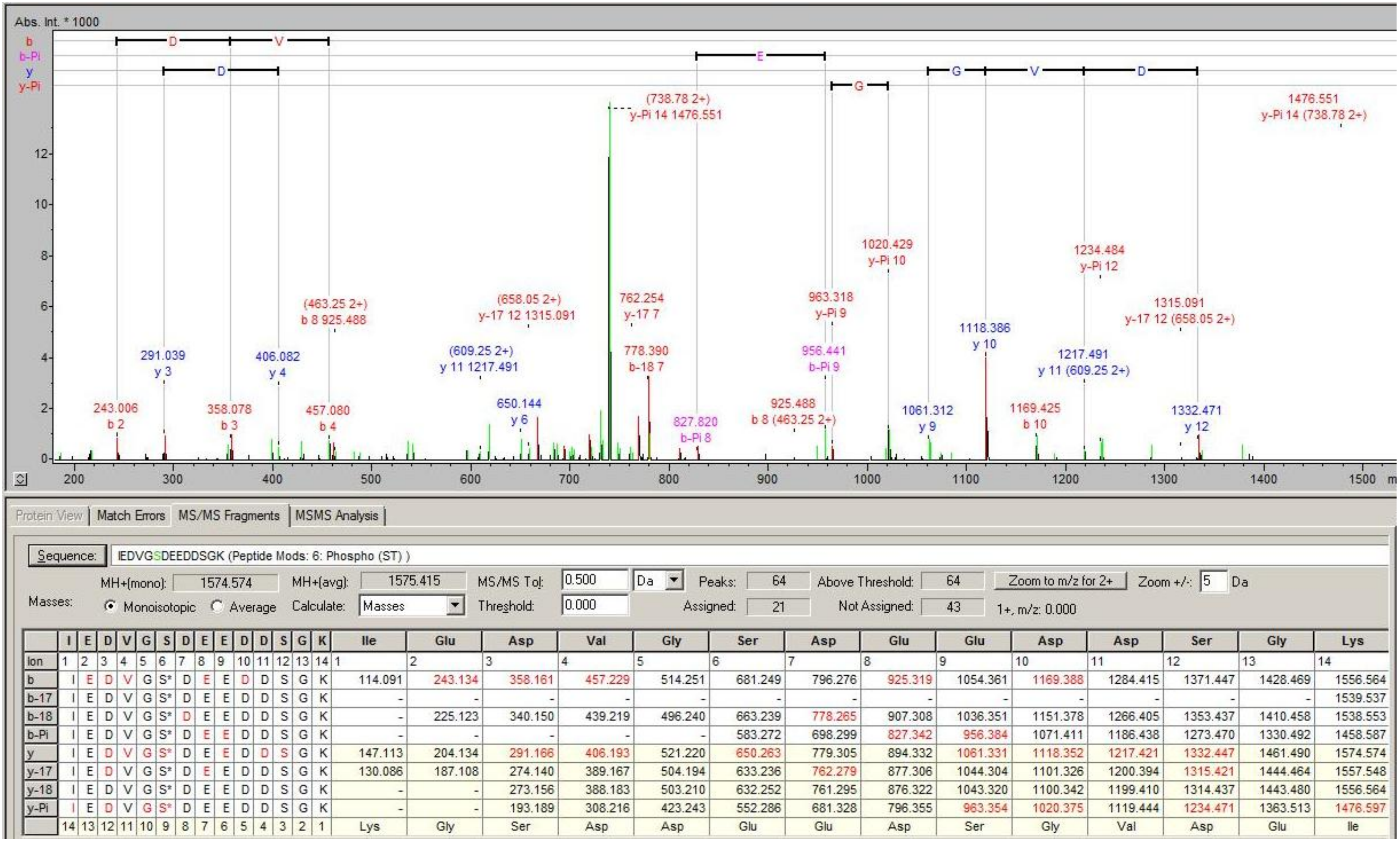
SPOT ID #	cmpd	ID	Description	Modified residue	Phosphosite	range	Modified position	peptide score (	Sequence	Mass	Charge	Rt(min)	MS/MS mode
70	102	HS90B_RAT	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4	S255	Y	250 - 263	Phospho: 6	34.6 (M:34.6)	K.IEDVGSDEEDDSGK.D	787.7692	2	15.44	CID
76	100	HS90B_RAT	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4	S255	Y	250 - 265	Phospho: 6	46.6 (M:46.6)	K.IEDVGSDEEDDSGKDK.K	606.5377	3	16.48	ETD
147	298	PGM1_RAT	Phosphoglucomutase-1 OS=Rattus norvegicus GN=Pgm1 PE=1 SV=2	T115	N	108 - 130	Phospho: 8; Deamidated: 17	59.7 (M:59.7)	K.AIGGIILTASHNPGGPNGDFGIK.F	763.0286	3	30.67	CID
169	121	FETUA_RAT	Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2	S138	Y	127 - 143	Carbamidomethyl: 6; Phospho: 12	55.4 (M:55.4)	R.VLHAQCHSTPDSAEDVR.K	667.9140	3	17.99	ETD
184	**128**	**FETUA_RAT**	**Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2**	**S138**	**Y**	**127 - 143**	**Carbamidomethyl: 6; Phospho: 12**	**36.6 (M:36.6)**	**R.VLHAQCHSTPDSAEDVR.K**	**667.9659**	**3**	**18.24**	**CID**
184	**108**	**FETUA_RAT**	**Alpha-2-HS-glycoprotein OS=Rattus norvegicus GN=Ahsg PE=1 SV=2**	**S138**	**Y**	**127 - 144**	**Carbamidomethyl: 6; Phospho: 12**	**76.4 (M:76.4)**	**R.VLHAQCHSTPDSAEDVRK.F**	**533.2272**	**4**	**16.87**	**ETD**
210	279	PDIA3_RAT	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2	S176	N	162 - 179	Phospho: 15	25.7 (M:25.7)	R.DLFSDGHSEFLKAASNLR.D	695.9822	3	29.83	CID
213	316	CH60_RAT	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1	T540	Y	524 - 551	Phospho: 14, 18	25.1 (M:25.1)	K.VVRTALLDAAGVASLLTTAEAVVTEI	743.2784	4	31.65	CID
411	**123**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T334; S335; S338**	**Y**	**328 - 343**	**Phospho: 7, 8, 11**	**32.5 (M:32.5)**	**R.SRTASLTSAASIDGSR.S**	**607.1690**	**3**	**21.49**	**CID**
411	**126**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T330; S332; T334**	**Y**	**328 - 343**	**Phospho: 3, 5, 7**	**33.2 (M:33.2)**	**R.SRTASLTSAASIDGSR.S**	**607.1581**	**3**	**21.67**	**ETD**
411	130	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S338	**Y**	330 - 343	Phospho: 1, 9	58.1 (M:58.1)	R.TASLTSAASIDGSR.S	748.7292	2	21.91	CID
411	150	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S332	**Y**	330 - 343	Phospho: 1, 3	48.6 (M:48.6)	R.TASLTSAASIDGSR.S	748.7062	2	23.15	CID
411	151	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S332	**Y**	330 - 343	Phospho: 3	73.4 (M:73.4)	R.TASLTSAASIDGSR.S	708.7679	2	23.19	CID
411	**139**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S338**	**Y**	**330 - 343**	**Phospho: 9**	**58.4 (M:58.4)**	**R.TASLTSAASIDGSR.S**	**708.7250**	**2**	**22.44**	**CID**
411	**134**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S332; S338**	**Y**	**330 - 343**	**Phospho: 3, 9**	**25.8 (M:25.8)**	**R.TASLTSAASIDGSR.S**	**748.7131**	**2**	**22.13**	**ETD**
411	194	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S352; S353	**Y**	348 - 371	Carbamidomethyl: 24; Phospho: 5, 6	56.4 (M:56.4)	R.TLSQSSESGTLPSGPPGHTMEVS	869.2446	3	25.64	CID
419	**158**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S328; T330**	**Y**	**328 - 343**	**Phospho: 1, 3**	**71.2 (M:71.2)**	**R.SRTASLTSAASIDGSR.S**	**580.5163**	**3**	**23.07**	**CID**
419	**158**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T330; S332**	**Y**	**328 - 343**	**Phospho: 3, 5**	**78.1 (M:78.1)**	**R.SRTASLTSAASIDGSR.S**	**580.5163**	**3**	**23.07**	**ETD**
419	139	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	**T330; S332; T334**	**Y**	328 - 343	Phospho: 3, 5, 7	39.4 (M:39.4)	R.SRTASLTSAASIDGSR.S	910.2264	2	21.87	CID
419	138	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	**T334; S335; S338**	**Y**	328 - 343	Phospho: 7, 8, 11	27.8 (M:27.8)	R.SRTASLTSAASIDGSR.S	607.1534	3	21.82	CID
419	166	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S332	**Y**	330 - 343	Phospho: 1, 3	49.2 (M:49.2)	R.TASLTSAASIDGSR.S	748.6921	2	23.47	CID
419	145	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S328	**Y**	330 - 343	Phospho: 1, 9	59.4 (M:59.4)	R.TASLTSAASIDGSR.S	748.7105	2	22.22	CID
419	141	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S332; S338	**Y**	330 - 343	Phospho: 3, 9	40.5 (M:40.5)	R.TASLTSAASIDGSR.S	748.7145	2	22.00	CID
419	165	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S332	**Y**	330 - 343	Phospho: 3	72.4 (M:72.4)	R.TASLTSAASIDGSR.S	708.7203	2	23.43	CID
419	152	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S338	**Y**	330 - 343	Phospho: 9	69.0 (M:69.0)	R.TASLTSAASIDGSR.S	708.7050	2	22.70	CID
427	309	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	K13	**N**	2 - 25	Acetyl: 12	22.2 (M:22.2)	M.AELQEVQITEEKPLLPGQTPEAAK.	887.7748	3	31.55	CID
427	154	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T334; S335	**Y**	328 - 343	Phospho: 7, 8	71.0 (M:71.0)	R.SRTASLTSAASIDGSR.S	580.4868	3	23.02	CID
427	**152**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T330; S328**	**Y**	**328 - 343**	**Phospho: 3, 5**	**89.0 (M:89.0)**	**R.SRTASLTSAASIDGSR.S**	**580.7692**	**3**	**22.90**	**ETD**
427	**152**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S328; T330**	**Y**	**328 - 343**	**Phospho: 1, 3**	**73.5 (M:73.5)**	**R.SRTASLTSAASIDGSR.S**	**580.7692**	**3**	**22.90**	**CID**
427	133	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S;332; T334; S338	**Y**	328 - 343	Phospho: 3, 5, 7	25.8 (M:25.8)	R.SRTASLTSAASIDGSR.S	910.2408	2	21.78	CID
427	147	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S338	**Y**	330 - 343	Phospho: 9	70.5 (M:70.5)	R.TASLTSAASIDGSR.S	708.7231	2	22.59	CID
427	140	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S332; S338	**Y**	330 - 343	Phospho: 3, 9	67.0 (M:67.0)	R.TASLTSAASIDGSR.S	748.6841	2	22.19	CID
427	135	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S328	**Y**	330 - 343	Phospho: 1, 9	63.7 (M:63.7)	R.TASLTSAASIDGSR.S	748.6947	2	21.91	CID
431	290	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	K13	**N**	2 - 25	Acetyl: 12	23.2 (M:23.2)	M.AELQEVQITEEKPLLPGQTPEAAK.	887.7730	3	31.27	CID
431	**157**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S328; T330**	**Y**	**328 - 343**	**Phospho: 1, 3**	**53.1 (M:53.1)**	**R.SRTASLTSAASIDGSR.S**	**580.5322**	**3**	**22.59**	**CID**
431	**157**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T330; S332**	**Y**	**328 - 343**	**Phospho: 3, 5**	**77.4 (M:77.4)**	**R.SRTASLTSAASIDGSR.S**	**580.5322**	**3**	**22.59**	**ETD**
431	154	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S338	**Y**	330 - 343	Phospho: 9	57.7 (M:57.7)	R.TASLTSAASIDGSR.S	708.7833	2	22.26	CID
433	**121**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**T330; S332**	**Y**	**328 - 343**	**Phospho: 3, 5**	**87.1 (M:87.1)**	**R.SRTASLTSAASIDGSR.S**	**580.4877**	**3**	**22.54**	**ETD**
433	**122**	**NDRG2_RAT**	**Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1**	**S332; T334**	**Y**	**328 - 343**	**Phospho: 5, 7**	**37.6 (M:37.6)**	**R.SRTASLTSAASIDGSR.S**	**580.5126**	**3**	**22.70**	**CID**
433	108	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330; S338	**Y**	330 - 343	Phospho: 1, 9	53.7 (M:53.7)	R.TASLTSAASIDGSR.S	748.7238	2	21.61	CID
433	118	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	S338	**Y**	330 - 343	Phospho: 9	83.2 (M:83.2)	R.TASLTSAASIDGSR.S	708.7621	2	22.35	CID
433	135	NDRG2_RAT	Protein NDRG2 OS=Rattus norvegicus GN=Ndrg2 PE=1 SV=1	T330	**Y**	330 - 343	Phospho: 1	59.1 (M:59.1)	R.TASLTSAASIDGSR.S	708.7250	2	23.43	CID
448	129	ODPA_RAT	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Ra	S331	**Y**	227 - 235	Phospho: 6	49.4 (M:49.4)	R.YGMGTSVER.A	540.1724	2	19.19	CID
463	253	ACTS_RAT	Actin, alpha skeletal muscle - Rattus norvegicus (Rat)	K330	**Y**	329 - 337	Acetyl: 2	30.6 (M:30.6)	K.IKIIAPPER.K	540.3601	2	25.98	CID
523	129	AATM_RAT	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2	K59	**N**	59 - 68	Acetyl: 1; Oxidation: 2	42.4 (M:42.4)	K.KMNLGVGAYR.D	389.7716	3	21.02	CID
523	226	AATM_RAT	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2	K122	**Y**	108 - 125	Acetyl: 15	92.2 (M:92.2)	K.ASAELALGENSEVLKSGR.F	624.9014	3	26.88	CID
523	128	AATM_RAT	Aspartate aminotransferase, mitochondrial OS=Rattus norvegicus GN=Got2 PE=1 SV=2	K363	**Y**	356 - 364	Acetyl: 8	34.8 (M:34.8)	R.TQLVSNLKK.E	358.1051	3	20.97	ETD
532	418	TPM2_RAT	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=2 SV=1	S283	**N**	269 - 284	Phospho: 15	57.0 (M:57.0)	K.AISEELDNALNDITSL.-	899.3913	2	35.82	CID
561	434	TPM2_RAT	Tropomyosin beta chain OS=Rattus norvegicus GN=Tpm2 PE=2 SV=1	S283	**N**	269 - 284	Phospho: 15	79.1 (M:79.1)	K.AISEELDNALNDITSL.-	899.3806	2	35.42	CID
614	146	MDHM_RAT	Malate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Mdh2 PE=1 SV=2	K239	**Y**	230 - 239	Acetyl: 10	35.0 (M:35.0)	R.IQEAGTEVVK.A	558.2736	2	20.13	CID
626	169	MDHC_RAT	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3	K121	**N**	111 - 121	Acetyl: 11	27.1 (M:27.1)	K.SQGAALEKYAK.K	403.4771	3	22.52	ETD
626	126	MDHC_RAT	Malate dehydrogenase, cytoplasmic OS=Rattus norvegicus GN=Mdh1 PE=1 SV=3	K239	**N**	239 - 248	Acetyl: 1	26.4 (M:26.4)	R.KLSSAMSAAK.A	518.7616	2	19.21	CID
677	396	3HIDH_RAT	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Hibadh PE	K55; K59	**N**	39 - 59	Acetyl: 17, 21	35.5 (M:35.5)	K.TPVGFIGLGNMGNPMAKNLIK.H	752.5969	3	35.28	CID
735	164	1433Z_RAT	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1	K2	**Y**	1 - 9	Acetyl: 3	39.7 (M:39.7)	-.MDKNELVQK.A	573.7547	2	21.18	CID
740	200	CAH3_RAT	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3	S99	**Y**	92 - 113	Phospho: 8	57.4 (M:57.4)	R.QFHLHWGSSDDHGSEHTVDGVK.	639.4749	4	25.45	ETD
742	232	CAH3_RAT	Carbonic anhydrase 3 OS=Rattus norvegicus GN=Ca3 PE=1 SV=3	S100	**N**	92 - 113	Phospho: 9	49.8 (M:49.8)	R.QFHLHWGSSDDHGSEHTVDGVK.	639.4534	4	25.26	ETD
763	**281**	**HSPB1_RAT**	**Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1**	**S15**	**Y**	**13 - 20**	**Phospho: 3**	**29.2 (M:29.2)**	**R.SPSWEPFR.D**	**543.2070**	**2**	**28.33**	**ETD**
763	**350**	**HSPB1_RAT**	**Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1**	**S15**	**Y**	**13 - 28**	**Phospho: 3**	**41.6 (M:41.6)**	**R.SPSWEPFRDWYPAHSR.L**	**699.9471**	**3**	**32.30**	**CID**
763	182	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S86	**Y**	84 - 93	Phospho: 3	69.4 (M:69.4)	R.QLSSGVSEIR.Q	578.2173	2	21.89	CID
789	222	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S86	**Y**	80 - 93	Phospho: 7	41.1 (M:41.1)	R.ALNRQLSSGVSEIR.Q	537.2801	3	24.60	CID
798	285	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S15	**Y**	13 - 20	Phospho: 3	35.9 (M:35.9)	R.SPSWEPFR.D	543.2000	2	28.50	CID
798	366	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S15	**Y**	13 - 28	Phospho: 3	60.1 (M:60.1)	R.SPSWEPFRDWYPAHSR.L	699.9021	3	32.75	CID
798	186	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S87	**Y**	84 - 93	Phospho: 4	51.4 (M:51.4)	R.QLSSGVSEIR.Q	578.1996	2	22.31	CID
798	188	HSPB1_RAT	Heat shock protein beta-1 OS=Rattus norvegicus GN=Hspb1 PE=1 SV=1	S86	**Y**	84 - 93	Phospho: 3	67.1 (M:67.1)	R.QLSSGVSEIR.Q	578.2206	2	22.44	CID
870	330	CRYAB_RAT	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1	S59	**Y**	57 - 69	Phospho: 3	88.0 (M:88.0)	R.APSWIDTGLSEMR.M	771.8131	2	32.18	CID
871	204	CRYAB_RAT	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1	K90	**Y**	83 - 92	Acetyl: 8	20.5 (M:20.5)	K.HFSPEELKVK.V	419.5171	3	24.47	CID
871	259	CRYAB_RAT	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1	K92	**Y**	91 - 103	Acetyl: 2	30.8 (M:30.8)	K.VKVLGDVIEVHGK.H	479.2377	3	27.60	ETD
871	83	CRYAB_RAT	Alpha-crystallin B chain OS=Rattus norvegicus GN=Cryab PE=1 SV=1	K166	**Y**	164 - 174	Acetyl: 3	42.5 (M:42.5)	R.EEKPAVTAAPK.K	394.8648	3	15.83	ETD
885	398	MLRV_RAT	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform OS=Rattus norvegicus	S15	**Y**	10 - 30	Phospho: 6; Deamidated: 14	32.1 (M:32.1)	R.LEGGSSNVFSMFEQTQIQEFK.E	829.6632	3	37.11	CID
889	266	HSPB6_RAT	Heat shock protein beta-6 OS=Rattus norvegicus GN=Hspb6 PE=1 SV=1	S16	**Y**	14 - 27	Phospho: 3	61.3 (M:61.3)	R.RASAPLPGFSTPGR.L	747.2755	2	27.40	CID

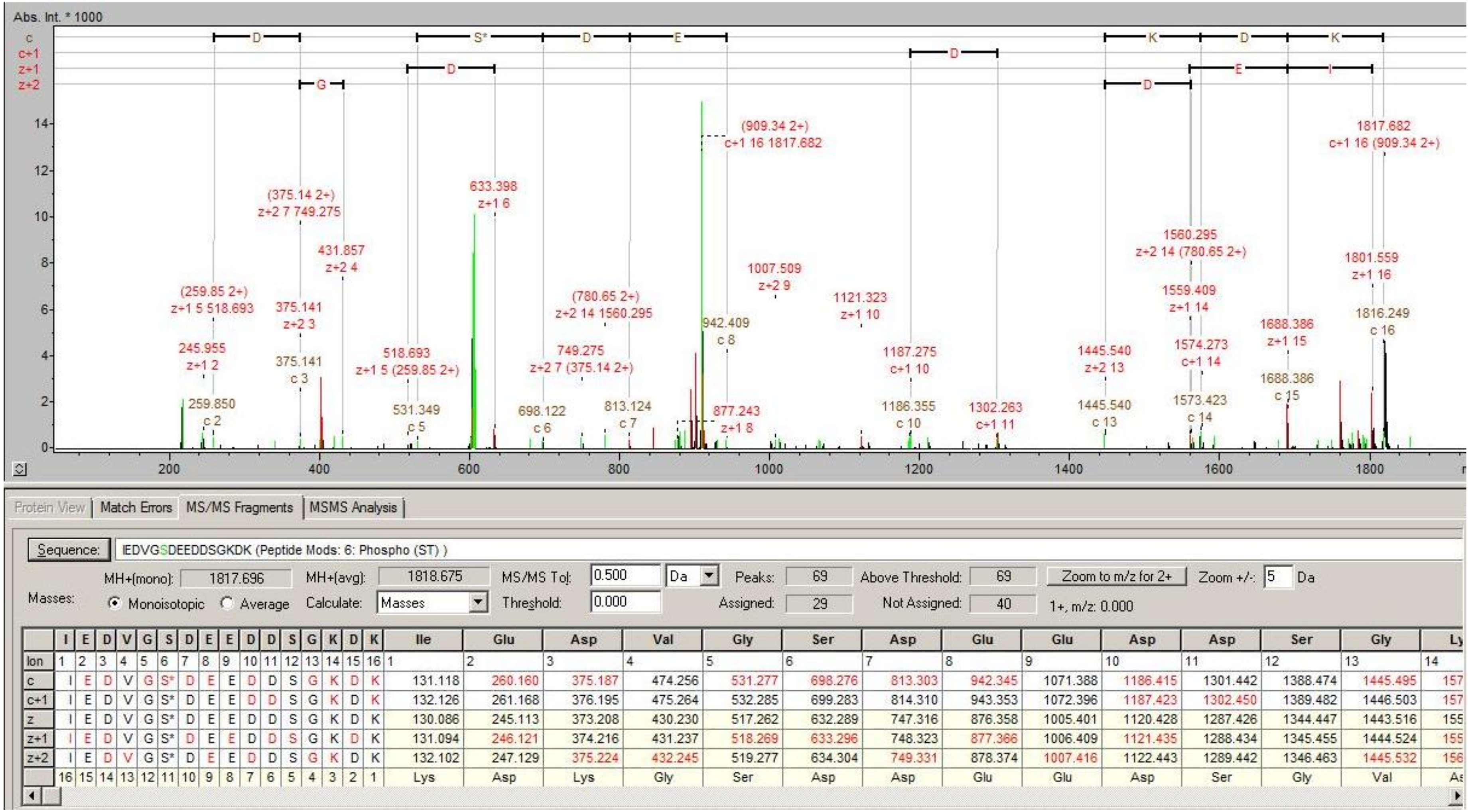


Sequence: IEDVGSDEEDDSGK (Peptide Mods: 6: Phospho (ST))

MH+(mono): 1574.574
MH+(avg): 1575.415
MS/MS Tol: 0.500 Da
Peaks: 64
Above Threshold: 64
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 21
Not Assigned: 43
1+, m/z: 0.000

	I	E	D	V	G	S	D	E	E	D	D	S	G	K	Ile	Glu	Asp	Val	Gly	Ser	Asp	Glu	Glu	Asp	Asp	Ser	Gly	Lys
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	114.091	243.134	358.161	457.229	514.251	681.249	796.276	925.319	1054.361	1169.388	1284.415	1371.447	1428.469	1556.564
b-17	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	-	-	-	-	-	-	-	-	-	-	-	-	-	1539.537
b-18	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	-	225.123	340.150	439.219	496.240	663.239	778.265	907.308	1036.351	1151.378	1266.405	1353.437	1410.458	1538.553
b-Pi	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	-	-	-	-	-	583.272	698.299	827.342	956.384	1071.411	1186.438	1273.470	1330.492	1458.587
y	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	147.113	204.134	291.166	406.193	521.220	650.263	779.305	894.332	1061.331	1118.352	1217.421	1332.447	1461.490	1574.574
y-17	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	130.086	187.108	274.140	389.167	504.194	633.236	762.279	877.306	1044.304	1101.326	1200.394	1315.421	1444.464	1557.548
y-18	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	-	-	273.156	388.183	503.210	632.252	761.295	876.322	1043.320	1100.342	1199.410	1314.437	1443.480	1556.564
y-Pi	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	-	-	193.189	308.216	423.243	552.286	681.328	796.355	963.354	1020.375	1119.444	1234.471	1363.513	1476.597
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Gly	Ser	Asp	Asp	Glu	Glu	Asp	Ser	Gly	Val	Asp	Glu	Ile



Sequence: IEDVGSDEEDDSGKDK (Peptide Mods: 6: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1817.696

MH+(avg): 1818.675

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 69

Assigned: 29

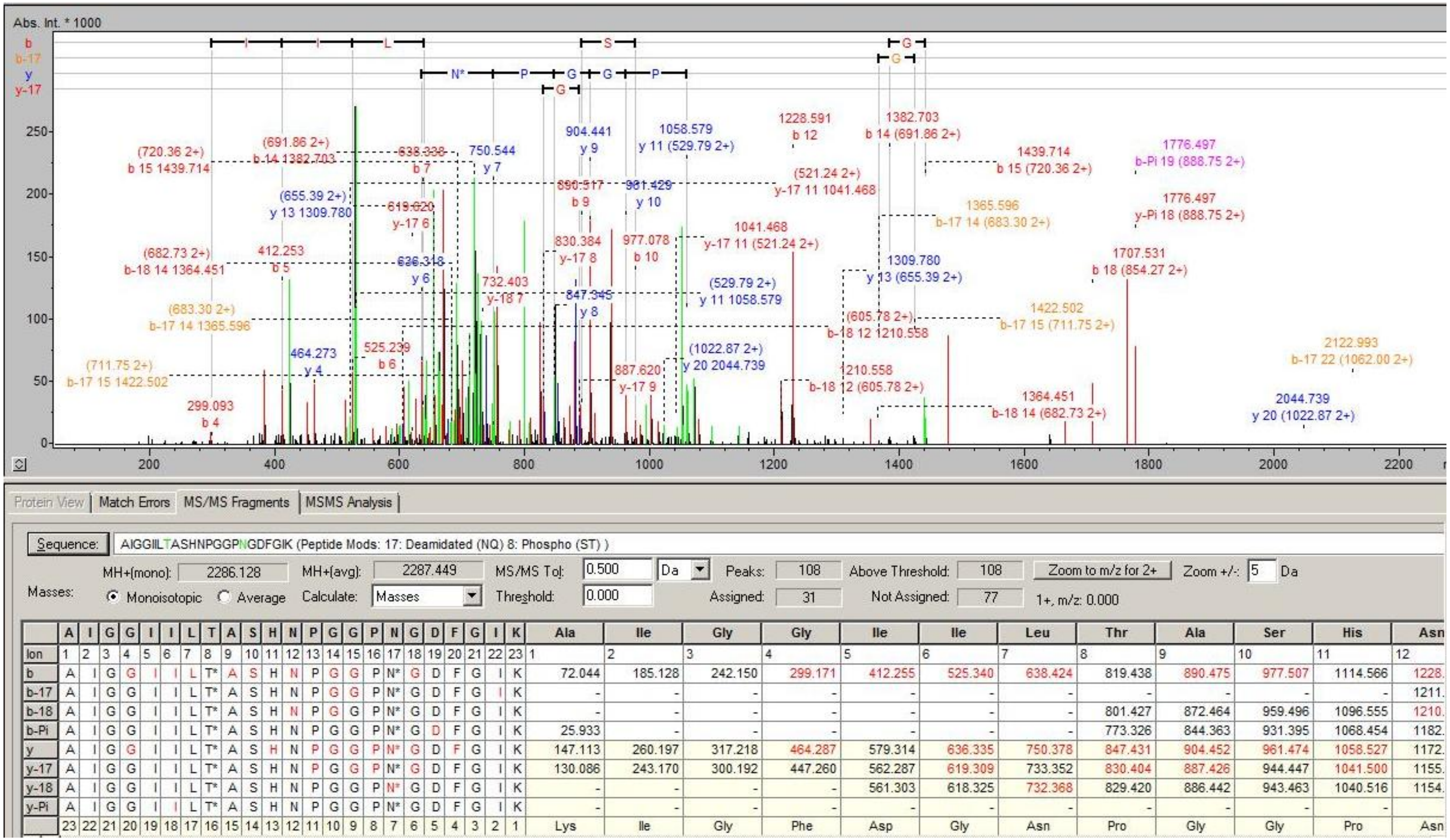
Above Threshold: 69

Not Assigned: 40

Zoom +/-: 5 Da

1+, m/z: 0.000

	I	E	D	V	G	S	D	E	E	D	D	S	G	K	D	K	Ile	Glu	Asp	Val	Gly	Ser	Asp	Glu	Glu	Asp	Asp	Ser	Gly	Ly
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	D	K	131.118	260.160	375.187	474.256	531.277	698.276	813.303	942.345	1071.388	1186.415	1301.442	1388.474	1445.495	157
c+1	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	D	K	132.126	261.168	376.195	475.264	532.285	699.283	814.310	943.353	1072.396	1187.423	1302.450	1389.482	1446.503	157
z	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	D	K	130.086	245.113	373.208	430.230	517.262	632.289	747.316	876.358	1005.401	1120.428	1287.426	1344.447	1443.516	155
z+1	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	D	K	131.094	246.121	374.216	431.237	518.269	633.296	748.323	877.366	1006.409	1121.435	1288.434	1345.455	1444.524	155
z+2	I	E	D	V	G	S*	D	E	E	D	D	S	G	K	D	K	132.102	247.129	375.224	432.245	519.277	634.304	749.331	878.374	1007.416	1122.443	1289.442	1346.463	1445.532	156
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Asp	Lys	Gly	Ser	Asp	Asp	Glu	Glu	Asp	Ser	Gly	Val	As



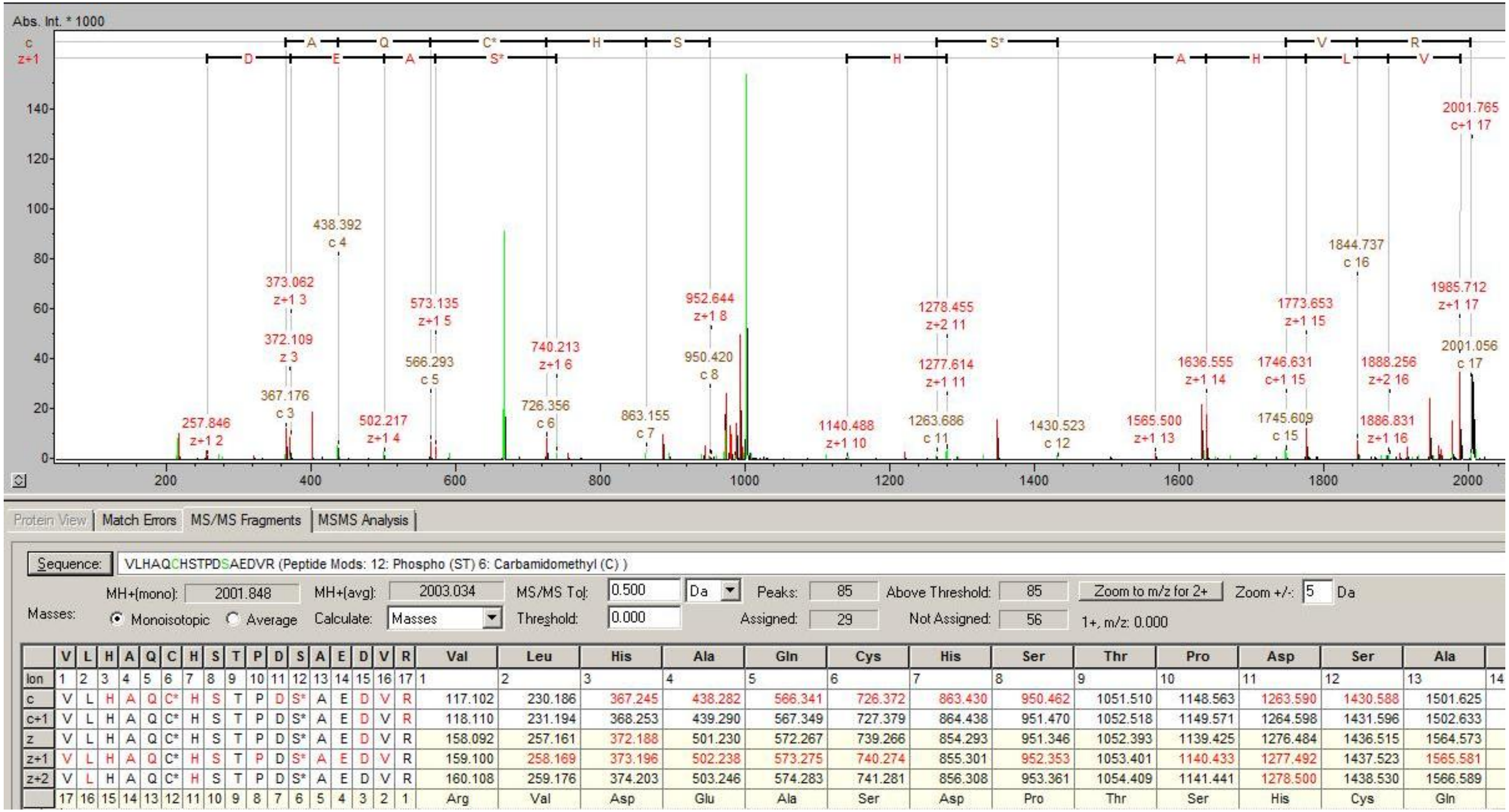
Sequence: AIGGIILTASHNPGGPNGDFGIK (Peptide Mods: 17: Deamidated (NQ) 8: Phospho (ST))

MH+(mono): 2286.128
MH+(avg): 2287.449
MS/MS Tol: 0.500 Da
Peaks: 108
Above Threshold: 108
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 31
Not Assigned: 77
1+, m/z: 0.000

	A	I	G	G	I	I	L	T	A	S	H	N	P	G	G	P	N	G	D	F	G	I	K
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
b	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
b-17	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
b-18	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
b-Pi	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
y	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
y-17	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
y-18	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
y-Pi	A	I	G	G	I	I	L	T*	A	S	H	N	P	G	G	P	N*	G	D	F	G	I	K
	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

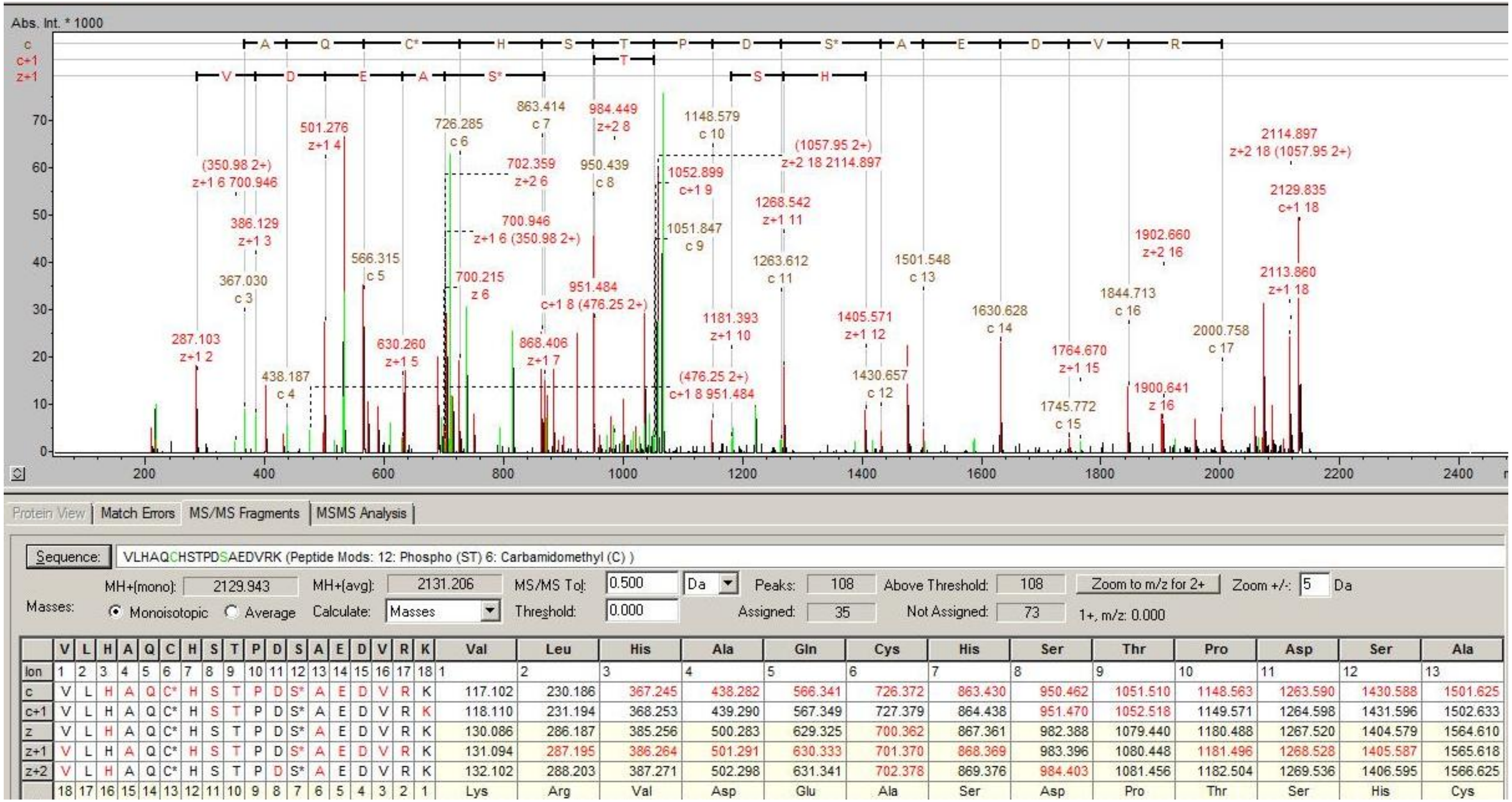
	Ala	Ile	Gly	Gly	Ile	Ile	Leu	Thr	Ala	Ser	His	Asn
Ion	1	2	3	4	5	6	7	8	9	10	11	12
b	72.044	185.128	242.150	299.171	412.255	525.340	638.424	819.438	890.475	977.507	1114.566	1228.
b-17	-	-	-	-	-	-	-	-	-	-	-	1211.
b-18	-	-	-	-	-	-	-	801.427	872.464	959.496	1096.555	1210.
b-Pi	25.933	-	-	-	-	-	-	773.326	844.363	931.395	1068.454	1182.
y	147.113	260.197	317.218	464.287	579.314	636.335	750.378	847.431	904.452	961.474	1058.527	1172.
y-17	130.086	243.170	300.192	447.260	562.287	619.309	733.352	830.404	887.426	944.447	1041.500	1155.
y-18	-	-	-	-	561.303	618.325	732.368	829.420	886.442	943.463	1040.516	1154.
y-Pi	-	-	-	-	-	-	-	-	-	-	-	
	Lys	Ile	Gly	Phe	Asp	Gly	Asn	Pro	Gly	Gly	Pro	Asn



Sequence: VLHAQCHSTPDSAEDVR (Peptide Mods: 12: Phospho (ST) 6: Carbamidomethyl (C))

Masses:
MH+(mono): 2001.848
MH+(avg): 2003.034
● Monoisotopic ○ Average
Calculate: Masses
MS/MS Tol: 0.500 Da
Threshold: 0.000
Peaks: 85
Above Threshold: 85
Assigned: 29
Not Assigned: 56
Zoom +/-: 5 Da
1+, m/z: 0.000

	V	L	H	A	Q	C	H	S	T	P	D	S	A	E	D	V	R	Val	Leu	His	Ala	Gln	Cys	His	Ser	Thr	Pro	Asp	Ser	Ala	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	117.102	230.186	367.245	438.282	566.341	726.372	863.430	950.462	1051.510	1148.563	1263.590	1430.588	1501.625	
c+1	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	118.110	231.194	368.253	439.290	567.349	727.379	864.438	951.470	1052.518	1149.571	1264.598	1431.596	1502.633	
z	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	158.092	257.161	372.188	501.230	572.267	739.266	854.293	951.346	1052.393	1139.425	1276.484	1436.515	1564.573	
z+1	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	159.100	258.169	373.196	502.238	573.275	740.274	855.301	952.353	1053.401	1140.433	1277.492	1437.523	1565.581	
z+2	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	160.108	259.176	374.203	503.246	574.283	741.281	856.308	953.361	1054.409	1141.441	1278.500	1438.530	1566.589	
	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Val	Asp	Glu	Ala	Ser	Asp	Pro	Thr	Ser	His	Cys	Gln	



Sequence: VLHAQCHSTPDSAEDVRK (Peptide Mods: 12: Phospho (ST) 6: Carbamidomethyl (C))

Masses:

MH+(mono): 2129.943

MH+(avg): 2131.206

MS/MS Tol: 0.500 Da

Peaks: 108

Above Threshold: 108

● Monoisotopic ○ Average

Calculate: Masses

Threshold: 0.000

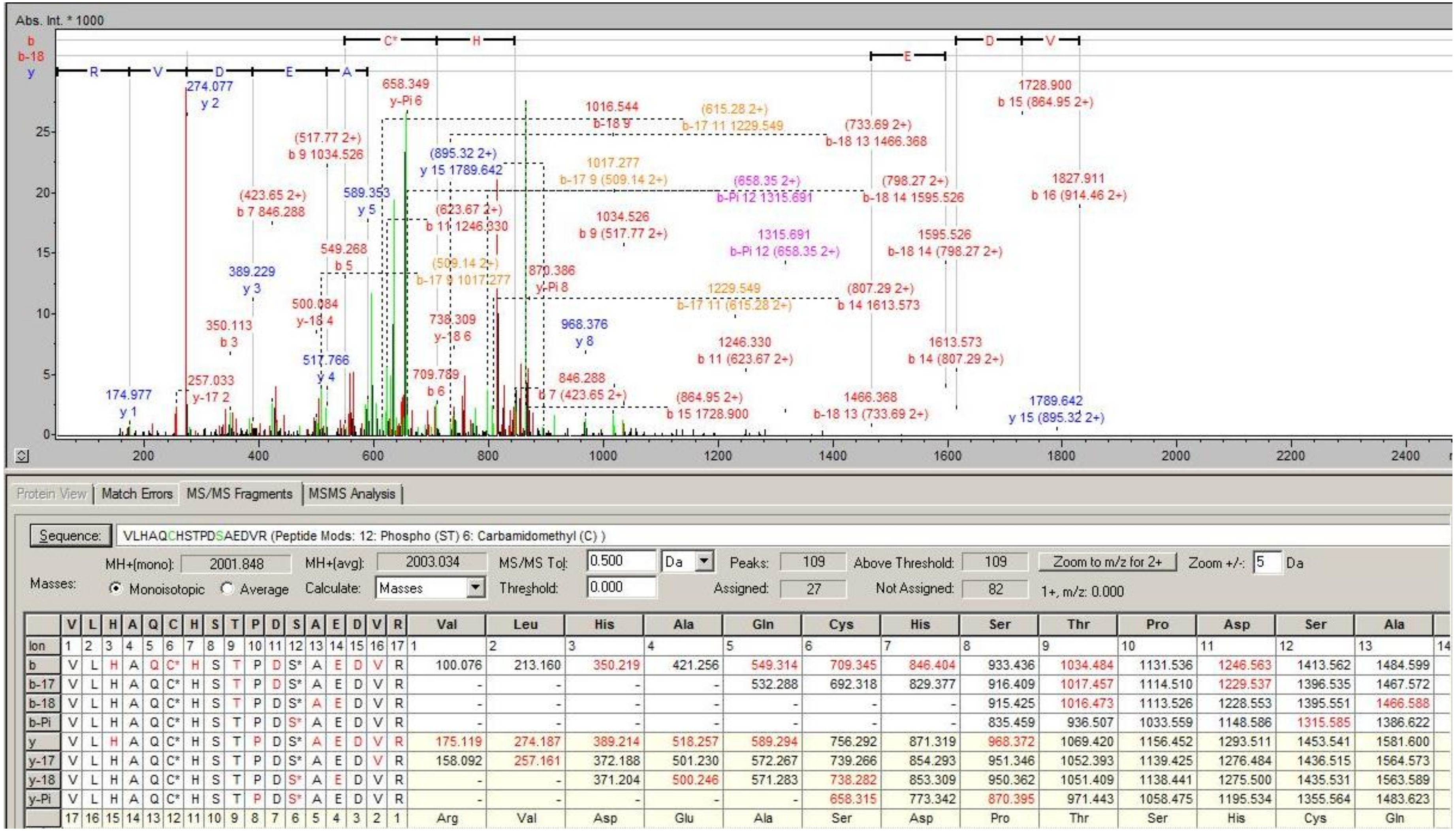
Assigned: 35

Not Assigned: 73

1+, m/z: 0.000

Zoom +/-: 5 Da

	V	L	H	A	Q	C	H	S	T	P	D	S	A	E	D	V	R	K	Val	Leu	His	Ala	Gln	Cys	His	Ser	Thr	Pro	Asp	Ser	Ala
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	1	2	3	4	5	6	7	8	9	10	11	12	13
c	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	K	117.102	230.186	367.245	438.282	566.341	726.372	863.430	950.462	1051.510	1148.563	1263.590	1430.588	1501.625
c+1	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	K	118.110	231.194	368.253	439.290	567.349	727.379	864.438	951.470	1052.518	1149.571	1264.598	1431.596	1502.633
z	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	K	130.086	286.187	385.256	500.283	629.325	700.362	867.361	982.388	1079.440	1180.488	1267.520	1404.579	1564.610
z+1	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	K	131.094	287.195	386.264	501.291	630.333	701.370	868.369	983.396	1080.448	1181.496	1268.528	1405.587	1565.618
z+2	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	K	132.102	288.203	387.271	502.298	631.341	702.378	869.376	984.403	1081.456	1182.504	1269.536	1406.595	1566.625
	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Arg	Val	Asp	Glu	Ala	Ser	Asp	Pro	Thr	Ser	His	Cys

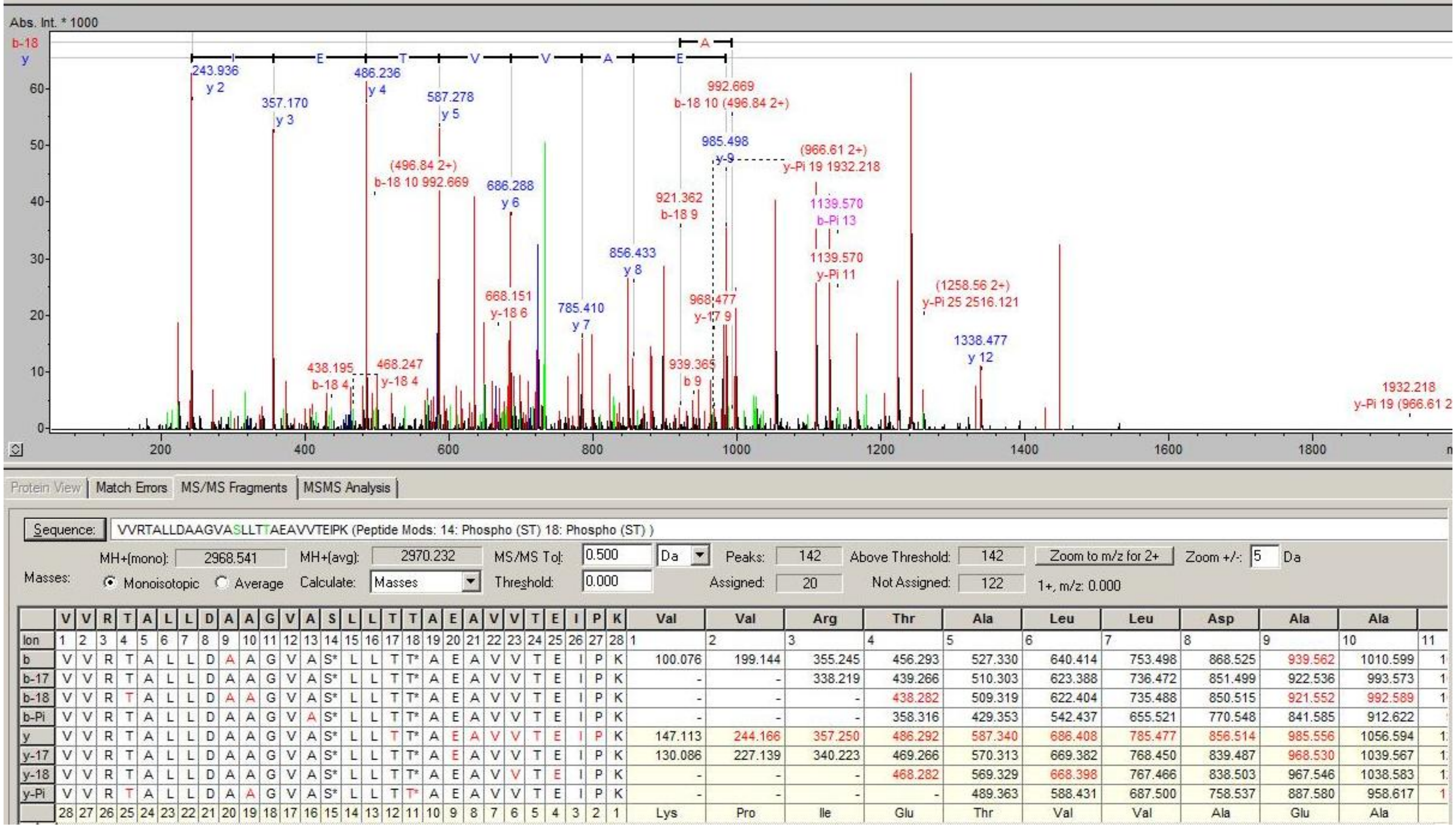


Sequence: VLHAQCHSTPDSAEDVR (Peptide Mods: 12: Phospho (ST) 6: Carbamidomethyl (C))

MH+(mono): 2001.848
MH+(avg): 2003.034
MS/MS Tol: 0.500 Da
Peaks: 109
Above Threshold: 109
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 27
Not Assigned: 82
1+, m/z: 0.000

	V	L	H	A	Q	C	H	S	T	P	D	S	A	E	D	V	R	Val	Leu	His	Ala	Gln	Cys	His	Ser	Thr	Pro	Asp	Ser	Ala	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	100.076	213.160	350.219	421.256	549.314	709.345	846.404	933.436	1034.484	1131.536	1246.563	1413.562	1484.599	
b-17	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	-	-	-	-	532.288	692.318	829.377	916.409	1017.457	1114.510	1229.537	1396.535	1467.572	
b-18	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	-	-	-	-	-	-	-	915.425	1016.473	1113.526	1228.553	1395.551	1466.588	
b-Pi	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	-	-	-	-	-	-	-	835.459	936.507	1033.559	1148.586	1315.585	1386.622	
y	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	175.119	274.187	389.214	518.257	589.294	756.292	871.319	968.372	1069.420	1156.452	1293.511	1453.541	1581.600	
y-17	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	158.092	257.161	372.188	501.230	572.267	739.266	854.293	951.346	1052.393	1139.425	1276.484	1436.515	1564.573	
y-18	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	-	-	371.204	500.246	571.283	738.282	853.309	950.362	1051.409	1138.441	1275.500	1435.531	1563.589	
y-Pi	V	L	H	A	Q	C*	H	S	T	P	D	S*	A	E	D	V	R	-	-	-	-	-	658.315	773.342	870.395	971.443	1058.475	1195.534	1355.564	1483.623	
	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Val	Asp	Glu	Ala	Ser	Asp	Pro	Thr	Ser	His	Cys	Gln	

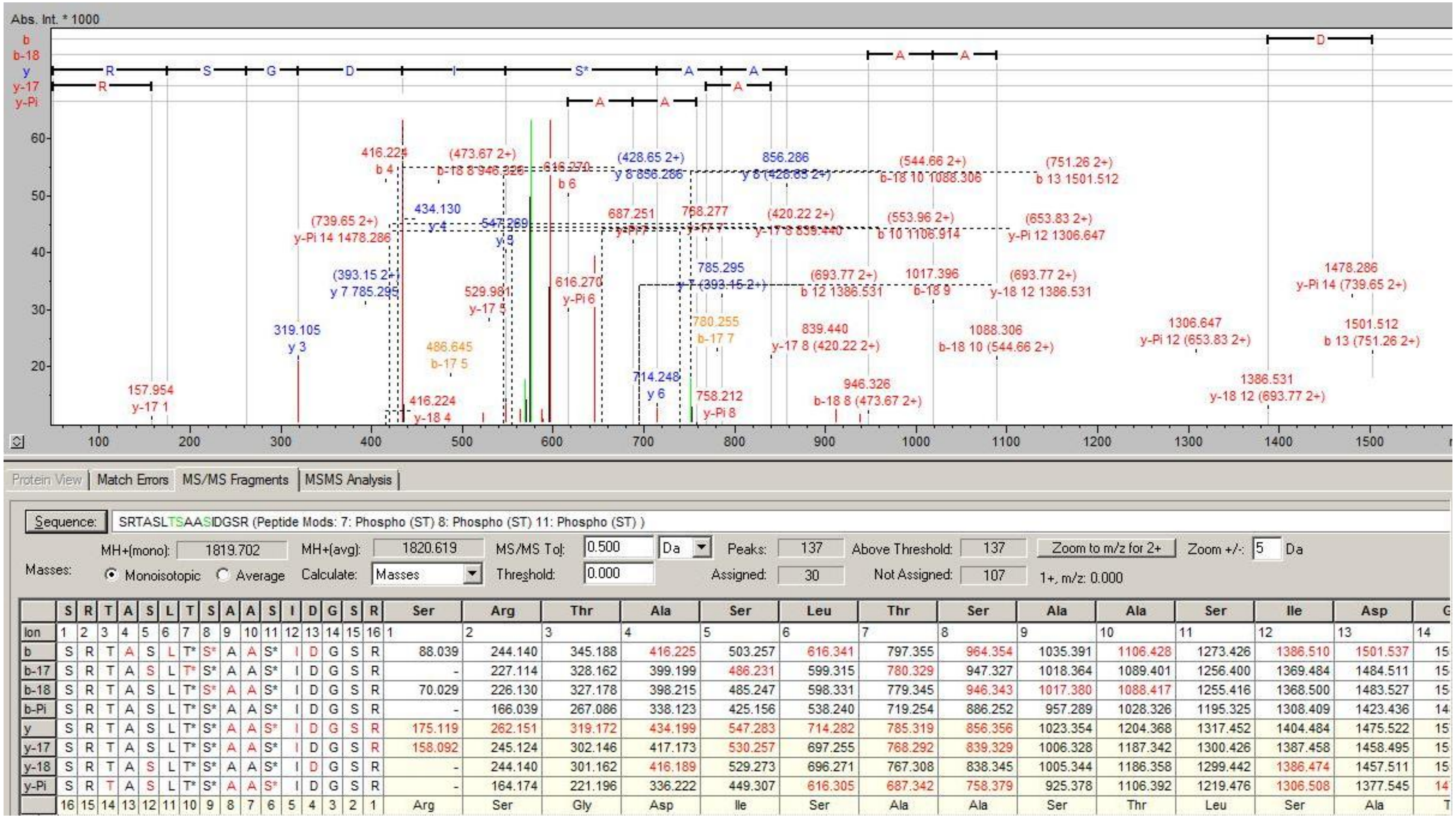


Sequence: VVRTALLDAAGVASLLTTAEAVVTEIPK (Peptide Mods: 14: Phospho (ST) 18: Phospho (ST))

Masses: MH+(mono): 2968.541 MH+(avg): 2970.232 MS/MS Tol: 0.500 Da Peaks: 142 Above Threshold: 142 Zoom +/-: 5 Da

● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 20 Not Assigned: 122 1+, m/z: 0.000

	V	V	R	T	A	L	L	D	A	A	G	V	A	S	L	L	T	T	A	E	A	V	V	T	E	I	P	K	Val	Val	Arg	Thr	Ala	Leu	Leu	Asp	Ala	Ala	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	1	2	3	4	5	6	7	8	9	10	11
b	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	100.076	199.144	355.245	456.293	527.330	640.414	753.498	868.525	939.562	1010.599	1
b-17	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	-	-	338.219	439.266	510.303	623.388	736.472	851.499	922.536	993.573	1
b-18	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	-	-	-	438.282	509.319	622.404	735.488	850.515	921.552	992.589	1
b-Pi	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	-	-	-	358.316	429.353	542.437	655.521	770.548	841.585	912.622	
y	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	147.113	244.166	357.250	486.292	587.340	686.408	785.477	856.514	985.556	1056.594	1
y-17	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	130.086	227.139	340.223	469.266	570.313	669.382	768.450	839.487	968.530	1039.567	1
y-18	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	-	-	-	468.282	569.329	668.398	767.466	838.503	967.546	1038.583	1
y-Pi	V	V	R	T	A	L	L	D	A	A	G	V	A	S*	L	L	T	T*	A	E	A	V	V	T	E	I	P	K	-	-	-	-	489.363	588.431	687.500	758.537	887.580	958.617	1
	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Pro	Ile	Glu	Thr	Val	Val	Ala	Glu	Ala	

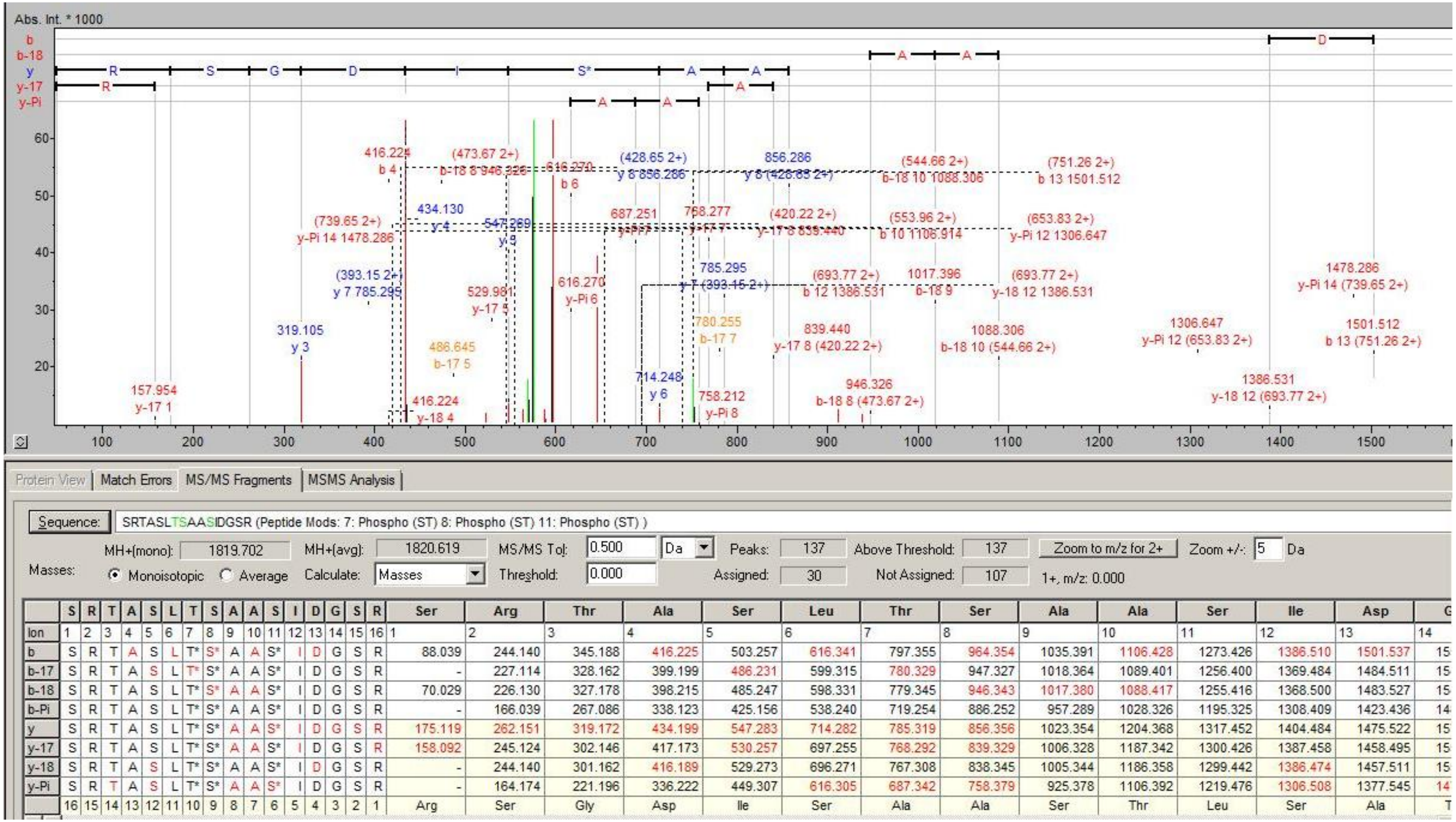


SRTASLTSAASIDGSR (Peptide Mods: 7: Phospho (ST) 8: Phospho (ST) 11: Phospho (ST))

Masses: MH+(mono): 1819.702 MH+(avg): 1820.619 MS/MS Tol: 0.500 Da Peaks: 137 Above Threshold: 137 Zoom +/-: 5 Da

● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 30 Not Assigned: 107 1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	88.039	244.140	345.188	416.225	503.257	616.341	797.355	964.354	1035.391	1106.428	1273.426	1386.510	1501.537	15
b-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	227.114	328.162	399.199	486.231	599.315	780.329	947.327	1018.364	1089.401	1256.400	1369.484	1484.511	15
b-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	70.029	226.130	327.178	398.215	485.247	598.331	779.345	946.343	1017.380	1088.417	1255.416	1368.500	1483.527	15
b-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	166.039	267.086	338.123	425.156	538.240	719.254	886.252	957.289	1028.326	1195.325	1308.409	1423.436	14
y	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	1023.354	1204.368	1317.452	1404.484	1475.522	15
y-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	1006.328	1187.342	1300.426	1387.458	1458.495	15
y-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	1005.344	1186.358	1299.442	1386.474	1457.511	15
y-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	925.378	1106.392	1219.476	1306.508	1377.545	14
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T

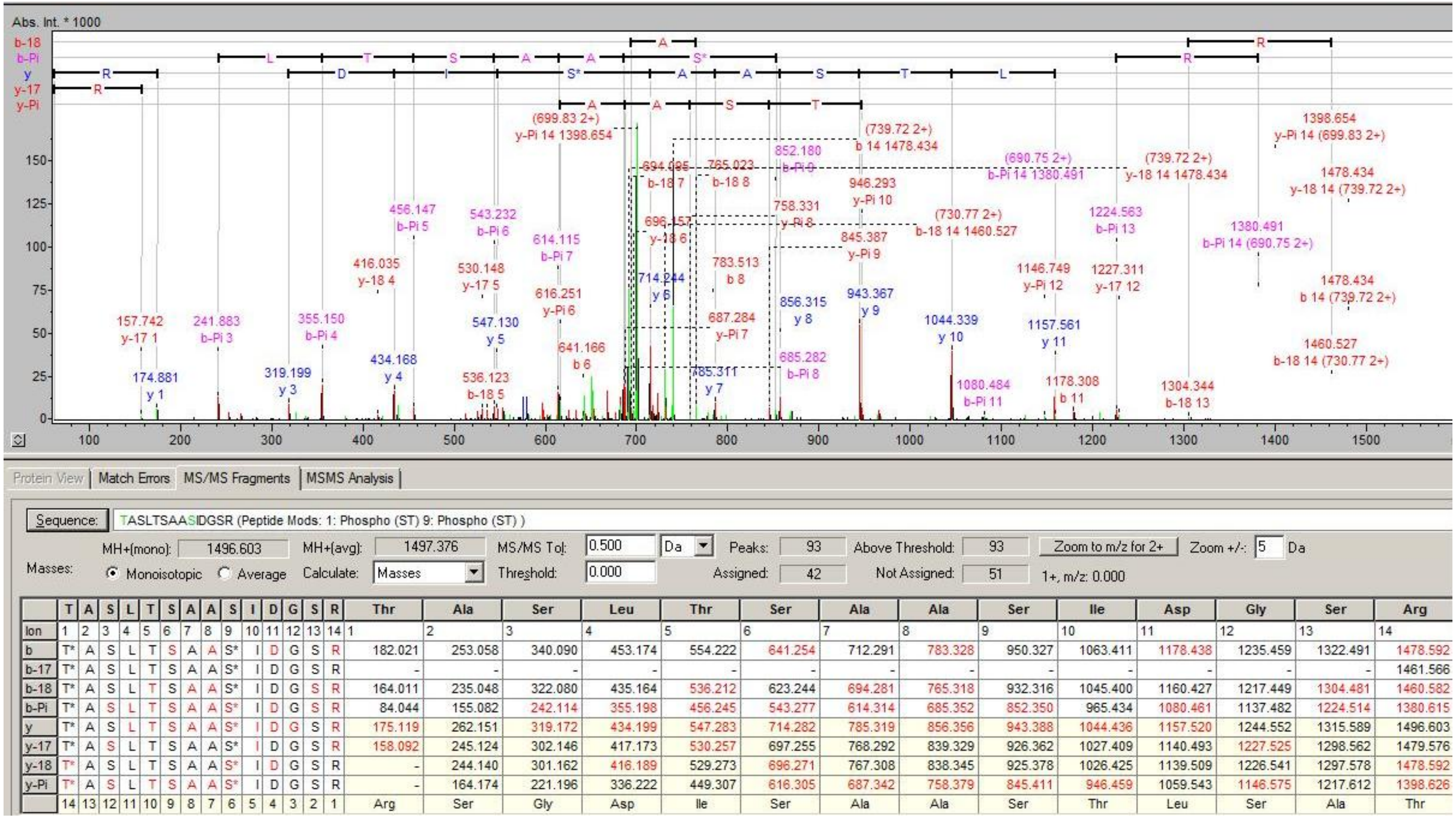


SRTASLTSAASIDGSR (Peptide Mods: 7: Phospho (ST) 8: Phospho (ST) 11: Phospho (ST))

MH+(mono): 1819.702
MH+(avg): 1820.619
MS/MS Tol: 0.500 Da
Peaks: 137
Above Threshold: 137
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 30
Not Assigned: 107
1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	88.039	244.140	345.188	416.225	503.257	616.341	797.355	964.354	1035.391	1106.428	1273.426	1386.510	1501.537	15
b-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	227.114	328.162	399.199	486.231	599.315	780.329	947.327	1018.364	1089.401	1256.400	1369.484	1484.511	15
b-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	70.029	226.130	327.178	398.215	485.247	598.331	779.345	946.343	1017.380	1088.417	1255.416	1368.500	1483.527	15
b-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	166.039	267.086	338.123	425.156	538.240	719.254	886.252	957.289	1028.326	1195.325	1308.409	1423.436	14
y	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	1023.354	1204.368	1317.452	1404.484	1475.522	15
y-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	1006.328	1187.342	1300.426	1387.458	1458.495	15
y-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	1005.344	1186.358	1299.442	1386.474	1457.511	15
y-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	925.378	1106.392	1219.476	1306.508	1377.545	14
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T



Sequence: TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 9: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1496.603

MH+(avg): 1497.376

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 93

Above Threshold: 93

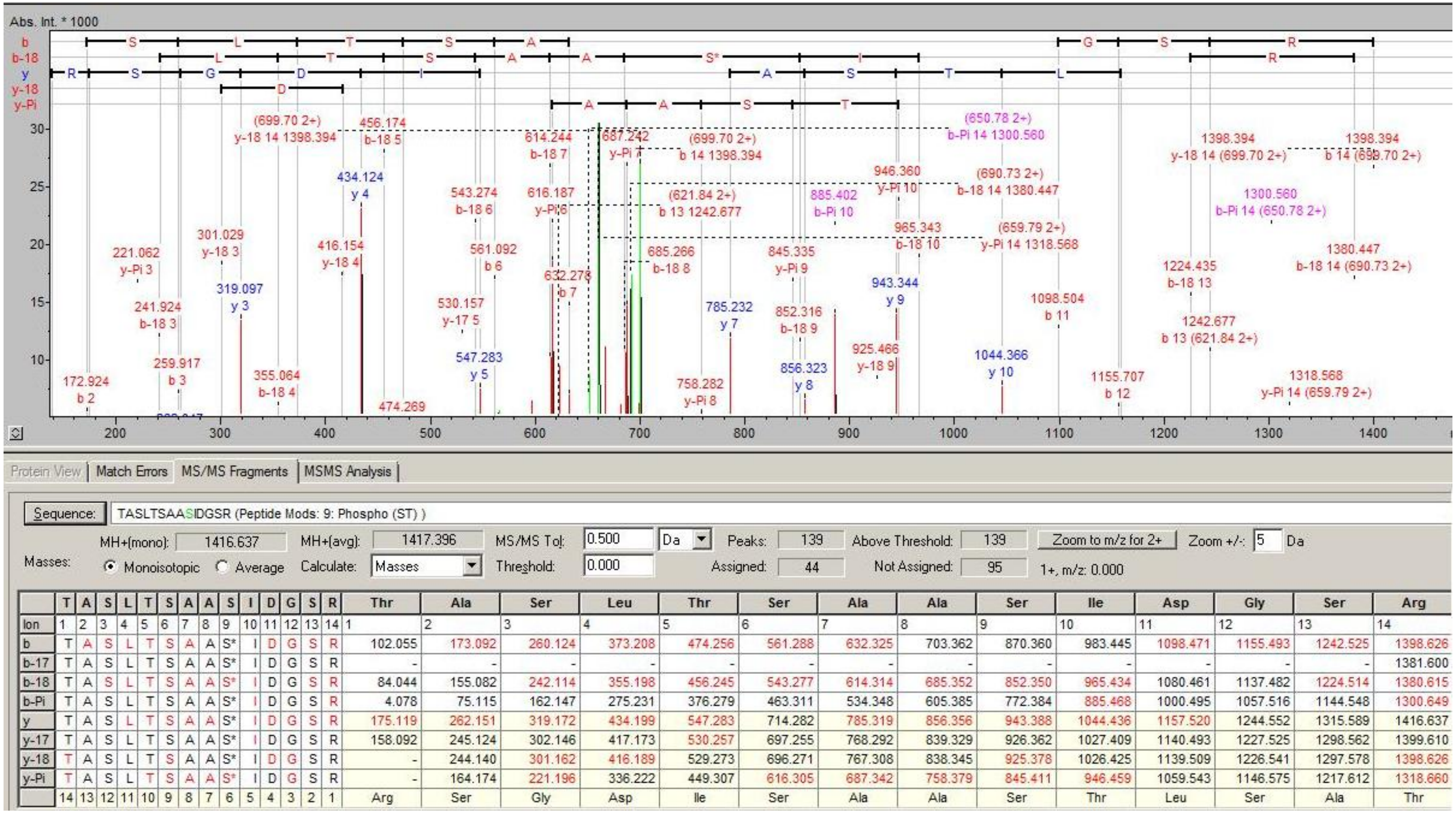
Assigned: 42

Not Assigned: 51

Zoom +/-: 5 Da

1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	182.021	253.058	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	164.011	235.048	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1496.603
y-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1479.576
y-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1478.592
y-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

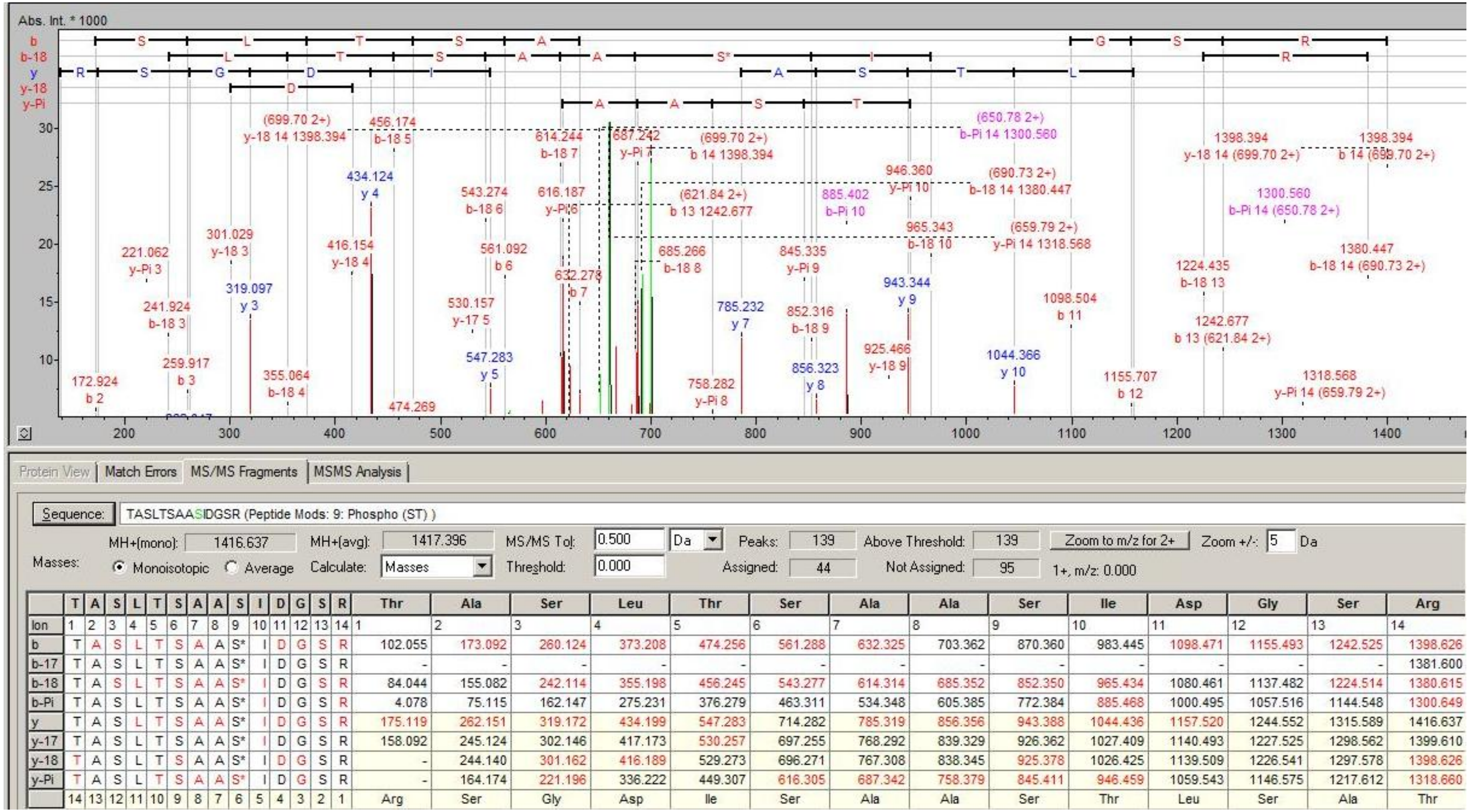


Sequence: TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

Masses: MH+(mono): 1416.637 MH+(avg): 1417.396 MS/MS Tol: 0.500 Da Peaks: 139 Above Threshold: 139 Zoom to m/z for 2+ Zoom +/-: 5 Da

● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 44 Not Assigned: 95 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



Sequence: TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

MH+(mono): 1416.637

MH+(avg): 1417.396

MS/MS Tol: 0.500 Da

Peaks: 139

Above Threshold: 139

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

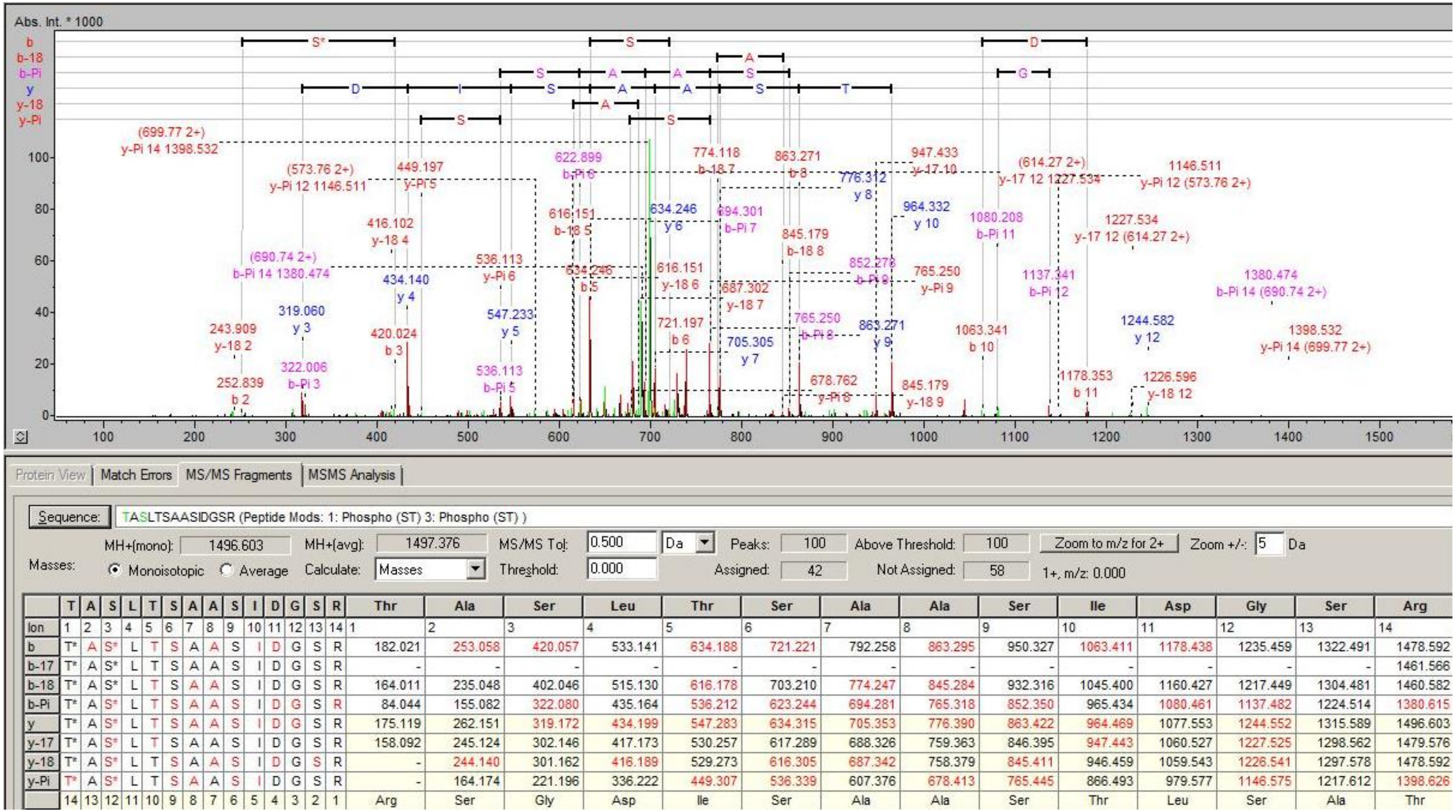
Threshold: 0.000

Assigned: 44

Not Assigned: 95

1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

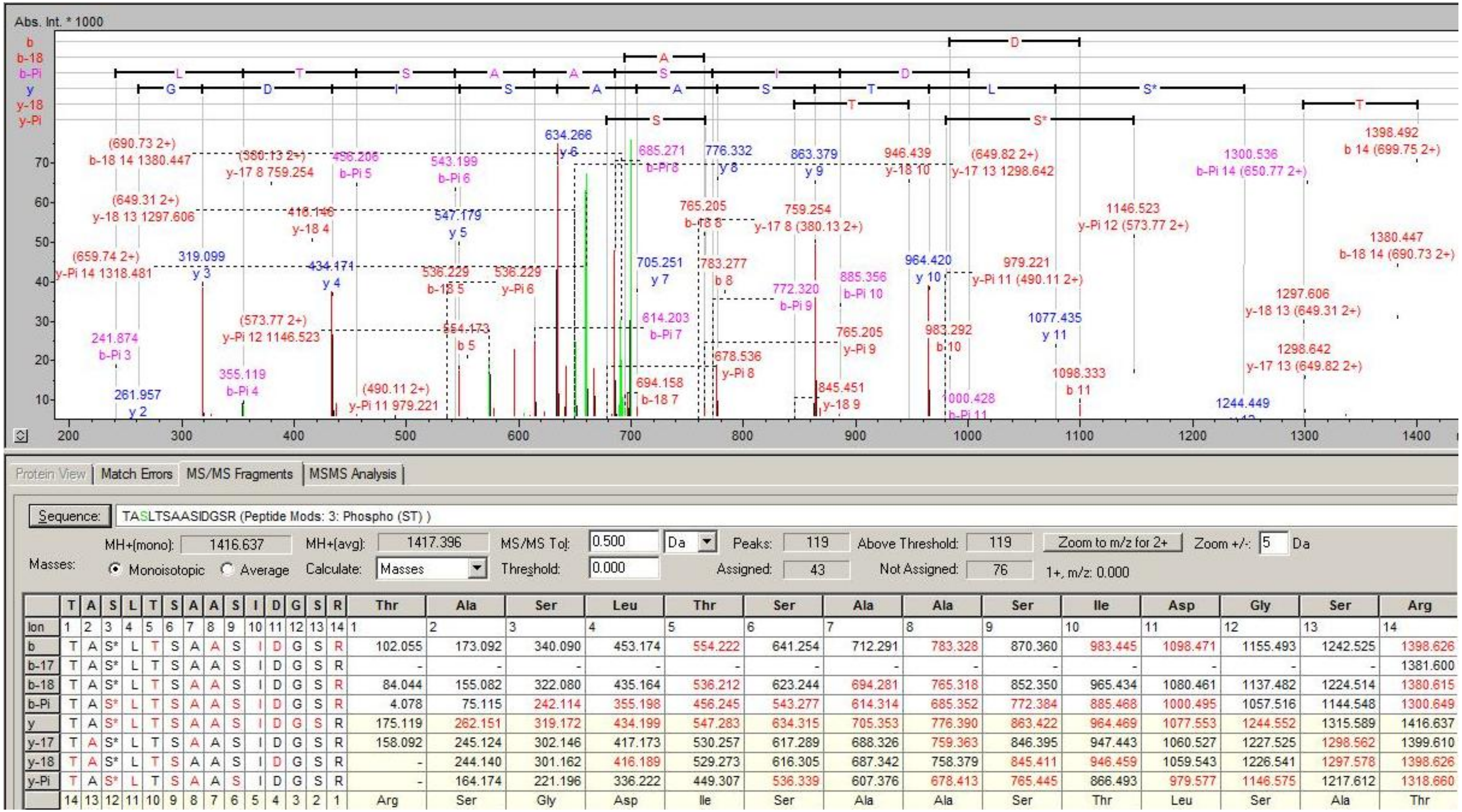


TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 3: Phospho (ST))

MH+(mono): 1496.603
MH+(avg): 1497.376
MS/MS Tol: 0.500 Da
Peaks: 100
Above Threshold: 100
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 42
Not Assigned: 58
1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	182.021	253.058	420.057	533.141	634.188	721.221	792.258	863.295	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	164.011	235.048	402.046	515.130	616.178	703.210	774.247	845.284	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1244.552	1315.589	1496.603
y-17	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1479.576
y-18	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1478.592
y-Pi	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



