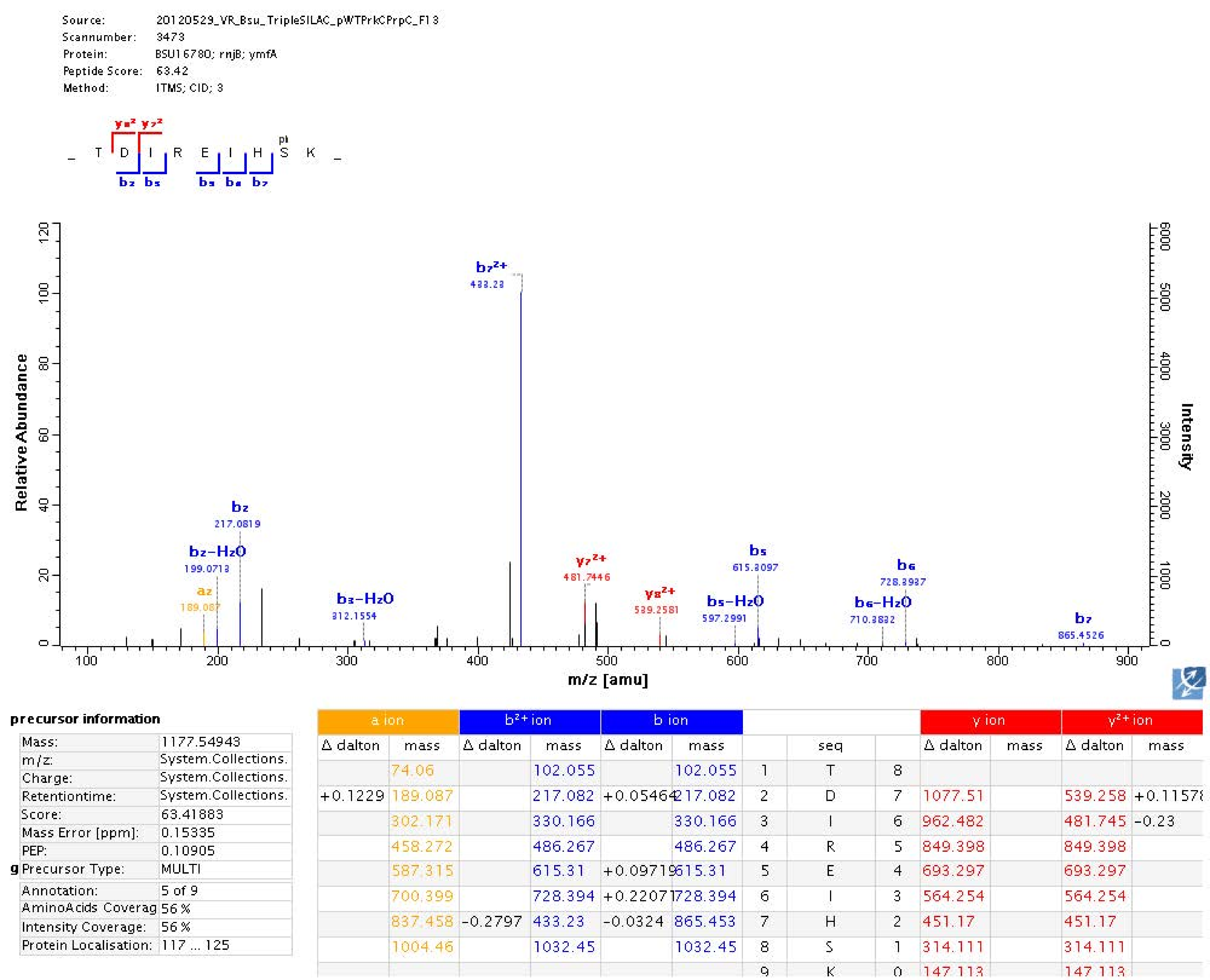


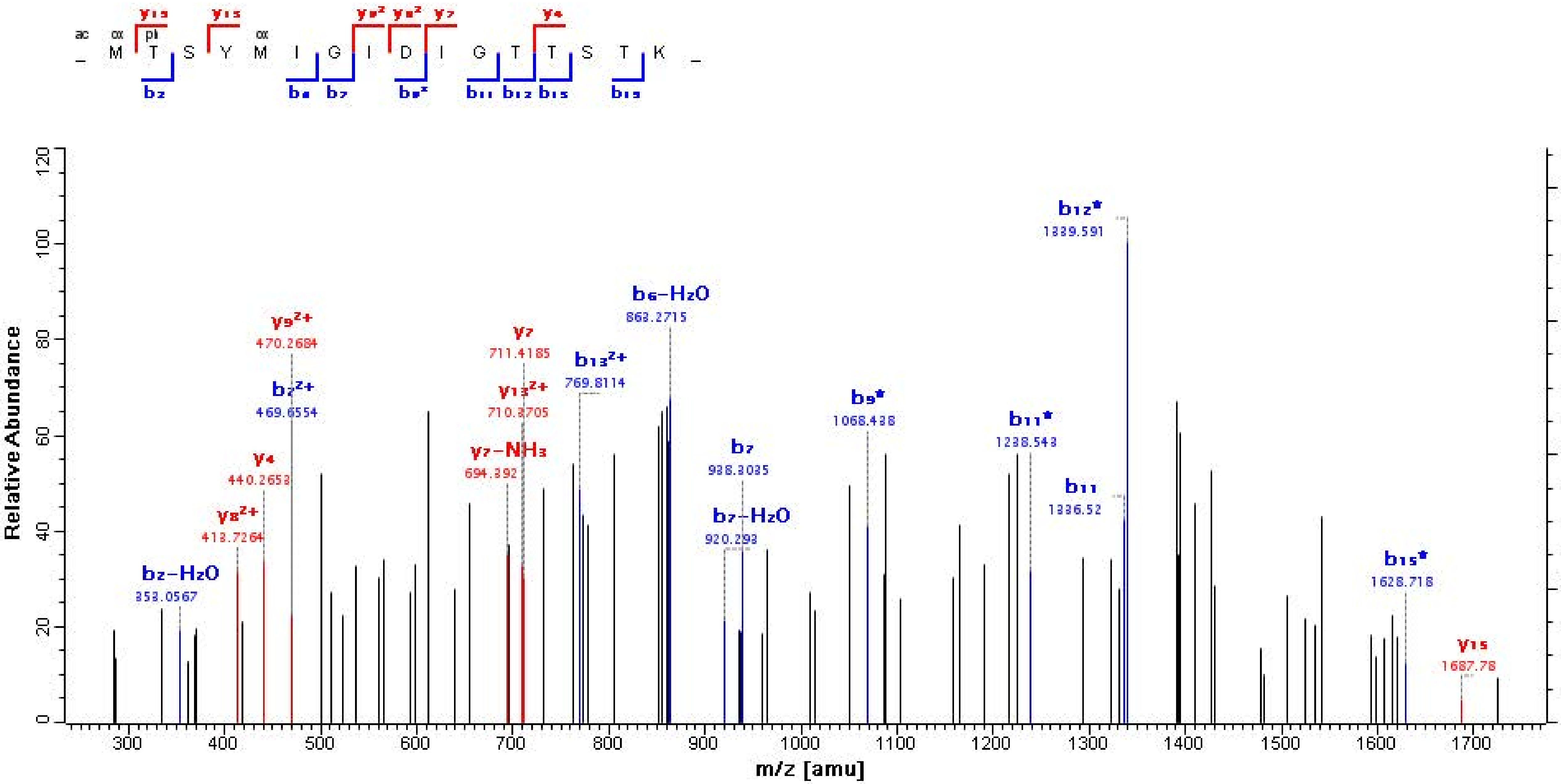
Source: 20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F13
Scannumber: 3473
Protein: BSU16780; rnjB; ymfA
Peptide Score: 63.42
Method: ITMS; CID; 3

precursor information

Mass:	1177.54943
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.41883
Mass Error [ppm]:	0.15335
PEP:	0.10905
g Precursor Type:	MULTI
Annotation:	5 of 9
AminoAcids Coverag	56 %
Intensity Coverage:	56 %
Protein Localisation:	117 ... 125

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.055		102.055	1	T	8				
+0.1229	189.087		217.082	+0.05464	217.082	2	D	7	1077.51		539.258	+0.1157
	302.171		330.166		330.166	3	I	6	962.482		481.745	-0.23
	458.272		486.267		486.267	4	R	5	849.398		849.398	
	587.315		615.31	+0.09719	615.31	5	E	4	693.297		693.297	
	700.399		728.394	+0.22071	728.394	6	I	3	564.254		564.254	
	837.458	-0.2797	433.23	-0.0324	865.453	7	H	2	451.17		451.17	
	1004.46		1032.45		1032.45	8	S	1	314.111		314.111	
						9	K	0	147.113		147.113	

Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F13
Scannumber:	5401
Protein:	BSU40060; gntK
Peptide Score:	57.97
Method:	ITMS; CID; 3



precursor information

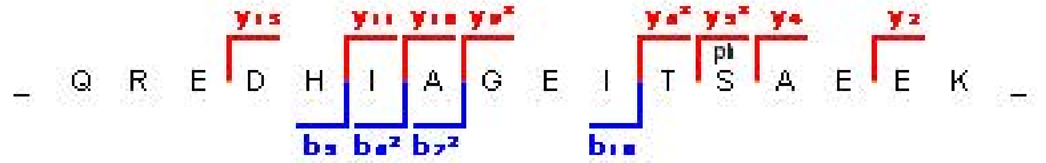
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	57.97267
Mass Error [ppm]:	5.6828
PEP:	0.023751
Precursor Type:	PEAK

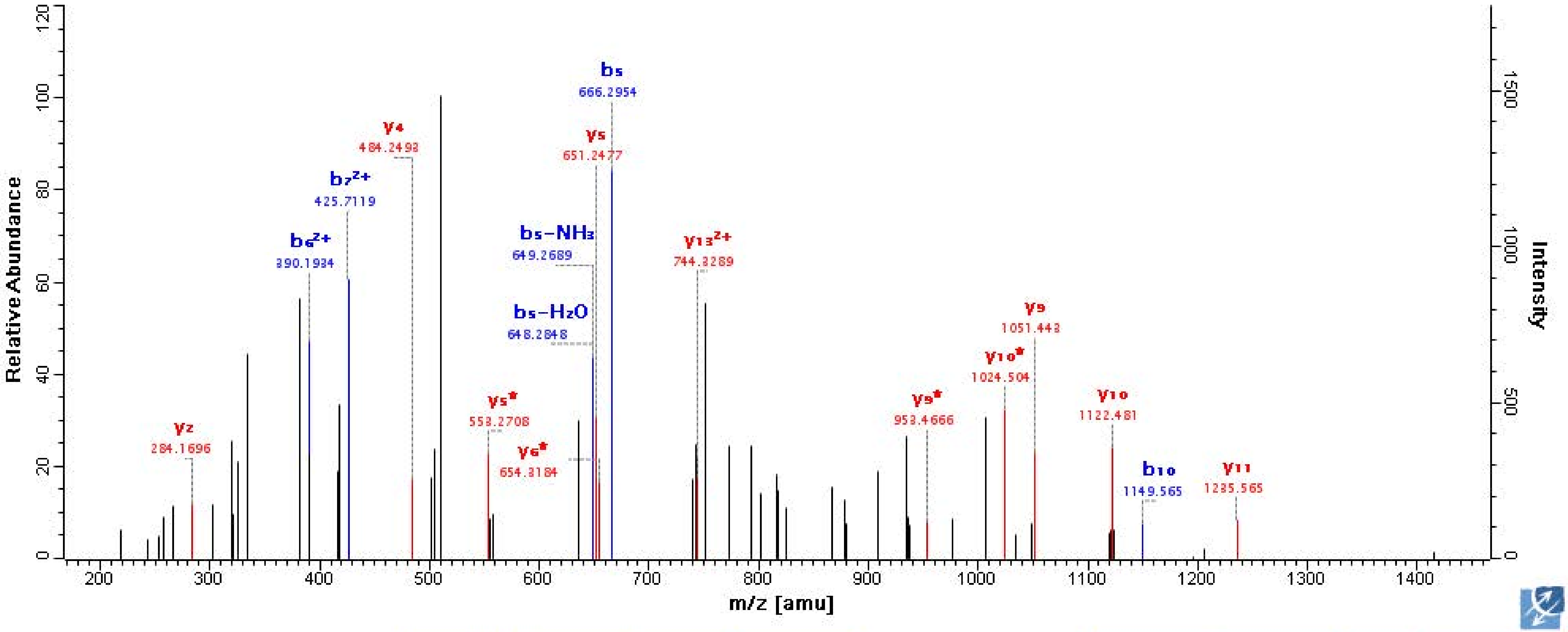
general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	21 %
Protein Localisation:	1 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	190.0532		190.0532	1	M	15				
	371.0672		371.0672	2	T	14	1687.78	+0.114485	1687.78	
	458.0993		458.0993	3	S	13	1506.766		1506.766	
	621.1626		621.1626	4	Y	12	1419.734		710.3705	+0.054284
	768.198		768.198	5	M	11	1256.67		1256.67	
	881.2821		881.2821	6	I	10	1109.635		1109.635	
-0.420847	469.6554	+0.10174	938.3035	7	G	9	996.551		996.551	
	1051.388		1051.388	8	I	8	939.5295		470.2684	-0.07894
	1166.415		1166.415	9	D	7	826.4454		413.7264	-0.315472
	1279.499		1279.499	10	I	6	711.4185	+0.047012	711.4185	
	1336.52	+0.216626	1336.52	11	G	5	598.3344		598.3344	
	1437.568		1437.568	12	T	4	541.313		541.313	
+0.387441	769.8114		1538.615	13	T	3	440.2653	-0.026161	440.2653	
	1625.647		1625.647	14	S	2	339.2176		339.2176	
	1726.695		1726.695	15	T	1	252.1856		252.1856	
				16	K	0	151.1379		151.1379	

Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F13
Scannumber:	5576
Protein:	atpF; BSU36850
Peptide Score:	57.6
Method:	ITMS; CID; 3





precursor information

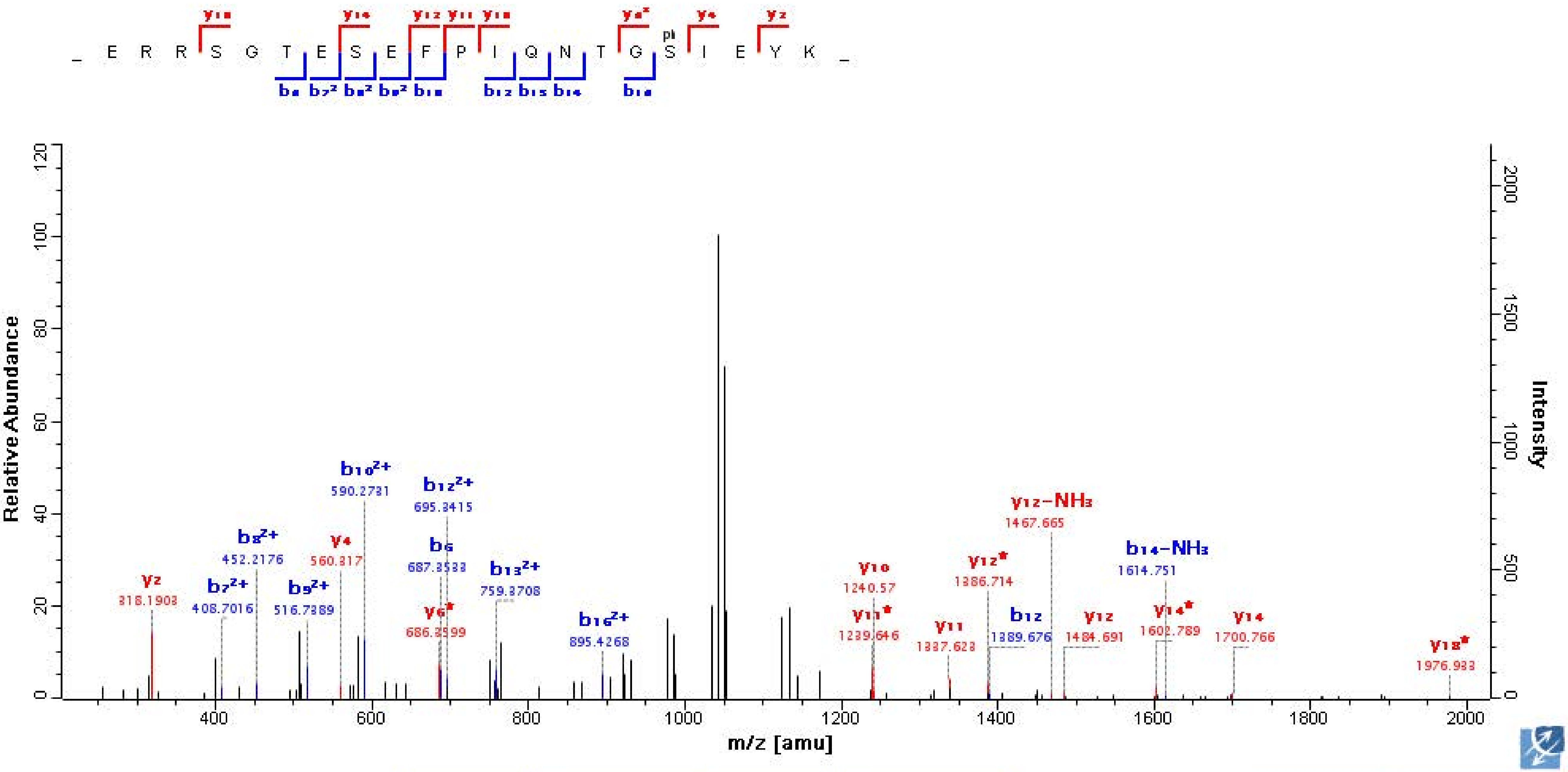
Mass:	1891.83119
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	57.59521
Mass Error [ppm]:	-0.055498
PEP:	0.016173
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	35 %
Protein Localisation:	45 ... 60

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659		129.0659	1	Q	15				
	285.167		285.167	2	R	14	1772.794		1772.794	
	414.2096		414.2096	3	E	13	1616.693		1616.693	
	529.2365		529.2365	4	D	12	1487.65		744.3289	+0.219882
	666.2954	+0.026425	666.2954	5	H	11	1372.624		1372.624	
+0.014631	390.1934		779.3795	6	I	10	1235.565	+0.112119	1235.565	
+0.336406	425.7119		850.4166	7	A	9	1122.481	+0.037003	1122.481	
	907.4381		907.4381	8	G	8	1051.443	+0.148092	1051.443	
	1036.481		1036.481	9	E	7	994.422		994.422	
	1149.565	+0.247788	1149.565	10	I	6	865.3794		865.3794	
	1250.612		1250.612	11	T	5	752.2953		752.2953	
	1417.611		1417.611	12	S	4	651.2477	+0.086994	651.2477	
	1488.648		1488.648	13	A	3	484.2493	+0.01974	484.2493	
	1617.69		1617.69	14	E	2	413.2122		413.2122	
	1746.733		1746.733	15	E	1	284.1696	+0.132894	284.1696	
				16	K	0	155.127		155.127	

Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F15
Scannumber:	7467
Protein:	BSU35720; rodC; tag3; tagF
Peptide Score:	98.27
Method:	ITMS; CID; 3



precursor information

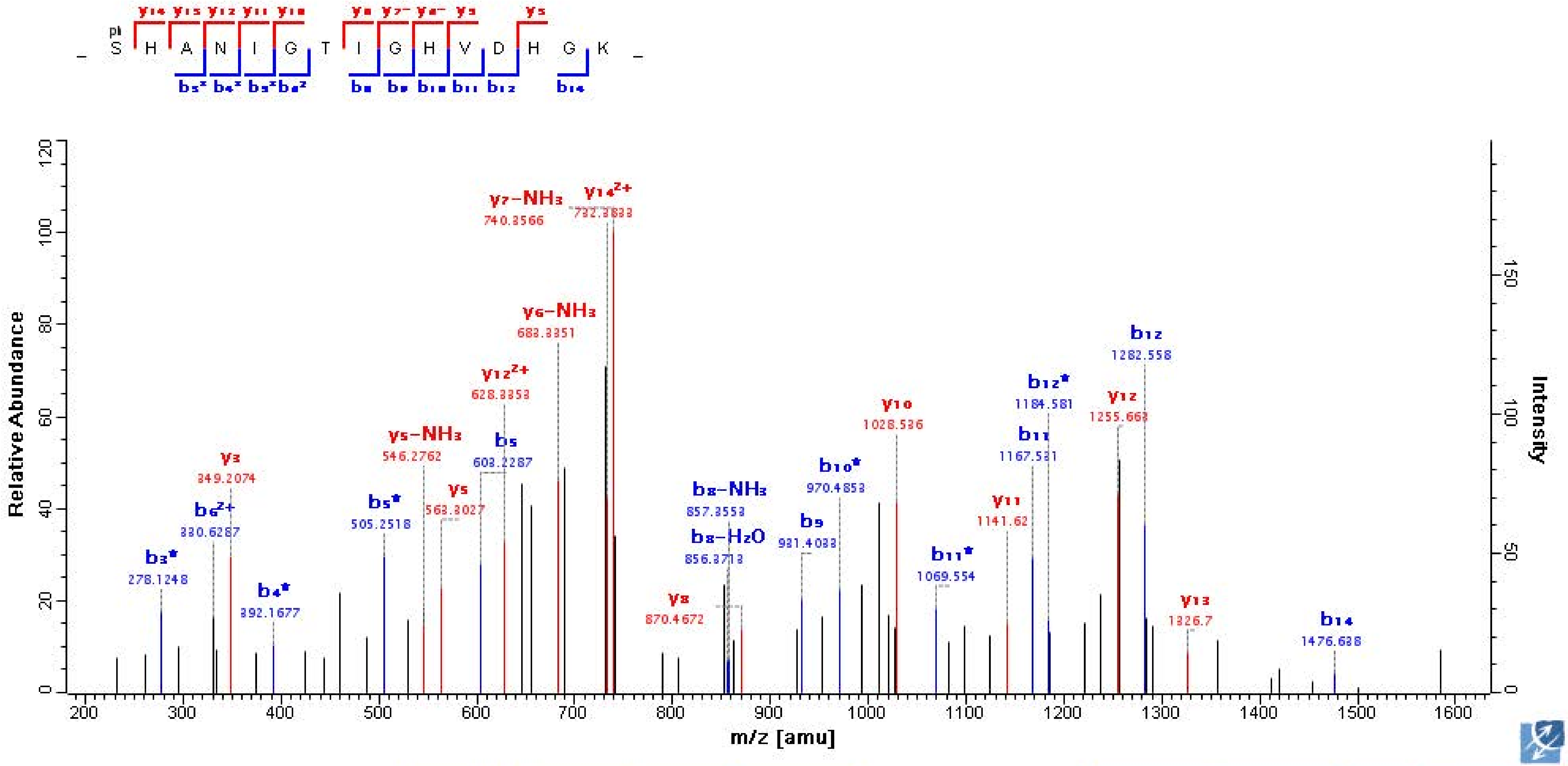
Mass:	2507.13314
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	98.26882
Mass Error [ppm]:	0.070058
PEP:	1.7653E-10
Precursor Type:	MULTI

general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	16 %
Protein Localisation:	70 ... 90

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	20		
	286.15098059		286.15098059	2	R	19	2387.1118436	
	442.25209162		442.25209162	3	R	18	2231.0107326	
	529.28412003		529.28412003	4	S	17	2074.9096215	
	586.30558375		586.30558375	5	G	16	1987.8775931	
	687.35326223	-0.2061065	687.35326223	6	T	15	1930.8561294	
+0.0575283	408.70156589		816.39585532	7	E	14	1829.8084509	
+0.3137309	452.2175801		903.42788373	8	S	13	1700.7658578	-0.3266488
+0.4420926	516.73887665		1032.4704768	9	E	12	1613.7338294	
+0.1704589	590.27308361		1179.5388907	10	F	11	1484.6912363	+0.2673818
	1276.5916546		1276.5916546	11	P	10	1337.6228224	+0.1076463
+0.3914737	695.34149752	+0.1832902	1389.6757186	12	I	9	1240.5700586	+0.1753028
+0.4021629	759.37078628		1517.7342961	13	Q	8	1127.4859946	
	1631.7772235		1631.7772235	14	N	7	999.42741706	
	1732.824902		1732.824902	15	T	6	885.38448961	
+0.2064186	895.4268211		1789.8463657	16	G	5	784.33681114	
	1956.8447246		1956.8447246	17	S	4	727.31534742	
	2069.9287885		2069.9287885	18	I	3	560.3169886	-0.0614344
	2198.9713816		2198.9713816	19	E	2	447.23292462	
	2362.0347102		2362.0347102	20	Y	1	318.19033152	+0.1878423
				21	K	0	155.12700298	

Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F17
Scannumber:	4044
Protein:	BSU01130; tuf; tufA
Peptide Score:	109.35
Method:	ITMS; CID; 3



precursor information

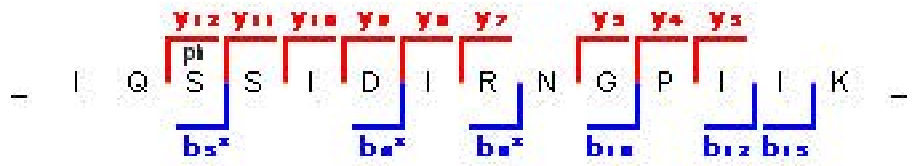
Mass:	1621.73672
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.352
Mass Error [ppm]:	0.30957
PEP:	5.0653E-07
Precursor Type:	MULTI

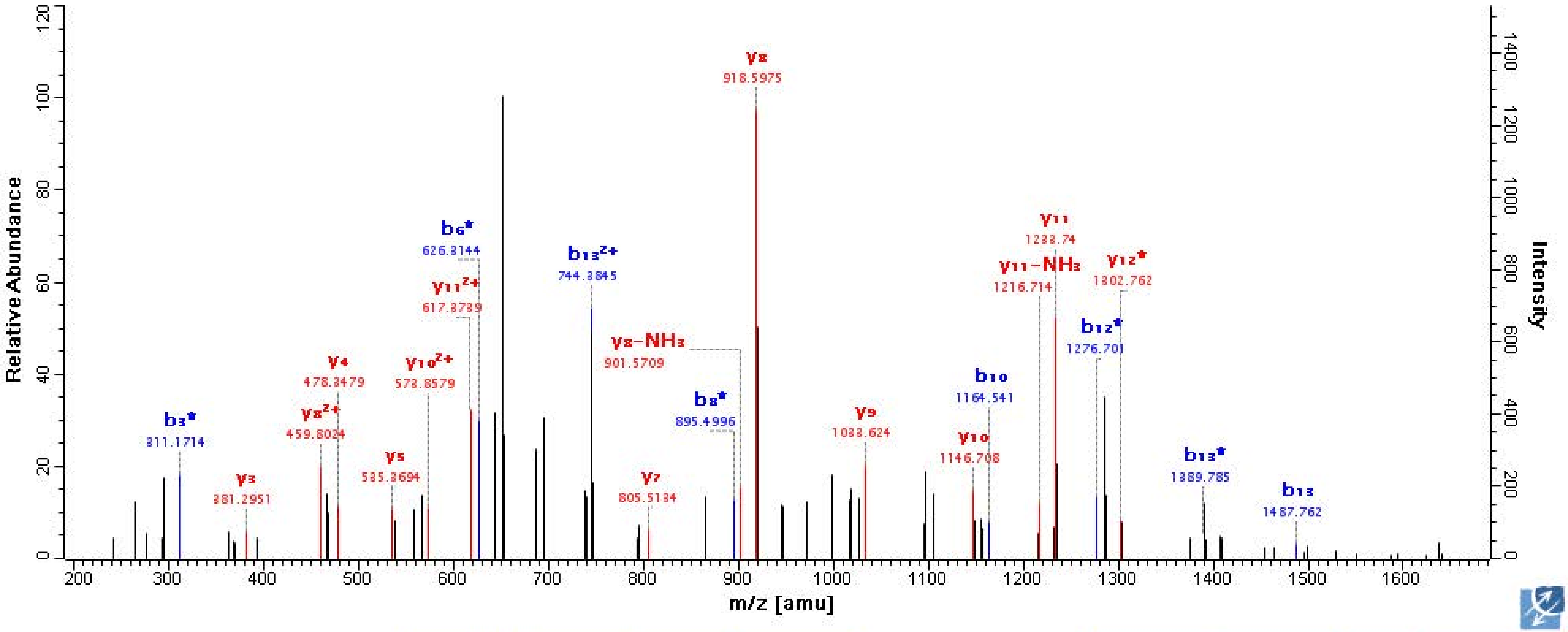
general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	45 %
Protein Localisation:	11 ... 25

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	14				
	305.0645		305.0645	2	H	13	1463.759		732.3833	+0.026485
	376.1017		376.1017	3	A	12	1326.7	+0.037126	1326.7	
	490.1446		490.1446	4	N	11	1255.663	-0.075174	628.3353	+0.140293
	603.2287	+0.410081	603.2287	5	I	10	1141.62	-0.055318	1141.62	
-0.249271	330.6287		660.2501	6	G	9	1028.536	+0.157286	1028.536	
	761.2978		761.2978	7	T	8	971.5149		971.5149	
	874.3819		874.3819	8	I	7	870.4672	+0.024707	870.4672	
	931.4033	+0.119444	931.4033	9	G	6	757.3831		757.3831	
	1068.462		1068.462	10	H	5	700.3616		700.3616	
	1167.531	-0.039437	1167.531	11	V	4	563.3027	+0.146972	563.3027	
	1282.558	-0.25742	1282.558	12	D	3	464.2343		464.2343	
	1419.617		1419.617	13	H	2	349.2074	+0.005756	349.2074	
	1476.638	-0.357571	1476.638	14	G	1	212.1485		212.1485	
				15	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	10006
Protein:	BSU03490; comL; srfA2; srfAB
Peptide Score:	121.45
Method:	ITMS; CID; 3





precursor information

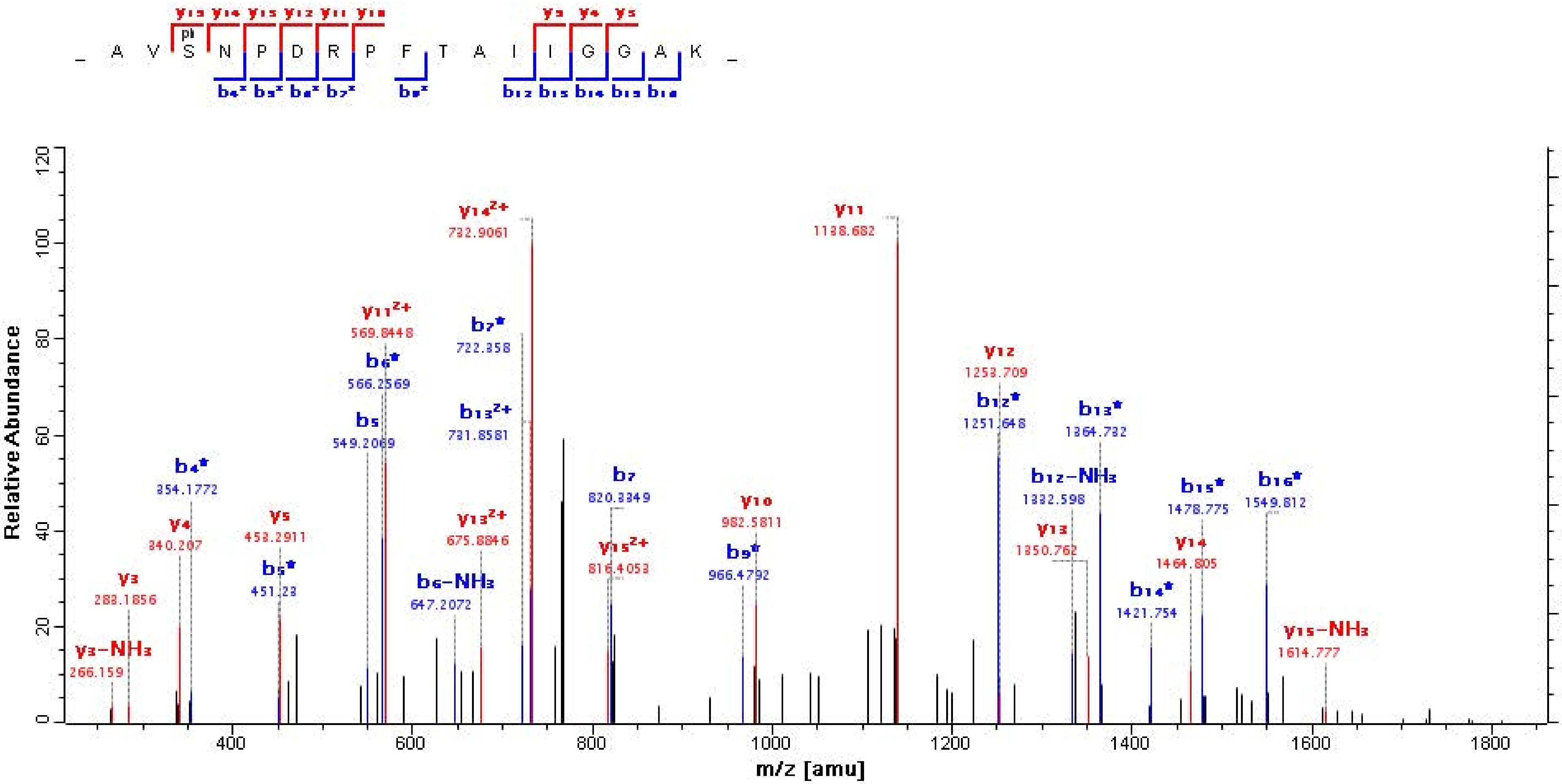
Mass:	1632.86008
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	121.4488
Mass Error [ppm]:	0.037494
PEP:	2.1968E-10
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	36 %
Protein Localisation:	3221 ... 3234

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	13				
	242.1499		242.1499	2	Q	12	1528.797		1528.797	
	409.1483		409.1483	3	S	11	1400.739		1400.739	
	496.1803		496.1803	4	S	10	1233.74	+0.005353	617.3739	+0.045547
	609.2644		609.2644	5	I	9	1146.708	-0.063326	573.8579	-0.214684
	724.2913		724.2913	6	D	8	1033.624	+0.13524	1033.624	
	837.3754		837.3754	7	I	7	918.5975	-0.007556	459.8024	-0.163086
	993.4765		993.4765	8	R	6	805.5134	+0.138092	805.5134	
	1107.519		1107.519	9	N	5	649.4123		649.4123	
	1164.541	-0.036484	1164.541	10	G	4	535.3694	-0.054051	535.3694	
	1261.594		1261.594	11	P	3	478.3479	+0.207464	478.3479	
	1374.678		1374.678	12	I	2	381.2951	+0.007909	381.2951	
+0.443907	744.3845	+0.419016	1487.762	13	I	1	268.2111		268.2111	
				14	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 10010
Protein: BSU33930; pgk
Peptide Score: 136.63
Method: ITMS; CID; 3



precursor information

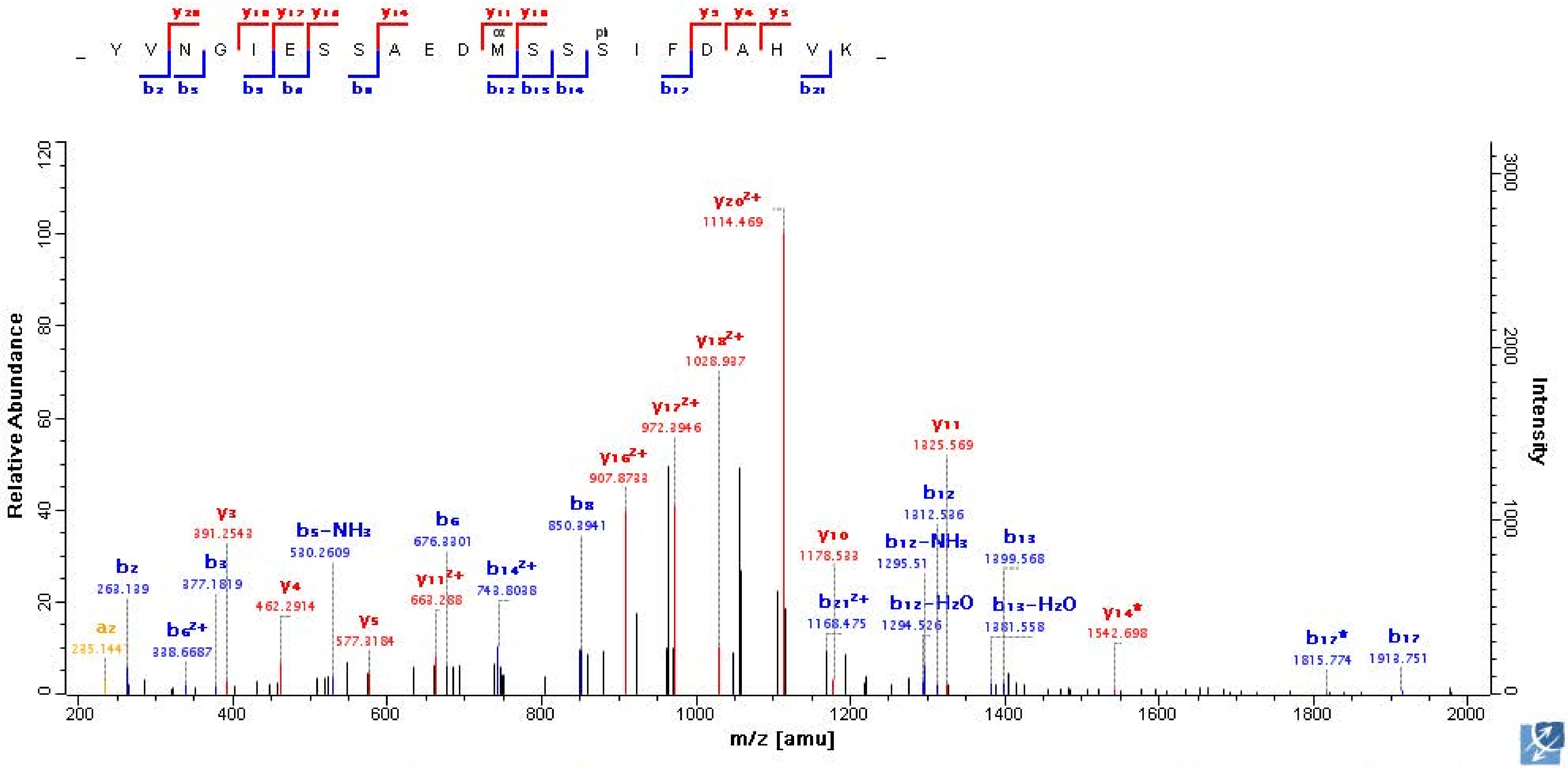
Mass:	1792.88712
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.6299
Mass Error [ppm]:	-0.097746
PEP:	8.2911E-18
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	55 %
Protein Localisation:	181 ... 197

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	16				
	171.1128		171.1128	2	V	15	1730.872		1730.872	
	338.1112		338.1112	3	S	14	1631.803		816.4053	+0.373303
	452.1541		452.1541	4	N	13	1464.805	+0.111983	732.9061	+0.082871
	549.2069	+0.202814	549.2069	5	P	12	1350.762	+0.110843	675.8846	+0.079554
	664.2338		664.2338	6	D	11	1253.709	-0.044401	1253.709	
	820.3349	+0.180656	820.3349	7	R	10	1138.682	+0.053587	569.8448	-0.141762
	917.3877		917.3877	8	P	9	982.5811	+0.15073	982.5811	
	1064.456		1064.456	9	F	8	885.5284		885.5284	
	1165.504		1165.504	10	T	7	738.46		738.46	
	1236.541		1236.541	11	A	6	637.4123		637.4123	
	1349.625		1349.625	12	I	5	566.3752		566.3752	
-0.119128	731.8581		1462.709	13	I	4	453.2911	+0.108428	453.2911	
	1519.73		1519.73	14	G	3	340.207	+0.082568	340.207	
	1576.752		1576.752	15	G	2	283.1856	+0.15704	283.1856	
	1647.789		1647.789	16	A	1	226.1641		226.1641	
				17	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 10244
Protein: BSU28440; citF; sdhA
Peptide Score: 120.9
Method: ITMS; CID; 3



precursor information

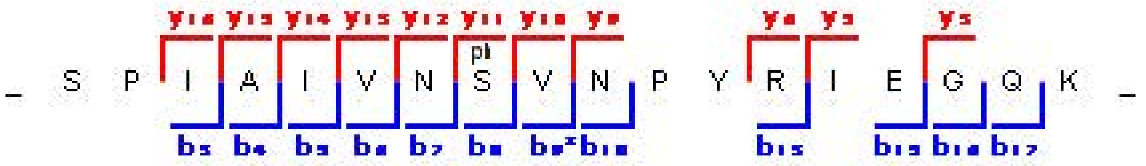
Mass:	2481.03987
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	120.8965
Mass Error [ppm]:	-0.3342
PEP:	1.3434E-16
Precursor Type:	MULTI

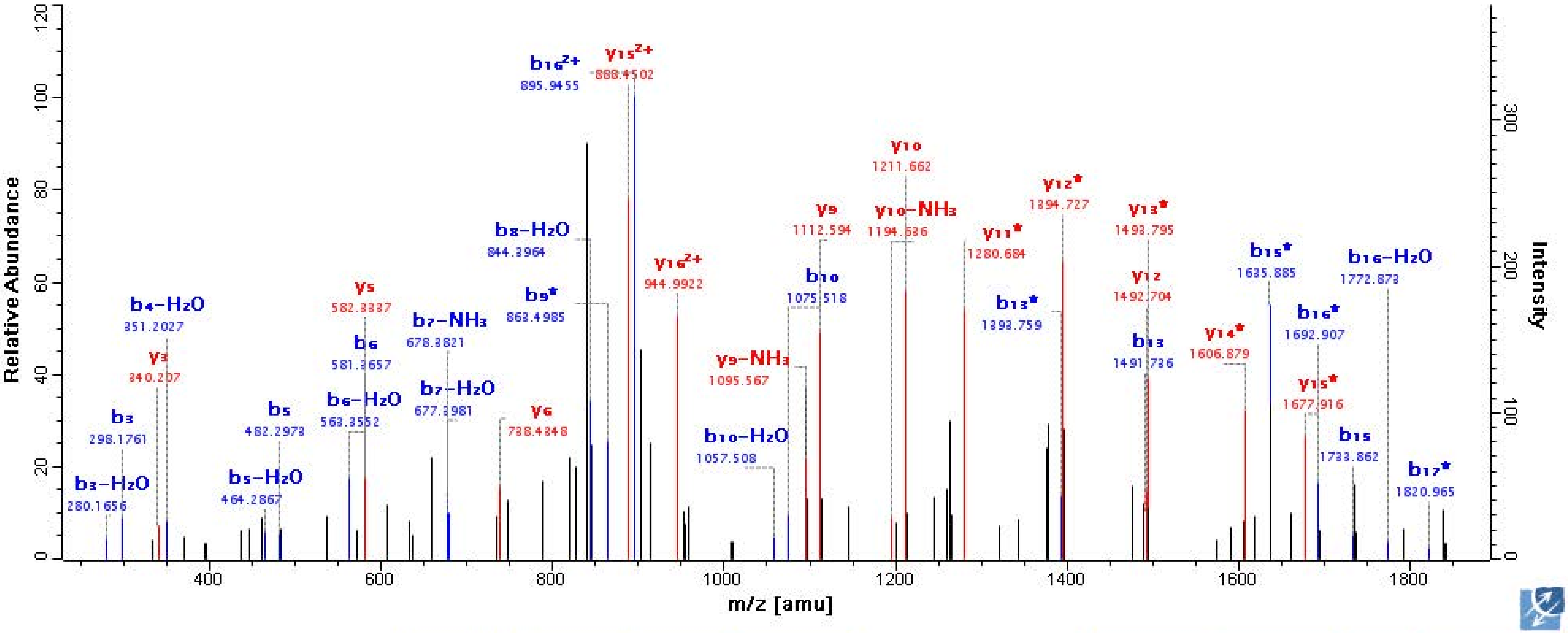
general information

Annotation:	15 of 22
AminoAcids Coverag	68 %
Intensity Coverage:	40 %
Protein Localisation:	409 ... 430

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.076		164.071		164.071	1	Y	21				
+0.06247	235.144		263.139	+0.04897	263.139	2	V	20	2327		2327	
	349.187		377.182	+0.12274	377.182	3	N	19	2227.93		1114.47	+0.2210
	406.208		434.203		434.203	4	G	18	2113.89		2113.89	
	519.293		547.287		547.287	5	I	17	2056.87		1028.94	+0.0060
	648.335	+0.40622	338.669	+0.10151	676.33	6	E	16	1943.78		972.395	+0.2231
	735.367		763.362		763.362	7	S	15	1814.74		907.873	+0.0412
	822.399		850.394	+0.2653	850.394	8	S	14	1727.71		1727.71	
	893.436		921.431		921.431	9	A	13	1640.68		1640.68	
	1022.48		1050.47		1050.47	10	E	12	1569.64		1569.64	
	1137.51		1165.5		1165.5	11	D	11	1440.6		1440.6	
	1284.54		1312.54	+0.14571	1312.54	12	M	10	1325.57	+0.09807	663.288	+0.0884
	1371.57		1399.57	+0.04752	1399.57	13	S	9	1178.53	-0.4727	1178.53	
	1458.61	-0.2217	743.804		1486.6	14	S	8	1091.5		1091.5	
	1625.6		1653.6		1653.6	15	S	7	1004.47		1004.47	
	1738.69		1766.68		1766.68	16	I	6	837.471		837.471	
	1885.76		1913.75	+0.35819	1913.75	17	F	5	724.387		724.387	
	2000.78		2028.78		2028.78	18	D	4	577.318	+0.23563	577.318	
	2071.82		2099.82		2099.82	19	A	3	462.291	+0.34552	462.291	
	2208.88		2236.87		2236.87	20	H	2	391.254	+0.20166	391.254	
	2307.95	+0.24804	1168.47		2335.94	21	V	1	254.195		254.195	
						22	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	10499
Protein:	BSU32250; thrC
Peptide Score:	152.94
Method:	ITMS; CID; 3





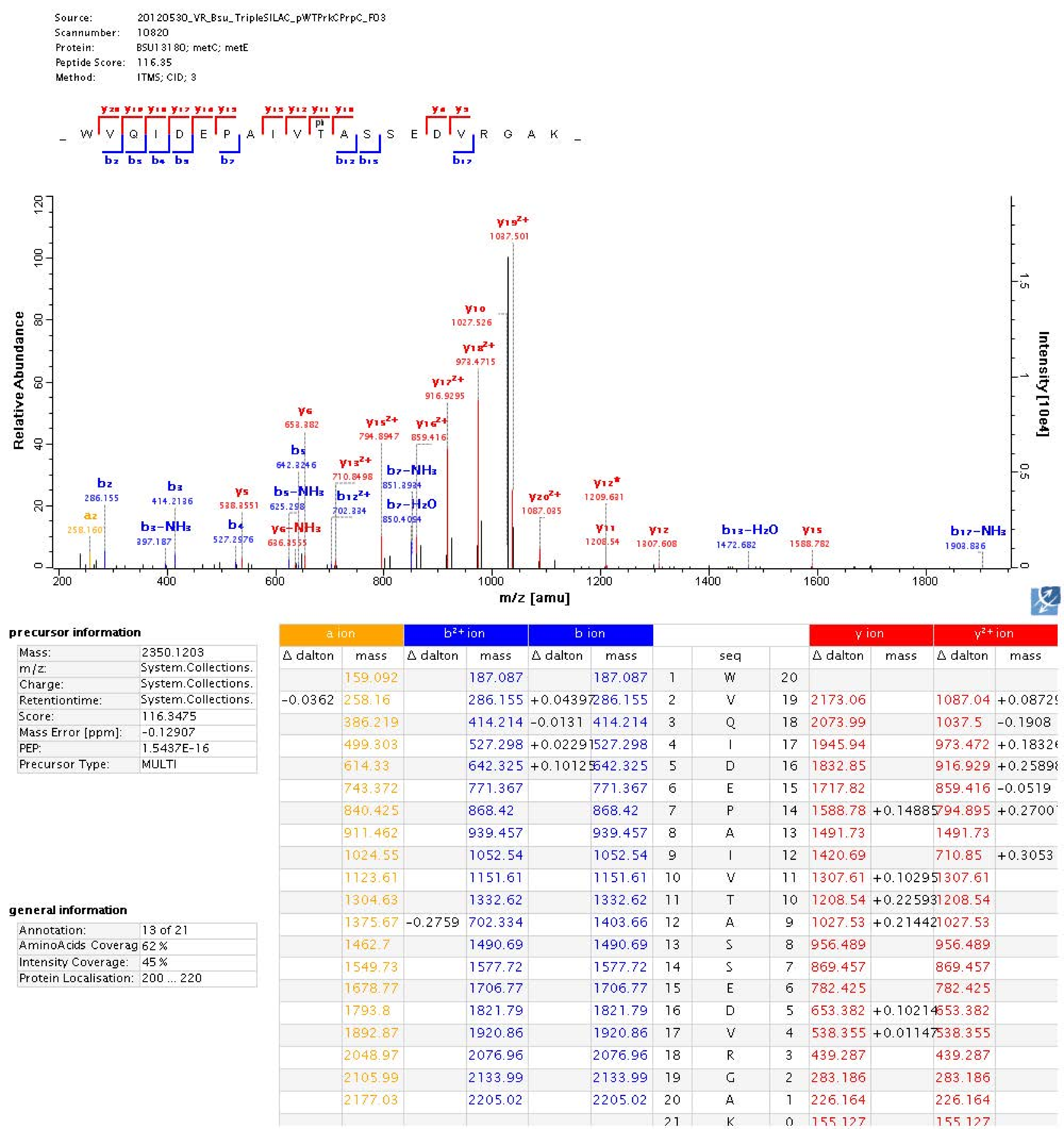
precursor information

Mass:	2064.04042
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	152.9385
Mass Error [ppm]:	-0.043228
PEP:	1.7474E-27
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	52 %
Protein Localisation:	146 ... 163

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	17				
	185.0921		185.0921	2	P	16	1986.03		1986.03	
	298.1761	+0.175827	298.1761	3	I	15	1888.977		944.9922	+0.013017
	369.2132		369.2132	4	A	14	1775.893		888.4502	+0.102046
	482.2973	+0.100334	482.2973	5	I	13	1704.856		1704.856	
	581.3657	-0.384889	581.3657	6	V	12	1591.772		1591.772	
	695.4087		695.4087	7	N	11	1492.704	+0.067586	1492.704	
	862.407		862.407	8	S	10	1378.661		1378.661	
	961.4754		961.4754	9	V	9	1211.662	+0.007065	1211.662	
	1075.518	+0.145466	1075.518	10	N	8	1112.594	+0.061807	1112.594	
	1172.571		1172.571	11	P	7	998.5509		998.5509	
	1335.634		1335.634	12	Y	6	901.4981		901.4981	
	1491.736	+0.212565	1491.736	13	R	5	738.4348	-0.150511	738.4348	
	1604.82		1604.82	14	I	4	582.3337	-0.24398	582.3337	
	1733.862	-0.319366	1733.862	15	E	3	469.2496		469.2496	
+0.154743	895.9455		1790.884	16	G	2	340.207	+0.174029	340.207	
	1918.942		1918.942	17	Q	1	283.1856		283.1856	
				18	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 10820
Protein: BSU13180; metC; metE
Peptide Score: 116.35
Method: ITMS; CID; 3

precursor information

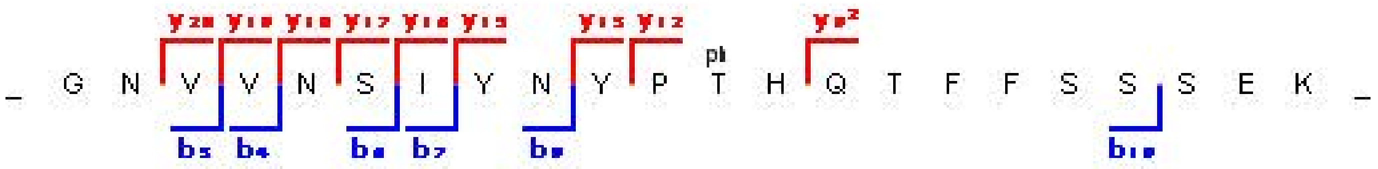
Mass:	2350.1203
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.3475
Mass Error [ppm]:	-0.12907
PEP:	1.5437E-16
Precursor Type:	MULTI

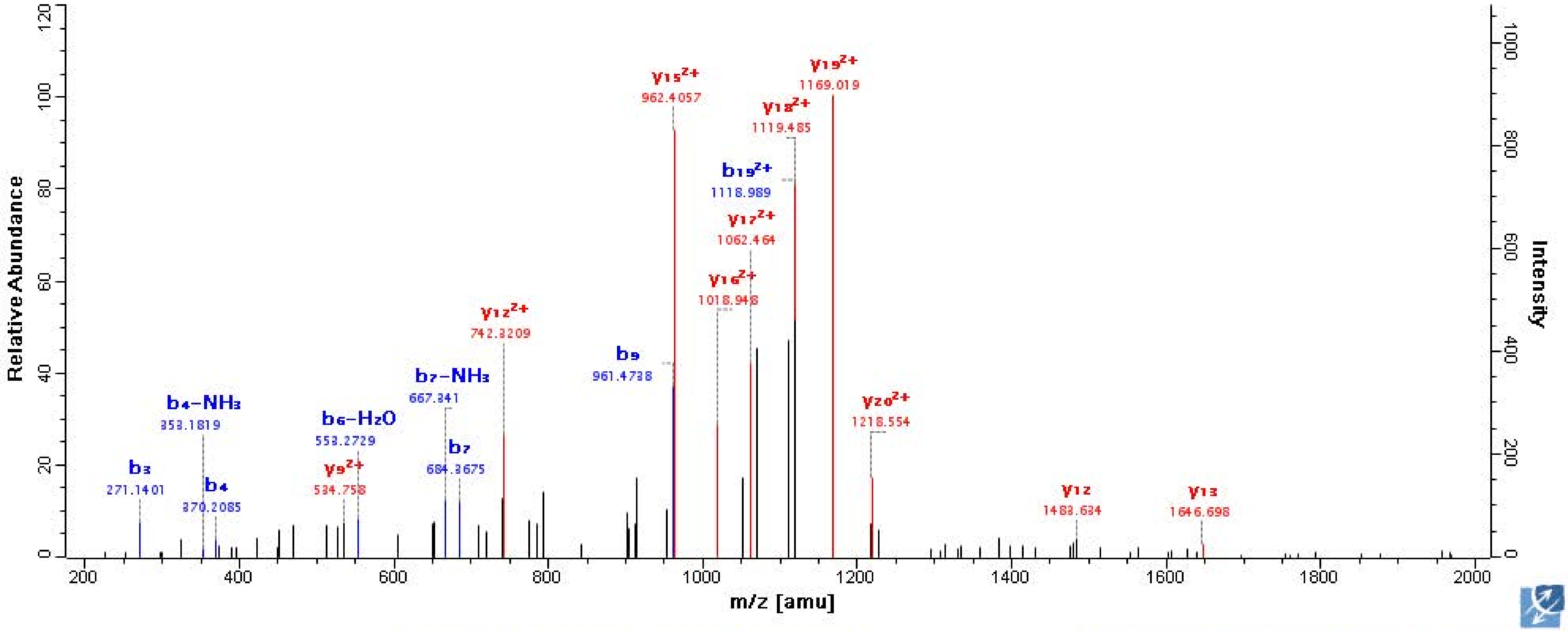
general information

Annotation:	13 of 21
AminoAcids Coverag	62 %
Intensity Coverage:	45 %
Protein Localisation:	200 ... 220

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.092		187.087		187.087	1	W	20				
-0.0362	258.16		286.155	+0.04397	286.155	2	V	19	2173.06		1087.04	+0.0872
	386.219		414.214	-0.0131	414.214	3	Q	18	2073.99		1037.5	-0.1908
	499.303		527.298	+0.0229	1527.298	4	I	17	1945.94		973.472	+0.1832
	614.33		642.325	+0.10125	642.325	5	D	16	1832.85		916.929	+0.2589
	743.372		771.367		771.367	6	E	15	1717.82		859.416	-0.0519
	840.425		868.42		868.42	7	P	14	1588.78	+0.14885	794.895	+0.2700
	911.462		939.457		939.457	8	A	13	1491.73		1491.73	
	1024.55		1052.54		1052.54	9	I	12	1420.69		710.85	+0.3053
	1123.61		1151.61		1151.61	10	V	11	1307.61	+0.10295	1307.61	
	1304.63		1332.62		1332.62	11	T	10	1208.54	+0.22593	1208.54	
	1375.67	-0.2759	702.334		1403.66	12	A	9	1027.53	+0.21442	1027.53	
	1462.7		1490.69		1490.69	13	S	8	956.489		956.489	
	1549.73		1577.72		1577.72	14	S	7	869.457		869.457	
	1678.77		1706.77		1706.77	15	E	6	782.425		782.425	
	1793.8		1821.79		1821.79	16	D	5	653.382	+0.10214	653.382	
	1892.87		1920.86		1920.86	17	V	4	538.355	+0.01147	538.355	
	2048.97		2076.96		2076.96	18	R	3	439.287		439.287	
	2105.99		2133.99		2133.99	19	G	2	283.186		283.186	
	2177.03		2205.02		2205.02	20	A	1	226.164		226.164	
						21	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	11019
Protein:	BSU22950; ypdA
Peptide Score:	76.71
Method:	ITMS; CID; 3





precursor information

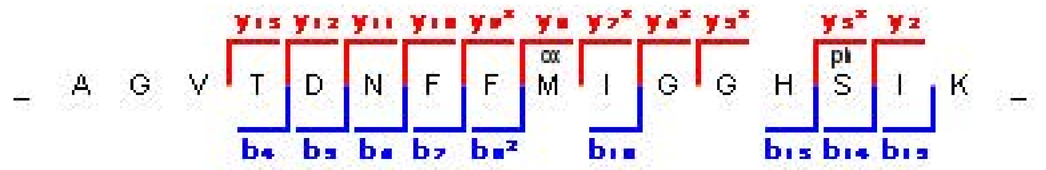
Mass:	2598.14223
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	76.71334
Mass Error [ppm]:	-0.21944
PEP:	0.00019749
Precursor Type:	MULTI

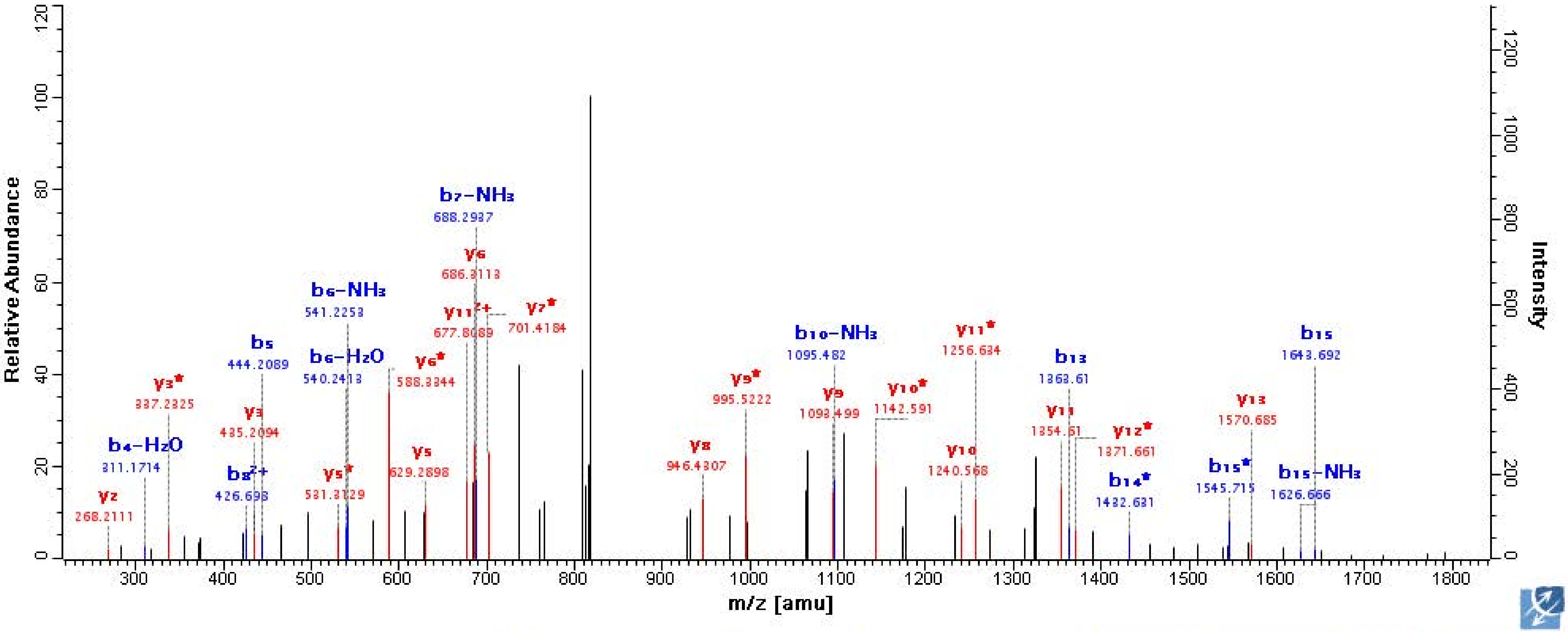
general information

Annotation:	11 of 22
AminoAcids Coverag	50 %
Intensity Coverage:	52 %
Protein Localisation:	35 ... 56

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	21				
	172.0717		172.0717	2	N	20	2550.143		2550.143	
	271.1401	-0.150061	271.1401	3	V	19	2436.1		1218.554	+0.244272
	370.2085	+0.072022	370.2085	4	V	18	2337.031		1169.019	+0.320716
	484.2514		484.2514	5	N	17	2237.963		1119.485	-0.029233
	571.2835		571.2835	6	S	16	2123.92		1062.464	+0.087934
	684.3675	-0.070213	684.3675	7	I	15	2036.888		1018.948	+0.240606
	847.4308		847.4308	8	Y	14	1923.804		962.4057	+0.222518
	961.4738	+0.037276	961.4738	9	N	13	1760.741		1760.741	
	1124.537		1124.537	10	Y	12	1646.698	+0.126074	1646.698	
	1221.59		1221.59	11	P	11	1483.634	+0.122997	742.3209	-0.047975
	1402.604		1402.604	12	T	10	1386.582		1386.582	
	1539.663		1539.663	13	H	9	1205.568		1205.568	
	1667.721		1667.721	14	Q	8	1068.509		534.758	+0.313207
	1768.769		1768.769	15	T	7	940.4502		940.4502	
	1915.837		1915.837	16	F	6	839.4025		839.4025	
	2062.906		2062.906	17	F	5	692.3341		692.3341	
	2149.938		2149.938	18	S	4	545.2657		545.2657	
-0.459548	1118.989		2236.97	19	S	3	458.2337		458.2337	
	2324.002		2324.002	20	S	2	371.2016		371.2016	
	2453.045		2453.045	21	E	1	284.1696		284.1696	
				22	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	11248
Protein:	BSU03490; comL; srfA2; srfAB
Peptide Score:	115.38
Method:	ITMS; CID; 3





precursor information

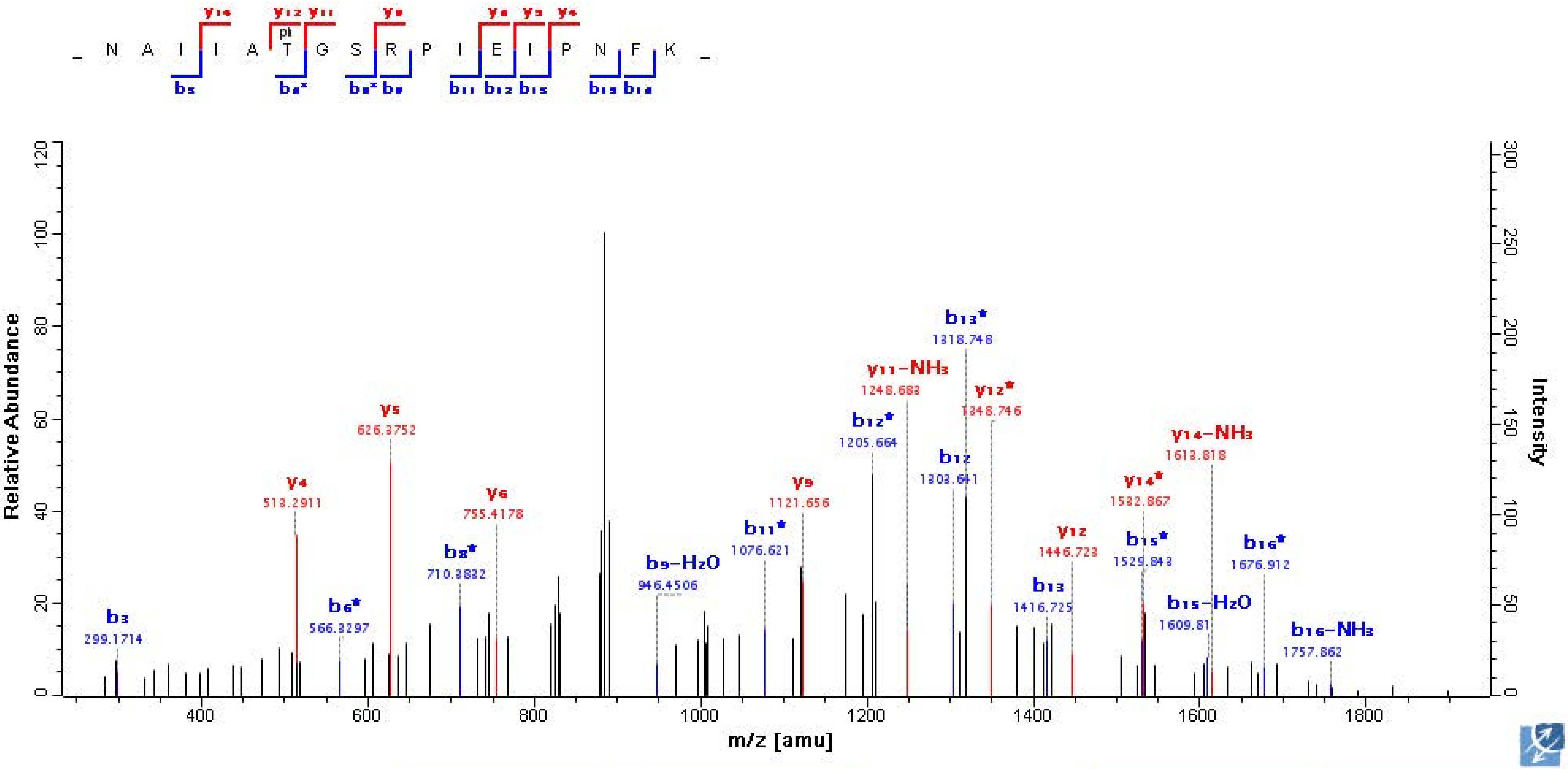
Mass:	1788.79098
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.3842
Mass Error [ppm]:	0.20244
PEP:	5.1896E-11
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	34 %
Protein Localisation:	986 ... 1001

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	15				
	129.0659		129.0659	2	G	14	1726.775		1726.775	
	228.1343		228.1343	3	V	13	1669.754		1669.754	
	329.1819		329.1819	4	T	12	1570.685	+0.096755	1570.685	
	444.2089	+0.150119	444.2089	5	D	11	1469.637		1469.637	
	558.2518		558.2518	6	N	10	1354.61	-0.114756	677.8089	-0.333416
	705.3202		705.3202	7	F	9	1240.568	-0.40032	1240.568	
-0.242821	426.698		852.3886	8	F	8	1093.499	+0.428958	1093.499	
	999.424		999.424	9	M	7	946.4307	-0.076053	946.4307	
	1112.508		1112.508	10	I	6	799.3953		799.3953	
	1169.53		1169.53	11	G	5	686.3113	+0.052504	686.3113	
	1226.551		1226.551	12	G	4	629.2898	+0.130426	629.2898	
	1363.61	+0.183388	1363.61	13	H	3	572.2683		572.2683	
	1530.608		1530.608	14	S	2	435.2094	+0.141893	435.2094	
	1643.692	+0.202283	1643.692	15	I	1	268.2111	+0.012871	268.2111	
				16	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 11320
Protein: aceD; BSU14610; citL; pdhD
Peptide Score: 64.27
Method: ITMS; CID; 3



precursor information

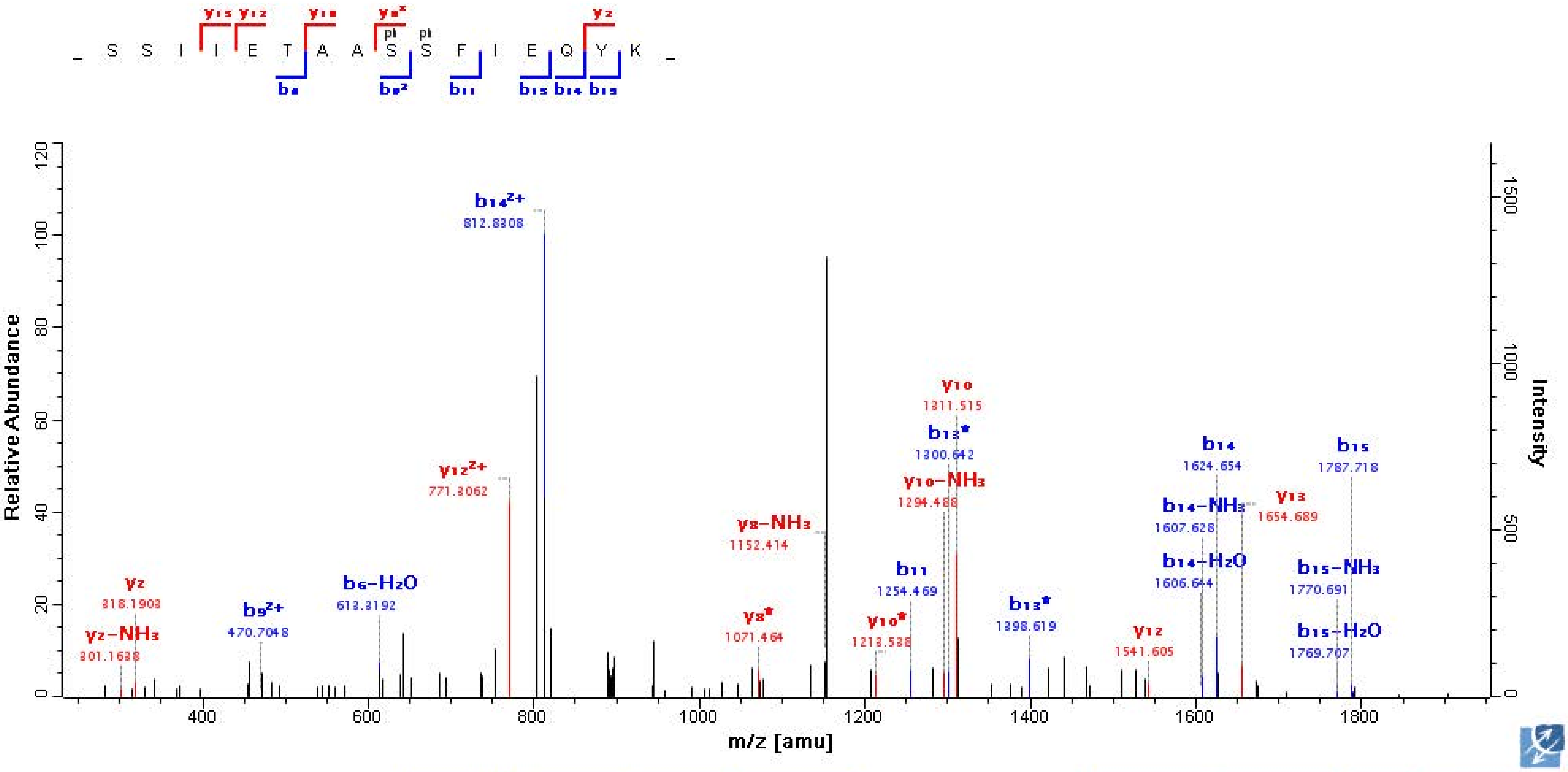
Mass:	1919.98635
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.27496
Mass Error [ppm]:	-0.34383
PEP:	0.0049098
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	28 %
Protein Localisation:	142 ... 158

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	16		
	186.087317702	2	A	15	1814.965560689	
-0.0806529	299.171381682	3	I	14	1743.928446901	
	412.255445662	4	I	13	1630.84438292	
	483.29255945	5	A	12	1517.76031894	
	664.306568333	6	T	11	1446.723205152	+0.2168583
	721.328032056	7	G	10	1265.70919627	
	808.360060466	8	S	9	1208.687732546	
	964.461171494	9	R	8	1121.655704136	+0.0092129
	1061.513935346	10	P	7	965.554593108	
	1174.597999327	11	I	6	868.501829256	
-0.009611	1303.640592423	12	E	5	755.417765276	-0.0428263
-0.1472638	1416.724656403	13	I	4	626.37517218	+0.0015368
	1513.777420255	14	P	3	513.291108199	+0.113738
	1627.820347703	15	N	2	416.238344347	
	1774.888761619	16	F	1	302.1954169	
		17	K	0	155.127002984	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 12335
Protein: BSU08320; yfiM
Peptide Score: 71.78
Method: ITMS; CID; 3



precursor information

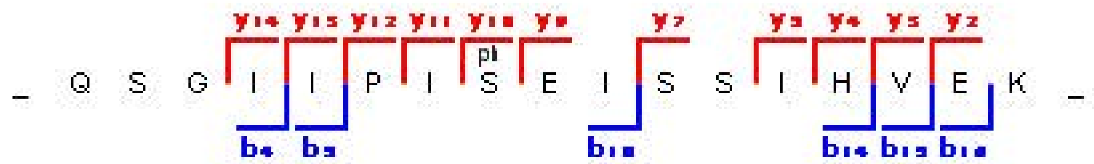
Mass:	1932.817
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.78071
Mass Error [ppm]:	0.5642
PEP:	0.0012491
Precursor Type:	MULTI

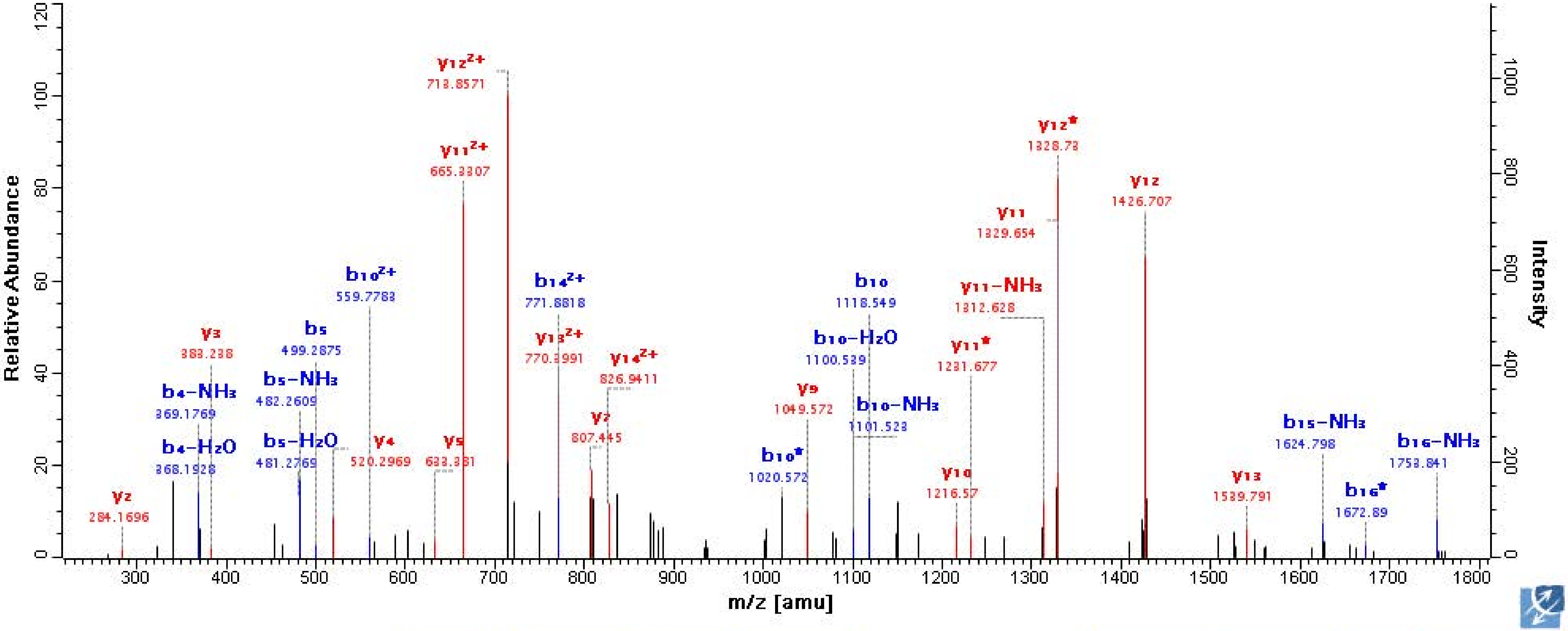
general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	31 %
Protein Localisation:	129 ... 144

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	15				
	175.0713		175.0713	2	S	14	1854.805		1854.805	
	288.1554		288.1554	3	I	13	1767.773		1767.773	
	401.2395		401.2395	4	I	12	1654.689	+0.002756	1654.689	
	530.2821		530.2821	5	E	11	1541.605	+0.255887	771.3062	+0.097023
	631.3297		631.3297	6	T	10	1412.563		1412.563	
	702.3668		702.3668	7	A	9	1311.515	+0.142912	1311.515	
	773.404		773.404	8	A	8	1240.478		1240.478	
+0.380957	470.7048		940.4023	9	S	7	1169.441		1169.441	
	1107.401		1107.401	10	S	6	1002.442		1002.442	
	1254.469	+0.146631	1254.469	11	F	5	835.444		835.444	
	1367.553		1367.553	12	I	4	688.3756		688.3756	
	1496.596		1496.596	13	E	3	575.2915		575.2915	
+0.033151	812.8308	-0.077056	1624.654	14	Q	2	446.2489		446.2489	
	1787.718	+0.246334	1787.718	15	Y	1	318.1903	-0.042871	318.1903	
				16	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 12359
Protein: BSU22880; jofD; ypfD
Peptide Score: 135.23
Method: ITMS; CID; 3





precursor information

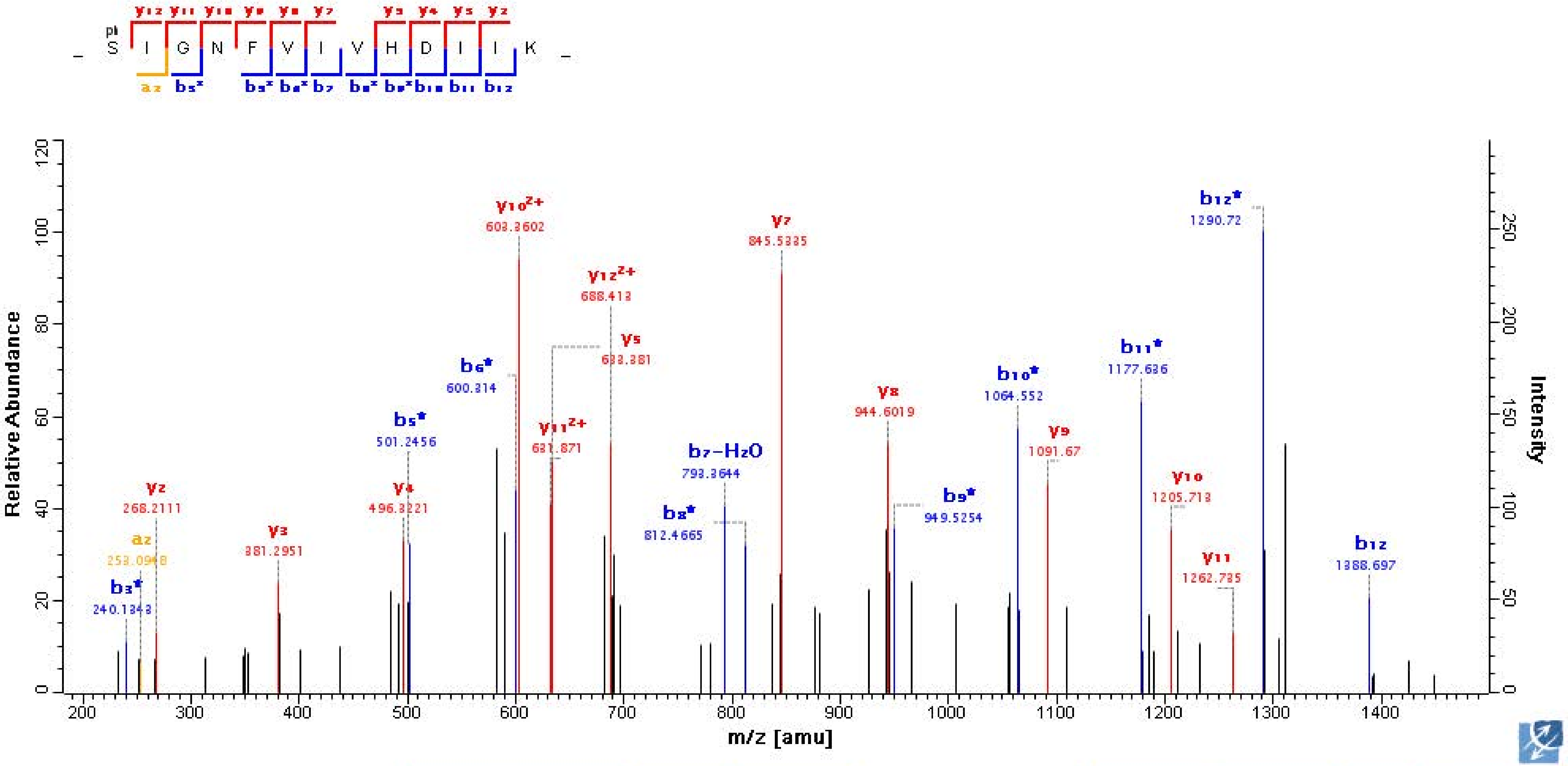
Mass:	1915.96744
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.2347
Mass Error [ppm]:	0.95169
PEP:	1.0352E-17
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	62 %
Protein Localisation:	40 ... 56

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659		129.0659	1	Q	16				
	216.0979		216.0979	2	S	15	1796.929		1796.929	
	273.1193		273.1193	3	G	14	1709.896		1709.896	
	386.2034		386.2034	4	I	13	1652.875		826.9411	+0.201128
	499.2875	+0.086366	499.2875	5	I	12	1539.791	+0.369328	770.3991	+0.051387
	596.3402		596.3402	6	P	11	1426.707	+0.060081	713.8571	-0.046779
	709.4243		709.4243	7	I	10	1329.654	+0.127494	665.3307	-0.359203
	876.4227		876.4227	8	S	9	1216.57	+0.131357	1216.57	
	1005.465		1005.465	9	E	8	1049.572	+0.186845	1049.572	
+0.135643	559.7783	-0.150026	1118.549	10	I	7	920.5291		920.5291	
	1205.581		1205.581	11	S	6	807.445	+0.10226	807.445	
	1292.613		1292.613	12	S	5	720.413		720.413	
	1405.697		1405.697	13	I	4	633.381	+0.02386	633.381	
-0.324013	771.8818		1542.756	14	H	3	520.2969	+0.043837	520.2969	
	1641.825		1641.825	15	V	2	383.238	+0.066403	383.238	
	1770.867		1770.867	16	E	1	284.1696	-0.0189	284.1696	
				17	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	13148
Protein:	BSU00940; cysS; spnA
Peptide Score:	145.17
Method:	ITMS; CID; 3



precursor information

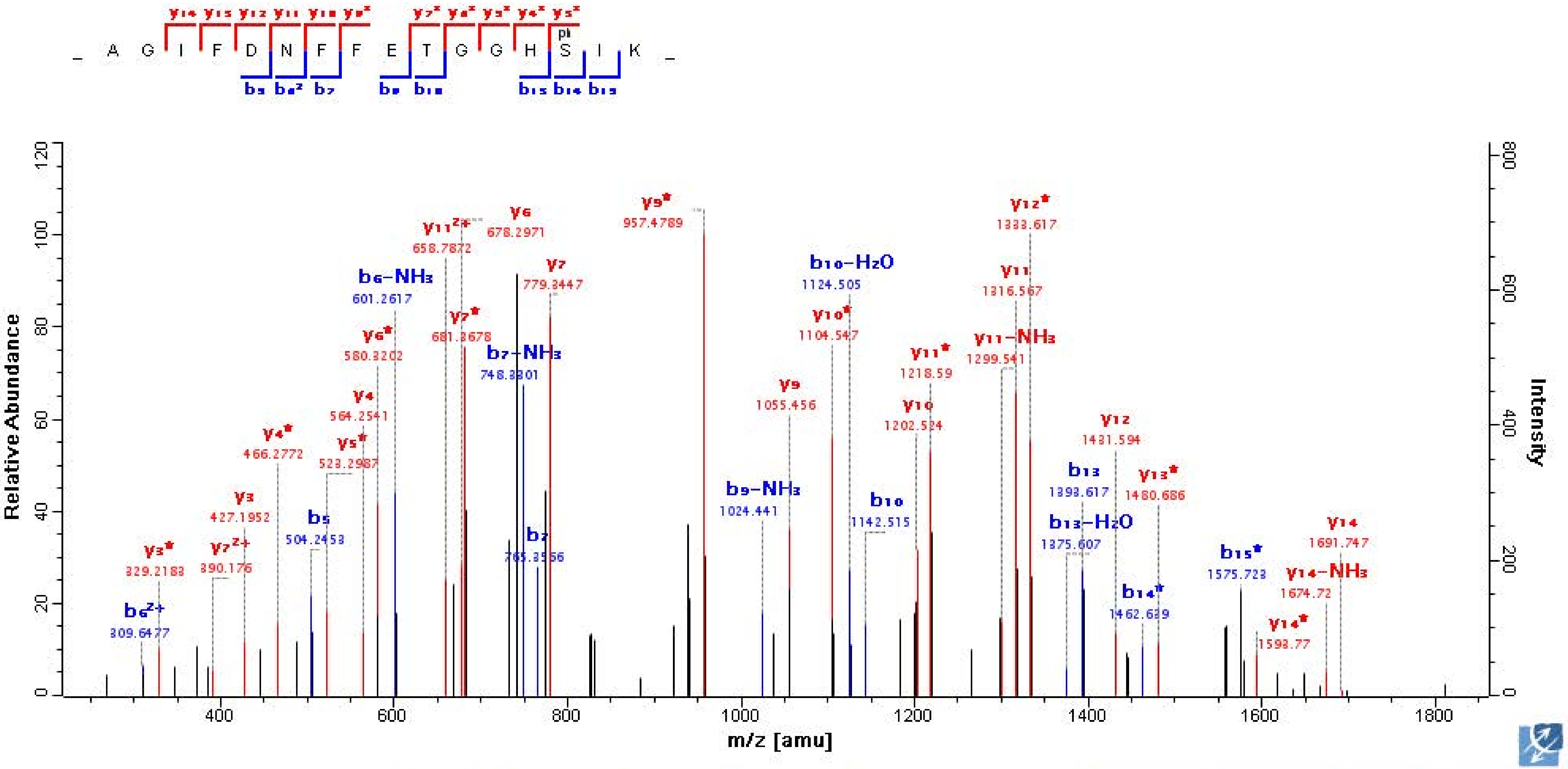
Mass:	1533.79606
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	145.1657
Mass Error [ppm]:	0.2775
PEP:	3.8387E-19
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	54 %
Protein Localisation:	270 ... 282

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	140.0107		168.0056	1	S	12				
+0.227603	253.0948		281.0897	2	I	11	1375.819		688.413	+0.032972
	310.1162		338.1112	3	G	10	1262.735	+0.017637	631.871	-0.078621
	424.1592		452.1541	4	N	9	1205.713	+0.075111	603.3602	+0.080365
	571.2276		599.2225	5	F	8	1091.67	+0.046749	1091.67	
	670.296		698.2909	6	V	7	944.6019	-0.111155	944.6019	
	783.3801		811.375	7	I	6	845.5335	+0.193709	845.5335	
	882.4485		910.4434	8	V	5	732.4494		732.4494	
	1019.507		1047.502	9	H	4	633.381	-0.099064	633.381	
	1134.534		1162.529	10	D	3	496.3221	+0.05848	496.3221	
	1247.618		1275.613	11	I	2	381.2951	+0.0416	381.2951	
	1360.702	+0.05079	1388.697	12	I	1	268.2111	+0.175896	268.2111	
				13	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	13295
Protein:	BSU03480; srfA; srfA1; srfAA
Peptide Score:	198.87
Method:	ITMS; CID; 3



precursor information

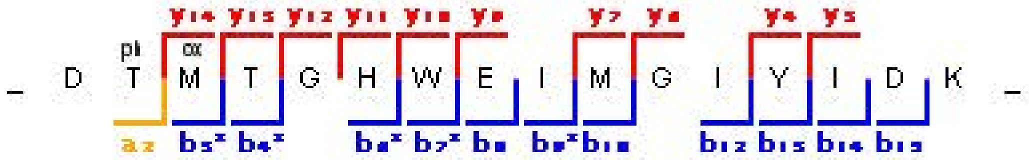
Mass:	1818.79783
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	198.8673
Mass Error [ppm]:	0.007619
PEP:	3.1608E-57
Precursor Type:	MULTI

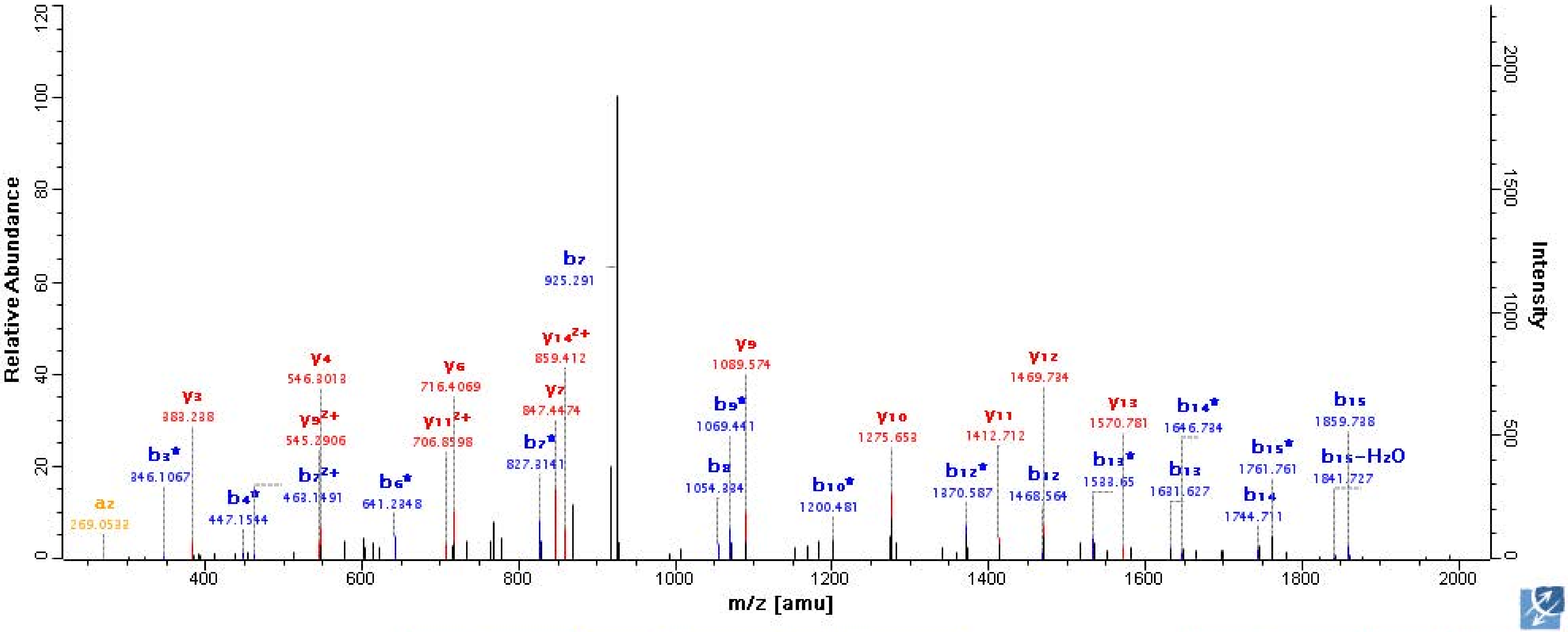
general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	55 %
Protein Localisation:	993 ... 1008

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	15				
	129.0659		129.0659	2	G	14	1748.768		1748.768	
	242.1499		242.1499	3	I	13	1691.747	+0.143379	1691.747	
	389.2183		389.2183	4	F	12	1578.662		1578.662	
	504.2453	+0.031703	504.2453	5	D	11	1431.594	-0.037762	1431.594	
+0.411098	309.6477		618.2882	6	N	10	1316.567	+0.139328	658.7872	+0.393296
	765.3566	+0.015515	765.3566	7	F	9	1202.524	+0.179326	1202.524	
	912.425		912.425	8	F	8	1055.456	+0.100156	1055.456	
	1041.468		1041.468	9	E	7	908.3873		908.3873	
	1142.515	-0.127362	1142.515	10	T	6	779.3447	+0.19035	390.176	+0.162429
	1199.537		1199.537	11	G	5	678.2971	-0.067147	678.2971	
	1256.558		1256.558	12	G	4	621.2756		621.2756	
	1393.617	+0.126023	1393.617	13	H	3	564.2541	+0.107372	564.2541	
	1560.615		1560.615	14	S	2	427.1952	+0.111841	427.1952	
	1673.7		1673.7	15	I	1	260.1969		260.1969	
				16	K	0	147.1128		147.1128	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 13415
Protein: BSU23500; drm; yqkN
Peptide Score: 171.08
Method: ITMS; CID; 3





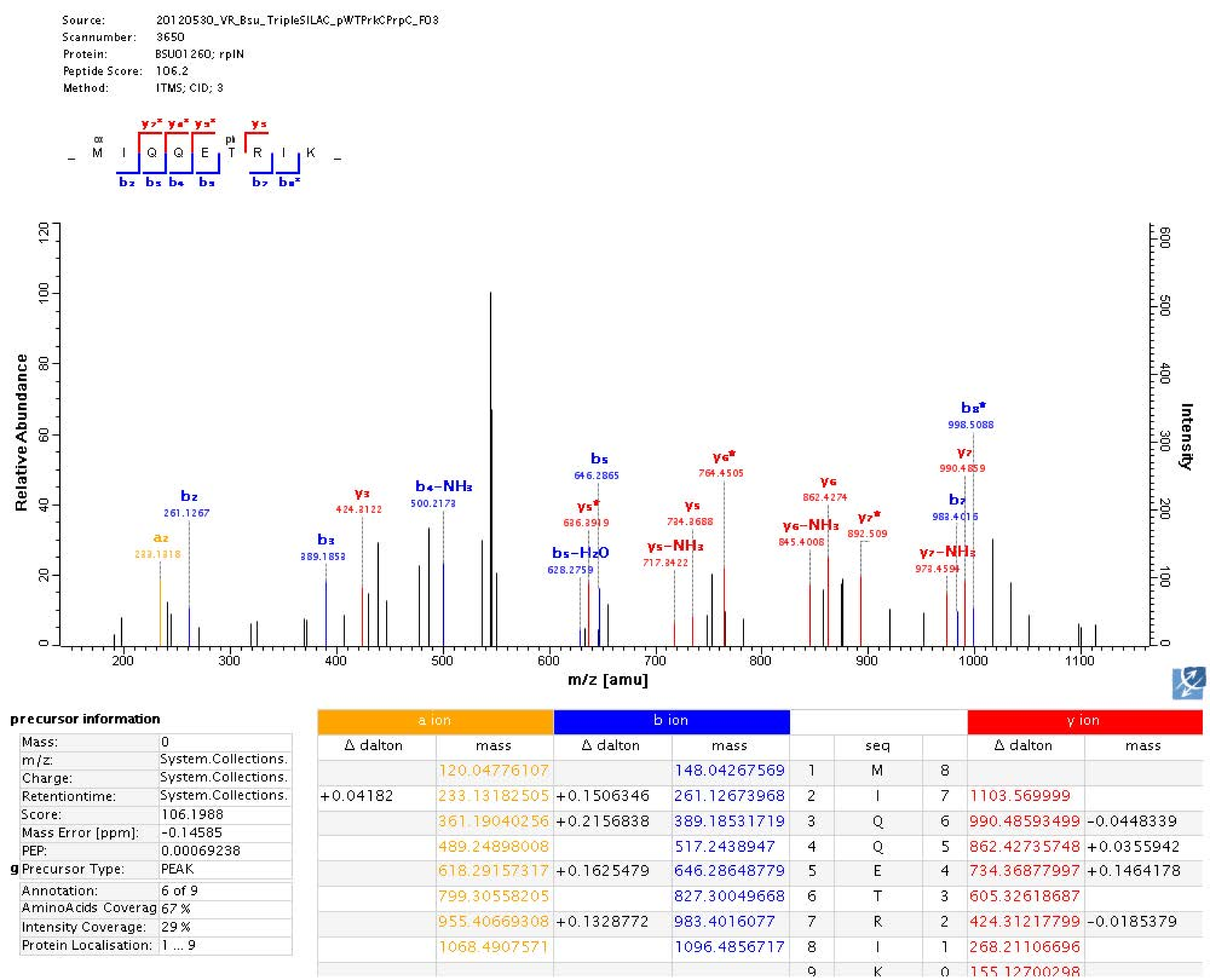
precursor information

Mass:	2004.83703
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	171.0793
Mass Error [ppm]:	0.38705
PEP:	6.2258E-34
Precursor Type:	MULTI

general information

Annotation:	14 of 16
AminoAcids Coverag	88 %
Intensity Coverage:	33 %
Protein Localisation:	86 ... 101

a ion		b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		116.034		116.034	1	D	15				
+0.11316	269.053		297.048		297.048	2	T	14	1898.83		1898.83	
	416.089		444.084		444.084	3	M	13	1717.82		859.412	-0.1044
	517.136		545.131		545.131	4	T	12	1570.78	-0.0127	1570.78	
	574.158		602.153		602.153	5	G	11	1469.73	-0.076	1469.73	
	711.217		739.212		739.212	6	H	10	1412.71	+0.09282	706.86	+0.476
	897.296	-0.2428	463.149	-0.1811	925.291	7	W	9	1275.65	+0.05981	1275.65	
	1026.34		1054.33	+0.15469	1054.33	8	E	8	1089.57	+0.08859	545.291	+0.4748
	1139.42		1167.42		1167.42	9	I	7	960.531		960.531	
	1270.46		1298.46		1298.46	10	M	6	847.447	+0.13236	847.447	
	1327.48		1355.48		1355.48	11	G	5	716.407	+0.04186	716.407	
	1440.57		1468.56	+0.14617	1468.56	12	I	4	659.385		659.385	
	1603.63		1631.63	+0.03499	1631.63	13	Y	3	546.301	+0.09527	546.301	
	1716.72		1744.71	+0.03711	1744.71	14	I	2	383.238	+0.02334	383.238	
	1831.74		1859.74	+0.3195	1859.74	15	D	1	270.154		270.154	
						16	K	0	155.127		155.127	



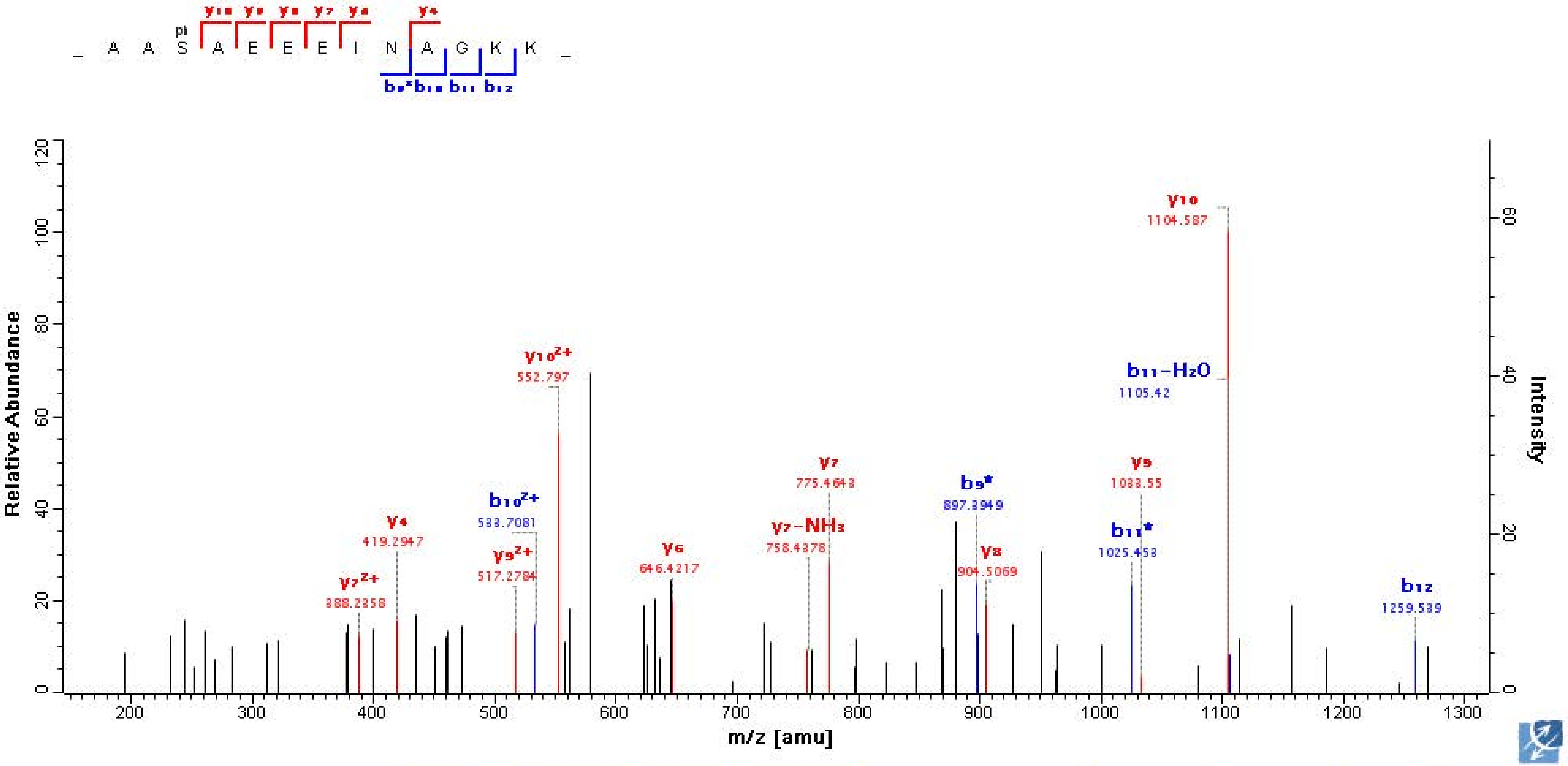
Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	3650
Protein:	BSU01260; rplN
Peptide Score:	106.2
Method:	ITMS; CID; 3

precursor information

Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	106.1988
Mass Error [ppm]:	-0.14585
PEP:	0.00069238
Precursor Type:	PEAK
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	29 %
Protein Localisation:	1 ... 9

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.04776107		148.04267569	1	M	8		
+0.04182	233.13182505	+0.1506346	261.12673968	2	I	7	1103.569999	
	361.19040256	+0.2156838	389.18531719	3	Q	6	990.48593499	-0.0448339
	489.24898008		517.2438947	4	Q	5	862.42735748	+0.0355942
	618.29157317	+0.1625479	646.28648779	5	E	4	734.36877997	+0.1464178
	799.30558205		827.30049668	6	T	3	605.32618687	
	955.40669308	+0.1328772	983.4016077	7	R	2	424.31217799	-0.0185379
	1068.4907571		1096.4856717	8	I	1	268.21106696	
				9	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 3909
Protein: BSU41000; gidB; rsmG
Peptide Score: 52.5
Method: ITMS; CID; 3



precursor information

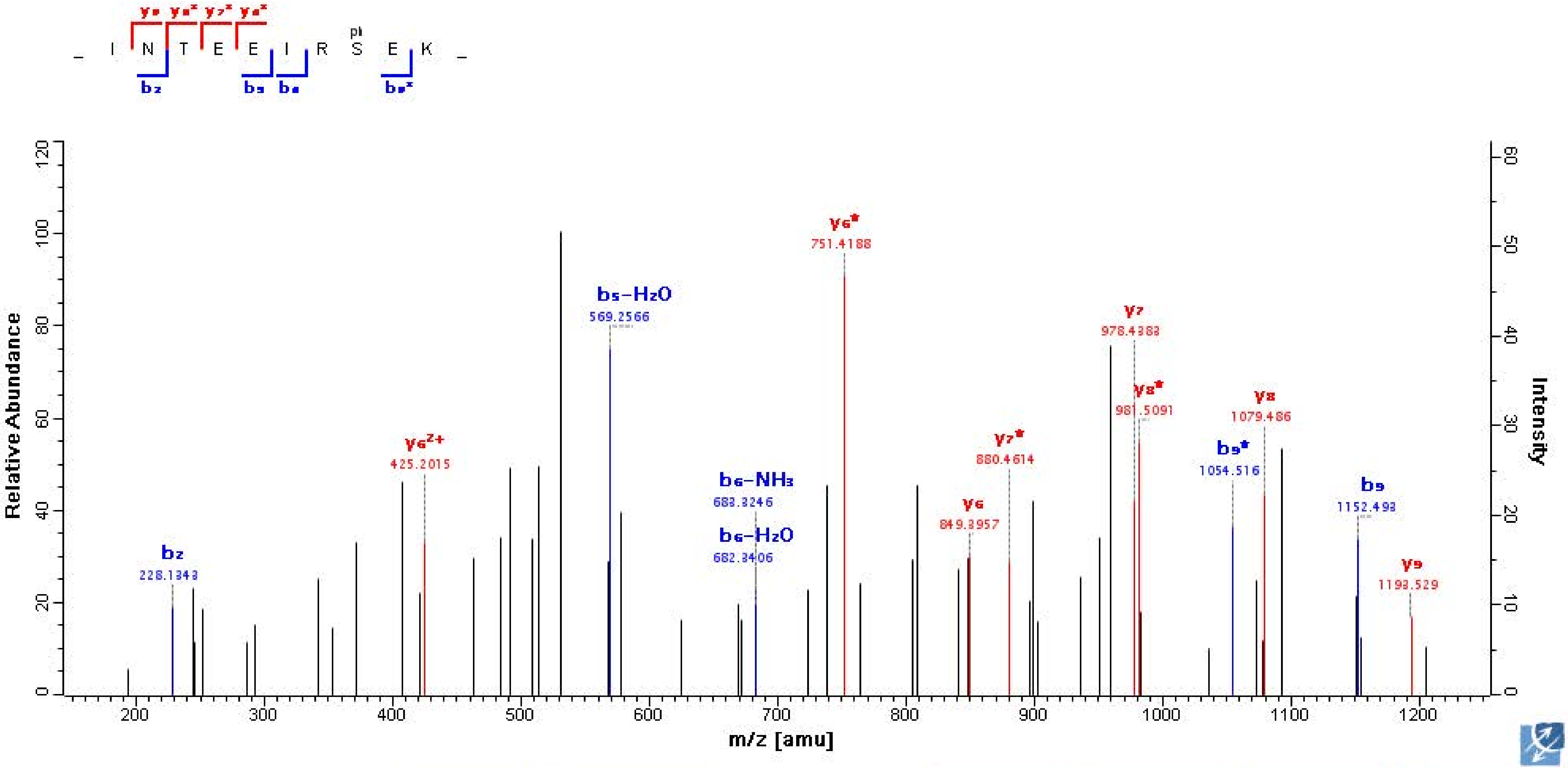
Mass:	1396.62431
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	52.5002
Mass Error [ppm]:	0.54254
PEP:	0.028761
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	35 %
Protein Localisation:	174 ... 186

