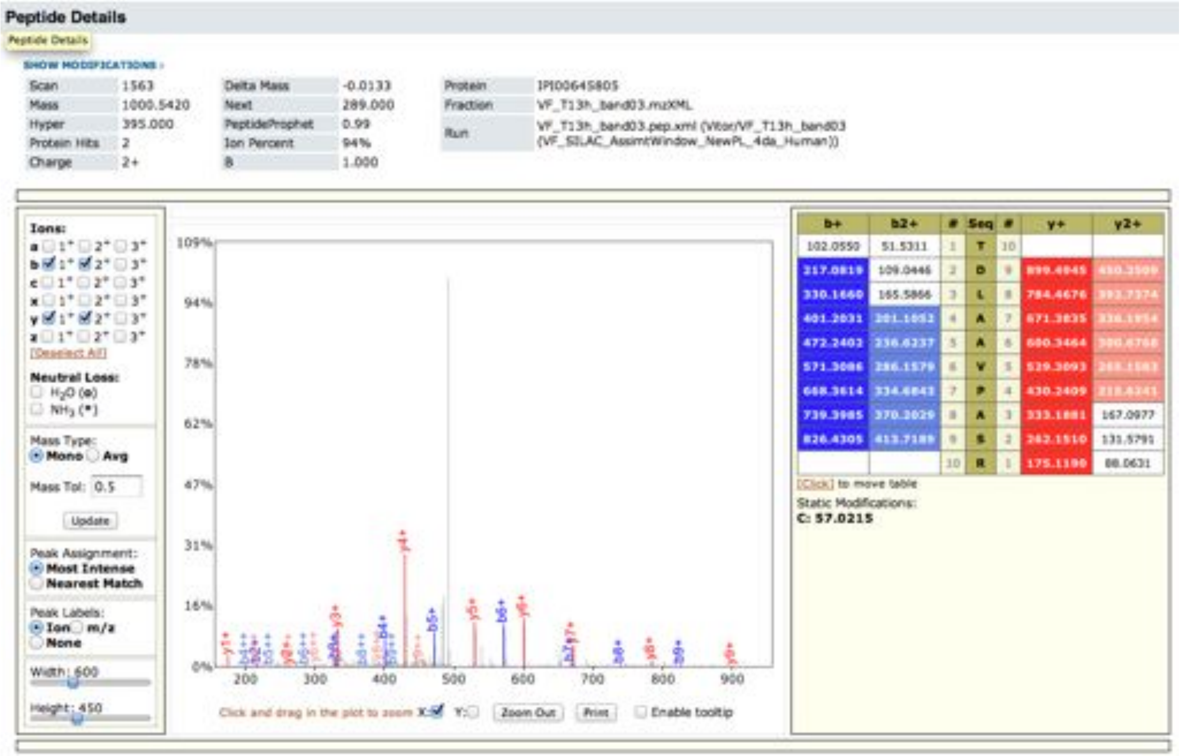
Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	14		
199.1441	100.0757	2	V	13	1429.6819	715.3446
314.1710	157.5892	3	D	12	1330.6135	665.8104
428.2140	214.6106	4	N	11	1215.5865	608.2969
515.2460	258.1266	5	S	10	1101.5436	551.2754
586.2831	293.6452	6	A	9	1014.5116	507.7594
699.3672	350.1872	7	L	8	943.4744	472.2409
756.3886	378.6980	8	G	7	830.3904	415.6988
870.4316	435.7194	9	N	6	773.3689	387.1881
957.4636	479.2354	10	S	5	659.3260	330.1666
1054.5164	527.7618	11	P	4	572.2940	286.6506
1217.5797	609.2935	12	Y	3	475.2413	238.1243
1354.6386	677.8229	13	H	2	312.1779	156.5926
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9205	IPI00645805, IPI00789848	1	1	IVD, IVD	1563	2+	-0.0133	0.9939	K.TDLAAVPASR.G



Scan	1563
Mass	1000.5420
Hyper	395.000
Protein Hits	2
Charge	2+

Delta Mass	-0.0133
Next	289.000
PeptideProphet	0.99
Ion Percent	94%
B	1.000

Protein	IPI00645805
Fraction	VF_T13h_band03.mzXML
Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	10		
217.0819	109.0446	2	D	9	899.4945	450.2509
330.1660	165.5866	3	L	8	784.4676	392.7374
401.2031	201.1052	4	A	7	671.3835	336.1954
472.2402	236.6237	5	A	6	600.3464	300.6768
571.3086	286.1579	6	V	5	529.3093	265.1583
668.3614	334.6843	7	P	4	430.2409	215.6241
739.3985	370.2029	8	A	3	333.1881	167.0977
826.4305	413.7189	9	S	2	262.1510	131.5791
		10	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8619	IPI00216569	1	1	CST7	1598	2+	-0.0121	0.9883	K.TNDPGVLQAAR.Y

Peptide Details

SHOW MODIFICATIONS ›

Scan	1598	Delta Mass	-0.0121	Protein	IPI00216569
Mass	1141.5960	Next	243.000	Fraction	VF_T13h_band05.mzXML
Hyper	334.000	PeptideProphet	0.99	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	1	Ion Percent	70%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
216.0979	108.5526	2	N	10	1040.5483	520.7778
331.1248	166.0661	3	D	9	926.5054	463.7563
428.1776	214.5924	4	P	8	811.4785	406.2429
485.1991	243.1032	5	G	7	714.4257	357.7165
584.2675	292.6374	6	V	6	657.4042	329.2058
697.3515	349.1794	7	L	5	558.3358	279.6715
825.4101	413.2087	8	Q	4	445.2518	223.1295
896.4472	448.7272	9	A	3	317.1932	159.1002
967.4843	484.2458	10	A	2	246.1561	123.5817
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9870	IPI00216569	1	1	CST7	1603	2+	-0.0134	0.9998	K.TNDPGVLQAAR.Y

Peptide Details

SHOW MODIFICATIONS ›

Scan	1603	Delta Mass	-0.0134	Protein	IPI00216569
Mass	1141.5960	Next	362.000	Fraction	VF_T13h_band06.mzXML
Hyper	629.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	95%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

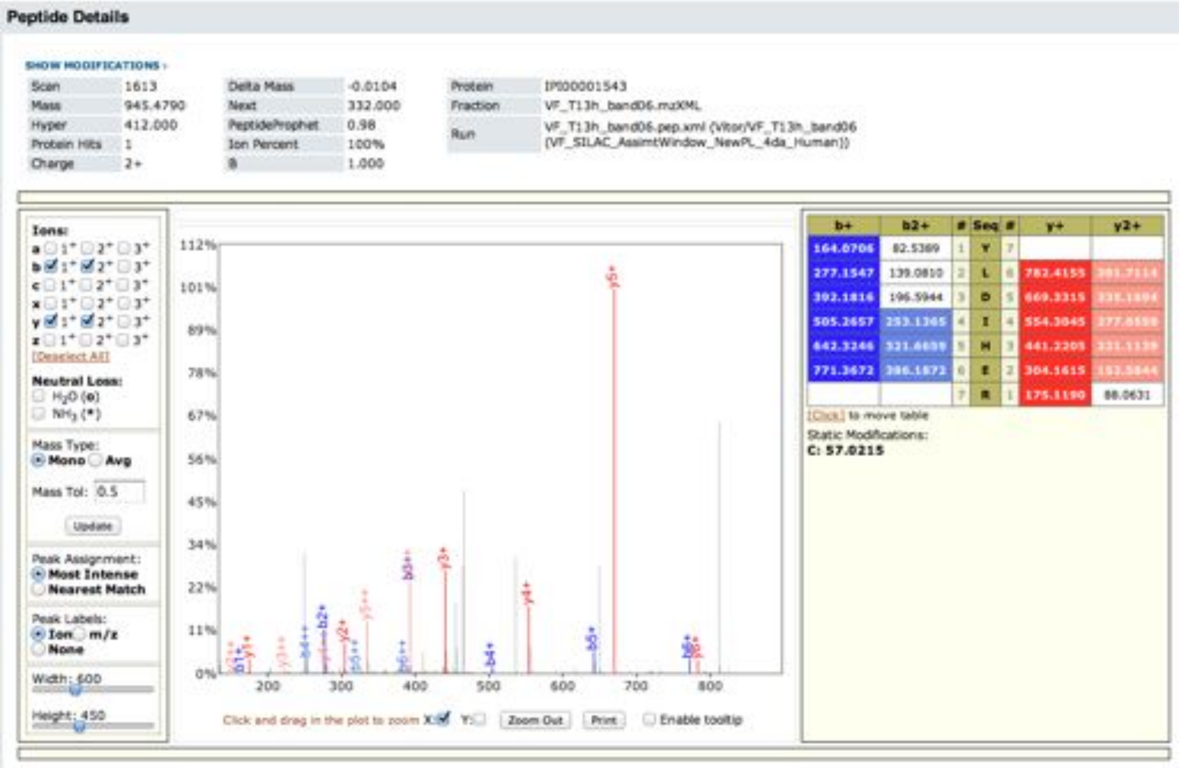
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
216.0979	108.5526	2	N	10	1040.5483	520.7779
331.1248	166.0661	3	D	9	926.5054	463.7563
428.1776	214.5924	4	P	8	811.4785	406.2429
485.1991	243.1032	5	G	7	714.4257	357.7165
584.2675	292.6374	6	V	6	657.4042	329.2058
697.3515	349.1794	7	L	5	558.3358	279.6715
825.4101	413.2087	8	Q	4	445.2518	223.1295
896.4472	448.7272	9	A	3	317.1932	159.1002
967.4843	484.2458	10	A	2	246.1561	123.5817
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8345	IPI00001543	1	1	TIMM10	1613	2+	-0,0104	0,9832	K.YLDIHER.M



Peptide Details

SHOW MODIFICATIONS ›

Scan	1613	Delta Mass	-0.0104	Protein	IPI00001543
Mass	945.4790	Next	332.000	Fraction	VF_T13h_band06.mzXML
Hyper	412.000	PeptideProphet	0.98	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	100%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	7		
277.1547	139.0810	2	L	6	782.4155	391.7114
392.1816	196.5944	3	D	5	669.3315	335.1694
505.2657	253.1365	4	I	4	554.3045	277.6559
642.3246	321.6659	5	H	3	441.2205	221.1139
771.3672	386.1872	6	E	2	304.1615	152.5844
		7	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9230	IPI00645966, IPI00645010, IPI00304596	1	1	NONO, NONO, NONO	1676	2+	-0,0130	0,9965	R.FACHSASLTVR.N

Peptide Details

SHOW MODIFICATIONS ›

Scan	1676	Delta Mass	-0.0130	Protein	IPI00304596
Mass	1248.6150	Next	312.000	Fraction	VF_T13h_band02.mzXML
Hyper	429.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

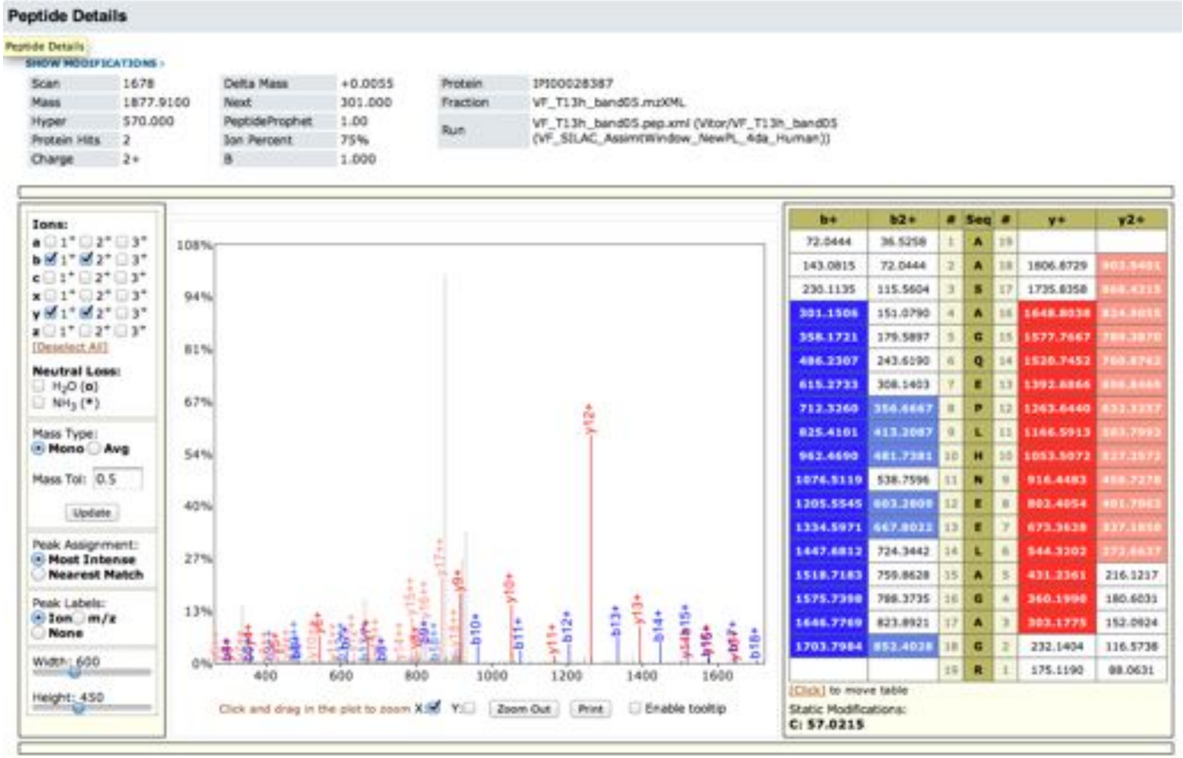
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
219.1128	110.0600	2	A	10	1101.5470	551.2771
379.1435	190.0754	3	C	9	1030.5099	515.7586
516.2024	258.6048	4	H	8	870.4792	435.7433
603.2344	302.1209	5	S	7	733.4203	367.2138
674.2715	337.6394	6	A	6	646.3883	323.6978
761.3036	381.1554	7	S	5	575.3511	288.1792
874.3876	437.6975	8	L	4	488.3191	244.6632
975.4353	488.2213	9	T	3	375.2350	188.1212
1074.5037	537.7555	10	V	2	274.1874	137.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9756	IPI00375407, IPI00028387	1	1	C20orf116, C20orf116	1678	2+	+0,0055	0,9990	R.AASAGQEPLHNEELAGAGR.V



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

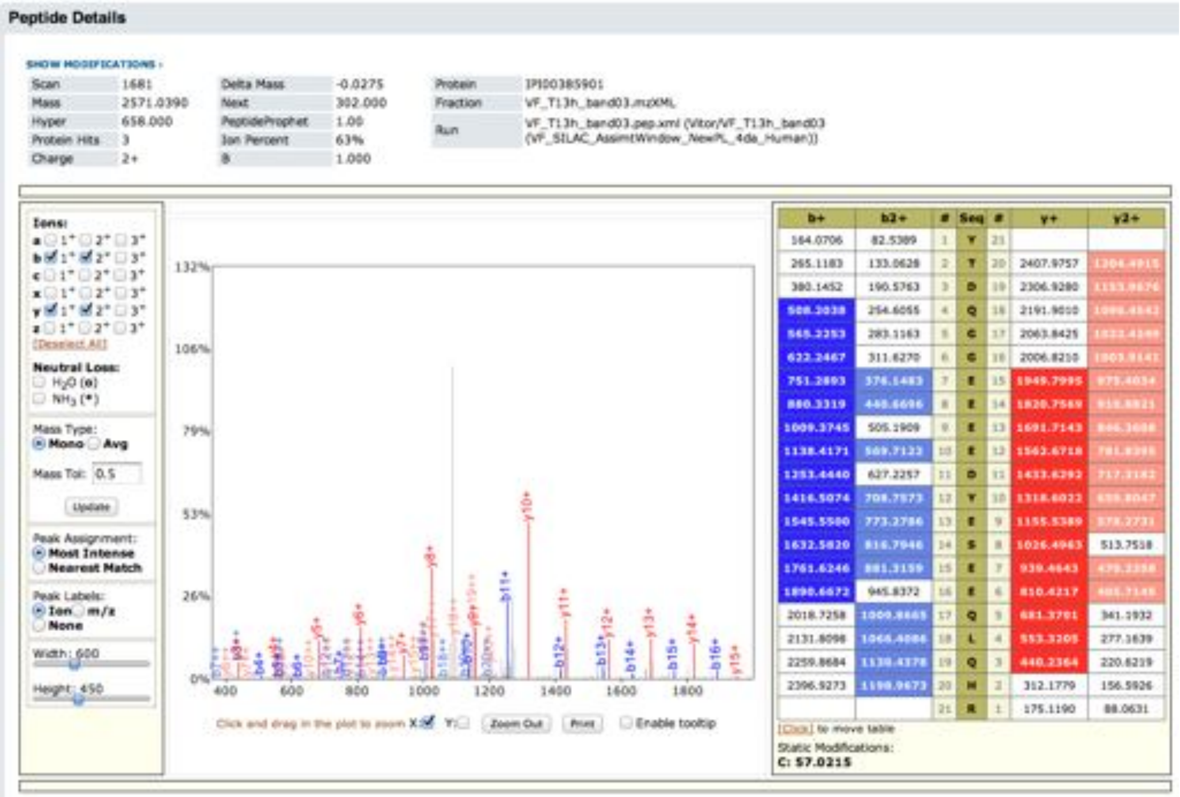
Scan	1678	Delta Mass	+0.0055	Protein	IPI00028387
Mass	1877.9100	Next	301.000	Fraction	VF_T13h_band05.mzXML
Hyper	570.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	19		
143.0815	72.0444	2	A	18	1806.8729	903.9401
230.1135	115.5604	3	S	17	1735.8358	868.4215
301.1506	151.0790	4	A	16	1648.8038	824.9055
358.1721	179.5897	5	G	15	1577.7667	789.3870
486.2307	243.6190	6	Q	14	1520.7452	760.8762
615.2733	308.1403	7	E	13	1392.6866	696.8469
712.3260	356.6667	8	P	12	1263.6440	632.3257
825.4101	413.2087	9	L	11	1166.5913	583.7993
962.4690	481.7381	10	H	10	1053.5072	527.2573
1076.5119	538.7596	11	N	9	916.4483	458.7278
1205.5545	603.2809	12	E	8	802.4054	401.7063
1334.5971	667.8022	13	E	7	673.3628	337.1850
1447.6812	724.3442	14	L	6	544.3202	272.6637
1518.7183	759.8628	15	A	5	431.2361	216.1217
1575.7398	788.3735	16	G	4	360.1990	180.6031
1646.7769	823.8921	17	A	3	303.1775	152.0924
1703.7984	852.4028	18	G	2	232.1404	116.5738
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00385901, IPI00908298, IPI00470631	1	1	COQ9, -, COQ9	2+	1681	-0,0275	1,0000	R.YTDQGGEEEEDYESEEQLQHR.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	1681	Delta Mass	-0.0275	Protein	IPI00385901
Mass	2571.0390	Next	302.000	Fraction	VF_T13h_band03.mzXML
Hyper	658.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	63%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

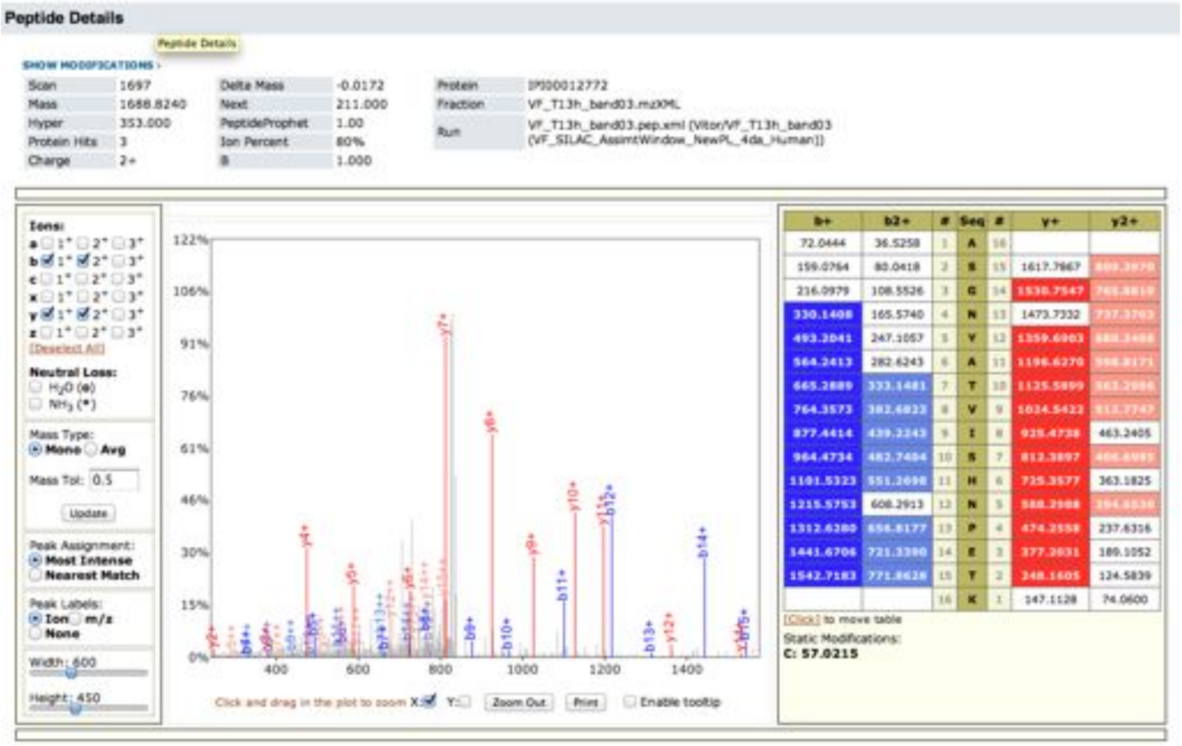
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	21		
265.1183	133.0628	2	T	20	2407.9757	1204.4915
380.1452	190.5763	3	D	19	2306.9280	1153.9676
508.2038	254.6055	4	Q	18	2191.9010	1096.4542
565.2253	283.1163	5	G	17	2063.8425	1032.4249
622.2467	311.6270	6	G	16	2006.8210	1003.9141
751.2893	376.1483	7	E	15	1949.7995	975.4034
880.3319	440.6696	8	E	14	1820.7569	910.8821
1009.3745	505.1909	9	E	13	1691.7143	846.3608
1138.4171	569.7122	10	E	12	1562.6718	781.8395
1253.4440	627.2257	11	D	11	1433.6292	717.3182
1416.5074	708.7573	12	Y	10	1318.6022	659.8047
1545.5500	773.2786	13	E	9	1155.5389	578.2731
1632.5820	816.7946	14	S	8	1026.4963	513.7518
1761.6246	881.3159	15	E	7	939.4643	470.2358
1890.6672	945.8372	16	E	6	810.4217	405.7145
2018.7258	1009.8665	17	Q	5	681.3701	341.1932
2131.8098	1066.4086	18	L	4	553.3205	277.1639
2259.8684	1130.4378	19	Q	3	440.2364	220.6219
2396.9273	1198.9673	20	H	2	312.1779	156.5926
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9672	IPI00909884, IPI00012772, IPI00797230	1	1	-, RPL8, RPL8	2+	1697	-0,0172	0,9982	R.ASGNYATVISHNPETK.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	1697	Delta Mass	-0.0172	Protein	IPI00012772
Mass	1688.8240	Next	211.000	Fraction	VF_T13h_band03.mzXML
Hyper	353.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

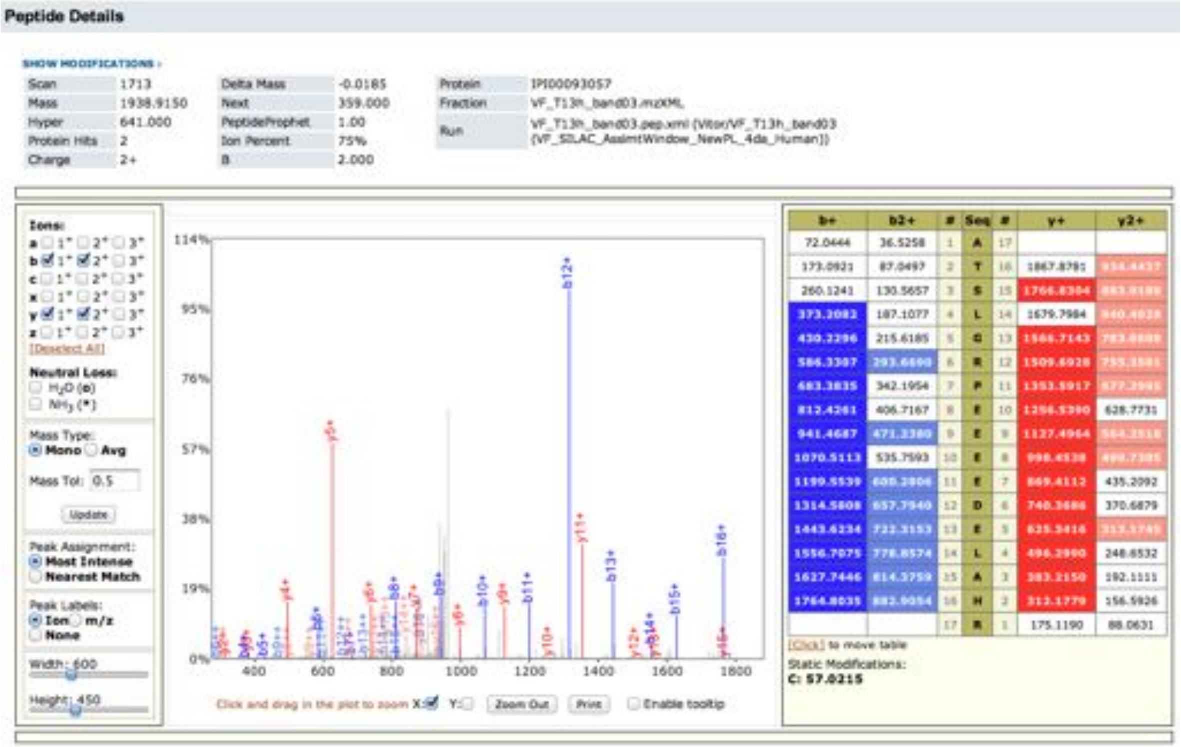
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	16		
159.0764	80.0418	2	S	15	1617.7867	809.3970
216.0979	108.5526	3	G	14	1530.7547	765.8810
330.1408	165.5740	4	N	13	1473.7332	737.3703
493.2041	247.1057	5	Y	12	1359.6903	680.3488
564.2413	282.6243	6	A	11	1196.6270	598.8171
665.2889	333.1481	7	T	10	1125.5899	563.2986
764.3573	382.6823	8	V	9	1024.5422	512.7747
877.4414	439.2243	9	I	8	925.4738	463.2405
964.4734	482.7404	10	S	7	812.3897	406.6985
1101.5323	551.2698	11	H	6	725.3577	363.1825
1215.5753	608.2913	12	N	5	588.2988	294.6530
1312.6280	656.8177	13	P	4	474.2558	237.6316
1441.6706	721.3390	14	E	3	377.2031	189.1052
1542.7183	771.8628	15	T	2	248.1605	124.5839
		16	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00794067, IPI00093057	1	1	CPOX, CPOX	1713	2+	-0,0185	0,9999	R.ATSLGRPEEEEEDELAHR.C



Peptide Details

SHOW MODIFICATIONS ›

Scan	1713	Delta Mass	-0.0185	Protein	IPI00093057
Mass	1938.9150	Next	359.000	Fraction	VF_T13h_band03.mzXML
Hyper	641.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	2.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	17		
173.0921	87.0497	2	T	16	1867.8791	934.4427
260.1241	130.5657	3	S	15	1766.8304	883.9188
373.2082	187.1077	4	L	14	1679.7984	840.4028
430.2296	215.6185	5	G	13	1566.7143	783.8608
586.3307	293.6690	6	R	12	1509.6928	755.3501
683.3835	342.1954	7	P	11	1353.5917	677.2995
812.4261	406.7167	8	E	10	1256.5390	628.7731
941.4687	471.2380	9	E	9	1127.4964	564.2518
1070.5113	535.7593	10	E	8	998.4538	499.7305
1199.5539	600.2806	11	E	7	869.4112	435.2092
1314.5808	657.7940	12	D	6	740.3686	370.6879
1443.6234	722.3153	13	E	5	625.3416	313.1745
1556.7075	778.8574	14	L	4	496.2990	248.6532
1627.7446	814.3759	15	A	3	383.2150	192.1111
1764.8035	882.9054	16	H	2	312.1779	156.5926
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8713	IPI00643765, IPI00886965, IPI00888198, IPI00410496, IPI00550900, IPI00009943, IPI00014402	1	1	TPT1, LOC389787, LOC389787, FLJ44635, TPT1, TPT1, HUWE1	1767	2+	-0,0137	0,9913	R.VK'PFM"TGAAEQIK'.H

Peptide Details

SHOW MODIFICATIONS ›

Scan	1767	Delta Mass	-0.0137	Protein	IPI00009943
Mass	1447.8020	Next	270.000	Fraction	VF_T13h_band04.mzXML
Hyper	367.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

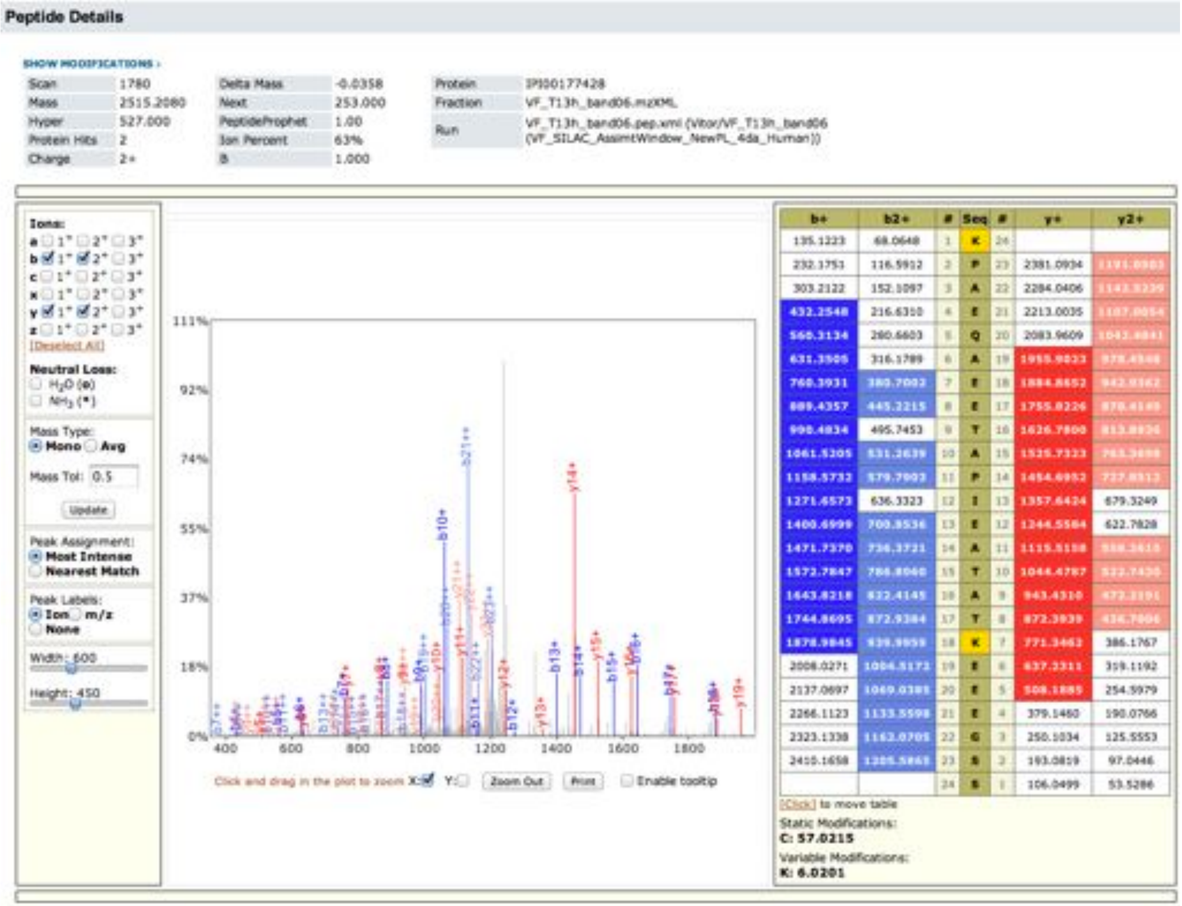
b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	13		
234.1908	117.5990	2	K	12	1348.7331	674.8702
331.2435	166.1254	3	P	11	1214.6181	607.8127
478.3119	239.6596	4	F	10	1117.5653	559.2863
625.3473	313.1773	5	M	9	970.4969	485.7521
726.3950	363.7011	6	T	8	823.4615	412.2344
783.4165	392.2119	7	G	7	722.4138	361.7106
854.4536	427.7304	8	A	6	665.3924	333.1998
925.4907	463.2490	9	A	5	594.3553	297.6813
1054.5333	527.7703	10	E	4	523.3181	262.1627
1182.5919	591.7996	11	Q	3	394.2755	197.6414
1295.6759	648.3416	12	I	2	266.2170	133.6121
		13	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9743	IPI00748354, IPI00177428	1	1	CHCHD4, CHCHD4	1780	2+	-0,0358	0,9986	K.K'PAEQAEETAPIEATATK'EEEGSS.-



Scan	1780	Delta Mass	-0.0358	Protein	IPI00177428
Mass	2515.2080	Next	253.000	Fraction	VF_T13h_band06.mzXML
Hyper	527.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	63%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
135.1223	68.0648	1	K	24		
232.1751	116.5912	2	P	23	2381.0934	1191.0503
303.2122	152.1097	3	A	22	2284.0406	1142.5239
432.2548	216.6310	4	E	21	2213.0035	1107.0054
560.3134	280.6603	5	Q	20	2083.9609	1042.4841
631.3505	316.1789	6	A	19	1955.9023	978.4548
760.3931	380.7002	7	E	18	1884.8652	942.9362
889.4357	445.2215	8	E	17	1755.8226	878.4149
990.4834	495.7453	9	T	16	1626.7800	813.8936
1061.5205	531.2639	10	A	15	1525.7323	763.3698
1158.5732	579.7903	11	P	14	1454.6952	727.8513
1271.6573	636.3323	12	I	13	1357.6424	679.3249
1400.6999	700.8536	13	E	12	1244.5584	622.7828
1471.7370	736.3721	14	A	11	1115.5158	558.2615
1572.7847	786.8960	15	T	10	1044.4787	522.7430
1643.8218	822.4145	16	A	9	943.4310	472.2191
1744.8695	872.9384	17	T	8	872.3939	436.7006
1878.9845	939.9959	18	K	7	771.3463	386.1767
2008.0271	1004.5173	19	E	6	637.2311	319.1192
2137.0697	1069.0385	20	E	5	508.1885	254.5979
2266.1123	1133.5598	21	E	4	379.1460	190.0766
2323.1338	1162.0705	22	G	3	250.1034	125.5553
2410.1658	1205.5865	23	S	2	193.0819	97.0446
		24	S	1	106.0499	53.5286

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9792	IPI00329321, IPI00873110	1	1	LYRM7, LYRM7	1798	2+	-0,0195	0,9993	R.TSVIQGIHTDHNTLK'.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	1798	Delta Mass	-0.0195	Protein	IPI00329321
Mass	1669.8960	Next	219.000	Fraction	VF_T13h_band05.mzXML
Hyper	378.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml [Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human)]
Protein Hits	2	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

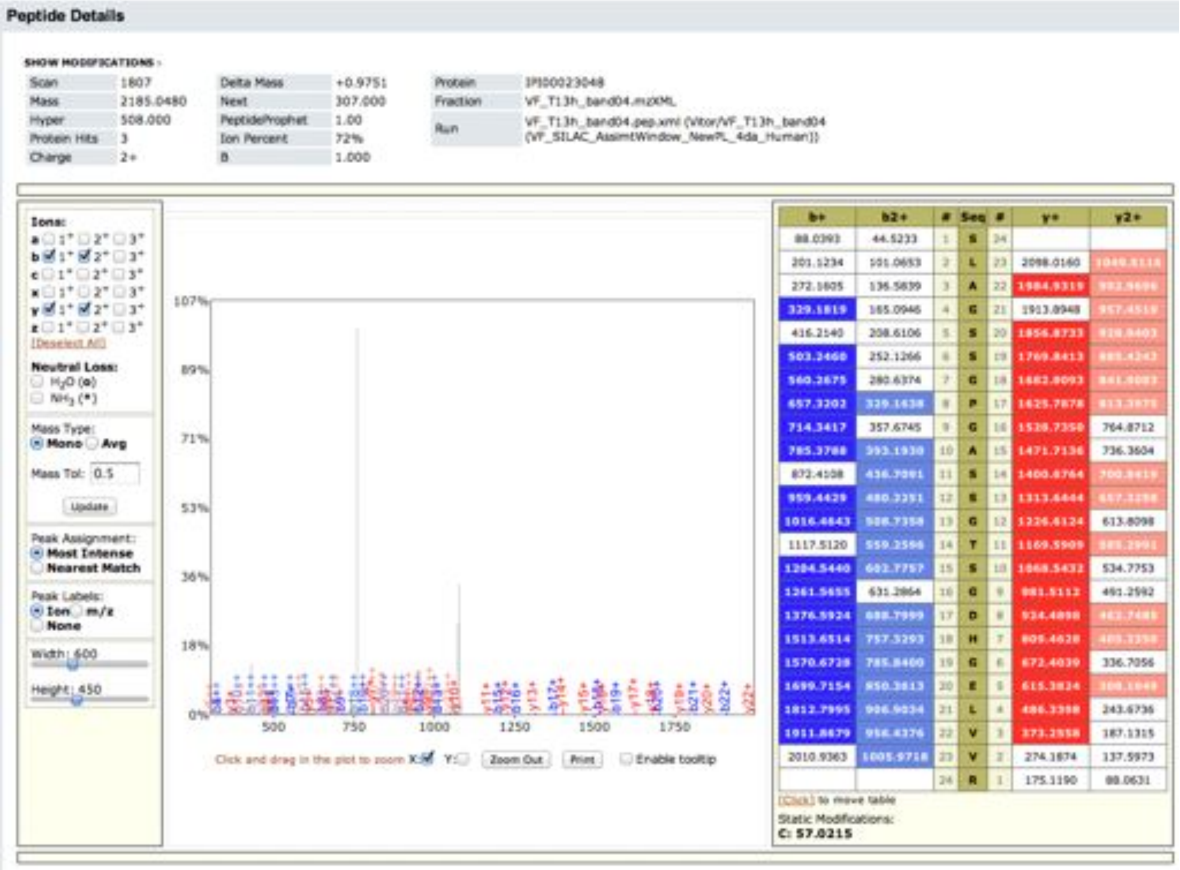
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	15		
189.0870	95.0471	2	S	14	1568.8486	784.9280
288.1554	144.5813	3	V	13	1481.8166	741.4119
401.2395	201.1234	4	I	12	1382.7482	691.8777
529.2980	265.1527	5	Q	11	1269.6641	635.3357
586.3195	293.6634	6	G	10	1141.6055	571.3064
699.4036	350.2054	7	I	9	1084.5841	542.7957
836.4625	418.7349	8	H	8	971.5000	486.2536
937.5102	469.2587	9	T	7	834.4411	417.7242
1052.5371	526.7722	10	D	6	733.3934	367.2004
1189.5960	595.3016	11	H	5	618.3665	309.6869
1303.6389	652.3231	12	N	4	481.3076	241.1574
1404.6866	702.8469	13	T	3	367.2646	184.1360
1517.7707	759.3890	14	L	2	266.2170	133.6121
		15	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9362	IPI00023048, IPI00789435, IPI00642971	1	1	EEF1D, EEF1D, EEF1D	1807	2+	+0,9751	0,9965	K.SLAGSSGPGASSGTSGDHGELVVR.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	1807	Delta Mass	+0.9751	Protein	IPI00023048
Mass	2185.0480	Next	307.000	Fraction	VF_T13h_band04.mzXML
Hyper	508.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	72%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

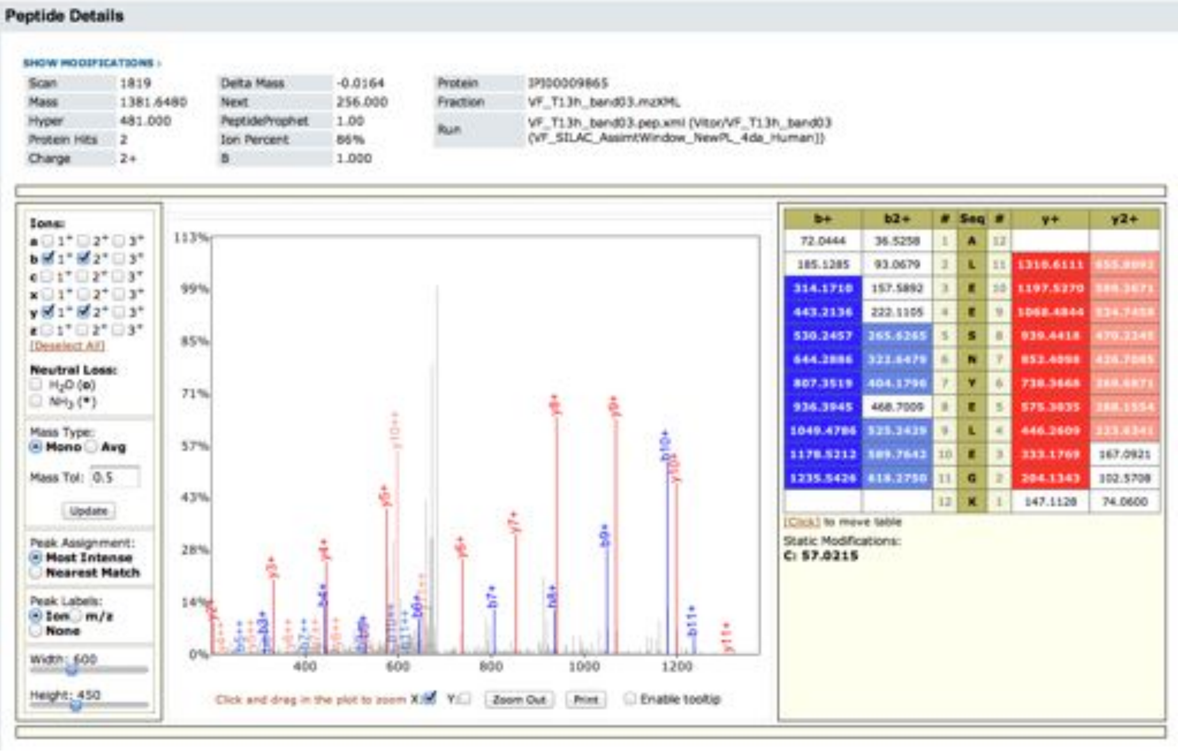
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	24		
201.1234	101.0653	2	L	23	2098.0160	1049.5114
272.1605	136.5839	3	A	22	1984.9319	992.9696
329.1819	165.0946	4	G	21	1913.8948	957.4519
416.2140	208.6106	5	S	20	1856.8733	928.9403
503.2460	252.1266	6	S	19	1769.8413	885.4243
560.2675	280.6374	7	G	18	1682.8093	841.9083
657.3202	329.1638	8	P	17	1625.7878	813.3975
714.3417	357.6745	9	G	16	1528.7350	764.8712
785.3788	393.1930	10	A	15	1471.7136	736.3604
872.4108	436.7091	11	S	14	1400.6764	700.8419
959.4429	480.2251	12	S	13	1313.6444	657.3258
1016.4643	508.7358	13	G	12	1226.6124	613.8098
1117.5120	559.2596	14	T	11	1169.5909	585.2991
1204.5440	602.7757	15	S	10	1068.5432	534.7753
1261.5655	631.2864	16	G	9	981.5112	491.2592
1376.5924	688.7999	17	D	8	924.4898	462.7485
1513.6514	757.3293	18	H	7	809.4628	405.2350
1570.6728	785.8400	19	G	6	672.4039	336.7056
1699.7154	850.3613	20	E	5	615.3824	308.1948
1812.7995	906.9034	21	L	4	486.3398	243.6736
1911.8679	956.4376	22	V	3	373.2558	187.1315
2010.9363	1005.9718	23	V	2	274.1874	137.5973
		24	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9857	IPI00884222, IPI00009865	1	1	KRT10, KRT10	1819	2+	-0,0164	0,9998	R.ALEESNYELEGK.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	1819	Delta Mass	-0.0164	Protein	IPI00009865
Mass	1381.6480	Next	256.000	Fraction	VF_T13h_band03.mzXML
Hyper	481.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

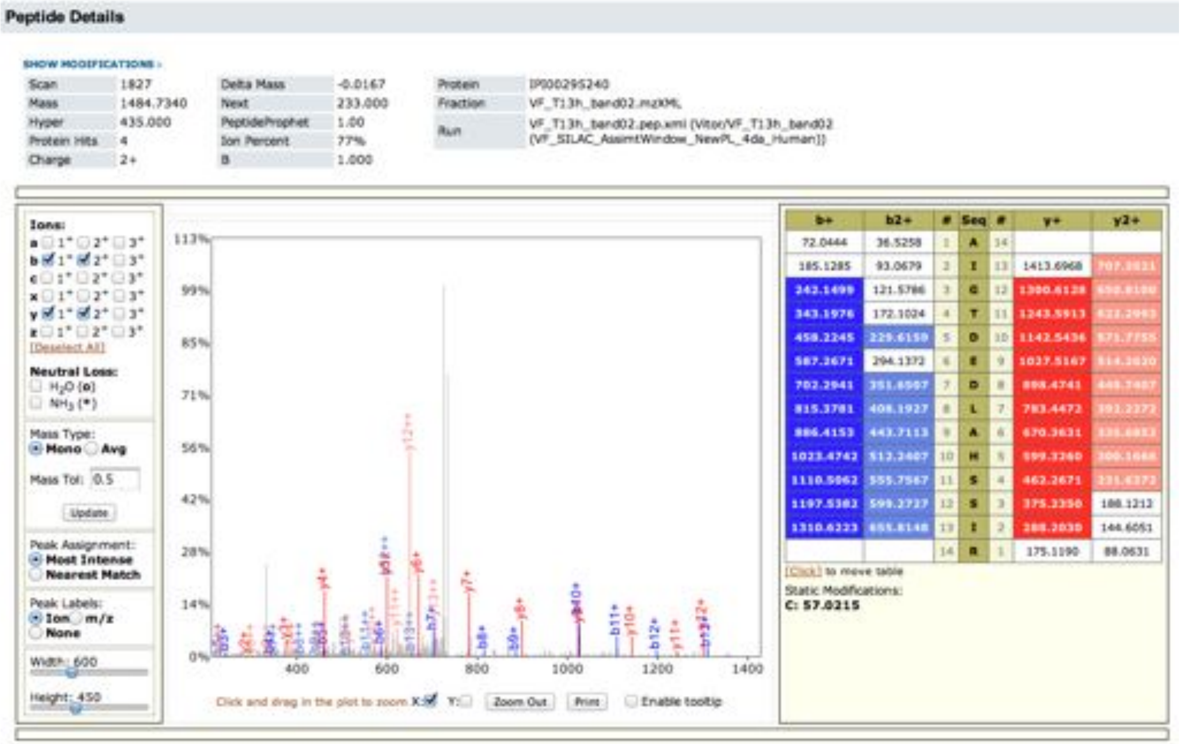
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
185.1285	93.0679	2	L	11	1310.6111	655.8092
314.1710	157.5892	3	E	10	1197.5270	599.2671
443.2136	222.1105	4	E	9	1068.4844	534.7458
530.2457	265.6265	5	S	8	939.4418	470.2245
644.2886	322.6479	6	N	7	852.4098	426.7085
807.3519	404.1796	7	Y	6	738.3668	369.6871
936.3945	468.7009	8	E	5	575.3035	288.1554
1049.4786	525.2429	9	L	4	446.2609	223.6341
1178.5212	589.7642	10	E	3	333.1769	167.0921
1235.5426	618.2750	11	G	2	204.1343	102.5708
		12	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9765	IPI00894086, IPI00892745, IPI00643101, IPI00295240	1	1	CPNE1, CPNE1, NFS1, NFS1	1827	2+	-0,0167	0,9997	R.AIGTDEDLAHSSIR.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	1827	Delta Mass	-0.0167	Protein	IPI00295240
Mass	1484.7340	Next	233.000	Fraction	VF_T13h_band02.mzXML
Hyper	435.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	14		
185.1285	93.0679	2	I	13	1413.6968	707.3521
242.1499	121.5786	3	G	12	1300.6128	650.8100
343.1976	172.1024	4	T	11	1243.5913	622.2993
458.2245	229.6159	5	D	10	1142.5436	571.7755
587.2671	294.1372	6	E	9	1027.5167	514.2620
702.2941	351.6507	7	D	8	898.4741	449.7407
815.3781	408.1927	8	L	7	783.4472	392.2272
886.4153	443.7113	9	A	6	670.3631	335.6853
1023.4742	512.2407	10	H	5	599.3260	300.1666
1110.5062	555.7567	11	S	4	462.2671	231.6372
1197.5382	599.2727	12	S	3	375.2350	188.1212
1310.6223	655.8148	13	I	2	288.2030	144.6051
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9255	IPI00744902, IPI00024670	1	1	DP1, REEP5	1849	2+	-0,0170	0,9937	K.KATVNLLGEEK.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	1849	Delta Mass	-0.0170	Protein	IPI00024670
Mass	1201.6790	Next	320.000	Fraction	VF_T13h_band06.mzXML
Hyper	427.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 [VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	2	Ion Percent	90%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	11		
200.1394	100.5733	2	A	10	1073.5837	537.2955
301.1870	151.0972	3	T	9	1002.5466	501.7769
400.2554	200.6314	4	V	8	901.4989	451.2531
514.2984	257.6528	5	N	7	802.4305	401.7189
627.3824	314.1949	6	L	6	688.3876	344.6974
740.4665	370.7369	7	L	5	575.3035	288.1554
797.4880	399.2476	8	G	4	462.2195	231.6134
926.5306	463.7689	9	E	3	405.1980	203.1026
1055.5732	528.2902	10	E	2	276.1554	138.5813
		11	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9840	IPI00301364	1	1	SKP1A	1865	2+	-0,0169	0,9997	K.NDFTEEEEAQVR.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	1865	Delta Mass	-0.0169	Protein	IPI00301364
Mass	1466.6390	Next	263.000	Fraction	VF_T13h_band05.mzXML
Hyper	445.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	12		
230.0771	115.5422	2	D	11	1352.5965	676.8019
377.1456	189.0764	3	F	10	1237.5695	619.2884
478.1932	239.6003	4	T	9	1090.5011	545.7542
607.2358	304.1216	5	E	8	989.4534	495.2304
736.2784	368.6429	6	E	7	860.4108	430.7091
865.3210	433.1641	7	E	6	731.3682	366.1878
994.3636	497.6854	8	E	5	602.3257	301.6665
1065.4007	533.2040	9	A	4	473.2831	237.1452
1193.4593	597.2333	10	Q	3	402.2459	201.6266
1292.5277	646.7675	11	V	2	274.1874	137.5973
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐

☐ Enable tooltip

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8635	IPI00414696, IPI00396378, IPI00874030	1	1	HNRNPA2B1, HNRPA2B1, HNRNPA2B1	1920	2+	-0,0136	0,9925	R.GGGGNFGPGPGSNFR.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	1920	Delta Mass	-0.0136	Protein	IPI00396378
Mass	1377.6290	Next	283.000	Fraction	VF_T13h_band02.mzXML
Hyper	387.000	PeptideProphet	0.99	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	61%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

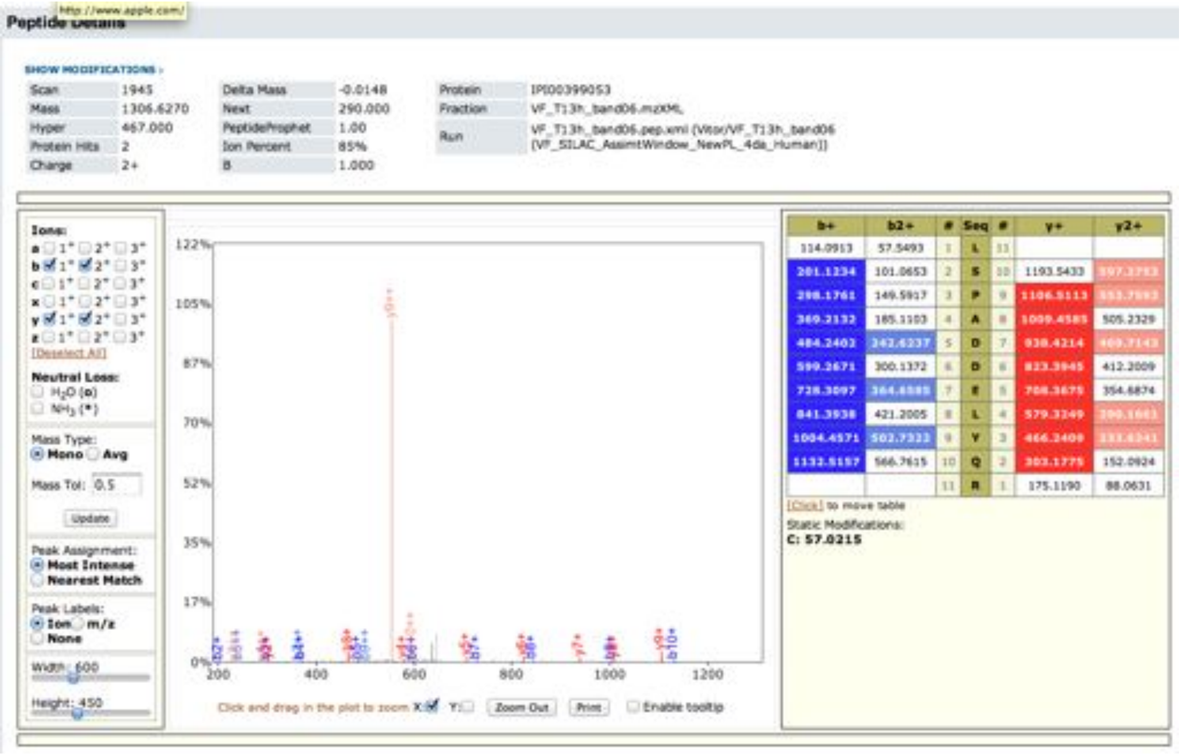
☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	15		
115.0502	58.0287	2	G	14	1320.6080	660.8076
172.0717	86.5395	3	G	13	1263.5865	632.2969
229.0931	115.0502	4	G	12	1206.5650	603.7863
343.1361	172.0717	5	N	11	1149.5436	575.2754
490.2045	245.6059	6	F	10	1035.5007	518.2540
547.2259	274.1166	7	G	9	888.4322	444.7198
644.2787	322.6430	8	P	8	831.4108	416.2090
701.3002	351.1537	9	G	7	734.3580	367.6826
798.3529	399.6801	10	P	6	677.3365	339.1719
855.3744	428.1908	11	G	5	580.2838	290.6455
942.4064	471.7068	12	S	4	523.2623	262.1348
1056.4493	528.7283	13	N	3	436.2303	218.6188
1203.5178	602.2625	14	F	2	322.1874	161.5973
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9796	IPI00797958, IPI00399053	1	1	C3orf60, C3orf60	1945	2+	-0,0148	0,9991	R.LSPADDELYQR.T



Scan	1945	Delta Mass	-0.0148	Protein	IPI00399053
Mass	1306.6270	Next	290.000	Fraction	VF_T13h_band06.mzXML
Hyper	467.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

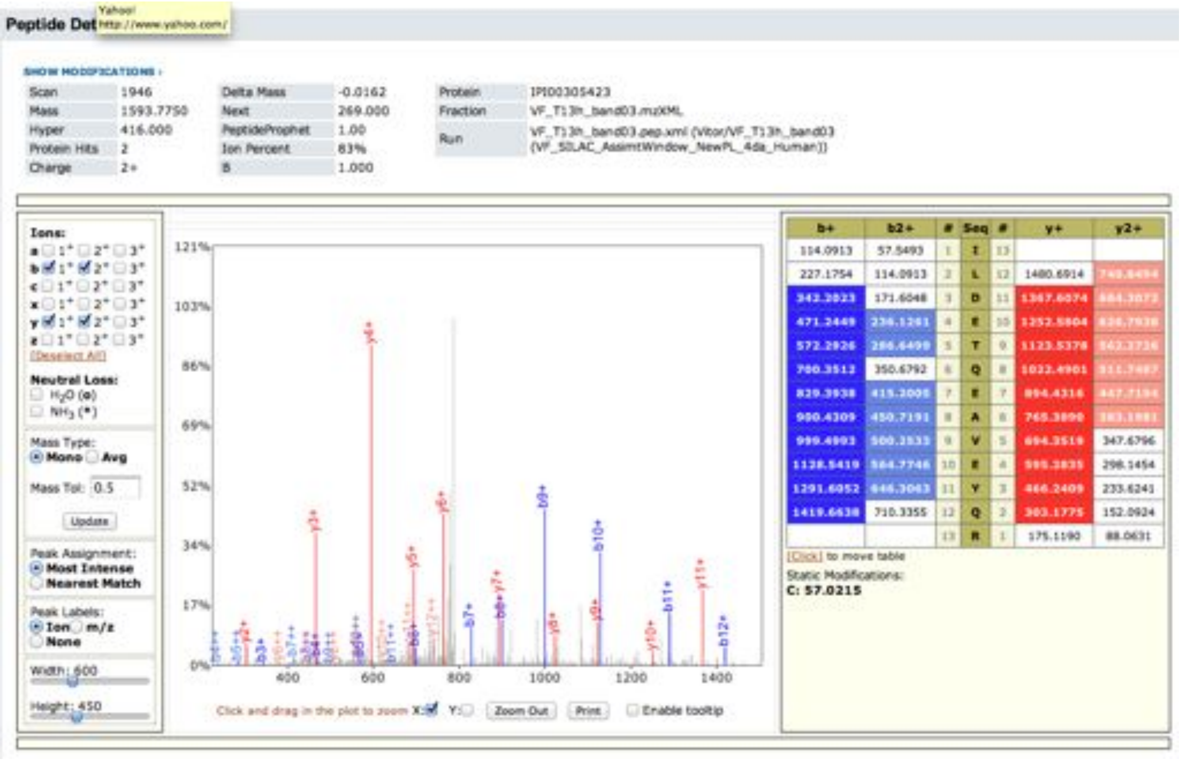
Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	11		
201.1234	101.0653	2	S	10	1193.5433	597.2753
298.1761	149.5917	3	P	9	1106.5113	553.7593
369.2132	185.1103	4	A	8	1009.4585	505.2329
484.2402	242.6237	5	D	7	938.4214	469.7143
599.2671	300.1372	6	D	6	823.3945	412.2009
728.3097	364.6585	7	E	5	708.3675	354.6874
841.3938	421.2005	8	L	4	579.3249	290.1661
1004.4571	502.7322	9	Y	3	466.2409	233.6241
1132.5157	566.7615	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9729	IPI00796868, IPI00305423	1	1	CHMP6, CHMP6	1946	2+	-0,0162	0,9987	R.ILDETQEAVEYQR.Q



Scan	1946	Delta Mass	-0.0162	Protein	IPI00305423
Mass	1593.7750	Next	269.000	Fraction	VF_T13h_band03.mzXML
Hyper	416.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

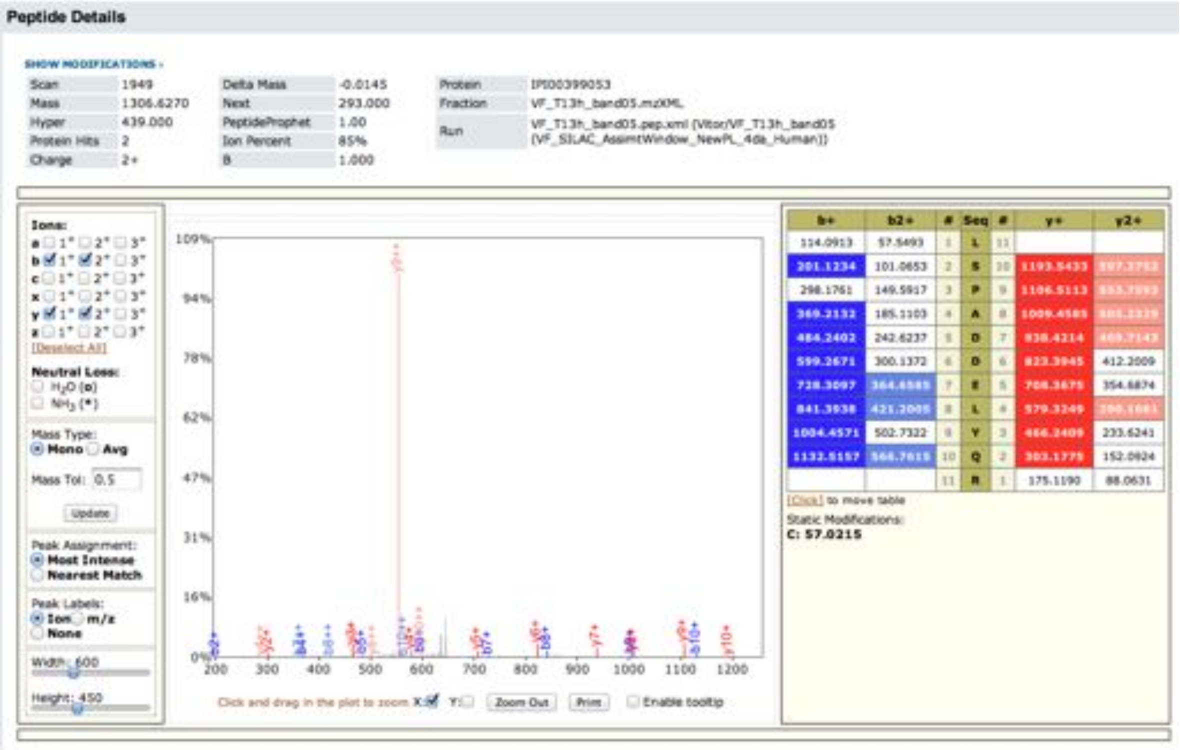
Width: 600
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	13		
227.1754	114.0913	2	L	12	1480.6914	740.8494
342.2023	171.6048	3	D	11	1367.6074	684.3073
471.2449	236.1261	4	E	10	1252.5804	626.7938
572.2926	286.6499	5	T	9	1123.5378	562.2726
700.3512	350.6792	6	Q	8	1022.4901	511.7487
829.3938	415.2005	7	E	7	894.4316	447.7194
900.4309	450.7191	8	A	6	765.3890	383.1981
999.4993	500.2533	9	V	5	694.3519	347.6796
1128.5419	564.7746	10	E	4	595.3835	298.1454
1291.6052	646.3063	11	Y	3	466.2409	233.6241
1419.6638	710.3355	12	Q	2	303.1775	152.0924
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9768	IPI00797958, IPI00399053	1	1	C3orf60, C3orf60	1949	2+	-0,0145	0,9991	R.LSPADDELYQR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	1949	Delta Mass	-0.0145	Protein	IPI00399053
Mass	1306.6270	Next	293.000	Fraction	VF_T13h_band05.mzXML
Hyper	439.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

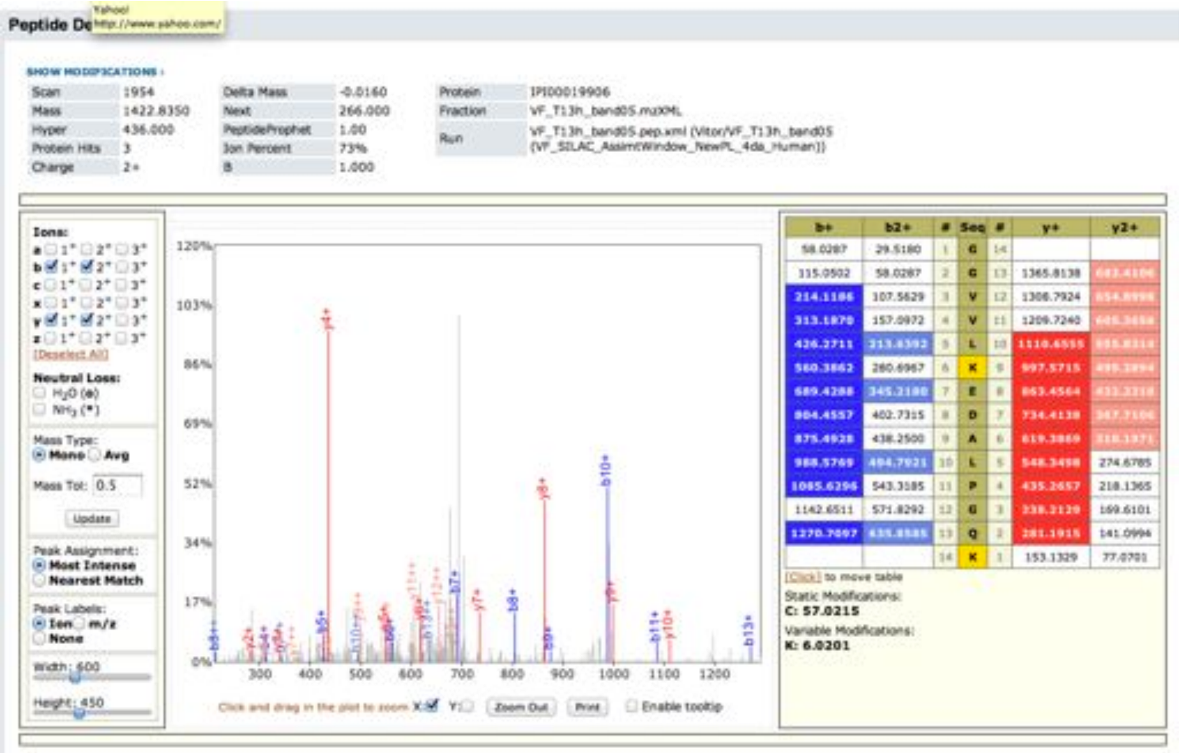
Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	11		
201.1234	101.0653	2	S	10	1193.5433	597.2752
298.1761	149.5917	3	P	9	1106.5113	553.7593
369.2132	185.1103	4	A	8	1009.4585	505.2329
484.2402	242.6237	5	D	7	938.4214	469.7143
599.2671	300.1372	6	D	6	823.3945	412.2009
728.3097	364.6585	7	E	5	708.3675	354.6874
841.3938	421.2005	8	L	4	579.3249	290.1661
1004.4571	502.7322	9	Y	3	466.2409	233.6241
1132.5157	566.7615	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	**Protein**	**Tot. Peptides**	**Unique Peptides**	**Best Gene Name**	**Scan #**	**Charge**	**Delta Mass**	**Peptide Prophet Score**	**Peptide Sequence**
0,9433	IPI00908477, IPI00019906, IPI00218019	1	1	-, hEMMPRIN, BSG	1954	2+	-0,0160	0,9962	K.GGVVLK'EDALPGQK'.T



Peptide De

Yahoo!
http://www.yahoo.com/

SHOW MODIFICATIONS ›

Scan	1954	Delta Mass	-0.0160	Protein	IPI00019906
Mass	1422.8350	Next	266.000	Fraction	VF_T13h_band05.mzXML
Hyper	436.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	73%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	14		
115.0502	58.0287	2	G	13	1365.8138	683.4106
214.1186	107.5629	3	V	12	1308.7924	654.8998
313.1870	157.0972	4	V	11	1209.7240	605.3658
426.2711	213.6392	5	L	10	1110.6555	555.8314
560.3862	280.6967	6	K	9	997.5715	499.2894
689.4288	345.2180	7	E	8	863.4564	432.2318
804.4557	402.7315	8	D	7	734.4138	367.7106
875.4928	438.2500	9	A	6	619.3869	310.1971
988.5769	494.7921	10	L	5	548.3498	274.6785
1085.6296	543.3185	11	P	4	435.2657	218.1365
1142.6511	571.8292	12	G	3	338.2129	169.6101
1270.7097	635.8585	13	Q	2	281.1915	141.0994
		14	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8607	IPI00853215, IPI00027430	1	1	SPN, SPN	1982	2+	-0,0149	0,9923	R.TSGAPVTTAASSLETSR.G


Peptide Details

SHOW MODIFICATIONS ›

Scan	1982	Delta Mass	-0.0149	Protein	IPI00027430
Mass	1635.8180	Next	234.000	Fraction	VF_T13h_band02.mzXML
Hyper	344.000	PeptideProphet	0.99	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	66%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

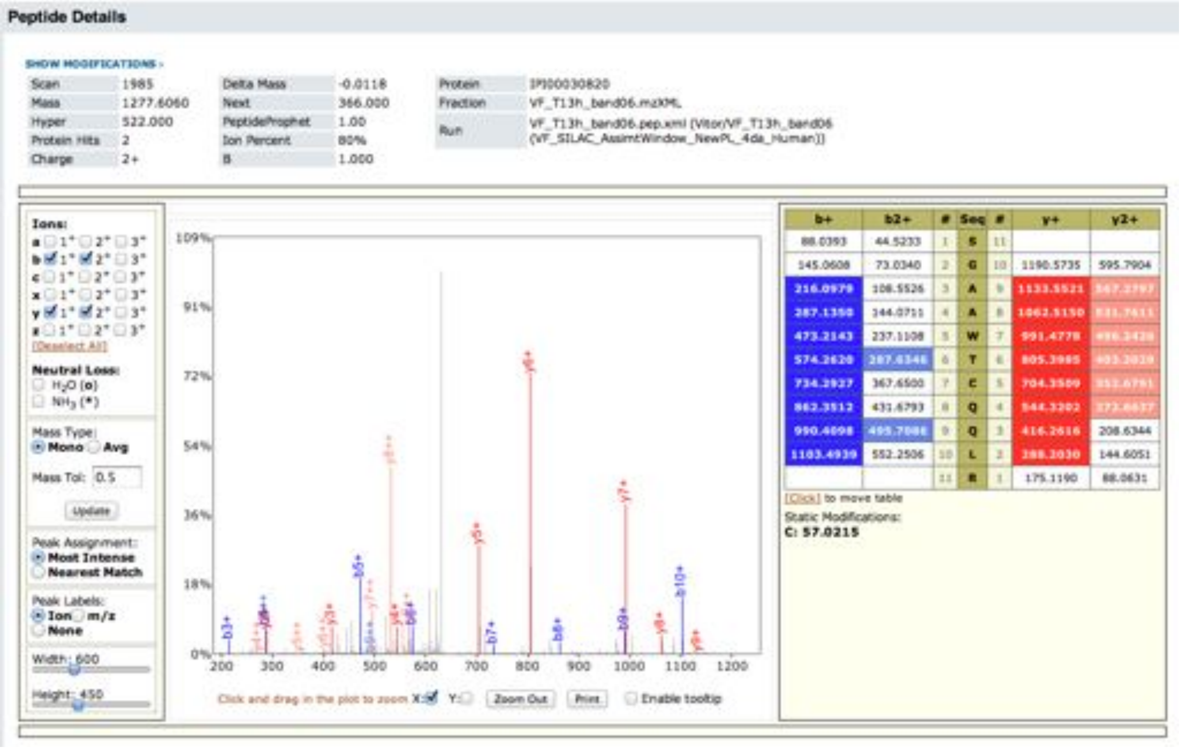
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	17		
189.0870	95.0471	2	S	16	1534.7707	767.8890
246.1084	123.5579	3	G	15	1447.7387	724.3730
317.1456	159.0764	4	A	14	1390.7172	695.8623
414.1983	207.6028	5	P	13	1319.6801	660.3437
513.2667	257.1370	6	V	12	1222.6274	611.8173
614.3144	307.6608	7	T	11	1123.5590	562.2831
715.3621	358.1847	8	T	10	1022.5113	511.7593
786.3992	393.7032	9	A	9	921.4636	461.2354
857.4363	429.2218	10	A	8	850.4265	425.7169
944.4684	472.7378	11	S	7	779.3894	390.1983
1031.5004	516.2538	12	S	6	692.3573	346.6823
1144.5844	572.7959	13	L	5	605.3253	303.1663
1273.6270	637.3172	14	E	4	492.2413	246.6243
1374.6747	687.8410	15	T	3	363.1987	182.1030
1461.7067	731.3570	16	S	2	262.1510	131.5791
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9764	IPI00794978, IPI00030820	1	1	MRPL47, MRPL47	1985	2+	-0,0118	0,9988	K.SGAAWTCQQLR.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	1985	Delta Mass	-0.0118	Protein	IPI00030820
Mass	1277.6060	Next	366.000	Fraction	VF_T13h_band06.mzXML
Hyper	522.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	80%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	11		
145.0608	73.0340	2	G	10	1190.5735	595.7904
216.0979	108.5526	3	A	9	1133.5521	567.2797
287.1350	144.0711	4	A	8	1062.5150	531.7611
473.2143	237.1108	5	W	7	991.4778	496.2426
574.2620	287.6346	6	T	6	805.3985	403.2029
734.2927	367.6500	7	C	5	704.3509	352.6791
862.3512	431.6793	8	Q	4	544.3202	272.6637
990.4098	495.7086	9	Q	3	416.2616	208.6344
1103.4939	552.2506	10	L	2	288.2030	144.6051
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9174	IPI00382804, IPI00556204, IPI00025447, IPI00396485, IPI00472724, IPI00014424	1	1	EEF1A, EEF1A2, EEF1A1, EEF1A1, EEF1AL3, EEF1A2	1987	2+	-0,0118	0,9959	K.IGGIGTVPVGR.V

Peptide Details

Scan	1987	Delta Mass	-0.0118	Protein	IPI00014424
Mass	1025.6100	Next	383.000	Fraction	VF_T13h_band01.mzXML
Hyper	484.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	95%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

☑ X ☐ Y

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	11		
171.1128	86.0600	2	G	10	912.5261	456.7667
228.1343	114.5708	3	G	9	855.5047	428.2560
341.2183	171.1128	4	I	8	798.4832	399.7452
398.2398	199.6235	5	G	7	685.3991	343.2032
499.2875	250.1474	6	T	6	628.3777	314.6925
598.3559	299.6816	7	V	5	527.3300	264.1686
695.4087	348.2080	8	P	4	428.2616	214.6344
794.4771	397.7422	9	V	3	331.2088	166.1081
851.4985	426.2529	10	G	2	232.1404	116.5738
		11	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9718	IPI00402184, IPI00910614, IPI00856037, IPI00402183, IPI00402182, IPI00018140, IPI00012074, IPI00644055	1	1	SYNCRIP, HNRNPR, HNRNPR, RP1-3J17.2, SYNCRIP, SYNCRIP, HNRPR, HNRPR	1995	2+	-0,0182	0,9986	R.TGYTLDVTTGQR.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	1995	Delta Mass	-0.0182	Protein	IPI00012074
Mass	1311.6540	Next	291.000	Fraction	VF_T13h_band03.mzXML
Hyper	433.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	8	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	12		
159.0764	80.0418	2	G	11	1210.6062	605.8068
322.1397	161.5735	3	Y	10	1153.5848	577.2960
423.1874	212.0974	4	T	9	990.5214	495.7644
536.2715	268.6394	5	L	8	889.4738	445.2405
651.2984	326.1529	6	D	7	776.3897	388.6985
750.3668	375.6871	7	V	6	661.3628	331.1850
851.4145	426.2109	8	T	5	562.2944	281.6509
952.4622	476.7347	9	T	4	461.2467	231.1270
1009.4837	505.2455	10	G	3	360.1990	180.6031
1137.5422	569.2748	11	Q	2	303.1775	152.0924
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9234	IPI00217465, IPI00217467, IPI00217466	1	1	HIST1H1C, HIST1H1E, HIST1H1D	2003	2+	+0,9852	0,9963	R.KASGPPVSELITK.A

Peptide Details

Scan	2003	Delta Mass	+0.9852	Protein	IPI00217465
Mass	1326.7630	Next	330.000	Fraction	VF_T13h_band01.mzXML
Hyper	553.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

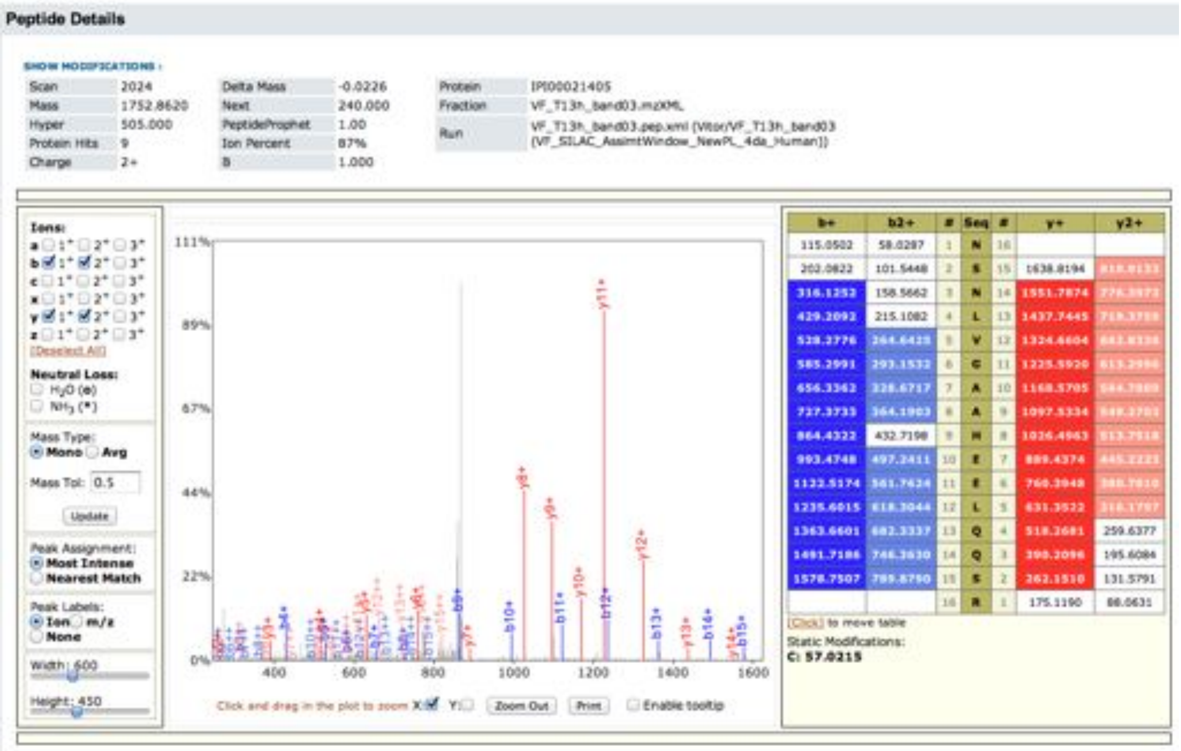
Height: 450

X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.1022	65.0548	1	K	13		
200.1394	100.5733	2	A	12	1198.6678	599.8375
287.1714	144.0893	3	S	11	1127.6307	564.3190
344.1928	172.6001	4	G	10	1040.5986	520.8030
441.2456	221.1264	5	P	9	983.5772	492.2922
538.2984	269.6528	6	P	8	886.5244	443.7658
637.3668	319.1870	7	V	7	789.4716	395.2395
724.3988	362.7030	8	S	6	690.4032	345.7053
853.4414	427.2243	9	E	5	603.3712	302.1892
966.5255	483.7664	10	L	4	474.3286	237.6679
1079.6095	540.3084	11	I	3	361.2445	181.1259
1180.6572	590.8322	12	T	2	248.1605	124.5839
		13	K	1	147.1128	74.0600

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00514204, IPI00655812, IPI00514817, IPI00514320, IPI00216952, IPI00910241, IPI00644087, IPI00216953, IPI00021405	1	1	LMNA, LMNA, LMNA, LMNA, LMNA, -, LMNA, LMNA, LMNA	2024	2+	-0,0226	0,9999	R.NSNLVGAAHEELQQSR.I



Peptide Details

SHOW MODIFICATIONS :

Scan	2024	Delta Mass	-0.0226	Protein	IPI00021405
Mass	1752.8620	Next	240.000	Fraction	VF_T13h_band03.mzXML
Hyper	505.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	9	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

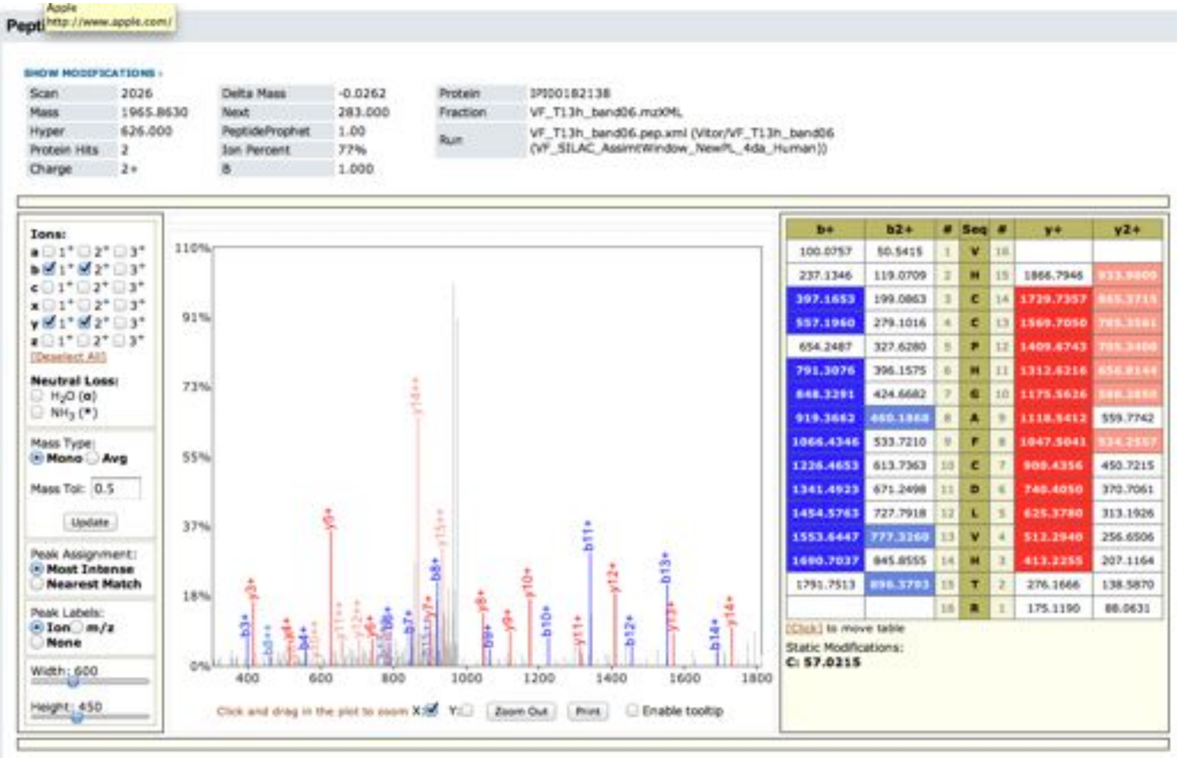
Click and drag in the plot to zoom X ☑ Y ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	16		
202.0822	101.5448	2	S	15	1638.8194	819.9133
316.1252	158.5662	3	N	14	1551.7874	776.3973
429.2092	215.1082	4	L	13	1437.7445	719.3759
528.2776	264.6425	5	V	12	1324.6604	662.8338
585.2991	293.1532	6	G	11	1225.5920	613.2996
656.3362	328.6717	7	A	10	1168.5705	584.7889
727.3733	364.1903	8	A	9	1097.5334	549.2703
864.4322	432.7198	9	H	8	1026.4963	513.7518
993.4748	497.2411	10	E	7	889.4374	445.2223
1122.5174	561.7624	11	E	6	760.3948	380.7010
1235.6015	618.3044	12	L	5	631.3522	316.1797
1363.6601	682.3337	13	Q	4	518.2681	259.6377
1491.7186	746.3630	14	Q	3	390.2096	195.6084
1578.7507	789.8790	15	S	2	262.1510	131.5791
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00182138, IPI00296713	1	1	GRN, GRN	2026	2+	-0,0262	0,9999	R.VHCCPHGAFCDLVHTR.C



Scan	2026	Delta Mass	-0.0262	Protein	IPI00182138
Mass	1965.8630	Next	283.000	Fraction	VF_T13h_band06.mzXML
Hyper	626.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

X: ☑ Y: ☐

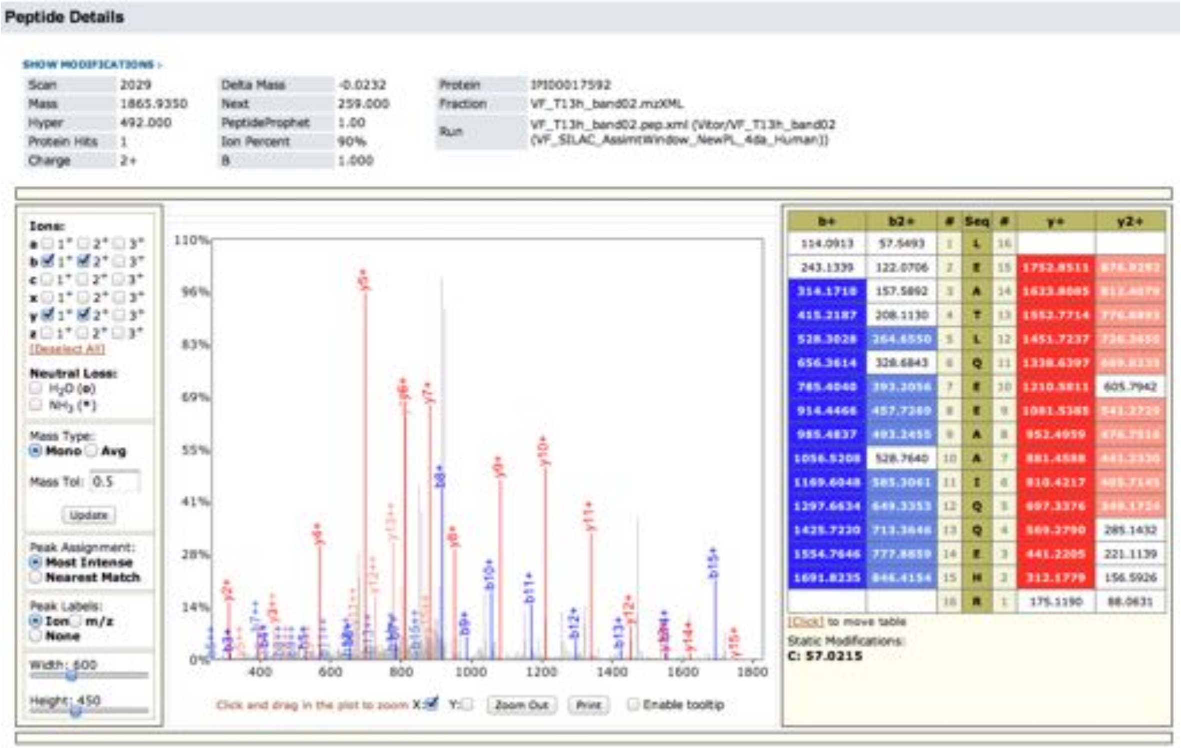
☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	16		
237.1346	119.0709	2	H	15	1866.7946	933.9009
397.1653	199.0863	3	C	14	1729.7357	865.3715
557.1960	279.1016	4	C	13	1569.7050	785.3561
654.2487	327.6280	5	P	12	1409.6743	705.3408
791.3076	396.1575	6	H	11	1312.6216	656.8144
848.3291	424.6682	7	G	10	1175.5626	588.2850
919.3662	460.1868	8	A	9	1118.5412	559.7742
1066.4346	533.7210	9	F	8	1047.5041	524.2557
1226.4653	613.7363	10	C	7	900.4356	450.7215
1341.4923	671.2498	11	D	6	740.4050	370.7061
1454.5763	727.7918	12	L	5	625.3780	313.1926
1553.6447	777.3260	13	V	4	512.2940	256.6506
1690.7037	845.8555	14	H	3	413.2255	207.1164
1791.7513	896.3793	15	T	2	276.1666	138.5870
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00017592	1	1	LETM1	2029	2+	-0,0232	0,9999	K.LEATLQEEAAIQQEHR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	2029	Delta Mass	-0.0232	Protein	IPI00017592
Mass	1865.9350	Next	259.000	Fraction	VF_T13h_band02.mzXML
Hyper	492.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
243.1339	122.0706	2	E	15	1752.8511	876.9292
314.1710	157.5892	3	A	14	1623.8085	812.4079
415.2187	208.1130	4	T	13	1552.7714	776.8893
528.3028	264.6550	5	L	12	1451.7237	726.3655
656.3614	328.6843	6	Q	11	1338.6397	669.8235
785.4040	393.2056	7	E	10	1210.5811	605.7942
914.4466	457.7269	8	E	9	1081.5365	541.2719
985.4837	493.2455	9	A	8	952.4959	476.7516
1056.5208	528.7640	10	A	7	881.4588	441.2330
1169.6048	585.3061	11	I	6	810.4217	405.7145
1297.6634	649.3353	12	Q	5	697.3376	349.1724
1425.7220	713.3646	13	Q	4	569.2790	285.1432
1554.7646	777.8859	14	E	3	441.2205	221.1139
1691.8235	846.4154	15	H	2	312.1779	156.5926
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9578	IPI00217468	1	1	HIST1H1B	2041	2+	-0,0168	0,9985	R.K'ATGPPVSELITK'.A

Peptide Details

Scan	2041	Delta Mass	-0.0168	Protein	IPI00217468
Mass	1352.8190	Next	264.000	Fraction	VF_T13h_band01.mzXML
Hyper	413.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
135.1223	68.0648	1	K	13		
206.1595	103.5834	2	A	12	1218.7035	609.8554
307.2071	154.1072	3	T	11	1147.6664	574.3368
364.2286	182.6179	4	G	10	1046.6187	523.8130
461.2814	231.1443	5	P	9	989.5973	495.3023
558.3341	279.6707	6	P	8	892.5445	446.7759
657.4025	329.2049	7	V	7	795.4917	398.2495
744.4346	372.7209	8	S	6	696.4233	348.7153
873.4772	437.2422	9	E	5	609.3913	305.1993
986.5612	493.7842	10	L	4	480.3487	240.6780
1099.6453	550.3263	11	I	3	367.2646	184.1360
1200.6930	600.8501	12	T	2	254.1806	127.5939
		13	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9785	IPI00026167, IPI00893746	1	1	NHP2L1, NHP2L1	2047	2+	-0,0185	0,9990	K.QQIQSIQQSIER.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	2047	Delta Mass	-0.0185	Protein	IPI00026167
Mass	1457.7710	Next	315.000	Fraction	VF_T13h_band06.mzXML
Hyper	485.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

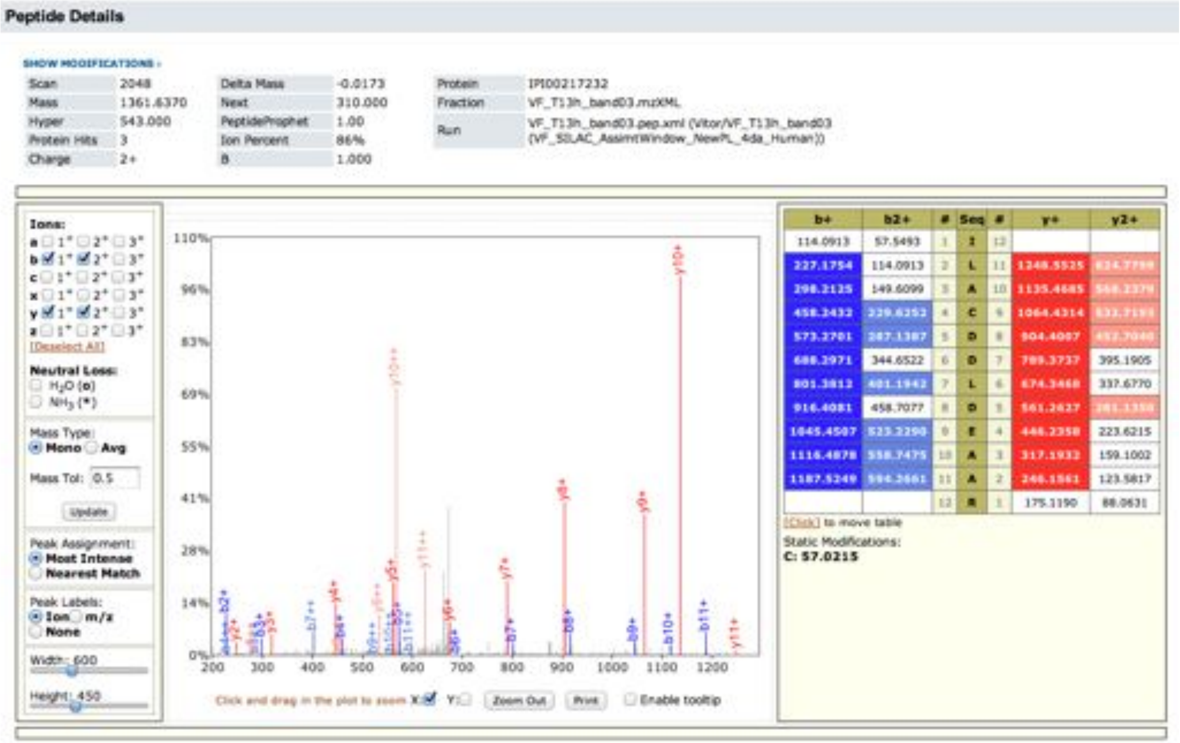
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	12		
257.1244	129.0659	2	Q	11	1329.7121	665.3597
370.2085	185.6079	3	I	10	1201.6535	601.3304
498.2671	249.6372	4	Q	9	1088.5695	544.7884
585.2991	293.1532	5	S	8	960.5109	480.7591
698.3832	349.6952	6	I	7	873.4789	437.2431
826.4417	413.7245	7	Q	6	760.3948	380.7010
954.5003	477.7538	8	Q	5	632.3362	316.6717
1041.5323	521.2698	9	S	4	504.2776	252.6425
1154.6164	577.8118	10	I	3	417.2456	209.1264
1283.6590	642.3331	11	E	2	304.1615	152.5844
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00514217, IPI00217232, IPI00464979	1	1	SUCLA2, SUCLA2, SUCLA2	2048	2+	-0,0173	0,9999	K.ILACDDLDEAAR.M



Peptide Details

SHOW MODIFICATIONS ›

Scan	2048	Delta Mass	-0.0173	Protein	IPI00217232
Mass	1361.6370	Next	310.000	Fraction	VF_T13h_band03.mzXML
Hyper	543.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	12		
227.1754	114.0913	2	L	11	1248.5525	624.7799
298.2125	149.6099	3	A	10	1135.4685	568.2379
458.2432	229.6252	4	C	9	1064.4314	532.7193
573.2701	287.1387	5	D	8	904.4007	452.7040
688.2971	344.6522	6	D	7	789.3737	395.1905
801.3812	401.1942	7	L	6	674.3468	337.6770
916.4081	458.7077	8	D	5	561.2627	281.1350
1045.4507	523.2290	9	E	4	446.2358	223.6215
1116.4878	558.7475	10	A	3	317.1932	159.1002
1187.5249	594.2661	11	A	2	246.1561	123.5817
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9840	IPI00646750, IPI00045660, IPI00552131, IPI00830136	1	1	C1orf31, C1orf31, C1orf31, C1orf31	2061	2+	-0,0131	0,9997	K.FEAGQFEPSETTAK'.S

Peptide Details

Yahoo!
http://www.yahoo.com/

SHOW MODIFICATIONS ›

Scan	2061	Delta Mass	-0.0131	Protein	IPI00045660
Mass	1547.7320	Next	297.000	Fraction	VF_T13h_band05.mzXML
Hyper	482.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	14		
277.1183	139.0628	2	E	13	1400.6635	700.8354
348.1554	174.5813	3	A	12	1271.6209	636.3141
405.1769	203.0921	4	G	11	1200.5838	600.7955
533.2354	267.1214	5	Q	10	1143.5623	572.2848
680.3039	340.6556	6	F	9	1015.5038	508.2555
809.3464	405.1769	7	E	8	868.4354	434.7213
906.3992	453.7032	8	P	7	739.3928	370.2000
993.4312	497.2193	9	S	6	642.3400	321.6736
1122.4738	561.7406	10	E	5	555.3080	278.1576
1223.5215	612.2644	11	T	4	426.2654	213.6363
1324.5692	662.7882	12	T	3	325.2177	163.1125
1395.6063	698.3068	13	A	2	224.1700	112.5886
		14	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9524	IPI00026167, IPI00893746	1	1	NHP2L1, NHP2L1	2062	2+	-0,0146	0,9970	K.QQIQSIQQSIER.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	2062	Delta Mass	-0.0146	Protein	IPI00026167
Mass	1457.7710	Next	265.000	Fraction	VF_T13h_band05.mzXML
Hyper	382.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	91%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

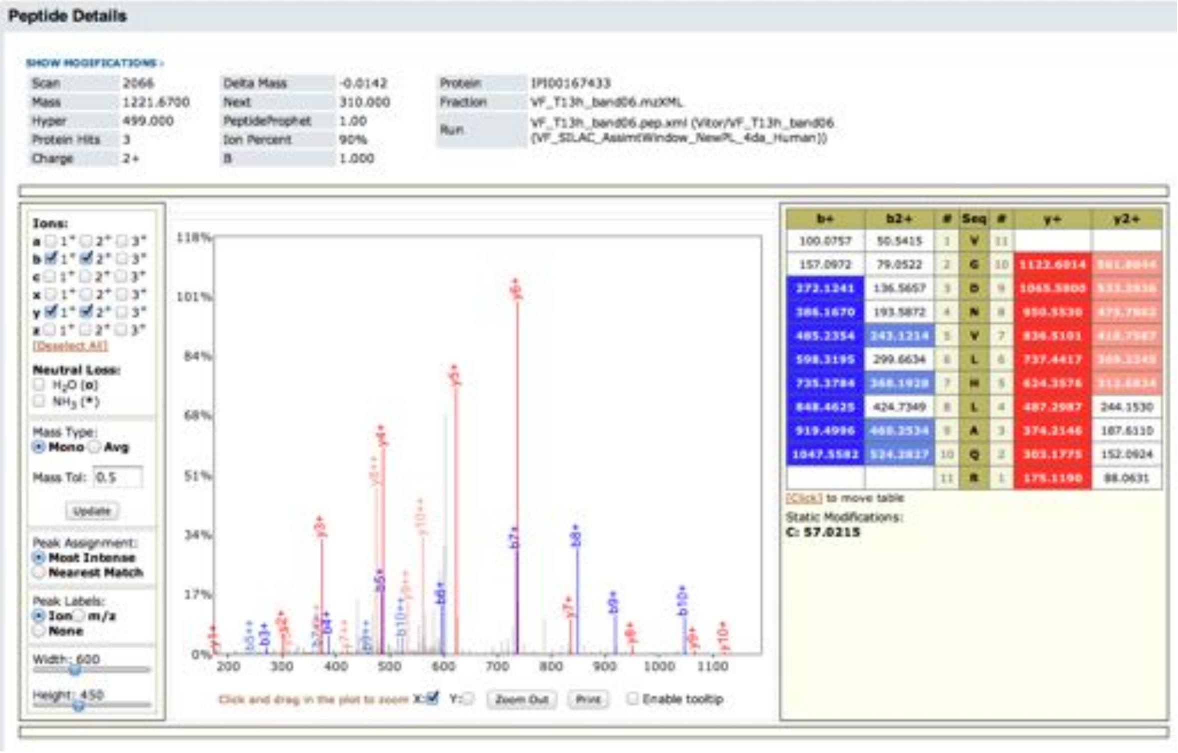
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	12		
257.1244	129.0659	2	Q	11	1329.7121	665.3597
370.2085	185.6079	3	I	10	1201.6535	601.3304
498.2671	249.6372	4	Q	9	1088.5695	544.7884
585.2991	293.1532	5	S	8	960.5109	480.7591
698.3832	349.6952	6	I	7	873.4789	437.2431
826.4417	413.7245	7	Q	6	760.3948	380.7010
954.5003	477.7538	8	Q	5	632.3362	316.6717
1041.5323	521.2698	9	S	4	504.2776	252.6425
1154.6164	577.8118	10	I	3	417.2456	209.1264
1283.6590	642.3331	11	E	2	304.1615	152.5844
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9817	IPI00167433, IPI00894257, IPI00440693	1	1	FDX1L, MGC19604, FDX1L	2066	2+	-0,0142	0,9993	R.VGDNVLHLAQR.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	2066	Delta Mass	-0.0142	Protein	IPI00167433
Mass	1221.6700	Next	310.000	Fraction	VF_T13h_band06.mzXML
Hyper	499.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
157.0972	79.0522	2	G	10	1122.6014	561.8044
272.1241	136.5657	3	D	9	1065.5800	533.2936
386.1670	193.5872	4	N	8	950.5530	475.7802
485.2354	243.1214	5	V	7	836.5101	418.7587
598.3195	299.6634	6	L	6	737.4417	369.2245
735.3784	368.1928	7	H	5	624.3576	312.6824
848.4625	424.7349	8	L	4	487.2987	244.1530
919.4996	460.2534	9	A	3	374.2146	187.6110
1047.5582	524.2827	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9865	IPI00384659, IPI00071334, IPI00555748	1	1	-, ND3, NADH3	2079	2+	-0,0193	0,9999	K.STPYECGFDPM"SPAR.V

Peptide Details

Scan	2079	Delta Mass	-0.0193	Protein	IPI00071334
Mass	1730.7150	Next	387.000	Fraction	VF_T13h_band05.mzXML
Hyper	633.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600
Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

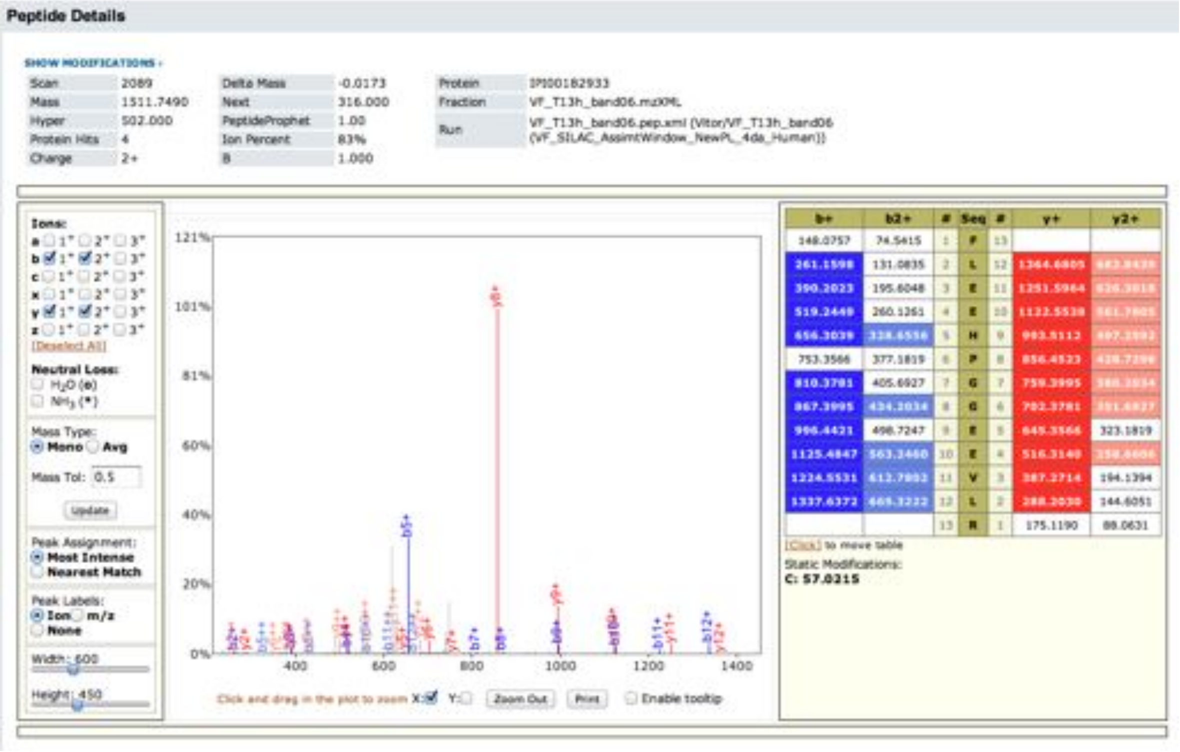
b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	15		
189.0870	95.0471	2	T	14	1643.6829	822.3451
286.1397	143.5735	3	P	13	1542.6352	771.8212
449.2031	225.1052	4	Y	12	1445.5824	723.2969
578.2457	289.6265	5	E	11	1282.5191	641.7633
738.2764	369.6418	6	C	10	1153.4765	577.2419
795.2978	398.1525	7	G	9	993.4458	497.2266
942.3662	471.6868	8	F	8	936.4244	468.7158
1057.3932	529.2002	9	D	7	789.3559	395.1816
1154.4459	577.7266	10	P	6	674.3290	337.6681
1301.4813	651.2443	11	M	5	577.2762	289.1418
1388.5134	694.7603	12	S	4	430.2409	215.6241
1485.5661	743.2867	13	P	3	343.2088	172.1081
1556.6032	778.8053	14	A	2	246.1561	123.5817
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9817	IPI00182933, IPI00871858, IPI00645474, IPI00397860	1	1	CYB5A, CYB5A, CYB5A, CYB5	2089	2+	-0,0173	0,9993	K.FLEEHPGGEEVLR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	2089	Delta Mass	-0.0173	Protein	IPI00182933
Mass	1511.7490	Next	316.000	Fraction	VF_T13h_band06.mzXML
Hyper	502.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	13		
261.1598	131.0835	2	L	12	1364.6805	682.8439
390.2023	195.6048	3	E	11	1251.5964	626.3018
519.2449	260.1261	4	E	10	1122.5538	561.7805
656.3039	328.6556	5	H	9	993.5112	497.2592
753.3566	377.1819	6	P	8	856.4523	428.7298
810.3781	405.6927	7	G	7	759.3995	380.2034
867.3995	434.2034	8	G	6	702.3781	351.6927
996.4421	498.7247	9	E	5	645.3566	323.1819
1125.4847	563.3460	10	E	4	516.3140	258.6606
1224.5531	612.7802	11	V	3	387.2714	194.1394
1337.6372	669.3222	12	L	2	288.2030	144.6051
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9798	IPI00910941, IPI00908389, IPI00747497, IPI00000875	1	1	-, -, EEF1G, EEF1G	2102	2+	-0,0166	0,9993	K.ALIAAQYSGAQVR.V

Peptide Details

SHOW MODIFICATIONS ›

Scan	2102	Delta Mass	-0.0166	Protein	IPI00000875
Mass	1347.7380	Next	260.000	Fraction	VF_T13h_band03.mzXML
Hyper	425.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

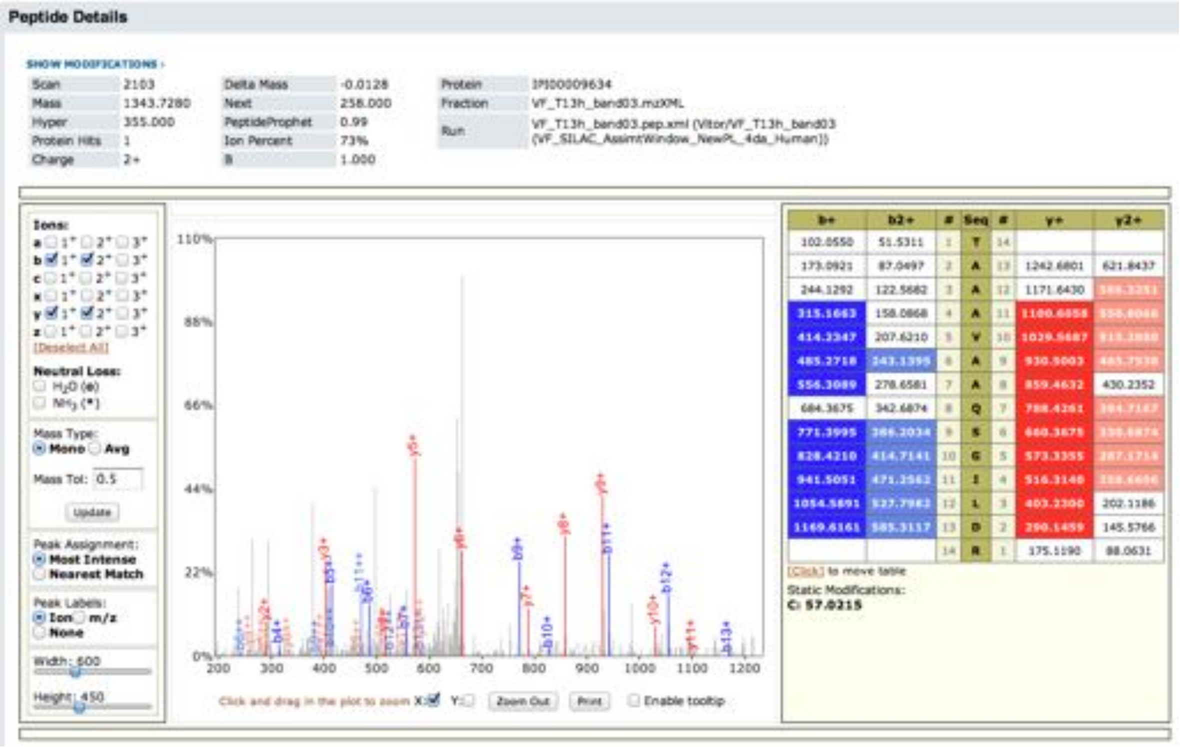
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	13		
185.1285	93.0679	2	L	12	1276.7008	638.8540
298.2125	149.6099	3	I	11	1163.6167	582.3120
369.2496	185.1285	4	A	10	1050.5327	525.7700
440.2867	220.6470	5	A	9	979.4956	490.2514
568.3453	284.6763	6	Q	8	908.4585	454.7329
731.4087	366.2080	7	Y	7	780.3999	390.7036
818.4407	409.7240	8	S	6	617.3365	309.1719
875.4621	438.2347	9	G	5	530.3045	265.6559
946.4993	473.7533	10	A	4	473.2831	237.1452
1074.5578	537.7826	11	Q	3	402.2459	201.6266
1173.6262	587.3168	12	V	2	274.1874	137.5973
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8628	IPI00009634	1	1	SQRDL	2103	2+	-0,0128	0,9880	K.TAAAVAAQSGILDR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	2103	Delta Mass	-0.0128	Protein	IPI00009634
Mass	1343.7280	Next	258.000	Fraction	VF_T13h_band03.mzXML
Hyper	355.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPt_4da_Human))
Protein Hits	1	Ion Percent	73%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

