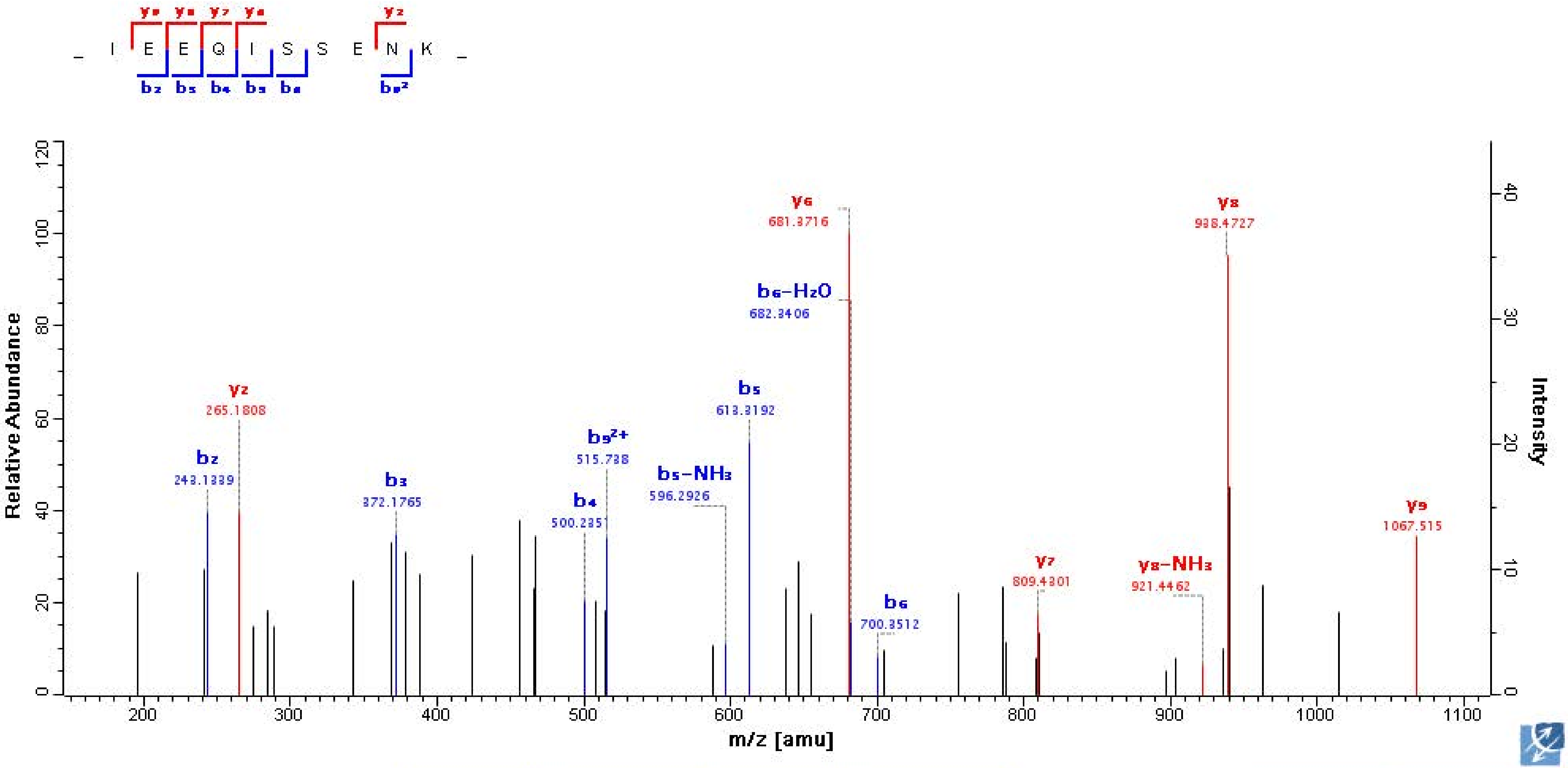
Source:	20120314_VR_TripleSILAC_pT1L1T2_F04
Scannumber:	2376
Protein:	BSU15150; ftsL; yllD; ylxB
Peptide Score:	75.51
Method:	ITMS; CID; 3



precursor information

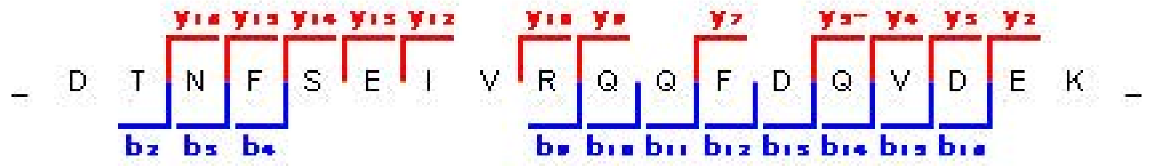
Mass:	1175.56683
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	75.50899
Mass Error [ppm]:	-0.14292
PEP:	0.0046244
Precursor Type:	MULTI

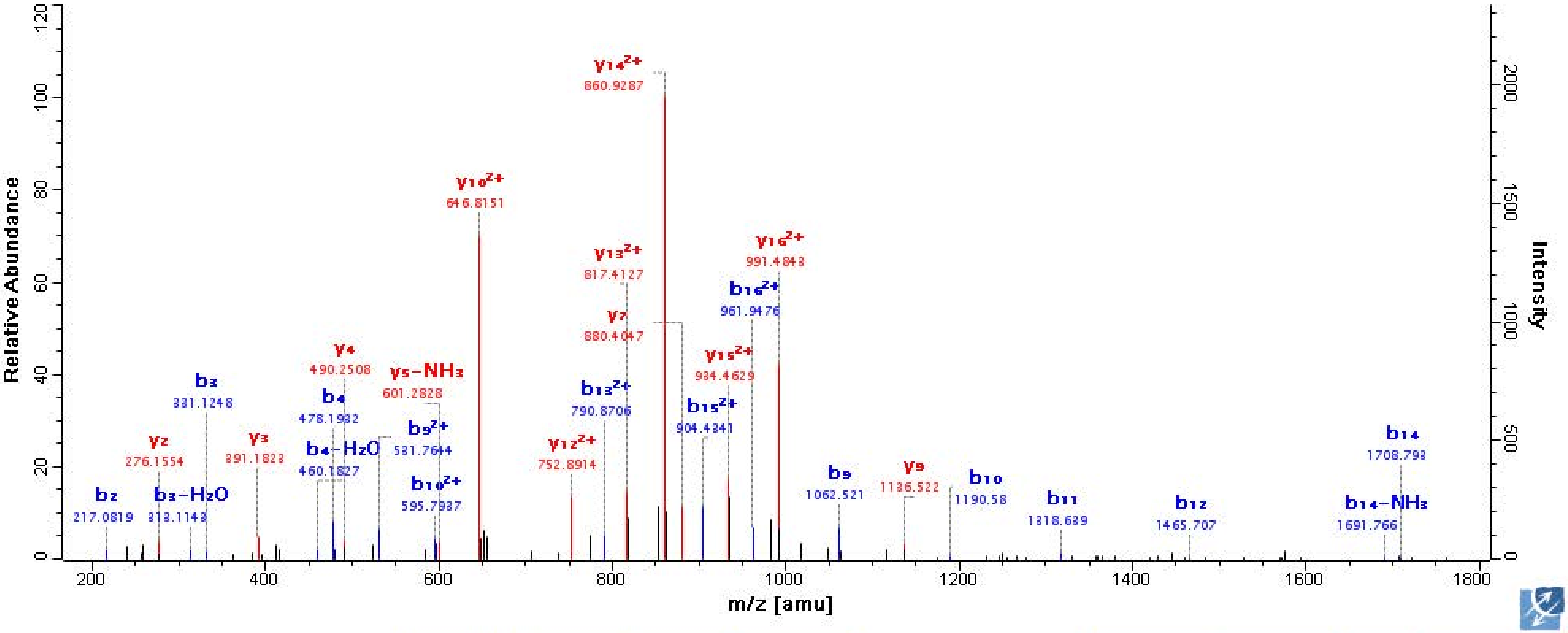
general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	44 %
Protein Localisation:	69 ... 78

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	9		
	243.13393354	+0.18998	243.13393354	2	E	8	1067.5153162	-0.0073816
	372.17652664	-0.0183235	372.17652664	3	E	7	938.47272311	+0.2158145
	500.23510415	+0.1014437	500.23510415	4	Q	6	809.43013001	+0.2433929
	613.31916813	-0.0084992	613.31916813	5	I	5	681.3715525	+0.0201711
	700.35119654	+0.1171262	700.35119654	6	S	4	568.28748852	
	787.38322495		787.38322495	7	S	3	481.25546011	
	916.42581805		916.42581805	8	E	2	394.2234317	
-0.3417097	515.73801098		1030.4687455	9	N	1	265.1808386	-0.159873
				10	K	0	151.13791115	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F09
Scannumber:	9284
Protein:	BSU36390; flhP; yvyB
Peptide Score:	156.17
Method:	ITMS; CID; 3





precursor information

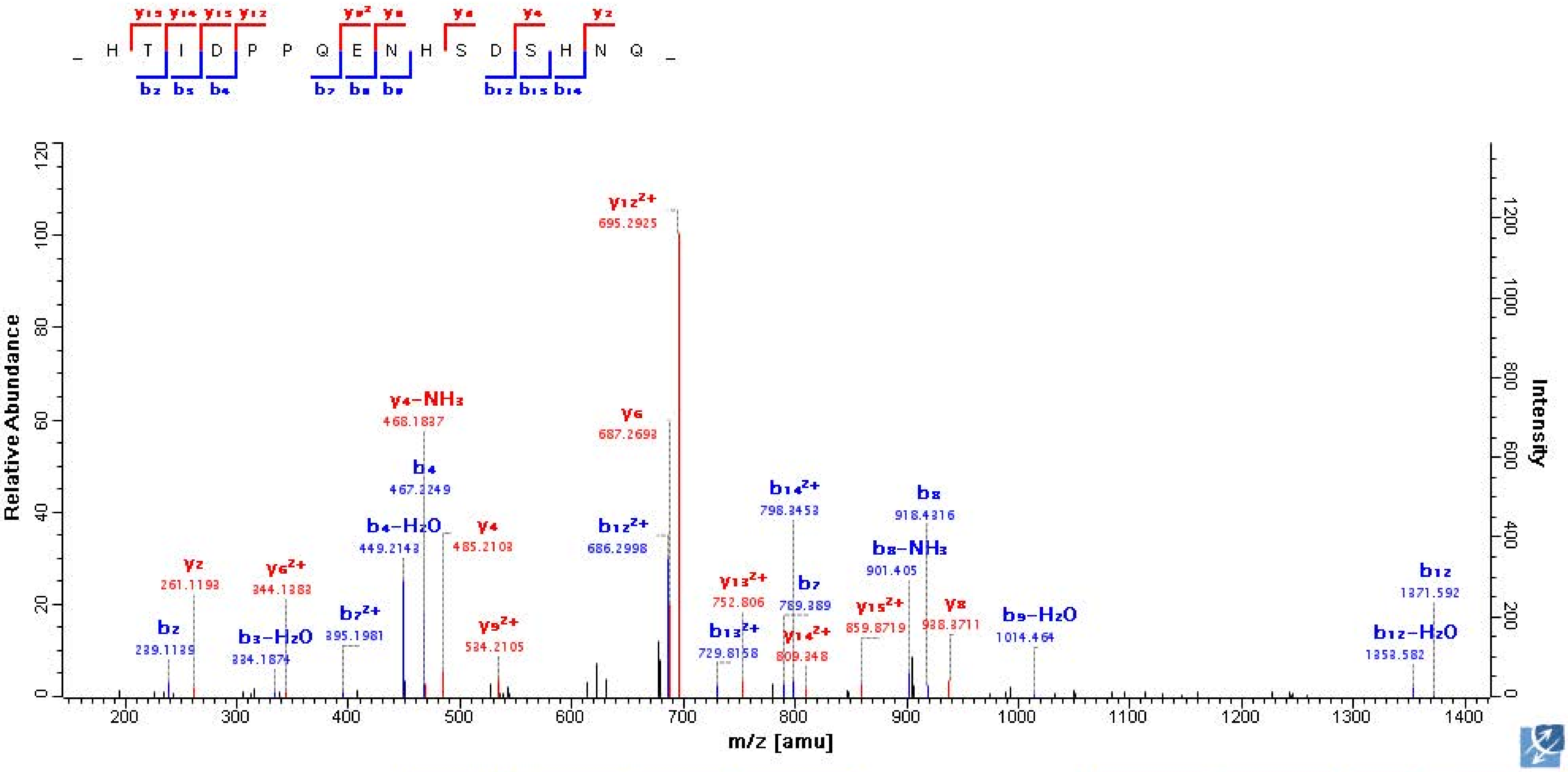
Mass:	2197.02784
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.1734
Mass Error [ppm]:	-0.41025
PEP:	2.3514E-21
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	70 %
Protein Localisation:	38 ... 55

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	17				
	217.0819	+0.122265	217.0819	2	T	16	2083.009		2083.009	
	331.1248	+0.141532	331.1248	3	N	15	1981.961		991.4843	+0.313271
	478.1932	+0.057005	478.1932	4	F	14	1867.918		934.4629	-0.052716
	565.2253		565.2253	5	S	13	1720.85		860.9287	+0.246933
	694.2679		694.2679	6	E	12	1633.818		817.4127	-0.000359
	807.3519		807.3519	7	I	11	1504.775		752.8914	+0.256167
	906.4203		906.4203	8	V	10	1391.691		1391.691	
+0.243938	531.7644	+0.067539	1062.521	9	R	9	1292.623		646.8151	+0.204782
-0.102185	595.7937	-0.002513	1190.58	10	Q	8	1136.522	-0.03283	1136.522	
	1318.639	+0.104925	1318.639	11	Q	7	1008.463		1008.463	
	1465.707	+0.238294	1465.707	12	F	6	880.4047	-0.015956	880.4047	
-0.316664	790.8706		1580.734	13	D	5	733.3363		733.3363	
	1708.793	+0.22333	1708.793	14	Q	4	618.3093		618.3093	
+0.212309	904.4341		1807.861	15	V	3	490.2508	+0.066018	490.2508	
+0.167709	961.9476		1922.888	16	D	2	391.1823	+0.220858	391.1823	
	2051.93		2051.93	17	E	1	276.1554	+0.000548	276.1554	
				18	K	0	147.1128		147.1128	

Source:	20120314_VR_TripleSILAC_pT1L1T2_F16
Scannumber:	1840
Protein:	BSU30659; ytzI
Peptide Score:	139.78
Method:	ITMS; CID; 3



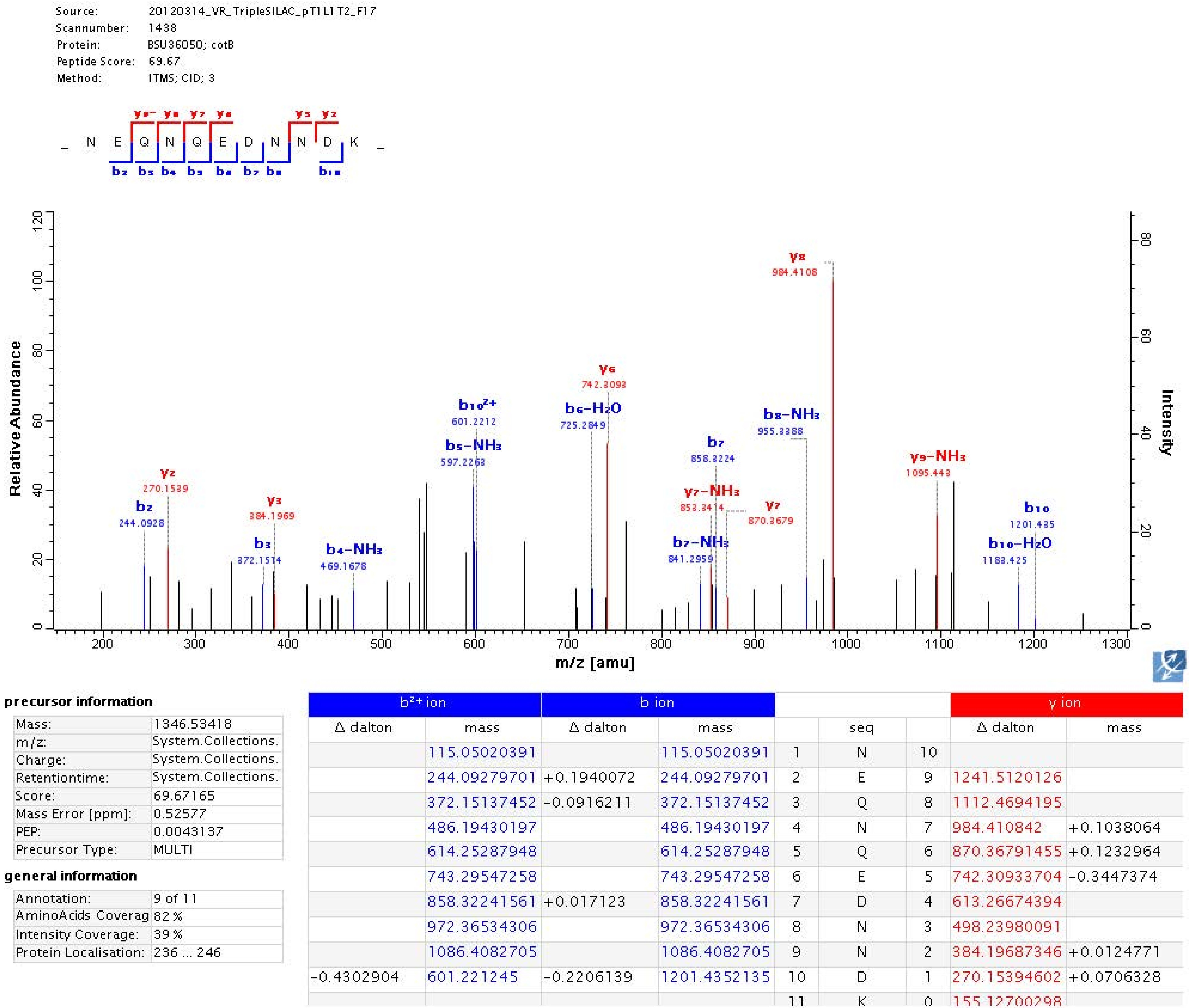
precursor information

Mass:	1854.78777
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	139.7806
Mass Error [ppm]:	-0.18772
PEP:	2.7457E-10
Precursor Type:	ISO

general information

Annotation:	12 of 16
AminoAcids Coverag	75 %
Intensity Coverage:	73 %
Protein Localisation:	43 ... 58

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	15				
	239.1139	+0.116846	239.1139	2	T	14	1718.736		859.8719	+0.114755
	352.1979		352.1979	3	I	13	1617.689		809.348	+0.140791
	467.2249	-0.0519	467.2249	4	D	12	1504.605		752.806	+0.208824
	564.2776		564.2776	5	P	11	1389.578		695.2925	+0.228704
	661.3304		661.3304	6	P	10	1292.525		1292.525	
+0.217033	395.1981	+0.086973	789.389	7	Q	9	1195.472		1195.472	
	918.4316	+0.054756	918.4316	8	E	8	1067.414		534.2105	-0.128452
	1032.474		1032.474	9	N	7	938.3711	-0.057621	938.3711	
	1169.533		1169.533	10	H	6	824.3282		824.3282	
	1256.565		1256.565	11	S	5	687.2693	+0.031584	344.1383	+0.093544
+0.335974	686.2998	+0.376977	1371.592	12	D	4	600.2372		600.2372	
+0.039076	729.8158		1458.624	13	S	3	485.2103	-0.065389	485.2103	
+0.322791	798.3453		1595.683	14	H	2	398.1783		398.1783	
	1709.726		1709.726	15	N	1	261.1193	+0.06614	261.1193	
				16	Q	0	147.0764		147.0764	



Source:	20120314_VR_TripleSILAC_pT1L1T2_F17
Scannumber:	1438
Protein:	BSU36050; cotB
Peptide Score:	69.67
Method:	ITMS; CID; 3

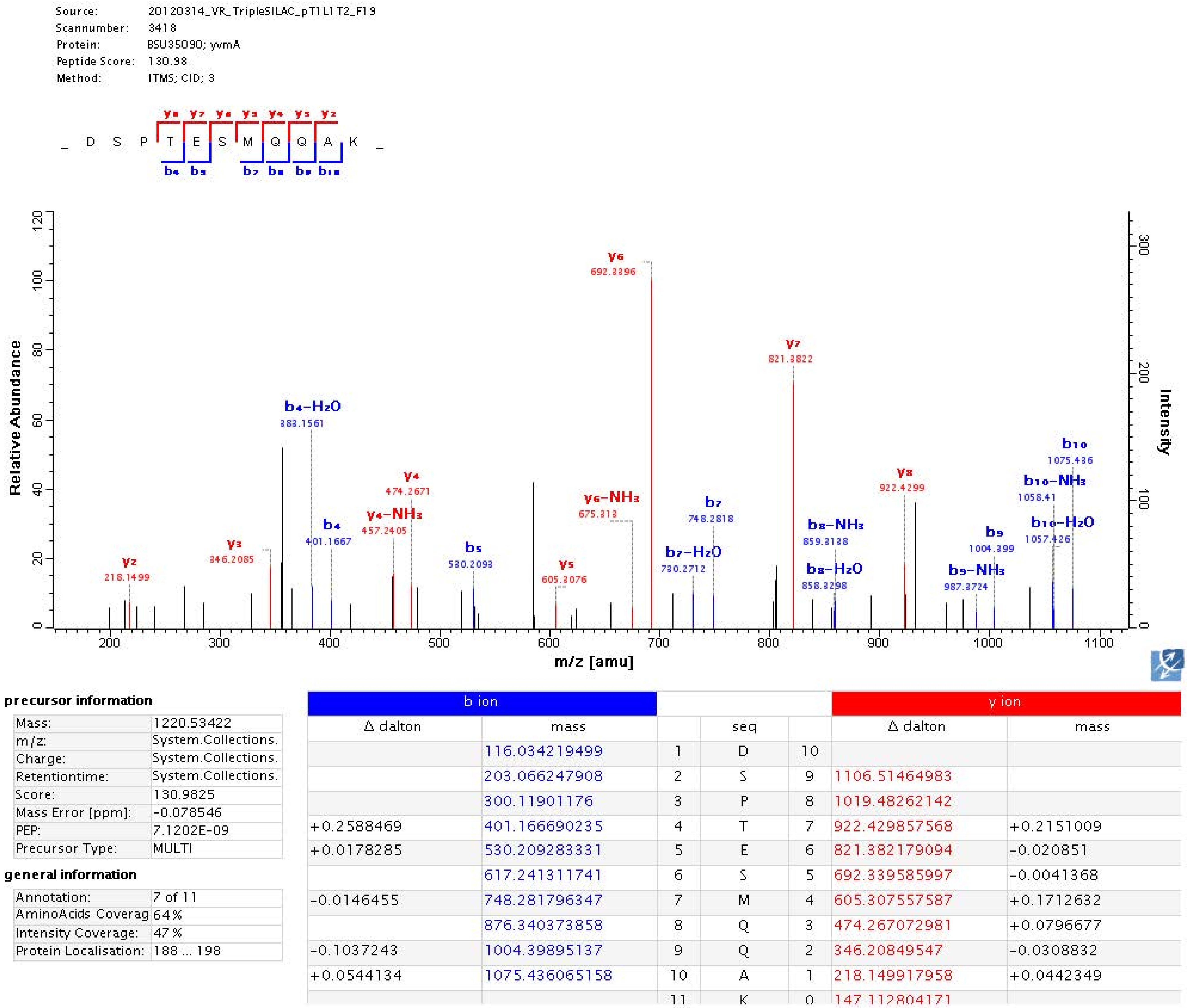
precursor information

Mass:	1346.53418
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	69.67165
Mass Error [ppm]:	0.52577
PEP:	0.0043137
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	39 %
Protein Localisation:	236 ... 246

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	115.05020391		115.05020391	1	N	10		
	244.09279701	+0.1940072	244.09279701	2	E	9	1241.5120126	
	372.15137452	-0.0916211	372.15137452	3	Q	8	1112.4694195	
	486.19430197		486.19430197	4	N	7	984.410842	+0.1038064
	614.25287948		614.25287948	5	Q	6	870.36791455	+0.1232964
	743.29547258		743.29547258	6	E	5	742.30933704	-0.3447374
	858.32241561	+0.017123	858.32241561	7	D	4	613.26674394	
	972.36534306		972.36534306	8	N	3	498.23980091	
	1086.4082705		1086.4082705	9	N	2	384.19687346	+0.0124771
-0.4302904	601.221245	-0.2206139	1201.4352135	10	D	1	270.15394602	+0.0706328
				11	K	0	155.12700298	



Source: 20120314_VR_TripleSILAC_pT1L1T2_F19
Scannumber: 3418
Protein: BSU35090; yvmA
Peptide Score: 130.98
Method: ITMS; CID; 3

precursor information

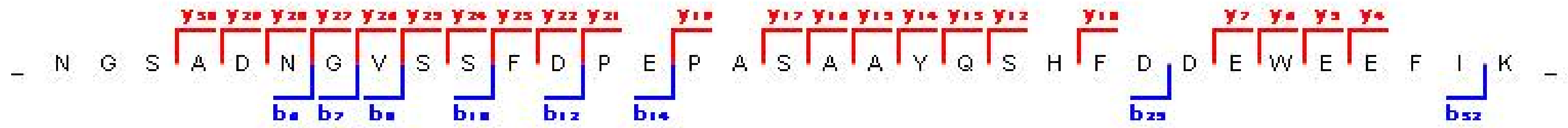
Mass:	1220.53422
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	130.9825
Mass Error [ppm]:	-0.078546
PEP:	7.1202E-09
Precursor Type:	MULTI

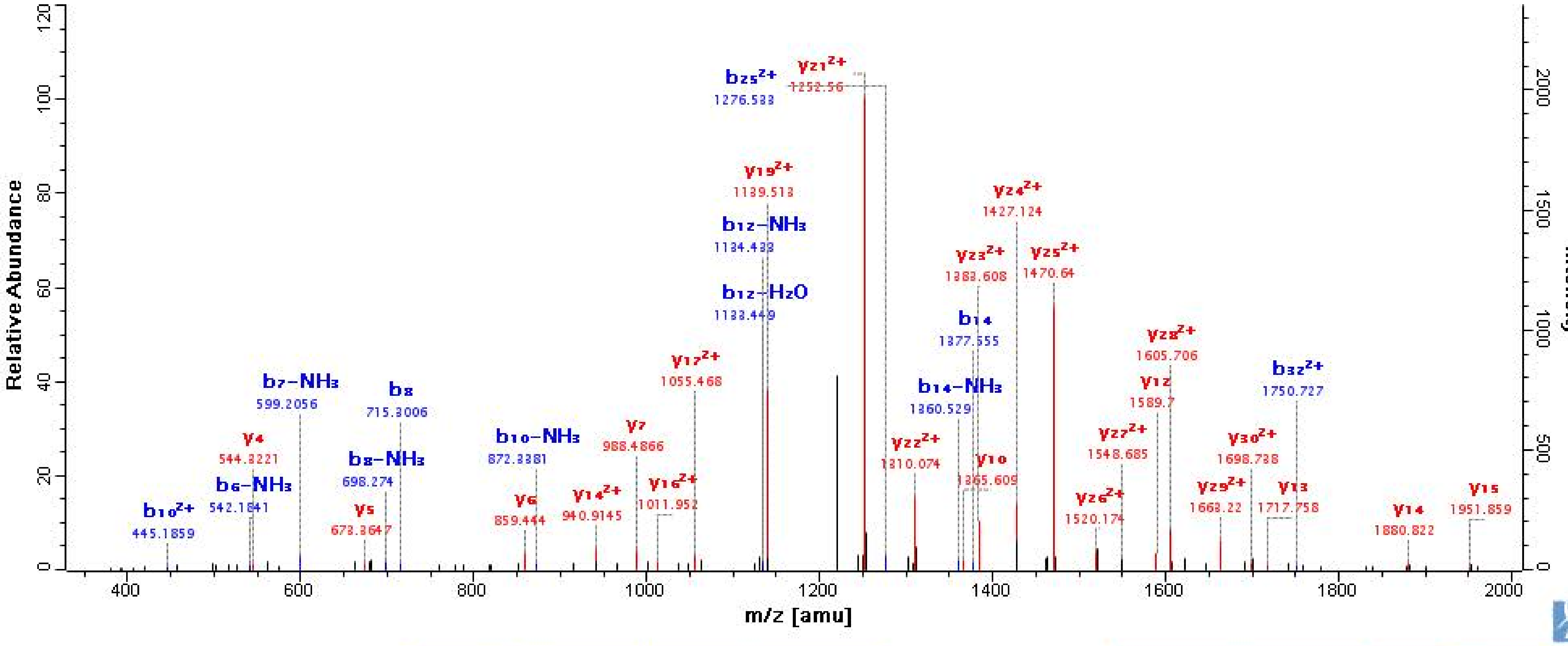
general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	47 %
Protein Localisation:	188 ... 198

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	10		
	203.066247908	2	S	9	1106.51464983	
	300.11901176	3	P	8	1019.48262142	
+0.2588469	401.166690235	4	T	7	922.429857568	+0.2151009
+0.0178285	530.209283331	5	E	6	821.382179094	-0.020851
	617.241311741	6	S	5	692.339585997	-0.0041368
-0.0146455	748.281796347	7	M	4	605.307557587	+0.1712632
	876.340373858	8	Q	3	474.267072981	+0.0796677
-0.1037243	1004.39895137	9	Q	2	346.20849547	-0.0308832
+0.0544134	1075.436065158	10	A	1	218.149917958	+0.0442349
		11	K	0	147.112804171	

Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F05
Scannumber: 12209
Protein: BSU33130; liaI; yvqI
Peptide Score: 114.9
Method: ITMS; CID; 3





precursor information

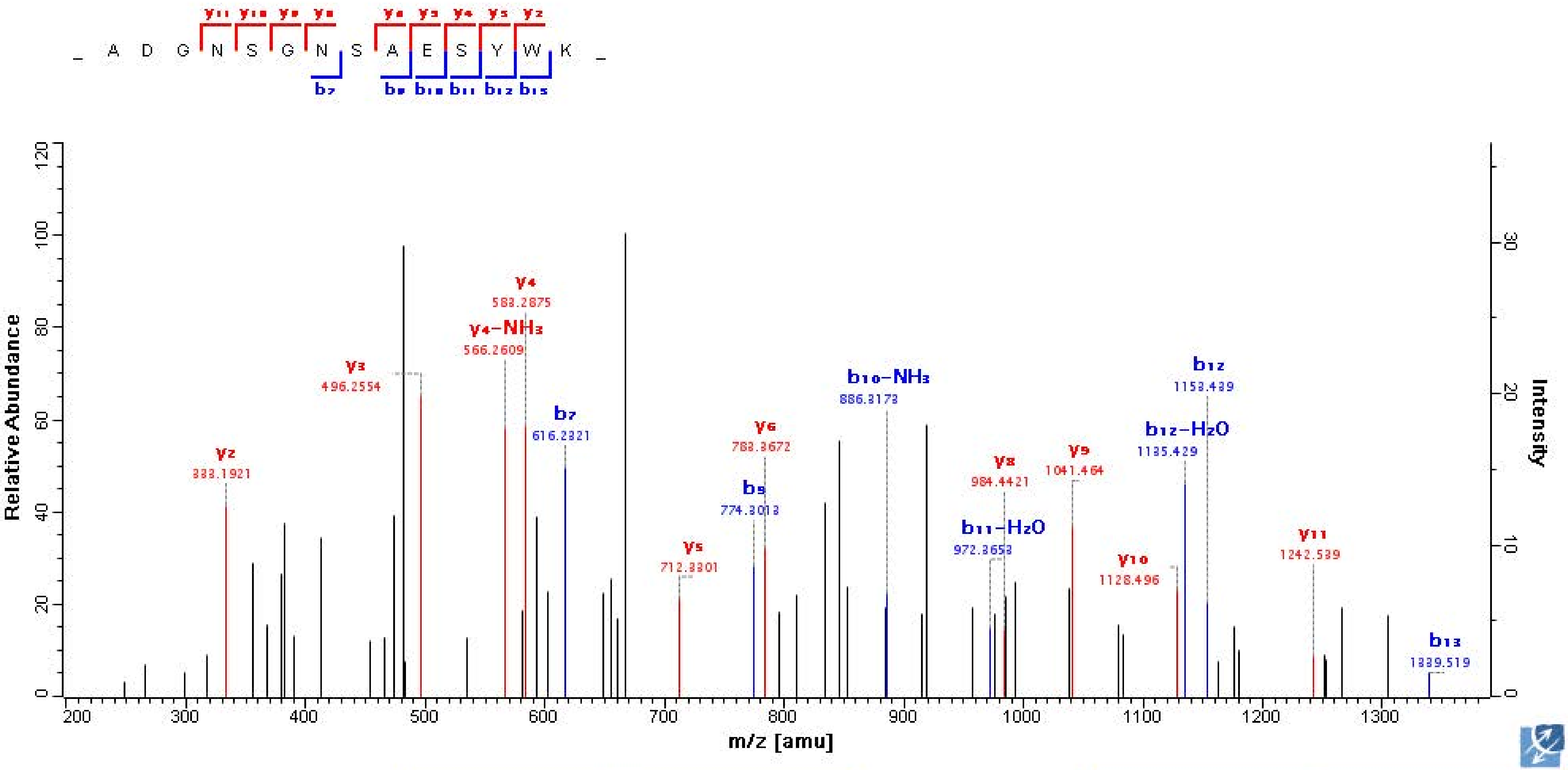
Mass:	3653.55829
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	114.8969
Mass Error [ppm]:	-0.094004
PEP:	2.1877E-27
Precursor Type:	ISO

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	32				
	172.0717		172.0717	2	G	31	3540.523		3540.523	
	259.1037		259.1037	3	S	30	3483.502		3483.502	
	330.1408		330.1408	4	A	29	3396.469		1698.738	+0.139915
	445.1678		445.1678	5	D	28	3325.432		1663.22	+0.334253
	559.2107		559.2107	6	N	27	3210.405		1605.706	-0.016167
	616.2321		616.2321	7	G	26	3096.363		1548.685	+0.204637
	715.3006	+0.264872	715.3006	8	V	25	3039.341		1520.174	+0.038245
	802.3326		802.3326	9	S	24	2940.273		1470.64	+0.289005
+0.044523	445.1859		889.3646	10	S	23	2853.241		1427.124	-0.027867
	1036.433		1036.433	11	F	22	2766.209		1383.608	+0.331409
	1151.46		1151.46	12	D	21	2619.14		1310.074	+0.270035
	1248.513		1248.513	13	P	20	2504.113		1252.56	+0.298155
	1377.555	+0.062469	1377.555	14	E	19	2407.06		2407.06	
	1474.608		1474.608	15	P	18	2278.018		1139.513	+0.182992
	1545.645		1545.645	16	A	17	2180.965		2180.965	
	1632.677		1632.677	17	S	16	2109.928		1055.468	-0.032079
	1703.714		1703.714	18	A	15	2022.896		1011.952	+0.045214
	1774.751		1774.751	19	A	14	1951.859	+0.08123	1951.859	
	1937.815		1937.815	20	Y	13	1880.822	+0.314389	940.9145	+0.181449
	2065.873		2065.873	21	Q	12	1717.758	+0.352083	1717.758	
	2152.905		2152.905	22	S	11	1589.7	-0.164535	1589.7	
	2289.964		2289.964	23	H	10	1502.668		1502.668	
	2437.033		2437.033	24	F	9	1365.609	+0.08705	1365.609	
+0.317115	1276.533		2552.06	25	D	8	1218.54		1218.54	
	2667.087		2667.087	26	D	7	1103.514		1103.514	
	2796.129		2796.129	27	E	6	988.4866	-0.087525	988.4866	
	2982.209		2982.209	28	W	5	859.444	-0.005259	859.444	
	3111.251		3111.251	29	E	4	673.3647	+0.013507	673.3647	
	3240.294		3240.294	30	E	3	544.3221	-0.007255	544.3221	
	3387.362		3387.362	31	F	2	415.2795		415.2795	
+0.077105	1750.727		3500.446	32	I	1	268.2111		268.2111	
				33	K	0	155.127		155.127	

general information

Annotation:	25 of 33
AminoAcids Coverag	76 %
Intensity Coverage:	68 %
Protein Localisation:	92 ... 124

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F06
Scannumber:	5658
Protein:	BSU11900; yjcL
Peptide Score:	87.5
Method:	ITMS; CID; 3



precursor information

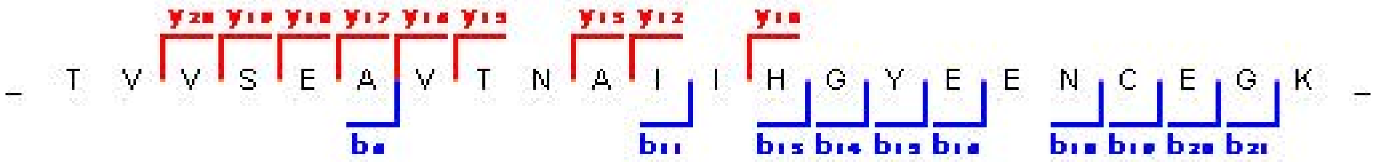
Mass:	1484.61705
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.4985
Mass Error [ppm]:	0.16536
PEP:	0.013591
Precursor Type:	ISO

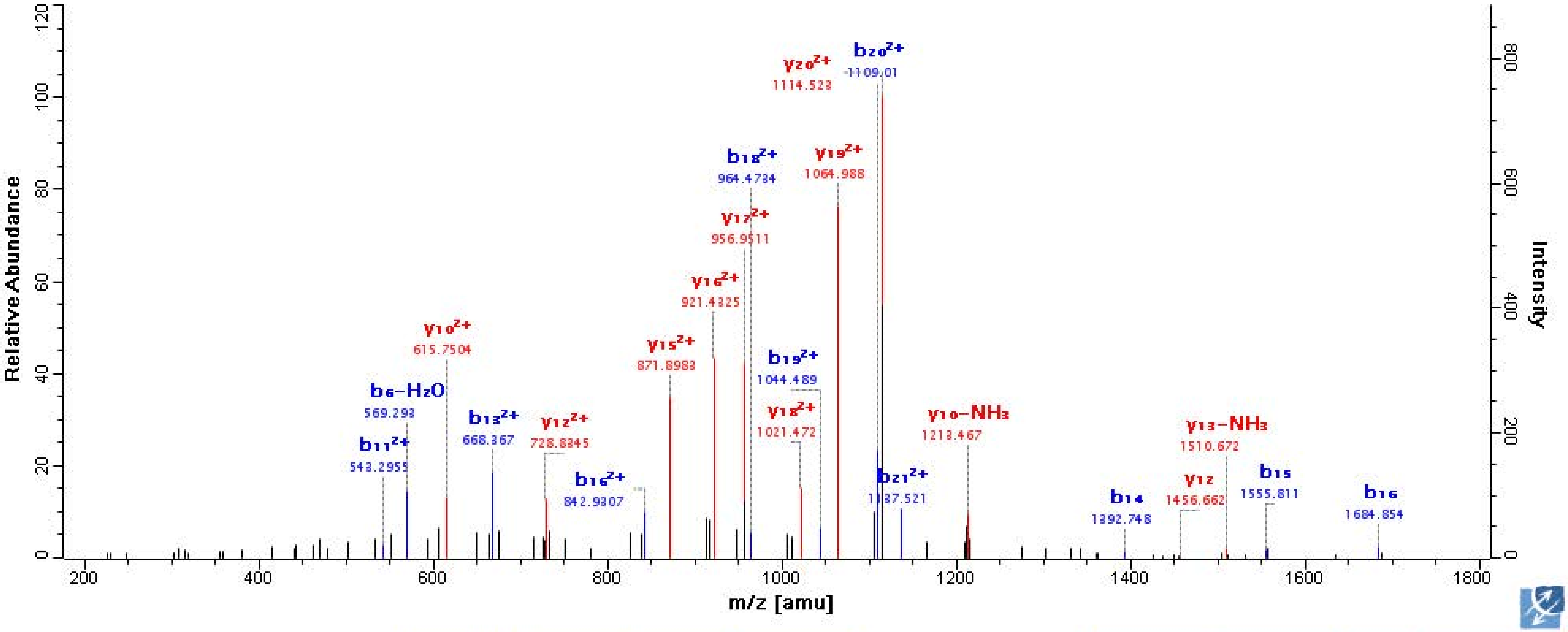
general information

Annotation:	9 of 14
AminoAcids Coverag	64%
Intensity Coverage:	33%
Protein Localisation:	196 ... 209

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	72.044390254	1	A	13		
	187.071333286	2	D	12	1414.58696315	
	244.09279701	3	G	11	1299.560020118	
	358.135724457	4	N	10	1242.538556394	+0.302386
	445.167752867	5	S	9	1128.495628947	-0.1966788
	502.189216591	6	G	8	1041.463600537	+0.0984112
+0.0291475	616.232144038	7	N	7	984.442136813	-0.0210553
	703.264172448	8	S	6	870.399209366	
+0.0524125	774.301286236	9	A	5	783.367180956	+0.226447
	903.343879332	10	E	4	712.330067168	+0.2018542
	990.375907742	11	S	3	583.28747407 2	-0.0036606
+0.1258272	1153.43923628	12	Y	2	496.255445662	-0.0845472
+0.0614068	1339.518549234	13	W	1	333.192117124	+0.0892549
		14	K	0	147.112804171	

Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F07
Scannumber:	10935
Protein:	BSU23460; spoIIAB
Peptide Score:	70.34
Method:	ITMS; CID; 3





precursor information

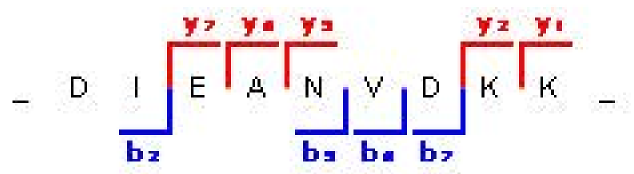
Mass:	2427.14526
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	70.33514
Mass Error [ppm]:	-0.61358
PEP:	0.0069702
Precursor Type:	ISO

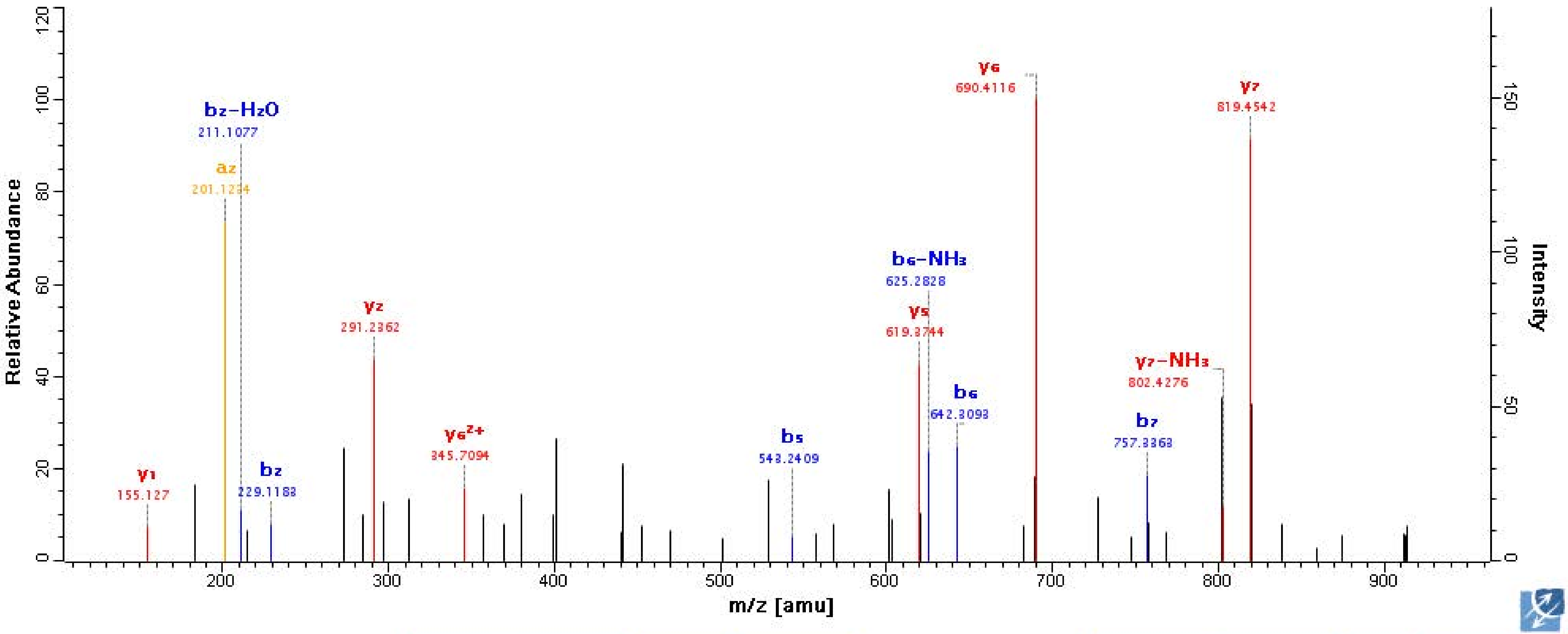
general information

Annotation:	16 of 22
AminoAcids Coverag	73 %
Intensity Coverage:	63 %
Protein Localisation:	42 ... 63

b^{2+} ion		b ion					y ion		y^{2+} 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		300.1918	3	V	19	2228.038		1114.523	+0.013282
	387.2238		387.2238	4	S	18	2128.97		1064.988	+0.193729
	516.2664		516.2664	5	E	17	2041.937		1021.472	+0.323757
	587.3035		587.3035	6	A	16	1912.895		956.9511	+0.018699
	686.3719		686.3719	7	V	15	1841.858		921.4325	+0.278345
	787.4196		787.4196	8	T	14	1742.789		871.8983	+0.109304
	901.4625		901.4625	9	N	13	1641.742		1641.742	
	972.4997		972.4997	10	A	12	1527.699		1527.699	
-0.246851	543.2955		1085.584	11	I	11	1456.662	+0.206144	728.8345	+0.177559
	1198.668		1198.668	12	I	10	1343.578		1343.578	
+0.170492	668.367		1335.727	13	H	9	1230.494		615.7504	-0.047581
	1392.748	+0.029555	1392.748	14	G	8	1093.435		1093.435	
	1555.811	+0.336588	1555.811	15	Y	7	1036.413		1036.413	
-0.09596	842.9307	-0.009594	1684.854	16	E	6	873.3498		873.3498	
	1813.897		1813.897	17	E	5	744.3072		744.3072	
+0.354139	964.4734		1927.94	18	N	4	615.2646		615.2646	
-0.00048	1044.489		2087.97	19	C	3	501.2217		501.2217	
+0.195631	1109.01		2217.013	20	E	2	341.1911		341.1911	
-0.040565	1137.521		2274.034	21	G	1	212.1485		212.1485	
				22	K	0	155.127		155.127	

Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F12
Scannumber: 3023
Protein: BSU15320; sigE; spoIIGB
Peptide Score: 94.85
Method: ITMS; CID; 3

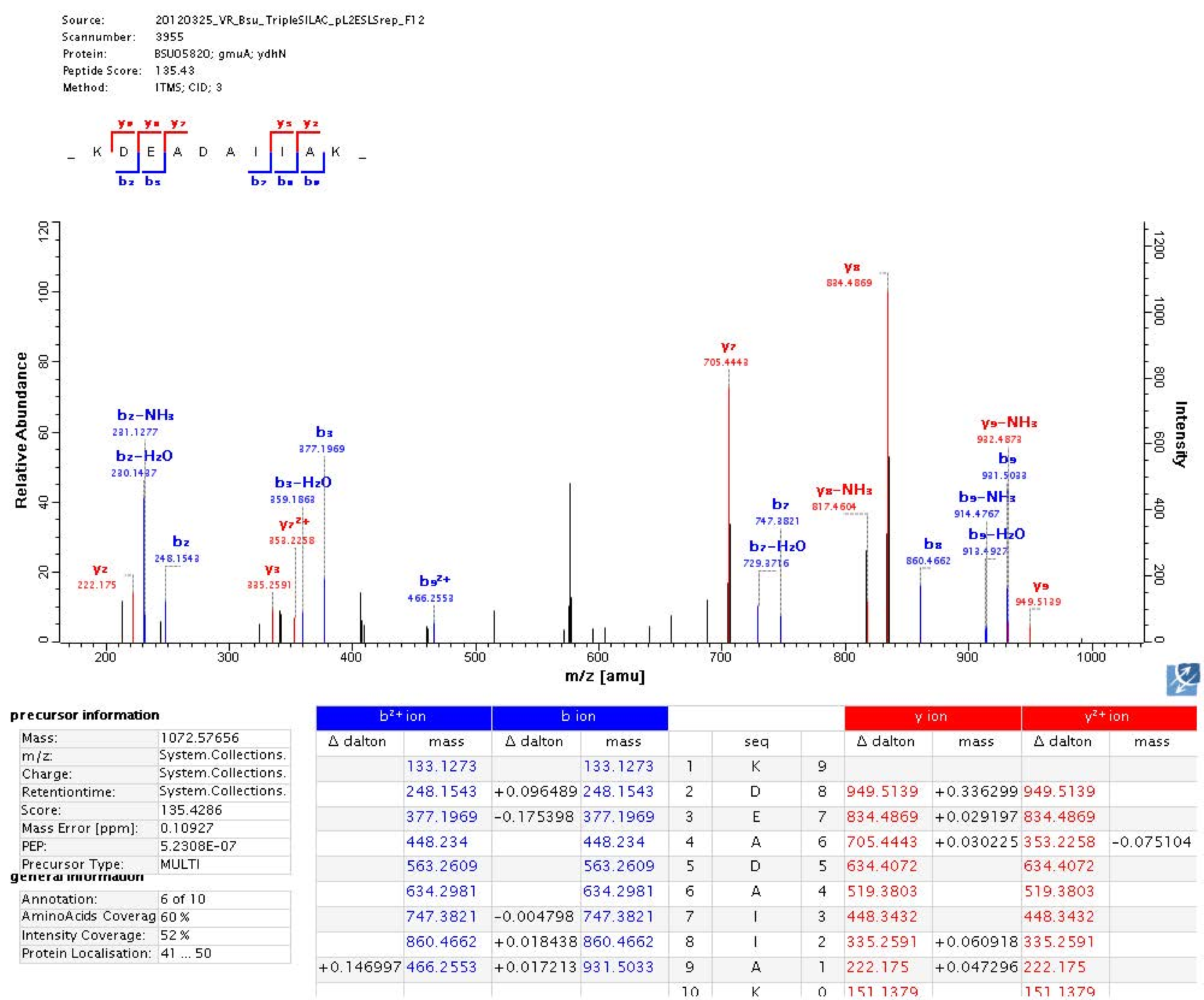




precursor information

Mass:	1030.52929
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.84981
Mass Error [ppm]:	-0.18665
PEP:	0.0018395
Precursor Type:	MULTI
Annotation:	8 of 9
AminoAcids Coverag	89 %
Intensity Coverage:	53 %
Protein Localisation:	167 ... 175

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		116.0342	1	D	8				
+0.04492	201.1234	-0.009076	229.1183	2	I	7	932.5382		932.5382	
	330.166		358.1609	3	E	6	819.4542	-0.00451	819.4542	
	401.2031		429.198	4	A	5	690.4116	+0.058347	345.7094	+0.025627
	515.246	+0.04198	543.2409	5	N	4	619.3744	-0.064574	619.3744	
	614.3144	+0.0003	642.3093	6	V	3	505.3315		505.3315	
	729.3414	+0.052092	757.3363	7	D	2	406.2631		406.2631	
	865.4505		893.4454	8	K	1	291.2362	-0.089986	291.2362	
				9	K	0	155.127	-0.093052	155.127	



Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F12
Scannumber: 3955
Protein: BSU05820; gmuA; ydhN
Peptide Score: 135.43
Method: ITMS; CID; 3

precursor information

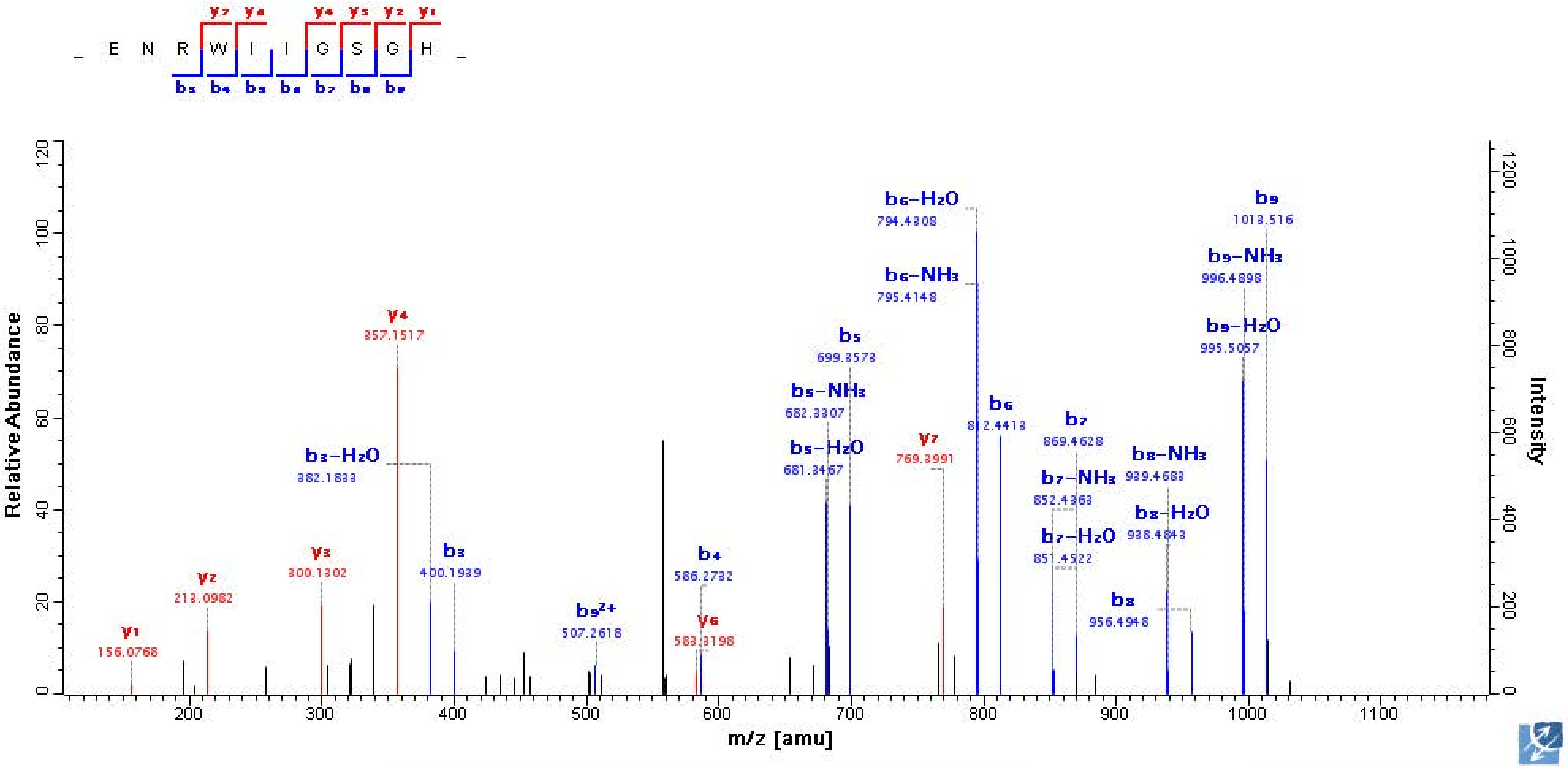
Mass:	1072.57656
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.4286
Mass Error [ppm]:	0.10927
PEP:	5.2308E-07
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	52 %
Protein Localisation:	41 ... 50

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	133.1273		133.1273	1	K	9				
	248.1543	+0.096489	248.1543	2	D	8	949.5139	+0.336299	949.5139	
	377.1969	-0.175398	377.1969	3	E	7	834.4869	+0.029197	834.4869	
	448.234		448.234	4	A	6	705.4443	+0.030225	353.2258	-0.075104
	563.2609		563.2609	5	D	5	634.4072		634.4072	
	634.2981		634.2981	6	A	4	519.3803		519.3803	
	747.3821	-0.004798	747.3821	7	I	3	448.3432		448.3432	
	860.4662	+0.018438	860.4662	8	I	2	335.2591	+0.060918	335.2591	
+0.146997	466.2553	+0.017213	931.5033	9	A	1	222.175	+0.047296	222.175	
				10	K	0	151.1379		151.1379	

Source: 20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F13
Scannumber: 7813
Protein: BSU40180; yydF
Peptide Score: 245.99
Method: ITMS; CID; 3



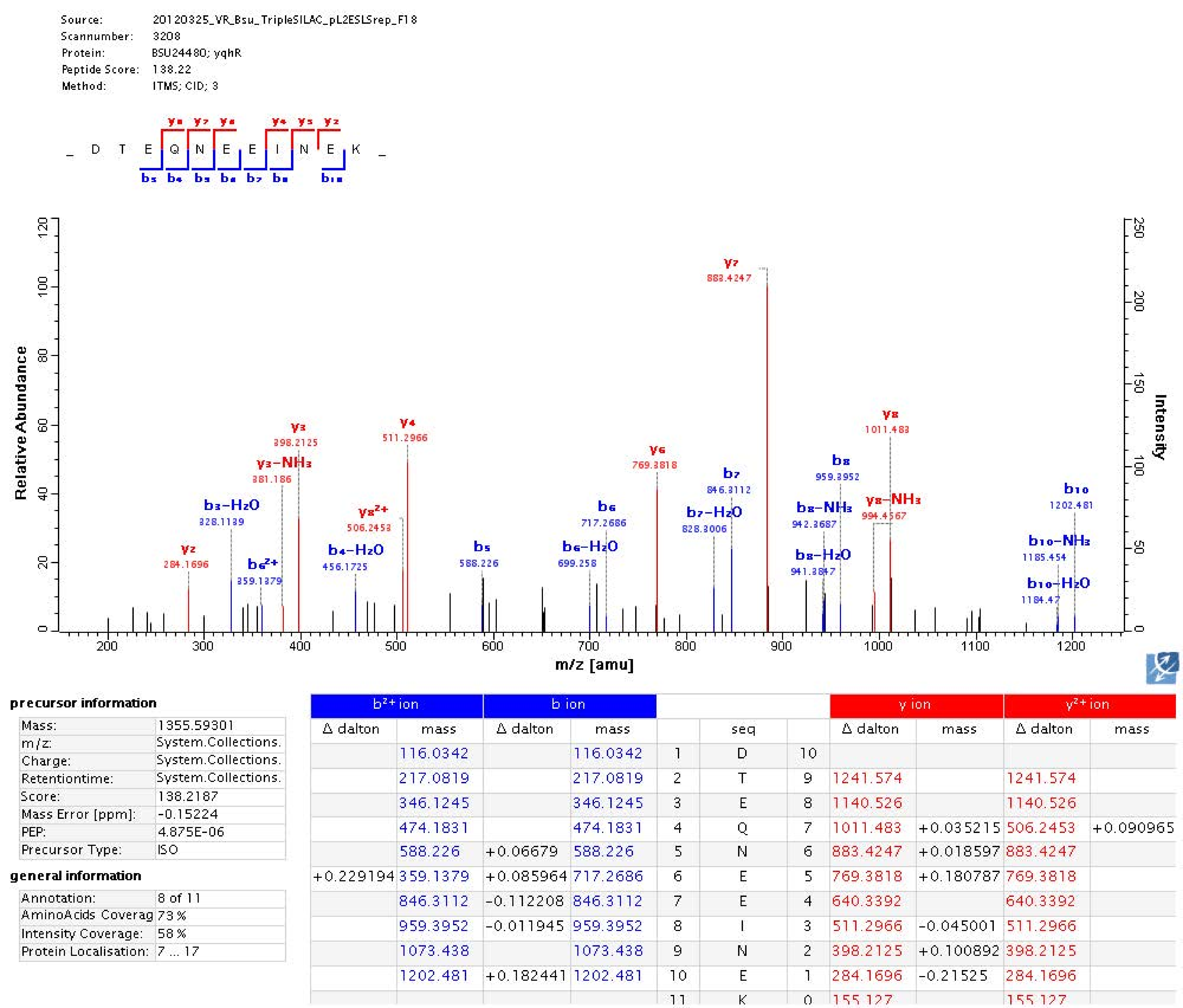
precursor information

Mass:	1167.57812
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	245.9939
Mass Error [ppm]:	-0.33308
PEP:	5.5092E-230
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	75 %
Protein Localisation:	40 ... 49

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	9		
	244.09279701		244.09279701	2	N	8	1039.5431883	
	400.19390804	+0.0132453	400.19390804	3	R	7	925.50026081	
	586.27322099	+0.0943327	586.27322099	4	W	6	769.39914979	+0.0739337
	699.35728497	+0.0045925	699.35728497	5	I	5	583.31983683	+0.077441
	812.44134895	+0.0095177	812.44134895	6	I	4	470.23577285	
	869.46281268	-0.1567214	869.46281268	7	G	3	357.15170887	+0.0371949
	956.49484109	+0.0635696	956.49484109	8	S	2	300.13024515	+0.0213357
-0.3182482	507.26179064	-0.0067833	1013.5163048	9	G	1	213.09821674	-0.0016133
				10	H	0	156.07675302	-0.1472944



Source:	20120325_VR_Bsu_TripleSILAC_pL2ESLSrep_F18
Scannumber:	3208
Protein:	BSU24480; yqhR
Peptide Score:	138.22
Method:	ITMS; CID; 3

precursor information

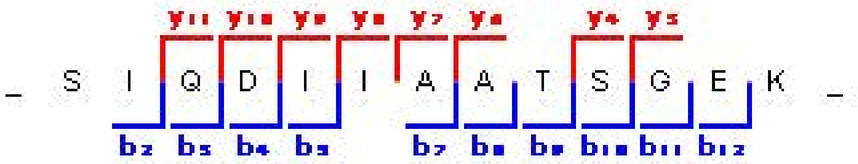
Mass:	1355.59301
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.2187
Mass Error [ppm]:	-0.15224
PEP:	4.875E-06
Precursor Type:	ISO

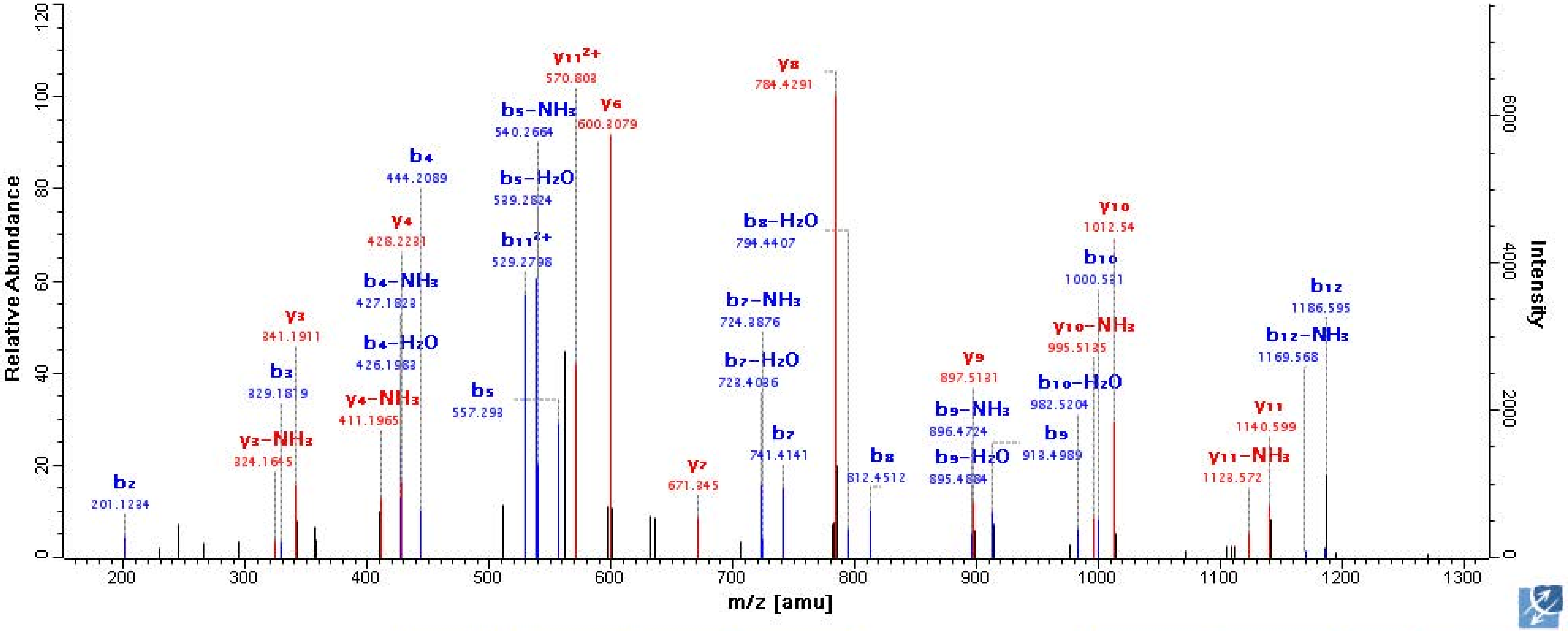
general information

Annotation:	8 of 11
AminoAcids Coverag	73 %
Intensity Coverage:	58 %
Protein Localisation:	7 ... 17

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	10				
	217.0819		217.0819	2	T	9	1241.574		1241.574	
	346.1245		346.1245	3	E	8	1140.526		1140.526	
	474.1831		474.1831	4	Q	7	1011.483	+0.035215	506.2453	+0.090965
	588.226	+0.06679	588.226	5	N	6	883.4247	+0.018597	883.4247	
+0.229194	359.1379	+0.085964	717.2686	6	E	5	769.3818	+0.180787	769.3818	
	846.3112	-0.112208	846.3112	7	E	4	640.3392		640.3392	
	959.3952	-0.011945	959.3952	8	I	3	511.2966	-0.045001	511.2966	
	1073.438		1073.438	9	N	2	398.2125	+0.100892	398.2125	
	1202.481	+0.182441	1202.481	10	E	1	284.1696	-0.21525	284.1696	
				11	K	0	155.127		155.127	

Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F02
Scannumber: 19971
Protein: BSU09460; yhdG
Peptide Score: 241.15
Method: ITMS; CID; 3





precursor information

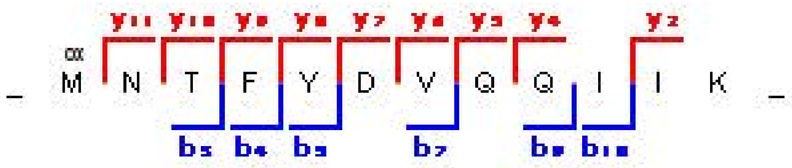
Mass:	1339.70763
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	241.1508
Mass Error [ppm]:	0.12643
PEP:	1.011E-94
Precursor Type:	ISO

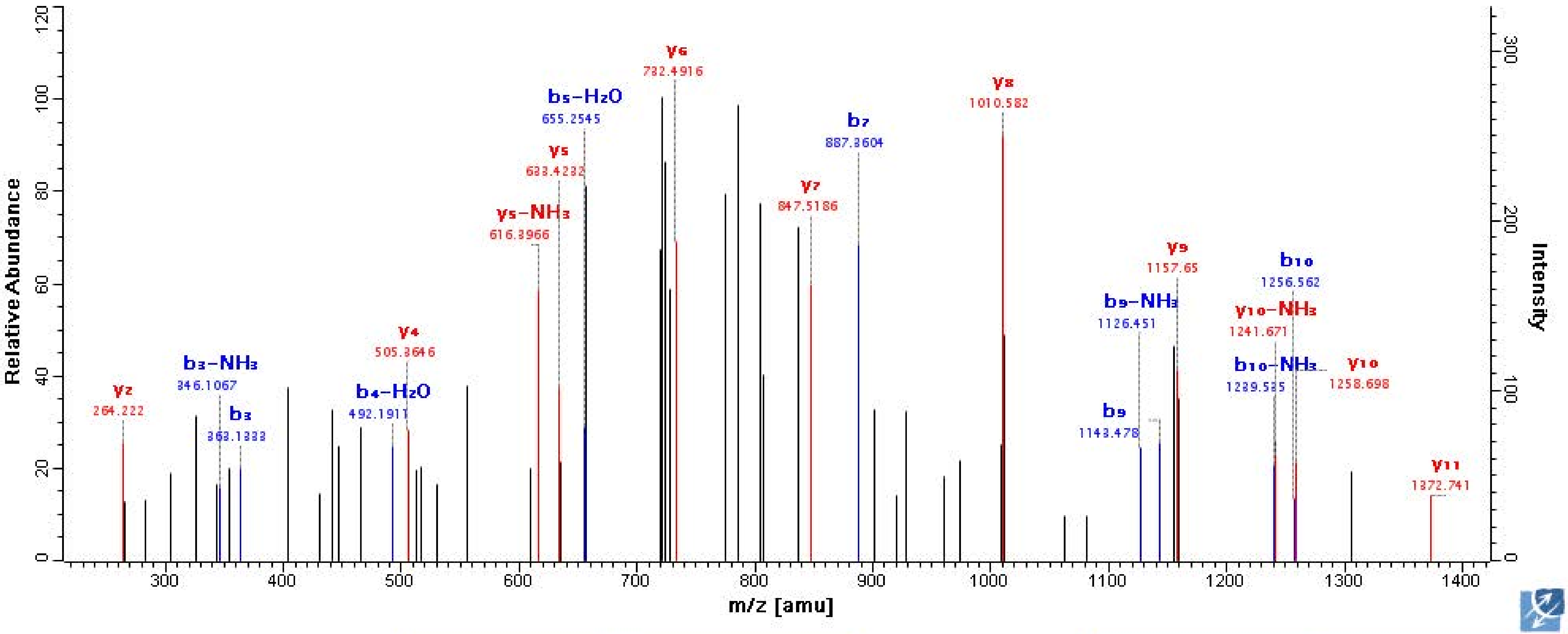
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	74 %
Protein Localisation:	10 ... 22

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		88.0393	1	S	12				
	201.1234	+0.148039	201.1234	2	I	11	1253.683		1253.683	
	329.1819	+0.11145	329.1819	3	Q	10	1140.599	+0.009878	570.803	+0.275104
	444.2089	+0.163913	444.2089	4	D	9	1012.54	-0.018398	1012.54	
	557.293	-0.046188	557.293	5	I	8	897.5131	+0.112061	897.5131	
	670.377		670.377	6	I	7	784.4291	-0.020733	784.4291	
	741.4141	-0.001411	741.4141	7	A	6	671.345	+0.149513	671.345	
	812.4512	+0.094531	812.4512	8	A	5	600.3079	+0.031597	600.3079	
	913.4989	+0.037393	913.4989	9	T	4	529.2708		529.2708	
	1000.531	+0.044427	1000.531	10	S	3	428.2231	+0.000972	428.2231	
+0.048645	529.2798		1057.552	11	G	2	341.1911	+0.134441	341.1911	
	1186.595	-0.094276	1186.595	12	E	1	284.1696		284.1696	
				13	K	0	155.127		155.127	

Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F04
Scannumber: 24270
Protein: BSU24860; yqgQ
Peptide Score: 93.84
Method: ITMS; CID; 3





precursor information

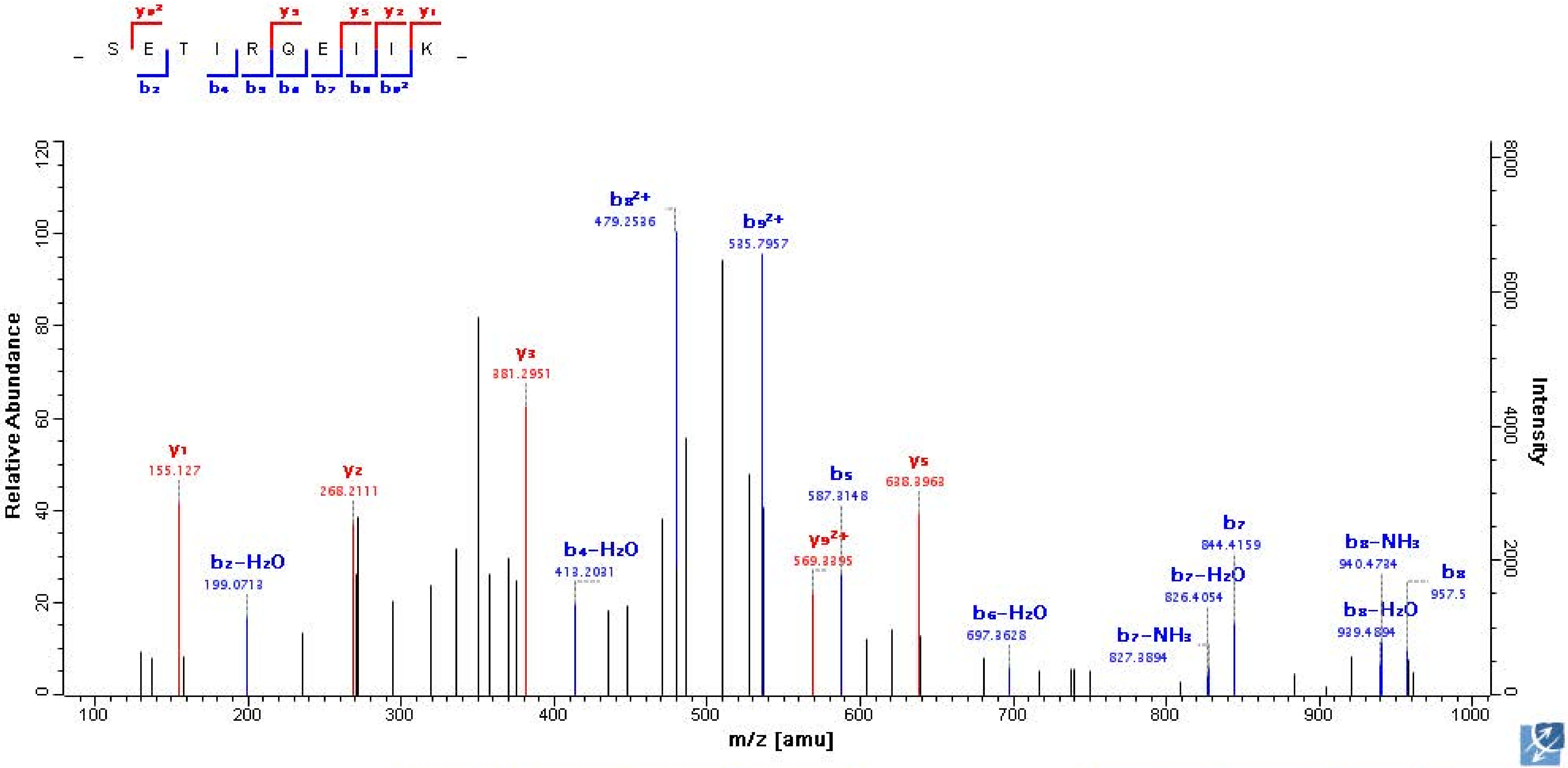
Mass:	1518.77175
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.83924
Mass Error [ppm]:	1.7971
PEP:	0.00077256
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	32 %
Protein Localisation:	1 ... 12

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.042675695	1	M	11		
	262.085603142	2	N	10	1372.740899462	+0.2121035
-0.0248832	363.133281616	3	T	9	1258.697972015	+0.3274186
	510.201695532	4	F	8	1157.65029354	+0.1531733
	673.265024071	5	Y	7	1010.581879624	+0.1303396
	788.291967103	6	D	6	847.518551086	+0.1538732
+0.2532054	887.360381019	7	V	5	732.491608054	+0.1481625
	1015.41895853	8	Q	4	633.423194138	+0.4007805
+0.1709015	1143.477536042	9	Q	3	505.364616626	+0.0283887
+0.3601529	1256.561600022	10	I	2	377.306039115	
	1369.645664002	11	I	1	264.221975135	+0.0940039
		12	K	0	151.137911154	

Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F05
Scannumber:	11321
Protein:	BSU14730; ylaC
Peptide Score:	101.11
Method:	ITMS; CID; 3



precursor information

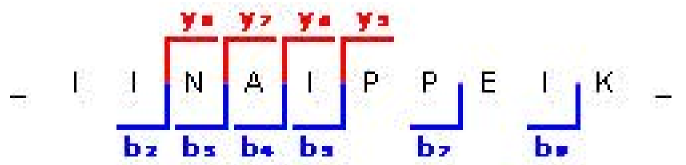
Mass:	1215.68237
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.1051
Mass Error [ppm]:	0.059098
PEP:	0.0021765
Precursor Type:	MULTI

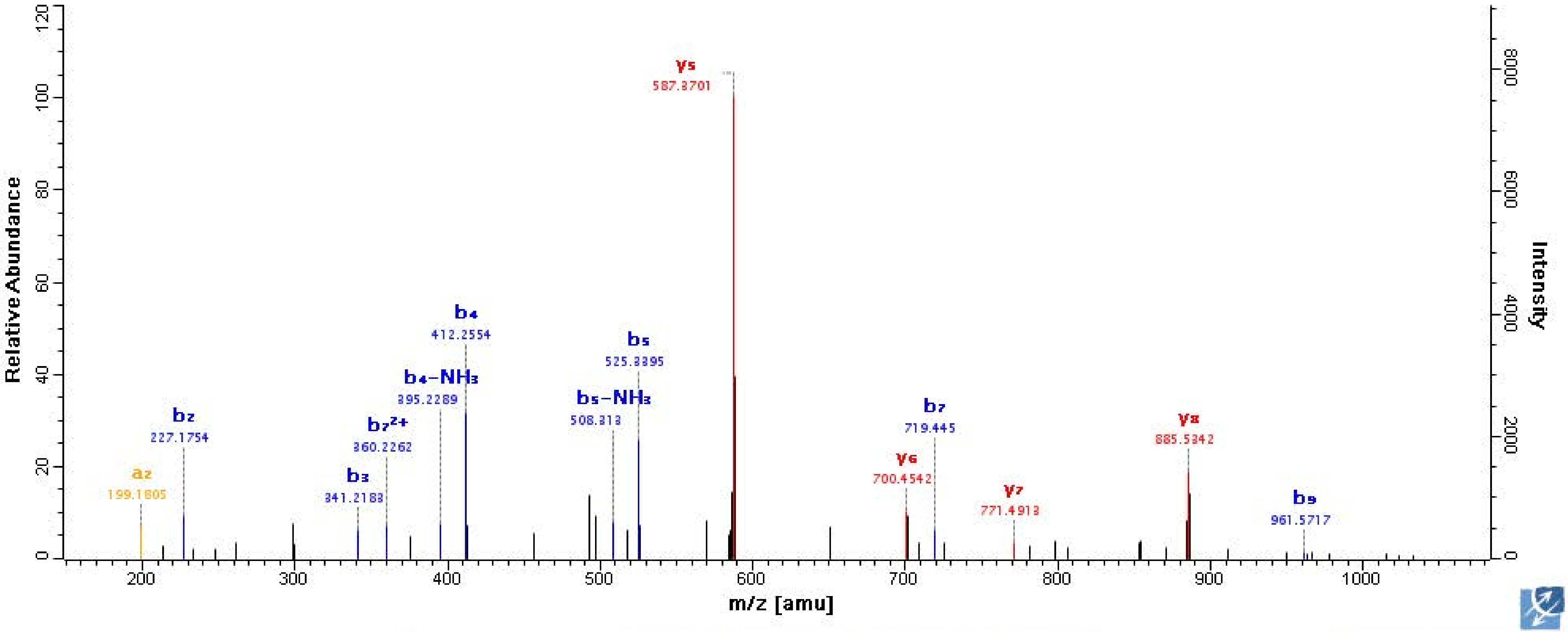
general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	40 %
Protein Localisation:	107 ... 116

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	9				
	217.0819		217.0819	2	E	8	1137.672		569.3395	+0.027919
	318.1296		318.1296	3	T	7	1008.629		1008.629	
	431.2136		431.2136	4	I	6	907.5815		907.5815	
	587.3148	+0.051032	587.3148	5	R	5	794.4974		794.4974	
	715.3733		715.3733	6	Q	4	638.3963	+0.029663	638.3963	
	844.4159	+0.295992	844.4159	7	E	3	510.3377		510.3377	
+0.074066	479.2536	+0.203444	957.5	8	I	2	381.2951	+0.017491	381.2951	
+0.010123	535.7957		1070.584	9	I	1	268.2111	+0.035485	268.2111	
				10	K	0	155.127	+0.021129	155.127	

Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F05
Scannumber:	18753
Protein:	BSU06370; pbuG; yebB
Peptide Score:	107.15
Method:	ITMS; CID; 3





precursor information

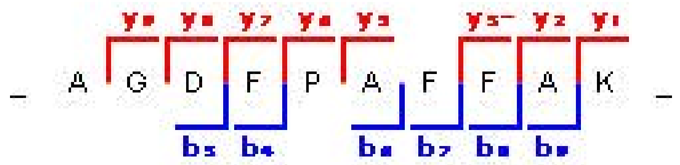
Mass:	1106.6699
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.154
Mass Error [ppm]:	-0.041328
PEP:	0.0019493
Precursor Type:	MULTI

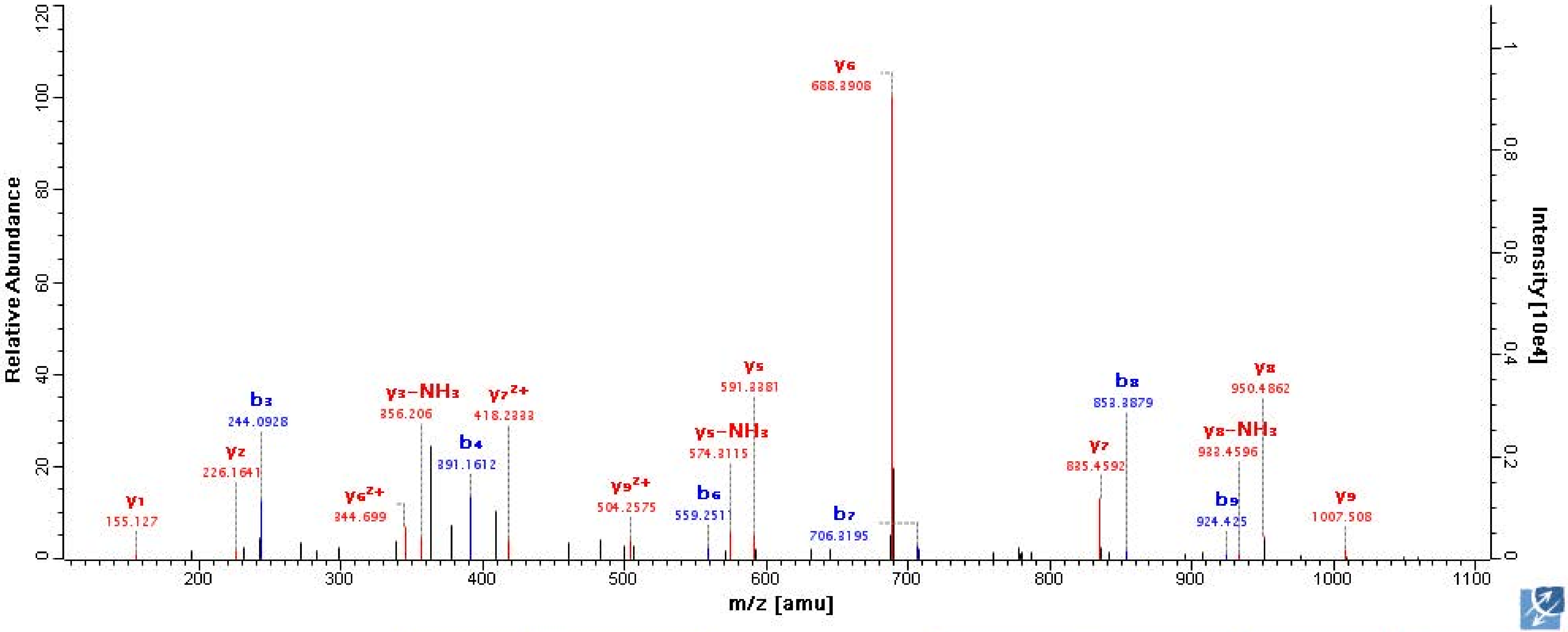
general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	52 %
Protein Localisation:	131 ... 140

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	9		
+0.039298	199.1805		227.1754	-0.003194	227.1754	2	I	8	998.6183	
	313.2234		341.2183	+0.205801	341.2183	3	N	7	885.5342	-0.020773
	384.2605		412.2554	+0.050157	412.2554	4	A	6	771.4913	+0.168516
	497.3446		525.3395	+0.105131	525.3395	5	I	5	700.4542	+0.089846
	594.3974		622.3923		622.3923	6	P	4	587.3701	+0.057577
	691.4501	+0.154214	360.2262	+0.155365	719.445	7	P	3	490.3173	
	820.4927		848.4876		848.4876	8	E	2	393.2646	
	933.5768		961.5717	+0.006247	961.5717	9	I	1	264.222	
						10	K	0	151.1379	

Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F05
Scannumber: 22532
Protein: BSU33330; yvsH
Peptide Score: 130.66
Method: ITMS; CID; 3





precursor information

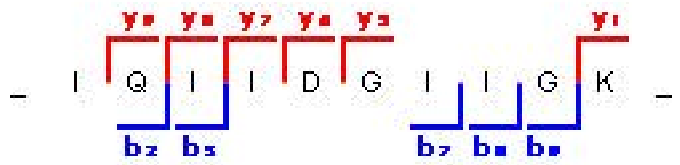
Mass:	1069.52395
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	130.6557
Mass Error [ppm]:	0.61795
PEP:	0.00010818
Precursor Type:	MULTI

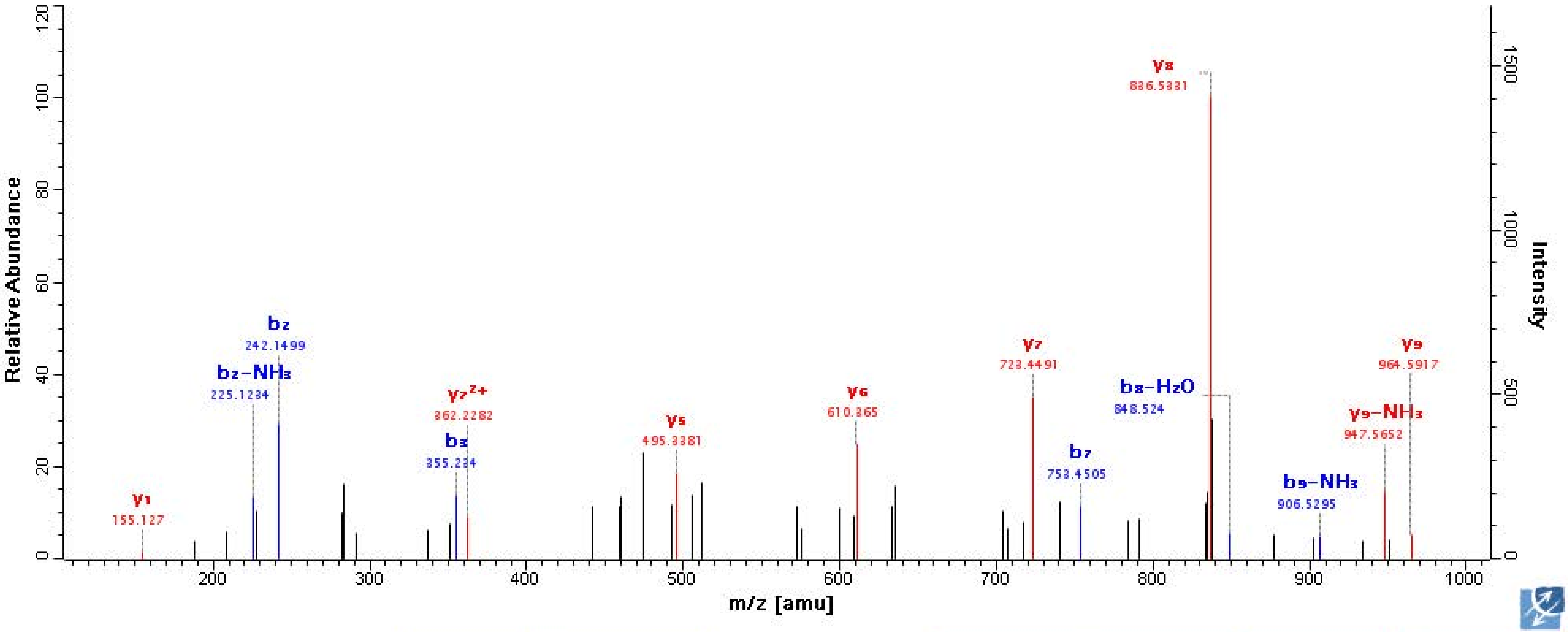
general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	59 %
Protein Localisation:	332 ... 341

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	9				
	129.06585398	2	G	8	1007.5076429	+0.1066149	504.25745969	+0.2659778
-0.0709769	244.09279701	3	D	7	950.48617919	+0.0519678	950.48617919	
-0.0275745	391.16121093	4	F	6	835.45923616	-0.0409012	418.23325631	-0.050334
	488.21397478	5	P	5	688.39082224	-0.0244892	344.69904936	+0.4203049
-0.4301047	559.25108857	6	A	4	591.33805839	+0.0699006	591.33805839	
+0.0445112	706.31950248	7	F	3	520.3009446		520.3009446	
+0.2189562	853.3879164	8	F	2	373.23253069		373.23253069	
+0.2705265	924.42503019	9	A	1	226.16411677	+0.0121375	226.16411677	
		10	K	0	155.12700298	+0.1223104	155.12700298	

Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F05
Scannumber: 24507
Protein: albE; BSU37410; ywhO
Peptide Score: 101.11
Method: ITMS; CID; 3





precursor information

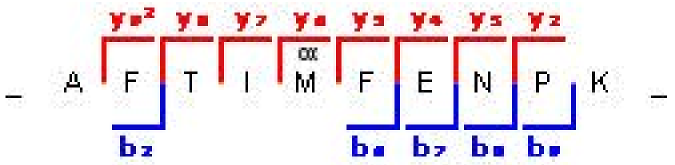
Mass:	1076.66869
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.1051
Mass Error [ppm]:	0.17705
PEP:	0.0052591
Precursor Type:	ISO