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	12				
	143.0815		143.0815	2	A	11	1342.622		1342.622	
	310.0799		310.0799	3	S	10	1271.585		1271.585	
	381.117		381.117	4	A	9	1104.587	+0.171918	552.797	+0.115097
	510.1596		510.1596	5	E	8	1033.55	-0.215529	517.2784	-0.290907
	639.2022		639.2022	6	E	7	904.5069	+0.0839	904.5069	
	768.2448		768.2448	7	E	6	775.4643	+0.208647	388.2358	+0.119972
	881.3288		881.3288	8	I	5	646.4217	+0.367878	646.4217	
	995.3717		995.3717	9	N	4	533.3377		533.3377	
-0.157227	533.7081		1066.409	10	A	3	419.2947	+0.035275	419.2947	
	1123.43		1123.43	11	G	2	348.2576		348.2576	
	1259.539	-0.00433	1259.539	12	K	1	291.2362		291.2362	
				13	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 4378
Protein: BSU23850; yqjI; zwf
Peptide Score: 64.44
Method: ITMS; CID; 3



precursor information

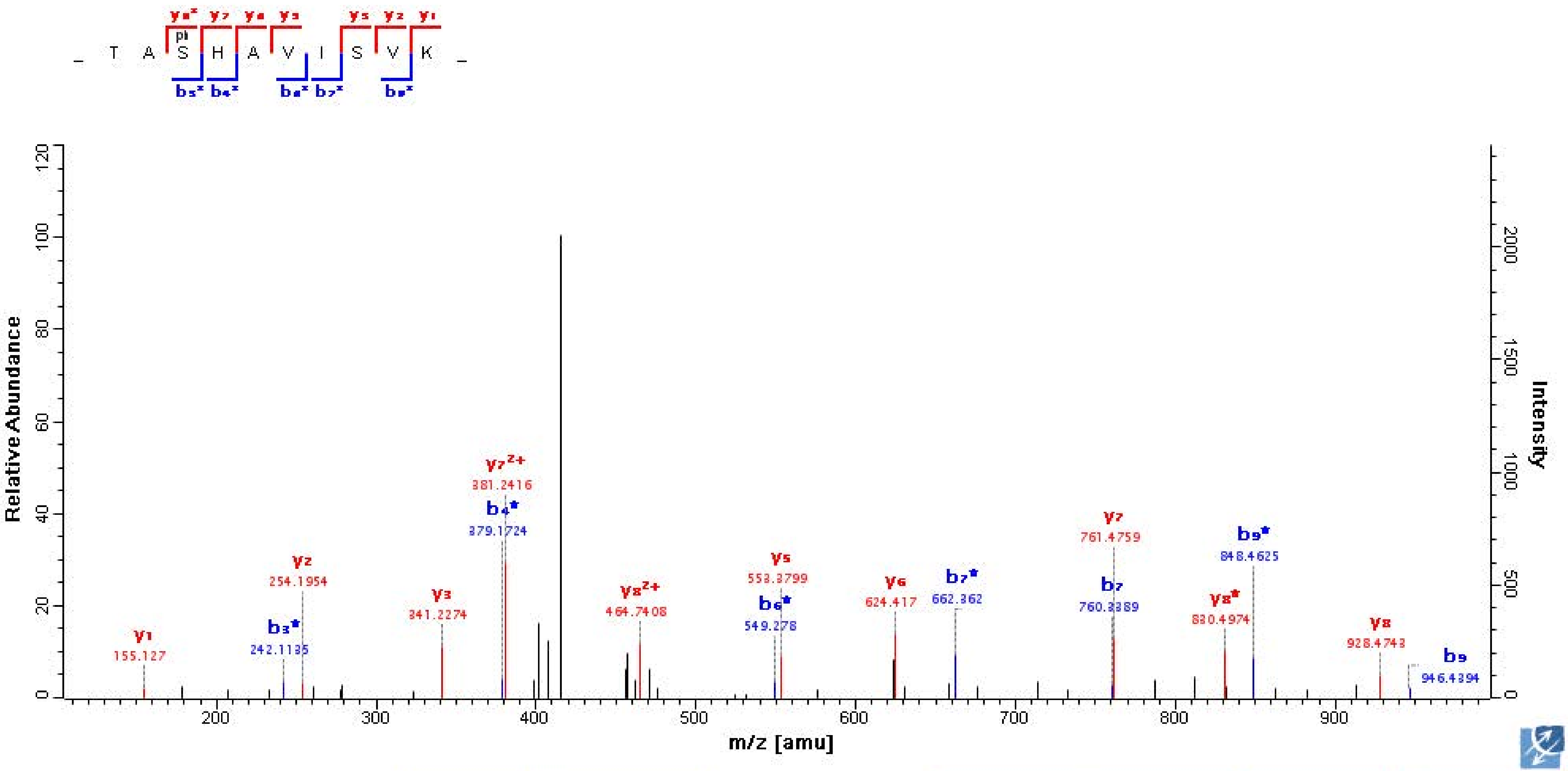
Mass:	1297.5925
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.43861
Mass Error [ppm]:	0.7613
PEP:	0.028807
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	31 %
Protein Localisation:	257 ... 266

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	9				
+0.0007419	228.13426789	2	N	8	1193.528922	+0.2396327	1193.528922	
	329.18194637	3	T	7	1079.4859946	+0.1241128	1079.4859946	
	458.22453946	4	E	6	978.4383161	-0.0142438	978.4383161	
	587.26713256	5	E	5	849.395723	+0.1708053	425.20149973	-0.2518537
	700.35119654	6	I	4	720.35312991		720.35312991	
	856.45230757	7	R	3	607.26906593		607.26906593	
	1023.4506664	8	S	2	451.1679549		451.1679549	
-0.2704812	1152.4932595	9	E	1	284.16959608		284.16959608	
		10	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	4454
Protein:	BSU14490; kinC; mskA; ssb
Peptide Score:	129.7
Method:	ITMS; CID; 3



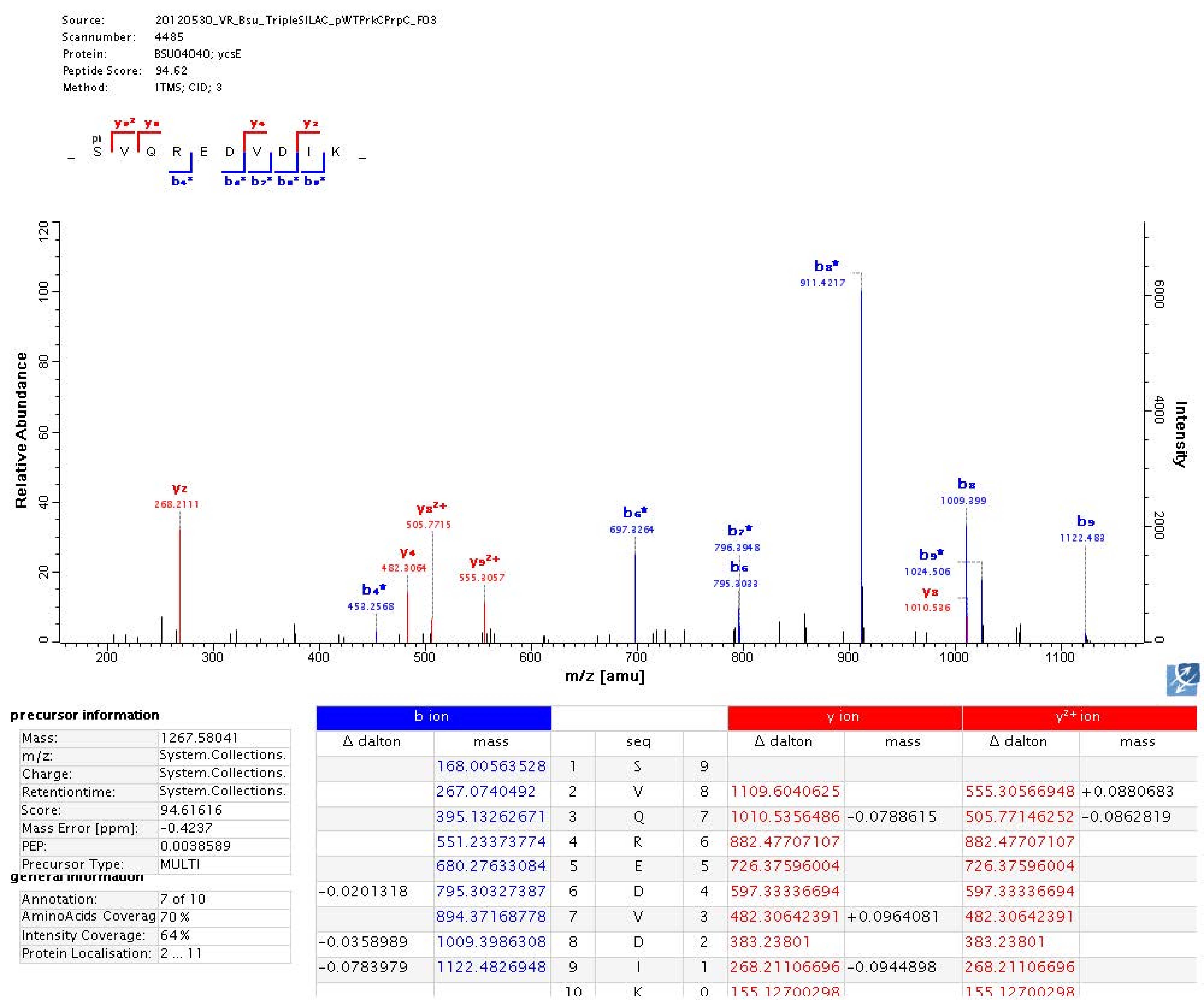
precursor information

Mass:	1099.55179
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	129.7024
Mass Error [ppm]:	-0.026871
PEP:	0.040016
Precursor Type:	ISO

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	39 %
Protein Localisation:	353 ... 362

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494	1	T	9				
	173.09206873	2	A	8	999.51142146		999.51142146	
	340.09042755	3	S	7	928.47430768	-0.0207554	464.74079207	+0.1818764
	477.14933941	4	H	6	761.47594886	+0.1318392	381.24161266	+0.0031994
	548.1864532	5	A	5	624.41703699	+0.0929728	624.41703699	
	647.25486711	6	V	4	553.37992321	+0.1225182	553.37992321	
+0.0983858	760.33893109	7	I	3	454.31150929		454.31150929	
	847.3709595	8	S	2	341.22744531	+0.0367759	341.22744531	
+0.0848575	946.43937342	9	V	1	254.1954169	+0.0675683	254.1954169	
		10	K	0	155.12700298	+0.020046	155.12700298	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 4485
Protein: BSU04040; ycsE
Peptide Score: 94.62
Method: ITMS; CID; 3

precursor information

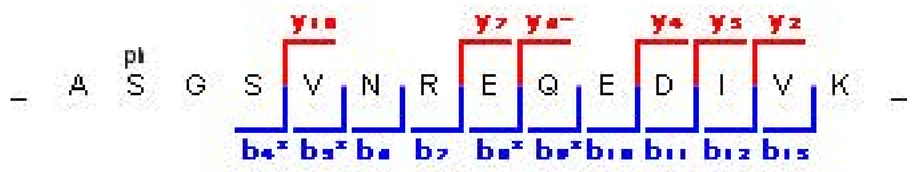
Mass:	1267.58041
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.61616
Mass Error [ppm]:	-0.4237
PEP:	0.0038589
Precursor Type:	MULTI

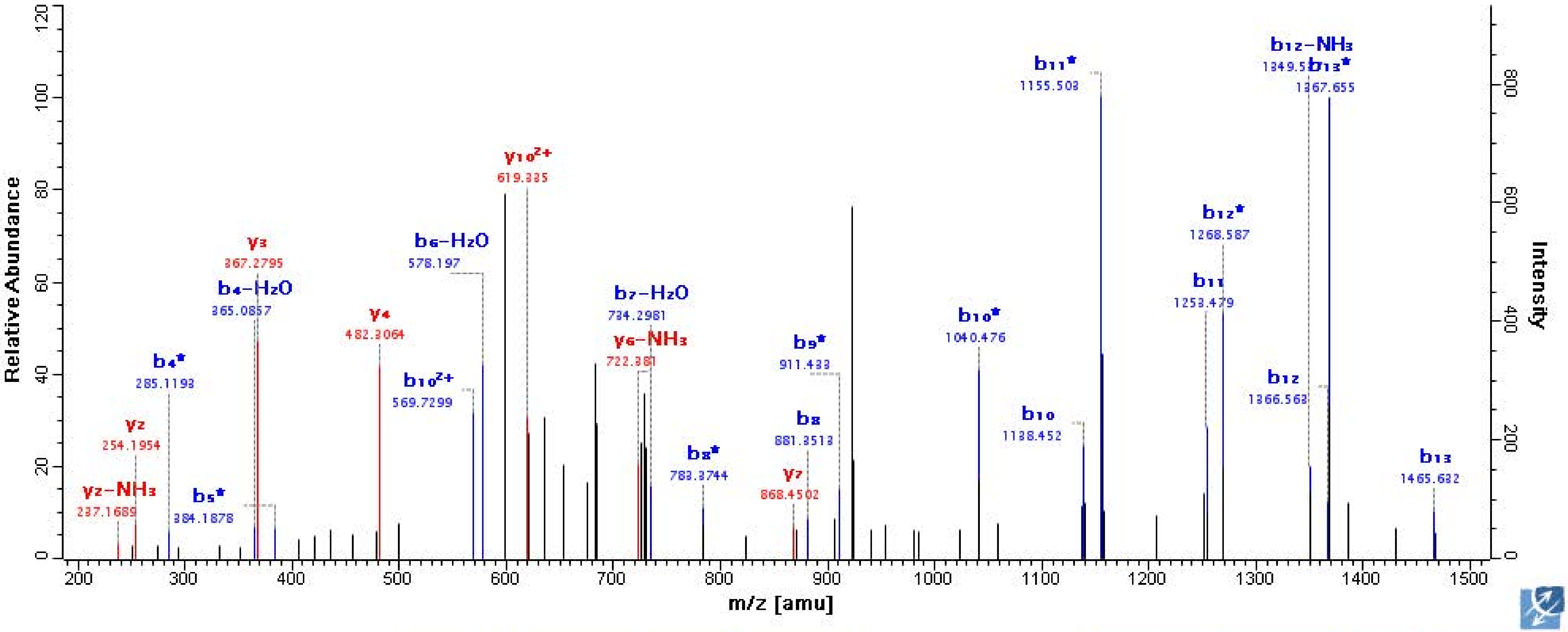
general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	64 %
Protein Localisation:	2 ... 11

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	9				
	267.0740492	2	V	8	1109.6040625		555.30566948	+0.0880683
	395.13262671	3	Q	7	1010.5356486	-0.0788615	505.77146252	-0.0862819
	551.23373774	4	R	6	882.47707107		882.47707107	
	680.27633084	5	E	5	726.37596004		726.37596004	
-0.0201318	795.30327387	6	D	4	597.33336694		597.33336694	
	894.37168778	7	V	3	482.30642391	+0.0964081	482.30642391	
-0.0358989	1009.3986308	8	D	2	383.23801		383.23801	
-0.0783979	1122.4826948	9	I	1	268.21106696	-0.0944898	268.21106696	
		10	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	4580
Protein:	BSU13890; crr; ptsG; ptsX
Peptide Score:	106.42
Method:	ITMS; CID; 3





precursor information

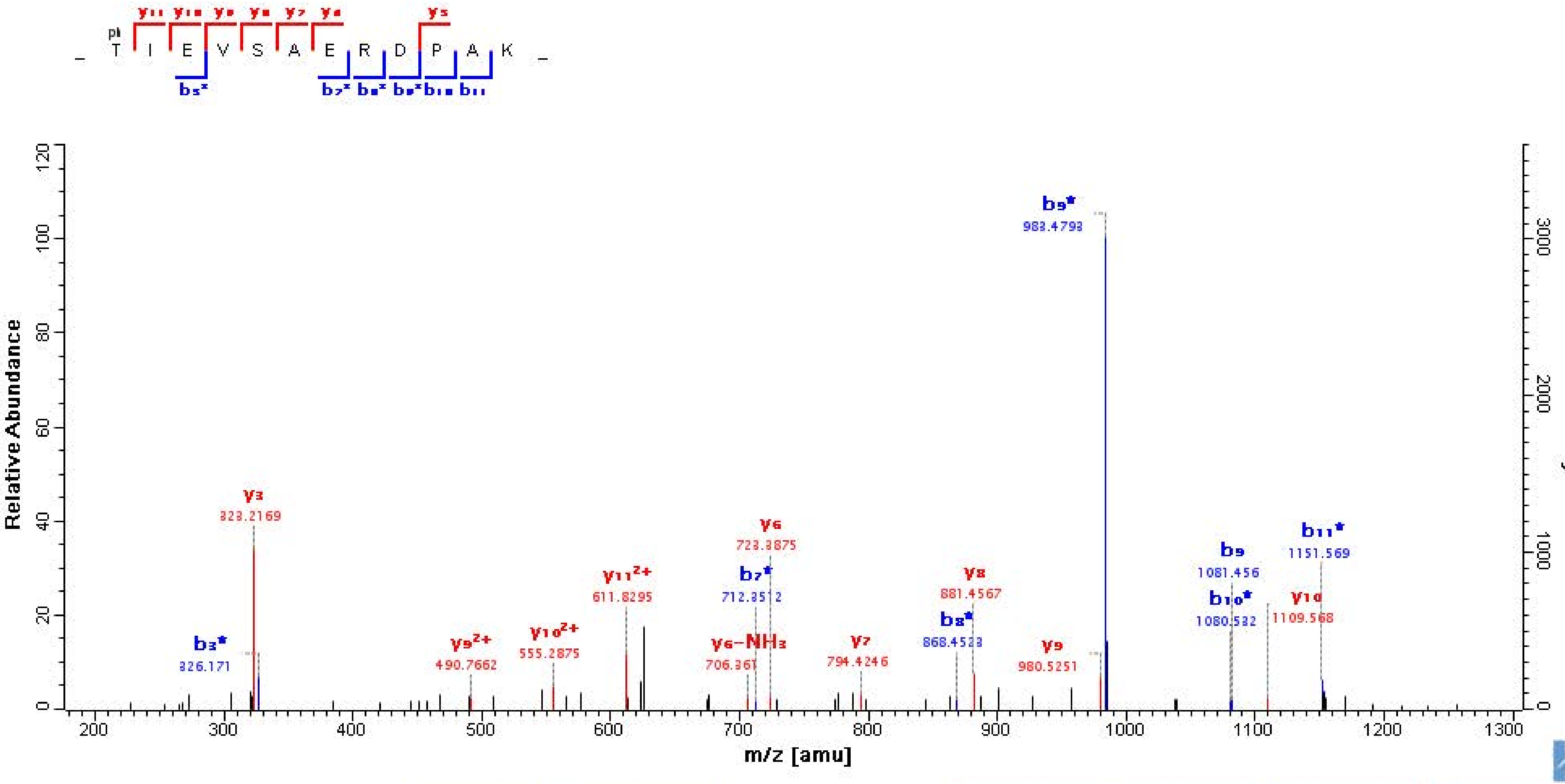
Mass:	1610.73007
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	106.4236
Mass Error [ppm]:	-0.038029
PEP:	1.6306E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	47 %
Protein Localisation:	683 ... 696

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	13				
	239.0427		239.0427	2	S	12	1548.714		1548.714	
	296.0642		296.0642	3	G	11	1381.716		1381.716	
	383.0962		383.0962	4	S	10	1324.695		1324.695	
	482.1647		482.1647	5	V	9	1237.663		619.335	-0.017514
	596.2076		596.2076	6	N	8	1138.594		1138.594	
	752.3087		752.3087	7	R	7	1024.551		1024.551	
	881.3513	-0.009795	881.3513	8	E	6	868.4502	+0.101082	868.4502	
	1009.41		1009.41	9	Q	5	739.4076		739.4076	
-0.247628	569.7299	+0.063656	1138.452	10	E	4	611.349		611.349	
	1253.479	+0.176483	1253.479	11	D	3	482.3064	+0.110751	482.3064	
	1366.563	-0.104602	1366.563	12	I	2	367.2795	+0.050109	367.2795	
	1465.632	+0.065509	1465.632	13	V	1	254.1954	+0.012789	254.1954	
				14	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	4718
Protein:	BSU33940; gap; gapA
Peptide Score:	81.71
Method:	ITMS; CID; 3



precursor information

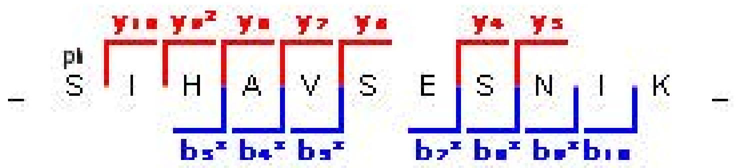
Mass:	1394.64228
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	81.70898
Mass Error [ppm]:	-1.4249
PEP:	0.0032482
Precursor Type:	MULTI

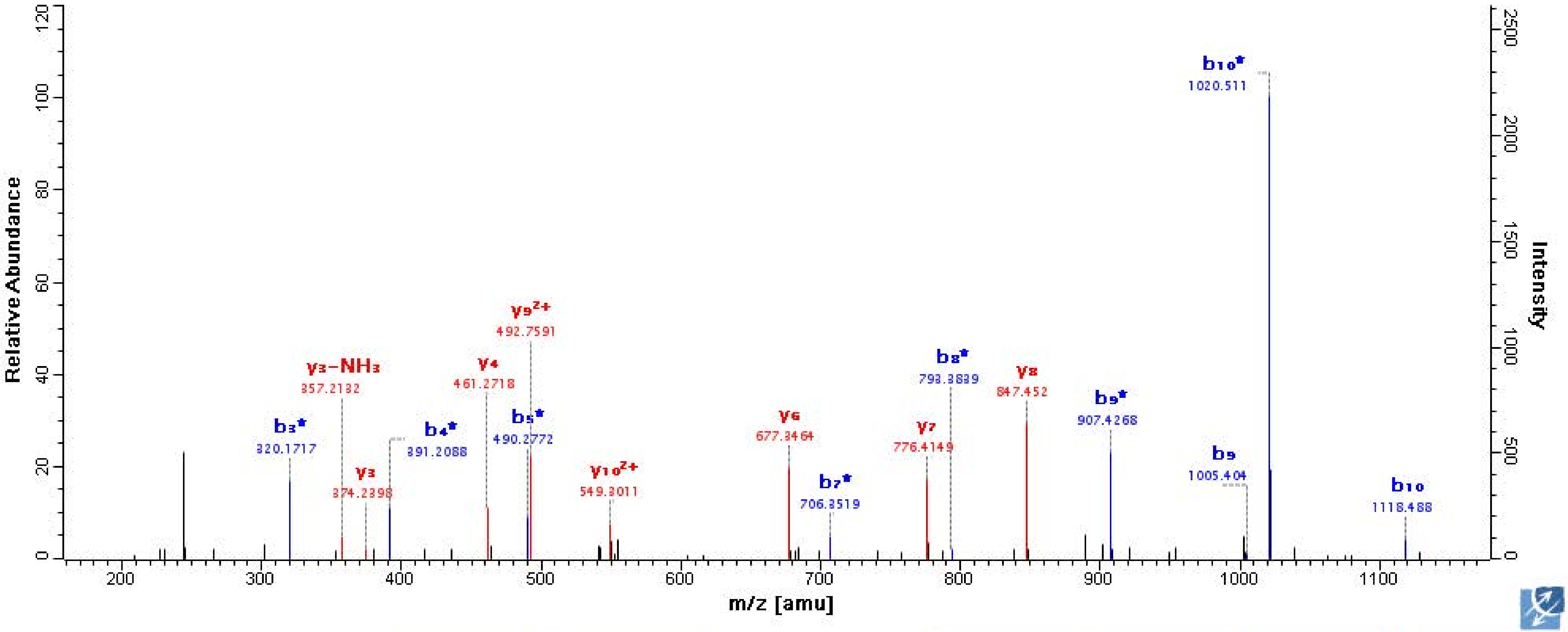
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Protein Localisation:	71 ... 82

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.02128535	1	T	11				
	295.10534933	2	I	10	1222.651741		611.82950872	-0.0252485
	424.14794243	3	E	9	1109.567677	+0.0811267	555.28747673	+0.1674183
	523.21635634	4	V	8	980.52508389	+0.1453263	490.76618018	+0.4070986
	610.24838475	5	S	7	881.45666998	+0.0533398	881.45666998	
	681.28549854	6	A	6	794.42464157	-0.0007524	794.42464157	
	810.32809164	7	E	5	723.38752778	-0.0410922	723.38752778	
	966.42920266	8	R	4	594.34493468		594.34493468	
+0.1011053	1081.4561457	9	D	3	438.24382366		438.24382366	
	1178.5089095	10	P	2	323.21688062	+0.1075823	323.21688062	
	1249.5460233	11	A	1	226.16411677		226.16411677	
		12	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	5056
Protein:	BSU35730; gtaA; rodD; tagE
Peptide Score:	122.51
Method:	ITMS; CID; 3





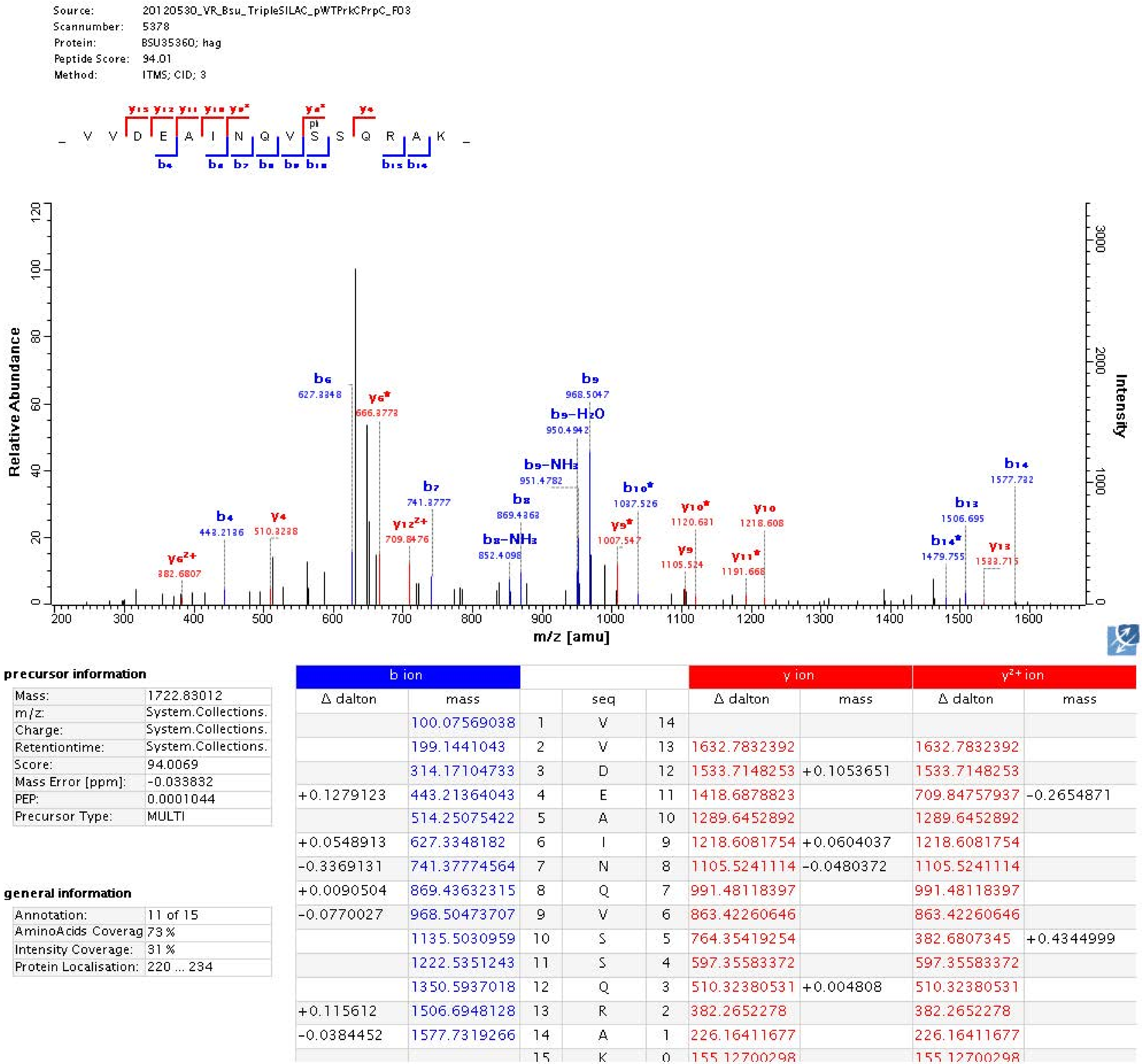
precursor information

Mass:	1263.5857
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	122.5105
Mass Error [ppm]:	-0.25832
PEP:	6.213E-07
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	69 %
Protein Localisation:	2 ... 12

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	10				
	281.08969927	2	I	9	1097.5949491		549.30111276	+0.1961407
	418.14861113	3	H	8	984.51088508		492.75908077	+0.1133557
	489.18572492	4	A	7	847.45197322	+0.0180585	847.45197322	
	588.25413883	5	V	6	776.41485943	-0.0448033	776.41485943	
	675.28616724	6	S	5	677.34644551	+0.0628562	677.34644551	
	804.32876034	7	E	4	590.3144171		590.3144171	
	891.36078875	8	S	3	461.27182401	+0.2306784	461.27182401	
-0.4686576	1005.4037162	9	N	2	374.2397956	-0.1842536	374.2397956	
-0.018664	1118.4877802	10	I	1	260.19686815		260.19686815	
		11	K	0	147.11280417		147.11280417	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	5378
Protein:	BSU35360; hag
Peptide Score:	94.01
Method:	ITMS; CID; 3

precursor information

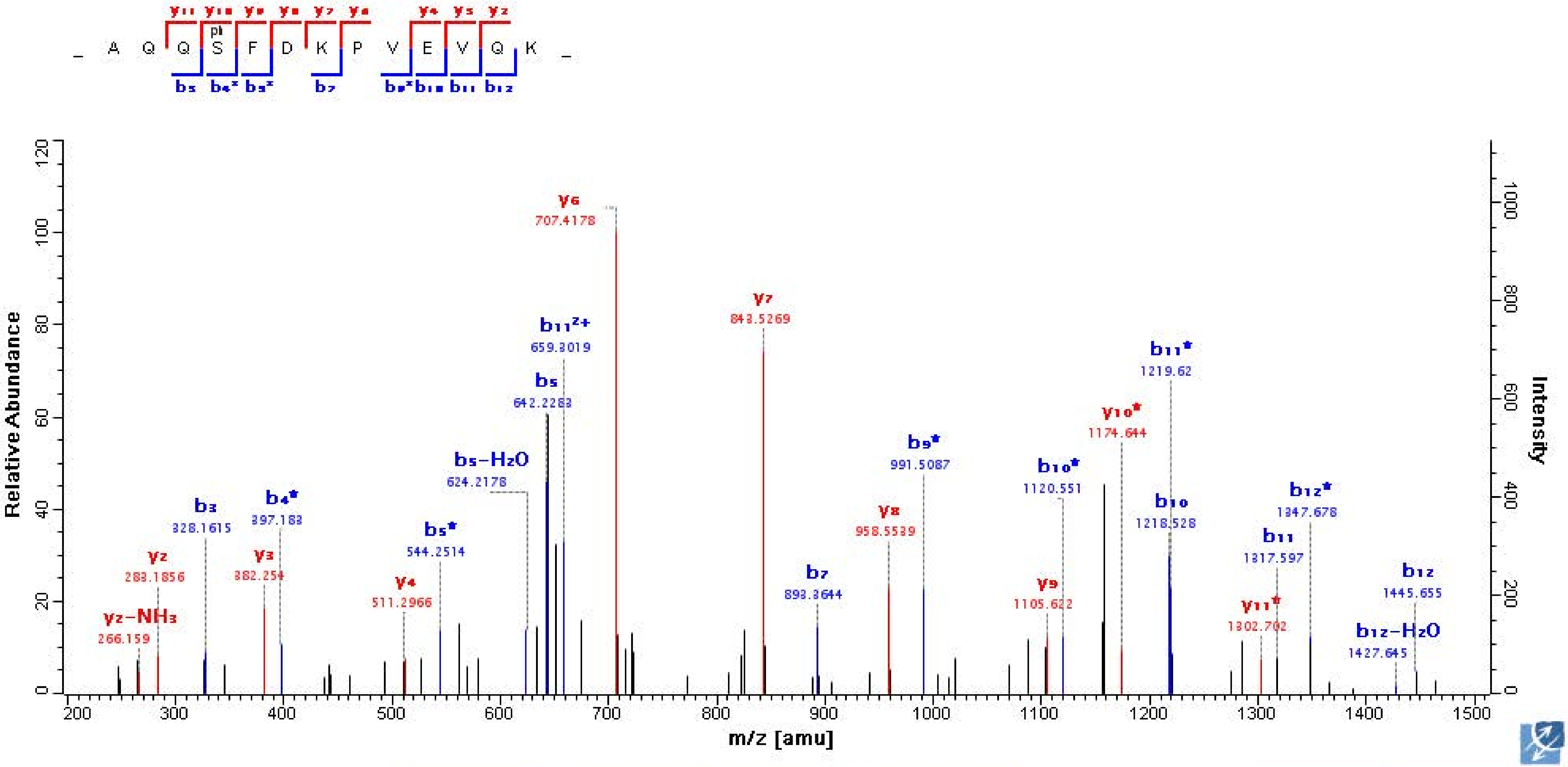
Mass:	1722.83012
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.0069
Mass Error [ppm]:	-0.033832
PEP:	0.0001044
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	31 %
Protein Localisation:	220 ... 234

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	14				
	199.1441043	2	V	13	1632.7832392		1632.7832392	
	314.17104733	3	D	12	1533.7148253	+0.1053651	1533.7148253	
+0.1279123	443.21364043	4	E	11	1418.6878823		709.84757937	-0.2654871
	514.25075422	5	A	10	1289.6452892		1289.6452892	
+0.0548913	627.3348182	6	I	9	1218.6081754	+0.0604037	1218.6081754	
-0.3369131	741.37774564	7	N	8	1105.5241114	-0.0480372	1105.5241114	
+0.0090504	869.43632315	8	Q	7	991.48118397		991.48118397	
-0.0770027	968.50473707	9	V	6	863.42260646		863.42260646	
	1135.5030959	10	S	5	764.35419254		382.6807345	+0.4344999
	1222.5351243	11	S	4	597.35583372		597.35583372	
	1350.5937018	12	Q	3	510.32380531	+0.004808	510.32380531	
+0.115612	1506.6948128	13	R	2	382.2652278		382.2652278	
-0.0384452	1577.7319266	14	A	1	226.16411677		226.16411677	
		15	K	0	155.12700298		155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 5397
Protein: BSU19360; citM; odhB
Peptide Score: 132.31
Method: ITMS; CID; 3



precursor information

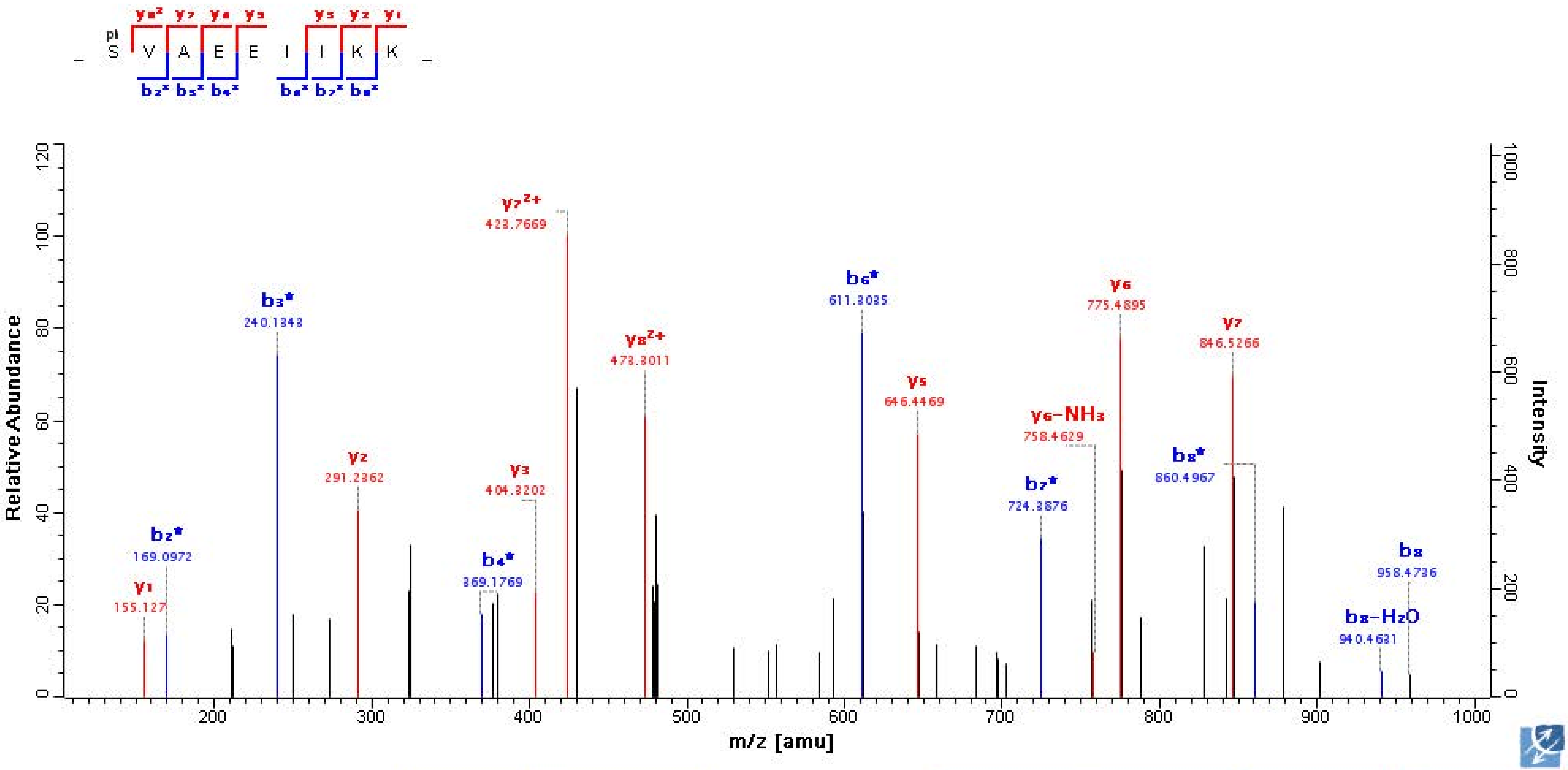
Mass:	1582.74018
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.3096
Mass Error [ppm]:	0.5918
PEP:	1.6273E-13
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	51 %
Protein Localisation:	179 ... 191

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	12		
	200.10296777		200.10296777	2	Q	11	1528.7377979	
	328.16154528	+0.1341701	328.16154528	3	Q	10	1400.6792204	
	495.1599041		495.1599041	4	S	9	1272.6206429	
	642.22831801	+0.4092552	642.22831801	5	F	8	1105.6222841	+0.0283507
	757.25526104		757.25526104	6	D	7	958.55387014	+0.1082392
	893.36442287	+0.0727719	893.36442287	7	K	6	843.52692711	+0.02361
	990.41718673		990.41718673	8	P	5	707.41776528	-0.0483195
	1089.4856006		1089.4856006	9	V	4	610.36500142	
	1218.5281937	+0.0374801	1218.5281937	10	E	3	511.29658751	+0.2124457
+0.0048817	659.30194206	-0.2417493	1317.5966077	11	V	2	382.25399441	+0.048862
	1445.6551852	+0.1891752	1445.6551852	12	Q	1	283.1855805	+0.0154083
				13	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 5592
Protein: BSU01120; fus; fusA
Peptide Score: 116.3
Method: ITMS; CID; 3

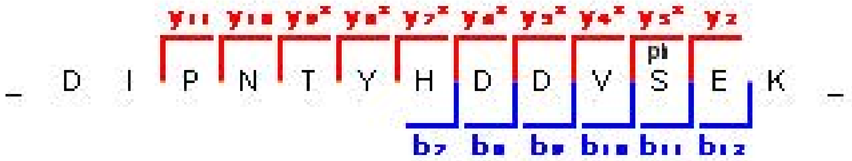


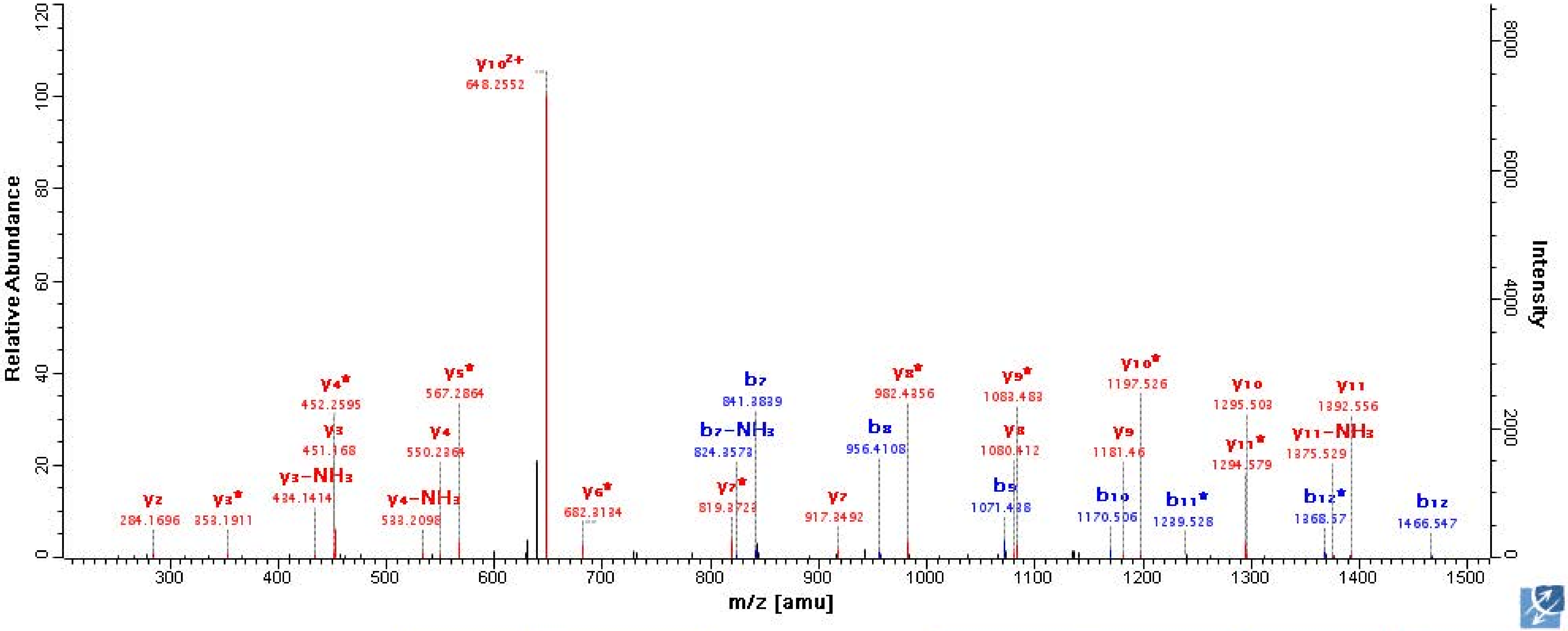
precursor information

Mass:	1095.55765
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.3045
Mass Error [ppm]:	-0.039527
PEP:	0.0001479
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	49 %
Protein Localisation:	680 ... 688

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	8				
	267.0740492	2	V	7	945.59500667		473.30114157	+0.0136167
	338.11116299	3	A	6	846.52659276	+0.0188174	423.76693461	+0.1477382
	467.15375609	4	E	5	775.48947897	+0.022545	775.48947897	
	596.19634918	5	E	4	646.44688587	+0.0589735	646.44688587	
	709.28041316	6	I	3	517.40429278		517.40429278	
	822.36447714	7	I	2	404.3202288	-0.100136	404.3202288	
+0.2148376	958.47363897	8	K	1	291.23616481	-0.1302688	291.23616481	
		9	K	0	155.12700298	+0.060497	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 5626
Protein: BSU16910; ymfM
Peptide Score: 196.11
Method: ITMS; CID; 3





precursor information

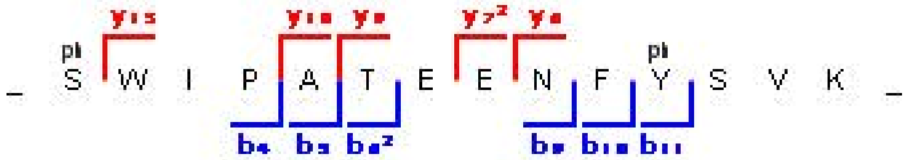
Mass:	1619.65884
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	196.1098
Mass Error [ppm]:	-0.46732
PEP:	6.1846E-88
Precursor Type:	ISO

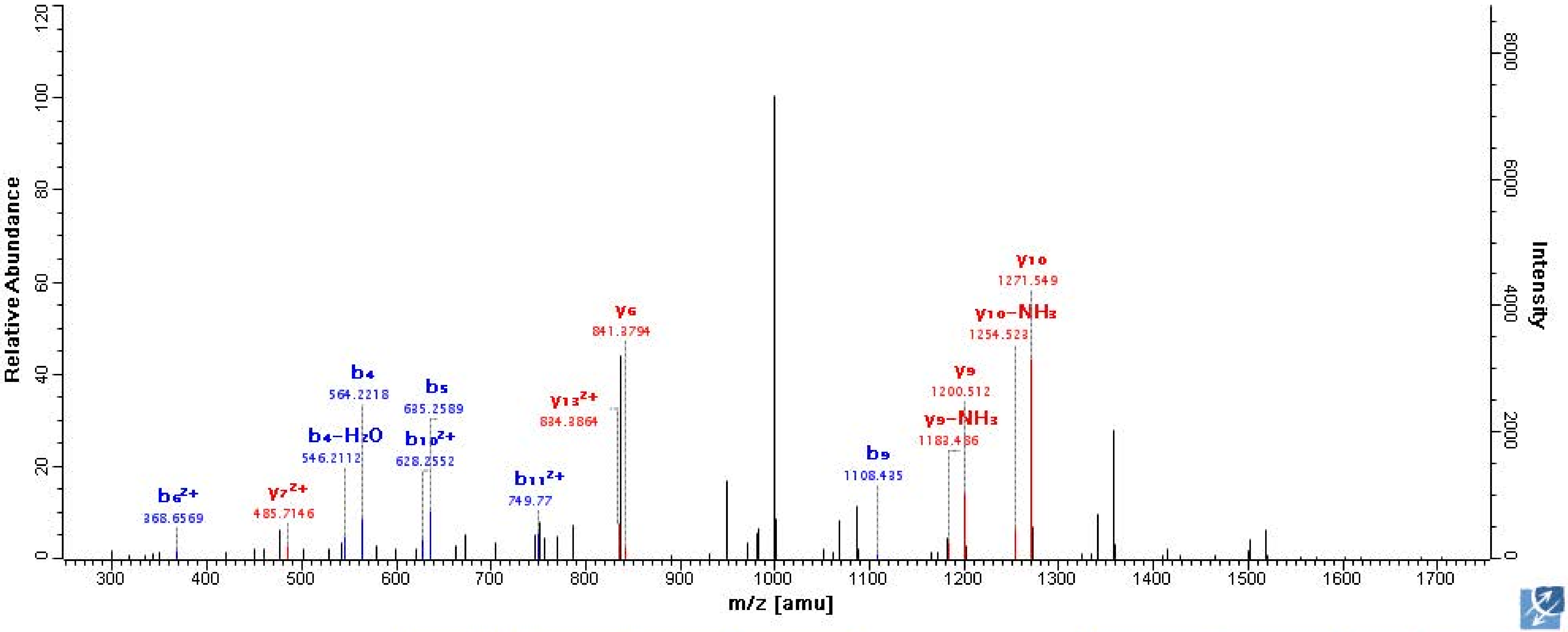
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	73 %
Protein Localisation:	59 ... 71

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	12				
	229.11828348	2	I	11	1505.639929		1505.639929	
	326.17104733	3	P	10	1392.5558651	+0.1747258	1392.5558651	
	440.21397478	4	N	9	1295.5031012	+0.049267	648.25518883	-0.3431405
	541.26165325	5	T	8	1181.4601738	+0.0278634	1181.4601738	
	704.32498179	6	Y	7	1080.4124953	+0.0784715	1080.4124953	
+0.0463432	841.38389365	7	H	6	917.34916674	+0.1102449	917.34916674	
+0.036612	956.41083668	8	D	5	780.29025488		780.29025488	
-0.042516	1071.4377797	9	D	4	665.26331185		665.26331185	
-0.0982346	1170.5061936	10	V	3	550.23636881	-0.0142619	550.23636881	
	1337.5045525	11	S	2	451.1679549	+0.0081315	451.1679549	
-0.0772969	1466.5471455	12	E	1	284.16959608	+0.0826622	284.16959608	
		13	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	5804
Protein:	BSU20590; yoqL
Peptide Score:	76.52
Method:	ITMS; CID; 3





precursor information

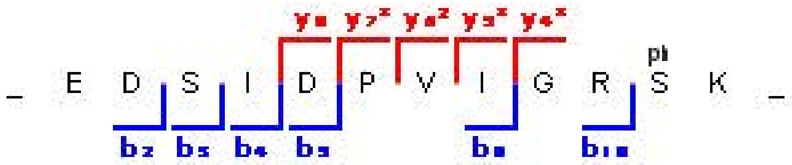
Mass:	1833.75815
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	76.52248
Mass Error [ppm]:	0.87184
PEP:	0.10526
Precursor Type:	ISO

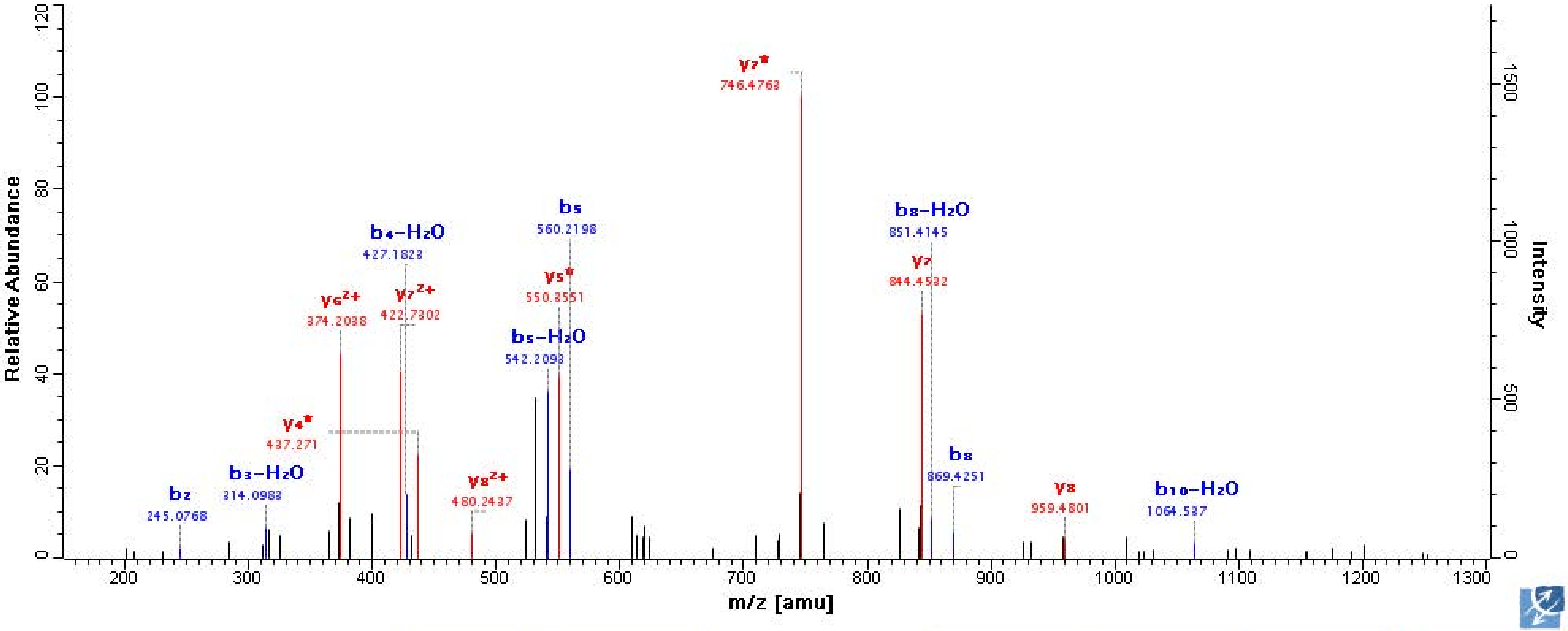
general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	23 %
Protein Localisation:	22 ... 35

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	13				
	354.0849		354.0849	2	W	12	1667.765		834.3864	+0.092019
	467.169		467.169	3	I	11	1481.686		1481.686	
	564.2218	+0.069911	564.2218	4	P	10	1368.602		1368.602	
	635.2589	-0.002359	635.2589	5	A	9	1271.549	-0.031144	1271.549	
-0.412721	368.6569		736.3066	6	T	8	1200.512	+0.072376	1200.512	
	865.3492		865.3492	7	E	7	1099.465		1099.465	
	994.3918		994.3918	8	E	6	970.4219		485.7146	-0.254529
	1108.435	-0.008657	1108.435	9	N	5	841.3794	-0.043721	841.3794	
-0.298948	628.2552		1255.503	10	F	4	727.3364		727.3364	
-0.421871	749.77		1498.533	11	Y	3	580.268		580.268	
	1585.565		1585.565	12	S	2	337.2384		337.2384	
	1684.633		1684.633	13	V	1	250.2063		250.2063	
				14	K	0	151.1379		151.1379	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	6688
Protein:	BSU00860; clpC; mecB
Peptide Score:	63.09
Method:	ITMS; CID; 3





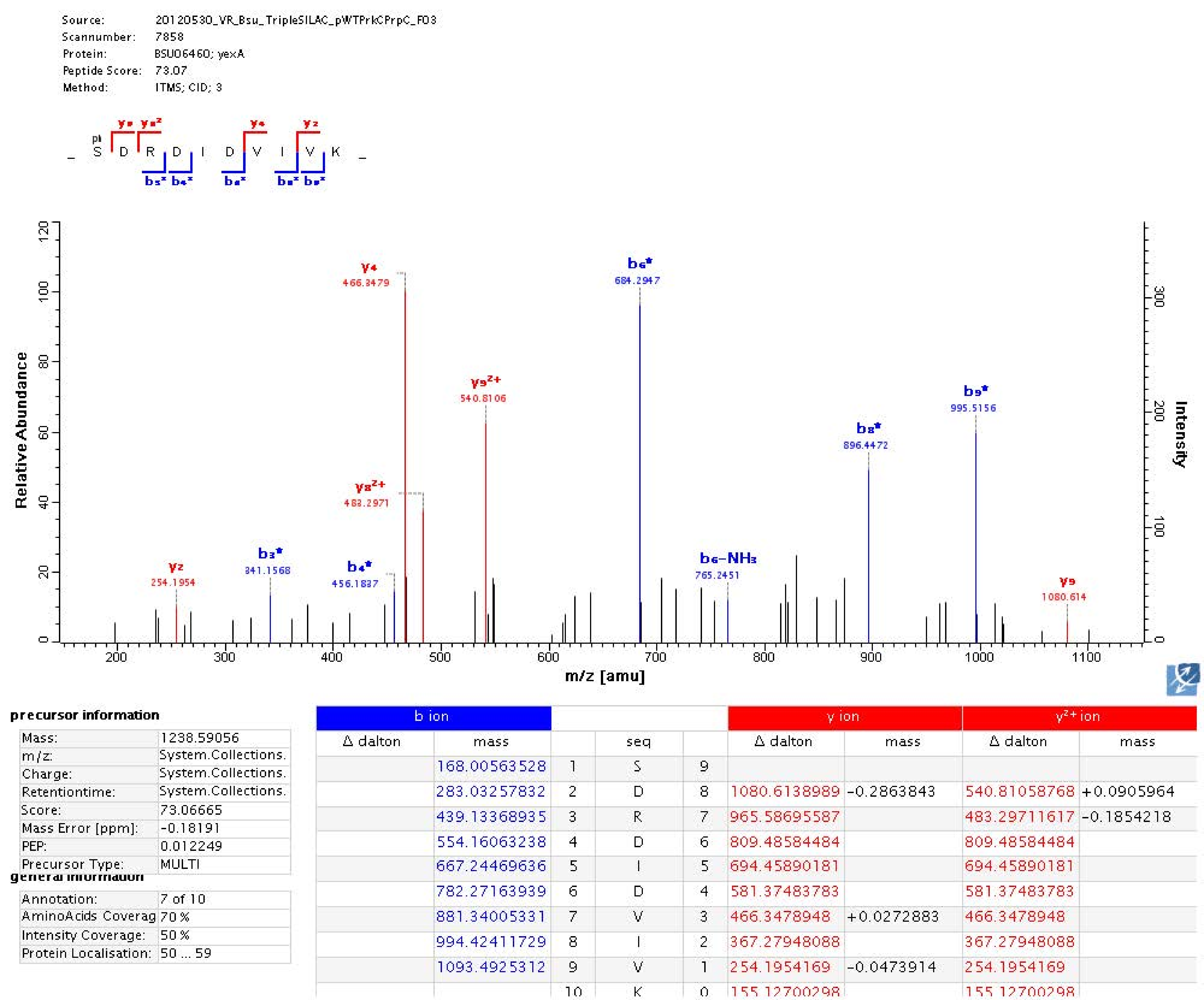
precursor information

Mass:	1394.6445
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.09117
Mass Error [ppm]:	0.16029
PEP:	0.034099
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	62 %
Protein Localisation:	176 ... 187

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	11				
-0.3177641	245.07681259	2	D	10	1274.6231568		1274.6231568	
	332.108841	3	S	9	1159.5962137		1159.5962137	
	445.19290499	4	I	8	1072.5641853		1072.5641853	
+0.0448615	560.21984802	5	D	7	959.48012133	+0.2103694	480.2436989	-0.106675
	657.27261187	6	P	6	844.4531783	-0.0004805	422.73022738	-0.1091336
	756.34102579	7	V	5	747.40041445		374.20384546	-0.4905886
+0.2035113	869.42508977	8	I	4	648.33200053		648.33200053	
	926.44655349	9	G	3	535.24793655		535.24793655	
	1082.5476645	10	R	2	478.22647283		478.22647283	
	1249.5460233	11	S	1	322.1253618		322.1253618	
		12	K	0	155.12700298		155.12700298	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	7858
Protein:	BSU06460; yexA
Peptide Score:	73.07
Method:	ITMS; CID; 3

precursor information

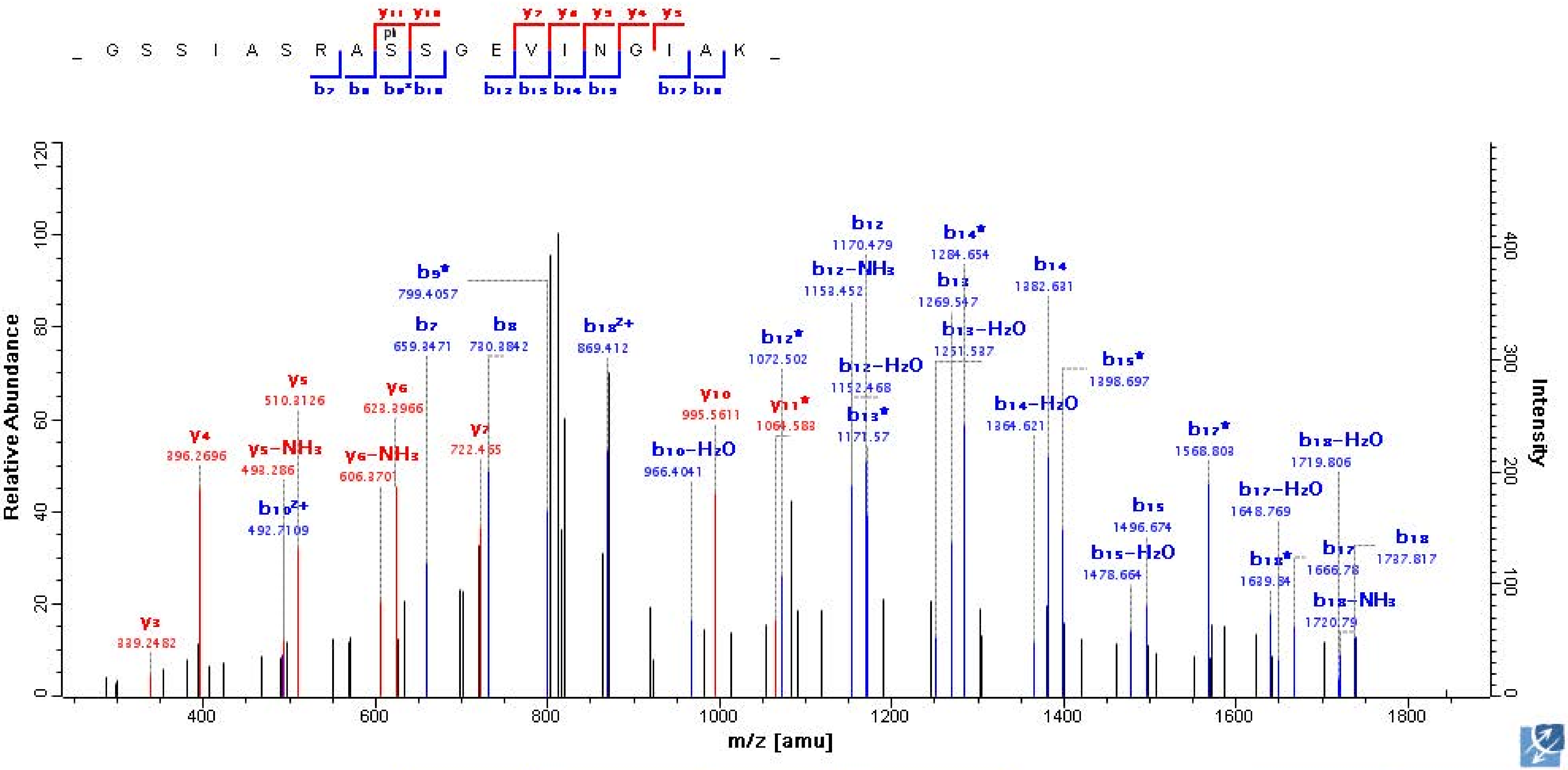
Mass:	1238.59056
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	73.06665
Mass Error [ppm]:	-0.18191
PEP:	0.012249
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	50 %
Protein Localisation:	50 ... 59

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	9				
	283.03257832	2	D	8	1080.6138989	-0.2863843	540.81058768	+0.0905964
	439.13368935	3	R	7	965.58695587		483.29711617	-0.1854218
	554.16063238	4	D	6	809.48584484		809.48584484	
	667.24469636	5	I	5	694.45890181		694.45890181	
	782.27163939	6	D	4	581.37483783		581.37483783	
	881.34005331	7	V	3	466.3478948	+0.0272883	466.3478948	
	994.42411729	8	I	2	367.27948088		367.27948088	
	1093.4925312	9	V	1	254.1954169	-0.0473914	254.1954169	
		10	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	8636
Protein:	BSU17890; tkt; tktA
Peptide Score:	176.11
Method:	ITMS; CID; 3



precursor information

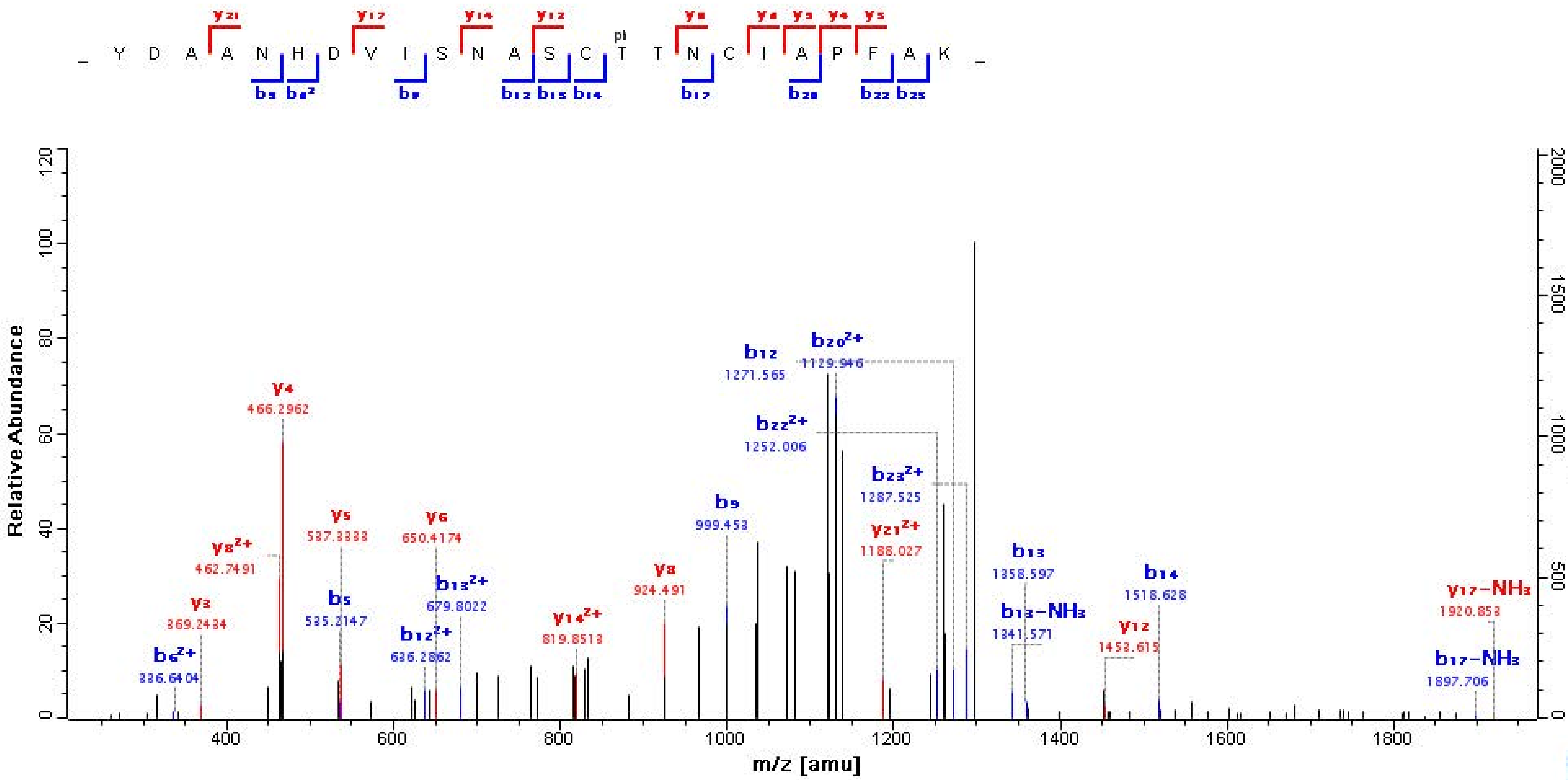
Mass:	1882.91458
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	176.1133
Mass Error [ppm]:	-0.20367
PEP:	1.9529E-47
Precursor Type:	MULTI

general information

Annotation:	11 of 19
AminoAcids Coverag	58 %
Intensity Coverage:	47 %
Protein Localisation:	351 ... 369

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	58.02874019		58.02874019	1	G	18		
	145.0607686		145.0607686	2	S	17	1834.9149817	
	232.09279701		232.09279701	3	S	16	1747.8829533	
	345.17686099		345.17686099	4	I	15	1660.8509249	
	416.21397478		416.21397478	5	A	14	1547.7668609	
	503.24600319		503.24600319	6	S	13	1476.7297471	
	659.34711422	+0.0023731	659.34711422	7	R	12	1389.6977187	
	730.384228	+0.022022	730.384228	8	A	11	1233.5966077	
	897.38258682		897.38258682	9	S	10	1162.5594939	
-0.282418	492.71094585		984.41461523	10	S	9	995.56113505	+0.0393899
	1041.436079		1041.436079	11	G	8	908.52910664	
	1170.4786721	-0.0491066	1170.4786721	12	E	7	851.50764292	
	1269.547086	+0.2208584	1269.547086	13	V	6	722.46504982	-0.0613633
	1382.6311499	+0.0192407	1382.6311499	14	I	5	623.3966359	+0.0664989
	1496.6740774	+0.1297556	1496.6740774	15	N	4	510.31257192	+0.0767713
	1553.6955411		1553.6955411	16	G	3	396.26964448	+0.1145718
	1666.7796051	+0.0518158	1666.7796051	17	I	2	339.24818075	-0.0440182
+0.4453021	869.41199768	+0.0252001	1737.8167189	18	A	1	226.16411677	
				19	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber: 9685
Protein: BSU33940; gap; gapA
Peptide Score: 65.16
Method: ITMS; CID; 3



precursor information

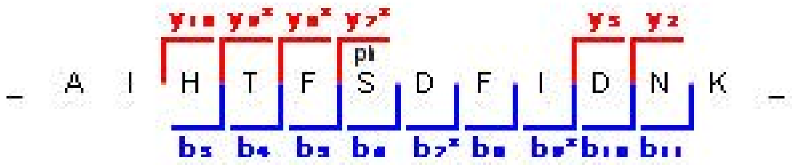
Mass:	2719.13983
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	65.15955
Mass Error [ppm]:	-0.34319
PEP:	0.0012778
Precursor Type:	MULTI

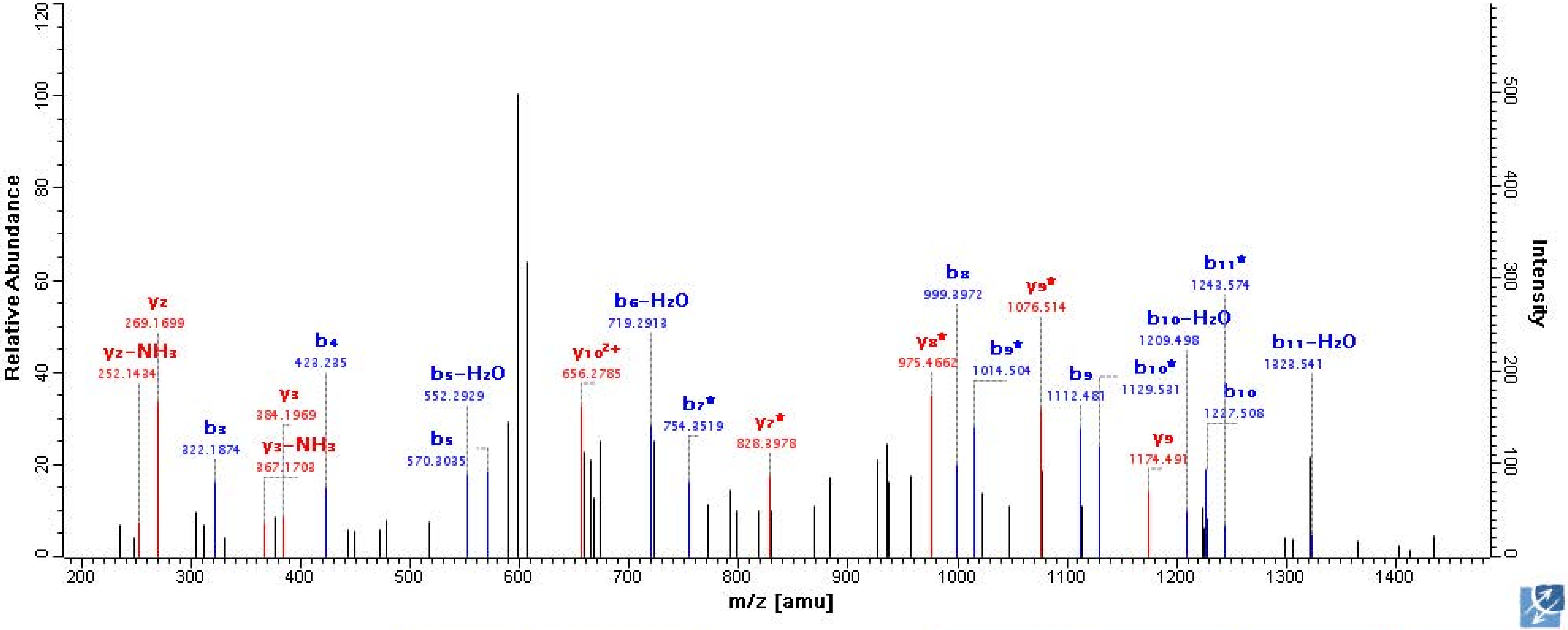
general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	27 %
Protein Localisation:	139 ... 162

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.0706		164.0706	1	Y	23				
	279.0975		279.0975	2	D	22	2561.11		2561.11	
	350.1347		350.1347	3	A	21	2446.083		2446.083	
	421.1718		421.1718	4	A	20	2375.046		1188.027	-0.456086
	535.2147	+0.231525	535.2147	5	N	19	2304.009		2304.009	
-0.352299	336.6404		672.2736	6	H	18	2189.966		2189.966	
	787.3006		787.3006	7	D	17	2052.907		2052.907	
	886.369		886.369	8	V	16	1937.88		1937.88	
	999.453	-0.096163	999.453	9	I	15	1838.811		1838.811	
	1086.485		1086.485	10	S	14	1725.727		1725.727	
	1200.528		1200.528	11	N	13	1638.695		819.8513	+0.293151
+0.129092	636.2862	+0.065266	1271.565	12	A	12	1524.652		1524.652	
+0.08903	679.8022	+0.22208	1358.597	13	S	11	1453.615	+0.15531	1453.615	
	1518.628	+0.058741	1518.628	14	C	10	1366.583		1366.583	
	1699.642		1699.642	15	T	9	1206.553		1206.553	
	1800.689		1800.689	16	T	8	1025.539		1025.539	
	1914.732		1914.732	17	N	7	924.491	+0.081126	462.7491	-0.387239
	2074.763		2074.763	18	C	6	810.448		810.448	
	2187.847		2187.847	19	I	5	650.4174	+0.009683	650.4174	
-0.118845	1129.946		2258.884	20	A	4	537.3333	+0.106747	537.3333	
	2355.937		2355.937	21	P	3	466.2962	+0.016236	466.2962	
+0.182138	1252.006		2503.005	22	F	2	369.2434	+0.154449	369.2434	
-0.129876	1287.525		2574.043	23	A	1	222.175		222.175	
				24	K	0	151.1379		151.1379	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 10343
Protein: BSU35070; ywmC
Peptide Score: 134.98
Method: ITMS; CID; 3





precursor information

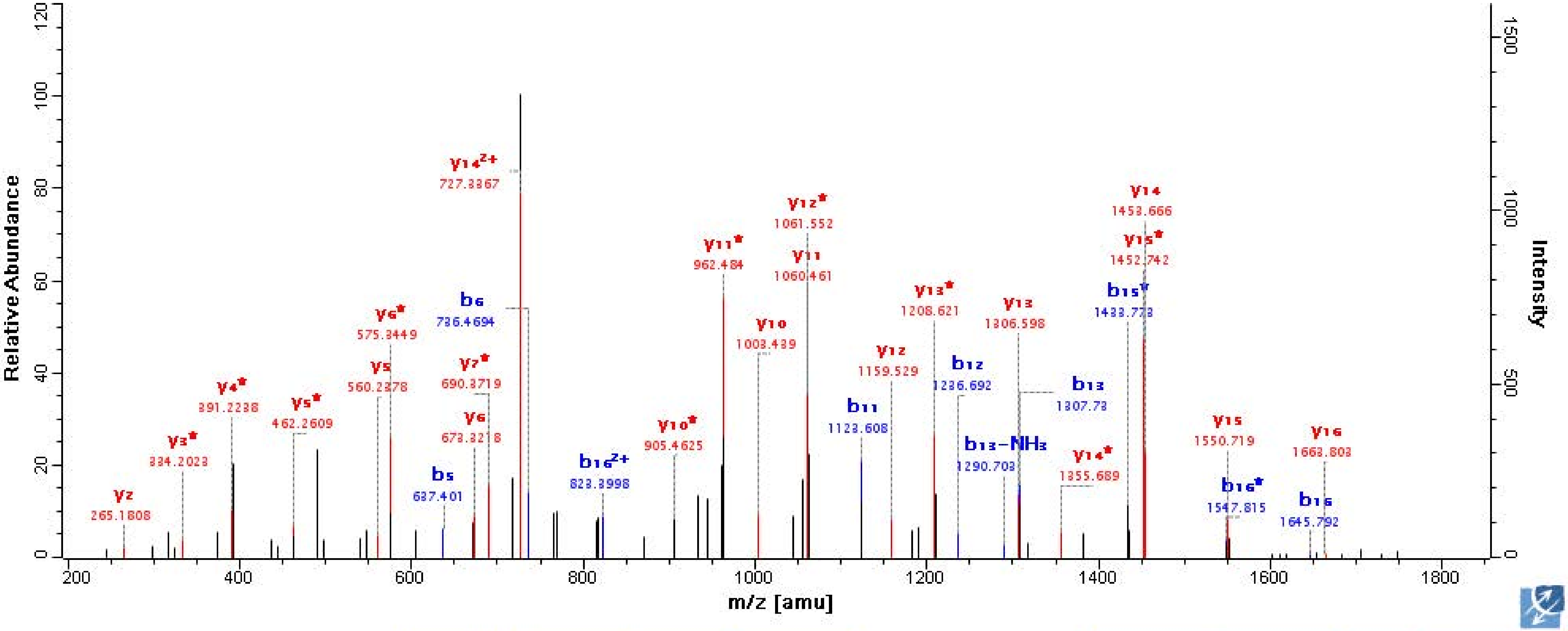
Mass:	1494.66404
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	134.9769
Mass Error [ppm]:	0.32451
PEP:	6.6698E-06
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	39 %
Protein Localisation:	113 ... 124

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	11				
	185.12845423	2	I	10	1424.6337214		1424.6337214	
+0.0806088	322.1873661	3	H	9	1311.5496575		656.27846696	+0.0884154
-0.2403546	423.23504457	4	T	8	1174.4907456	-0.1649399	1174.4907456	
+0.0490806	570.30345849	5	F	7	1073.4430671		1073.4430671	
	737.30181731	6	S	6	926.37465321		926.37465321	
	852.32876034	7	D	5	759.37629439		759.37629439	
+0.2013975	999.39717425	8	F	4	644.34935136		644.34935136	
+0.1143428	1112.4812382	9	I	3	497.28093744		497.28093744	
-0.3176295	1227.5081813	10	D	2	384.19687346	+0.2140152	384.19687346	
	1341.5511087	11	N	1	269.16993043	+0.0402441	269.16993043	
		12	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	10484
Protein:	BSU17890; tkt; tktA
Peptide Score:	164.93
Method:	ITMS; CID; 3



precursor information

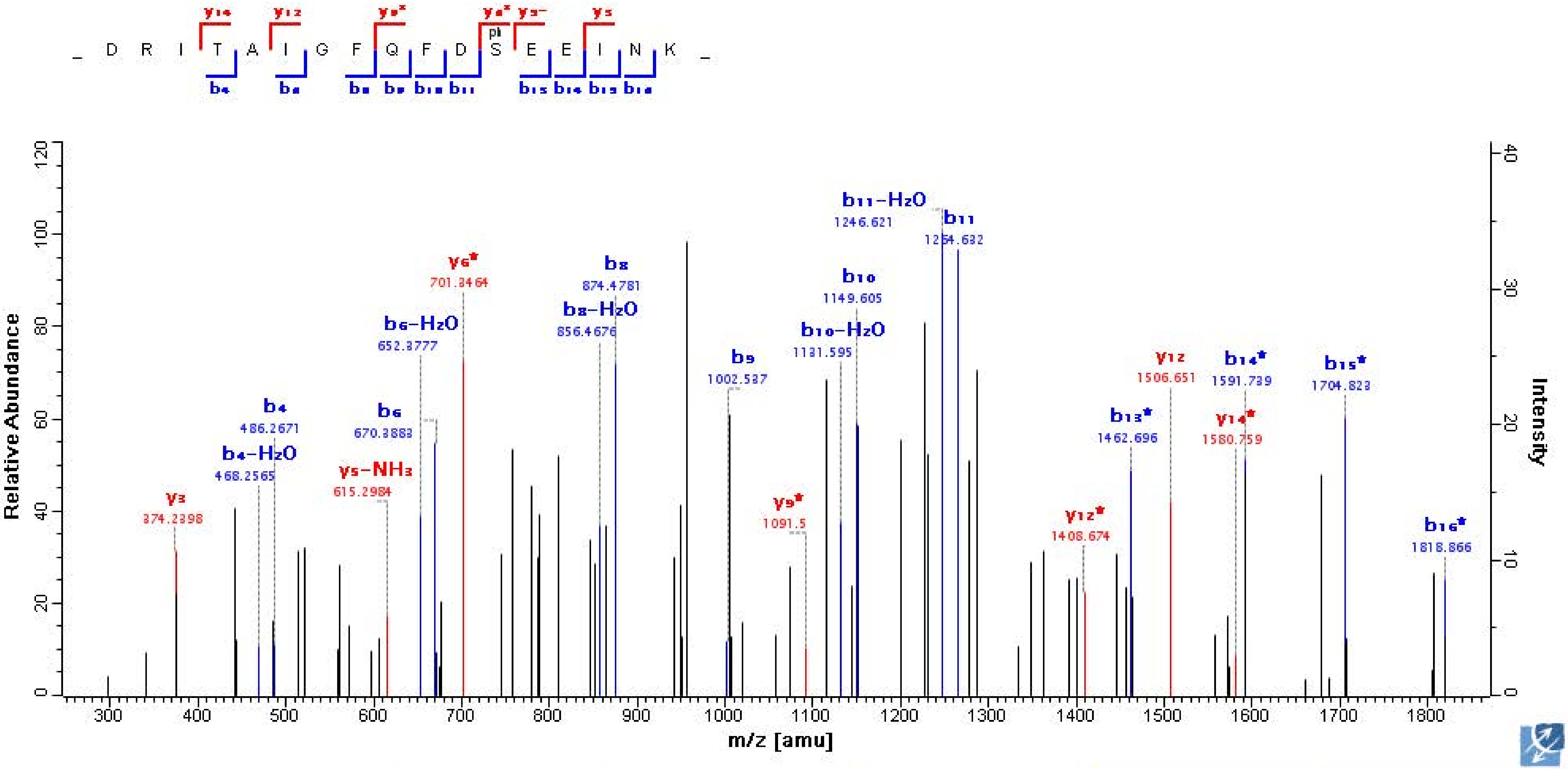
Mass:	1786.86625
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	164.9298
Mass Error [ppm]:	0.41699
PEP:	2.4551E-34
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	49 %
Protein Localisation:	370 ... 386

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133.1273		133.1273	1	K	16				
	246.2114		246.2114	2	I	15	1663.803	+0.422909	1663.803	
	343.2642		343.2642	3	P	14	1550.719	+0.019302	1550.719	
	490.3326		490.3326	4	F	13	1453.666	+0.12834	727.3367	+0.18895
	637.401	-0.078614	637.401	5	F	12	1306.598	+0.059669	1306.598	
	736.4694	-0.075983	736.4694	6	V	11	1159.529	+0.073029	1159.529	
	793.4909		793.4909	7	G	10	1060.461	-0.05509	1060.461	
	850.5123		850.5123	8	G	9	1003.439	-0.115169	1003.439	
	937.5444		937.5444	9	S	8	946.4179		946.4179	
	1008.581		1008.581	10	A	7	859.3859		859.3859	
	1123.608	+0.1633	1123.608	11	D	6	788.3488		788.3488	
	1236.692	+0.252576	1236.692	12	I	5	673.3218	-0.047547	673.3218	
	1307.73	+0.023201	1307.73	13	A	4	560.2378	-0.03819	560.2378	
	1364.751		1364.751	14	G	3	489.2007		489.2007	
	1531.749		1531.749	15	S	2	432.1792		432.1792	
-0.121557	823.3998	-0.04492	1645.792	16	N	1	265.1808	-0.05178	265.1808	
				17	K	0	151.1379		151.1379	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 11550
Protein: BSU28280; leuA
Peptide Score: 77.51
Method: ITMS; CID; 3



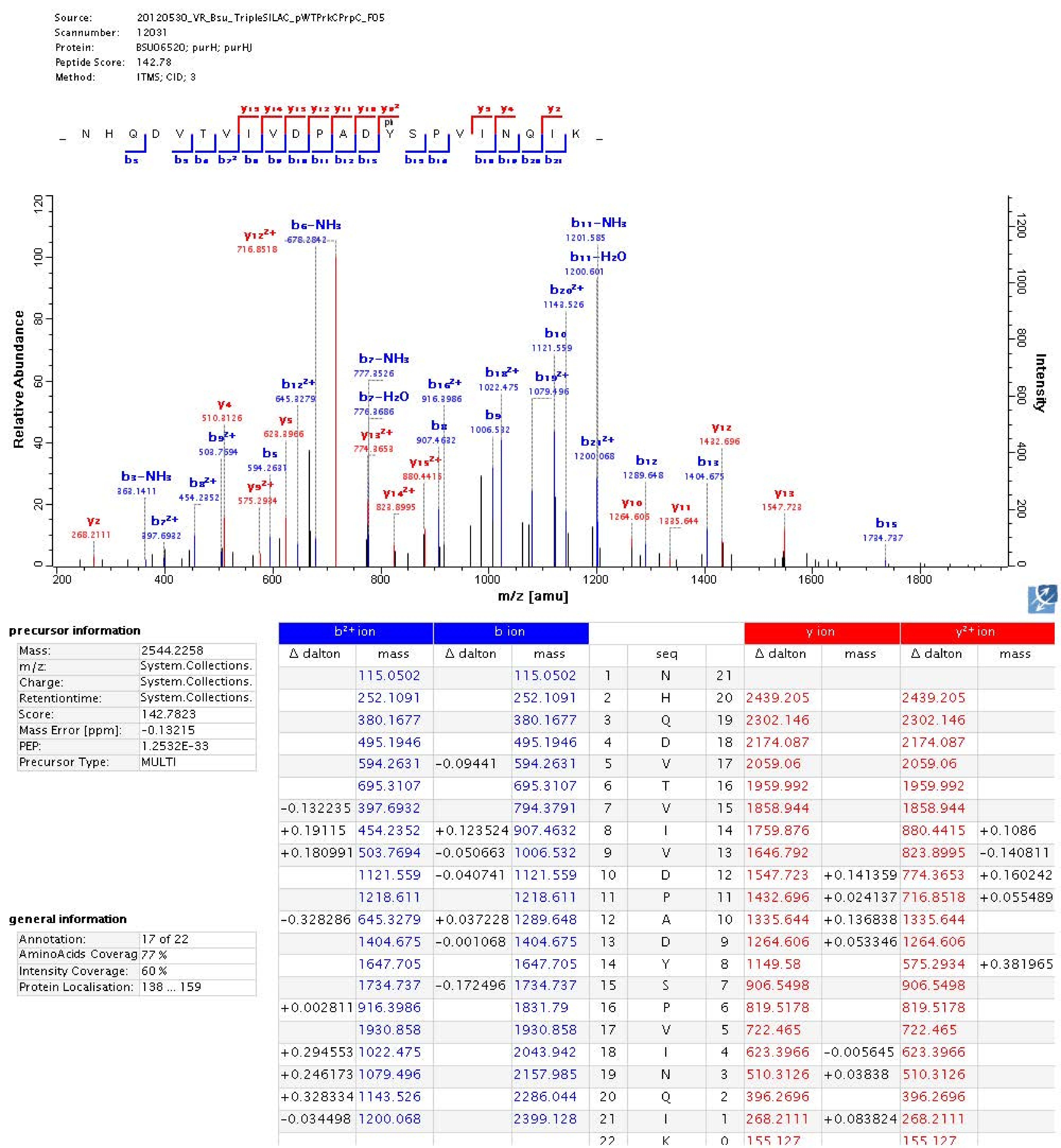
precursor information

Mass:	2061.94066
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.50517
Mass Error [ppm]:	-0.09198
PEP:	0.00019063
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	33 %
Protein Localisation:	338 ... 354

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	16		
	272.135330527	2	R	15	1947.921183959	
	385.219394507	3	I	14	1791.820072931	
+0.211992	486.267072981	4	T	13	1678.736008951	
	557.304186769	5	A	12	1577.688330477	
-0.0164856	670.388250749	6	I	11	1506.651216689	+0.0574015
	727.409714473	7	G	10	1393.567152708	
+0.0128384	874.478128389	8	F	9	1336.545688985	
-0.259118	1002.536705901	9	Q	8	1189.477275069	
+0.1719798	1149.605119817	10	F	7	1061.418697557	
+0.166277	1264.632062849	11	D	6	914.350283641	
	1431.630421667	12	S	5	799.323340609	
	1560.673014763	13	E	4	632.324981791	
	1689.71560786	14	E	3	503.282388694	
	1802.79967184	15	I	2	374.239795598	+0.1665154
	1916.842599287	16	N	1	261.155731618	
		17	K	0	147.112804171	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	12031
Protein:	BSU06520; purH; purHJ
Peptide Score:	142.78
Method:	ITMS; CID; 3

precursor information

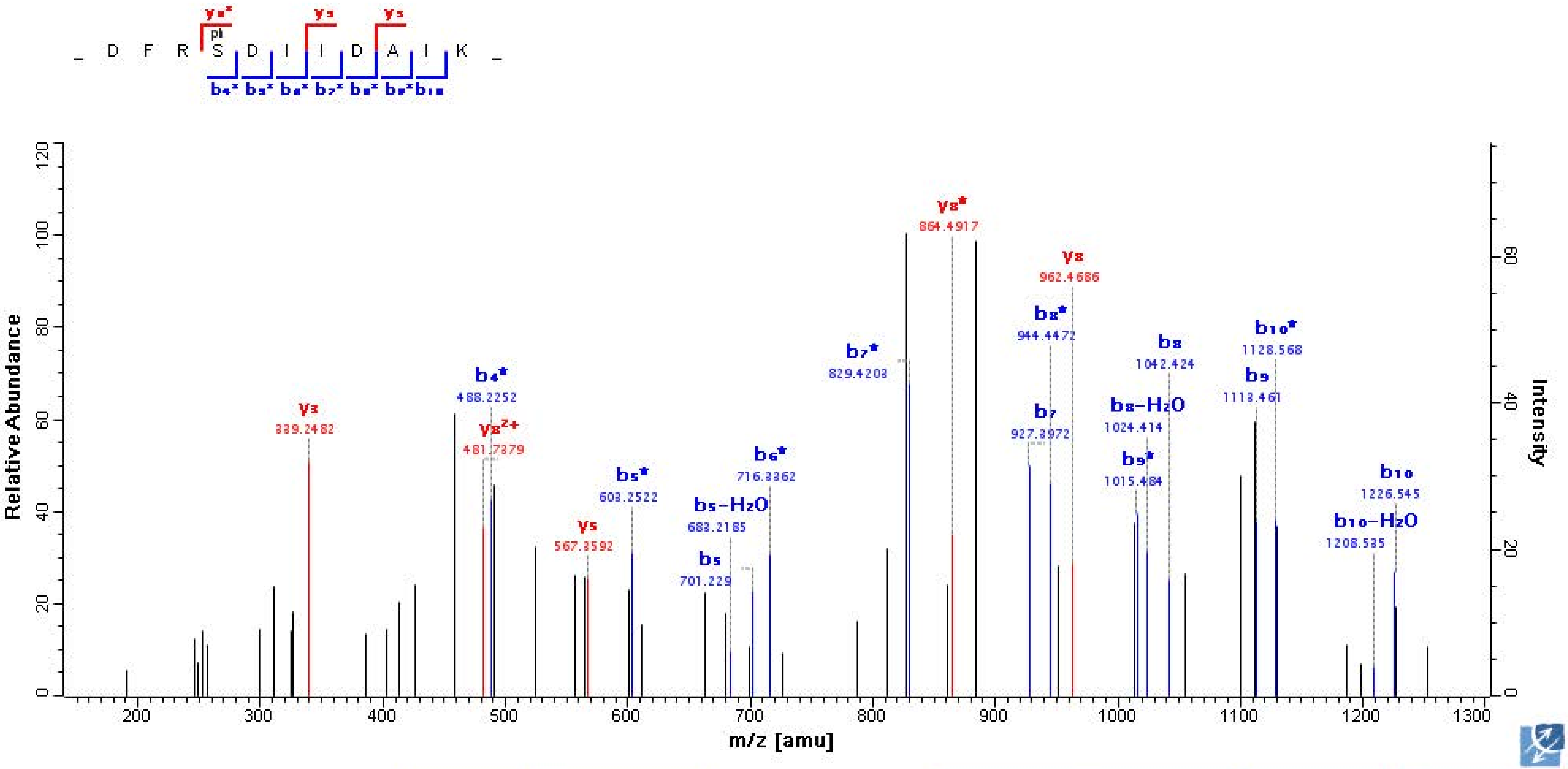
Mass:	2544.2258
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	142.7823
Mass Error [ppm]:	-0.13215
PEP:	1.2532E-33
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	60 %
Protein Localisation:	138 ... 159

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	21				
	252.1091		252.1091	2	H	20	2439.205		2439.205	
	380.1677		380.1677	3	Q	19	2302.146		2302.146	
	495.1946		495.1946	4	D	18	2174.087		2174.087	
	594.2631	-0.09441	594.2631	5	V	17	2059.06		2059.06	
	695.3107		695.3107	6	T	16	1959.992		1959.992	
-0.132235	397.6932		794.3791	7	V	15	1858.944		1858.944	
+0.19115	454.2352	+0.123524	907.4632	8	I	14	1759.876		880.4415	+0.1086
+0.180991	503.7694	-0.050663	1006.532	9	V	13	1646.792		823.8995	-0.140811
	1121.559	-0.040741	1121.559	10	D	12	1547.723	+0.141359	774.3653	+0.160242
	1218.611		1218.611	11	P	11	1432.696	+0.024137	716.8518	+0.055489
-0.328286	645.3279	+0.037228	1289.648	12	A	10	1335.644	+0.136838	1335.644	
	1404.675	-0.001068	1404.675	13	D	9	1264.606	+0.053346	1264.606	
	1647.705		1647.705	14	Y	8	1149.58		575.2934	+0.381965
	1734.737	-0.172496	1734.737	15	S	7	906.5498		906.5498	
+0.002811	916.3986		1831.79	16	P	6	819.5178		819.5178	
	1930.858		1930.858	17	V	5	722.465		722.465	
+0.294553	1022.475		2043.942	18	I	4	623.3966	-0.005645	623.3966	
+0.246173	1079.496		2157.985	19	N	3	510.3126	+0.03838	510.3126	
+0.328334	1143.526		2286.044	20	Q	2	396.2696		396.2696	
-0.034498	1200.068		2399.128	21	I	1	268.2111	+0.083824	268.2111	
				22	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 13136
Protein: BSU15430; ileS
Peptide Score: 109.72
Method: ITMS; CID; 3



precursor information

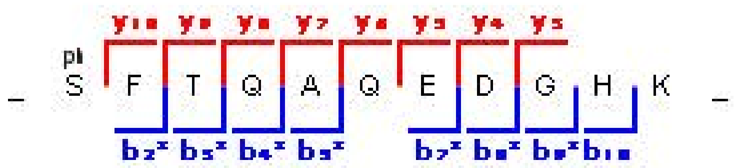
Mass:	1371.64327
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.7213
Mass Error [ppm]:	-0.20238
PEP:	5.6505E-05
Precursor Type:	MULTI

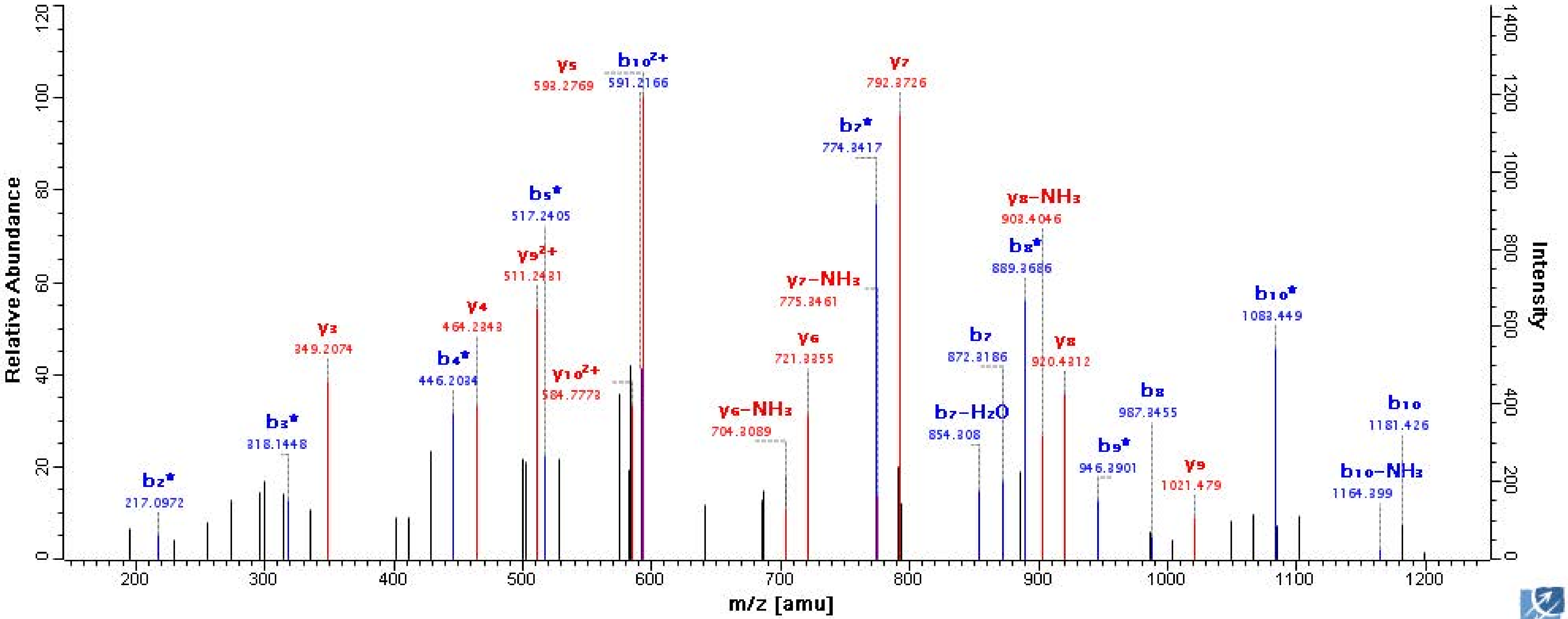
general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	40 %
Protein Localisation:	417 ... 427

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	10				
	263.10263341	2	F	9	1265.6380785		1265.6380785	
	419.20374444	3	R	8	1118.5696646		1118.5696646	
	586.20210326	4	S	7	962.4685536	+0.0802745	481.73791503	+0.2752686
+0.0437198	701.22904629	5	D	6	795.47019478		795.47019478	
	814.31311027	6	I	5	680.44325174		680.44325174	
+0.1999937	927.39717425	7	I	4	567.35918776	-0.1655232	567.35918776	
-0.0483849	1042.4241173	8	D	3	454.27512378		454.27512378	
-0.0205572	1113.4612311	9	A	2	339.24818075	+0.1699101	339.24818075	
-0.2667306	1226.5452951	10	I	1	268.21106696		268.21106696	
		11	K	0	155.12700298		155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 2900
Protein: BSU28290; ilvC
Peptide Score: 194.17
Method: ITMS; CID; 3





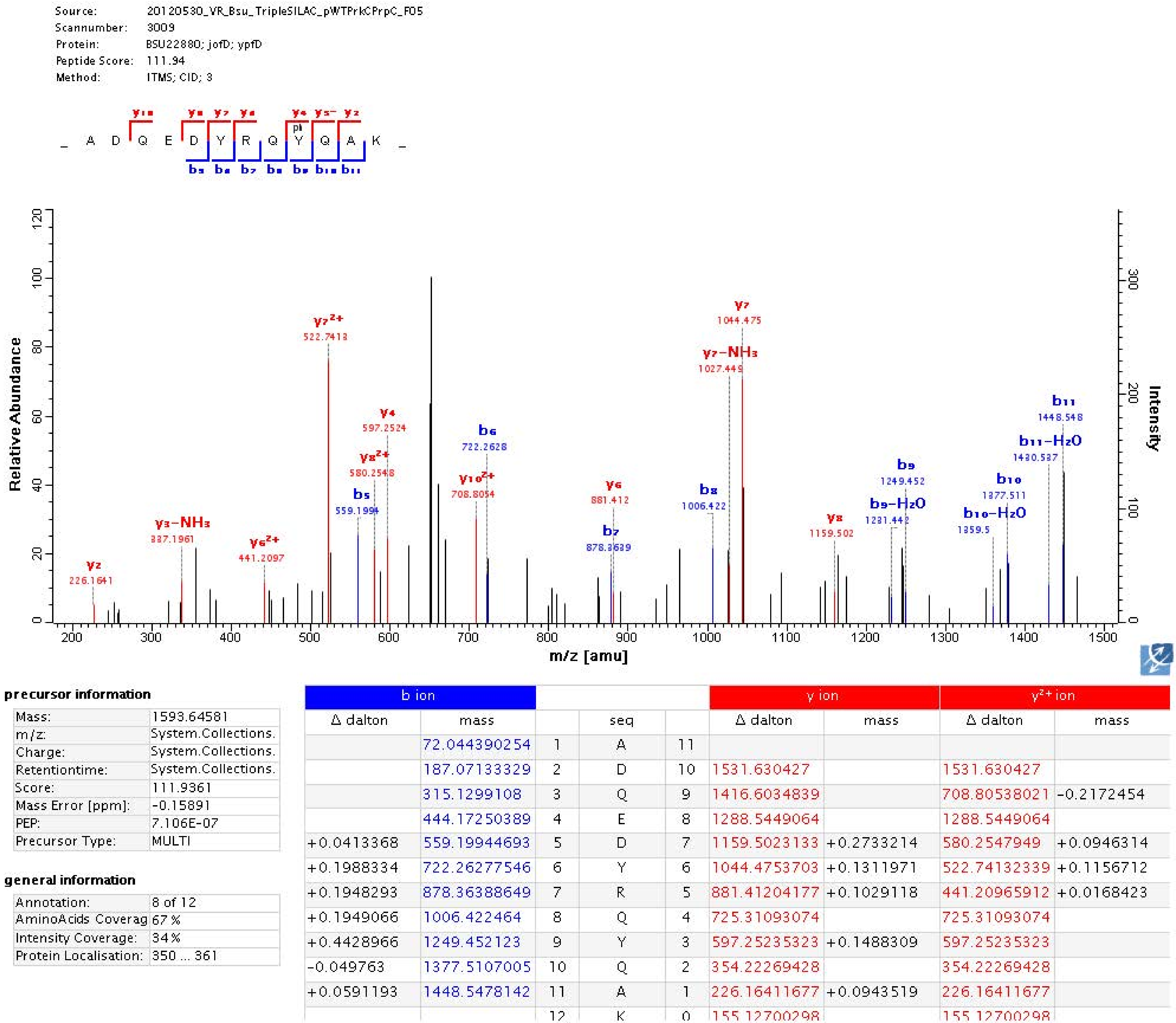
precursor information

Mass:	1326.52417
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	194.1653
Mass Error [ppm]:	0.0044655
PEP:	9.6528E-39
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	64 %
Protein Localisation:	52 ... 62

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	10				
	315.074		315.074	2	F	9	1168.547		584.7773	+0.119269
	416.1217		416.1217	3	T	8	1021.479	+0.136433	511.2431	+0.010776
	544.1803		544.1803	4	Q	7	920.4312	+0.06314	920.4312	
	615.2174		615.2174	5	A	6	792.3726	+0.102064	792.3726	
	743.276		743.276	6	Q	5	721.3355	+0.016131	721.3355	
	872.3186	+0.044509	872.3186	7	E	4	593.2769	-0.428221	593.2769	
	987.3455	+0.230334	987.3455	8	D	3	464.2343	+0.061699	464.2343	
	1044.367		1044.367	9	G	2	349.2074	+0.072346	349.2074	
+0.492941	591.2166	+0.109126	1181.426	10	H	1	292.1859		292.1859	
				11	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 3009
Protein: BSU22880; jofD; ypfD
Peptide Score: 111.94
Method: ITMS; CID; 3

precursor information

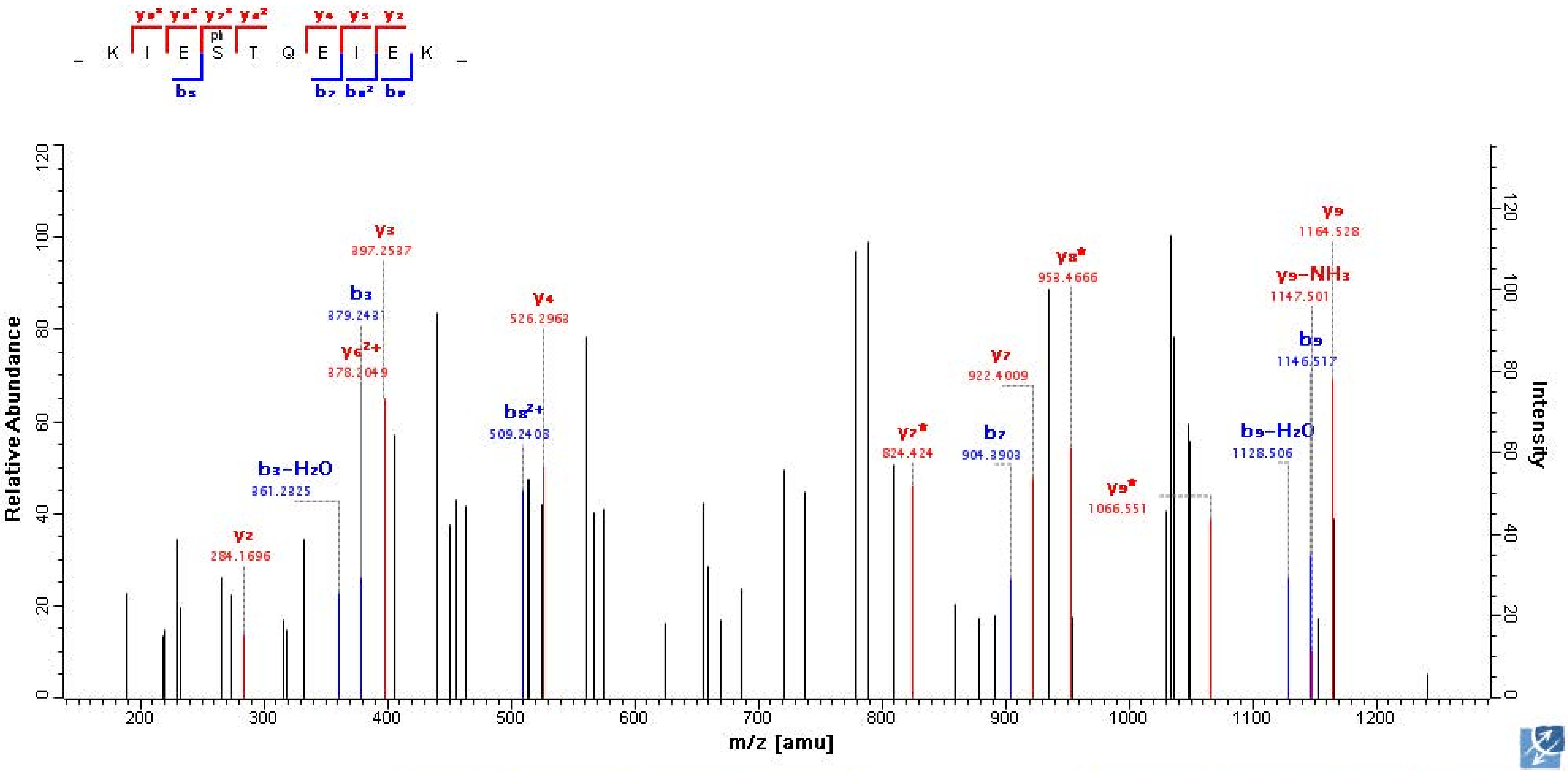
Mass:	1593.64581
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.9361
Mass Error [ppm]:	-0.15891
PEP:	7.106E-07
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	34 %
Protein Localisation:	350 ... 361

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	11				
	187.07133329	2	D	10	1531.630427		1531.630427	
	315.1299108	3	Q	9	1416.6034839		708.80538021	-0.2172454
	444.17250389	4	E	8	1288.5449064		1288.5449064	
+0.0413368	559.19944693	5	D	7	1159.5023133	+0.2733214	580.2547949	+0.0946314
+0.1988334	722.26277546	6	Y	6	1044.4753703	+0.1311971	522.74132339	+0.1156712
+0.1948293	878.36388649	7	R	5	881.41204177	+0.1029118	441.20965912	+0.0168423
+0.1949066	1006.422464	8	Q	4	725.31093074		725.31093074	
+0.4428966	1249.452123	9	Y	3	597.25235323	+0.1488309	597.25235323	
-0.049763	1377.5107005	10	Q	2	354.22269428		354.22269428	
+0.0591193	1448.5478142	11	A	1	226.16411677	+0.0943519	226.16411677	
		12	K	0	155.12700298		155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 3502
Protein: BSU29840; ytpP
Peptide Score: 83.08
Method: ITMS; CID; 3



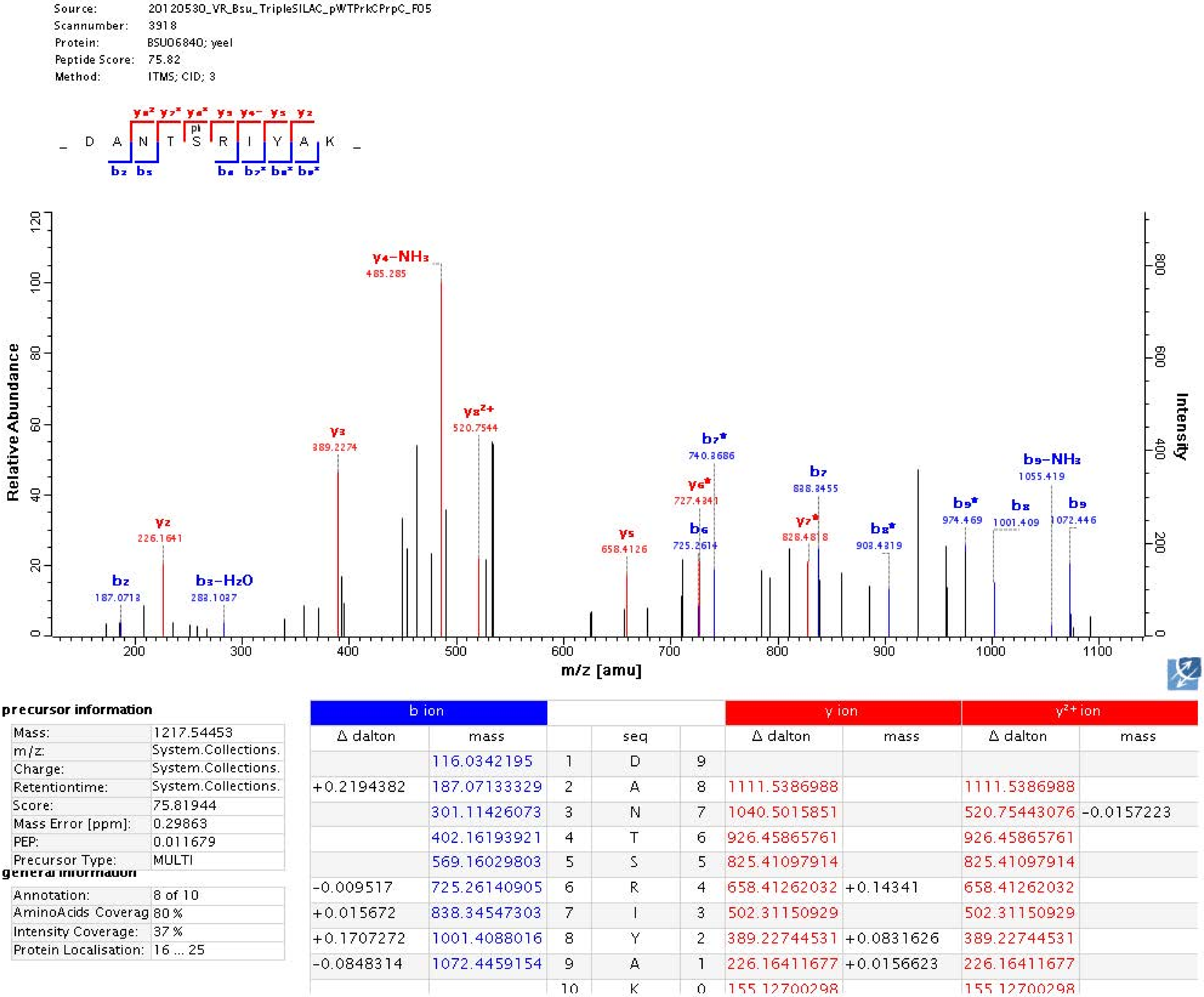
precursor information

Mass:	1283.59863
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	83.08141
Mass Error [ppm]:	-1.8346
PEP:	0.005258
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	24 %
Protein Localisation:	3 ... 12