Sequence: TASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1416.637

MH+(avg): 1417.396

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 119

Above Threshold: 119

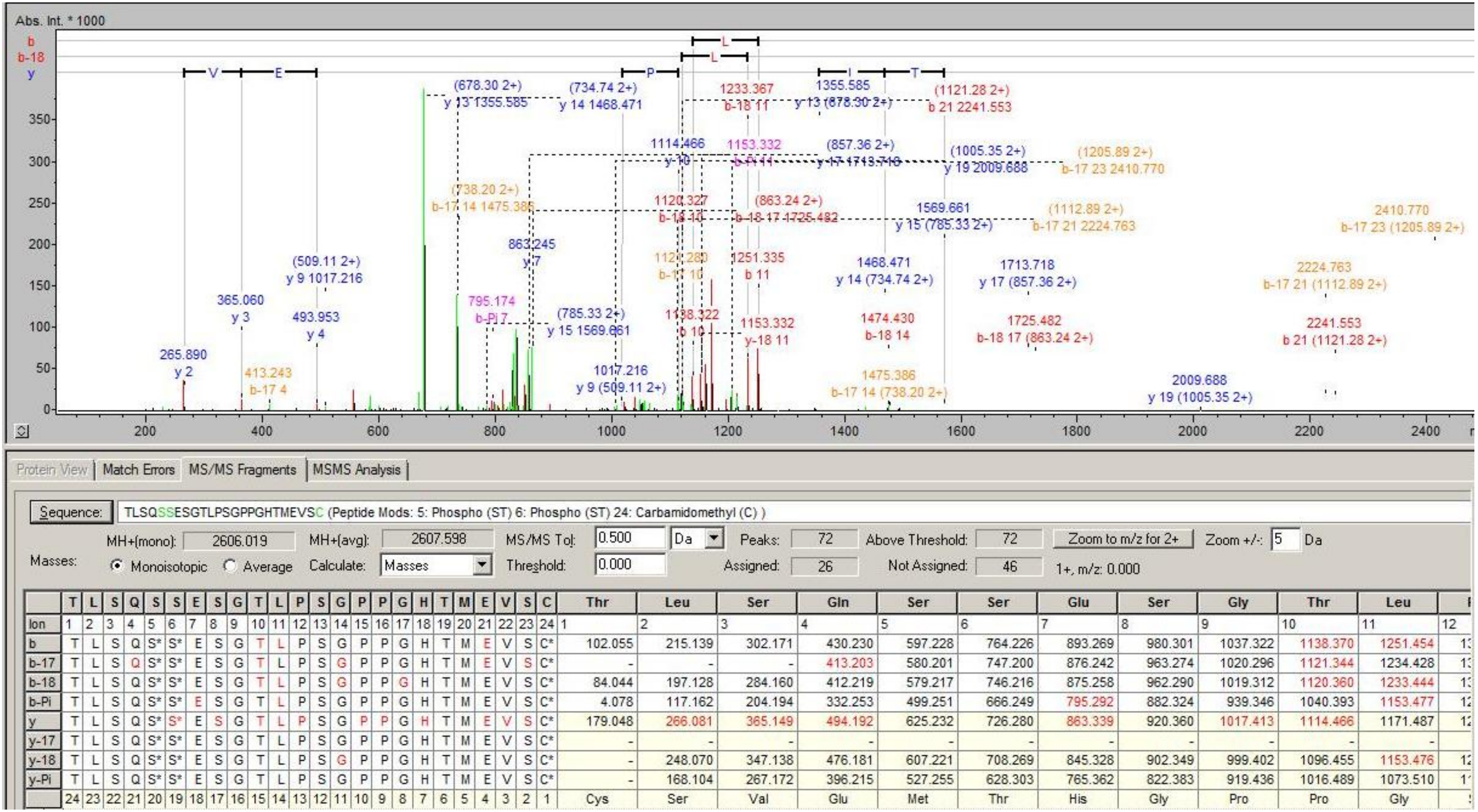
Assigned: 43

Not Assigned: 76

Zoom +/-: 5 Da

1+, m/z: 0.000

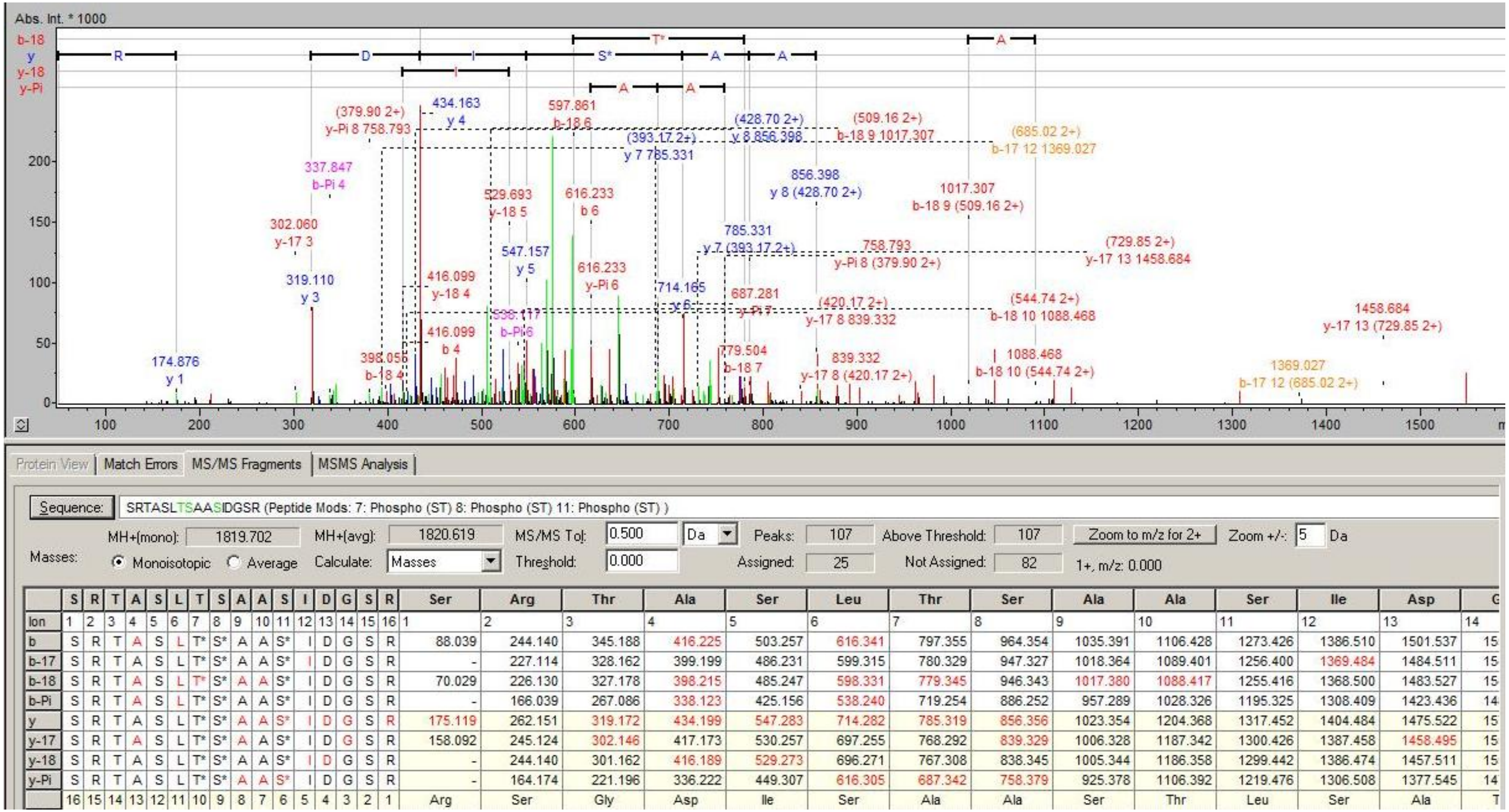
	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	102.055	173.092	340.090	453.174	554.222	641.254	712.291	783.328	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	4.078	75.115	242.114	355.198	456.245	543.277	614.314	685.352	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1244.552	1315.589	1416.637
y-17	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1399.610
y-18	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1398.626
y-Pi	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



Sequence: TLSQSSESGTLPSGPPGHTMEVSC (Peptide Mods: 5: Phospho (ST) 6: Phospho (ST) 24: Carbamidomethyl (C))

MH+(mono): 2606.019
MH+(avg): 2607.598
MS/MS Tol: 0.500 Da
Peaks: 72
Above Threshold: 72
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 26
Not Assigned: 46
Zoom +/-: 5 Da
1+, m/z: 0.000

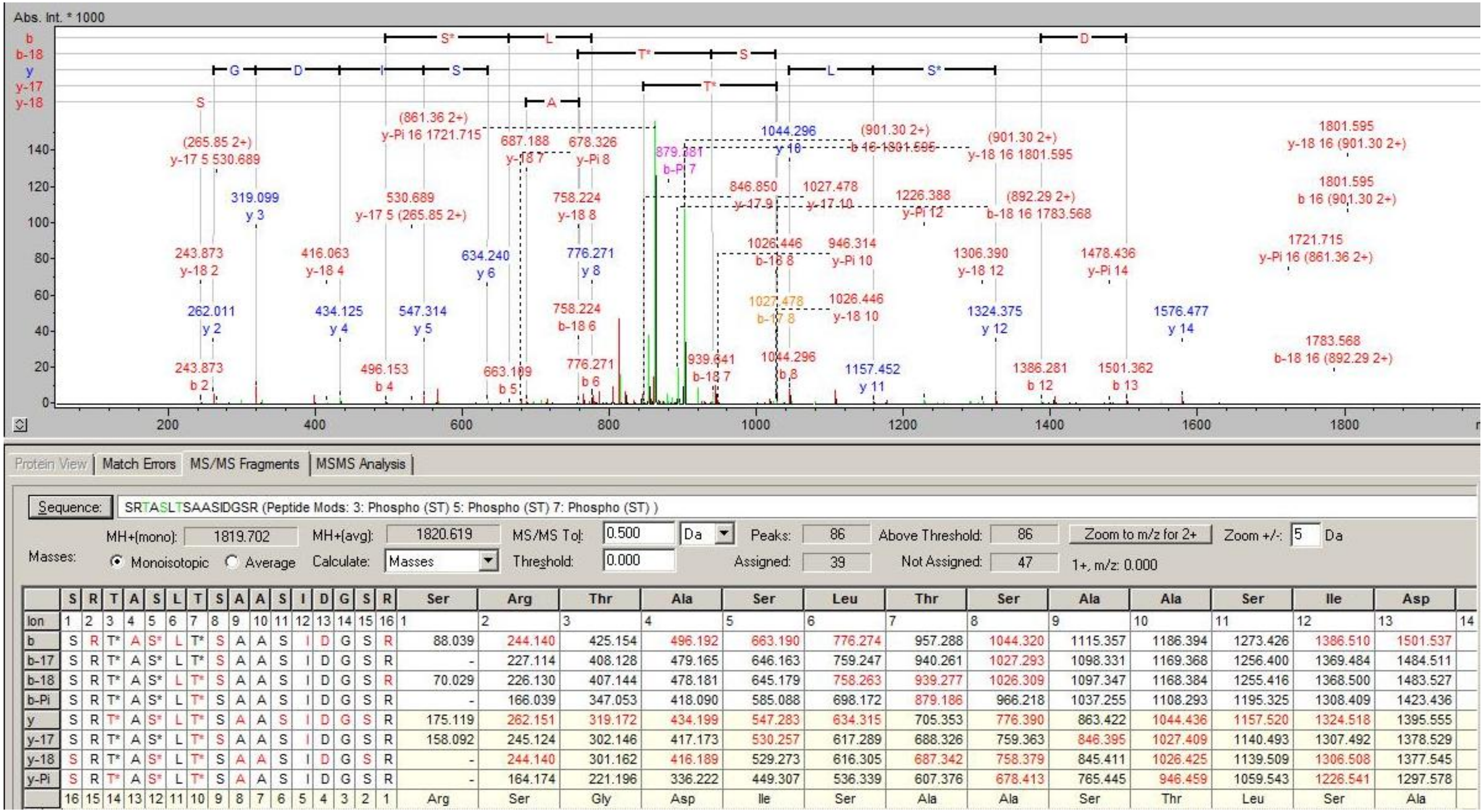
	T	L	S	Q	S	S	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C	Thr	Leu	Ser	Gln	Ser	Ser	Glu	Ser	Gly	Thr	Leu
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	1	2	3	4	5	6	7	8	9	10	11
b	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	102.055	215.139	302.171	430.230	597.228	764.226	893.269	980.301	1037.322	1138.370	1251.454
b-17	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	-	-	-	413.203	580.201	747.200	876.242	963.274	1020.296	1121.344	1234.428
b-18	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	84.044	197.128	284.160	412.219	579.217	746.216	875.258	962.290	1019.312	1120.360	1233.444
b-Pi	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	4.078	117.162	204.194	332.253	499.251	666.249	795.292	882.324	939.346	1040.393	1153.477
y	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	179.048	266.081	365.149	494.192	625.232	726.280	863.339	920.360	1017.413	1114.466	1171.487
y-17	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	-	-	-	-	-	-	-	-	-	-	-
y-18	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	-	248.070	347.138	476.181	607.221	708.269	845.328	902.349	999.402	1096.455	1153.476
y-Pi	T	L	S	Q	S*	S*	E	S	G	T	L	P	S	G	P	P	G	H	T	M	E	V	S	C*	-	168.104	267.172	396.215	527.255	628.303	765.362	822.383	919.436	1016.489	1073.510
	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Cys	Ser	Val	Glu	Met	Thr	His	Gly	Pro	Pro	Gly



SRTASLTSAASIDGSR (Peptide Mods: 7: Phospho (ST) 8: Phospho (ST) 11: Phospho (ST))

MH+(mono): 1819.702
MH+(avg): 1820.619
MS/MS Tol: 0.500 Da
Peaks: 107
Above Threshold: 107
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 25
Not Assigned: 82
1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	88.039	244.140	345.188	416.225	503.257	616.341	797.355	964.354	1035.391	1106.428	1273.426	1386.510	1501.537	15
b-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	227.114	328.162	399.199	486.231	599.315	780.329	947.327	1018.364	1089.401	1256.400	1369.484	1484.511	15
b-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	70.029	226.130	327.178	398.215	485.247	598.331	779.345	946.343	1017.380	1088.417	1255.416	1368.500	1483.527	15
b-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	166.039	267.086	338.123	425.156	538.240	719.254	886.252	957.289	1028.326	1195.325	1308.409	1423.436	14
y	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	1023.354	1204.368	1317.452	1404.484	1475.522	15
y-17	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	1006.328	1187.342	1300.426	1387.458	1458.495	15
y-18	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	1005.344	1186.358	1299.442	1386.474	1457.511	15
y-Pi	S	R	T	A	S	L	T*	S*	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	925.378	1106.392	1219.476	1306.508	1377.545	14
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T



Sequence: SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST) 7: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1819.702

MH+(avg): 1820.619

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 86

Above Threshold: 86

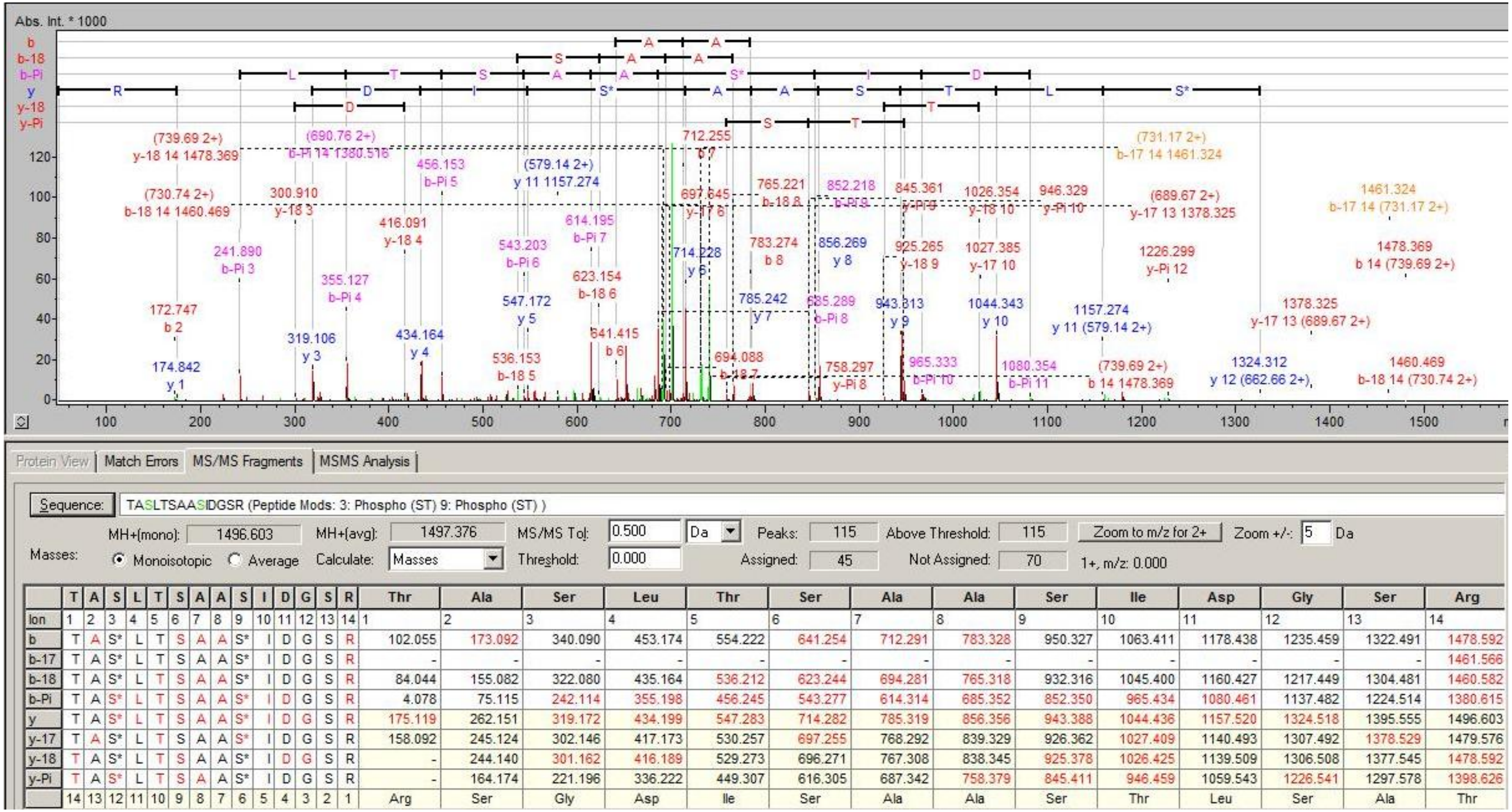
Assigned: 39

Not Assigned: 47

Zoom +/-: 5 Da

1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	88.039	244.140	425.154	496.192	663.190	776.274	957.288	1044.320	1115.357	1186.394	1273.426	1386.510	1501.537	
b-17	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	227.114	408.128	479.165	646.163	759.247	940.261	1027.293	1098.331	1169.368	1256.400	1369.484	1484.511	
b-18	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	70.029	226.130	407.144	478.181	645.179	758.263	939.277	1026.309	1097.347	1168.384	1255.416	1368.500	1483.527	
b-Pi	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	166.039	347.053	418.090	585.088	698.172	879.186	966.218	1037.255	1108.293	1195.325	1308.409	1423.436	
y	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	1044.436	1157.520	1324.518	1395.555	
y-17	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	1027.409	1140.493	1307.492	1378.529	
y-18	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	1026.425	1139.509	1306.508	1377.545	
y-Pi	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	946.459	1059.543	1226.541	1297.578	
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	

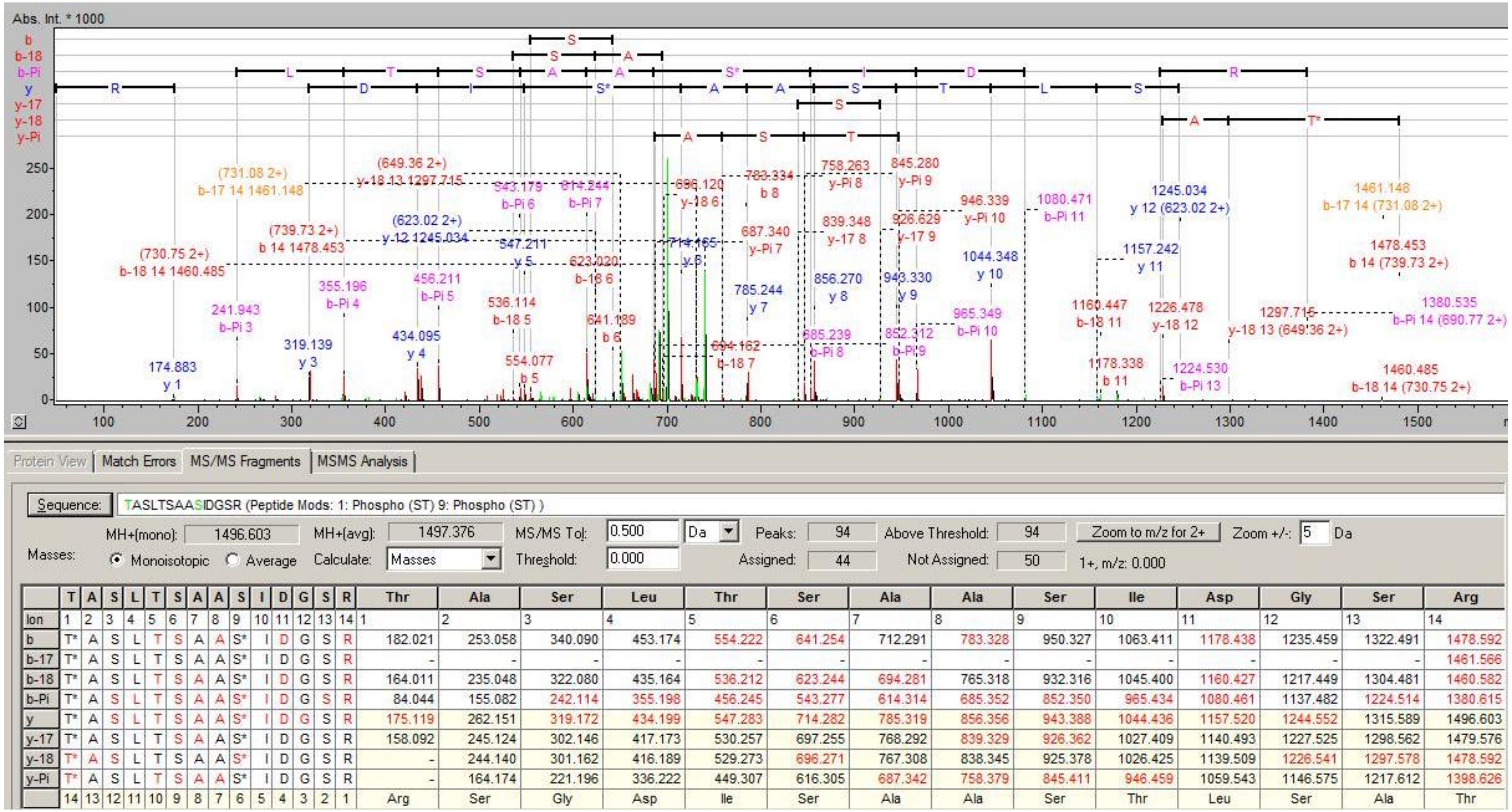


TASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 9: Phospho (ST))

MH+(mono): 1496.603
MH+(avg): 1497.376
MS/MS Tol: 0.500 Da
Peaks: 115
Above Threshold: 115
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 45
Not Assigned: 70
1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1324.518	1395.555	1496.603
y-17	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1307.492	1378.529	1479.576
y-18	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1306.508	1377.545	1478.592
y-Pi	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

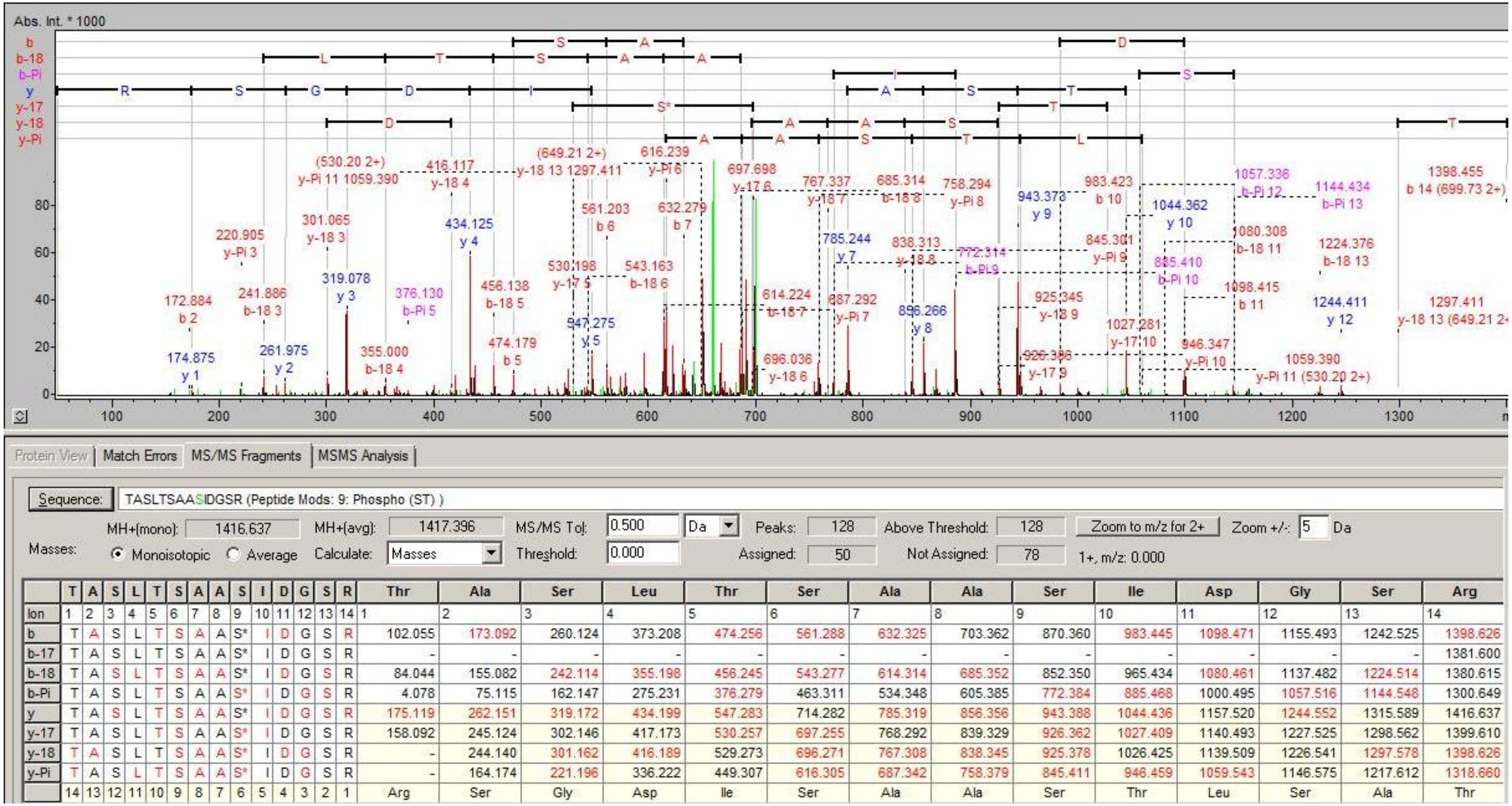


Sequence: TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 9: Phospho (ST))

MH+(mono): 1496.603
MH+(avg): 1497.376
MS/MS Tol: 0.500 Da
Peaks: 94
Above Threshold: 94
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 44
Not Assigned: 50
1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	182.021	253.058	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	164.011	235.048	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1496.603
y-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1479.576
y-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1478.592
y-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

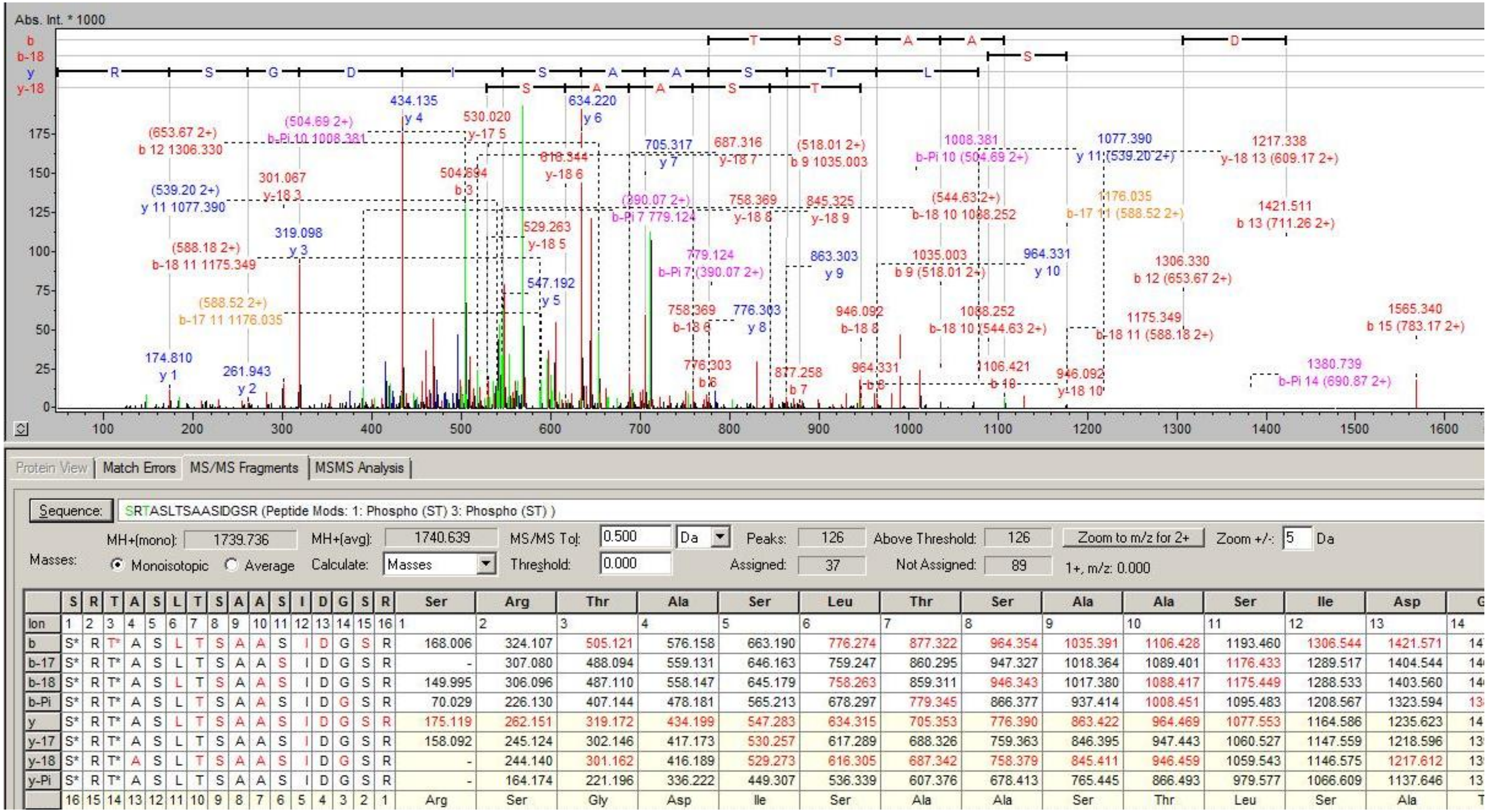


Sequence: TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

MH+(mono): 1416.637
MH+(avg): 1417.396
MS/MS Tol: 0.500 Da
Peaks: 128
Above Threshold: 128
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 50
Not Assigned: 78
1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

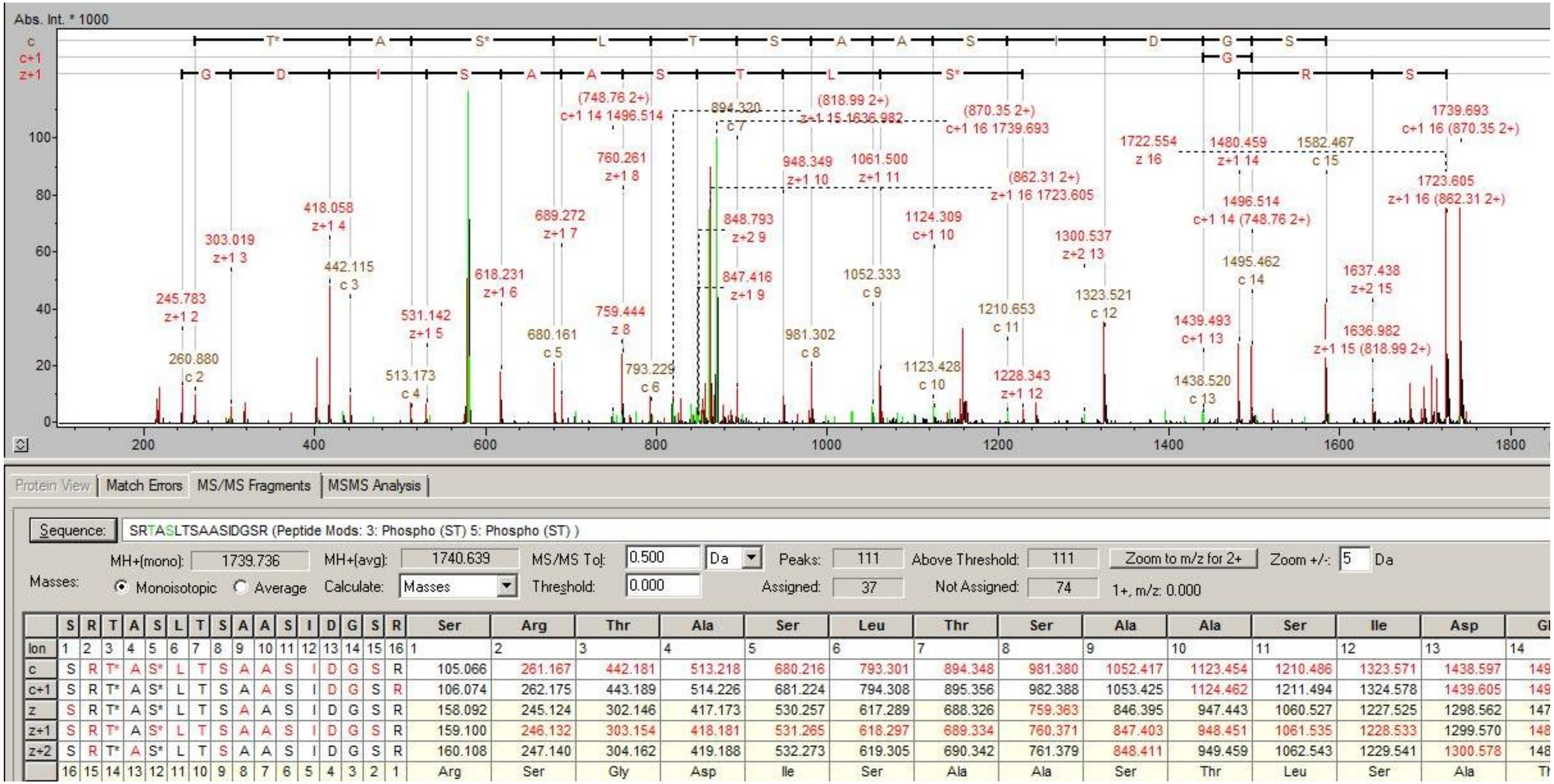


SRTASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 3: Phospho (ST))

MH+(mono): 1739.736 MH+(avg): 1740.639 MS/MS Tol: 0.500 Da Peaks: 126 Above Threshold: 126 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 37 Not Assigned: 89 1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	168.006	324.107	505.121	576.158	663.190	776.274	877.322	964.354	1035.391	1106.428	1193.460	1306.544	1421.571	14
b-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	307.080	488.094	559.131	646.163	759.247	860.295	947.327	1018.364	1089.401	1176.433	1289.517	1404.544	14
b-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	149.995	306.096	487.110	558.147	645.179	758.263	859.311	946.343	1017.380	1088.417	1175.449	1288.533	1403.560	14
b-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	70.029	226.130	407.144	478.181	565.213	678.297	779.345	866.377	937.414	1008.451	1095.483	1208.567	1323.594	13
y	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1164.586	1235.623	14
y-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1147.559	1218.596	13
y-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	13
y-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1066.609	1137.646	13
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T



SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST))

MH+(mono): 1739.736

MH+(avg): 1740.639

MS/MS Tol: 0.500 Da

Peaks: 111

Above Threshold: 111

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

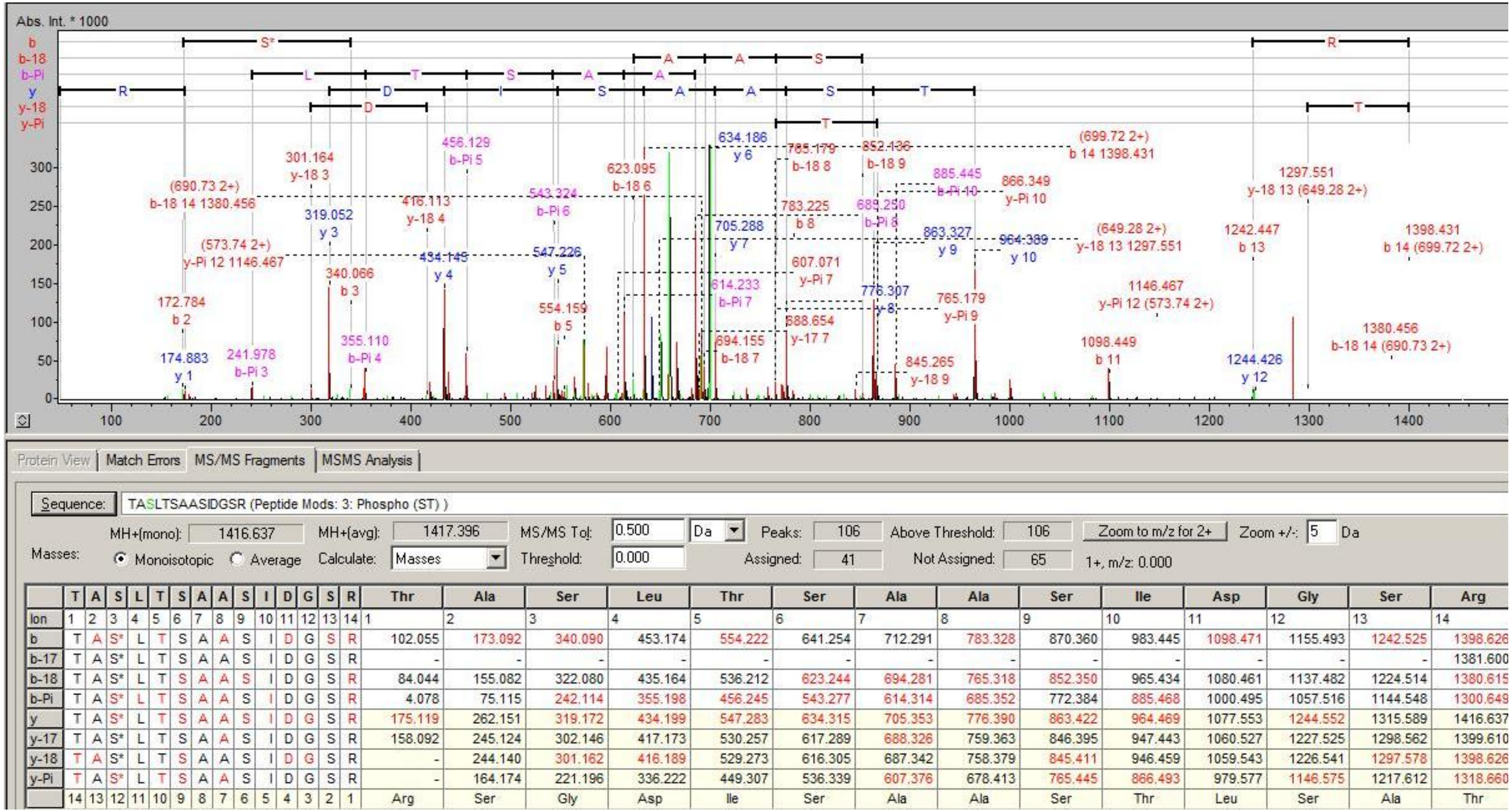
Threshold: 0.000

Assigned: 37

Not Assigned: 74

1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gl
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	105.066	261.167	442.181	513.218	680.216	793.301	894.348	981.380	1052.417	1123.454	1210.486	1323.571	1438.597	149
c+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	106.074	262.175	443.189	514.226	681.224	794.308	895.356	982.388	1053.425	1124.462	1211.494	1324.578	1439.605	149
z	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	147
z+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	159.100	246.132	303.154	418.181	531.265	618.297	689.334	760.371	847.403	948.451	1061.535	1228.533	1299.570	148
z+2	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	160.108	247.140	304.162	419.188	532.273	619.305	690.342	761.379	848.411	949.459	1062.543	1229.541	1300.578	148
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Th

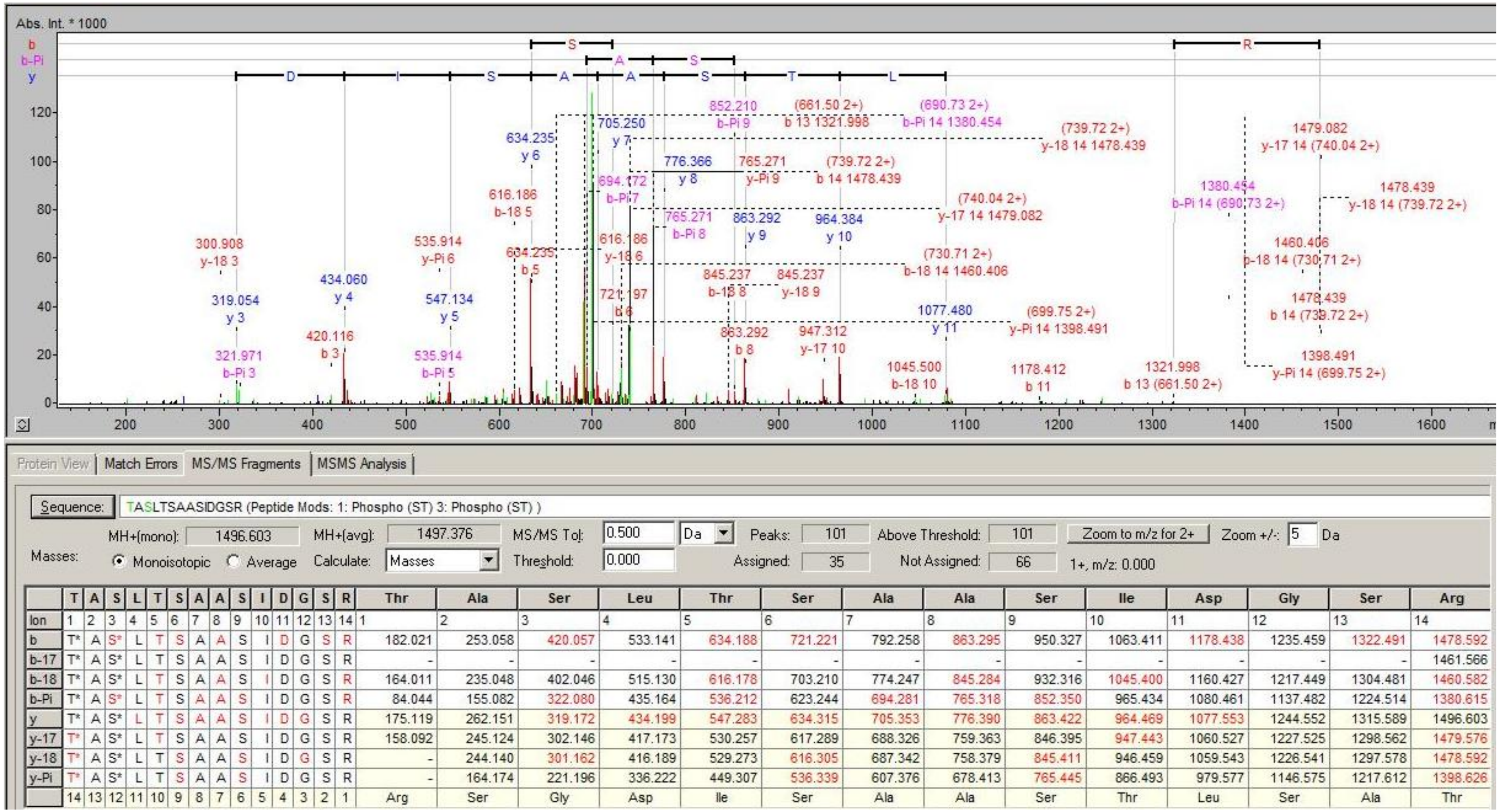


Sequence: TASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1416.637 MH+(avg): 1417.396 MS/MS Tol: 0.500 Da Peaks: 106 Above Threshold: 106 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 41 Not Assigned: 65 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	102.055	173.092	340.090	453.174	554.222	641.254	712.291	783.328	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	4.078	75.115	242.114	355.198	456.245	543.277	614.314	685.352	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1244.552	1315.589	1416.637
y-17	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1399.610
y-18	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1398.626
y-Pi	T	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