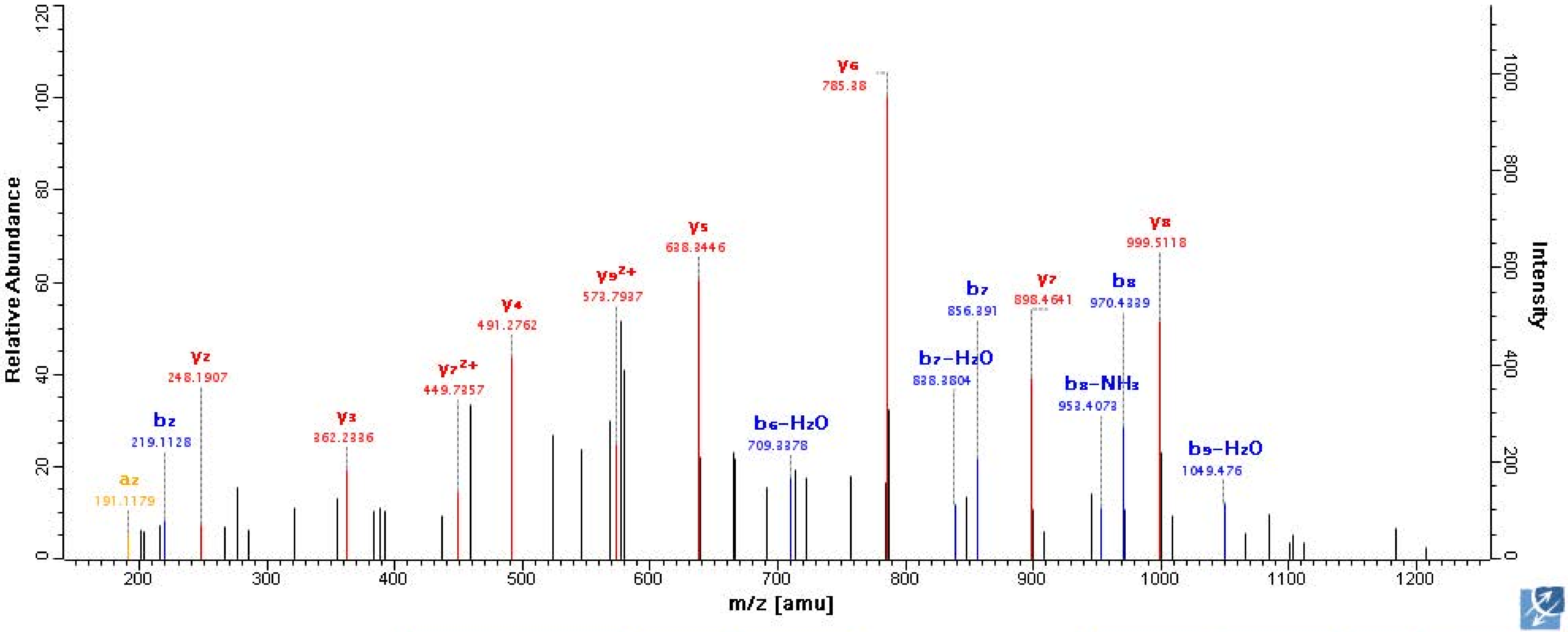
general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	44 %
Protein Localisation:	247 ... 256

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	9				
+0.0286709	242.14991796	2	Q	8	964.5917069	+0.0933517	964.5917069	
+0.1143457	355.23398194	3	I	7	836.53312938	+0.0407232	836.53312938	
	468.31804592	4	I	6	723.4490654	+0.173249	362.22817094	+0.3313383
	583.34498895	5	D	5	610.36500142	+0.1804087	610.36500142	
	640.36645267	6	G	4	495.33805839	+0.2246247	495.33805839	
+0.1153403	753.45051666	7	I	3	438.31659467		438.31659467	
	866.53458064	8	I	2	325.23253069		325.23253069	
	923.55604436	9	G	1	212.14846671		212.14846671	
		10	K	0	155.12700298	+0.0660512	155.12700298	

Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F06
Scannumber:	19264
Protein:	BSU27760; csbX
Peptide Score:	102.07
Method:	ITMS; CID; 3





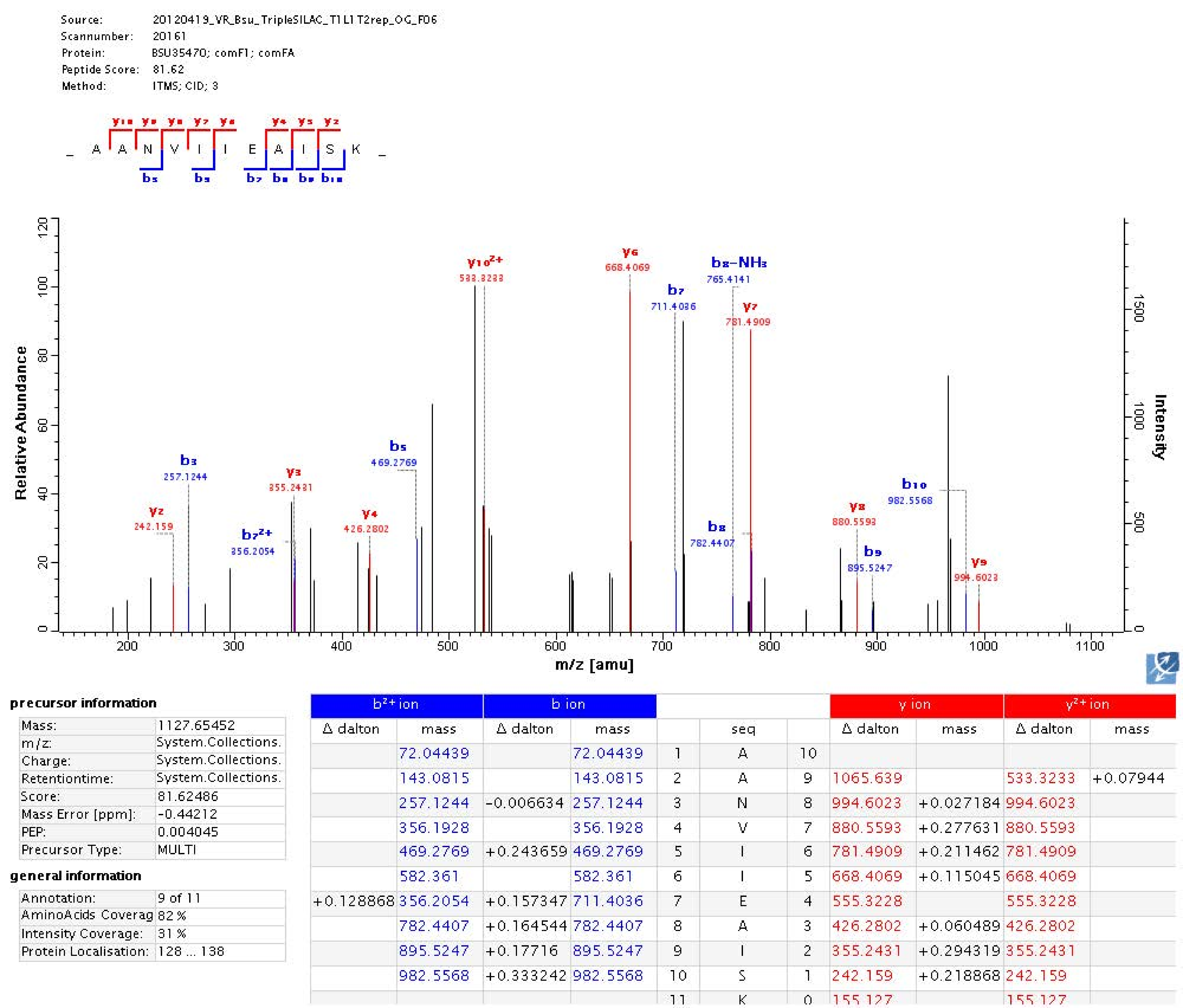
precursor information

Mass:	1216.6113
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.0672
Mass Error [ppm]:	1.0671
PEP:	0.0030018
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	42 %
Protein Localisation:	219 ... 228

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.04948		72.04439	1	A	9				
+0.06897	191.1179	-0.067562	219.1128	2	F	8	1146.58		573.7937	-0.21645
	292.1656		320.1605	3	T	7	999.5118	+0.075773	999.5118	
	405.2496		433.2445	4	I	6	898.4641	+0.071206	449.7357	-0.430499
	552.285		580.2799	5	M	5	785.38	-0.012272	785.38	
	699.3534		727.3484	6	F	4	638.3446	-0.008245	638.3446	
	828.396	+0.423439	856.391	7	E	3	491.2762	+0.00658	491.2762	
	942.439	+0.087787	970.4339	8	N	2	362.2336	+0.036844	362.2336	
	1039.492		1067.487	9	P	1	248.1907	+0.015471	248.1907	
				10	K	0	151.1379		151.1379	



Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F06
Scannumber: 20161
Protein: BSU35470; comFI; comFA
Peptide Score: 81.62
Method: ITMS; CID; 3

precursor information

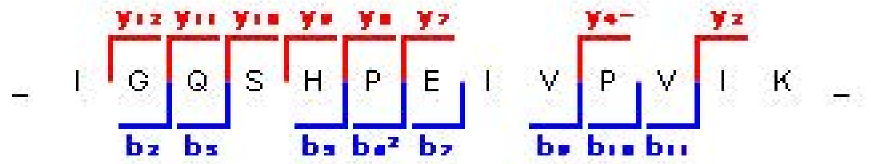
Mass:	1127.65452
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	81.62486
Mass Error [ppm]:	-0.44212
PEP:	0.004045
Precursor Type:	MULTI

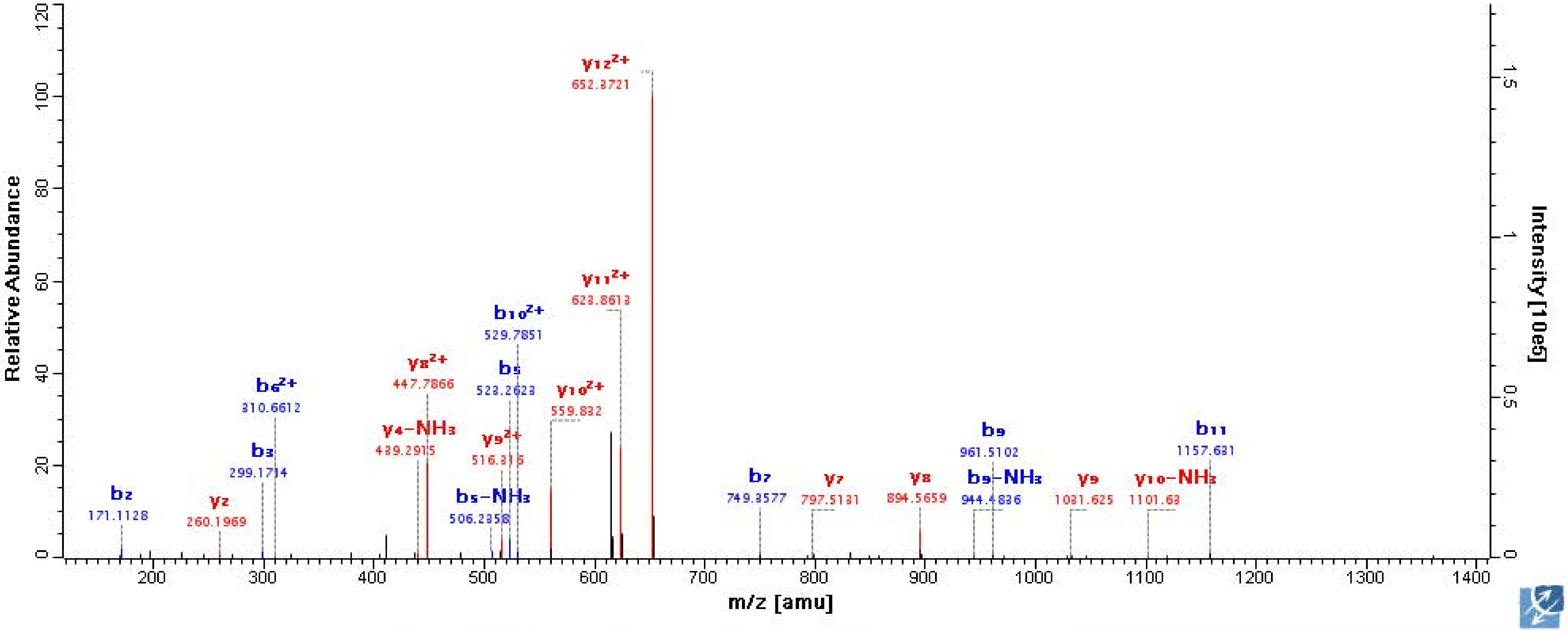
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	31 %
Protein Localisation:	128 ... 138

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	10				
	143.0815		143.0815	2	A	9	1065.639		533.3233	+0.07944
	257.1244	-0.006634	257.1244	3	N	8	994.6023	+0.027184	994.6023	
	356.1928		356.1928	4	V	7	880.5593	+0.277631	880.5593	
	469.2769	+0.243659	469.2769	5	I	6	781.4909	+0.211462	781.4909	
	582.361		582.361	6	I	5	668.4069	+0.115045	668.4069	
+0.128868	356.2054	+0.157347	711.4036	7	E	4	555.3228		555.3228	
	782.4407	+0.164544	782.4407	8	A	3	426.2802	+0.060489	426.2802	
	895.5247	+0.17716	895.5247	9	I	2	355.2431	+0.294319	355.2431	
	982.5568	+0.333242	982.5568	10	S	1	242.159	+0.218868	242.159	
				11	K	0	155.127		155.127	

Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F08
Scannumber:	16393
Protein:	BSU35710; tagG
Peptide Score:	117.09
Method:	ITMS; CID; 3





precursor information

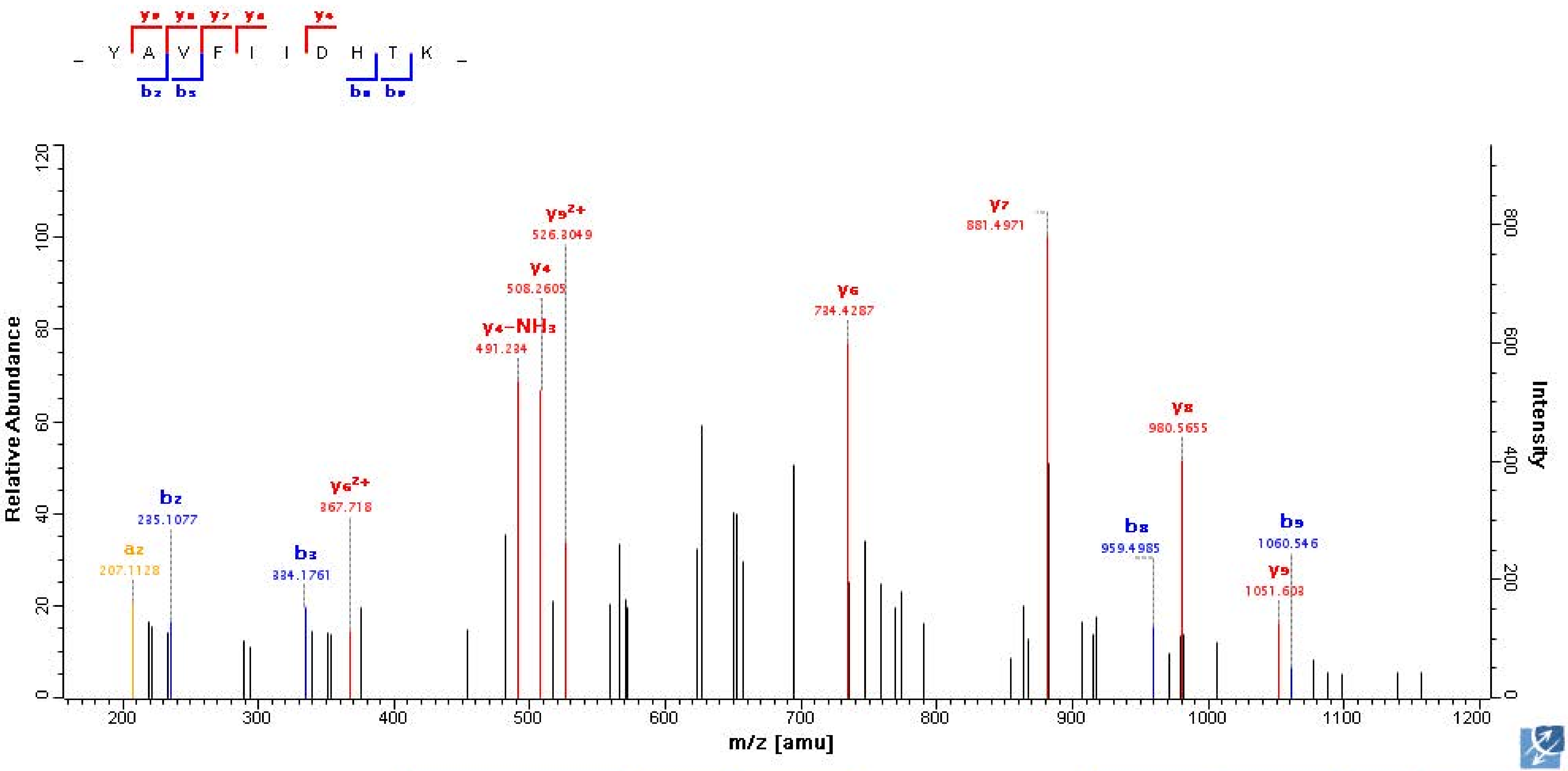
Mass:	1415.81339
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	117.0911
Mass Error [ppm]:	-0.18148
PEP:	0.00034545
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	72 %
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	+0.182682	171.1128	2	G	11	1303.737		652.3721	+0.201539
	299.1714	+0.082952	299.1714	3	Q	10	1246.715		623.8613	+0.154471
	386.2034		386.2034	4	S	9	1118.657		559.832	+0.222822
	523.2623	+0.025947	523.2623	5	H	8	1031.625	+0.342981	516.316	-0.001093
-0.224963	310.6612		620.3151	6	P	7	894.5659	+0.090003	447.7866	+0.220379
	749.3577	+0.385241	749.3577	7	E	6	797.5131	-0.05871	797.5131	
	862.4417		862.4417	8	I	5	668.4705		668.4705	
	961.5102	+0.129003	961.5102	9	V	4	555.3865		555.3865	
+0.475949	529.7851		1058.563	10	P	3	456.318		456.318	
	1157.631	+0.269422	1157.631	11	V	2	359.2653		359.2653	
	1270.715		1270.715	12	I	1	260.1969	+0.067475	260.1969	
				13	K	0	147.1128		147.1128	

Source: 20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F08
Scannumber: 18013
Protein: BSU20010; yojV; yosT
Peptide Score: 99.8
Method: ITMS; CID; 3



precursor information

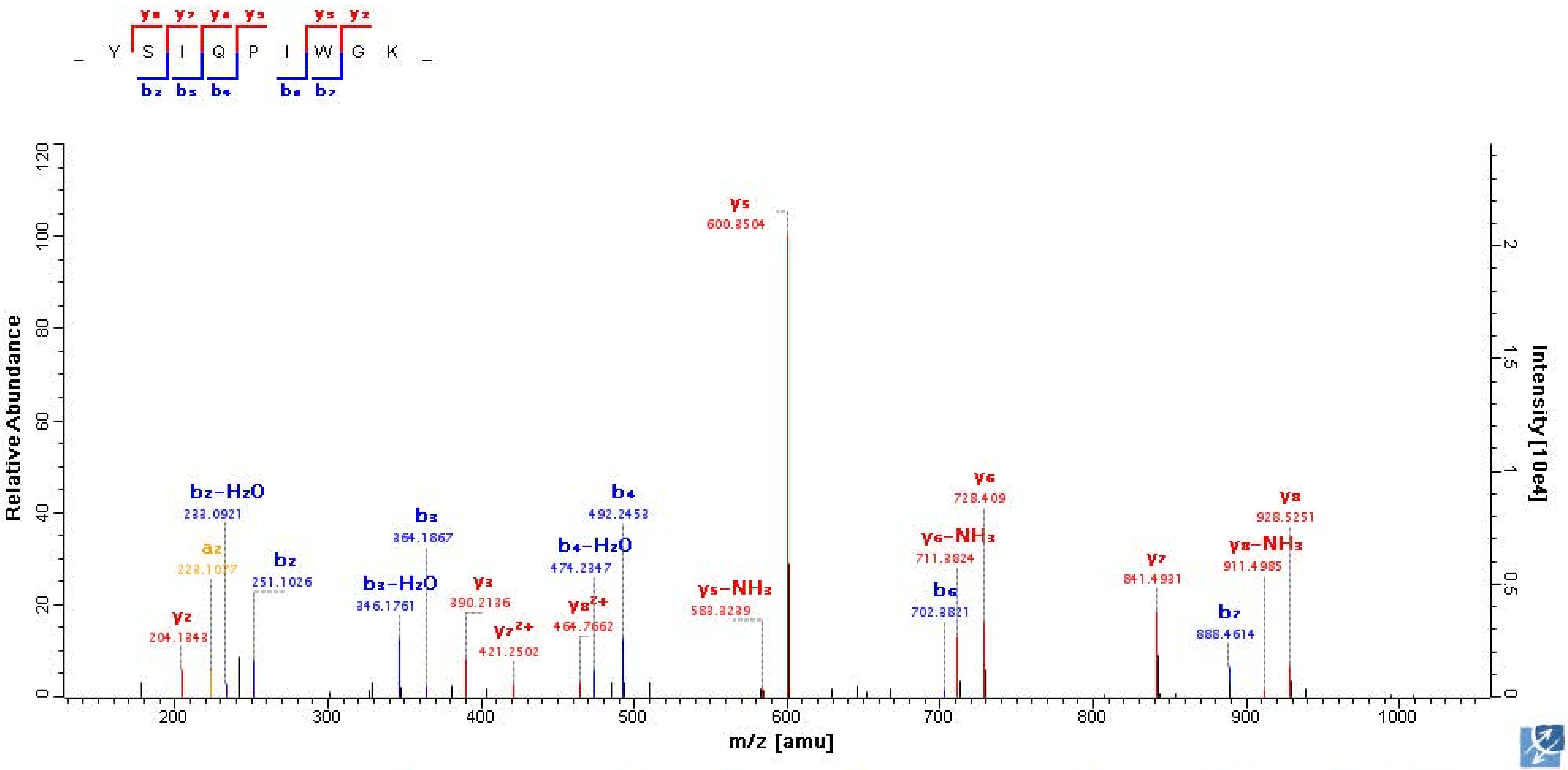
Mass:	1205.64539
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	99.80212
Mass Error [ppm]:	0.76606
PEP:	0.0022185
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	36 %
Protein Localisation:	93 ... 102

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	9				
+0.242604	207.1128	-0.066398	235.1077	2	A	8	1051.603	+0.179743	526.3049	+0.318045
	306.1812	+0.290634	334.1761	3	V	7	980.5655	+0.073851	980.5655	
	453.2496		481.2445	4	F	6	881.4971	+0.058647	881.4971	
	566.3337		594.3286	5	I	5	734.4287	+0.27794	367.718	+0.24727
	679.4178		707.4127	6	I	4	621.3446		621.3446	
	794.4447		822.4396	7	D	3	508.2605	-0.121681	508.2605	
	931.5036	+0.067083	959.4985	8	H	2	393.2336		393.2336	
	1032.551	+0.260555	1060.546	9	T	1	256.1747		256.1747	
				10	K	0	155.127		155.127	

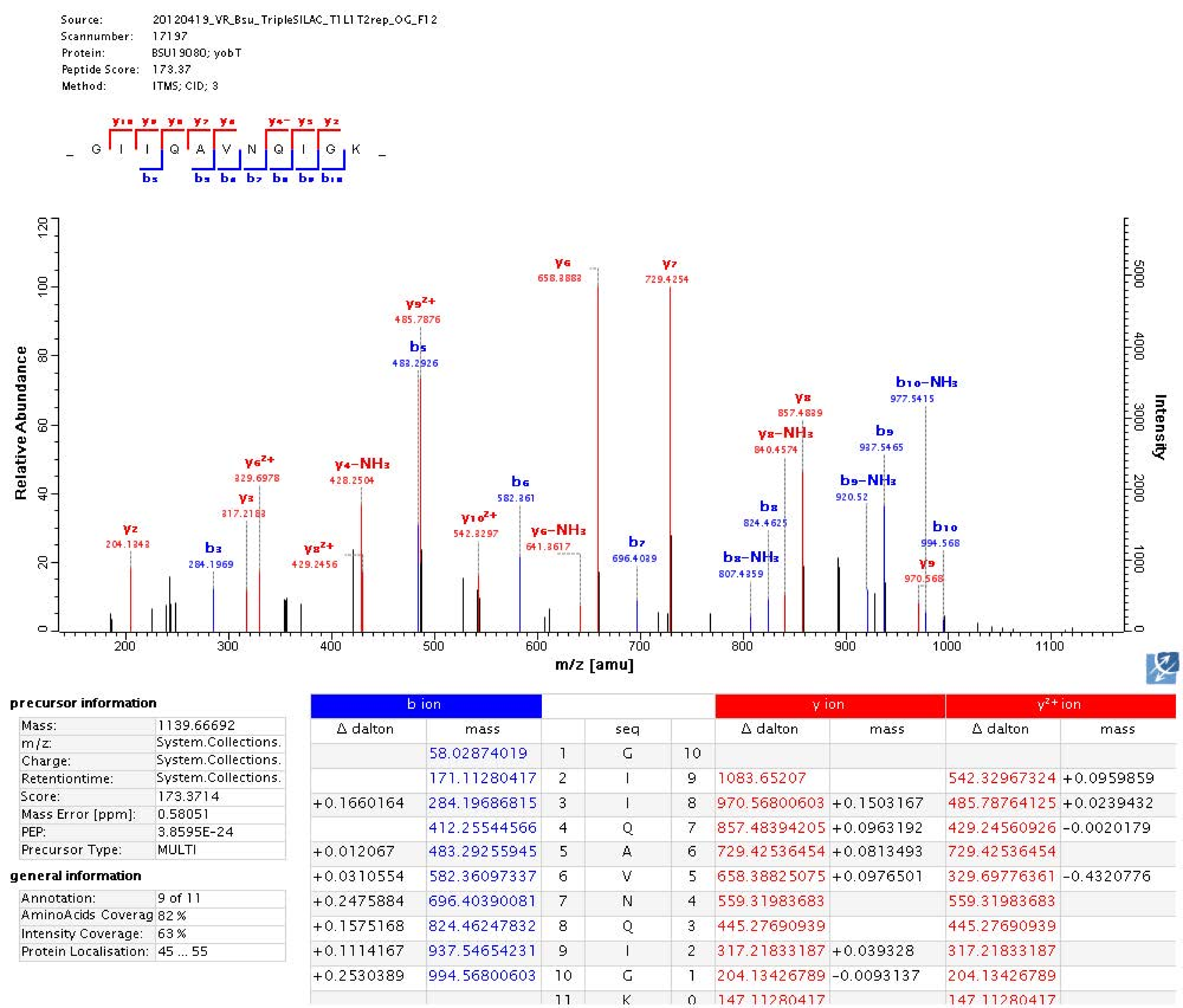
Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F11
Scannumber:	19621
Protein:	BSU22350; dnaD
Peptide Score:	149.82
Method:	ITMS; CID; 3



precursor information

Mass:	1090.58107
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	149.816
Mass Error [ppm]:	-0.054867
PEP:	6.898E-11
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	70 %
Protein Localisation:	97 ... 105

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	136.0757		164.0706	1	Y	8				
+0.13633	223.1077	-0.034854	251.1026	2	S	7	928.5251	+0.029426	464.7662	-0.380496
	336.1918	+0.131937	364.1867	3	I	6	841.4931	+0.009574	421.2502	+0.056538
	464.2504	-0.011632	492.2453	4	Q	5	728.409	+0.013133	728.409	
	561.3031		589.298	5	P	4	600.3504	+0.064875	600.3504	
	674.3872	+0.34391	702.3821	6	I	3	503.2976		503.2976	
	860.4665	+0.151866	888.4614	7	W	2	390.2136	+0.113781	390.2136	
	917.488		945.4829	8	G	1	204.1343	+0.137216	204.1343	
				9	K	0	147.1128		147.1128	



Source:	20120419_VR_Bsu_TripleSILAC_T1L1T2rep_OG_F12
Scannumber:	17197
Protein:	BSU19080; yobT
Peptide Score:	173.37
Method:	ITMS; CID; 3

precursor information

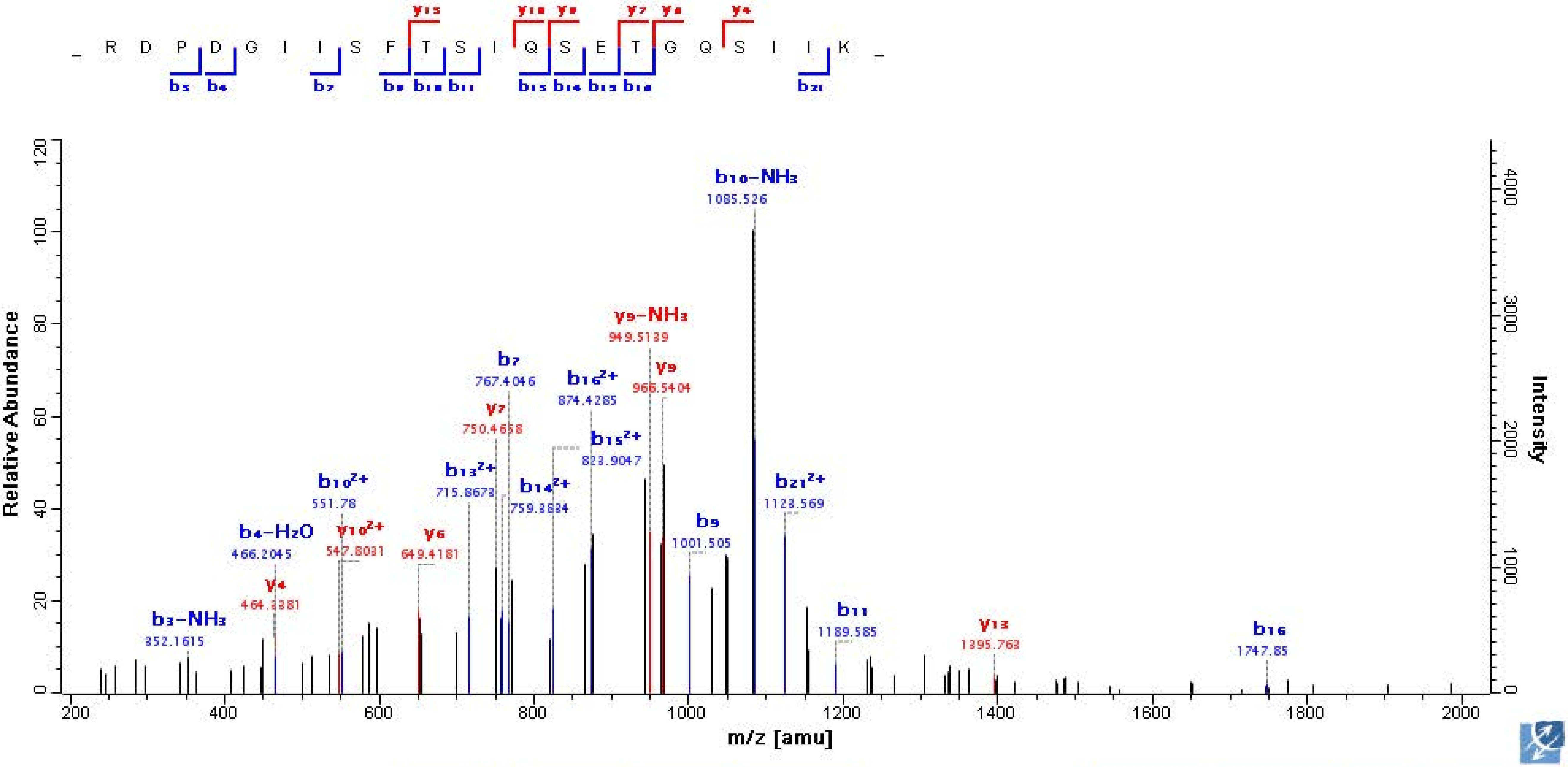
Mass:	1139.66692
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	173.3714
Mass Error [ppm]:	0.58051
PEP:	3.8595E-24
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	63 %
Protein Localisation:	45 ... 55

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	10				
	171.11280417	2	I	9	1083.65207		542.32967324	+0.0959859
+0.1660164	284.19686815	3	I	8	970.56800603	+0.1503167	485.78764125	+0.0239432
	412.25544566	4	Q	7	857.48394205	+0.0963192	429.24560926	-0.0020179
+0.012067	483.29255945	5	A	6	729.42536454	+0.0813493	729.42536454	
+0.0310554	582.36097337	6	V	5	658.38825075	+0.0976501	329.69776361	-0.4320776
+0.2475884	696.40390081	7	N	4	559.31983683		559.31983683	
+0.1575168	824.46247832	8	Q	3	445.27690939		445.27690939	
+0.1114167	937.54654231	9	I	2	317.21833187	+0.039328	317.21833187	
+0.2530389	994.56800603	10	G	1	204.13426789	-0.0093137	204.13426789	
		11	K	0	147.11280417		147.11280417	

Source:	20120420_VR_Bsu_TripleSILAC_L2ESLSrep_OG_F02
Scannumber:	25582
Protein:	BSU31500; yugD; yuxK
Peptide Score:	50.36
Method:	ITMS; CID; 3



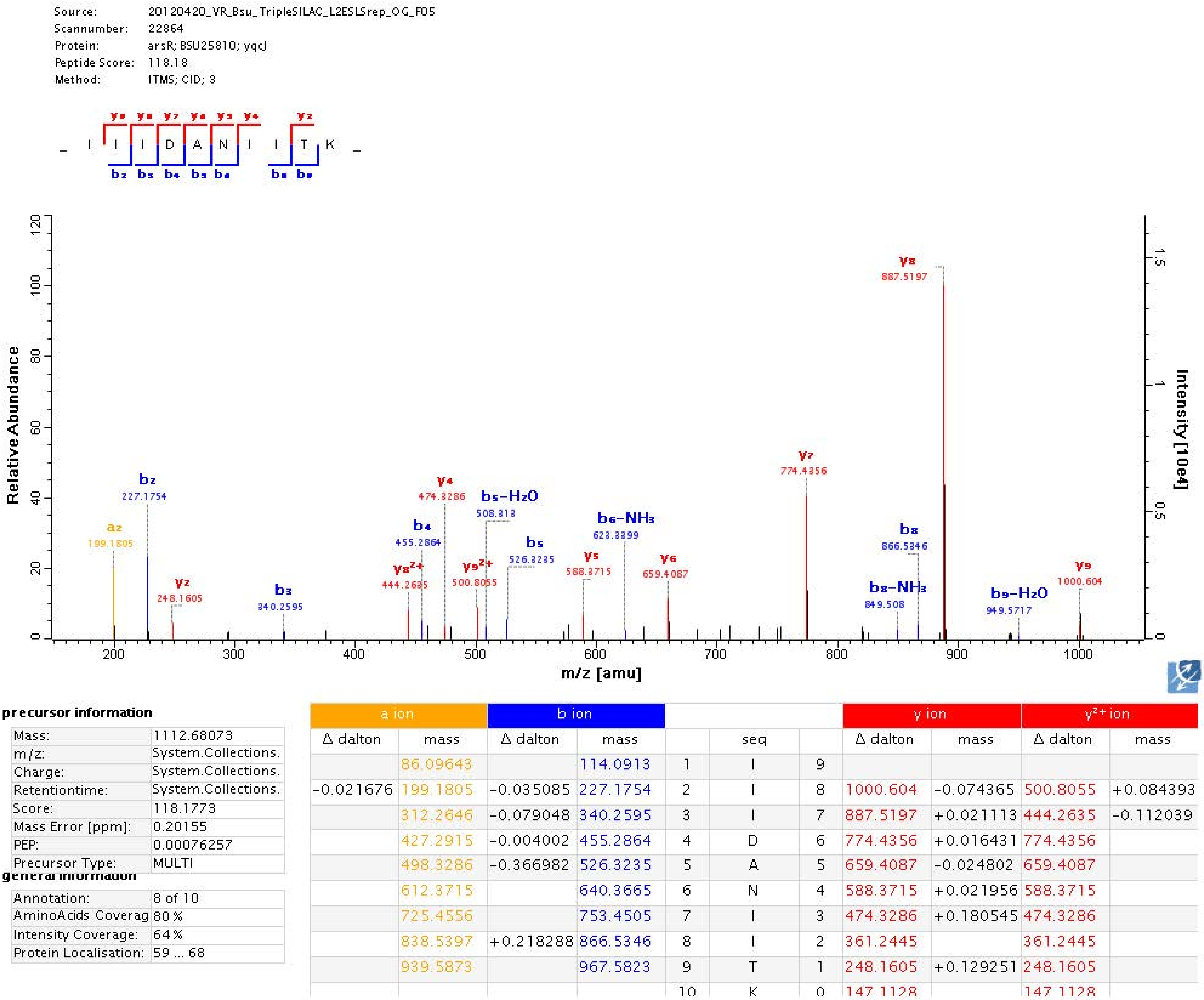
precursor information

Mass:	2391.22987
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	50.35817
Mass Error [ppm]:	0.71048
PEP:	0.002555
Precursor Type:	MULTI

general information

Annotation:	14 of 22
AminoAcids Coverag	64 %
Intensity Coverage:	32 %
Protein Localisation:	30 ... 51

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	21				
	272.1353		272.1353	2	D	20	2240.159		2240.159	
	369.1881		369.1881	3	P	19	2125.132		2125.132	
	484.215		484.215	4	D	18	2028.08		2028.08	
	541.2365		541.2365	5	G	17	1913.053		1913.053	
	654.3206		654.3206	6	I	16	1856.031		1856.031	
	767.4046	+0.138828	767.4046	7	I	15	1742.947		1742.947	
	854.4367		854.4367	8	S	14	1629.863		1629.863	
	1001.505	+0.170954	1001.505	9	F	13	1542.831		1542.831	
-0.02983	551.78		1102.553	10	T	12	1395.763	+0.354064	1395.763	
	1189.585	+0.115783	1189.585	11	S	11	1294.715		1294.715	
	1302.669		1302.669	12	I	10	1207.683		1207.683	
+0.441978	715.8673		1430.727	13	Q	9	1094.599		547.8031	-0.36911
+0.355224	759.3834		1517.759	14	S	8	966.5404	+0.09277	966.5404	
-0.199154	823.9047		1646.802	15	E	7	879.5084		879.5084	
+0.018218	874.4285	+0.29945	1747.85	16	T	6	750.4658	-0.013151	750.4658	
	1804.871		1804.871	17	G	5	649.4181	+0.122113	649.4181	
	1932.93		1932.93	18	Q	4	592.3966		592.3966	
	2019.962		2019.962	19	S	3	464.3381	+0.107001	464.3381	
	2133.046		2133.046	20	I	2	377.306		377.306	
+0.088141	1123.569		2246.13	21	I	1	264.222		264.222	
				22	K	0	151.1379		151.1379	



Source: 20120420_VR_Bsu_TripleSILAC_L2ESLSrep_OG_F05
Scannumber: 22864
Protein: arsR; BSU25810; yqcJ
Peptide Score: 118.18
Method: ITMS; CID; 3

precursor information

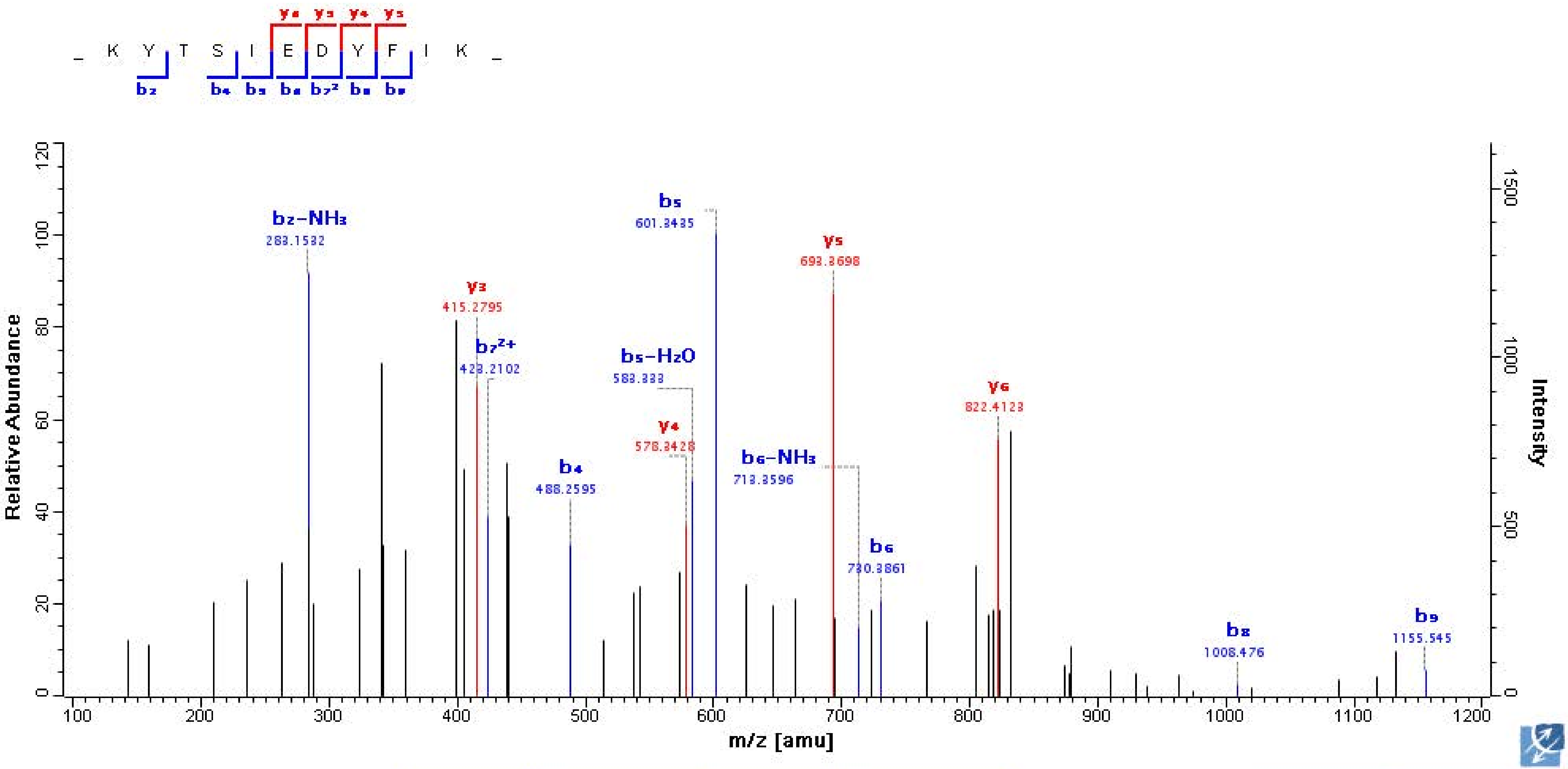
Mass:	1112.68073
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.1773
Mass Error [ppm]:	0.20155
PEP:	0.00076257
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	64 %
Protein Localisation:	59 ... 68

a ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	9				
-0.021676	199.1805	-0.035085	227.1754	2	I	8	1000.604	-0.074365	500.8055	+0.084393
	312.2646	-0.079048	340.2595	3	I	7	887.5197	+0.021113	444.2635	-0.112039
	427.2915	-0.004002	455.2864	4	D	6	774.4356	+0.016431	774.4356	
	498.3286	-0.366982	526.3235	5	A	5	659.4087	-0.024802	659.4087	
	612.3715		640.3665	6	N	4	588.3715	+0.021956	588.3715	
	725.4556		753.4505	7	I	3	474.3286	+0.180545	474.3286	
	838.5397	+0.218288	866.5346	8	I	2	361.2445		361.2445	
	939.5873		967.5823	9	T	1	248.1605	+0.129251	248.1605	
				10	K	0	147.1128		147.1128	

Source: 20120420_VR_Bsu_TripleSILAC_L2ESLSrep_OG_F05
Scannumber: 22995
Protein: BSU02570; ycbN
Peptide Score: 67.15
Method: ITMS; CID; 3



precursor information

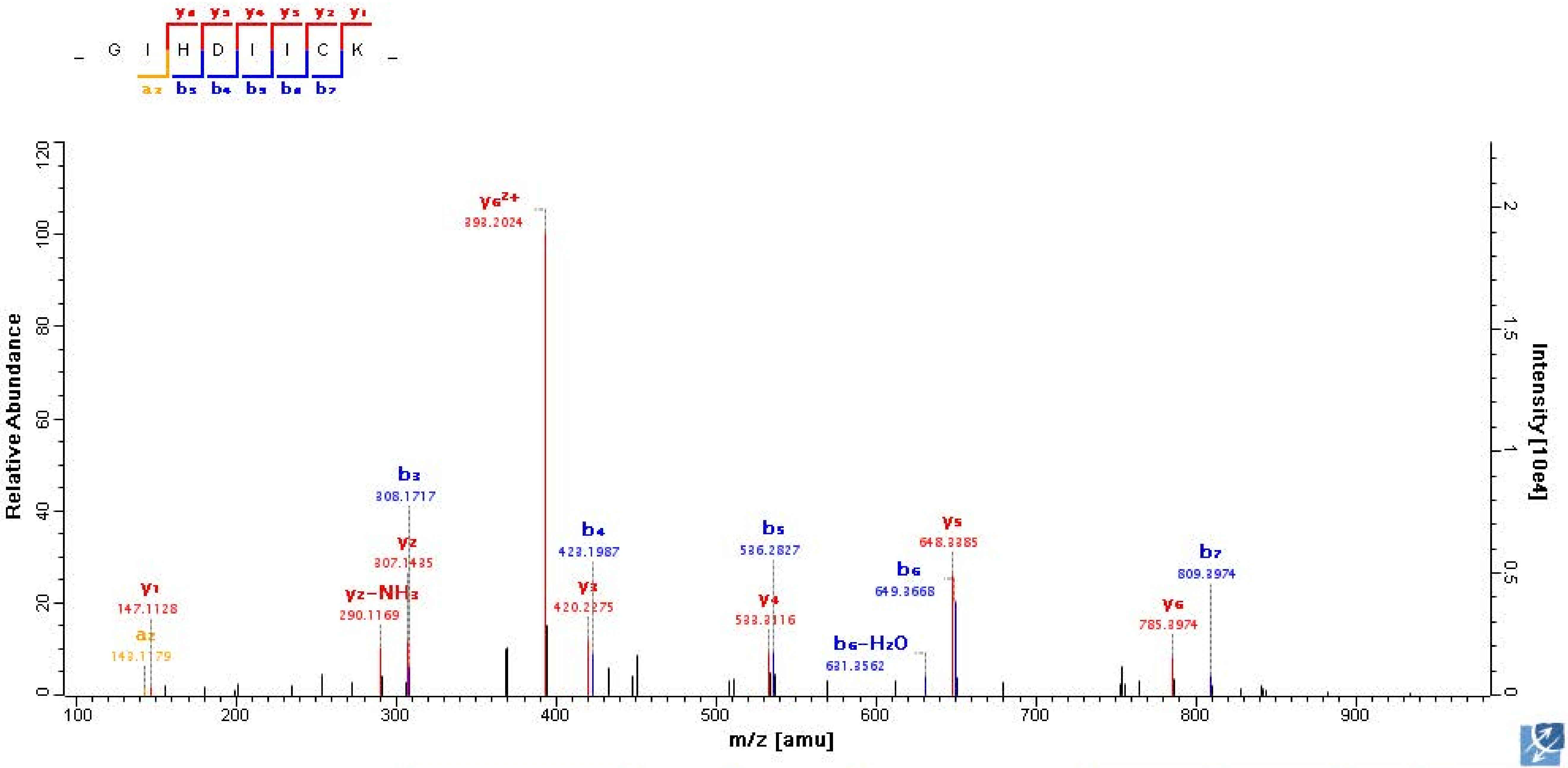
Mass:	1405.71122
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	67.15321
Mass Error [ppm]:	-1.2064
PEP:	0.0045994
Precursor Type:	MULTI

general information

Annotation:	7 of 11
AminoAcids Coverag	64 %
Intensity Coverage:	39 %
Protein Localisation:	288 ... 298

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	137.1164383		137.1164383	1	K	10		
	300.17976684		300.17976684	2	Y	9	1286.6394449	
	401.22744531		401.22744531	3	T	8	1123.5761164	
	488.25947372	+0.1617909	488.25947372	4	S	7	1022.5284379	
	601.3435377	+0.1689135	601.3435377	5	I	6	935.49640953	
	730.3861308	+0.1561666	730.3861308	6	E	5	822.41234555	+0.1605304
+0.0544733	423.21017515		845.41307383	7	D	4	693.36975245	-0.0253311
	1008.4764024	+0.3095473	1008.4764024	8	Y	3	578.34280942	+0.2577765
	1155.5448163	+0.2189777	1155.5448163	9	F	2	415.27948088	-0.0128183
	1268.6288803		1268.6288803	10	I	1	268.21106696	
				11	K	0	155.12700298	

Source: 20120420_VR_Bsu_TripleSILAC_L2ESLSrep_OG_F09
Scannumber: 10370
Protein: BSU39960; S141R; yxaI
Peptide Score: 136.11
Method: ITMS; CID; 3



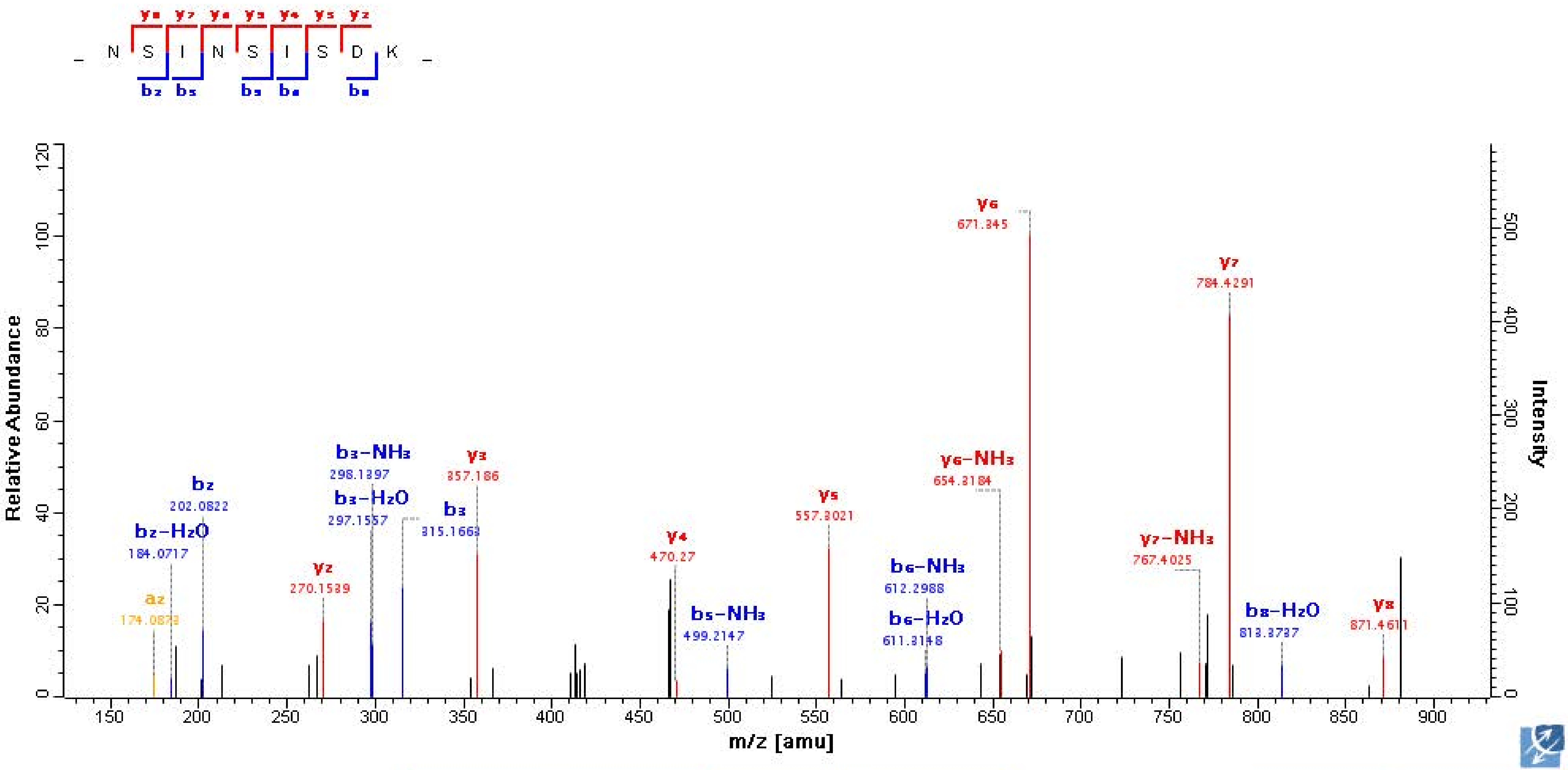
precursor information

Mass:	954.49604
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.1133
Mass Error [ppm]:	0.37076
PEP:	0.00037902
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	64 %
Protein Localisation:	138 ... 145

g

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	30.03383		58.02874	1	G	7				
+0.070572	143.1179		171.1128	2	I	6	898.4815		898.4815	
	280.1768	+0.077643	308.1717	3	H	5	785.3974	+0.07693	393.2024	+0.077796
	395.2037	+0.06782	423.1987	4	D	4	648.3385	+0.020607	648.3385	
	508.2878	+0.109367	536.2827	5	I	3	533.3116	+0.029728	533.3116	
	621.3719	+0.012852	649.3668	6	I	2	420.2275	-0.000221	420.2275	
	781.4025	+0.05746	809.3974	7	C	1	307.1435	+0.027629	307.1435	
				8	K	0	147.1128	+0.023579	147.1128	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F06
Scannumber: 5003
Protein: BSU40160; yydH
Peptide Score: 108.74
Method: ITMS; CID; 3

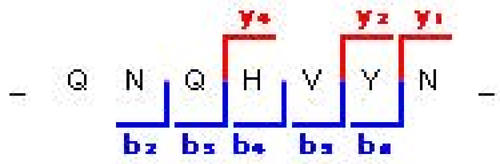


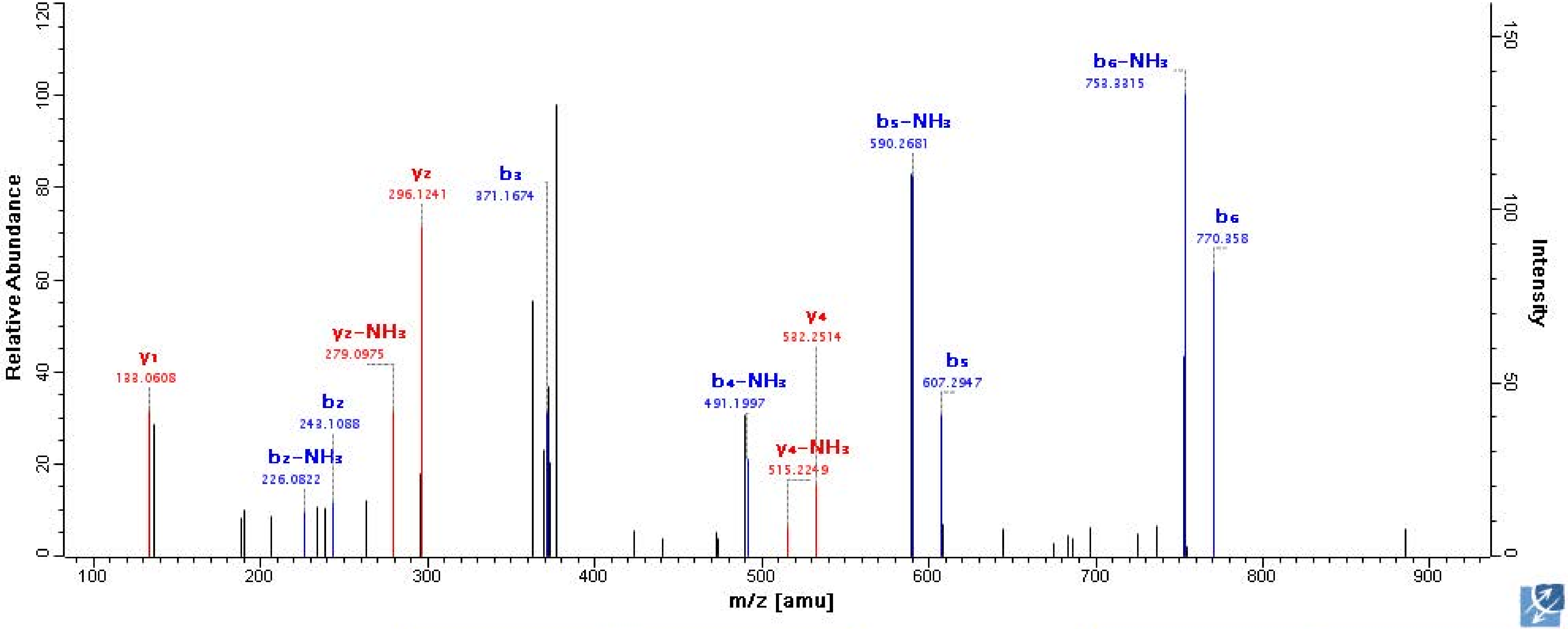
precursor information

Mass:	976.48204
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.7426
Mass Error [ppm]:	-0.50893
PEP:	0.0015294
Precursor Type:	MULTI
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	60 %
Protein Localisation:	32 ... 40

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	87.055289292		115.05020391	1	N	8		
+0.0746086	174.0873177	-0.0622433	202.08223232	2	S	7	871.46108665	-0.0442776
	287.17138168	+0.0590455	315.1662963	3	I	6	784.42905824	-0.006817
	401.21430913		429.20922375	4	N	5	671.34499426	-0.0577018
	488.24633754		516.24125216	5	S	4	557.30206682	+0.1005821
	601.33040152		629.32531614	6	I	3	470.27003841	+0.1260187
	688.36242993		716.35734455	7	S	2	357.18597443	+0.0183408
	803.38937296		831.38428758	8	D	1	270.15394602	+0.0452117
				9	K	0	155.12700298	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F08
Scannumber:	1968
Protein:	bdbB; BSU21440; yolK
Peptide Score:	99.92
Method:	ITMS; CID; 3

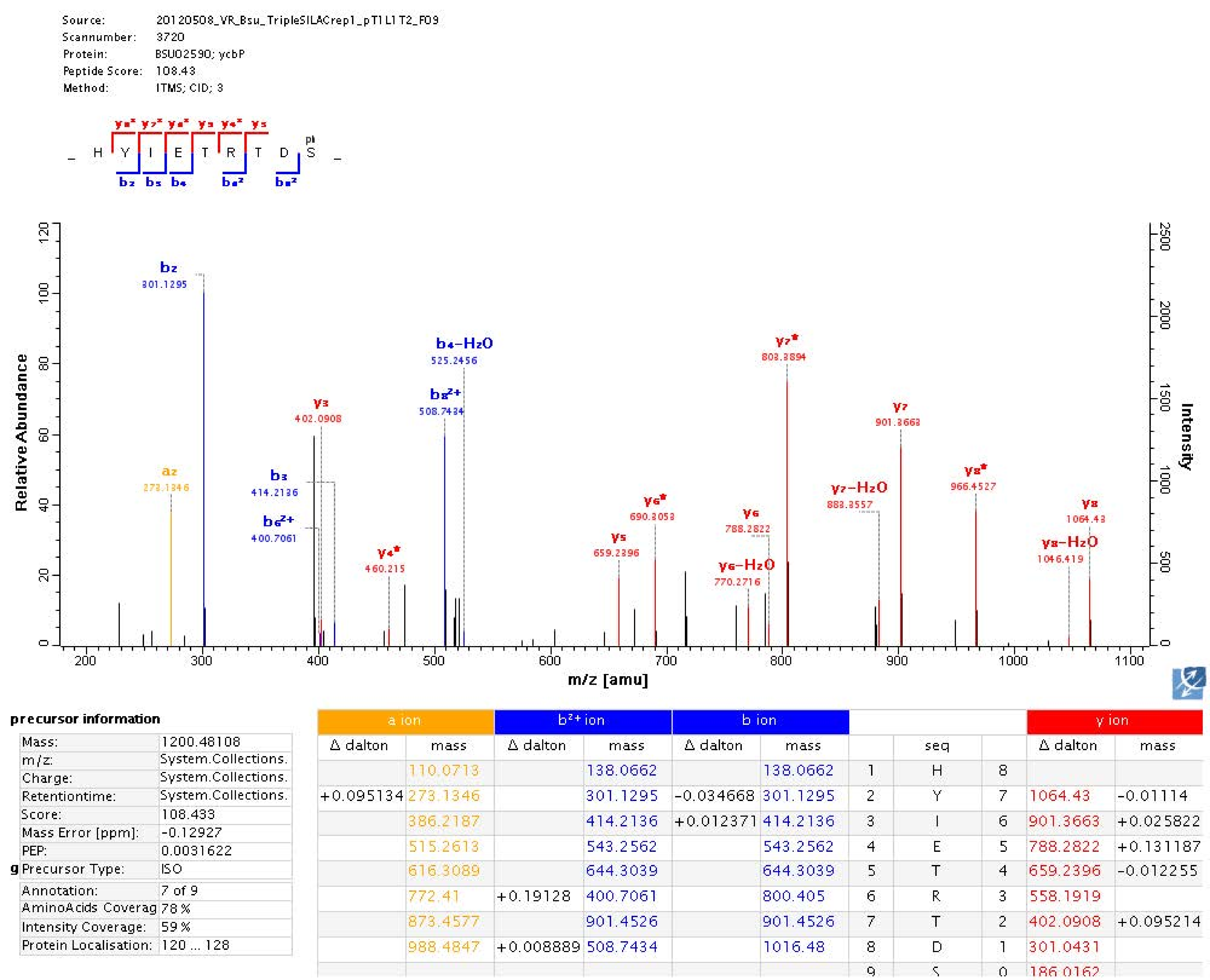




precursor information

Mass:	901.40406
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	99.91949
Mass Error [ppm]:	-0.18307
PEP:	0.0041422
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	47 %
Protein Localisation:	142 ... 148

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	129.065853978	1	Q	6		
+0.4079422	243.108781425	2	N	5	774.352927876	
-0.036347	371.167358937	3	Q	4	660.310000428	
	508.226270799	4	H	3	532.251422917	-0.0869332
-0.1474069	607.294684715	5	V	2	395.192511055	
-0.1070977	770.358013254	6	Y	1	296.124097138	+0.0615718
		7	N	0	133.0607686	+0.0711284



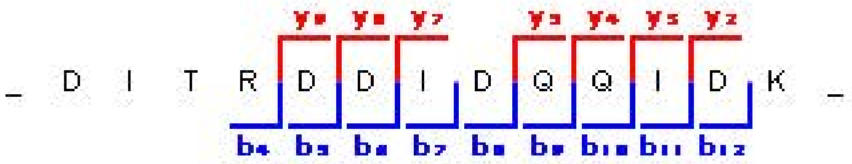
Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F09
Scannumber: 3720
Protein: BSU02590; ycbP
Peptide Score: 108.43
Method: ITMS; CID; 3

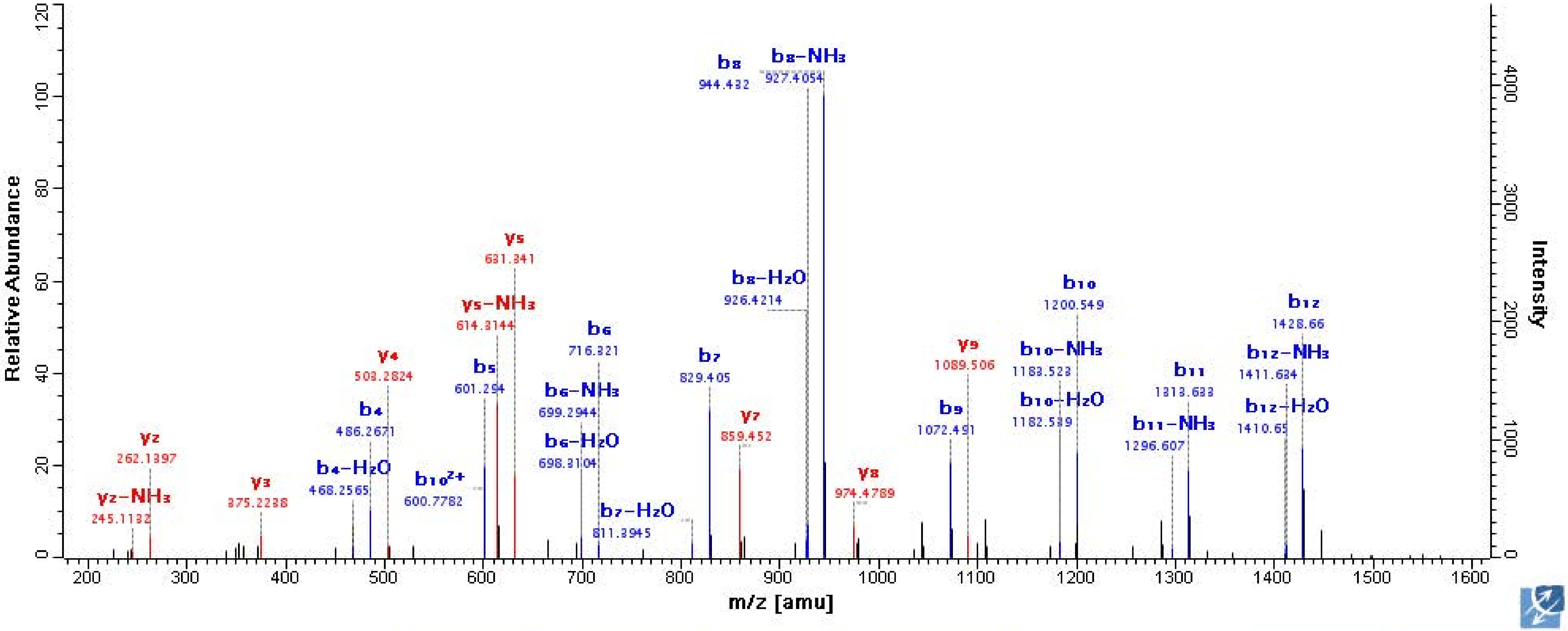
precursor information

Mass:	1200.48108
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.433
Mass Error [ppm]:	-0.12927
PEP:	0.0031622
Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	59 %
Protein Localisation:	120 ... 128

a ion		b²⁺ 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	8		
+0.095134	273.1346		301.1295	-0.034668	301.1295	2	Y	7	1064.43	-0.01114
	386.2187		414.2136	+0.012371	414.2136	3	I	6	901.3663	+0.025822
	515.2613		543.2562		543.2562	4	E	5	788.2822	+0.131187
	616.3089		644.3039		644.3039	5	T	4	659.2396	-0.012255
	772.41	+0.19128	400.7061		800.405	6	R	3	558.1919	
	873.4577		901.4526		901.4526	7	T	2	402.0908	+0.095214
	988.4847	+0.008889	508.7434		1016.48	8	D	1	301.0431	
						9	S	0	186.0162	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F10
Scannumber:	5982
Protein:	BSU14570; ykrC; ykyA
Peptide Score:	195.77
Method:	ITMS; CID; 3





precursor information

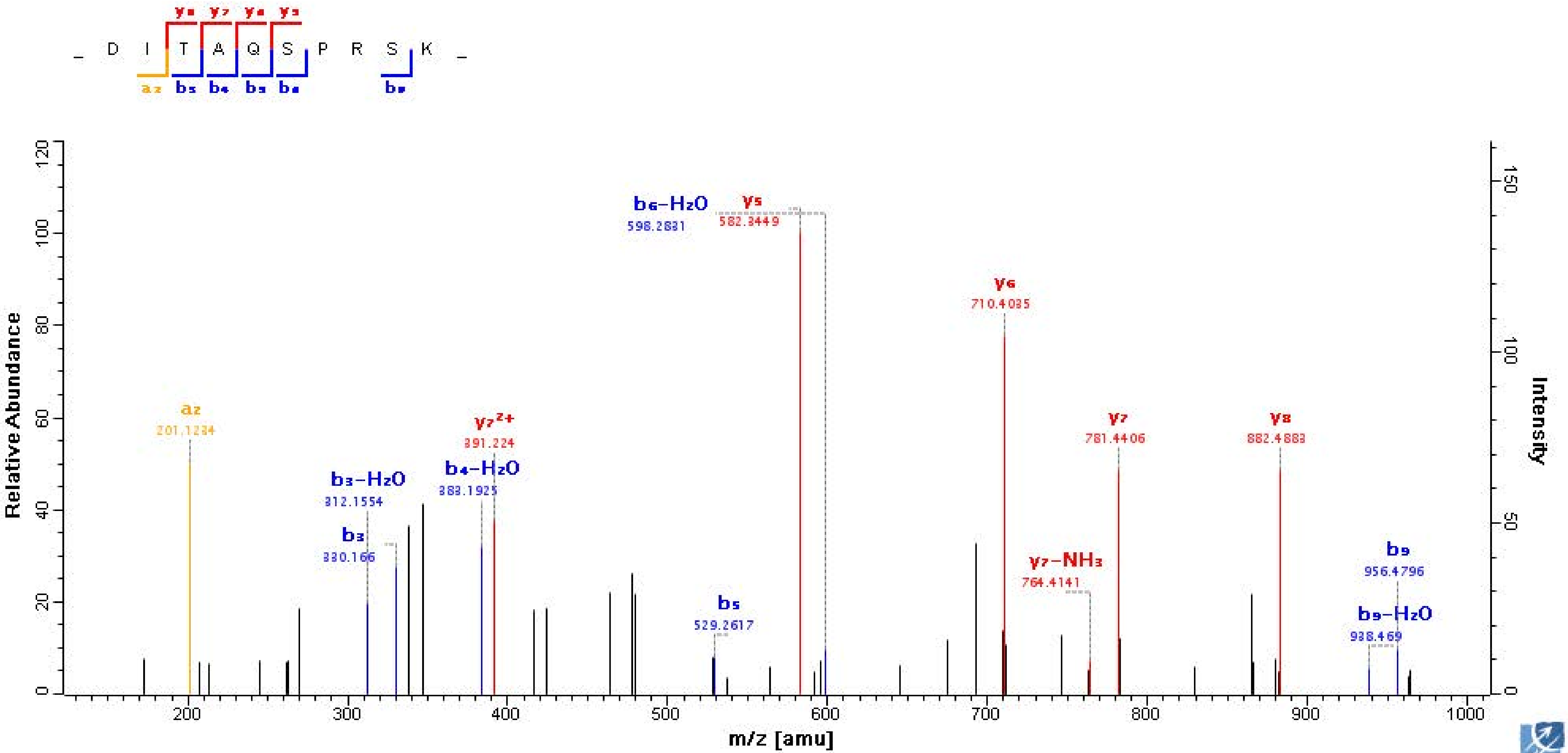
Mass:	1573.75853
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	195.7693
Mass Error [ppm]:	0.096837
PEP:	6.4774E-47
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	67 %
Protein Localisation:	171 ... 183

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	12		
	229.11828348		229.11828348	2	I	11	1459.7387128	
	330.16596195		330.16596195	3	T	10	1346.6546488	
	486.26707298	+0.0868699	486.26707298	4	R	9	1245.6069703	
	601.29401601	+0.1491603	601.29401601	5	D	8	1089.5058593	+0.0909425
	716.32095905	+0.0873051	716.32095905	6	D	7	974.47891625	+0.0644797
	829.40502303	-0.0365538	829.40502303	7	I	6	859.45197322	+0.0452802
	944.43196606	+0.0147503	944.43196606	8	D	5	746.36790924	
	1072.4905436	+0.0062826	1072.4905436	9	Q	4	631.34096621	+0.0373297
+0.0011591	600.77819877	+0.020459	1200.5491211	10	Q	3	503.28238869	+0.1161098
	1313.6331851	+0.0749448	1313.6331851	11	I	2	375.22381118	-0.1339064
	1428.6601281	+0.1217323	1428.6601281	12	D	1	262.1397472	+0.1157154
				13	K	0	147.11280417	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F12
Scannumber: 2514
Protein: BSU04360; mntH; ydaR
Peptide Score: 82.29
Method: ITMS; CID; 3



precursor information

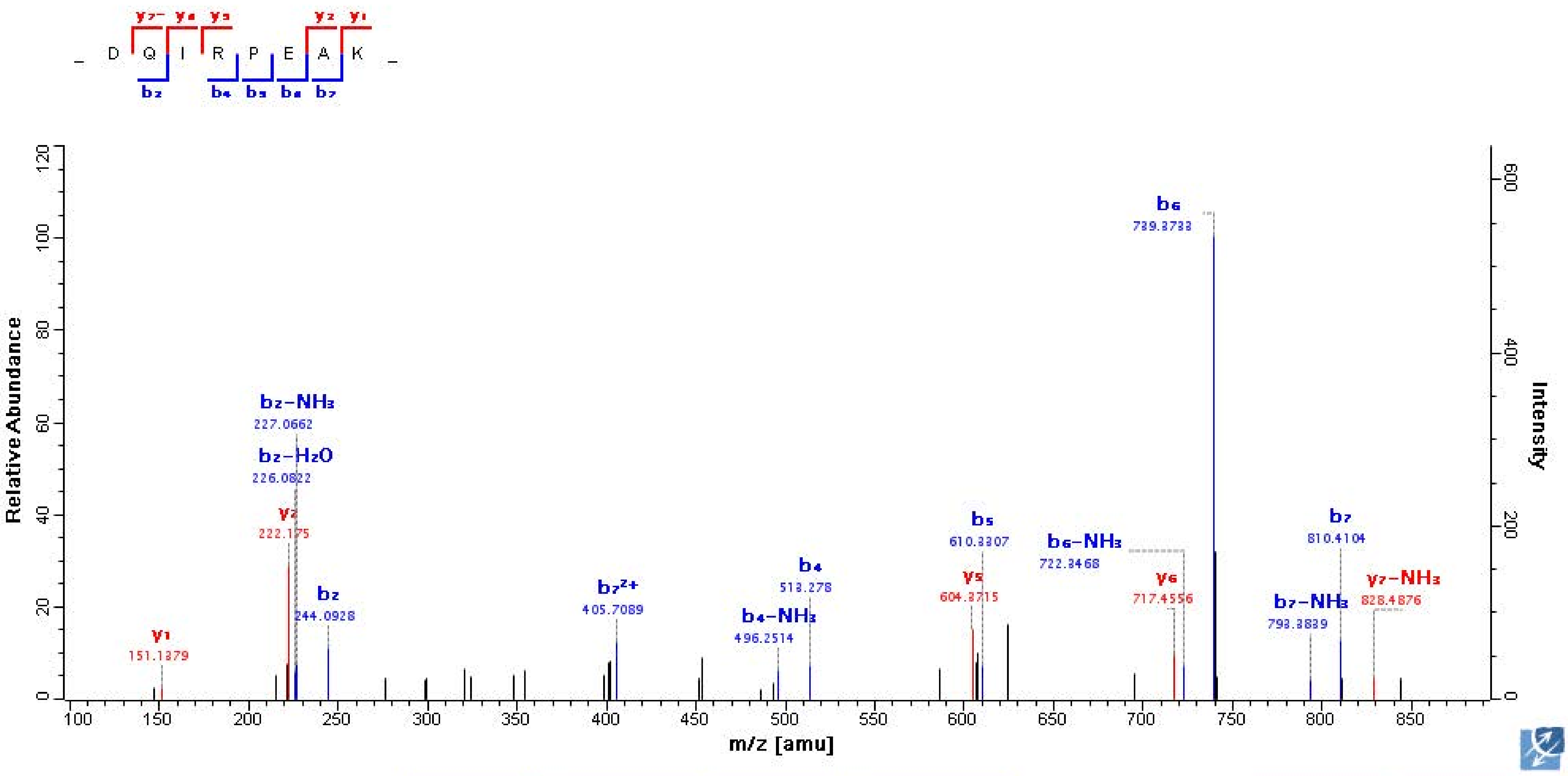
Mass:	1101.57838
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	82.28683
Mass Error [ppm]:	0.4886
PEP:	0.0025702
Precursor Type:	MULTI

general information

Annotation:	6 of 10
AminoAcids Coverag	60 %
Intensity Coverage:	53 %
Protein Localisation:	5 ... 14

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.0393		116.0342	1	D	9				
+0.102736	201.1234		229.1183	2	I	8	995.5724		995.5724	
	302.171	+0.070977	330.166	3	T	7	882.4883	+0.087928	882.4883	
	373.2082		401.2031	4	A	6	781.4406	+0.212755	391.224	+0.242052
	501.2667	-0.346797	529.2617	5	Q	5	710.4035	+0.115958	710.4035	
	588.2988		616.2937	6	S	4	582.3449	+0.112341	582.3449	
	685.3515		713.3464	7	P	3	495.3129		495.3129	
	841.4526		869.4476	8	R	2	398.2601		398.2601	
	928.4847	+0.112151	956.4796	9	S	1	242.159		242.159	
				10	K	0	155.127		155.127	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F13
Scannumber:	2684
Protein:	BSU13850; ykvW; zosA
Peptide Score:	111.17
Method:	ITMS; CID; 3



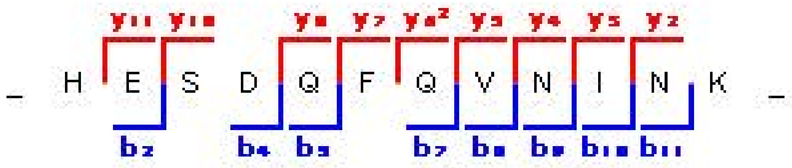
precursor information

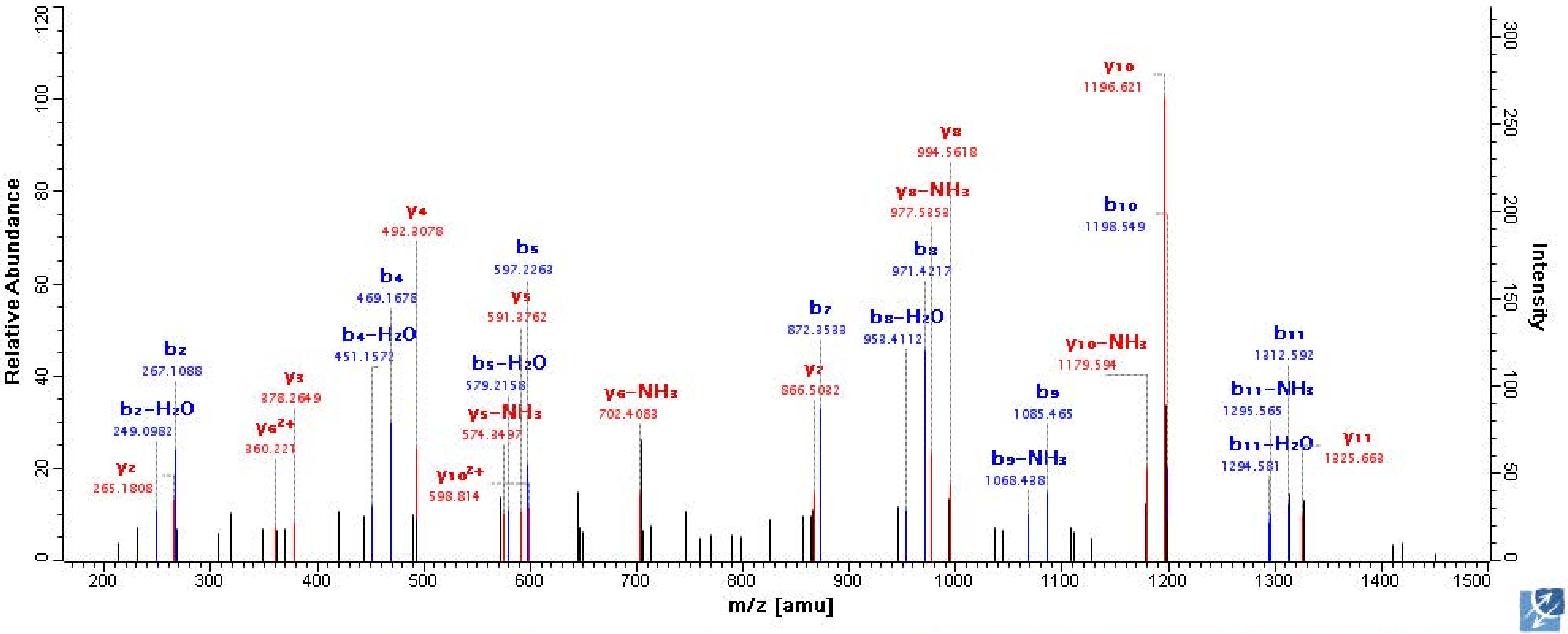
g

Mass:	959.53381
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.1672
Mass Error [ppm]:	0.010896
PEP:	0.0035053
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	57 %
Protein Localisation:	464 ... 471

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	116.0342195		116.0342195	1	D	7		
	244.09279701	+0.0329812	244.09279701	2	Q	6	845.51413441	
	357.17686099		357.17686099	3	I	5	717.4555569	+0.1963596
	513.27797202	+0.010297	513.27797202	4	R	4	604.37149292	+0.1227698
	610.33073587	-0.1408555	610.33073587	5	P	3	448.27038189	
	739.37332897	-0.0272596	739.37332897	6	E	2	351.21761804	
-0.1317722	405.70885961	+0.0712467	810.41044275	7	A	1	222.17502494	+0.0065699
				8	K	0	151.13791115	+0.251661

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F13
Scannumber: 6950
Protein: BSU09640; yhdY
Peptide Score: 190.53
Method: ITMS; CID; 3





precursor information

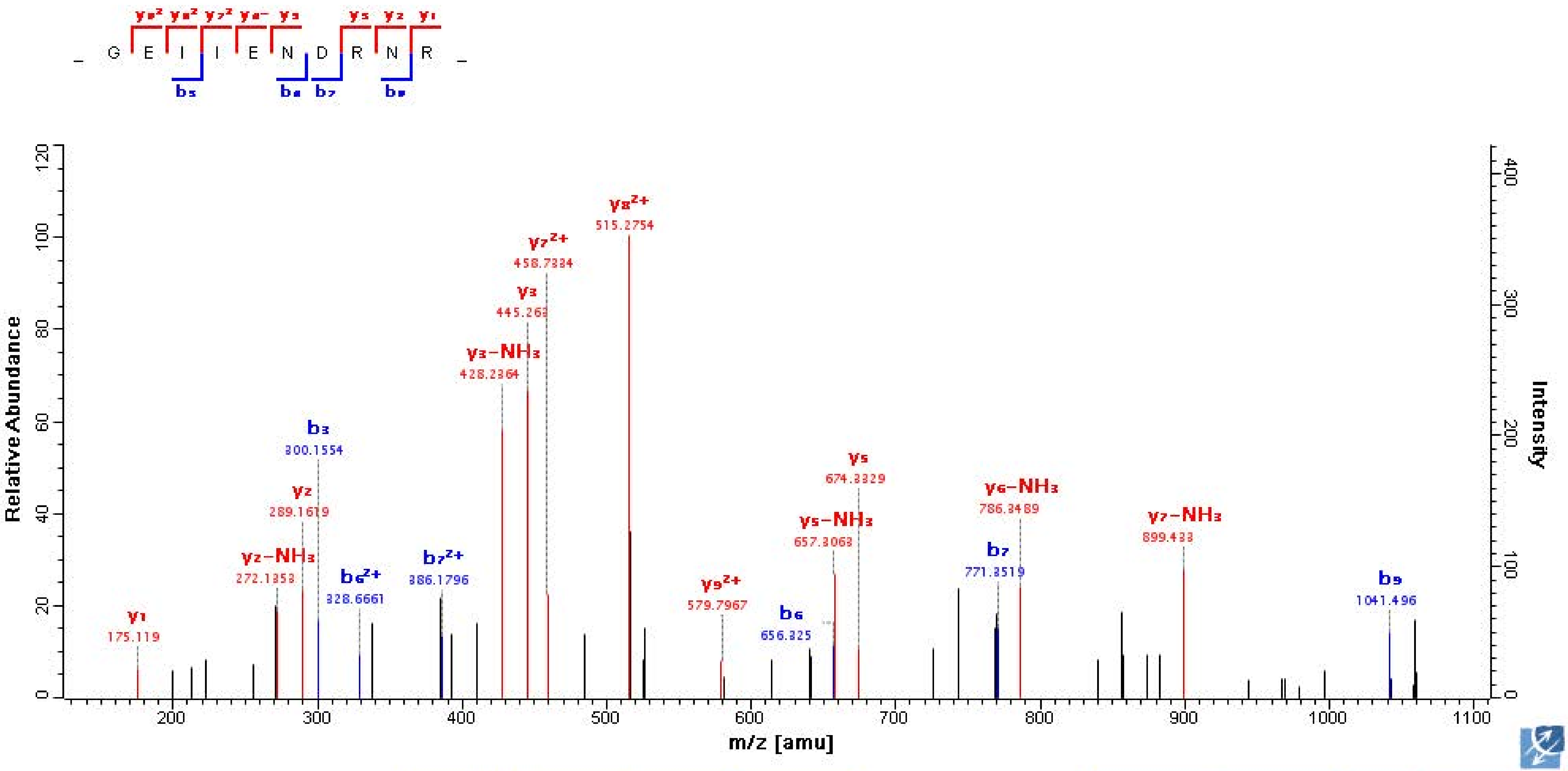
Mass:	1457.68986
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	190.531
Mass Error [ppm]:	-0.031783
PEP:	2.3837E-45
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	58 %
Protein Localisation:	354 ... 365

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833	1	H	11				
+0.1166214	267.10878143	2	E	10	1325.6633774	+0.0937027	1325.6633774	
	354.14080984	3	S	9	1196.6207843	+0.0991864	598.8140304	-0.4666793
-0.1110512	469.16775287	4	D	8	1109.5887559		1109.5887559	
+0.1148561	597.22633038	5	Q	7	994.56181288	+0.0382237	994.56181288	
	744.29474429	6	F	6	866.50323537	+0.0029292	866.50323537	
-0.0331314	872.35332181	7	Q	5	719.43482146		360.22104896	-0.1318766
+0.117632	971.42173572	8	V	4	591.37624395	-0.3563465	591.37624395	
+0.0848974	1085.4646632	9	N	3	492.30783003	+0.0163887	492.30783003	
+0.2054232	1198.5487271	10	I	2	378.26490258	+0.0361228	378.26490258	
+0.0400593	1312.5916546	11	N	1	265.1808386	+0.1373377	265.1808386	
		12	K	0	151.13791115		151.13791115	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F14
Scannumber:	4008
Protein:	BSU31650; mrpF; yufC
Peptide Score:	101.65
Method:	ITMS; CID; 3



precursor information

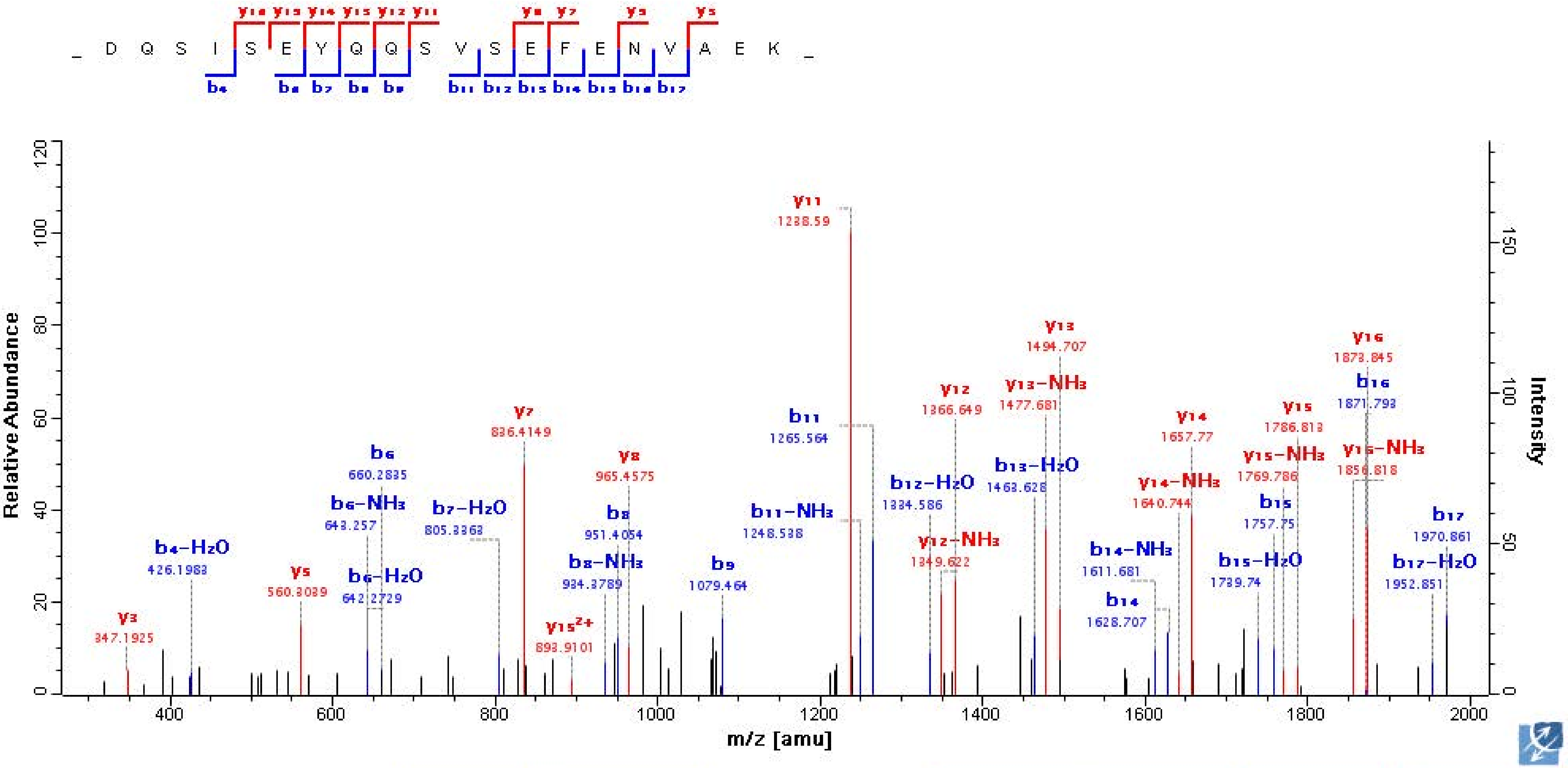
Mass:	1214.6
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	101.6462
Mass Error [ppm]:	-0.29569
PEP:	0.0013278
Precursor Type:	ISO