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164		137.1164	1	K	9				
	250.2005		250.2005	2	I	8	1164.528	+0.051821	1164.528	
	379.2431	-0.036797	379.2431	3	E	7	1051.443		1051.443	
	546.2415		546.2415	4	S	6	922.4009	+0.008556	922.4009	
	647.2891		647.2891	5	T	5	755.4025		378.2049	+0.266665
	775.3477		775.3477	6	Q	4	654.3548		654.3548	
	904.3903	+0.045183	904.3903	7	E	3	526.2963	+0.046642	526.2963	
+0.456993	509.2408		1017.474	8	I	2	397.2537	+0.145144	397.2537	
	1146.517	-0.109123	1146.517	9	E	1	284.1696	-0.1439	284.1696	
				10	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 3918
Protein: BSU06840; yeeI
Peptide Score: 75.82
Method: ITMS; CID; 3

precursor information

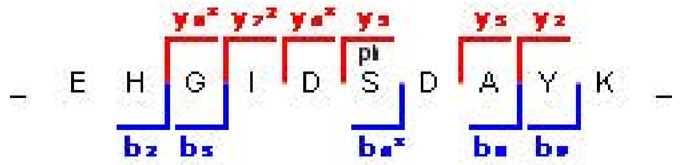
Mass:	1217.54453
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	75.81944
Mass Error [ppm]:	0.29863
PEP:	0.011679
Precursor Type:	MULTI

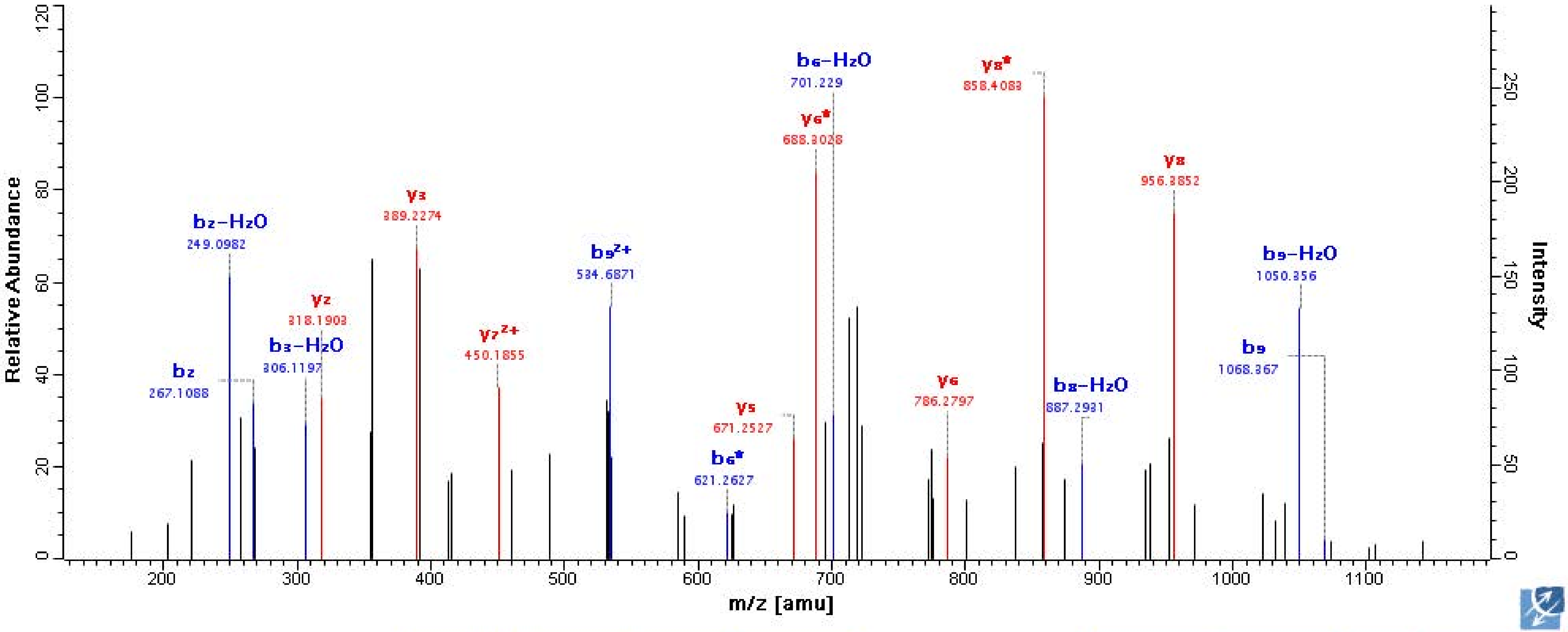
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	37 %
Protein Localisation:	16 ... 25

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	9				
+0.2194382	187.07133329	2	A	8	1111.5386988		1111.5386988	
	301.11426073	3	N	7	1040.5015851		520.75443076	-0.0157223
	402.16193921	4	T	6	926.45865761		926.45865761	
	569.16029803	5	S	5	825.41097914		825.41097914	
-0.009517	725.26140905	6	R	4	658.41262032	+0.14341	658.41262032	
+0.015672	838.34547303	7	I	3	502.31150929		502.31150929	
+0.1707272	1001.4088016	8	Y	2	389.22744531	+0.0831626	389.22744531	
-0.0848314	1072.4459154	9	A	1	226.16411677	+0.0156623	226.16411677	
		10	K	0	155.12700298		155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 4276
Protein: asnS; BSU22360
Peptide Score: 93.06
Method: ITMS; CID; 3





precursor information

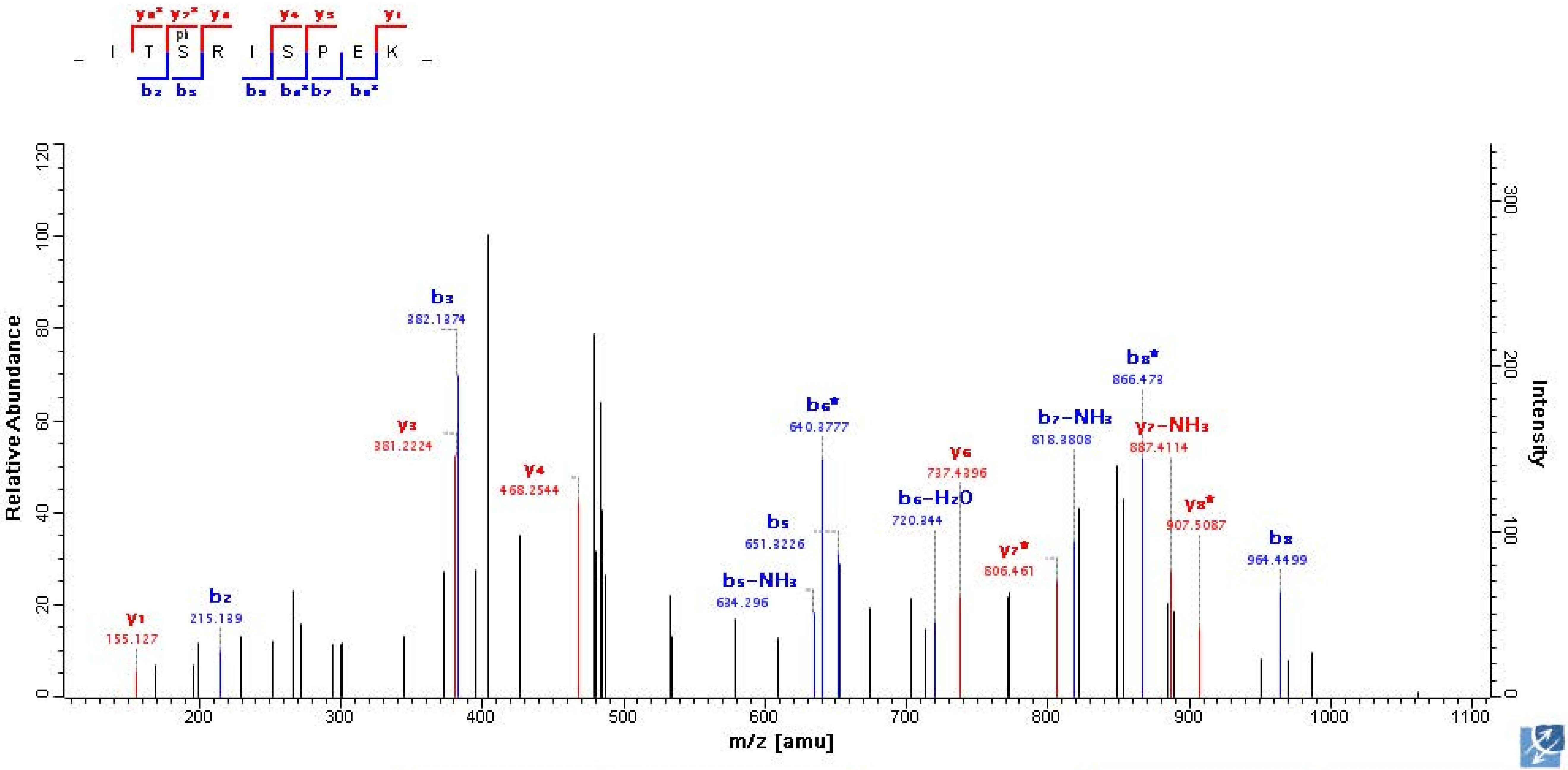
Mass:	1221.47922
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.05779
Mass Error [ppm]:	-0.18917
PEP:	0.010369
Precursor Type:	ISO

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	46 %
Protein Localisation:	373 ... 382

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	9				
	267.1088	-0.359911	267.1088	2	H	8	1093.444		1093.444	
	324.1302		324.1302	3	G	7	956.3852	+0.065527	956.3852	
	437.2143		437.2143	4	I	6	899.3638		450.1855	+0.405854
	552.2413		552.2413	5	D	5	786.2797	+0.074924	786.2797	
	719.2396		719.2396	6	S	4	671.2527	-0.041688	671.2527	
	834.2666		834.2666	7	D	3	504.2544		504.2544	
	905.3037		905.3037	8	A	2	389.2274	+0.136263	389.2274	
-0.309695	534.6871	+0.055611	1068.367	9	Y	1	318.1903	+0.09928	318.1903	
				10	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	4629
Protein:	BSU06440; purB; purE
Peptide Score:	83.87
Method:	ITMS; CID; 3

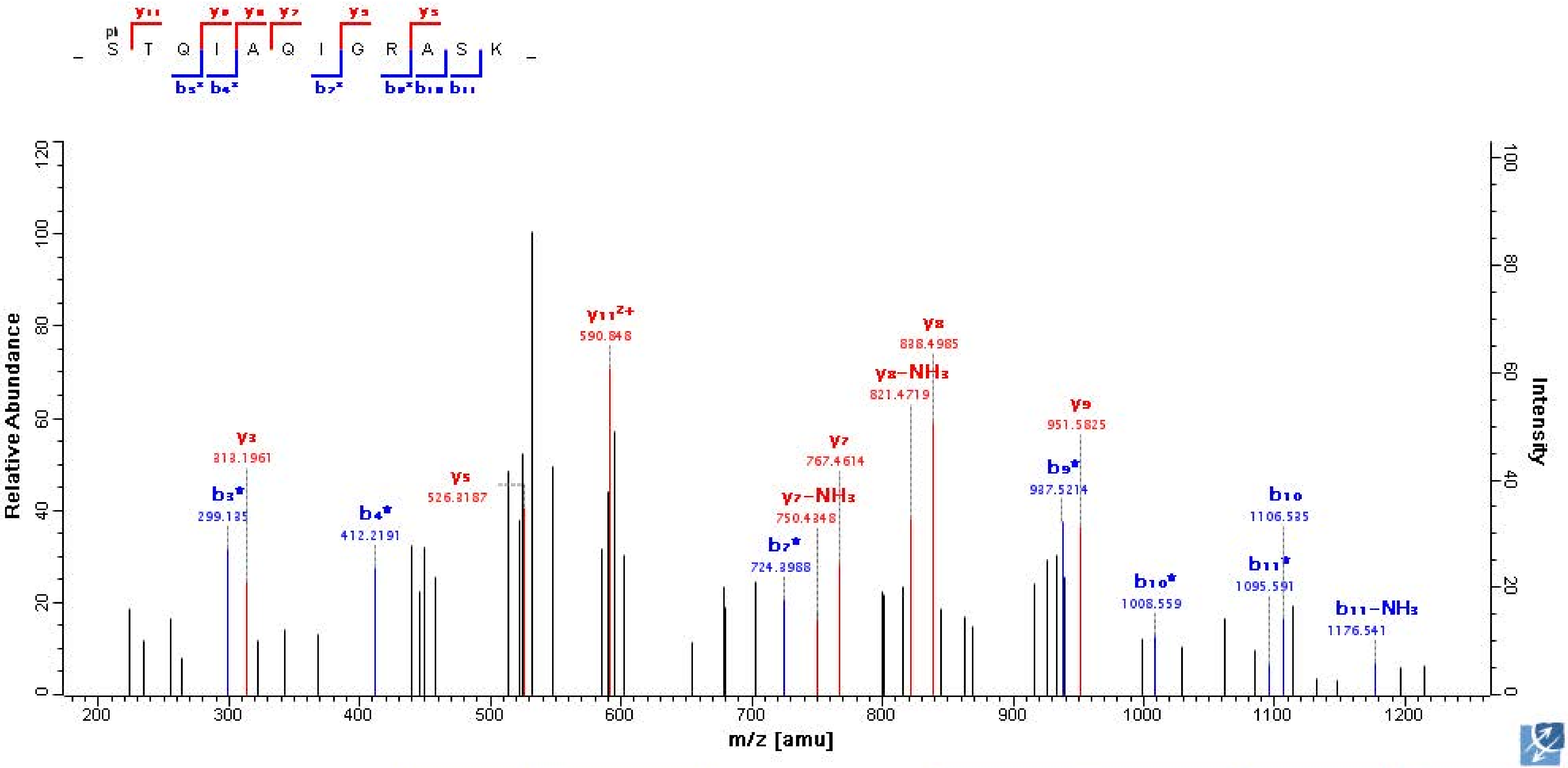


precursor information

Mass:	1109.54821
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	83.86861
Mass Error [ppm]:	0.0169
PEP:	0.031184
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	34 %
Protein Localisation:	399 ... 407

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	8		
+0.0668221	215.139018921	2	T	7	1005.485600643	
+0.1758547	382.137377739	3	S	6	904.437922169	
	538.238488768	4	R	5	737.43956335	+0.1003536
-0.0462466	651.322552748	5	I	4	581.338452322	
	738.354581158	6	S	3	468.254388342	+0.1608338
	835.40734501	7	P	2	381.222359932	-0.1232999
+0.0456063	964.449938106	8	E	1	284.16959608	
		9	K	0	155.127002984	-0.115742

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 5194
Protein: BSU06030; groEL; groL; mopA
Peptide Score: 76.33
Method: ITMS; CID; 3



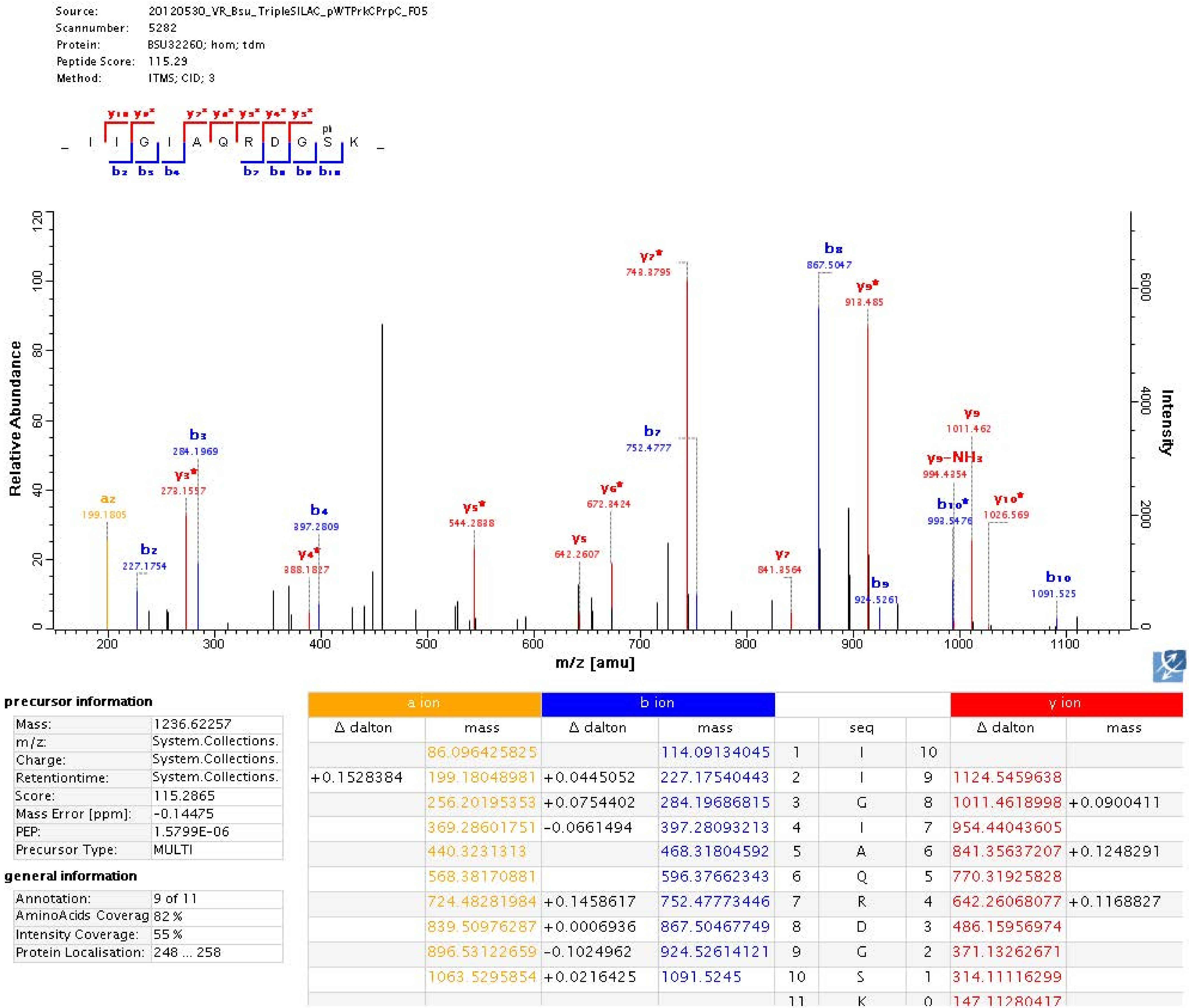
precursor information

Mass:	1338.66519
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	76.32578
Mass Error [ppm]:	-0.35984
PEP:	0.0094223
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoActds Coverag	83 %
Intensity Coverage:	31 %
Protein Localisation:	309 ... 320

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	11				
	269.05331376	2	T	10	1180.6887952		590.84803582	+0.2437
	397.11189127	3	Q	9	1079.6411167		1079.6411167	
	510.19595525	4	I	8	951.58253919	+0.1433519	951.58253919	
	581.23306904	5	A	7	838.49847521	-0.2316905	838.49847521	
	709.29164655	6	Q	6	767.46136142	+0.0644564	767.46136142	
	822.37571053	7	I	5	639.40278391		639.40278391	
	879.39717425	8	G	4	526.31871993	+0.0219783	526.31871993	
	1035.4982853	9	R	3	469.29725621		469.29725621	
+0.417848	1106.5353991	10	A	2	313.19614518	+0.0884618	313.19614518	
	1193.5674275	11	S	1	242.15903139		242.15903139	
		12	K	0	155.12700298		155.12700298	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 5282
Protein: BSU32260; hom; tdm
Peptide Score: 115.29
Method: ITMS; CID; 3

precursor information

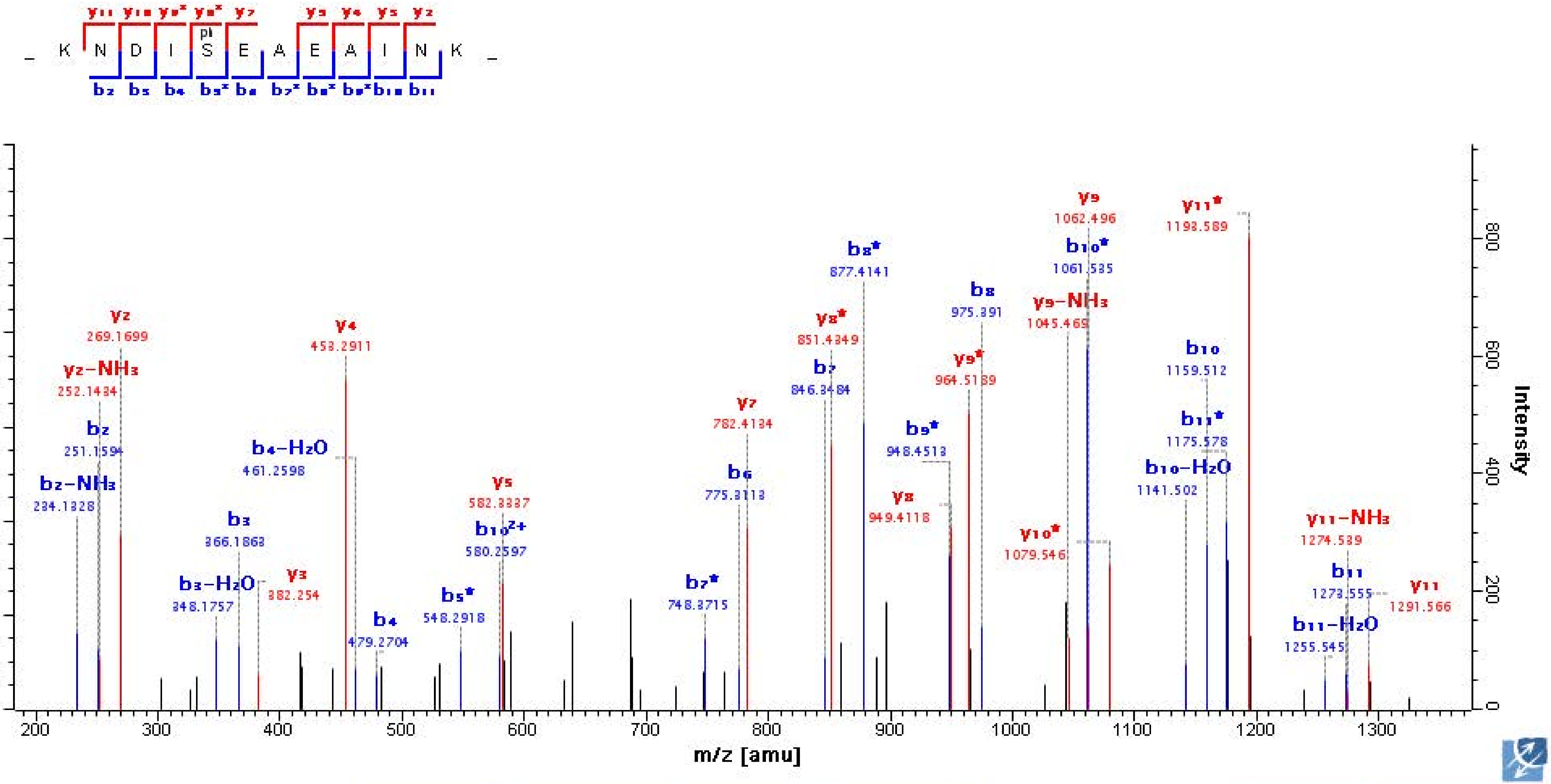
Mass:	1236.62257
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.2865
Mass Error [ppm]:	-0.14475
PEP:	1.5799E-06
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	55 %
Protein Localisation:	248 ... 258

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096425825		114.09134045	1	I	10		
+0.1528384	199.18048981	+0.0445052	227.17540443	2	I	9	1124.5459638	
	256.20195353	+0.0754402	284.19686815	3	G	8	1011.4618998	+0.0900411
	369.28601751	-0.0661494	397.28093213	4	I	7	954.44043605	
	440.3231313		468.31804592	5	A	6	841.35637207	+0.1248291
	568.38170881		596.37662343	6	Q	5	770.31925828	
	724.48281984	+0.1458617	752.47773446	7	R	4	642.26068077	+0.1168827
	839.50976287	+0.0006936	867.50467749	8	D	3	486.15956974	
	896.53122659	-0.1024962	924.52614121	9	G	2	371.13262671	
	1063.5295854	+0.0216425	1091.5245	10	S	1	314.11116299	
				11	K	0	147.11280417	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	5774
Protein:	BSU08790; thiA; thiC
Peptide Score:	242.48
Method:	ITMS; CID; 3



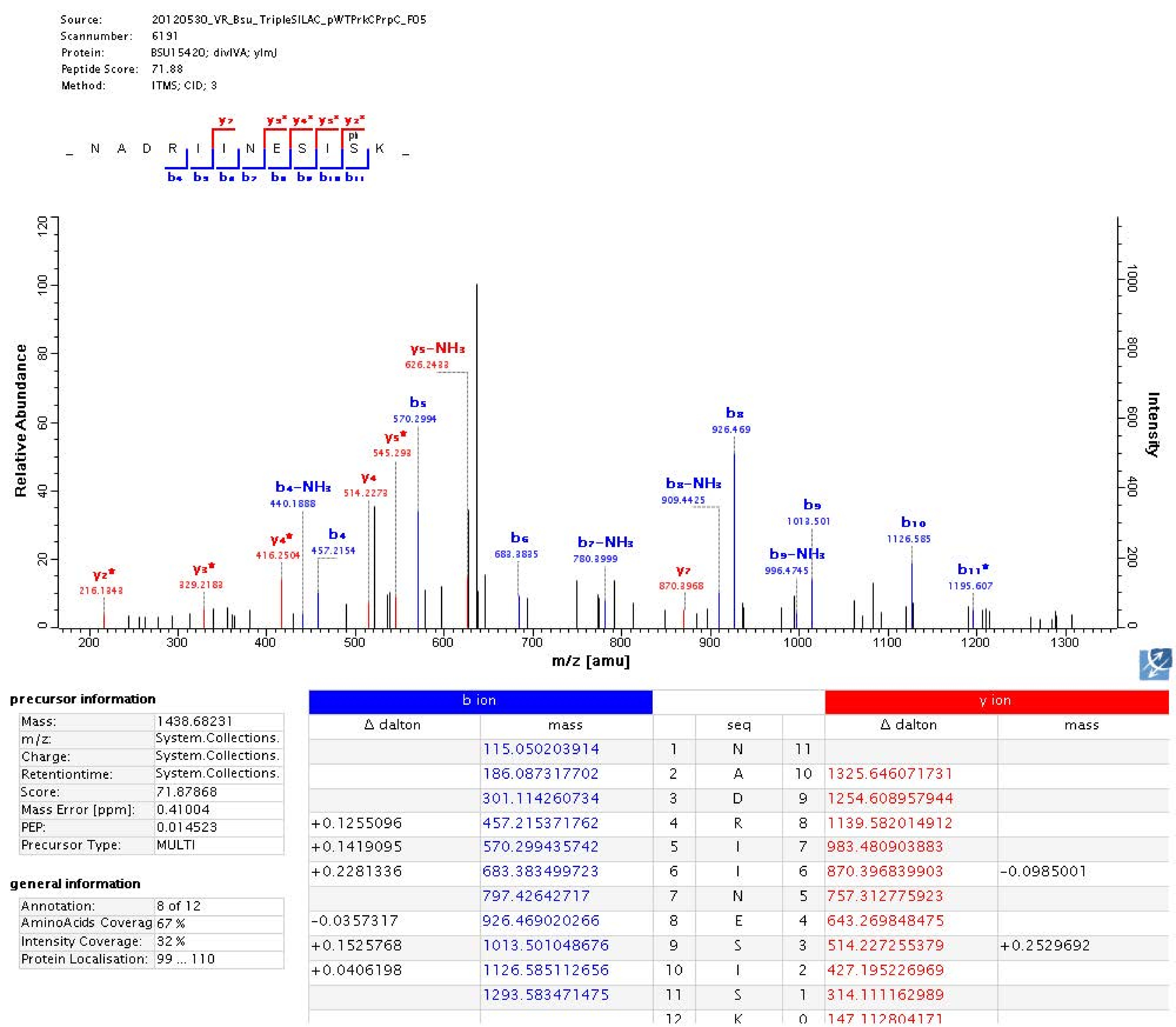
precursor information

Mass:	1410.63878
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	242.4801
Mass Error [ppm]:	-0.2873
PEP:	5.77E-81
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	72 %
Protein Localisation:	561 ... 572

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	137.1164383		137.1164383	1	K	11		
	251.15936574	+0.2621736	251.15936574	2	N	10	1291.5657015	+0.0647917
	366.18630878	+0.0429393	366.18630878	3	D	9	1177.522774	
	479.27037276	+0.1471077	479.27037276	4	I	8	1062.495831	+0.0155216
	646.26873158		646.26873158	5	S	7	949.411767	+0.0729132
	775.31132467	+0.0291905	775.31132467	6	E	6	782.41340818	+0.0743238
	846.34843846	-0.1417734	846.34843846	7	A	5	653.37081508	
	975.39103156	-0.0116981	975.39103156	8	E	4	582.3337013	+0.0911034
	1046.4281453		1046.4281453	9	A	3	453.2911082	-0.0041209
-0.2710344	580.2597429	+0.0125709	1159.5122093	10	I	2	382.25399441	+0.1347385
	1273.5551368	-0.1685401	1273.5551368	11	N	1	269.16993043	+0.0344763
				12	K	0	155.12700298	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	6191
Protein:	BSU15420; divIVA; ylmJ
Peptide Score:	71.88
Method:	ITMS; CID; 3

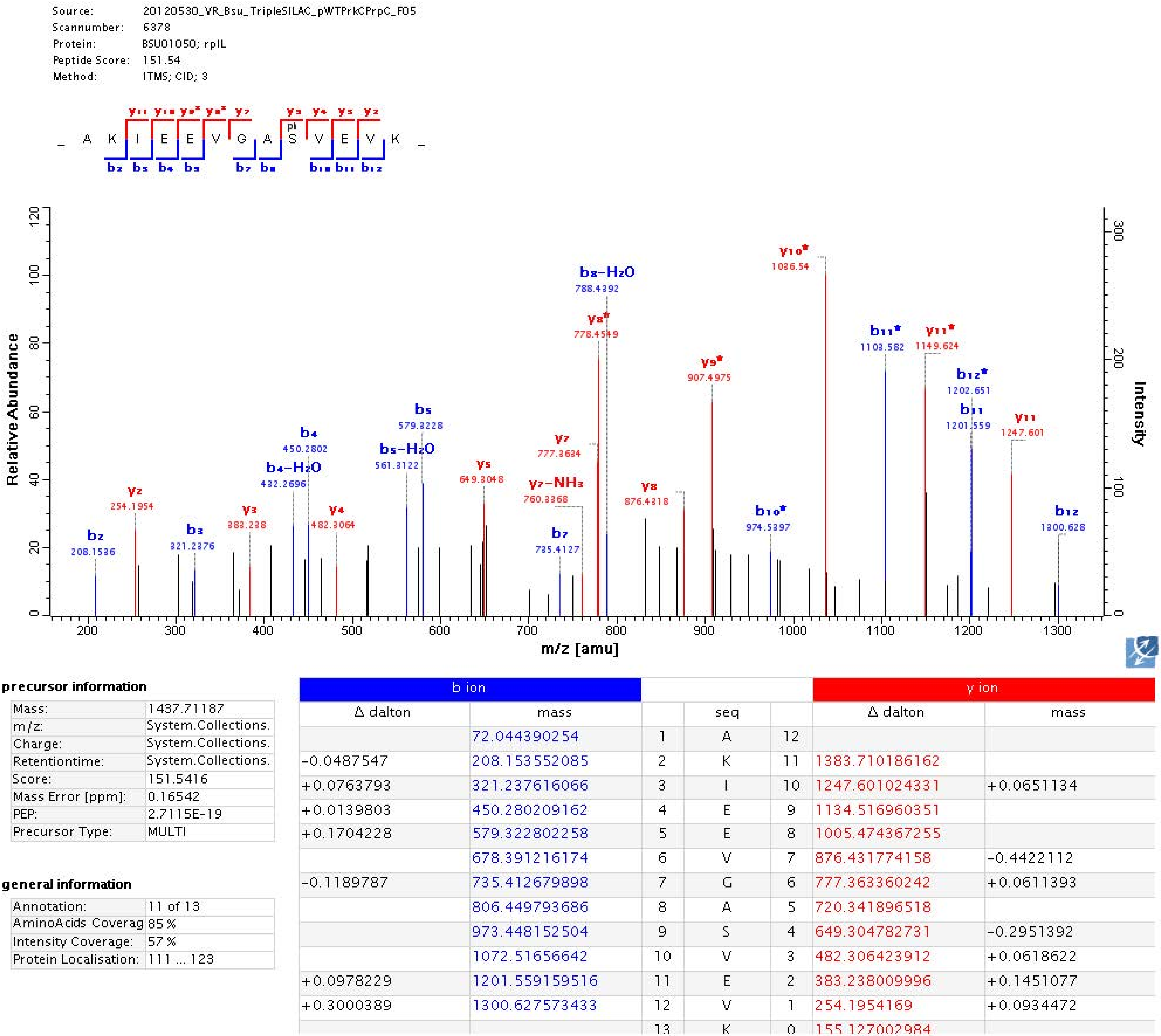
precursor information

Mass:	1438.68231
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.87868
Mass Error [ppm]:	0.41004
PEP:	0.014523
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	32 %
Protein Localisation:	99 ... 110

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	11		
	186.087317702	2	A	10	1325.646071731	
	301.114260734	3	D	9	1254.608957944	
+0.1255096	457.215371762	4	R	8	1139.582014912	
+0.1419095	570.299435742	5	I	7	983.480903883	
+0.2281336	683.383499723	6	I	6	870.396839903	-0.0985001
	797.42642717	7	N	5	757.312775923	
-0.0357317	926.469020266	8	E	4	643.269848475	
+0.1525768	1013.501048676	9	S	3	514.227255379	+0.2529692
+0.0406198	1126.585112656	10	I	2	427.195226969	
	1293.583471475	11	S	1	314.111162989	
		12	K	0	147.112804171	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	6378
Protein:	BSU01050; rplL
Peptide Score:	151.54
Method:	ITMS; CID; 3

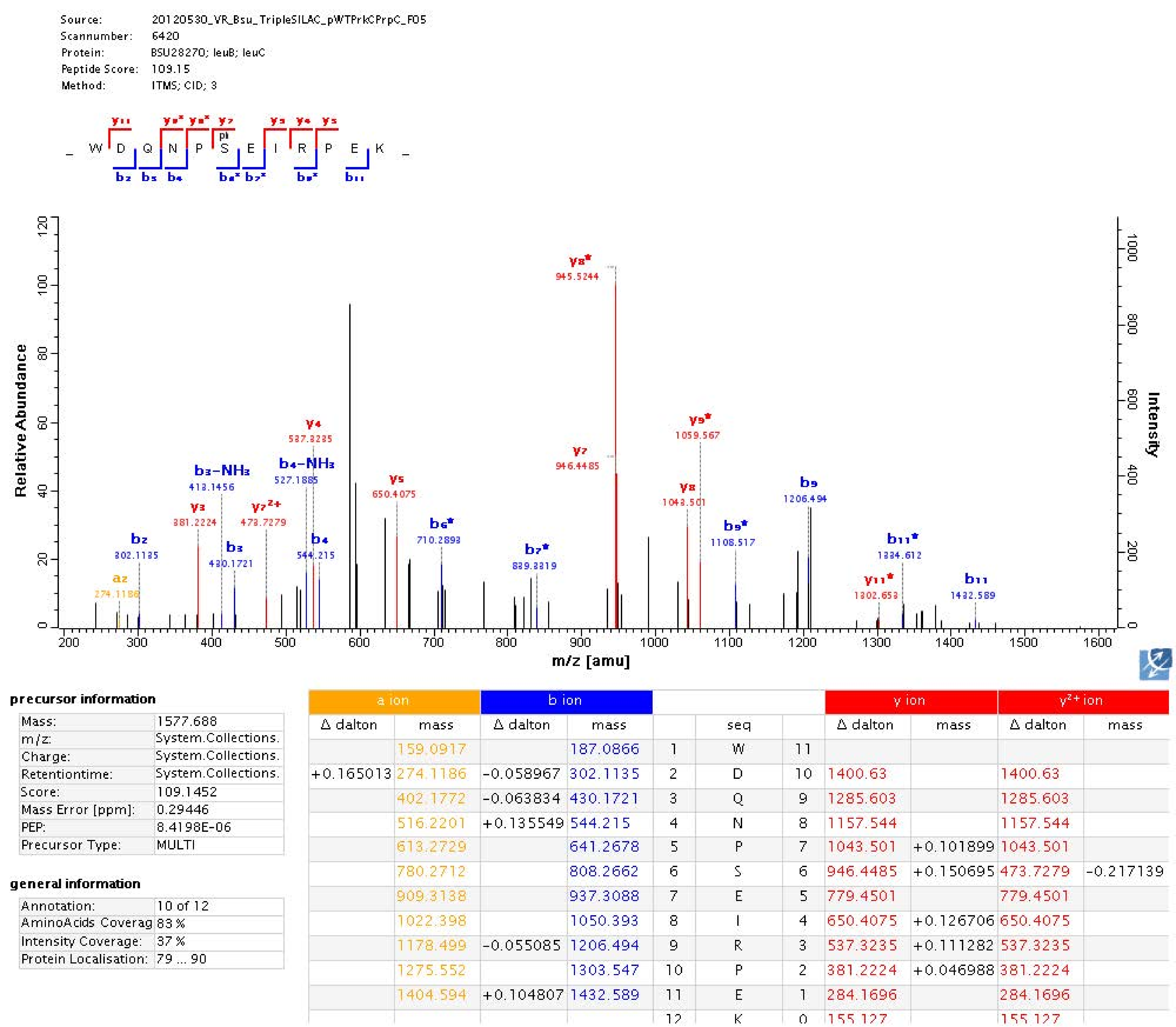
precursor information

Mass:	1437.71187
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.5416
Mass Error [ppm]:	0.16542
PEP:	2.7115E-19
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	57 %
Protein Localisation:	111 ... 123

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	12		
-0.0487547	208.153552085	2	K	11	1383.710186162	
+0.0763793	321.237616066	3	I	10	1247.601024331	+0.0651134
+0.0139803	450.280209162	4	E	9	1134.516960351	
+0.1704228	579.322802258	5	E	8	1005.474367255	
	678.391216174	6	V	7	876.431774158	-0.4422112
-0.1189787	735.412679898	7	G	6	777.363360242	+0.0611393
	806.449793686	8	A	5	720.341896518	
	973.448152504	9	S	4	649.304782731	-0.2951392
	1072.51656642	10	V	3	482.306423912	+0.0618622
+0.0978229	1201.559159516	11	E	2	383.238009996	+0.1451077
+0.3000389	1300.627573433	12	V	1	254.1954169	+0.0934472
		13	K	0	155.127002984	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 6420
Protein: BSU28270; leuB; leuC
Peptide Score: 109.15
Method: ITMS; CID; 3

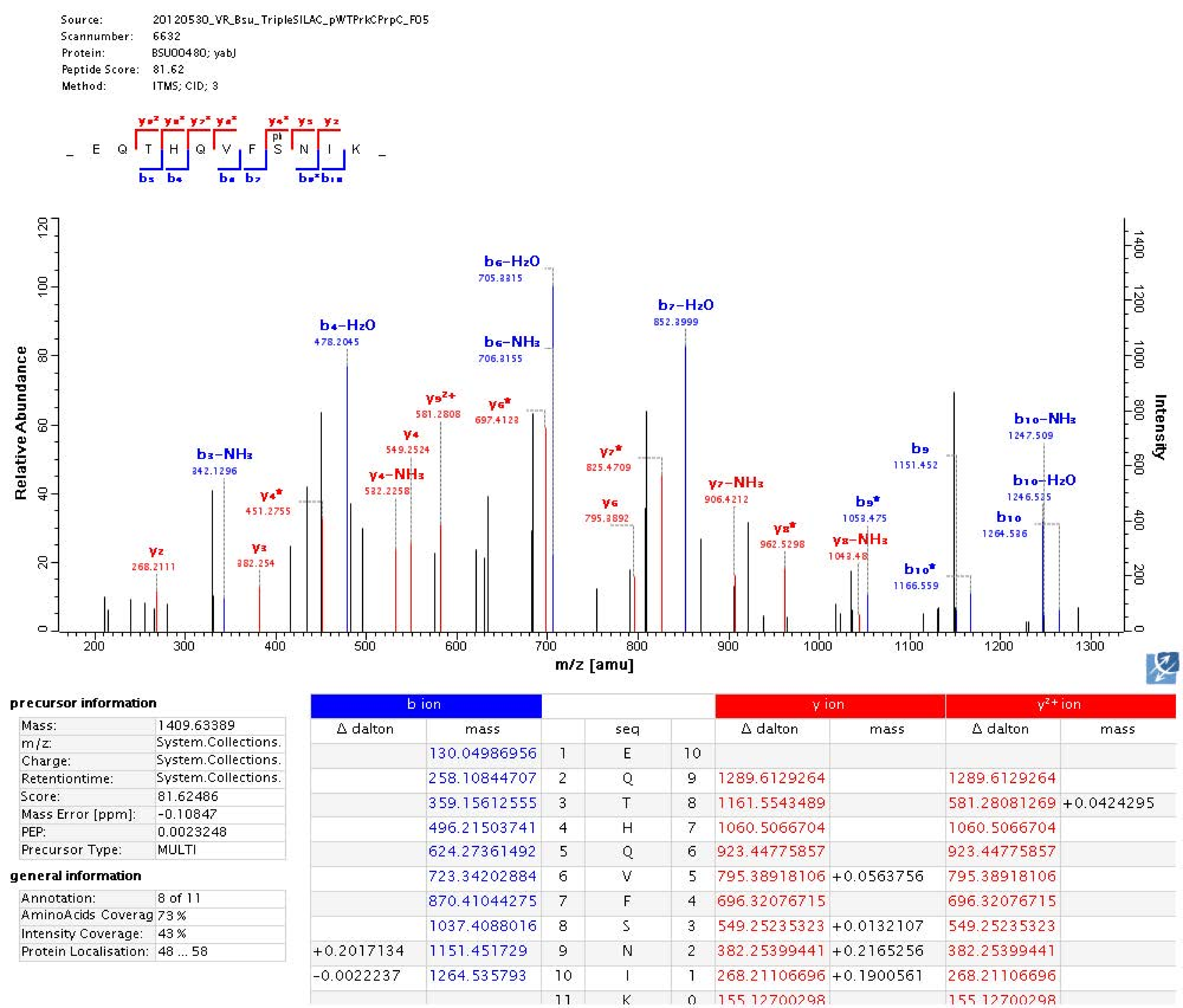
precursor information

Mass:	1577.688
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.1452
Mass Error [ppm]:	0.29446
PEP:	8.4198E-06
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	37 %
Protein Localisation:	79 ... 90

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	159.0917		187.0866	1	W	11				
+0.165013	274.1186	-0.058967	302.1135	2	D	10	1400.63		1400.63	
	402.1772	-0.063834	430.1721	3	Q	9	1285.603		1285.603	
	516.2201	+0.135549	544.215	4	N	8	1157.544		1157.544	
	613.2729		641.2678	5	P	7	1043.501	+0.101899	1043.501	
	780.2712		808.2662	6	S	6	946.4485	+0.150695	473.7279	-0.217139
	909.3138		937.3088	7	E	5	779.4501		779.4501	
	1022.398		1050.393	8	I	4	650.4075	+0.126706	650.4075	
	1178.499	-0.055085	1206.494	9	R	3	537.3235	+0.111282	537.3235	
	1275.552		1303.547	10	P	2	381.2224	+0.046988	381.2224	
	1404.594	+0.104807	1432.589	11	E	1	284.1696		284.1696	
				12	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 6632
Protein: BSU00480; yabJ
Peptide Score: 81.62
Method: ITMS; CID; 3

precursor information

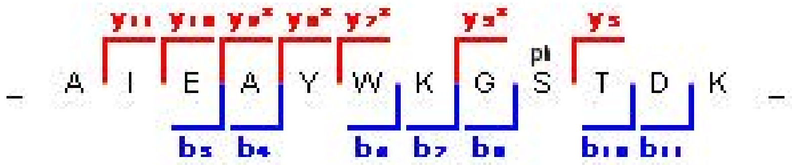
Mass:	1409.63389
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	81.62486
Mass Error [ppm]:	-0.10847
PEP:	0.0023248
Precursor Type:	MULTI

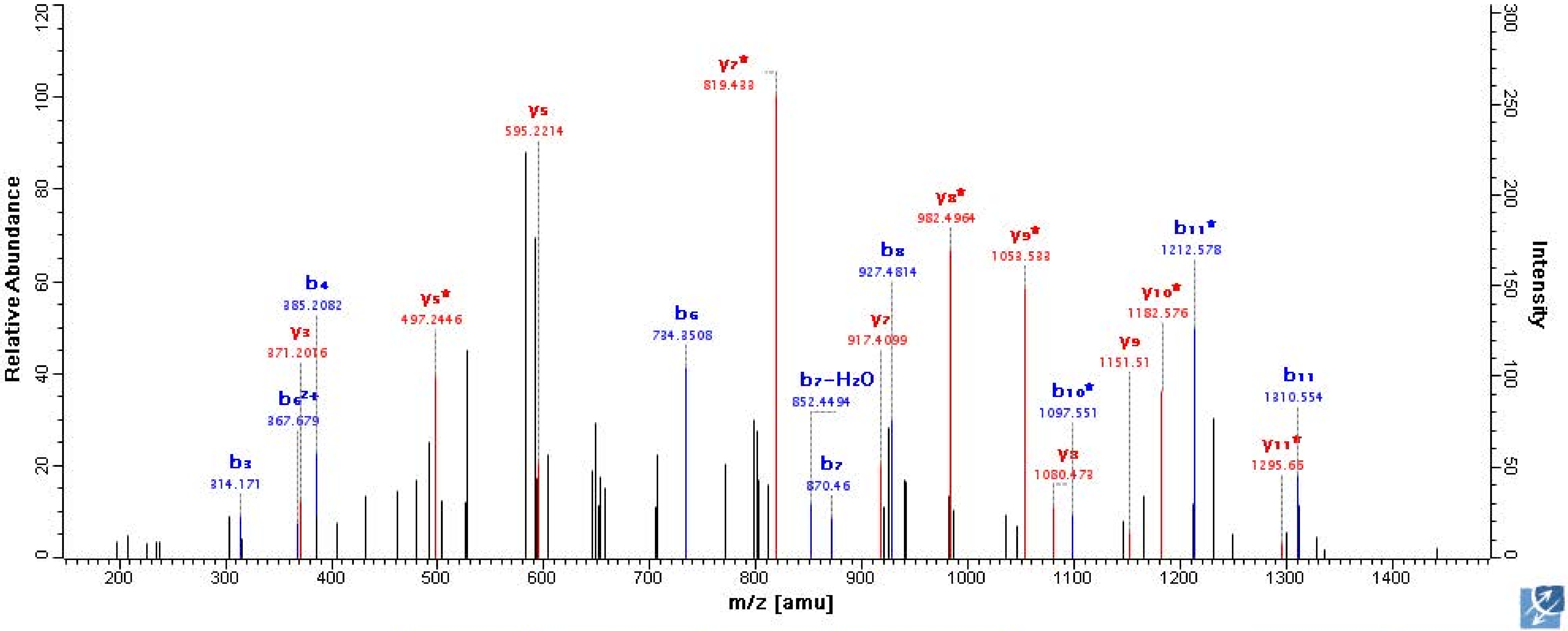
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	43 %
Protein Localisation:	48 ... 58

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	10				
	258.10844707	2	Q	9	1289.6129264		1289.6129264	
	359.15612555	3	T	8	1161.5543489		581.28081269	+0.0424295
	496.21503741	4	H	7	1060.5066704		1060.5066704	
	624.27361492	5	Q	6	923.44775857		923.44775857	
	723.34202884	6	V	5	795.38918106	+0.0563756	795.38918106	
	870.41044275	7	F	4	696.32076715		696.32076715	
	1037.4088016	8	S	3	549.25235323	+0.0132107	549.25235323	
+0.2017134	1151.451729	9	N	2	382.25399441	+0.2165256	382.25399441	
-0.0022237	1264.535793	10	I	1	268.21106696	+0.1900561	268.21106696	
		11	K	0	155.12700298		155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 7118
Protein: BSU13180; metC; metE
Peptide Score: 131.69
Method: ITMS; CID; 3





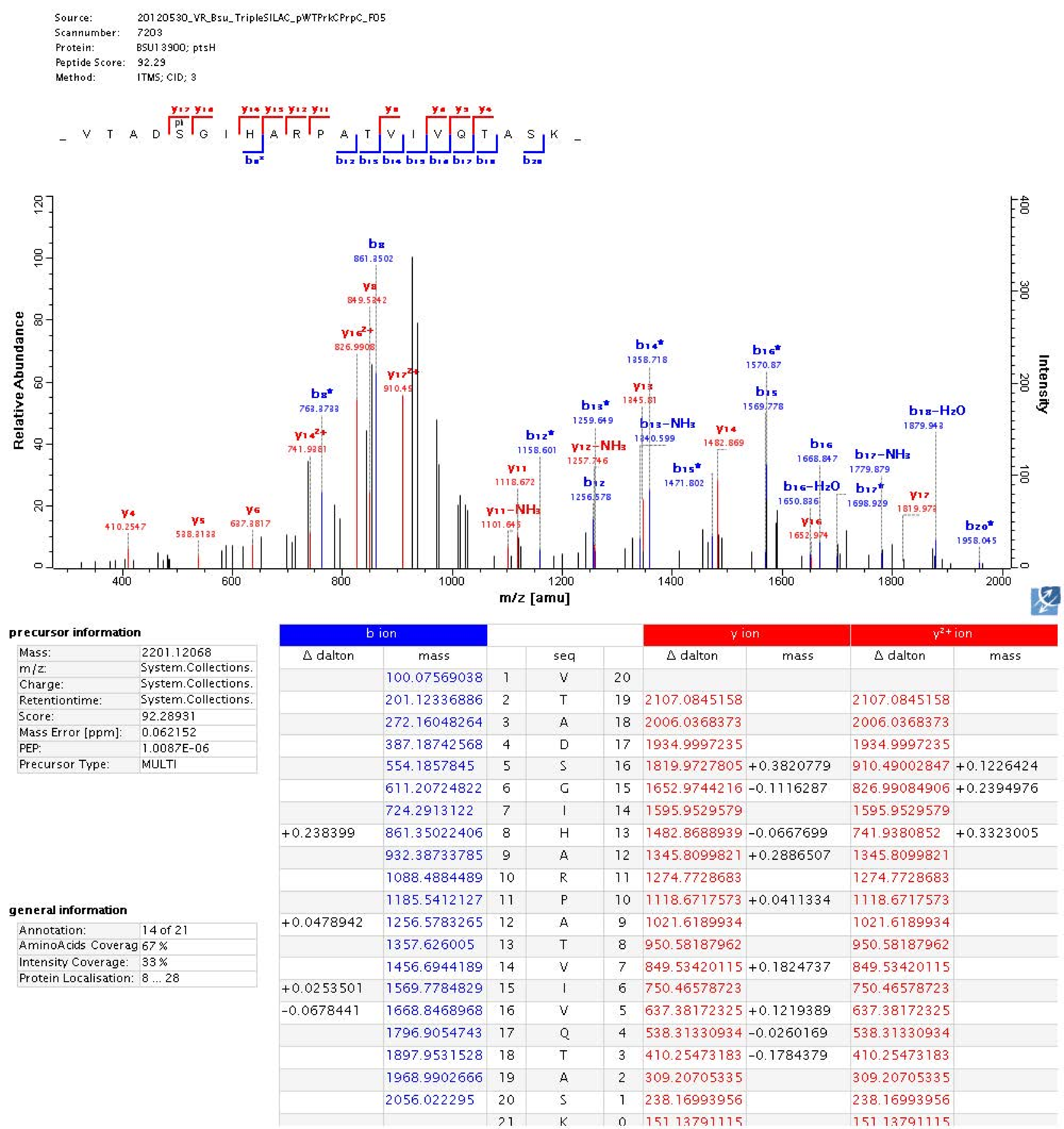
precursor information

Mass:	1447.6384
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	131.6914
Mass Error [ppm]:	-0.04008
PEP:	1.9598E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	41 %
Protein Localisation:	23 ... 34

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	11		
	185.12845423		185.12845423	2	I	10	1393.6370212	
	314.17104733	+0.0533789	314.17104733	3	E	9	1280.5529572	
	385.20816112	-0.0637519	385.20816112	4	A	8	1151.5103641	-0.2164188
	548.27148966		548.27148966	5	Y	7	1080.4732504	+0.0848551
-0.4084707	367.67903954	-0.1077606	734.35080261	6	W	6	917.40992182	+0.0549219
	870.45996444	-0.0441319	870.45996444	7	K	5	731.33060886	
	927.48142817	+0.294878	927.48142817	8	G	4	595.22144703	+0.2043953
	1094.479787		1094.479787	9	S	3	538.19998331	
	1195.5274655		1195.5274655	10	T	2	371.20162449	+0.1468252
	1310.5544085	+0.0181013	1310.5544085	11	D	1	270.15394602	
				12	K	0	155.12700298	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 7203
Protein: BSU13900; ptsH
Peptide Score: 92.29
Method: ITMS; CID; 3

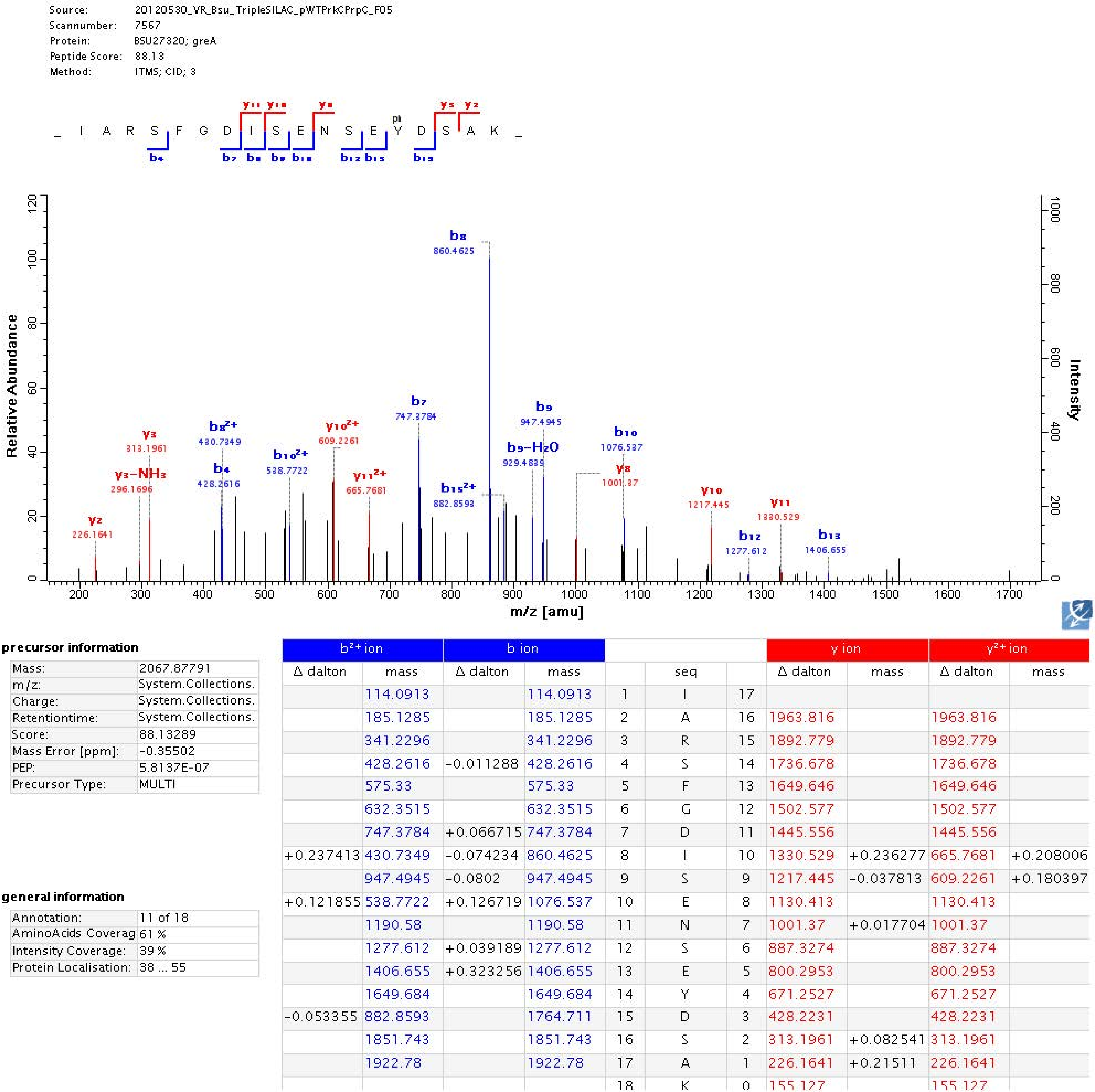
precursor information

Mass:	2201.12068
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	92.28931
Mass Error [ppm]:	0.062152
PEP:	1.0087E-06
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	33 %
Protein Localisation:	8 ... 28

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	20				
	201.12336886	2	T	19	2107.0845158		2107.0845158	
	272.16048264	3	A	18	2006.0368373		2006.0368373	
	387.18742568	4	D	17	1934.9997235		1934.9997235	
	554.1857845	5	S	16	1819.9727805	+0.3820779	910.49002847	+0.1226424
	611.20724822	6	G	15	1652.9744216	-0.1116287	826.99084906	+0.2394976
	724.2913122	7	I	14	1595.9529579		1595.9529579	
+0.238399	861.35022406	8	H	13	1482.8688939	-0.0667699	741.9380852	+0.3323005
	932.38733785	9	A	12	1345.8099821	+0.2886507	1345.8099821	
	1088.4884489	10	R	11	1274.7728683		1274.7728683	
	1185.5412127	11	P	10	1118.6717573	+0.0411334	1118.6717573	
+0.0478942	1256.5783265	12	A	9	1021.6189934		1021.6189934	
	1357.626005	13	T	8	950.58187962		950.58187962	
	1456.6944189	14	V	7	849.53420115	+0.1824737	849.53420115	
+0.0253501	1569.7784829	15	I	6	750.46578723		750.46578723	
-0.0678441	1668.8468968	16	V	5	637.38172325	+0.1219389	637.38172325	
	1796.9054743	17	Q	4	538.31330934	-0.0260169	538.31330934	
	1897.9531528	18	T	3	410.25473183	-0.1784379	410.25473183	
	1968.9902666	19	A	2	309.20705335		309.20705335	
	2056.022295	20	S	1	238.16993956		238.16993956	
		21	K	0	151.13791115		151.13791115	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 7567
Protein: BSU27320; greA
Peptide Score: 88.13
Method: ITMS; CID; 3

precursor information

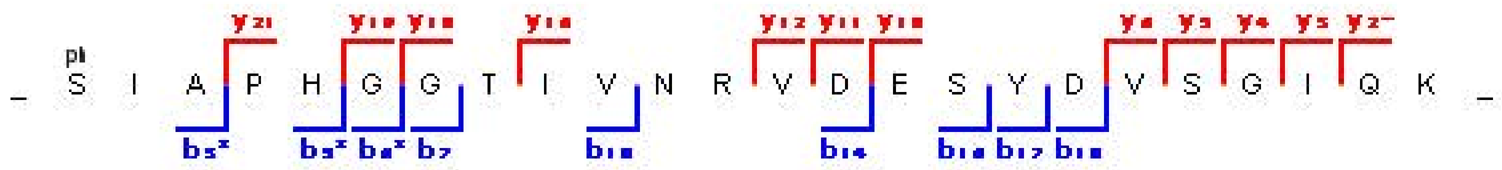
Mass:	2067.87791
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	88.13289
Mass Error [ppm]:	-0.35502
PEP:	5.8137E-07
Precursor Type:	MULTI

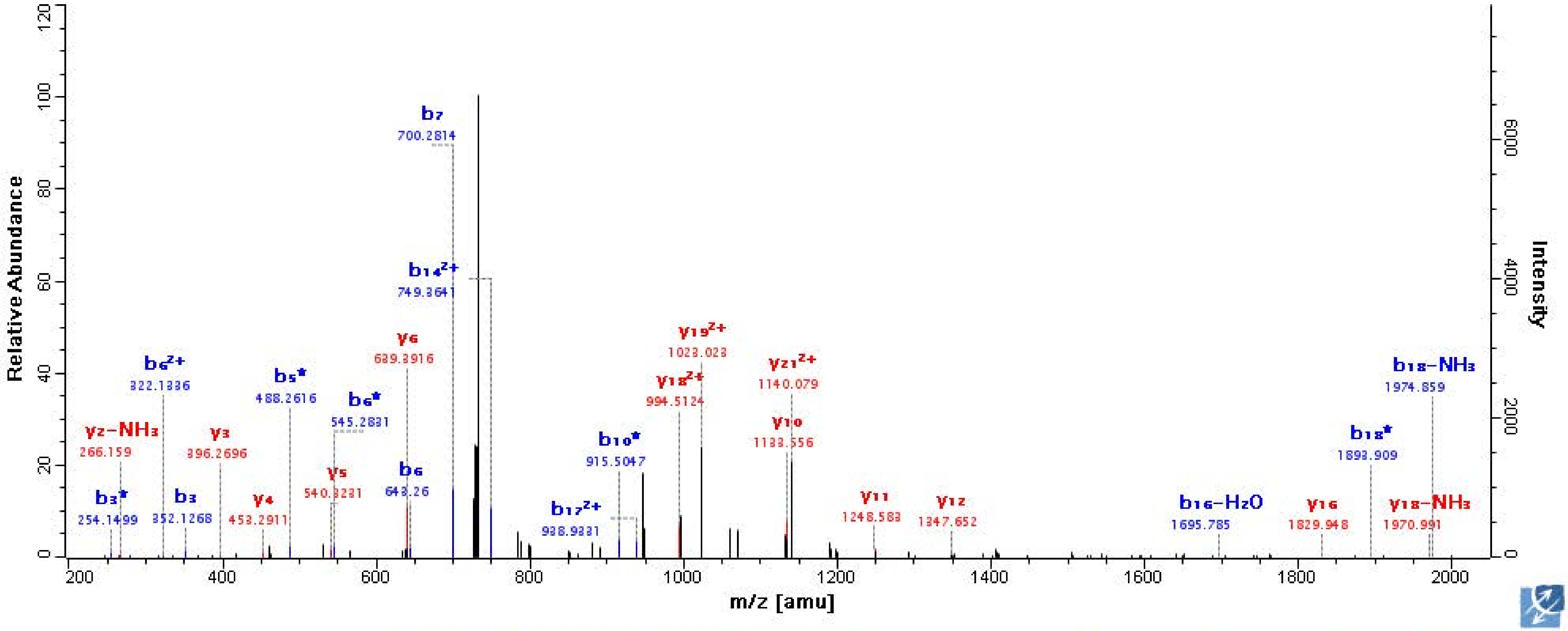
general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	39 %
Protein Localisation:	38 ... 55

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	17				
	185.1285		185.1285	2	A	16	1963.816		1963.816	
	341.2296		341.2296	3	R	15	1892.779		1892.779	
	428.2616	-0.011288	428.2616	4	S	14	1736.678		1736.678	
	575.33		575.33	5	F	13	1649.646		1649.646	
	632.3515		632.3515	6	G	12	1502.577		1502.577	
	747.3784	+0.066715	747.3784	7	D	11	1445.556		1445.556	
+0.237413	430.7349	-0.074234	860.4625	8	I	10	1330.529	+0.236277	665.7681	+0.208006
	947.4945	-0.0802	947.4945	9	S	9	1217.445	-0.037813	609.2261	+0.180397
+0.121855	538.7722	+0.126719	1076.537	10	E	8	1130.413		1130.413	
	1190.58		1190.58	11	N	7	1001.37	+0.017704	1001.37	
	1277.612	+0.039189	1277.612	12	S	6	887.3274		887.3274	
	1406.655	+0.323256	1406.655	13	E	5	800.2953		800.2953	
	1649.684		1649.684	14	Y	4	671.2527		671.2527	
-0.053355	882.8593		1764.711	15	D	3	428.2231		428.2231	
	1851.743		1851.743	16	S	2	313.1961	+0.082541	313.1961	
	1922.78		1922.78	17	A	1	226.1641	+0.21511	226.1641	
				18	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber:	8868
Protein:	BSU15590; sat; ylnB
Peptide Score:	67.22
Method:	ITMS; CID; 3





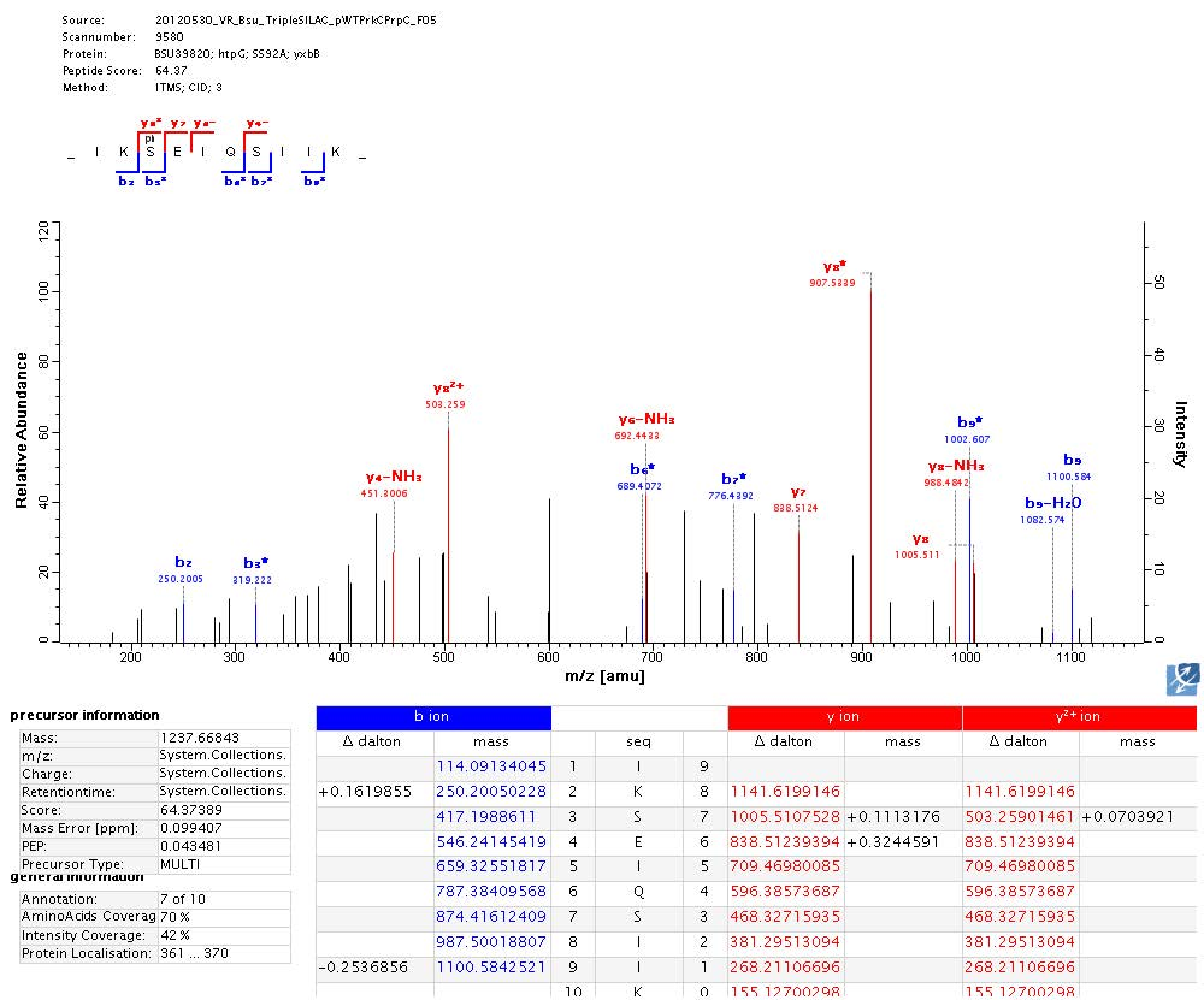
precursor information

Mass:	2621.2481
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	67.21661
Mass Error [ppm]:	-0.21279
PEP:	8.8529E-05
Precursor Type:	MULTI

general information

Annotation:	18 of 24
AminoAcids Coverag	75 %
Intensity Coverage:	25 %
Protein Localisation:	2 ... 25

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	23				
	281.0897		281.0897	2	I	22	2463.272		2463.272	
	352.1268	+0.094867	352.1268	3	A	21	2350.188		2350.188	
	449.1796		449.1796	4	P	20	2279.151		1140.079	-0.054035
	586.2385		586.2385	5	H	19	2182.098		2182.098	
+0.07476	322.1336	+0.0061	643.26	6	G	18	2045.039		1023.023	+0.152132
	700.2814	+0.313066	700.2814	7	G	17	1988.017		994.5124	+0.117698
	801.3291		801.3291	8	T	16	1930.996		1930.996	
	914.4132		914.4132	9	I	15	1829.948	+0.044725	1829.948	
	1013.482		1013.482	10	V	14	1716.864		1716.864	
	1127.525		1127.525	11	N	13	1617.796		1617.796	
	1283.626		1283.626	12	R	12	1503.753		1503.753	
	1382.694		1382.694	13	V	11	1347.652	+0.417169	1347.652	
-0.381212	749.3641		1497.721	14	D	10	1248.583	+0.081897	1248.583	
	1626.764		1626.764	15	E	9	1133.556	+0.05049	1133.556	
	1713.796		1713.796	16	S	8	1004.514		1004.514	
-0.186454	938.9331		1876.859	17	Y	7	917.4818		917.4818	
	1991.886		1991.886	18	D	6	754.4185		754.4185	
	2090.954		2090.954	19	V	5	639.3916	+0.174551	639.3916	
	2177.986		2177.986	20	S	4	540.3231	+0.035506	540.3231	
	2235.008		2235.008	21	G	3	453.2911	-0.071076	453.2911	
	2348.092		2348.092	22	I	2	396.2696	-0.035056	396.2696	
	2476.15		2476.15	23	Q	1	283.1856		283.1856	
				24	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F05
Scannumber: 9580
Protein: BSU39820; htpG; S592A; yxbB
Peptide Score: 64.37
Method: ITMS; CID; 3

precursor information

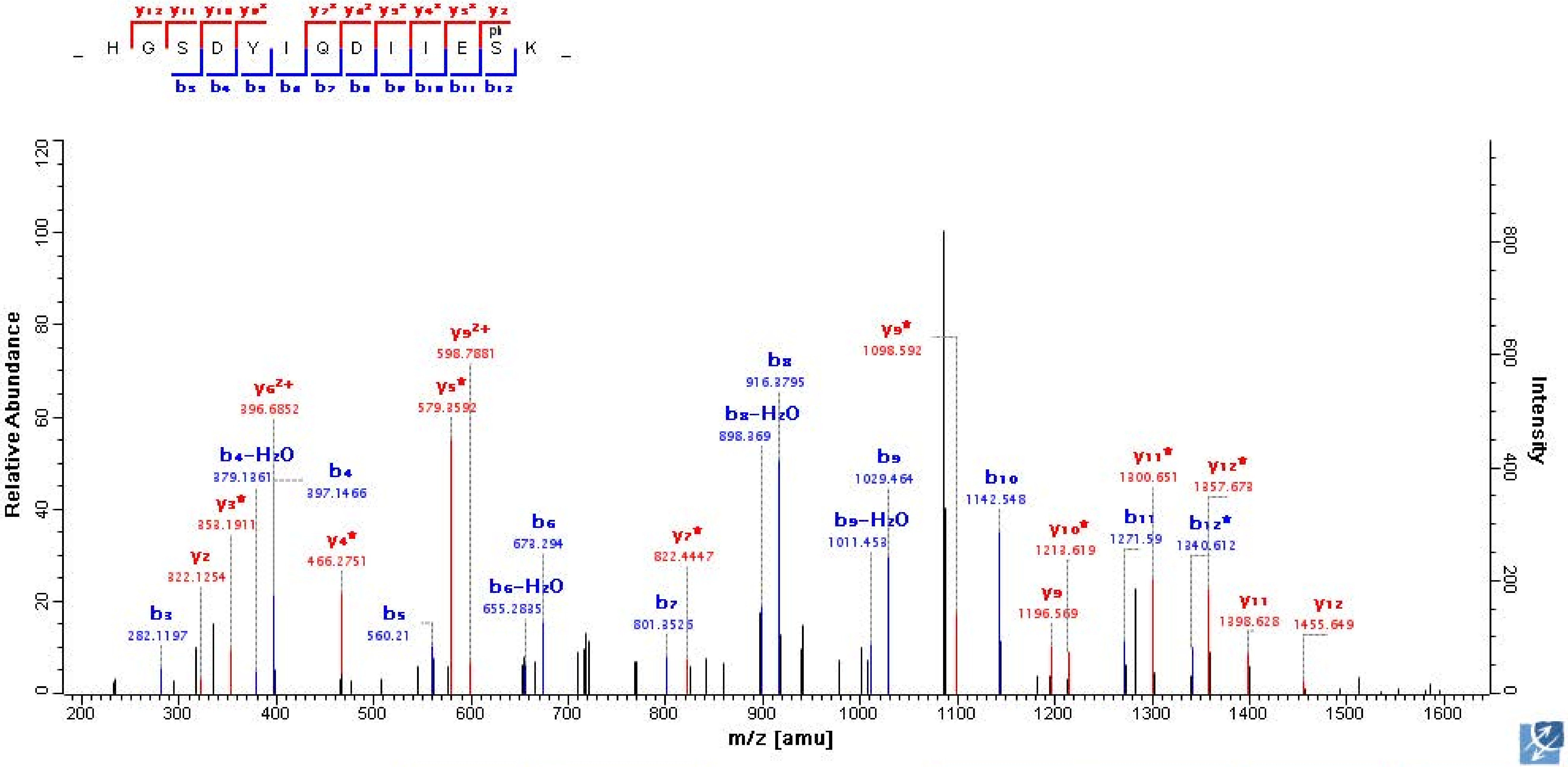
Mass:	1237.66843
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.37389
Mass Error [ppm]:	0.099407
PEP:	0.043481
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	42 %
Protein Localisation:	361 ... 370

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	9				
+0.1619855	250.20050228	2	K	8	1141.6199146		1141.6199146	
	417.1988611	3	S	7	1005.5107528	+0.1113176	503.25901461	+0.0703921
	546.24145419	4	E	6	838.51239394	+0.3244591	838.51239394	
	659.32551817	5	I	5	709.46980085		709.46980085	
	787.38409568	6	Q	4	596.38573687		596.38573687	
	874.41612409	7	S	3	468.32715935		468.32715935	
	987.50018807	8	I	2	381.29513094		381.29513094	
-0.2536856	1100.5842521	9	I	1	268.21106696		268.21106696	
		10	K	0	155.12700298		155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber:	10768
Protein:	BSU25870; yqcF
Peptide Score:	182.89
Method:	ITMS; CID; 3



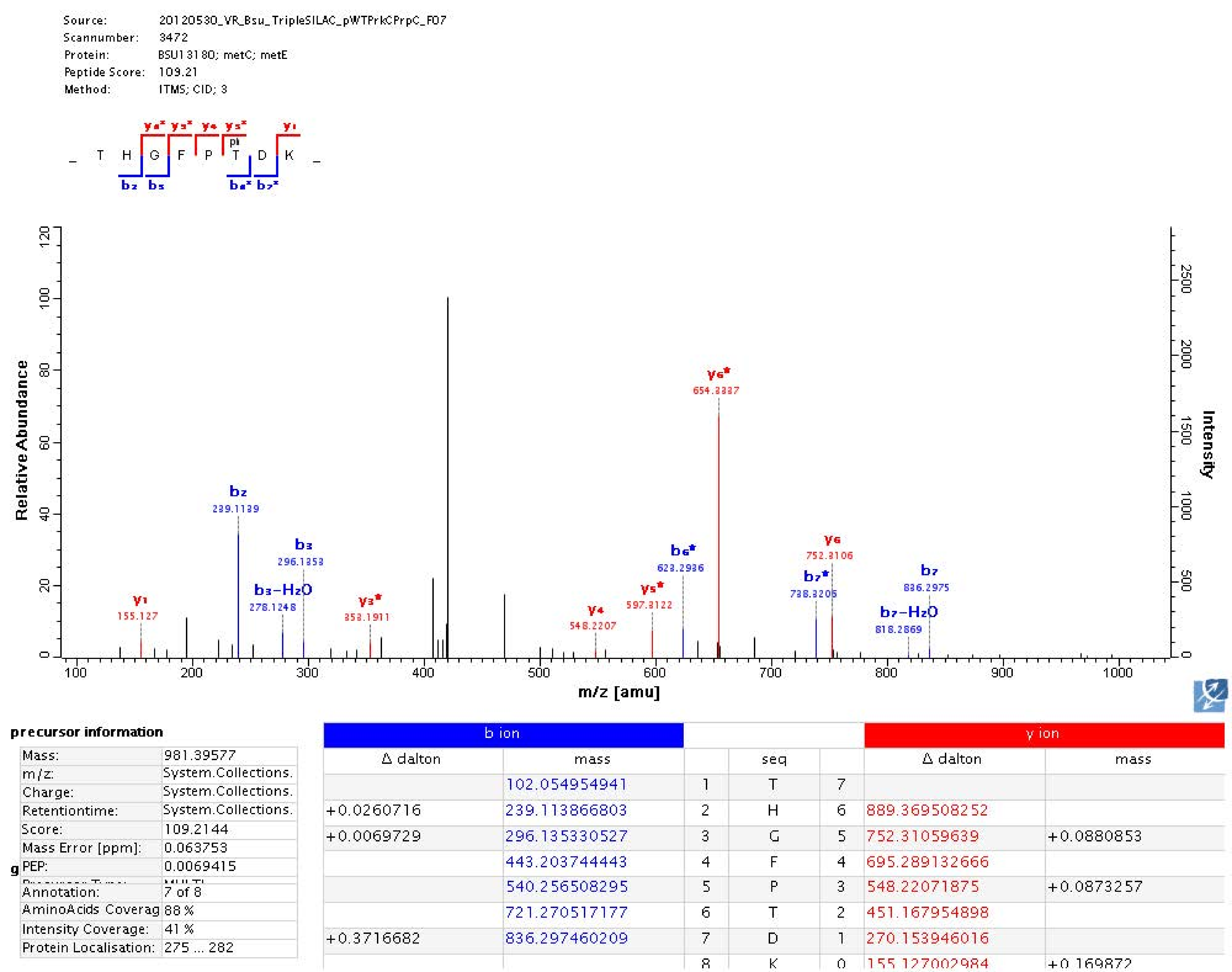
precursor information

Mass:	1583.68696
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	182.8864
Mass Error [ppm]:	0.059133
PEP:	1.0181E-35
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	45 %
Protein Localisation:	167 ... 179

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833	1	H	12				
	195.08765205	2	G	11	1455.6494311	+0.4315015	1455.6494311	
-0.0040799	282.11968046	3	S	10	1398.6279674	+0.1023793	1398.6279674	
+0.099104	397.14662349	4	D	9	1311.595939		1311.595939	
+0.0705045	560.20995203	5	Y	8	1196.5689959	-0.0520281	598.78813619	+0.347545
+0.1443995	673.29401601	6	I	7	1033.5056674		1033.5056674	
+0.1511907	801.35259352	7	Q	6	920.4216034		920.4216034	
+0.197856	916.37953656	8	D	5	792.36302589		396.68515118	-0.0514842
+0.0835186	1029.4636005	9	I	4	677.33608286		677.33608286	
-0.0038413	1142.5476645	10	I	3	564.25201888		564.25201888	
+0.1715832	1271.5902576	11	E	2	451.1679549		451.1679549	
	1438.5886164	12	S	1	322.1253618	+0.2249495	322.1253618	
		13	K	0	155.12700298		155.12700298	

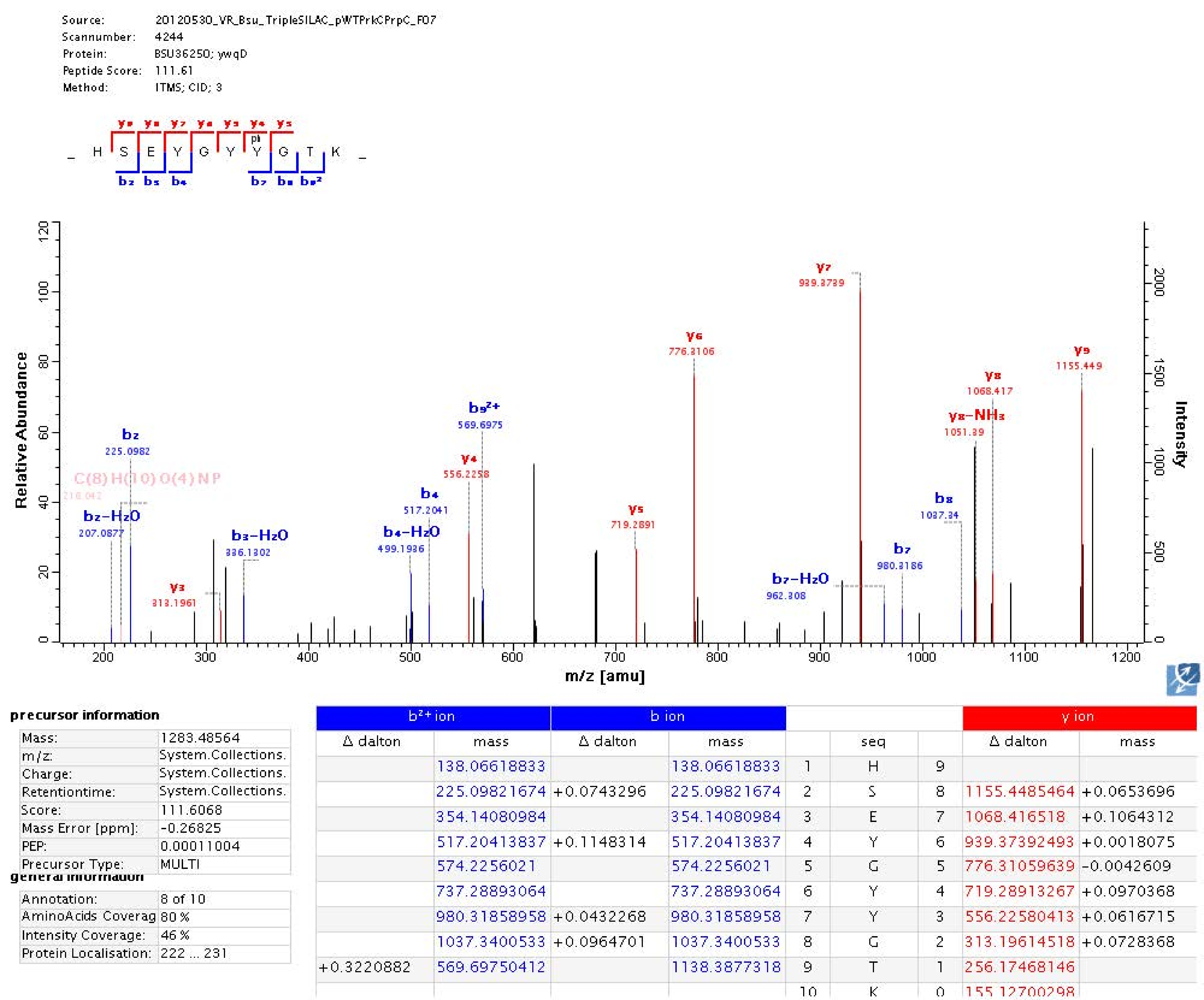


Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber: 3472
Protein: BSU13180; metC; metE
Peptide Score: 109.21
Method: ITMS; CID; 3

precursor information

Mass:	981.39577
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.2144
Mass Error [ppm]:	0.063753
PEP:	0.0069415
Precursor Type:	MULTI
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	41 %
Protein Localisation:	275 ... 282

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	102.054954941	1	T	7		
+0.0260716	239.113866803	2	H	6	889.369508252	
+0.0069729	296.135330527	3	G	5	752.31059639	+0.0880853
	443.203744443	4	F	4	695.289132666	
	540.256508295	5	P	3	548.22071875	+0.0873257
	721.270517177	6	T	2	451.167954898	
+0.3716682	836.297460209	7	D	1	270.153946016	
		8	K	0	155.127002984	+0.169872



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber:	4244
Protein:	BSU36250; ywqD
Peptide Score:	111.61
Method:	ITMS; CID; 3

precursor information

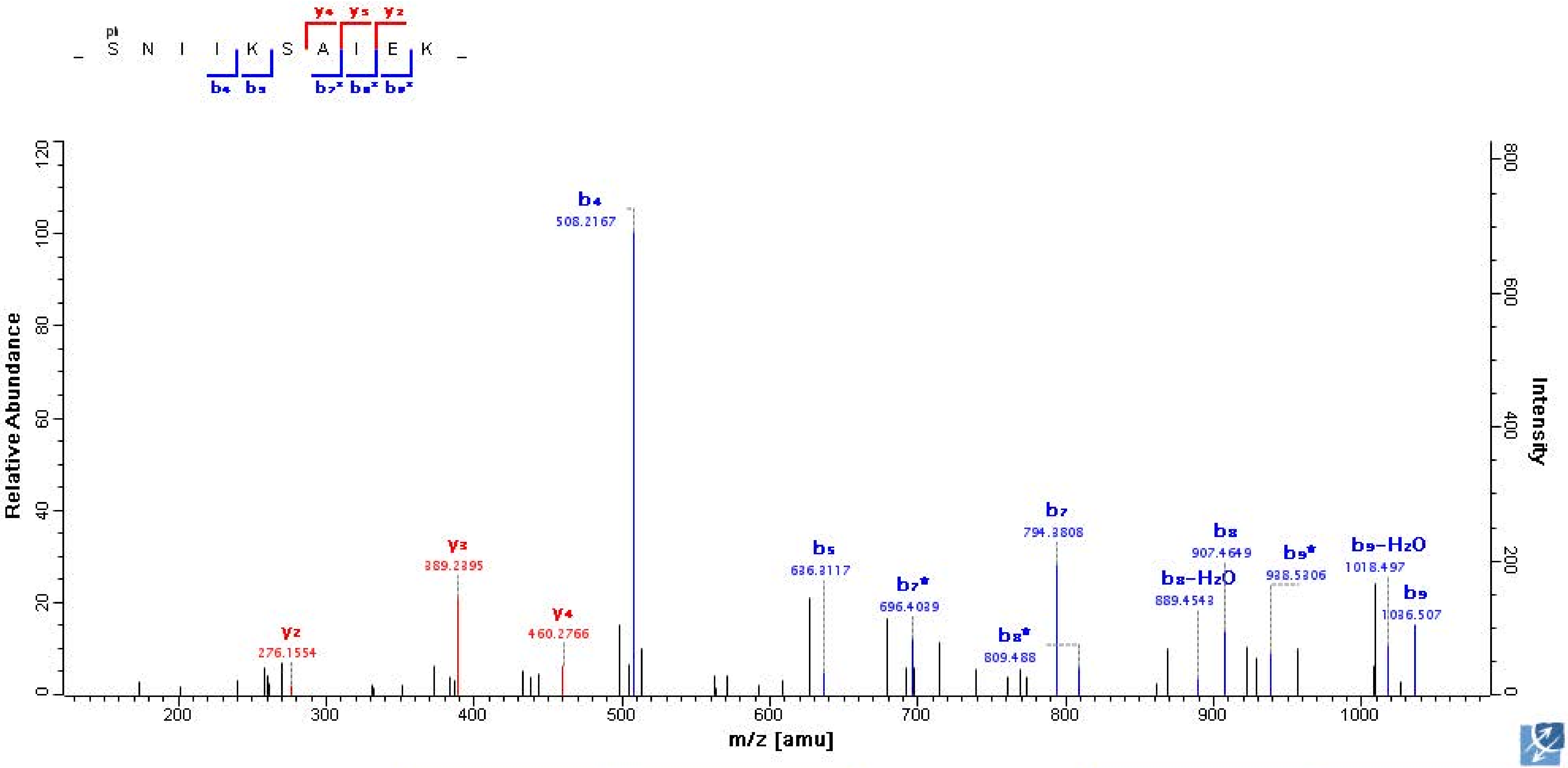
Mass:	1283.48564
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.6068
Mass Error [ppm]:	-0.26825
PEP:	0.00011004
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	46 %
Protein Localisation:	222 ... 231

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.06618833		138.06618833	1	H	9		
	225.09821674	+0.0743296	225.09821674	2	S	8	1155.4485464	+0.0653696
	354.14080984		354.14080984	3	E	7	1068.416518	+0.1064312
	517.20413837	+0.1148314	517.20413837	4	Y	6	939.37392493	+0.0018075
	574.2256021		574.2256021	5	G	5	776.31059639	-0.0042609
	737.28893064		737.28893064	6	Y	4	719.28913267	+0.0970368
	980.31858958	+0.0432268	980.31858958	7	Y	3	556.22580413	+0.0616715
	1037.3400533	+0.0964701	1037.3400533	8	G	2	313.19614518	+0.0728368
+0.3220882	569.69750412		1138.3877318	9	T	1	256.17468146	
				10	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber: 6090
Protein: BSU13330; ykoL
Peptide Score: 56.2
Method: ITMS; CID; 3



precursor information

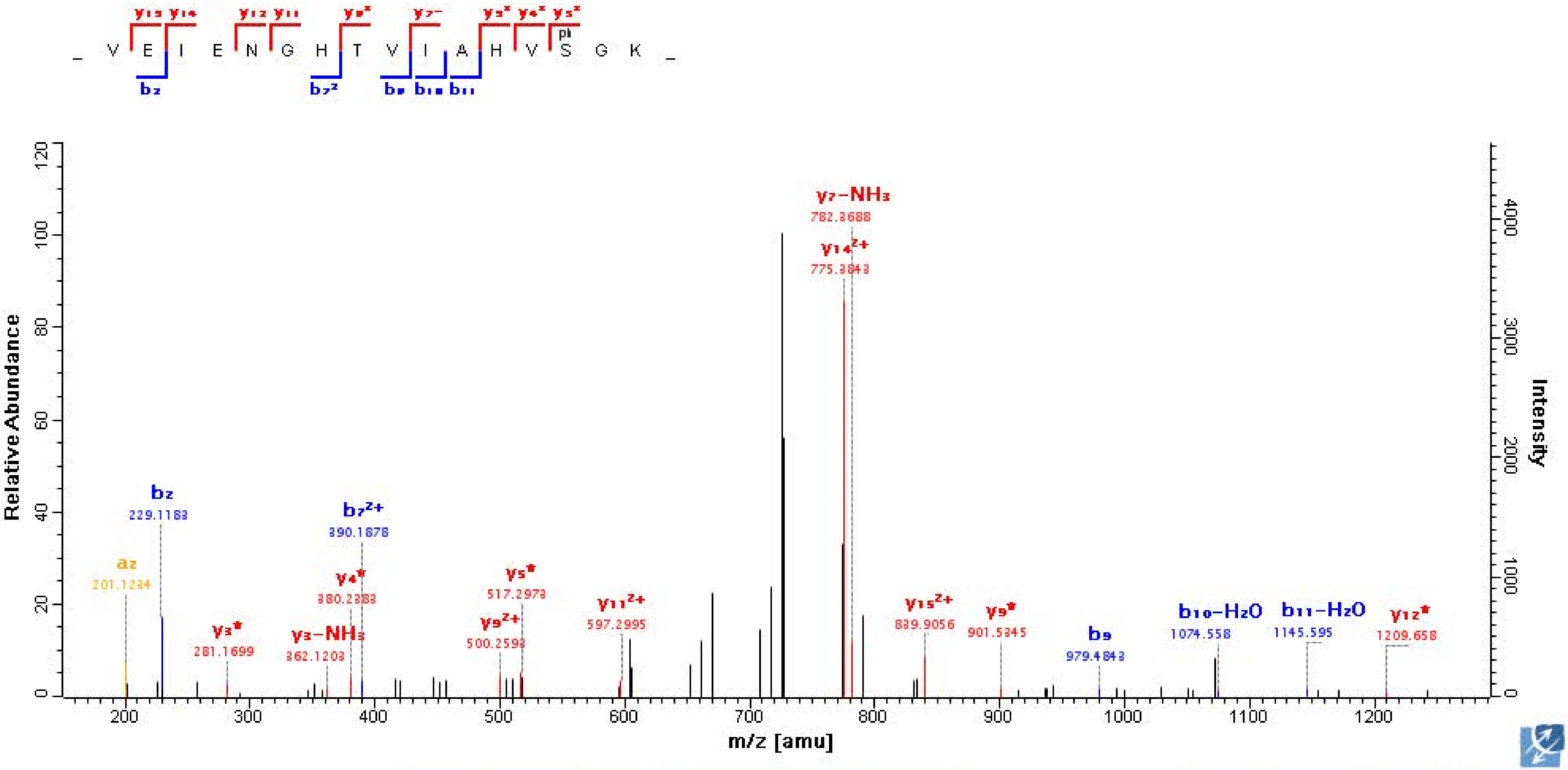
Mass:	1181.60603
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	56.20483
Mass Error [ppm]:	0.27174
PEP:	0.11663
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	47 %
Protein Localisation:	2 ... 11

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	168.005635285	1	S	9		
	282.048562732	2	N	8	1015.614621871	
	395.132626712	3	I	7	901.571694423	
-0.2542273	508.216690693	4	I	6	788.487630443	
+0.1111979	636.311653711	5	K	5	675.403566463	
	723.34368212	6	S	4	547.308603445	
+0.0697656	794.380795908	7	A	3	460.276575035	-0.2804813
+0.2877646	907.464859889	8	I	2	389.239461247	+0.0697429
+0.0982599	1036.507452985	9	E	1	276.155397267	+0.2708112
		10	K	0	147.112804171	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber: 6256
Protein: BSU01390; infA
Peptide Score: 60.92
Method: ITMS; CID; 3



precursor information

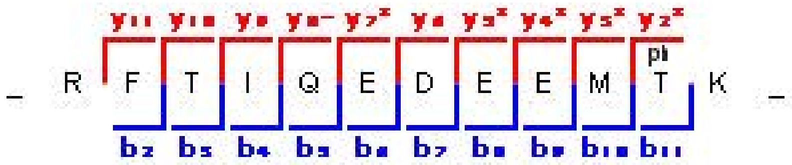
Mass:	1768.852
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	60.91842
Mass Error [ppm]:	0.61402
PEP:	0.010692
Precursor Type:	MULTI

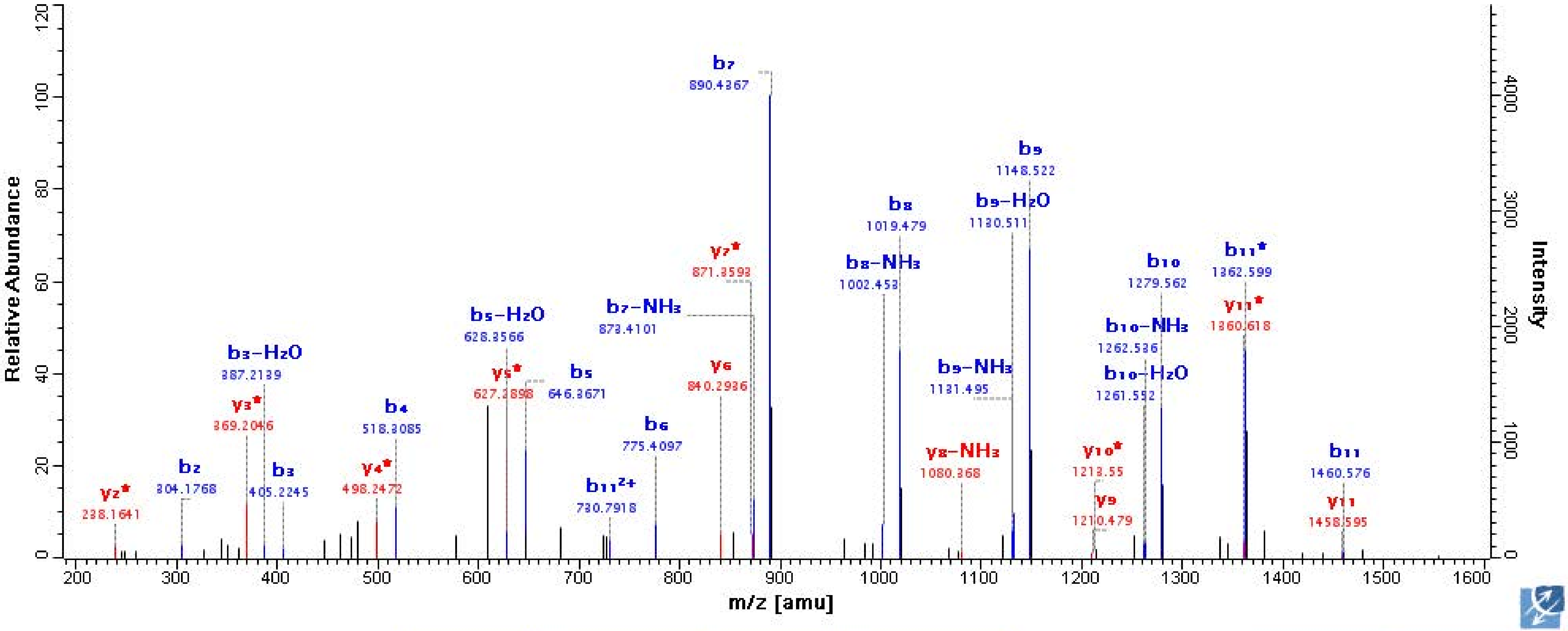
general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	28 %
Protein Localisation:	24 ... 39

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.0808		100.076		100.076	1	V	15				
-0.0334	201.123		229.118	+0.07044	229.118	2	E	14	1678.8		839.906	+0.2096
	314.207		342.202		342.202	3	I	13	1549.76		775.384	+0.2212
	443.25		471.245		471.245	4	E	12	1436.68		1436.68	
	557.293		585.288		585.288	5	N	11	1307.63		1307.63	
	614.314		642.309		642.309	6	G	10	1193.59		597.3	-0.4575
	751.373	+0.05492	390.188		779.368	7	H	9	1136.57		1136.57	
	852.421		880.416		880.416	8	T	8	999.511		500.259	+0.2465
	951.489		979.484	+0.16142	979.484	9	V	7	898.464		898.464	
	1064.57		1092.57		1092.57	10	I	6	799.395		799.395	
	1135.61		1163.61		1163.61	11	A	5	686.311		686.311	
	1272.67		1300.66		1300.66	12	H	4	615.274		615.274	
	1371.74		1399.73		1399.73	13	V	3	478.215		478.215	
	1538.74		1566.73		1566.73	14	S	2	379.147		379.147	
	1595.76		1623.75		1623.75	15	G	1	212.148		212.148	
						16	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber: 6537
Protein: BSU15770; prkC; yloP
Peptide Score: 186.16
Method: ITMS; CID; 3





precursor information

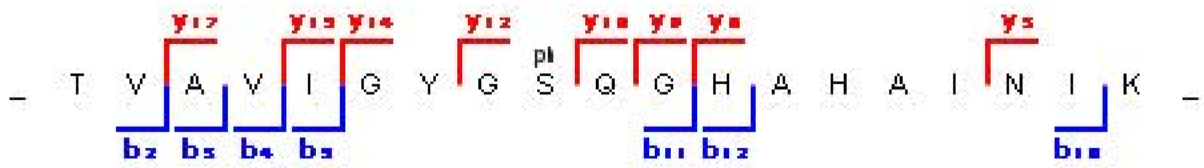
Mass:	1613.68922
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	186.1593
Mass Error [ppm]:	0.27027
PEP:	1.3064E-71
Precursor Type:	ISO

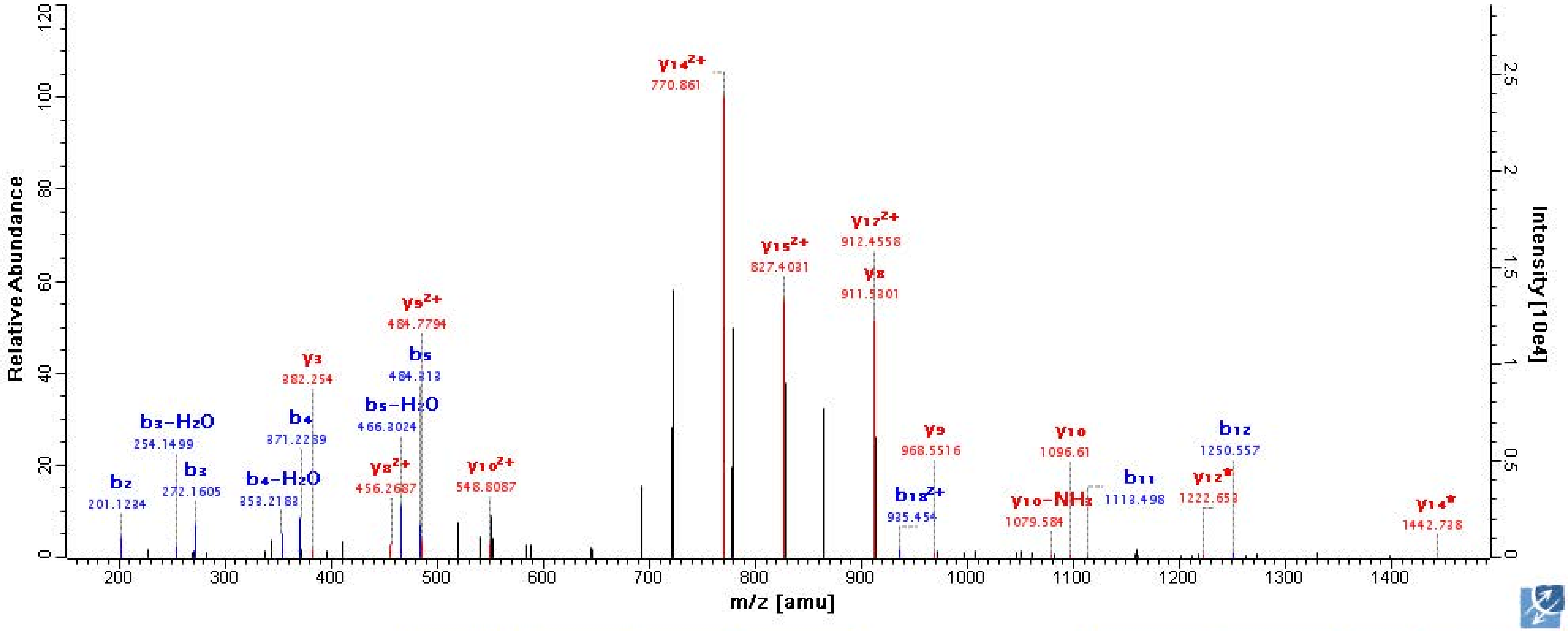
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	64 %
Protein Localisation:	280 ... 291

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.10838749		157.10838749	1	R	11		
	304.17680141	+0.0821402	304.17680141	2	F	10	1458.5949527	+0.3021421
	405.22447988	+0.0070875	405.22447988	3	T	9	1311.5265388	
	518.30854387	+0.0503429	518.30854387	4	I	8	1210.4788603	-0.1595243
	646.36712138	+0.1165212	646.36712138	5	Q	7	1097.3947963	
	775.40971447	+0.0466454	775.40971447	6	E	6	969.33621879	
	890.43665751	-0.0269285	890.43665751	7	D	5	840.2936257	+0.1278221
	1019.4792506	+0.0335057	1019.4792506	8	E	4	725.26668266	
	1148.5218437	+0.1263497	1148.5218437	9	E	3	596.22408957	
	1279.5623283	+0.0775643	1279.5623283	10	M	2	467.18149647	
-0.4428688	730.79180683	-0.4105657	1460.5763372	11	T	1	336.14101187	
				12	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber: 7532
Protein: BSU28290; ilvC
Peptide Score: 93.91
Method: ITMS; CID; 3





precursor information

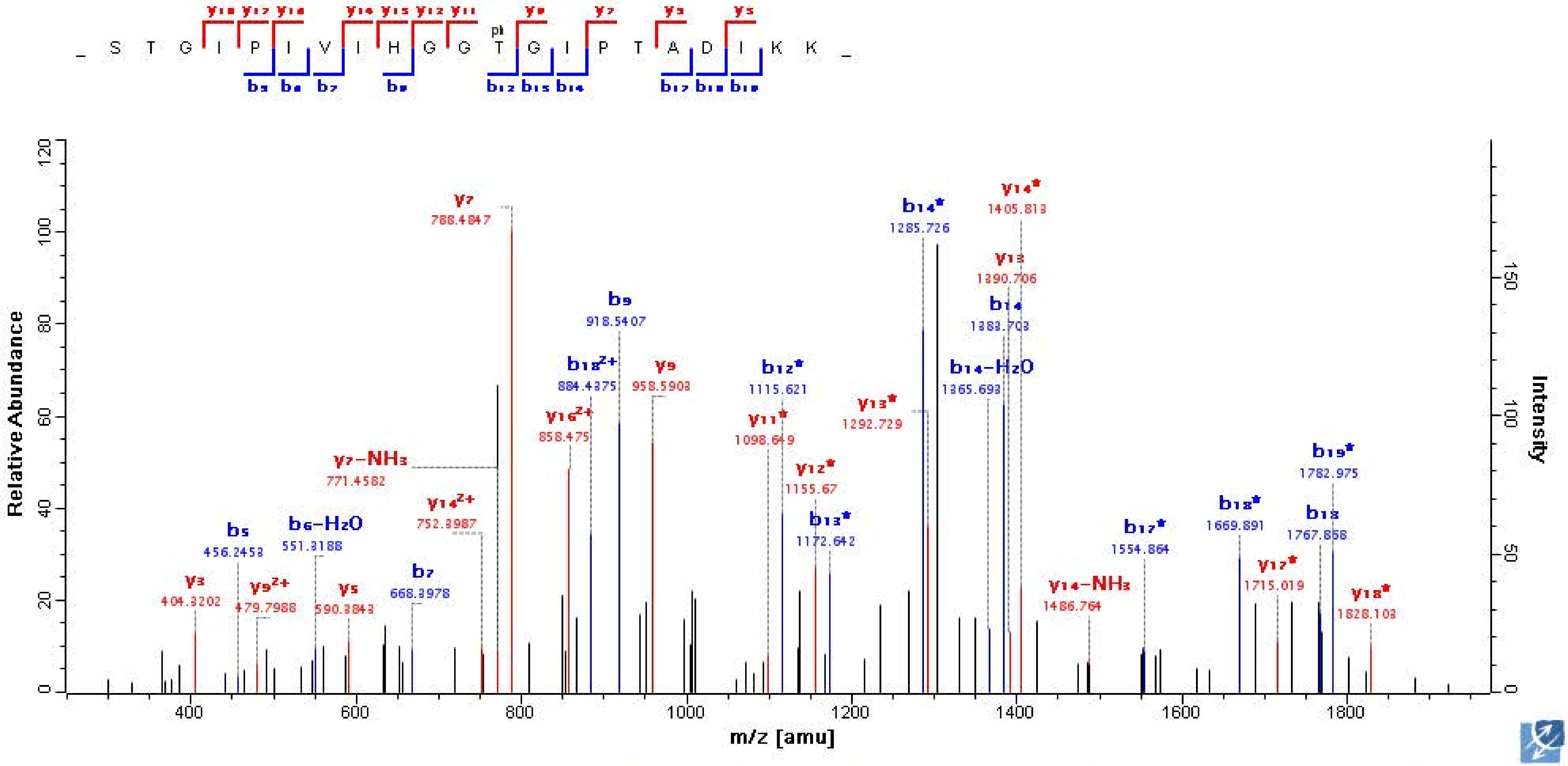
Mass:	2014.99861
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.90913
Mass Error [ppm]:	-0.17926
PEP:	2.8119E-07
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	43 %
Protein Localisation:	19 ... 37

