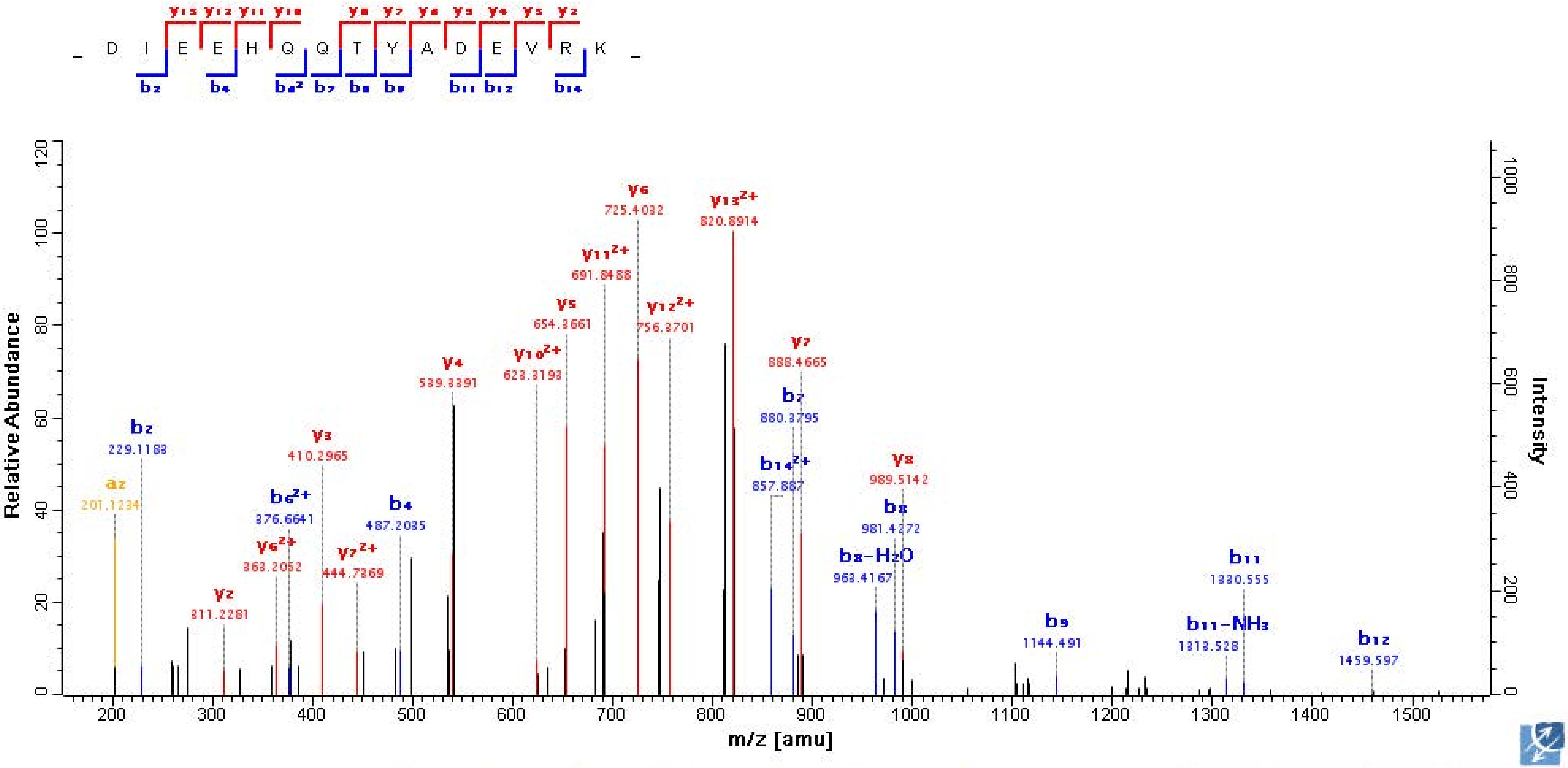
Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F15
Scannumber:	4810
Protein:	BSU36600; mta; ywnD
Peptide Score:	137.62
Method:	ITMS; CID; 3



precursor information

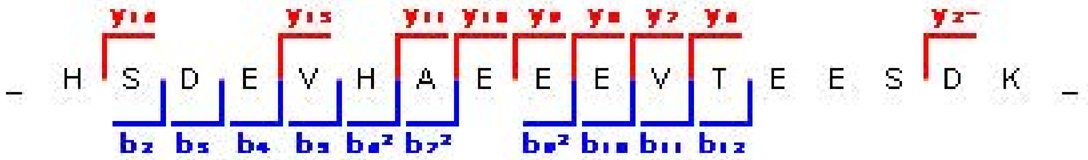
Mass:	1859.86509
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	137.6248
Mass Error [ppm]:	0.064723
PEP:	6.1707E-17
Precursor Type:	MULTI

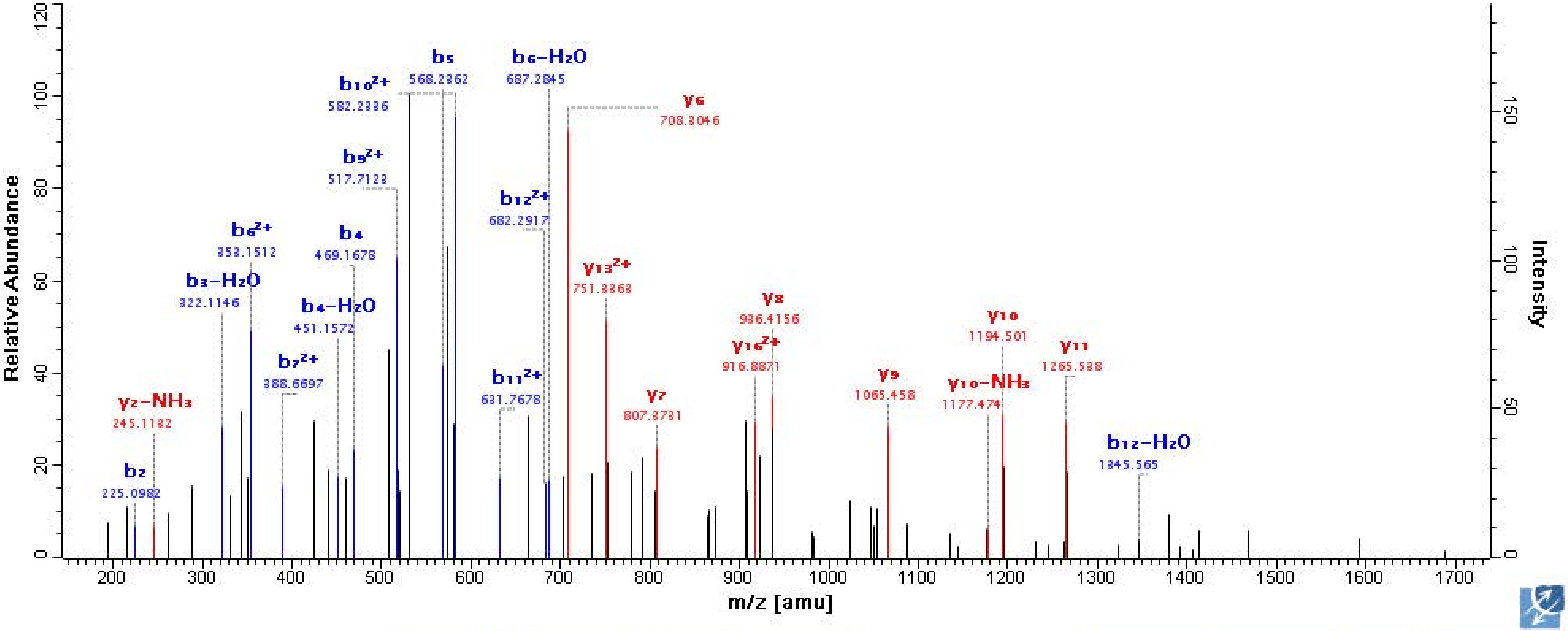
general information

Annotation:	13 of 15
AminoAcids Coverag	87 %
Intensity Coverage:	47 %
Protein Localisation:	127 ... 141

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				
+0.04297	201.123		229.118	-0.0792	229.118	2	I	13	1753.86		1753.86	
	330.166		358.161		358.161	3	E	12	1640.78		820.891	+0.0082
	459.209		487.203	+0.00991	487.203	4	E	11	1511.73		756.37	+0.1854
	596.267		624.262		624.262	5	H	10	1382.69		691.849	+0.1044
	724.326	+0.18744	376.664		752.321	6	Q	9	1245.63		623.319	+0.2977
	852.385		880.38	+0.03453	880.38	7	Q	8	1117.57		1117.57	
	953.432		981.427	+0.00107	981.427	8	T	7	989.514	+0.14554	989.514	
	1116.5		1144.49	+0.05877	1144.49	9	Y	6	888.467	-0.0214	444.737	+0.2668
	1187.53		1215.53		1215.53	10	A	5	725.403	-0.0165	363.205	+0.2179
	1302.56		1330.55	+0.0173	1330.55	11	D	4	654.366	+0.06173	654.366	
	1431.6		1459.6	+0.24827	1459.6	12	E	3	539.339	+0.04766	539.339	
	1530.67		1558.67		1558.67	13	V	2	410.297	+0.09245	410.297	
	1686.77	+0.2211	857.887		1714.77	14	R	1	311.228	-0.0168	311.228	
						15	K	0	155.127		155.127	

Source:	20120529_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F17
Scannumber:	4516
Protein:	BSU09030; yhcC
Peptide Score:	98.59
Method:	ITMS; CID; 3





precursor information

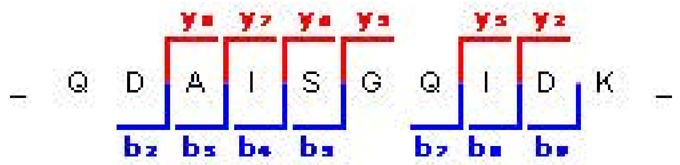
Mass:	1968.81813
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	98.59244
Mass Error [ppm]:	-0.17213
PEP:	1.9605E-08
Precursor Type:	MULTI

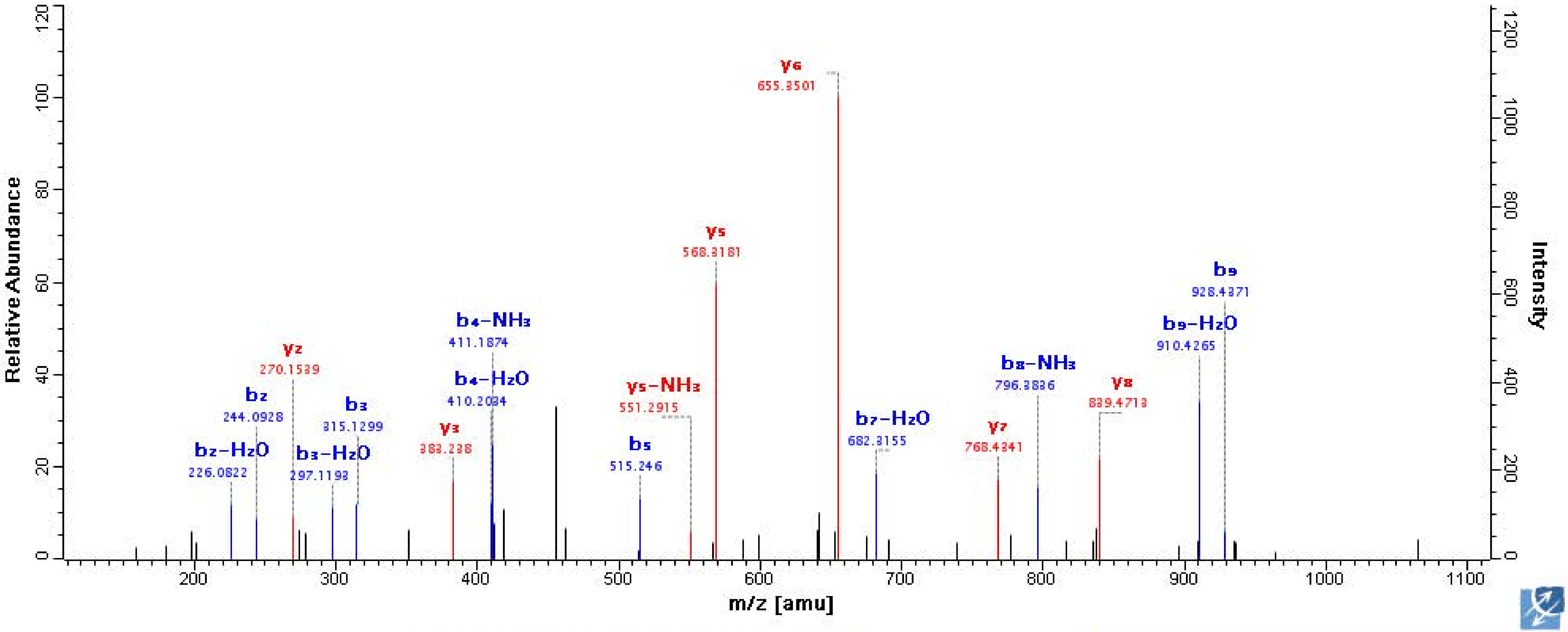
general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	45 %
Protein Localisation:	90 ... 106

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	16				
	225.0982	-0.155361	225.0982	2	S	15	1832.767		916.8871	+0.073575
	340.1252		340.1252	3	D	14	1745.735		1745.735	
	469.1678	+0.180758	469.1678	4	E	13	1630.708		1630.708	
	568.2362	-0.087058	568.2362	5	V	12	1501.665		751.3363	-0.018648
+0.088935	353.1512		705.2951	6	H	11	1402.597		1402.597	
-0.110897	388.6697		776.3322	7	A	10	1265.538	-0.065413	1265.538	
	905.3748		905.3748	8	E	9	1194.501	-0.036356	1194.501	
-0.111803	517.7123		1034.417	9	E	8	1065.458	+0.172131	1065.458	
+0.167316	582.2336		1163.46	10	E	7	936.4156	+0.101015	936.4156	
+0.30596	631.7678		1262.528	11	V	6	807.3731	+0.013481	807.3731	
+0.449358	682.2917		1363.576	12	T	5	708.3046	+0.012865	708.3046	
	1492.619		1492.619	13	E	4	607.257		607.257	
	1621.661		1621.661	14	E	3	478.2144		478.2144	
	1708.693		1708.693	15	S	2	349.1718		349.1718	
	1823.72		1823.72	16	D	1	262.1397		262.1397	
				17	K	0	147.1128		147.1128	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F03
Scannumber:	4862
Protein:	BSU18350; dacC; pbp
Peptide Score:	100.48
Method:	ITMS; CID; 3





precursor information

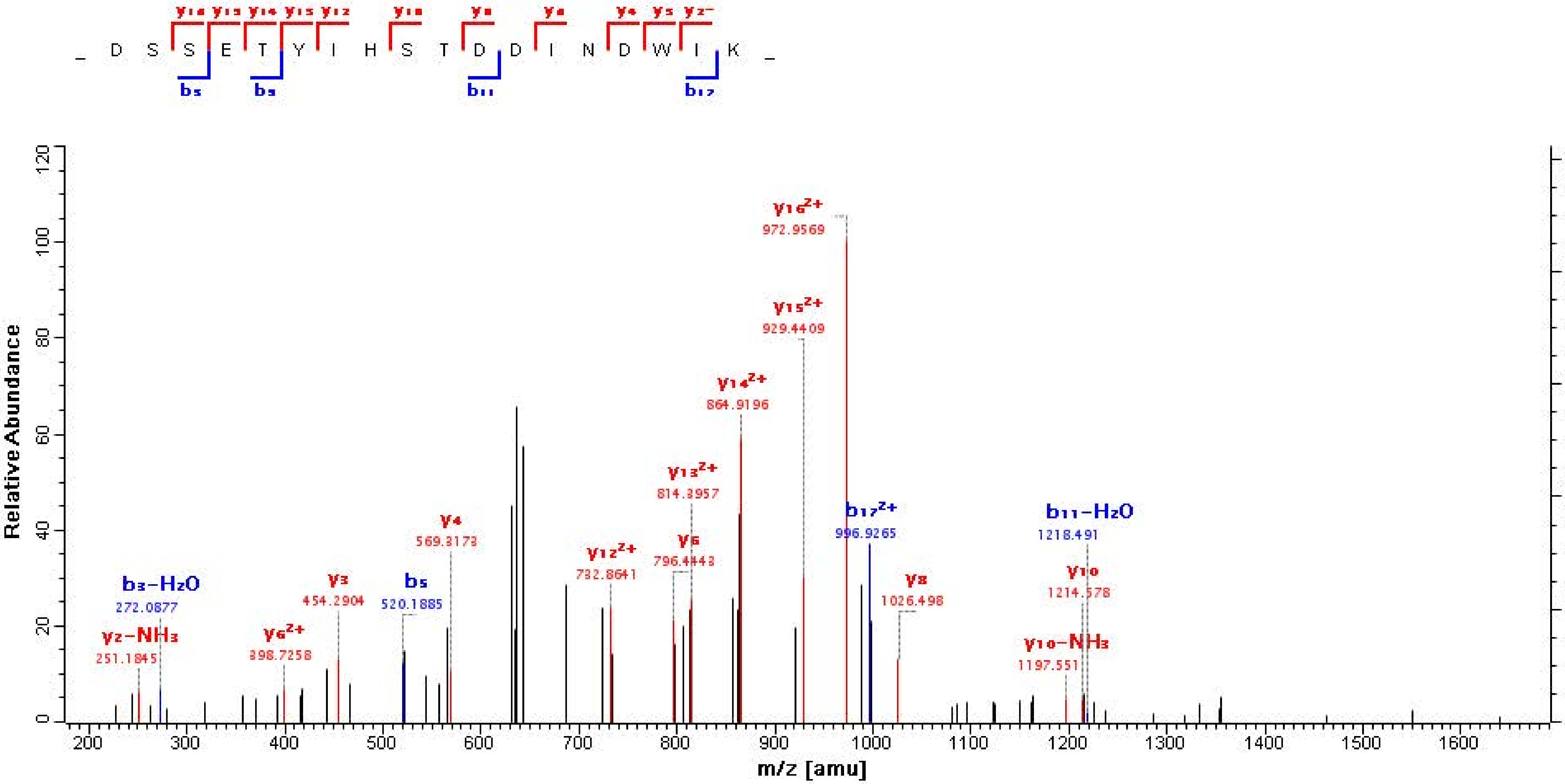
Mass:	1081.54979
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	100.4767
Mass Error [ppm]:	0.2713
PEP:	0.0011819
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	68 %
Protein Localisation:	33 ... 42

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	9		
+0.0385812	244.09279701	2	D	8	954.498200441	
-0.1800817	315.129910798	3	A	7	839.471257409	+0.0626781
	428.213974778	4	I	6	768.434143622	-0.0800787
+0.1116018	515.246003188	5	S	5	655.350079641	+0.0032529
	572.267466912	6	G	4	568.318051231	+0.1179839
	700.326044423	7	Q	3	511.296587508	
	813.410108404	8	I	2	383.238009996	+0.058865
+0.2957977	928.437051435	9	D	1	270.153946016	-0.0373689
		10	K	0	155.127002984	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F07
Scannumber:	10865
Protein:	BSU39200; yxzC
Peptide Score:	66.25
Method:	ITMS; CID; 3



precursor information

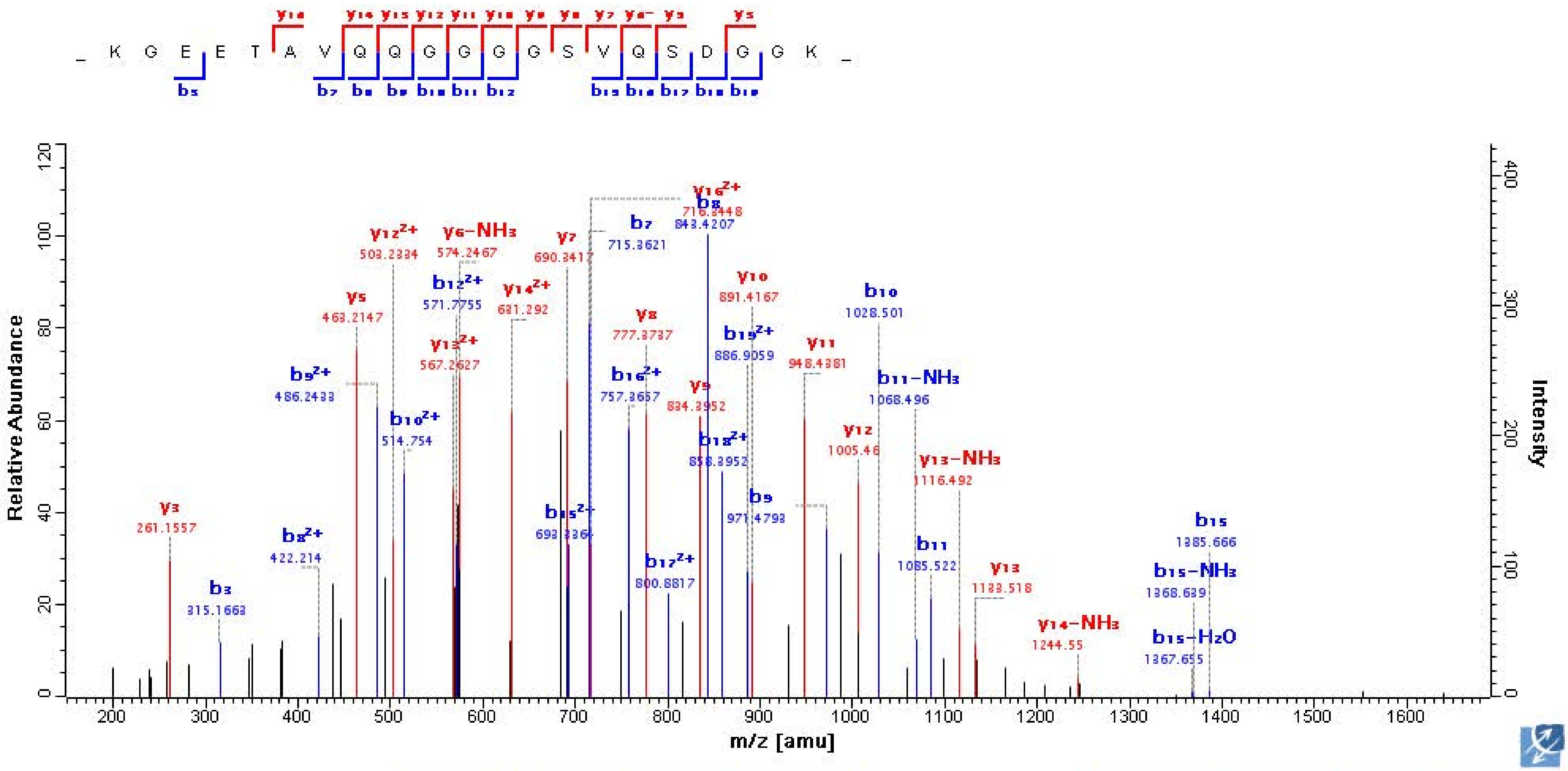
Mass:	2137.94518
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	66.24619
Mass Error [ppm]:	0.54465
PEP:	0.00063464
Precursor Type:	MULTI

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	31 %
Protein Localisation:	101 ... 118

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				
	203.0662		203.0662	2	S	16	2031.939		2031.939	
	290.0983		290.0983	3	S	15	1944.907		972.9569	+0.217117
	419.1409		419.1409	4	E	14	1857.874		929.4409	+0.268166
	520.1885	-0.039317	520.1885	5	T	13	1728.832		864.9196	+0.352695
	683.2519		683.2519	6	Y	12	1627.784		814.3957	+0.177925
	796.3359		796.3359	7	I	11	1464.721		732.8641	+0.179072
	933.3949		933.3949	8	H	10	1351.637		1351.637	
	1020.427		1020.427	9	S	9	1214.578	-0.044826	1214.578	
	1121.475		1121.475	10	T	8	1127.546		1127.546	
	1236.502		1236.502	11	D	7	1026.498	-0.396394	1026.498	
	1351.528		1351.528	12	D	6	911.4713		911.4713	
	1464.613		1464.613	13	I	5	796.4443	+0.029074	398.7258	+0.481785
	1578.655		1578.655	14	N	4	683.3603		683.3603	
	1693.682		1693.682	15	D	3	569.3173	+0.112059	569.3173	
	1879.762		1879.762	16	W	2	454.2904	+0.047877	454.2904	
-0.033694	996.9265		1992.846	17	I	1	268.2111		268.2111	
				18	K	0	155.127		155.127	

Source:	20120530_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F09
Scannumber:	3173
Protein:	BSU25590; comE1; comEA
Peptide Score:	190.24
Method:	ITMS; CID; 3



precursor information

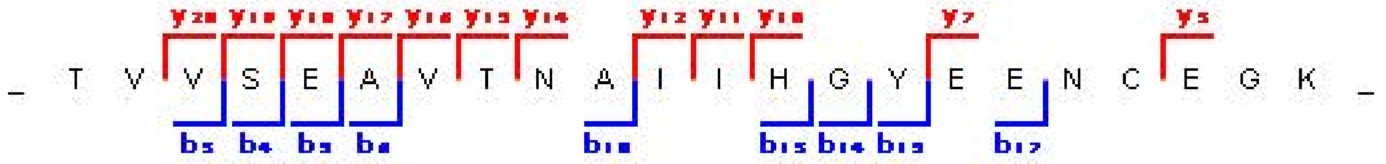
Mass:	1974.92393
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	190.2405
Mass Error [ppm]:	-0.1769
PEP:	6.4704E-65
Precursor Type:	MULTI

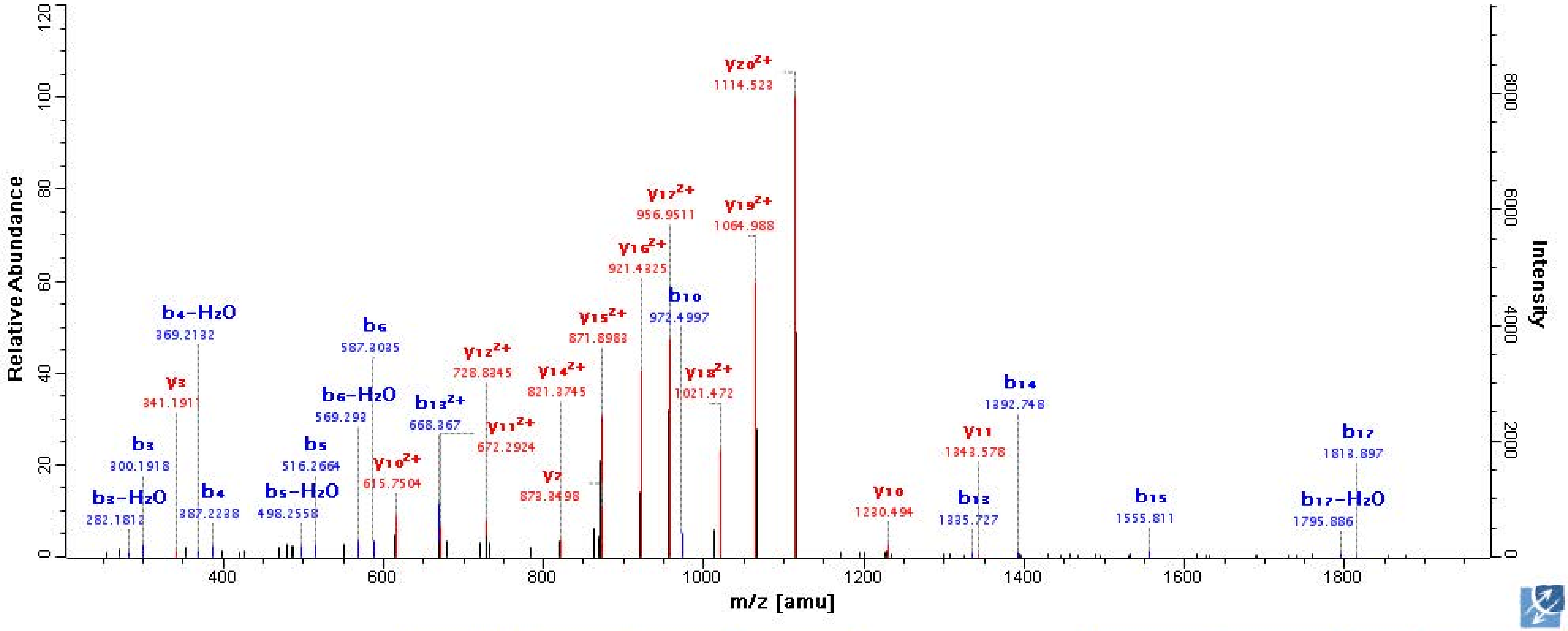
general information

Annotation:	15 of 21
AminoAcids Coverag	71 %
Intensity Coverage:	74 %
Protein Localisation:	120 ... 140

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	20				
	186.1237		186.1237	2	G	19	1847.837		1847.837	
	315.1663	+0.193689	315.1663	3	E	18	1790.815		1790.815	
	444.2089		444.2089	4	E	17	1661.773		1661.773	
	545.2566		545.2566	5	T	16	1532.73		1532.73	
	616.2937		616.2937	6	A	15	1431.682		716.3448	+0.155109
	715.3621	-0.004491	715.3621	7	V	14	1360.645		1360.645	
+0.102248	422.214	-0.04134	843.4207	8	Q	13	1261.577		631.292	+0.170581
+0.09835	486.2433	+0.007016	971.4793	9	Q	12	1133.518	-0.040982	567.2627	+0.076823
+0.193514	514.754	+0.049457	1028.501	10	G	11	1005.46	+0.191789	503.2334	+0.129793
	1085.522	+0.044472	1085.522	11	G	10	948.4381	-0.040958	948.4381	
+0.253227	571.7755		1142.544	12	G	9	891.4167	-0.084436	891.4167	
	1199.565		1199.565	13	G	8	834.3952	+0.036759	834.3952	
	1286.597		1286.597	14	S	7	777.3737	+0.146175	777.3737	
+0.106764	693.3364	+0.23289	1385.666	15	V	6	690.3417	-0.053425	690.3417	
+0.144675	757.3657		1513.724	16	Q	5	591.2733		591.2733	
+0.092345	800.8817		1600.756	17	S	4	463.2147	+0.104145	463.2147	
+0.367692	858.3952		1715.783	18	D	3	376.1827		376.1827	
+0.235012	886.9059		1772.805	19	G	2	261.1557	+0.014099	261.1557	
	1829.826		1829.826	20	G	1	204.1343		204.1343	
				21	K	0	147.1128		147.1128	

Source:	20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F06
Scannumber:	11449
Protein:	BSU23460; spoIIAB
Peptide Score:	132.51
Method:	ITMS; CID; 3





precursor information

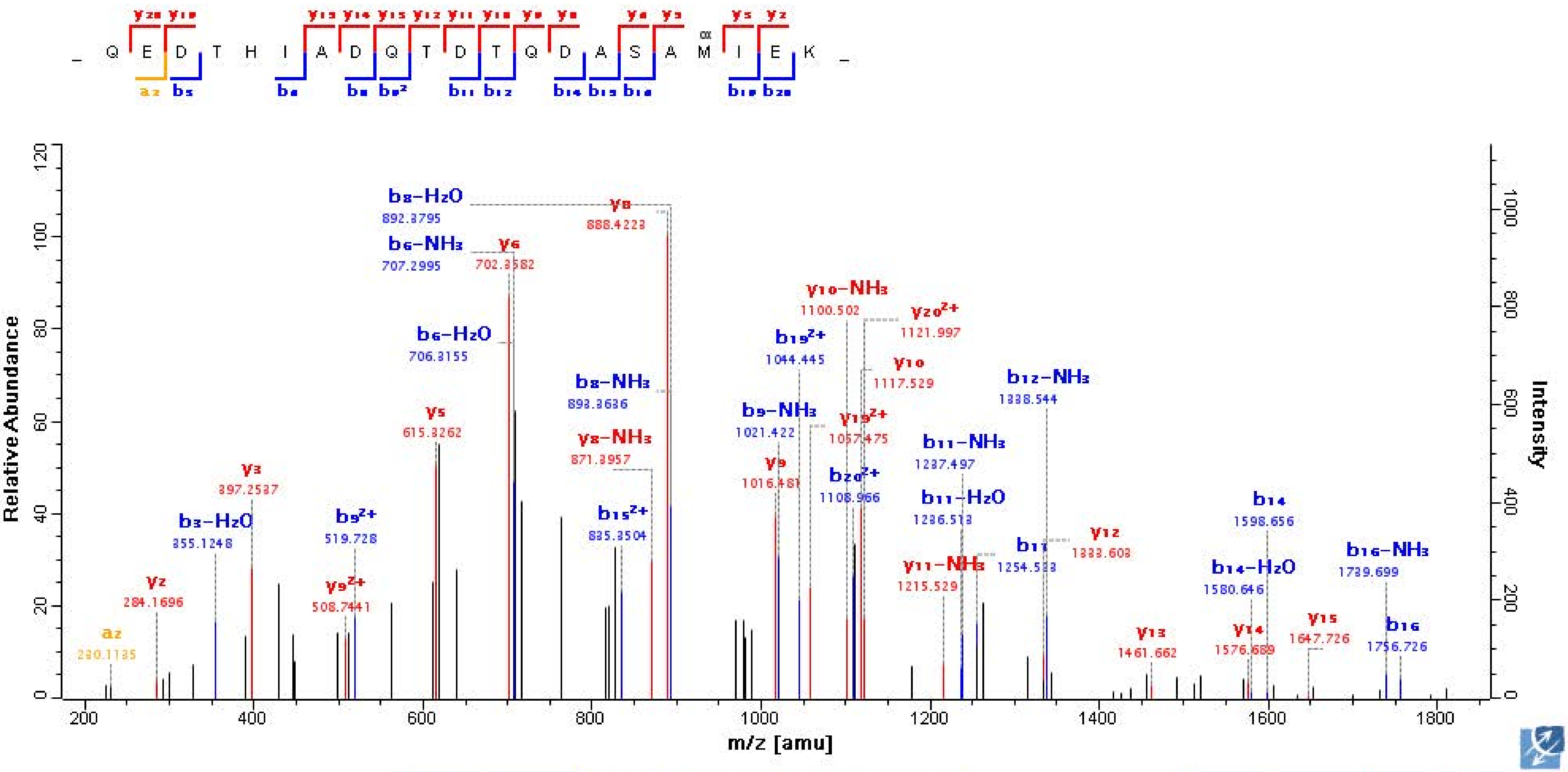
Mass:	2419.13246
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.5055
Mass Error [ppm]:	-0.040367
PEP:	6.7431E-25
Precursor Type:	MULTI

general information

Annotation:	17 of 22
AminoAcids Coverag	77 %
Intensity Coverage:	53 %
Protein Localisation:	42 ... 63

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	21				
	201.1234		201.1234	2	V	20	2327.106		2327.106	
	300.1918	-0.034739	300.1918	3	V	19	2228.038		1114.523	+0.034156
	387.2238	+0.154729	387.2238	4	S	18	2128.97		1064.988	-0.071407
	516.2664	-0.043565	516.2664	5	E	17	2041.937		1021.472	+0.355984
	587.3035	+0.097056	587.3035	6	A	16	1912.895		956.9511	+0.208518
	686.3719		686.3719	7	V	15	1841.858		921.4325	+0.185205
	787.4196		787.4196	8	T	14	1742.789		871.8983	-0.05073
	901.4625		901.4625	9	N	13	1641.742		821.3745	+0.00027
	972.4997	+0.045575	972.4997	10	A	12	1527.699		1527.699	
	1085.584		1085.584	11	I	11	1456.662		728.8345	+0.052925
	1198.668		1198.668	12	I	10	1343.578	+0.09575	672.2924	-0.163649
+0.091573	668.367	+0.011101	1335.727	13	H	9	1230.494	+0.021367	615.7504	-0.131993
	1392.748	+0.014662	1392.748	14	G	8	1093.435		1093.435	
	1555.811	+0.478677	1555.811	15	Y	7	1036.413		1036.413	
	1684.854		1684.854	16	E	6	873.3498	+0.057893	873.3498	
	1813.897	+0.057554	1813.897	17	E	5	744.3072		744.3072	
	1927.94		1927.94	18	N	4	615.2646		615.2646	
	2087.97		2087.97	19	C	3	501.2217		501.2217	
	2217.013		2217.013	20	E	2	341.1911	+0.158183	341.1911	
	2274.034		2274.034	21	G	1	212.1485		212.1485	
				22	K	0	155.127		155.127	

Source:	20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F06
Scannumber:	5708
Protein:	BSU27630; yrvD
Peptide Score:	140.46
Method:	ITMS; CID; 3



precursor information

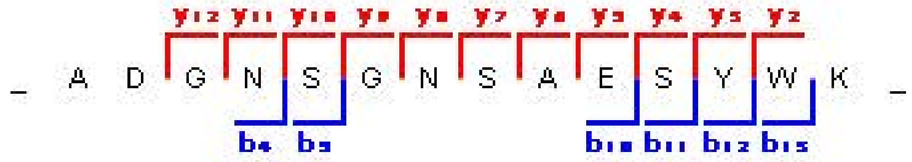
Mass:	2362.02247
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.4611
Mass Error [ppm]:	-0.24978
PEP:	5.6133E-25
Precursor Type:	MULTI

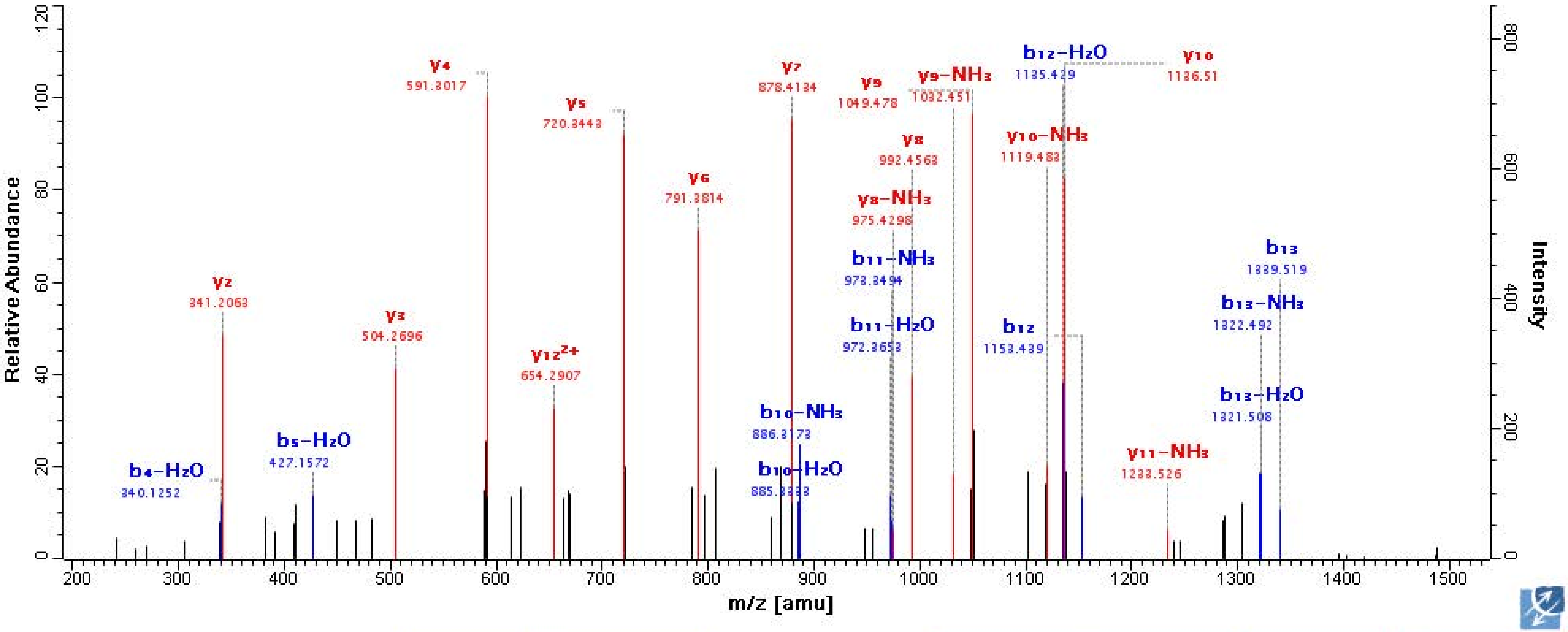
general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	54 %
Protein Localisation:	85 ... 105

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
	101.071		129.066		129.066	1	Q	20				
+0.08529	230.114		258.108		258.108	2	E	19	2242.99		1122	+0.4277
	345.14		373.135		373.135	3	D	18	2113.94		1057.48	+0.2016
	446.188		474.183		474.183	4	T	17	1998.92		1998.92	
	583.247		611.242		611.242	5	H	16	1897.87		1897.87	
	696.331		724.326		724.326	6	I	15	1760.81		1760.81	
	767.368		795.363		795.363	7	A	14	1647.73	+0.22894	1647.73	
	882.395		910.39		910.39	8	D	13	1576.69	+0.29596	1576.69	
	1010.45	+0.29644	519.728		1038.45	9	Q	12	1461.66	-0.3156	1461.66	
	1111.5		1139.5		1139.5	10	T	11	1333.6	-0.0779	1333.6	
	1226.53		1254.52	+0.01295	1254.52	11	D	10	1232.56		1232.56	
	1327.58		1355.57		1355.57	12	T	9	1117.53	+0.12835	1117.53	
	1455.63		1483.63		1483.63	13	Q	8	1016.48	-0.0063	508.744	-0.1729
	1570.66		1598.66	+0.10498	1598.66	14	D	7	888.422	+0.05412	888.422	
	1641.7	+0.12105	835.35		1669.69	15	A	6	773.395		773.395	
	1728.73		1756.73	-0.2673	1756.73	16	S	5	702.358	+0.00612	702.358	
	1799.77		1827.76		1827.76	17	A	4	615.326	+0.06695	615.326	
	1946.8		1974.8		1974.8	18	M	3	544.289		544.289	
	2059.89	+0.10017	1044.44		2087.88	19	I	2	397.254	+0.00202	397.254	
	2188.93	+0.12136	1108.97		2216.92	20	E	1	284.17	+0.01745	284.17	
						21	K	0	155.127		155.127	

Source:	20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F06
Scannumber:	5976
Protein:	BSU11900; yjcL
Peptide Score:	105.65
Method:	ITMS; CID; 3





precursor information

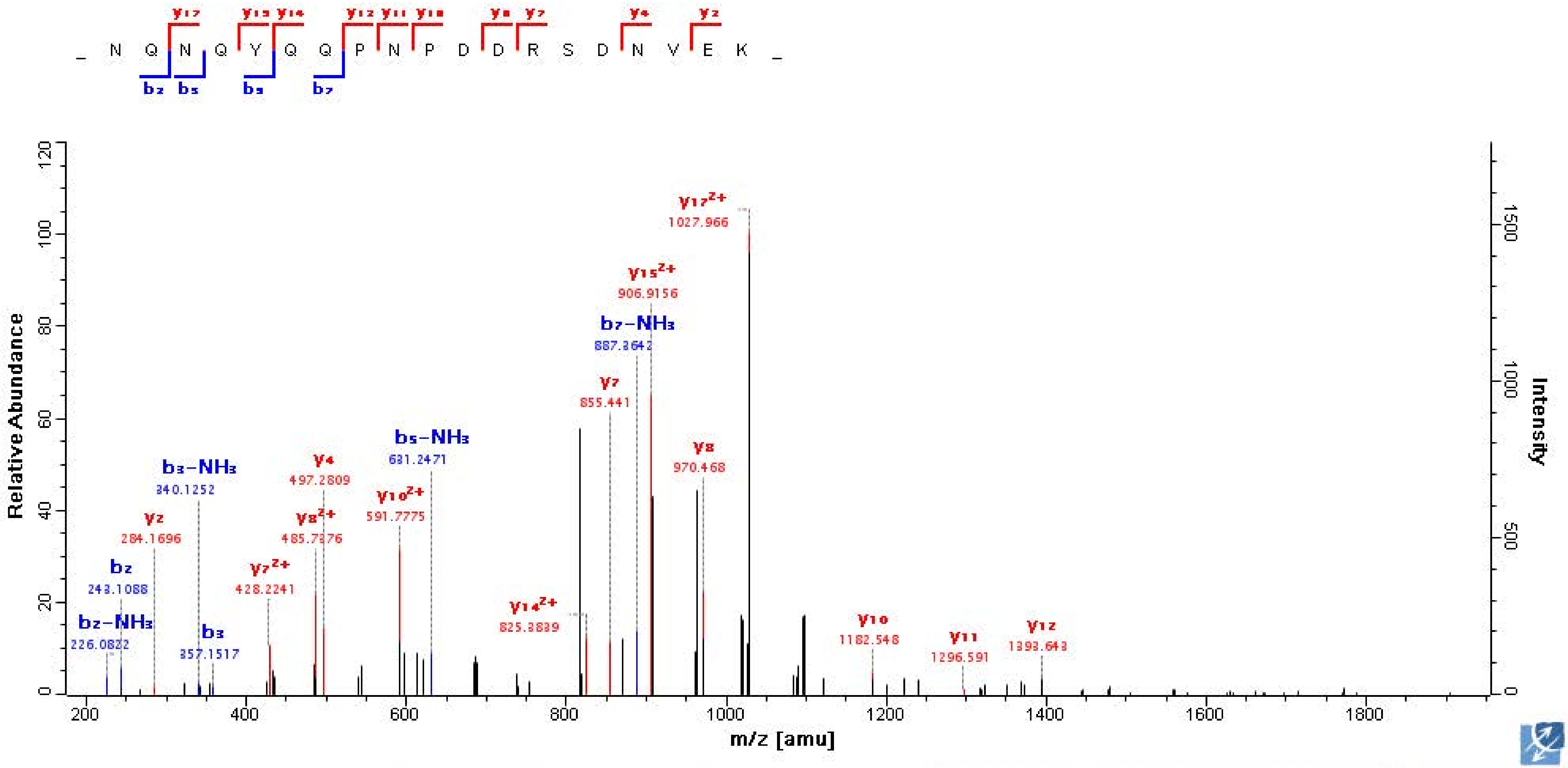
Mass:	1484.61639
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.649
Mass Error [ppm]:	-0.27384
PEP:	7.0117E-07
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	64 %
Protein Localisation:	196 ... 209

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	13				
	187.07133329	2	D	12	1422.601162		1422.601162	
	244.09279701	3	G	11	1307.5742189		654.2907477	+0.2217645
	358.13572446	4	N	10	1250.5527552		1250.5527552	
	445.16775287	5	S	9	1136.5098278	+0.0087269	1136.5098278	
	502.18921659	6	G	8	1049.4777994	+0.050521	1049.4777994	
	616.23214404	7	N	7	992.45633563	-0.0649782	992.45633563	
	703.26417245	8	S	6	878.41340818	-1.71E-05	878.41340818	
	774.30128624	9	A	5	791.38137977	-0.0077836	791.38137977	
	903.34387933	10	E	4	720.34426598	+0.1133146	720.34426598	
	990.37590774	11	S	3	591.30167289	+0.061059	591.30167289	
-0.0229765	1153.4392363	12	Y	2	504.26964448	+0.066171	504.26964448	
+0.2298639	1339.5185492	13	W	1	341.20631594	+0.0616284	341.20631594	
		14	K	0	155.12700298		155.12700298	

Source: 20120601_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F08
Scannumber: 3486
Protein: BSU18030; tlp; tlpA
Peptide Score: 76.85
Method: ITMS; CID; 3



precursor information

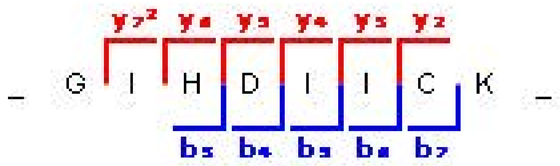
Mass:	2288.00437
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	76.85023
Mass Error [ppm]:	-0.44142
PEP:	8.7053E-05
Precursor Type:	MULTI

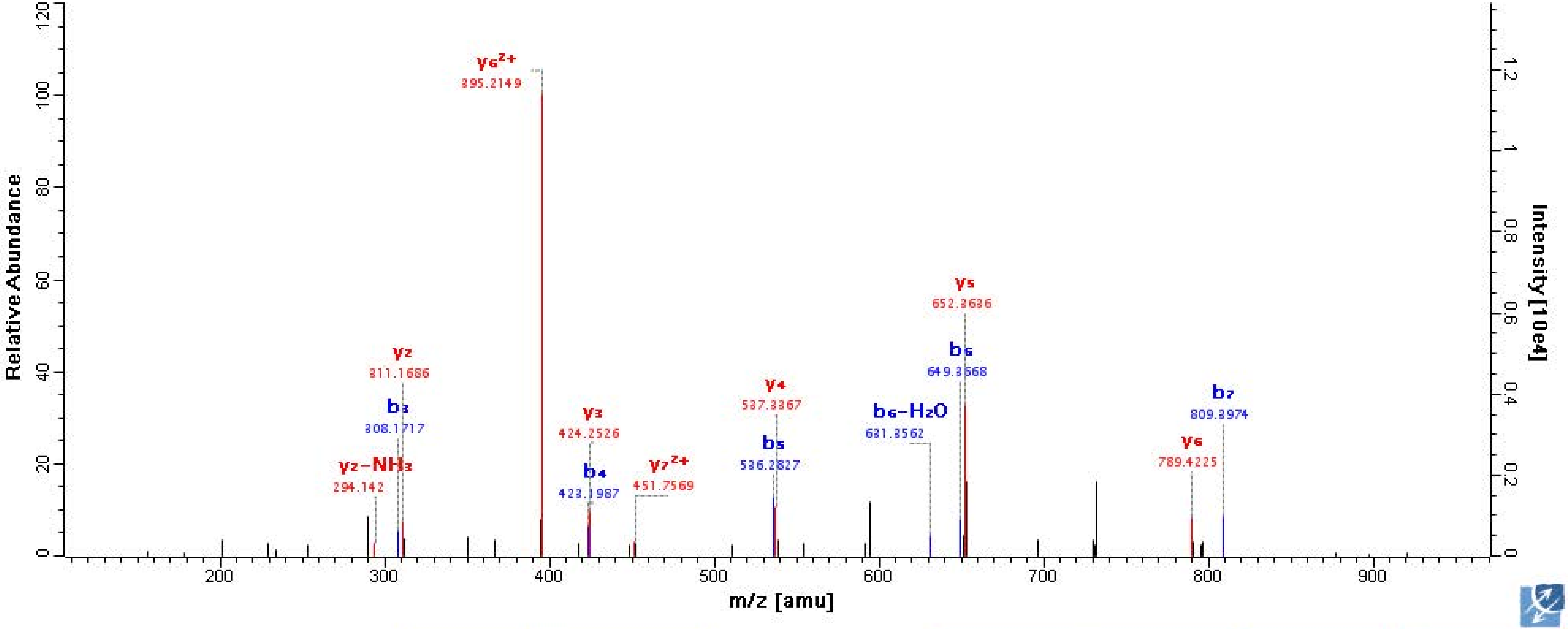
general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	37 %
Protein Localisation:	4 ... 22

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	18				
+0.1013931	243.10878143	2	Q	17	2182.9839272		2182.9839272	
-0.0102904	357.15170887	3	N	16	2054.9253496		1027.9663131	-0.0211226
	485.21028638	4	Q	15	1940.8824222		1940.8824222	
	648.27361492	5	Y	14	1812.8238447		906.91556058	+0.0165073
	776.33219243	6	Q	13	1649.7605162		825.38389631	+0.2228542
	904.39076994	7	Q	12	1521.7019386		1521.7019386	
	1001.4435338	8	P	11	1393.6433611	+0.0396223	1393.6433611	
	1115.4864612	9	N	10	1296.5905973	+0.1834506	1296.5905973	
	1212.5392251	10	P	9	1182.5476698	+0.1607042	591.77747315	+0.0256885
	1327.5661681	11	D	8	1085.494906		1085.494906	
	1442.5931112	12	D	7	970.46796295	+0.1683286	485.73761971	-0.074961
	1598.6942222	13	R	6	855.44101991	+0.0649615	428.22414819	+0.1694675
	1685.7262506	14	S	5	699.33990889		699.33990889	
	1800.7531936	15	D	4	612.30788048		612.30788048	
	1914.7961211	16	N	3	497.28093744	+0.0662305	497.28093744	
	2013.864535	17	V	2	383.23801		383.23801	
	2142.9071281	18	E	1	284.16959608	-0.1323646	284.16959608	
		19	K	0	155.12700298		155.12700298	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber:	10599
Protein:	BSU39960; S141R; yxaI
Peptide Score:	111.82
Method:	ITMS; CID; 3