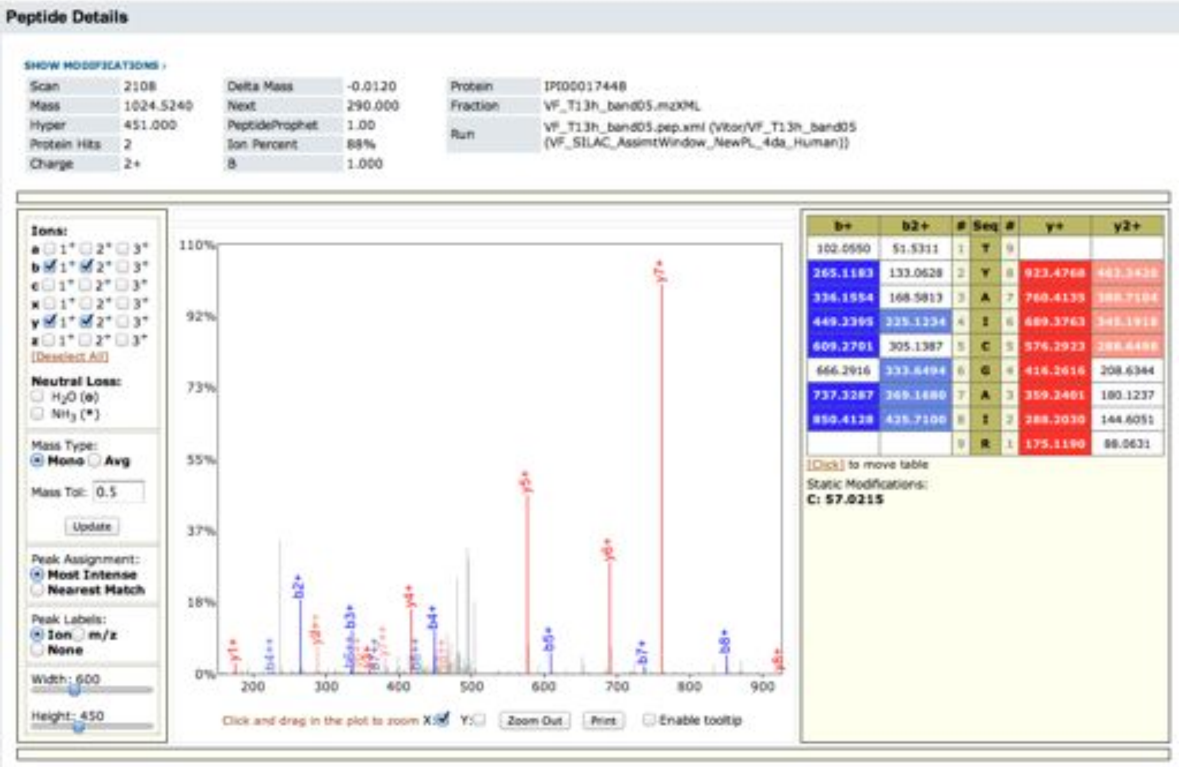
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
173.0921	87.0497	2	A	13	1242.6801	621.8437
244.1292	122.5682	3	A	12	1171.6430	586.3251
315.1663	158.0868	4	A	11	1100.6058	550.8066
414.2347	207.6210	5	V	10	1029.5687	515.2880
485.2718	243.1395	6	A	9	930.5003	465.7538
556.3089	278.6581	7	A	8	859.4632	430.2352
684.3675	342.6874	8	Q	7	788.4261	394.7167
771.3995	386.2034	9	S	6	660.3675	330.6874
828.4210	414.7141	10	G	5	573.3355	287.1714
941.5051	471.2562	11	I	4	516.3140	258.6606
1054.5891	527.7982	12	L	3	403.2300	202.1186
1169.6161	585.3117	13	D	2	290.1459	145.5766
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9804	IPI00017448, IPI00387084	1	1	RPS21, RPS21	2108	2+	-0,0120	0,9994	K.TYAICGAIR.R



Peptide Details

SHOW MODIFICATIONS ›

Scan	2108	Delta Mass	-0.0120	Protein	IPI00017448
Mass	1024.5240	Next	290.000	Fraction	VF_T13h_band05.mzXML
Hyper	451.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

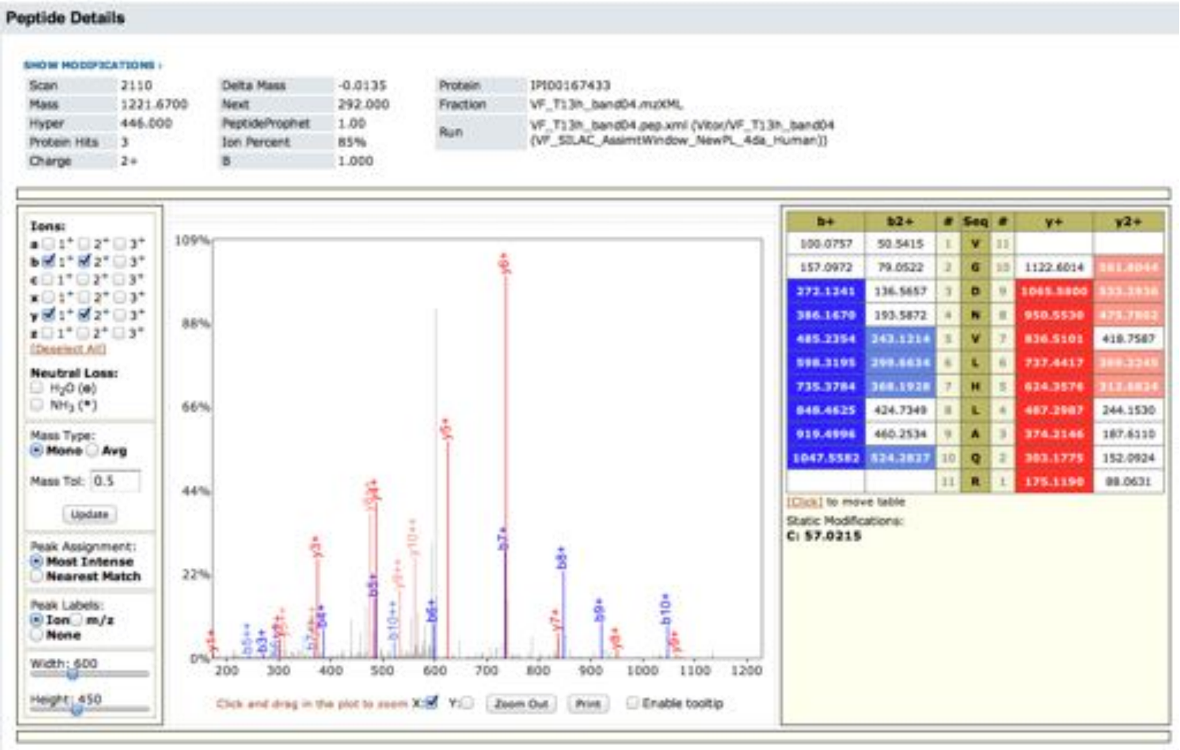
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	9		
265.1183	133.0628	2	Y	8	923.4768	462.2420
336.1554	168.5813	3	A	7	760.4135	380.7104
449.2395	225.1234	4	I	6	689.3763	345.1918
609.2701	305.1387	5	C	5	576.2923	288.6498
666.2916	333.6494	6	G	4	416.2616	208.6344
737.3287	369.1680	7	A	3	359.2401	180.1237
850.4128	425.7100	8	I	2	288.2030	144.6051
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9721	IPI00167433, IPI00894257, IPI00440693	1	1	FDX1L, MGC19604, FDX1L	2110	2+	-0,0135	0,9991	R.VGDNVLHLAQR.H



Peptide Details

SHOW MODIFICATIONS ›

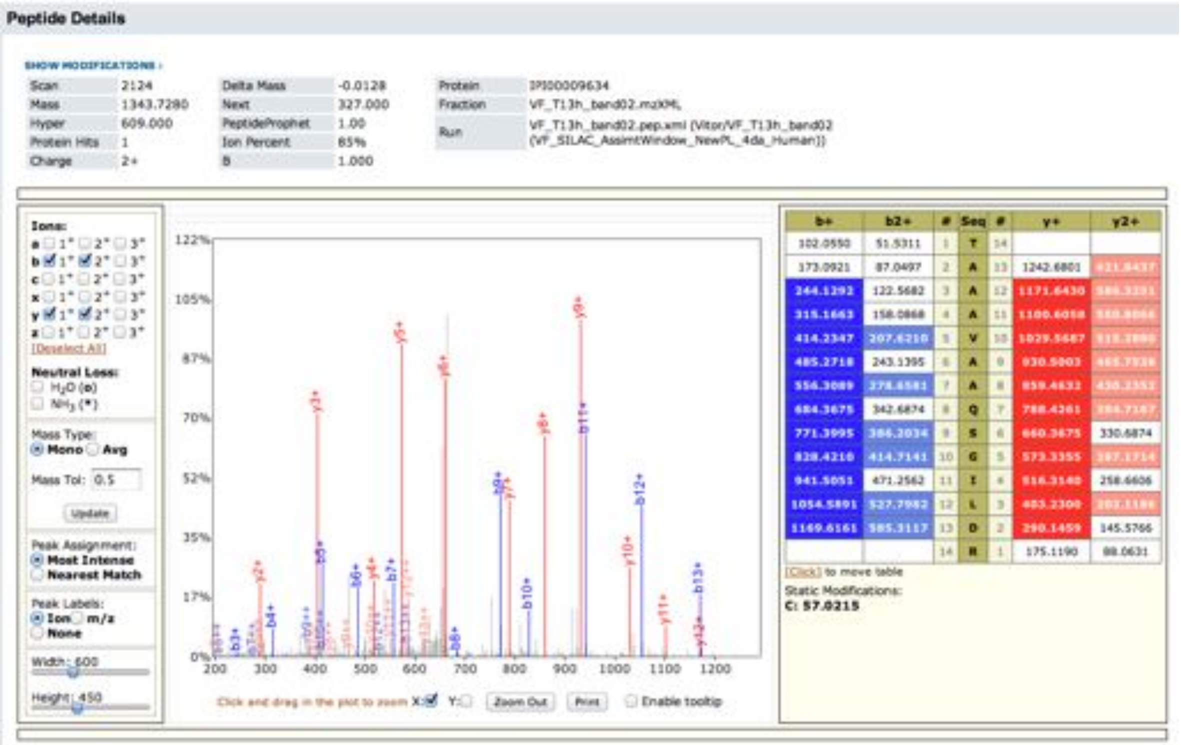
Scan	2110	Delta Mass	-0.0135	Protein	IPI00167433
Mass	1221.6700	Next	292.000	Fraction	VF_T13h_band04.mzXML
Hyper	446.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	85%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
157.0972	79.0522	2	G	10	1122.6014	561.8044
272.1241	136.5657	3	D	9	1065.5800	533.2936
386.1670	193.5872	4	N	8	950.5530	475.7802
485.2354	243.1214	5	V	7	836.5101	418.7587
598.3195	299.6634	6	L	6	737.4417	369.2245
735.3784	368.1928	7	H	5	624.3576	312.6824
848.4625	424.7349	8	L	4	487.2987	244.1530
919.4996	460.2534	9	A	3	374.2146	187.6110
1047.5582	524.2827	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00009634	1	1	SQRDL	2124	2+	-0,0128	0,9999	K.TAAAVAAQSGILDR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	2124	Delta Mass	-0.0128	Protein	IPI00009634
Mass	1343.7280	Next	327.000	Fraction	VF_T13h_band02.mzXML
Hyper	609.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

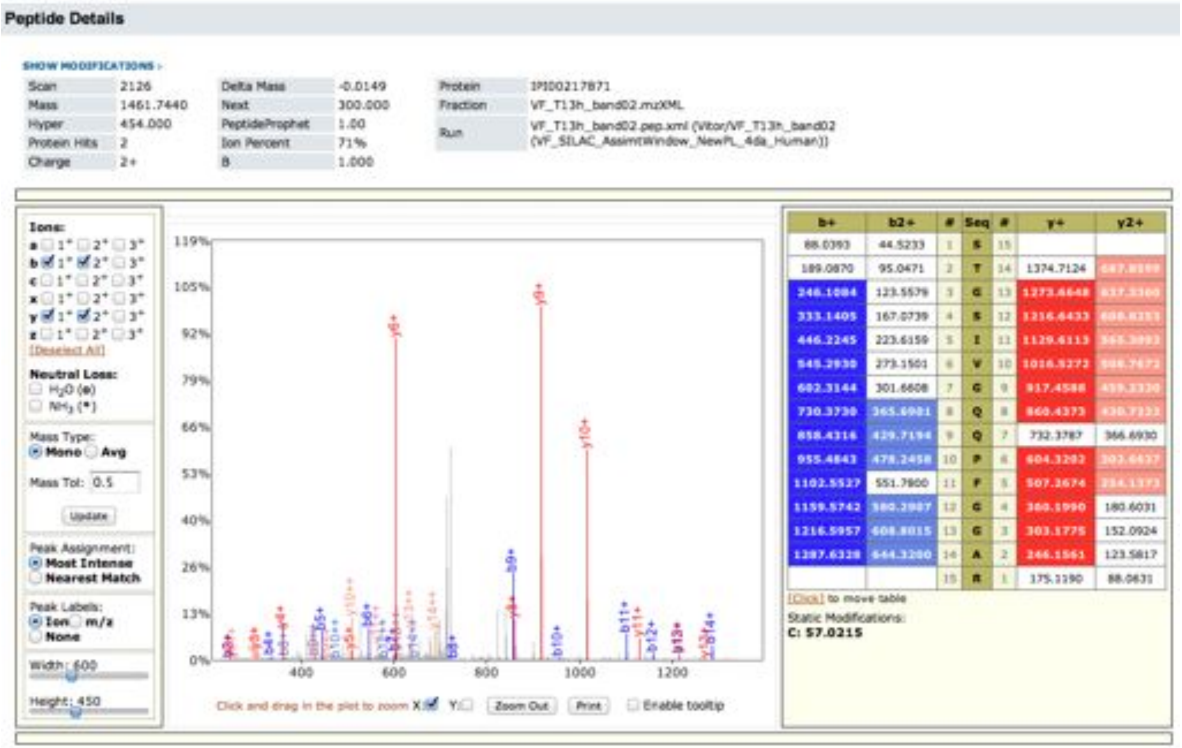
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
173.0921	87.0497	2	A	13	1242.6801	621.8437
244.1292	122.5682	3	A	12	1171.6430	586.3251
315.1663	158.0868	4	A	11	1100.6058	550.8066
414.2347	207.6210	5	V	10	1029.5687	515.2880
485.2718	243.1395	6	A	9	930.5003	465.7538
556.3089	278.6581	7	A	8	859.4632	430.2352
684.3675	342.6874	8	Q	7	788.4261	394.7167
771.3995	386.2034	9	S	6	660.3675	330.6874
828.4210	414.7141	10	G	5	573.3355	287.1714
941.5051	471.2562	11	I	4	516.3140	258.6606
1054.5891	527.7982	12	L	3	403.2300	202.1186
1169.6161	585.3117	13	D	2	290.1459	145.5766
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9661	IPI00647328, IPI00217871	1	1	ALDH4A1, ALDH4A1	2126	2+	-0,0149	0,9991	K.STGSIVGQQPFGGAR.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	2126	Delta Mass	-0.0149	Protein	IPI00217871
Mass	1461.7440	Next	300.000	Fraction	VF_T13h_band02.mzXML
Hyper	454.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

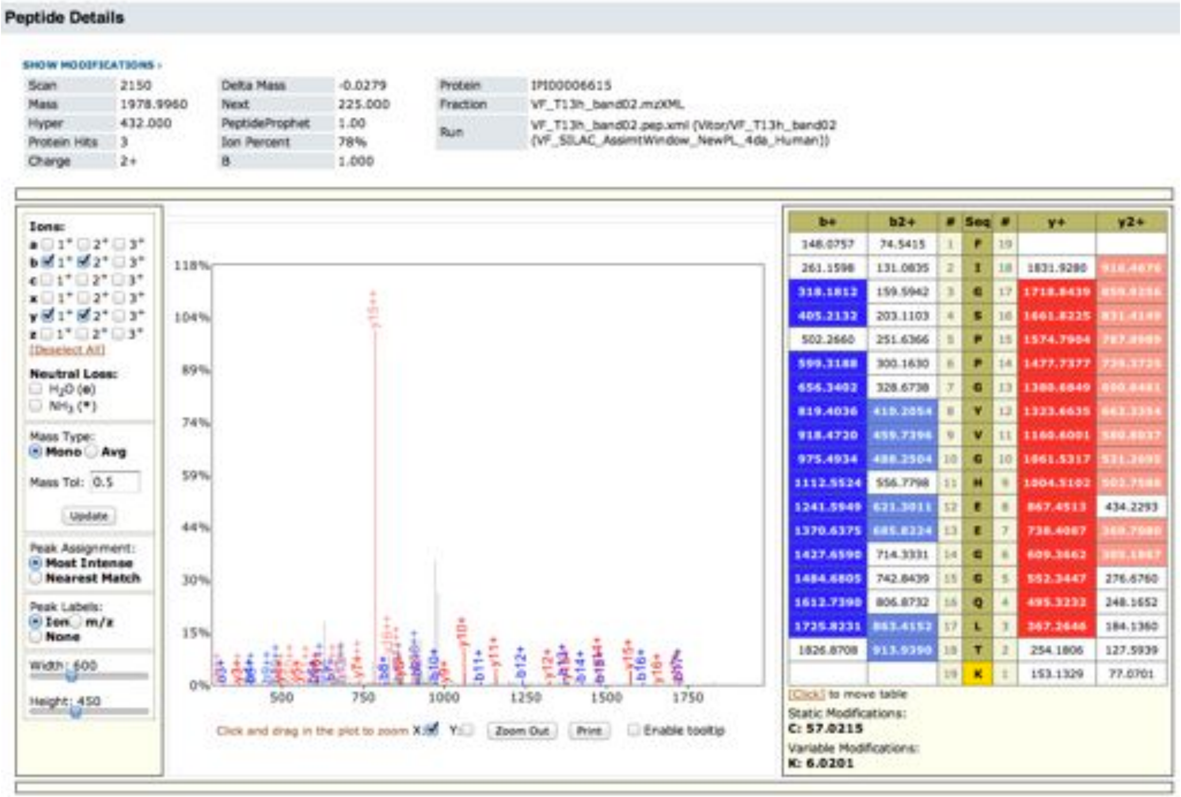
Height: 450

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	15		
189.0870	95.0471	2	T	14	1374.7124	687.8599
246.1084	123.5579	3	G	13	1273.6648	637.3360
333.1405	167.0739	4	S	12	1216.6433	608.8253
446.2245	223.6159	5	I	11	1129.6113	565.3093
545.2930	273.1501	6	V	10	1016.5272	508.7672
602.3144	301.6608	7	G	9	917.4588	459.2330
730.3730	365.6901	8	Q	8	860.4373	430.7223
858.4316	429.7194	9	Q	7	732.3787	366.6930
955.4843	478.2458	10	P	6	604.3202	302.6637
1102.5527	551.7800	11	F	5	507.2674	254.1373
1159.5742	580.2907	12	G	4	360.1990	180.6031
1216.5957	608.8015	13	G	3	303.1775	152.0924
1287.6328	644.3200	14	A	2	246.1561	123.5817
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9783	IPI00910365, IPI00216192, IPI00006615	1	1	-, CLPB, CLPB	2150	2+	-0,0279	0,9998	K.FIGSPPGYVGHEEGGQLTK'.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2150	Delta Mass	-0.0279	Protein	IPI00006615
Mass	1978.9960	Next	225.000	Fraction	VF_T13h_band02.mzXML
Hyper	432.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

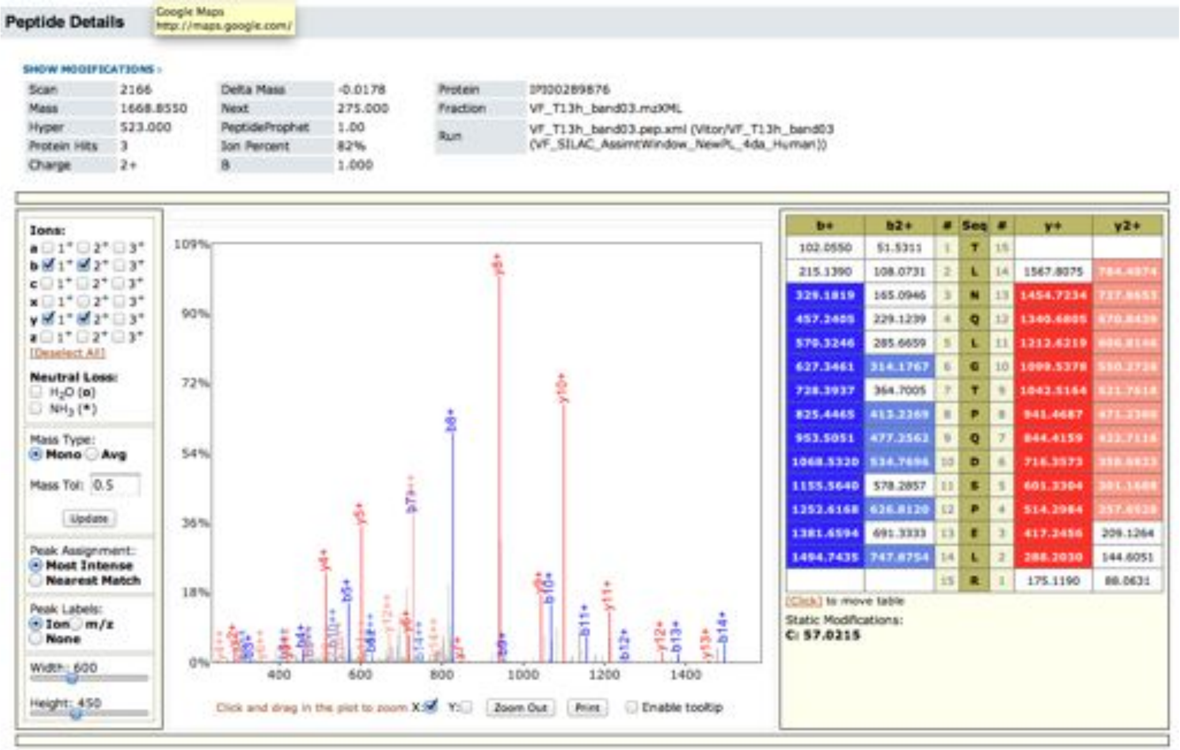
b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	19		
261.1598	131.0835	2	I	18	1831.9280	916.4676
318.1812	159.5942	3	G	17	1718.8439	859.9256
405.2132	203.1103	4	S	16	1661.8225	831.4149
502.2660	251.6366	5	P	15	1574.7904	787.8989
599.3188	300.1630	6	P	14	1477.7377	739.3725
656.3402	328.6738	7	G	13	1380.6849	690.8461
819.4036	410.2054	8	Y	12	1323.6635	662.3354
918.4720	459.7396	9	V	11	1160.6001	580.8037
975.4934	488.2504	10	G	10	1061.5317	531.2695
1112.5524	556.7798	11	H	9	1004.5102	502.7588
1241.5949	621.3011	12	E	8	867.4513	434.2293
1370.6375	685.8224	13	E	7	738.4087	369.7080
1427.6590	714.3331	14	G	6	609.3662	305.1867
1484.6805	742.8439	15	G	5	552.3447	276.6760
1612.7390	806.8732	16	Q	4	495.3232	248.1652
1725.8231	863.4152	17	L	3	367.2646	184.1360
1826.8708	913.9390	18	T	2	254.1806	127.5939
		19	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00909094, IPI00552913, IPI00289876	1	1	-, STX7, STX7	2166	2+	-0,0178	0,9999	R.TLNQLGTPQDSPELR.Q



Peptide Details

Google Maps
http://maps.google.com/

SHOW MODIFICATIONS ›

Scan	2166	Delta Mass	-0.0178	Protein	IPI00289876
Mass	1668.8550	Next	275.000	Fraction	VF_T13h_band03.mzXML
Hyper	523.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

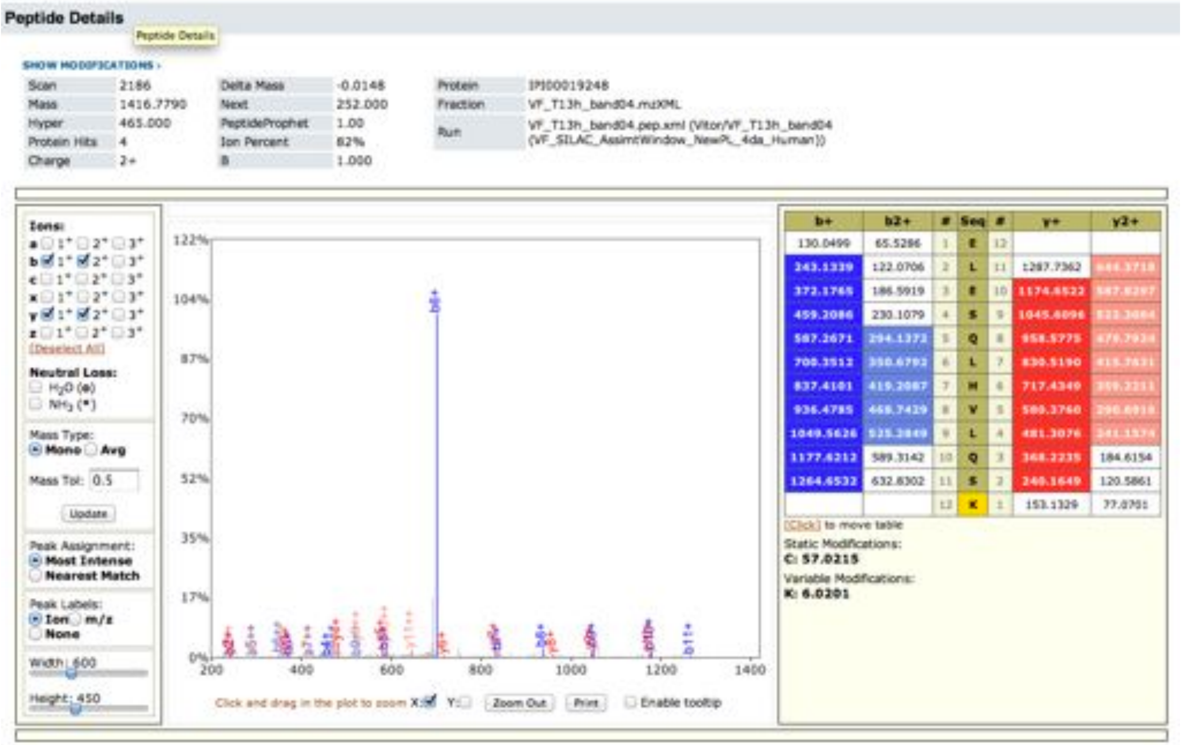
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	15		
215.1390	108.0731	2	L	14	1567.8075	784.4074
329.1819	165.0946	3	N	13	1454.7234	727.8653
457.2405	229.1239	4	Q	12	1340.6805	670.8439
570.3246	285.6659	5	L	11	1212.6219	606.8146
627.3461	314.1767	6	G	10	1099.5378	550.2726
728.3937	364.7005	7	T	9	1042.5164	521.7618
825.4465	413.2269	8	P	8	941.4687	471.2380
953.5051	477.2562	9	Q	7	844.4159	422.7116
1068.5320	534.7696	10	D	6	716.3573	358.6823
1155.5640	578.2857	11	S	5	601.3304	301.1688
1252.6168	626.8120	12	P	4	514.2984	257.6528
1381.6594	691.3333	13	E	3	417.2456	209.1264
1494.7435	747.8754	14	L	2	288.2030	144.6051
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9822	IPI00640511, IPI00019248, IPI00645440, IPI00719170	1	1	TRAF3IP3, TRAF3IP3, T3JAM, TRAF3IP3	2186	2+	-0,0148	0,9998	R.ELESQLHVLQSK'.L



Peptide Details

Scan	2186	Delta Mass	-0.0148	Protein	IPI00019248
Mass	1416.7790	Next	252.000	Fraction	VF_T13h_band04.mzXML
Hyper	465.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ ☐ Enable tooltip

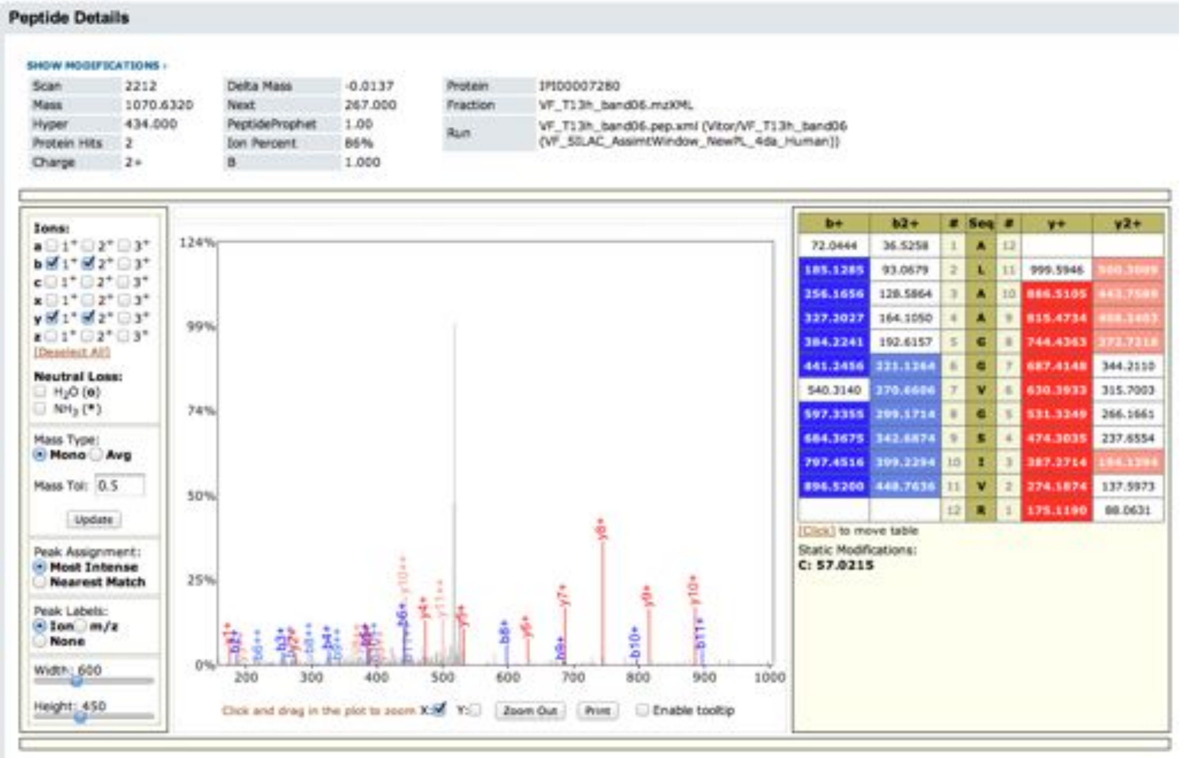
b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	12		
243.1339	122.0706	2	L	11	1287.7362	644.3718
372.1765	186.5919	3	E	10	1174.6522	587.8297
459.2086	230.1079	4	S	9	1045.6096	523.3084
587.2671	294.1372	5	Q	8	958.5775	479.7924
700.3512	350.6792	6	L	7	830.5190	415.7631
837.4101	419.2087	7	H	6	717.4349	359.2211
936.4785	468.7429	8	V	5	580.3760	290.6919
1049.5626	525.2849	9	L	4	481.3076	241.1574
1177.6212	589.3142	10	Q	3	368.2235	184.6154
1264.6532	632.8302	11	S	2	240.1649	120.5861
		12	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9764	IPI00550234, IPI00007280	1	1	ARPC5, ARPC5	2212	2+	-0,0137	0,9988	K.ALAAGGVGSIVR.V



Peptide Details

SHOW MODIFICATIONS ›

Scan	2212	Delta Mass	-0.0137	Protein	IPI00007280
Mass	1070.6320	Next	267.000	Fraction	VF_T13h_band06.mzXML
Hyper	434.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	2	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
185.1285	93.0679	2	L	11	999.5946	500.3009
256.1656	128.5864	3	A	10	886.5105	443.7589
327.2027	164.1050	4	A	9	815.4734	408.2403
384.2241	192.6157	5	G	8	744.4363	372.7218
441.2456	221.1264	6	G	7	687.4148	344.2110
540.3140	270.6606	7	V	6	630.3933	315.7003
597.3355	299.1714	8	G	5	531.3249	266.1661
684.3675	342.6874	9	S	4	474.3035	237.6554
797.4516	399.2294	10	I	3	387.2714	194.1394
896.5200	448.7636	11	V	2	274.1874	137.5973
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00796659, IPI00025049	1	1	M6PR, M6PR	2220	2+	-0,0140	0,9999	R.HTLADNFNPVSEER.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	2220	Delta Mass	-0.0140	Protein	IPI00025049
Mass	1628.7660	Next	299.000	Fraction	VF_T13h_band02.mzXML
Hyper	580.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	92%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	14		
239.1139	120.0606	2	T	13	1491.7074	746.3573
352.1979	176.6026	3	L	12	1390.6597	695.8335
423.2350	212.1212	4	A	11	1277.5757	639.2915
538.2620	269.6346	5	D	10	1206.5386	603.7729
652.3049	326.6561	6	N	9	1091.5116	546.2594
799.3733	400.1903	7	F	8	977.4687	489.2380
913.4163	457.2118	8	N	7	830.4003	415.7038
1010.4690	505.7381	9	P	6	716.3573	358.6823
1109.5374	555.2724	10	V	5	619.3046	310.1559
1196.5695	598.7884	11	S	4	520.2362	260.6217
1325.6121	663.3097	12	E	3	433.2041	217.1057
1454.6546	727.8310	13	E	2	304.1615	152.5844
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9810	IPI00911004, IPI00878551, IPI00010796	1	1	-, P4HB, P4HB	2255	2+	-0,0189	0,9999	K.VDATEESDLAQQYGVR.G

Peptide Details

Scan	2255	Delta Mass	-0.0189	Protein	IPI00010796
Mass	1780.8350	Next	259.000	Fraction	VF_T13h_band01.mzXML
Hyper	568.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

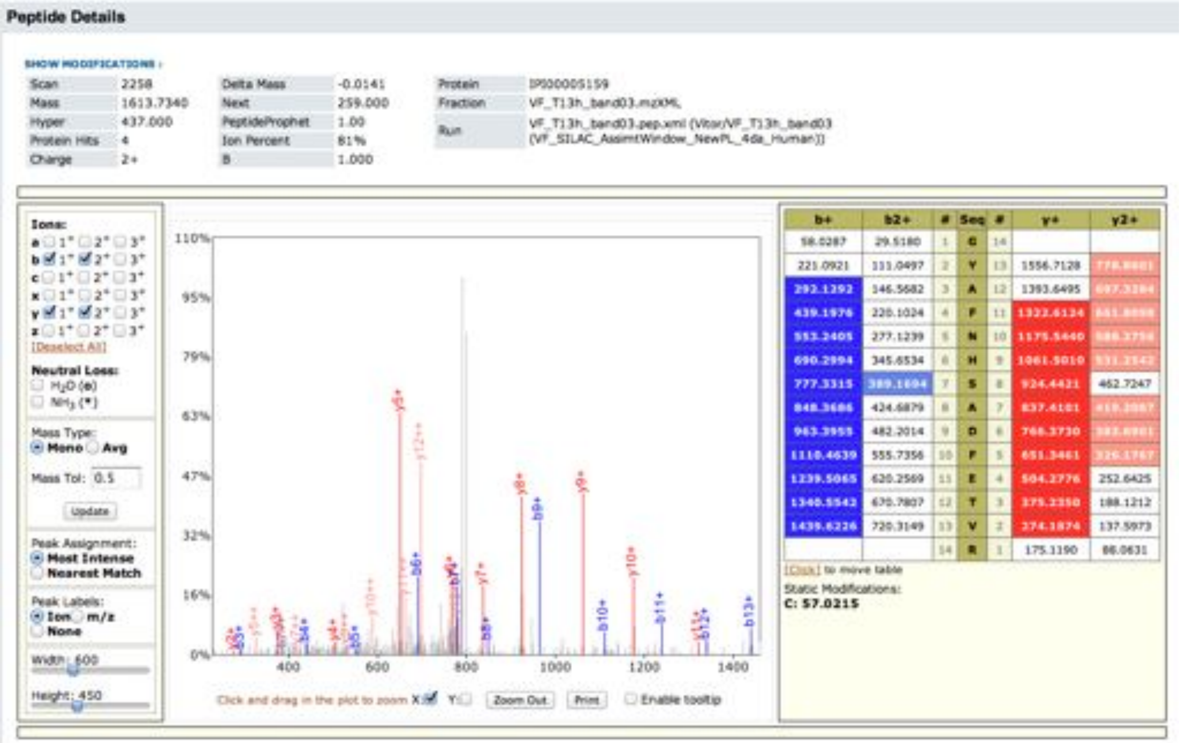
Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	16		
215.1026	108.0550	2	D	15	1681.7664	841.3868
286.1397	143.5735	3	A	14	1566.7394	783.8734
387.1874	194.0974	4	T	13	1495.7023	748.3548
516.2300	258.6186	5	E	12	1394.6546	697.8310
645.2726	323.1399	6	E	11	1265.6121	633.3097
732.3046	366.6560	7	S	10	1136.5695	568.7884
847.3316	424.1694	8	D	9	1049.5374	525.2734
960.4156	480.7115	9	L	8	934.5105	467.7589
1031.4528	516.2300	10	A	7	821.4264	411.2169
1159.5113	580.2593	11	Q	6	750.3893	375.6983
1287.5699	644.2886	12	Q	5	622.3307	311.6690
1450.6332	725.8203	13	Y	4	494.2722	247.6397
1507.6547	754.3310	14	G	3	331.2088	166.1081
1606.7231	803.8652	15	V	2	274.1874	137.5973
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9822	IPI00909247, IPI00005159, IPI00470573, IPI00749250	1	1	-, ACTR2, ACTR2, ACTR2	2258	2+	-0,0141	0,9995	R.GYAFNHSADFETVR.M



Peptide Details

SHOW MODIFICATIONS :

Scan	2258	Delta Mass	-0.0141	Protein	IPI00005159
Mass	1613.7340	Next	259.000	Fraction	VF_T13h_band03.mzXML
Hyper	437.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	14		
221.0921	111.0497	2	Y	13	1556.7128	778.8601
292.1292	146.5682	3	A	12	1393.6495	697.3284
439.1976	220.1024	4	F	11	1322.6124	661.8098
553.2405	277.1239	5	N	10	1175.5440	588.2756
690.2994	345.6534	6	H	9	1061.5010	531.2542
777.3315	389.1694	7	S	8	924.4421	462.7247
848.3686	424.6879	8	A	7	837.4101	419.2087
963.3955	482.2014	9	D	6	766.3730	383.6901
1110.4639	555.7356	10	F	5	651.3461	326.1767
1239.5065	620.2569	11	E	4	504.2776	252.6425
1340.5542	670.7807	12	T	3	375.2350	188.1212
1439.6226	720.3149	13	V	2	274.1874	137.5973
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8213	IPI00219160, IPI00741167	1	1	RPL34, LOC651249	2260	2+	-0,0103	0,9815	R.AFLIEEQK.I

Peptide Details

SHOW MODIFICATIONS ›

Scan	2260	Delta Mass	-0.0103	Protein	IPI00219160
Mass	977.5300	Next	476.000	Fraction	VF_T13h_band06.mzXML
Hyper	519.000	PeptideProphet	0.98	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	93%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

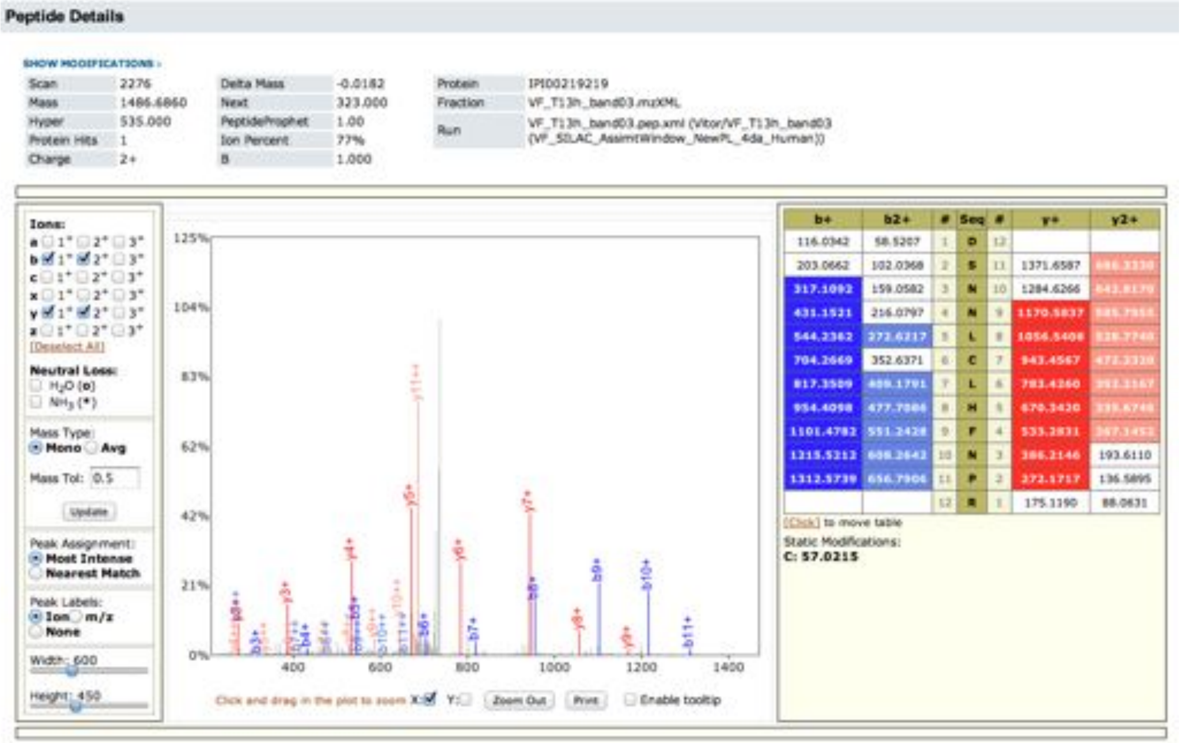
☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	8		
219.1128	110.0600	2	F	7	906.4931	453.7502
332.1969	166.6021	3	L	6	759.4247	380.2160
445.2809	223.1441	4	I	5	646.3406	323.6740
574.3235	287.6654	5	E	4	533.2566	267.1319
703.3661	352.1867	6	E	3	404.2140	202.6106
831.4247	416.2160	7	Q	2	275.1714	138.0893
		8	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9857	IPI00219219	1	1	LGALS1	2276	2+	-0,0182	0,9998	K.DSNNLCLHFNPR.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	2276	Delta Mass	-0.0182	Protein	IPI00219219
Mass	1486.6860	Next	323.000	Fraction	VF_T13h_band03.mzXML
Hyper	535.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	12		
203.0662	102.0368	2	S	11	1371.6587	686.3330
317.1092	159.0582	3	N	10	1284.6266	642.8170
431.1521	216.0797	4	N	9	1170.5837	585.7955
544.2362	272.6217	5	L	8	1056.5408	528.7740
704.2669	352.6371	6	C	7	943.4567	472.2320
817.3509	409.1791	7	L	6	783.4260	392.2167
954.4098	477.7086	8	H	5	670.3420	335.6746
1101.4782	551.2428	9	F	4	533.2831	267.1452
1215.5212	608.2642	10	N	3	386.2146	193.6110
1312.5739	656.7906	11	P	2	272.1717	136.5895
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9859	IPI00019329, IPI00062037	1	1	DNCL1, DYNLL2	2308	2+	-0,0185	0,9997	K.YNPTWHCIVGR.N

Peptide Details

SHOW MODIFICATIONS ›

Scan	2308	Delta Mass	-0.0185	Protein	IPI00019329
Mass	1402.6680	Next	275.000	Fraction	VF_T13h_band06.mzXML
Hyper	499.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	11		
278.1135	139.5604	2	N	10	1239.6052	620.3062
375.1663	188.0868	3	P	9	1125.5622	563.2848
476.2140	238.6106	4	T	8	1028.5095	514.7584
662.2933	331.6503	5	W	7	927.4618	464.2340
799.3522	400.1797	6	H	6	741.3825	371.1949
959.3829	480.1951	7	C	5	604.3236	302.6654
1072.4669	536.7371	8	I	4	444.2929	222.6501
1171.5354	586.2713	9	V	3	331.2088	166.1081
1228.5568	614.7821	10	G	2	232.1404	116.5738
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8411	IPI00902623, IPI00797025, IPI00022284, IPI00382843	1	1	-, PRNP, PRNP, PRNP	2315	2+	-0,0147	0,9856	R.VVEQMCITQYER.E

Peptide Details

SHOW MODIFICATIONS ›

Scan	2315	Delta Mass	-0.0147	Protein	IPI00022284
Mass	1555.7240	Next	268.000	Fraction	VF_T13h_band03.mzXML
Hyper	360.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600
Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	12		
199.1441	100.0757	2	V	11	1456.6559	728.8318
328.1867	164.5970	3	E	10	1357.5875	679.2974
456.2453	228.6263	4	Q	9	1228.5449	614.7761
587.2858	294.1465	5	M	8	1100.4864	550.7468
747.3164	374.1619	6	C	7	969.4459	485.2266
860.4005	430.7039	7	I	6	809.4152	405.2112
961.4482	481.2277	8	T	5	696.3311	348.6692
1089.5068	545.2570	9	Q	4	595.2835	298.1454
1252.5701	626.7887	10	Y	3	467.2249	234.1161
1381.6127	691.3100	11	E	2	304.1615	152.5844
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9566	IPI00003362	1	1	HSPA5	2378	2+	-0,0206	0,9980	K.NQLTSNPENTVFDAK.R

Peptide Details

SHOW MODIFICATIONS ›

Scan	2378	Delta Mass	-0.0206	Protein	IPI00003362
Mass	1677.8080	Next	239.000	Fraction	VF_T13h_band04.mzXML
Hyper	374.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

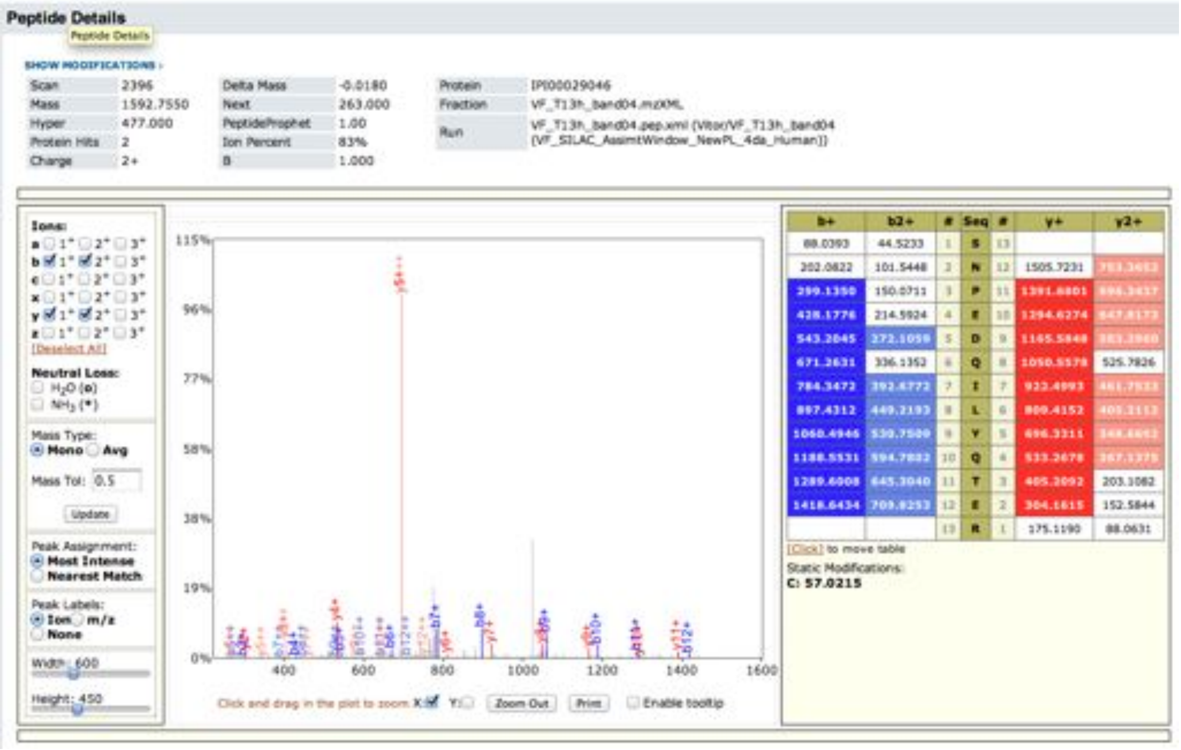
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	15		
243.1088	122.0580	2	Q	14	1563.7649	782.3861
356.1928	178.6001	3	L	13	1435.7063	718.3568
457.2405	229.1239	4	T	12	1322.6223	661.8148
544.2726	272.6399	5	S	11	1221.5746	611.2909
658.3155	329.6614	6	N	10	1134.5426	567.7749
755.3682	378.1878	7	P	9	1020.4997	510.7535
884.4108	442.7091	8	E	8	923.4469	462.2271
998.4538	499.7305	9	N	7	794.4043	397.7058
1099.5014	550.2544	10	T	6	680.3614	340.6843
1198.5699	599.7886	11	V	5	579.3137	290.1605
1345.6383	673.3228	12	F	4	480.2453	240.6263
1460.6652	730.8362	13	D	3	333.1769	167.0921
1531.7023	766.3548	14	A	2	218.1499	109.5786
		15	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9822	IPI00798088, IPI00029046	1	1	KIAA0152, KIAA0152	2396	2+	-0,0180	0,9998	R.SNPEDQILYQTER.Y



Peptide Details

SHOW MODIFICATIONS ›

Scan	2396	Delta Mass	-0.0180	Protein	IPI00029046
Mass	1592.7550	Next	263.000	Fraction	VF_T13h_band04.mzXML
Hyper	477.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	13		
202.0822	101.5448	2	N	12	1505.7231	753.3652
299.1350	150.0711	3	P	11	1391.6801	696.3437
428.1776	214.5924	4	E	10	1294.6274	647.8173
543.2045	272.1059	5	D	9	1165.5848	583.2960
671.2631	336.1352	6	Q	8	1050.5578	525.7826
784.3472	392.6772	7	I	7	922.4993	461.7533
897.4312	449.2193	8	L	6	809.4152	405.2113
1060.4946	530.7500	9	Y	5	696.3311	348.6692
1188.5531	594.7802	10	Q	4	533.2678	267.1375
1289.6008	645.3040	11	T	3	405.2092	203.1082
1418.6434	709.8253	12	E	2	304.1615	152.5844
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9776	IPI00748835, IPI00795504, IPI00807403, IPI00015102	1	1	ALCAM, ALCAM, ALCAM, ALCAM	2413	2+	-0,0192	0,9997	R.QIGDALPVSCTISASR.N

Peptide Details

Scan	2413	Delta Mass	-0.0192	Protein	IPI00015102
Mass	1674.8480	Next	317.000	Fraction	VF_T13h_band01.mzXML
Hyper	531.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

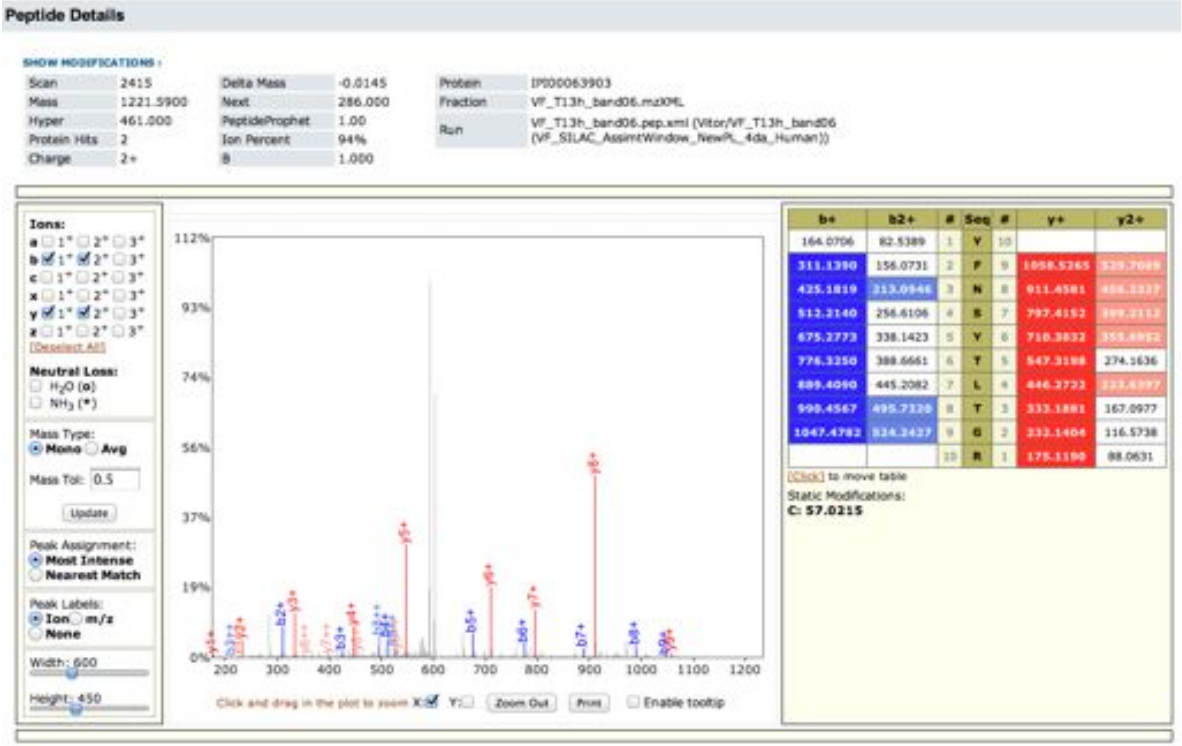
Height: 450

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	16		
242.1499	121.5786	2	I	15	1546.7894	773.8983
299.1714	150.0893	3	G	14	1433.7053	717.3563
414.1983	207.6028	4	D	13	1376.6839	688.8456
485.2354	243.1214	5	A	12	1261.6569	631.3321
598.3195	299.6634	6	L	11	1190.6198	595.8135
695.3723	348.1898	7	P	10	1077.5358	539.2715
794.4407	397.7240	8	V	9	980.4830	490.7451
881.4727	441.2400	9	S	8	881.4146	441.2109
1041.5034	521.2553	10	C	7	794.3825	397.6949
1142.5511	571.7792	11	T	6	634.3519	317.6796
1255.6351	628.3213	12	I	5	533.3042	267.1557
1342.6672	671.8372	13	S	4	420.2201	210.6137
1413.7043	707.3558	14	A	3	333.1881	167.0977
1500.7363	750.8718	15	S	2	262.1510	131.5791
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9796	IPI00063903, IPI00640630	1	1	USMG5, USMG5P1	2415	2+	-0,0145	0,9991	K.YFNSYTLTGR.M



Peptide Details

SHOW MODIFICATIONS ›

Scan	2415	Delta Mass	-0.0145	Protein	IPI00063903
Mass	1221.5900	Next	286.000	Fraction	VF_T13h_band06.mzXML
Hyper	461.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPt_4da_Human))
Protein Hits	2	Ion Percent	94%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

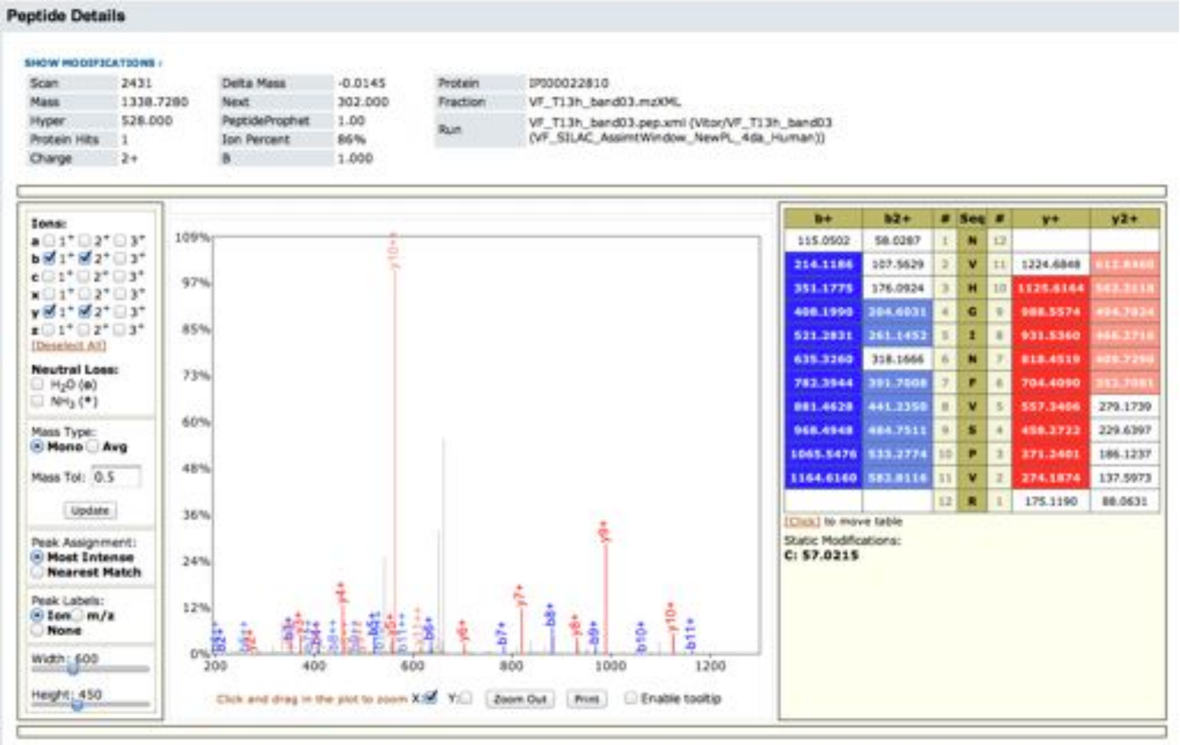
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	10		
311.1390	156.0731	2	F	9	1058.5265	529.7669
425.1819	213.0946	3	N	8	911.4581	456.2327
512.2140	256.6106	4	S	7	797.4152	399.2112
675.2773	338.1423	5	Y	6	710.3832	355.6952
776.3250	388.6661	6	T	5	547.3198	274.1636
889.4090	445.2082	7	L	4	446.2722	223.6397
990.4567	495.7320	8	T	3	333.1881	167.0977
1047.4782	524.2427	9	G	2	232.1404	116.5738
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9857	IPI00022810	1	1	CTSC	2431	2+	-0.0145	0.9998	R.NVHGINFVSPVR.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	2431	Delta Mass	-0.0145	Protein	IPI00022810
Mass	1338.7280	Next	302.000	Fraction	VF_T13h_band03.mzXML
Hyper	528.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

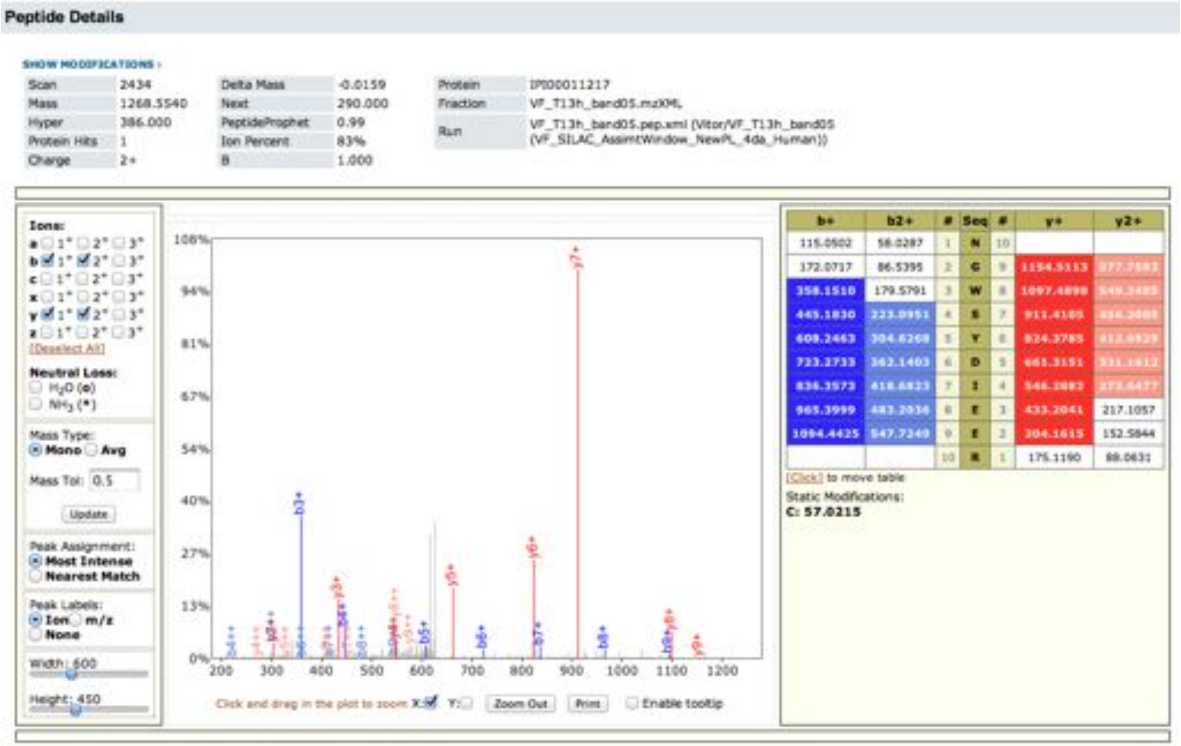
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	12		
214.1186	107.5629	2	V	11	1224.6848	612.8460
351.1775	176.0924	3	H	10	1125.6164	563.3118
408.1990	204.6031	4	G	9	988.5574	494.7824
521.2831	261.1452	5	I	8	931.5360	466.2716
635.3260	318.1666	6	N	7	818.4519	409.7296
782.3944	391.7008	7	F	6	704.4090	352.7081
881.4628	441.2350	8	V	5	557.3406	279.1739
968.4948	484.7511	9	S	4	458.2722	229.6397
1065.5476	533.2774	10	P	3	371.2401	186.1237
1164.6160	583.8116	11	V	2	274.1874	137.5973
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9161	IPI00011217	1	1	NDUFS4	2434	2+	-0.0159	0.9937	K.NGWSYDIEER.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2434	Delta Mass	-0.0159	Protein	IPI00011217
Mass	1268.5540	Next	290.000	Fraction	VF_T13h_band05.mzXML
Hyper	386.000	PeptideProphet	0.99	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

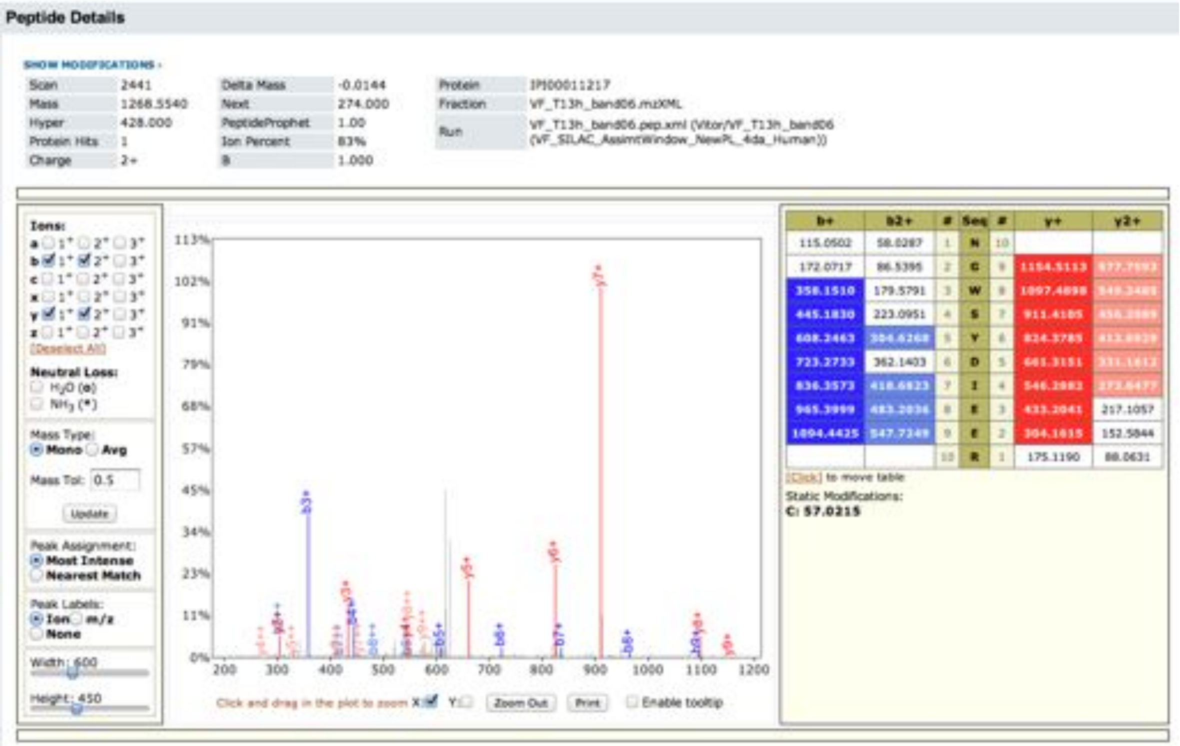
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	10		
172.0717	86.5395	2	G	9	1154.5113	577.7593
358.1510	179.5791	3	W	8	1097.4898	549.2485
445.1830	223.0951	4	S	7	911.4105	456.2089
608.2463	304.6268	5	Y	6	824.3785	412.6929
723.2733	362.1403	6	D	5	661.3151	331.1612
836.3573	418.6823	7	I	4	546.2882	273.6477
965.3999	483.2036	8	E	3	433.2041	217.1057
1094.4425	547.7249	9	E	2	304.1615	152.5844
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9712	IPI00011217	1	1	NDUFS4	2441	2+	-0.0144	0.9983	K.NGWSYDIEER.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2441	Delta Mass	-0.0144	Protein	IPI00011217
Mass	1268.5540	Next	274.000	Fraction	VF_T13h_band06.mzXML
Hyper	428.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	10		
172.0717	86.5395	2	G	9	1154.5113	577.7593
358.1510	179.5791	3	W	8	1097.4898	549.2485
445.1830	223.0951	4	S	7	911.4105	456.2089
608.2463	304.6268	5	Y	6	824.3785	412.6929
723.2733	362.1403	6	D	5	661.3151	331.1612
836.3573	418.6823	7	I	4	546.2882	273.6477
965.3999	483.2036	8	E	3	433.2041	217.1057
1094.4425	547.7249	9	E	2	304.1615	152.5844
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9695	IPI00908950, IPI00215719	1	1	-, RPL18	2442	2+	-0.0143	0.9984	K.TAVVVGTITDDVR.V

Peptide Details

Scan	2442	Delta Mass	-0.0143	Protein	IPI00215719
Mass	1345.7320	Next	368.000	Fraction	VF_T13h_band03.mzXML
Hyper	496.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	13		
173.0921	87.0497	2	A	12	1244.6845	622.8459
272.1605	136.5839	3	V	11	1173.6474	587.3273
371.2289	186.1181	4	V	10	1074.5790	537.7931
470.2973	235.6523	5	V	9	975.5106	488.2589
527.3188	264.1630	6	G	8	876.4421	438.7247
628.3665	314.6869	7	T	7	819.4207	410.3140
741.4505	371.2289	8	I	6	718.3730	359.6901
842.4982	421.7527	9	T	5	605.2889	303.1481
957.5251	479.2662	10	D	4	504.2413	252.6243
1072.5521	536.7797	11	D	3	389.2143	195.1106
1171.6205	586.3139	12	V	2	274.1874	137.5973
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9775	IPI00024619	1	1	C16orf61	2444	2+	-0.0136	0.9989	K.FFGYCNDVDR.E

Peptide Details

SHOW MODIFICATIONS ›

Scan	2444	Delta Mass	-0.0136	Protein	IPI00024619
Mass	1292.5360	Next	270.000	Fraction	VF_T13h_band06.mzXML
Hyper	439.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	89%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	10		
295.1441	148.0757	2	F	9	1145.4681	573.2377
352.1656	176.5864	3	G	8	998.3997	499.7035
515.2289	258.1181	4	Y	7	941.3782	471.1927
675.2596	338.1334	5	C	6	778.3149	389.6611
789.3025	395.1549	6	N	5	618.2842	309.6457
904.3295	452.6684	7	D	4	504.2413	252.6243
1003.3979	502.2026	8	V	3	389.2143	195.1108
1118.4248	559.7160	9	D	2	290.1459	145.5766
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9881	IPI00021794, IPI00640525	1	1	CTSA, PPGB	2446	2+	-0.0166	0.9999	K.YGDSGEQIAGFVK.E

Peptide Details

SHOW MODIFICATIONS ›

Scan	2446	Delta Mass	-0.0166	Protein	IPI00021794
Mass	1370.6590	Next	322.000	Fraction	VF_T13h_band06.mzXML
Hyper	665.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	92%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	13		
221.0921	111.0497	2	G	12	1207.5953	604.3013
336.1190	168.5631	3	D	11	1150.5739	575.7906
423.1510	212.0792	4	S	10	1035.5469	518.2771
480.1725	240.5899	5	G	9	948.5149	474.7611
609.2151	305.1112	6	E	8	891.4934	446.2504
737.2737	369.1405	7	Q	7	762.4509	381.7291
850.3577	425.6825	8	I	6	634.3923	317.6998
921.3949	461.2011	9	A	5	521.3082	261.1577
978.4163	489.7118	10	G	4	450.2711	225.6392
1125.4847	563.2460	11	F	3	393.2496	197.1285
1224.5531	612.7802	12	V	2	246.1812	123.5942
		13	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9810	IPI00796250, IPI00794986, IPI00217906, IPI00748145, IPI00465121	1	1	GNAI2, GNAI2, GNAI2, GNAI2, GNAI2	2452	2+	-0.0184	0.9999	R.IAQSDYIPTQQDVLR.T

Peptide Details

Scan	2452	Delta Mass	-0.0184	Protein	IPI00217906
Mass	1746.9020	Next	286.000	Fraction	VF_T13h_band01.mzXML
Hyper	563.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

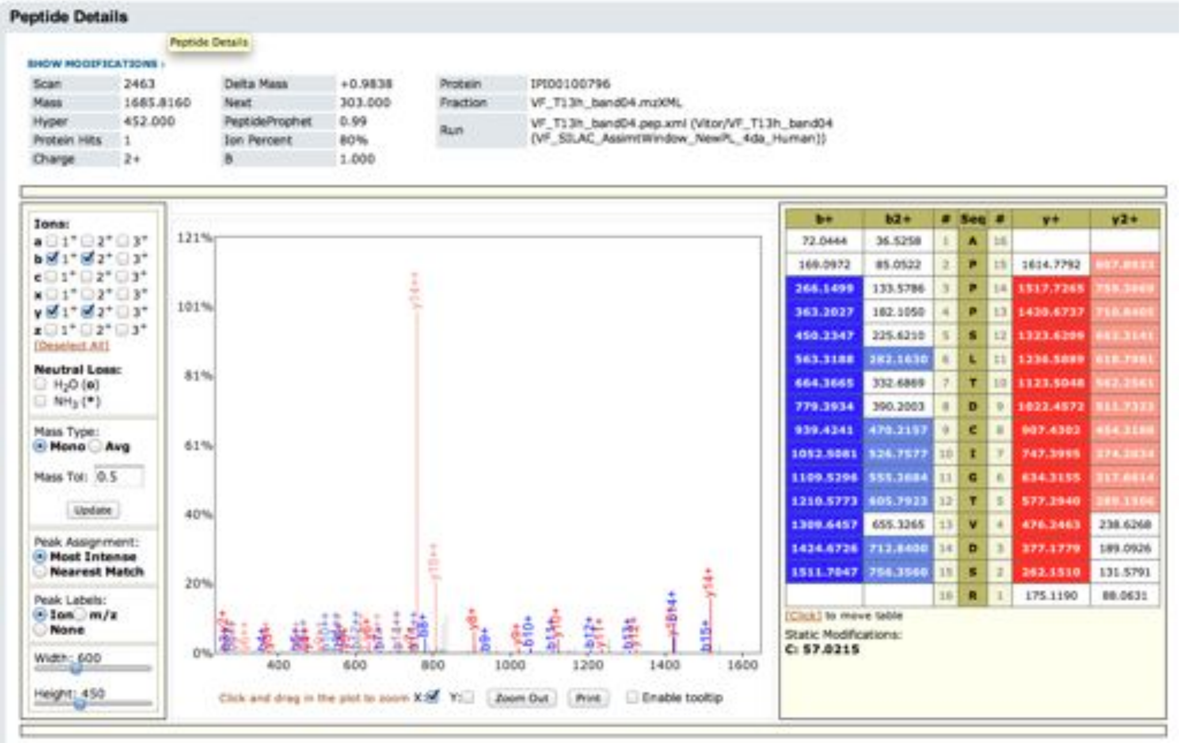
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	15		
185.1285	93.0679	2	A	14	1633.8180	817.4127
313.1870	157.0972	3	Q	13	1562.7809	781.8941
400.2191	200.6132	4	S	12	1434.7223	717.8648
515.2460	258.1266	5	D	11	1347.6903	674.3488
678.3093	339.6583	6	Y	10	1232.6634	616.8353
791.3934	396.2003	7	I	9	1069.6000	535.3037
888.4462	444.7267	8	P	8	956.5160	478.7616
989.4938	495.2506	9	T	7	859.4632	430.2352
1117.5524	559.2798	10	Q	6	758.4155	379.7114
1245.6110	623.3091	11	Q	5	630.3570	315.6821
1360.6379	680.8226	12	D	4	502.2984	251.6528
1459.7063	730.3568	13	V	3	387.2714	194.1394
1572.7904	786.8988	14	L	2	288.2030	144.6051
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8237	IPI00100796	1	1	CHMP5	2463	2+	+0.9838	0.9870	K.APPPSLTDCIGTVDSR.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	2463	Delta Mass	+0.9838	Protein	IPI00100796
Mass	1685.8160	Next	303.000	Fraction	VF_T13h_band04.mzXML
Hyper	452.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	1	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

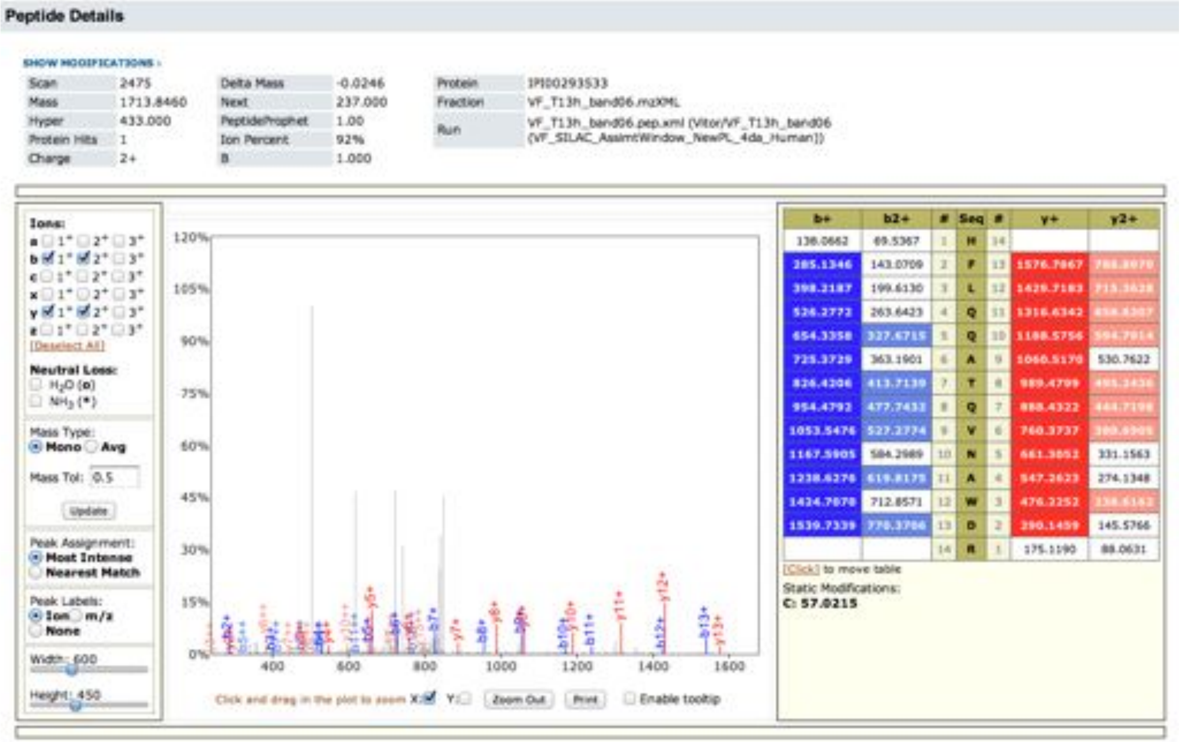
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	16		
169.0972	85.0522	2	P	15	1614.7792	807.8933
266.1499	133.5786	3	P	14	1517.7265	759.3669
363.2027	182.1050	4	P	13	1420.6737	710.8405
450.2347	225.6210	5	S	12	1323.6209	662.3141
563.3188	282.1630	6	L	11	1236.5889	618.7981
664.3665	332.6869	7	T	10	1123.5048	562.2561
779.3934	390.2003	8	D	9	1022.4572	511.7323
939.4241	470.2157	9	C	8	907.4302	454.2188
1052.5081	526.7577	10	I	7	747.3995	374.2034
1109.5296	555.2684	11	G	6	634.3155	317.6614
1210.5773	605.7923	12	T	5	577.2940	289.1506
1309.6457	655.3265	13	V	4	476.2463	238.6268
1424.6726	712.8400	14	D	3	377.1779	189.0926
1511.7047	756.3560	15	S	2	262.1510	131.5791
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9828	IPI00293533	1	1	NUP62	2475	2+	-0.0246	0.9994	R.HFLQQATQVNAWDR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	2475	Delta Mass	-0.0246	Protein	IPI00293533
Mass	1713.8460	Next	237.000	Fraction	VF_T13h_band06.mzXML
Hyper	433.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	92%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	14		
285.1346	143.0709	2	F	13	1576.7867	788.8970
398.2187	199.6130	3	L	12	1429.7183	715.3628
526.2772	263.6423	4	Q	11	1316.6342	658.8207
654.3358	327.6715	5	Q	10	1188.5756	594.7914
725.3729	363.1901	6	A	9	1060.5170	530.7622
826.4206	413.7139	7	T	8	989.4799	495.2436
954.4792	477.7433	8	Q	7	888.4322	444.7198
1053.5476	527.2774	9	V	6	760.3737	380.6905
1167.5905	584.2989	10	N	5	661.3052	331.1563
1238.6276	619.8175	11	A	4	547.2623	274.1348
1424.7070	712.8571	12	W	3	476.2252	238.6162
1539.7339	770.3706	13	D	2	290.1459	145.5766
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9733	IPI00293533	1	1	NUP62	2483	2+	-0.0222	0.9988	R.HFLQQATQVNAWDR.T

Peptide Details

SHOW MODIFICATIONS ›

Scan	2483	Delta Mass	-0.0222	Protein	IPI00293533
Mass	1713.8460	Next	235.000	Fraction	VF_T13h_band05.mzXML
Hyper	379.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	92%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	14		
285.1346	143.0709	2	F	13	1576.7867	788.8970
398.2187	199.6130	3	L	12	1429.7183	715.3628
526.2772	263.6423	4	Q	11	1316.6342	658.8207
654.3358	327.6715	5	Q	10	1188.5756	594.7914
725.3729	363.1901	6	A	9	1060.5170	530.7622
826.4206	413.7139	7	T	8	989.4799	495.2436
954.4792	477.7432	8	Q	7	888.4322	444.7198
1053.5476	527.2774	9	V	6	760.3737	380.6905
1167.5905	584.2989	10	N	5	661.3052	331.1563
1238.6276	619.8175	11	A	4	547.2623	274.1348
1424.7070	712.8571	12	W	3	476.2252	238.6162
1539.7339	770.3706	13	D	2	290.1459	145.5766
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9234	IPI00879638, IPI00798375, IPI00017617, IPI00651653, IPI00651677, IPI00889541, IPI00023785	1	1	DDX17, DDX5, DDX5, DDX17, DKFZp761H2016, DDX17, DDX17	2484	2+	-0.0116	0.9963	K.APILIATDVASR.G

Peptide Details

Scan	2484	Delta Mass	-0.0116	Protein	IPI00017617
Mass	1226.7100	Next	291.000	Fraction	VF_T13h_band01.mzXML
Hyper	410.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	73%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X ☑ Y ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
169.0972	85.0522	2	P	11	1155.6732	578.3402
282.1812	141.5942	3	I	10	1058.6204	529.8139
395.2653	198.1363	4	L	9	945.5364	473.2718
508.3493	254.6783	5	I	8	832.4523	416.7298
579.3865	290.1969	6	A	7	719.3682	360.1878
680.4341	340.7207	7	T	6	648.3311	324.6692
795.4611	398.2342	8	D	5	547.2835	274.1454
894.5295	447.7684	9	V	4	432.2565	216.6319
965.5666	483.2869	10	A	3	333.1881	167.0977
1052.5986	526.8030	11	S	2	262.1510	131.5791
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8236	IPI00795286, IPI00795693, IPI00181409, IPI00873716, IPI00791301, IPI00030131	1	1	TMPO, TMPO, TMPO, TMPO, TMPO, TMPO	2515	2+	-0.0140	0.9841	K.GAAGRPLELSDFR.M

Peptide Details

SHOW MODIFICATIONS ›

Scan	2515	Delta Mass	-0.0140	Protein	IPI00030131
Mass	1388.7280	Next	251.000	Fraction	VF_T13h_band05.mzXML
Hyper	335.000	PeptideProphet	0.98	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	6	Ion Percent	67%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	13		
129.0659	65.0366	2	A	12	1331.7066	666.3570
200.1030	100.5551	3	A	11	1260.6695	630.8384
257.1244	129.0659	4	G	10	1189.6324	595.3198
413.2255	207.1164	5	R	9	1132.6109	566.8091
510.2783	255.6428	6	P	8	976.5098	488.7585
623.3624	312.1848	7	L	7	879.4571	440.2322
752.4050	376.7061	8	E	6	766.3730	383.6901
865.4890	433.2482	9	L	5	637.3304	319.1688
952.5211	476.7642	10	S	4	524.2463	262.6268
1067.5480	534.2776	11	D	3	437.2143	219.1108
1214.6164	607.8118	12	F	2	322.1874	161.5973
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9643	IPI00807609, IPI00033466	1	1	CLEC11A, CLEC11A	2516	2+	-0.0071	0.9990	R.LAGLDAGLHQLHVR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	2516	Delta Mass	-0.0071	Protein	IPI00033466
Mass	1499.8441	Next	234.000	Fraction	VF_T13h_band02.mzXML
Hyper	392.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

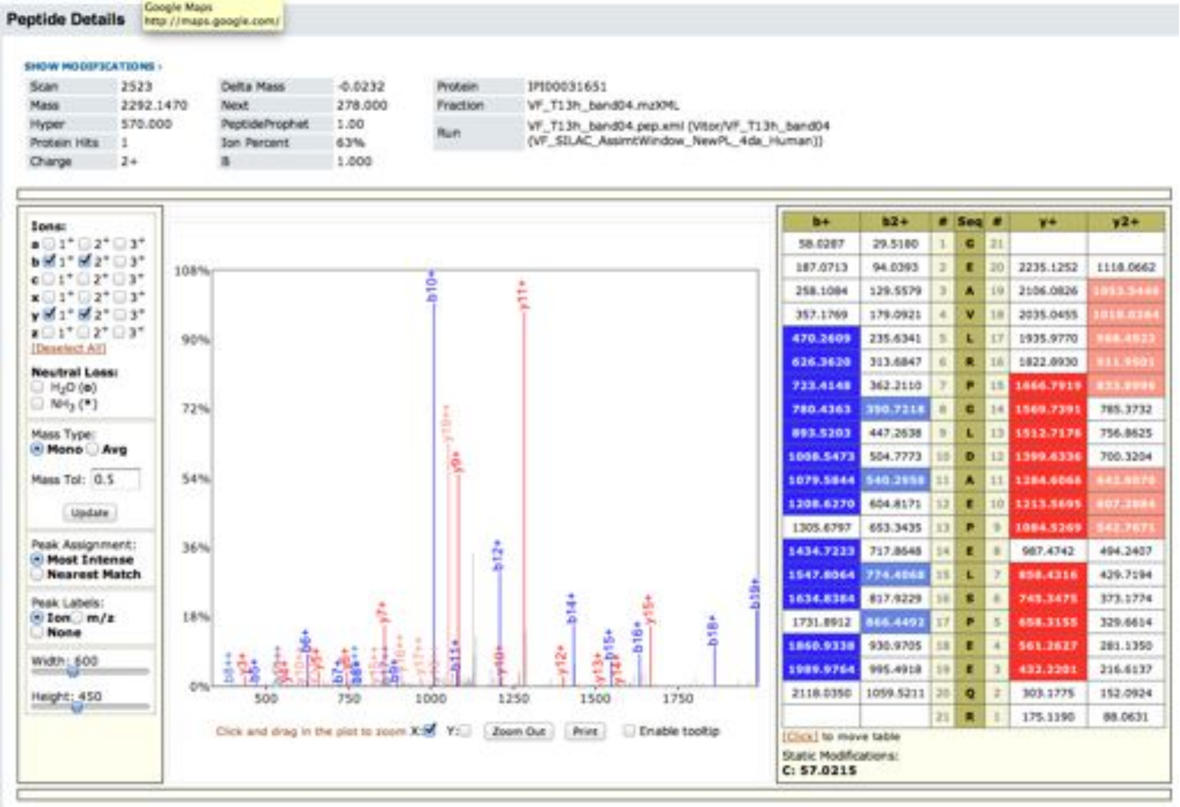
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	14		
185.1285	93.0679	2	A	13	1386.7601	693.8837
242.1499	121.5786	3	G	12	1315.7229	658.3651
355.2340	178.1206	4	L	11	1258.7015	629.8544
470.2609	235.6341	5	D	10	1145.6174	573.3123
541.2980	271.1527	6	A	9	1030.5905	515.7989
598.3195	299.6634	7	G	8	959.5534	480.2803
711.4036	356.2054	8	L	7	902.5319	451.7696
848.4625	424.7349	9	H	6	789.4478	395.2276
976.5211	488.7642	10	Q	5	652.3889	326.6981
1089.6051	545.3062	11	L	4	524.3303	262.6688
1226.6640	613.8357	12	H	3	411.2463	206.1268
1325.7324	663.3699	13	V	2	274.1874	137.5973
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00031651	1	1	FP15621	2523	2+	-0.0232	0.9999	K.GEAVLRPGLDAEPELSPEEQR.V



Scan	2523	Delta Mass	-0.0232	Protein	IPI00031651
Mass	2292.1470	Next	278.000	Fraction	VF_T13h_band04.mzXML
Hyper	570.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	63%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

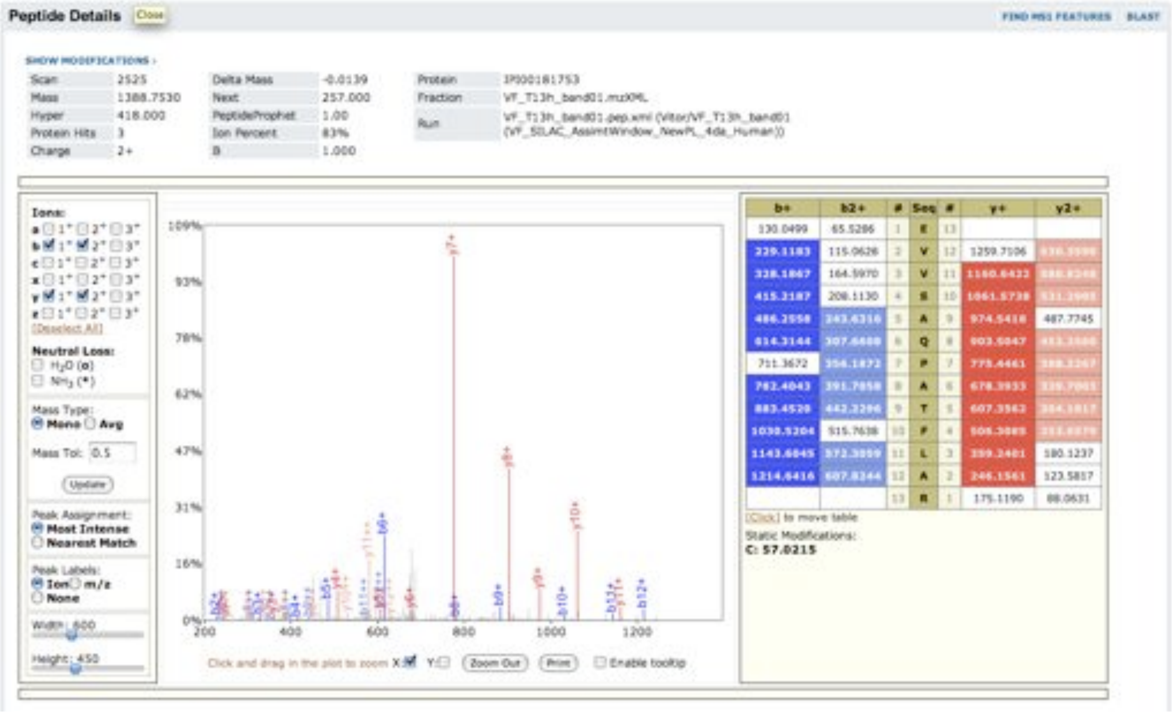
Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	21		
187.0713	94.0393	2	E	20	2235.1252	1118.0662
258.1084	129.5579	3	A	19	2106.0826	1053.5448
357.1769	179.0921	4	V	18	2035.0455	1018.0264
470.2609	235.6341	5	L	17	1935.9770	968.4923
626.3620	313.6847	6	R	16	1822.8930	911.9501
723.4148	362.2110	7	P	15	1666.7919	833.8996
780.4363	390.7218	8	G	14	1569.7391	785.3732
893.5203	447.2638	9	L	13	1512.7176	756.8625
1008.5473	504.7773	10	D	12	1399.6336	700.3204
1079.5844	540.2958	11	A	11	1284.6066	642.8070
1208.6270	604.8171	12	E	10	1213.5695	607.2884
1305.6797	653.3435	13	P	9	1084.5269	542.7671
1434.7223	717.8648	14	E	8	987.4742	494.2407
1547.8064	774.4068	15	L	7	858.4316	429.7194
1634.8384	817.9229	16	S	6	745.3475	373.1774
1731.8912	866.4492	17	P	5	658.3155	329.6614
1860.9338	930.9705	18	E	4	561.2827	281.1350
1989.9764	995.4918	19	E	3	432.2201	216.6137
2118.0350	1059.5211	20	Q	2	303.1775	152.0924
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9643	IPI00181753, IPI00909124, IPI00296713	1	1	GRN, -, GRN	2525	2+	-0.0139	0.9989	K.EVVSAQPATFLAR.S



Peptide Details

Scan	2525	Delta Mass	-0.0139	Protein	IPI00181753
Mass	1388.7530	Next	257.000	Fraction	VF_T13h_band01.mzXML
Hyper	418.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	13		
229.1183	115.0626	2	V	12	1259.7106	[illegible]
328.1867	164.5970	3	V	11	1160.6422	[illegible]
415.2187	208.1130	4	S	10	1061.5738	[illegible]
486.2558	243.6316	5	A	9	974.5418	487.7745
614.3144	307.6608	6	Q	8	903.5047	[illegible]
711.3672	356.1872	7	P	7	775.4461	[illegible]
782.4043	391.7058	8	A	6	678.3933	[illegible]
883.4520	442.2296	9	T	5	607.3562	[illegible]
1030.5204	515.7638	10	F	4	506.3085	[illegible]
1143.6045	572.3059	11	L	3	359.2401	180.1237
1214.6416	607.8244	12	A	2	246.1561	123.5817
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8759	IPI00793922, IPI00747273, IPI00789134, IPI00797221, IPI00795257, IPI00219018, IPI00788737	1	1	GAPDH, -, GAPDH, GAPDH, GAPDH, GAPD, GAPDH	2532	2+	+1.0000	0.9930	R.VPTANVSVVDLTCR.L

Peptide Details

Scan	2532	Delta Mass	+1.0000	Protein	IPI00219018
Mass	1530.7940	Next	300.000	Fraction	VF_T13h_band01.mzXML
Hyper	491.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	81%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	14		
197.1285	99.0679	2	P	13	1431.7261	716.3667
298.1761	149.5917	3	T	12	1334.6733	667.8403
369.2132	185.1103	4	A	11	1233.6256	617.3165
483.2562	242.1317	5	N	10	1162.5885	581.7979
582.3246	291.6659	6	V	9	1048.5456	524.7764
669.3566	335.1819	7	S	8	949.4772	475.2423
768.4250	384.7162	8	V	7	862.4451	431.7262
867.4934	434.2504	9	V	6	763.3767	382.1920
982.5204	491.7638	10	D	5	664.3083	332.6578
1095.6045	548.3059	11	L	4	549.2814	275.1443
1196.6521	598.8297	12	T	3	436.1973	218.6023
1356.6828	678.8450	13	C	2	335.1496	168.0785
		14	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Mass Type: ● Mono ○ Avg
Mass Tol: 0.5
Peak Assignment: ● Most Intense ○ Nearest Match
Peak Labels: ● Ion ○ m/z ○ None
Width: 600
Height: 450

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9759	IPI00902496, IPI00218922	1	1	-, SEC63	2537	2+	-0.0119	0.9996	R.VLLLSHLAR.M

Peptide Details

Scan	2537	Delta Mass	-0.0119	Protein	IPI00218922
Mass	1021.6520	Next	390.000	Fraction	VF_T13h_band01.mzXML
Hyper	581.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	88%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

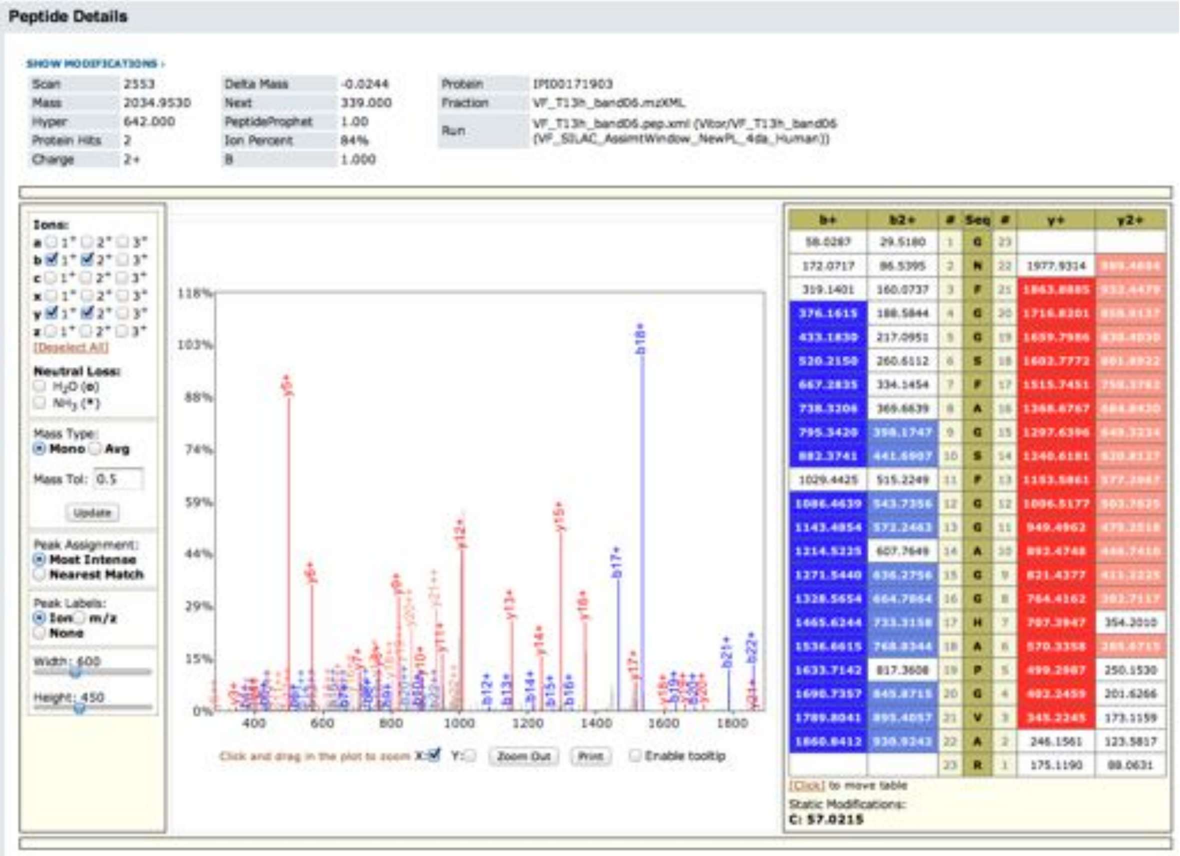
Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	9		
213.1598	107.0835	2	L	8	922.5833	461.7953
326.2438	163.6255	3	L	7	809.4992	405.2532
439.3279	220.1676	4	L	6	696.4151	348.7112
526.3599	263.6836	5	S	5	583.3311	292.1692
663.4188	332.2130	6	H	4	496.2990	248.6532
776.5029	388.7551	7	L	3	359.2401	180.1237
847.5400	424.2736	8	A	2	246.1561	123.5817
		9	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9881	IPI00383296, IPI00171903	1	1	HNRPM, HNRPM	2553	2+	-0.0244	0.9999	R.GNFGGSFAGSFGGAGGHAPGVAR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2553	Delta Mass	-0.0244	Protein	IPI00171903
Mass	2034.9530	Next	339.000	Fraction	VF_T13h_band06.mzXML
Hyper	642.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	84%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	23		
172.0717	86.5395	2	N	22	1977.9314	989.4684
319.1401	160.0737	3	F	21	1863.8885	932.4479
376.1615	188.5844	4	G	20	1716.8201	858.9137
433.1830	217.0951	5	G	19	1659.7986	830.4030
520.2150	260.6112	6	S	18	1602.7772	801.8922
667.2835	334.1454	7	F	17	1515.7451	758.3762
738.3206	369.6639	8	A	16	1368.6767	684.8420
795.3420	398.1747	9	G	15	1297.6396	649.3234
882.3741	441.6907	10	S	14	1240.6181	620.8127
1029.4425	515.2249	11	F	13	1153.5861	577.2967
1086.4639	543.7356	12	G	12	1006.5177	503.7625
1143.4854	572.2463	13	G	11	949.4962	475.2518
1214.5225	607.7649	14	A	10	892.4748	446.7410
1271.5440	636.2756	15	G	9	821.4377	411.2225
1328.5654	664.7864	16	G	8	764.4162	382.7117
1465.6244	733.3158	17	H	7	707.3947	354.2010
1536.6615	768.8344	18	A	6	570.3358	285.6715
1633.7142	817.3608	19	P	5	499.2987	250.1530
1690.7357	845.8715	20	G	4	402.2459	201.6266
1789.8041	895.4057	21	V	3	345.2245	173.1159
1860.8412	930.9242	22	A	2	246.1561	123.5817
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9639	IPI00302850, IPI00889157, IPI00903286	1	1	SNRPD1, LOC100129492, SNRPD1	2554	2+	-0.0174	0.9980	K.NREPVQLETLSIR.G

Peptide Details

Scan	2554	Delta Mass	-0.0174	Protein	IPI00302850
Mass	1554.8600	Next	264.000	Fraction	VF_T13h_band05.mzXML
Hyper	458.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

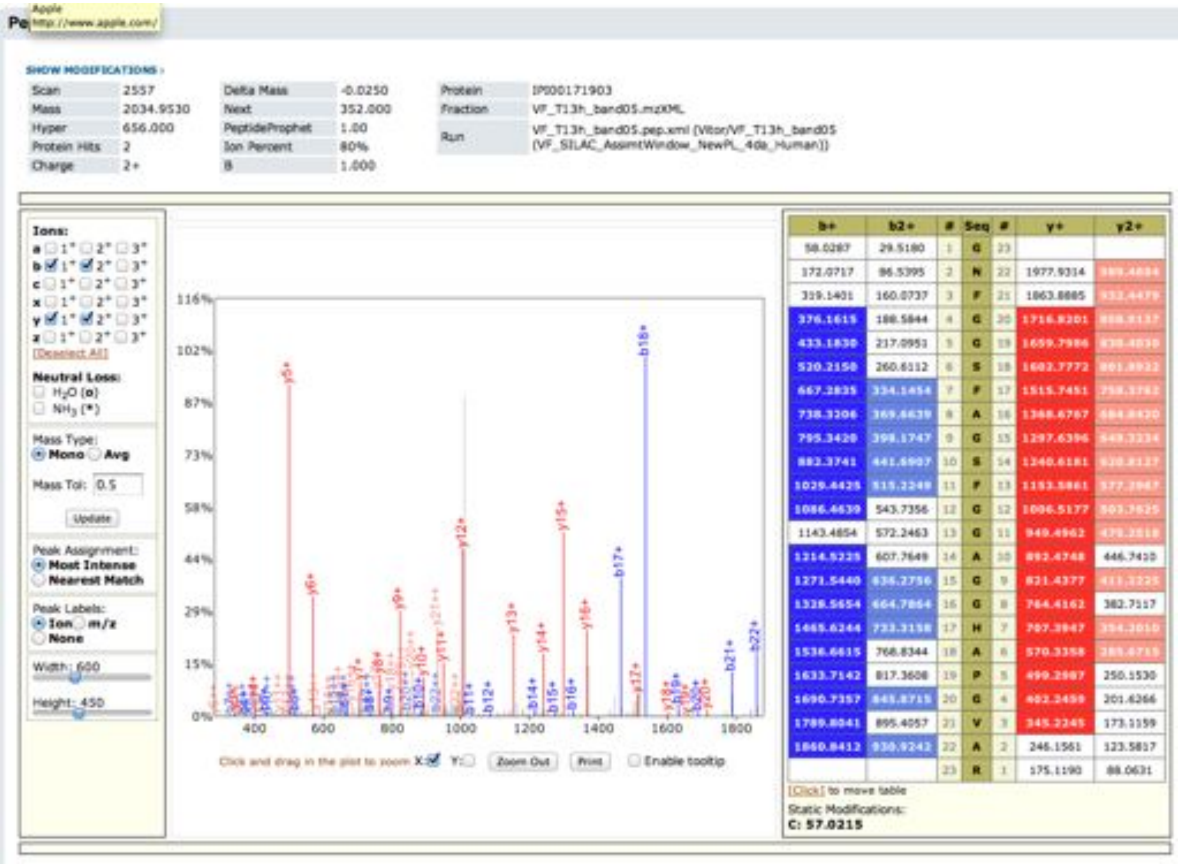
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	13		
271.1513	136.0793	2	R	12	1440.8169	720.9121
400.1939	200.6006	3	E	11	1284.7158	642.8615
497.2467	249.1270	4	P	10	1155.6732	578.3402
596.3151	298.6612	5	V	9	1058.6204	529.8139
724.3737	362.6905	6	Q	8	959.5520	480.2796
837.4577	419.2325	7	L	7	831.4934	416.2504
966.5003	483.7538	8	E	6	718.4094	359.7083
1067.5480	534.2776	9	T	5	589.3668	295.1870
1180.6321	590.8197	10	L	4	488.3191	244.6632
1267.6641	634.3357	11	S	3	375.2350	188.1212
1380.7482	690.8777	12	I	2	288.2030	144.6051
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9877	IPI00383296, IPI00171903	1	1	HNRPM, HNRPM	2557	2+	-0.0250	1.0000	R.GNFGGSFAGSFGGAGGHAPGVAR.K



Scan	2557	Delta Mass	-0.0250	Protein	IPI00171903
Mass	2034.9530	Next	352.000	Fraction	VF_T13h_band05.mzXML
Hyper	656.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	80%		
Charge	2+	B	1.000		

a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg
Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

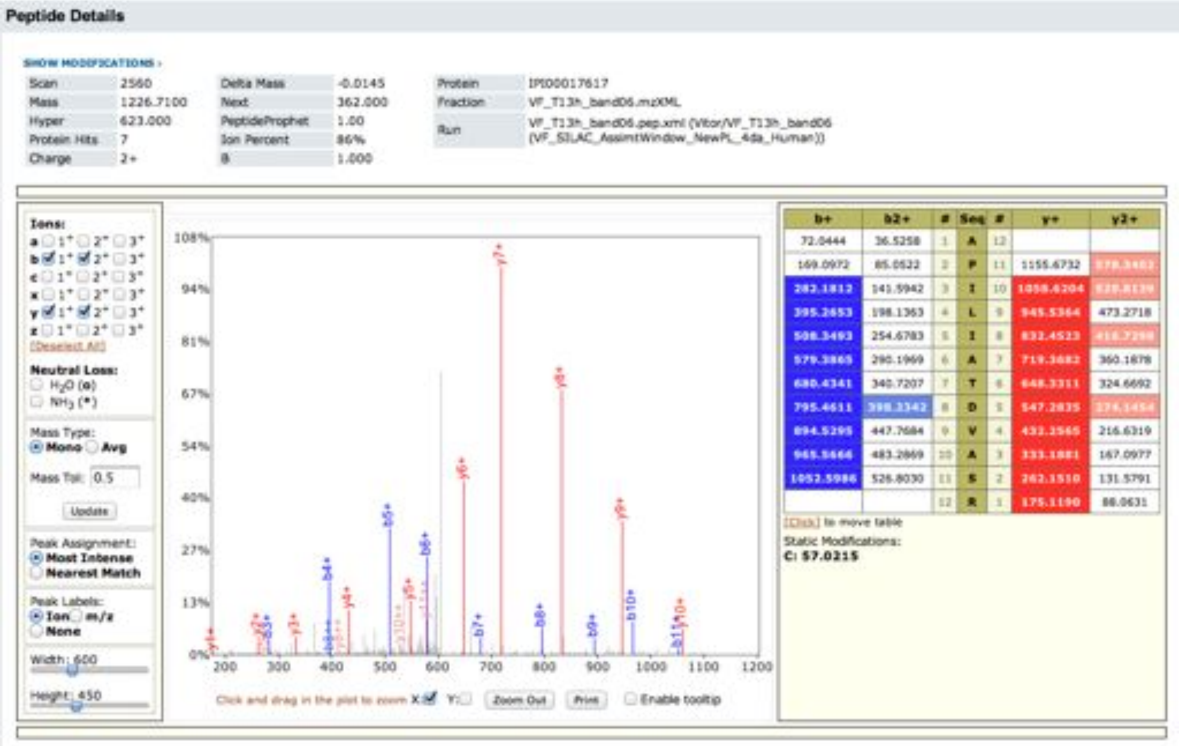
Peak Labels: ● Ion ○ m/z ○ None

Width: 600
Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	23		
172.0717	86.5395	2	N	22	1977.9314	989.4694
319.1401	160.0737	3	F	21	1863.8885	932.4479
376.1615	188.5844	4	G	20	1716.8201	858.9137
433.1830	217.0951	5	G	19	1659.7986	830.4030
520.2150	260.6112	6	S	18	1602.7772	801.8922
667.2835	334.1454	7	F	17	1515.7451	758.3762
738.3206	369.6639	8	A	16	1368.6767	684.8420
795.3420	398.1747	9	G	15	1297.6396	649.3234
882.3741	441.6907	10	S	14	1240.6181	620.8127
1029.4425	515.2249	11	F	13	1153.5861	577.2967
1086.4639	543.7356	12	G	12	1006.5177	503.7625
1143.4854	572.2463	13	G	11	949.4962	475.2518
1214.5225	607.7649	14	A	10	892.4748	446.7410
1271.5440	636.2756	15	G	9	821.4377	411.2225
1328.5654	664.7864	16	G	8	764.4162	382.7117
1465.6244	733.3158	17	H	7	707.3947	354.2010
1536.6615	768.8344	18	A	6	570.3358	285.6715
1633.7142	817.3608	19	P	5	499.2987	250.1530
1690.7357	845.8715	20	G	4	402.2459	201.6266
1789.8041	895.4057	21	V	3	345.2245	173.1159
1860.8412	930.9242	22	A	2	246.1561	123.5817
		23	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9870	IPI00879638, IPI00798375, IPI00017617, IPI00651653, IPI00651677, IPI00889541, IPI00023785	1	1	DDX17, DDX5, DDX5, DDX17, DKFZp761H2016, DDX17, DDX17	2560	2+	-0.0145	0.9998	K.APILIATDVASR.G



Peptide Details

SHOW MODIFICATIONS ›

Scan	2560	Delta Mass	-0.0145	Protein	IPI00017617
Mass	1226.7100	Next	362.000	Fraction	VF_T13h_band06.mzXML
Hyper	623.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