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	18				
	201.1234	-0.000719	201.1234	2	V	17	1922.973		1922.973	
	272.1605	+0.044992	272.1605	3	A	16	1823.904		912.4558	+0.000726
	371.2289	-0.120925	371.2289	4	V	15	1752.867		1752.867	
	484.313	-0.152072	484.313	5	I	14	1653.799		827.4031	+0.018761
	541.3344		541.3344	6	G	13	1540.715		770.861	+0.190065
	704.3978		704.3978	7	Y	12	1483.693		1483.693	
	761.4192		761.4192	8	G	11	1320.63		1320.63	
	928.4176		928.4176	9	S	10	1263.609		1263.609	
	1056.476		1056.476	10	Q	9	1096.61	+0.011797	548.8087	+0.077334
	1113.498	+0.211734	1113.498	11	G	8	968.5516	+0.086915	484.7794	+0.381403
	1250.557	+0.196035	1250.557	12	H	7	911.5301	-0.155049	456.2687	-0.220475
	1321.594		1321.594	13	A	6	774.4712		774.4712	
	1458.653		1458.653	14	H	5	703.4341		703.4341	
	1529.69		1529.69	15	A	4	566.3752		566.3752	
	1642.774		1642.774	16	I	3	495.3381		495.3381	
	1756.817		1756.817	17	N	2	382.254	+0.208713	382.254	
+0.338786	935.454		1869.901	18	I	1	268.2111		268.2111	
				19	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber:	9544
Protein:	BSU37120; fba; fba1; fbaA; tsr
Peptide Score:	119.38
Method:	ITMS; CID; 3



precursor information

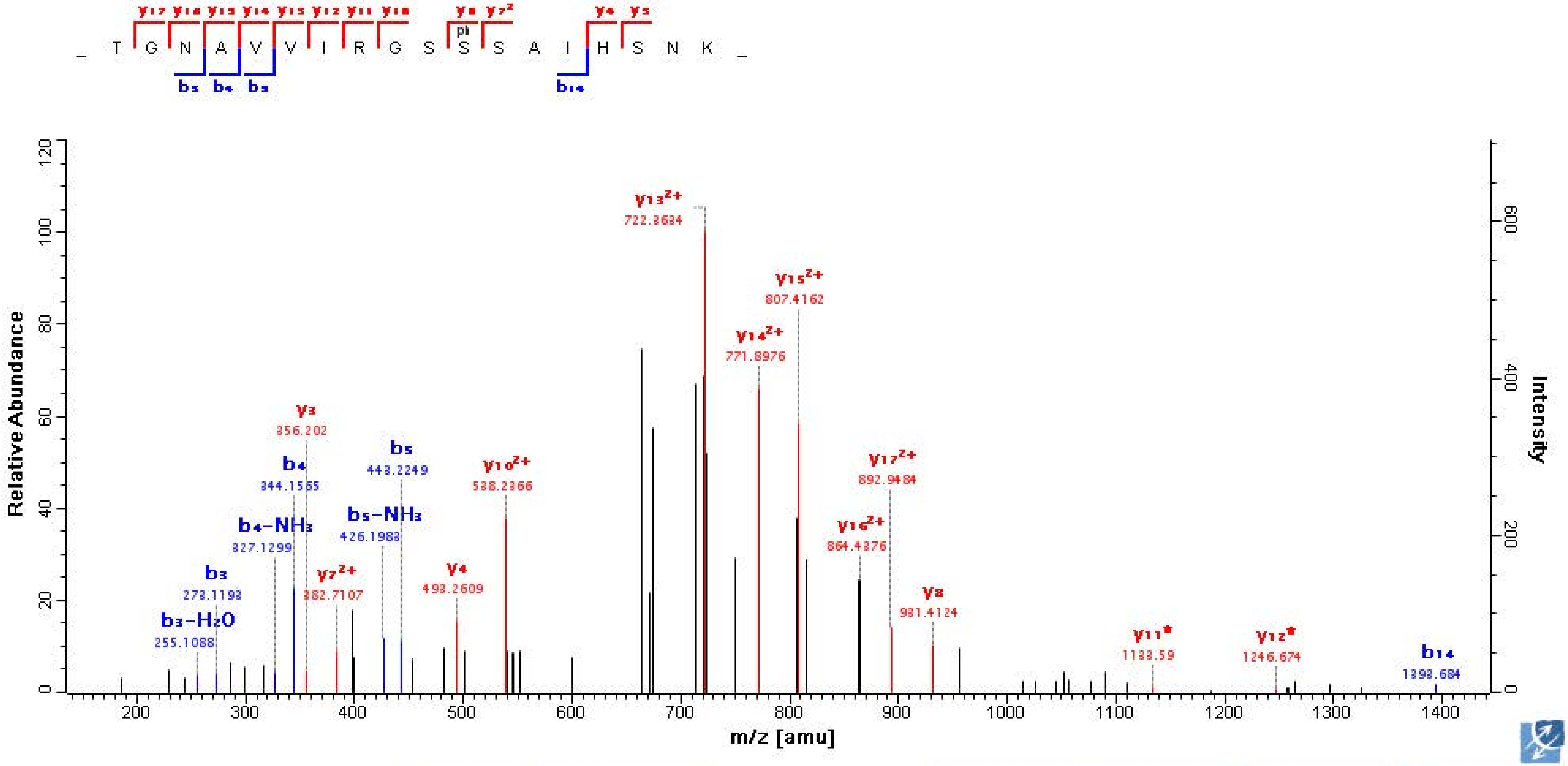
Mass:	2154.14536
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	119.3771
Mass Error [ppm]:	0.17765
PEP:	5.9379E-17
Precursor Type:	MULTI

general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	51 %
Protein Localisation:	201 ... 221

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	20				
	189.087		189.087	2	T	19	2084.149		2084.149	
	246.1084		246.1084	3	G	18	1983.101		1983.101	
	359.1925		359.1925	4	I	17	1926.079		1926.079	
	456.2453	-0.06162	456.2453	5	P	16	1812.995		1812.995	
	569.3293		569.3293	6	I	15	1715.943		858.475	-0.484971
	668.3978	-0.071642	668.3978	7	V	14	1602.859		1602.859	
	781.4818		781.4818	8	I	13	1503.79		752.3987	+0.022665
	918.5407	+0.166791	918.5407	9	H	12	1390.706	+0.090283	1390.706	
	975.5622		975.5622	10	G	11	1253.647		1253.647	
	1032.584		1032.584	11	G	10	1196.626		1196.626	
	1213.598		1213.598	12	T	9	1139.604		1139.604	
	1270.619		1270.619	13	G	8	958.5903	-0.00737	479.7988	+0.17682
	1383.703	+0.022515	1383.703	14	I	7	901.5688		901.5688	
	1480.756		1480.756	15	P	6	788.4847	+0.097547	788.4847	
	1581.804		1581.804	16	T	5	691.432		691.432	
	1652.841		1652.841	17	A	4	590.3843	+0.101676	590.3843	
-0.297469	884.4375	+0.094588	1767.868	18	D	3	519.3472		519.3472	
	1880.952		1880.952	19	I	2	404.3202	+0.038597	404.3202	
	2017.061		2017.061	20	K	1	291.2362		291.2362	
				21	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F09
Scannumber: 5003
Protein: BSU13130; proA
Peptide Score: 63.06
Method: ITMS; CID; 3



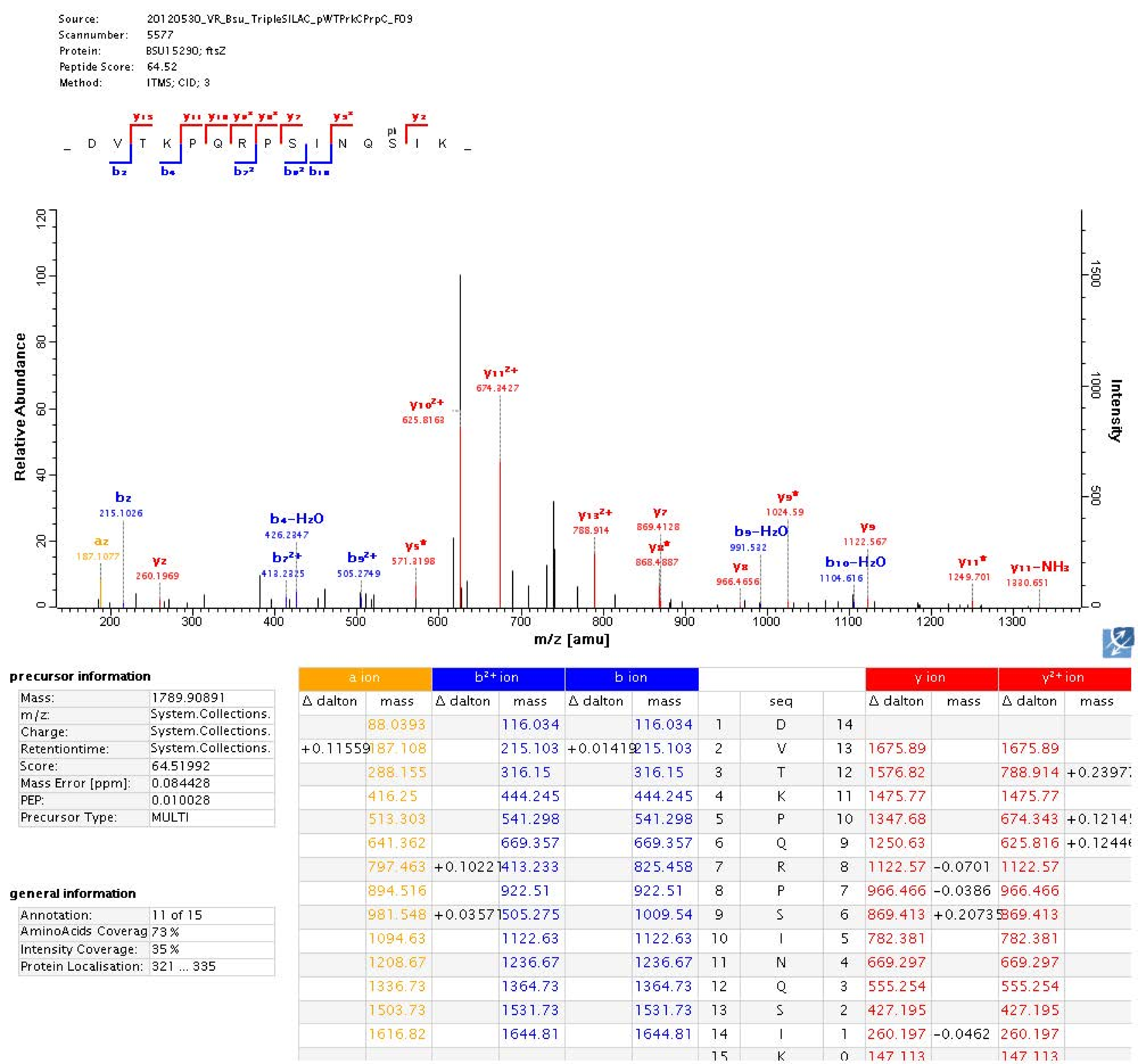
precursor information

Mass:	1876.91581
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.06153
Mass Error [ppm]:	0.089223
PEP:	0.0062925
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	37 %
Protein Localisation:	138 ... 155

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.05495494	1	T	17				
	159.07641866	2	G	16	1784.8894356		892.94835605	+0.2676474
-0.0804057	273.11934611	3	N	15	1727.8679719		864.43762419	-0.0482199
+0.2035255	344.1564599	4	A	14	1613.8250445		807.41616046	+0.3923723
+0.1476848	443.22487382	5	V	13	1542.7879307		771.89760357	+0.0074868
	542.29328773	6	V	12	1443.7195168		722.36339661	-0.0476617
	655.37735171	7	I	11	1344.6511028		1344.6511028	
	811.47846274	8	R	10	1231.5670389		1231.5670389	
	868.49992646	9	G	9	1075.4659278		538.23660215	+0.0473944
	955.53195487	10	S	8	1018.4444641		1018.4444641	
	1122.5303137	11	S	7	931.4124357	+0.0355623	931.4124357	
	1209.5623421	12	S	6	764.41407688		382.71067667	+0.1063399
	1280.5994559	13	A	5	677.38204847		677.38204847	
-0.3060785	1393.6835199	14	I	4	606.34493468		606.34493468	
	1530.7424317	15	H	3	493.2608707	+0.0980771	493.2608707	
	1617.7744601	16	S	2	356.20195884	+0.0215519	356.20195884	
	1731.8173876	17	N	1	269.16993043		269.16993043	
		18	K	0	155.12700298		155.12700298	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F09
Scannumber: 5577
Protein: BSU15290; ftsZ
Peptide Score: 64.52
Method: ITMS; CID; 3

precursor information

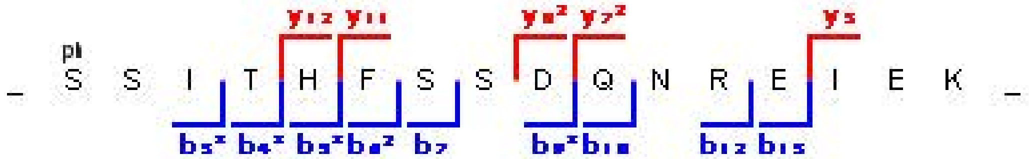
Mass:	1789.90891
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.51992
Mass Error [ppm]:	0.084428
PEP:	0.010028
Precursor Type:	MULTI

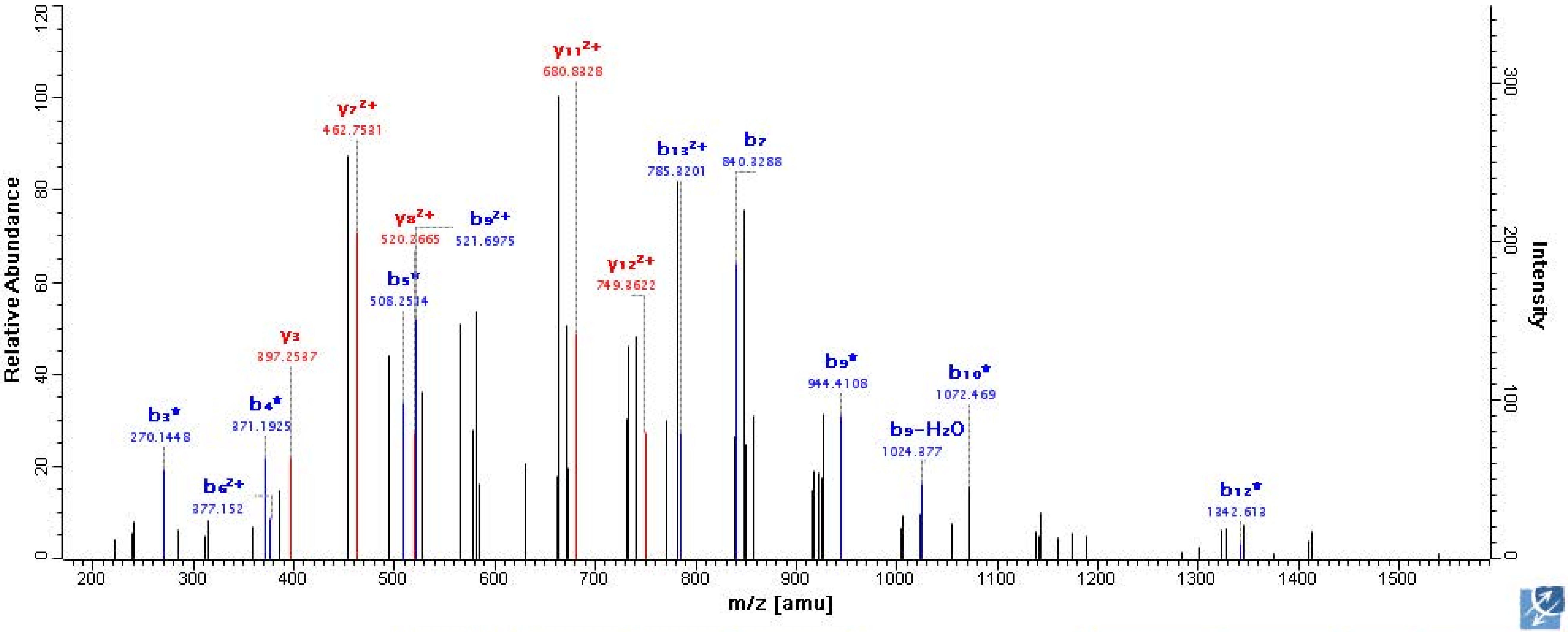
general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	35 %
Protein Localisation:	321 ... 335

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		116.034		116.034	1	D	14				
+0.11559	187.108		215.103	+0.01419	215.103	2	V	13	1675.89		1675.89	
	288.155		316.15		316.15	3	T	12	1576.82		788.914	+0.2397
	416.25		444.245		444.245	4	K	11	1475.77		1475.77	
	513.303		541.298		541.298	5	P	10	1347.68		674.343	+0.1214
	641.362		669.357		669.357	6	Q	9	1250.63		625.816	+0.1244
	797.463	+0.10221	413.233		825.458	7	R	8	1122.57	-0.0701	1122.57	
	894.516		922.51		922.51	8	P	7	966.466	-0.0386	966.466	
	981.548	+0.03571	505.275		1009.54	9	S	6	869.413	+0.20735	869.413	
	1094.63		1122.63		1122.63	10	I	5	782.381		782.381	
	1208.67		1236.67		1236.67	11	N	4	669.297		669.297	
	1336.73		1364.73		1364.73	12	Q	3	555.254		555.254	
	1503.73		1531.73		1531.73	13	S	2	427.195		427.195	
	1616.82		1644.81		1644.81	14	I	1	260.197	-0.0462	260.197	
						15	K	0	147.113		147.113	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F09
Scannumber:	5787
Protein:	BSU05000; yddK
Peptide Score:	50.87
Method:	ITMS; CID; 3





precursor information

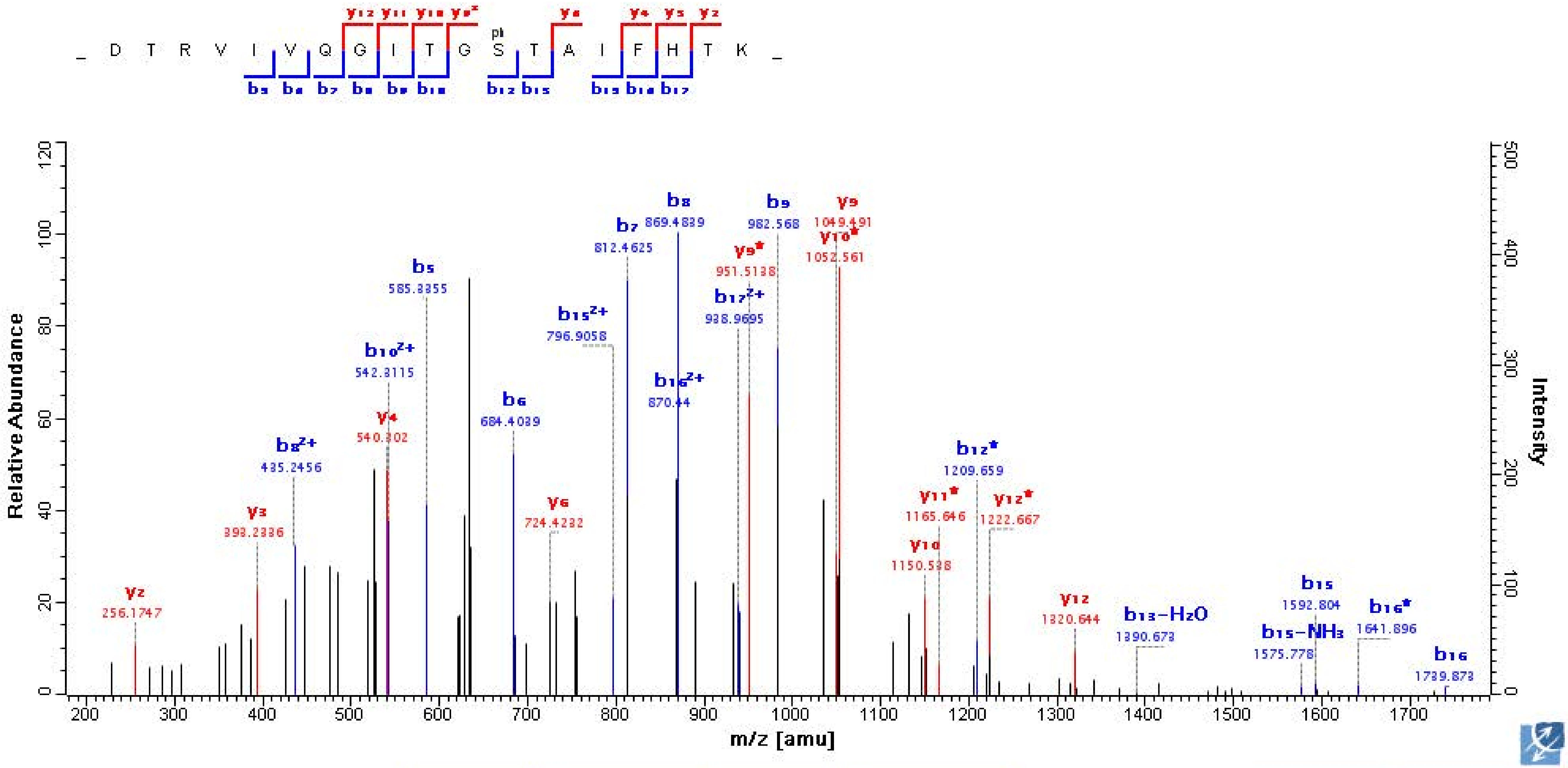
Mass:	1956.85791
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	50.87437
Mass Error [ppm]:	0.033205
PEP:	0.044176
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	28 %
Protein Localisation:	99 ... 114

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	15				
	255.0377		255.0377	2	S	14	1798.881		1798.881	
	368.1217		368.1217	3	I	13	1711.849		1711.849	
	469.1694		469.1694	4	T	12	1598.765		1598.765	
	606.2283		606.2283	5	H	11	1497.717		749.3622	+0.370736
-0.463894	377.152		753.2967	6	F	10	1360.658		680.8328	+0.155563
	840.3288	-0.363367	840.3288	7	S	9	1213.59		1213.59	
	927.3608		927.3608	8	S	8	1126.558		1126.558	
-0.03631	521.6975		1042.388	9	D	7	1039.526		520.2665	+0.212765
	1170.446		1170.446	10	Q	6	924.4989		462.7531	+0.169718
	1284.489		1284.489	11	N	5	796.4403		796.4403	
	1440.59		1440.59	12	R	4	682.3974		682.3974	
-0.062723	785.3201		1569.633	13	E	3	526.2963		526.2963	
	1682.717		1682.717	14	I	2	397.2537	+0.115603	397.2537	
	1811.76		1811.76	15	E	1	284.1696		284.1696	
				16	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F09
Scannumber:	9885
Protein:	BSU16100; sucD
Peptide Score:	127.5
Method:	ITMS; CID; 3



precursor information

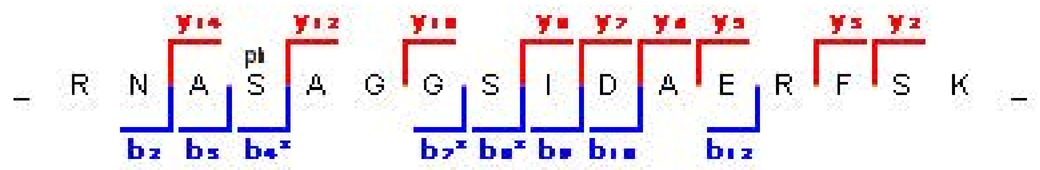
Mass:	2123.07742
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	127.4995
Mass Error [ppm]:	-0.094755
PEP:	1.58E-20
Precursor Type:	MULTI

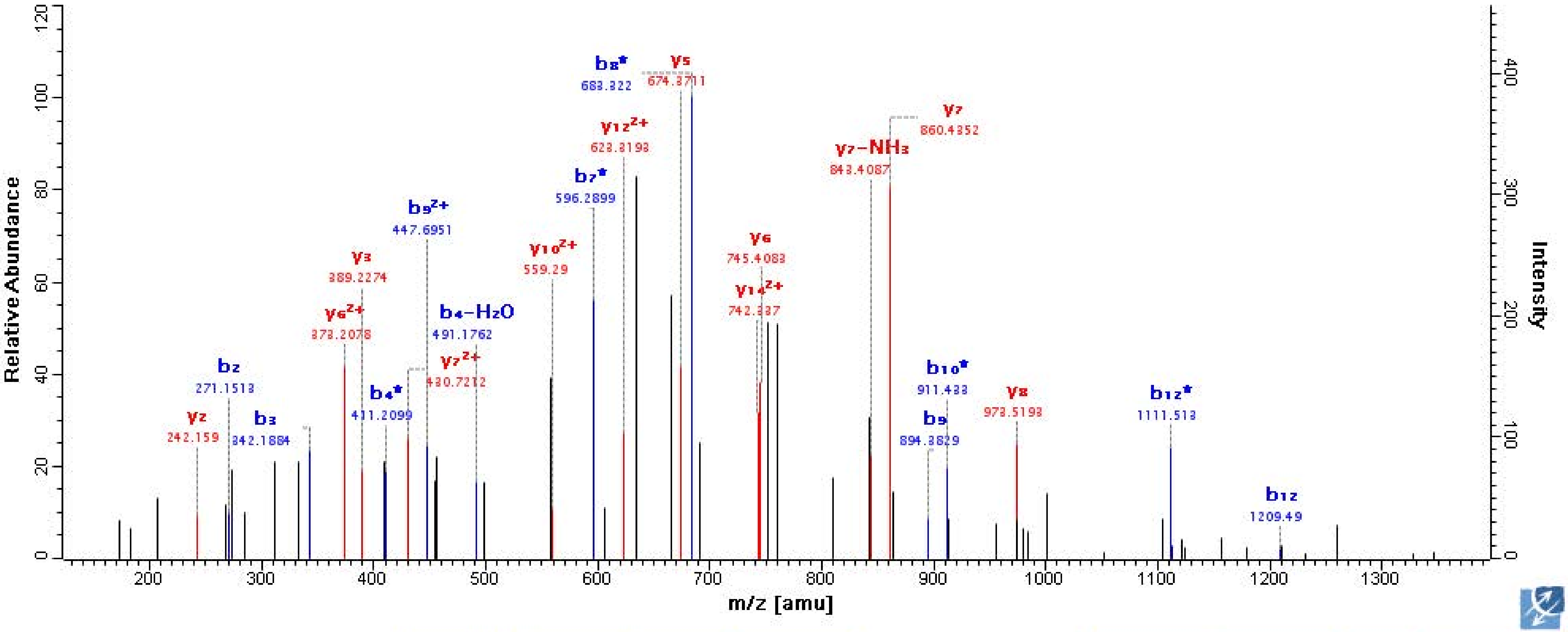
general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	46 %
Protein Localisation:	8 ... 26

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	18		
	217.08189797		217.08189797	2	T	17	2017.072151	
	373.183009		373.183009	3	R	16	1916.0244726	
	472.25142292		472.25142292	4	V	15	1759.9233615	
	585.3354869	-0.0881114	585.3354869	5	I	14	1660.8549476	
	684.40390081	-0.0683906	684.40390081	6	V	13	1547.7708836	
	812.46247833	+0.1201022	812.46247833	7	Q	12	1448.7024697	
+0.2584191	435.24560926	+0.2595272	869.48394205	8	G	11	1320.6438922	+0.0824262
	982.56800603	-0.0311408	982.56800603	9	I	10	1263.6224285	
+0.1724062	542.31148048		1083.6156845	10	T	9	1150.5383645	+0.097866
	1140.6371482		1140.6371482	11	G	8	1049.490686	+0.1224732
	1307.635507		1307.635507	12	S	7	992.4692223	
	1408.6831855		1408.6831855	13	T	6	825.47086348	
	1479.7202993		1479.7202993	14	A	5	724.423185	-0.1206337
+0.4615507	796.90581988	-0.0438652	1592.8043633	15	I	4	653.38607122	
+0.1692871	870.44002684	+0.1488292	1739.8727772	16	F	3	540.30200724	+0.0289254
-0.0908207	938.96948277		1876.9316891	17	H	2	393.23359332	+0.1426884
	1977.9793675		1977.9793675	18	T	1	256.17468146	-0.0794971
				19	K	0	155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber:	5267
Protein:	BSU03480; srfA; srfA1; srfAA
Peptide Score:	92.8
Method:	ITMS; CID; 3





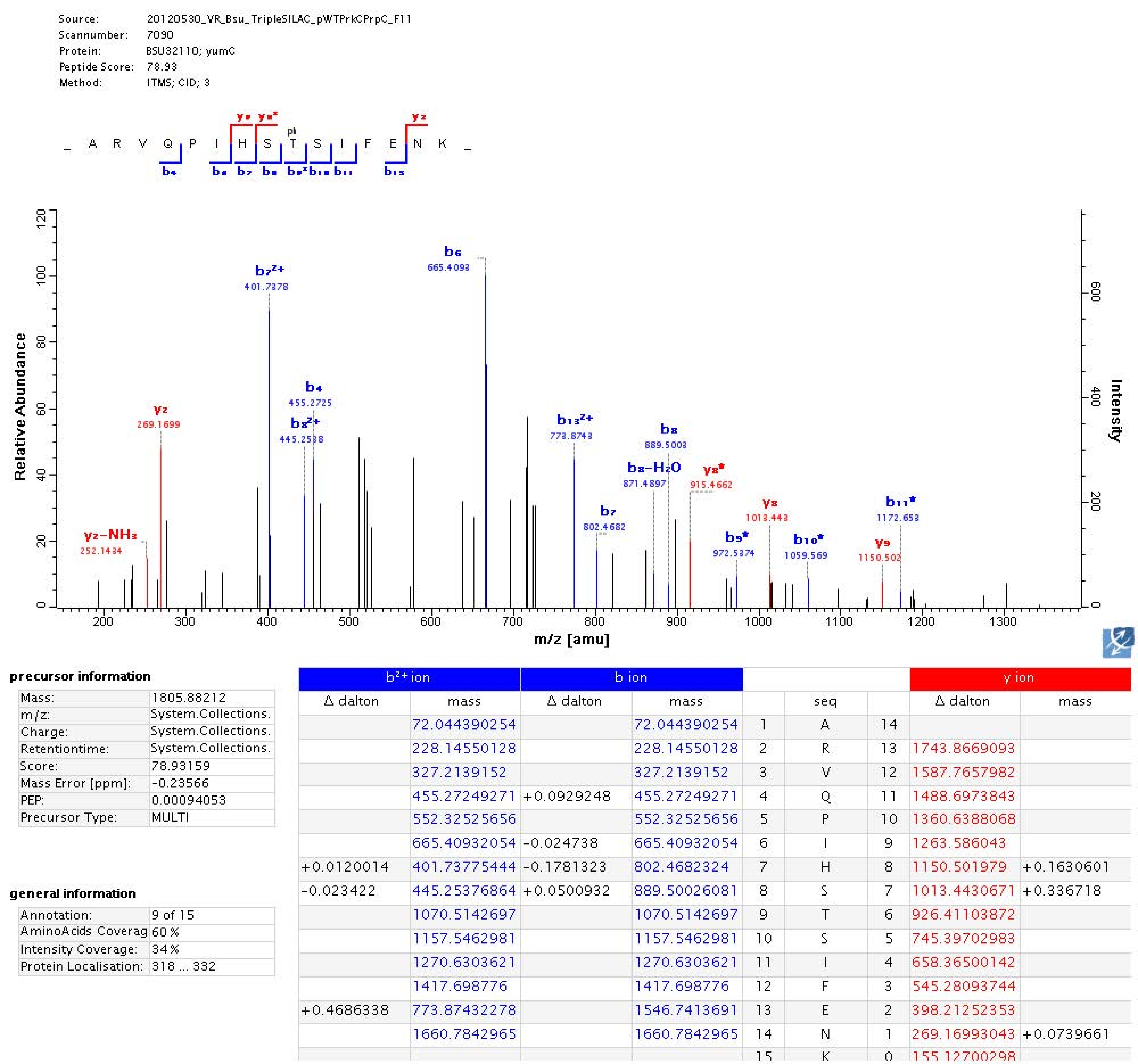
precursor information

Mass:	1744.7891
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	92.80044
Mass Error [ppm]:	-0.15486
PEP:	6.7929E-06
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	48 %
Protein Localisation:	214 ... 229

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	15				
	271.1513	-0.320504	271.1513	2	N	14	1597.71		1597.71	
	342.1884	-0.03108	342.1884	3	A	13	1483.667		742.337	+0.299369
	509.1868		509.1868	4	S	12	1412.63		1412.63	
	580.2239		580.2239	5	A	11	1245.631		623.3193	+0.335904
	637.2454		637.2454	6	G	10	1174.594		1174.594	
	694.2668		694.2668	7	G	9	1117.573		559.29	-0.178996
	781.2989		781.2989	8	S	8	1060.551		1060.551	
-0.276642	447.6951	+0.035353	894.3829	9	I	7	973.5193	+0.003496	973.5193	
	1009.41		1009.41	10	D	6	860.4352	-0.076991	430.7212	-0.145863
	1080.447		1080.447	11	A	5	745.4083	-0.028441	373.2078	+0.126947
	1209.49	-0.246529	1209.49	12	E	4	674.3711	+0.132879	674.3711	
	1365.591		1365.591	13	R	3	545.3286		545.3286	
	1512.659		1512.659	14	F	2	389.2274	+0.432589	389.2274	
	1599.691		1599.691	15	S	1	242.159	-0.222065	242.159	
				16	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber: 7090
Protein: BSU32110; yumC
Peptide Score: 78.93
Method: ITMS; CID; 3

precursor information

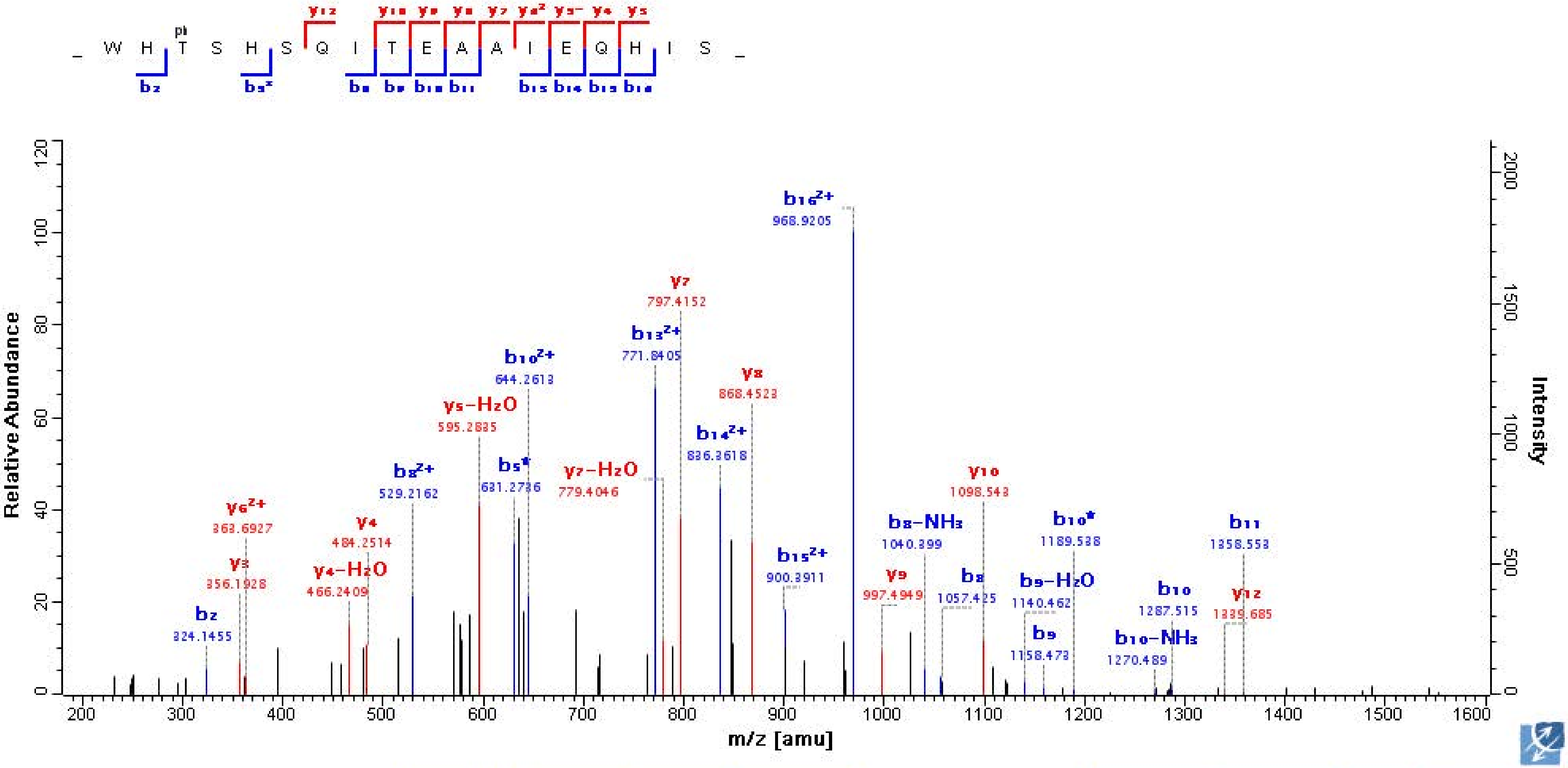
Mass:	1805.88212
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	78.93159
Mass Error [ppm]:	-0.23566
PEP:	0.00094053
Precursor Type:	MULTI

general information

Annotation:	9 of 15
AminoAcids Coverag	60 %
Intensity Coverage:	34 %
Protein Localisation:	318 ... 332

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	14		
	228.14550128		228.14550128	2	R	13	1743.8669093	
	327.2139152		327.2139152	3	V	12	1587.7657982	
	455.27249271	+0.0929248	455.27249271	4	Q	11	1488.6973843	
	552.32525656		552.32525656	5	P	10	1360.6388068	
	665.40932054	-0.024738	665.40932054	6	I	9	1263.586043	
+0.0120014	401.73775444	-0.1781323	802.4682324	7	H	8	1150.501979	+0.1630601
-0.023422	445.25376864	+0.0500932	889.50026081	8	S	7	1013.4430671	+0.336718
	1070.5142697		1070.5142697	9	T	6	926.41103872	
	1157.5462981		1157.5462981	10	S	5	745.39702983	
	1270.6303621		1270.6303621	11	I	4	658.36500142	
	1417.698776		1417.698776	12	F	3	545.28093744	
+0.4686338	773.87432278		1546.7413691	13	E	2	398.21252353	
	1660.7842965		1660.7842965	14	N	1	269.16993043	+0.0739661
				15	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber: 8292
Protein: BSU29760; ytxJ
Peptide Score: 122.33
Method: ITMS; CID; 3



precursor information

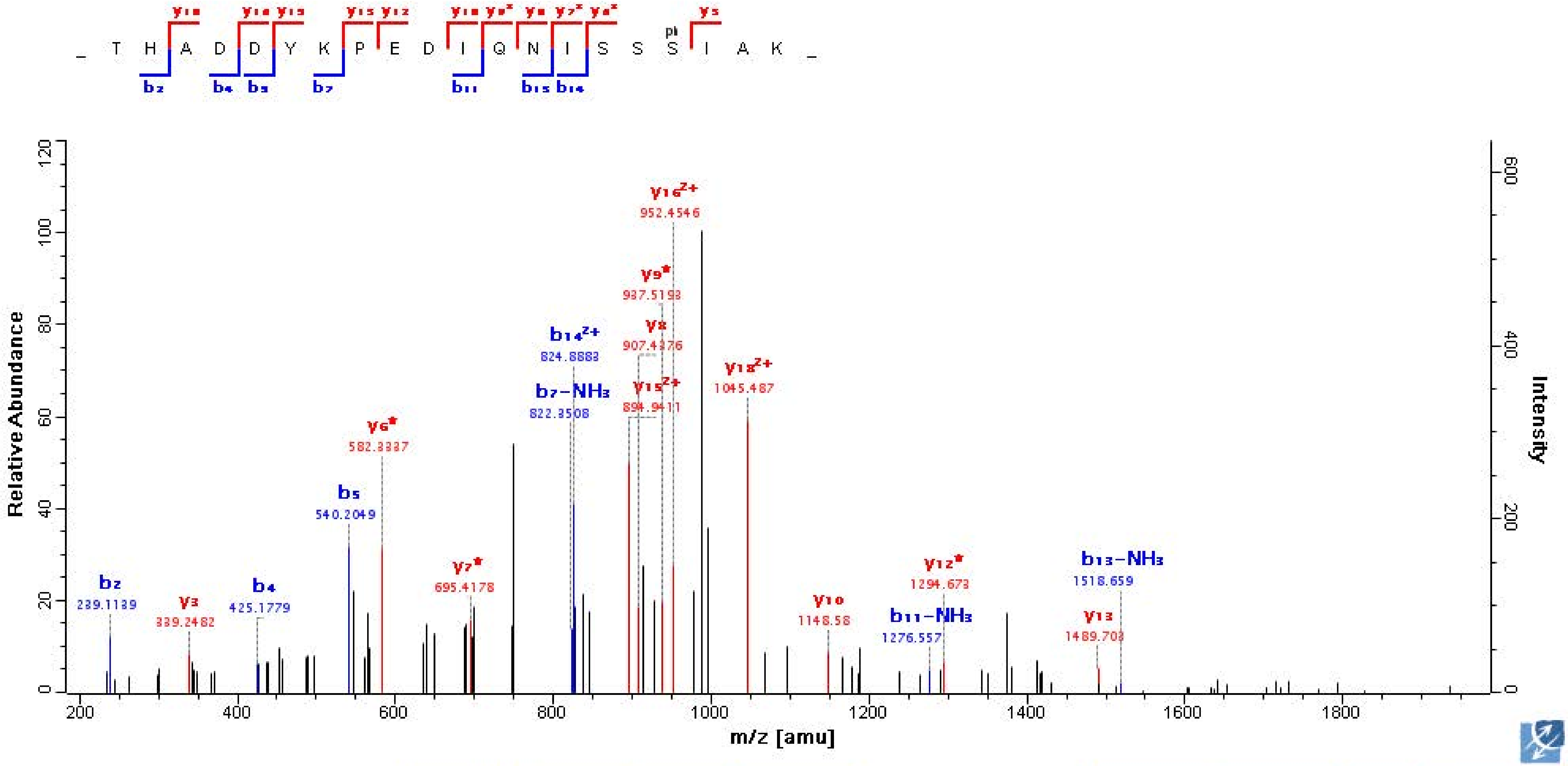
Mass:	2153.95342
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	122.327
Mass Error [ppm]:	0.12468
PEP:	2.4696E-07
Precursor Type:	ISO

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	58 %
Protein Localisation:	91 ... 108

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866		187.0866	1	W	17				
	324.1455	+0.088202	324.1455	2	H	16	1968.881		1968.881	
	505.1595		505.1595	3	T	15	1831.822		1831.822	
	592.1915		592.1915	4	S	14	1650.808		1650.808	
	729.2505		729.2505	5	H	13	1563.776		1563.776	
	816.2825		816.2825	6	S	12	1426.717		1426.717	
	944.3411		944.3411	7	Q	11	1339.685	-0.043741	1339.685	
+0.147815	529.2162	-0.345897	1057.425	8	I	10	1211.627		1211.627	
	1158.473	+0.29661	1158.473	9	T	9	1098.543	+0.058251	1098.543	
-0.095746	644.2613	+0.136952	1287.515	10	E	8	997.4949	+0.108188	997.4949	
	1358.553	+0.32579	1358.553	11	A	7	868.4523	-0.04563	868.4523	
	1429.59		1429.59	12	A	6	797.4152	+0.079984	797.4152	
+0.314366	771.8405		1542.674	13	I	5	726.3781		363.6927	-0.131826
+0.131693	836.3618		1671.716	14	E	4	613.294		613.294	
+0.22423	900.3911		1799.775	15	Q	3	484.2514	-0.069172	484.2514	
+0.243785	968.9205		1936.834	16	H	2	356.1928	+0.090968	356.1928	
	2049.918		2049.918	17	I	1	219.1339		219.1339	
				18	S	0	106.0499		106.0499	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber: 8392
Protein: BSU10030; hit; yhaE
Peptide Score: 56.06
Method: ITMS; CID; 3



precursor information

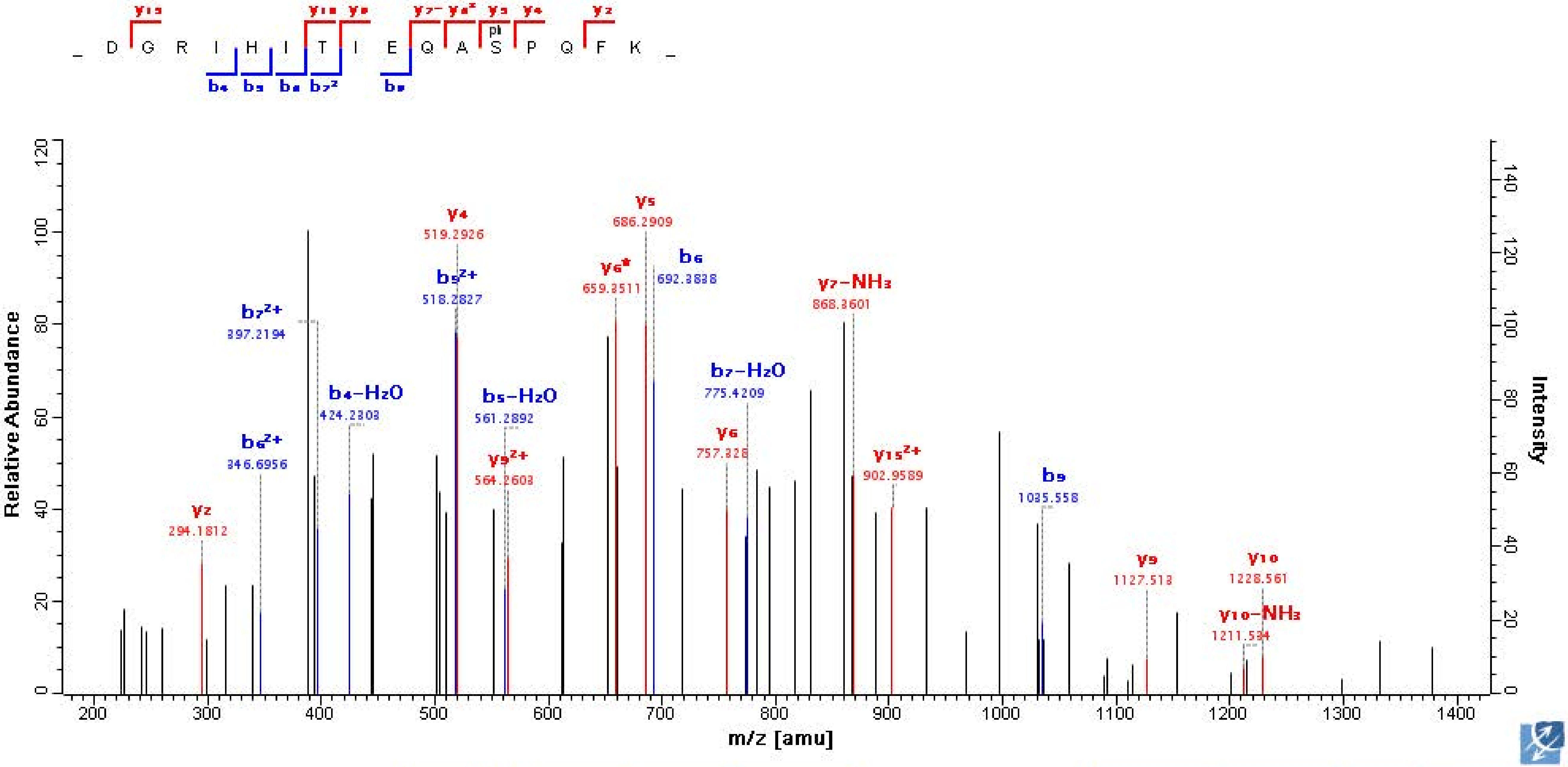
Mass:	2311.03536
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	56.05522
Mass Error [ppm]:	-0.67569
PEP:	0.0197
Precursor Type:	MULTI

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	32 %
Protein Localisation:	121 ... 140

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	19				
	239.1139	+0.007013	239.1139	2	H	18	2227.025		2227.025	
	310.151		310.151	3	A	17	2089.966		1045.487	+0.475754
	425.1779	+0.326227	425.1779	4	D	16	2018.929		2018.929	
	540.2049	+0.051359	540.2049	5	D	15	1903.902		952.4546	-0.245818
	703.2682		703.2682	6	Y	14	1788.875		894.9411	+0.142897
	839.3774		839.3774	7	K	13	1625.812		1625.812	
	936.4301		936.4301	8	P	12	1489.703	+0.336411	1489.703	
	1065.473		1065.473	9	E	11	1392.65		1392.65	
	1180.5		1180.5	10	D	10	1263.607		1263.607	
	1293.584		1293.584	11	I	9	1148.58	+0.215059	1148.58	
	1421.642		1421.642	12	Q	8	1035.496		1035.496	
	1535.685		1535.685	13	N	7	907.4376	-0.09158	907.4376	
+0.205894	824.8883		1648.769	14	I	6	793.3947		793.3947	
	1735.801		1735.801	15	S	5	680.3106		680.3106	
	1822.833		1822.833	16	S	4	593.2786		593.2786	
	1989.832		1989.832	17	S	3	506.2465		506.2465	
	2102.916		2102.916	18	I	2	339.2482	+0.136249	339.2482	
	2173.953		2173.953	19	A	1	226.1641		226.1641	
				20	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber:	8424
Protein:	BSU08470; yfhB
Peptide Score:	50.1
Method:	ITMS; CID; 3



precursor information

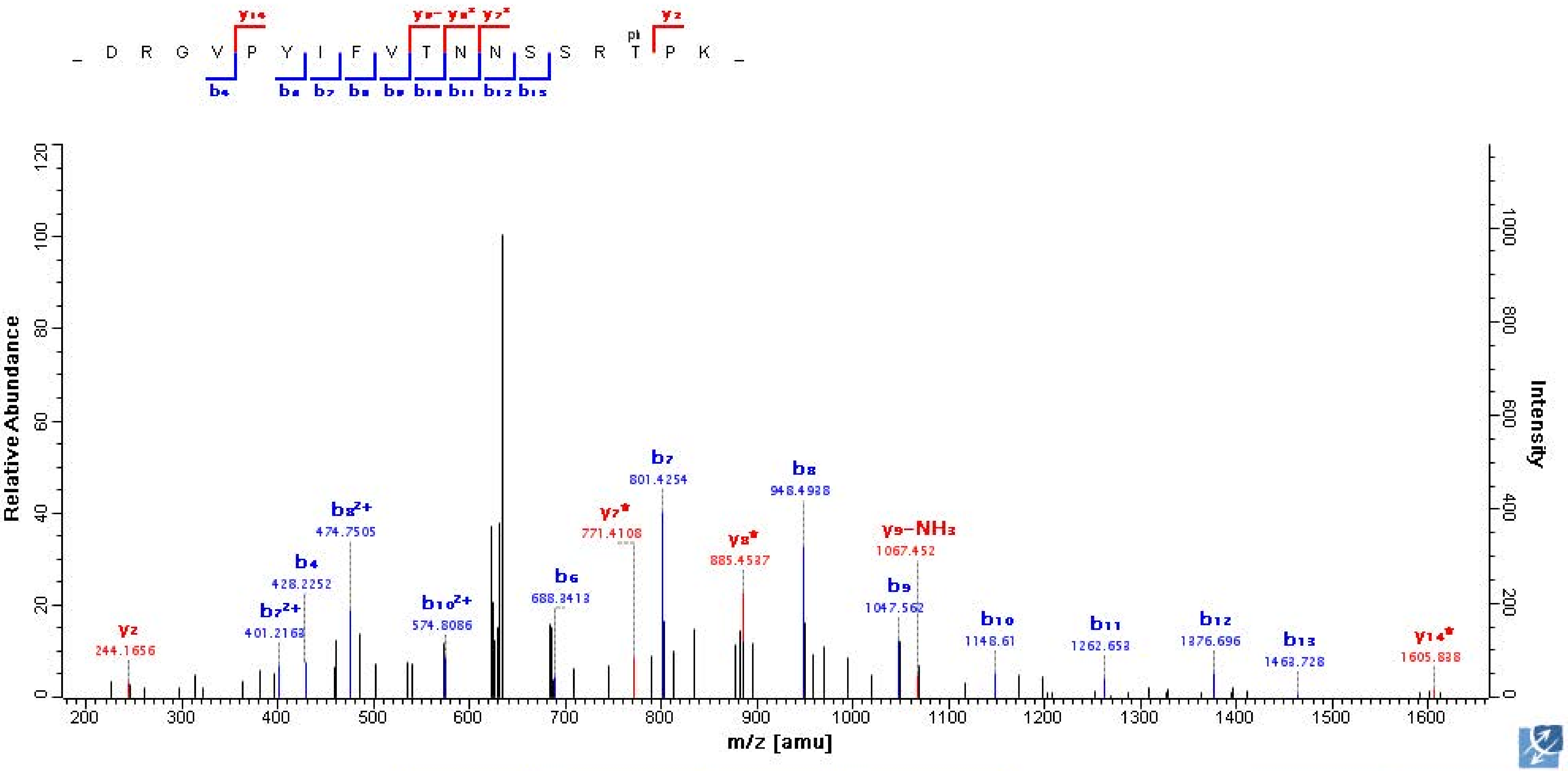
Mass:	1918.9299
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	50.10182
Mass Error [ppm]:	-0.17091
PEP:	0.057813
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	33 %
Protein Localisation:	113 ... 128

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	15				
	173.0557		173.0557	2	G	14	1804.911		902.9589	-0.142573
	329.1568		329.1568	3	R	13	1747.889		1747.889	
	442.2409		442.2409	4	I	12	1591.788		1591.788	
	579.2998		579.2998	5	H	11	1478.704		1478.704	
+0.225831	346.6956	+0.208573	692.3838	6	I	10	1341.645		1341.645	
+0.162869	397.2194		793.4315	7	T	9	1228.561	+0.330534	1228.561	
	906.5156		906.5156	8	I	8	1127.513	+0.062783	564.2603	+0.165571
-0.015267	518.2827	-0.096866	1035.558	9	E	7	1014.429		1014.429	
	1163.617		1163.617	10	Q	6	885.3866		885.3866	
	1234.654		1234.654	11	A	5	757.328	+0.142183	757.328	
	1401.652		1401.652	12	S	4	686.2909	+0.026342	686.2909	
	1498.705		1498.705	13	P	3	519.2926	-0.115252	519.2926	
	1626.764		1626.764	14	Q	2	422.2398		422.2398	
	1773.832		1773.832	15	F	1	294.1812	+0.072566	294.1812	
				16	K	0	147.1128		147.1128	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F11
Scannumber:	8851
Protein:	BSU32290; yutF
Peptide Score:	63.69
Method:	ITMS; CID; 3



precursor information

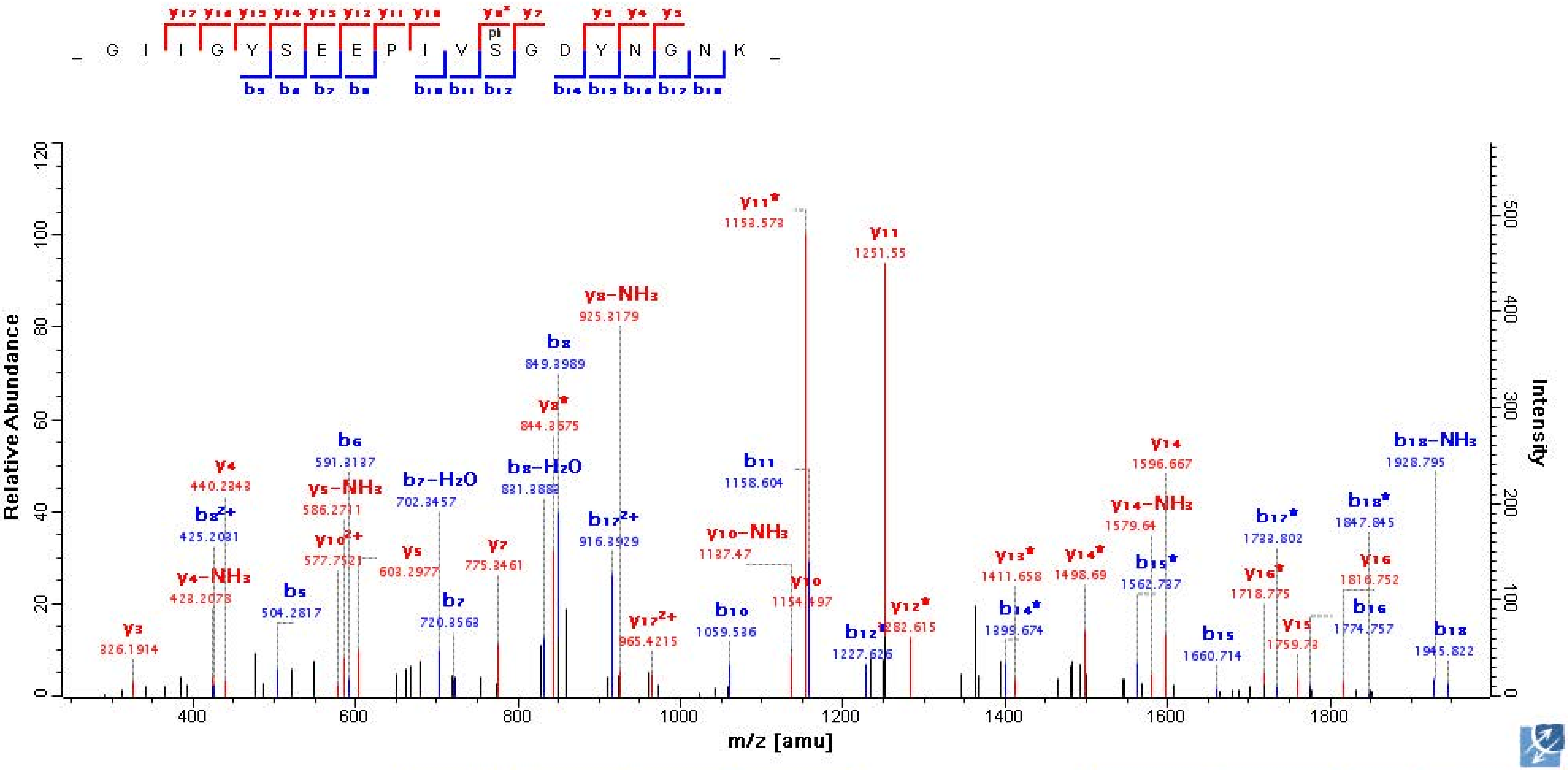
Mass:	2130.02517
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.68993
Mass Error [ppm]:	-0.34926
PEP:	0.0053816
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	25 %
Protein Localisation:	34 ... 51

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	17		
	272.13533053		272.13533053	2	R	16	2016.006251	
	329.15679425		329.15679425	3	G	15	1859.90514	
	428.22520817	+0.1731073	428.22520817	4	V	14	1802.8836762	
	525.27797202		525.27797202	5	P	13	1703.8152623	
	688.34130056	+0.0564045	688.34130056	6	Y	12	1606.7624985	
+0.0792117	401.2163205	+0.0464983	801.42536454	7	I	11	1443.6991699	
+0.4012059	474.75052746	-0.0165446	948.49377845	8	F	10	1330.615106	
	1047.5621924	+0.1284815	1047.5621924	9	V	9	1183.546692	
-0.4608564	574.80857366	+0.0213547	1148.6098708	10	T	8	1084.4782781	
	1262.6527983	+0.0858492	1262.6527983	11	N	7	983.43059965	
	1376.6957257	+0.0973651	1376.6957257	12	N	6	869.3876722	
	1463.7277541	+0.4232468	1463.7277541	13	S	5	755.34474475	
	1550.7597826		1550.7597826	14	S	4	668.31271634	
	1706.8608936		1706.8608936	15	R	3	581.28068793	
	1887.8749025		1887.8749025	16	T	2	425.17957691	
	1984.9276663		1984.9276663	17	P	1	244.16556802	+0.0411581
				18	K	0	147.11280417	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	10678
Protein:	BSU33940; gap; gapA
Peptide Score:	232.15
Method:	ITMS; CID; 3



precursor information

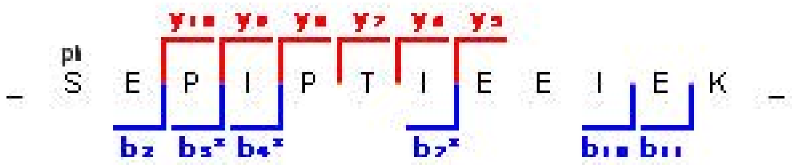
Mass:	2090.91984
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	232.1485
Mass Error [ppm]:	0.030007
PEP:	2.4486E-91
Precursor Type:	MULTI

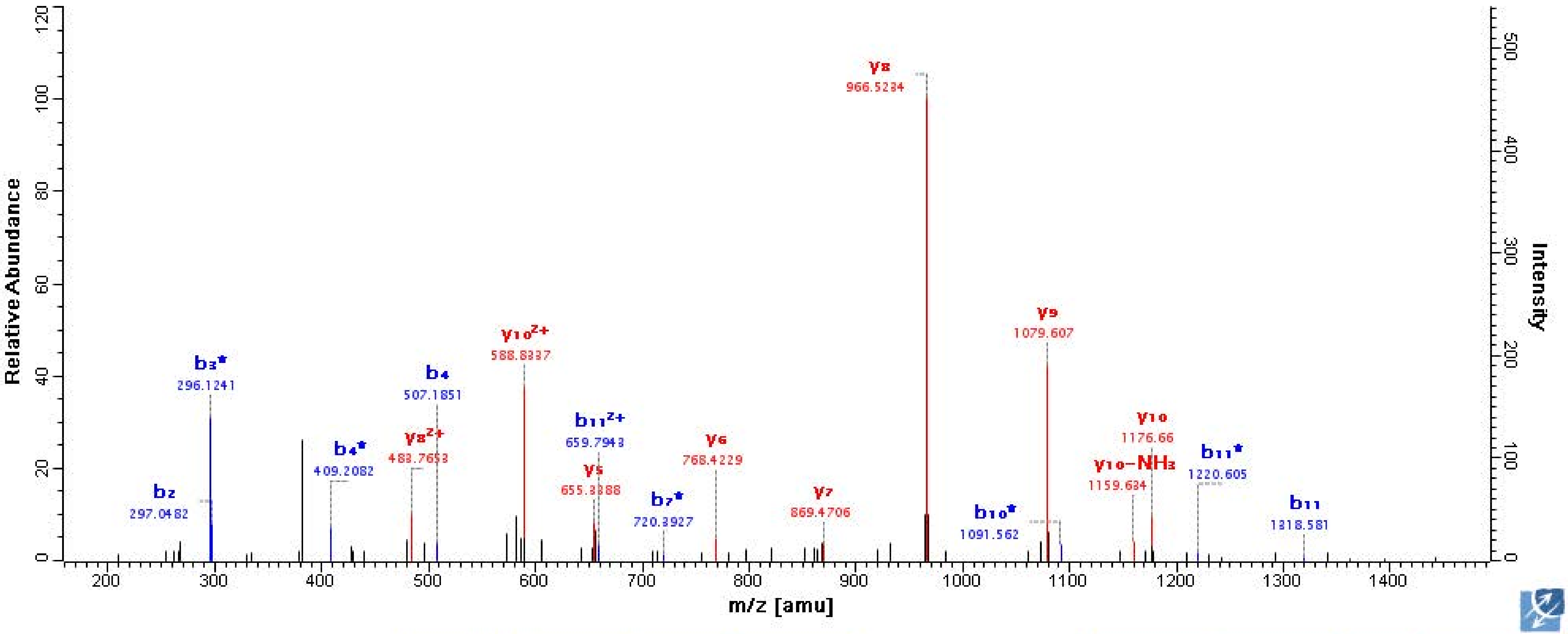
general information

Annotation:	16 of 19
AminoAcids Coverag	84 %
Intensity Coverage:	65 %
Protein Localisation:	271 ... 289

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	18				
	171.1128		171.1128	2	I	17	2042.92		2042.92	
	284.1969		284.1969	3	I	16	1929.836		965.4215	-0.140252
	341.2183		341.2183	4	G	15	1816.752	+0.148604	1816.752	
	504.2817	+0.041277	504.2817	5	Y	14	1759.73	+0.482812	1759.73	
	591.3137	-0.265471	591.3137	6	S	13	1596.667	+0.015135	1596.667	
	720.3563	+0.222026	720.3563	7	E	12	1509.635		1509.635	
+0.071064	425.2031	-0.02827	849.3989	8	E	11	1380.592		1380.592	
	946.4516		946.4516	9	P	10	1251.55	-0.015966	1251.55	
	1059.536	+0.052676	1059.536	10	I	9	1154.497	+0.10003	577.7521	-0.191721
	1158.604	+0.007456	1158.604	11	V	8	1041.413		1041.413	
	1325.602		1325.602	12	S	7	942.3444		942.3444	
	1382.624		1382.624	13	G	6	775.3461	+0.140576	775.3461	
	1497.651		1497.651	14	D	5	718.3246		718.3246	
	1660.714	+0.00637	1660.714	15	Y	4	603.2977	-0.0341	603.2977	
	1774.757	-0.184751	1774.757	16	N	3	440.2343	-0.080757	440.2343	
+0.029912	916.3929		1831.779	17	G	2	326.1914	+0.161664	326.1914	
	1945.822	+0.154423	1945.822	18	N	1	269.1699		269.1699	
				19	K	0	155.127		155.127	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 10687
Protein: BSU20420; yorD
Peptide Score: 103.88
Method: ITMS; CID; 3





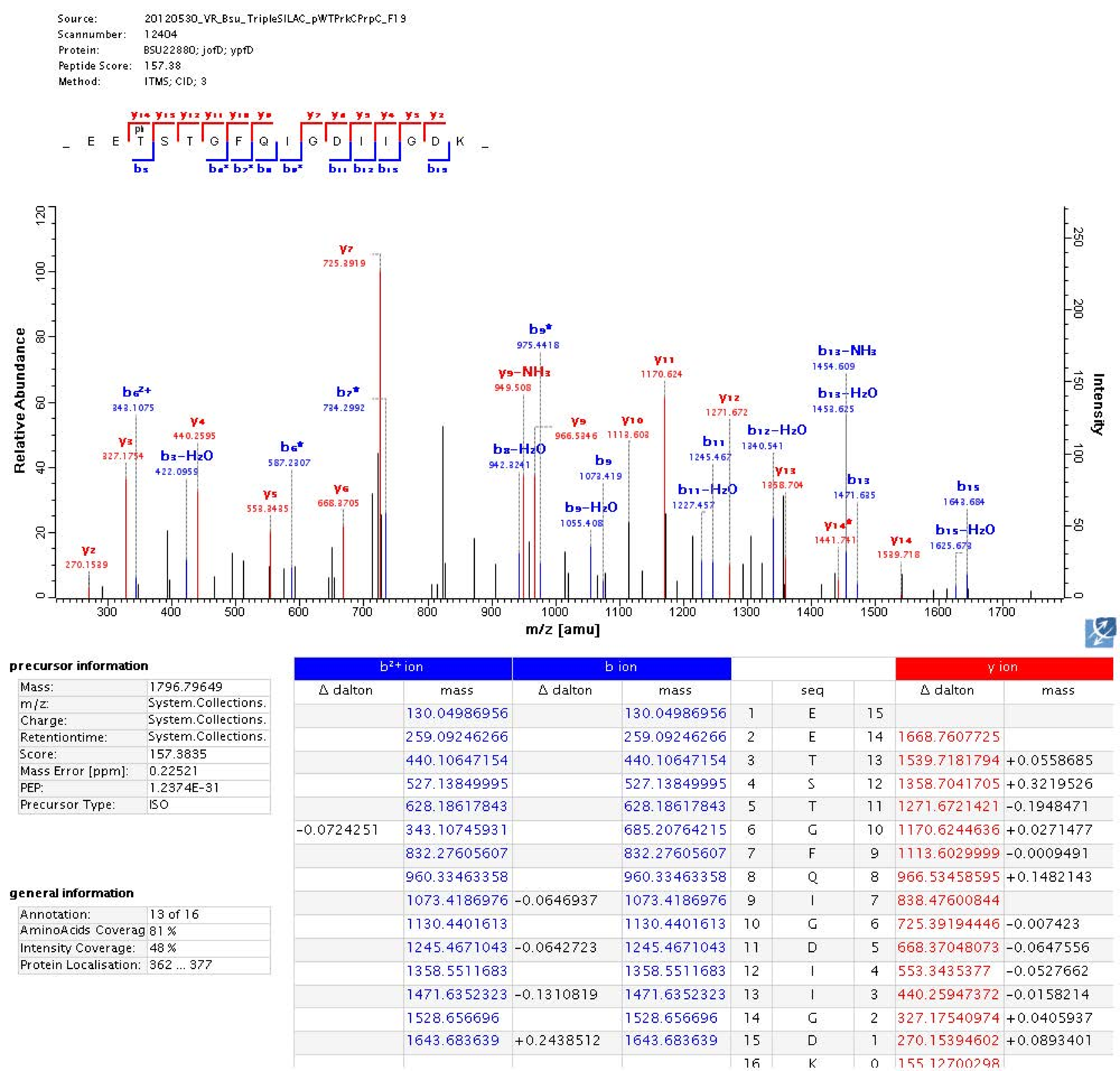
precursor information

Mass:	1471.69417
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	103.8804
Mass Error [ppm]:	0.21246
PEP:	0.0094539
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	60 %
Protein Localisation:	54 ... 65

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	11				
	297.0482	+0.20403	297.0482	2	E	10	1305.703		1305.703	
	394.101		394.101	3	P	9	1176.66	-0.179956	588.8337	+0.029614
	507.1851	-0.022092	507.1851	4	I	8	1079.607	-0.014399	1079.607	
	604.2378		604.2378	5	P	7	966.5234	+0.061303	483.7653	-0.064204
	705.2855		705.2855	6	T	6	869.4706	-0.093147	869.4706	
	818.3696		818.3696	7	I	5	768.4229	+0.035708	768.4229	
	947.4122		947.4122	8	E	4	655.3388	+0.001059	655.3388	
	1076.455		1076.455	9	E	3	526.2963		526.2963	
	1189.539		1189.539	10	I	2	397.2537		397.2537	
-0.372466	659.7943	+0.38002	1318.581	11	E	1	284.1696		284.1696	
				12	K	0	155.127		155.127	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 12404
Protein: BSU22880; jofD; ypfD
Peptide Score: 157.38
Method: ITMS; CID; 3

precursor information

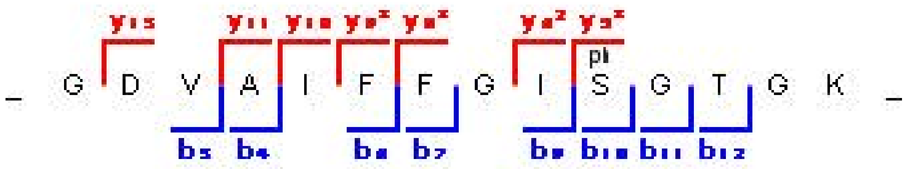
Mass:	1796.79649
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	157.3835
Mass Error [ppm]:	0.22521
PEP:	1.2374E-31
Precursor Type:	ISO

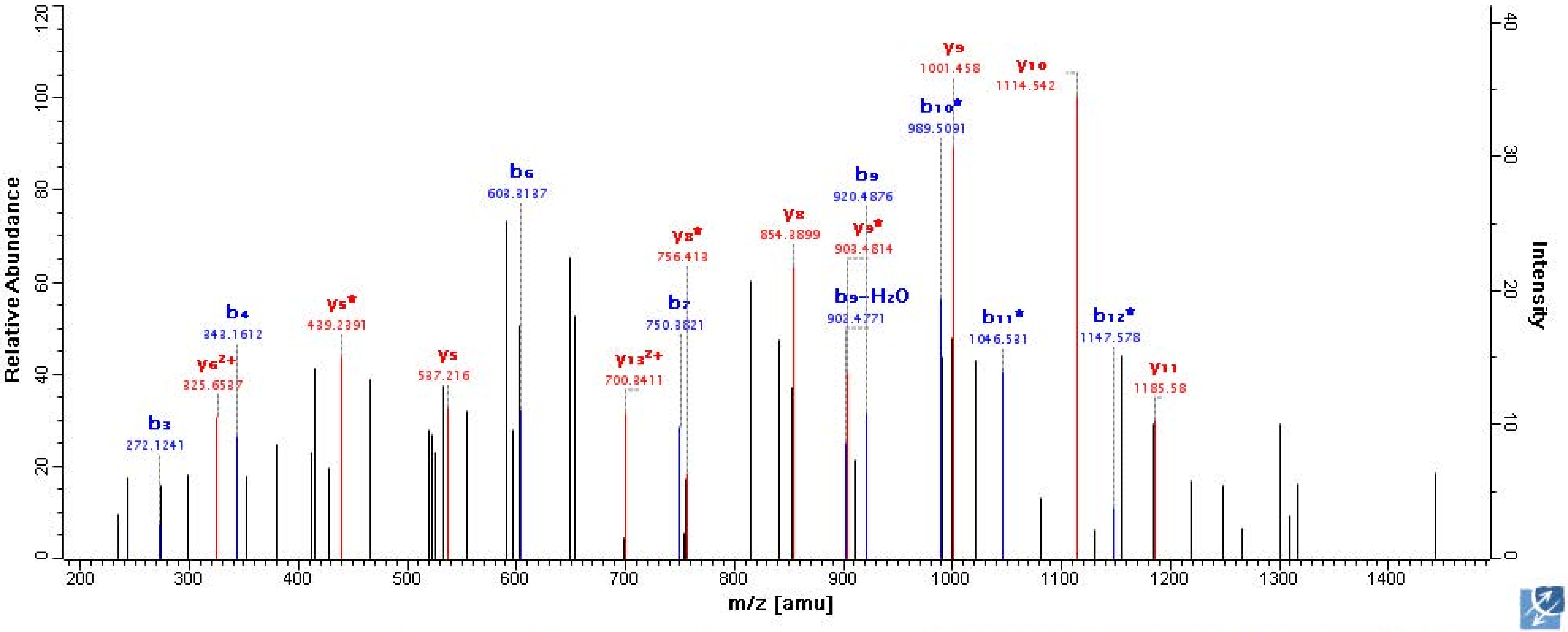
general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	48 %
Protein Localisation:	362 ... 377

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	15		
	259.09246266		259.09246266	2	E	14	1668.7607725	
	440.10647154		440.10647154	3	T	13	1539.7181794	+0.0558685
	527.13849995		527.13849995	4	S	12	1358.7041705	+0.3219526
	628.18617843		628.18617843	5	T	11	1271.6721421	-0.1948471
-0.0724251	343.10745931		685.20764215	6	G	10	1170.6244636	+0.0271477
	832.27605607		832.27605607	7	F	9	1113.6029999	-0.0009491
	960.33463358		960.33463358	8	Q	8	966.53458595	+0.1482143
	1073.4186976	-0.0646937	1073.4186976	9	I	7	838.47600844	
	1130.4401613		1130.4401613	10	G	6	725.39194446	-0.007423
	1245.4671043	-0.0642723	1245.4671043	11	D	5	668.37048073	-0.0647556
	1358.5511683		1358.5511683	12	I	4	553.3435377	-0.0527662
	1471.6352323	-0.1310819	1471.6352323	13	I	3	440.25947372	-0.0158214
	1528.656696		1528.656696	14	G	2	327.17540974	+0.0405937
	1643.683639	+0.2438512	1643.683639	15	D	1	270.15394602	+0.0893401
				16	K	0	155.12700298	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 12819
Protein: BSU30560; pckA; ppc
Peptide Score: 95.98
Method: ITMS; CID; 3





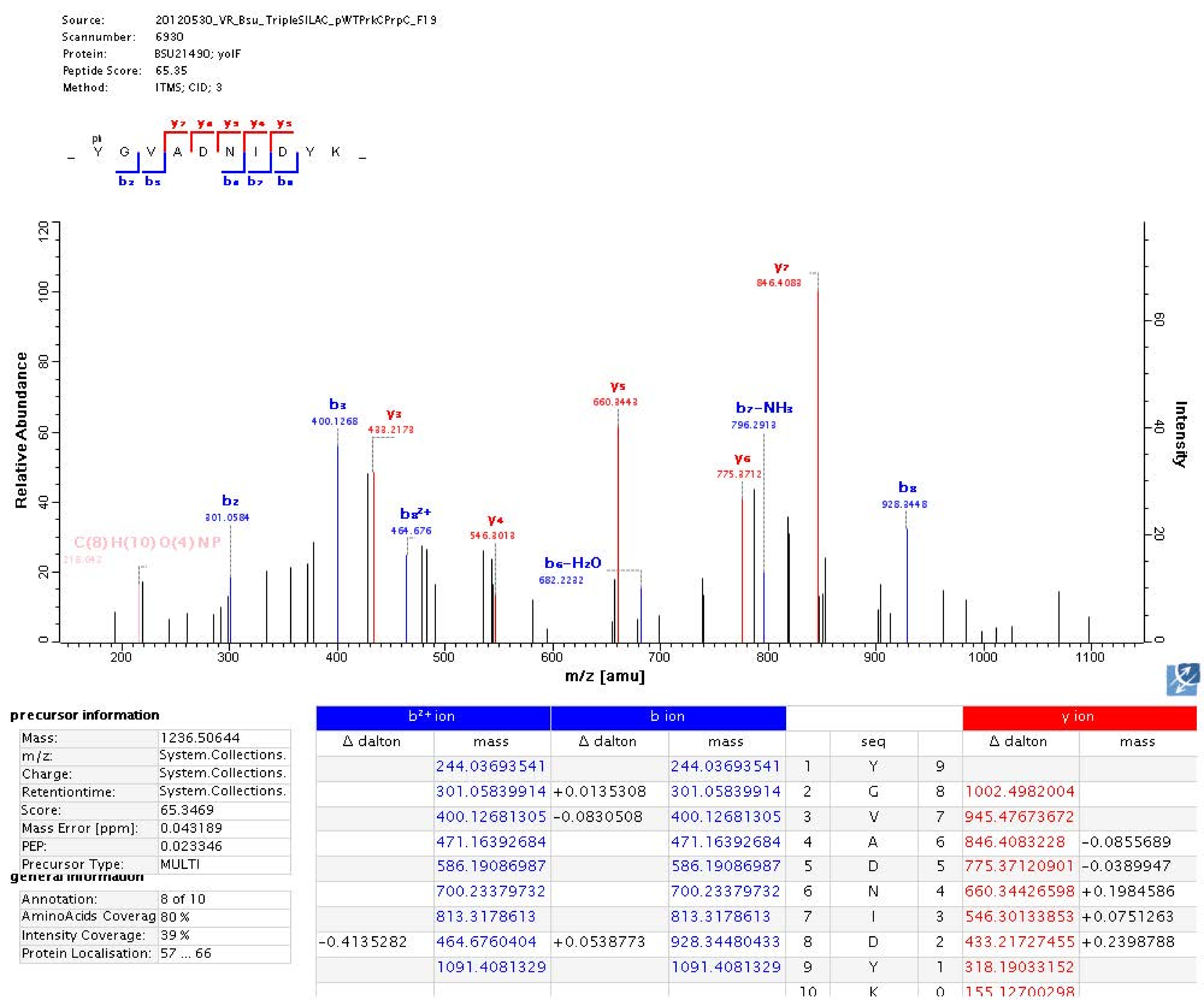
precursor information

Mass:	1447.67569
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.98126
Mass Error [ppm]:	0.57773
PEP:	6.2944E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	36 %
Protein Localisation:	226 ... 239

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	13				
	173.05568322	2	D	12	1399.674858		700.34106722	-0.0430936
+0.1966121	272.12409714	3	V	11	1284.6479149		1284.6479149	
+0.0521069	343.16121093	4	A	10	1185.579501	-0.14371	1185.579501	
	456.24527491	5	I	9	1114.5423872	+0.1761186	1114.5423872	
+0.0752272	603.31368882	6	F	8	1001.4583233	+0.0356343	1001.4583233	
-0.297447	750.38210274	7	F	7	854.38990934	+0.2393021	854.38990934	
	807.40356646	8	G	6	707.32149543		707.32149543	
+0.1564125	920.48763044	9	I	5	650.3000317		325.65365409	-0.4840374
	1087.4859893	10	S	4	537.21596772	+0.2167105	537.21596772	
	1144.507453	11	G	3	370.21760891		370.21760891	
	1245.5551315	12	T	2	313.19614518		313.19614518	
	1302.5765952	13	G	1	212.14846671		212.14846671	
		14	K	0	155.12700298		155.12700298	



Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	6930
Protein:	BSU21490; yolF
Peptide Score:	65.35
Method:	ITMS; CID; 3

precursor information

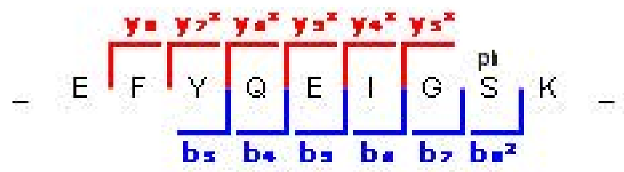
Mass:	1236.50644
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	65.3469
Mass Error [ppm]:	0.043189
PEP:	0.023346
Precursor Type:	MULTI

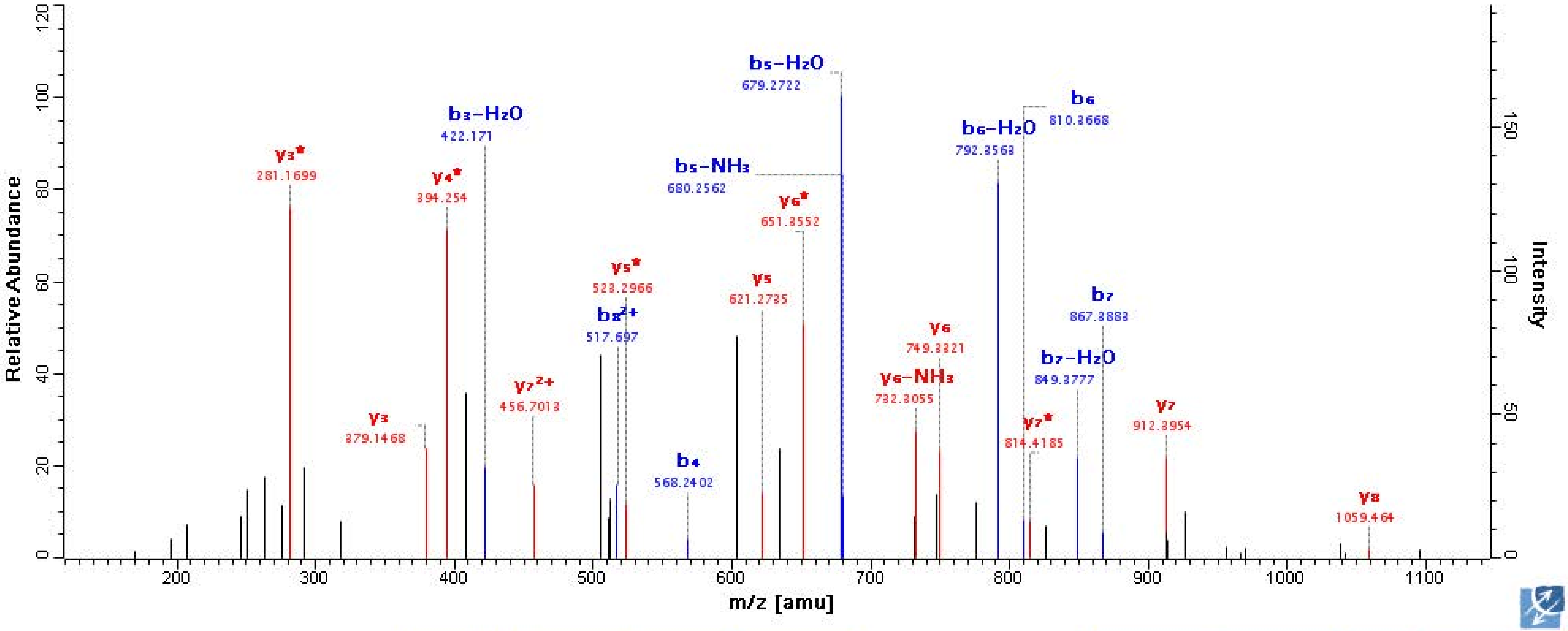
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	39 %
Protein Localisation:	57 ... 66

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	244.03693541		244.03693541	1	Y	9		
	301.05839914	+0.0135308	301.05839914	2	G	8	1002.4982004	
	400.12681305	-0.0830508	400.12681305	3	V	7	945.47673672	
	471.16392684		471.16392684	4	A	6	846.4083228	-0.0855689
	586.19086987		586.19086987	5	D	5	775.37120901	-0.0389947
	700.23379732		700.23379732	6	N	4	660.34426598	+0.1984586
	813.3178613		813.3178613	7	I	3	546.30133853	+0.0751263
-0.4135282	464.6760404	+0.0538773	928.34480433	8	D	2	433.21727455	+0.2398788
	1091.4081329		1091.4081329	9	Y	1	318.19033152	
				10	K	0	155.12700298	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	7421
Protein:	BSU04400; gsiB
Peptide Score:	129.85
Method:	ITMS; CID; 3



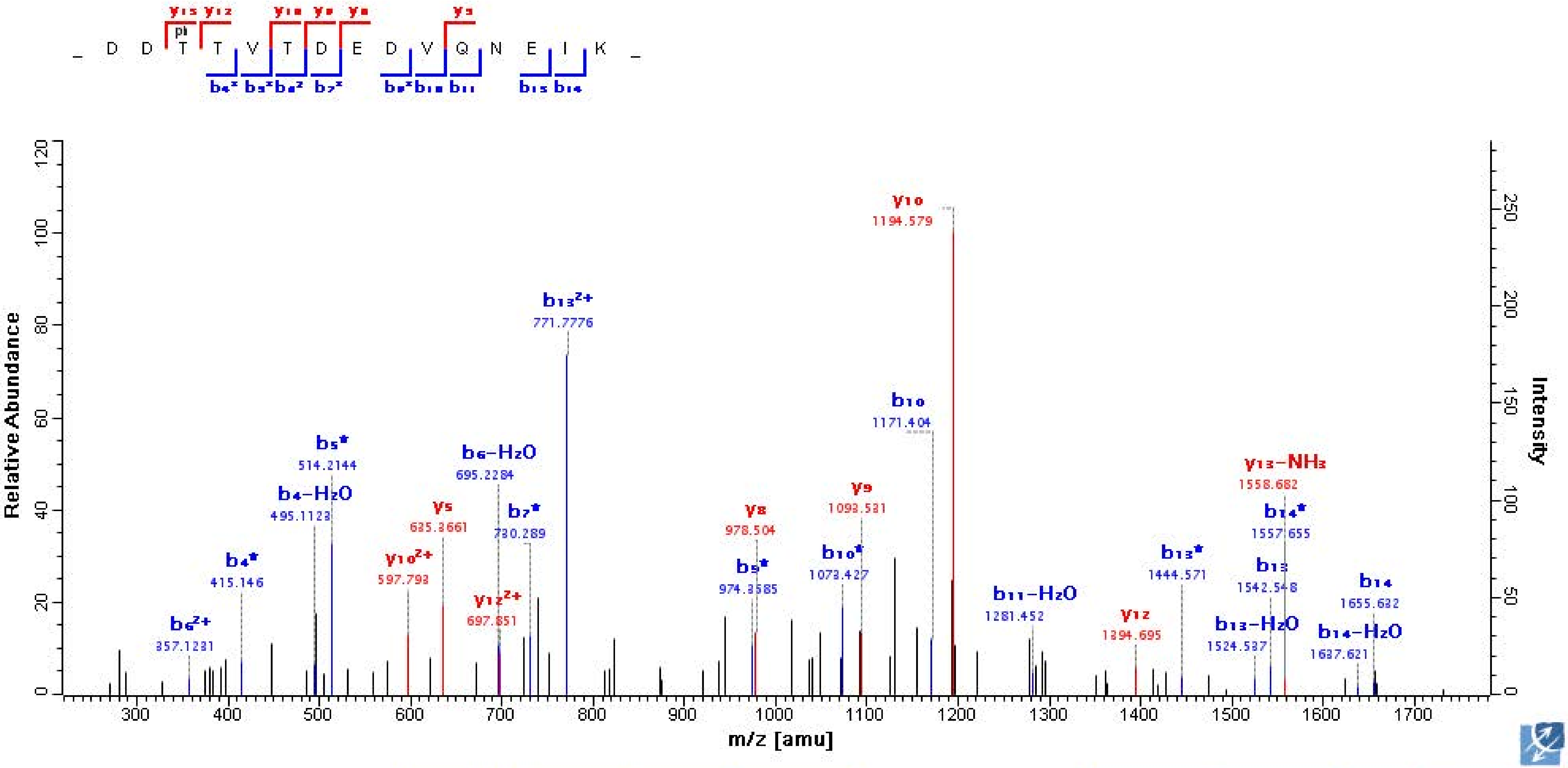


precursor information

Mass:	1179.48459
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	129.8513
Mass Error [ppm]:	-0.27535
PEP:	7.5472E-07
g Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	64 %
Protein Localisation:	107 ... 115

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	8				
	277.1183		277.1183	2	F	7	1059.464	-0.059017	1059.464	
	440.1816		440.1816	3	Y	6	912.3954	+0.046445	456.7013	+0.185325
	568.2402	+0.039168	568.2402	4	Q	5	749.3321	+0.161531	749.3321	
	697.2828		697.2828	5	E	4	621.2735	+0.05214	621.2735	
	810.3668	-0.06576	810.3668	6	I	3	492.2309		492.2309	
	867.3883	+0.189571	867.3883	7	G	2	379.1468	+0.240809	379.1468	
-0.387036	517.697		1034.387	8	S	1	322.1254		322.1254	
				9	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	8196
Protein:	BSU28230; tig; yzzH
Peptide Score:	98.68
Method:	ITMS; CID; 3



precursor information

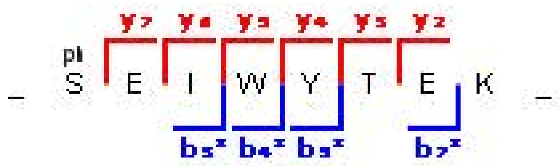
Mass:	1800.73088
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	98.67624
Mass Error [ppm]:	0.35205
PEP:	2.4459E-06
Precursor Type:	MULTI

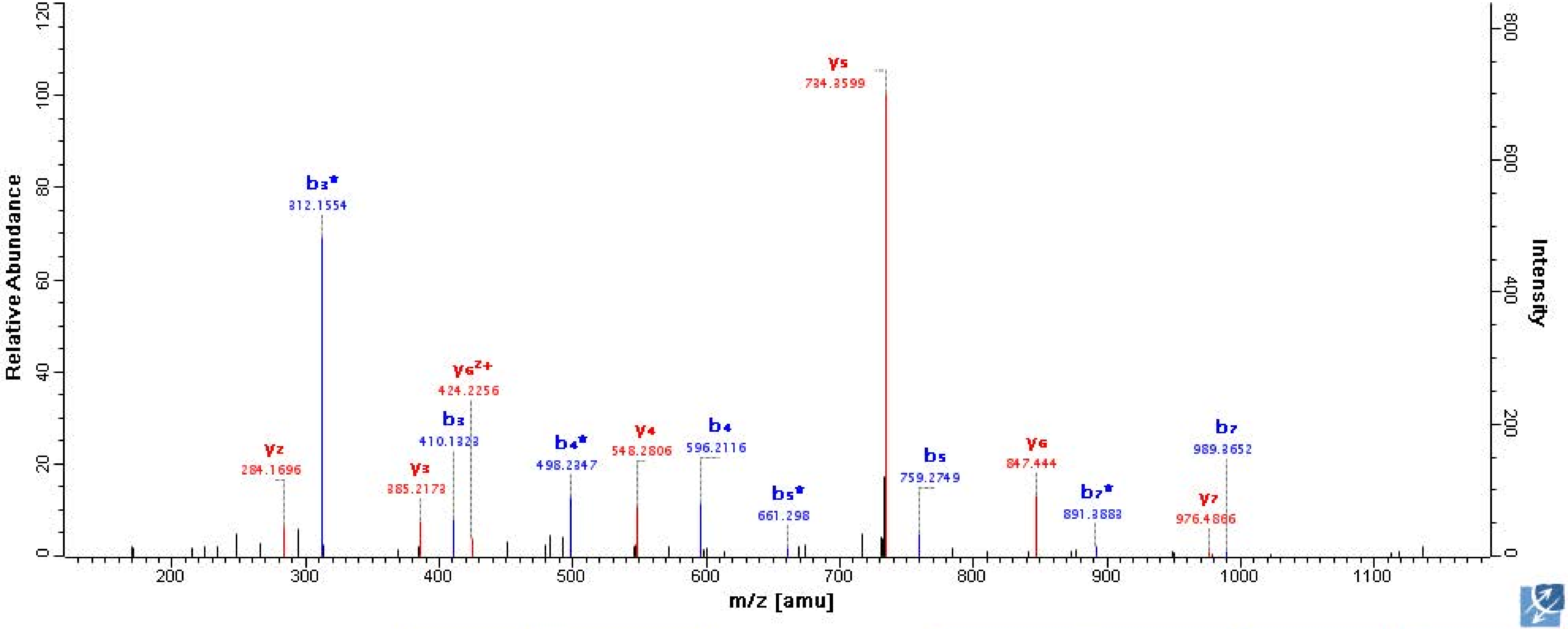
general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	44 %
Protein Localisation:	129 ... 143

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	14				
	231.0612		231.0612	2	D	13	1690.736		1690.736	
	412.0752		412.0752	3	T	12	1575.709		1575.709	
	513.1228		513.1228	4	T	11	1394.695	+0.080165	697.851	+0.208808
	612.1913		612.1913	5	V	10	1293.647		1293.647	
-0.010683	357.1231		713.2389	6	T	9	1194.579	-0.029328	597.793	-0.387382
	828.2659		828.2659	7	D	8	1093.531	+0.11796	1093.531	
	957.3085		957.3085	8	E	7	978.504	-0.077815	978.504	
	1072.335		1072.335	9	D	6	849.4614		849.4614	
	1171.404	-0.023464	1171.404	10	V	5	734.4345		734.4345	
	1299.462		1299.462	11	Q	4	635.3661	+0.13118	635.3661	
	1413.505		1413.505	12	N	3	507.3075		507.3075	
-0.363176	771.7776	-0.024862	1542.548	13	E	2	393.2646		393.2646	
	1655.632	+0.170127	1655.632	14	I	1	264.222		264.222	
				15	K	0	151.1379		151.1379	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 8424
Protein: BSU37500; speE; ywhF
Peptide Score: 135.79
Method: ITMS; CID; 3



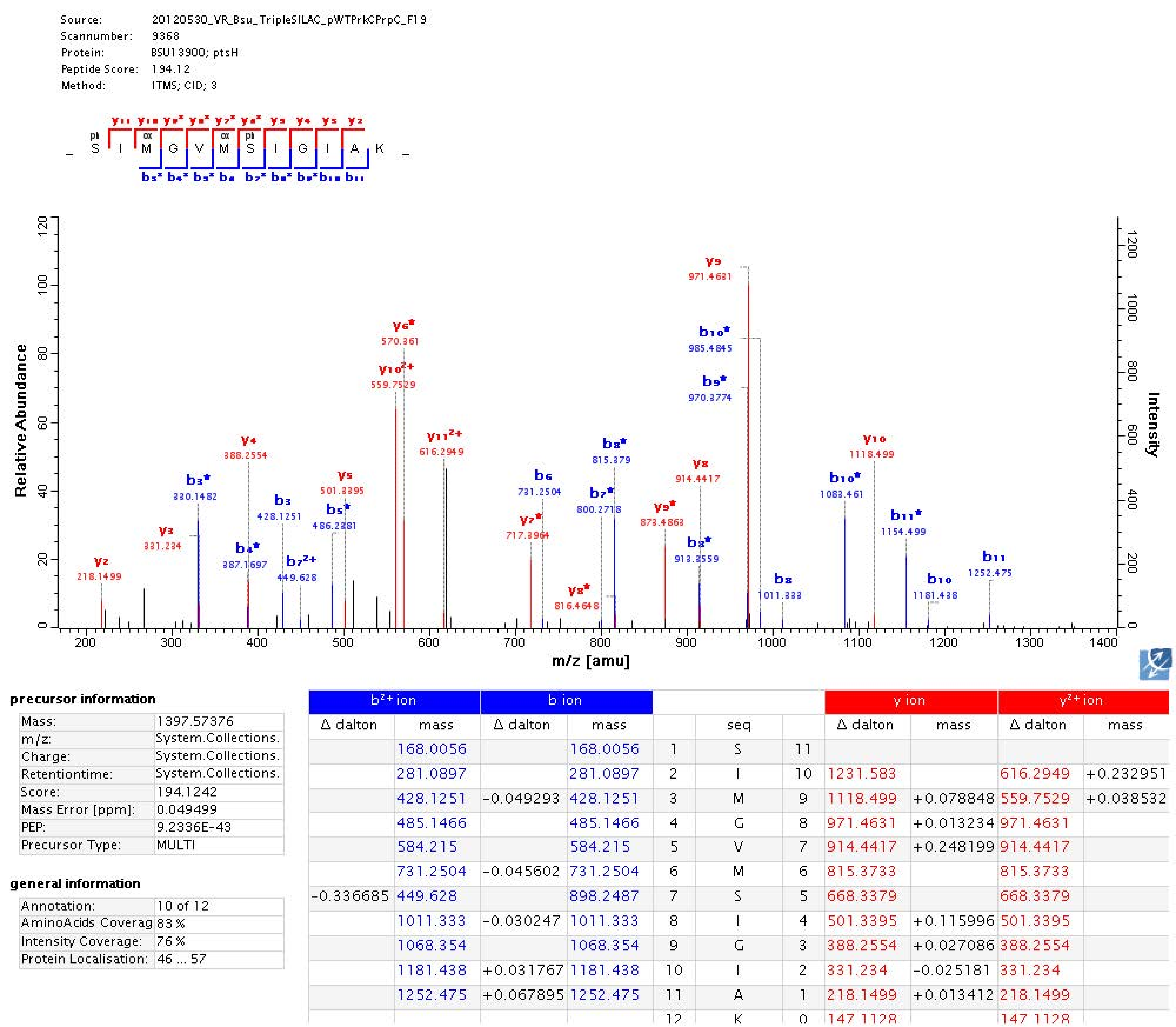


precursor information

g

Mass:	1134.46277
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.7909
Mass Error [ppm]:	-0.59924
PEP:	1.3946E-06
Precursor Type:	MULTI
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	72 %
Protein Localisation:	2 ... 9

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	7				
	297.04822838	2	E	6	976.48657312	+0.0868522	976.48657312	
+0.0173048	410.13229236	3	I	5	847.44398003	-0.0556133	424.22562825	+0.1477848
-0.0568812	596.21160532	4	W	4	734.35991605	+0.1133506	734.35991605	
-0.3743601	759.27493385	5	Y	3	548.28060309	+0.0938476	548.28060309	
	860.32261233	6	T	2	385.21727455	-0.011403	385.21727455	
+0.1817306	989.36520542	7	E	1	284.16959608	-0.3014931	284.16959608	
		8	K	0	155.12700298		155.12700298	



Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 9368
Protein: BSU13900; ptsH
Peptide Score: 194.12
Method: ITMS; CID; 3

precursor information

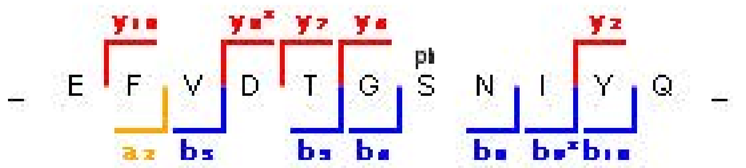
Mass:	1397.57376
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	194.1242
Mass Error [ppm]:	0.049499
PEP:	9.2336E-43
Precursor Type:	MULTI

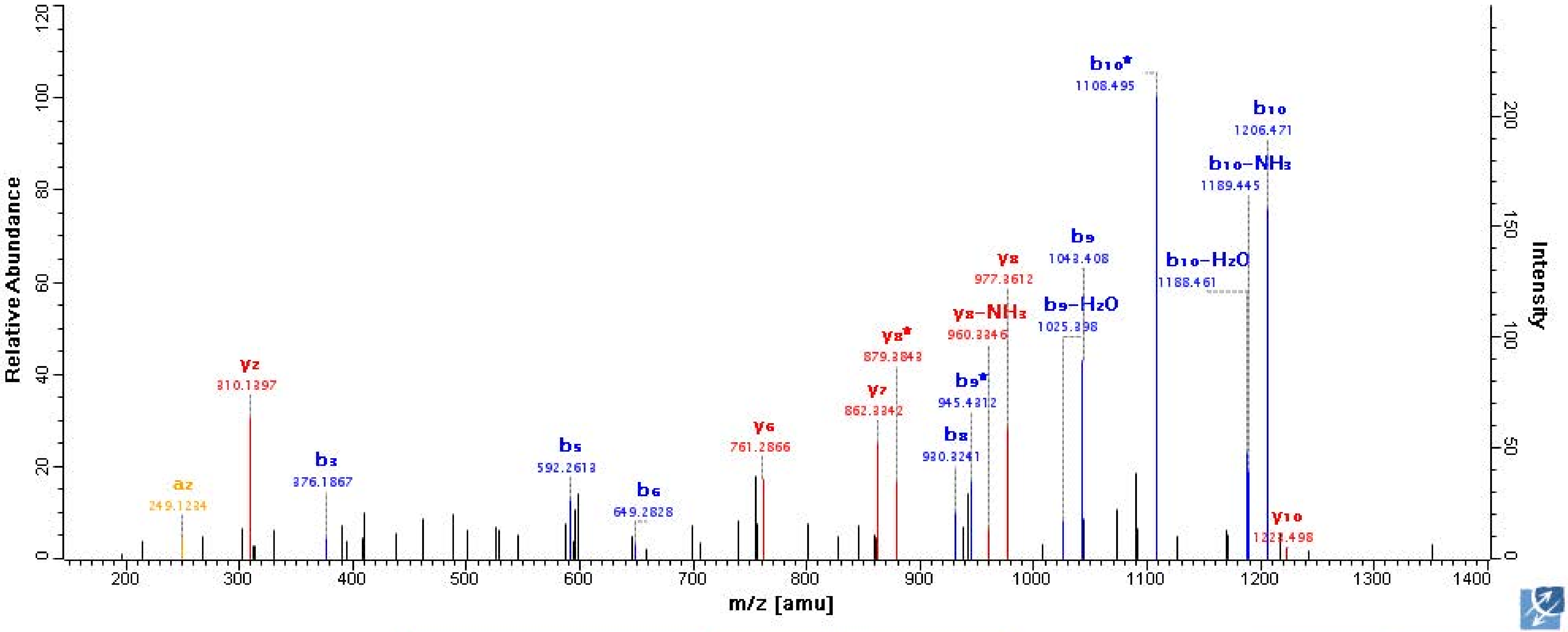
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	76 %
Protein Localisation:	46 ... 57

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	11				
	281.0897		281.0897	2	I	10	1231.583		616.2949	+0.232951
	428.1251	-0.049293	428.1251	3	M	9	1118.499	+0.078848	559.7529	+0.038532
	485.1466		485.1466	4	G	8	971.4631	+0.013234	971.4631	
	584.215		584.215	5	V	7	914.4417	+0.248199	914.4417	
	731.2504	-0.045602	731.2504	6	M	6	815.3733		815.3733	
-0.336685	449.628		898.2487	7	S	5	668.3379		668.3379	
	1011.333	-0.030247	1011.333	8	I	4	501.3395	+0.115996	501.3395	
	1068.354		1068.354	9	G	3	388.2554	+0.027086	388.2554	
	1181.438	+0.031767	1181.438	10	I	2	331.234	-0.025181	331.234	
	1252.475	+0.067895	1252.475	11	A	1	218.1499	+0.013412	218.1499	
				12	K	0	147.1128		147.1128	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	9375
Protein:	BSU08790; thiA; thiC
Peptide Score:	101.89
Method:	ITMS; CID; 3





precursor information

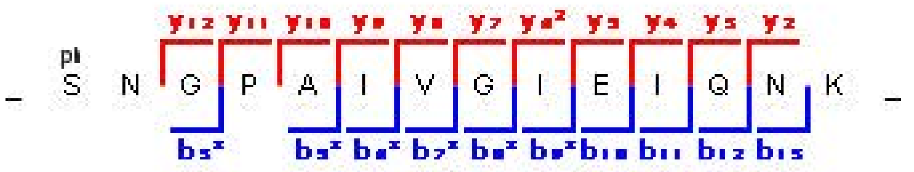
Mass:	1351.53345
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.8882
Mass Error [ppm]:	0.092978
PEP:	0.0094527
Precursor Type:	ISO

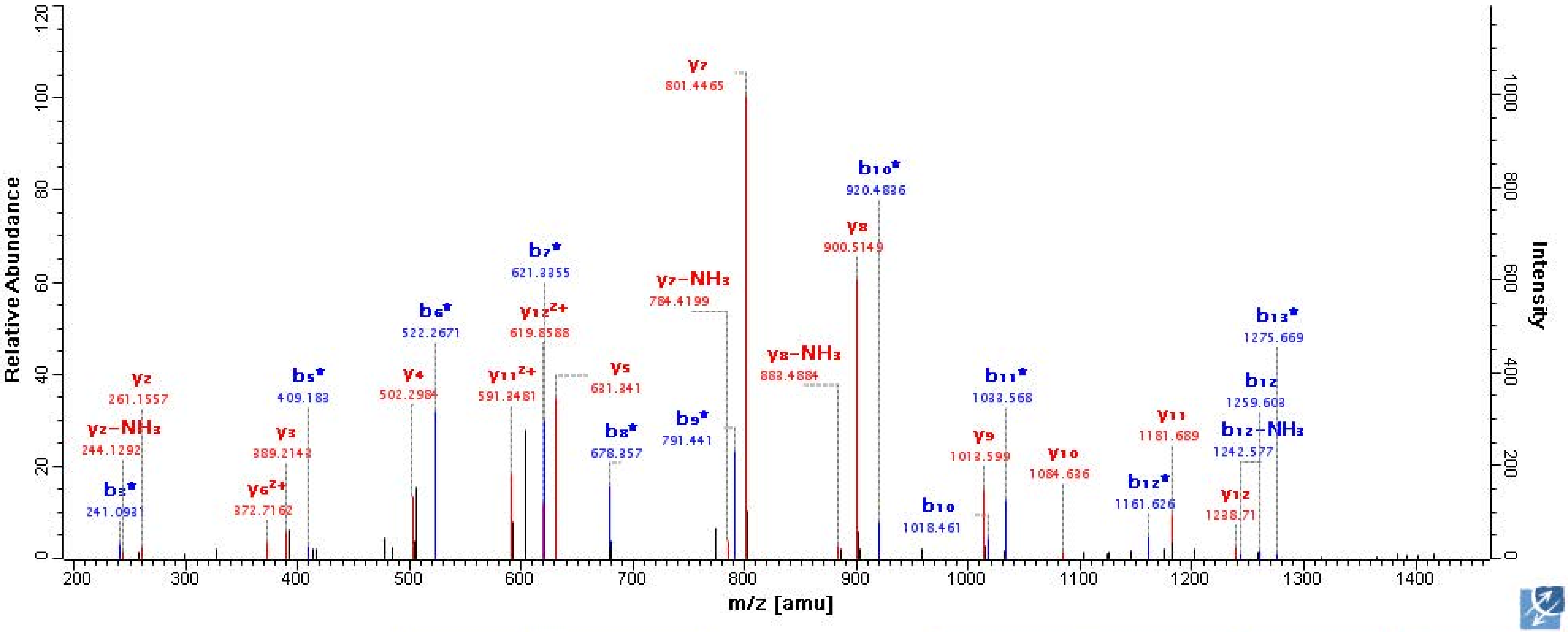
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	58 %
Protein Localisation:	580 ... 590

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.05495494		130.04986956	1	E	10		
+0.0780777	249.12336886		277.11828348	2	F	9	1223.4980105	-0.2806033
	348.19178277	-0.2008576	376.1866974	3	V	8	1076.4295966	
	463.21872581		491.21364043	4	D	7	977.36118268	+0.1300893
	564.26640428	+0.0511201	592.2613189	5	T	6	862.33423965	-0.0944325
	621.287868	+0.1188287	649.28278262	6	G	5	761.28656117	+0.0971669
	788.28622682		816.28114144	7	S	4	704.26509745	
	902.32915427	+0.0019199	930.32406889	8	N	3	537.26673863	
	1015.4132182	-0.0831817	1043.4081329	9	I	2	423.22381118	
	1178.4765468	-0.0843764	1206.4714614	10	Y	1	310.1397472	-0.0176159
				11	Q	0	147.07641866	

Source: 20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber: 9734
Protein: BSU21770; ilvA
Peptide Score: 167.32
Method: ITMS; CID; 3





precursor information

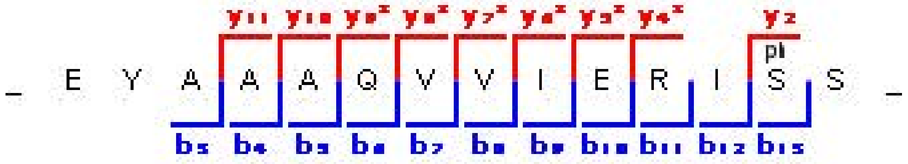
Mass:	1518.74457
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	167.3248
Mass Error [ppm]:	0.15996
PEP:	2.9713E-30
Precursor Type:	MULTI

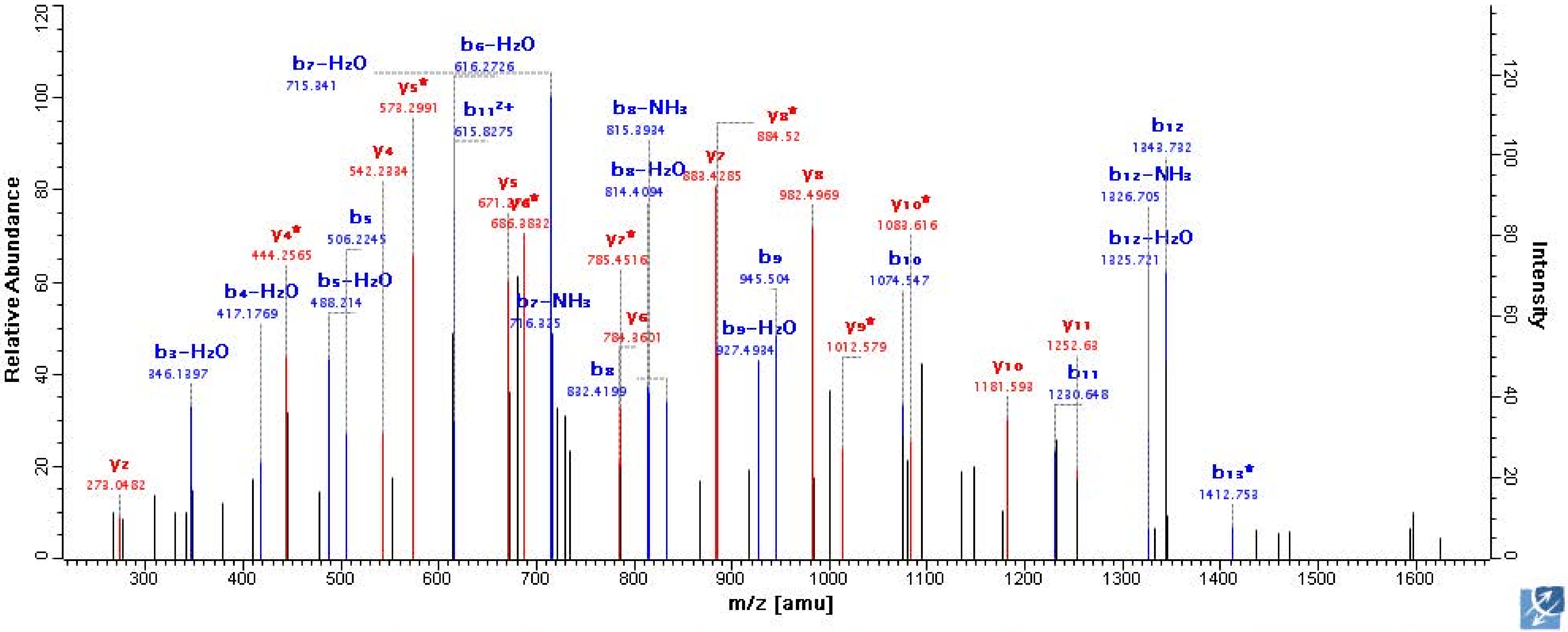
general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	75 %
Protein Localisation:	378 ... 391