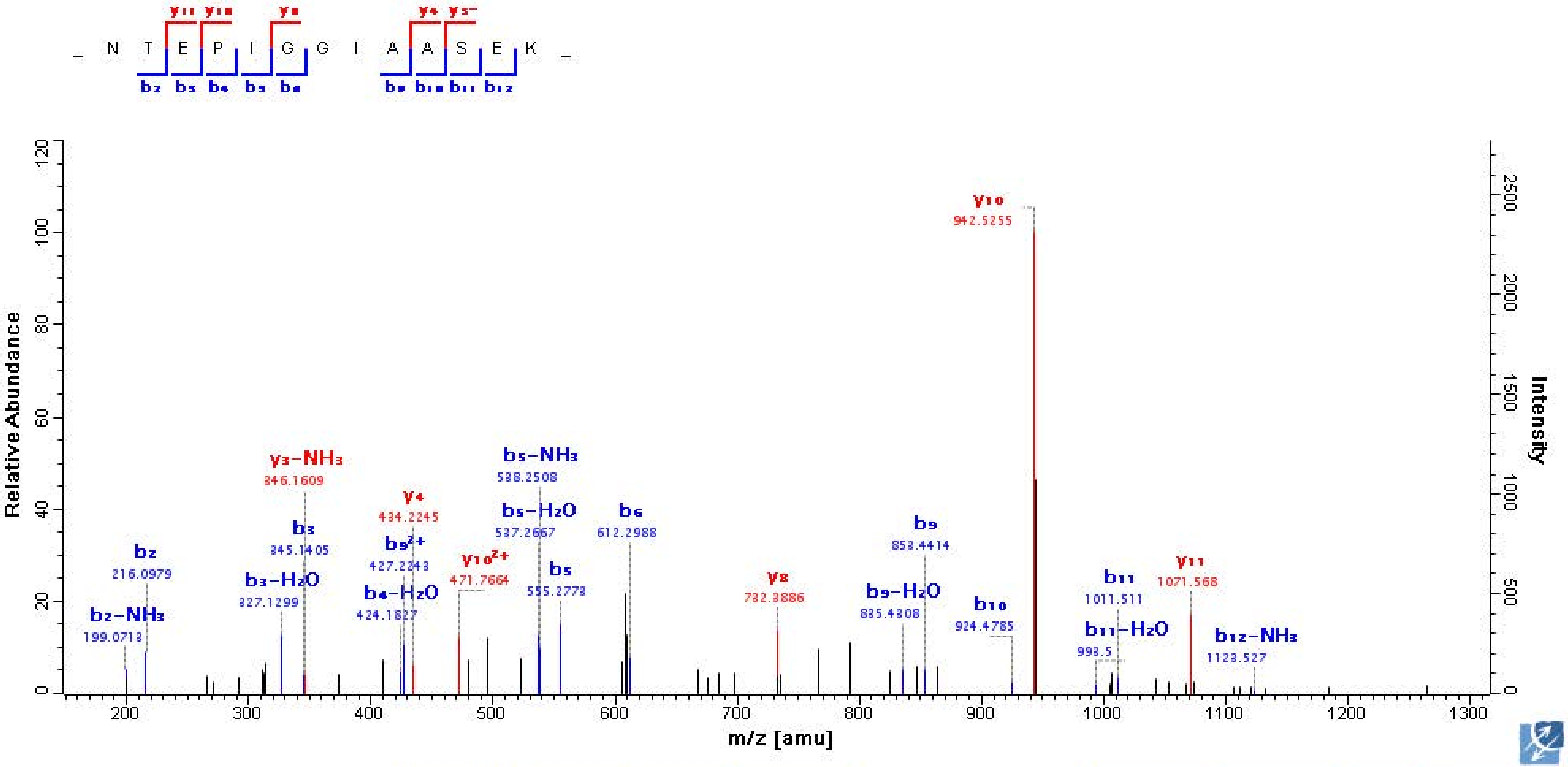
precursor information

Mass:	954.49569
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.8157
Mass Error [ppm]:	0.0062653
PEP:	0.0039394
Annotation:	6 of 8
AminoAcids Coverag	75 %
Intensity Coverage:	63 %
Protein Localisation:	138 ... 145

g

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	7				
	171.11280417	2	I	6	902.50660619		451.75694133	-0.2960649
-0.0876706	308.17171603	3	H	5	789.42254221	+0.0447429	395.21490934	+0.1750443
-0.0035907	423.19865906	4	D	4	652.36363035	+0.0367603	652.36363035	
-0.0071493	536.28272305	5	I	3	537.33668732	-0.0401175	537.33668732	
-0.017788	649.36678703	6	I	2	424.25262334	-0.0447986	424.25262334	
-0.006383	809.39743523	7	C	1	311.16855936	+0.078572	311.16855936	
		8	K	0	151.13791115		151.13791115	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber:	11480
Protein:	BSU02170; ybfB
Peptide Score:	95.27
Method:	ITMS; CID; 3



precursor information

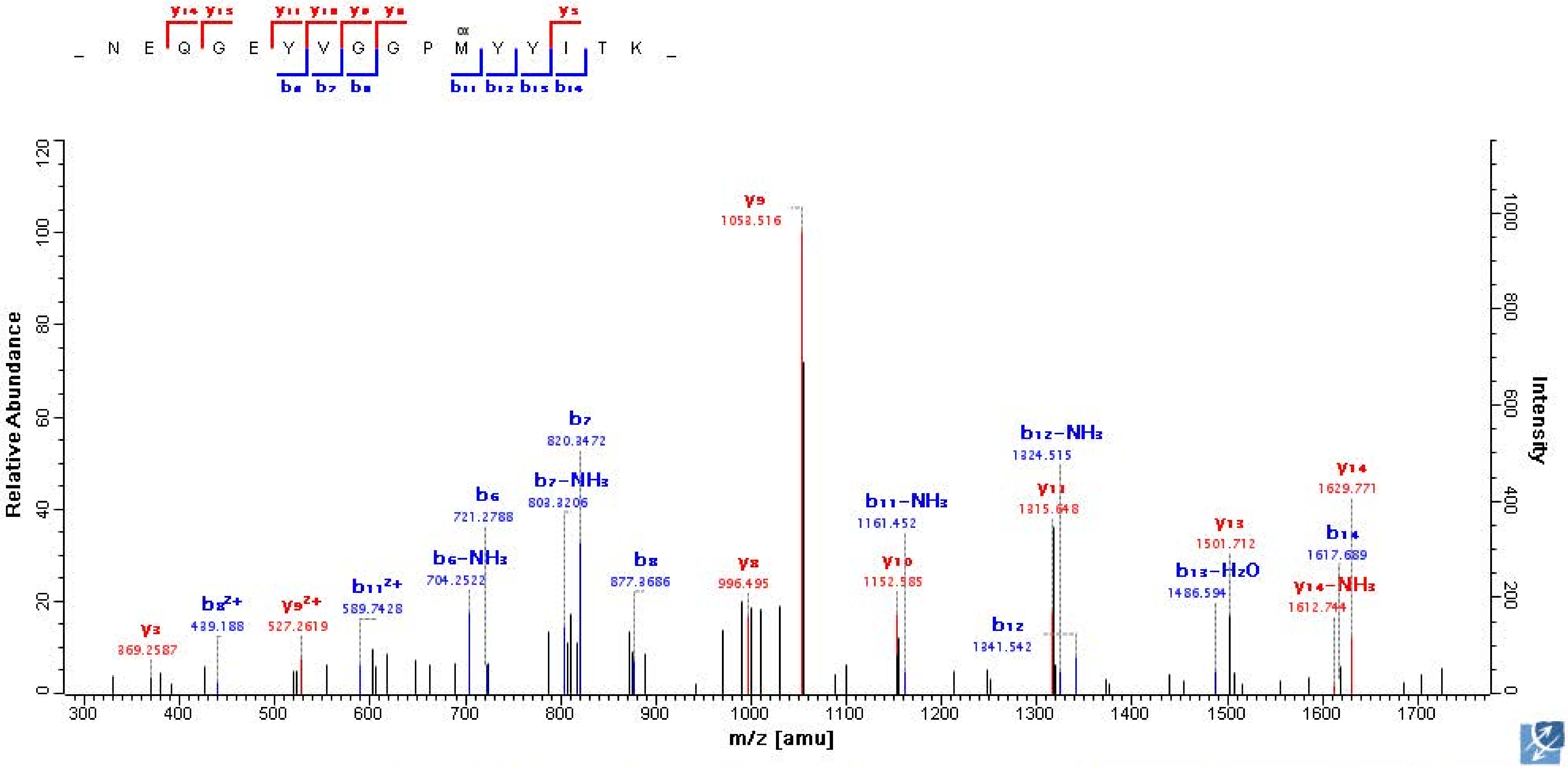
Mass:	1285.65152
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.27338
Mass Error [ppm]:	0.096467
PEP:	0.0003969
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	51 %
Protein Localisation:	194 ... 206

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	12				
	216.0979	-0.108747	216.0979	2	T	11	1172.616		1172.616	
	345.1405	+0.017422	345.1405	3	E	10	1071.568	+0.124805	1071.568	
	442.1932		442.1932	4	P	9	942.5255	+0.08317	471.7664	-0.209185
	555.2773	+0.106669	555.2773	5	I	8	845.4727		845.4727	
	612.2988	+0.275696	612.2988	6	G	7	732.3886	+0.058865	732.3886	
	669.3202		669.3202	7	G	6	675.3672		675.3672	
	782.4043		782.4043	8	I	5	618.3457		618.3457	
+0.154137	427.2243	+0.158567	853.4414	9	A	4	505.2617		505.2617	
	924.4785	+0.296929	924.4785	10	A	3	434.2245	+0.378549	434.2245	
	1011.511	+0.259042	1011.511	11	S	2	363.1874		363.1874	
	1140.553		1140.553	12	E	1	276.1554		276.1554	
				13	K	0	147.1128		147.1128	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber: 16174
Protein: BSU07750; yflA
Peptide Score: 93.48
Method: ITMS; CID; 3



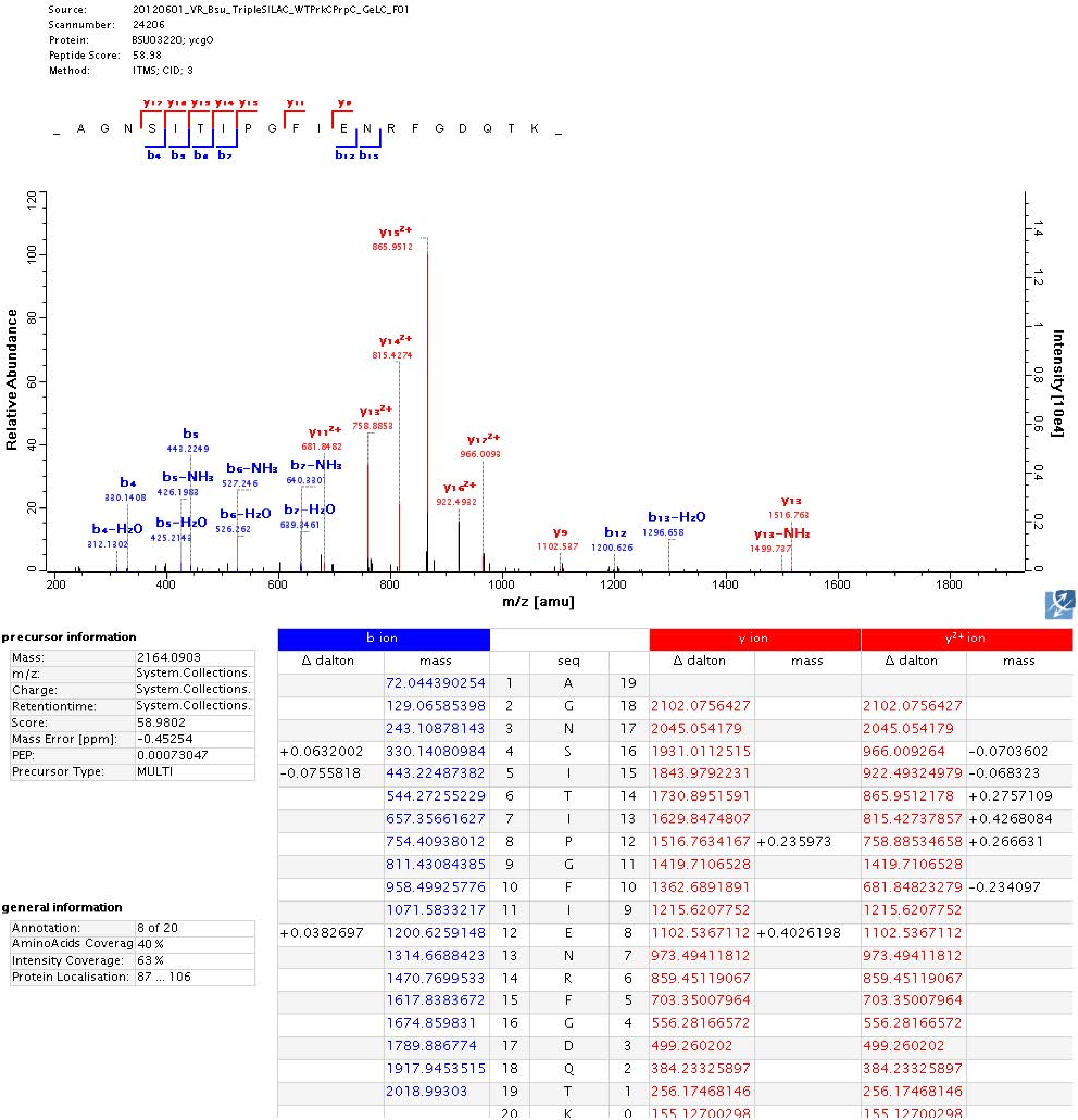
precursor information

Mass:	1871.85024
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.47838
Mass Error [ppm]:	0.60346
PEP:	0.0024812
Precursor Type:	ISO

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	38 %
Protein Localisation:	126 ... 141

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	15				
	244.0928		244.0928	2	E	14	1758.813		1758.813	
	372.1514		372.1514	3	Q	13	1629.771	+0.457524	1629.771	
	429.1728		429.1728	4	G	12	1501.712	+0.206043	1501.712	
	558.2154		558.2154	5	E	11	1444.691		1444.691	
	721.2788	+0.358752	721.2788	6	Y	10	1315.648	+0.236042	1315.648	
	820.3472	+0.151911	820.3472	7	V	9	1152.585	-0.126533	1152.585	
+0.20102	439.188	+0.207046	877.3686	8	G	8	1053.516	+0.028673	527.2619	+0.2903
	934.3901		934.3901	9	G	7	996.495	+0.153469	996.495	
	1031.443		1031.443	10	P	6	939.4736		939.4736	
-0.470309	589.7428		1178.478	11	M	5	842.4208		842.4208	
	1341.542	+0.261142	1341.542	12	Y	4	695.3854		695.3854	
	1504.605		1504.605	13	Y	3	532.3221		532.3221	
	1617.689	+0.220805	1617.689	14	I	2	369.2587	-0.101488	369.2587	
	1718.737		1718.737	15	T	1	256.1747		256.1747	
				16	K	0	155.127		155.127	



Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber: 24206
Protein: BSU03220; ycgO
Peptide Score: 58.98
Method: ITMS; CID; 3

precursor information

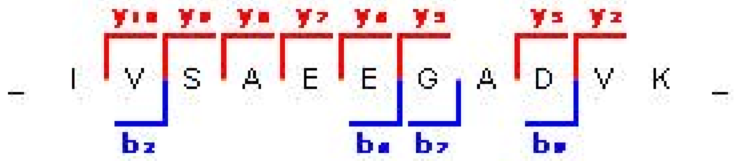
Mass:	2164.0903
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	58.9802
Mass Error [ppm]:	-0.45254
PEP:	0.00073047
Precursor Type:	MULTI

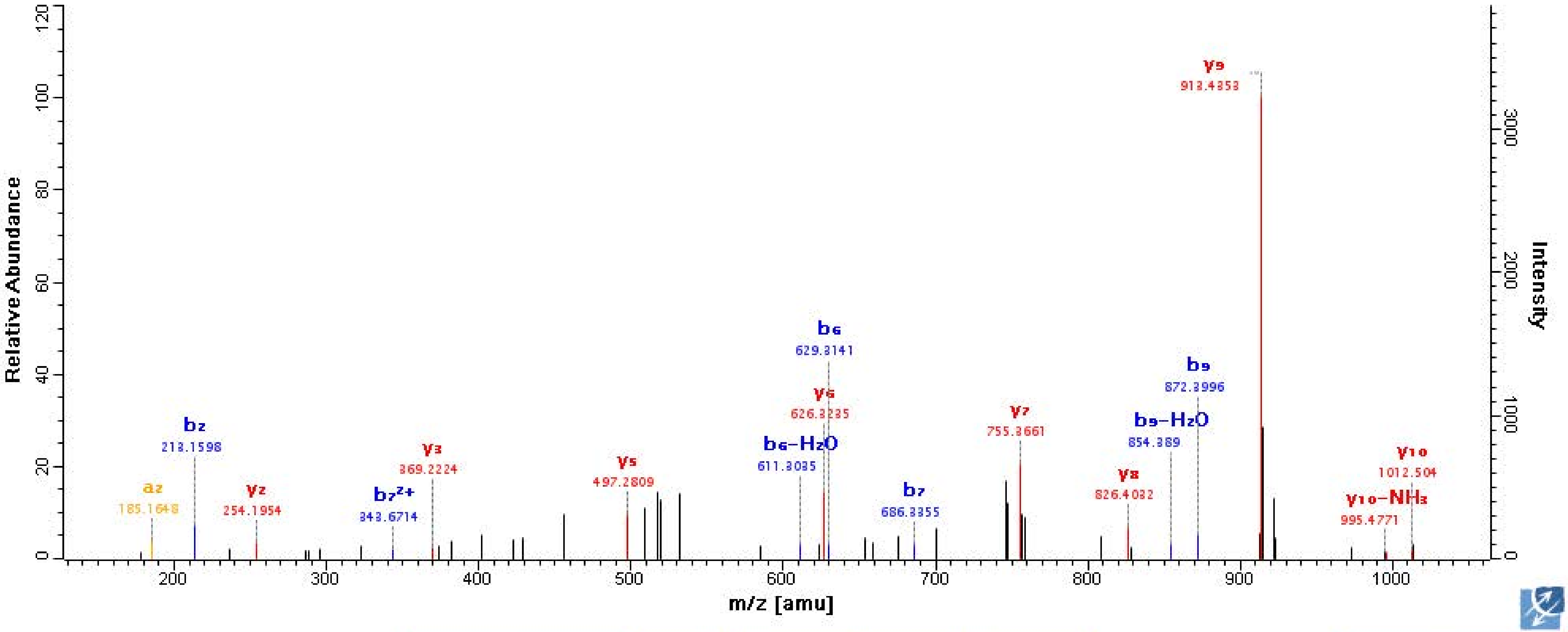
general information

Annotation:	8 of 20
AminoAcids Coverag	40 %
Intensity Coverage:	63 %
Protein Localisation:	87 ... 106

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	19				
	129.06585398	2	G	18	2102.0756427		2102.0756427	
	243.10878143	3	N	17	2045.054179		2045.054179	
+0.0632002	330.14080984	4	S	16	1931.0112515		966.009264	-0.0703602
-0.0755818	443.22487382	5	I	15	1843.9792231		922.49324979	-0.068323
	544.27255229	6	T	14	1730.8951591		865.9512178	+0.2757109
	657.35661627	7	I	13	1629.8474807		815.42737857	+0.4268084
	754.40938012	8	P	12	1516.7634167	+0.235973	758.88534658	+0.266631
	811.43084385	9	G	11	1419.7106528		1419.7106528	
	958.49925776	10	F	10	1362.6891891		681.84823279	-0.234097
	1071.5833217	11	I	9	1215.6207752		1215.6207752	
+0.0382697	1200.6259148	12	E	8	1102.5367112	+0.4026198	1102.5367112	
	1314.6688423	13	N	7	973.49411812		973.49411812	
	1470.7699533	14	R	6	859.45119067		859.45119067	
	1617.8383672	15	F	5	703.35007964		703.35007964	
	1674.859831	16	G	4	556.28166572		556.28166572	
	1789.886774	17	D	3	499.260202		499.260202	
	1917.9453515	18	Q	2	384.23325897		384.23325897	
	2018.99303	19	T	1	256.17468146		256.17468146	
		20	K	0	155.12700298		155.12700298	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber: 7906
Protein: BSU01680; ybbF
Peptide Score: 101.97
Method: ITMS; CID; 3





precursor information

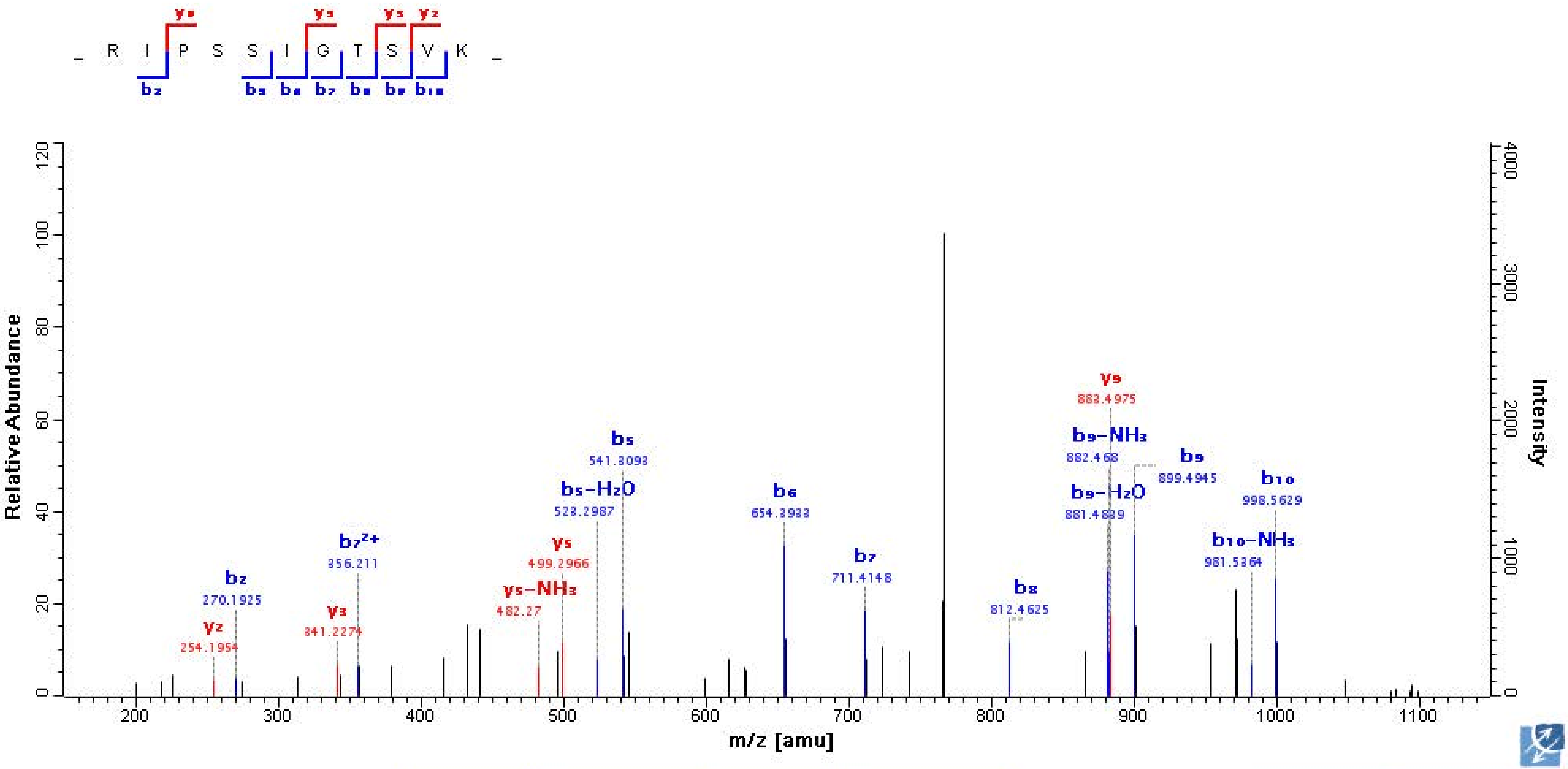
Mass:	1116.56649
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.9741
Mass Error [ppm]:	0.19375
PEP:	0.00041337
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	45 %
Protein Localisation:	83 ... 93

a ion		b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.09643		114.0913		114.0913	1	I	10		
-0.028335	185.1648		213.1598	+0.037908	213.1598	2	V	9	1012.504	+0.369489
	272.1969		300.1918		300.1918	3	S	8	913.4353	+0.00669
	343.234		371.2289		371.2289	4	A	7	826.4032	+0.019248
	472.2766		500.2715		500.2715	5	E	6	755.3661	-0.005589
	601.3192		629.3141	-0.003719	629.3141	6	E	5	626.3235	-0.020613
	658.3406	-0.428553	343.6714	+0.05514	686.3355	7	G	4	497.2809	+0.468513
	729.3777		757.3727		757.3727	8	A	3	440.2595	
	844.4047		872.3996	+0.322992	872.3996	9	D	2	369.2224	+0.051749
	943.4731		971.468		971.468	10	V	1	254.1954	+0.151156
						11	K	0	155.127	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F01
Scannumber:	8668
Protein:	BSU05680; ydgK
Peptide Score:	90.91
Method:	ITMS; CID; 3



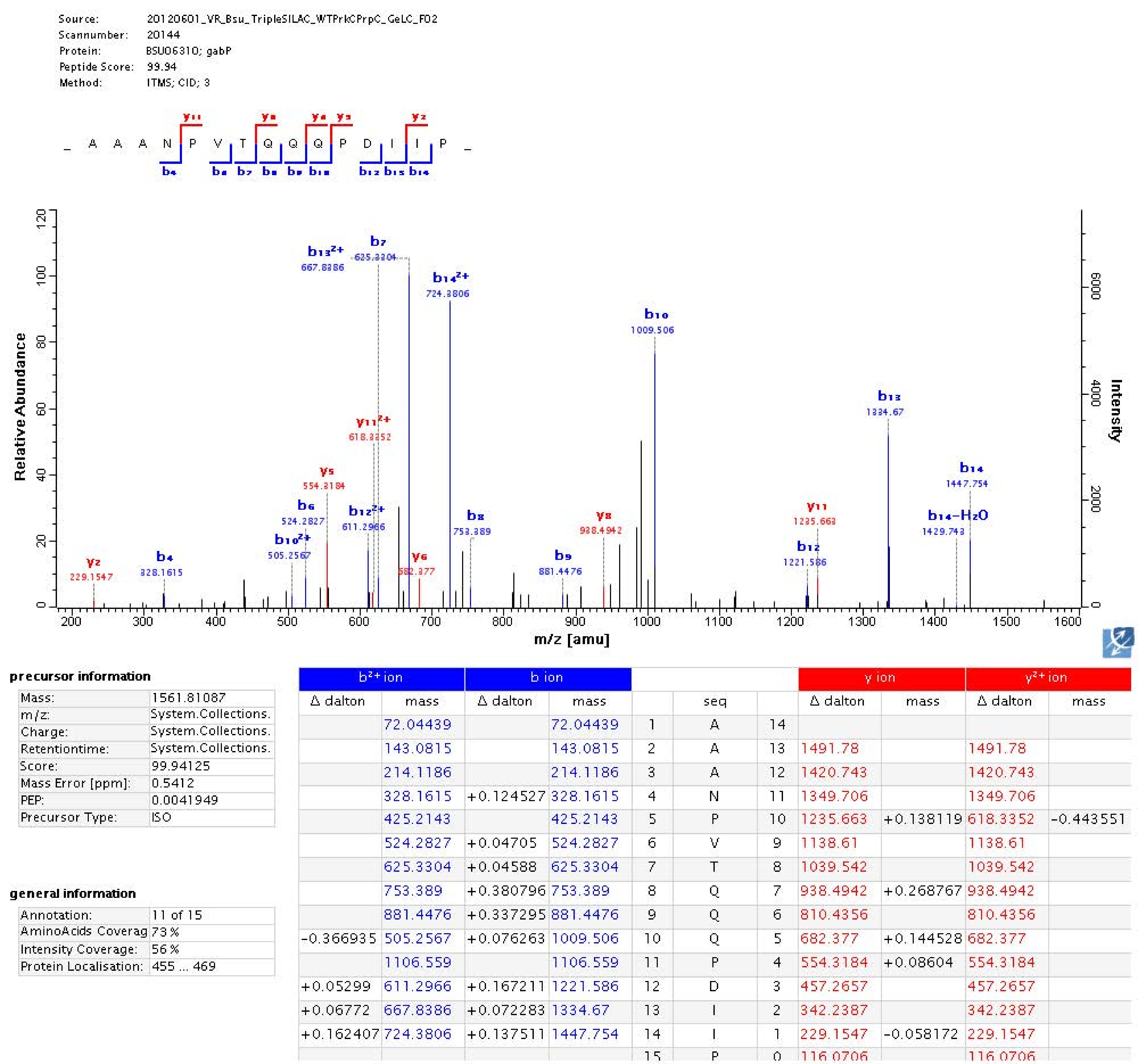
precursor information

Mass:	1143.66125
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.91307
Mass Error [ppm]:	0.071516
PEP:	0.0016635
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	38 %
Protein Localisation:	198 ... 208

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	157.10838749		157.10838749	1	R	10		
	270.19245148	+0.0606918	270.19245148	2	I	9	996.58153614	
	367.24521533		367.24521533	3	P	8	883.49747216	+0.0647227
	454.27724374		454.27724374	4	S	7	786.44470831	
	541.30927215	+0.0076834	541.30927215	5	S	6	699.4126799	
	654.39333613	+0.1401722	654.39333613	6	I	5	612.38065149	
-0.0316558	356.21103816	-0.0025684	711.41479985	7	G	4	499.29658751	+0.0970893
	812.46247833	+0.0169528	812.46247833	8	T	3	442.27512378	
	899.49450673	-0.0045775	899.49450673	9	S	2	341.22744531	+0.1413901
	998.56292065	+0.011054	998.56292065	10	V	1	254.1954169	+0.0381036
				11	K	0	155.12700298	



Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F02
Scannumber:	20144
Protein:	BSU06310; gabP
Peptide Score:	99.94
Method:	ITMS; CID; 3

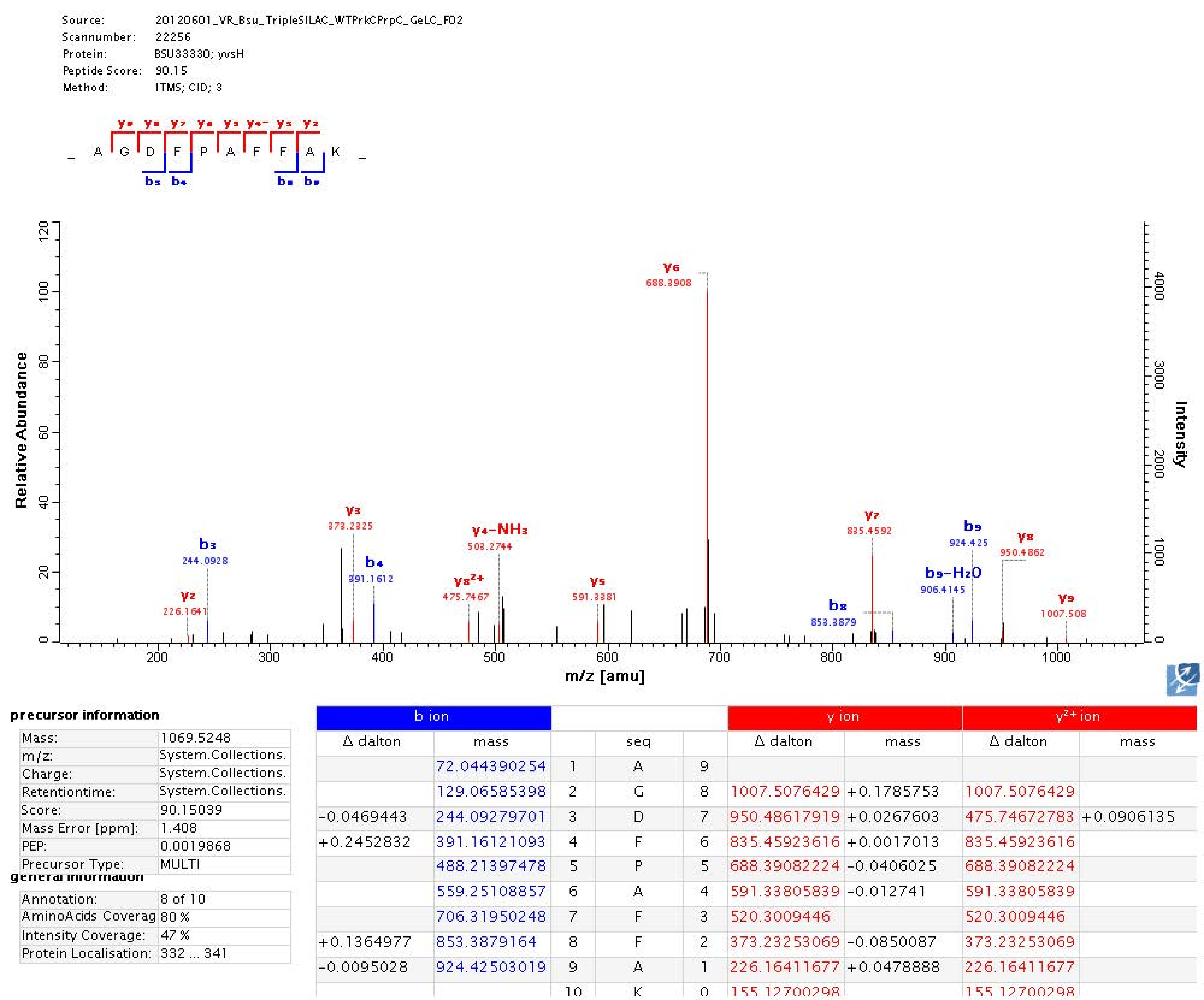
precursor information

Mass:	1561.81087
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	99.94125
Mass Error [ppm]:	0.5412
PEP:	0.0041949
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	56 %
Protein Localisation:	455 ... 469

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	14				
	143.0815		143.0815	2	A	13	1491.78		1491.78	
	214.1186		214.1186	3	A	12	1420.743		1420.743	
	328.1615	+0.124527	328.1615	4	N	11	1349.706		1349.706	
	425.2143		425.2143	5	P	10	1235.663	+0.138119	618.3352	-0.443551
	524.2827	+0.04705	524.2827	6	V	9	1138.61		1138.61	
	625.3304	+0.04588	625.3304	7	T	8	1039.542		1039.542	
	753.389	+0.380796	753.389	8	Q	7	938.4942	+0.268767	938.4942	
	881.4476	+0.337295	881.4476	9	Q	6	810.4356		810.4356	
-0.366935	505.2567	+0.076263	1009.506	10	Q	5	682.377	+0.144528	682.377	
	1106.559		1106.559	11	P	4	554.3184	+0.08604	554.3184	
+0.05299	611.2966	+0.167211	1221.586	12	D	3	457.2657		457.2657	
+0.06772	667.8386	+0.072283	1334.67	13	I	2	342.2387		342.2387	
+0.162407	724.3806	+0.137511	1447.754	14	I	1	229.1547	-0.058172	229.1547	
				15	P	0	116.0706		116.0706	



Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F02
Scannumber:	22256
Protein:	BSU33330; yvsH
Peptide Score:	90.15
Method:	ITMS; CID; 3

precursor information

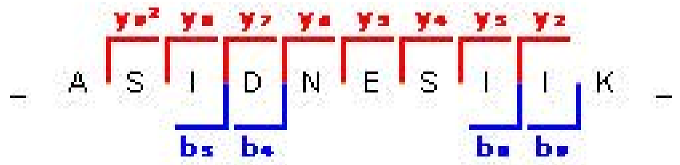
Mass:	1069.5248
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.15039
Mass Error [ppm]:	1.408
PEP:	0.0019868
Precursor Type:	MULTI

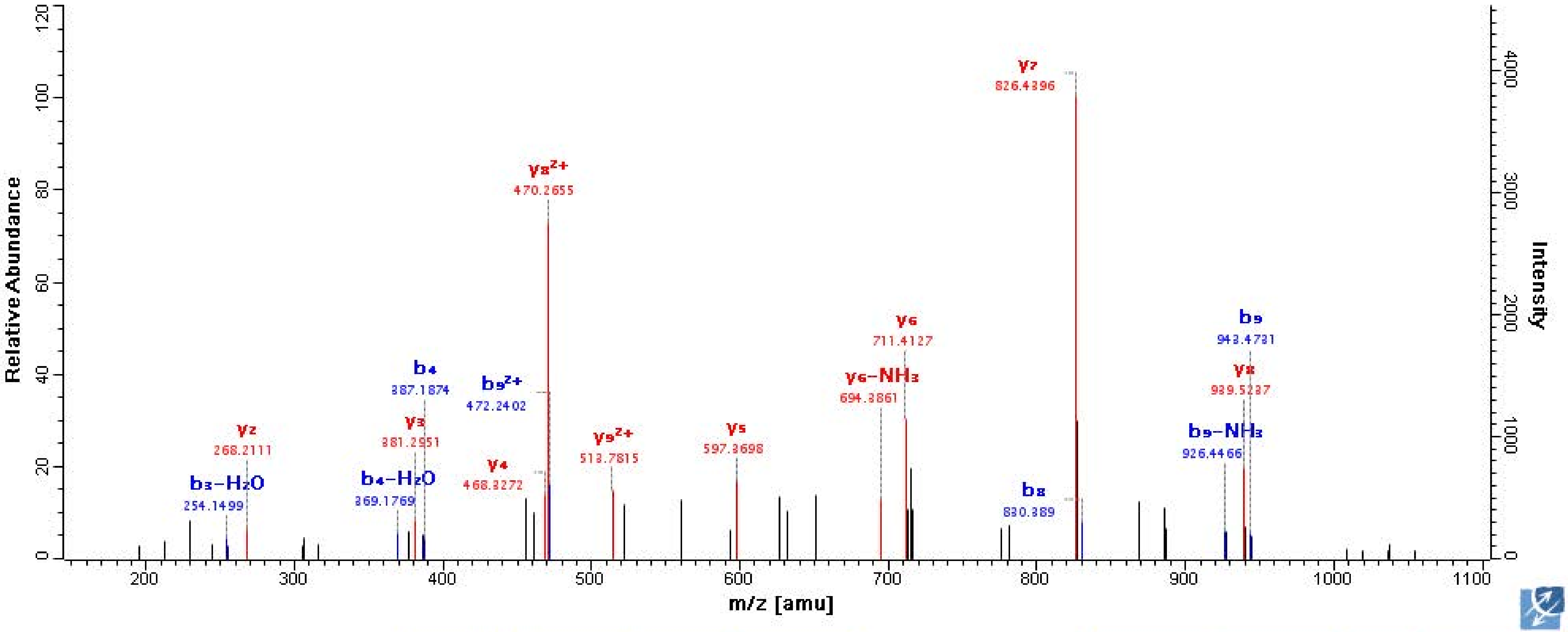
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	47 %
Protein Localisation:	332 ... 341

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	9				
	129.06585398	2	G	8	1007.5076429	+0.1785753	1007.5076429	
-0.0469443	244.09279701	3	D	7	950.48617919	+0.0267603	475.74672783	+0.0906135
+0.2452832	391.16121093	4	F	6	835.45923616	+0.0017013	835.45923616	
	488.21397478	5	P	5	688.39082224	-0.0406025	688.39082224	
	559.25108857	6	A	4	591.33805839	-0.012741	591.33805839	
	706.31950248	7	F	3	520.3009446		520.3009446	
+0.1364977	853.3879164	8	F	2	373.23253069	-0.0850087	373.23253069	
-0.0095028	924.42503019	9	A	1	226.16411677	+0.0478888	226.16411677	
		10	K	0	155.12700298		155.12700298	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F03
Scannumber: 12622
Protein: BSU03670; yclF
Peptide Score: 109.29
Method: ITMS; CID; 3





precursor information

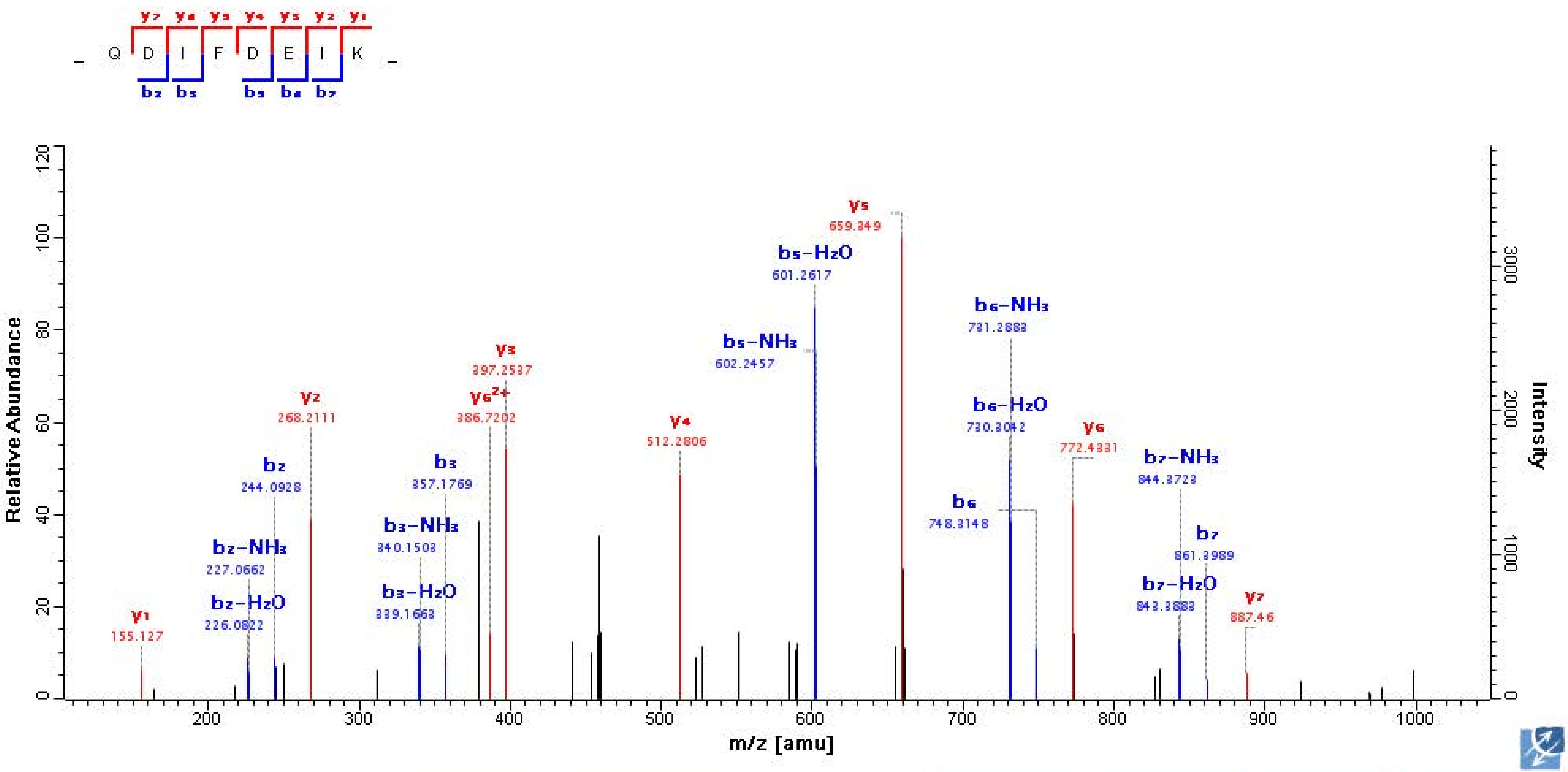
Mass:	1088.5701
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.2901
Mass Error [ppm]:	-1.1439
PEP:	1.6686E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	55 %
Protein Localisation:	2 ... 11

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				
	159.0764		159.0764	2	S	8	1026.556		513.7815	+0.397581
	272.1605		272.1605	3	I	7	939.5237	+0.227656	470.2655	+0.165671
	387.1874	-0.071306	387.1874	4	D	6	826.4396	+0.068983	826.4396	
	501.2304		501.2304	5	N	5	711.4127	+0.043863	711.4127	
	630.2729		630.2729	6	E	4	597.3698	+0.255614	597.3698	
	717.305		717.305	7	S	3	468.3272	+0.208668	468.3272	
	830.389	+0.398071	830.389	8	I	2	381.2951	+0.002782	381.2951	
-0.497392	472.2402	+0.205181	943.4731	9	I	1	268.2111	+0.06408	268.2111	
				10	K	0	155.127		155.127	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F04
Scannumber:	21953
Protein:	BSU19340; yocR
Peptide Score:	160.11
Method:	ITMS; CID; 3

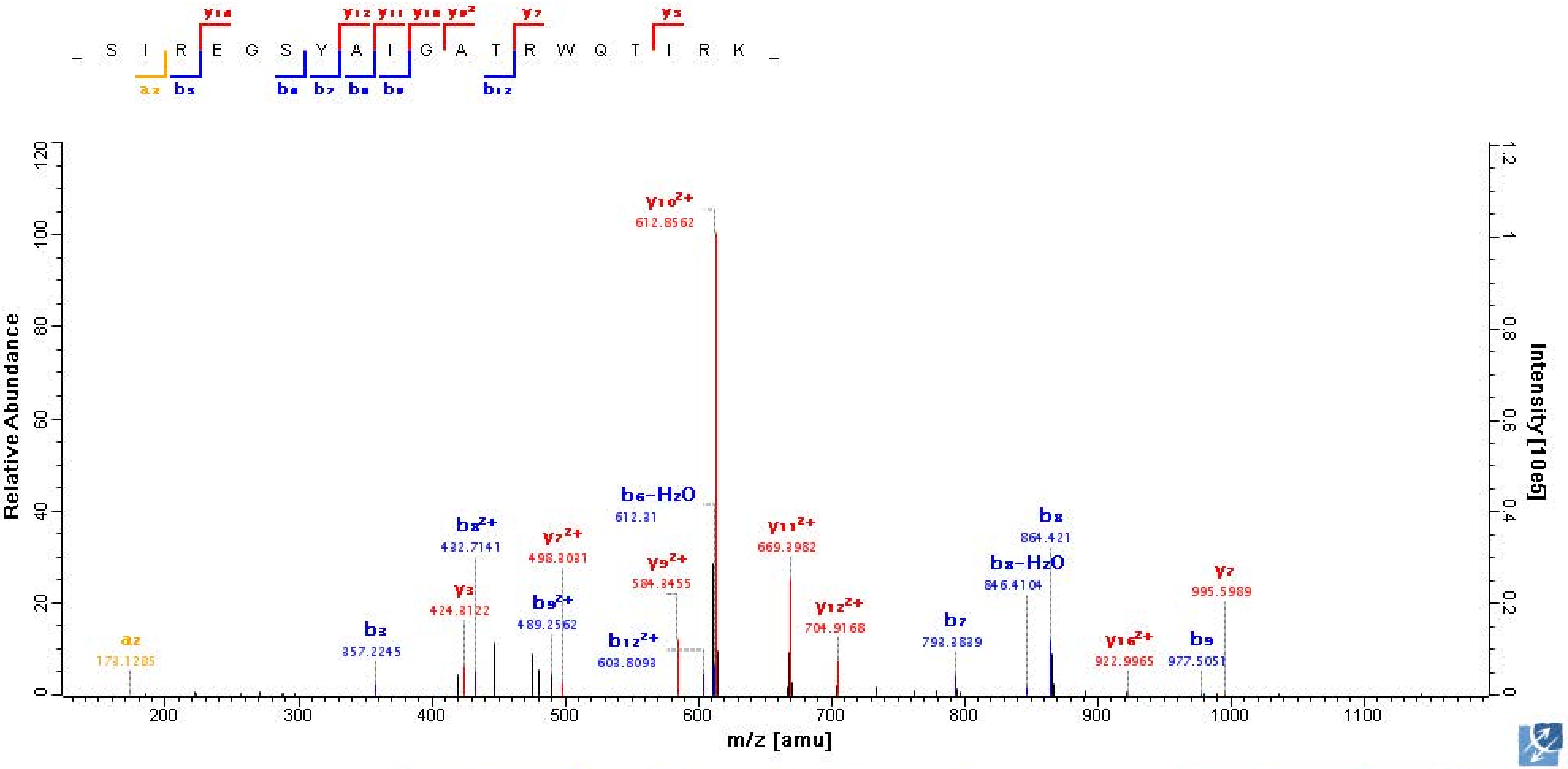


precursor information

Mass:	1014.51089
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.1061
Mass Error [ppm]:	-0.42646
PEP:	6.7702E-20
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	67 %
Protein Localisation:	402 ... 409

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398	1	Q	7				
+0.1287148	244.09279701	2	D	6	887.46002402	+0.361204	887.46002402	
+0.1053656	357.17686099	3	I	5	772.43308099	+0.0243165	386.72017873	-0.0203496
	504.24527491	4	F	4	659.34901701	+0.0063907	659.34901701	
	619.27221794	5	D	3	512.28060309	-0.0275513	512.28060309	
+0.1211021	748.31481103	6	E	2	397.25366006	-0.0252055	397.25366006	
+0.2546284	861.39887502	7	I	1	268.21106696	+0.0383227	268.21106696	
		8	K	0	155.12700298	+0.0842244	155.12700298	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F06
Scannumber: 14655
Protein: BSU24980; yqgH; yzmC
Peptide Score: 63.68
Method: ITMS; CID; 3



precursor information

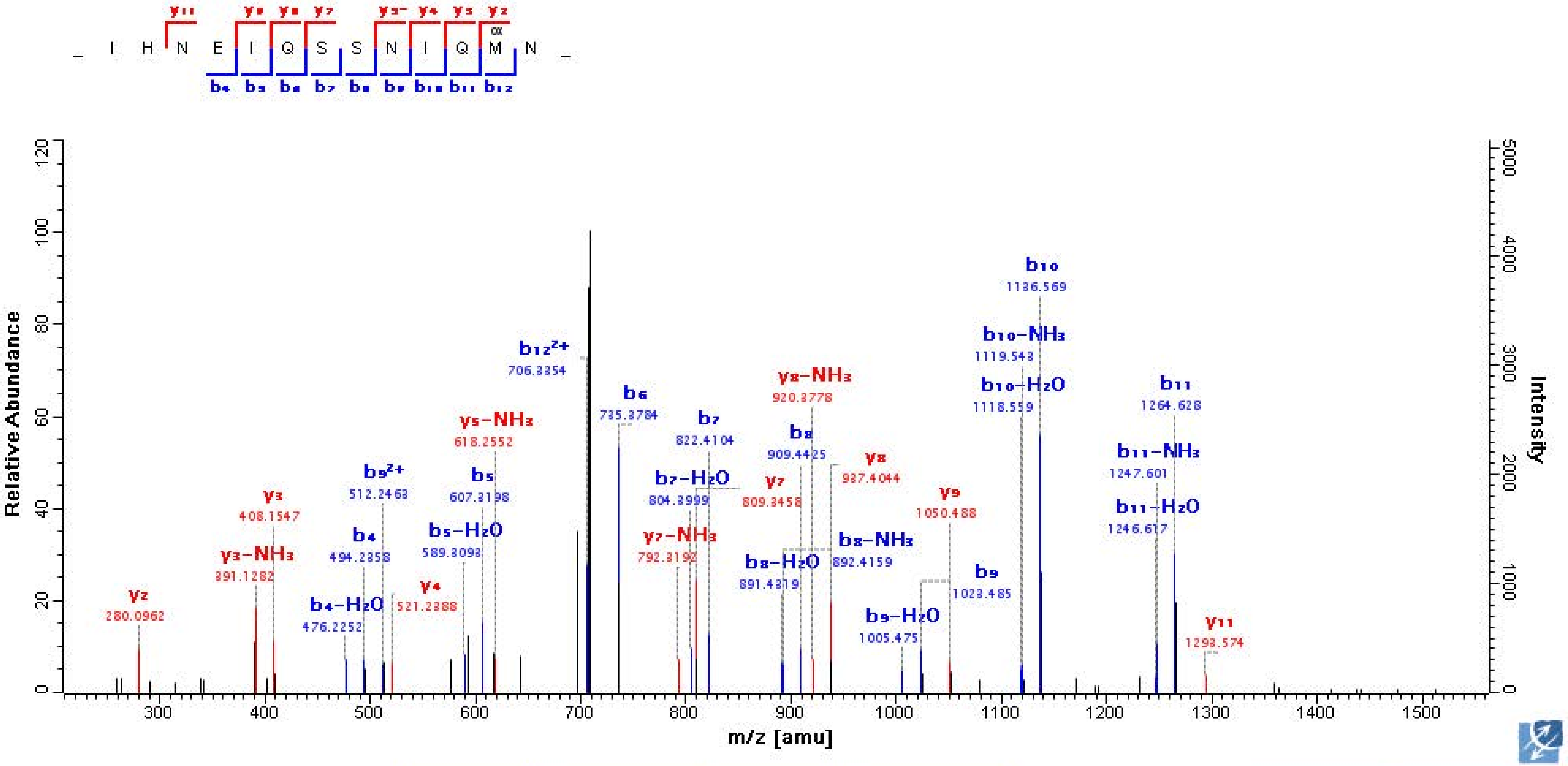
Mass:	2192.18274
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.68069
Mass Error [ppm]:	0.59222
PEP:	0.00045821
Precursor Type:	MULTI

general information

Annotation:	12 of 19
AminoAcids Coverag	63 %
Intensity Coverage:	63 %
Protein Localisation:	194 ... 212

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
	60.0444		88.0393		88.0393	1	S	18				
+0.14788	173.128		201.123		201.123	2	I	17	2114.17		2114.17	
	329.23		357.224	+0.05268	357.224	3	R	16	2001.09		2001.09	
	458.272		486.267		486.267	4	E	15	1844.99		922.996	-0.3499
	515.294		543.289		543.289	5	G	14	1715.94		1715.94	
	602.326		630.321		630.321	6	S	13	1658.92		1658.92	
	765.389		793.384	+0.1714	793.384	7	Y	12	1571.89		1571.89	
	836.426	+0.13632	432.714	+0.21663	864.421	8	A	11	1408.83		704.917	+0.3130
	949.51	+0.06737	489.256	+0.21203	977.505	9	I	10	1337.79		669.398	+0.3127
	1006.53		1034.53		1034.53	10	G	9	1224.71		612.856	+0.3164
	1077.57		1105.56		1105.56	11	A	8	1167.68		584.345	+0.2550
	1178.62	+0.20925	603.809		1206.61	12	T	7	1096.65		1096.65	
	1334.72		1362.71		1362.71	13	R	6	995.599	+0.1335	498.303	+0.2509
	1520.8		1548.79		1548.79	14	W	5	839.498		839.498	
	1648.86		1676.85		1676.85	15	Q	4	653.418		653.418	
	1749.9		1777.9		1777.9	16	T	3	525.36		525.36	
	1862.99		1890.98		1890.98	17	I	2	424.312	-0.3879	424.312	
	2019.09		2047.08		2047.08	18	R	1	311.228		311.228	
						19	K	0	155.127		155.127	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F11
Scannumber:	10834
Protein:	BSU17950; ccdC; yneJ; yoxI
Peptide Score:	210.79
Method:	ITMS; CID; 3



precursor information

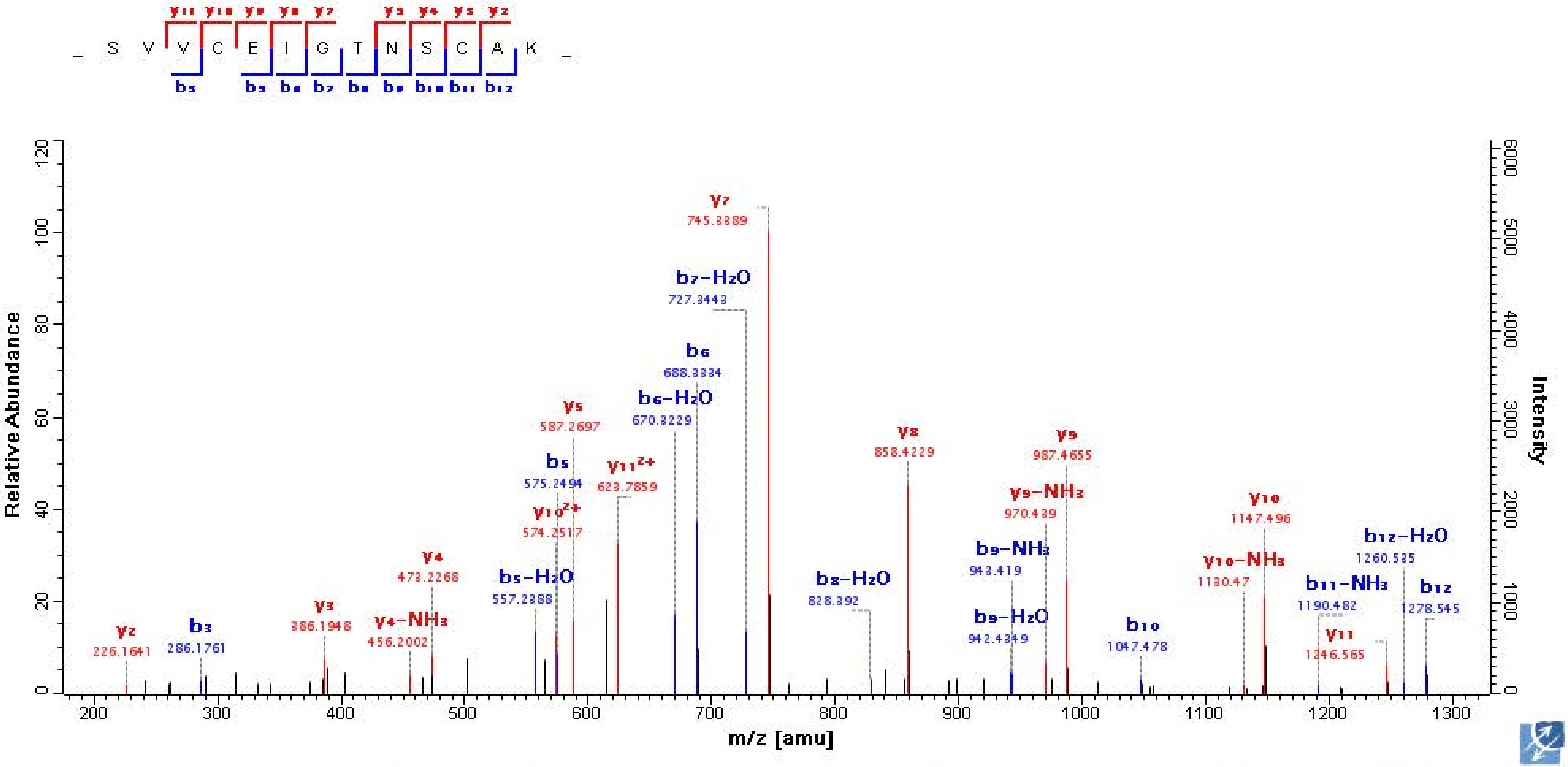
Mass:	1542.70884
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	210.7892
Mass Error [ppm]:	-0.52736
PEP:	3.2071E-151
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	50 %
Protein Localisation:	148 ... 160