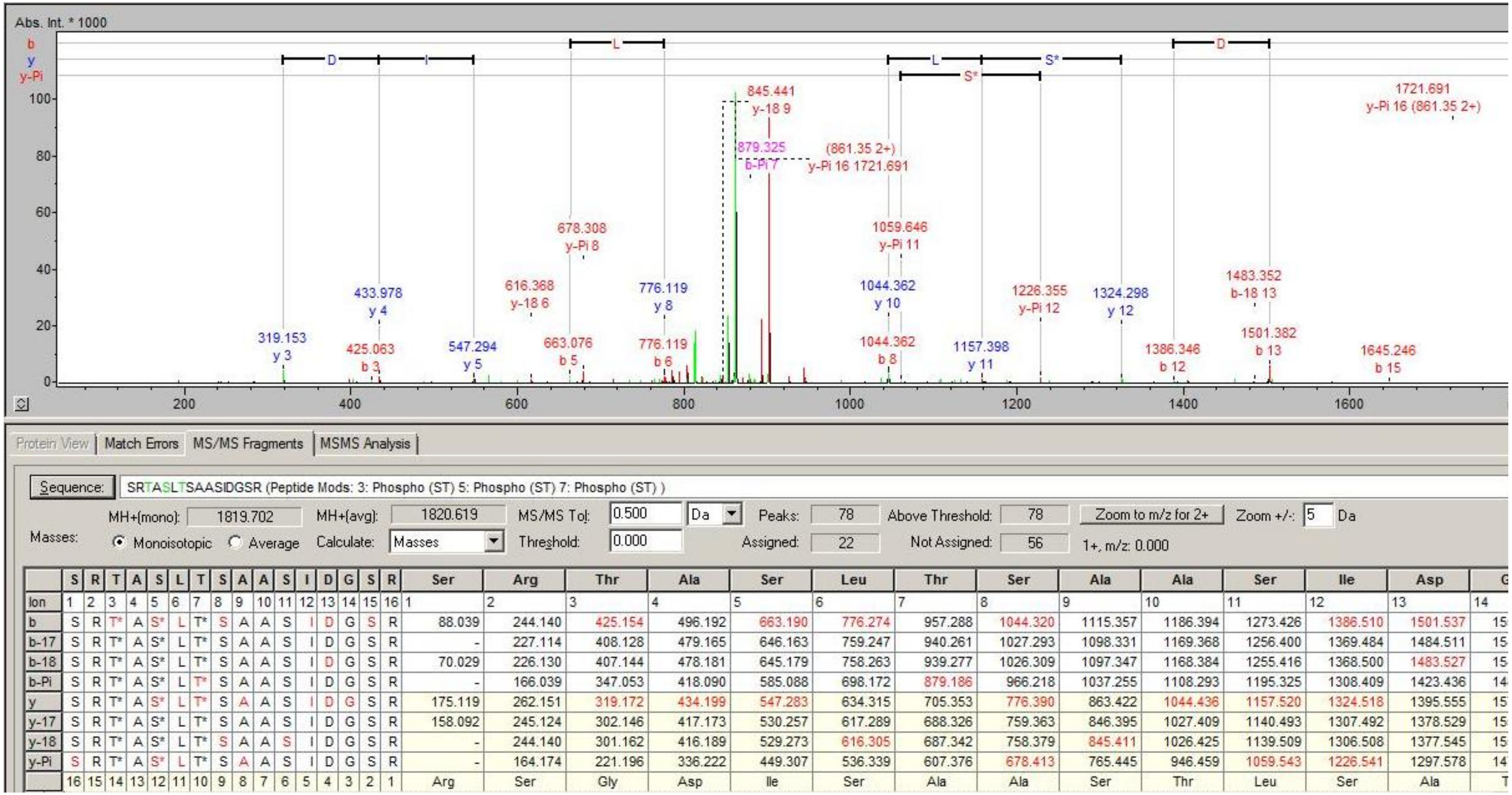


TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 3: Phospho (ST))

MH+(mono): 1496.603 MH+(avg): 1497.376 MS/MS Tol: 0.500 Da Peaks: 101 Above Threshold: 101 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 35 Not Assigned: 66 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	182.021	253.058	420.057	533.141	634.188	721.221	792.258	863.295	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	164.011	235.048	402.046	515.130	616.178	703.210	774.247	845.284	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1244.552	1315.589	1496.603
y-17	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1479.576
y-18	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1478.592
y-Pi	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



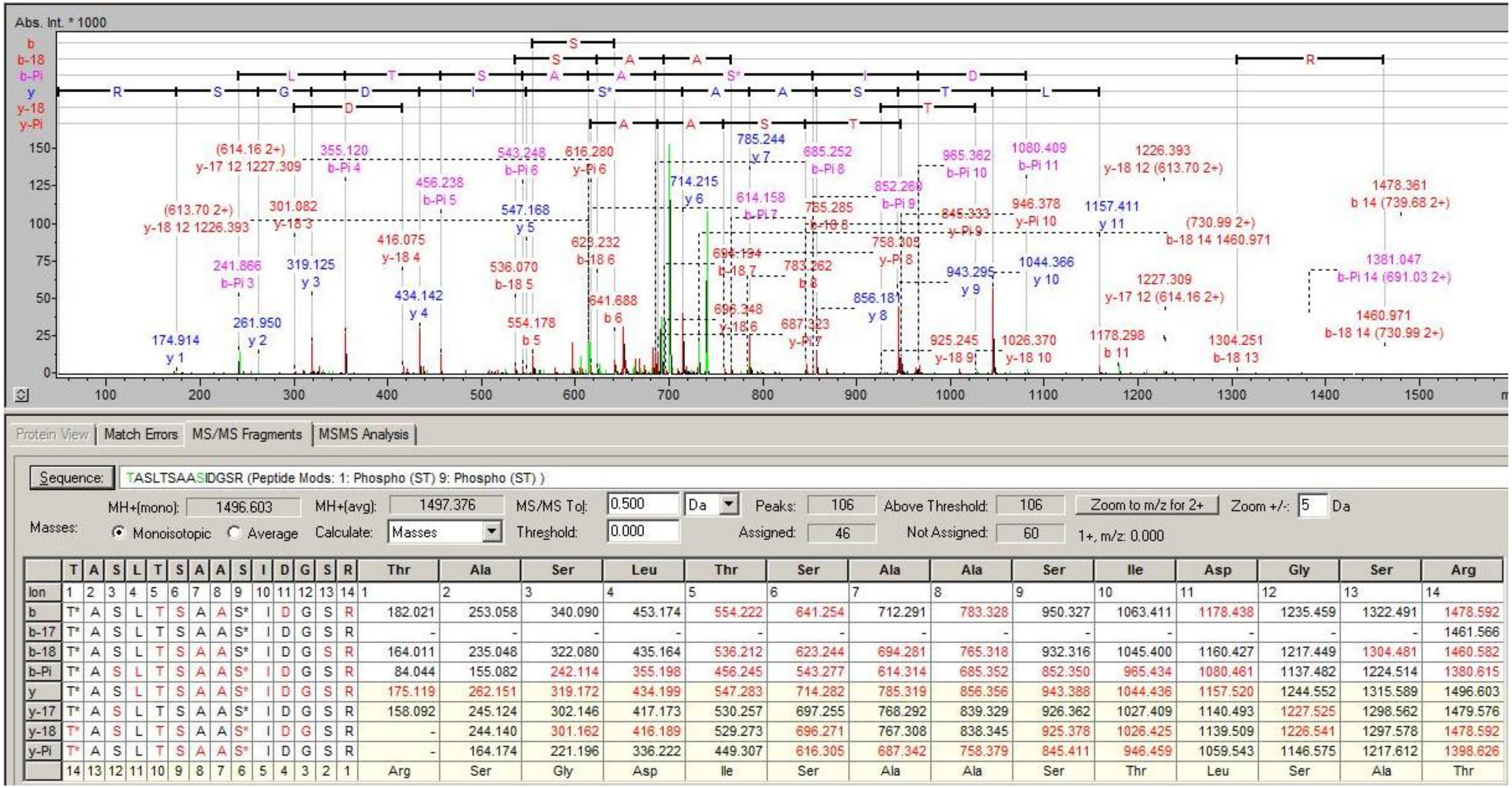
Sequence: SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST) 7: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1819.702 MH+(avg): 1820.619 MS/MS Tol: 0.500 Da Peaks: 78 Above Threshold: 78 Zoom +/-: 5 Da

Calculate: Masses Threshold: 0.000 Assigned: 22 Not Assigned: 56 1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	88.039	244.140	425.154	496.192	663.190	776.274	957.288	1044.320	1115.357	1186.394	1273.426	1386.510	1501.537	15
b-17	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	227.114	408.128	479.165	646.163	759.247	940.261	1027.293	1098.331	1169.368	1256.400	1369.484	1484.511	15
b-18	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	70.029	226.130	407.144	478.181	645.179	758.263	939.277	1026.309	1097.347	1168.384	1255.416	1368.500	1483.527	15
b-Pi	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	166.039	347.053	418.090	585.088	698.172	879.186	966.218	1037.255	1108.293	1195.325	1308.409	1423.436	14
y	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	1044.436	1157.520	1324.518	1395.555	15
y-17	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	1027.409	1140.493	1307.492	1378.529	15
y-18	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	1026.425	1139.509	1306.508	1377.545	15
y-Pi	S	R	T*	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	946.459	1059.543	1226.541	1297.578	14
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T

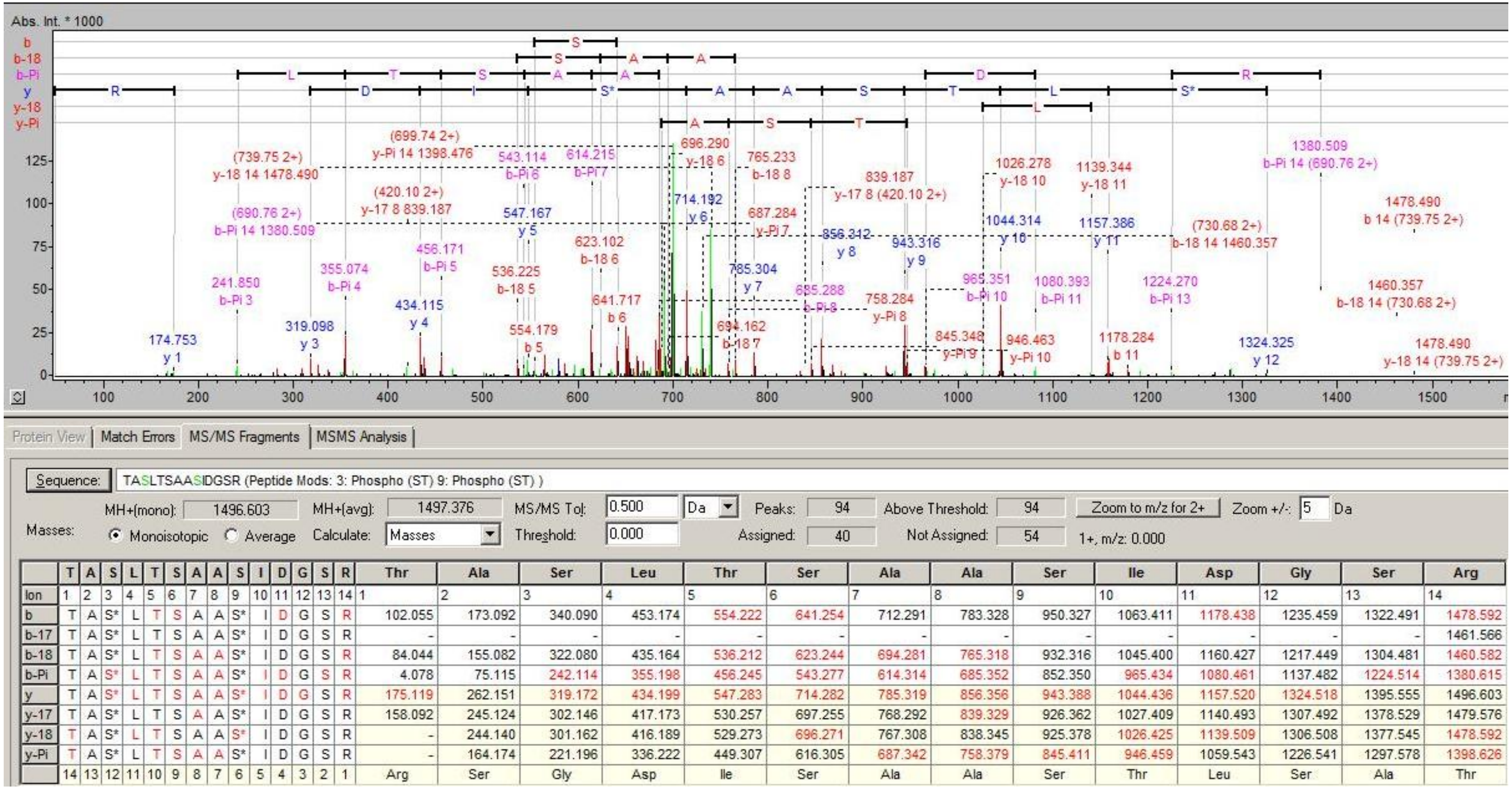


Sequence: TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 9: Phospho (ST))

MH+(mono): 1496.603 MH+(avg): 1497.376 MS/MS Tol: 0.500 Da Peaks: 106 Above Threshold: 106 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 46 Not Assigned: 60 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	182.021	253.058	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	164.011	235.048	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1496.603
y-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1479.576
y-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1478.592
y-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

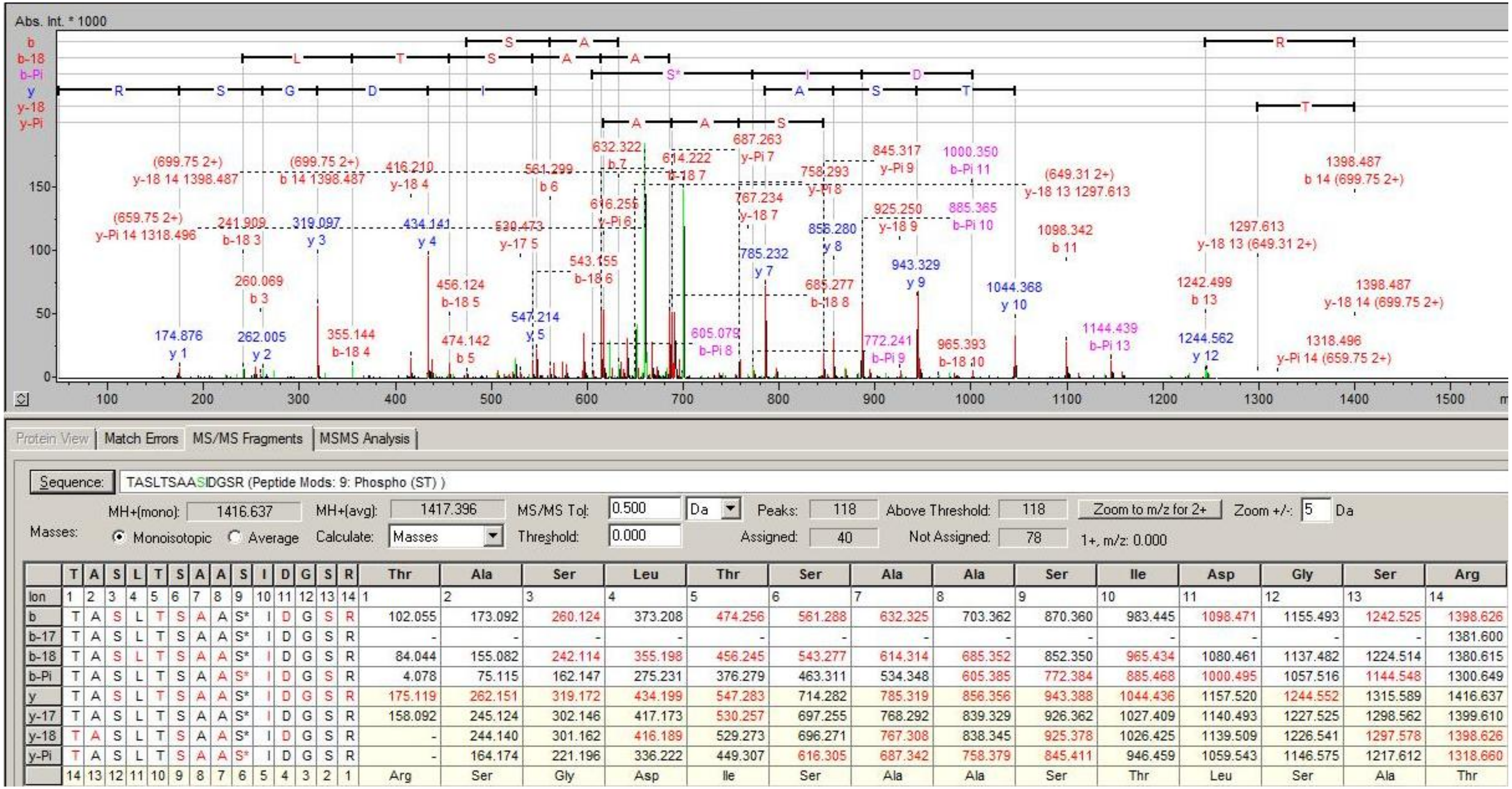


Sequence: TASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 9: Phospho (ST))

MH+(mono): 1496.603 MH+(avg): 1497.376 MS/MS Tol: 0.500 Da Peaks: 94 Above Threshold: 94 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 40 Not Assigned: 54 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1324.518	1395.555	1496.603
y-17	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1307.492	1378.529	1479.576
y-18	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1306.508	1377.545	1478.592
y-Pi	T	A	S*	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1226.541	1297.578	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

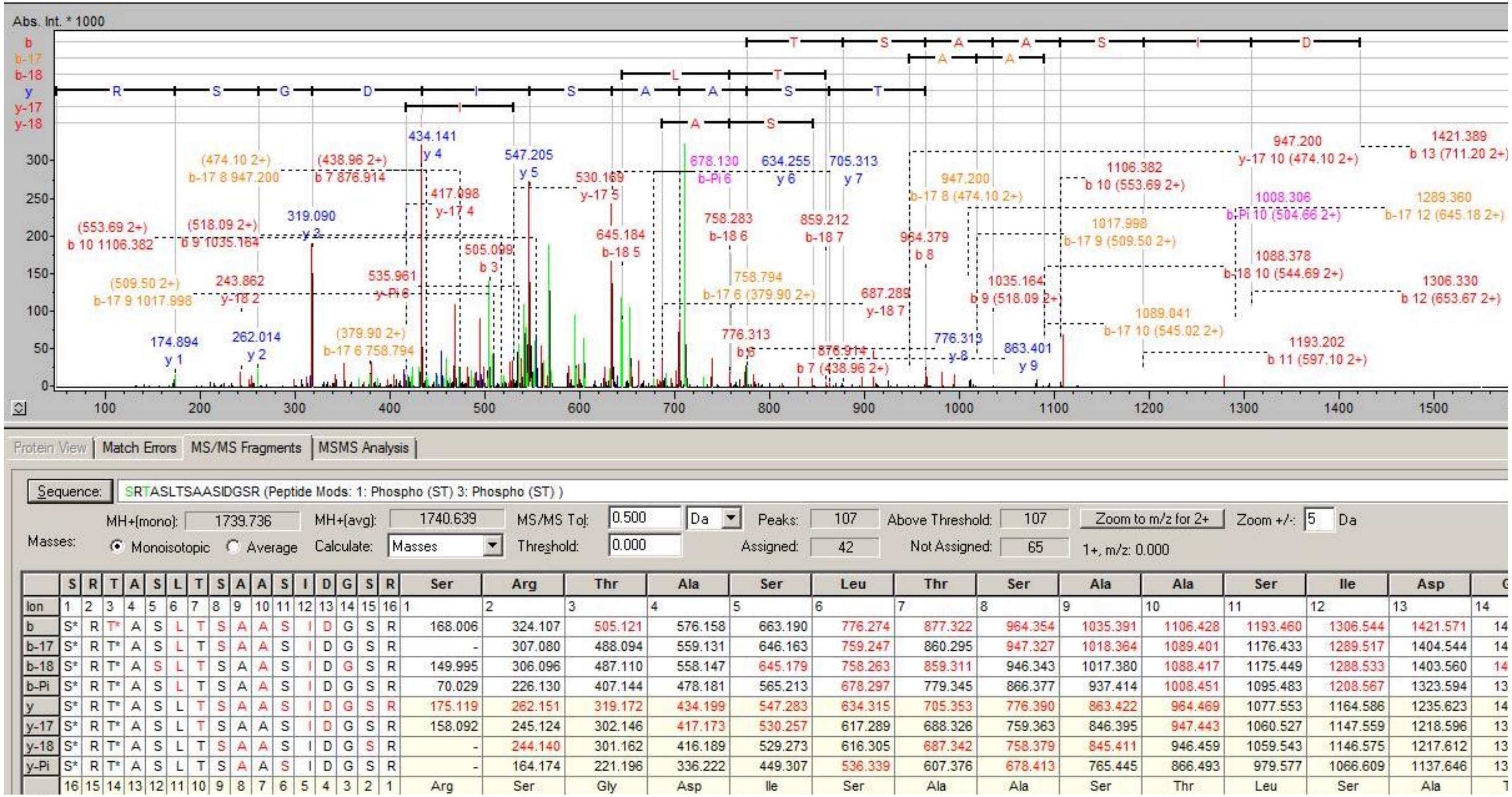


Sequence: TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

MH+(mono): 1416.637 MH+(avg): 1417.396 MS/MS Tol: 0.500 Da Peaks: 118 Above Threshold: 118 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 40 Not Assigned: 78 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



SRTASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 3: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1739.736

MH+(avg): 1740.639

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 107

Assigned: 42

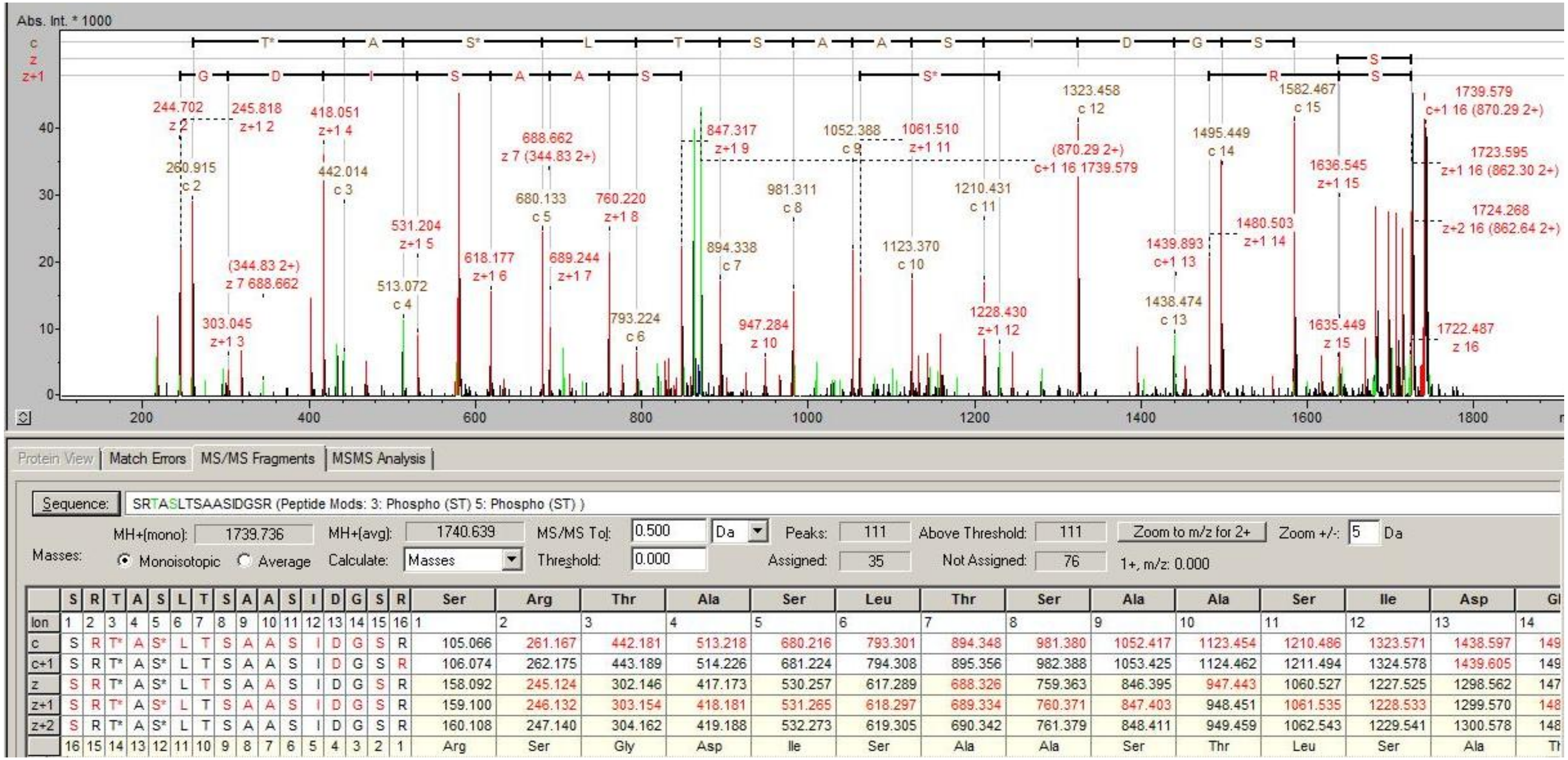
Above Threshold: 107

Not Assigned: 65

Zoom +/-: 5 Da

1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	168.006	324.107	505.121	576.158	663.190	776.274	877.322	964.354	1035.391	1106.428	1193.460	1306.544	1421.571	14
b-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	307.080	488.094	559.131	646.163	759.247	860.295	947.327	1018.364	1089.401	1176.433	1289.517	1404.544	14
b-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	149.995	306.096	487.110	558.147	645.179	758.263	859.311	946.343	1017.380	1088.417	1175.449	1288.533	1403.560	14
b-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	70.029	226.130	407.144	478.181	565.213	678.297	779.345	866.377	937.414	1008.451	1095.483	1208.567	1323.594	13
y	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1164.586	1235.623	14
y-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1147.559	1218.596	13
y-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	13
y-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1066.609	1137.646	13
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T

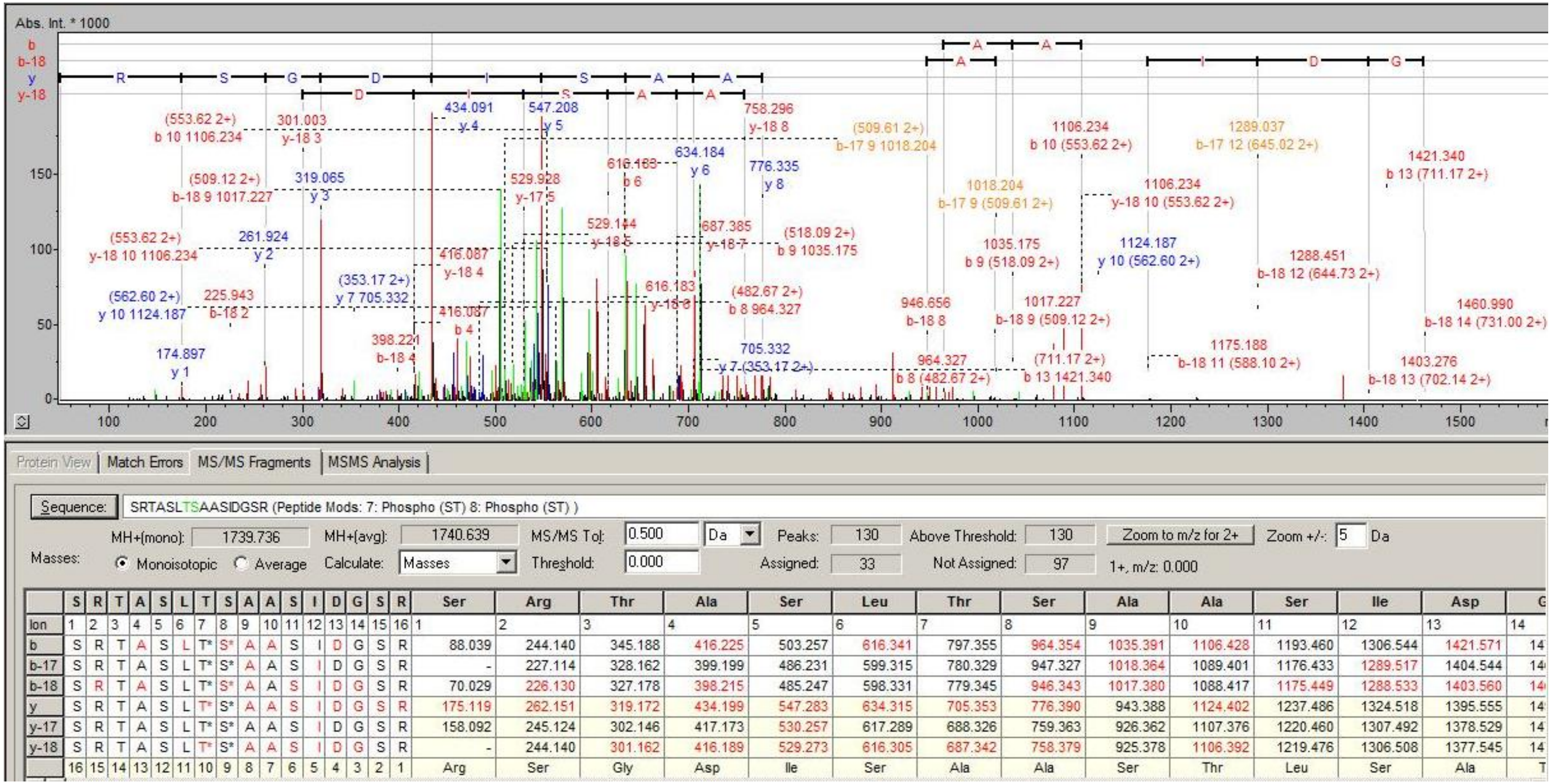


Sequence: SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST))

MH+(mono): 1739.736
MH+(avg): 1740.639
MS/MS Tol: 0.500 Da
Peaks: 111
Above Threshold: 111
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 35
Not Assigned: 76
1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gl
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	105.066	261.167	442.181	513.218	680.216	793.301	894.348	981.380	1052.417	1123.454	1210.486	1323.571	1438.597	149
c+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	106.074	262.175	443.189	514.226	681.224	794.308	895.356	982.388	1053.425	1124.462	1211.494	1324.578	1439.605	149
z	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	147
z+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	159.100	246.132	303.154	418.181	531.265	618.297	689.334	760.371	847.403	948.451	1061.535	1228.533	1299.570	148
z+2	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	160.108	247.140	304.162	419.188	532.273	619.305	690.342	761.379	848.411	949.459	1062.543	1229.541	1300.578	148
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Th

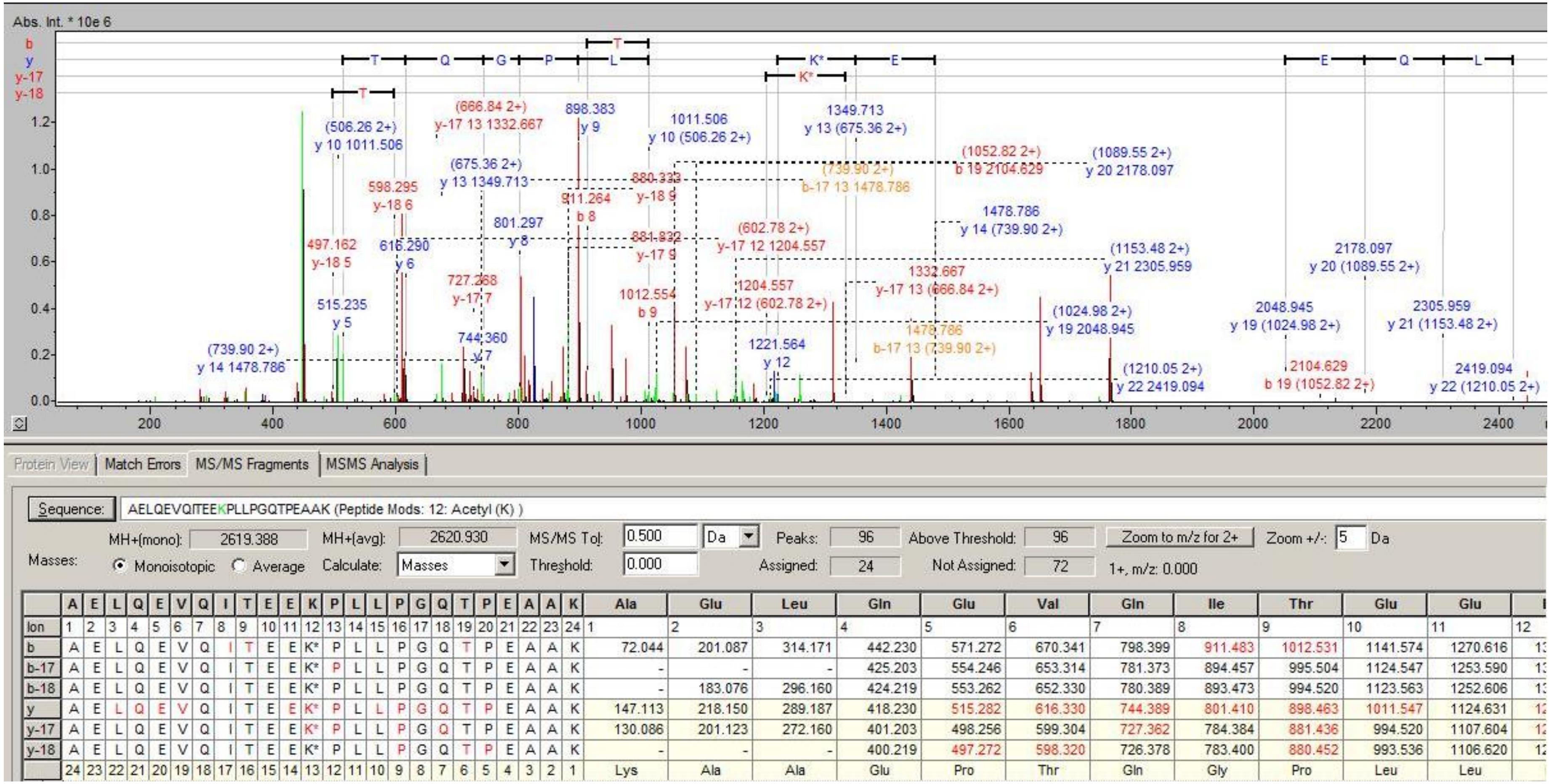


SRTASLTSAASIDGSR (Peptide Mods: 7: Phospho (ST) 8: Phospho (ST))

MH+(mono): 1739.736 MH+(avg): 1740.639 MS/MS Tol: 0.500 Da Peaks: 130 Above Threshold: 130 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 33 Not Assigned: 97 1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	G
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	88.039	244.140	345.188	416.225	503.257	616.341	797.355	964.354	1035.391	1106.428	1193.460	1306.544	1421.571	14
b-17	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	-	227.114	328.162	399.199	486.231	599.315	780.329	947.327	1018.364	1089.401	1176.433	1289.517	1404.544	14
b-18	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	70.029	226.130	327.178	398.215	485.247	598.331	779.345	946.343	1017.380	1088.417	1175.449	1288.533	1403.560	14
y	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	943.388	1124.402	1237.486	1324.518	1395.555	14
y-17	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	926.362	1107.376	1220.460	1307.492	1378.529	14
y-18	S	R	T	A	S	L	T*	S*	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	925.378	1106.392	1219.476	1306.508	1377.545	14
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	T

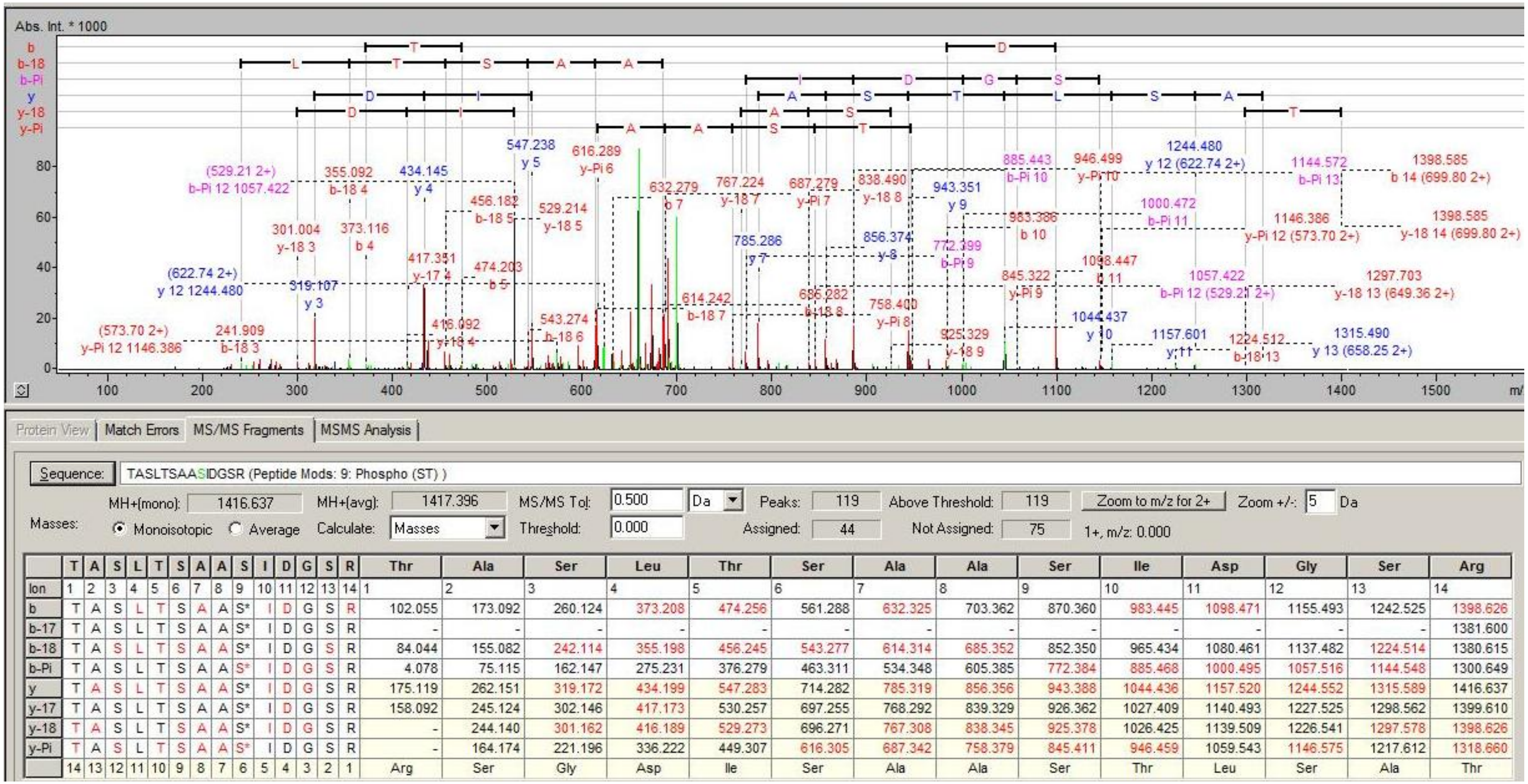


Sequence: AELQEVQITEEKPLLPGQTPEAAK (Peptide Mods: 12: Acetyl (K))

MH+(mono): 2619.388 MH+(avg): 2620.930 MS/MS Tol: 0.500 Da Peaks: 96 Above Threshold: 96 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 24 Not Assigned: 72 1+, m/z: 0.000

	A	E	L	Q	E	V	Q	I	T	E	E	K	P	L	L	P	G	Q	T	P	E	A	A	K	Ala	Glu	Leu	Gln	Glu	Val	Gln	Ile	Thr	Glu	Glu	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	1	2	3	4	5	6	7	8	9	10	11	12
b	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	72.044	201.087	314.171	442.230	571.272	670.341	798.399	911.483	1012.531	1141.574	1270.616	
b-17	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	-	-	425.203	554.246	653.314	781.373	894.457	995.504	1124.547	1253.590	
b-18	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	183.076	296.160	424.219	553.262	652.330	780.389	893.473	994.520	1123.563	1252.606	
y	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	147.113	218.150	289.187	418.230	515.282	616.330	744.389	801.410	898.463	1011.547	1124.631	
y-17	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	130.086	201.123	272.160	401.203	498.256	599.304	727.362	784.384	881.436	994.520	1107.604	
y-18	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	-	-	400.219	497.272	598.320	726.378	783.400	880.452	993.536	1106.620	
	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Ala	Ala	Glu	Pro	Thr	Gln	Gly	Pro	Leu	Leu	

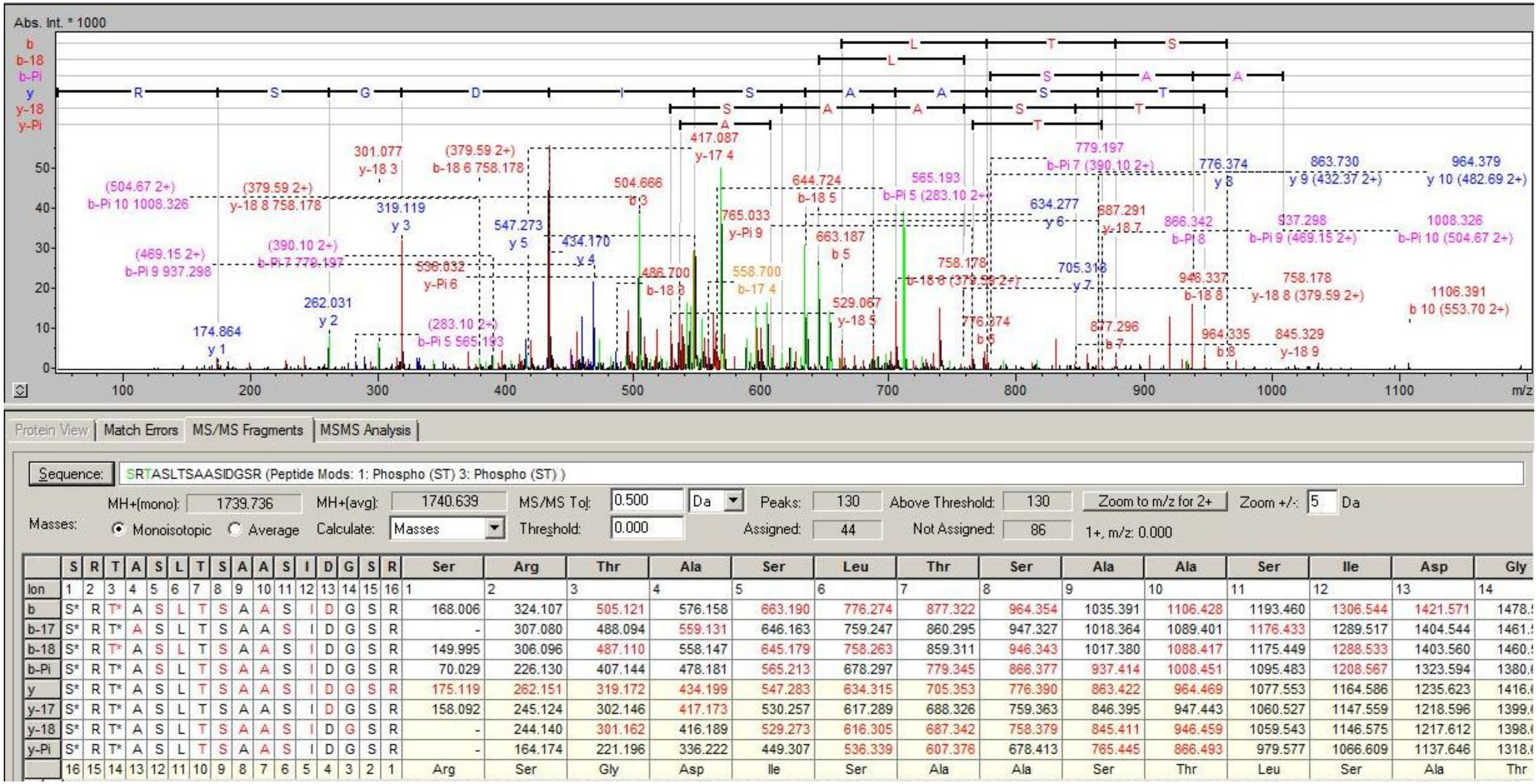


Sequence: TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

MH+(mono): 1416.637
MH+(avg): 1417.396
MS/MS Tol: 0.500 Da
Peaks: 119
Above Threshold: 119
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 44
Not Assigned: 75
1+, m/z: 0.000