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	13				
	282.04856273	2	N	12	1352.7532406		1352.7532406	
	339.07002646	3	G	11	1238.7103132	+0.26039	619.85879482	+0.034943
	436.12279031	4	P	10	1181.6888494	+0.0548029	591.34806296	-0.0774941
	507.1599041	5	A	9	1084.6360856	-0.0982438	1084.6360856	
	620.24396808	6	I	8	1013.5989718	-0.000278	1013.5989718	
	719.31238199	7	V	7	900.51490783	+0.045578	900.51490783	
	776.33384572	8	G	6	801.44649391	+0.0232937	801.44649391	
	889.4179097	9	I	5	744.42503019		372.71615333	-0.3160679
+0.0135573	1018.4605028	10	E	4	631.34096621	+0.0290289	631.34096621	
	1131.5445668	11	I	3	502.29837311	+0.1136142	502.29837311	
+0.3002981	1259.6031443	12	Q	2	389.21430913	+0.0544897	389.21430913	
	1373.6460717	13	N	1	261.15573162	+0.0933529	261.15573162	
		14	K	0	147.11280417		147.11280417	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F19
Scannumber:	9977
Protein:	acpS; BSU04620; ydcB
Peptide Score:	184.76
Method:	ITMS; CID; 3





precursor information

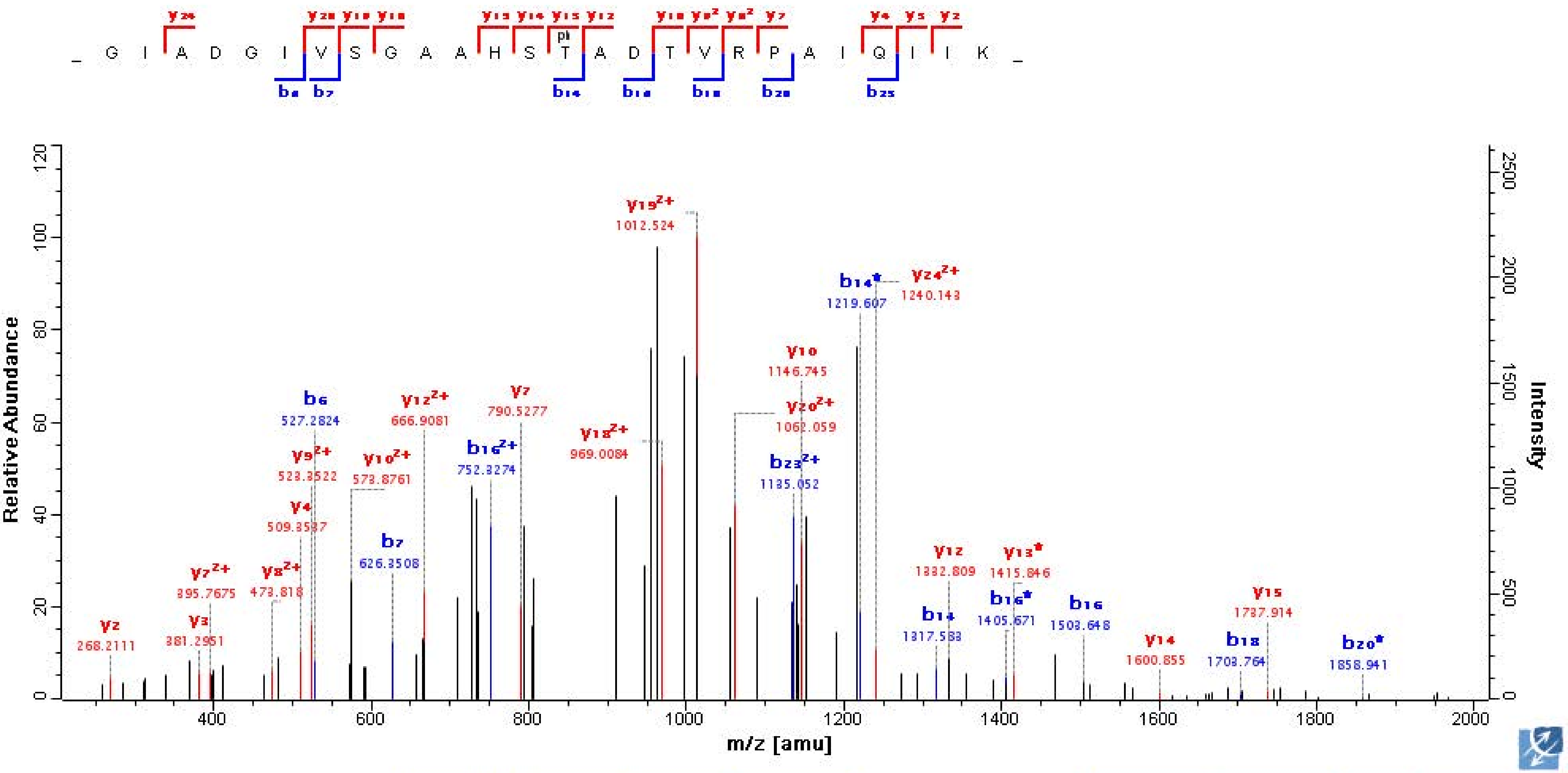
Mass:	1614.76474
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	184.7638
Mass Error [ppm]:	-0.4396
PEP:	1.7362E-63
Precursor Type:	ISO

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	64 %
Protein Localisation:	108 ... 121

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	13		
	293.1131981		293.1131981	2	Y	12	1486.7301357	
	364.15031189		364.15031189	3	A	11	1323.6668072	
	435.18742568		435.18742568	4	A	10	1252.6296934	+0.0930849
	506.22453946	-0.0527865	506.22453946	5	A	9	1181.5925796	+0.2743638
	634.28311698		634.28311698	6	Q	8	1110.5554658	
	733.35153089		733.35153089	7	V	7	982.4968883	-0.0281993
	832.41994481	-0.0460434	832.41994481	8	V	6	883.42847438	+0.0537034
	945.50400879	+0.0688062	945.50400879	9	I	5	784.36006047	+0.40471
	1074.5466019	+0.0776657	1074.5466019	10	E	4	671.27599649	-0.0377763
+0.0272416	615.82749469	-0.0094072	1230.6477129	11	R	3	542.23340339	-0.1383106
	1343.7317769	-0.01144	1343.7317769	12	I	2	386.13229236	
	1510.7301357		1510.7301357	13	S	1	273.04822838	-0.0036422
				14	S	0	106.04986956	

Source: 20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F06
Scannumber: 10764
Protein: BSU37660; ipa-88d; pta; ywfJ
Peptide Score: 87.88
Method: ITMS; CID; 3



precursor information

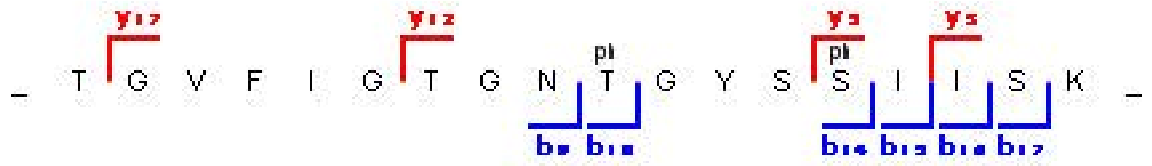
Mass:	2648.37789
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.88075
Mass Error [ppm]:	0.024362
PEP:	6.2465E-13
Precursor Type:	ISO

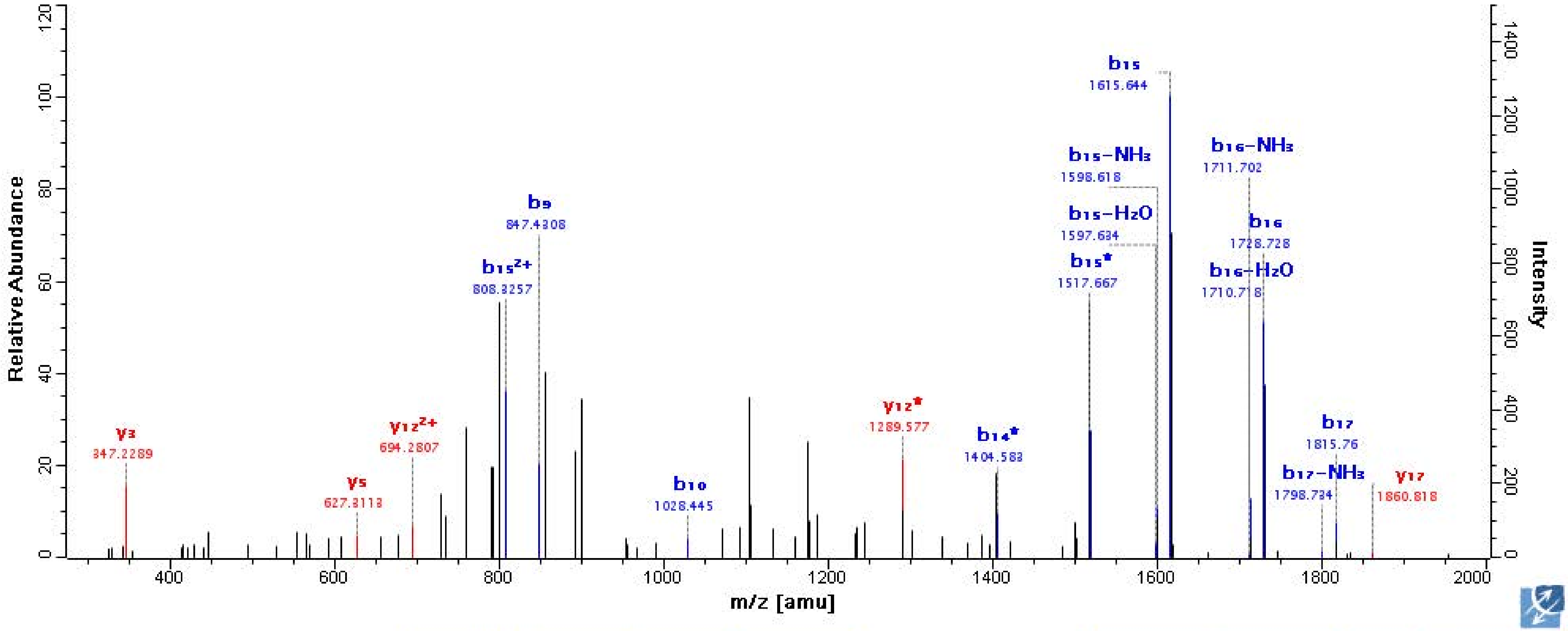
general information

Annotation:	18 of 26
AminoAcids Coverag	69 %
Intensity Coverage:	32 %
Protein Localisation:	116 ... 141

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	25				
	171.1128		171.1128	2	I	24	2592.364		2592.364	
	242.1499		242.1499	3	A	23	2479.28		1240.143	+0.239385
	357.1769		357.1769	4	D	22	2408.242		2408.242	
	414.1983		414.1983	5	G	21	2293.216		2293.216	
	527.2824	+0.006124	527.2824	6	I	20	2236.194		2236.194	
	626.3508	+0.035611	626.3508	7	V	19	2123.11		1062.059	+0.262654
	713.3828		713.3828	8	S	18	2024.042		1012.524	+0.36516
	770.4043		770.4043	9	G	17	1937.01		969.0084	+0.288706
	841.4414		841.4414	10	A	16	1879.988		1879.988	
	912.4785		912.4785	11	A	15	1808.951		1808.951	
	1049.537		1049.537	12	H	14	1737.914	+0.104451	1737.914	
	1136.569		1136.569	13	S	13	1600.855	+0.080355	1600.855	
	1317.583	+0.201563	1317.583	14	T	12	1513.823		1513.823	
	1388.621		1388.621	15	A	11	1332.809	+0.079639	666.9081	-0.051587
+0.200369	752.3274	+0.045221	1503.648	16	D	10	1261.772		1261.772	
	1604.695		1604.695	17	T	9	1146.745	+0.105977	573.8761	-0.061307
	1703.764	+0.346487	1703.764	18	V	8	1045.697		523.3522	-0.030937
	1859.865		1859.865	19	R	7	946.6288		473.818	+0.226598
	1956.917		1956.917	20	P	6	790.5277	-0.270509	395.7675	+0.44793
	2027.955		2027.955	21	A	5	693.4749		693.4749	
	2141.039		2141.039	22	I	4	622.4378		622.4378	
+0.100813	1135.052		2269.097	23	Q	3	509.3537	-0.007883	509.3537	
	2382.181		2382.181	24	I	2	381.2951	-0.117885	381.2951	
	2495.265		2495.265	25	I	1	268.2111	+0.068657	268.2111	
				26	K	0	155.127		155.127	

Source: 20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F06
Scannumber: 8656
Protein: BSU17210; pksN
Peptide Score: 69.76
Method: ITMS; CID; 3





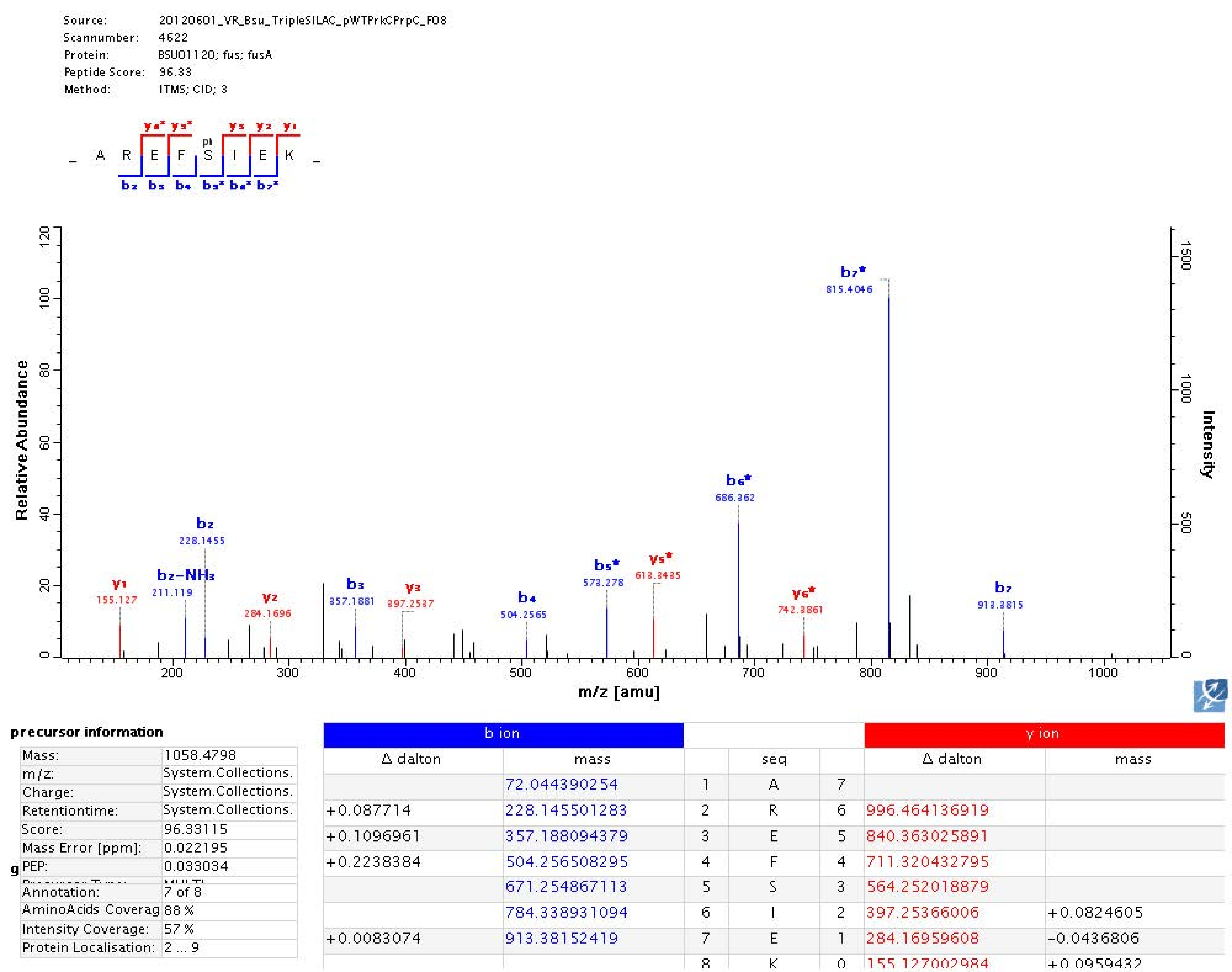
precursor information

Mass:	1960.85885
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	69.76321
Mass Error [ppm]:	0.21141
PEP:	0.12437
Precursor Type:	ISO

general information

Annotation:	8 of 18
AminoAcids Coverag	44 %
Intensity Coverage:	31 %
Protein Localisation:	2691 ... 2708

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	17				
	159.0764		159.0764	2	G	16	1860.818	+0.155717	1860.818	
	258.1448		258.1448	3	V	15	1803.797		1803.797	
	405.2132		405.2132	4	F	14	1704.728		1704.728	
	518.2973		518.2973	5	I	13	1557.66		1557.66	
	575.3188		575.3188	6	G	12	1444.576		1444.576	
	676.3665		676.3665	7	T	11	1387.554		694.2807	+0.231337
	733.3879		733.3879	8	G	10	1286.507		1286.507	
	847.4308	-0.140439	847.4308	9	N	9	1229.485		1229.485	
	1028.445	+0.204805	1028.445	10	T	8	1115.442		1115.442	
	1085.466		1085.466	11	G	7	934.4281		934.4281	
	1248.53		1248.53	12	Y	6	877.4067		877.4067	
	1335.562		1335.562	13	S	5	714.3433		714.3433	
	1502.56		1502.56	14	S	4	627.3113	-0.078287	627.3113	
-0.00574	808.3257	+0.079292	1615.644	15	I	3	460.313		460.313	
	1728.728	+0.176259	1728.728	16	I	2	347.2289	+0.03444	347.2289	
	1815.76	+0.182927	1815.76	17	S	1	234.1448		234.1448	
				18	K	0	147.1128		147.1128	



Source:	20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F08
Scannumber:	4622
Protein:	BSU01120; fus; fusA
Peptide Score:	96.33
Method:	ITMS; CID; 3

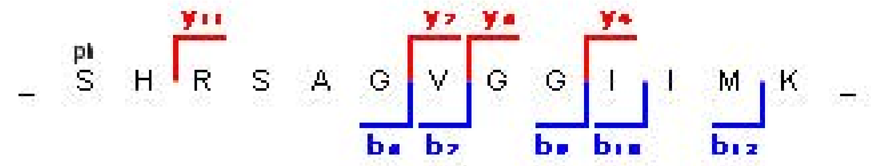
precursor information

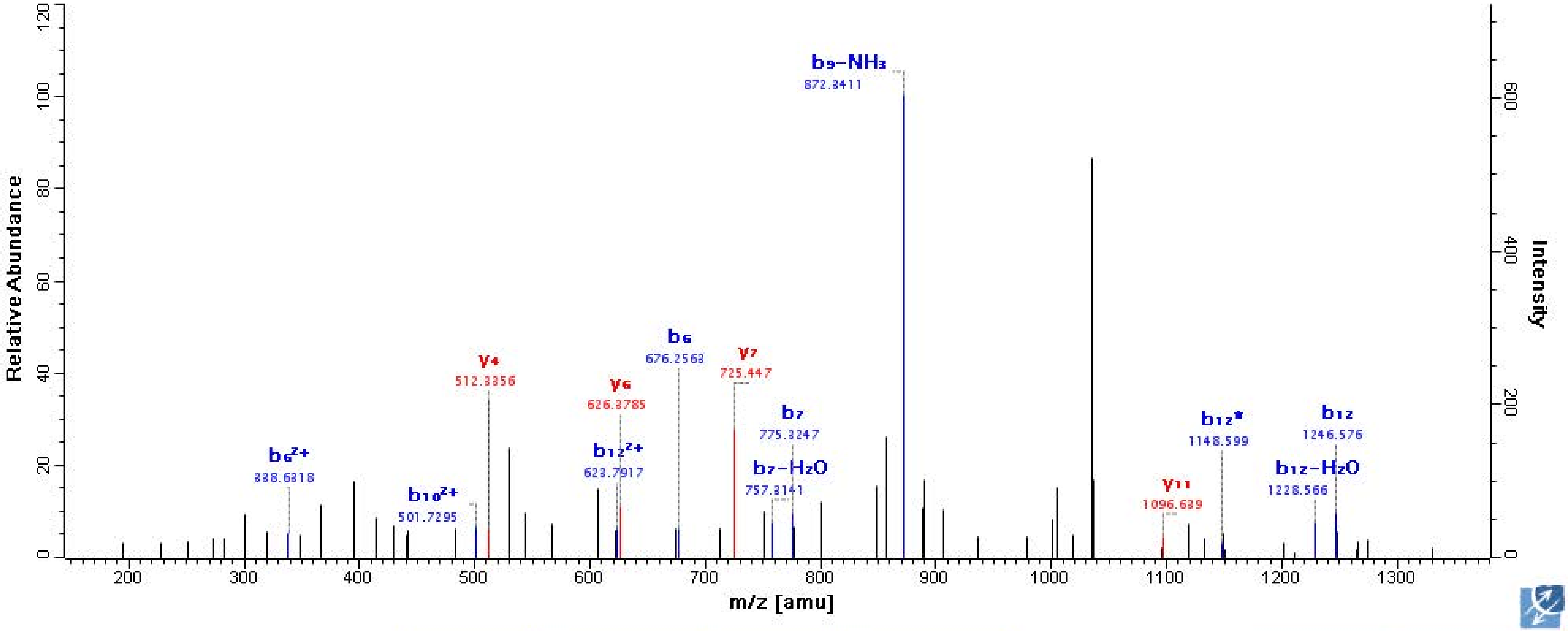
g

Mass:	1058.4798
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	96.33115
Mass Error [ppm]:	0.022195
PEP:	0.033034
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	57 %
Protein Localisation:	2 ... 9

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	7		
+0.087714	228.145501283	2	R	6	996.464136919	
+0.1096961	357.188094379	3	E	5	840.363025891	
+0.2238384	504.256508295	4	F	4	711.320432795	
	671.254867113	5	S	3	564.252018879	
	784.338931094	6	I	2	397.25366006	+0.0824605
+0.0083074	913.38152419	7	E	1	284.16959608	-0.0436806
		8	K	0	155.127002984	+0.0959432

Source: 20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F08
Scannumber: 9474
Protein: BSU11840; yjcF
Peptide Score: 55.04
Method: ITMS; CID; 3





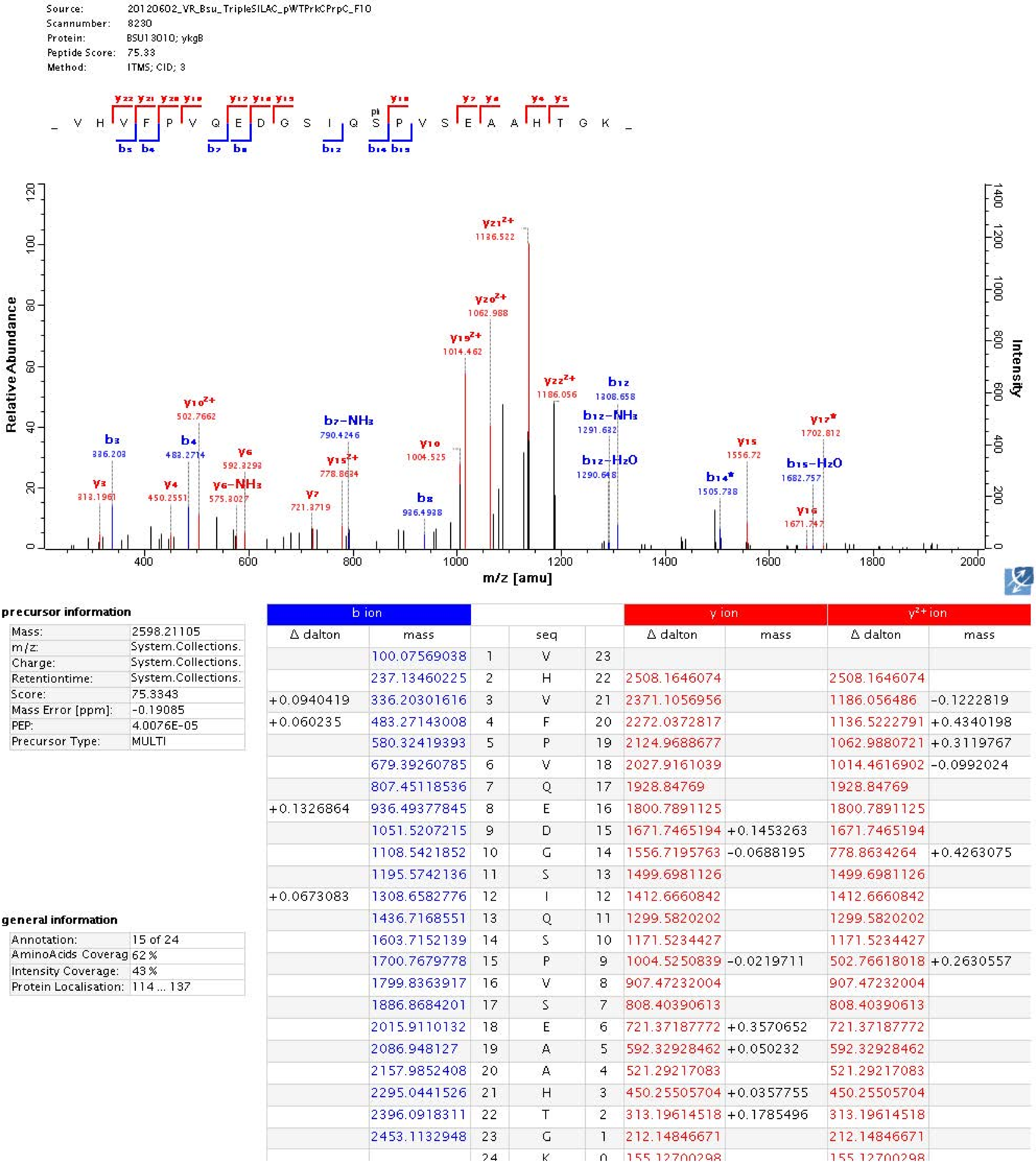
precursor information

Mass:	1391.67334
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	55.0402
Mass Error [ppm]:	-0.80357
PEP:	0.046952
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54%
Intensity Coverage:	29%
Protein Localisation:	76 ... 88

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	168.00563528		168.00563528	1	S	12		
	305.06454715		305.06454715	2	H	11	1233.6975857	
	461.16565818		461.16565818	3	R	10	1096.6386739	-0.1145039
	548.19768659		548.19768659	4	S	9	940.53756284	
	619.23480037		619.23480037	5	A	8	853.50553443	
-0.4338333	338.63177028	+0.2130352	676.2562641	6	G	7	782.46842064	
	775.32467801	+0.2134079	775.32467801	7	V	6	725.44695691	+0.0151403
	832.34614174		832.34614174	8	G	5	626.378543	+0.0021943
	889.36760546		889.36760546	9	G	4	569.35707927	
-0.4300345	501.72947295		1002.4516694	10	I	3	512.33561555	+0.130571
	1115.5357334		1115.5357334	11	I	2	399.25155157	
-0.1000358	623.79174725	+0.3227078	1246.576218	12	M	1	286.16748759	
				13	K	0	155.12700298	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F10
Scannumber: 8230
Protein: BSU13010; ykgB
Peptide Score: 75.33
Method: ITMS; CID; 3

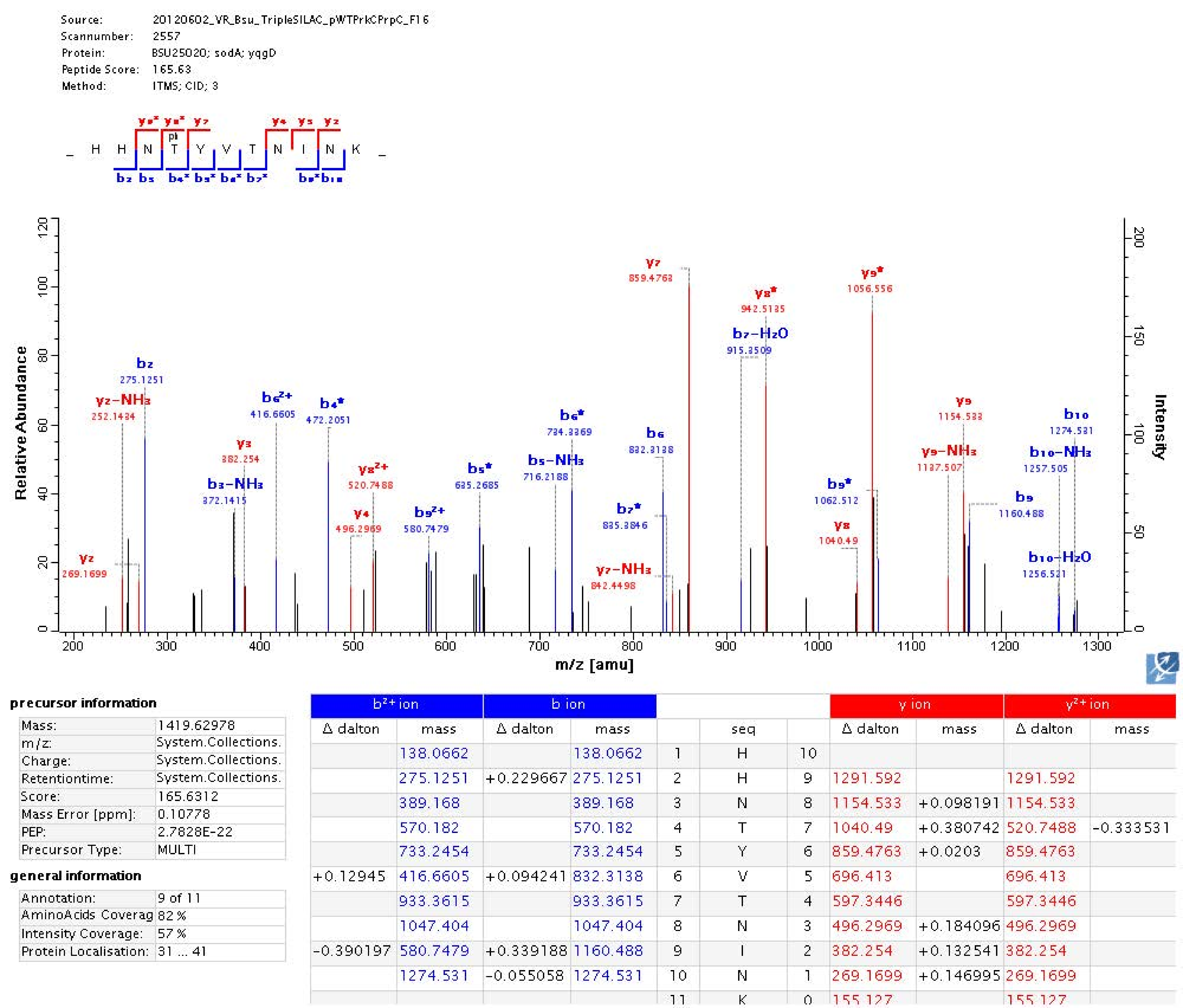
precursor information

Mass:	2598.21105
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	75.3343
Mass Error [ppm]:	-0.19085
PEP:	4.0076E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	43 %
Protein Localisation:	114 ... 137

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	23				
	237.13460225	2	H	22	2508.1646074		2508.1646074	
+0.0940419	336.20301616	3	V	21	2371.1056956		1186.056486	-0.1222819
+0.060235	483.27143008	4	F	20	2272.0372817		1136.5222791	+0.4340198
	580.32419393	5	P	19	2124.9688677		1062.9880721	+0.3119767
	679.39260785	6	V	18	2027.9161039		1014.4616902	-0.0992024
	807.45118536	7	Q	17	1928.84769		1928.84769	
+0.1326864	936.49377845	8	E	16	1800.7891125		1800.7891125	
	1051.5207215	9	D	15	1671.7465194	+0.1453263	1671.7465194	
	1108.5421852	10	G	14	1556.7195763	-0.0688195	778.8634264	+0.4263075
	1195.5742136	11	S	13	1499.6981126		1499.6981126	
+0.0673083	1308.6582776	12	I	12	1412.6660842		1412.6660842	
	1436.7168551	13	Q	11	1299.5820202		1299.5820202	
	1603.7152139	14	S	10	1171.5234427		1171.5234427	
	1700.7679778	15	P	9	1004.5250839	-0.0219711	502.76618018	+0.2630557
	1799.8363917	16	V	8	907.47232004		907.47232004	
	1886.8684201	17	S	7	808.40390613		808.40390613	
	2015.9110132	18	E	6	721.37187772	+0.3570652	721.37187772	
	2086.948127	19	A	5	592.32928462	+0.050232	592.32928462	
	2157.9852408	20	A	4	521.29217083		521.29217083	
	2295.0441526	21	H	3	450.25505704	+0.0357755	450.25505704	
	2396.0918311	22	T	2	313.19614518	+0.1785496	313.19614518	
	2453.1132948	23	G	1	212.14846671		212.14846671	
		24	K	0	155.12700298		155.12700298	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F16
Scannumber: 2557
Protein: BSU25020; sodA; yqgD
Peptide Score: 165.63
Method: ITMS; CID; 3

precursor information

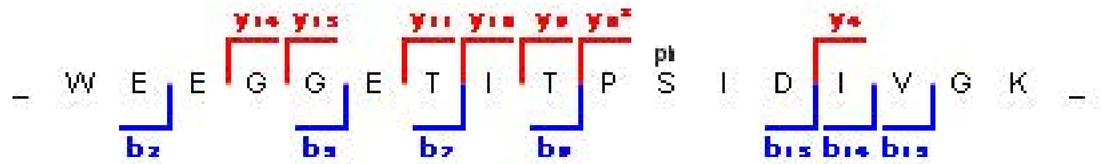
Mass:	1419.62978
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	165.6312
Mass Error [ppm]:	0.10778
PEP:	2.7828E-22
Precursor Type:	MULTI

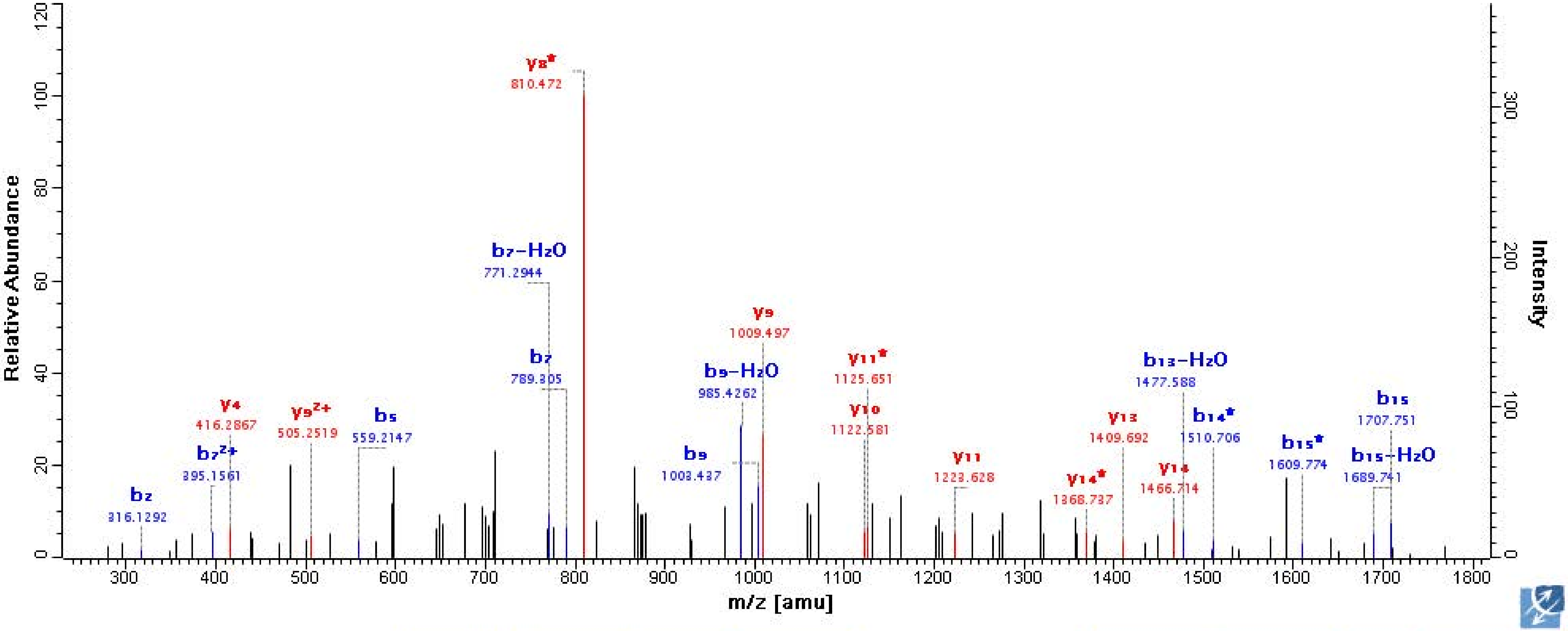
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	57 %
Protein Localisation:	31 ... 41

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.0662		138.0662	1	H	10				
	275.1251	+0.229667	275.1251	2	H	9	1291.592		1291.592	
	389.168		389.168	3	N	8	1154.533	+0.098191	1154.533	
	570.182		570.182	4	T	7	1040.49	+0.380742	520.7488	-0.333531
	733.2454		733.2454	5	Y	6	859.4763	+0.0203	859.4763	
+0.12945	416.6605	+0.094241	832.3138	6	V	5	696.413		696.413	
	933.3615		933.3615	7	T	4	597.3446		597.3446	
	1047.404		1047.404	8	N	3	496.2969	+0.184096	496.2969	
-0.390197	580.7479	+0.339188	1160.488	9	I	2	382.254	+0.132541	382.254	
	1274.531	-0.055058	1274.531	10	N	1	269.1699	+0.146995	269.1699	
				11	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber:	11318
Protein:	ahpC; BSU40090
Peptide Score:	80.54
Method:	ITMS; CID; 3





precursor information

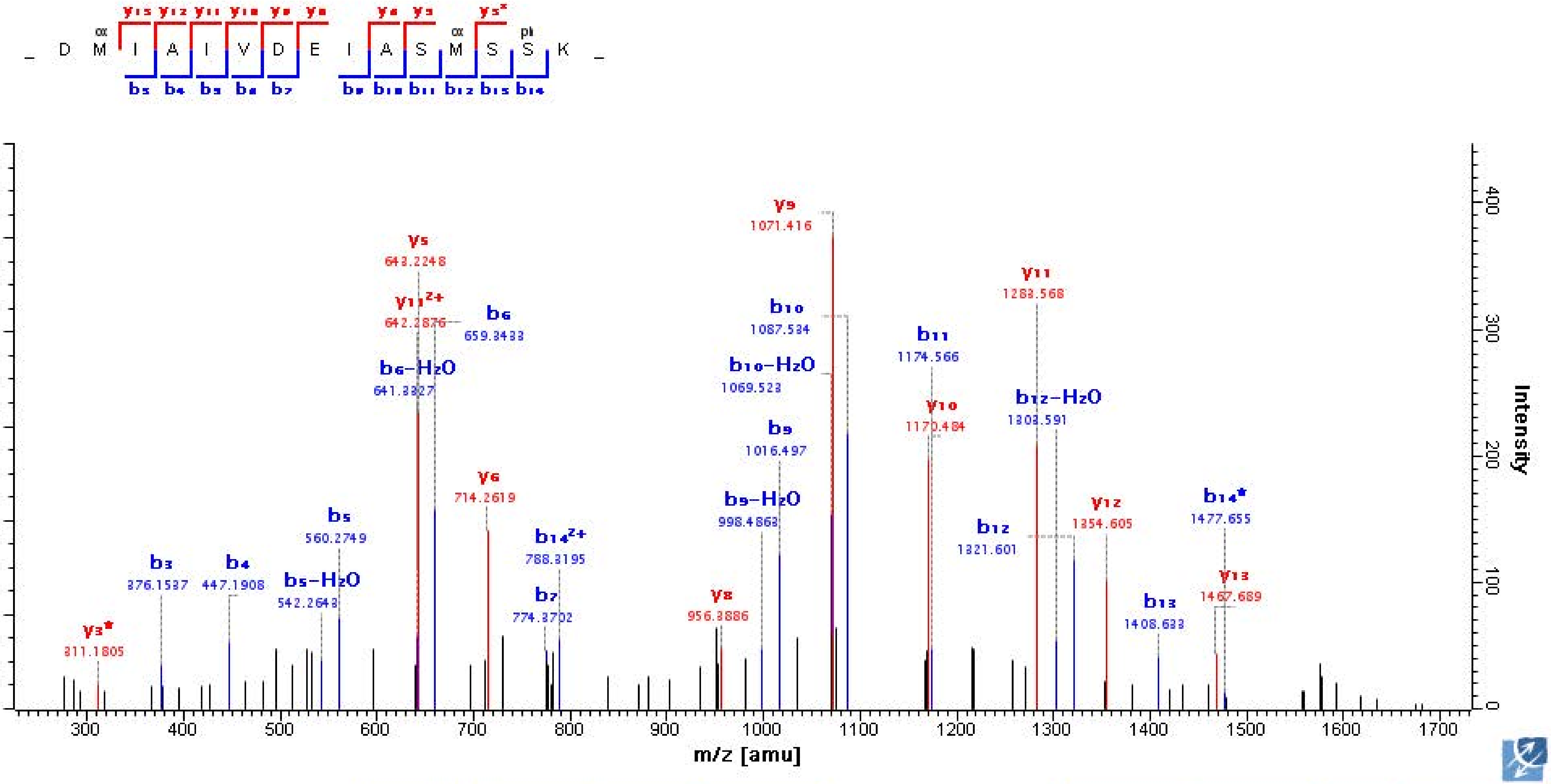
Mass:	1909.87035
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	80.54491
Mass Error [ppm]:	-0.36322
PEP:	6.8224E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	34 %
Protein Localisation:	170 ... 186

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.0866		187.0866	1	W	16				
	316.1292	+0.178435	316.1292	2	E	15	1724.799		1724.799	
	445.1718		445.1718	3	E	14	1595.756		1595.756	
	502.1932		502.1932	4	G	13	1466.714	+0.171681	1466.714	
	559.2147	+0.195514	559.2147	5	G	12	1409.692	+0.145415	1409.692	
	688.2573		688.2573	6	E	11	1352.671		1352.671	
+0.346713	395.1561	+0.165301	789.305	7	T	10	1223.628	+0.067871	1223.628	
	902.389		902.389	8	I	9	1122.581	+0.223093	1122.581	
	1003.437	-0.045787	1003.437	9	T	8	1009.497	+0.122098	505.2519	-0.217491
	1100.489		1100.489	10	P	7	908.4489		908.4489	
	1267.488		1267.488	11	S	6	811.3961		811.3961	
	1380.572		1380.572	12	I	5	644.3978		644.3978	
	1495.599		1495.599	13	D	4	531.3137		531.3137	
	1608.683		1608.683	14	I	3	416.2867	+0.24072	416.2867	
	1707.751	+0.384051	1707.751	15	V	2	303.2027		303.2027	
	1764.773		1764.773	16	G	1	204.1343		204.1343	
				17	K	0	147.1128		147.1128	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber:	11511
Protein:	ahpF; BSU40100; ndh
Peptide Score:	171.29
Method:	ITMS; CID; 3



precursor information

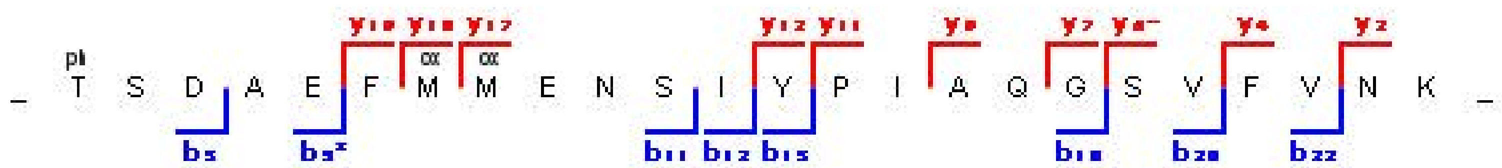
Mass:	1720.73097
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	171.288
Mass Error [ppm]:	0.53109
PEP:	1.5262E-33
Precursor Type:	MULTI

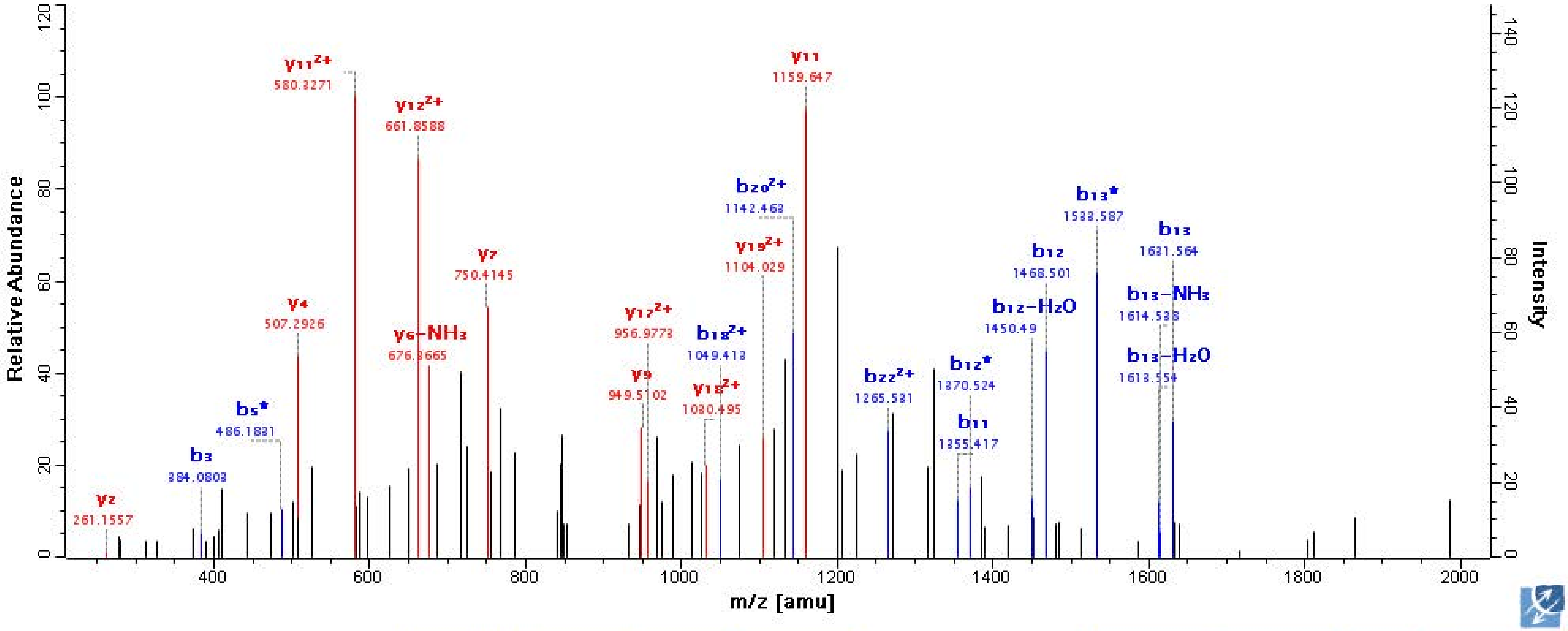
general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	62 %
Protein Localisation:	36 ... 50

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	14				
	263.0696		263.0696	2	M	13	1614.725		1614.725	
	376.1537	+0.07169	376.1537	3	I	12	1467.689	+0.230734	1467.689	
	447.1908	+0.005432	447.1908	4	A	11	1354.605	+0.240702	1354.605	
	560.2749	+0.054058	560.2749	5	I	10	1283.568	+0.069319	642.2876	+0.27089
	659.3433	-0.007398	659.3433	6	V	9	1170.484	+0.135195	1170.484	
	774.3702	+0.387168	774.3702	7	D	8	1071.416	-0.022954	1071.416	
	903.4128		903.4128	8	E	7	956.3886	+0.109885	956.3886	
	1016.497	-0.042712	1016.497	9	I	6	827.346		827.346	
	1087.534	-0.011405	1087.534	10	A	5	714.2619	+0.229279	714.2619	
	1174.566	-0.008644	1174.566	11	S	4	643.2248	+0.120885	643.2248	
	1321.601	+0.064966	1321.601	12	M	3	556.1928		556.1928	
	1408.633	+0.447	1408.633	13	S	2	409.1574		409.1574	
+0.396952	788.3195		1575.632	14	S	1	322.1254		322.1254	
				15	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 12189
Protein: BSU07710; ltaS2; yflE
Peptide Score: 77.69
Method: ITMS; CID; 3





precursor information

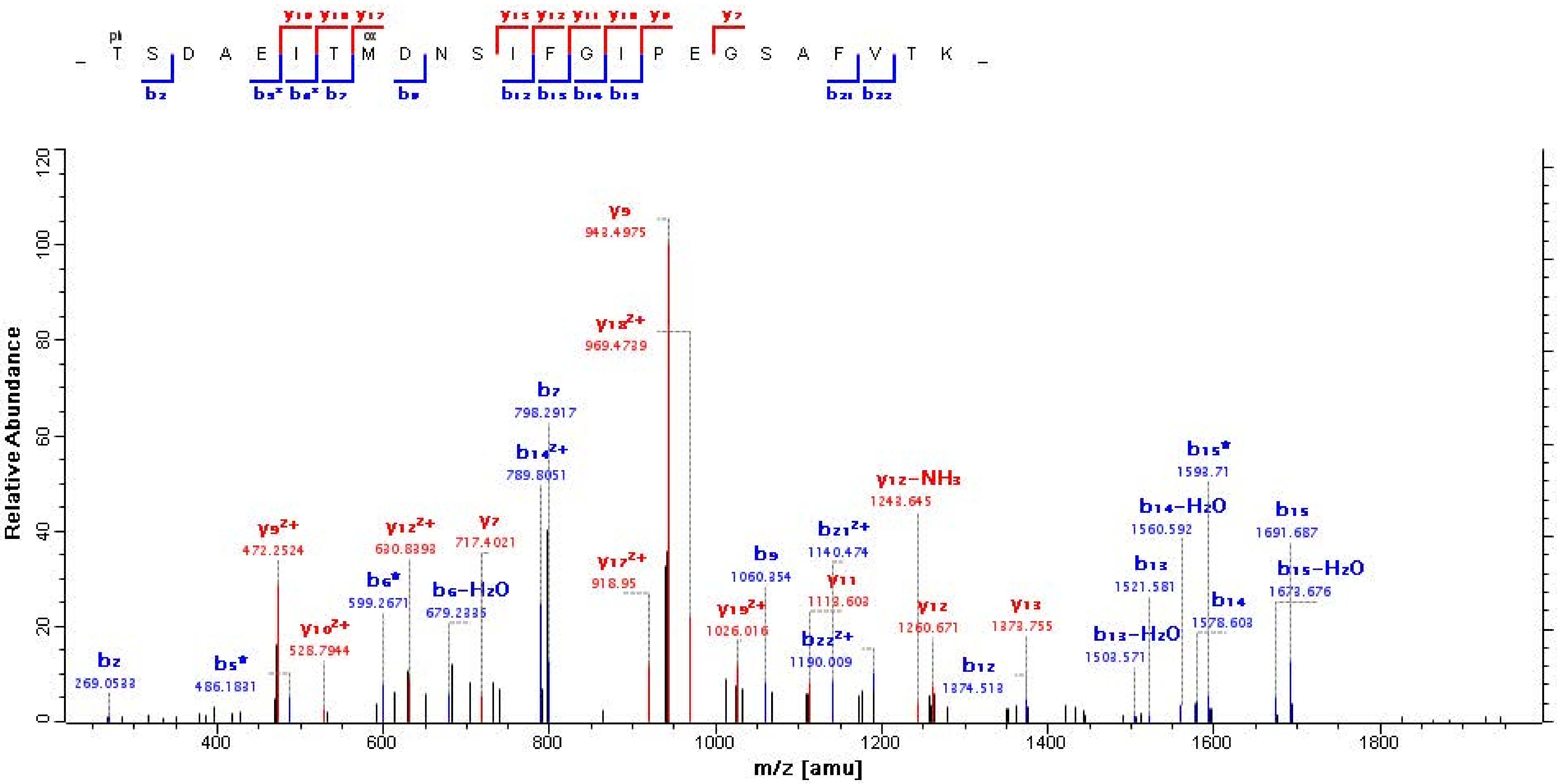
Mass:	2789.19709
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.689
Mass Error [ppm]:	0.19417
PEP:	4.2175E-05
Precursor Type:	MULTI

general information

Annotation:	16 of 24
AminoAcids Coverag	67 %
Intensity Coverage:	46 %
Protein Localisation:	297 ... 320

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.0213		182.0213	1	T	23				
	269.0533		269.0533	2	S	22	2609.19		2609.19	
	384.0803	+0.094243	384.0803	3	D	21	2522.158		2522.158	
	455.1174		455.1174	4	A	20	2407.131		2407.131	
	584.16		584.16	5	E	19	2336.094		2336.094	
	731.2284		731.2284	6	F	18	2207.051		1104.029	+0.165861
	878.2638		878.2638	7	M	17	2059.983		1030.495	+0.319453
	1025.299		1025.299	8	M	16	1912.947		956.9773	+0.357965
	1154.342		1154.342	9	E	15	1765.912		1765.912	
	1268.385		1268.385	10	N	14	1636.869		1636.869	
	1355.417	-0.461403	1355.417	11	S	13	1522.826		1522.826	
	1468.501	+0.081486	1468.501	12	I	12	1435.794		1435.794	
	1631.564	+0.10788	1631.564	13	Y	11	1322.71		661.8588	+0.029328
	1728.617		1728.617	14	P	10	1159.647	+0.101306	580.3271	+0.273394
	1841.701		1841.701	15	I	9	1062.594		1062.594	
	1912.738		1912.738	16	A	8	949.5102	-0.016199	949.5102	
	2040.797		2040.797	17	Q	7	878.473		878.473	
-0.15805	1049.413		2097.818	18	G	6	750.4145	+0.288537	750.4145	
	2184.85		2184.85	19	S	5	693.393		693.393	
+0.325054	1142.463		2283.919	20	V	4	606.361		606.361	
	2430.987		2430.987	21	F	3	507.2926	+0.068463	507.2926	
-0.24458	1265.531		2530.055	22	V	2	360.2241		360.2241	
	2644.098		2644.098	23	N	1	261.1557	+0.051391	261.1557	
				24	K	0	147.1128		147.1128	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 12834
Protein: BSU07260; ltaS1; yfnI
Peptide Score: 108.57
Method: ITMS; CID; 3



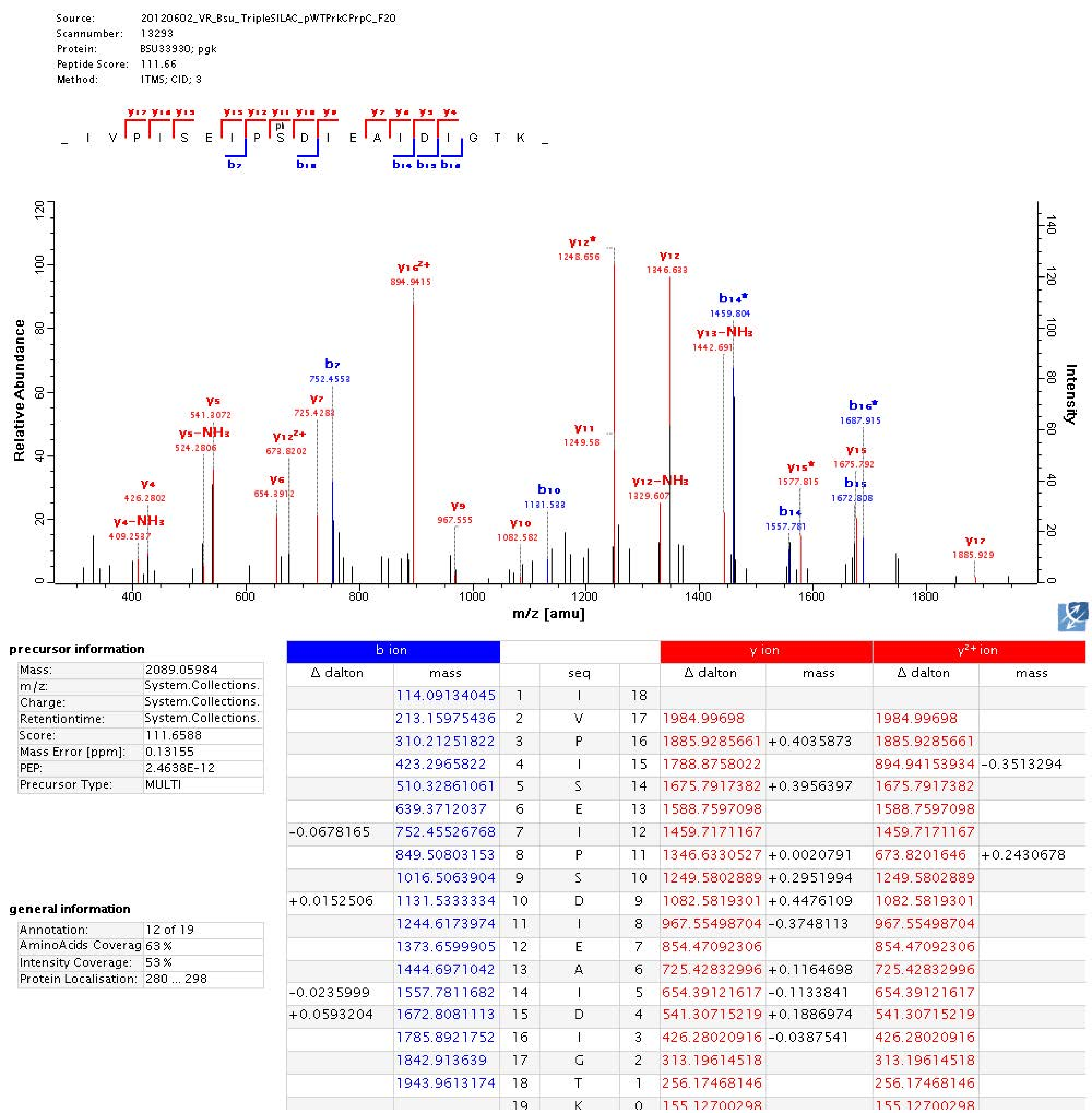
precursor information

Mass:	2633.16948
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.574
Mass Error [ppm]:	-0.17175
PEP:	3.1111E-08
Precursor Type:	ISO

general information

Annotation:	15 of 24
AminoAcids Coverag	62 %
Intensity Coverage:	45 %
Protein Localisation:	297 ... 320

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.0213		182.0213	1	T	23				
	269.0533	+0.144593	269.0533	2	S	22	2453.163		2453.163	
	384.0803		384.0803	3	D	21	2366.131		2366.131	
	455.1174		455.1174	4	A	20	2251.104		2251.104	
	584.16		584.16	5	E	19	2180.067		2180.067	
	697.244		697.244	6	I	18	2051.025		1026.016	+0.311251
	798.2917	+0.267315	798.2917	7	T	17	1937.94		969.4739	-0.203358
	945.3271		945.3271	8	M	16	1836.893		918.95	+0.19182
	1060.354	-0.45146	1060.354	9	D	15	1689.857		1689.857	
	1174.397		1174.397	10	N	14	1574.83		1574.83	
	1261.429		1261.429	11	S	13	1460.788		1460.788	
	1374.513	+0.163323	1374.513	12	I	12	1373.755	+0.167252	1373.755	
	1521.581	+0.331482	1521.581	13	F	11	1260.671	+0.009372	630.8393	+0.02473
+0.043827	789.8051	-0.409831	1578.603	14	G	10	1113.603	+0.03616	1113.603	
	1691.687	-0.047117	1691.687	15	I	9	1056.582		528.7944	-0.189487
	1788.74		1788.74	16	P	8	943.4975	+0.059657	472.2524	+0.154425
	1917.782		1917.782	17	E	7	846.4447		846.4447	
	1974.804		1974.804	18	G	6	717.4021	+0.221664	717.4021	
	2061.836		2061.836	19	S	5	660.3807		660.3807	
	2132.873		2132.873	20	A	4	573.3486		573.3486	
+0.392612	1140.474		2279.941	21	F	3	502.3115		502.3115	
-0.106683	1190.009		2379.01	22	V	2	355.2431		355.2431	
	2480.057		2480.057	23	T	1	256.1747		256.1747	
				24	K	0	155.127		155.127	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 13293
Protein: BSU33930; pgk
Peptide Score: 111.66
Method: ITMS; CID; 3

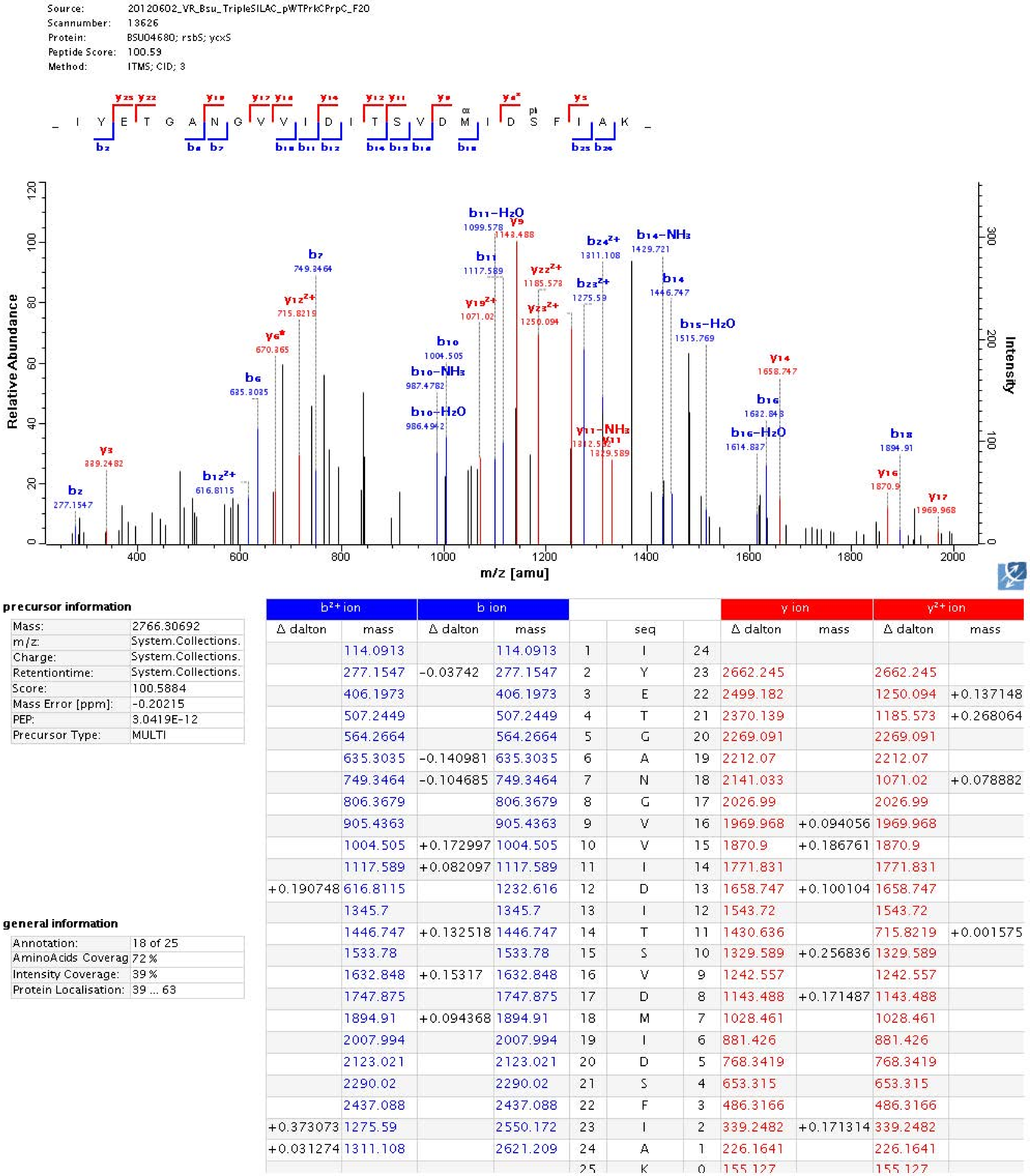
precursor information

Mass:	2089.05984
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.6588
Mass Error [ppm]:	0.13155
PEP:	2.4638E-12
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	53 %
Protein Localisation:	280 ... 298

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	18				
	213.15975436	2	V	17	1984.99698		1984.99698	
	310.21251822	3	P	16	1885.9285661	+0.4035873	1885.9285661	
	423.2965822	4	I	15	1788.8758022		894.94153934	-0.3513294
	510.32861061	5	S	14	1675.7917382	+0.3956397	1675.7917382	
	639.3712037	6	E	13	1588.7597098		1588.7597098	
-0.0678165	752.45526768	7	I	12	1459.7171167		1459.7171167	
	849.50803153	8	P	11	1346.6330527	+0.0020791	673.8201646	+0.2430678
	1016.5063904	9	S	10	1249.5802889	+0.2951994	1249.5802889	
+0.0152506	1131.5333334	10	D	9	1082.5819301	+0.4476109	1082.5819301	
	1244.6173974	11	I	8	967.55498704	-0.3748113	967.55498704	
	1373.6599905	12	E	7	854.47092306		854.47092306	
	1444.6971042	13	A	6	725.42832996	+0.1164698	725.42832996	
-0.0235999	1557.7811682	14	I	5	654.39121617	-0.1133841	654.39121617	
+0.0593204	1672.8081113	15	D	4	541.30715219	+0.1886974	541.30715219	
	1785.8921752	16	I	3	426.28020916	-0.0387541	426.28020916	
	1842.913639	17	G	2	313.19614518		313.19614518	
	1943.9613174	18	T	1	256.17468146		256.17468146	
		19	K	0	155.12700298		155.12700298	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 13626
Protein: BSU04680; rsbS; ycxS
Peptide Score: 100.59
Method: ITMS; CID; 3

precursor information

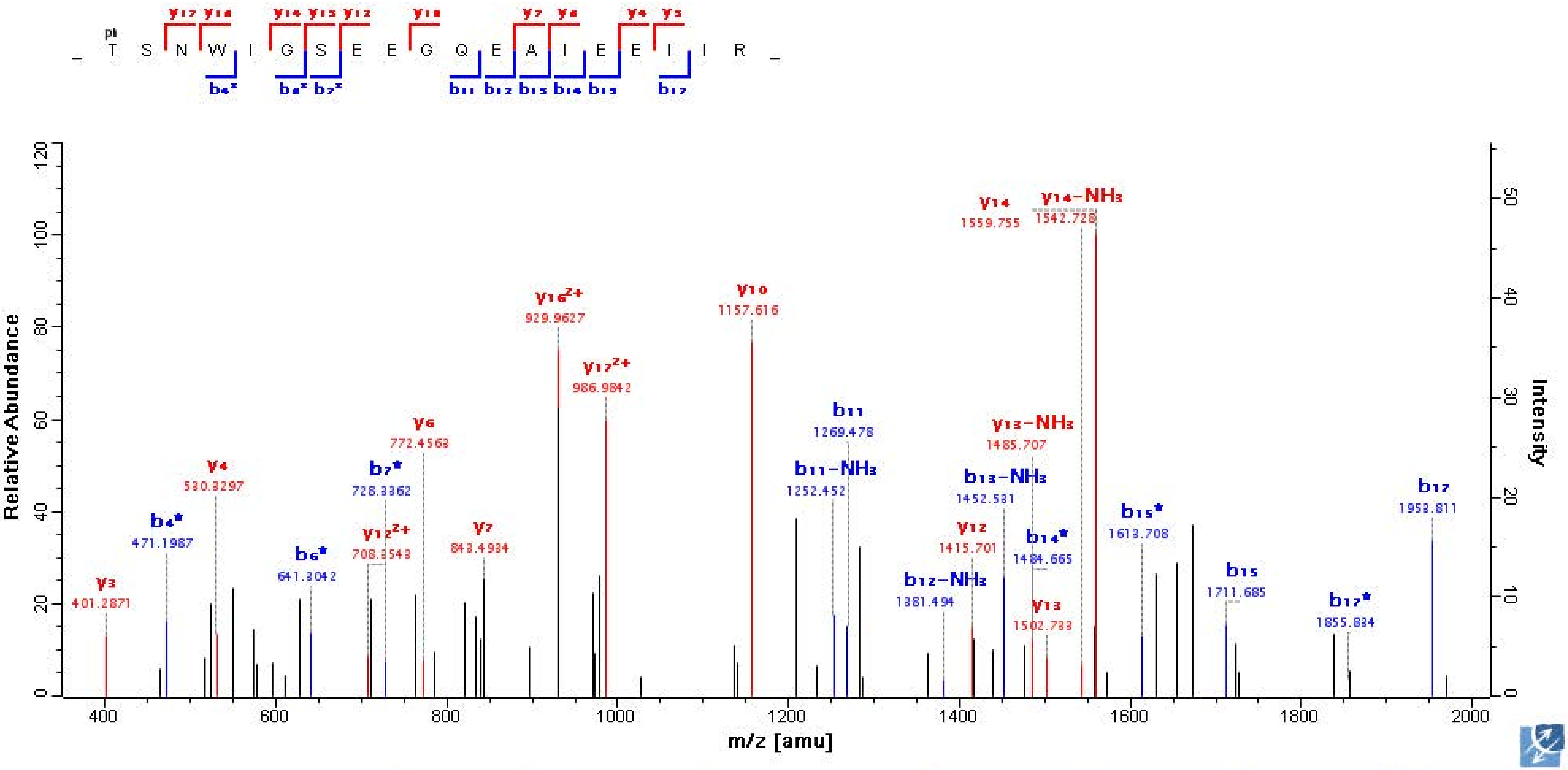
Mass:	2766.30692
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	100.5884
Mass Error [ppm]:	-0.20215
PEP:	3.0419E-12
Precursor Type:	MULTI

general information

Annotation:	18 of 25
AminoAcids Coverag	72 %
Intensity Coverage:	39 %
Protein Localisation:	39 ... 63

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	24				
	277.1547	-0.03742	277.1547	2	Y	23	2662.245		2662.245	
	406.1973		406.1973	3	E	22	2499.182		1250.094	+0.137148
	507.2449		507.2449	4	T	21	2370.139		1185.573	+0.268064
	564.2664		564.2664	5	G	20	2269.091		2269.091	
	635.3035	-0.140981	635.3035	6	A	19	2212.07		2212.07	
	749.3464	-0.104685	749.3464	7	N	18	2141.033		1071.02	+0.078882
	806.3679		806.3679	8	G	17	2026.99		2026.99	
	905.4363		905.4363	9	V	16	1969.968	+0.094056	1969.968	
	1004.505	+0.172997	1004.505	10	V	15	1870.9	+0.186761	1870.9	
	1117.589	+0.082097	1117.589	11	I	14	1771.831		1771.831	
+0.190748	616.8115		1232.616	12	D	13	1658.747	+0.100104	1658.747	
	1345.7		1345.7	13	I	12	1543.72		1543.72	
	1446.747	+0.132518	1446.747	14	T	11	1430.636		715.8219	+0.001575
	1533.78		1533.78	15	S	10	1329.589	+0.256836	1329.589	
	1632.848	+0.15317	1632.848	16	V	9	1242.557		1242.557	
	1747.875		1747.875	17	D	8	1143.488	+0.171487	1143.488	
	1894.91	+0.094368	1894.91	18	M	7	1028.461		1028.461	
	2007.994		2007.994	19	I	6	881.426		881.426	
	2123.021		2123.021	20	D	5	768.3419		768.3419	
	2290.02		2290.02	21	S	4	653.315		653.315	
	2437.088		2437.088	22	F	3	486.3166		486.3166	
+0.373073	1275.59		2550.172	23	I	2	339.2482	+0.171314	339.2482	
+0.031274	1311.108		2621.209	24	A	1	226.1641		226.1641	
				25	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber:	13692
Protein:	BSU27660; yrzD
Peptide Score:	90.72
Method:	ITMS; CID; 3



precursor information

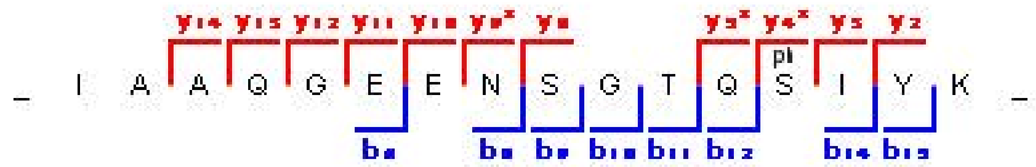
Mass:	2240.00042
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.7179
Mass Error [ppm]:	0.26549
PEP:	0.022506
Precursor Type:	ISO

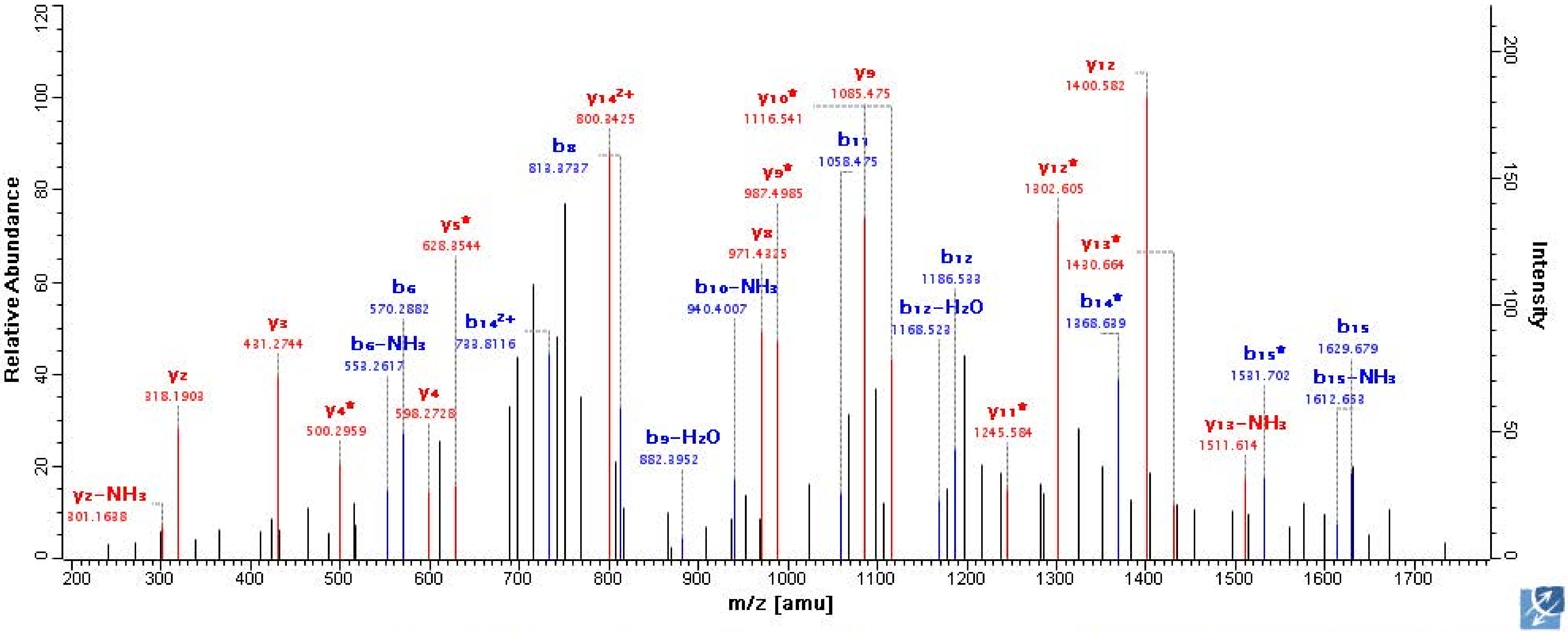
general information

Annotation:	14 of 19
AminoAcids Coverag	74 %
Intensity Coverage:	46 %
Protein Localisation:	80 ... 98

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	182.02128535	1	T	18				
	269.05331376	2	S	17	2059.9930896		2059.9930896	
	383.09624121	3	N	16	1972.9610611		986.9841688	-0.1335829
	569.17555416	4	W	15	1858.9181337		929.96270508	-0.0081152
	682.25961814	5	I	14	1672.8388207		1672.8388207	
	739.28108186	6	G	13	1559.7547568	+0.222294	1559.7547568	
	826.31311027	7	S	12	1502.733293	+0.0961747	1502.733293	
	955.35570337	8	E	11	1415.7012646	-0.0461133	708.35427055	-0.4182354
	1084.3982965	9	E	10	1286.6586715		1286.6586715	
	1141.4197602	10	G	9	1157.6160784	+0.0454206	1157.6160784	
-0.3178152	1269.4783377	11	Q	8	1100.5946147		1100.5946147	
	1398.5209308	12	E	7	972.5360372		972.5360372	
	1469.5580446	13	A	6	843.4934441	-0.3253533	843.4934441	
	1582.6421086	14	I	5	772.45633031	-0.2458811	772.45633031	
+0.3349517	1711.6847017	15	E	4	659.37226633		659.37226633	
	1840.7272948	16	E	3	530.32967324	+0.2582174	530.32967324	
+0.1514098	1953.8113587	17	I	2	401.28708014	+0.037871	401.28708014	
	2066.8954227	18	I	1	288.20301616		288.20301616	
		19	R	0	175.11895218		175.11895218	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 6072
Protein: BSU13960; ykwC
Peptide Score: 139.49
Method: ITMS; CID; 3





precursor information

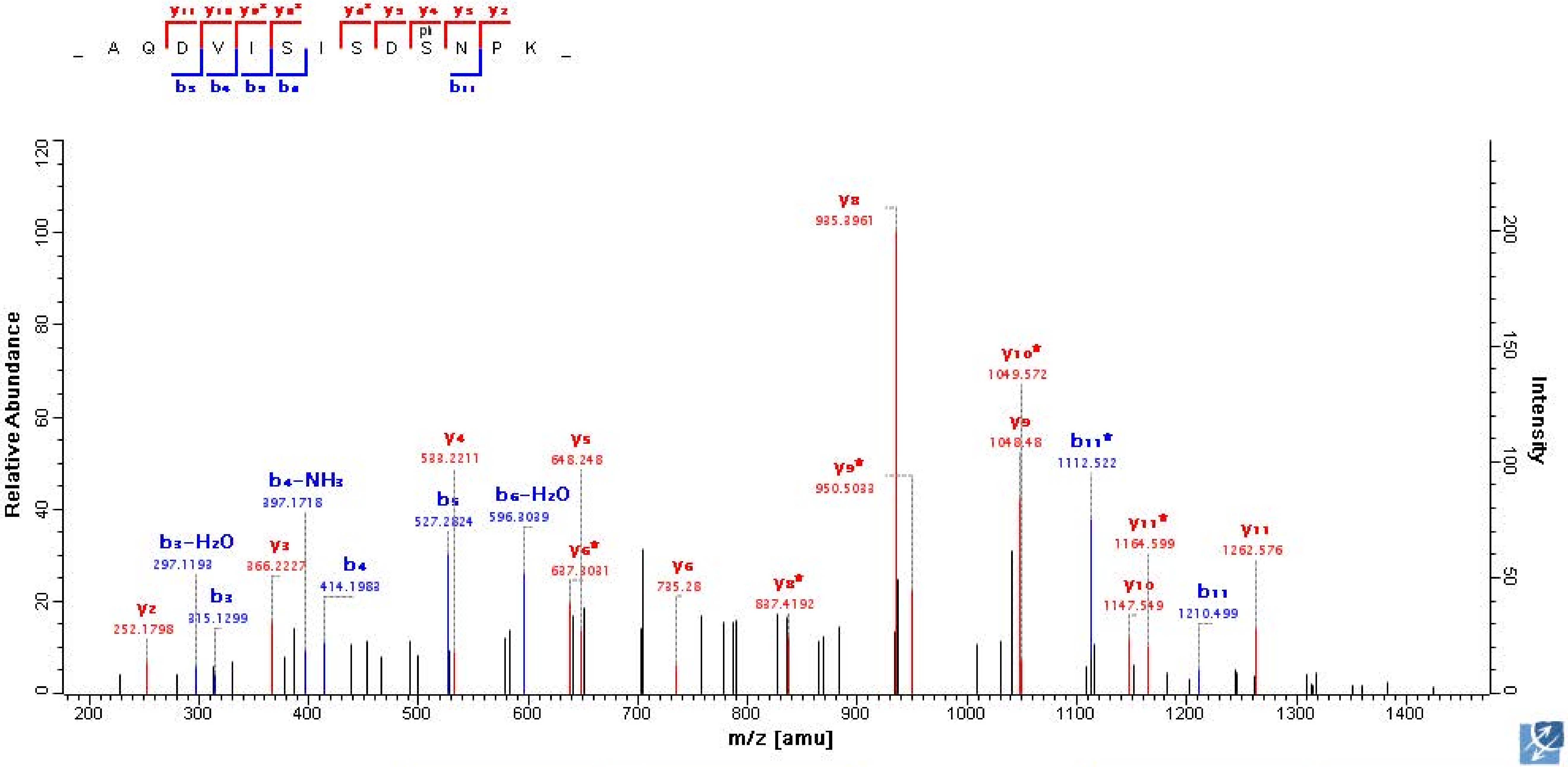
Mass:	1782.79117
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	139.4914
Mass Error [ppm]:	-0.28247
PEP:	7.6866E-23
Precursor Type:	ISO

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	49 %
Protein Localisation:	269 ... 284

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	15				
	185.1285		185.1285	2	A	14	1670.715		1670.715	
	256.1656		256.1656	3	A	13	1599.678		800.3425	+0.104681
	384.2241		384.2241	4	Q	12	1528.641		1528.641	
	441.2456		441.2456	5	G	11	1400.582	+0.196607	1400.582	
	570.2882	+0.045599	570.2882	6	E	10	1343.561		1343.561	
	699.3308		699.3308	7	E	9	1214.518		1214.518	
	813.3737	+0.172237	813.3737	8	N	8	1085.475	+0.065464	1085.475	
	900.4058		900.4058	9	S	7	971.4325	+0.056023	971.4325	
	957.4272		957.4272	10	G	6	884.4005		884.4005	
	1058.475	+0.053915	1058.475	11	T	5	827.379		827.379	
	1186.533	-0.081323	1186.533	12	Q	4	726.3313		726.3313	
	1353.532		1353.532	13	S	3	598.2728	+0.12196	598.2728	
-0.106873	733.8116		1466.616	14	I	2	431.2744	+0.012897	431.2744	
	1629.679	-0.070091	1629.679	15	Y	1	318.1903	+0.100806	318.1903	
				16	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 7500
Protein: BSU13620; mtnD; ykrZ
Peptide Score: 102.5
Method: ITMS; CID; 3



precursor information

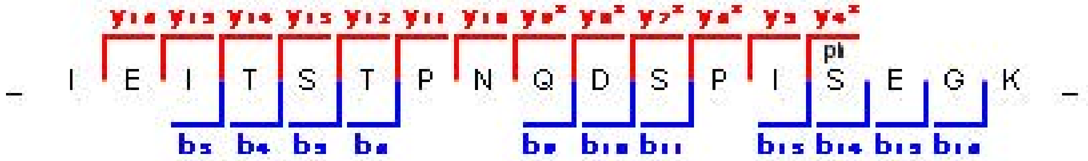
Mass:	1452.6498
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.505
Mass Error [ppm]:	0.029874
PEP:	5.2887E-06
Precursor Type:	MULTI

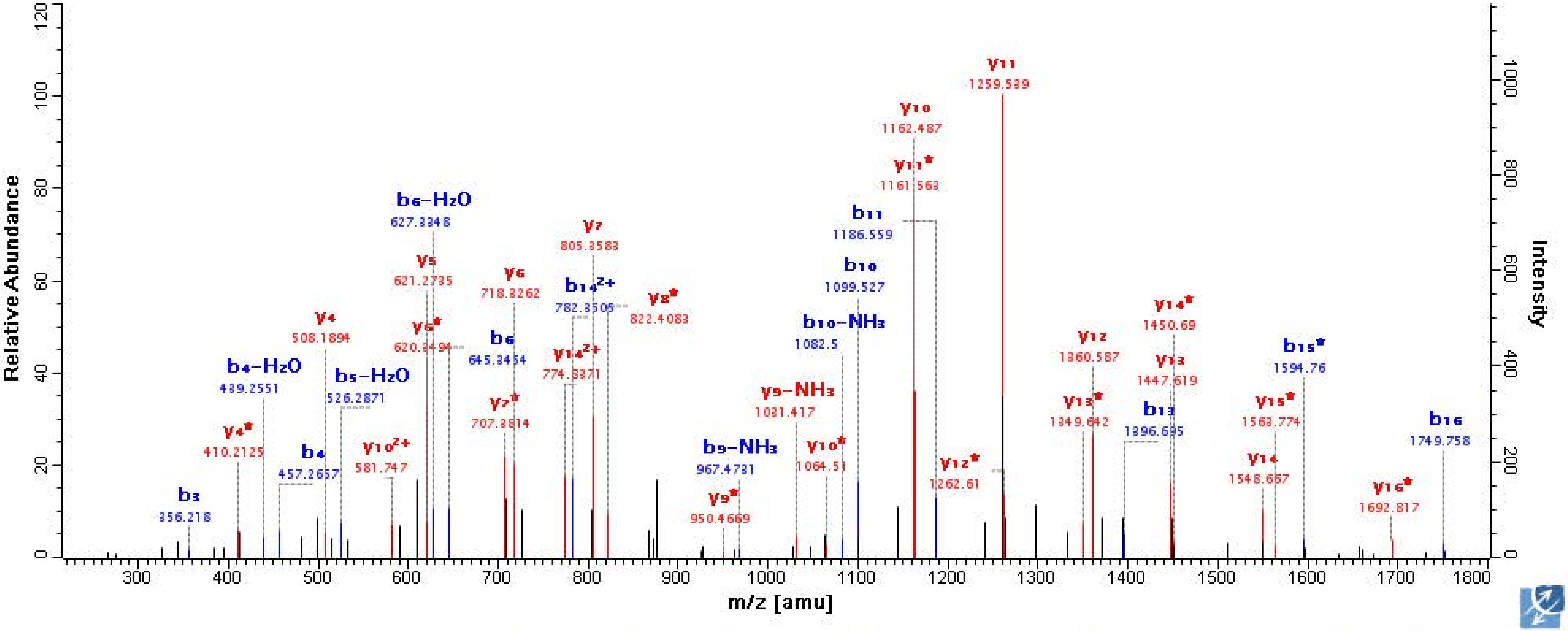
general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	44 %
Protein Localisation:	76 ... 88

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	12		
	200.102967766	2	Q	11	1390.634115374	
+0.0538661	315.129910798	3	D	10	1262.575537862	+0.1875237
-0.0822969	414.198324714	4	V	9	1147.54859483	+0.2292372
+0.151022	527.282388694	5	I	8	1048.480180914	+0.0662058
	614.314417104	6	S	7	935.396116933	+0.1979382
	727.398481085	7	I	6	848.364088524	
	814.430509495	8	S	5	735.280024543	+0.085576
	929.457452527	9	D	4	648.247996133	+0.1436665
	1096.455811345	10	S	3	533.221053101	+0.0704508
+0.3877358	1210.498738792	11	N	2	366.222694283	+0.1091539
	1307.551502644	12	P	1	252.179766836	-0.048999
		13	K	0	155.127002984	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber:	8105
Protein:	BSU25020; sodA; yqgD
Peptide Score:	202.34
Method:	ITMS; CID; 3





precursor information

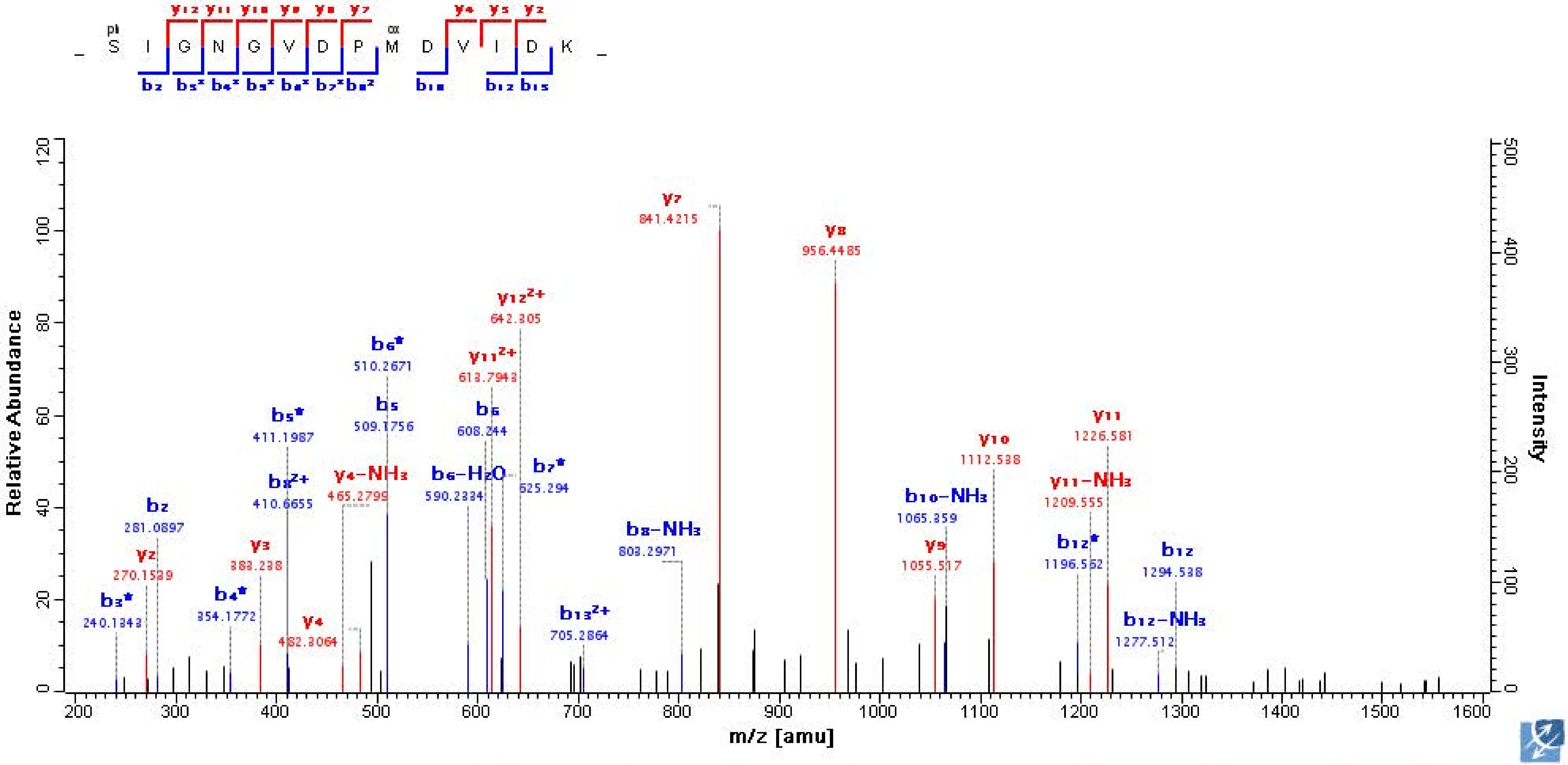
Mass:	1894.85534
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	202.3416
Mass Error [ppm]:	-0.41016
PEP:	3.1651E-59
Precursor Type:	MULTI

general information

Annotation:	15 of 17
AminoAcids Coverag	88 %
Intensity Coverage:	66 %
Protein Localisation:	141 ... 157

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	16				
	243.1339		243.1339	2	E	15	1790.794		1790.794	
	356.218	-0.199473	356.218	3	I	14	1661.751		1661.751	
	457.2657	+0.07429	457.2657	4	T	13	1548.667	+0.119139	774.8371	+0.009972
	544.2977		544.2977	5	S	12	1447.619	+0.13044	1447.619	
	645.3454	+0.057388	645.3454	6	T	11	1360.587	+0.059075	1360.587	
	742.3981		742.3981	7	P	10	1259.539	+0.071475	1259.539	
	856.4411		856.4411	8	N	9	1162.487	+0.150972	581.747	-0.304922
	984.4997		984.4997	9	Q	8	1048.444		1048.444	
	1099.527	-0.021956	1099.527	10	D	7	920.3852		920.3852	
	1186.559	+0.115205	1186.559	11	S	6	805.3583	+0.064394	805.3583	
	1283.611		1283.611	12	P	5	718.3262	-0.00984	718.3262	
	1396.695	+0.005233	1396.695	13	I	4	621.2735	+0.122941	621.2735	
+0.104779	782.3505		1563.694	14	S	3	508.1894	-0.203823	508.1894	
	1692.736		1692.736	15	E	2	341.1911		341.1911	
	1749.758	+0.254096	1749.758	16	G	1	212.1485		212.1485	
				17	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F20
Scannumber: 8730
Protein: BSU28090; valS
Peptide Score: 157.2
Method: ITMS; CID; 3



precursor information

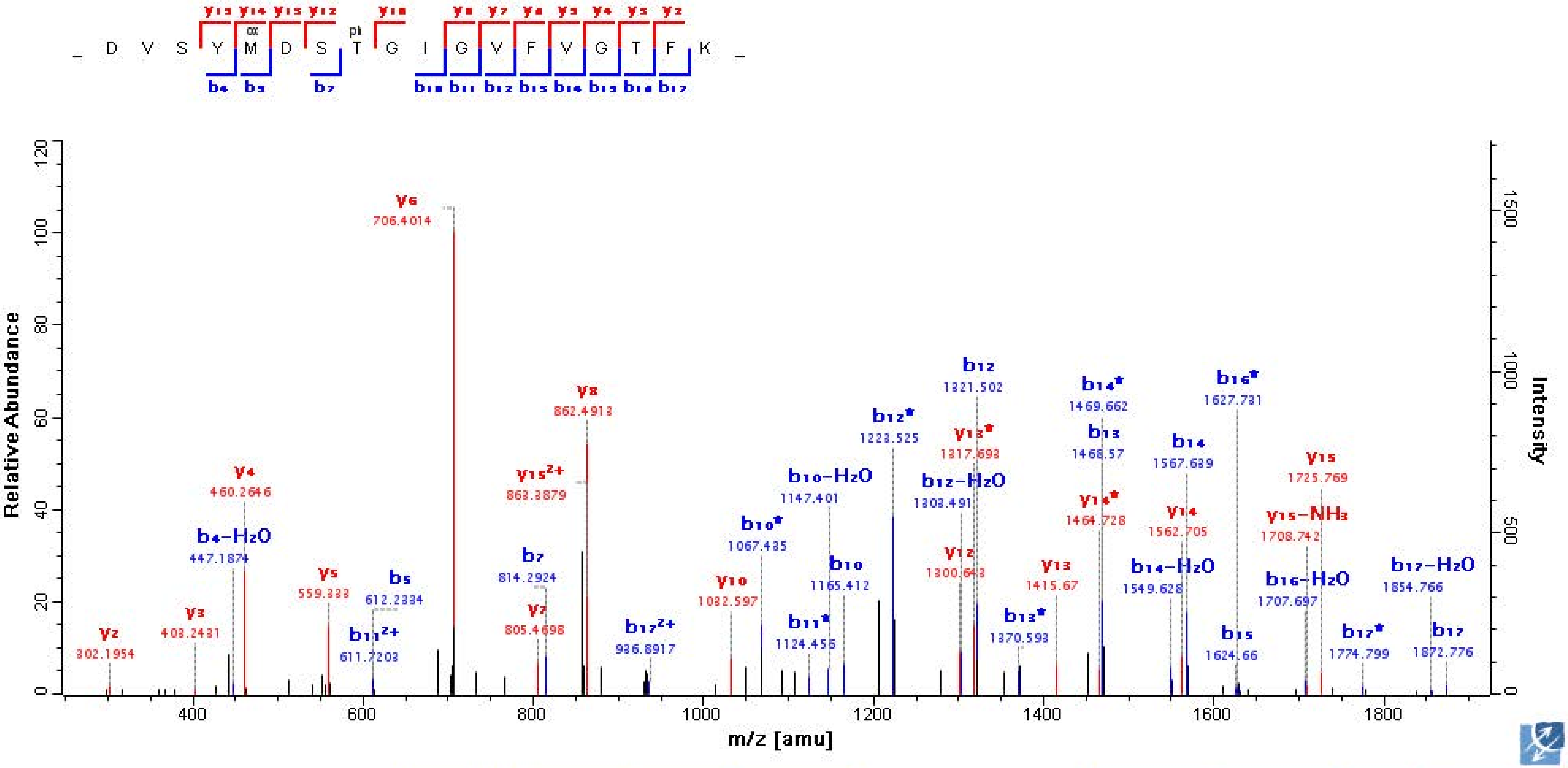
Mass:	1554.66322
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	157.2003
Mass Error [ppm]:	-0.30131
PEP:	3.724E-24
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	61 %
Protein Localisation:	529 ... 542

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	13				
	281.0897	+0.022727	281.0897	2	I	12	1396.687		1396.687	
	338.1112		338.1112	3	G	11	1283.603		642.305	+0.101912
	452.1541		452.1541	4	N	10	1226.581	+0.071554	613.7943	-0.043362
	509.1756	+0.022505	509.1756	5	G	9	1112.538	-0.041036	1112.538	
	608.244	+0.113759	608.244	6	V	8	1055.517	+0.080647	1055.517	
	723.2709		723.2709	7	D	7	956.4485	-0.045885	956.4485	
-0.431711	410.6655		820.3237	8	P	6	841.4215	+0.036844	841.4215	
	967.3591		967.3591	9	M	5	744.3688		744.3688	
	1082.386		1082.386	10	D	4	597.3334		597.3334	
	1181.454		1181.454	11	V	3	482.3064	+0.08414	482.3064	
	1294.538	-0.301679	1294.538	12	I	2	383.238	-0.052829	383.238	
+0.147664	705.2864		1409.565	13	D	1	270.1539	+0.042953	270.1539	
				14	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F21
Scannumber: 14991
Protein: BSU04710; rsbV
Peptide Score: 235.95
Method: ITMS; CID; 3



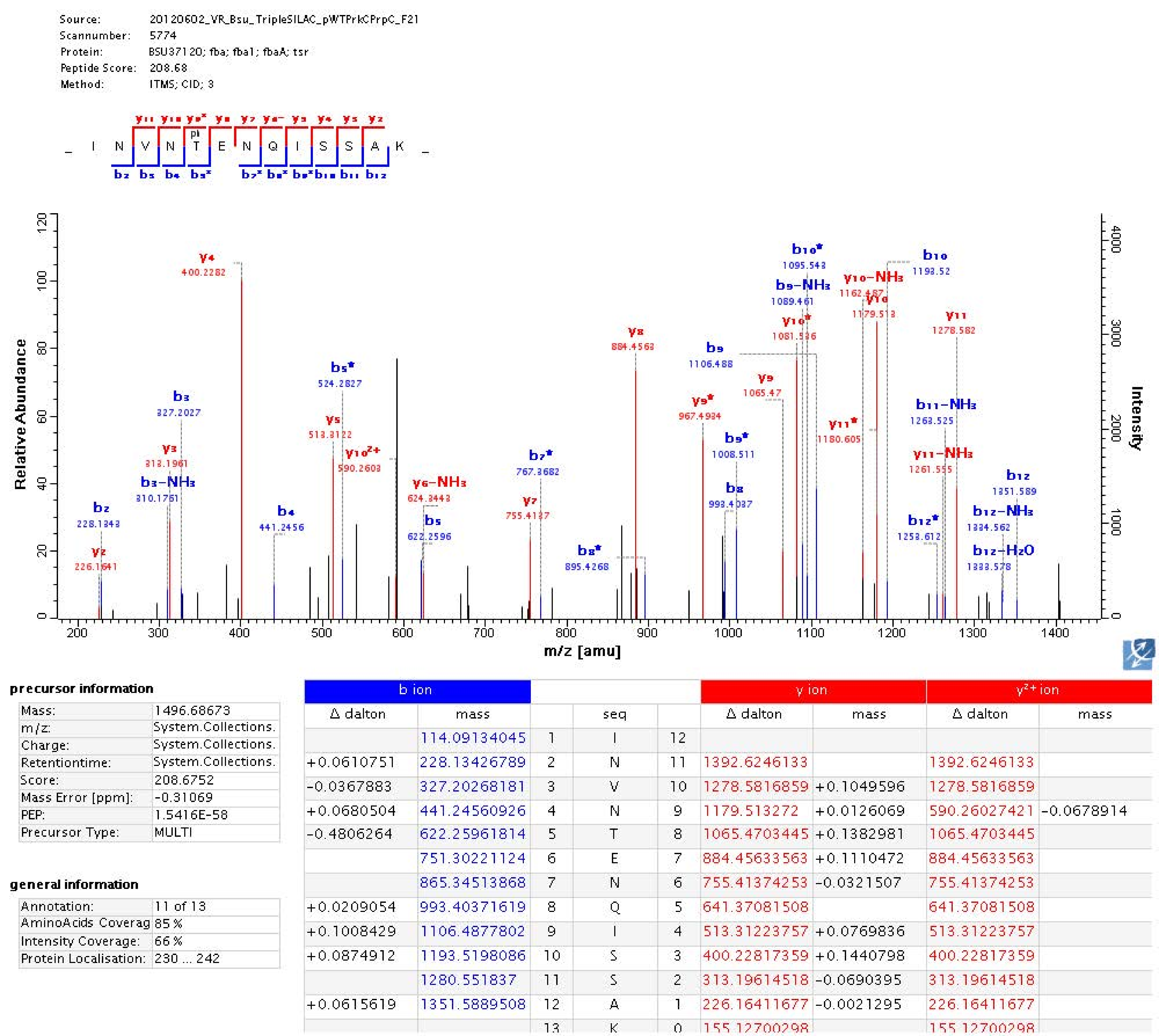
precursor information

Mass:	2017.87279
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	235.9495
Mass Error [ppm]:	-0.79917
PEP:	3.0587E-106
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	63 %
Protein Localisation:	50 ... 67

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	17				
	215.1026		215.1026	2	V	16	1911.869		1911.869	
	302.1347		302.1347	3	S	15	1812.801		1812.801	
	465.198		465.198	4	Y	14	1725.769	+0.004815	863.3879	+0.099172
	612.2334	-0.076651	612.2334	5	M	13	1562.705	-0.00815	1562.705	
	727.2603		727.2603	6	D	12	1415.67	+0.115506	1415.67	
	814.2924	+0.141477	814.2924	7	S	11	1300.643	+0.068352	1300.643	
	995.3064		995.3064	8	T	10	1213.611		1213.611	
	1052.328		1052.328	9	G	9	1032.597	+0.173471	1032.597	
	1165.412	-0.06827	1165.412	10	I	8	975.5753		975.5753	
-0.308576	611.7203		1222.433	11	G	7	862.4913	-0.06939	862.4913	
	1321.502	-0.138616	1321.502	12	V	6	805.4698	-0.008497	805.4698	
	1468.57	+0.021974	1468.57	13	F	5	706.4014	-0.046406	706.4014	
	1567.639	+0.059517	1567.639	14	V	4	559.333	+0.033116	559.333	
	1624.66	+0.117521	1624.66	15	G	3	460.2646	+0.093626	460.2646	
	1725.708		1725.708	16	T	2	403.2431	+0.262215	403.2431	
-0.371698	936.8917	+0.091761	1872.776	17	F	1	302.1954	+0.063708	302.1954	
				18	K	0	155.127		155.127	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F21
Scannumber: 5774
Protein: BSU37120; fba; fba1; fbaA; tsr
Peptide Score: 208.68
Method: ITMS; CID; 3

precursor information

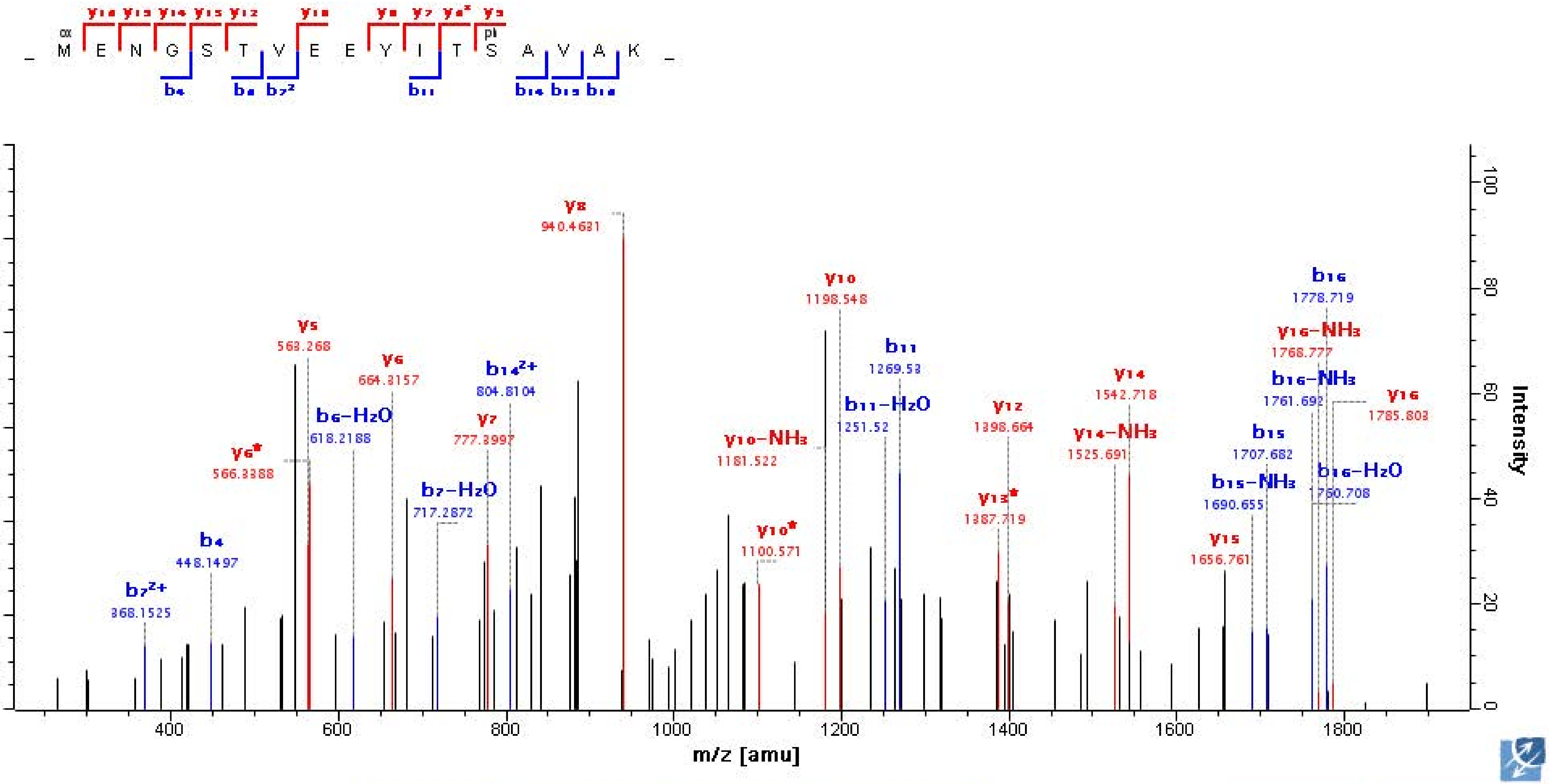
Mass:	1496.68673
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	208.6752
Mass Error [ppm]:	-0.31069
PEP:	1.5416E-58
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	66 %
Protein Localisation:	230 ... 242