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	12		
	251.15025231		251.15025231	2	H	11	1430.6328675	
	365.19317976		365.19317976	3	N	10	1293.5739556	+0.1664008
	494.23577285	+0.1236021	494.23577285	4	E	9	1179.5310282	
	607.31983683	+0.0541256	607.31983683	5	I	8	1050.4884351	-0.0895093
	735.37841434	+0.0329626	735.37841434	6	Q	7	937.4043711	+0.0601064
	822.41044275	+0.0074039	822.41044275	7	S	6	809.34579359	+0.2085277
	909.44247116	+0.0027803	909.44247116	8	S	5	722.31376518	
+0.0977787	512.24633754	+0.1534564	1023.4853986	9	N	4	635.28173677	
	1136.5694626	+0.1021683	1136.5694626	10	I	3	521.23880932	+0.1695159
	1264.6280401	+0.2149775	1264.6280401	11	Q	2	408.15474534	+0.1047151
+0.2632139	706.3353579		1411.6634393	12	M	1	280.09616783	-0.0202706
				13	N	0	133.0607686	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F14
Scannumber: 12061
Protein: bdbB; BSU21440; yolK
Peptide Score: 148.18
Method: ITMS; CID; 3



precursor information

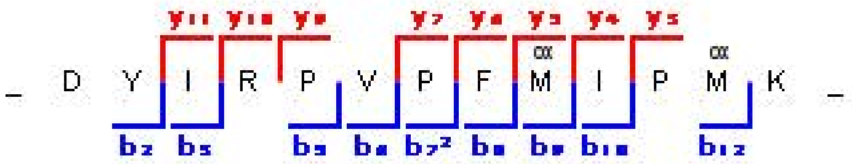
Mass:	1431.65779
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	148.1832
Mass Error [ppm]:	0.031506
PEP:	4.2653E-26
Precursor Type:	ISO

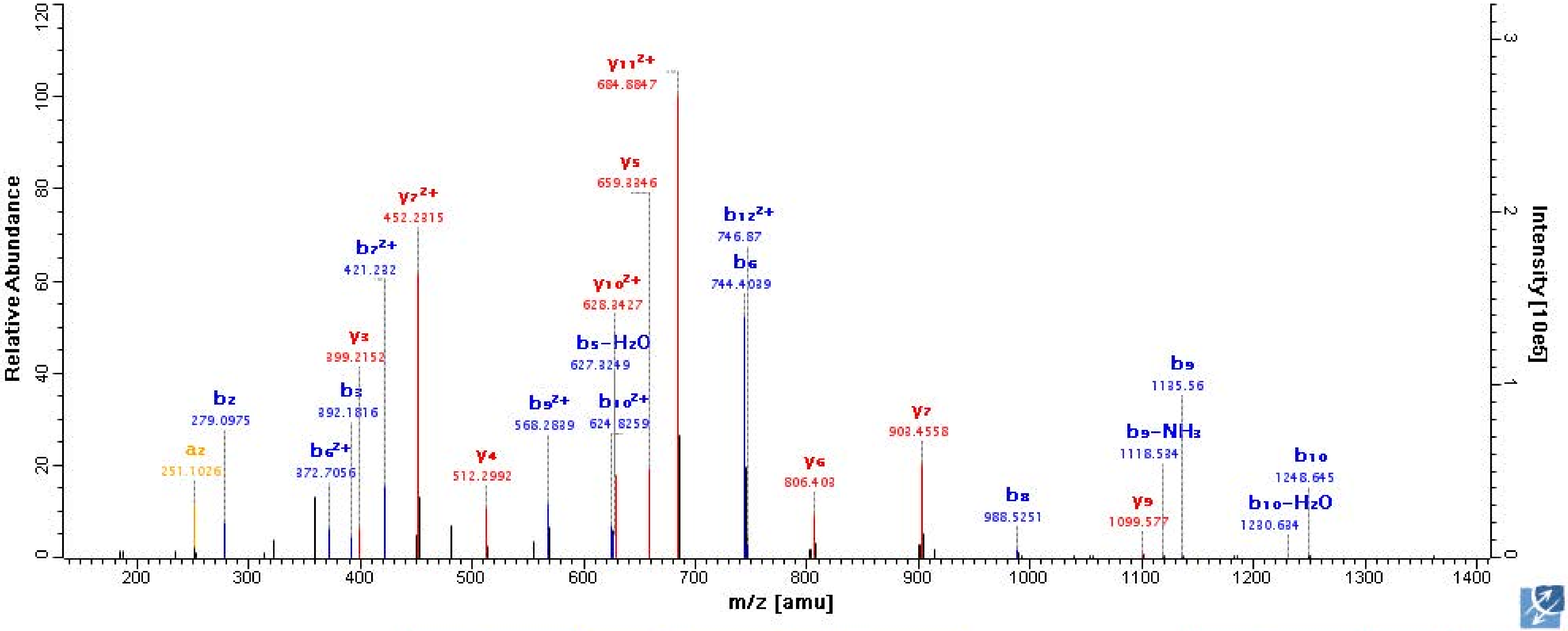
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	68 %
Protein Localisation:	92 ... 104

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	12				
	187.10771879	2	V	11	1345.6329961		1345.6329961	
+0.141067	286.17613271	3	V	10	1246.5645822	+0.0342947	623.78592934	-0.0417887
	446.20678091	4	C	9	1147.4961683	+0.094652	574.25172239	-0.2395154
-0.0501553	575.24937401	5	E	8	987.4655201	+0.0216625	987.4655201	
+0.1475801	688.33343799	6	I	7	858.42292701	-0.0813132	858.42292701	
	745.35490171	7	G	6	745.33886303	-0.0256306	745.33886303	
	846.40258018	8	T	5	688.3173993		688.3173993	
	960.44550763	9	N	4	587.26972083	+0.0501644	587.26972083	
+0.0448028	1047.477536	10	S	3	473.22679338	+0.117567	473.22679338	
	1207.5081842	11	C	2	386.19476497	+0.0209333	386.19476497	
-0.1344094	1278.545298	12	A	1	226.16411677	-0.1666802	226.16411677	
		13	K	0	155.12700298		155.12700298	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F14
Scannumber:	23661
Protein:	atpB; BSU36870
Peptide Score:	151.98
Method:	ITMS; CID; 3





precursor information

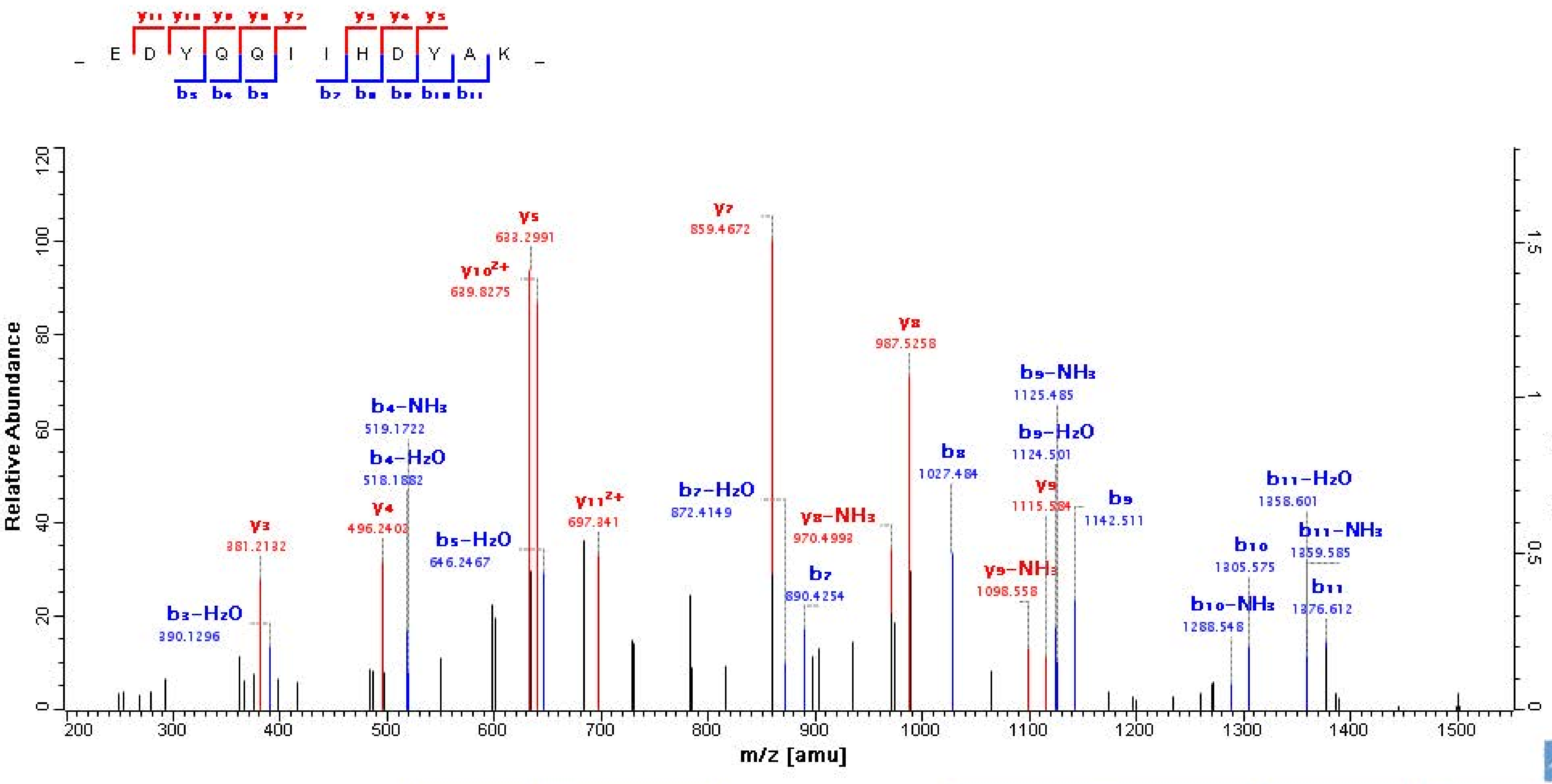
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	151.9761
Mass Error [ppm]:	-0.47648
PEP:	6.2859E-55
Precursor Type:	PEAK

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	64 %
Protein Localisation:	143 ... 155

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				
-0.0306	251.103		279.098	-0.0072	279.098	2	Y	11	1531.83		1531.83	
	364.187		392.182	+0.03671	392.182	3	I	10	1368.76		684.885	+0.0579
	520.288		548.283		548.283	4	R	9	1255.68		628.343	+0.2763
	617.341		645.335		645.335	5	P	8	1099.58	+0.15812	1099.58	
	716.409	+0.04289	372.706	+0.13156	744.404	6	V	7	1002.52		1002.52	
	813.462	+0.04488	421.232		841.457	7	P	6	903.456	+0.10266	452.232	+0.0714
	960.53		988.525	+0.18128	988.525	8	F	5	806.403	+0.12778	806.403	
	1107.57	+0.03363	568.284	+0.26057	1135.56	9	M	4	659.335	+0.06662	659.335	
	1220.65	+0.15145	624.826	+0.23095	1248.64	10	I	3	512.299	+0.09939	512.299	
	1317.7		1345.7		1345.7	11	P	2	399.215	+0.08739	399.215	
	1464.74	+0.22364	746.87		1492.73	12	M	1	302.162		302.162	
						13	K	0	155.127		155.127	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F16
Scannumber:	20538
Protein:	BSU12069; yjzH
Peptide Score:	135.99
Method:	ITMS; CID; 3



precursor information

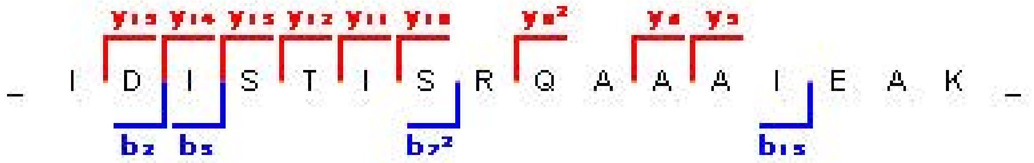
Mass:	1521.7086
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.9866
Mass Error [ppm]:	-0.90106
PEP:	1.9687E-16
Precursor Type:	MULTI

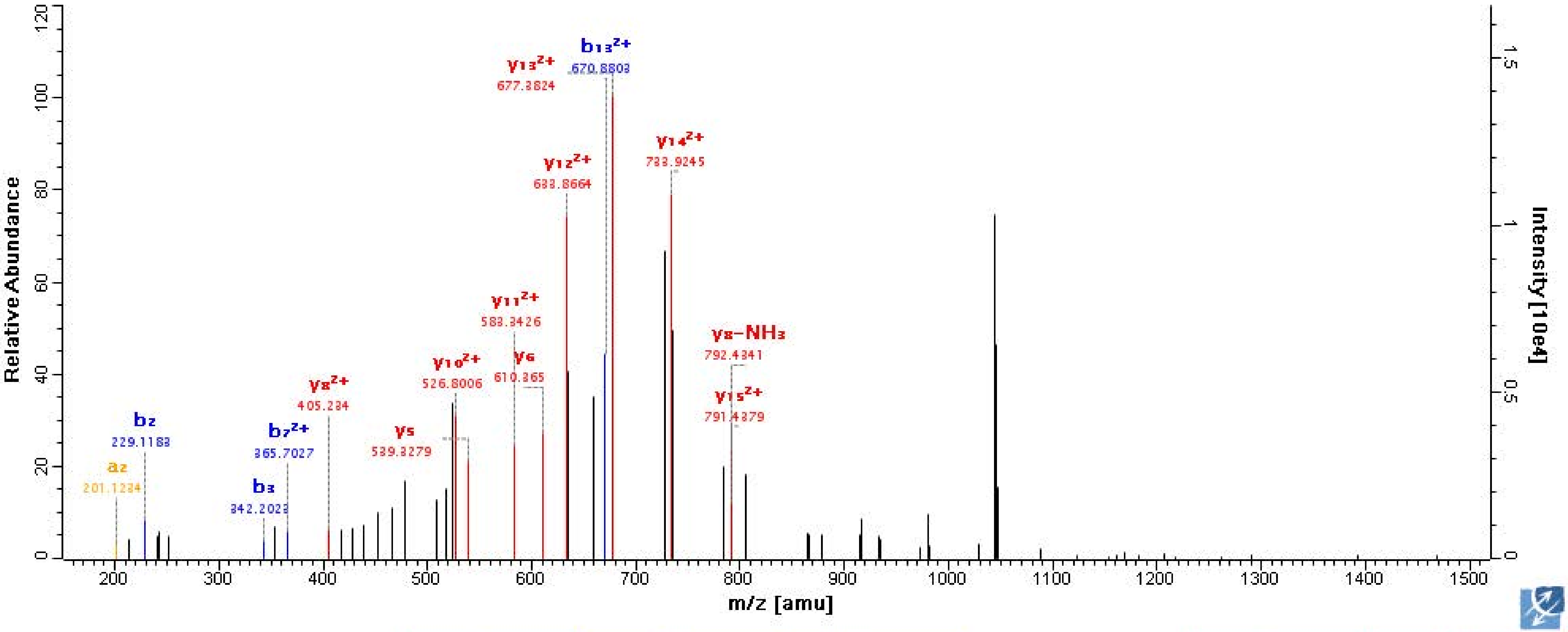
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	60 %
Protein Localisation:	20 ... 31

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	11				
	245.07681259	2	D	10	1393.6746559		697.34096621	+0.2408819
	408.14014113	3	Y	9	1278.6477129		639.82749469	+0.0582475
	536.19871864	4	Q	8	1115.5843844	+0.0364652	1115.5843844	
	664.25729616	5	Q	7	987.52580686	+0.0643421	987.52580686	
	777.34136014	6	I	6	859.46722935	+0.0498605	859.46722935	
+0.0486359	890.42542412	7	I	5	746.38316537		746.38316537	
+0.0342187	1027.484336	8	H	4	633.29910139	-0.0157762	633.29910139	
+0.1981936	1142.511279	9	D	3	496.24018953	-0.0195474	496.24018953	
+0.2045673	1305.5746075	10	Y	2	381.2132465	-0.063039	381.2132465	
+0.1175267	1376.6117213	11	A	1	218.14991796		218.14991796	
		12	K	0	147.11280417		147.11280417	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F16
Scannumber: 24698
Protein: BSU40010; S14D; yxaD
Peptide Score: 68
Method: ITMS; CID; 3





precursor information

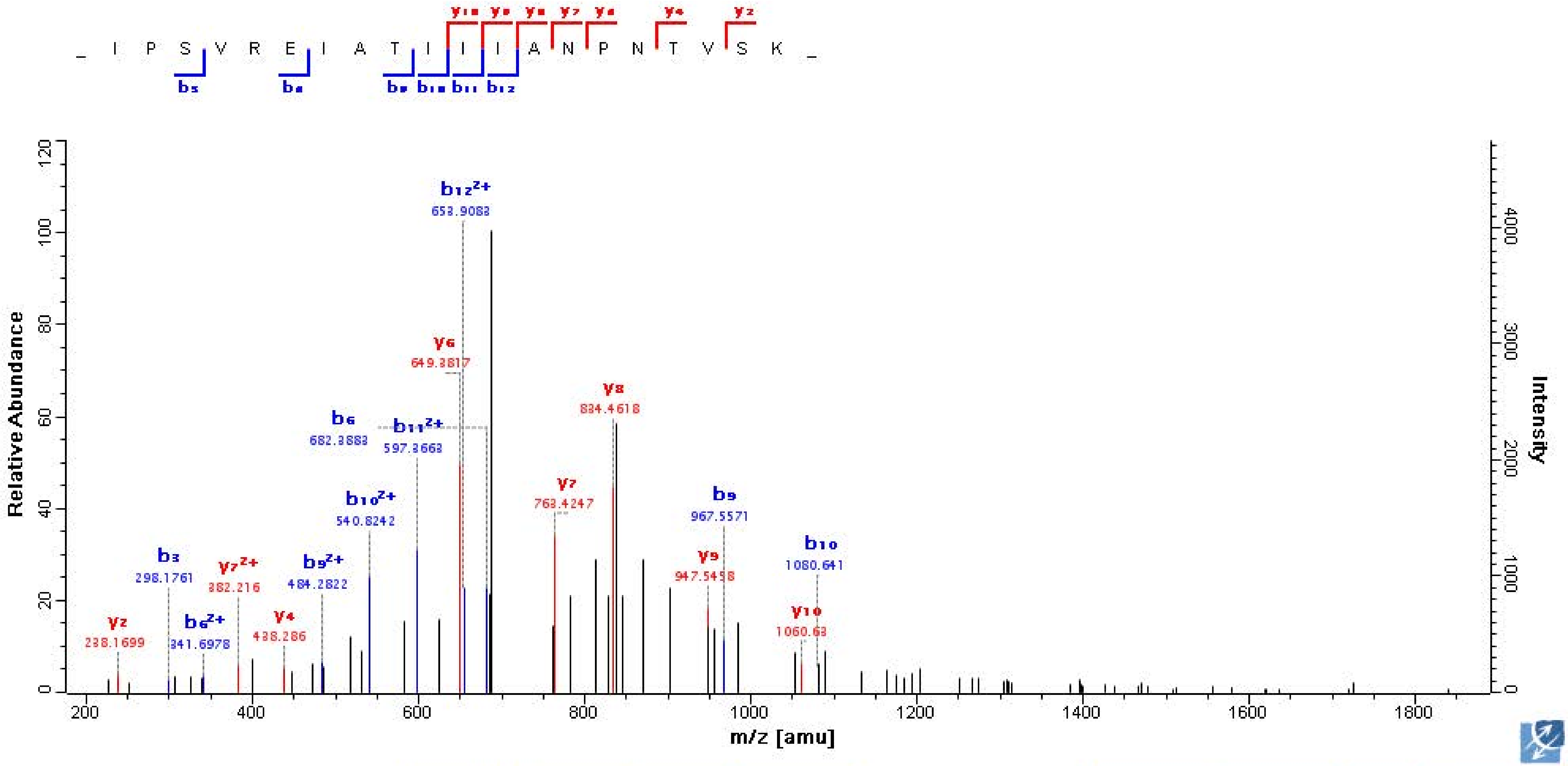
Mass:	1685.92989
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	67.99693
Mass Error [ppm]:	-0.77245
PEP:	0.00038885
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	43 %
Protein Localisation:	62 ... 77

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
	86.0964		114.091		114.091	1	I	15				
+0.13237	201.123		229.118	+0.07253	229.118	2	D	14	1581.87		791.438	+0.1685
	314.207		342.202	+0.16045	342.202	3	I	13	1466.84		733.924	+0.0870
	401.239		429.234		429.234	4	S	12	1353.76		677.382	+0.1050
	502.287		530.282		530.282	5	T	11	1266.73		633.866	-0.1194
	615.371		643.366		643.366	6	I	10	1165.68		583.343	+0.2849
	702.403	-0.202	365.703		730.398	7	S	9	1052.59		526.801	+0.2856
	858.504		886.499		886.499	8	R	8	965.562		965.562	
	986.563		1014.56		1014.56	9	Q	7	809.461		405.234	+0.3778
	1057.6		1085.59		1085.59	10	A	6	681.402		681.402	
	1128.64		1156.63		1156.63	11	A	5	610.365	+0.07311	610.365	
	1199.67		1227.67		1227.67	12	A	4	539.328	+0.10442	539.328	
	1312.76	-0.19	670.88		1340.75	13	I	3	468.291		468.291	
	1441.8		1469.8		1469.8	14	E	2	355.207		355.207	
	1512.84		1540.83		1540.83	15	A	1	226.164		226.164	
						16	K	0	155.127		155.127	

Source: 20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F16
Scannumber: 29503
Protein: BSU30460; ytrA
Peptide Score: 64.27
Method: ITMS; CID; 3



precursor information

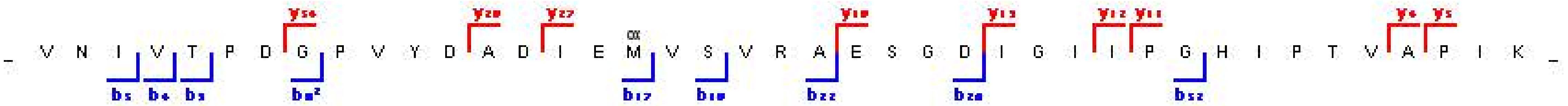
Mass:	2135.23393
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	64.27496
Mass Error [ppm]:	1.1825
PEP:	0.00030871
Precursor Type:	MULTI

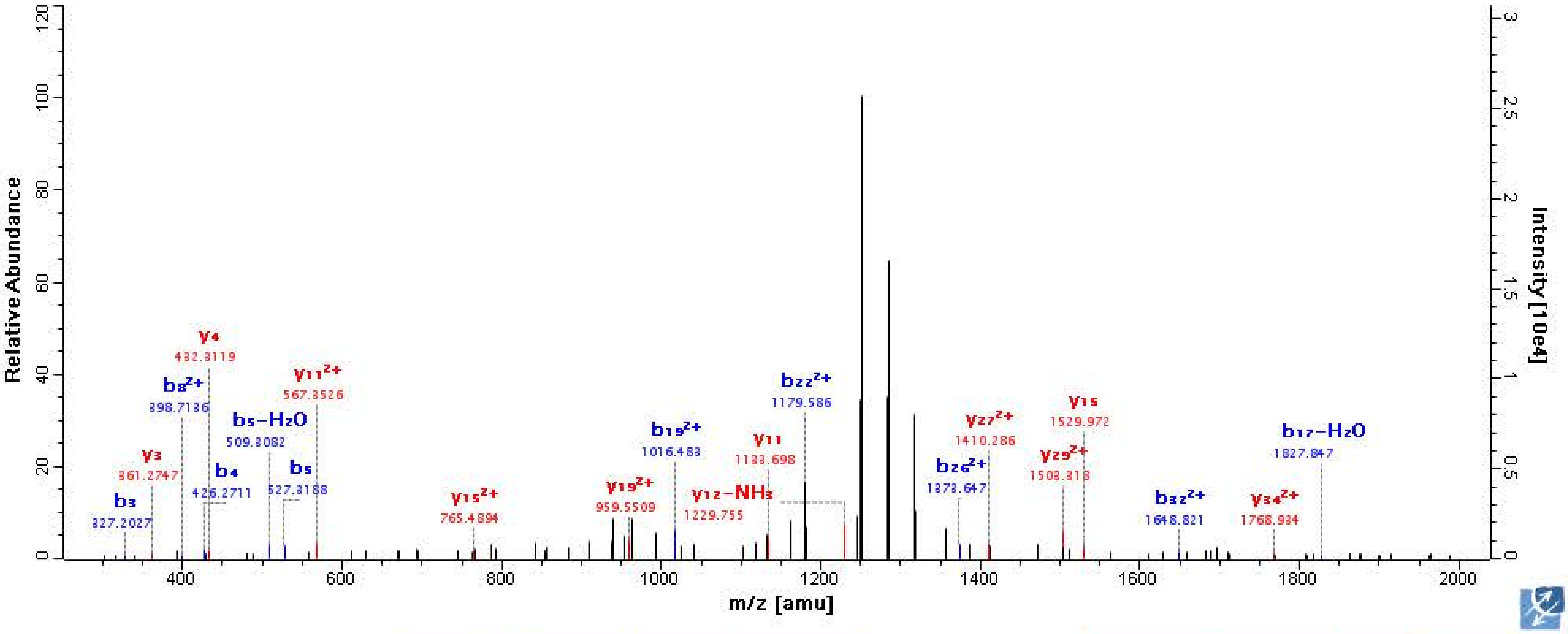
general information

Annotation:	11 of 20
AminoAcids Coverag	55 %
Intensity Coverage:	35 %
Protein Localisation:	35 ... 54

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	19				
	211.1441		211.1441	2	P	18	2027.18		2027.18	
	298.1761	+0.068496	298.1761	3	S	17	1930.127		1930.127	
	397.2445		397.2445	4	V	16	1843.095		1843.095	
	553.3457		553.3457	5	R	15	1744.027		1744.027	
-0.146006	341.6978	-0.010687	682.3883	6	E	14	1587.925		1587.925	
	795.4723		795.4723	7	I	13	1458.883		1458.883	
	866.5094		866.5094	8	A	12	1345.799		1345.799	
-0.018032	484.2822	+0.14083	967.5571	9	T	11	1274.762		1274.762	
-0.032354	540.8242	+0.136539	1080.641	10	I	10	1173.714		1173.714	
+0.044938	597.3663		1193.725	11	I	9	1060.63	+0.205801	1060.63	
+0.373695	653.9083		1306.809	12	I	8	947.5458	-0.009146	947.5458	
	1377.846		1377.846	13	A	7	834.4618	+0.021085	834.4618	
	1491.889		1491.889	14	N	6	763.4247	+0.024019	382.216	+0.021402
	1588.942		1588.942	15	P	5	649.3817	-0.000315	649.3817	
	1702.985		1702.985	16	N	4	552.329		552.329	
	1804.033		1804.033	17	T	3	438.286	-0.01943	438.286	
	1903.101		1903.101	18	V	2	337.2384		337.2384	
	1990.133		1990.133	19	S	1	238.1699	+0.06619	238.1699	
				20	K	0	151.1379		151.1379	

Source:	20120601_VR_Bsu_TripleSILAC_WTPrkCPrpC_GeLC_F16
Scannumber:	30996
Protein:	atpC; BSU36800
Peptide Score:	40.41
Method:	ITMS; CID; 3





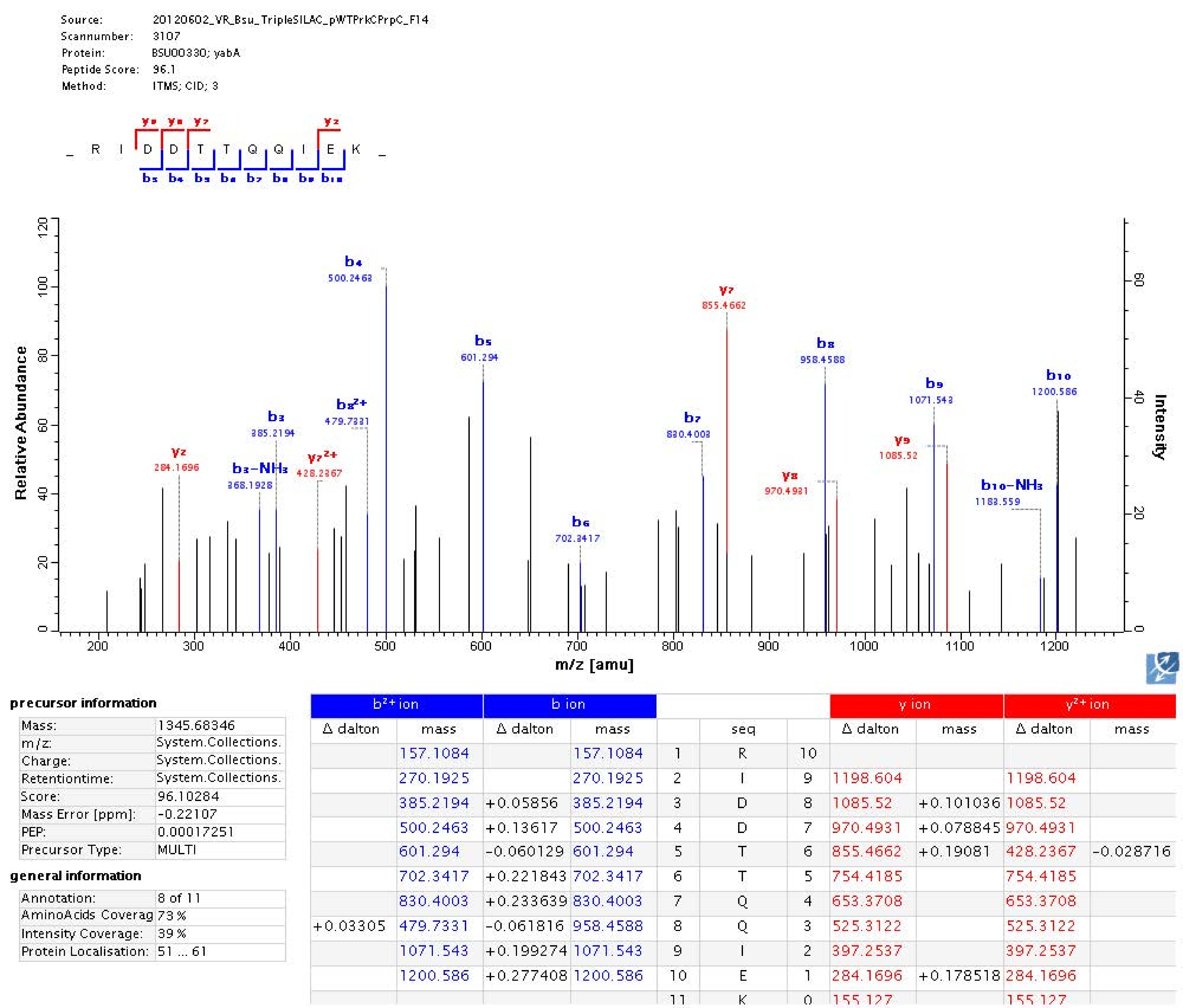
precursor information

Mass:	4274.2371
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	40.40741
Mass Error [ppm]:	-1.7632
PEP:	0.0037391
Precursor Type:	ISO

general information

Annotation:	17 of 41
AminoAcids Coverag	41 %
Intensity Coverage:	11 %
Protein Localisation:	6 ... 46

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	40				
	214.1186		214.1186	2	N	39	4176.183		4176.183	
	327.2027	+0.082078	327.2027	3	I	38	4062.141		4062.141	
	426.2711	+0.120262	426.2711	4	V	37	3949.057		3949.057	
	527.3188	+0.232984	527.3188	5	T	36	3849.988		3849.988	
	624.3715		624.3715	6	P	35	3748.94		3748.94	
	739.3985		739.3985	7	D	34	3651.888		3651.888	
-0.277972	398.7136		796.4199	8	G	33	3536.861		1768.934	+0.107026
	893.4727		893.4727	9	P	32	3479.839		3479.839	
	992.5411		992.5411	10	V	31	3382.786		3382.786	
	1155.604		1155.604	11	Y	30	3283.718		3283.718	
	1270.631		1270.631	12	D	29	3120.655		3120.655	
	1341.669		1341.669	13	A	28	3005.628		1503.318	+0.009615
	1456.695		1456.695	14	D	27	2934.591		2934.591	
	1569.78		1569.78	15	I	26	2819.564		1410.286	+0.331072
	1698.822		1698.822	16	E	25	2706.48		2706.48	
	1845.858		1845.858	17	M	24	2577.437		2577.437	
	1944.926		1944.926	18	V	23	2430.402		2430.402	
+0.485527	1016.483		2031.958	19	S	22	2331.333		2331.333	
	2131.026		2131.026	20	V	21	2244.301		2244.301	
	2287.127		2287.127	21	R	20	2145.233		2145.233	
+0.188604	1179.586		2358.165	22	A	19	1989.132		1989.132	
	2487.207		2487.207	23	E	18	1918.095		959.5509	+0.162687
	2574.239		2574.239	24	S	17	1789.052		1789.052	
	2631.261		2631.261	25	G	16	1702.02		1702.02	
+0.219131	1373.647		2746.288	26	D	15	1644.999		1644.999	
	2859.372		2859.372	27	I	14	1529.972	+0.039174	765.4894	+0.284809
	2916.393		2916.393	28	G	13	1416.888		1416.888	
	3029.477		3029.477	29	I	12	1359.866		1359.866	
	3142.561		3142.561	30	I	11	1246.782		1246.782	
	3239.614		3239.614	31	P	10	1133.698	+0.205042	567.3526	+0.498968
+0.105614	1648.821		3296.635	32	G	9	1036.645		1036.645	
	3433.694		3433.694	33	H	8	979.6237		979.6237	
	3546.778		3546.778	34	I	7	842.5648		842.5648	
	3643.831		3643.831	35	P	6	729.4807		729.4807	
	3744.879		3744.879	36	T	5	632.4279		632.4279	
	3843.947		3843.947	37	V	4	531.3803		531.3803	
	3914.984		3914.984	38	A	3	432.3119	+0.300299	432.3119	
	4012.037		4012.037	39	P	2	361.2747	+0.147319	361.2747	
	4125.121		4125.121	40	I	1	264.222		264.222	
				41	K	0	151.1379		151.1379	



Source:	20120602_VR_Bsu_TripleSILAC_pWTPrkCPrpC_F14
Scannumber:	3107
Protein:	BSU00330; yabA
Peptide Score:	96.1
Method:	ITMS; CID; 3

precursor information

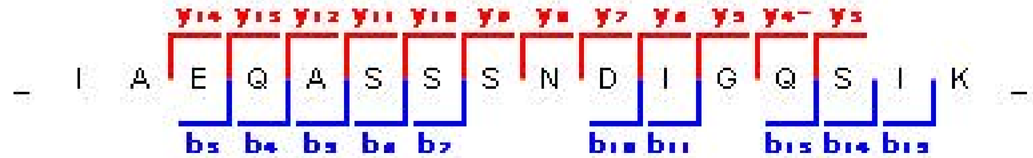
Mass:	1345.68346
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	96.10284
Mass Error [ppm]:	-0.22107
PEP:	0.00017251
Precursor Type:	MULTI

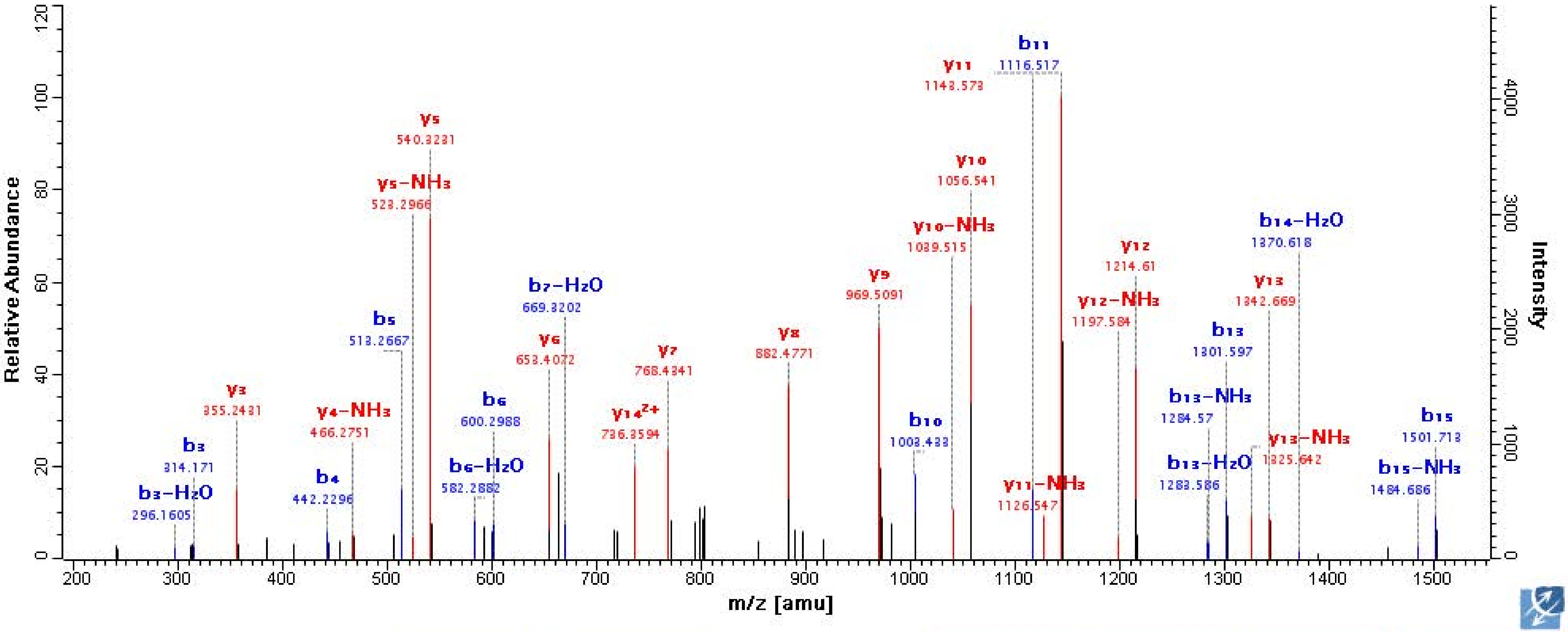
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	39 %
Protein Localisation:	51 ... 61

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	10				
	270.1925		270.1925	2	I	9	1198.604		1198.604	
	385.2194	+0.05856	385.2194	3	D	8	1085.52	+0.101036	1085.52	
	500.2463	+0.13617	500.2463	4	D	7	970.4931	+0.078845	970.4931	
	601.294	-0.060129	601.294	5	T	6	855.4662	+0.19081	428.2367	-0.028716
	702.3417	+0.221843	702.3417	6	T	5	754.4185		754.4185	
	830.4003	+0.233639	830.4003	7	Q	4	653.3708		653.3708	
+0.03305	479.7331	-0.061816	958.4588	8	Q	3	525.3122		525.3122	
	1071.543	+0.199274	1071.543	9	I	2	397.2537		397.2537	
	1200.586	+0.277408	1200.586	10	E	1	284.1696	+0.178518	284.1696	
				11	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F02
Scannumber: 10741
Protein: BSU34710; yvcQ
Peptide Score: 169.4
Method: ITMS; CID; 3





precursor information

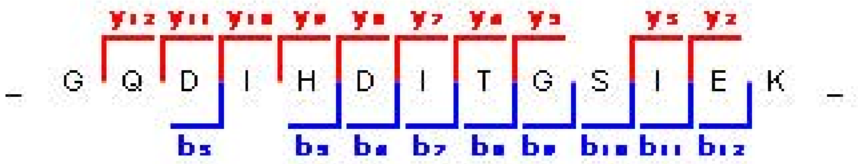
Mass:	1654.82517
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	169.3951
Mass Error [ppm]:	-0.10603
PEP:	3.8022E-65
Precursor Type:	ISO

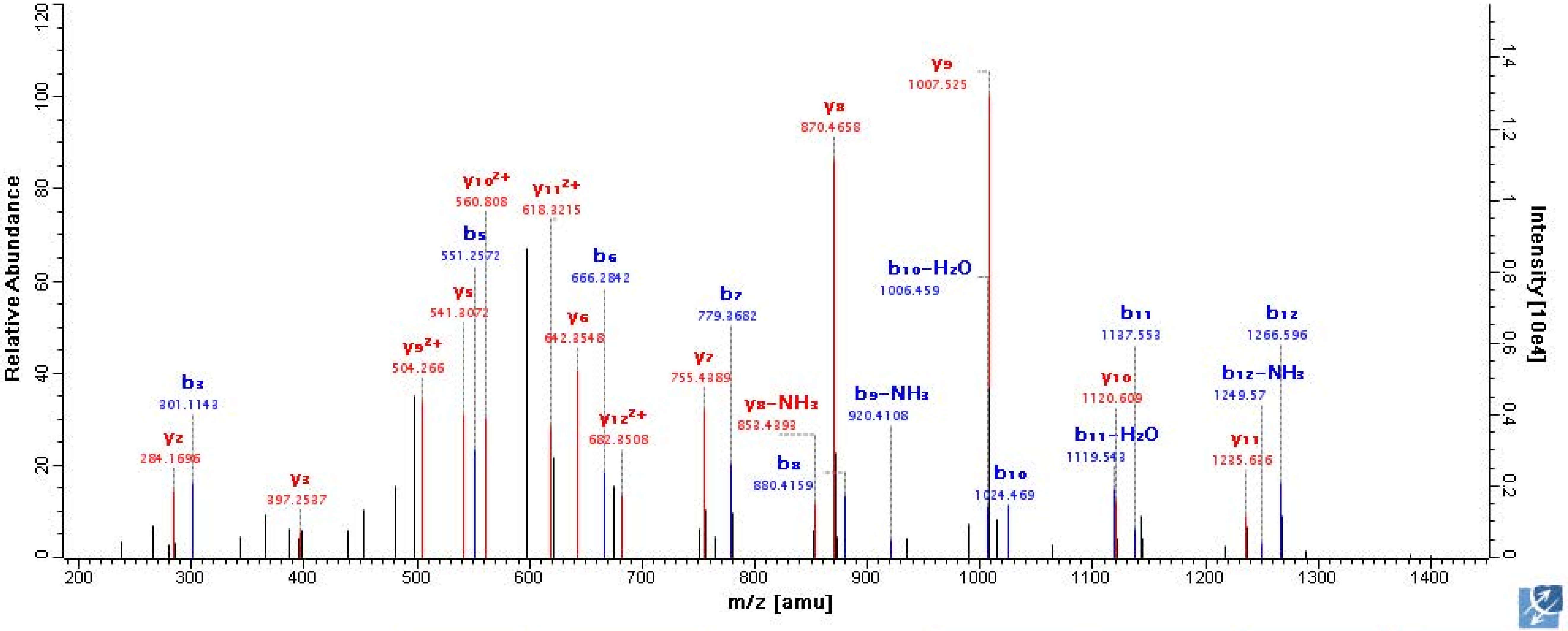
general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	62 %
Protein Localisation:	75 ... 90

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	15				
	185.12845423	2	A	14	1542.7485545		1542.7485545	
+0.0346106	314.17104733	3	E	13	1471.7114407		736.35935858	+0.1779339
-0.0043441	442.22962484	4	Q	12	1342.6688476	+0.1645264	1342.6688476	
-0.0196683	513.26673863	5	A	11	1214.6102701	+0.0736899	1214.6102701	
+0.0184937	600.29876704	6	S	10	1143.5731563	+0.0658818	1143.5731563	
	687.33079545	7	S	9	1056.5411279	-0.0128076	1056.5411279	
	774.36282386	8	S	8	969.50909948	+0.0198312	969.50909948	
	888.40575131	9	N	7	882.47707107	-0.0418294	882.47707107	
+0.0849448	1003.4326943	10	D	6	768.43414362	+0.0169062	768.43414362	
+0.0257221	1116.5167583	11	I	5	653.40720059	+0.0763199	653.40720059	
	1173.538222	12	G	4	540.32313661	-0.061662	540.32313661	
+0.0738547	1301.5967996	13	Q	3	483.30167289		483.30167289	
	1388.628828	14	S	2	355.24309537	-0.0425339	355.24309537	
+0.0830065	1501.7128919	15	I	1	268.21106696		268.21106696	
		16	K	0	155.12700298		155.12700298	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F02
Scannumber: 12276
Protein: BSU06920; yeeN; yesJ; yfxC; yfxD
Peptide Score: 159.5
Method: ITMS; CID; 3





precursor information

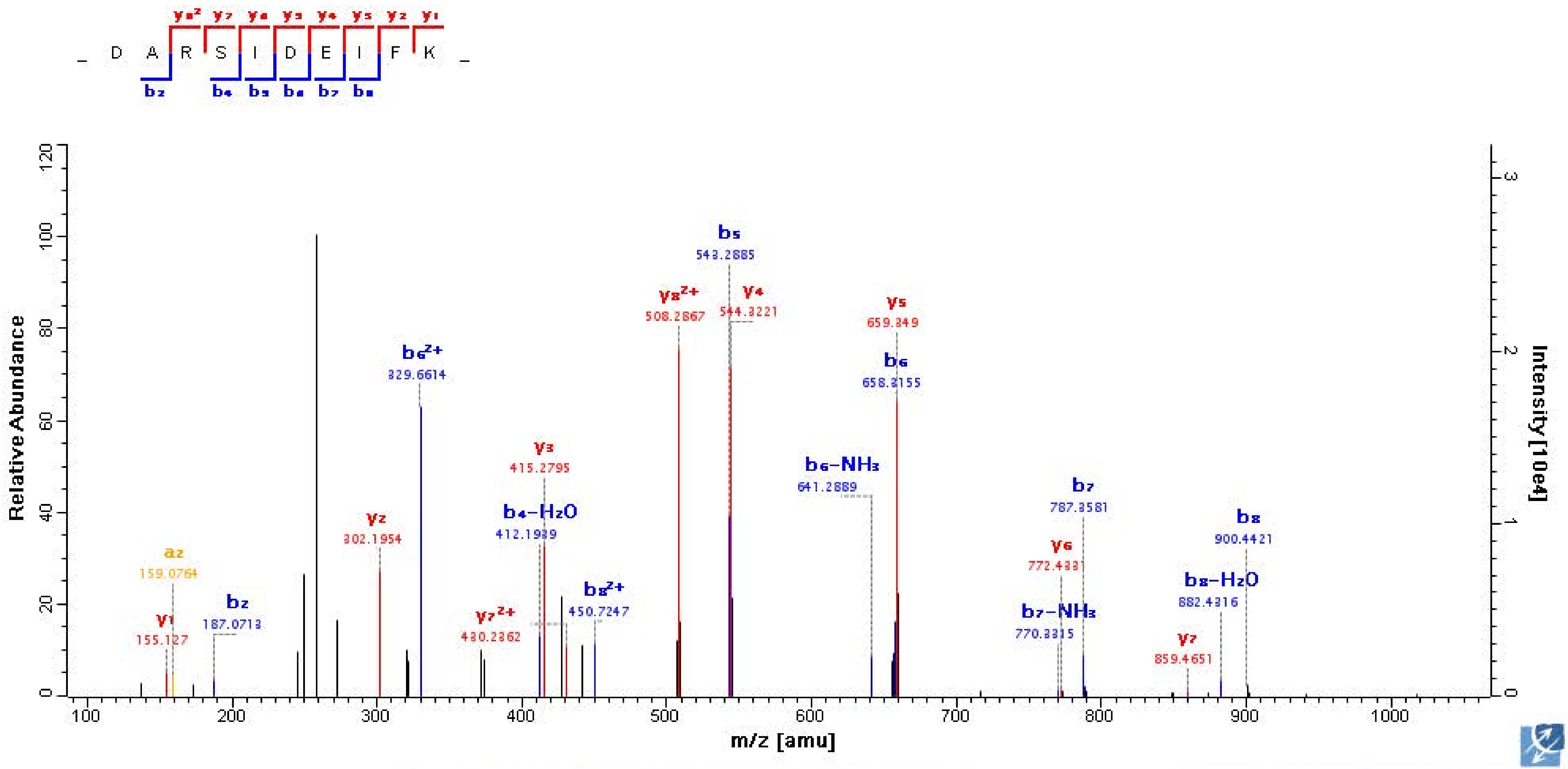
Mass:	1419.70894
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	159.496
Mass Error [ppm]:	0.29172
PEP:	7.6366E-37
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	62 %
Protein Localisation:	53 ... 65

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	12				
	186.0873177	2	Q	11	1363.6943341		682.35080527	+0.1744023
+0.1513337	301.11426073	3	D	10	1235.6357566	+0.0617532	618.32151651	+0.2630782
	414.19832471	4	I	9	1120.6088135	-0.0012696	560.80804499	+0.188537
+0.1330222	551.25723658	5	H	8	1007.5247495	+0.1166079	504.266013	-0.0011204
+0.0430299	666.28417961	6	D	7	870.46583768	+0.1023386	870.46583768	
+0.0648619	779.36824359	7	I	6	755.43889465	+0.0947357	755.43889465	
+0.1130696	880.41592206	8	T	5	642.35483067	+0.0948153	642.35483067	
	937.43738579	9	G	4	541.30715219	+0.0146251	541.30715219	
+0.2215038	1024.4694142	10	S	3	484.28568847		484.28568847	
+0.0059701	1137.5534782	11	I	2	397.25366006	-0.0355204	397.25366006	
+0.1763897	1266.5960713	12	E	1	284.16959608	-0.1344398	284.16959608	
		13	K	0	155.12700298		155.12700298	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F02
Scannumber:	18645
Protein:	BSU33230; sigO; yvrI
Peptide Score:	148.32
Method:	ITMS; CID; 3



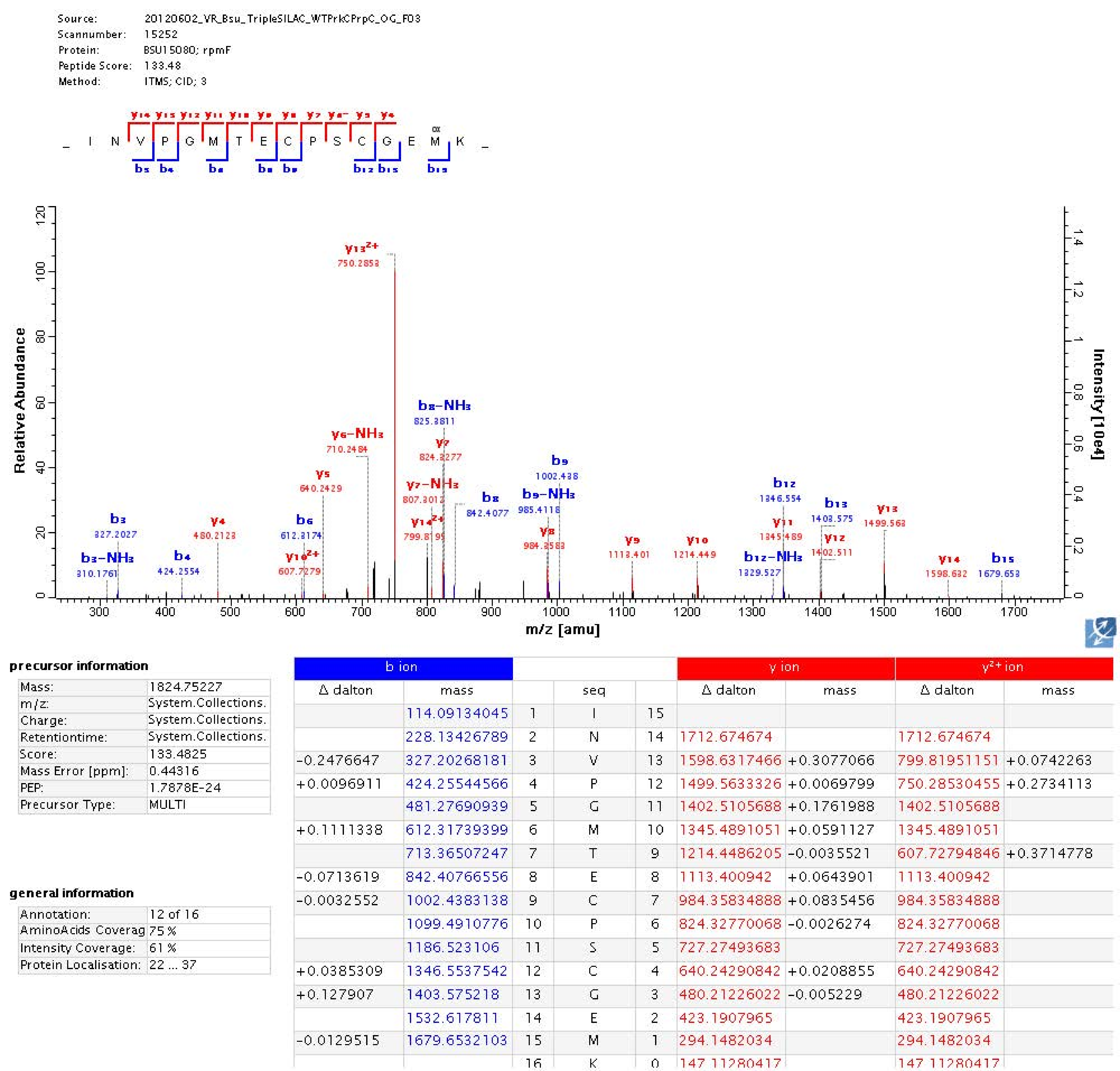
precursor information

Mass:	1192.60836
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	148.321
Mass Error [ppm]:	-0.36405
PEP:	4.6446E-17
Precursor Type:	MULTI

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	58 %
Protein Localisation:	30 ... 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
	88.0393		116.034		116.034	1	D	9				
+0.08038	159.076		187.071	+0.02281	187.071	2	A	8	1086.6		1086.6	
	315.178		343.172		343.172	3	R	7	1015.57		508.287	+0.0479
	402.21		430.204		430.204	4	S	6	859.465	+0.25804	430.236	+0.1458
	515.294		543.289	-0.0197	543.289	5	I	5	772.433	+0.16329	772.433	
	630.321	+0.23352	329.661	-0.0608	658.315	6	D	4	659.349	-0.0355	659.349	
	759.363		787.358	-0.0202	787.358	7	E	3	544.322	-0.0609	544.322	
	872.447	+0.10958	450.725	+0.07123	900.442	8	I	2	415.279	-0.0189	415.279	
	1019.52		1047.51		1047.51	9	F	1	302.195	+0.02736	302.195	
						10	K	0	155.127	+0.07681	155.127	



Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F03
Scannumber:	15252
Protein:	BSU15080; rpmF
Peptide Score:	133.48
Method:	ITMS; CID; 3