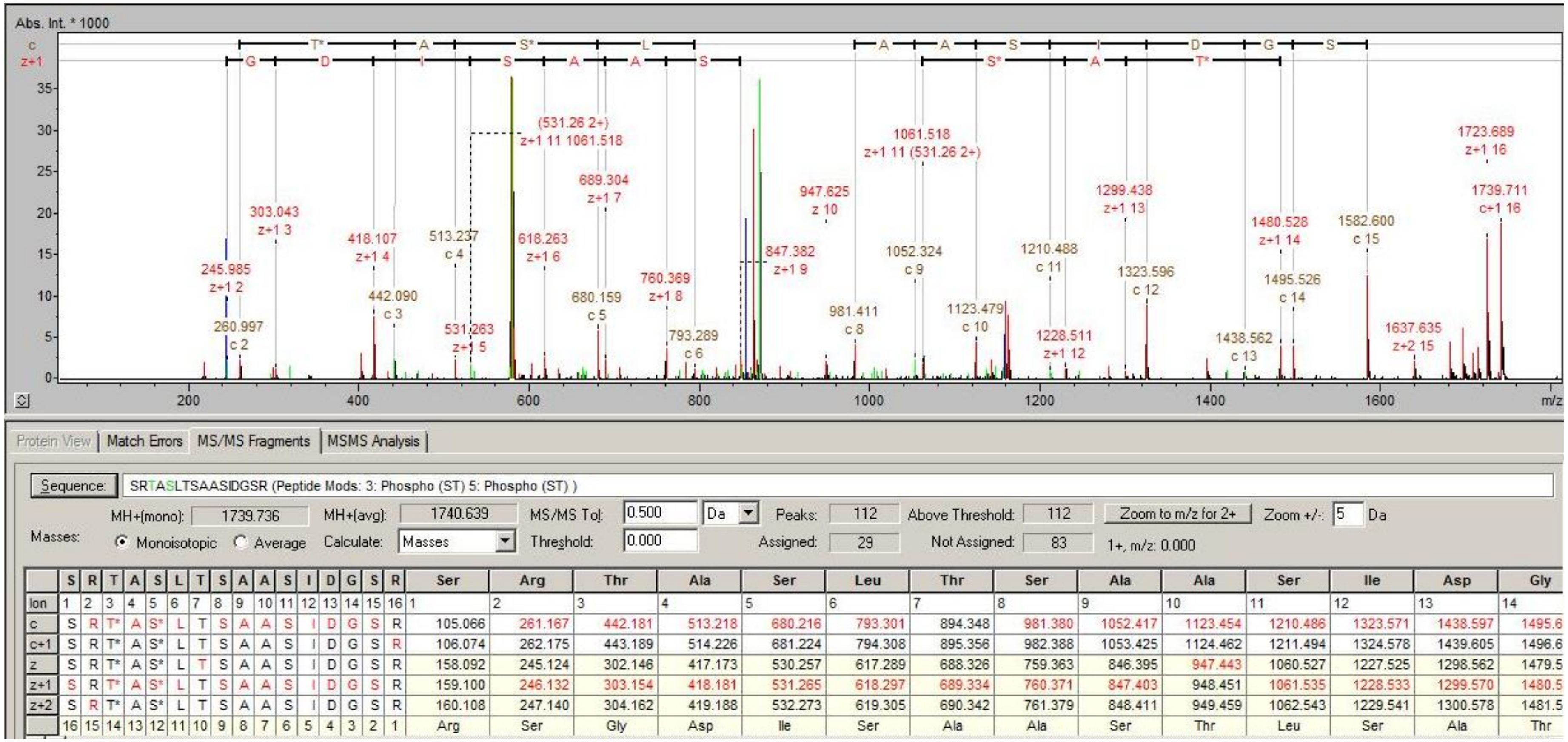
	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



SRTASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 3: Phospho (ST))

MH+(mono): 1739.736
MH+(avg): 1740.639
MS/MS Tol: 0.500 Da
Peaks: 130
Above Threshold: 130
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 44
Not Assigned: 86
1+, m/z: 0.000

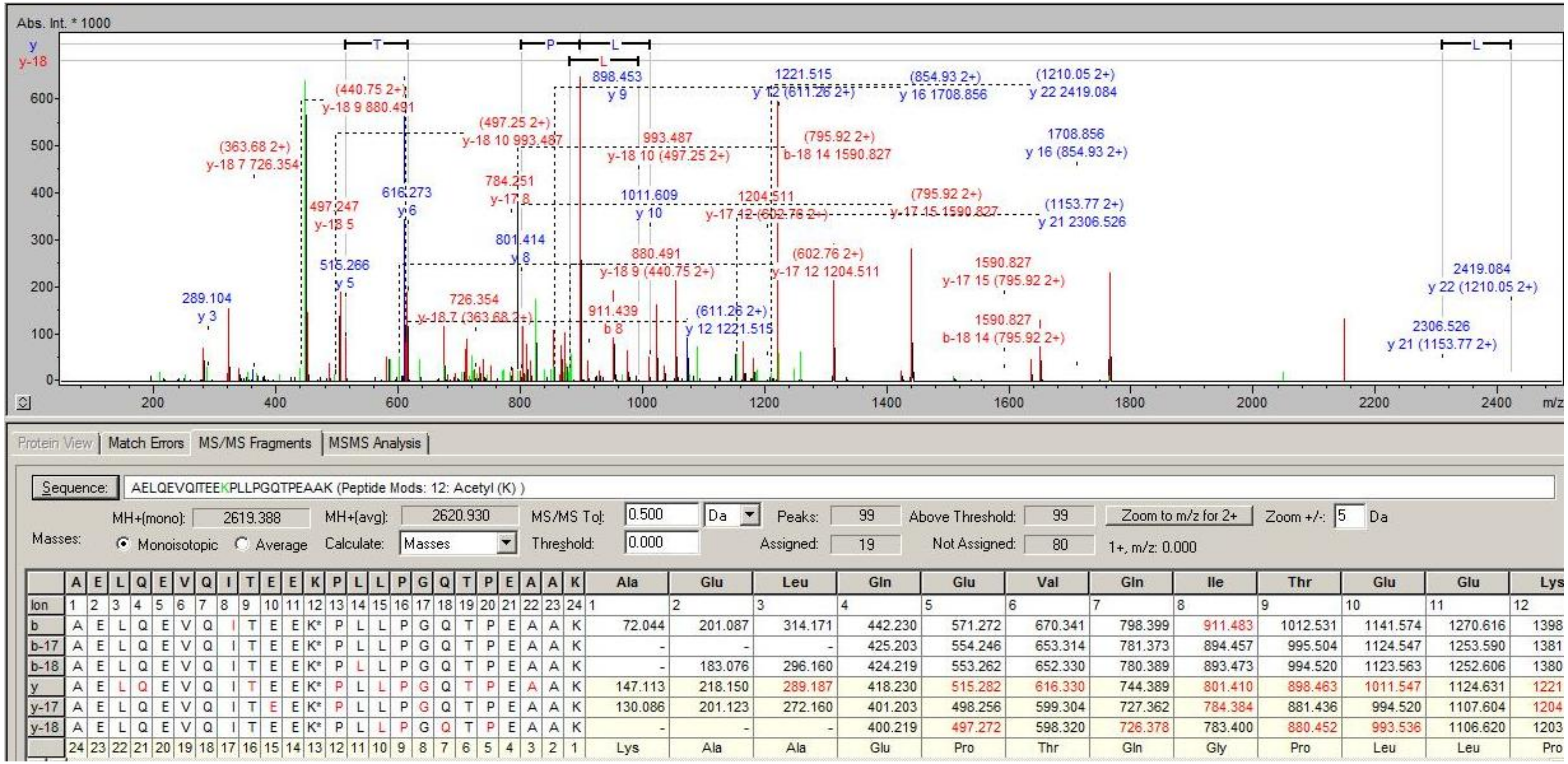
	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	168.006	324.107	505.121	576.158	663.190	776.274	877.322	964.354	1035.391	1106.428	1193.460	1306.544	1421.571	1478.
b-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	307.080	488.094	559.131	646.163	759.247	860.295	947.327	1018.364	1089.401	1176.433	1289.517	1404.544	1461.
b-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	149.995	306.096	487.110	558.147	645.179	758.263	859.311	946.343	1017.380	1088.417	1175.449	1288.533	1403.560	1460.
b-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	70.029	226.130	407.144	478.181	565.213	678.297	779.345	866.377	937.414	1008.451	1095.483	1208.567	1323.594	1380.
y	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1164.586	1235.623	1416.
y-17	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1147.559	1218.596	1399.
y-18	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.
y-Pi	S*	R	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1066.609	1137.646	1318.
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST))

MH+(mono): 1739.736
MH+(avg): 1740.639
MS/MS Tol: 0.500 Da
Peaks: 112
Above Threshold: 112
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 29
Not Assigned: 83
1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	105.066	261.167	442.181	513.218	680.216	793.301	894.348	981.380	1052.417	1123.454	1210.486	1323.571	1438.597	1495.6
c+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	106.074	262.175	443.189	514.226	681.224	794.308	895.356	982.388	1053.425	1124.462	1211.494	1324.578	1439.605	1496.6
z	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1479.5
z+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	159.100	246.132	303.154	418.181	531.265	618.297	689.334	760.371	847.403	948.451	1061.535	1228.533	1299.570	1480.5
z+2	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R	160.108	247.140	304.162	419.188	532.273	619.305	690.342	761.379	848.411	949.459	1062.543	1229.541	1300.578	1481.5
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

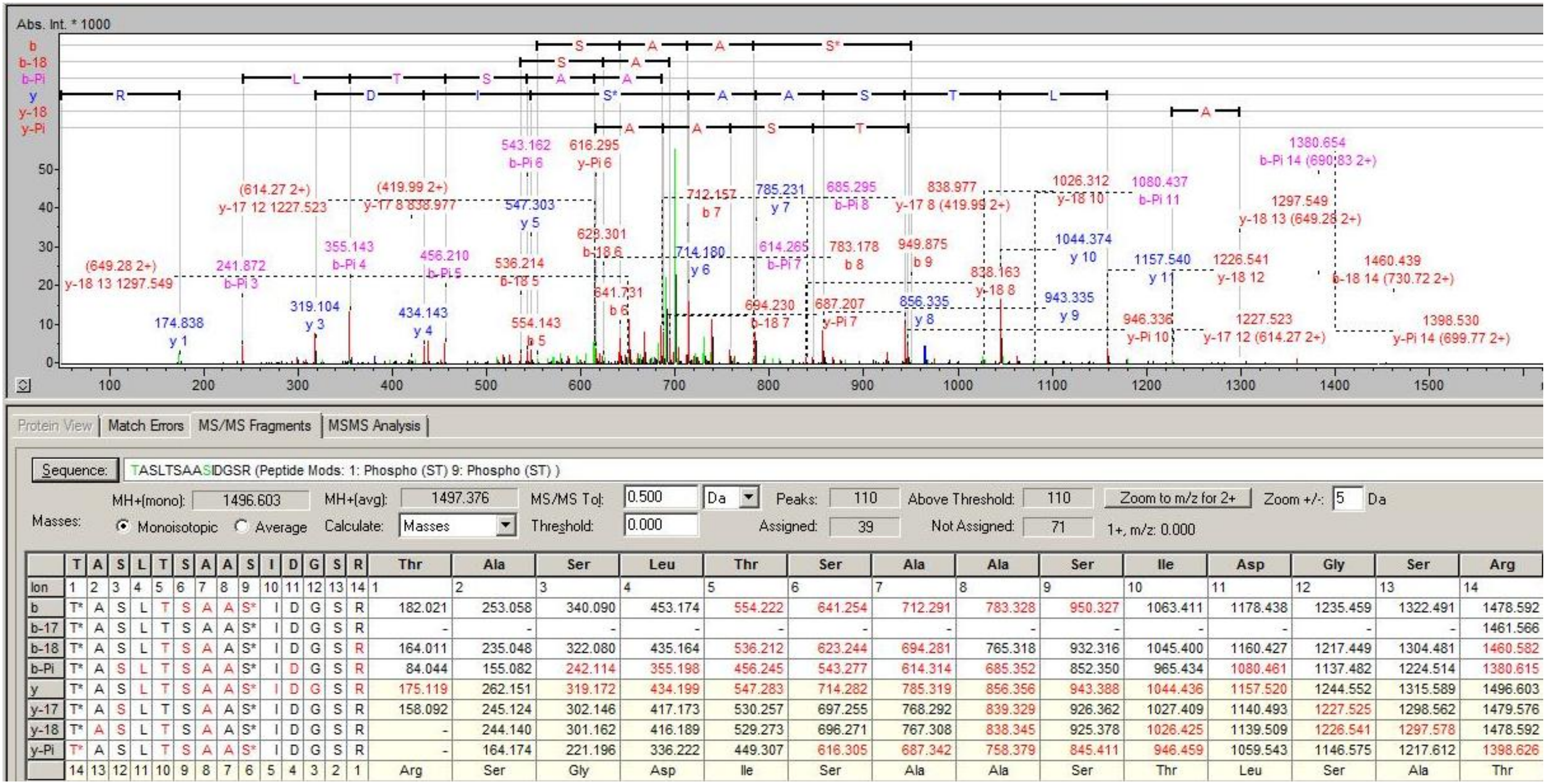


Sequence: AELQEVQITEEKPLLPGQTPEAAK (Peptide Mods: 12: Acetyl (K))

MH+(mono): 2619.388 MH+(avg): 2620.930 MS/MS Tol: 0.500 Da Peaks: 99 Above Threshold: 99 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 19 Not Assigned: 80 1+, m/z: 0.000

	A	E	L	Q	E	V	Q	I	T	E	E	K	P	L	L	P	G	Q	T	P	E	A	A	K	Ala	Glu	Leu	Gln	Glu	Val	Gln	Ile	Thr	Glu	Glu	Lys
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	1	2	3	4	5	6	7	8	9	10	11	12
b	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	72.044	201.087	314.171	442.230	571.272	670.341	798.399	911.483	1012.531	1141.574	1270.616	1398
b-17	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	-	-	425.203	554.246	653.314	781.373	894.457	995.504	1124.547	1253.590	1381
b-18	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	183.076	296.160	424.219	553.262	652.330	780.389	893.473	994.520	1123.563	1252.606	1380
y	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	147.113	218.150	289.187	418.230	515.282	616.330	744.389	801.410	898.463	1011.547	1124.631	1221
y-17	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	130.086	201.123	272.160	401.203	498.256	599.304	727.362	784.384	881.436	994.520	1107.604	1204
y-18	A	E	L	Q	E	V	Q	I	T	E	E	K*	P	L	L	P	G	Q	T	P	E	A	A	K	-	-	-	400.219	497.272	598.320	726.378	783.400	880.452	993.536	1106.620	1203
	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Ala	Ala	Glu	Pro	Thr	Gln	Gly	Pro	Leu	Leu	Pro

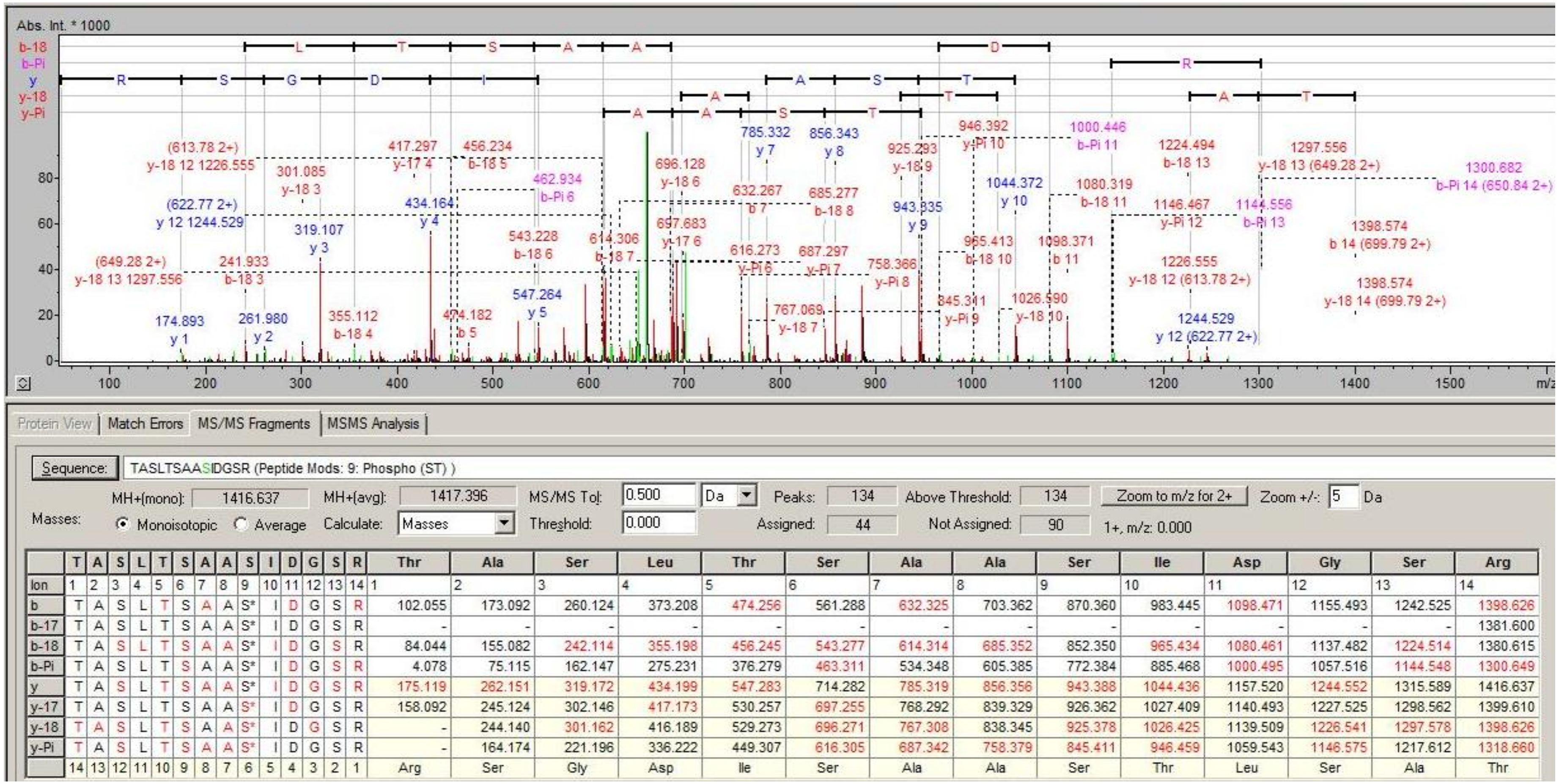


Sequence: TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST) 9: Phospho (ST))

MH+(mono): 1496.603 MH+(avg): 1497.376 MS/MS Tol: 0.500 Da Peaks: 110 Above Threshold: 110 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 39 Not Assigned: 71 1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	182.021	253.058	340.090	453.174	554.222	641.254	712.291	783.328	950.327	1063.411	1178.438	1235.459	1322.491	1478.592
b-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1461.566
b-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	164.011	235.048	322.080	435.164	536.212	623.244	694.281	765.318	932.316	1045.400	1160.427	1217.449	1304.481	1460.582
b-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
y	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1496.603
y-17	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1479.576
y-18	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1478.592
y-Pi	T*	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.626
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



TASLTSAASIDGSR (Peptide Mods: 9: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1416.637

MH+(avg): 1417.396

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 134

Above Threshold: 134

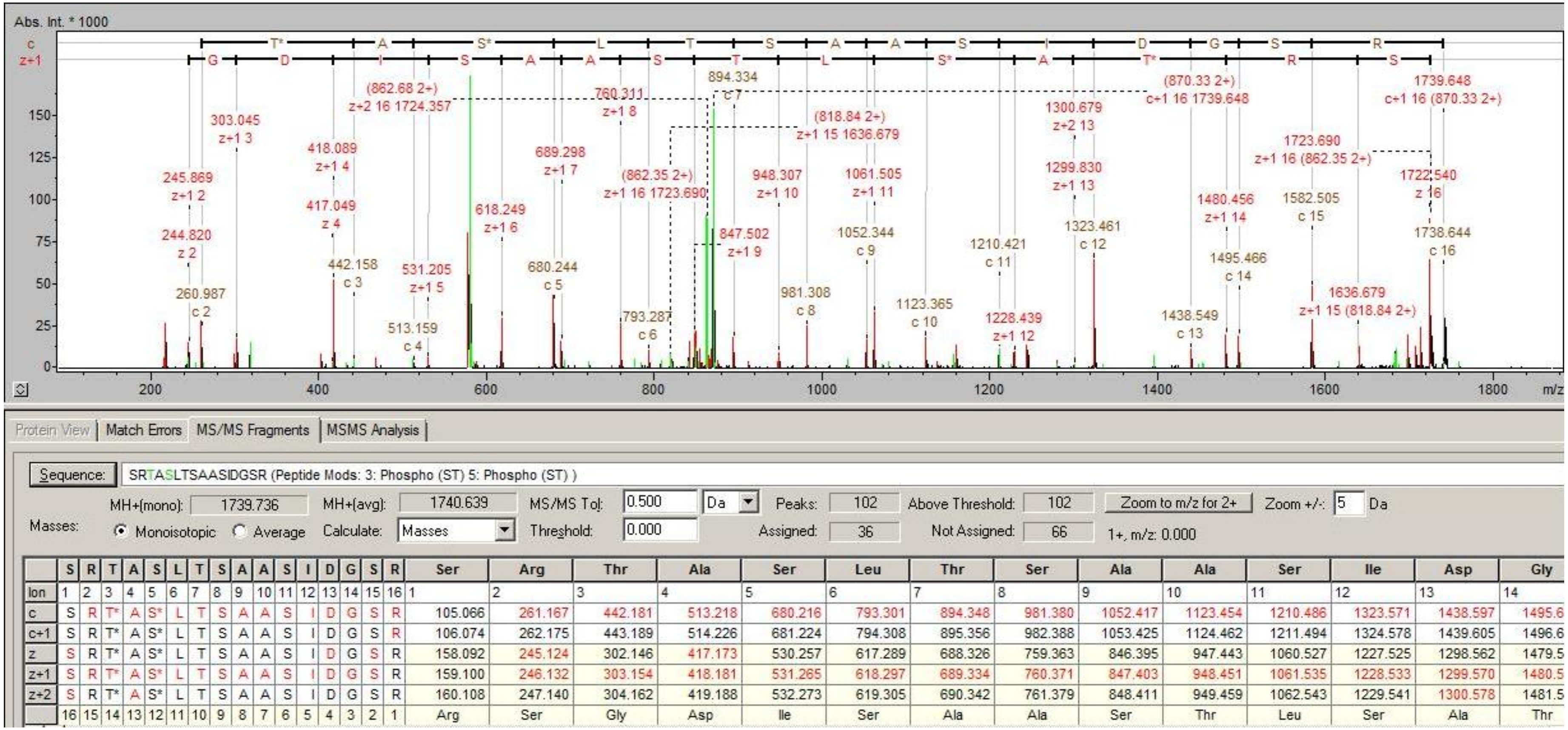
Assigned: 44

Not Assigned: 90

Zoom +/-: 5 Da

1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	102.055	173.092	260.124	373.208	474.256	561.288	632.325	703.362	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	4.078	75.115	162.147	275.231	376.279	463.311	534.348	605.385	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	714.282	785.319	856.356	943.388	1044.436	1157.520	1244.552	1315.589	1416.637
y-17	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	697.255	768.292	839.329	926.362	1027.409	1140.493	1227.525	1298.562	1399.610
y-18	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	244.140	301.162	416.189	529.273	696.271	767.308	838.345	925.378	1026.425	1139.509	1226.541	1297.578	1398.626
y-Pi	T	A	S	L	T	S	A	A	S*	I	D	G	S	R	-	164.174	221.196	336.222	449.307	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



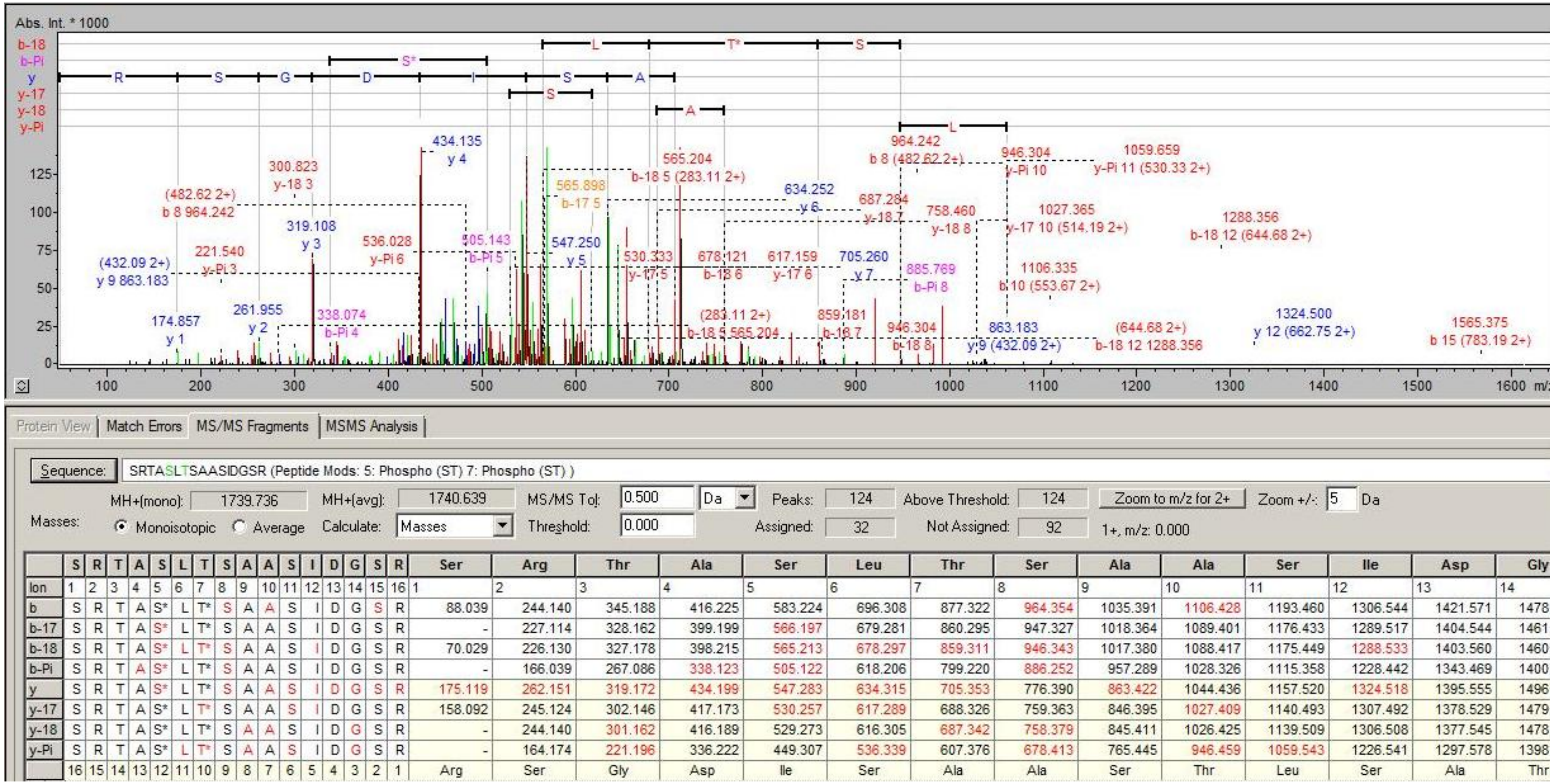
Sequence: SRTASLTSAASIDGSR (Peptide Mods: 3: Phospho (ST) 5: Phospho (ST))

MH+(mono): 1739.736 MH+(avg): 1740.639 MS/MS Tol: 0.500 Da Peaks: 102 Above Threshold: 102 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 36 Not Assigned: 66 1+, m/z: 0.000

	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
c	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R
c+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R
z	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R
z+1	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R
z+2	S	R	T*	A	S*	L	T	S	A	A	S	I	D	G	S	R
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14
c	105.066	261.167	442.181	513.218	680.216	793.301	894.348	981.380	1052.417	1123.454	1210.486	1323.571	1438.597	1495.6
c+1	106.074	262.175	443.189	514.226	681.224	794.308	895.356	982.388	1053.425	1124.462	1211.494	1324.578	1439.605	1496.6
z	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1227.525	1298.562	1479.5
z+1	159.100	246.132	303.154	418.181	531.265	618.297	689.334	760.371	847.403	948.451	1061.535	1228.533	1299.570	1480.5
z+2	160.108	247.140	304.162	419.188	532.273	619.305	690.342	761.379	848.411	949.459	1062.543	1229.541	1300.578	1481.5
	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



SRTASLTSAASIDGSR (Peptide Mods: 5: Phospho (ST) 7: Phospho (ST))

MH+(mono): 1739.736

MH+(avg): 1740.639

MS/MS Tol: 0.500 Da

Peaks: 124

Above Threshold: 124

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

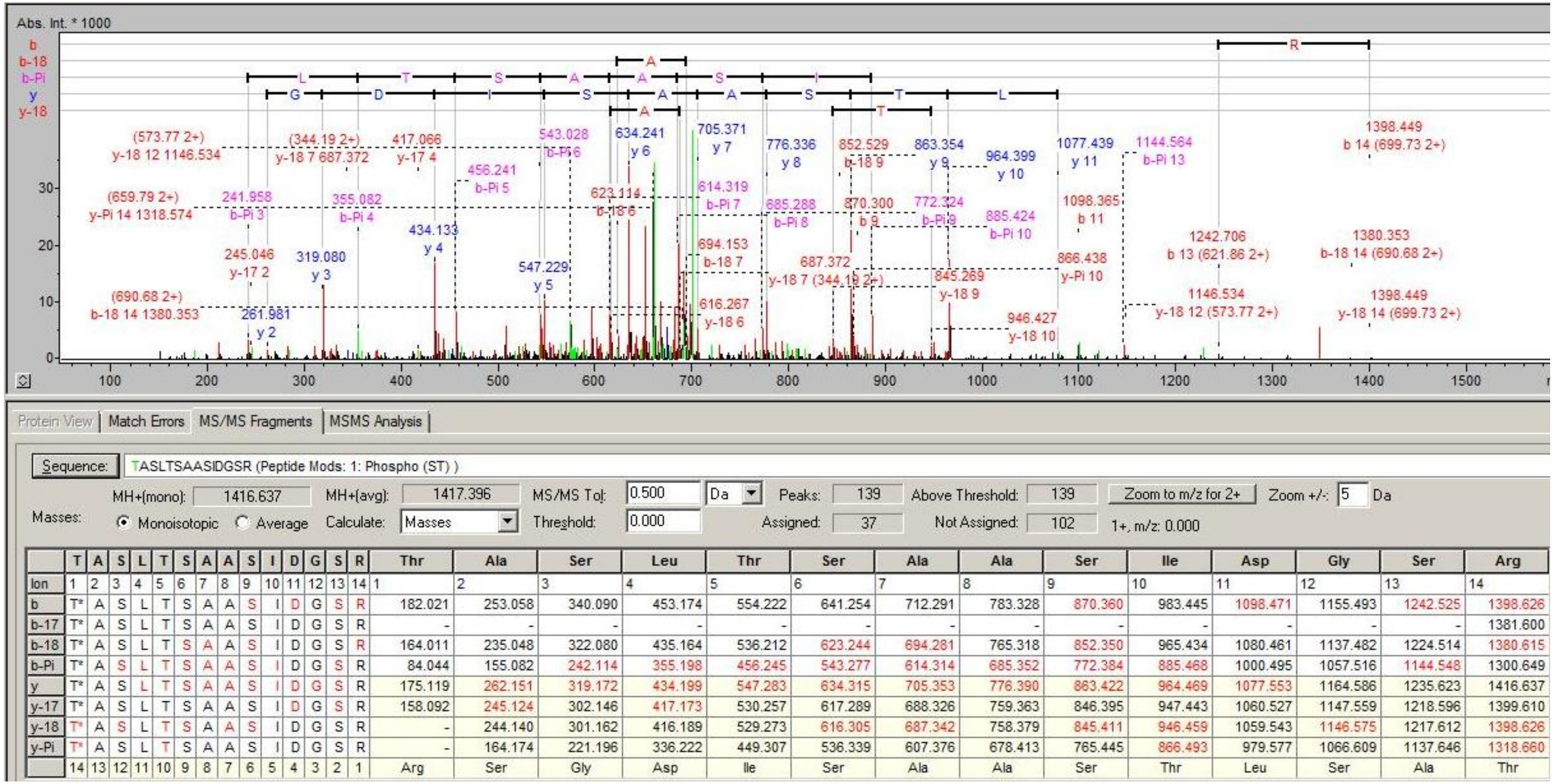
Threshold: 0.000

Assigned: 32

Not Assigned: 92

1+, m/z: 0.000

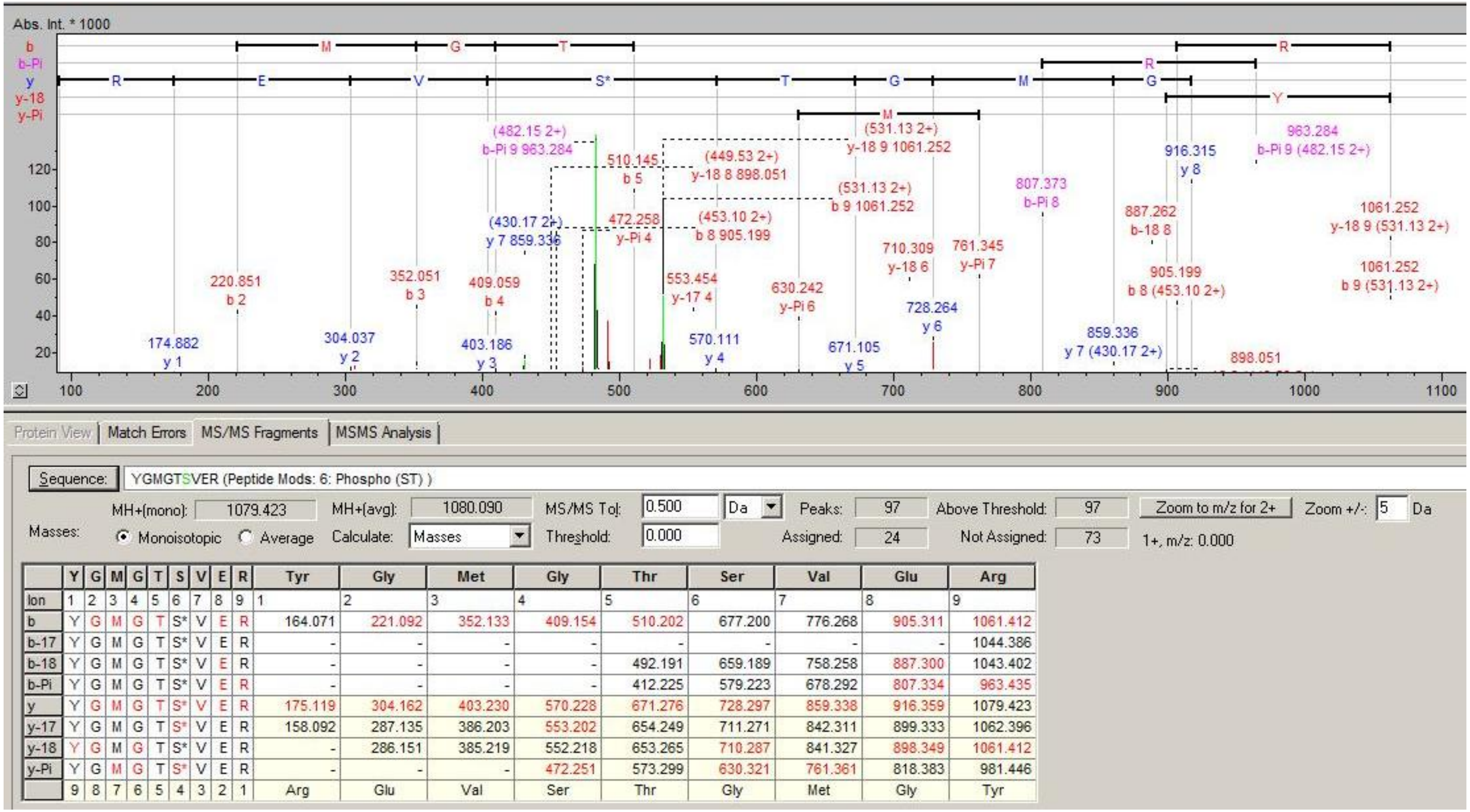
	S	R	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Ser	Arg	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	88.039	244.140	345.188	416.225	583.224	696.308	877.322	964.354	1035.391	1106.428	1193.460	1306.544	1421.571	1478
b-17	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	227.114	328.162	399.199	566.197	679.281	860.295	947.327	1018.364	1089.401	1176.433	1289.517	1404.544	1461
b-18	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	70.029	226.130	327.178	398.215	565.213	678.297	859.311	946.343	1017.380	1088.417	1175.449	1288.533	1403.560	1460
b-Pi	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	166.039	267.086	338.123	505.122	618.206	799.220	886.252	957.289	1028.326	1115.358	1228.442	1343.469	1400
y	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	1044.436	1157.520	1324.518	1395.555	1496
y-17	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	1027.409	1140.493	1307.492	1378.529	1479
y-18	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	1026.425	1139.509	1306.508	1377.545	1478
y-Pi	S	R	T	A	S*	L	T*	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	946.459	1059.543	1226.541	1297.578	1398
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr



Sequence: TASLTSAASIDGSR (Peptide Mods: 1: Phospho (ST))

Masses:
MH+(mono): 1416.637
MH+(avg): 1417.396
MS/MS Tol: 0.500 Da
Peaks: 139
Above Threshold: 139
Zoom +/-: 5 Da
● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 37
Not Assigned: 102
1+, m/z: 0.000

	T	A	S	L	T	S	A	A	S	I	D	G	S	R	Thr	Ala	Ser	Leu	Thr	Ser	Ala	Ala	Ser	Ile	Asp	Gly	Ser	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	182.021	253.058	340.090	453.174	554.222	641.254	712.291	783.328	870.360	983.445	1098.471	1155.493	1242.525	1398.626
b-17	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	1381.600
b-18	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	164.011	235.048	322.080	435.164	536.212	623.244	694.281	765.318	852.350	965.434	1080.461	1137.482	1224.514	1380.615
b-Pi	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	84.044	155.082	242.114	355.198	456.245	543.277	614.314	685.352	772.384	885.468	1000.495	1057.516	1144.548	1300.649
y	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	175.119	262.151	319.172	434.199	547.283	634.315	705.353	776.390	863.422	964.469	1077.553	1164.586	1235.623	1416.637
y-17	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	158.092	245.124	302.146	417.173	530.257	617.289	688.326	759.363	846.395	947.443	1060.527	1147.559	1218.596	1399.610
y-18	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	244.140	301.162	416.189	529.273	616.305	687.342	758.379	845.411	946.459	1059.543	1146.575	1217.612	1398.626
y-Pi	T*	A	S	L	T	S	A	A	S	I	D	G	S	R	-	164.174	221.196	336.222	449.307	536.339	607.376	678.413	765.445	866.493	979.577	1066.609	1137.646	1318.660
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	Gly	Asp	Ile	Ser	Ala	Ala	Ser	Thr	Leu	Ser	Ala	Thr

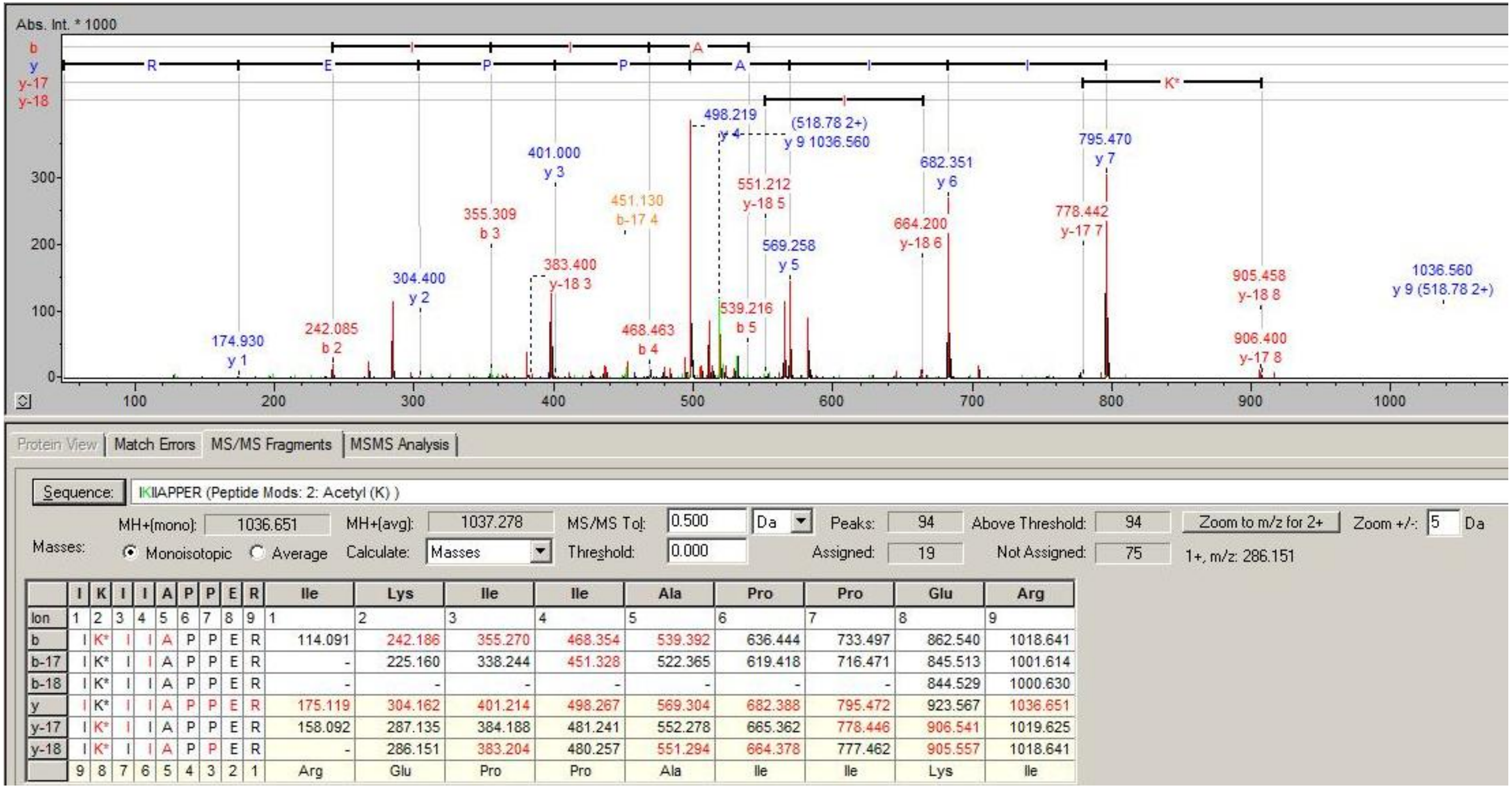


Sequence: YGMGTSVER (Peptide Mods: 6: Phospho (ST))