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	12				
+0.0610751	228.13426789	2	N	11	1392.6246133		1392.6246133	
-0.0367883	327.20268181	3	V	10	1278.5816859	+0.1049596	1278.5816859	
+0.0680504	441.24560926	4	N	9	1179.513272	+0.0126069	590.26027421	-0.0678914
-0.4806264	622.25961814	5	T	8	1065.4703445	+0.1382981	1065.4703445	
	751.30221124	6	E	7	884.45633563	+0.1110472	884.45633563	
	865.34513868	7	N	6	755.41374253	-0.0321507	755.41374253	
+0.0209054	993.40371619	8	Q	5	641.37081508		641.37081508	
+0.1008429	1106.4877802	9	I	4	513.31223757	+0.0769836	513.31223757	
+0.0874912	1193.5198086	10	S	3	400.22817359	+0.1440798	400.22817359	
	1280.551837	11	S	2	313.19614518	-0.0690395	313.19614518	
+0.0615619	1351.5889508	12	A	1	226.16411677	-0.0021295	226.16411677	
		13	K	0	155.12700298		155.12700298	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F22
Scannumber: 10096
Protein: BSU16500; tsf
Peptide Score: 105.06
Method: ITMS; CID; 3



precursor information

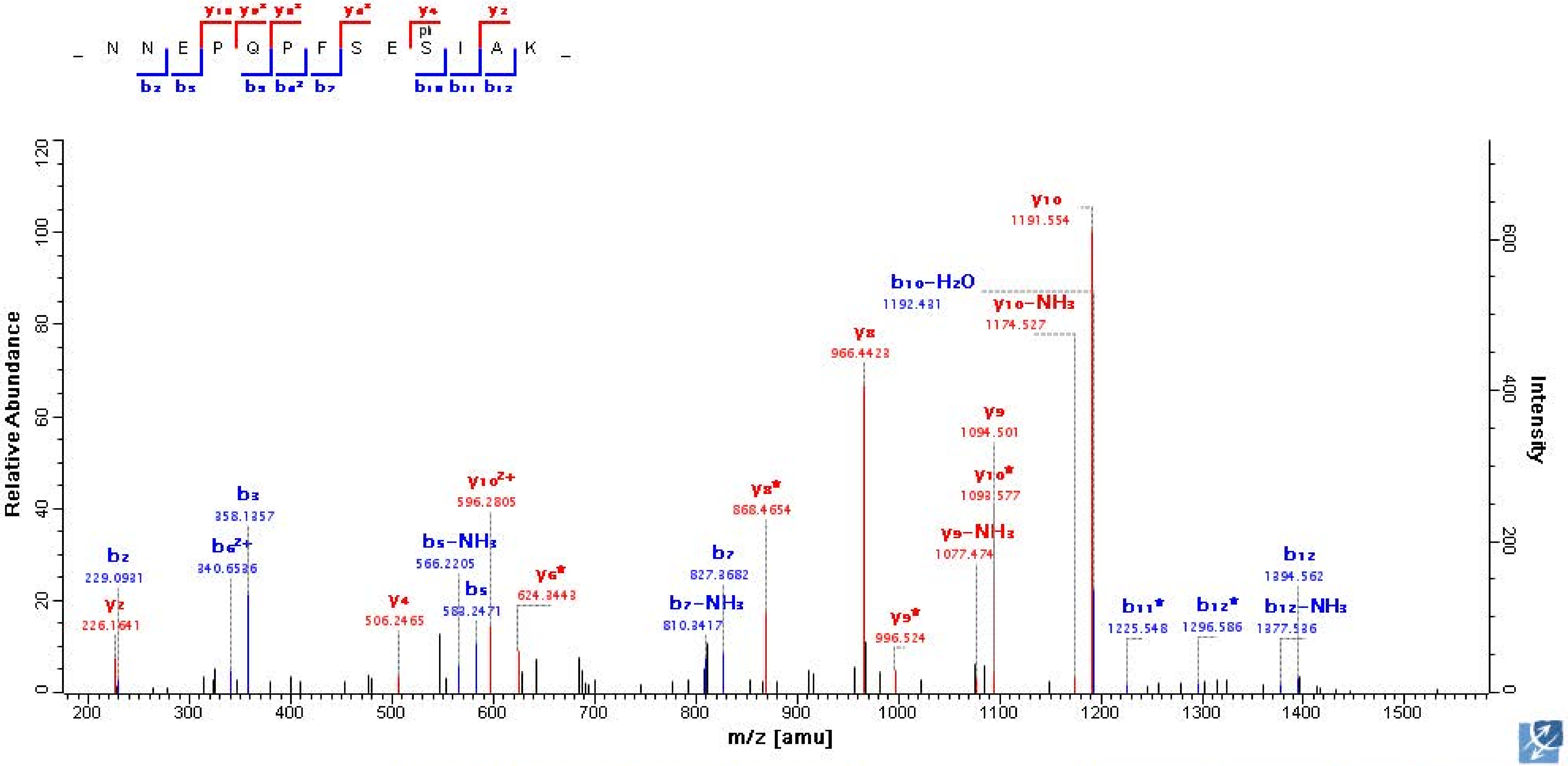
Mass:	1923.81749
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.0601
Mass Error [ppm]:	0.10277
PEP:	7.0915E-08
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	33 %
Protein Localisation:	115 ... 131

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.04267569		148.04267569	1	M	16		
	277.08526879		277.08526879	2	E	15	1785.8033655	+0.1381628
	391.12819624		391.12819624	3	N	14	1656.7607725	-0.3251035
	448.14965996	+0.1422712	448.14965996	4	G	13	1542.717845	+0.0872087
	535.18168837		535.18168837	5	S	12	1485.6963813	
	636.22936685		636.22936685	6	T	11	1398.6643529	+0.0534206
-0.0336932	368.15252861		735.29778076	7	V	10	1297.6166744	
	864.34037386		864.34037386	8	E	9	1198.5482605	-0.4856384
	993.38296695		993.38296695	9	E	8	1069.5056674	
	1156.4462955		1156.4462955	10	Y	7	940.46307429	-0.0665289
	1269.5303595	+0.0784052	1269.5303595	11	I	6	777.39974575	-0.0364035
	1370.5780379		1370.5780379	12	T	5	664.31568177	+0.107475
	1537.5763968		1537.5763968	13	S	4	563.26800329	+0.2327291
+0.4218453	804.81039351		1608.6135106	14	A	3	396.26964448	
	1707.6819245	+0.2032074	1707.6819245	15	V	2	325.23253069	
	1778.7190383	+0.1863573	1778.7190383	16	A	1	226.16411677	
				17	K	0	155.12700298	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F22
Scannumber: 7086
Protein: argJ; BSU11200
Peptide Score: 136.3
Method: ITMS; CID; 3



precursor information

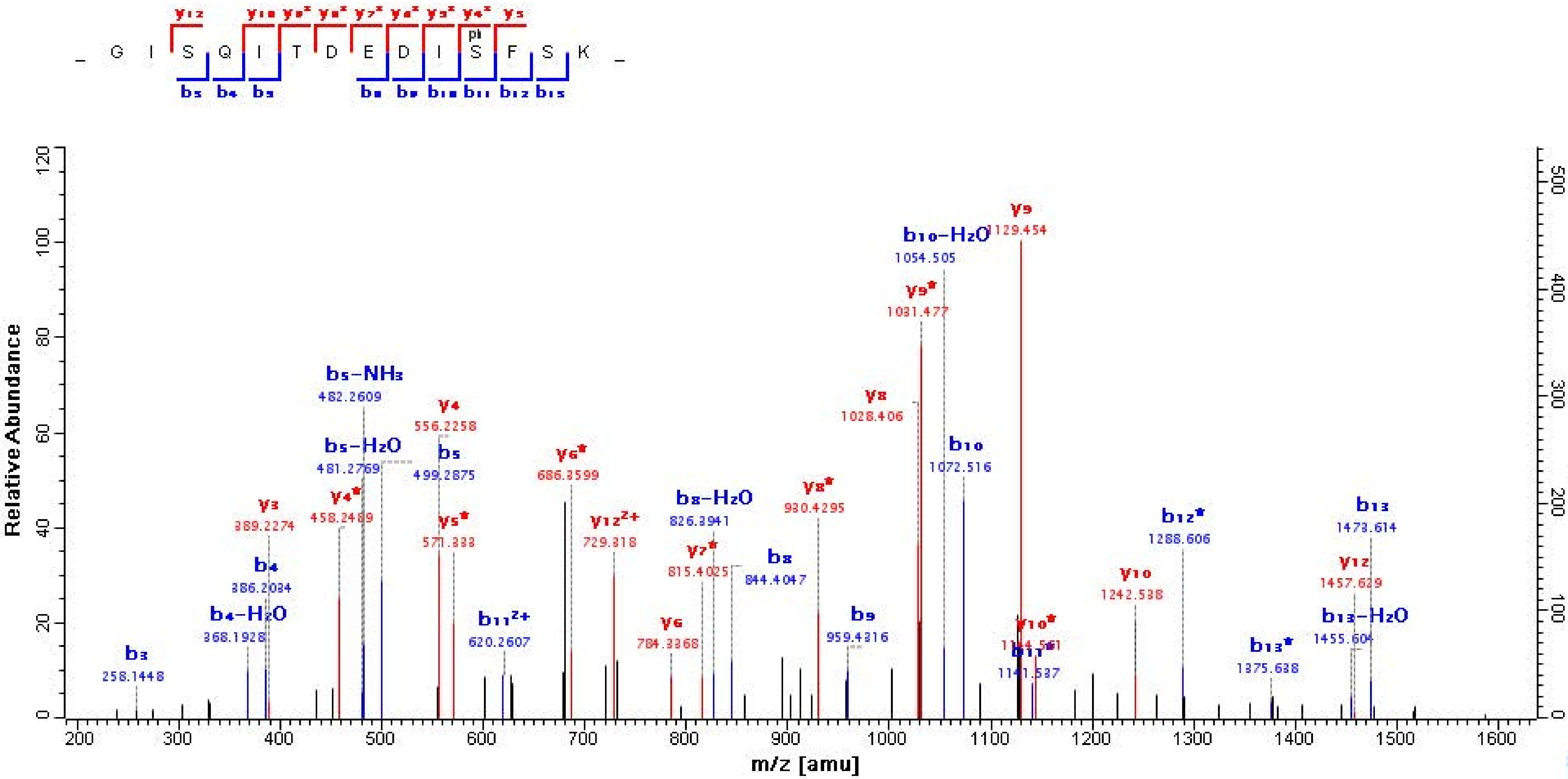
Mass:	1539.6605
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.2988
Mass Error [ppm]:	-0.098316
PEP:	6.5382E-14
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	64 %
Protein Localisation:	353 ... 365

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	12				
	229.0931	+0.046227	229.0931	2	N	11	1434.639		1434.639	
	358.1357	-0.046308	358.1357	3	E	10	1320.596		1320.596	
	455.1885		455.1885	4	P	9	1191.554	+0.092194	596.2805	+0.15574
	583.2471	+0.103093	583.2471	5	Q	8	1094.501	+0.342345	1094.501	
+0.471996	340.6536		680.2998	6	P	7	966.4423	+0.032698	966.4423	
	827.3682	+0.087811	827.3682	7	F	6	869.3896		869.3896	
	914.4003		914.4003	8	S	5	722.3212		722.3212	
	1043.443		1043.443	9	E	4	635.2891		635.2891	
	1210.441		1210.441	10	S	3	506.2465	+0.066632	506.2465	
	1323.525		1323.525	11	I	2	339.2482		339.2482	
	1394.562	-0.027856	1394.562	12	A	1	226.1641	+0.168296	226.1641	
				13	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F22
Scannumber:	8981
Protein:	BSU32260; hom; tdm
Peptide Score:	194.48
Method:	ITMS; CID; 3



precursor information

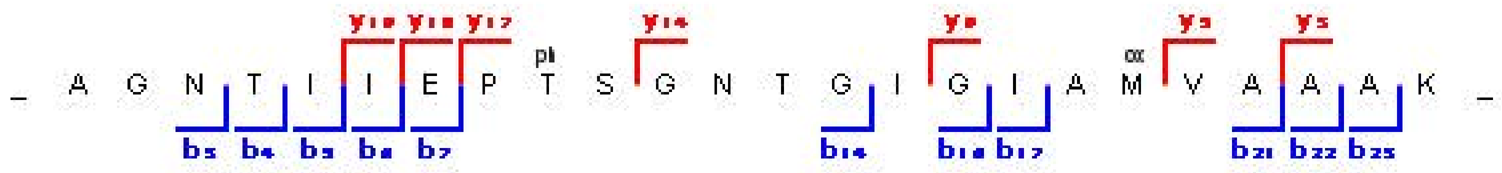
Mass:	1618.71271
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	194.4753
Mass Error [ppm]:	-0.021827
PEP:	1.7443E-49
Precursor Type:	MULTI

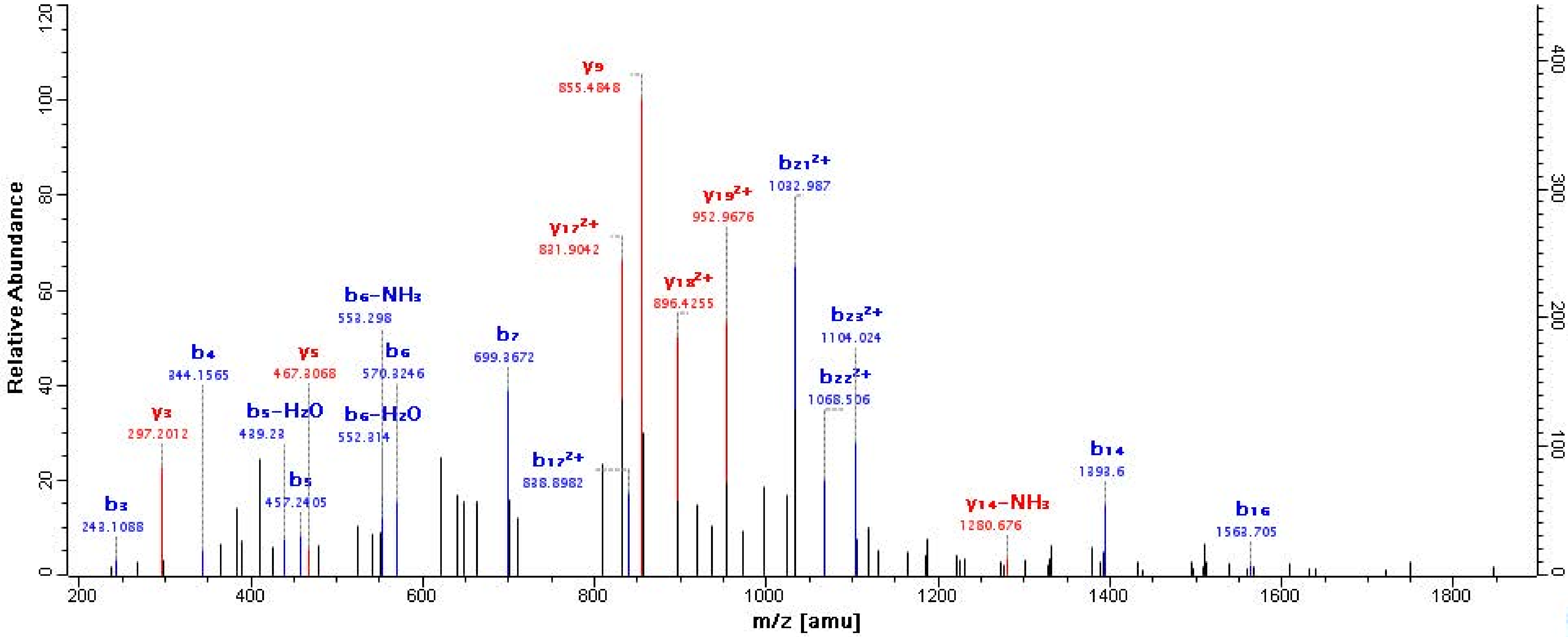
general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	63 %
Protein Localisation:	227 ... 240

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	13				
	171.1128		171.1128	2	I	12	1570.713		1570.713	
	258.1448	+0.083866	258.1448	3	S	11	1457.629	-0.145908	729.318	+0.074043
	386.2034	+0.065023	386.2034	4	Q	10	1370.597		1370.597	
	499.2875	+0.017519	499.2875	5	I	9	1242.538	+0.288448	1242.538	
	600.3352		600.3352	6	T	8	1129.454	-0.012131	1129.454	
	715.3621		715.3621	7	D	7	1028.406	+0.231836	1028.406	
	844.4047	-0.101161	844.4047	8	E	6	913.3794		913.3794	
	959.4316	-0.073783	959.4316	9	D	5	784.3368	-0.013935	784.3368	
	1072.516	-0.005442	1072.516	10	I	4	669.3099		669.3099	
-0.32164	620.2607		1239.514	11	S	3	556.2258	+0.193324	556.2258	
	1386.582		1386.582	12	F	2	389.2274	+0.185702	389.2274	
	1473.614	-0.151972	1473.614	13	S	1	242.159		242.159	
				14	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F22
Scannumber: 9397
Protein: BSU00730; cysK
Peptide Score: 74.05
Method: ITMS; CID; 3





precursor information

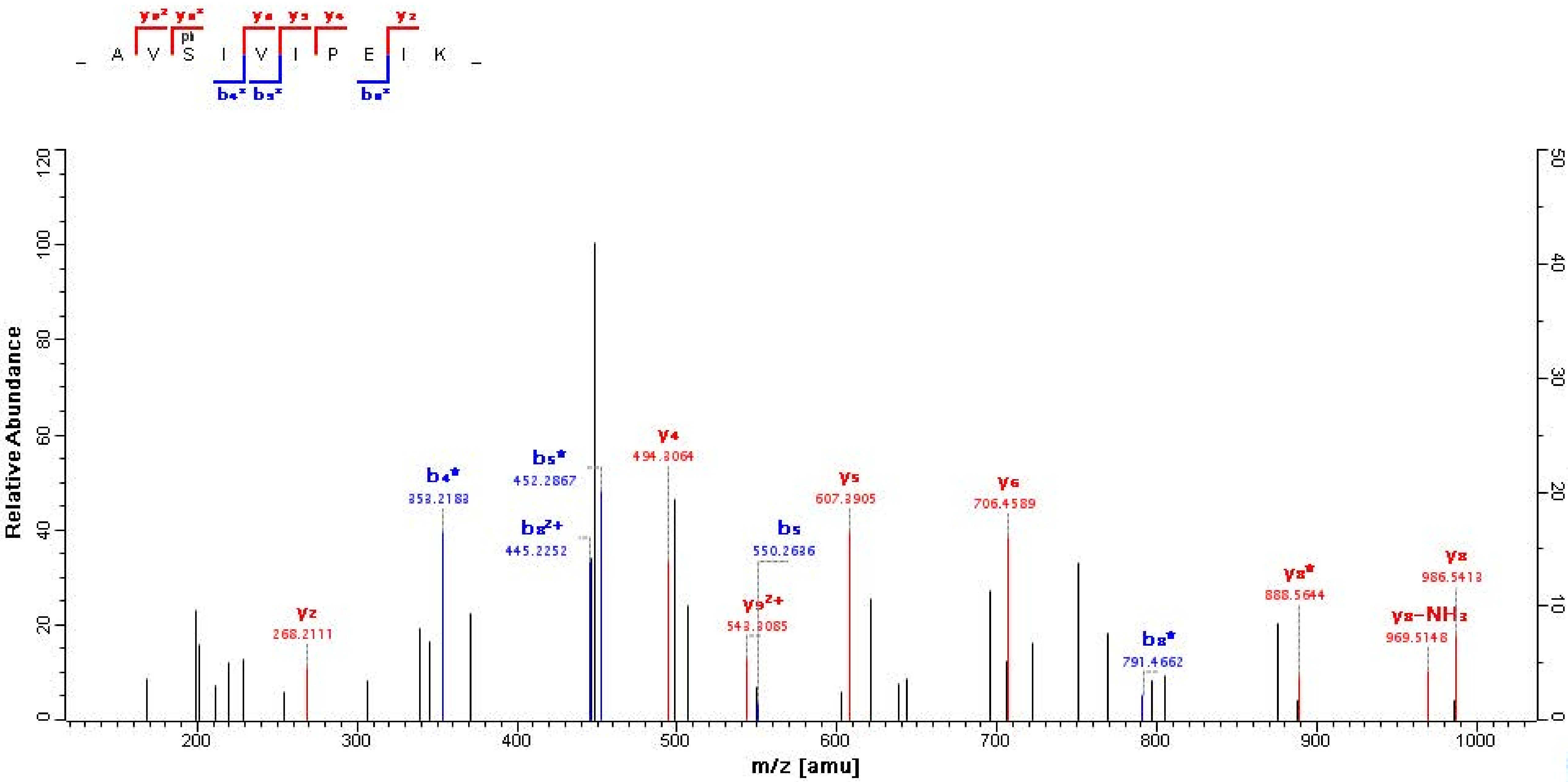
Mass:	2352.13884
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	74.0475
Mass Error [ppm]:	-0.33302
PEP:	0.00012517
Precursor Type:	MULTI

general information

Annotation:	14 of 24
AminoAcids Coverag	58 %
Intensity Coverage:	49 %
Protein Localisation:	64 ... 87

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	23				
	129.0659		129.0659	2	G	22	2290.124		2290.124	
	243.1088	+0.0605	243.1088	3	N	21	2233.103		2233.103	
	344.1565	+0.073643	344.1565	4	T	20	2119.06		2119.06	
	457.2405	+0.001725	457.2405	5	I	19	2018.012		2018.012	
	570.3246	-0.066348	570.3246	6	I	18	1904.928		952.9676	-0.046667
	699.3672	+0.048529	699.3672	7	E	17	1791.844		896.4255	+0.179996
	796.4199		796.4199	8	P	16	1662.801		831.9042	-0.044069
	977.434		977.434	9	T	15	1565.748		1565.748	
	1064.466		1064.466	10	S	14	1384.734		1384.734	
	1121.487		1121.487	11	G	13	1297.702		1297.702	
	1235.53		1235.53	12	N	12	1240.681		1240.681	
	1336.578		1336.578	13	T	11	1126.638		1126.638	
	1393.6	+0.102145	1393.6	14	G	10	1025.59		1025.59	
	1506.684		1506.684	15	I	9	968.5689		968.5689	
	1563.705	-0.043788	1563.705	16	G	8	855.4848	+0.125125	855.4848	
+0.282045	838.8982		1676.789	17	I	7	798.4633		798.4633	
	1747.826		1747.826	18	A	6	685.3793		685.3793	
	1894.862		1894.862	19	M	5	614.3422		614.3422	
	1993.93		1993.93	20	V	4	467.3068	+0.060673	467.3068	
+0.366426	1032.987		2064.967	21	A	3	368.2383		368.2383	
-0.013826	1068.506		2136.004	22	A	2	297.2012	+0.021395	297.2012	
+0.402676	1104.024		2207.041	23	A	1	226.1641		226.1641	
				24	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber:	10277
Protein:	BSU33940; gap; gapA
Peptide Score:	72.43
Method:	ITMS; CID; 3



precursor information

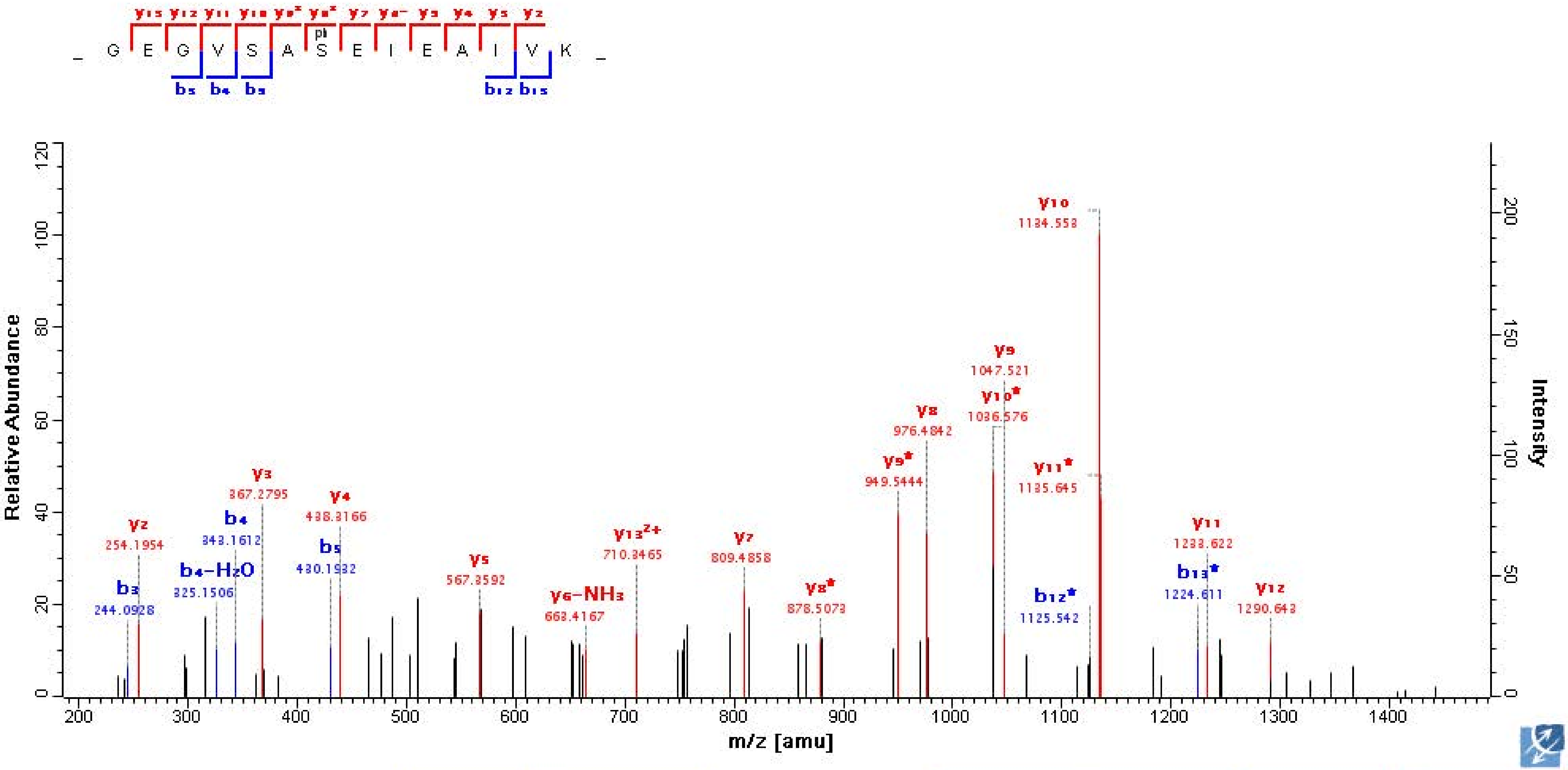
Mass:	1147.62511
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	72.43395
Mass Error [ppm]:	-0.22882
PEP:	0.012379
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	35 %
Protein Localisation:	215 ... 224

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	9				
	171.1128		171.1128	2	V	8	1085.61		543.3085	-0.006994
	338.1112		338.1112	3	S	7	986.5413	+0.410336	986.5413	
	451.1952		451.1952	4	I	6	819.543		819.543	
	550.2636	+0.026215	550.2636	5	V	5	706.4589	+0.170127	706.4589	
	663.3477		663.3477	6	I	4	607.3905	+0.164627	607.3905	
	760.4005		760.4005	7	P	3	494.3064	+0.057651	494.3064	
-0.252513	445.2252		889.4431	8	E	2	397.2537		397.2537	
	1002.527		1002.527	9	I	1	268.2111	+0.022728	268.2111	
				10	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber:	10606
Protein:	BSU13140; ohrA; yklA
Peptide Score:	119.32
Method:	ITMS; CID; 3



precursor information

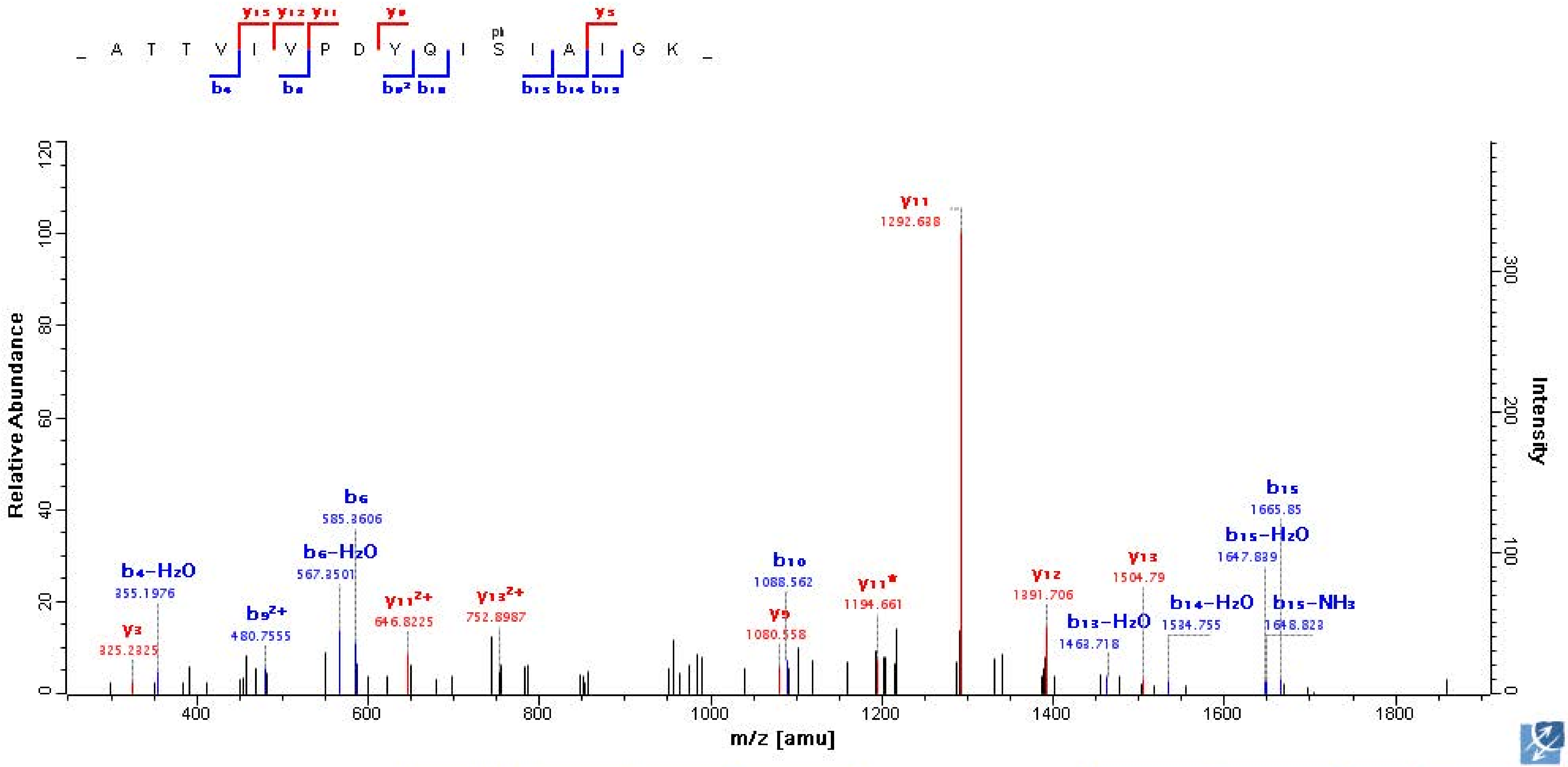
Mass:	1467.686
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	119.3155
Mass Error [ppm]:	0.12909
PEP:	3.013E-10
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	47 %
Protein Localisation:	104 ... 117

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	13				
	187.07133329	2	E	12	1419.6858166		710.34654653	+0.4435536
+0.2120889	244.09279701	3	G	11	1290.6432235	-0.1521346	1290.6432235	
-0.3954639	343.16121093	4	V	10	1233.6217598	-0.2815498	1233.6217598	
+0.1052226	430.19323934	5	S	9	1134.5533459	-0.1083996	1134.5533459	
	501.23035312	6	A	8	1047.5213174	-0.0498819	1047.5213174	
	668.22871194	7	S	7	976.48420366	-0.0015987	976.48420366	
	797.27130504	8	E	6	809.48584484	+0.0479076	809.48584484	
	910.35536902	9	I	5	680.44325174		680.44325174	
	1039.3979621	10	E	4	567.35918776	+0.0059245	567.35918776	
	1110.4350759	11	A	3	438.31659467	+0.0337471	438.31659467	
	1223.5191399	12	I	2	367.27948088	+0.0632315	367.27948088	
	1322.5875538	13	V	1	254.1954169	-0.040998	254.1954169	
		14	K	0	155.12700298		155.12700298	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 10788
Protein: BSU16600; nusA
Peptide Score: 62.38
Method: ITMS; CID; 3



precursor information

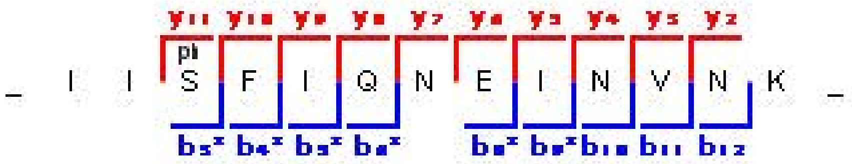
Mass:	1867.96985
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	62.37828
Mass Error [ppm]:	0.11591
PEP:	0.007918
Precursor Type:	MULTI

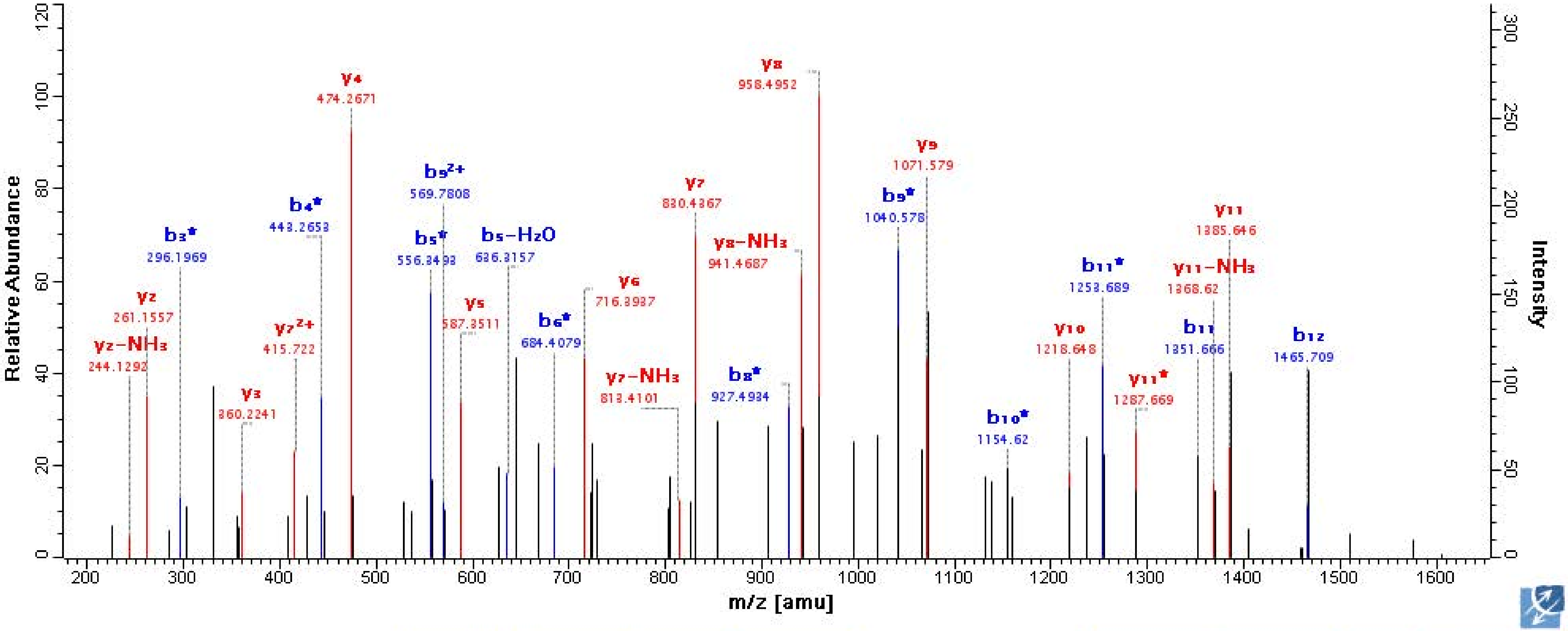
general information

Annotation:	9 of 17
AminoAcids Coverag	53 %
Intensity Coverage:	36 %
Protein Localisation:	303 ... 319

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	16				
	173.0921		173.0921	2	T	15	1805.954		1805.954	
	274.1397		274.1397	3	T	14	1704.906		1704.906	
	373.2082		373.2082	4	V	13	1603.859		1603.859	
	486.2922		486.2922	5	I	12	1504.79	+0.282776	752.8987	-0.018195
	585.3606	-0.10777	585.3606	6	V	11	1391.706	+0.191913	1391.706	
	682.4134		682.4134	7	P	10	1292.638	+0.013257	646.8225	-0.394288
	797.4403		797.4403	8	D	9	1195.585		1195.585	
-0.02934	480.7555		960.5037	9	Y	8	1080.558	-0.200005	1080.558	
	1088.562	+0.295536	1088.562	10	Q	7	917.4947		917.4947	
	1201.646		1201.646	11	I	6	789.4361		789.4361	
	1368.645		1368.645	12	S	5	676.3521		676.3521	
	1481.729		1481.729	13	I	4	509.3537		509.3537	
	1552.766		1552.766	14	A	3	396.2696		396.2696	
	1665.85	+0.194761	1665.85	15	I	2	325.2325	-0.080034	325.2325	
	1722.871		1722.871	16	G	1	212.1485		212.1485	
				17	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 11885
Protein: BSU29130; citC; icd
Peptide Score: 168.61
Method: ITMS; CID; 3





precursor information

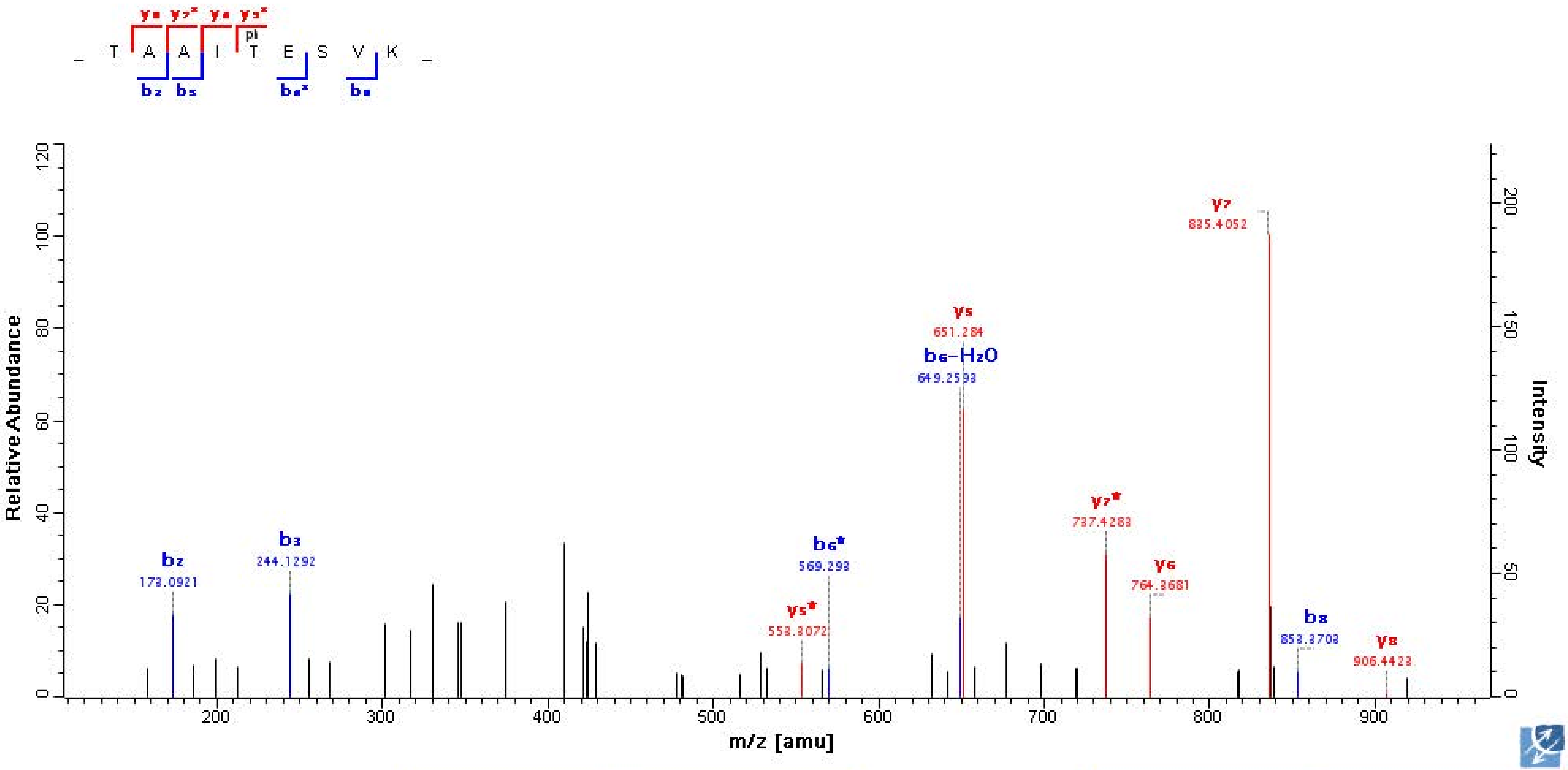
Mass:	1610.80697
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	168.6075
Mass Error [ppm]:	0.027936
PEP:	7.0909E-27
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	49 %
Protein Localisation:	166 ... 178

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	12				
	227.1754		227.1754	2	I	11	1498.73		1498.73	
	394.1738		394.1738	3	S	10	1385.646	-0.005569	1385.646	
	541.2422		541.2422	4	F	9	1218.648	-0.038948	1218.648	
	654.3262		654.3262	5	I	8	1071.579	+0.051194	1071.579	
	782.3848		782.3848	6	Q	7	958.4952	+0.010441	958.4952	
	896.4277		896.4277	7	N	6	830.4367	-0.011365	415.722	-0.257489
	1025.47		1025.47	8	E	5	716.3937	-0.025383	716.3937	
-0.246172	569.7808		1138.554	9	I	4	587.3511	-0.009767	587.3511	
	1252.597		1252.597	10	N	3	474.2671	-0.001631	474.2671	
	1351.666	-0.024997	1351.666	11	V	2	360.2241	+0.081885	360.2241	
	1465.709	+0.063911	1465.709	12	N	1	261.1557	-0.016114	261.1557	
				13	K	0	147.1128		147.1128	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 4081
Protein: BSU23890; oxaA2
Peptide Score: 62.3
Method: ITMS; CID; 3

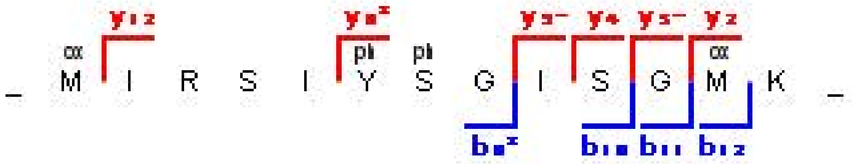


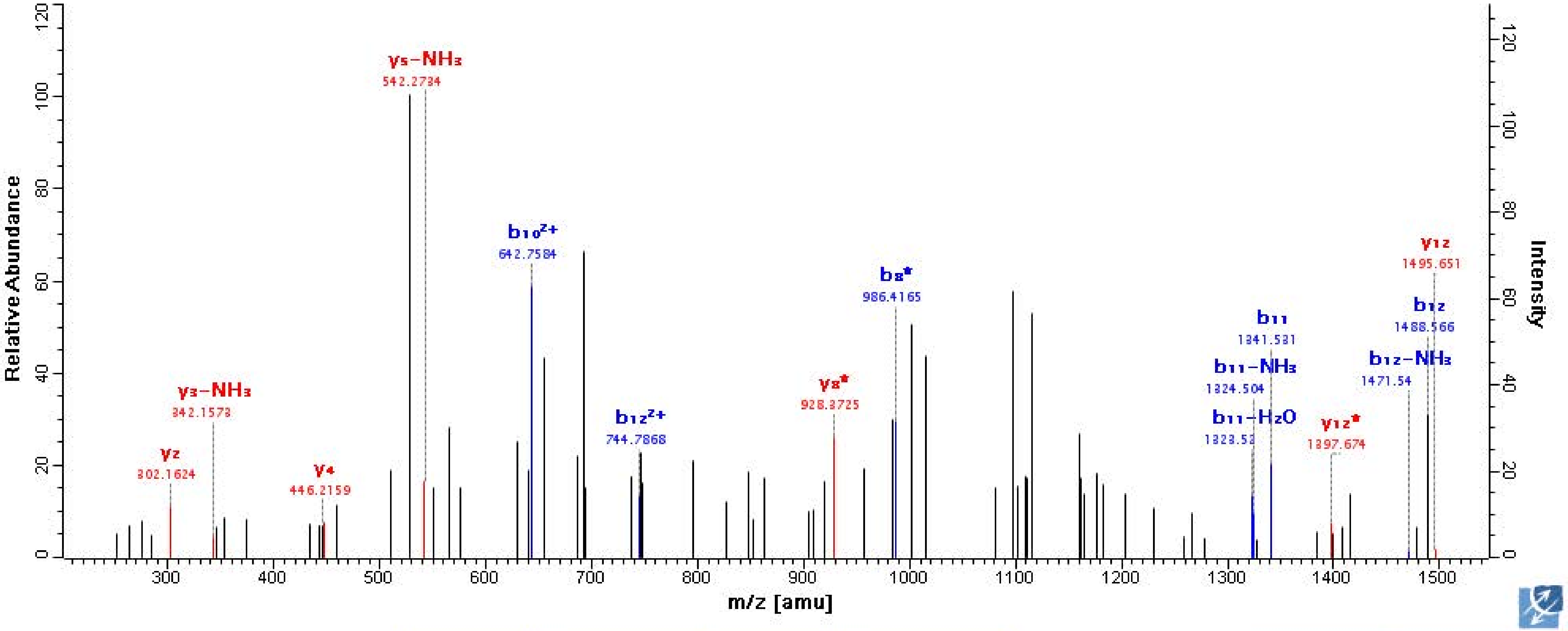
precursor information

Mass:	998.46858
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	62.30259
Mass Error [ppm]:	0.040724
PEP:	0.12106
Precursor Type:	MULTI
Annotation:	6 of 9
AminoAcids Coverag	67 %
Intensity Coverage:	43 %
Protein Localisation:	267 ... 275

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	102.054954941	1	T	8		
+0.0192899	173.092068728	2	A	7	906.442338845	+0.1695386
+0.0485213	244.129182516	3	A	6	835.405225057	+0.0941036
	357.213246497	4	I	5	764.368111269	+0.0742105
	538.227255379	5	T	4	651.284047289	+0.0735577
	667.269848475	6	E	3	470.270038406	
	754.301876885	7	S	2	341.22744531	
-0.0349026	853.370290802	8	V	1	254.1954169	
		9	K	0	155.127002984	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 7587
Protein: BSU16290; flgE; flgG
Peptide Score: 55.72
Method: ITMS; CID; 3





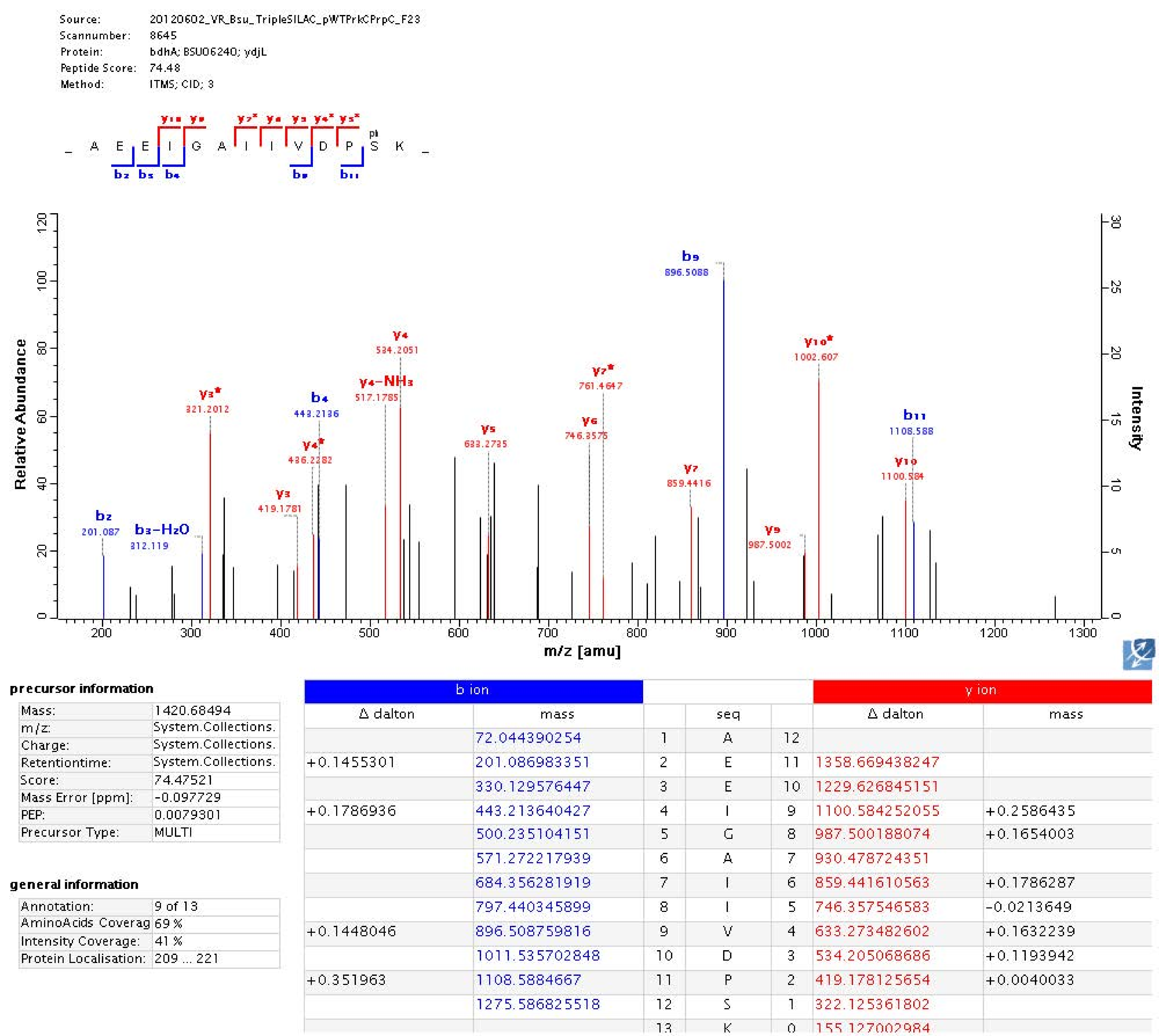
precursor information

Mass:	1633.66504
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	55.72391
Mass Error [ppm]:	0.24692
PEP:	0.10591
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54%
Intensity Coverage:	17%
Protein Localisation:	1 ... 13

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.04267569		148.04267569	1	M	12		
	261.12673968		261.12673968	2	I	11	1495.6507072	+0.1377449
	417.2278507		417.2278507	3	R	10	1382.5666432	
	504.25987911		504.25987911	4	S	9	1226.4655322	
	617.34394309		617.34394309	5	I	8	1139.4335038	
	860.37360204		860.37360204	6	Y	7	1026.3494398	
	1027.3719609		1027.3719609	7	S	6	783.31978087	
	1084.3934246		1084.3934246	8	G	5	616.32142205	
	1197.4774886		1197.4774886	9	I	4	559.29995833	
-0.434239	642.75839672		1284.509517	10	S	3	446.21589435	+0.341967
	1341.5309807	-0.1556145	1341.5309807	11	G	2	359.18386594	
+0.0185307	744.7868282	-0.1277813	1488.5663799	12	M	1	302.16240221	+0.1847658
				13	K	0	155.12700298	



Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 8645
Protein: bdhA; BSU06240; ydjL
Peptide Score: 74.48
Method: ITMS; CID; 3

precursor information

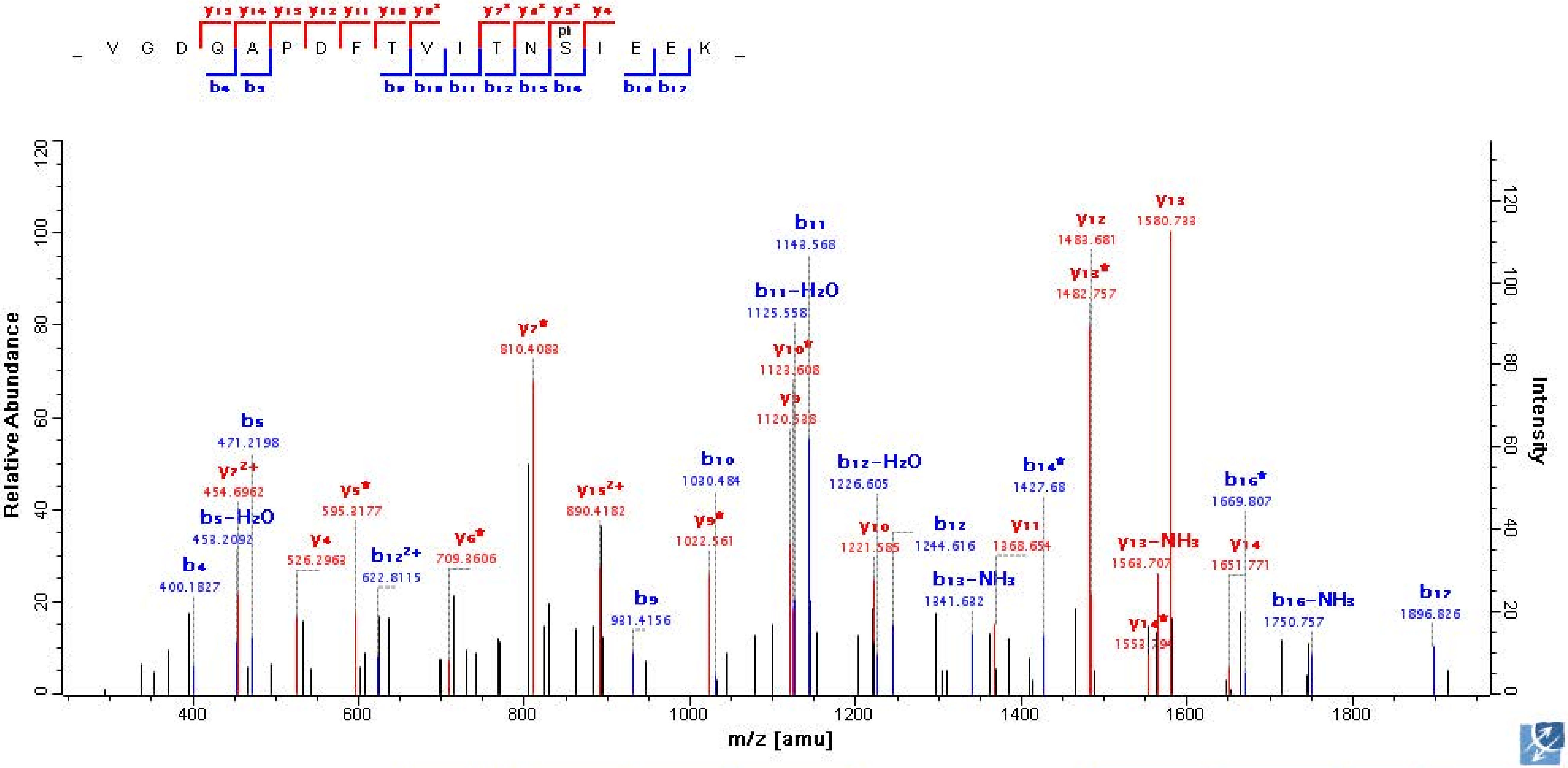
Mass:	1420.68494
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	74.47521
Mass Error [ppm]:	-0.097729
PEP:	0.0079301
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	41 %
Protein Localisation:	209 ... 221

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	12		
+0.1455301	201.086983351	2	E	11	1358.669438247	
	330.129576447	3	E	10	1229.626845151	
+0.1786936	443.213640427	4	I	9	1100.584252055	+0.2586435
	500.235104151	5	G	8	987.500188074	+0.1654003
	571.272217939	6	A	7	930.478724351	
	684.356281919	7	I	6	859.441610563	+0.1786287
	797.440345899	8	I	5	746.357546583	-0.0213649
+0.1448046	896.508759816	9	V	4	633.273482602	+0.1632239
	1011.535702848	10	D	3	534.205068686	+0.1193942
+0.351963	1108.5884667	11	P	2	419.178125654	+0.0040033
	1275.586825518	12	S	1	322.125361802	
		13	K	0	155.127002984	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 9610
Protein: BSU29490; tpx; ytgI
Peptide Score: 135.29
Method: ITMS; CID; 3



precursor information

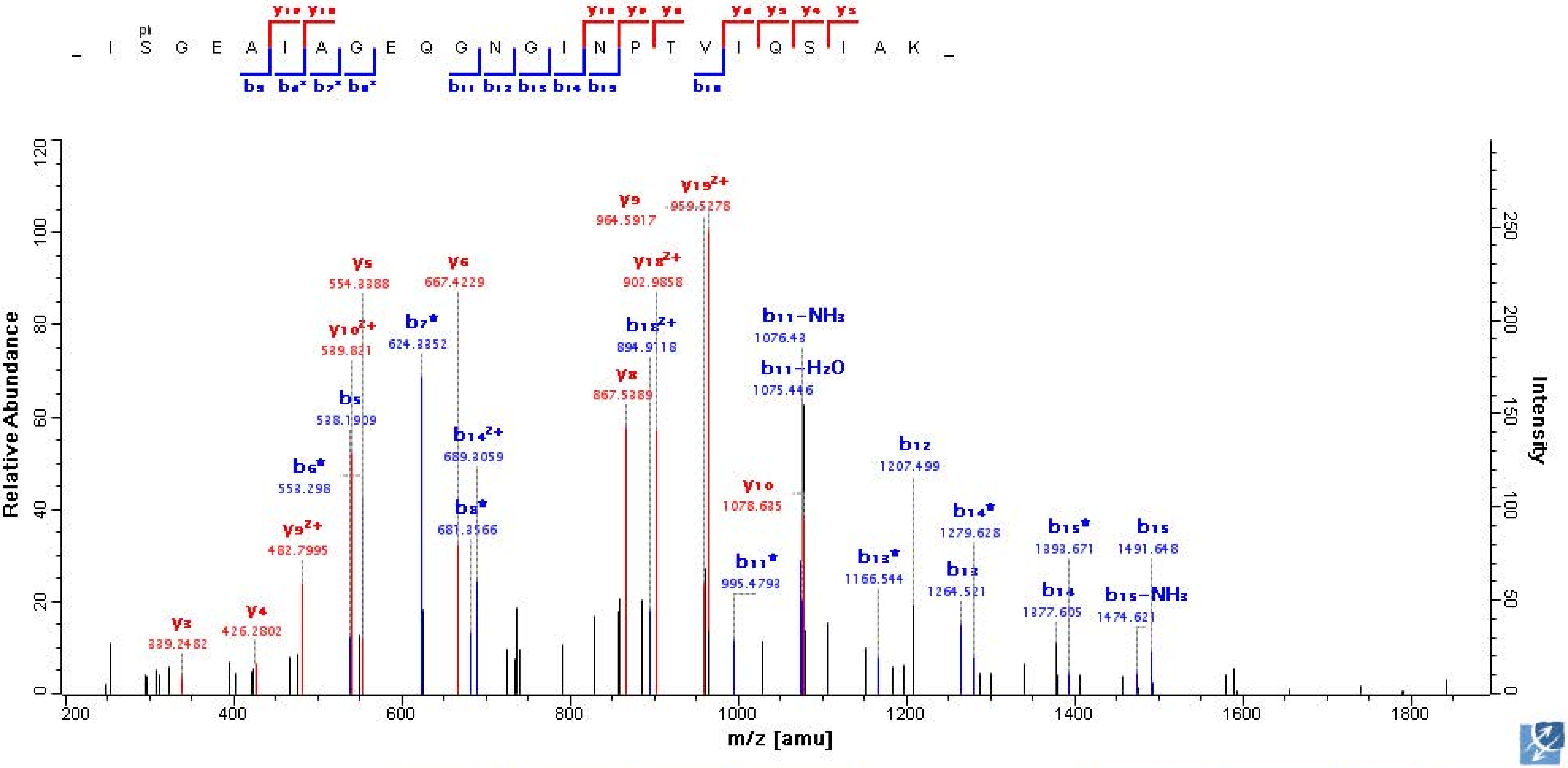
Mass:	2041.92372
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.2923
Mass Error [ppm]:	-0.39608
PEP:	4.6547E-20
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	51 %
Protein Localisation:	20 ... 37

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	17				
	157.0972		157.0972	2	G	16	1951.878		1951.878	
	272.1241		272.1241	3	D	15	1894.856		1894.856	
	400.1827	-0.028134	400.1827	4	Q	14	1779.829		890.4182	+0.117779
	471.2198	-0.085481	471.2198	5	A	13	1651.771	-0.082499	1651.771	
	568.2726		568.2726	6	P	12	1580.733	+0.0917	1580.733	
	683.2995		683.2995	7	D	11	1483.681	+0.192804	1483.681	
	830.3679		830.3679	8	F	10	1368.654	-0.454447	1368.654	
	931.4156	+0.052674	931.4156	9	T	9	1221.585	+0.136916	1221.585	
	1030.484	+0.060066	1030.484	10	V	8	1120.538	-0.133155	1120.538	
	1143.568	+0.134571	1143.568	11	I	7	1021.469		1021.469	
-0.207201	622.8115	-0.372092	1244.616	12	T	6	908.3852		454.6962	-0.355305
	1358.659		1358.659	13	N	5	807.3375		807.3375	
	1525.657		1525.657	14	S	4	693.2946		693.2946	
	1638.741		1638.741	15	I	3	526.2963	-0.105701	526.2963	
	1767.784		1767.784	16	E	2	413.2122		413.2122	
	1896.826	+0.377577	1896.826	17	E	1	284.1696		284.1696	
				18	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F23
Scannumber: 9911
Protein: BSU16510; pyrH; smbA
Peptide Score: 88.5
Method: ITMS; CID; 3



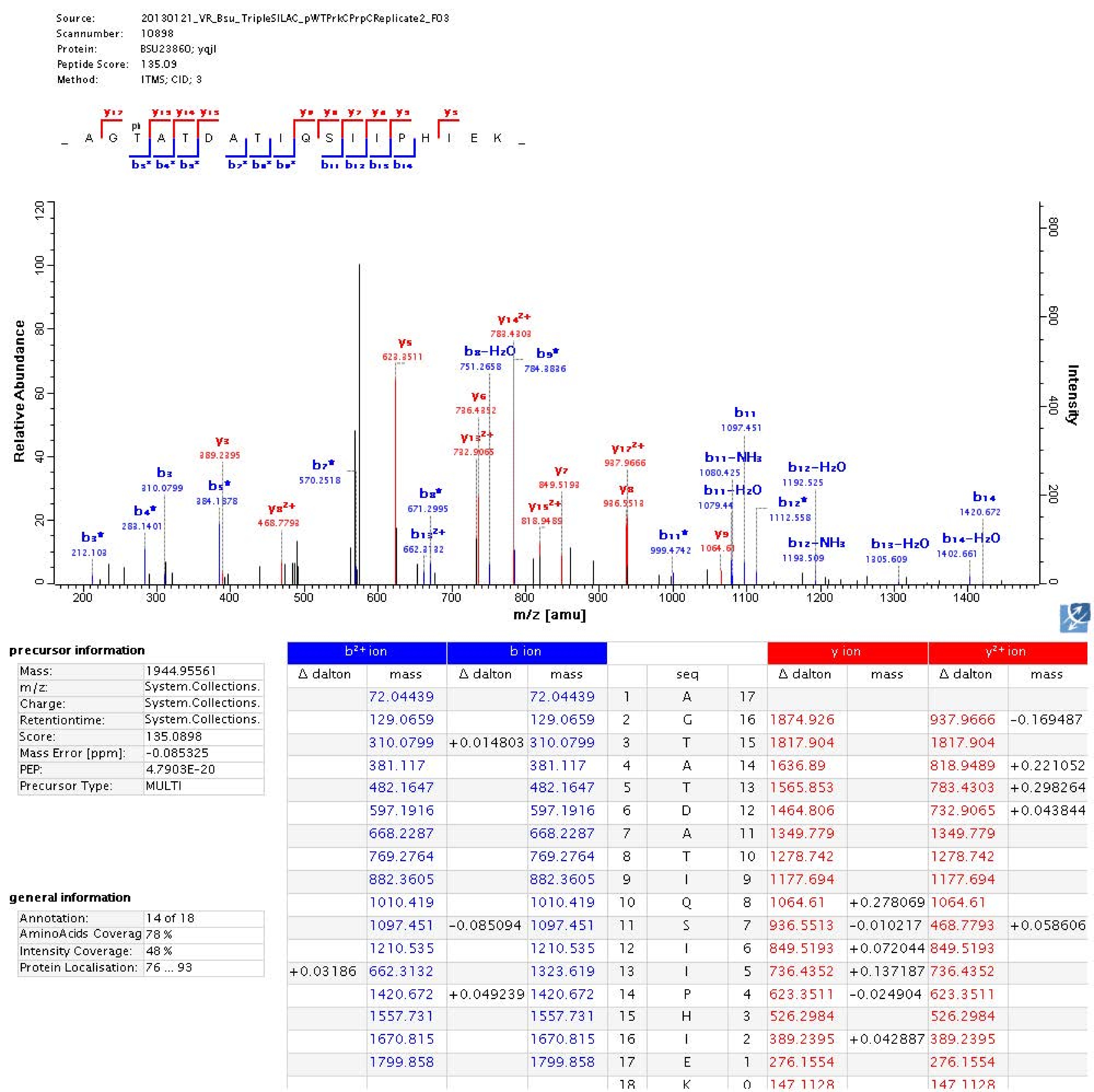
precursor information

Mass:	2446.20979
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	88.50416
Mass Error [ppm]:	-0.28186
PEP:	4.569E-08
Precursor Type:	MULTI

general information

Annotation:	16 of 24
AminoAcids Coverag	67 %
Intensity Coverage:	58 %
Protein Localisation:	13 ... 36

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	23				
	281.0897		281.0897	2	S	22	2342.148		2342.148	
	338.1112		338.1112	3	G	21	2175.15		2175.15	
	467.1538		467.1538	4	E	20	2118.128		2118.128	
	538.1909	-0.00984	538.1909	5	A	19	1989.085		1989.085	
	651.2749		651.2749	6	I	18	1918.048		959.5278	+0.046215
	722.312		722.312	7	A	17	1804.964		902.9858	+0.193227
	779.3335		779.3335	8	G	16	1733.927		1733.927	
	908.3761		908.3761	9	E	15	1676.906		1676.906	
	1036.435		1036.435	10	Q	14	1547.863		1547.863	
	1093.456		1093.456	11	G	13	1419.805		1419.805	
	1207.499	+0.153026	1207.499	12	N	12	1362.783		1362.783	
	1264.521	-0.076567	1264.521	13	G	11	1248.74		1248.74	
+0.051971	689.3059	+0.103529	1377.605	14	I	10	1191.719		1191.719	
	1491.648	+0.05169	1491.648	15	N	9	1078.635	+0.340952	539.821	+0.073515
	1588.7		1588.7	16	P	8	964.5917	+0.00479	482.7995	+0.042671
	1689.748		1689.748	17	T	7	867.5389	+0.027341	867.5389	
-0.428859	894.9118		1788.816	18	V	6	766.4913		766.4913	
	1901.9		1901.9	19	I	5	667.4229	+0.143128	667.4229	
	2029.959		2029.959	20	Q	4	554.3388	+0.080891	554.3388	
	2116.991		2116.991	21	S	3	426.2802	+0.334476	426.2802	
	2230.075		2230.075	22	I	2	339.2482	+0.196582	339.2482	
	2301.112		2301.112	23	A	1	226.1641		226.1641	
				24	K	0	155.127		155.127	



Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F03
Scannumber: 10898
Protein: BSU23860; yqjl
Peptide Score: 135.09
Method: ITMS; CID; 3

precursor information

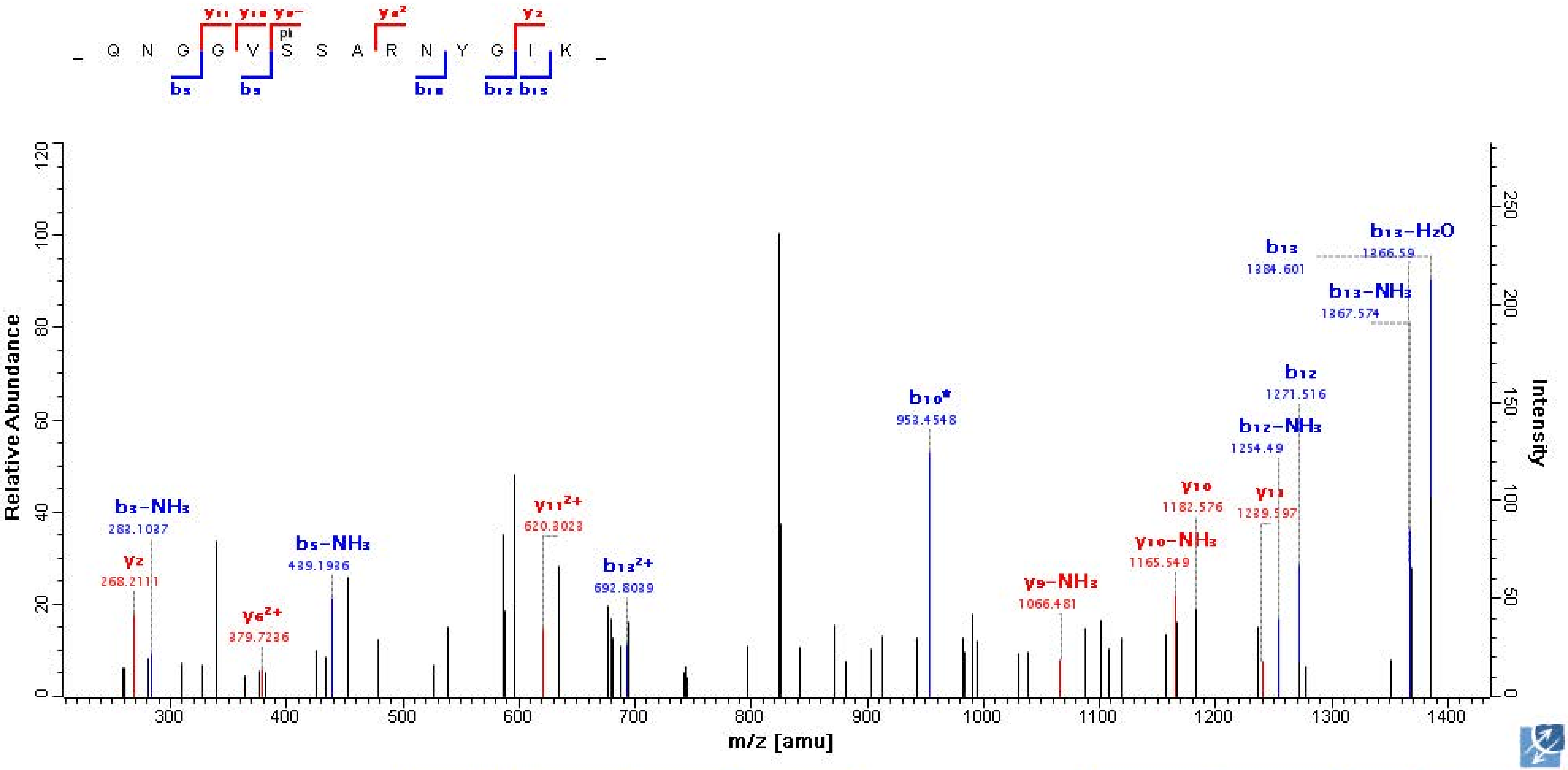
Mass:	1944.95561
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.0898
Mass Error [ppm]:	-0.085325
PEP:	4.7903E-20
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	48 %
Protein Localisation:	76 ... 93

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	17				
	129.0659		129.0659	2	G	16	1874.926		937.9666	-0.169487
	310.0799	+0.014803	310.0799	3	T	15	1817.904		1817.904	
	381.117		381.117	4	A	14	1636.89		818.9489	+0.221052
	482.1647		482.1647	5	T	13	1565.853		783.4303	+0.298264
	597.1916		597.1916	6	D	12	1464.806		732.9065	+0.043844
	668.2287		668.2287	7	A	11	1349.779		1349.779	
	769.2764		769.2764	8	T	10	1278.742		1278.742	
	882.3605		882.3605	9	I	9	1177.694		1177.694	
	1010.419		1010.419	10	Q	8	1064.61	+0.278069	1064.61	
	1097.451	-0.085094	1097.451	11	S	7	936.5513	-0.010217	468.7793	+0.058606
	1210.535		1210.535	12	I	6	849.5193	+0.072044	849.5193	
+0.03186	662.3132		1323.619	13	I	5	736.4352	+0.137187	736.4352	
	1420.672	+0.049239	1420.672	14	P	4	623.3511	-0.024904	623.3511	
	1557.731		1557.731	15	H	3	526.2984		526.2984	
	1670.815		1670.815	16	I	2	389.2395	+0.042887	389.2395	
	1799.858		1799.858	17	E	1	276.1554		276.1554	
				18	K	0	147.1128		147.1128	

Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F03
Scannumber: 6230
Protein: BSU35680; ggaB
Peptide Score: 54.02
Method: ITMS; CID; 3



precursor information

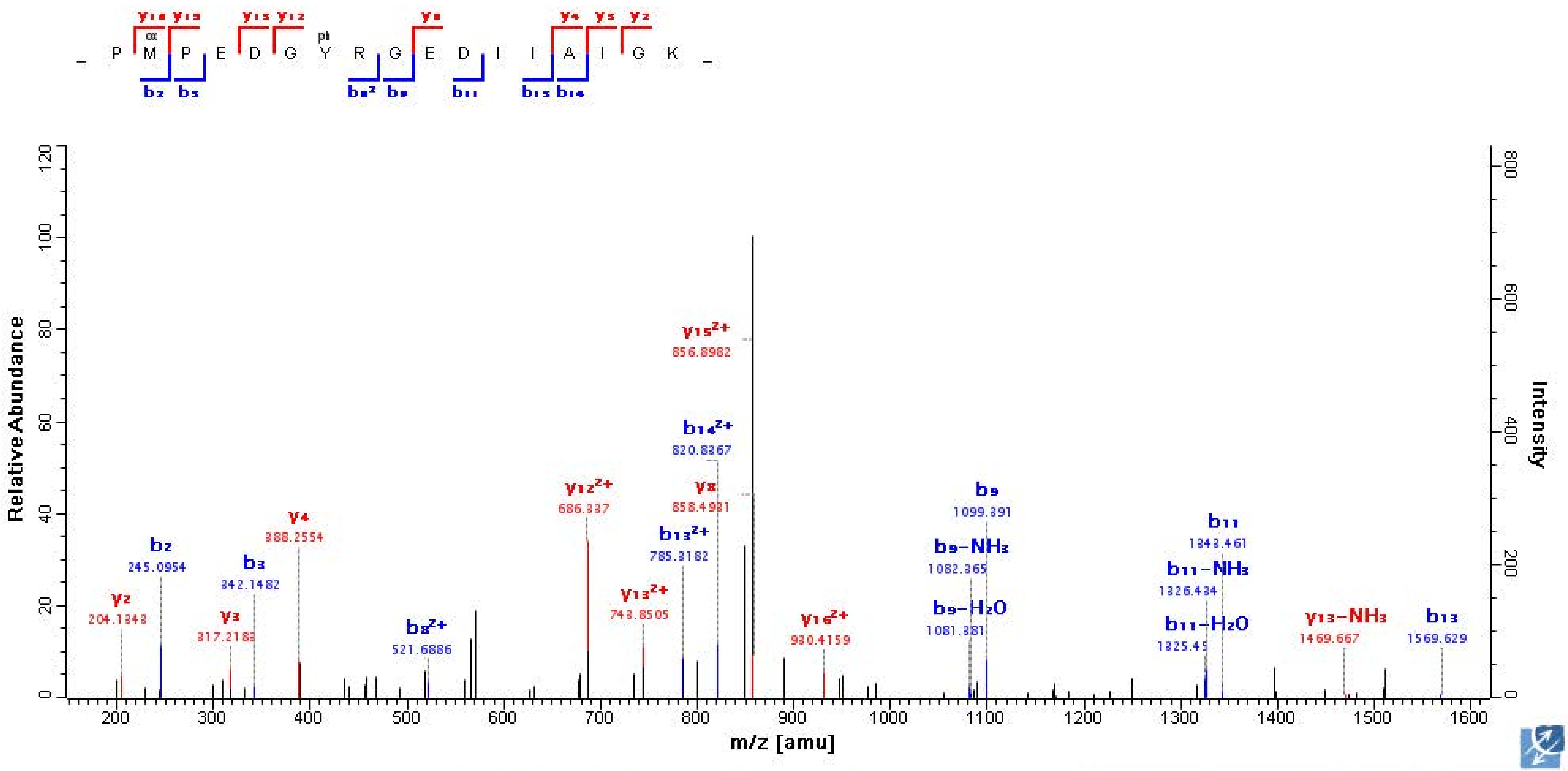
Mass:	1529.70026
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	54.02306
Mass Error [ppm]:	0.97119
PEP:	0.033448
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64%
Intensity Coverage:	29%
Protein Localisation:	74 ... 87

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659		129.0659	1	Q	13				
	243.1088		243.1088	2	N	12	1410.662		1410.662	
	300.1302		300.1302	3	G	11	1296.619		1296.619	
	357.1517		357.1517	4	G	10	1239.597	+0.418715	620.3023	+0.192902
	456.2201		456.2201	5	V	9	1182.576	+0.056145	1182.576	
	623.2185		623.2185	6	S	8	1083.507		1083.507	
	710.2505		710.2505	7	S	7	916.509		916.509	
	781.2876		781.2876	8	A	6	829.477		829.477	
	937.3887		937.3887	9	R	5	758.4399		379.7236	-0.096329
	1051.432		1051.432	10	N	4	602.3388		602.3388	
	1214.495		1214.495	11	Y	3	488.2959		488.2959	
	1271.516	-0.097998	1271.516	12	G	2	325.2325		325.2325	
-0.126529	692.8039	-0.01983	1384.601	13	I	1	268.2111	+0.106346	268.2111	
				14	K	0	155.127		155.127	

Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F03
Scannumber: 6247
Protein: argS; BSU37330
Peptide Score: 91.31
Method: ITMS; CID; 3



precursor information

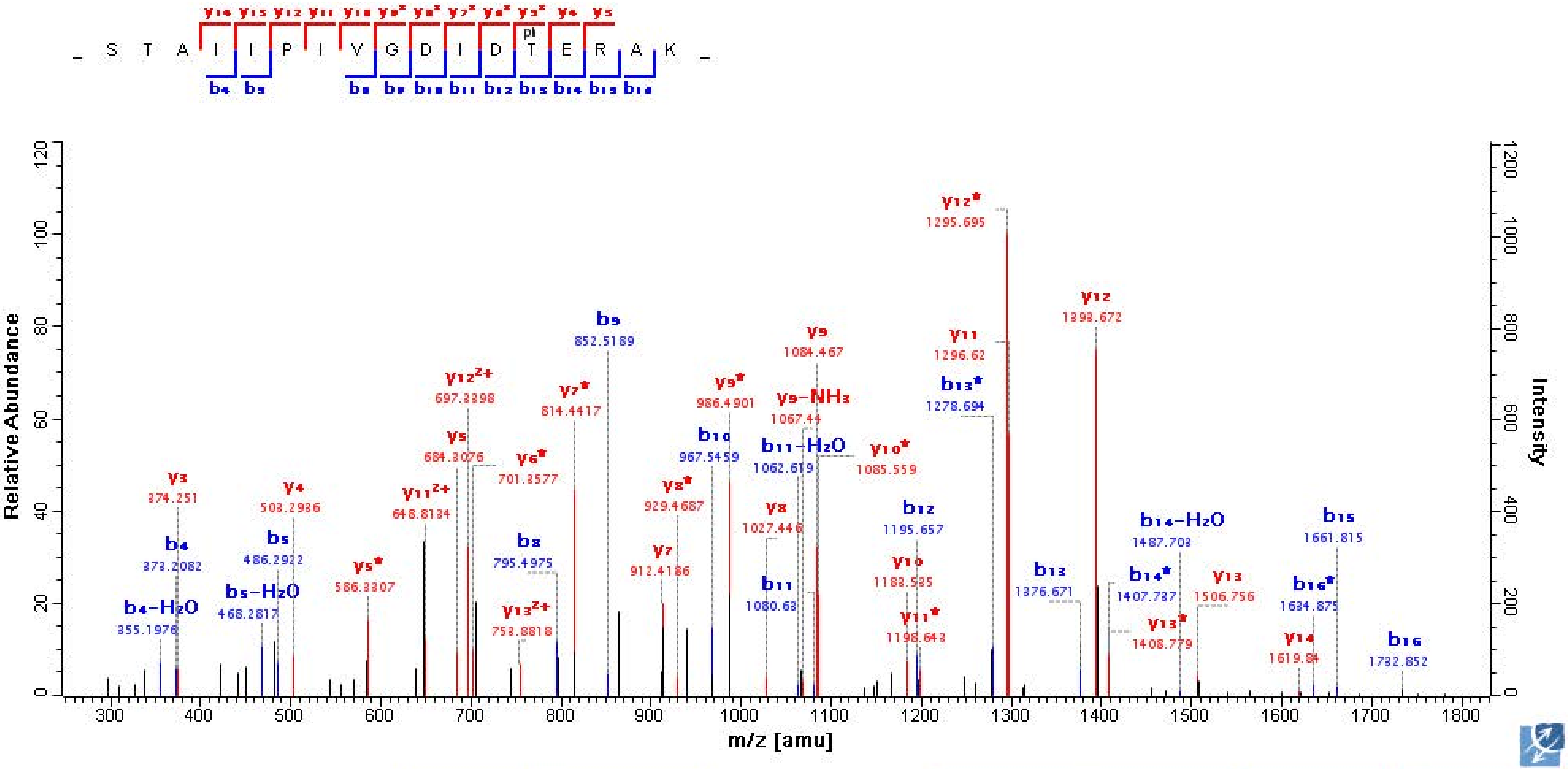
Mass:	1955.86903
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	91.30651
Mass Error [ppm]:	-0.49271
PEP:	8.3642E-06
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	36 %
Protein Localisation:	196 ... 212

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06004		98.06004	1	P	16				
	245.0954	+0.142033	245.0954	2	M	15	1859.825		930.4159	+0.147646
	342.1482	+0.042959	342.1482	3	P	14	1712.789		856.8982	-0.004637
	471.1908		471.1908	4	E	13	1615.736		1615.736	
	586.2177		586.2177	5	D	12	1486.694		743.8505	+0.408703
	643.2392		643.2392	6	G	11	1371.667		686.337	+0.16839
	886.2689		886.2689	7	Y	10	1314.645		1314.645	
-0.321743	521.6886		1042.37	8	R	9	1071.616		1071.616	
	1099.391	+0.074505	1099.391	9	G	8	915.5146		915.5146	
	1228.434		1228.434	10	E	7	858.4931	-0.355109	858.4931	
	1343.461	+0.041102	1343.461	11	D	6	729.4505		729.4505	
	1456.545		1456.545	12	I	5	614.4236		614.4236	
+0.012927	785.3182	-0.120434	1569.629	13	I	4	501.3395		501.3395	
+0.288682	820.8367		1640.666	14	A	3	388.2554	+0.118089	388.2554	
	1753.75		1753.75	15	I	2	317.2183	+0.173514	317.2183	
	1810.772		1810.772	16	G	1	204.1343	-0.015249	204.1343	
				17	K	0	147.1128		147.1128	

Source:	20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F03
Scannumber:	9877
Protein:	BSU13200; rsbRB; ykoB
Peptide Score:	237.4
Method:	ITMS; CID; 3



precursor information

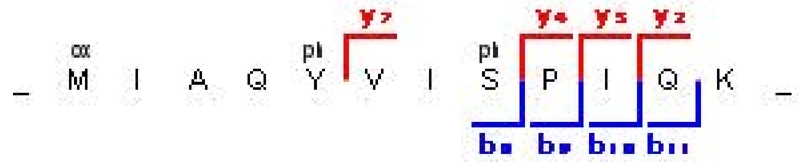
Mass:	1877.94945
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	237.4024
Mass Error [ppm]:	-0.27071
PEP:	9.6593E-103
Precursor Type:	MULTI

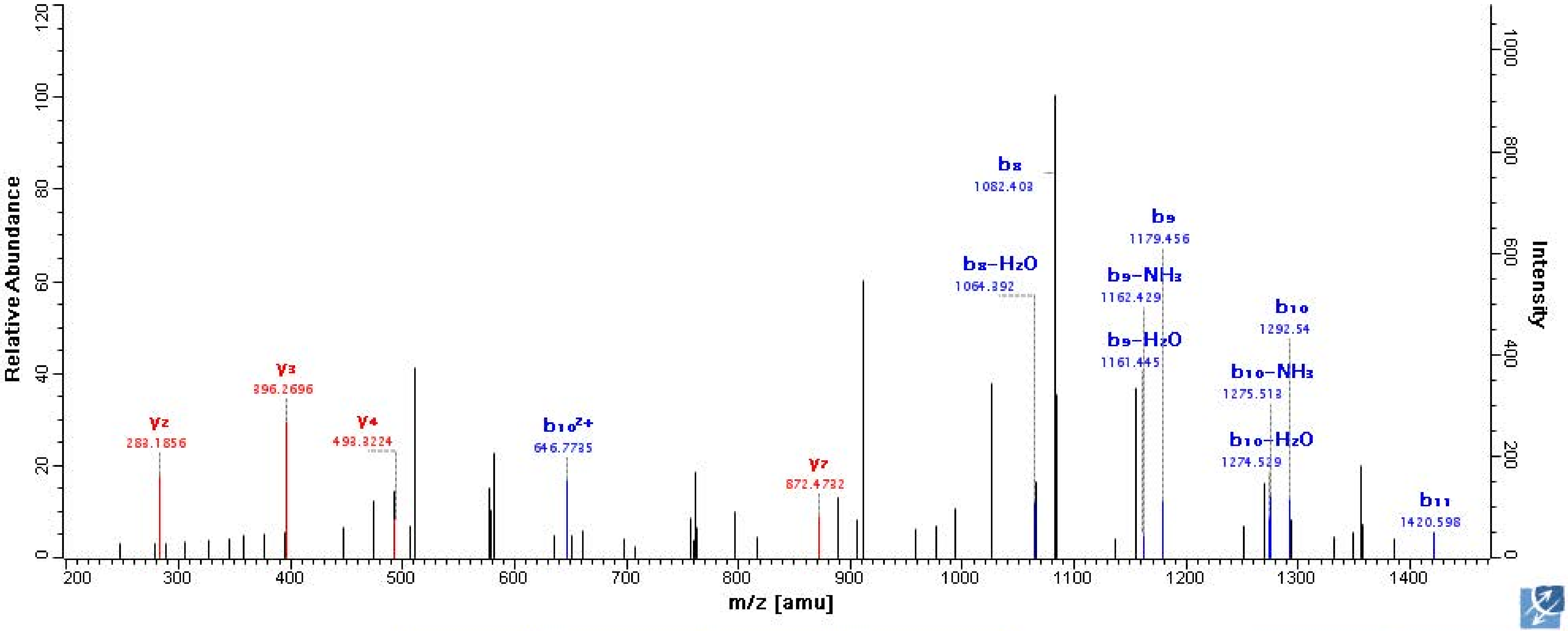
general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	67 %
Protein Localisation:	174 ... 190

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	16				
	189.08698335	2	T	15	1791.9252067		1791.9252067	
	260.12409714	3	A	14	1690.8775282		1690.8775282	
+0.173156	373.20816112	4	I	13	1619.8404144	-0.0312103	1619.8404144	
+0.0420034	486.2922251	5	I	12	1506.7563505	-0.2796659	753.88181346	+0.257835
	583.34498895	6	P	11	1393.6722865	+0.1057897	697.33978147	+0.1528943
	696.42905293	7	I	10	1296.6195226	+0.1900477	648.81339955	+0.3740394
+0.069916	795.49746685	8	V	9	1183.5354586	+0.1156644	1183.5354586	
+0.0491847	852.51893057	9	G	8	1084.4670447	+0.0657922	1084.4670447	
+0.3138066	967.5458736	10	D	7	1027.445581	+0.182837	1027.445581	
+0.2509218	1080.6299376	11	I	6	912.41863798	+0.1927512	912.41863798	
+0.0604045	1195.6568806	12	D	5	799.334574		799.334574	
-0.0379549	1376.6708895	13	T	4	684.30763097	+0.0090805	684.30763097	
	1505.7134826	14	E	3	503.29362208	+0.0897397	503.29362208	
+0.0987365	1661.8145936	15	R	2	374.25102899	+0.2017298	374.25102899	
+0.1856461	1732.8517074	16	A	1	218.14991796		218.14991796	
		17	K	0	147.11280417		147.11280417	

Source:	20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F04
Scannumber:	3635
Protein:	BSU35800; gerBA
Peptide Score:	66.27
Method:	ITMS; CID; 3





precursor information

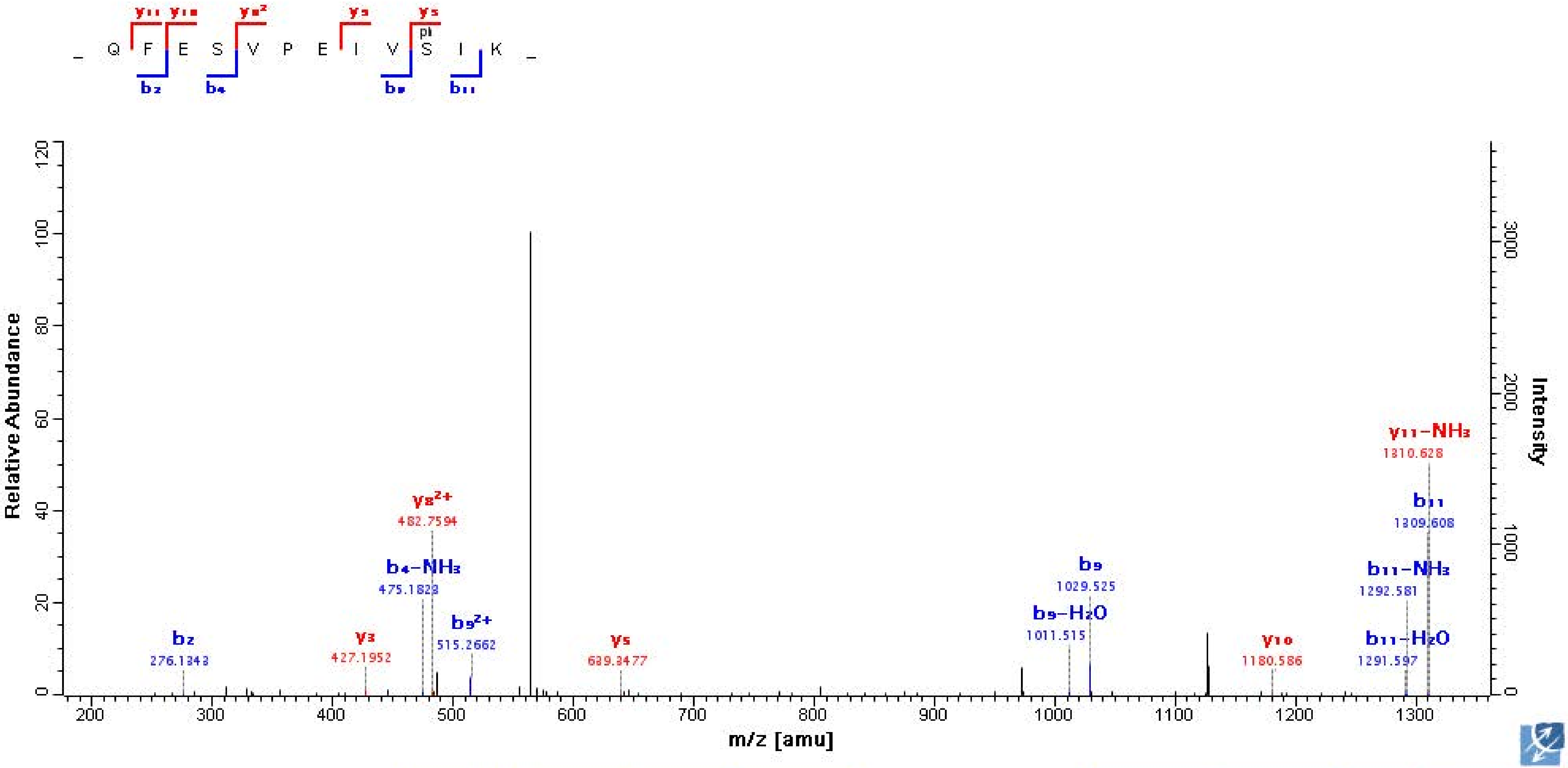
Mass:	1565.69608
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	66.26665
Mass Error [ppm]:	-0.32142
PEP:	0.036805
Precursor Type:	MULTI

general information

Annotation:	5 of 12
AminoAcids Coverag	42 %
Intensity Coverage:	21 %
Protein Localisation:	51 ... 62

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	148.04267569		148.04267569	1	M	11		
	261.12673968		261.12673968	2	I	10	1427.6826593	
	332.16385346		332.16385346	3	A	9	1314.5985953	
	460.22243097		460.22243097	4	Q	8	1243.5614815	
	703.25208992		703.25208992	5	Y	7	1115.502904	
	802.32050384		802.32050384	6	V	6	872.47324504	-0.0483183
	915.40456782		915.40456782	7	I	5	773.40483113	
	1082.4029266	+0.4841583	1082.4029266	8	S	4	660.32076715	
	1179.4556905	+0.0306376	1179.4556905	9	P	3	493.32240833	-0.0630089
-0.3319261	646.77351547	+0.1854653	1292.5397545	10	I	2	396.26964448	+0.1129239
	1420.598332	+0.1517901	1420.598332	11	Q	1	283.1855805	+0.0859649
				12	K	0	155.12700298	

Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F04
Scannumber: 9018
Protein: BSU03480; srfA; srfA1; srfAA
Peptide Score: 53.08
Method: ITMS; CID; 3



precursor information

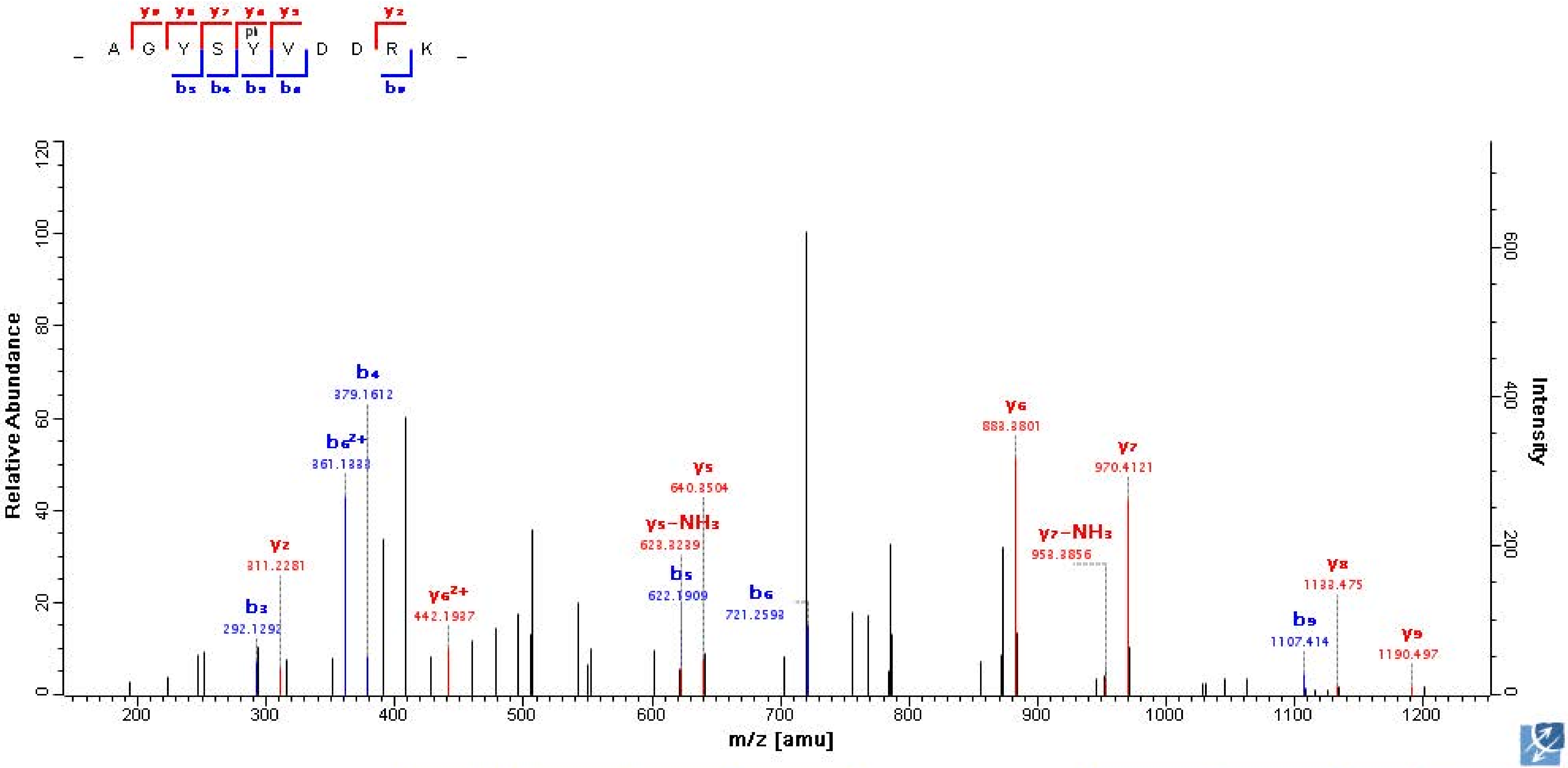
Mass:	1454.70562
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	53.08014
Mass Error [ppm]:	-0.12942
PEP:	0.070012
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	9 %
Protein Localisation:	202 ... 213

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659		129.0659	1	Q	11				
	276.1343	-0.220816	276.1343	2	F	10	1327.655		1327.655	
	405.1769		405.1769	3	E	9	1180.586	-0.106483	1180.586	
	492.2089		492.2089	4	S	8	1051.544		1051.544	
	591.2773		591.2773	5	V	7	964.5115		482.7594	-0.310096
	688.3301		688.3301	6	P	6	865.4431		865.4431	
	817.3727		817.3727	7	E	5	768.3903		768.3903	
	930.4567		930.4567	8	I	4	639.3477	-0.106982	639.3477	
-0.254794	515.2662	+0.097665	1029.525	9	V	3	526.2636		526.2636	
	1196.523		1196.523	10	S	2	427.1952	-0.185767	427.1952	
	1309.608	+0.116926	1309.608	11	I	1	260.1969		260.1969	
				12	K	0	147.1128		147.1128	

Source:	20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F05
Scannumber:	2540
Protein:	BSU05740; phoAIII; phoB
Peptide Score:	87.15
Method:	ITMS; CID; 3



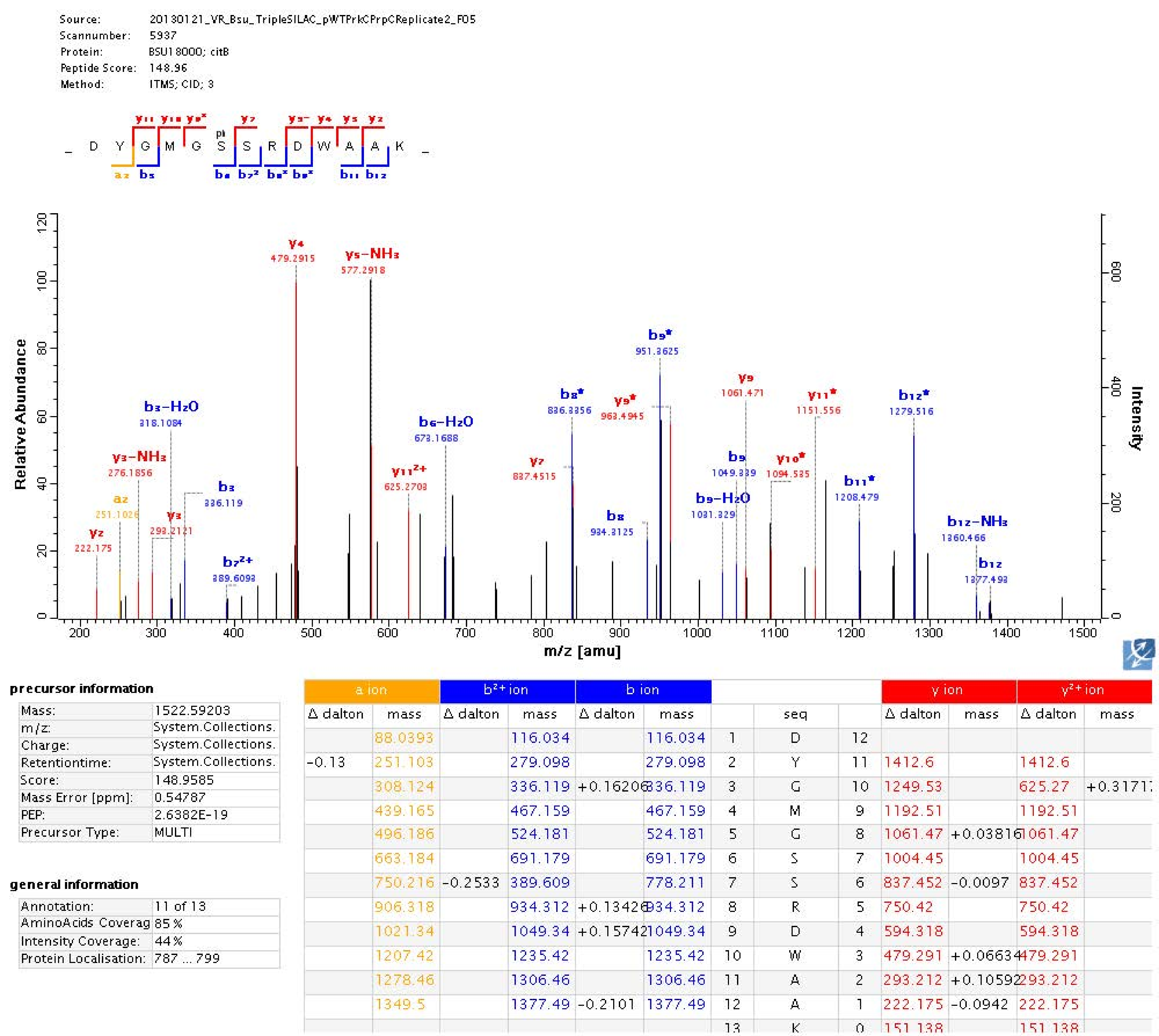
precursor information

Mass:	1260.527
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.14896
Mass Error [ppm]:	0.21448
PEP:	0.054988
Precursor Type:	ISO

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	27 %
Protein Localisation:	211 ... 220

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	9				
	129.0659		129.0659	2	G	8	1190.497	+0.027887	1190.497	
	292.1292	-0.063326	292.1292	3	Y	7	1133.475	+0.072055	1133.475	
	379.1612	+0.145308	379.1612	4	S	6	970.4121	+0.162117	970.4121	
	622.1909	+0.312121	622.1909	5	Y	5	883.3801	+0.045769	442.1937	-0.135386
+0.004842	361.1333	+0.298822	721.2593	6	V	4	640.3504	+0.136647	640.3504	
	836.2862		836.2862	7	D	3	541.282		541.282	
	951.3132		951.3132	8	D	2	426.2551		426.2551	
	1107.414	-0.010472	1107.414	9	R	1	311.2281	+0.033361	311.2281	
				10	K	0	155.127		155.127	



Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F05
Scannumber: 5937
Protein: BSU18000; citB
Peptide Score: 148.96
Method: ITMS; CID; 3

precursor information

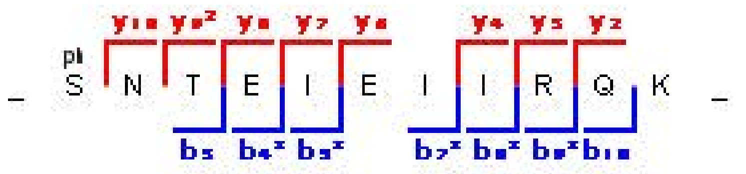
Mass:	1522.59203
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	148.9585
Mass Error [ppm]:	0.54787
PEP:	2.6382E-19
Precursor Type:	MULTI

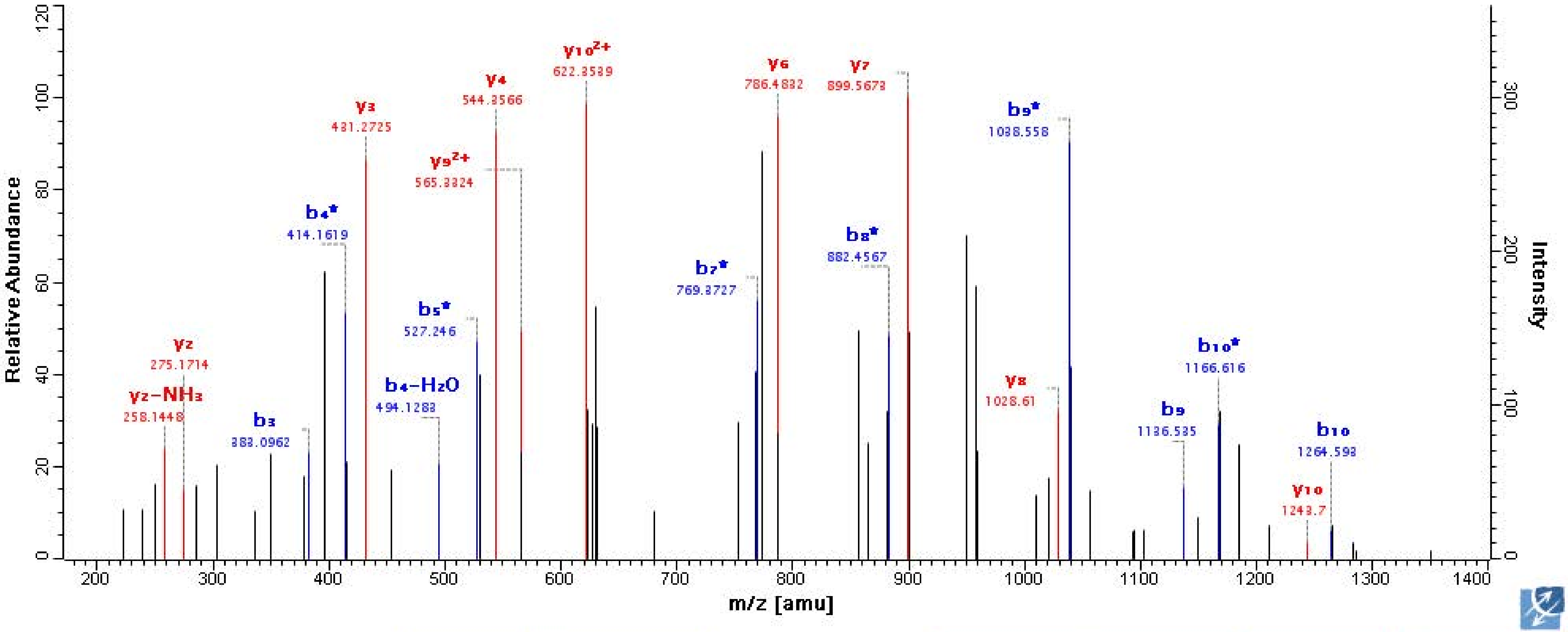
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	44 %
Protein Localisation:	787 ... 799

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		116.034		116.034	1	D	12				
-0.13	251.103		279.098		279.098	2	Y	11	1412.6		1412.6	
	308.124		336.119	+0.16206	336.119	3	G	10	1249.53		625.27	+0.3171
	439.165		467.159		467.159	4	M	9	1192.51		1192.51	
	496.186		524.181		524.181	5	G	8	1061.47	+0.03816	1061.47	
	663.184		691.179		691.179	6	S	7	1004.45		1004.45	
	750.216	-0.2533	389.609		778.211	7	S	6	837.452	-0.0097	837.452	
	906.318		934.312	+0.13426	934.312	8	R	5	750.42		750.42	
	1021.34		1049.34	+0.15742	1049.34	9	D	4	594.318		594.318	
	1207.42		1235.42		1235.42	10	W	3	479.291	+0.06634	479.291	
	1278.46		1306.46		1306.46	11	A	2	293.212	+0.10592	293.212	
	1349.5		1377.49	-0.2101	1377.49	12	A	1	222.175	-0.0942	222.175	
						13	K	0	151.138		151.138	

Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F05
Scannumber: 6902
Protein: aroA; BSU29750
Peptide Score: 113.61
Method: ITMS; CID; 3





precursor information

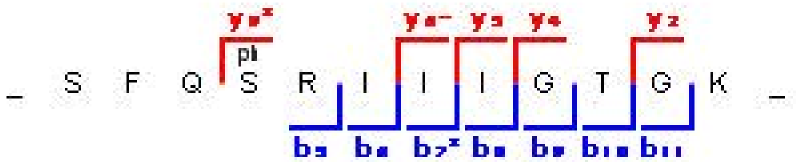
Mass:	1409.69154
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.609
Mass Error [ppm]:	-0.011434
PEP:	1.8025E-06
Precursor Type:	MULTI