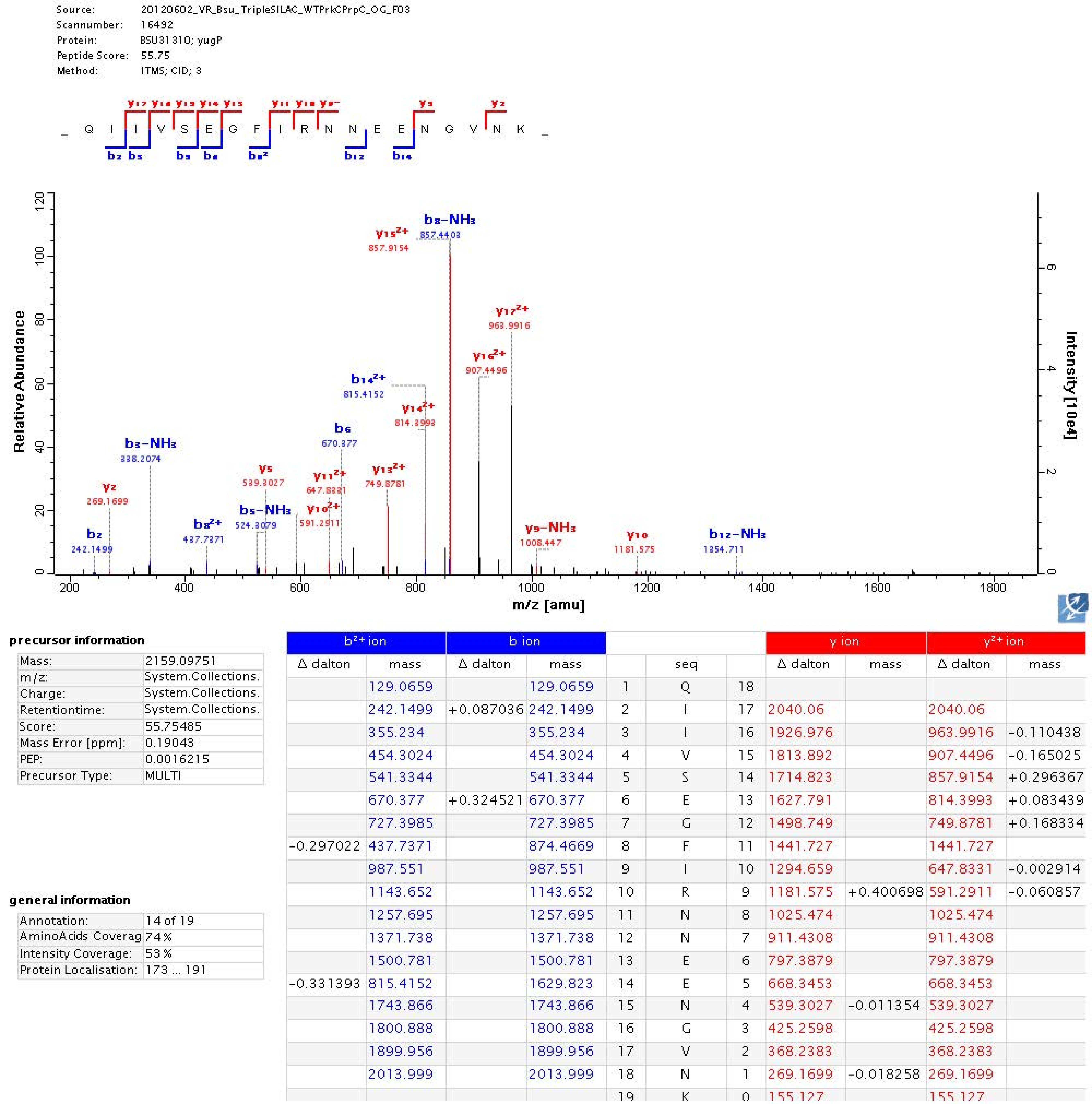
precursor information

Mass:	1824.75227
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	133.4825
Mass Error [ppm]:	0.44316
PEP:	1.7878E-24
Precursor Type:	MULTI

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	61 %
Protein Localisation:	22 ... 37

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	15				
	228.13426789	2	N	14	1712.674674		1712.674674	
-0.2476647	327.20268181	3	V	13	1598.6317466	+0.3077066	799.81951151	+0.0742263
+0.0096911	424.25544566	4	P	12	1499.5633326	+0.0069799	750.28530455	+0.2734113
	481.27690939	5	G	11	1402.5105688	+0.1761988	1402.5105688	
+0.1111338	612.31739399	6	M	10	1345.4891051	+0.0591127	1345.4891051	
	713.36507247	7	T	9	1214.4486205	-0.0035521	607.72794846	+0.3714778
-0.0713619	842.40766556	8	E	8	1113.400942	+0.0643901	1113.400942	
-0.0032552	1002.4383138	9	C	7	984.35834888	+0.0835456	984.35834888	
	1099.4910776	10	P	6	824.32770068	-0.0026274	824.32770068	
	1186.523106	11	S	5	727.27493683		727.27493683	
+0.0385309	1346.5537542	12	C	4	640.24290842	+0.0208855	640.24290842	
+0.127907	1403.575218	13	G	3	480.21226022	-0.005229	480.21226022	
	1532.617811	14	E	2	423.1907965		423.1907965	
-0.0129515	1679.6532103	15	M	1	294.1482034		294.1482034	
		16	K	0	147.11280417		147.11280417	



Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F03
Scannumber: 16492
Protein: BSU31310; yugP
Peptide Score: 55.75
Method: ITMS; CID; 3

precursor information

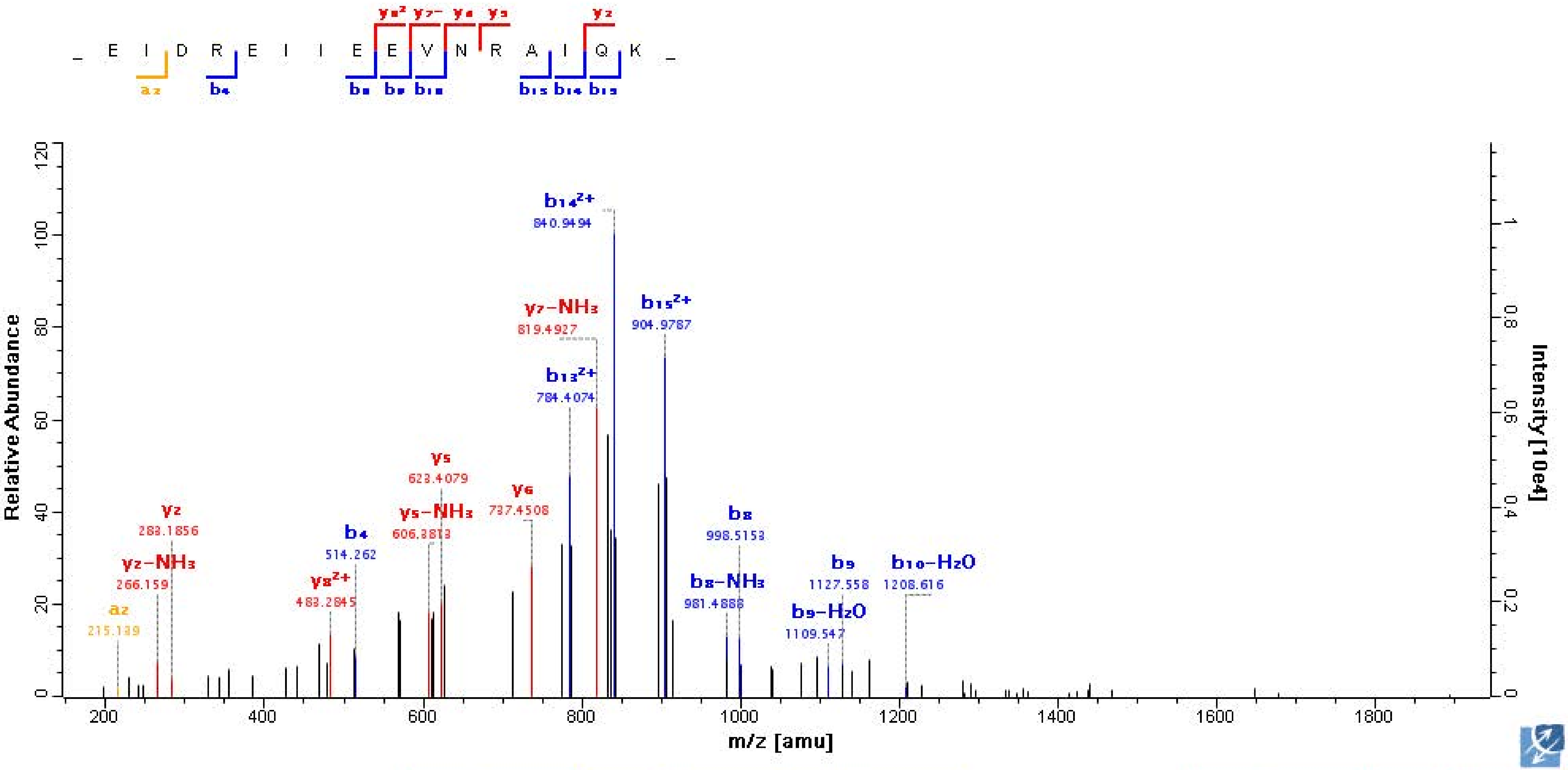
Mass:	2159.09751
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	55.75485
Mass Error [ppm]:	0.19043
PEP:	0.0016215
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74%
Intensity Coverage:	53%
Protein Localisation:	173 ... 191

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.0659		129.0659	1	Q	18				
	242.1499	+0.087036	242.1499	2	I	17	2040.06		2040.06	
	355.234		355.234	3	I	16	1926.976		963.9916	-0.110438
	454.3024		454.3024	4	V	15	1813.892		907.4496	-0.165025
	541.3344		541.3344	5	S	14	1714.823		857.9154	+0.296367
	670.377	+0.324521	670.377	6	E	13	1627.791		814.3993	+0.083439
	727.3985		727.3985	7	G	12	1498.749		749.8781	+0.168334
-0.297022	437.7371		874.4669	8	F	11	1441.727		1441.727	
	987.551		987.551	9	I	10	1294.659		647.8331	-0.002914
	1143.652		1143.652	10	R	9	1181.575	+0.400698	591.2911	-0.060857
	1257.695		1257.695	11	N	8	1025.474		1025.474	
	1371.738		1371.738	12	N	7	911.4308		911.4308	
	1500.781		1500.781	13	E	6	797.3879		797.3879	
-0.331393	815.4152		1629.823	14	E	5	668.3453		668.3453	
	1743.866		1743.866	15	N	4	539.3027	-0.011354	539.3027	
	1800.888		1800.888	16	G	3	425.2598		425.2598	
	1899.956		1899.956	17	V	2	368.2383		368.2383	
	2013.999		2013.999	18	N	1	269.1699	-0.018258	269.1699	
				19	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F03
Scannumber: 25921
Protein: BSU19240; yocK
Peptide Score: 68.28
Method: ITMS; CID; 3



precursor information

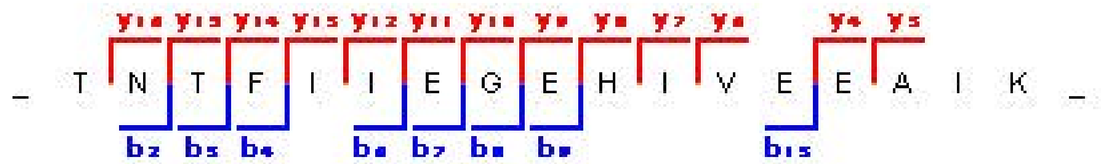
Mass:	1954.04934
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	68.27738
Mass Error [ppm]:	0.50432
PEP:	0.00037955
Precursor Type:	MULTI

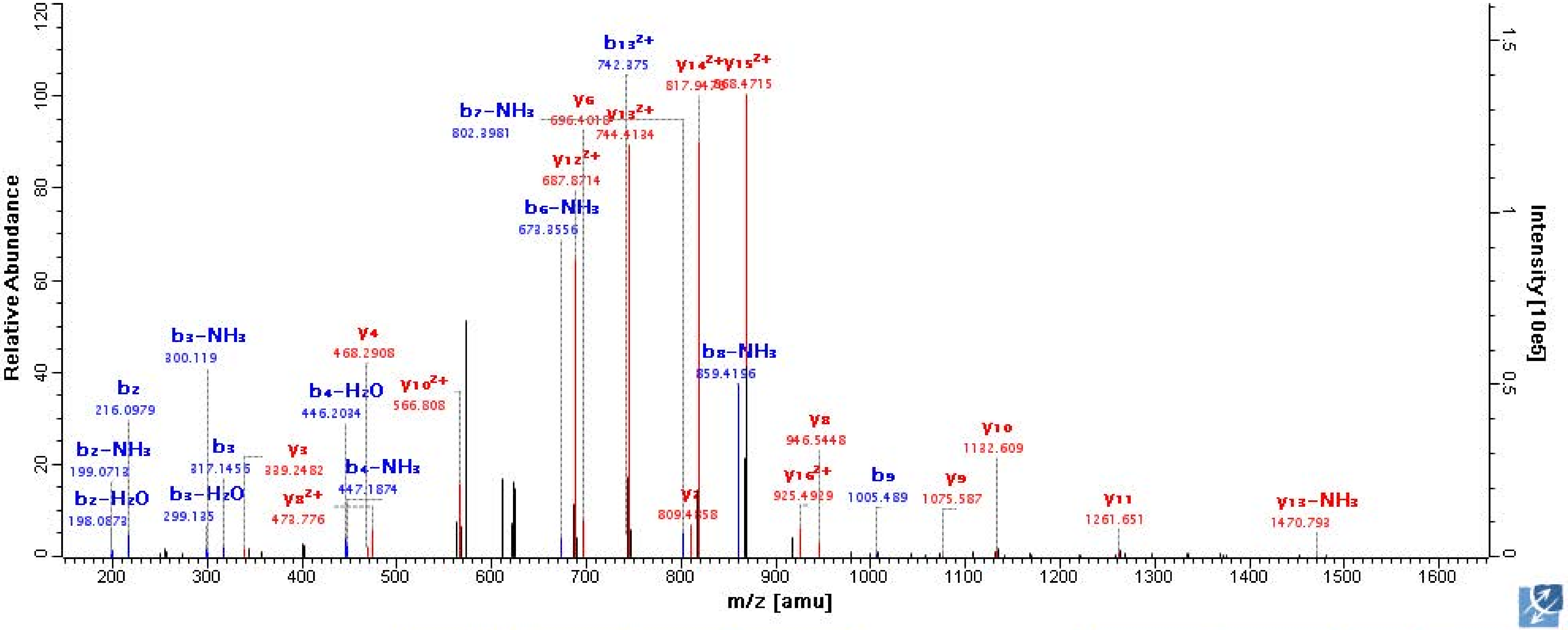
general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	41 %
Protein Localisation:	65 ... 80

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
	102.055		130.05		130.05	1	E	15				
+0.00132	215.139		243.134		243.134	2	I	14	1834.03		1834.03	
	330.166		358.161		358.161	3	D	13	1720.94		1720.94	
	486.267		514.262	+0.06644	514.262	4	R	12	1605.92		1605.92	
	615.31		643.305		643.305	5	E	11	1449.82		1449.82	
	728.394		756.389		756.389	6	I	10	1320.77		1320.77	
	841.478		869.473		869.473	7	I	9	1207.69		1207.69	
	970.52		998.515	+0.11208	998.515	8	E	8	1094.6		1094.6	
	1099.56		1127.56	+0.21579	1127.56	9	E	7	965.562		483.285	+0.2367
	1198.63		1226.63		1226.63	10	V	6	836.519		836.519	
	1312.67		1340.67		1340.67	11	N	5	737.451	+0.14393	737.451	
	1468.78		1496.77		1496.77	12	R	4	623.408	+0.20523	623.408	
	1539.81	+0.30564	784.407		1567.81	13	A	3	467.307		467.307	
	1652.9	+0.41248	840.949		1680.89	14	I	2	396.27		396.27	
	1780.96	+0.141	904.979		1808.95	15	Q	1	283.186	+0.07437	283.186	
						16	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F03
Scannumber:	31638
Protein:	BSU28650; ysgA
Peptide Score:	119.96
Method:	ITMS; CID; 3





precursor information

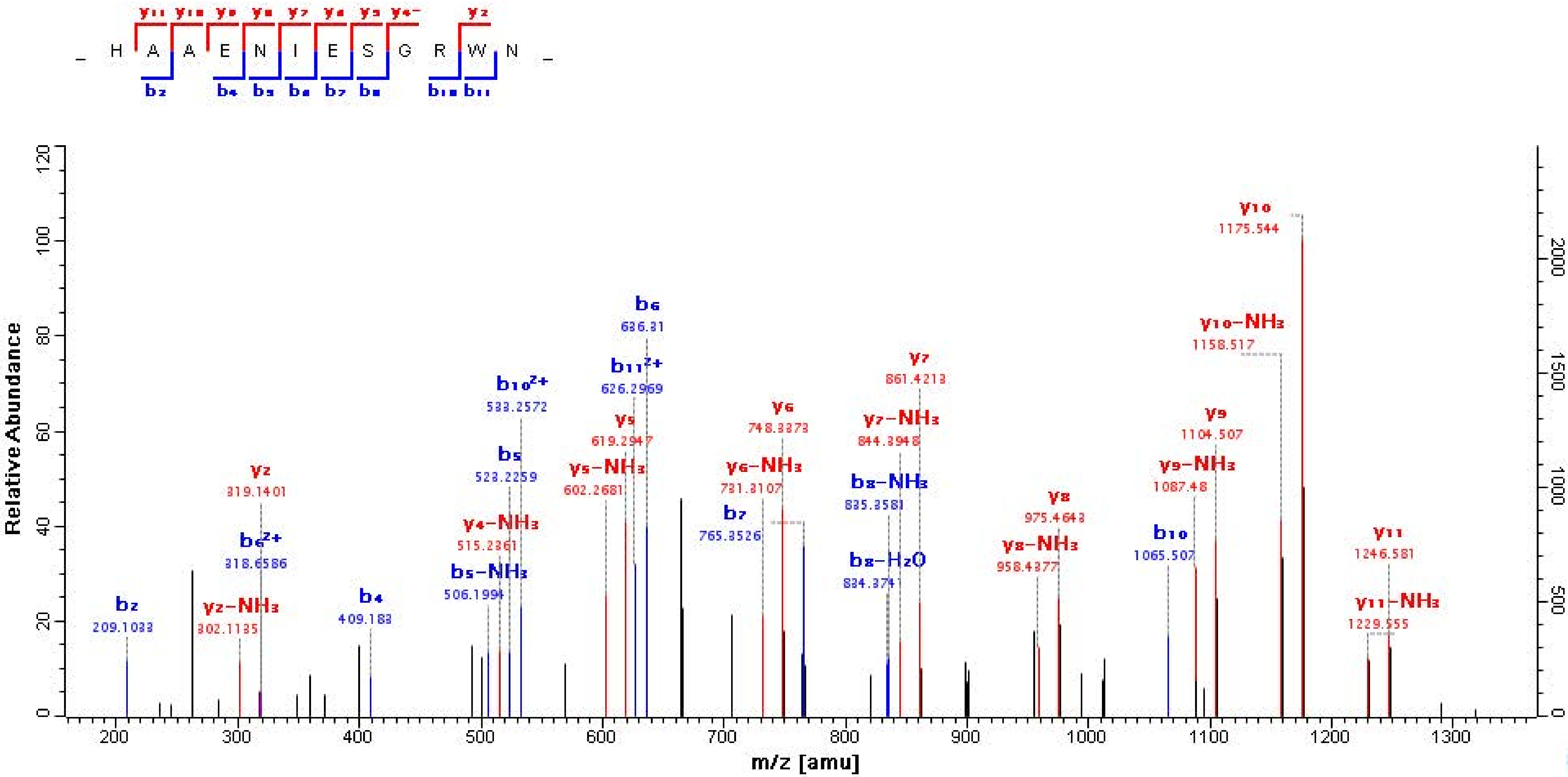
Mass:	1942.00467
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	119.9631
Mass Error [ppm]:	-0.04474
PEP:	2.6342E-15
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	62 %
Protein Localisation:	27 ... 43

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	16				
	216.0979	-0.063306	216.0979	2	N	15	1849.979		925.4929	+0.340825
	317.1456	+0.068306	317.1456	3	T	14	1735.936		868.4715	+0.19963
	464.214		464.214	4	F	13	1634.888		817.9476	+0.38094
	577.298		577.298	5	I	12	1487.82		744.4134	+0.359422
	690.3821		690.3821	6	I	11	1374.735		687.8714	+0.290431
	819.4247		819.4247	7	E	10	1261.651	+0.167929	1261.651	
	876.4462		876.4462	8	G	9	1132.609	+0.174145	566.808	+0.152038
	1005.489	+0.310564	1005.489	9	E	8	1075.587	+0.087577	1075.587	
	1142.548		1142.548	10	H	7	946.5448	-0.011309	473.776	+0.197677
	1255.632		1255.632	11	I	6	809.4858	+0.153743	809.4858	
	1354.7		1354.7	12	V	5	696.4018	+0.133436	696.4018	
+0.450372	742.375		1483.743	13	E	4	597.3334		597.3334	
	1612.785		1612.785	14	E	3	468.2908	+0.091184	468.2908	
	1683.822		1683.822	15	A	2	339.2482	-0.012616	339.2482	
	1796.907		1796.907	16	I	1	268.2111		268.2111	
				17	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F04
Scannumber:	11041
Protein:	BSU02270; pss; pssA
Peptide Score:	209.97
Method:	ITMS; CID; 3



precursor information

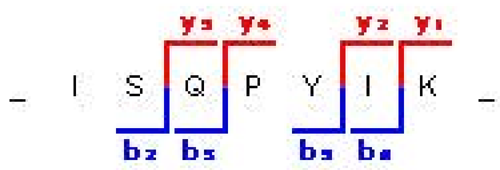
Mass:	1382.63112
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	209.9664
Mass Error [ppm]:	-1.1589
PEP:	5.9292E-126
Precursor Type:	ISO

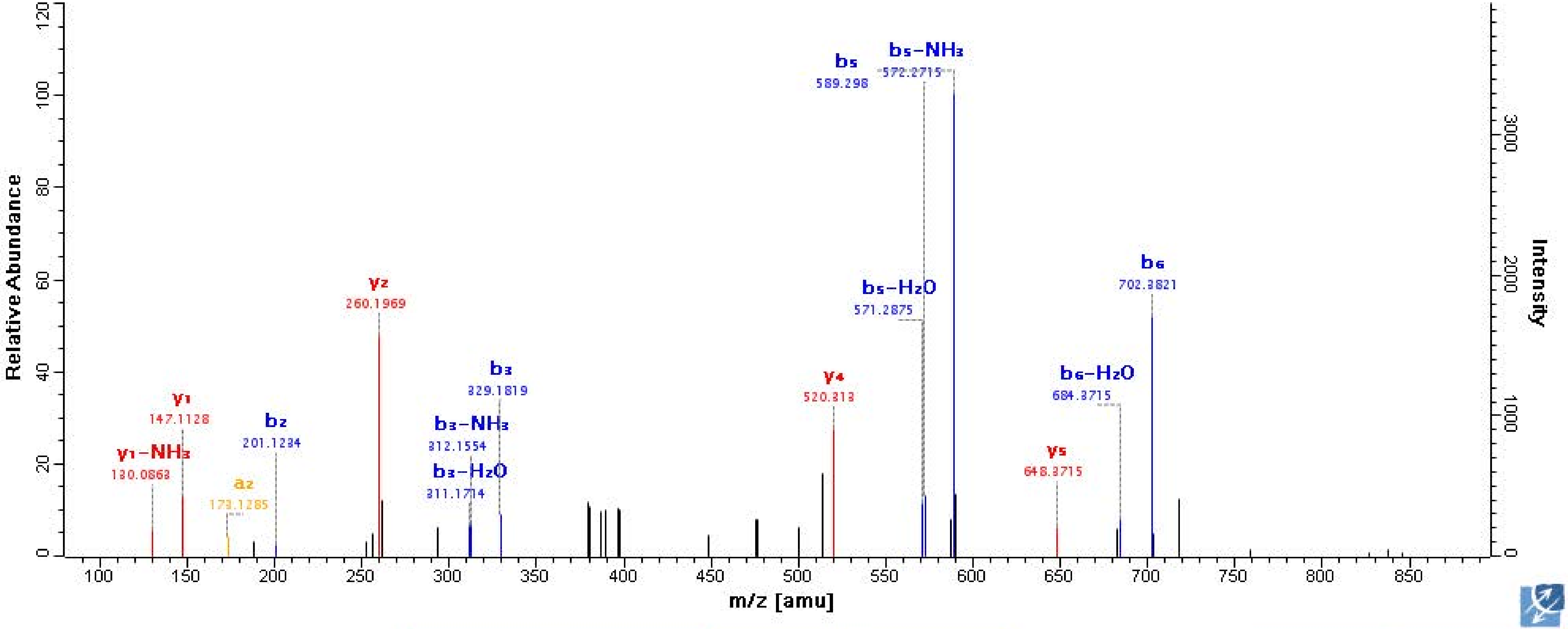
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Protein Localisation:	166 ... 177

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	138.06618833		138.06618833	1	H	11		
	209.10330212	-0.0873567	209.10330212	2	A	10	1246.5810899	+0.1211806
	280.1404159		280.1404159	3	A	9	1175.5439761	+0.0038754
	409.183009	-0.0118664	409.183009	4	E	8	1104.5068623	+0.172459
	523.22593645	+0.167252	523.22593645	5	N	7	975.46426924	+0.1613411
-0.3445515	318.65863845	+0.0567598	636.31000043	6	I	6	861.42134179	+0.0841514
	765.35259352	+0.1729192	765.35259352	7	E	5	748.33727781	+0.1212183
	852.38462193		852.38462193	8	S	4	619.29468472	+0.1500785
	909.40608566		909.40608566	9	G	3	532.2626563	
+0.1102561	533.25723658	+0.2915094	1065.5071967	10	R	2	475.24119258	
+0.0775576	626.29689305		1251.5865096	11	W	1	319.14008155	+0.2095889
				12	N	0	133.0607686	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F04
Scannumber: 26979
Protein: BSU31140; cdoA; yubC
Peptide Score: 148.07
Method: ITMS; CID; 3





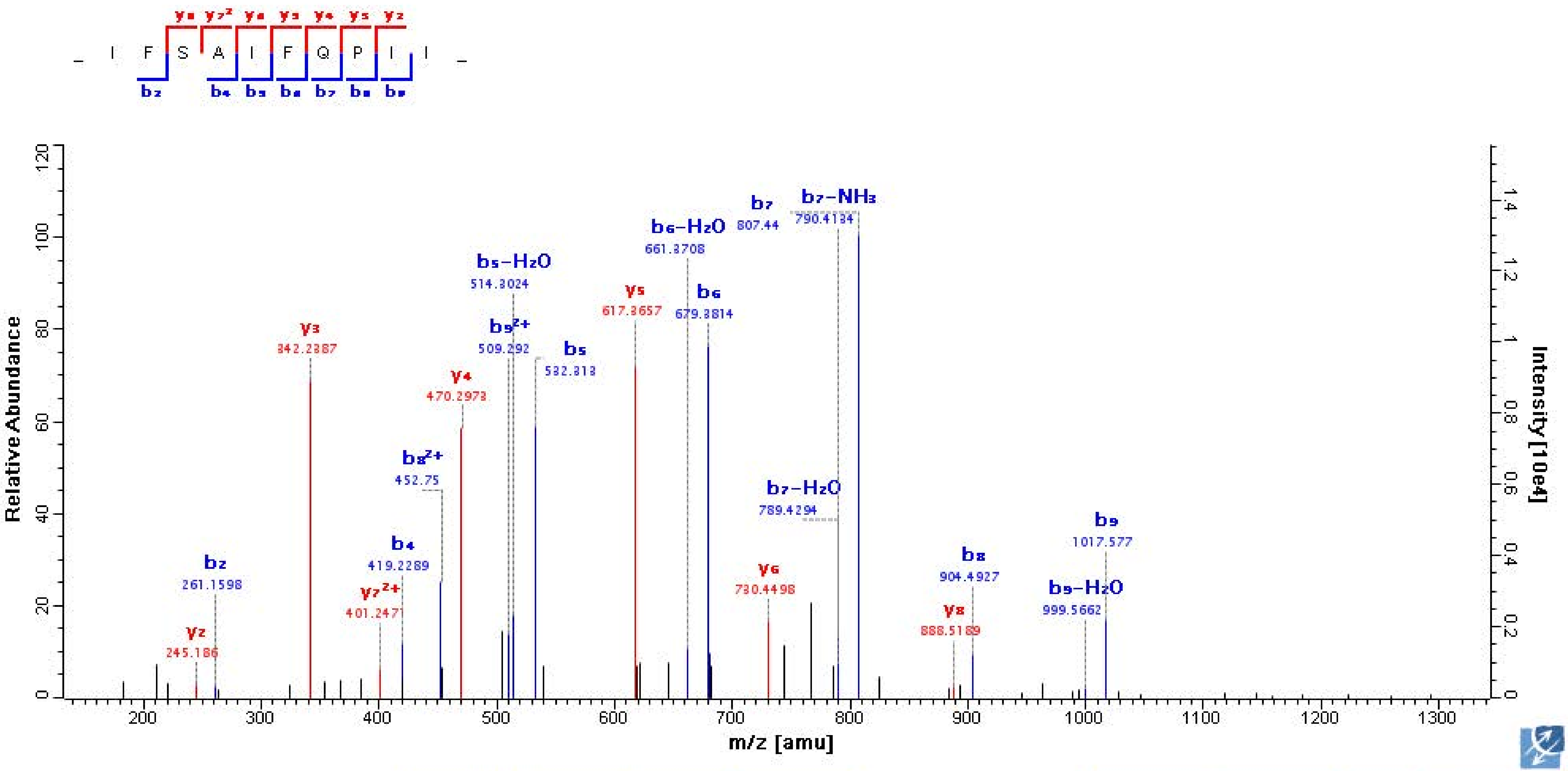
precursor information

g

Mass:	847.48065
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	148.068
Mass Error [ppm]:	0.35071
PEP:	1.5327E-14
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	63 %
Protein Localisation:	35 ... 41

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	86.096425825		114.09134045	1	I	6		
+0.2128849	173.12845423	+0.0325149	201.12336886	2	S	5	735.40356646	
	301.18703175	+0.0186762	329.18194637	3	Q	4	648.37153805	+0.1174756
	398.2397956		426.23471022	4	P	3	520.31296054	+0.0360995
	561.30312414	+0.0958211	589.29803876	5	Y	2	423.26019669	
	674.38718812	+0.1120379	702.38210274	6	I	1	260.19686815	-0.0686638
				7	K	0	147.11280417	+0.0188334

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F04
Scannumber:	32653
Protein:	BSU37530; ywhC
Peptide Score:	195.27
Method:	ITMS; CID; 3



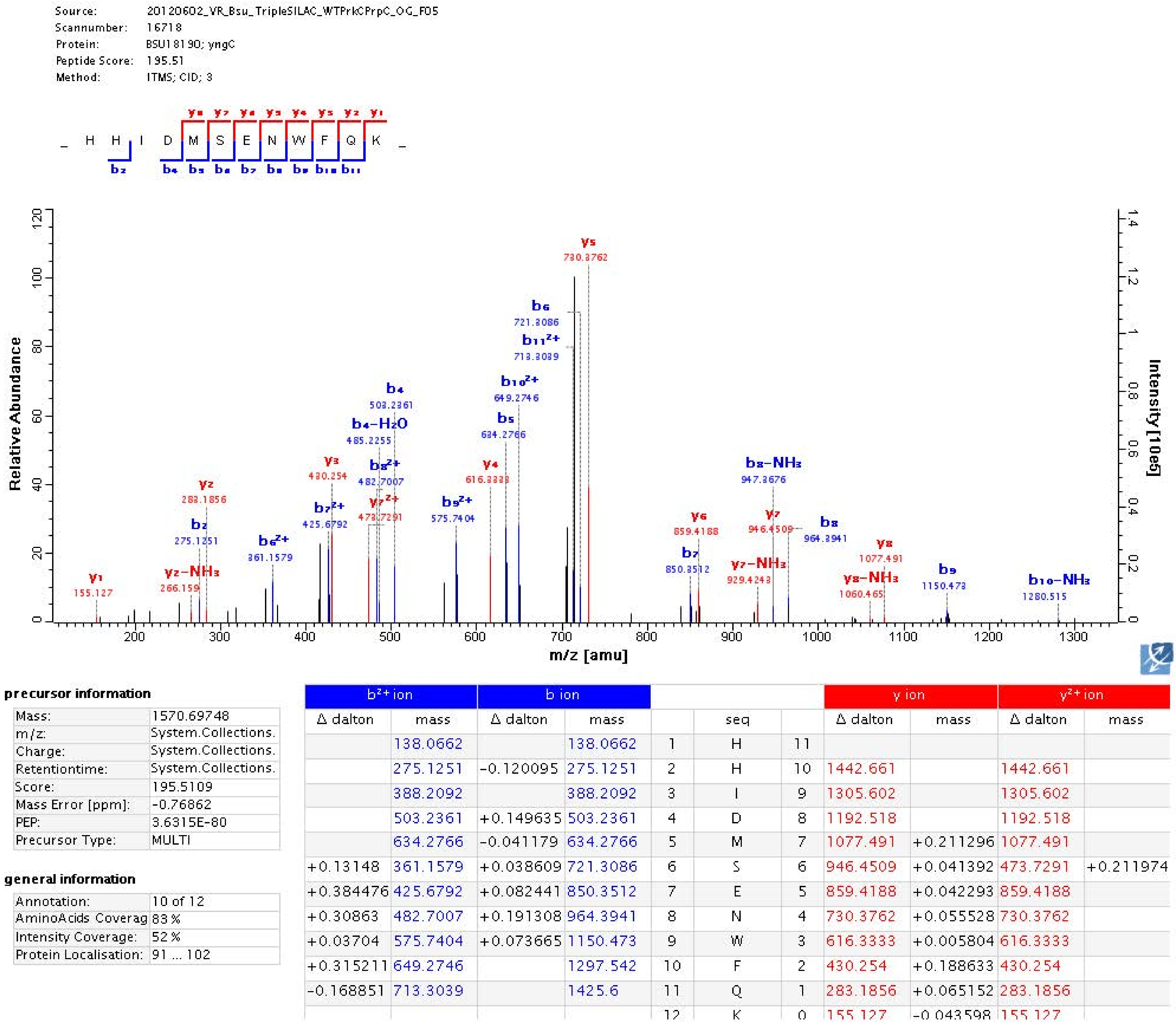
precursor information

Mass:	1147.66349
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	195.2698
Mass Error [ppm]:	-0.56135
PEP:	4.6121E-82
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	78 %
Protein Localisation:	210 ... 219

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	9				
	261.1598	+0.107915	261.1598	2	F	8	1035.587		1035.587	
	348.1918		348.1918	3	S	7	888.5189	+0.147512	888.5189	
	419.2289	+0.172654	419.2289	4	A	6	801.4869		401.2471	-0.002399
	532.313	-0.014682	532.313	5	I	5	730.4498	+0.074504	730.4498	
	679.3814	+0.032322	679.3814	6	F	4	617.3657	-0.002748	617.3657	
	807.44	+0.026662	807.44	7	Q	3	470.2973	-0.070931	470.2973	
-0.239742	452.75	+0.042196	904.4927	8	P	2	342.2387	-0.050623	342.2387	
+0.041956	509.292	-0.057371	1017.577	9	I	1	245.186	-0.128321	245.186	
				10	I	0	132.1019		132.1019	



Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F05
Scannumber: 16718
Protein: BSU18190; yngC
Peptide Score: 195.51
Method: ITMS; CID; 3

precursor information

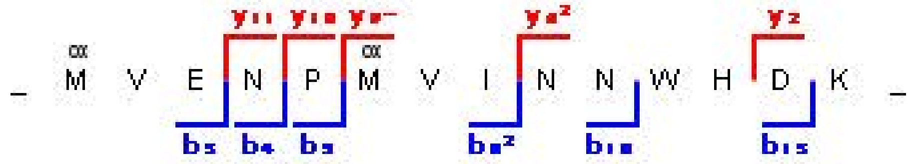
Mass:	1570.69748
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	195.5109
Mass Error [ppm]:	-0.76862
PEP:	3.6315E-80
Precursor Type:	MULTI

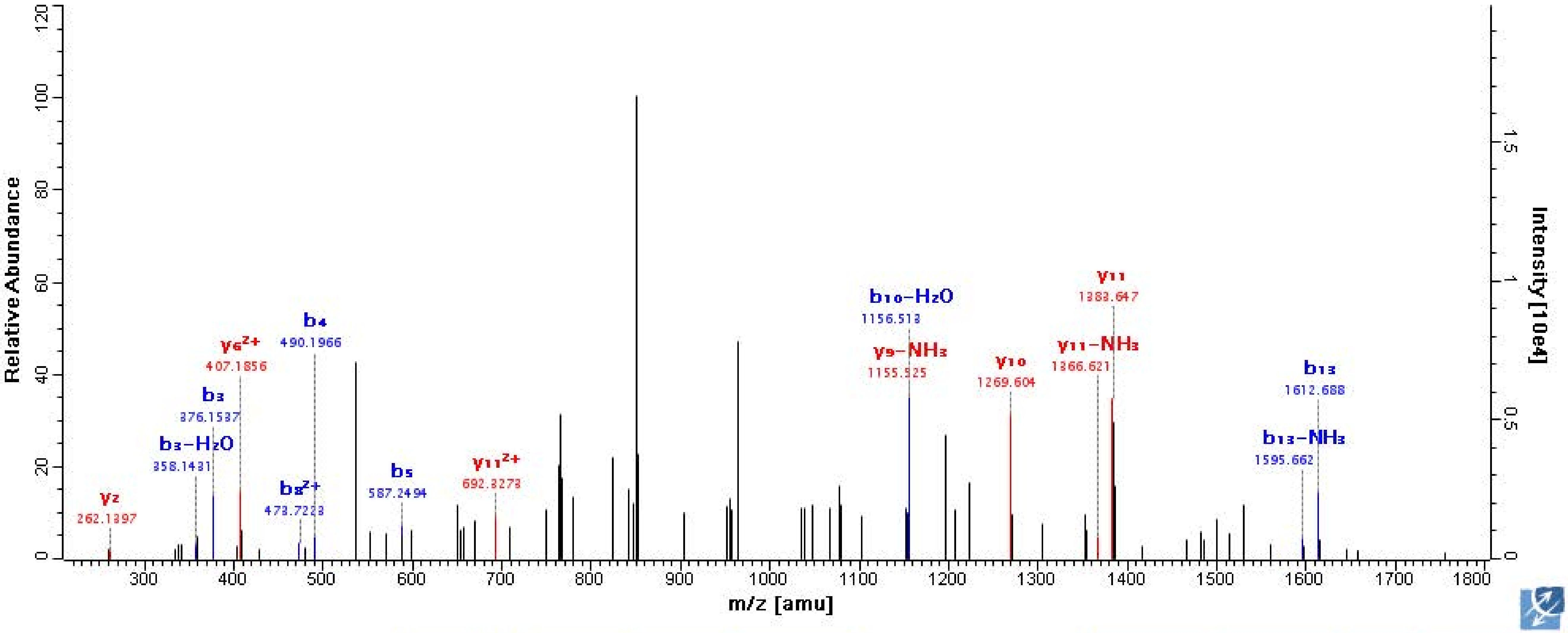
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Protein Localisation:	91 ... 102

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	11				
	275.1251	-0.120095	275.1251	2	H	10	1442.661		1442.661	
	388.2092		388.2092	3	I	9	1305.602		1305.602	
	503.2361	+0.149635	503.2361	4	D	8	1192.518		1192.518	
	634.2766	-0.041179	634.2766	5	M	7	1077.491	+0.211296	1077.491	
+0.13148	361.1579	+0.038609	721.3086	6	S	6	946.4509	+0.041392	473.7291	+0.211974
+0.384476	425.6792	+0.082441	850.3512	7	E	5	859.4188	+0.042293	859.4188	
+0.30863	482.7007	+0.191308	964.3941	8	N	4	730.3762	+0.055528	730.3762	
+0.03704	575.7404	+0.073665	1150.473	9	W	3	616.3333	+0.005804	616.3333	
+0.315211	649.2746		1297.542	10	F	2	430.254	+0.188633	430.254	
-0.168851	713.3039		1425.6	11	Q	1	283.1856	+0.065152	283.1856	
				12	K	0	155.127	-0.043598	155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F05
Scannumber:	26746
Protein:	BSU26300; yqal
Peptide Score:	71.24
Method:	ITMS; CID; 3





precursor information

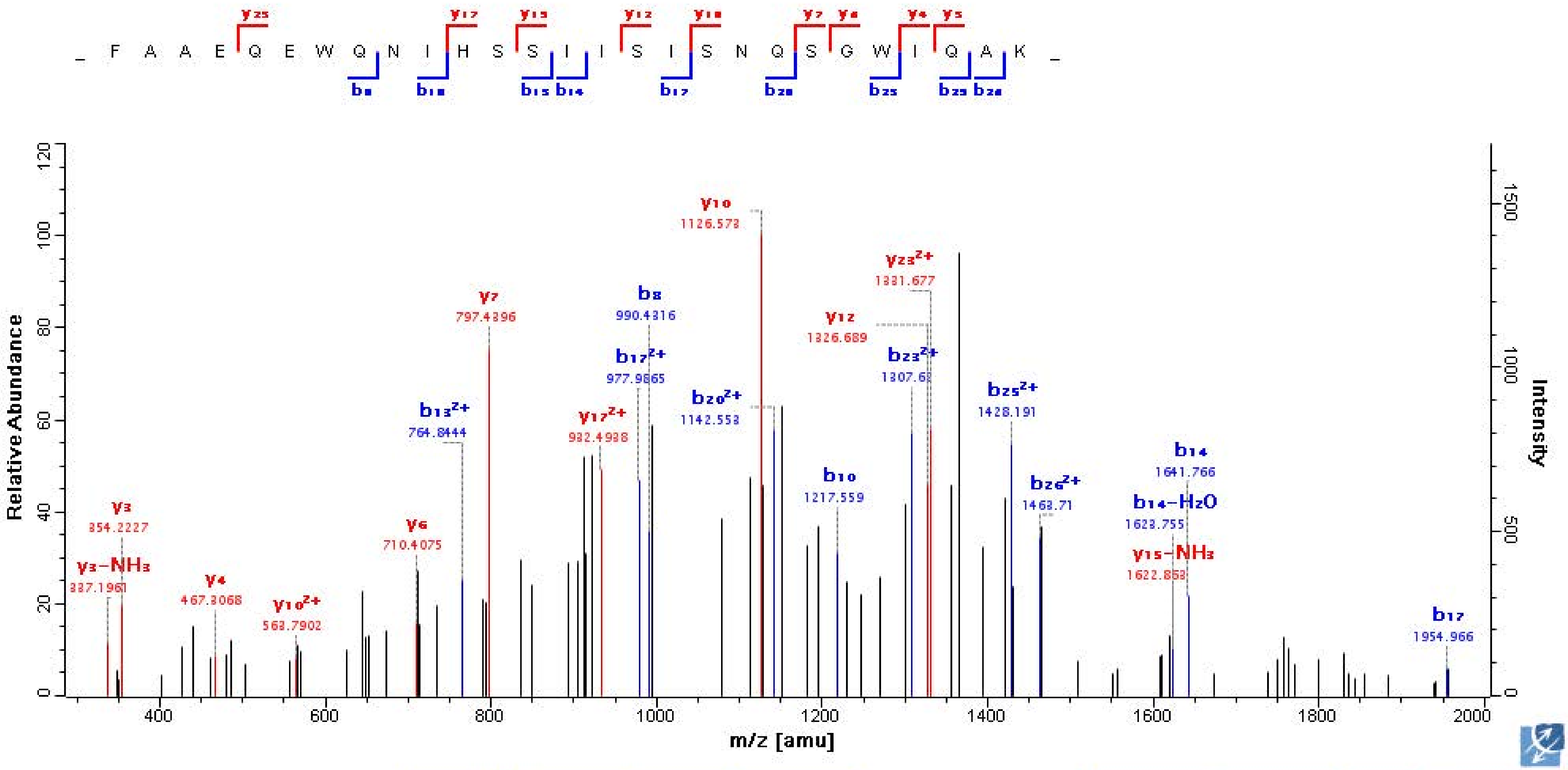
Mass:	1757.78786
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.24082
Mass Error [ppm]:	0.75685
PEP:	0.0012877
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	19 %
Protein Localisation:	1 ... 14

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.0427		148.0427	1	M	13				
	247.1111		247.1111	2	V	12	1611.758		1611.758	
	376.1537	-0.042294	376.1537	3	E	11	1512.69		1512.69	
	490.1966	+0.131088	490.1966	4	N	10	1383.647	-0.067561	692.3273	+0.152767
	587.2494	+0.106827	587.2494	5	P	9	1269.604	+0.084863	1269.604	
	734.2848		734.2848	6	M	8	1172.552		1172.552	
	833.3532		833.3532	7	V	7	1025.516		1025.516	
-0.412541	473.7223		946.4373	8	I	6	926.4479		926.4479	
	1060.48		1060.48	9	N	5	813.3638		407.1856	+0.026362
	1174.523		1174.523	10	N	4	699.3209		699.3209	
	1360.602		1360.602	11	W	3	585.278		585.278	
	1497.661		1497.661	12	H	2	399.1987		399.1987	
	1612.688	-0.020793	1612.688	13	D	1	262.1397	+0.103966	262.1397	
				14	K	0	147.1128		147.1128	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F05
Scannumber: 32342
Protein: BSU23830; yqjL
Peptide Score: 79.69
Method: ITMS; CID; 3



precursor information

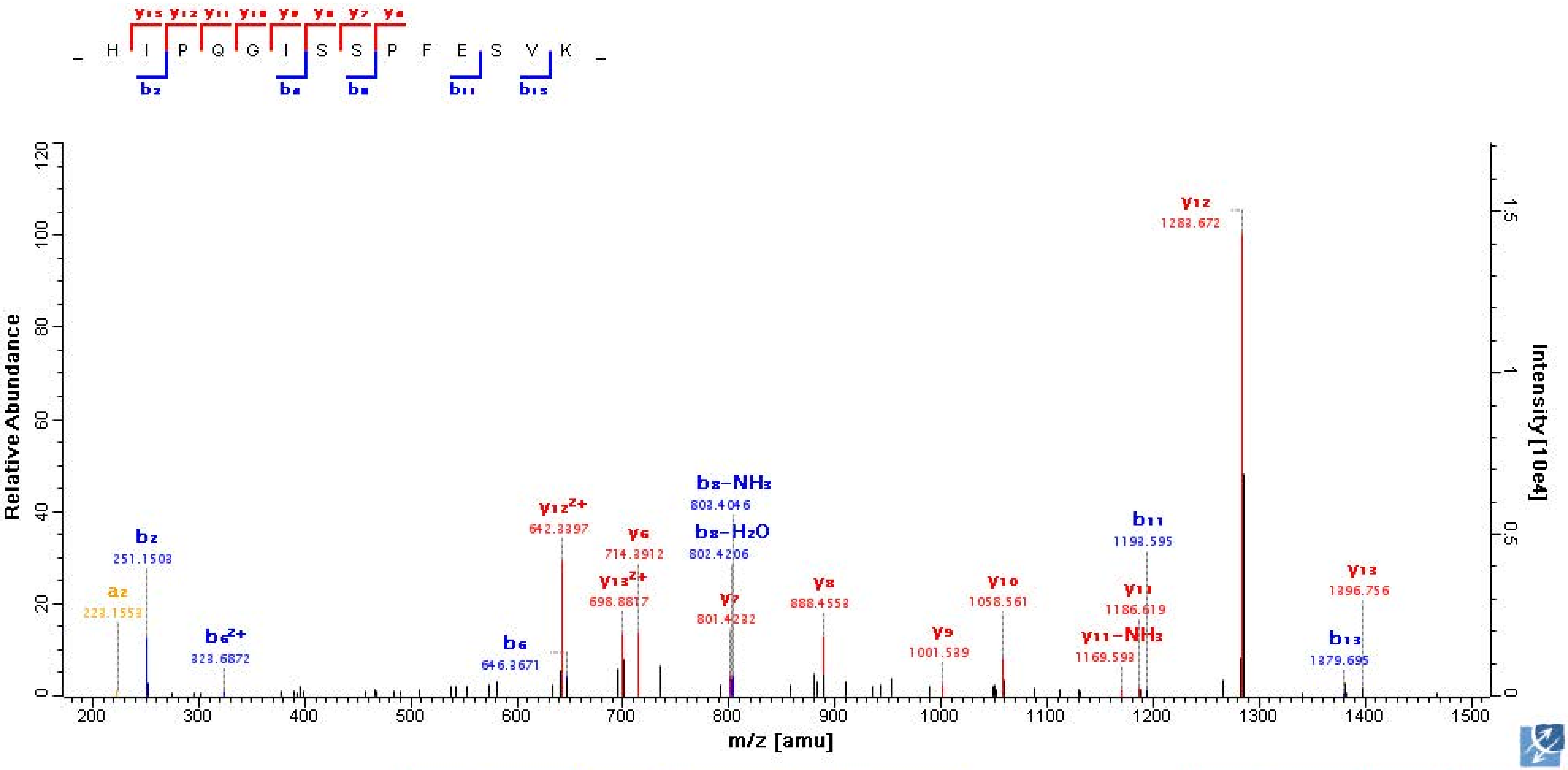
Mass:	3079.52613
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	79.6897
Mass Error [ppm]:	0.59394
PEP:	5.8448E-08
Precursor Type:	ISO

general information

Annotation:	16 of 27
AminoAcids Coverag	59 %
Intensity Coverage:	34 %
Protein Localisation:	190 ... 216

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.0757		148.0757	1	F	26				
	219.1128		219.1128	2	A	25	2933.463		2933.463	
	290.1499		290.1499	3	A	24	2862.426		2862.426	
	419.1925		419.1925	4	E	23	2791.389		2791.389	
	547.2511		547.2511	5	Q	22	2662.346		1331.677	+0.472363
	676.2937		676.2937	6	E	21	2534.288		2534.288	
	862.373		862.373	7	W	20	2405.245		2405.245	
	990.4316	+0.229317	990.4316	8	Q	19	2219.166		2219.166	
	1104.474		1104.474	9	N	18	2091.107		2091.107	
	1217.559	+0.199981	1217.559	10	I	17	1977.064		1977.064	
	1354.617		1354.617	11	H	16	1863.98		932.4938	+0.188958
	1441.65		1441.65	12	S	15	1726.921		1726.921	
+0.415483	764.8444		1528.682	13	S	14	1639.889		1639.889	
	1641.766	+0.343168	1641.766	14	I	13	1552.857		1552.857	
	1754.85		1754.85	15	I	12	1439.773		1439.773	
	1841.882		1841.882	16	S	11	1326.689	+0.086812	1326.689	
+0.495419	977.9865	+0.076606	1954.966	17	I	10	1239.657		1239.657	
	2041.998		2041.998	18	S	9	1126.573	+0.098778	563.7902	+0.254735
	2156.041		2156.041	19	N	8	1039.541		1039.541	
+0.308779	1142.553		2284.099	20	Q	7	925.4981		925.4981	
	2371.131		2371.131	21	S	6	797.4396	+0.107922	797.4396	
	2428.153		2428.153	22	G	5	710.4075	+0.06384	710.4075	
+0.383246	1307.62		2614.232	23	W	4	653.3861		653.3861	
	2727.316		2727.316	24	I	3	467.3068	+0.105931	467.3068	
-0.010707	1428.191		2855.375	25	Q	2	354.2227	-0.007179	354.2227	
+0.097323	1463.71		2926.412	26	A	1	226.1641		226.1641	
				27	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F06
Scannumber:	18078
Protein:	BSU04080; kipI; ycsJ
Peptide Score:	90.79
Method:	ITMS; CID; 3



precursor information

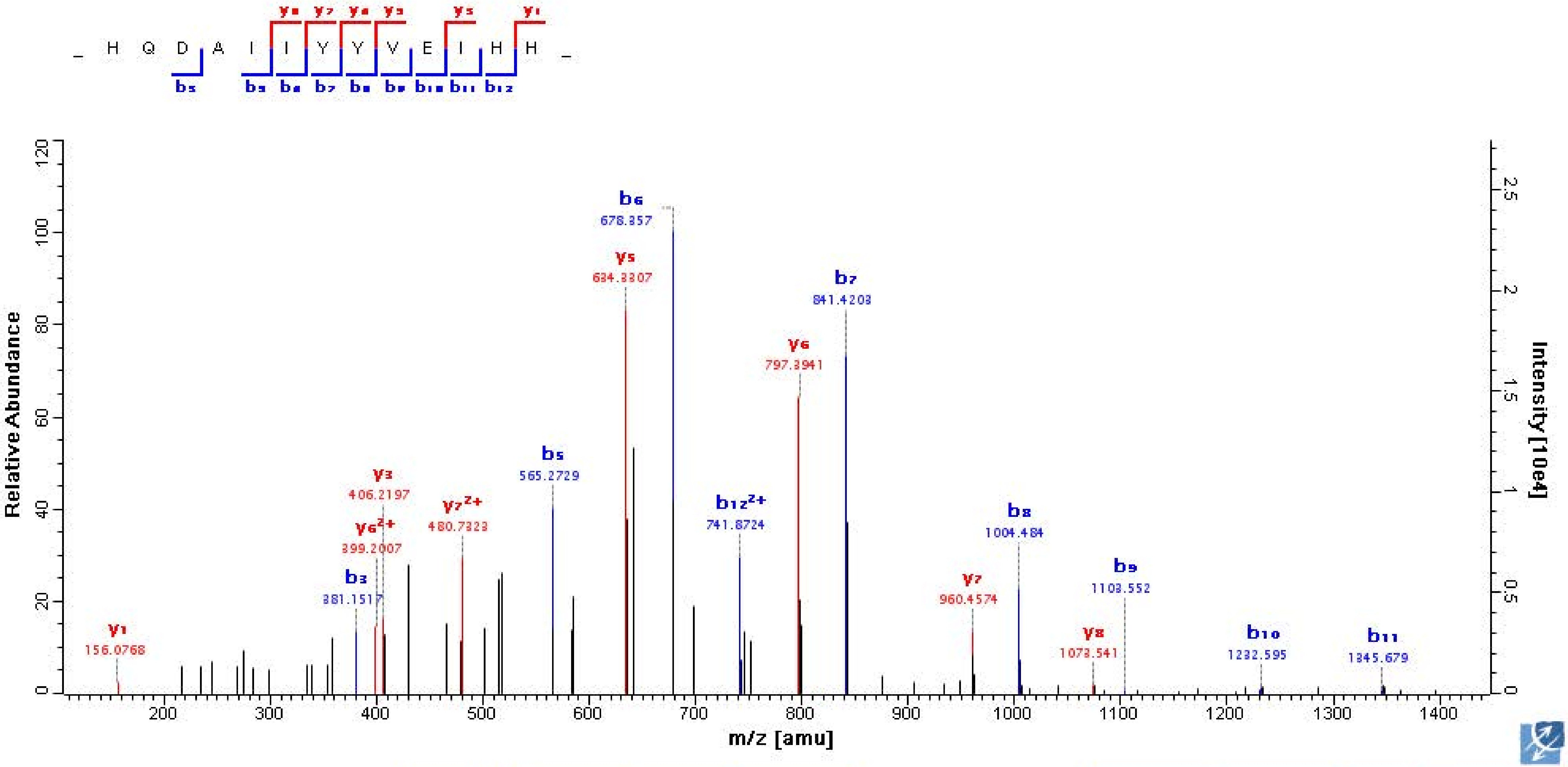
Mass:	1532.80681
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.79278
Mass Error [ppm]:	-0.67392
PEP:	0.0034969
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	54 %
Protein Localisation:	68 ... 81

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
	110.071		138.066		138.066	1	H	13				
-0.1665	223.155		251.15	-0.1453	251.15	2	I	12	1396.76	+0.01088	698.882	-0.0381
	320.208		348.203		348.203	3	P	11	1283.67	+0.02378	642.34	+0.0727
	448.267		476.262		476.262	4	Q	10	1186.62	+0.1477	1186.62	
	505.288		533.283		533.283	5	G	9	1058.56	+0.02807	1058.56	
	618.372	-0.0609	323.687	-0.0651	646.367	6	I	8	1001.54	+0.1293	1001.54	
	705.404		733.399		733.399	7	S	7	888.455	-0.0535	888.455	
	792.436		820.431		820.431	8	S	6	801.423	-0.0257	801.423	
	889.489		917.484		917.484	9	P	5	714.391	-0.3107	714.391	
	1036.56		1064.55		1064.55	10	F	4	617.338		617.338	
	1165.6		1193.59	+0.26809	1193.59	11	E	3	470.27		470.27	
	1252.63		1280.63		1280.63	12	S	2	341.227		341.227	
	1351.7		1379.7	+0.23564	1379.7	13	V	1	254.195		254.195	
						14	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F06
Scannumber: 21247
Protein: BSU08870; ygaN
Peptide Score: 103.88
Method: ITMS; CID; 3



precursor information

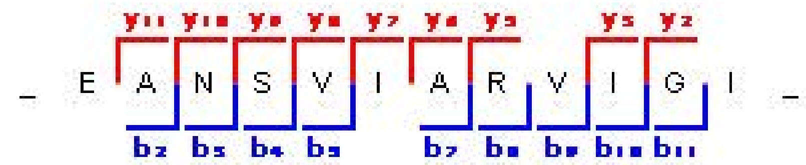
Mass:	1636.80069
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	103.8804
Mass Error [ppm]:	0.54908
PEP:	0.0024185
Precursor Type:	ISO