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	55 %
Protein Localisation:	85 ... 94

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	9				
	187.0713		187.0713	2	E	8	1158.586		579.7967	-0.255222
	300.1554	+0.018095	300.1554	3	I	7	1029.544		515.2754	+0.048973
	413.2395		413.2395	4	I	6	916.4595		458.7334	+0.274232
	542.2821		542.2821	5	E	5	803.3755		803.3755	
+0.478036	328.6661	-0.030914	656.325	6	N	4	674.3329	+0.009729	674.3329	
-0.081639	386.1796	-0.416439	771.3519	7	D	3	560.2899		560.2899	
	927.453		927.453	8	R	2	445.263	-0.000662	445.263	
	1041.496	-0.150626	1041.496	9	N	1	289.1619	+0.054246	289.1619	
				10	R	0	175.119	+0.013036	175.119	

Source: 20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F21
Scannumber: 10591
Protein: BSU16250; cheF; fliJ
Peptide Score: 167.28
Method: ITMS; CID; 3



precursor information

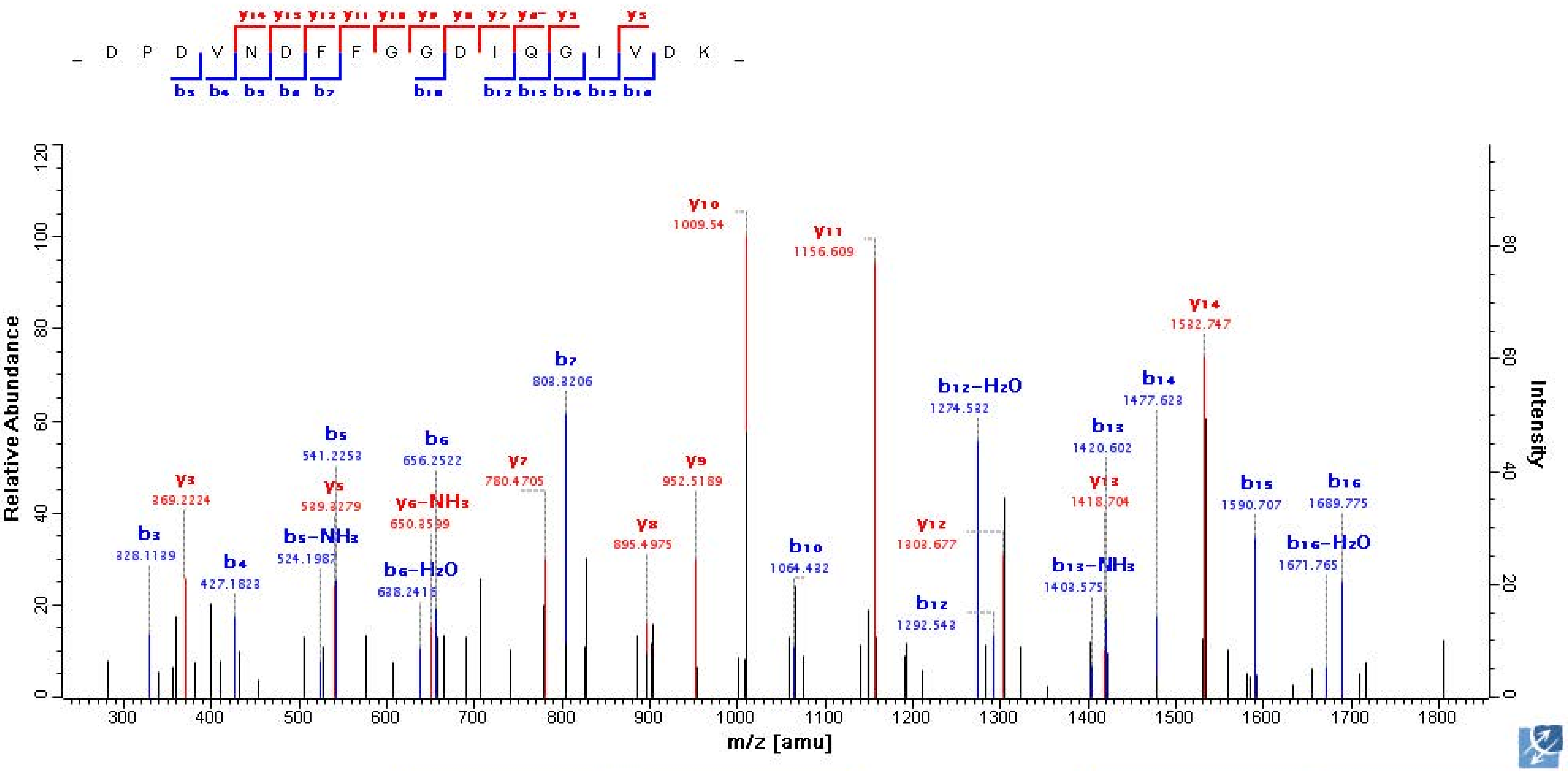
Mass:	2316.04154
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	167.2807
Mass Error [ppm]:	0.9405
PEP:	1.1492E-45
Precursor Type:	ISO

general information

Annotation:	15 of 20
AminoAcids Coverag	75 %
Intensity Coverage:	62 %
Protein Localisation:	19 ... 38

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	19				
	244.09279701	2	Q	18	2202.0196982		2202.0196982	
	331.12482542	3	S	17	2073.9611207		2073.9611207	
	444.2088894	4	I	16	1986.9290923		1986.9290923	
	531.24091781	5	S	15	1873.8450283	+0.1615635	1873.8450283	
+0.086118	660.28351091	6	E	14	1786.8129999	+0.1247442	893.91013819	+0.041644
	823.34683944	7	Y	13	1657.7704068	+0.0912875	1657.7704068	
+0.143167	951.40541696	8	Q	12	1494.7070783	+0.1275164	1494.7070783	
+0.1768747	1079.4639945	9	Q	11	1366.6485008	+0.2411477	1366.6485008	
	1166.4960229	10	S	10	1238.5899233	-0.0325502	1238.5899233	
+0.0962077	1265.5644368	11	V	9	1151.5578949		1151.5578949	
	1352.5964652	12	S	8	1052.4894809		1052.4894809	
	1481.6390583	13	E	7	965.45745253	-0.0387514	965.45745253	
-0.1072525	1628.7074722	14	F	6	836.41485943	-0.0359532	836.41485943	
+0.3253741	1757.7500653	15	E	5	689.34644551		689.34644551	
+0.1374272	1871.7929928	16	N	4	560.30385242	+0.0975148	560.30385242	
-0.1829399	1970.8614067	17	V	3	446.26092497		446.26092497	
	2041.8985205	18	A	2	347.19251105	+0.0618835	347.19251105	
	2170.9411136	19	E	1	276.15539727		276.15539727	
		20	K	0	147.11280417		147.11280417	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F21
Scannumber:	12082
Protein:	bbmA; BSU34620; yvdF
Peptide Score:	128.26
Method:	ITMS; CID; 3



precursor information

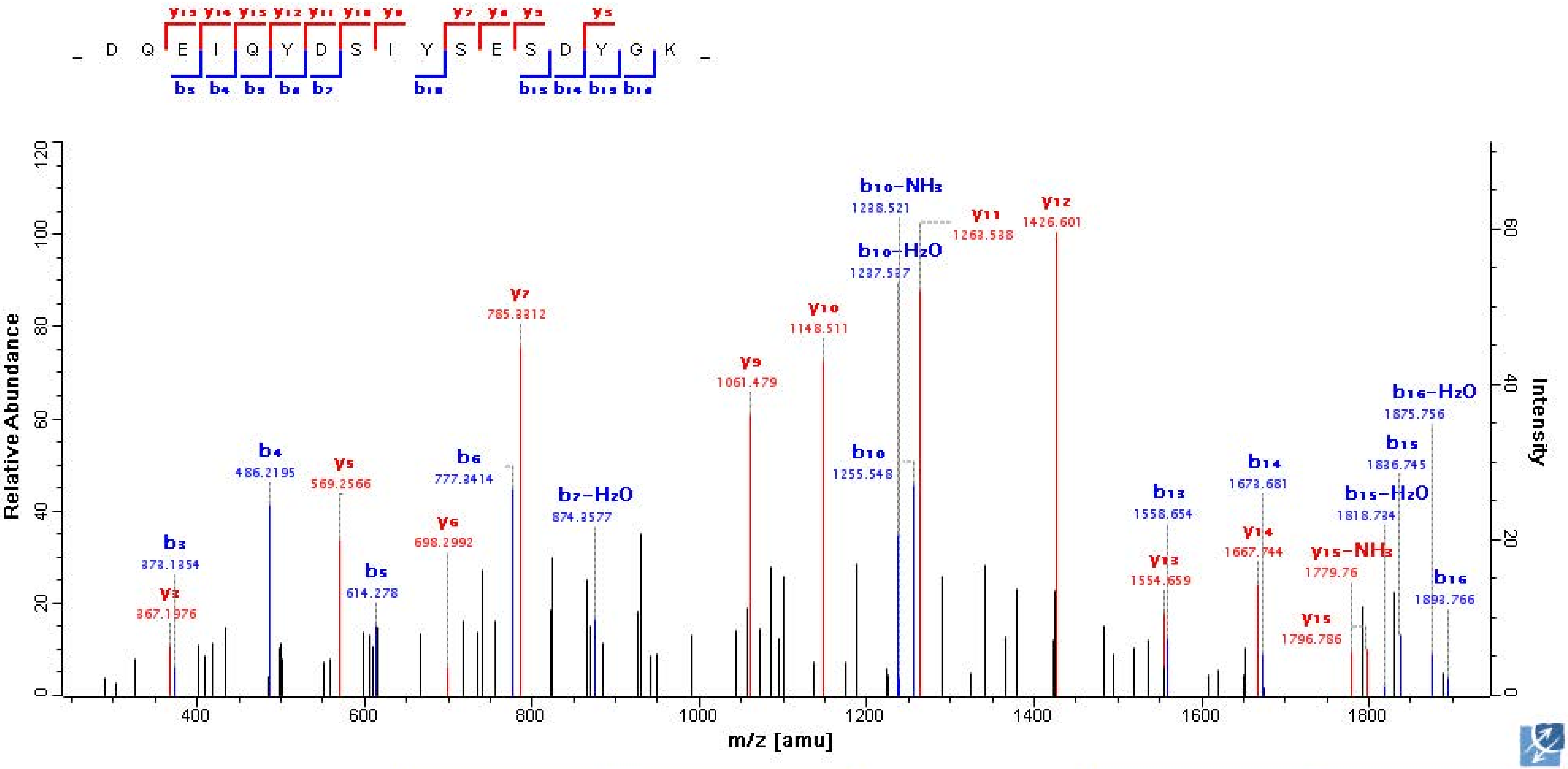
Mass:	1949.90082
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	128.2604
Mass Error [ppm]:	0.066286
PEP:	4.4885E-11
Precursor Type:	MULTI

general information

Annotation:	14 of 18
AminoAcids Coverag	78 %
Intensity Coverage:	50 %
Protein Localisation:	166 ... 183

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	17		
	213.086983351	2	P	16	1843.895218719	
+0.1192279	328.113926383	3	D	15	1746.842454867	
-0.0317666	427.182340299	4	V	14	1631.815511835	
-0.0839103	541.225267746	5	N	13	1532.747097919	-0.1039094
+0.0753039	656.252210778	6	D	12	1418.704170471	+0.2461469
+0.0670706	803.320624694	7	F	11	1303.677227439	+0.1605411
	950.38903861	8	F	10	1156.608813523	+0.2818115
	1007.410502334	9	G	9	1009.540399607	+0.1091976
+0.0870769	1064.431966058	10	G	8	952.518935883	+0.1246798
	1179.45890909	11	D	7	895.49747216	+0.2028452
-0.0008588	1292.54297307	12	I	6	780.470529128	+0.0955109
+0.2076535	1420.601550581	13	Q	5	667.386465147	
-0.0524577	1477.623014305	14	G	4	539.327887636	+0.1688775
+0.2699725	1590.707078285	15	I	3	482.306423912	
+0.0588584	1689.775492202	16	V	2	369.222359932	+0.2295138
	1804.802435234	17	D	1	270.153946016	
		18	K	0	155.127002984	

Source:	20120508_VR_Bsu_TripleSILACrep1_pT1L1T2_F21
Scannumber:	8126
Protein:	BSU26420; yrkQ
Peptide Score:	113.29
Method:	ITMS; CID; 3



precursor information

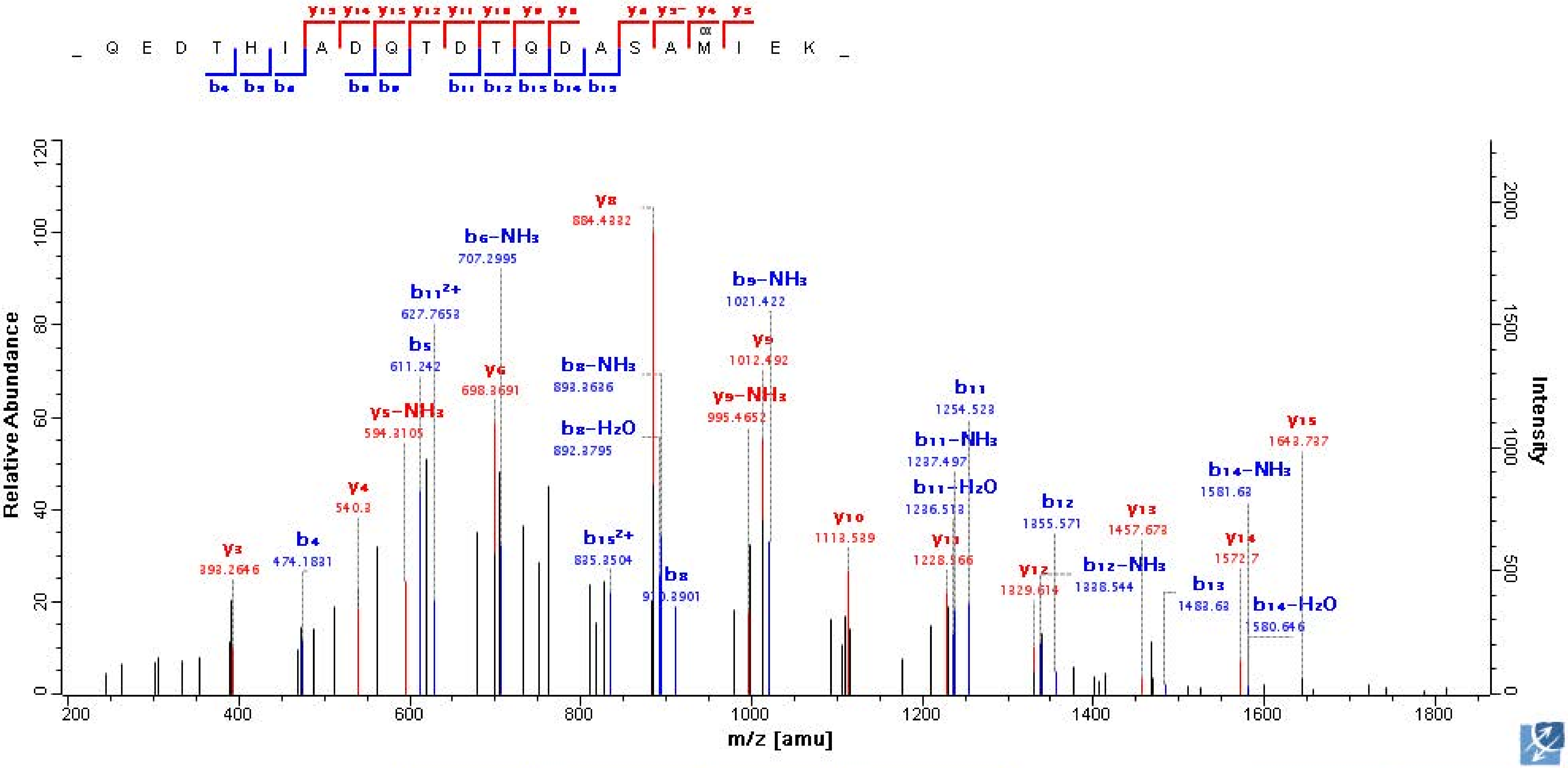
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.2877
Mass Error [ppm]:	-3.3026
PEP:	5.0875E-22
Precursor Type:	PEAK

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	47 %
Protein Localisation:	93 ... 109

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	116.034219499	1	D	16		
	244.09279701	2	Q	15	1924.844693979	
-0.1228169	373.135390106	3	E	14	1796.786116467	+0.266862
-0.1230796	486.219454087	4	I	13	1667.743523371	+0.0664132
-0.1299603	614.278031598	5	Q	12	1554.659459391	+0.1966197
-0.1227932	777.341360136	6	Y	11	1426.600881879	+0.0738007
	892.368303168	7	D	10	1263.537553341	-0.0597701
	979.400331578	8	S	9	1148.510610309	+0.0451758
	1092.484395559	9	I	8	1061.478581899	+0.2372384
+0.1618706	1255.547724097	10	Y	7	948.394517919	
	1342.579752507	11	S	6	785.33118938	+0.1882198
	1471.622345603	12	E	5	698.299160971	-0.2101717
+0.2368613	1558.654374013	13	S	4	569.256567874	+0.017541
-0.4180114	1673.681317045	14	D	3	482.224539464	
+0.1597734	1836.744645583	15	Y	2	367.197596432	+0.2442981
+0.1374551	1893.766109307	16	G	1	204.134267894	
		17	K	0	147.112804171	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F01
Scannumber: 8926
Protein: BSU27630; yrvD
Peptide Score: 104.84
Method: ITMS; CID; 3



precursor information

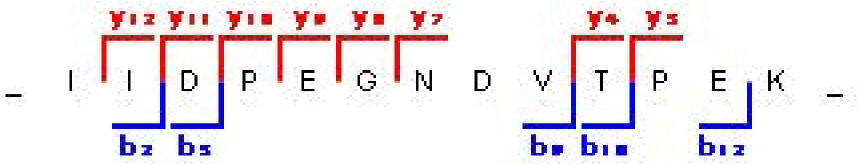
Mass:	2362.0218
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	104.8373
Mass Error [ppm]:	-0.53299
PEP:	1.5101E-12
Precursor Type:	MULTI

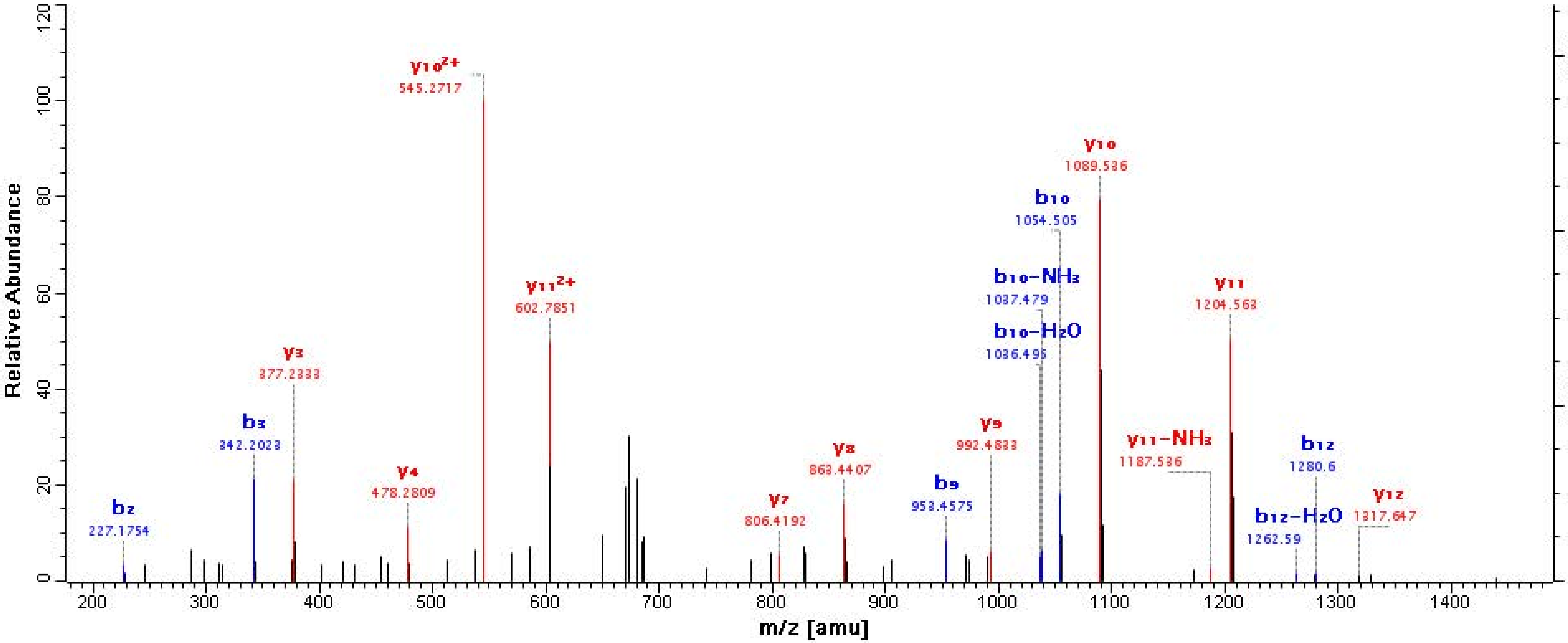
general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	43 %
Protein Localisation:	85 ... 105

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	129.06585398		129.06585398	1	Q	20		
	258.10844707		258.10844707	2	E	19	2238.9968687	
	373.13539011		373.13539011	3	D	18	2109.9542756	
	474.18306858	+0.0707766	474.18306858	4	T	17	1994.9273326	
	611.24198044	-0.0302495	611.24198044	5	H	16	1893.8796541	
	724.32604442		724.32604442	6	I	15	1756.8207423	
	795.36315821		795.36315821	7	A	14	1643.7366783	+0.0892494
	910.39010124	+0.0144398	910.39010124	8	D	13	1572.6995645	+0.0675253
	1038.4486788		1038.4486788	9	Q	12	1457.6726215	+0.0464947
	1139.4963572		1139.4963572	10	T	11	1329.614044	+0.2583926
+0.2116403	627.76528836	-0.0267182	1254.5233003	11	D	10	1228.5663655	+0.0006511
	1355.5709787	+0.0766043	1355.5709787	12	T	9	1113.5394225	+0.0350404
	1483.6295562	+0.3280854	1483.6295562	13	Q	8	1012.491744	-0.0444173
	1598.6564993		1598.6564993	14	D	7	884.43316648	+0.0020752
+0.1773873	835.35044477		1669.6936131	15	A	6	769.40622344	
	1756.7256415		1756.7256415	16	S	5	698.36910966	-0.0663753
	1827.7627553		1827.7627553	17	A	4	611.33708125	
	1974.7981545		1974.7981545	18	M	3	540.29996746	+0.1120809
	2087.8822185		2087.8822185	19	I	2	393.26456823	+0.0458261
	2216.9248116		2216.9248116	20	E	1	280.18050425	
				21	K	0	151.13791115	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F01
Scannumber:	9418
Protein:	BSU17880; ynzC
Peptide Score:	108.56
Method:	ITMS; CID; 3





precursor information

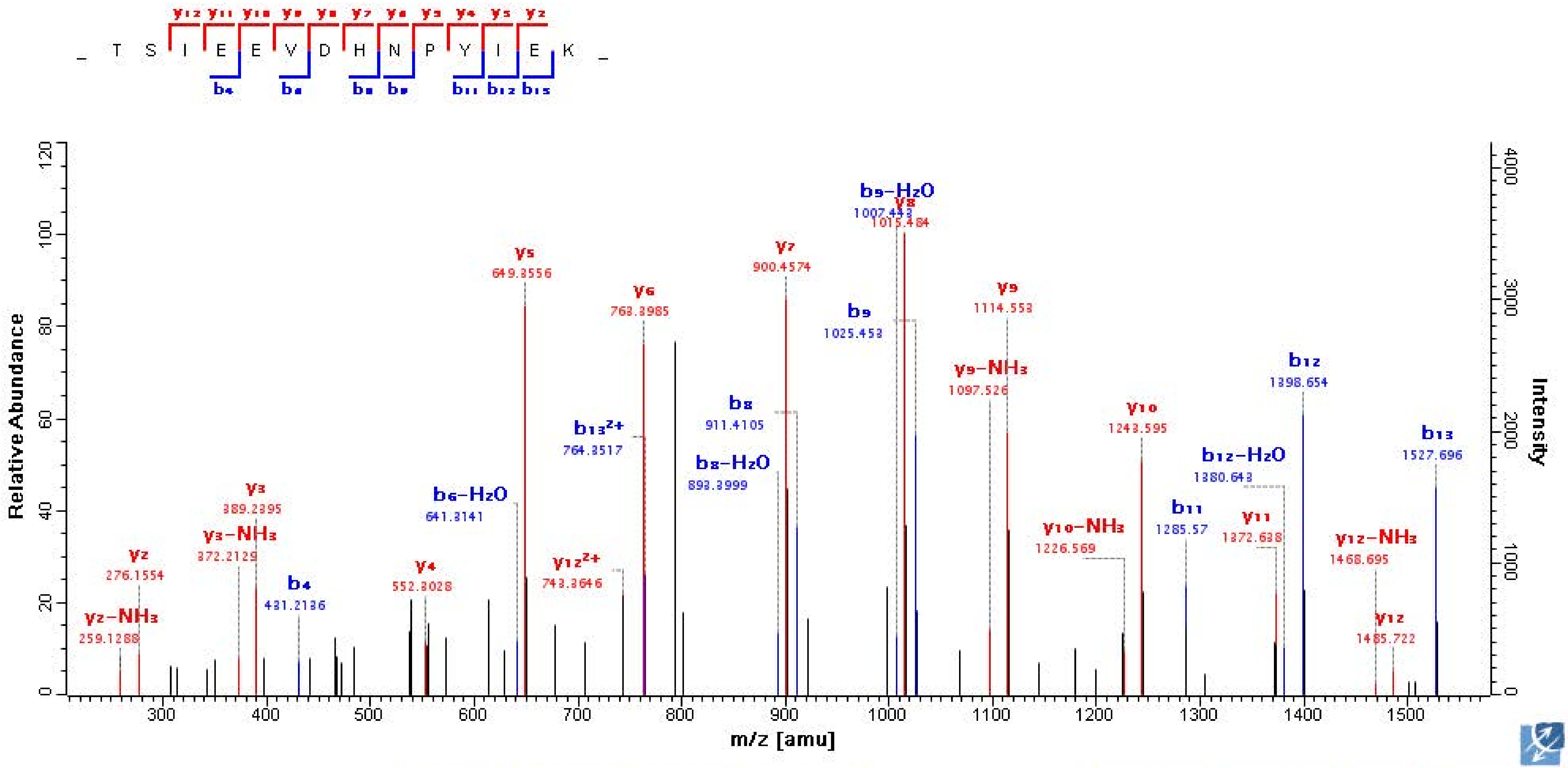
Mass:	1429.72455
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.5638
Mass Error [ppm]:	0.48965
PEP:	0.00015696
Precursor Type:	ISO

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	50 %
Protein Localisation:	54 ... 66

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	12				
+0.1237136	227.17540443	2	I	11	1317.6470587	+0.2405146	1317.6470587	
-0.0379798	342.20234746	3	D	10	1204.5629947	+0.0241635	602.78513557	+0.0669762
	439.25511131	4	P	9	1089.5360516	+0.034505	545.27166406	+0.3956943
	568.29770441	5	E	8	992.48328779	+0.2071419	992.48328779	
	625.31916813	6	G	7	863.4406947	-0.0538539	863.4406947	
	739.36209558	7	N	6	806.41923097	-0.0493579	806.41923097	
	854.38903861	8	D	5	692.37630352		692.37630352	
+0.1416075	953.45745253	9	V	4	577.34936049		577.34936049	
+0.0657919	1054.505131	10	T	3	478.28094658	-0.0150774	478.28094658	
	1151.5578949	11	P	2	377.2332681	+0.0224082	377.2332681	
-0.0610592	1280.6004879	12	E	1	280.18050425		280.18050425	
		13	K	0	151.13791115		151.13791115	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F02
Scannumber: 13263
Protein: BSU00140; dak; dck; yaaF
Peptide Score: 162.31
Method: ITMS; CID; 3



precursor information

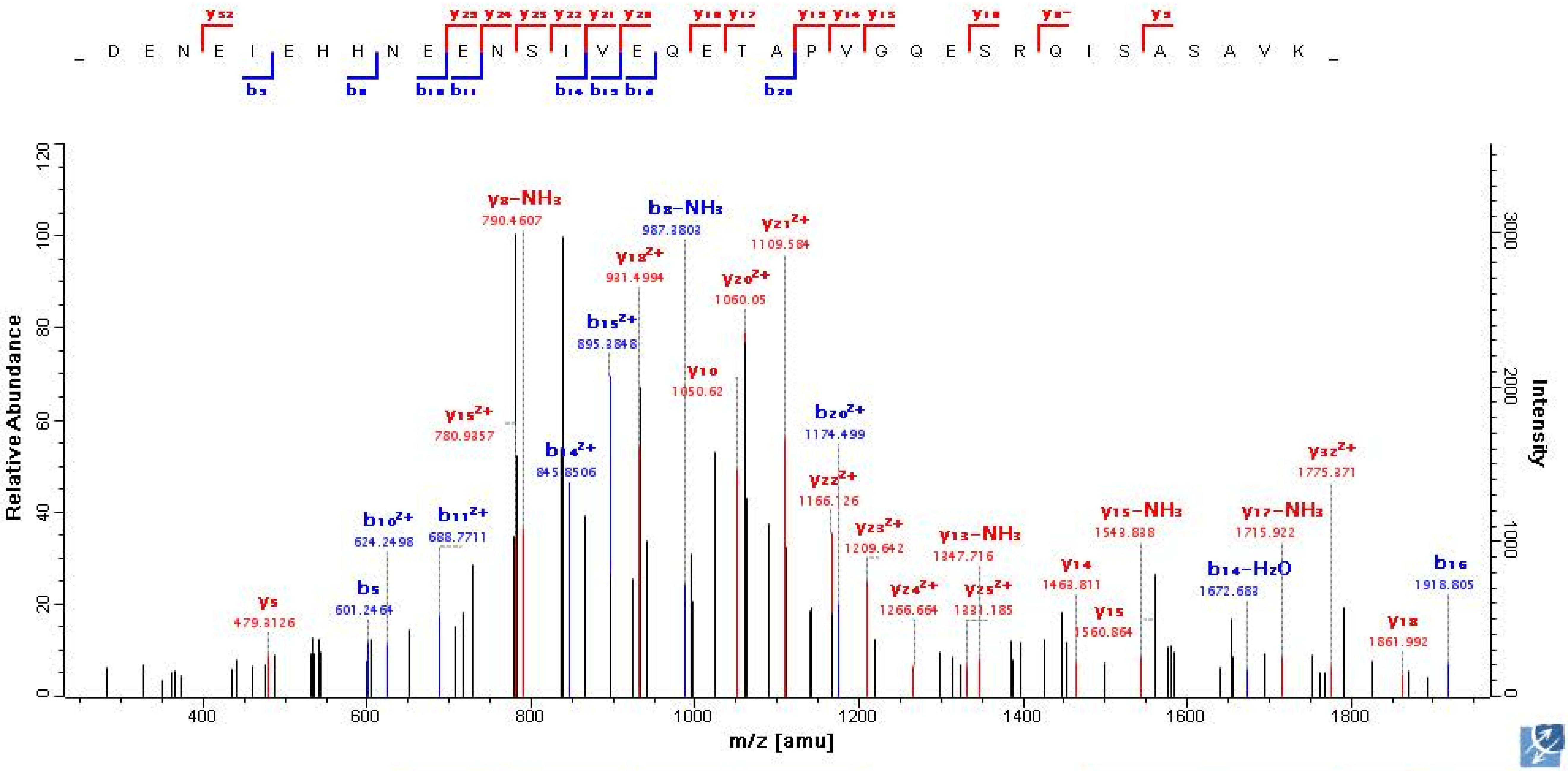
Mass:	1672.79286
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	162.3062
Mass Error [ppm]:	-0.93856
PEP:	9.7344E-19
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	54 %
Protein Localisation:	37 ... 50

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	13				
	189.087		189.087	2	S	12	1572.754		1572.754	
	302.171		302.171	3	I	11	1485.722	+0.233688	743.3646	+0.048142
	431.2136	+0.059126	431.2136	4	E	10	1372.638	+0.062503	1372.638	
	560.2562		560.2562	5	E	9	1243.595	-0.020758	1243.595	
	659.3246		659.3246	6	V	8	1114.553	-0.018814	1114.553	
	774.3516		774.3516	7	D	7	1015.484	+0.038735	1015.484	
	911.4105	+0.069783	911.4105	8	H	6	900.4574	+0.019353	900.4574	
	1025.453	+0.043763	1025.453	9	N	5	763.3985	-0.009687	763.3985	
	1122.506		1122.506	10	P	4	649.3556	+0.029883	649.3556	
	1285.57	+0.053281	1285.57	11	Y	3	552.3028	-0.023127	552.3028	
	1398.654	+0.132913	1398.654	12	I	2	389.2395	-0.076925	389.2395	
+0.005938	764.3517	+0.093127	1527.696	13	E	1	276.1554	+0.069243	276.1554	
				14	K	0	147.1128		147.1128	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F02
Scannumber: 15407
Protein: BSU36570; ywnG
Peptide Score: 56.85
Method: ITMS; CID; 3



precursor information

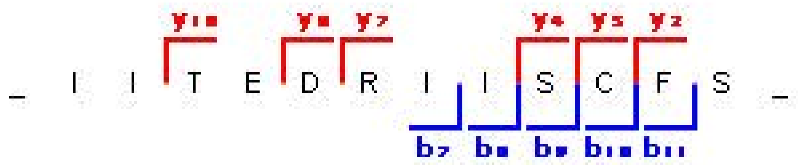
Mass:	3902.81387
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	56.85416
Mass Error [ppm]:	-0.40735
PEP:	4.6257E-07
Precursor Type:	MULTI

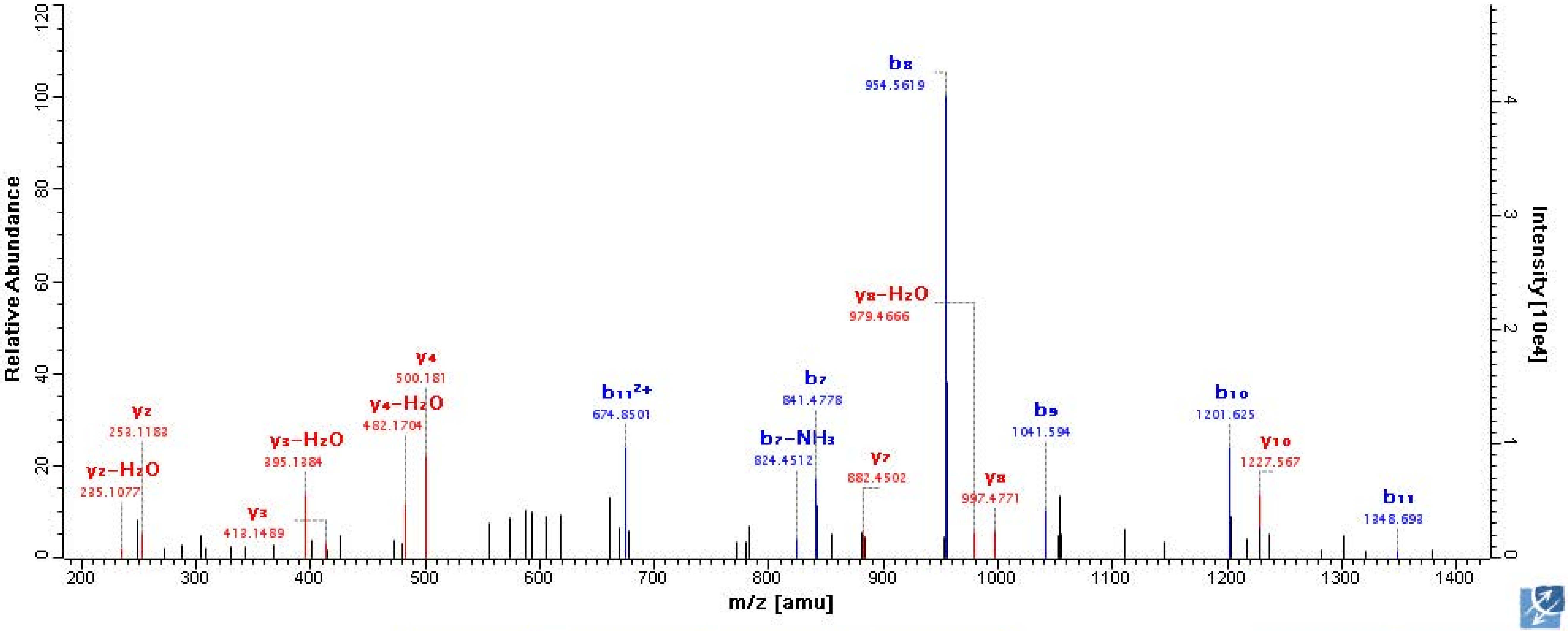
b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342		116.0342	1	D	34				
	245.0768		245.0768	2	E	33	3792.821		3792.821	
	359.1197		359.1197	3	N	32	3663.778		3663.778	
	488.1623		488.1623	4	E	31	3549.735		1775.371	-0.343496
	601.2464	+0.202272	601.2464	5	I	30	3420.693		3420.693	
	730.289		730.289	6	E	29	3307.609		3307.609	
	867.3479		867.3479	7	H	28	3178.566		3178.566	
	1004.407		1004.407	8	H	27	3041.507		3041.507	
	1118.45		1118.45	9	N	26	2904.448		2904.448	
+0.073009	624.2498		1247.492	10	E	25	2790.405		2790.405	
+0.042314	688.7711		1376.535	11	E	24	2661.363		1331.185	+0.158841
	1490.578		1490.578	12	N	23	2532.32		1266.664	-0.45414
	1577.61		1577.61	13	S	22	2418.277		1209.642	+0.375185
-0.094569	845.8506		1690.694	14	I	21	2331.245		1166.126	+0.132533
+0.390511	895.3848		1789.762	15	V	20	2218.161		1109.584	+0.159428
	1918.805	-0.001854	1918.805	16	E	19	2119.093		1060.05	+0.057771
	2046.864		2046.864	17	Q	18	1990.05		1990.05	
	2175.906		2175.906	18	E	17	1861.992	-0.244273	931.4994	+0.036945
	2276.954		2276.954	19	T	16	1732.949		1732.949	
+0.172656	1174.499		2347.991	20	A	15	1631.901		1631.901	
	2445.044		2445.044	21	P	14	1560.864	-0.161077	780.9357	+0.286612
	2544.112		2544.112	22	V	13	1463.811	-0.060096	1463.811	
	2601.134		2601.134	23	G	12	1364.743		1364.743	
	2729.192		2729.192	24	Q	11	1307.722		1307.722	
	2858.235		2858.235	25	E	10	1179.663		1179.663	
	2945.267		2945.267	26	S	9	1050.62	-0.155669	1050.62	
	3101.368		3101.368	27	R	8	963.5884		963.5884	
	3229.426		3229.426	28	Q	7	807.4873		807.4873	
	3342.511		3342.511	29	I	6	679.4287		679.4287	
	3429.543		3429.543	30	S	5	566.3446		566.3446	
	3500.58		3500.58	31	A	4	479.3126	+0.132121	479.3126	
	3587.612		3587.612	32	S	3	408.2755		408.2755	
	3658.649		3658.649	33	A	2	321.2434		321.2434	
	3757.717		3757.717	34	V	1	250.2063		250.2063	
				35	K	0	151.1379		151.1379	

general information

Annotation:	19 of 35
AminoAcids Coverag	54 %
Intensity Coverage:	32 %
Protein Localisation:	7 ... 41

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F02
Scannumber: 21008
Protein: BSU24890; yqgN
Peptide Score: 98.16
Method: ITMS; CID; 3





precursor information

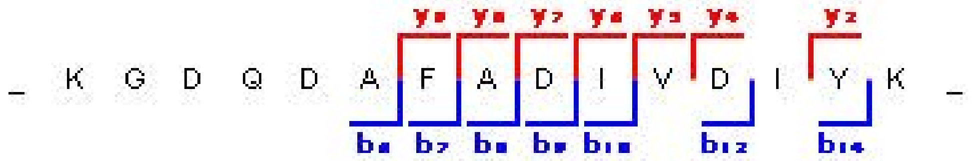
Mass:	1452.72788
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	98.15634
Mass Error [ppm]:	-0.26373
PEP:	0.0019519
Precursor Type:	ISO

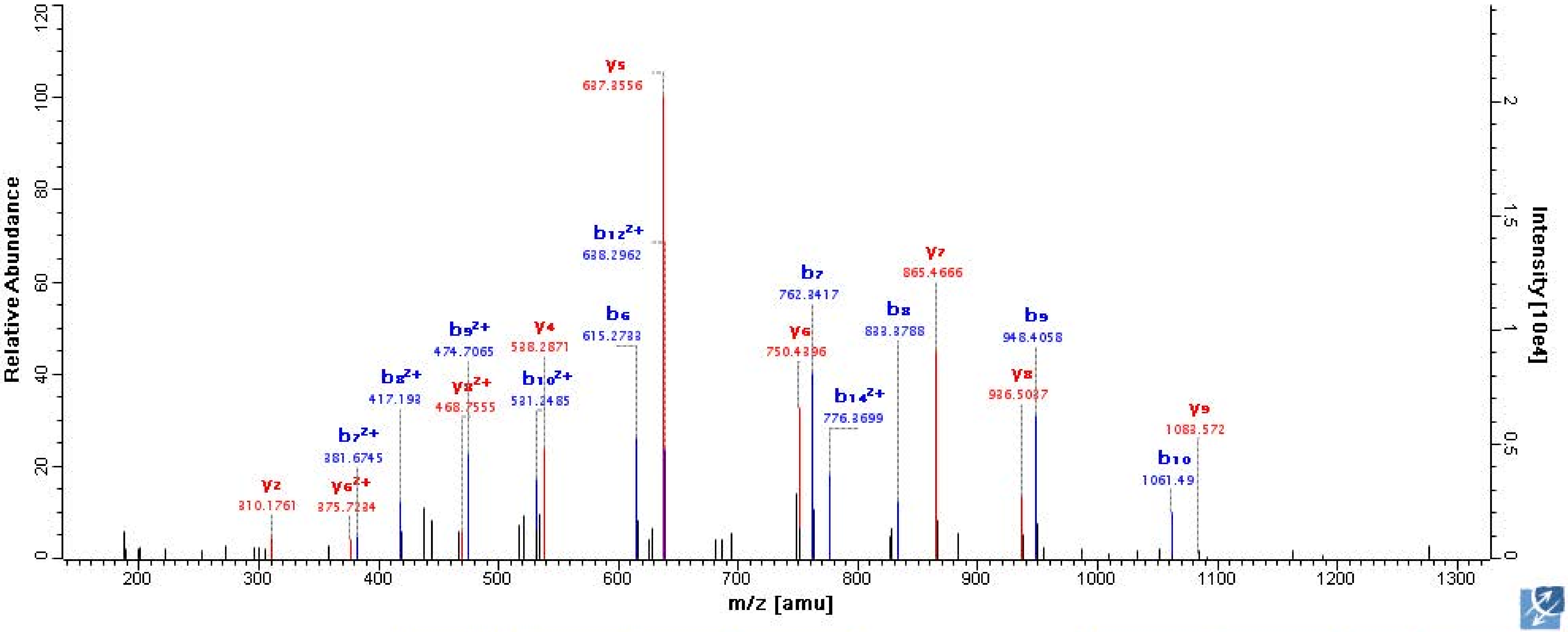
general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	48 %
Protein Localisation:	176 ... 187

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	114.09134045		114.09134045	1	I	11		
	227.17540443		227.17540443	2	I	10	1340.6514777	
	328.2230829		328.2230829	3	T	9	1227.5674137	+0.1060482
	457.265676		457.265676	4	E	8	1126.5197352	
	572.29261903		572.29261903	5	D	7	997.47714211	+0.2605288
	728.39373006		728.39373006	6	R	6	882.45019908	+0.1112633
	841.47779404	-0.0102647	841.47779404	7	I	5	726.34908805	
	954.56185802	+0.0243236	954.56185802	8	I	4	613.26502407	
	1041.5938864	+0.1542825	1041.5938864	9	S	3	500.18096009	-0.0439972
	1201.6245346	+0.1846695	1201.6245346	10	C	2	413.14893168	+0.2542666
+0.4602513	674.85011251	+0.2621296	1348.6929485	11	F	1	253.11828348	-0.0486576
				12	S	0	106.04986956	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F02
Scannumber:	22311
Protein:	BSU01730; sigW; ybbL
Peptide Score:	115.12
Method:	ITMS; CID; 3





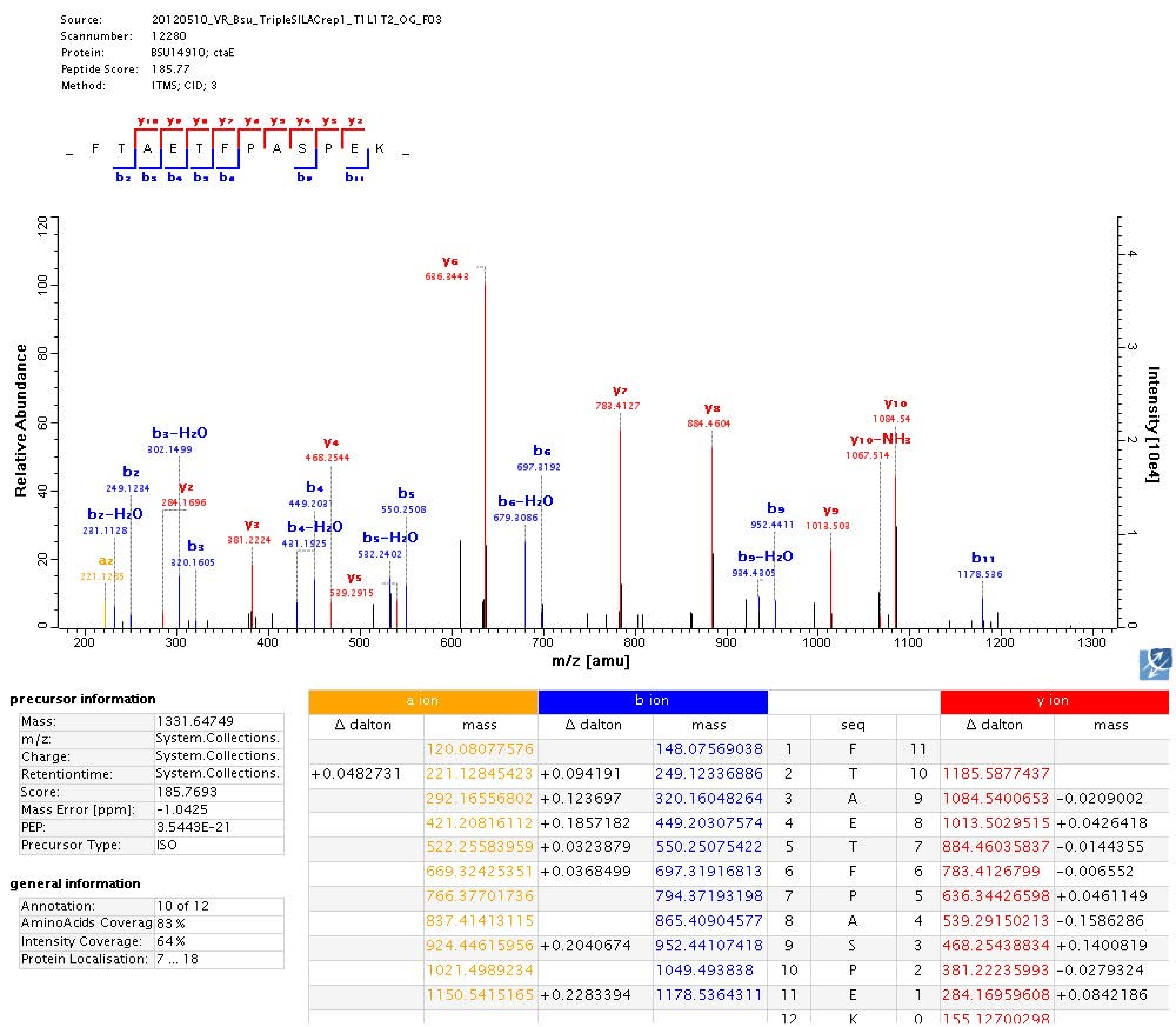
precursor information

Mass:	1696.83023
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.1193
Mass Error [ppm]:	-0.34805
PEP:	1.4376E-05
Precursor Type:	MULTI

general information

Annotation:	8 of 15
AminoAcids Coverag	53 %
Intensity Coverage:	68 %
Protein Localisation:	14 ... 28

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	14				
	186.1237		186.1237	2	G	13	1569.743		1569.743	
	301.1506		301.1506	3	D	12	1512.722		1512.722	
	429.2092		429.2092	4	Q	11	1397.695		1397.695	
	544.2362		544.2362	5	D	10	1269.636		1269.636	
	615.2733	+0.080784	615.2733	6	A	9	1154.609		1154.609	
+0.272109	381.6745	+0.078899	762.3417	7	F	8	1083.572	+0.482721	1083.572	
+0.138989	417.193	+0.119666	833.3788	8	A	7	936.5037	+0.047534	468.7555	+0.089068
+0.030547	474.7065	+0.20045	948.4058	9	D	6	865.4666	-0.019112	865.4666	
+0.097218	531.2485	+0.121879	1061.49	10	I	5	750.4396	+0.274677	375.7234	+0.390933
	1160.558		1160.558	11	V	4	637.3556	+0.044044	637.3556	
+0.052225	638.2962		1275.585	12	D	3	538.2871	+0.065888	538.2871	
	1388.669		1388.669	13	I	2	423.2602		423.2602	
+0.232802	776.3699		1551.733	14	Y	1	310.1761	+0.027175	310.1761	
				15	K	0	147.1128		147.1128	



Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F03
Scannumber: 12280
Protein: BSU14910; ctaE
Peptide Score: 185.77
Method: ITMS; CID; 3

precursor information

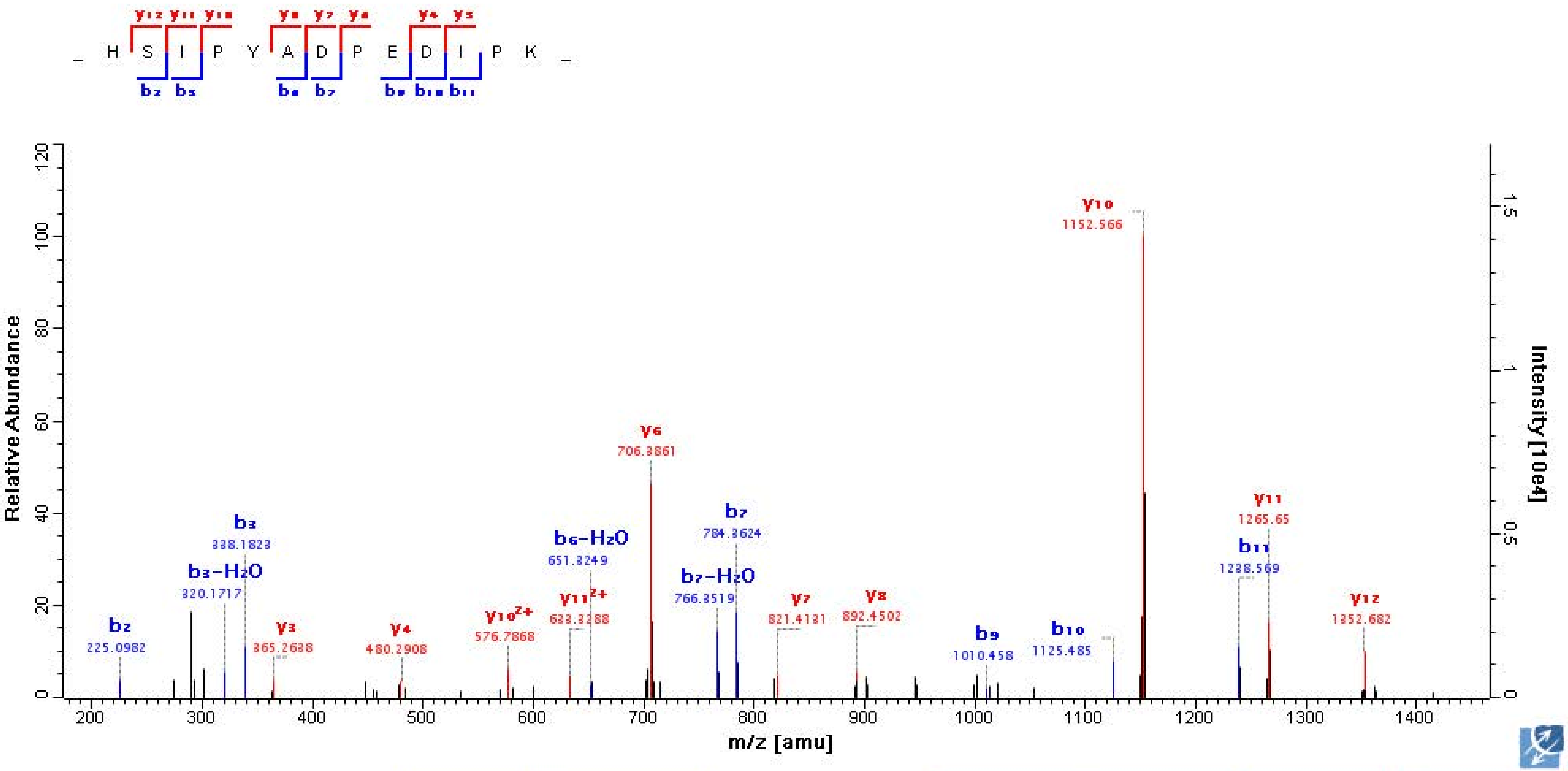
Mass:	1331.64749
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	185.7693
Mass Error [ppm]:	-1.0425
PEP:	3.5443E-21
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	64 %
Protein Localisation:	7 ... 18

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	120.08077576		148.07569038	1	F	11		
+0.0482731	221.12845423	+0.094191	249.12336886	2	T	10	1185.5877437	
	292.16556802	+0.123697	320.16048264	3	A	9	1084.5400653	-0.0209002
	421.20816112	+0.1857182	449.20307574	4	E	8	1013.5029515	+0.0426418
	522.25583959	+0.0323879	550.25075422	5	T	7	884.46035837	-0.0144355
	669.32425351	+0.0368499	697.31916813	6	F	6	783.4126799	-0.006552
	766.37701736		794.37193198	7	P	5	636.34426598	+0.0461149
	837.41413115		865.40904577	8	A	4	539.29150213	-0.1586286
	924.44615956	+0.2040674	952.44107418	9	S	3	468.25438834	+0.1400819
	1021.4989234		1049.493838	10	P	2	381.22235993	-0.0279324
	1150.5415165	+0.2283394	1178.5364311	11	E	1	284.16959608	+0.0842186
				12	K	0	155.12700298	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F03
Scannumber: 13106
Protein: BSU01510; ybaJ
Peptide Score: 106.49
Method: ITMS; CID; 3



precursor information

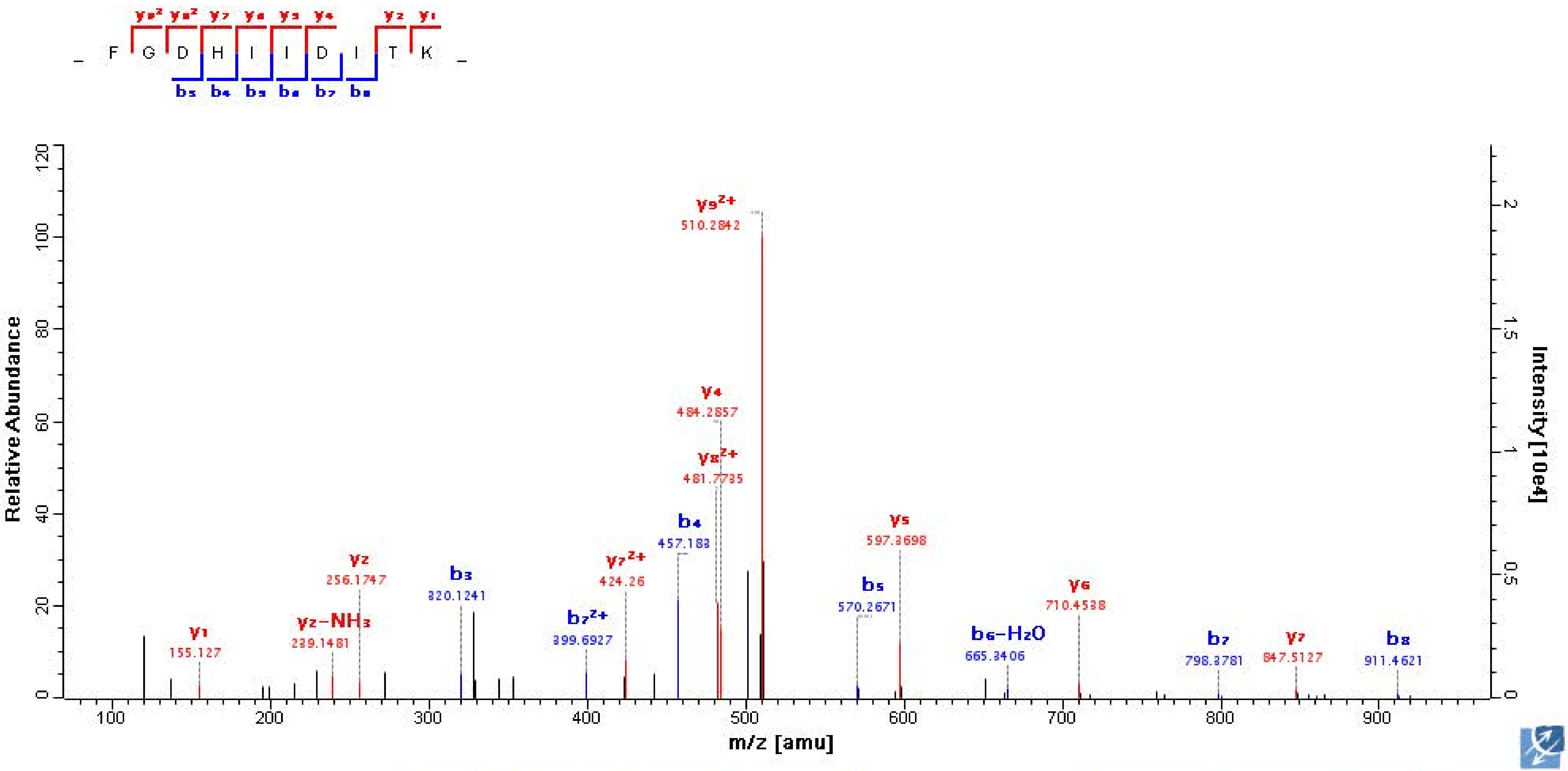
Mass:	1480.72003
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	106.492
Mass Error [ppm]:	0.15079
PEP:	0.0011513
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	52 %
Protein Localisation:	183 ... 195

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	138.06618833	1	H	12				
+0.1496318	225.09821674	2	S	11	1352.6823724	+0.2260749	1352.6823724	
-0.0212395	338.18228072	3	I	10	1265.650344	-0.0015403	633.32881023	-0.1457048
	435.23504457	4	P	9	1152.56628	+0.0070843	576.78677824	-0.0469711
	598.29837311	5	Y	8	1055.5135162		1055.5135162	
	669.3354869	6	A	7	892.45018762	+0.0263749	892.45018762	
+0.0535857	784.36242993	7	D	6	821.41307383	+0.2686278	821.41307383	
	881.41519378	8	P	5	706.3861308	-0.0314555	706.3861308	
+0.2080456	1010.4577869	9	E	4	609.33336694		609.33336694	
+0.0308951	1125.4847299	10	D	3	480.29077385	-0.1460595	480.29077385	
+0.021294	1238.5687939	11	I	2	365.26383082	+0.106439	365.26383082	
	1335.6215577	12	P	1	252.17976684		252.17976684	
		13	K	0	155.12700298		155.12700298	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F04
Scannumber:	16594
Protein:	BSU17610; xylB; yncA
Peptide Score:	105.4
Method:	ITMS; CID; 3



precursor information

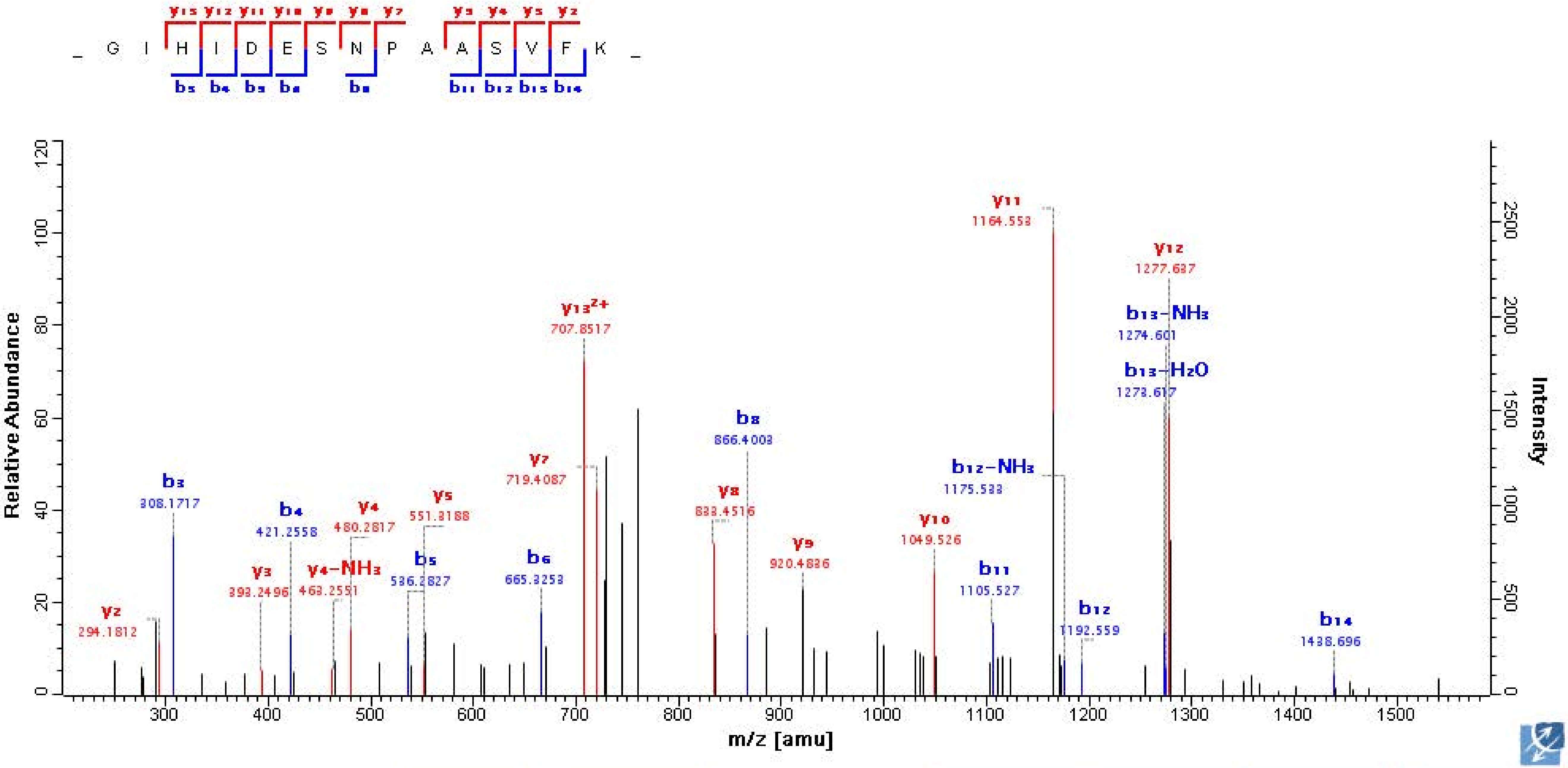
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.3963
Mass Error [ppm]:	-0.45675
PEP:	0.00017912
Precursor Type:	PEAK

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	56 %
Protein Localisation:	116 ... 125

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.0757		148.0757	1	F	9				
	205.0972		205.0972	2	G	8	1019.561		510.2842	+0.034764
	320.1241	+0.041674	320.1241	3	D	7	962.5397		481.7735	+0.297022
	457.183	-0.064601	457.183	4	H	6	847.5127	+0.250883	424.26	+0.233406
	570.2671	-0.022078	570.2671	5	I	5	710.4538	+0.130473	710.4538	
	683.3511		683.3511	6	I	4	597.3698	+0.084715	597.3698	
-0.05657	399.6927	+0.375277	798.3781	7	D	3	484.2857	+0.03084	484.2857	
	911.4621	+0.095839	911.4621	8	I	2	369.2587		369.2587	
	1012.51		1012.51	9	T	1	256.1747	+0.0011	256.1747	
				10	K	0	155.127	+0.173702	155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F04
Scannumber:	17509
Protein:	BSU04060; ycsG; ycsH
Peptide Score:	113.25
Method:	ITMS; CID; 3



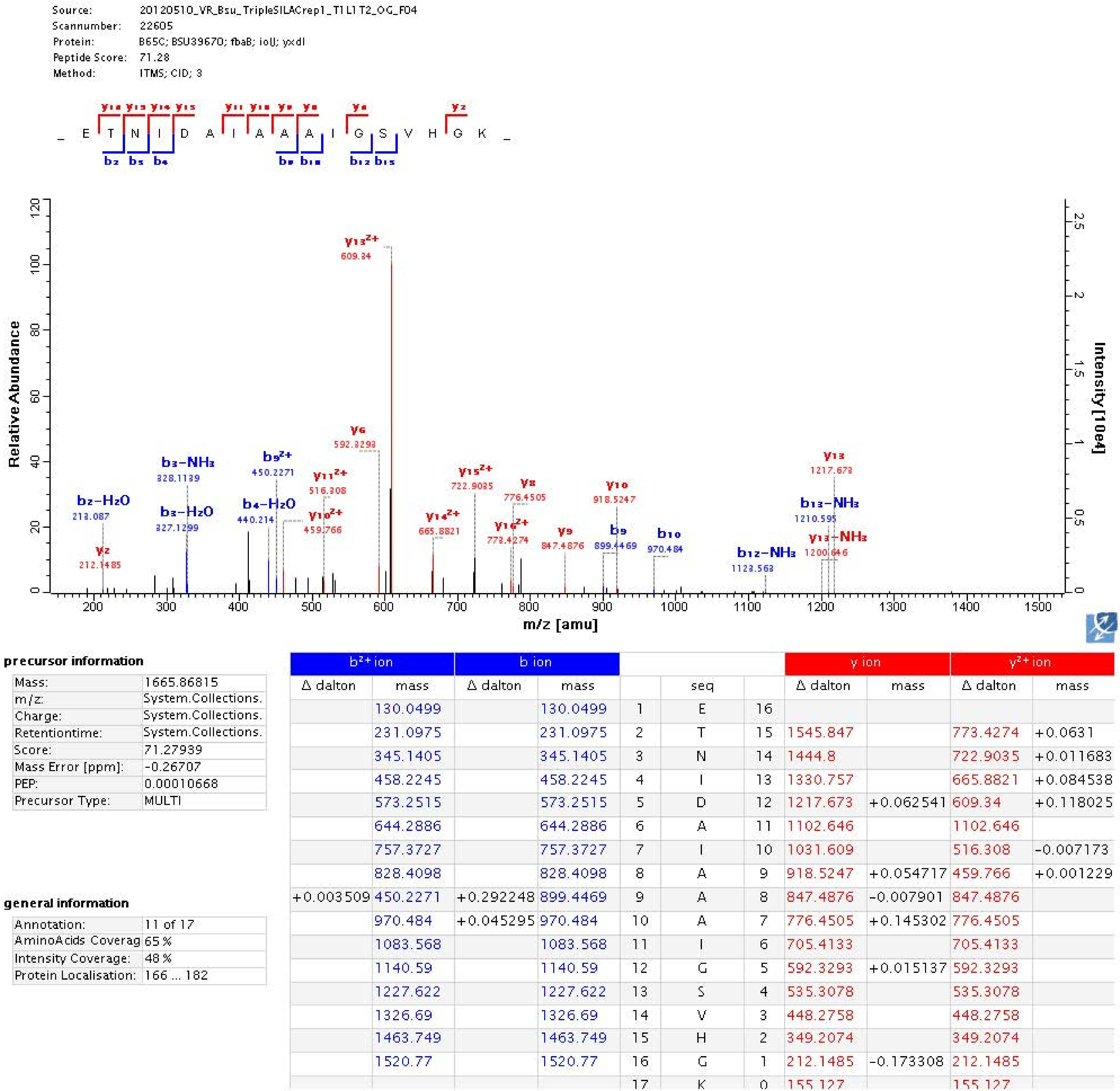
precursor information

Mass:	1583.79476
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.2528
Mass Error [ppm]:	0.24395
PEP:	3.7413E-07
Precursor Type:	ISO

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	47 %
Protein Localisation:	255 ... 269

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	14				
	171.11280417	2	I	13	1527.7801836		1527.7801836	
+0.1403567	308.17171603	3	H	12	1414.6961197		707.85169807	+0.2475451
+0.1324646	421.25578001	4	I	11	1277.6372078	+0.1051018	1277.6372078	
+0.0113443	536.28272305	5	D	10	1164.5531438	+0.095782	1164.5531438	
-0.0098865	665.32531614	6	E	9	1049.5262008	+0.129683	1049.5262008	
	752.35734455	7	S	8	920.4836077	-0.0022234	920.4836077	
+0.0463833	866.400272	8	N	7	833.45157929	+0.2279251	833.45157929	
	963.45303585	9	P	6	719.40865184	+0.0312285	719.40865184	
	1034.4901496	10	A	5	622.35588799		622.35588799	
+0.3296702	1105.5272634	11	A	4	551.3187742	-0.2374143	551.3187742	
+0.2230568	1192.5592918	12	S	3	480.28166041	+0.25197	480.28166041	
	1291.6277058	13	V	2	393.249632	+0.1968707	393.249632	
+0.2416245	1438.6961197	14	F	1	294.18121809	+0.1250258	294.18121809	
		15	K	0	147.11280417		147.11280417	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F04
Scannumber:	22605
Protein:	B65C; BSU39670; fbaB; iolJ; yxdI
Peptide Score:	71.28
Method:	ITMS; CID; 3

precursor information

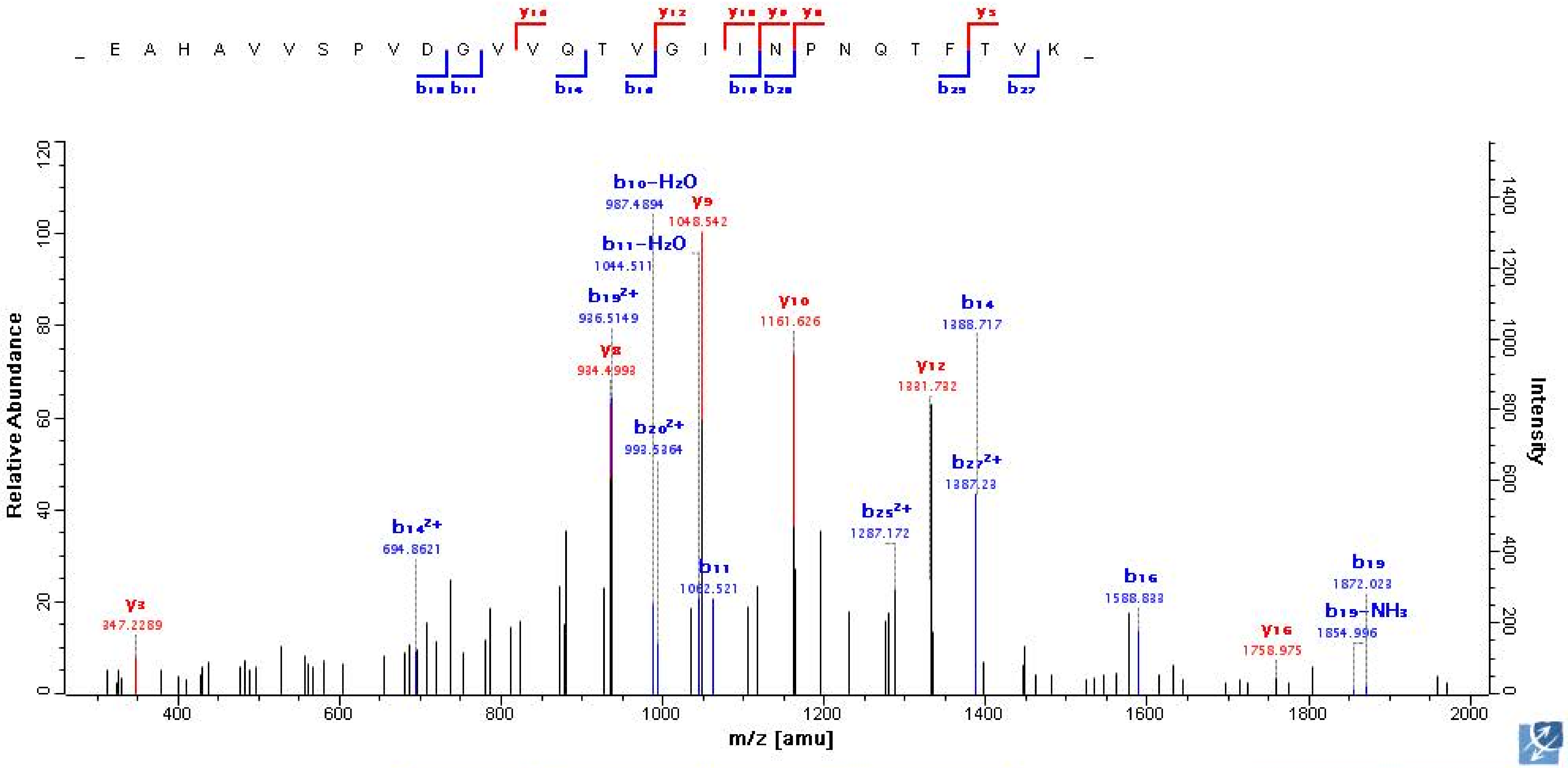
Mass:	1665.86815
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.27939
Mass Error [ppm]:	-0.26707
PEP:	0.00010668
Precursor Type:	MULTI

general information

Annotation:	11 of 17
AminoAcids Coverag	65 %
Intensity Coverage:	48 %
Protein Localisation:	166 ... 182

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	16				
	231.0975		231.0975	2	T	15	1545.847		773.4274	+0.0631
	345.1405		345.1405	3	N	14	1444.8		722.9035	+0.011683
	458.2245		458.2245	4	I	13	1330.757		665.8821	+0.084538
	573.2515		573.2515	5	D	12	1217.673	+0.062541	609.34	+0.118025
	644.2886		644.2886	6	A	11	1102.646		1102.646	
	757.3727		757.3727	7	I	10	1031.609		516.308	-0.007173
	828.4098		828.4098	8	A	9	918.5247	+0.054717	459.766	+0.001229
+0.003509	450.2271	+0.292248	899.4469	9	A	8	847.4876	-0.007901	847.4876	
	970.484	+0.045295	970.484	10	A	7	776.4505	+0.145302	776.4505	
	1083.568		1083.568	11	I	6	705.4133		705.4133	
	1140.59		1140.59	12	G	5	592.3293	+0.015137	592.3293	
	1227.622		1227.622	13	S	4	535.3078		535.3078	
	1326.69		1326.69	14	V	3	448.2758		448.2758	
	1463.749		1463.749	15	H	2	349.2074		349.2074	
	1520.77		1520.77	16	G	1	212.1485	-0.173308	212.1485	
				17	K	0	155.127		155.127	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F04
Scannumber: 25713
Protein: BSU02290; psd
Peptide Score: 50.5
Method: ITMS; CID; 3



precursor information

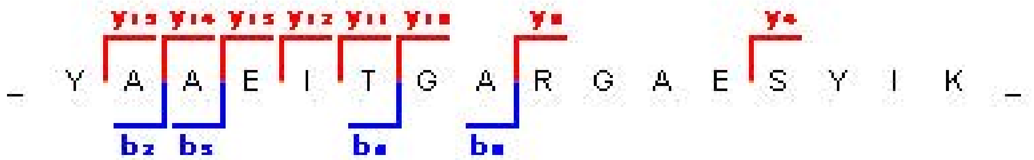
Mass:	2918.55126
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	50.4978
Mass Error [ppm]:	0.37273
PEP:	0.0015926
Precursor Type:	ISO

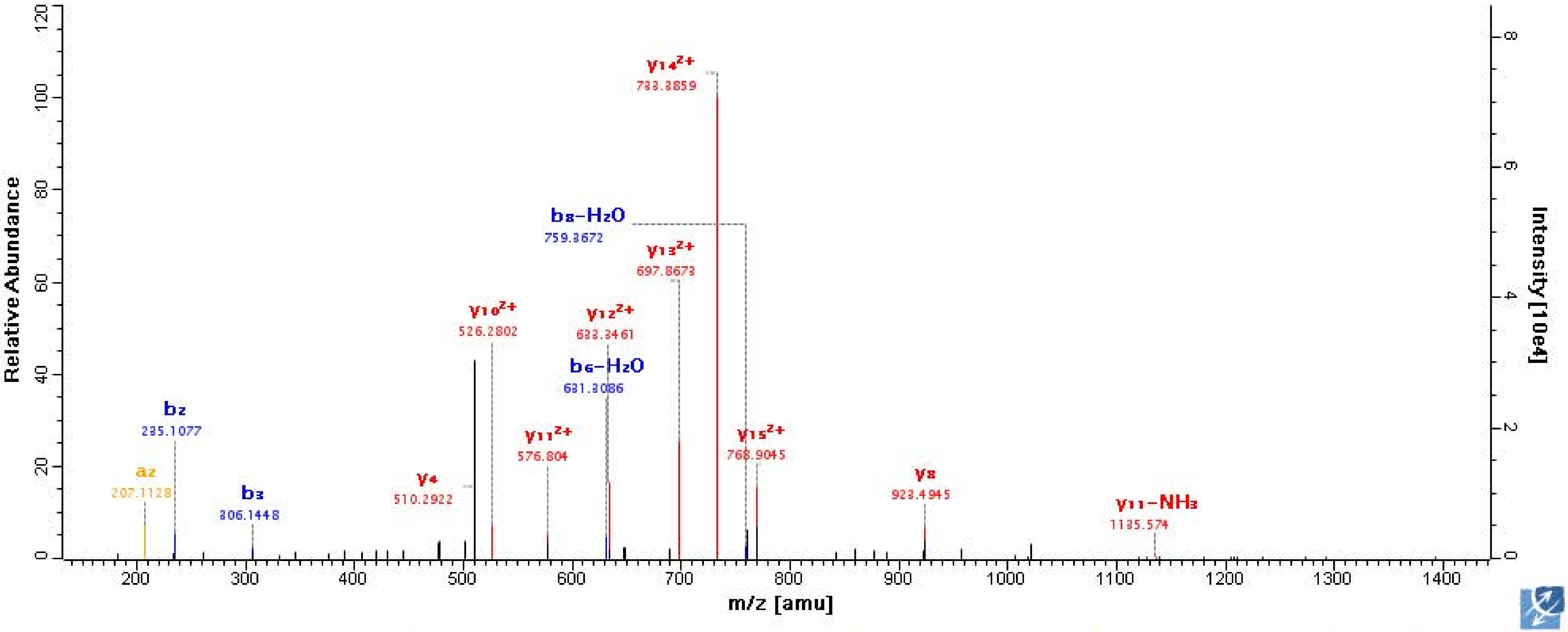
general information

Annotation:	15 of 28
AminoAcids Coverag	54 %
Intensity Coverage:	35 %
Protein Localisation:	81 ... 108

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	130.04986956		130.04986956	1	E	27		
	201.08698335		201.08698335	2	A	26	2790.5148548	
	338.14589521		338.14589521	3	H	25	2719.477741	
	409.183009		409.183009	4	A	24	2582.4188292	
	508.25142292		508.25142292	5	V	23	2511.3817154	
	607.31983683		607.31983683	6	V	22	2412.3133015	
	694.35186524		694.35186524	7	S	21	2313.2448876	
	791.4046291		791.4046291	8	P	20	2226.2128592	
	890.47304301		890.47304301	9	V	19	2129.1600953	
	1005.499986		1005.499986	10	D	18	2030.0916814	
	1062.5214498	-0.1838033	1062.5214498	11	G	17	1915.0647384	
	1161.5898637		1161.5898637	12	V	16	1858.0432746	
	1260.6582776		1260.6582776	13	V	15	1758.9748607	+0.2755055
+0.2095895	694.86206579	-0.4308444	1388.7168551	14	Q	14	1659.9064468	
	1489.7645336		1489.7645336	15	T	13	1531.8478693	
	1588.8329475	+0.0896599	1588.8329475	16	V	12	1430.8001908	
	1645.8544112		1645.8544112	17	G	11	1331.7317769	+0.2148784
	1758.9384752		1758.9384752	18	I	10	1274.7103132	
+0.3921967	936.51490783	+0.2826366	1872.0225392	19	I	9	1161.6262492	+0.0206014
+0.4442803	993.53637155		1986.0654666	20	N	8	1048.5421852	+0.0637718
	2083.1182305		2083.1182305	21	P	7	934.49925776	+0.1786597
	2197.1611579		2197.1611579	22	N	6	837.44649391	
	2325.2197354		2325.2197354	23	Q	5	723.40356646	
	2426.2674139		2426.2674139	24	T	4	595.34498895	
+0.1452203	1287.1715522		2573.3358278	25	F	3	494.29731048	
	2674.3835063		2674.3835063	26	T	2	347.22889656	+0.1514745
-0.0278161	1387.2295983		2773.4519202	27	V	1	246.18121809	
				28	K	0	147.11280417	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber: 15712
Protein: BSU02260; ybfK
Peptide Score: 71.24
Method: ITMS; CID; 3





precursor information

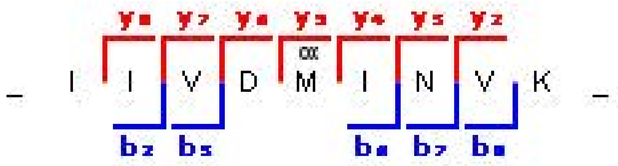
Mass:	1698.85965
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	71.24082
Mass Error [ppm]:	1.1465
PEP:	0.011645
Precursor Type:	ISO

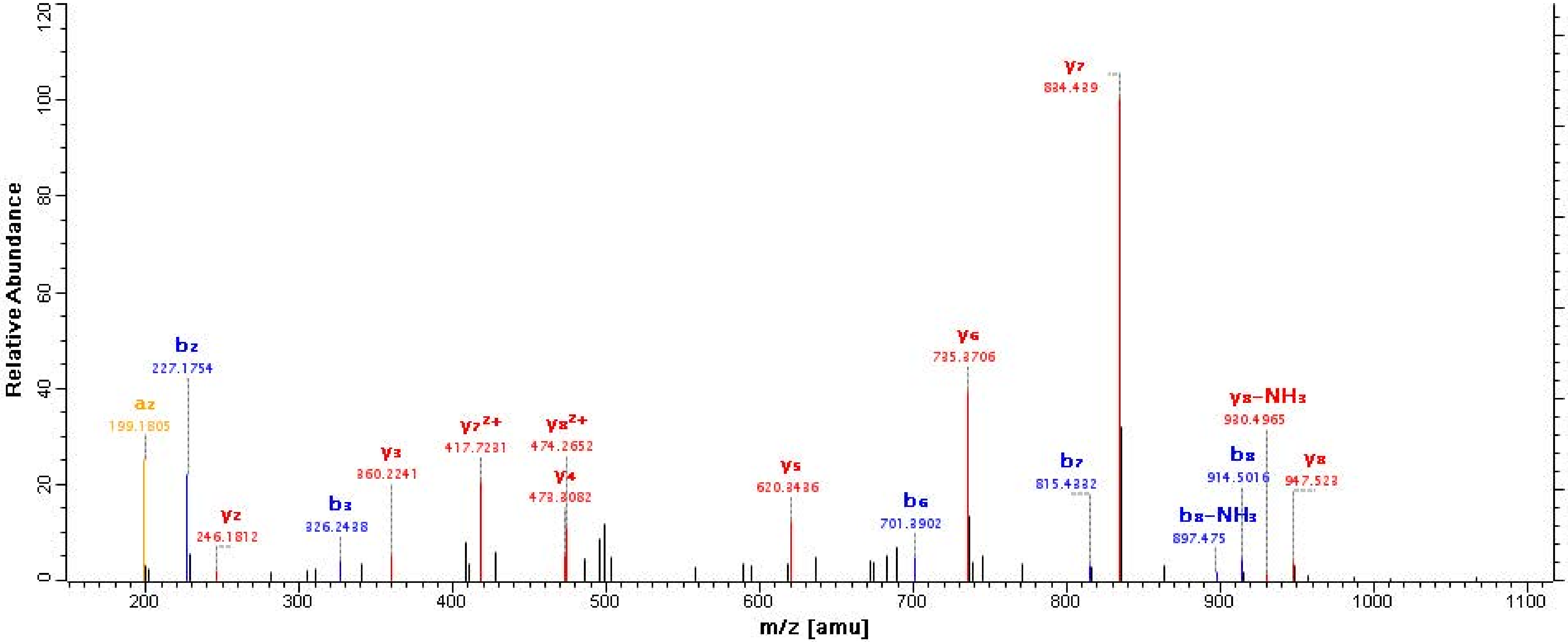
general information

Annotation:	9 of 16
AminoAcids Coverag	56 %
Intensity Coverage:	63 %
Protein Localisation:	168 ... 183

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	15				
+0.16634	207.1128	-0.046424	235.1077	2	A	14	1536.802		768.9045	+0.105914
	278.1499	+0.049107	306.1448	3	A	13	1465.765		733.3859	+0.261739
	407.1925		435.1874	4	E	12	1394.727		697.8673	+0.289268
	520.2766		548.2715	5	I	11	1265.685		633.3461	+0.077105
	621.3243		649.3192	6	T	10	1152.601		576.804	+0.040158
	678.3457		706.3406	7	G	9	1051.553		526.2802	+0.089388
	749.3828		777.3777	8	A	8	994.5316		994.5316	
	905.4839		933.4789	9	R	7	923.4945	+0.046814	923.4945	
	962.5054		990.5003	10	G	6	767.3934		767.3934	
	1033.543		1061.537	11	A	5	710.3719		710.3719	
	1162.585		1190.58	12	E	4	639.3348		639.3348	
	1249.617		1277.612	13	S	3	510.2922	-0.165272	510.2922	
	1412.68		1440.675	14	Y	2	423.2602		423.2602	
	1525.765		1553.759	15	I	1	260.1969		260.1969	
				16	K	0	147.1128		147.1128	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber: 17408
Protein: BSU03460; hxlA; yckG
Peptide Score: 118.33
Method: ITMS; CID; 3



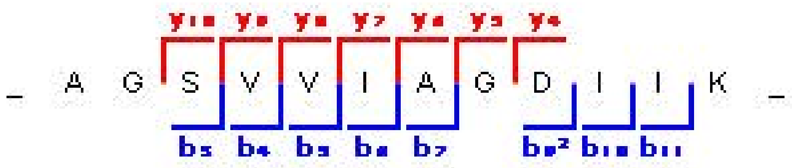


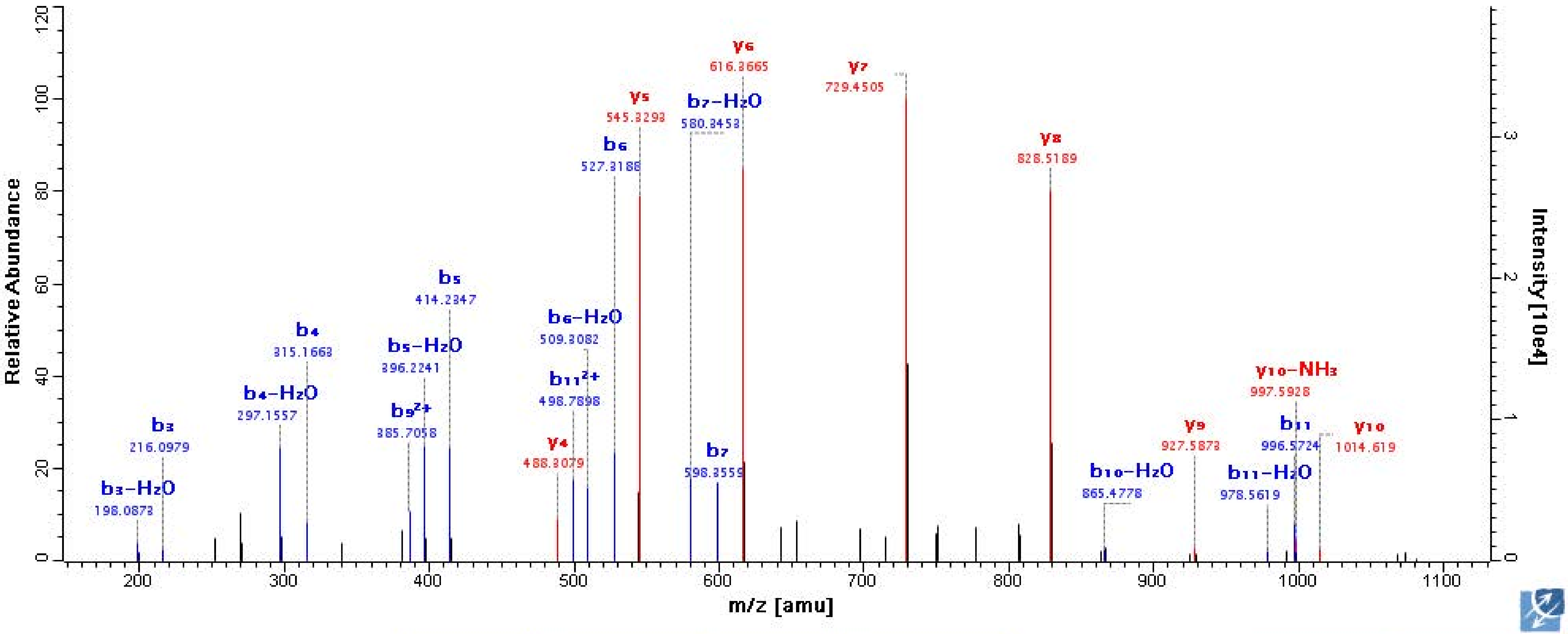
precursor information

Mass:	1059.60022
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	118.3341
Mass Error [ppm]:	0.37768
PEP:	0.0015587
g Precursor Type:	ISO
Annotation:	7 of 9
AminoAcids Coverag	78 %
Intensity Coverage:	60 %
Protein Localisation:	106 ... 114