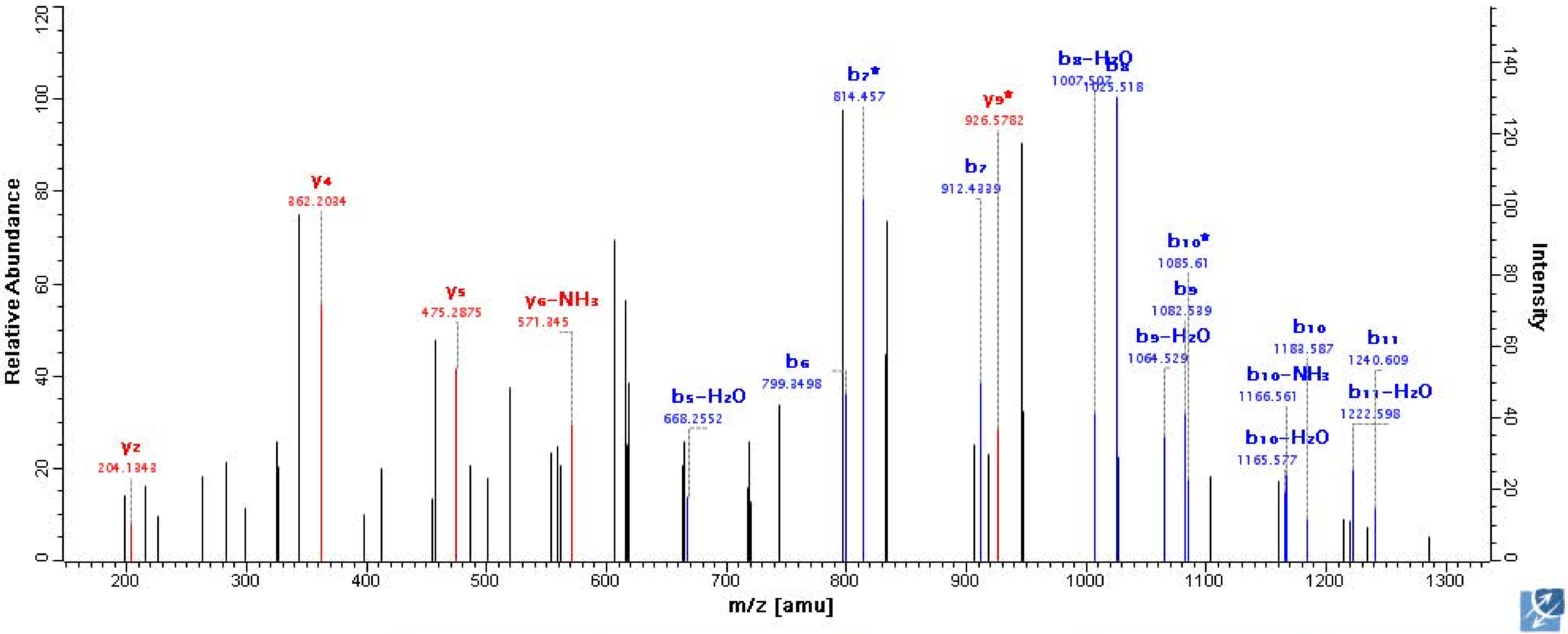
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	45 %
Protein Localisation:	2 ... 12

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.00563528	1	S	10				
	282.04856273	2	N	9	1243.7004768	+0.1934441	622.35387662	-0.0414987
+0.1173818	383.09624121	3	T	8	1129.6575493		565.33241289	-0.0137483
	512.1388343	4	E	7	1028.6098708	+0.1198655	1028.6098708	
	625.22289828	5	I	6	899.56727775	-0.0524462	899.56727775	
	754.26549138	6	E	5	786.48321377	+0.0294815	786.48321377	
	867.34955536	7	I	4	657.44062067		657.44062067	
	980.43361934	8	I	3	544.35655669	-0.1630142	544.35655669	
+0.0147081	1136.5347304	9	R	2	431.27249271	+0.1254565	431.27249271	
+0.0618435	1264.5933079	10	Q	1	275.17138168	-0.0934398	275.17138168	
		11	K	0	147.11280417		147.11280417	

Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F05
Scannumber: 8397
Protein: BSU11690; thiG; yjbT
Peptide Score: 79.87
Method: ITMS; CID; 3





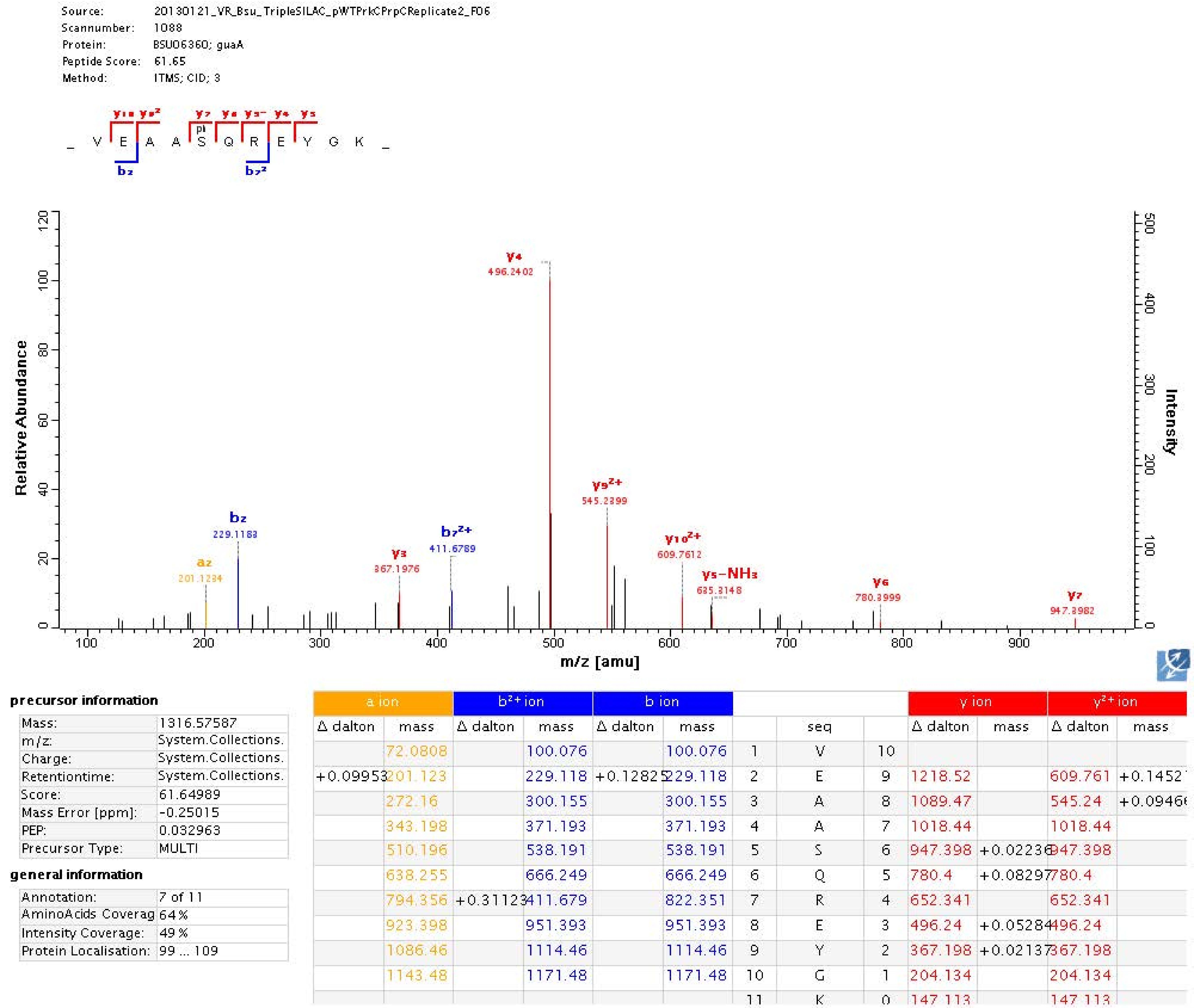
precursor information

Mass:	1385.70622
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	79.87488
Mass Error [ppm]:	-0.43088
PEP:	0.0053518
Precursor Type:	MULTI

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	32 %
Protein Localisation:	10 ... 21

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	88.039304876	1	S	11		
	235.107718793	2	F	10	1299.682063307	
	363.166296304	3	Q	9	1152.613649391	
	530.164655122	4	S	8	1024.55507188	
	686.265766151	5	R	7	857.556713061	
+0.0068593	799.349830131	6	I	6	701.455602033	
+0.1095629	912.433894111	7	I	5	588.371538053	
+0.1087509	1025.517958092	8	I	4	475.287474072	-0.1408066
+0.2763741	1082.539421815	9	G	3	362.203410092	+0.0998736
+0.189511	1183.587100289	10	T	2	305.181946368	
+0.4176811	1240.608564013	11	G	1	204.134267894	-0.1459561
		12	K	0	147.112804171	



Source: 20130121_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F06
Scannumber: 1088
Protein: BSU06360; guaA
Peptide Score: 61.65
Method: ITMS; CID; 3

precursor information

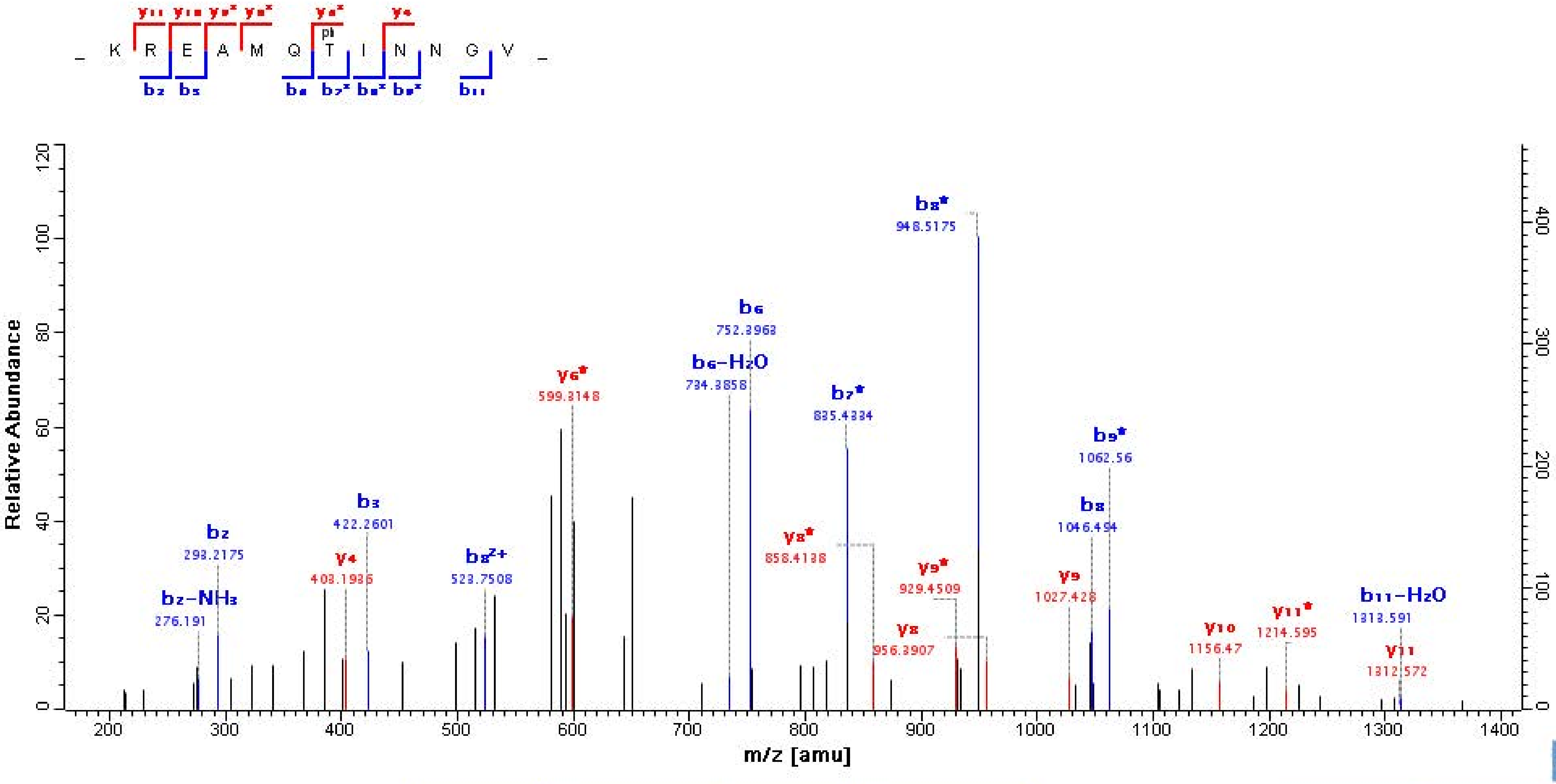
Mass:	1316.57587
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	61.64989
Mass Error [ppm]:	-0.25015
PEP:	0.032963
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	49 %
Protein Localisation:	99 ... 109

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.0808		100.076		100.076	1	V	10				
+0.09953	201.123		229.118	+0.12825	229.118	2	E	9	1218.52		609.761	+0.1452
	272.16		300.155		300.155	3	A	8	1089.47		545.24	+0.0946
	343.198		371.193		371.193	4	A	7	1018.44		1018.44	
	510.196		538.191		538.191	5	S	6	947.398	+0.02236	947.398	
	638.255		666.249		666.249	6	Q	5	780.4	+0.08297	780.4	
	794.356	+0.31123	411.679		822.351	7	R	4	652.341		652.341	
	923.398		951.393		951.393	8	E	3	496.24	+0.05284	496.24	
	1086.46		1114.46		1114.46	9	Y	2	367.198	+0.02137	367.198	
	1143.48		1171.48		1171.48	10	G	1	204.134		204.134	
						11	K	0	147.113		147.113	

Source:	20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F09
Scannumber:	3017
Protein:	BSU14000; patA; uat
Peptide Score:	115.33
Method:	ITMS; CID; 3



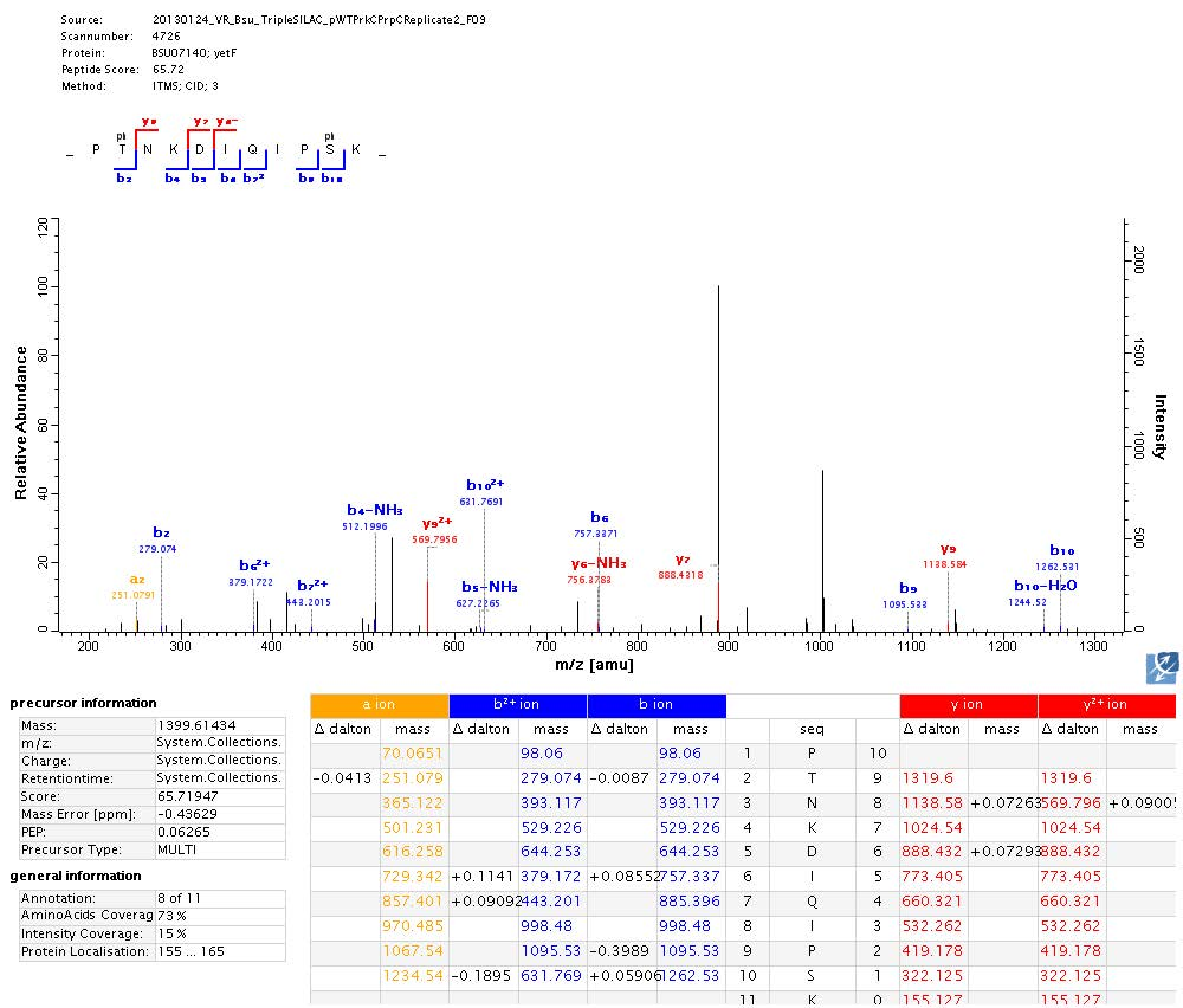
precursor information

Mass:	1447.6732
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.3266
Mass Error [ppm]:	-0.14651
PEP:	5.0267E-05
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	39 %
Protein Localisation:	382 ... 393

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	137.1164383		137.1164383	1	K	11		
	293.21754933	-0.0078325	293.21754933	2	R	10	1312.5715266	+0.1416082
	422.26014242	+0.3356828	422.26014242	3	E	9	1156.4704156	+0.2360053
	493.29725621		493.29725621	4	A	8	1027.4278225	-0.0531887
	624.33774082		624.33774082	5	M	7	956.39070867	-0.0399396
	752.39631833	-0.0741137	752.39631833	6	Q	6	825.35022406	
	933.41032721		933.41032721	7	T	5	697.29164655	
-0.1232704	523.75083383	+0.2510922	1046.4943912	8	I	4	516.27763767	
	1160.5373186		1160.5373186	9	N	3	403.19357369	-0.0084541
	1274.5802461		1274.5802461	10	N	2	289.15064624	
	1331.6017098		1331.6017098	11	G	1	175.10771879	
				12	V	0	118.08625507	



Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F09
Scannumber: 4726
Protein: BSU07140; yetF
Peptide Score: 65.72
Method: ITMS; CID; 3

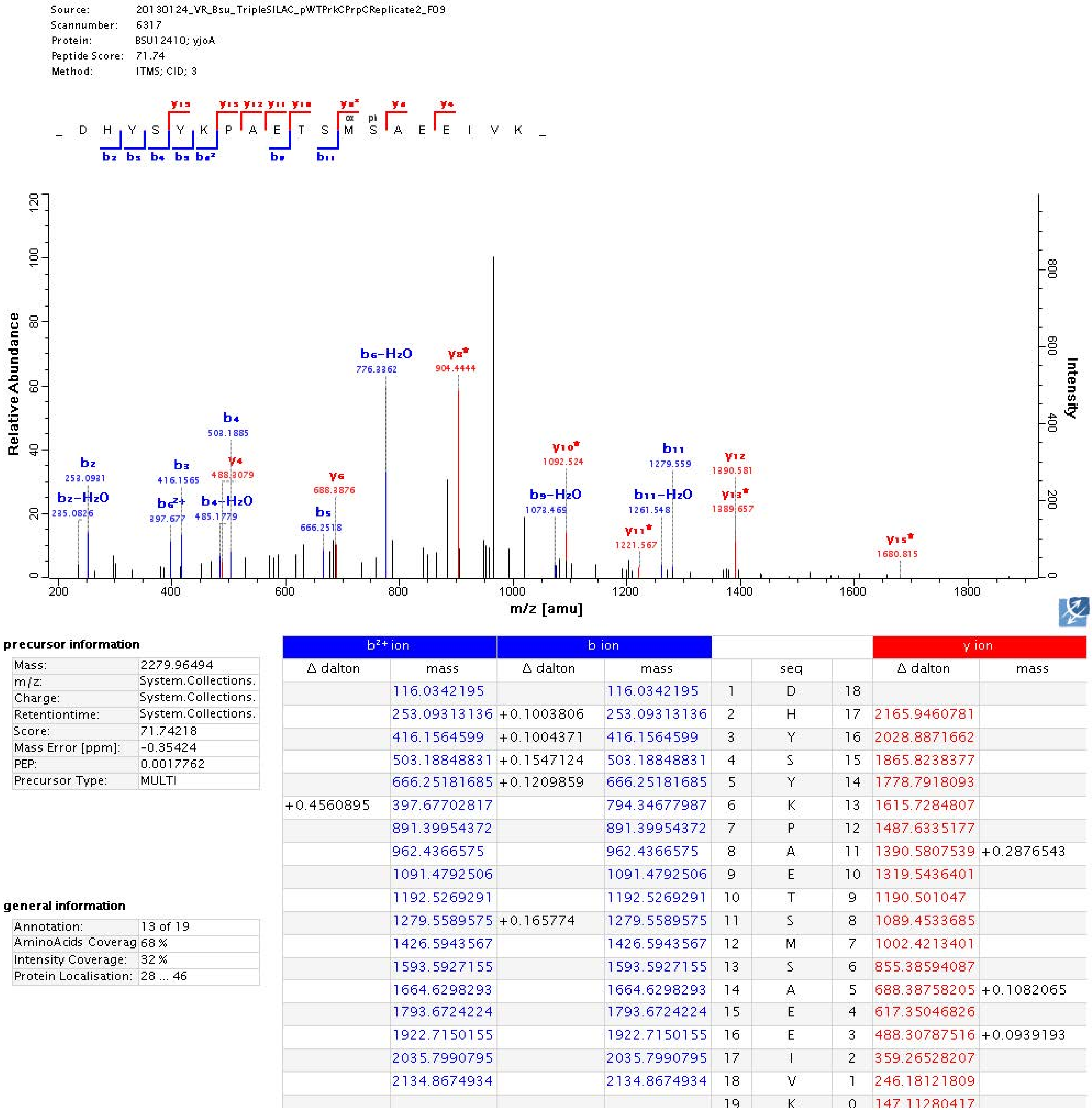
precursor information

Mass:	1399.61434
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	65.71947
Mass Error [ppm]:	-0.43629
PEP:	0.06265
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	15 %
Protein Localisation:	155 ... 165

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	70.0651		98.06		98.06	1	P	10				
-0.0413	251.079		279.074	-0.0087	279.074	2	T	9	1319.6		1319.6	
	365.122		393.117		393.117	3	N	8	1138.58	+0.07263	569.796	+0.0900
	501.231		529.226		529.226	4	K	7	1024.54		1024.54	
	616.258		644.253		644.253	5	D	6	888.432	+0.07293	888.432	
	729.342	+0.1141	379.172	+0.08552	757.337	6	I	5	773.405		773.405	
	857.401	+0.09092	443.201		885.396	7	Q	4	660.321		660.321	
	970.485		998.48		998.48	8	I	3	532.262		532.262	
	1067.54		1095.53	-0.3989	1095.53	9	P	2	419.178		419.178	
	1234.54	-0.1895	631.769	+0.05906	1262.53	10	S	1	322.125		322.125	
						11	K	0	155.127		155.127	



Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F09
Scannumber: 6317
Protein: BSU12410; yjoA
Peptide Score: 71.74
Method: ITMS; CID; 3

precursor information

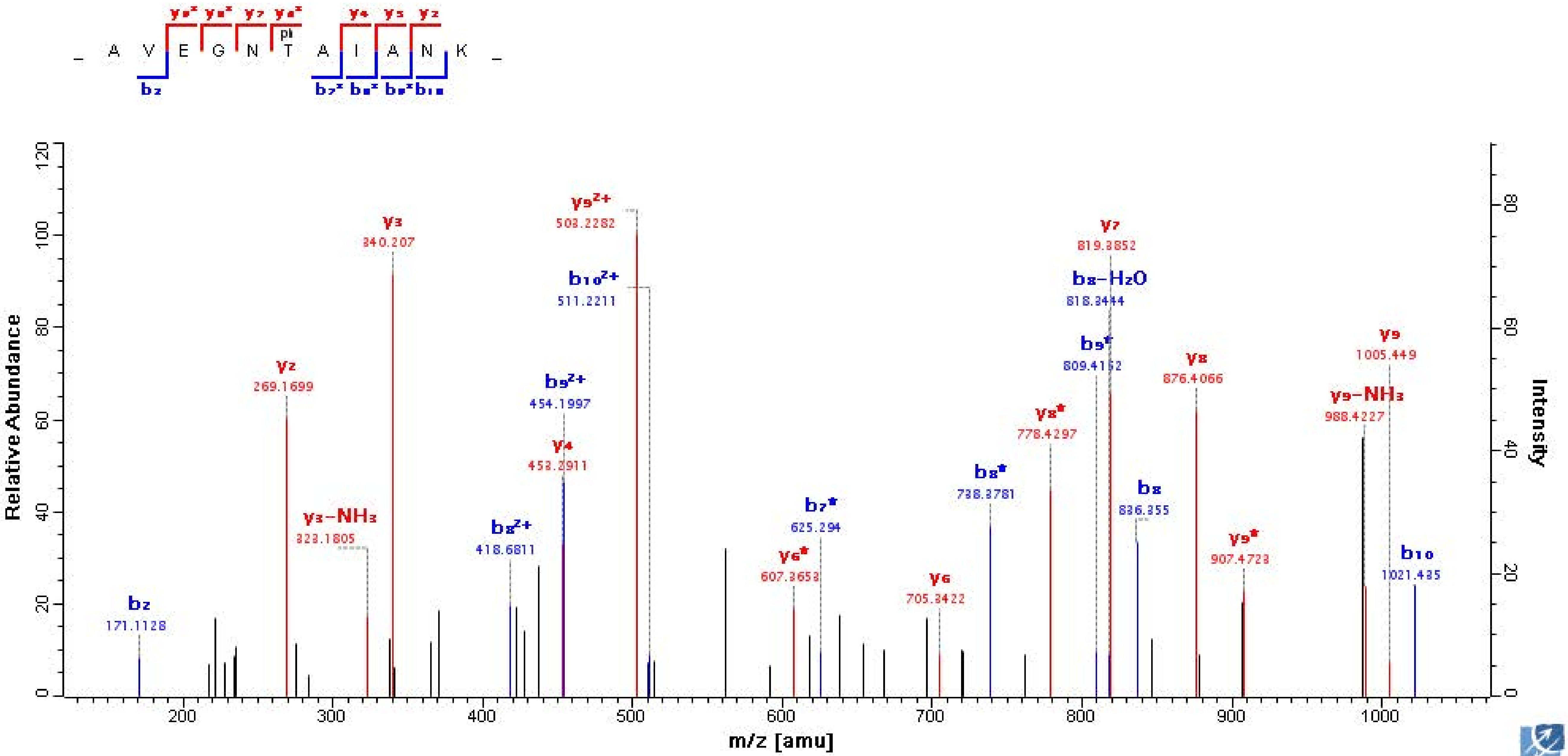
Mass:	2279.96494
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.74218
Mass Error [ppm]:	-0.35424
PEP:	0.0017762
Precursor Type:	MULTI

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	32 %
Protein Localisation:	28 ... 46

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	18		
	253.09313136	+0.1003806	253.09313136	2	H	17	2165.9460781	
	416.1564599	+0.1004371	416.1564599	3	Y	16	2028.8871662	
	503.18848831	+0.1547124	503.18848831	4	S	15	1865.8238377	
	666.25181685	+0.1209859	666.25181685	5	Y	14	1778.7918093	
+0.4560895	397.67702817		794.34677987	6	K	13	1615.7284807	
	891.39954372		891.39954372	7	P	12	1487.6335177	
	962.4366575		962.4366575	8	A	11	1390.5807539	+0.2876543
	1091.4792506		1091.4792506	9	E	10	1319.5436401	
	1192.5269291		1192.5269291	10	T	9	1190.501047	
	1279.5589575	+0.165774	1279.5589575	11	S	8	1089.4533685	
	1426.5943567		1426.5943567	12	M	7	1002.4213401	
	1593.5927155		1593.5927155	13	S	6	855.38594087	
	1664.6298293		1664.6298293	14	A	5	688.38758205	+0.1082065
	1793.6724224		1793.6724224	15	E	4	617.35046826	
	1922.7150155		1922.7150155	16	E	3	488.30787516	+0.0939193
	2035.7990795		2035.7990795	17	I	2	359.26528207	
	2134.8674934		2134.8674934	18	V	1	246.18121809	
				19	K	0	147.11280417	

Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F20
Scannumber: 1500
Protein: BSU25020; sodA; yqgD
Peptide Score: 140.78
Method: ITMS; CID; 3



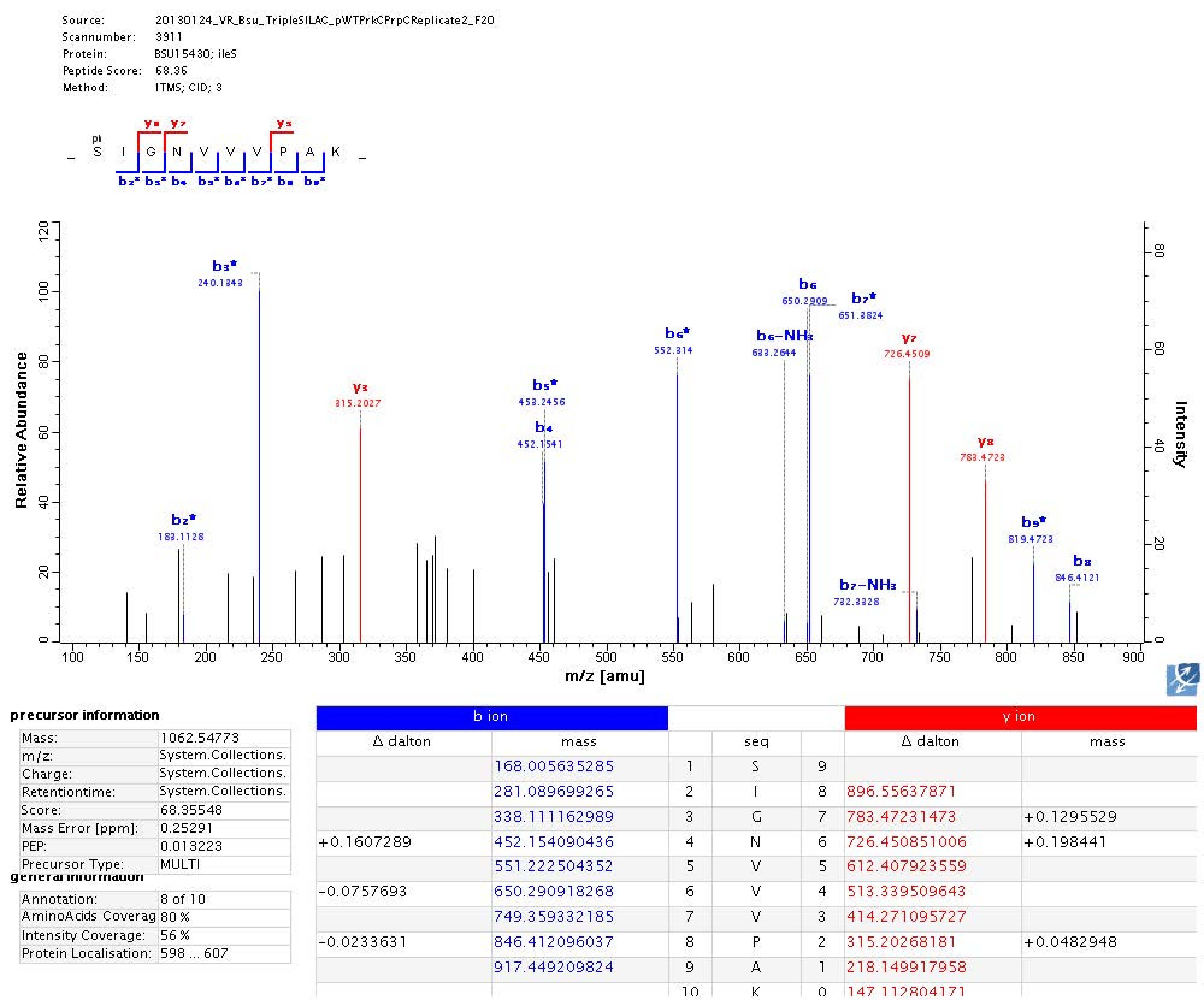
precursor information

Mass:	1166.5335
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.7803
Mass Error [ppm]:	0.19973
PEP:	2.8126E-11
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	64 %
Protein Localisation:	42 ... 52

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	10				
	171.1128	+0.077183	171.1128	2	V	9	1104.518		1104.518	
	300.1554		300.1554	3	E	8	1005.449	+0.064701	503.2282	+0.146327
	357.1769		357.1769	4	G	7	876.4066	-0.105291	876.4066	
	471.2198		471.2198	5	N	6	819.3852	-0.037685	819.3852	
	652.2338		652.2338	6	T	5	705.3422	-0.143378	705.3422	
	723.2709		723.2709	7	A	4	524.3282		524.3282	
-0.332676	418.6811	+0.315679	836.355	8	I	3	453.2911	+0.001861	453.2911	
+0.236902	454.1997		907.3921	9	A	2	340.207	-0.069837	340.207	
-0.307938	511.2211	+0.320111	1021.435	10	N	1	269.1699	-0.05259	269.1699	
				11	K	0	155.127		155.127	



Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F20
Scannumber: 3911
Protein: BSU15430; ileS
Peptide Score: 68.36
Method: ITMS; CID; 3

precursor information

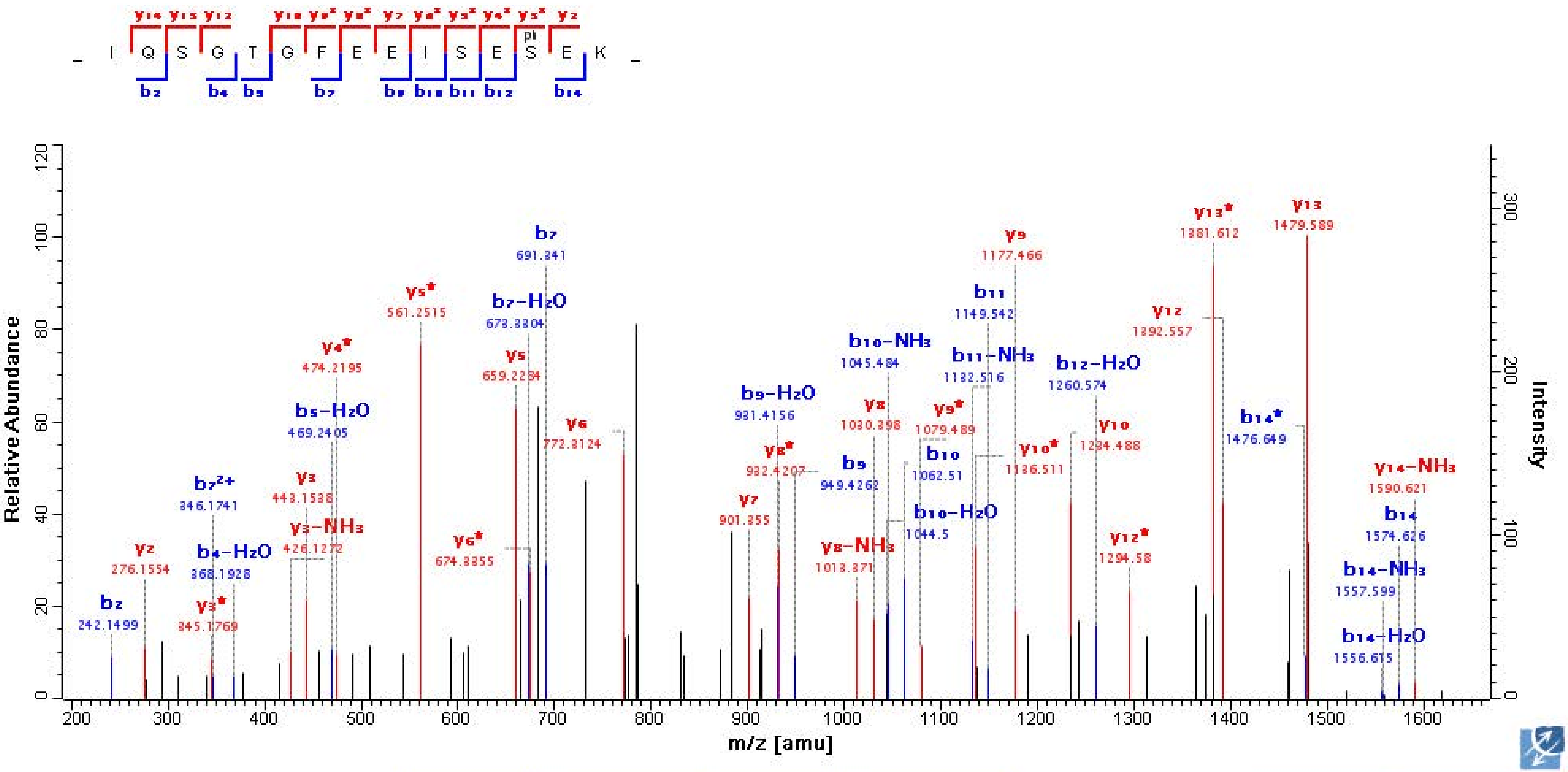
Mass:	1062.54773
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	68.35548
Mass Error [ppm]:	0.25291
PEP:	0.013223
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	56 %
Protein Localisation:	598 ... 607

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	168.005635285	1	S	9		
	281.089699265	2	I	8	896.55637871	
	338.111162989	3	G	7	783.47231473	+0.1295529
+0.1607289	452.154090436	4	N	6	726.450851006	+0.198441
	551.222504352	5	V	5	612.407923559	
-0.0757693	650.290918268	6	V	4	513.339509643	
	749.359332185	7	V	3	414.271095727	
-0.0233631	846.412096037	8	P	2	315.20268181	+0.0482948
	917.449209824	9	A	1	218.149917958	
		10	K	0	147.112804171	

Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F20
Scannumber: 4682
Protein: azoR2; BSU33540; yvaB
Peptide Score: 220.46
Method: ITMS; CID; 3



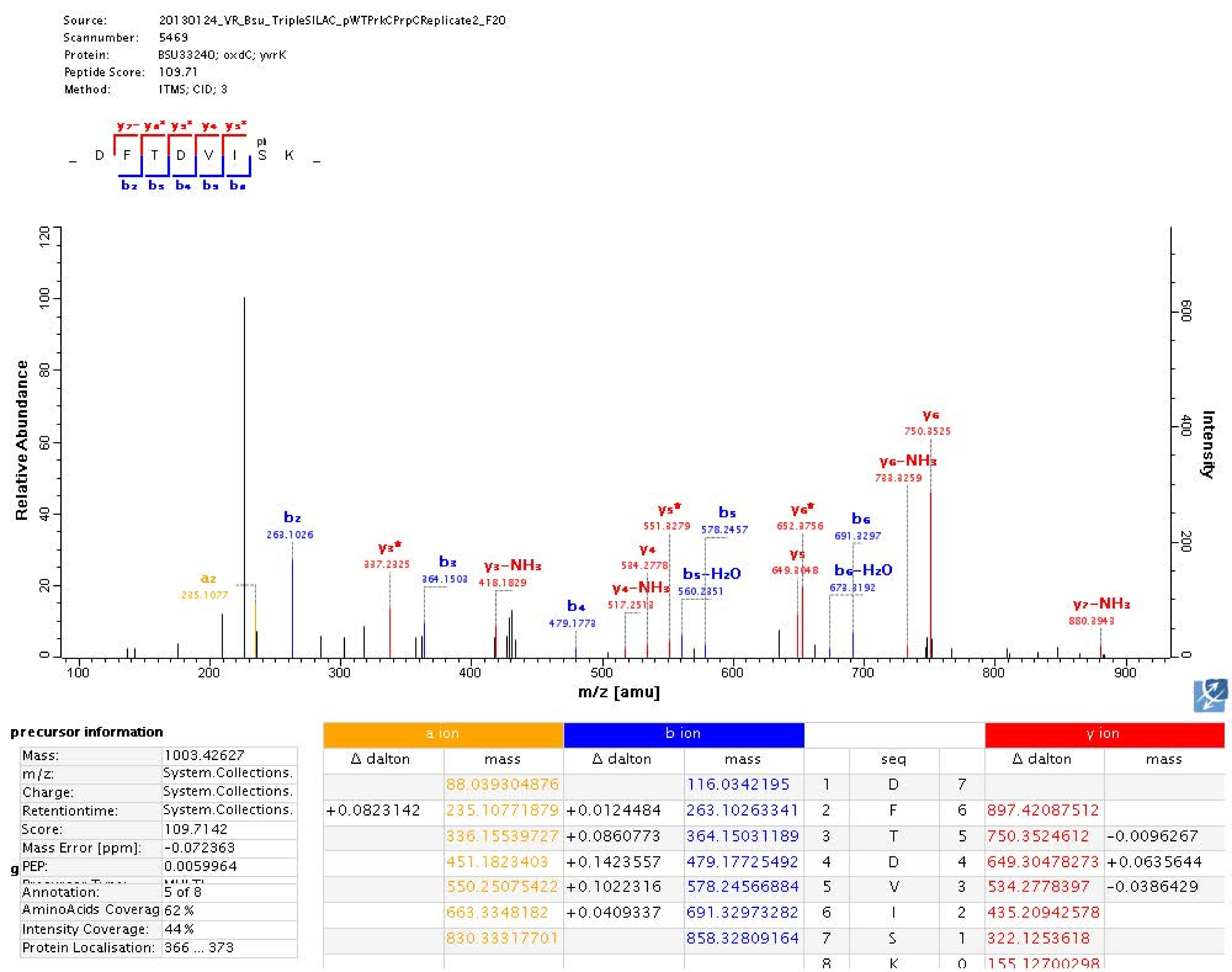
precursor information

Mass:	1719.72498
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	220.4599
Mass Error [ppm]:	0.54634
PEP:	2.8756E-80
Precursor Type:	MULTI

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	58 %
Protein Localisation:	63 ... 77

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	14		
	242.14991796	-0.0176853	242.14991796	2	Q	13	1607.6472535	
	329.18194637		329.18194637	3	S	12	1479.588676	+0.1406941
	386.20341009		386.20341009	4	G	11	1392.5566476	+0.2752616
	487.25108857		487.25108857	5	T	10	1335.5351839	
	544.27255229		544.27255229	6	G	9	1234.4875054	-0.050982
+0.1547056	346.17412134	+0.1844855	691.34096621	7	F	8	1177.4660417	+0.0362777
	820.3835593		820.3835593	8	E	7	1030.3976278	-0.0322713
	949.4261524	+0.2101391	949.4261524	9	E	6	901.35503467	+0.0909492
	1062.5102164	-0.0883414	1062.5102164	10	I	5	772.31244157	+0.0966771
	1149.5422448	+0.3044349	1149.5422448	11	S	4	659.22837759	+0.1899574
	1278.5848379		1278.5848379	12	E	3	572.19634918	
	1445.5831967		1445.5831967	13	S	2	443.15375609	+0.0637732
	1574.6257898	+0.0476721	1574.6257898	14	E	1	276.15539727	+0.1309492
				15	K	0	147.11280417	

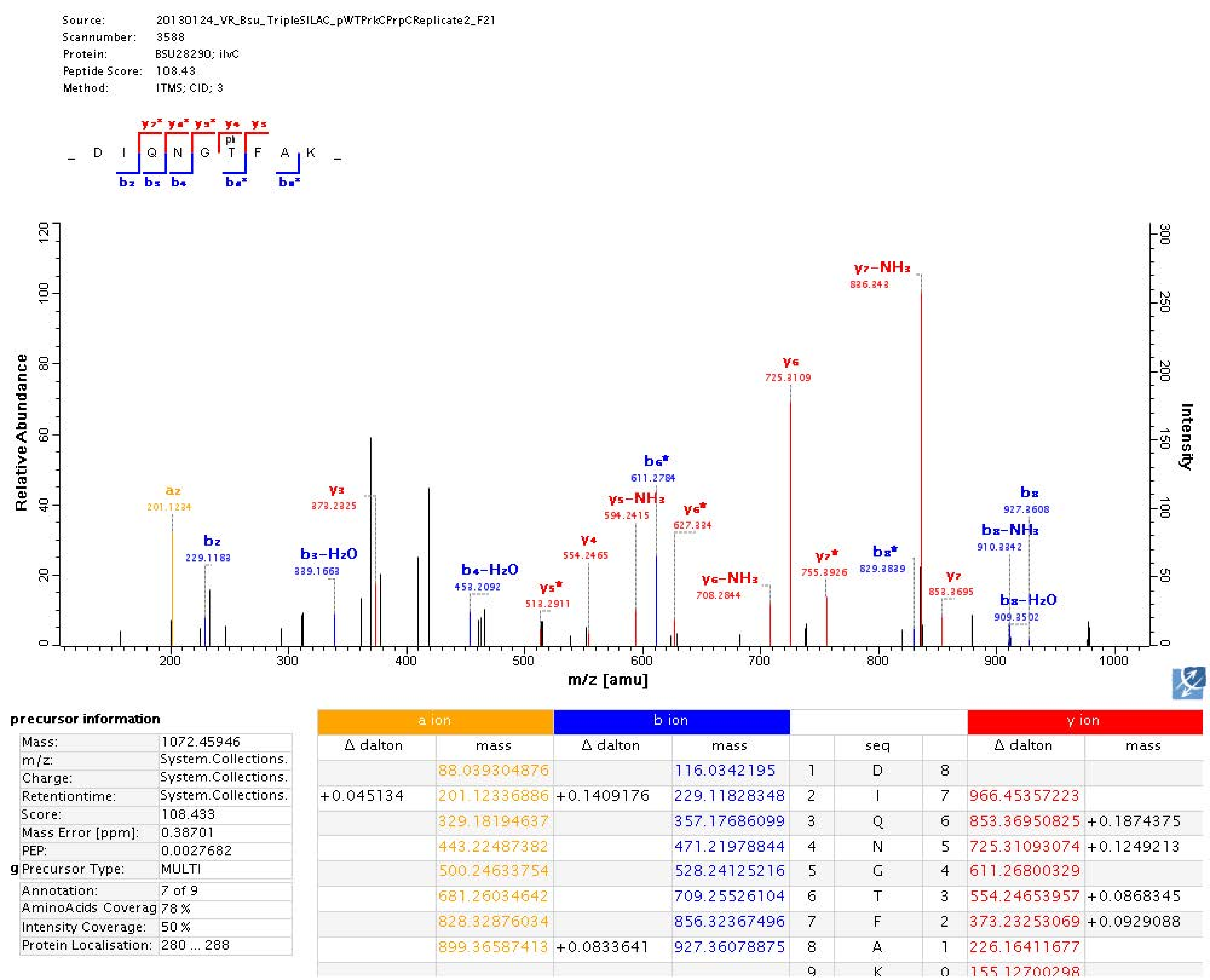


Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F20
Scannumber: 5469
Protein: BSU33240; oxdC; yvrK
Peptide Score: 109.71
Method: ITMS; CID; 3

precursor information

Mass:	1003.42627
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.7142
Mass Error [ppm]:	-0.072363
PEP:	0.0059964
Precursor Type:	MULTI
Annotation:	5 of 8
AminoAcids Coverag	62 %
Intensity Coverage:	44 %
Protein Localisation:	366 ... 373

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.0342195	1	D	7		
+0.0823142	235.10771879	+0.0124484	263.10263341	2	F	6	897.42087512	
	336.15539727	+0.0860773	364.15031189	3	T	5	750.3524612	-0.0096267
	451.1823403	+0.1423557	479.17725492	4	D	4	649.30478273	+0.0635644
	550.25075422	+0.1022316	578.24566884	5	V	3	534.2778397	-0.0386429
	663.3348182	+0.0409337	691.32973282	6	I	2	435.20942578	
	830.33317701		858.32809164	7	S	1	322.1253618	
				8	K	0	155.12700298	



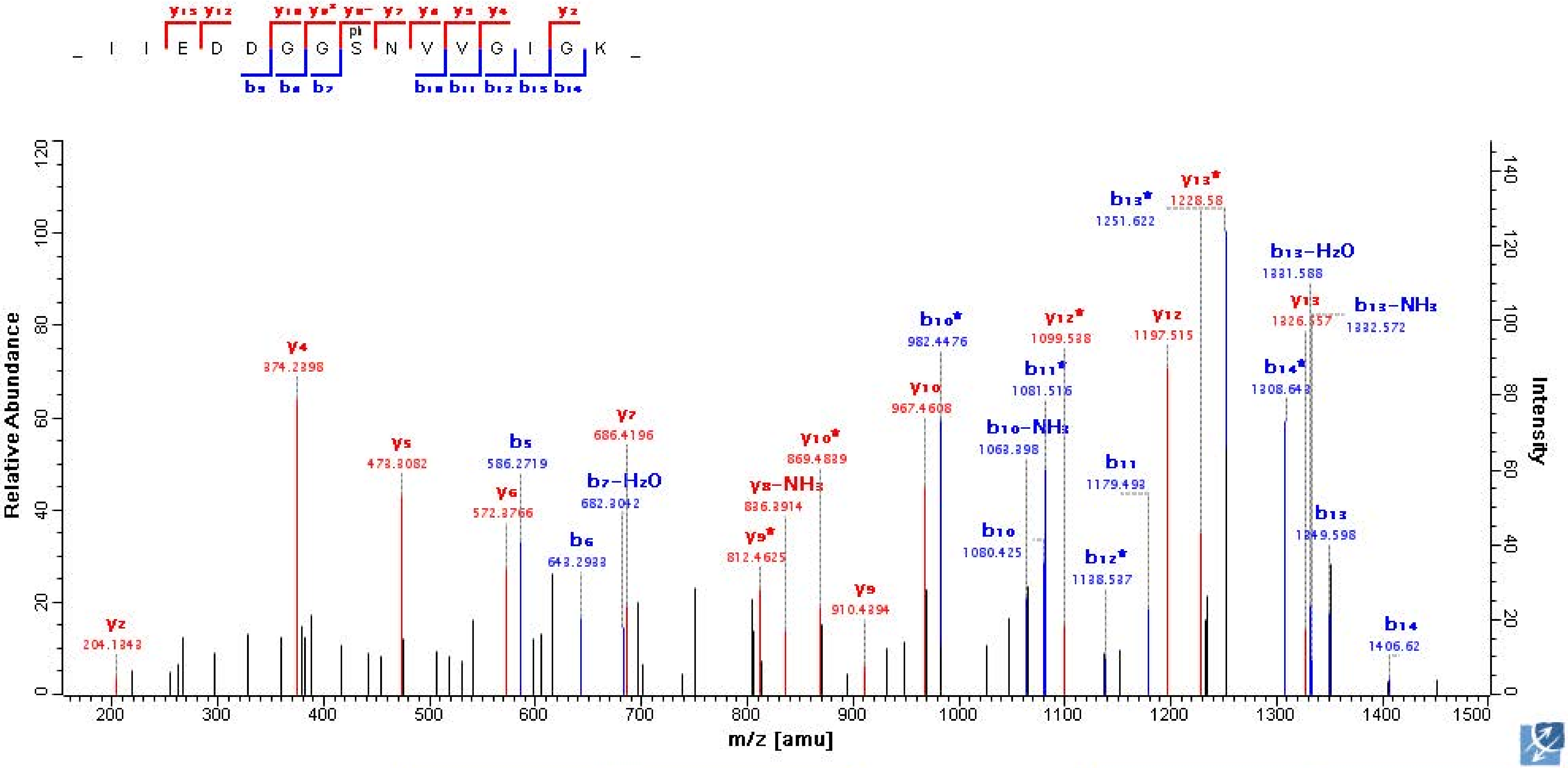
Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F21
Scannumber: 3588
Protein: BSU28290; ilvC
Peptide Score: 108.43
Method: ITMS; CID; 3

precursor information

Mass:	1072.45946
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.433
Mass Error [ppm]:	0.38701
PEP:	0.0027682
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	50 %
Protein Localisation:	280 ... 288

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.0342195	1	D	8		
+0.045134	201.12336886	+0.1409176	229.11828348	2	I	7	966.45357223	
	329.18194637		357.17686099	3	Q	6	853.36950825	+0.1874375
	443.22487382		471.21978844	4	N	5	725.31093074	+0.1249213
	500.24633754		528.24125216	5	G	4	611.26800329	
	681.26034642		709.25526104	6	T	3	554.24653957	+0.0868345
	828.32876034		856.32367496	7	F	2	373.23253069	+0.0929088
	899.36587413	+0.0833641	927.36078875	8	A	1	226.16411677	
				9	K	0	155.12700298	

Source: 20130124_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate2_F21
Scannumber: 5074
Protein: BSU27320; greA
Peptide Score: 142.45
Method: ITMS; CID; 3



precursor information

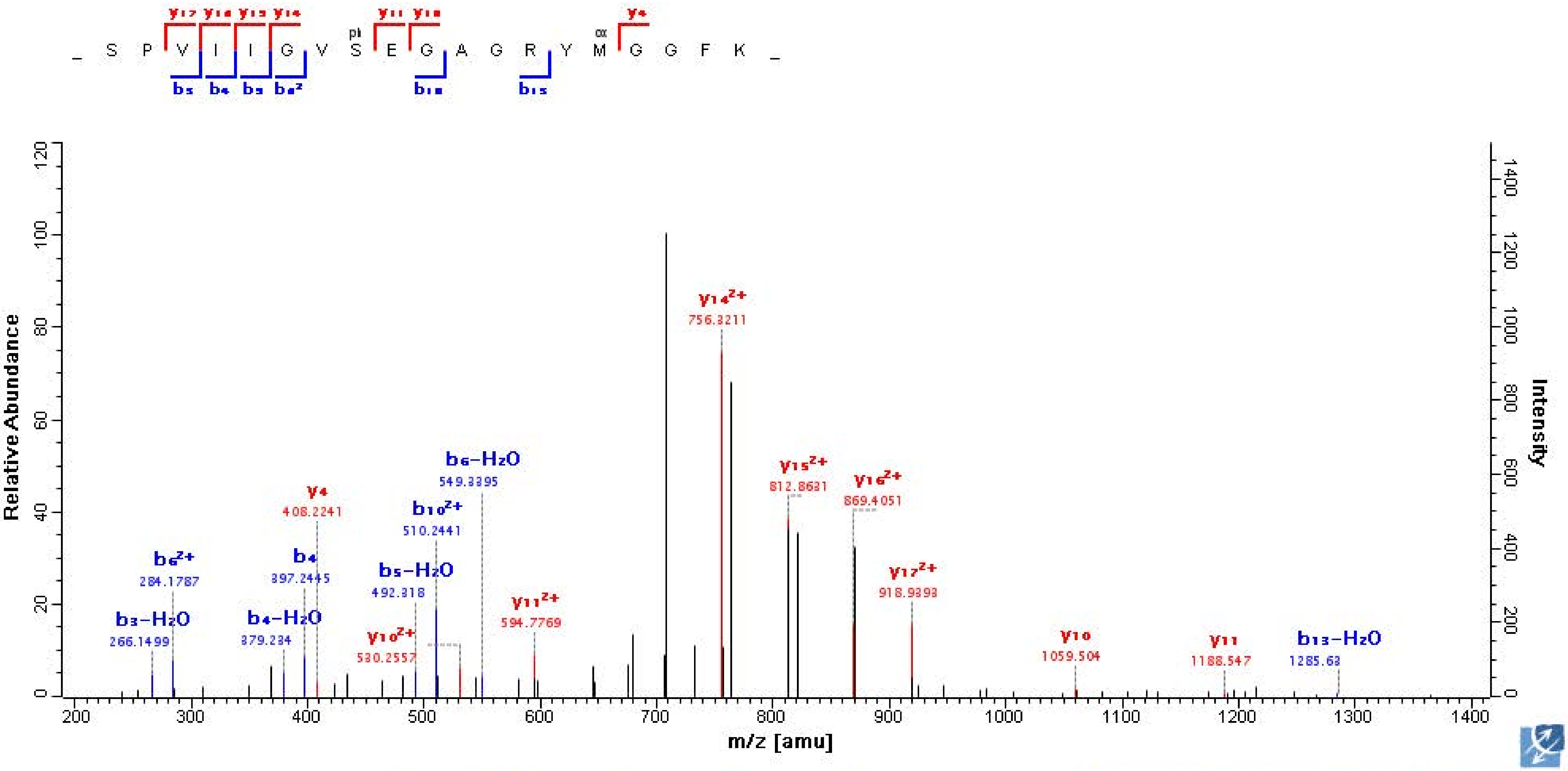
Mass:	1551.71817
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	142.4528
Mass Error [ppm]:	-0.0011177
PEP:	1.8158E-23
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	58 %
Protein Localisation:	77 ... 91

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	114.091340447	1	I	14		
	227.175404427	2	I	13	1439.641380284	
	356.217997524	3	E	12	1326.557316304	+0.0931964
	471.244940556	4	D	11	1197.514723207	+0.1146713
+0.0128454	586.271883588	5	D	10	1082.487780175	
+0.0289793	643.293347311	6	G	9	967.460837143	+0.0647976
	700.314811035	7	G	8	910.43937342	+0.0042301
	867.313169853	8	S	7	853.417909696	
	981.3560973	9	N	6	686.419550878	-0.0585279
-0.1907466	1080.424511216	10	V	5	572.376623431	-0.000952
+0.1087594	1179.492925133	11	V	4	473.308209514	+0.0736264
	1236.514388856	12	G	3	374.239795598	+0.0941277
-0.0609773	1349.598452837	13	I	2	317.218331875	
-0.2025582	1406.61991656	14	G	1	204.134267894	+0.2205905
		15	K	0	147.112804171	

Source: 20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F03
Scannumber: 8808
Protein: BSU37120; fba; fba1; fbaA; tsr
Peptide Score: 69.73
Method: ITMS; CID; 3



precursor information

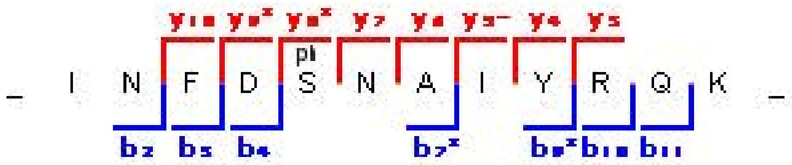
Mass:	2019.94998
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	69.72889
Mass Error [ppm]:	0.53029
PEP:	0.0014252
Precursor Type:	MULTI

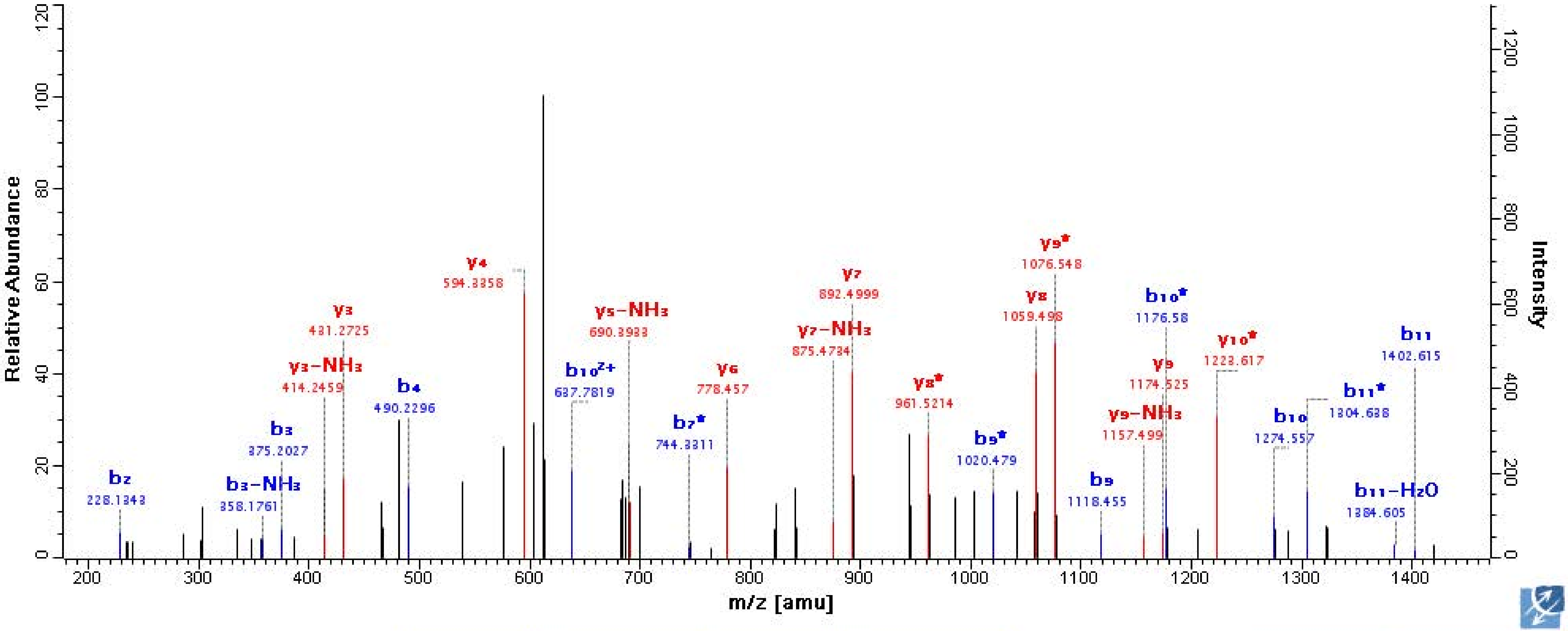
general information

Annotation:	8 of 19
AminoAcids Coverag	42 %
Intensity Coverage:	33 %
Protein Localisation:	43 ... 61

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	18				
	185.0921		185.0921	2	P	17	1933.924		1933.924	
	284.1605		284.1605	3	V	16	1836.871		918.9393	+0.197321
	397.2445	-0.01481	397.2445	4	I	15	1737.803		869.4051	-0.208047
	510.3286		510.3286	5	I	14	1624.719		812.8631	-0.14331
+0.096776	284.1787		567.3501	6	G	13	1511.635		756.3211	+0.116251
	666.4185		666.4185	7	V	12	1454.613		1454.613	
	833.4168		833.4168	8	S	11	1355.545		1355.545	
	962.4594		962.4594	9	E	10	1188.547	-0.376697	594.7769	-0.301545
-0.088939	510.2441		1019.481	10	G	9	1059.504	-0.017942	530.2557	+0.124781
	1090.518		1090.518	11	A	8	1002.483		1002.483	
	1147.539		1147.539	12	G	7	931.4454		931.4454	
	1303.641		1303.641	13	R	6	874.424		874.424	
	1466.704		1466.704	14	Y	5	718.3229		718.3229	
	1613.739		1613.739	15	M	4	555.2595		555.2595	
	1670.761		1670.761	16	G	3	408.2241	+0.029578	408.2241	
	1727.782		1727.782	17	G	2	351.2027		351.2027	
	1874.851		1874.851	18	F	1	294.1812		294.1812	
				19	K	0	147.1128		147.1128	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F05
Scannumber:	8117
Protein:	BSU16090; sucC
Peptide Score:	145.29
Method:	ITMS; CID; 3





precursor information

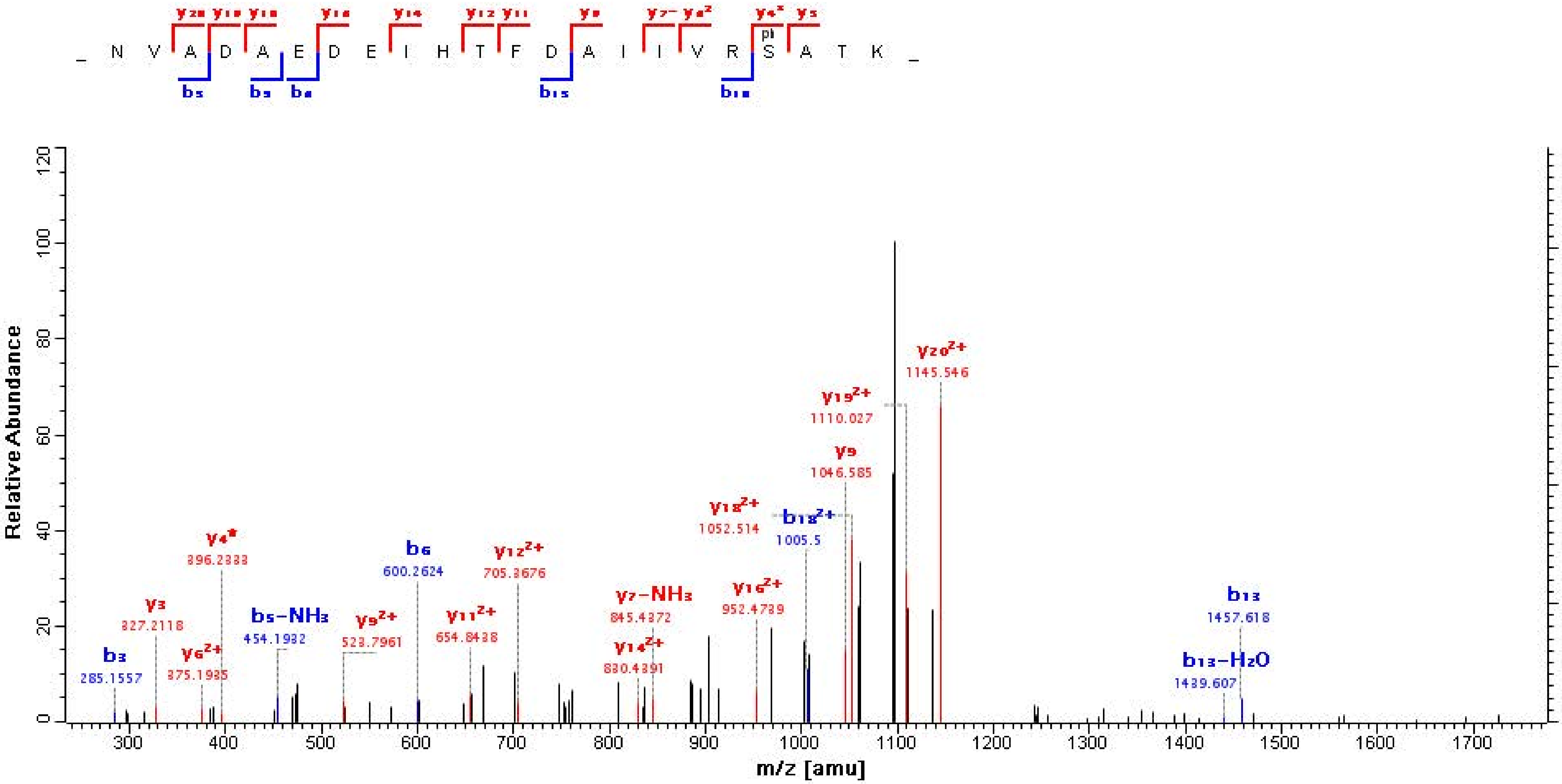
Mass:	1547.71324
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	145.2936
Mass Error [ppm]:	-0.076532
PEP:	3.8379E-17
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	40 %
Protein Localisation:	216 ... 227

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	11		
	228.13426789	+0.0841464	228.13426789	2	N	10	1435.6365697	
	375.20268181	+0.0274818	375.20268181	3	F	9	1321.5936422	
	490.22962484	-0.1181136	490.22962484	4	D	8	1174.5252283	+0.1046545
	657.22798366		657.22798366	5	S	7	1059.4982853	-0.0212345
	771.27091111		771.27091111	6	N	6	892.49992646	-0.1979855
	842.3080249		842.3080249	7	A	5	778.45699902	-0.078459
	955.39208888		955.39208888	8	I	4	707.41988523	
	1118.4554174	+0.1415064	1118.4554174	9	Y	3	594.33582125	+0.1071109
+0.1850775	637.78190245	+0.0214745	1274.5565284	10	R	2	431.27249271	-0.0831006
	1402.615106	-0.122186	1402.615106	11	Q	1	275.17138168	
				12	K	0	147.11280417	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F07
Scannumber:	13360
Protein:	BSU23070; serA
Peptide Score:	46.51
Method:	ITMS; CID; 3



precursor information

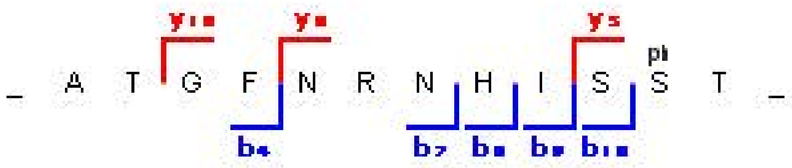
Mass:	2494.17369
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	46.5141
Mass Error [ppm]:	-0.16248
PEP:	0.071551
Precursor Type:	MULTI

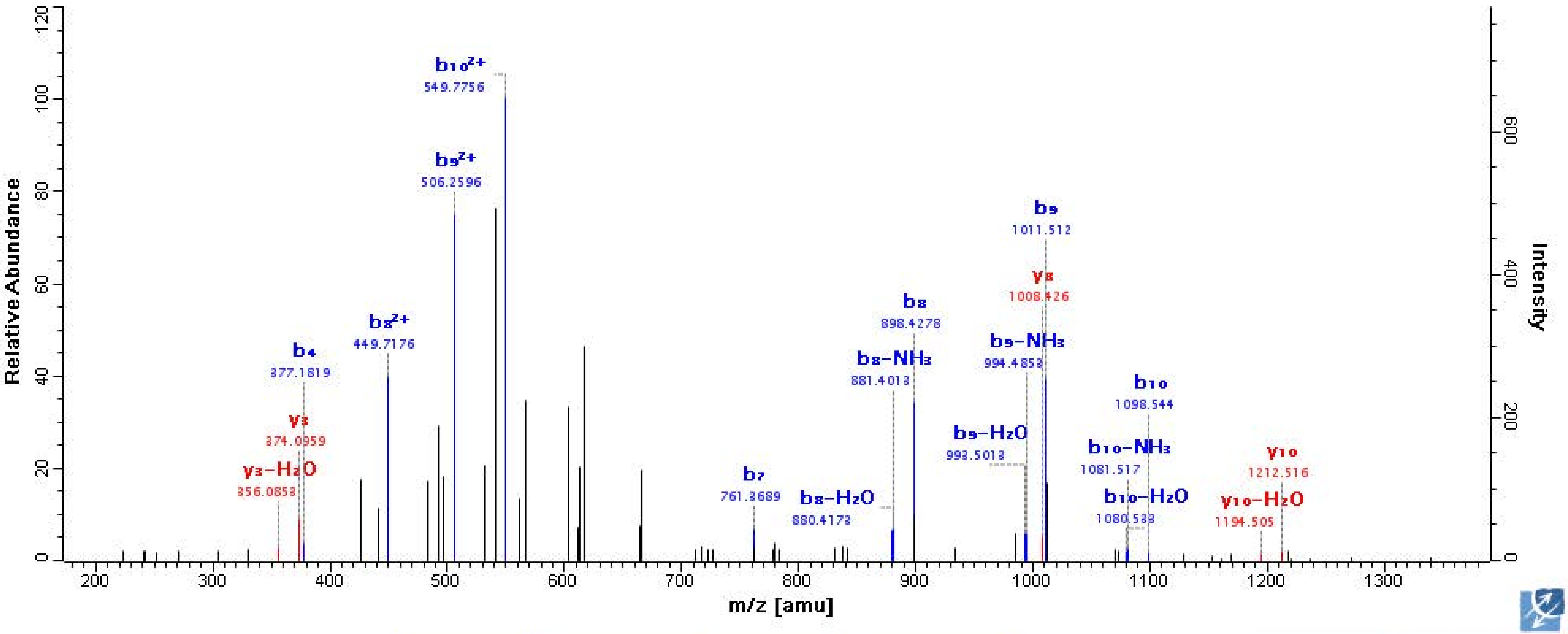
general information

Annotation:	15 of 22
AminoAcids Coverag	68 %
Intensity Coverage:	30 %
Protein Localisation:	30 ... 51

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.0502		115.0502	1	N	21				
	214.1186		214.1186	2	V	20	2389.153		2389.153	
	285.1557	-0.013855	285.1557	3	A	19	2290.084		1145.546	+0.223411
	400.1827		400.1827	4	D	18	2219.047		1110.027	-0.236914
	471.2198		471.2198	5	A	17	2104.02		1052.514	+0.108955
	600.2624	+0.071603	600.2624	6	E	16	2032.983		2032.983	
	715.2893		715.2893	7	D	15	1903.94		952.4739	+0.427678
	844.3319		844.3319	8	E	14	1788.914		1788.914	
	957.416		957.416	9	I	13	1659.871		830.4391	-0.253008
	1094.475		1094.475	10	H	12	1546.787		1546.787	
	1195.523		1195.523	11	T	11	1409.728		705.3676	+0.091063
	1342.591		1342.591	12	F	10	1308.68		654.8438	+0.245639
	1457.618	+0.386954	1457.618	13	D	9	1161.612		1161.612	
	1528.655		1528.655	14	A	8	1046.585	-0.038046	523.7961	-0.013018
	1641.739		1641.739	15	I	7	975.5478		975.5478	
	1754.823		1754.823	16	I	6	862.4637		862.4637	
	1853.892		1853.892	17	V	5	749.3797		375.1935	-0.097469
+0.271193	1005.5		2009.993	18	R	4	650.3113		650.3113	
	2176.991		2176.991	19	S	3	494.2102		494.2102	
	2248.028		2248.028	20	A	2	327.2118	+0.036587	327.2118	
	2349.076		2349.076	21	T	1	256.1747		256.1747	
				22	K	0	155.127		155.127	

Source: 20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F07
Scannumber: 3197
Protein: bioYB; BSU32030; yuiG
Peptide Score: 115.57
Method: ITMS; CID; 3





precursor information

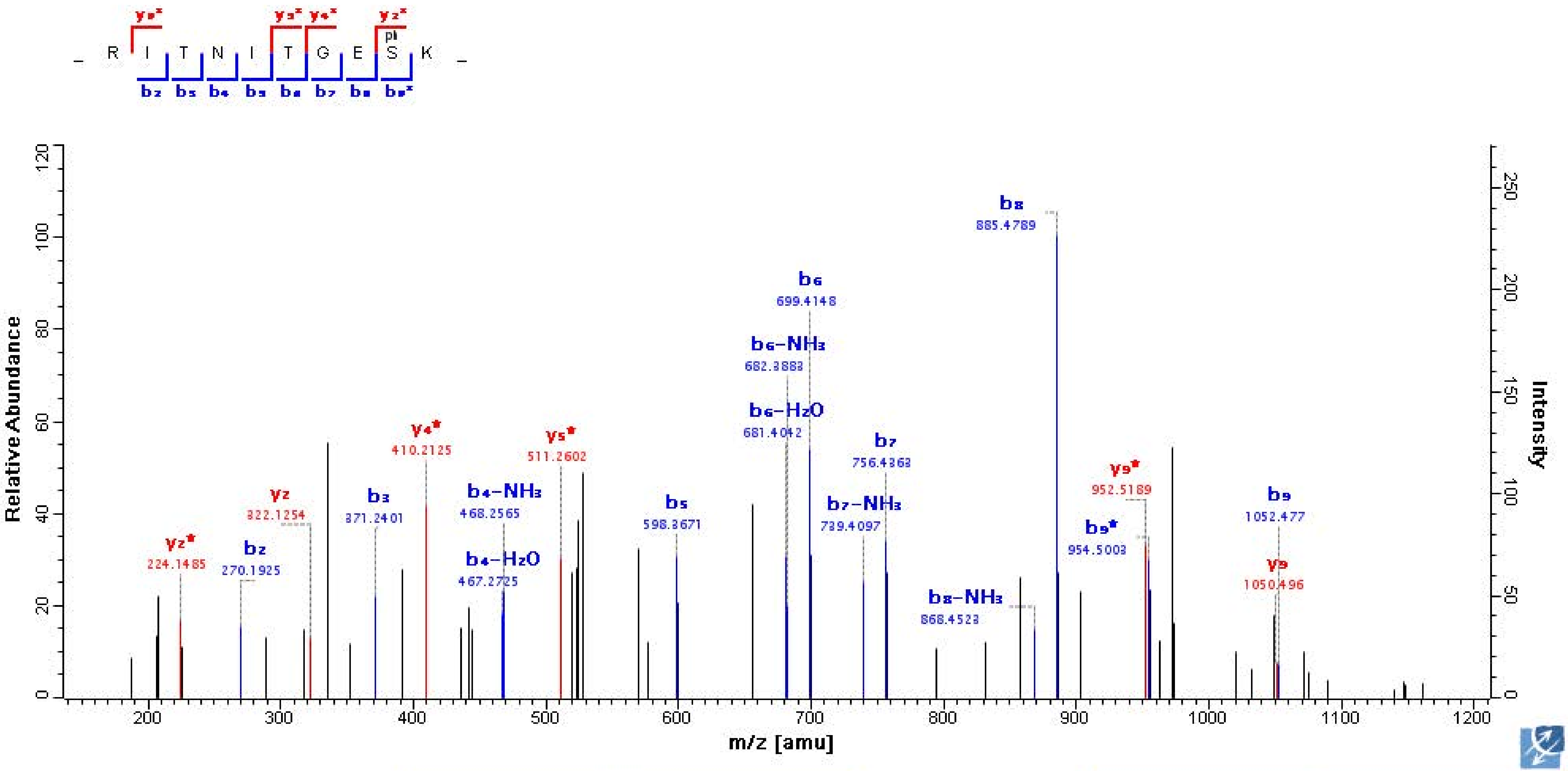
Mass:	1383.59257
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.5738
Mass Error [ppm]:	-0.48497
PEP:	1.1879E-05
Precursor Type:	ISO

general information

Annotation:	7 of 12
AminoAcids Coverag	58 %
Intensity Coverage:	42 %
Protein Localisation:	189 ... 200

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	11		
	173.09206873		173.09206873	2	T	10	1313.5634047	
	230.11353245		230.11353245	3	G	9	1212.5157263	-0.2436315
	377.18194637	-0.0978399	377.18194637	4	F	8	1155.4942625	
	491.22487382		491.22487382	5	N	7	1008.4258486	-0.320624
	647.32598484		647.32598484	6	R	6	894.38292117	
	761.36891229	+0.0839075	761.36891229	7	N	5	738.28181015	
+0.0967197	449.71755031	-0.017912	898.42782415	8	H	4	624.2388827	
+0.1416628	506.2595823	-0.1766831	1011.5118881	9	I	3	487.17997084	
+0.1380998	549.77559651	-0.3210162	1098.5439165	10	S	2	374.09590686	+0.0918373
	1265.5422754		1265.5422754	11	S	1	287.06387845	
				12	T	0	120.06551963	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F07
Scannumber:	3720
Protein:	BSU29140; citA2; citZ
Peptide Score:	108.35
Method:	ITMS; CID; 3



precursor information

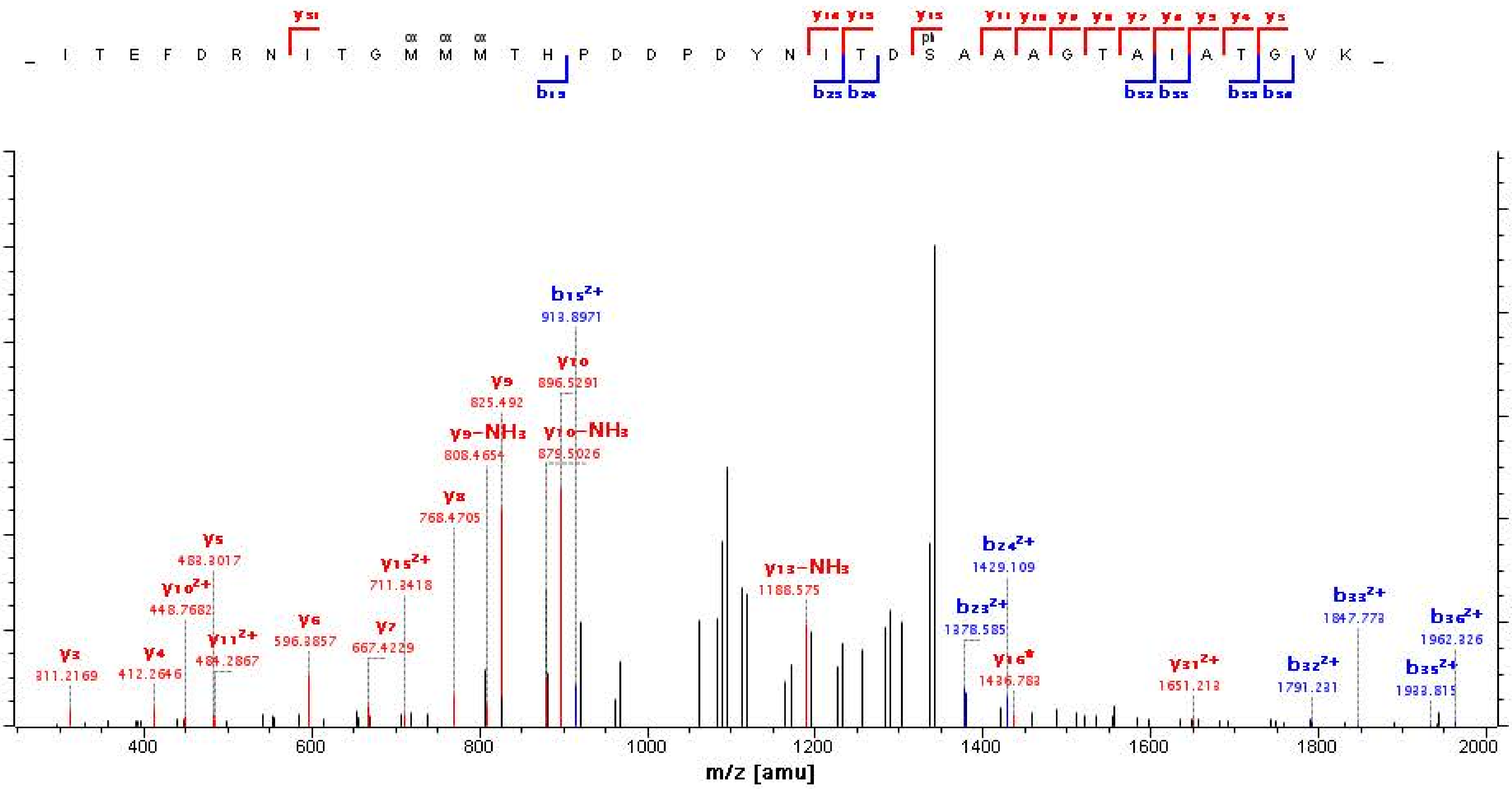
Mass:	1197.57481
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.3483
Mass Error [ppm]:	-0.5428
PEP:	0.09038
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	41 %
Protein Localisation:	276 ... 285

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	157.108387495	1	R	9		
-0.0594559	270.192451475	2	I	8	1050.495830978	+0.274921
-0.290545	371.240129949	3	T	7	937.411766998	
	485.283057396	4	N	6	836.364088524	
-0.2197215	598.367121377	5	I	5	722.321161076	
-0.0555469	699.414799851	6	T	4	609.237097096	
-0.0218959	756.436263575	7	G	3	508.189418622	
-0.024572	885.478856671	8	E	2	451.167954898	
-0.3096129	1052.477215489	9	S	1	322.125361802	-0.0393022
		10	K	0	155.127002984	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F08
Scannumber:	10292
Protein:	BSU09410; phoA; phoAIV
Peptide Score:	43.58
Method:	ITMS; CID; 3



precursor information

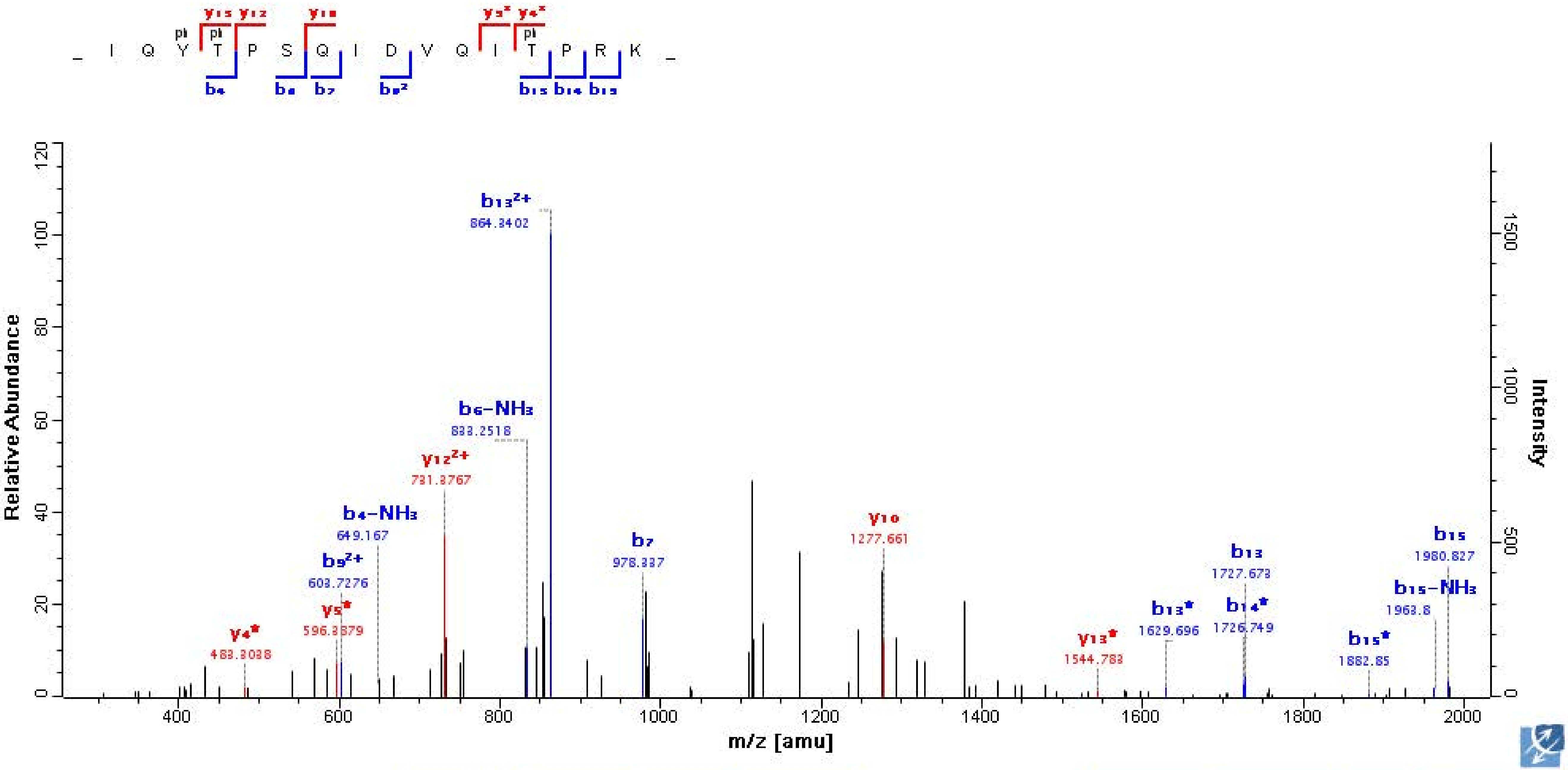
Mass:	4175.82478
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	43.58282
Mass Error [ppm]:	-0.15815
PEP:	0.00024447
Precursor Type:	ISO

general information

Annotation:	15 of 38
AminoAcids Coverag	39 %
Intensity Coverage:	22 %
Protein Localisation:	83 ... 120

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	37				
	215.139		215.139	2	T	36	4063.749		4063.749	
	344.1816		344.1816	3	E	35	3962.701		3962.701	
	491.25		491.25	4	F	34	3833.658		3833.658	
	606.277		606.277	5	D	33	3686.59		3686.59	
	762.3781		762.3781	6	R	32	3571.563		3571.563	
	876.421		876.421	7	N	31	3415.462		3415.462	
	989.5051		989.5051	8	I	30	3301.419		1651.213	+0.398441
	1090.553		1090.553	9	T	29	3188.335		3188.335	
	1147.574		1147.574	10	G	28	3087.287		3087.287	
	1294.61		1294.61	11	M	27	3030.266		3030.266	
	1441.645		1441.645	12	M	26	2883.23		2883.23	
	1588.68		1588.68	13	M	25	2736.195		2736.195	
	1689.728		1689.728	14	T	24	2589.16		2589.16	
+0.342729	913.8971		1826.787	15	H	23	2488.112		2488.112	
	1923.84		1923.84	16	P	22	2351.053		2351.053	
	2038.867		2038.867	17	D	21	2254		2254	
	2153.894		2153.894	18	D	20	2138.973		2138.973	
	2250.946		2250.946	19	P	19	2023.946		2023.946	
	2365.973		2365.973	20	D	18	1926.894		1926.894	
	2529.037		2529.037	21	Y	17	1811.867		1811.867	
	2643.08		2643.08	22	N	16	1648.803		1648.803	
+0.166842	1378.585		2756.164	23	I	15	1534.76		1534.76	
-0.343936	1429.109		2857.211	24	T	14	1421.676		711.3418	-0.036986
	2972.238		2972.238	25	D	13	1320.629		1320.629	
	3139.237		3139.237	26	S	12	1205.602		1205.602	
	3210.274		3210.274	27	A	11	1038.603		1038.603	
	3281.311		3281.311	28	A	10	967.5662		484.2867	+0.040522
	3352.348		3352.348	29	A	9	896.5291	-0.077569	448.7682	-0.045474
	3409.369		3409.369	30	G	8	825.492	-0.173878	825.492	
	3510.417		3510.417	31	T	7	768.4705	+0.102957	768.4705	
-0.139824	1791.231		3581.454	32	A	6	667.4229	-0.020873	667.4229	
-0.056246	1847.773		3694.538	33	I	5	596.3857	+0.068975	596.3857	
	3765.575		3765.575	34	A	4	483.3017	-0.00373	483.3017	
-0.321786	1933.815		3866.623	35	T	3	412.2646	-0.057589	412.2646	
-0.417845	1962.326		3923.645	36	G	2	311.2169	+0.132179	311.2169	
	4022.713		4022.713	37	V	1	254.1954		254.1954	
				38	K	0	155.127		155.127	

Source: 20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F08
Scannumber: 7262
Protein: BSU35390; yviE
Peptide Score: 53.45
Method: ITMS; CID; 3



precursor information

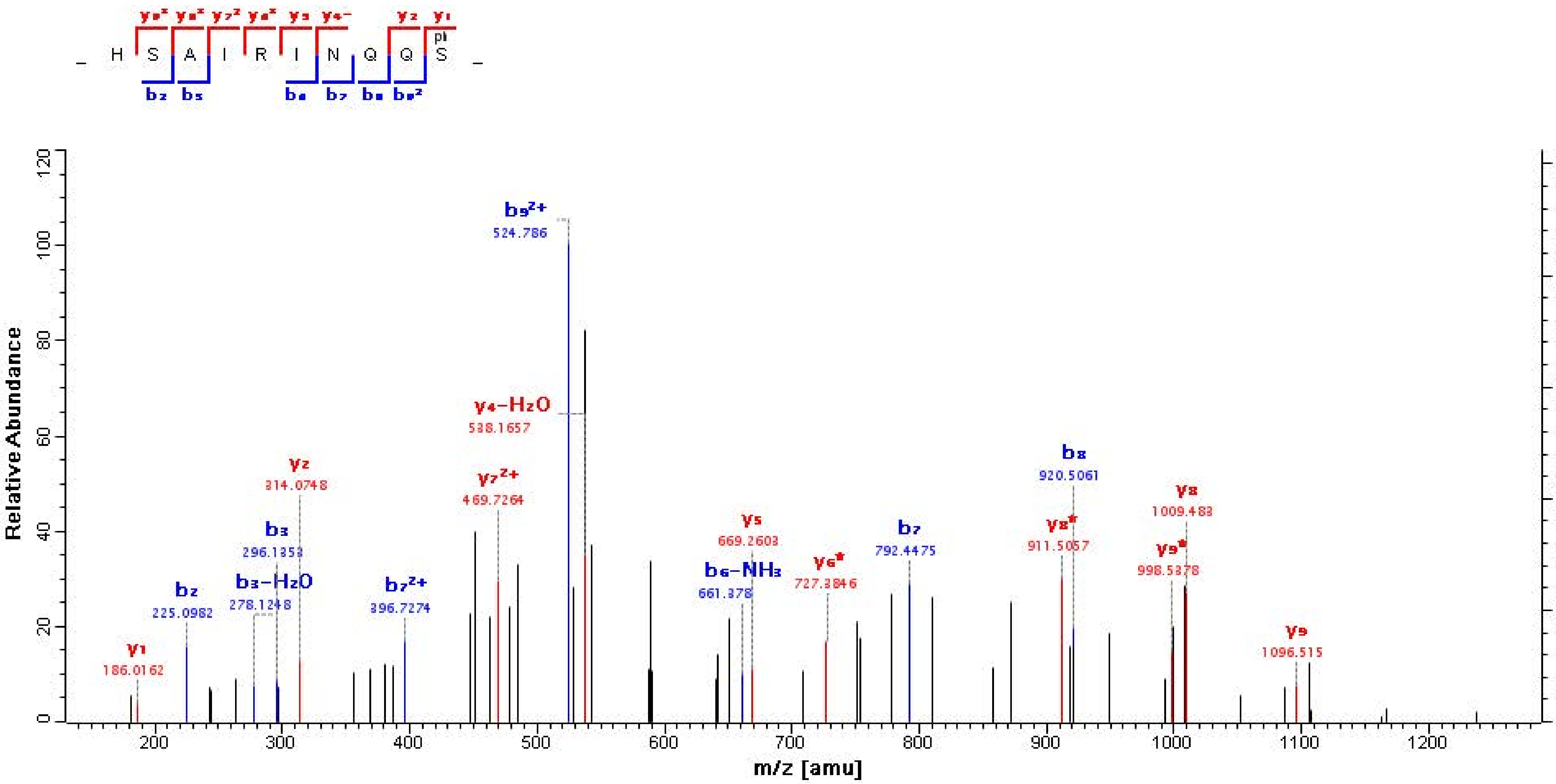
Mass:	2125.92618
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	53.45319
Mass Error [ppm]:	0.4818
PEP:	0.037286
Precursor Type:	MULTI

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	28 %
Protein Localisation:	134 ... 149

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	15				
	242.1499		242.1499	2	Q	14	2013.848		2013.848	
	485.1796		485.1796	3	Y	13	1885.79		1885.79	
	666.1936		666.1936	4	T	12	1642.76		1642.76	
	763.2463		763.2463	5	P	11	1461.746		731.3767	-0.006947
	850.2784		850.2784	6	S	10	1364.693		1364.693	
	978.337	+0.113484	978.337	7	Q	9	1277.661	+0.010791	1277.661	
	1091.421		1091.421	8	I	8	1149.603		1149.603	
-0.470723	603.7276		1206.448	9	D	7	1036.519		1036.519	
	1305.516		1305.516	10	V	6	921.4917		921.4917	
	1433.575		1433.575	11	Q	5	822.4233		822.4233	
	1546.659		1546.659	12	I	4	694.3648		694.3648	
-0.387149	864.3402	+0.199288	1727.673	13	T	3	581.2807		581.2807	
	1824.726		1824.726	14	P	2	400.2667		400.2667	
	1980.827	+0.288211	1980.827	15	R	1	303.2139		303.2139	
				16	K	0	147.1128		147.1128	

Source: 20130211_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F09
Scannumber: 3185
Protein: BSU38020; ipa-52r; pdxK; ywdB
Peptide Score: 103.34
Method: ITMS; CID; 3



precursor information

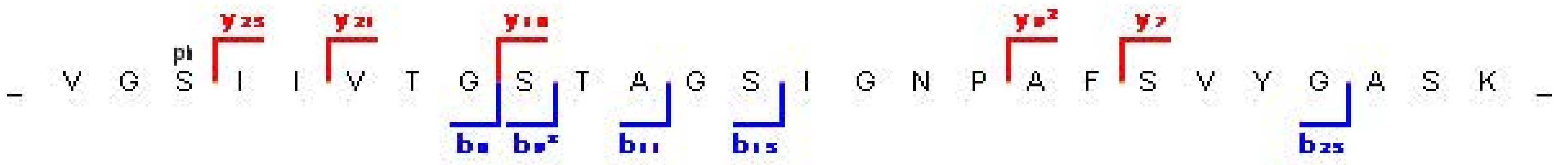
Mass:	1232.56647
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	103.3417
Mass Error [ppm]:	0.14093
PEP:	0.0089679
Precursor Type:	ISO

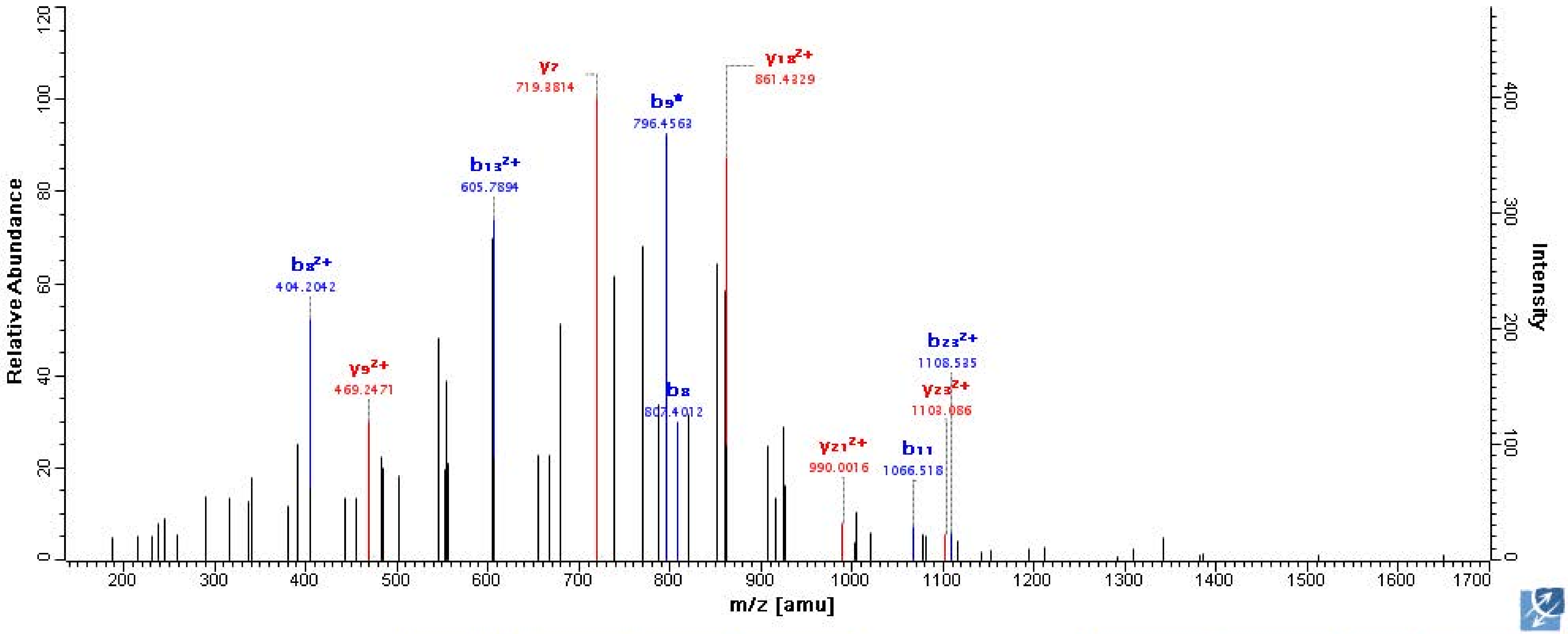
general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	34 %
Protein Localisation:	262 ... 271

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.0662		138.0662	1	H	9				
	225.0982	-0.12585	225.0982	2	S	8	1096.515	-0.036392	1096.515	
	296.1353	+0.029831	296.1353	3	A	7	1009.483	-0.020172	1009.483	
	409.2194		409.2194	4	I	6	938.4455		469.7264	-0.127888
	565.3205		565.3205	5	R	5	825.3615		825.3615	
	678.4046		678.4046	6	I	4	669.2603	-0.131013	669.2603	
-0.459015	396.7274	-0.039843	792.4475	7	N	3	556.1763		556.1763	
	920.5061	-0.136873	920.5061	8	Q	2	442.1334		442.1334	
+0.125718	524.786		1048.565	9	Q	1	314.0748	-0.178293	314.0748	
				10	S	0	186.0162	-0.13679	186.0162	

Source:	20130211_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F13
Scannumber:	8790
Protein:	BSU13770; ykvO
Peptide Score:	39.65
Method:	ITMS; CID; 3





precursor information

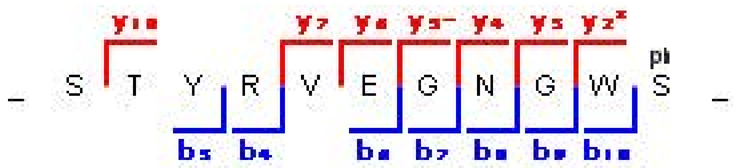
Mass:	2519.22886
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	39.64721
Mass Error [ppm]:	-0.80238
PEP:	0.08806
Precursor Type:	MULTI

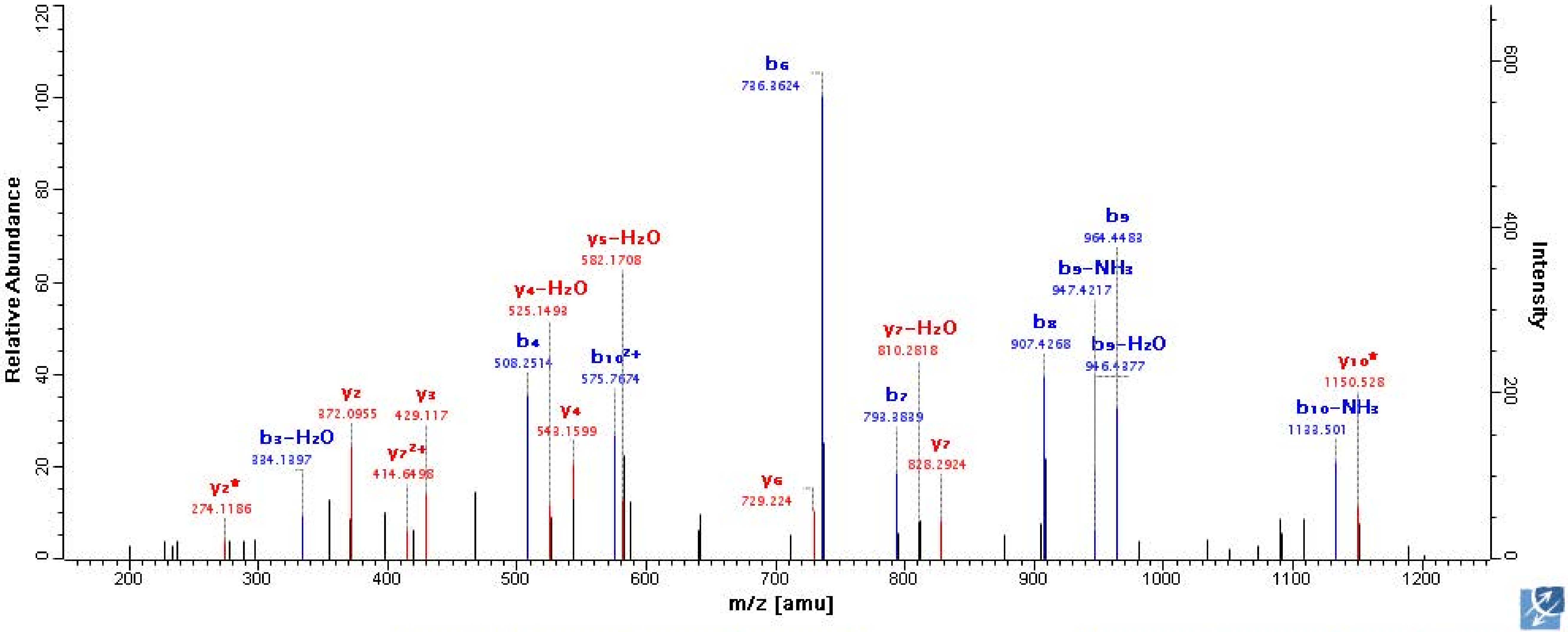
general information

Annotation:	10 of 26
AminoAcids Coverag	38 %
Intensity Coverage:	31 %
Protein Localisation:	130 ... 155

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	25				
	157.0972		157.0972	2	G	24	2429.184		2429.184	
	324.0955		324.0955	3	S	23	2372.162		2372.162	
	437.1796		437.1796	4	I	22	2205.164		1103.086	-0.489753
	550.2636		550.2636	5	I	21	2092.08		2092.08	
	649.3321		649.3321	6	V	20	1978.996		990.0016	-0.255725
	750.3797		750.3797	7	T	19	1879.928		1879.928	
+0.13341	404.2042	-0.002759	807.4012	8	G	18	1778.88		1778.88	
	894.4332		894.4332	9	S	17	1721.858		861.4329	+0.045353
	995.4809		995.4809	10	T	16	1634.826		1634.826	
	1066.518	+0.098804	1066.518	11	A	15	1533.779		1533.779	
	1123.539		1123.539	12	G	14	1462.742		1462.742	
+0.075048	605.7894		1210.572	13	S	13	1405.72		1405.72	
	1323.656		1323.656	14	I	12	1318.688		1318.688	
	1380.677		1380.677	15	G	11	1205.604		1205.604	
	1494.72		1494.72	16	N	10	1148.583		1148.583	
	1591.773		1591.773	17	P	9	1034.54		1034.54	
	1662.81		1662.81	18	A	8	937.4869		469.2471	-0.435996
	1809.878		1809.878	19	F	7	866.4498		866.4498	
	1896.91		1896.91	20	S	6	719.3814	-0.371553	719.3814	
	1995.979		1995.979	21	V	5	632.3494		632.3494	
	2159.042		2159.042	22	Y	4	533.2809		533.2809	
+0.305192	1108.535		2216.063	23	G	3	370.2176		370.2176	
	2287.101		2287.101	24	A	2	313.1961		313.1961	
	2374.133		2374.133	25	S	1	242.159		242.159	
				26	K	0	155.127		155.127	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F20
Scannumber:	5689
Protein:	BSU32260; hom; tdm
Peptide Score:	100.69
Method:	ITMS; CID; 3





precursor information

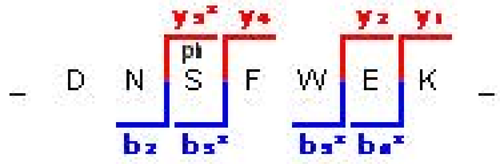
Mass:	1334.52923
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	100.6867
Mass Error [ppm]:	-0.011995
PEP:	0.017012
Precursor Type:	ISO

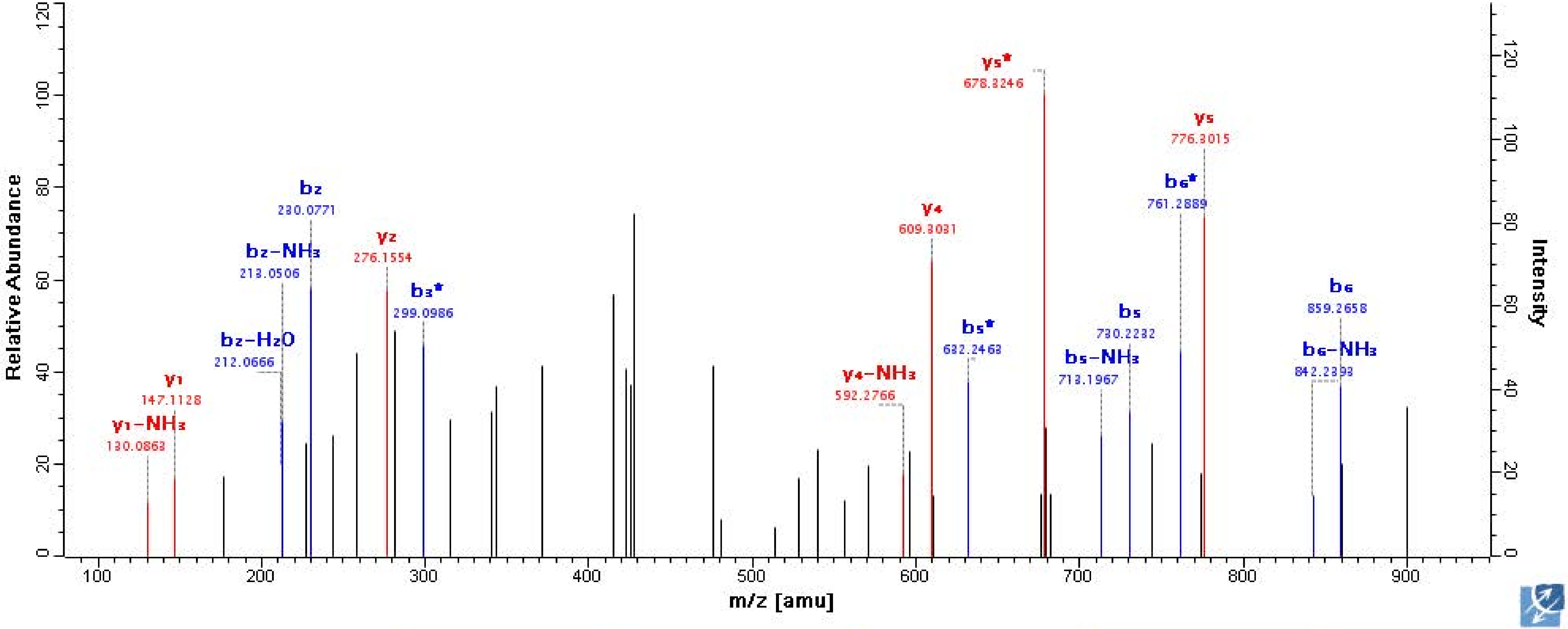
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	60 %
Protein Localisation:	423 ... 433

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	10				
	189.087		189.087	2	T	9	1248.504		1248.504	
	352.1503		352.1503	3	Y	8	1147.457		1147.457	
	508.2514	+0.01347	508.2514	4	R	7	984.3935		984.3935	
	607.3198		607.3198	5	V	6	828.2924	-0.050248	414.6498	+0.210099
	736.3624	+0.004941	736.3624	6	E	5	729.224	+0.10685	729.224	
	793.3839	+0.008501	793.3839	7	G	4	600.1814		600.1814	
	907.4268	-0.185122	907.4268	8	N	3	543.1599	-0.135917	543.1599	
	964.4483	-0.037152	964.4483	9	G	2	429.117	-0.024753	429.117	
+0.068806	575.7674		1150.528	10	W	1	372.0955	-0.205437	372.0955	
				11	S	0	186.0162		186.0162	

Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F20
Scannumber: 6269
Protein: BSU29540; ppnK2; ytdI
Peptide Score: 133.55
Method: ITMS; CID; 3