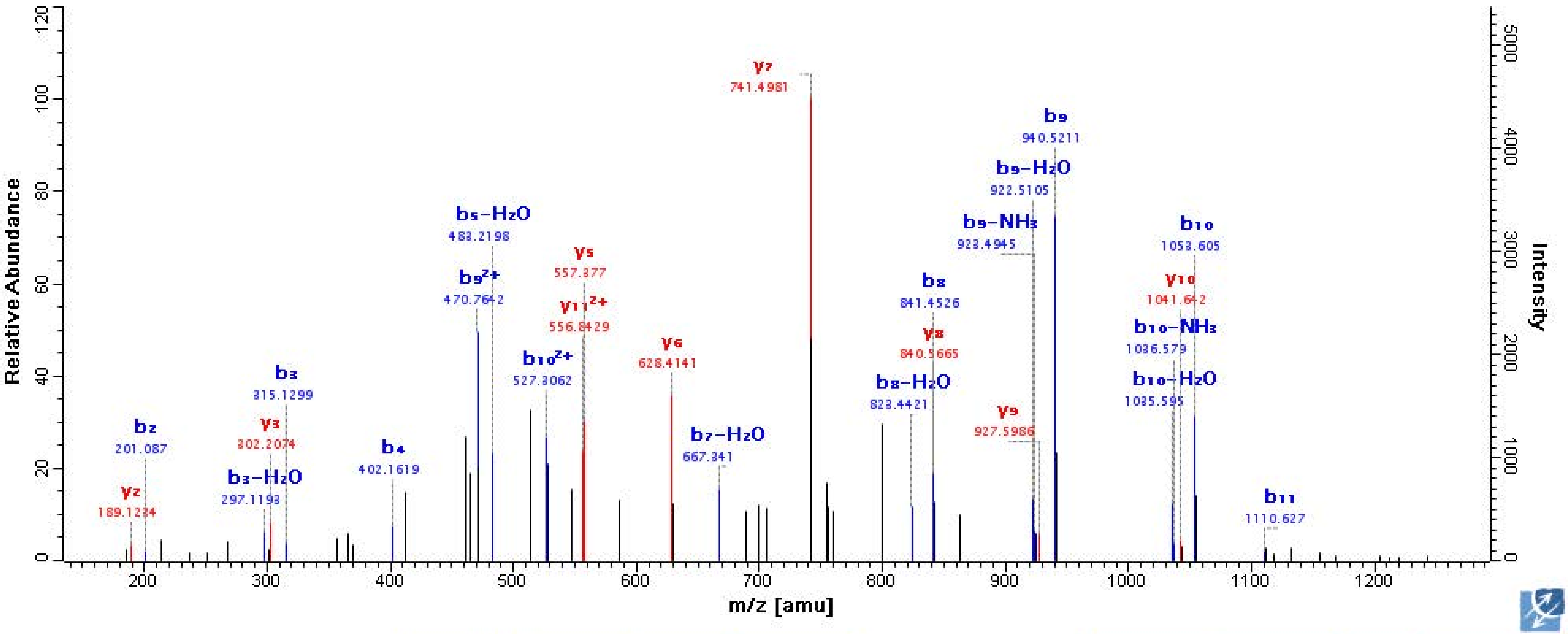
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	45 %
Protein Localisation:	166 ... 178

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	12				
	266.1248		266.1248	2	Q	11	1500.748		1500.748	
	381.1517	-0.014136	381.1517	3	D	10	1372.69		1372.69	
	452.1888		452.1888	4	A	9	1257.663		1257.663	
	565.2729	-0.026915	565.2729	5	I	8	1186.626		1186.626	
	678.357	+0.00334	678.357	6	I	7	1073.541	+0.070359	1073.541	
	841.4203	-0.010794	841.4203	7	Y	6	960.4574	+0.209477	480.7323	+0.103542
	1004.484	+0.020176	1004.484	8	Y	5	797.3941	-0.047751	399.2007	-0.029528
	1103.552	+0.140361	1103.552	9	V	4	634.3307	-0.030382	634.3307	
	1232.595	+0.028798	1232.595	10	E	3	535.2623		535.2623	
	1345.679	+0.144075	1345.679	11	I	2	406.2197	-0.054812	406.2197	
+0.059146	741.8724		1482.738	12	H	1	293.1357		293.1357	
				13	H	0	156.0768	+0.055785	156.0768	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F06
Scannumber: 28794
Protein: BSU14270; moeB
Peptide Score: 185.08
Method: ITMS; CID; 3





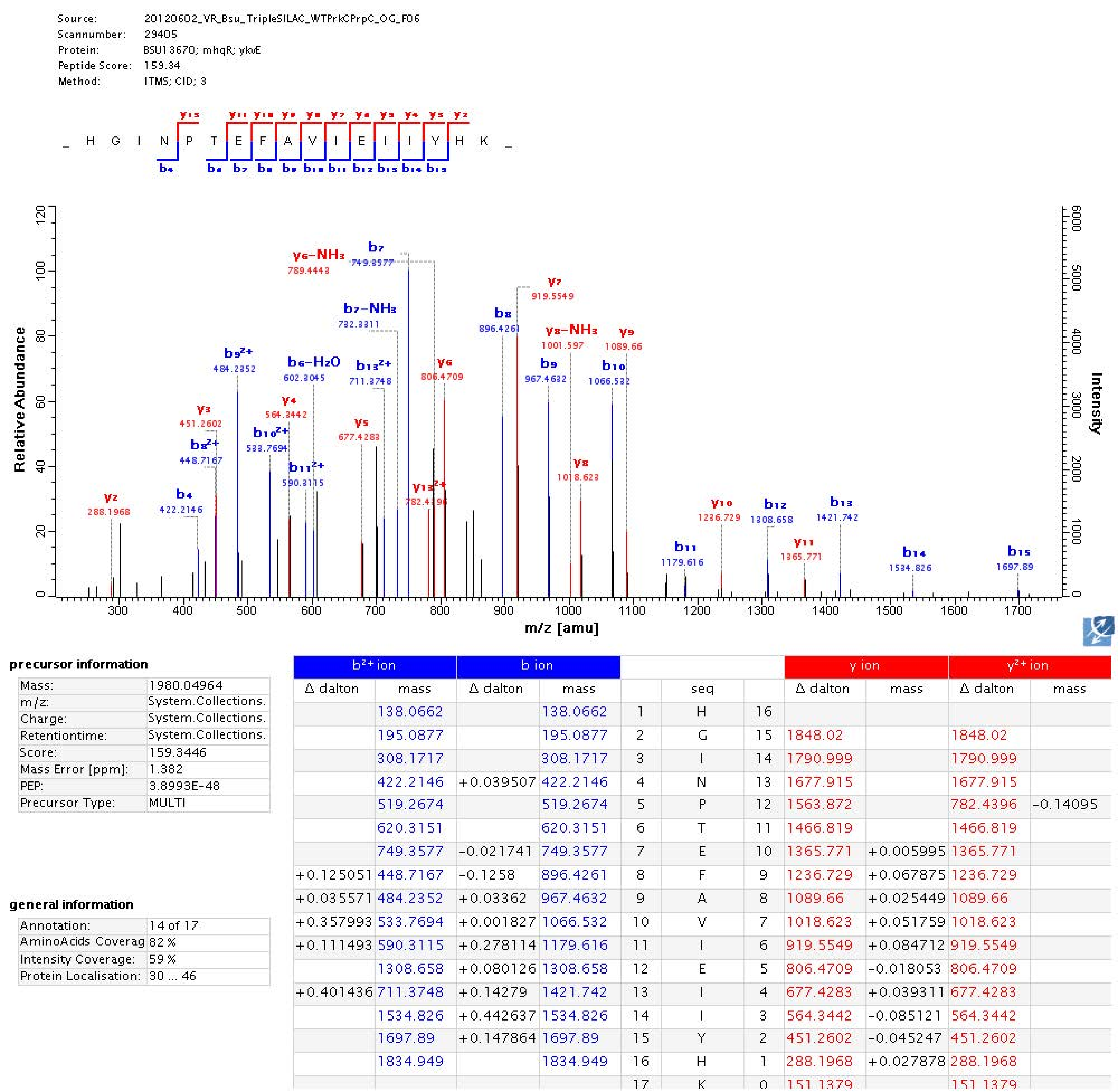
precursor information

Mass:	1240.71419
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	185.0814
Mass Error [ppm]:	0.20174
PEP:	8.3122E-74
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	55 %
Protein Localisation:	328 ... 339

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	11				
	201.087	+0.007102	201.087	2	A	10	1112.679		556.8429	-0.451285
	315.1299	+0.112643	315.1299	3	N	9	1041.642	+0.175755	1041.642	
	402.1619	+0.05443	402.1619	4	S	8	927.5986	+0.150079	927.5986	
	501.2304		501.2304	5	V	7	840.5665	+0.15275	840.5665	
	614.3144		614.3144	6	I	6	741.4981	+0.082187	741.4981	
	685.3515		685.3515	7	A	5	628.4141	+0.14324	628.4141	
	841.4526	+0.138178	841.4526	8	R	4	557.377	+0.06689	557.377	
+0.052362	470.7642	+0.119325	940.5211	9	V	3	401.2758		401.2758	
+0.049881	527.3062	+0.067121	1053.605	10	I	2	302.2074	-0.020299	302.2074	
	1110.627	+0.268558	1110.627	11	G	1	189.1234	-0.050905	189.1234	
				12	I	0	132.1019		132.1019	



Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F06
Scannumber:	29405
Protein:	BSU13670; mhqR; ykvE
Peptide Score:	159.34
Method:	ITMS; CID; 3

precursor information

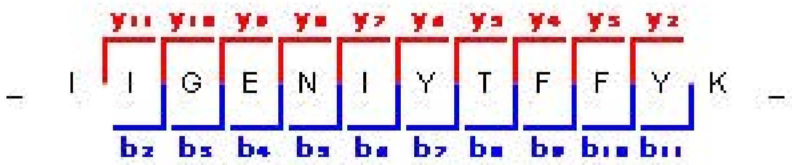
Mass:	1980.04964
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	159.3446
Mass Error [ppm]:	1.382
PEP:	3.8993E-48
Precursor Type:	MULTI

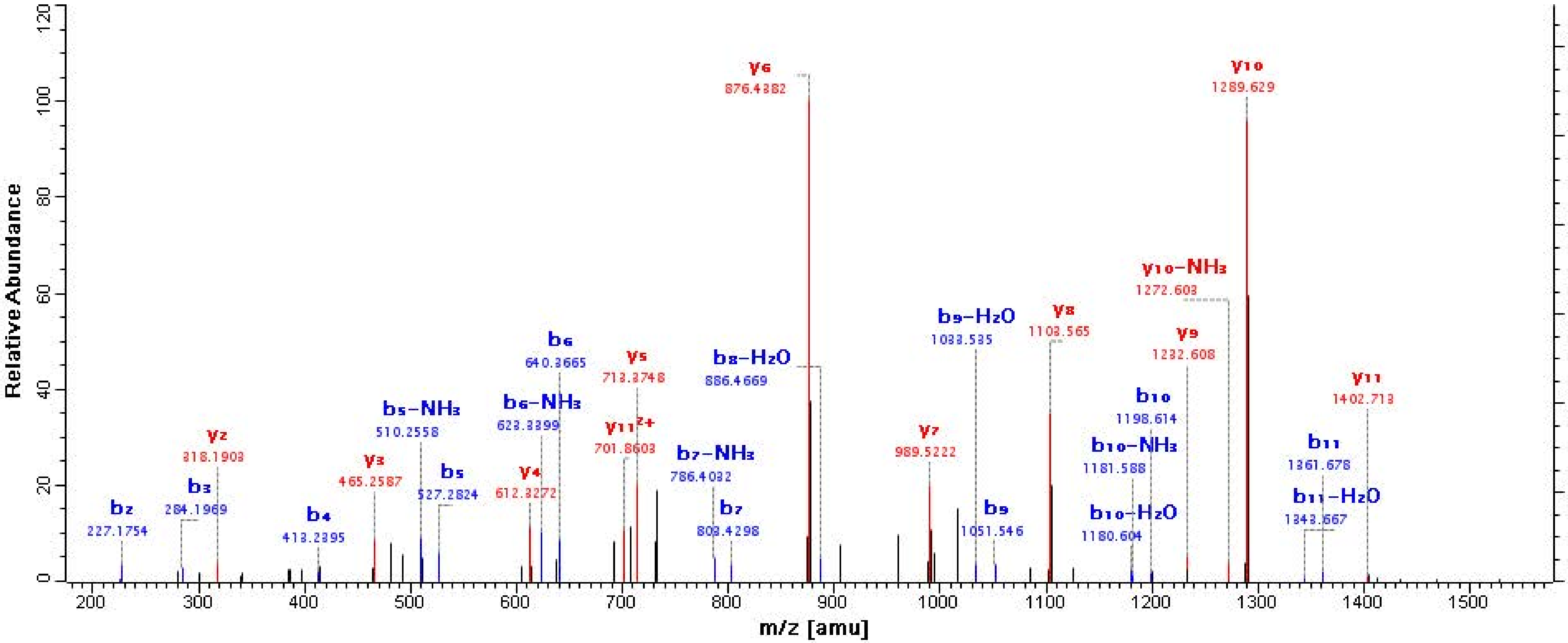
general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	59 %
Protein Localisation:	30 ... 46

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.0662		138.0662	1	H	16				
	195.0877		195.0877	2	G	15	1848.02		1848.02	
	308.1717		308.1717	3	I	14	1790.999		1790.999	
	422.2146	+0.039507	422.2146	4	N	13	1677.915		1677.915	
	519.2674		519.2674	5	P	12	1563.872		782.4396	-0.14095
	620.3151		620.3151	6	T	11	1466.819		1466.819	
	749.3577	-0.021741	749.3577	7	E	10	1365.771	+0.005995	1365.771	
+0.125051	448.7167	-0.1258	896.4261	8	F	9	1236.729	+0.067875	1236.729	
+0.035571	484.2352	+0.03362	967.4632	9	A	8	1089.66	+0.025449	1089.66	
+0.357993	533.7694	+0.001827	1066.532	10	V	7	1018.623	+0.051759	1018.623	
+0.111493	590.3115	+0.278114	1179.616	11	I	6	919.5549	+0.084712	919.5549	
	1308.658	+0.080126	1308.658	12	E	5	806.4709	-0.018053	806.4709	
+0.401436	711.3748	+0.14279	1421.742	13	I	4	677.4283	+0.039311	677.4283	
	1534.826	+0.442637	1534.826	14	I	3	564.3442	-0.085121	564.3442	
	1697.89	+0.147864	1697.89	15	Y	2	451.2602	-0.045247	451.2602	
	1834.949		1834.949	16	H	1	288.1968	+0.027878	288.1968	
				17	K	0	151.1379		151.1379	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F06
Scannumber:	30799
Protein:	BSU40140; yydJ
Peptide Score:	196.24
Method:	ITMS; CID; 3





precursor information

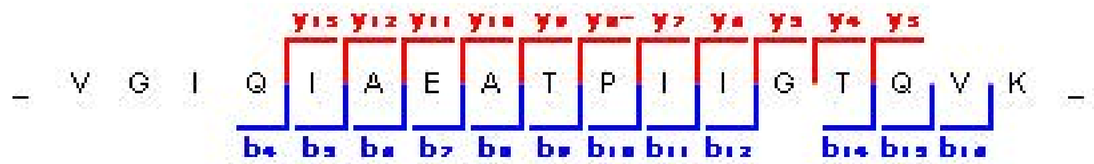
Mass:	1514.79071
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	196.239
Mass Error [ppm]:	0.42302
PEP:	4.8069E-90
Precursor Type:	ISO

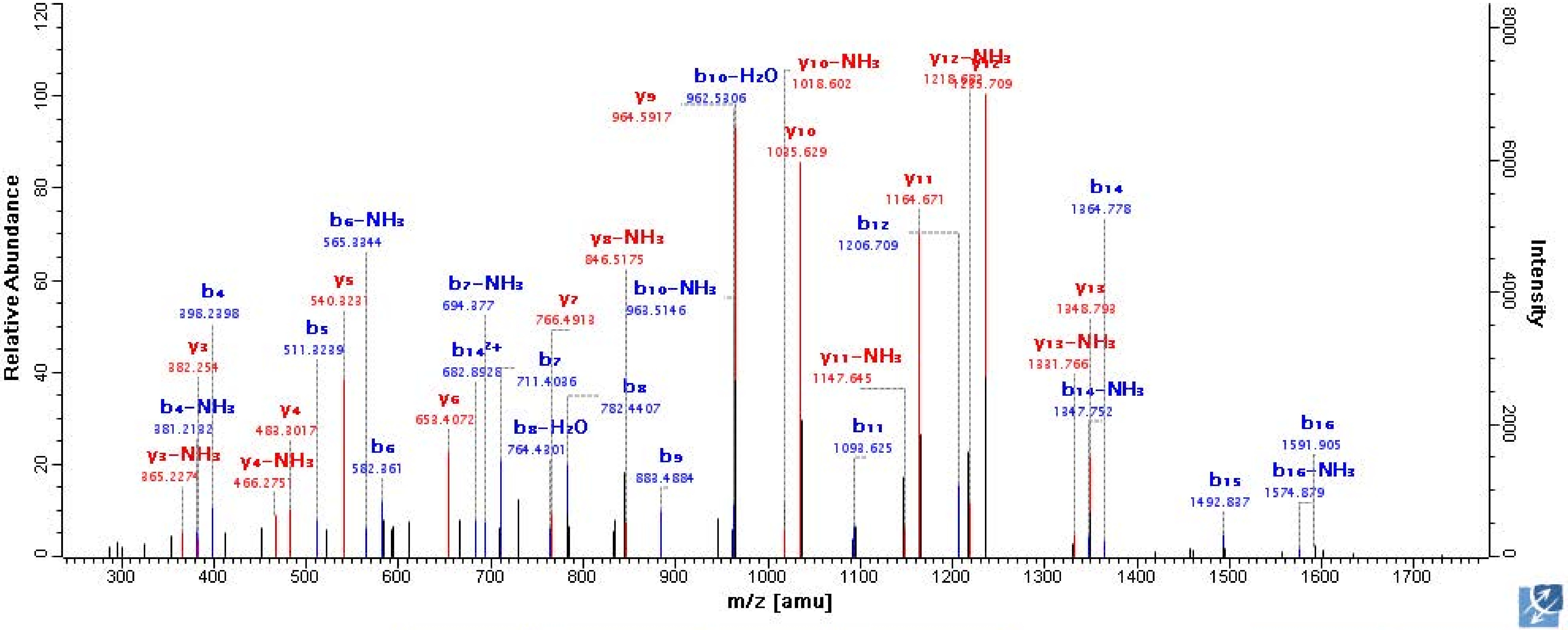
general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	55 %
Protein Localisation:	84 ... 95

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	11				
-0.2707719	227.17540443	2	I	10	1402.7132786	+0.1568386	701.86027753	-0.0256828
+0.1197212	284.19686815	3	G	9	1289.6292146	+0.0573088	1289.6292146	
-0.0034383	413.23946125	4	E	8	1232.6077509	+0.0586309	1232.6077509	
+0.0257168	527.28238869	5	N	7	1103.5651578	+0.0134555	1103.5651578	
-0.0099463	640.36645267	6	I	6	989.52223035	+0.0271471	989.52223035	
-0.0834067	803.42978121	7	Y	5	876.43816637	+0.0084889	876.43816637	
	904.47745969	8	T	4	713.37483783	+0.0821934	713.37483783	
+0.1814213	1051.5458736	9	F	3	612.32715935	+0.0222669	612.32715935	
+0.301484	1198.6142875	10	F	2	465.25874544	-0.0536673	465.25874544	
+0.0191613	1361.6776161	11	Y	1	318.19033152	+0.1568059	318.19033152	
		12	K	0	155.12700298		155.12700298	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F07
Scannumber: 24443
Protein: bfcB; BSU22550; qcrB
Peptide Score: 194.77
Method: ITMS; CID; 3





precursor information

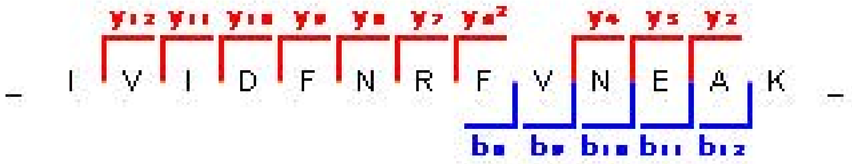
Mass:	1737.00359
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	194.773
Mass Error [ppm]:	-0.028233
PEP:	2.9127E-89
Precursor Type:	MULTI

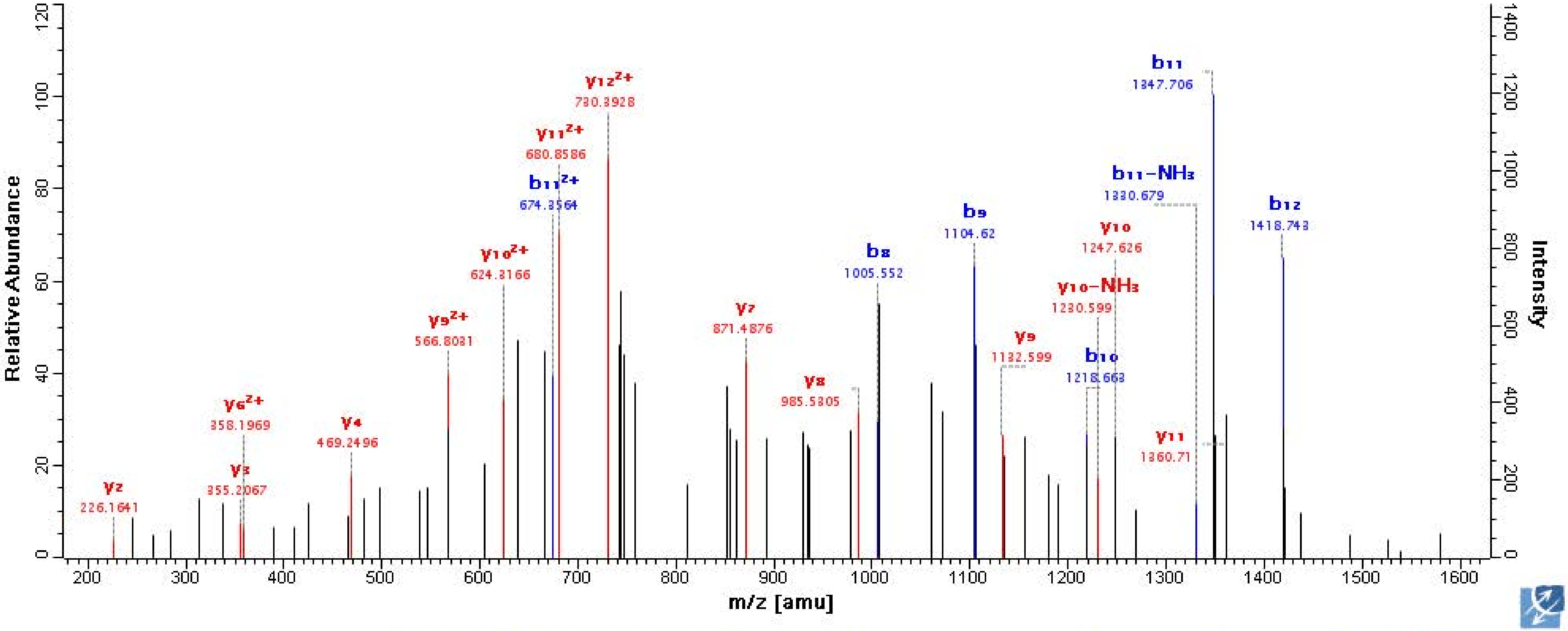
general information

Annotation:	13 of 17
AminoAcids Coverag	76 %
Intensity Coverage:	64 %
Protein Localisation:	158 ... 174

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	100.07569038		100.07569038	1	V	16		
	157.09715411		157.09715411	2	G	15	1646.9566968	
	270.18121809		270.18121809	3	I	14	1589.935233	
	398.2397956	-0.098194	398.2397956	4	Q	13	1476.8511691	
	511.32385958	-0.0717233	511.32385958	5	I	12	1348.7925915	-0.0013318
	582.36097337	-0.0816155	582.36097337	6	A	11	1235.7085276	+0.0061941
	711.40356646	-0.0125142	711.40356646	7	E	10	1164.6714138	+0.0005833
	782.44068025	-0.0274722	782.44068025	8	A	9	1035.6288207	+0.0041139
	883.48835872	+0.051009	883.48835872	9	T	8	964.5917069	-0.0151078
	980.54112258		980.54112258	10	P	7	863.54402842	
	1093.6251866	-0.0592686	1093.6251866	11	I	6	766.49126457	-0.1429369
	1206.7092505	+0.0135278	1206.7092505	12	I	5	653.40720059	-0.0322616
	1263.7307143		1263.7307143	13	G	4	540.32313661	-0.1046918
+0.4871092	682.8928346	+0.0642586	1364.7783927	14	T	3	483.30167289	-0.0749883
	1492.8369702	+0.1470385	1492.8369702	15	Q	2	382.25399441	+0.0868259
	1591.9053842	+0.101818	1591.9053842	16	V	1	254.1954169	
				17	K	0	155.12700298	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F07
Scannumber:	24907
Protein:	BSU32060; yuiD
Peptide Score:	118.87
Method:	ITMS; CID; 3





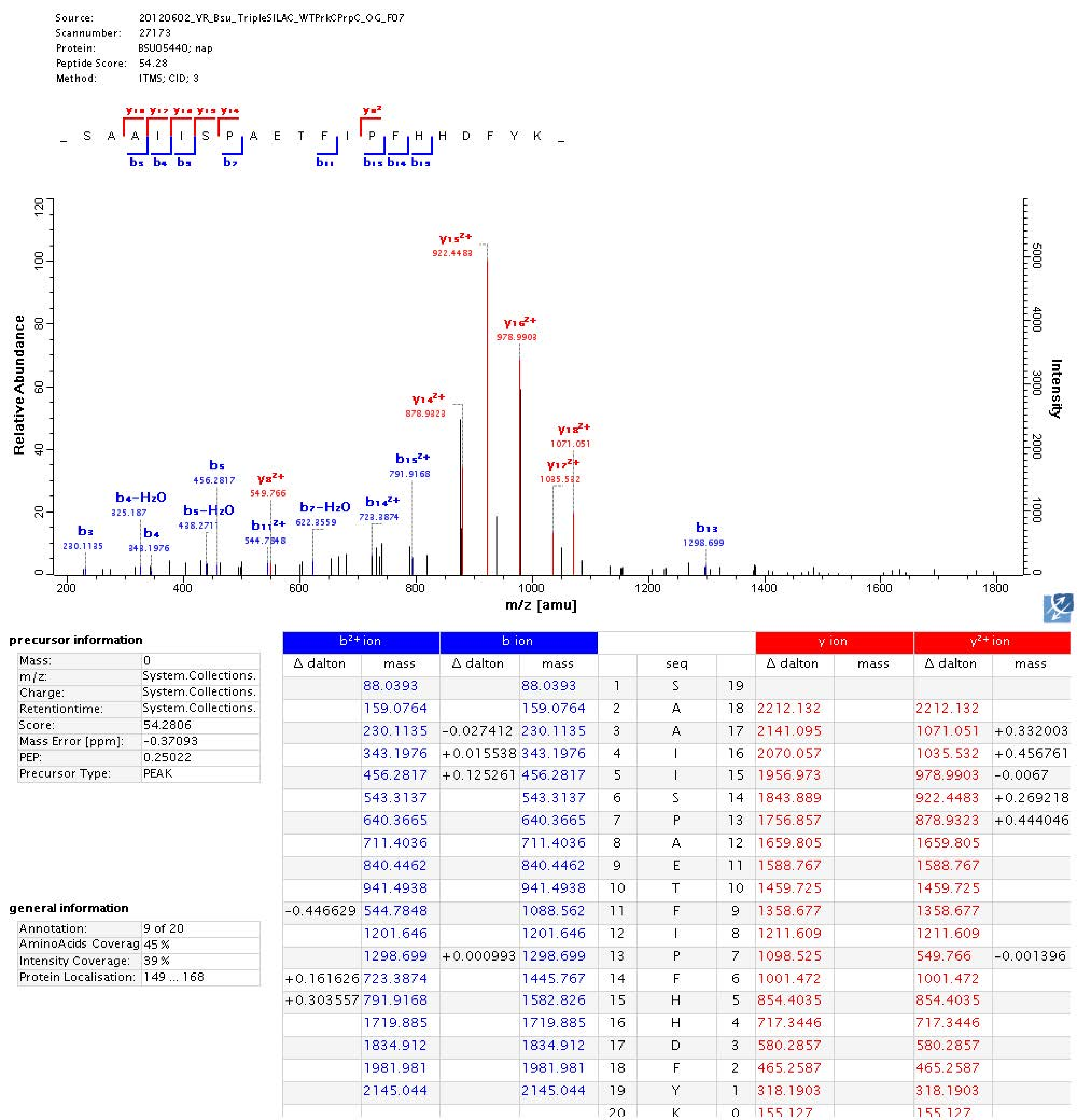
precursor information

Mass:	1571.8548
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.8658
Mass Error [ppm]:	-0.20998
PEP:	6.5467E-09
Precursor Type:	ISO

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	38 %
Protein Localisation:	102 ... 114

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				
	213.1598		213.1598	2	V	11	1459.778		730.3928	+0.379409
	326.2438		326.2438	3	I	10	1360.71	+0.178625	680.8586	-0.076069
	441.2708		441.2708	4	D	9	1247.626	+0.100824	624.3166	+0.250448
	588.3392		588.3392	5	F	8	1132.599	+0.192098	566.8031	+0.025211
	702.3821		702.3821	6	N	7	985.5305	+0.223891	985.5305	
	858.4832		858.4832	7	R	6	871.4876	+0.275607	871.4876	
	1005.552	+0.065987	1005.552	8	F	5	715.3865		358.1969	+0.104277
	1104.62	+0.167922	1104.62	9	V	4	568.3181		568.3181	
	1218.663	+0.130244	1218.663	10	N	3	469.2496	+0.140072	469.2496	
+0.428127	674.3564	+0.097905	1347.706	11	E	2	355.2067	-0.031905	355.2067	
	1418.743	+0.158569	1418.743	12	A	1	226.1641	-0.037972	226.1641	
				13	K	0	155.127		155.127	



Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F07
Scannumber: 27173
Protein: BSU05440; nap
Peptide Score: 54.28
Method: ITMS; CID; 3

precursor information

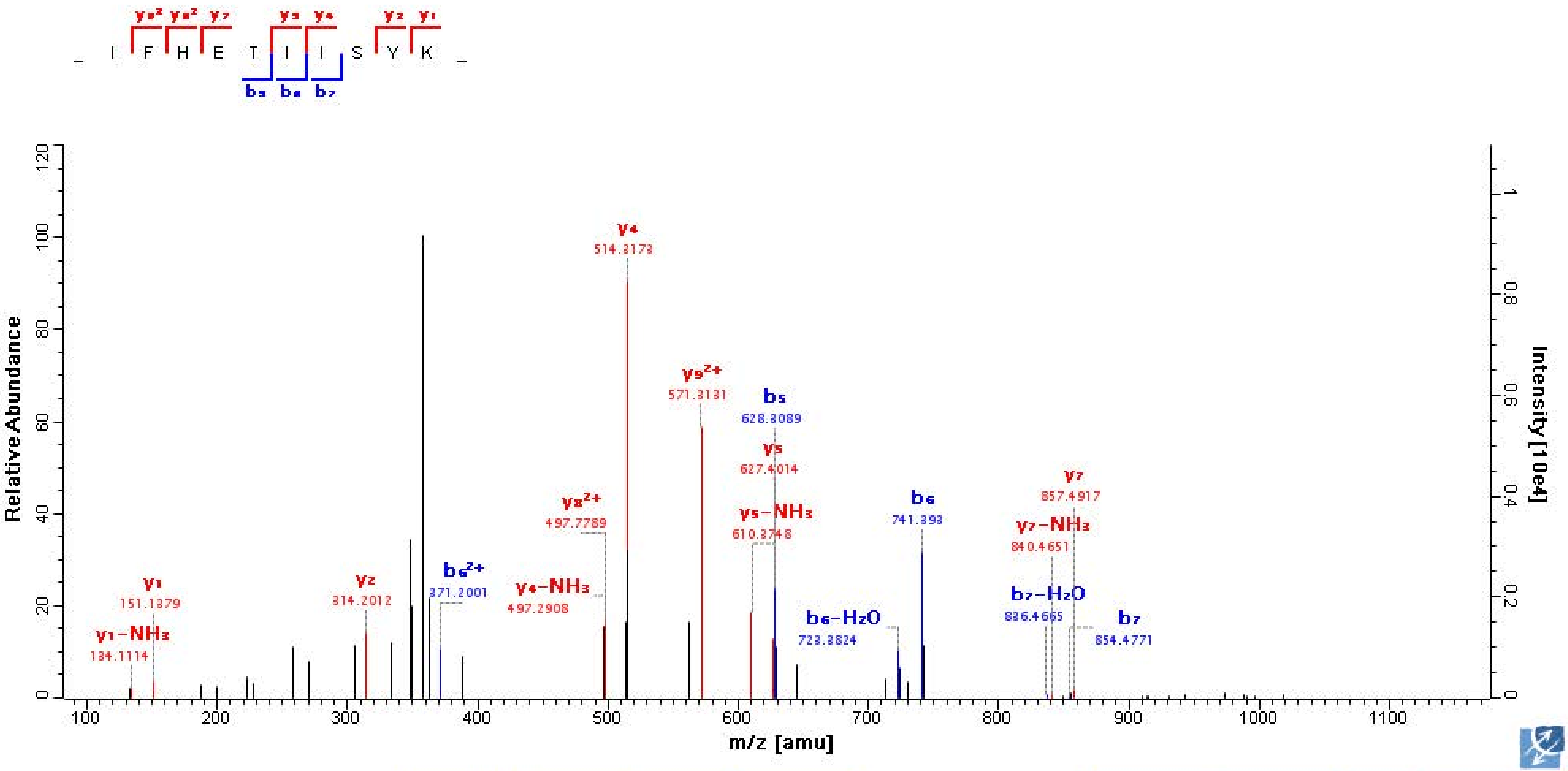
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	54.2806
Mass Error [ppm]:	-0.37093
PEP:	0.25022
Precursor Type:	PEAK

general information

Annotation:	9 of 20
AminoAcids Coverag	45 %
Intensity Coverage:	39 %
Protein Localisation:	149 ... 168

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	19				
	159.0764		159.0764	2	A	18	2212.132		2212.132	
	230.1135	-0.027412	230.1135	3	A	17	2141.095		1071.051	+0.332003
	343.1976	+0.015538	343.1976	4	I	16	2070.057		1035.532	+0.456761
	456.2817	+0.125261	456.2817	5	I	15	1956.973		978.9903	-0.0067
	543.3137		543.3137	6	S	14	1843.889		922.4483	+0.269218
	640.3665		640.3665	7	P	13	1756.857		878.9323	+0.444046
	711.4036		711.4036	8	A	12	1659.805		1659.805	
	840.4462		840.4462	9	E	11	1588.767		1588.767	
	941.4938		941.4938	10	T	10	1459.725		1459.725	
-0.446629	544.7848		1088.562	11	F	9	1358.677		1358.677	
	1201.646		1201.646	12	I	8	1211.609		1211.609	
	1298.699	+0.000993	1298.699	13	P	7	1098.525		549.766	-0.001396
+0.161626	723.3874		1445.767	14	F	6	1001.472		1001.472	
+0.303557	791.9168		1582.826	15	H	5	854.4035		854.4035	
	1719.885		1719.885	16	H	4	717.3446		717.3446	
	1834.912		1834.912	17	D	3	580.2857		580.2857	
	1981.981		1981.981	18	F	2	465.2587		465.2587	
	2145.044		2145.044	19	Y	1	318.1903		318.1903	
				20	K	0	155.127		155.127	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F08
Scannumber: 16578
Protein: BSU14250; cse15; yknT
Peptide Score: 118.5
Method: ITMS; CID; 3



precursor information

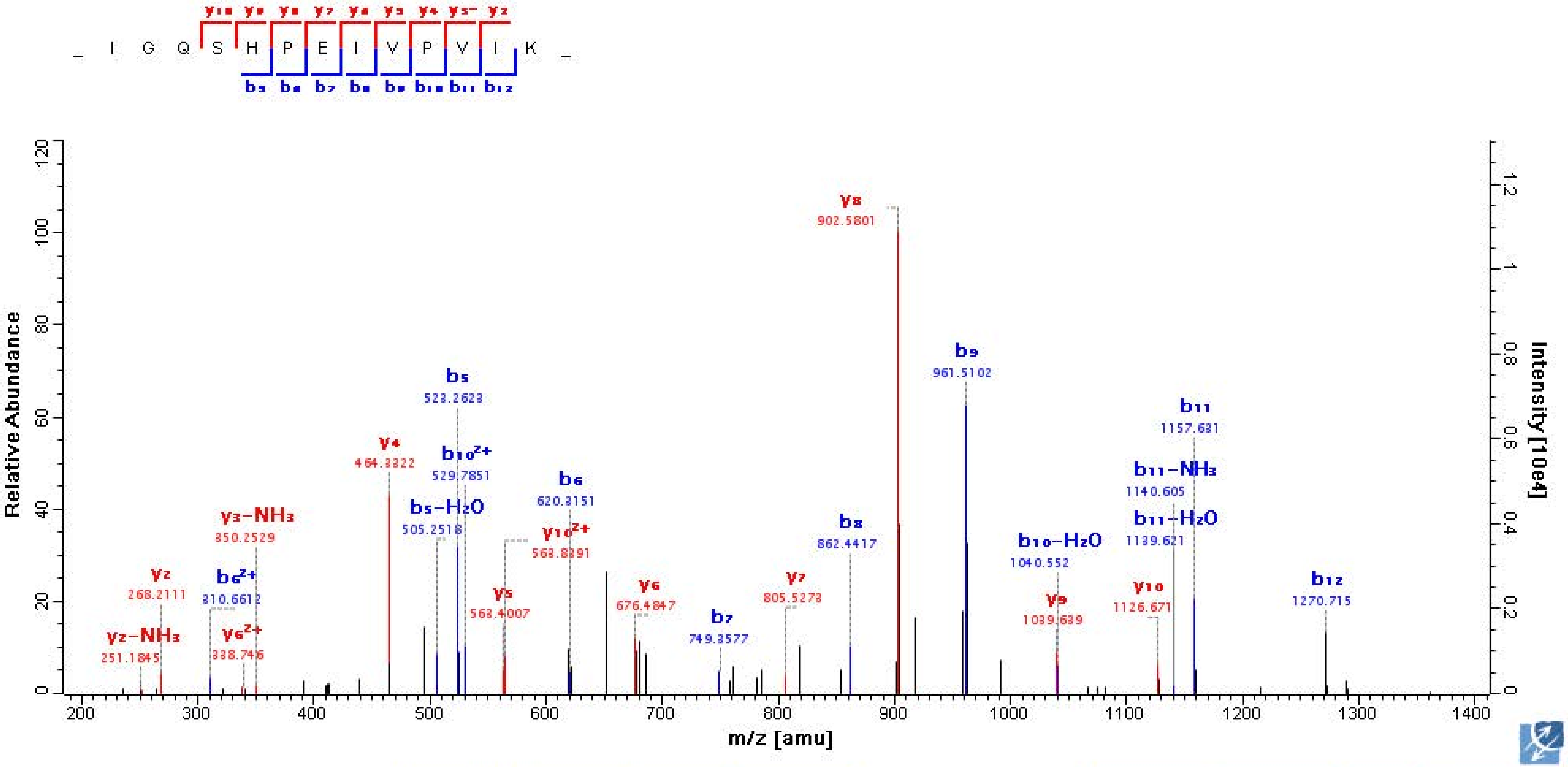
Mass:	1253.69593
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.4951
Mass Error [ppm]:	0.12088
PEP:	0.00040182
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	46 %
Protein Localisation:	205 ... 214

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	9				
	261.1598		261.1598	2	F	8	1141.619		571.3131	+0.3151
	398.2187		398.2187	3	H	7	994.5506		497.7789	+0.398562
	527.2613		527.2613	4	E	6	857.4917	+0.277436	857.4917	
	628.3089	+0.115073	628.3089	5	T	5	728.4491		728.4491	
+0.114985	371.2001	+0.143436	741.393	6	I	4	627.4014	-0.022917	627.4014	
	854.4771	+0.085678	854.4771	7	I	3	514.3173	+0.097036	514.3173	
	941.5091		941.5091	8	S	2	401.2333		401.2333	
	1104.572		1104.572	9	Y	1	314.2012	+0.286431	314.2012	
				10	K	0	151.1379	+0.10977	151.1379	

Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F08
Scannumber: 16777
Protein: BSU35710; tagG
Peptide Score: 126.83
Method: ITMS; CID; 3



precursor information

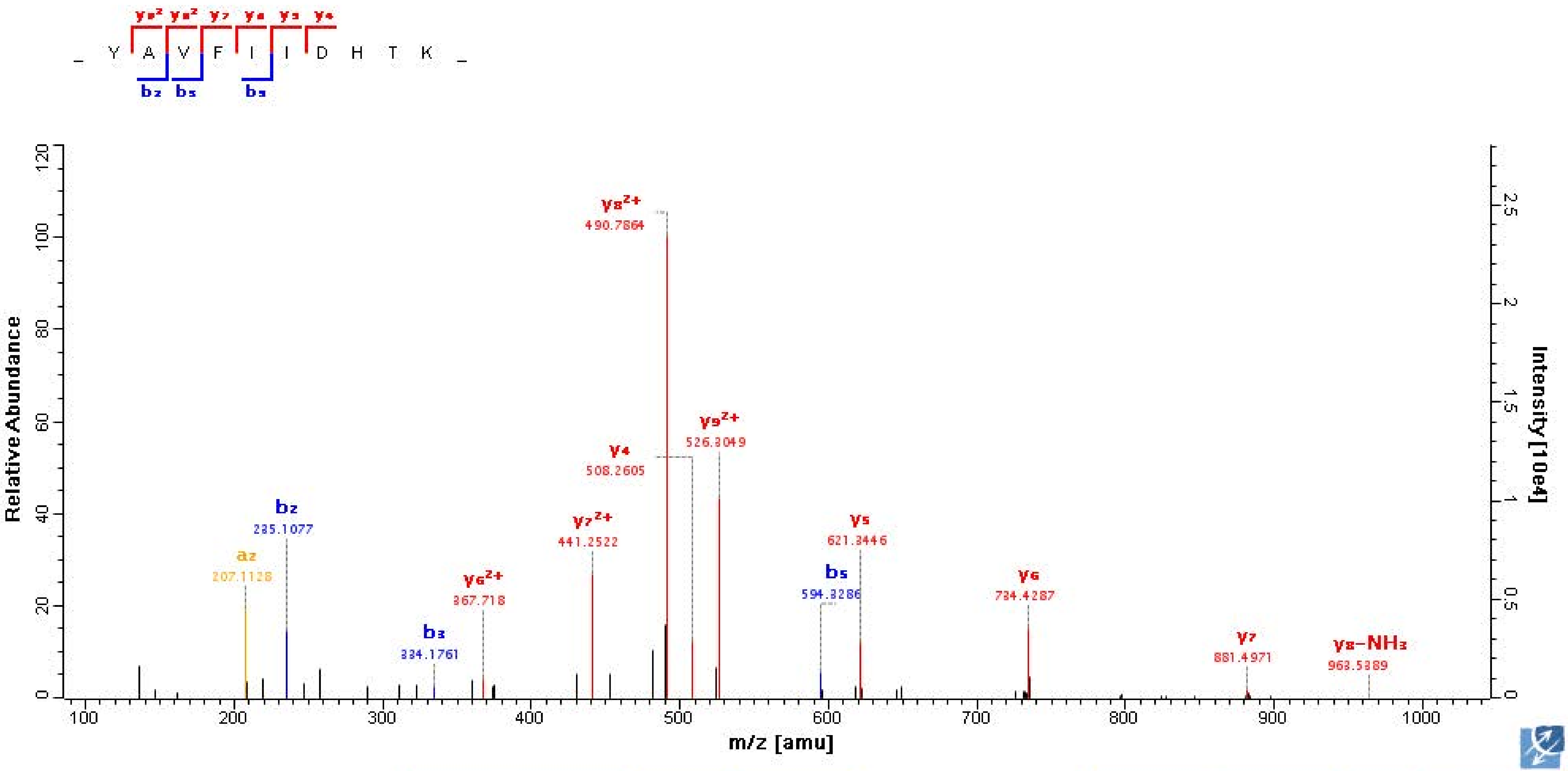
Mass:	1415.81365
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	126.8319
Mass Error [ppm]:	0.0014104
PEP:	2.5817E-13
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoActids Coverag	69 %
Intensity Coverage:	56 %
Protein Localisation:	206 ... 218

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.0913		114.0913	1	I	12				
	171.1128		171.1128	2	G	11	1311.751		1311.751	
	299.1714		299.1714	3	Q	10	1254.73		1254.73	
	386.2034		386.2034	4	S	9	1126.671	+0.129151	563.8391	-0.059058
	523.2623	-0.018425	523.2623	5	H	8	1039.639	+0.025437	1039.639	
-0.400225	310.6612	-0.080284	620.3151	6	P	7	902.5801	+0.035216	902.5801	
	749.3577	-0.041273	749.3577	7	E	6	805.5273	-0.00632	805.5273	
	862.4417	-0.028352	862.4417	8	I	5	676.4847	+0.005023	338.746	-0.406217
	961.5102	+0.040441	961.5102	9	V	4	563.4007	-0.263696	563.4007	
+0.095944	529.7851		1058.563	10	P	3	464.3322	-0.036102	464.3322	
	1157.631	+0.023206	1157.631	11	V	2	367.2795		367.2795	
	1270.715	-0.011541	1270.715	12	I	1	268.2111	-0.091743	268.2111	
				13	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F08
Scannumber:	19218
Protein:	BSU20010; yojV; yosT
Peptide Score:	96.71
Method:	ITMS; CID; 3



precursor information

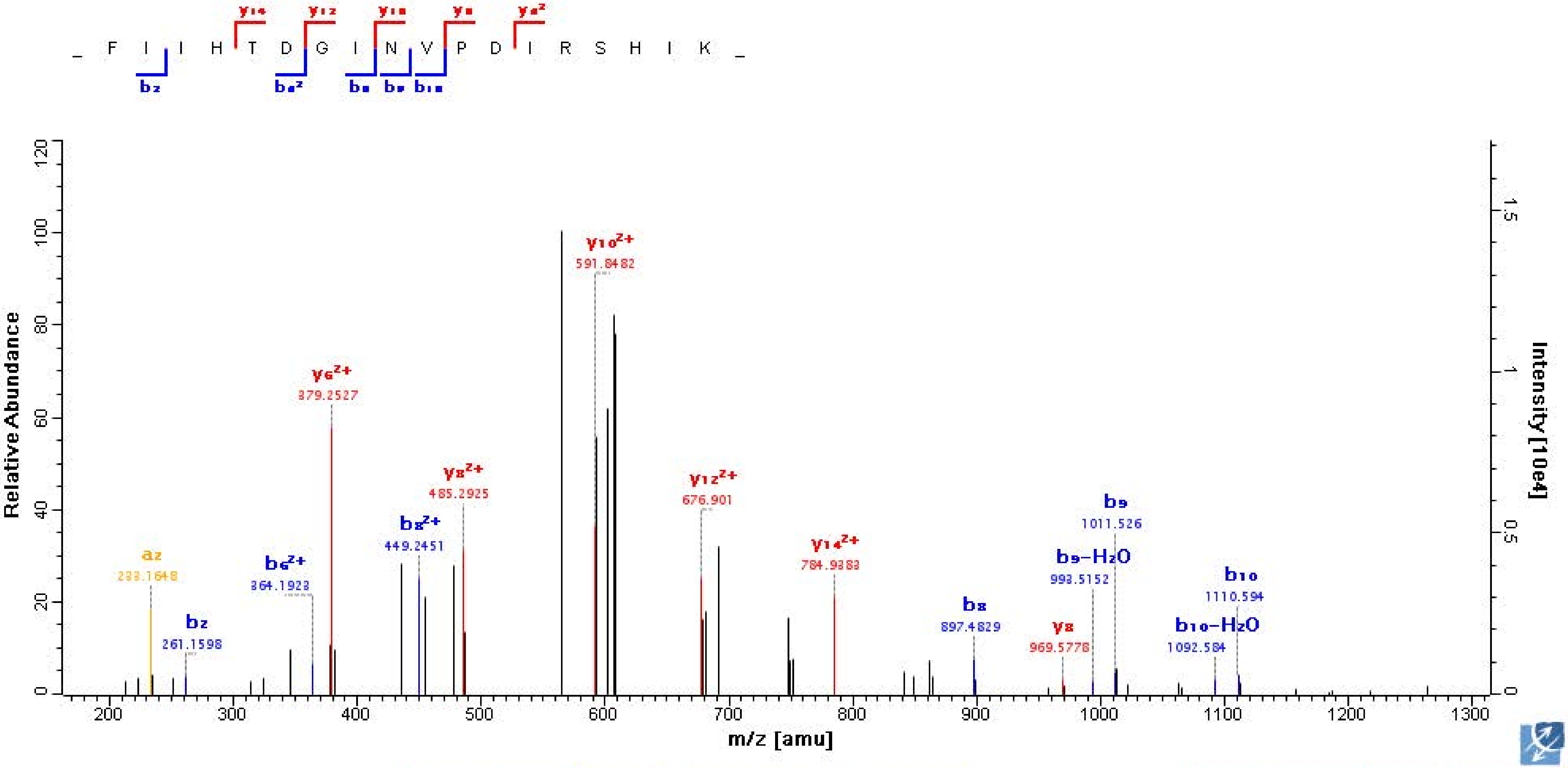
Mass:	1205.64496
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	96.71067
Mass Error [ppm]:	0.4167
PEP:	0.00072653
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	70 %
Protein Localisation:	93 ... 102

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	9				
-0.039837	207.1128	-0.054801	235.1077	2	A	8	1051.603		526.3049	+0.2022
	306.1812	+0.015213	334.1761	3	V	7	980.5655		490.7864	+0.13134
	453.2496		481.2445	4	F	6	881.4971	+0.220939	441.2522	+0.154561
	566.3337	+0.043948	594.3286	5	I	5	734.4287	+0.046739	367.718	+0.289537
	679.4178		707.4127	6	I	4	621.3446	+0.23499	621.3446	
	794.4447		822.4396	7	D	3	508.2605	-0.010536	508.2605	
	931.5036		959.4985	8	H	2	393.2336		393.2336	
	1032.551		1060.546	9	T	1	256.1747		256.1747	
				10	K	0	155.127		155.127	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F08
Scannumber:	21775
Protein:	BSU04740; rsbX
Peptide Score:	58.89
Method:	ITMS; CID; 3



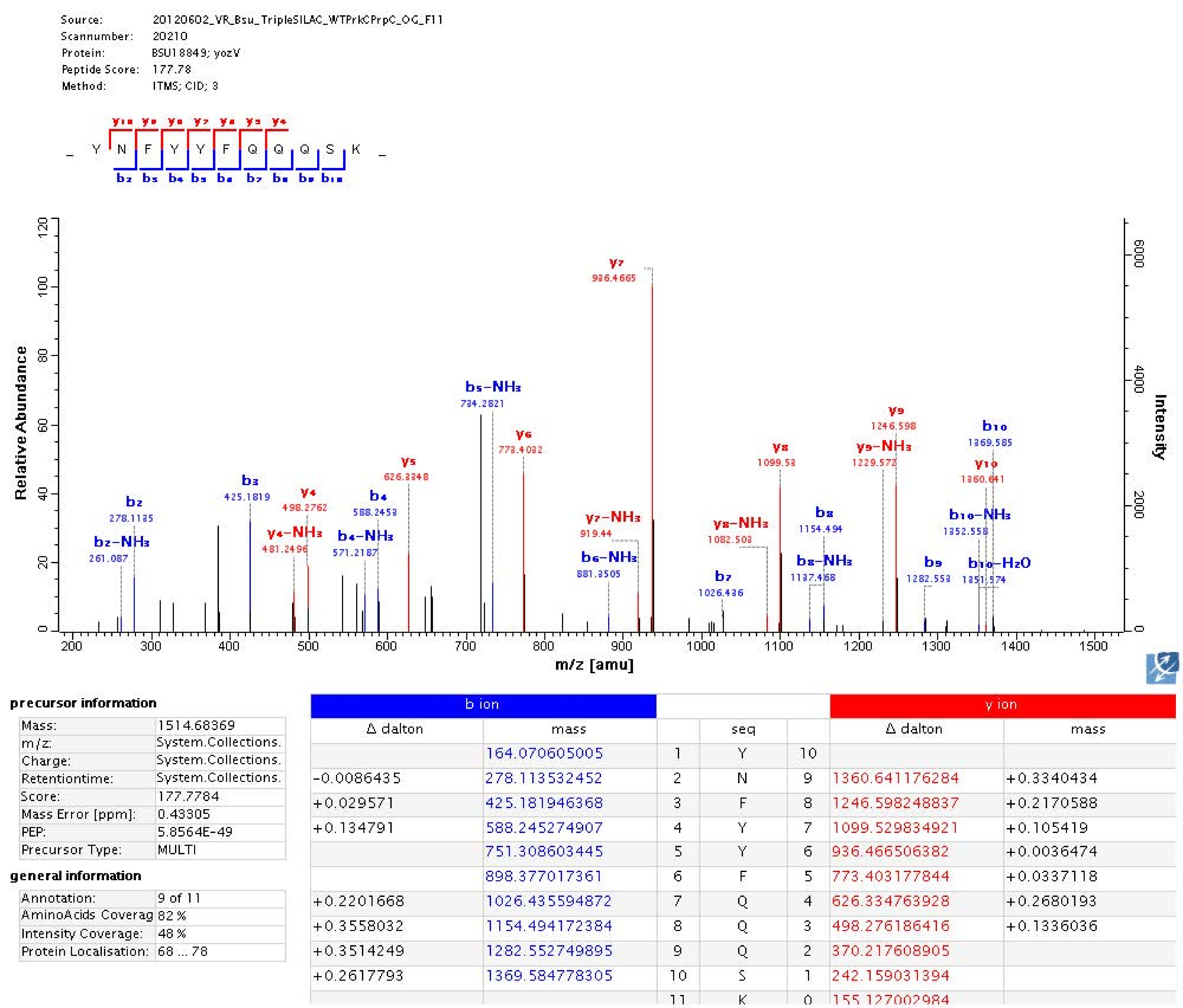
precursor information

Mass:	2074.13255
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	58.88521
Mass Error [ppm]:	0.092511
PEP:	0.001564
Precursor Type:	MULTI

general information

Annotation:	9 of 18
AminoAcids Coverag	50 %
Intensity Coverage:	27 %
Protein Localisation:	151 ... 168