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	8				
-0.07496	199.1805	-0.064015	227.1754	2	I	7	947.523	+0.09605	474.2652	+0.050521
	298.2489	+0.174639	326.2438	3	V	6	834.439	+0.009704	417.7231	+0.195885
	413.2758		441.2708	4	D	5	735.3706	+0.031182	735.3706	
	560.3112		588.3062	5	M	4	620.3436	+0.0201	620.3436	
	673.3953	+0.081028	701.3902	6	I	3	473.3082	+0.202655	473.3082	
	787.4382	-0.066087	815.4332	7	N	2	360.2241	-0.026483	360.2241	
	886.5067	+0.047262	914.5016	8	V	1	246.1812	+0.123042	246.1812	
				9	K	0	147.1128		147.1128	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber: 19845
Protein: BSU18070; plsY; yneS
Peptide Score: 180.07
Method: ITMS; CID; 3





precursor information

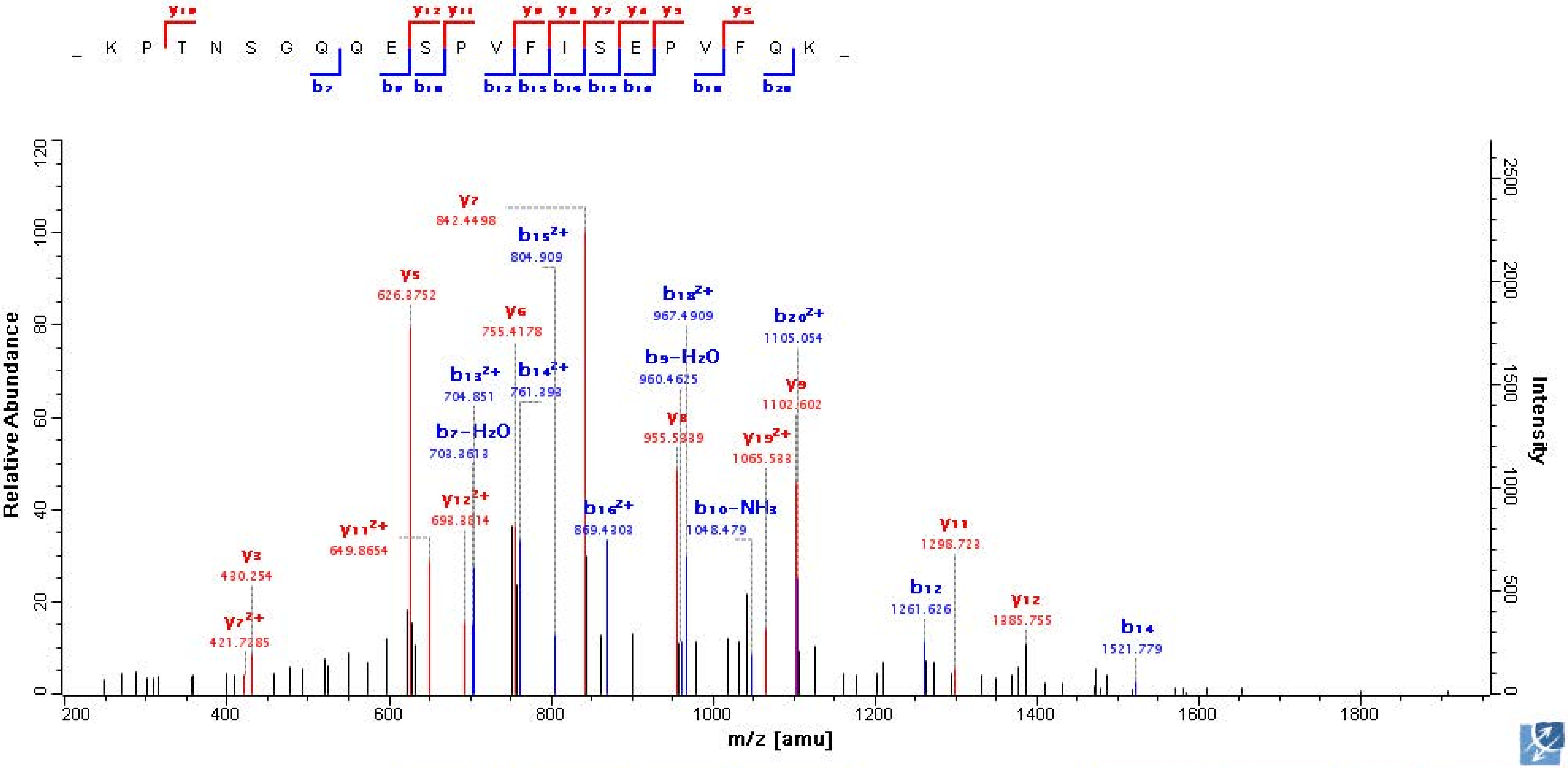
Mass:	1141.67048
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	180.0659
Mass Error [ppm]:	-0.17149
PEP:	4.0071E-26
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	72 %
Protein Localisation:	52 ... 63

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	11		
	129.06585398		129.06585398	2	G	10	1071.6408366	
	216.09788239	+0.0317258	216.09788239	3	S	9	1014.6193729	+0.1070065
	315.1662963	-0.0906737	315.1662963	4	V	8	927.58734449	+0.1655852
	414.23471022	-0.0854182	414.23471022	5	V	7	828.51893057	+0.018545
	527.3187742	-0.0201902	527.3187742	6	I	6	729.45051666	+0.0200034
	598.35588799	+0.0513996	598.35588799	7	A	5	616.36645267	+0.011416
	655.37735171		655.37735171	8	G	4	545.32933889	+0.0283882
+0.4445745	385.70578561		770.40429474	9	D	3	488.30787516	+0.1211409
	883.48835872		883.48835872	10	I	2	373.28093213	
+0.4466616	498.78984959	+0.2027848	996.5724227	11	I	1	260.19686815	
				12	K	0	147.11280417	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber:	20170
Protein:	BSU07860; yfkL
Peptide Score:	91.32
Method:	ITMS; CID; 3



precursor information

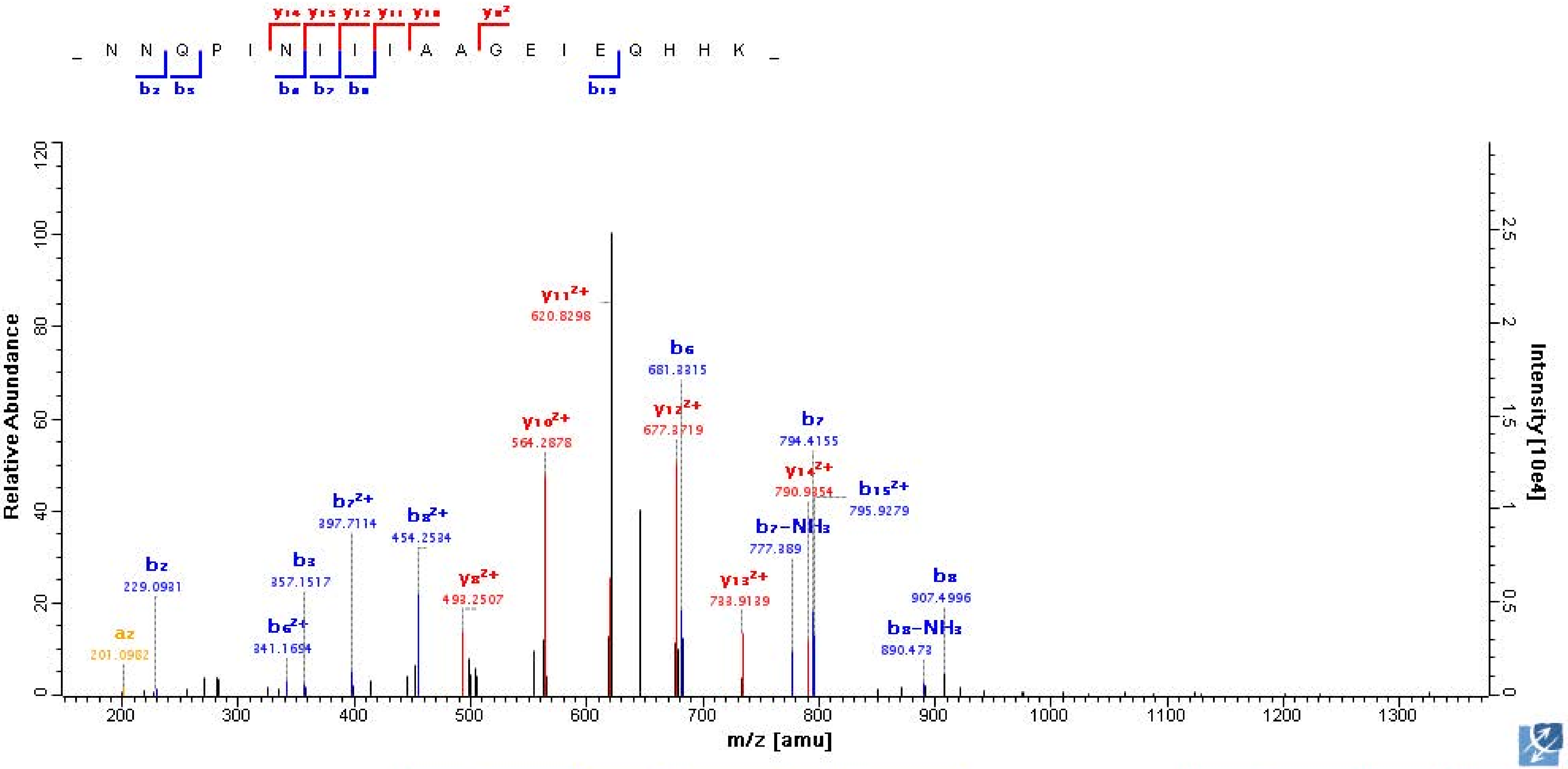
Mass:	2346.18571
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	91.31718
Mass Error [ppm]:	0.056087
PEP:	2.5057E-08
Precursor Type:	MULTI

general information

Annotation:	14 of 21
AminoAcids Coverag	67 %
Intensity Coverage:	57 %
Protein Localisation:	189 ... 209

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164		137.1164	1	K	20				
	234.1692		234.1692	2	P	19	2227.112		2227.112	
	335.2169		335.2169	3	T	18	2130.059		1065.533	+0.191797
	449.2598		449.2598	4	N	17	2029.012		2029.012	
	536.2918		536.2918	5	S	16	1914.969		1914.969	
	593.3133		593.3133	6	G	15	1827.937		1827.937	
	721.3719		721.3719	7	Q	14	1770.915		1770.915	
	849.4305		849.4305	8	Q	13	1642.857		1642.857	
	978.473		978.473	9	E	12	1514.798		1514.798	
	1065.505		1065.505	10	S	11	1385.755	+0.136612	693.3814	+0.127839
	1162.558		1162.558	11	P	10	1298.723	+0.129212	649.8654	+0.003717
	1261.626	+0.212369	1261.626	12	V	9	1201.671		1201.671	
+0.062541	704.851		1408.695	13	F	8	1102.602	+0.077538	1102.602	
-0.037963	761.393	+0.264847	1521.779	14	I	7	955.5339	+0.24727	955.5339	
-0.139365	804.909		1608.811	15	S	6	842.4498	+0.124669	421.7285	-0.370045
+0.309187	869.4303		1737.853	16	E	5	755.4178	+0.065023	755.4178	
	1834.906		1834.906	17	P	4	626.3752	+0.005931	626.3752	
+0.487978	967.4909		1933.975	18	V	3	529.3224		529.3224	
	2081.043		2081.043	19	F	2	430.254	-0.047574	430.254	
+0.251386	1105.054		2209.102	20	Q	1	283.1856		283.1856	
				21	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber:	24002
Protein:	besA; BSU32010; yuiI
Peptide Score:	108.71
Method:	ITMS; CID; 3



precursor information

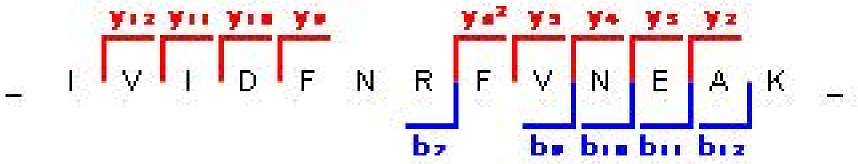
Mass:	2138.12388
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.7129
Mass Error [ppm]:	0.29502
PEP:	1.3262E-16
Precursor Type:	MULTI

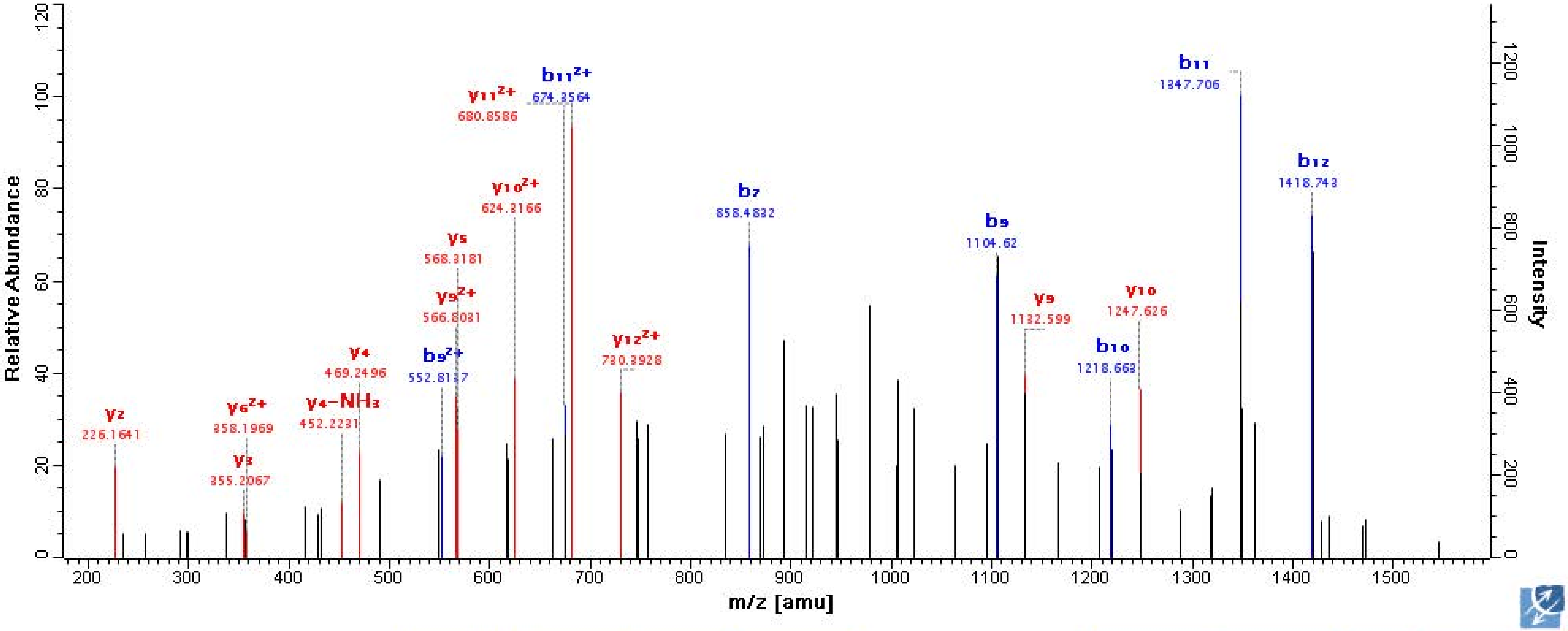
general information

Annotation:	10 of 19
AminoAcids Coverag	53 %
Intensity Coverage:	47 %
Protein Localisation:	211 ... 229

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
	87.0553		115.05		115.05	1	N	18				
+0.19062	201.098		229.093	+0.09414	229.093	2	N	17	2033.1		2033.1	
	329.157		357.152	+0.03158	357.152	3	Q	16	1919.06		1919.06	
	426.21		454.204		454.204	4	P	15	1791		1791	
	539.294		567.289		567.289	5	I	14	1693.95		1693.95	
	653.337	+0.14438	341.169	+0.02974	681.331	6	N	13	1580.86		790.935	+0.2194
	766.421	+0.24947	397.711	+0.11078	794.416	7	I	12	1466.82		733.914	+0.2855
	879.505	+0.30986	454.253	+0.09526	907.5	8	I	11	1353.74		677.372	+0.3490
	992.589		1020.58		1020.58	9	I	10	1240.65		620.83	-0.3815
	1063.63		1091.62		1091.62	10	A	9	1127.57		564.288	+0.2056
	1134.66		1162.66		1162.66	11	A	8	1056.53		1056.53	
	1191.68		1219.68		1219.68	12	G	7	985.494		493.251	+0.0676
	1320.73		1348.72		1348.72	13	E	6	928.473		928.473	
	1433.81		1461.81		1461.81	14	I	5	799.43		799.43	
	1562.85	-0.4005	795.928		1590.85	15	E	4	686.346		686.346	
	1690.91		1718.91		1718.91	16	Q	3	557.303		557.303	
	1827.97		1855.97		1855.97	17	H	2	429.245		429.245	
	1965.03		1993.02		1993.02	18	H	1	292.186		292.186	
						19	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber:	24407
Protein:	BSU32060; yuiD
Peptide Score:	126.76
Method:	ITMS; CID; 3





precursor information

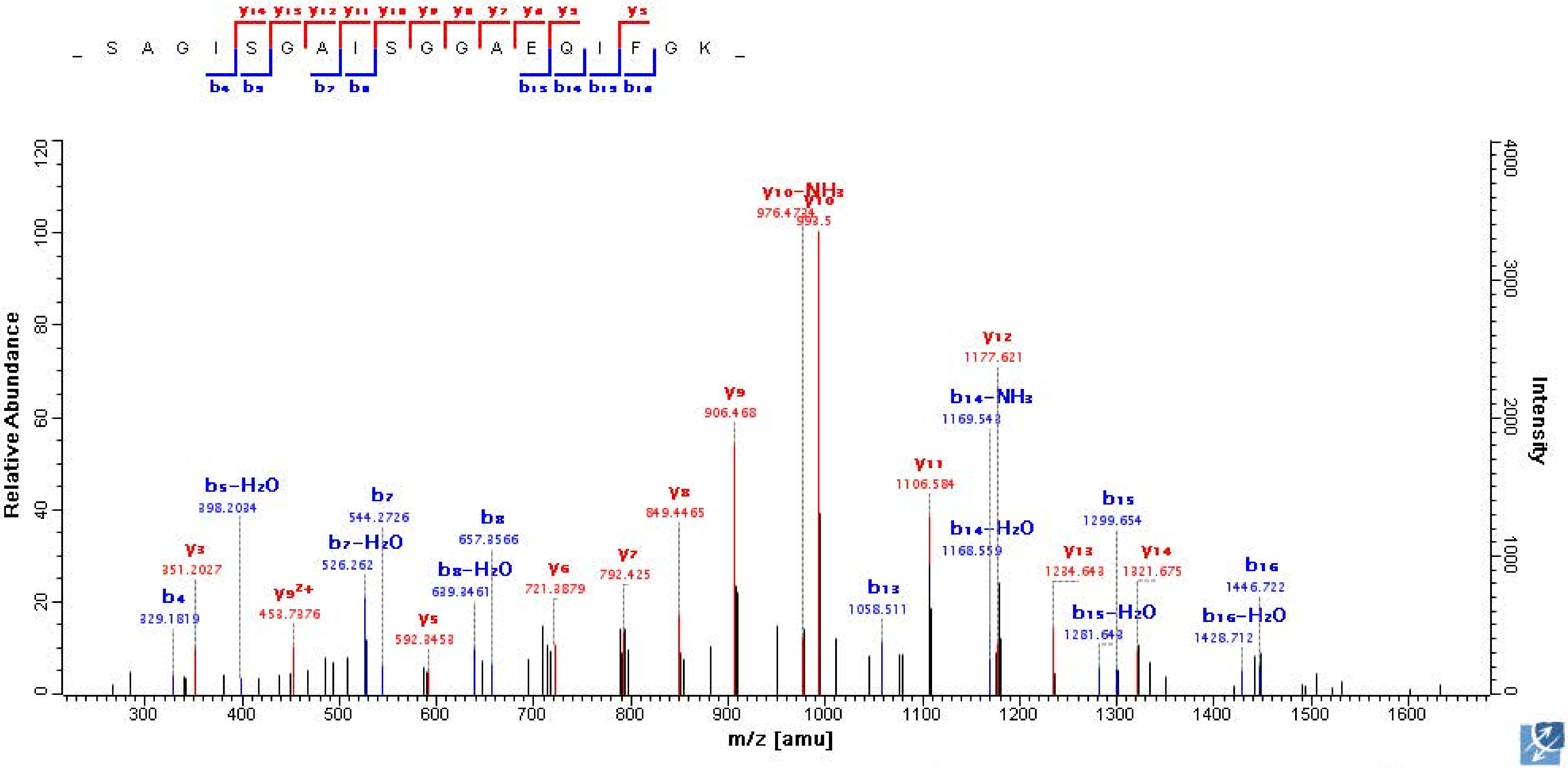
Mass:	1563.84026
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	126.765
Mass Error [ppm]:	-0.4213
PEP:	6.0188E-05
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
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	+0.004287
	326.2438		326.2438	3	I	10	1360.71		680.8586	+0.335491
	441.2708		441.2708	4	D	9	1247.626	+0.129755	624.3166	-0.01774
	588.3392		588.3392	5	F	8	1132.599	+0.103597	566.8031	+0.073002
	702.3821		702.3821	6	N	7	985.5305		985.5305	
	858.4832	-0.002745	858.4832	7	R	6	871.4876		871.4876	
	1005.552		1005.552	8	F	5	715.3865		358.1969	+0.211027
-0.167114	552.8137	-0.026047	1104.62	9	V	4	568.3181	+0.278689	568.3181	
	1218.663	+0.179682	1218.663	10	N	3	469.2496	+0.051937	469.2496	
+0.414882	674.3564	+0.031132	1347.706	11	E	2	355.2067	+0.173326	355.2067	
	1418.743	+0.023193	1418.743	12	A	1	226.1641	+0.099311	226.1641	
				13	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber:	24655
Protein:	BSU33630; secG; yvaL
Peptide Score:	116.86
Method:	ITMS; CID; 3



precursor information

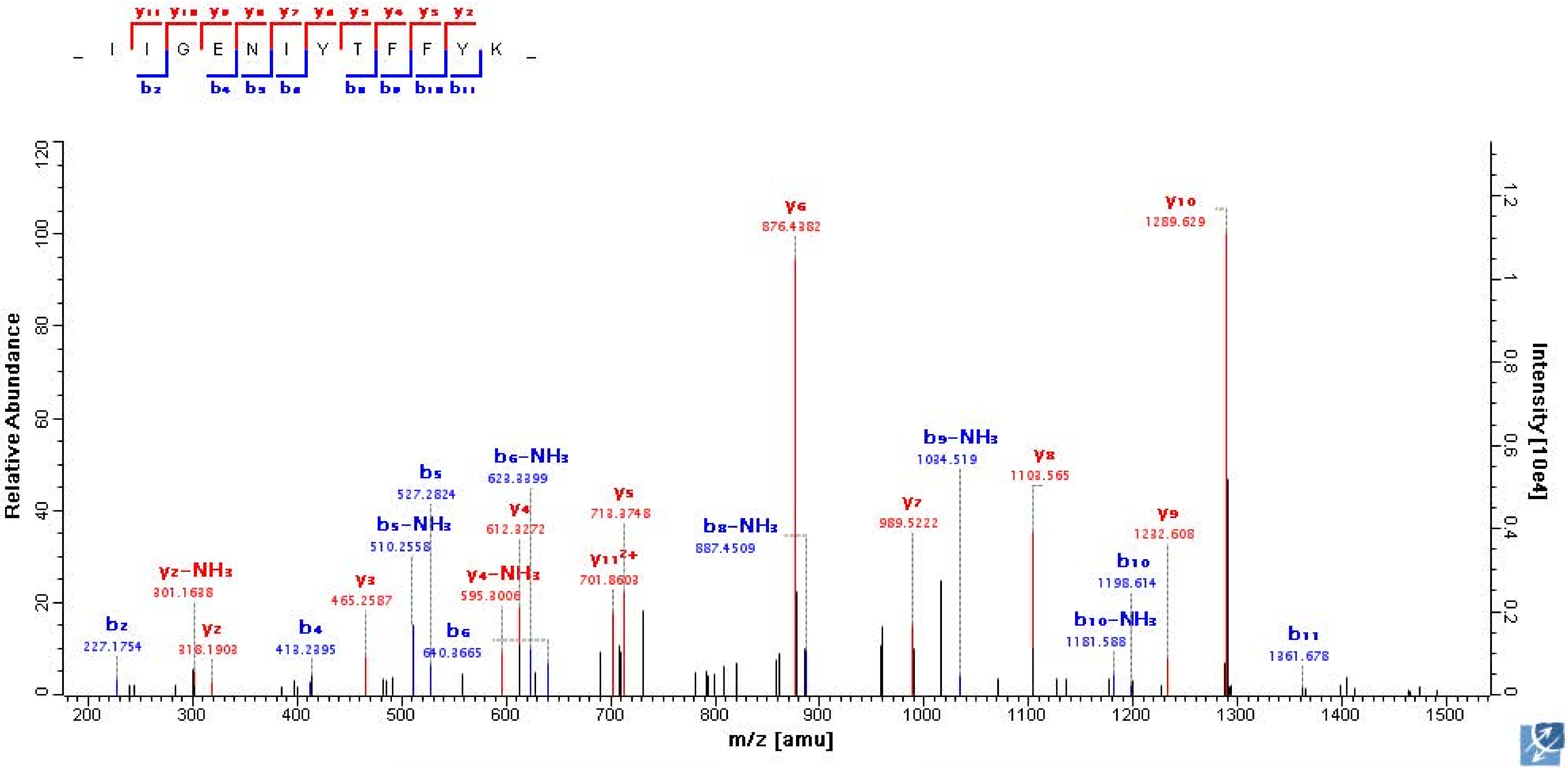
Mass:	1648.84198
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	116.8621
Mass Error [ppm]:	-0.043833
PEP:	7.7955E-12
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	44 %
Protein Localisation:	27 ... 44

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	88.039304876	1	S	17				
	159.07641866	2	A	16	1562.8172974		1562.8172974	
	216.09788239	3	G	15	1491.7801836		1491.7801836	
+0.3128656	329.18194637	4	I	14	1434.7587199		1434.7587199	
	416.21397478	5	S	13	1321.6746559	+0.1126976	1321.6746559	
	473.2354385	6	G	12	1234.6426275	+0.2168695	1234.6426275	
-0.12619	544.27255229	7	A	11	1177.6211638	+0.1281038	1177.6211638	
+0.3154418	657.35661627	8	I	10	1106.58405	+0.0853836	1106.58405	
	744.38864468	9	S	9	993.49998604	+0.1419207	993.49998604	
	801.4101084	10	G	8	906.46795763	+0.0343007	453.73761705	-0.4336009
	858.43157213	11	G	7	849.44649391	-0.1234348	849.44649391	
	929.46868591	12	A	6	792.42503019	+0.0280948	792.42503019	
+0.1978274	1058.511279	13	E	5	721.3879164	+0.2116319	721.3879164	
	1186.5698565	14	Q	4	592.3453233	+0.1269667	592.3453233	
+0.2233988	1299.6539205	15	I	3	464.28674579		464.28674579	
+0.2693648	1446.7223344	16	F	2	351.20268181	+0.0028236	351.20268181	
	1503.7437981	17	G	1	204.13426789		204.13426789	
		18	K	0	147.11280417		147.11280417	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F06
Scannumber:	29342
Protein:	BSU40140; yydJ
Peptide Score:	142.07
Method:	ITMS; CID; 3



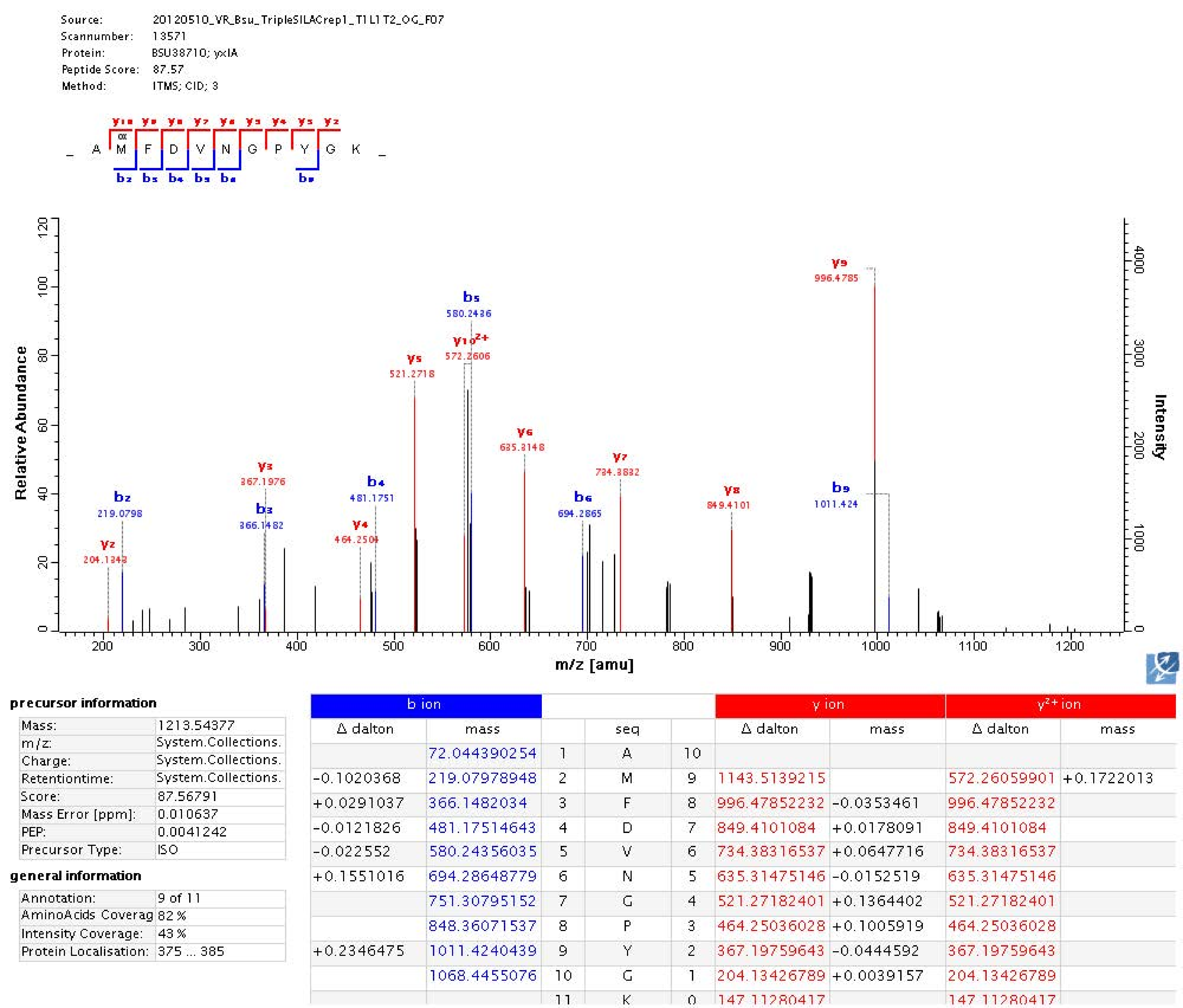
precursor information

Mass:	1506.77564
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	142.0682
Mass Error [ppm]:	-0.15214
PEP:	5.8785E-08
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	52 %
Protein Localisation:	84 ... 95

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	114.09134045	1	I	11				
+0.1176101	227.17540443	2	I	10	1402.7132786		701.86027753	+0.4125496
	284.19686815	3	G	9	1289.6292146	+0.0930754	1289.6292146	
-0.0816243	413.23946125	4	E	8	1232.6077509	+0.3008184	1232.6077509	
-0.1868076	527.28238869	5	N	7	1103.5651578	-0.0136441	1103.5651578	
+0.2398095	640.36645267	6	I	6	989.52223035	+0.0175035	989.52223035	
	803.42978121	7	Y	5	876.43816637	+0.0189259	876.43816637	
	904.47745969	8	T	4	713.37483783	+0.045084	713.37483783	
	1051.5458736	9	F	3	612.32715935	+0.0107923	612.32715935	
+0.1188668	1198.6142875	10	F	2	465.25874544	-0.0552542	465.25874544	
-0.3236122	1361.6776161	11	Y	1	318.19033152	+0.1315374	318.19033152	
		12	K	0	155.12700298		155.12700298	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F07
Scannumber:	13571
Protein:	BSU38710; yxlA
Peptide Score:	87.57
Method:	ITMS; CID; 3

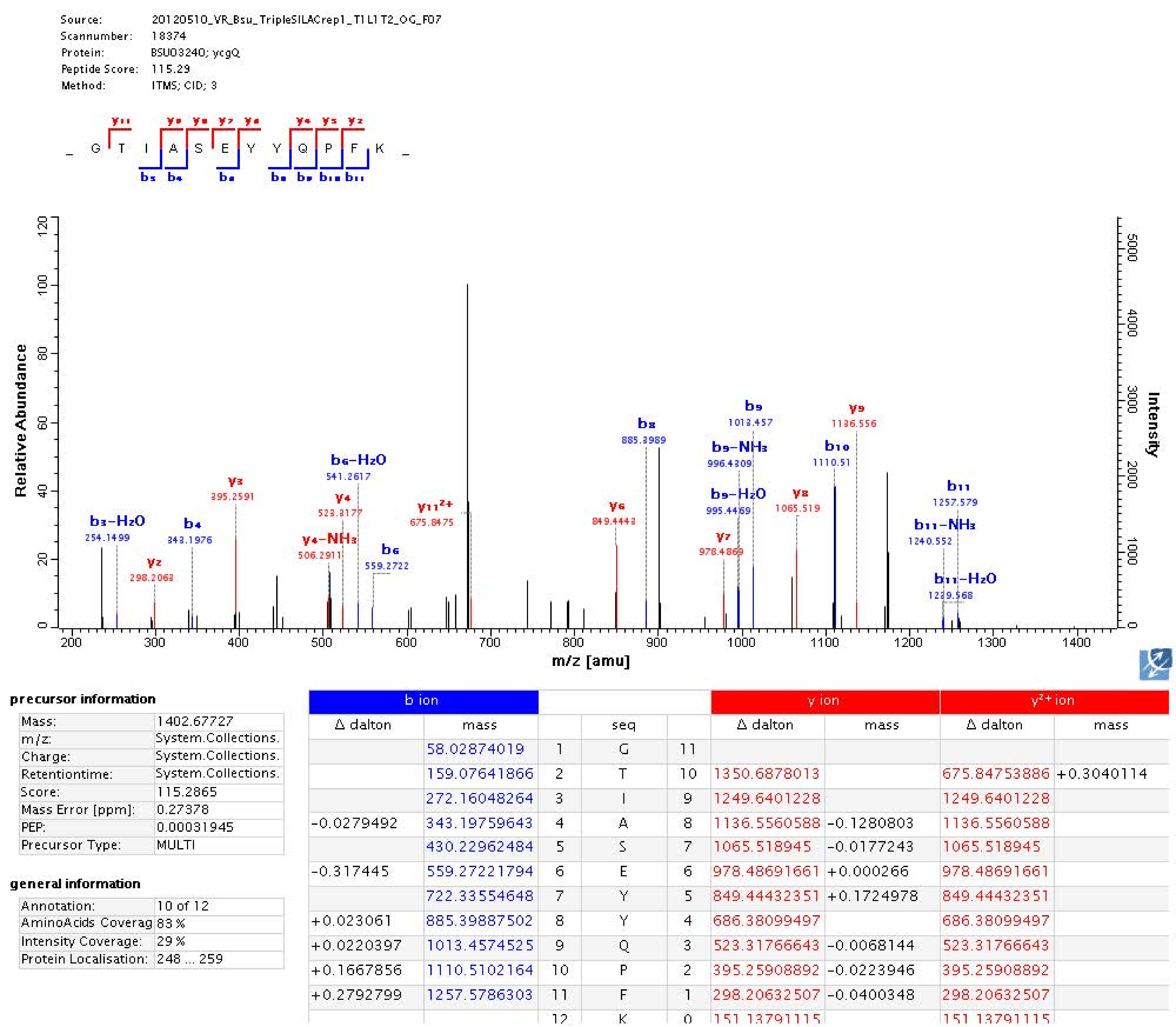
precursor information

Mass:	1213.54377
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.56791
Mass Error [ppm]:	0.010637
PEP:	0.0041242
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	43 %
Protein Localisation:	375 ... 385

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	10				
-0.1020368	219.07978948	2	M	9	1143.5139215		572.26059901	+0.1722013
+0.0291037	366.1482034	3	F	8	996.47852232	-0.0353461	996.47852232	
-0.0121826	481.17514643	4	D	7	849.4101084	+0.0178091	849.4101084	
-0.022552	580.24356035	5	V	6	734.38316537	+0.0647716	734.38316537	
+0.1551016	694.28648779	6	N	5	635.31475146	-0.0152519	635.31475146	
	751.30795152	7	G	4	521.27182401	+0.1364402	521.27182401	
	848.36071537	8	P	3	464.25036028	+0.1005919	464.25036028	
+0.2346475	1011.4240439	9	Y	2	367.19759643	-0.0444592	367.19759643	
	1068.4455076	10	G	1	204.13426789	+0.0039157	204.13426789	
		11	K	0	147.11280417		147.11280417	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F07
Scannumber:	18374
Protein:	BSU03240; ycgQ
Peptide Score:	115.29
Method:	ITMS; CID; 3

precursor information

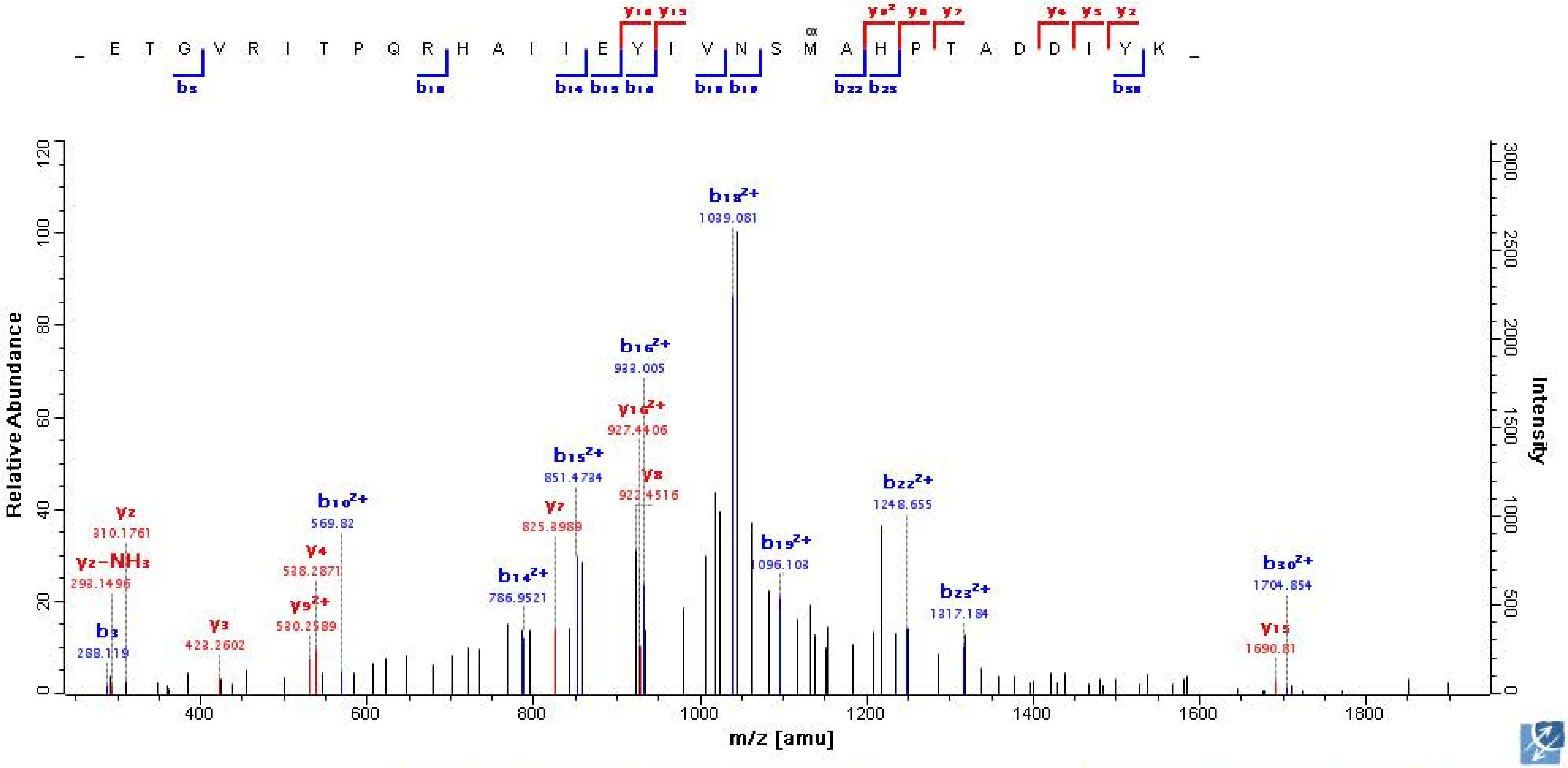
Mass:	1402.67727
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.2865
Mass Error [ppm]:	0.27378
PEP:	0.00031945
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	29 %
Protein Localisation:	248 ... 259

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	11				
	159.07641866	2	T	10	1350.6878013		675.84753886	+0.3040114
	272.16048264	3	I	9	1249.6401228		1249.6401228	
-0.0279492	343.19759643	4	A	8	1136.5560588	-0.1280803	1136.5560588	
	430.22962484	5	S	7	1065.518945	-0.0177243	1065.518945	
-0.317445	559.27221794	6	E	6	978.48691661	+0.000266	978.48691661	
	722.33554648	7	Y	5	849.44432351	+0.1724978	849.44432351	
+0.023061	885.39887502	8	Y	4	686.38099497		686.38099497	
+0.0220397	1013.4574525	9	Q	3	523.31766643	-0.0068144	523.31766643	
+0.1667856	1110.5102164	10	P	2	395.25908892	-0.0223946	395.25908892	
+0.2792799	1257.5786303	11	F	1	298.20632507	-0.0400348	298.20632507	
		12	K	0	151.13791115		151.13791115	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F07
Scannumber: 20891
Protein: BSU08730; perR; ygaG
Peptide Score: 47.33
Method: ITMS; CID; 3



precursor information

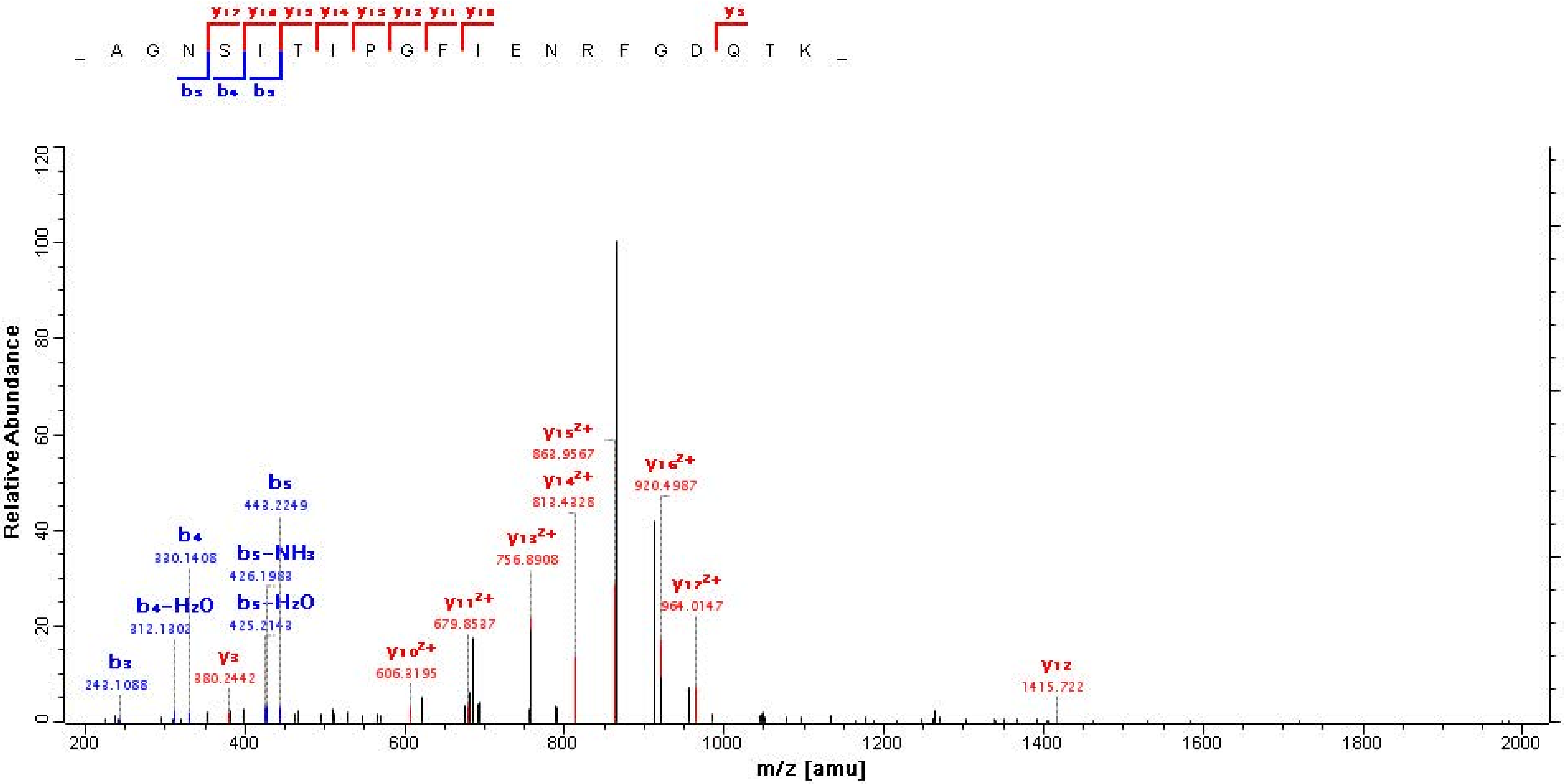
Mass:	3553.80044
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	47.33092
Mass Error [ppm]:	0.47382
PEP:	8.4421E-05
Precursor Type:	MULTI

general information

Annotation:	15 of 31
AminoAcids Coverag	48 %
Intensity Coverage:	26 %
Protein Localisation:	15 ... 45

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	30				
	231.0975		231.0975	2	T	29	3425.763		3425.763	
	288.119	-0.043084	288.119	3	G	28	3324.716		3324.716	
	387.1874		387.1874	4	V	27	3267.694		3267.694	
	543.2885		543.2885	5	R	26	3168.626		3168.626	
	656.3726		656.3726	6	I	25	3012.525		3012.525	
	757.4203		757.4203	7	T	24	2899.441		2899.441	
	854.473		854.473	8	P	23	2798.393		2798.393	
	982.5316		982.5316	9	Q	22	2701.34		2701.34	
-0.017148	569.82		1138.633	10	R	21	2573.282		2573.282	
	1275.692		1275.692	11	H	20	2417.181		2417.181	
	1346.729		1346.729	12	A	19	2280.122		2280.122	
	1459.813		1459.813	13	I	18	2209.085		2209.085	
-0.273919	786.9521		1572.897	14	I	17	2096		2096	
+0.281322	851.4734		1701.939	15	E	16	1982.916		1982.916	
-0.42771	933.005		1865.003	16	Y	15	1853.874		927.4406	+0.28003
	1978.087		1978.087	17	I	14	1690.81	+0.159107	1690.81	
+0.316669	1039.081		2077.155	18	V	13	1577.726		1577.726	
+0.297646	1096.103		2191.198	19	N	12	1478.658		1478.658	
	2278.23		2278.23	20	S	11	1364.615		1364.615	
	2425.266		2425.266	21	M	10	1277.583		1277.583	
+0.140517	1248.655		2496.303	22	A	9	1130.548		1130.548	
+0.133888	1317.184		2633.362	23	H	8	1059.511		530.2589	-0.07355
	2730.414		2730.414	24	P	7	922.4516	-0.038431	922.4516	
	2831.462		2831.462	25	T	6	825.3989	+0.266591	825.3989	
	2902.499		2902.499	26	A	5	724.3512		724.3512	
	3017.526		3017.526	27	D	4	653.3141		653.3141	
	3132.553		3132.553	28	D	3	538.2871	+0.082428	538.2871	
	3245.637		3245.637	29	I	2	423.2602	+0.030575	423.2602	
+0.142083	1704.854		3408.701	30	Y	1	310.1761	-0.000351	310.1761	
				31	K	0	147.1128		147.1128	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F07
Scannumber:	24039
Protein:	BSU03220; ycgO
Peptide Score:	57.5
Method:	ITMS; CID; 3



precursor information

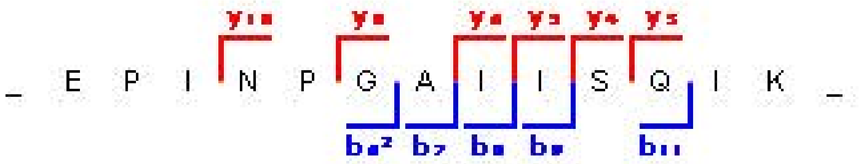
Mass:	2164.09133
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	57.49924
Mass Error [ppm]:	0.021906
PEP:	0.0017846
Precursor Type:	MULTI

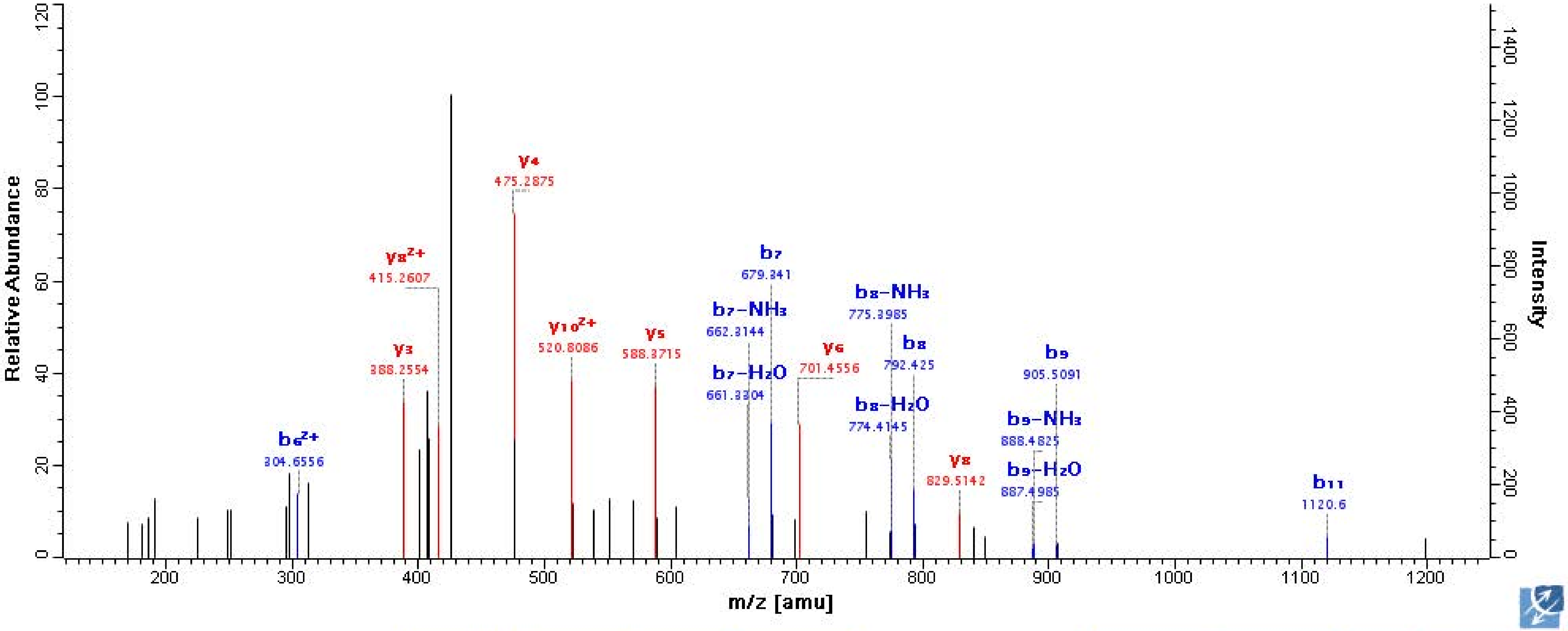
general information

Annotation:	10 of 20
AminoAcids Coverag	50 %
Intensity Coverage:	27 %
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	2098.0865509		2098.0865509	
+0.0591721	243.10878143	3	N	17	2041.0650871		2041.0650871	
+0.1115705	330.14080984	4	S	16	1927.0221597		964.01471808	+0.334464
+0.0059611	443.22487382	5	I	15	1839.9901313		920.49870388	+0.0255271
	544.27255229	6	T	14	1726.9060673		863.95667189	-0.1966621
	657.35661627	7	I	13	1625.8583888		813.43283265	+0.4742718
	754.40938012	8	P	12	1512.7743249		756.89080066	-0.170891
	811.43084385	9	G	11	1415.721561	+0.1802945	1415.721561	
	958.49925776	10	F	10	1358.7000973		679.85368687	+0.4303097
	1071.5833217	11	I	9	1211.6316834		606.31947992	+0.4542017
	1200.6259148	12	E	8	1098.5476194		1098.5476194	
	1314.6688423	13	N	7	969.50502629		969.50502629	
	1470.7699533	14	R	6	855.46209884		855.46209884	
	1617.8383672	15	F	5	699.36098781		699.36098781	
	1674.859831	16	G	4	552.2925739		552.2925739	
	1789.886774	17	D	3	495.27111017		495.27111017	
	1917.9453515	18	Q	2	380.24416714	+0.0056498	380.24416714	
	2018.99303	19	T	1	252.18558963		252.18558963	
		20	K	0	151.13791115		151.13791115	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F07
Scannumber:	25894
Protein:	BSU29920; ytmP
Peptide Score:	93.84
Method:	ITMS; CID; 3





precursor information

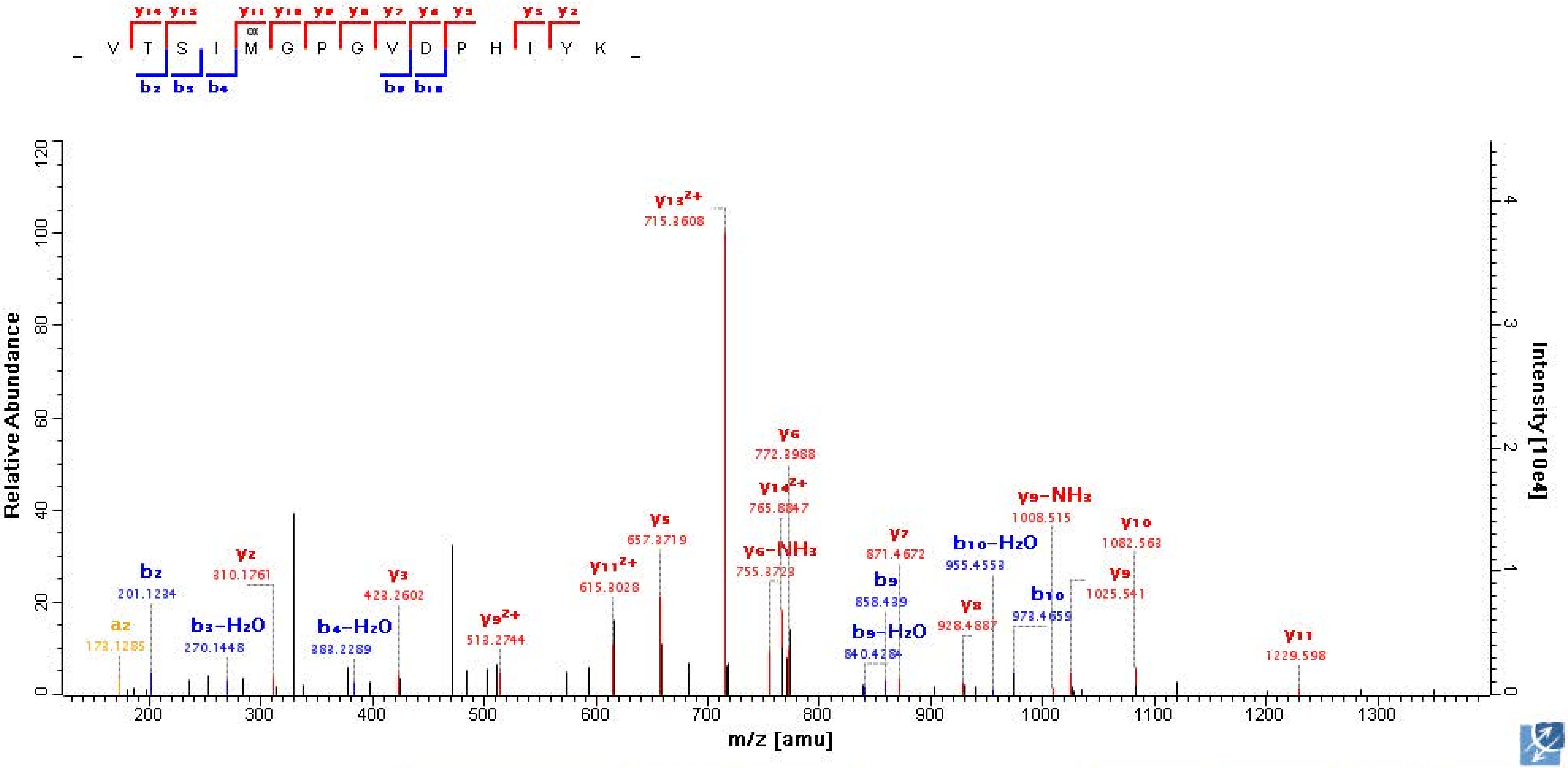
Mass:	1378.7828
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.83924
Mass Error [ppm]:	0.56946
PEP:	0.00074333
Precursor Type:	MULTI

general information

Annotation:	7 of 13
AminoAcids Coverag	54 %
Intensity Coverage:	45 %
Protein Localisation:	51 ... 63

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	12				
	227.1026		227.1026	2	P	11	1250.747		1250.747	
	340.1867		340.1867	3	I	10	1153.694		1153.694	
	454.2296		454.2296	4	N	9	1040.61		520.8086	+0.063314
	551.2824		551.2824	5	P	8	926.5669		926.5669	
-0.361924	304.6556		608.3039	6	G	7	829.5142	+0.157024	415.2607	+0.123305
	679.341	+0.242347	679.341	7	A	6	772.4927		772.4927	
	792.425	+0.178058	792.425	8	I	5	701.4556	+0.26919	701.4556	
	905.5091	+0.460388	905.5091	9	I	4	588.3715	+0.082014	588.3715	
	992.5411		992.5411	10	S	3	475.2875	+0.214357	475.2875	
	1120.6	+0.011506	1120.6	11	Q	2	388.2554	-0.190077	388.2554	
	1233.684		1233.684	12	I	1	260.1969		260.1969	
				13	K	0	147.1128		147.1128	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F08
Scannumber: 14154
Protein: BSU30770; mntA; ytgA
Peptide Score: 110.8
Method: ITMS; CID; 3



precursor information

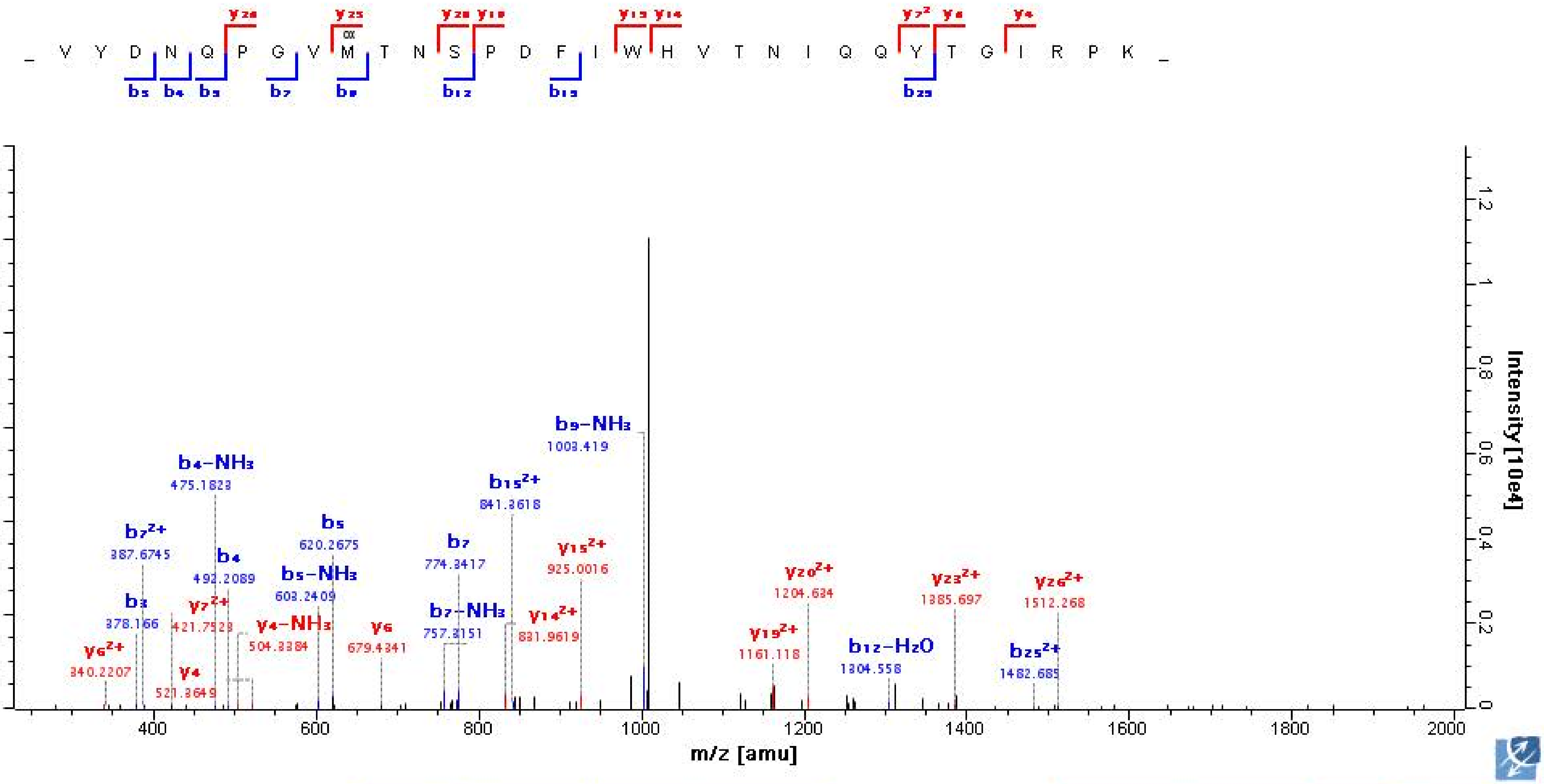
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	110.8011
Mass Error [ppm]:	0.091146
PEP:	1.5136E-12
Precursor Type:	PEAK

general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	49 %
Protein Localisation:	55 ... 69

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.08078		100.0757	1	V	14				
+0.304789	173.1285	+0.151472	201.1234	2	T	13	1530.762		765.8847	+0.145956
	260.1605		288.1554	3	S	12	1429.714		715.3608	+0.264949
	373.2445		401.2395	4	I	11	1342.682		1342.682	
	520.2799		548.2749	5	M	10	1229.598	-0.146416	615.3028	-0.099246
	577.3014		605.2963	6	G	9	1082.563	+0.175727	1082.563	
	674.3542		702.3491	7	P	8	1025.541	+0.090745	513.2744	-0.054518
	731.3756		759.3706	8	G	7	928.4887	+0.13588	928.4887	
	830.4441	+0.220336	858.439	9	V	6	871.4672	+0.235468	871.4672	
	945.471	-0.021085	973.4659	10	D	5	772.3988	+0.200977	772.3988	
	1042.524		1070.519	11	P	4	657.3719	+0.072341	657.3719	
	1179.583		1207.578	12	H	3	560.3191		560.3191	
	1292.667		1320.662	13	I	2	423.2602	-0.086857	423.2602	
	1455.73		1483.725	14	Y	1	310.1761	+0.066726	310.1761	
				15	K	0	147.1128		147.1128	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F08
Scannumber:	24308
Protein:	BSU39540; LP9A; yxel
Peptide Score:	63.27
Method:	ITMS; CID; 3



precursor information

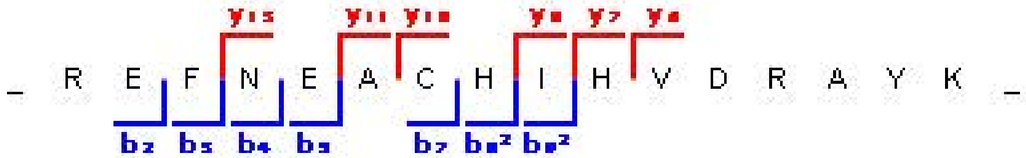
Mass:	3641.78402
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	63.27224
Mass Error [ppm]:	0.6497
PEP:	3.5367E-06
Precursor Type:	ISO

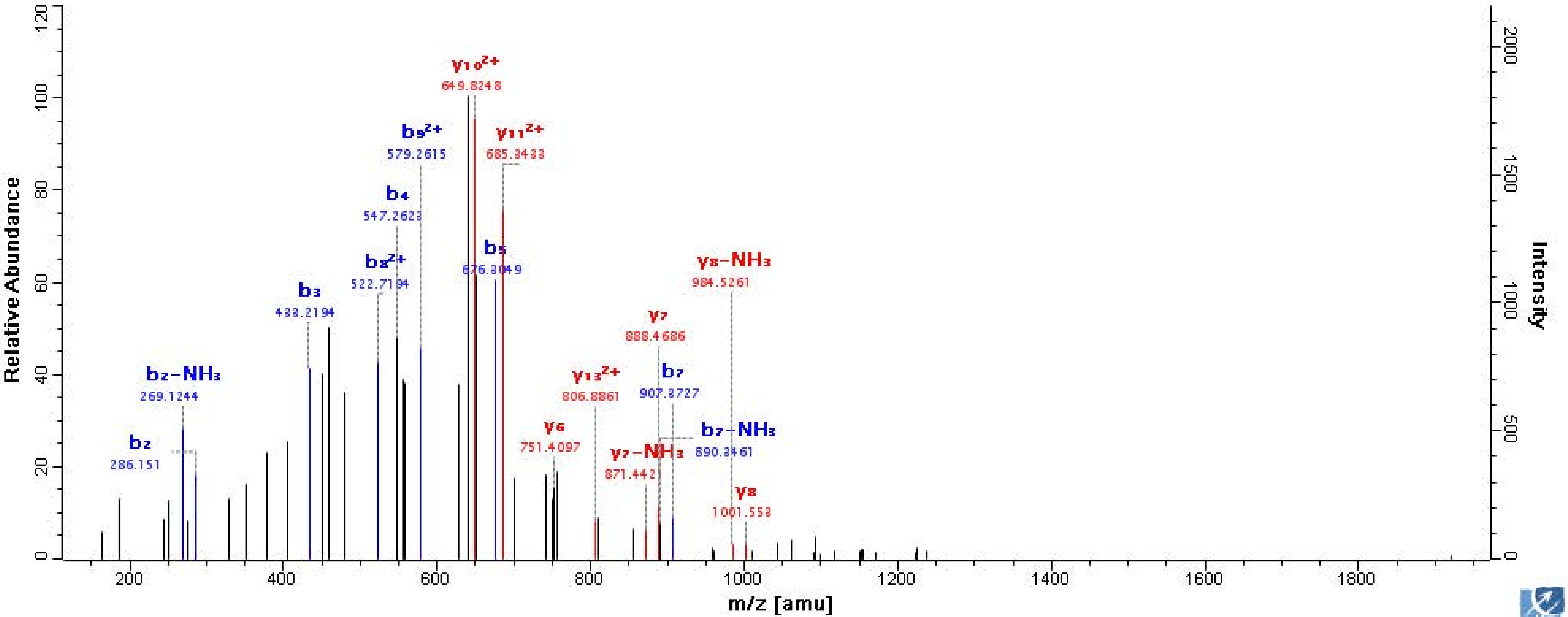
general information

Annotation:	14 of 31
AminoAcids Coverag	45 %
Intensity Coverage:	18 %
Protein Localisation:	164 ... 194

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	30				
	263.139		263.139	2	Y	29	3543.721		3543.721	
	378.166	+0.075585	378.166	3	D	28	3380.657		3380.657	
	492.2089	+0.101352	492.2089	4	N	27	3265.63		3265.63	
	620.2675	+0.041432	620.2675	5	Q	26	3151.587		3151.587	
	717.3202		717.3202	6	P	25	3023.529		1512.268	-0.366029
+0.476149	387.6745	+0.138469	774.3417	7	G	24	2926.476		2926.476	
	873.4101		873.4101	8	V	23	2869.455		2869.455	
	1020.446		1020.446	9	M	22	2770.386		1385.697	+0.089691
	1121.493		1121.493	10	T	21	2623.351		2623.351	
	1235.536		1235.536	11	N	20	2522.303		2522.303	
	1322.568		1322.568	12	S	19	2408.26		1204.634	+0.48204
	1419.621		1419.621	13	P	18	2321.228		1161.118	+0.080085
	1534.648		1534.648	14	D	17	2224.175		2224.175	
+0.428636	841.3618		1681.716	15	F	16	2109.148		2109.148	
	1794.8		1794.8	16	I	15	1962.08		1962.08	
	1980.88		1980.88	17	W	14	1848.996		925.0016	+0.027904
	2117.939		2117.939	18	H	13	1662.917		831.9619	+0.284662
	2217.007		2217.007	19	V	12	1525.858		1525.858	
	2318.055		2318.055	20	T	11	1426.789		1426.789	
	2432.098		2432.098	21	N	10	1325.742		1325.742	
	2545.182		2545.182	22	I	9	1211.699		1211.699	
	2673.24		2673.24	23	Q	8	1098.615		1098.615	
	2801.299		2801.299	24	Q	7	970.556		970.556	
-0.183111	1482.685		2964.362	25	Y	6	842.4974		421.7523	+0.494848
	3065.41		3065.41	26	T	5	679.4341	+0.258299	340.2207	-0.059731
	3122.431		3122.431	27	G	4	578.3864		578.3864	
	3235.515		3235.515	28	I	3	521.3649	+0.060046	521.3649	
	3391.616		3391.616	29	R	2	408.2809		408.2809	
	3488.669		3488.669	30	P	1	252.1798		252.1798	
				31	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F08
Scannumber:	8707
Protein:	BSU32780; yusF
Peptide Score:	73.89
Method:	ITMS; CID; 3





precursor information

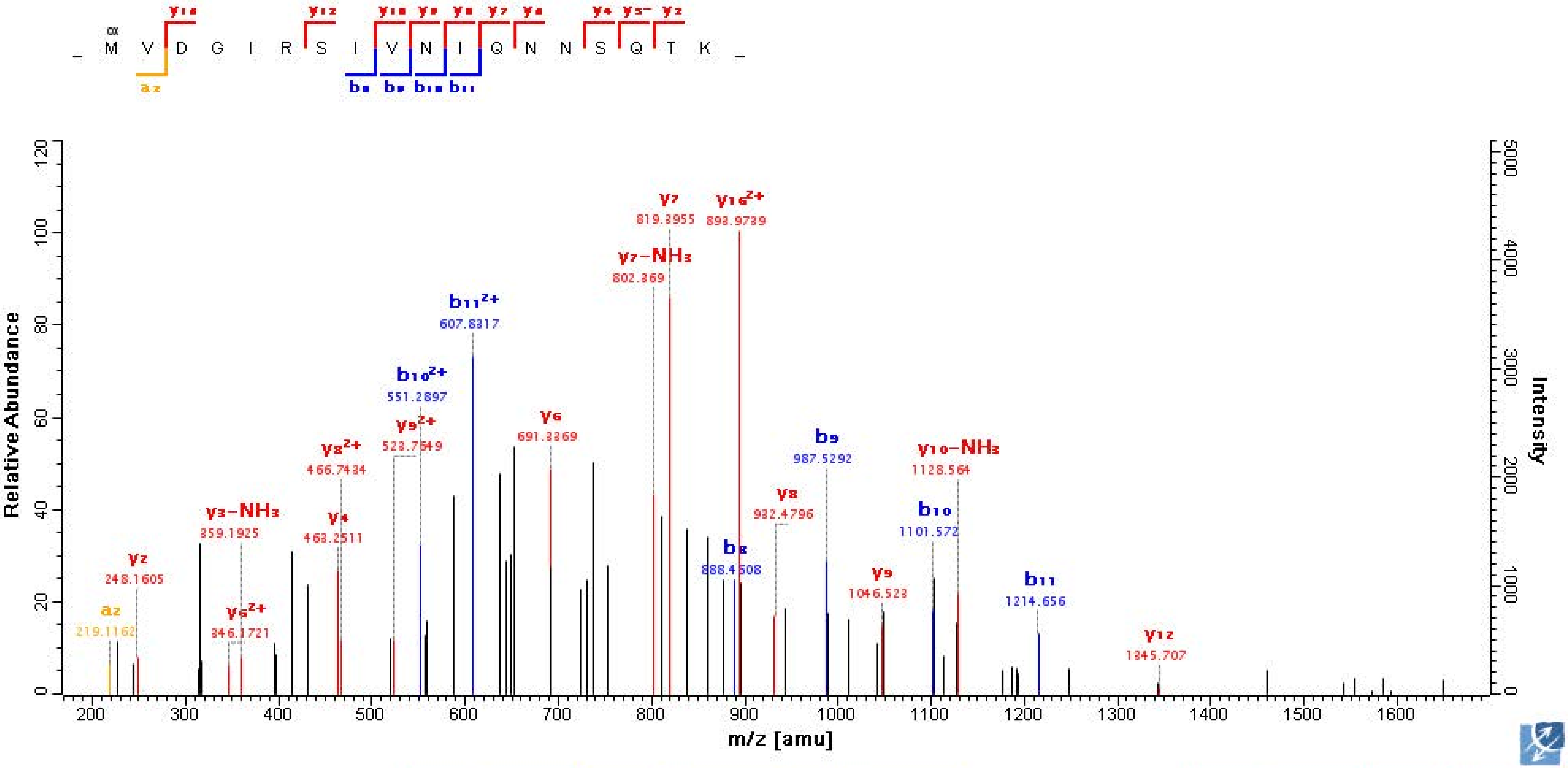
Mass:	2043.97061
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	73.88673
Mass Error [ppm]:	0.43295
PEP:	0.00055851
Precursor Type:	MULTI

general information

Annotation:	10 of 16
AminoAcids Coverag	62 %
Intensity Coverage:	41 %
Protein Localisation:	98 ... 113

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	15				
	286.151	-0.005473	286.151	2	E	14	1888.876		1888.876	
	433.2194	+0.210171	433.2194	3	F	13	1759.833		1759.833	
	547.2623	-0.02813	547.2623	4	N	12	1612.765		806.8861	+0.060941
	676.3049	+0.028093	676.3049	5	E	11	1498.722		1498.722	
	747.342		747.342	6	A	10	1369.679		685.3433	+0.18738
	907.3727	+0.12305	907.3727	7	C	9	1298.642		649.8248	+0.076054
+0.432362	522.7194		1044.432	8	H	8	1138.612		1138.612	
-0.22582	579.2615		1157.516	9	I	7	1001.553	+0.056257	1001.553	
	1294.575		1294.575	10	H	6	888.4686	-0.11981	888.4686	
	1393.643		1393.643	11	V	5	751.4097	+0.240615	751.4097	
	1508.67		1508.67	12	D	4	652.3413		652.3413	
	1664.771		1664.771	13	R	3	537.3144		537.3144	
	1735.808		1735.808	14	A	2	381.2132		381.2132	
	1898.871		1898.871	15	Y	1	310.1761		310.1761	
				16	K	0	147.1128		147.1128	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F09
Scannumber:	17672
Protein:	BSU06270; ydjO
Peptide Score:	93.51
Method:	ITMS; CID; 3



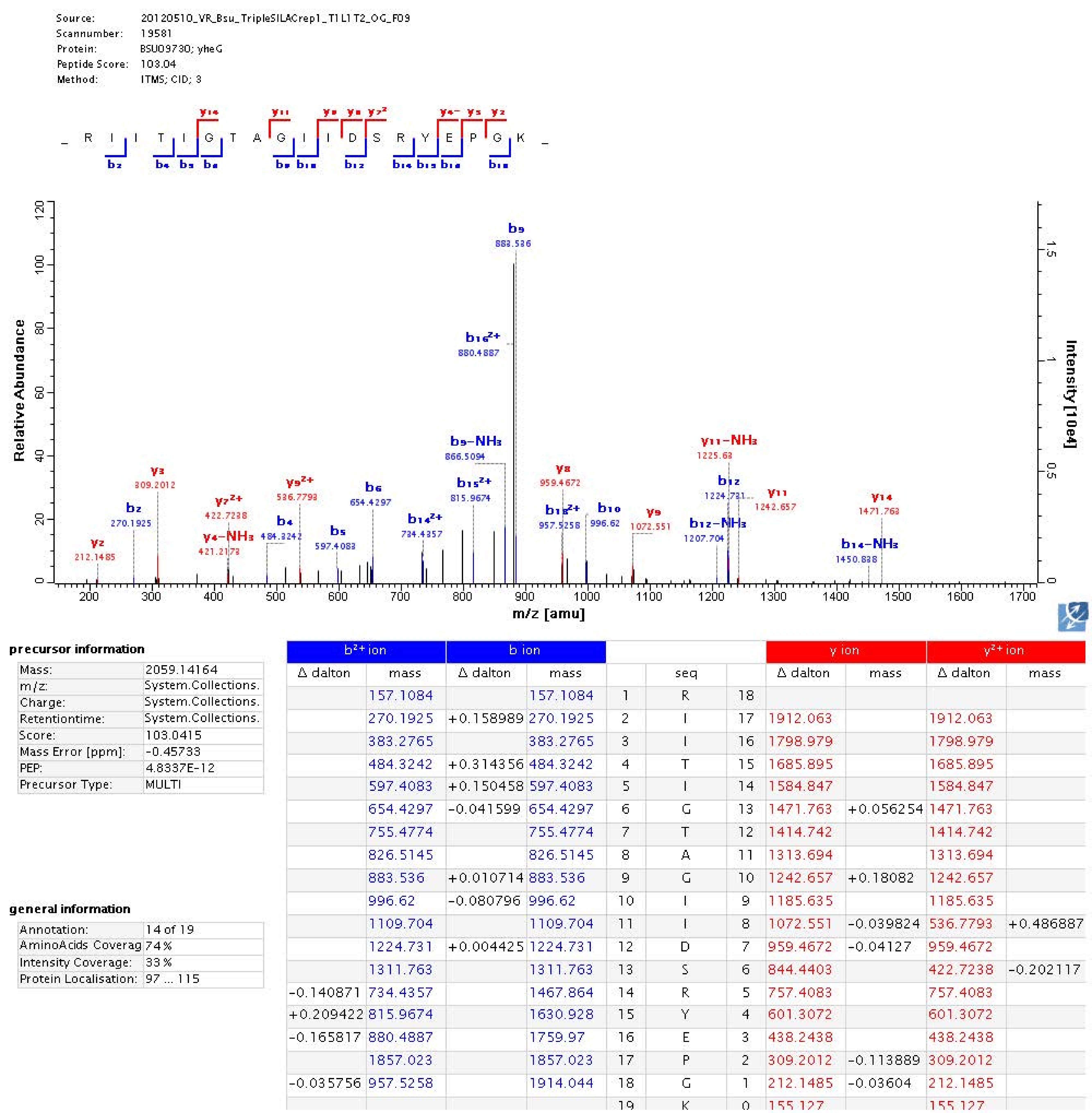
precursor information

Mass:	2032.03507
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	93.50977
Mass Error [ppm]:	-1.0184
PEP:	2.3134E-09
Precursor Type:	MULTI

general information

Annotation:	12 of 18
AminoAcids Coverag	67 %
Intensity Coverage:	39 %
Protein Localisation:	50 ... 67

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
	120.048		148.043		148.043	1	M	17				
+0.06153	219.116		247.111		247.111	2	V	16	1886.01		1886.01	
	334.143		362.138		362.138	3	D	15	1786.94		893.974	+0.2286
	391.165		419.159		419.159	4	G	14	1671.91		1671.91	
	504.249		532.244		532.244	5	I	13	1614.89		1614.89	
	660.35		688.345		688.345	6	R	12	1501.81		1501.81	
	747.382		775.377		775.377	7	S	11	1345.71	-0.0066	1345.71	
	860.466		888.461	-0.1188	888.461	8	I	10	1258.67		1258.67	
	959.534		987.529	+0.1134	987.529	9	V	9	1145.59		1145.59	
	1073.58	+0.26628	551.29	+0.04801	1101.57	10	N	8	1046.52	+0.10566	523.765	-0.0353
	1186.66	+0.38495	607.832	+0.18111	1214.66	11	I	7	932.48	-0.2967	466.743	+0.4956
	1314.72		1342.71		1342.71	12	Q	6	819.396	-0.005	819.396	
	1428.76		1456.76		1456.76	13	N	5	691.337	-0.0314	346.172	-0.1031
	1542.81		1570.8		1570.8	14	N	4	577.294		577.294	
	1629.84		1657.83		1657.83	15	S	3	463.251	+0.00111	463.251	
	1757.9		1785.89		1785.89	16	Q	2	376.219		376.219	
	1858.94		1886.94		1886.94	17	T	1	248.16	+0.29002	248.16	
						18	K	0	147.113		147.113	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F09
Scannumber:	19581
Protein:	BSU09730; yheG
Peptide Score:	103.04
Method:	ITMS; CID; 3

precursor information

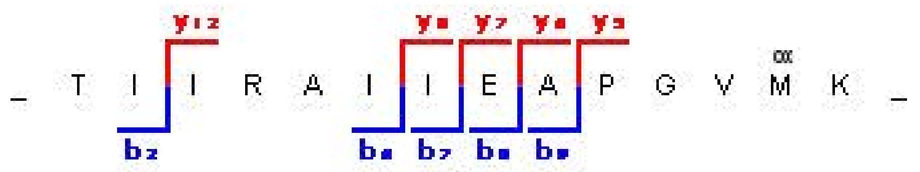
Mass:	2059.14164
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	103.0415
Mass Error [ppm]:	-0.45733
PEP:	4.8337E-12
Precursor Type:	MULTI

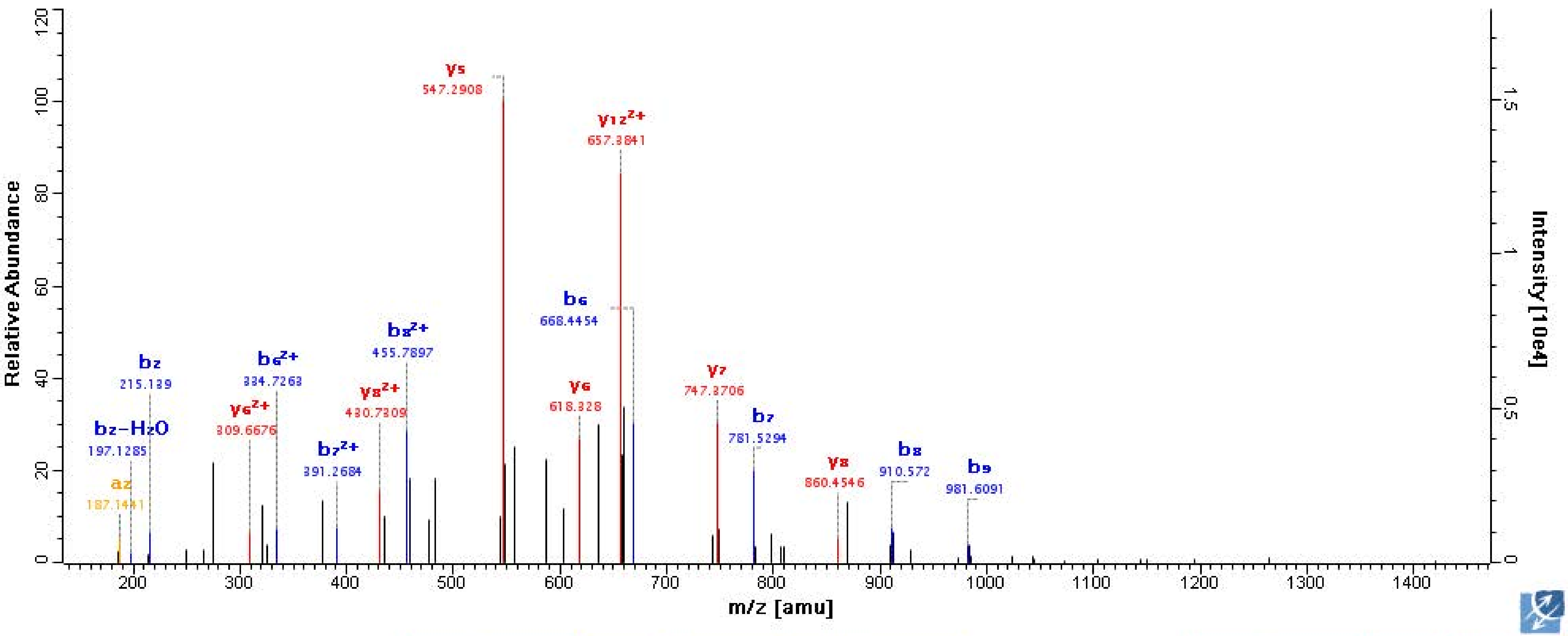
general information

Annotation:	14 of 19
AminoAcids Coverag	74%
Intensity Coverage:	33%
Protein Localisation:	97 ... 115

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	18				
	270.1925	+0.158989	270.1925	2	I	17	1912.063		1912.063	
	383.2765		383.2765	3	I	16	1798.979		1798.979	
	484.3242	+0.314356	484.3242	4	T	15	1685.895		1685.895	
	597.4083	+0.150458	597.4083	5	I	14	1584.847		1584.847	
	654.4297	-0.041599	654.4297	6	G	13	1471.763	+0.056254	1471.763	
	755.4774		755.4774	7	T	12	1414.742		1414.742	
	826.5145		826.5145	8	A	11	1313.694		1313.694	
	883.536	+0.010714	883.536	9	G	10	1242.657	+0.18082	1242.657	
	996.62	-0.080796	996.62	10	I	9	1185.635		1185.635	
	1109.704		1109.704	11	I	8	1072.551	-0.039824	536.7793	+0.486887
	1224.731	+0.004425	1224.731	12	D	7	959.4672	-0.04127	959.4672	
	1311.763		1311.763	13	S	6	844.4403		422.7238	-0.202117
-0.140871	734.4357		1467.864	14	R	5	757.4083		757.4083	
+0.209422	815.9674		1630.928	15	Y	4	601.3072		601.3072	
-0.165817	880.4887		1759.97	16	E	3	438.2438		438.2438	
	1857.023		1857.023	17	P	2	309.2012	-0.113889	309.2012	
-0.035756	957.5258		1914.044	18	G	1	212.1485	-0.03604	212.1485	
				19	K	0	155.127		155.127	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F10
Scannumber: 20288
Protein: BSU11640; yjbQ
Peptide Score: 105.65
Method: ITMS; CID; 3





precursor information

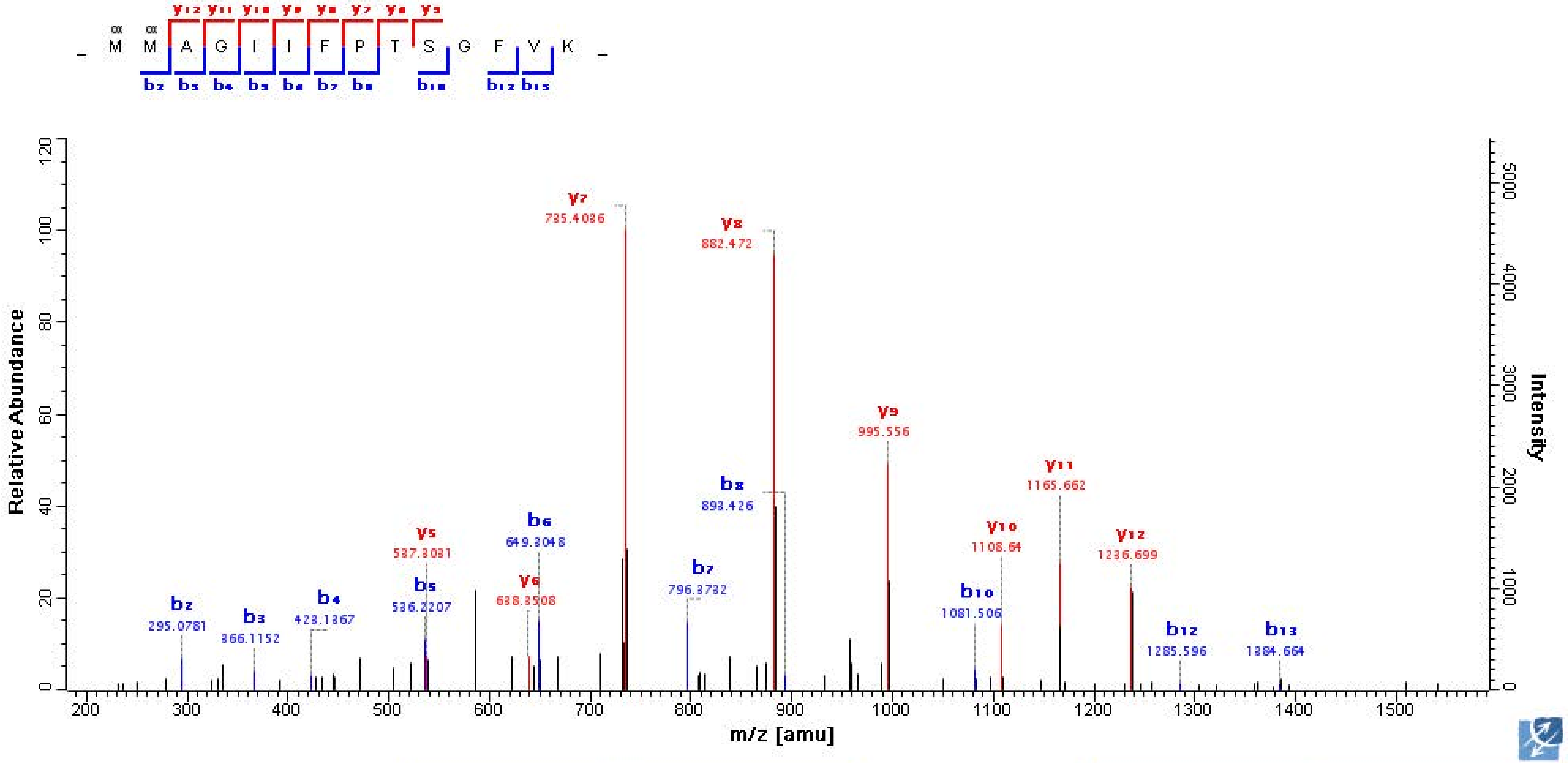
Mass:	1526.88488
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.649
Mass Error [ppm]:	-0.36148
PEP:	0.00021999
Precursor Type:	MULTI

general information

Annotation:	8 of 14
AminoAcids Coverag	57 %
Intensity Coverage:	51 %
Protein Localisation:	524 ... 537