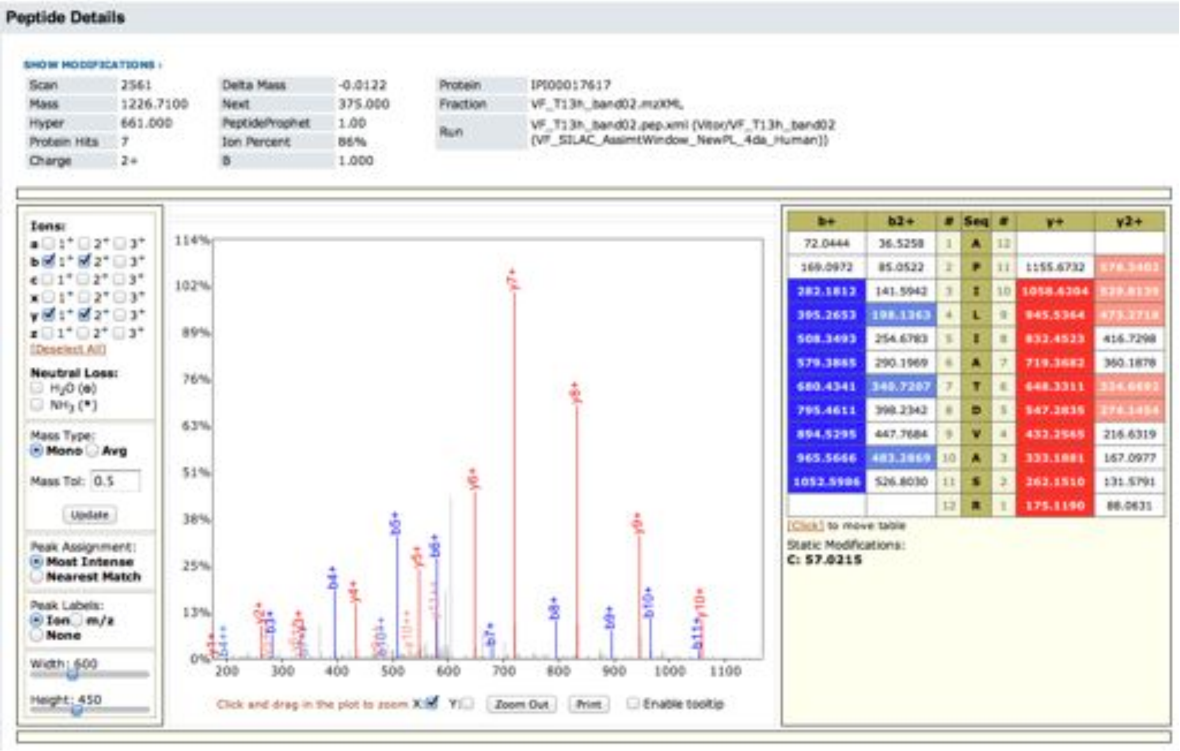
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
169.0972	85.0522	2	P	11	1155.6732	578.3402
282.1812	141.5942	3	I	10	1058.6204	529.8139
395.2653	198.1363	4	L	9	945.5364	473.2718
508.3493	254.6783	5	I	8	832.4523	416.7298
579.3865	290.1969	6	A	7	719.3682	360.1878
680.4341	340.7207	7	T	6	648.3311	324.6692
795.4611	398.2342	8	D	5	547.2835	274.1454
894.5295	447.7684	9	V	4	432.2565	216.6319
965.5666	483.2869	10	A	3	333.1881	167.0977
1052.5986	526.8030	11	S	2	262.1510	131.5791
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9801	IPI00879638, IPI00798375, IPI00017617, IPI00651653, IPI00651677, IPI00889541, IPI00023785	1	1	DDX17, DDX5, DDX5, DDX17, DKFZp761H2016, DDX17, DDX17	2561	2+	-0.0122	0.9999	K.APILIATDVASR.G



Peptide Details

SHOW MODIFICATIONS ›

Scan	2561	Delta Mass	-0.0122	Protein	IPI00017617
Mass	1226.7100	Next	375.000	Fraction	VF_T13h_band02.mzXML
Hyper	661.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
169.0972	85.0522	2	P	11	1155.6732	578.3402
282.1812	141.5942	3	I	10	1058.6204	529.8139
395.2653	198.1363	4	L	9	945.5364	473.2718
508.3493	254.6783	5	I	8	832.4523	416.7298
579.3865	290.1969	6	A	7	719.3682	360.1878
680.4341	340.7207	7	T	6	648.3311	324.6692
795.4611	398.2342	8	D	5	547.2835	274.1454
894.5295	447.7684	9	V	4	432.2565	216.6319
965.5666	483.2869	10	A	3	333.1881	167.0977
1052.5986	526.8030	11	S	2	262.1510	131.5791
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9865	IPI00220573, IPI00033494, IPI00719669, IPI00604523, IPI00888129	1	1	MRLC3, MRLC2, MRLC2, MRCL3, LOC642076	2571	2+	-0.0147	0.9999	R.FTDEEVDELYR.E

Peptide Details

SHOW MODIFICATIONS ›

Scan	2571	Delta Mass	-0.0147	Protein	IPI00033494
Mass	1415.6330	Next	373.000	Fraction	VF_T13h_band05.mzXML
Hyper	601.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H$_2$O (o)
☐ NH$_3$ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

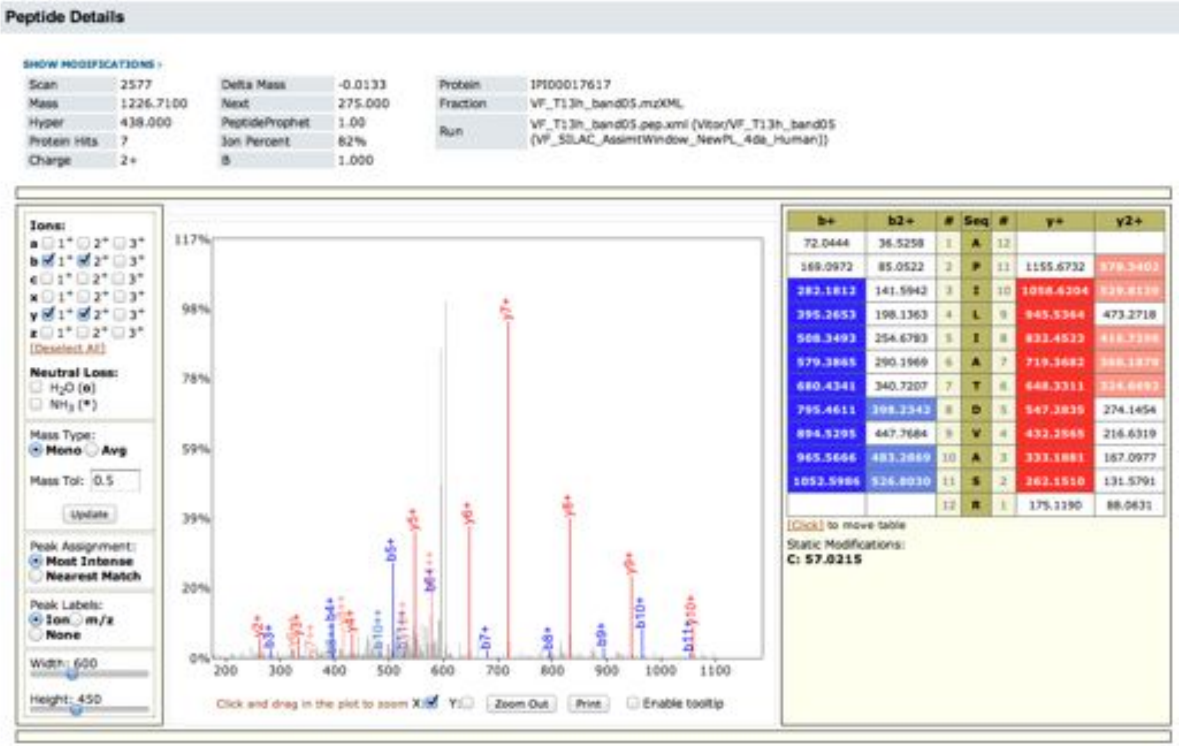
Height: 450

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
249.1234	125.0653	2	T	10	1268.5641	634.7857
364.1503	182.5788	3	D	9	1167.5164	584.2618
493.1929	247.1001	4	E	8	1052.4895	526.7484
622.2355	311.6214	5	E	7	923.4469	462.2271
721.3039	361.1556	6	V	6	794.4043	397.7058
836.3309	418.6691	7	D	5	695.3359	348.1716
965.3734	483.1904	8	E	4	580.3089	290.6581
1078.4575	539.7324	9	L	3	451.2663	226.1368
1241.5208	621.2641	10	Y	2	338.1823	169.5948
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9804	IPI00879638, IPI00798375, IPI00017617, IPI00651653, IPI00651677, IPI00889541, IPI00023785	1	1	DDX17, DDX5, DDX5, DDX17, DKFZp761 H2016, DDX17, DDX17	2577	2+	-0.0133	0.9994	K.APILIATDVASR.G



Peptide Details

SHOW MODIFICATIONS ›

Scan	2577	Delta Mass	-0.0133	Protein	IPI00017617
Mass	1226.7100	Next	275.000	Fraction	VF_T13h_band05.mzXML
Hyper	438.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	12		
169.0972	85.0522	2	P	11	1155.6732	578.3403
282.1812	141.5942	3	I	10	1058.6204	529.8139
395.2653	198.1363	4	L	9	945.5364	473.2718
508.3493	254.6783	5	I	8	832.4523	416.7298
579.3865	290.1969	6	A	7	719.3682	360.1878
680.4341	340.7207	7	T	6	648.3311	324.6692
795.4611	398.2342	8	D	5	547.2835	274.1454
894.5295	447.7684	9	V	4	432.2565	216.6319
965.5666	483.2869	10	A	3	333.1881	167.0977
1052.5986	526.8030	11	S	2	262.1510	131.5791
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9592	IPI00893179, IPI00893062, IPI00889791, IPI00644712, IPI00888181, IPI00888013	1	1	XRCC6, XRCC6, XRCC6, XRCC6, LOC389901, LOC389901	2577	2+	-0.0141	0.9987	R.SDSFENPVLQQHFR.N

Peptide Details

SHOW MODIFICATIONS ›

Scan	2577	Delta Mass	-0.0141	Protein	IPI00644712
Mass	1703.8140	Next	266.000	Fraction	VF_T13h_band02.mzXML
Hyper	415.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	14		
203.0662	102.0368	2	D	13	1616.7816	808.8944
290.0983	145.5528	3	S	12	1501.7546	751.3810
437.1667	219.0870	4	F	11	1414.7226	707.8649
566.2093	283.6083	5	E	10	1267.6542	634.3307
680.2522	340.6297	6	N	9	1138.6116	569.8094
777.3050	389.1561	7	P	8	1024.5687	512.7880
876.3734	438.6903	8	V	7	927.5159	464.2616
989.4575	495.2324	9	L	6	828.4475	414.7274
1117.5160	559.2617	10	Q	5	715.3634	358.1854
1245.5746	623.2909	11	Q	4	587.3049	294.1561
1382.6335	691.8204	12	H	3	459.2463	230.1268
1529.7019	765.3546	13	F	2	322.1874	161.5973
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9721	IPI00029114, IPI00791262	1	1	ICT1, ICT1	2578	2+	-0.0148	0.9987	R.LGELILTSESSR.Y

Peptide Details

SHOW MODIFICATIONS »

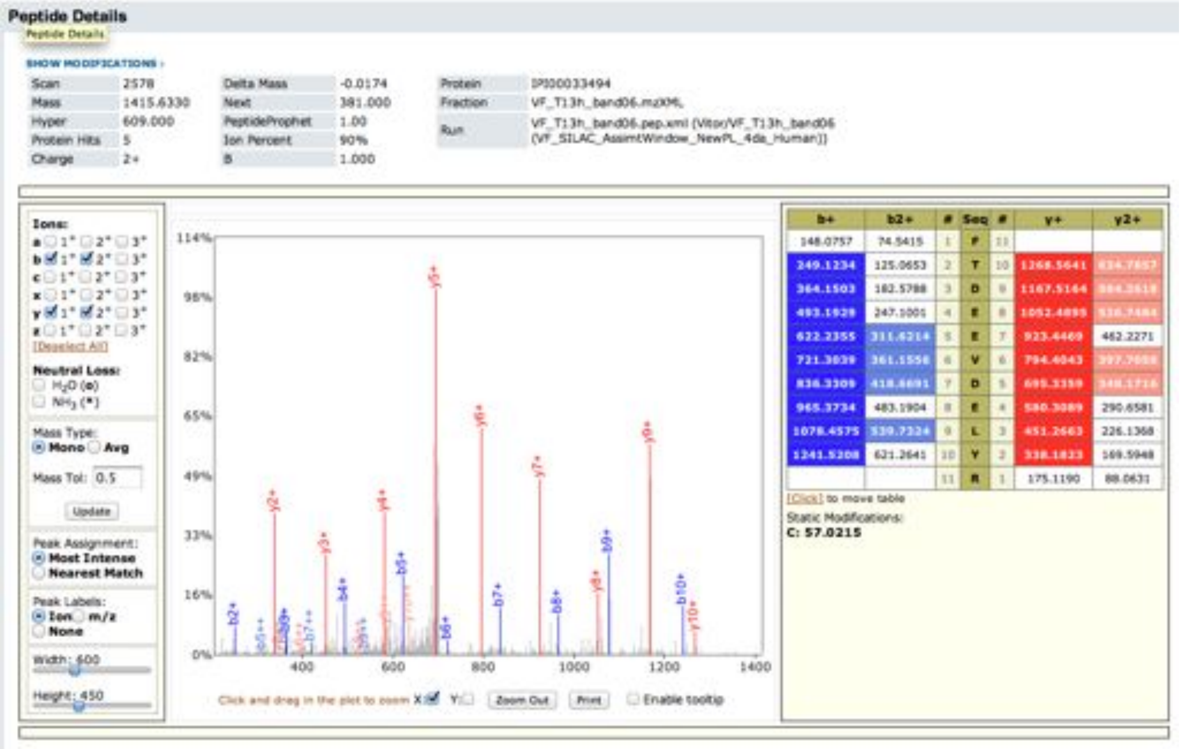
Scan	2578	Delta Mass	-0.0148	Protein	IPI00029114
Mass	1304.7060	Next	295.000	Fraction	VF_T13h_band05.mzXML
Hyper	431.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	82%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	12		
171.1128	86.0600	2	G	11	1191.6216	596.3144
300.1554	150.5813	3	E	10	1134.6001	567.8037
413.2395	207.1234	4	L	9	1005.5575	503.2824
526.3235	263.6654	5	I	8	892.4734	446.7404
639.4076	320.2074	6	L	7	779.3894	390.1983
740.4553	370.7313	7	T	6	666.3053	333.6563
827.4873	414.2473	8	S	5	565.2576	283.1325
956.5299	478.7686	9	E	4	478.2256	239.6164
1043.5619	522.2846	10	S	3	349.1830	175.0951
1130.5939	565.8006	11	S	2	262.1510	131.5791
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9859	IPI00220573, IPI00033494, IPI00719669, IPI00604523, IPI00888129	1	1	MRLC3, MRLC2, MRLC2, MRCL3, LOC642076	2578	2+	-0.0174	0.9997	R.FTDEEVDELYR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	2578	Delta Mass	-0.0174	Protein	IPI00033494
Mass	1415.6330	Next	381.000	Fraction	VF_T13h_band06.mzXML
Hyper	609.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

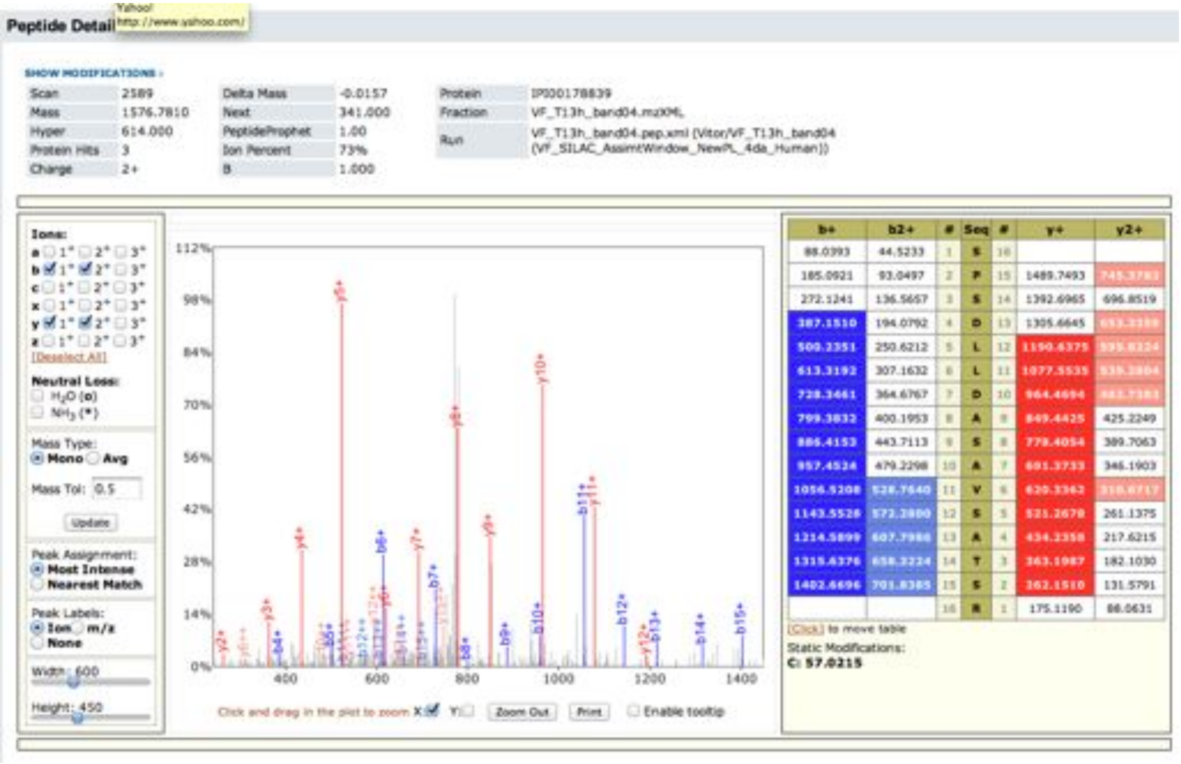
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
249.1234	125.0653	2	T	10	1268.5641	634.7857
364.1503	182.5788	3	D	9	1167.5164	584.2618
493.1929	247.1001	4	E	8	1052.4895	526.7484
622.2355	311.6214	5	E	7	923.4469	462.2271
721.3039	361.1556	6	V	6	794.4043	397.7058
836.3309	418.6691	7	D	5	695.3359	348.1716
965.3734	483.1904	8	E	4	580.3089	290.6581
1078.4575	539.7324	9	L	3	451.2663	226.1368
1241.5208	621.2641	10	Y	2	338.1823	169.5948
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00178839, IPI00477418, IPI00293402	1	1	STX10, STX10, STX10	2589	2+	-0.0157	0.9999	K.SPSDLLDASAVSATSR.Y



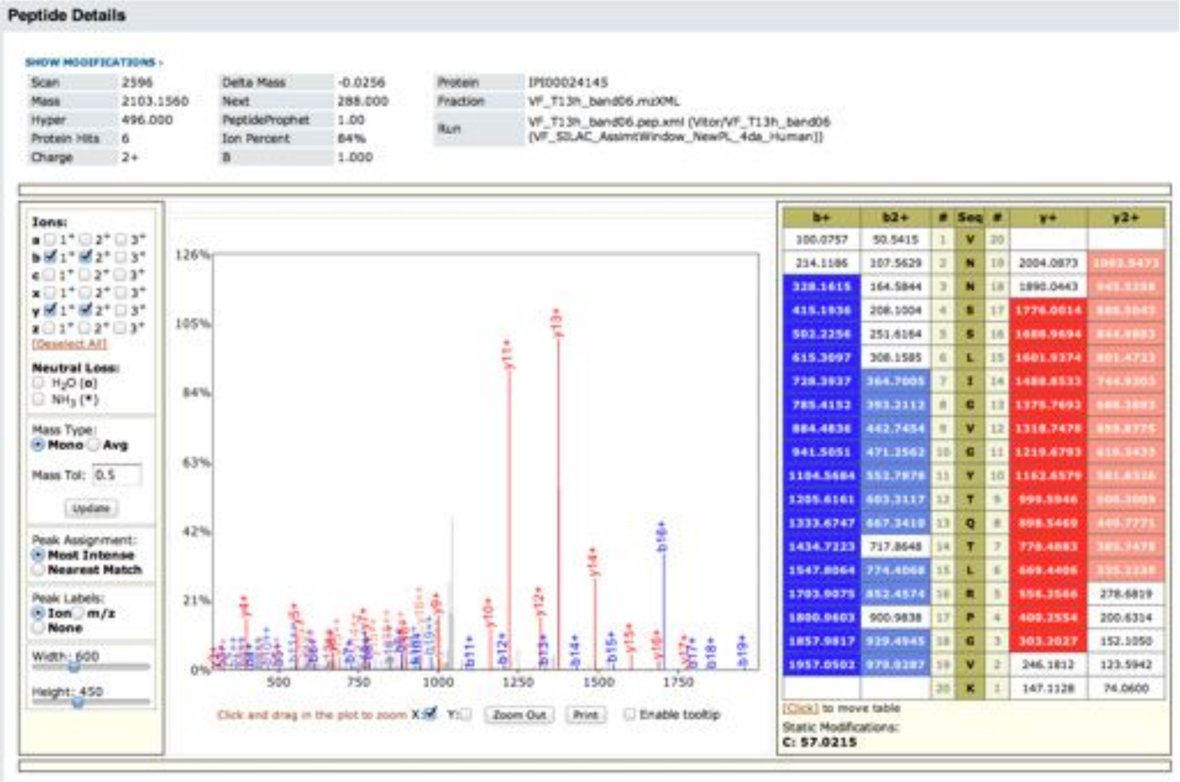
Peptide Detail

Scan	2589	Delta Mass	-0.0157	Protein	IPI00178839
Mass	1576.7810	Next	341.000	Fraction	VF_T13h_band04.mzXML
Hyper	614.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	73%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	16		
185.0921	93.0497	2	P	15	1489.7493	745.3783
272.1241	136.5657	3	S	14	1392.6965	696.8519
387.1510	194.0792	4	D	13	1305.6645	653.3359
500.2351	250.6212	5	L	12	1190.6375	595.8224
613.3192	307.1632	6	L	11	1077.5535	539.2804
728.3461	364.6767	7	D	10	964.4694	482.7383
799.3832	400.1953	8	A	9	849.4425	425.2249
886.4153	443.7113	9	S	8	778.4054	389.7063
957.4524	479.2298	10	A	7	691.3733	346.1903
1056.5208	528.7640	11	V	6	620.3362	310.6717
1143.5528	572.2800	12	S	5	521.2678	261.1375
1214.5899	607.7986	13	A	4	434.2358	217.6215
1315.6376	658.3224	14	T	3	363.1987	182.1030
1402.6696	701.8385	15	S	2	262.1510	131.5791
		16	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9838	IPI00455531, IPI00737171, IPI00888783, IPI00216026, IPI00902560, IPI00024145	1	1	LOC729317, LOC729317, LOC729317, VDAC2, VDAC2, VDAC2	2596	2+	-0.0256	0.9995	K.VNNSSLIGVGYTQTLRPGVK.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	2596	Delta Mass	-0.0256	Protein	IPI00024145
Mass	2103.1560	Next	288.000	Fraction	VF_T13h_band06.mzXML
Hyper	496.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	84%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	20		
214.1186	107.5629	2	N	19	2004.0873	1002.5473
328.1615	164.5844	3	N	18	1890.0443	945.5258
415.1936	208.1004	4	S	17	1776.0014	888.5043
502.2256	251.6164	5	S	16	1688.9694	844.9883
615.3097	308.1585	6	L	15	1601.9374	801.4723
728.3937	364.7005	7	I	14	1488.8533	744.9303
785.4152	393.2112	8	G	13	1375.7693	688.3883
884.4836	442.7454	9	V	12	1318.7478	659.8775
941.5051	471.2562	10	G	11	1219.6793	610.3433
1104.5684	552.7878	11	Y	10	1162.6579	581.8326
1205.6161	603.3117	12	T	9	999.5946	500.3009
1333.6747	667.3410	13	Q	8	898.5469	449.7771
1434.7223	717.8648	14	T	7	770.4883	385.7478
1547.8064	774.4068	15	L	6	669.4406	335.2238
1703.9075	852.4574	16	R	5	556.3566	278.6819
1800.9603	900.9838	17	P	4	400.2554	200.6314
1857.9817	929.4945	18	G	3	303.2027	152.1050
1957.0502	979.0287	19	V	2	246.1812	123.5942
		20	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9796	IPI00646310, IPI00060107	1	1	CHCHD1, CHCHD1	2608	2+	-0.0145	0.9991	K.EIQGFLDCAAR.A

Peptide Details

SHOW MODIFICATIONS ›

Scan	2608	Delta Mass	-0.0145	Protein	IPI00060107
Mass	1279.6100	Next	229.000	Fraction	VF_T13h_band06.mzXML
Hyper	407.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

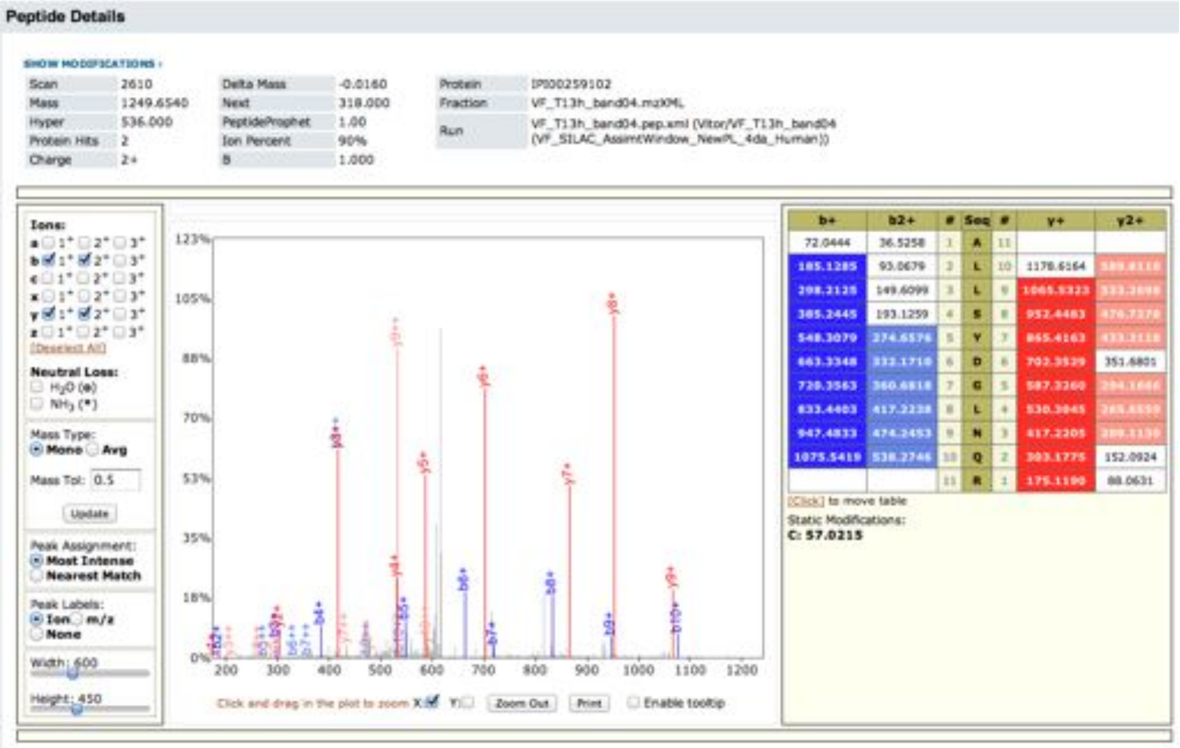
Click and drag in the plot to zoom X ☑ Y ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	11		
243.1339	122.0706	2	I	10	1150.5674	575.7873
371.1925	186.0999	3	Q	9	1037.4833	519.2453
428.2140	214.6106	4	G	8	909.4247	455.2160
575.2824	288.1448	5	F	7	852.4033	426.7053
688.3665	344.6869	6	L	6	705.3349	353.1711
803.3934	402.2003	7	D	5	592.2508	296.6290
963.4241	482.2157	8	C	4	477.2239	239.1156
1034.4612	517.7342	9	A	3	317.1932	159.1002
1105.4983	553.2528	10	A	2	246.1561	123.5817
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00259102, IPI00657648	1	1	EPDR1, UCC1	2610	2+	-0.0160	0.9998	R.ALLSYDGLNQR.V



Peptide Details

SHOW MODIFICATIONS ›

Scan	2610	Delta Mass	-0.0160	Protein	IPI00259102
Mass	1249.6540	Next	318.000	Fraction	VF_T13h_band04.mzXML
Hyper	536.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	11		
185.1285	93.0679	2	L	10	1178.6164	589.8118
298.2125	149.6099	3	L	9	1065.5323	533.2698
385.2445	193.1259	4	S	8	952.4483	476.7278
548.3079	274.6576	5	Y	7	865.4163	433.2118
663.3348	332.1710	6	D	6	702.3529	351.6801
720.3563	360.6818	7	G	5	587.3260	294.1666
833.4403	417.2238	8	L	4	530.3045	265.6559
947.4833	474.2453	9	N	3	417.2205	209.1139
1075.5419	538.2746	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9730	IPI00793922, IPI00747273, IPI00789134, IPI00797221, IPI00795257, IPI00219018, IPI00788737	1	1	GAPDH, -, GAPDH, GAPDH, GAPDH, GAPD, GAPDH	2613	2+	-0.0186	0.9995	R.VPTANVSVVDLTCR.L

Scan	2613
Mass	1530.7940
Hyper	443.000
Protein Hits	7
Charge	2+

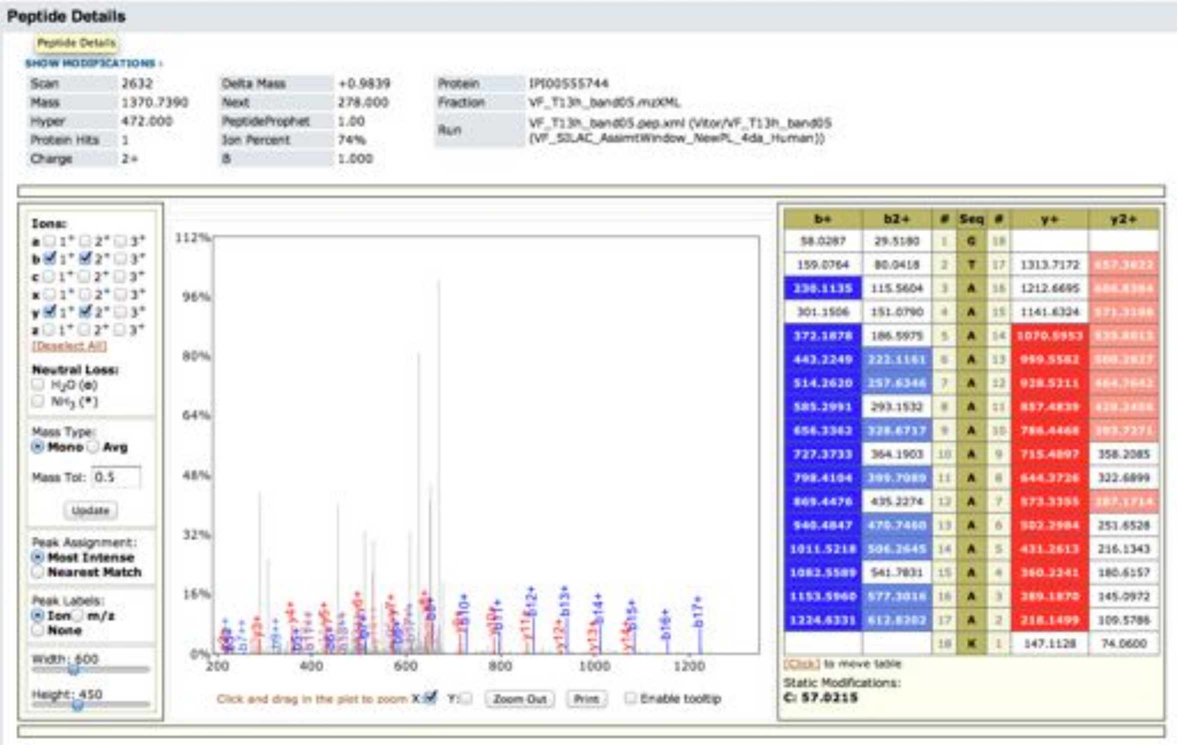
Delta Mass	-0.0186
Next	268.000
PeptideProphet	1.00
Ion Percent	58%
B	1.000

Protein	IPI00219018
Fraction	VF_T13h_band02.mzXML
Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimWindow_NewPL_4da_Human))

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	14		
197.1285	99.0679	2	P	13	1431.7261	716.3667
298.1761	149.5917	3	T	12	1334.6733	667.8403
369.2132	185.1103	4	A	11	1233.6256	617.3165
483.2562	242.1317	5	N	10	1162.5885	581.7979
582.3246	291.6659	6	V	9	1048.5456	524.7764
669.3566	335.1819	7	S	8	949.4772	475.2422
768.4250	384.7162	8	V	7	862.4451	431.7262
867.4934	434.2504	9	V	6	763.3767	382.1920
982.5204	491.7638	10	D	5	664.3083	332.6578
1095.6045	548.3059	11	L	4	549.2814	275.1443
1196.6521	598.8297	12	T	3	436.1973	218.6023
1356.6828	678.8450	13	C	2	335.1496	168.0785
		14	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9422	IPI00555744	1	1	RPL14	2632	2+	+0.9839	0.9961	K.GTAAAAAAAAAAAAAAAK.V



Peptide Details

Scan	2632	Delta Mass	+0.9839	Protein	IPI00555744
Mass	1370.7390	Next	278.000	Fraction	VF_T13h_band05.mzXML
Hyper	472.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	74%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

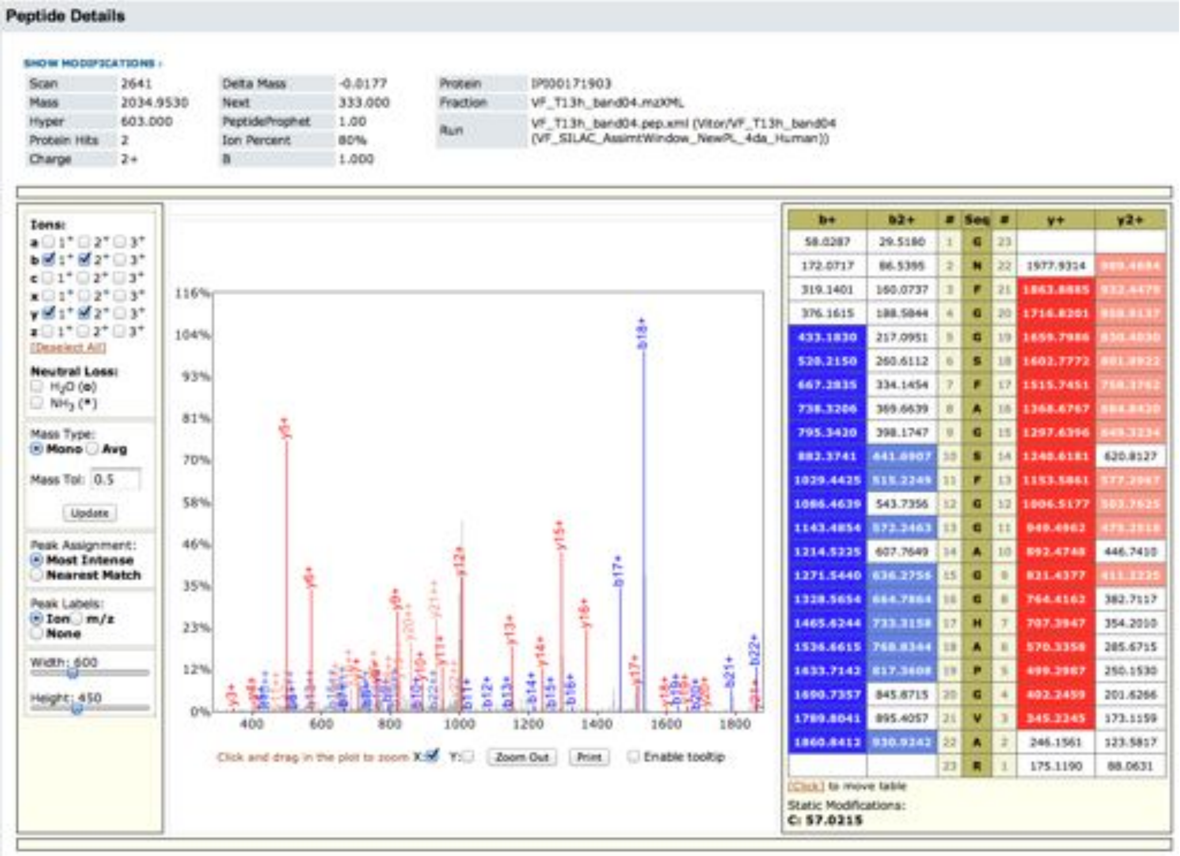
Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	18		
159.0764	80.0418	2	T	17	1313.7172	657.3622
230.1135	115.5604	3	A	16	1212.6695	606.8384
301.1506	151.0790	4	A	15	1141.6324	571.3198
372.1878	186.5975	5	A	14	1070.5953	535.8013
443.2249	222.1161	6	A	13	999.5582	500.2827
514.2620	257.6346	7	A	12	928.5211	464.7642
585.2991	293.1532	8	A	11	857.4839	429.2456
656.3362	328.6717	9	A	10	786.4468	393.7271
727.3733	364.1903	10	A	9	715.4097	358.2085
798.4104	399.7089	11	A	8	644.3726	322.6899
869.4476	435.2274	12	A	7	573.3355	287.1714
940.4847	470.7460	13	A	6	502.2984	251.6528
1011.5218	506.2645	14	A	5	431.2613	216.1343
1082.5589	541.7831	15	A	4	360.2241	180.6157
1153.5960	577.3016	16	A	3	289.1870	145.0972
1224.6331	612.8202	17	A	2	218.1499	109.5786
		18	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00383296, IPI00171903	1	1	HNRPM, HNRPM	2641	2+	-0.0177	0.9999	R.GNFGGSFAGSFGGAGGHAPGVAR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2641	Delta Mass	-0.0177	Protein	IPI00171903
Mass	2034.9530	Next	333.000	Fraction	VF_T13h_band04.mzXML
Hyper	603.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	80%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	23		
172.0717	86.5395	2	N	22	1977.9314	989.4684
319.1401	160.0737	3	F	21	1863.8885	932.4479
376.1615	188.5844	4	G	20	1716.8201	858.9137
433.1830	217.0951	5	G	19	1659.7986	830.4030
520.2150	260.6112	6	S	18	1602.7772	801.8922
667.2835	334.1454	7	F	17	1515.7451	758.3762
738.3206	369.6639	8	A	16	1368.6767	684.8420
795.3420	398.1747	9	G	15	1297.6396	649.3234
882.3741	441.0907	10	S	14	1240.6181	620.8127
1029.4425	515.2249	11	F	13	1153.5861	577.2967
1086.4639	543.7356	12	G	12	1006.5177	503.7625
1143.4854	572.2463	13	G	11	949.4962	475.2518
1214.5225	607.7649	14	A	10	892.4748	446.7410
1271.5440	636.2756	15	G	9	821.4377	411.2225
1328.5654	664.7864	16	G	8	764.4162	382.7117
1465.6244	733.3158	17	H	7	707.3947	354.2010
1536.6615	768.8344	18	A	6	570.3358	285.6715
1633.7142	817.3608	19	P	5	499.2987	250.1530
1690.7357	845.8715	20	G	4	402.2459	201.6266
1789.8041	895.4057	21	V	3	345.2245	173.1159
1860.8412	930.9242	22	A	2	246.1561	123.5817
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9810	IPI00293254, IPI00065554, IPI00879242, IPI00879259, IPI00872855, IPI00009841	1	1	EWSR1, EWSR1, EWSR1, EWSR1, EWSR1, EWSR1	2641	2+	-0.0248	0.9999	R.AGDWQCPNPGCGNQNFAWR.T

Peptide Details

Scan	2641
Mass	2234.9240
Hyper	596.000
Protein Hits	6
Charge	2+

Delta Mass	-0.0248
Next	321.000
PeptideProphet	1.00
Ion Percent	78%
B	1.000

Protein	IPI00009841
Fraction	VF_T13h_band01.mzXML
Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	19		
129.0659	65.0366	2	G	18	2163.8873	1082.4473
244.0928	122.5500	3	D	17	2106.8658	1053.9365
430.1721	215.5897	4	W	16	1991.8389	996.4231
558.2307	279.6190	5	Q	15	1805.7596	903.3834
718.2614	359.6343	6	C	14	1677.7010	839.3541
815.3141	408.1607	7	P	13	1517.6703	759.3388
929.3571	465.1822	8	N	12	1420.6175	710.8124
1026.4098	513.7086	9	P	11	1306.5746	653.7909
1083.4313	542.2193	10	G	10	1209.5218	605.2646
1243.4620	622.2346	11	C	9	1152.5004	576.7538
1300.4834	650.7454	12	G	8	992.4697	496.7385
1414.5264	707.7668	13	N	7	935.4482	468.2279
1542.5849	771.7961	14	Q	6	821.4053	411.2063
1656.6279	828.8176	15	N	5	693.3467	347.1770
1803.6963	902.3518	16	F	4	579.3038	290.1555
1874.7334	937.8703	17	A	3	432.2354	216.6213
2060.8127	1030.9100	18	W	2	361.1983	181.1028
		19	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9535	IPI00556640, IPI00012503, IPI00873201, IPI00744835, IPI00873020, IPI00219825	1	1	PSAP, PSAP, PSAP, PSAP, PSAP, PSAP	2644	2+	-0.0129	0.9971	K.GCSFLPDPYQK.Q

Peptide Details

SHOW MODIFICATIONS ›

Scan	2644	Delta Mass	-0.0129	Protein	IPI00012503
Mass	1311.6040	Next	324.000	Fraction	VF_T13h_band05.mzXML
Hyper	433.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4de_Human))
Protein Hits	6	Ion Percent	60%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	11		
218.0594	109.5334	2	C	10	1254.5824	627.7948
305.0915	153.0494	3	S	9	1094.5517	547.7795
452.1599	226.5836	4	F	8	1007.5197	504.2635
565.2439	283.1256	5	L	7	860.4512	430.7293
662.2967	331.6520	6	P	6	747.3672	374.1872
777.3236	389.1655	7	D	5	650.3144	325.6608
874.3764	437.6918	8	P	4	535.2875	268.1474
1037.4397	519.2235	9	Y	3	438.2347	219.6210
1165.4983	583.2528	10	Q	2	275.1714	138.0893
		11	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9865	IPI00009407	1	1	DAD1	2659	2+	-0.0164	0.9999	R.FLEEYLSSTPQR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	2659	Delta Mass	-0.0164	Protein	IPI00009407
Mass	1469.7270	Next	349.000	Fraction	VF_T13h_band05.mzXML
Hyper	577.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	91%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

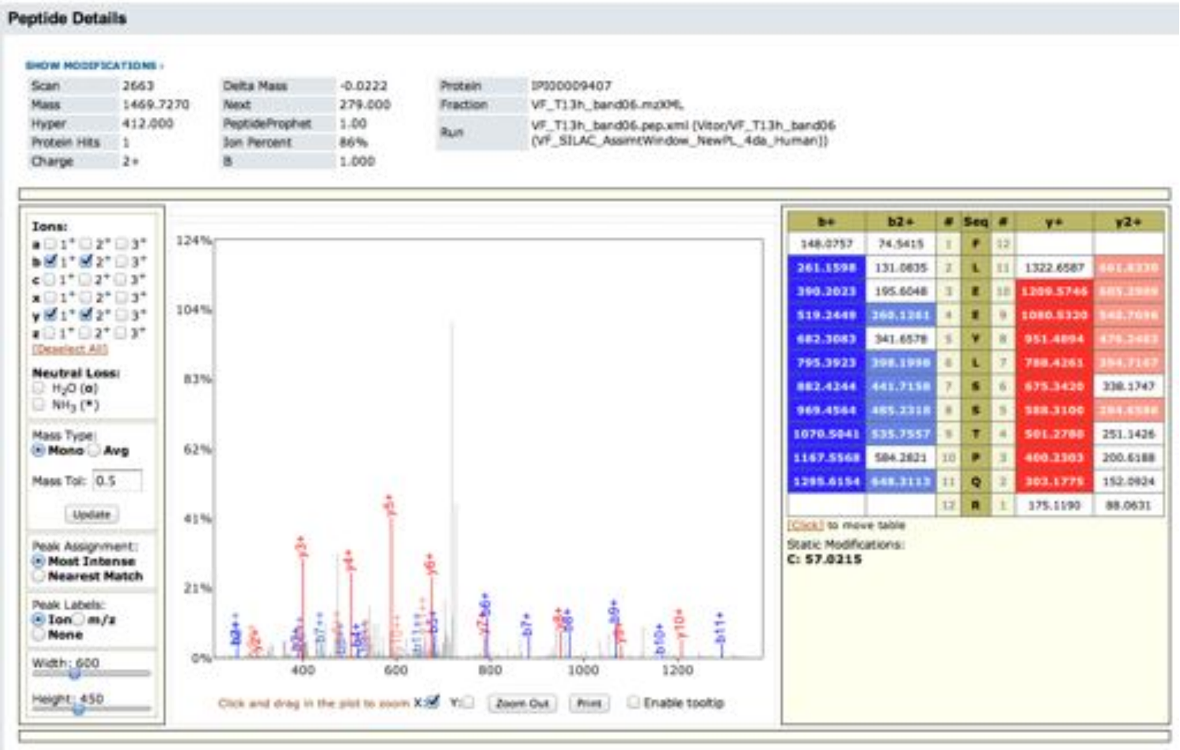
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	12		
261.1598	131.0835	2	L	11	1322.6587	661.8330
390.2023	195.6048	3	E	10	1209.5746	605.2909
519.2449	260.1261	4	E	9	1080.5320	540.7696
682.3083	341.6578	5	Y	8	951.4894	476.2483
795.3923	398.1998	6	L	7	788.4261	394.7167
882.4244	441.7158	7	S	6	675.3420	338.1747
969.4564	485.2318	8	S	5	588.3100	294.6586
1070.5041	535.7557	9	T	4	501.2780	251.1426
1167.5568	584.2821	10	P	3	400.2303	200.6188
1295.6154	648.3113	11	Q	2	303.1775	152.0924
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9569	IPI00009407	1	1	DAD1	2663	2+	-0.0222	0.9969	R.FLEEYLSSTPQR.L



Scan	2663	Delta Mass	-0.0222	Protein	IPI00009407
Mass	1469.7270	Next	279.000	Fraction	VF_T13h_band06.mzXML
Hyper	412.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

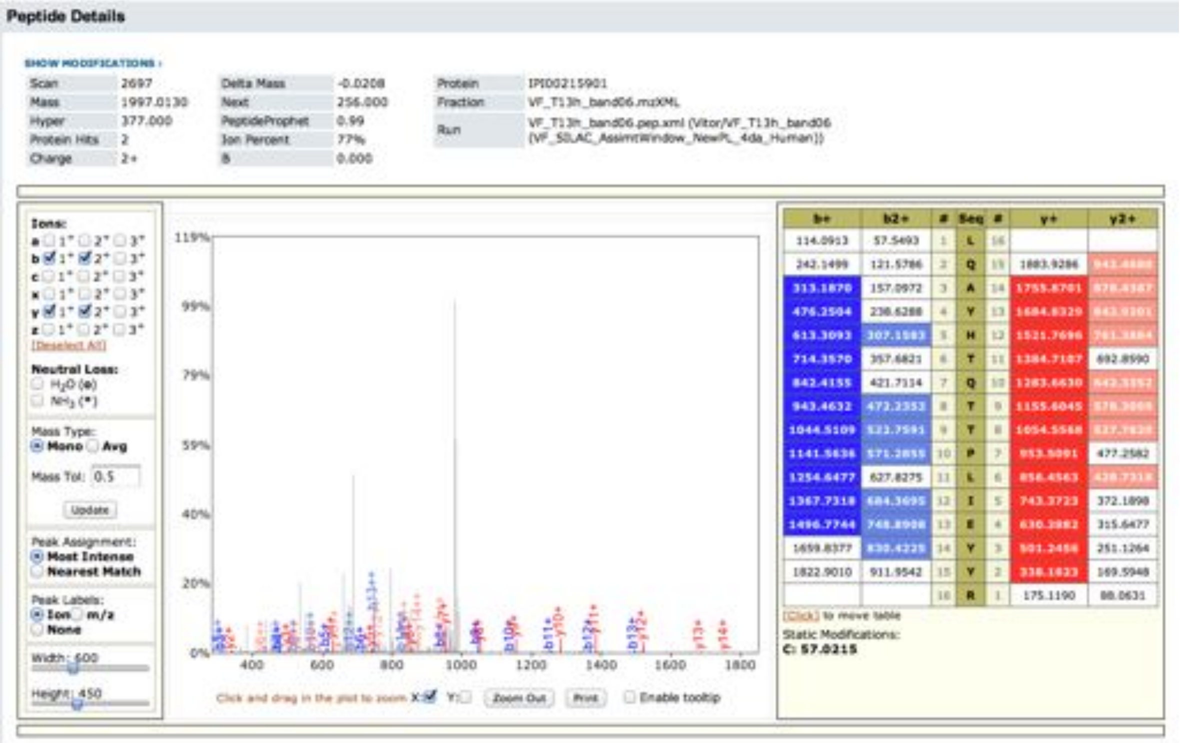
Height: 450

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	12		
261.1598	131.0835	2	L	11	1322.6587	661.8330
390.2023	195.6048	3	E	10	1209.5746	605.2909
519.2449	260.1261	4	E	9	1080.5320	540.7696
682.3083	341.6578	5	Y	8	951.4894	476.2483
795.3923	398.1998	6	L	7	788.4261	394.7167
882.4244	441.7158	7	S	6	675.3420	338.1747
969.4564	485.2318	8	S	5	588.3100	294.6586
1070.5041	535.7557	9	T	4	501.2780	251.1426
1167.5568	584.2821	10	P	3	400.2303	200.6188
1295.6154	648.3113	11	Q	2	303.1775	152.0924
		12	R	1	175.1190	88.0631

Static Modifications:

C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9361	IPI00218988, IPI00215901	1	1	AK2, AK2	2697	2+	-0.0208	0.9948	R.LQAYHTQTTPLIEYYR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2697	Delta Mass	-0.0208	Protein	IPI00215901
Mass	1997.0130	Next	256.000	Fraction	VF_T13h_band06.mzXML
Hyper	377.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	77%		
Charge	2+	B	0.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

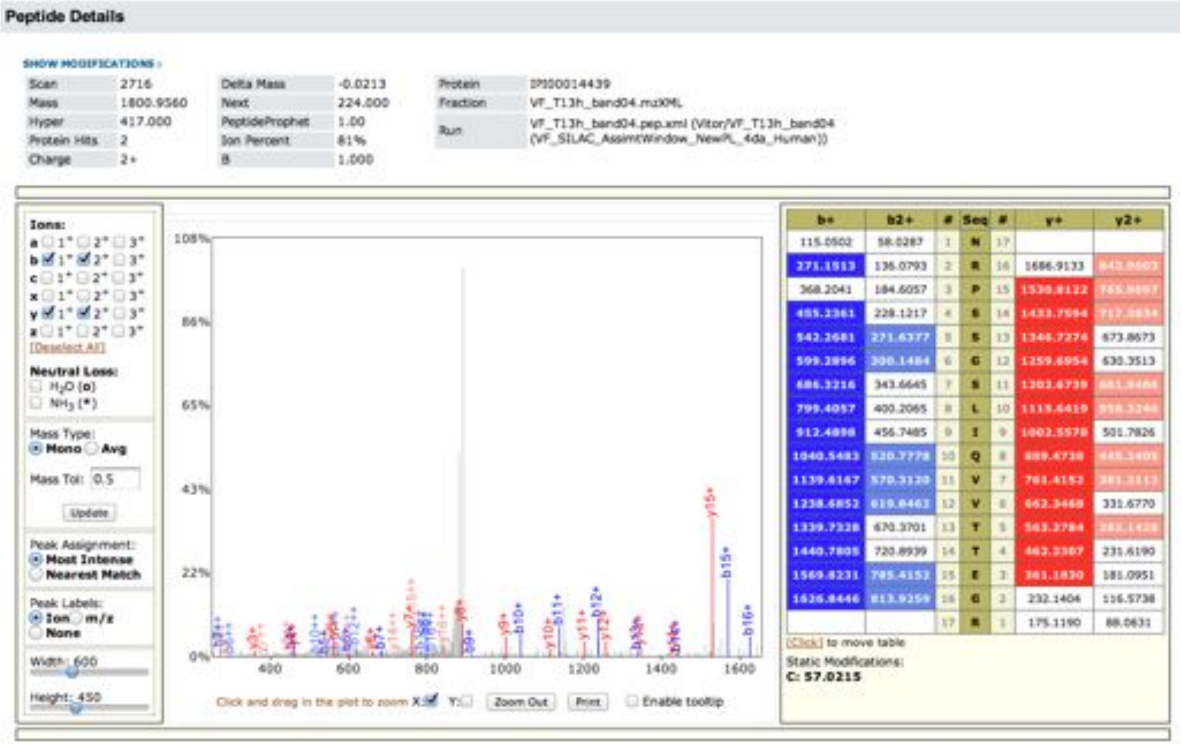
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
242.1499	121.5786	2	Q	15	1883.9286	942.4680
313.1870	157.0972	3	A	14	1755.8701	878.4387
476.2504	238.6288	4	Y	13	1684.8329	842.9201
613.3093	307.1583	5	H	12	1521.7696	761.3884
714.3570	357.6821	6	T	11	1384.7107	692.8590
842.4155	421.7114	7	Q	10	1283.6630	642.3352
943.4632	472.2353	8	T	9	1155.6045	578.3059
1044.5109	522.7591	9	T	8	1054.5568	527.7820
1141.5636	571.2855	10	P	7	953.5091	477.2582
1254.6477	627.8275	11	L	6	856.4563	428.7318
1367.7318	684.3695	12	I	5	743.3723	372.1898
1496.7744	748.8908	13	E	4	630.2882	315.6477
1659.8377	830.4225	14	Y	3	501.2456	251.1264
1822.9010	911.9542	15	Y	2	338.1823	169.5948
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9807	IPI00902534, IPI00014439	1	1	-, QDPR	2716	2+	-0.0213	0.9997	K.NRPSSGSLIQVVTTEGR.T



Peptide Details

SHOW MODIFICATIONS »

Scan	2716	Delta Mass	-0.0213	Protein	IPI00014439
Mass	1800.9560	Next	224.000	Fraction	VF_T13h_band04.mzXML
Hyper	417.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

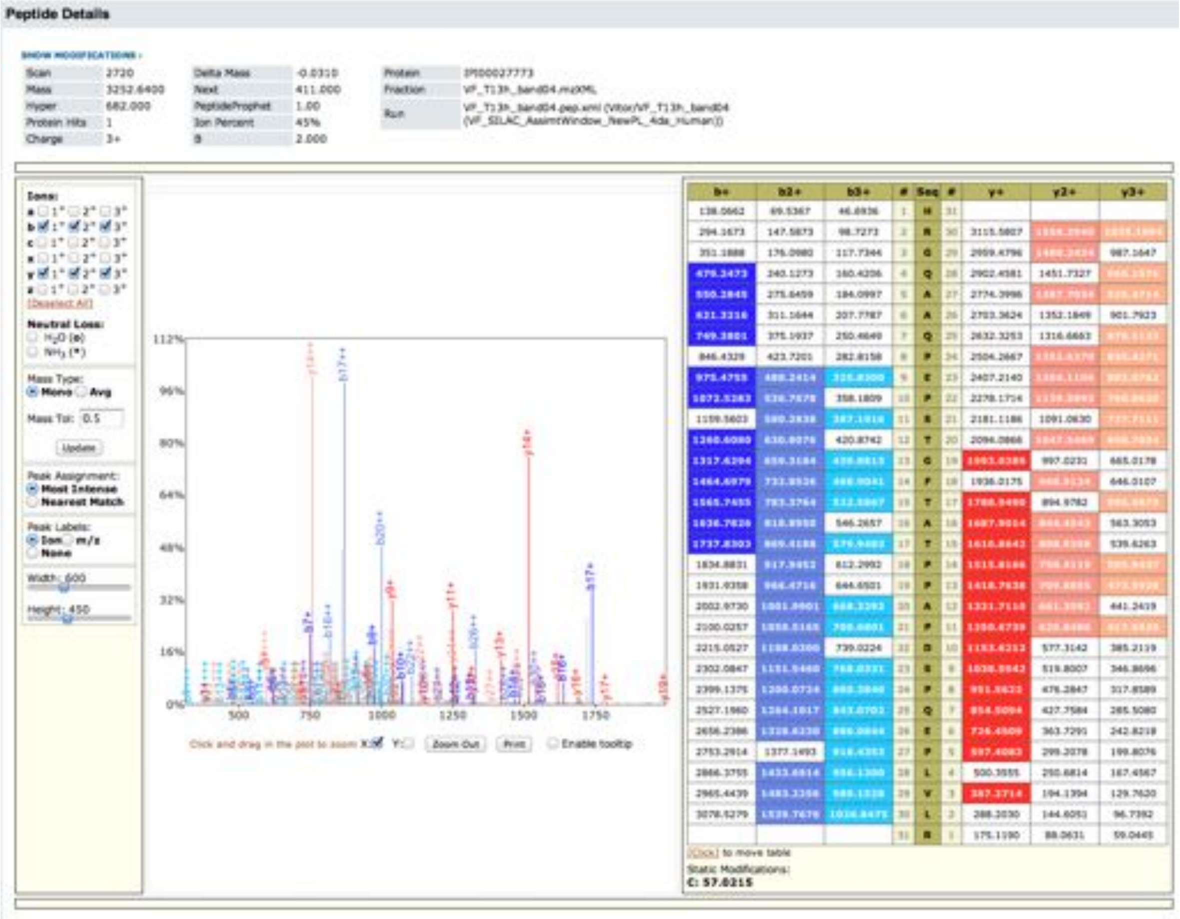
Click and drag in the plot to zoom X: ☑ Y: ☐

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	17		
271.1513	136.0793	2	R	16	1686.9133	843.9603
368.2041	184.6057	3	P	15	1530.8122	765.9097
455.2361	228.1217	4	S	14	1433.7594	717.3834
542.2681	271.6377	5	S	13	1346.7274	673.8673
599.2896	300.1484	6	G	12	1259.6954	630.3513
686.3216	343.6645	7	S	11	1202.6739	601.8406
799.4057	400.2065	8	L	10	1115.6419	558.3246
912.4898	456.7485	9	I	9	1002.5578	501.7826
1040.5483	520.7778	10	Q	8	889.4738	445.2405
1139.6167	570.3120	11	V	7	761.4152	381.2113
1238.6852	619.8463	12	V	6	662.3468	331.6770
1339.7328	670.3701	13	T	5	563.2784	282.1428
1440.7805	720.8939	14	T	4	462.2307	231.6190
1569.8231	785.4152	15	E	3	361.1830	181.0951
1626.8446	813.9259	16	G	2	232.1404	116.5738
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9851	IPI00027773	1	1	HOPS	2720	3+	-0.0310	1.0000	R.HRGQAAQPEPSTGFTATPPAPDSPQEPLVLR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	2720	Delta Mass	-0.0310	Protein	IPI00027773
Mass	3252.6400	Next	411.000	Fraction	VF_T13h_band04.mzXML
Hyper	682.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	45%		
Charge	3+	B	2.000		

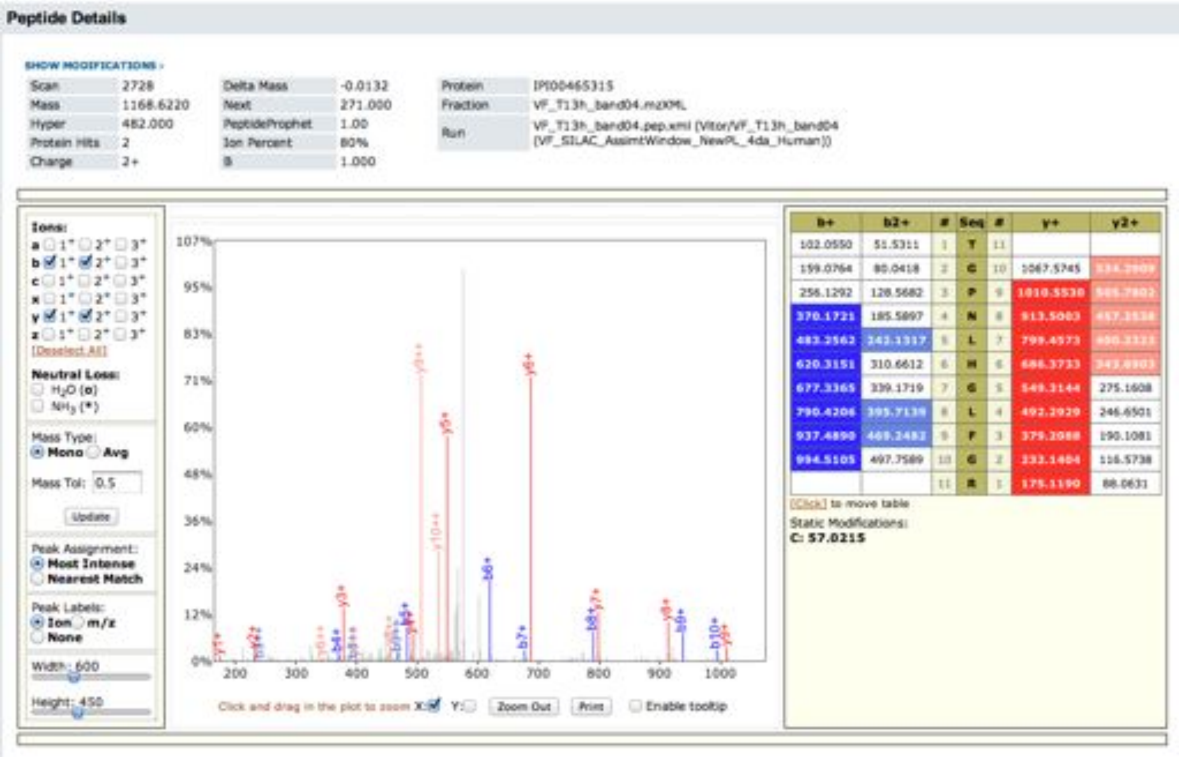
b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
138.0662	69.5367	46.6936	1	H	31			
294.1673	147.5873	98.7273	2	R	30	3115.5807	[illegible]	[illegible]
351.1888	176.0980	117.7344	3	G	29	2959.4796	[illegible]	987.1647
479.2473	240.1273	160.4206	4	Q	28	2902.4581	1451.7327	[illegible]
550.2845	275.6459	184.0997	5	A	27	2774.3996	[illegible]	[illegible]
621.3216	311.1644	207.7787	6	A	26	2703.3624	1352.1849	901.7923
749.3801	375.1937	250.4649	7	Q	25	2632.3253	1316.6663	[illegible]
846.4329	423.7201	282.8158	8	P	24	2504.2667	[illegible]	[illegible]
975.4755	488.2414	325.8300	9	E	23	2407.2140	[illegible]	[illegible]
1072.5283	536.7678	358.1809	10	P	22	2278.1714	[illegible]	[illegible]
1159.5603	580.2838	387.1916	11	S	21	2181.1186	1091.0630	[illegible]
1260.6080	630.8076	420.8742	12	T	20	2094.0866	[illegible]	[illegible]
1317.6294	659.3184	439.8813	13	G	19	1993.0389	997.0231	665.0178
1464.6979	732.8526	489.9041	14	F	18	1936.0175	[illegible]	646.0107
1565.7455	783.3764	522.5867	15	T	17	1788.9490	894.9782	[illegible]
1636.7826	818.8950	546.2657	16	A	16	1687.9014	[illegible]	563.3053
1737.8303	869.4188	579.9483	17	T	15	1616.8642	[illegible]	539.6263
1834.8831	917.9452	612.2992	18	P	14	1515.8166	[illegible]	[illegible]
1931.9358	966.4716	644.6501	19	P	13	1418.7638	[illegible]	[illegible]
2002.9730	1001.9901	668.3292	20	A	12	1321.7110	[illegible]	441.2419
2100.0257	1050.5165	700.6801	21	P	11	1250.6739	[illegible]	[illegible]
2215.0527	1108.0300	739.0224	22	D	10	1153.6212	577.3142	385.2119
2302.0847	1151.5460	768.0331	23	S	9	1038.5942	519.8007	346.8696
2399.1375	1200.0724	800.3840	24	P	8	951.5622	476.2847	317.8589
2527.1960	1264.1017	843.0702	25	Q	7	854.5094	427.7584	285.5080
2656.2386	1328.6230	886.0844	26	E	6	726.4509	363.7291	242.8218
2753.2914	1377.1493	918.4353	27	P	5	597.4083	299.2078	199.8076
2866.3755	1433.6914	956.1300	28	L	4	500.3555	250.6814	167.4567
2965.4439	1483.2256	989.1528	29	V	3	387.2714	194.1394	129.7620
3078.5279	1539.7676	1026.8475	30	L	2	288.2030	144.6051	96.7392
			31	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:

C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00465315, IPI00872914	1	1	CYCS, -	2728	2+	-0.0132	0.9998	K.TGPNLHGLFGR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	2728	Delta Mass	-0.0132	Protein	IPI00465315
Mass	1168.6220	Next	271.000	Fraction	VF_T13h_band04.mzXML
Hyper	482.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	80%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
159.0764	80.0418	2	G	10	1067.5745	534.2909
256.1292	128.5682	3	P	9	1010.5530	505.7802
370.1721	185.5897	4	N	8	913.5003	457.2538
483.2562	242.1317	5	L	7	799.4573	400.2323
620.3151	310.6612	6	H	6	686.3733	343.6903
677.3365	339.1719	7	G	5	549.3144	275.1608
790.4206	395.7139	8	L	4	492.2929	246.6501
937.4890	469.2482	9	F	3	379.2088	190.1081
994.5105	497.7589	10	G	2	232.1404	116.5738
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9819	IPI00743775, IPI00024642	1	1	CCDC47, CCDC47	2748	2+	-0.0186	1.0000	K.LNQENEHIYNLWCSGR.V

Peptide Details

SHOW MODIFICATIONS ›

Scan	2748	Delta Mass	-0.0186	Protein	IPI00024642
Mass	2032.9290	Next	361.000	Fraction	VF_T13h_band02.mzXML
Hyper	667.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
228.1343	114.5708	2	N	15	1919.8454	960.4263
356.1928	178.6001	3	Q	14	1805.8024	903.4049
485.2354	243.1214	4	E	13	1677.7439	839.3756
599.2784	300.1428	5	N	12	1548.7013	774.8543
728.3210	364.6641	6	E	11	1434.6583	717.8328
865.3799	433.1936	7	H	10	1305.6157	653.3115
978.4639	489.7356	8	I	9	1168.5568	584.7821
1141.5273	571.2673	9	Y	8	1055.4728	528.2400
1255.5702	628.2887	10	N	7	892.4094	446.7084
1368.6543	684.8308	11	L	6	778.3665	389.6869
1554.7336	777.8704	12	W	5	665.2824	333.1449
1714.7643	857.8858	13	C	4	479.2031	240.1052
1801.7963	901.4018	14	S	3	319.1724	160.0899
1858.8177	929.9125	15	G	2	232.1404	116.5738
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9776	IPI00747225, IPI00217113, IPI00027172, IPI00013455	1	1	CLIP1, CLIP1, CLIP1, CLIP1	2770	2+	-0.0190	0.9997	K.ATSHVGEIEQELALAR.D

Peptide Details

Scan	2770	Delta Mass	-0.0190	Protein	IPI00013455
Mass	1723.8970	Next	274.000	Fraction	VF_T13h_band01.mzXML
Hyper	495.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

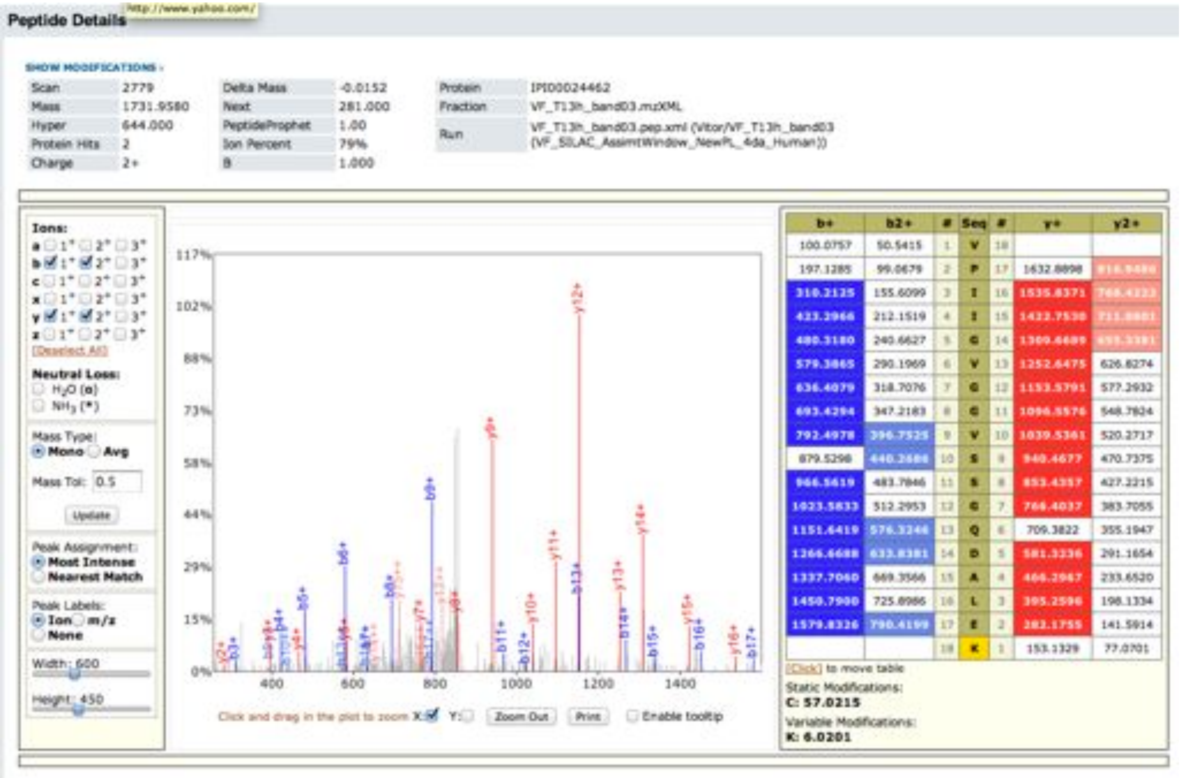
Click and drag in the plot to zoom X ☑ Y ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	16		
173.0921	87.0497	2	T	15	1652.8602	826.9338
260.1241	130.5657	3	S	14	1551.8125	776.4099
397.1830	199.0951	4	H	13	1464.7805	732.8938
496.2514	248.6293	5	V	12	1327.7216	664.3644
553.2729	277.1401	6	G	11	1228.6532	614.8302
682.3155	341.6614	7	E	10	1171.6317	586.3195
795.3995	398.2034	8	I	9	1042.5891	521.7983
924.4421	462.7247	9	E	8	929.5051	465.2562
1052.5007	526.7540	10	Q	7	800.4625	400.7349
1181.5433	591.2753	11	E	6	672.4039	336.7056
1294.6274	647.8173	12	L	5	543.3613	272.1843
1365.6645	683.3359	13	A	4	430.2772	215.6423
1478.7485	739.8779	14	L	3	359.2401	180.1237
1549.7857	775.3965	15	A	2	246.1561	123.5817
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9880	IPI00642644, IPI00024462	1	1	DHODH, DHODH	2779	2+	-0.0152	1.0000	R.VPIIGVGGVSSGQDALEK'.I



Peptide Details

Scan	2779	Delta Mass	-0.0152	Protein	IPI00024462
Mass	1731.9580	Next	281.000	Fraction	VF_T13h_band03.mzXML
Hyper	644.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	79%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	18		
197.1285	99.0679	2	P	17	1632.8898	816.9486
310.2125	155.6099	3	I	16	1535.8371	768.4222
423.2966	212.1519	4	I	15	1422.7530	711.8801
480.3180	240.6627	5	G	14	1309.6689	655.3381
579.3865	290.1969	6	V	13	1252.6475	626.8274
636.4079	318.7076	7	G	12	1153.5791	577.2932
693.4294	347.2183	8	G	11	1096.5576	548.7824
792.4978	396.7525	9	V	10	1039.5361	520.2717
879.5298	440.2686	10	S	9	940.4677	470.7375
966.5619	483.7846	11	S	8	853.4357	427.2215
1023.5833	512.2953	12	G	7	766.4037	383.7055
1151.6419	576.3246	13	Q	6	709.3822	355.1947
1266.6688	633.8381	14	D	5	581.3236	291.1654
1337.7060	669.3566	15	A	4	466.2967	233.6520
1450.7900	725.8986	16	L	3	395.2596	198.1334
1579.8326	790.4199	17	E	2	282.1755	141.5914
		18	K	1	153.1329	77.0701

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9419	IPI00027448	1	1	ATP5L	2811	2+	-0.0159	0.9954	K.VELVPPTPAEIPR.A


Peptide Details

SHOW MODIFICATIONS ›

Scan	2811	Delta Mass	-0.0159	Protein	IPI00027448
Mass	1417.8050	Next	250.000	Fraction	VF_T13h_band06.mzXML
Hyper	375.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

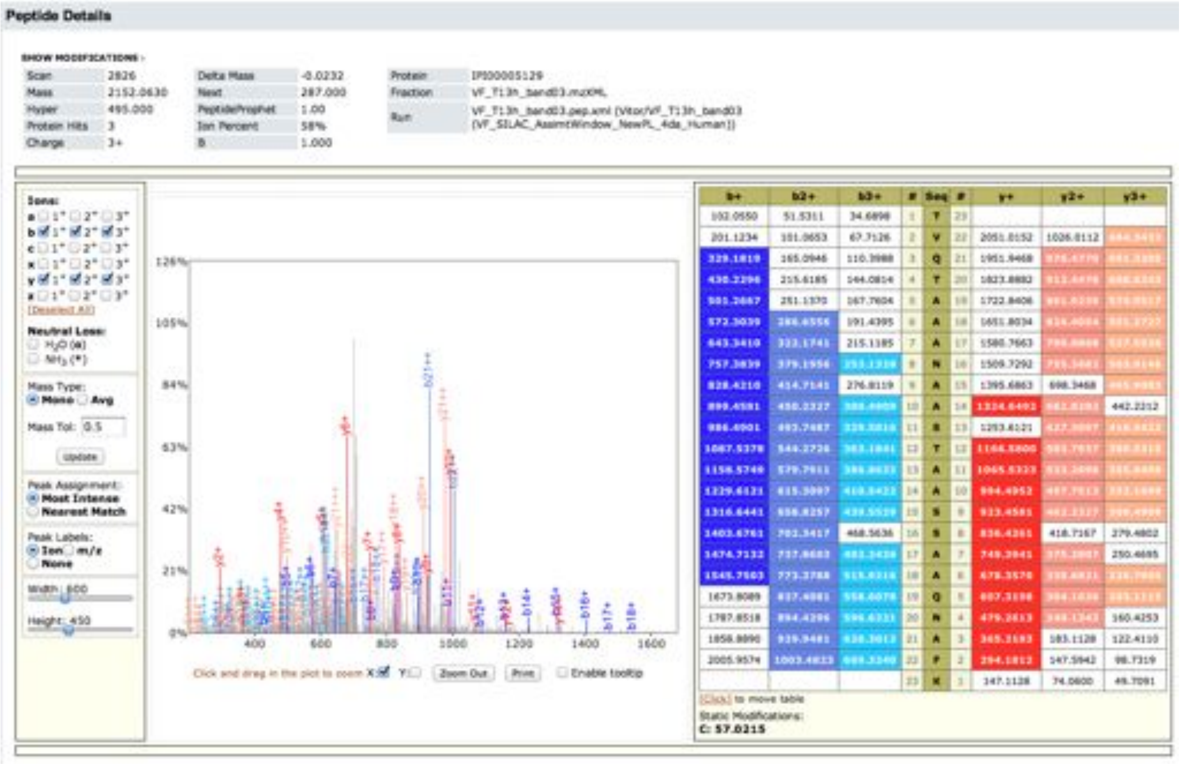
X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	13		
229.1183	115.0628	2	E	12	1318.7365	659.8719
342.2023	171.6048	3	L	11	1189.6939	595.3506
441.2708	221.1390	4	V	10	1076.6099	538.8086
538.3235	269.6654	5	P	9	977.5415	489.2744
635.3763	318.1918	6	P	8	880.4887	440.7480
736.4240	368.7156	7	T	7	783.4359	392.2216
833.4767	417.2420	8	P	6	682.3883	341.6979
904.5138	452.7606	9	A	5	585.3355	293.1714
1033.5564	517.2819	10	E	4	514.2984	257.6528
1146.6405	573.8239	11	I	3	385.2558	193.1315
1243.6933	622.3503	12	P	2	272.1717	136.5895
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9880	IPI00059809, IPI00909127, IPI00005129	1	1	SCAMP1, -, SCAMP1	2826	3+	-0.0232	1.0000	K.TVQTAAANAASTAASSAAQNAFK.G



Peptide Details

SHOW MODIFICATIONS :

Scan	2826	Delta Mass	-0.0232	Protein	IPI00005129
Mass	2152.0630	Next	287.000	Fraction	VF_T13h_band03.mzXML
Hyper	495.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	58%		
Charge	3+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☑ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

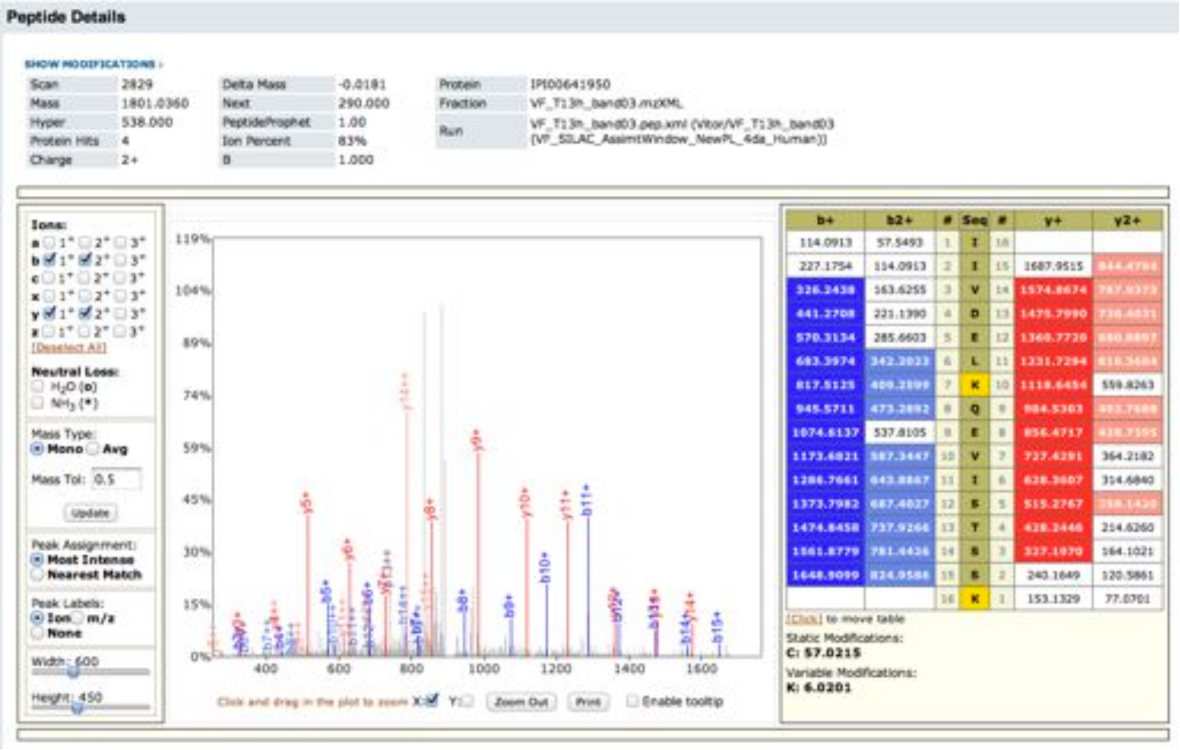
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
102.0550	51.5311	34.6898	1	T	23			
201.1234	101.0653	67.7126	2	V	22	2051.0152	1026.0112	684.3433
329.1819	165.0946	110.3988	3	Q	21	1951.9468	976.4770	651.3205
430.2296	215.6185	144.0814	4	T	20	1823.8882	912.4478	608.6343
501.2667	251.1370	167.7604	5	A	19	1722.8406	861.9239	574.9517
572.3039	286.6556	191.4395	6	A	18	1651.8034	826.4054	551.2727
643.3410	322.1741	215.1185	7	A	17	1580.7663	790.8868	527.5936
757.3839	379.1956	253.1328	8	N	16	1509.7292	755.3683	503.9146
828.4210	414.7141	276.8119	9	A	15	1395.6863	698.3468	465.9003
899.4581	450.2327	300.4909	10	A	14	1324.6491	662.8283	442.2212
986.4901	493.7487	329.5016	11	S	13	1253.6121	627.3097	418.5422
1087.5378	544.2726	363.1841	12	T	12	1166.5800	583.7937	389.5315
1158.5749	579.7911	386.8633	13	A	11	1065.5323	533.2698	355.8490
1229.6121	615.3097	410.5422	14	A	10	994.4952	497.7513	332.1699
1316.6441	658.8257	439.5529	15	S	9	923.4581	462.2327	308.4909
1403.6761	702.3417	468.5636	16	S	8	836.4261	418.7167	279.4802
1474.7132	737.8603	492.2426	17	A	7	749.3941	375.2007	250.4695
1545.7503	773.3788	515.9216	18	A	6	678.3570	339.6821	226.7906
1673.8089	837.4081	558.6078	19	Q	5	607.3198	304.1636	203.1123
1787.8518	894.4296	596.6231	20	N	4	479.2613	240.1343	160.4253
1858.8890	929.9481	620.3013	21	A	3	365.2183	183.1128	122.4110
2005.9574	1003.4823	669.3240	22	F	2	294.1812	147.5942	98.7319
			23	K	1	147.1128	74.0600	49.7091

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9729	IPI00784408, IPI00902520, IPI00848226, IPI00641950	1	1	GNB2L1, -, GNB2L1, GNB2L1	2829	2+	-0.0181	0.9987	K.IIVDELK'QEVISTSSK'.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	2829	Delta Mass	-0.0181	Protein	IPI00641950
Mass	1801.0360	Next	290.000	Fraction	VF_T13h_band03.mzXML
Hyper	538.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 [VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	4	Ion Percent	83%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	16		
227.1754	114.0913	2	I	15	1687.9515	844.4794
326.2438	163.6255	3	V	14	1574.8674	787.9373
441.2708	221.1390	4	D	13	1475.7990	738.4031
570.3134	285.6603	5	E	12	1360.7720	680.8897
683.3974	342.2023	6	L	11	1231.7294	616.3684
817.5125	409.2599	7	K	10	1118.6454	559.8263
945.5711	473.2892	8	Q	9	984.5303	492.7688
1074.6137	537.8105	9	E	8	856.4717	428.7395
1173.6821	587.3447	10	V	7	727.4291	364.2182
1286.7661	643.8867	11	I	6	628.3607	314.6840
1373.7982	687.4027	12	S	5	515.2767	258.1420
1474.8458	737.9266	13	T	4	428.2446	214.6260
1561.8779	781.4426	14	S	3	327.1970	164.1021
1648.9099	824.9586	15	S	2	240.1649	120.5861
		16	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8298	IPI00027448	1	1	ATP5L	2833	2+	-0.0154	0.9848	K.VELVPPTPAEIPR.A

Peptide Details

SHOW MODIFICATIONS ›

Scan	2833	Delta Mass	-0.0154	Protein	IPI00027448
Mass	1417.8050	Next	273.000	Fraction	VF_T13h_band05.mzXML
Hyper	354.000	PeptideProphet	0.98	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

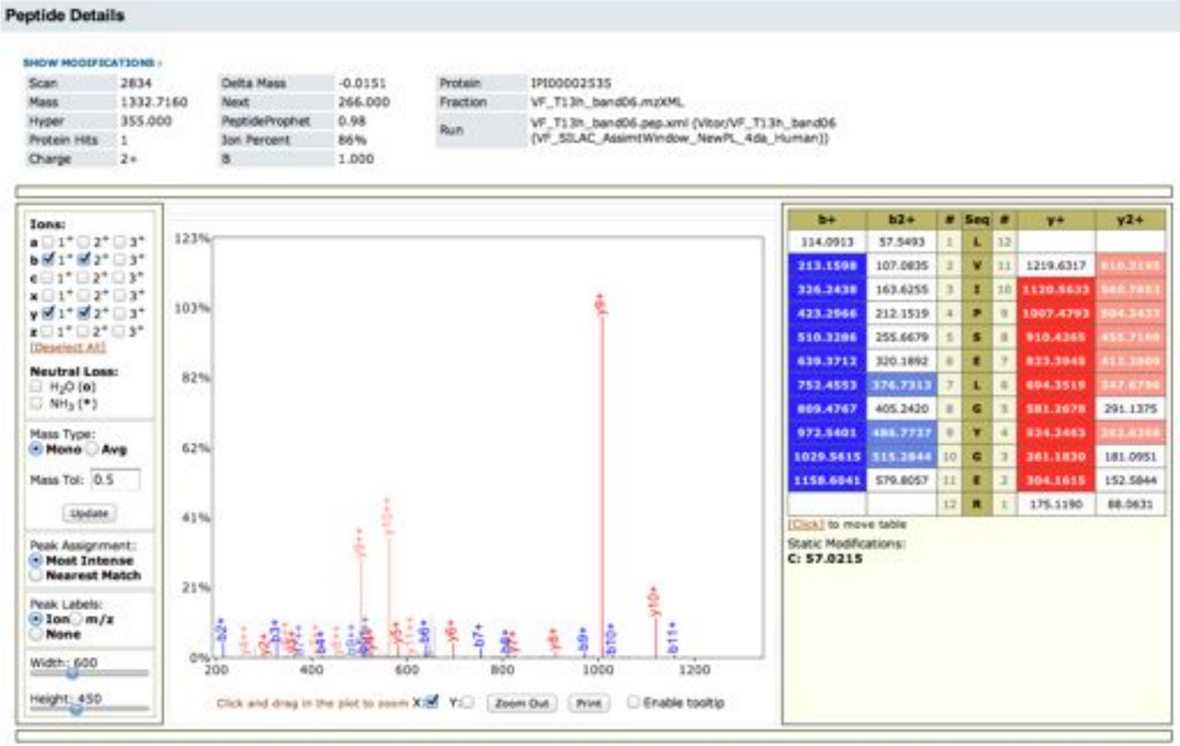
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	13		
229.1183	115.0628	2	E	12	1318.7365	659.8719
342.2023	171.6048	3	L	11	1189.6939	595.3506
441.2708	221.1390	4	V	10	1076.6099	538.8086
538.3235	269.6654	5	P	9	977.5415	489.2744
635.3763	318.1918	6	P	8	880.4887	440.7480
736.4240	368.7156	7	T	7	783.4359	392.2216
833.4767	417.2420	8	P	6	682.3883	341.6979
904.5138	452.7606	9	A	5	585.3355	293.1714
1033.5564	517.2819	10	E	4	514.2984	257.6528
1146.6405	573.8239	11	I	3	385.2558	193.1315
1243.6933	622.3503	12	P	2	272.1717	136.5895
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8136	IPI00002535	1	1	FKBP2	2834	2+	-0.0151	0.9805	K.LVIPSELGYGER.G



Peptide Details

Scan	2834	Delta Mass	-0.0151	Protein	IPI00002535
Mass	1332.7160	Next	266.000	Fraction	VF_T13h_band06.mzXML
Hyper	355.000	PeptideProphet	0.98	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

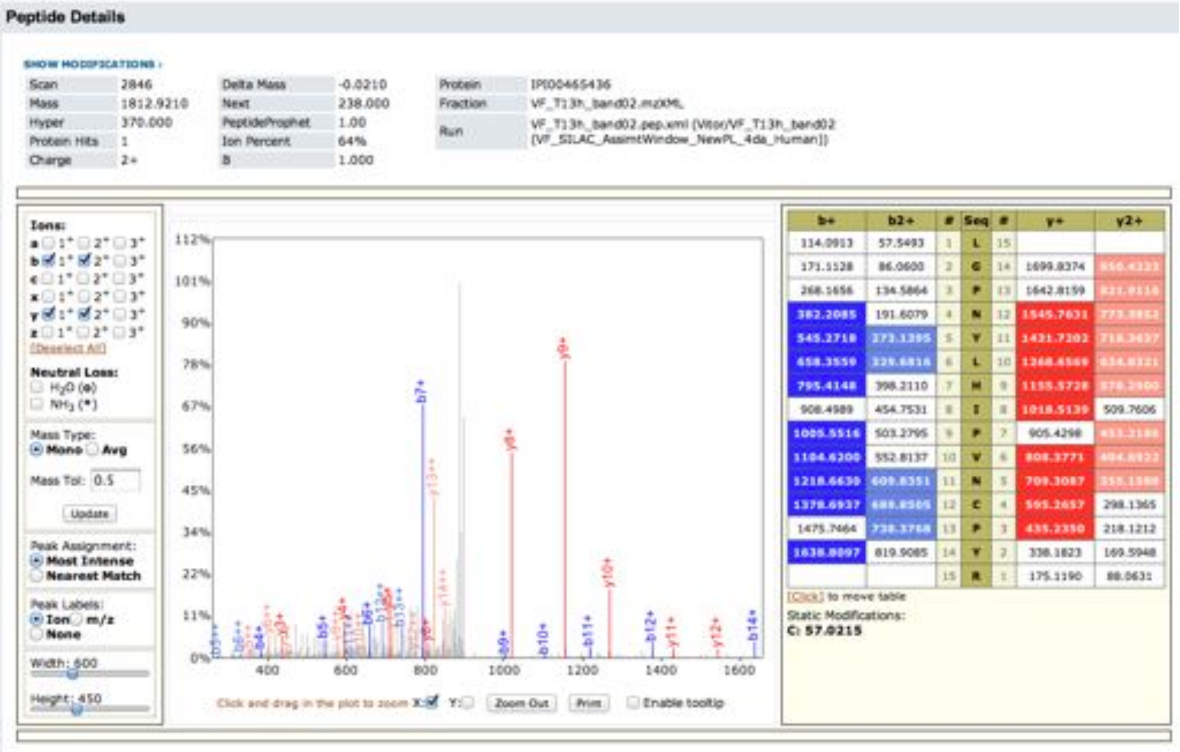
Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	12		
213.1598	107.0835	2	V	11	1219.6317	610.3195
326.2438	163.6255	3	I	10	1120.5633	560.7853
423.2966	212.1519	4	P	9	1007.4793	504.2433
510.3286	255.6679	5	S	8	910.4265	455.7169
639.3712	320.1892	6	E	7	823.3945	412.2009
752.4553	376.7313	7	L	6	694.3519	347.6796
809.4767	405.2420	8	G	5	581.2678	291.1375
972.5401	486.7737	9	Y	4	524.2463	262.6268
1029.5615	515.2844	10	G	3	361.1830	181.0951
1158.6041	579.8057	11	E	2	304.1615	152.5844
		12	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9359	IPI00465436	1	1	CAT	2846	2+	-0.0210	0.9973	R.LGPNYLHIPVNCPYR.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	2846	Delta Mass	-0.0210	Protein	IPI00465436
Mass	1812.9210	Next	238.000	Fraction	VF_T13h_band02.mzXML
Hyper	370.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	64%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
171.1128	86.0600	2	G	14	1699.8374	850.4223
268.1656	134.5864	3	P	13	1642.8159	821.9116
382.2085	191.6079	4	N	12	1545.7631	773.3852
545.2718	273.1395	5	Y	11	1431.7202	716.3637
658.3559	329.6816	6	L	10	1268.6569	634.8321
795.4148	398.2110	7	H	9	1155.5728	578.2900
908.4989	454.7531	8	I	8	1018.5139	509.7606
1005.5516	503.2795	9	P	7	905.4298	453.2186
1104.6200	552.8137	10	V	6	808.3771	404.6922
1218.6630	609.8351	11	N	5	709.3087	355.1580
1378.6937	689.8505	12	C	4	595.2657	298.1365
1475.7464	738.3768	13	P	3	435.2350	218.1212
1638.8097	819.9085	14	Y	2	338.1823	169.5948
		15	R	1	175.1190	88.0631

[Click] to move table

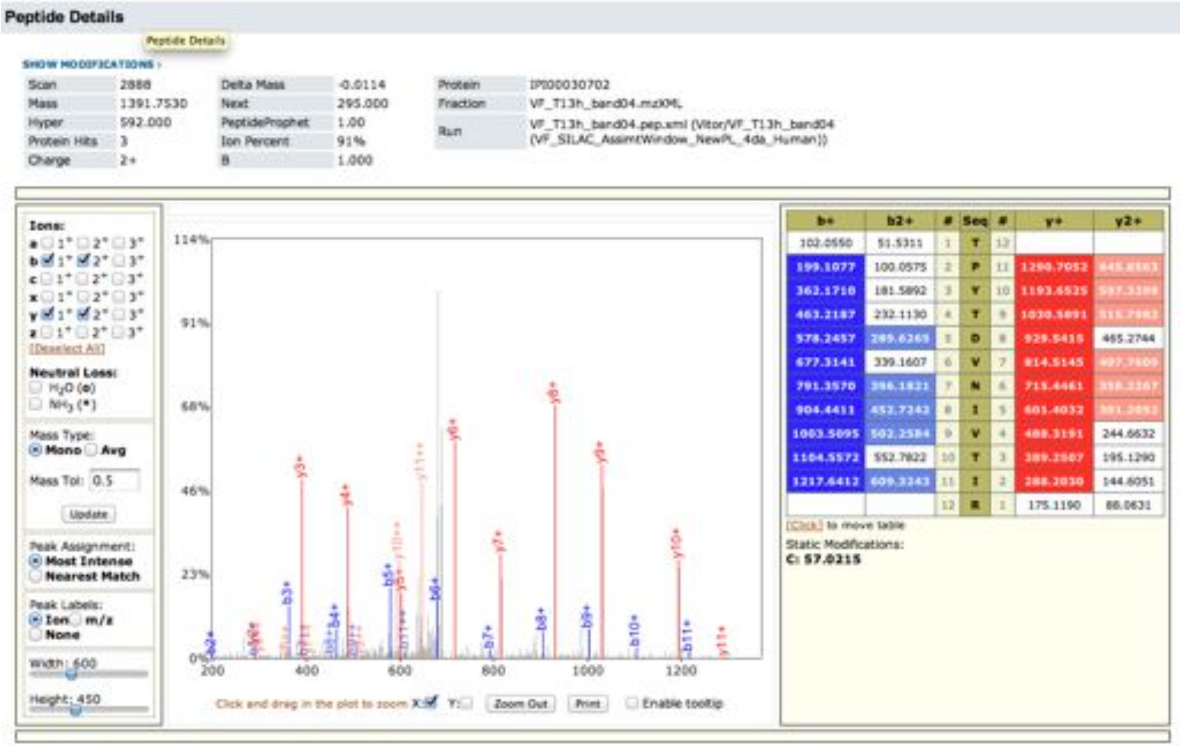
Static Modifications:
C: 57.0215

Mass Tol: 0.5

Width: 600

Height: 450

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00792971, IPI00909577, IPI00030702	1	1	DKFZp761L1216, -, IDH3A	2888	2+	-0.0114	0.9999	K.TPYTDVNIVTIR.E



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	2888	Delta Mass	-0.0114	Protein	IPI00030702
Mass	1391.7530	Next	295.000	Fraction	VF_T13h_band04.mzXML
Hyper	592.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	91%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	12		
199.1077	100.0575	2	P	11	1290.7052	645.8563
362.1710	181.5892	3	Y	10	1193.6525	597.3299
463.2187	232.1130	4	T	9	1030.5891	515.7982
578.2457	289.6265	5	D	8	929.5415	465.2744
677.3141	339.1607	6	V	7	814.5145	407.7609
791.3570	396.1821	7	N	6	715.4461	358.2267
904.4411	452.7242	8	I	5	601.4032	301.2052
1003.5095	502.2584	9	V	4	488.3191	244.6632
1104.5572	552.7822	10	T	3	389.2507	195.1290
1217.6412	609.3243	11	I	2	288.2030	144.6051
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.8924	IPI00465361	1	1	RPL13	2895	2+	-0.0099	0.9901	R.GFSLEELR.V

Peptide Details

SHOW MODIFICATIONS ›

Scan	2895	Delta Mass	-0.0099	Protein	IPI00465361
Mass	950.4940	Next	273.000	Fraction	VF_T13h_band06.mzXML
Hyper	376.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	8		
205.0972	103.0522	2	F	7	893.4727	447.2400
292.1292	146.5682	3	S	6	746.4043	373.7058
405.2132	203.1103	4	L	5	659.3723	330.1898
534.2558	267.6316	5	E	4	546.2882	273.6477
663.2984	332.1529	6	E	3	417.2456	209.1264
776.3825	388.6949	7	L	2	288.2030	144.6051
		8	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00909970, IPI00023748, IPI00797259, IPI00797126	1	1	-, NACA, NACA, NACA	2900	2+	-0.0177	0.9999	K.SPASDTYIVFGEAK'.I

Peptide Details

SHOW MODIFICATIONS ›

Scan	2900	Delta Mass	-0.0177	Protein	IPI00023748
Mass	1490.7470	Next	315.000	Fraction	VF_T13h_band04.mzXML
Hyper	618.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	85%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	14		
185.0921	93.0497	2	P	13	1403.7148	702.3610
256.1292	128.5682	3	A	12	1306.6621	653.8347
343.1612	172.0842	4	S	11	1235.6249	618.3161
458.1882	229.5977	5	D	10	1148.5929	574.8001
559.2358	280.1216	6	T	9	1033.5660	517.2866
722.2992	361.6532	7	Y	8	932.5183	466.7628
835.3832	418.1953	8	I	7	769.4550	385.2311
934.4516	467.7295	9	V	6	656.3709	328.6891
1081.5201	541.2637	10	F	5	557.3025	279.1549
1138.5415	569.7744	11	G	4	410.2341	205.6207
1267.5841	634.2957	12	E	3	353.2126	177.1099
1338.6212	669.8142	13	A	2	224.1700	112.5886
		14	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9592	IPI00443537, IPI00877095, IPI00419604, IPI00385965, IPI00848151, IPI00444090, IPI00307749	1	1	NDUFS7, -, NDUFS7, NDUFS7, -, NDUFS7, NDUFS7	2909	2+	-0.0150	0.9976	K.LDDLVNWAR.R

Peptide Details

SHOW MODIFICATIONS ›

Scan	2909	Delta Mass	-0.0150	Protein	IPI00307749
Mass	1101.5690	Next	286.000	Fraction	VF_T13h_band05.mzXML
Hyper	406.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	7	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

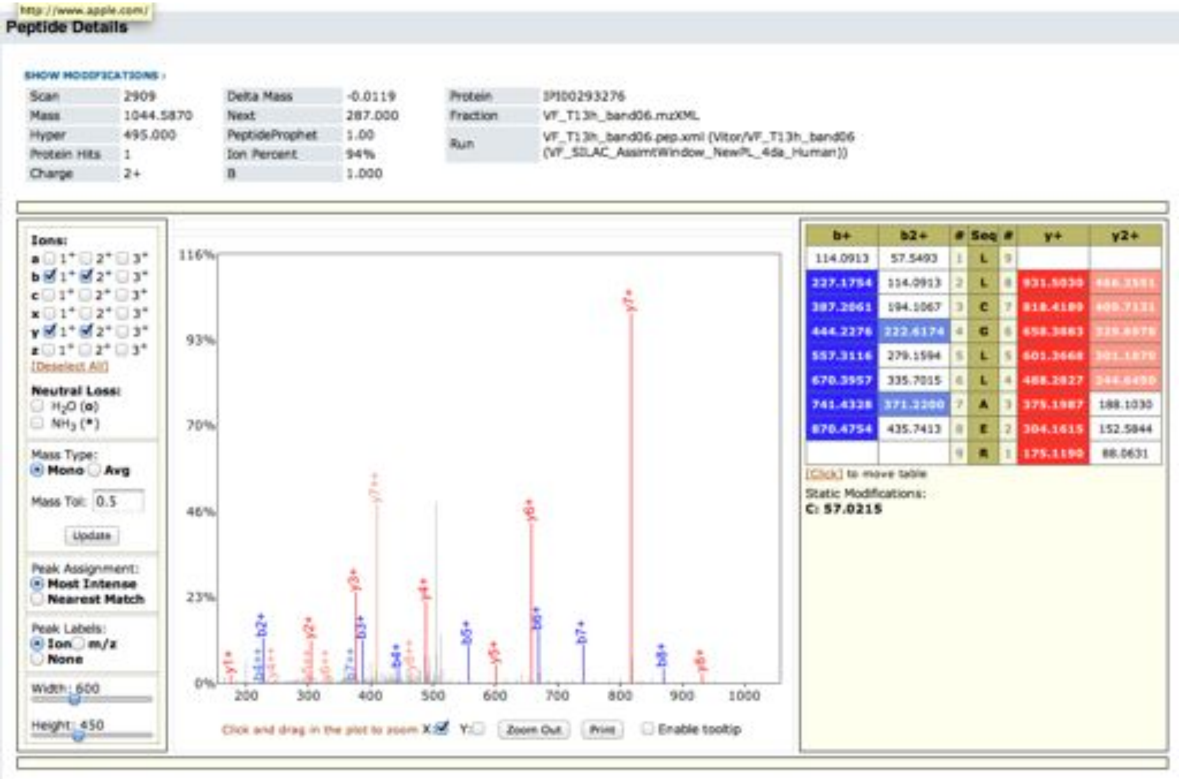
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	9		
229.1183	115.0628	2	D	8	988.4847	494.7460
344.1452	172.5763	3	D	7	873.4577	437.2325
457.2293	229.1183	4	L	6	758.4308	379.7190
556.2977	278.6525	5	V	5	645.3467	323.1770
670.3406	335.6740	6	N	4	546.2783	273.6428
856.4199	428.7136	7	W	3	432.2354	216.6213
927.4571	464.2322	8	A	2	246.1561	123.5817
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9838	IPI00293276	1	1	MIF	2909	2+	-0.0119	0.9995	K.LLCGLLAER.L



http://www.apple.com/

Peptide Details

SHOW MODIFICATIONS ›

Scan	2909	Delta Mass	-0.0119	Protein	IPI00293276
Mass	1044.5870	Next	287.000	Fraction	VF_T13h_band06.mzXML
Hyper	495.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	94%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	9		
227.1754	114.0913	2	L	8	931.5030	466.2551
387.2061	194.1067	3	C	7	818.4189	409.7131
444.2276	222.6174	4	G	6	658.3883	329.6978
557.3116	279.1594	5	L	5	601.3668	301.1870
670.3957	335.7015	6	L	4	488.2827	244.6450
741.4328	371.2200	7	A	3	375.1987	188.1030
870.4754	435.7413	8	E	2	304.1615	152.5844
		9	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9837	IPI00792139, IPI00654754, IPI00798155, IPI00793330, IPI00456429, IPI00789823, IPI00784990, IPI00796007, IPI00179330, IPI00794211, IPI00796600, IPI00797400, IPI00793810, IPI00795527, IPI00794925, IPI00790633, IPI00418813, IPI00719280, IPI00794205, IPI00789107, IPI00793729, IPI00792712, IPI00743241, IPI00743650, IPI00744274, IPI00798127	1	1	RPS27A, RPS27A, RPS27A, RPS27A, UBA52, RPS27A, UBC, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, -, UBB, -, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A, RPS27A	2942	2+	-0.0182	0.9999	K.TITLEVEPSDTIENVK'.A

Peptide Details

Scan	2942	Delta Mass	-0.0182	Protein	IPI00179330
Mass	1793.9470	Next	316.000	Fraction	VF_T13h_band04.mzXML
Hyper	582.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	69	Ion Percent	83%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	16		
215.1390	108.0731	2	I	15	1692.8997	846.9535
316.1867	158.5970	3	T	14	1579.8157	790.4115
429.2708	215.1390	4	L	13	1478.7680	739.8876
558.3134	279.6603	5	E	12	1365.6839	683.3456
657.3818	329.1945	6	V	11	1236.6413	618.8243
786.4244	393.7158	7	E	10	1137.5729	569.2901
883.4771	442.2422	8	P	9	1008.5303	504.7688
970.5092	485.7582	9	S	8	911.4776	456.2424
1085.5361	543.2717	10	D	7	824.4455	412.7264
1186.5838	593.7955	11	T	6	709.4186	355.2129
1299.6678	650.3376	12	I	5	608.3709	304.6891
1428.7104	714.8589	13	E	4	495.2868	248.1471
1542.7534	771.8803	14	N	3	366.2442	183.6258
1641.8218	821.4145	15	V	2	252.2013	126.6043
		16	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9870	IPI00001589	1	1	TIMM13	2956	2+	-0.0172	0.9998	K.VQIAVANAQELLQR.M

Peptide Details

SHOW MODIFICATIONS ›

Scan	2956	Delta Mass	-0.0172	Protein	IPI00001589
Mass	1552.8810	Next	334.000	Fraction	VF_T13h_band06.mzXML
Hyper	608.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

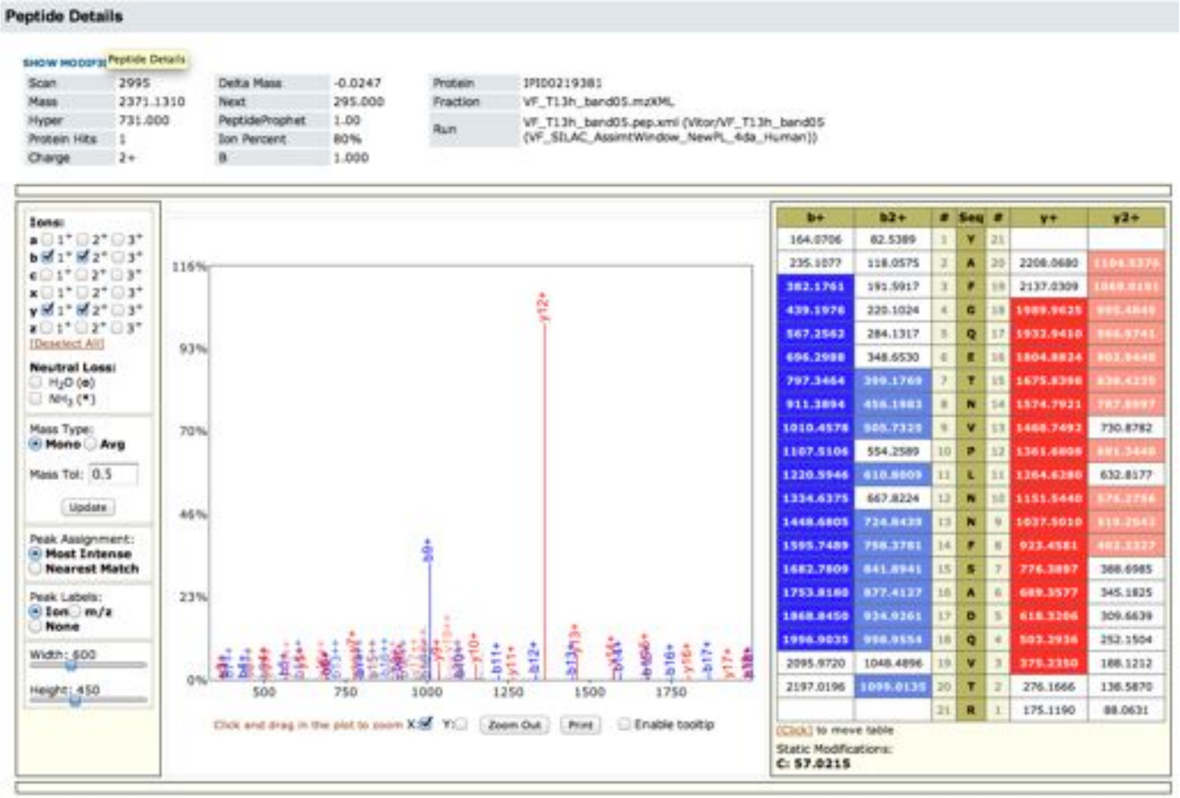
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	14		
228.1343	114.5708	2	Q	13	1453.8122	727.4097
341.2183	171.1128	3	I	12	1325.7536	663.3804
412.2554	206.6314	4	A	11	1212.6695	606.8384
511.3239	256.1656	5	V	10	1141.6324	571.3198
582.3610	291.6841	6	A	9	1042.5640	521.7856
696.4039	348.7056	7	N	8	971.5269	486.2671
767.4410	384.2241	8	A	7	857.4839	429.2456
895.4996	448.2534	9	Q	6	786.4468	393.7271
1024.5422	512.7747	10	E	5	658.3883	329.6978
1137.6262	569.3168	11	L	4	529.3457	265.1765
1250.7103	625.8588	12	L	3	416.2616	208.6344
1378.7689	689.8881	13	Q	2	303.1775	152.0924
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9877	IPI00219381	1	1	NDUFA2	2995	2+	-0.0247	1.0000	R.YAFGQETNVPLNNFSADQVTR.A



Scan	2995	Delta Mass	-0.0247	Protein	IPI00219381
Mass	2371.1310	Next	295.000	Fraction	VF_T13h_band05.mzXML
Hyper	731.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	21		
235.1077	118.0575	2	A	20	2208.0680	1104.5376
382.1761	191.5917	3	F	19	2137.0309	1069.0191
439.1976	220.1024	4	G	18	1989.9625	995.4849
567.2562	284.1317	5	Q	17	1932.9410	966.9741
696.2988	348.6530	6	E	16	1804.8824	903.9448
797.3464	399.1769	7	T	15	1675.8398	838.4235
911.3894	456.1983	8	N	14	1574.7921	787.8997
1010.4578	505.7325	9	V	13	1460.7492	730.8782
1107.5106	554.2589	10	P	12	1361.6808	681.3440
1220.5946	610.8009	11	L	11	1264.6280	632.8177
1334.6375	667.8224	12	N	10	1151.5440	576.2756
1448.6805	724.8439	13	N	9	1037.5010	519.2541
1595.7489	798.3781	14	F	8	923.4581	462.2327
1682.7809	841.8941	15	S	7	776.3897	388.6985
1753.8180	877.4127	16	A	6	689.3577	345.1825
1868.8450	934.9261	17	D	5	618.3206	309.6639
1996.9035	998.9554	18	Q	4	503.2936	252.1504
2095.9720	1048.4896	19	V	3	375.2350	188.1212
2197.0196	1099.0135	20	T	2	276.1666	138.5870
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9819	IPI00335277, IPI00009507	1	1	SYPL, SYPL	3020	2+	-0.0126	1.0000	K.TVTATFGYPFR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	3020	Delta Mass	-0.0126	Protein	IPI00009507
Mass	1259.6420	Next	268.000	Fraction	VF_T13h_band02.mzXML
Hyper	561.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