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
	120.081		148.076		148.076	1	F	17				
-0.0156	233.165		261.16	+0.14161	261.16	2	I	16	1932.1		1932.1	
	346.249		374.244		374.244	3	I	15	1819.01		1819.01	
	483.308		511.303		511.303	4	H	14	1705.93		1705.93	
	584.355		612.35		612.35	5	T	13	1568.87		784.938	+0.0083
	699.382	+0.02418	864.192		727.377	6	D	12	1467.82		1467.82	
	756.404		784.399		784.399	7	G	11	1352.79		676.901	+0.4538
	869.488	+0.11204	449.245	+0.26016	897.483	8	I	10	1295.77		1295.77	
	983.531		1011.53	+0.32997	1011.53	9	N	9	1182.69		591.848	-0.0542
	1082.6		1110.59	+0.33461	1110.59	10	V	8	1068.65		1068.65	
	1179.65		1207.65		1207.65	11	P	7	969.578	+0.15884	485.293	+0.0911
	1294.68		1322.67		1322.67	12	D	6	872.525		872.525	
	1407.76		1435.76		1435.76	13	I	5	757.498		379.253	+0.4060
	1563.86		1591.86		1591.86	14	R	4	644.414		644.414	
	1650.9		1678.89		1678.89	15	S	3	488.313		488.313	
	1787.96		1815.95		1815.95	16	H	2	401.281		401.281	
	1901.04		1929.03		1929.03	17	I	1	264.222		264.222	
						18	K	0	151.138		151.138	



Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F11
Scannumber: 20210
Protein: BSU18849; yozV
Peptide Score: 177.78
Method: ITMS; CID; 3

precursor information

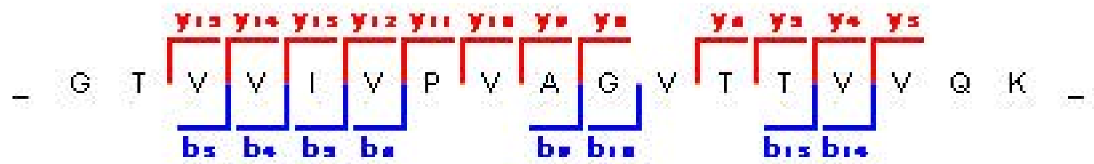
Mass:	1514.68369
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	177.7784
Mass Error [ppm]:	0.43305
PEP:	5.8564E-49
Precursor Type:	MULTI

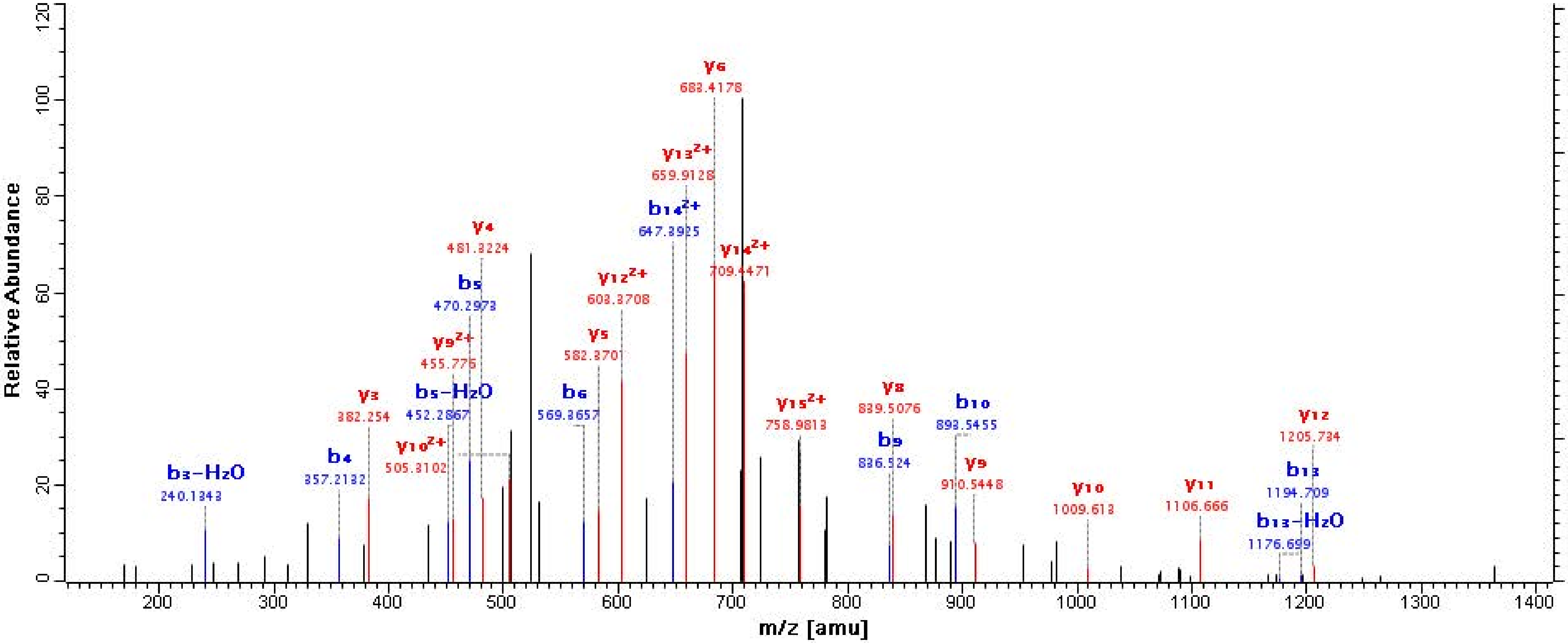
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	48 %
Protein Localisation:	68 ... 78

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	164.070605005	1	Y	10		
-0.0086435	278.113532452	2	N	9	1360.641176284	+0.3340434
+0.029571	425.181946368	3	F	8	1246.598248837	+0.2170588
+0.134791	588.245274907	4	Y	7	1099.529834921	+0.105419
	751.308603445	5	Y	6	936.466506382	+0.0036474
	898.377017361	6	F	5	773.403177844	+0.0337118
+0.2201668	1026.435594872	7	Q	4	626.334763928	+0.2680193
+0.3558032	1154.494172384	8	Q	3	498.276186416	+0.1336036
+0.3514249	1282.552749895	9	Q	2	370.217608905	
+0.2617793	1369.584778305	10	S	1	242.159031394	
		11	K	0	155.127002984	

Source:	20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F12
Scannumber:	21791
Protein:	BSU04320; ydaO
Peptide Score:	121.18
Method:	ITMS; CID; 3





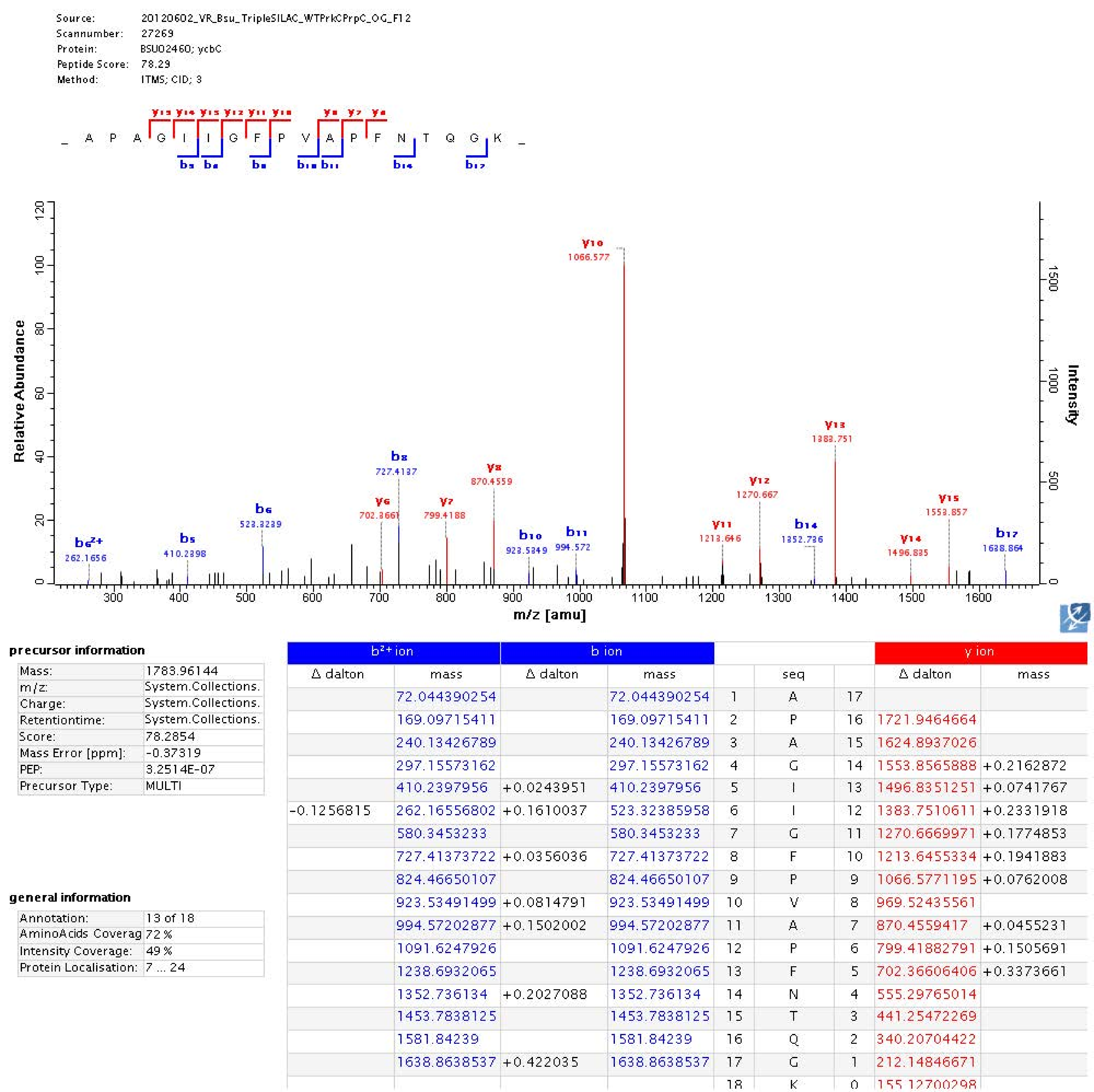
precursor information

Mass:	1666.00307
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	121.1825
Mass Error [ppm]:	0.0984
PEP:	4.8181E-20
Precursor Type:	MULTI

general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	47 %
Protein Localisation:	473 ... 489

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	16				
	159.0764		159.0764	2	T	15	1618.003		1618.003	
	258.1448		258.1448	3	V	14	1516.955		758.9813	+0.335148
	357.2132	-0.039907	357.2132	4	V	13	1417.887		709.4471	-0.058807
	470.2973	+0.032829	470.2973	5	I	12	1318.818		659.9128	+0.078916
	569.3657	+0.051146	569.3657	6	V	11	1205.734	+0.236721	603.3708	+0.354163
	666.4185		666.4185	7	P	10	1106.666	+0.227864	1106.666	
	765.4869		765.4869	8	V	9	1009.613	+0.329029	505.3102	-0.056317
	836.524	+0.250215	836.524	9	A	8	910.5448	+0.144147	455.776	+0.124374
	893.5455	+0.241325	893.5455	10	G	7	839.5076	+0.240648	839.5076	
	992.6139		992.6139	11	V	6	782.4862		782.4862	
	1093.662		1093.662	12	T	5	683.4178	+0.027608	683.4178	
	1194.709	+0.320657	1194.709	13	T	4	582.3701	-0.016693	582.3701	
+0.177293	647.3925		1293.778	14	V	3	481.3224	+0.161845	481.3224	
	1392.846		1392.846	15	V	2	382.254	+0.210056	382.254	
	1520.905		1520.905	16	Q	1	283.1856		283.1856	
				17	K	0	155.127		155.127	



Source: 20120602_VR_Bsu_TripleSILAC_WTPrkCPrpC_OG_F12
Scannumber: 27269
Protein: BSU02460; ycbC
Peptide Score: 78.29
Method: ITMS; CID; 3

precursor information

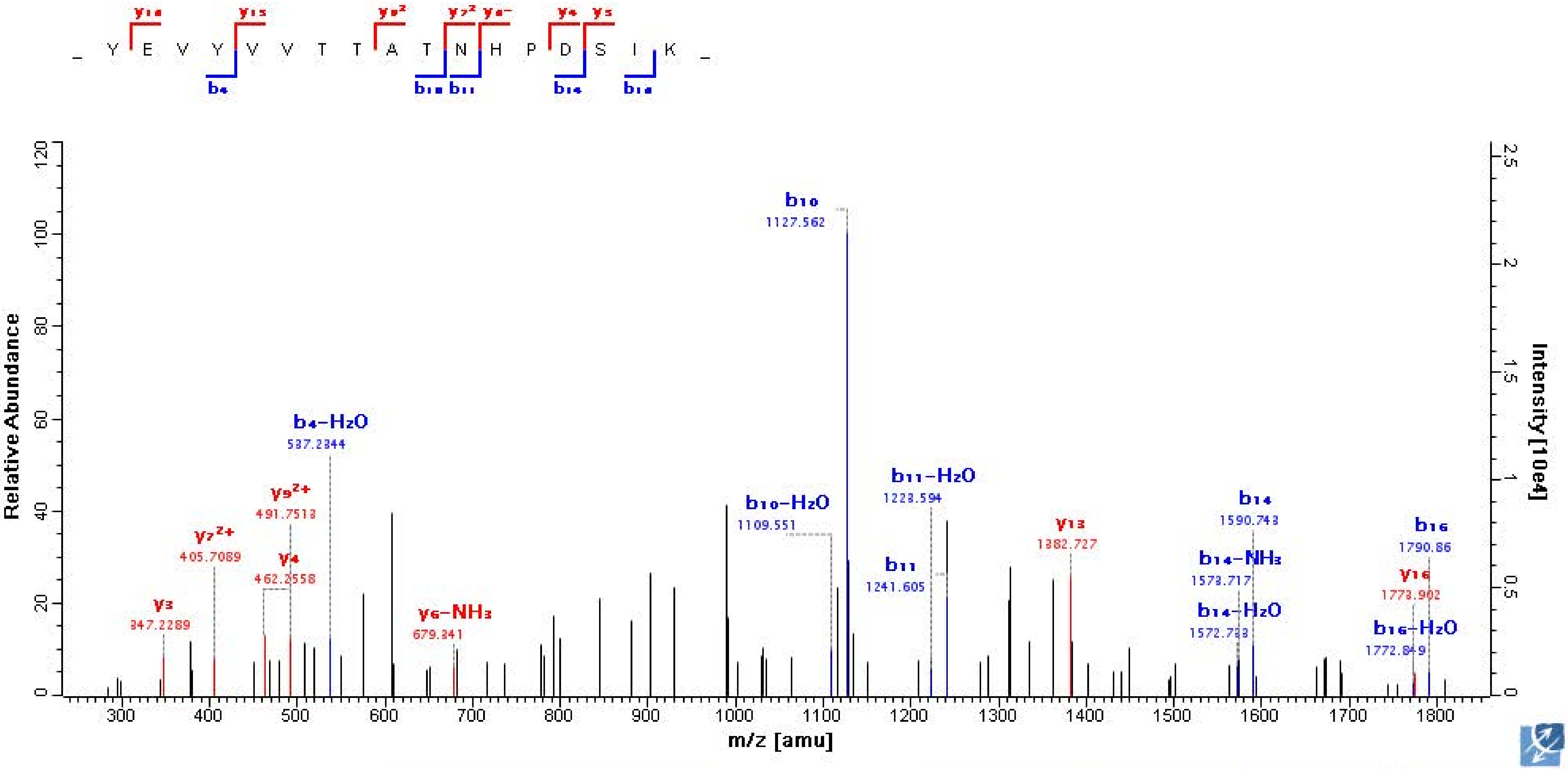
Mass:	1783.96144
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	78.2854
Mass Error [ppm]:	-0.37319
PEP:	3.2514E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	49 %
Protein Localisation:	7 ... 24

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	17		
	169.09715411		169.09715411	2	P	16	1721.9464664	
	240.13426789		240.13426789	3	A	15	1624.8937026	
	297.15573162		297.15573162	4	G	14	1553.8565888	+0.2162872
	410.2397956	+0.0243951	410.2397956	5	I	13	1496.8351251	+0.0741767
-0.1256815	262.16556802	+0.1610037	523.32385958	6	I	12	1383.7510611	+0.2331918
	580.3453233		580.3453233	7	G	11	1270.6669971	+0.1774853
	727.41373722	+0.0356036	727.41373722	8	F	10	1213.6455334	+0.1941883
	824.46650107		824.46650107	9	P	9	1066.5771195	+0.0762008
	923.53491499	+0.0814791	923.53491499	10	V	8	969.52435561	
	994.57202877	+0.1502002	994.57202877	11	A	7	870.4559417	+0.0455231
	1091.6247926		1091.6247926	12	P	6	799.41882791	+0.1505691
	1238.6932065		1238.6932065	13	F	5	702.36606406	+0.3373661
	1352.736134	+0.2027088	1352.736134	14	N	4	555.29765014	
	1453.7838125		1453.7838125	15	T	3	441.25472269	
	1581.84239		1581.84239	16	Q	2	340.20704422	
	1638.8638537	+0.422035	1638.8638537	17	G	1	212.14846671	
				18	K	0	155.12700298	

Source: 20130124_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_OG_F02
Scannumber: 19169
Protein: BSU20270; yorS
Peptide Score: 62.36
Method: ITMS; CID; 3



precursor information

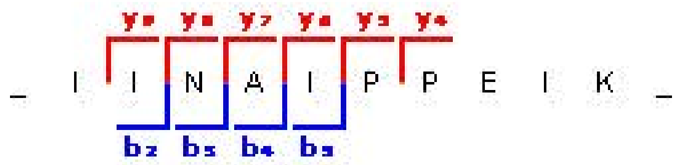
Mass:	1935.95558
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	62.35712
Mass Error [ppm]:	-1.1505
PEP:	0.0010923
Precursor Type:	MULTI

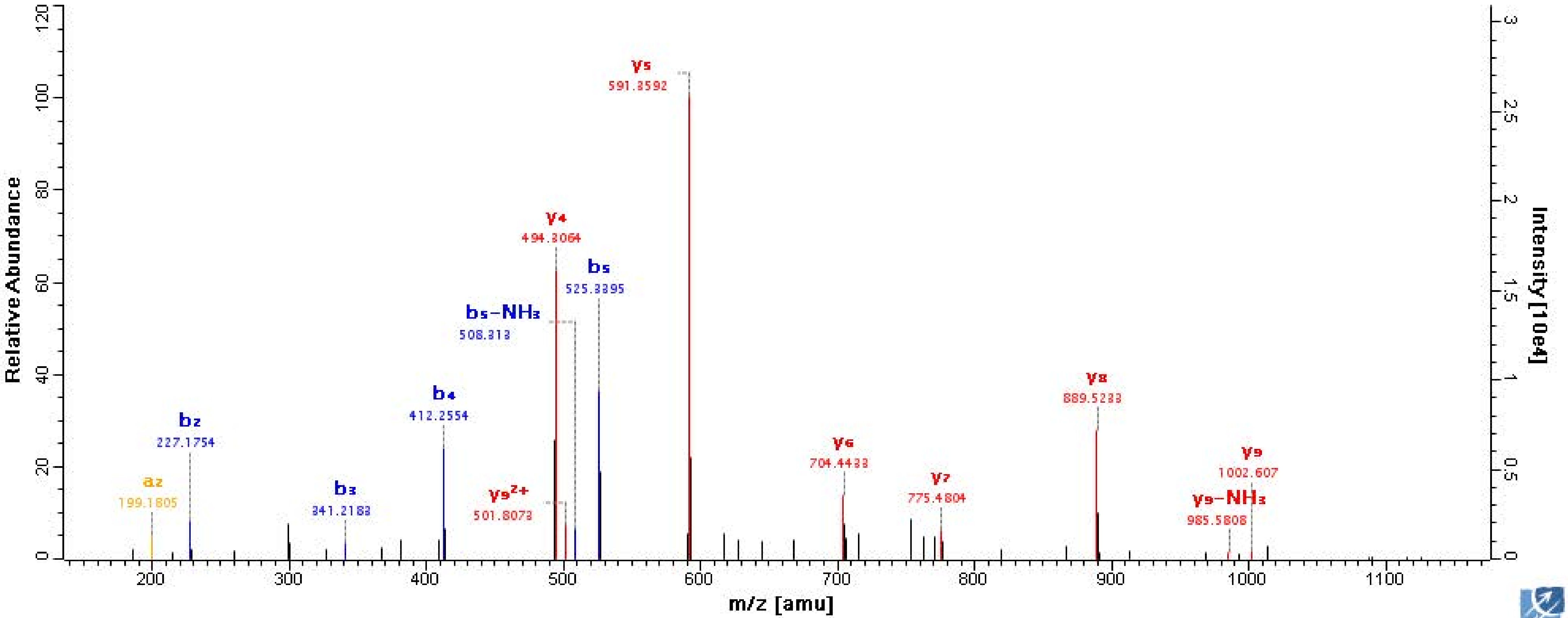
general information

Annotation:	10 of 17
AminoAcids Coverag	59 %
Intensity Coverage:	25 %
Protein Localisation:	81 ... 97

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	164.070605	1	Y	16				
	293.1131981	2	E	15	1773.9017553	+0.1251001	1773.9017553	
	392.18161202	3	V	14	1644.8591623		1644.8591623	
	555.24494056	4	Y	13	1545.7907483		1545.7907483	
	654.31335447	5	V	12	1382.7274198	+0.100339	1382.7274198	
	753.38176839	6	V	11	1283.6590059		1283.6590059	
	854.42944686	7	T	10	1184.590592		1184.590592	
	955.47712534	8	T	9	1083.5429135		1083.5429135	
	1026.5142391	9	A	8	982.49523502		491.75125574	-0.4125717
-0.0425084	1127.5619176	10	T	7	911.45812123		911.45812123	
-0.1183948	1241.604845	11	N	6	810.41044275		405.70885961	+0.3287686
	1378.6637569	12	H	5	696.36751531		696.36751531	
	1475.7165208	13	P	4	559.30860344		559.30860344	
+0.4413507	1590.7434638	14	D	3	462.25583959	+0.0790298	462.25583959	
	1677.7754922	15	S	2	347.22889656	-0.003158	347.22889656	
-0.1296978	1790.8595562	16	I	1	260.19686815		260.19686815	
		17	K	0	147.11280417		147.11280417	

Source: 20130124_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_OG_F05
Scannumber: 20168
Protein: BSU06370; pbuG; yebB
Peptide Score: 89.25
Method: ITMS; CID; 3





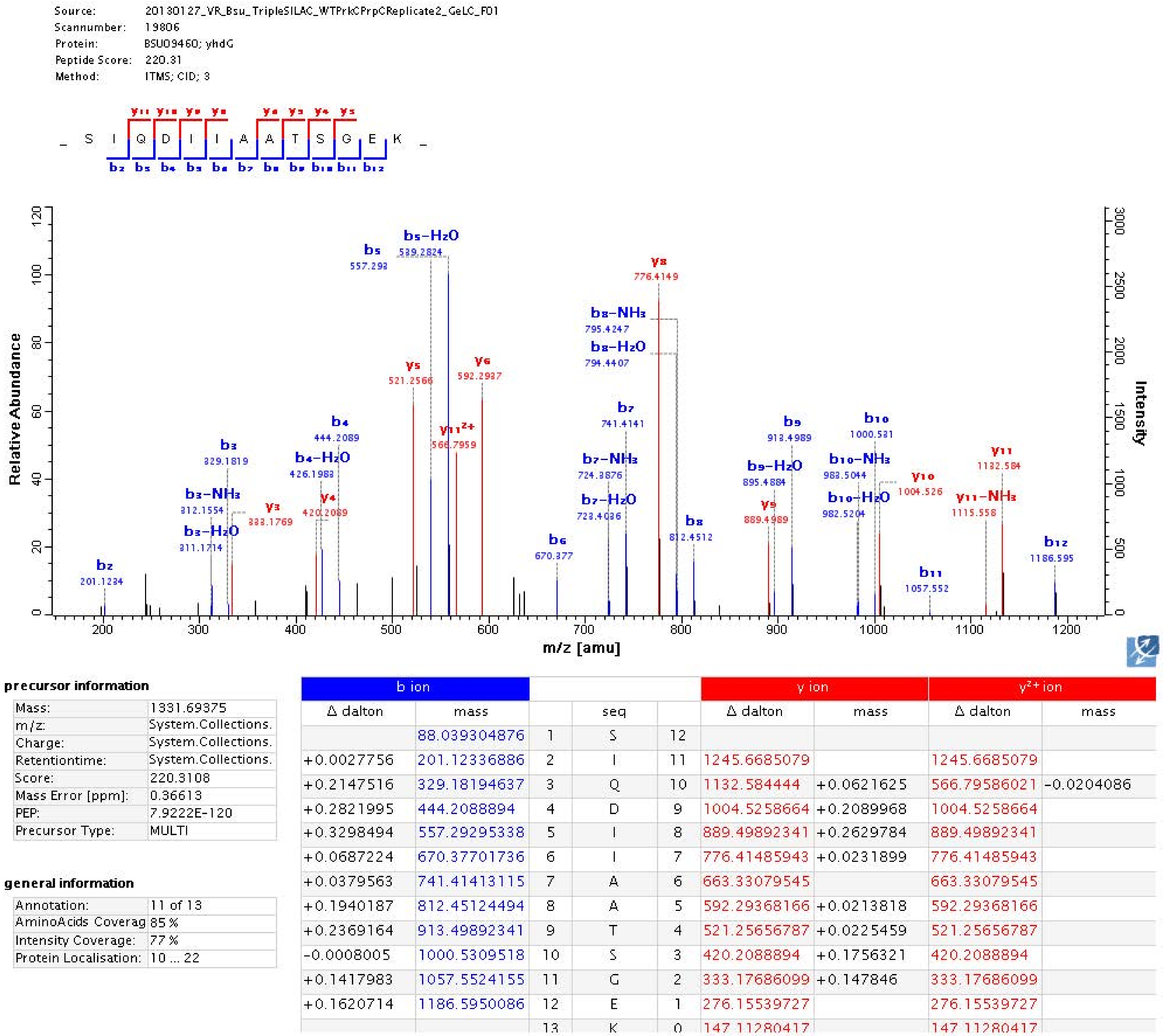
precursor information

Mass:	1106.67016
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	89.24719
Mass Error [ppm]:	0.19507
PEP:	0.0021603
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	61 %
Protein Localisation:	131 ... 140

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	9				
+0.003394	199.1805	-0.130284	227.1754	2	I	8	1002.607	+0.006291	501.8073	+0.022578
	313.2234	-0.05134	341.2183	3	N	7	889.5233	-0.11332	889.5233	
	384.2605	-0.048475	412.2554	4	A	6	775.4804	-0.039081	775.4804	
	497.3446	-0.077181	525.3395	5	I	5	704.4433	-0.075515	704.4433	
	594.3974		622.3923	6	P	4	591.3592	-0.053585	591.3592	
	691.4501		719.445	7	P	3	494.3064	+0.355502	494.3064	
	820.4927		848.4876	8	E	2	397.2537		397.2537	
	933.5768		961.5717	9	I	1	268.2111		268.2111	
				10	K	0	155.127		155.127	



Source: 20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F01
Scannumber: 19806
Protein: BSU09460; yhdG
Peptide Score: 220.31
Method: ITMS; CID; 3

precursor information

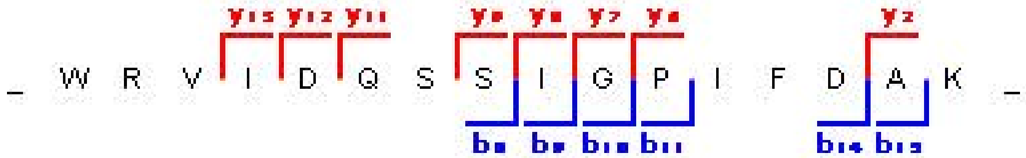
Mass:	1331.69375
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	220.3108
Mass Error [ppm]:	0.36613
PEP:	7.9222E-120
Precursor Type:	MULTI

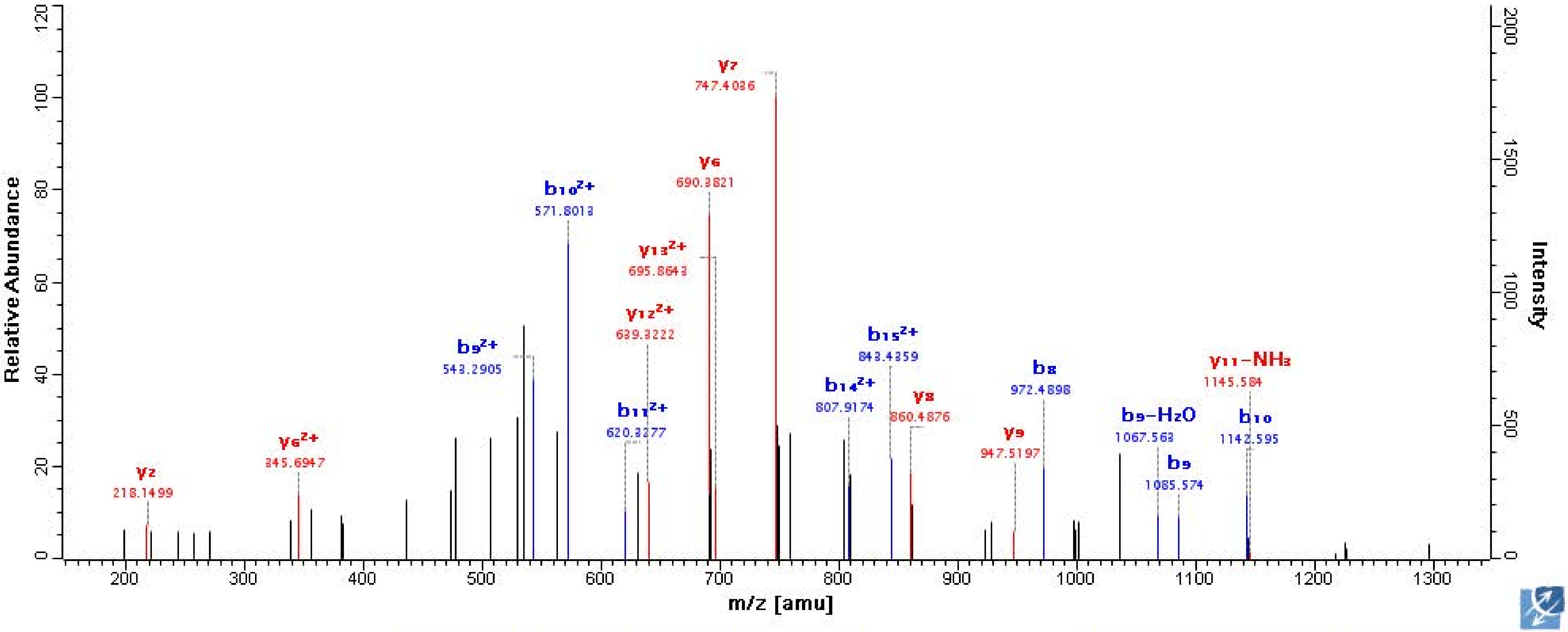
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	77 %
Protein Localisation:	10 ... 22

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	12				
+0.0027756	201.12336886	2	I	11	1245.6685079		1245.6685079	
+0.2147516	329.18194637	3	Q	10	1132.584444	+0.0621625	566.79586021	-0.0204086
+0.2821995	444.2088894	4	D	9	1004.5258664	+0.2089968	1004.5258664	
+0.3298494	557.29295338	5	I	8	889.49892341	+0.2629784	889.49892341	
+0.0687224	670.37701736	6	I	7	776.41485943	+0.0231899	776.41485943	
+0.0379563	741.41413115	7	A	6	663.33079545		663.33079545	
+0.1940187	812.45124494	8	A	5	592.29368166	+0.0213818	592.29368166	
+0.2369164	913.49892341	9	T	4	521.25656787	+0.0225459	521.25656787	
-0.0008005	1000.5309518	10	S	3	420.2088894	+0.1756321	420.2088894	
+0.1417983	1057.5524155	11	G	2	333.17686099	+0.147846	333.17686099	
+0.1620714	1186.5950086	12	E	1	276.15539727		276.15539727	
		13	K	0	147.11280417		147.11280417	

Source: 20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F14
Scannumber: 27794
Protein: BSU37640; ipa-90d; ywfL
Peptide Score: 88.08
Method: ITMS; CID; 3





precursor information

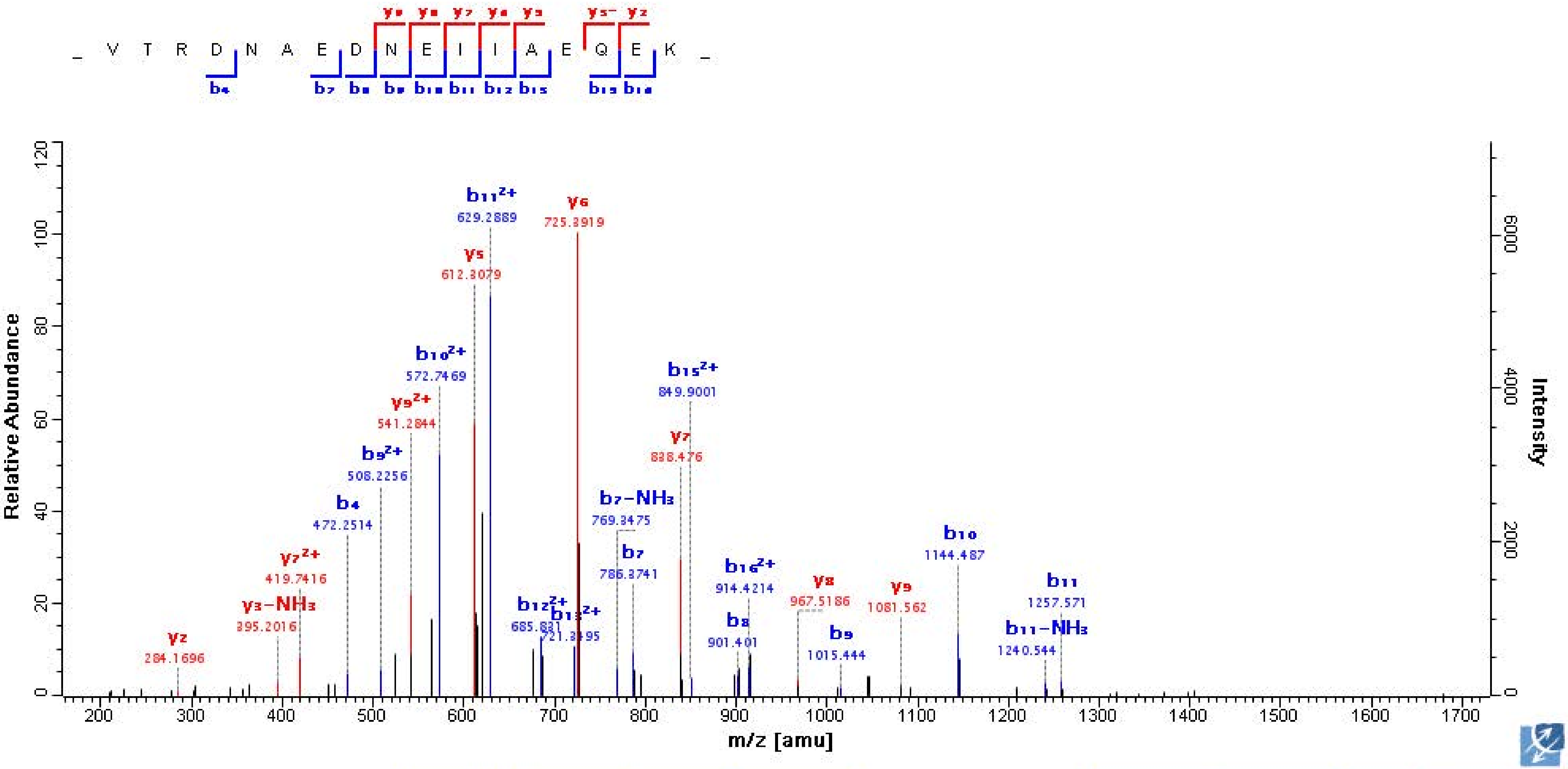
Mass:	1830.96248
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	88.07503
Mass Error [ppm]:	-0.19399
PEP:	0.0011347
Precursor Type:	ISO

general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	46 %
Protein Localisation:	14 ... 29

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	15				
	343.1877		343.1877	2	R	14	1645.891		1645.891	
	442.2561		442.2561	3	V	13	1489.79		1489.79	
	555.3402		555.3402	4	I	12	1390.721		695.8643	-0.276384
	670.3671		670.3671	5	D	11	1277.637		639.3222	+0.339745
	798.4257		798.4257	6	Q	10	1162.61		1162.61	
	885.4577		885.4577	7	S	9	1034.552		1034.552	
	972.4898	+0.191824	972.4898	8	S	8	947.5197	-0.205694	947.5197	
-0.00173	543.2905	+0.054354	1085.574	9	I	7	860.4876	-0.01534	860.4876	
+0.340322	571.8013	+0.122734	1142.595	10	G	6	747.4036	-0.076662	747.4036	
+0.155553	620.3277		1239.648	11	P	5	690.3821	-0.080772	345.6947	-0.082751
	1352.732		1352.732	12	I	4	593.3293		593.3293	
	1499.801		1499.801	13	F	3	480.2453		480.2453	
-0.013381	807.9174		1614.827	14	D	2	333.1769		333.1769	
+0.301314	843.4359		1685.865	15	A	1	218.1499	-0.009461	218.1499	
				16	K	0	147.1128		147.1128	

Source:	20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F15
Scannumber:	11770
Protein:	BSU31110; yubF
Peptide Score:	122.33
Method:	ITMS; CID; 3



precursor information

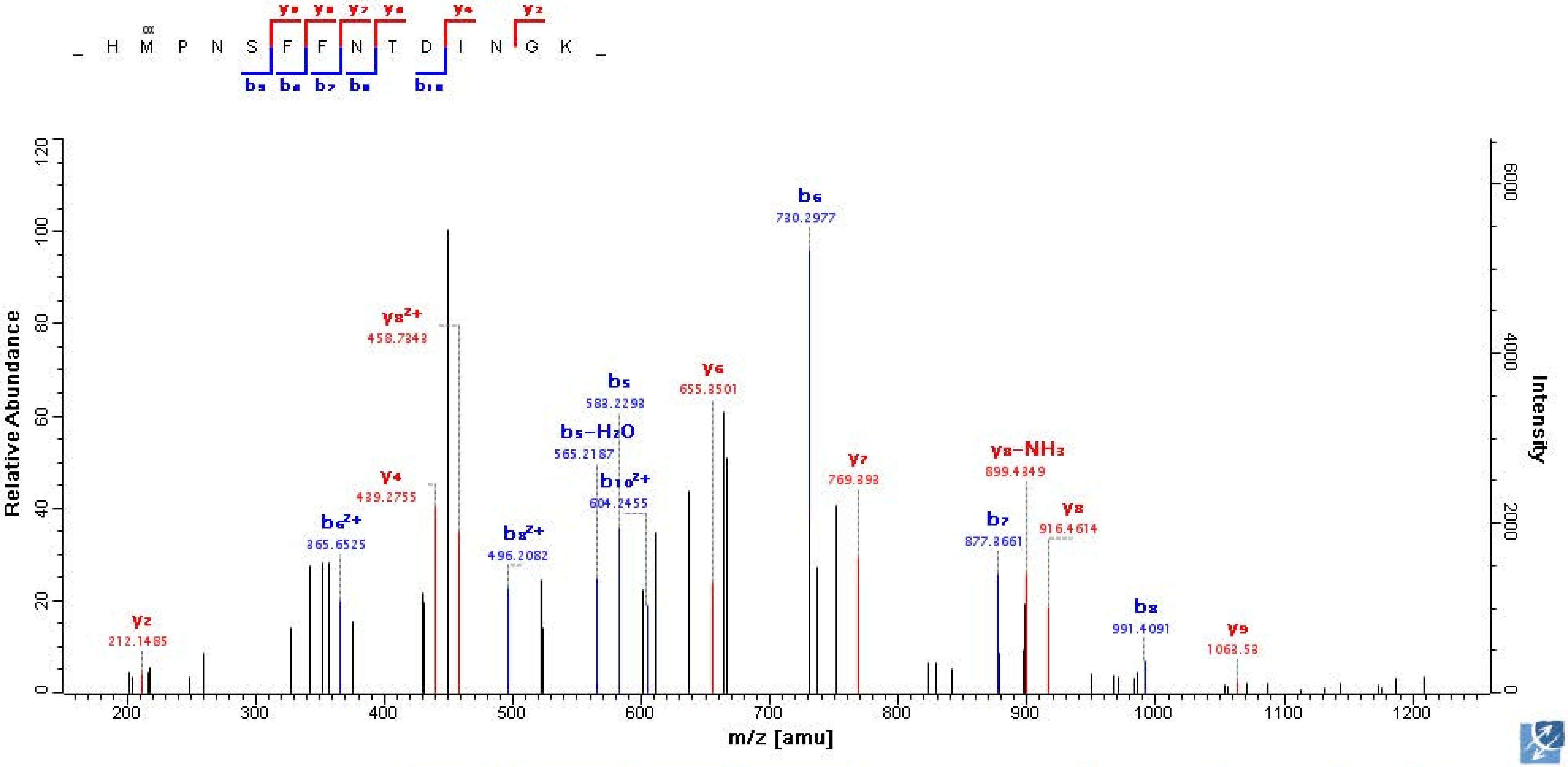
Mass:	1972.93351
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	122.327
Mass Error [ppm]:	-0.13313
PEP:	4.2807E-20
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	63 %
Protein Localisation:	62 ... 78

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	16				
	201.1234		201.1234	2	T	15	1882.887		1882.887	
	357.2245		357.2245	3	R	14	1781.839		1781.839	
	472.2514	-0.070087	472.2514	4	D	13	1625.738		1625.738	
	586.2944		586.2944	5	N	12	1510.711		1510.711	
	657.3315		657.3315	6	A	11	1396.668		1396.668	
	786.3741	+0.094021	786.3741	7	E	10	1325.631		1325.631	
	901.401	+0.084901	901.401	8	D	9	1196.588		1196.588	
-0.002946	508.2256	+0.031902	1015.444	9	N	8	1081.562	+0.016108	541.2844	+0.012289
+0.321766	572.7469	+0.047903	1144.487	10	E	7	967.5186	+0.052443	967.5186	
+0.43104	629.2889	+0.06235	1257.571	11	I	6	838.476	+0.069707	419.7416	-0.037999
-0.016387	685.831		1370.655	12	I	5	725.3919	+0.062035	725.3919	
+0.11801	721.3495		1441.692	13	A	4	612.3079	+0.047649	612.3079	
	1570.734		1570.734	14	E	3	541.2708		541.2708	
+0.427227	849.9001		1698.793	15	Q	2	412.2282		412.2282	
-0.051284	914.4214		1827.836	16	E	1	284.1696	+0.292013	284.1696	
				17	K	0	155.127		155.127	

Source: 20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F15
Scannumber: 17312
Protein: BSU05070; yddQ
Peptide Score: 70.44
Method: ITMS; CID; 3



precursor information

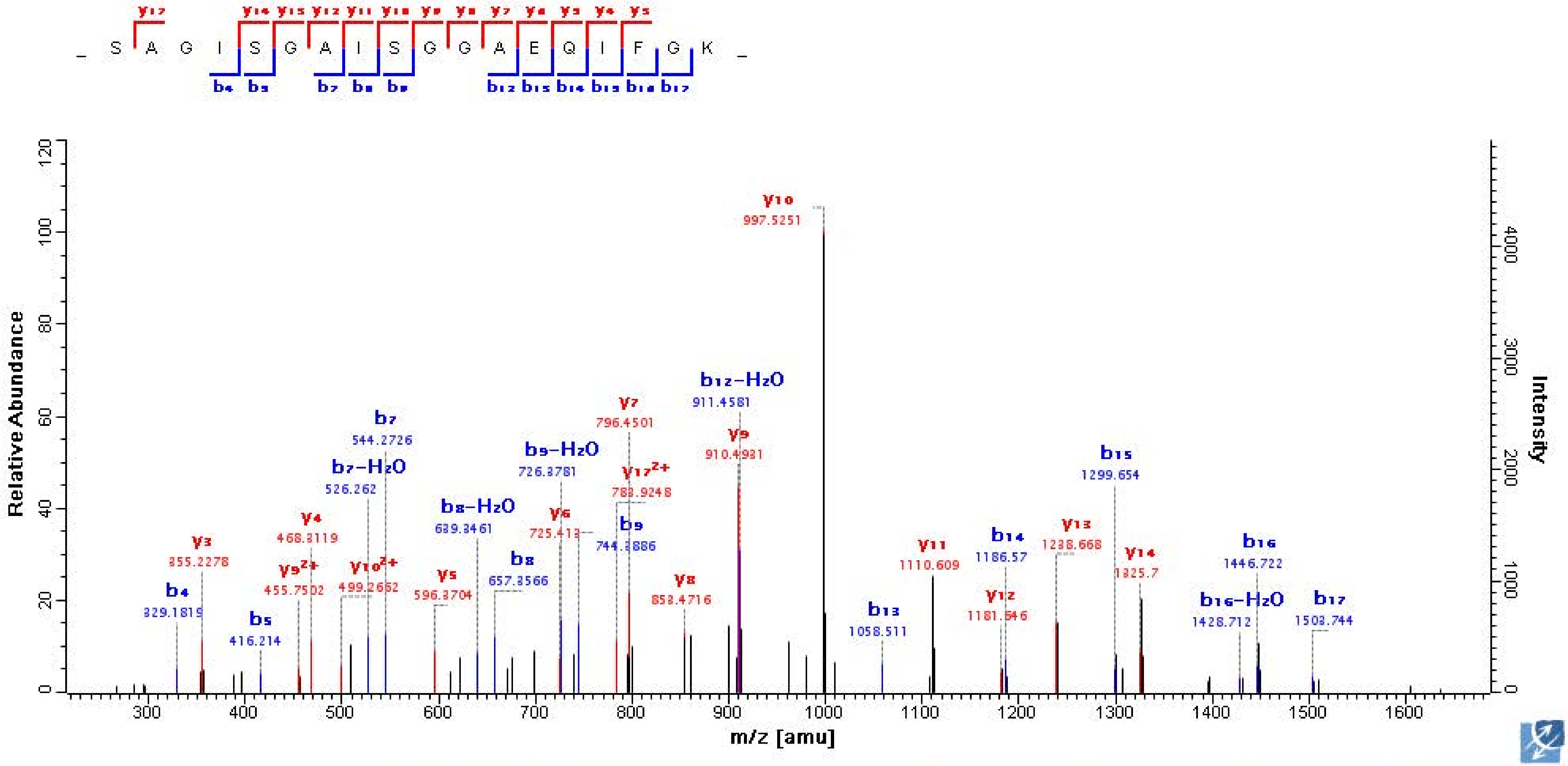
Mass:	1636.73003
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	70.43787
Mass Error [ppm]:	-0.21884
PEP:	0.00139
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	37 %
Protein Localisation:	86 ... 99

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.0662		138.0662	1	H	13				
	285.1016		285.1016	2	M	12	1508.693		1508.693	
	382.1544		382.1544	3	P	11	1361.658		1361.658	
	496.1973		496.1973	4	N	10	1264.605		1264.605	
	583.2293	-0.025084	583.2293	5	S	9	1150.562		1150.562	
-0.021884	365.6525	-0.043876	730.2977	6	F	8	1063.53	+0.07539	1063.53	
	877.3661	+0.05812	877.3661	7	F	7	916.4614	+0.17603	458.7343	-0.110814
+0.404684	496.2082	+0.183589	991.4091	8	N	6	769.393	+0.003416	769.393	
	1092.457		1092.457	9	T	5	655.3501	+0.006244	655.3501	
+0.034305	604.2455		1207.484	10	D	4	554.3024		554.3024	
	1320.568		1320.568	11	I	3	439.2755	+0.083856	439.2755	
	1434.611		1434.611	12	N	2	326.1914		326.1914	
	1491.632		1491.632	13	G	1	212.1485	+0.024904	212.1485	
				14	K	0	155.127		155.127	

Source:	20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F15
Scannumber:	25850
Protein:	BSU33630; secG; yvaL
Peptide Score:	176.33
Method:	ITMS; CID; 3



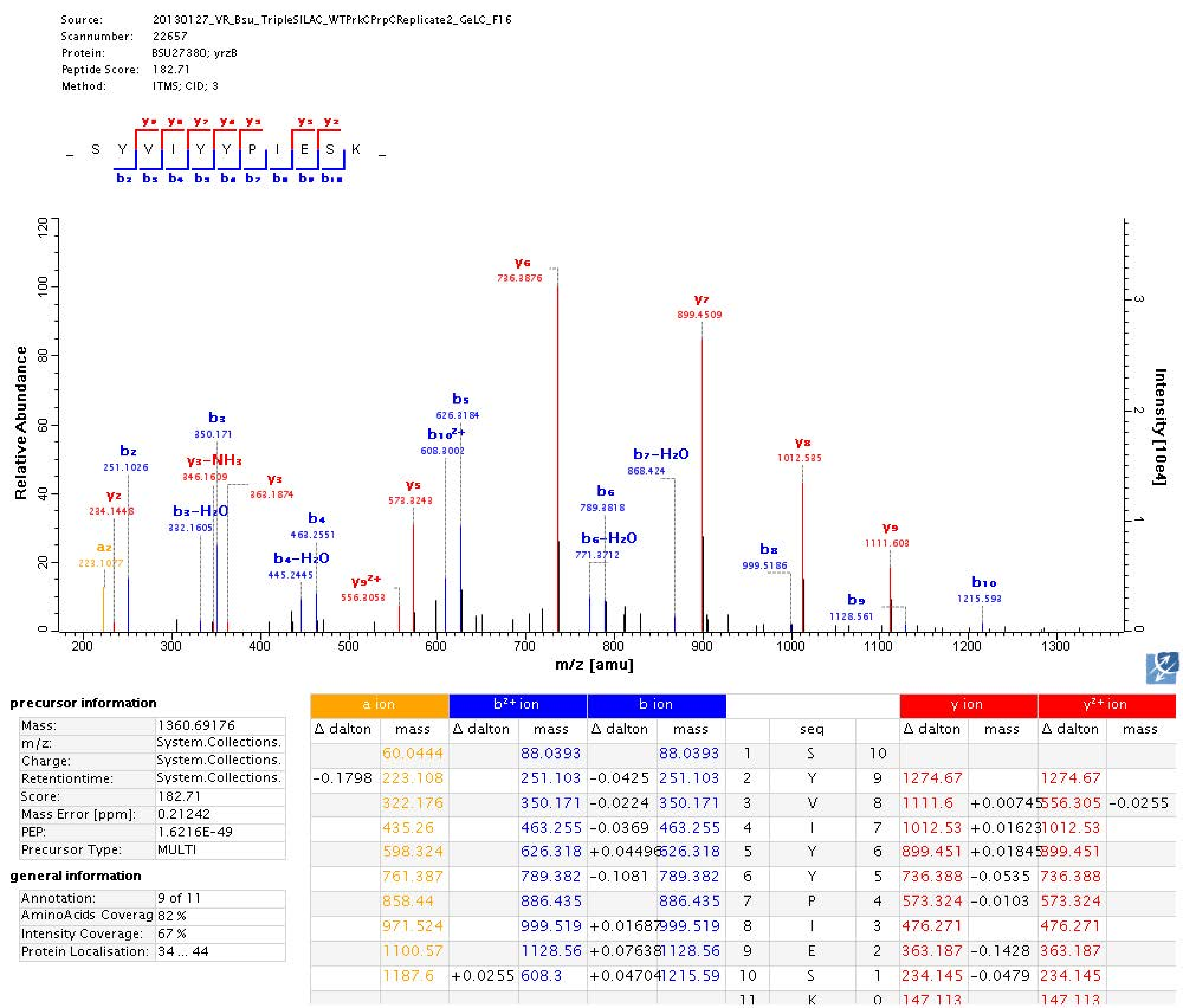
precursor information

Mass:	1648.84234
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	176.3325
Mass Error [ppm]:	0.17283
PEP:	1.4924E-79
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	49 %
Protein Localisation:	27 ... 44

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	17				
	159.07641866	2	A	16	1566.8424044		783.92484044	-0.1951652
	216.09788239	3	G	15	1495.8052906		1495.8052906	
-0.0191961	329.18194637	4	I	14	1438.7838269		1438.7838269	
+0.0840904	416.21397478	5	S	13	1325.6997629	+0.0980886	1325.6997629	
	473.2354385	6	G	12	1238.6677345	-0.0044044	1238.6677345	
-0.0444639	544.27255229	7	A	11	1181.6462708	-0.0169983	1181.6462708	
+0.0841186	657.35661627	8	I	10	1110.609157	+0.0166975	1110.609157	
-0.0339084	744.38864468	9	S	9	997.52509303	-0.0357131	499.26618475	+0.1436663
	801.4101084	10	G	8	910.49306462	+0.0170062	455.75017054	-0.4064816
	858.43157213	11	G	7	853.47160089	+0.0098444	853.47160089	
	929.46868591	12	A	6	796.45013717	-0.014041	796.45013717	
-0.0814694	1058.511279	13	E	5	725.41302338	+0.1115738	725.41302338	
-0.0278643	1186.5698565	14	Q	4	596.37043029	+0.0557782	596.37043029	
-0.0397848	1299.6539205	15	I	3	468.31185277	-0.015344	468.31185277	
-0.0325151	1446.7223344	16	F	2	355.22778879	+0.028864	355.22778879	
+0.0230476	1503.7437981	17	G	1	208.15937488		208.15937488	
		18	K	0	151.13791115		151.13791115	



Source:	20130127_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate2_GeLC_F16
Scannumber:	22657
Protein:	BSU27380; yrzB
Peptide Score:	182.71
Method:	ITMS; CID; 3

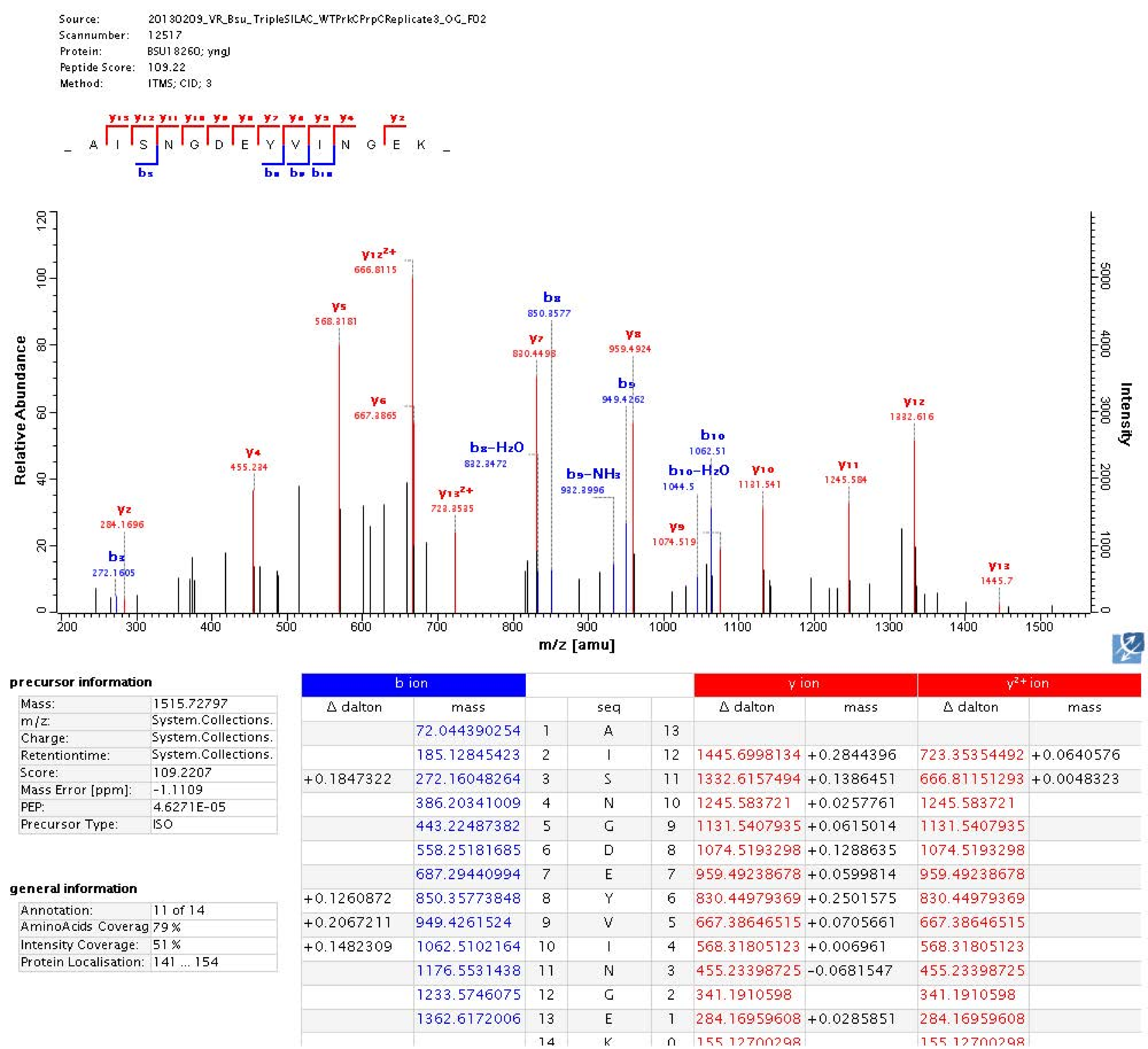
precursor information

Mass:	1360.69176
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	182.71
Mass Error [ppm]:	0.21242
PEP:	1.6216E-49
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	67 %
Protein Localisation:	34 ... 44