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.055		102.055	1	T	13				
+0.06953	187.144		215.139	+0.11211	215.139	2	I	12	1426.85		1426.85	
	300.228		328.223		328.223	3	I	11	1313.76		657.384	+0.0721
	456.329		484.324		484.324	4	R	10	1200.68		1200.68	
	527.366		555.361		555.361	5	A	9	1044.58		1044.58	
	640.45	+0.21725	334.726	-0.0195	668.445	6	I	8	973.539		973.539	
	753.535	-0.0721	391.268	+0.20616	781.529	7	I	7	860.455	+0.21714	430.731	+0.4324
	882.577	-0.0112	455.79	+0.05187	910.572	8	E	6	747.371	+0.17986	747.371	
	953.614		981.609	+0.1455	981.609	9	A	5	618.328	-0.0303	309.668	+0.1259
	1050.67		1078.66		1078.66	10	P	4	547.291	+0.00133	547.291	
	1107.69		1135.68		1135.68	11	G	3	450.238		450.238	
	1206.76		1234.75		1234.75	12	V	2	393.217		393.217	
	1353.79		1381.79		1381.79	13	M	1	294.148		294.148	
						14	K	0	147.113		147.113	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F10
Scannumber:	24134
Protein:	BSU09070; yhcG
Peptide Score:	108.56
Method:	ITMS; CID; 3



precursor information

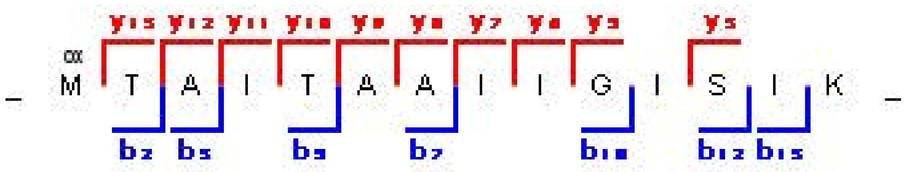
Mass:	1529.76241
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.5638
Mass Error [ppm]:	0.13029
PEP:	0.00017484
Precursor Type:	MULTI

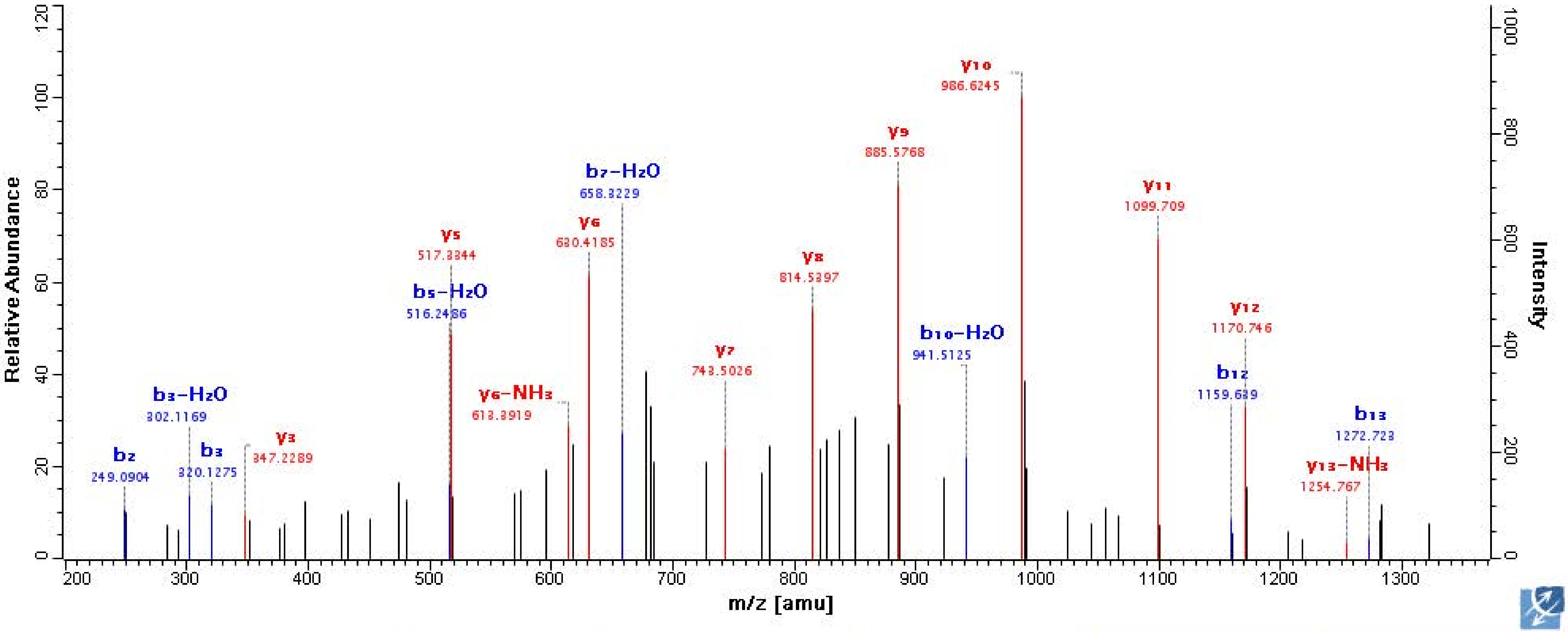
general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	51 %
Protein Localisation:	47 ... 60

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.042675695	1	M	13		
-0.1410937	295.078074923	2	M	12	1383.734085079	
+0.1942595	366.115188711	3	A	11	1236.698685851	+0.0199421
+0.0783439	423.136652435	4	G	10	1165.661572063	+0.0913576
+0.05089	536.220716415	5	I	9	1108.64010834	+0.0855997
-0.0527662	649.304780395	6	I	8	995.556044359	+0.0229351
-0.0248056	796.373194312	7	F	7	882.471980379	-0.0162309
-0.3465514	893.425958164	8	P	6	735.403566463	-0.0087911
	994.473636638	9	T	5	638.350802611	+0.1786774
+0.1778066	1081.505665048	10	S	4	537.303124136	-0.0011832
	1138.527128771	11	G	3	450.271095727	
-0.0205915	1285.595542687	12	F	2	393.249632003	
+0.2070151	1384.663956604	13	V	1	246.181218087	
		14	K	0	147.112804171	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F10
Scannumber:	27486
Protein:	BSU39490; LP9F; yxeN
Peptide Score:	90.93
Method:	ITMS; CID; 3





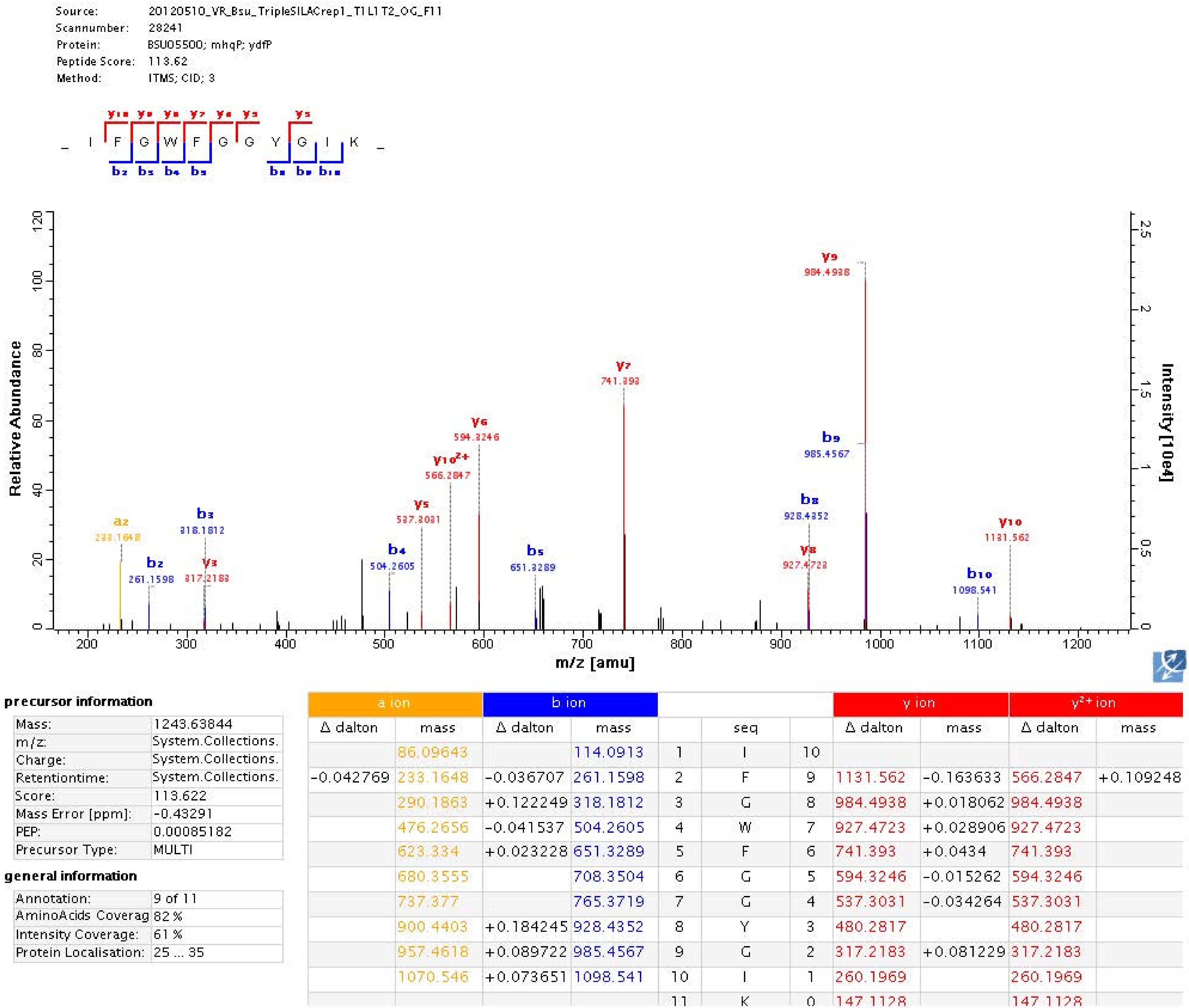
precursor information

Mass:	1417.82119
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	90.92576
Mass Error [ppm]:	-0.17533
PEP:	0.00026182
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	46 %
Protein Localisation:	89 ... 102

b ion					y ion	
Δ dalton	mass		seq		Δ dalton	mass
	148.042675695	1	M	13		
+0.0606163	249.090354169	2	T	12	1271.793314518	
+0.3396341	320.127467957	3	A	11	1170.745636044	+0.1191101
	433.211531937	4	I	10	1099.708522256	+0.1562238
	534.259210411	5	T	9	986.624458275	+0.2390671
	605.296324199	6	A	8	885.576779801	+0.077334
	676.333437987	7	A	7	814.539666014	+0.0598213
	789.417501967	8	I	6	743.502552226	+0.1869009
	902.501565948	9	I	5	630.418488245	+0.0303643
	959.523029671	10	G	4	517.334424265	-0.0143559
	1072.607093652	11	I	3	460.312960541	
+0.0818252	1159.639122062	12	S	2	347.228896561	+0.0580297
-0.42802	1272.723186042	13	I	1	260.196868151	
		14	K	0	147.112804171	



Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F11
Scannumber: 28241
Protein: BSU05500; mhqP; ydfP
Peptide Score: 113.62
Method: ITMS; CID; 3

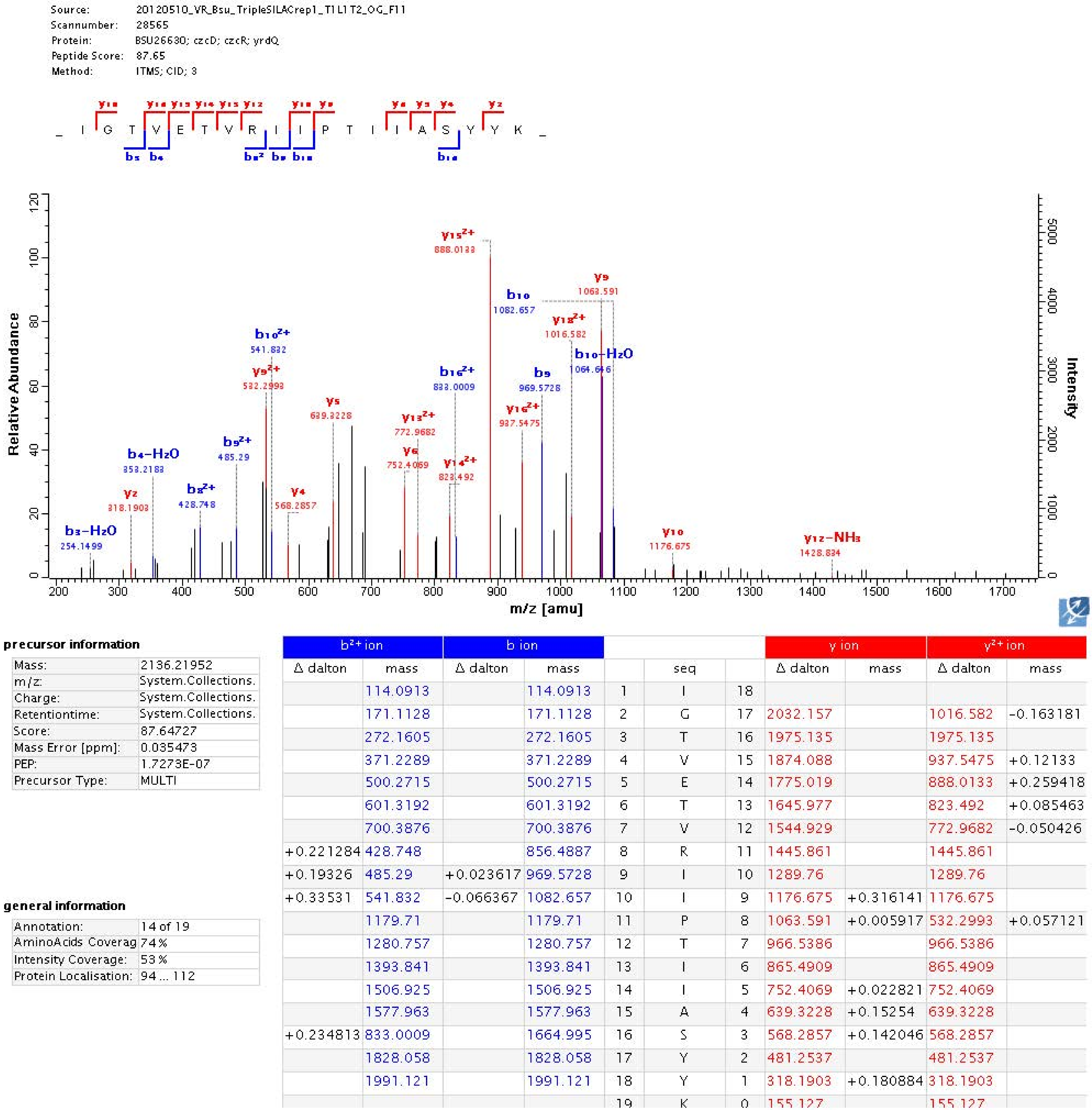
precursor information

Mass:	1243.63844
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	113.622
Mass Error [ppm]:	-0.43291
PEP:	0.00085182
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	61 %
Protein Localisation:	25 ... 35

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	10				
-0.042769	233.1648	-0.036707	261.1598	2	F	9	1131.562	-0.163633	566.2847	+0.109248
	290.1863	+0.122249	318.1812	3	G	8	984.4938	+0.018062	984.4938	
	476.2656	-0.041537	504.2605	4	W	7	927.4723	+0.028906	927.4723	
	623.334	+0.023228	651.3289	5	F	6	741.393	+0.0434	741.393	
	680.3555		708.3504	6	G	5	594.3246	-0.015262	594.3246	
	737.377		765.3719	7	G	4	537.3031	-0.034264	537.3031	
	900.4403	+0.184245	928.4352	8	Y	3	480.2817		480.2817	
	957.4618	+0.089722	985.4567	9	G	2	317.2183	+0.081229	317.2183	
	1070.546	+0.073651	1098.541	10	I	1	260.1969		260.1969	
				11	K	0	147.1128		147.1128	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F11
Scannumber:	28565
Protein:	BSU26630; czcD; czcR; yrdQ
Peptide Score:	87.65
Method:	ITMS; CID; 3

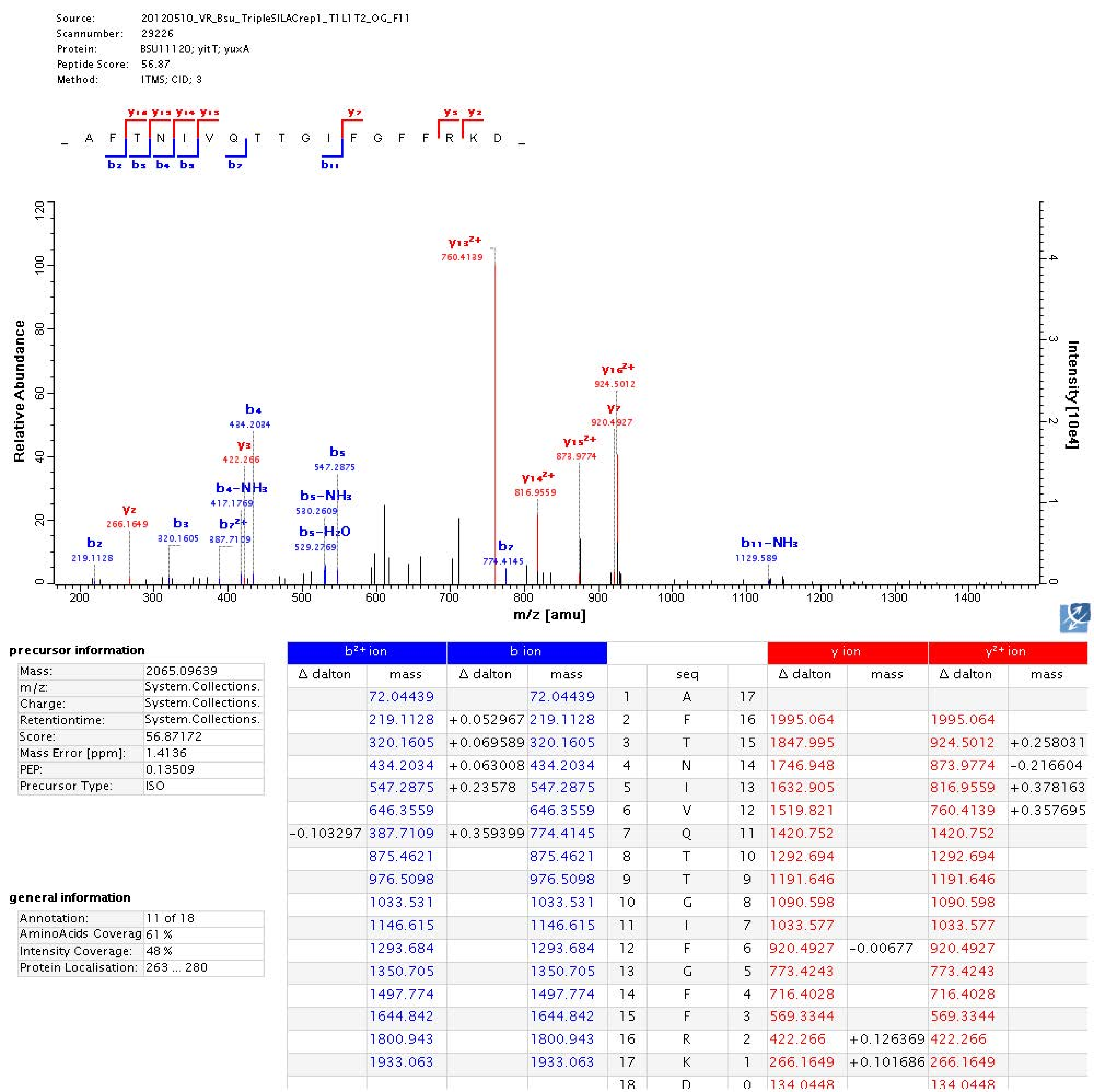
precursor information

Mass:	2136.21952
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	87.64727
Mass Error [ppm]:	0.035473
PEP:	1.7273E-07
Precursor Type:	MULTI

general information

Annotation:	14 of 19
AminoAcids Coverag	74%
Intensity Coverage:	53%
Protein Localisation:	94 ... 112

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	18				
	171.1128		171.1128	2	G	17	2032.157		1016.582	-0.163181
	272.1605		272.1605	3	T	16	1975.135		1975.135	
	371.2289		371.2289	4	V	15	1874.088		937.5475	+0.12133
	500.2715		500.2715	5	E	14	1775.019		888.0133	+0.259418
	601.3192		601.3192	6	T	13	1645.977		823.492	+0.085463
	700.3876		700.3876	7	V	12	1544.929		772.9682	-0.050426
+0.221284	428.748		856.4887	8	R	11	1445.861		1445.861	
+0.19326	485.29	+0.023617	969.5728	9	I	10	1289.76		1289.76	
+0.33531	541.832	-0.066367	1082.657	10	I	9	1176.675	+0.316141	1176.675	
	1179.71		1179.71	11	P	8	1063.591	+0.005917	532.2993	+0.057121
	1280.757		1280.757	12	T	7	966.5386		966.5386	
	1393.841		1393.841	13	I	6	865.4909		865.4909	
	1506.925		1506.925	14	I	5	752.4069	+0.022821	752.4069	
	1577.963		1577.963	15	A	4	639.3228	+0.15254	639.3228	
+0.234813	833.0009		1664.995	16	S	3	568.2857	+0.142046	568.2857	
	1828.058		1828.058	17	Y	2	481.2537		481.2537	
	1991.121		1991.121	18	Y	1	318.1903	+0.180884	318.1903	
				19	K	0	155.127		155.127	



Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F11
Scannumber: 29226
Protein: BSU11120; yitT; yuxA
Peptide Score: 56.87
Method: ITMS; CID; 3

precursor information

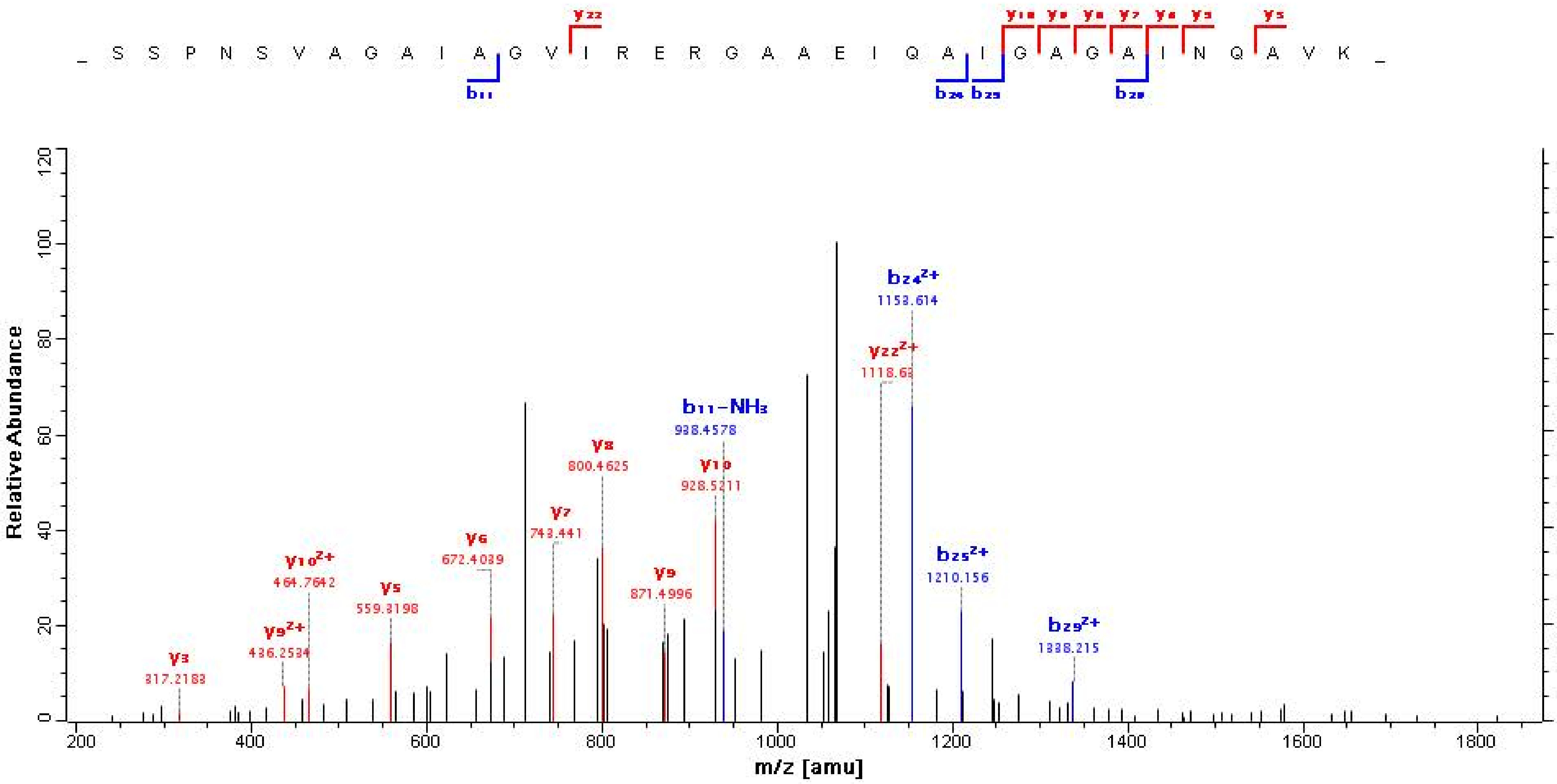
Mass:	2065.09639
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	56.87172
Mass Error [ppm]:	1.4136
PEP:	0.13509
Precursor Type:	ISO

general information

Annotation:	11 of 18
AminoAcids Coverag	61 %
Intensity Coverage:	48 %
Protein Localisation:	263 ... 280

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	17				
	219.1128	+0.052967	219.1128	2	F	16	1995.064		1995.064	
	320.1605	+0.069589	320.1605	3	T	15	1847.995		924.5012	+0.258031
	434.2034	+0.063008	434.2034	4	N	14	1746.948		873.9774	-0.216604
	547.2875	+0.23578	547.2875	5	I	13	1632.905		816.9559	+0.378163
	646.3559		646.3559	6	V	12	1519.821		760.4139	+0.357695
-0.103297	387.7109	+0.359399	774.4145	7	Q	11	1420.752		1420.752	
	875.4621		875.4621	8	T	10	1292.694		1292.694	
	976.5098		976.5098	9	T	9	1191.646		1191.646	
	1033.531		1033.531	10	G	8	1090.598		1090.598	
	1146.615		1146.615	11	I	7	1033.577		1033.577	
	1293.684		1293.684	12	F	6	920.4927	-0.00677	920.4927	
	1350.705		1350.705	13	G	5	773.4243		773.4243	
	1497.774		1497.774	14	F	4	716.4028		716.4028	
	1644.842		1644.842	15	F	3	569.3344		569.3344	
	1800.943		1800.943	16	R	2	422.266	+0.126369	422.266	
	1933.063		1933.063	17	K	1	266.1649	+0.101686	266.1649	
				18	D	0	134.0448		134.0448	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F11
Scannumber: 29536
Protein: BSU16980; spoVS
Peptide Score: 40.84
Method: ITMS; CID; 3



precursor information

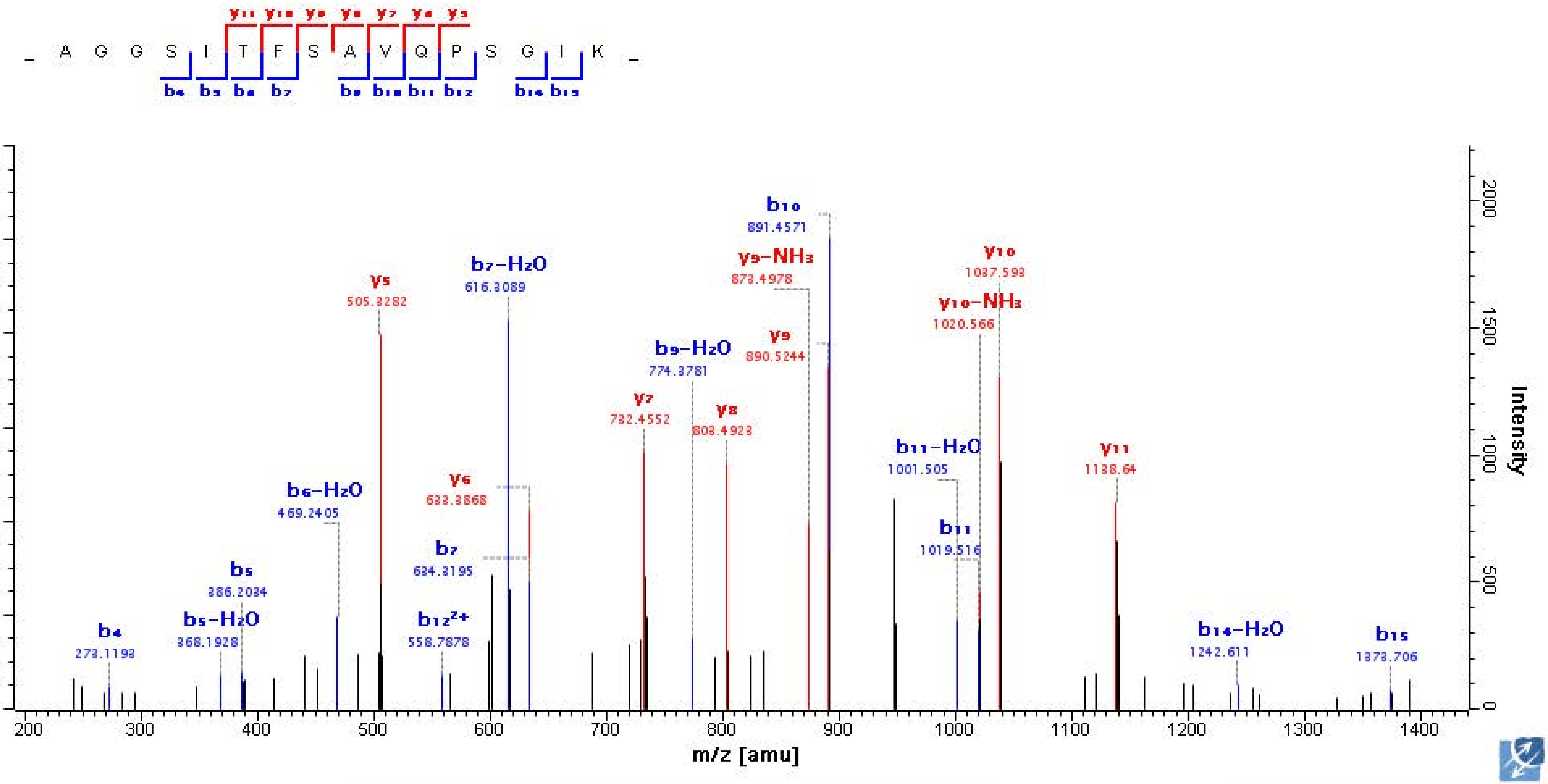
Mass:	3345.8147
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	40.83715
Mass Error [ppm]:	0.89719
PEP:	0.00075562
Precursor Type:	MULTI

general information

Annotation:	12 of 35
AminoAcids Coverag	34 %
Intensity Coverage:	28 %
Protein Localisation:	10 ... 44

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	34				
	175.0713		175.0713	2	S	33	3259.787		3259.787	
	272.1241		272.1241	3	P	32	3172.755		3172.755	
	386.167		386.167	4	N	31	3075.702		3075.702	
	473.1991		473.1991	5	S	30	2961.659		2961.659	
	572.2675		572.2675	6	V	29	2874.627		2874.627	
	643.3046		643.3046	7	A	28	2775.559		2775.559	
	700.326		700.326	8	G	27	2704.522		2704.522	
	771.3632		771.3632	9	A	26	2647.5		2647.5	
	884.4472		884.4472	10	I	25	2576.463		2576.463	
	955.4843		955.4843	11	A	24	2463.379		2463.379	
	1012.506		1012.506	12	G	23	2392.342		2392.342	
	1111.574		1111.574	13	V	22	2335.32		2335.32	
	1224.658		1224.658	14	I	21	2236.252		1118.63	-0.187641
	1380.759		1380.759	15	R	20	2123.168		2123.168	
	1509.802		1509.802	16	E	19	1967.067		1967.067	
	1665.903		1665.903	17	R	18	1838.024		1838.024	
	1722.925		1722.925	18	G	17	1681.923		1681.923	
	1793.962		1793.962	19	A	16	1624.902		1624.902	
	1864.999		1864.999	20	A	15	1553.865		1553.865	
	1994.041		1994.041	21	E	14	1482.827		1482.827	
	2107.125		2107.125	22	I	13	1353.785		1353.785	
	2235.184		2235.184	23	Q	12	1240.701		1240.701	
+0.240654	1153.614		2306.221	24	A	11	1112.642		1112.642	
+0.206923	1210.156		2419.305	25	I	10	1041.605		1041.605	
	2476.327		2476.327	26	G	9	928.5211	-0.003539	464.7642	+0.021417
	2547.364		2547.364	27	A	8	871.4996	+0.123699	436.2534	+0.260787
	2604.385		2604.385	28	G	7	800.4625	+0.019638	800.4625	
-0.239716	1338.215		2675.422	29	A	6	743.441	+0.13827	743.441	
	2788.506		2788.506	30	I	5	672.4039	+0.165557	672.4039	
	2902.549		2902.549	31	N	4	559.3198	+0.15697	559.3198	
	3030.608		3030.608	32	Q	3	445.2769		445.2769	
	3101.645		3101.645	33	A	2	317.2183	+0.115408	317.2183	
	3200.713		3200.713	34	V	1	246.1812		246.1812	
				35	K	0	147.1128		147.1128	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F12b
Scannumber:	18552
Protein:	BSU38900; yxjM
Peptide Score:	102.52
Method:	ITMS; CID; 3



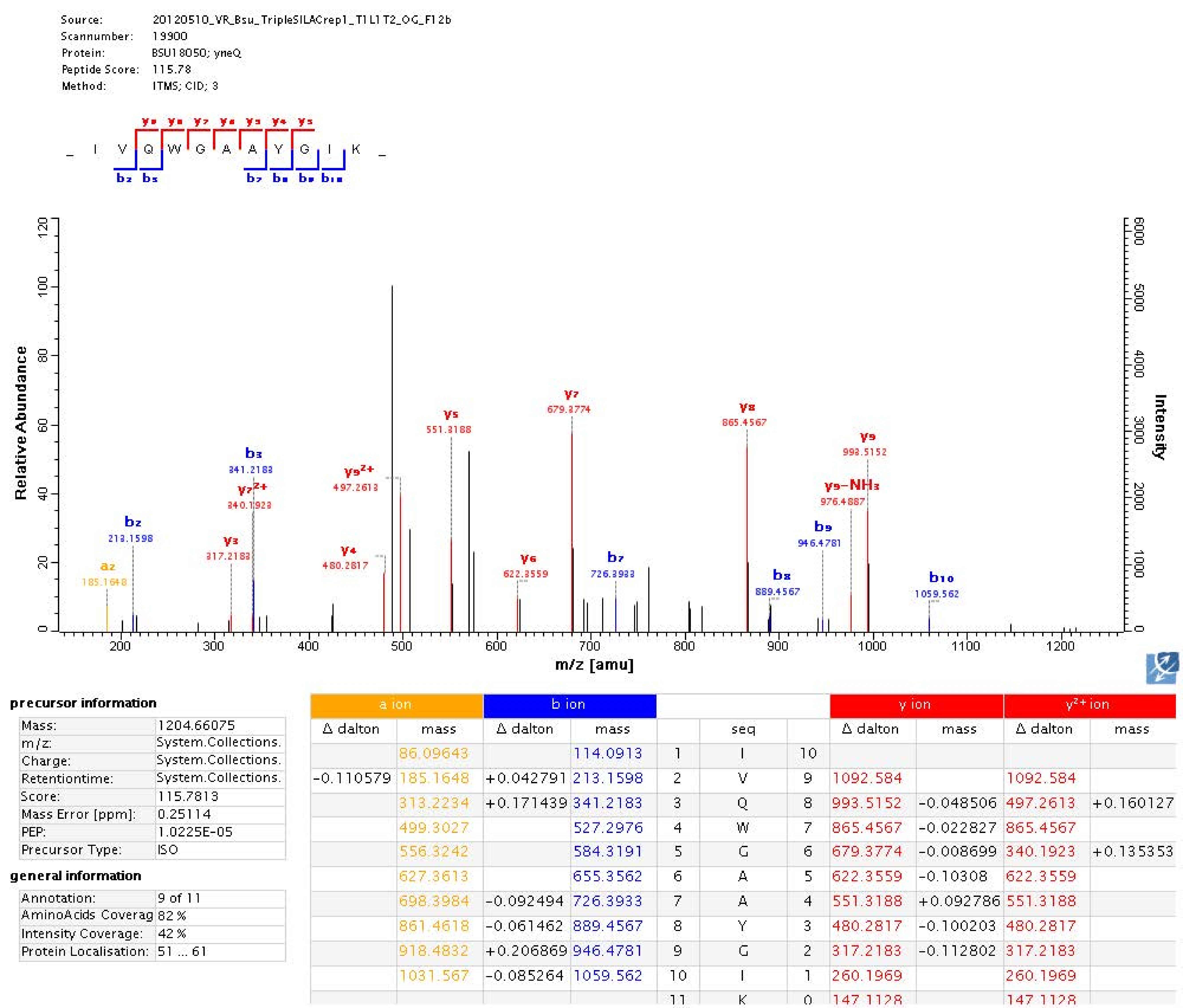
precursor information

Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.52
Mass Error [ppm]:	-1.6103
PEP:	5.5357E-09
Precursor Type:	PEAK

general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	56 %
Protein Localisation:	372 ... 387

b²⁺ ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	72.044390254		72.044390254	1	A	15		
	129.06585398		129.06585398	2	G	14	1452.799477	
	186.0873177		186.0873177	3	G	13	1395.7780132	
	273.11934611	-0.0003886	273.11934611	4	S	12	1338.7565495	
	386.20341009	-0.0077924	386.20341009	5	I	11	1251.7245211	
	487.25108857		487.25108857	6	T	10	1138.6404571	-0.112503
	634.31950248	+0.0766157	634.31950248	7	F	9	1037.5927787	-0.0401664
	721.35153089		721.35153089	8	S	8	890.52436475	-0.0479854
	792.38864468		792.38864468	9	A	7	803.49233634	-0.0763817
	891.4570586	-0.0248687	891.4570586	10	V	6	732.45522255	-0.0261454
	1019.5156361	+0.2375377	1019.5156361	11	Q	5	633.38680863	-0.0989668
+0.4293859	558.78783821		1116.5684	12	P	4	505.32823112	+0.2027747
	1203.6004284		1203.6004284	13	S	3	408.27546727	
	1260.6218921		1260.6218921	14	G	2	321.24343886	
	1373.7059561	+0.3823008	1373.7059561	15	I	1	264.22197513	
				16	K	0	151.13791115	



Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F12b
Scannumber:	19900
Protein:	BSU18050; yneQ
Peptide Score:	115.78
Method:	ITMS; CID; 3

precursor information

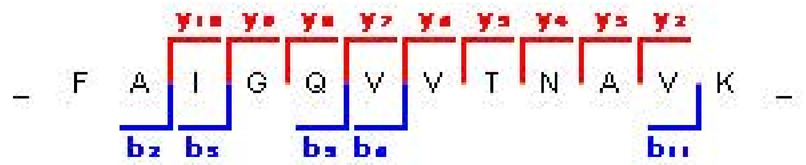
Mass:	1204.66075
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	115.7813
Mass Error [ppm]:	0.25114
PEP:	1.0225E-05
Precursor Type:	ISO

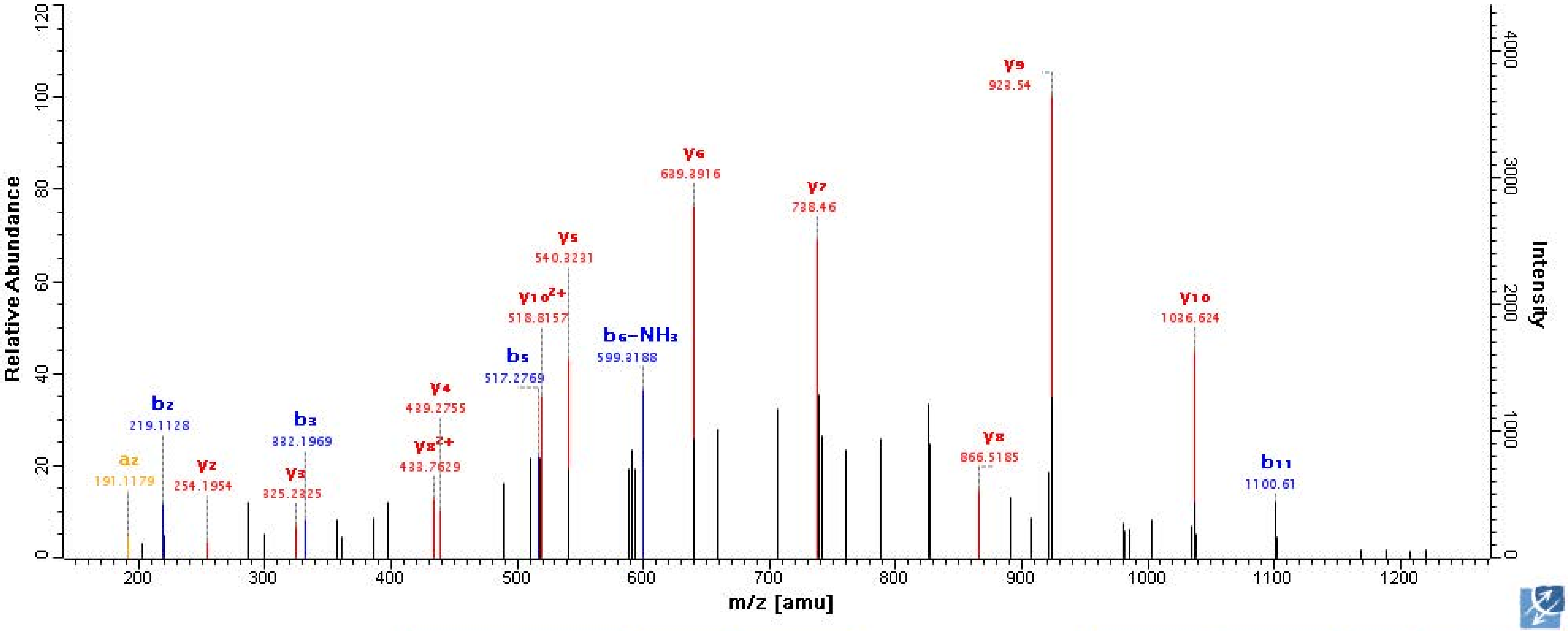
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	42 %
Protein Localisation:	51 ... 61

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	10				
-0.110579	185.1648	+0.042791	213.1598	2	V	9	1092.584		1092.584	
	313.2234	+0.171439	341.2183	3	Q	8	993.5152	-0.048506	497.2613	+0.160127
	499.3027		527.2976	4	W	7	865.4567	-0.022827	865.4567	
	556.3242		584.3191	5	G	6	679.3774	-0.008699	340.1923	+0.135353
	627.3613		655.3562	6	A	5	622.3559	-0.10308	622.3559	
	698.3984	-0.092494	726.3933	7	A	4	551.3188	+0.092786	551.3188	
	861.4618	-0.061462	889.4567	8	Y	3	480.2817	-0.100203	480.2817	
	918.4832	+0.206869	946.4781	9	G	2	317.2183	-0.112802	317.2183	
	1031.567	-0.085264	1059.562	10	I	1	260.1969		260.1969	
				11	K	0	147.1128		147.1128	

Source: 20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F12b
Scannumber: 20399
Protein: B65E; BSU39650; yxdK
Peptide Score: 97.73
Method: ITMS; CID; 3





precursor information

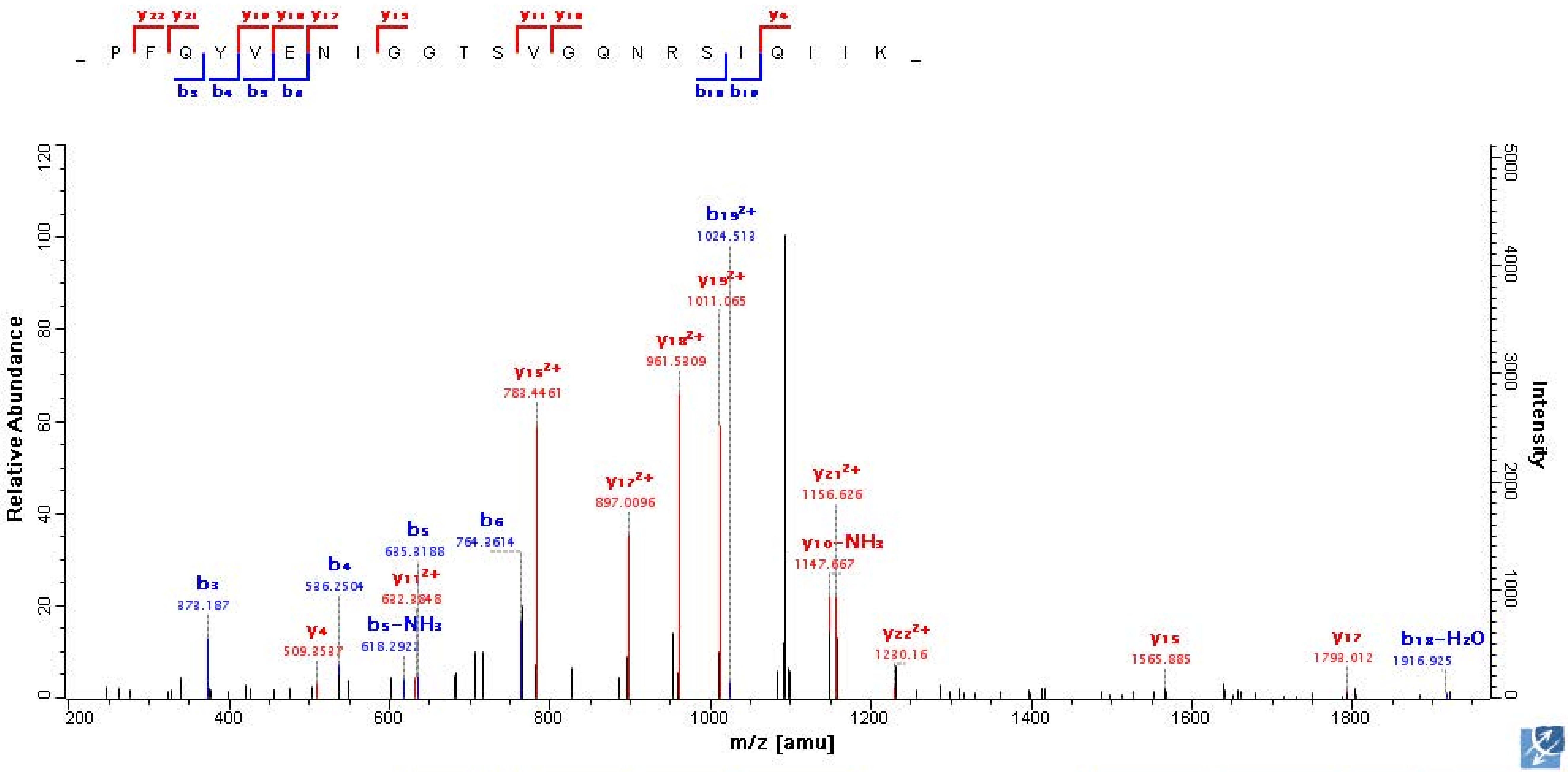
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	97.73378
Mass Error [ppm]:	-0.39056
PEP:	0.00049104
Precursor Type:	PEAK

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	45 %
Protein Localisation:	220 ... 231

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.0808		148.0757	1	F	11				
+0.034012	191.1179	+0.09055	219.1128	2	A	10	1107.661		1107.661	
	304.202	-0.068206	332.1969	3	I	9	1036.624	+0.034256	518.8157	+0.12494
	361.2234		389.2183	4	G	8	923.54	-0.004849	923.54	
	489.282	+0.138374	517.2769	5	Q	7	866.5185	+0.012342	433.7629	-0.035736
	588.3504		616.3453	6	V	6	738.46	+0.070492	738.46	
	687.4188		715.4137	7	V	5	639.3916	-0.014597	639.3916	
	788.4665		816.4614	8	T	4	540.3231	+0.00743	540.3231	
	902.5094		930.5043	9	N	3	439.2755	+0.170465	439.2755	
	973.5465		1001.541	10	A	2	325.2325	-0.103808	325.2325	
	1072.615	+0.061394	1100.61	11	V	1	254.1954	+0.120165	254.1954	
				12	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F12b
Scannumber:	21533
Protein:	BSU16340; cheA; fliZ
Peptide Score:	58.02
Method:	ITMS; CID; 3



precursor information

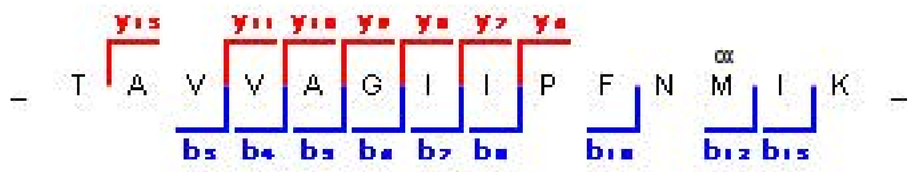
Mass:	2547.34102
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	58.02433
Mass Error [ppm]:	-1.3777
PEP:	0.00019953
Precursor Type:	MULTI

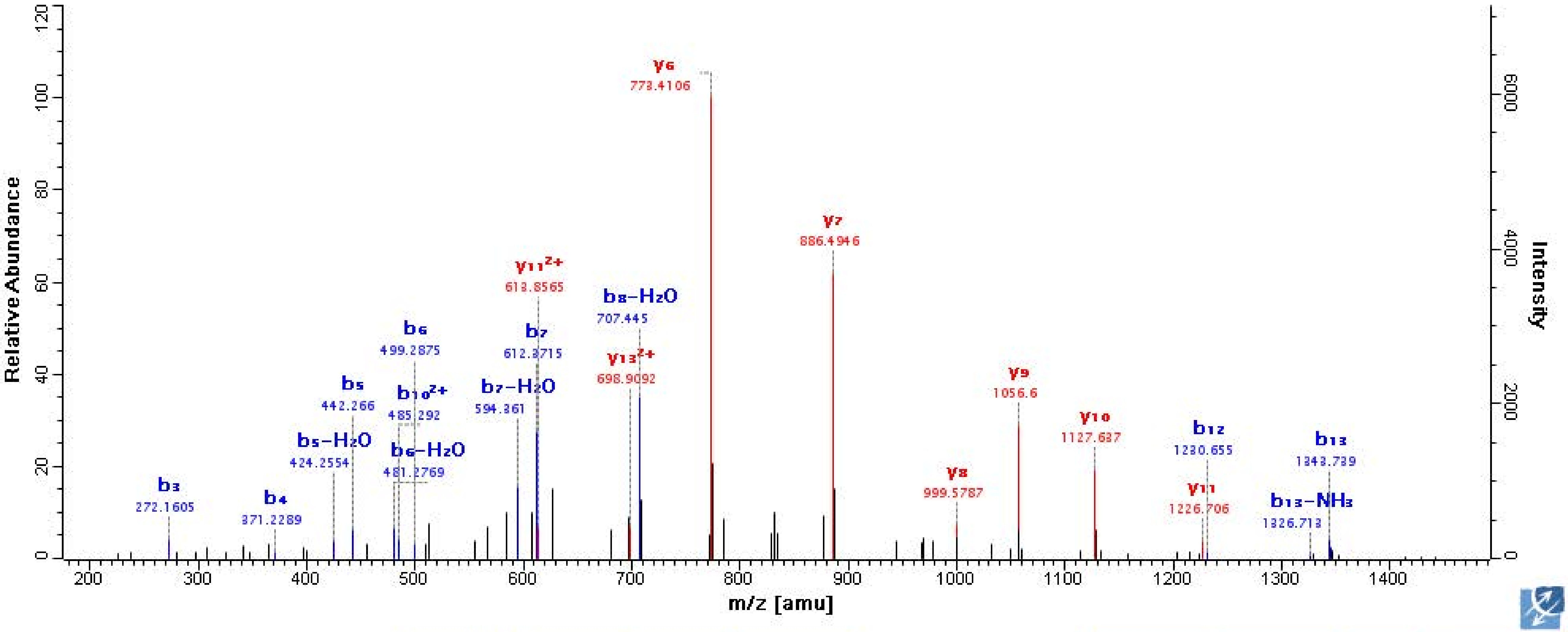
general information

Annotation:	12 of 23
AminoAcids Coverag	52 %
Intensity Coverage:	44 %
Protein Localisation:	106 ... 128

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	98.06004		98.06004	1	P	22				
	245.1285		245.1285	2	F	21	2459.313		1230.16	-0.070784
	373.187	-0.03365	373.187	3	Q	20	2312.245		1156.626	-0.224444
	536.2504	-0.113458	536.2504	4	Y	19	2184.186		2184.186	
	635.3188	+0.141248	635.3188	5	V	18	2021.123		1011.065	+0.375694
	764.3614	-0.135415	764.3614	6	E	17	1922.055		961.5309	+0.2365
	878.4043		878.4043	7	N	16	1793.012	+0.318036	897.0096	+0.315841
	991.4884		991.4884	8	I	15	1678.969		1678.969	
	1048.51		1048.51	9	G	14	1565.885	+0.189778	783.4461	+0.326358
	1105.531		1105.531	10	G	13	1508.863		1508.863	
	1206.579		1206.579	11	T	12	1451.842		1451.842	
	1293.611		1293.611	12	S	11	1350.794		1350.794	
	1392.679		1392.679	13	V	10	1263.762		632.3848	-0.202718
	1449.701		1449.701	14	G	9	1164.694		1164.694	
	1577.759		1577.759	15	Q	8	1107.672		1107.672	
	1691.802		1691.802	16	N	7	979.6138		979.6138	
	1847.903		1847.903	17	R	6	865.5709		865.5709	
	1934.936		1934.936	18	S	5	709.4698		709.4698	
-0.017212	1024.513		2048.02	19	I	4	622.4378		622.4378	
	2176.078		2176.078	20	Q	3	509.3537	+0.179495	509.3537	
	2289.162		2289.162	21	I	2	381.2951		381.2951	
	2402.246		2402.246	22	I	1	268.2111		268.2111	
				23	K	0	155.127		155.127	

Source:	20120510_VR_Bsu_TripleSILACrep1_T1L1T2_OG_F12b
Scannumber:	25202
Protein:	BSU23050; ypaA
Peptide Score:	102.97
Method:	ITMS; CID; 3





precursor information

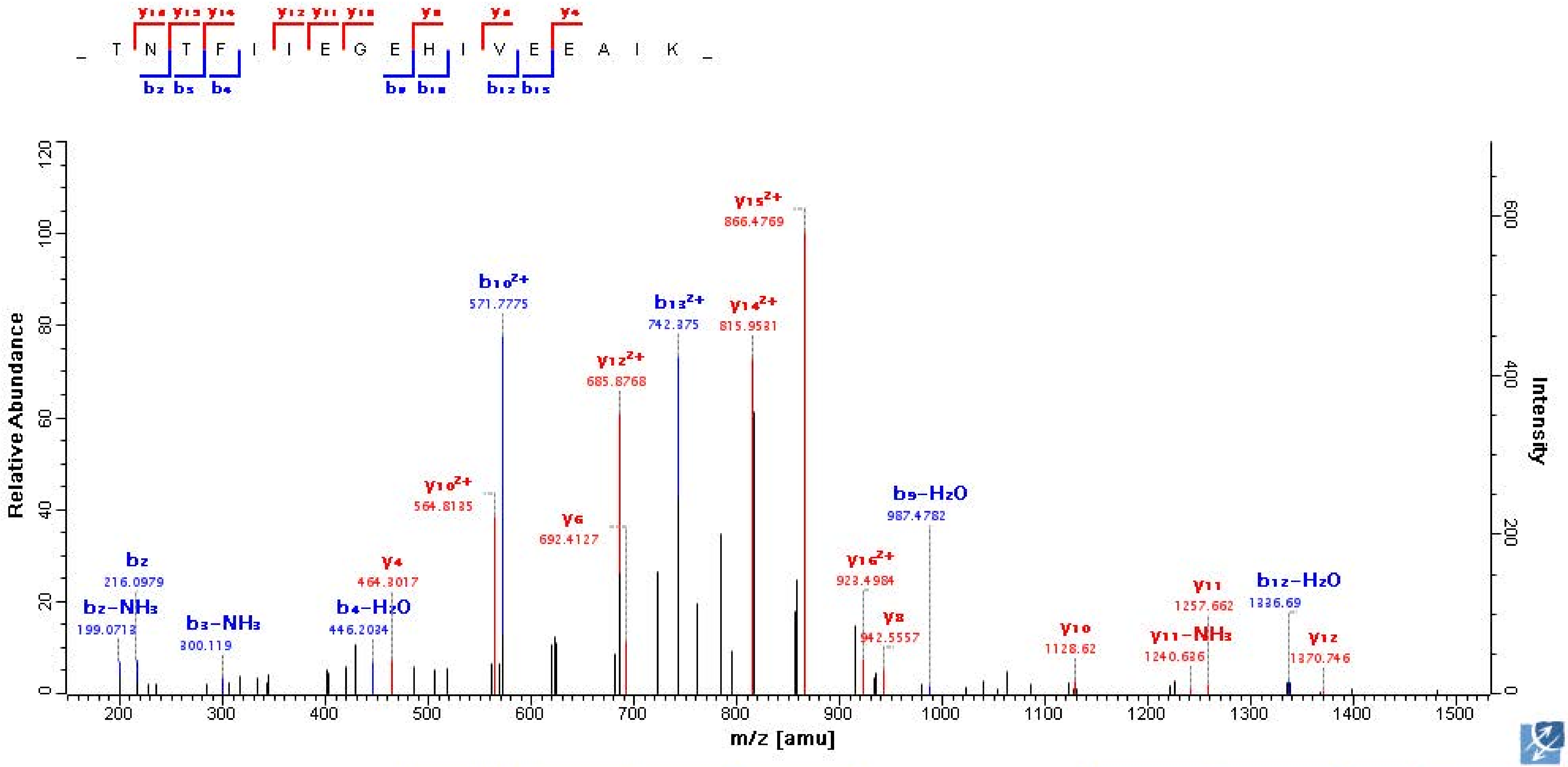
Mass:	1488.83912
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	102.9703
Mass Error [ppm]:	1.1354
PEP:	0.00020104
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	57 %
Protein Localisation:	149 ... 162

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	13				
	173.0921		173.0921	2	A	12	1396.811		698.9092	-0.453925
	272.1605	+0.062692	272.1605	3	V	11	1325.774		1325.774	
	371.2289	-0.038955	371.2289	4	V	10	1226.706	+0.211057	613.8565	-0.056923
	442.266	+0.020367	442.266	5	A	9	1127.637	+0.008353	1127.637	
	499.2875	+0.073183	499.2875	6	G	8	1056.6	-0.123723	1056.6	
	612.3715	-0.079363	612.3715	7	I	7	999.5787	-0.007593	999.5787	
	725.4556		725.4556	8	I	6	886.4946	-0.07569	886.4946	
	822.5084		822.5084	9	P	5	773.4106	-0.045093	773.4106	
-0.242468	485.292		969.5768	10	F	4	676.3578		676.3578	
	1083.62		1083.62	11	N	3	529.2894		529.2894	
	1230.655	+0.270553	1230.655	12	M	2	415.2465		415.2465	
	1343.739	-0.081578	1343.739	13	I	1	268.2111		268.2111	
				14	K	0	155.127		155.127	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F08
Scannumber:	13641
Protein:	BSU28650; ysgA
Peptide Score:	82.91
Method:	ITMS; CID; 3



precursor information

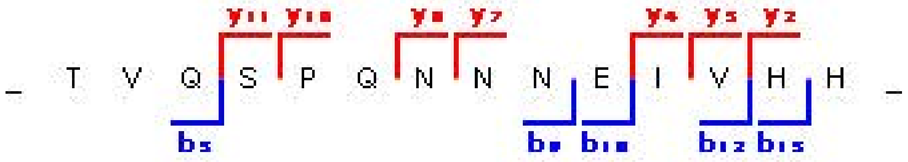
Mass:	1942.00476
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	82.90767
Mass Error [ppm]:	-0.0009983
PEP:	0.0006632
Precursor Type:	MULTI

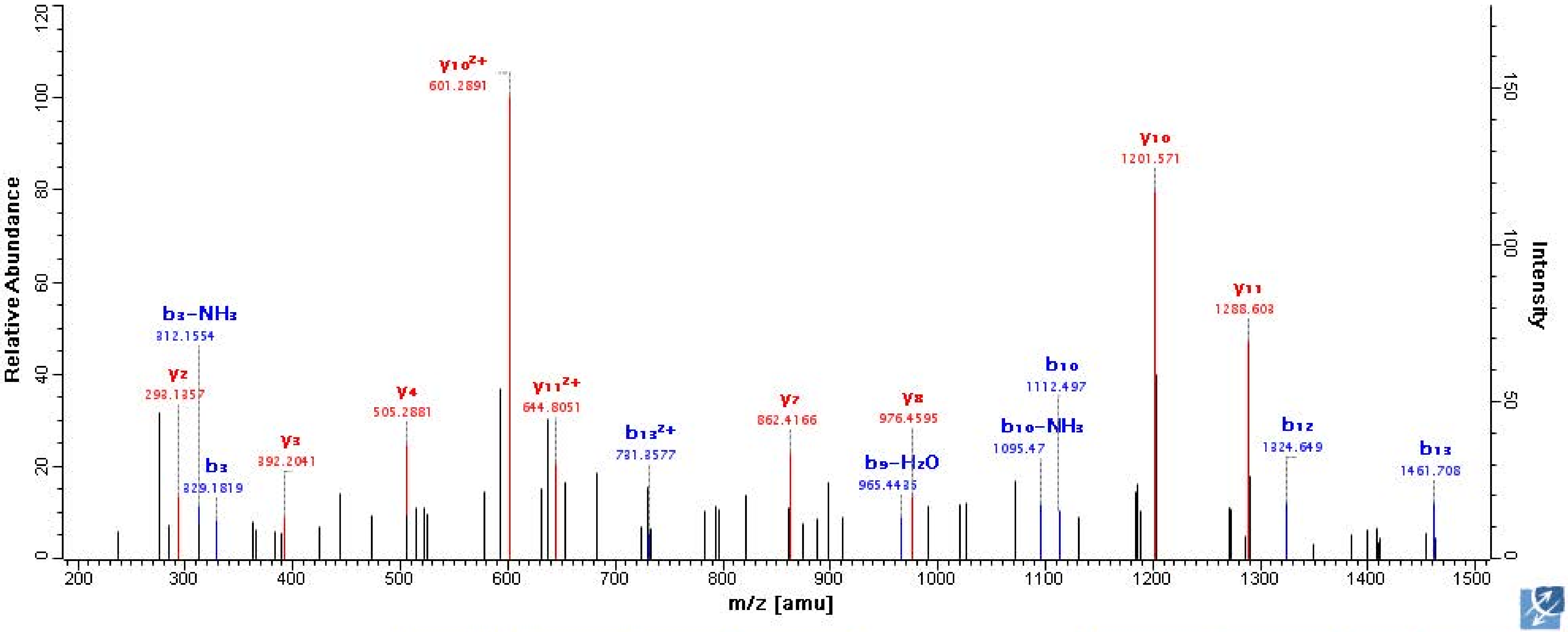
general information

Annotation:	12 of 17
AminoAcids Coverag	71 %
Intensity Coverage:	49 %
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	+0.132586	216.0979	2	N	15	1845.989		923.4984	+0.157392
	317.1456		317.1456	3	T	14	1731.947		866.4769	+0.254051
	464.214		464.214	4	F	13	1630.899		815.9531	-0.037356
	577.298		577.298	5	I	12	1483.83		1483.83	
	690.3821		690.3821	6	I	11	1370.746	-0.033854	685.8768	+0.039127
	819.4247		819.4247	7	E	10	1257.662	+0.18937	1257.662	
	876.4462		876.4462	8	G	9	1128.62	-0.25522	564.8135	+0.23954
	1005.489		1005.489	9	E	8	1071.598		1071.598	
+0.347591	571.7775		1142.548	10	H	7	942.5557	+0.091735	942.5557	
	1255.632		1255.632	11	I	6	805.4968		805.4968	
	1354.7		1354.7	12	V	5	692.4127	+0.186188	692.4127	
-0.088934	742.375		1483.743	13	E	4	593.3443		593.3443	
	1612.785		1612.785	14	E	3	464.3017	+0.037857	464.3017	
	1683.822		1683.822	15	A	2	335.2591		335.2591	
	1796.907		1796.907	16	I	1	264.222		264.222	
				17	K	0	151.1379		151.1379	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F08
Scannumber:	3675
Protein:	BSU28910; lrgA; ysbA
Peptide Score:	109.24
Method:	ITMS; CID; 3





precursor information

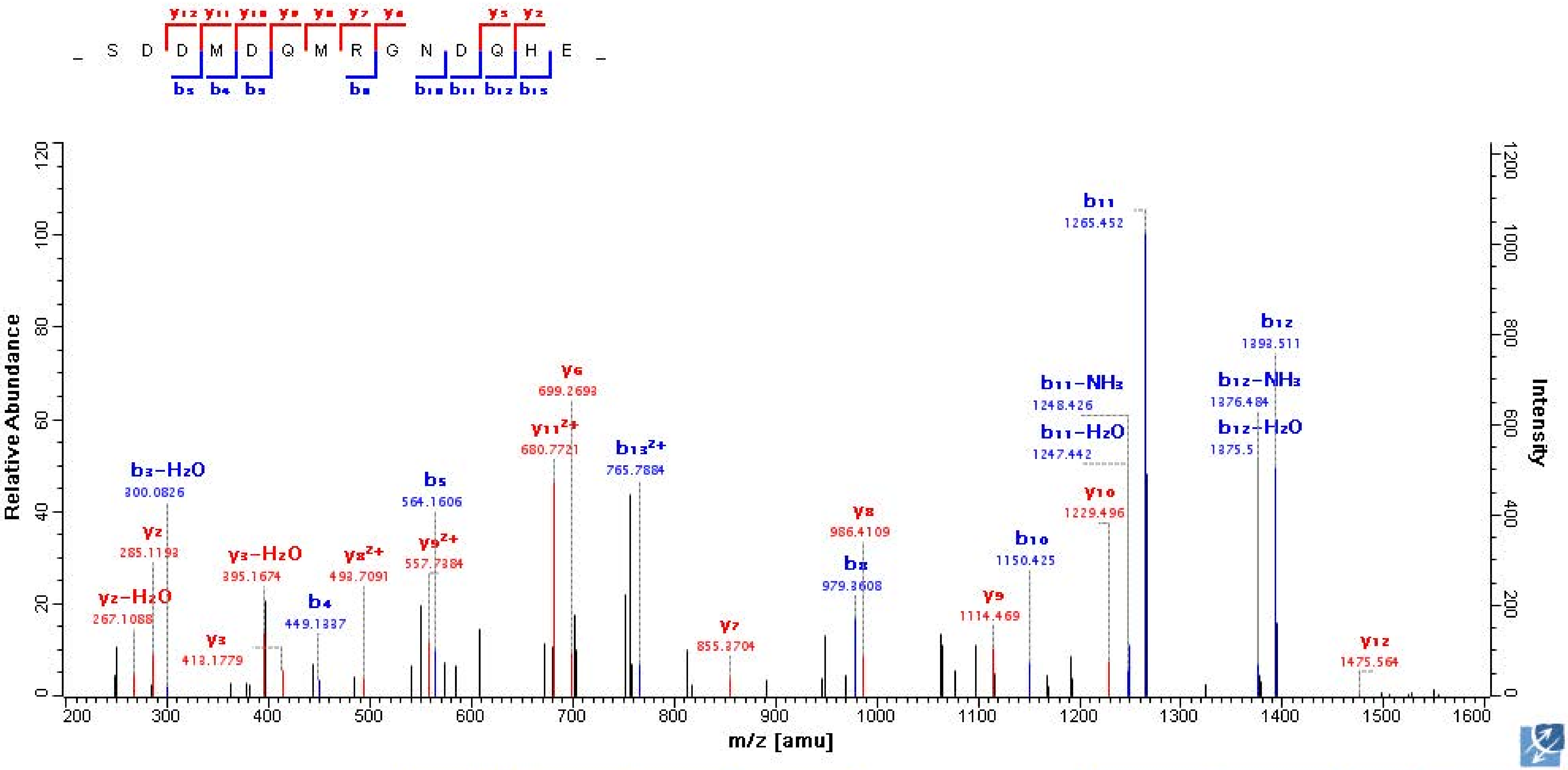
Mass:	1615.77012
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.236
Mass Error [ppm]:	-0.098832
PEP:	0.0021293
Precursor Type:	ISO

general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	38 %
Protein Localisation:	133 ... 146

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	13				
	201.1234		201.1234	2	V	12	1515.73		1515.73	
	329.1819	-0.063965	329.1819	3	Q	11	1416.661		1416.661	
	416.214		416.214	4	S	10	1288.603	+0.00905	644.8051	+0.086092
	513.2667		513.2667	5	P	9	1201.571	-0.061582	601.2891	+0.253535
	641.3253		641.3253	6	Q	8	1104.518		1104.518	
	755.3682		755.3682	7	N	7	976.4595	+0.114029	976.4595	
	869.4112		869.4112	8	N	6	862.4166	+0.114171	862.4166	
	983.4541		983.4541	9	N	5	748.3737		748.3737	
	1112.497	+0.14198	1112.497	10	E	4	634.3307		634.3307	
	1225.581		1225.581	11	I	3	505.2881	-0.122127	505.2881	
	1324.649	+0.005494	1324.649	12	V	2	392.2041	+0.102989	392.2041	
-0.117628	731.3577	-0.096753	1461.708	13	H	1	293.1357	-0.057967	293.1357	
				14	H	0	156.0768		156.0768	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F09
Scannumber:	5077
Protein:	BSU31620; mrpC; yufV
Peptide Score:	136.93
Method:	ITMS; CID; 3



precursor information

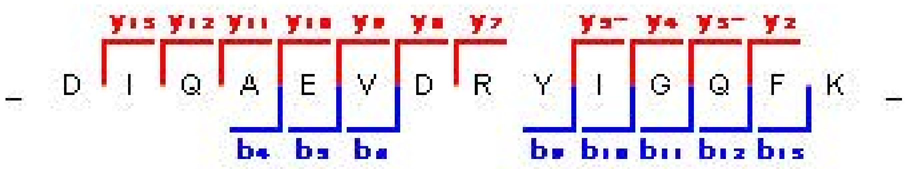
Mass:	1676.61583
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	136.9324
Mass Error [ppm]:	0.19706
PEP:	2.0946E-06
Precursor Type:	ISO

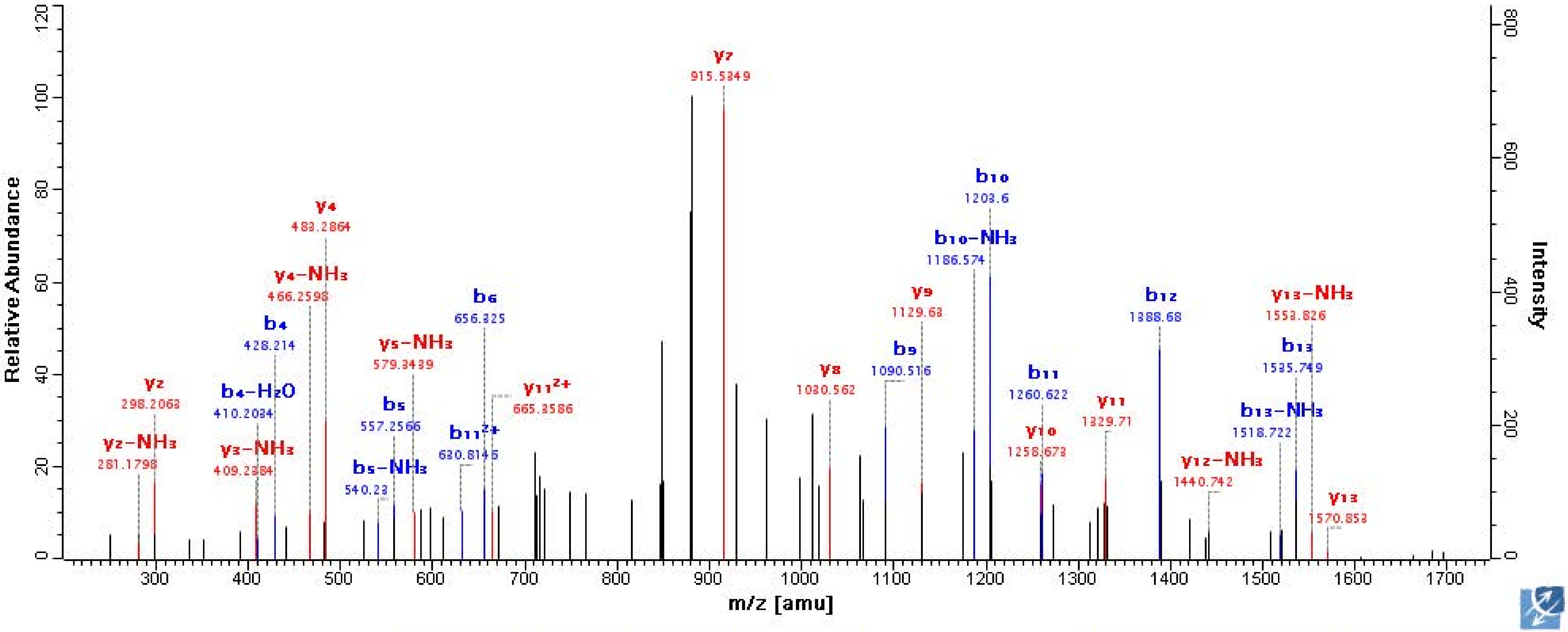
general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	46 %
Protein Localisation:	100 ... 113

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	13				
	203.0662		203.0662	2	D	12	1590.591		1590.591	
	318.0932		318.0932	3	D	11	1475.564	+0.37028	1475.564	
	449.1337	+0.177787	449.1337	4	M	10	1360.537		680.7721	+0.163357
	564.1606	+0.035854	564.1606	5	D	9	1229.496	+0.043665	1229.496	
	692.2192		692.2192	6	Q	8	1114.469	+0.131765	557.7384	+0.04546
	823.2597		823.2597	7	M	7	986.4109	+0.067235	493.7091	-0.249409
	979.3608	-0.041944	979.3608	8	R	6	855.3704	+0.105522	855.3704	
	1036.382		1036.382	9	G	5	699.2693	+0.128874	699.2693	
	1150.425	+0.066028	1150.425	10	N	4	642.2478		642.2478	
	1265.452	+0.014549	1265.452	11	D	3	528.2049		528.2049	
	1393.511	-0.086875	1393.511	12	Q	2	413.1779	+0.170831	413.1779	
-0.041437	765.7884		1530.57	13	H	1	285.1193	+0.184456	285.1193	
				14	E	0	148.0604		148.0604	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F10
Scannumber:	12505
Protein:	BSU22500; jojD; ypjD
Peptide Score:	135.81
Method:	ITMS; CID; 3





precursor information

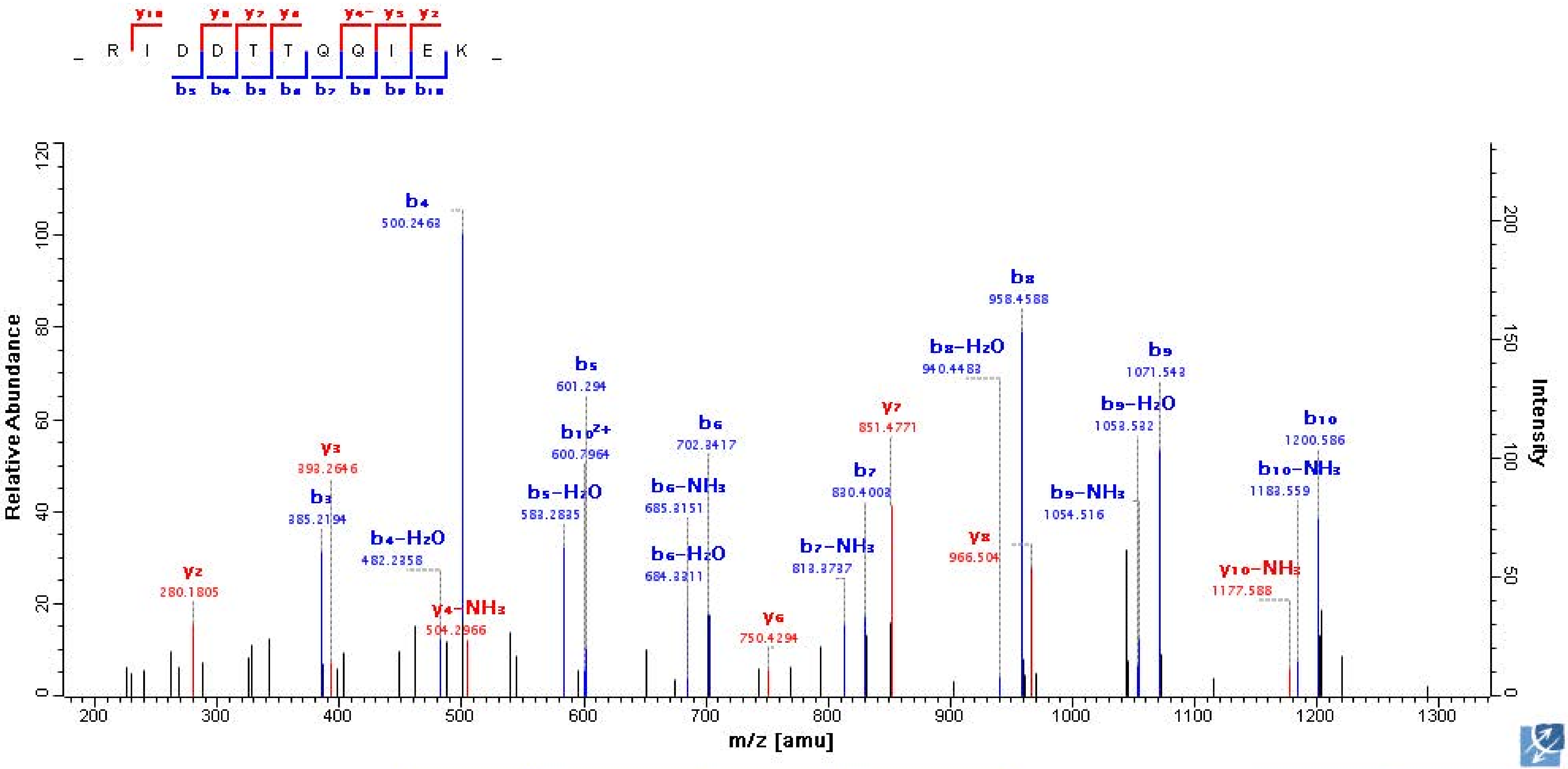
Mass:	1680.84569
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.8143
Mass Error [ppm]:	-0.85799
PEP:	3.7566E-08
Precursor Type:	MULTI

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	37 %
Protein Localisation:	8 ... 21

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	13				
	229.1183		229.1183	2	I	12	1570.853	-0.01444	1570.853	
	357.1769		357.1769	3	Q	11	1457.769		1457.769	
	428.214	-0.03978	428.214	4	A	10	1329.71	+0.070706	665.3586	-0.177514
	557.2566	+0.102014	557.2566	5	E	9	1258.673	+0.105622	1258.673	
	656.325	+0.073028	656.325	6	V	8	1129.63	+0.066306	1129.63	
	771.3519		771.3519	7	D	7	1030.562	+0.061356	1030.562	
	927.453		927.453	8	R	6	915.5349	+0.225872	915.5349	
	1090.516	+0.21679	1090.516	9	Y	5	759.4338		759.4338	
	1203.6	+0.061071	1203.6	10	I	4	596.3704		596.3704	
+0.403555	630.8146	+0.200862	1260.622	11	G	3	483.2864	+0.079967	483.2864	
	1388.68	+0.076488	1388.68	12	Q	2	426.2649		426.2649	
	1535.749	-0.007551	1535.749	13	F	1	298.2063	+0.19077	298.2063	
				14	K	0	151.1379		151.1379	

Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F10
Scannumber:	4317
Protein:	BSU00330; yabA
Peptide Score:	145.28
Method:	ITMS; CID; 3



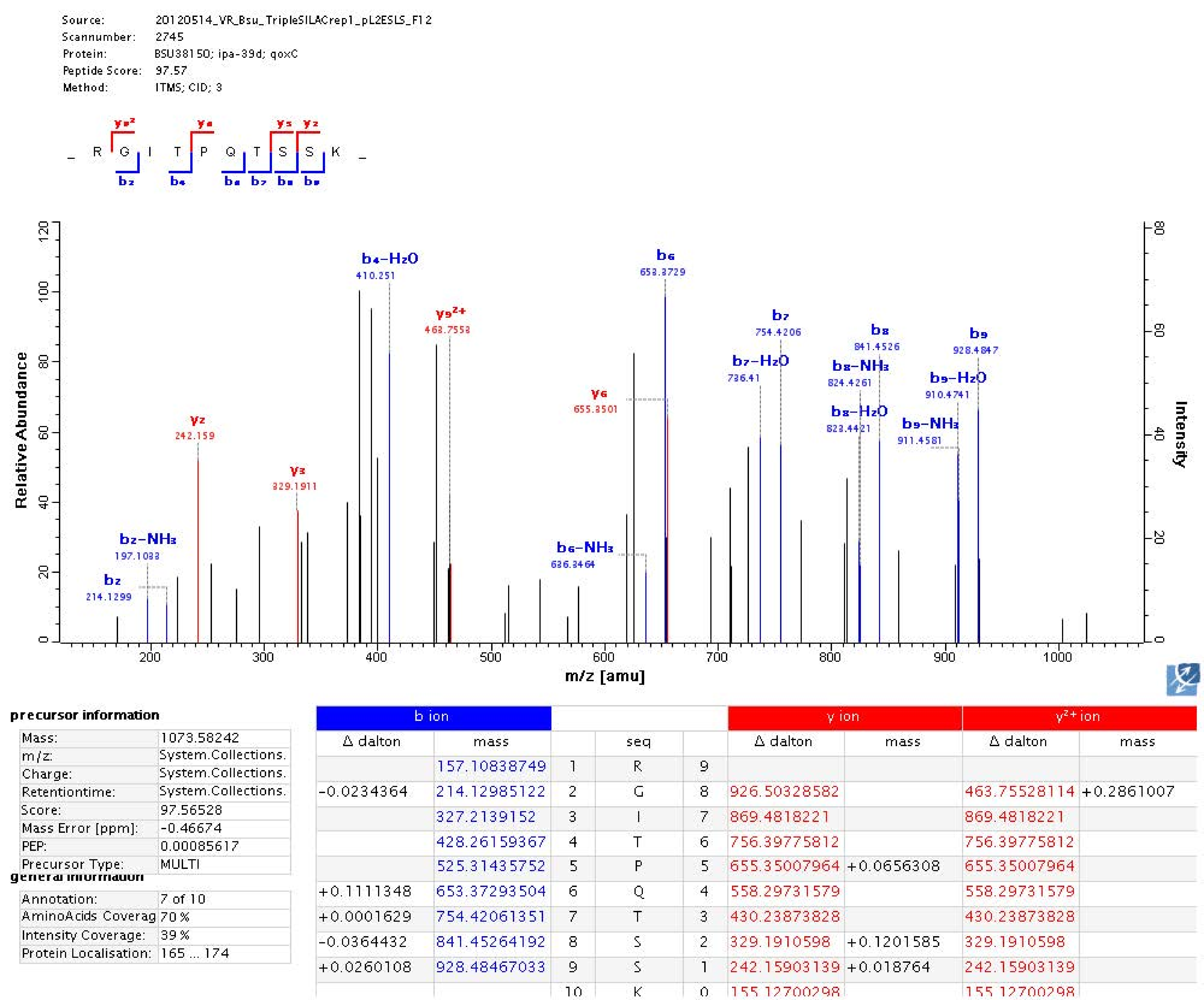
precursor information

Mass:	1349.70851
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	145.2753
Mass Error [ppm]:	-0.26568
PEP:	3.0193E-10
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	61 %
Protein Localisation:	51 ... 61

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		270.19245148	2	I	9	1194.6150302	
	385.21939451	+0.1535913	385.21939451	3	D	8	1081.5309663	
	500.24633754	-0.0176388	500.24633754	4	D	7	966.50402323	+0.1539358
	601.29401601	+0.1581324	601.29401601	5	T	6	851.4770802	+0.1592723
	702.34169449	+0.0976976	702.34169449	6	T	5	750.42940173	+0.0953175
	830.400272	+0.1753506	830.400272	7	Q	4	649.38172325	
	958.45884951	+0.0830816	958.45884951	8	Q	3	521.32314574	
	1071.5429135	+0.0852603	1071.5429135	9	I	2	393.26456823	+0.3881417
-0.4936572	600.79639153	+0.0675696	1200.5855066	10	E	1	280.18050425	-0.0484242
				11	K	0	151.13791115	



Source:	20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F12
Scannumber:	2745
Protein:	BSU38150; ipa-39d; qoxC
Peptide Score:	97.57
Method:	ITMS; CID; 3

precursor information

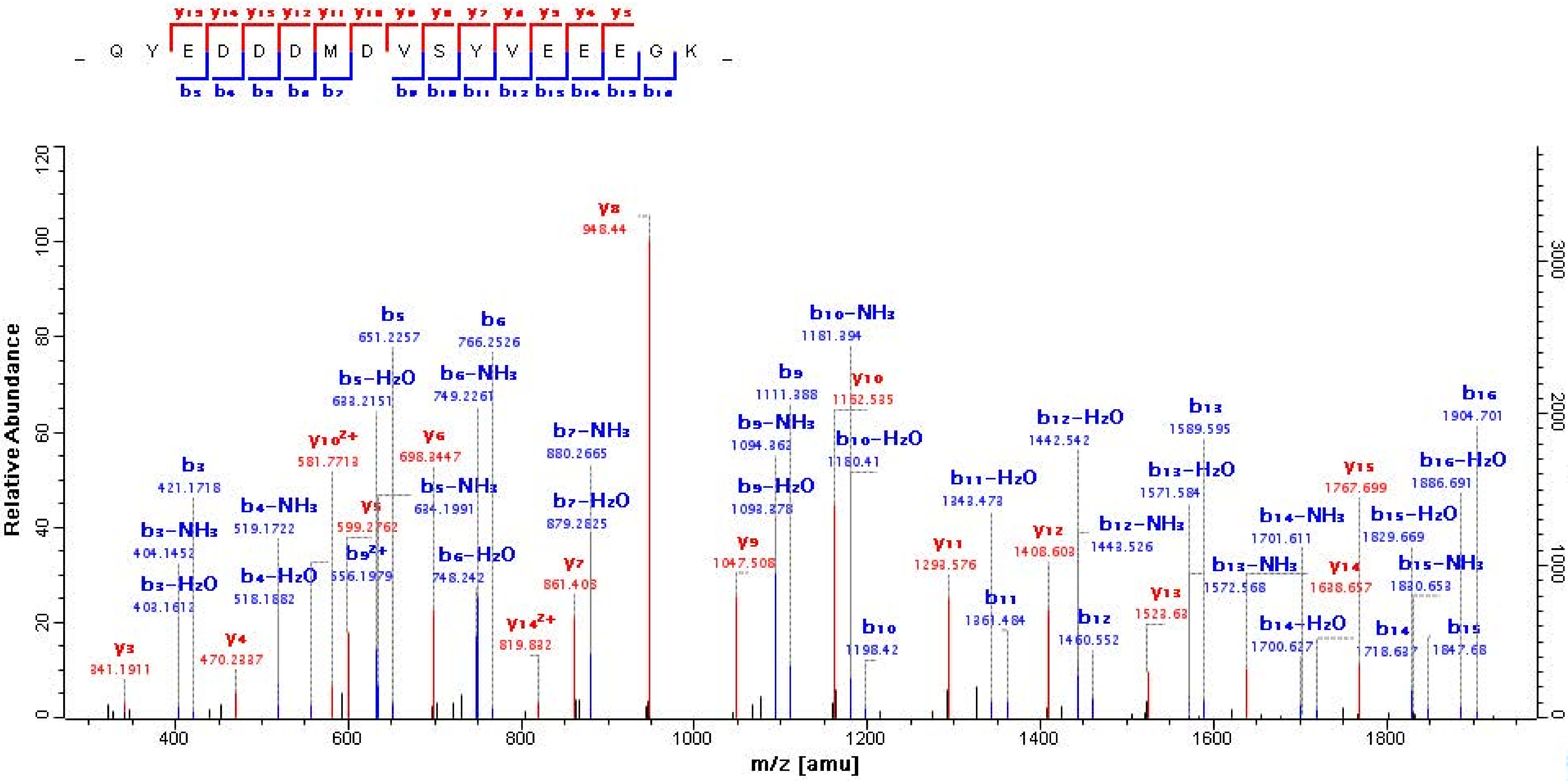
Mass:	1073.58242
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	97.56528
Mass Error [ppm]:	-0.46674
PEP:	0.00085617
Precursor Type:	MULTI

general information

Annotation:	7 of 10
AminoAcids Coverag	70 %
Intensity Coverage:	39 %
Protein Localisation:	165 ... 174