MH+(mono): 1079.423
MH+(avg): 1080.090
MS/MS Tol: 0.500 Da
Peaks: 97
Above Threshold: 97
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 24
Not Assigned: 73
1+, m/z: 0.000

	Y	G	M	G	T	S	V	E	R	Tyr	Gly	Met	Gly	Thr	Ser	Val	Glu	Arg
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
b	Y	G	M	G	T	S*	V	E	R	164.071	221.092	352.133	409.154	510.202	677.200	776.268	905.311	1061.412
b-17	Y	G	M	G	T	S*	V	E	R	-	-	-	-	-	-	-	-	1044.386
b-18	Y	G	M	G	T	S*	V	E	R	-	-	-	-	492.191	659.189	758.258	887.300	1043.402
b-Pi	Y	G	M	G	T	S*	V	E	R	-	-	-	-	412.225	579.223	678.292	807.334	963.435
y	Y	G	M	G	T	S*	V	E	R	175.119	304.162	403.230	570.228	671.276	728.297	859.338	916.359	1079.423
y-17	Y	G	M	G	T	S*	V	E	R	158.092	287.135	386.203	553.202	654.249	711.271	842.311	899.333	1062.396
y-18	Y	G	M	G	T	S*	V	E	R	-	286.151	385.219	552.218	653.265	710.287	841.327	898.349	1061.412
y-Pi	Y	G	M	G	T	S*	V	E	R	-	-	-	472.251	573.299	630.321	761.361	818.383	981.446
	9	8	7	6	5	4	3	2	1	Arg	Glu	Val	Ser	Thr	Gly	Met	Gly	Tyr

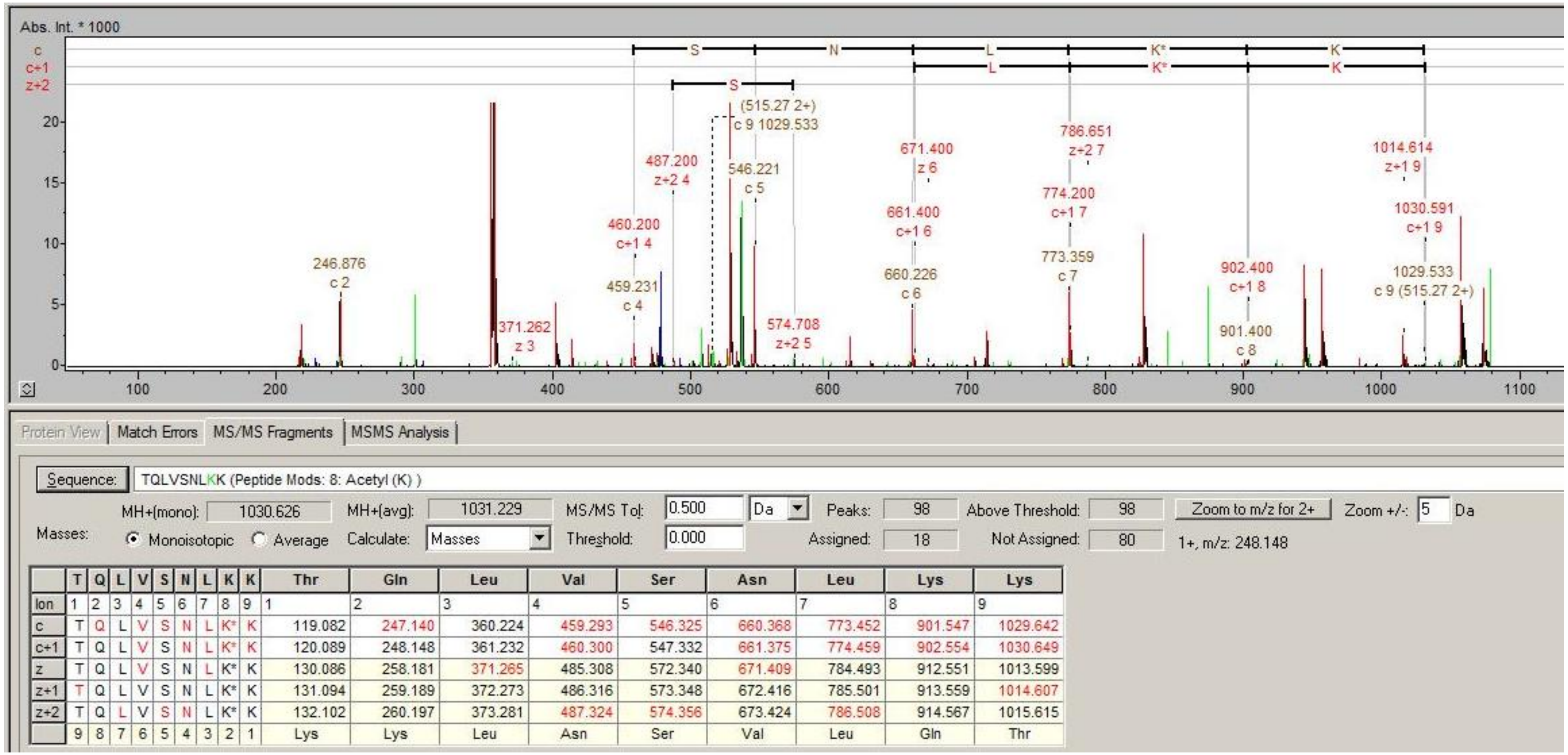


Sequence: IKIIAPPER (Peptide Mods: 2: Acetyl (K))

MH+(mono): 1036.651 MH+(avg): 1037.278 MS/MS Tol: 0.500 Da Peaks: 94 Above Threshold: 94 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 19 Not Assigned: 75 1+, m/z: 286.151

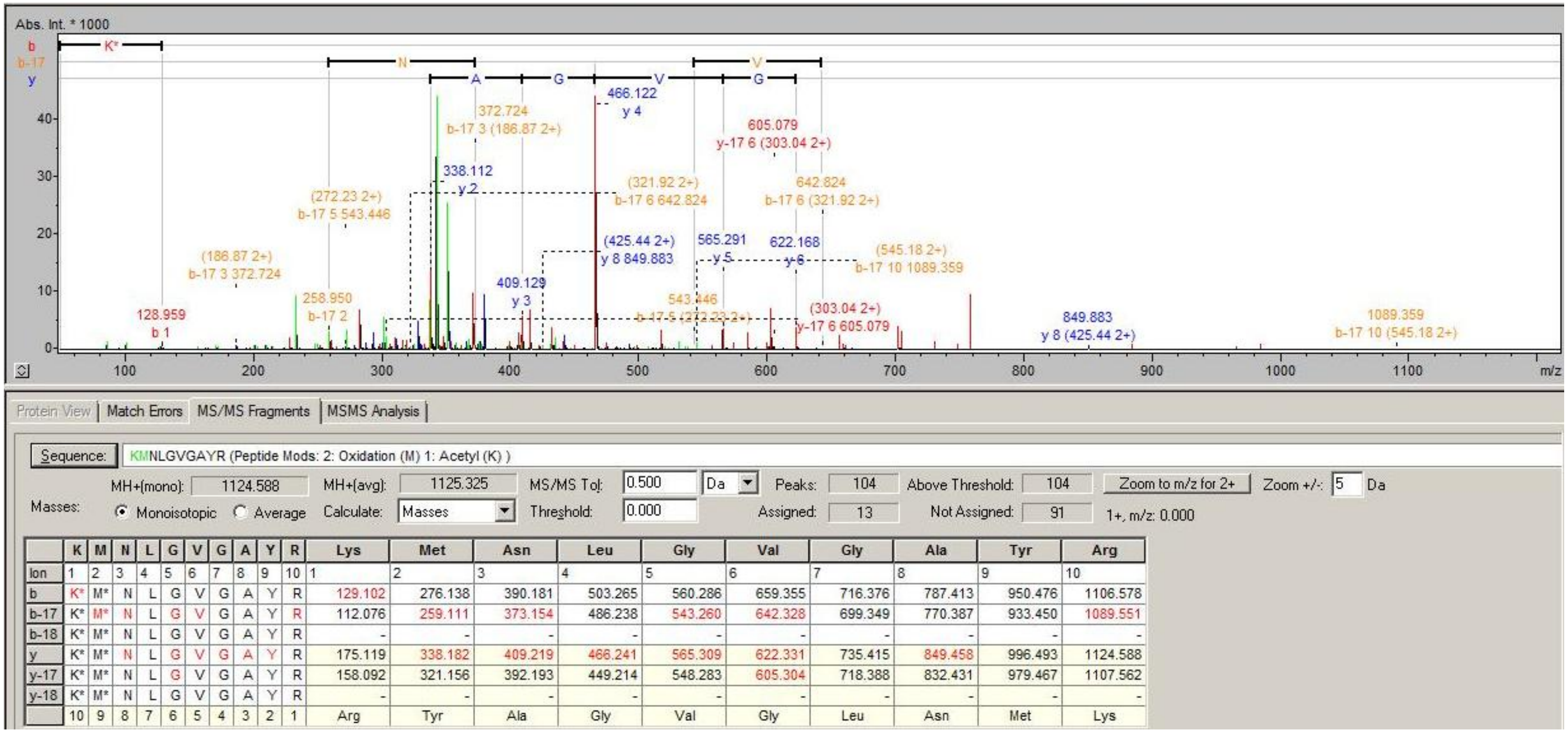
	I	K	I	I	A	P	P	E	R	Ile	Lys	Ile	Ile	Ala	Pro	Pro	Glu	Arg
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
b	I	K*	I	I	A	P	P	E	R	114.091	242.186	355.270	468.354	539.392	636.444	733.497	862.540	1018.641
b-17	I	K*	I	I	A	P	P	E	R	-	225.160	338.244	451.328	522.365	619.418	716.471	845.513	1001.614
b-18	I	K*	I	I	A	P	P	E	R	-	-	-	-	-	-	-	844.529	1000.630
y	I	K*	I	I	A	P	P	E	R	175.119	304.162	401.214	498.267	569.304	682.388	795.472	923.567	1036.651
y-17	I	K*	I	I	A	P	P	E	R	158.092	287.135	384.188	481.241	552.278	665.362	778.446	906.541	1019.625
y-18	I	K*	I	I	A	P	P	E	R	-	286.151	383.204	480.257	551.294	664.378	777.462	905.557	1018.641
	9	8	7	6	5	4	3	2	1	Arg	Glu	Pro	Pro	Ala	Ile	Ile	Lys	Ile



TQLVSNLKK (Peptide Mods: 8: Acetyl (K))

MH+(mono): 1030.626
MH+(avg): 1031.229
MS/MS Tol: 0.500 Da
Peaks: 98
Above Threshold: 98
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 18
Not Assigned: 80
1+, m/z: 248.148

	T	Q	L	V	S	N	L	K	K	Thr	Gln	Leu	Val	Ser	Asn	Leu	Lys	Lys
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
c	T	Q	L	V	S	N	L	K*	K	119.082	247.140	360.224	459.293	546.325	660.368	773.452	901.547	1029.642
c+1	T	Q	L	V	S	N	L	K*	K	120.089	248.148	361.232	460.300	547.332	661.375	774.459	902.554	1030.649
z	T	Q	L	V	S	N	L	K*	K	130.086	258.181	371.265	485.308	572.340	671.409	784.493	912.551	1013.599
z+1	T	Q	L	V	S	N	L	K*	K	131.094	259.189	372.273	486.316	573.348	672.416	785.501	913.559	1014.607
z+2	T	Q	L	V	S	N	L	K*	K	132.102	260.197	373.281	487.324	574.356	673.424	786.508	914.567	1015.615
	9	8	7	6	5	4	3	2	1	Lys	Lys	Leu	Asn	Ser	Val	Leu	Gln	Thr



Sequence: KMNLGVGAYR (Peptide Mods: 2: Oxidation (M) 1: Acetyl (K))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1124.588

MH+(avg): 1125.325

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 104

Assigned: 13

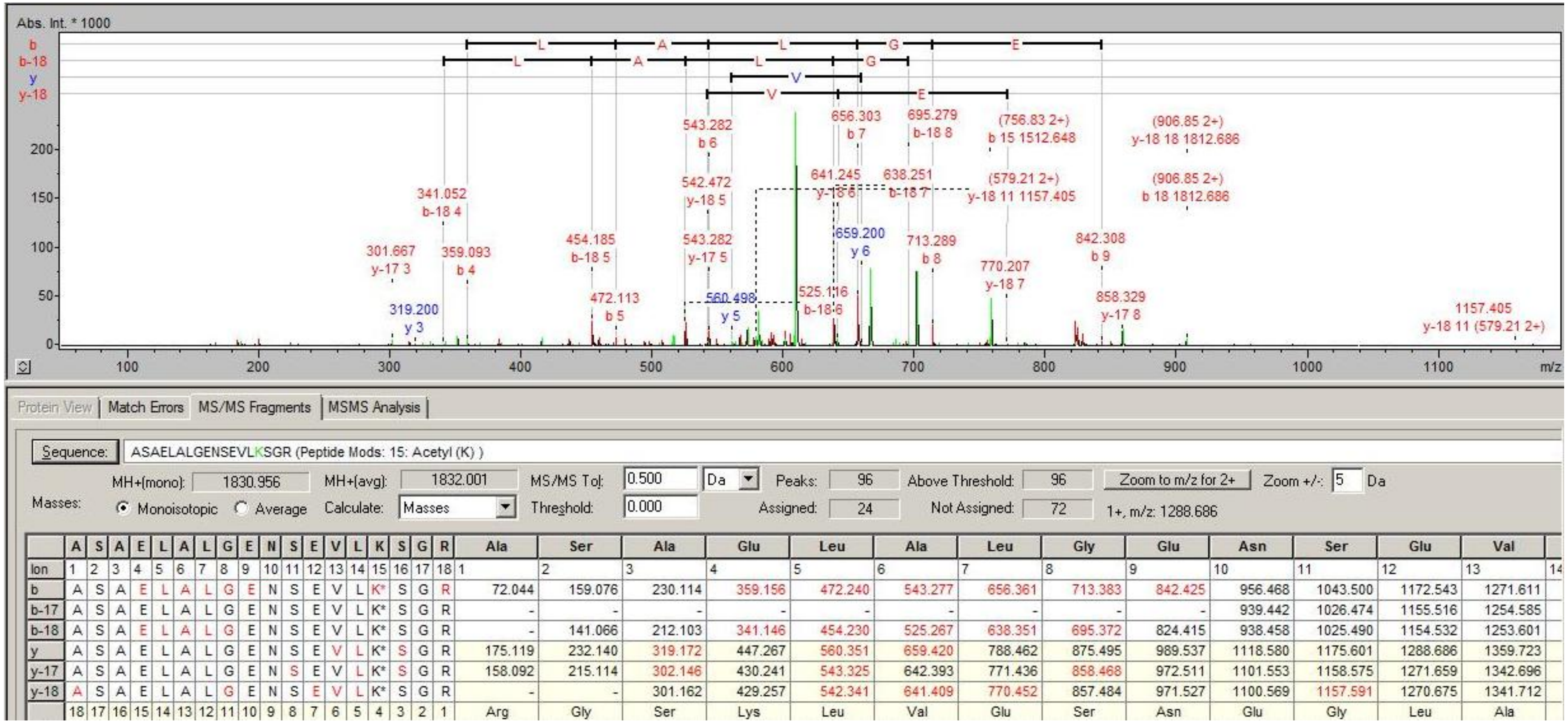
Above Threshold: 104

Not Assigned: 91

Zoom +/-: 5 Da

1+, m/z: 0.000

	K	M	N	L	G	V	G	A	Y	R	Lys	Met	Asn	Leu	Gly	Val	Gly	Ala	Tyr	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	K*	M*	N	L	G	V	G	A	Y	R	129.102	276.138	390.181	503.265	560.286	659.355	716.376	787.413	950.476	1106.578
b-17	K*	M*	N	L	G	V	G	A	Y	R	112.076	259.111	373.154	486.238	543.260	642.328	699.349	770.387	933.450	1089.551
b-18	K*	M*	N	L	G	V	G	A	Y	R	-	-	-	-	-	-	-	-	-	-
y	K*	M*	N	L	G	V	G	A	Y	R	175.119	338.182	409.219	466.241	565.309	622.331	735.415	849.458	996.493	1124.588
y-17	K*	M*	N	L	G	V	G	A	Y	R	158.092	321.156	392.193	449.214	548.283	605.304	718.388	832.431	979.467	1107.562
y-18	K*	M*	N	L	G	V	G	A	Y	R	-	-	-	-	-	-	-	-	-	-
	10	9	8	7	6	5	4	3	2	1	Arg	Tyr	Ala	Gly	Val	Gly	Leu	Asn	Met	Lys



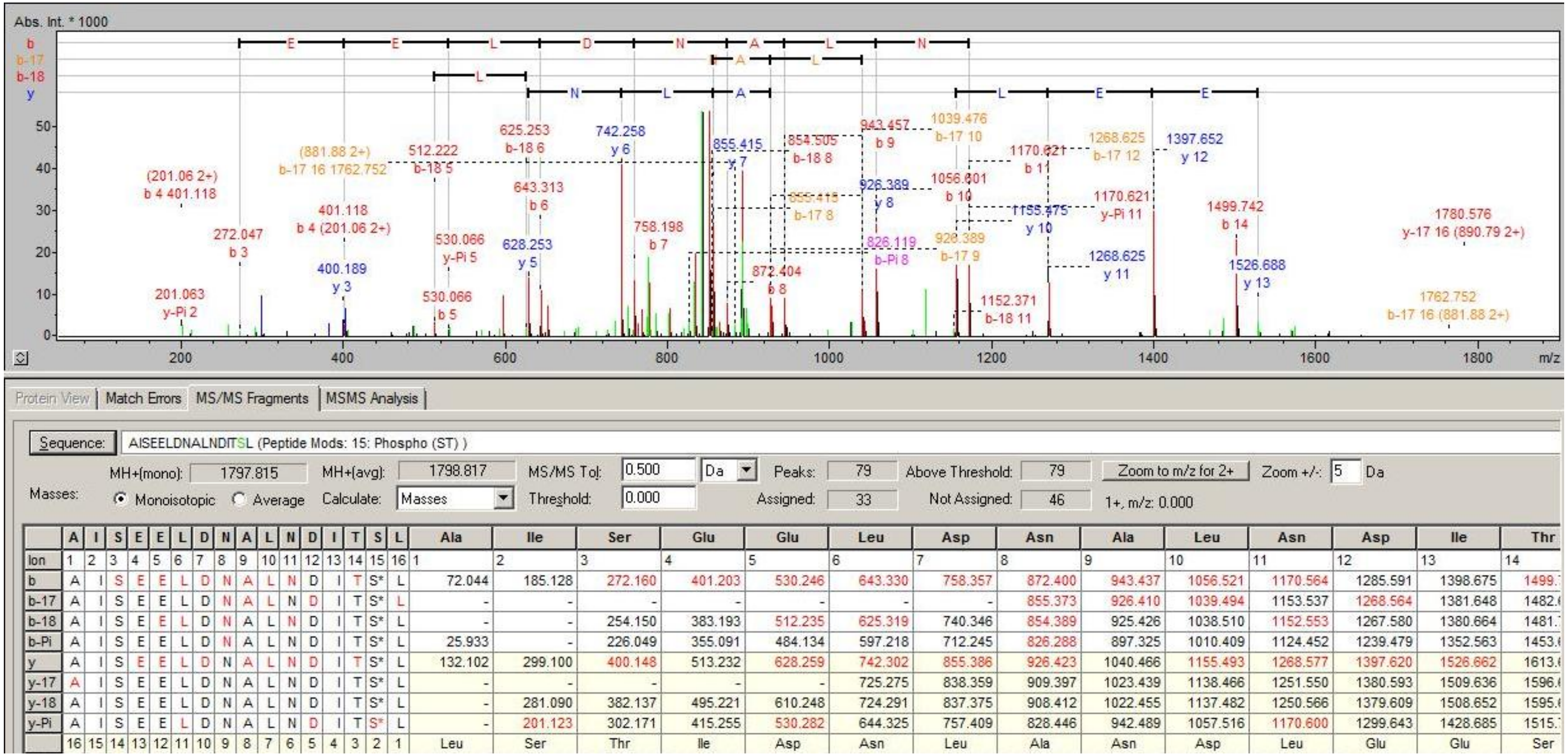
Sequence: ASAELALGENSEVLKSGR (Peptide Mods: 15: Acetyl (K))

MH+(mono): 1830.956 MH+(avg): 1832.001 MS/MS Tol: 0.500 Da Peaks: 96 Above Threshold: 96 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 24 Not Assigned: 72 1+, m/z: 1288.686

	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K	S	G	R
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
b	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
b-17	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
b-18	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
y	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
y-17	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
y-18	A	S	A	E	L	A	L	G	E	N	S	E	V	L	K*	S	G	R
	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

	Ala	Ser	Ala	Glu	Leu	Ala	Leu	Gly	Glu	Asn	Ser	Glu	Val
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13
b	72.044	159.076	230.114	359.156	472.240	543.277	656.361	713.383	842.425	956.468	1043.500	1172.543	1271.611
b-17	-	-	-	-	-	-	-	-	-	939.442	1026.474	1155.516	1254.585
b-18	-	141.066	212.103	341.146	454.230	525.267	638.351	695.372	824.415	938.458	1025.490	1154.532	1253.601
y	175.119	232.140	319.172	447.267	560.351	659.420	788.462	875.495	989.537	1118.580	1175.601	1288.686	1359.723
y-17	158.092	215.114	302.146	430.241	543.325	642.393	771.436	858.468	972.511	1101.553	1158.575	1271.659	1342.696
y-18	-	-	301.162	429.257	542.341	641.409	770.452	857.484	971.527	1100.569	1157.591	1270.675	1341.712
	Arg	Gly	Ser	Lys	Leu	Val	Glu	Ser	Asn	Glu	Gly	Leu	Ala

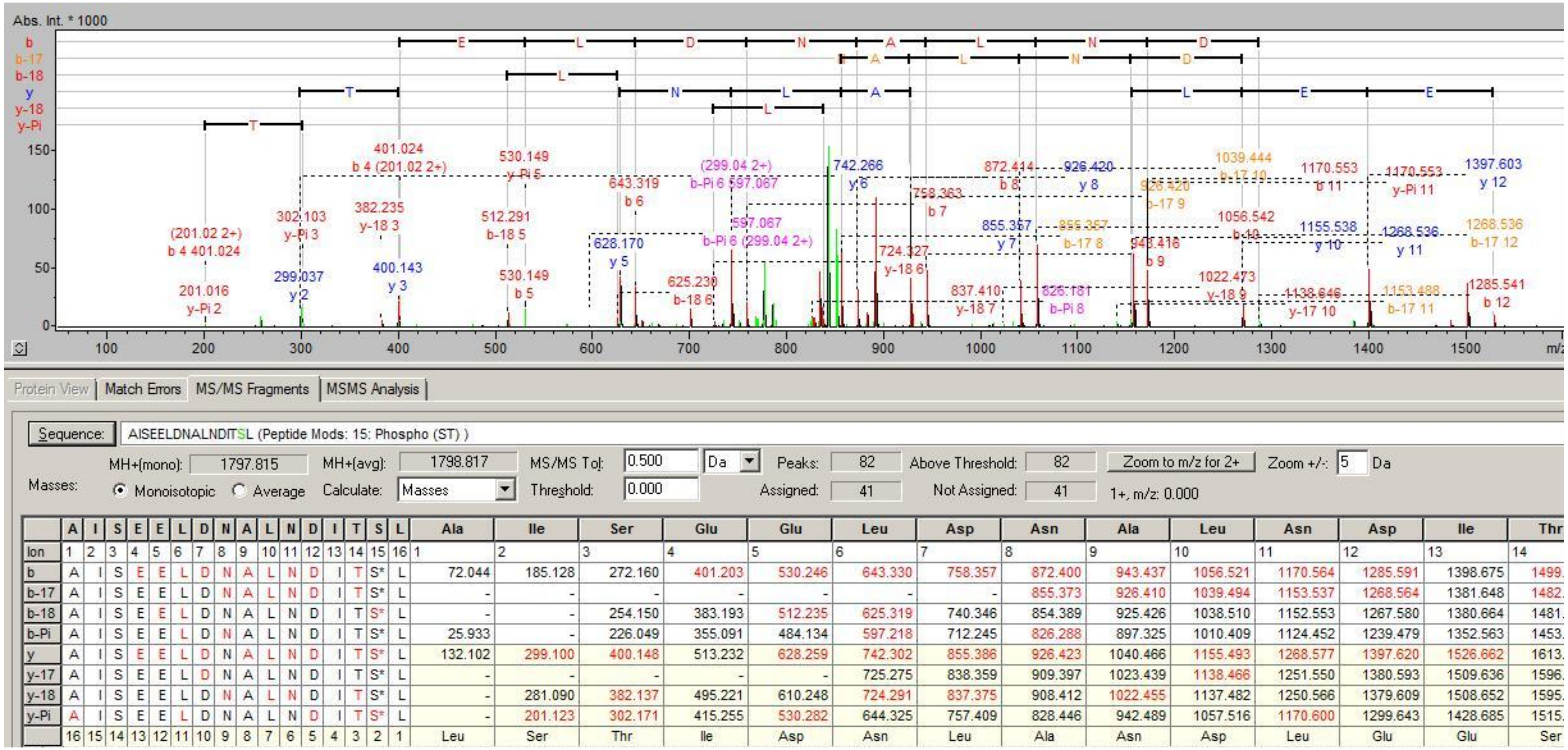


Sequence: AISEELDNALNDITSL (Peptide Mods: 15: Phospho (ST))

MH+(mono): 1797.815
MH+(avg): 1798.817
MS/MS Tol: 0.500 Da
Peaks: 79
Above Threshold: 79
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 33
Not Assigned: 46
1+, m/z: 0.000

	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S	L	Ala	Ile	Ser	Glu	Glu	Leu	Asp	Asn	Ala	Leu	Asn	Asp	Ile	Thr
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	72.044	185.128	272.160	401.203	530.246	643.330	758.357	872.400	943.437	1056.521	1170.564	1285.591	1398.675	1499.
b-17	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	-	-	-	-	-	855.373	926.410	1039.494	1153.537	1268.564	1381.648	1482.
b-18	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	254.150	383.193	512.235	625.319	740.346	854.389	925.426	1038.510	1152.553	1267.580	1380.664	1481.
b-Pi	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	25.933	-	226.049	355.091	484.134	597.218	712.245	826.288	897.325	1010.409	1124.452	1239.479	1352.563	1453.
y	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	132.102	299.100	400.148	513.232	628.259	742.302	855.386	926.423	1040.466	1155.493	1268.577	1397.620	1526.662	1613.
y-17	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	-	-	-	725.275	838.359	909.397	1023.439	1138.466	1251.550	1380.593	1509.636	1596.
y-18	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	281.090	382.137	495.221	610.248	724.291	837.375	908.412	1022.455	1137.482	1250.566	1379.609	1508.652	1595.
y-Pi	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	201.123	302.171	415.255	530.282	644.325	757.409	828.446	942.489	1057.516	1170.600	1299.643	1428.685	1515.
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Leu	Ser	Thr	Ile	Asp	Asn	Leu	Ala	Asn	Asp	Leu	Glu	Glu	Ser

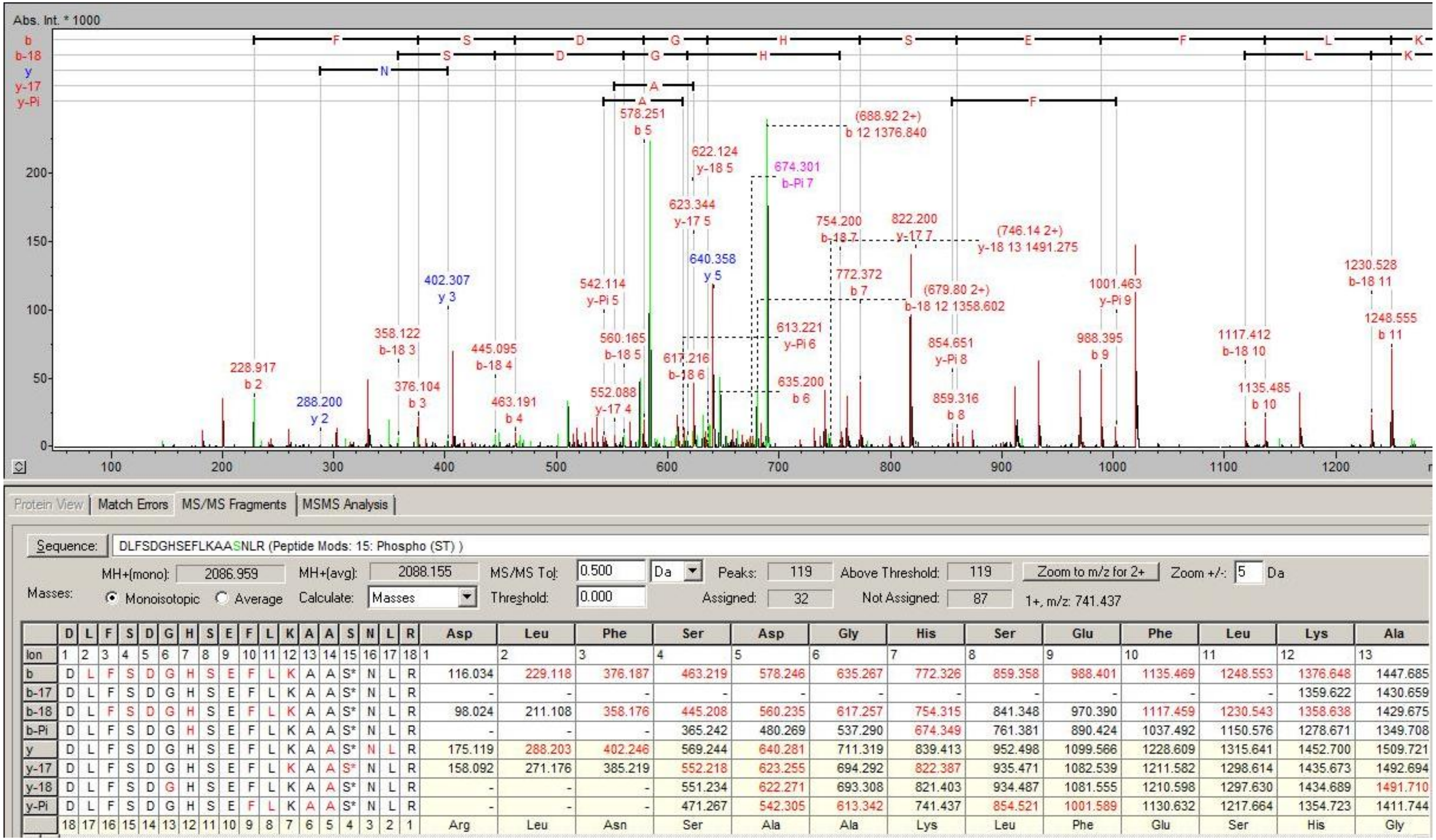


Sequence: AISEELDNALNDITSL (Peptide Mods: 15: Phospho (ST))

MH+(mono): 1797.815
MH+(avg): 1798.817
MS/MS Tol: 0.500 Da
Peaks: 82
Above Threshold: 82
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 41
Not Assigned: 41
1+, m/z: 0.000

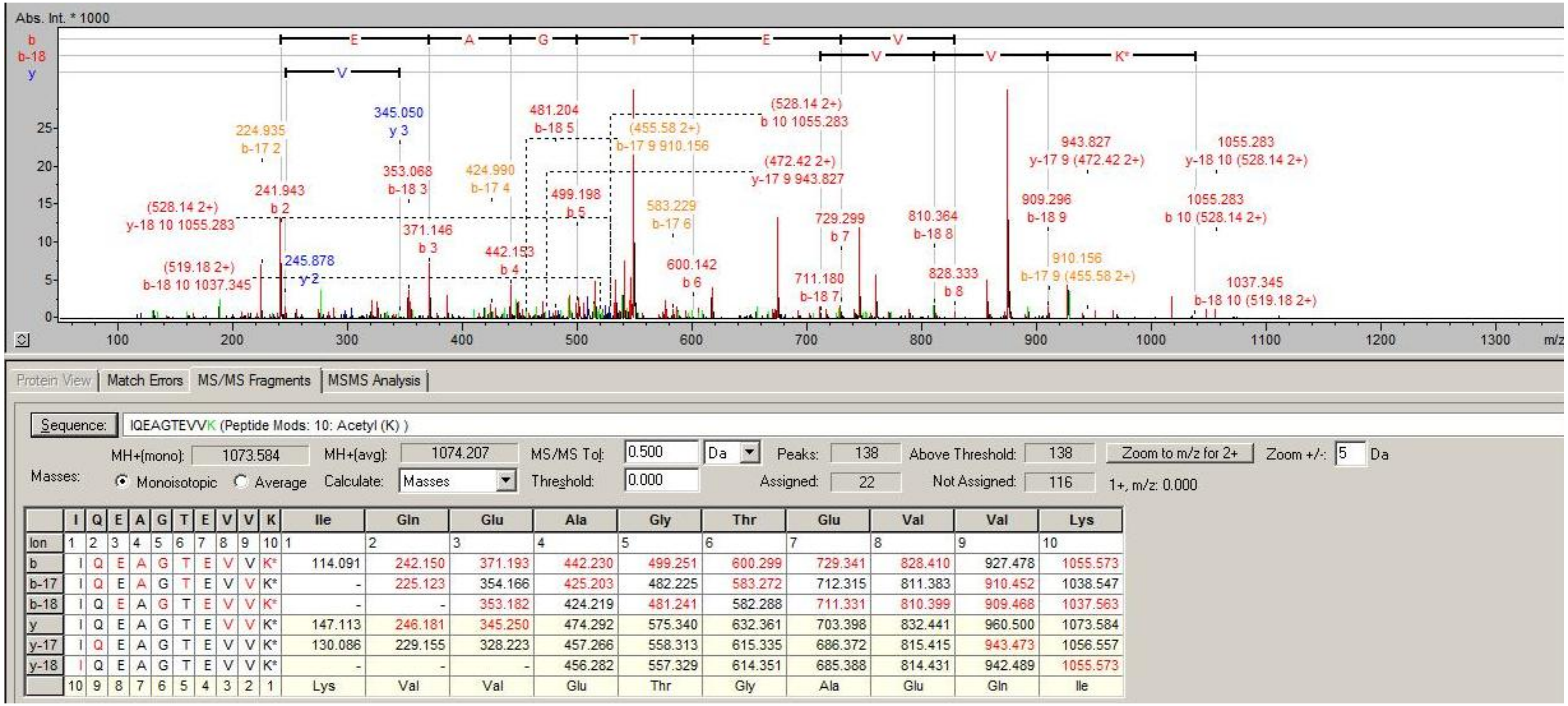
	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S	L	Ala	Ile	Ser	Glu	Glu	Leu	Asp	Asn	Ala	Leu	Asn	Asp	Ile	Thr
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	72.044	185.128	272.160	401.203	530.246	643.330	758.357	872.400	943.437	1056.521	1170.564	1285.591	1398.675	1499.
b-17	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	-	-	-	-	-	855.373	926.410	1039.494	1153.537	1268.564	1381.648	1482.
b-18	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	254.150	383.193	512.235	625.319	740.346	854.389	925.426	1038.510	1152.553	1267.580	1380.664	1481.
b-Pi	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	25.933	-	226.049	355.091	484.134	597.218	712.245	826.288	897.325	1010.409	1124.452	1239.479	1352.563	1453.
y	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	132.102	299.100	400.148	513.232	628.259	742.302	855.386	926.423	1040.466	1155.493	1268.577	1397.620	1526.662	1613.
y-17	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	-	-	-	-	725.275	838.359	909.397	1023.439	1138.466	1251.550	1380.593	1509.636	1596.
y-18	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	281.090	382.137	495.221	610.248	724.291	837.375	908.412	1022.455	1137.482	1250.566	1379.609	1508.652	1595.
y-Pi	A	I	S	E	E	L	D	N	A	L	N	D	I	T	S*	L	-	201.123	302.171	415.255	530.282	644.325	757.409	828.446	942.489	1057.516	1170.600	1299.643	1428.685	1515.
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Leu	Ser	Thr	Ile	Asp	Asn	Leu	Ala	Asn	Asp	Leu	Glu	Glu	Ser



Sequence: DLFSDGHSEFLKAASNLR (Peptide Mods: 15: Phospho (ST))

MH+(mono): 2086.959
MH+(avg): 2088.155
MS/MS Tol: 0.500 Da
Peaks: 119
Above Threshold: 119
Zoom to m/z for 2+
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 32
Not Assigned: 87
1+, m/z: 741.437

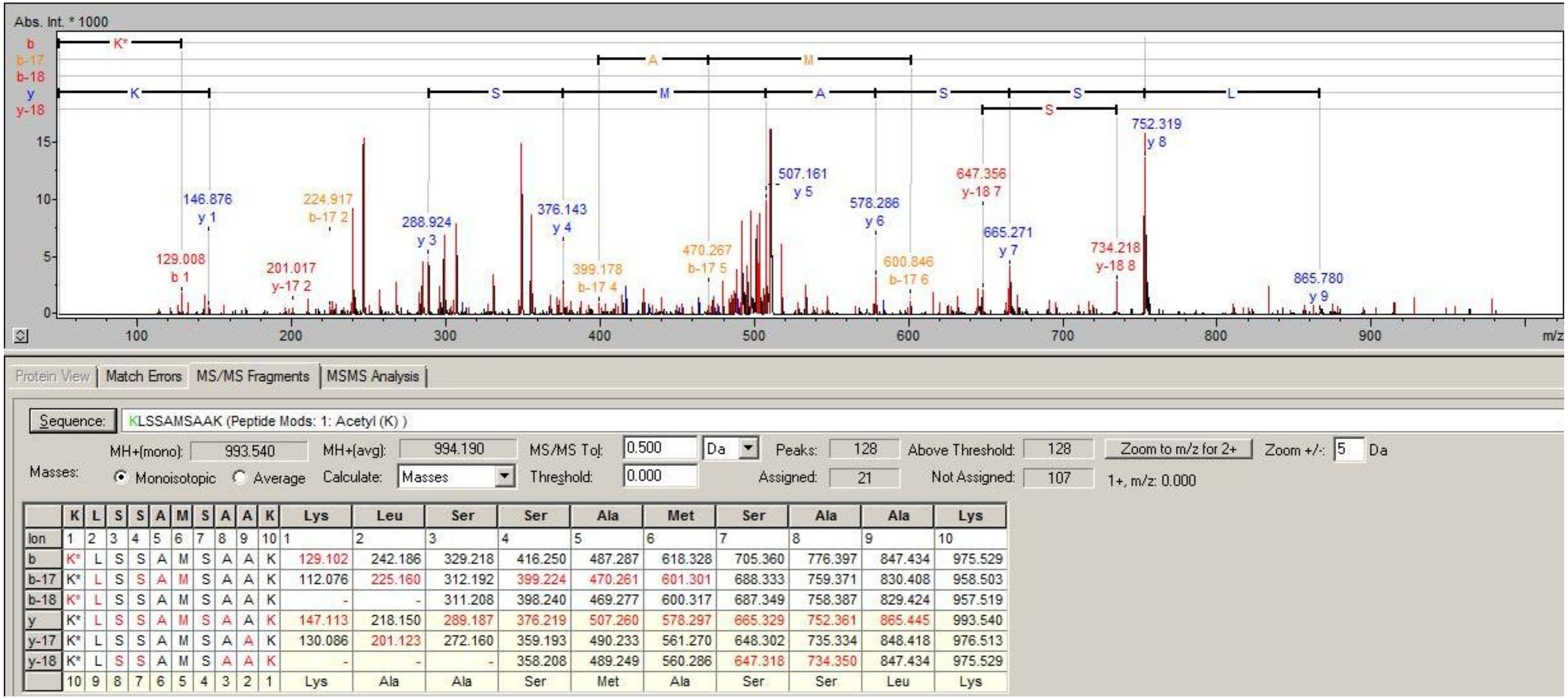
	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S	N	L	R	Asp	Leu	Phe	Ser	Asp	Gly	His	Ser	Glu	Phe	Leu	Lys	Ala
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	1	2	3	4	5	6	7	8	9	10	11	12	13
b	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	116.034	229.118	376.187	463.219	578.246	635.267	772.326	859.358	988.401	1135.469	1248.553	1376.648	1447.685
b-17	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	-	-	-	-	-	-	-	-	-	-	-	1359.622	1430.659
b-18	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	98.024	211.108	358.176	445.208	560.235	617.257	754.315	841.348	970.390	1117.459	1230.543	1358.638	1429.675
b-Pi	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	-	-	-	365.242	480.269	537.290	674.349	761.381	890.424	1037.492	1150.576	1278.671	1349.708
y	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	175.119	288.203	402.246	569.244	640.281	711.319	839.413	952.498	1099.566	1228.609	1315.641	1452.700	1509.721
y-17	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	158.092	271.176	385.219	552.218	623.255	694.292	822.387	935.471	1082.539	1211.582	1298.614	1435.673	1492.694
y-18	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	-	-	-	551.234	622.271	693.308	821.403	934.487	1081.555	1210.598	1297.630	1434.689	1491.710
y-Pi	D	L	F	S	D	G	H	S	E	F	L	K	A	A	S*	N	L	R	-	-	-	471.267	542.305	613.342	741.437	854.521	1001.589	1130.632	1217.664	1354.723	1411.744
	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Leu	Asn	Ser	Ala	Ala	Lys	Leu	Phe	Glu	Ser	His	Gly



IQEAGTEVVK (Peptide Mods: 10: Acetyl (K))

MH+(mono): 1073.584
MH+(avg): 1074.207
MS/MS Tol: 0.500 Da
Peaks: 138
Above Threshold: 138
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 22
Not Assigned: 116
1+, m/z: 0.000