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
	60.0444		88.0393		88.0393	1	S	10				
-0.1798	223.108		251.103	-0.0425	251.103	2	Y	9	1274.67		1274.67	
	322.176		350.171	-0.0224	350.171	3	V	8	1111.6	+0.00745	556.305	-0.0255
	435.26		463.255	-0.0369	463.255	4	I	7	1012.53	+0.01623	1012.53	
	598.324		626.318	+0.04496	626.318	5	Y	6	899.451	+0.01845	899.451	
	761.387		789.382	-0.1081	789.382	6	Y	5	736.388	-0.0535	736.388	
	858.44		886.435		886.435	7	P	4	573.324	-0.0103	573.324	
	971.524		999.519	+0.01687	999.519	8	I	3	476.271		476.271	
	1100.57		1128.56	+0.07638	1128.56	9	E	2	363.187	-0.1428	363.187	
	1187.6	+0.0255	608.3	+0.04704	1215.59	10	S	1	234.145	-0.0479	234.145	
						11	K	0	147.113		147.113	



Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F02
Scannumber:	12517
Protein:	BSU18260; yngJ
Peptide Score:	109.22
Method:	ITMS; CID; 3

precursor information

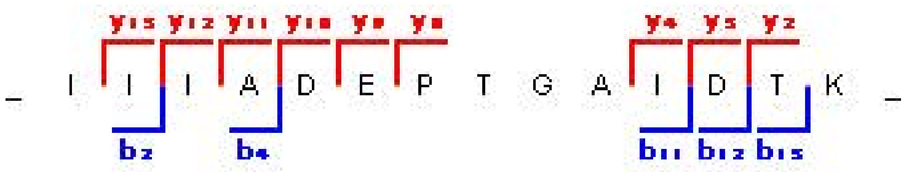
Mass:	1515.72797
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.2207
Mass Error [ppm]:	-1.1109
PEP:	4.6271E-05
Precursor Type:	ISO

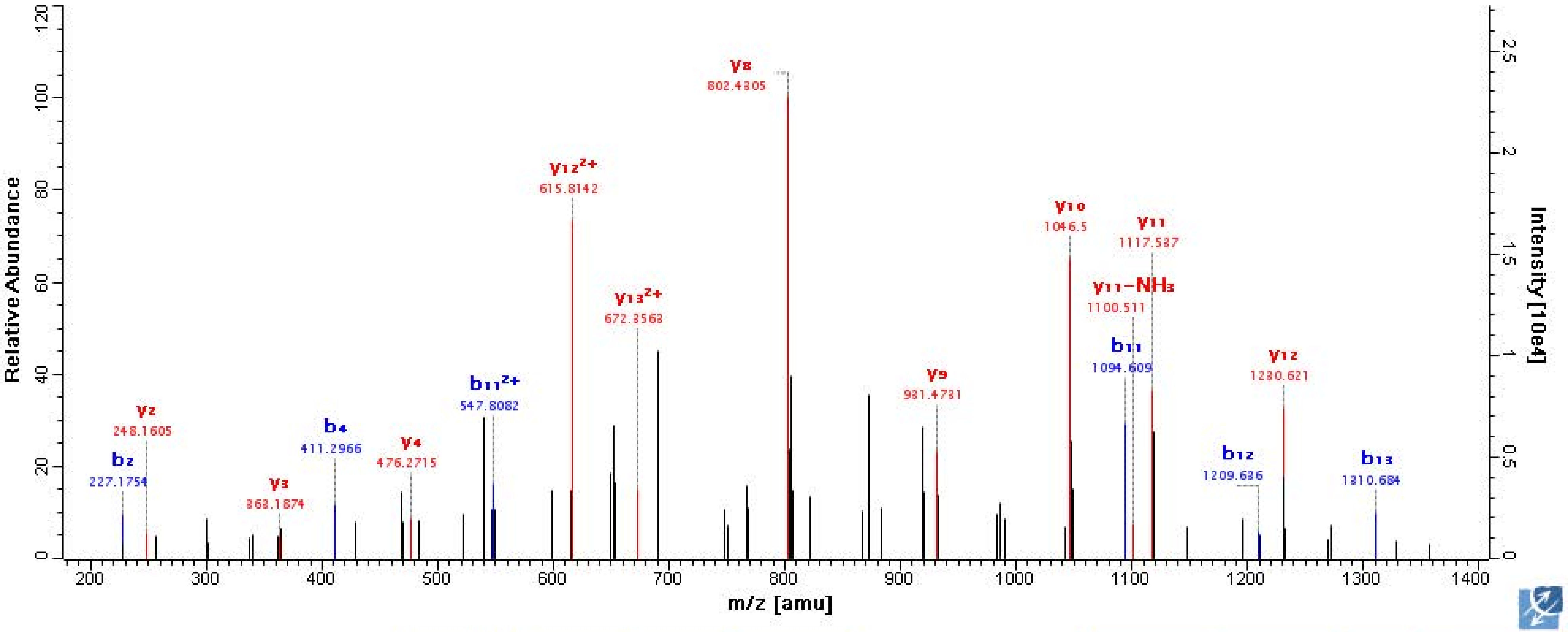
general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	51 %
Protein Localisation:	141 ... 154

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	13				
	185.12845423	2	I	12	1445.6998134	+0.2844396	723.35354492	+0.0640576
+0.1847322	272.16048264	3	S	11	1332.6157494	+0.1386451	666.81151293	+0.0048323
	386.20341009	4	N	10	1245.583721	+0.0257761	1245.583721	
	443.22487382	5	G	9	1131.5407935	+0.0615014	1131.5407935	
	558.25181685	6	D	8	1074.5193298	+0.1288635	1074.5193298	
	687.29440994	7	E	7	959.49238678	+0.0599814	959.49238678	
+0.1260872	850.35773848	8	Y	6	830.44979369	+0.2501575	830.44979369	
+0.2067211	949.4261524	9	V	5	667.38646515	+0.0705661	667.38646515	
+0.1482309	1062.5102164	10	I	4	568.31805123	+0.006961	568.31805123	
	1176.5531438	11	N	3	455.23398725	-0.0681547	455.23398725	
	1233.5746075	12	G	2	341.1910598		341.1910598	
	1362.6172006	13	E	1	284.16959608	+0.0285851	284.16959608	
		14	K	0	155.12700298		155.12700298	

Source: 20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F02
Scannumber: 18740
Protein: BSU14360; yknY
Peptide Score: 92.19
Method: ITMS; CID; 3





precursor information

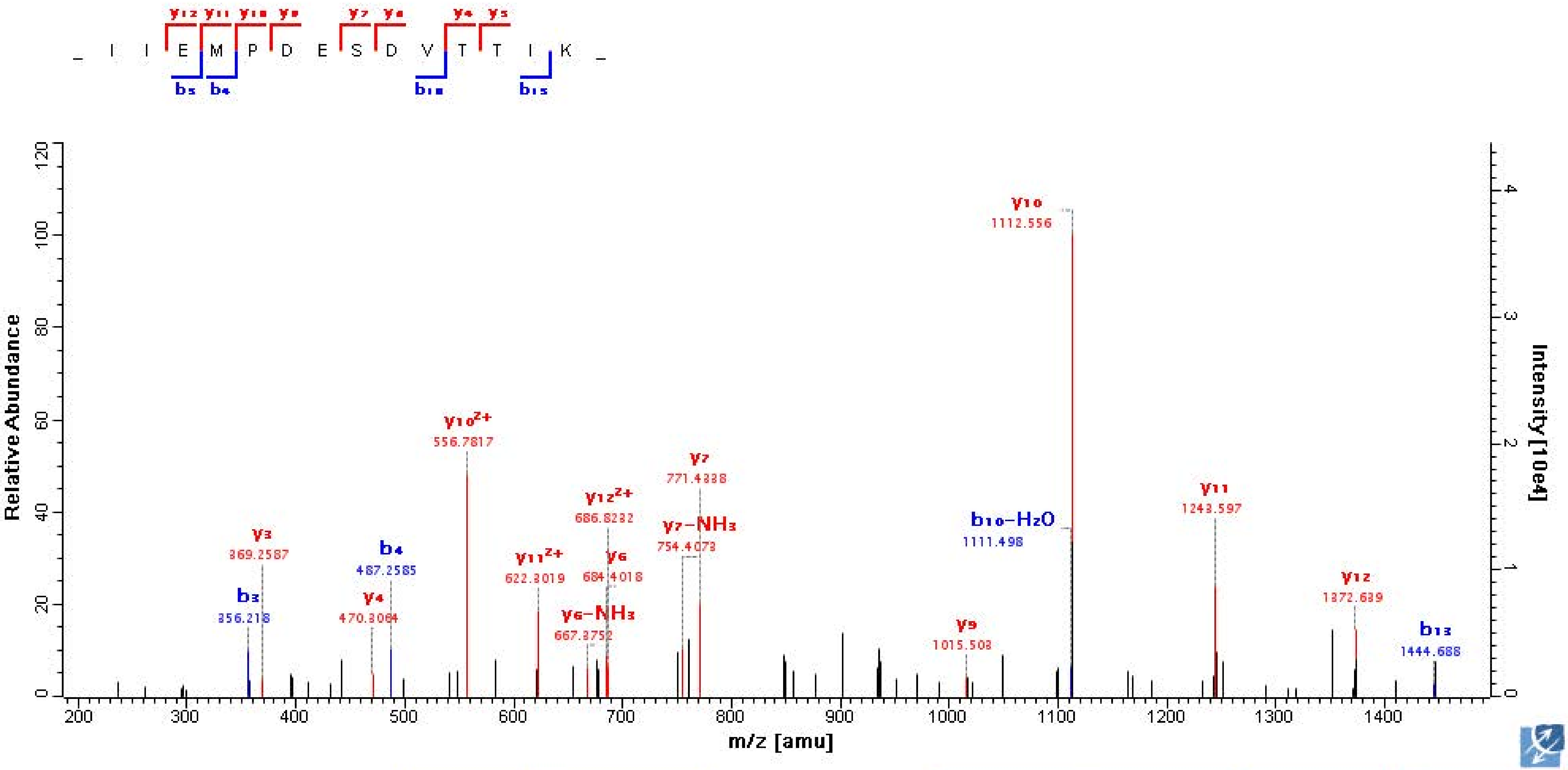
Mass:	1455.78219
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	92.18982
Mass Error [ppm]:	0.075686
PEP:	0.0003863
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	39 %
Protein Localisation:	162 ... 175

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				
	227.1754	-0.087895	227.1754	2	I	12	1343.705		672.3563	+0.089031
	340.2595		340.2595	3	I	11	1230.621	+0.05407	615.8142	+0.28127
	411.2966	+0.161975	411.2966	4	A	10	1117.537	+0.057323	1117.537	
	526.3235		526.3235	5	D	9	1046.5	+0.06221	1046.5	
	655.3661		655.3661	6	E	8	931.4731	+0.055218	931.4731	
	752.4189		752.4189	7	P	7	802.4305	+0.057528	802.4305	
	853.4666		853.4666	8	T	6	705.3777		705.3777	
	910.488		910.488	9	G	5	604.3301		604.3301	
	981.5251		981.5251	10	A	4	547.3086		547.3086	
-0.184582	547.8082	-0.001536	1094.609	11	I	3	476.2715	+0.075007	476.2715	
	1209.636	-0.001013	1209.636	12	D	2	363.1874	+0.090742	363.1874	
	1310.684	+0.109878	1310.684	13	T	1	248.1605	+0.008081	248.1605	
				14	K	0	147.1128		147.1128	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F02
Scannumber:	20293
Protein:	BSU20820; yopO
Peptide Score:	88.02
Method:	ITMS; CID; 3



precursor information

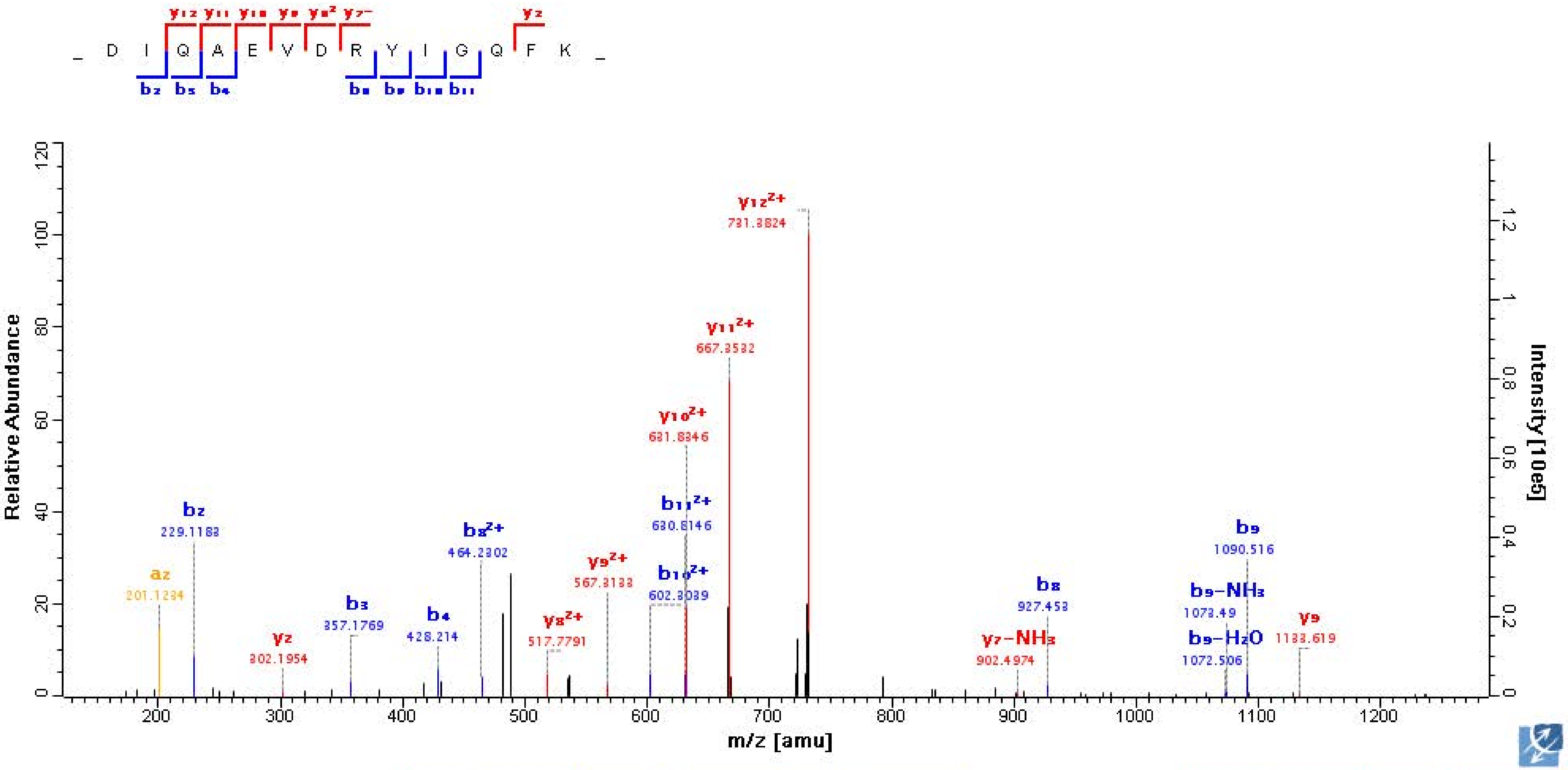
Mass:	1589.78582
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	88.02058
Mass Error [ppm]:	-0.0098175
PEP:	0.00060395
Precursor Type:	MULTI

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	47 %
Protein Localisation:	33 ... 46

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	13				
	227.17540443	2	I	12	1485.7232509		1485.7232509	
+0.0421648	356.21799752	3	E	11	1372.639187	+0.3532447	686.82323171	+0.1410017
+0.3053606	487.25848213	4	M	10	1243.5965939	+0.071497	622.30193516	+0.3361264
	584.31124598	5	P	9	1112.5561093	+0.1499454	556.78169286	+0.3307339
	699.33818901	6	D	8	1015.5033454	+0.1799432	1015.5033454	
	828.38078211	7	E	7	900.47640237		900.47640237	
	915.41281052	8	S	6	771.43380927	+0.1067791	771.43380927	
	1030.4397536	9	D	5	684.40178086	+0.2578871	684.40178086	
	1129.5081675	10	V	4	569.37483783		569.37483783	
	1230.5558459	11	T	3	470.30642391	+0.2041352	470.30642391	
	1331.6035244	12	T	2	369.25874544	+0.215101	369.25874544	
+0.0832856	1444.6875884	13	I	1	268.21106696		268.21106696	
		14	K	0	155.12700298		155.12700298	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F03
Scannumber:	30230
Protein:	BSU22500; jojD; ypjD
Peptide Score:	108.56
Method:	ITMS; CID; 3



precursor information

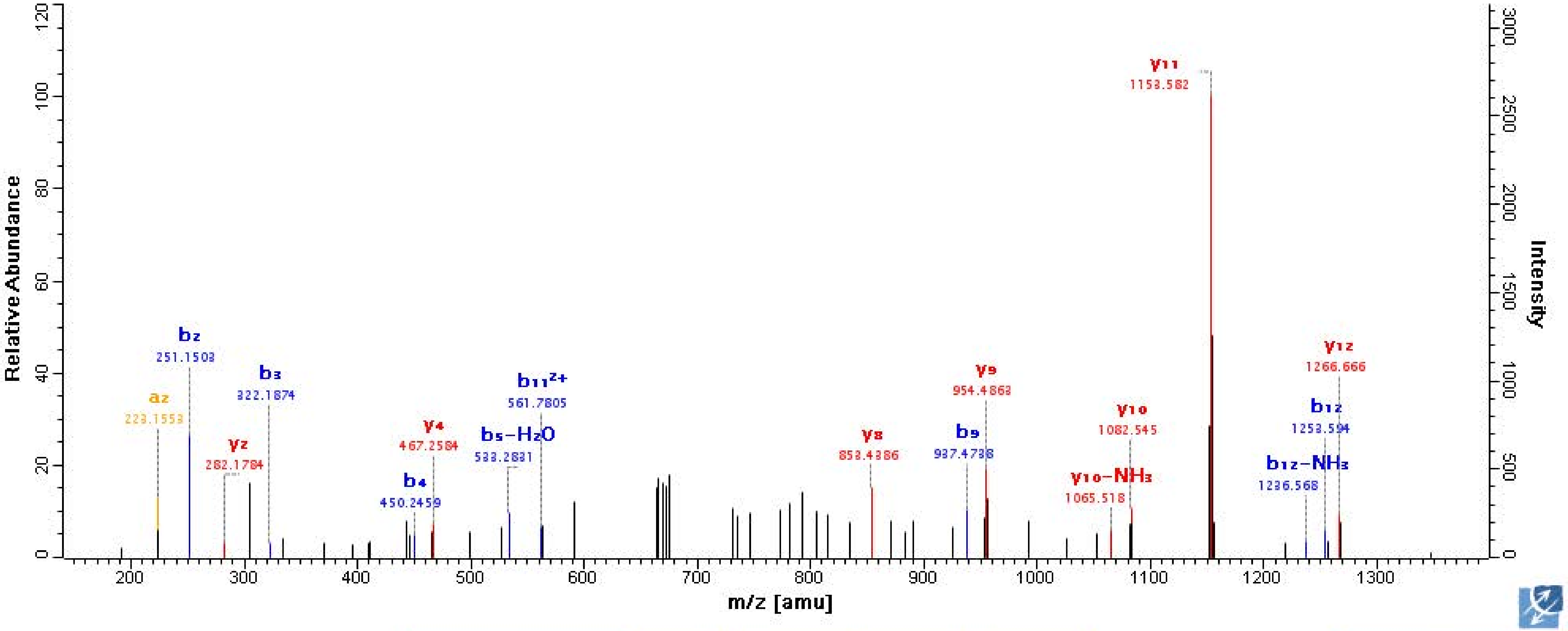
Mass:	1680.84688
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.5638
Mass Error [ppm]:	-0.14841
PEP:	1.4305E-06
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	60 %
Protein Localisation:	8 ... 21

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	13				
-0.1656	201.123		229.118	-0.1413	229.118	2	I	12	1574.84		1574.84	
	329.182		357.177	+0.09261	357.177	3	Q	11	1461.76		731.382	+0.0343
	400.219		428.214	+0.03993	428.214	4	A	10	1333.7		667.353	+0.1375
	529.262		557.257		557.257	5	E	9	1262.66		631.835	+0.2218
	628.33		656.325		656.325	6	V	8	1133.62	+0.11225	567.313	+0.2372
	743.357		771.352		771.352	7	D	7	1034.55		517.779	-0.1519
	899.458	+0.19764	464.23	-0.0686	927.453	8	R	6	919.524		919.524	
	1062.52		1090.52	+0.14013	1090.52	9	Y	5	763.423		763.423	
	1175.61	+0.39396	602.304		1203.6	10	I	4	600.36		600.36	
	1232.63	-0.3464	630.815		1260.62	11	G	3	487.275		487.275	
	1360.69		1388.68		1388.68	12	Q	2	430.254		430.254	
	1507.75		1535.75		1535.75	13	F	1	302.195	-0.0147	302.195	
						14	K	0	155.127		155.127	

Source: 20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F06
Scannumber: 10301
Protein: BSU39310; J3C; yxiC
Peptide Score: 88.34
Method: ITMS; CID; 3



precursor information

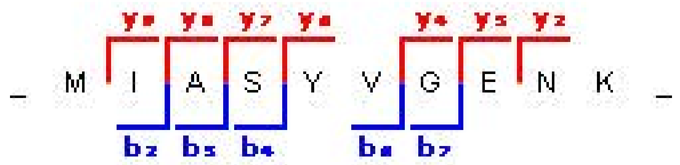
Mass:	1398.69257
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	88.33767
Mass Error [ppm]:	0.017757
PEP:	0.0010638
Precursor Type:	MULTI

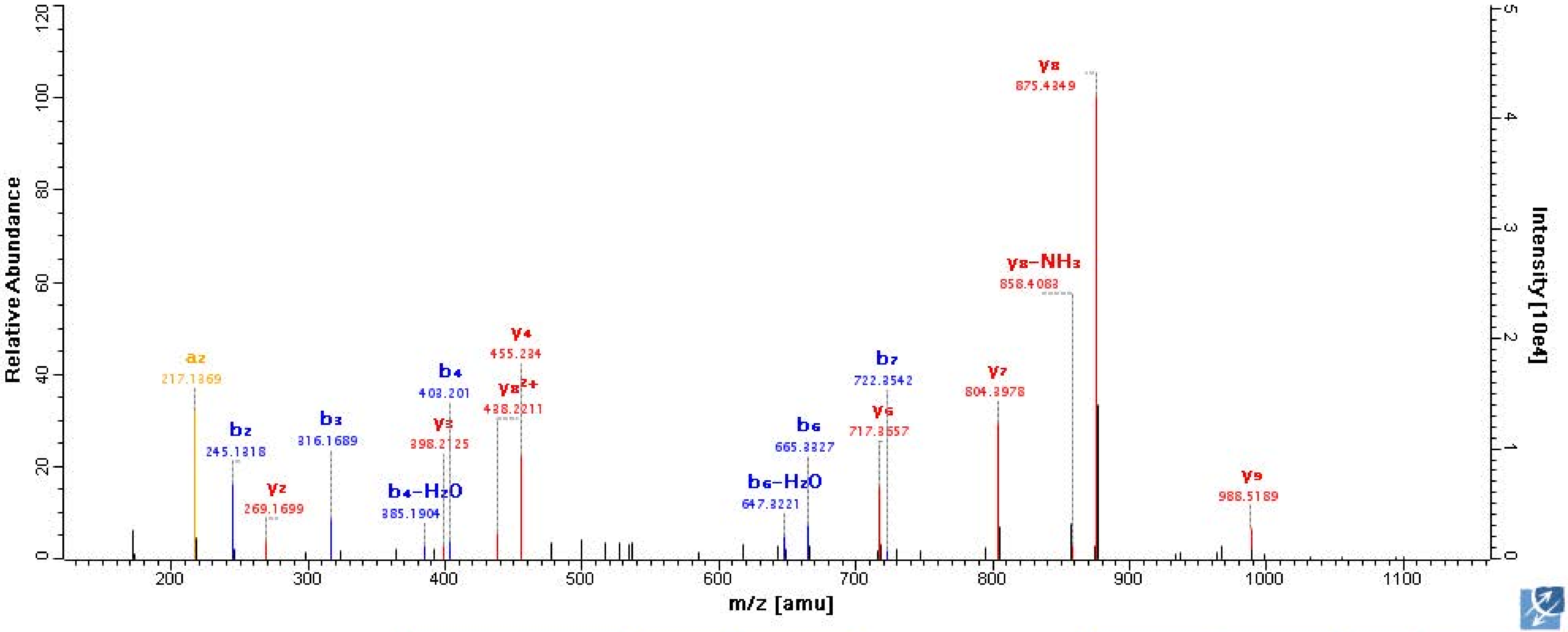
general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	34 %
Protein Localisation:	66 ... 78

a ion		b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	110.0713		138.0662		138.0662	1	H	12		
-0.092044	223.1553		251.1503	-0.043014	251.1503	2	I	11	1266.666	+0.018306
	294.1925		322.1874	+0.168042	322.1874	3	A	10	1153.582	+0.040725
	422.251		450.2459	+0.224882	450.2459	4	Q	9	1082.545	+0.19466
	523.2987		551.2936		551.2936	5	T	8	954.4863	+0.021243
	652.3413		680.3362		680.3362	6	E	7	853.4386	+0.147229
	739.3733		767.3682		767.3682	7	S	6	724.396	
	810.4104		838.4054		838.4054	8	A	5	637.364	
	909.4789		937.4738	+0.008651	937.4738	9	V	4	566.3269	
	1023.522		1051.517		1051.517	10	N	3	467.2584	-0.000136
	1094.559	+0.013767	561.7805		1122.554	11	A	2	353.2155	
	1225.599		1253.594	+0.177676	1253.594	12	M	1	282.1784	+0.063914
						13	K	0	151.1379	

Source: 20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F06
Scannumber: 13125
Protein: BSU38990; N15K; scoA; yxjD
Peptide Score: 129.1
Method: ITMS; CID; 3





precursor information

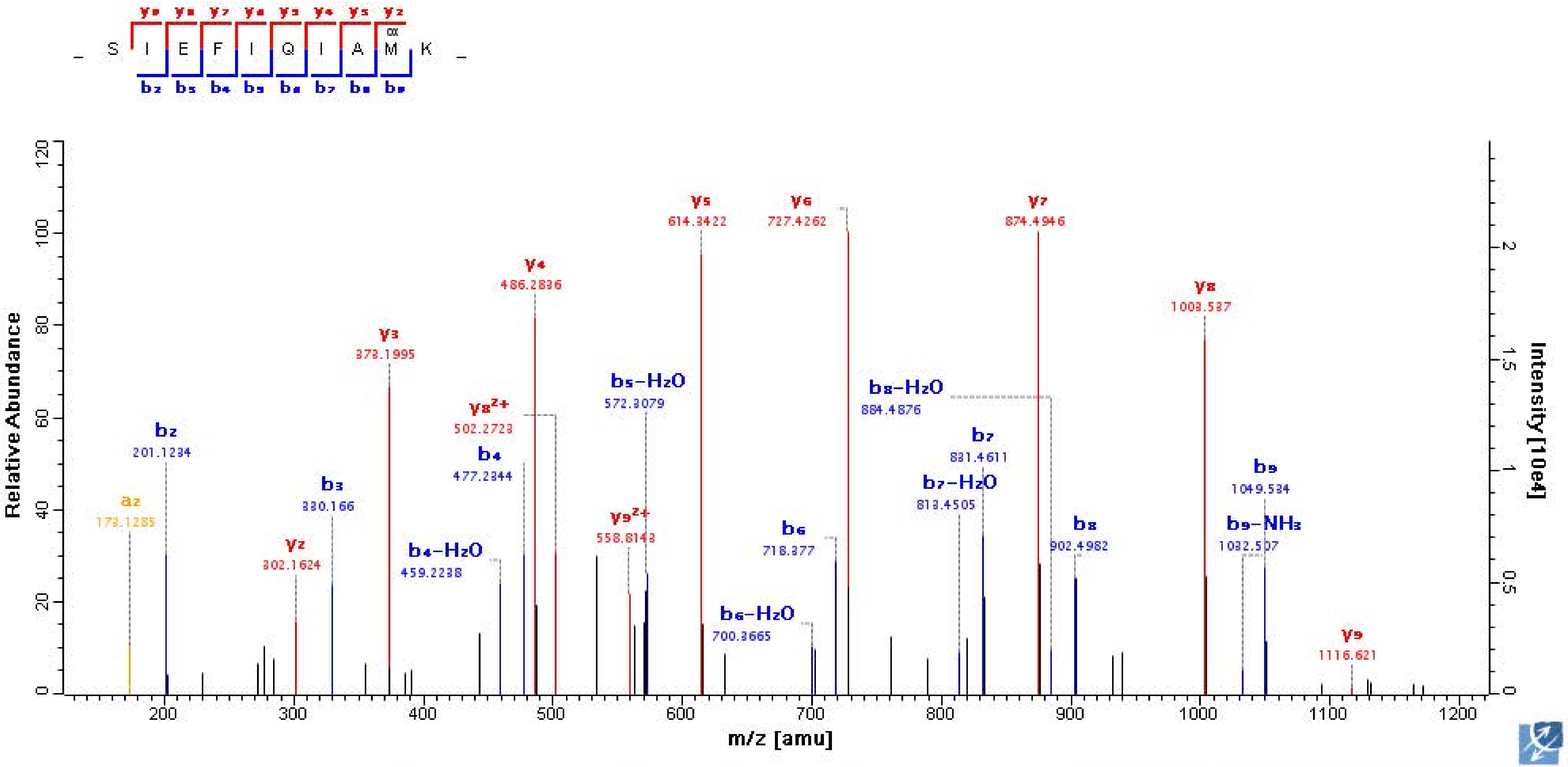
Mass:	1118.55164
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	129.099
Mass Error [ppm]:	-0.45055
PEP:	2.4153E-10
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	67 %
Protein Localisation:	73 ... 82

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	104.0528		132.0478	1	M	9				
-0.024743	217.1369	-0.008931	245.1318	2	I	8	988.5189	+0.068589	988.5189	
	288.174	+0.003424	316.1689	3	A	7	875.4349	+0.122745	438.2211	+0.181453
	375.2061	+0.053977	403.201	4	S	6	804.3978	+0.068612	804.3978	
	538.2694		566.2643	5	Y	5	717.3657	+0.07293	717.3657	
	637.3378	+0.112664	665.3327	6	V	4	554.3024		554.3024	
	694.3593	+0.22505	722.3542	7	G	3	455.234	+0.054465	455.234	
	823.4019		851.3968	8	E	2	398.2125	+0.199403	398.2125	
	937.4448		965.4397	9	N	1	269.1699	-0.021218	269.1699	
				10	K	0	155.127		155.127	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F06
Scannumber:	26046
Protein:	BSU11310; comZ
Peptide Score:	177.78
Method:	ITMS; CID; 3



precursor information

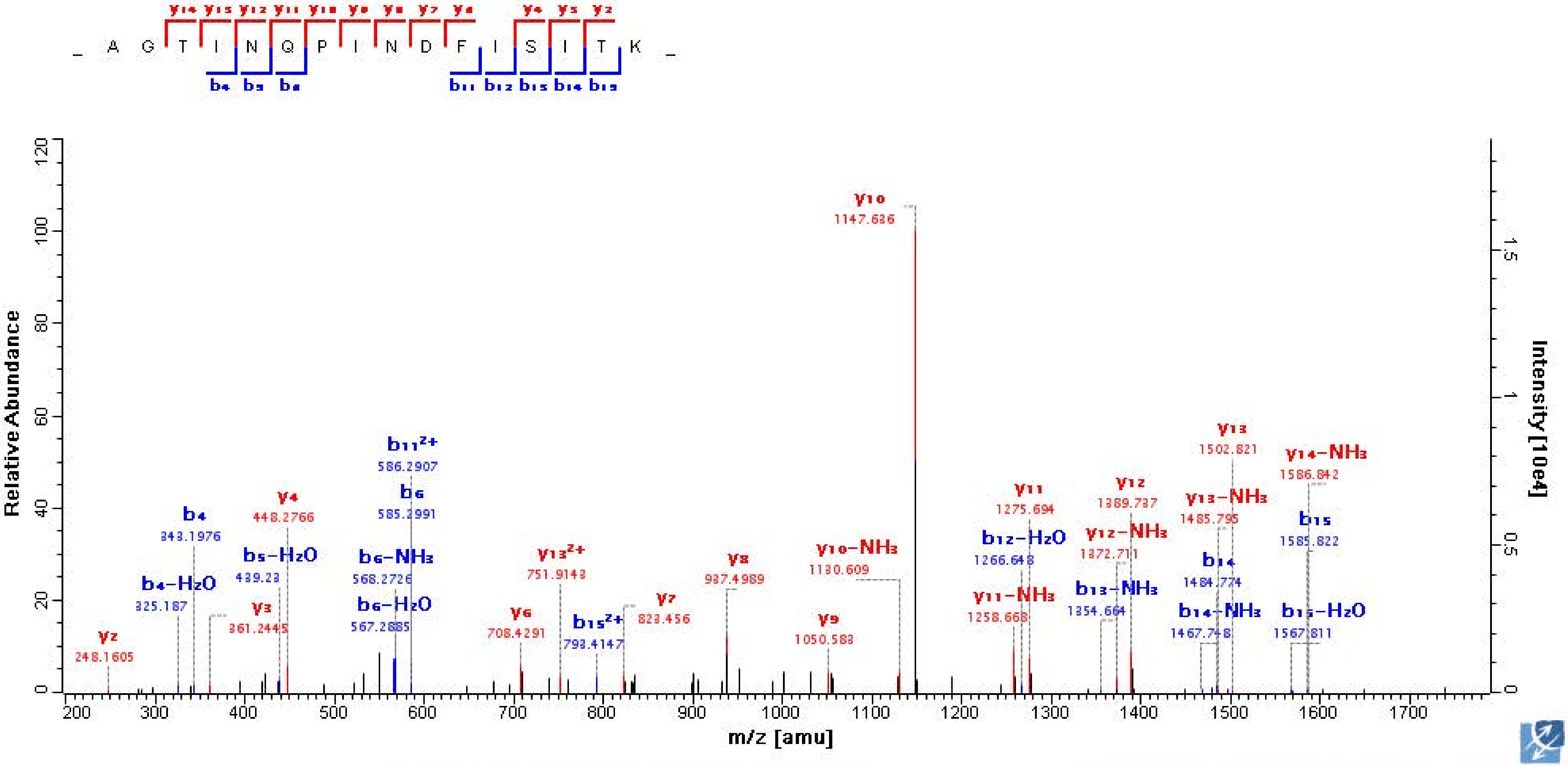
Mass:	1202.64576
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	177.7784
Mass Error [ppm]:	-0.23789
PEP:	2.0228E-52
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	69 %
Protein Localisation:	6 ... 15

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	60.04439		88.0393	1	S	9				
+0.04719	173.1285	-0.023958	201.1234	2	I	8	1116.621	-0.338211	558.8143	+0.212144
	302.171	+0.011833	330.166	3	E	7	1003.537	+0.136111	502.2723	+0.371668
	449.2395	+0.044494	477.2344	4	F	6	874.4946	+0.101007	874.4946	
	562.3235		590.3184	5	I	5	727.4262	+0.13164	727.4262	
	690.3821	+0.015256	718.377	6	Q	4	614.3422	+0.098089	614.3422	
	803.4662	+0.070413	831.4611	7	I	3	486.2836	+0.081593	486.2836	
	874.5033	+0.069127	902.4982	8	A	2	373.1995	+0.055703	373.1995	
	1021.539	+0.068823	1049.534	9	M	1	302.1624	+0.021436	302.1624	
				10	K	0	155.127		155.127	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F06
Scannumber:	31774
Protein:	BSU34830; yvzA
Peptide Score:	161.21
Method:	ITMS; CID; 3



precursor information

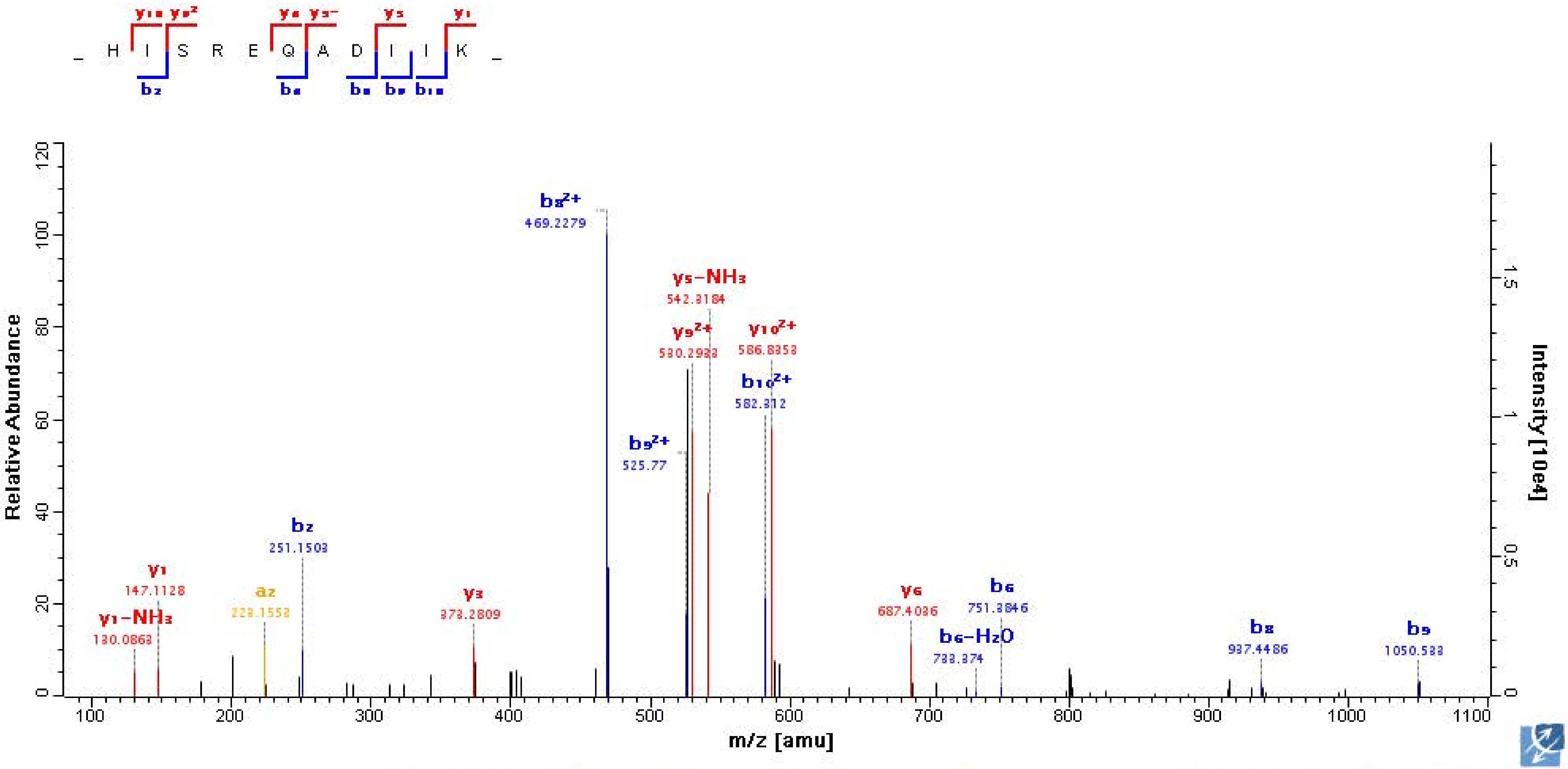
Mass:	1730.92086
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	161.2056
Mass Error [ppm]:	0.32562
PEP:	4.6573E-44
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	53 %
Protein Localisation:	29 ... 44

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	15				
	129.0659		129.0659	2	G	14	1660.89		1660.89	
	230.1135		230.1135	3	T	13	1603.869		1603.869	
	343.1976	-0.005702	343.1976	4	I	12	1502.821	+0.174774	751.9143	-0.195182
	457.2405		457.2405	5	N	11	1389.737	+0.044848	1389.737	
	585.2991	+0.157442	585.2991	6	Q	10	1275.694	+0.098762	1275.694	
	682.3519		682.3519	7	P	9	1147.636	-0.007699	1147.636	
	795.4359		795.4359	8	I	8	1050.583	+0.030782	1050.583	
	909.4789		909.4789	9	N	7	937.4989	+0.031411	937.4989	
	1024.506		1024.506	10	D	6	823.456	+0.075071	823.456	
+0.022182	586.2907		1171.574	11	F	5	708.4291	-0.01615	708.4291	
	1284.658		1284.658	12	I	4	561.3606		561.3606	
	1371.69		1371.69	13	S	3	448.2766	+0.010229	448.2766	
	1484.774	+0.088789	1484.774	14	I	2	361.2445	+0.035971	361.2445	
-0.094045	793.4147	+0.276096	1585.822	15	T	1	248.1605	+0.063791	248.1605	
				16	K	0	147.1128		147.1128	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F06
Scannumber:	9863
Protein:	BSU05640; ydgG
Peptide Score:	98.05
Method:	ITMS; CID; 3



precursor information

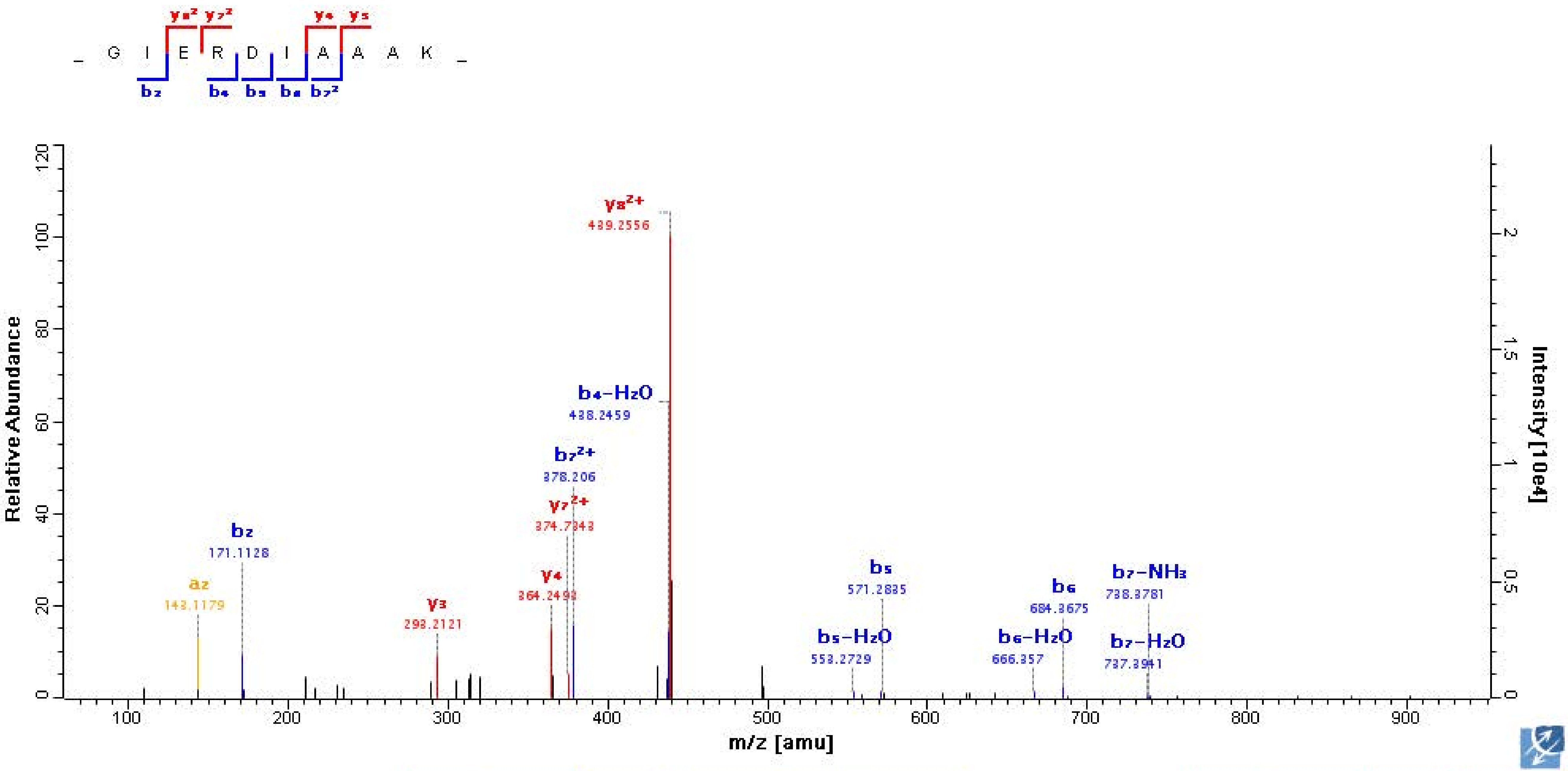
Mass:	1308.71588
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	98.04827
Mass Error [ppm]:	0.6766
PEP:	0.00073012
Precursor Type:	MULTI

general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	61 %
Protein Localisation:	35 ... 45

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
	110.071		138.066		138.066	1	H	10				
+0.04158	223.155		251.15	-0.0314	251.15	2	I	9	1172.66		586.835	+0.2219
	310.187		338.182		338.182	3	S	8	1059.58		530.293	+0.2123
	466.288		494.283		494.283	4	R	7	972.547		972.547	
	595.331		623.326		623.326	5	E	6	816.446		816.446	
	723.39		751.385	+0.45614	751.385	6	Q	5	687.404	-0.0638	687.404	
	794.427		822.422		822.422	7	A	4	559.345		559.345	
	909.454	+0.08074	469.228	+0.27453	937.449	8	D	3	488.308		488.308	
	1022.54	-0.1698	525.77	+0.12418	1050.53	9	I	2	373.281	+0.00599	373.281	
	1135.62	+0.2345	582.312		1163.62	10	I	1	260.197		260.197	
						11	K	0	147.113	+0.07096	147.113	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F07
Scannumber:	10911
Protein:	BSU25370; yqfB
Peptide Score:	93.55
Method:	ITMS; CID; 3



precursor information

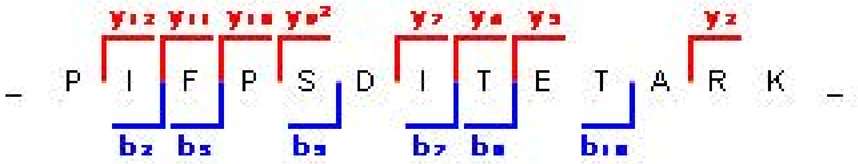
Mass:	1042.57709
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.55083
Mass Error [ppm]:	-0.018594
PEP:	0.0013336
Precursor Type:	MULTI

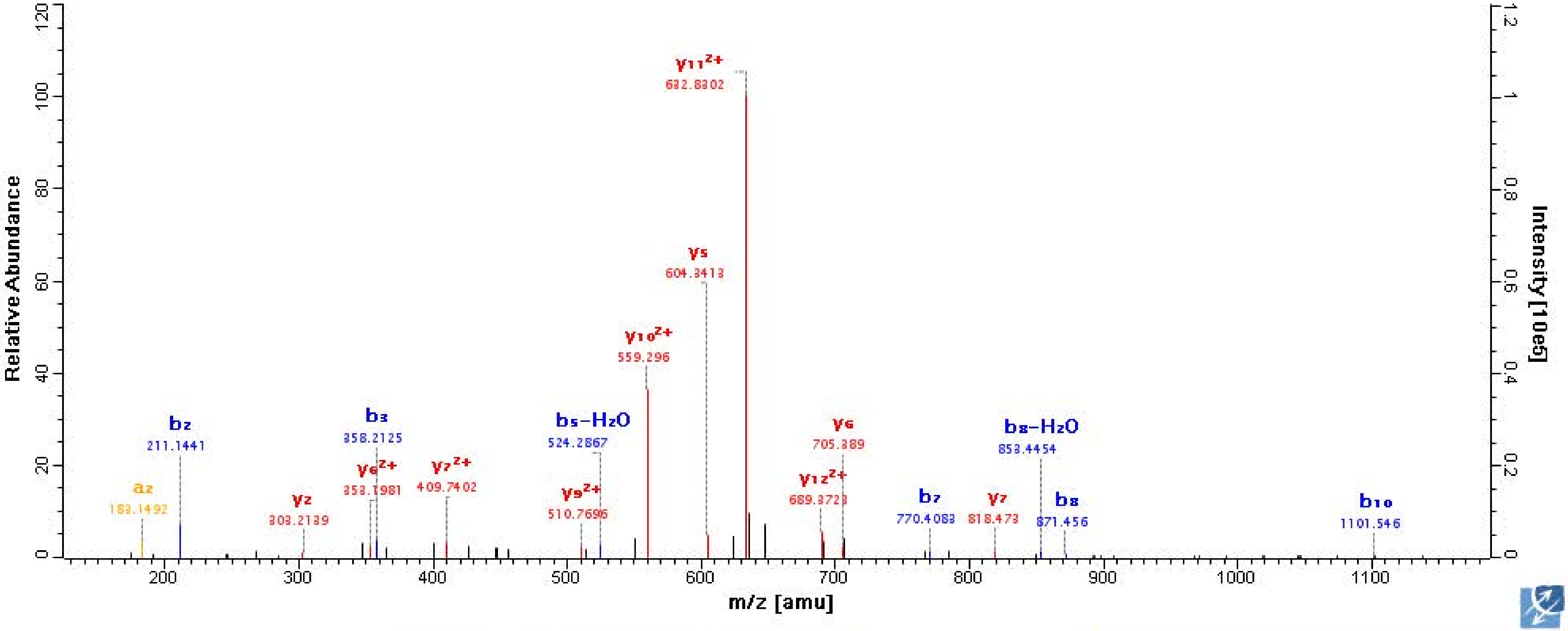
general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	66 %
Protein Localisation:	84 ... 93

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
	30.0338		58.0287		58.0287	1	G	9				
-0.1236	143.118		171.113	-0.083	171.113	2	I	8	990.588		990.588	
	272.16		300.155		300.155	3	E	7	877.504		439.256	-0.0085
	428.262		456.257		456.257	4	R	6	748.461		374.734	+0.3655
	543.289		571.283	-0.0301	571.283	5	D	5	592.36		592.36	
	656.373		684.368	+0.36564	684.368	6	I	4	477.333		477.333	
	727.41	+0.40791	378.206		755.405	7	A	3	364.249	+0.02049	364.249	
	798.447		826.442		826.442	8	A	2	293.212	-0.0635	293.212	
	869.484		897.479		897.479	9	A	1	222.175		222.175	
						10	K	0	151.138		151.138	

Source: 20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F09
Scannumber: 18753
Protein: BSU11560; yjbI
Peptide Score: 110.39
Method: ITMS; CID; 3





precursor information

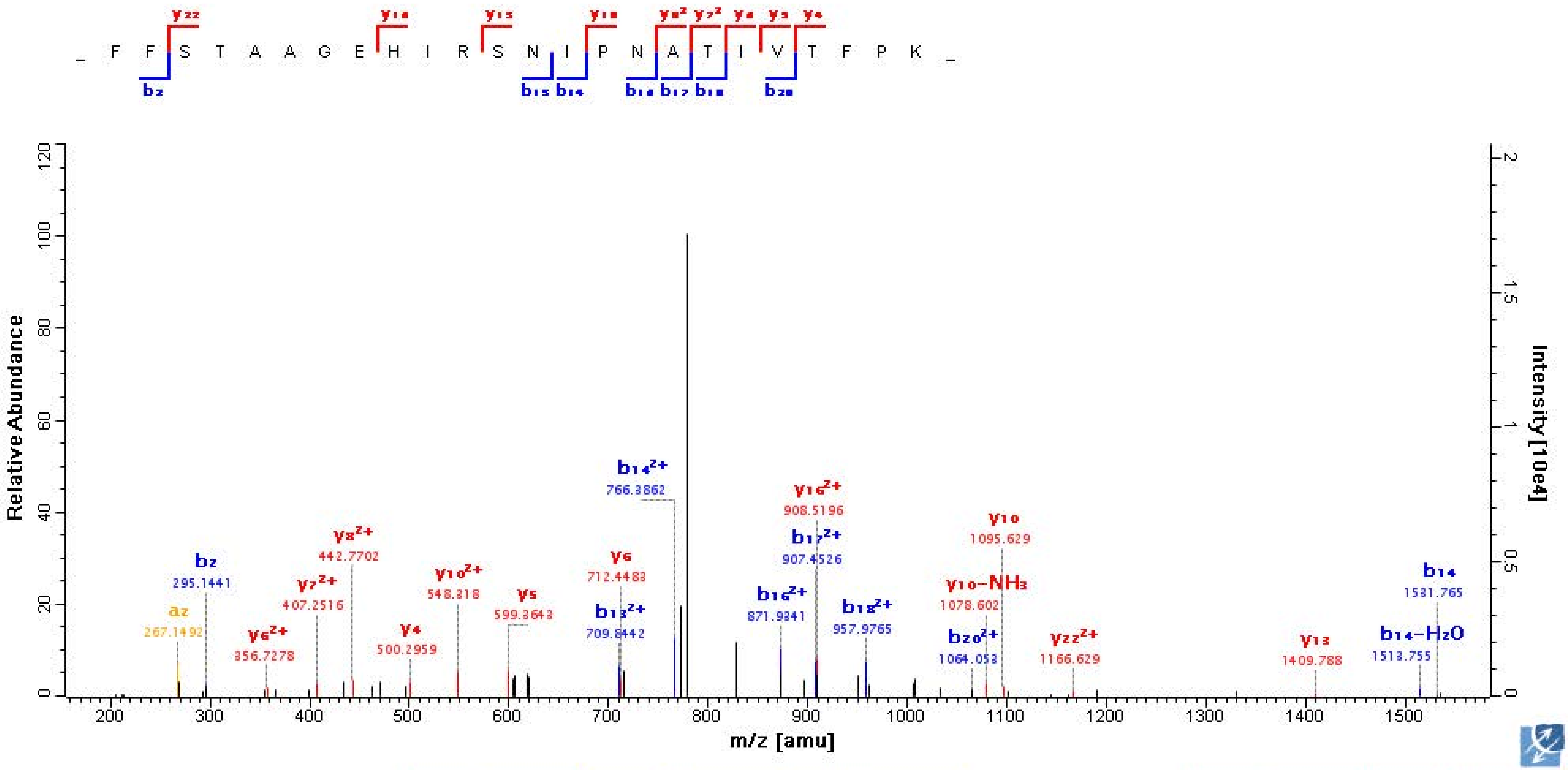
Mass:	1473.78294
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.3872
Mass Error [ppm]:	0.13453
PEP:	2.9445E-08
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	72 %
Protein Localisation:	36 ... 48