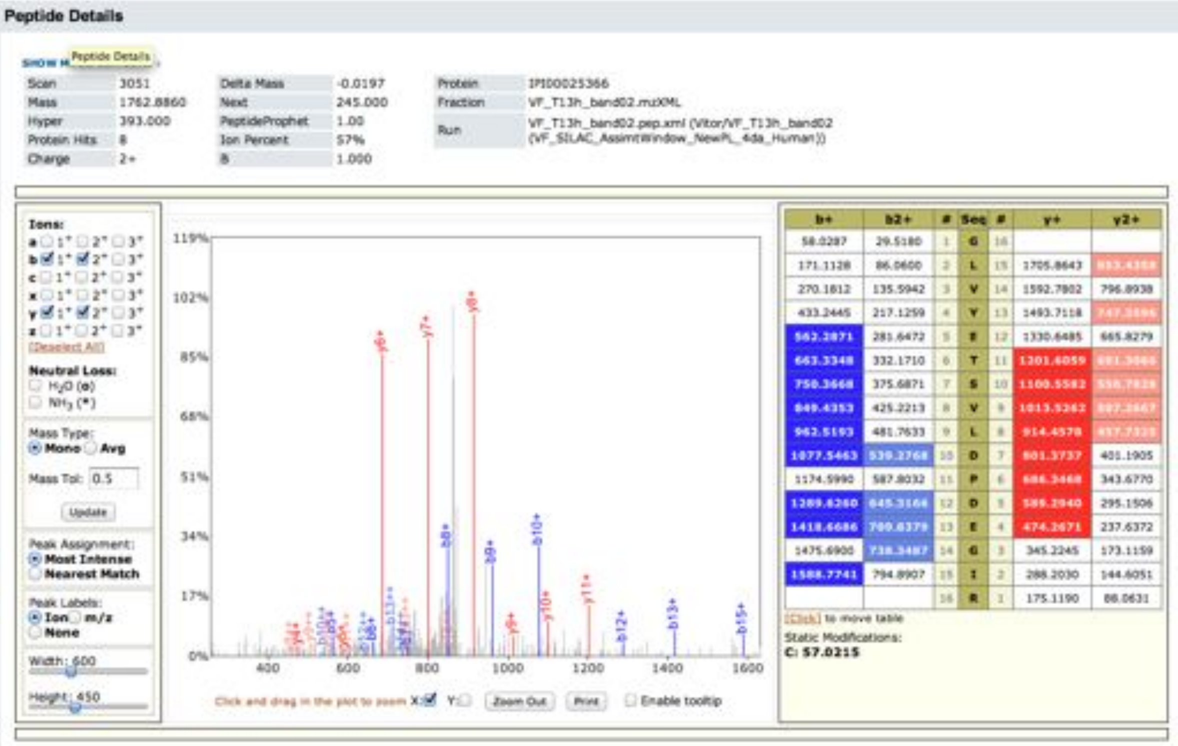
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
201.1234	101.0653	2	V	10	1158.5942	579.8007
302.1710	151.5892	3	T	9	1059.5258	530.2665
373.2082	187.1077	4	A	8	958.4781	479.7427
474.2558	237.6316	5	T	7	887.4410	444.2241
621.3243	311.1658	6	F	6	786.3933	393.7003
678.3457	339.6765	7	G	5	639.3249	320.1661
841.4090	421.2082	8	Y	4	582.3035	291.6554
938.4618	469.7345	9	P	3	419.2401	210.1237
1085.5302	543.2687	10	F	2	322.1874	161.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:

C: 57.0215

Protein Probab.	**Protein**	**Tot. Peptides**	**Unique Peptides**	**Best Gene Name**	**Scan #**	**Charge**	**Delta Mass**	**Peptide Prophet Score**	**Peptide Sequence**
0.9575	IPI00792509, IPI00795682, IPI00791211, IPI00791780, IPI00795080, IPI00383539, IPI00793839, IPI00025366	1	1	CS, CS, CS, CS, CS, CS, CS, CS	3051	2+	-0.0197	0.9986	K.GLVYETSVLDPDEGIR.F



Peptide Details

Scan	3051	Delta Mass	-0.0197	Protein	IPI00025366
Mass	1762.8860	Next	245.000	Fraction	VF_T13h_band02.mzXML
Hyper	393.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	8	Ion Percent	57%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

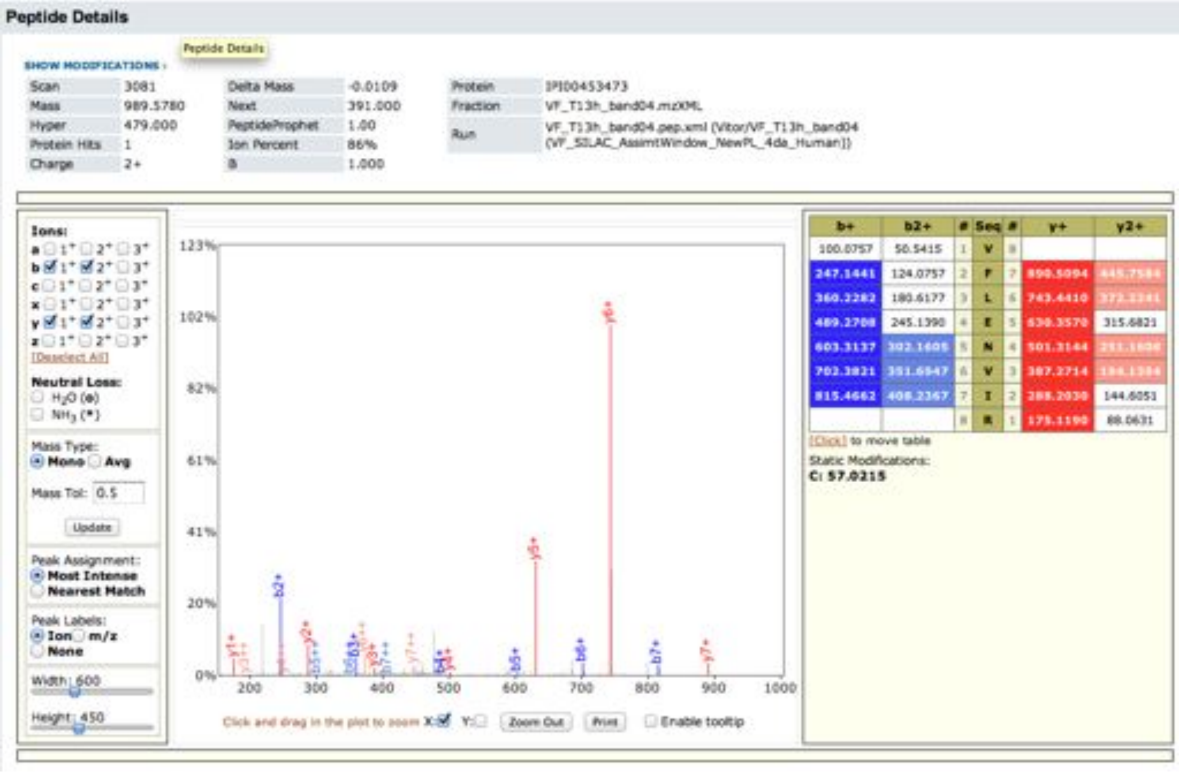
Height: 450

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	16		
171.1128	86.0600	2	L	15	1705.8643	853.4358
270.1812	135.5942	3	V	14	1592.7802	796.8938
433.2445	217.1259	4	Y	13	1493.7118	747.3596
562.2871	281.6472	5	E	12	1330.6485	665.8279
663.3348	332.1710	6	T	11	1201.6059	651.3066
750.3668	375.6871	7	S	10	1100.5582	550.7828
849.4353	425.2213	8	V	9	1013.5262	507.2667
962.5193	481.7633	9	L	8	914.4578	457.7325
1077.5463	539.2768	10	D	7	801.3737	401.1905
1174.5990	587.8032	11	P	6	686.3468	343.6770
1289.6260	645.3166	12	D	5	589.2940	295.1506
1418.6686	709.8379	13	E	4	474.2671	237.6372
1475.6900	738.3487	14	G	3	345.2245	173.1159
1588.7741	794.8907	15	I	2	288.2030	144.6051
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9179	IPI00453473	1	1	HIST1H4I	3081	2+	-0.0109	0.9951	K.VFLENVIR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	3081	Delta Mass	-0.0109	Protein	IPI00453473
Mass	989.5780	Next	391.000	Fraction	VF_T13h_band04.mzXML
Hyper	479.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	8		
247.1441	124.0757	2	F	7	890.5094	445.7584
360.2282	180.6177	3	L	6	743.4410	372.2241
489.2708	245.1390	4	E	5	630.3570	315.6821
603.3137	302.1605	5	N	4	501.3144	251.1608
702.3821	351.6947	6	V	3	387.2714	194.1394
815.4662	408.2367	7	I	2	288.2030	144.6051
		8	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9869	IPI00335277, IPI00009507	1	1	SYPL, SYPL	3083	2+	-0.0141	0.9999	K.TVTATFGYPFR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	3083	Delta Mass	-0.0141	Protein	IPI00009507
Mass	1259.6420	Next	280.000	Fraction	VF_T13h_band03.mzXML
Hyper	562.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

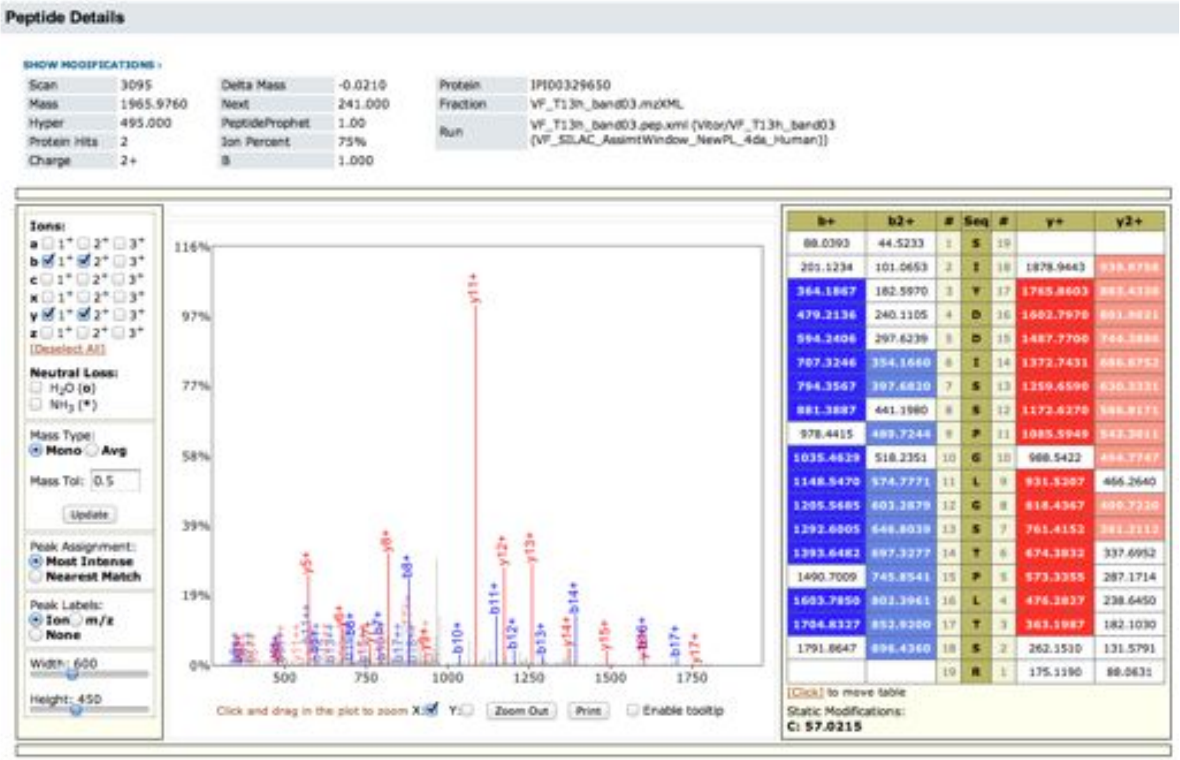
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
201.1234	101.0653	2	V	10	1158.5942	579.8007
302.1710	151.5892	3	T	9	1059.5258	530.2665
373.2082	187.1077	4	A	8	958.4781	479.7427
474.2558	237.6316	5	T	7	887.4410	444.2241
621.3243	311.1658	6	F	6	786.3933	393.7003
678.3457	339.6765	7	G	5	639.3249	320.1661
841.4090	421.2082	8	Y	4	582.3035	291.6554
938.4618	469.7345	9	P	3	419.2401	210.1237
1085.5302	543.2687	10	F	2	322.1874	161.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9869	IPI00550291, IPI00329650	1	1	NUP35, NUP35	3095	2+	-0.0210	0.9999	R.SIYDDISSPGLGSTPLTSR.R



Peptide Details

SHOW MODIFICATIONS ›

Scan	3095	Delta Mass	-0.0210	Protein	IPI00329650
Mass	1965.9760	Next	241.000	Fraction	VF_T13h_band03.mzXML
Hyper	495.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

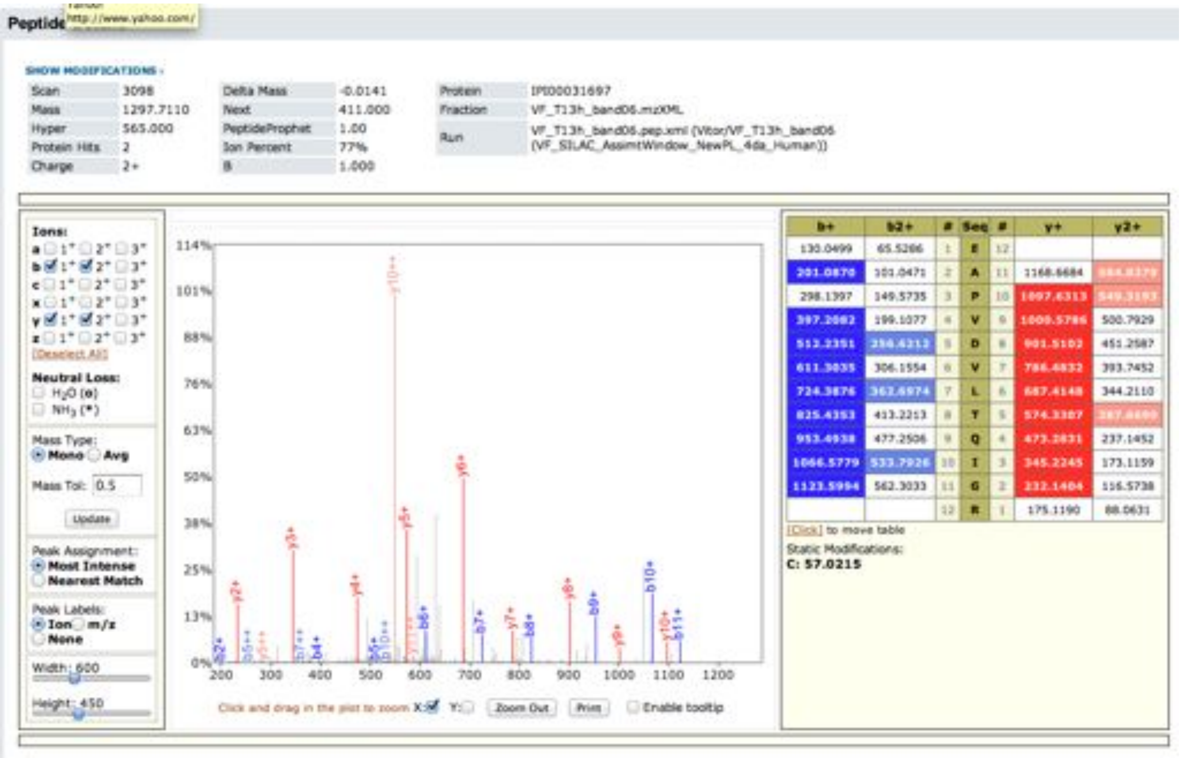
Height: 450

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	19		
201.1234	101.0653	2	I	18	1878.9443	939.9758
364.1867	182.5970	3	Y	17	1765.8603	883.4338
479.2136	240.1105	4	D	16	1602.7970	801.9021
594.2406	297.6239	5	D	15	1487.7700	744.3886
707.3246	354.1660	6	I	14	1372.7431	686.8752
794.3567	397.6820	7	S	13	1259.6590	630.3331
881.3887	441.1980	8	S	12	1172.6270	586.8171
978.4415	489.7244	9	P	11	1085.5949	543.3011
1035.4629	518.2351	10	G	10	988.5422	494.7747
1148.5470	574.7771	11	L	9	931.5207	466.2640
1205.5685	603.2879	12	G	8	818.4367	409.7220
1292.6005	646.8039	13	S	7	761.4152	381.2113
1393.6482	697.3277	14	T	6	674.3832	337.6952
1490.7009	745.8541	15	P	5	573.3355	287.1714
1603.7850	802.3961	16	L	4	476.2827	238.6450
1704.8327	852.9200	17	T	3	363.1987	182.1030
1791.8647	896.4360	18	S	2	262.1510	131.5791
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9775	IPI00908304, IPI00031697	1	1	-, TMEM109	3098	2+	-0.0141	0.9989	R.EAPVDVLTQIGR.S



Scan	3098	Delta Mass	-0.0141	Protein	IPI00031697
Mass	1297.7110	Next	411.000	Fraction	VF_T13h_band06.mzXML
Hyper	565.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

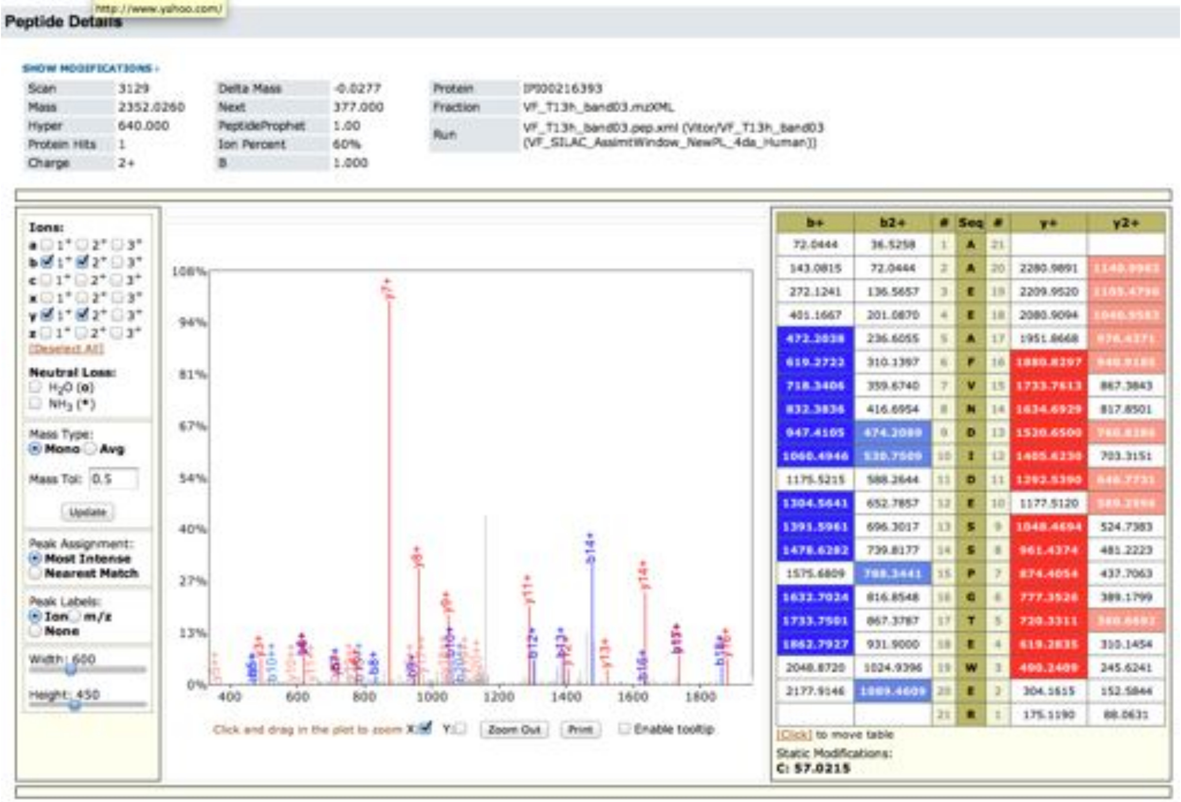
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	12		
201.0870	101.0471	2	A	11	1168.6684	584.8379
298.1397	149.5735	3	P	10	1097.6313	549.3193
397.2082	199.1077	4	V	9	1000.5786	500.7929
512.2351	256.6212	5	D	8	901.5102	451.2587
611.3035	306.1554	6	V	7	786.4832	393.7452
724.3876	362.6974	7	L	6	687.4148	344.2110
825.4353	413.2213	8	T	5	574.3307	287.6690
953.4938	477.2506	9	Q	4	473.2831	237.1452
1066.5779	533.7926	10	I	3	345.2245	173.1159
1123.5994	562.3033	11	G	2	232.1404	116.5738
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9869	IPI00216393	1	1	CLTA	3129	2+	-0.0277	0.9999	R.AAEEAFVNDIDESSPGTEWER.V



Peptide Details

Scan	3129	Delta Mass	-0.0277	Protein	IPI00216393
Mass	2352.0260	Next	377.000	Fraction	VF_T13h_band03.mzXML
Hyper	640.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	60%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense

Peak Labels: ● Ion

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	21		
143.0815	72.0444	2	A	20	2280.9891	1140.9983
272.1241	136.5657	3	E	19	2209.9520	1105.4796
401.1667	201.0870	4	E	18	2080.9094	1040.9583
472.2038	236.6055	5	A	17	1951.8668	976.4371
619.2723	310.1397	6	F	16	1880.8297	940.9185
718.3406	359.6740	7	V	15	1733.7613	867.3843
832.3836	416.6954	8	N	14	1634.6929	817.8501
947.4105	474.2089	9	D	13	1520.6500	760.8286
1060.4946	530.7509	10	I	12	1405.6230	703.3151
1175.5215	588.2644	11	D	11	1292.5390	646.7731
1304.5641	652.7857	12	E	10	1177.5120	589.2596
1391.5961	696.3017	13	S	9	1048.4694	524.7383
1478.6282	739.8177	14	S	8	961.4374	481.2223
1575.6809	788.3441	15	P	7	874.4054	437.7063
1632.7024	816.8548	16	G	6	777.3526	389.1799
1733.7501	867.3787	17	T	5	720.3311	360.6692
1862.7927	931.9000	18	E	4	619.2835	310.1454
2048.8720	1024.9396	19	W	3	490.2409	245.6241
2177.9146	1089.4609	20	E	2	304.1615	152.5844
		21	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	**Protein**	**Tot. Peptides**	**Unique Peptides**	**Best Gene Name**	**Scan #**	**Charge**	**Delta Mass**	**Peptide Prophet Score**	**Peptide Sequence**
0.9750	IPI00335277, IPI00009507	1	1	SYPL, SYPL	3178	2+	-0.0171	0.9993	K.TVTATFGYPFR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	3178	Delta Mass	-0.0171	Protein	IPI00009507
Mass	1259.6420	Next	268.000	Fraction	VF_T13h_band04.mzXML
Hyper	432.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

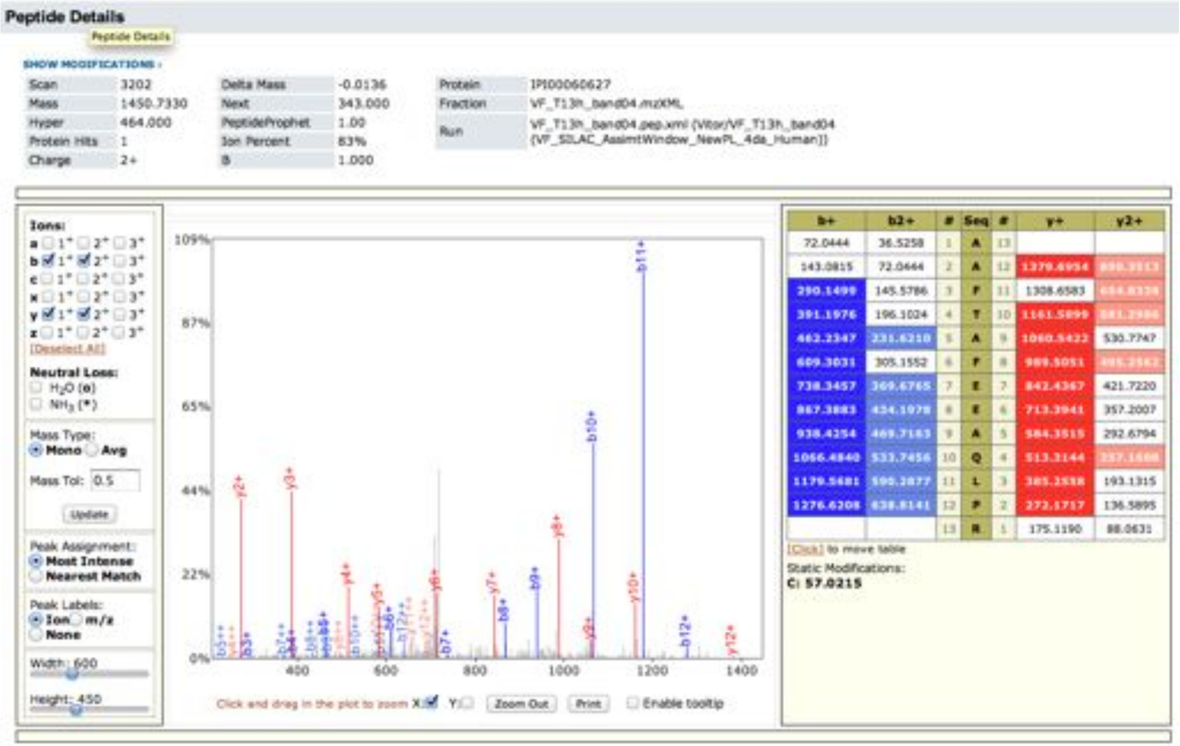
Click and drag in the plot to zoom X: ☑ Y: ☐

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	11		
201.1234	101.0653	2	V	10	1158.5942	579.8007
302.1710	151.5892	3	T	9	1059.5258	530.2665
373.2082	187.1077	4	A	8	958.4781	479.7427
474.2558	237.6316	5	T	7	887.4410	444.2241
621.3243	311.1658	6	F	6	786.3933	393.7003
678.3457	339.6765	7	G	5	639.3249	320.1661
841.4090	421.2082	8	Y	4	582.3035	291.6554
938.4618	469.7345	9	P	3	419.2401	210.1237
1085.5302	543.2687	10	F	2	322.1874	161.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	DeltaMass	PeptideProphet Score	Peptide Sequence
0.9552	IPI00060627	1	1	CCDC124	3202	2+	-0.0136	0.9979	R.AAFTAFEEAQLPR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	3202	Delta Mass	-0.0136	Protein	IPI00060627
Mass	1450.7330	Next	343.000	Fraction	VF_T13h_band04.mzXML
Hyper	464.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

Height: 450

Zoom X: ☑ Y: ☐

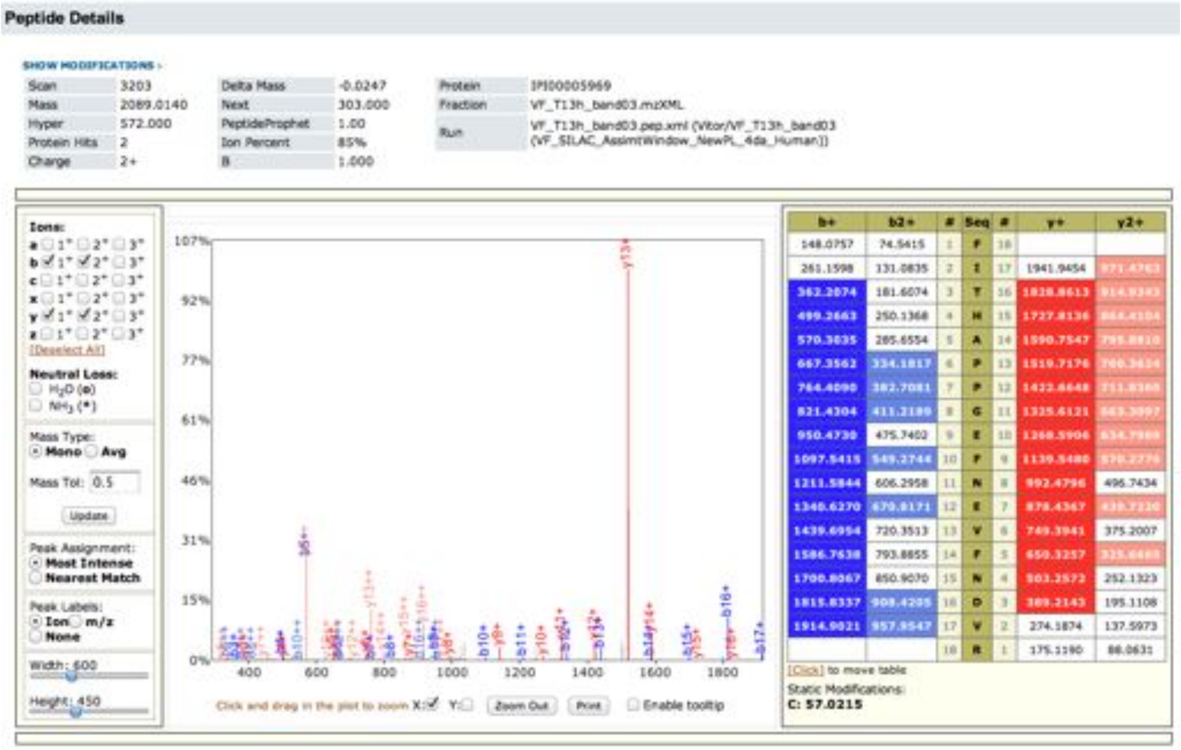
☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	13		
143.0815	72.0444	2	A	12	1379.6954	690.3513
290.1499	145.5786	3	F	11	1308.6583	654.8328
391.1976	196.1024	4	T	10	1161.5899	581.2986
462.2347	231.6210	5	A	9	1060.5422	530.7747
609.3031	305.1552	6	F	8	989.5051	495.2562
738.3457	369.6765	7	E	7	842.4367	421.7220
867.3883	434.1978	8	E	6	713.3941	357.2007
938.4254	469.7163	9	A	5	584.3515	292.6794
1066.4840	533.7456	10	Q	4	513.3144	257.1608
1179.5681	590.2877	11	L	3	385.2558	193.1315
1276.6208	638.8141	12	P	2	272.1717	136.5895
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9869	IPI00873484, IPI00005969	1	1	CAPZA1, CAPZA1	3203	2+	-0.0247	0.9999	K.FITHAPPGEFNEVFNDVR.L



Peptide Details

SHOW MODIFICATIONS ›

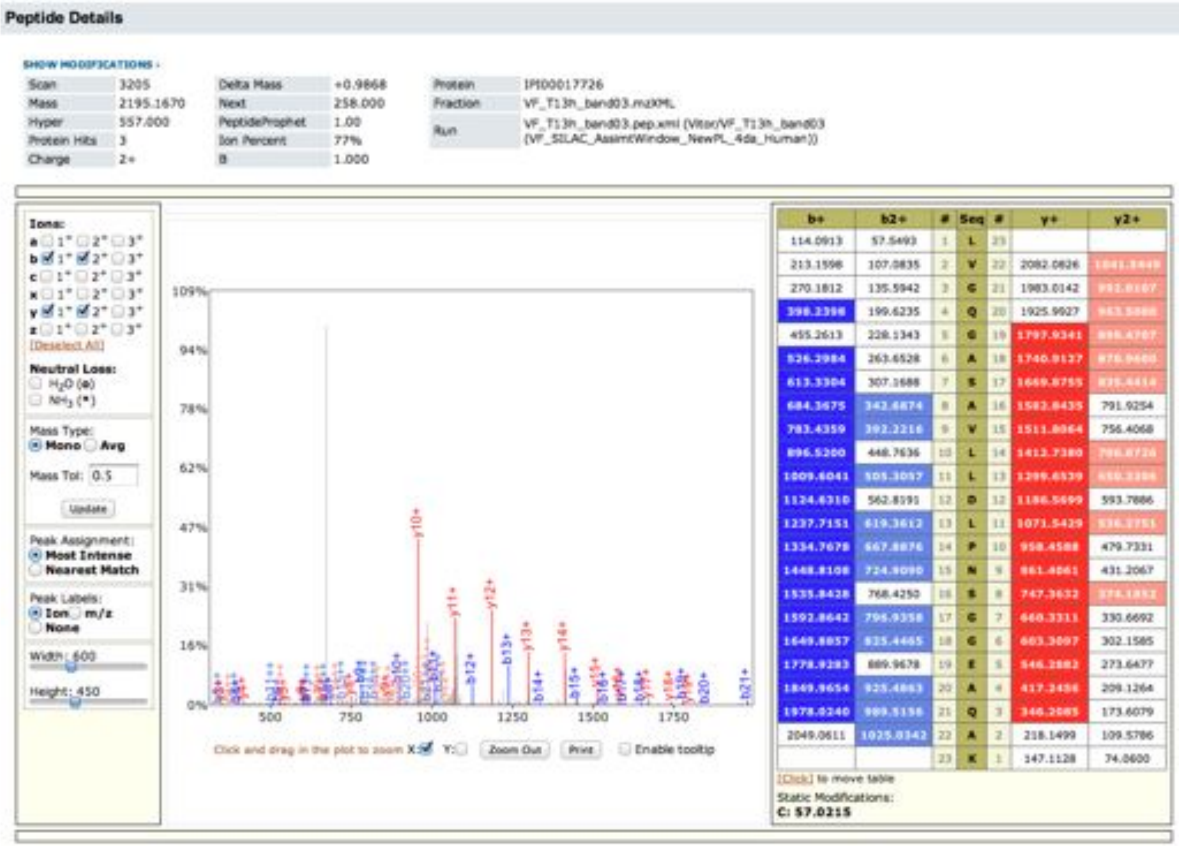
Scan	3203	Delta Mass	-0.0247	Protein	IPI00005969
Mass	2089.0140	Next	303.000	Fraction	VF_T13h_band03.mzXML
Hyper	572.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	2	Ion Percent	85%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	18		
261.1598	131.0835	2	I	17	1941.9454	971.4763
362.2074	181.6074	3	T	16	1828.8613	914.9343
499.2663	250.1368	4	H	15	1727.8136	864.4104
570.3035	285.6554	5	A	14	1590.7547	795.8810
667.3562	334.1817	6	P	13	1519.7176	760.3624
764.4090	382.7081	7	P	12	1422.6648	711.8360
821.4304	411.2189	8	G	11	1325.6121	663.3097
950.4730	475.7402	9	E	10	1268.5906	634.7989
1097.5415	549.2744	10	F	9	1139.5480	570.2776
1211.5844	606.2958	11	N	8	992.4796	496.7434
1340.6270	670.8171	12	E	7	878.4367	439.7220
1439.6954	720.3513	13	V	6	749.3941	375.2007
1586.7638	793.8855	14	F	5	650.3257	325.6665
1700.8067	850.9070	15	N	4	503.2573	252.1323
1815.8337	908.4205	16	D	3	389.2143	195.1108
1914.9021	957.9547	17	V	2	274.1874	137.5973
		18	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00639797, IPI00336094, IPI00017726	1	1	HSD17B10, HSD17B10, HADH2	3205	2+	+0.9868	0.9995	R.LVGQGASAVLLDLPNSGGEAQAK.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	3205	Delta Mass	+0.9868	Protein	IPI00017726
Mass	2195.1670	Next	258.000	Fraction	VF_T13h_band03.mzXML
Hyper	557.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

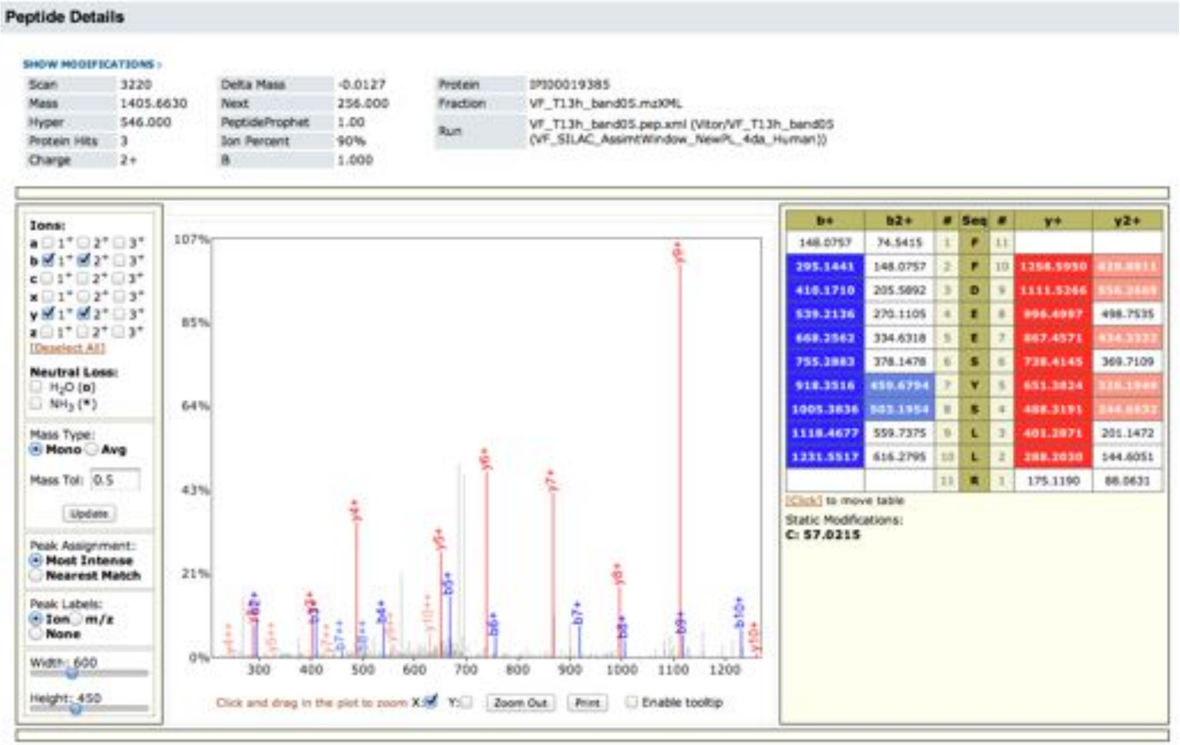
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	23		
213.1598	107.0835	2	V	22	2082.0826	1041.5449
270.1812	135.5942	3	G	21	1983.0142	992.0107
398.2398	199.6235	4	Q	20	1925.9927	963.5000
455.2613	228.1343	5	G	19	1797.9341	899.4707
526.2984	263.6528	6	A	18	1740.9127	870.9600
613.3304	307.1688	7	S	17	1669.8755	835.4414
684.3675	342.6874	8	A	16	1582.8435	791.9254
783.4359	392.2216	9	V	15	1511.8064	756.4068
896.5200	448.7636	10	L	14	1412.7380	706.8726
1009.6041	505.3057	11	L	13	1299.6539	650.3306
1124.6310	562.8191	12	D	12	1186.5699	593.7886
1237.7151	619.3612	13	L	11	1071.5429	536.2751
1334.7678	667.8876	14	P	10	958.4588	479.7331
1448.8108	724.9090	15	N	9	861.4061	431.2067
1535.8428	768.4250	16	S	8	747.3632	374.1852
1592.8642	796.9358	17	G	7	660.3311	330.6692
1649.8857	825.4465	18	G	6	603.3097	302.1585
1778.9283	889.9678	19	E	5	546.2882	273.6477
1849.9654	925.4863	20	A	4	417.2456	209.1264
1978.0240	989.5156	21	Q	3	346.2085	173.6079
2049.0611	1025.0342	22	A	2	218.1499	109.5786
		23	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9877	IPI00646864, IPI00647421, IPI00019385	1	1	SSR4, SSR4, SSR4	3220	2+	-0.0127	1.0000	R.FFDEESYSLLR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	3220	Delta Mass	-0.0127	Protein	IPI00019385
Mass	1405.6630	Next	256.000	Fraction	VF_T13h_band05.mzXML
Hyper	546.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	90%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
295.1441	148.0757	2	F	10	1258.5950	629.8011
410.1710	205.5892	3	D	9	1111.5266	556.2669
539.2136	270.1105	4	E	8	996.4997	498.7535
668.2562	334.6318	5	E	7	867.4571	434.2322
755.2883	378.1478	6	S	6	738.4145	369.7109
918.3516	459.6794	7	Y	5	651.3824	326.1948
1005.3836	503.1954	8	S	4	488.3191	244.6632
1118.4677	559.7375	9	L	3	401.2871	201.1472
1231.5517	616.2795	10	L	2	288.2030	144.6051
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9849	IPI00646864, IPI00647421, IPI00019385	1	1	SSR4, SSR4, SSR4	3225	2+	-0.0145	0.9996	R.FFDEESYSLLR.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	3225	Delta Mass	-0.0145	Protein	IPI00019385
Mass	1405.6630	Next	244.000	Fraction	VF_T13h_band06.mzXML
Hyper	462.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

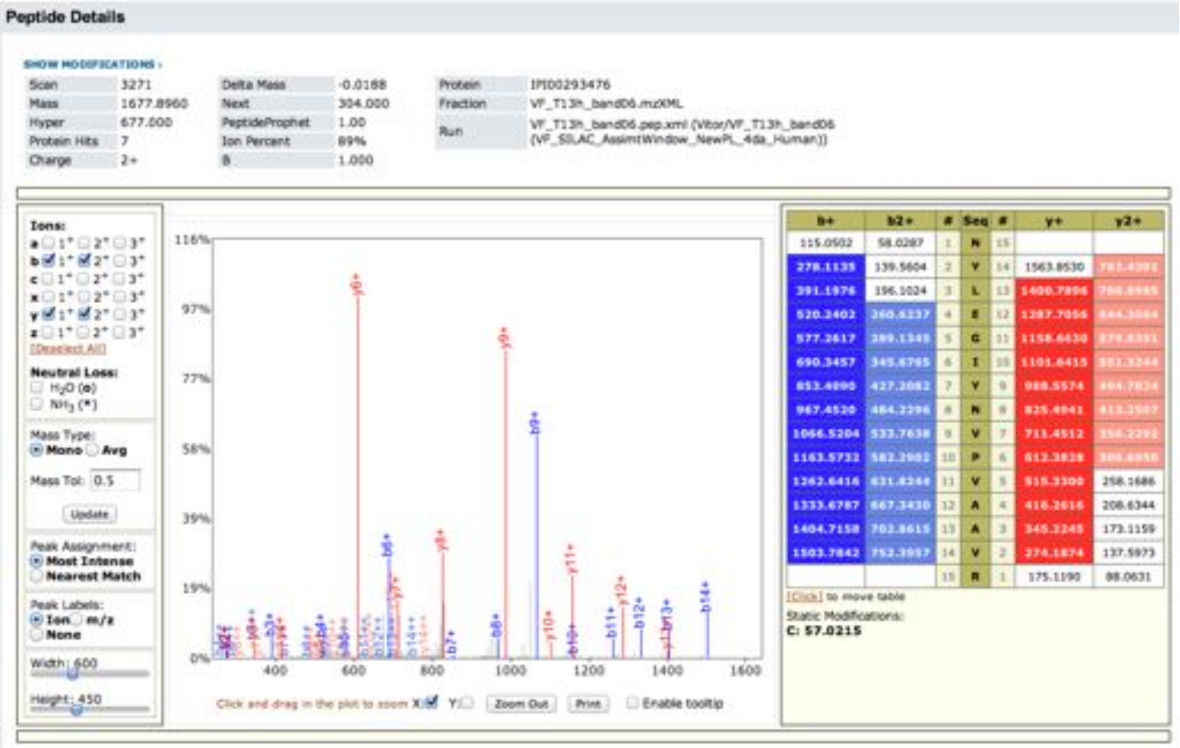
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	11		
295.1441	148.0757	2	F	10	1258.5950	629.8011
410.1710	205.5892	3	D	9	1111.5266	556.2669
539.2136	270.1105	4	E	8	996.4997	498.7535
668.2562	334.6318	5	E	7	867.4571	434.2322
755.2883	378.1478	6	S	6	738.4145	369.7109
918.3516	459.6794	7	Y	5	651.3824	326.1949
1005.3836	503.1954	8	S	4	488.3191	244.6632
1118.4677	559.7375	9	L	3	401.2871	201.1472
1231.5517	616.2795	10	L	2	288.2030	144.6051
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9881	IPI00894530, IPI00293476, IPI00871573, IPI00872806, IPI00658024, IPI00853031, IPI00853201	1	1	MRPL23, MRPL23, MRPL23, MRPL23, MRPL23, MRPL23, MRPL23	3271	2+	-0.0188	0.9999	R.NYLEGIYNVPVAAVR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	3271	Delta Mass	-0.0188	Protein	IPI00293476
Mass	1677.8960	Next	304.000	Fraction	VF_T13h_band06.mzXML
Hyper	677.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	7	Ion Percent	89%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

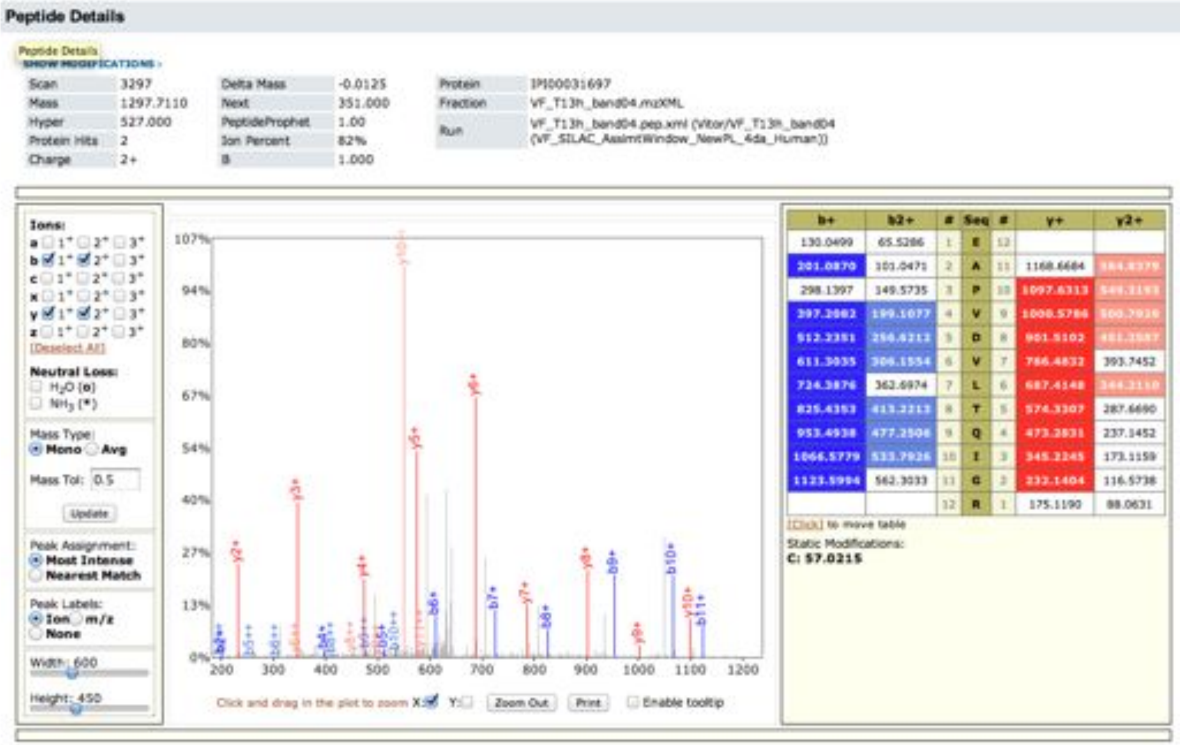
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	15		
278.1135	139.5604	2	Y	14	1563.8530	782.4301
391.1976	196.1024	3	L	13	1400.7896	700.8985
520.2402	260.6237	4	E	12	1287.7056	644.3564
577.2617	289.1345	5	G	11	1158.6630	579.8351
690.3457	345.6765	6	I	10	1101.6415	551.3244
853.4090	427.2082	7	Y	9	988.5574	494.7824
967.4520	484.2296	8	N	8	825.4941	413.2507
1066.5204	533.7638	9	V	7	711.4512	356.2292
1163.5732	582.2902	10	P	6	612.3828	306.6950
1262.6416	631.8244	11	V	5	515.3300	258.1686
1333.6787	667.3430	12	A	4	416.2616	208.6344
1404.7158	702.8615	13	A	3	345.2245	173.1159
1503.7842	752.3957	14	V	2	274.1874	137.5973
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9793	IPI00908304, IPI00031697	1	1	-, TMEM109	3297	2+	-0.0125	0.9996	R.EAPVDVLTQIGR.S



Peptide Details

Peptide Details
SHOW MODIFICATIONS ›

Scan	3297	Delta Mass	-0.0125	Protein	IPI00031697
Mass	1297.7110	Next	351.000	Fraction	VF_T13h_band04.mzXML
Hyper	527.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

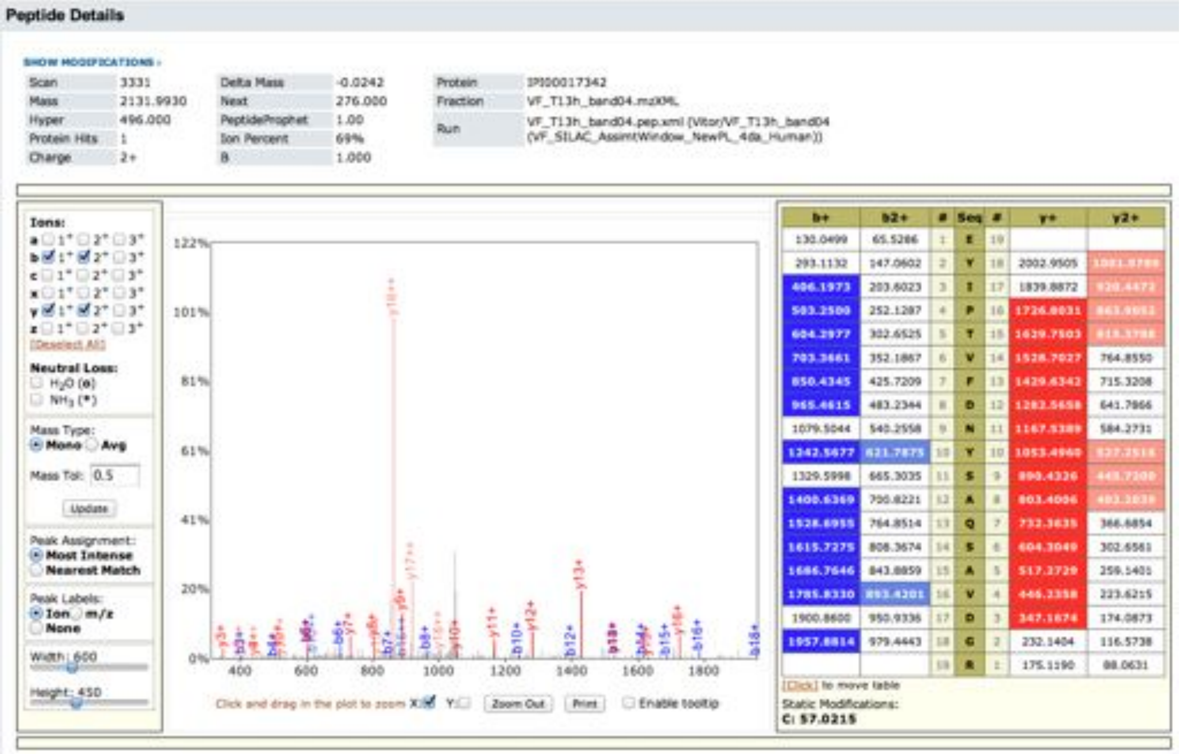
Click and drag in the plot to zoom X: ☑ Y: ☐

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	12		
201.0870	101.0471	2	A	11	1168.6684	584.8379
298.1397	149.5735	3	P	10	1097.6313	549.3193
397.2082	199.1077	4	V	9	1000.5786	500.7929
512.2351	256.6212	5	D	8	901.5102	451.2587
611.3035	306.1554	6	V	7	786.4832	393.7452
724.3876	362.6974	7	L	6	687.4148	344.2110
825.4353	413.2213	8	T	5	574.3307	287.6690
953.4938	477.2506	9	Q	4	473.2831	237.1452
1066.5779	533.7926	10	I	3	345.2245	173.1159
1123.5994	562.3033	11	G	2	232.1404	116.5738
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9822	IPI00017342	1	1	ARHG	3331	2+	-0.0242	0.9998	K.EYIPTVFDNYSAQSAVDGR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	3331	Delta Mass	-0.0242	Protein	IPI00017342
Mass	2131.9930	Next	276.000	Fraction	VF_T13h_band04.mzXML
Hyper	496.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	69%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	19		
293.1132	147.0602	2	Y	18	2002.9505	1001.9789
406.1973	203.6023	3	I	17	1839.8872	920.4472
503.2500	252.1287	4	P	16	1726.8031	863.9052
604.2977	302.6525	5	T	15	1629.7503	815.3788
703.3661	352.1867	6	V	14	1528.7027	764.8550
850.4345	425.7209	7	F	13	1429.6342	715.3208
965.4615	483.2344	8	D	12	1282.5658	641.7866
1079.5044	540.2558	9	N	11	1167.5389	584.2731
1242.5677	621.7875	10	Y	10	1053.4960	527.2516
1329.5998	665.3035	11	S	9	890.4326	445.7200
1400.6369	700.8221	12	A	8	803.4006	402.2039
1528.6955	764.8514	13	Q	7	732.3635	366.6854
1615.7275	808.3674	14	S	6	604.3049	302.6561
1686.7646	843.8859	15	A	5	517.2729	259.1401
1785.8330	893.4201	16	V	4	446.2358	223.6215
1900.8600	950.9336	17	D	3	347.1674	174.0873
1957.8814	979.4443	18	G	2	232.1404	116.5738
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9877	IPI00032460	1	1	LSM2	3335	2+	-0.0221	1.0000	R.YVQLPADEVDTQLLQDAAR.K

Peptide Details

SHOW MODIFICATIONS ›

Scan	3335	Delta Mass	-0.0221	Protein	IPI00032460
Mass	2145.0820	Next	369.000	Fraction	VF_T13h_band05.mzXML
Hyper	719.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

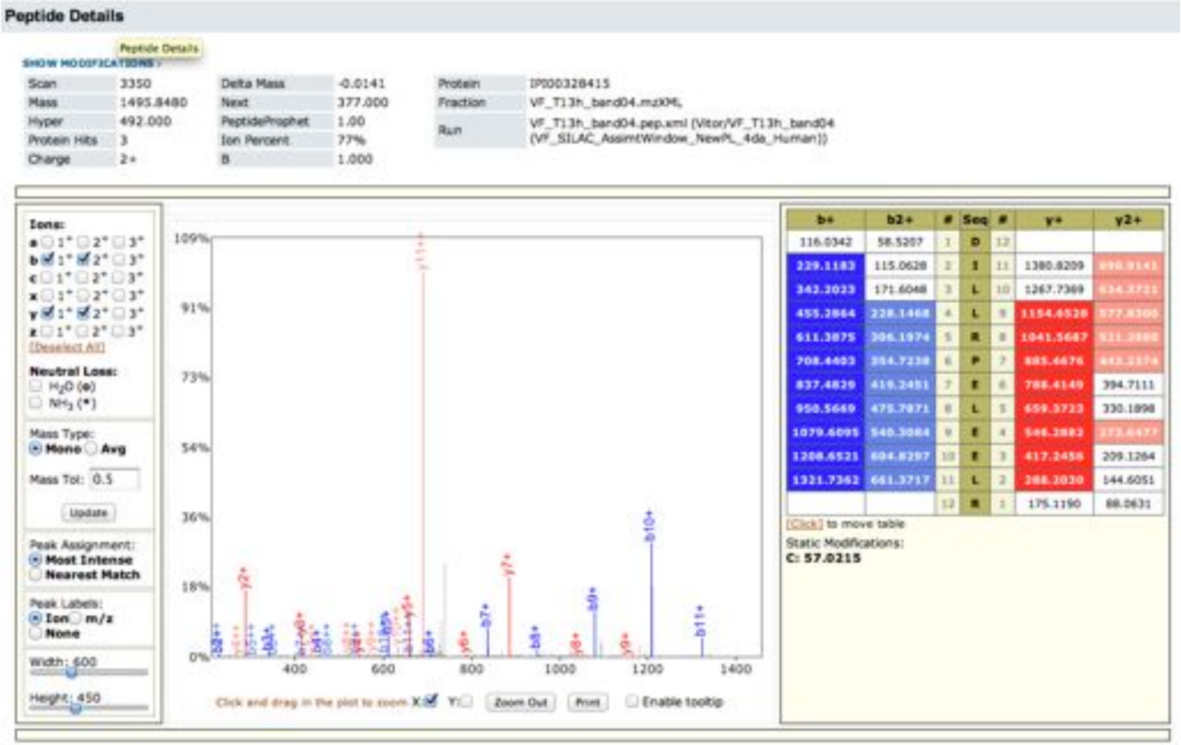
Height: 450

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	19		
263.1390	132.0731	2	V	18	1982.0189	991.5131
391.1976	196.1024	3	Q	17	1882.9505	941.9789
504.2817	252.6445	4	L	16	1754.8919	877.9496
601.3344	301.1708	5	P	15	1641.8079	821.4076
672.3715	336.6894	6	A	14	1544.7551	772.8812
787.3985	394.2029	7	D	13	1473.7180	737.3626
916.4411	458.7242	8	E	12	1358.6910	679.8492
1015.5095	508.2584	9	V	11	1229.6484	615.3279
1130.5364	565.7719	10	D	10	1130.5800	565.7937
1231.5841	616.2957	11	T	9	1015.5531	508.2803
1359.6427	680.3250	12	Q	8	914.5054	457.7563
1472.7268	736.8670	13	L	7	786.4468	393.7271
1585.8108	793.4090	14	L	6	673.3628	337.1850
1713.8694	857.4383	15	Q	5	560.2787	280.6430
1828.8963	914.9518	16	D	4	432.2201	216.6137
1899.9334	950.4704	17	A	3	317.1932	159.1002
1970.9706	985.9889	18	A	2	246.1561	123.5817
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9552	IPI00446235, IPI00871319, IPI00328415	1	1	CYB5R3, CYB5R3, CYB5R3	3350	2+	-0.0141	0.9979	K.DILLRPELEELR.N



Peptide Details

SHOW MODIFICATIONS

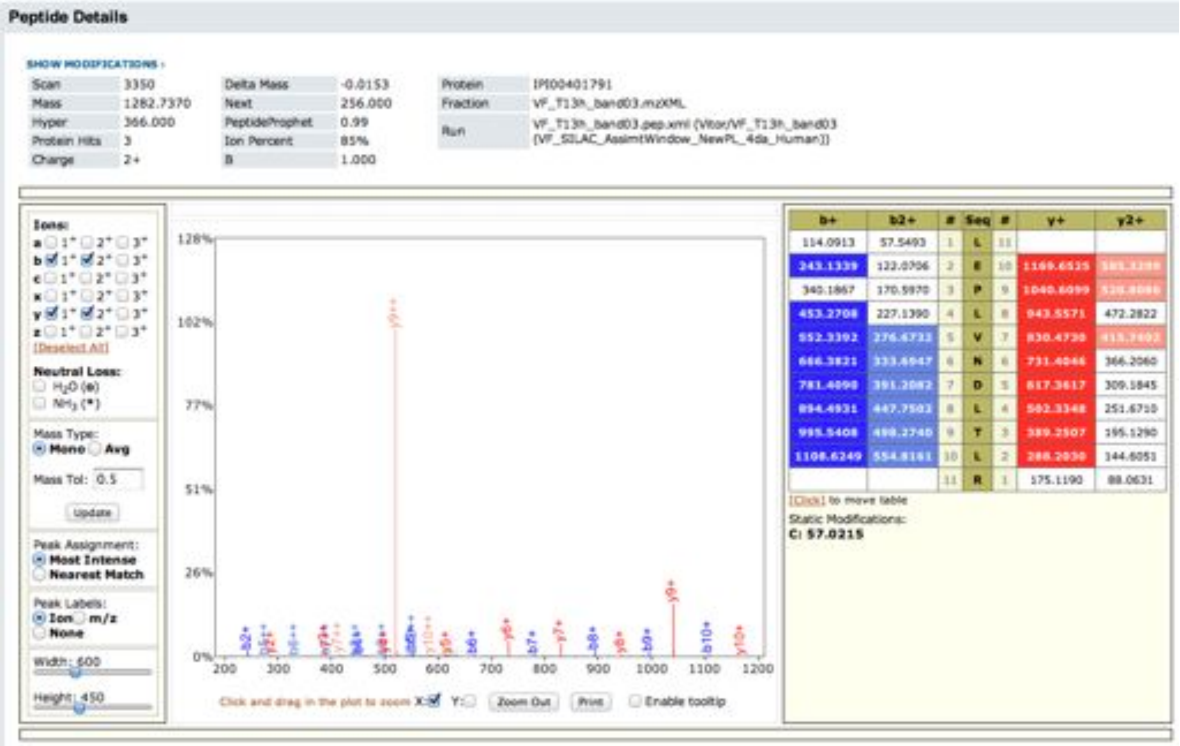
Scan	3350	Delta Mass	-0.0141	Protein	IPI00328415
Mass	1495.8480	Next	377.000	Fraction	VF_T13h_band04.mzXML
Hyper	492.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	12		
229.1183	115.0628	2	I	11	1380.8209	690.9141
342.2023	171.6048	3	L	10	1267.7369	634.3721
455.2864	228.1468	4	L	9	1154.6528	577.8300
611.3875	306.1974	5	R	8	1041.5687	521.2880
708.4403	354.7238	6	P	7	885.4676	443.2374
837.4829	419.2451	7	E	6	788.4149	394.7111
950.5669	475.7871	8	L	5	659.3723	330.1898
1079.6095	540.3084	9	E	4	546.2882	273.6477
1208.6521	604.8297	10	E	3	417.2456	209.1264
1321.7362	661.3717	11	L	2	288.2030	144.6051
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9184	IPI00896464, IPI00401791, IPI00797136	1	1	IKIP, IKIP, IKIP	3350	2+	-0.0153	0.9937	R.LEPLVNDLTLR.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	3350	Delta Mass	-0.0153	Protein	IPI00401791
Mass	1282.7370	Next	256.000	Fraction	VF_T13h_band03.mzXML
Hyper	366.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 [VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	3	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

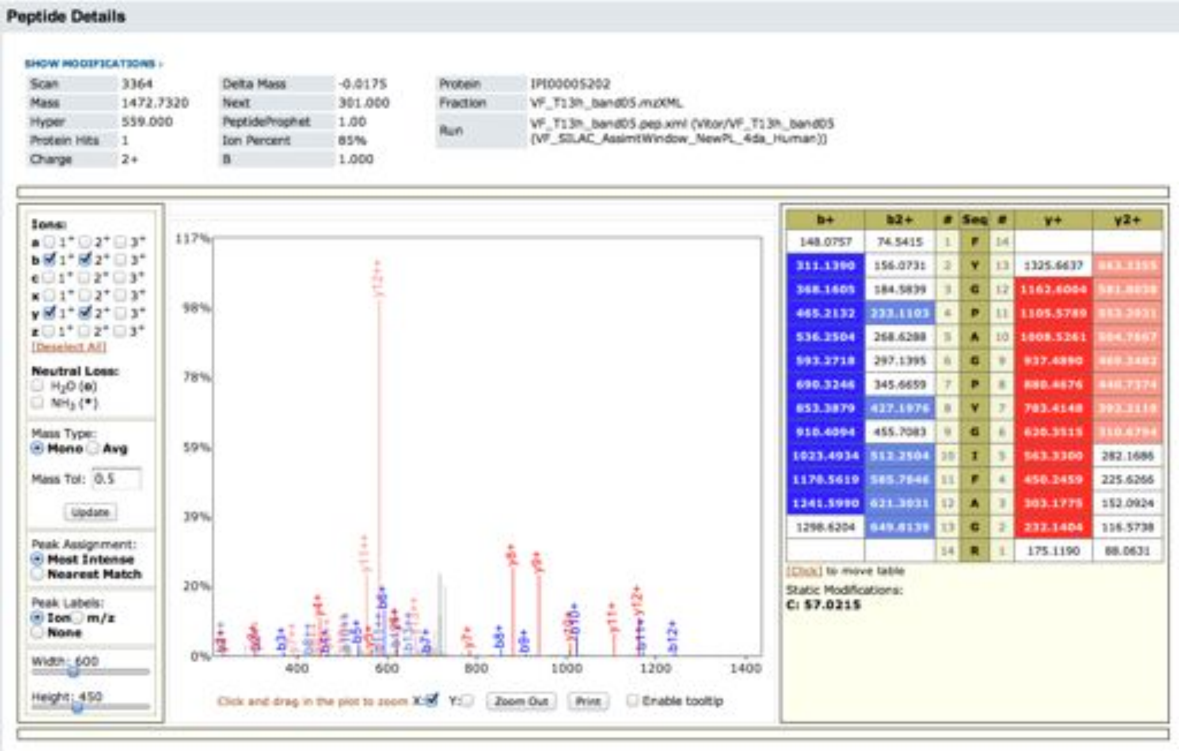
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	11		
243.1339	122.0706	2	E	10	1169.6525	585.3299
340.1867	170.5970	3	P	9	1040.6099	520.8086
453.2708	227.1390	4	L	8	943.5571	472.2822
552.3392	276.6733	5	V	7	830.4730	415.7402
666.3821	333.6947	6	N	6	731.4046	366.2060
781.4090	391.2082	7	D	5	617.3617	309.1845
894.4931	447.7503	8	L	4	502.3348	251.6710
995.5408	498.2740	9	T	3	389.2507	195.1290
1108.6249	554.8161	10	L	2	288.2030	144.6051
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9865	IPI00005202	1	1	PGRMC2	3364	2+	-0.0175	0.9999	K.FYGPAGPYGIFAGR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	3364	Delta Mass	-0.0175	Protein	IPI00005202
Mass	1472.7320	Next	301.000	Fraction	VF_T13h_band05.mzXML
Hyper	559.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

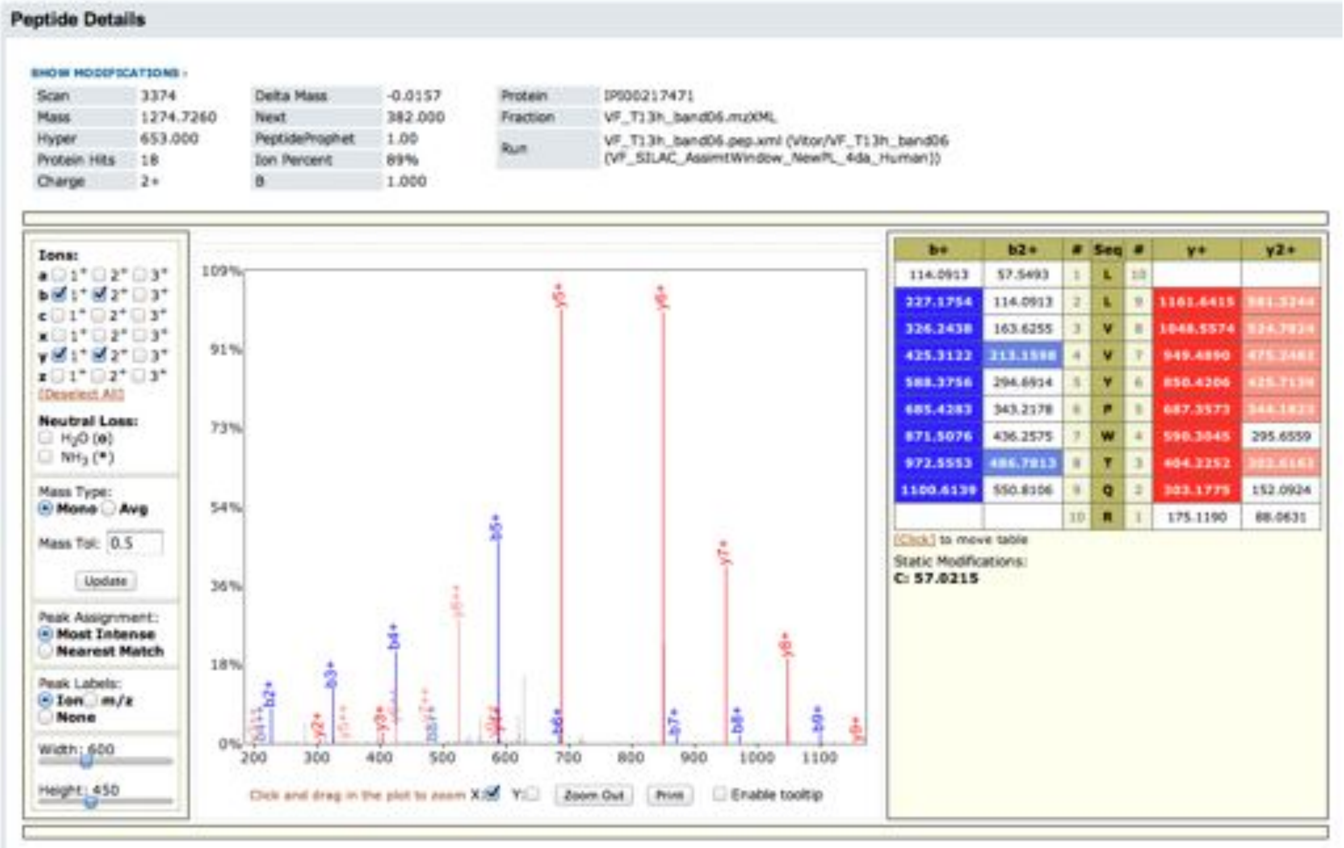
Height: 450

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	14		
311.1390	156.0731	2	Y	13	1325.6637	663.3355
368.1605	184.5839	3	G	12	1162.6004	581.8038
465.2132	233.1103	4	P	11	1105.5789	553.2931
536.2504	268.6288	5	A	10	1008.5261	504.7667
593.2718	297.1395	6	G	9	937.4890	469.2482
690.3246	345.6659	7	P	8	880.4676	440.7374
853.3879	427.1976	8	Y	7	783.4148	392.2110
910.4094	455.7083	9	G	6	620.3515	310.6794
1023.4934	512.2504	10	I	5	563.3300	282.1686
1170.5619	585.7846	11	F	4	450.2459	225.6266
1241.5990	621.3031	12	A	3	303.1775	152.0924
1298.6204	649.8139	13	G	2	232.1404	116.5738
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0.9870	IPI00815947, IPI00853641, IPI00884436, IPI00791558, IPI00796636, IPI00829896, IPI00915024, IPI00657911, IPI00657660, IPI00217471, IPI00220706, IPI00473011, IPI00554676, IPI00654755, IPI00816618, IPI00744503, IPI00749035, IPI00884107	1	1	HBB, HBE1, -, HBB, HBB, HBD, HBD, HBG2, HBB, HBE1, HBG1, HBD, HBG1, HBB, HBG2, HBG1, HBG2, HBB	3374	2+	-0.0157	0.9998	R.LLVVYPWTQR.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	3374	Delta Mass	-0.0157	Protein	IPI00217471
Mass	1274.7260	Next	382.000	Fraction	VF_T13h_band06.mzXML
Hyper	653.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	18	Ion Percent	89%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

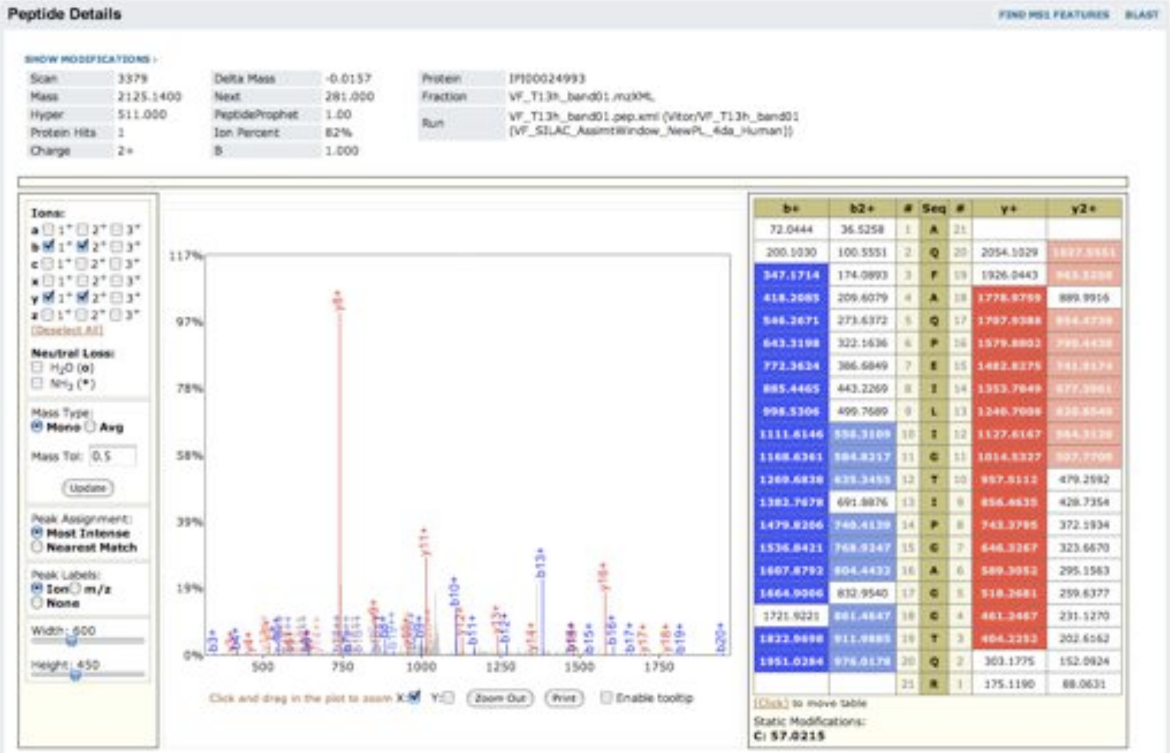
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	10		
227.1754	114.0913	2	L	9	1161.6415	581.3244
326.2438	163.6255	3	V	8	1048.5574	524.7824
425.3122	213.1598	4	V	7	949.4890	475.2482
588.3756	294.6914	5	Y	6	850.4206	425.7138
685.4283	343.2178	6	P	5	687.3573	344.1823
871.5076	436.2575	7	W	4	590.3045	295.6559
972.5553	486.7813	8	T	3	404.2252	302.6163
1100.6139	550.8106	9	Q	2	303.1775	152.0924
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9793	IPI00024993	1	1	ECHS1	3379	2+	-0,0157	0,9998	K.AQFAQPEILIGTIPGAGGTQR.L



Peptide Details

Scan	3379	Delta Mass	-0.0157	Protein	IPI00024993
Mass	2125.1400	Next	281.000	Fraction	VF_T13h_band01.mzXML
Hyper	511.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	82%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	21		
200.1030	100.5551	2	Q	20	2054.1029	1027.5551
347.1714	174.0893	3	F	19	1926.0443	963.5258
418.2085	209.6079	4	A	18	1778.9759	889.9916
546.2671	273.6372	5	Q	17	1707.9388	854.4730
643.3198	322.1636	6	P	16	1579.8802	790.4438
772.3624	386.6849	7	E	15	1482.8275	741.9174
885.4465	443.2269	8	I	14	1353.7649	677.3861
998.5306	499.7689	9	L	13	1240.7008	620.8540
1111.6146	556.3109	10	I	12	1127.6167	564.3120
1168.6361	584.8217	11	G	11	1014.5327	507.7700
1269.6838	635.3455	12	T	10	957.5112	479.2592
1382.7678	691.8876	13	I	9	856.4635	428.7354
1479.8206	740.4139	14	P	8	743.3795	372.1934
1536.8421	768.9247	15	G	7	646.3267	323.6670
1607.8792	804.4433	16	A	6	589.3052	295.1563
1664.9006	832.9540	17	G	5	518.2681	259.6377
1721.9221	861.4647	18	G	4	461.2467	231.1270
1822.0698	911.9885	19	T	3	404.2252	202.6162
1951.0284	976.0178	20	Q	2	303.1775	152.0924
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9323	IPI00386294	1	1	OBTP	3392	2+	-0,0155	0,9952	R.NLSDIDLMAPQPGV.-

Pep

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http://www.yahoo.com/

SHOW MODIFICATIONS ›

Scan	3392	Delta Mass	-0.0155	Protein	IPI00386294
Mass	1469.7300	Next	256.000	Fraction	VF_T13h_band05.mzXML
Hyper	363.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	73%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	14		
228.1343	114.5708	2	L	13	1355.6875	678.3474
315.1663	158.0868	3	S	12	1242.6035	621.8054
430.1932	215.6003	4	D	11	1155.5714	578.2894
543.2773	272.1423	5	I	10	1040.5445	520.7759
658.3042	329.6558	6	D	9	927.4604	464.2339
771.3883	386.1978	7	L	8	812.4335	406.7204
902.4288	451.7180	8	M	7	699.3494	350.1783
973.4659	487.2366	9	A	6	568.3089	284.6581
1070.5187	535.7630	10	P	5	497.2718	249.1395
1198.5772	599.7923	11	Q	4	400.2191	200.6132
1295.6300	648.3186	12	P	3	272.1605	136.5839
1352.6515	676.8294	13	G	2	175.1077	88.0575
		14	V	1	118.0863	59.5468

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00023086	1	1	MRPL15	3413	2+	-0,0158	0,9999	R.LGFEGGQTPFYIR.I

Peptide Details

SHOW MODIFICATIONS ›

Scan	3413	Delta Mass	-0.0158	Protein	IPI00023086
Mass	1484.7530	Next	261.000	Fraction	VF_T13h_band03.mzXML
Hyper	524.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	1	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

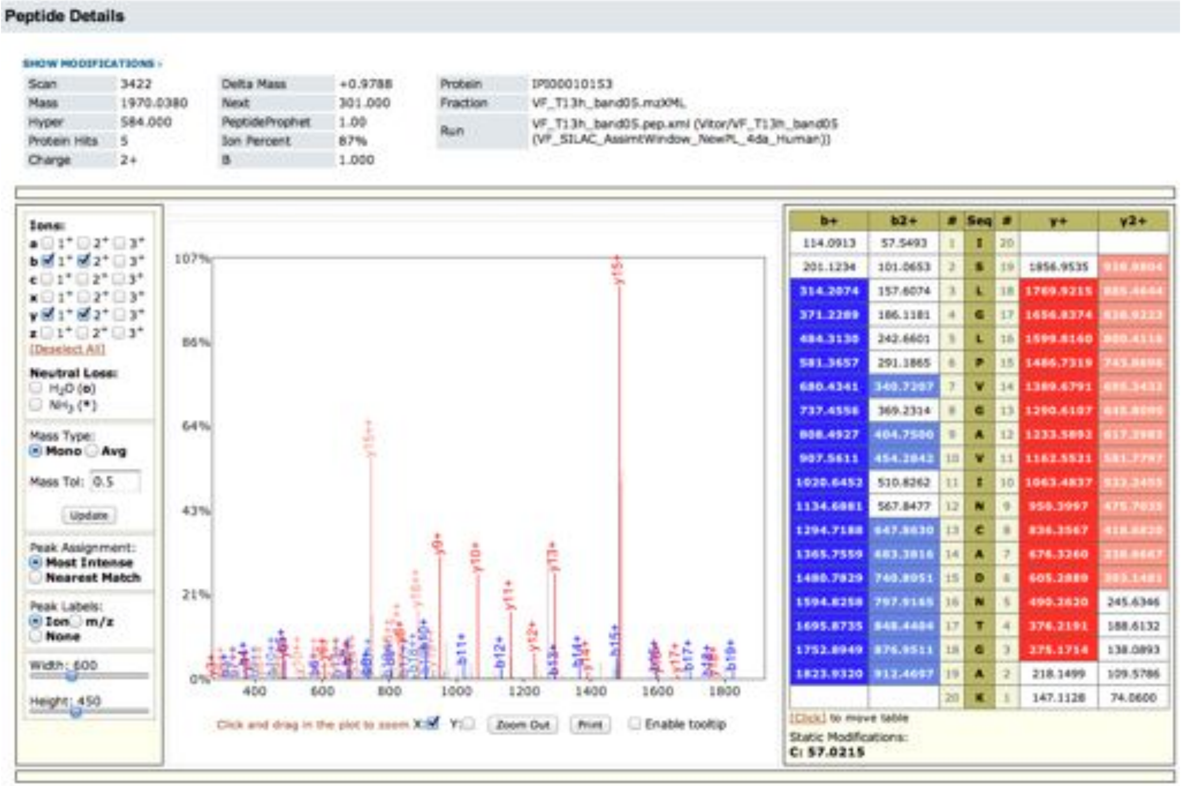
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	13		
171.1128	86.0600	2	G	12	1371.6692	686.3383
318.1812	159.5942	3	F	11	1314.6477	657.8275
447.2238	224.1155	4	E	10	1167.5793	584.2933
504.2453	252.6263	5	G	9	1038.5367	519.7720
561.2667	281.1370	6	G	8	981.5152	491.2613
689.3253	345.1663	7	Q	7	924.4938	462.7505
790.3730	395.6901	8	T	6	796.4352	398.7212
887.4258	444.2165	9	P	5	695.3875	348.1974
1034.4942	517.7507	10	F	4	598.3348	299.6710
1197.5575	599.2824	11	Y	3	451.2663	226.1368
1310.6416	655.8244	12	I	2	288.2030	144.6051
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9780	IPI00795751, IPI00794091, IPI00791920, IPI00010153, IPI00795408	1	1	RPL23, RPL23, RPL23, RPL23, RPL23	3422	2+	+0,9788	0,9992	R.ISLGLPVGAVINCADNTGAK.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	3422	Delta Mass	+0.9788	Protein	IPI00010153
Mass	1970.0380	Next	301.000	Fraction	VF_T13h_band05.mzXML
Hyper	584.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

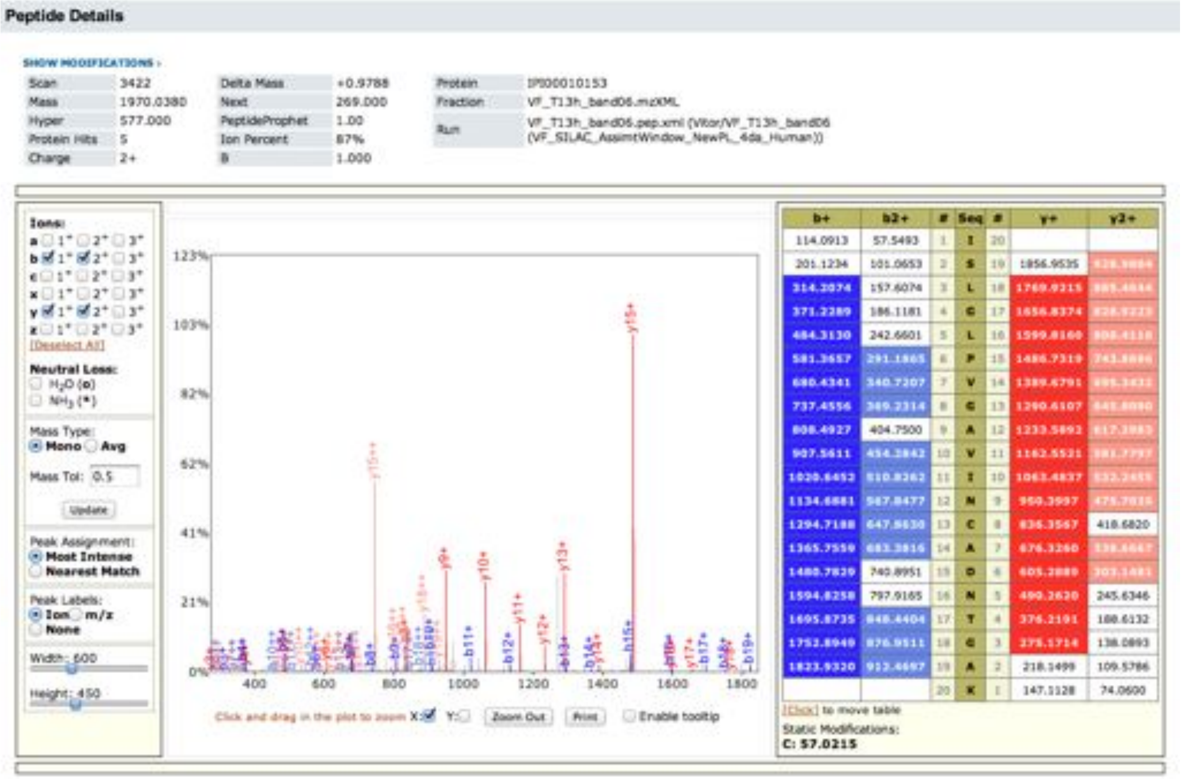
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	20		
201.1234	101.0653	2	S	19	1856.9535	928.9804
314.2074	157.6074	3	L	18	1769.9215	885.4644
371.2289	186.1181	4	G	17	1656.8374	828.9223
484.3130	242.6601	5	L	16	1599.8160	800.4116
581.3657	291.1865	6	P	15	1486.7319	743.8696
680.4341	340.7207	7	V	14	1389.6791	695.3432
737.4556	369.2314	8	G	13	1290.6107	645.8090
808.4927	404.7500	9	A	12	1233.5892	617.2983
907.5611	454.2842	10	V	11	1162.5521	581.7797
1020.6452	510.8262	11	I	10	1063.4837	532.2455
1134.6881	567.8477	12	N	9	950.3997	475.7035
1294.7188	647.8630	13	C	8	836.3567	418.6820
1365.7559	683.3816	14	A	7	676.3260	338.6667
1480.7829	740.8951	15	D	6	605.2889	303.1481
1594.8258	797.9165	16	N	5	490.2620	245.6346
1695.8735	848.4404	17	T	4	376.2191	188.6132
1752.8949	876.9511	18	G	3	275.1714	138.0893
1823.9320	912.4697	19	A	2	218.1499	109.5786
		20	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9723	IPI00795751, IPI00794091, IPI00791920, IPI00010153, IPI00795408	1	1	RPL23, RPL23, RPL23, RPL23, RPL23	3422	2+	+0,9788	0,9984	R.ISLGLPVGAVINCADNTGAK.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	3422	Delta Mass	+0.9788	Protein	IPI00010153
Mass	1970.0380	Next	269.000	Fraction	VF_T13h_band06.mzXML
Hyper	577.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

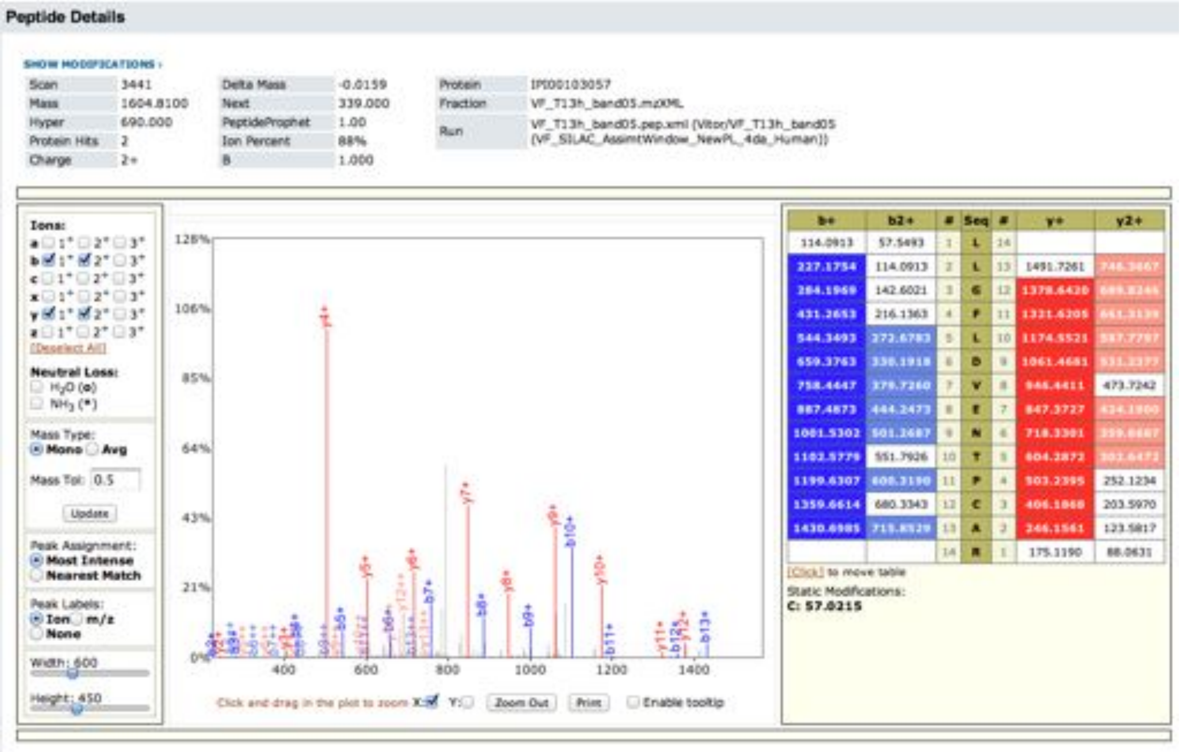
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	20		
201.1234	101.0653	2	S	19	1856.9535	928.9804
314.2074	157.6074	3	L	18	1769.9215	885.4644
371.2289	186.1181	4	G	17	1656.8374	828.9223
484.3130	242.6601	5	L	16	1599.8160	800.4118
581.3657	291.1865	6	P	15	1486.7319	743.8696
680.4341	340.7207	7	V	14	1389.6791	695.3432
737.4556	369.2314	8	G	13	1290.6107	645.8090
808.4927	404.7500	9	A	12	1233.5892	617.2983
907.5611	454.2842	10	V	11	1162.5521	581.7797
1020.6452	510.8262	11	I	10	1063.4837	532.2455
1134.6881	567.8477	12	N	9	950.3997	475.7035
1294.7188	647.8630	13	C	8	836.3567	418.6820
1365.7559	683.3816	14	A	7	676.3260	338.6667
1480.7829	740.8951	15	D	6	605.2889	303.1481
1594.8258	797.9165	16	N	5	490.2620	245.6346
1695.8735	848.4404	17	T	4	376.2191	188.6132
1752.8949	876.9511	18	G	3	275.1714	138.0893
1823.9320	912.4697	19	A	2	218.1499	109.5786
		20	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00607610, IPI00103057	1	1	FAM36A, FAM36A	3441	2+	-0,0159	1,0000	K.LLGFLDVENTPCAR.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	3441	Delta Mass	-0.0159	Protein	IPI00103057
Mass	1604.8100	Next	339.000	Fraction	VF_T13h_band05.mzXML
Hyper	690.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

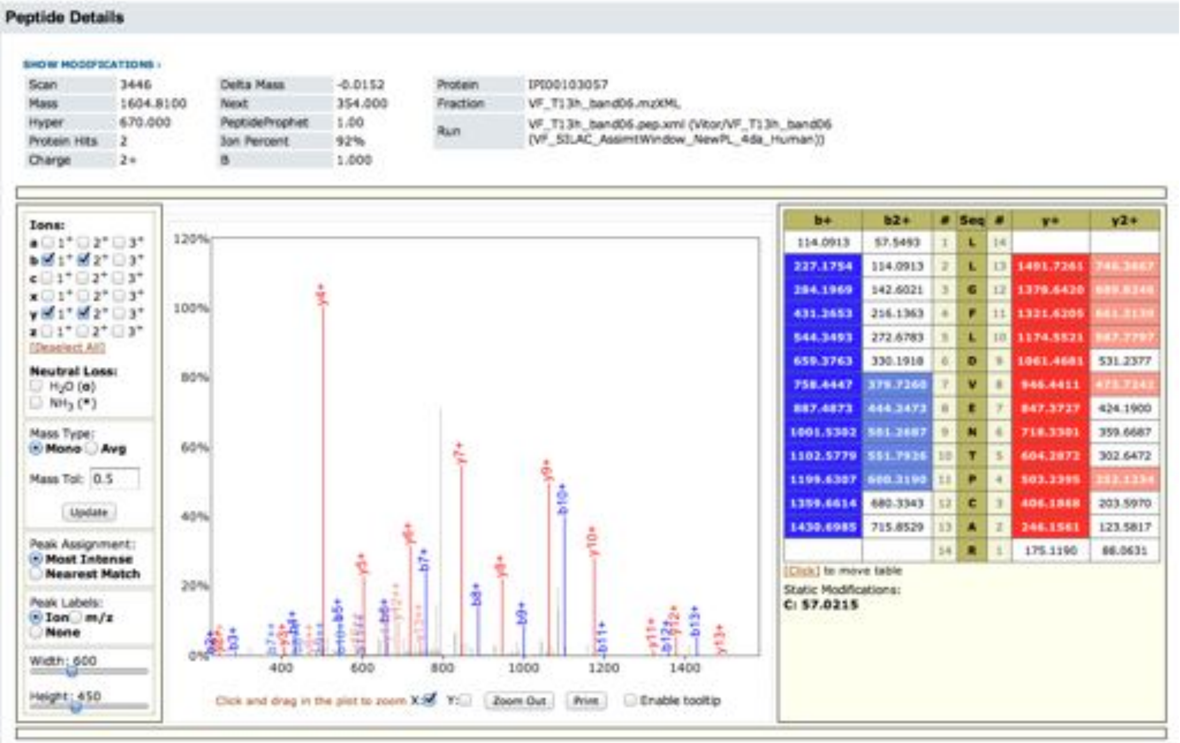
Width: 600
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	14		
227.1754	114.0913	2	L	13	1491.7261	746.3667
284.1969	142.6021	3	G	12	1378.6420	689.8246
431.2653	216.1363	4	F	11	1321.6205	661.3139
544.3493	272.6783	5	L	10	1174.5521	587.7797
659.3763	330.1918	6	D	9	1061.4681	531.2377
758.4447	379.7260	7	V	8	946.4411	473.7242
887.4873	444.2473	8	E	7	847.3727	424.1900
1001.5302	501.2687	9	N	6	718.3301	359.6687
1102.5779	551.7926	10	T	5	604.2872	302.6472
1199.6307	600.3190	11	P	4	503.2395	252.1234
1359.6614	680.3343	12	C	3	406.1860	203.5970
1430.6985	715.8529	13	A	2	246.1561	123.5817
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00607610, IPI00103057	1	1	FAM36A, FAM36A	3446	2+	-0,0152	0,9999	K.LLGFLDVENTPCAR.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	3446	Delta Mass	-0.0152	Protein	IPI00103057
Mass	1604.8100	Next	354.000	Fraction	VF_T13h_band06.mzXML
Hyper	670.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	92%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

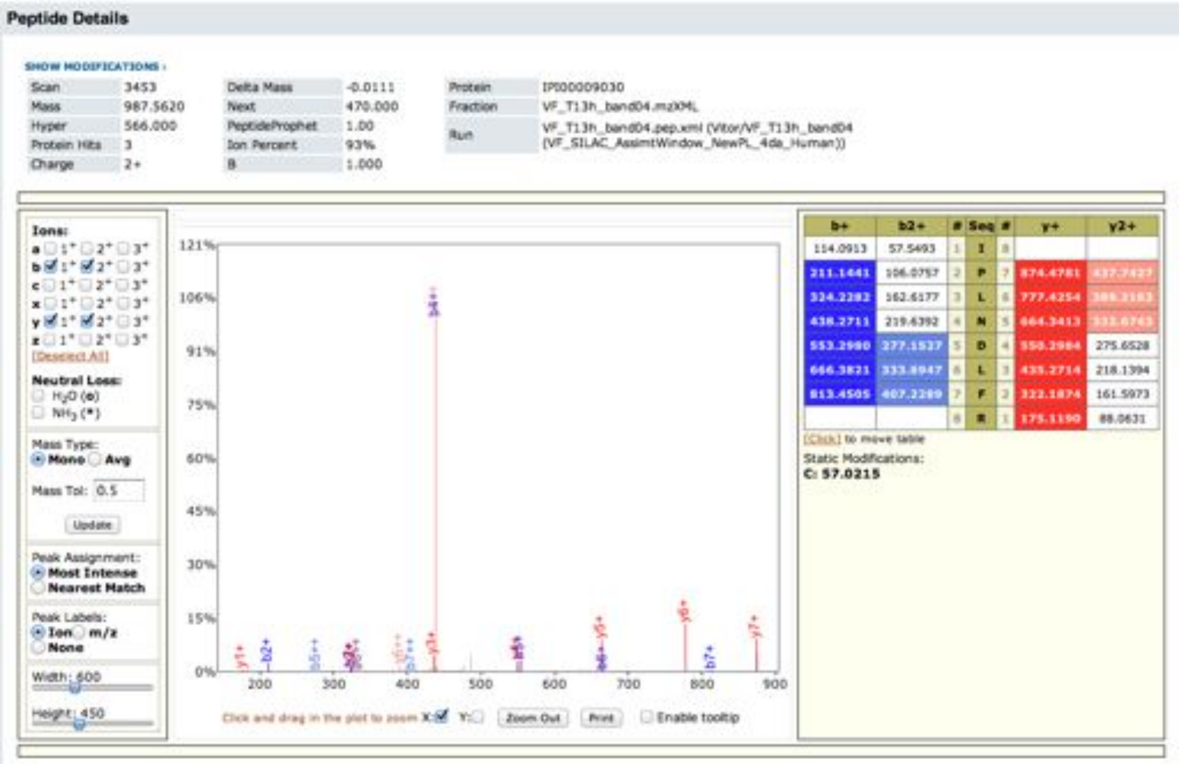
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	14		
227.1754	114.0913	2	L	13	1491.7261	746.3667
284.1969	142.6021	3	G	12	1378.6420	689.8246
431.2653	216.1363	4	F	11	1321.6205	661.3139
544.3493	272.6783	5	L	10	1174.5521	587.7797
659.3763	330.1918	6	D	9	1061.4681	531.2377
758.4447	379.7260	7	V	8	946.4411	473.7242
887.4873	444.2473	8	E	7	847.3727	424.1900
1001.5302	501.2687	9	N	6	718.3301	359.6687
1102.5779	551.7926	10	T	5	604.2872	302.6472
1199.6307	600.3190	11	P	4	503.2395	252.1234
1359.6614	680.3343	12	C	3	406.1868	203.5970
1430.6985	715.8529	13	A	2	246.1561	123.5817
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9552	IPI00009030, IPI00739827, IPI00216172	1	1	LAMP2, LAMP2, LAMP2	3453	2+	-0,0111	0,9979	R.IPLNDLFR.C



Peptide Details

SHOW MODIFICATIONS ›

Scan	3453	Delta Mass	-0.0111	Protein	IPI00009030
Mass	987.5620	Next	470.000	Fraction	VF_T13h_band04.mzXML
Hyper	566.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	93%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

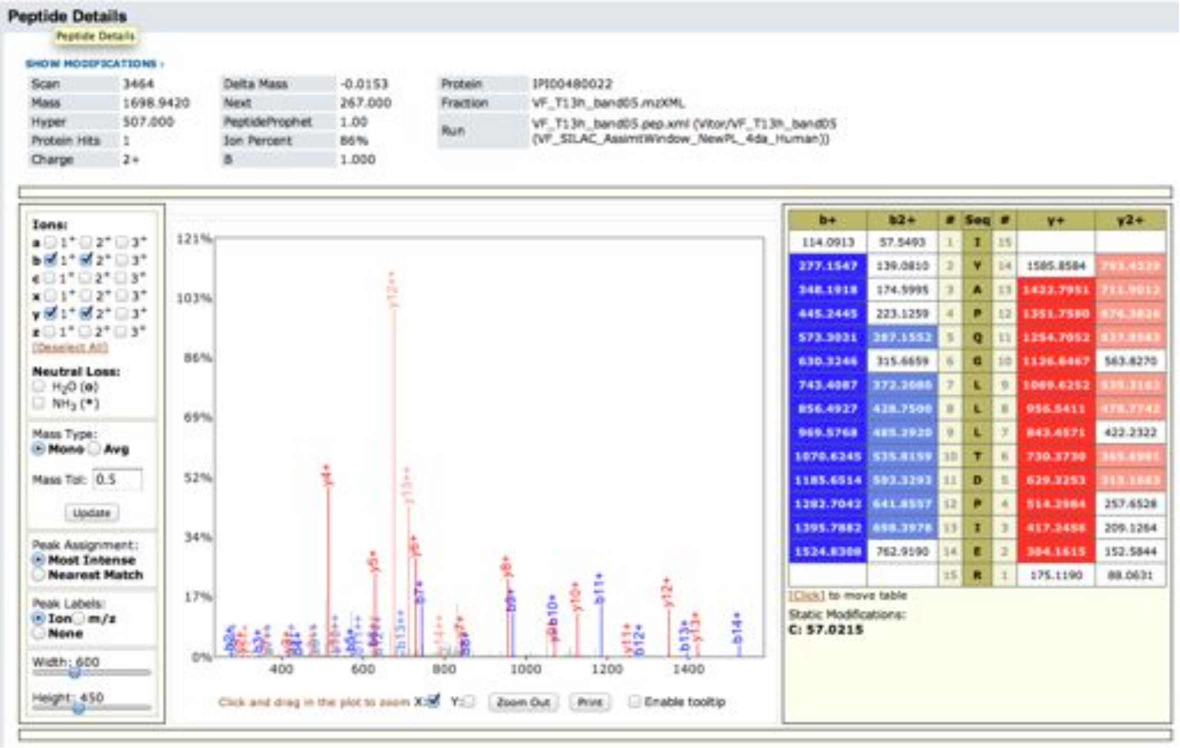
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	8		
211.1441	106.0757	2	P	7	874.4781	437.7427
324.2282	162.6177	3	L	6	777.4254	389.2163
438.2711	219.6392	4	N	5	664.3413	332.6743
553.2980	277.1527	5	D	4	550.2984	275.6528
666.3821	333.6947	6	L	3	435.2714	218.1394
813.4505	407.2289	7	F	2	322.1874	161.5973
		8	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9865	IPI00480022	1	1	GOLGA7	3464	2+	-0,0153	0,9999	K.IYAPQGLLLTDPIER.G



Scan	3464	Delta Mass	-0.0153	Protein	IPI00480022
Mass	1698.9420	Next	267.000	Fraction	VF_T13h_band05.mzXML
Hyper	507.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

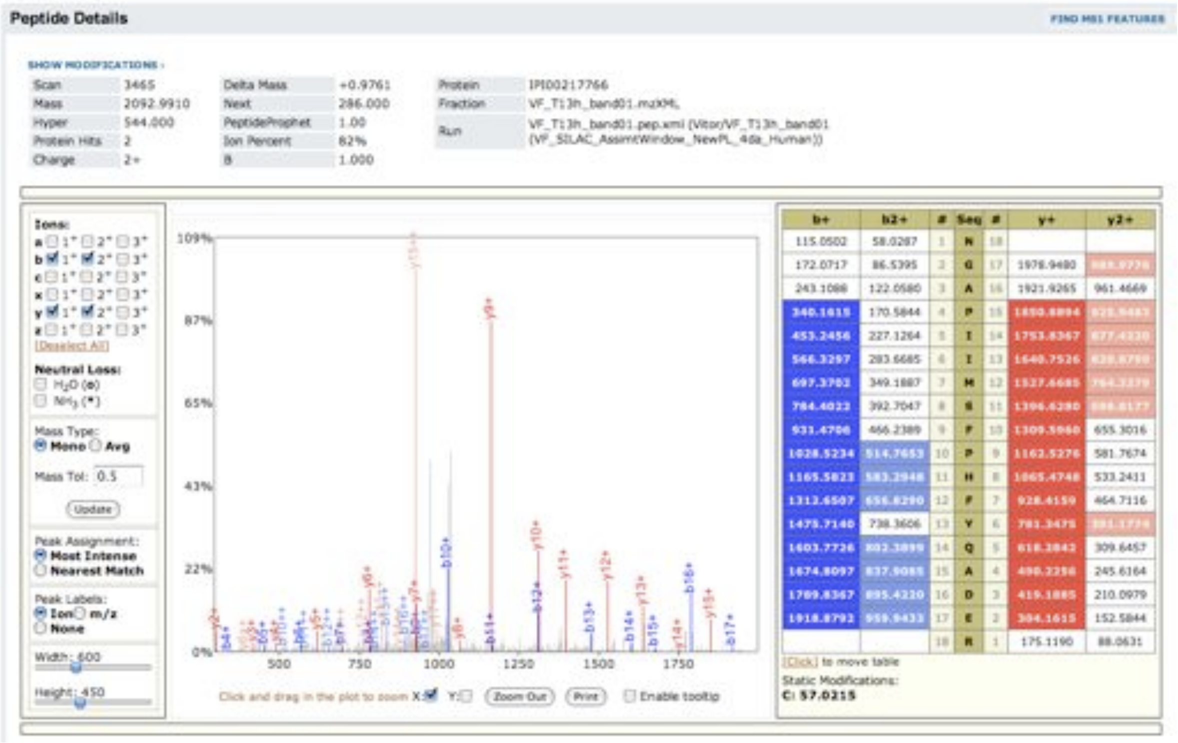
Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	15		
277.1547	139.0810	2	Y	14	1585.8584	793.4329
348.1918	174.5995	3	A	13	1422.7951	711.9012
445.2445	223.1259	4	P	12	1351.7580	676.3826
573.3031	287.1552	5	Q	11	1254.7052	627.8563
630.3246	315.6659	6	G	10	1126.6467	563.8270
743.4087	372.2080	7	L	9	1069.6252	535.3162
856.4927	428.7500	8	L	8	956.5411	478.7742
969.5768	485.2920	9	L	7	843.4571	422.2322
1070.6245	535.8159	10	T	6	730.3730	365.6901
1185.6514	593.3293	11	D	5	629.3253	315.1663
1282.7042	641.8557	12	P	4	514.2984	257.6528
1395.7882	698.3978	13	I	3	417.2456	209.1264
1524.8308	762.9190	14	E	2	304.1615	152.5844
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9466	IPI00909338, IPI00217766	1	1	-, SCARB2	3465	2+	+0,9761	0,9978	K.NGAPIIMSFPHFYQADER.F



Peptide Details

Scan	3465	Delta Mass	+0.9761	Protein	IPI00217766
Mass	2092.9910	Next	286.000	Fraction	VF_T13h_band01.mzXML
Hyper	544.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

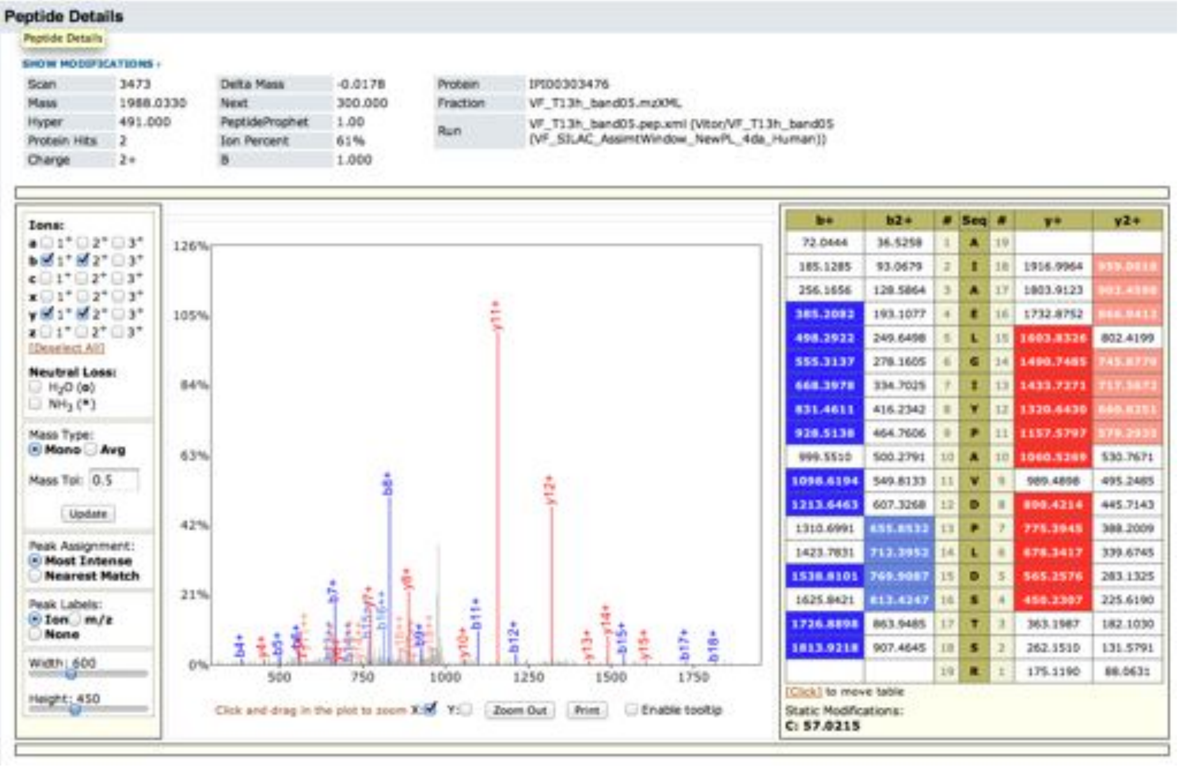
☑ X ☐ Y

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	18		
172.0717	86.5395	2	G	17	1978.9480	989.9776
243.1088	122.0580	3	A	16	1921.9265	961.4669
340.1615	170.5844	4	P	15	1850.8894	925.9483
453.2456	227.1264	5	I	14	1753.8367	877.4220
566.3297	283.6685	6	I	13	1640.7526	820.8799
697.3702	349.1887	7	M	12	1527.6685	764.3379
784.4022	392.7047	8	S	11	1396.6280	698.8177
931.4706	466.2389	9	F	10	1309.5960	655.3016
1028.5234	514.7653	10	P	9	1162.5276	581.7674
1165.5823	583.2948	11	H	8	1065.4748	533.2411
1312.6507	656.8290	12	F	7	928.4159	464.7116
1475.7140	738.3606	13	Y	6	781.3475	391.1774
1603.7726	802.3899	14	Q	5	618.2842	309.6457
1674.8097	837.9085	15	A	4	490.2256	245.6164
1789.8367	895.4220	16	D	3	419.1885	210.0979
1918.8793	959.9433	17	E	2	304.1615	152.5844
		18	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9840	IPI00790847, IPI00303476	1	1	ATP5B, ATP5B	3473	2+	-0,0178	0,9997	R.AIAELGIYPAVDPLDSTSR.I