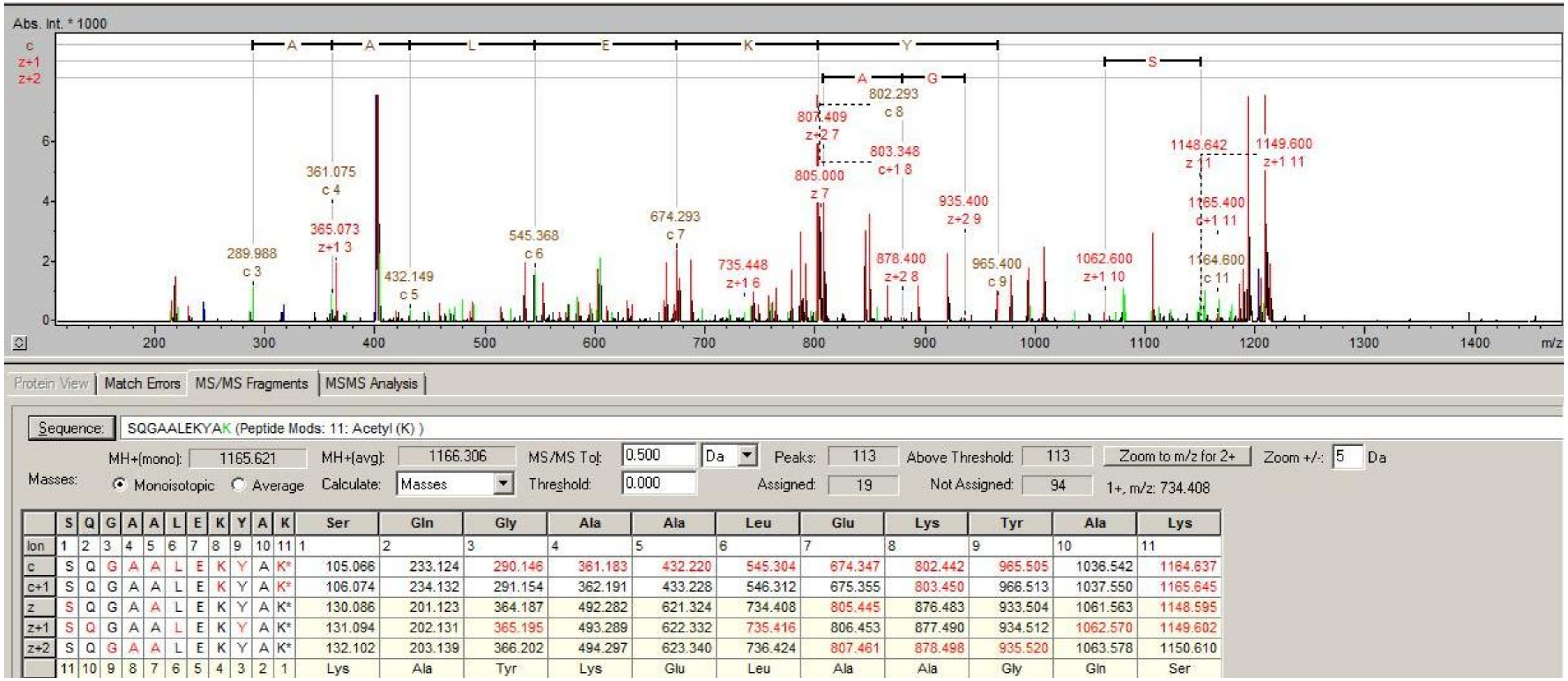
	I	Q	E	A	G	T	E	V	V	K	Ile	Gln	Glu	Ala	Gly	Thr	Glu	Val	Val	Lys
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	I	Q	E	A	G	T	E	V	V	K*	114.091	242.150	371.193	442.230	499.251	600.299	729.341	828.410	927.478	1055.573
b-17	I	Q	E	A	G	T	E	V	V	K*	-	225.123	354.166	425.203	482.225	583.272	712.315	811.383	910.452	1038.547
b-18	I	Q	E	A	G	T	E	V	V	K*	-	-	353.182	424.219	481.241	582.288	711.331	810.399	909.468	1037.563
y	I	Q	E	A	G	T	E	V	V	K*	147.113	246.181	345.250	474.292	575.340	632.361	703.398	832.441	960.500	1073.584
y-17	I	Q	E	A	G	T	E	V	V	K*	130.086	229.155	328.223	457.266	558.313	615.335	686.372	815.415	943.473	1056.557
y-18	I	Q	E	A	G	T	E	V	V	K*	-	-	-	456.282	557.329	614.351	685.388	814.431	942.489	1055.573
	10	9	8	7	6	5	4	3	2	1	Lys	Val	Val	Glu	Thr	Gly	Ala	Glu	Gln	Ile



Sequence: KLSSAMSAAK (Peptide Mods: 1: Acetyl (K))

MH+(mono): 993.540
MH+(avg): 994.190
MS/MS Tol: 0.500 Da
Peaks: 128
Above Threshold: 128
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 21
Not Assigned: 107
1+, m/z: 0.000

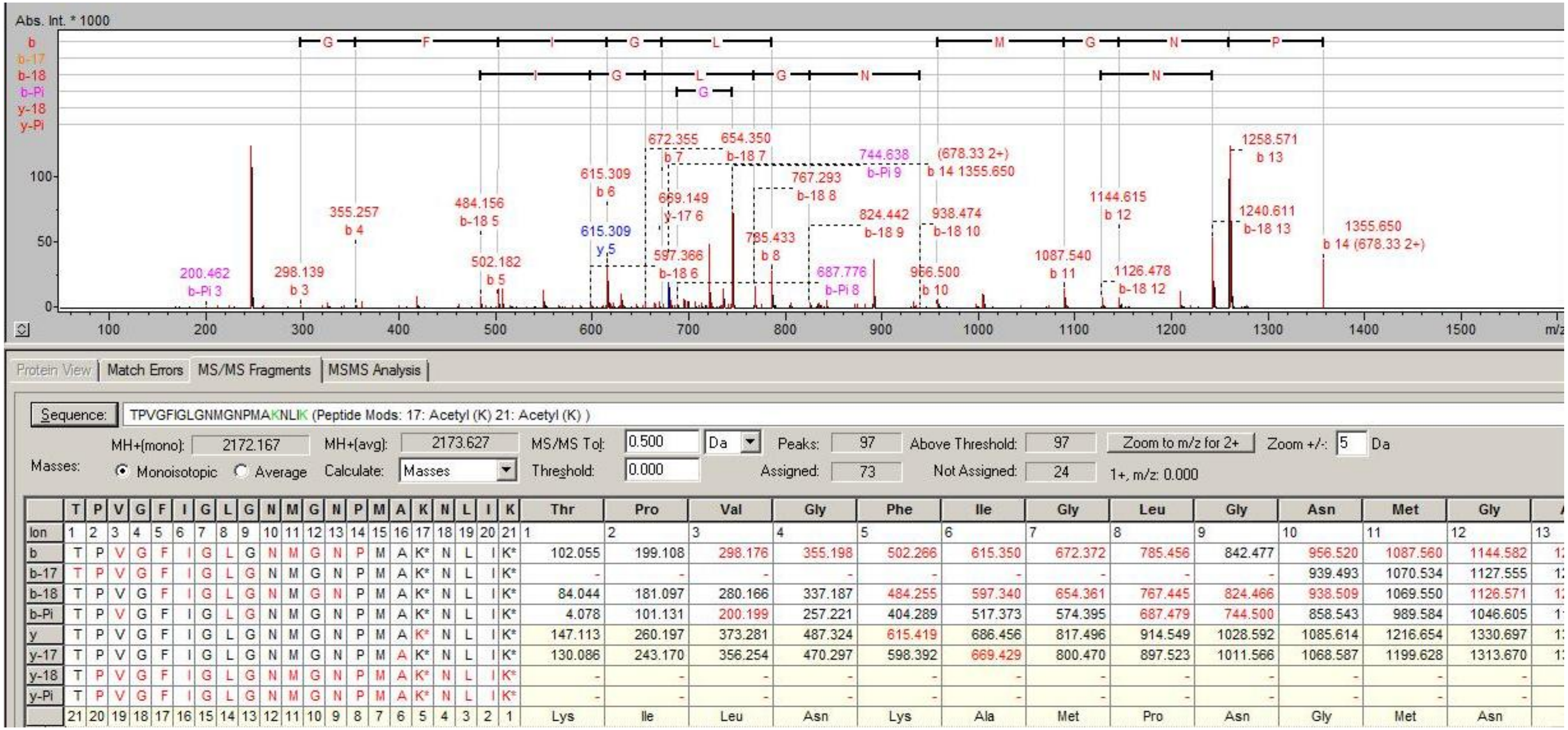
	K	L	S	S	A	M	S	A	A	K	Lys	Leu	Ser	Ser	Ala	Met	Ser	Ala	Ala	Lys
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	K*	L	S	S	A	M	S	A	A	K	129.102	242.186	329.218	416.250	487.287	618.328	705.360	776.397	847.434	975.529
b-17	K*	L	S	S	A	M	S	A	A	K	112.076	225.160	312.192	399.224	470.261	601.301	688.333	759.371	830.408	958.503
b-18	K*	L	S	S	A	M	S	A	A	K	-	-	311.208	398.240	469.277	600.317	687.349	758.387	829.424	957.519
y	K*	L	S	S	A	M	S	A	A	K	147.113	218.150	289.187	376.219	507.260	578.297	665.329	752.361	865.445	993.540
y-17	K*	L	S	S	A	M	S	A	A	K	130.086	201.123	272.160	359.193	490.233	561.270	648.302	735.334	848.418	976.513
y-18	K*	L	S	S	A	M	S	A	A	K	-	-	-	358.208	489.249	560.286	647.318	734.350	847.434	975.529
	10	9	8	7	6	5	4	3	2	1	Lys	Ala	Ala	Ser	Met	Ala	Ser	Ser	Leu	Lys



Sequence: SQGAALEKYAK (Peptide Mods: 11: Acetyl (K))

MH+(mono): 1165.621
MH+(avg): 1166.306
MS/MS Tol: 0.500 Da
Peaks: 113
Above Threshold: 113
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 19
Not Assigned: 94
1+, m/z: 734.408

	S	Q	G	A	A	L	E	K	Y	A	K	Ser	Gln	Gly	Ala	Ala	Leu	Glu	Lys	Tyr	Ala	Lys
Ion	1	2	3	4	5	6	7	8	9	10	11	1	2	3	4	5	6	7	8	9	10	11
c	S	Q	G	A	A	L	E	K	Y	A	K*	105.066	233.124	290.146	361.183	432.220	545.304	674.347	802.442	965.505	1036.542	1164.637
c+1	S	Q	G	A	A	L	E	K	Y	A	K*	106.074	234.132	291.154	362.191	433.228	546.312	675.355	803.450	966.513	1037.550	1165.645
z	S	Q	G	A	A	L	E	K	Y	A	K*	130.086	201.123	364.187	492.282	621.324	734.408	805.445	876.483	933.504	1061.563	1148.595
z+1	S	Q	G	A	A	L	E	K	Y	A	K*	131.094	202.131	365.195	493.289	622.332	735.416	806.453	877.490	934.512	1062.570	1149.602
z+2	S	Q	G	A	A	L	E	K	Y	A	K*	132.102	203.139	366.202	494.297	623.340	736.424	807.461	878.498	935.520	1063.578	1150.610
	11	10	9	8	7	6	5	4	3	2	1	Lys	Ala	Tyr	Lys	Glu	Leu	Ala	Ala	Gly	Gln	Ser

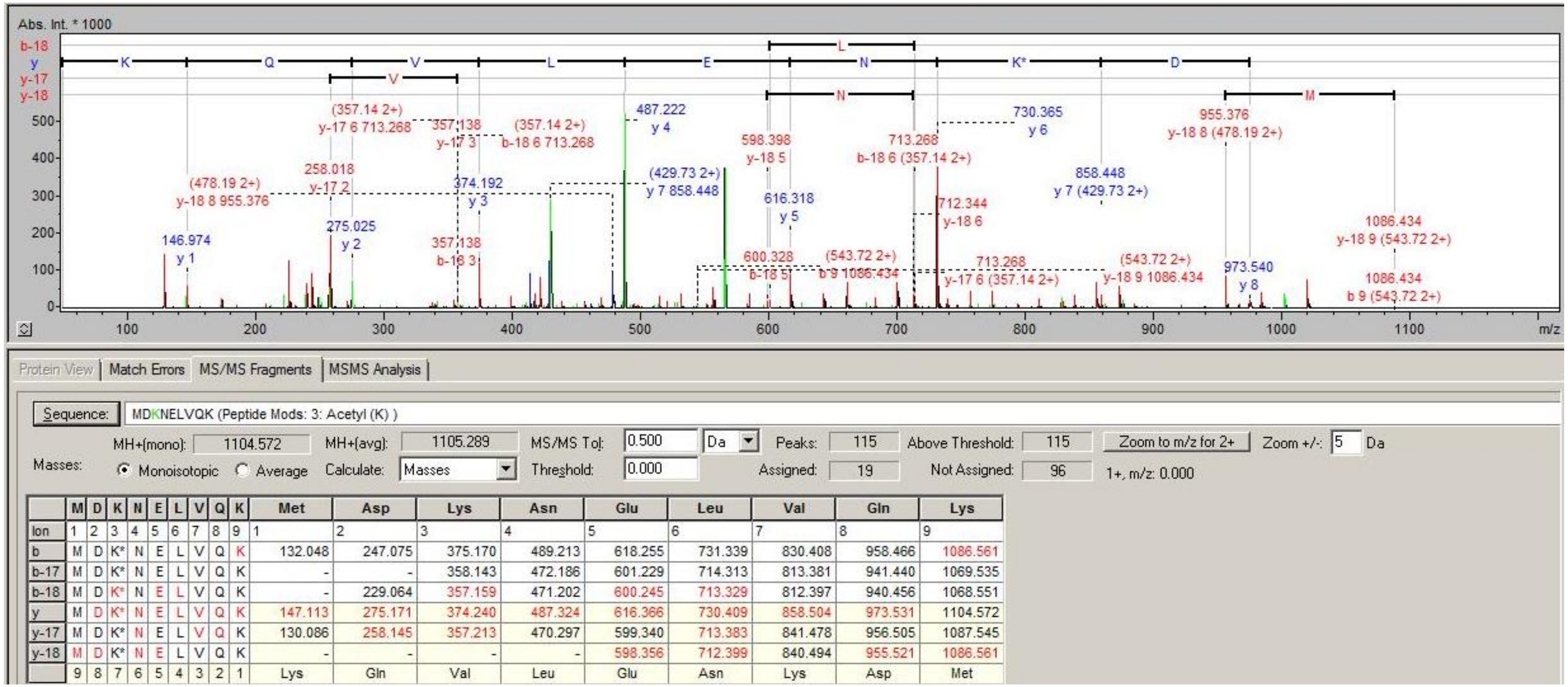


Sequence: TPVGFIGLGNMGNPMAKNLIK (Peptide Mods: 17: Acetyl (K) 21: Acetyl (K))

MH+(mono): 2172.167 MH+(avg): 2173.627 MS/MS Tol: 0.500 Da Peaks: 97 Above Threshold: 97 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 73 Not Assigned: 24 1+, m/z: 0.000

	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K	N	L	I	K	Thr	Pro	Val	Gly	Phe	Ile	Gly	Leu	Gly	Asn	Met	Gly	
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	1	2	3	4	5	6	7	8	9	10	11	12	13
b	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	102.055	199.108	298.176	355.198	502.266	615.350	672.372	785.456	842.477	956.520	1087.560	1144.582	
b-17	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	-	-	-	-	-	-	-	-	-	939.493	1070.534	1127.555	
b-18	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	84.044	181.097	280.166	337.187	484.255	597.340	654.361	767.445	824.466	938.509	1069.550	1126.571	
b-Pi	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	4.078	101.131	200.199	257.221	404.289	517.373	574.395	687.479	744.500	858.543	989.584	1046.605	
y	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	147.113	260.197	373.281	487.324	615.419	686.456	817.496	914.549	1028.592	1085.614	1216.654	1330.697	
y-17	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	130.086	243.170	356.254	470.297	598.392	669.429	800.470	897.523	1011.566	1068.587	1199.628	1313.670	
y-18	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	-	-	-	-	-	-	-	-	-	-	-	-	
y-Pi	T	P	V	G	F	I	G	L	G	N	M	G	N	P	M	A	K*	N	L	I	K*	-	-	-	-	-	-	-	-	-	-	-	-	
	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Ile	Leu	Asn	Lys	Ala	Met	Pro	Asn	Gly	Met	Asn	

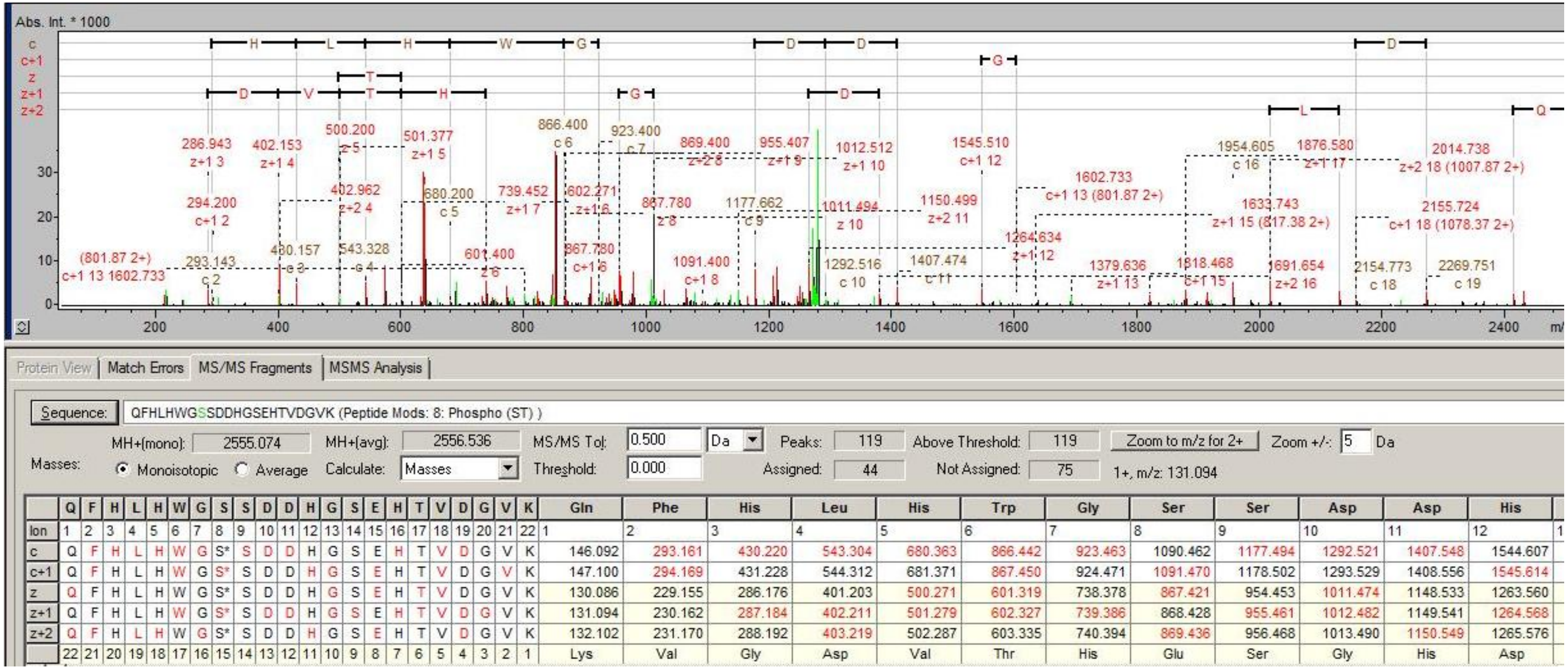


Sequence: MDKNELVQK (Peptide Mods: 3: Acetyl (K))

Masses: MH+(mono): 1104.572 MH+(avg): 1105.289 MS/MS Tol: 0.500 Da Peaks: 115 Above Threshold: 115 Zoom +/-: 5 Da

● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 19 Not Assigned: 96 1+, m/z: 0.000

	M	D	K	N	E	L	V	Q	K	Met	Asp	Lys	Asn	Glu	Leu	Val	Gln	Lys
Ion	1	2	3	4	5	6	7	8	9	1	2	3	4	5	6	7	8	9
b	M	D	K*	N	E	L	V	Q	K	132.048	247.075	375.170	489.213	618.255	731.339	830.408	958.466	1086.561
b-17	M	D	K*	N	E	L	V	Q	K	-	-	358.143	472.186	601.229	714.313	813.381	941.440	1069.535
b-18	M	D	K*	N	E	L	V	Q	K	-	229.064	357.159	471.202	600.245	713.329	812.397	940.456	1068.551
y	M	D	K*	N	E	L	V	Q	K	147.113	275.171	374.240	487.324	616.366	730.409	858.504	973.531	1104.572
y-17	M	D	K*	N	E	L	V	Q	K	130.086	258.145	357.213	470.297	599.340	713.383	841.478	956.505	1087.545
y-18	M	D	K*	N	E	L	V	Q	K	-	-	-	-	598.356	712.399	840.494	955.521	1086.561
	9	8	7	6	5	4	3	2	1	Lys	Gln	Val	Leu	Glu	Asn	Lys	Asp	Met

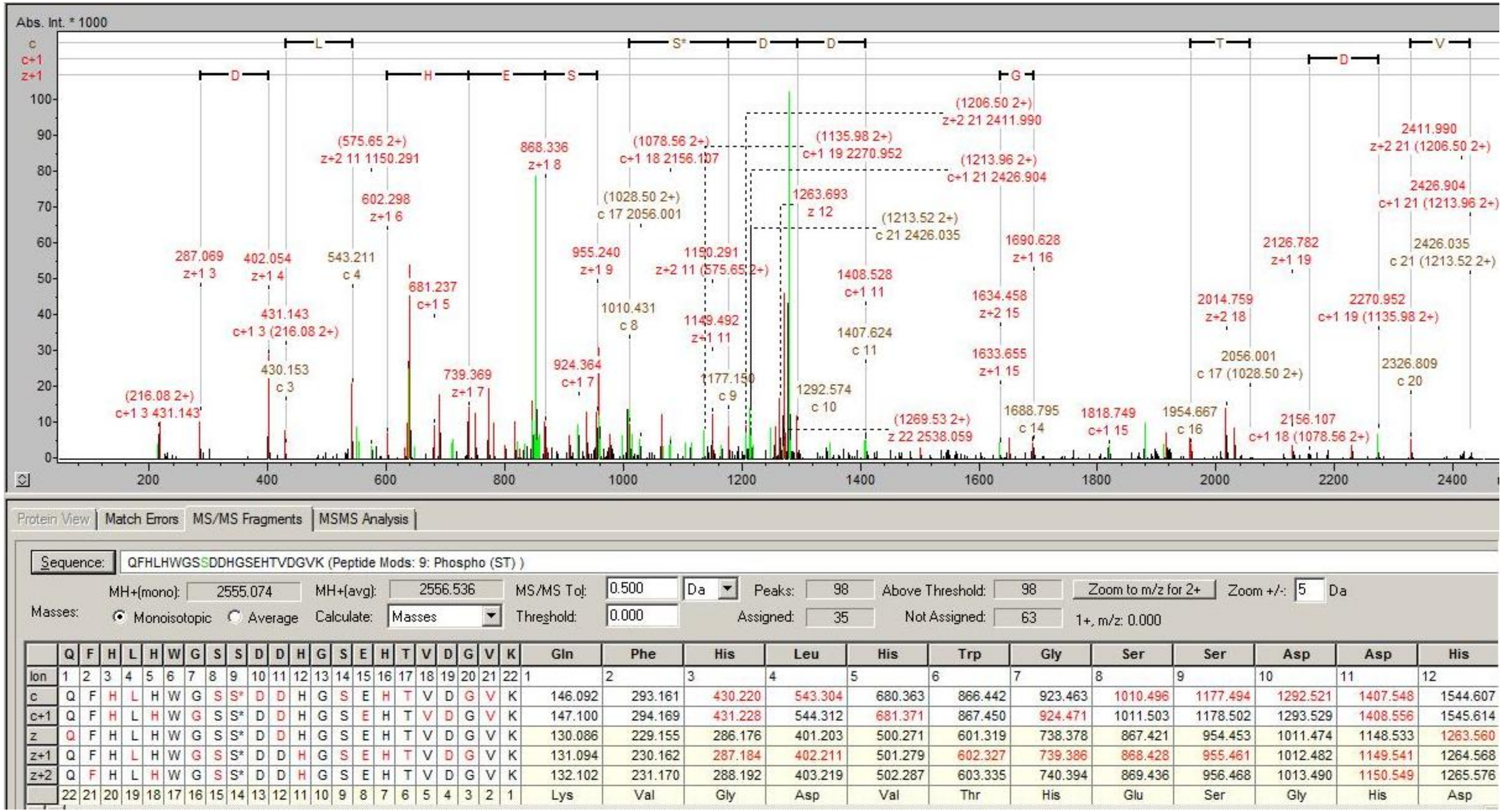


Sequence: QFHLHWGSSDDHGSEHTVDGVK (Peptide Mods: 8: Phospho (ST))

MH+(mono): 2555.074
MH+(avg): 2556.536
MS/MS Tol: 0.500 Da
Peaks: 119
Above Threshold: 119
Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 44
Not Assigned: 75
1+, m/z: 131.094

	Q	F	H	L	H	W	G	S	S	D	D	H	G	S	E	H	T	V	D	G	V	K	Gln	Phe	His	Leu	His	Trp	Gly	Ser	Ser	Asp	Asp	His
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	1	2	3	4	5	6	7	8	9	10	11	12
c	Q	F	H	L	H	W	G	S*	S	D	D	H	G	S	E	H	T	V	D	G	V	K	146.092	293.161	430.220	543.304	680.363	866.442	923.463	1090.462	1177.494	1292.521	1407.548	1544.607
c+1	Q	F	H	L	H	W	G	S*	S	D	D	H	G	S	E	H	T	V	D	G	V	K	147.100	294.169	431.228	544.312	681.371	867.450	924.471	1091.470	1178.502	1293.529	1408.556	1545.614
z	Q	F	H	L	H	W	G	S*	S	D	D	H	G	S	E	H	T	V	D	G	V	K	130.086	229.155	286.176	401.203	500.271	601.319	738.378	867.421	954.453	1011.474	1148.533	1263.560
z+1	Q	F	H	L	H	W	G	S*	S	D	D	H	G	S	E	H	T	V	D	G	V	K	131.094	230.162	287.184	402.211	501.279	602.327	739.386	868.428	955.461	1012.482	1149.541	1264.568
z+2	Q	F	H	L	H	W	G	S*	S	D	D	H	G	S	E	H	T	V	D	G	V	K	132.102	231.170	288.192	403.219	502.287	603.335	740.394	869.436	956.468	1013.490	1150.549	1265.576
	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Val	Gly	Asp	Val	Thr	His	Glu	Ser	Gly	His	Asp



Sequence: QFHLHWGSSDDHGSEHTVDGVK (Peptide Mods: 9: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 2555.074

MH+(avg): 2556.536

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 98

Above Threshold: 98

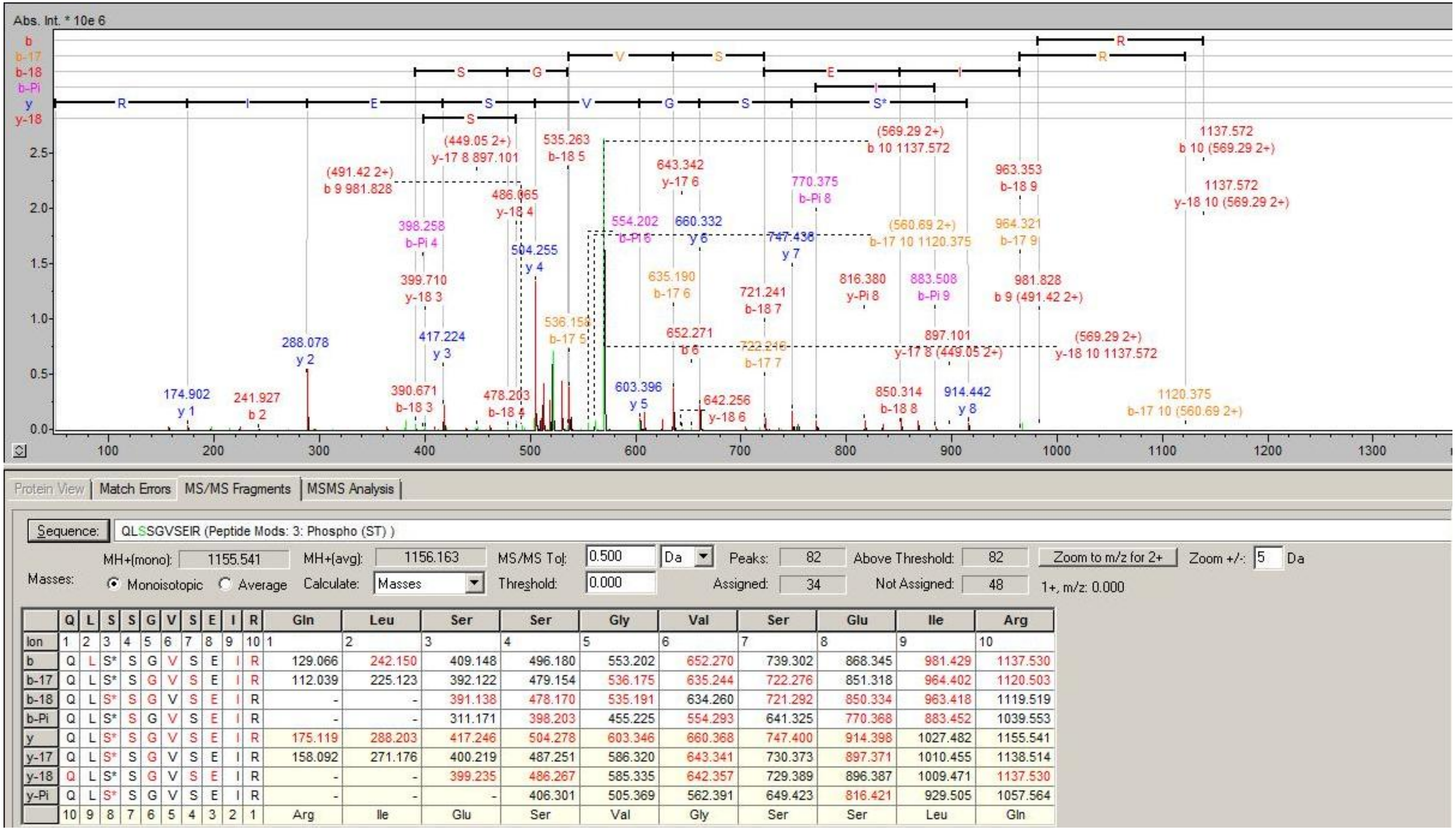
Assigned: 35

Not Assigned: 63

Zoom +/-: 5 Da

1+, m/z: 0.000

	Q	F	H	L	H	W	G	S	S	D	D	H	G	S	E	H	T	V	D	G	V	K	Gln	Phe	His	Leu	His	Trp	Gly	Ser	Ser	Asp	Asp	His
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	1	2	3	4	5	6	7	8	9	10	11	12
c	Q	F	H	L	H	W	G	S	S*	D	D	H	G	S	E	H	T	V	D	G	V	K	146.092	293.161	430.220	543.304	680.363	866.442	923.463	1010.496	1177.494	1292.521	1407.548	1544.607
c+1	Q	F	H	L	H	W	G	S	S*	D	D	H	G	S	E	H	T	V	D	G	V	K	147.100	294.169	431.228	544.312	681.371	867.450	924.471	1011.503	1178.502	1293.529	1408.556	1545.614
z	Q	F	H	L	H	W	G	S	S*	D	D	H	G	S	E	H	T	V	D	G	V	K	130.086	229.155	286.176	401.203	500.271	601.319	738.378	867.421	954.453	1011.474	1148.533	1263.560
z+1	Q	F	H	L	H	W	G	S	S*	D	D	H	G	S	E	H	T	V	D	G	V	K	131.094	230.162	287.184	402.211	501.279	602.327	739.386	868.428	955.461	1012.482	1149.541	1264.568
z+2	Q	F	H	L	H	W	G	S	S*	D	D	H	G	S	E	H	T	V	D	G	V	K	132.102	231.170	288.192	403.219	502.287	603.335	740.394	869.436	956.468	1013.490	1150.549	1265.576
	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Val	Gly	Asp	Val	Thr	His	Glu	Ser	Gly	His	Asp



Sequence: QLSSGVSEIR (Peptide Mods: 3: Phospho (ST))

Masses:

MH+(mono): 1155.541

● Monoisotopic ○ Average

MH+(avg): 1156.163

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 82

Assigned: 34

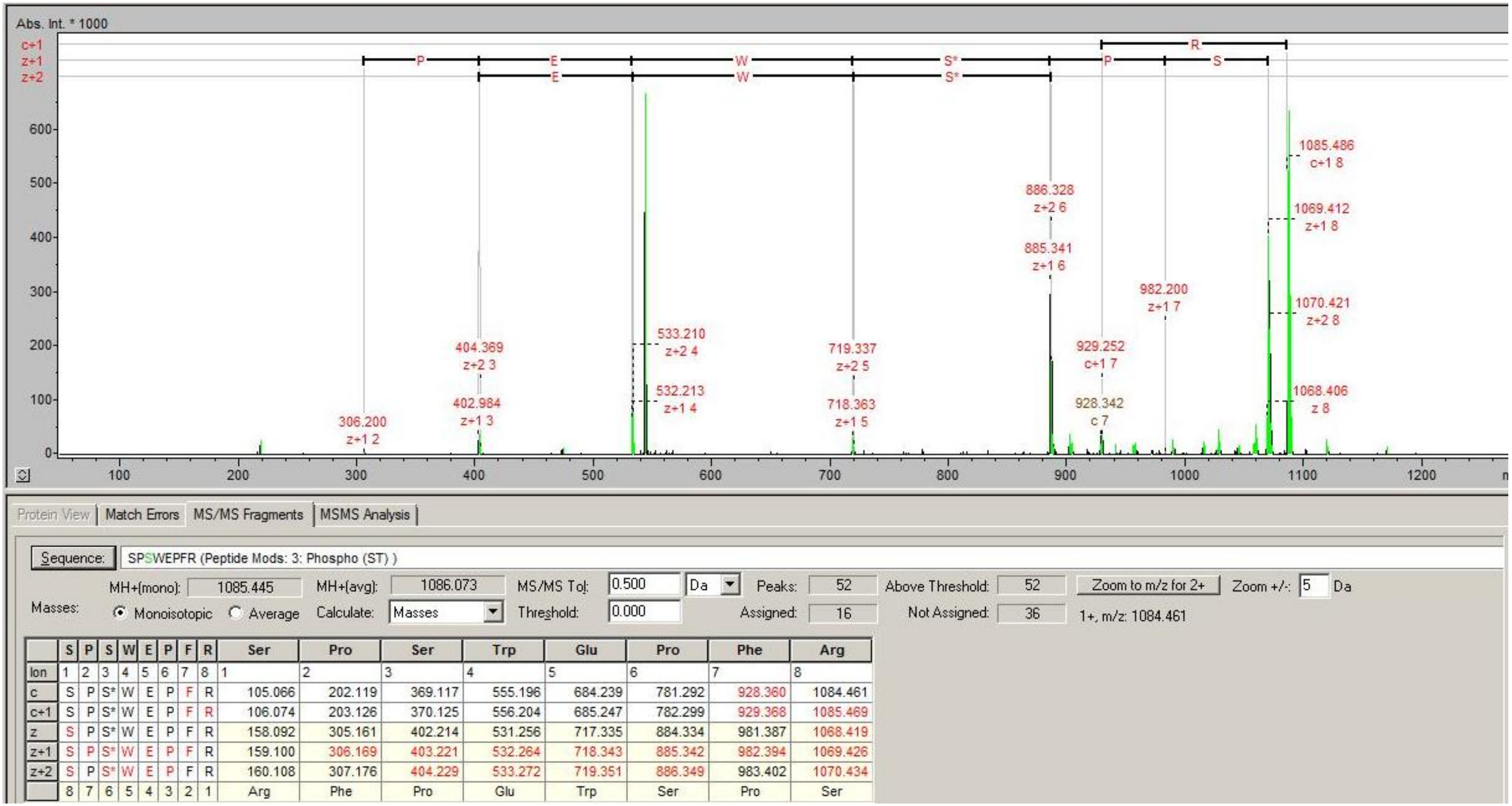
Above Threshold: 82

Not Assigned: 48

Zoom +/-: 5 Da

1+, m/z: 0.000

	Q	L	S	S	G	V	S	E	I	R	Gln	Leu	Ser	Ser	Gly	Val	Ser	Glu	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	Q	L	S*	S	G	V	S	E	I	R	129.066	242.150	409.148	496.180	553.202	652.270	739.302	868.345	981.429	1137.530
b-17	Q	L	S*	S	G	V	S	E	I	R	112.039	225.123	392.122	479.154	536.175	635.244	722.276	851.318	964.402	1120.503
b-18	Q	L	S*	S	G	V	S	E	I	R	-	-	391.138	478.170	535.191	634.260	721.292	850.334	963.418	1119.519
b-Pi	Q	L	S*	S	G	V	S	E	I	R	-	-	311.171	398.203	455.225	554.293	641.325	770.368	883.452	1039.553
y	Q	L	S*	S	G	V	S	E	I	R	175.119	288.203	417.246	504.278	603.346	660.368	747.400	914.398	1027.482	1155.541
y-17	Q	L	S*	S	G	V	S	E	I	R	158.092	271.176	400.219	487.251	586.320	643.341	730.373	897.371	1010.455	1138.514
y-18	Q	L	S*	S	G	V	S	E	I	R	-	-	399.235	486.267	585.335	642.357	729.389	896.387	1009.471	1137.530
y-Pi	Q	L	S*	S	G	V	S	E	I	R	-	-	-	406.301	505.369	562.391	649.423	816.421	929.505	1057.564
	10	9	8	7	6	5	4	3	2	1	Arg	Ile	Glu	Ser	Val	Gly	Ser	Ser	Leu	Gln



SPSWEPFR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1085.445

MH+(avg): 1086.073

MS/MS Tol: 0.500 Da

Peaks: 52

Above Threshold: 52

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

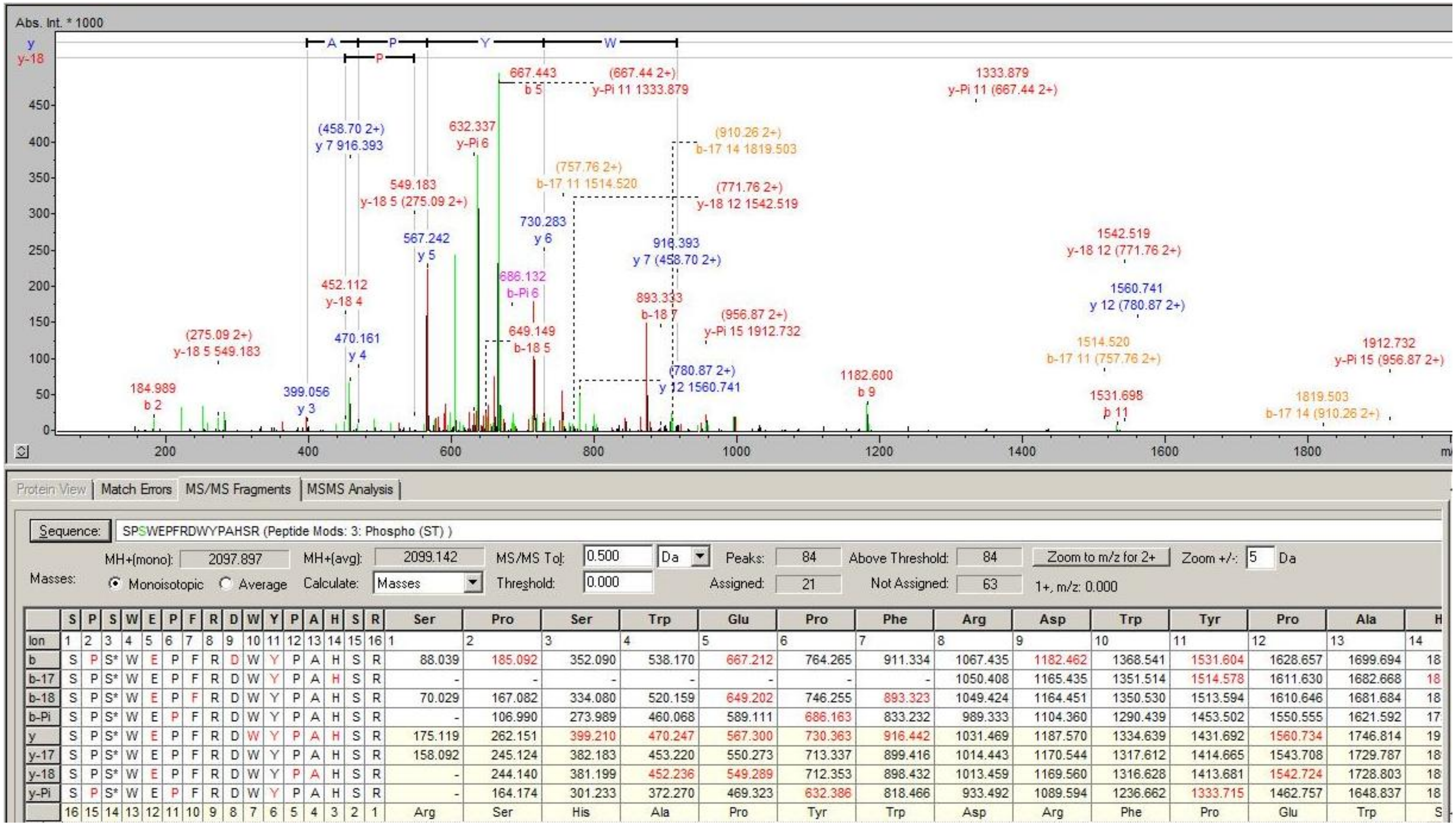
Threshold: 0.000

Assigned: 16

Not Assigned: 36

1+, m/z: 1084.461

	S	P	S	W	E	P	F	R	Ser	Pro	Ser	Trp	Glu	Pro	Phe	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
c	S	P	S*	W	E	P	F	R	105.066	202.119	369.117	555.196	684.239	781.292	928.360	1084.461
c+1	S	P	S*	W	E	P	F	R	106.074	203.126	370.125	556.204	685.247	782.299	929.368	1085.469
z	S	P	S*	W	E	P	F	R	158.092	305.161	402.214	531.256	717.335	884.334	981.387	1068.419
z+1	S	P	S*	W	E	P	F	R	159.100	306.169	403.221	532.264	718.343	885.342	982.394	1069.426
z+2	S	P	S*	W	E	P	F	R	160.108	307.176	404.229	533.272	719.351	886.349	983.402	1070.434
	8	7	6	5	4	3	2	1	Arg	Phe	Pro	Glu	Trp	Ser	Pro	Ser