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	70.06513		98.06004	1	P	12				
-0.09879	183.1492	-0.064545	211.1441	2	I	11	1377.737		689.3723	+0.15172
	330.2176	-0.073602	358.2125	3	F	10	1264.653		632.8302	+0.458645
	427.2704		455.2653	4	P	9	1117.585		559.296	+0.293023
	514.3024		542.2973	5	S	8	1020.532		510.7696	+0.06913
	629.3293		657.3243	6	D	7	933.5		933.5	
	742.4134	+0.129402	770.4083	7	I	6	818.473	+0.242899	409.7402	+0.043379
	843.4611	+0.225401	871.456	8	T	5	705.389	+0.032103	353.1981	-0.188118
	972.5037		1000.499	9	E	4	604.3413	+0.054146	604.3413	
	1073.551	-0.167239	1101.546	10	T	3	475.2987		475.2987	
	1144.588		1172.583	11	A	2	374.251		374.251	
	1300.69		1328.684	12	R	1	303.2139	-0.439593	303.2139	
				13	K	0	147.1128		147.1128	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F09
Scannumber:	24395
Protein:	BSU06280; ydjP
Peptide Score:	127.22
Method:	ITMS; CID; 3



precursor information

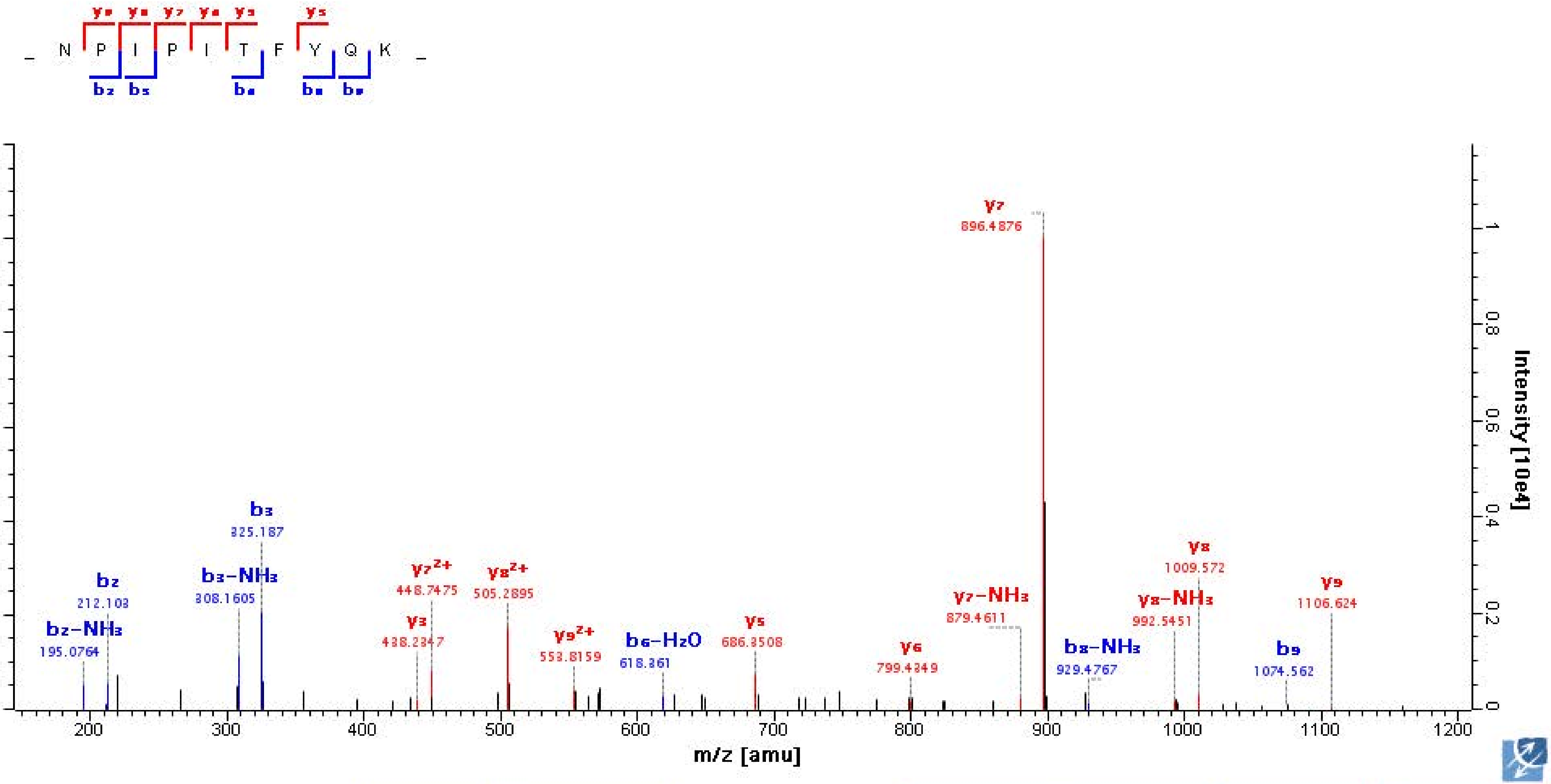
Mass:	2625.37783
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	127.2172
Mass Error [ppm]:	-0.62406
PEP:	1.6802E-29
Precursor Type:	ISO

general information

Annotation:	13 of 24
AminoAcids Coverag	54%
Intensity Coverage:	30%
Protein Localisation:	220 ... 243

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
	120.081		148.076		148.076	1	F	23				
-0.0998	267.149		295.144	+0.08279	295.144	2	F	22	2479.32		2479.32	
	354.181		382.176		382.176	3	S	21	2332.25		1166.63	-0.0582
	455.229		483.224		483.224	4	T	20	2245.22		2245.22	
	526.266		554.261		554.261	5	A	19	2144.17		2144.17	
	597.303		625.298		625.298	6	A	18	2073.13		2073.13	
	654.325		682.32		682.32	7	G	17	2002.1		2002.1	
	783.367		811.362		811.362	8	E	16	1945.07		1945.07	
	920.426		948.421		948.421	9	H	15	1816.03		908.52	-0.2087
	1033.51		1061.51		1061.51	10	I	14	1678.97		1678.97	
	1189.61		1217.61		1217.61	11	R	13	1565.89		1565.89	
	1276.64		1304.64		1304.64	12	S	12	1409.79	+0.35266	1409.79	
	1390.69	+0.10764	709.844		1418.68	13	N	11	1322.76		1322.76	
	1503.77	+0.4284	766.386	+0.03277	1531.77	14	I	10	1208.71		1208.71	
	1600.82		1628.82		1628.82	15	P	9	1095.63	+0.30868	548.318	+0.4477
	1714.87	+0.48388	871.934		1742.86	16	N	8	998.576		998.576	
	1785.9	-0.0413	907.453		1813.9	17	A	7	884.533		442.77	+0.0886
	1886.95	+0.3893	957.976		1914.95	18	T	6	813.496		407.252	+0.0391
	2000.03		2028.03		2028.03	19	I	5	712.448	-0.0845	356.728	+0.4524
	2099.1	+0.15993	1064.05		2127.1	20	V	4	599.364	+0.26311	599.364	
	2200.15		2228.15		2228.15	21	T	3	500.296	-0.0457	500.296	
	2347.22		2375.21		2375.21	22	F	2	399.248		399.248	
	2444.27		2472.27		2472.27	23	P	1	252.18		252.18	
						24	K	0	155.127		155.127	

Source:	20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F12
Scannumber:	21624
Protein:	BSU38620; yxlJ
Peptide Score:	113.71
Method:	ITMS; CID; 3



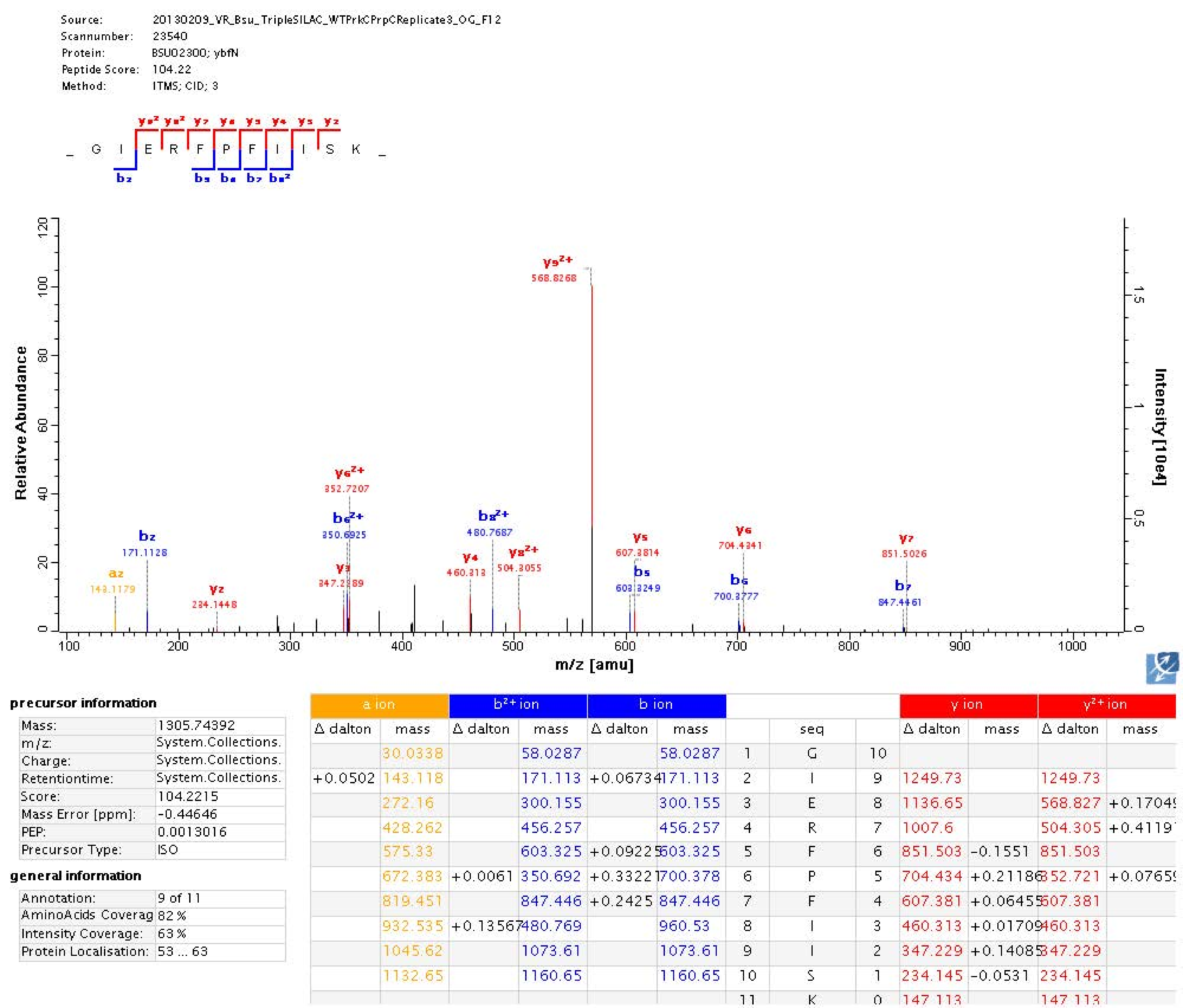
precursor information

Mass:	1219.66008
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.7065
Mass Error [ppm]:	-0.020702
PEP:	1.104E-06
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	56 %
Protein Localisation:	6 ... 15

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	9				
+0.076674	212.10296777	2	P	8	1106.6244583	+0.1279831	553.81586737	-0.1233625
-0.0569658	325.18703175	3	I	7	1009.5716944	+0.1717138	505.28948545	+0.0287519
	422.2397956	4	P	6	896.48763044	+0.0541176	448.74745345	+0.0677931
	535.32385958	5	I	5	799.43486659	-0.1163851	799.43486659	
	636.37153805	6	T	4	686.35080261	-0.0690033	686.35080261	
	783.43995197	7	F	3	585.30312414		585.30312414	
	946.50328051	8	Y	2	438.23471022	+0.1850896	438.23471022	
+0.1196605	1074.561858	9	Q	1	275.17138168		275.17138168	
		10	K	0	147.11280417		147.11280417	



Source: 20130209_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_OG_F12
Scannumber: 23540
Protein: BSU02300; ybfN
Peptide Score: 104.22
Method: ITMS; CID; 3

precursor information

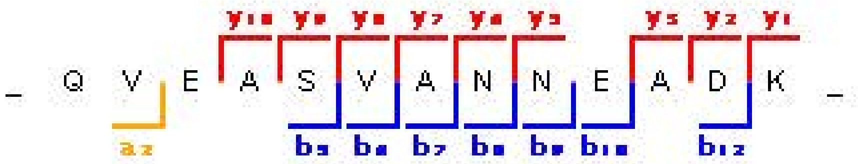
Mass:	1305.74392
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	104.2215
Mass Error [ppm]:	-0.44646
PEP:	0.0013016
Precursor Type:	ISO

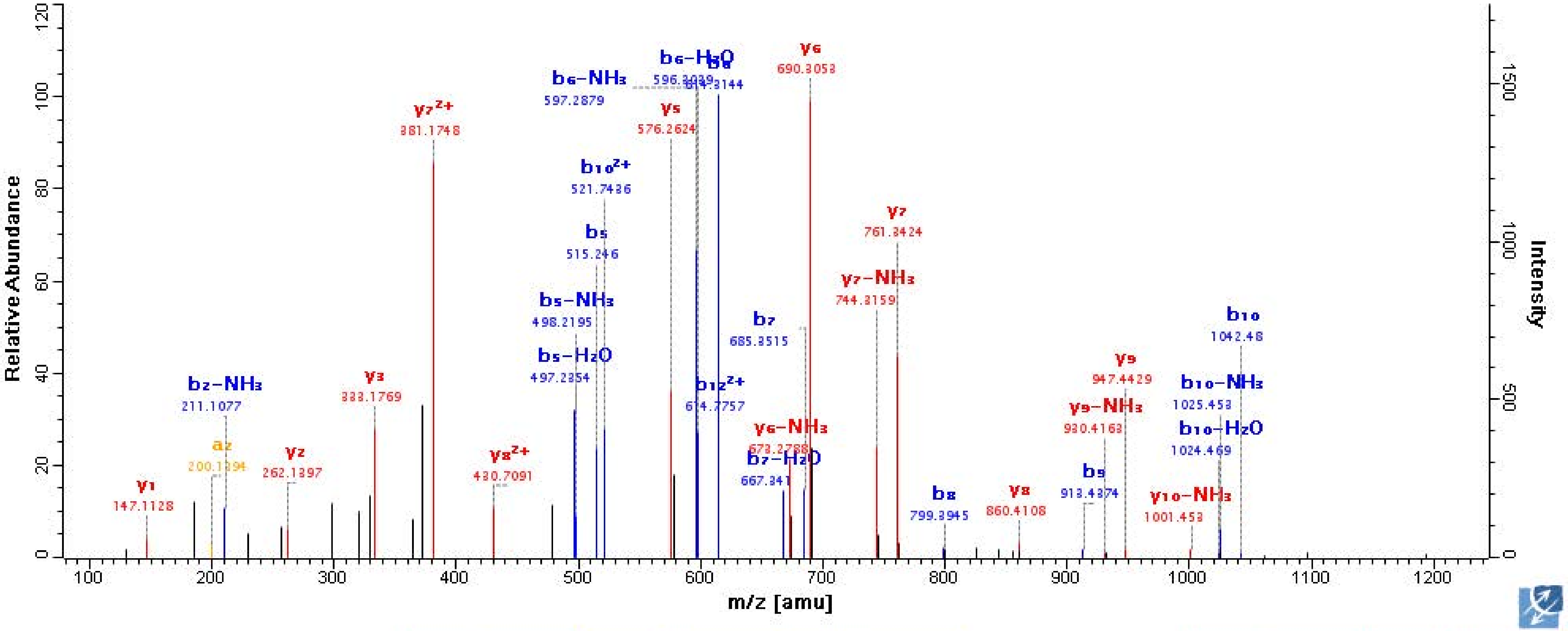
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	63 %
Protein Localisation:	53 ... 63

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
	30.0338		58.0287		58.0287	1	G	10				
+0.0502	143.118		171.113	+0.06734	171.113	2	I	9	1249.73		1249.73	
	272.16		300.155		300.155	3	E	8	1136.65		568.827	+0.1704
	428.262		456.257		456.257	4	R	7	1007.6		504.305	+0.4119
	575.33		603.325	+0.09225	603.325	5	F	6	851.503	-0.1551	851.503	
	672.383	+0.0061	350.692	+0.33221	700.378	6	P	5	704.434	+0.21186	352.721	+0.0765
	819.451		847.446	+0.2425	847.446	7	F	4	607.381	+0.06455	607.381	
	932.535	+0.13567	480.769		960.53	8	I	3	460.313	+0.01709	460.313	
	1045.62		1073.61		1073.61	9	I	2	347.229	+0.14085	347.229	
	1132.65		1160.65		1160.65	10	S	1	234.145	-0.0531	234.145	
						11	K	0	147.113		147.113	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F03
Scannumber:	2244
Protein:	BSU25550; rpsT; yqeO
Peptide Score:	218.75
Method:	ITMS; CID; 3





precursor information

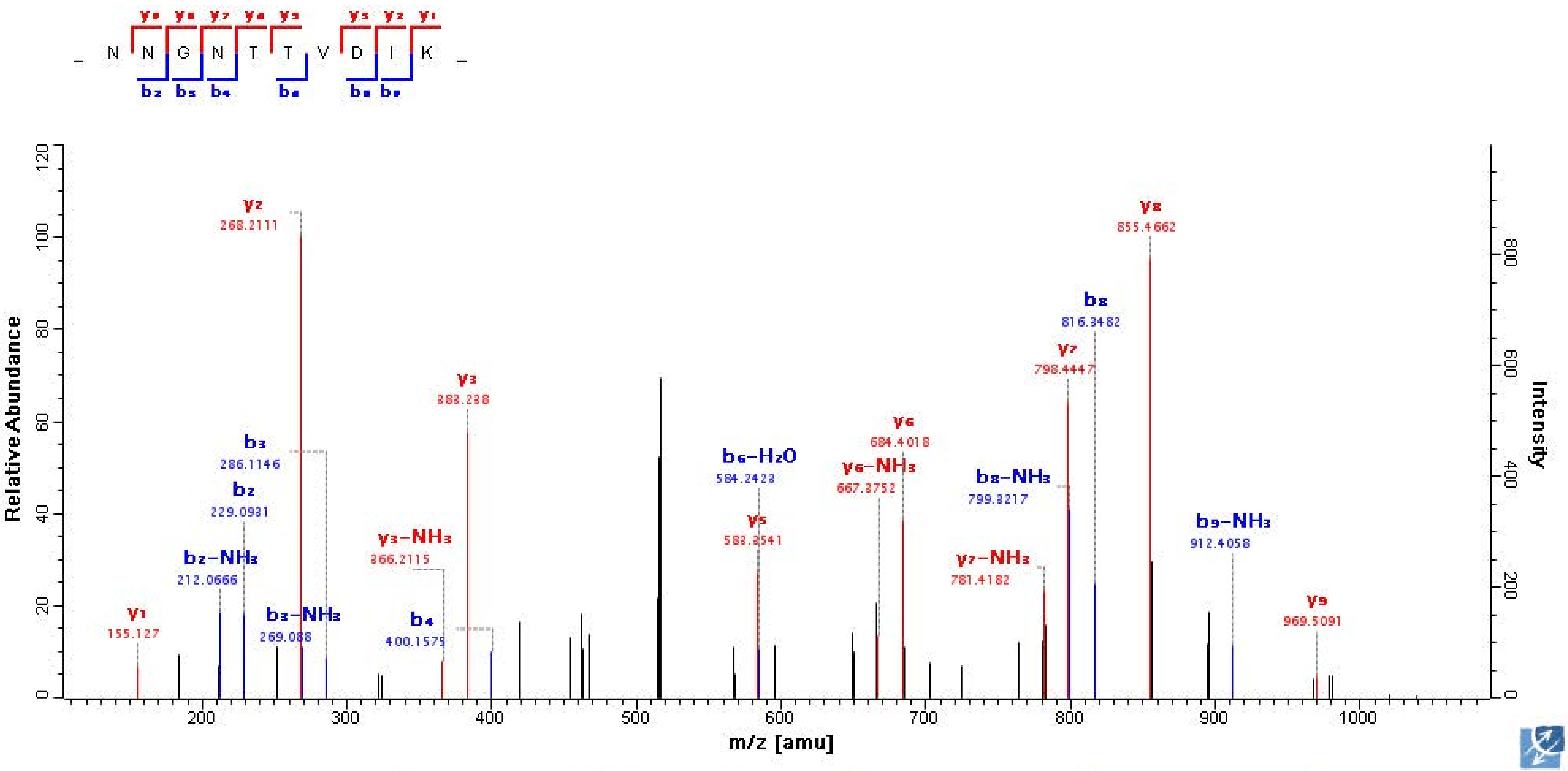
Mass:	1373.64208
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	218.752
Mass Error [ppm]:	-0.15364
PEP:	2.7029E-72
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	79 %
Protein Localisation:	34 ... 46

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
	101.071		129.066		129.066	1	Q	12				
-0.0635	200.139		228.134		228.134	2	V	11	1246.59		1246.59	
	329.182		357.177		357.177	3	E	10	1147.52		1147.52	
	400.219		428.214		428.214	4	A	9	1018.48		1018.48	
	487.251		515.246	-0.1753	515.246	5	S	8	947.443	-0.1287	947.443	
	586.32		614.314	-0.0575	614.314	6	V	7	860.411	-0.0729	430.709	-0.0664
	657.357		685.352	-0.1992	685.352	7	A	6	761.342	-0.1427	381.175	+0.0697
	771.4		799.394	-0.1908	799.394	8	N	5	690.305	-0.0764	690.305	
	885.442		913.437	-0.372	913.437	9	N	4	576.262	-0.0315	576.262	
	1014.49	+0.10256	521.744	-0.1174	1042.48	10	E	3	462.219		462.219	
	1085.52		1113.52		1113.52	11	A	2	333.177	+0.01619	333.177	
	1200.55	+0.37614	614.776		1228.54	12	D	1	262.14	+0.07409	262.14	
						13	K	0	147.113	-0.009	147.113	

Source:	20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F06
Scannumber:	2402
Protein:	bglC; BSU18130; eglS; gld
Peptide Score:	134.25
Method:	ITMS; CID; 3



precursor information

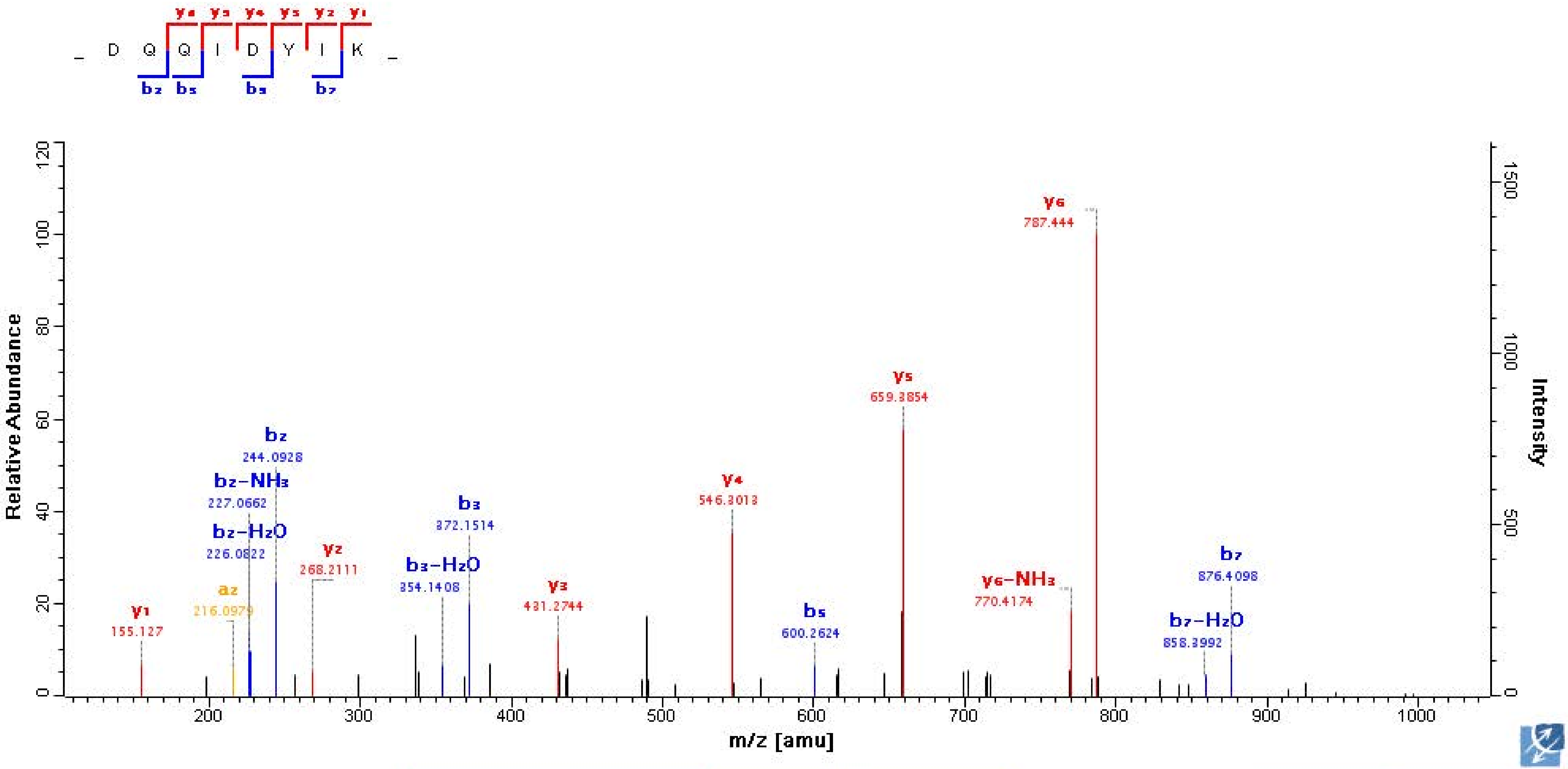
Mass:	1074.53052
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	134.2468
Mass Error [ppm]:	-0.026994
PEP:	2.1321E-09
Precursor Type:	MULTI

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	55 %
Protein Localisation:	378 ... 387

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	115.050203914	1	N	9		
+0.0644004	229.093131361	2	N	8	969.509099479	+0.1188302
+0.152861	286.114595085	3	G	7	855.466172031	-0.0944069
-0.1051544	400.157522532	4	N	6	798.444708308	-0.1926941
	501.205201006	5	T	5	684.401780861	-0.1407945
	602.25287948	6	T	4	583.354102386	-0.1461556
	701.321293396	7	V	3	482.306423912	
-0.0562442	816.348236428	8	D	2	383.238009996	-0.0812107
	929.432300409	9	I	1	268.211066964	-0.0486524
		10	K	0	155.127002984	-0.0326121

Source: 20130210_VR_Bsu_TripleSILAC_pWTPrkCPrpCReplicate3_F06
Scannumber: 5624
Protein: BSU07970; yfjT
Peptide Score: 138.54
Method: ITMS; CID; 3



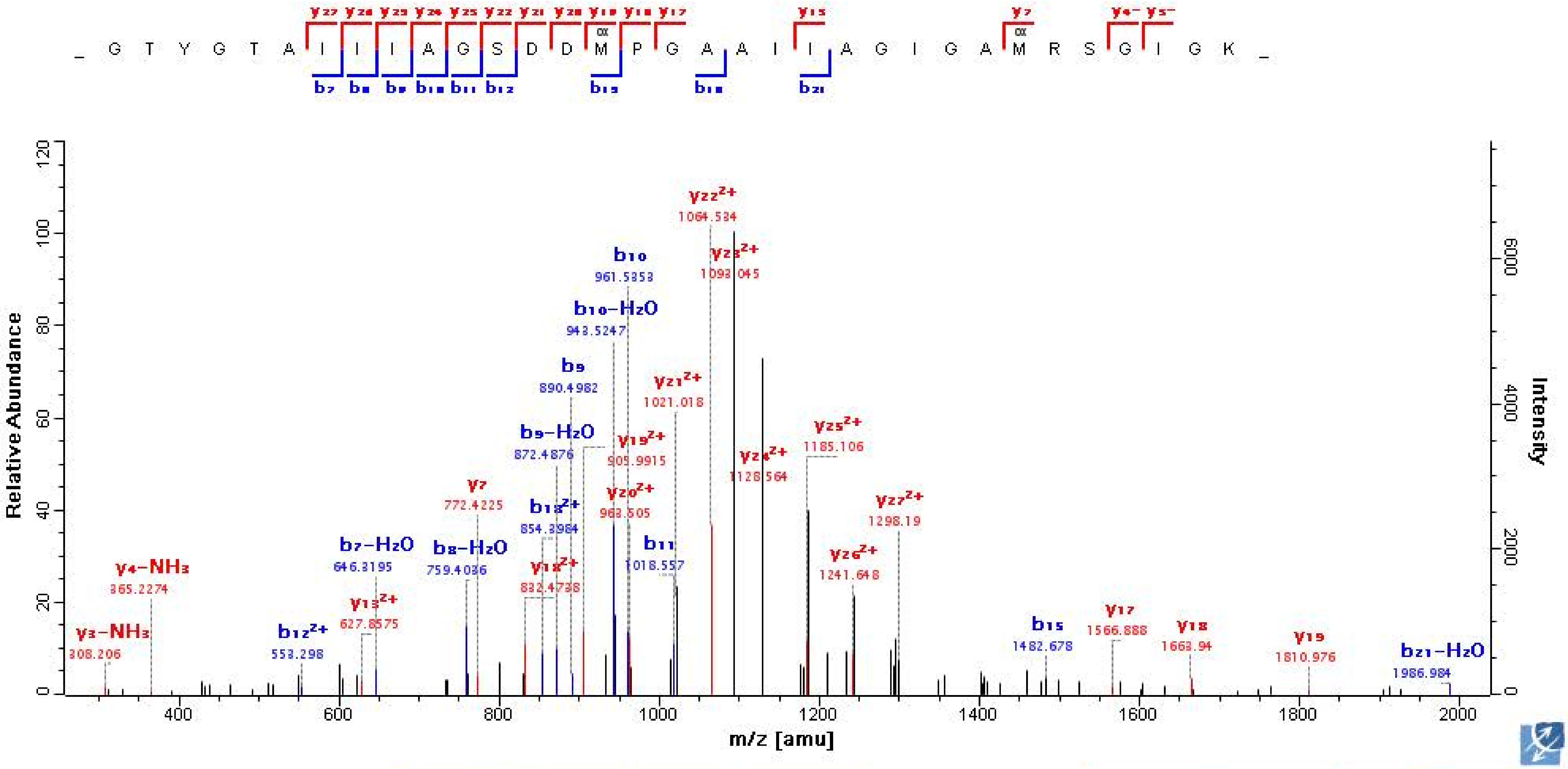
precursor information

g

Mass:	1021.50799
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.5448
Mass Error [ppm]:	-0.031027
PEP:	3.0272E-07
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	65 %
Protein Localisation:	9 ... 16

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.0342195	1	D	7		
+0.005679	216.09788239	-0.0347068	244.09279701	2	Q	6	915.50255754	
	344.1564599	+0.153313	372.15137452	3	Q	5	787.44398003	-0.1070049
	457.24052388		485.2354385	4	I	4	659.38540251	+0.0500833
	572.26746691	+0.0789271	600.26238153	5	D	3	546.30133853	-0.1401447
	735.33079545		763.32571007	6	Y	2	431.2743955	-0.1028257
	848.41485943	+0.0125282	876.40977405	7	I	1	268.21106696	+0.2143786
				8	K	0	155.12700298	-0.0715831

Source: 20130211_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_GeLC_F13
Scannumber: 28666
Protein: BSU38720; yxkO
Peptide Score: 71.42
Method: ITMS; CID; 3



precursor information

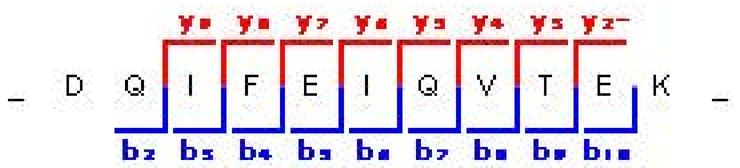
Mass:	3136.58862
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.41802
Mass Error [ppm]:	-0.33234
PEP:	1.4846E-13
Precursor Type:	MULTI

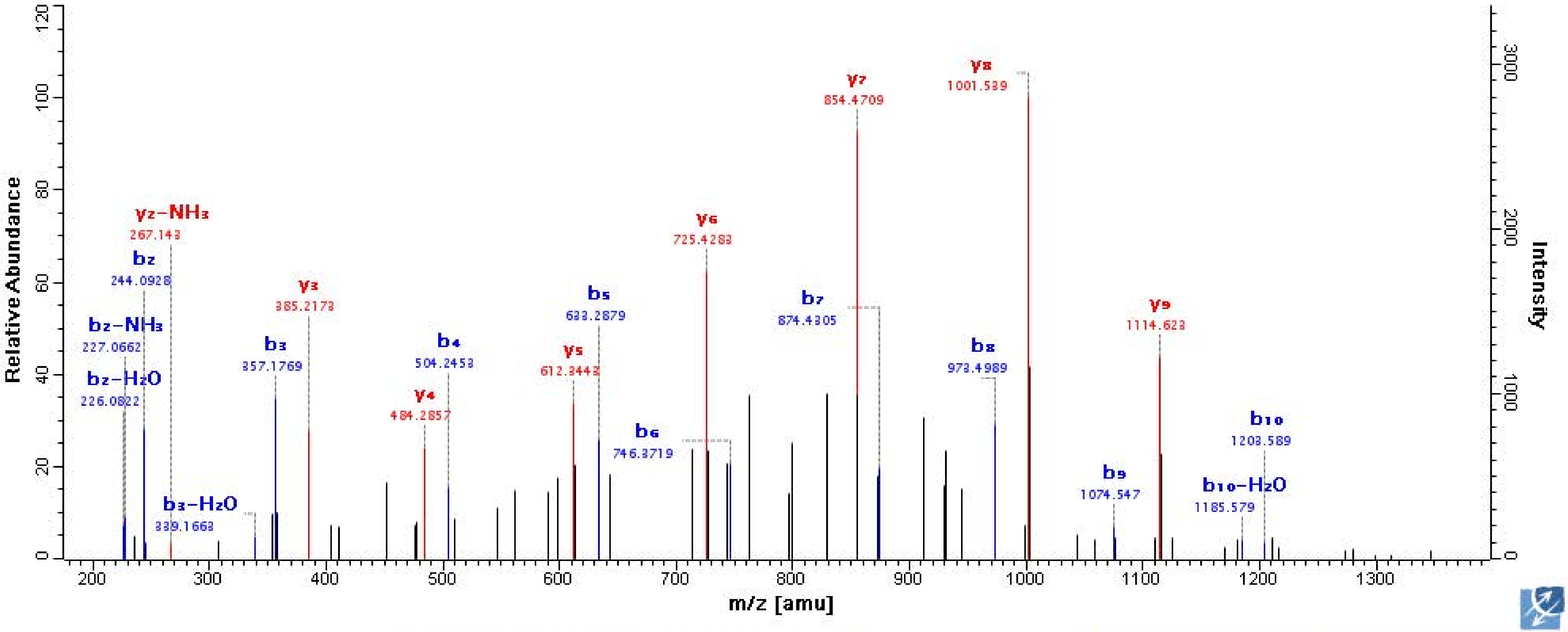
general information

Annotation:	16 of 33
AminoAcids Coverag	48 %
Intensity Coverage:	42 %
Protein Localisation:	25 ... 57

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	32				
	159.0764		159.0764	2	T	31	3088.59		3088.59	
	322.1397		322.1397	3	Y	30	2987.542		2987.542	
	379.1612		379.1612	4	G	29	2824.479		2824.479	
	480.2089		480.2089	5	T	28	2767.457		2767.457	
	551.246		551.246	6	A	27	2666.41		2666.41	
	664.3301		664.3301	7	I	26	2595.372		1298.19	+0.335177
	777.4141		777.4141	8	I	25	2482.288		1241.648	+0.141491
	890.4982	+0.125218	890.4982	9	I	24	2369.204		1185.106	+0.069632
	961.5353	+0.084442	961.5353	10	A	23	2256.12		1128.564	+0.047455
	1018.557	+0.446157	1018.557	11	G	22	2185.083		1093.045	+0.188448
+0.35992	553.298		1105.589	12	S	21	2128.062		1064.534	+0.470542
	1220.616		1220.616	13	D	20	2041.03		1021.018	+0.148422
	1335.643		1335.643	14	D	19	1926.003		963.505	-0.115817
	1482.678	-0.339952	1482.678	15	M	18	1810.976	+0.05698	905.9915	+0.35432
	1579.731		1579.731	16	P	17	1663.94	+0.247409	832.4738	+0.437083
	1636.752		1636.752	17	G	16	1566.888	+0.101931	1566.888	
+0.407556	854.3984		1707.789	18	A	15	1509.866		1509.866	
	1778.827		1778.827	19	A	14	1438.829		1438.829	
	1891.911		1891.911	20	I	13	1367.792		1367.792	
	2004.995		2004.995	21	I	12	1254.708		627.8575	+0.194273
	2076.032		2076.032	22	A	11	1141.624		1141.624	
	2133.053		2133.053	23	G	10	1070.587		1070.587	
	2246.137		2246.137	24	I	9	1013.565		1013.565	
	2303.159		2303.159	25	G	8	900.4811		900.4811	
	2374.196		2374.196	26	A	7	843.4596		843.4596	
	2521.231		2521.231	27	M	6	772.4225	+0.389112	772.4225	
	2677.332		2677.332	28	R	5	625.3871		625.3871	
	2764.364		2764.364	29	S	4	469.286		469.286	
	2821.386		2821.386	30	G	3	382.254		382.254	
	2934.47		2934.47	31	I	2	325.2325		325.2325	
	2991.491		2991.491	32	G	1	212.1485		212.1485	
				33	K	0	155.127		155.127	

Source:	20130211_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_GeLC_F14
Scannumber:	19645
Protein:	BSU11290; yjaV
Peptide Score:	113.77
Method:	ITMS; CID; 3





precursor information

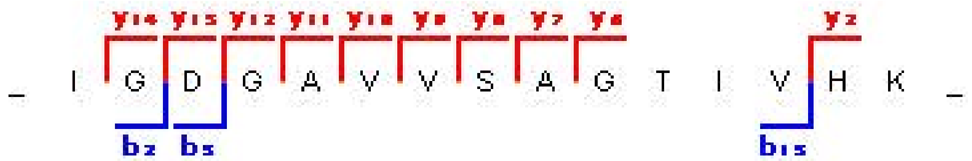
Mass:	1348.68701
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.7672
Mass Error [ppm]:	-0.3228
PEP:	4.3205E-06
Precursor Type:	MULTI

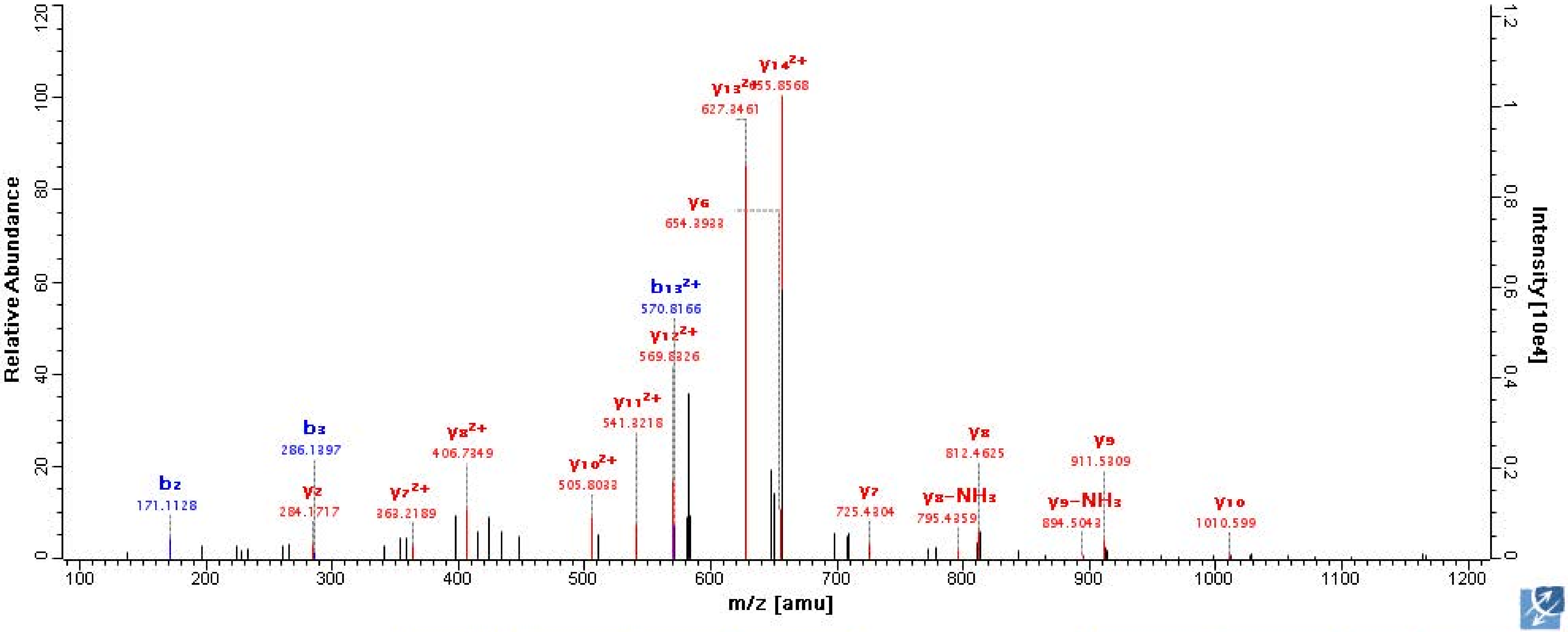
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	49 %
Protein Localisation:	151 ... 161

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	10		
-0.0786674	244.09279701	2	Q	9	1242.681978466	
-0.0385858	357.17686099	3	I	8	1114.623400955	-0.0097535
+0.1117197	504.245274907	4	F	7	1001.539336974	+0.0442812
-0.0399432	633.287868003	5	E	6	854.470923058	+0.0354246
-0.0371542	746.371931983	6	I	5	725.428329962	+0.0565333
+0.0119344	874.430509495	7	Q	4	612.344265982	-0.0285922
+0.0155419	973.498923411	8	V	3	484.28568847	-0.0319043
+0.2333053	1074.546601885	9	T	2	385.217274554	+0.0272018
+0.1888812	1203.589194981	10	E	1	284.16959608	
		11	K	0	155.127002984	

Source:	20130211_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_GeLC_F16
Scannumber:	12327
Protein:	BSU34960; yvoF
Peptide Score:	90.7
Method:	ITMS; CID; 3





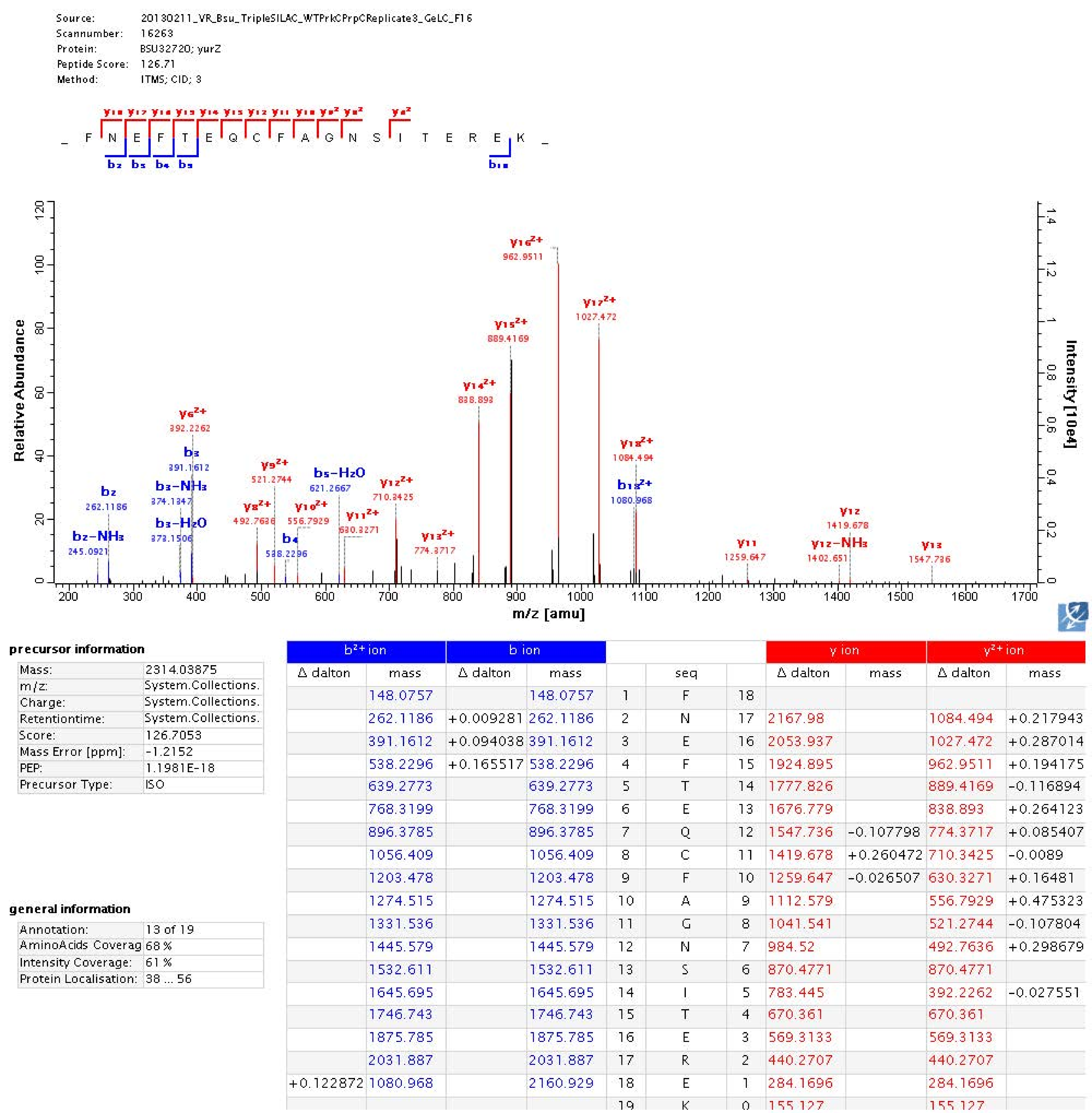
precursor information

Mass:	1422.783
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.69701
Mass Error [ppm]:	-0.056173
PEP:	8.367E-05
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	52 %
Protein Localisation:	127 ... 141

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	14				
	171.1128	+0.03841	171.1128	2	G	13	1310.706		655.8568	-0.001315
	286.1397	+0.14013	286.1397	3	D	12	1253.685		627.3461	+0.175433
	343.1612		343.1612	4	G	11	1138.658		569.8326	+0.006714
	414.1983		414.1983	5	A	10	1081.636		541.3218	+0.075796
	513.2667		513.2667	6	V	9	1010.599	-0.016787	505.8033	-0.040108
	612.3352		612.3352	7	V	8	911.5309	-0.005074	911.5309	
	699.3672		699.3672	8	S	7	812.4625	+0.175461	406.7349	+0.011583
	770.4043		770.4043	9	A	6	725.4304	+0.108674	363.2189	-0.041495
	827.4258		827.4258	10	G	5	654.3933	+0.227513	654.3933	
	928.4734		928.4734	11	T	4	597.3719		597.3719	
	1041.558		1041.558	12	I	3	496.3242		496.3242	
-0.310858	570.8166		1140.626	13	V	2	383.2401		383.2401	
	1277.685		1277.685	14	H	1	284.1717	-0.012353	284.1717	
				15	K	0	147.1128		147.1128	



Source: 20130211_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_GeLC_F16
Scannumber: 16263
Protein: BSU32720; yurZ
Peptide Score: 126.71
Method: ITMS; CID; 3

precursor information

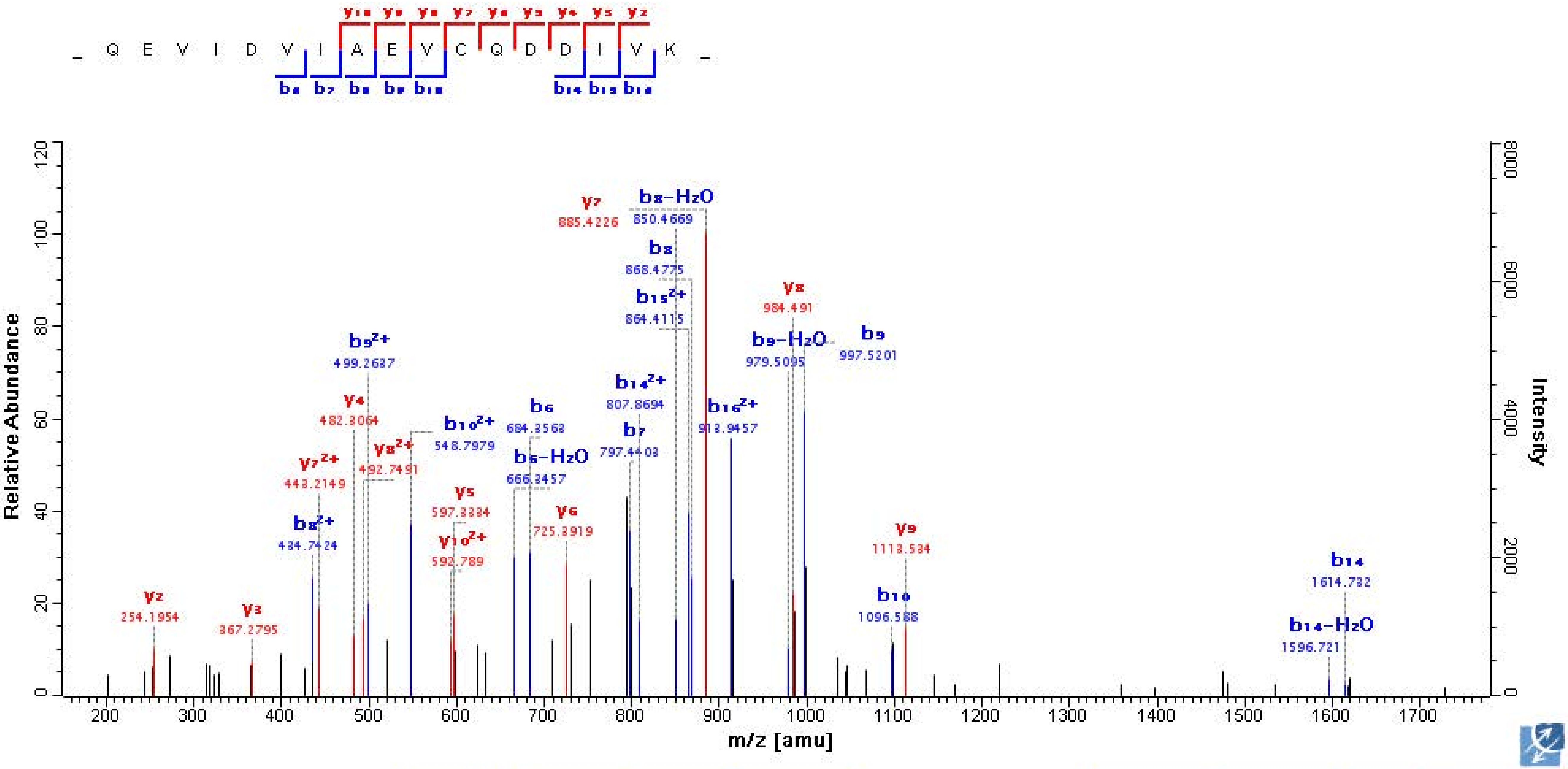
Mass:	2314.03875
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	126.7053
Mass Error [ppm]:	-1.2152
PEP:	1.1981E-18
Precursor Type:	ISO

general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	61 %
Protein Localisation:	38 ... 56

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.0757		148.0757	1	F	18				
	262.1186	+0.009281	262.1186	2	N	17	2167.98		1084.494	+0.217943
	391.1612	+0.094038	391.1612	3	E	16	2053.937		1027.472	+0.287014
	538.2296	+0.165517	538.2296	4	F	15	1924.895		962.9511	+0.194175
	639.2773		639.2773	5	T	14	1777.826		889.4169	-0.116894
	768.3199		768.3199	6	E	13	1676.779		838.893	+0.264123
	896.3785		896.3785	7	Q	12	1547.736	-0.107798	774.3717	+0.085407
	1056.409		1056.409	8	C	11	1419.678	+0.260472	710.3425	-0.0089
	1203.478		1203.478	9	F	10	1259.647	-0.026507	630.3271	+0.16481
	1274.515		1274.515	10	A	9	1112.579		556.7929	+0.475323
	1331.536		1331.536	11	G	8	1041.541		521.2744	-0.107804
	1445.579		1445.579	12	N	7	984.52		492.7636	+0.298679
	1532.611		1532.611	13	S	6	870.4771		870.4771	
	1645.695		1645.695	14	I	5	783.445		392.2262	-0.027551
	1746.743		1746.743	15	T	4	670.361		670.361	
	1875.785		1875.785	16	E	3	569.3133		569.3133	
	2031.887		2031.887	17	R	2	440.2707		440.2707	
+0.122872	1080.968		2160.929	18	E	1	284.1696		284.1696	
				19	K	0	155.127		155.127	

Source:	20130211_VR_Bsu_TripleSILAC_WTPrkCPrpCReplicate3_GeLC_F16
Scannumber:	28604
Protein:	BSU38520; dltC; ipa-3r
Peptide Score:	160.65
Method:	ITMS; CID; 3



precursor information

Mass:	1971.98214
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	160.6495
Mass Error [ppm]:	-0.086543
PEP:	2.6248E-48
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	63 %
Protein Localisation:	5 ... 21

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				
	258.1084		258.1084	2	E	15	1852.945		1852.945	
	357.1769		357.1769	3	V	14	1723.903		1723.903	
	470.2609		470.2609	4	I	13	1624.834		1624.834	
	585.2879		585.2879	5	D	12	1511.75		1511.75	
	684.3563	+0.074199	684.3563	6	V	11	1396.723		1396.723	
	797.4403	-0.050453	797.4403	7	I	10	1297.655		1297.655	
+0.361819	434.7424	-0.046857	868.4775	8	A	9	1184.571		592.789	+0.058844
-0.094109	499.2637	+0.110074	997.5201	9	E	8	1113.534	-0.027618	1113.534	
-0.084676	548.7979	+0.218662	1096.588	10	V	7	984.491	+0.075278	492.7491	+0.326237
	1256.619		1256.619	11	C	6	885.4226	-0.048386	443.2149	+0.201997
	1384.678		1384.678	12	Q	5	725.3919	+0.151513	725.3919	
	1499.705		1499.705	13	D	4	597.3334	-0.144768	597.3334	
+0.14632	807.8694	-0.004039	1614.732	14	D	3	482.3064	+0.122165	482.3064	
+0.09086	864.4115		1727.816	15	I	2	367.2795	-0.138246	367.2795	
+0.052197	913.9457		1826.884	16	V	1	254.1954	+0.13283	254.1954	
				17	K	0	155.127		155.127	