Peptide Details

Scan	3473	Delta Mass	-0.0178	Protein	IPI00303476
Mass	1988.0330	Next	300.000	Fraction	VF_T13h_band05.mzXML
Hyper	491.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	61%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

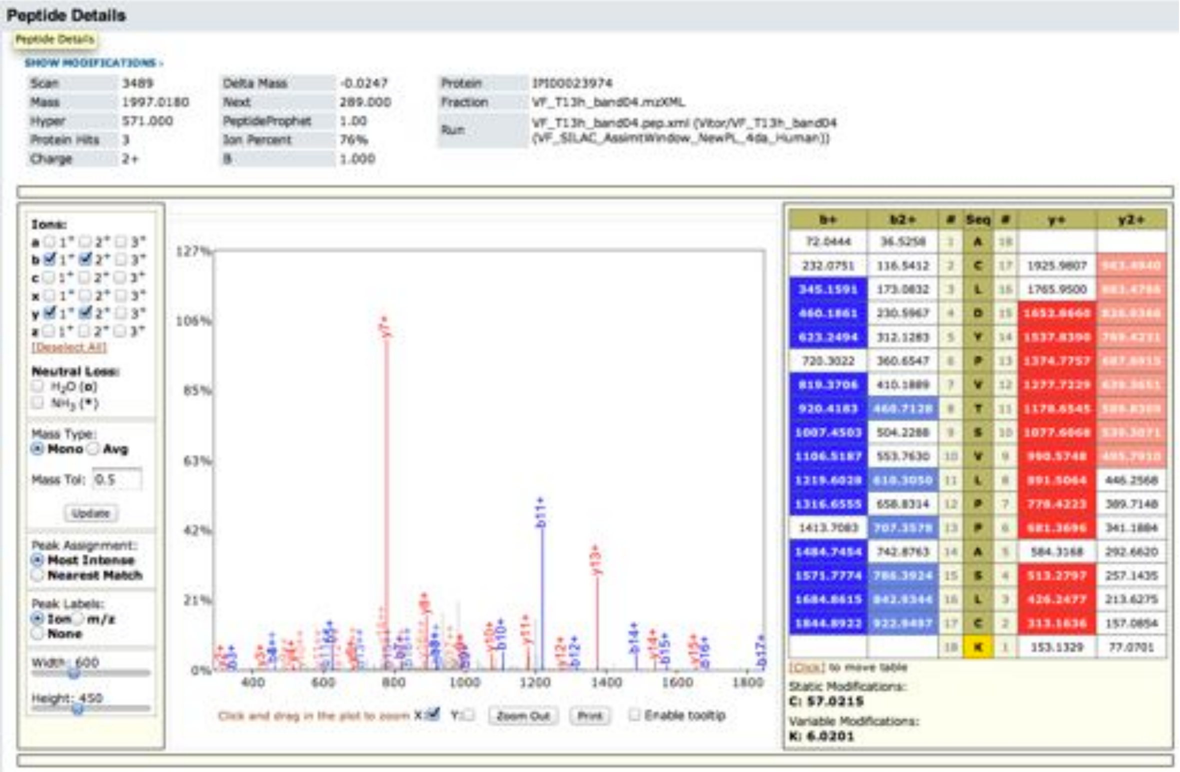
Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	19		
185.1285	93.0679	2	I	18	1916.9964	959.0018
256.1656	128.5864	3	A	17	1803.9123	902.4598
385.2082	193.1077	4	E	16	1732.8752	866.9412
498.2922	249.6498	5	L	15	1603.8326	802.4199
555.3137	278.1605	6	G	14	1490.7485	745.8779
668.3978	334.7025	7	I	13	1433.7271	717.3672
831.4611	416.2342	8	Y	12	1320.6430	660.8251
928.5138	464.7606	9	P	11	1157.5797	579.2935
999.5510	500.2791	10	A	10	1060.5269	530.7671
1098.6194	549.8133	11	V	9	989.4898	495.2485
1213.6463	607.3268	12	D	8	900.4214	445.7143
1310.6991	655.8532	13	P	7	775.3945	388.2009
1423.7831	712.3952	14	L	6	678.3417	339.6745
1538.8101	769.9087	15	D	5	565.2576	283.1325
1625.8421	813.4247	16	S	4	450.2307	225.6190
1726.8898	863.9485	17	T	3	363.1987	182.1030
1813.9218	907.4645	18	S	2	262.1510	131.5791
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9837	IPI00795434, IPI00794805, IPI00023974	1	1	PTTG1IP, PTTG1IP, PTTG1IP	3489	2+	-0,0247	0,9999	K.ACLDYPVTSVLPPASLCK'.L


Peptide Details

Scan	3489	Delta Mass	-0.0247	Protein	IPI00023974
Mass	1997.0180	Next	289.000	Fraction	VF_T13h_band04.mzXML
Hyper	571.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	76%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

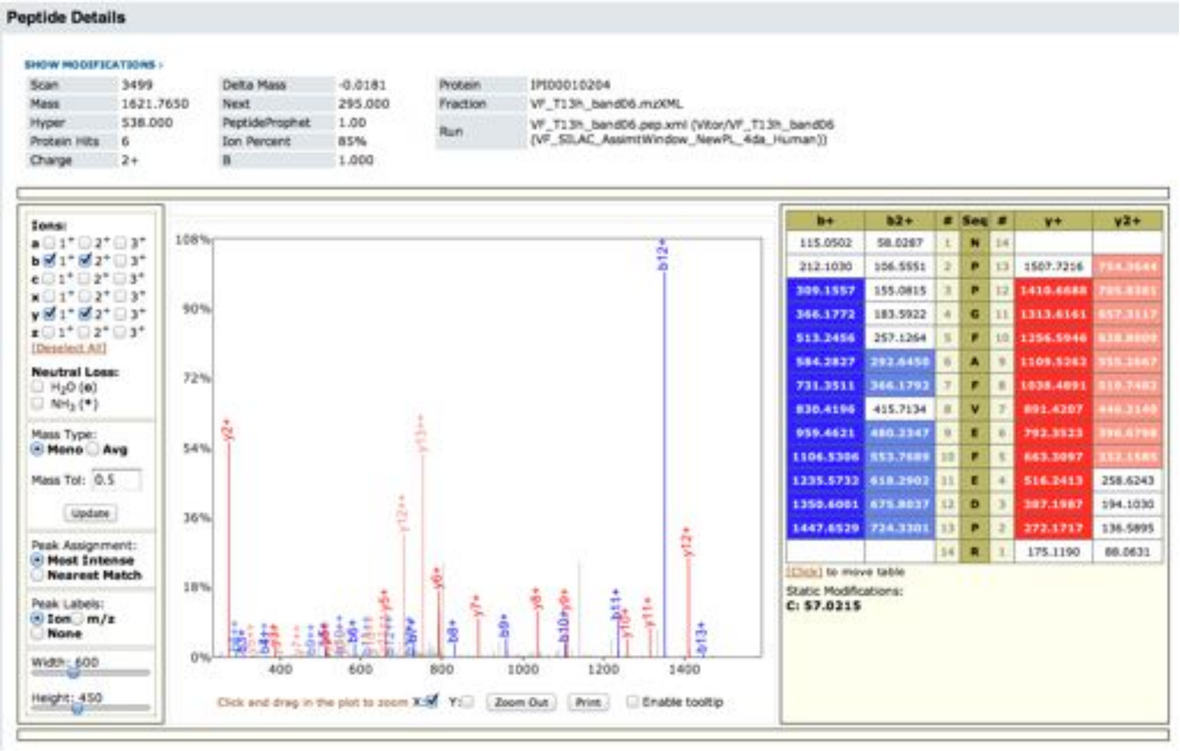
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	18		
232.0751	116.5412	2	C	17	1925.9807	963.4940
345.1591	173.0832	3	L	16	1765.9500	883.4786
460.1861	230.5967	4	D	15	1652.8660	826.9366
623.2494	312.1283	5	Y	14	1537.8390	769.4231
720.3022	360.6547	6	P	13	1374.7757	687.8915
819.3706	410.1889	7	V	12	1277.7229	639.3651
920.4183	460.7128	8	T	11	1178.6545	589.8309
1007.4503	504.2288	9	S	10	1077.6068	539.3071
1106.5187	553.7630	10	V	9	990.5748	495.7910
1219.6028	610.3050	11	L	8	891.5064	446.2568
1316.6555	658.8314	12	P	7	778.4223	389.7148
1413.7083	707.3579	13	P	6	681.3696	341.1884
1484.7454	742.8763	14	A	5	584.3168	292.6620
1571.7774	786.3924	15	S	4	513.2797	257.1435
1684.8615	842.9344	16	L	3	426.2477	213.6275
1844.8922	922.9497	17	C	2	313.1636	157.0854
		18	K	1	153.1329	77.0701

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9859	IPI00843996, IPI00332419, IPI00215907, IPI00010204, IPI00744364, IPI00003377	1	1	SFRS3, SFRS7, SFRS7, SFRS3, SFRS7, SFRS7	3499	2+	-0,0181	0,9997	R.NPPGFAFVEFEDPR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	3499	Delta Mass	-0.0181	Protein	IPI00010204
Mass	1621.7650	Next	295.000	Fraction	VF_T13h_band06.mzXML
Hyper	538.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	85%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

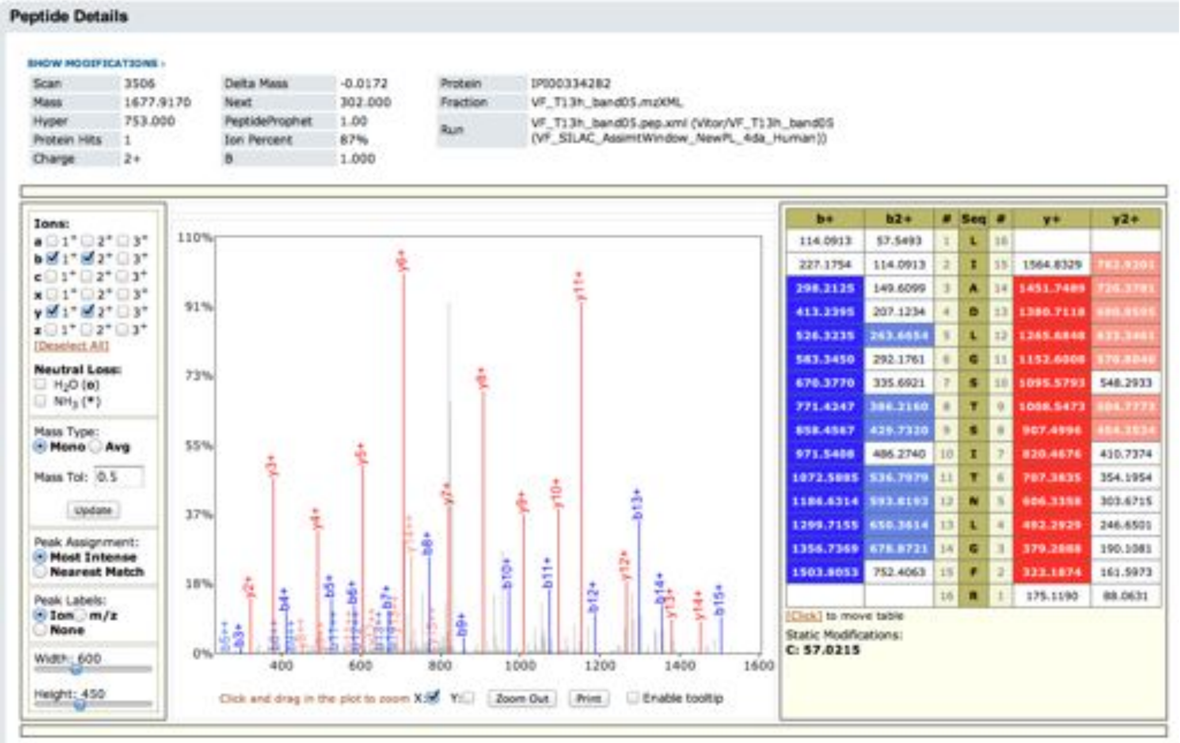
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	14		
212.1030	106.5551	2	P	13	1507.7216	754.3644
309.1557	155.0815	3	P	12	1410.6688	705.8381
366.1772	183.5922	4	G	11	1313.6161	657.3117
513.2456	257.1264	5	F	10	1256.5946	628.8009
584.2827	292.6450	6	A	9	1109.5262	555.2667
731.3511	366.1792	7	F	8	1038.4891	519.7482
830.4196	415.7134	8	V	7	891.4207	446.2140
959.4621	480.2347	9	E	6	792.3523	396.6798
1106.5306	553.7689	10	F	5	663.3097	332.1585
1235.5732	618.2902	11	E	4	516.2413	258.6243
1350.6001	675.8037	12	D	3	387.1987	194.1030
1447.6529	724.3301	13	P	2	272.1717	136.5895
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00334282	1	1	FAM3C	3506	2+	-0,0172	1,0000	R.LIADLGSTSITNLGFR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	3506	Delta Mass	-0.0172	Protein	IPI00334282
Mass	1677.9170	Next	302.000	Fraction	VF_T13h_band05.mzXML
Hyper	753.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
227.1754	114.0913	2	I	15	1564.8329	782.9201
298.2125	149.6099	3	A	14	1451.7489	726.3781
413.2395	207.1234	4	D	13	1380.7118	690.8595
526.3235	263.6654	5	L	12	1265.6848	633.3461
583.3450	292.1761	6	G	11	1152.6008	576.8040
670.3770	335.6921	7	S	10	1095.5793	548.2933
771.4247	386.2160	8	T	9	1008.5473	504.7773
858.4567	429.7320	9	S	8	907.4996	454.2534
971.5408	486.2740	10	I	7	820.4676	410.7374
1072.5885	536.7979	11	T	6	707.3835	354.1954
1186.6314	593.8193	12	N	5	606.3358	303.6715
1299.7155	650.3614	13	L	4	493.2929	246.6501
1356.7369	678.8721	14	G	3	379.2088	190.1081
1503.8053	752.4063	15	F	2	322.1874	161.5973
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8983	IPI00016342	1	1	RAB7A	3528	2+	-0,0120	0,9946	K.EAINVEQAFQTIAR.N

Peptide Details

SHOW MODIFICATIONS »

Scan	3528	Delta Mass	-0.0120	Protein	IPI00016342
Mass	1589.8280	Next	250.000	Fraction	VF_T13h_band01.mzXML
Hyper	365.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	58%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

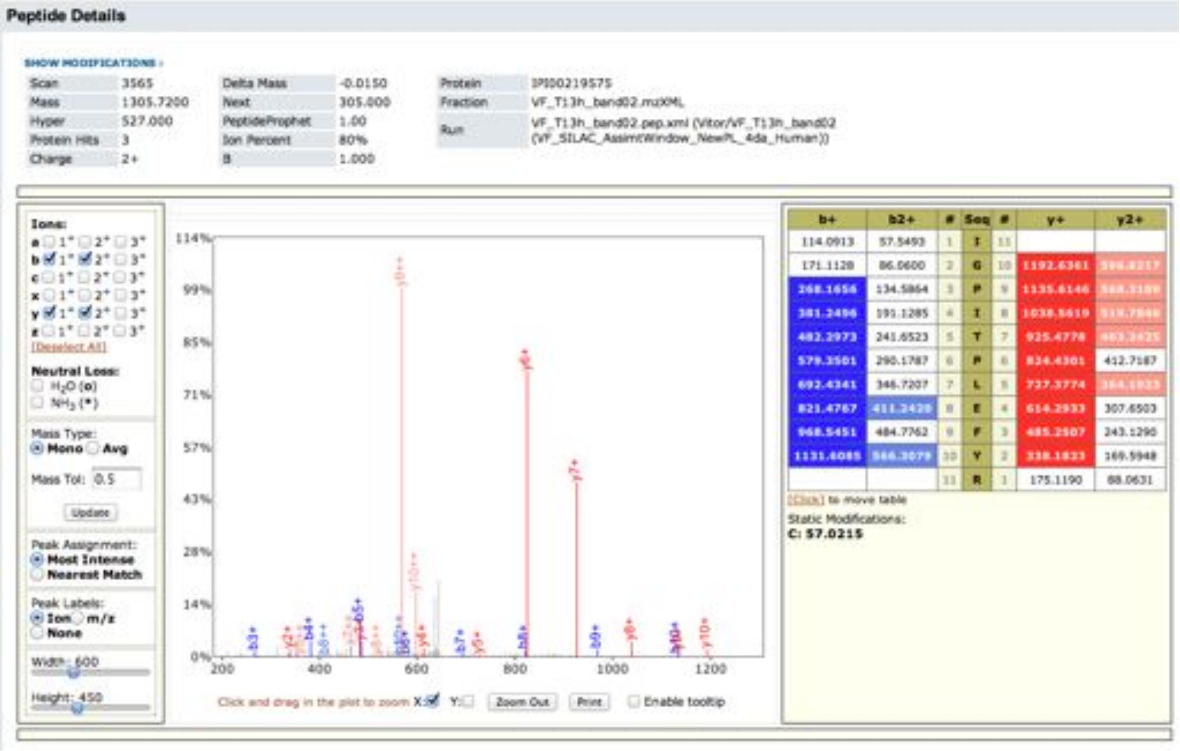
Height: 450

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	14		
201.0870	101.0471	2	A	13	1460.7856	730.8964
314.1710	157.5892	3	I	12	1389.7485	695.3779
428.2140	214.6106	4	N	11	1276.6644	638.8359
527.2824	264.1448	5	V	10	1162.6215	581.8144
656.3250	328.6661	6	E	9	1063.5531	532.2802
784.3836	392.6954	7	Q	8	934.5105	467.7589
855.4207	428.2140	8	A	7	806.4519	403.7296
1002.4891	501.7482	9	F	6	735.4148	368.2110
1130.5477	565.7775	10	Q	5	588.3464	294.6768
1231.5953	616.3013	11	T	4	460.2878	230.6475
1344.6794	672.8433	12	I	3	359.2401	180.1237
1415.7165	708.3619	13	A	2	246.1561	123.5817
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9783	IPI00794082, IPI00219575, IPI00873294	1	1	BLMH, BLMH, BLMH	3565	2+	-0,0150	0,9998	K.IGPITPLEFYR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	3565	Delta Mass	-0.0150	Protein	IPI00219575
Mass	1305.7200	Next	305.000	Fraction	VF_T13h_band02.mzXML
Hyper	527.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

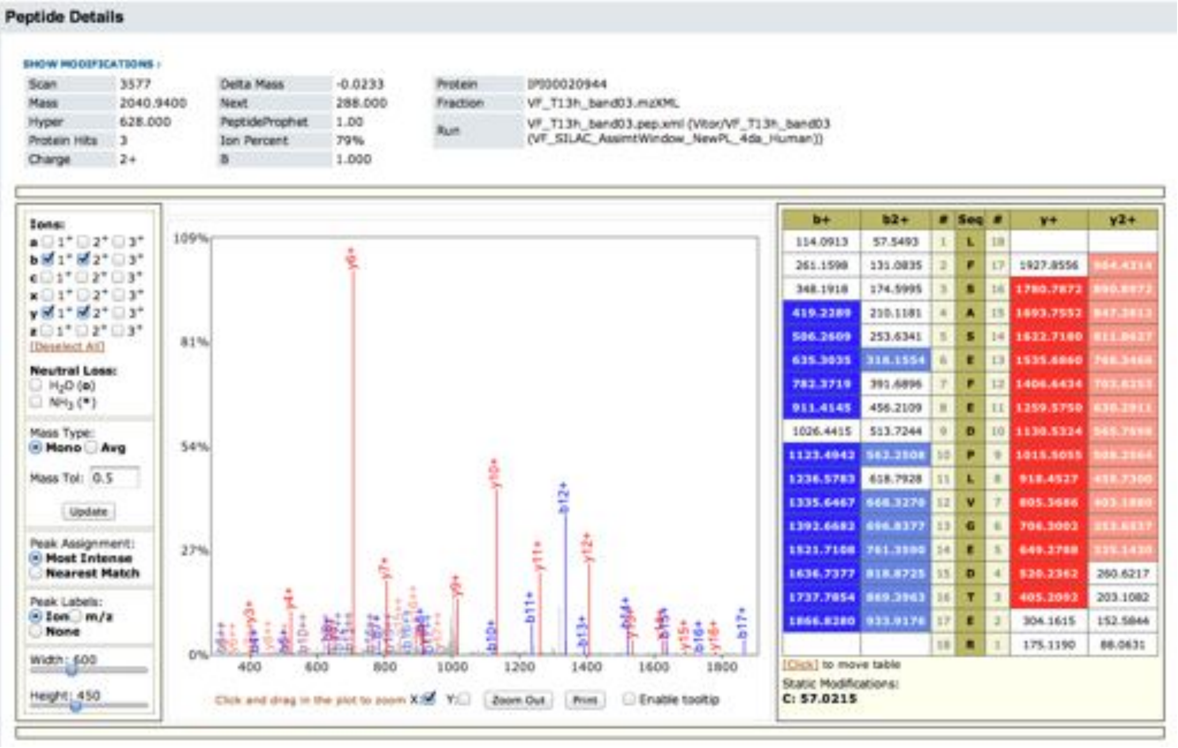
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	11		
171.1128	86.0600	2	G	10	1192.6361	596.8217
268.1656	134.5864	3	P	9	1135.6146	568.3109
381.2496	191.1285	4	I	8	1038.5619	519.7846
482.2973	241.6523	5	T	7	925.4778	463.2425
579.3501	290.1787	6	P	6	824.4301	412.7187
692.4341	346.7207	7	L	5	727.3774	364.1923
821.4767	411.2420	8	E	4	614.2933	307.6503
968.5451	484.7762	9	F	3	485.2507	243.1290
1131.6085	566.3079	10	Y	2	338.1823	169.5948
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00908715, IPI00020944, IPI00909060	1	1	-, FDFT1, -	3577	2+	-0,0233	1,0000	R.LFSASEFEDPLVGEDTER.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	3577	Delta Mass	-0.0233	Protein	IPI00020944
Mass	2040.9400	Next	288.000	Fraction	VF_T13h_band03.mzXML
Hyper	628.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

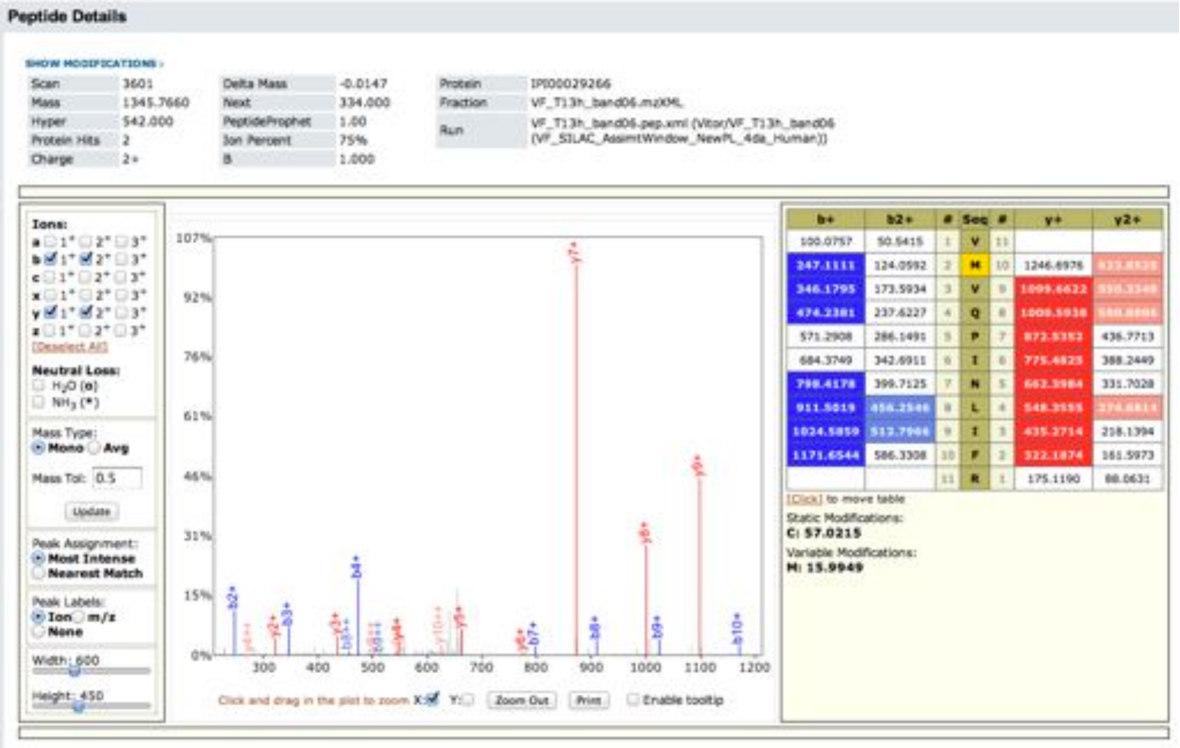
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	18		
261.1598	131.0835	2	F	17	1927.8556	964.4314
348.1918	174.5995	3	S	16	1780.7872	890.8972
419.2289	210.1181	4	A	15	1693.7552	847.3813
506.2609	253.6341	5	S	14	1622.7180	811.8627
635.3035	318.1554	6	E	13	1535.6860	768.3466
782.3719	391.6896	7	F	12	1406.6434	703.8253
911.4145	456.2109	8	E	11	1259.5750	630.2911
1026.4415	513.7244	9	D	10	1130.5324	565.7698
1123.4942	562.2508	10	P	9	1015.5055	508.2564
1236.5783	618.7928	11	L	8	918.4527	459.7300
1335.6467	668.3270	12	V	7	805.3686	403.1880
1392.6682	696.8377	13	G	6	706.3002	353.6537
1521.7108	761.3590	14	E	5	649.2788	325.1430
1636.7377	818.8725	15	D	4	520.2362	260.6217
1737.7854	869.3963	16	T	3	405.2092	203.1082
1866.8280	933.9176	17	E	2	304.1615	152.5844
		18	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9849	IPI00029266, IPI00068430	1	1	SNRPE, SNRPEL1	3601	2+	-0,0147	0,9996	K.VM"VQPINLIFR.Y



Peptide Details

SHOW MODIFICATIONS ›

Scan	3601	Delta Mass	-0.0147	Protein	IPI00029266
Mass	1345.7660	Next	334.000	Fraction	VF_T13h_band06.mzXML
Hyper	542.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐

☐ Enable tooltip

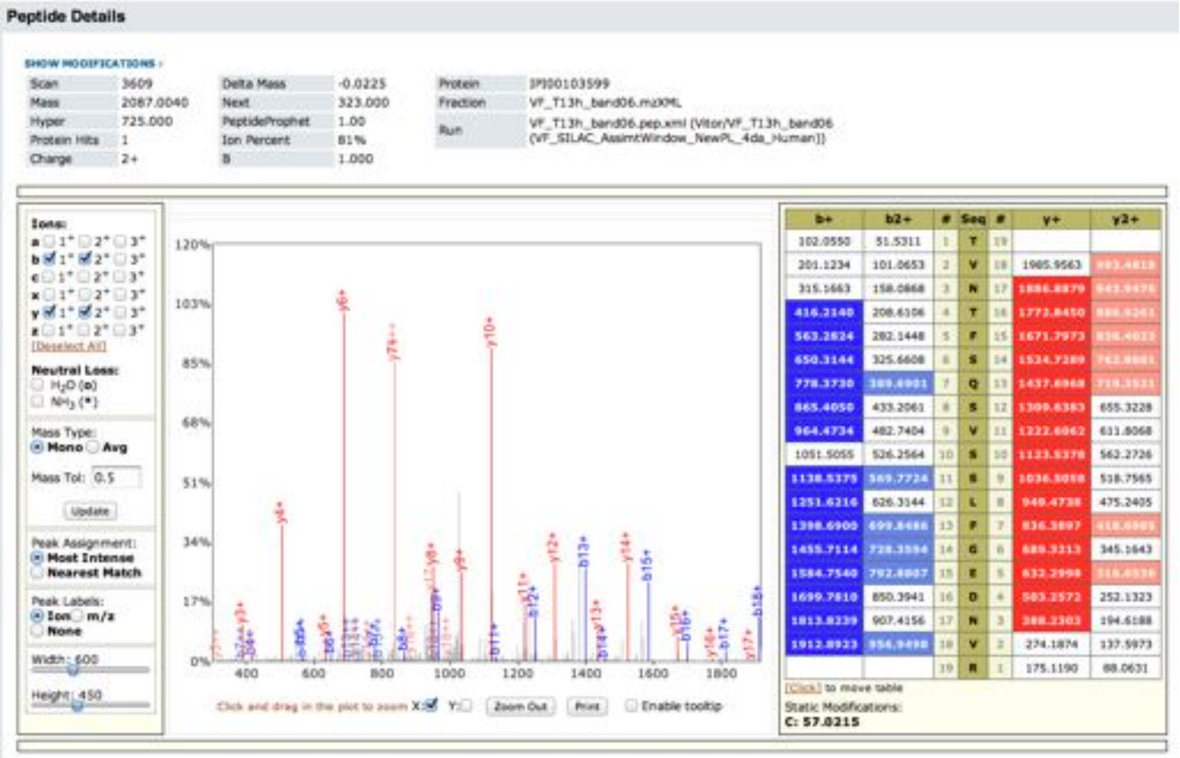
b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
247.1111	124.0592	2	M	10	1246.6976	623.8523
346.1795	173.5934	3	V	9	1099.6622	550.3348
474.2381	237.6227	4	Q	8	1000.5938	500.8006
571.2908	286.1491	5	P	7	872.5352	436.7713
684.3749	342.6911	6	I	6	775.4825	388.2449
798.4178	399.7125	7	N	5	662.3984	331.7028
911.5019	456.2546	8	L	4	548.3555	274.6814
1024.5859	512.7966	9	I	3	435.2714	218.1394
1171.6544	586.3308	10	F	2	322.1874	161.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00103599	1	1	BRI3BP	3609	2+	-0,0225	0,9999	R.TVNTFSQSVSSLFGEDNVR.A



Peptide Details

SHOW MODIFICATIONS ›

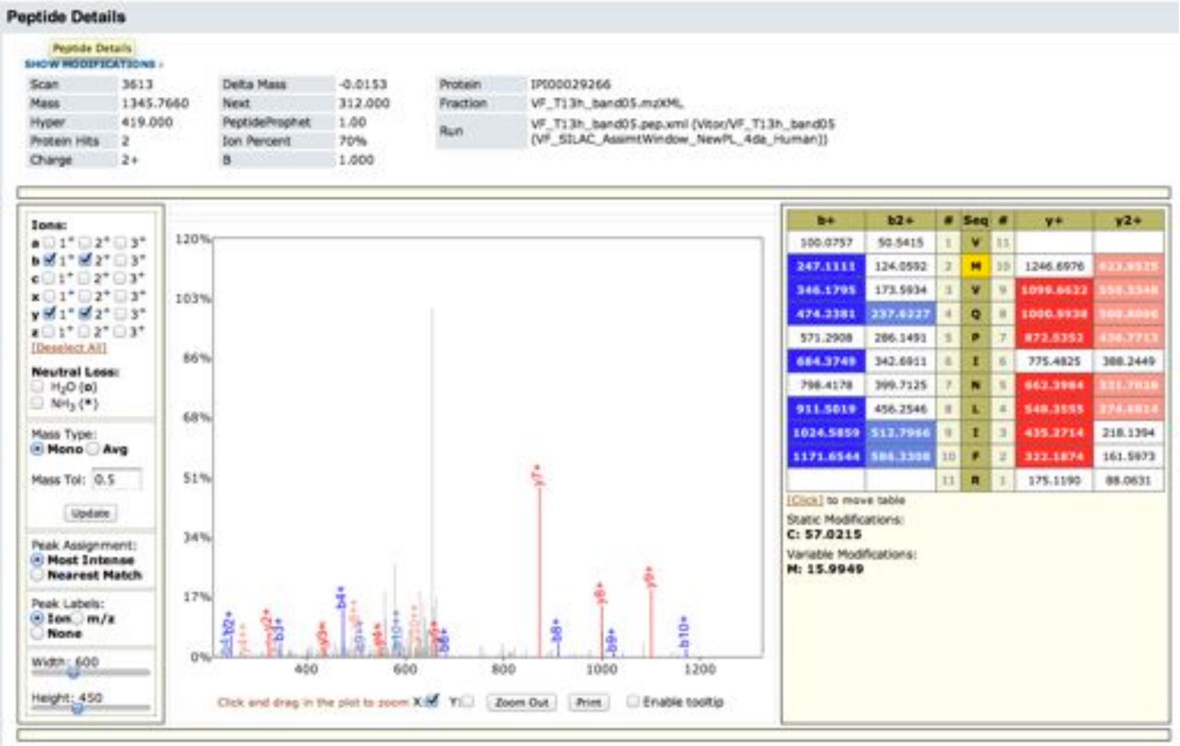
Scan	3609	Delta Mass	-0.0225	Protein	IPI00103599
Mass	2087.0040	Next	323.000	Fraction	VF_T13h_band06.mzXML
Hyper	725.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Viton/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	81%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	19		
201.1234	101.0653	2	V	18	1985.9563	993.4818
315.1663	158.0868	3	N	17	1886.8879	943.9476
416.2140	208.6106	4	T	16	1772.8450	886.9261
563.2824	282.1448	5	F	15	1671.7973	836.4023
650.3144	325.6608	6	S	14	1524.7289	762.8681
778.3730	389.6901	7	Q	13	1437.6968	719.3521
865.4050	433.2061	8	S	12	1309.6383	655.3228
964.4734	482.7404	9	V	11	1222.6062	611.8068
1051.5055	526.2564	10	S	10	1123.5378	562.2726
1138.5375	569.7724	11	S	9	1036.5058	518.7565
1251.6216	626.3144	12	L	8	949.4738	475.2405
1398.6900	699.8486	13	F	7	836.3897	418.6985
1455.7114	728.3594	14	G	6	689.3213	345.1643
1584.7540	792.8807	15	E	5	632.2998	316.6536
1699.7810	850.3941	16	D	4	503.2572	252.1323
1813.8239	907.4156	17	N	3	388.2303	194.6188
1912.8923	956.9498	18	V	2	274.1874	137.5973
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9478	IPI00029266, IPI00068430	1	1	SNRPE, SNRPEL1	3613	2+	-0,0153	0,9966	K.VM"VQPINLIFR.Y



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	3613	Delta Mass	-0.0153	Protein	IPI00029266
Mass	1345.7660	Next	312.000	Fraction	VF_T13h_band05.mzXML
Hyper	419.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4de_Human))
Protein Hits	2	Ion Percent	70%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
247.1111	124.0592	2	M	10	1246.6976	623.8525
346.1795	173.5934	3	V	9	1099.6632	550.3348
474.2381	237.6227	4	Q	8	1000.5938	500.8006
571.2908	286.1491	5	P	7	872.5352	436.7713
684.3749	342.6911	6	I	6	775.4825	388.2449
798.4178	399.7125	7	N	5	662.3984	331.7028
911.5019	456.2546	8	L	4	548.3555	274.6814
1024.5859	512.7966	9	I	3	435.2714	218.1394
1171.6544	586.3308	10	F	2	322.1874	161.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9301	IPI00791418, IPI00025252	1	1	PDIA3, PDIA3	3616	2+	-0,0134	0,9950	R.ELSDFISYLQR.E

Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	3616	Delta Mass	-0.0134	Protein	IPI00025252
Mass	1370.6950	Next	266.000	Fraction	VF_T13h_band05.mzXML
Hyper	371.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	70%		
Charge	2+	B	0.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

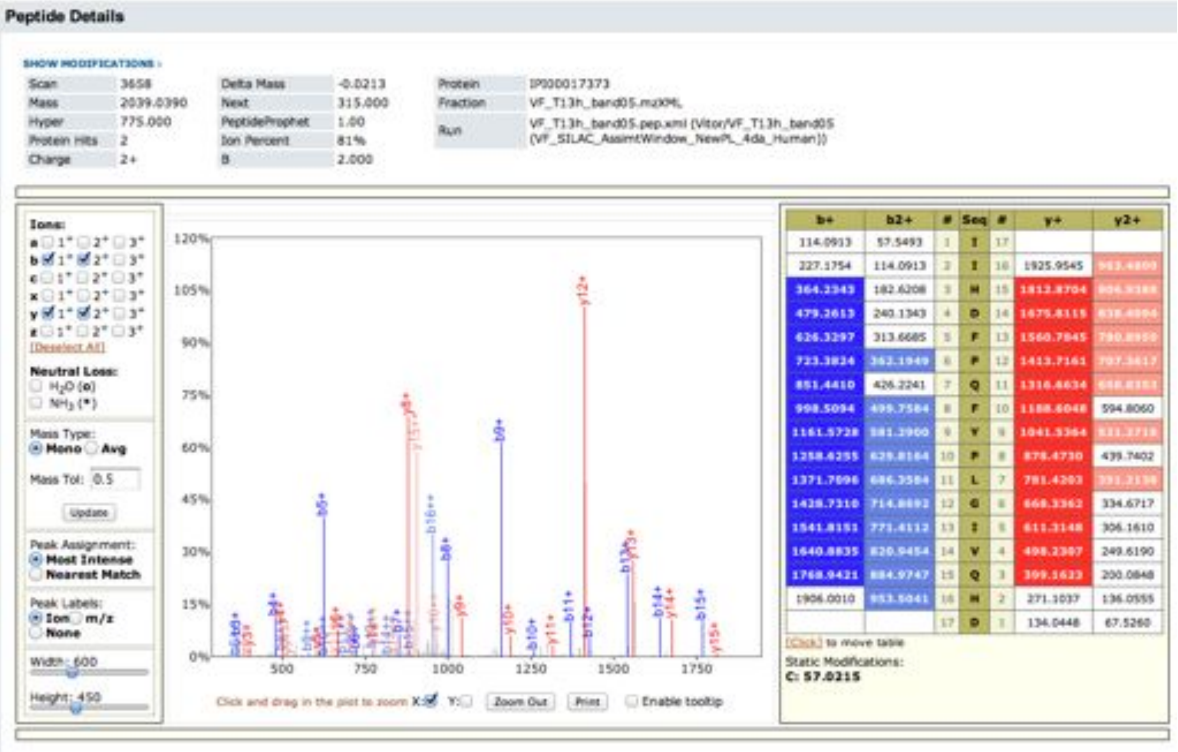
b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	11		
243.1339	122.0706	2	L	10	1241.6525	621.3299
330.1660	165.5866	3	S	9	1128.5684	564.7878
445.1929	223.1001	4	D	8	1041.5364	521.2718
592.2613	296.6343	5	F	7	926.5094	463.7584
705.3454	353.1763	6	I	6	779.4410	390.2241
792.3774	396.6923	7	S	5	666.3570	333.6821
955.4407	478.2240	8	Y	4	579.3249	290.1661
1068.5248	534.7660	9	L	3	416.2616	208.6344
1196.5834	598.7953	10	Q	2	303.1775	152.0924
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00894460, IPI00017373	1	1	RPA3, RPA3	3658	2+	-0,0213	1,0000	K.IIHDFPQFYPLGIVQHD.-



Peptide Details

SHOW MODIFICATIONS ›

Scan	3658	Delta Mass	-0.0213	Protein	IPI00017373
Mass	2039.0390	Next	315.000	Fraction	VF_T13h_band05.mzXML
Hyper	775.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	81%		
Charge	2+	B	2.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	17		
227.1754	114.0913	2	I	16	1925.9545	963.4809
364.2343	182.6208	3	H	15	1812.8704	906.9388
479.2613	240.1343	4	D	14	1675.8115	838.4094
626.3297	313.6685	5	F	13	1560.7845	780.8959
723.3824	362.1949	6	P	12	1413.7161	707.3617
851.4410	426.2241	7	Q	11	1316.6634	658.8353
998.5094	499.7584	8	F	10	1188.6048	594.8060
1161.5728	581.2900	9	Y	9	1041.5364	521.2718
1258.6255	629.8164	10	P	8	878.4730	439.7402
1371.7096	686.3584	11	L	7	781.4203	391.2138
1428.7310	714.8692	12	G	6	668.3362	334.6717
1541.8151	771.4112	13	I	5	611.3148	306.1610
1640.8835	820.9454	14	V	4	498.2307	249.6190
1768.9421	884.9747	15	Q	3	399.1623	200.0848
1906.0010	953.5041	16	H	2	271.1037	136.0555
		17	D	1	134.0448	67.5260

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9636	IPI00029665	1	1	MMAB	3685	2+	-0,0130	0,9985	R.LSDYLFTLAR.Y

Peptide Details

SHOW MODIFICATIONS ›

Scan	3685	Delta Mass	-0.0130	Protein	IPI00029665
Mass	1198.6470	Next	341.000	Fraction	VF_T13h_band04.mzXML
Hyper	473.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	94%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

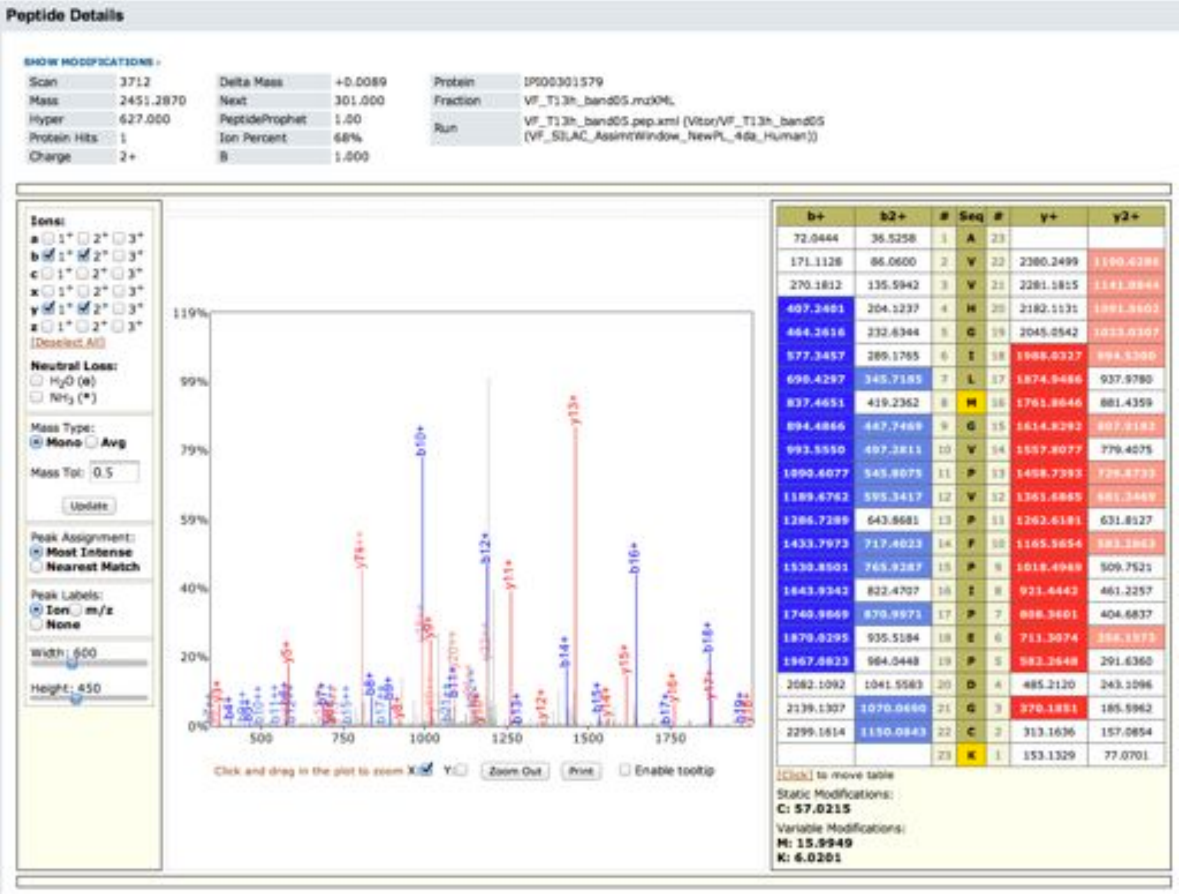
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	10		
201.1234	101.0653	2	S	9	1085.5626	543.2849
316.1503	158.5788	3	D	8	998.5306	499.7689
479.2136	240.1105	4	Y	7	883.5036	442.2554
592.2977	296.6525	5	L	6	720.4403	360.7238
739.3661	370.1867	6	F	5	607.3562	304.1817
840.4138	420.7105	7	T	4	460.2878	230.6475
953.4979	477.2526	8	L	3	359.2401	180.1237
1024.5350	512.7711	9	A	2	246.1561	123.5817
		10	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9816	IPI00301579	1	1	NPC2	3712	2+	+0,0089	0,9995	K.AVVHGILM"GVPVPFPIPEPDGCK'.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	3712	Delta Mass	+0.0089	Protein	IPI00301579
Mass	2451.2870	Next	301.000	Fraction	VF_T13h_band05.mzXML
Hyper	627.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

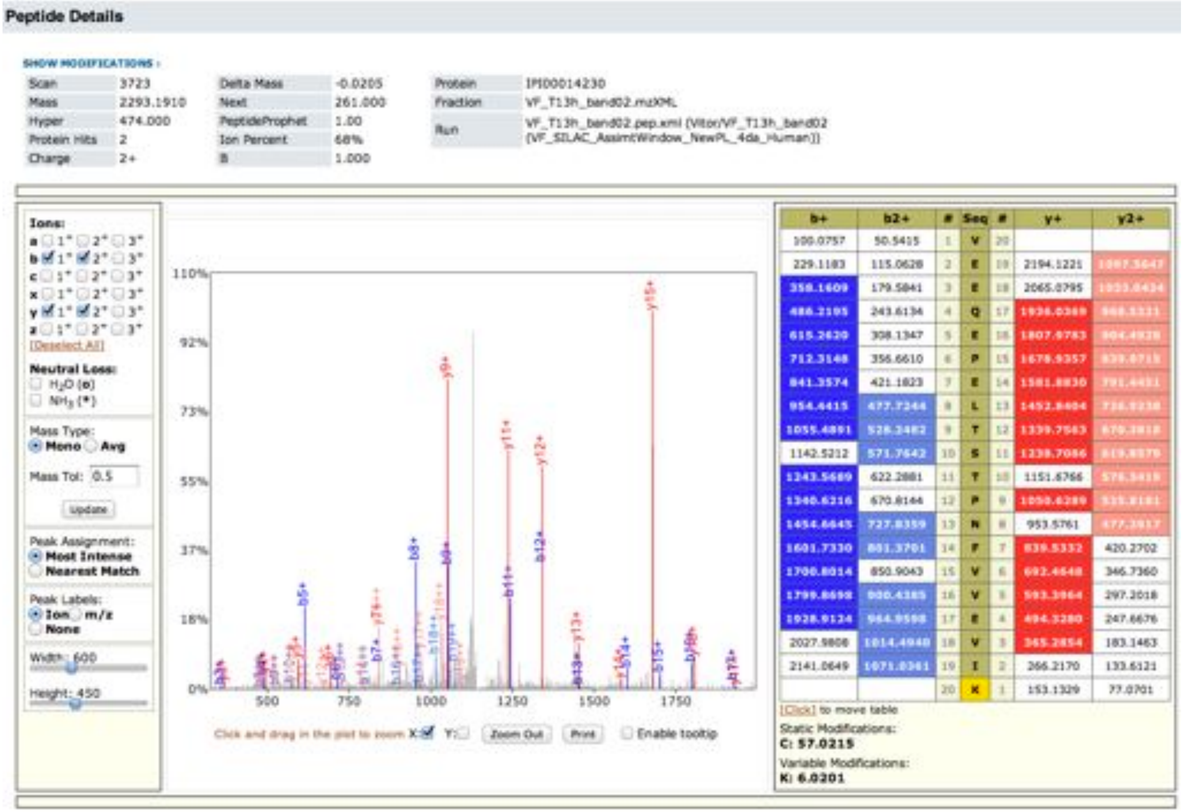
b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	23		
171.1128	86.0600	2	V	22	2380.2499	1190.6286
270.1812	135.5942	3	V	21	2281.1815	1141.0944
407.2401	204.1237	4	H	20	2182.1131	1091.5602
464.2616	232.6344	5	G	19	2045.0542	1023.0307
577.3457	289.1765	6	I	18	1988.0327	994.5200
690.4297	345.7185	7	L	17	1874.9486	937.9780
837.4651	419.2362	8	M	16	1761.8646	881.4359
894.4866	447.7469	9	G	15	1614.8292	807.9182
993.5550	497.2811	10	V	14	1557.8077	779.4075
1090.6077	545.8075	11	P	13	1458.7393	729.8733
1189.6762	595.3417	12	V	12	1361.6865	681.3469
1286.7289	643.8681	13	P	11	1262.6181	631.8127
1433.7973	717.4023	14	F	10	1165.5654	583.2863
1530.8501	765.9287	15	P	9	1018.4969	509.7521
1643.9342	822.4707	16	I	8	921.4442	461.2257
1740.9869	870.9971	17	P	7	808.3601	404.6837
1870.0295	935.5184	18	E	6	711.3074	356.1573
1967.0823	984.0448	19	P	5	582.2648	291.6360
2082.1092	1041.5583	20	D	4	485.2120	243.1096
2139.1307	1070.0690	21	G	3	370.1851	185.5962
2299.1614	1150.0843	22	C	2	313.1636	157.0854
		23	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9783	IPI00796075, IPI00014230	1	1	C1QBP, C1QBP	3723	2+	-0,0205	0,9998	K.VEEQEPELTSTPNFVVEVIK'.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	3723	Delta Mass	-0.0205	Protein	IPI00014230
Mass	2293.1910	Next	261.000	Fraction	VF_T13h_band02.mzXML
Hyper	474.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

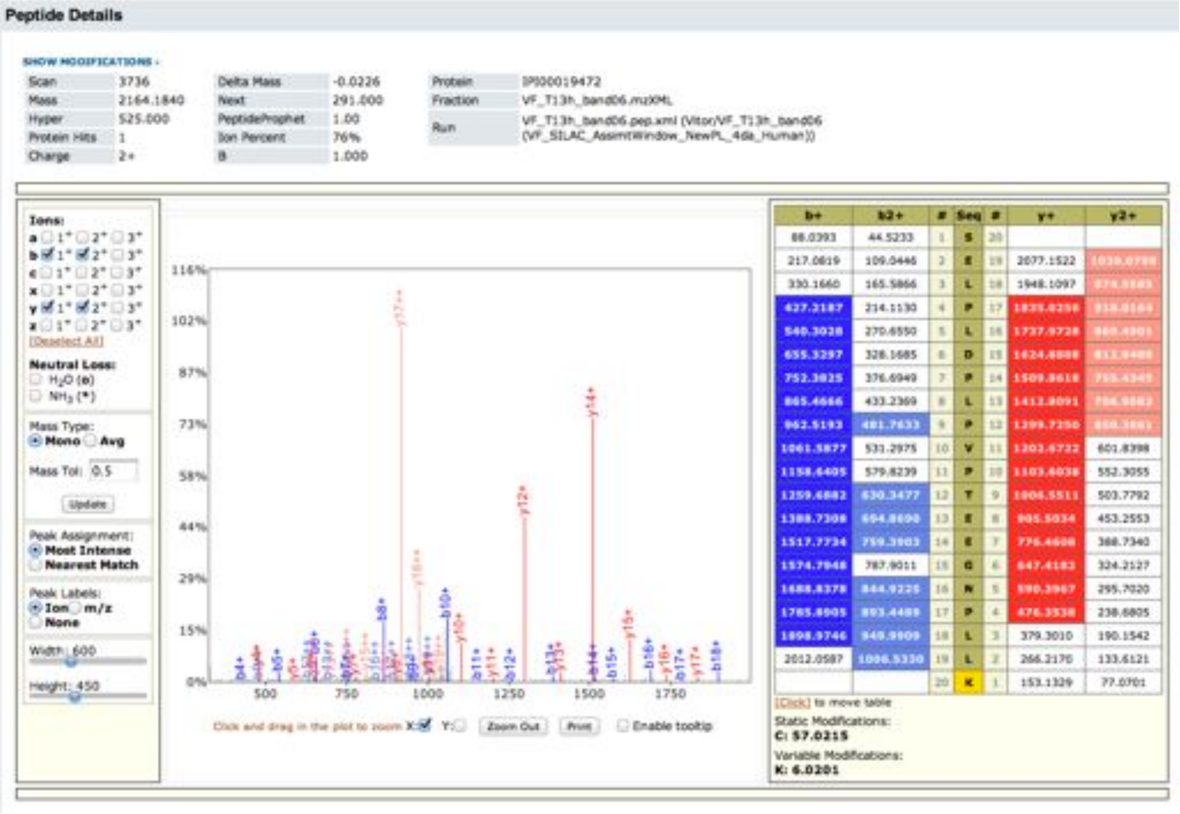
b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	20		
229.1183	115.0628	2	E	19	2194.1221	1097.5647
358.1609	179.5841	3	E	18	2065.0795	1033.0434
486.2195	243.6134	4	Q	17	1936.0369	968.5221
615.2620	308.1347	5	E	16	1807.9783	904.4928
712.3148	356.6610	6	P	15	1678.9357	839.9715
841.3574	421.1823	7	E	14	1581.8830	791.4451
954.4415	477.7244	8	L	13	1452.8404	726.9238
1055.4891	528.2482	9	T	12	1339.7563	670.3818
1142.5212	571.7642	10	S	11	1238.7086	619.8579
1243.5689	622.2881	11	T	10	1151.6766	576.3419
1340.6216	670.8144	12	P	9	1050.6289	525.8181
1454.6645	727.8359	13	N	8	953.5761	477.2917
1601.7330	801.3701	14	F	7	839.5332	420.2702
1700.8014	850.9043	15	V	6	692.4648	346.7360
1799.8698	900.4385	16	V	5	593.3964	297.2018
1928.9124	964.9598	17	E	4	494.3280	247.6676
2027.9808	1014.4940	18	V	3	365.2854	183.1463
2141.0649	1071.0361	19	I	2	266.2170	133.6121
		20	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9859	IPI00019472	1	1	SLC1A5	3736	2+	-0,0226	0,9997	K.SELPLDPLPVPTEEGNPLLK'.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	3736	Delta Mass	-0.0226	Protein	IPI00019472
Mass	2164.1840	Next	291.000	Fraction	VF_T13h_band06.mzXML
Hyper	525.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	76%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	20		
217.0819	109.0446	2	E	19	2077.1522	1039.0798
330.1660	165.5866	3	L	18	1948.1097	974.5583
427.2187	214.1130	4	P	17	1835.0256	918.0164
540.3028	270.6550	5	L	16	1737.9728	869.4901
655.3297	328.1685	6	D	15	1624.8888	812.9480
752.3825	376.6949	7	P	14	1509.8618	755.4345
865.4666	433.2369	8	L	13	1412.8091	706.9082
962.5193	481.7633	9	P	12	1299.7250	650.3661
1061.5877	531.2975	10	V	11	1202.6722	601.8398
1158.6405	579.8239	11	P	10	1103.6038	552.3055
1259.6882	630.3477	12	T	9	1006.5511	503.7792
1388.7308	694.8690	13	E	8	905.5034	453.2553
1517.7734	759.3903	14	E	7	776.4608	388.7340
1574.7948	787.9011	15	G	6	647.4182	324.2127
1688.8378	844.9225	16	N	5	590.3967	295.7020
1785.8905	893.4489	17	P	4	476.3538	238.6805
1898.9746	949.9909	18	L	3	379.3010	190.1542
2012.0587	1006.5330	19	L	2	266.2170	133.6121
		20	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9865	IPI00328978	1	1	CTSW	3741	2+	-0,0213	0,9999	K.VAWIQDFIM"LQNNEHR.I

Peptide Details

SHOW MODIFICATIONS ›

Scan	3741	Delta Mass	-0.0213	Protein	IPI00328978
Mass	2029.9910	Next	254.000	Fraction	VF_T13h_band05.mzXML
Hyper	489.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	16		
171.1128	86.0600	2	A	15	1930.9228	965.9651
357.1921	179.0997	3	W	14	1859.8857	930.4465
470.2762	235.6417	4	I	13	1673.8064	837.4068
598.3348	299.6710	5	Q	12	1560.7223	780.8648
713.3617	357.1845	6	D	11	1432.6638	716.8355
860.4301	430.7187	7	F	10	1317.6368	659.3220
973.5142	487.2607	8	I	9	1170.5684	585.7878
1120.5496	560.7784	9	M	8	1057.4843	529.2458
1233.6336	617.3205	10	L	7	910.4490	455.7281
1361.6922	681.3497	11	Q	6	797.3649	399.1861
1475.7351	738.3712	12	N	5	669.3063	335.1568
1589.7781	795.3927	13	N	4	555.2634	278.1353
1718.8207	859.9140	14	E	3	441.2205	221.1139
1855.8796	928.4434	15	H	2	312.1779	156.5926
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9849	IPI00719814, IPI00456013, IPI00219291, IPI00873259, IPI00220300, IPI00171925	1	1	ATP5J2, ATP5J2, ATP5J2, ATP5J2, ATP5J2, PTCD1	3745	2+	-0,0161	0,9996	R.DFSPSGIFGAFQR.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	3745	Delta Mass	-0.0161	Protein	IPI00171925
Mass	1428.6910	Next	282.000	Fraction	VF_T13h_band06.mzXML
Hyper	493.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	88%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	13		
263.1026	132.0550	2	F	12	1313.6637	657.3355
350.1347	175.5710	3	S	11	1166.5953	583.8013
447.1874	224.0974	4	P	10	1079.5633	540.2853
534.2195	267.6134	5	S	9	982.5105	491.7589
591.2409	296.1241	6	G	8	895.4785	448.2429
704.3250	352.6661	7	I	7	838.4570	419.7321
851.3934	426.2003	8	F	6	725.3729	363.1901
908.4149	454.7111	9	G	5	578.3045	289.6559
979.4520	490.2296	10	A	4	521.2831	261.1452
1126.5204	563.7638	11	F	3	450.2459	225.6266
1254.5790	627.7931	12	Q	2	303.1775	152.0924
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

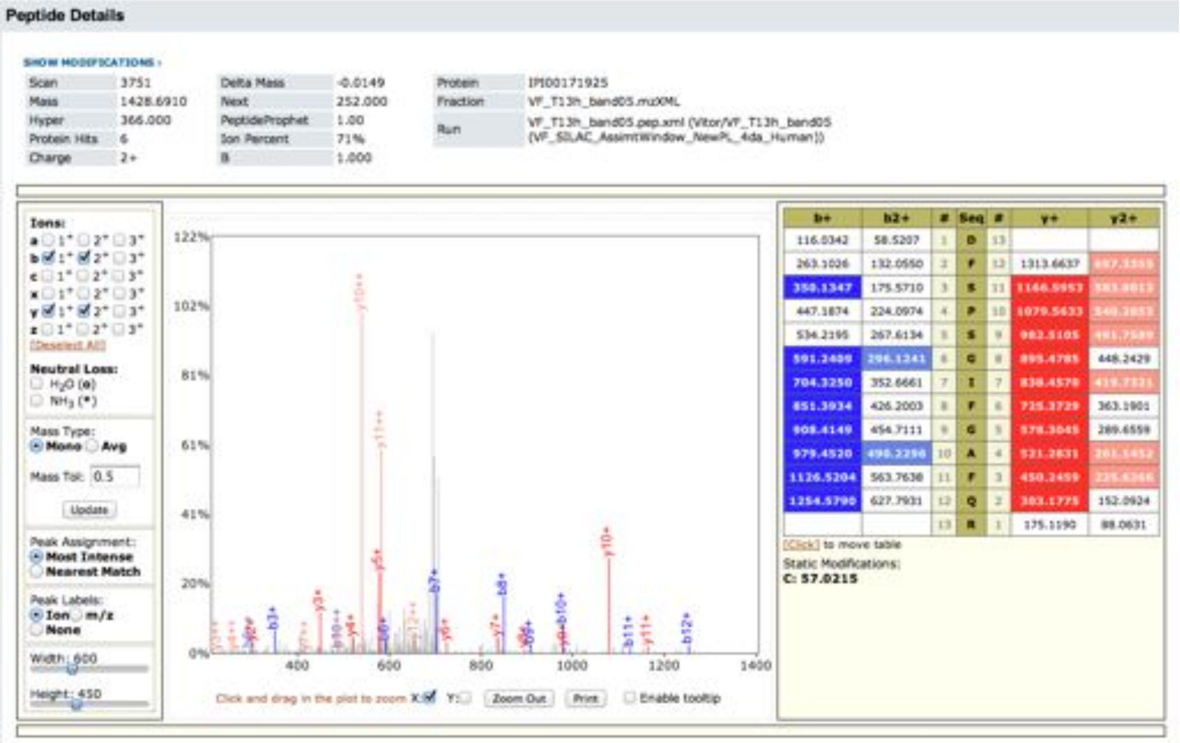
Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9456	IPI00719814, IPI00456013, IPI00219291, IPI00873259, IPI00220300, IPI00171925	1	1	ATP5J2, ATP5J2, ATP5J2, ATP5J2, ATP5J2, PTCD1	3751	2+	-0,0149	0,9964	R.DFSPSGIFGAFQR.G



Peptide Details

SHOW MODIFICATIONS ›

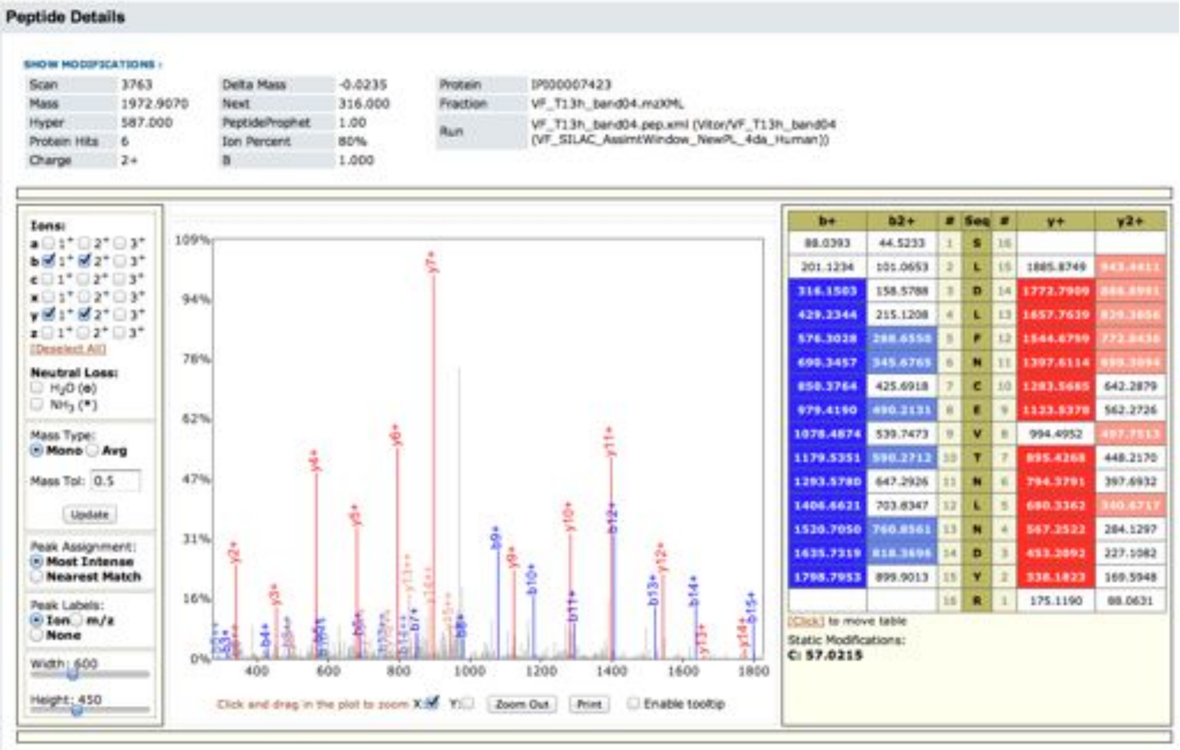
Scan	3751	Delta Mass	-0.0149	Protein	IPI00171925
Mass	1428.6910	Next	252.000	Fraction	VF_T13h_band05.mzXML
Hyper	366.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	71%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	13		
263.1026	132.0550	2	F	12	1313.6637	657.3355
350.1347	175.5710	3	S	11	1166.5953	583.8012
447.1874	224.0974	4	P	10	1079.5633	540.2853
534.2195	267.6134	5	S	9	982.5105	491.7589
591.2409	296.1241	6	G	8	895.4785	448.2429
704.3250	352.6661	7	I	7	838.4570	419.7321
851.3934	426.2003	8	F	6	725.3729	363.1901
908.4149	454.7111	9	G	5	578.3045	289.6559
979.4520	490.2296	10	A	4	521.2831	261.1452
1126.5204	563.7638	11	F	3	450.2459	225.6266
1254.5790	627.7931	12	Q	2	303.1775	152.0924
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9837	IPI00647001, IPI00759824, IPI00449263, IPI00760940, IPI00025849, IPI00007423	1	1	ANP32B, ANP32B, ANP32A, LOC723972, ANP32A, ANP32B	3763	2+	-0,0235	0,9999	K.SLDLFNCEVTNLNDYR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	3763	Delta Mass	-0.0235	Protein	IPI00007423
Mass	1972.9070	Next	316.000	Fraction	VF_T13h_band04.mzXML
Hyper	587.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	16		
201.1234	101.0653	2	L	15	1885.8749	943.4411
316.1503	158.5788	3	D	14	1772.7909	886.8991
429.2344	215.1208	4	L	13	1657.7639	829.3856
576.3028	288.6550	5	F	12	1544.6799	772.8436
690.3457	345.6765	6	N	11	1397.6114	699.3094
850.3764	425.6918	7	C	10	1283.5685	642.2879
979.4190	490.2131	8	E	9	1123.5378	562.2726
1078.4874	539.7473	9	V	8	994.4952	497.7513
1179.5351	590.2712	10	T	7	895.4268	448.2170
1293.5780	647.2926	11	N	6	794.3791	397.6932
1406.6621	703.8347	12	L	5	680.3362	340.6717
1520.7050	760.8561	13	N	4	567.2522	284.1297
1635.7319	818.3696	14	D	3	453.2092	227.1082
1798.7953	899.9013	15	Y	2	338.1823	169.5948
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9695	IPI00791194, IPI00789063, IPI00789999, IPI00789792, IPI00220503	1	1	DCTN2, DCTN2, DCTN2, DCTN2, DCTN2	3774	2+	-0,0154	0,9984	K.VSALDLAVLDQVEAR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	3774	Delta Mass	-0.0154	Protein	IPI00220503
Mass	1598.8750	Next	246.000	Fraction	VF_T13h_band03.mzXML
Hyper	389.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	15		
187.1077	94.0575	2	S	14	1499.8064	750.4068
258.1448	129.5761	3	A	13	1412.7744	706.8908
371.2289	186.1181	4	L	12	1341.7373	671.3733
486.2558	243.6316	5	D	11	1228.6532	614.8302
599.3399	300.1736	6	L	10	1113.6262	557.3168
670.3770	335.6921	7	A	9	1000.5422	500.7747
769.4454	385.2264	8	V	8	929.5051	465.2562
882.5295	441.7684	9	L	7	830.4367	415.7220
997.5564	499.2819	10	D	6	717.3526	359.1799
1125.6150	563.3111	11	Q	5	602.3257	301.6665
1224.6834	612.8454	12	V	4	474.2671	237.6372
1353.7260	677.3666	13	E	3	375.1987	188.1030
1424.7631	712.8852	14	A	2	246.1561	123.5817
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9837	IPI00334282	1	1	FAM3C	3777	2+	-0,0241	0,9999	R.LIADLGSTSITNLGFR.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	3777	Delta Mass	-0.0241	Protein	IPI00334282
Mass	1677.9170	Next	281.000	Fraction	VF_T13h_band04.mzXML
Hyper	594.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	87%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	16		
227.1754	114.0913	2	I	15	1564.8329	782.9201
298.2125	149.6099	3	A	14	1451.7489	726.3781
413.2395	207.1234	4	D	13	1380.7118	690.8595
526.3235	263.6654	5	L	12	1265.6848	633.3481
583.3450	292.1761	6	G	11	1152.6008	576.8040
670.3770	335.6921	7	S	10	1095.5793	548.2933
771.4247	386.2160	8	T	9	1008.5473	504.7773
858.4567	429.7320	9	S	8	907.4996	454.2534
971.5408	486.2740	10	I	7	820.4676	410.7374
1072.5885	536.7979	11	T	6	707.3835	354.1954
1186.6314	593.8193	12	N	5	606.3358	303.6715
1299.7155	650.3614	13	L	4	492.2929	246.6501
1356.7369	678.8721	14	G	3	379.2088	190.1081
1503.8053	752.4063	15	F	2	322.1874	161.5973
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9776	IPI00790135, IPI00394737, IPI00873898, IPI00163644	1	1	OSBPL8, OSBPL8, OSBPL8, DKFZp686C0249	3784	2+	-0,0152	0,9997	K.VVLPTFILEPR.S

Peptide Details

SHOW MODIFICATIONS ›

Scan	3784	Delta Mass	-0.0152	Protein	IPI00163644
Mass	1283.7720	Next	301.000	Fraction	VF_T13h_band01.mzXML
Hyper	511.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	4	Ion Percent	65%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	11		
199.1441	100.0757	2	V	10	1184.7038	592.8555
312.2282	156.6177	3	L	9	1085.6354	543.3213
409.2809	205.1441	4	P	8	972.5513	486.7793
510.3286	255.6679	5	T	7	875.4985	438.2529
657.3970	329.2022	6	F	6	774.4509	387.7291
770.4811	385.7442	7	I	5	627.3834	314.1949
883.5652	442.2862	8	L	4	514.2984	257.6528
1012.6077	506.8075	9	E	3	401.2143	201.1108
1109.6605	555.3339	10	P	2	272.1717	136.5895
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9056	IPI00025257	1	1	SEMA7A	3785	2+	-0,0156	0,9951	R.LQDVFLLPDPSGQWR.D

Peptide Details

Scan	3785	Delta Mass	-0.0156	Protein	IPI00025257
Mass	1770.9170	Next	327.000	Fraction	VF_T13h_band01.mzXML
Hyper	433.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	75%		
Charge	2+	B	1.000		

Ions: b ☑ 1⁺ ☑ 2⁺; y ☑ 1⁺ ☑ 2⁺

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
242.1499	121.5786	2	Q	14	1657.8333	829.4203
357.1769	179.0921	3	D	13	1529.7747	765.3910
456.2453	228.6263	4	V	12	1414.7478	707.8775
603.3137	302.1605	5	F	11	1315.6793	658.3433
716.3978	358.7025	6	L	10	1168.6109	584.8091
829.4818	415.2445	7	L	9	1055.5269	528.2671
926.5346	463.7709	8	P	8	942.4428	471.7250
1041.5615	521.2844	9	D	7	845.3900	423.1987
1138.6143	569.8108	10	P	6	730.3631	365.6852
1225.6463	613.3268	11	S	5	633.3103	317.1588
1282.6678	641.8375	12	G	4	546.2783	273.6428
1410.7264	705.8668	13	Q	3	489.2568	245.1321
1596.8057	798.9065	14	W	2	361.1983	181.1028
		15	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9793	IPI00789521, IPI00788784, IPI00008167	1	1	ATP1B3, ATP1B3, ATP1B3	3812	2+	-0,0083	0,9996	K.LFIYNPTTGEFLGR.T

Peptide Details

SHOW MODIFICATIONS ›

Scan	3812	Delta Mass	-0.0083	Protein	IPI00008167
Mass	1627.8479	Next	371.000	Fraction	VF_T13h_band04.mzXML
Hyper	554.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

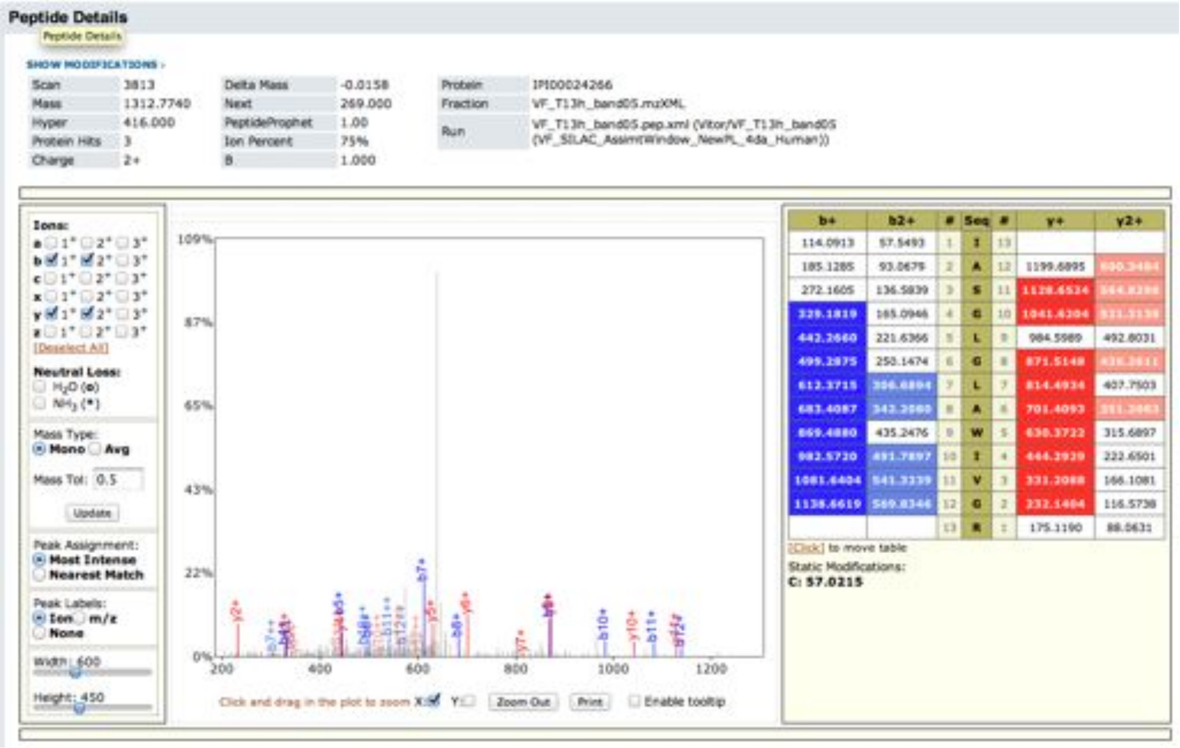
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	14		
261.1598	131.0835	2	F	13	1514.7638	757.8855
374.2438	187.6255	3	I	12	1367.6954	684.3513
537.3071	269.1572	4	Y	11	1254.6113	627.8093
651.3501	326.1787	5	N	10	1091.5480	546.2776
748.4028	374.7051	6	P	9	977.5051	489.2562
849.4505	425.2289	7	T	8	880.4523	440.7298
950.4982	475.7527	8	T	7	779.4046	390.2060
1007.5197	504.2635	9	G	6	678.3570	339.6821
1136.5623	568.7848	10	E	5	621.3355	311.1714
1283.6307	642.3190	11	F	4	492.2929	246.6501
1396.7147	698.8610	12	L	3	345.2245	173.1159
1453.7362	727.3717	13	G	2	232.1404	116.5738
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9756	IPI00647044, IPI00024266, IPI00639812	1	1	MGST3, MGST3, MGST3	3813	2+	-0,0158	0,9990	R.IASGLGLAWIVGR.V



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	3813	Delta Mass	-0.0158	Protein	IPI00024266
Mass	1312.7740	Next	269.000	Fraction	VF_T13h_band05.mzXML
Hyper	416.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

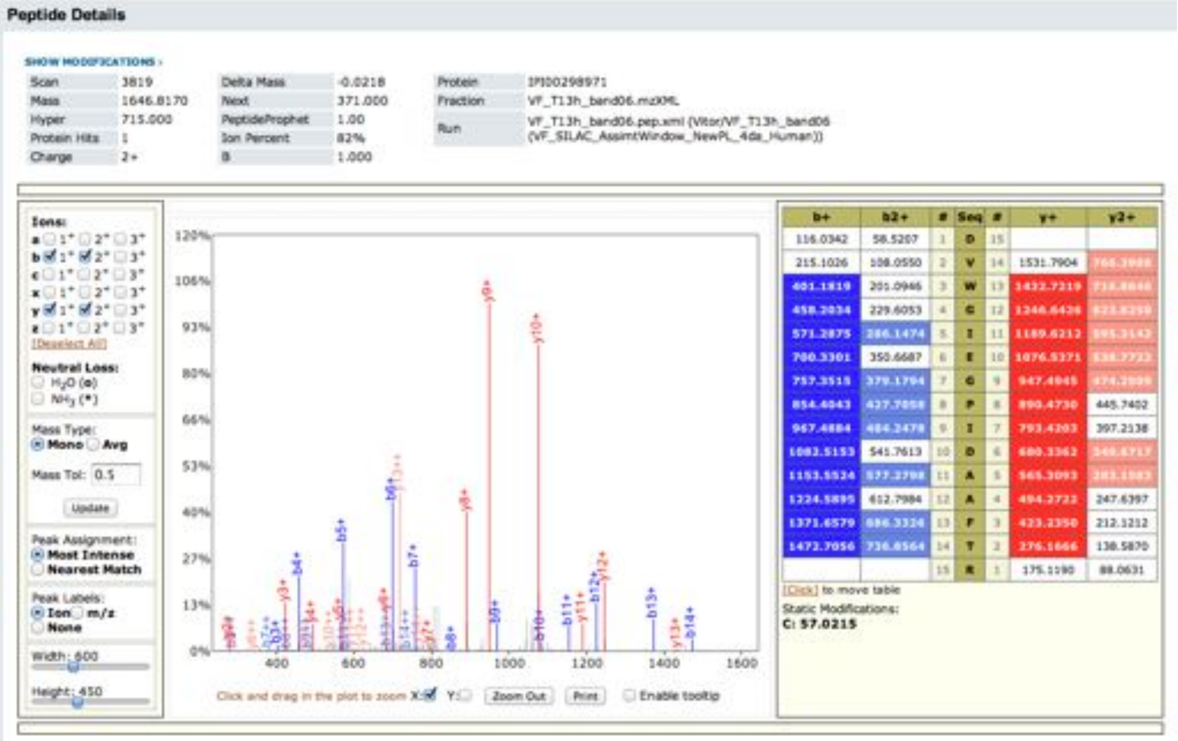
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	13		
185.1285	93.0679	2	A	12	1199.6895	600.3484
272.1605	136.5839	3	S	11	1128.6534	564.8298
329.1819	165.0946	4	G	10	1041.6204	521.3138
442.2660	221.6366	5	L	9	984.5989	492.8031
499.2875	250.1474	6	G	8	871.5148	436.2611
612.3715	306.6894	7	L	7	814.4934	407.7503
683.4087	342.2080	8	A	6	701.4093	351.2083
869.4880	435.2476	9	W	5	630.3722	315.6897
982.5720	491.7897	10	I	4	444.2929	222.6501
1081.6404	541.3339	11	V	3	331.2088	166.1081
1138.6619	569.8346	12	G	2	232.1404	116.5738
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00298971	1	1	VTN	3819	2+	-0,0218	0,9999	R.DVWGIEGPIDAAFTR.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	3819	Delta Mass	-0.0218	Protein	IPI00298971
Mass	1646.8170	Next	371.000	Fraction	VF_T13h_band06.mzXML
Hyper	715.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	15		
215.1026	108.0550	2	V	14	1531.7904	766.3988
401.1819	201.0946	3	W	13	1432.7219	716.8646
458.2034	229.6053	4	G	12	1246.6426	623.8250
571.2875	286.1474	5	I	11	1189.6212	595.3142
700.3301	350.6687	6	E	10	1076.5371	538.7722
757.3515	379.1794	7	G	9	947.4945	474.2509
854.4043	427.7058	8	P	8	890.4730	445.7402
967.4884	484.2478	9	I	7	793.4203	397.2138
1082.5153	541.7613	10	D	6	680.3362	340.6717
1153.5524	577.2798	11	A	5	565.3093	283.1583
1224.5895	612.7984	12	A	4	494.2722	247.6397
1371.6579	686.3324	13	F	3	423.2350	212.1212
1472.7056	736.8564	14	T	2	276.1666	138.5870
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9827	IPI00238081, IPI00053288, IPI00171127	1	1	UBAP2, UBAP2, UBAP2	3821	2+	-0,0173	1,0000	R.LPVDYYGIPFAAPTALASR.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	3821	Delta Mass	-0.0173	Protein	IPI00053288
Mass	2022.0690	Next	299.000	Fraction	VF_T13h_band01.mzXML
Hyper	728.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

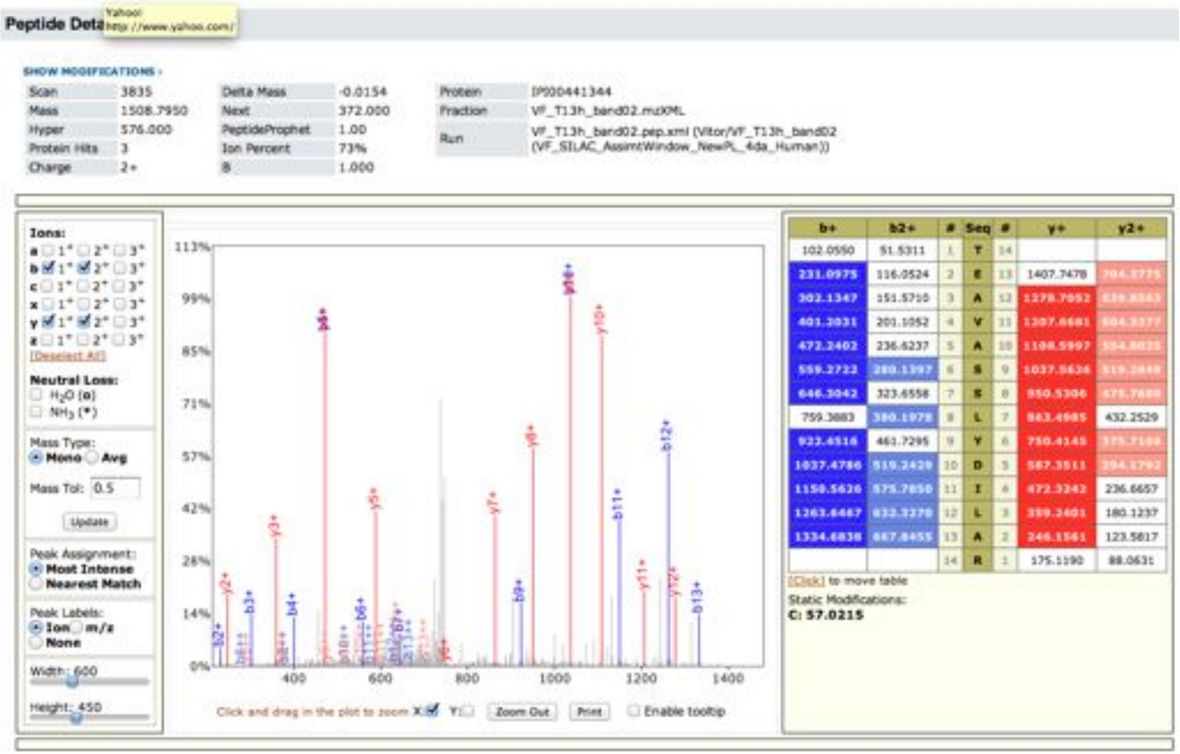
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	19		
211.1441	106.0757	2	P	18	1908.9854	954.9964
310.2125	155.6099	3	V	17	1811.9327	906.4700
425.2395	213.1234	4	D	16	1712.8642	856.9358
588.3028	294.6550	5	Y	15	1597.8373	799.4223
751.3661	376.1867	6	Y	14	1434.7740	717.8906
808.3876	404.6974	7	G	13	1271.7106	636.3590
921.4716	461.2395	8	I	12	1214.6892	607.8482
1018.5244	509.7658	9	P	11	1101.6051	551.3062
1165.5928	583.3000	10	F	10	1004.5524	502.7798
1236.6299	618.8186	11	A	9	857.4839	429.2456
1307.6671	654.3372	12	A	8	786.4468	393.7271
1404.7198	702.8635	13	P	7	715.4097	358.2085
1505.7675	753.3874	14	T	6	618.3570	309.6821
1576.8046	788.9059	15	A	5	517.3093	259.1583
1689.8887	845.4480	16	L	4	446.2722	223.6397
1760.9258	880.9665	17	A	3	333.1881	167.0977
1847.9578	924.4825	18	S	2	262.1510	131.5791
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9783	IPI00441550, IPI00797646, IPI00441344	1	1	GLB1, GLB1, GLB1	3835	2+	-0,0154	0,9998	K.TEAVASSLYDILAR.G



Peptide Deta

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SHOW MODIFICATIONS ›

Scan	3835	Delta Mass	-0.0154	Protein	IPI00441344
Mass	1508.7950	Next	372.000	Fraction	VF_T13h_band02.mzXML
Hyper	576.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	73%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X ☑ Y ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
231.0975	116.0524	2	E	13	1407.7478	704.3775
302.1347	151.5710	3	A	12	1278.7052	639.8563
401.2031	201.1052	4	V	11	1207.6681	604.3377
472.2402	236.6237	5	A	10	1108.5997	554.8035
559.2722	280.1397	6	S	9	1037.5626	519.2849
646.3042	323.6558	7	S	8	950.5306	475.7689
759.3883	380.1978	8	L	7	863.4985	432.2529
922.4516	461.7295	9	Y	6	750.4145	375.7109
1037.4786	519.2429	10	D	5	587.3511	294.1792
1150.5626	575.7850	11	I	4	472.3242	236.6657
1263.6467	632.3270	12	L	3	359.2401	180.1237
1334.6838	667.8455	13	A	2	246.1561	123.5817
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9691	IPI00644989, IPI00299571	1	1	P5, PDIA6	3842	2+	-0,0163	0,9981	R.TGEAIVDAALSALR.Q

Peptide Details

SHOW MODIFICATIONS ›

Scan	3842	Delta Mass	-0.0163	Protein	IPI00299571
Mass	1386.7590	Next	306.000	Fraction	VF_T13h_band06.mzXML
Hyper	452.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	58%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
159.0764	80.0418	2	G	13	1285.7110	643.3592
288.1190	144.5631	3	E	12	1228.6896	614.8484
359.1561	180.0817	4	A	11	1099.6470	550.3271
472.2402	236.6237	5	I	10	1028.6099	514.8086
571.3086	286.1579	6	V	9	915.5258	458.2665
686.3355	343.6714	7	D	8	816.4574	408.7323
757.3727	379.1900	8	A	7	701.4304	351.2189
828.4098	414.7085	9	A	6	630.3933	315.7003
941.4938	471.2506	10	L	5	559.3562	280.1817
1028.5259	514.7666	11	S	4	446.2722	223.6397
1099.5630	550.2851	12	A	3	359.2401	180.1237
1212.6470	606.8272	13	L	2	288.2030	144.6051
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9870	IPI00761107, IPI00026111	1	1	TMCO1, TMCO1	3845	2+	-0,0179	0,9998	K.LPFTPLSYIQGLSHR.N

Peptide Details

SHOW MODIFICATIONS ›

Scan	3845	Delta Mass	-0.0179	Protein	IPI00026111
Mass	1728.9430	Next	288.000	Fraction	VF_T13h_band06.mzXML
Hyper	569.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	89%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

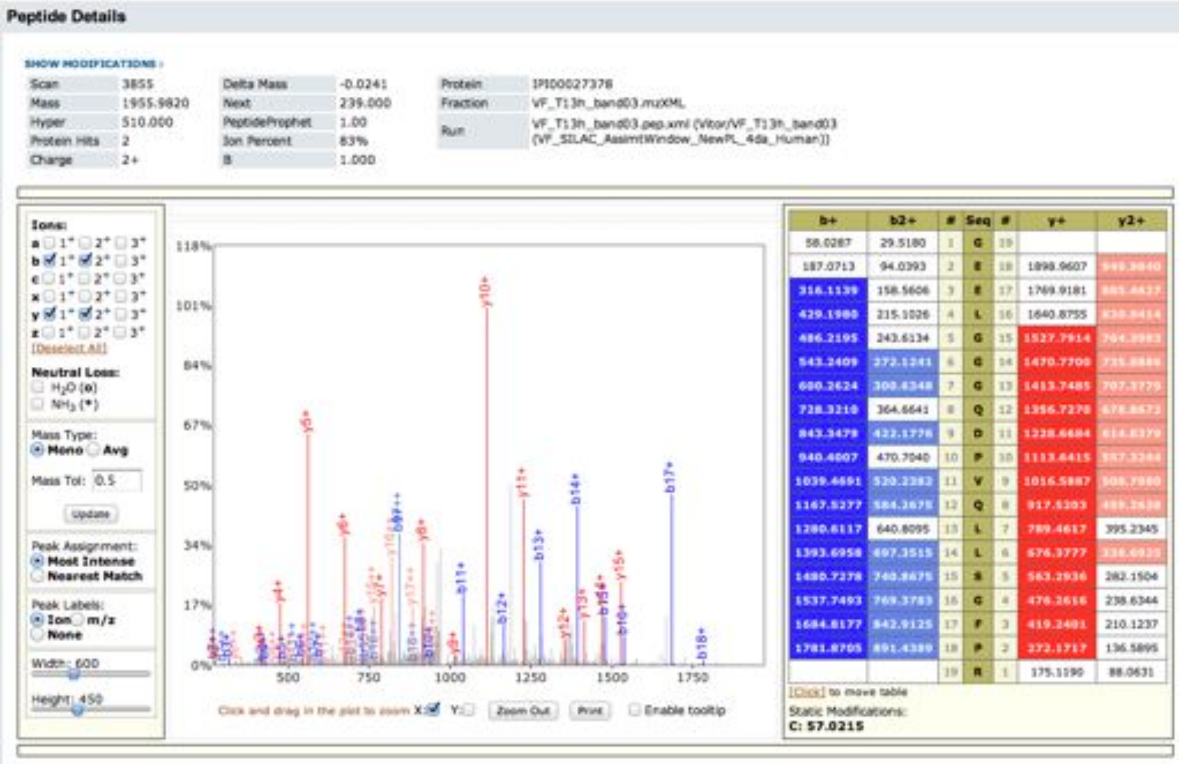
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
211.1441	106.0757	2	P	14	1615.8591	808.4333
358.2125	179.6099	3	F	13	1518.8063	759.9068
459.2602	230.1337	4	T	12	1371.7379	686.3726
556.3130	278.6601	5	P	11	1270.6902	635.8488
669.3970	335.2022	6	L	10	1173.6375	587.3224
756.4291	378.7182	7	S	9	1060.5534	530.7803
919.4924	460.2498	8	Y	8	973.5214	487.2643
1032.5764	516.7919	9	I	7	810.4581	405.7327
1160.6350	580.8211	10	Q	6	697.3740	349.1906
1217.6565	609.3319	11	G	5	569.3154	285.1613
1330.7406	665.8739	12	L	4	512.2940	256.6506
1417.7726	709.3899	13	S	3	399.2099	200.1086
1554.8315	777.9194	14	H	2	312.1779	156.5926
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00027378, IPI00396563	1	1	SAKS1, LOC51035	3855	2+	-0,0241	0,9999	R.GEELGGGQDPVQLLSGFPR.R



Peptide Details

SHOW MODIFICATIONS »

Scan	3855	Delta Mass	-0.0241	Protein	IPI00027378
Mass	1955.9820	Next	239.000	Fraction	VF_T13h_band03.mzXML
Hyper	510.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	19		
187.0713	94.0393	2	E	18	1898.9607	949.9840
316.1139	158.5606	3	E	17	1769.9181	885.4627
429.1980	215.1026	4	L	16	1640.8755	820.9414
486.2195	243.6134	5	G	15	1527.7914	764.3993
543.2409	272.1241	6	G	14	1470.7700	735.8886
600.2624	300.6348	7	G	13	1413.7485	707.3779
728.3210	364.6641	8	Q	12	1356.7270	678.8672
843.3479	422.1776	9	D	11	1228.6684	614.8379
940.4007	470.7040	10	P	10	1113.6415	557.3244
1039.4691	520.2382	11	V	9	1016.5887	508.7980
1167.5277	584.2675	12	Q	8	917.5203	459.2638
1280.6117	640.8095	13	L	7	789.4617	395.2345
1393.6958	697.3515	14	L	6	676.3777	338.6925
1480.7278	740.8675	15	S	5	563.2936	282.1504
1537.7493	769.3783	16	G	4	476.2616	238.6344
1684.8177	842.9125	17	F	3	419.2401	210.1237
1781.8705	891.4389	18	P	2	272.1717	136.5895
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9594	IPI00218853, IPI00029159	1	1	MRE11A, MRE11A	3863	2+	-0,0153	0,9986	R.GNDTFVTLDEILR.L

Peptide Details

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Peptide Details

Scan	3863	Delta Mass	-0.0153	Protein	IPI00029159
Mass	1492.7640	Next	330.000	Fraction	VF_T13h_band01.mzXML
Hyper	474.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	13		
172.0717	86.5395	2	N	12	1435.7427	718.3750
287.0986	144.0529	3	D	11	1321.6998	661.3535
388.1463	194.5768	4	T	10	1206.6729	603.8401
535.2147	268.1110	5	F	9	1105.6252	553.3162
634.2831	317.6452	6	V	8	958.5568	479.7820
735.3308	368.1690	7	T	7	859.4884	430.2478
848.4149	424.7111	8	L	6	758.4407	379.7240
963.4418	482.2245	9	D	5	645.3566	323.1819
1092.4844	546.7458	10	E	4	530.3297	265.6685
1205.5685	603.2879	11	I	3	401.2871	201.1472
1318.6525	659.8299	12	L	2	288.2030	144.6051
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9434	IPI00644131, IPI00012989	1	1	MAN2B1, MAN2B1	3870	2+	-0,0131	0,9976	K.ELVDYFLNVATAQGR.Y

Scan	3870	Delta Mass	-0.0131	Protein	IPI00012989
Mass	1695.8700	Next	260.000	Fraction	VF_T13h_band01.mzXML
Hyper	395.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg
Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

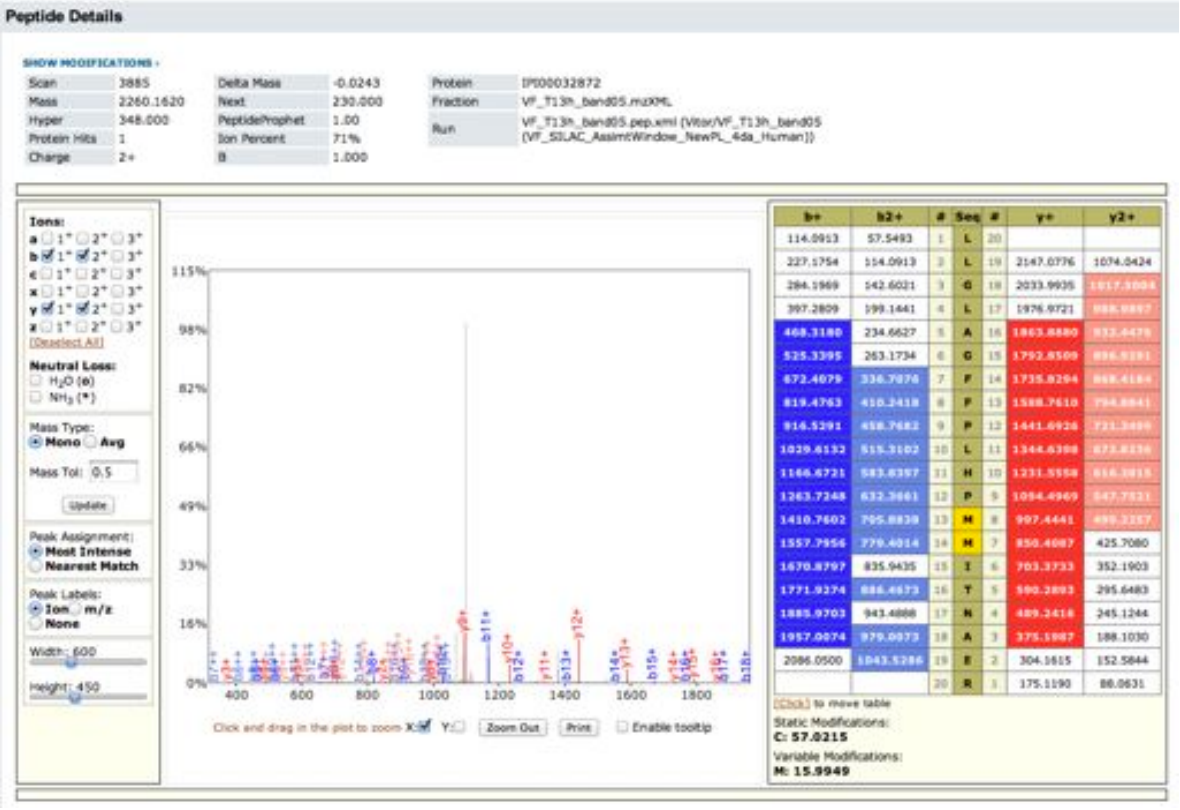
Width: 600
Height: 450

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	15		
243.1339	122.0706	2	L	14	1566.8275	783.9174
342.2023	171.6048	3	V	13	1453.7434	727.3753
457.2293	229.1183	4	D	12	1354.6750	677.8411
620.2936	310.6499	5	Y	11	1239.6480	620.3277
767.3610	384.1842	6	F	10	1076.5847	538.7960
880.4451	440.7262	7	L	9	929.5163	465.2618
994.4880	497.7477	8	N	8	816.4322	408.7198
1093.5564	547.2819	9	V	7	702.3893	351.6983
1164.5936	582.8004	10	A	6	603.3209	302.1641
1265.6412	633.3243	11	T	5	532.2838	266.6455
1336.6783	668.8428	12	A	4	431.2361	216.1217
1464.7369	732.8721	13	Q	3	360.1990	180.6031
1521.7584	761.3828	14	G	2	232.1404	116.5738
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9478	IPI00032872	1	1	MRPS16	3885	2+	-0,0243	0,9966	K.LLGLAGFFPLHPM"M"ITNAER.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	3885	Delta Mass	-0.0243	Protein	IPI00032872
Mass	2260.1620	Next	230.000	Fraction	VF_T13h_band05.mzXML
Hyper	348.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	71%		
Charge	2+	B	1.000		

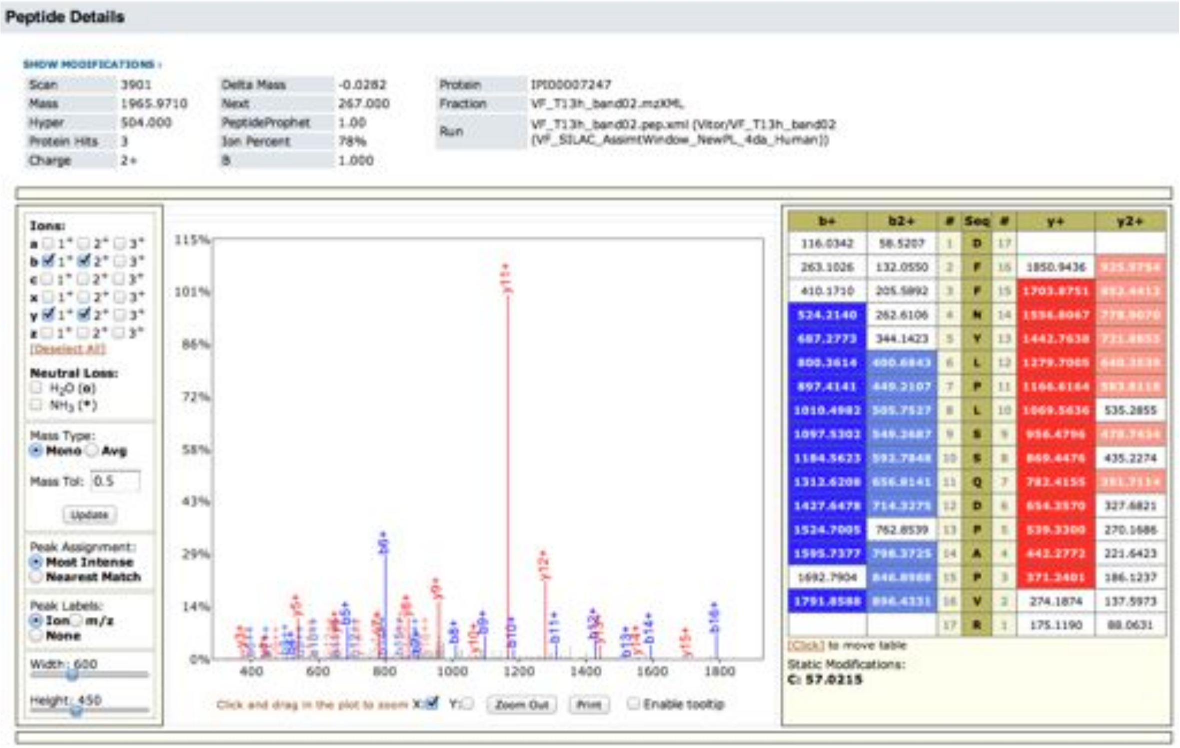
b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	20		
227.1754	114.0913	2	L	19	2147.0776	1074.0424
284.1969	142.6021	3	G	18	2033.9935	1017.5004
397.2809	199.1441	4	L	17	1976.9721	988.9897
468.3180	234.6627	5	A	16	1863.8880	932.4476
525.3395	263.1734	6	G	15	1792.8509	896.9291
672.4079	336.7076	7	F	14	1735.8294	868.4184
819.4763	410.2418	8	F	13	1588.7610	794.8841
916.5291	458.7682	9	P	12	1441.6926	721.3499
1029.6132	515.3102	10	L	11	1344.6398	672.8236
1166.6721	583.8397	11	H	10	1231.5558	616.2815
1263.7248	632.3661	12	P	9	1094.4969	547.7521
1410.7602	705.8838	13	M	8	997.4441	499.2257
1557.7956	779.4014	14	M	7	850.4087	425.7080
1670.8797	835.9435	15	I	6	703.3733	352.1903
1771.9274	886.4673	16	T	5	590.2893	295.6483
1885.9703	943.4888	17	N	4	489.2416	245.1244
1957.0074	979.0073	18	A	3	375.1987	188.1030
2086.0500	1043.5286	19	E	2	304.1615	152.5844
		20	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00387103, IPI00792361, IPI00007247	1	1	PCCB, PCCB, PCCB	3901	2+	-0,0282	0,9999	R.DFFNYLPLSSQDPAPVR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	3901	Delta Mass	-0.0282	Protein	IPI00007247
Mass	1965.9710	Next	267.000	Fraction	VF_T13h_band02.mzXML
Hyper	504.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

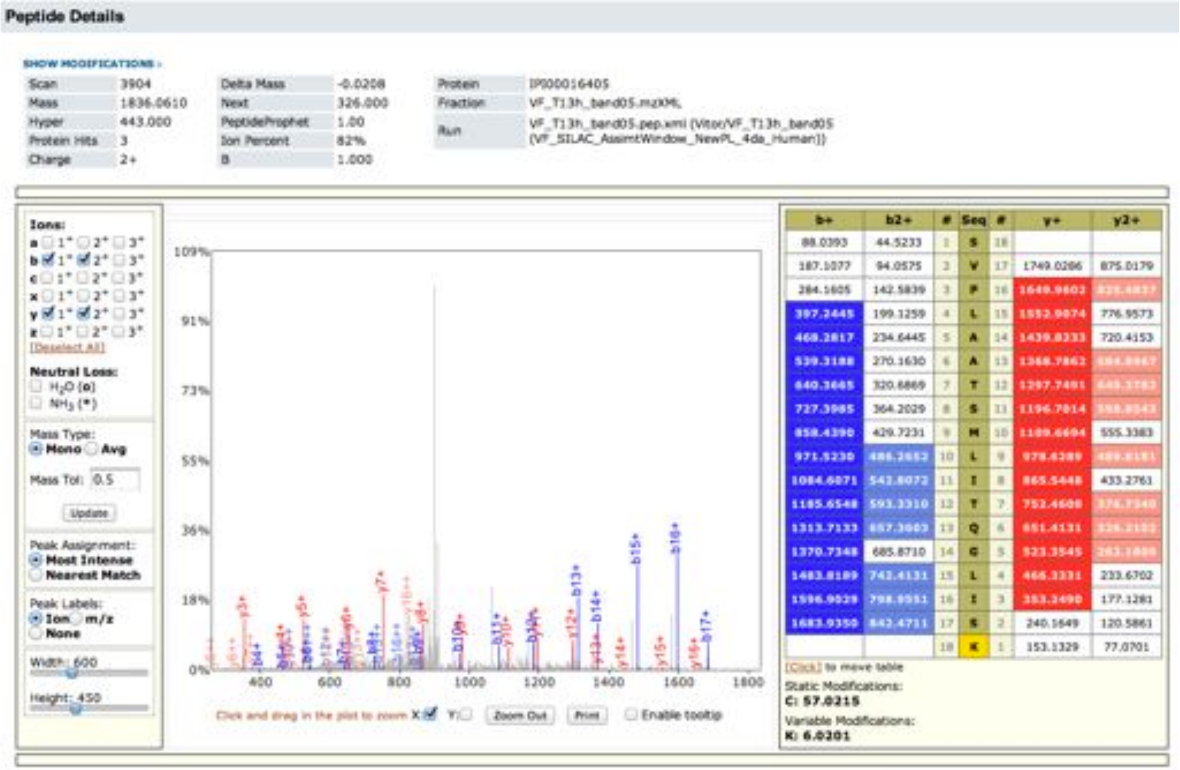
Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	17		
263.1026	132.0550	2	F	16	1850.9436	925.9754
410.1710	205.5892	3	F	15	1703.8751	852.4413
524.2140	262.6106	4	N	14	1556.8067	778.9070
687.2773	344.1423	5	Y	13	1442.7638	721.8855
800.3614	400.6843	6	L	12	1279.7005	640.3538
897.4141	449.2107	7	P	11	1166.6164	583.8118
1010.4982	505.7527	8	L	10	1069.5636	535.2855
1097.5302	549.2687	9	S	9	956.4796	478.7434
1184.5623	592.7848	10	S	8	869.4476	435.2274
1312.6208	656.8141	11	Q	7	782.4155	391.7114
1427.6478	714.3275	12	D	6	654.3570	327.6821
1524.7005	762.8539	13	P	5	539.3300	270.1686
1595.7377	798.3725	14	A	4	442.2772	221.6423
1692.7904	846.8988	15	P	3	371.2401	186.1237
1791.8588	896.4331	16	V	2	274.1874	137.5973
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9627	IPI00816371, IPI00816523, IPI00016405	1	1	OCIAD1, OCIAD1, OCIAD1	3904	2+	-0,0208	0,9979	R.SVPLAATSMLITQGLISK'.G



Peptide Details

SHOW MODIFICATIONS »

Scan	3904	Delta Mass	-0.0208	Protein	IPI00016405
Mass	1836.0610	Next	326.000	Fraction	VF_T13h_band05.mzXML
Hyper	443.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

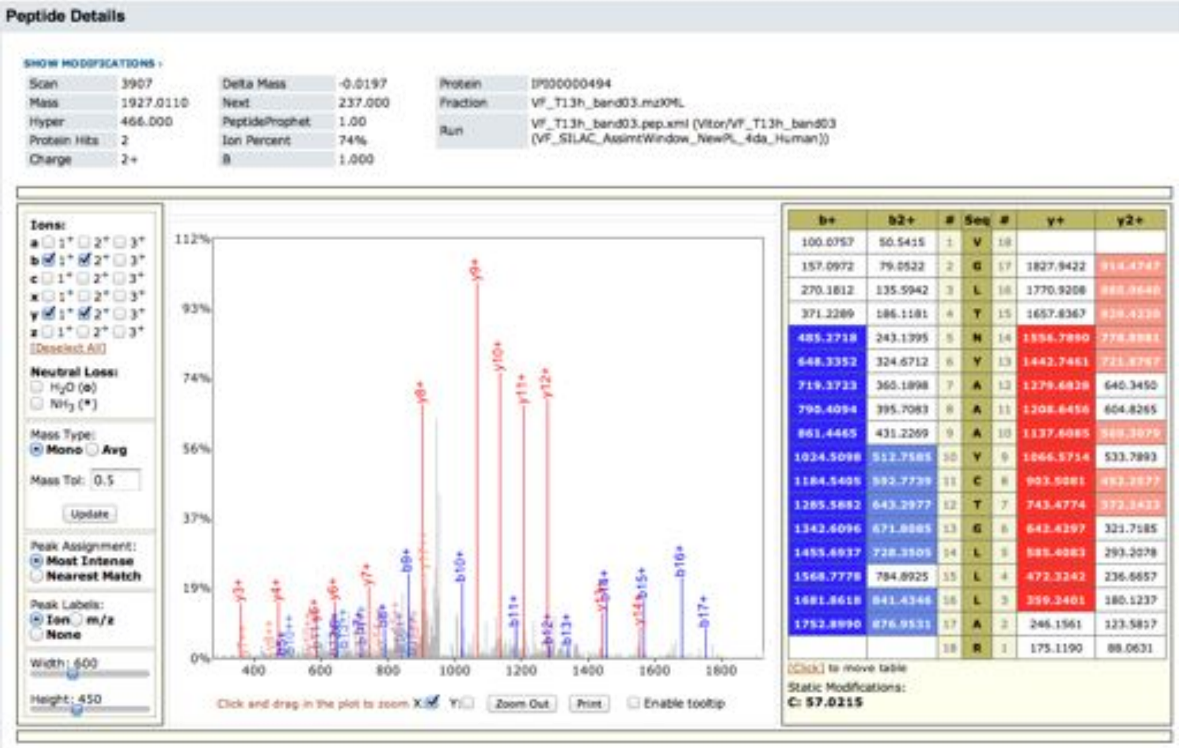
b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	18		
187.1077	94.0575	2	V	17	1749.0286	875.0179
284.1605	142.5839	3	P	16	1649.9602	825.4837
397.2445	199.1259	4	L	15	1552.9074	776.9573
468.2817	234.6445	5	A	14	1439.8233	720.4153
539.3188	270.1630	6	A	13	1368.7862	684.8967
640.3665	320.6869	7	T	12	1297.7491	649.3782
727.3985	364.2029	8	S	11	1196.7014	598.8543
858.4390	429.7231	9	M	10	1109.6694	555.3383
971.5230	486.2652	10	L	9	978.6289	489.8181
1084.6071	542.8072	11	I	8	865.5448	433.2761
1185.6548	593.3310	12	T	7	752.4608	376.7340
1313.7133	657.3603	13	Q	6	651.4131	326.2102
1370.7348	685.8710	14	G	5	523.3545	262.1809
1483.8189	742.4131	15	L	4	466.3331	233.6702
1596.9029	798.9551	16	I	3	353.2490	177.1281
1683.9350	842.4711	17	S	2	240.1649	120.5861
		18	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9857	IPI00640037, IPI00000494	1	1	RPL5, RPL5	3907	2+	-0,0197	0,9998	K.VGLTNYAAAYCTGLLLAR.R