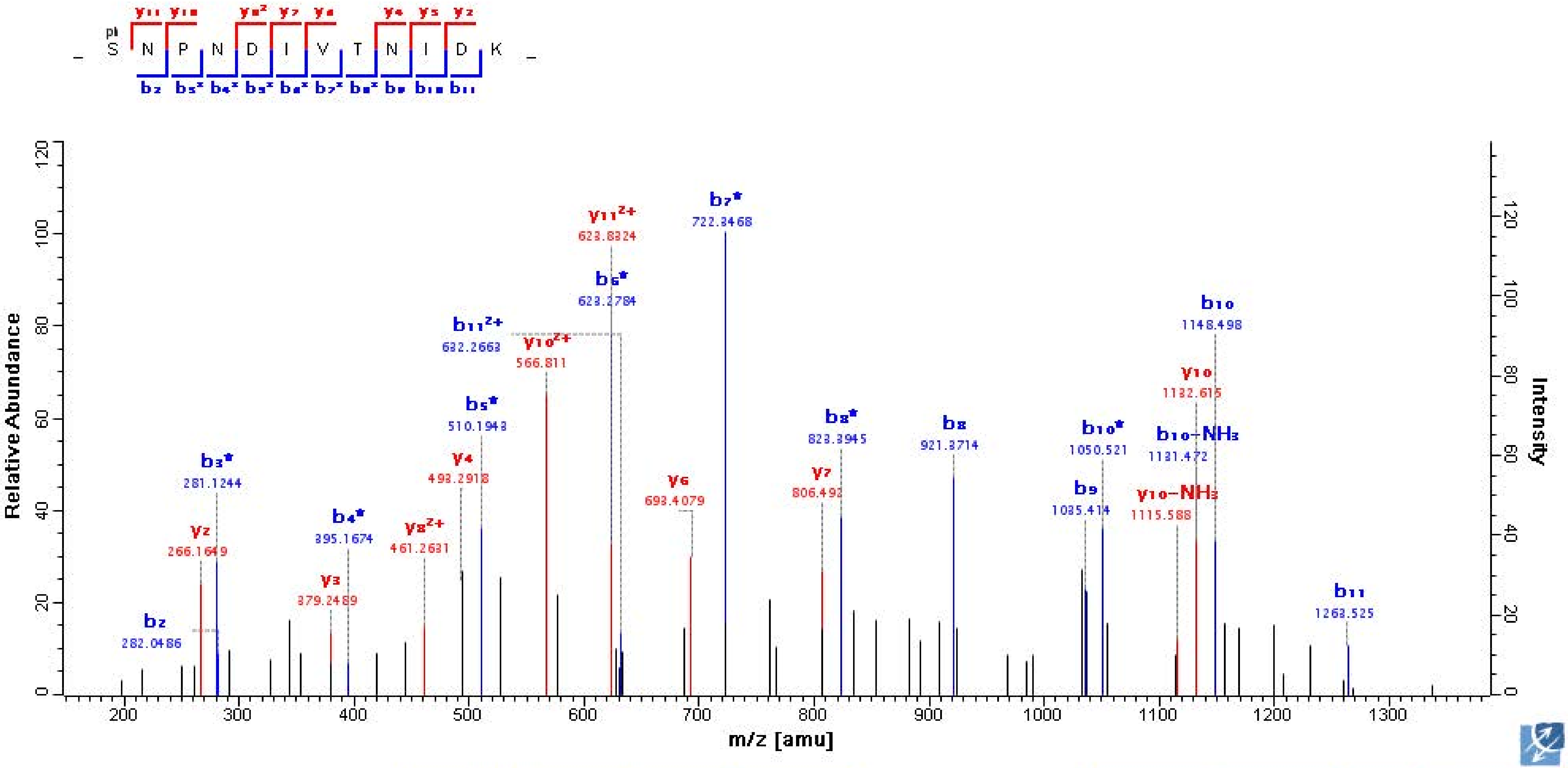


precursor information

Mass:	1004.36411
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	133.5481
Mass Error [ppm]:	0.029983
PEP:	1.8118E-07
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	45 %
Protein Localisation:	255 ... 261

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	6		
+0.0337845	230.077146946	2	N	5	890.344410402	
	397.075505764	3	S	4	776.301482955	+0.0131533
	544.14391968	4	F	3	609.303124136	-0.1260611
-0.1209987	730.223232634	5	W	2	462.23471022	
-0.1613946	859.26582573	6	E	1	276.155397267	+0.1271345
		7	K	0	147.112804171	+0.0224192

Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F20
Scannumber: 6440
Protein: BSU14670; suhB; yktC
Peptide Score: 140.82
Method: ITMS; CID; 3



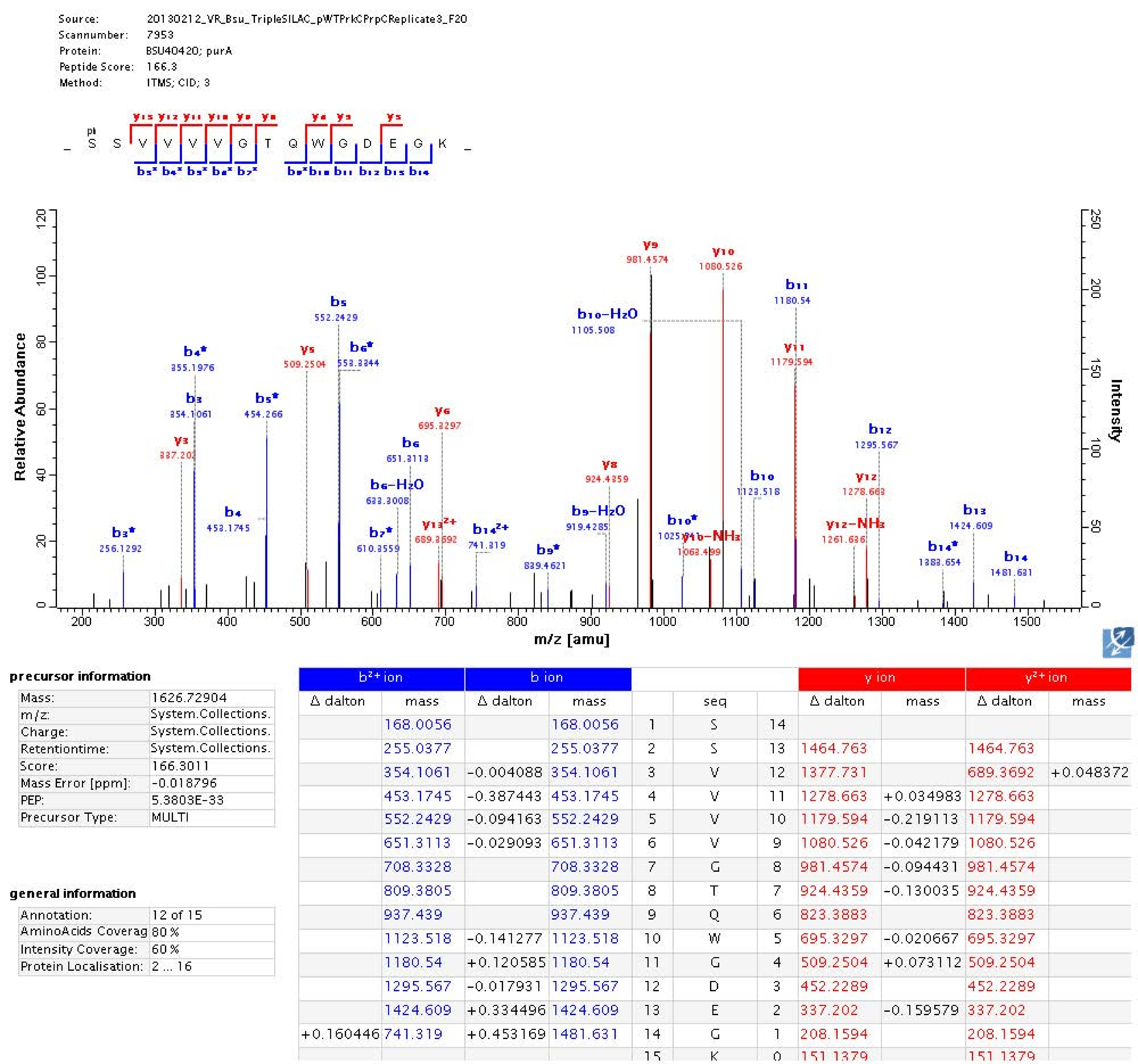
precursor information

Mass:	1408.62374
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.8238
Mass Error [ppm]:	0.14278
PEP:	1.7693E-12
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	57 %
Protein Localisation:	36 ... 47

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	11				
	282.0486	+0.031576	282.0486	2	N	10	1246.658		623.8324	+0.444985
	379.1013		379.1013	3	P	9	1132.615	-0.090833	566.811	-0.151166
	493.1443		493.1443	4	N	8	1035.562		1035.562	
	608.1712		608.1712	5	D	7	921.5189		461.2631	+0.100781
	721.2553		721.2553	6	I	6	806.492	-0.162351	806.492	
	820.3237		820.3237	7	V	5	693.4079	-0.261209	693.4079	
	921.3714	-0.245377	921.3714	8	T	4	594.3395		594.3395	
	1035.414	+0.009059	1035.414	9	N	3	493.2918	+0.170801	493.2918	
	1148.498	+0.013618	1148.498	10	I	2	379.2489	-0.029131	379.2489	
-0.112657	632.2663	+0.156719	1263.525	11	D	1	266.1649	+0.017397	266.1649	
				12	K	0	151.1379		151.1379	



Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F20
Scannumber: 7953
Protein: BSU40420; purA
Peptide Score: 166.3
Method: ITMS; CID; 3

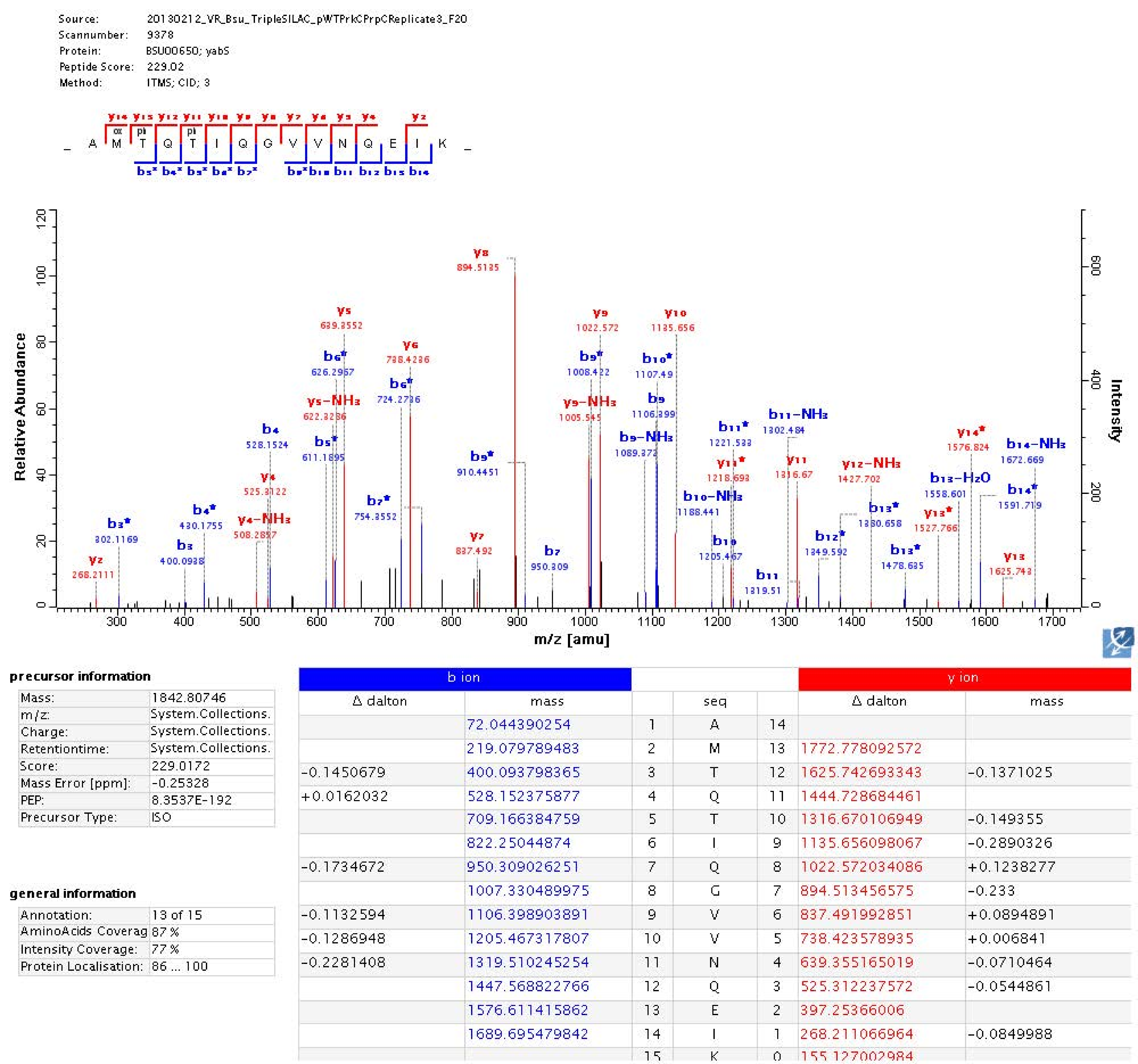
precursor information

Mass:	1626.72904
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	166.3011
Mass Error [ppm]:	-0.018796
PEP:	5.3803E-33
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	60 %
Protein Localisation:	2 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	14				
	255.0377		255.0377	2	S	13	1464.763		1464.763	
	354.1061	-0.004088	354.1061	3	V	12	1377.731		689.3692	+0.048372
	453.1745	-0.387443	453.1745	4	V	11	1278.663	+0.034983	1278.663	
	552.2429	-0.094163	552.2429	5	V	10	1179.594	-0.219113	1179.594	
	651.3113	-0.029093	651.3113	6	V	9	1080.526	-0.042179	1080.526	
	708.3328		708.3328	7	G	8	981.4574	-0.094431	981.4574	
	809.3805		809.3805	8	T	7	924.4359	-0.130035	924.4359	
	937.439		937.439	9	Q	6	823.3883		823.3883	
	1123.518	-0.141277	1123.518	10	W	5	695.3297	-0.020667	695.3297	
	1180.54	+0.120585	1180.54	11	G	4	509.2504	+0.073112	509.2504	
	1295.567	-0.017931	1295.567	12	D	3	452.2289		452.2289	
	1424.609	+0.334496	1424.609	13	E	2	337.202	-0.159579	337.202	
+0.160446	741.319	+0.453169	1481.631	14	G	1	208.1594		208.1594	
				15	K	0	151.1379		151.1379	



Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F20
Scannumber: 9378
Protein: BSU00650; yabS
Peptide Score: 229.02
Method: ITMS; CID; 3

precursor information

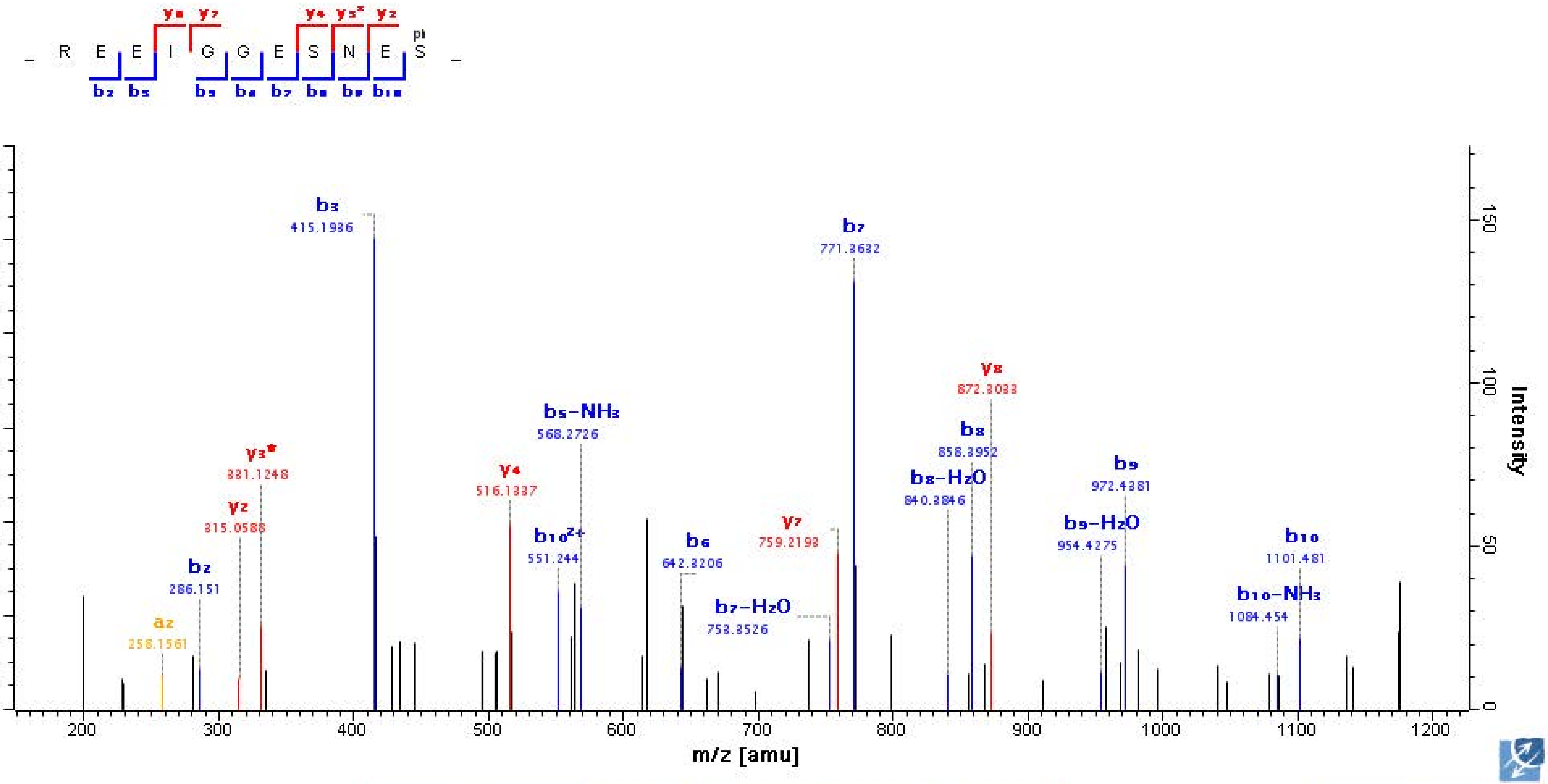
Mass:	1842.80746
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	229.0172
Mass Error [ppm]:	-0.25328
PEP:	8.3537E-192
Precursor Type:	ISO

general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	77 %
Protein Localisation:	86 ... 100

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	14		
	219.079789483	2	M	13	1772.778092572	
-0.1450679	400.093798365	3	T	12	1625.742693343	-0.1371025
+0.0162032	528.152375877	4	Q	11	1444.728684461	
	709.166384759	5	T	10	1316.670106949	-0.149355
	822.25044874	6	I	9	1135.656098067	-0.2890326
-0.1734672	950.309026251	7	Q	8	1022.572034086	+0.1238277
	1007.330489975	8	G	7	894.513456575	-0.233
-0.1132594	1106.398903891	9	V	6	837.491992851	+0.0894891
-0.1286948	1205.467317807	10	V	5	738.423578935	+0.006841
-0.2281408	1319.510245254	11	N	4	639.355165019	-0.0710464
	1447.568822766	12	Q	3	525.312237572	-0.0544861
	1576.611415862	13	E	2	397.25366006	
	1689.695479842	14	I	1	268.211066964	-0.0849988
		15	K	0	155.127002984	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F21
Scannumber:	1623
Protein:	BSU01230; rplP
Peptide Score:	89.27
Method:	ITMS; CID; 3



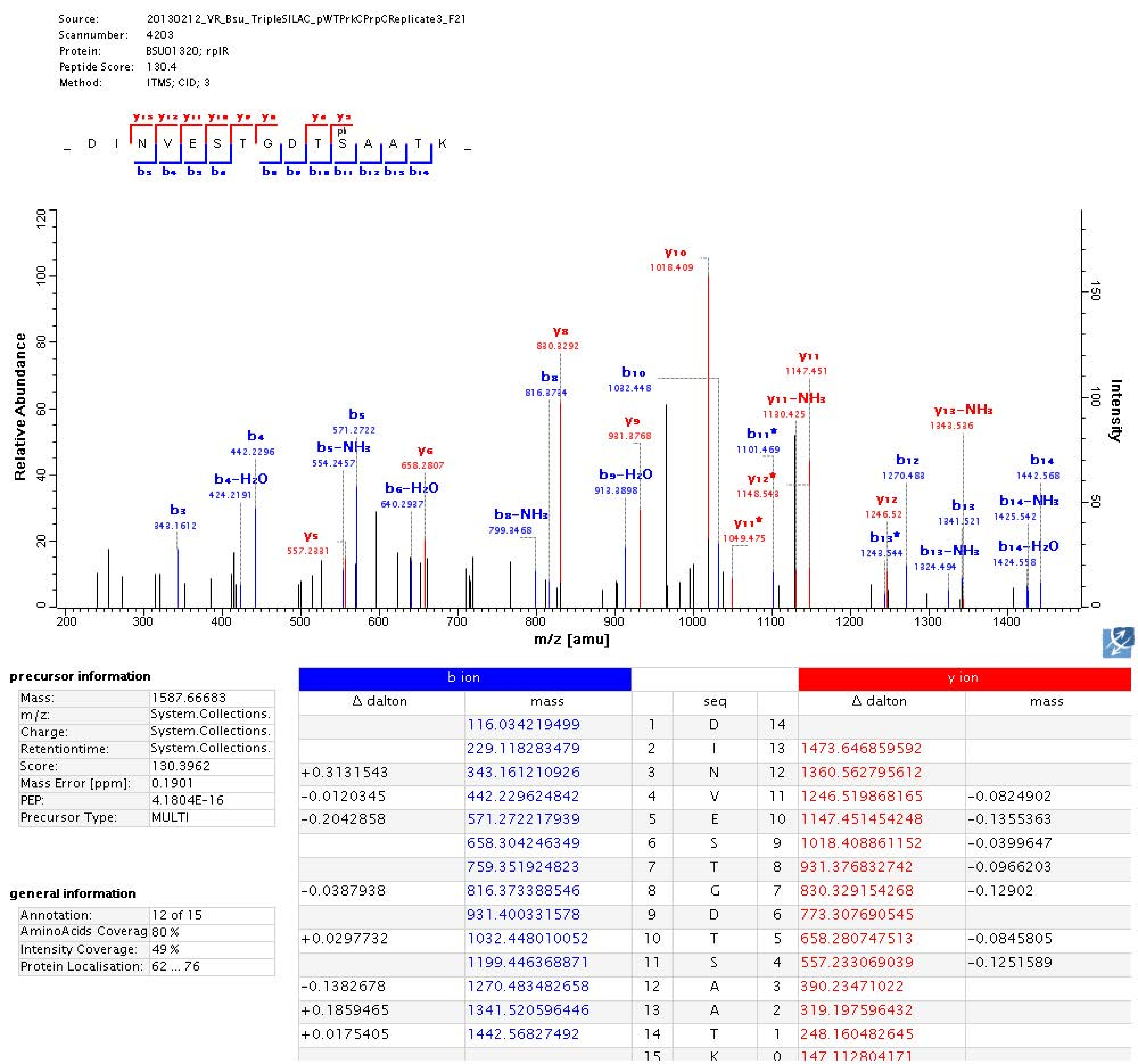
precursor information

Mass:	1285.48205
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.26604
Mass Error [ppm]:	-0.23737
PEP:	0.032461
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	47 %
Protein Localisation:	134 ... 144

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.1135		157.1084		157.1084	1	R	10		
-0.347716	258.1561		286.151	-0.041728	286.151	2	E	9	1130.389	
	387.1987		415.1936	+0.015533	415.1936	3	E	8	1001.346	
	500.2827		528.2776		528.2776	4	I	7	872.3033	+0.087841
	557.3042		585.2991		585.2991	5	G	6	759.2193	-0.118012
	614.3257		642.3206	+0.086661	642.3206	6	G	5	702.1978	
	743.3682		771.3632	+0.01764	771.3632	7	E	4	645.1763	
	830.4003		858.3952	+0.085587	858.3952	8	S	3	516.1337	-0.085348
	944.4432		972.4381	-0.138126	972.4381	9	N	2	429.1017	
	1073.486	-0.175327	551.244	-0.051142	1101.481	10	E	1	315.0588	-0.185563
						11	S	0	186.0162	



Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F21
Scannumber: 4203
Protein: BSU01320; rplR
Peptide Score: 130.4
Method: ITMS; CID; 3

precursor information

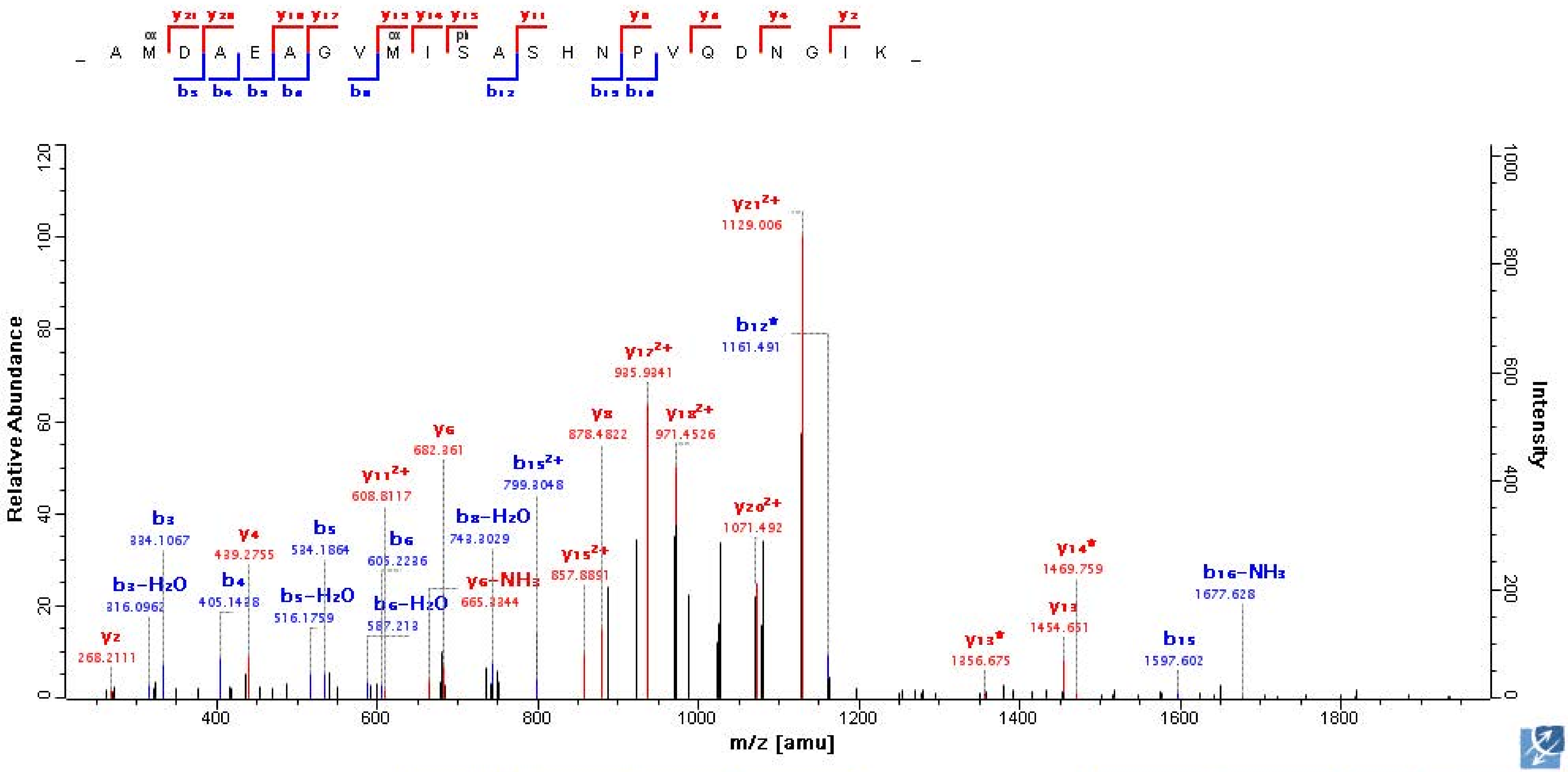
Mass:	1587.66683
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	130.3962
Mass Error [ppm]:	0.1901
PEP:	4.1804E-16
Precursor Type:	MULTI

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	49 %
Protein Localisation:	62 ... 76

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	14		
	229.118283479	2	I	13	1473.646859592	
+0.3131543	343.161210926	3	N	12	1360.562795612	
-0.0120345	442.229624842	4	V	11	1246.519868165	-0.0824902
-0.2042858	571.272217939	5	E	10	1147.451454248	-0.1355363
	658.304246349	6	S	9	1018.408861152	-0.0399647
	759.351924823	7	T	8	931.376832742	-0.0966203
-0.0387938	816.373388546	8	G	7	830.329154268	-0.12902
	931.400331578	9	D	6	773.307690545	
+0.0297732	1032.448010052	10	T	5	658.280747513	-0.0845805
	1199.446368871	11	S	4	557.233069039	-0.1251589
-0.1382678	1270.483482658	12	A	3	390.23471022	
+0.1859465	1341.520596446	13	A	2	319.197596432	
+0.0175405	1442.56827492	14	T	1	248.160482645	
		15	K	0	147.112804171	

Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F21
Scannumber: 7039
Protein: BSU01770; glmM; ybbT
Peptide Score: 116.29
Method: ITMS; CID; 3



precursor information

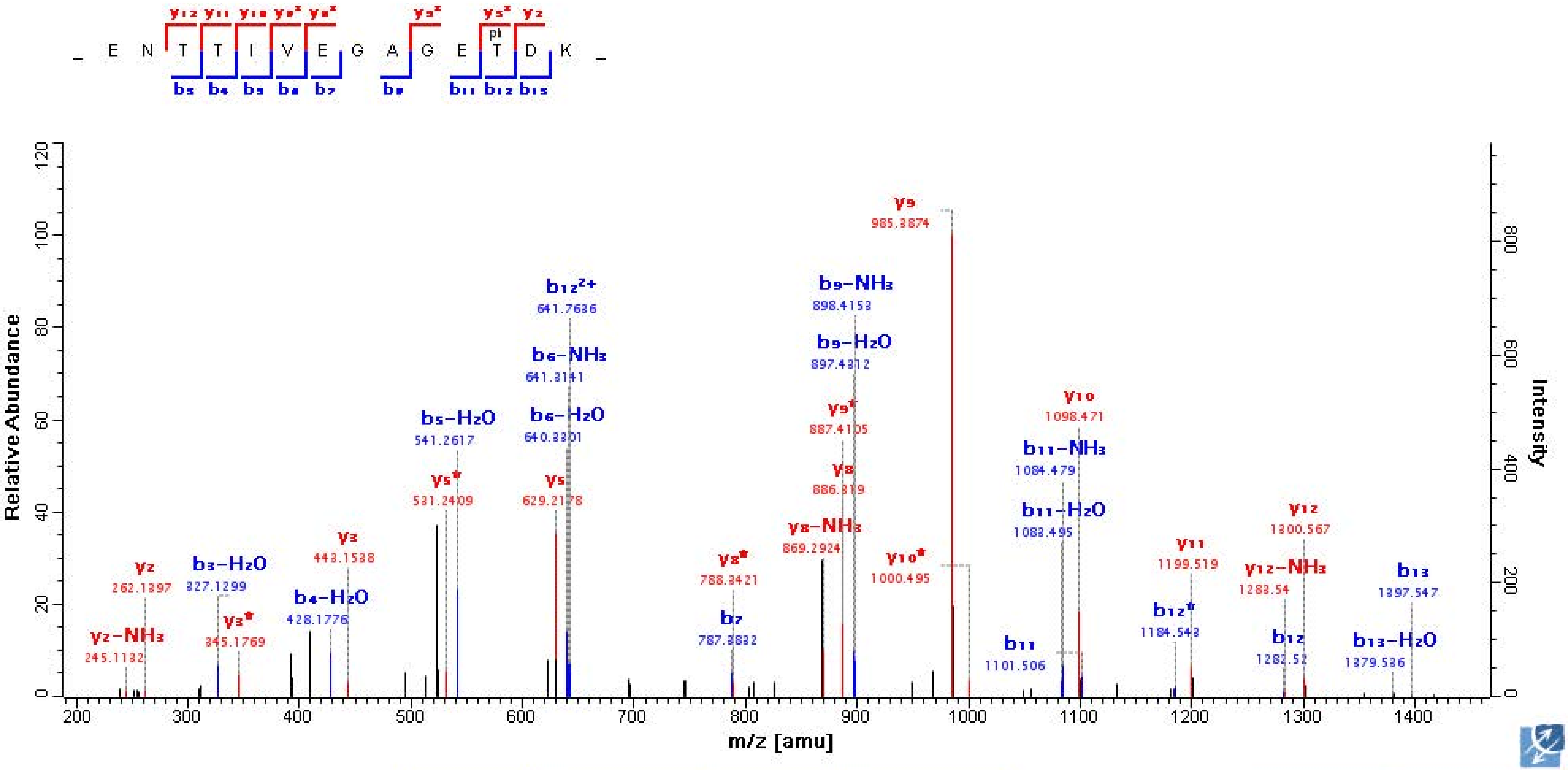
Mass:	2466.05475
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.2923
Mass Error [ppm]:	-0.35912
PEP:	3.1534E-17
Precursor Type:	MULTI

general information

Annotation:	17 of 23
AminoAcids Coverag	74%
Intensity Coverage:	41 %
Protein Localisation:	88 ... 110

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	22				
	219.0798		219.0798	2	M	21	2404.04		2404.04	
	334.1067	-0.177594	334.1067	3	D	20	2257.005		1129.006	+0.175213
	405.1438	-0.081346	405.1438	4	A	19	2141.978		1071.492	+0.303675
	534.1864	-0.054787	534.1864	5	E	18	2070.941		2070.941	
	605.2236	+0.091144	605.2236	6	A	17	1941.898		971.4526	-0.083473
	662.245		662.245	7	G	16	1870.861		935.9341	-0.044348
	761.3134		761.3134	8	V	15	1813.839		1813.839	
	908.3488		908.3488	9	M	14	1714.771		857.8891	+0.316631
	1021.433		1021.433	10	I	13	1567.736		1567.736	
	1188.431		1188.431	11	S	12	1454.651	-0.225105	1454.651	
	1259.468		1259.468	12	A	11	1287.653		1287.653	
	1346.5		1346.5	13	S	10	1216.616		608.8117	-0.43665
	1483.559		1483.559	14	H	9	1129.584		1129.584	
-0.212592	799.3048	-0.084046	1597.602	15	N	8	992.5251		992.5251	
	1694.655		1694.655	16	P	7	878.4822	+0.077231	878.4822	
	1793.723		1793.723	17	V	6	781.4294		781.4294	
	1921.782		1921.782	18	Q	5	682.361	+0.454878	682.361	
	2036.809		2036.809	19	D	4	554.3024		554.3024	
	2150.852		2150.852	20	N	3	439.2755	-0.115607	439.2755	
	2207.873		2207.873	21	G	2	325.2325		325.2325	
	2320.957		2320.957	22	I	1	268.2111	-0.264656	268.2111	
				23	K	0	155.127		155.127	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F22
Scannumber:	3905
Protein:	BSU06030; groEL; groL; mopA
Peptide Score:	141.85
Method:	ITMS; CID; 3



precursor information

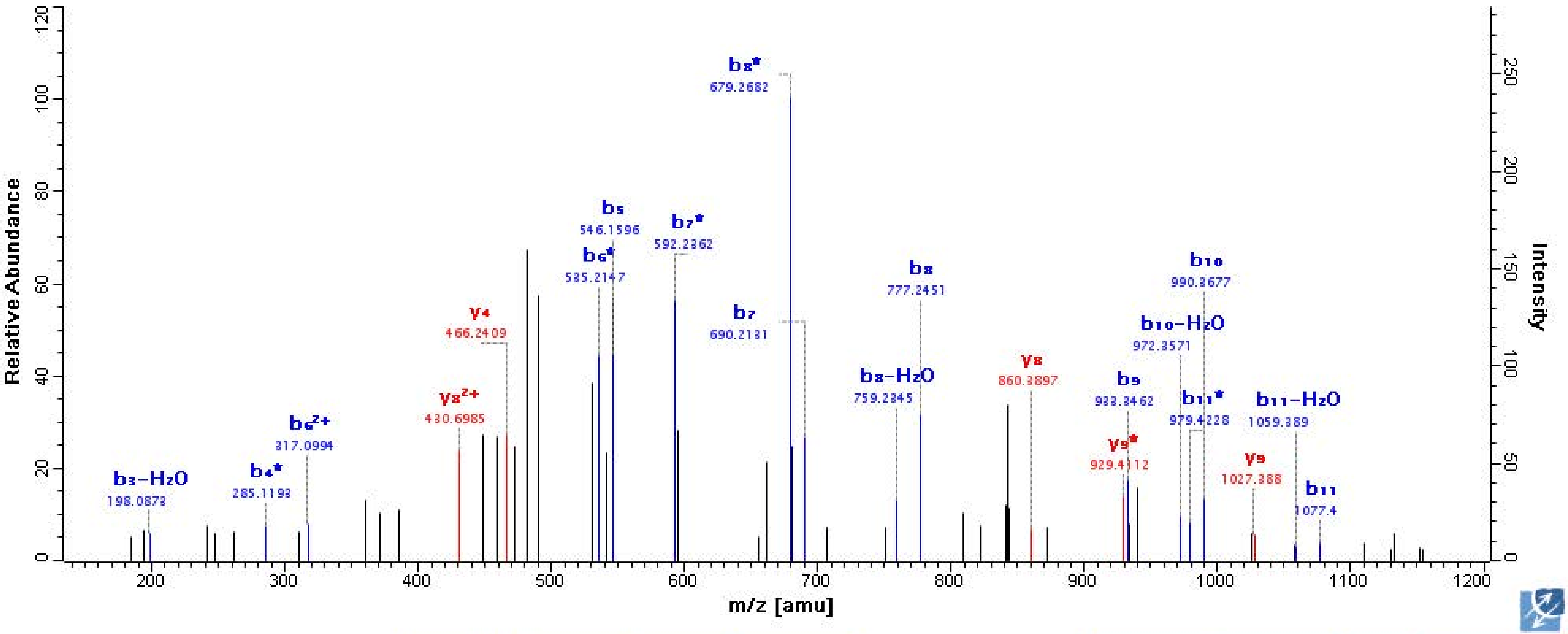
Mass:	1542.64474
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	141.8514
Mass Error [ppm]:	-0.21061
PEP:	4.6994E-17
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	62 %
Protein Localisation:	326 ... 339

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	13		
	244.09279701		244.09279701	2	N	12	1414.6097458	
	345.14047548		345.14047548	3	T	11	1300.5668184	-0.11821
	446.18815396		446.18815396	4	T	10	1199.5191399	-0.1565911
	559.27221794		559.27221794	5	I	9	1098.4714614	+0.003148
	658.34063185		658.34063185	6	V	8	985.38739743	-0.0507275
	787.38322495	-0.1762547	787.38322495	7	E	7	886.31898351	-0.031569
	844.40468867		844.40468867	8	G	6	757.27639042	
	915.44180246		915.44180246	9	A	5	700.25492669	
	972.46326619		972.46326619	10	G	4	629.2178129	-0.0777372
	1101.5058593	-0.0515136	1101.5058593	11	E	3	572.19634918	
+0.4116596	641.76357232	-0.0240186	1282.5198682	12	T	2	443.15375609	-0.0327234
	1397.5468112	-0.2261325	1397.5468112	13	D	1	262.1397472	+0.0071339
				14	K	0	147.11280417	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F22
Scannumber:	4468
Protein:	BSU06200; ydjH
Peptide Score:	107.97
Method:	ITMS; CID; 3



precursor information

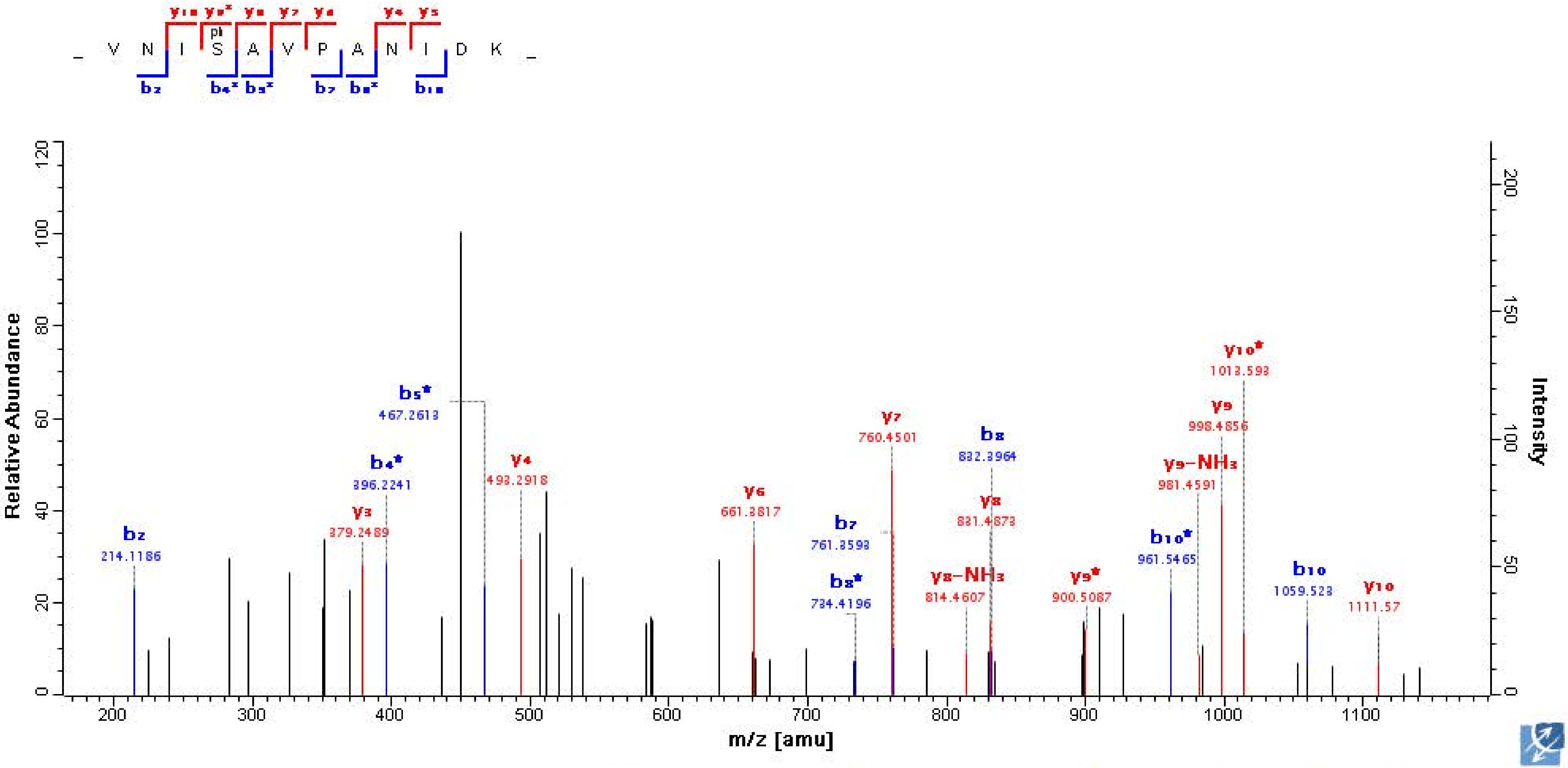
Mass:	1241.47151
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.9664
Mass Error [ppm]:	0.09264
PEP:	0.0030823
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	42 %
Protein Localisation:	243 ... 254

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	11				
	115.0502		115.0502	2	G	10	1185.457		1185.457	
	216.0979		216.0979	3	T	9	1128.436		1128.436	
	383.0962		383.0962	4	S	8	1027.388	+0.090205	1027.388	
	546.1596	+0.366981	546.1596	5	Y	7	860.3897	-0.047361	430.6985	-0.432318
+0.044362	317.0994		633.1916	6	S	6	697.3264		697.3264	
	690.2131	-0.208118	690.2131	7	G	5	610.2944		610.2944	
	777.2451	-0.026035	777.2451	8	S	4	553.2729		553.2729	
	933.3462	-0.108225	933.3462	9	R	3	466.2409	-0.168898	466.2409	
	990.3677	-0.070485	990.3677	10	G	2	310.1397		310.1397	
	1077.4	-0.135289	1077.4	11	S	1	253.1183		253.1183	
				12	F	0	166.0863		166.0863	

Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F22
Scannumber: 7247
Protein: BSU02900; yceD
Peptide Score: 104.17
Method: ITMS; CID; 3



precursor information

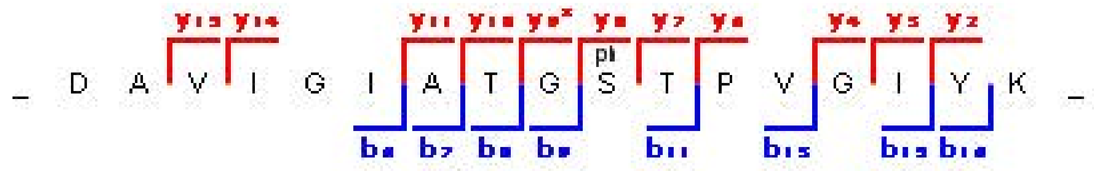
Mass:	1319.64877
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	104.1745
Mass Error [ppm]:	0.10229
PEP:	2.215E-05
Precursor Type:	MULTI

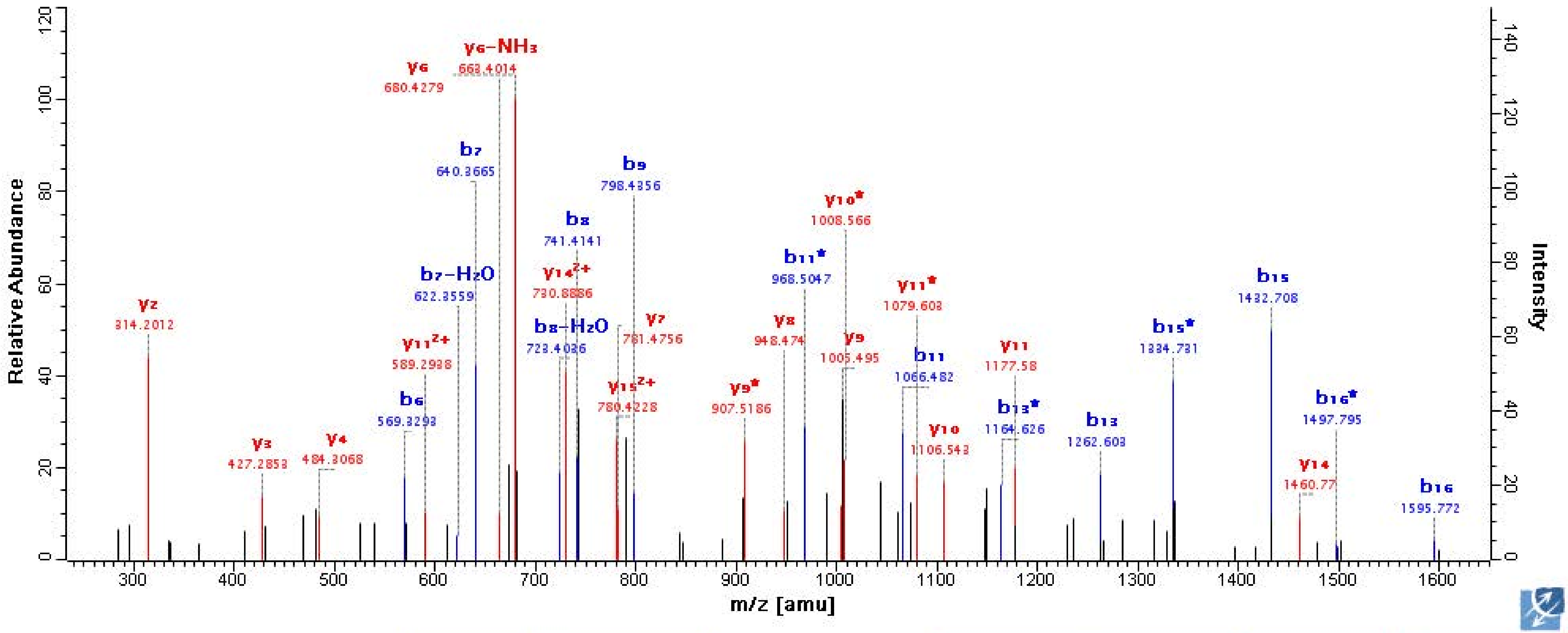
general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	36 %
Protein Localisation:	94 ... 105

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	100.075690383	1	V	11		
+0.2449686	214.11861783	2	N	10	1225.612601204	
	327.20268181	3	I	9	1111.569673756	+0.0216348
	494.201040629	4	S	8	998.485609776	-0.1302021
	565.238154416	5	A	7	831.487250958	-0.2440869
	664.306568333	6	V	6	760.45013717	-0.099124
-0.0520812	761.359332185	7	P	5	661.381723254	+0.0088407
+0.1531756	832.396445972	8	A	4	564.328959402	
	946.43937342	9	N	3	493.291845614	-0.094519
+0.1550294	1059.5234374	10	I	2	379.248918167	+0.0420364
	1174.550380432	11	D	1	266.164854186	
		12	K	0	151.137911154	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	10955
Protein:	BSU02360; gamA; ybfT
Peptide Score:	156.11
Method:	ITMS; CID; 3





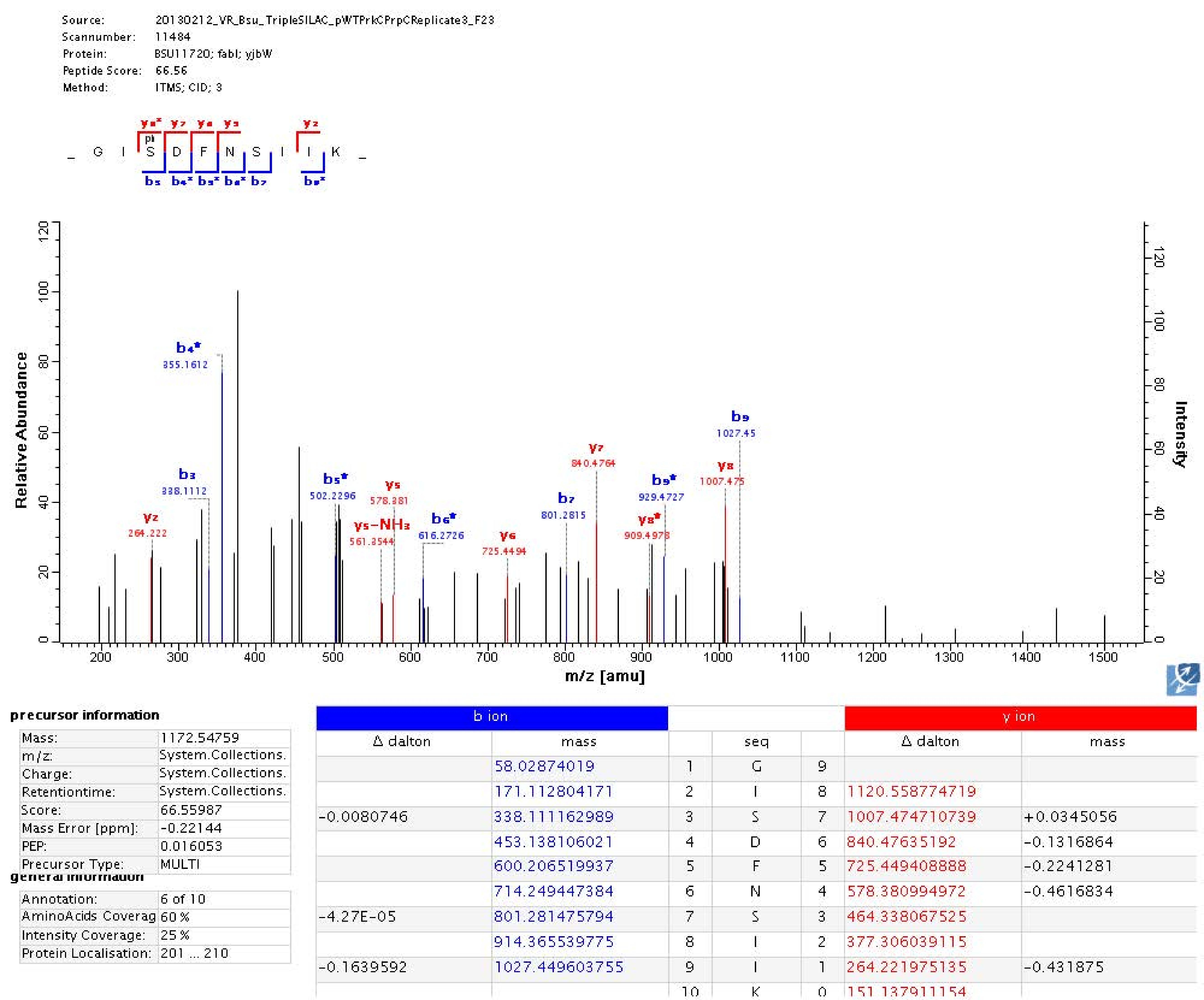
precursor information

Mass:	1740.86992
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.114
Mass Error [ppm]:	0.0018236
PEP:	8.1091E-26
Precursor Type:	MULTI

general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	61 %
Protein Localisation:	29 ... 45

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	16				
	187.07133329	2	A	15	1630.8753578		1630.8753578	
	286.1397472	3	V	14	1559.838244		780.42276025	-0.196564
	399.22381118	4	I	13	1460.7698301	+0.3384462	730.8885533	-0.0559117
	456.24527491	5	G	12	1347.6857661		1347.6857661	
-0.0002373	569.32933889	6	I	11	1290.6643024		1290.6643024	
-0.1884131	640.36645267	7	A	10	1177.5802384	+0.0413436	589.29375745	+0.2542772
+0.0086594	741.41413115	8	T	9	1106.5431247	-0.2530856	1106.5431247	
+0.2086312	798.43559487	9	G	8	1005.4954462	-0.4678583	1005.4954462	
	965.43395369	10	S	7	948.47398246	-0.1529986	948.47398246	
-0.1525306	1066.4816322	11	T	6	781.47562364	-0.014381	781.47562364	
	1163.534396	12	P	5	680.42794516	-0.070096	680.42794516	
-0.2728539	1262.6028099	13	V	4	583.37518131		583.37518131	
	1319.6242737	14	G	3	484.3067674	+0.0950881	484.3067674	
-0.071741	1432.7083376	15	I	2	427.28530367	-0.1512705	427.28530367	
+0.2785047	1595.7716662	16	Y	1	314.20123969	-0.0092841	314.20123969	
		17	K	0	151.13791115		151.13791115	



Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	11484
Protein:	BSU11720; fabI; yjbW
Peptide Score:	66.56
Method:	ITMS; CID; 3

precursor information

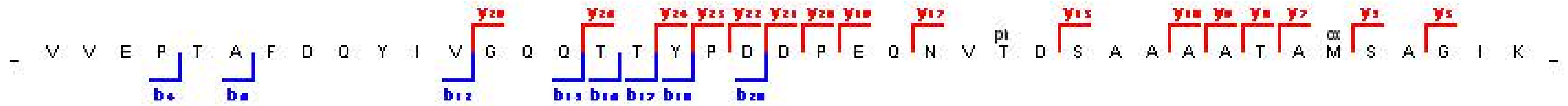
Mass:	1172.54759
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	66.55987
Mass Error [ppm]:	-0.22144
PEP:	0.016053
Precursor Type:	MULTI

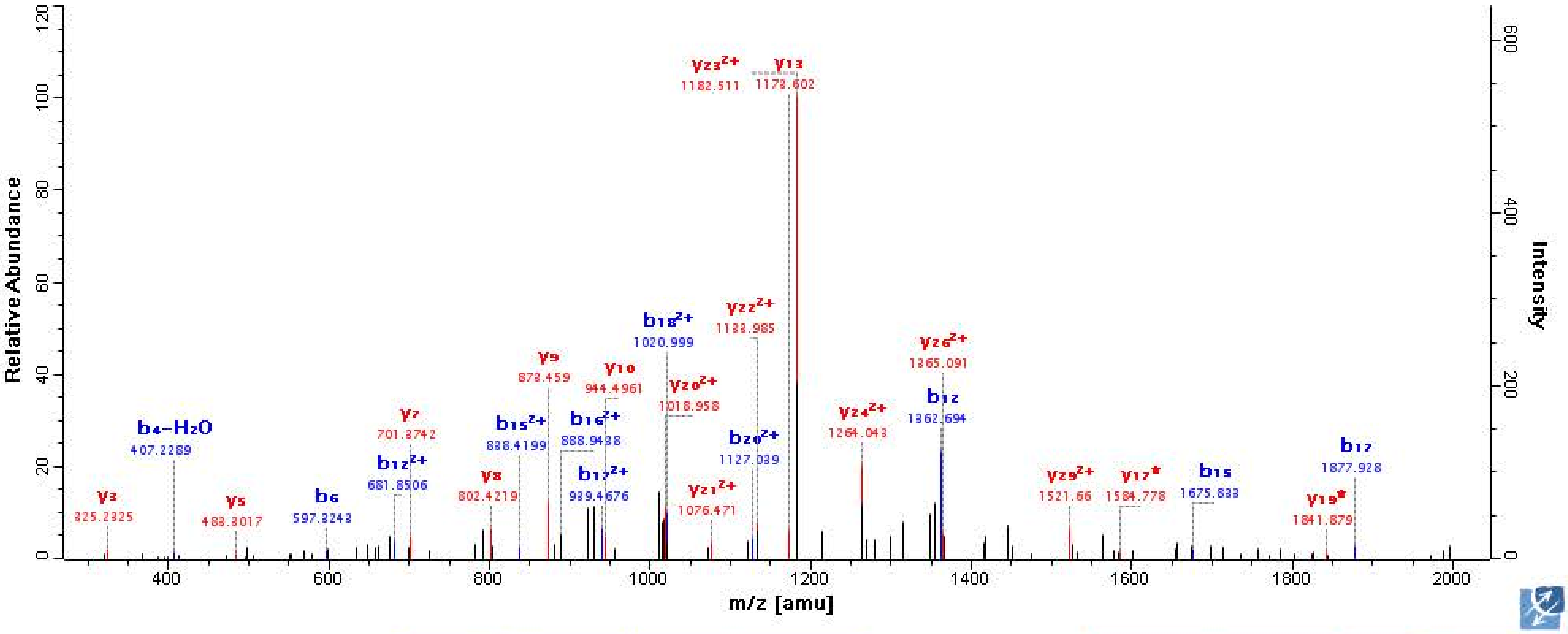
general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	25 %
Protein Localisation:	201 ... 210

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	58.02874019	1	G	9		
	171.112804171	2	I	8	1120.558774719	
-0.0080746	338.111162989	3	S	7	1007.474710739	+0.0345056
	453.138106021	4	D	6	840.47635192	-0.1316864
	600.206519937	5	F	5	725.449408888	-0.2241281
	714.249447384	6	N	4	578.380994972	-0.4616834
-4.27E-05	801.281475794	7	S	3	464.338067525	
	914.365539775	8	I	2	377.306039115	
-0.1639592	1027.449603755	9	I	1	264.221975135	-0.431875
		10	K	0	151.137911154	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	12114
Protein:	BSU05740; phoAIII; phoB
Peptide Score:	45.02
Method:	ITMS; CID; 3





precursor information

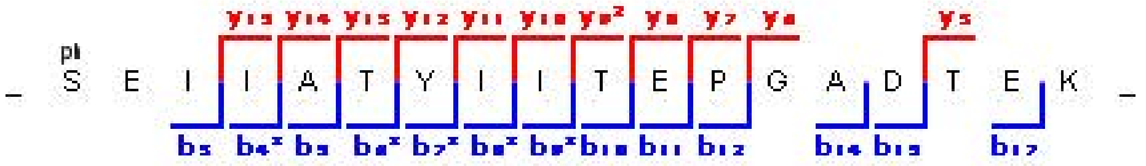
Mass:	4402.99109
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	45.02093
Mass Error [ppm]:	-0.2008
PEP:	5.0551E-05
Precursor Type:	ISO

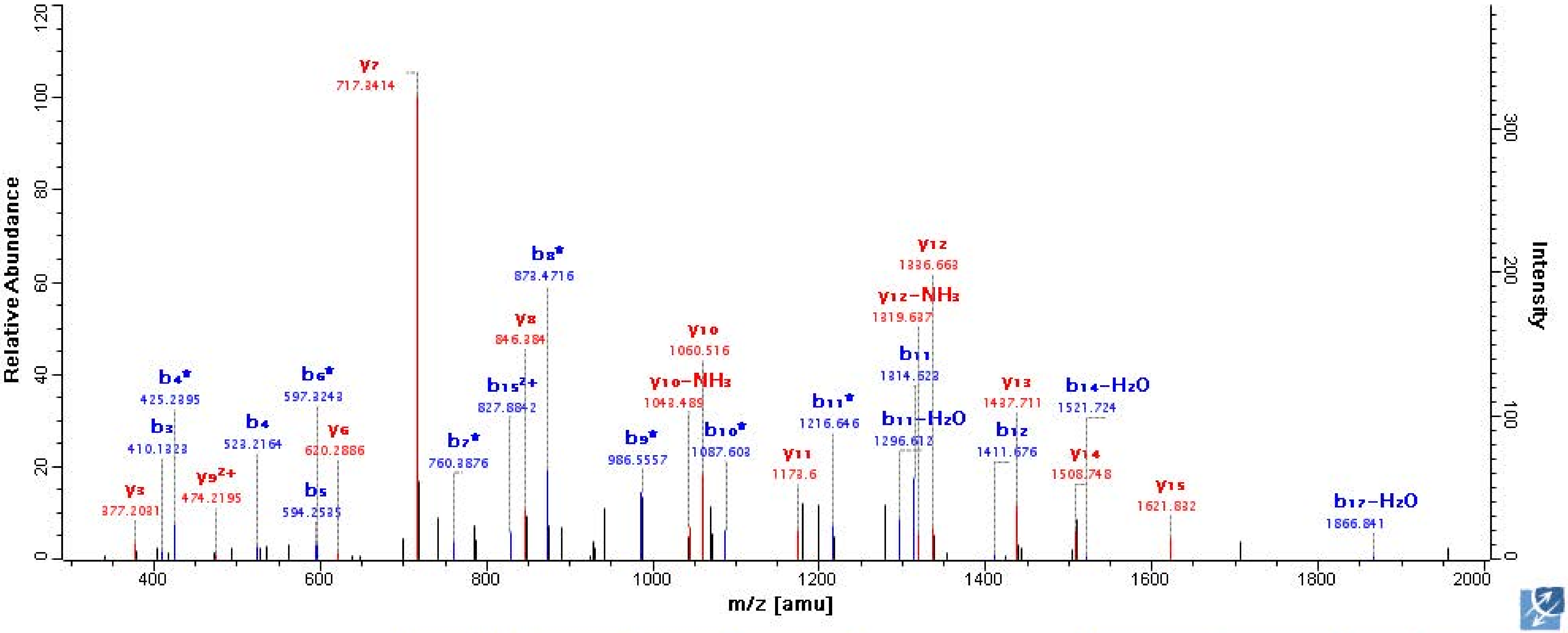
general information

Annotation:	23 of 41
AminoAcids Coverag	56 %
Intensity Coverage:	46 %
Protein Localisation:	73 ... 113

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	40				
	199.1441		199.1441	2	V	39	4304.931		4304.931	
	328.1867		328.1867	3	E	38	4205.862		4205.862	
	425.2395		425.2395	4	P	37	4076.82		4076.82	
	526.2871		526.2871	5	T	36	3979.767		3979.767	
	597.3243	-0.100865	597.3243	6	A	35	3878.719		3878.719	
	744.3927		744.3927	7	F	34	3807.682		3807.682	
	859.4196		859.4196	8	D	33	3660.614		3660.614	
	987.4782		987.4782	9	Q	32	3545.587		3545.587	
	1150.542		1150.542	10	Y	31	3417.528		3417.528	
	1263.626		1263.626	11	I	30	3254.465		3254.465	
+0.242504	681.8506	-0.002344	1362.694	12	V	29	3141.381		3141.381	
	1419.715		1419.715	13	G	28	3042.313		1521.66	+0.189706
	1547.774		1547.774	14	Q	27	2985.291		2985.291	
-0.083641	838.4199	+0.057768	1675.833	15	Q	26	2857.232		2857.232	
-0.110776	888.9438		1776.88	16	T	25	2729.174		1365.091	-0.176043
+0.121244	939.4676	-0.20983	1877.928	17	T	24	2628.126		2628.126	
+0.152202	1020.999		2040.991	18	Y	23	2527.079		1264.043	-0.195137
	2138.044		2138.044	19	P	22	2364.015		1182.511	-0.253439
-0.279375	1127.039		2253.071	20	D	21	2266.962		1133.985	-0.463141
	2368.098		2368.098	21	D	20	2151.936		1076.471	-0.079918
	2465.151		2465.151	22	P	19	2036.909		1018.958	+0.190389
	2594.193		2594.193	23	E	18	1939.856		1939.856	
	2722.252		2722.252	24	Q	17	1810.813		1810.813	
	2836.295		2836.295	25	N	16	1682.755		1682.755	
	2935.363		2935.363	26	V	15	1568.712		1568.712	
	3116.377		3116.377	27	T	14	1469.643		1469.643	
	3231.404		3231.404	28	D	13	1288.629		1288.629	
	3318.436		3318.436	29	S	12	1173.602	+0.0821	1173.602	
	3389.473		3389.473	30	A	11	1086.57		1086.57	
	3460.51		3460.51	31	A	10	1015.533		1015.533	
	3531.548		3531.548	32	A	9	944.4961	-0.088743	944.4961	
	3602.585		3602.585	33	A	8	873.459	-0.06994	873.459	
	3703.632		3703.632	34	T	7	802.4219	-0.096059	802.4219	
	3774.669		3774.669	35	A	6	701.3742	-0.18278	701.3742	
	3921.705		3921.705	36	M	5	630.3371		630.3371	
	4008.737		4008.737	37	S	4	483.3017	+0.177484	483.3017	
	4079.774		4079.774	38	A	3	396.2696		396.2696	
	4136.795		4136.795	39	G	2	325.2325	-0.222582	325.2325	
	4249.88		4249.88	40	I	1	268.2111		268.2111	
				41	K	0	155.127		155.127	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	12599
Protein:	BSU13590; mtnW; ykrW
Peptide Score:	118.48
Method:	ITMS; CID; 3





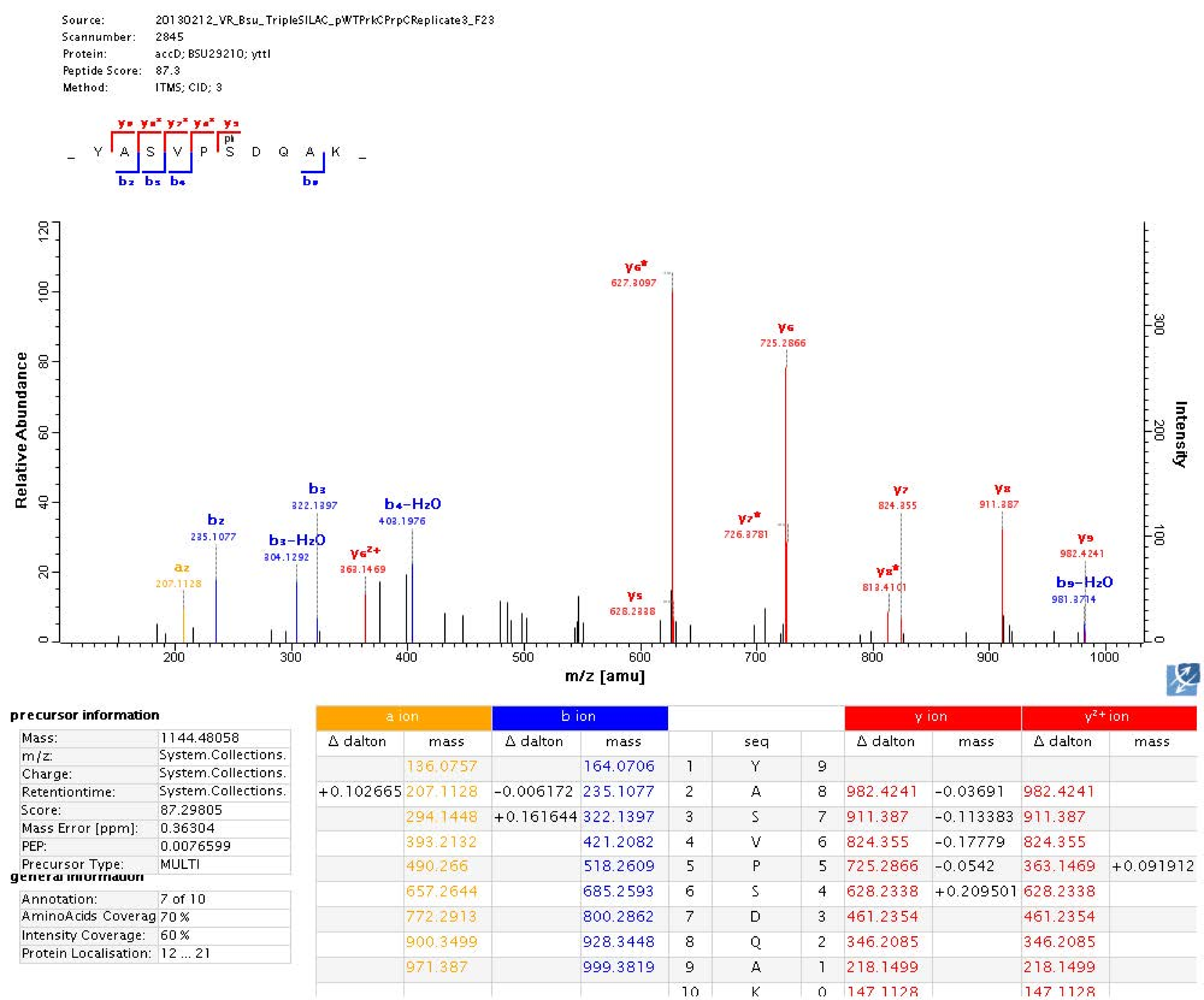
precursor information

Mass:	2029.94961
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.4799
Mass Error [ppm]:	-0.034226
PEP:	1.5772E-14
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	57 %
Protein Localisation:	2 ... 19

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	168.0056		168.0056	1	S	17				
	297.0482		297.0482	2	E	16	1863.959		1863.959	
	410.1323	-0.007445	410.1323	3	I	15	1734.916		1734.916	
	523.2164	+0.033094	523.2164	4	I	14	1621.832	-0.203404	1621.832	
	594.2535	+0.278085	594.2535	5	A	13	1508.748	-0.248979	1508.748	
	695.3011		695.3011	6	T	12	1437.711	-0.058301	1437.711	
	858.3645		858.3645	7	Y	11	1336.663	-0.13782	1336.663	
	971.4485		971.4485	8	I	10	1173.6	-0.13455	1173.6	
	1084.533		1084.533	9	I	9	1060.516	-0.240671	1060.516	
	1185.58		1185.58	10	T	8	947.4316		474.2195	-0.055605
	1314.623	-0.202711	1314.623	11	E	7	846.384	+0.002155	846.384	
	1411.676	-0.004376	1411.676	12	P	6	717.3414	-0.040457	717.3414	
	1468.697		1468.697	13	G	5	620.2886	+0.036782	620.2886	
	1539.734		1539.734	14	A	4	563.2671		563.2671	
+0.369321	827.8842		1654.761	15	D	3	492.23		492.23	
	1755.809		1755.809	16	T	2	377.2031	+0.035541	377.2031	
	1884.851		1884.851	17	E	1	276.1554		276.1554	
				18	K	0	147.1128		147.1128	



Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	2845
Protein:	accD; BSU29210; yttI
Peptide Score:	87.3
Method:	ITMS; CID; 3

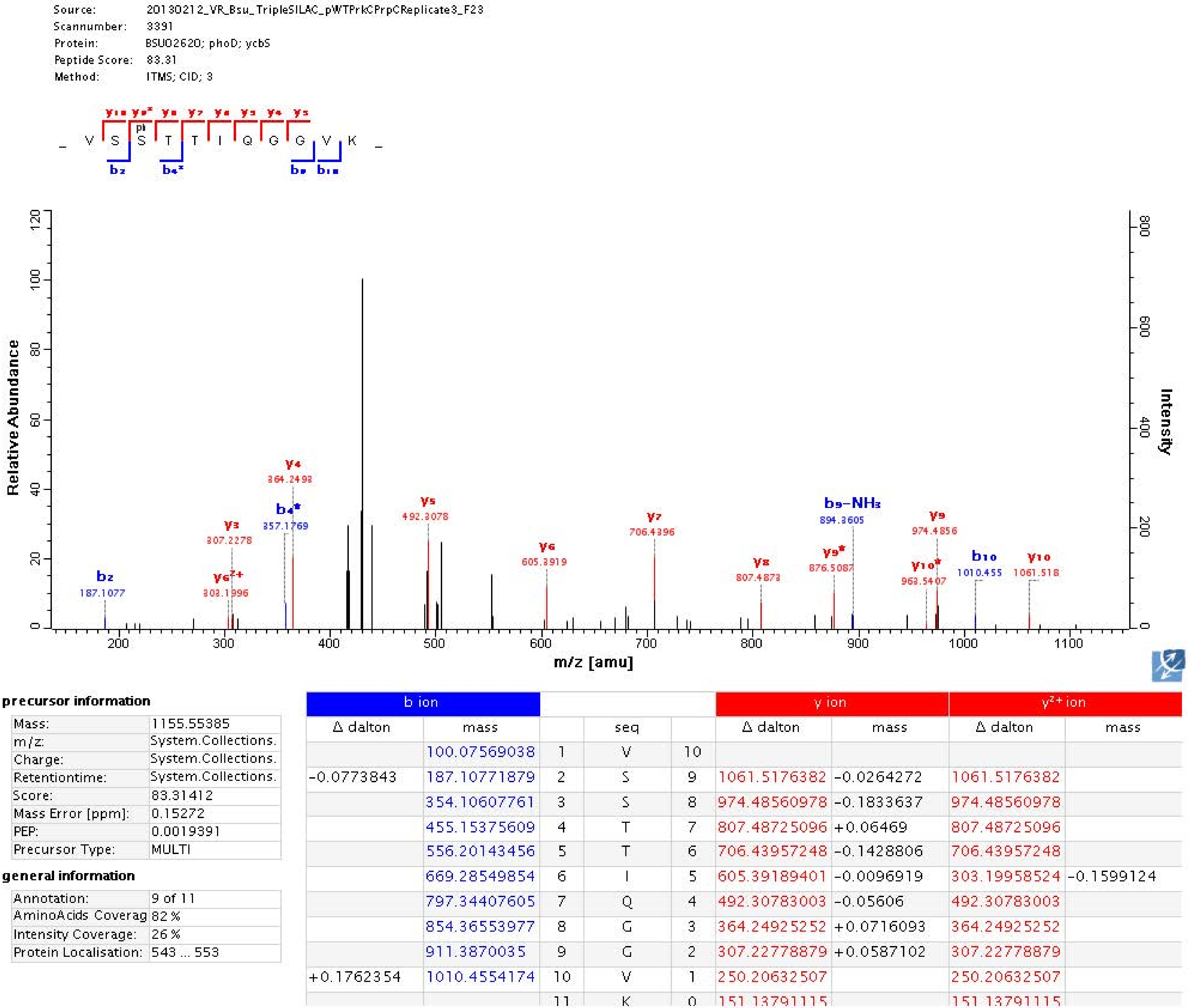
precursor information

Mass:	1144.48058
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.29805
Mass Error [ppm]:	0.36304
PEP:	0.0076599
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	60 %
Protein Localisation:	12 ... 21

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	9				
+0.102665	207.1128	-0.006172	235.1077	2	A	8	982.4241	-0.03691	982.4241	
	294.1448	+0.161644	322.1397	3	S	7	911.387	-0.113383	911.387	
	393.2132		421.2082	4	V	6	824.355	-0.17779	824.355	
	490.266		518.2609	5	P	5	725.2866	-0.0542	363.1469	+0.091912
	657.2644		685.2593	6	S	4	628.2338	+0.209501	628.2338	
	772.2913		800.2862	7	D	3	461.2354		461.2354	
	900.3499		928.3448	8	Q	2	346.2085		346.2085	
	971.387		999.3819	9	A	1	218.1499		218.1499	
				10	K	0	147.1128		147.1128	



Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber: 3391
Protein: BSU02620; phoD; ycbS
Peptide Score: 83.31
Method: ITMS; CID; 3

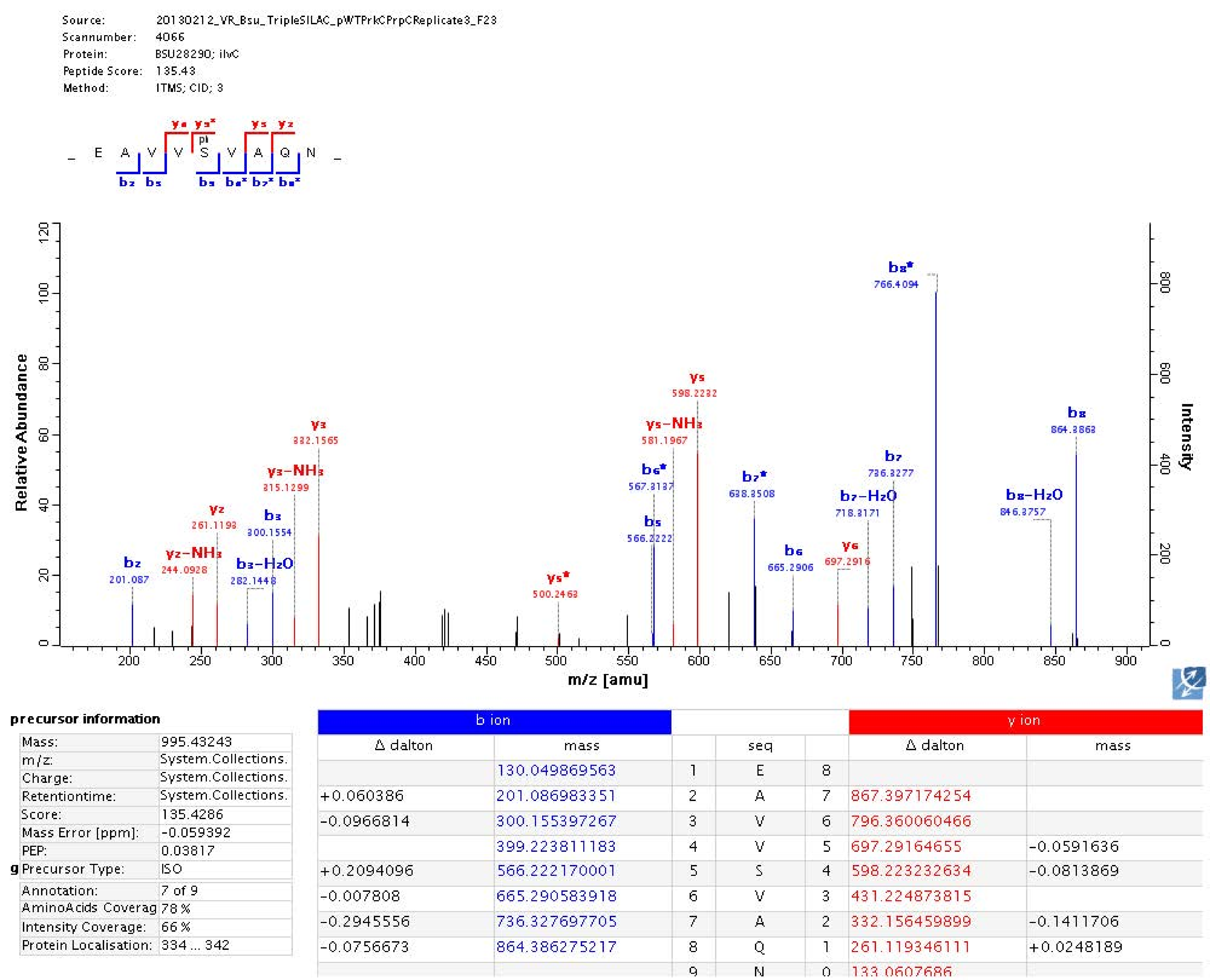
precursor information

Mass:	1155.55385
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	83.31412
Mass Error [ppm]:	0.15272
PEP:	0.0019391
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	26 %
Protein Localisation:	543 ... 553

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	10				
-0.0773843	187.10771879	2	S	9	1061.5176382	-0.0264272	1061.5176382	
	354.10607761	3	S	8	974.48560978	-0.1833637	974.48560978	
	455.15375609	4	T	7	807.48725096	+0.06469	807.48725096	
	556.20143456	5	T	6	706.43957248	-0.1428806	706.43957248	
	669.28549854	6	I	5	605.39189401	-0.0096919	303.19958524	-0.1599124
	797.34407605	7	Q	4	492.30783003	-0.05606	492.30783003	
	854.36553977	8	G	3	364.24925252	+0.0716093	364.24925252	
	911.3870035	9	G	2	307.22778879	+0.0587102	307.22778879	
+0.1762354	1010.4554174	10	V	1	250.20632507		250.20632507	
		11	K	0	151.13791115		151.13791115	



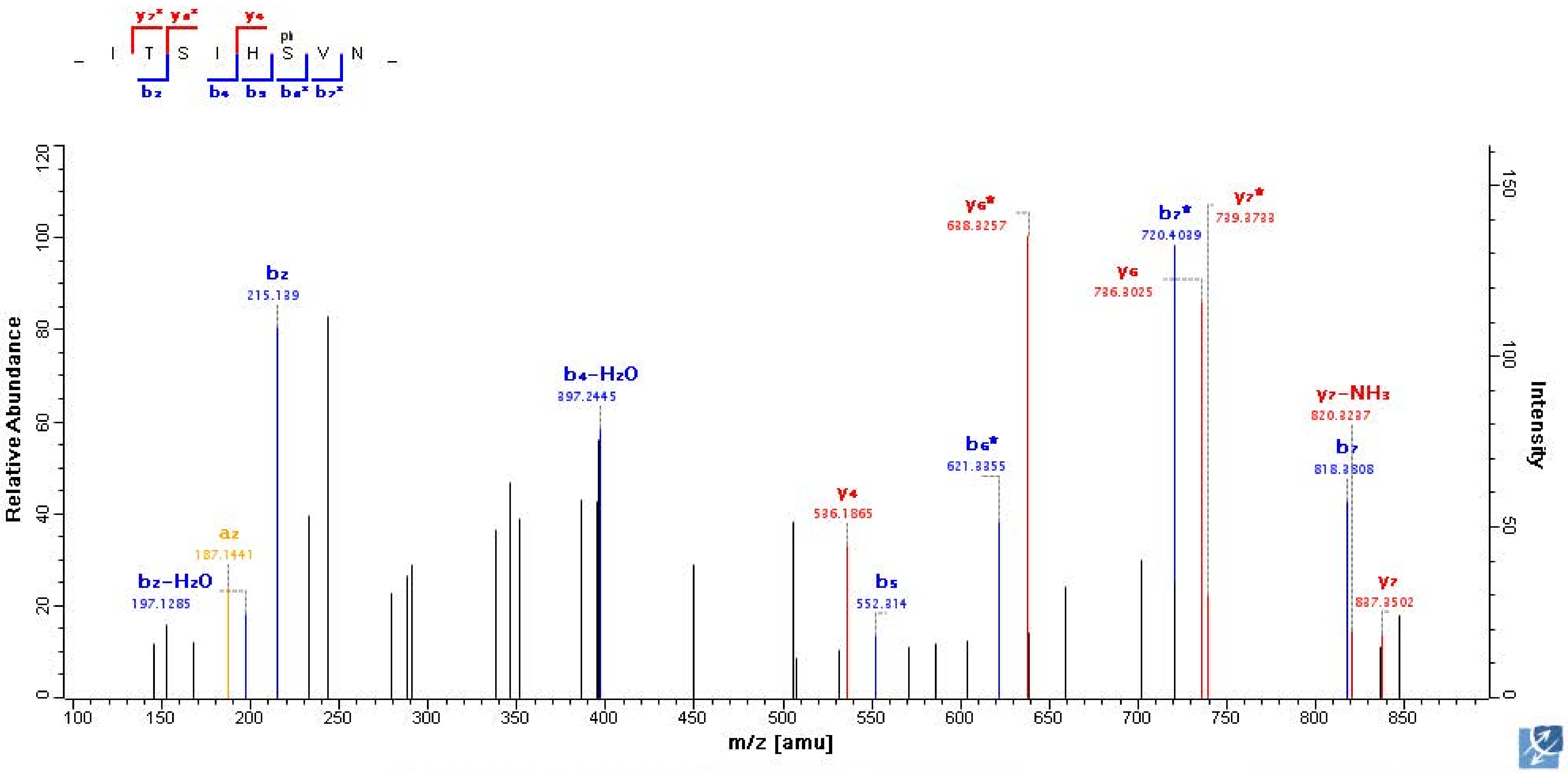
Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	4066
Protein:	BSU28290; ilvC
Peptide Score:	135.43
Method:	ITMS; CID; 3

precursor information

Mass:	995.43243
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.4286
Mass Error [ppm]:	-0.059392
PEP:	0.03817
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	66 %
Protein Localisation:	334 ... 342

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	130.049869563	1	E	8		
+0.060386	201.086983351	2	A	7	867.397174254	
-0.0966814	300.155397267	3	V	6	796.360060466	
	399.223811183	4	V	5	697.29164655	-0.0591636
+0.2094096	566.222170001	5	S	4	598.223232634	-0.0813869
-0.007808	665.290583918	6	V	3	431.224873815	
-0.2945556	736.327697705	7	A	2	332.156459899	-0.1411706
-0.0756673	864.386275217	8	Q	1	261.119346111	+0.0248189
		9	N	0	133.0607686	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	4116
Protein:	BSU30570; ytmB
Peptide Score:	89.7
Method:	ITMS; CID; 3

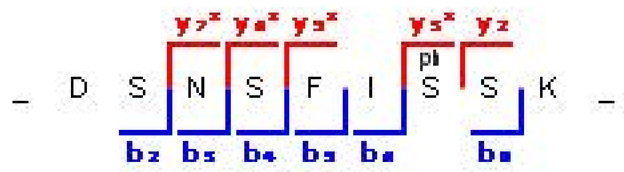


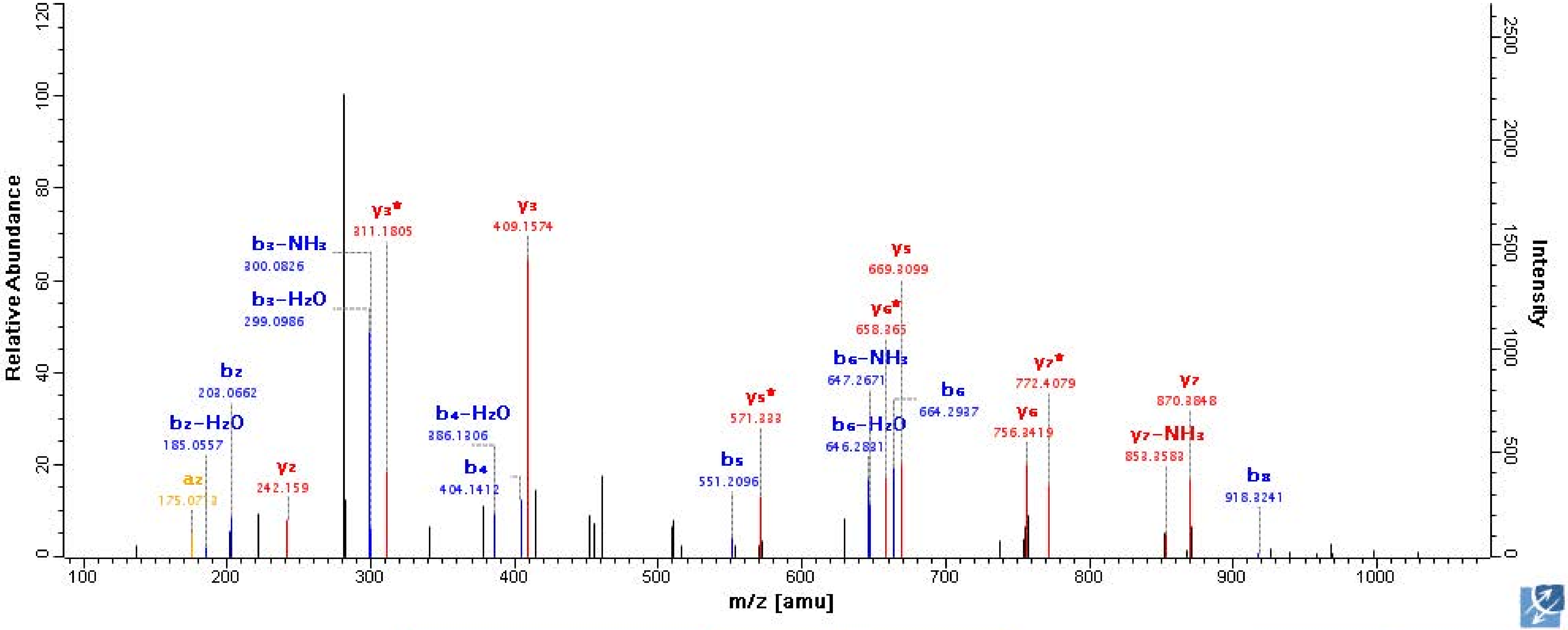
precursor information

Mass:	949.42724
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.69799
Mass Error [ppm]:	0.24321
PEP:	0.0452
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	46 %
Protein Localisation:	73 ... 80

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096425825		114.09134045	1	I	7		
+0.1284177	187.1441043	-0.0014762	215.13901892	2	T	6	837.35022406	+0.1701006
	274.17613271		302.17104733	3	S	5	736.30254559	-0.1185856
	387.26019669		415.25511131	4	I	4	649.27051718	
	524.31910855	-0.2091037	552.31402317	5	H	3	536.1864532	-0.2978424
	691.31746737		719.31238199	6	S	2	399.12754133	
	790.38588129	-0.094419	818.38079591	7	V	1	232.12918252	
				8	N	0	133.0607686	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	4213
Protein:	BSU36050; cotB
Peptide Score:	128.03
Method:	ITMS; CID; 3



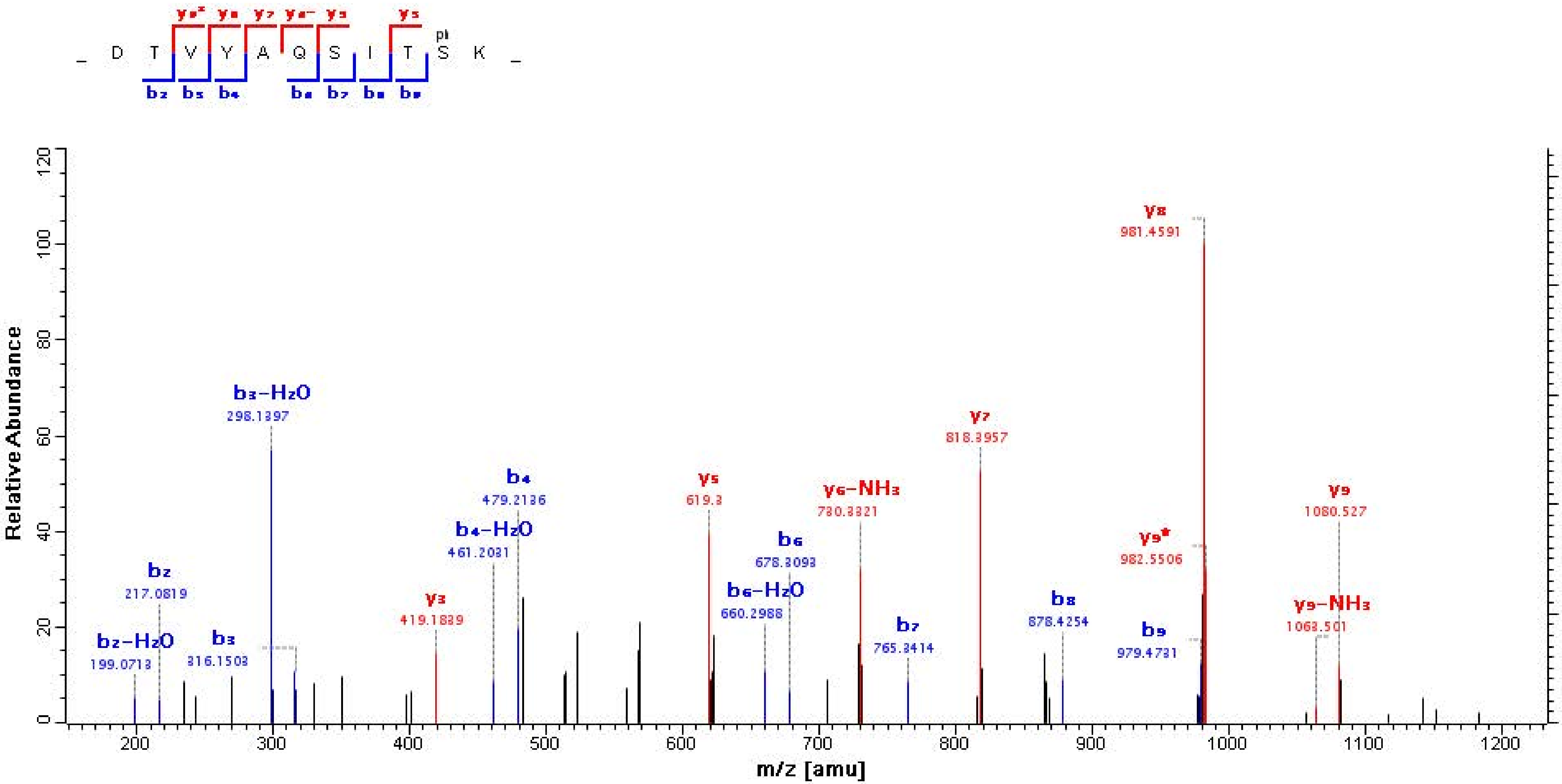


precursor information

Mass:	1063.42208
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.0347
Mass Error [ppm]:	-0.22308
PEP:	8.6535E-07
g Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	54 %
Protein Localisation:	247 ... 255

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.0342195	1	D	8		
-0.0342087	175.07133329	+0.0761166	203.06624791	2	S	7	957.41685238	
	289.11426073		317.10917536	3	N	6	870.38482397	-0.0686619
	376.14628914	+0.0185863	404.14120377	4	S	5	756.34189652	-0.0915303
	523.21470306	+0.0485	551.20961768	5	F	4	669.30986811	-0.0823901
	636.29876704	-0.1529346	664.29368166	6	I	3	522.24145419	
	803.29712586		831.29204048	7	S	2	409.15739021	-0.1376148
	890.32915427	-0.4330166	918.32406889	8	S	1	242.15903139	-0.2371564
				9	K	0	155.12700298	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	5205
Protein:	BSU13180; metC; metE
Peptide Score:	120.06
Method:	ITMS; CID; 3



precursor information

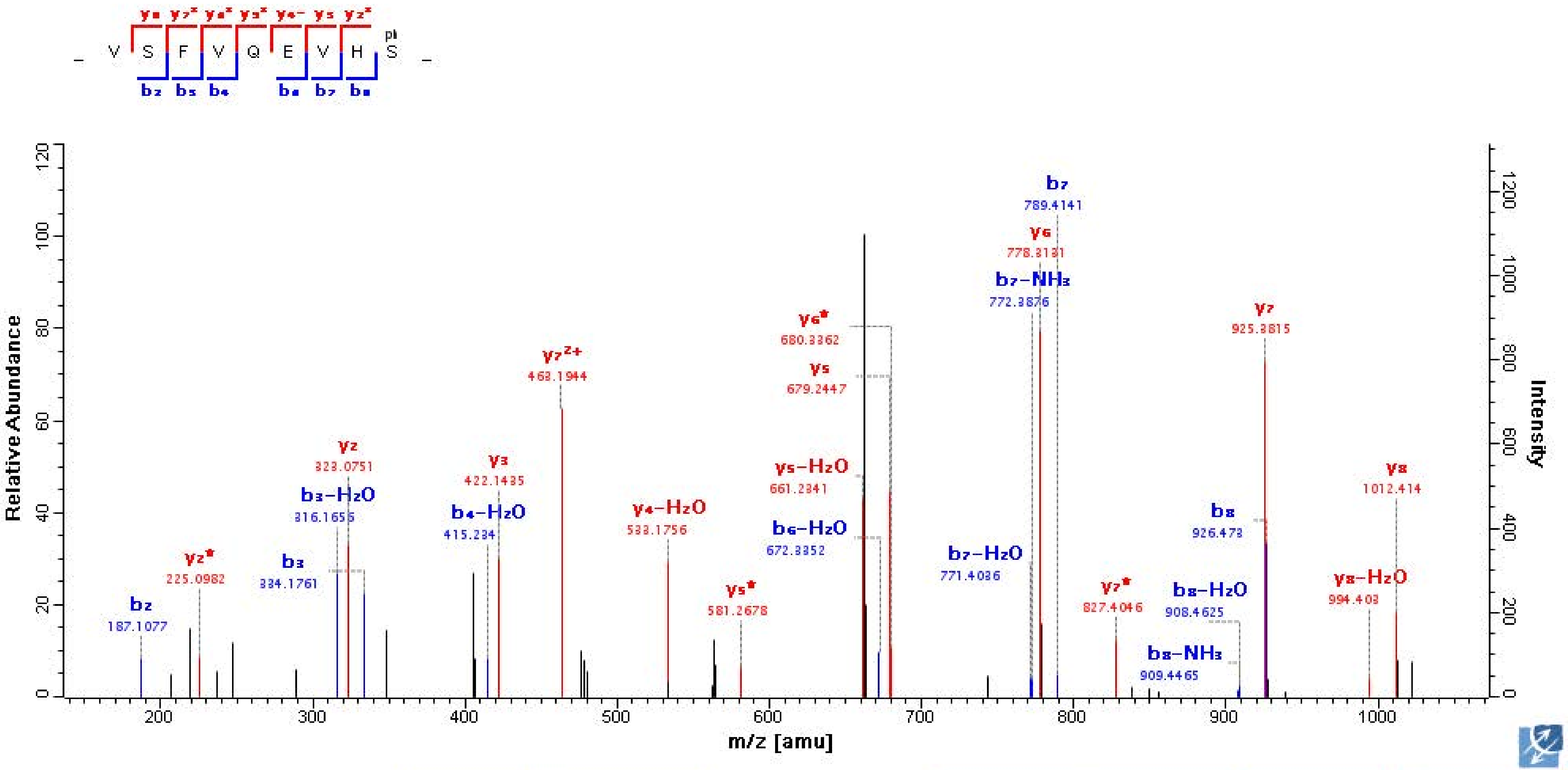
Mass:	1291.56962
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	120.0616
Mass Error [ppm]:	-0.071657
PEP:	9.4626E-07
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	54 %
Protein Localisation:	540 ... 550

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	10		
-0.045109	217.081897973	2	T	9	1181.575153065	
-0.2158636	316.150311889	3	V	8	1080.527474591	-0.1480801
-0.0424978	479.213640427	4	Y	7	981.459060674	-0.1345978
	550.250754215	5	A	6	818.395732136	-0.051799
+0.0420477	678.309331726	6	Q	5	747.358618348	
-0.2581692	765.341360136	7	S	4	619.300040837	-0.0599896
-0.055368	878.425424117	8	I	3	532.268012427	
+0.07304	979.473102591	9	T	2	419.183948447	-0.0068244
	1146.471461409	10	S	1	318.136269973	
		11	K	0	151.137911154	

Source:	20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber:	6140
Protein:	BSU22070; xpt
Peptide Score:	160.36
Method:	ITMS; CID; 3

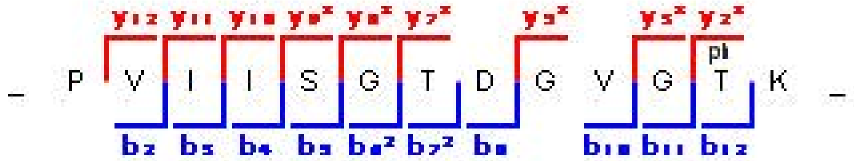


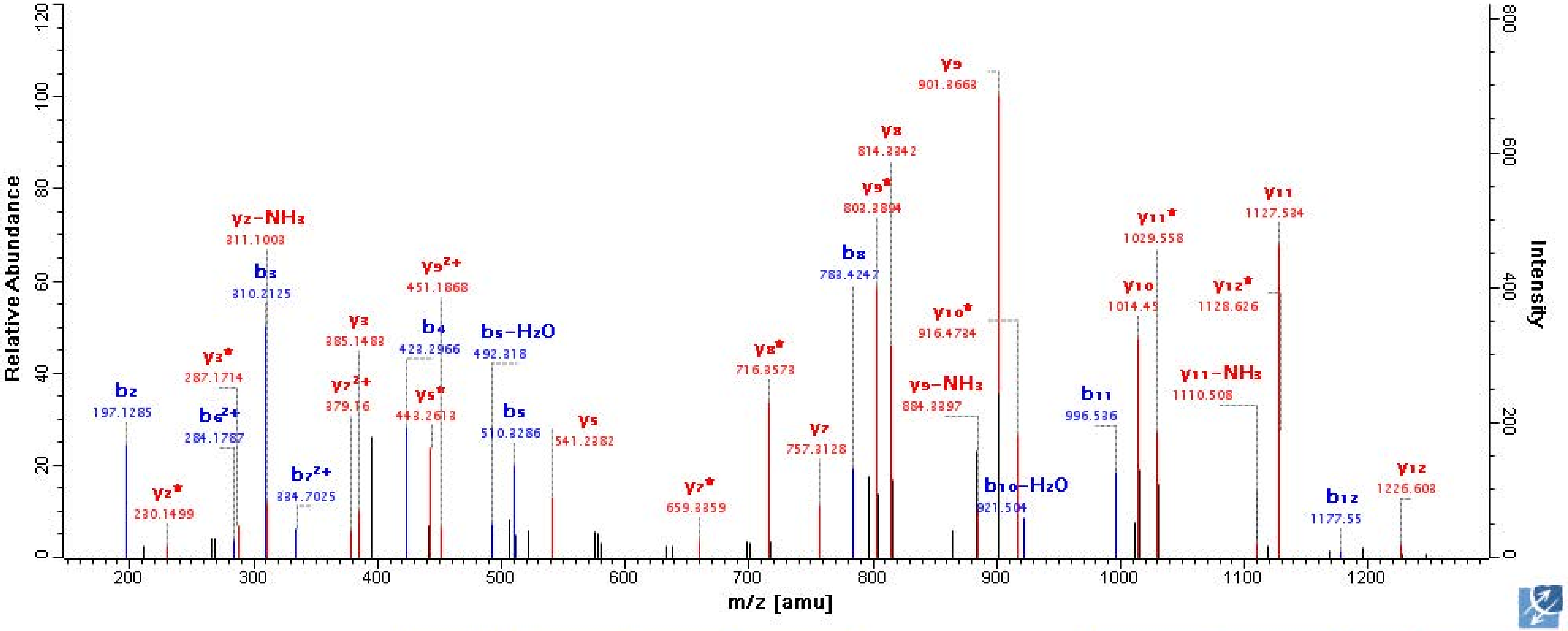
precursor information

Mass:	1110.47471
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.3616
Mass Error [ppm]:	0.021044
PEP:	8.1257E-23
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	65 %
Protein Localisation:	186 ... 194

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	8				
+0.007363	187.10771879	2	S	7	1012.4135526	-0.2012113	1012.4135526	
-0.0922704	334.17613271	3	F	6	925.38152419	-0.0261165	463.19440033	+0.1560635
	433.24454663	4	V	5	778.31311027	-0.1014404	778.31311027	
	561.30312414	5	Q	4	679.24469636	-0.0246646	679.24469636	
	690.34571723	6	E	3	551.18611885		551.18611885	
+0.0757981	789.41413115	7	V	2	422.14352575	-0.0771805	422.14352575	
-0.1103111	926.47304301	8	H	1	323.07511183	+0.0801006	323.07511183	
		9	S	0	186.01619997		186.01619997	

Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber: 6326
Protein: ath; BSU06500; purM
Peptide Score: 210.15
Method: ITMS; CID; 3





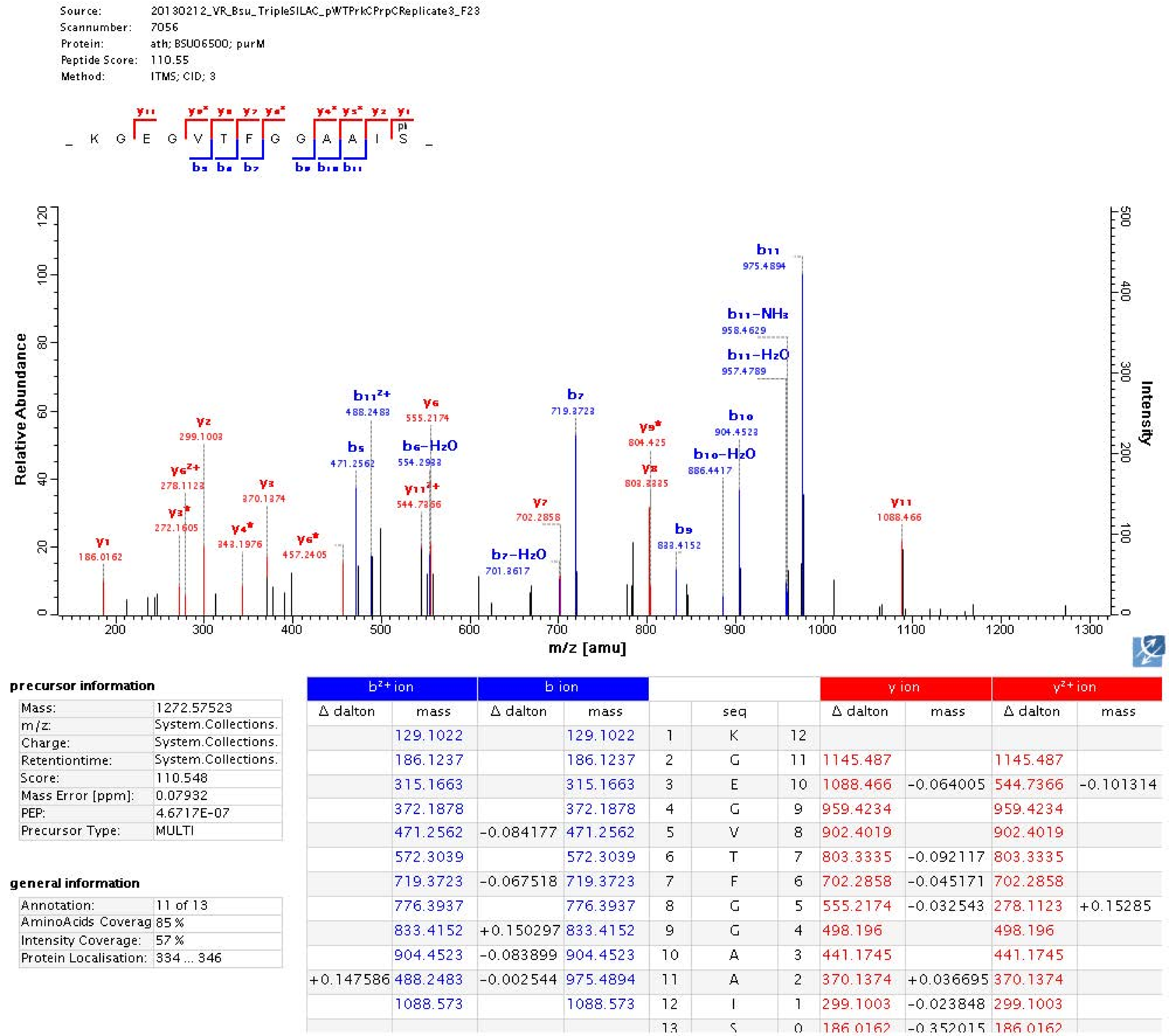
precursor information

Mass:	1322.64853
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	210.1489
Mass Error [ppm]:	0.17564
PEP:	1.9371E-121
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	73 %
Protein Localisation:	55 ... 67

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06004		98.06004	1	P	12				
	197.1285	+0.065882	197.1285	2	V	11	1226.603	-0.034695	1226.603	
	310.2125	-0.135858	310.2125	3	I	10	1127.534	-0.192111	1127.534	
	423.2966	-0.13313	423.2966	4	I	9	1014.45	-0.057998	1014.45	
	510.3286	+0.056277	510.3286	5	S	8	901.3663	-0.090633	451.1868	-0.248174
+0.022985	284.1787		567.3501	6	G	7	814.3342	-0.001415	814.3342	
-0.380859	334.7025		668.3978	7	T	6	757.3128	-0.027803	379.16	-0.048698
	783.4247	+0.056444	783.4247	8	D	5	656.2651		656.2651	
	840.4462		840.4462	9	G	4	541.2382	+0.107793	541.2382	
	939.5146		939.5146	10	V	3	484.2167		484.2167	
	996.536	-0.088222	996.536	11	G	2	385.1483	-0.313072	385.1483	
	1177.55	-0.438108	1177.55	12	T	1	328.1268		328.1268	
				13	K	0	147.1128		147.1128	



Source: 20130212_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F23
Scannumber: 7056
Protein: ath; BSU06500; purM
Peptide Score: 110.55
Method: ITMS; CID; 3

precursor information

Mass:	1272.57523
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.548
Mass Error [ppm]:	0.07932
PEP:	4.6717E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	57 %
Protein Localisation:	334 ... 346

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.1022		129.1022	1	K	12				
	186.1237		186.1237	2	G	11	1145.487		1145.487	
	315.1663		315.1663	3	E	10	1088.466	-0.064005	544.7366	-0.101314
	372.1878		372.1878	4	G	9	959.4234		959.4234	
	471.2562	-0.084177	471.2562	5	V	8	902.4019		902.4019	
	572.3039		572.3039	6	T	7	803.3335	-0.092117	803.3335	
	719.3723	-0.067518	719.3723	7	F	6	702.2858	-0.045171	702.2858	
	776.3937		776.3937	8	G	5	555.2174	-0.032543	278.1123	+0.15285
	833.4152	+0.150297	833.4152	9	G	4	498.196		498.196	
	904.4523	-0.083899	904.4523	10	A	3	441.1745		441.1745	
+0.147586	488.2483	-0.002544	975.4894	11	A	2	370.1374	+0.036695	370.1374	
	1088.573		1088.573	12	I	1	299.1003	-0.023848	299.1003	
				13	S	0	186.0162	-0.352015	186.0162	