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.10838749	1	R	9				
-0.0234364	214.12985122	2	G	8	926.50328582		463.75528114	+0.2861007
	327.2139152	3	I	7	869.4818221		869.4818221	
	428.26159367	4	T	6	756.39775812		756.39775812	
	525.31435752	5	P	5	655.35007964	+0.0656308	655.35007964	
+0.1111348	653.37293504	6	Q	4	558.29731579		558.29731579	
+0.0001629	754.42061351	7	T	3	430.23873828		430.23873828	
-0.0364432	841.45264192	8	S	2	329.1910598	+0.1201585	329.1910598	
+0.0260108	928.48467033	9	S	1	242.15903139	+0.018764	242.15903139	
		10	K	0	155.12700298		155.12700298	

Source: 20120514_VR_Bsu_TripleSILACrep1_pL2ESLS_F20
Scannumber: 8919
Protein: BSU40740; yyaR
Peptide Score: 328.73
Method: ITMS; CID; 3



precursor information

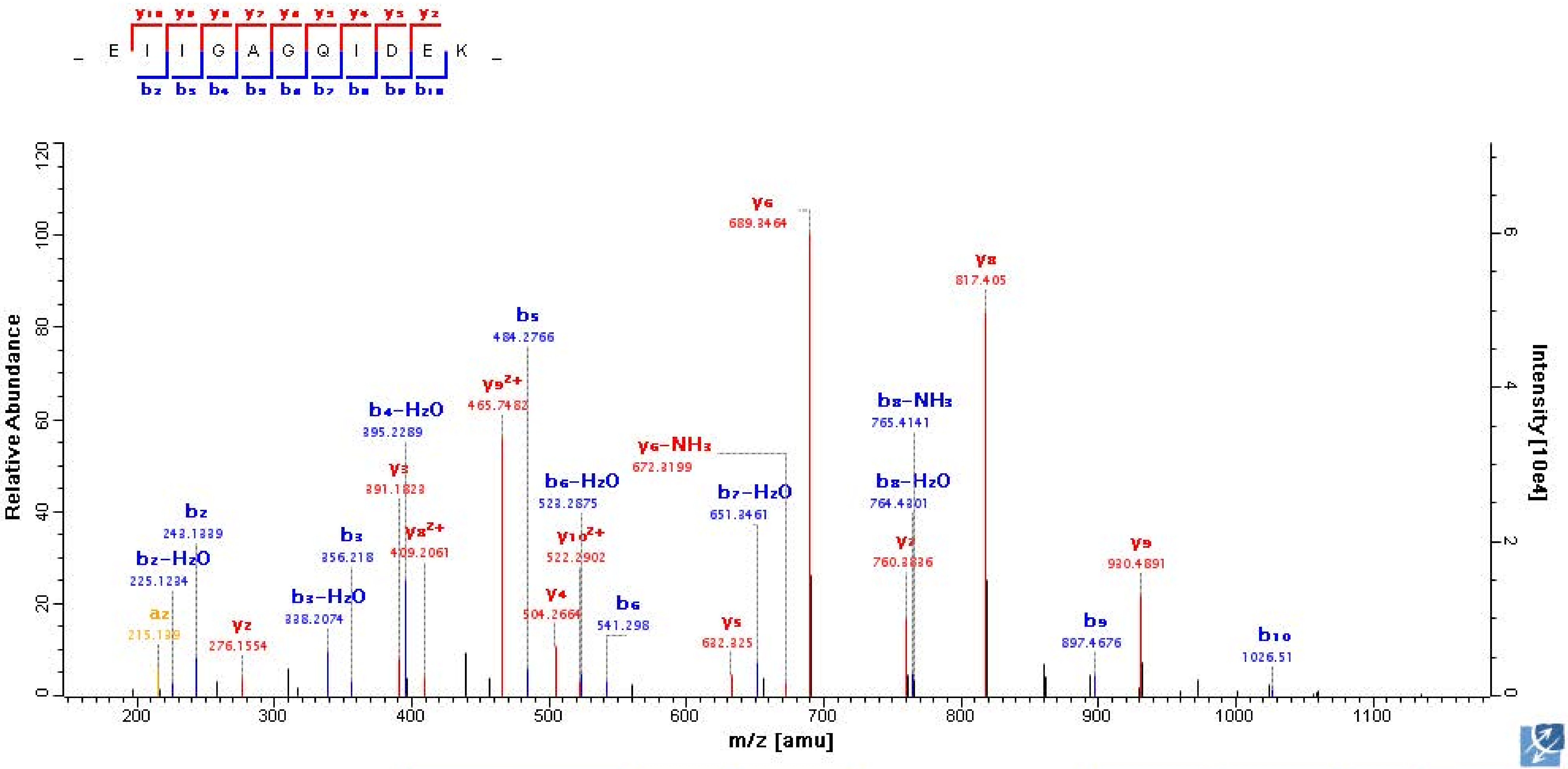
Mass:	2049.79959
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	328.7328
Mass Error [ppm]:	-0.060873
PEP:	2.3161E-255
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	83 %
Protein Localisation:	49 ... 65

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	16				
	292.1292		292.1292	2	Y	15	1930.763		1930.763	
	421.1718	-0.145164	421.1718	3	E	14	1767.699	+0.05194	1767.699	
	536.1987		536.1987	4	D	13	1638.657	+0.18694	819.832	-0.055493
	651.2257	+0.10344	651.2257	5	D	12	1523.63	+0.193864	1523.63	
	766.2526	-0.053325	766.2526	6	D	11	1408.603	+0.045636	1408.603	
	897.2931		897.2931	7	M	10	1293.576	+0.159493	1293.576	
	1012.32		1012.32	8	D	9	1162.535	-0.041599	581.7713	-0.456262
+0.152603	556.1979	+0.050641	1111.388	9	V	8	1047.508	-0.035286	1047.508	
	1198.42	+0.067562	1198.42	10	S	7	948.44	+0.030564	948.44	
	1361.484	+0.151207	1361.484	11	Y	6	861.408	+0.087739	861.408	
	1460.552	-0.044283	1460.552	12	V	5	698.3447	+0.007452	698.3447	
	1589.595	-0.078575	1589.595	13	E	4	599.2762	+0.068358	599.2762	
	1718.637	-0.026808	1718.637	14	E	3	470.2337	+0.046621	470.2337	
	1847.68	+0.196102	1847.68	15	E	2	341.1911	+0.135295	341.1911	
	1904.701	+0.232988	1904.701	16	G	1	212.1485		212.1485	
				17	K	0	155.127		155.127	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F01
Scannumber:	10653
Protein:	BSU05320; ydeS
Peptide Score:	156.48
Method:	ITMS; CID; 3



precursor information

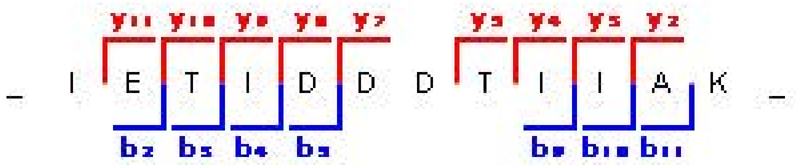
Mass:	1171.60736
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	156.4802
Mass Error [ppm]:	-0.94317
PEP:	1.5294E-11
Precursor Type:	MULTI

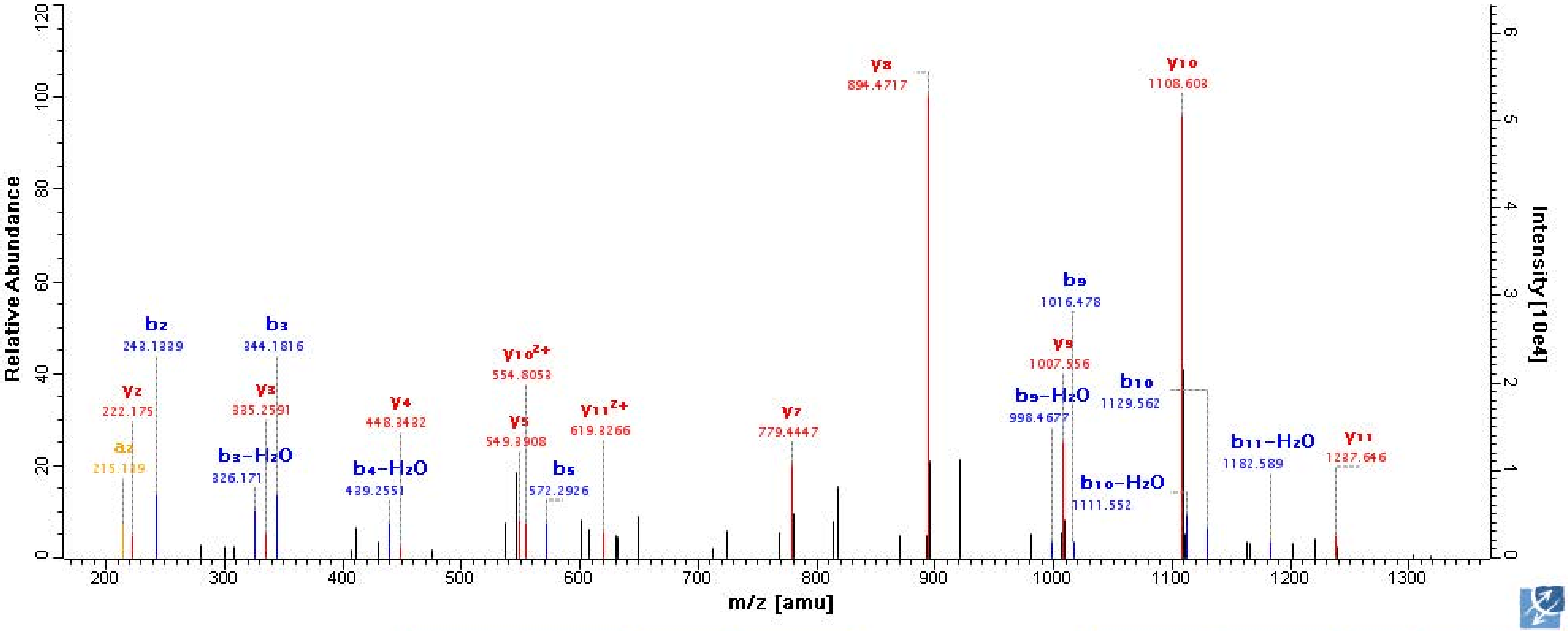
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	76 %
Protein Localisation:	105 ... 115

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		130.0499	1	E	10				
-0.077236	215.139	-0.00991	243.1339	2	I	9	1043.573		522.2902	+0.010079
	328.2231	+0.104268	356.218	3	I	8	930.4891	+0.106372	465.7482	+0.308032
	385.2445		413.2395	4	G	7	817.405	+0.06507	409.2061	+0.219204
	456.2817	+0.150122	484.2766	5	A	6	760.3836	+0.020738	760.3836	
	513.3031	+0.156063	541.298	6	G	5	689.3464	+0.031179	689.3464	
	641.3617		669.3566	7	Q	4	632.325	+0.136688	632.325	
	754.4458		782.4407	8	I	3	504.2664	+0.061049	504.2664	
	869.4727	+0.129972	897.4676	9	D	2	391.1823	+0.00165	391.1823	
	998.5153	+0.272865	1026.51	10	E	1	276.1554	+0.160734	276.1554	
				11	K	0	147.1128		147.1128	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F01
Scannumber: 13782
Protein: BSU14790; ylaI
Peptide Score: 122.69
Method: ITMS; CID; 3





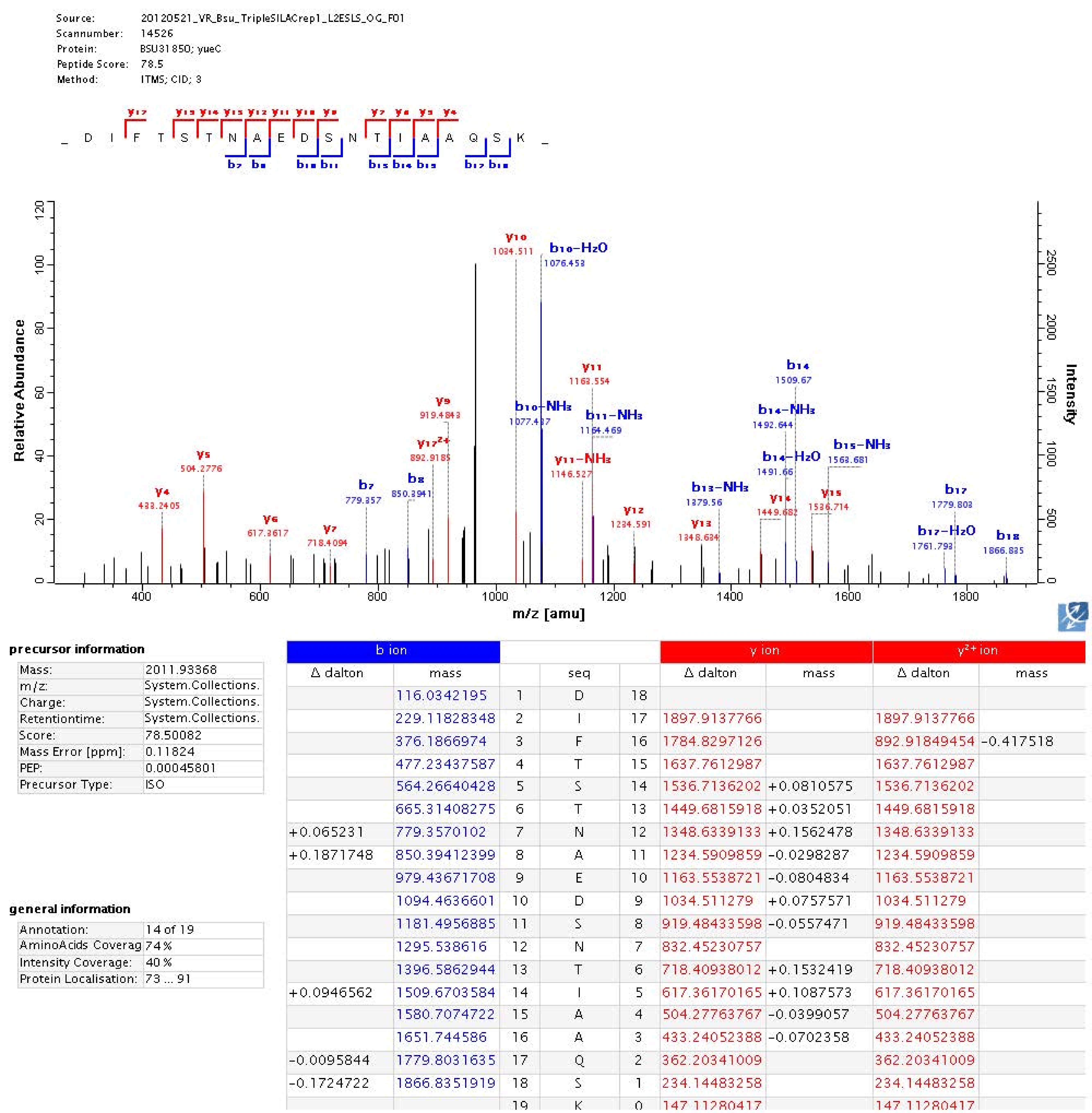
precursor information

Mass:	1349.72412
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	122.6907
Mass Error [ppm]:	0.99263
PEP:	9.3994E-07
Precursor Type:	ISO

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	54 %
Protein Localisation:	12 ... 23

a ion		b ion					y ion		y^{z+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	86.09643		114.0913	1	I	11				
+0.033222	215.139	-0.070549	243.1339	2	E	10	1237.646	-0.036377	619.3266	+0.13955
	316.1867	+0.072783	344.1816	3	T	9	1108.603	+0.054434	554.8053	-0.081646
	429.2708		457.2657	4	I	8	1007.556	+0.128052	1007.556	
	544.2977	+0.156172	572.2926	5	D	7	894.4717	+0.058735	894.4717	
	659.3246		687.3196	6	D	6	779.4447	+0.09581	779.4447	
	774.3516		802.3465	7	D	5	664.4178		664.4178	
	875.3993		903.3942	8	T	4	549.3908	+0.000831	549.3908	
	988.4833	+0.097741	1016.478	9	I	3	448.3432	+0.048632	448.3432	
	1101.567	+0.10346	1129.562	10	I	2	335.2591	+0.111761	335.2591	
	1172.605		1200.599	11	A	1	222.175	-0.122947	222.175	
				12	K	0	151.1379		151.1379	



Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F01
Scannumber: 14526
Protein: BSU31850; yueC
Peptide Score: 78.5
Method: ITMS; CID; 3

precursor information

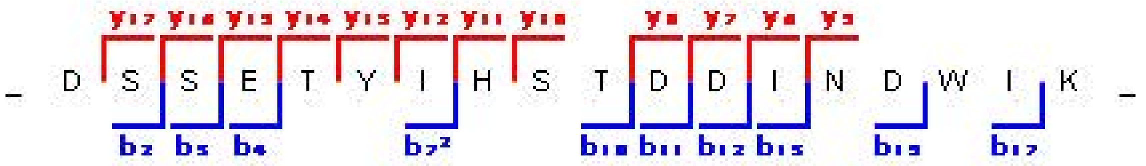
Mass:	2011.93368
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	78.50082
Mass Error [ppm]:	0.11824
PEP:	0.00045801
Precursor Type:	ISO

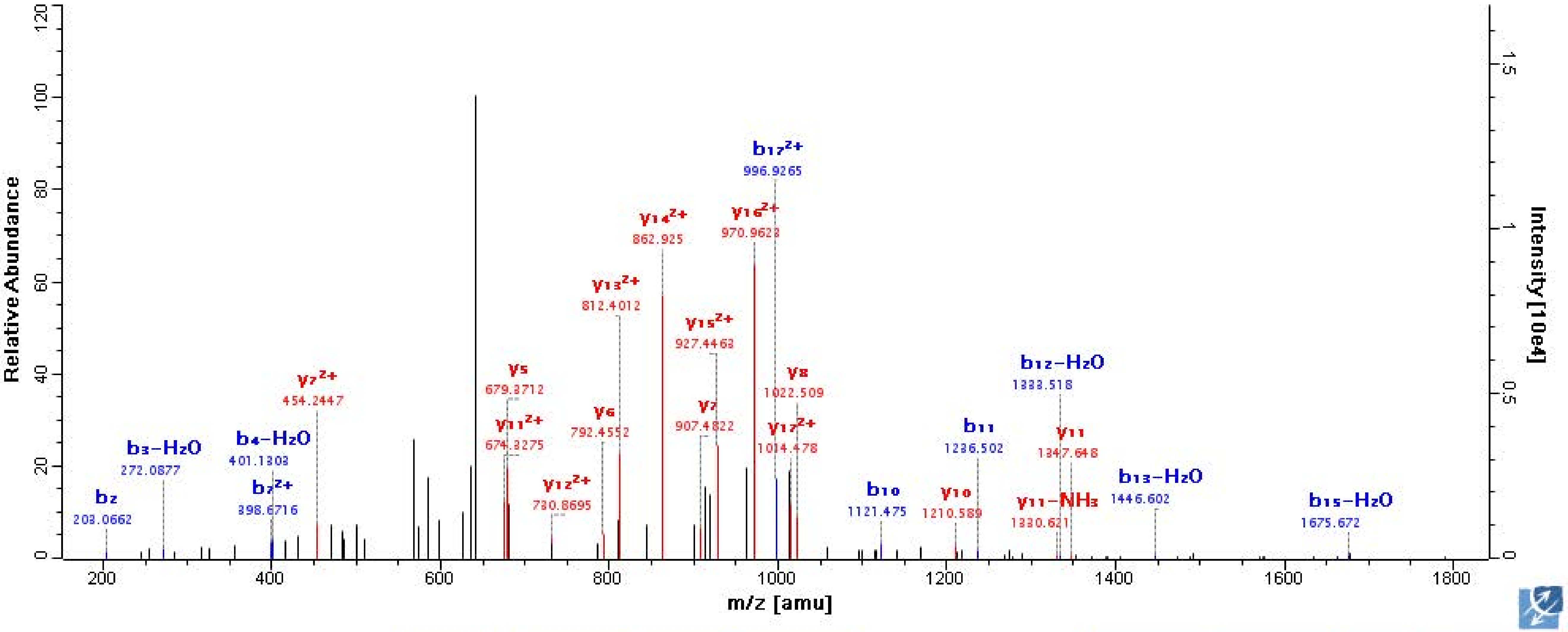
general information

Annotation:	14 of 19
AminoAcids Coverag	74%
Intensity Coverage:	40%
Protein Localisation:	73 ... 91

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	18				
	229.11828348	2	I	17	1897.9137766		1897.9137766	
	376.1866974	3	F	16	1784.8297126		892.91849454	-0.417518
	477.23437587	4	T	15	1637.7612987		1637.7612987	
	564.26640428	5	S	14	1536.7136202	+0.0810575	1536.7136202	
	665.31408275	6	T	13	1449.6815918	+0.0352051	1449.6815918	
+0.065231	779.3570102	7	N	12	1348.6339133	+0.1562478	1348.6339133	
+0.1871748	850.39412399	8	A	11	1234.5909859	-0.0298287	1234.5909859	
	979.43671708	9	E	10	1163.5538721	-0.0804834	1163.5538721	
	1094.4636601	10	D	9	1034.511279	+0.0757571	1034.511279	
	1181.4956885	11	S	8	919.48433598	-0.0557471	919.48433598	
	1295.538616	12	N	7	832.45230757		832.45230757	
	1396.5862944	13	T	6	718.40938012	+0.1532419	718.40938012	
+0.0946562	1509.6703584	14	I	5	617.36170165	+0.1087573	617.36170165	
	1580.7074722	15	A	4	504.27763767	-0.0399057	504.27763767	
	1651.744586	16	A	3	433.24052388	-0.0702358	433.24052388	
-0.0095844	1779.8031635	17	Q	2	362.20341009		362.20341009	
-0.1724722	1866.8351919	18	S	1	234.14483258		234.14483258	
		19	K	0	147.11280417		147.11280417	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F01
Scannumber: 20185
Protein: BSU39200; yxzC
Peptide Score: 109.83
Method: ITMS; CID; 3





precursor information

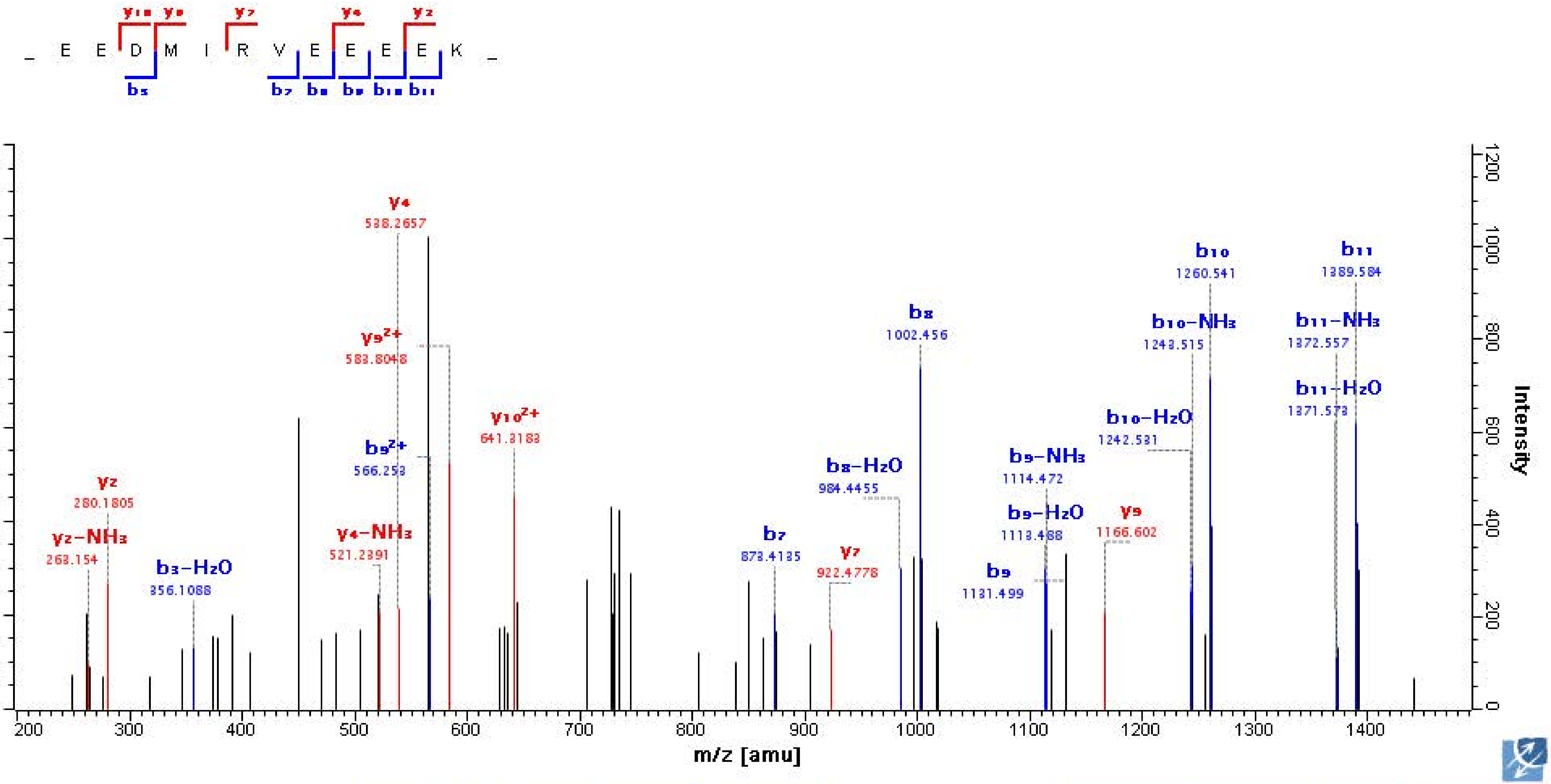
Mass:	2137.94461
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	109.8349
Mass Error [ppm]:	0.28169
PEP:	2.155E-11
Precursor Type:	MULTI

general information

Annotation:	15 of 18
AminoAcids Coverag	83 %
Intensity Coverage:	42 %
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	+0.085836	203.0662	2	S	16	2027.949		1014.478	+0.280488
	290.0983		290.0983	3	S	15	1940.917		970.9623	+0.303643
	419.1409		419.1409	4	E	14	1853.885		927.4463	+0.431168
	520.1885		520.1885	5	T	13	1724.843		862.925	+0.238659
	683.2519		683.2519	6	Y	12	1623.795		812.4012	+0.337205
-0.468667	398.6716		796.3359	7	I	11	1460.732		730.8695	+0.093357
	933.3949		933.3949	8	H	10	1347.648	+0.124489	674.3275	+0.246106
	1020.427		1020.427	9	S	9	1210.589	+0.037283	1210.589	
	1121.475	+0.285206	1121.475	10	T	8	1123.557		1123.557	
	1236.502	+0.105431	1236.502	11	D	7	1022.509	+0.044053	1022.509	
	1351.528		1351.528	12	D	6	907.4822	+0.220105	454.2447	+0.089141
	1464.613		1464.613	13	I	5	792.4552	+0.197671	792.4552	
	1578.655		1578.655	14	N	4	679.3712	+0.035763	679.3712	
	1693.682		1693.682	15	D	3	565.3282		565.3282	
	1879.762		1879.762	16	W	2	450.3013		450.3013	
+0.392209	996.9265		1992.846	17	I	1	264.222		264.222	
				18	K	0	151.1379		151.1379	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F01
Scannumber: 9250
Protein: BSU39410; nupC
Peptide Score: 130.01
Method: ITMS; CID; 3



precursor information

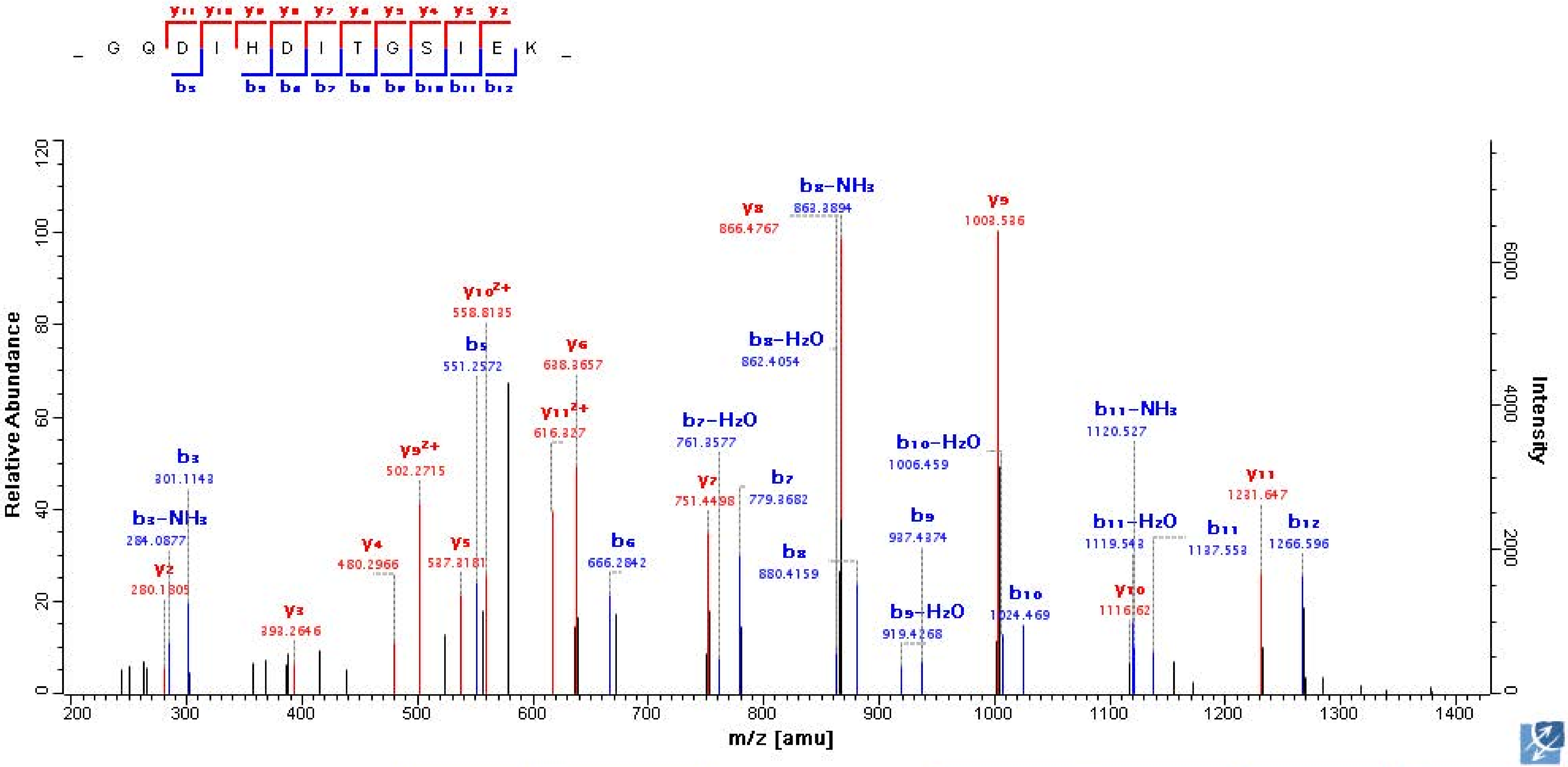
Mass:	1538.7077
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	130.006
Mass Error [ppm]:	0.31733
PEP:	0.0002665
Precursor Type:	ISO

general information

Annotation:	8 of 12
AminoAcids Coverag	67 %
Intensity Coverage:	38 %
Protein Localisation:	219 ... 230

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				
	259.0925		259.0925	2	E	10	1410.672		1410.672	
	374.1194		374.1194	3	D	9	1281.629		641.3183	+0.178965
	505.1599		505.1599	4	M	8	1166.602	+0.204894	583.8048	+0.217278
	618.244		618.244	5	I	7	1035.562		1035.562	
	774.3451		774.3451	6	R	6	922.4778	+0.251806	922.4778	
	873.4135	+0.087986	873.4135	7	V	5	766.3767		766.3767	
	1002.456	+0.098371	1002.456	8	E	4	667.3083		667.3083	
+0.108662	566.253	+0.032951	1131.499	9	E	3	538.2657	+0.181392	538.2657	
	1260.541	+0.030519	1260.541	10	E	2	409.2231		409.2231	
	1389.584	+0.057262	1389.584	11	E	1	280.1805	+0.16465	280.1805	
				12	K	0	151.1379		151.1379	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	11443
Protein:	BSU06920; yeeN; yesJ; yfxC; yfxD
Peptide Score:	188.48
Method:	ITMS; CID; 3



precursor information

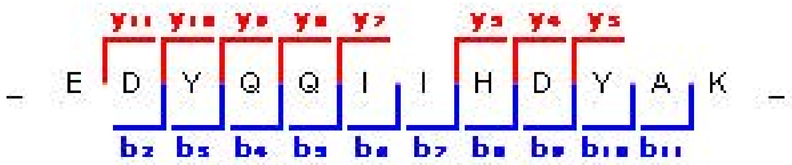
Mass:	1415.71963
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	188.4789
Mass Error [ppm]:	0.14212
PEP:	1.4842E-21
Precursor Type:	ISO

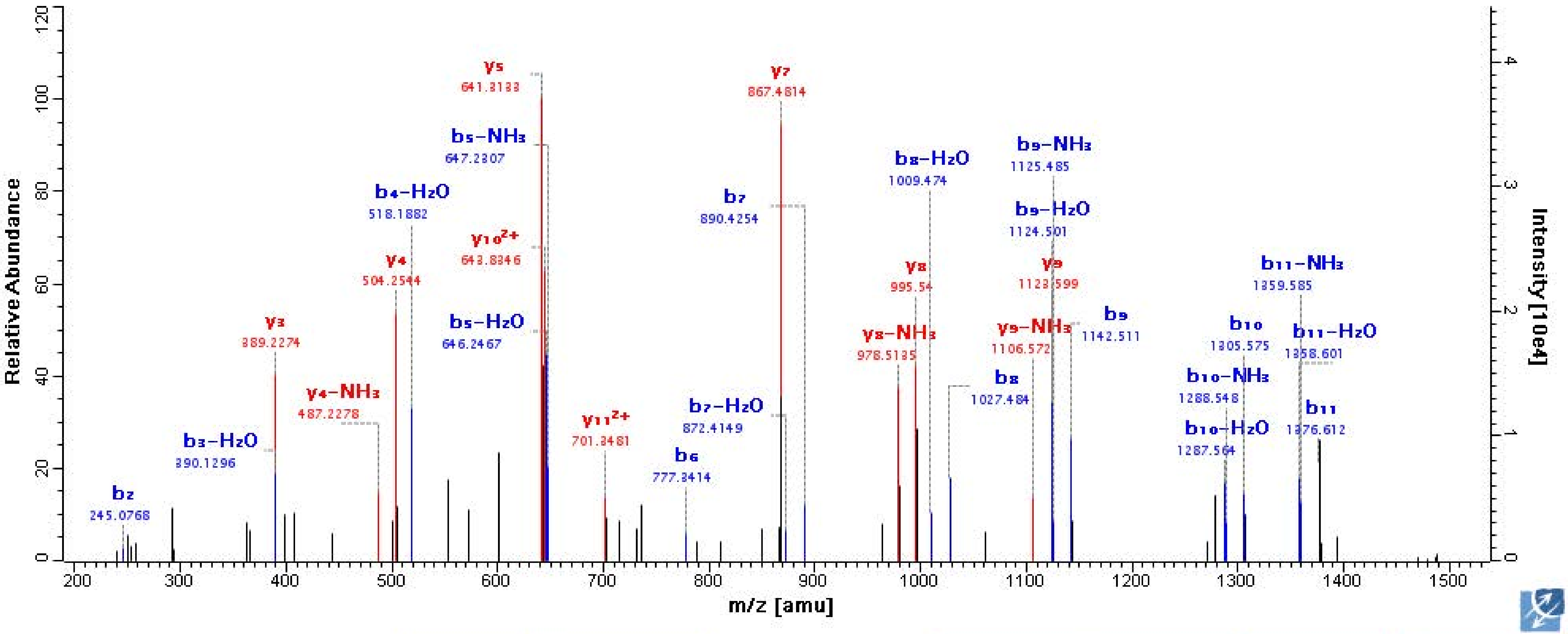
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	61 %
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	1359.7052422		1359.7052422	
-0.0762358	301.11426073	3	D	10	1231.6466647	+0.0669583	616.3269706	+0.1256661
	414.19832471	4	I	9	1116.6197217	+0.0240771	558.81349908	+0.3426899
+0.0374412	551.25723658	5	H	8	1003.5356577	+0.03673	502.27146709	+0.0566579
-0.0008544	666.28417961	6	D	7	866.47674585	+0.031738	866.47674585	
+0.0290342	779.36824359	7	I	6	751.44980282	+0.0129657	751.44980282	
+0.0190755	880.41592206	8	T	5	638.36573884	-0.0016641	638.36573884	
+0.2665327	937.43738579	9	G	4	537.31806036	-0.0067811	537.31806036	
+0.0895458	1024.4694142	10	S	3	480.29659664	-0.07156	480.29659664	
+0.1323128	1137.5534782	11	I	2	393.26456823	+0.1312448	393.26456823	
+0.0892315	1266.5960713	12	E	1	280.18050425	-0.058617	280.18050425	
		13	K	0	151.13791115		151.13791115	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	15763
Protein:	BSU12069; yjzH
Peptide Score:	174.77
Method:	ITMS; CID; 3





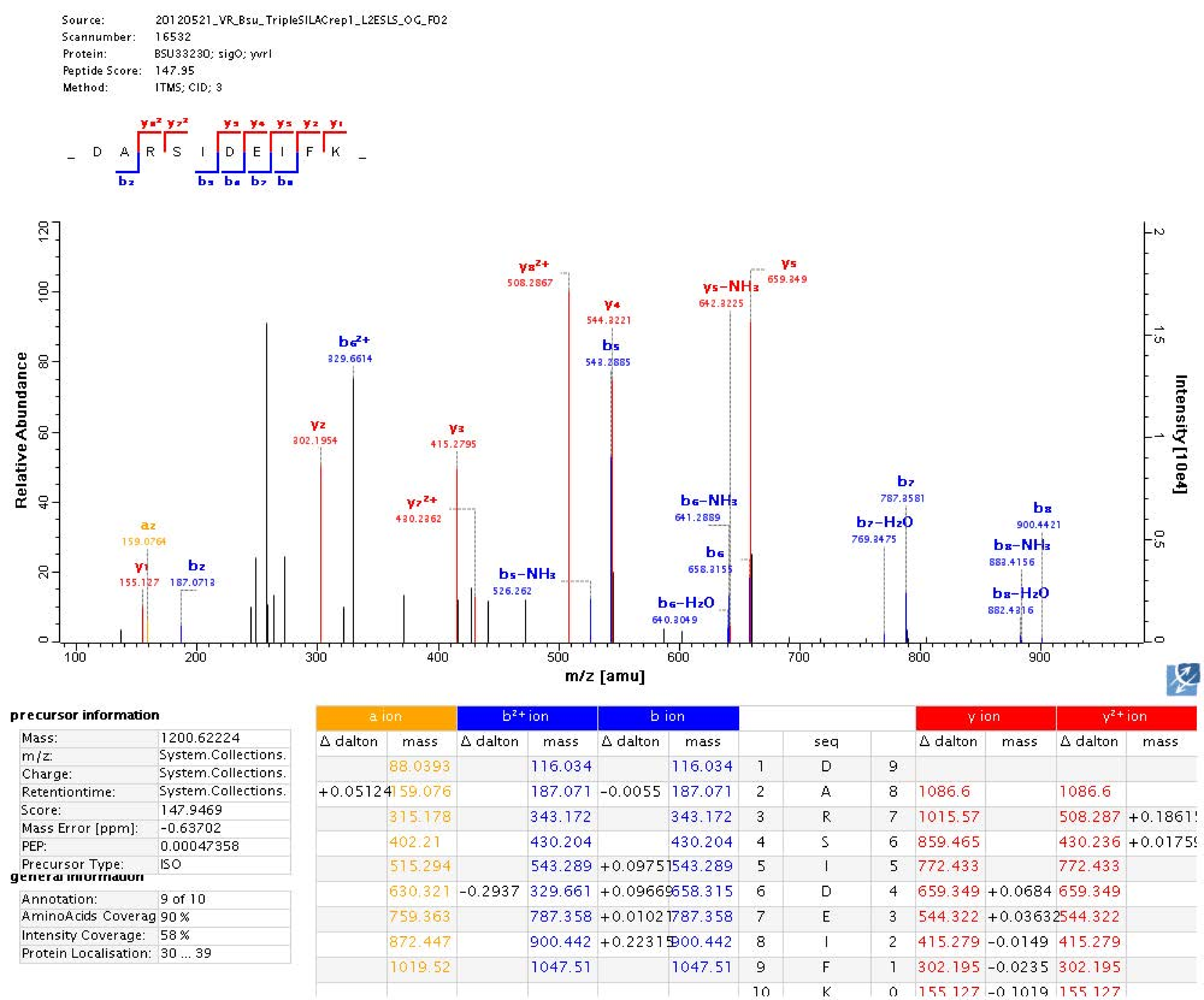
precursor information

Mass:	1521.70986
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	174.7679
Mass Error [ppm]:	-0.073898
PEP:	7.7726E-26
Precursor Type:	MULTI

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	67 %
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				
+0.0216524	245.07681259	2	D	10	1401.6888548		701.34806561	+0.1554744
	408.14014113	3	Y	9	1286.6619117		643.8345941	+0.0936896
	536.19871864	4	Q	8	1123.5985832	+0.0712166	1123.5985832	
	664.25729616	5	Q	7	995.54000568	+0.0868254	995.54000568	
+0.0756931	777.34136014	6	I	6	867.48142817	+0.0868091	867.48142817	
+0.0726838	890.42542412	7	I	5	754.39736418		754.39736418	
+0.1133203	1027.484336	8	H	4	641.3133002	+0.0569391	641.3133002	
+0.1413089	1142.511279	9	D	3	504.25438834	+0.0415101	504.25438834	
+0.1563495	1305.5746075	10	Y	2	389.22744531	+0.0068076	389.22744531	
+0.2295873	1376.6117213	11	A	1	226.16411677		226.16411677	
		12	K	0	155.12700298		155.12700298	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	16532
Protein:	BSU33230; sigO; yvrI
Peptide Score:	147.95
Method:	ITMS; CID; 3

precursor information

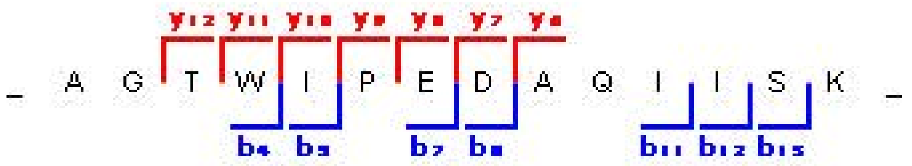
Mass:	1200.62224
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	147.9469
Mass Error [ppm]:	-0.63702
PEP:	0.00047358
Precursor Type:	ISO

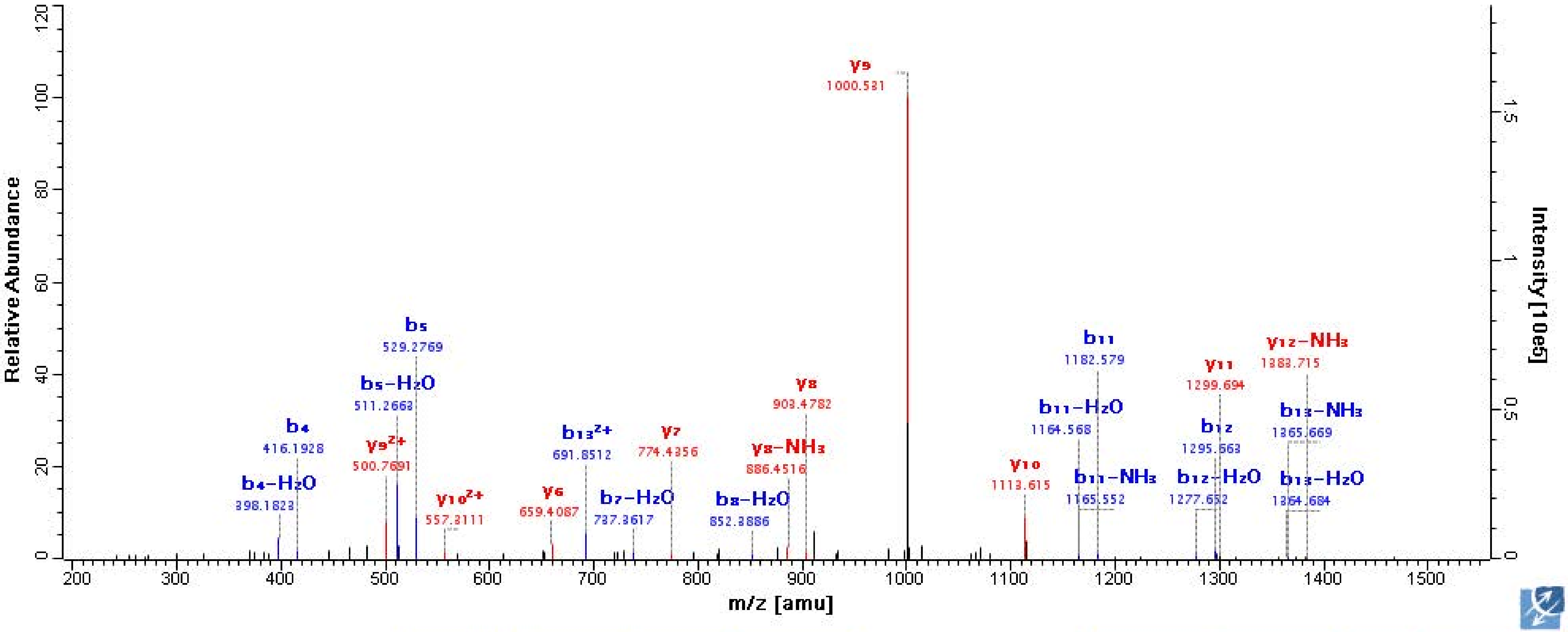
general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	58 %
Protein Localisation:	30 ... 39

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	9				
+0.05124	159.076		187.071	-0.0055	187.071	2	A	8	1086.6		1086.6	
	315.178		343.172		343.172	3	R	7	1015.57		508.287	+0.1861
	402.21		430.204		430.204	4	S	6	859.465		430.236	+0.0175
	515.294		543.289	+0.0975	543.289	5	I	5	772.433		772.433	
	630.321	-0.2937	329.661	+0.09669	658.315	6	D	4	659.349	+0.0684	659.349	
	759.363		787.358	+0.0102	787.358	7	E	3	544.322	+0.03632	544.322	
	872.447		900.442	+0.22315	900.442	8	I	2	415.279	-0.0149	415.279	
	1019.52		1047.51		1047.51	9	F	1	302.195	-0.0235	302.195	
						10	K	0	155.127	-0.1019	155.127	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	19312
Protein:	BSU40290; yycN
Peptide Score:	107.09
Method:	ITMS; CID; 3





precursor information

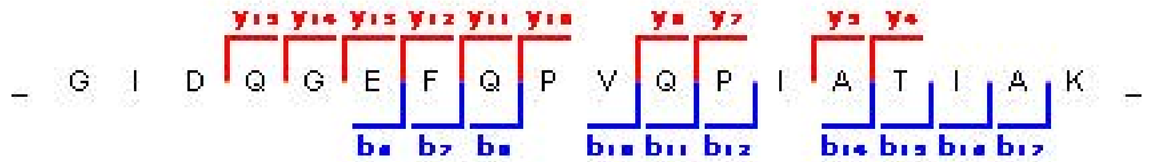
Mass:	1527.79843
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	107.0884
Mass Error [ppm]:	3.3514
PEP:	0.00032931
Precursor Type:	MULTI

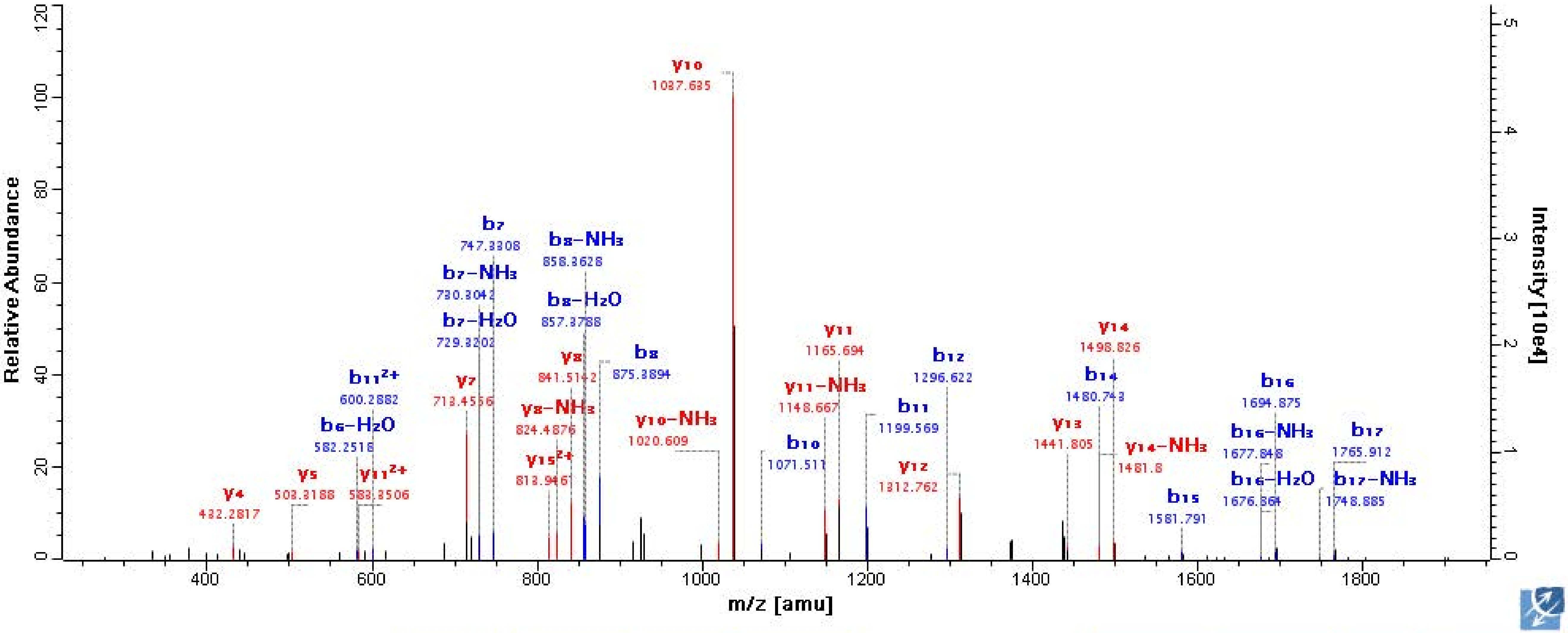
general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	63 %
Protein Localisation:	31 ... 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	13				
	129.0659		129.0659	2	G	12	1457.763		1457.763	
	230.1135		230.1135	3	T	11	1400.742		1400.742	
	416.1928	-0.123632	416.1928	4	W	10	1299.694	+0.167732	1299.694	
	529.2769	+0.014045	529.2769	5	I	9	1113.615	+0.083471	557.3111	+0.076915
	626.3297		626.3297	6	P	8	1000.531	+0.067437	500.7691	+0.4652
	755.3723		755.3723	7	E	7	903.4782	+0.184471	903.4782	
	870.3992		870.3992	8	D	6	774.4356	+0.164198	774.4356	
	941.4363		941.4363	9	A	5	659.4087	+0.208475	659.4087	
	1069.495		1069.495	10	Q	4	588.3715		588.3715	
	1182.579	+0.309951	1182.579	11	I	3	460.313		460.313	
	1295.663	+0.241512	1295.663	12	I	2	347.2289		347.2289	
+0.100799	691.8512		1382.695	13	S	1	234.1448		234.1448	
				14	K	0	147.1128		147.1128	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	19356
Protein:	BSU08370; yfiR
Peptide Score:	179.81
Method:	ITMS; CID; 3





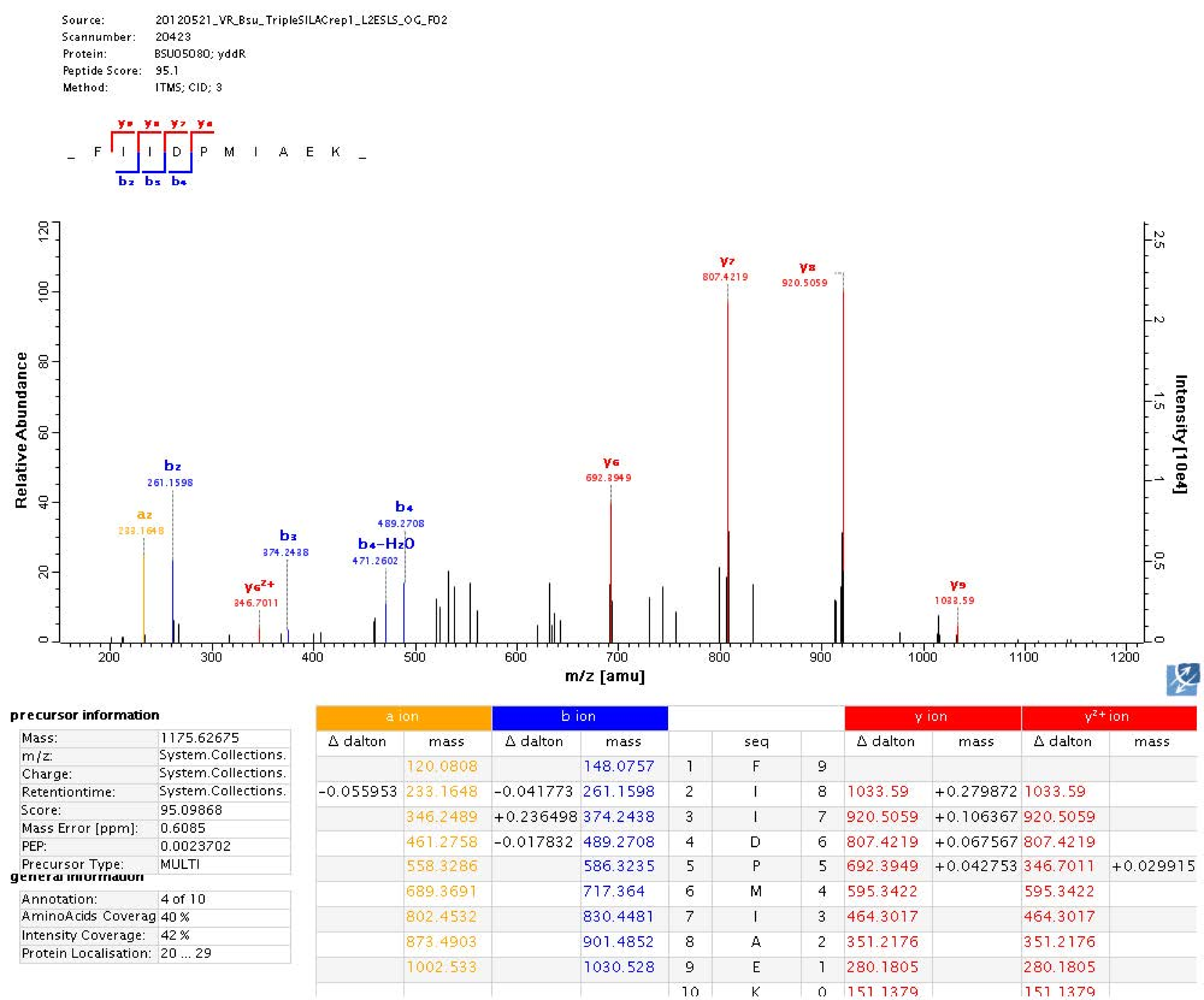
precursor information

Mass:	1911.00905
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	179.8072
Mass Error [ppm]:	-0.58912
PEP:	8.5891E-35
Precursor Type:	MULTI

general information

Annotation:	13 of 18
AminoAcids Coverag	72 %
Intensity Coverage:	58 %
Protein Localisation:	145 ... 162

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	17				
	171.1128		171.1128	2	I	16	1854.996		1854.996	
	286.1397		286.1397	3	D	15	1741.912		1741.912	
	414.1983		414.1983	4	Q	14	1626.885		813.9461	+0.006385
	471.2198		471.2198	5	G	13	1498.826	+0.216807	1498.826	
	600.2624		600.2624	6	E	12	1441.805	+0.129751	1441.805	
	747.3308	+0.014908	747.3308	7	F	11	1312.762	+0.190654	1312.762	
	875.3894	+0.022309	875.3894	8	Q	10	1165.694	+0.216343	583.3506	+0.019389
	972.4421		972.4421	9	P	9	1037.635	+0.066303	1037.635	
	1071.511	-0.021293	1071.511	10	V	8	940.5826		940.5826	
+0.020636	600.2882	+0.021082	1199.569	11	Q	7	841.5142	-0.007405	841.5142	
	1296.622	+0.369075	1296.622	12	P	6	713.4556	+0.159876	713.4556	
	1409.706		1409.706	13	I	5	616.4028		616.4028	
	1480.743	+0.229342	1480.743	14	A	4	503.3188	-0.018908	503.3188	
	1581.791	+0.085228	1581.791	15	T	3	432.2817	-0.130415	432.2817	
	1694.875	+0.022649	1694.875	16	I	2	331.234		331.234	
	1765.912	-0.111755	1765.912	17	A	1	218.1499		218.1499	
				18	K	0	147.1128		147.1128	



Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber: 20423
Protein: BSU05080; yddR
Peptide Score: 95.1
Method: ITMS; CID; 3

precursor information

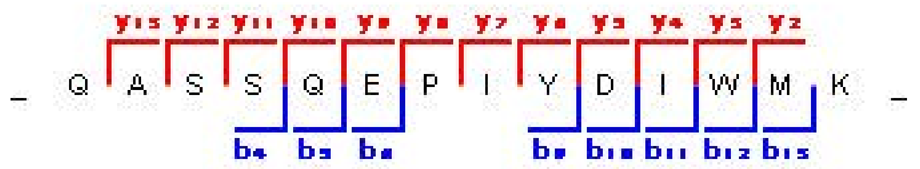
Mass:	1175.62675
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.09868
Mass Error [ppm]:	0.6085
PEP:	0.0023702
Precursor Type:	MULTI

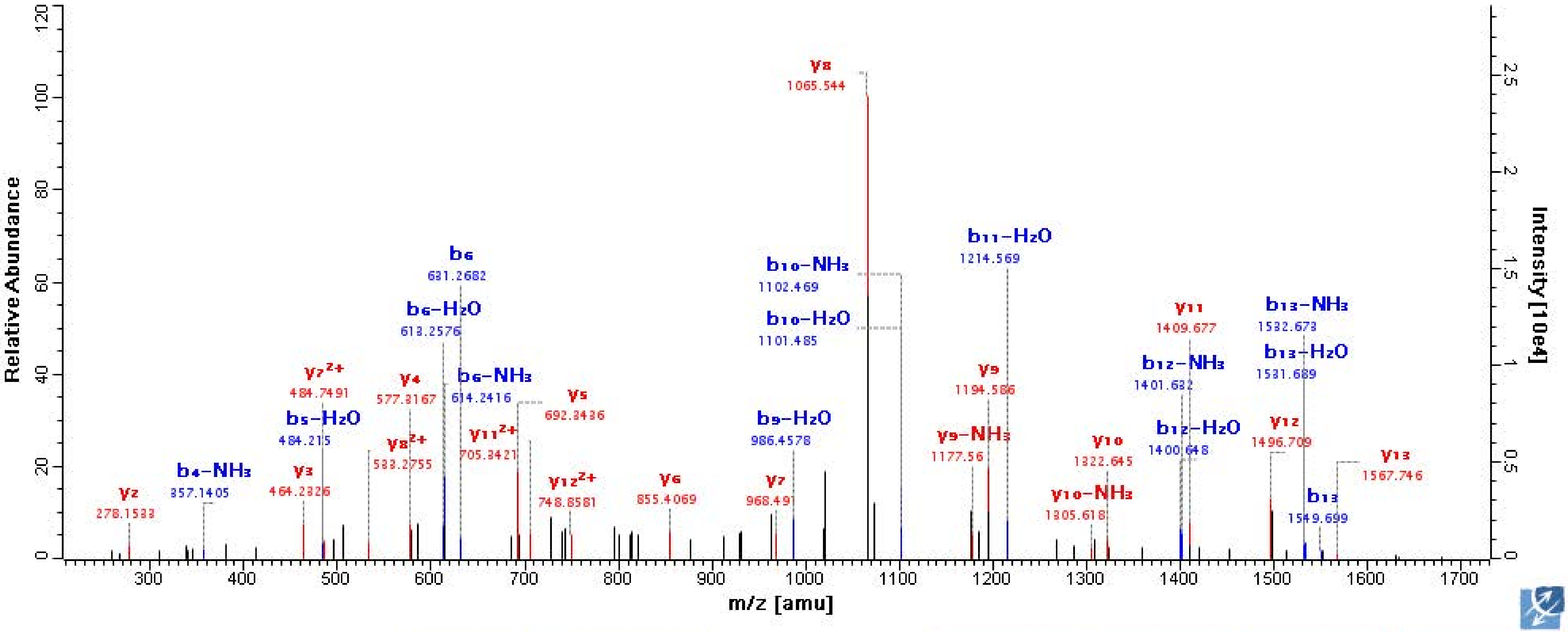
general information

Annotation:	4 of 10
AminoAcids Coverag	40 %
Intensity Coverage:	42 %
Protein Localisation:	20 ... 29

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	120.0808		148.0757	1	F	9				
-0.055953	233.1648	-0.041773	261.1598	2	I	8	1033.59	+0.279872	1033.59	
	346.2489	+0.236498	374.2438	3	I	7	920.5059	+0.106367	920.5059	
	461.2758	-0.017832	489.2708	4	D	6	807.4219	+0.067567	807.4219	
	558.3286		586.3235	5	P	5	692.3949	+0.042753	346.7011	+0.029915
	689.3691		717.364	6	M	4	595.3422		595.3422	
	802.4532		830.4481	7	I	3	464.3017		464.3017	
	873.4903		901.4852	8	A	2	351.2176		351.2176	
	1002.533		1030.528	9	E	1	280.1805		280.1805	
				10	K	0	151.1379		151.1379	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber:	21939
Protein:	BSU17160; pksH
Peptide Score:	140.91
Method:	ITMS; CID; 3





precursor information

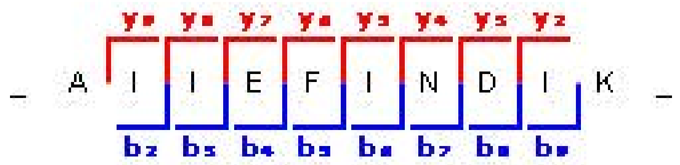
Mass:	1694.79662
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.9054
Mass Error [ppm]:	-0.46545
PEP:	0.00071549
Precursor Type:	ISO

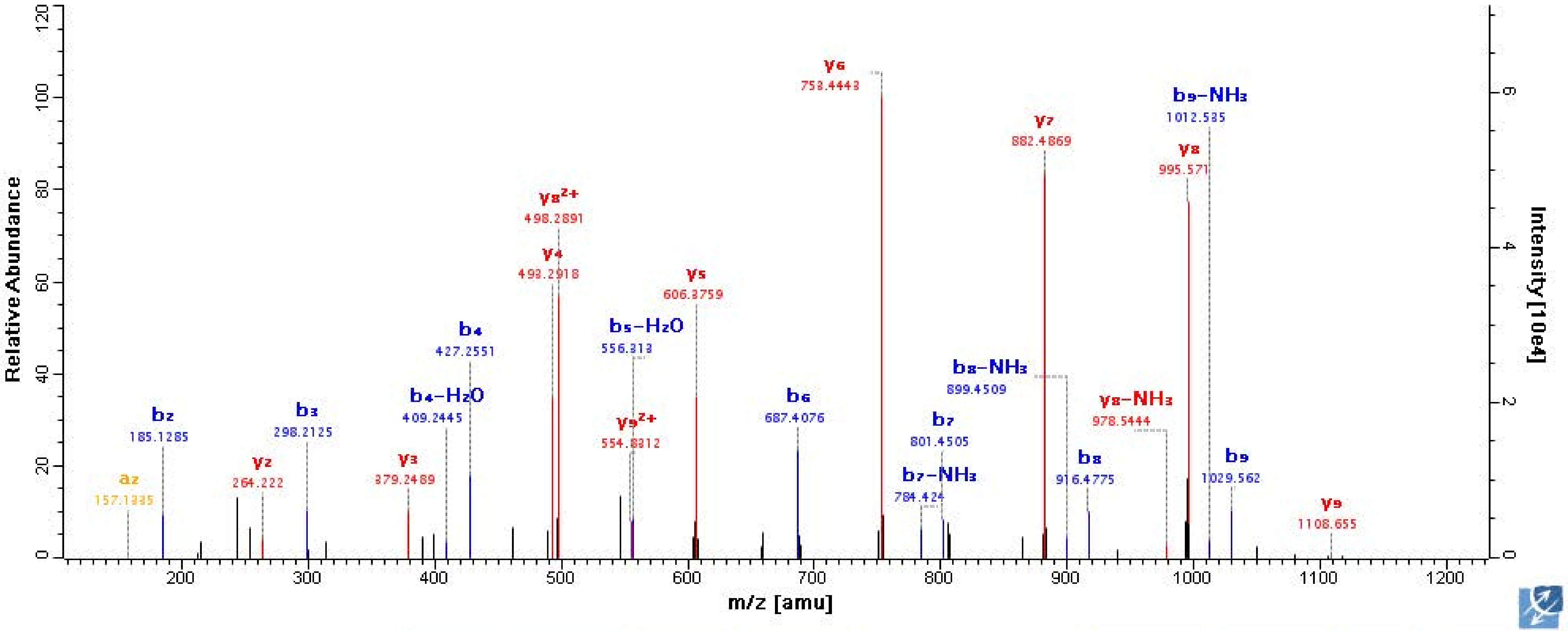
general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	50 %
Protein Localisation:	82 ... 95

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	129.06585398	1	Q	13				
	200.10296777	2	A	12	1567.7461063	+0.2515743	1567.7461063	
	287.13499618	3	S	11	1496.7089925	+0.0977702	748.8581345	+0.2506301
	374.16702459	4	S	10	1409.6769641	+0.0676648	705.3421203	+0.1446351
	502.2256021	5	Q	9	1322.6449357	+0.1368026	1322.6449357	
+0.0678033	631.26819519	6	E	8	1194.5863582	+0.0927189	1194.5863582	
	728.32095905	7	P	7	1065.5437651	+0.0518159	533.27552079	+0.3358073
	841.40502303	8	I	6	968.49100126	+0.1290549	484.74913886	+0.4551458
	1004.4683516	9	Y	5	855.40693728	+4.51E-05	855.40693728	
	1119.4952946	10	D	4	692.34360874	+0.0484201	692.34360874	
	1232.5793586	11	I	3	577.31666571	+0.0045623	577.31666571	
	1418.6586715	12	W	2	464.23260173	-0.0686613	464.23260173	
+0.0744034	1549.6991561	13	M	1	278.15328878	+0.1593028	278.15328878	
		14	K	0	147.11280417		147.11280417	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F02
Scannumber: 25445
Protein: BSU23760; coaA; yqjS
Peptide Score: 169.41
Method: ITMS; CID; 3





precursor information

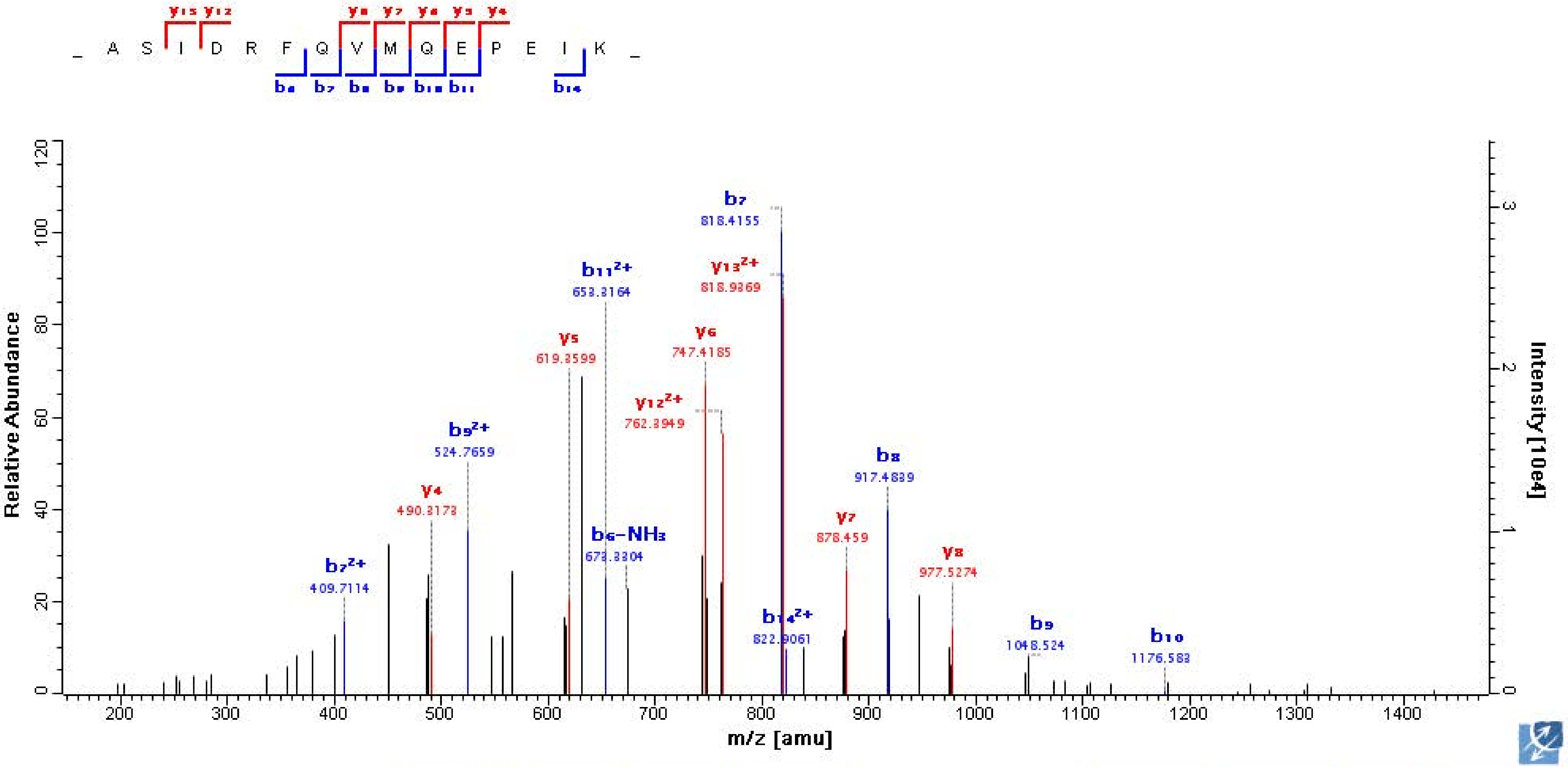
Mass:	1174.65994
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	169.4059
Mass Error [ppm]:	0.13894
PEP:	2.6786E-16
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	69 %
Protein Localisation:	156 ... 165

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	44.04948		72.04439	1	A	9				
-0.000422	157.1335	+0.092844	185.1285	2	I	8	1108.655	+0.377548	554.8312	+0.178361
	270.2176	+0.010474	298.2125	3	I	7	995.571	+0.146732	498.2891	-0.017522
	399.2602	+0.246415	427.2551	4	E	6	882.4869	+0.095481	882.4869	
	546.3286		574.3235	5	F	5	753.4443	+0.112317	753.4443	
	659.4127	+0.09943	687.4076	6	I	4	606.3759	+0.104681	606.3759	
	773.4556	+0.254134	801.4505	7	N	3	493.2918	+0.065088	493.2918	
	888.4825	+0.300372	916.4775	8	D	2	379.2489	+0.024977	379.2489	
	1001.567	+0.304565	1029.562	9	I	1	264.222	-0.043417	264.222	
				10	K	0	151.1379		151.1379	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F03
Scannumber:	15273
Protein:	BSU07440; yfmK
Peptide Score:	77.53
Method:	ITMS; CID; 3



precursor information

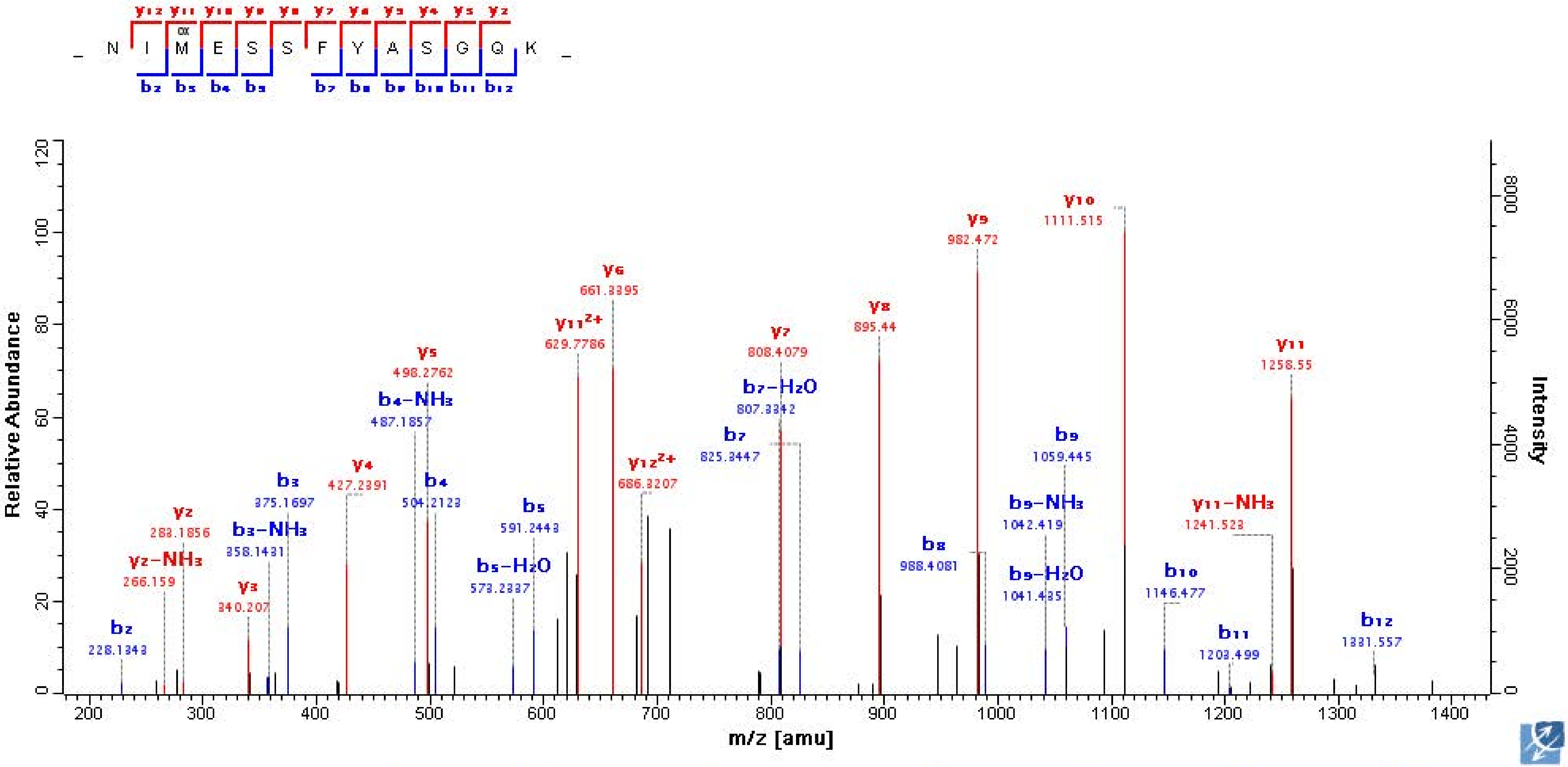
Mass:	1789.90316
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	77.52677
Mass Error [ppm]:	-0.062429
PEP:	0.00069607
Precursor Type:	MULTI

general information

Annotation:	11 of 15
AminoAcids Coverag	73 %
Intensity Coverage:	49 %
Protein Localisation:	2 ... 16

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.04439		72.04439	1	A	14				
	159.0764		159.0764	2	S	13	1723.899		1723.899	
	272.1605		272.1605	3	I	12	1636.867		818.9369	+0.477718
	387.1874		387.1874	4	D	11	1523.782		762.3949	+0.295751
	543.2885		543.2885	5	R	10	1408.756		1408.756	
	690.357		690.357	6	F	9	1252.654		1252.654	
-0.047218	409.7114	-0.35608	818.4155	7	Q	8	1105.586		1105.586	
	917.4839	+0.04212	917.4839	8	V	7	977.5274	+0.138492	977.5274	
+0.13521	524.7659	+0.055407	1048.524	9	M	6	878.459	+0.015012	878.459	
	1176.583	+0.379276	1176.583	10	Q	5	747.4185	-0.012131	747.4185	
+0.386627	653.3164		1305.626	11	E	4	619.3599	+0.282836	619.3599	
	1402.678		1402.678	12	P	3	490.3173	+0.138784	490.3173	
	1531.721		1531.721	13	E	2	393.2646		393.2646	
-0.003559	822.9061		1644.805	14	I	1	264.222		264.222	
				15	K	0	151.1379		151.1379	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber: 12016
Protein: BSU33410; yvgO
Peptide Score: 210.64
Method: ITMS; CID; 3



precursor information

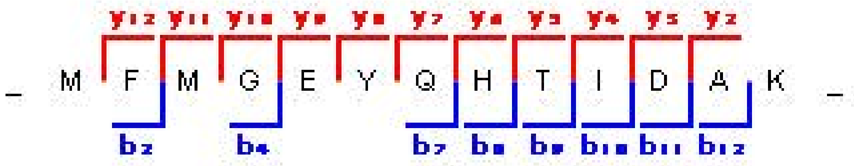
Mass:	1484.66918
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	210.6389
Mass Error [ppm]:	-0.34277
PEP:	2.2485E-52
Precursor Type:	ISO

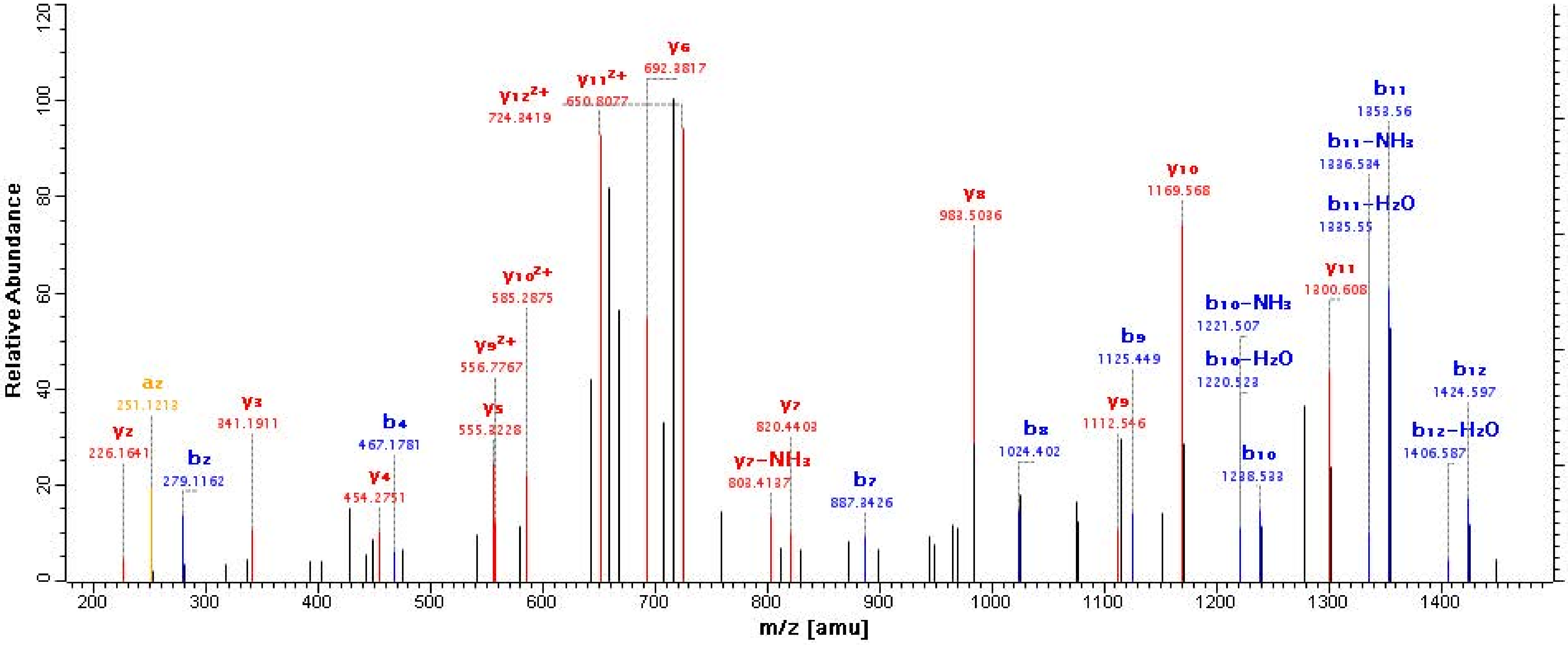
general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	65 %
Protein Localisation:	78 ... 90

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	12				
+0.0203342	228.13426789	2	I	11	1371.634042		686.32065923	+0.1508984
-0.0173234	375.16966712	3	M	10	1258.549978	+0.1331275	629.77862724	+0.0530378
+0.0275469	504.21226022	4	E	9	1111.5145788	+0.0759974	1111.5145788	
+0.0351914	591.24428863	5	S	8	982.47198569	+0.0994865	982.47198569	
	678.27631704	6	S	7	895.43995728	+0.0541223	895.43995728	
+0.2185625	825.34473095	7	F	6	808.40792887	+0.0400081	808.40792887	
+0.0561739	988.40805949	8	Y	5	661.33951495	+0.0507438	661.33951495	
+0.1461353	1059.4451733	9	A	4	498.27618642	-0.018496	498.27618642	
+0.2616899	1146.4772017	10	S	3	427.23907263	-0.0151346	427.23907263	
+0.1288981	1203.4986654	11	G	2	340.20704422	+0.0325798	340.20704422	
+0.20472	1331.5572429	12	Q	1	283.1855805	+0.140805	283.1855805	
		13	K	0	155.12700298		155.12700298	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	13782
Protein:	BSU15130; mraZ; ylIB
Peptide Score:	191.79
Method:	ITMS; CID; 3





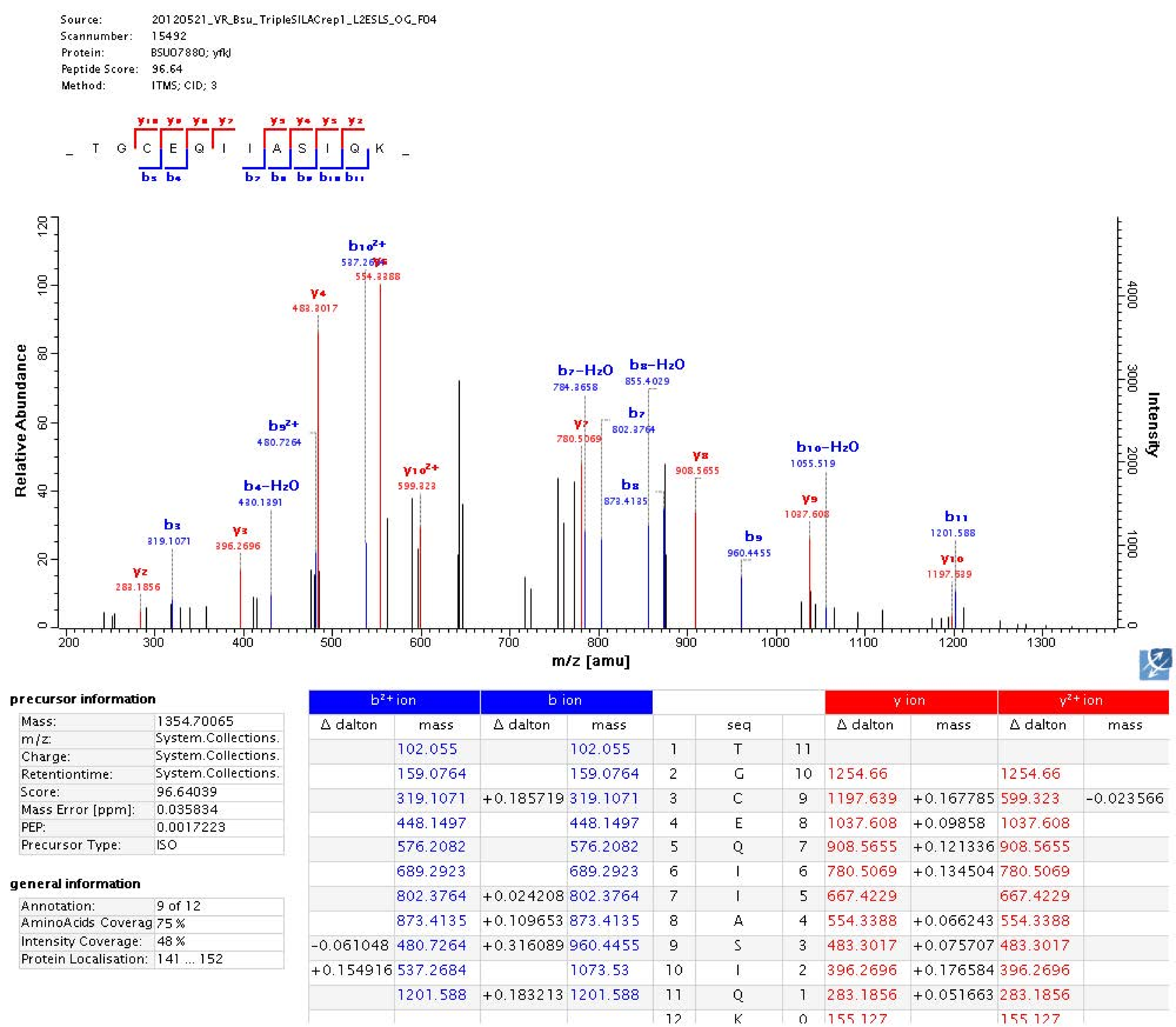
precursor information

Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	191.7854
Mass Error [ppm]:	-0.40656
PEP:	4.3458E-166
Precursor Type:	PEAK

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	50 %
Protein Localisation:	1 ... 13

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	12				
+0.005128	251.1213	-0.139796	279.1162	2	F	11	1447.677		724.3419	+0.310174
	382.1617		410.1567	3	M	10	1300.608	+0.060051	650.8077	+0.126546
	439.1832	+0.163246	467.1781	4	G	9	1169.568	+0.015697	585.2875	-0.00232
	568.2258		596.2207	5	E	8	1112.546	+0.04241	556.7767	+0.42223
	731.2891		759.284	6	Y	7	983.5036	+0.044353	983.5036	
	859.3477	+0.073332	887.3426	7	Q	6	820.4403	+0.164872	820.4403	
	996.4066	+0.066239	1024.402	8	H	5	692.3817	+0.063781	692.3817	
	1097.454	+0.088019	1125.449	9	T	4	555.3228	+0.108716	555.3228	
	1210.538	+0.043017	1238.533	10	I	3	454.2751	-0.042153	454.2751	
	1325.565	+0.011191	1353.56	11	D	2	341.1911	-0.000905	341.1911	
	1396.602	+0.087603	1424.597	12	A	1	226.1641	-0.004205	226.1641	
				13	K	0	155.127		155.127	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	15492
Protein:	BSU07880; yfkJ
Peptide Score:	96.64
Method:	ITMS; CID; 3

precursor information

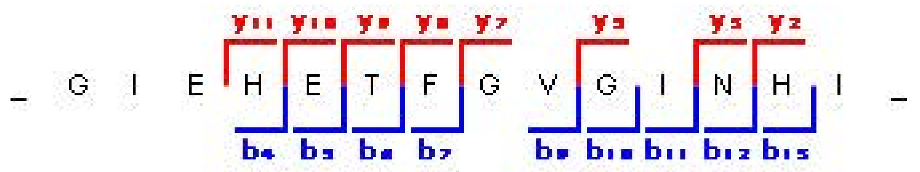
Mass:	1354.70065
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	96.64039
Mass Error [ppm]:	0.035834
PEP:	0.0017223
Precursor Type:	ISO