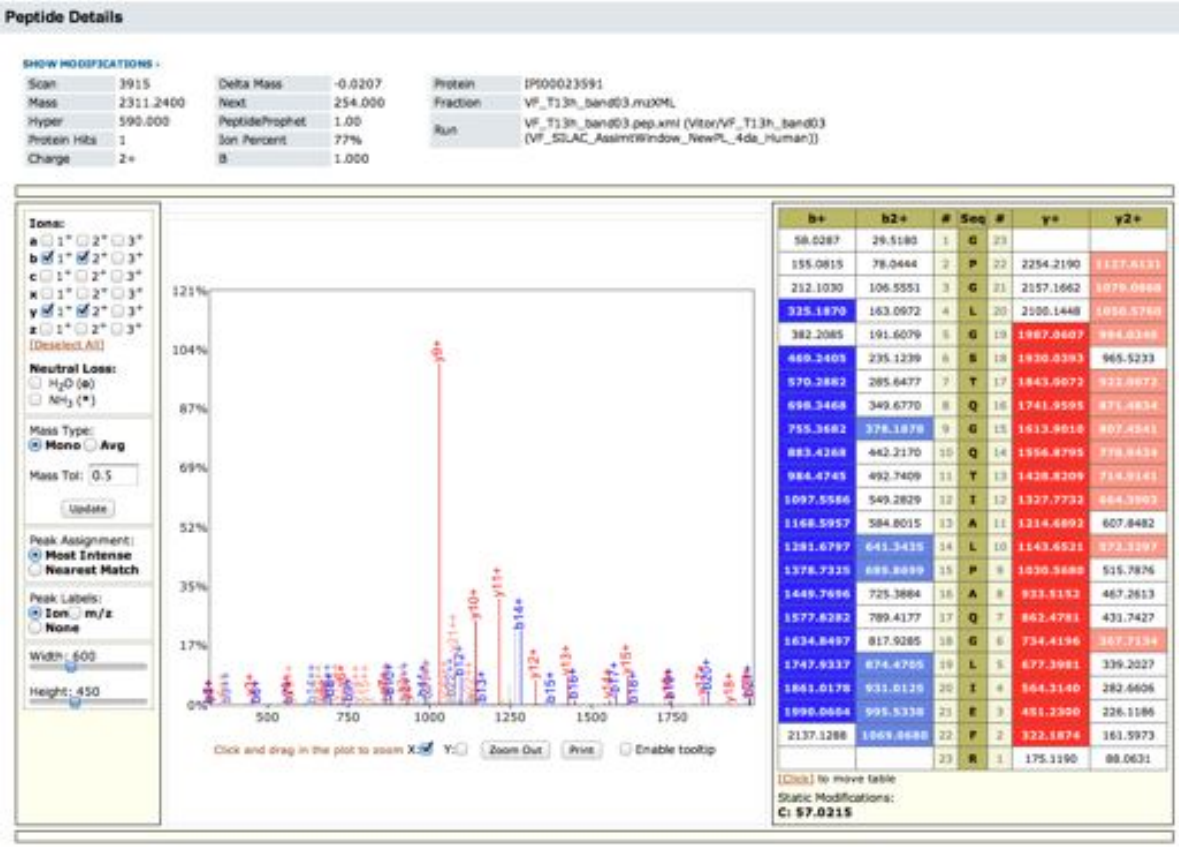
Peptide Details

Scan	3907	Delta Mass	-0.0197	Protein	IPI00000494
Mass	1927.0110	Next	237.000	Fraction	VF_T13h_band03.mzXML
Hyper	466.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	74%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	18		
157.0972	79.0522	2	G	17	1827.9422	914.4747
270.1812	135.5942	3	L	16	1770.9208	885.9640
371.2289	186.1181	4	T	15	1657.8367	829.4220
485.2718	243.1395	5	N	14	1556.7890	778.8981
648.3352	324.6712	6	Y	13	1442.7461	721.8767
719.3723	360.1898	7	A	12	1279.6828	640.3450
790.4094	395.7083	8	A	11	1208.6456	604.8265
861.4465	431.2269	9	A	10	1137.6085	569.3079
1024.5098	512.7585	10	Y	9	1066.5714	533.7893
1184.5405	592.7739	11	C	8	903.5081	452.2577
1285.5882	643.2977	12	T	7	743.4774	372.2423
1342.6096	671.8085	13	G	6	642.4297	321.7185
1455.6937	728.3505	14	L	5	585.4083	293.2078
1568.7778	784.8925	15	L	4	472.3242	236.6657
1681.8618	841.4346	16	L	3	359.2401	180.1237
1752.8990	876.9531	17	A	2	246.1561	123.5817
		18	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00023591	1	1	PURA	3915	2+	-0,0207	1,0000	R.GPGLGSTQGQTIALPAQGLIEFR.D



Peptide Details

SHOW MODIFICATIONS ›

Scan	3915	Delta Mass	-0.0207	Protein	IPI00023591
Mass	2311.2400	Next	254.000	Fraction	VF_T13h_band03.mzXML
Hyper	590.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	77%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	23		
155.0815	78.0444	2	P	22	2254.2190	1127.6131
212.1030	106.5551	3	G	21	2157.1662	1079.0868
325.1870	163.0972	4	L	20	2100.1448	1050.5760
382.2085	191.6079	5	G	19	1987.0607	994.0340
469.2405	235.1239	6	S	18	1930.0393	965.5233
570.2882	285.6477	7	T	17	1843.0073	922.0073
698.3468	349.6770	8	Q	16	1741.9595	871.4834
755.3682	378.1878	9	G	15	1613.9010	807.4541
883.4268	442.2170	10	Q	14	1556.8795	778.9434
984.4745	492.7409	11	T	13	1428.8209	714.9141
1097.5586	549.2829	12	I	12	1327.7732	664.3903
1168.5957	584.8015	13	A	11	1214.6892	607.8482
1281.6797	641.3435	14	L	10	1143.6521	572.3297
1378.7325	689.8699	15	P	9	1030.5680	515.7876
1449.7696	725.3884	16	A	8	933.5152	467.2613
1577.8282	789.4177	17	Q	7	862.4781	431.7427
1634.8497	817.9285	18	G	6	734.4196	367.7134
1747.9337	874.4705	19	L	5	677.3981	339.2027
1861.0178	931.0125	20	I	4	564.3140	282.6606
1990.0604	995.5338	21	E	3	451.2300	226.1186
2137.1288	1069.0680	22	F	2	322.1874	161.5973
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9594	IPI00019502	1	1	MYH9	3922	2+	-0,0260	0,9986	K.DFSALESQLQDTQELLQEENR.Q

Peptide Details

Scan	3922	Delta Mass	-0.0260	Protein	IPI00019502
Mass	2493.1740	Next	263.000	Fraction	VF_T13h_band01.mzXML
Hyper	414.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	55%		
Charge	2+	B	1.000		

Ions: b ☑ 1⁺ ☑ 2⁺; y ☑ 1⁺ ☑ 2⁺

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

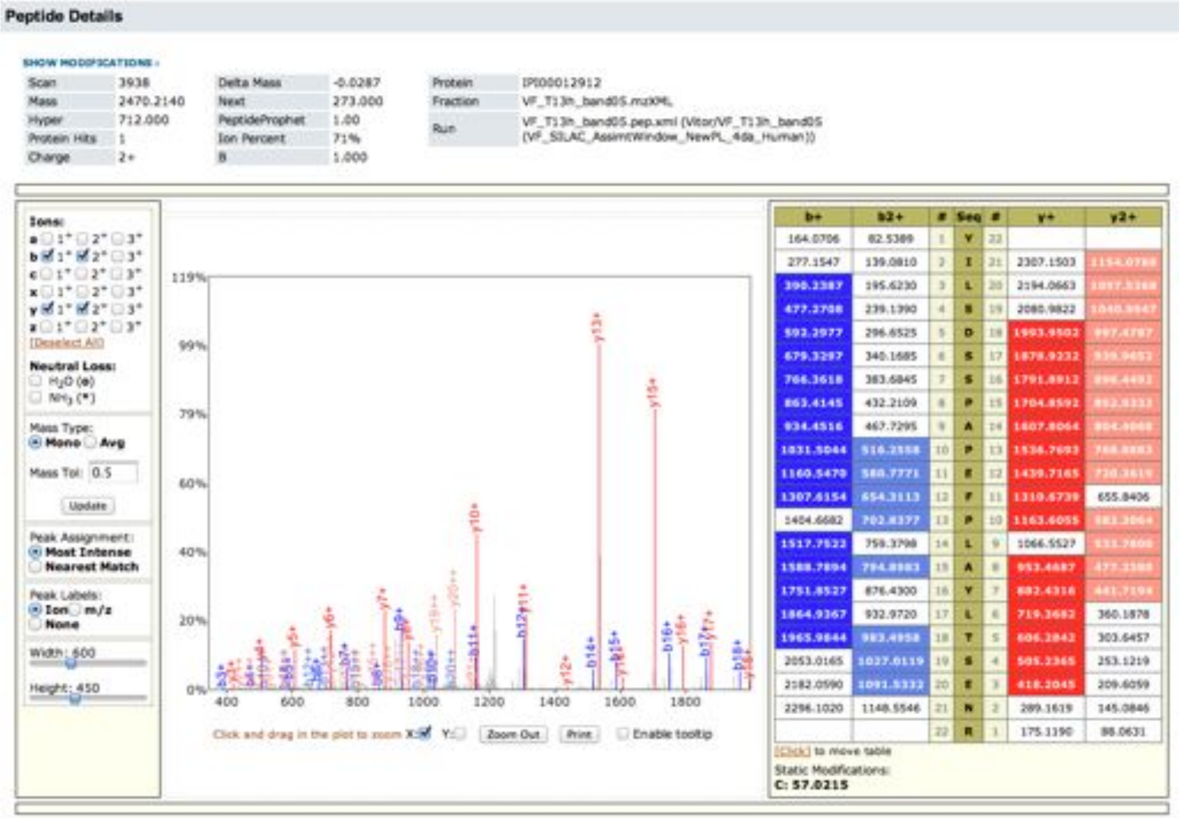
Height: 450

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	21		
263.1026	132.0550	2	F	20	2378.1470	1189.5772
350.1347	175.5710	3	S	19	2231.0786	1116.0429
421.1718	211.0895	4	A	18	2144.0466	1072.5269
534.2558	267.6316	5	L	17	2073.0095	1037.0084
663.2984	332.1529	6	E	16	1959.9254	980.4663
750.3305	375.6689	7	S	15	1830.8826	915.9450
878.3890	439.6982	8	Q	14	1743.8508	872.4290
991.4731	496.2402	9	L	13	1615.7922	808.3997
1119.5317	560.2695	10	Q	12	1502.7081	751.8577
1234.5586	617.7829	11	D	11	1374.6496	687.8284
1335.6063	668.3068	12	T	10	1259.6226	630.3149
1463.6649	732.3361	13	Q	9	1158.5749	579.7911
1592.7075	796.8574	14	E	8	1030.5164	515.7618
1705.7915	853.3994	15	L	7	901.4738	451.2405
1818.8756	909.9414	16	L	6	788.3897	394.6985
1946.9342	973.9707	17	Q	5	675.3056	338.1565
2075.9768	1038.4920	18	E	4	547.2471	274.1272
2205.0194	1103.0133	19	E	3	418.2045	209.6059
2319.0623	1160.0348	20	N	2	289.1619	145.0846
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00012912	1	1	CPT2	3938	2+	-0,0287	1,0000	K.YILSDSSPAPEFPLAYLTSENR.D



Peptide Details

SHOW MODIFICATIONS »

Scan	3938	Delta Mass	-0.0287	Protein	IPI00012912
Mass	2470.2140	Next	273.000	Fraction	VF_T13h_band05.mzXML
Hyper	712.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

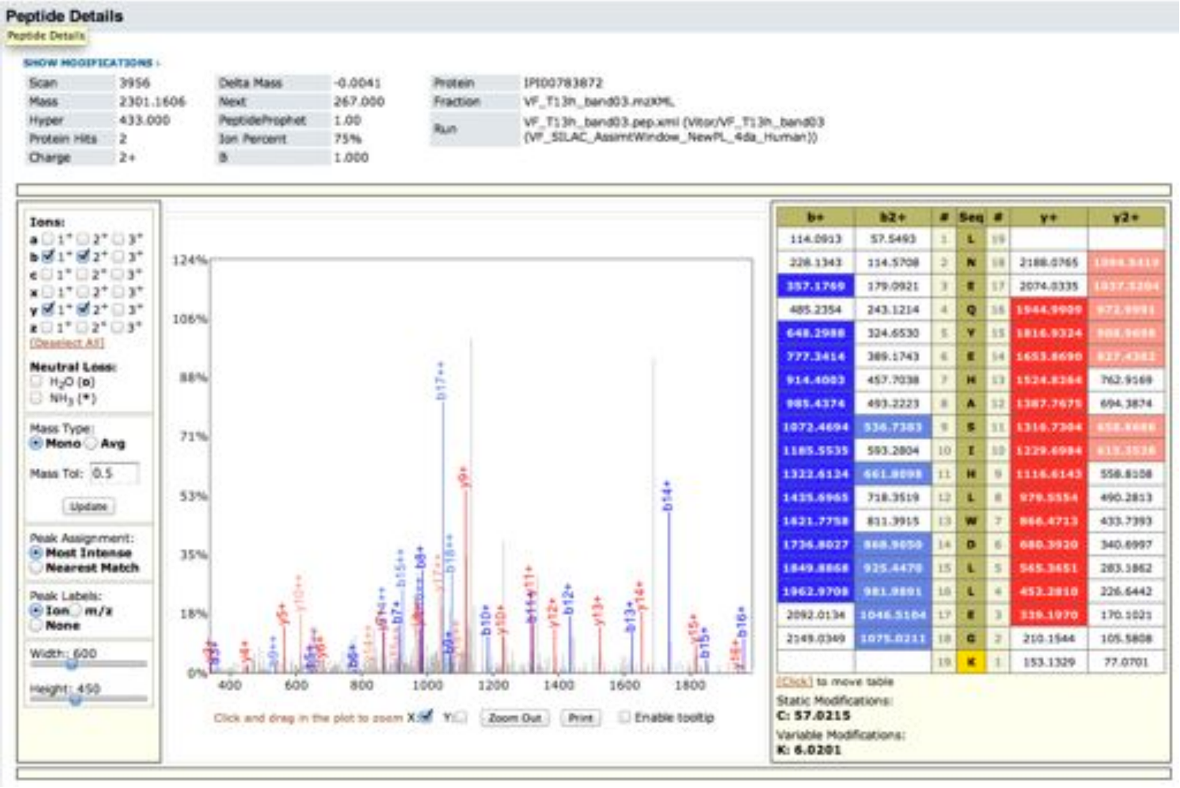
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
164.0706	82.5389	1	Y	22		
277.1547	139.0810	2	I	21	2307.1503	1154.0788
390.2387	195.6230	3	L	20	2194.0663	1097.5368
477.2708	239.1390	4	S	19	2080.9822	1040.9947
592.2977	296.6525	5	D	18	1993.9502	997.4787
679.3297	340.1685	6	S	17	1878.9232	939.9653
766.3618	383.6845	7	S	16	1791.8912	896.4492
863.4145	432.2109	8	P	15	1704.8592	852.9332
934.4516	467.7295	9	A	14	1607.8064	804.4068
1031.5044	516.2558	10	P	13	1536.7693	768.8883
1160.5470	580.7771	11	E	12	1439.7165	720.3619
1307.6154	654.3113	12	F	11	1310.6739	655.8406
1404.6682	702.8377	13	P	10	1163.6055	582.3064
1517.7522	759.3798	14	L	9	1066.5527	533.7800
1588.7894	794.8983	15	A	8	953.4687	477.2388
1751.8527	876.4300	16	Y	7	882.4316	441.7194
1864.9367	932.9720	17	L	6	719.3682	360.1878
1965.9844	983.4958	18	T	5	606.2842	303.6457
2053.0165	1027.0119	19	S	4	505.2365	253.1219
2182.0590	1091.5332	20	E	3	418.2045	209.6059
2296.1020	1148.5546	21	N	2	289.1619	145.0846
		22	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9798	IPI00873926, IPI00783872	1	1	CAPRIN1, CAPRIN1	3956	2+	-0,0041	0,9993	R.LNEQYEHASIHLWDLLEGK'.E



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	3956	Delta Mass	-0.0041	Protein	IPI00783872
Mass	2301.1606	Next	267.000	Fraction	VF_T13h_band03.mzXML
Hyper	433.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

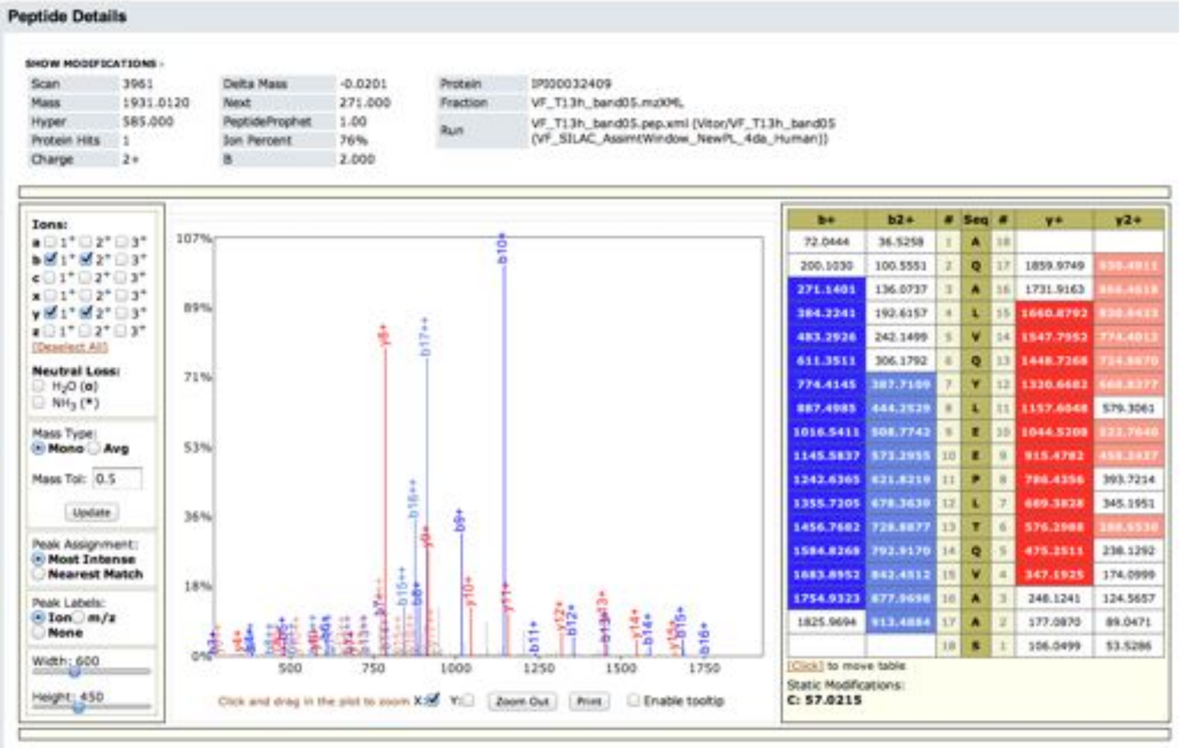
b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	19		
228.1343	114.5708	2	N	18	2188.0765	1094.5419
357.1769	179.0921	3	E	17	2074.0335	1037.5204
485.2354	243.1214	4	Q	16	1944.9909	972.9991
648.2988	324.6530	5	Y	15	1816.9324	908.9698
777.3414	389.1743	6	E	14	1653.8690	827.4382
914.4003	457.7038	7	H	13	1524.8264	762.9169
985.4374	493.2223	8	A	12	1387.7675	694.3874
1072.4694	536.7383	9	S	11	1316.7304	658.8688
1185.5535	593.2804	10	I	10	1229.6984	615.3528
1322.6124	661.8098	11	H	9	1116.6143	558.8108
1435.6965	718.3519	12	L	8	979.5554	490.2813
1621.7758	811.3915	13	W	7	866.4713	433.7393
1736.8027	868.9050	14	D	6	680.3920	340.6997
1849.8868	925.4470	15	L	5	565.3651	283.1862
1962.9708	981.9891	16	L	4	452.2810	226.6442
2092.0134	1046.5104	17	E	3	339.1970	170.1021
2149.0349	1075.0211	18	G	2	210.1544	105.5808
		19	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00032409	1	1	MAPBPIP	3961	2+	-0,0201	1,0000	K.AQALVQYLEEPLTQVAAS.-



Peptide Details

SHOW MODIFICATIONS -

Scan	3961	Delta Mass	-0.0201	Protein	IPI00032409
Mass	1931.0120	Next	271.000	Fraction	VF_T13h_band05.mzXML
Hyper	585.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	76%		
Charge	2+	B	2.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600
Height: 450

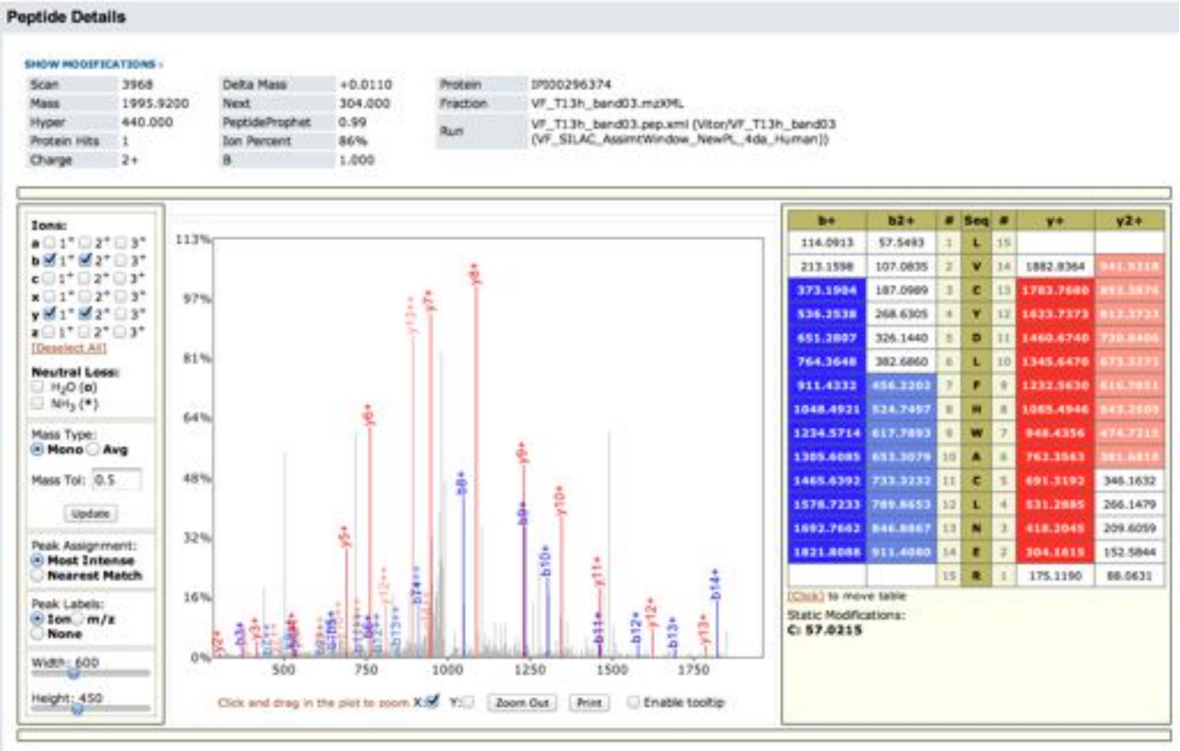
Click and drag in the plot to zoom X:☑ Y:☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	18		
200.1030	100.5551	2	Q	17	1859.9749	930.4911
271.1401	136.0737	3	A	16	1731.9163	866.4618
384.2241	192.6157	4	L	15	1660.8792	830.9433
483.2926	242.1499	5	V	14	1547.7952	774.4013
611.3511	306.1792	6	Q	13	1448.7268	724.8670
774.4145	387.7109	7	Y	12	1320.6682	660.8377
887.4985	444.2529	8	L	11	1157.6048	579.3061
1016.5411	508.7742	9	E	10	1044.5208	522.7640
1145.5837	573.2955	10	E	9	915.4782	458.2427
1242.6365	621.8219	11	P	8	786.4356	393.7214
1355.7205	678.3639	12	L	7	689.3828	345.1951
1456.7682	728.8877	13	T	6	576.2988	288.6530
1584.8268	792.9170	14	Q	5	475.2511	238.1292
1683.8952	842.4512	15	V	4	347.1925	174.0999
1754.9323	877.9698	16	A	3	248.1241	124.5657
1825.9694	913.4884	17	A	2	177.0870	89.0471
		18	S	1	106.0499	53.5286

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8447	IPI00296374	1	1	ZFPL1	3968	2+	+0,0110	0,9860	R.LVCYDLFHWACLNER.A


Peptide Details

SHOW MODIFICATIONS ›

Scan	3968	Delta Mass	+0.0110	Protein	IPI00296374
Mass	1995.9200	Next	304.000	Fraction	VF_T13h_band03.mzXML
Hyper	440.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

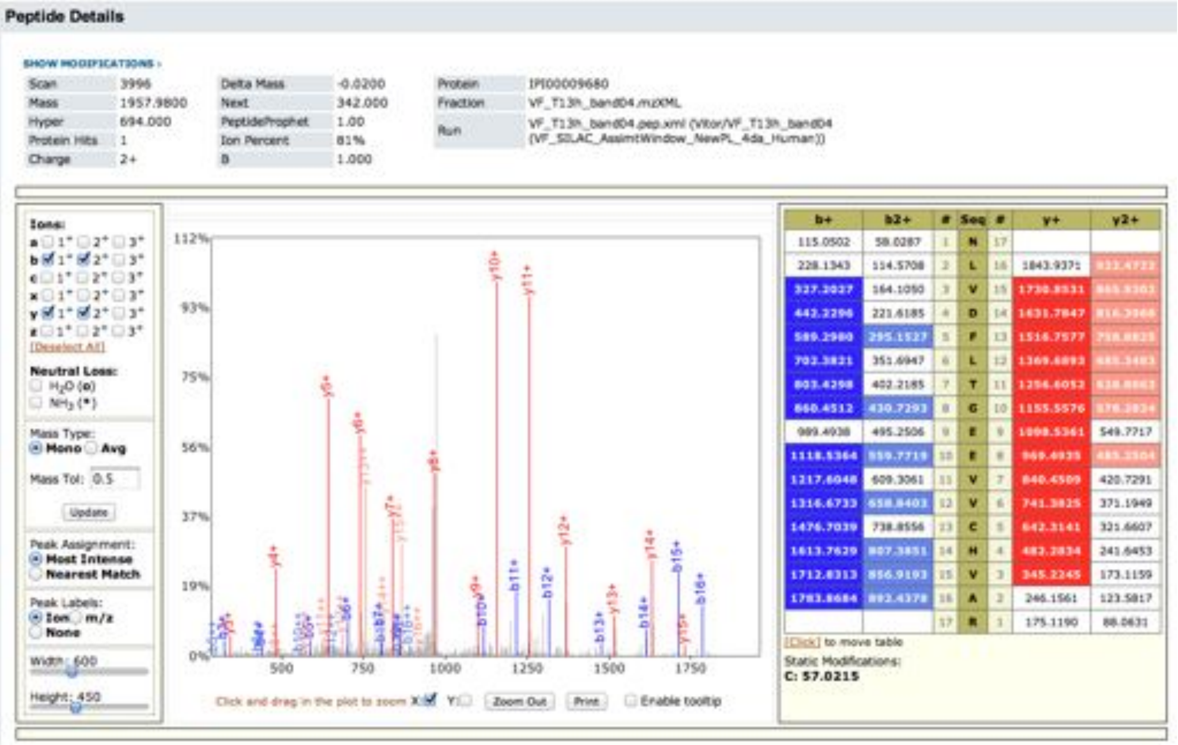
Enable tooltip: ☐

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
213.1598	107.0835	2	V	14	1882.8364	941.9218
373.1904	187.0989	3	C	13	1783.7680	892.3876
536.2538	268.6305	4	Y	12	1623.7373	812.3723
651.2807	326.1440	5	D	11	1460.6740	730.8406
764.3648	382.6860	6	L	10	1345.6470	673.3271
911.4332	456.2202	7	F	9	1232.5630	616.7851
1048.4921	524.7497	8	H	8	1085.4946	543.2509
1234.5714	617.7893	9	W	7	948.4356	474.7215
1305.6085	653.3079	10	A	6	762.3563	381.6818
1465.6392	733.3232	11	C	5	691.3192	346.1632
1578.7233	789.8653	12	L	4	531.2885	266.1479
1692.7662	846.8867	13	N	3	418.2045	209.6059
1821.8088	911.4080	14	E	2	304.1615	152.5844
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9851	IPI00009680	1	1	MRPL44	3996	2+	-0,0200	1,0000	K.NLVDFLTGEEVVCHVAR.N



Peptide Details

SHOW MODIFICATIONS ›

Scan	3996	Delta Mass	-0.0200	Protein	IPI00009680
Mass	1957.9800	Next	342.000	Fraction	VF_T13h_band04.mzXML
Hyper	694.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	81%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	17		
228.1343	114.5708	2	L	16	1843.9371	922.4722
327.2027	164.1050	3	V	15	1730.8531	865.9302
442.2296	221.6185	4	D	14	1631.7847	816.3960
589.2980	295.1527	5	F	13	1516.7577	758.8825
702.3821	351.6947	6	L	12	1369.6893	685.3483
803.4298	402.2185	7	T	11	1256.6052	628.8063
860.4512	430.7293	8	G	10	1155.5576	578.2824
989.4938	495.2506	9	E	9	1098.5361	549.7717
1118.5364	559.7719	10	E	8	969.4935	485.2504
1217.6048	609.3061	11	V	7	840.4509	420.7291
1316.6733	658.8403	12	V	6	741.3825	371.1949
1476.7039	738.8556	13	C	5	642.3141	321.6607
1613.7629	807.3851	14	H	4	482.2834	241.6453
1712.8313	856.9193	15	V	3	345.2245	173.1159
1783.8684	892.4378	16	A	2	246.1561	123.5817
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00007049	1	1	MRPS18C	4021	2+	-0,0203	0,9999	K.NVQLLSQFVSPFTGCIYGR.H

Apple
http://www.apple.com/

SHOW MODIFICATIONS ›

Scan	4021	Delta Mass	-0.0203	Protein	IPI00007049
Mass	2186.1060	Next	334.000	Fraction	VF_T13h_band06.mzXML
Hyper	750.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

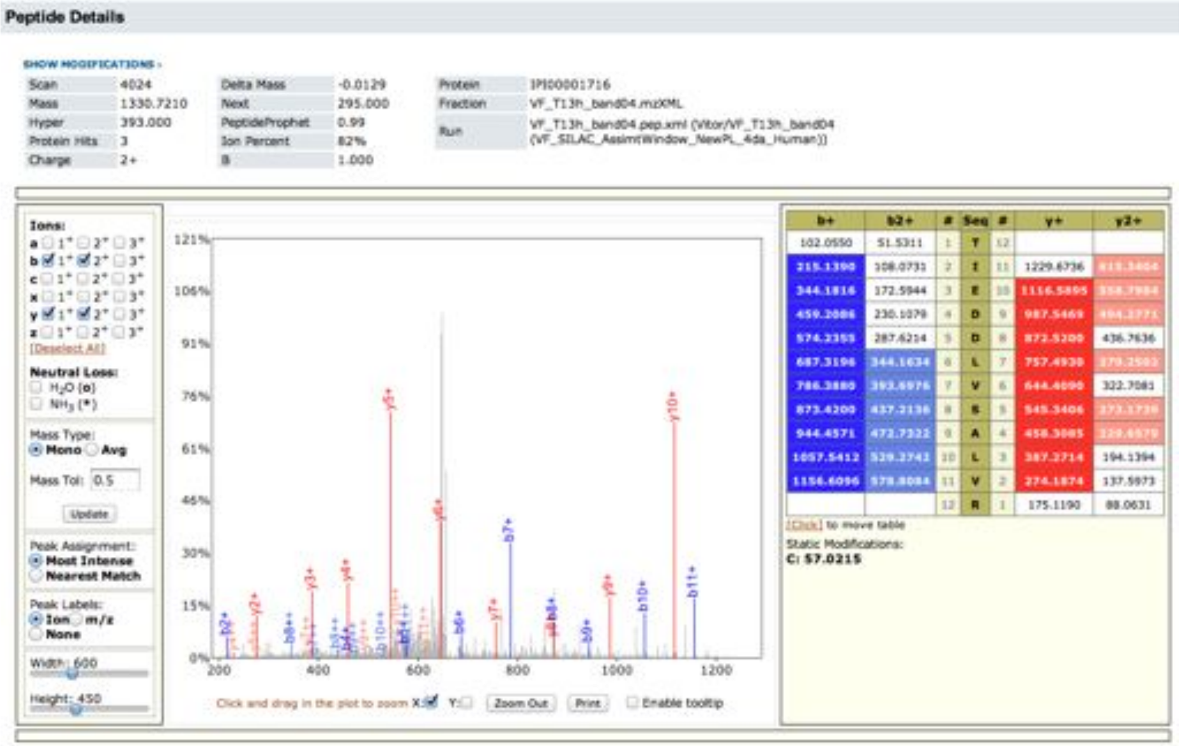
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	19		
214.1186	107.5629	2	V	18	2072.0634	1036.5353
342.1772	171.5922	3	Q	17	1972.9950	987.0011
455.2613	228.1343	4	L	16	1844.9364	922.9718
568.3453	284.6763	5	L	15	1731.8523	866.4298
655.3774	328.1923	6	S	14	1618.7683	809.8879
783.4359	392.2216	7	Q	13	1531.7362	766.3718
930.5043	465.7558	8	F	12	1403.6777	702.3425
1029.5728	515.2900	9	V	11	1256.6093	628.8083
1116.6048	558.8060	10	S	10	1157.5408	579.2741
1213.6575	607.3324	11	P	9	1070.5088	535.7580
1360.7260	680.8666	12	F	8	973.4560	487.2317
1461.7736	731.3905	13	T	7	826.3876	413.6975
1518.7951	759.9012	14	G	6	725.3400	363.1736
1678.8258	839.9165	15	C	5	668.3185	334.6629
1791.9099	896.4586	16	I	4	508.2878	254.6475
1954.9732	977.9902	17	Y	3	395.2037	198.1055
2011.9946	1006.5010	18	G	2	232.1404	116.5738
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8928	IPI00795171, IPI00001716, IPI00619930	1	1	PUS1, PUS1, PUS1	4024	2+	-0,0129	0,9931	K.TIEDDLVSALVR.S



Peptide Details

SHOW MODIFICATIONS »

Scan	4024	Delta Mass	-0.0129	Protein	IPI00001716
Mass	1330.7210	Next	295.000	Fraction	VF_T13h_band04.mzXML
Hyper	393.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	12		
215.1390	108.0731	2	I	11	1229.6736	615.3404
344.1816	172.5944	3	E	10	1116.5895	558.7984
459.2086	230.1079	4	D	9	987.5469	494.2771
574.2355	287.6214	5	D	8	872.5200	436.7636
687.3196	344.1634	6	L	7	757.4930	379.2501
786.3880	393.6976	7	V	6	644.4090	322.7081
873.4200	437.2136	8	S	5	545.3406	273.1739
944.4571	472.7322	9	A	4	458.3085	229.6579
1057.5412	529.2742	10	L	3	387.2714	194.1394
1156.6096	578.8084	11	V	2	274.1874	137.5973
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9741	IPI00646262, IPI00019407	1	1	NSDHL, NSDHL	4027	2+	-0,0136	0,9988	R.DPQLVPILIEAAR.N

Peptide Details

Scan	4027	Delta Mass	-0.0136	Protein	IPI00019407
Mass	1434.8310	Next	283.000	Fraction	VF_T13h_band03.mzXML
Hyper	432.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

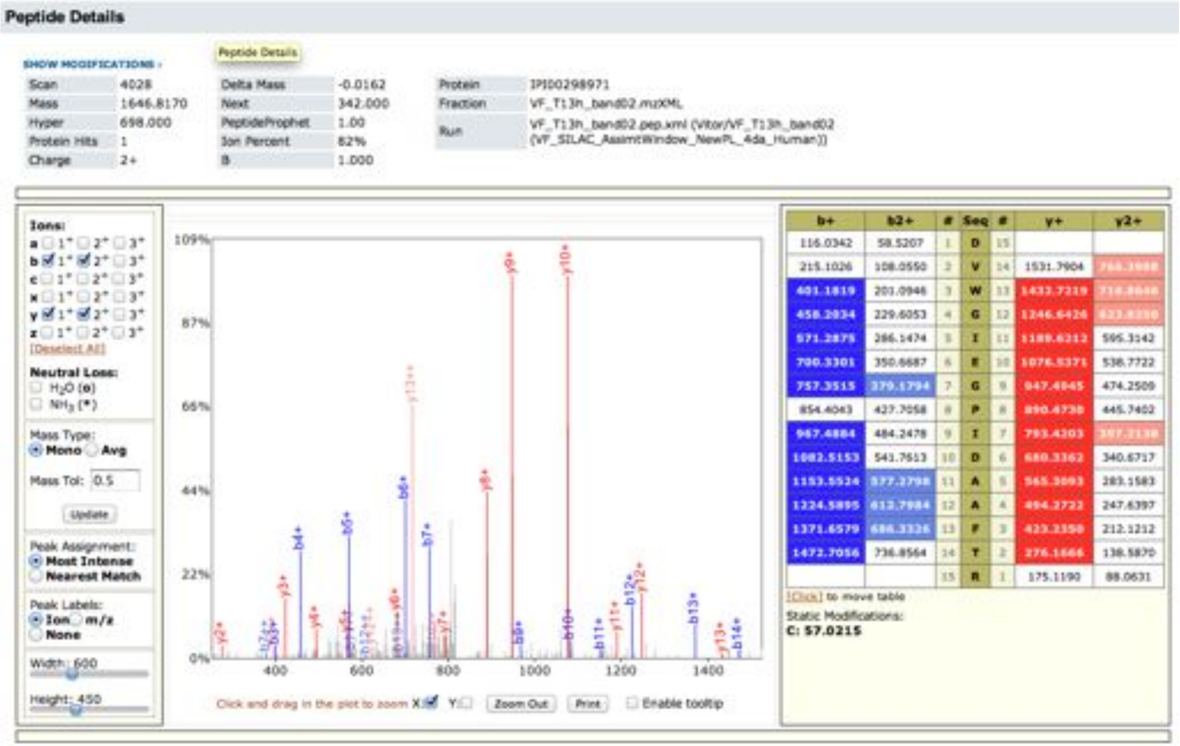
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	13		
213.0870	107.0471	2	P	12	1319.8045	660.4059
341.1456	171.0764	3	Q	11	1222.7518	611.8795
454.2296	227.6185	4	L	10	1094.6932	547.8502
553.2980	277.1527	5	V	9	981.6091	491.3083
650.3508	325.6790	6	P	8	882.5407	441.7740
763.4349	382.2211	7	I	7	785.4880	393.2476
876.5189	438.7631	8	L	6	672.4039	336.7056
989.6030	495.3051	9	I	5	559.3198	280.1636
1118.6456	559.8264	10	E	4	446.2358	223.6215
1189.6827	595.3450	11	A	3	317.1932	159.1002
1260.7198	630.8635	12	A	2	246.1561	123.5817
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9819	IPI00298971	1	1	VTN	4028	2+	-0,0162	1,0000	R.DVWGIEGPIDAAFTR.I



Peptide Details

Scan	4028	Delta Mass	-0.0162	Protein	IPI00298971
Mass	1646.8170	Next	342.000	Fraction	VF_T13h_band02.mzXML
Hyper	698.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

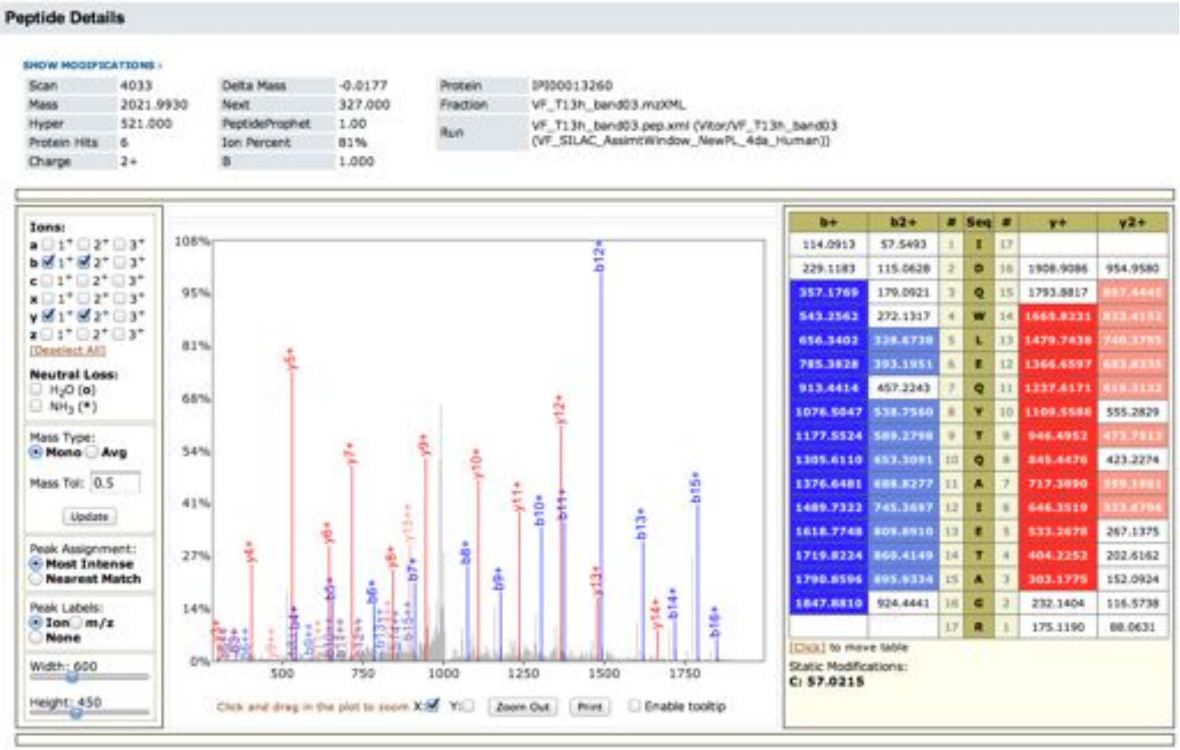
Height: 450

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	15		
215.1026	108.0550	2	V	14	1531.7904	766.3988
401.1819	201.0946	3	W	13	1432.7219	716.8646
458.2034	229.6053	4	G	12	1246.6426	623.8250
571.2875	286.1474	5	I	11	1189.6212	595.3142
700.3301	350.6687	6	E	10	1076.5371	538.7722
757.3515	379.1794	7	G	9	947.4945	474.2509
854.4043	427.7058	8	P	8	890.4730	445.7402
967.4884	484.2478	9	I	7	793.4203	397.2138
1082.5153	541.7613	10	D	6	680.3362	340.6717
1153.5524	577.2798	11	A	5	565.3093	283.1583
1224.5895	612.7984	12	A	4	494.2722	247.6397
1371.6579	686.3326	13	F	3	423.2350	212.1212
1472.7056	736.8564	14	T	2	276.1666	138.5870
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9845	IPI00790783, IPI00657664, IPI00789393, IPI00013260, IPI00902983, IPI00554652	1	1	LSP1, LSP1, LSP1, LSP1, LSP1, LSP1	4033	2+	-0,0177	0,9997	K.IDQWLEQYTQAIETAGR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	4033	Delta Mass	-0.0177	Protein	IPI00013260
Mass	2021.9930	Next	327.000	Fraction	VF_T13h_band03.mzXML
Hyper	521.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human])
Protein Hits	6	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	17		
229.1183	115.0628	2	D	16	1908.9086	954.9580
357.1769	179.0921	3	Q	15	1793.8817	897.4445
543.2562	272.1317	4	W	14	1665.8231	833.4153
656.3402	328.6738	5	L	13	1479.7438	740.3755
785.3828	393.1951	6	E	12	1366.6597	683.8335
913.4414	457.2243	7	Q	11	1237.6171	619.3122
1076.5047	538.7560	8	Y	10	1109.5586	555.2829
1177.5524	589.2798	9	T	9	946.4952	473.7513
1305.6110	653.3091	10	Q	8	845.4476	423.2274
1376.6481	688.8277	11	A	7	717.3890	359.1981
1489.7322	745.3697	12	I	6	646.3519	323.6796
1618.7748	809.8910	13	E	5	533.2678	267.1375
1719.8224	860.4149	14	T	4	404.2252	202.6162
1790.8596	895.9334	15	A	3	303.1775	152.0924
1847.8810	924.4441	16	G	2	232.1404	116.5738
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9756	IPI00790114, IPI00472168, IPI00796313, IPI00009444, IPI00873328	1	1	MRPL27, MRPL27, MRPL27, MRPL27, MRPL27	4043	2+	-0,0152	0,9990	K.C^LYALEEGIVR.Y

Peptide Details

SHOW MODIFICATIONS ›

Scan	4043	Delta Mass	-0.0152	Protein	IPI00009444
Mass	1305.6510	Next	443.000	Fraction	VF_T13h_band05.mzXML
Hyper	565.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	80%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

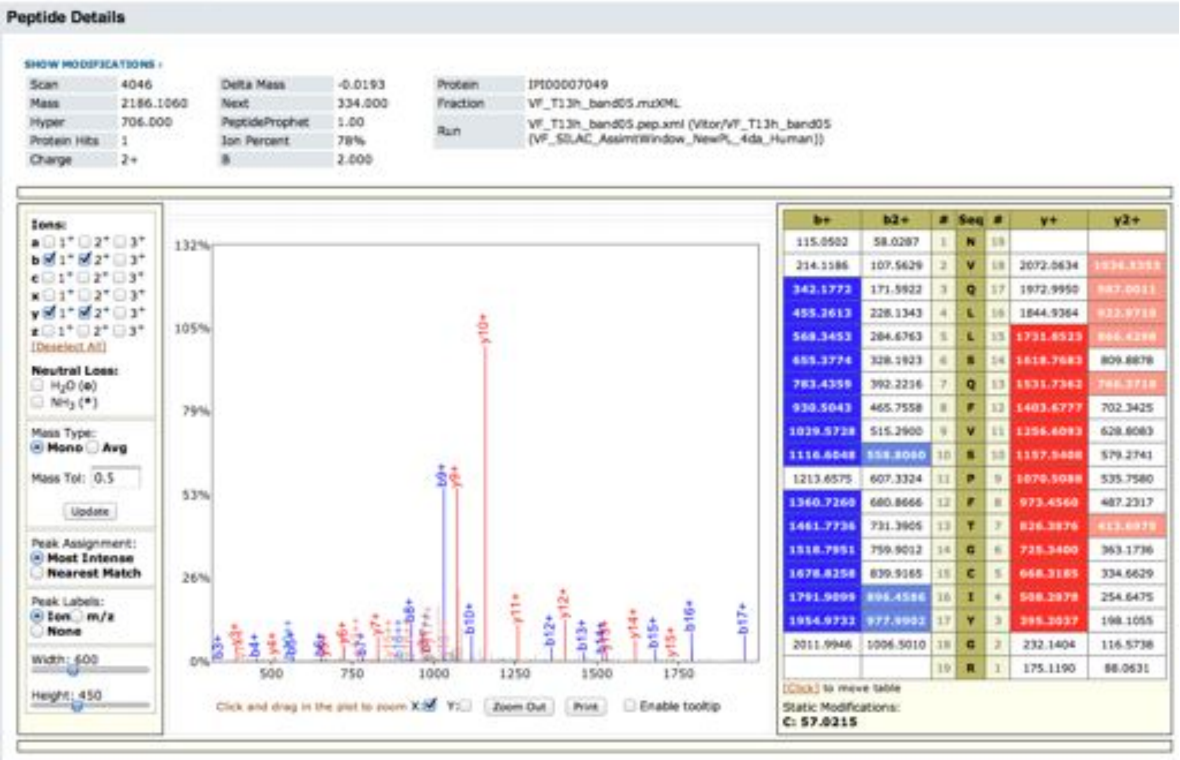
b+	b2+	#	Seq	#	y+	y2+
144.0115	72.5094	1	C	11		
357.0955	129.0514	2	L	10	1162.6467	581.8270
420.1589	210.5831	3	Y	9	1049.5626	525.2849
491.1960	246.1016	4	A	8	886.4993	443.7533
604.2800	302.6437	5	L	7	815.4621	408.2347
733.3226	367.1650	6	E	6	702.3781	351.6927
862.3652	431.6862	7	E	5	573.3355	287.1714
919.3867	460.1970	8	G	4	444.2929	222.6501
1032.4707	516.7390	9	I	3	387.2714	194.1394
1131.5392	566.2732	10	V	2	274.1874	137.5973
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
C: -17.0265

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00007049	1	1	MRPS18C	4046	2+	-0,0193	1,0000	K.NVQLLSQFVSPFTGCIYGR.H


Peptide Details

SHOW MODIFICATIONS ›

Scan	4046	Delta Mass	-0.0193	Protein	IPI00007049
Mass	2186.1060	Next	334.000	Fraction	VF_T13h_band05.mzXML
Hyper	706.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	78%		
Charge	2+	B	2.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	19		
214.1186	107.5629	2	V	18	2072.0634	1036.5353
342.1772	171.5922	3	Q	17	1972.9950	987.0011
455.2613	228.1343	4	L	16	1844.9364	922.9718
568.3453	284.6763	5	L	15	1731.8523	866.4298
655.3774	328.1923	6	S	14	1618.7683	809.8878
783.4359	392.2216	7	Q	13	1531.7362	766.3718
930.5043	465.7558	8	F	12	1403.6777	702.3425
1029.5728	515.2900	9	V	11	1256.6093	628.8083
1116.6048	558.8060	10	S	10	1157.5408	579.2741
1213.6575	607.3324	11	P	9	1070.5088	535.7580
1360.7260	680.8666	12	F	8	973.4560	487.2317
1461.7736	731.3905	13	T	7	826.3876	413.6975
1518.7951	759.9012	14	G	6	725.3400	363.1736
1678.8258	839.9165	15	C	5	668.3185	334.6629
1791.9099	896.4586	16	I	4	508.2878	254.6475
1954.9732	977.9902	17	Y	3	395.2037	198.1055
2011.9946	1006.5010	18	G	2	232.1404	116.5738
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00879142, IPI00430781, IPI00166638	1	1	MGC70857, MGC70857, MGC70857	4064	2+	-0,0176	0,9999	R.LALTM"DLAPLLLAAR.S

Scan	4064
Mass	1597.9350
Hyper	686.000
Protein Hits	3
Charge	2+

Delta Mass	-0.0176
Next	356.000
PeptideProphet	1.00
Ion Percent	86%
B	1.000

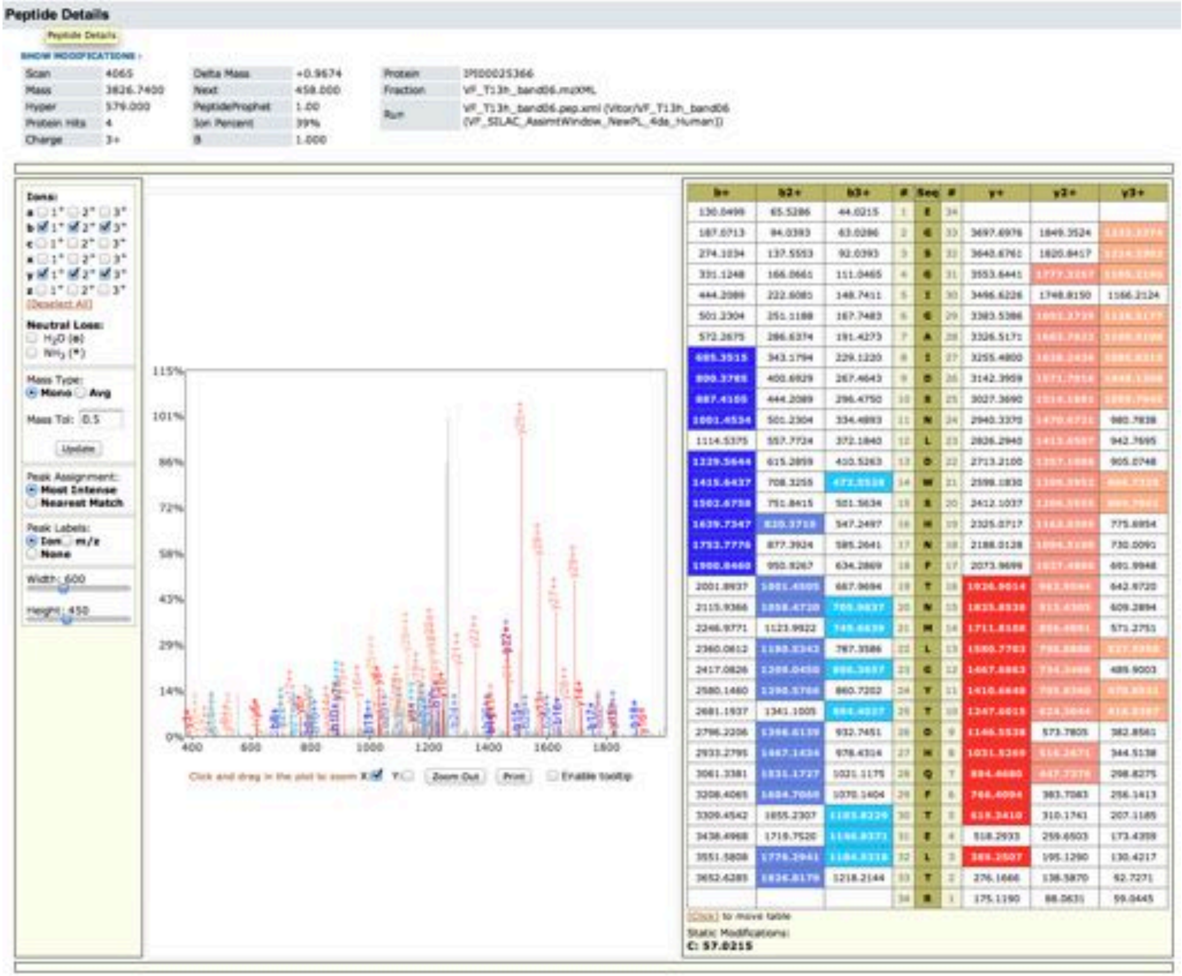
Protein	IPI00166638
Fraction	VF_T13h_band06.mzXML
Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
185.1285	93.0679	2	A	14	1484.8505	742.9289
298.2125	149.6099	3	L	13	1413.8134	707.4103
399.2602	200.1337	4	T	12	1300.7293	650.8683
546.2956	273.6514	5	M	11	1199.6816	600.3445
661.3225	331.1649	6	D	10	1052.6463	526.8268
774.4066	387.7069	7	L	9	937.6193	469.3133
845.4437	423.2255	8	A	8	824.5352	412.7713
942.4965	471.7519	9	P	7	753.4981	377.2527
1055.5805	528.2939	10	L	6	656.4454	328.7263
1168.6646	584.8359	11	L	5	543.3613	272.1843
1281.7487	641.3780	12	L	4	430.2772	215.6423
1352.7858	676.8965	13	A	3	317.1932	159.1002
1423.8229	712.4151	14	A	2	246.1561	123.5817
		15	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9400	IPI00796979, IPI00383539, IPI00793839, IPI00025366	1	1	CS, CS, CS, CS	4065	3+	+0,9674	0,9952	R.EGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELTR.L

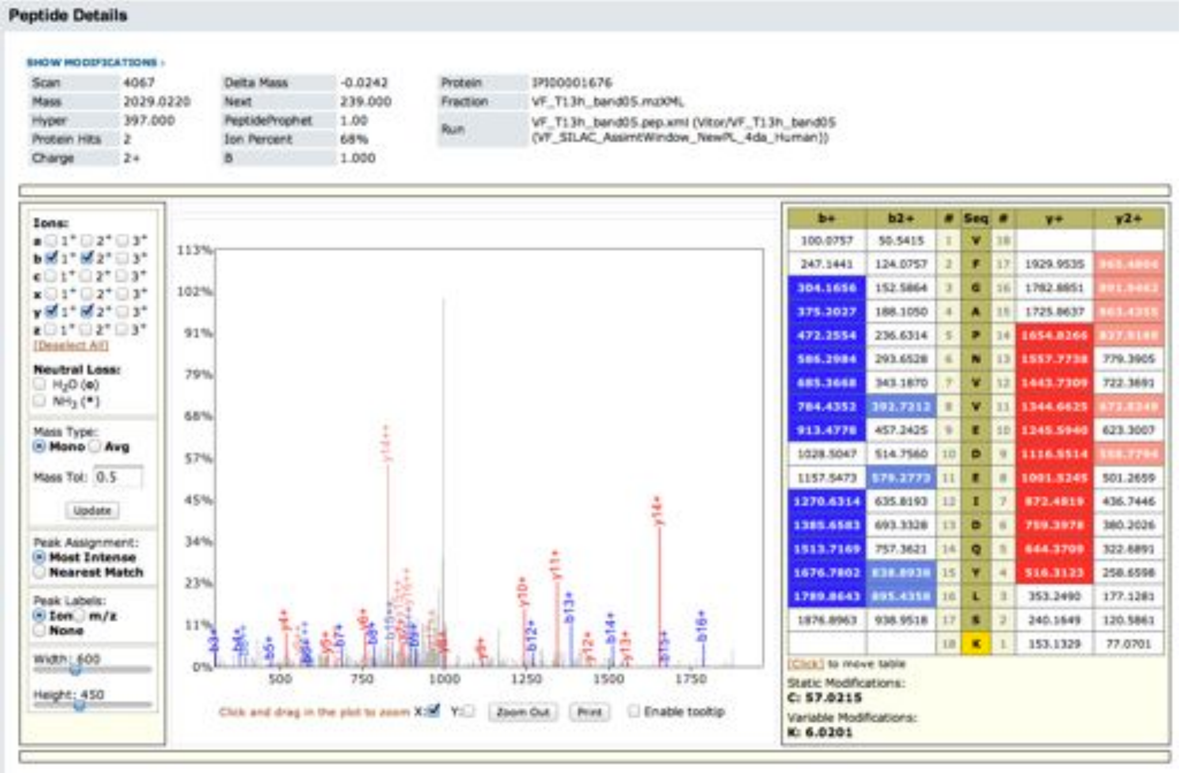


Peptide Details

Scan	4065	Delta Mass	+0.9674	Protein	IPI00025366
Mass	3826.7400	Next	458.000	Fraction	VF_T13h_band06.mzXML
Hyper	579.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	39%		
Charge	3+	B	1.000		

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9792	IPI00290543, IPI00001676	1	1	NPLOC4, NPLOC4	4067	2+	-0,0242	0,9993	K.VFGAPNVVEDEIDQYLSK'.Q



Peptide Details

SHOW MODIFICATIONS ›

Scan	4067	Delta Mass	-0.0242	Protein	IPI00001676
Mass	2029.0220	Next	239.000	Fraction	VF_T13h_band05.mzXML
Hyper	397.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

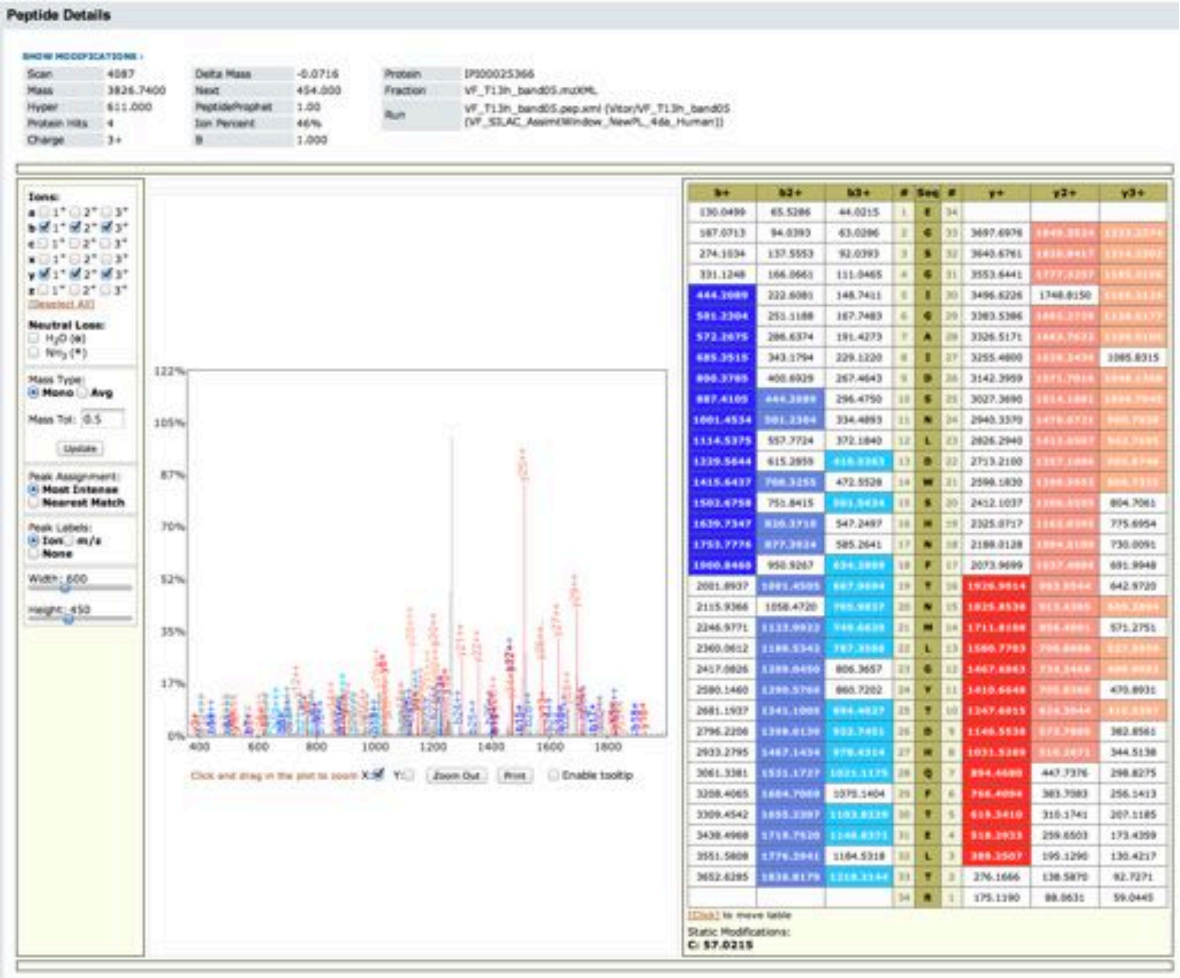
b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	18		
247.1441	124.0757	2	F	17	1929.9535	965.4804
304.1656	152.5864	3	G	16	1782.8851	891.9463
375.2027	188.1050	4	A	15	1725.8637	863.4355
472.2554	236.6314	5	P	14	1654.8266	827.9169
586.2984	293.6528	6	N	13	1557.7738	779.3905
685.3668	343.1870	7	V	12	1443.7309	722.3691
784.4352	392.7212	8	V	11	1344.6625	672.8349
913.4778	457.2425	9	E	10	1245.5940	623.3007
1028.5047	514.7560	10	D	9	1116.5514	558.7794
1157.5473	579.2773	11	E	8	1001.5245	501.2659
1270.6314	635.8193	12	I	7	872.4819	436.7446
1385.6583	693.3328	13	D	6	759.3978	380.2026
1513.7169	757.3621	14	Q	5	644.3709	322.6891
1676.7802	838.8938	15	Y	4	516.3123	258.6598
1789.8643	895.4358	16	L	3	353.2490	177.1281
1876.8963	938.9518	17	S	2	240.1649	120.5861
		18	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9840	IPI00796979, IPI00383539, IPI00793839, IPI00025366	1	1	CS, CS, CS, CS	4087	3+	-0,0716	0,9997	R.EGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELTR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4087	Delta Mass	-0.0716	Protein	IPI00025366
Mass	3826.7400	Next	454.000	Fraction	VF_T13h_band05.mzXML
Hyper	611.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4de_Human))
Protein Hits	4	Ion Percent	46%		
Charge	3+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☑ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

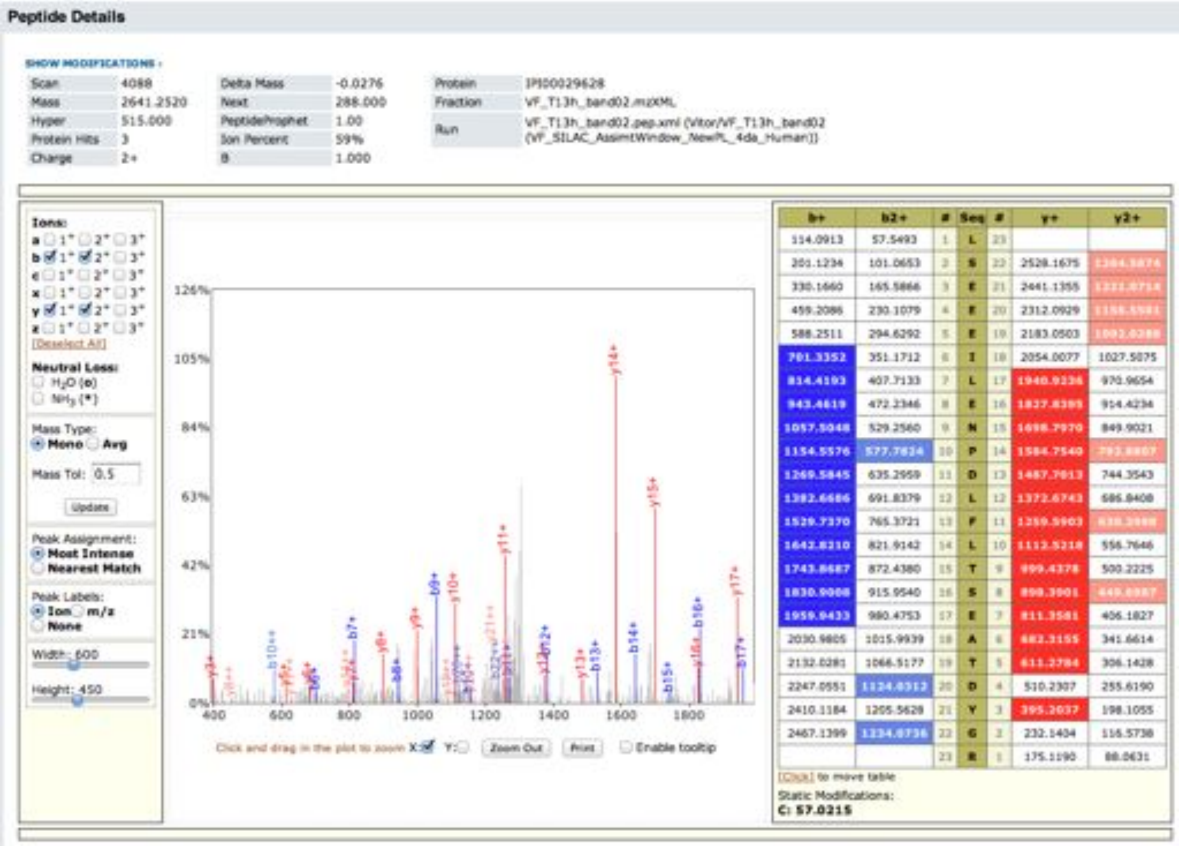
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
130.0499	65.5286	44.0215	1	E	34			
187.0713	94.0393	63.0286	2	G	33	3697.6976	[illegible]	[illegible]
274.1034	137.5553	92.0393	3	S	32	3640.6761	[illegible]	[illegible]
331.1248	166.0661	111.0465	4	G	31	3553.6441	[illegible]	[illegible]
444.2089	222.6081	148.7411	5	I	30	3496.6226	1748.8150	[illegible]
501.2304	251.1188	167.7483	6	G	29	3383.5386	[illegible]	[illegible]
572.2675	286.6374	191.4273	7	A	28	3326.5171	[illegible]	[illegible]
685.3515	343.1794	229.1220	8	I	27	3255.4800	[illegible]	1085.8315
800.3785	400.6929	267.4643	9	D	26	3142.3959	[illegible]	[illegible]
887.4105	444.2089	296.4750	10	S	25	3027.3690	[illegible]	[illegible]
1001.4534	501.2304	334.4893	11	N	24	2940.3370	[illegible]	[illegible]
1114.5375	557.7724	372.1840	12	L	23	2826.2940	[illegible]	[illegible]
1229.5644	615.2859	410.5263	13	D	22	2713.2100	[illegible]	[illegible]
1415.6437	708.3255	472.5528	14	W	21	2598.1830	[illegible]	[illegible]
1502.6758	751.8415	501.5434	15	S	20	2412.1037	[illegible]	804.7061
1639.7347	820.3710	547.2487	16	H	19	2325.0717	[illegible]	775.6954
1753.7776	877.3924	585.2641	17	N	18	2188.0128	[illegible]	730.0091
1900.8460	950.9267	634.2889	18	F	17	2073.9699	[illegible]	691.9948
2001.8937	1001.4505	667.9684	19	T	16	1926.9814	[illegible]	642.9720
2115.9366	1058.4720	705.9837	20	N	15	1825.8538	[illegible]	[illegible]
2246.9771	1123.9922	749.6639	21	M	14	1711.8108	[illegible]	571.2751
2360.0612	1180.5343	787.3588	22	L	13	1580.7703	[illegible]	[illegible]
2417.0826	1209.0450	806.3657	23	G	12	1467.6863	[illegible]	[illegible]
2580.1460	1290.5768	860.7202	24	Y	11	1410.6648	[illegible]	470.8931
2681.1937	1341.1008	894.4027	25	T	10	1247.6015	[illegible]	[illegible]
2796.2206	1398.6139	932.7451	26	D	9	1146.5538	[illegible]	382.8561
2933.2795	1467.1434	978.4314	27	H	8	1031.5269	[illegible]	344.5138
3061.3381	1531.1727	1021.1175	28	Q	7	894.4680	447.7376	298.8275
3208.4065	1604.7068	1070.1404	29	F	6	766.4094	383.7083	256.1413
3309.4542	1655.2307	1103.8119	30	T	5	619.3410	310.1741	207.1185
3438.4968	1719.7520	1146.8371	31	E	4	518.2933	259.6503	173.4359
3551.5808	1776.2941	1184.5318	32	L	3	389.2507	195.1290	130.4217
3652.6285	1826.8179	1218.2144	33	T	2	276.1666	138.5870	92.7271
			34	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00853306, IPI00029628, IPI00790214	1	1	RCN2, RCN2, RCN2	4088	2+	-0,0276	0,9999	K.LSEEEILENPDLFLTSEATDYGR.Q



Peptide Details

SHOW MODIFICATIONS ›

Scan	4088	Delta Mass	-0.0276	Protein	IPI00029628
Mass	2641.2520	Next	288.000	Fraction	VF_T13h_band02.mzXML
Hyper	515.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	59%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	23		
201.1234	101.0653	2	S	22	2528.1675	1264.5874
330.1660	165.5866	3	E	21	2441.1355	1221.0714
459.2086	230.1079	4	E	20	2312.0929	1156.5501
588.2511	294.6292	5	E	19	2183.0503	1092.0288
701.3352	351.1712	6	I	18	2054.0077	1027.5075
814.4193	407.7133	7	L	17	1940.9236	970.9654
943.4619	472.2346	8	E	16	1827.8395	914.4234
1057.5048	529.2560	9	N	15	1698.7970	849.9021
1154.5576	577.7824	10	P	14	1584.7540	792.8807
1269.5845	635.2959	11	D	13	1487.7013	744.3543
1382.6686	691.8379	12	L	12	1372.6743	686.8408
1529.7370	765.3721	13	F	11	1259.5903	630.2988
1642.8210	821.9142	14	L	10	1112.5218	556.7646
1743.8687	872.4380	15	T	9	999.4378	500.2225
1830.9008	915.9540	16	S	8	898.3901	449.6987
1959.9433	980.4753	17	E	7	811.3581	406.1827
2030.9805	1015.9939	18	A	6	682.3155	341.6614
2132.0281	1066.5177	19	T	5	611.2784	306.1428
2247.0551	1124.0312	20	D	4	510.2307	255.6190
2410.1184	1205.5628	21	Y	3	395.2037	198.1055
2467.1399	1234.0736	22	G	2	232.1404	116.5738
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9709	IPI00914952, IPI00914938, IPI00016621, IPI00256684, IPI00304577	1	1	AP2A2, AP2A2, AP2A2, AP2A1, AP2A1	4099	2+	-0,0220	0,9993	K.VGGYILGEFGNLIAGDPR.S

Scan	4099
Mass	1847.9650
Hyper	445.000
Protein Hits	5
Charge	2+

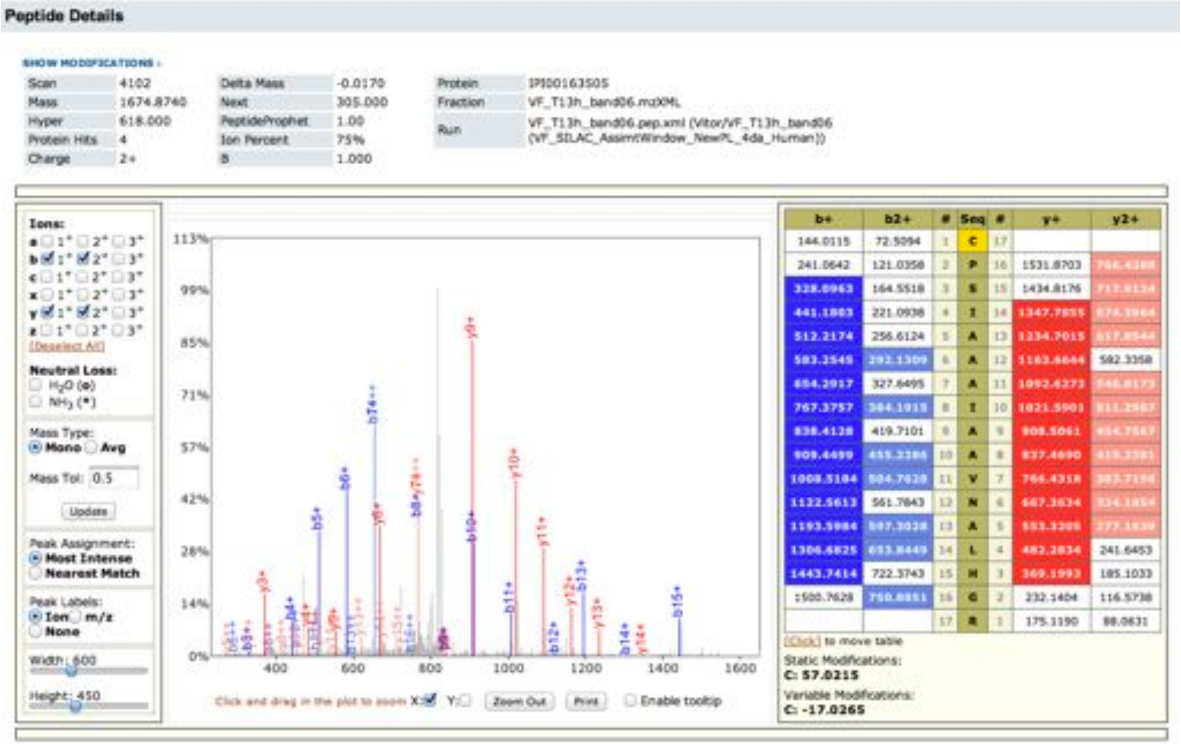
Delta Mass	-0.0220
Next	268.000
PeptideProphet	1.00
Ion Percent	71%
B	1.000

Protein	IPI00016621
Fraction	VF_T13h_band01.mzXML
Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	18		
157.0972	79.0522	2	G	17	1748.8966	874.9519
214.1186	107.5629	3	G	16	1691.8751	846.4412
377.1819	189.0946	4	Y	15	1634.8537	817.9305
490.2660	245.6366	5	I	14	1471.7904	736.3988
603.3501	302.1787	6	L	13	1358.7063	679.8568
660.3715	330.6894	7	G	12	1245.6222	623.3148
789.4141	395.2107	8	E	11	1188.6008	594.8040
936.4825	468.7449	9	F	10	1059.5582	530.2827
993.5040	497.2556	10	G	9	912.4898	456.7485
1107.5469	554.2771	11	N	8	855.4683	428.2378
1220.6310	610.8191	12	L	7	741.4254	371.2163
1333.7151	667.3612	13	I	6	628.3413	314.6743
1404.7522	702.8797	14	A	5	515.2572	258.1323
1461.7736	731.3905	15	G	4	444.2201	222.6137
1576.8006	788.9039	16	D	3	387.1987	194.1030
1673.8533	837.4303	17	P	2	272.1717	136.5895
		18	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9881	IPI00843773, IPI00513959, IPI00215801, IPI00163505	1	1	RBM39, RBM39, RBM39, RBM39	4102	2+	-0,0170	0,9999	K.C^PSIAAAIAAVNALHGR.W



Peptide Details

SHOW MODIFICATIONS ›

Scan	4102	Delta Mass	-0.0170	Protein	IPI00163505
Mass	1674.8740	Next	305.000	Fraction	VF_T13h_band06.mzXML
Hyper	618.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
144.0115	72.5094	1	C	17		
241.0642	121.0358	2	P	16	1531.8703	766.4388
328.0963	164.5518	3	S	15	1434.8176	717.9124
441.1803	221.0938	4	I	14	1347.7855	674.3964
512.2174	256.6124	5	A	13	1234.7015	617.8544
583.2545	292.1309	6	A	12	1163.6644	582.3358
654.2917	327.6495	7	A	11	1092.6273	546.8173
767.3757	384.1915	8	I	10	1021.5901	511.2987
838.4128	419.7101	9	A	9	908.5061	454.7567
909.4499	455.2286	10	A	8	837.4690	419.2381
1008.5184	504.7628	11	V	7	766.4318	383.7196
1122.5613	561.7843	12	N	6	667.3634	334.1854
1193.5984	597.3028	13	A	5	553.3205	277.1639
1306.6825	653.8449	14	L	4	482.2834	241.6453
1443.7414	722.3743	15	H	3	369.1993	185.1033
1500.7628	750.8851	16	G	2	232.1404	116.5738
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
C: -17.0265

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9870	IPI00794777, IPI00909207, IPI00027350	1	1	PRDX2, -, PRDX2	4107	2+	-0,0281	0,9998	K.EGGLGPLNIPLLADVTR.R

Peptide Details

SHOW MODIFICATIONS ›

Scan	4107	Delta Mass	-0.0281	Protein	IPI00027350
Mass	1734.9750	Next	270.000	Fraction	VF_T13h_band06.mzXML
Hyper	536.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	75%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

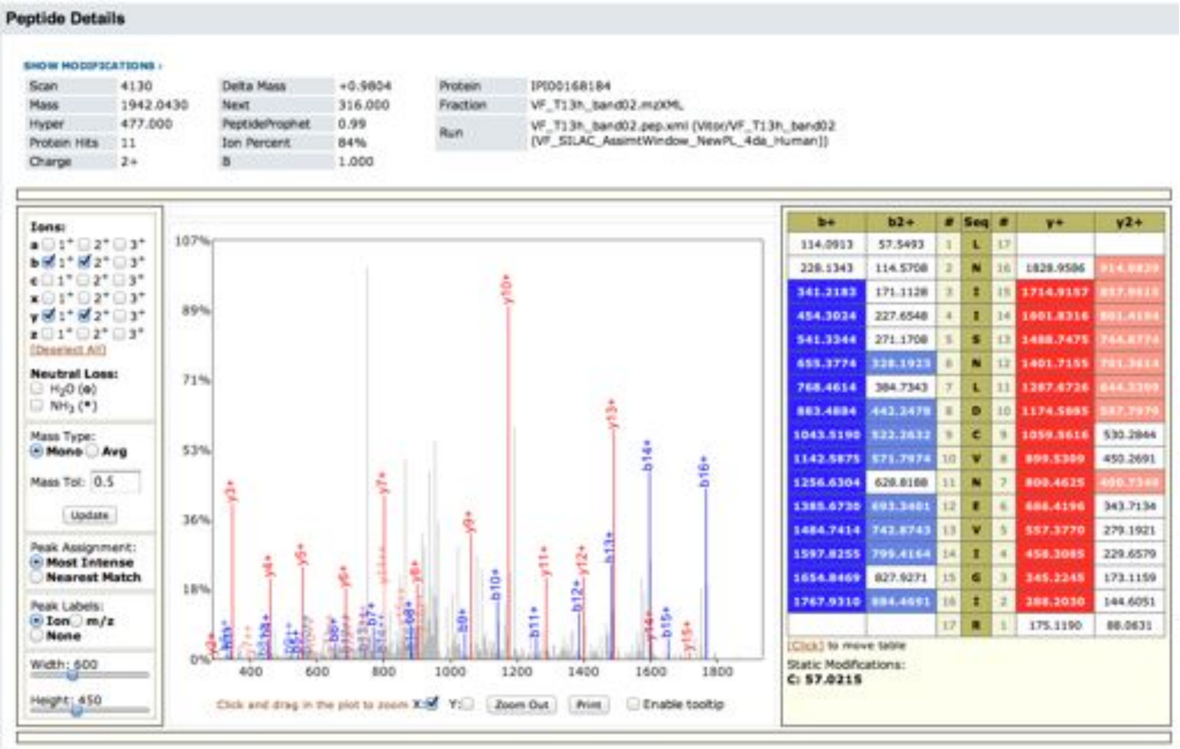
X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	17		
187.0713	94.0393	2	G	16	1605.9323	803.4698
244.0928	122.5500	3	G	15	1548.9108	774.9590
357.1769	179.0921	4	L	14	1491.8893	746.4483
414.1983	207.6028	5	G	13	1378.8053	689.9063
511.2511	256.1292	6	P	12	1321.7838	661.3955
624.3352	312.6712	7	L	11	1224.7310	612.8692
738.3781	369.6927	8	N	10	1111.6470	556.3271
851.4621	426.2347	9	I	9	997.6041	499.3057
948.5149	474.7611	10	P	8	884.5200	442.7636
1061.5990	531.3031	11	L	7	787.4672	394.2373
1174.6830	587.8452	12	L	6	674.3832	337.6952
1245.7201	623.3637	13	A	5	561.2991	281.1532
1360.7471	680.8772	14	D	4	490.2620	245.6346
1459.8155	730.4114	15	V	3	375.2350	188.1212
1560.8632	780.9352	16	T	2	276.1666	138.5870
		17	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8820	IPI00798040, IPI00909011, IPI00168184, IPI00910732, IPI00908543, IPI00910814, IPI00554737, IPI00294178, IPI00874039, IPI00909316, IPI00335449	1	1	PPP2R1A, -, PPP2R1A, -, -, -, PPP2R1A, PPP2R1B, PPP2R1B, -, PPP2R1B	4130	2+	+0,9804	0,9938	R.LNIISNLDCVNEVIGIR.Q



Peptide Details

SHOW MODIFICATIONS ›

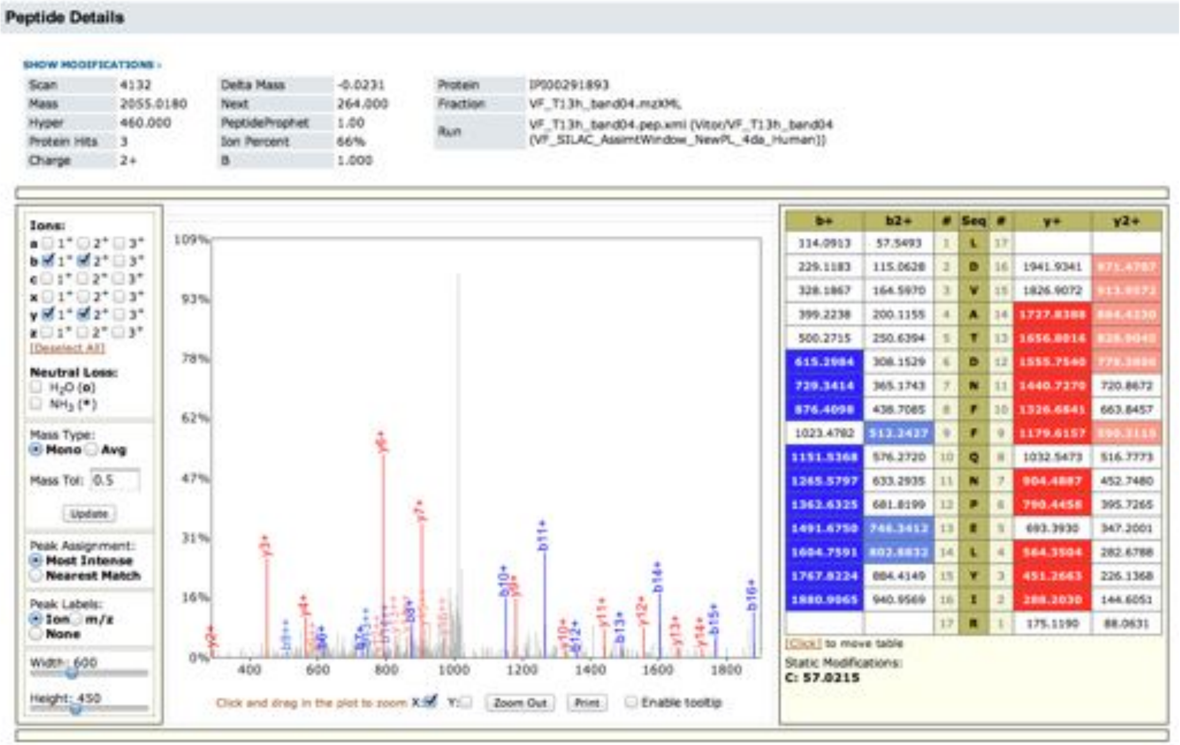
Scan	4130	Delta Mass	+0.9804	Protein	IPI00168184
Mass	1942.0430	Next	316.000	Fraction	VF_T13h_band02.mzXML
Hyper	477.000	PeptideProphet	0.99	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	11	Ion Percent	84%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	17		
228.1343	114.5708	2	N	16	1828.9586	914.9829
341.2183	171.1128	3	I	15	1714.9157	857.9615
454.3024	227.6548	4	I	14	1601.8316	801.4194
541.3344	271.1708	5	S	13	1488.7475	744.8774
655.3774	328.1923	6	N	12	1401.7155	701.3614
768.4614	384.7343	7	L	11	1287.6726	644.3399
883.4884	442.2478	8	D	10	1174.5885	587.7979
1043.5190	522.2632	9	C	9	1059.5616	530.2844
1142.5875	571.7974	10	V	8	899.5309	450.2691
1256.6304	628.8188	11	N	7	800.4625	400.7348
1385.6730	693.3401	12	E	6	686.4196	343.7134
1484.7414	742.8743	13	V	5	557.3770	279.1921
1597.8255	799.4164	14	I	4	458.3085	229.6579
1654.8469	827.9271	15	G	3	345.2245	173.1159
1767.9310	884.4691	16	I	2	288.2030	144.6051
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9807	IPI00749447, IPI00910838, IPI00291893	1	1	DCUN1D1, -, DCUN1D1	4132	2+	-0,0231	0,9997	K.LDVATDNFFQNPELYIR.E



Peptide Details

SHOW MODIFICATIONS »

Scan	4132	Delta Mass	-0.0231	Protein	IPI00291893
Mass	2055.0180	Next	264.000	Fraction	VF_T13h_band04.mzXML
Hyper	460.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	66%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

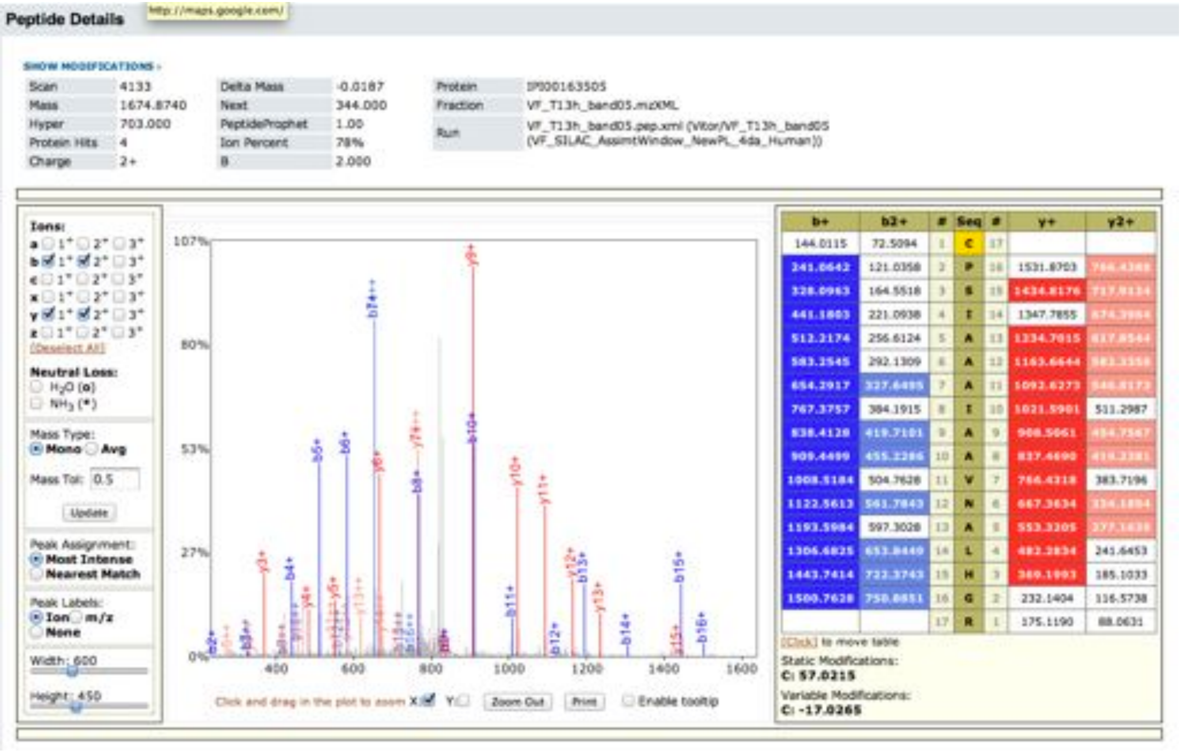
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	17		
229.1183	115.0628	2	D	16	1941.9341	971.4707
328.1867	164.5970	3	V	15	1826.9072	913.9572
399.2238	200.1155	4	A	14	1727.8388	864.4230
500.2715	250.6394	5	T	13	1656.8016	828.9045
615.2984	308.1529	6	D	12	1555.7540	778.3806
729.3414	365.1743	7	N	11	1440.7270	720.8672
876.4098	438.7085	8	F	10	1326.6841	663.8457
1023.4782	512.2427	9	F	9	1179.6157	590.3115
1151.5368	576.2720	10	Q	8	1032.5473	516.7773
1265.5797	633.2935	11	N	7	904.4887	452.7480
1362.6325	681.8199	12	P	6	790.4458	395.7265
1491.6750	746.3412	13	E	5	693.3930	347.2001
1604.7591	802.8832	14	L	4	564.3504	282.6788
1767.8224	884.4149	15	Y	3	451.2663	226.1368
1880.9065	940.9569	16	I	2	288.2030	144.6051
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9877	IPI00843773, IPI00513959, IPI00215801, IPI00163505	1	1	RBM39, RBM39, RBM39, RBM39	4133	2+	-0,0187	1,0000	K.C^PSIAAAIAAVNALHGR.W



Peptide Details

http://maps.google.com/

SHOW MODIFICATIONS ›

Scan	4133	Delta Mass	-0.0187	Protein	IPI00163505
Mass	1674.8740	Next	344.000	Fraction	VF_T13h_band05.mzXML
Hyper	703.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	78%		
Charge	2+	B	2.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600
Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
144.0115	72.5094	1	C	17		
241.0642	121.0358	2	P	16	1531.8703	766.4388
328.0963	164.5518	3	S	15	1434.8176	717.9124
441.1803	221.0938	4	I	14	1347.7855	674.3964
512.2174	256.6124	5	A	13	1234.7015	617.8544
583.2545	292.1309	6	A	12	1163.6644	582.3358
654.2917	327.6495	7	A	11	1092.6273	546.8173
767.3757	384.1915	8	I	10	1021.5901	511.2987
838.4128	419.7101	9	A	9	908.5061	454.7567
909.4499	455.2286	10	A	8	837.4690	419.2381
1008.5184	504.7628	11	V	7	766.4318	383.7196
1122.5613	561.7843	12	N	6	667.3634	334.1854
1193.5984	597.3028	13	A	5	553.3205	277.1639
1306.6825	653.8449	14	L	4	482.2834	241.6453
1443.7414	722.3743	15	H	3	369.1993	185.1033
1500.7628	750.8851	16	G	2	232.1404	116.5738
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
C: -17.0265

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9793	IPI00236575, IPI00216423, IPI00892957, IPI00396534, IPI00414027	1	1	ITSN2, ITSN2, ITSN2, ITSN2, ITSN2	4151	2+	-0,0208	0,9998	K.AGQPLPLTLPPELVPPSFR.G

Peptide Details

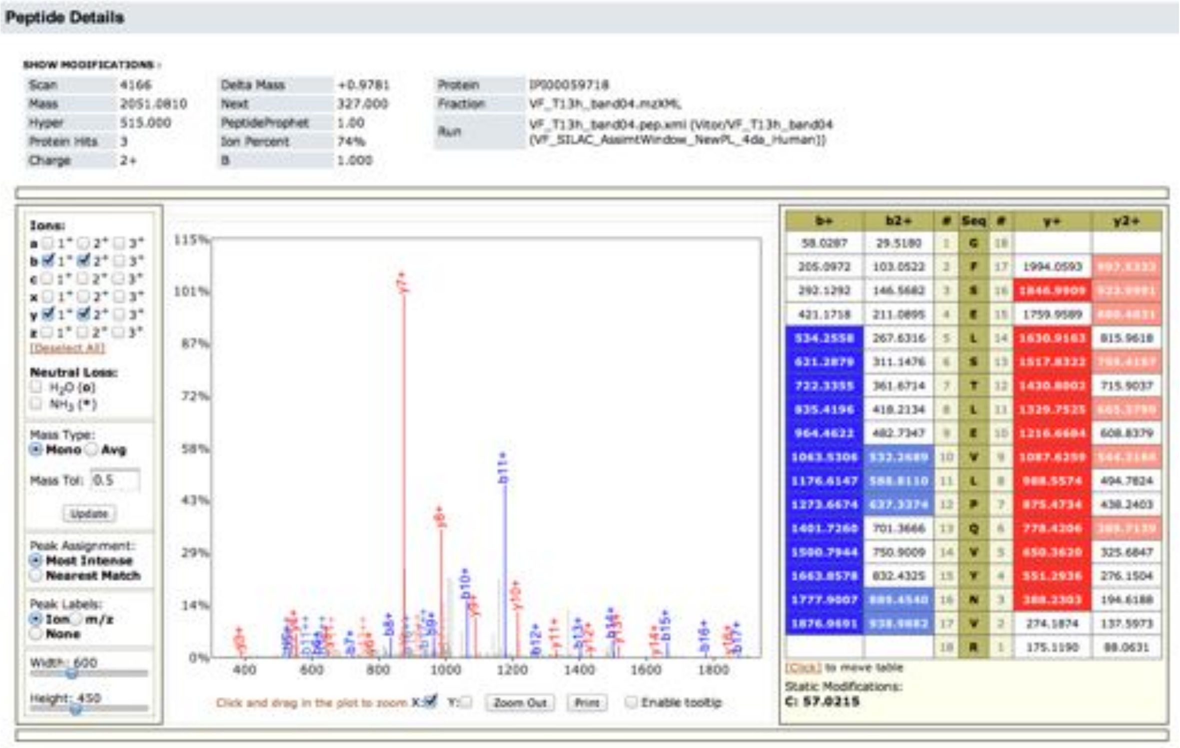
Scan	4151	Delta Mass	-0.0208	Protein	IPI00216423
Mass	2029.1480	Next	288.000	Fraction	VF_T13h_band01.mzXML
Hyper	523.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	67%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	19		
129.0659	65.0366	2	G	18	1958.1110	979.5591
257.1244	129.0659	3	Q	17	1901.0895	951.0484
354.1772	177.5922	4	P	16	1773.0309	887.0191
467.2613	234.1343	5	L	15	1675.9782	838.4927
564.3140	282.6606	6	P	14	1562.8941	781.9507
677.3981	339.2027	7	L	13	1465.8413	733.4243
778.4458	389.7265	8	T	12	1352.7573	676.8823
891.5298	446.2686	9	L	11	1251.7096	626.3584
988.5826	494.7949	10	P	10	1138.6255	569.8164
1085.6354	543.3213	11	P	9	1041.5728	521.2900
1214.6780	607.8426	12	E	8	944.5200	472.7636
1327.7620	664.3846	13	L	7	815.4774	408.2423
1426.8304	713.9189	14	V	6	702.3933	351.7003
1523.8832	762.4452	15	P	5	603.3249	302.1661
1620.9360	810.9716	16	P	4	506.2722	253.6397
1707.9680	854.4876	17	S	3	409.2194	205.1133
1855.0364	928.0218	18	P	2	322.1874	161.5973
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9230	IPI00059718, IPI00783197, IPI00177856	1	1	C14orf172, TRM61, C14orf172	4166	2+	+0,9781	0,9955	R.GFSELSTLEVLPQVYNVR.T



Peptide Details

SHOW MODIFICATIONS :

Scan	4166	Delta Mass	+0.9781	Protein	IPI00059718
Mass	2051.0810	Next	327.000	Fraction	VF_T13h_band04.mzXML
Hyper	515.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	74%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	18		
205.0972	103.0522	2	F	17	1994.0593	997.5333
292.1292	146.5682	3	S	16	1846.9909	923.9991
421.1718	211.0895	4	E	15	1759.9589	880.4831
534.2558	267.6316	5	L	14	1630.9163	815.9618
621.2879	311.1476	6	S	13	1517.8322	759.4197
722.3355	361.6714	7	T	12	1430.8002	715.9037
835.4196	418.2134	8	L	11	1329.7525	665.3799
964.4622	482.7347	9	E	10	1216.6684	608.8379
1063.5306	532.2689	10	V	9	1087.6259	544.3166
1176.6147	588.8110	11	L	8	988.5574	494.7824
1273.6674	637.3374	12	P	7	875.4734	438.2403
1401.7260	701.3666	13	Q	6	778.4206	389.7139
1500.7944	750.9009	14	V	5	650.3620	325.6847
1663.8578	832.4325	15	Y	4	551.2936	276.1504
1777.9007	889.4540	16	N	3	388.2303	194.6188
1876.9691	938.9882	17	V	2	274.1874	137.5973
		18	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00027493, IPI00554722, IPI00554702, IPI00604710, IPI00554611, IPI00554481	1	1	SLC3A2, LOC442497, LOC442497, LOC442497, LOC442497, LOC442497	4177	2+	-0,0132	1,0000	K.GQSEDPGSLLSLFR.R

Peptide Details

SHOW MODIFICATIONS ›

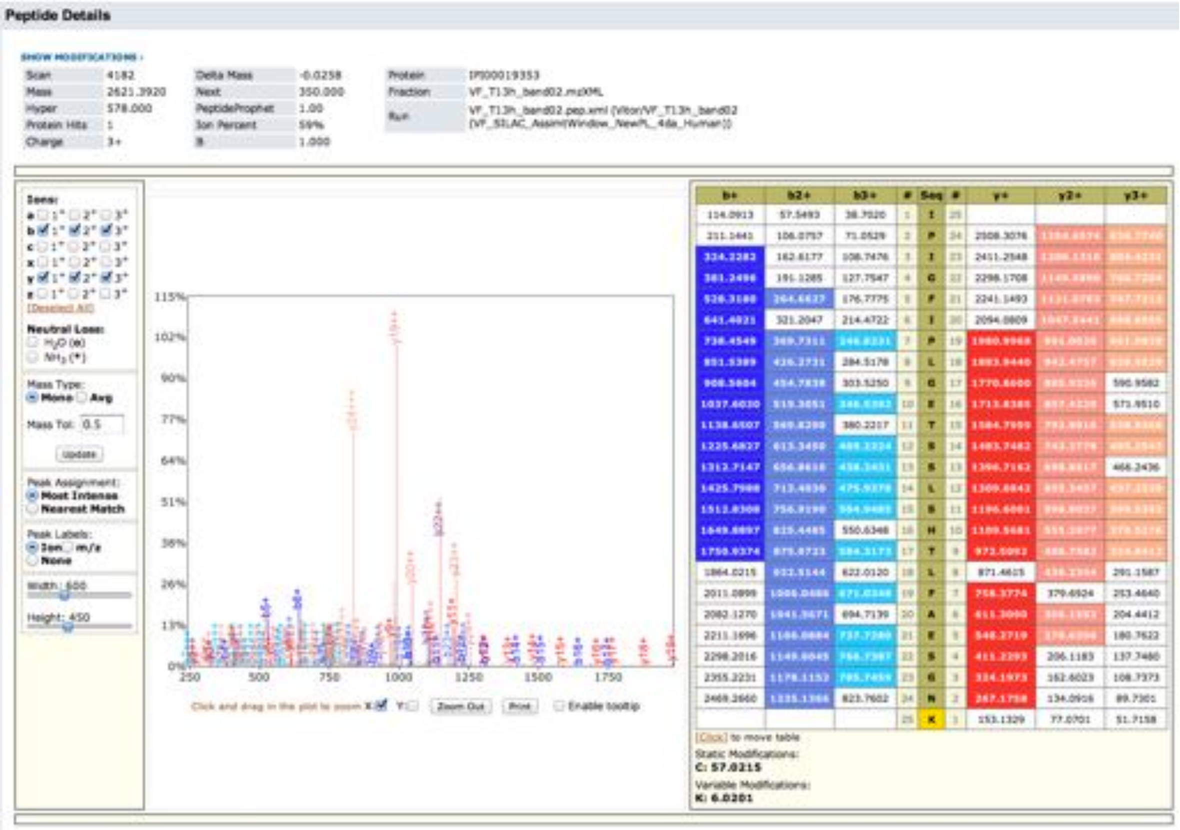
Scan	4177	Delta Mass	-0.0132	Protein	IPI00027493
Mass	1505.7590	Next	269.000	Fraction	VF_T13h_band03.mzXML
Hyper	603.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	81%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	14		
186.0873	93.5473	2	Q	13	1448.7380	724.8726
273.1193	137.0633	3	S	12	1320.6794	660.8433
402.1619	201.5846	4	E	11	1233.6474	617.3273
517.1889	259.0981	5	D	10	1104.6048	552.8060
614.2416	307.6245	6	P	9	989.5778	495.2926
671.2631	336.1352	7	G	8	892.5251	446.7662
758.2951	379.6512	8	S	7	835.5036	418.2554
871.3792	436.1932	9	L	6	748.4716	374.7394
984.4633	492.7353	10	L	5	635.3875	318.1974
1071.4953	536.2513	11	S	4	522.3035	261.6554
1184.5794	592.7933	12	L	3	435.2714	218.1394
1331.6478	666.3275	13	F	2	322.1874	161.5973
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9819	IPI00019353	1	1	FLJ10842	4182	3+	-0,0258	1,0000	K.IPIGFIPLGETSSLSHTLFAESGNK'.V



Peptide Details

SHOW MODIFICATIONS ›

Scan	4182	Delta Mass	-0.0258	Protein	IPI00019353
Mass	2621.3920	Next	350.000	Fraction	VF_T13h_band02.mzXML
Hyper	578.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Viton/VF_T13h_band02 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	59%		
Charge	3+	B	1.000		

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
114.0913	57.5493	38.7020	1	I	25			
211.1441	106.0757	71.0529	2	P	24	2508.3076	1254.6574	836.7740
324.2282	162.6177	108.7476	3	I	23	2411.2548	1206.1310	804.4231
381.2496	191.1285	127.7547	4	G	22	2298.1708	1149.5890	766.7284
528.3180	264.6627	176.7775	5	F	21	2241.1493	1121.0783	747.7212
641.4021	321.2047	214.4722	6	I	20	2094.0809	1047.5441	698.6985
738.4549	369.7311	246.8231	7	P	19	1980.9968	991.0020	661.0038
851.5389	426.2731	284.5178	8	L	18	1883.9440	942.4757	628.6529
908.5604	454.7838	303.5250	9	G	17	1770.8600	885.9336	590.9582
1037.6030	519.3051	346.5392	10	E	16	1713.8385	857.4228	571.9510
1138.6507	569.8290	380.2217	11	T	15	1584.7959	792.9016	528.9368
1225.6827	613.3450	409.2324	12	S	14	1483.7482	742.3778	495.2547
1312.7147	656.8610	438.2431	13	S	13	1396.7162	698.8617	466.2436
1425.7988	713.4030	475.9378	14	L	12	1309.6842	655.3457	437.2328
1512.8308	756.9190	504.9485	15	S	11	1196.6001	598.8037	399.5382
1649.8897	825.4485	550.6348	16	H	10	1109.5681	555.2877	370.5278
1750.9374	875.9723	584.3173	17	T	9	972.5092	486.7582	324.8412
1864.0215	932.5144	622.0120	18	L	8	871.4615	436.2344	291.1587
2011.0899	1006.0486	671.0348	19	F	7	758.3774	379.6924	253.4640
2082.1270	1041.5671	694.7139	20	A	6	611.3090	306.1581	204.4412
2211.1696	1106.0884	737.7280	21	E	5	540.2719	270.6396	180.7622
2298.2016	1149.6045	766.7387	22	S	4	411.2293	206.1183	137.7480
2355.2231	1178.1152	785.7459	23	G	3	324.1973	162.6023	108.7373
2469.2660	1235.1366	823.7602	24	N	2	267.1758	134.0916	89.7301
			25	K	1	153.1329	77.0701	51.7158

[Click] to move table

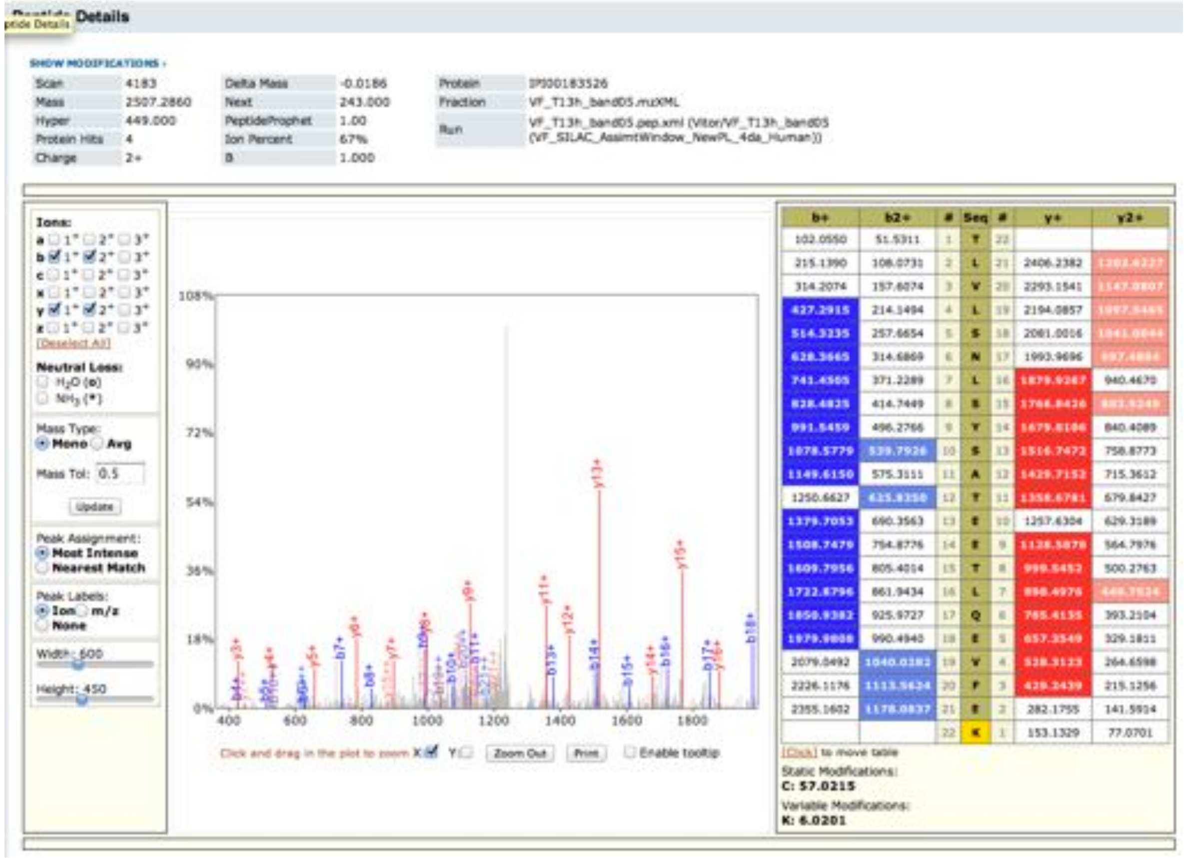
Static Modifications:

C: 57.0215

Variable Modifications:

K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9852	IPI00183526, IPI00444262, IPI00827674, IPI00604620	1	1	NCL, NCL, NCL, NCL	4183	2+	-0,0186	0,9998	K.TLVLSNLSYSATEETLQEVFEK'.A



Scan	4183	Delta Mass	-0.0186
Mass	2507.2860	Next	243.000
Hyper	449.000	PeptideProphet	1.00
Protein Hits	4	Ion Percent	67%
Charge	2+	B	1.000

Protein	IPI00183526
Fraction	VF_T13h_bandD5.mzXML
Run	VF_T13h_bandD5.pep.xml (Vitor/VF_T13h_bandD5 (VF_SILAC_AssimtWindow_NewPL_4da_Human))