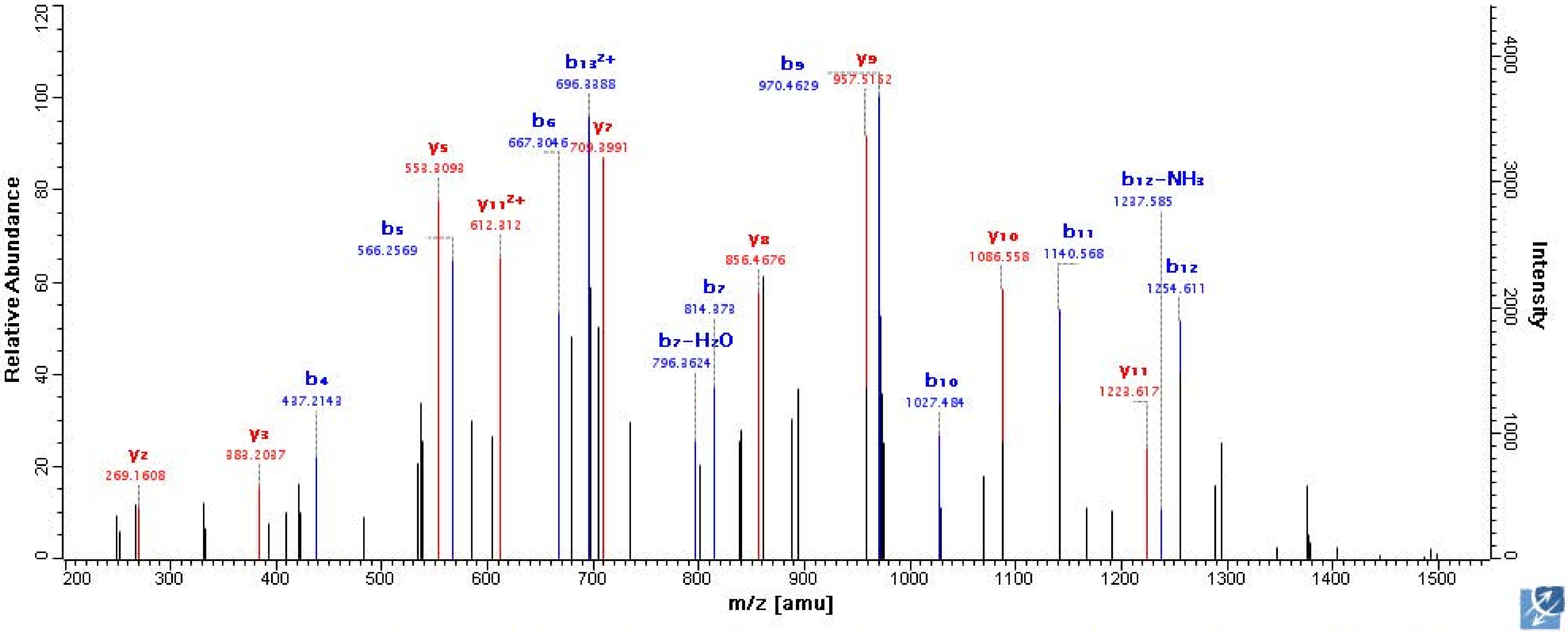
general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	48 %
Protein Localisation:	141 ... 152

b^{2+} ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		102.055	1	T	11				
	159.0764		159.0764	2	G	10	1254.66		1254.66	
	319.1071	+0.185719	319.1071	3	C	9	1197.639	+0.167785	599.323	-0.023566
	448.1497		448.1497	4	E	8	1037.608	+0.09858	1037.608	
	576.2082		576.2082	5	Q	7	908.5655	+0.121336	908.5655	
	689.2923		689.2923	6	I	6	780.5069	+0.134504	780.5069	
	802.3764	+0.024208	802.3764	7	I	5	667.4229		667.4229	
	873.4135	+0.109653	873.4135	8	A	4	554.3388	+0.066243	554.3388	
-0.061048	480.7264	+0.316089	960.4455	9	S	3	483.3017	+0.075707	483.3017	
+0.154916	537.2684		1073.53	10	I	2	396.2696	+0.176584	396.2696	
	1201.588	+0.183213	1201.588	11	Q	1	283.1856	+0.051663	283.1856	
				12	K	0	155.127		155.127	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	16266
Protein:	BSU39340; hutP
Peptide Score:	145.91
Method:	ITMS; CID; 3





precursor information

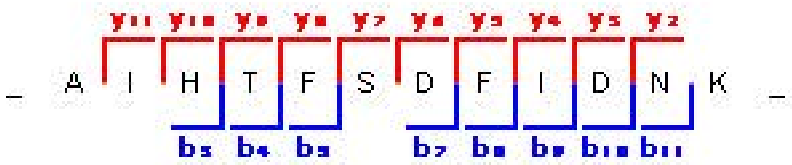
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	145.9146
Mass Error [ppm]:	2.2852
PEP:	1.9488E-63
Precursor Type:	PEAK

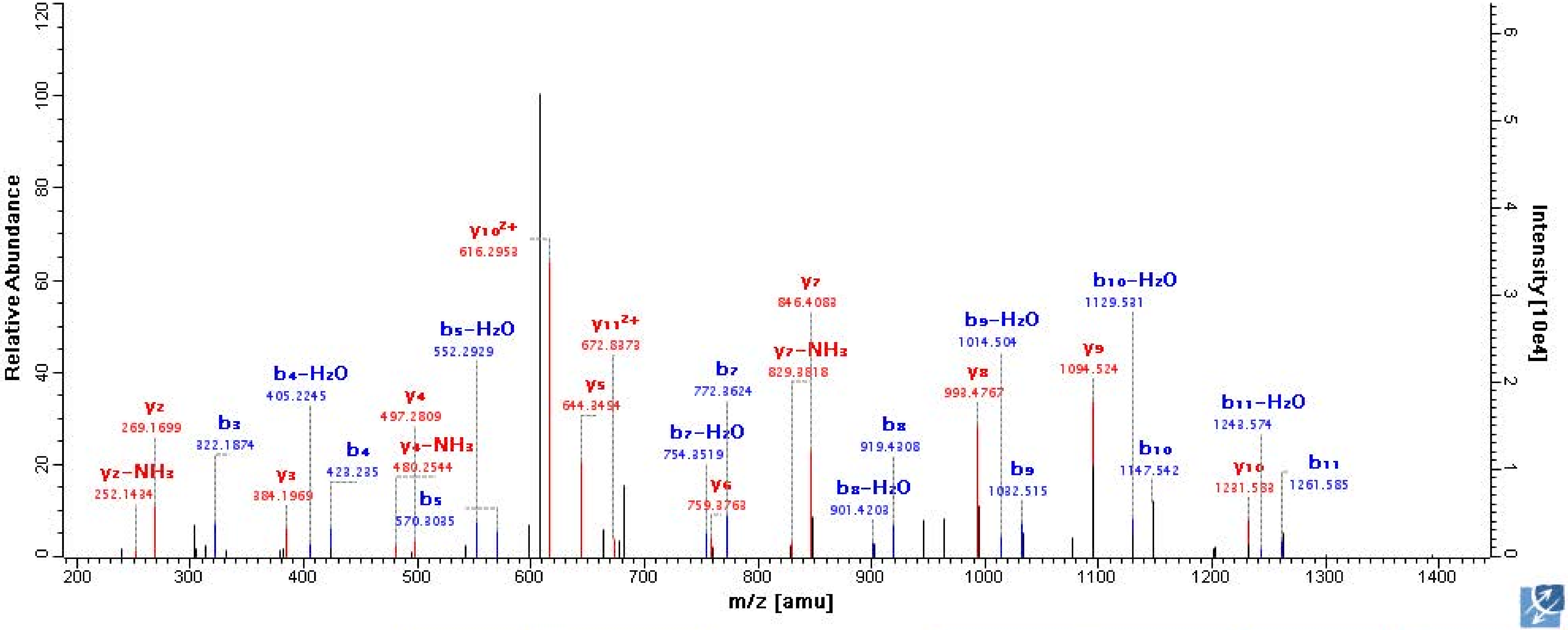
general information

Annotation:	10 of 14
AminoAcids Coverag	71 %
Intensity Coverage:	50 %
Protein Localisation:	135 ... 148

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874		58.02874	1	G	13				
	171.1128		171.1128	2	I	12	1465.743		1465.743	
	300.1554		300.1554	3	E	11	1352.659		1352.659	
	437.2143	+0.200852	437.2143	4	H	10	1223.617	+0.110914	612.312	+0.177002
	566.2569	+0.108332	566.2569	5	E	9	1086.558	+0.120509	1086.558	
	667.3046	+0.217636	667.3046	6	T	8	957.5152	+0.097124	957.5152	
	814.373	+0.092276	814.373	7	F	7	856.4676	+0.089016	856.4676	
	871.3945		871.3945	8	G	6	709.3991	+0.094808	709.3991	
	970.4629	+0.137286	970.4629	9	V	5	652.3777		652.3777	
	1027.484	-0.074058	1027.484	10	G	4	553.3093	+0.06823	553.3093	
	1140.568	+0.125326	1140.568	11	I	3	496.2878		496.2878	
	1254.611	+0.133057	1254.611	12	N	2	383.2037	+0.24285	383.2037	
+0.16881	696.3388		1391.67	13	H	1	269.1608	+0.11378	269.1608	
				14	I	0	132.1019		132.1019	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	16647
Protein:	BSU35070; yvmC
Peptide Score:	226.29
Method:	ITMS; CID; 3





precursor information

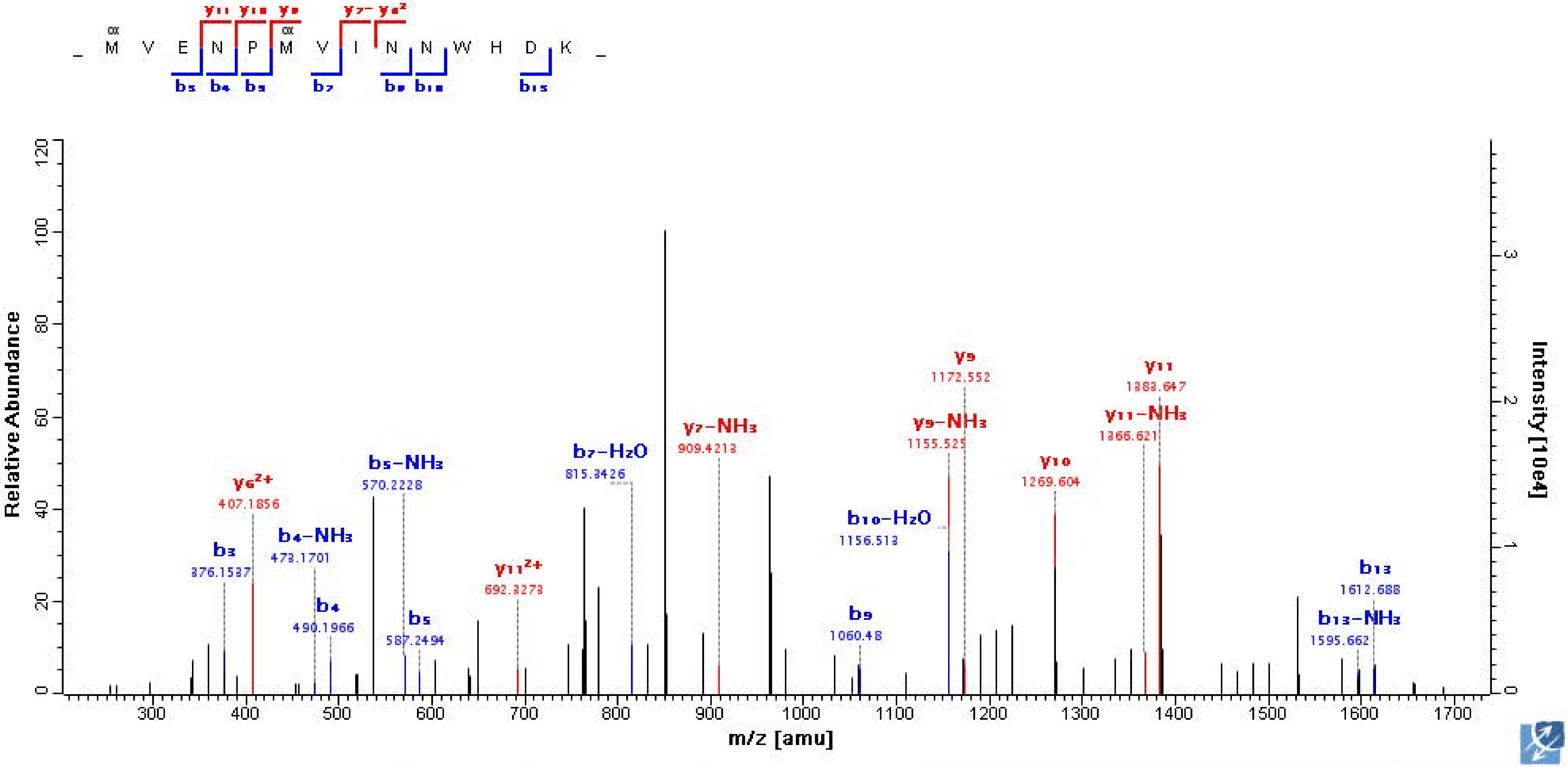
Mass:	1414.69764
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	226.2873
Mass Error [ppm]:	0.29122
PEP:	1.0945E-74
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	53 %
Protein Localisation:	113 ... 124

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	11				
	185.12845423	2	I	10	1344.667391		672.83733375	+0.2199783
-0.0818363	322.1873661	3	H	9	1231.5833271	+0.0623028	616.29530176	+0.1393296
-0.0027142	423.23504457	4	T	8	1094.5244152	+0.0333241	1094.5244152	
+0.0268027	570.30345849	5	F	7	993.47673672	+0.0550626	993.47673672	
	657.3354869	6	S	6	846.4083228	+0.0703149	846.4083228	
+0.0869109	772.36242993	7	D	5	759.37629439	+0.0363033	759.37629439	
+0.1056552	919.43084385	8	F	4	644.34935136	+0.0828996	644.34935136	
+0.088974	1032.5149078	9	I	3	497.28093744	+0.1149366	497.28093744	
+0.0329782	1147.5418509	10	D	2	384.19687346	-0.0140121	384.19687346	
+0.0098262	1261.5847783	11	N	1	269.16993043	-0.0643396	269.16993043	
		12	K	0	155.12700298		155.12700298	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	21151
Protein:	BSU26300; yqaI
Peptide Score:	65.29
Method:	ITMS; CID; 3



precursor information

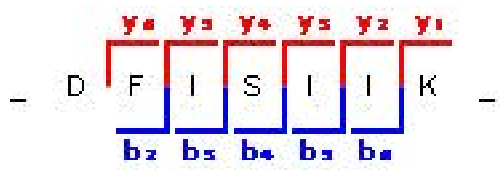
Mass:	1757.78755
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	65.2948
Mass Error [ppm]:	0.58555
PEP:	0.002097
Precursor Type:	MULTI

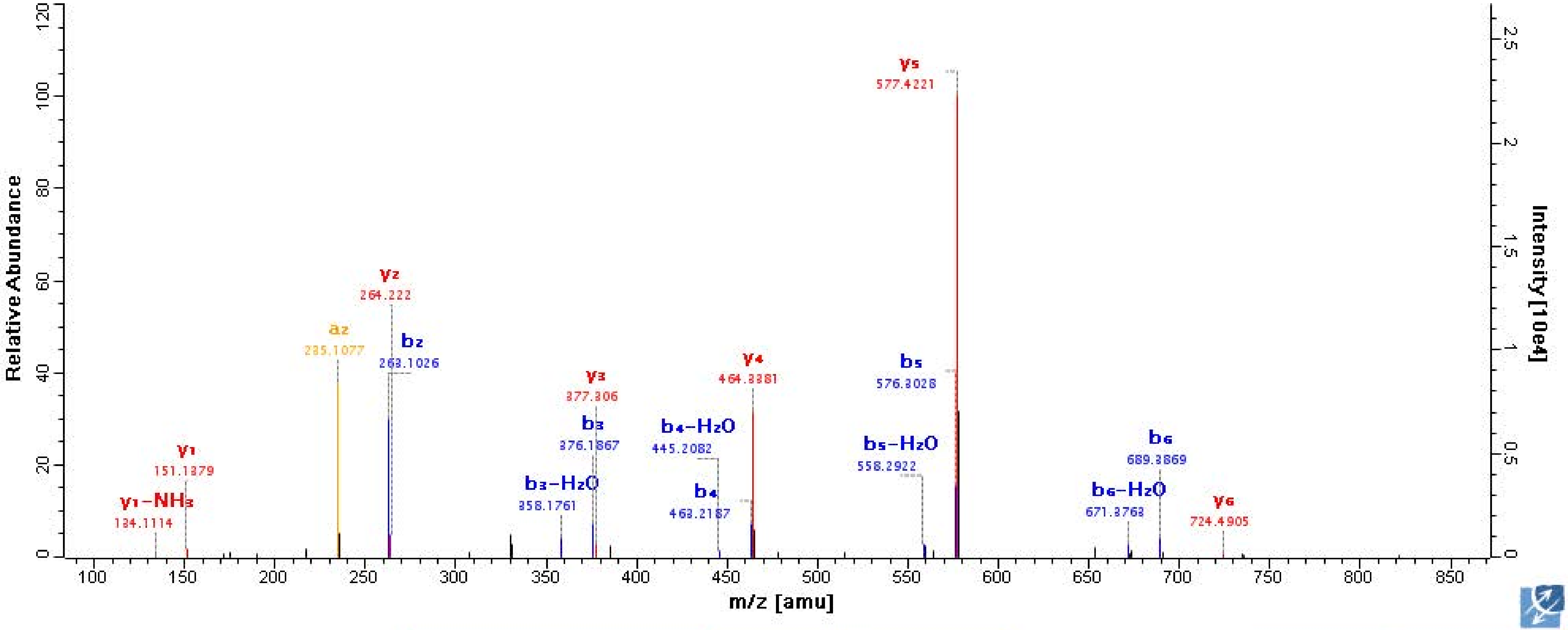
general information

Annotation:	9 of 14
AminoAcids Coverag	64%
Intensity Coverage:	25%
Protein Localisation:	1 ... 14

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	148.04267569	1	M	13				
	247.11108961	2	V	12	1611.7584023		1611.7584023	
+0.1123695	376.15368271	3	E	11	1512.6899884		1512.6899884	
+0.1105798	490.19661015	4	N	10	1383.6473953	+0.0238693	692.3273359	-0.0266157
+0.0453037	587.24937401	5	P	9	1269.6044679	+0.0193114	1269.6044679	
	734.28477323	6	M	8	1172.551704	+0.043877	1172.551704	
	833.35318715	7	V	7	1025.5163048		1025.5163048	
	946.43725113	8	I	6	926.44789089		926.44789089	
-0.2249296	1060.4801786	9	N	5	813.36382691		407.18555169	+0.2124891
	1174.523106	10	N	4	699.32089947		699.32089947	
	1360.602419	11	W	3	585.27797202		585.27797202	
	1497.6613308	12	H	2	399.19865906		399.19865906	
+0.0518384	1612.6882739	13	D	1	262.1397472		262.1397472	
		14	K	0	147.11280417		147.11280417	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber: 22726
Protein: BSU14880; ctaB2
Peptide Score: 178.65
Method: ITMS; CID; 3

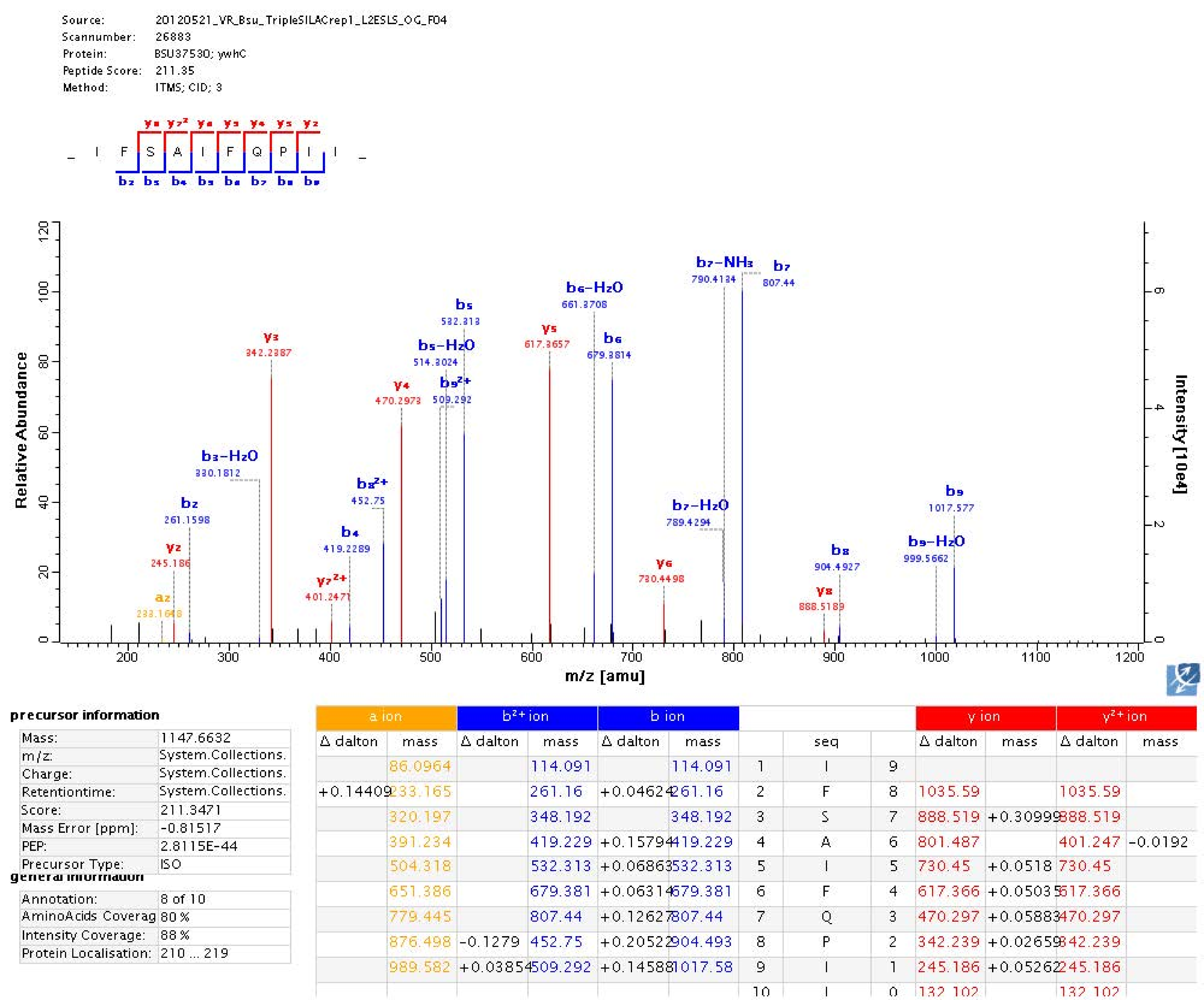




precursor information

Mass:	834.48541
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	178.6466
Mass Error [ppm]:	0.36679
PEP:	1.7664E-14
Annotation:	6 of 7
AminoAcids Coverag	86 %
Intensity Coverage:	79 %
Protein Localisation:	24 ... 30

a ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	88.039304876		116.0342195	1	D	6		
-0.0541757	235.10771879	-0.0660734	263.10263341	2	F	5	724.49054542	-0.2066709
	348.19178277	-0.000235	376.1866974	3	I	4	577.42213151	+0.0347166
	435.22381118	+0.1518186	463.21872581	4	S	3	464.33806752	+0.0206361
	548.30787516	+0.1527156	576.30278979	5	I	2	377.30603912	-0.0214932
	661.39193914	+0.0593132	689.38685377	6	I	1	264.22197513	-0.1741541
				7	K	0	151.13791115	+0.0584389



Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber: 26883
Protein: BSU37530; ywhC
Peptide Score: 211.35
Method: ITMS; CID; 3

precursor information

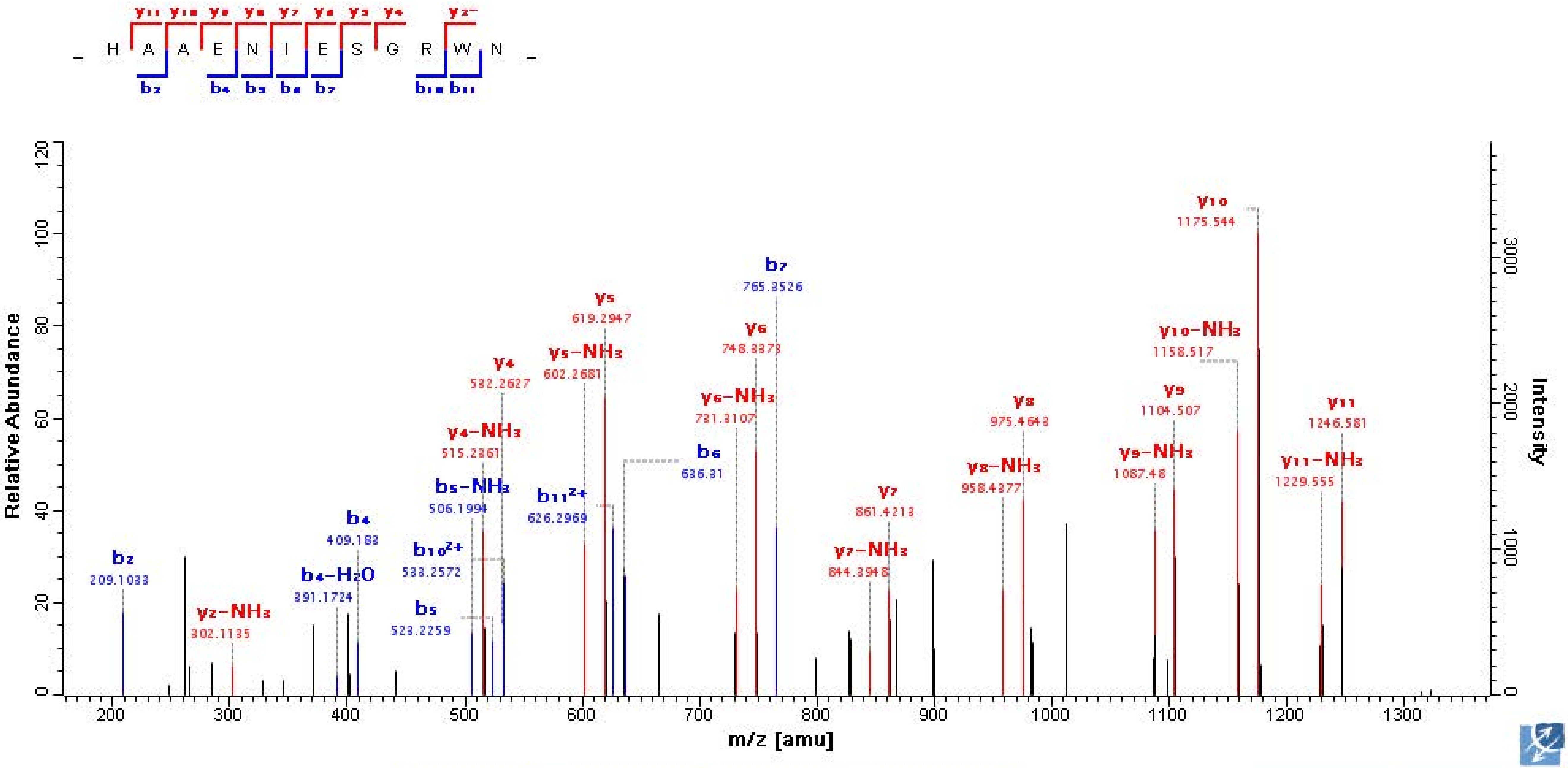
Mass:	1147.6632
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	211.3471
Mass Error [ppm]:	-0.81517
PEP:	2.8115E-44
Precursor Type:	ISO

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	88 %
Protein Localisation:	210 ... 219

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	9				
+0.14409	233.165		261.16	+0.04624	261.16	2	F	8	1035.59		1035.59	
	320.197		348.192		348.192	3	S	7	888.519	+0.30999	888.519	
	391.234		419.229	+0.15794	419.229	4	A	6	801.487		401.247	-0.0192
	504.318		532.313	+0.06863	532.313	5	I	5	730.45	+0.0518	730.45	
	651.386		679.381	+0.06314	679.381	6	F	4	617.366	+0.05035	617.366	
	779.445		807.44	+0.12627	807.44	7	Q	3	470.297	+0.05883	470.297	
	876.498	-0.1279	452.75	+0.20522	904.493	8	P	2	342.239	+0.02659	342.239	
	989.582	+0.03854	509.292	+0.14588	1017.58	9	I	1	245.186	+0.05262	245.186	
						10	I	0	132.102		132.102	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F04
Scannumber:	9934
Protein:	BSU02270; pss; pssA
Peptide Score:	173.71
Method:	ITMS; CID; 3



precursor information

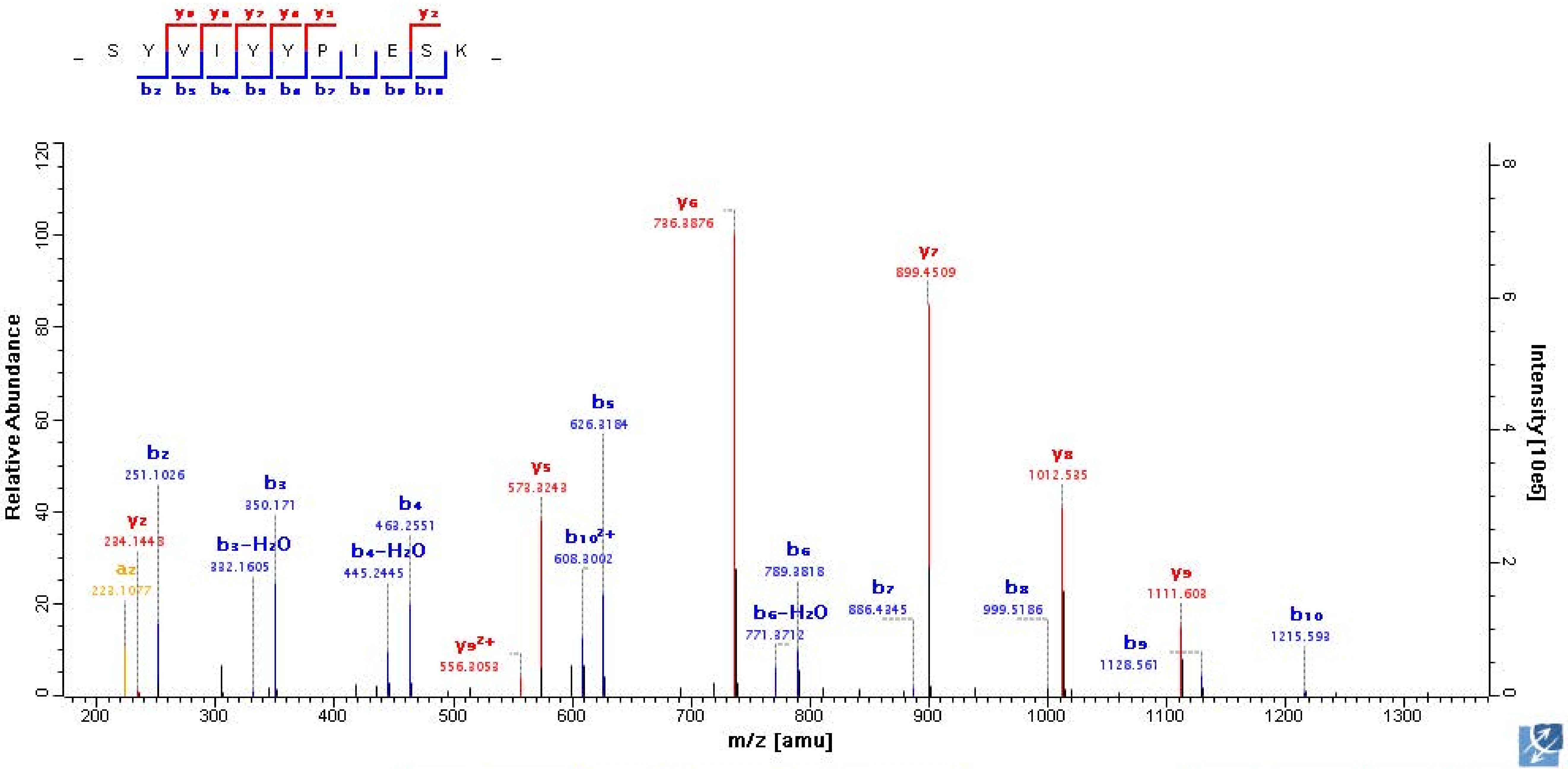
Mass:	1382.63142
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	173.7086
Mass Error [ppm]:	-0.9419
PEP:	2.5694E-09
Precursor Type:	ISO

general information

Annotation:	10 of 12
AminoAcids Coverag	83 %
Intensity Coverage:	56 %
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	-0.0440065	209.10330212	2	A	10	1246.5810899	+0.13058
	280.1404159		280.1404159	3	A	9	1175.5439761	+0.1257016
	409.183009	-0.0028332	409.183009	4	E	8	1104.5068623	+0.0824931
	523.22593645	+0.2145543	523.22593645	5	N	7	975.46426924	+0.105616
	636.31000043	+0.142209	636.31000043	6	I	6	861.42134179	+0.0893394
	765.35259352	+0.1346501	765.35259352	7	E	5	748.33727781	+0.0423609
	852.38462193		852.38462193	8	S	4	619.29468472	+0.0133597
	909.40608566		909.40608566	9	G	3	532.26265631	+0.161416
+0.2620505	533.25723658		1065.5071967	10	R	2	475.24119258	
+0.2669497	626.29689305		1251.5865096	11	W	1	319.14008155	
				12	N	0	133.0607686	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F05
Scannumber:	19318
Protein:	BSU27380; yrzB
Peptide Score:	158.79
Method:	ITMS; CID; 3



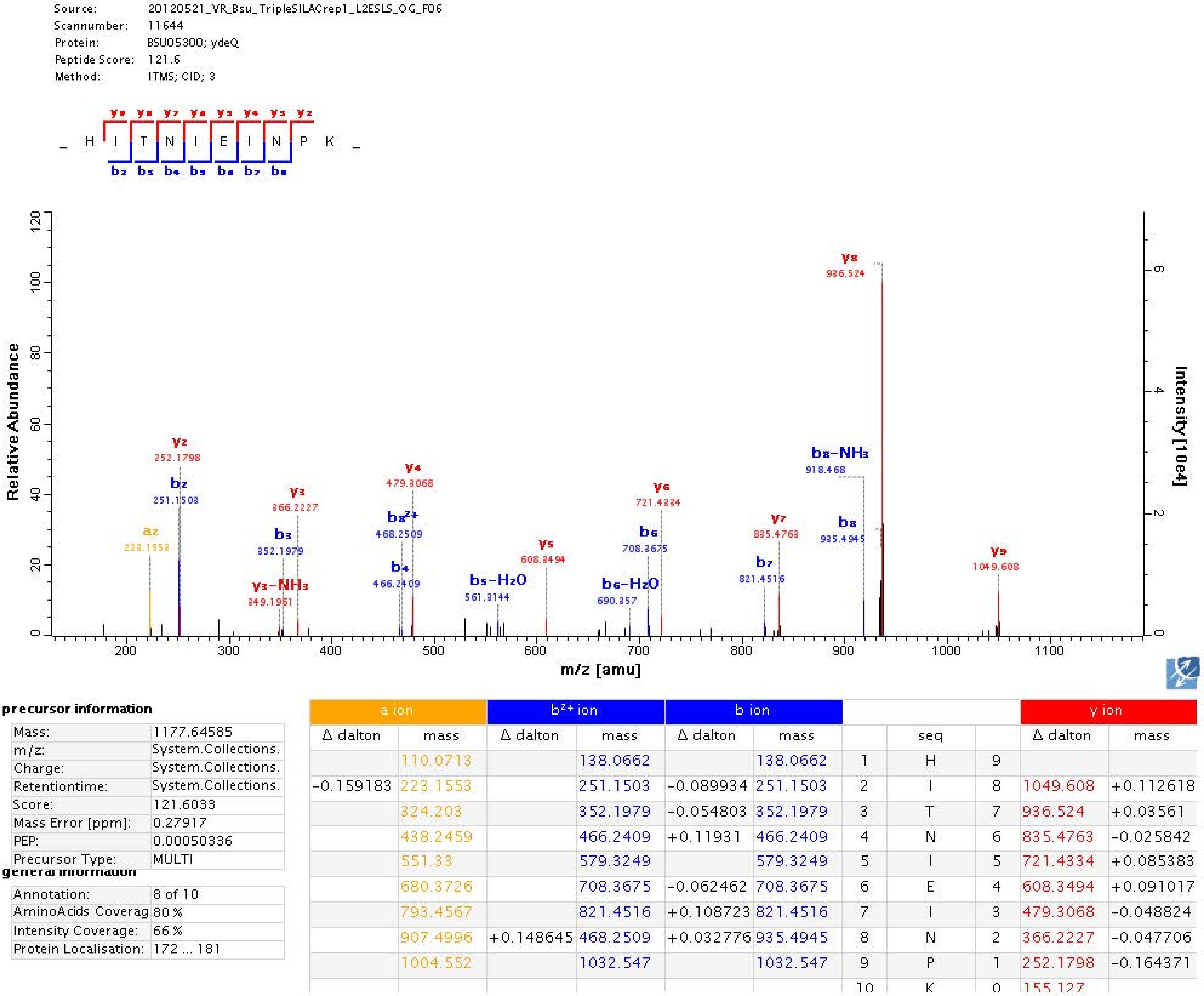
precursor information

Mass:	1360.69162
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	158.7898
Mass Error [ppm]:	0.11035
PEP:	3.1064E-12
Precursor Type:	MULTI

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	72 %
Protein Localisation:	34 ... 44

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	10				
-0.0486	223.108		251.103	-0.0543	251.103	2	Y	9	1274.67		1274.67	
	322.176		350.171	-0.0186	350.171	3	V	8	1111.6	+0.2594	556.305	+0.1011
	435.26		463.255	+0.03163	463.255	4	I	7	1012.53	+0.08209	1012.53	
	598.324		626.318	+0.04026	626.318	5	Y	6	899.451	+0.03316	899.451	
	761.387		789.382	+0.04322	789.382	6	Y	5	736.388	+0.03686	736.388	
	858.44		886.435	+0.23692	886.435	7	P	4	573.324	+0.06521	573.324	
	971.524		999.519	+0.16396	999.519	8	I	3	476.271		476.271	
	1100.57		1128.56	+0.22519	1128.56	9	E	2	363.187		363.187	
	1187.6	+0.06255	608.3	+0.19206	1215.59	10	S	1	234.145	+0.0499	234.145	
						11	K	0	147.113		147.113	



Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber: 11644
Protein: BSU05300; ydeQ
Peptide Score: 121.6
Method: ITMS; CID; 3

precursor information

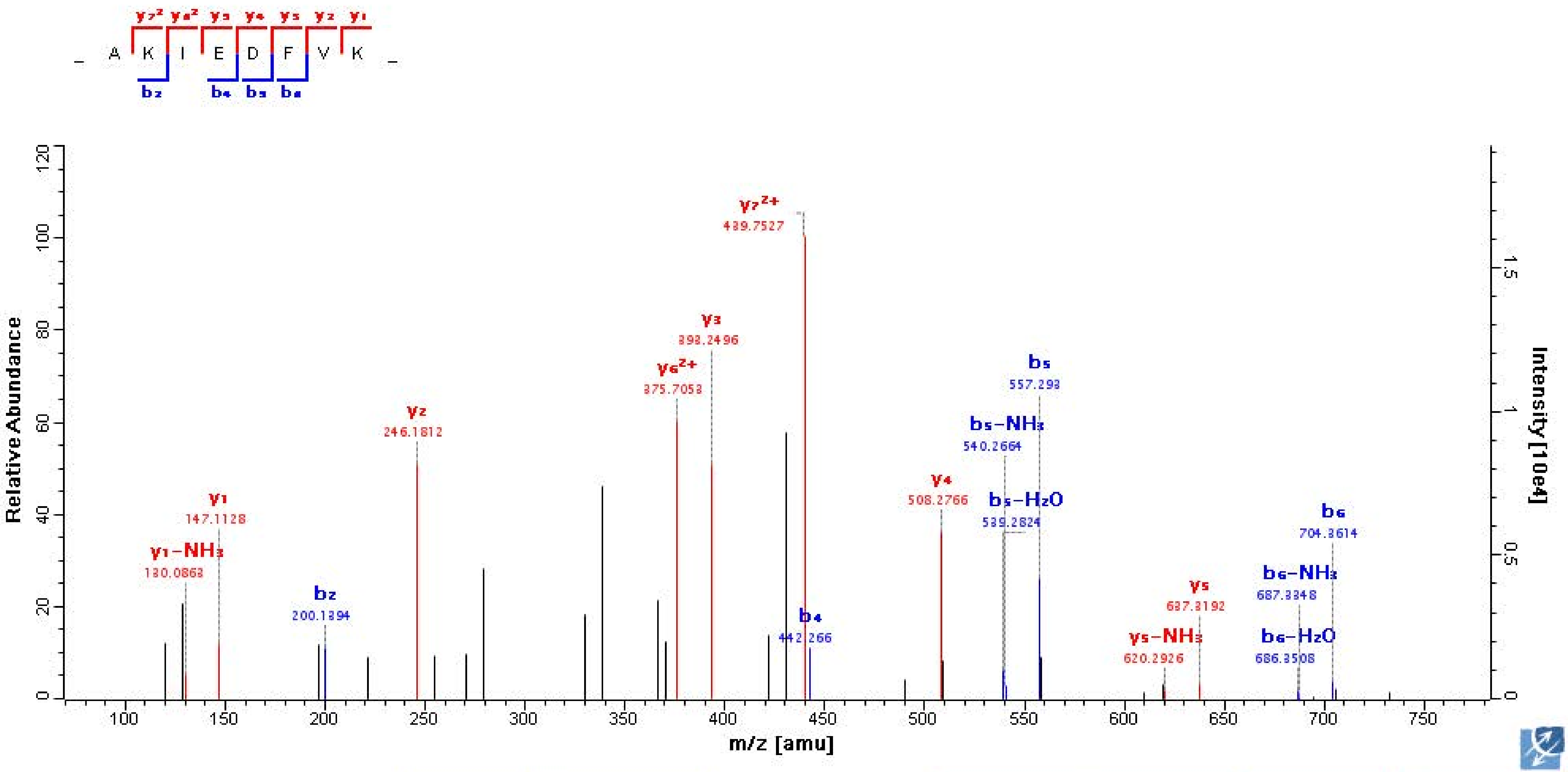
Mass:	1177.64585
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	121.6033
Mass Error [ppm]:	0.27917
PEP:	0.00050336
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	66 %
Protein Localisation:	172 ... 181

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	9		
-0.159183	223.1553		251.1503	-0.089934	251.1503	2	I	8	1049.608	+0.112618
	324.203		352.1979	-0.054803	352.1979	3	T	7	936.524	+0.03561
	438.2459		466.2409	+0.11931	466.2409	4	N	6	835.4763	-0.025842
	551.33		579.3249		579.3249	5	I	5	721.4334	+0.085383
	680.3726		708.3675	-0.062462	708.3675	6	E	4	608.3494	+0.091017
	793.4567		821.4516	+0.108723	821.4516	7	I	3	479.3068	-0.048824
	907.4996	+0.148645	468.2509	+0.032776	935.4945	8	N	2	366.2227	-0.047706
	1004.552		1032.547		1032.547	9	P	1	252.1798	-0.164371
						10	K	0	155.127	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber:	13908
Protein:	BSU33980; ywbT
Peptide Score:	130.22
Method:	ITMS; CID; 3



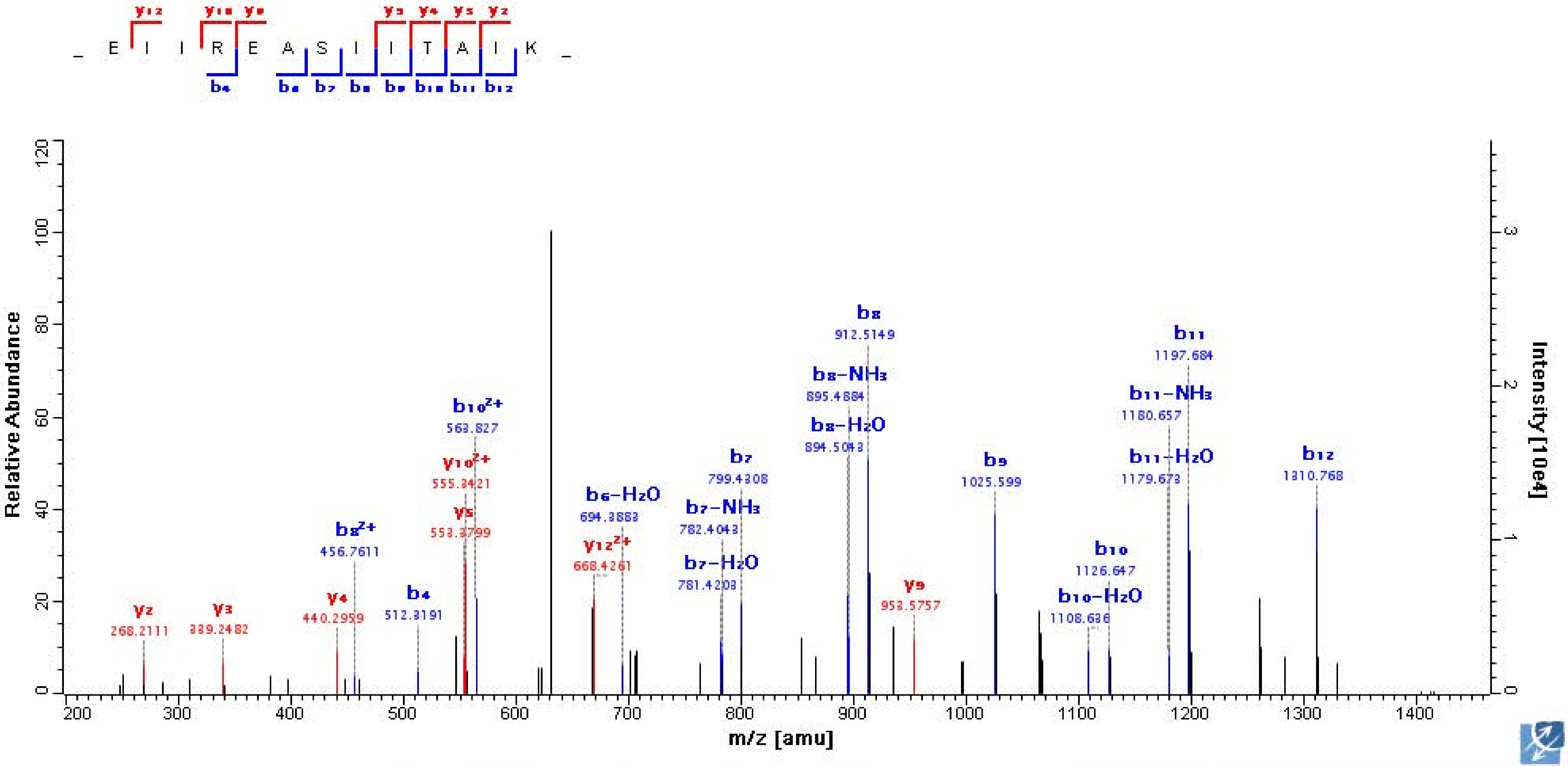
g

precursor information

Mass:	948.52747
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	130.2208
Mass Error [ppm]:	-0.592
PEP:	0.0019271
Annotation:	7 of 8
AminoAcids Coverag	88 %
Intensity Coverage:	56 %
Protein Localisation:	296 ... 303

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	72.044390254	1	A	7				
+0.1206565	200.13935327	2	K	6	878.49819513		439.7527358	+0.2661851
	313.22341725	3	I	5	750.40323211		375.70525429	+0.1926339
+0.0546073	442.26601035	4	E	4	637.31916813	+0.2667694	637.31916813	
+0.0804597	557.29295338	5	D	3	508.27657504	+0.0884762	508.27657504	
+0.1331395	704.3613673	6	F	2	393.249632	+0.0612811	393.249632	
	803.42978121	7	V	1	246.18121809	+0.0067855	246.18121809	
		8	K	0	147.11280417	-0.0336111	147.11280417	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber: 20043
Protein: BSU17360; ymzA
Peptide Score: 149.23
Method: ITMS; CID; 3



precursor information

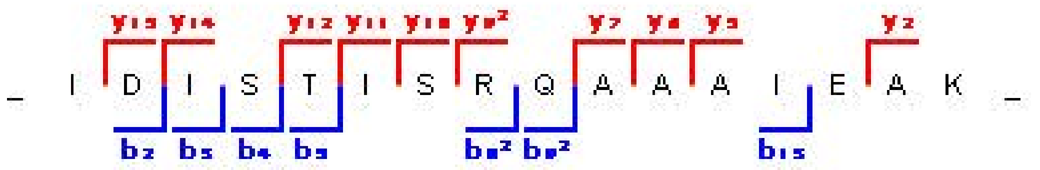
Mass:	1455.86698
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	149.2254
Mass Error [ppm]:	0.61272
PEP:	7.6456E-12
Precursor Type:	MULTI

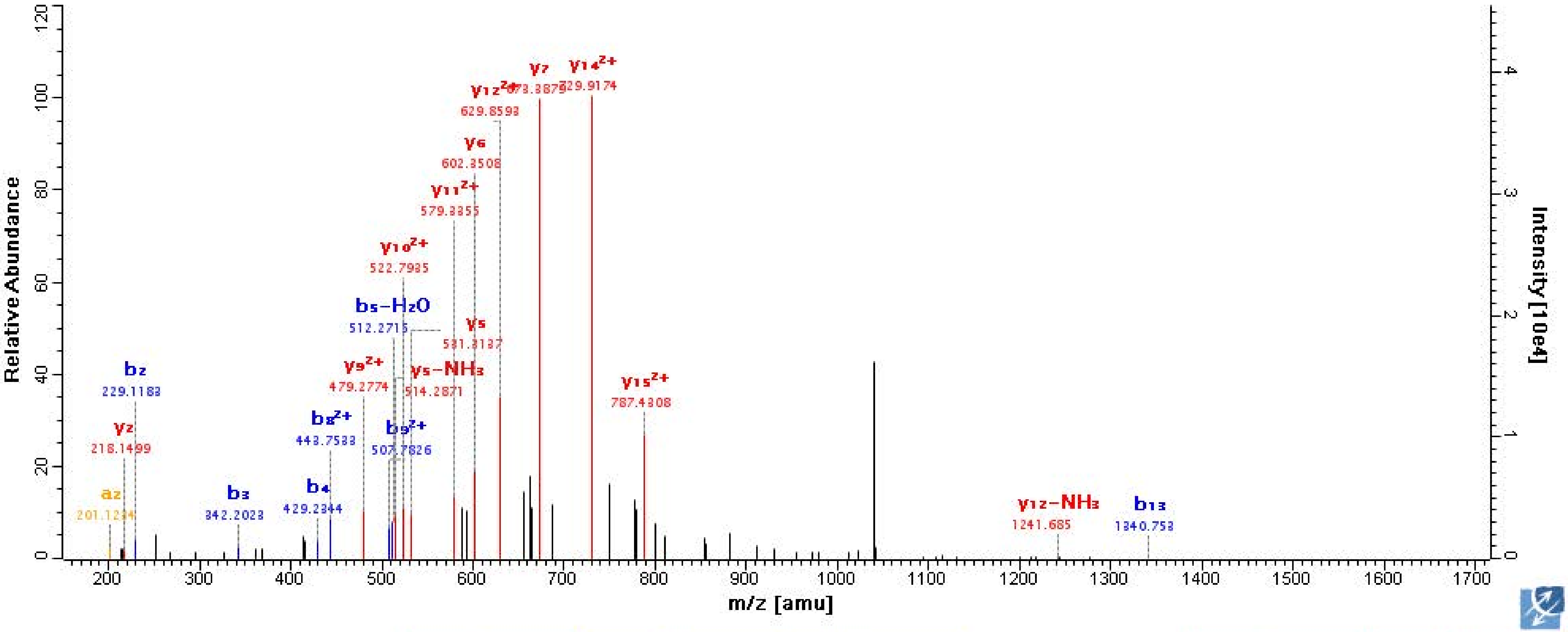
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	45 %
Protein Localisation:	32 ... 44

b2+ ion		b ion					y ion		y2+ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.0499		130.0499	1	E	12				
	243.1339		243.1339	2	I	11	1335.845		668.4261	+0.070768
	356.218		356.218	3	I	10	1222.761		1222.761	
	512.3191	-0.044694	512.3191	4	R	9	1109.677		555.3421	-0.361098
	641.3617		641.3617	5	E	8	953.5757	+0.019798	953.5757	
	712.3988		712.3988	6	A	7	824.5331		824.5331	
	799.4308	+0.05286	799.4308	7	S	6	753.496		753.496	
+0.030168	456.7611	+0.043015	912.5149	8	I	5	666.464		666.464	
	1025.599	+0.048855	1025.599	9	I	4	553.3799	+0.099691	553.3799	
+0.116945	563.827	+0.049028	1126.647	10	T	3	440.2959	+0.136575	440.2959	
	1197.684	+0.045606	1197.684	11	A	2	339.2482	-0.016552	339.2482	
	1310.768	+0.077387	1310.768	12	I	1	268.2111	-0.083198	268.2111	
				13	K	0	155.127		155.127	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber: 21988
Protein: BSU40010; S14D; yxaD
Peptide Score: 97.55
Method: ITMS; CID; 3





precursor information

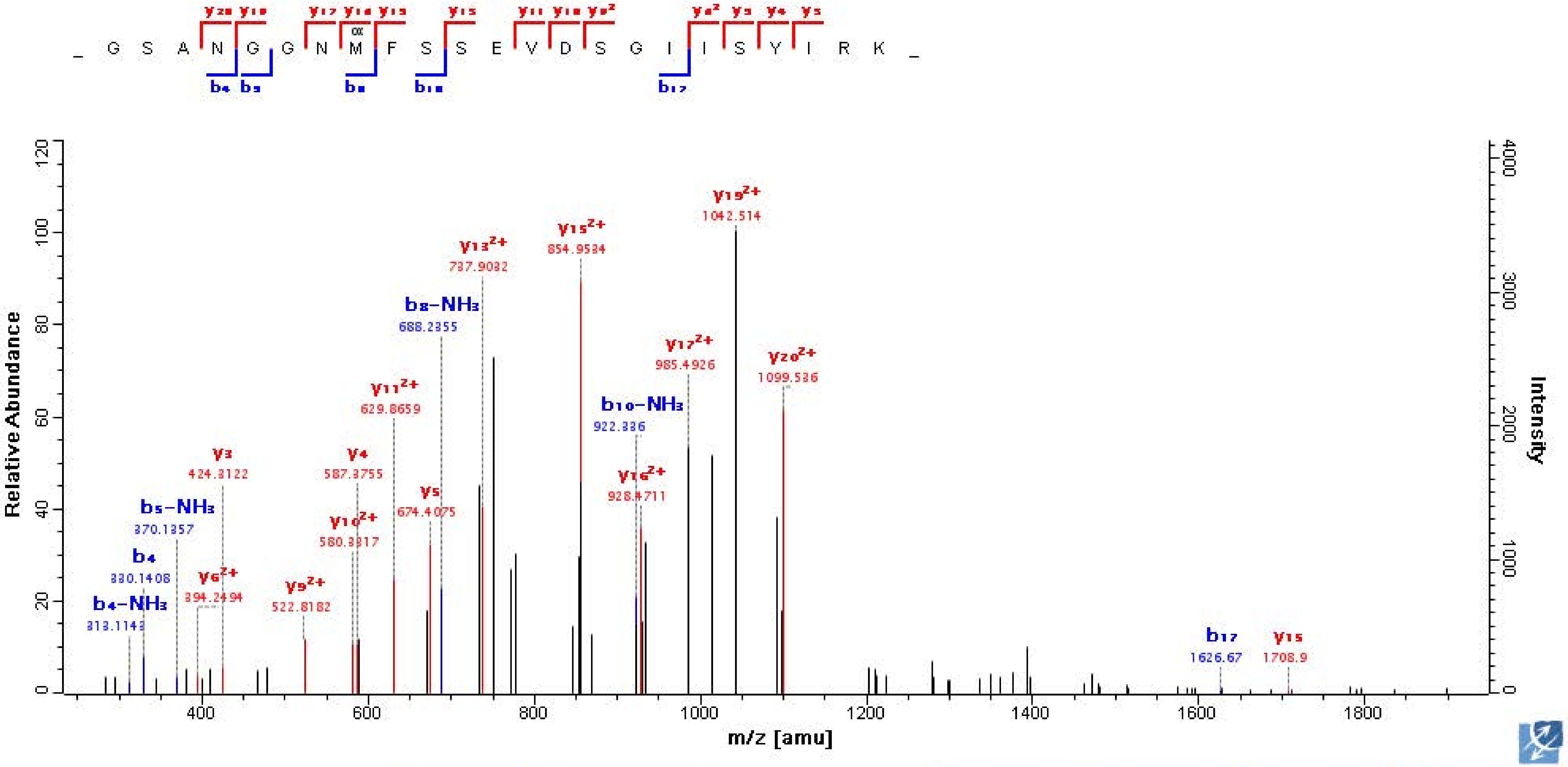
Mass:	1685.93304
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	97.55133
Mass Error [ppm]:	1.0924
PEP:	6.4832E-07
Precursor Type:	MULTI

general information

Annotation:	13 of 16
AminoAcids Coverag	81 %
Intensity Coverage:	60 %
Protein Localisation:	62 ... 77

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
	86.0964		114.091		114.091	1	I	15				
+0.08569	201.123		229.118	+0.03394	229.118	2	D	14	1573.85		787.431	+0.4006
	314.207		342.202	-0.0252	342.202	3	I	13	1458.83		729.917	+0.2207
	401.239		429.234	+0.2293	429.234	4	S	12	1345.74		1345.74	
	502.287		530.282		530.282	5	T	11	1258.71		629.859	+0.2176
	615.371		643.366		643.366	6	I	10	1157.66		579.335	+0.4040
	702.403		730.398		730.398	7	S	9	1044.58		522.793	+0.0482
	858.504	-0.4735	443.753		886.499	8	R	8	957.548		479.277	+0.0116
	986.563	+0.00858	507.783		1014.56	9	Q	7	801.446		801.446	
	1057.6		1085.59		1085.59	10	A	6	673.388	+0.21737	673.388	
	1128.64		1156.63		1156.63	11	A	5	602.351	+0.04855	602.351	
	1199.67		1227.67		1227.67	12	A	4	531.314	+0.00675	531.314	
	1312.76		1340.75	-0.1122	1340.75	13	I	3	460.277		460.277	
	1441.8		1469.8		1469.8	14	E	2	347.193		347.193	
	1512.84		1540.83		1540.83	15	A	1	218.15	-0.0037	218.15	
						16	K	0	147.113		147.113	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber:	23303
Protein:	BSU40490; yycA
Peptide Score:	59.59
Method:	ITMS; CID; 3



precursor information

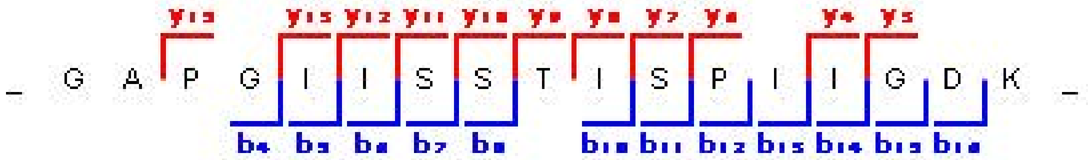
Mass:	2404.13219
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	59.58521
Mass Error [ppm]:	-0.29085
PEP:	0.00011328
Precursor Type:	MULTI

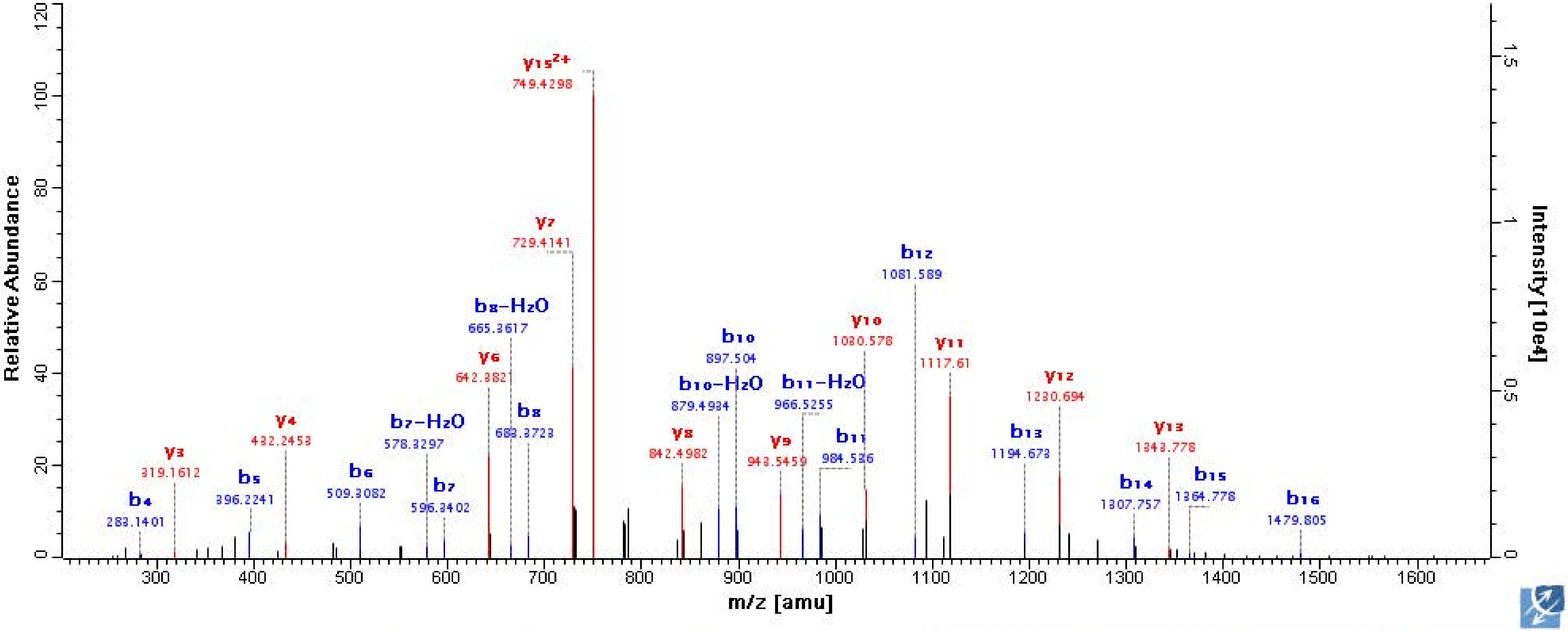
general information

Annotation:	15 of 23
AminoAcids Coverag	65 %
Intensity Coverage:	36 %
Protein Localisation:	548 ... 570

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	22				
	145.0607686	2	S	21	2356.1328996		2356.1328996	
	216.09788239	3	A	20	2269.1008712		2269.1008712	
+0.1305525	330.14080984	4	N	19	2198.0637574		1099.5355169	+0.4672907
	387.16227356	5	G	18	2084.0208299		1042.5140532	+0.2094575
	444.18373728	6	G	17	2026.9993662		2026.9993662	
	558.22666473	7	N	16	1969.9779025		985.49258948	-0.0452018
	705.26206396	8	M	15	1855.934975		928.47112576	+0.0639695
	852.33047787	9	F	14	1708.8995758	+0.1575531	854.95342614	+0.1630289
	939.36250628	10	S	13	1561.8311619		1561.8311619	
	1026.3945347	11	S	12	1474.7991335		737.90320498	+0.348443
	1155.4371278	12	E	11	1387.7671051		1387.7671051	
	1254.5055417	13	V	10	1258.724512		629.86589422	+0.3176385
	1369.5324847	14	D	9	1159.6560981		580.33168727	+0.366738
	1456.5645131	15	S	8	1044.629155		522.81821575	+0.3195406
	1513.5859769	16	G	7	957.59712662		957.59712662	
+0.3984406	1626.6700409	17	I	6	900.5756629		900.5756629	
	1739.7541048	18	I	5	787.49159892		394.24943769	+0.2642342
	1826.7861332	19	S	4	674.40753494	+0.1490446	674.40753494	
	1989.8494618	20	Y	3	587.37550653	+0.0113343	587.37550653	
	2102.9335258	21	I	2	424.31217799	+0.1223923	424.31217799	
	2259.0346368	22	R	1	311.22811401		311.22811401	
		23	K	0	155.12700298		155.12700298	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber: 24865
Protein: BSU30070; opuD; ytfQ
Peptide Score: 153.09
Method: ITMS; CID; 3





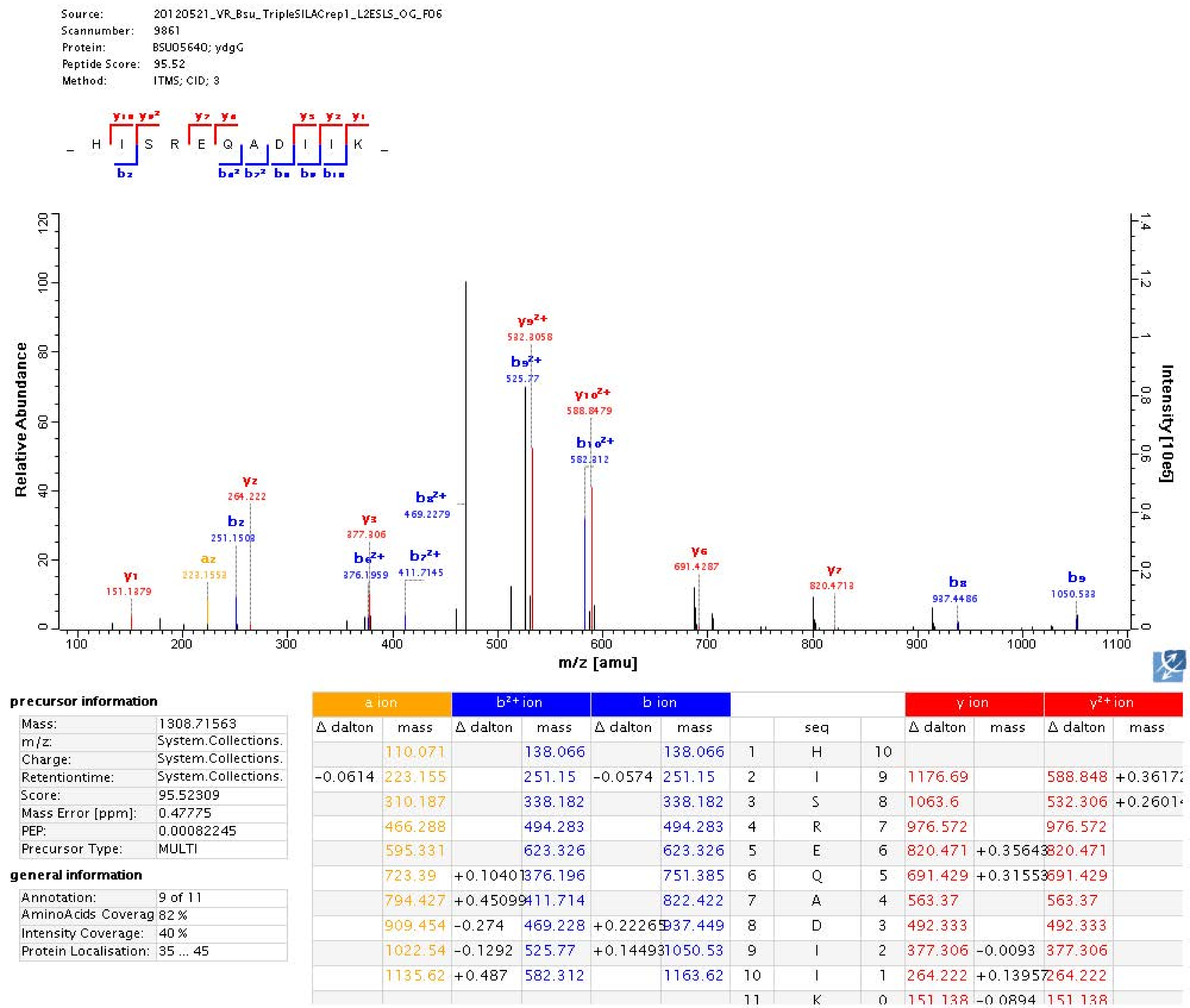
precursor information

Mass:	1624.90333
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	153.0896
Mass Error [ppm]:	-0.15576
PEP:	1.0535E-19
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	65 %
Protein Localisation:	161 ... 177

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	58.02874019	1	G	16				
	129.06585398	2	A	15	1568.8893997		1568.8893997	
	226.11861783	3	P	14	1497.852286		749.42978121	+0.211149
+0.1494082	283.14008155	4	G	13	1400.7995221		1400.7995221	
-0.0916992	396.22414553	5	I	12	1343.7780584	-0.0092596	1343.7780584	
-0.0171329	509.30820951	6	I	11	1230.6939944	+0.1124021	1230.6939944	
+0.0451991	596.34023792	7	S	10	1117.6099304	+0.0772034	1117.6099304	
+0.0353875	683.37226633	8	S	9	1030.577902	+0.1354769	1030.577902	
	784.41994481	9	T	8	943.5458736	+0.03335	943.5458736	
+0.0938306	897.50400879	10	I	7	842.49819513	+0.1098981	842.49819513	
+0.1144755	984.5360372	11	S	6	729.41413115	+0.0524826	729.41413115	
+0.0170339	1081.5888011	12	P	5	642.38210274	+0.0378802	642.38210274	
+0.0689563	1194.672865	13	I	4	545.32933889		545.32933889	
+0.0943893	1307.756929	14	I	3	432.24527491	+0.2126719	432.24527491	
+0.0634041	1364.7783927	15	G	2	319.16121093	+0.1694165	319.16121093	
+0.0406115	1479.8053358	16	D	1	262.1397472		262.1397472	
		17	K	0	147.11280417		147.11280417	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F06
Scannumber:	9861
Protein:	BSU05640; ydgG
Peptide Score:	95.52
Method:	ITMS; CID; 3

precursor information

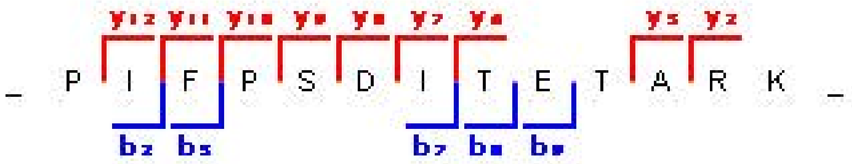
Mass:	1308.71563
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	95.52309
Mass Error [ppm]:	0.47775
PEP:	0.00082245
Precursor Type:	MULTI

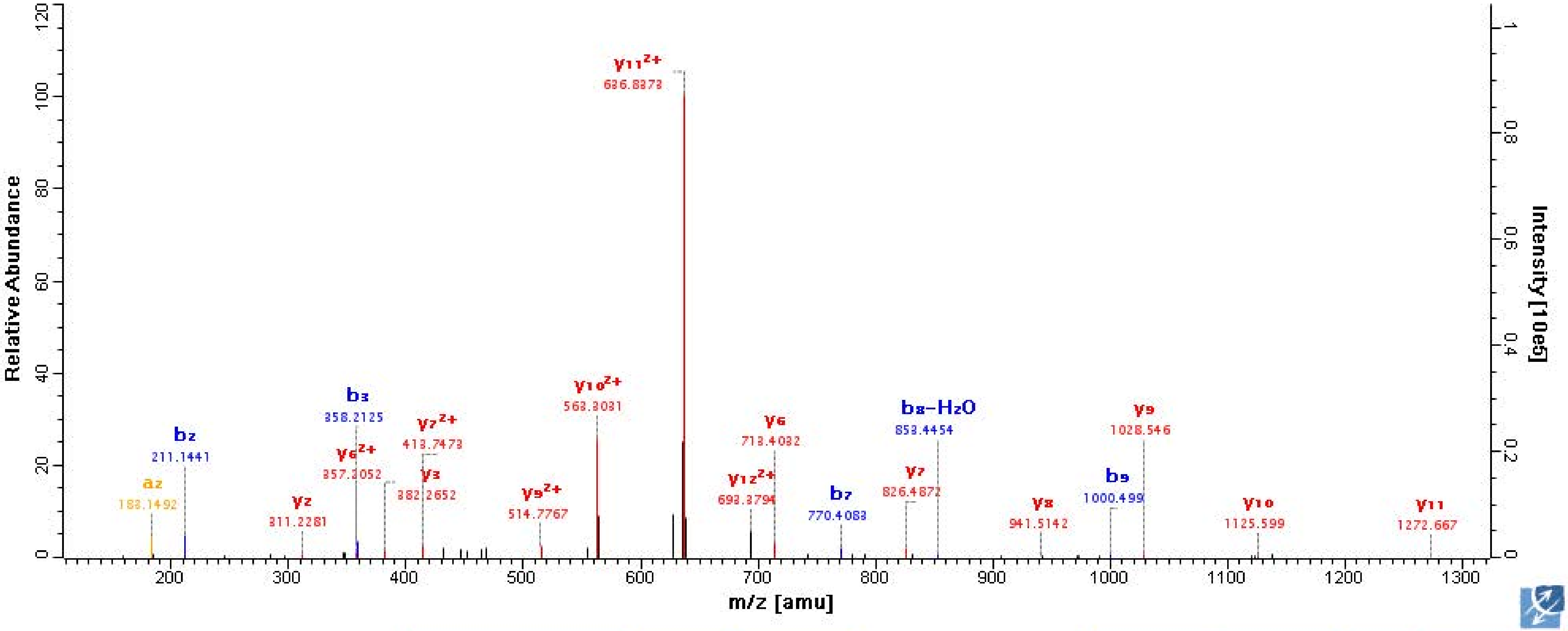
general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	40 %
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				
-0.0614	223.155		251.15	-0.0574	251.15	2	I	9	1176.69		588.848	+0.3617
	310.187		338.182		338.182	3	S	8	1063.6		532.306	+0.2601
	466.288		494.283		494.283	4	R	7	976.572		976.572	
	595.331		623.326		623.326	5	E	6	820.471	+0.35643	820.471	
	723.39	+0.10401	376.196		751.385	6	Q	5	691.429	+0.31553	691.429	
	794.427	+0.45099	411.714		822.422	7	A	4	563.37		563.37	
	909.454	-0.274	469.228	+0.22265	937.449	8	D	3	492.333		492.333	
	1022.54	-0.1292	525.77	+0.14493	1050.53	9	I	2	377.306	-0.0093	377.306	
	1135.62	+0.487	582.312		1163.62	10	I	1	264.222	+0.13957	264.222	
						11	K	0	151.138	-0.0894	151.138	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F07
Scannumber:	15013
Protein:	BSU11560; yjbI
Peptide Score:	111.86
Method:	ITMS; CID; 3





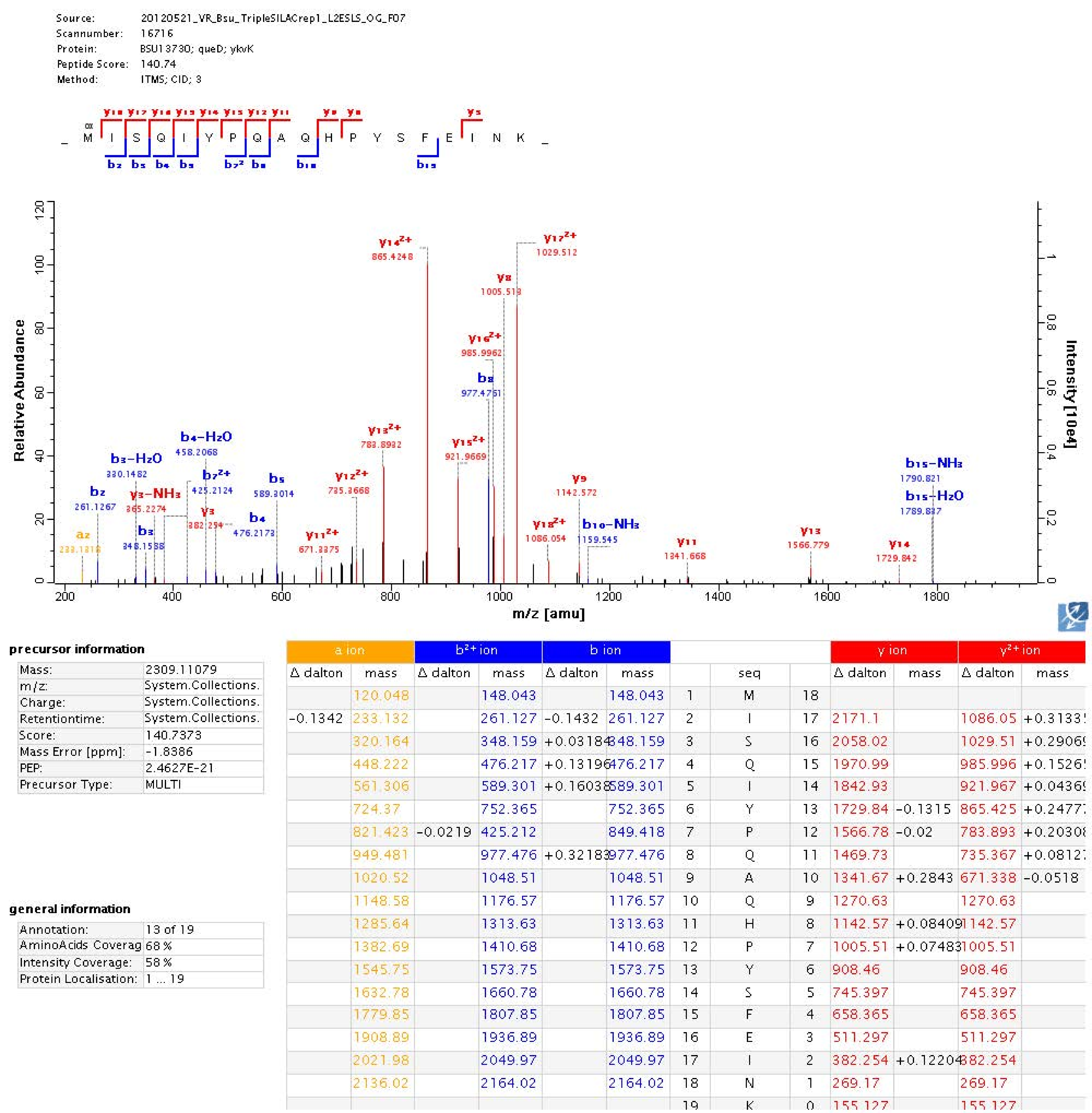
precursor information

Mass:	1473.78254
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.8553
Mass Error [ppm]:	-0.13412
PEP:	0.00075642
Precursor Type:	MULTI

general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	65 %
Protein Localisation:	36 ... 48

a ion		b ion					y ion		y^{2+} ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	70.06513		98.06004	1	P	12				
-0.051381	183.1492	-0.0094	211.1441	2	I	11	1385.751		693.3794	+0.11685
	330.2176	+0.032538	358.2125	3	F	10	1272.667	+0.363249	636.8373	+0.291939
	427.2704		455.2653	4	P	9	1125.599	+0.276023	563.3031	+0.163609
	514.3024		542.2973	5	S	8	1028.546	+0.159841	514.7767	+0.171802
	629.3293		657.3243	6	D	7	941.5142	+0.282019	941.5142	
	742.4134	+0.096199	770.4083	7	I	6	826.4872	+0.221804	413.7473	-0.120367
	843.4611		871.456	8	T	5	713.4032	+0.149312	357.2052	+0.077549
	972.5037	+0.349067	1000.499	9	E	4	612.3555		612.3555	
	1073.551		1101.546	10	T	3	483.3129		483.3129	
	1144.588		1172.583	11	A	2	382.2652	+0.197297	382.2652	
	1300.69		1328.684	12	R	1	311.2281	+0.158605	311.2281	
				13	K	0	155.127		155.127	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F07
Scannumber:	16716
Protein:	BSU13730; queD; ykvK
Peptide Score:	140.74
Method:	ITMS; CID; 3

precursor information

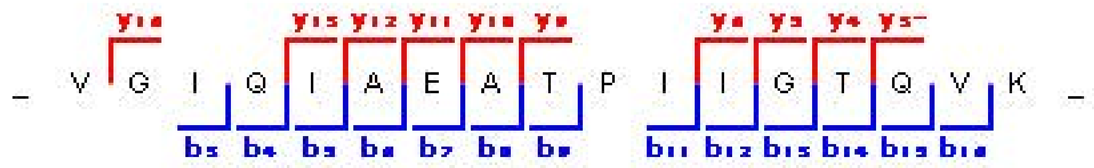
Mass:	2309.11079
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	140.7373
Mass Error [ppm]:	-1.8386
PEP:	2.4627E-21
Precursor Type:	MULTI

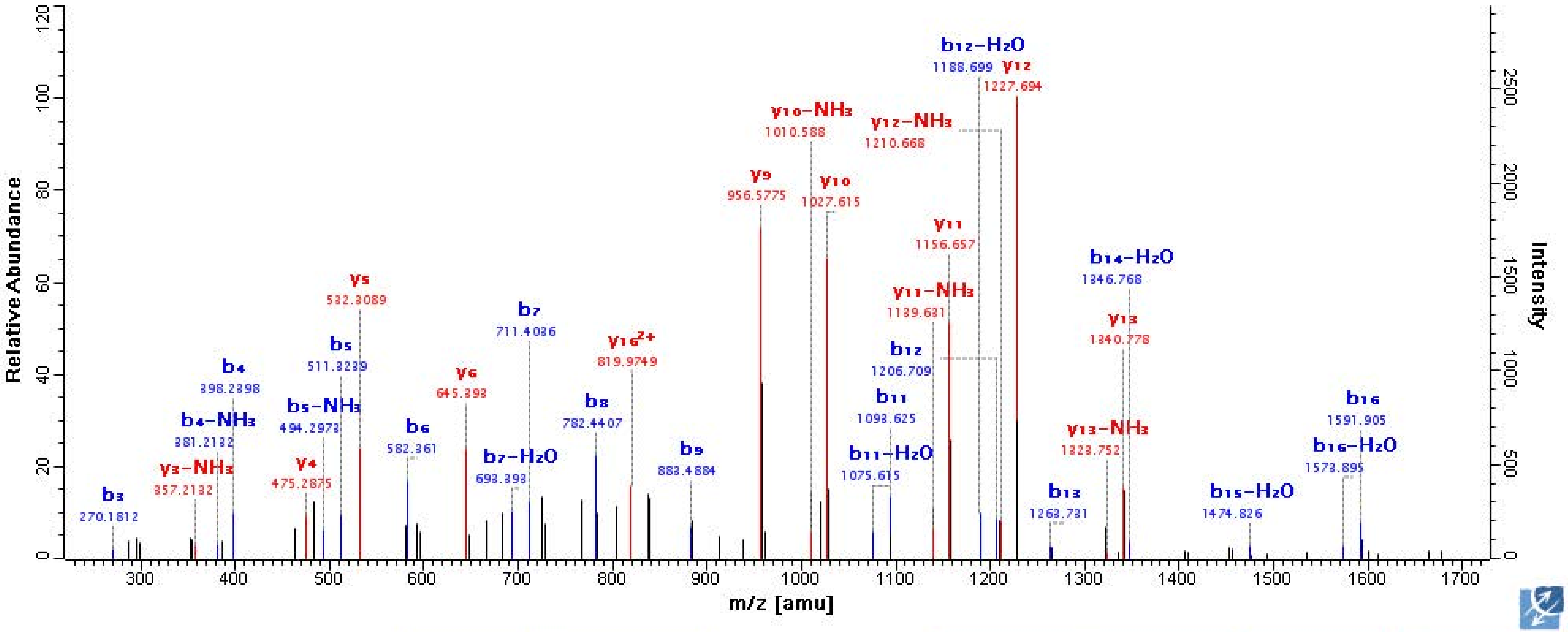
general information

Annotation:	13 of 19
AminoAcids Coverag	68 %
Intensity Coverage:	58 %
Protein Localisation:	1 ... 19

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
	120.048		148.043		148.043	1	M	18				
-0.1342	233.132		261.127	-0.1432	261.127	2	I	17	2171.1		1086.05	+0.3133
	320.164		348.159	+0.03184	348.159	3	S	16	2058.02		1029.51	+0.2906
	448.222		476.217	+0.13196	476.217	4	Q	15	1970.99		985.996	+0.1526
	561.306		589.301	+0.16038	589.301	5	I	14	1842.93		921.967	+0.0436
	724.37		752.365		752.365	6	Y	13	1729.84	-0.1315	865.425	+0.2477
	821.423	-0.0219	425.212		849.418	7	P	12	1566.78	-0.02	783.893	+0.2030
	949.481		977.476	+0.32183	977.476	8	Q	11	1469.73		735.367	+0.0812
	1020.52		1048.51		1048.51	9	A	10	1341.67	+0.2843	671.338	-0.0518
	1148.58		1176.57		1176.57	10	Q	9	1270.63		1270.63	
	1285.64		1313.63		1313.63	11	H	8	1142.57	+0.08409	1142.57	
	1382.69		1410.68		1410.68	12	P	7	1005.51	+0.07483	1005.51	
	1545.75		1573.75		1573.75	13	Y	6	908.46		908.46	
	1632.78		1660.78		1660.78	14	S	5	745.397		745.397	
	1779.85		1807.85		1807.85	15	F	4	658.365		658.365	
	1908.89		1936.89		1936.89	16	E	3	511.297		511.297	
	2021.98		2049.97		2049.97	17	I	2	382.254	+0.12204	382.254	
	2136.02		2164.02		2164.02	18	N	1	269.17		269.17	
						19	K	0	155.127		155.127	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F07
Scannumber: 19930
Protein: bfcB; BSU22550; qcrB
Peptide Score: 161.82
Method: ITMS; CID; 3





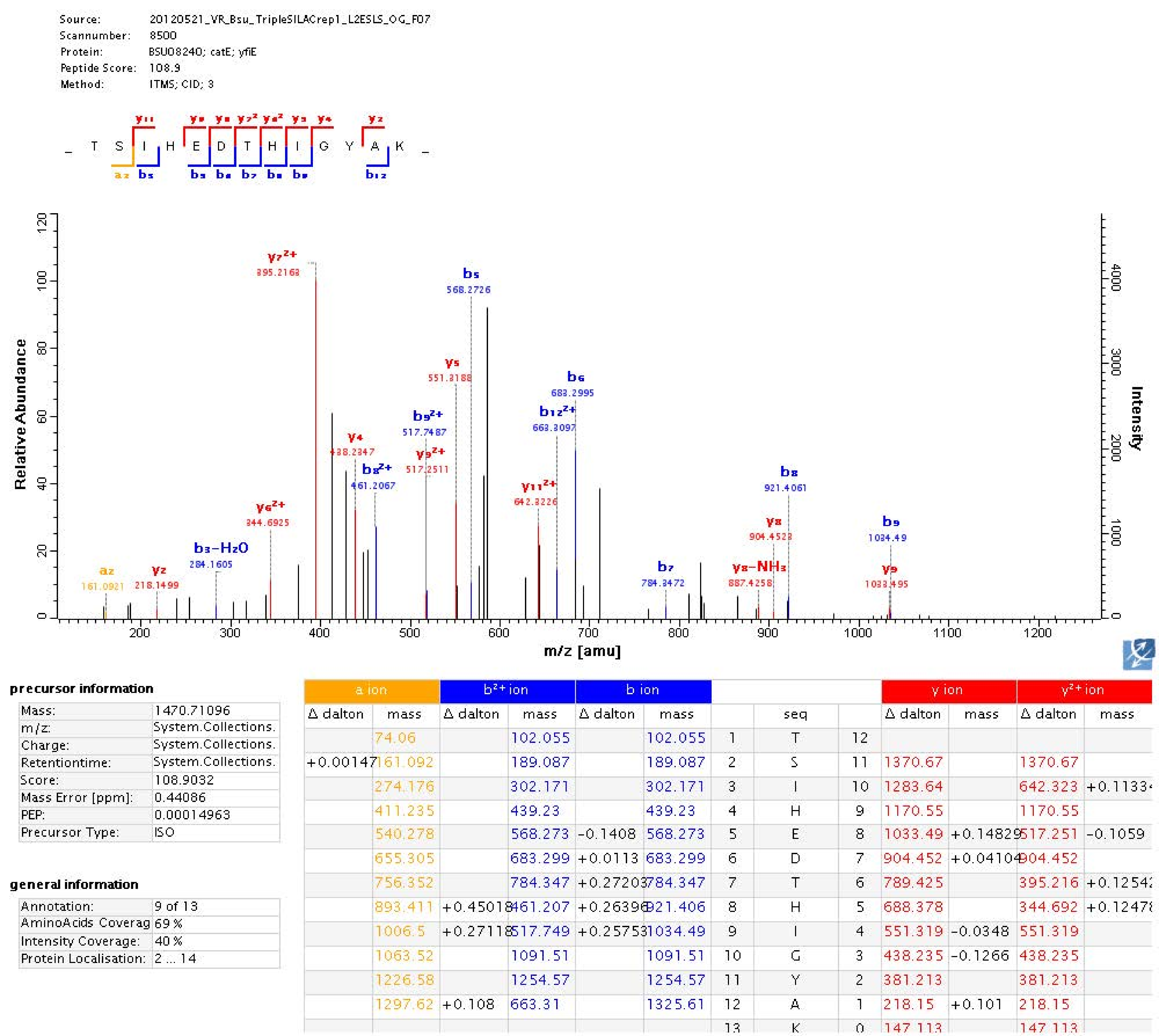
precursor information

Mass:	1737.00347
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	161.8241
Mass Error [ppm]:	-0.093087
PEP:	7.5833E-26
Precursor Type:	MULTI

general information

Annotation:	14 of 17
AminoAcids Coverag	82 %
Intensity Coverage:	58 %
Protein Localisation:	158 ... 174