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	22		
215.1390	108.0731	2	L	21	2406.2382	1203.6227
314.2074	157.6074	3	V	20	2293.1541	1147.0807
427.2915	214.1494	4	L	19	2194.0857	1097.5465
514.3235	257.6654	5	S	18	2081.0016	1041.0044
628.3665	314.6869	6	N	17	1993.9696	997.4884
741.4505	371.2289	7	L	16	1879.9267	940.4670
828.4825	414.7449	8	S	15	1766.8426	883.9249
991.5459	496.2766	9	Y	14	1679.8106	840.4089
1078.5779	539.7926	10	S	13	1516.7472	758.8773
1149.6150	575.3111	11	A	12	1429.7152	715.3612
1250.6627	625.8350	12	T	11	1358.6781	679.8427
1379.7053	690.3563	13	E	10	1257.6304	629.3189
1508.7479	754.8776	14	E	9	1128.5878	564.7976
1609.7956	805.4014	15	T	8	999.5452	500.2763
1722.8796	861.9434	16	L	7	898.4976	448.7524
1850.9382	925.9727	17	Q	6	785.4135	393.2104
1979.9808	990.4940	18	E	5	657.3549	329.1811
2079.0492	1040.0182	19	V	4	528.3123	264.6598
2226.1176	1113.5624	20	F	3	429.2439	215.1256
2355.1602	1178.0837	21	E	2	282.1755	141.5914
		22	K	1	153.1329	77.0701

Static Modifications:
C: 57.0215
Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9793	IPI00644989, IPI00299571	1	1	P5, PDIA6	4190	2+	-0,0157	0,9996	R.TGEAIVDAALSALR.Q

Peptide Details

Scan	4190	Delta Mass	-0.0157	Protein	IPI00299571
Mass	1386.7590	Next	363.000	Fraction	VF_T13h_band04.mzXML
Hyper	547.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	62%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

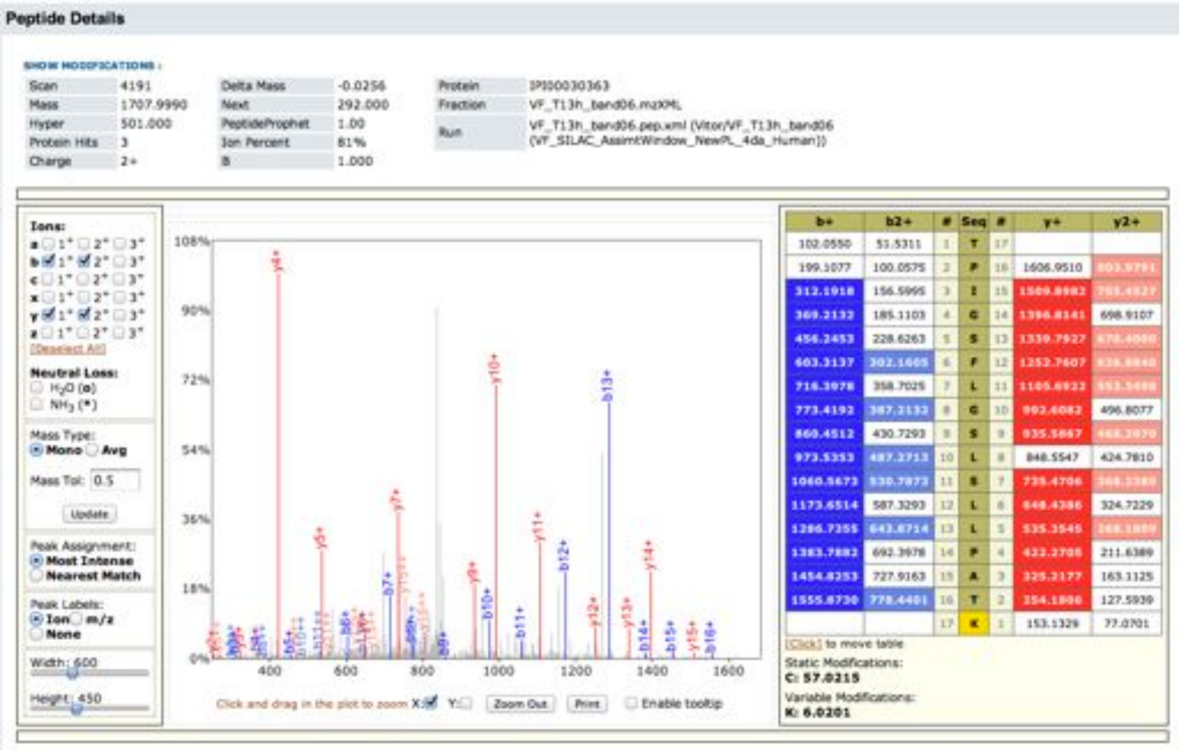
X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
159.0764	80.0418	2	G	13	1285.7110	643.3592
288.1190	144.5631	3	E	12	1228.6896	614.8484
359.1561	180.0817	4	A	11	1099.6470	550.3271
472.2402	236.6237	5	I	10	1028.6099	514.8086
571.3086	286.1579	6	V	9	915.5258	458.2665
686.3355	343.6714	7	D	8	816.4574	408.7323
757.3727	379.1900	8	A	7	701.4304	351.2189
828.4098	414.7085	9	A	6	630.3933	315.7003
941.4938	471.2506	10	L	5	559.3562	280.1817
1028.5259	514.7666	11	S	4	446.2722	223.6397
1099.5630	550.2851	12	A	3	359.2401	180.1237
1212.6470	606.8272	13	L	2	288.2030	144.6051
		14	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9849	IPI00062003, IPI00440499, IPI00030363	1	1	ACAT1, ACAT1, ACAT1	4191	2+	-0,0256	0,9996	R.TPIGSFLGSLSLLPATK'.L



Peptide Details

SHOW MODIFICATIONS :

Scan	4191	Delta Mass	-0.0256	Protein	IPI00030363
Mass	1707.9990	Next	292.000	Fraction	VF_T13h_band06.mzXML
Hyper	501.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

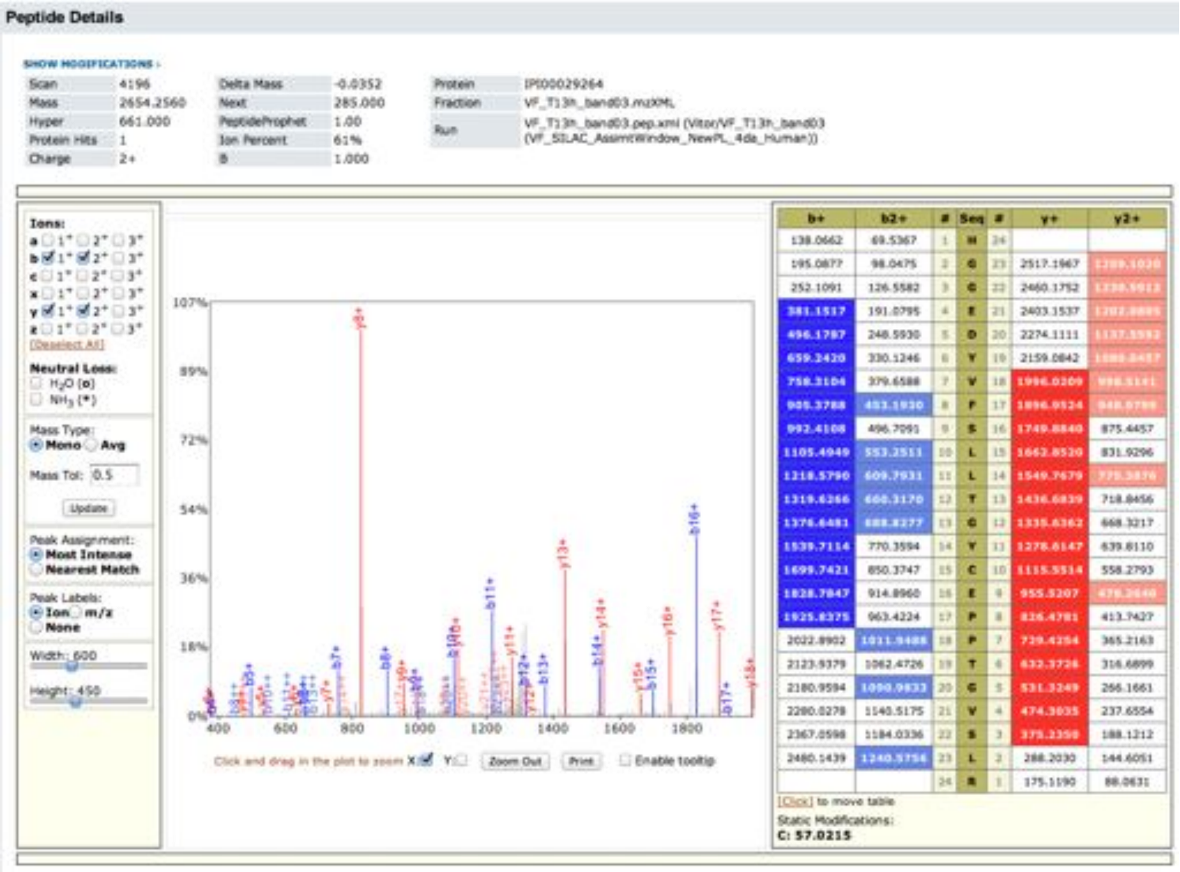
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	17		
199.1077	100.0575	2	P	16	1606.9510	803.9791
312.1918	156.5995	3	I	15	1509.8982	755.4527
369.2132	185.1103	4	G	14	1396.8141	698.9107
456.2453	228.6263	5	S	13	1339.7927	670.4000
603.3137	302.1605	6	F	12	1252.7607	626.8840
716.3978	358.7025	7	L	11	1105.6922	553.3498
773.4192	387.2132	8	G	10	992.6082	496.8077
860.4512	430.7293	9	S	9	935.5867	468.2970
973.5353	487.2713	10	L	8	848.5547	424.7810
1060.5673	530.7873	11	S	7	735.4706	368.2389
1173.6514	587.3293	12	L	6	648.4386	324.7229
1286.7355	643.8714	13	L	5	535.3545	268.1809
1383.7882	692.3978	14	P	4	422.2705	211.6389
1454.8253	727.9163	15	A	3	325.2177	163.1125
1555.8730	778.4401	16	T	2	254.1806	127.5939
		17	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00029264	1	1	CYC1	4196	2+	-0,0352	1,0000	R.HGGEDYVFSLLTGYCEPPTGVSLR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	4196	Delta Mass	-0.0352	Protein	IPI00029264
Mass	2654.2560	Next	285.000	Fraction	VF_T13h_band03.mzXML
Hyper	661.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	61%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

Height: 450

X ☑ Y ☐

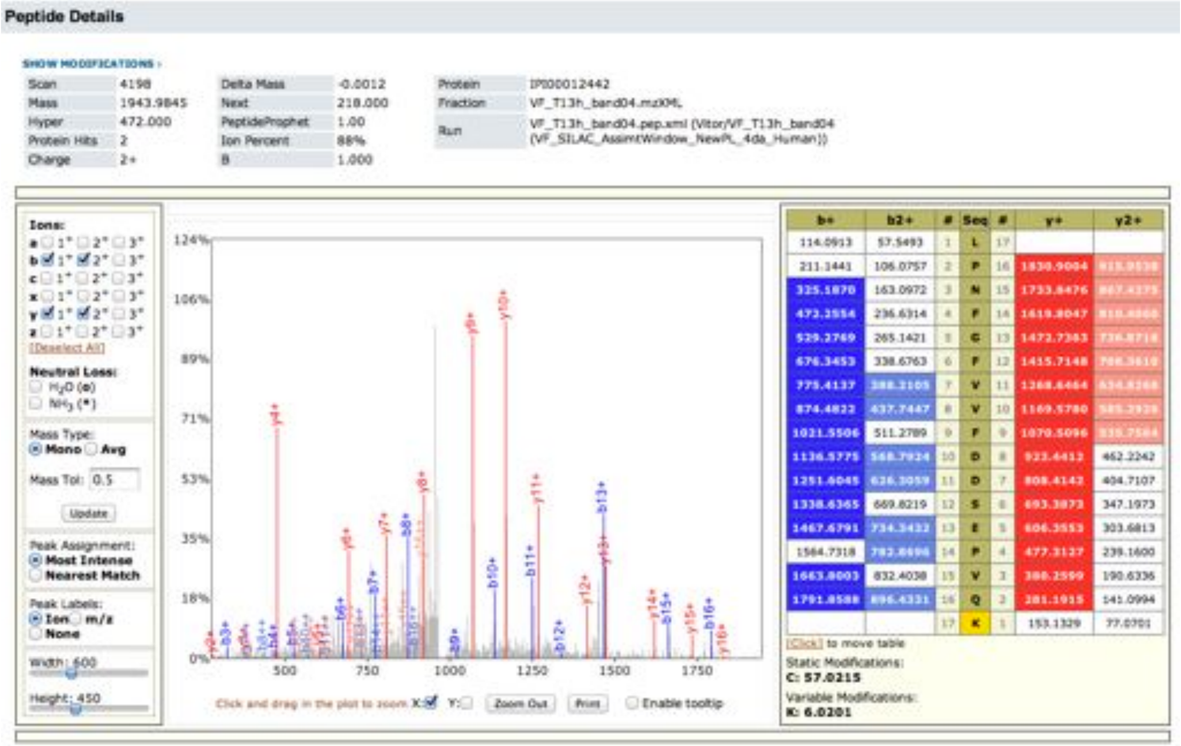
☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
138.0662	69.5367	1	H	24		
195.0877	98.0475	2	G	23	2517.1967	1259.1020
252.1091	126.5582	3	G	22	2460.1752	1230.5912
381.1517	191.0795	4	E	21	2403.1537	1202.0805
496.1787	248.5930	5	D	20	2274.1111	1137.5592
659.2420	330.1246	6	Y	19	2159.0842	1080.0457
758.3104	379.6588	7	V	18	1996.0209	998.5141
905.3788	453.1930	8	F	17	1896.9524	948.9798
992.4108	496.7091	9	S	16	1749.8840	875.4457
1105.4949	553.2511	10	L	15	1662.8520	831.9296
1218.5790	609.7931	11	L	14	1549.7679	775.3876
1319.6266	660.3170	12	T	13	1436.6839	718.8456
1376.6481	688.8277	13	G	12	1335.6362	668.3217
1539.7114	770.3594	14	Y	11	1278.6147	639.8110
1699.7421	850.3747	15	C	10	1115.5514	558.2793
1828.7847	914.8960	16	E	9	955.5207	478.2640
1925.8375	963.4224	17	P	8	826.4781	413.7427
2022.8902	1011.9488	18	P	7	729.4254	365.2163
2123.9379	1062.4726	19	T	6	632.3726	316.6899
2180.9594	1090.9833	20	G	5	531.3249	266.1661
2280.0278	1140.5175	21	V	4	474.3035	237.6554
2367.0598	1184.0336	22	S	3	375.2350	188.1212
2480.1439	1240.5756	23	L	2	288.2030	144.6051
		24	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9837	IPI00442863, IPI00012442	1	1	G3BP1, G3BP	4198	2+	-0,0012	0,9999	K.LPNFGFVVFDDSEPVQK'.V



Peptide Details

SHOW MODIFICATIONS ›

Scan	4198	Delta Mass	-0.0012	Protein	IPI00012442
Mass	1943.9845	Next	218.000	Fraction	VF_T13h_band04.mzXML
Hyper	472.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

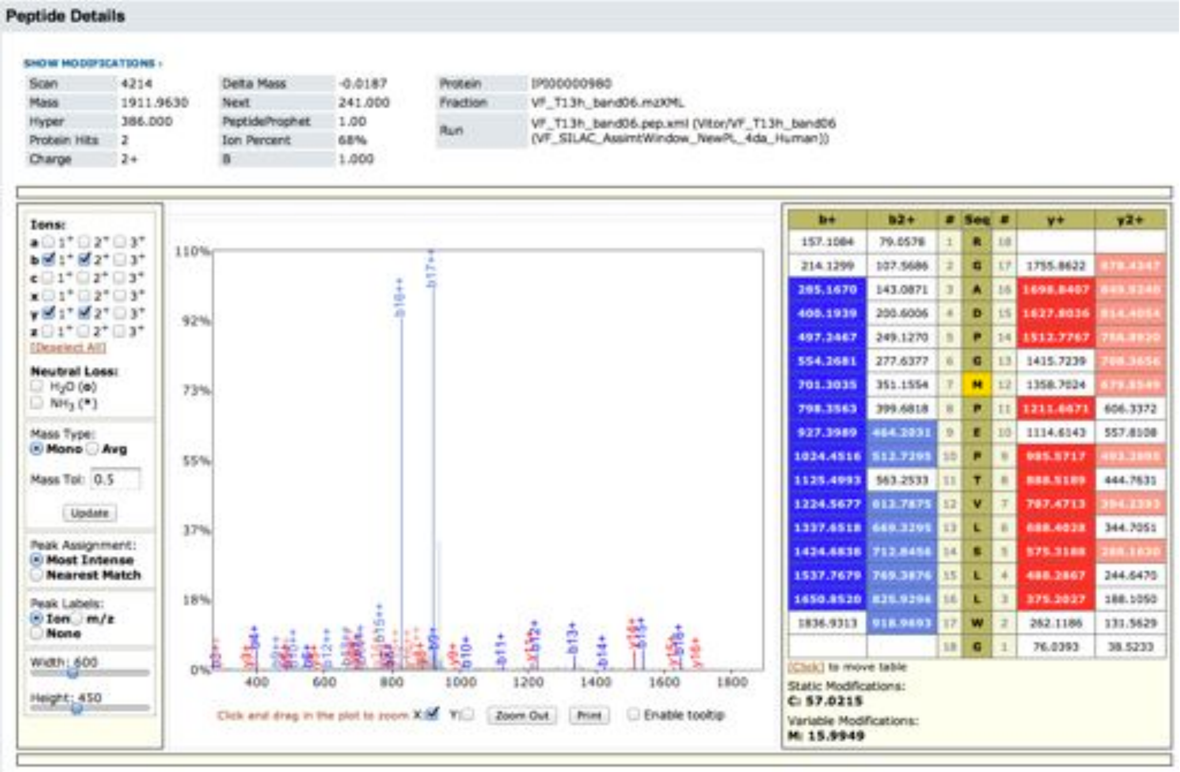
b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	17		
211.1441	106.0757	2	P	16	1830.9004	915.9538
325.1870	163.0972	3	N	15	1733.8476	867.4275
472.2554	236.6314	4	F	14	1619.8047	810.4060
529.2769	265.1421	5	G	13	1472.7363	736.8718
676.3453	338.6763	6	F	12	1415.7148	708.3610
775.4137	388.2105	7	V	11	1268.6464	634.8268
874.4822	437.7447	8	V	10	1169.5780	585.2928
1021.5506	511.2789	9	F	9	1070.5096	535.7584
1136.5775	568.7924	10	D	8	923.4412	462.2242
1251.6045	626.3059	11	D	7	808.4142	404.7107
1338.6365	669.8219	12	S	6	693.3873	347.1973
1467.6791	734.3432	13	E	5	606.3553	303.6813
1564.7318	782.8696	14	P	4	477.3127	239.1600
1663.8003	832.4038	15	V	3	380.2599	190.6336
1791.8588	896.4331	16	Q	2	281.1915	141.0994
		17	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9650	IPI00893222, IPI00000980	1	1	TOMM, TOM7	4214	2+	-0,0187	0,9977	K.RGADPGM"PEPTVLSLLWG.-



Peptide Details

SHOW MODIFICATIONS ›

Scan	4214	Delta Mass	-0.0187	Protein	IPI00000980
Mass	1911.9630	Next	241.000	Fraction	VF_T13h_band06.mzXML
Hyper	386.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	68%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
157.1084	79.0578	1	R	18		
214.1299	107.5686	2	G	17	1755.8622	878.4347
285.1670	143.0871	3	A	16	1698.8407	849.9240
400.1939	200.6006	4	D	15	1627.8036	814.4054
497.2467	249.1270	5	P	14	1512.7767	756.8920
554.2681	277.6377	6	G	13	1415.7239	708.3656
701.3035	351.1554	7	M	12	1358.7024	679.8549
798.3563	399.6818	8	P	11	1211.6471	606.3372
927.3989	464.2031	9	E	10	1114.6143	557.8108
1024.4516	512.7295	10	P	9	985.5717	493.2895
1125.4993	563.2533	11	T	8	888.5189	444.7631
1224.5677	612.7875	12	V	7	787.4713	394.2393
1337.6518	669.3295	13	L	6	688.4028	344.7051
1424.6838	712.8456	14	S	5	575.3188	288.1630
1537.7679	769.3876	15	L	4	488.2867	244.6470
1650.8520	825.9296	16	L	3	375.2027	188.1050
1836.9313	918.9693	17	W	2	262.1186	131.5629
		18	G	1	76.0393	38.5233

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00848150, IPI00909140, IPI00647896, IPI00640115, IPI00645452, IPI00011654, IPI00007752, IPI00013475, IPI00031370, IPI00646779, IPI00013683, IPI00152453	1	1	LOC92755, -, TUBB, TUBB3, TUBB, TUBB, TUBB2C, TUBB2A, TUBB2B, TUBB6, TUBB3, TUBB3	4217	2+	-0,0198	1,0000	K.GHYTEGAELVDSVLDVVR.K

Peptide Details

Scan	4217	Delta Mass	-0.0198	Protein	IPI00007752
Mass	1958.9820	Next	399.000	Fraction	VF_T13h_band03.mzXML
Hyper	861.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	12	Ion Percent	88%		
Charge	2+	B	2.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

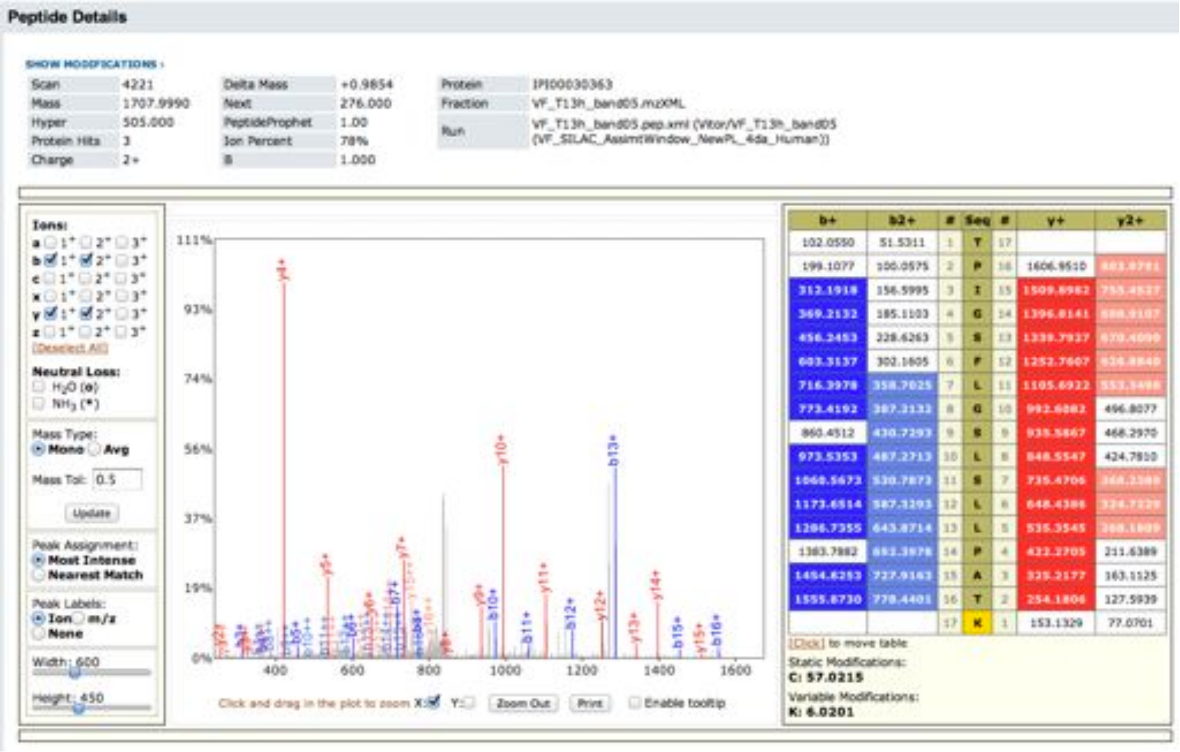
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	18		
195.0877	98.0475	2	H	17	1901.9603	951.4838
358.1510	179.5791	3	Y	16	1764.9014	882.9543
459.1987	230.1030	4	T	15	1601.8381	801.4227
588.2413	294.6243	5	E	14	1500.7904	750.8988
645.2627	323.1350	6	G	13	1371.7478	686.3775
716.2998	358.6536	7	A	12	1314.7264	657.8668
845.3424	423.1748	8	E	11	1243.6892	622.3483
958.4265	479.7169	9	L	10	1114.6467	557.8270
1057.4949	529.2511	10	V	9	1001.5626	501.2849
1172.5218	586.7646	11	D	8	902.4942	451.7507
1259.5539	630.2806	12	S	7	787.4672	394.2373
1358.6223	679.8148	13	V	6	700.4352	350.7212
1471.7063	736.3568	14	L	5	601.3668	301.1870
1586.7333	793.8703	15	D	4	488.2827	244.6450
1685.8017	843.4045	16	V	3	373.2558	187.1315
1784.8701	892.9387	17	V	2	274.1874	137.5973
		18	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9650	IPI00062003, IPI00440499, IPI00030363	1	1	ACAT1, ACAT1, ACAT1	4221	2+	+0,9854	0,9981	R.TPIGSFLGSLSLLPATK'.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4221	Delta Mass	+0.9854	Protein	IPI00030363
Mass	1707.9990	Next	276.000	Fraction	VF_T13h_band05.mzXML
Hyper	505.000	PeptideProphet	1.00	Run	VF_T13h_band05.pep.xml (Vitor/VF_T13h_band05 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

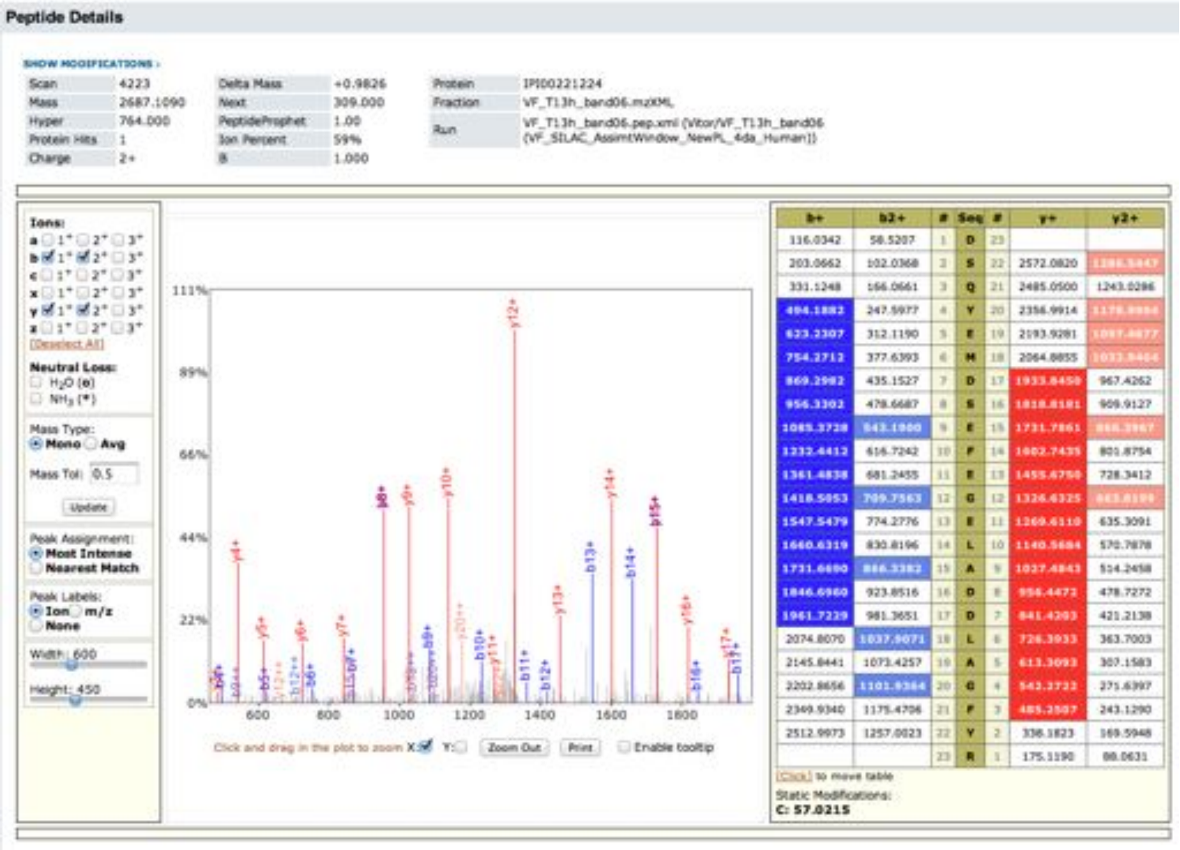
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	17		
199.1077	100.0575	2	P	16	1606.9510	803.9791
312.1918	156.5995	3	I	15	1509.8982	755.4527
369.2132	185.1103	4	G	14	1396.8141	698.9107
456.2453	228.6263	5	S	13	1339.7927	670.4000
603.3137	302.1605	6	F	12	1252.7607	626.8840
716.3978	358.7025	7	L	11	1105.6922	553.3498
773.4192	387.2133	8	G	10	992.6082	496.8077
860.4512	430.7293	9	S	9	935.5867	468.2970
973.5353	487.2713	10	L	8	848.5547	424.7810
1060.5673	530.7873	11	S	7	735.4706	368.2389
1173.6514	587.3293	12	L	6	648.4386	324.7229
1286.7355	643.8714	13	L	5	535.3545	268.1809
1383.7882	692.3978	14	P	4	422.2705	211.6389
1454.8253	727.9163	15	A	3	325.2177	163.1125
1555.8730	778.4401	16	T	2	254.1806	127.5939
		17	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9817	IPI00221224	1	1	ANPEP	4223	2+	+0,9826	0,9993	K.DSQYEMDSEFEGELADDLAGFYR.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	4223	Delta Mass	+0.9826	Protein	IPI00221224
Mass	2687.1090	Next	309.000	Fraction	VF_T13h_band06.mzXML
Hyper	764.000	PeptideProphet	1.00	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	59%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

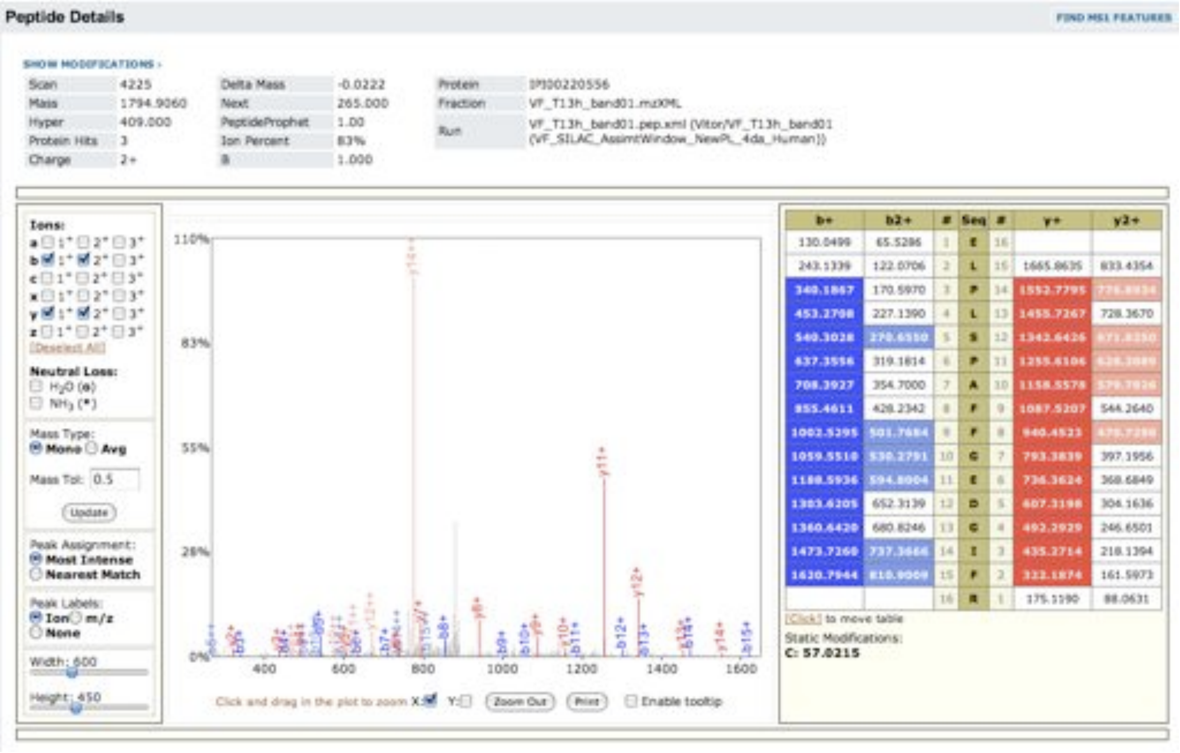
Click and drag in the plot to zoom X:☑ Y:☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	23		
203.0662	102.0368	2	S	22	2572.0820	1286.5447
331.1248	166.0661	3	Q	21	2485.0500	1243.0286
494.1882	247.5977	4	Y	20	2356.9914	1178.9994
623.2307	312.1190	5	E	19	2193.9281	1097.4677
754.2712	377.6393	6	M	18	2064.8855	1032.9464
869.2982	435.1527	7	D	17	1933.8450	967.4262
956.3302	478.6687	8	S	16	1818.8181	909.9127
1085.3728	543.1900	9	E	15	1731.7861	866.3967
1232.4412	616.7242	10	F	14	1602.7435	801.8754
1361.4838	681.2455	11	E	13	1455.6750	728.3412
1418.5053	709.7563	12	G	12	1326.6325	663.8199
1547.5479	774.2776	13	E	11	1269.6110	635.3091
1660.6319	830.8196	14	L	10	1140.5684	570.7878
1731.6690	866.3382	15	A	9	1027.4843	514.2458
1846.6960	923.8516	16	D	8	956.4472	478.7272
1961.7229	981.3651	17	D	7	841.4203	421.2138
2074.8070	1037.9071	18	L	6	726.3933	363.7003
2145.8441	1073.4257	19	A	5	613.3093	307.1583
2202.8656	1101.9364	20	G	4	542.2722	271.6397
2349.9340	1175.4706	21	F	3	485.2507	243.1290
2512.9973	1257.0023	22	Y	2	338.1823	169.5948
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9546	IPI00220556, IPI00645060, IPI00332106	1	1	PBXIP1, PBXIP1, PBXIP1	4225	2+	-0,0222	0,9983	K.ELPLSPAFFGEDGIFR.H

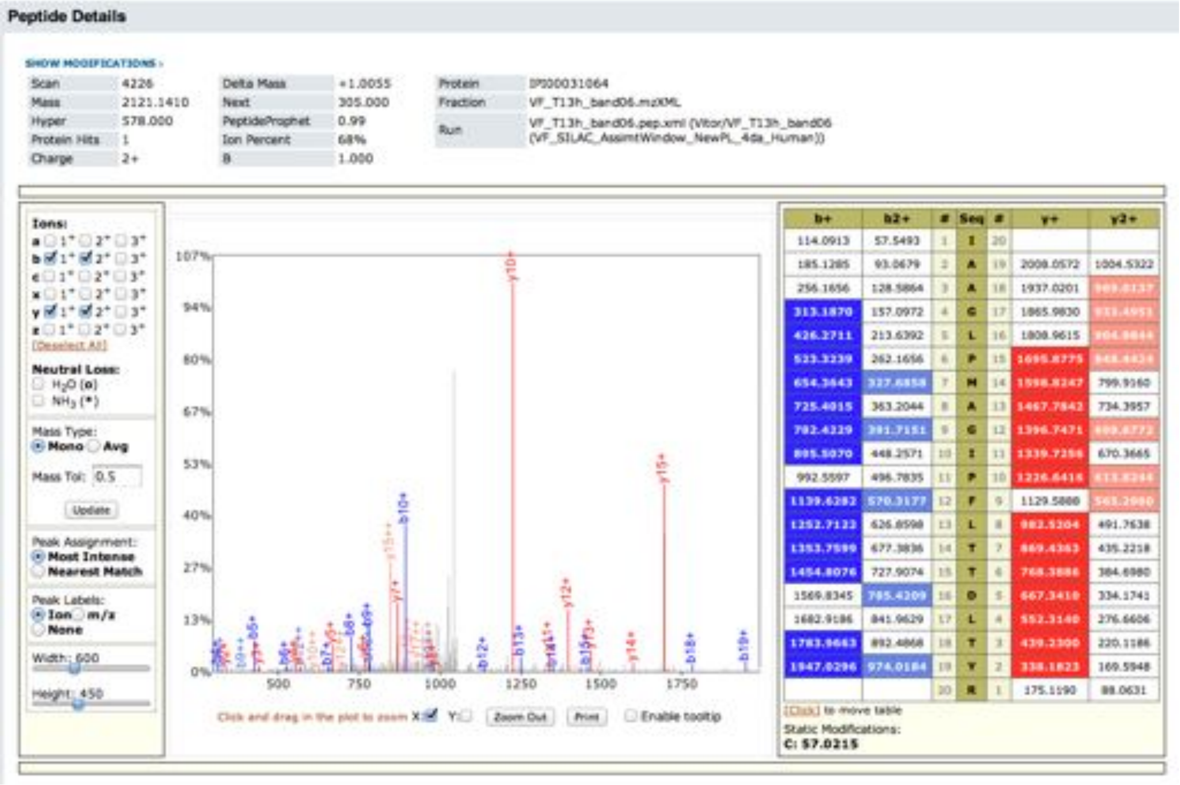


Scan	4225	Delta Mass	-0.0222	Protein	IPI00220556
Mass	1794.9060	Next	265.000	Fraction	VF_T13h_band01.mzXML
Hyper	409.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	83%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	16		
243.1339	122.0706	2	L	15	1665.8635	833.4354
340.1867	170.5970	3	P	14	1552.7795	776.8934
453.2708	227.1390	4	L	13	1455.7267	728.3670
540.3028	270.6550	5	S	12	1342.6426	671.8250
637.3556	319.1814	6	P	11	1255.6106	628.3089
708.3927	354.7000	7	A	10	1158.5578	579.7826
855.4611	428.2342	8	F	9	1087.5207	544.2640
1002.5295	501.7684	9	F	8	940.4523	470.7298
1059.5510	530.2791	10	G	7	793.3839	397.1956
1188.5936	594.8004	11	E	6	736.3624	368.6849
1303.6205	652.3139	12	D	5	607.3198	304.1636
1360.6420	680.8246	13	G	4	492.2929	246.6501
1473.7260	737.3666	14	I	3	435.2714	218.1394
1620.7944	810.9009	15	F	2	322.1874	161.5973
		16	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9322	IPI00031064	1	1	TMEM126A	4226	2+	+1,0055	0,9944	R.IAAGLPMAGIPFLTTDLTYR.C



Peptide Details

SHOW MODIFICATIONS ›

Scan	4226	Delta Mass	+1.0055	Protein	IPI00031064
Mass	2121.1410	Next	305.000	Fraction	VF_T13h_band06.mzXML
Hyper	578.000	PeptideProphet	0.99	Run	VF_T13h_band06.pep.xml (Vitor/VF_T13h_band06 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

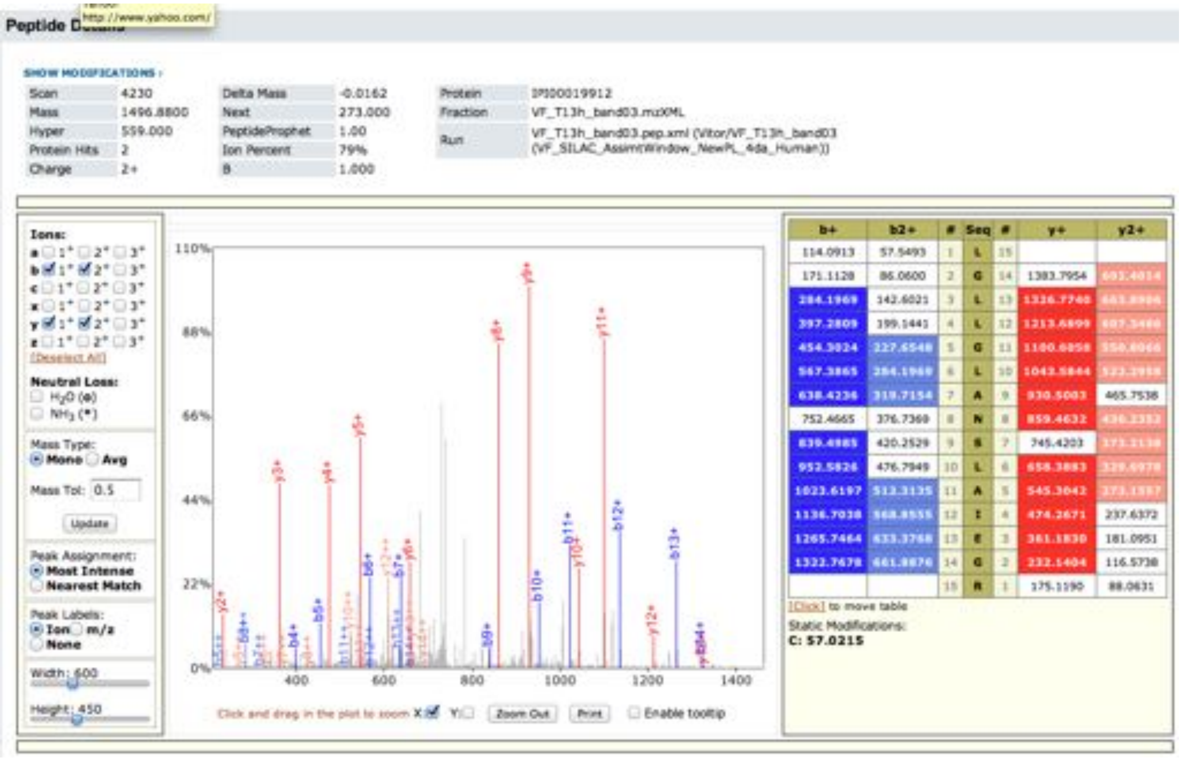
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	20		
185.1285	93.0679	2	A	19	2008.0572	1004.5322
256.1656	128.5864	3	A	18	1937.0201	969.0137
313.1870	157.0972	4	G	17	1865.9830	933.4951
426.2711	213.6392	5	L	16	1808.9615	904.9844
523.3239	262.1656	6	P	15	1695.8775	848.4424
654.3643	327.6858	7	M	14	1598.8247	799.9160
725.4015	363.2044	8	A	13	1467.7842	734.3957
782.4229	391.7151	9	G	12	1396.7471	698.8772
895.5070	448.2571	10	I	11	1339.7256	670.3665
992.5597	496.7835	11	P	10	1226.6416	613.8244
1139.6282	570.3177	12	F	9	1129.5880	565.2980
1252.7122	626.8598	13	L	8	982.5204	491.7638
1353.7599	677.3836	14	T	7	869.4363	435.2218
1454.8076	727.9074	15	T	6	768.3886	384.6980
1569.8345	785.4209	16	D	5	667.3410	334.1741
1682.9186	841.9629	17	L	4	552.3140	276.6606
1783.9663	892.4868	18	T	3	439.2300	220.1186
1947.0296	974.0184	19	Y	2	338.1823	169.5948
		20	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00019912, IPI00909582	1	1	HSD17B4, -	4230	2+	-0,0162	0,9999	K.LGLLGLANSLAIEGR.K



Peptide D

http://www.yahoo.com/

SHOW MODIFICATIONS ›

Scan	4230	Delta Mass	-0.0162	Protein	IPI00019912
Mass	1496.8800	Next	273.000	Fraction	VF_T13h_band03.mzXML
Hyper	559.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

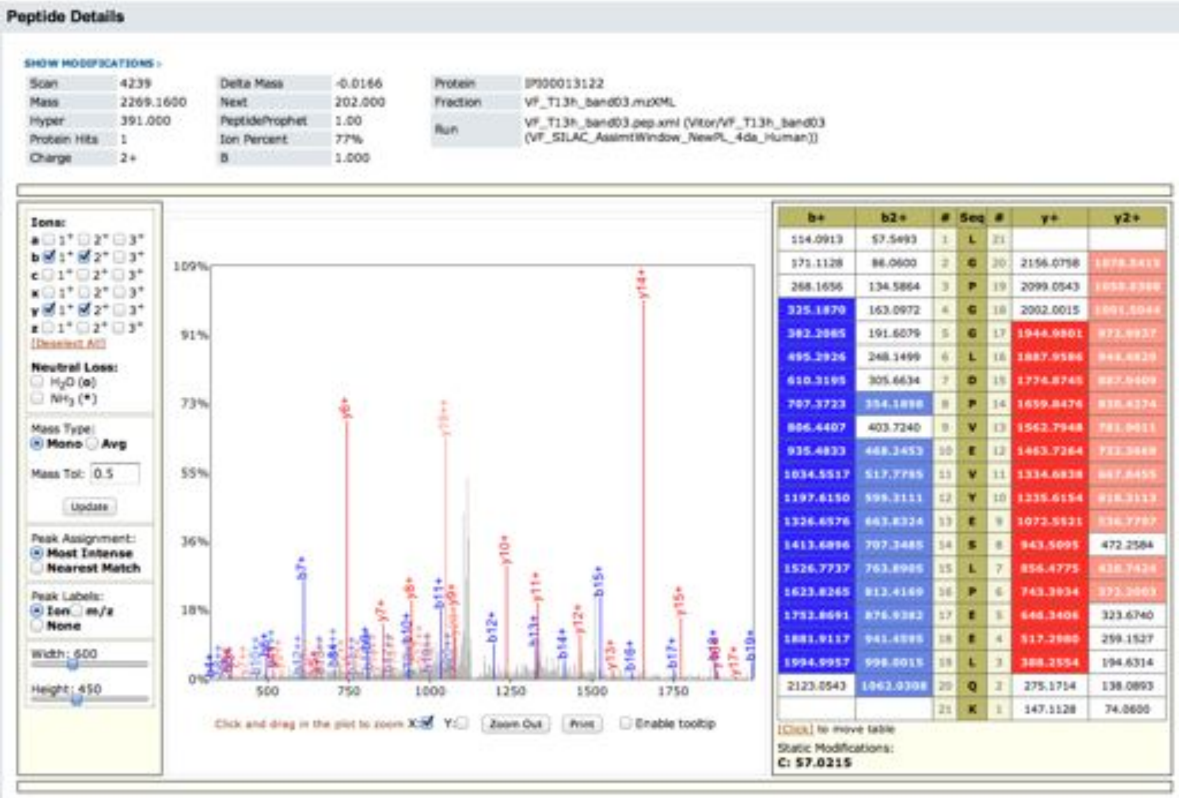
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	15		
171.1128	86.0600	2	G	14	1383.7954	692.4014
284.1969	142.6021	3	L	13	1326.7740	663.8906
397.2809	199.1441	4	L	12	1213.6899	607.3486
454.3024	227.6548	5	G	11	1100.6058	550.8066
567.3865	284.1969	6	L	10	1043.5844	522.2958
638.4236	319.7154	7	A	9	930.5003	465.7538
752.4665	376.7369	8	N	8	859.4632	430.2352
839.4985	420.2529	9	S	7	745.4203	373.2138
952.5826	476.7949	10	L	6	658.3883	329.6978
1023.6197	512.3135	11	A	5	545.3042	273.1557
1136.7038	568.8555	12	I	4	474.2671	237.6372
1265.7464	633.3768	13	E	3	361.1830	181.0951
1322.7678	661.8876	14	G	2	232.1404	116.5738
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9833	IPI00013122	1	1	CDC37	4239	2+	-0,0166	0,9996	R.LGPGGLDPVEVYESLPEELQK.C



Peptide Details

SHOW MODIFICATIONS ›

Scan	4239	Delta Mass	-0.0166	Protein	IPI00013122
Mass	2269.1600	Next	202.000	Fraction	VF_T13h_band03.mzXML
Hyper	391.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	77%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

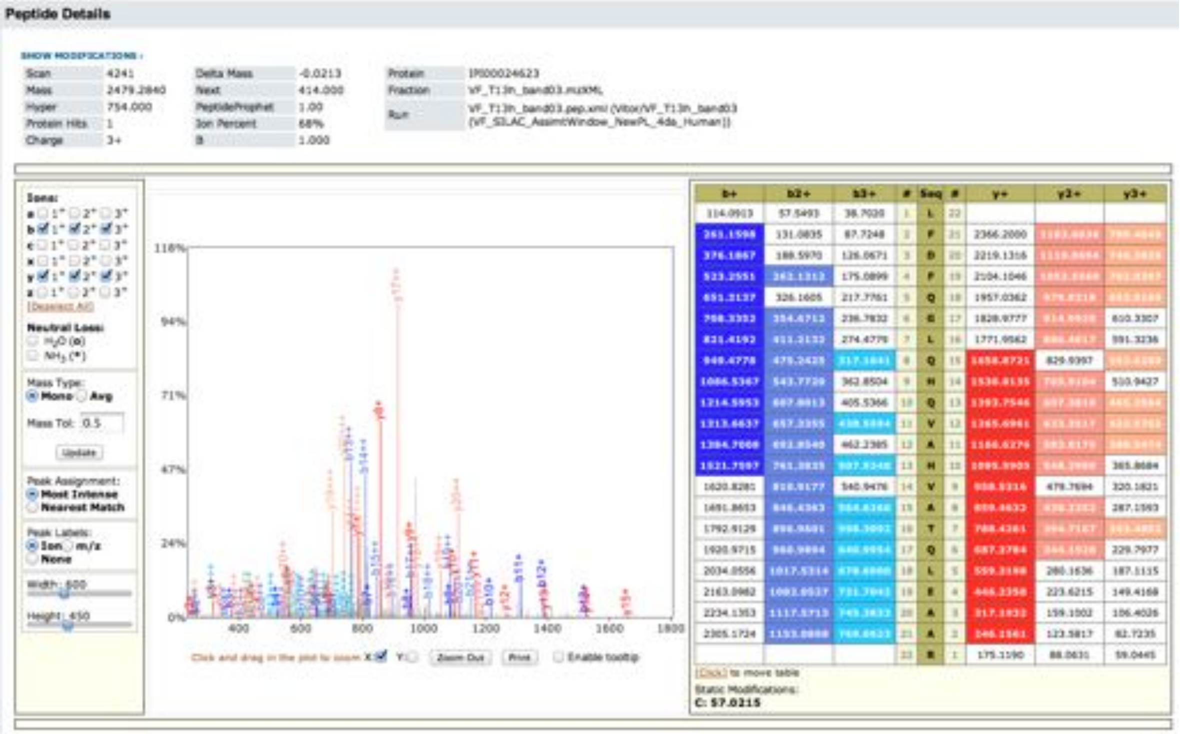
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	21		
171.1128	86.0600	2	G	20	2156.0758	1078.5415
268.1656	134.5864	3	P	19	2099.0543	1050.0308
325.1870	163.0972	4	G	18	2002.0015	1001.5044
382.2085	191.6079	5	G	17	1944.9801	972.9937
495.2926	248.1499	6	L	16	1887.9586	944.4829
610.3195	305.6634	7	D	15	1774.8745	887.9409
707.3723	354.1898	8	P	14	1659.8476	830.4274
806.4407	403.7240	9	V	13	1562.7948	781.9011
935.4833	468.2453	10	E	12	1463.7264	732.3669
1034.5517	517.7795	11	V	11	1334.6838	667.8455
1197.6150	599.3111	12	Y	10	1235.6154	618.3113
1326.6576	663.8324	13	E	9	1072.5521	536.7797
1413.6896	707.3485	14	S	8	943.5095	472.2584
1526.7737	763.8905	15	L	7	856.4775	428.7424
1623.8265	812.4169	16	P	6	743.3934	372.2003
1752.8691	876.9382	17	E	5	646.3406	323.6740
1881.9117	941.4595	18	E	4	517.2980	259.1527
1994.9957	998.0015	19	L	3	388.2554	194.6314
2123.0543	1062.0308	20	Q	2	275.1714	138.0893
		21	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00024623	1	1	ACADSB	4241	3+	-0,0213	1,0000	R.LFDFQGLQHQVAHVATQLEAAR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4241	Delta Mass	-0.0213	Protein	IPI00024623
Mass	2479.2840	Next	414.000	Fraction	VF_T13h_band03.mzXML
Hyper	754.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	68%		
Charge	3+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☑ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
114.0913	57.5493	38.7020	1	L	22			
261.1598	131.0835	87.7248	2	F	21	2366.2000	[illegible]	[illegible]
376.1867	188.5970	126.0671	3	D	20	2219.1316	[illegible]	[illegible]
523.2551	262.1312	175.0899	4	F	19	2104.1046	[illegible]	[illegible]
651.3137	326.1605	217.7761	5	Q	18	1957.0362	[illegible]	[illegible]
708.3352	354.6712	236.7832	6	G	17	1828.9777	[illegible]	610.3307
821.4192	411.2133	274.4779	7	L	16	1771.9562	[illegible]	591.3236
949.4778	475.2425	317.1641	8	Q	15	1658.8721	829.9397	[illegible]
1086.5367	543.7720	362.8504	9	H	14	1530.8135	[illegible]	510.9427
1214.5953	607.8013	405.5366	10	Q	13	1393.7546	[illegible]	[illegible]
1313.6637	657.3355	438.5594	11	V	12	1265.6961	[illegible]	[illegible]
1384.7008	692.8540	462.2385	12	A	11	1166.6276	[illegible]	[illegible]
1521.7597	761.3835	507.9248	13	H	10	1095.5905	[illegible]	365.8684
1620.8281	810.9177	540.9476	14	V	9	958.5316	479.7694	320.1821
1691.8653	846.4363	564.6266	15	A	8	859.4632	[illegible]	287.1593
1792.9129	896.9601	598.3092	16	T	7	788.4261	[illegible]	[illegible]
1920.9715	960.9894	640.9954	17	Q	6	687.3784	[illegible]	229.7977
2034.0556	1017.5314	678.6900	18	L	5	559.3198	280.1636	187.1115
2163.0982	1082.0527	721.7042	19	E	4	446.2358	223.6215	149.4168
2234.1353	1117.5713	745.3833	20	A	3	317.1932	159.1002	106.4026
2305.1724	1153.0898	769.0623	21	A	2	246.1561	123.5817	82.7235
			22	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9167	IPI00909038, IPI00328361	1	1	-, SARS2	4248	2+	-0,0192	0,9961	R.SADLPAIISTWQELR.Q

Peptide Details

SHOW MODIFICATIONS :

Scan	4248	Delta Mass	-0.0192	Protein	IPI00328361
Mass	1699.9010	Next	278.000	Fraction	VF_T13h_band02.mzXML
Hyper	397.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	61%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	15		
159.0764	80.0418	2	A	14	1612.8693	806.9383
274.1034	137.5553	3	D	13	1541.8322	771.4197
387.1874	194.0974	4	L	12	1426.8053	713.9063
484.2402	242.6237	5	P	11	1313.7212	657.3642
555.2773	278.1423	6	A	10	1216.6684	608.8379
668.3614	334.6843	7	I	9	1145.6313	573.3193
781.4454	391.2264	8	I	8	1032.5473	516.7773
868.4775	434.7424	9	S	7	919.4632	460.2352
969.5251	485.2662	10	T	6	832.4312	416.7192
1155.6045	578.3059	11	W	5	731.3835	366.1954
1283.6630	642.3352	12	Q	4	545.3042	273.1557
1412.7056	706.8564	13	E	3	417.2456	209.1264
1525.7897	763.3985	14	L	2	288.2030	144.6051
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8333	IPI00290614	1	1	ENDOG	4254	2+	-0,0153	0,9879	R.ASGLLFVPNILAR.A

Peptide Details

SHOW MODIFICATIONS ›

Scan	4254	Delta Mass	-0.0153	Protein	IPI00290614
Mass	1370.8150	Next	335.000	Fraction	VF_T13h_band04.mzXML
Hyper	413.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	75%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	13		
159.0764	80.0418	2	S	12	1299.7783	650.3928
216.0979	108.5526	3	G	11	1212.7463	606.8768
329.1819	165.0946	4	L	10	1155.7248	578.3661
442.2660	221.6366	5	L	9	1042.6408	521.8240
589.3344	295.1708	6	F	8	929.5567	465.2820
688.4028	344.7051	7	V	7	782.4883	391.7476
785.4556	393.2314	8	P	6	683.4199	342.2136
899.4985	450.2529	9	N	5	586.3671	293.6872
1012.5826	506.7949	10	I	4	472.3242	236.6657
1125.6667	563.3370	11	L	3	359.2401	180.1237
1196.7038	598.8555	12	A	2	246.1561	123.5817
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

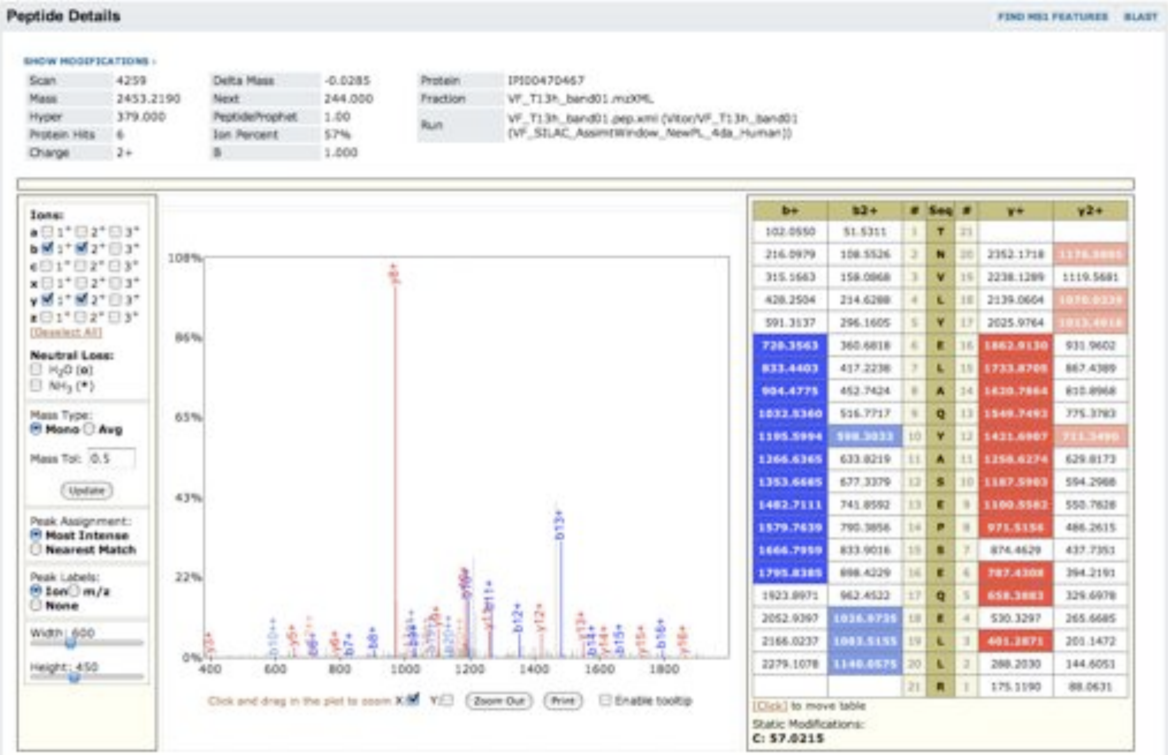
Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9419	IPI00908675, IPI00910178, IPI00903331, IPI00470467, IPI00792395, IPI00880028	1	1	-, -, POR, POR, DKFZp686G04235, -	4259	2+	-0,0285	0,9975	R.TNVLYELAQYASEPSEQELLR.K



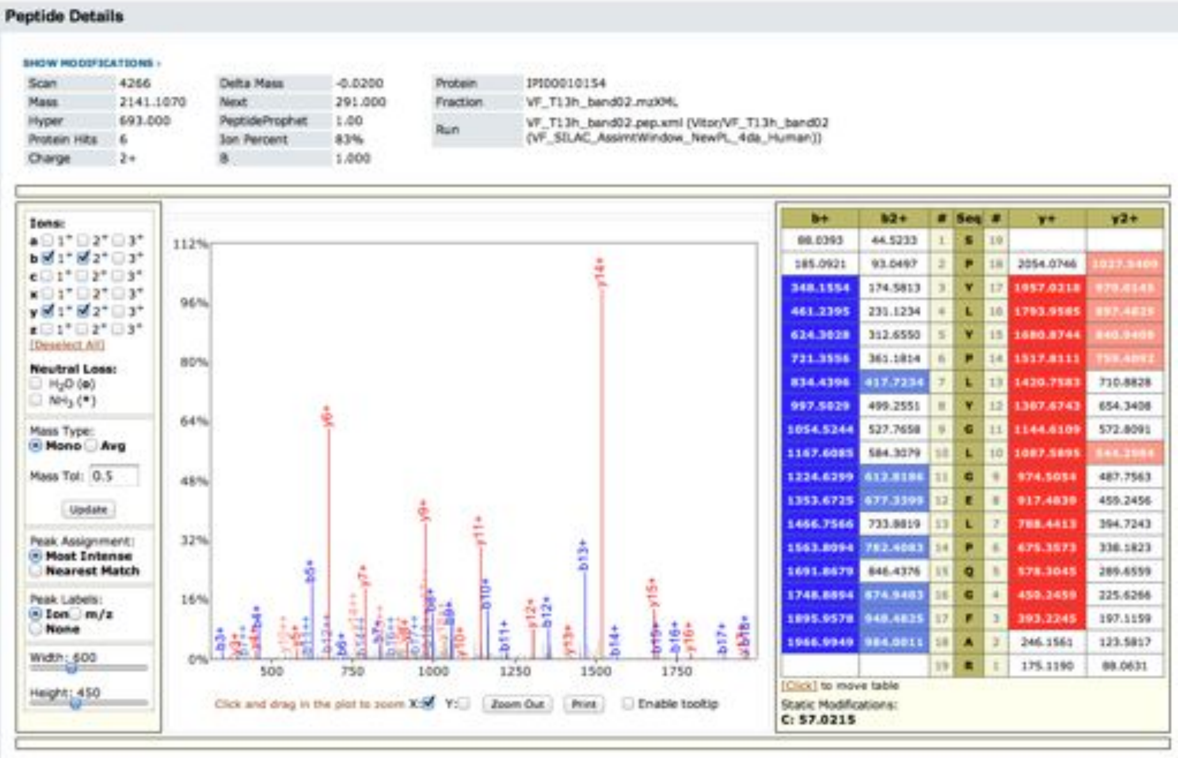
Scan	4259	Delta Mass	-0.0285	Protein	IPI00470467
Mass	2453.2190	Next	244.000	Fraction	VF_T13h_band01.mzXML
Hyper	379.000	PeptideProphet	1.00	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	57%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	21		
216.0979	108.5526	2	N	20	2352.1718	1176.5895
315.1663	158.0868	3	V	19	2238.1289	1119.5681
428.2504	214.6288	4	L	18	2139.0604	1070.0339
591.3137	296.1605	5	Y	17	2025.9764	1013.4918
720.3563	360.6818	6	E	16	1862.9130	931.9602
833.4403	417.2238	7	L	15	1733.8705	867.4389
904.4775	452.7424	8	A	14	1620.7864	810.8968
1032.5360	516.7717	9	Q	13	1549.7493	775.3783
1195.5994	598.3033	10	Y	12	1421.6907	711.3490
1266.6365	633.8219	11	A	11	1258.6274	629.8173
1353.6685	677.3379	12	S	10	1187.5903	594.2988
1482.7111	741.8592	13	E	9	1100.5582	550.7828
1579.7639	790.3856	14	P	8	971.5156	486.2615
1666.7959	833.9016	15	S	7	874.4629	437.7351
1795.8385	898.4229	16	E	6	787.4308	394.2191
1923.8971	962.4522	17	Q	5	658.3883	329.6978
2052.9397	1026.9735	18	E	4	530.3297	265.6685
2166.0237	1083.5155	19	L	3	401.2871	201.1472
2279.1078	1140.0575	20	L	2	288.2030	144.6051
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9819	IPI00514395, IPI00645255, IPI00640006, IPI00910113, IPI00010154, IPI00031461	1	1	GDI2, GDI2, GDI2, -, GDI1, GDI2	4266	2+	-0,0200	1,0000	K.SPYLYPLYGLGELPQGFAR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4266	Delta Mass	-0.0200	Protein	IPI00010154
Mass	2141.1070	Next	291.000	Fraction	VF_T13h_band02.mzXML
Hyper	693.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H2O (o)
☐ NH3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

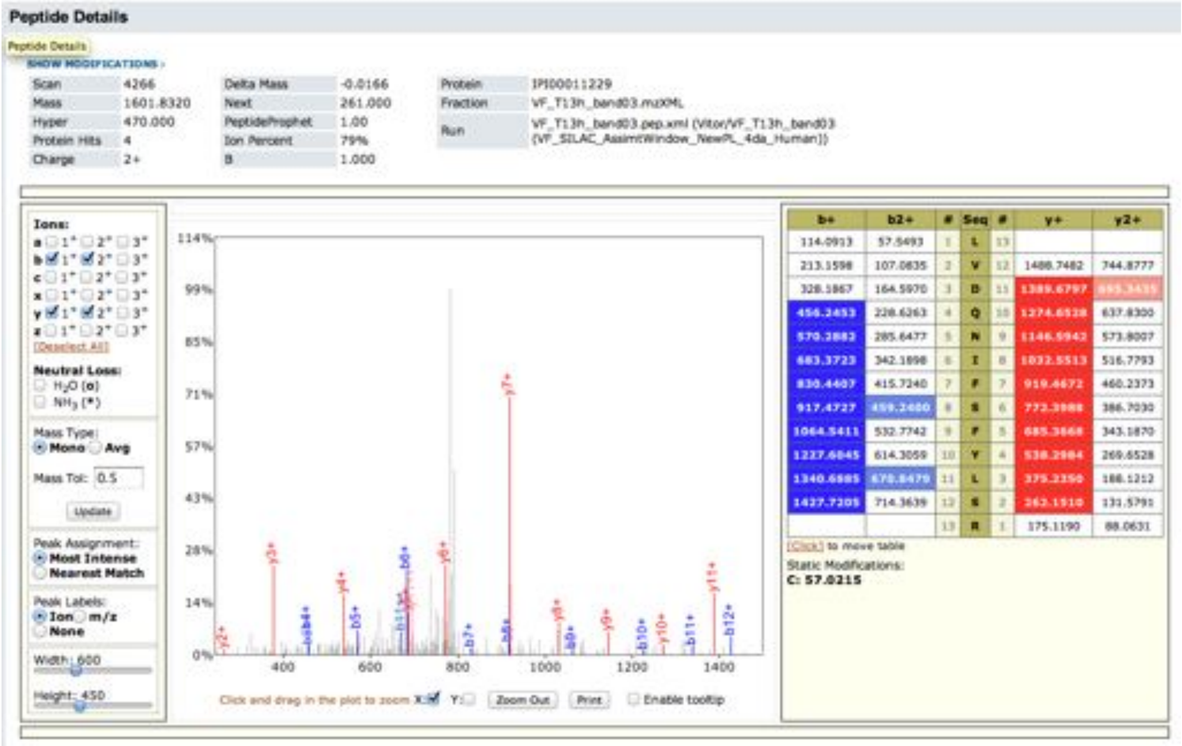
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	19		
185.0921	93.0497	2	P	18	2054.0746	1027.5409
348.1554	174.5813	3	Y	17	1957.0218	979.0145
461.2395	231.1234	4	L	16	1793.9585	897.4825
624.3028	312.6550	5	Y	15	1680.8744	840.9409
721.3556	361.1814	6	P	14	1517.8111	759.4092
834.4396	417.7234	7	L	13	1420.7583	710.8828
997.5029	499.2551	8	Y	12	1307.6743	654.3408
1054.5244	527.7658	9	G	11	1144.6109	572.8091
1167.6085	584.3079	10	L	10	1087.5895	544.2984
1224.6299	612.8186	11	G	9	974.5054	487.7563
1353.6725	677.3399	12	E	8	917.4839	459.2456
1466.7566	733.8819	13	L	7	788.4413	394.7243
1563.8094	782.4083	14	P	6	675.3573	338.1823
1691.8679	846.4376	15	Q	5	578.3045	289.6559
1748.8894	874.9483	16	G	4	450.2459	225.6266
1895.9578	948.4825	17	F	3	393.2245	197.1159
1966.9949	984.0011	18	A	2	246.1561	123.5817
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9857	IPI00879328, IPI00852597, IPI00853455, IPI00011229	1	1	CTSD, CTSD, CTSD, CTSD	4266	2+	-0,0166	0,9998	K.LVDQNIFSFYLSR.D



Peptide Details

Peptide Details

SHOW MODIFICATIONS ›

Scan	4266	Delta Mass	-0.0166	Protein	IPI00011229
Mass	1601.8320	Next	261.000	Fraction	VF_T13h_band03.mzXML
Hyper	470.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	13		
213.1598	107.0835	2	V	12	1488.7482	744.8777
328.1867	164.5970	3	D	11	1389.6797	695.3435
456.2453	228.6263	4	Q	10	1274.6528	637.8300
570.2882	285.6477	5	N	9	1146.5942	573.8007
683.3723	342.1898	6	I	8	1032.5513	516.7793
830.4407	415.7240	7	F	7	919.4672	460.2373
917.4727	459.2400	8	S	6	772.3988	386.7030
1064.5411	532.7742	9	F	5	685.3668	343.1870
1227.6045	614.3059	10	Y	4	538.2984	269.6528
1340.6885	670.8479	11	L	3	375.2350	188.1212
1427.7205	714.3639	12	S	2	262.1510	131.5791
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9730	IPI00887542, IPI00908881, IPI00027497, IPI00910781	1	1	LOC100133951, -, GPI, -	4278	2+	-0,0176	0,9995	K.ILLANFLAQTEALM"R.G

Peptide Details

SHOW MODIFICATIONS ›

Scan	4278	Delta Mass	-0.0176	Protein	IPI00027497
Mass	1719.9460	Next	277.000	Fraction	VF_T13h_band02.mzXML
Hyper	454.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	68%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

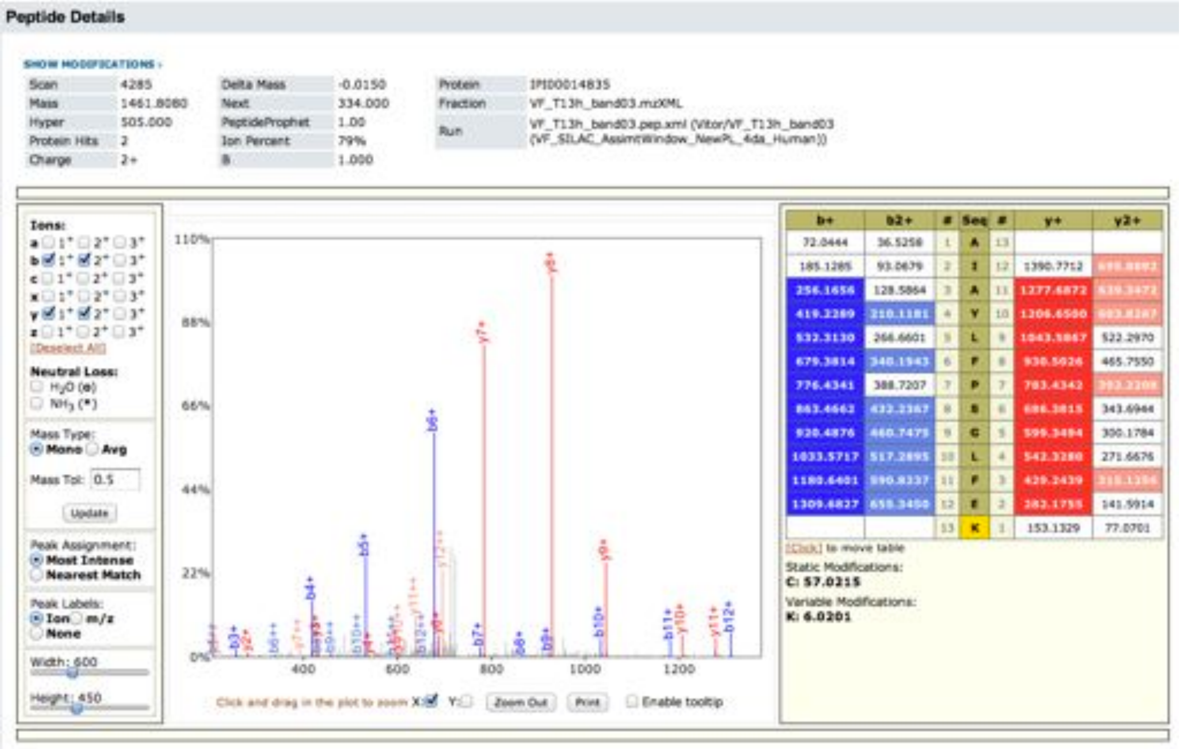
b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	15		
227.1754	114.0913	2	L	14	1606.8621	803.9347
340.2595	170.6334	3	L	13	1493.7781	747.3927
411.2966	206.1519	4	A	12	1380.6940	690.8506
525.3395	263.1734	5	N	11	1309.6569	655.3321
672.4079	336.7076	6	F	10	1195.6140	598.3106
785.4920	393.2496	7	L	9	1048.5455	524.7764
856.5291	428.7682	8	A	8	935.4615	468.2344
984.5877	492.7975	9	Q	7	864.4244	432.7158
1085.6354	543.3213	10	T	6	736.3658	368.6865
1214.6780	607.8426	11	E	5	635.3181	318.1627
1285.7151	643.3612	12	A	4	506.2755	253.6414
1398.7991	699.9032	13	L	3	435.2384	218.1228
1545.8345	773.4209	14	M	2	322.1543	161.5808
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9822	IPI00014835, IPI00641924	1	1	MRPS9, MRPS9	4285	2+	-0,0150	0,9995	R.AIAYLFPSGLFEK'.R



Peptide Details

SHOW MODIFICATIONS ›

Scan	4285	Delta Mass	-0.0150	Protein	IPI00014835
Mass	1461.8080	Next	334.000	Fraction	VF_T13h_band03.mzXML
Hyper	505.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	13		
185.1285	93.0679	2	I	12	1390.7712	695.8892
256.1656	128.5864	3	A	11	1277.6872	639.3472
419.2289	210.1181	4	Y	10	1206.6500	603.8287
532.3130	266.6601	5	L	9	1043.5867	522.2970
679.3814	340.1943	6	F	8	930.5026	465.7550
776.4341	388.7207	7	P	7	783.4342	392.2208
863.4662	432.2367	8	S	6	686.3815	343.6944
920.4876	460.7475	9	G	5	599.3494	300.1784
1033.5717	517.2895	10	L	4	542.3280	271.6676
1180.6401	590.8237	11	F	3	429.2439	215.1256
1309.6827	655.3450	12	E	2	282.1755	141.5914
		13	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8718	IPI00218547, IPI00008982	1	1	ALDH18A1, ALDH18A1	4302	2+	-0,0150	0,9927	R.TPLFDQIIDM"LR.V

Peptide Details

Scan	4302	Delta Mass	-0.0150	Protein	IPI00008982
Mass	1477.7720	Next	215.000	Fraction	VF_T13h_band01.mzXML
Hyper	327.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	55%		
Charge	2+	B	0.000		

Mass Tol: 0.5

Width: 600

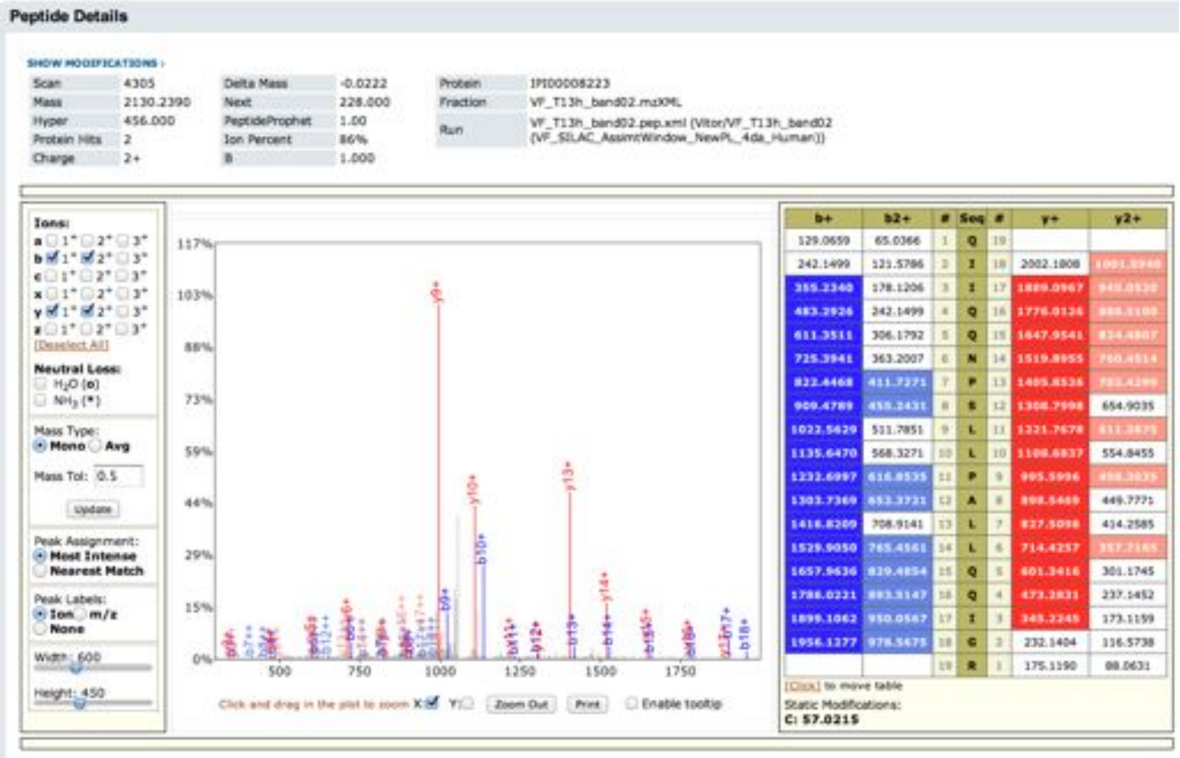
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	12		
199.1077	100.0575	2	P	11	1376.7242	688.8658
312.1918	156.5995	3	L	10	1279.6715	640.3394
459.2602	230.1337	4	F	9	1166.5874	583.7973
574.2871	287.6472	5	D	8	1019.5190	510.2631
702.3457	351.6765	6	Q	7	904.4920	452.7497
815.4298	408.2185	7	I	6	776.4335	388.7204
928.5138	464.7606	8	I	5	663.3494	332.1783
1043.5408	522.2740	9	D	4	550.2653	275.6363
1190.5762	595.7917	10	M	3	435.2384	218.1228
1303.6602	652.3338	11	L	2	288.2030	144.6051
		12	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00642549, IPI00008223	1	1	RAD23B, RAD23B	4305	2+	-0,0222	0,9999	R.QIIQQNPSLLPALLQQIGR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	4305	Delta Mass	-0.0222	Protein	IPI00008223
Mass	2130.2390	Next	228.000	Fraction	VF_T13h_band02.mzXML
Hyper	456.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Viton/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	19		
242.1499	121.5786	2	I	18	2002.1808	1001.5940
355.2340	178.1206	3	I	17	1889.0967	945.0520
483.2926	242.1499	4	Q	16	1776.0126	888.5100
611.3511	306.1792	5	Q	15	1647.9541	824.4807
725.3941	363.2007	6	N	14	1519.8955	760.4514
822.4468	411.7271	7	P	13	1405.8526	703.4299
909.4789	455.2431	8	S	12	1308.7998	654.9035
1022.5629	511.7851	9	L	11	1221.7678	611.3875
1135.6470	568.3271	10	L	10	1108.6837	554.8455
1232.6997	616.8535	11	P	9	995.5996	498.3035
1303.7369	652.3721	12	A	8	898.5469	449.7771
1416.8209	708.9141	13	L	7	827.5098	414.2585
1529.9050	765.4561	14	L	6	714.4257	357.7165
1657.9636	829.4854	15	Q	5	601.3416	301.1745
1786.0221	893.5147	16	Q	4	473.2831	237.1452
1899.1062	950.0567	17	I	3	345.2245	173.1159
1956.1277	978.5675	18	G	2	232.1404	116.5738
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8800	IPI00062003, IPI00440499, IPI00030363	1	1	ACAT1, ACAT1, ACAT1	4351	2+	-0,0197	0,9933	R.TPIGSFLGSLSLLPATK'.L

Scan	4351	Delta Mass	-0.0197	Protein	IPI00030363
Mass	1707.9990	Next	250.000	Fraction	VF_T13h_band01.mzXML
Hyper	360.000	PeptideProphet	0.99	Run	VF_T13h_band01.pep.xml (Vitor/VF_T13h_band01 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	72%		
Charge	2+	B	1.000		

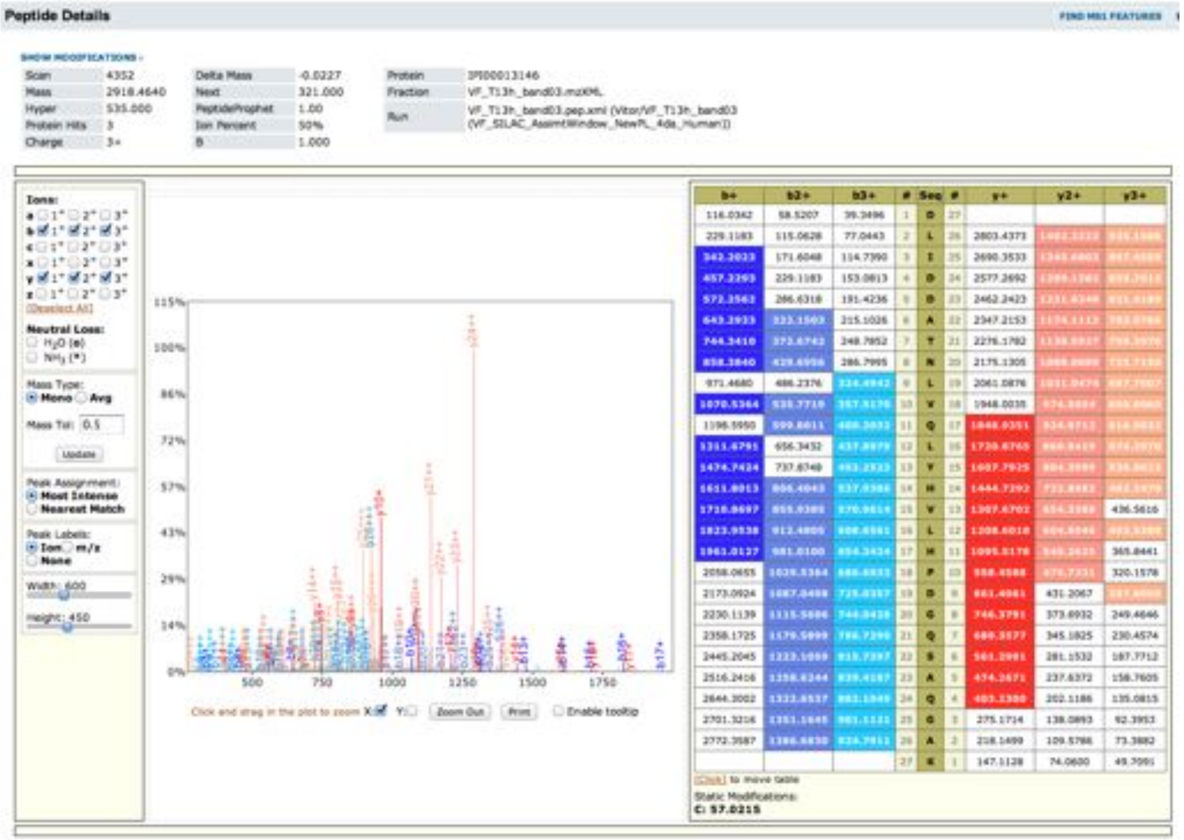
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	17		
199.1077	100.0575	2	P	16	1606.9510	803.9791
312.1918	156.5995	3	I	15	1509.8983	755.4527
369.2132	185.1103	4	G	14	1396.8141	698.9107
456.2453	228.6263	5	S	13	1339.7927	670.4000
603.3137	302.1605	6	F	12	1252.7607	626.8840
716.3978	358.7025	7	L	11	1105.6922	553.3498
773.4192	387.2132	8	G	10	992.6082	496.8077
860.4512	430.7293	9	S	9	935.5867	468.2970
973.5353	487.2713	10	L	8	848.5547	424.7810
1060.5673	530.7873	11	S	7	735.4706	368.2389
1173.6514	587.3293	12	L	6	648.4386	324.7229
1286.7355	643.8714	13	L	5	535.3545	268.1809
1383.7882	692.3978	14	P	4	422.2705	211.6389
1454.8253	727.9163	15	A	3	325.2177	163.1125
1555.8730	778.4401	16	T	2	254.1806	127.5939
		17	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00795908, IPI00791542, IPI00013146	1	1	MRPS22, MRPS22, MRPS22	4352	3+	-0,0227	1,0000	R.DLIDDATNLVQLYHVLHPDGQSAQGAK.D



Peptide Details

Scan	4352	Delta Mass	-0.0227	Protein	IPI00013146
Mass	2918.4640	Next	321.000	Fraction	VF_T13h_band03.mzXML
Hyper	535.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	50%		
Charge	3+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☑ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment: ● **Most Intense** ○ **Nearest Match**

Peak Labels: ● **Ion** ○ **m/z** ○ **None**

Width: 600

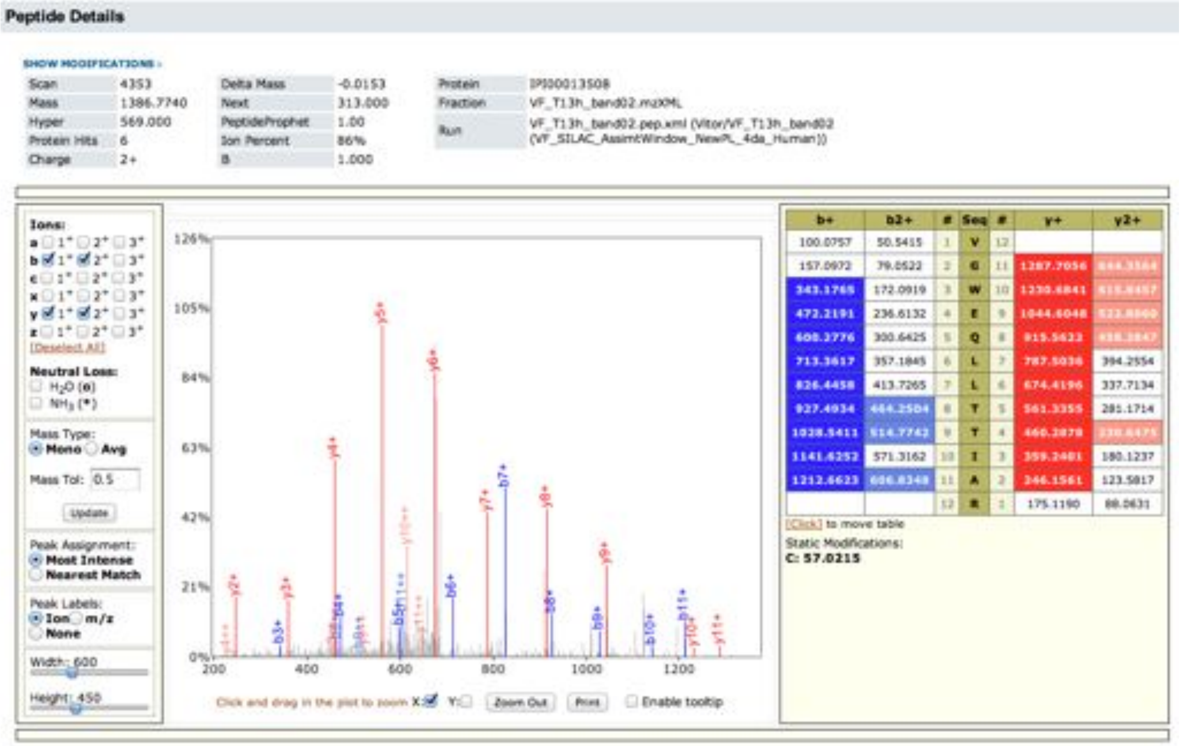
Height: 450

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
116.0342	58.5207	39.3496	1	D	27			
229.1183	115.0628	77.0443	2	L	26	2803.4373	1402.2223	935.1506
342.2023	171.6048	114.7390	3	I	25	2690.3533	1345.6803	897.4558
457.2293	229.1183	153.0813	4	D	24	2577.2692	1289.1383	859.7613
572.2562	286.6318	191.4236	5	D	23	2462.2423	1231.6248	821.4189
643.2933	322.1503	215.1026	6	A	22	2347.2153	1174.1113	783.0766
744.3410	372.6742	248.7852	7	T	21	2276.1782	1138.5927	759.3976
858.3840	429.6956	286.7995	8	N	20	2175.1305	1088.0689	725.7150
971.4680	486.2376	324.4942	9	L	19	2061.0876	1031.0474	687.7007
1070.5364	535.7719	357.5170	10	V	18	1948.0035	974.5054	650.0060
1198.5950	599.8011	400.2032	11	Q	17	1848.9351	924.9712	616.9831
1311.6791	656.3432	437.8979	12	L	16	1720.8765	860.9419	574.2970
1474.7424	737.8748	492.2523	13	Y	15	1607.7925	804.3999	536.6013
1611.8013	806.4043	537.9386	14	H	14	1444.7292	722.8682	482.2479
1710.8697	855.9385	570.9614	15	V	13	1307.6702	654.3388	436.5616
1823.9538	912.4805	608.6561	16	L	12	1208.6018	604.8046	403.5388
1961.0127	981.0100	654.3424	17	H	11	1095.5178	548.2625	365.8441
2058.0655	1029.5364	686.6933	18	P	10	958.4588	479.7331	320.1578
2173.0924	1087.0498	725.0357	19	D	9	861.4061	431.2067	287.8069
2230.1139	1115.5606	744.0428	20	G	8	746.3791	373.6932	249.4646
2358.1725	1179.5899	786.7290	21	Q	7	689.3577	345.1825	230.4574
2445.2045	1223.1059	815.7387	22	S	6	561.2991	281.1532	187.7712
2516.2416	1258.6244	839.4187	23	A	5	474.2671	237.6372	158.7605
2644.3002	1322.6537	882.1049	24	Q	4	403.2300	202.1186	135.0815
2701.3216	1351.1645	901.1121	25	G	3	275.1714	138.0893	92.3953
2772.3587	1386.6830	924.7911	26	A	2	218.1499	109.5786	73.3882
			27	K	1	147.1128	74.0600	49.7091

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9801	IPI00793285, IPI00845465, IPI00909239, IPI00013508, IPI00013808, IPI00759776	1	1	ACTN4, ACTN4, ACTN1, ACTN1, ACTN4, ACTN1	4353	2+	-0,0153	0,9999	R.VGWEQLLTTIAR.T



Peptide Details

SHOW MODIFICATIONS ›

Scan	4353	Delta Mass	-0.0153	Protein	IPI00013508
Mass	1386.7740	Next	313.000	Fraction	VF_T13h_band02.mzXML
Hyper	569.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	86%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	12		
157.0972	79.0522	2	G	11	1287.7056	644.3564
343.1765	172.0919	3	W	10	1230.6841	615.8457
472.2191	236.6132	4	E	9	1044.6048	522.8060
600.2776	300.6425	5	Q	8	915.5622	458.2847
713.3617	357.1845	6	L	7	787.5036	394.2554
826.4458	413.7265	7	L	6	674.4196	337.7134
927.4934	464.2504	8	T	5	561.3355	281.1714
1028.5411	514.7742	9	T	4	460.2879	230.6475
1141.6252	571.3162	10	I	3	359.2401	180.1237
1212.6623	606.8348	11	A	2	246.1561	123.5817
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9741	IPI00003935, IPI00018534, IPI00020101, IPI00152785, IPI00152906, IPI00166293, IPI00220403, IPI00303133, IPI00329665, IPI00477495, IPI00515061, IPI00554798, IPI00815755, IPI00816252, IPI00419833, IPI00646240, IPI00794461	1	1	HIST2H2BE, HIST1H2BL, HIST1H2BD, HIST1H2BO, HIST1H2BD, HIST3H2BB, HIST1H2BB, HIST1H2BH, HIST2H2BF, H2BFS, HIST1H2BJ, HIST1H2BM, HIST1H2BG, H2BFS, HIST1H2BK, HIST2H2BA, OTTHUMP00000039500	4353	2+	-0,0232	0,9988	K.AM"GIMNSFVNDIFER.I

Scan	4353	Delta Mass	-0.0232	Protein	IPI00003935
Mass	1759.8140	Next	482.000	Fraction	VF_T13h_band03.mzXML
Hyper	598.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	17	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

X: ☑ Y: ☐

☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	15		
219.0798	110.0435	2	M	14	1688.7771	844.8922
276.1012	138.5543	3	G	13	1541.7417	771.3745
389.1853	195.0963	4	I	12	1484.7202	742.8638
520.2258	260.6165	5	M	11	1371.6362	686.3217
634.2687	317.6380	6	N	10	1240.5957	620.8015
721.3007	361.1540	7	S	9	1126.5527	563.7800
868.3692	434.6882	8	F	8	1039.5207	520.2640
967.4376	484.2224	9	V	7	892.4523	446.7298
1081.4805	541.2439	10	N	6	793.3839	397.1956
1196.5074	598.7574	11	D	5	679.3410	340.1741
1309.5915	655.2994	12	I	4	564.3140	282.6606
1456.6599	728.8336	13	F	3	451.2300	226.1186
1585.7025	793.3549	14	E	2	304.1615	152.5844
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8649	IPI00645888, IPI00029605	1	1	GALNS, GALNS	4356	2+	-0,0191	0,9926	R.AIDGLNLLPTLLQGR.L

Peptide Details

SHOW MODIFICATIONS ›

Scan	4356	Delta Mass	-0.0191	Protein	IPI00029605
Mass	1593.9320	Next	270.000	Fraction	VF_T13h_band02.mzXML
Hyper	376.000	PeptideProphet	0.99	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	57%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

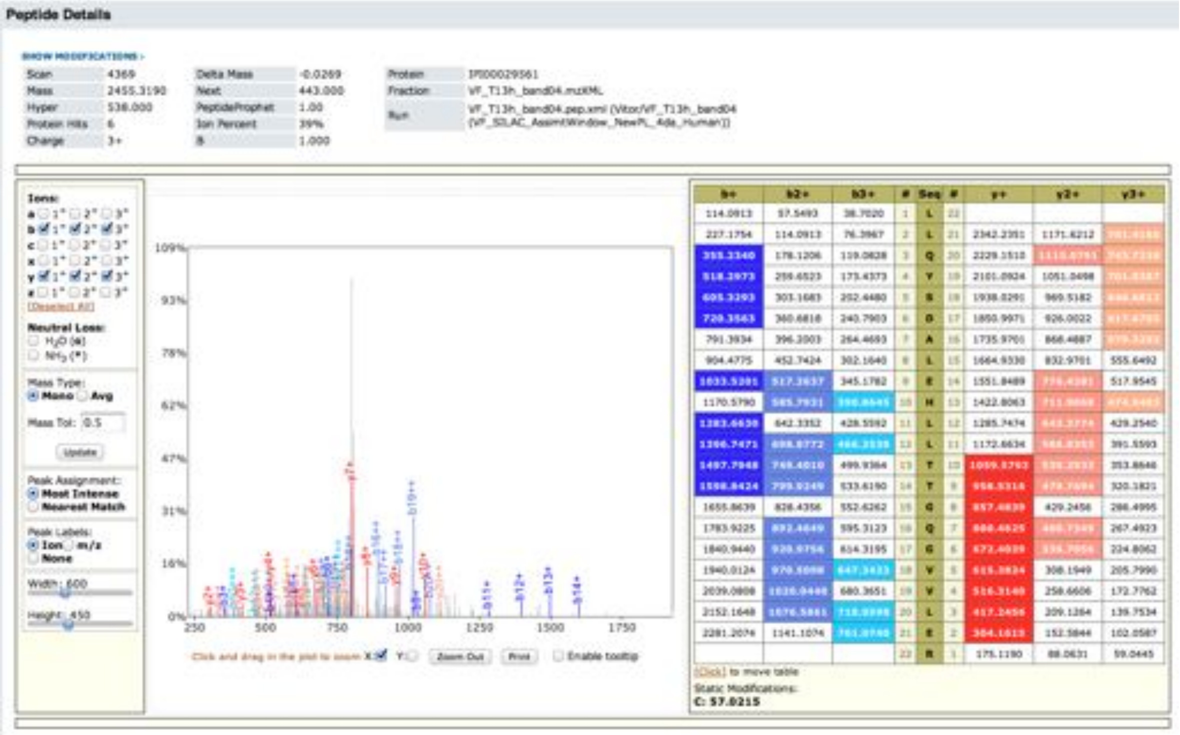
Height: 450

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	15		
185.1285	93.0679	2	I	14	1522.8952	761.9513
300.1554	150.5813	3	D	13	1409.8111	705.4092
357.1769	179.0921	4	G	12	1294.7841	647.8957
470.2609	235.6341	5	L	11	1237.7627	619.3850
584.3039	292.6556	6	N	10	1124.6786	562.8429
697.3879	349.1976	7	L	9	1010.6357	505.8215
810.4720	405.7396	8	L	8	897.5516	449.2795
907.5247	454.2660	9	P	7	784.4676	392.7374
1008.5724	504.7898	10	T	6	687.4148	344.2110
1121.6565	561.3319	11	L	5	586.3671	293.6872
1234.7406	617.8739	12	L	4	473.2831	237.1452
1362.7991	681.9032	13	Q	3	360.1990	180.6031
1419.8206	710.4139	14	G	2	232.1404	116.5738
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9443	IPI00894559, IPI00555877, IPI00894261, IPI00029561, IPI00894154, IPI00103509	1	1	NDUFA10, NDUFA10, NDUFA10, NDUFA10, NDUFA10, NDUFA10	4369	3+	-0,0269	0,9971	R.LLQYSDALEHLLTTGQGVVLER.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	4369	Delta Mass	-0.0269	Protein	IPI00029561
Mass	2455.3190	Next	443.000	Fraction	VF_T13h_band04.mzXML
Hyper	538.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	39%		
Charge	3+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☑ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

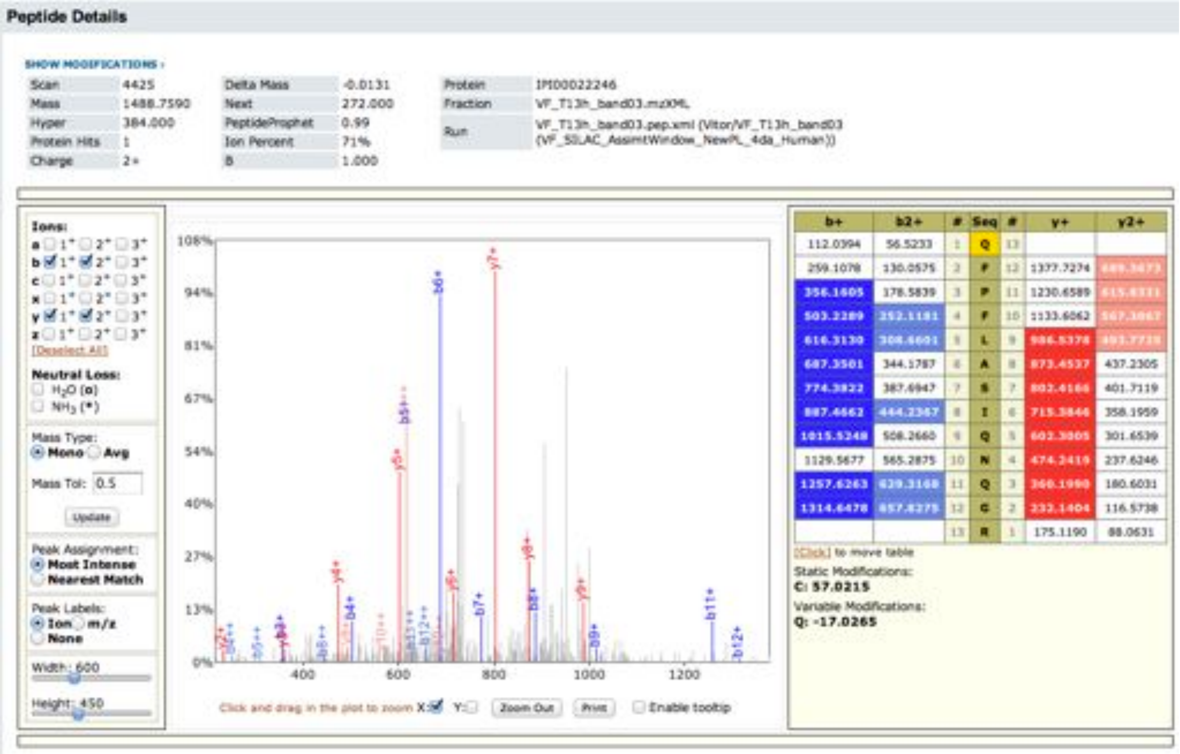
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
114.0913	57.5493	38.7020	1	L	22			
227.1754	114.0913	76.3967	2	L	21	2342.2351	1171.6212	[illegible]
355.2340	178.1206	119.0828	3	Q	20	2229.1510	1115.0791	[illegible]
518.2973	259.6523	173.4373	4	Y	19	2101.0924	1051.0498	[illegible]
605.3293	303.1683	202.4480	5	S	18	1938.0291	969.5182	[illegible]
720.3563	360.6818	240.7903	6	D	17	1850.9971	926.0022	[illegible]
791.3934	396.2003	264.4693	7	A	16	1735.9701	868.4887	[illegible]
904.4775	452.7424	302.1640	8	L	15	1664.9330	832.9701	555.6492
1033.5201	517.2637	345.1782	9	E	14	1551.8489	776.4281	517.9545
1170.5790	585.7931	390.8645	10	H	13	1422.8063	711.9068	[illegible]
1283.6630	642.3352	428.5592	11	L	12	1285.7474	643.3774	429.2540
1396.7471	698.8772	466.2539	12	L	11	1172.6634	586.8353	391.5593
1497.7948	749.4010	499.9364	13	T	10	1059.5792	530.2932	353.8646
1598.8424	799.9249	533.6190	14	T	9	958.5316	479.7694	320.1821
1655.8639	828.4356	552.6262	15	G	8	857.4839	429.2456	286.4995
1783.9225	892.4649	595.3123	16	Q	7	800.4625	400.7349	267.4923
1840.9440	920.9756	614.3195	17	G	6	672.4039	336.7056	224.8062
1940.0124	970.5098	647.3423	18	V	5	615.3824	308.1949	205.7990
2039.0808	1020.0440	680.3651	19	V	4	516.3140	258.6606	172.7762
2152.1648	1076.5861	[illegible]	20	L	3	417.2456	209.1264	139.7534
2281.2074	1141.1074	761.0740	21	E	2	304.1615	152.5844	102.0587
			22	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9299	IPI00022246	1	1	AZU1	4425	2+	-0,0131	0,9948	R.Q^FPFLASIQNQGR.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	4425	Delta Mass	-0.0131	Protein	IPI00022246
Mass	1488.7590	Next	272.000	Fraction	VF_T13h_band03.mzXML
Hyper	384.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
112.0394	56.5233	1	Q	13		
259.1078	130.0575	2	F	12	1377.7274	689.3673
356.1605	178.5839	3	P	11	1230.6589	615.8331
503.2289	252.1181	4	F	10	1133.6062	567.3067
616.3130	308.6601	5	L	9	986.5378	493.7728
687.3501	344.1787	6	A	8	873.4537	437.2305
774.3822	387.6947	7	S	7	802.4166	401.7119
887.4662	444.2367	8	I	6	715.3846	358.1959
1015.5248	508.2660	9	Q	5	602.3005	301.6539
1129.5677	565.2875	10	N	4	474.2419	237.6246
1257.6263	629.3168	11	Q	3	360.1990	180.6031
1314.6478	657.8275	12	G	2	232.1404	116.5738
		13	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
Q: -17.0265

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9764	IPI00217182, IPI00013933	1	1	DSP, DSP	4437	2+	-0,0161	0,9994	K.SAIYQLEEEYENLLK.A

Peptide Details

Scan	4437	Delta Mass	-0.0161	Protein	IPI00013933
Mass	1841.9170	Next	257.000	Fraction	VF_T13h_band04.mzXML
Hyper	426.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	71%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H$_2$O (o)
☐ NH$_3$ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

b+	b2+	#	Seq	#	y+	y2+
88.0393	44.5233	1	S	15		
159.0764	80.0418	2	A	14	1754.8847	877.9460
272.1605	136.5839	3	I	13	1683.8476	842.4274
435.2238	218.1155	4	Y	12	1570.7635	785.8854
563.2824	282.1448	5	Q	11	1407.7002	704.3537
676.3665	338.6869	6	L	10	1279.6416	640.3245
805.4090	403.2082	7	E	9	1166.5576	583.7824
934.4516	467.7295	8	E	8	1037.5150	519.2611
1063.4942	532.2508	9	E	7	908.4724	454.7398
1226.5576	613.7824	10	Y	6	779.4298	390.2185
1355.6002	678.3037	11	E	5	616.3665	308.6869
1469.6431	735.3253	12	N	4	487.3239	244.1656
1582.7271	791.8672	13	L	3	373.2809	187.1441
1695.8112	848.4002	14	L	2	260.1969	130.6021
		15	K	1	147.1128	74.0600

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9626	IPI00103467	1	1	ALDH 1B1	4443	2+	-0,0109	0,9989	R.LLNLLADLVER.D

Peptide Details

SHOW MODIFICATIONS ›

Scan	4443	Delta Mass	-0.0109	Protein	IPI00103467
Mass	1268.7570	Next	273.000	Fraction	VF_T13h_band02.mzXML
Hyper	424.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimtWindow_NewPL_4da_Human])
Protein Hits	1	Ion Percent	65%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

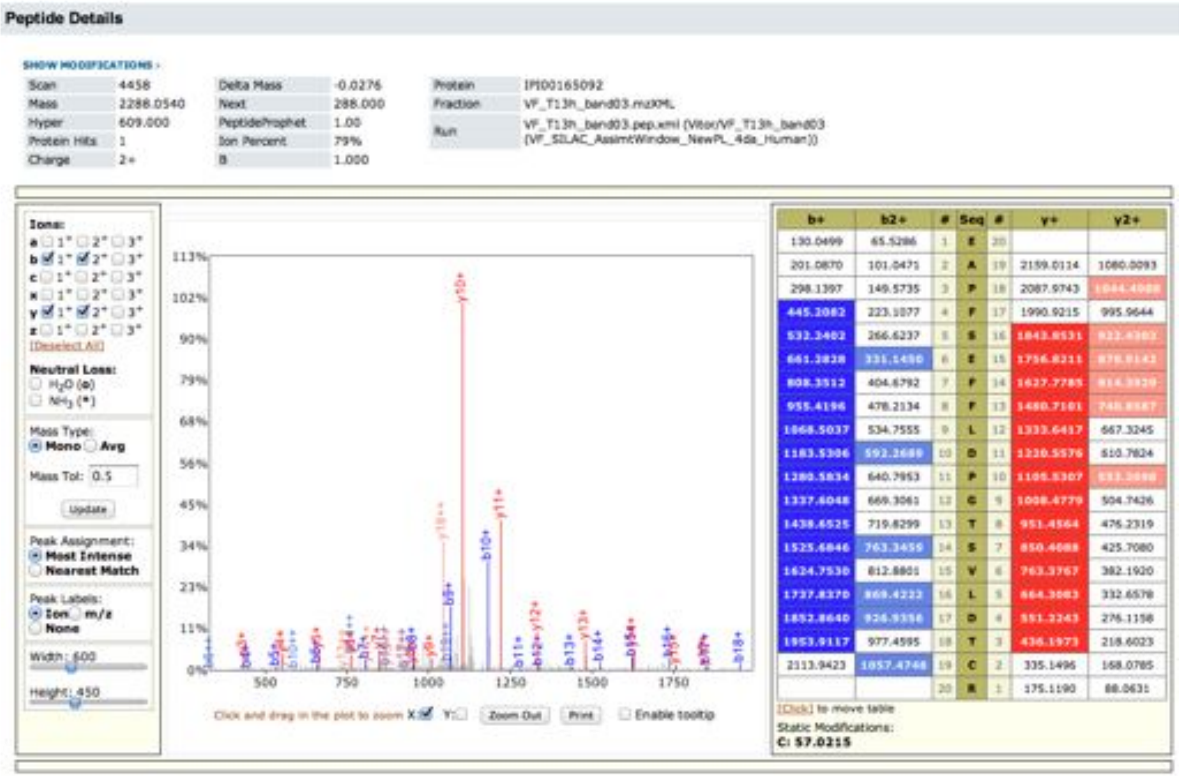
Height: 450

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	L	11		
227.1754	114.0913	2	L	10	1155.6732	578.3402
341.2183	171.1128	3	N	9	1042.5891	521.7982
454.3024	227.6548	4	L	8	928.5462	464.7767
567.3865	284.1969	5	L	7	815.4621	408.2347
638.4236	319.7154	6	A	6	702.3781	351.6927
753.4505	377.2289	7	D	5	631.3410	316.1741
866.5346	433.7709	8	L	4	516.3140	258.6606
965.6030	483.3051	9	V	3	403.2300	202.1186
1094.6456	547.8264	10	E	2	304.1615	152.5844
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00165092	1	1	YARS2	4458	2+	-0,0276	1,0000	K.EAPFSEFFLDPGTSVLDTCR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	4458	Delta Mass	-0.0276	Protein	IPI00165092
Mass	2288.0540	Next	288.000	Fraction	VF_T13h_band03.mzXML
Hyper	609.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

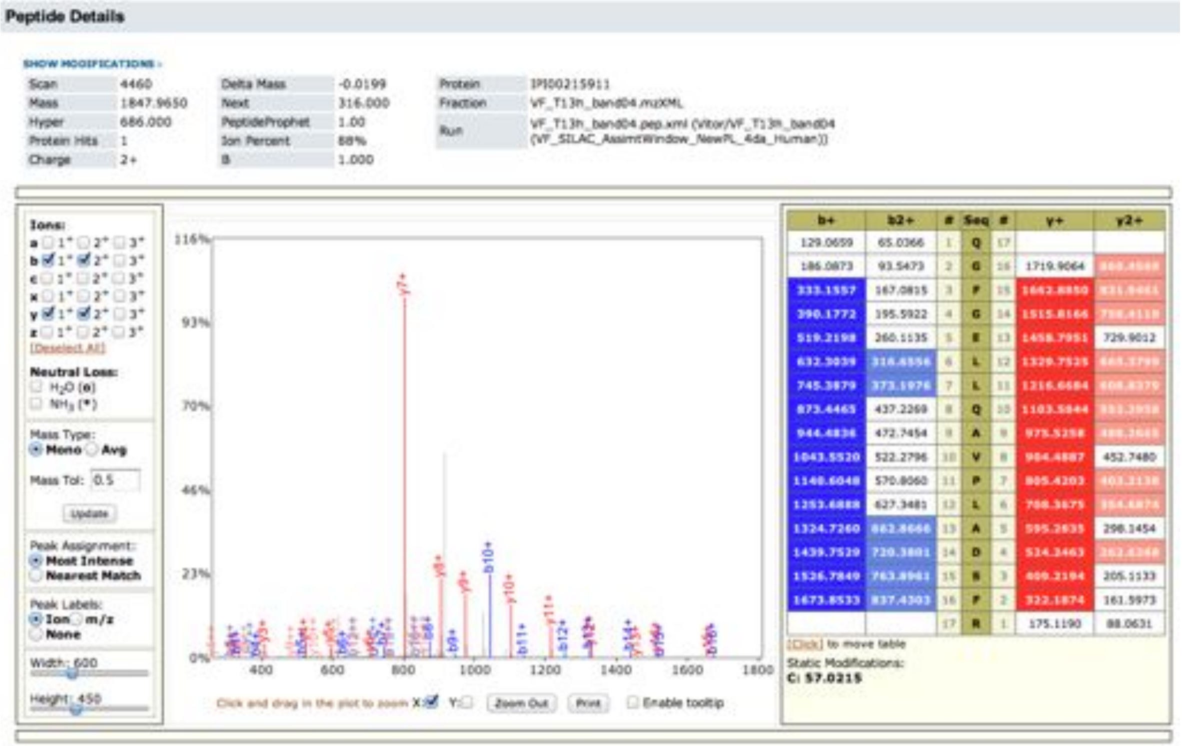
Height: 450

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	20		
201.0870	101.0471	2	A	19	2159.0114	1080.0093
298.1397	149.5735	3	P	18	2087.9743	1044.4908
445.2082	223.1077	4	F	17	1990.9215	995.9644
532.2402	266.6237	5	S	16	1843.8531	922.4302
661.2828	331.1450	6	E	15	1756.8211	878.9142
808.3512	404.6792	7	F	14	1627.7785	814.3929
955.4196	478.2134	8	F	13	1480.7101	740.8587
1068.5037	534.7555	9	L	12	1333.6417	667.3245
1183.5306	592.2689	10	D	11	1220.5576	610.7824
1280.5834	640.7953	11	P	10	1105.5307	553.2690
1337.6048	669.3061	12	G	9	1008.4779	504.7426
1438.6525	719.8299	13	T	8	951.4564	476.2319
1525.6846	763.3459	14	S	7	850.4088	425.7080
1624.7530	812.8801	15	V	6	763.3767	382.1920
1737.8370	869.4222	16	L	5	664.3083	332.6578
1852.8640	926.9356	17	D	4	551.2243	276.1158
1953.9117	977.4595	18	T	3	436.1973	218.6023
2113.9423	1057.4748	19	C	2	335.1496	168.0785
		20	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9851	IPI00215911	1	1	APEX1	4460	2+	-0,0199	1,0000	R.QGFGELLQAVPLADSFR.H



Peptide Details

SHOW MODIFICATIONS ›

Scan	4460	Delta Mass	-0.0199	Protein	IPI00215911
Mass	1847.9650	Next	316.000	Fraction	VF_T13h_band04.mzXML
Hyper	686.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

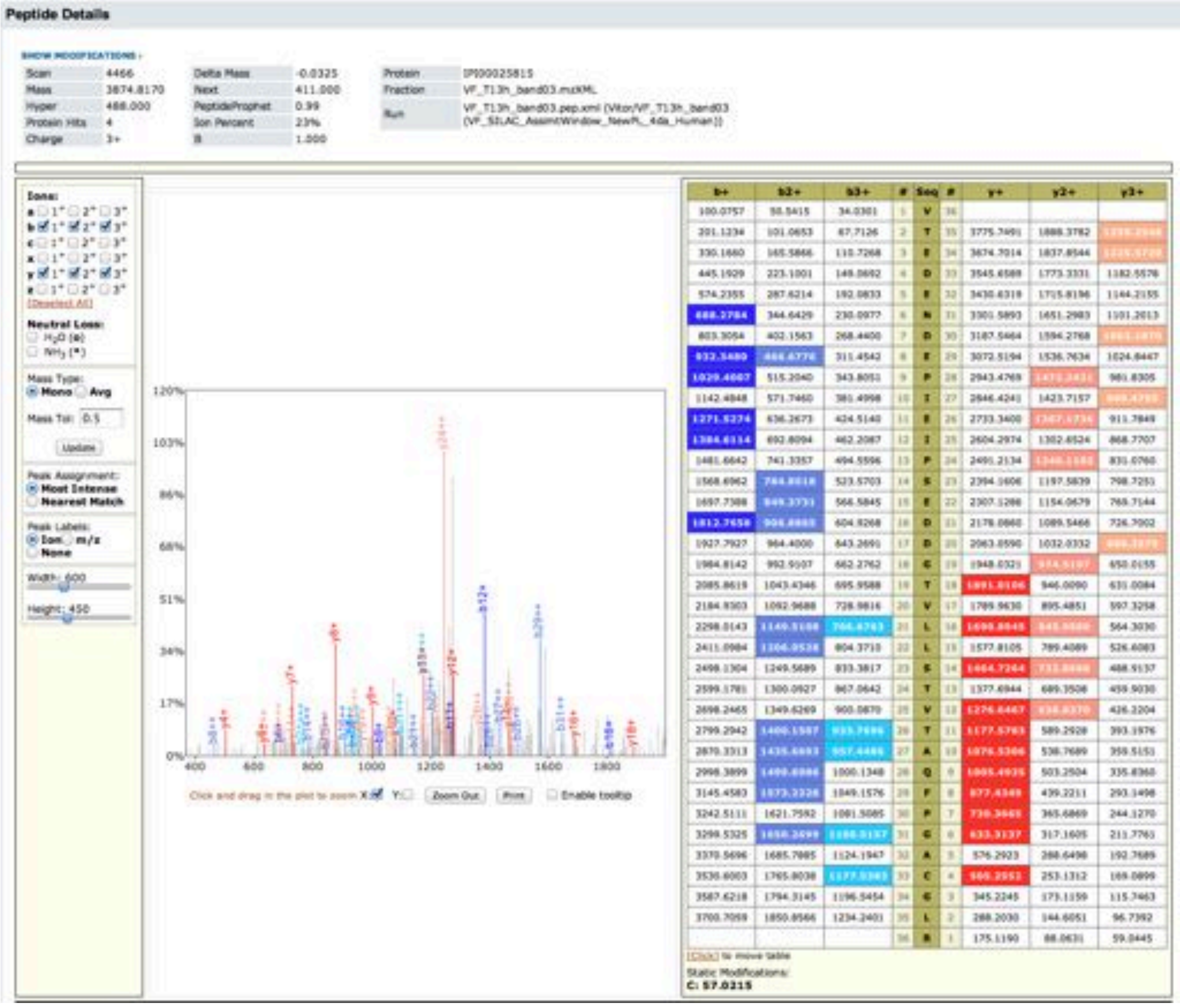
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	17		
186.0873	93.5473	2	G	16	1719.9064	860.4568
333.1557	167.0815	3	F	15	1662.8850	831.9461
390.1772	195.5922	4	G	14	1515.8166	758.4118
519.2198	260.1135	5	E	13	1458.7951	729.9012
632.3039	316.6556	6	L	12	1329.7525	665.3799
745.3879	373.1976	7	L	11	1216.6684	608.8379
873.4465	437.2269	8	Q	10	1103.5844	552.2958
944.4836	472.7454	9	A	9	975.5258	488.2665
1043.5520	522.2796	10	V	8	904.4887	452.7480
1140.6048	570.8060	11	P	7	805.4203	403.2138
1253.6888	627.3481	12	L	6	708.3675	354.6874
1324.7260	662.8666	13	A	5	595.2835	298.1454
1439.7529	720.3801	14	D	4	524.2463	262.6268
1526.7849	763.8961	15	S	3	409.2194	205.1133
1673.8533	837.4303	16	F	2	322.1874	161.5973
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,8835	IPI00844544, IPI00639819, IPI00642429, IPI00025815	1	1	-, TARDBP, TARDBP, TARDBP	4466	3+	-0,0325	0,9902	R.VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR.Y

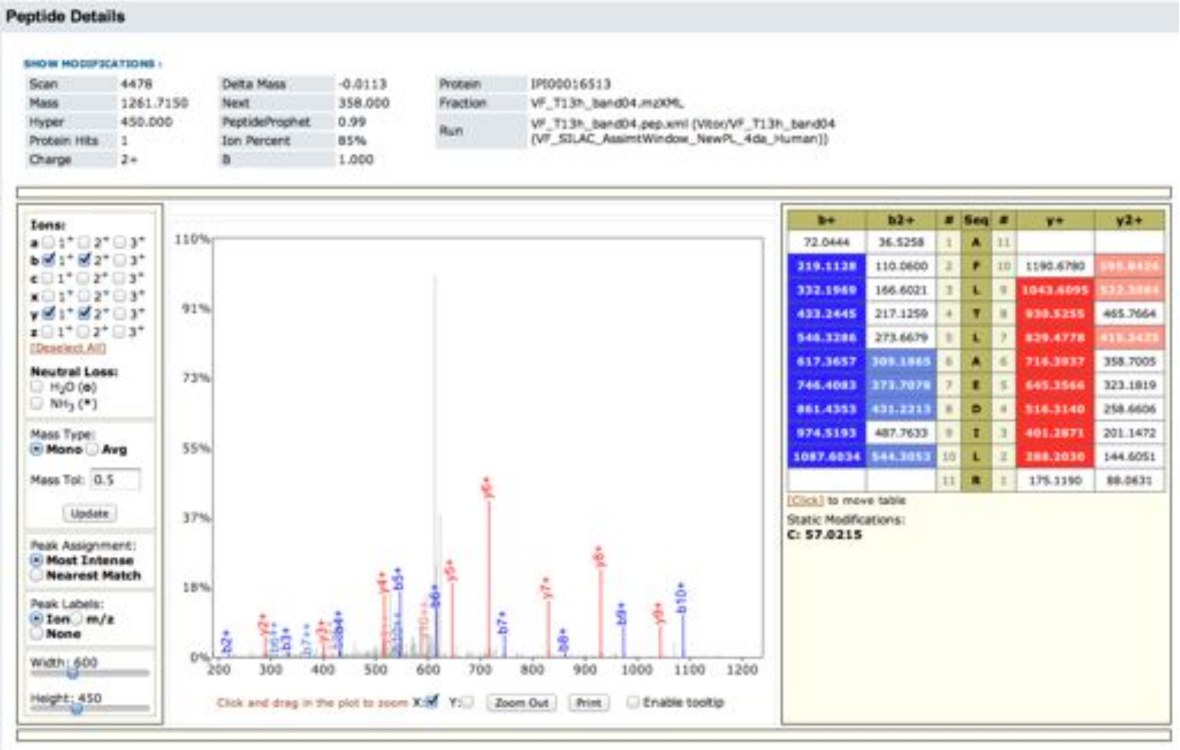


Peptide Details

Scan	4466	Delta Mass	-0.0325	Protein	IPI00025815
Mass	3874.8170	Next	411.000	Fraction	VF_T13h_band03.mzXML
Hyper	488.000	PeptideProphet	0.99	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	23%		
Charge	3+	B	1.000		

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9115	IPI00016513	1	1	RAB10	4478	2+	-0,0113	0,9946	K.AFLTLAEDILR.K



Peptide Details

SHOW MODIFICATIONS :

Scan	4478	Delta Mass	-0.0113	Protein	IPI00016513
Mass	1261.7150	Next	358.000	Fraction	VF_T13h_band04.mzXML
Hyper	450.000	PeptideProphet	0.99	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	85%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
72.0444	36.5258	1	A	11		
219.1128	110.0600	2	F	10	1190.6780	595.8426
332.1969	166.6021	3	L	9	1043.6095	522.3084
433.2445	217.1259	4	T	8	930.5255	465.7664
546.3286	273.6679	5	L	7	829.4778	415.2425
617.3657	309.1865	6	A	6	716.3937	358.7005
746.4083	373.7079	7	E	5	645.3566	323.1819
861.4353	431.2213	8	D	4	516.3140	258.6606
974.5193	487.7633	9	I	3	401.2871	201.1472
1087.6034	544.3053	10	L	2	288.2030	144.6051
		11	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Mass Type: Mono

Mass Tol: 0.5

Peak Assignment: Most Intense

Peak Labels: Ion

Width: 600

Height: 450

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00793285, IPI00845465, IPI00909239, IPI00013508, IPI00013808, IPI00759776	1	1	ACTN4, ACTN4, ACTN1, ACTN1, ACTN4, ACTN1	4478	2+	-0,0143	0,9999	R.VGWEQLLTTIAR.T

Peptide Details

SHOW MODIFICATIONS ›

Scan	4478	Delta Mass	-0.0143	Protein	IPI00013508
Mass	1386.7740	Next	338.000	Fraction	VF_T13h_band03.mzXML
Hyper	627.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	86%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

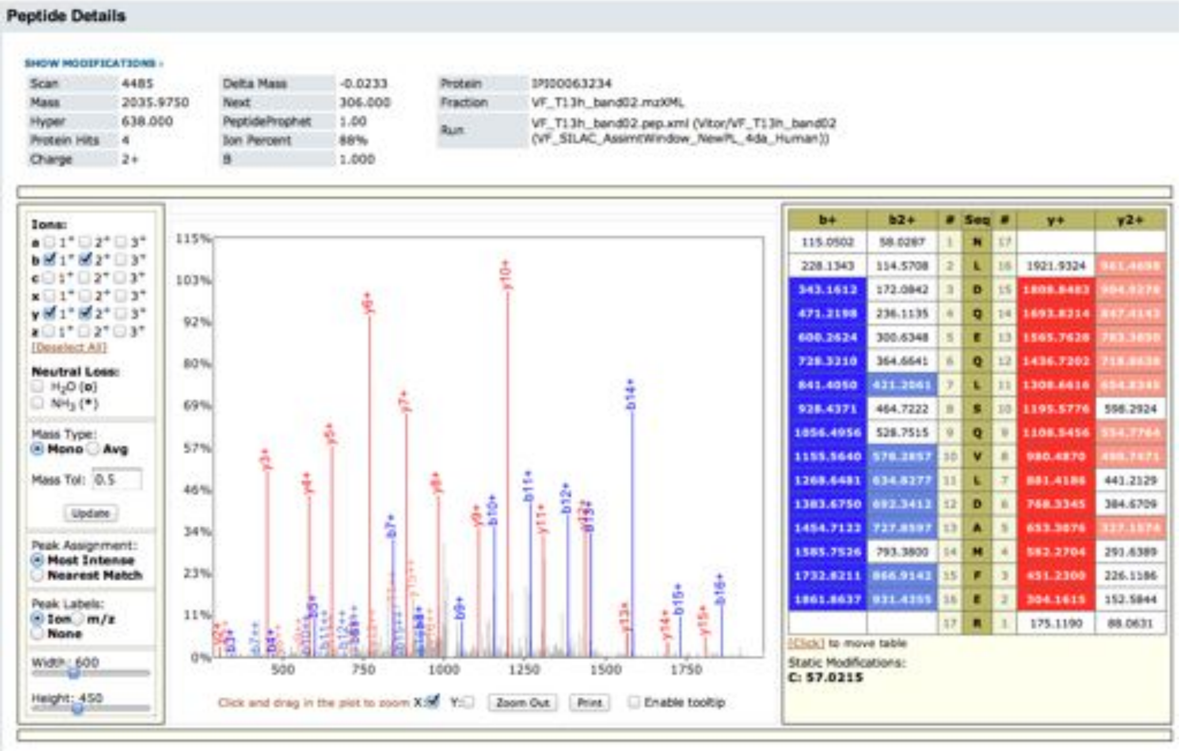
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	12		
157.0972	79.0522	2	G	11	1287.7056	644.3564
343.1765	172.0919	3	W	10	1230.6841	615.8457
472.2191	236.6132	4	E	9	1044.6048	522.8060
600.2776	300.6425	5	Q	8	915.5622	458.2847
713.3617	357.1845	6	L	7	787.5036	394.2554
826.4458	413.7265	7	L	6	674.4196	337.7134
927.4934	464.2504	8	T	5	561.3355	281.1714
1028.5411	514.7742	9	T	4	460.2878	230.6475
1141.6252	571.3162	10	I	3	359.2401	180.1237
1212.6623	606.8348	11	A	2	246.1561	123.5817
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9819	IPI00789242, IPI00788668, IPI00063234, IPI00219774	1	1	-, -, PRKAR2A, PRKAR2A	4485	2+	-0,0233	1,0000	K.NLDQEQLSQVLDAMFER.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	4485	Delta Mass	-0.0233	Protein	IPI00063234
Mass	2035.9750	Next	306.000	Fraction	VF_T13h_band02.mzXML
Hyper	638.000	PeptideProphet	1.00	Run	VF_T13h_band02.pep.xml (Vitor/VF_T13h_band02 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	88%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

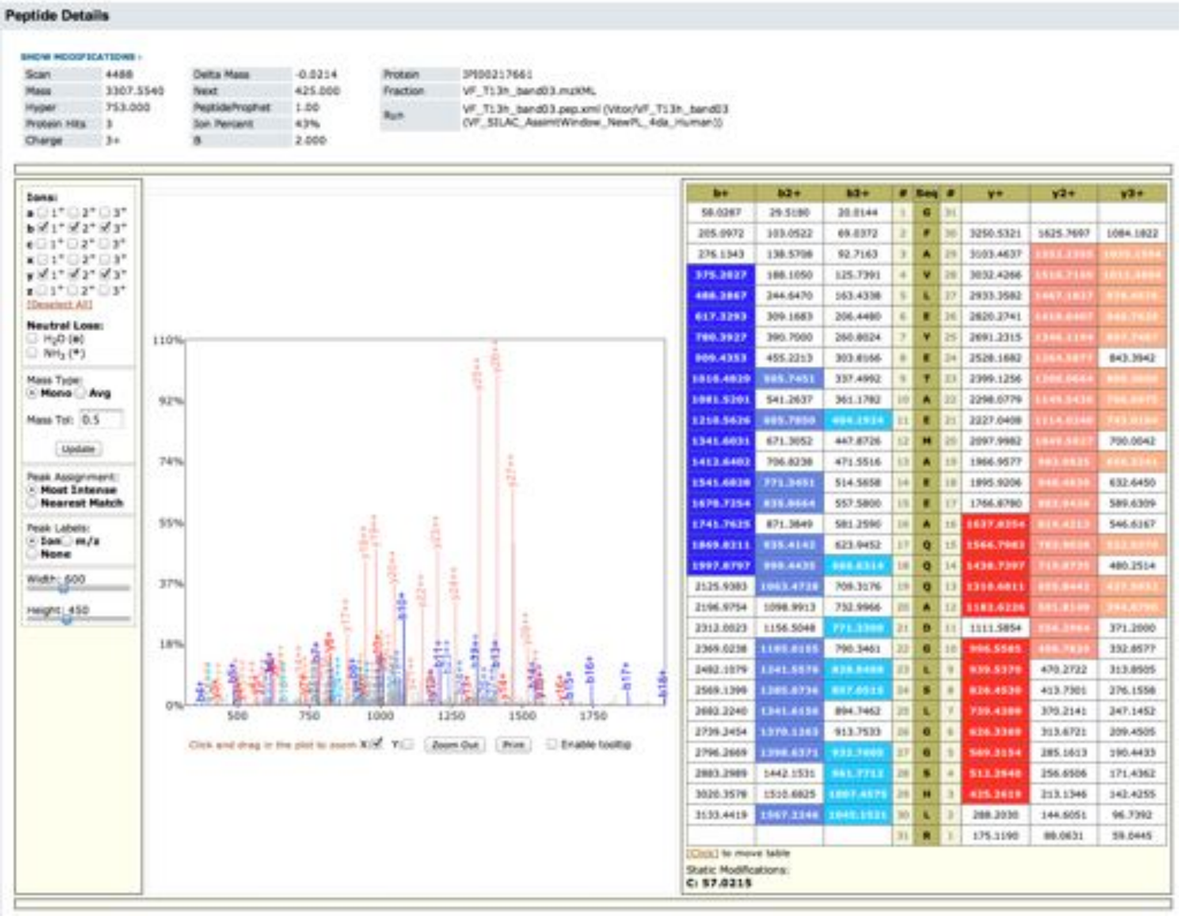
Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	17		
228.1343	114.5708	2	L	16	1921.9324	961.4698
343.1612	172.0842	3	D	15	1808.8483	904.9278
471.2198	236.1135	4	Q	14	1693.8214	847.4143
600.2624	300.6348	5	E	13	1565.7628	783.3850
728.3210	364.6641	6	Q	12	1436.7202	718.8638
841.4050	421.2061	7	L	11	1308.6616	654.8345
928.4371	464.7222	8	S	10	1195.5776	598.2924
1056.4956	528.7515	9	Q	9	1108.5456	554.7764
1155.5640	578.2857	10	V	8	980.4870	490.7471
1268.6481	634.8277	11	L	7	881.4186	441.2129
1383.6750	692.3412	12	D	6	768.3345	384.6709
1454.7122	727.8597	13	A	5	653.3076	327.1574
1585.7526	793.3800	14	M	4	582.2704	291.6389
1732.8211	866.9142	15	F	3	451.2300	226.1186
1861.8637	931.4355	16	E	2	304.1615	152.5844
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00643760, IPI00217670, IPI00217661	1	1	RAVER1, RAVER1, RAVER1	4488	3+	-0,0214	1,0000	K.GFAVLEYETAEMAEEAQQQADGLSLGGSHLR.V



Peptide Details

SHOW MODIFICATIONS ›

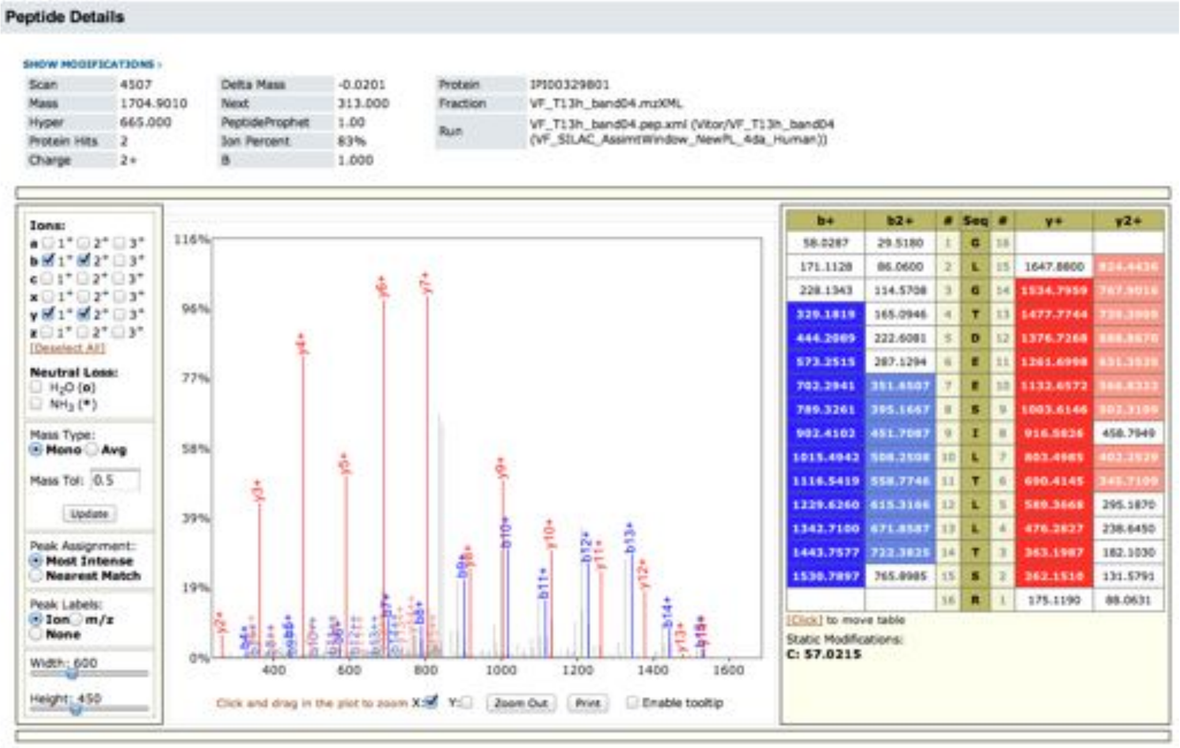
Scan	4488	Delta Mass	-0.0214	Protein	IPI00217661
Mass	3307.5540	Next	425.000	Fraction	VF_T13h_band03.mzXML
Hyper	753.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	43%		
Charge	3+	B	2.000		

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
58.0287	29.5180	20.0144	1	G	31			
205.0972	103.0522	69.0372	2	F	30	3250.5321	1625.7697	1084.1822
276.1343	138.5708	92.7163	3	A	29	3103.4637	[illegible]	[illegible]
375.2027	188.1050	125.7391	4	V	28	3032.4266	[illegible]	[illegible]
488.2867	244.6470	163.4338	5	L	27	2933.3582	[illegible]	[illegible]
617.3293	309.1683	206.4480	6	E	26	2820.2741	[illegible]	[illegible]
780.3927	390.7000	260.8024	7	Y	25	2691.2315	[illegible]	[illegible]
909.4353	455.2213	303.8166	8	E	24	2528.1682	[illegible]	843.3942
1010.4829	505.7451	337.4992	9	T	23	2399.1256	[illegible]	[illegible]
1081.5201	541.2637	361.1782	10	A	22	2298.0779	[illegible]	[illegible]
1210.5626	605.7850	404.1924	11	E	21	2227.0408	[illegible]	[illegible]
1341.6031	671.3052	447.8726	12	M	20	2097.9982	[illegible]	700.0042
1412.6402	706.8238	471.5516	13	A	19	1966.9577	[illegible]	[illegible]
1541.6828	771.3451	514.5658	14	E	18	1895.9206	[illegible]	632.6450
1670.7254	835.8664	557.5800	15	E	17	1766.8780	[illegible]	589.6309
1741.7625	871.3849	581.2590	16	A	16	1637.8354	[illegible]	546.6167
1869.8211	935.4142	623.9452	17	Q	15	1566.7983	[illegible]	[illegible]
1997.8797	999.4435	666.6314	18	Q	14	1438.7397	[illegible]	480.2514
2125.9383	1063.4728	709.3176	19	Q	13	1310.6811	[illegible]	[illegible]
2196.9754	1098.9913	732.9966	20	A	12	1182.6226	[illegible]	[illegible]
2312.0023	1156.5048	771.3388	21	D	11	1111.5854	[illegible]	371.2000
2369.0238	1185.0155	790.3461	22	G	10	996.5585	[illegible]	332.8577
2482.1079	1241.5576	828.0408	23	L	9	939.5370	470.2722	313.8505
2569.1399	1285.0736	857.0515	24	S	8	826.4530	413.7301	276.1558
2682.2240	1341.6156	894.7462	25	L	7	739.4209	370.2141	247.1452
2739.2454	1370.1263	913.7533	26	G	6	626.3369	313.6721	209.4505
2796.2669	1398.6371	932.7605	27	G	5	569.3154	285.1613	190.4433
2883.2989	1442.1531	961.7712	28	S	4	512.2940	256.6506	171.4362
3020.3578	1510.6825	1007.4575	29	H	3	425.2619	213.1346	142.4255
3133.4419	1567.2246	1045.1521	30	L	2	288.2030	144.6051	96.7392
			31	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9851	IPI00872379, IPI00329801	1	1	ANXA5, ANXA5	4507	2+	-0,0201	1,0000	K.GLGTDEESILTLLTSR.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	4507	Delta Mass	-0.0201	Protein	IPI00329801
Mass	1704.9010	Next	313.000	Fraction	VF_T13h_band04.mzXML
Hyper	665.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	83%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

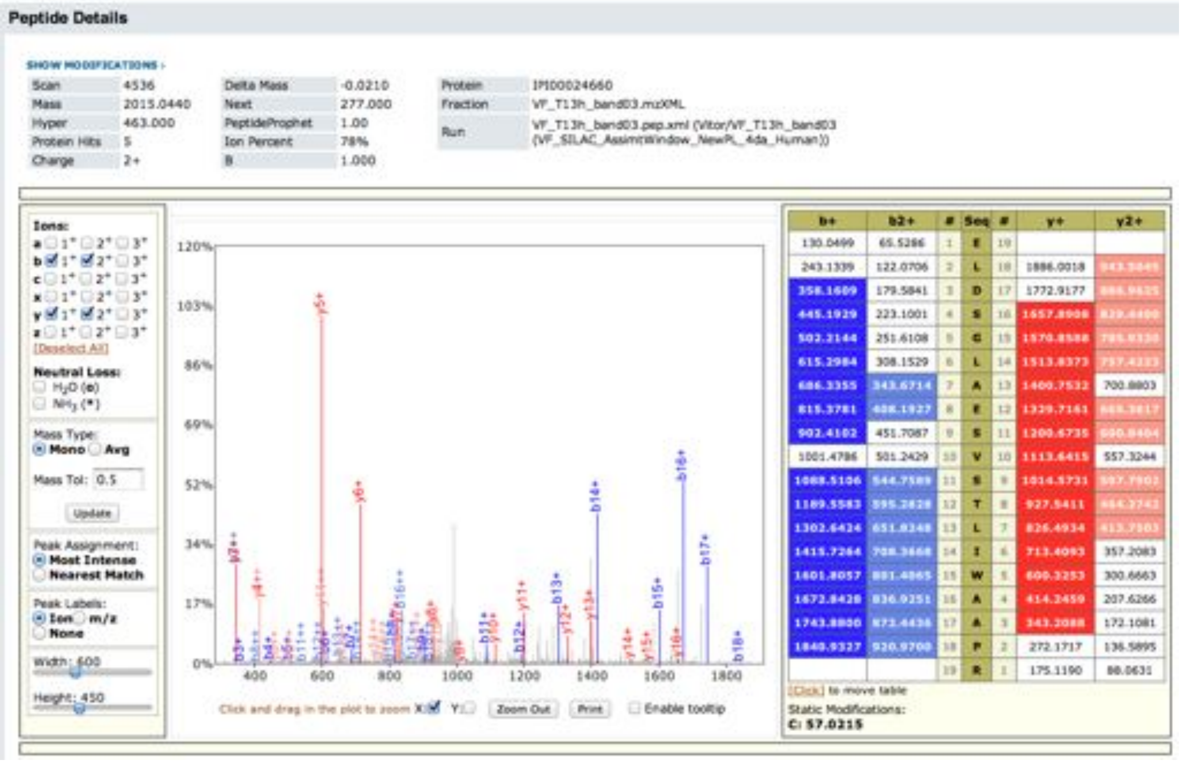
Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
58.0287	29.5180	1	G	16		
171.1128	86.0600	2	L	15	1647.8800	824.4436
228.1343	114.5708	3	G	14	1534.7959	767.9016
329.1819	165.0946	4	T	13	1477.7744	739.3908
444.2089	222.6081	5	D	12	1376.7268	688.8670
573.2515	287.1294	6	E	11	1261.6998	631.3535
702.2941	351.6507	7	E	10	1132.6572	566.8322
789.3261	395.1667	8	S	9	1003.6146	502.3109
902.4102	451.7087	9	I	8	916.5826	458.7949
1015.4942	508.2508	10	L	7	803.4985	402.2529
1116.5419	558.7746	11	T	6	690.4145	345.7109
1229.6260	615.3166	12	L	5	589.3668	295.1870
1342.7100	671.8587	13	L	4	476.2827	238.6450
1443.7577	722.3825	14	T	3	363.1987	182.1030
1530.7897	765.8985	15	S	2	262.1510	131.5791
		16	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9833	IPI00909013, IPI00420088, IPI00643007, IPI00024660, IPI00386516	1	1	-, KIAA0174, KIAA0174, KIAA0174, KIAA0174	4536	2+	-0,0210	0,9996	K.ELDSGLAESVSTLIWAAPR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4536	Delta Mass	-0.0210	Protein	IPI00024660
Mass	2015.0440	Next	277.000	Fraction	VF_T13h_band03.mzXML
Hyper	463.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	5	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

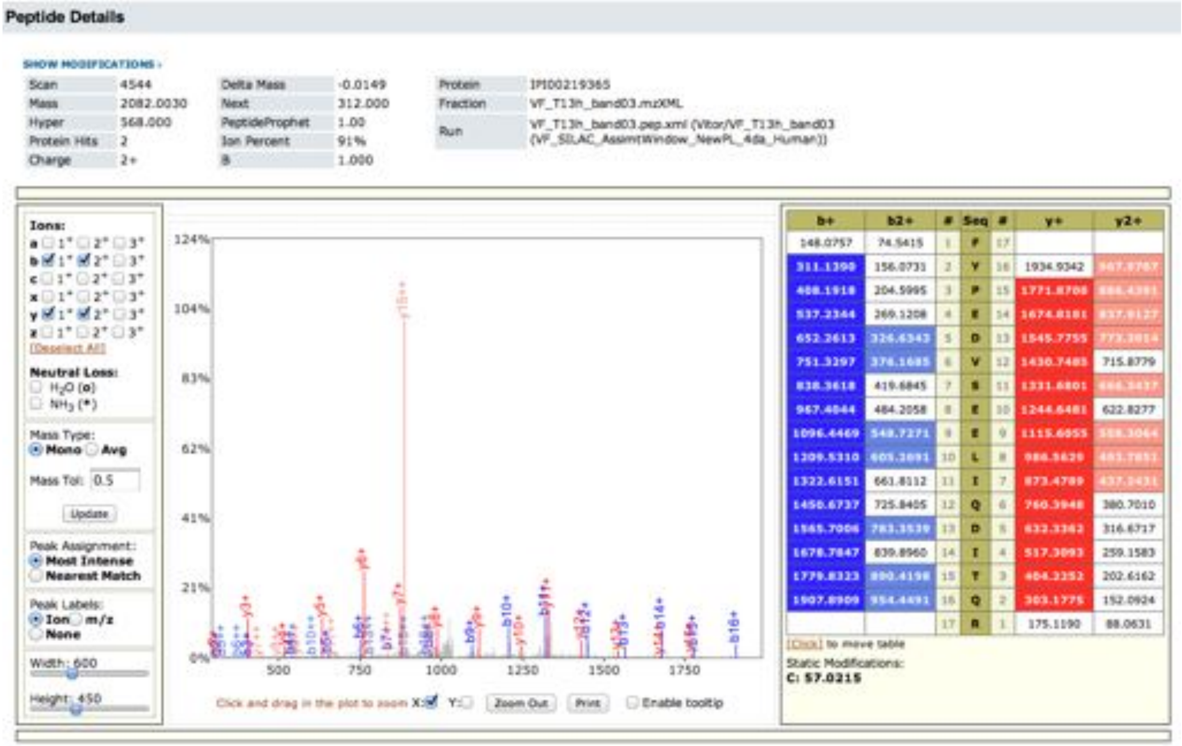
Height: 450

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	19		
243.1339	122.0706	2	L	18	1886.0018	943.5045
358.1609	179.5841	3	D	17	1772.9177	886.9625
445.1929	223.1001	4	S	16	1657.8906	829.4490
502.2144	251.6108	5	G	15	1570.8588	785.9330
615.2984	308.1529	6	L	14	1513.8373	757.4223
686.3355	343.6714	7	A	13	1400.7532	700.8803
815.3781	408.1927	8	E	12	1329.7161	665.3617
902.4102	451.7087	9	S	11	1200.6735	600.8404
1001.4786	501.2429	10	V	10	1113.6415	557.3244
1088.5106	544.7589	11	S	9	1014.5731	507.7902
1189.5583	595.2828	12	T	8	927.5411	464.2742
1302.6424	651.8248	13	L	7	826.4934	413.7503
1415.7264	708.3668	14	I	6	713.4093	357.2083
1601.8057	801.4065	15	W	5	600.3253	300.6663
1672.8428	836.9251	16	A	4	414.2459	207.6266
1743.8800	872.4436	17	A	3	343.2088	172.1081
1840.9327	920.9700	18	P	2	272.1717	136.5895
		19	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00872814, IPI00219365	1	1	MSN, MSN	4544	2+	-0,0149	0,9999	K.FYPEDVSEELIQDITQR.L



Peptide Details

SHOW MODIFICATIONS ›

Scan	4544	Delta Mass	-0.0149	Protein	IPI00219365
Mass	2082.0030	Next	312.000	Fraction	VF_T13h_band03.mzXML
Hyper	568.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	91%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type:
● **Mono** ○ **Avg**

Mass Tol: 0.5

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

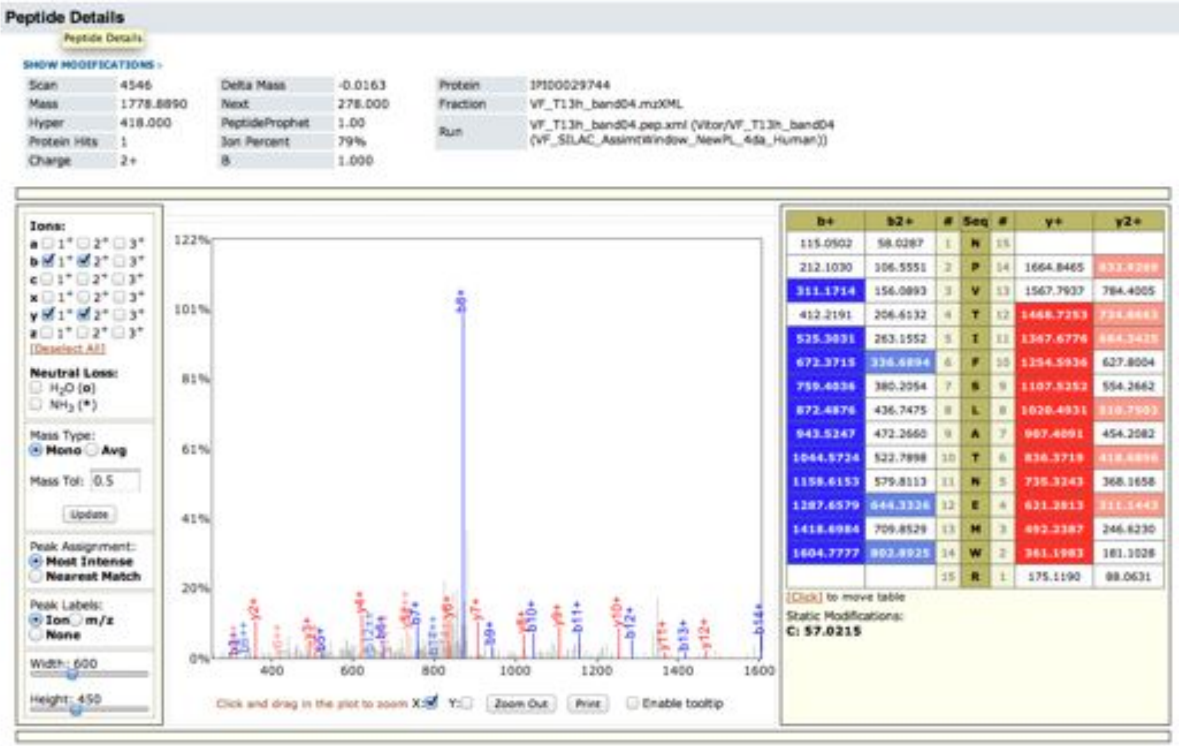
Height: 450

b+	b2+	#	Seq	#	y+	y2+
148.0757	74.5415	1	F	17		
311.1390	156.0731	2	Y	16	1934.9342	967.9707
408.1918	204.5995	3	P	15	1771.8708	886.4391
537.2344	269.1208	4	E	14	1674.8181	837.9127
652.2613	326.6343	5	D	13	1545.7755	773.3914
751.3297	376.1685	6	V	12	1430.7485	715.8779
838.3618	419.6845	7	S	11	1331.6801	666.3437
967.4044	484.2058	8	E	10	1244.6481	622.8277
1096.4469	548.7271	9	E	9	1115.6055	558.3064
1209.5310	605.2691	10	L	8	986.5629	493.7851
1322.6151	661.8112	11	I	7	873.4789	437.2431
1450.6737	725.8405	12	Q	6	760.3948	380.7010
1565.7006	783.3539	13	D	5	632.3362	316.6717
1678.7847	839.8960	14	I	4	517.3093	259.1583
1779.8323	890.4198	15	T	3	404.2252	202.6162
1907.8909	954.4491	16	Q	2	303.1775	152.0924
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9636	IPI00029744	1	1	SSBP1	4546	2+	-0,0163	0,9985	K.NPVTIFSLATNEMWR.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	4546	Delta Mass	-0.0163	Protein	IPI00029744
Mass	1778.8890	Next	278.000	Fraction	VF_T13h_band04.mzXML
Hyper	418.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	79%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

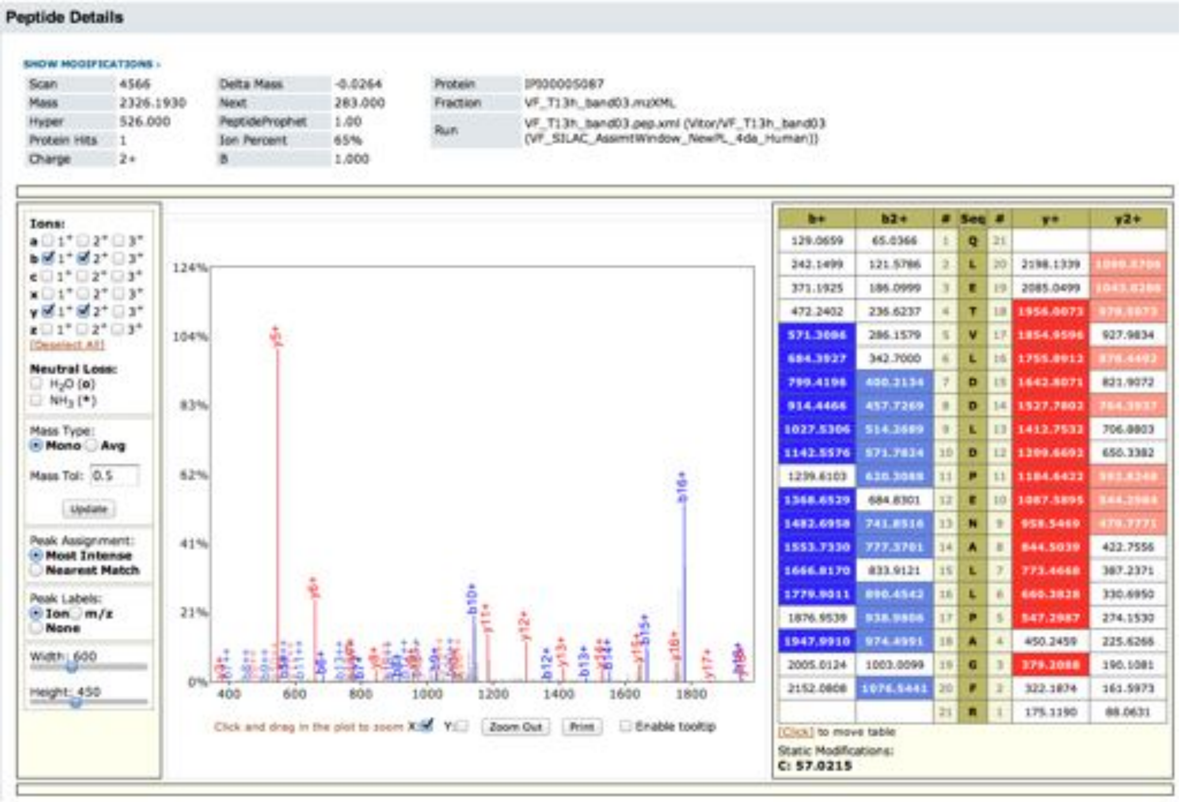
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	15		
212.1030	106.5551	2	P	14	1664.8465	832.9269
311.1714	156.0893	3	V	13	1567.7937	784.4005
412.2191	206.6132	4	T	12	1468.7253	734.8663
525.3031	263.1552	5	I	11	1367.6776	684.3425
672.3715	336.6894	6	F	10	1254.5936	627.8004
759.4036	380.2054	7	S	9	1107.5252	554.2662
872.4876	436.7475	8	L	8	1020.4931	510.7503
943.5247	472.2660	9	A	7	907.4091	454.2082
1044.5724	522.7898	10	T	6	836.3719	418.6896
1158.6153	579.8113	11	N	5	735.3243	368.1658
1287.6579	644.3326	12	E	4	621.2813	311.1443
1418.6984	709.8529	13	M	3	492.2387	246.6230
1604.7777	802.8925	14	W	2	361.1983	181.1028
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00005087	1	1	TMOD3	4566	2+	-0,0264	0,9999	K.QLETVLDDLDPENALLPAGFR.Q



Peptide Details

SHOW MODIFICATIONS ›

Scan	4566	Delta Mass	-0.0264	Protein	IPI00005087
Mass	2326.1930	Next	283.000	Fraction	VF_T13h_band03.mzXML
Hyper	526.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	65%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

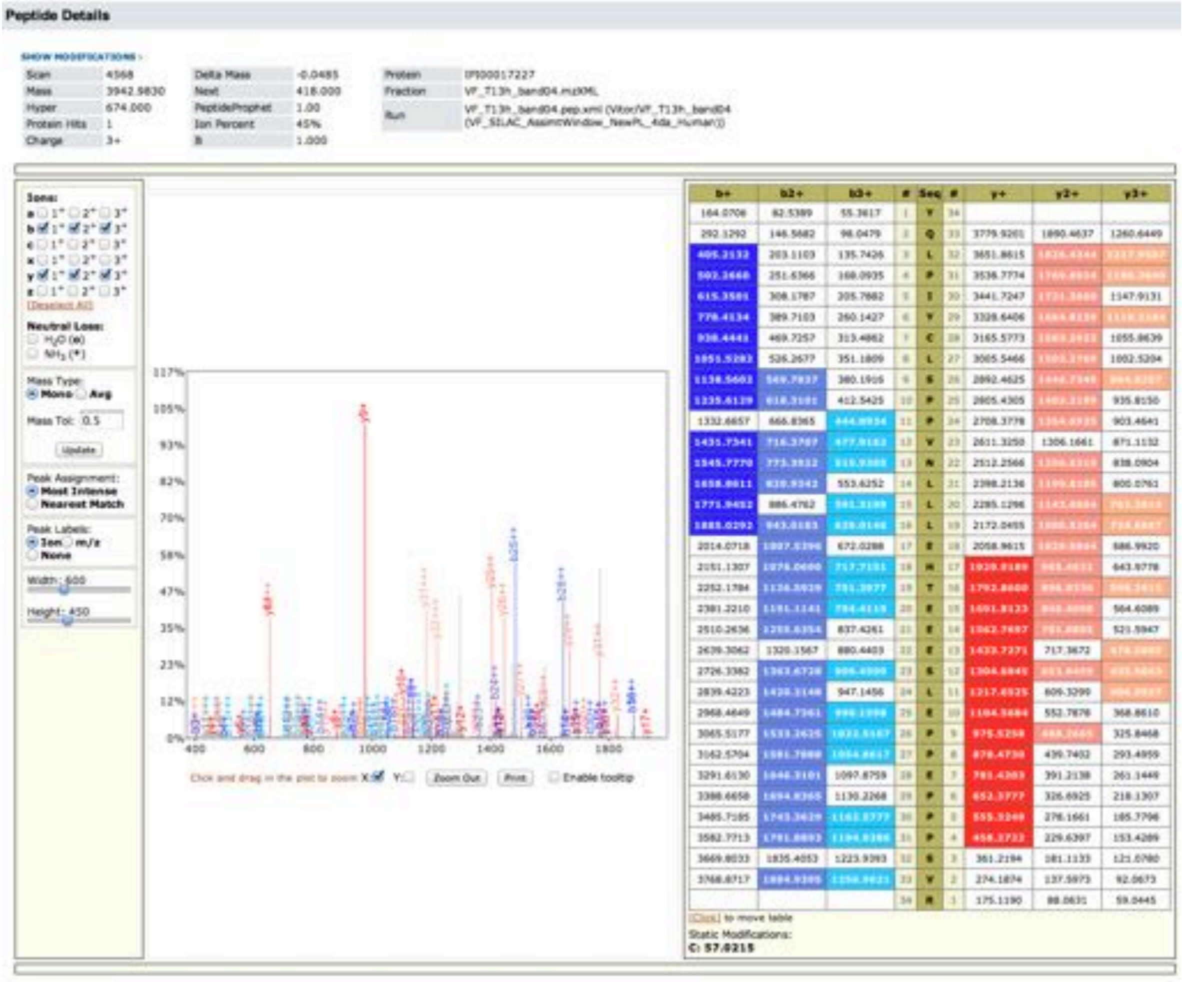
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip

b+	b2+	#	Seq	#	y+	y2+
129.0659	65.0366	1	Q	21		
242.1499	121.5786	2	L	20	2198.1339	1099.5706
371.1925	186.0999	3	E	19	2085.0499	1043.0286
472.2402	236.6237	4	T	18	1956.0073	978.5073
571.3086	286.1579	5	V	17	1854.9596	927.9834
684.3927	342.7000	6	L	16	1755.8912	878.4492
799.4196	400.2134	7	D	15	1642.8071	821.9072
914.4466	457.7269	8	D	14	1527.7802	764.3937
1027.5306	514.2689	9	L	13	1412.7532	706.8803
1142.5576	571.7824	10	D	12	1299.6691	650.3382
1239.6103	620.3088	11	P	11	1184.6422	592.8248
1368.6529	684.8301	12	E	10	1087.5895	544.2984
1482.6958	741.8516	13	N	9	958.5469	479.7771
1553.7330	777.3701	14	A	8	844.5039	422.7556
1666.8170	833.9121	15	L	7	773.4668	387.2371
1779.9011	890.4542	16	L	6	660.3828	330.6950
1876.9539	938.9806	17	P	5	547.2987	274.1530
1947.9910	974.4991	18	A	4	450.2459	225.6266
2005.0124	1003.0099	19	G	3	379.2088	190.1081
2152.0808	1076.5441	20	F	2	322.1874	161.5973
		21	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9851	IPI00017227	1	1	UBTD1	4568	3+	-0,0485	1,0000	R.YQLPIYCLSPPVNLLLEHTEEESLEPPEPPPSVR.R



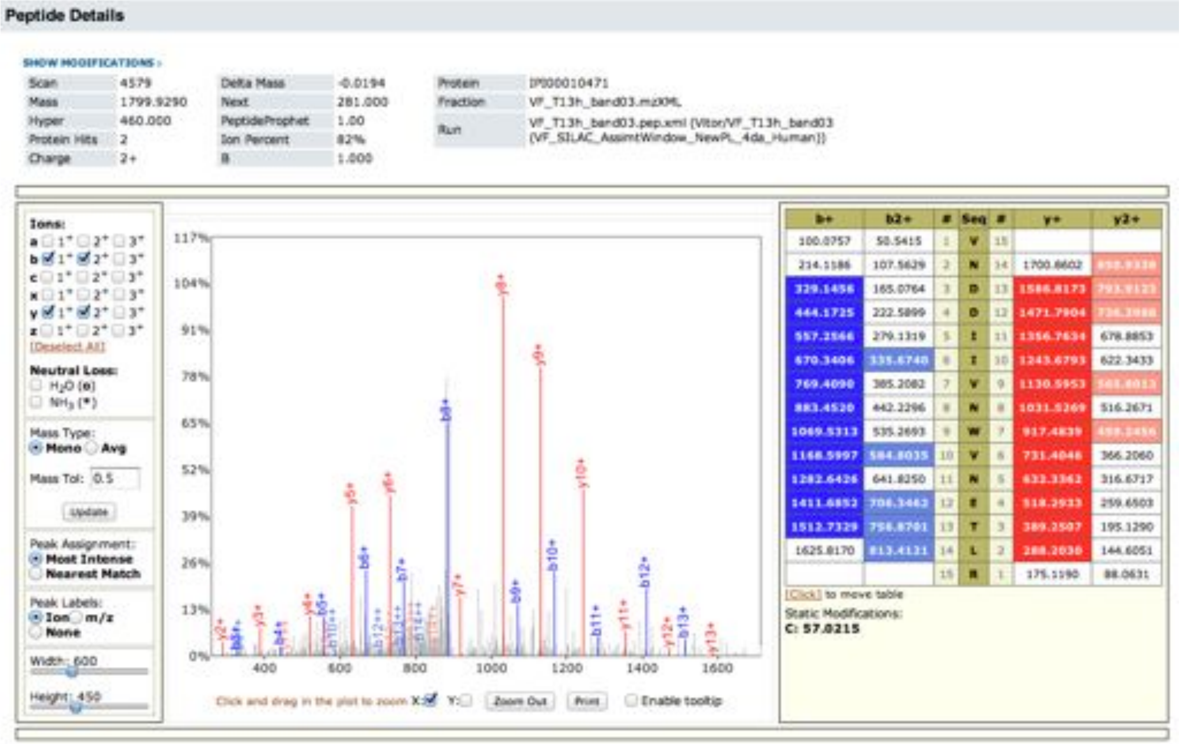
Peptide Details

SHOW MODIFICATIONS ›

Scan	4568	Delta Mass	-0.0485	Protein	IPI00017227
Mass	3942.9830	Next	418.000	Fraction	VF_T13h_band04.mzXML
Hyper	674.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	45%		
Charge	3+	B	1.000		

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9822	IPI00909658, IPI00010471	1	1	-, LCP1	4579	2+	-0,0194	0,9995	K.VNDDIIVNWVNETLR.E



Peptide Details

SHOW MODIFICATIONS ›

Scan	4579	Delta Mass	-0.0194	Protein	IPI00010471
Mass	1799.9290	Next	281.000	Fraction	VF_T13h_band03.mzXML
Hyper	460.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	82%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

Height: 450

Click and drag in the plot to zoom X: ☑ Y: ☐

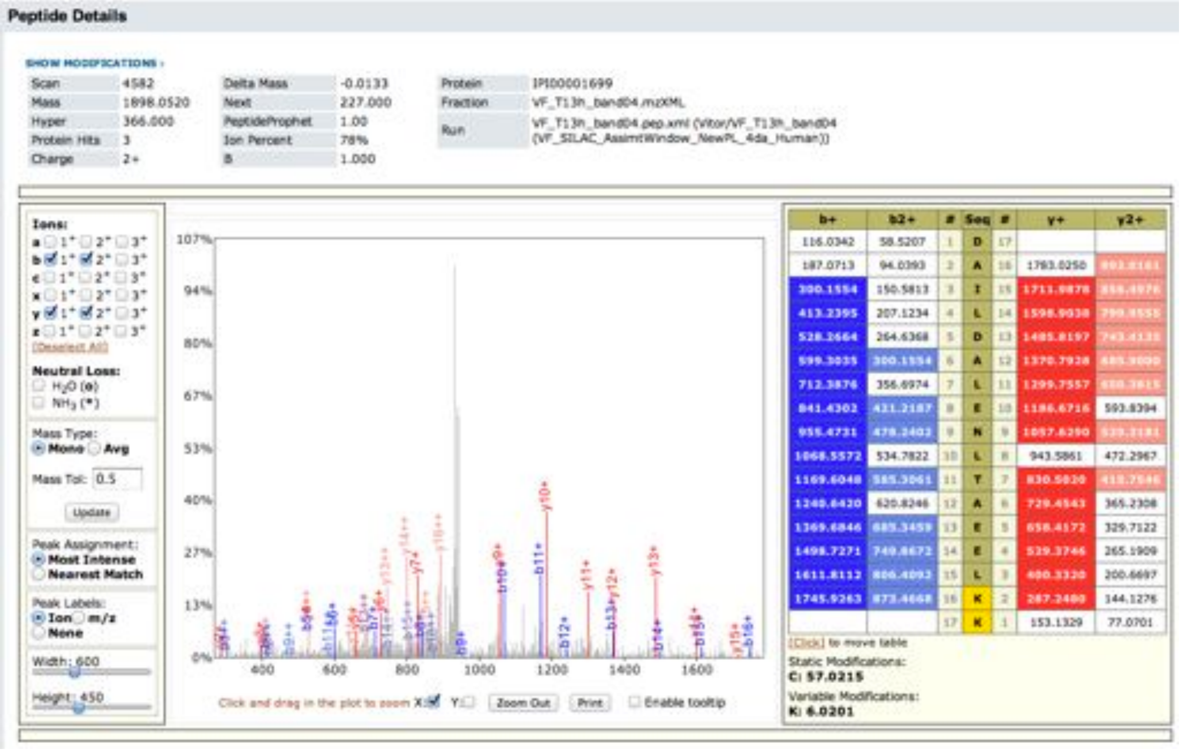
Enable tooltip ☐

b+	b2+	#	Seq	#	y+	y2+
100.0757	50.5415	1	V	15		
214.1186	107.5629	2	N	14	1700.8602	850.9338
329.1456	165.0764	3	D	13	1586.8173	793.9123
444.1725	222.5899	4	D	12	1471.7904	736.3988
557.2566	279.1319	5	I	11	1356.7634	678.8853
670.3406	335.6740	6	I	10	1243.6793	622.3433
769.4090	385.2082	7	V	9	1130.5953	565.8013
883.4520	442.2296	8	N	8	1031.5269	516.2671
1069.5313	535.2693	9	W	7	917.4839	459.2456
1168.5997	584.8035	10	V	6	731.4046	366.2060
1282.6426	641.8250	11	N	5	633.3362	316.6717
1411.6852	706.3462	12	E	4	518.2933	259.6503
1512.7329	756.8701	13	T	3	389.2507	195.1290
1625.8170	813.4121	14	L	2	288.2030	144.6051
		15	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9594	IPI00221362, IPI00221360, IPI00001699	1	1	PYCARD, PYCARD, PYCARD	4582	2+	-0,0133	0,9982	R.DAILDALENLTAEELK'K'.F



Peptide Details

SHOW MODIFICATIONS ›

Scan	4582	Delta Mass	-0.0133	Protein	IPI00001699
Mass	1898.0520	Next	227.000	Fraction	VF_T13h_band04.mzXML
Hyper	366.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	78%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● **Mono** ○ **Avg**

Mass Tol: 0.5

Update

Peak Assignment:
● **Most Intense**
○ **Nearest Match**

Peak Labels:
● **Ion** ○ **m/z**
○ **None**

Width: 600

Height: 450

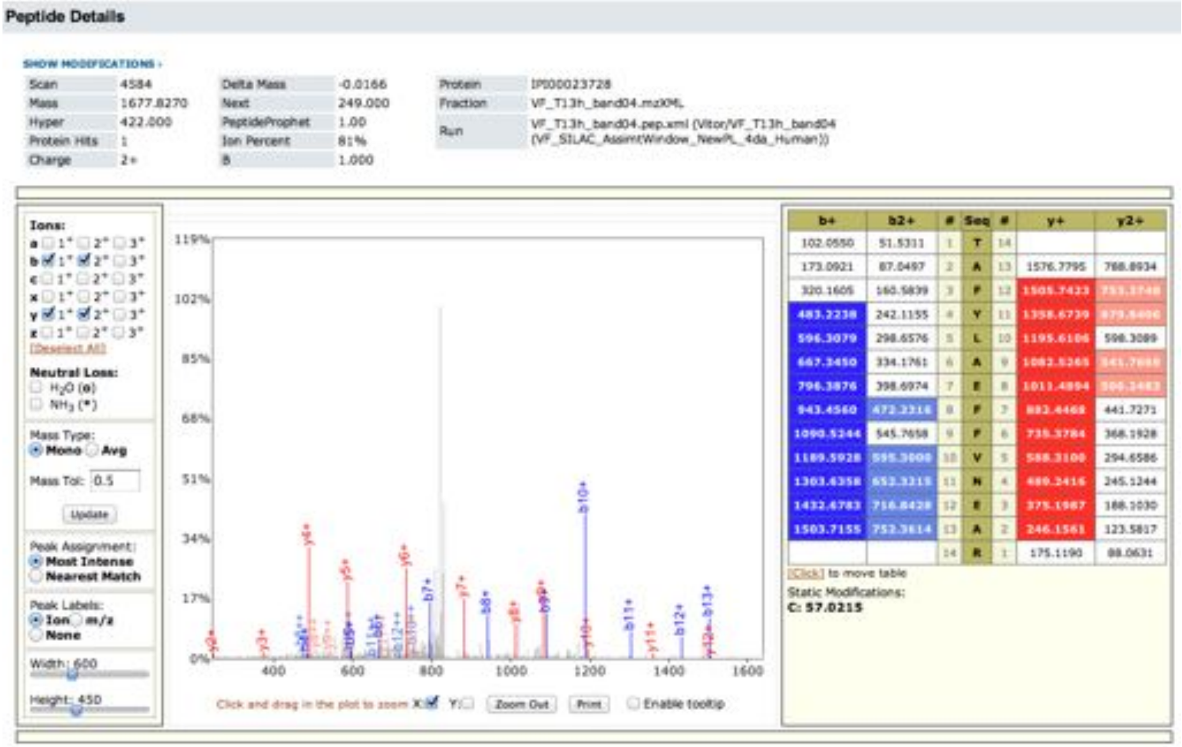
b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	17		
187.0713	94.0393	2	A	16	1783.0250	892.0161
300.1554	150.5813	3	I	15	1711.9878	856.4976
413.2395	207.1234	4	L	14	1598.9038	799.9555
528.2664	264.6368	5	D	13	1485.8197	743.4135
599.3035	300.1554	6	A	12	1370.7928	685.9000
712.3876	356.6974	7	L	11	1299.7557	650.3815
841.4302	421.2187	8	E	10	1186.6716	593.8394
955.4731	478.2402	9	N	9	1057.6290	529.3181
1068.5572	534.7822	10	L	8	943.5861	472.2967
1169.6048	585.3061	11	T	7	830.5020	415.7546
1240.6420	620.8246	12	A	6	729.4543	365.2308
1369.6846	685.3459	13	E	5	658.4172	329.7122
1498.7271	749.8672	14	E	4	529.3746	265.1909
1611.8112	806.4093	15	L	3	400.3320	200.6697
1745.9263	873.4668	16	K	2	287.2400	144.1276
		17	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9764	IPI00023728	1	1	GGH	4584	2+	-0,0166	0,9994	K.TAFYLAEFFVNEAR.K



Peptide Details

SHOW MODIFICATIONS ›

Scan	4584	Delta Mass	-0.0166	Protein	IPI00023728
Mass	1677.8270	Next	249.000	Fraction	VF_T13h_band04.mzXML
Hyper	422.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	81%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Update

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

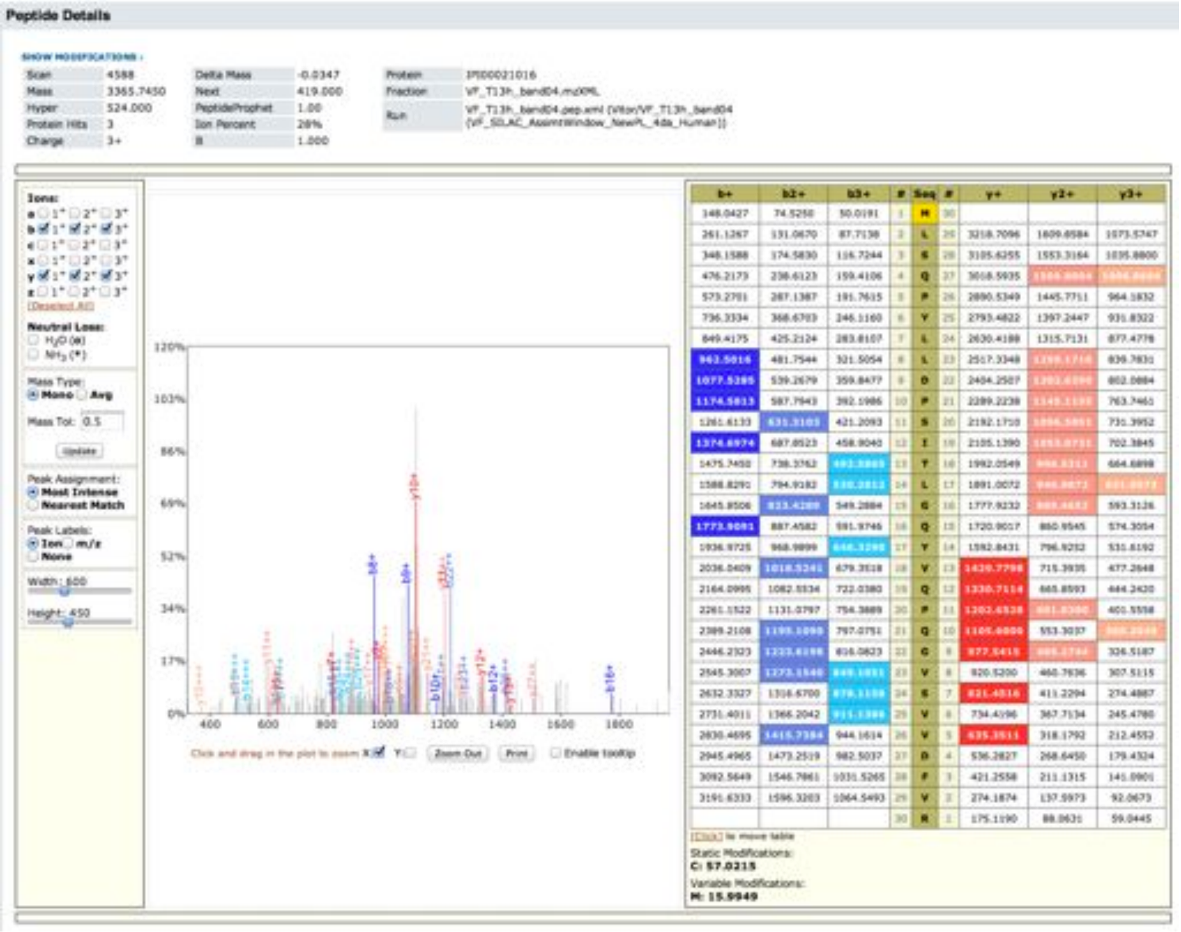
Height: 450

b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	14		
173.0921	87.0497	2	A	13	1576.7795	788.8934
320.1605	160.5839	3	F	12	1505.7423	753.3748
483.2238	242.1155	4	Y	11	1358.6739	679.8406
596.3079	298.6576	5	L	10	1195.6106	598.3089
667.3450	334.1761	6	A	9	1082.5265	541.7669
796.3876	398.6974	7	E	8	1011.4894	506.2483
943.4560	472.2316	8	F	7	882.4468	441.7271
1090.5244	545.7658	9	F	6	735.3784	368.1928
1189.5928	595.3000	10	V	5	588.3100	294.6586
1303.6358	652.3215	11	N	4	489.2416	245.1244
1432.6783	716.8428	12	E	3	375.1987	188.1030
1503.7155	752.3614	13	A	2	246.1561	123.5817
		14	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9594	IPI00910455, IPI00021016, IPI00216260	1	1	-, TSFM, TSFM	4588	3+	-0,0347	0,9982	K.M"LSQPYLLDPSITLGQYVQPQGVSVVDFVR.F



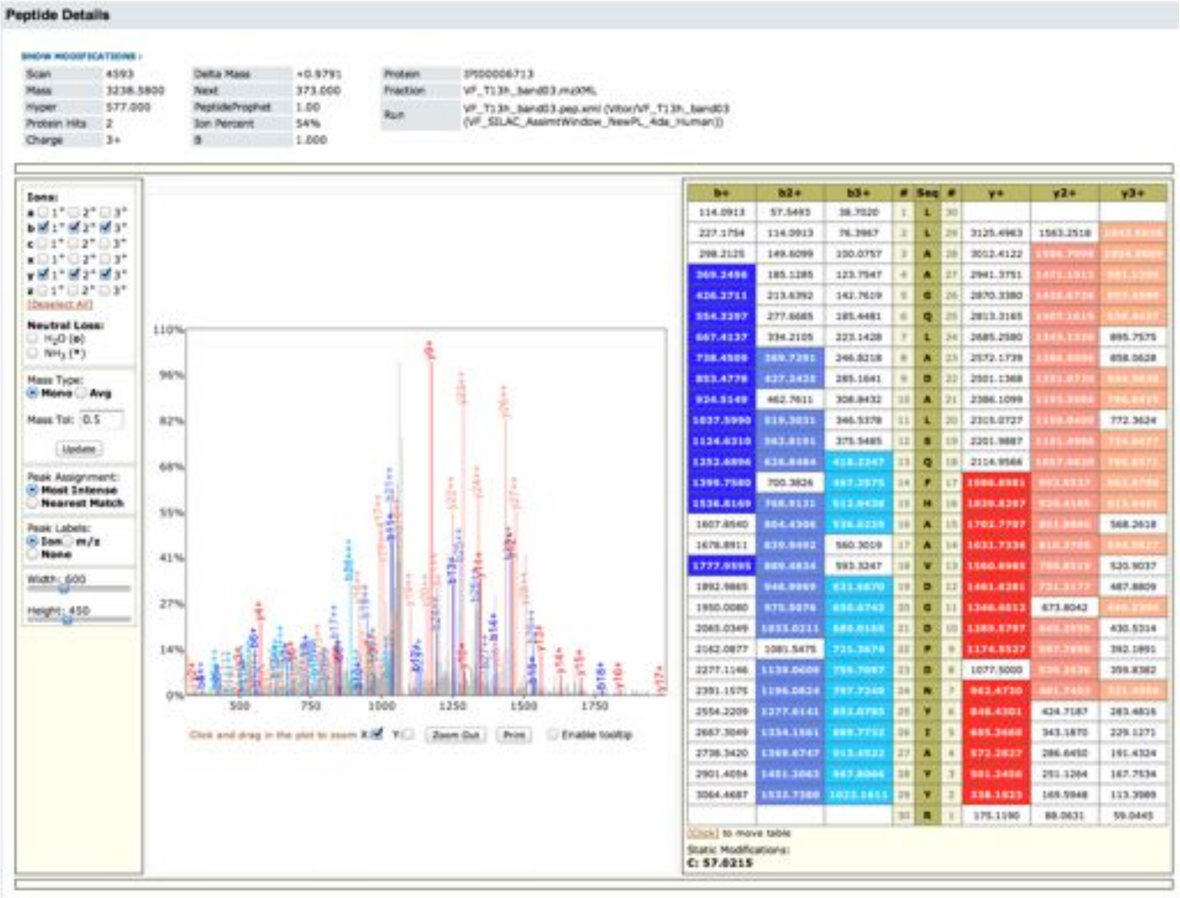
Scan	4588	Delta Mass	-0.0347	Protein	IPI00021016
Mass	3365.7450	Next	419.000	Fraction	VF_T13h_band04.mzXML
Hyper	524.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Viton/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	3	Ion Percent	28%		
Charge	3+	B	1.000		

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
148.0427	74.5250	50.0191	1	M	30			
261.1267	131.0670	87.7138	2	L	29	3218.7096	1609.8584	1073.5747
348.1588	174.5830	116.7244	3	S	28	3105.6255	1553.3164	1035.8800
476.2173	238.6123	159.4106	4	Q	27	3018.5935	1509.8004	1006.8694
573.2701	287.1387	191.7615	5	P	26	2890.5349	1445.7711	964.1832
736.3334	368.6703	246.1160	6	Y	25	2793.4822	1397.2447	931.8322
849.4175	425.2124	283.8107	7	L	24	2630.4188	1315.7131	877.4778
962.5016	481.7544	321.5054	8	L	23	2517.3348	1259.1710	839.7831
1077.5285	539.2679	359.8477	9	D	22	2404.2507	1202.6290	802.0884
1174.5813	587.7943	392.1986	10	P	21	2289.2238	1145.1155	763.7461
1261.6133	631.3103	421.2093	11	S	20	2192.1710	1096.5891	731.3952
1374.6974	687.8523	458.9040	12	I	19	2105.1390	1053.0731	702.3845
1475.7450	738.3762	492.5865	13	T	18	1992.0549	996.5311	664.6898
1588.8291	794.9182	530.2812	14	L	17	1891.0072	946.0072	631.0073
1645.8506	823.4289	549.2884	15	G	16	1777.9232	889.4652	593.3126
1773.9091	887.4582	591.9746	16	Q	15	1720.9017	860.9545	574.3054
1936.9725	968.9899	646.3290	17	Y	14	1592.8431	796.9252	531.6192
2036.0409	1018.5241	679.3518	18	V	13	1429.7798	715.3935	477.2648
2164.0995	1082.5534	722.0380	19	Q	12	1330.7114	665.8593	444.2420
2261.1522	1131.0797	754.3889	20	P	11	1202.6528	601.8300	401.5558
2389.2108	1195.1090	797.0751	21	Q	10	1105.6000	553.3037	369.2049
2446.2323	1223.6198	816.0823	22	G	9	977.5415	489.2744	326.5187
2545.3007	1273.1540	849.1051	23	V	8	920.5200	460.7636	307.5115
2632.3327	1316.6700	878.1158	24	S	7	821.4516	411.2294	274.4887
2731.4011	1366.2042	911.1386	25	V	6	734.4196	367.7134	245.4780
2830.4695	1415.7384	944.1614	26	V	5	635.3511	318.1792	212.4552
2945.4965	1473.2519	982.5037	27	D	4	536.2827	268.6450	179.4324
3092.5649	1546.7861	1031.5265	28	F	3	421.2558	211.1315	141.0901
3191.6333	1596.3203	1064.5493	29	V	2	274.1874	137.5973	92.0673
			30	R	1	175.1190	88.0631	59.0445

Static Modifications:
C: 57.0215

Variable Modifications:
M: 15.9949

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9869	IPI00166730, IPI00006713	1	1	DNAJC3, DNAJC3	4593	3+	+0,9791	0,9999	K.LLAAGQLADALSQFHAAVDGDPDNYIAYYR.R



Peptide Details

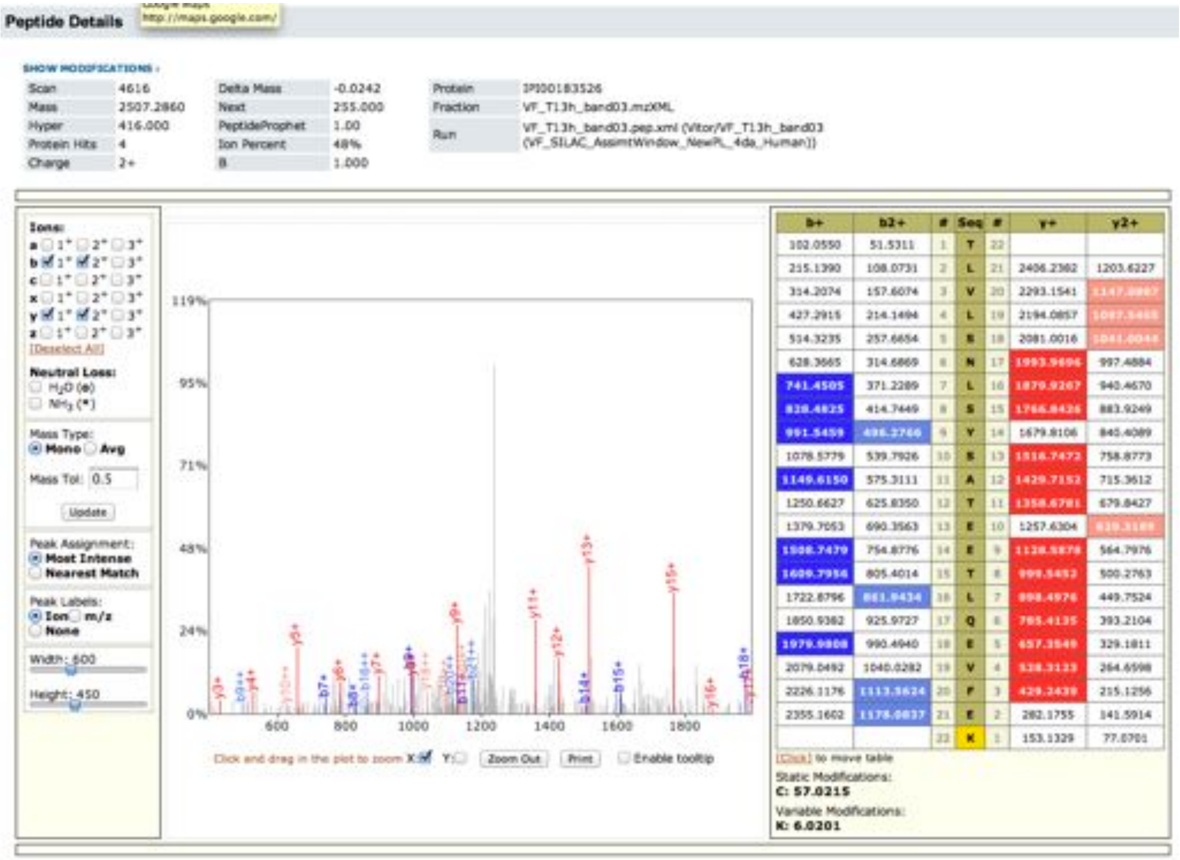
Scan	4593	Delta Mass	+0.9791	Protein	IPI00006713
Mass	3238.5800	Next	373.000	Fraction	VF_T13h_band03.mzXML
Hyper	577.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_human))
Protein Hits	2	Ion Percent	54%		
Charge	3+	B	1.000		

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
114.0913	57.5493	38.7020	1	L	30			
227.1754	114.0913	76.3867	2	L	29	3125.4963	1563.2518	[illegible]
298.2125	149.6099	100.0757	3	A	28	3012.4122	[illegible]	[illegible]
369.2496	185.1285	123.7547	4	A	27	2941.3751	[illegible]	[illegible]
426.2711	213.6392	142.7619	5	G	26	2870.3380	[illegible]	[illegible]
554.3297	277.6685	185.4481	6	Q	25	2813.3165	[illegible]	[illegible]
667.4137	334.2105	223.1428	7	L	24	2685.2580	[illegible]	895.7575
738.4509	[illegible]	246.8218	8	A	23	2572.1739	[illegible]	858.0628
853.4778	[illegible]	285.1641	9	D	22	2501.1368	[illegible]	[illegible]
924.5149	462.7611	308.8432	10	A	21	2386.1099	[illegible]	[illegible]
1037.5990	[illegible]	346.5378	11	L	20	2315.0727	[illegible]	772.3624
1124.6310	[illegible]	375.5485	12	S	19	2201.9887	[illegible]	[illegible]
1252.6896	[illegible]	[illegible]	13	Q	18	2114.9566	[illegible]	[illegible]
1398.7580	700.3826	[illegible]	14	F	17	1986.8981	[illegible]	[illegible]
1536.8169	[illegible]	[illegible]	15	H	16	1839.8297	[illegible]	[illegible]
1607.8540	[illegible]	[illegible]	16	A	15	1702.7707	[illegible]	568.2618
1678.8911	[illegible]	560.3019	17	A	14	1631.7336	[illegible]	[illegible]
1777.9595	[illegible]	593.3247	18	V	13	1560.6965	[illegible]	520.9037
1892.9865	[illegible]	[illegible]	19	D	12	1461.6281	[illegible]	487.8809
1950.0080	[illegible]	[illegible]	20	G	11	1346.6012	673.8042	[illegible]
2065.0349	[illegible]	[illegible]	21	D	10	1289.5797	[illegible]	430.5314
2162.0877	1081.5475	[illegible]	22	P	9	1174.5527	[illegible]	392.1891
2277.1146	[illegible]	[illegible]	23	D	8	1077.5000	[illegible]	359.8382
2391.1575	[illegible]	[illegible]	24	N	7	962.4730	[illegible]	[illegible]
2554.2209	[illegible]	[illegible]	25	Y	6	848.4301	424.7187	283.4816
2667.3049	[illegible]	[illegible]	26	I	5	685.3668	343.1870	229.1271
2738.3420	[illegible]	[illegible]	27	A	4	572.2827	286.6450	191.4324
2901.4054	[illegible]	[illegible]	28	Y	3	501.2456	251.1264	167.7534
3064.4687	[illegible]	[illegible]	29	Y	2	338.1823	169.5948	113.3989
			30	R	1	175.1190	88.0631	59.0445

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9787	IPI00183526, IPI00444262, IPI00827674, IPI00604620	1	1	NCL, NCL, NCL, NCL	4616	2+	-0,0242	0,9992	K.TLVLSNLSYSATEETLQEVFEK'.A



Peptide Details

SHOW MODIFICATIONS ›

Scan	4616	Delta Mass	-0.0242	Protein	IPI00183526
Mass	2507.2860	Next	255.000	Fraction	VF_T13h_band03.mzXML
Hyper	416.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	48%		
Charge	2+	B	1.000		

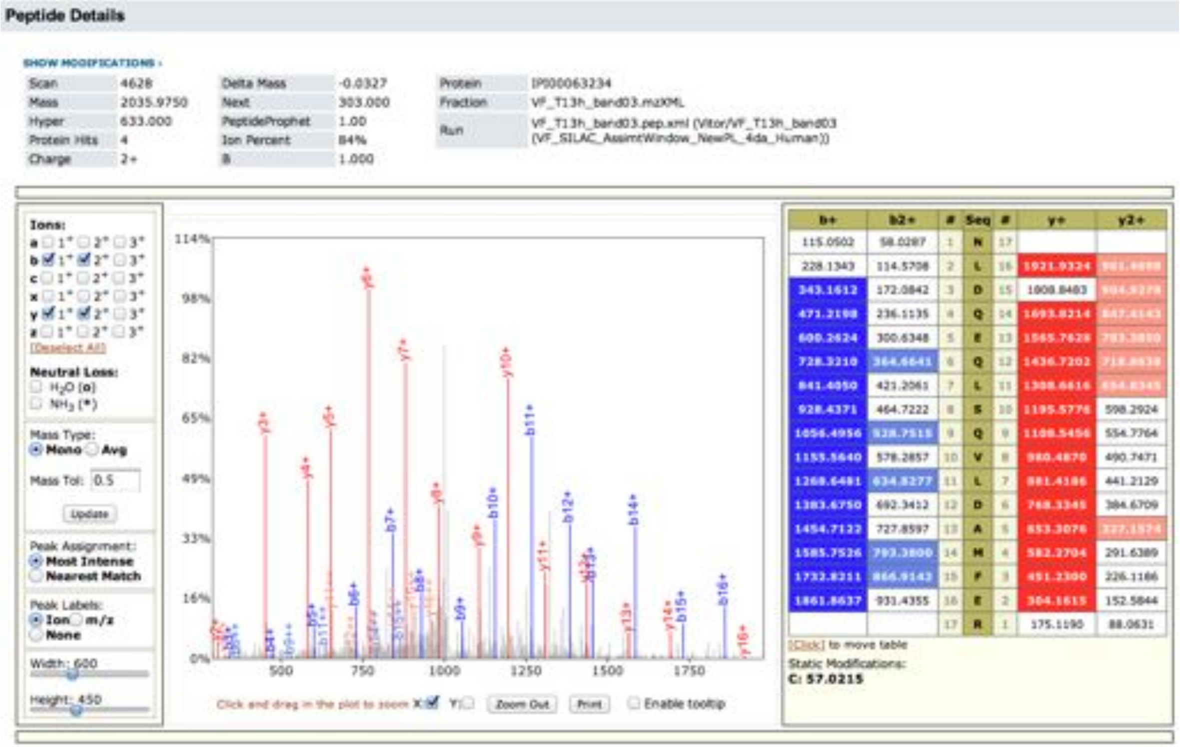
b+	b2+	#	Seq	#	y+	y2+
102.0550	51.5311	1	T	22		
215.1390	108.0731	2	L	21	2406.2362	1203.6227
314.2074	157.6074	3	V	20	2293.1541	1147.0867
427.2915	214.1494	4	L	19	2194.0857	1097.5465
514.3235	257.6654	5	S	18	2081.0016	1041.0044
628.3665	314.6869	6	N	17	1993.9696	997.4884
741.4505	371.2289	7	L	16	1879.9267	940.4670
828.4825	414.7449	8	S	15	1766.8426	883.9249
991.5459	496.2766	9	Y	14	1679.8106	840.4089
1078.5779	539.7926	10	S	13	1516.7472	758.8773
1149.6150	575.3111	11	A	12	1429.7152	715.3612
1250.6627	625.8350	12	T	11	1358.6781	679.8427
1379.7053	690.3563	13	E	10	1257.6304	629.3189
1508.7479	754.8776	14	E	9	1128.5878	564.7976
1609.7956	805.4014	15	T	8	999.5452	500.2763
1722.8796	861.9434	16	L	7	898.4976	449.7524
1850.9382	925.9727	17	Q	6	785.4135	393.2104
1979.9808	990.4940	18	E	5	657.3549	329.1811
2079.0492	1040.0282	19	V	4	528.3123	264.6598
2226.1176	1113.5624	20	F	3	429.2439	215.1256
2355.1602	1178.0837	21	E	2	282.1755	141.5914
		22	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00789242, IPI00788668, IPI00063234, IPI00219774	1	1	-, -, PRKAR2A, PRKAR2A	4628	2+	-0,0327	1,0000	K.NLDQEQLSQVLDAMFER.I



Peptide Details

SHOW MODIFICATIONS ›

Scan	4628	Delta Mass	-0.0327	Protein	IPI00063234
Mass	2035.9750	Next	303.000	Fraction	VF_T13h_band03.mzXML
Hyper	633.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	4	Ion Percent	84%		
Charge	2+	B	1.000		

Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

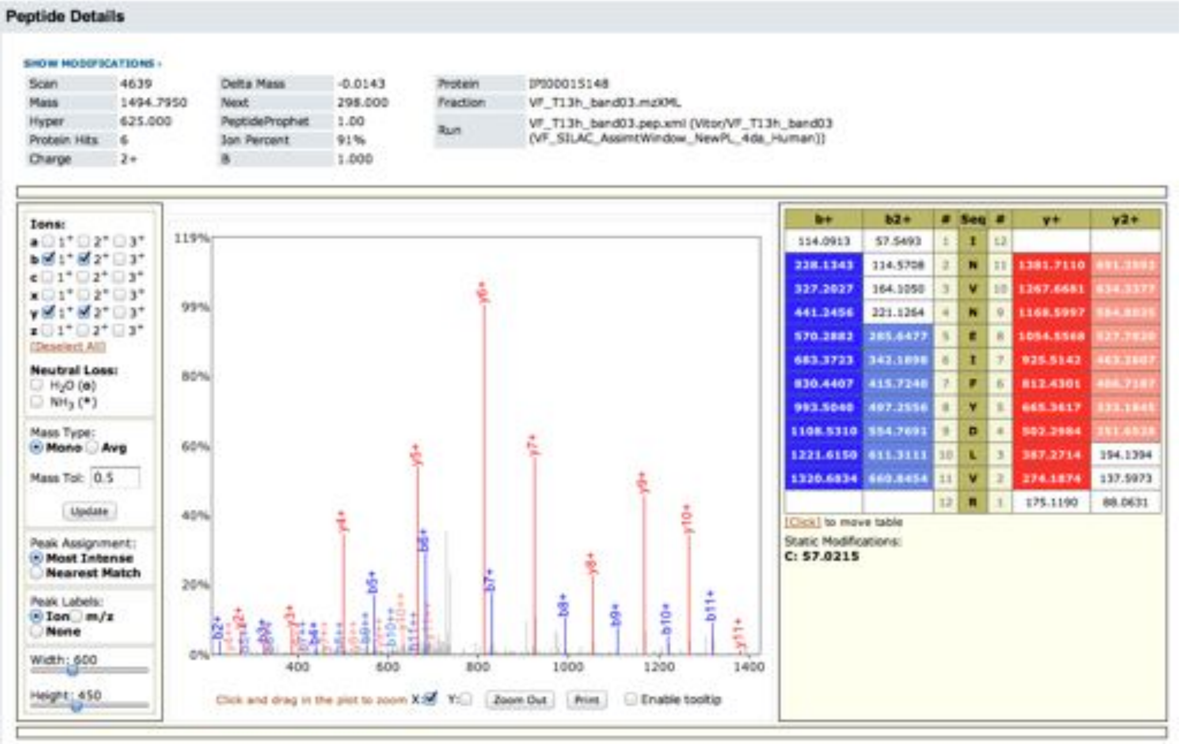
Height: 450

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	17		
228.1343	114.5708	2	L	16	1921.9324	961.4698
343.1612	172.0842	3	D	15	1808.8483	904.9278
471.2198	236.1135	4	Q	14	1693.8214	847.4143
600.2624	300.6348	5	E	13	1565.7628	783.3850
728.3210	364.6641	6	Q	12	1436.7202	718.8638
841.4050	421.2061	7	L	11	1308.6616	654.8345
928.4371	464.7222	8	S	10	1195.5776	598.2924
1056.4956	528.7515	9	Q	9	1108.5456	554.7764
1155.5640	578.2857	10	V	8	980.4870	490.7471
1268.6481	634.8277	11	L	7	881.4186	441.2129
1383.6750	692.3412	12	D	6	768.3345	384.6709
1454.7122	727.8597	13	A	5	653.3076	327.1574
1585.7526	793.3800	14	M	4	582.2704	291.6389
1732.8211	866.9142	15	F	3	451.2300	226.1186
1861.8637	931.4355	16	E	2	304.1615	152.5844
		17	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan#	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9880	IPI00908754, IPI00910592, IPI00015148, IPI00019345, IPI00412525, IPI00877120	1	1	-, -, RAP1B, RAP1A, hCG_1757335, RAP1A	4639	2+	-0,0143	1,0000	K.INVNEIFYDLVR.Q



Peptide Details

SHOW MODIFICATIONS ›

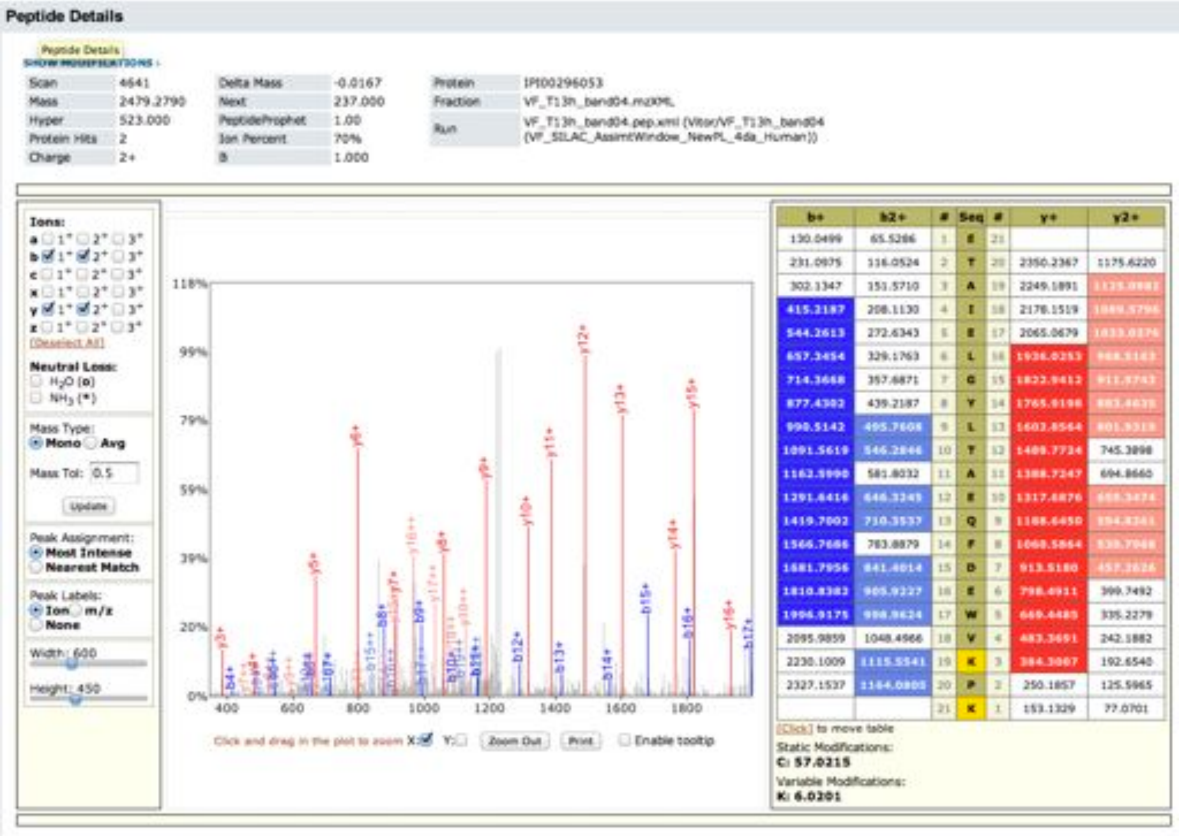
Scan	4639	Delta Mass	-0.0143	Protein	IPI00015148
Mass	1494.7950	Next	298.000	Fraction	VF_T13h_band03.mzXML
Hyper	625.000	PeptideProphet	1.00	Run	VF_T13h_band03.pep.xml (Vitor/VF_T13h_band03 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	6	Ion Percent	91%		
Charge	2+	B	1.000		

b+	b2+	#	Seq	#	y+	y2+
114.0913	57.5493	1	I	12		
228.1343	114.5708	2	N	11	1381.7110	691.3592
327.2027	164.1050	3	V	10	1267.6681	634.3377
441.2456	221.1264	4	N	9	1168.5997	584.8035
570.2882	285.6477	5	E	8	1054.5568	527.7820
683.3723	342.1898	6	I	7	925.5142	463.2607
830.4407	415.7240	7	F	6	812.4301	406.7187
993.5040	497.2556	8	Y	5	665.3617	333.1845
1108.5310	554.7691	9	D	4	502.2984	251.6528
1221.6150	611.3111	10	L	3	387.2714	194.1394
1320.6834	660.8454	11	V	2	274.1874	137.5973
		12	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9837	IPI00759715, IPI00296053	1	1	FH, FH	4641	2+	-0,0167	0,9999	K.ETAIELGYLTAEQFDEWVK'PK'.D



Peptide Details

Scan	4641	Delta Mass	-0.0167	Protein	IPI00296053
Mass	2479.2790	Next	237.000	Fraction	VF_T13h_band04.mzXML
Hyper	523.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	70%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

Width: 600

Height: 450

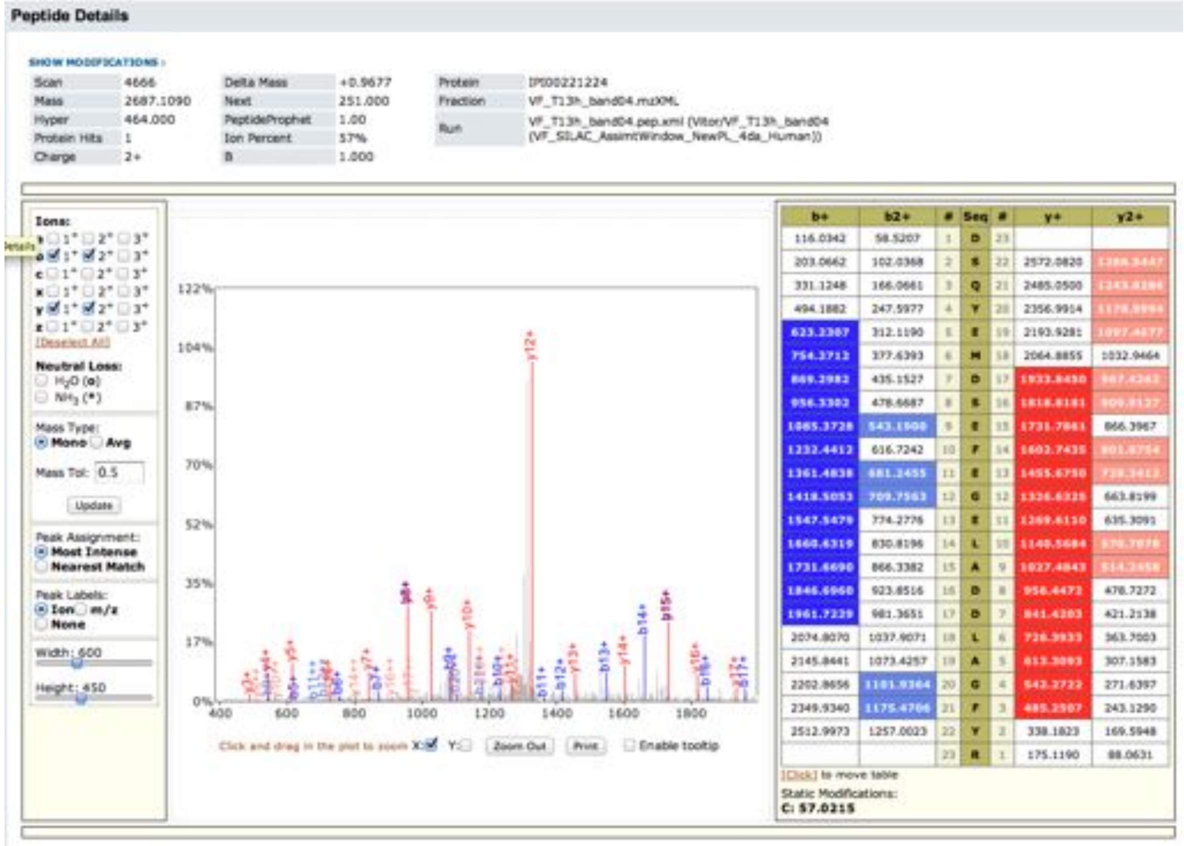
b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	E	21		
231.0975	116.0524	2	T	20	2350.2367	1175.6220
302.1347	151.5710	3	A	19	2249.1891	1125.0981
415.2187	208.1130	4	I	18	2178.1519	1089.5796
544.2613	272.6343	5	E	17	2065.0679	1033.0376
657.3454	329.1763	6	L	16	1936.0253	968.5163
714.3668	357.6871	7	G	15	1822.9412	911.9743
877.4302	439.2187	8	Y	14	1765.9198	883.4635
990.5142	495.7608	9	L	13	1602.8564	801.9319
1091.5619	546.2846	10	T	12	1489.7724	745.3898
1162.5990	581.8032	11	A	11	1388.7247	694.8660
1291.6416	646.3245	12	E	10	1317.6876	659.3474
1419.7002	710.3537	13	Q	9	1188.6450	594.8261
1566.7686	783.8879	14	F	8	1060.5864	530.7968
1681.7956	841.4014	15	D	7	913.5180	457.2626
1810.8382	905.9227	16	E	6	798.4911	399.7492
1996.9175	998.9624	17	W	5	669.4485	335.2279
2095.9859	1048.4966	18	V	4	483.3691	242.1882
2230.1009	1115.5541	19	K	3	384.3007	192.6540
2327.1537	1164.0805	20	P	2	250.1857	125.5965
		21	K	1	153.1329	77.0701

[Click] to move table

Static Modifications:
C: 57.0215

Variable Modifications:
K: 6.0201

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9456	IPI00221224	1	1	ANPEP	4666	2+	+0,9677	0,9972	K.DSQYEMDSEFEGELADDLAGFYR.S



Peptide Details

SHOW MODIFICATIONS ›

Scan	4666	Delta Mass	+0.9677	Protein	IPI00221224
Mass	2687.1090	Next	251.000	Fraction	VF_T13h_band04.mzXML
Hyper	464.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	1	Ion Percent	57%		
Charge	2+	B	1.000		

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ H₂O (o)
☐ NH₃ (*)

Mass Type:
● Mono ○ Avg

Mass Tol: 0.5

Peak Assignment:
● Most Intense
○ Nearest Match

Peak Labels:
● Ion ○ m/z
○ None

Width: 600

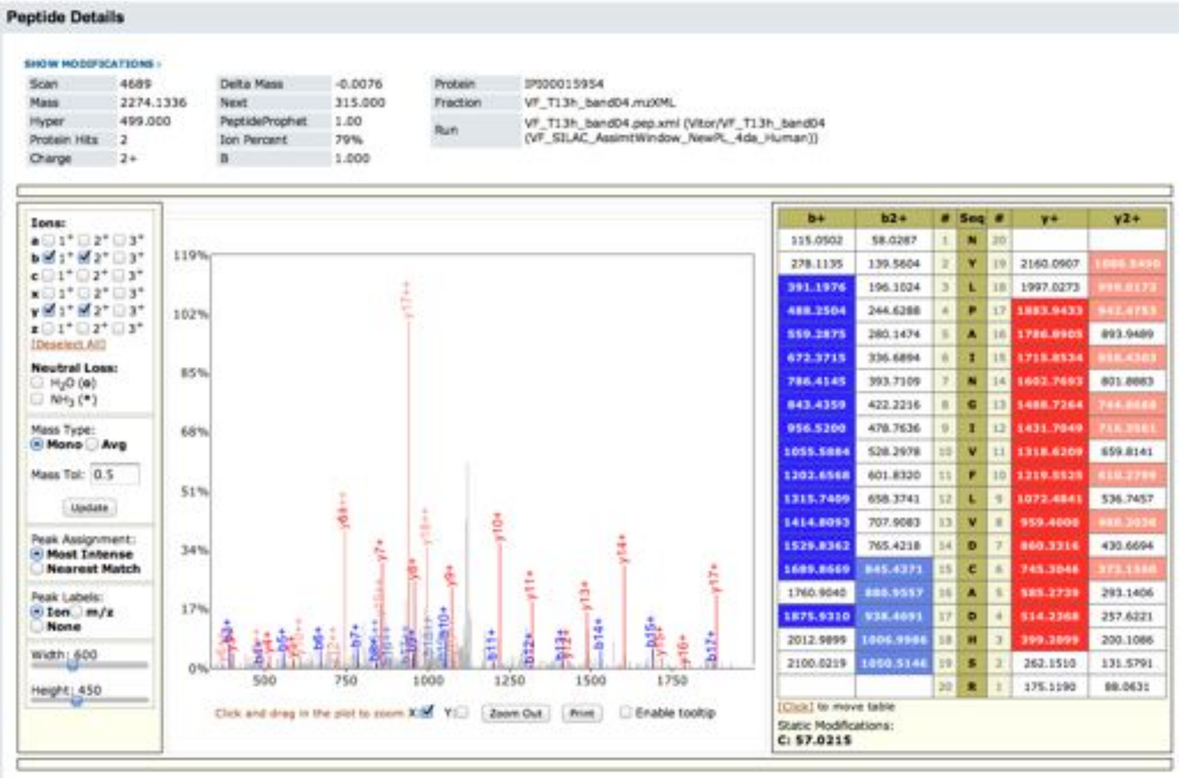
Height: 450

b+	b2+	#	Seq	#	y+	y2+
116.0342	58.5207	1	D	23		
203.0662	102.0368	2	S	22	2572.0820	1286.5447
331.1248	166.0661	3	Q	21	2485.0500	1243.0286
494.1882	247.5977	4	Y	20	2356.9914	1178.9994
623.2307	312.1190	5	E	19	2193.9281	1097.4677
754.2712	377.6393	6	M	18	2064.8855	1032.9464
869.2982	435.1527	7	D	17	1933.8450	967.4262
956.3302	478.6687	8	S	16	1818.8181	909.9127
1085.3728	543.1900	9	E	15	1731.7861	866.3967
1232.4412	616.7242	10	F	14	1602.7435	801.8754
1361.4838	681.2455	11	E	13	1455.6750	728.3412
1418.5053	709.7563	12	G	12	1326.6325	663.8199
1547.5479	774.2776	13	E	11	1269.6110	635.3091
1660.6319	830.8196	14	L	10	1140.5684	570.7878
1731.6690	866.3382	15	A	9	1027.4843	514.2458
1846.6960	923.8516	16	D	8	956.4472	478.7272
1961.7229	981.3651	17	D	7	841.4203	421.2138
2074.8070	1037.9071	18	L	6	726.3933	363.7003
2145.8441	1073.4257	19	A	5	613.3093	307.1583
2202.8656	1101.9364	20	G	4	542.2722	271.6397
2349.9340	1175.4706	21	F	3	485.2507	243.1290
2512.9973	1257.0023	22	Y	2	338.1823	169.5948
		23	R	1	175.1190	88.0631

[Click] to move table

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9793	IPI00644667, IPI00015954	1	1	SAR1A, SAR1A	4689	2+	-0,0076	0,9996	K.NYLPAINGIVFLVDCADHSR.L



Peptide Details

SHOW MODIFICATIONS »

Scan	4689	Delta Mass	-0.0076	Protein	IPI00015954
Mass	2274.1336	Next	315.000	Fraction	VF_T13h_band04.mzXML
Hyper	499.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vitor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_4da_Human))
Protein Hits	2	Ion Percent	79%		
Charge	2+	B	1.000		

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

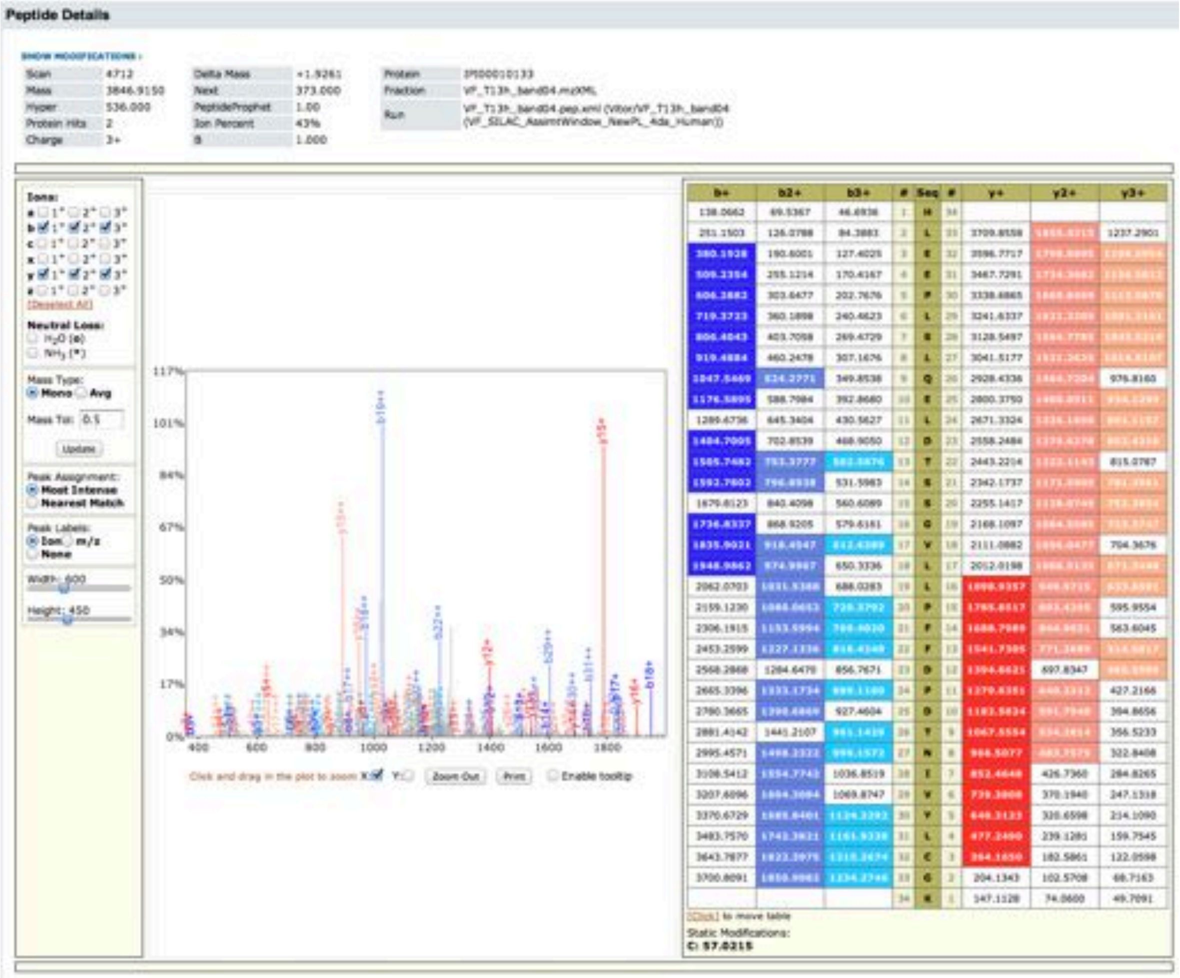
Peak Assignment: ● Most Intense ○ Nearest Match

Peak Labels: ● Ion ○ m/z ○ None

b+	b2+	#	Seq	#	y+	y2+
115.0502	58.0287	1	N	20		
278.1135	139.5604	2	Y	19	2160.0907	1080.5490
391.1976	196.1024	3	L	18	1997.0273	999.0173
488.2504	244.6288	4	P	17	1883.9433	942.4753
559.2875	280.1474	5	A	16	1786.8905	893.9489
672.3715	336.6894	6	I	15	1715.8534	858.4303
786.4145	393.7109	7	N	14	1602.7693	801.8883
843.4359	422.2216	8	G	13	1488.7264	744.8668
956.5200	478.7636	9	I	12	1431.7049	716.3561
1055.5884	528.2978	10	V	11	1318.6209	659.8141
1202.6568	601.8320	11	F	10	1219.5525	610.2799
1315.7409	658.3741	12	L	9	1072.4841	536.7457
1414.8093	707.9083	13	V	8	959.4000	480.2036
1529.8362	765.4218	14	D	7	860.3316	430.6694
1689.8669	845.4371	15	C	6	745.3046	373.1560
1760.9040	880.9557	16	A	5	585.2739	293.1406
1875.9310	938.4691	17	D	4	514.2368	257.6221
2012.9899	1006.9986	18	H	3	399.2099	200.1086
2100.0219	1050.5146	19	S	2	262.1510	131.5791
		20	R	1	175.1190	88.0631

Static Modifications:
C: 57.0215

Protein Probab.	Protein	Tot. Peptides	Unique Peptides	Best Gene Name	Scan #	Charge	Delta Mass	Peptide Prophet Score	Peptide Sequence
0,9636	IPI00642725, IPI00010133	1	1	CORO1A, CORO1A	4712	3+	+1,9261	0,9985	K.HLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGK.G



Peptide Details

Scan	4712	Delta Mass	+1.9261	Protein	IPI00010133
Mass	3846.9150	Next	373.000	Fraction	VF_T13h_band04.mzXML
Hyper	536.000	PeptideProphet	1.00	Run	VF_T13h_band04.pep.xml (Vibor/VF_T13h_band04 (VF_SILAC_AssimtWindow_NewPL_Ada_Human))
Protein Hits	2	Ion Percent	43%		
Charge	3+	B	1.000		

Static Modifications:
C: 57.0215