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.07569038	1	V	16				
	157.09715411	2	G	15	1638.942498		819.97488721	-0.2118257
+0.0287429	270.18121809	3	I	14	1581.9210342		1581.9210342	
-0.0042609	398.2397956	4	Q	13	1468.8369702		1468.8369702	
+0.1310965	511.32385958	5	I	12	1340.7783927	+0.2220955	1340.7783927	
+0.0800056	582.36097337	6	A	11	1227.6943288	+0.0723949	1227.6943288	
+0.293394	711.40356646	7	E	10	1156.657215	+0.0626337	1156.657215	
+0.1340878	782.44068025	8	A	9	1027.6146219	+0.0651877	1027.6146219	
+0.0138385	883.48835872	9	T	8	956.57750808	+0.0565862	956.57750808	
	980.54112258	10	P	7	855.52982961		855.52982961	
+0.1398281	1093.6251866	11	I	6	758.47706576		758.47706576	
+0.2072534	1206.7092505	12	I	5	645.39300178	+0.0057409	645.39300178	
+0.226317	1263.7307143	13	G	4	532.3089378	+0.0868752	532.3089378	
	1364.7783927	14	T	3	475.28747407	+0.1531082	475.28747407	
	1492.8369702	15	Q	2	374.2397956		374.2397956	
+0.1041373	1591.9053842	16	V	1	246.18121809		246.18121809	
		17	K	0	147.11280417		147.11280417	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F07
Scannumber:	8500
Protein:	BSU08240; catE; yfiE
Peptide Score:	108.9
Method:	ITMS; CID; 3

precursor information

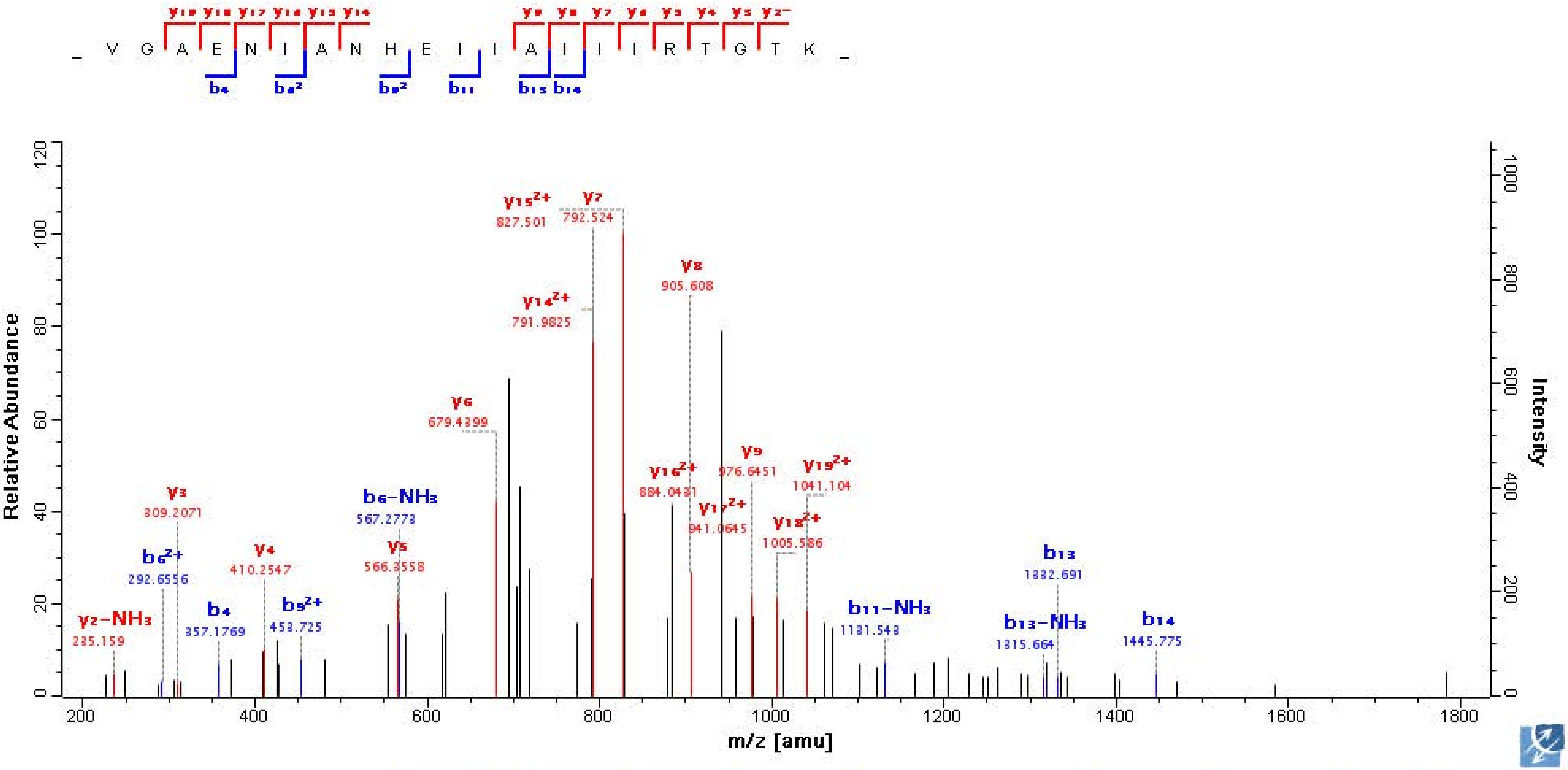
Mass:	1470.71096
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	108.9032
Mass Error [ppm]:	0.44086
PEP:	0.00014963
Precursor Type:	ISO

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	40 %
Protein Localisation:	2 ... 14

a ion		b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	74.06		102.055		102.055	1	T	12				
+0.00147	161.092		189.087		189.087	2	S	11	1370.67		1370.67	
	274.176		302.171		302.171	3	I	10	1283.64		642.323	+0.1133
	411.235		439.23		439.23	4	H	9	1170.55		1170.55	
	540.278		568.273	-0.1408	568.273	5	E	8	1033.49	+0.14829	517.251	-0.1059
	655.305		683.299	+0.0113	683.299	6	D	7	904.452	+0.04104	904.452	
	756.352		784.347	+0.27203	784.347	7	T	6	789.425		395.216	+0.1254
	893.411	+0.45018	461.207	+0.26396	921.406	8	H	5	688.378		344.692	+0.1247
	1006.5	+0.27118	517.749	+0.25753	1034.49	9	I	4	551.319	-0.0348	551.319	
	1063.52		1091.51		1091.51	10	G	3	438.235	-0.1266	438.235	
	1226.58		1254.57		1254.57	11	Y	2	381.213		381.213	
	1297.62	+0.108	663.31		1325.61	12	A	1	218.15	+0.101	218.15	
						13	K	0	147.113		147.113	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F08
Scannumber: 23798
Protein: BSU28040; ysxA
Peptide Score: 69.93
Method: ITMS; CID; 3



precursor information

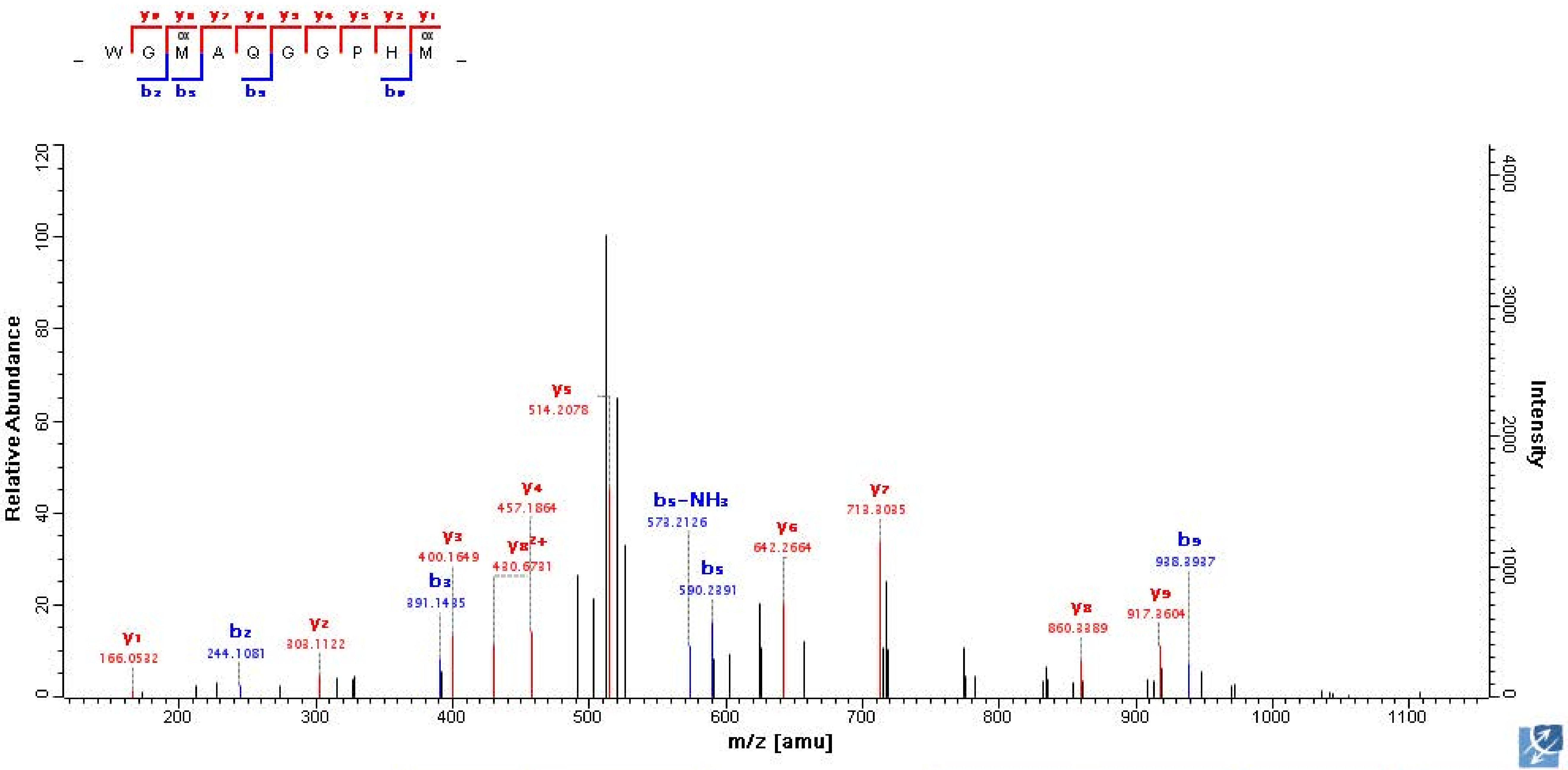
Mass:	2236.28046
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	69.93452
Mass Error [ppm]:	-1.6388
PEP:	0.003439
Precursor Type:	ISO

general information

Annotation:	16 of 21
AminoAcids Coverag	76 %
Intensity Coverage:	40 %
Protein Localisation:	26 ... 46

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	100.0757		100.0757	1	V	20				
	157.0972		157.0972	2	G	19	2138.223		2138.223	
	228.1343		228.1343	3	A	18	2081.202		1041.104	+0.475801
	357.1769	-0.065899	357.1769	4	E	17	2010.164		1005.586	-0.080898
	471.2198		471.2198	5	N	16	1881.122		941.0645	-0.195466
-0.444017	292.6556		584.3039	6	I	15	1767.079		884.0431	+0.036203
	655.341		655.341	7	A	14	1653.995		827.501	+0.341541
	769.3839		769.3839	8	N	13	1582.958		791.9825	+0.016103
+0.332759	453.725		906.4428	9	H	12	1468.915		1468.915	
	1035.485		1035.485	10	E	11	1331.856		1331.856	
	1148.569		1148.569	11	I	10	1202.813		1202.813	
	1261.654		1261.654	12	I	9	1089.729		1089.729	
	1332.691	+0.074252	1332.691	13	A	8	976.6451	+0.211358	976.6451	
	1445.775	+0.328445	1445.775	14	I	7	905.608	+0.111936	905.608	
	1558.859		1558.859	15	I	6	792.524	+0.233537	792.524	
	1671.943		1671.943	16	I	5	679.4399	+0.058201	679.4399	
	1828.044		1828.044	17	R	4	566.3558	+0.111076	566.3558	
	1929.092		1929.092	18	T	3	410.2547	+0.270598	410.2547	
	1986.113		1986.113	19	G	2	309.2071	+0.141579	309.2071	
	2087.161		2087.161	20	T	1	252.1856		252.1856	
				21	K	0	151.1379		151.1379	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F08
Scannumber: 6860
Protein: BSU05270; ydzF
Peptide Score: 138.9
Method: ITMS; CID; 3



precursor information

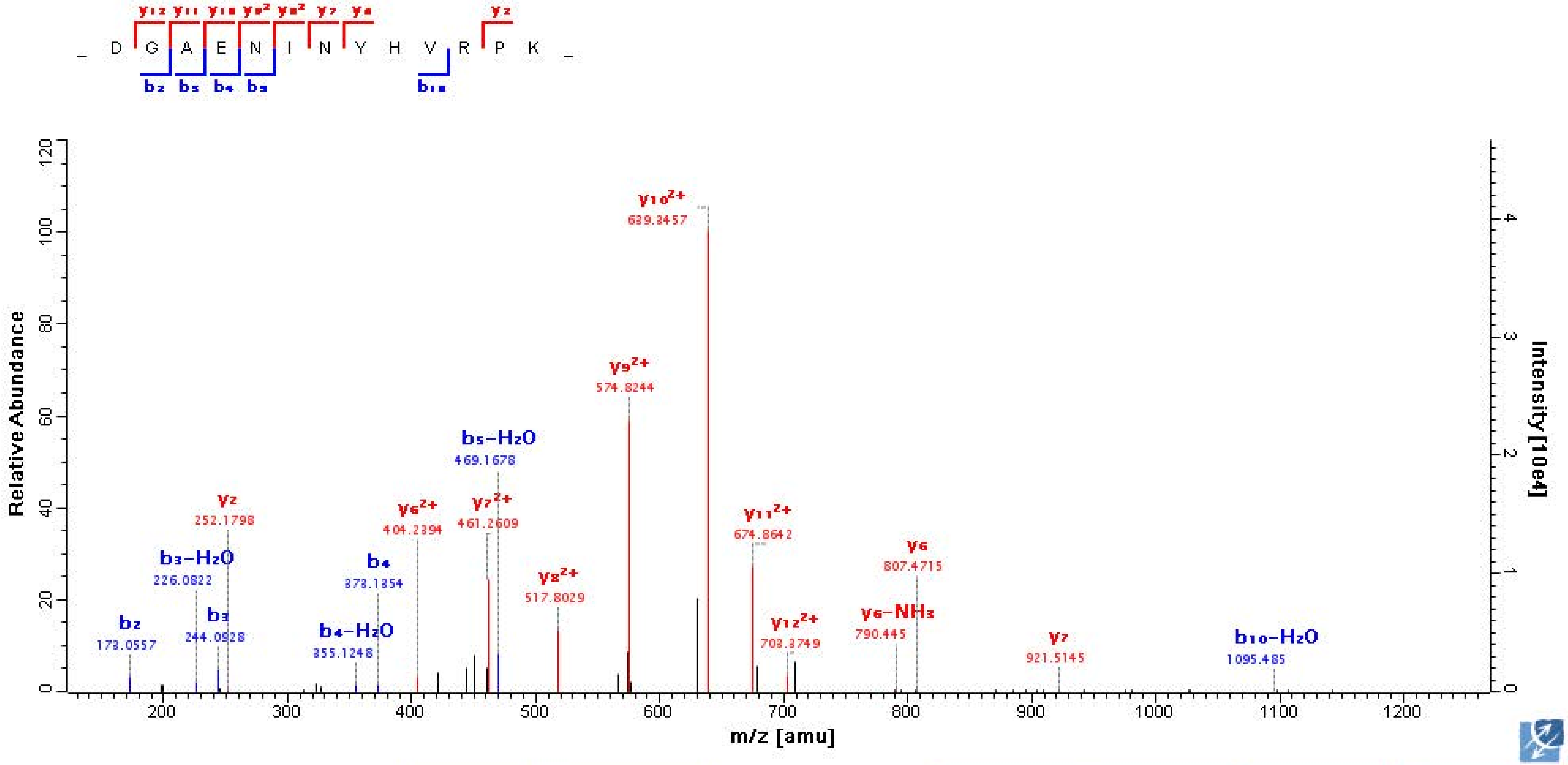
Mass:	1102.43237
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.895
Mass Error [ppm]:	-0.056646
PEP:	0.00040015
Precursor Type:	ISO

general information

Annotation:	9 of 10
AminoAcids Coverag	90 %
Intensity Coverage:	32 %
Protein Localisation:	100 ... 109

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	187.08658942	1	W	9				
+0.2311955	244.10805314	2	G	8	917.36039779	+0.0812526	917.36039779	
-0.113362	391.14345237	3	M	7	860.33893407	+0.2230166	430.67310527	-0.0028172
	462.18056616	4	A	6	713.30353484	+0.0535208	713.30353484	
+0.0046918	590.23914367	5	Q	5	642.26642105	+0.0319798	642.26642105	
	647.26060739	6	G	4	514.20784354	+0.022198	514.20784354	
	704.28207112	7	G	3	457.18637982	+0.2150484	457.18637982	
	801.33483497	8	P	2	400.1649161	+0.2055673	400.1649161	
+0.1475129	938.39374683	9	H	1	303.11215224	+0.0712279	303.11215224	
		10	M	0	166.05324038	+0.0659613	166.05324038	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F08
Scannumber: 7749
Protein: bltR; bmr2R; bmtR; BSU26580
Peptide Score: 100.88
Method: ITMS; CID; 3



precursor information

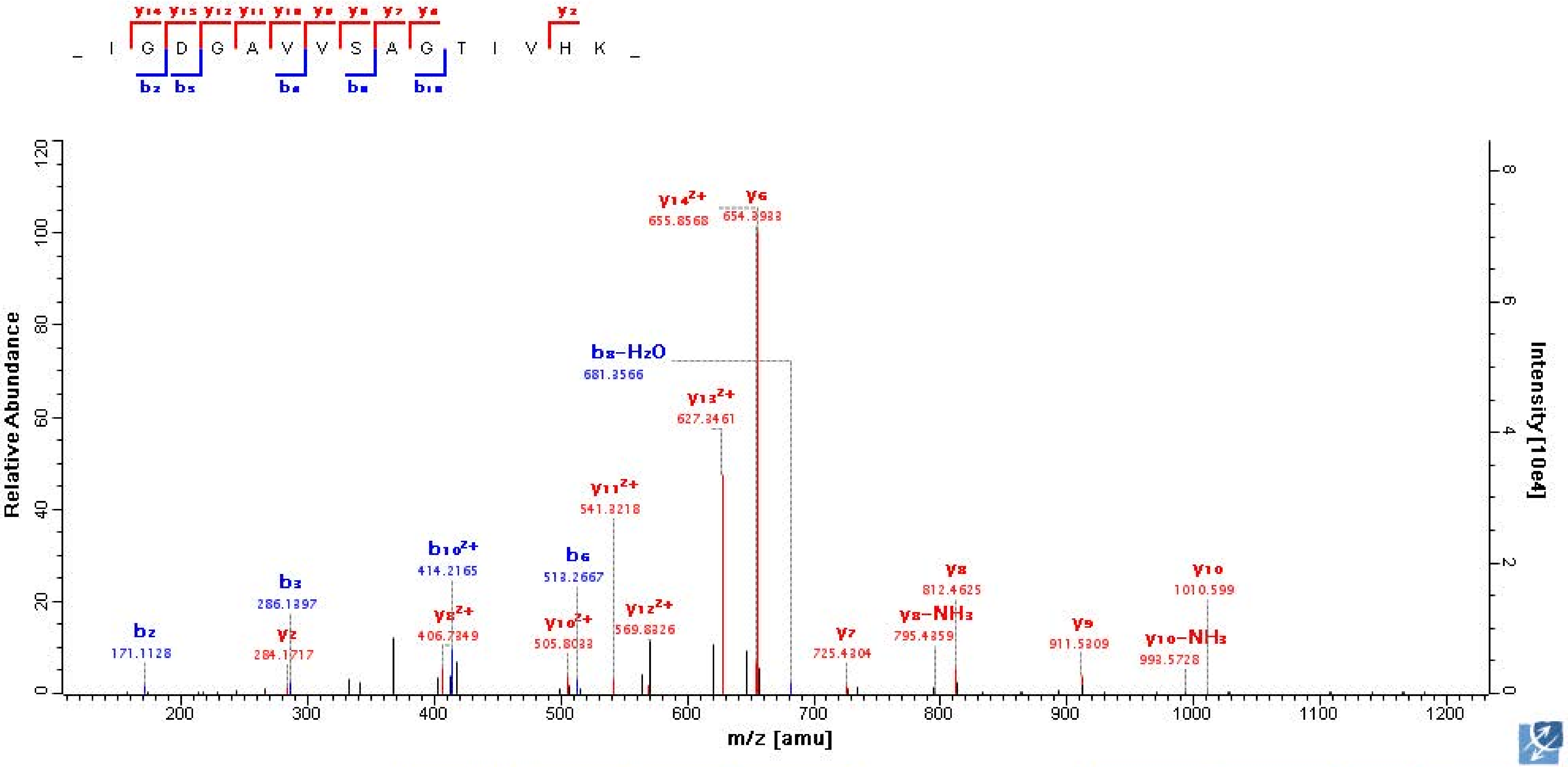
Mass:	1511.74687
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	100.8783
Mass Error [ppm]:	-0.80389
PEP:	0.00097028
Precursor Type:	MULTI

general information

Annotation:	9 of 13
AminoAcids Coverag	69 %
Intensity Coverage:	73 %
Protein Localisation:	198 ... 210

b ion					y ion		y²⁺ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	116.0342195	1	D	12				
-0.082264	173.05568322	2	G	11	1405.7426217		703.37494906	+0.1168722
-0.0512931	244.09279701	3	A	10	1348.7211579		674.8642172	+0.3215128
+0.0675518	373.13539011	4	E	9	1277.6840442		639.34566031	+0.2236146
	487.17831755	5	N	8	1148.6414511		574.82436376	+0.1949844
	600.26238153	6	I	7	1034.5985236		517.80290004	+0.2130912
	714.30530898	7	N	6	921.51445963	+0.1565609	461.26086805	+0.2232628
	877.36863752	8	Y	5	807.47153218	+0.2975108	404.23940432	-0.0654541
	1014.4275494	9	H	4	644.40820364		644.40820364	
	1113.4959633	10	V	3	507.34929178		507.34929178	
	1269.5970743	11	R	2	408.28087786		408.28087786	
	1366.6498382	12	P	1	252.17976684	-0.0337707	252.17976684	
		13	K	0	155.12700298		155.12700298	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F09
Scannumber: 11188
Protein: BSU34960; yvoF
Peptide Score: 105.65
Method: ITMS; CID; 3



precursor information

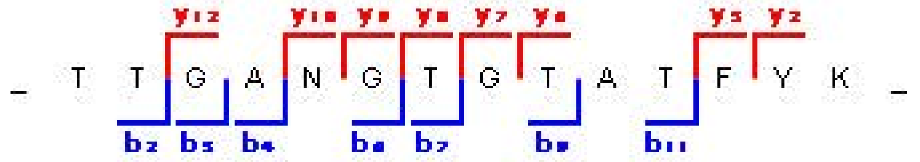
Mass:	1422.78371
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	105.649
Mass Error [ppm]:	0.44105
PEP:	7.7158E-05
Precursor Type:	MULTI

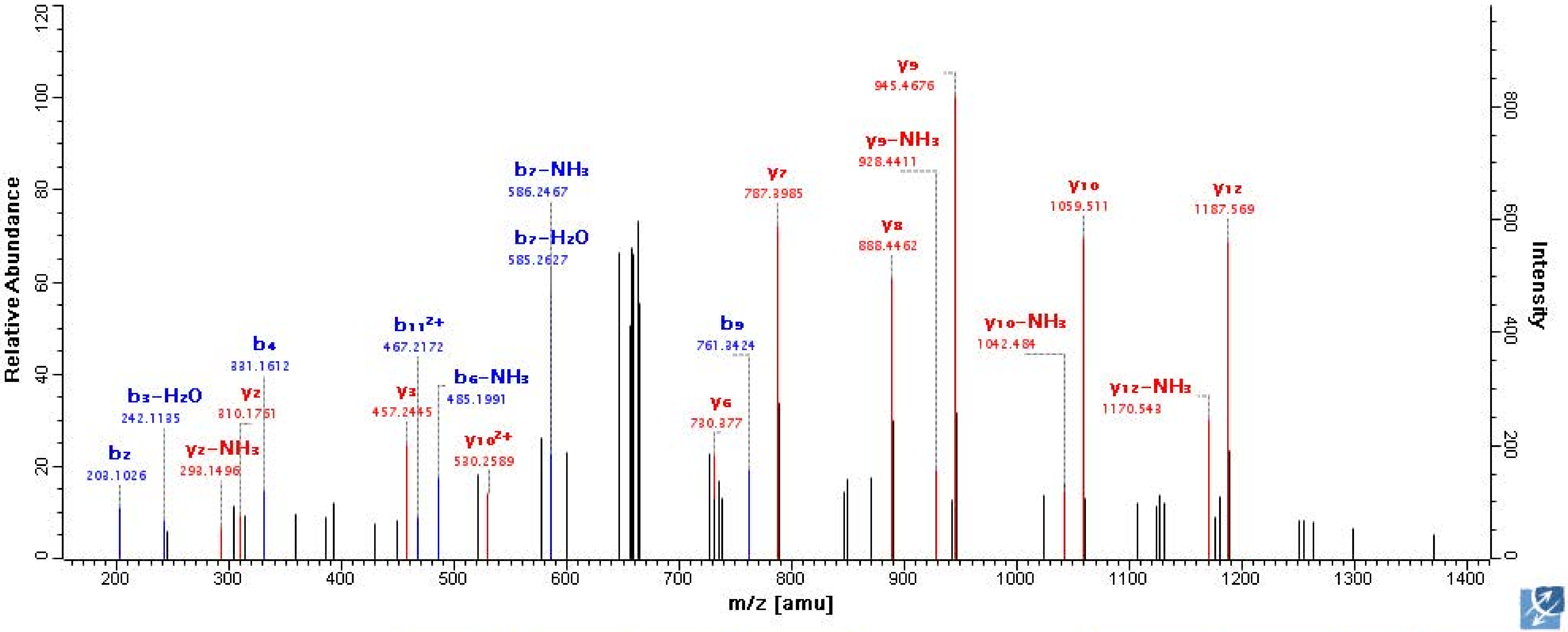
general information

Annotation:	10 of 15
AminoAcids Coverag	67 %
Intensity Coverage:	69 %
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	+0.127995	171.1128	2	G	13	1310.706		655.8568	+0.265043
	286.1397	-0.051612	286.1397	3	D	12	1253.685		627.3461	+0.277972
	343.1612		343.1612	4	G	11	1138.658		569.8326	-0.175537
	414.1983		414.1983	5	A	10	1081.636		541.3218	+0.350698
	513.2667	+0.147202	513.2667	6	V	9	1010.599	+0.090879	505.8033	+0.076164
	612.3352		612.3352	7	V	8	911.5309	+0.258781	911.5309	
	699.3672		699.3672	8	S	7	812.4625	+0.106247	406.7349	+0.165574
	770.4043		770.4043	9	A	6	725.4304	+0.084443	725.4304	
+0.013524	414.2165		827.4258	10	G	5	654.3933	+0.048986	654.3933	
	928.4734		928.4734	11	T	4	597.3719		597.3719	
	1041.558		1041.558	12	I	3	496.3242		496.3242	
	1140.626		1140.626	13	V	2	383.2401		383.2401	
	1277.685		1277.685	14	H	1	284.1717	+0.078559	284.1717	
				15	K	0	147.1128		147.1128	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F10
Scannumber:	10195
Protein:	BSU26060; yqbM; BSU12660; xkdM
Peptide Score:	92.19
Method:	ITMS; CID; 3





precursor information

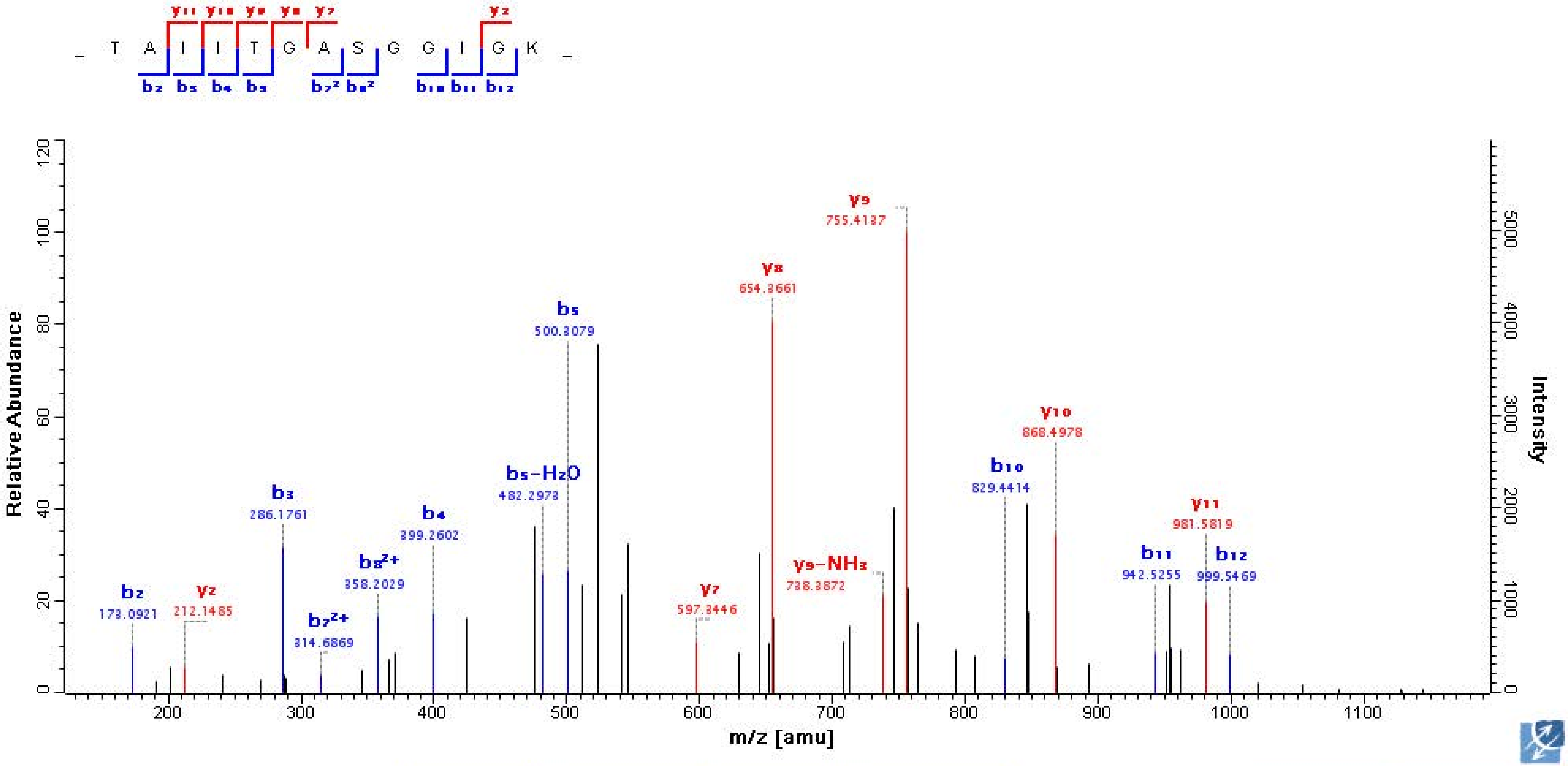
Mass:	1388.65686
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	92.18982
Mass Error [ppm]:	-0.25412
PEP:	0.00029799
Precursor Type:	MULTI

general information

Annotation:	11 of 14
AminoAcids Coverag	79 %
Intensity Coverage:	42 %
Protein Localisation:	52 ... 65

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	13				
	203.1026	+0.024915	203.1026	2	T	12	1288.617		1288.617	
	260.1241		260.1241	3	G	11	1187.569	+0.016443	1187.569	
	331.1612	+0.086775	331.1612	4	A	10	1130.548		1130.548	
	445.2041		445.2041	5	N	9	1059.511	-0.207328	530.2589	-0.148379
	502.2256		502.2256	6	G	8	945.4676	+0.169462	945.4676	
	603.2733		603.2733	7	T	7	888.4462	+0.198555	888.4462	
	660.2947		660.2947	8	G	6	787.3985	+0.22774	787.3985	
	761.3424	+0.264633	761.3424	9	T	5	730.377	+0.198239	730.377	
	832.3795		832.3795	10	A	4	629.3293		629.3293	
+0.124002	467.2172		933.4272	11	T	3	558.2922		558.2922	
	1080.496		1080.496	12	F	2	457.2445	+0.075644	457.2445	
	1243.559		1243.559	13	Y	1	310.1761	+0.049331	310.1761	
				14	K	0	147.1128		147.1128	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F10
Scannumber: 12623
Protein: BSU16870; ymfI
Peptide Score: 84.61
Method: ITMS; CID; 3



precursor information

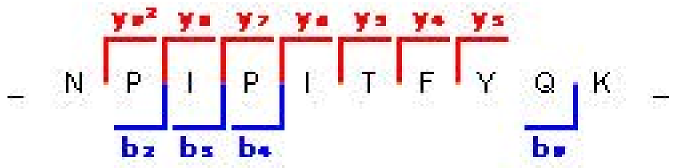
Mass:	1144.64437
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	84.60506
Mass Error [ppm]:	-0.71291
PEP:	0.0030795
Precursor Type:	MULTI

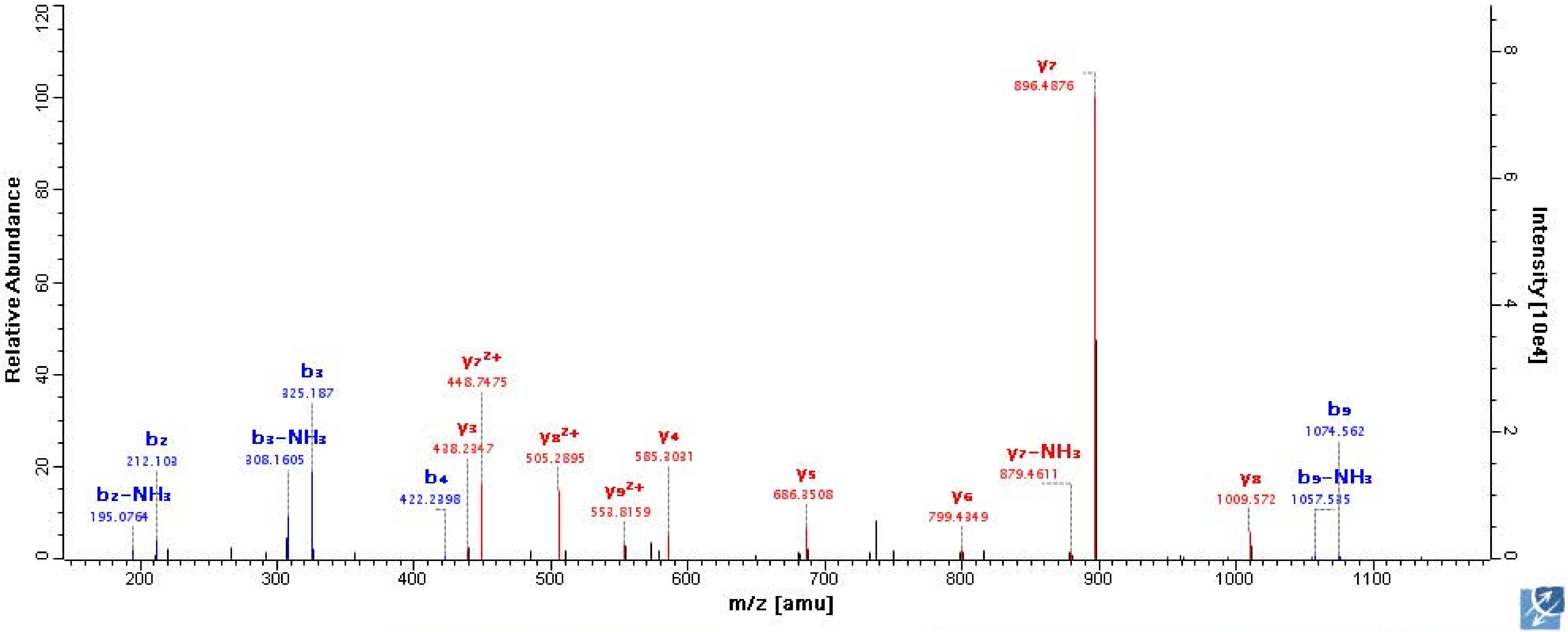
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	43 %
Protein Localisation:	4 ... 16

b^{2+} ion		b ion					y ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass
	102.05495494		102.05495494	1	T	12		
	173.09206873	-0.1327639	173.09206873	2	A	11	1052.6189843	
	286.17613271	-0.1179662	286.17613271	3	I	10	981.58187049	+0.1121603
	399.26019669	-0.0093422	399.26019669	4	I	9	868.49780651	+0.0198326
	500.30787516	+0.0124373	500.30787516	5	T	8	755.41374253	-0.0046849
	557.32933889		557.32933889	6	G	7	654.36606406	+0.0485478
+0.3866218	314.68686457		628.36645267	7	A	6	597.34460033	+0.2238201
-0.053953	358.20287878		715.39848108	8	S	5	526.30748654	
	772.41994481		772.41994481	9	G	4	439.27545813	
	829.44140853	+0.0259377	829.44140853	10	G	3	382.25399441	
	942.52547251	+0.0182897	942.52547251	11	I	2	325.23253069	
	999.54693624	+0.1033934	999.54693624	12	G	1	212.14846671	+0.0247511
				13	K	0	155.12700298	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F10
Scannumber: 18438
Protein: BSU38620; yxlJ
Peptide Score: 138.98
Method: ITMS; CID; 3





precursor information

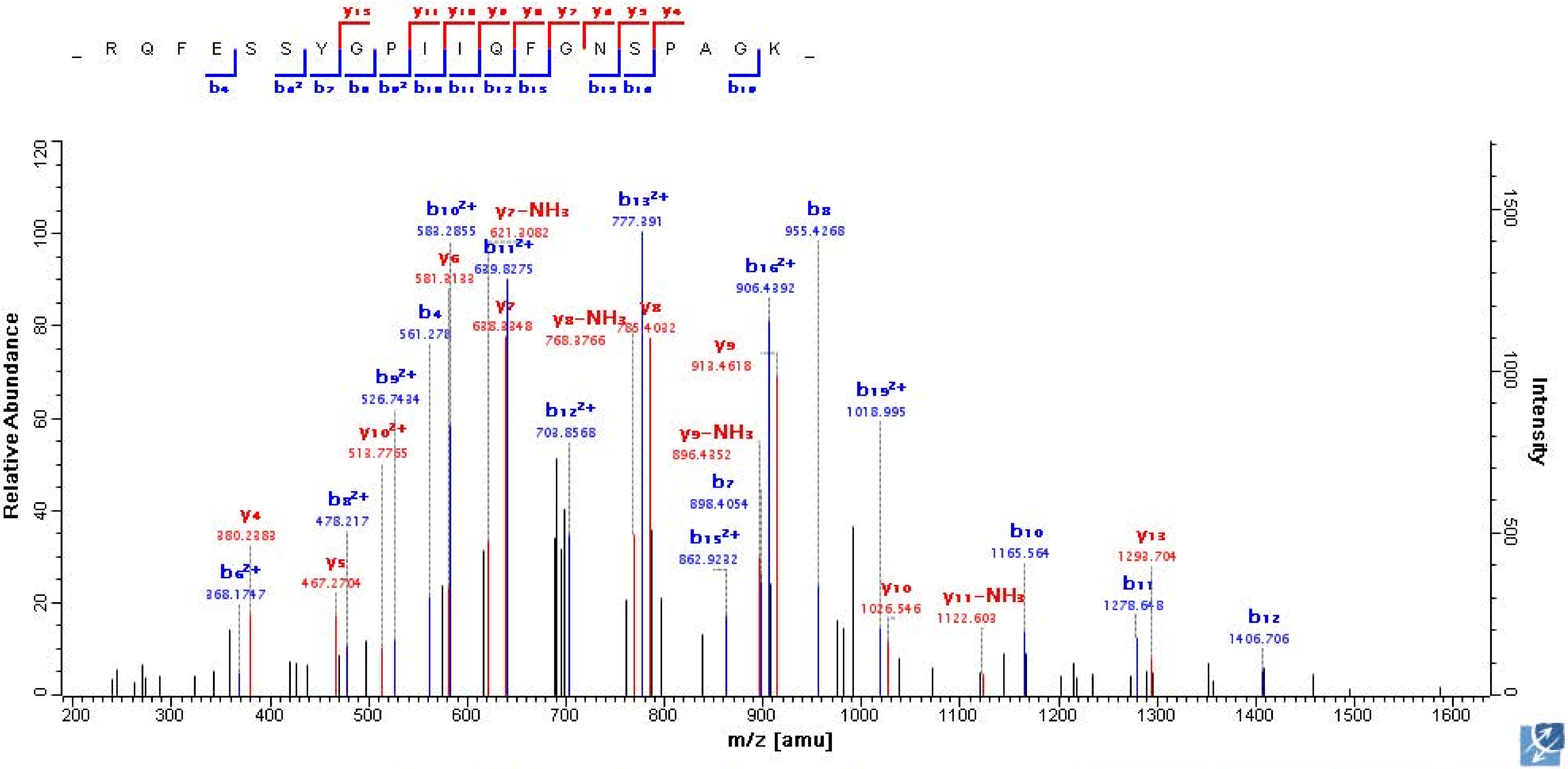
Mass:	1219.66043
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	138.9753
Mass Error [ppm]:	0.26206
PEP:	1.9343E-06
Precursor Type:	MULTI

general information

Annotation:	8 of 10
AminoAcids Coverag	80 %
Intensity Coverage:	65 %
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				
+0.0101609	212.10296777	2	P	8	1106.6244583		553.81586737	+0.0446063
+0.081706	325.18703175	3	I	7	1009.5716944	+0.0918798	505.28948545	+0.1543012
+0.2501336	422.2397956	4	P	6	896.48763044	+0.1014198	448.74745345	+0.2123244
	535.32385958	5	I	5	799.43486659	+0.1830533	799.43486659	
	636.37153805	6	T	4	686.35080261	+0.0112579	686.35080261	
	783.43995197	7	F	3	585.30312414	+0.0345223	585.30312414	
	946.50328051	8	Y	2	438.23471022	+0.1959538	438.23471022	
+0.1250316	1074.561858	9	Q	1	275.17138168		275.17138168	
		10	K	0	147.11280417		147.11280417	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F10
Scannumber: 19004
Protein: BSU06900; cotJB
Peptide Score: 132.51
Method: ITMS; CID; 3



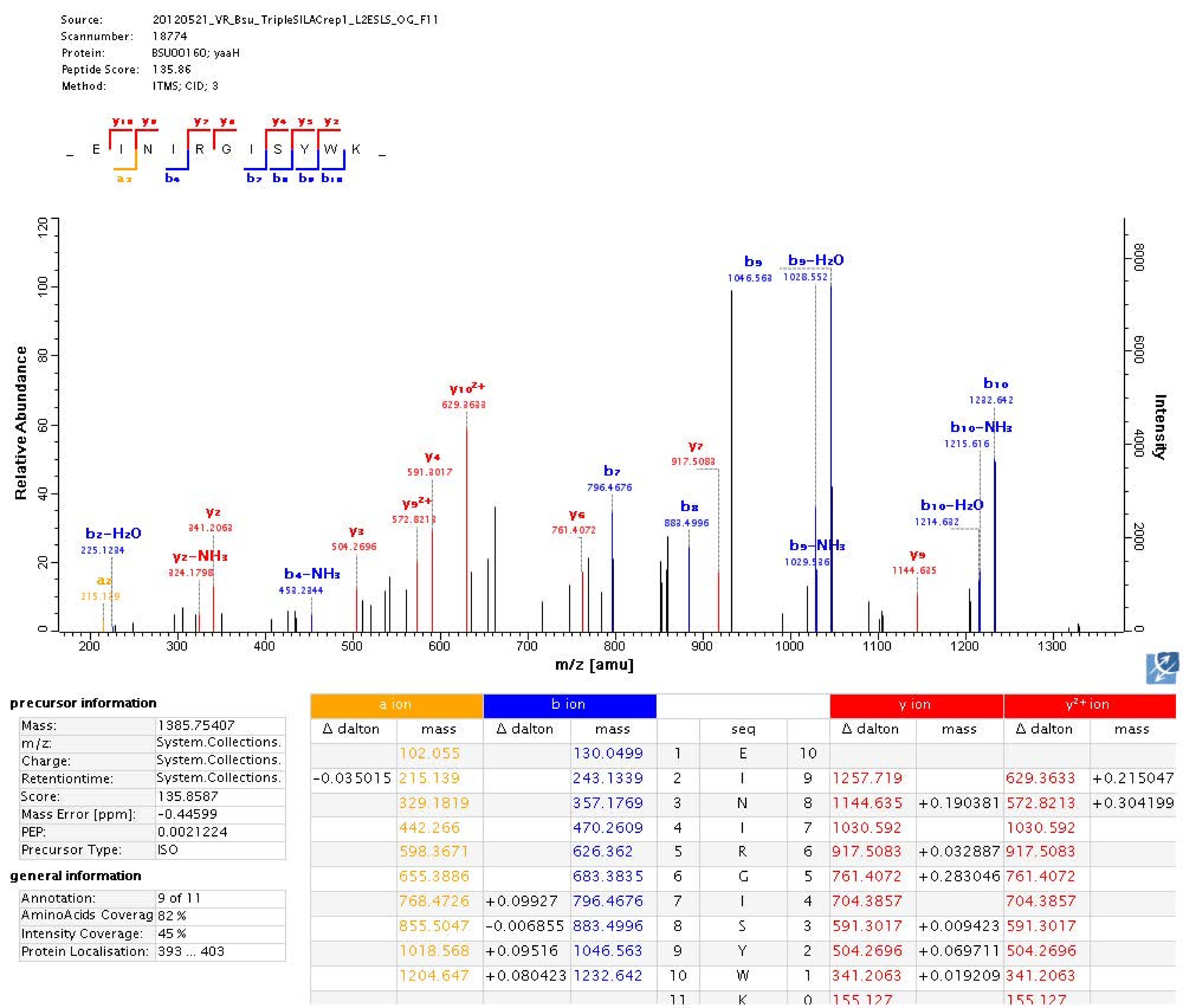
precursor information

Mass:	2190.09413
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	132.5122
Mass Error [ppm]:	-0.35814
PEP:	6.0981E-19
Precursor Type:	ISO

general information

Annotation:	14 of 20
AminoAcids Coverag	70 %
Intensity Coverage:	59 %
Protein Localisation:	55 ... 74

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	19				
	285.167		285.167	2	Q	18	2035.001		2035.001	
	432.2354		432.2354	3	F	17	1906.943		1906.943	
	561.278	+0.073224	561.278	4	E	16	1759.874		1759.874	
	648.31		648.31	5	S	15	1630.831		1630.831	
-0.082306	368.1747		735.342	6	S	14	1543.799		1543.799	
	898.4054	+0.327736	898.4054	7	Y	13	1456.767		1456.767	
+0.397636	478.217	+0.192625	955.4268	8	G	12	1293.704	+0.18566	1293.704	
+0.346474	526.7434		1052.48	9	P	11	1236.683		1236.683	
+0.109374	583.2855	+0.055248	1165.564	10	I	10	1139.63		1139.63	
+0.13503	639.8275	+0.301262	1278.648	11	I	9	1026.546	+0.366412	513.7765	+0.060793
-0.093051	703.8568	+0.283089	1406.706	12	Q	8	913.4618	-0.003198	913.4618	
+0.369447	777.391		1553.775	13	F	7	785.4032	+0.171895	785.4032	
	1610.796		1610.796	14	G	6	638.3348	+0.063002	638.3348	
+0.471284	862.9232		1724.839	15	N	5	581.3133	-0.010322	581.3133	
+0.062143	906.4392		1811.871	16	S	4	467.2704	+0.13368	467.2704	
	1908.924		1908.924	17	P	3	380.2383	+0.2442	380.2383	
	1979.961		1979.961	18	A	2	283.1856		283.1856	
+0.091677	1018.995		2036.982	19	G	1	212.1485		212.1485	
				20	K	0	155.127		155.127	



Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F11
Scannumber:	18774
Protein:	BSU00160; yaaH
Peptide Score:	135.86
Method:	ITMS; CID; 3

precursor information

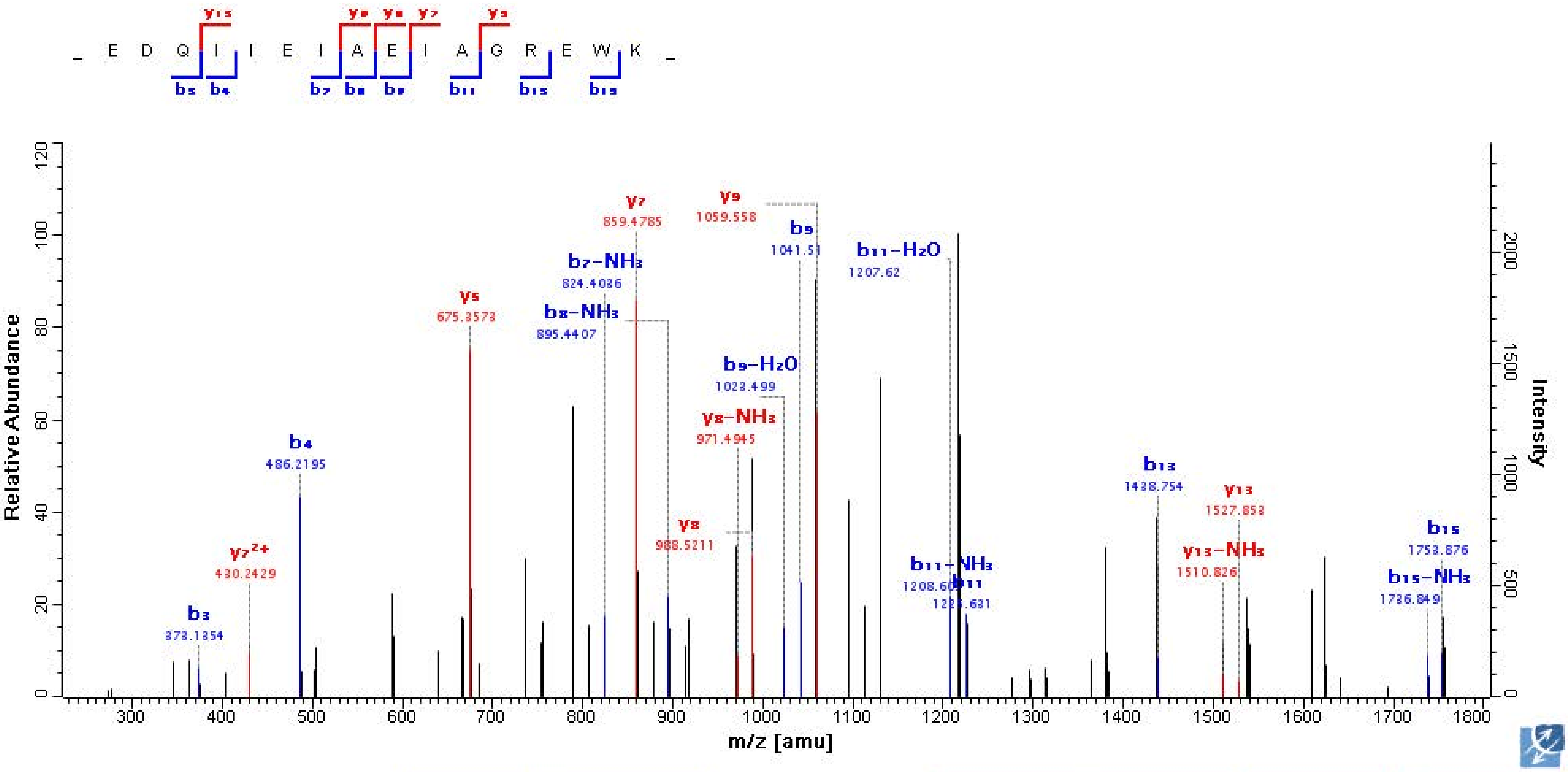
Mass:	1385.75407
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	135.8587
Mass Error [ppm]:	-0.44599
PEP:	0.0021224
Precursor Type:	ISO

general information

Annotation:	9 of 11
AminoAcids Coverag	82 %
Intensity Coverage:	45 %
Protein Localisation:	393 ... 403

a ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	102.055		130.0499	1	E	10				
-0.035015	215.139		243.1339	2	I	9	1257.719		629.3633	+0.215047
	329.1819		357.1769	3	N	8	1144.635	+0.190381	572.8213	+0.304199
	442.266		470.2609	4	I	7	1030.592		1030.592	
	598.3671		626.362	5	R	6	917.5083	+0.032887	917.5083	
	655.3886		683.3835	6	G	5	761.4072	+0.283046	761.4072	
	768.4726	+0.09927	796.4676	7	I	4	704.3857		704.3857	
	855.5047	-0.006855	883.4996	8	S	3	591.3017	+0.009423	591.3017	
	1018.568	+0.09516	1046.563	9	Y	2	504.2696	+0.069711	504.2696	
	1204.647	+0.080423	1232.642	10	W	1	341.2063	+0.019209	341.2063	
				11	K	0	155.127		155.127	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F11
Scannumber: 21842
Protein: BSU20680; yoqC
Peptide Score: 72.62
Method: ITMS; CID; 3



precursor information

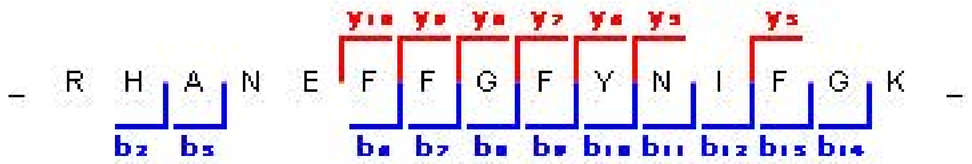
Mass:	1898.97431
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	72.61512
Mass Error [ppm]:	0.27194
PEP:	0.00065678
Precursor Type:	MULTI

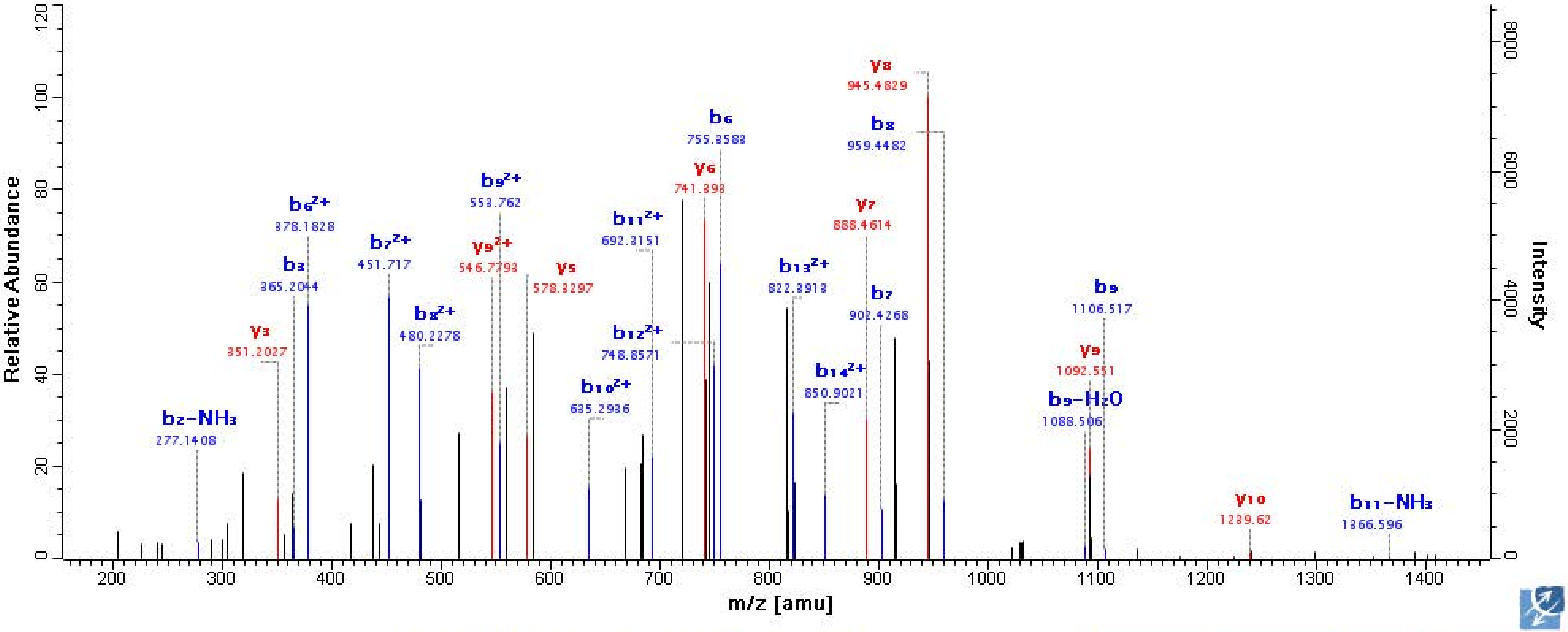
general information

Annotation:	11 of 16
AminoAcids Coverag	69 %
Intensity Coverage:	27 %
Protein Localisation:	67 ... 82

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	15				
	245.07681259	2	D	14	1770.9384752		1770.9384752	
+0.0988628	373.13539011	3	Q	13	1655.9115322		1655.9115322	
+0.1256997	486.21945409	4	I	12	1527.8529547	+0.148144	1527.8529547	
	599.30351807	5	I	11	1414.7688907		1414.7688907	
	728.34611116	6	E	10	1301.6848267		1301.6848267	
	841.43017514	7	I	9	1172.6422336		1172.6422336	
	912.46728893	8	A	8	1059.5581696	+0.212094	1059.5581696	
+0.1904354	1041.509882	9	E	7	988.52105584	+0.1860364	988.52105584	
	1154.593946	10	I	6	859.47846274	+0.1482462	430.2428696	+0.108937
+0.0384959	1225.6310598	11	A	5	746.39439876		746.39439876	
	1282.6525235	12	G	4	675.35728497	+0.1057277	675.35728497	
+0.1460237	1438.7536345	13	R	3	618.33582125		618.33582125	
	1567.7962276	14	E	2	462.23471022		462.23471022	
+0.224435	1753.8755406	15	W	1	333.19211712		333.19211712	
		16	K	0	147.11280417		147.11280417	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F11
Scannumber:	23153
Protein:	BSU39100; S3AR; yxiO
Peptide Score:	123.28
Method:	ITMS; CID; 3





precursor information

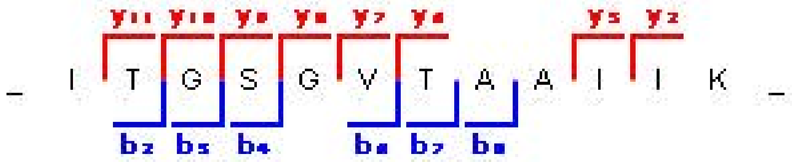
Mass:	1845.89551
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	123.2753
Mass Error [ppm]:	0.2296
PEP:	5.4218E-06
Precursor Type:	MULTI

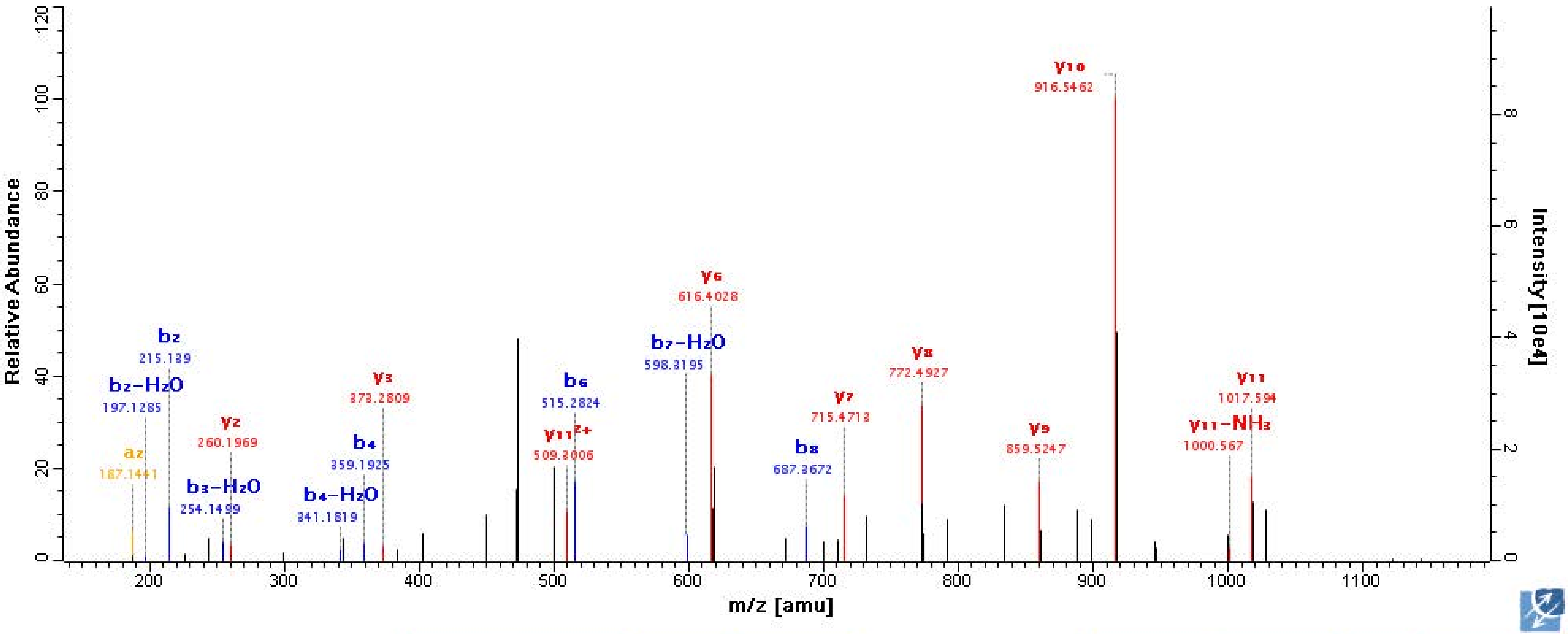
general information

Annotation:	12 of 15
AminoAcids Coverag	80 %
Intensity Coverage:	49 %
Protein Localisation:	356 ... 370

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	157.1084		157.1084	1	R	14				
	294.1673		294.1673	2	H	13	1690.801		1690.801	
	365.2044	+0.045526	365.2044	3	A	12	1553.742		1553.742	
	479.2473		479.2473	4	N	11	1482.705		1482.705	
	608.2899		608.2899	5	E	10	1368.662		1368.662	
+0.143604	378.1828	+0.042959	755.3583	6	F	9	1239.62	+0.247236	1239.62	
+0.041099	451.717	+0.039547	902.4268	7	F	8	1092.551	+0.114966	546.7793	+0.334729
+0.055757	480.2278	+0.070513	959.4482	8	G	7	945.4829	+0.053986	945.4829	
-0.046626	553.762	+0.451012	1106.517	9	F	6	888.4614	+0.050669	888.4614	
+0.224566	635.2936		1269.58	10	Y	5	741.393	+0.05048	741.393	
+0.203103	692.3151		1383.623	11	N	4	578.3297	+0.012429	578.3297	
+0.118468	748.8571		1496.707	12	I	3	464.2867		464.2867	
+0.256808	822.3913		1643.775	13	F	2	351.2027	+0.045243	351.2027	
+0.169293	850.9021		1700.797	14	G	1	204.1343		204.1343	
				15	K	0	147.1128		147.1128	

Source:	20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F12
Scannumber:	16008
Protein:	BSU01720; ybbK
Peptide Score:	111.86
Method:	ITMS; CID; 3





precursor information

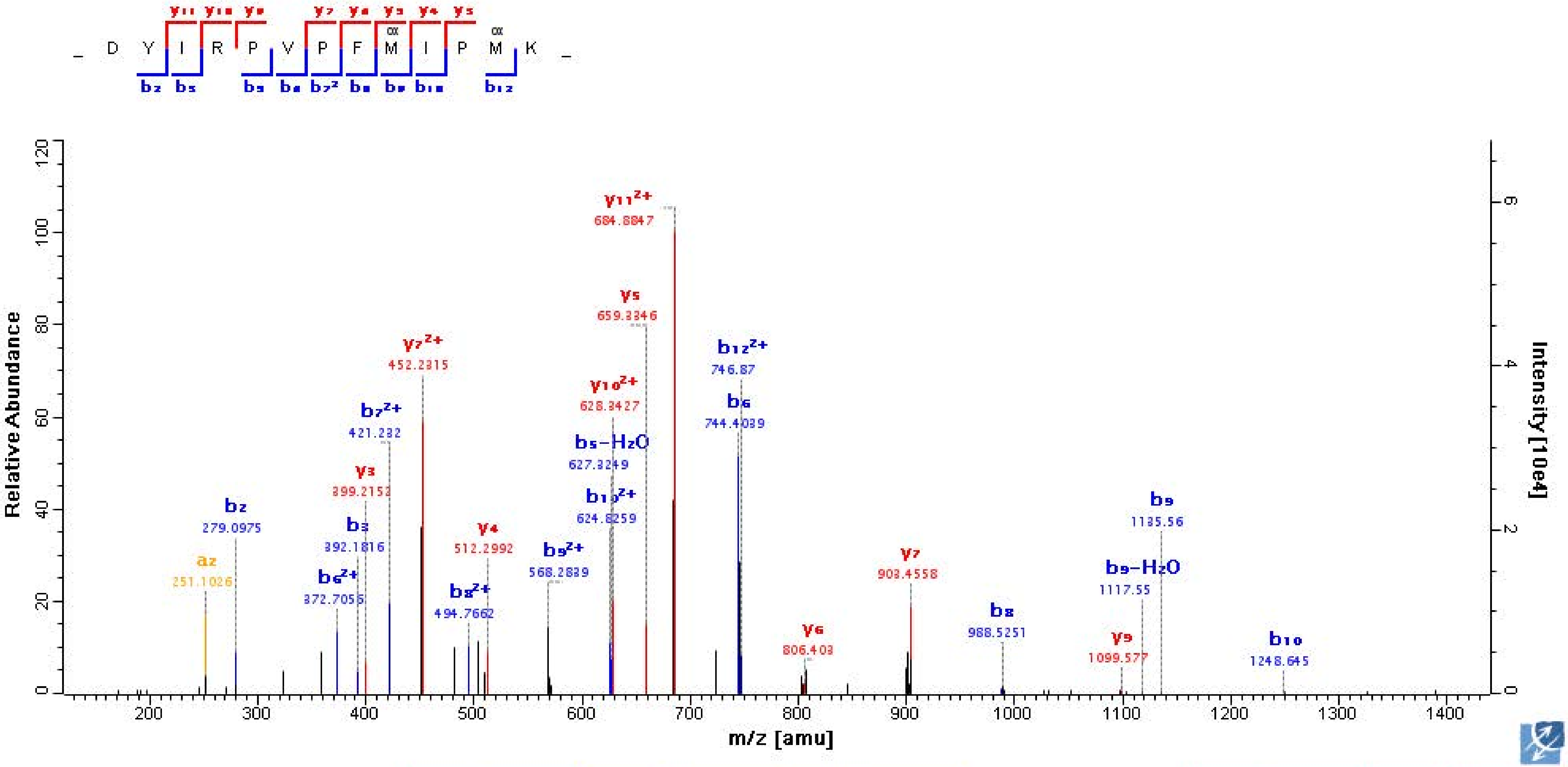
Mass:	1129.6696
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	111.8553
Mass Error [ppm]:	-0.95058
PEP:	0.00049291
Precursor Type:	MULTI

general information

Annotation:	9 of 12
AminoAcids Coverag	75 %
Intensity Coverage:	48 %
Protein Localisation:	124 ... 135

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	11				
-0.096619	187.1441	-0.107494	215.139	2	T	10	1017.594	+0.256516	509.3006	+0.440446
	244.1656		272.1605	3	G	9	916.5462	+0.071712	916.5462	
	331.1976	+0.003717	359.1925	4	S	8	859.5247	+0.258764	859.5247	
	388.2191		416.214	5	G	7	772.4927	+0.01351	772.4927	
	487.2875	+0.02236	515.2824	6	V	6	715.4713	+0.098267	715.4713	
	588.3352		616.3301	7	T	5	616.4028	+0.014398	616.4028	
	659.3723	+0.111518	687.3672	8	A	4	515.3552		515.3552	
	730.4094		758.4043	9	A	3	444.318		444.318	
	843.4934		871.4884	10	I	2	373.2809	+0.004834	373.2809	
	956.5775		984.5724	11	I	1	260.1969	+0.028626	260.1969	
				12	K	0	147.1128		147.1128	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F12
Scannumber: 20315
Protein: atpB; BSU36870
Peptide Score: 144.1
Method: ITMS; CID; 3



precursor information

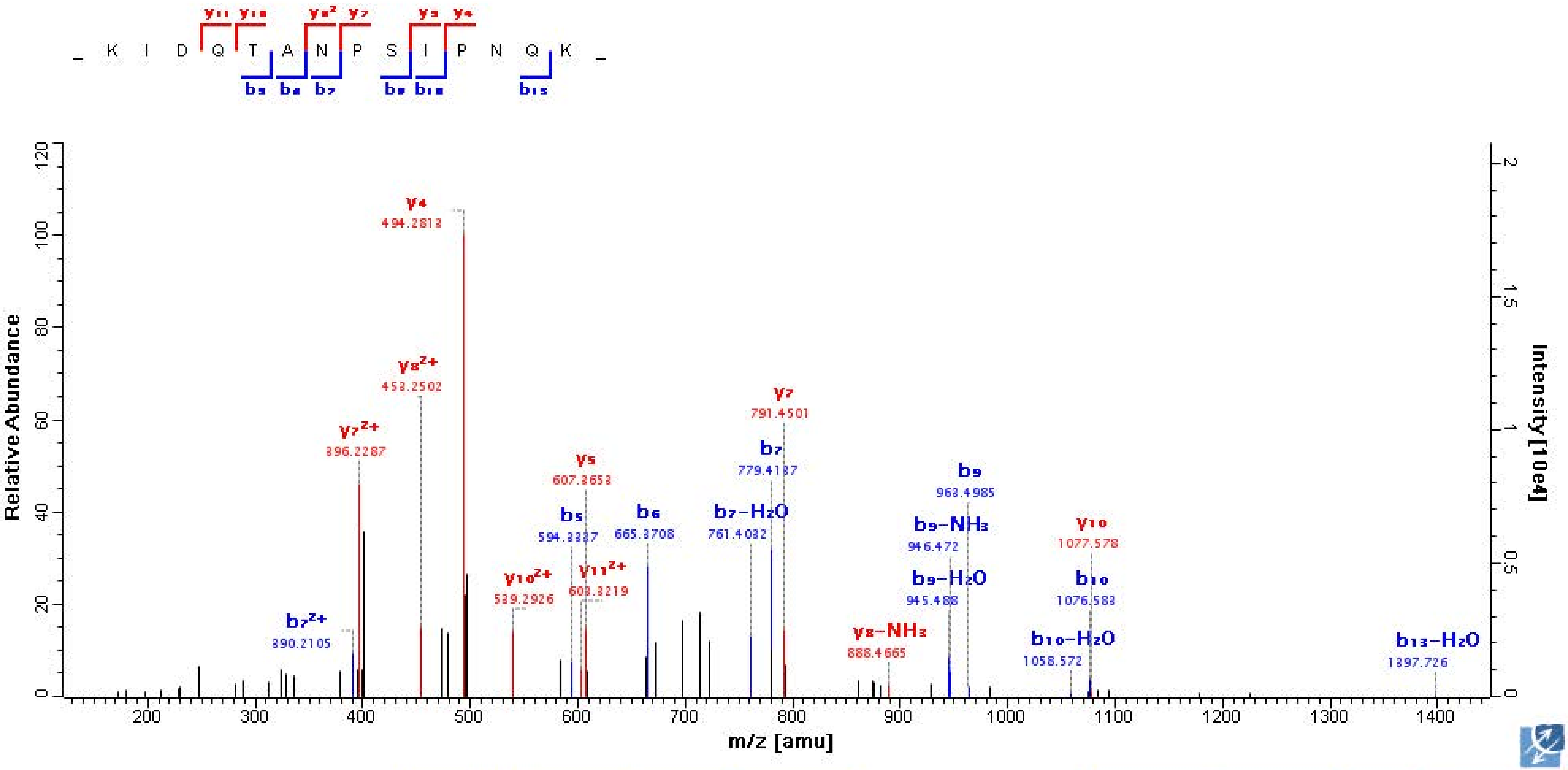
Mass:	1637.83038
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	144.1029
Mass Error [ppm]:	-0.34722
PEP:	2.3762E-08
Precursor Type:	MULTI

general information

Annotation:	11 of 13
AminoAcids Coverag	85 %
Intensity Coverage:	59 %
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				
-0.0232	251.103		279.098	+0.11797	279.098	2	Y	11	1531.83		1531.83	
	364.187		392.182	+0.07486	392.182	3	I	10	1368.76		684.885	+0.2690
	520.288		548.283		548.283	4	R	9	1255.68		628.343	+0.3150
	617.341		645.335		645.335	5	P	8	1099.58	-0.3576	1099.58	
	716.409	+0.2891	372.706	+0.16165	744.404	6	V	7	1002.52		1002.52	
	813.462	+0.18527	421.232		841.457	7	P	6	903.456	+0.13587	452.232	+0.0227
	960.53	+0.30481	494.766	-0.2981	988.525	8	F	5	806.403	-0.247	806.403	
	1107.57	+0.06762	568.284	-0.1012	1135.56	9	M	4	659.335	+0.09933	659.335	
	1220.65	+0.39315	624.826	+0.25036	1248.64	10	I	3	512.299	+0.33004	512.299	
	1317.7		1345.7		1345.7	11	P	2	399.215	+0.02427	399.215	
	1464.74	-0.4001	746.87		1492.73	12	M	1	302.162		302.162	
						13	K	0	155.127		155.127	

Source: 20120521_VR_Bsu_TripleSILACrep1_L2ESLS_OG_F12
Scannumber: 7040
Protein: BSU38690; yxlC
Peptide Score: 94.12
Method: ITMS; CID; 3



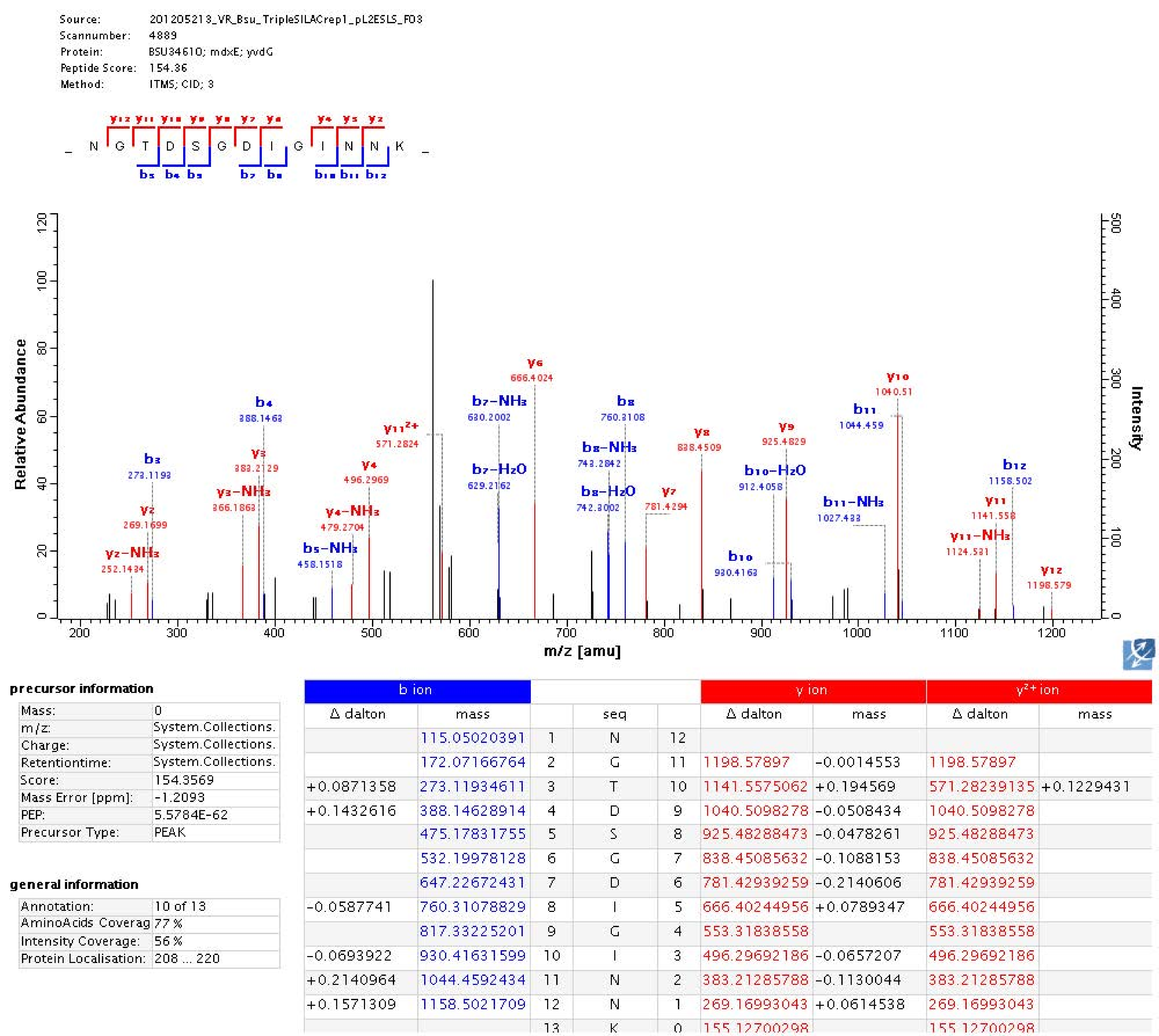
precursor information

Mass:	1552.82216
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	94.12169
Mass Error [ppm]:	0.79269
PEP:	8.7899E-05
Precursor Type:	MULTI

general information

Annotation:	9 of 14
AminoAcids Coverag	64 %
Intensity Coverage:	53 %
Protein Localisation:	16 ... 29

b²⁺ ion		b ion					y ion		y²⁺ ion	
Δ dalton	mass	Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	137.1164		137.1164	1	K	13				
	250.2005		250.2005	2	I	12	1433.747		1433.747	
	365.2274		365.2274	3	D	11	1320.663		1320.663	
	493.286		493.286	4	Q	10	1205.636		603.3219	+0.09508
	594.3337	+0.222207	594.3337	5	T	9	1077.578	+0.222323	539.2926	-0.180257
	665.3708	+0.029148	665.3708	6	A	8	976.5302		976.5302	
+0.109864	390.2105	+0.066543	779.4137	7	N	7	905.4931		453.2502	+0.261919
	876.4665		876.4665	8	P	6	791.4501	+0.019782	396.2287	+0.200314
	963.4985	+0.20691	963.4985	9	S	5	694.3974		694.3974	
	1076.583	+0.109296	1076.583	10	I	4	607.3653	+0.027853	607.3653	
	1173.635		1173.635	11	P	3	494.2813	+0.000528	494.2813	
	1287.678		1287.678	12	N	2	397.2285		397.2285	
	1415.737		1415.737	13	Q	1	283.1856		283.1856	
				14	K	0	155.127		155.127	



Source: 20120521 3_VR_Bsu_TripleSILACrep1_pL2ESLS_F03
Scannumber: 4889
Protein: BSU34610; mdxE; yvdG
Peptide Score: 154.36
Method: ITMS; CID; 3

precursor information

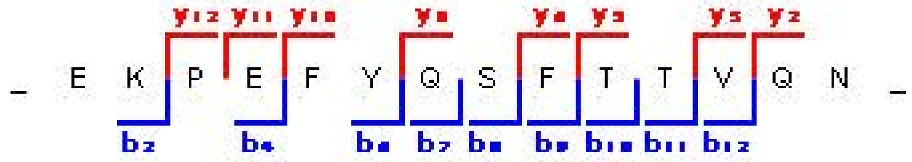
Mass:	0
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	154.3569
Mass Error [ppm]:	-1.2093
PEP:	5.5784E-62
Precursor Type:	PEAK

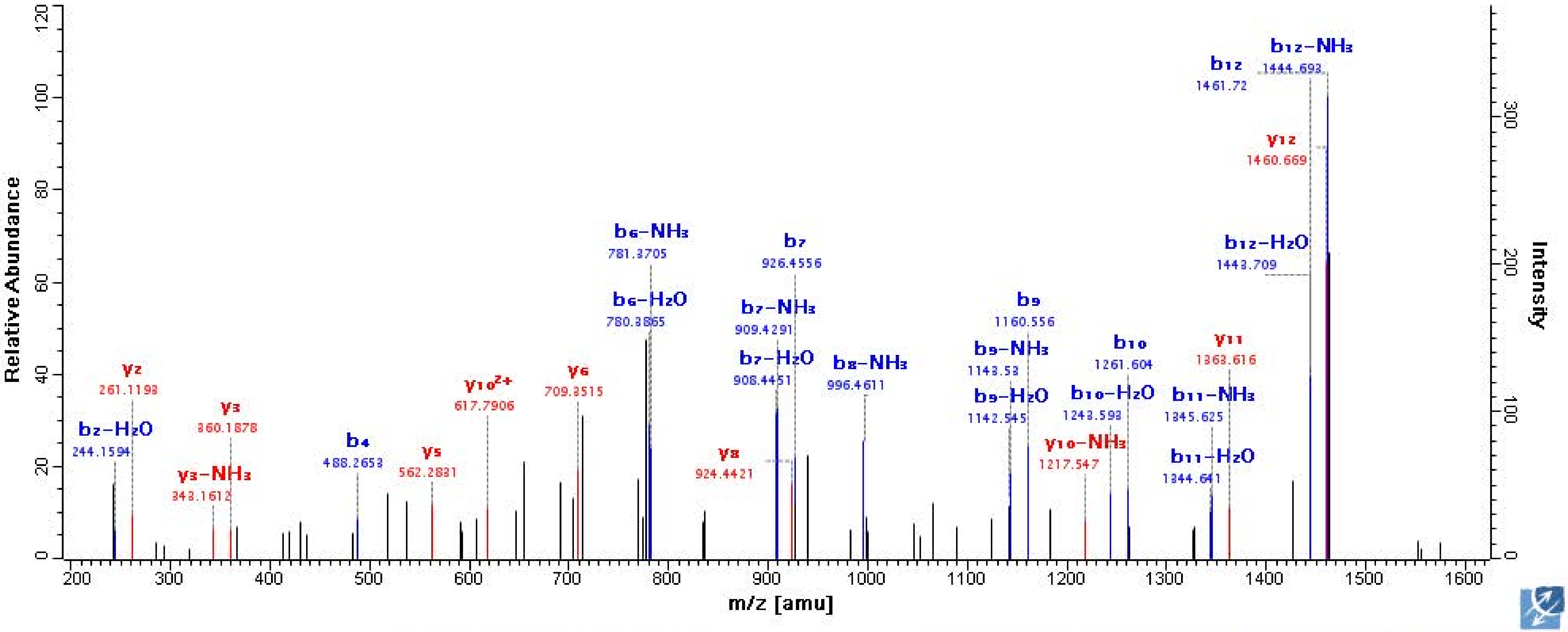
general information

Annotation:	10 of 13
AminoAcids Coverag	77 %
Intensity Coverage:	56 %
Protein Localisation:	208 ... 220

b ion					y ion		y2+ ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	115.05020391	1	N	12				
	172.07166764	2	G	11	1198.57897	-0.0014553	1198.57897	
+0.0871358	273.11934611	3	T	10	1141.5575062	+0.194569	571.28239135	+0.1229431
+0.1432616	388.14628914	4	D	9	1040.5098278	-0.0508434	1040.5098278	
	475.17831755	5	S	8	925.48288473	-0.0478261	925.48288473	
	532.19978128	6	G	7	838.45085632	-0.1088153	838.45085632	
	647.22672431	7	D	6	781.42939259	-0.2140606	781.42939259	
-0.0587741	760.31078829	8	I	5	666.40244956	+0.0789347	666.40244956	
	817.33225201	9	G	4	553.31838558		553.31838558	
-0.0693922	930.41631599	10	I	3	496.29692186	-0.0657207	496.29692186	
+0.2140964	1044.4592434	11	N	2	383.21285788	-0.1130044	383.21285788	
+0.1571309	1158.5021709	12	N	1	269.16993043	+0.0614538	269.16993043	
		13	K	0	155.12700298		155.12700298	

Source:	201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F04
Scannumber:	8526
Protein:	BSU39700; E83G; idh; iolG
Peptide Score:	134.56
Method:	ITMS; CID; 3





precursor information

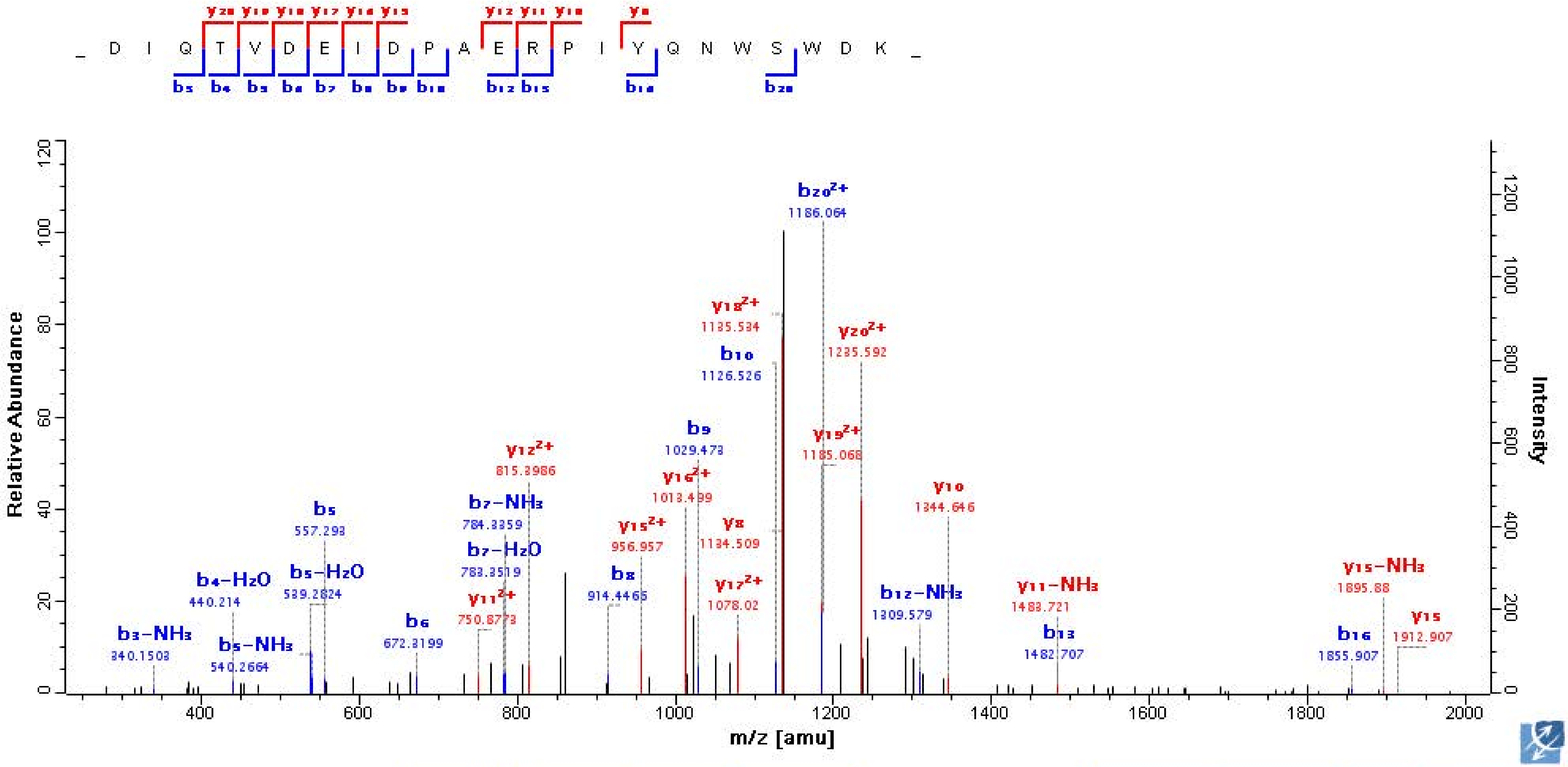
Mass:	1720.82489
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	134.5619
Mass Error [ppm]:	0.15373
PEP:	0.0021386
Precursor Type:	ISO

general information

Annotation:	12 of 14
AminoAcids Coverag	86 %
Intensity Coverage:	53 %
Protein Localisation:	331 ... 344

b ion					y ion		y^{2+} ion	
Δ dalton	mass		seq		Δ dalton	mass	Δ dalton	mass
	130.04986956	1	E	13				
	262.16993956	2	K	12	1592.7893062		1592.7893062	
	359.22270342	3	P	11	1460.6692362	-0.017869	1460.6692362	
+0.0191273	488.26529651	4	E	10	1363.6164724	-0.1563894	1363.6164724	
	635.33371043	5	F	9	1234.5738793		617.79057787	-0.3920183
	798.39703897	6	Y	8	1087.5054654		1087.5054654	
+0.0202136	926.45561648	7	Q	7	924.44213681	-0.0288678	924.44213681	
	1013.4876449	8	S	6	796.3835593		796.3835593	
-0.1610393	1160.5560588	9	F	5	709.35153089	-0.1220997	709.35153089	
+0.0604473	1261.6037373	10	T	4	562.28311698	-0.0907342	562.28311698	
	1362.6514158	11	T	3	461.2354385		461.2354385	
+0.0359076	1461.7198297	12	V	2	360.18776003	+0.0521081	360.18776003	
	1589.7784072	13	Q	1	261.11934611	-0.0770182	261.11934611	
		14	N	0	133.0607686		133.0607686	

Source: 201205213_VR_Bsu_TripleSILACrep1_pL2ESLS_F06
Scannumber: 11534
Protein: BSU34570; yvdK
Peptide Score: 81
Method: ITMS; CID; 3



precursor information

Mass:	2817.32475
m/z:	System.Collections.
Charge:	System.Collections.
Retentiontime:	System.Collections.
Score:	81.00344
Mass Error [ppm]:	0.05791
PEP:	3.3981E-05
Precursor Type:	MULTI

general information

Annotation:	13 of 23
AminoAcids Coverag	57 %
Intensity Coverage:	47 %
Protein Localisation:	558 ... 580

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	22				
	229.1183		229.1183	2	I	21	2711.319		2711.319	
	357.1769		357.1769	3	Q	20	2598.235		2598.235	
	458.2245		458.2245	4	T	19	2470.176		1235.592	+0.401042
	557.293	-0.019333	557.293	5	V	18	2369.129		1185.068	-0.040206
	672.3199	+0.016957	672.3199	6	D	17	2270.06		1135.534	-0.028216
	801.3625		801.3625	7	E	16	2155.033		1078.02	+0.315089
	914.4466	-0.064901	914.4466	8	I	15	2025.991		1013.499	+0.192648
	1029.473	-0.272081	1029.473	9	D	14	1912.907	-0.02727	956.957	+0.122741
	1126.526	+0.056747	1126.526	10	P	13	1797.88		1797.88	
	1197.563		1197.563	11	A	12	1700.827		1700.827	
	1326.606		1326.606	12	E	11	1629.79		815.3986	+0.222045
	1482.707	+0.122267	1482.707	13	R	10	1500.747		750.8773	-0.060857
	1579.76		1579.76	14	P	9	1344.646	+0.024515	1344.646	
	1692.844		1692.844	15	I	8	1247.593		1247.593	
	1855.907	+0.322013	1855.907	16	Y	7	1134.509	+0.142788	1134.509	
	1983.966		1983.966	17	Q	6	971.4461		971.4461	
	2098.009		2098.009	18	N	5	843.3875		843.3875	
	2284.088		2284.088	19	W	4	729.3446		729.3446	
-0.33028	1186.064		2371.12	20	S	3	543.2653		543.2653	
	2557.199		2557.199	21	W	2	456.2333		456.2333	
	2672.226		2672.226	22	D	1	270.1539		270.1539	
				23	K	0	155.127		155.127	