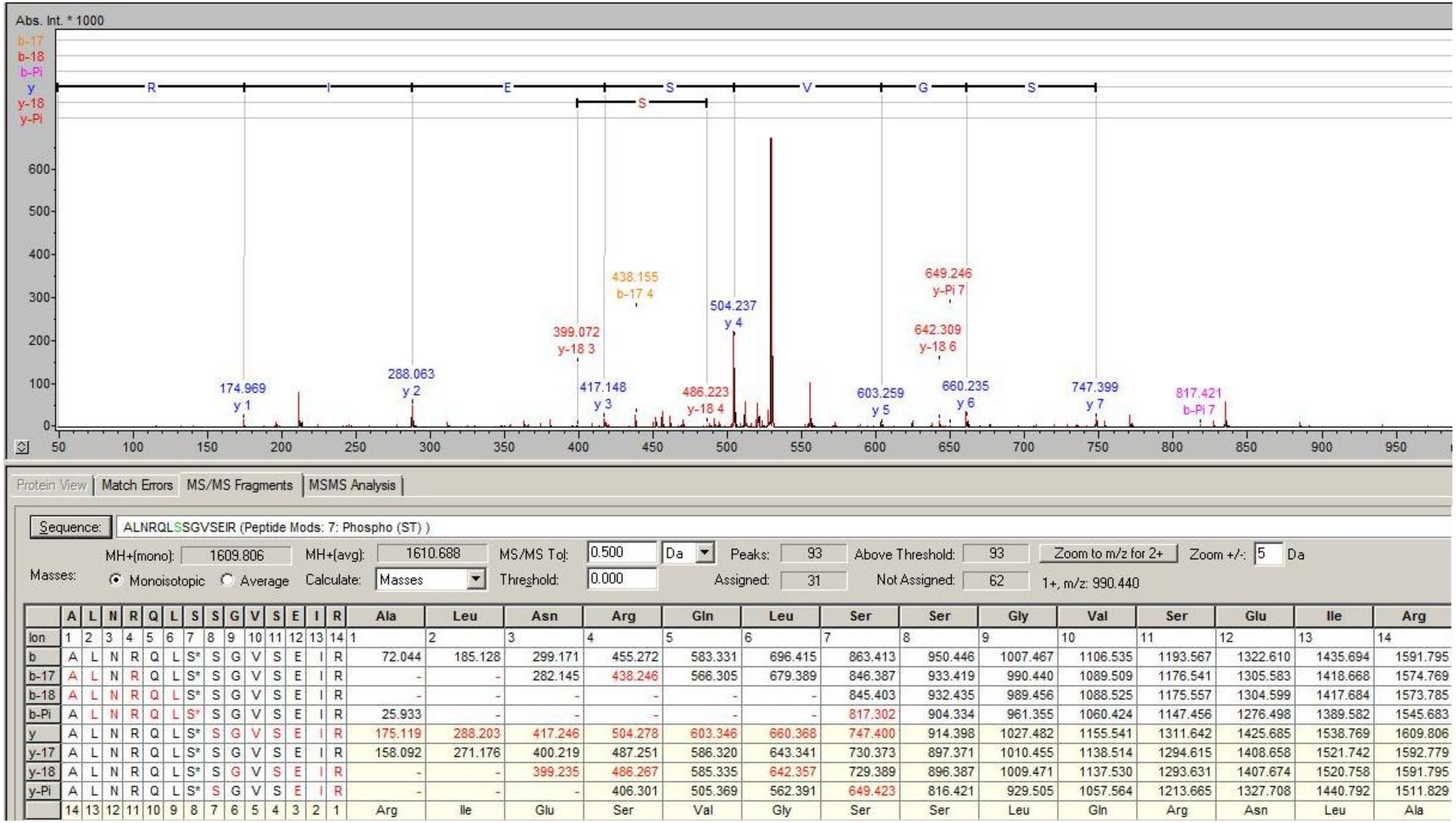


Sequence: SPSWEPFRDWYPAHSR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 2097.897 MH+(avg): 2099.142 MS/MS Tol: 0.500 Da Peaks: 84 Above Threshold: 84 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 21 Not Assigned: 63 1+, m/z: 0.000

	S	P	S	W	E	P	F	R	D	W	Y	P	A	H	S	R	Ser	Pro	Ser	Trp	Glu	Pro	Phe	Arg	Asp	Trp	Tyr	Pro	Ala	H
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	88.039	185.092	352.090	538.170	667.212	764.265	911.334	1067.435	1182.462	1368.541	1531.604	1628.657	1699.694	18
b-17	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	-	-	-	-	-	-	1050.408	1165.435	1351.514	1514.578	1611.630	1682.668	18
b-18	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	70.029	167.082	334.080	520.159	649.202	746.255	893.323	1049.424	1164.451	1350.530	1513.594	1610.646	1681.684	18
b-Pi	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	106.990	273.989	460.068	589.111	686.163	833.232	989.333	1104.360	1290.439	1453.502	1550.555	1621.592	17
y	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	175.119	262.151	399.210	470.247	567.300	730.363	916.442	1031.469	1187.570	1334.639	1431.692	1560.734	1746.814	19
y-17	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	158.092	245.124	382.183	453.220	550.273	713.337	899.416	1014.443	1170.544	1317.612	1414.665	1543.708	1729.787	18
y-18	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	244.140	381.199	452.236	549.289	712.353	898.432	1013.459	1169.560	1316.628	1413.681	1542.724	1728.803	18
y-Pi	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	164.174	301.233	372.270	469.323	632.386	818.466	933.492	1089.594	1236.662	1333.715	1462.757	1648.837	18
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	His	Ala	Pro	Tyr	Trp	Asp	Arg	Phe	Pro	Glu	Trp	S

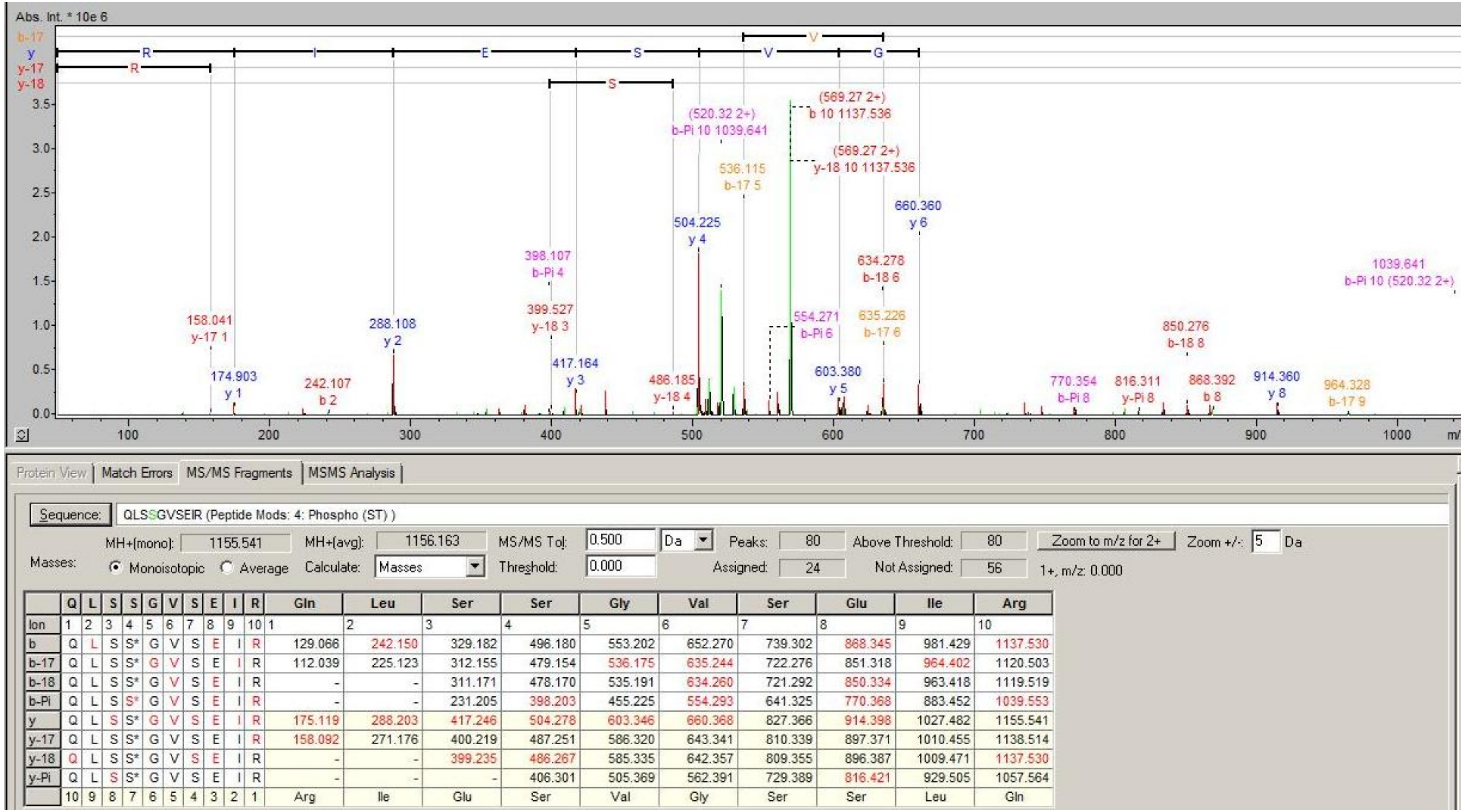


Sequence: ALNRQLSSGVSEIR (Peptide Mods: 7: Phospho (ST))

MH+(mono): 1609.806 MH+(avg): 1610.688 MS/MS Tol: 0.500 Da Peaks: 93 Above Threshold: 93 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 31 Not Assigned: 62 1+, m/z: 990.440

	A	L	N	R	Q	L	S	S	G	V	S	E	I	R	Ala	Leu	Asn	Arg	Gln	Leu	Ser	Ser	Gly	Val	Ser	Glu	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	72.044	185.128	299.171	455.272	583.331	696.415	863.413	950.446	1007.467	1106.535	1193.567	1322.610	1435.694	1591.795
b-17	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	-	-	282.145	438.246	566.305	679.389	846.387	933.419	990.440	1089.509	1176.541	1305.583	1418.668	1574.769
b-18	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	-	-	-	-	-	-	845.403	932.435	989.456	1088.525	1175.557	1304.599	1417.684	1573.785
b-Pi	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	25.933	-	-	-	-	-	817.302	904.334	961.355	1060.424	1147.456	1276.498	1389.582	1545.683
y	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	175.119	288.203	417.246	504.278	603.346	660.368	747.400	914.398	1027.482	1155.541	1311.642	1425.685	1538.769	1609.806
y-17	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	158.092	271.176	400.219	487.251	586.320	643.341	730.373	897.371	1010.455	1138.514	1294.615	1408.658	1521.742	1592.779
y-18	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	-	-	399.235	486.267	585.335	642.357	729.389	896.387	1009.471	1137.530	1293.631	1407.674	1520.758	1591.795
y-Pi	A	L	N	R	Q	L	S*	S	G	V	S	E	I	R	-	-	-	406.301	505.369	562.391	649.423	816.421	929.505	1057.564	1213.665	1327.708	1440.792	1511.829
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ile	Glu	Ser	Val	Gly	Ser	Ser	Leu	Gln	Arg	Asn	Leu	Ala

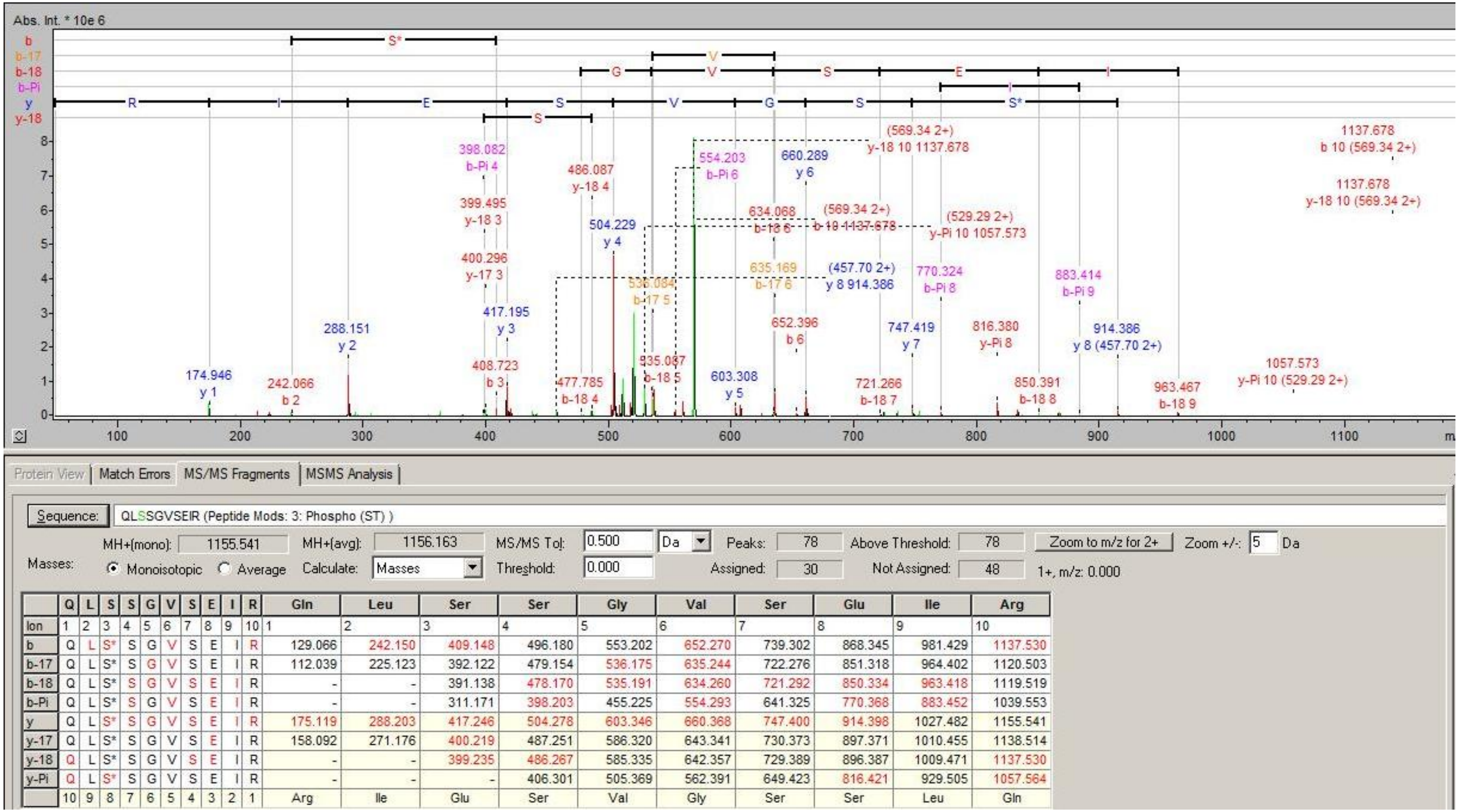


Sequence: QLSSGVSEIR (Peptide Mods: 4: Phospho (ST))

MH+(mono): 1155.541 MH+(avg): 1156.163 MS/MS Tol: 0.500 Da Peaks: 80 Above Threshold: 80 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 24 Not Assigned: 56 1+, m/z: 0.000

	Q	L	S	S	G	V	S	E	I	R	Gln	Leu	Ser	Ser	Gly	Val	Ser	Glu	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	Q	L	S	S*	G	V	S	E	I	R	129.066	242.150	329.182	496.180	553.202	652.270	739.302	868.345	981.429	1137.530
b-17	Q	L	S	S*	G	V	S	E	I	R	112.039	225.123	312.155	479.154	536.175	635.244	722.276	851.318	964.402	1120.503
b-18	Q	L	S	S*	G	V	S	E	I	R	-	-	311.171	478.170	535.191	634.260	721.292	850.334	963.418	1119.519
b-Pi	Q	L	S	S*	G	V	S	E	I	R	-	-	231.205	398.203	455.225	554.293	641.325	770.368	883.452	1039.553
y	Q	L	S	S*	G	V	S	E	I	R	175.119	288.203	417.246	504.278	603.346	660.368	827.366	914.398	1027.482	1155.541
y-17	Q	L	S	S*	G	V	S	E	I	R	158.092	271.176	400.219	487.251	586.320	643.341	810.339	897.371	1010.455	1138.514
y-18	Q	L	S	S*	G	V	S	E	I	R	-	-	399.235	486.267	585.335	642.357	809.355	896.387	1009.471	1137.530
y-Pi	Q	L	S	S*	G	V	S	E	I	R	-	-	-	406.301	505.369	562.391	729.389	816.421	929.505	1057.564
	10	9	8	7	6	5	4	3	2	1	Arg	Ile	Glu	Ser	Val	Gly	Ser	Ser	Leu	Gln

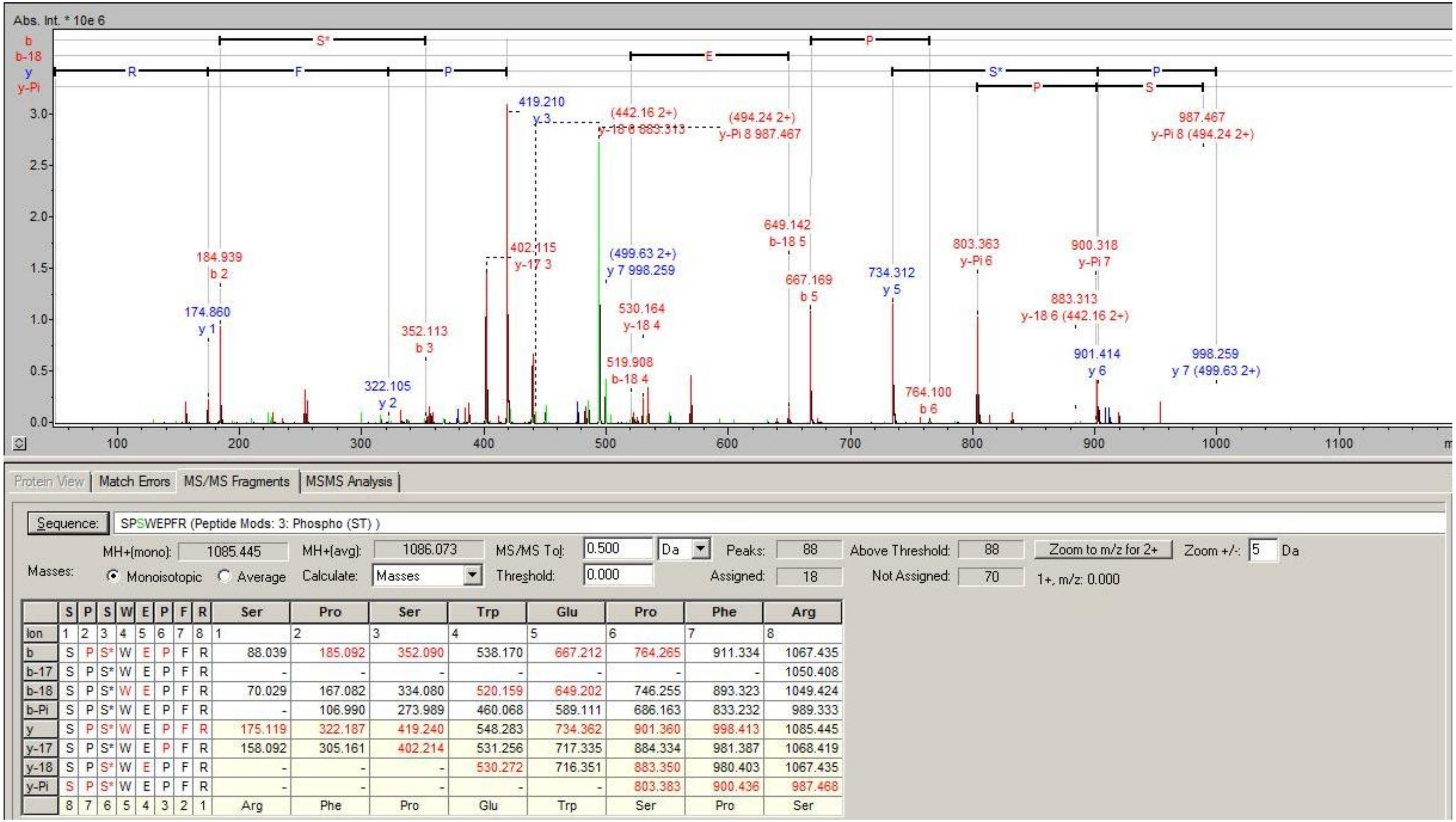


Sequence: QLSSGVSEIR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1155.541 MH+(avg): 1156.163 MS/MS Tol: 0.500 Da Peaks: 78 Above Threshold: 78 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 30 Not Assigned: 48 1+, m/z: 0.000

	Q	L	S	S	G	V	S	E	I	R	Gln	Leu	Ser	Ser	Gly	Val	Ser	Glu	Ile	Arg
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	Q	L	S*	S	G	V	S	E	I	R	129.066	242.150	409.148	496.180	553.202	652.270	739.302	868.345	981.429	1137.530
b-17	Q	L	S*	S	G	V	S	E	I	R	112.039	225.123	392.122	479.154	536.175	635.244	722.276	851.318	964.402	1120.503
b-18	Q	L	S*	S	G	V	S	E	I	R	-	-	391.138	478.170	535.191	634.260	721.292	850.334	963.418	1119.519
b-Pi	Q	L	S*	S	G	V	S	E	I	R	-	-	311.171	398.203	455.225	554.293	641.325	770.368	883.452	1039.553
y	Q	L	S*	S	G	V	S	E	I	R	175.119	288.203	417.246	504.278	603.346	660.368	747.400	914.398	1027.482	1155.541
y-17	Q	L	S*	S	G	V	S	E	I	R	158.092	271.176	400.219	487.251	586.320	643.341	730.373	897.371	1010.455	1138.514
y-18	Q	L	S*	S	G	V	S	E	I	R	-	-	399.235	486.267	585.335	642.357	729.389	896.387	1009.471	1137.530
y-Pi	Q	L	S*	S	G	V	S	E	I	R	-	-	-	406.301	505.369	562.391	649.423	816.421	929.505	1057.564
	10	9	8	7	6	5	4	3	2	1	Arg	Ile	Glu	Ser	Val	Gly	Ser	Ser	Leu	Gln



Sequence: SPSWEPFR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1085.445

MH+(avg): 1086.073

MS/MS Tol: 0.500 Da

Peaks: 88

Above Threshold: 88

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

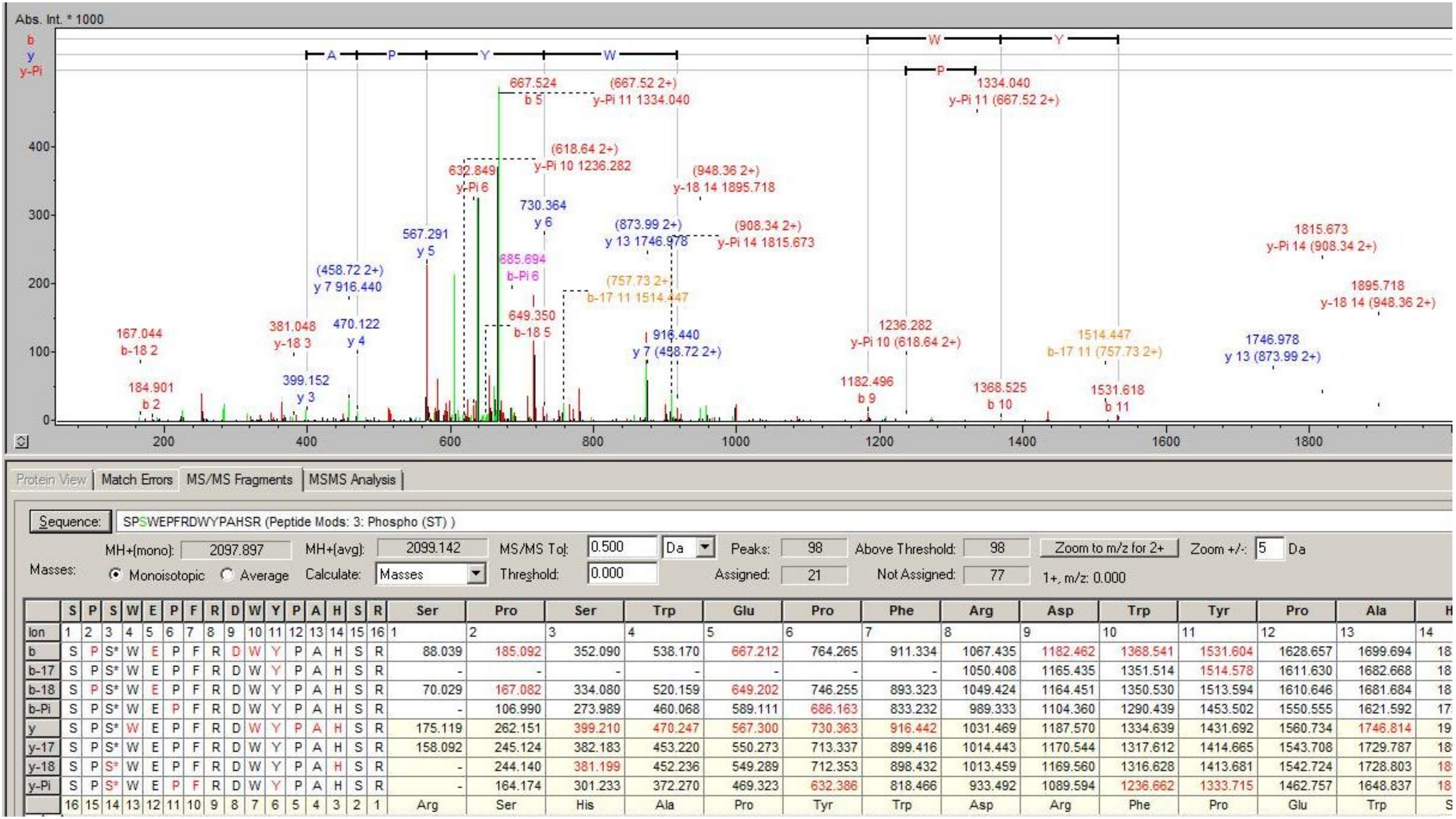
Threshold: 0.000

Assigned: 18

Not Assigned: 70

1+, m/z: 0.000

	S	P	S	W	E	P	F	R	Ser	Pro	Ser	Trp	Glu	Pro	Phe	Arg
Ion	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
b	S	P	S*	W	E	P	F	R	88.039	185.092	352.090	538.170	667.212	764.265	911.334	1067.435
b-17	S	P	S*	W	E	P	F	R	-	-	-	-	-	-	-	1050.408
b-18	S	P	S*	W	E	P	F	R	70.029	167.082	334.080	520.159	649.202	746.255	893.323	1049.424
b-Pi	S	P	S*	W	E	P	F	R	-	106.990	273.989	460.068	589.111	686.163	833.232	989.333
y	S	P	S*	W	E	P	F	R	175.119	322.187	419.240	548.283	734.362	901.360	998.413	1085.445
y-17	S	P	S*	W	E	P	F	R	158.092	305.161	402.214	531.256	717.335	884.334	981.387	1068.419
y-18	S	P	S*	W	E	P	F	R	-	-	-	530.272	716.351	883.350	980.403	1067.435
y-Pi	S	P	S*	W	E	P	F	R	-	-	-	-	-	803.383	900.436	987.468
	8	7	6	5	4	3	2	1	Arg	Phe	Pro	Glu	Trp	Ser	Pro	Ser



SPSWEPFRDWYPAHSR (Peptide Mods: 3: Phospho (ST))

Masses: ● Monoisotopic ○ Average

MH+(mono): 2097.897

MH+(avg): 2099.142

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 98

Above Threshold: 98

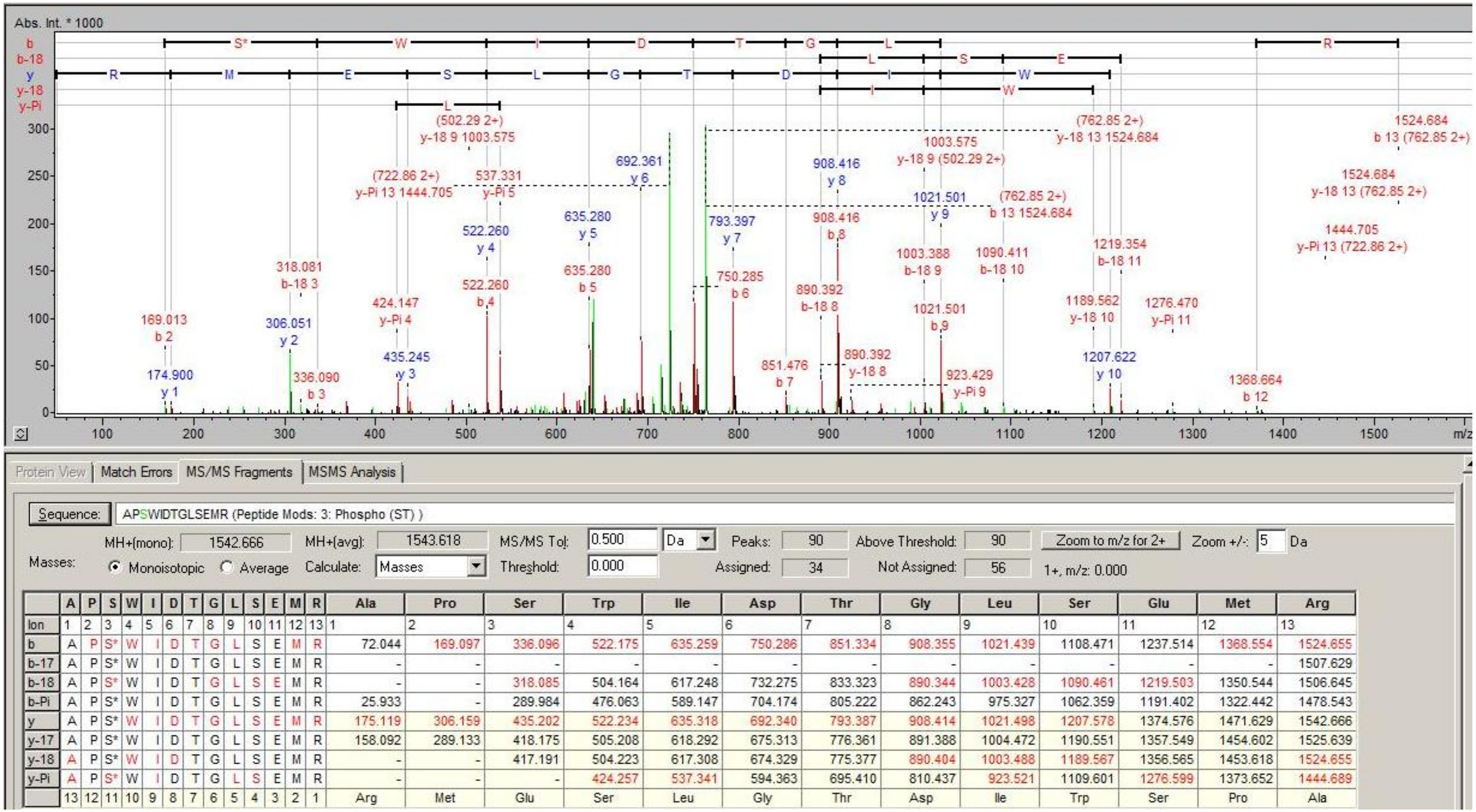
Assigned: 21

Not Assigned: 77

Zoom +/-: 5 Da

1+, m/z: 0.000

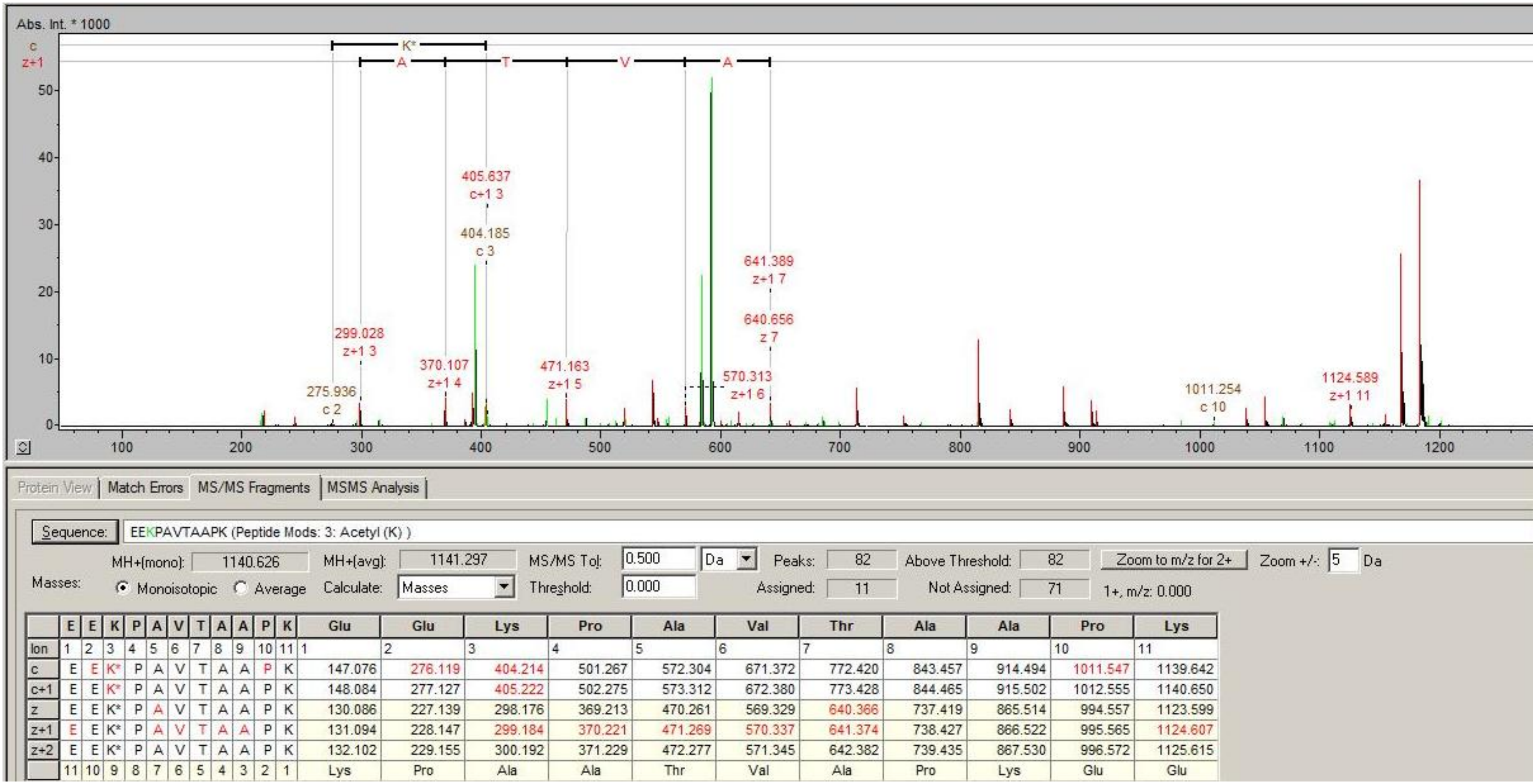
	S	P	S	W	E	P	F	R	D	W	Y	P	A	H	S	R	Ser	Pro	Ser	Trp	Glu	Pro	Phe	Arg	Asp	Trp	Tyr	Pro	Ala	H
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	88.039	185.092	352.090	538.170	667.212	764.265	911.334	1067.435	1182.462	1368.541	1531.604	1628.657	1699.694	18
b-17	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	-	-	-	-	-	-	1050.408	1165.435	1351.514	1514.578	1611.630	1682.668	18
b-18	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	70.029	167.082	334.080	520.159	649.202	746.255	893.323	1049.424	1164.451	1350.530	1513.594	1610.646	1681.684	18
b-Pi	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	106.990	273.989	460.068	589.111	686.163	833.232	989.333	1104.360	1290.439	1453.502	1550.555	1621.592	17
y	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	175.119	262.151	399.210	470.247	567.300	730.363	916.442	1031.469	1187.570	1334.639	1431.692	1560.734	1746.814	19
y-17	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	158.092	245.124	382.183	453.220	550.273	713.337	899.416	1014.443	1170.544	1317.612	1414.665	1543.708	1729.787	18
y-18	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	244.140	381.199	452.236	549.289	712.353	898.432	1013.459	1169.560	1316.628	1413.681	1542.724	1728.803	18
y-Pi	S	P	S*	W	E	P	F	R	D	W	Y	P	A	H	S	R	-	164.174	301.233	372.270	469.323	632.386	818.466	933.492	1089.594	1236.662	1333.715	1462.757	1648.837	18
	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Ser	His	Ala	Pro	Tyr	Trp	Asp	Arg	Phe	Pro	Glu	Trp	S



APSWIDTGLSEMR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1542.666
MH+(avg): 1543.618
MS/MS Tol: 0.500 Da
Peaks: 90
Above Threshold: 90
Zoom +/-: 5 Da
Masses: ● Monoisotopic ○ Average
Calculate: Masses
Threshold: 0.000
Assigned: 34
Not Assigned: 56
1+, m/z: 0.000

	A	P	S	W	I	D	T	G	L	S	E	M	R	Ala	Pro	Ser	Trp	Ile	Asp	Thr	Gly	Leu	Ser	Glu	Met	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	1	2	3	4	5	6	7	8	9	10	11	12	13
b	A	P	S*	W	I	D	T	G	L	S	E	M	R	72.044	169.097	336.096	522.175	635.259	750.286	851.334	908.355	1021.439	1108.471	1237.514	1368.554	1524.655
b-17	A	P	S*	W	I	D	T	G	L	S	E	M	R	-	-	-	-	-	-	-	-	-	-	-	-	1507.629
b-18	A	P	S*	W	I	D	T	G	L	S	E	M	R	-	-	318.085	504.164	617.248	732.275	833.323	890.344	1003.428	1090.461	1219.503	1350.544	1506.645
b-Pi	A	P	S*	W	I	D	T	G	L	S	E	M	R	25.933	-	289.984	476.063	589.147	704.174	805.222	862.243	975.327	1062.359	1191.402	1322.442	1478.543
y	A	P	S*	W	I	D	T	G	L	S	E	M	R	175.119	306.159	435.202	522.234	635.318	692.340	793.387	908.414	1021.498	1207.578	1374.576	1471.629	1542.666
y-17	A	P	S*	W	I	D	T	G	L	S	E	M	R	158.092	289.133	418.175	505.208	618.292	675.313	776.361	891.388	1004.472	1190.551	1357.549	1454.602	1525.639
y-18	A	P	S*	W	I	D	T	G	L	S	E	M	R	-	-	417.191	504.223	617.308	674.329	775.377	890.404	1003.488	1189.567	1356.565	1453.618	1524.655
y-Pi	A	P	S*	W	I	D	T	G	L	S	E	M	R	-	-	-	424.257	537.341	594.363	695.410	810.437	923.521	1109.601	1276.599	1373.652	1444.689
	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Met	Glu	Ser	Leu	Gly	Thr	Asp	Ile	Trp	Ser	Pro	Ala



EEKPAVTAAPK (Peptide Mods: 3: Acetyl (K))

Masses: ● Monoisotopic ○ Average

MH+(mono): 1140.626

MH+(avg): 1141.297

Calculate: Masses

MS/MS Tol: 0.500 Da

Threshold: 0.000

Peaks: 82

Assigned: 11

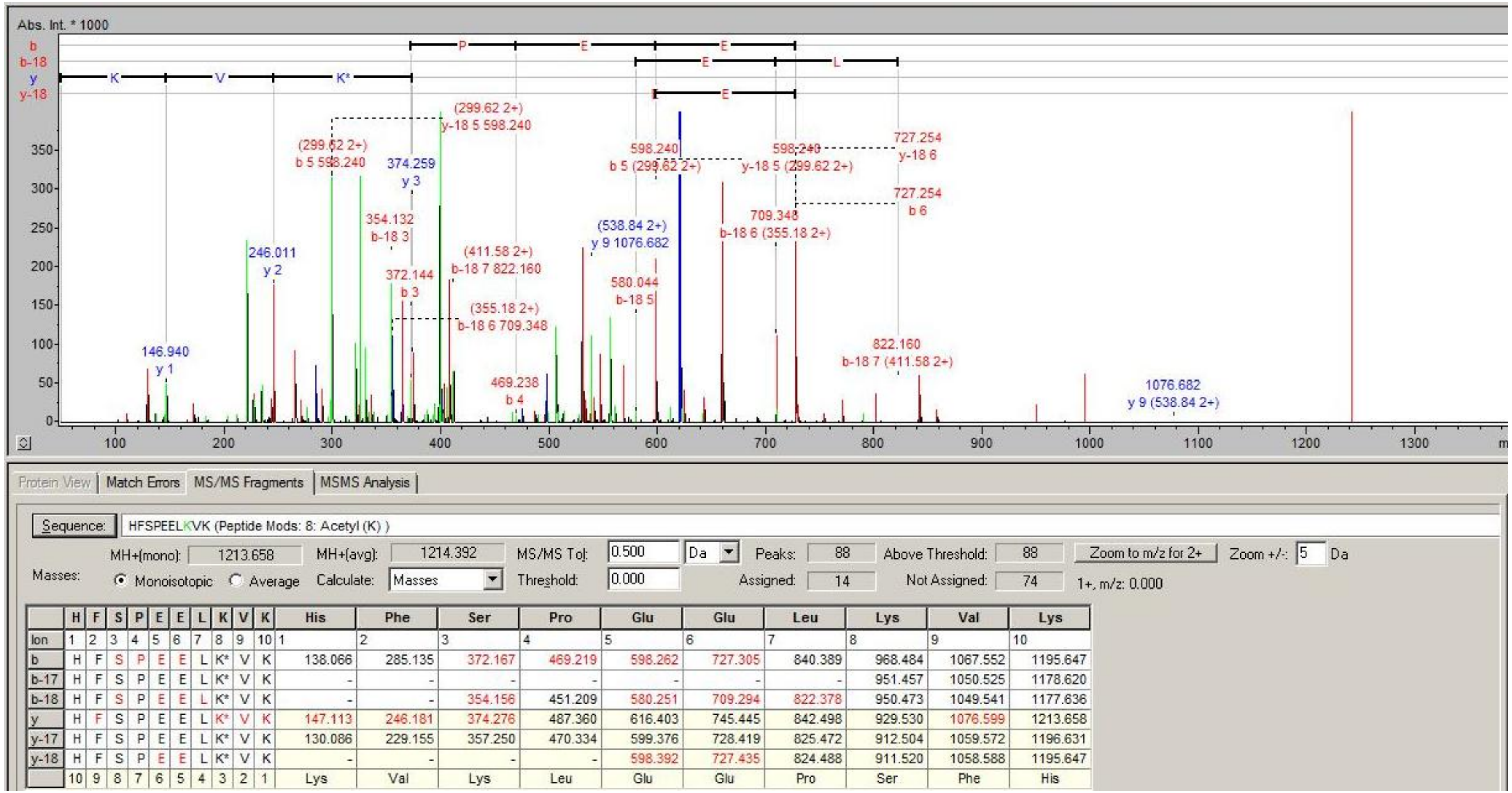
Above Threshold: 82

Not Assigned: 71

Zoom +/-: 5 Da

1+, m/z: 0.000

	E	E	K	P	A	V	T	A	A	P	K	Glu	Glu	Lys	Pro	Ala	Val	Thr	Ala	Ala	Pro	Lys
Ion	1	2	3	4	5	6	7	8	9	10	11	1	2	3	4	5	6	7	8	9	10	11
c	E	E	K*	P	A	V	T	A	A	P	K	147.076	276.119	404.214	501.267	572.304	671.372	772.420	843.457	914.494	1011.547	1139.642
c+1	E	E	K*	P	A	V	T	A	A	P	K	148.084	277.127	405.222	502.275	573.312	672.380	773.428	844.465	915.502	1012.555	1140.650
z	E	E	K*	P	A	V	T	A	A	P	K	130.086	227.139	298.176	369.213	470.261	569.329	640.366	737.419	865.514	994.557	1123.599
z+1	E	E	K*	P	A	V	T	A	A	P	K	131.094	228.147	299.184	370.221	471.269	570.337	641.374	738.427	866.522	995.565	1124.607
z+2	E	E	K*	P	A	V	T	A	A	P	K	132.102	229.155	300.192	371.229	472.277	571.345	642.382	739.435	867.530	996.572	1125.615
	11	10	9	8	7	6	5	4	3	2	1	Lys	Pro	Ala	Ala	Thr	Val	Ala	Pro	Lys	Glu	Glu



Sequence: HFSPEELKVK (Peptide Mods: 8: Acetyl (K))

MH+(mono): 1213.658

MH+(avg): 1214.392

MS/MS Tol: 0.500 Da

Peaks: 88

Above Threshold: 88

Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average

Calculate: Masses

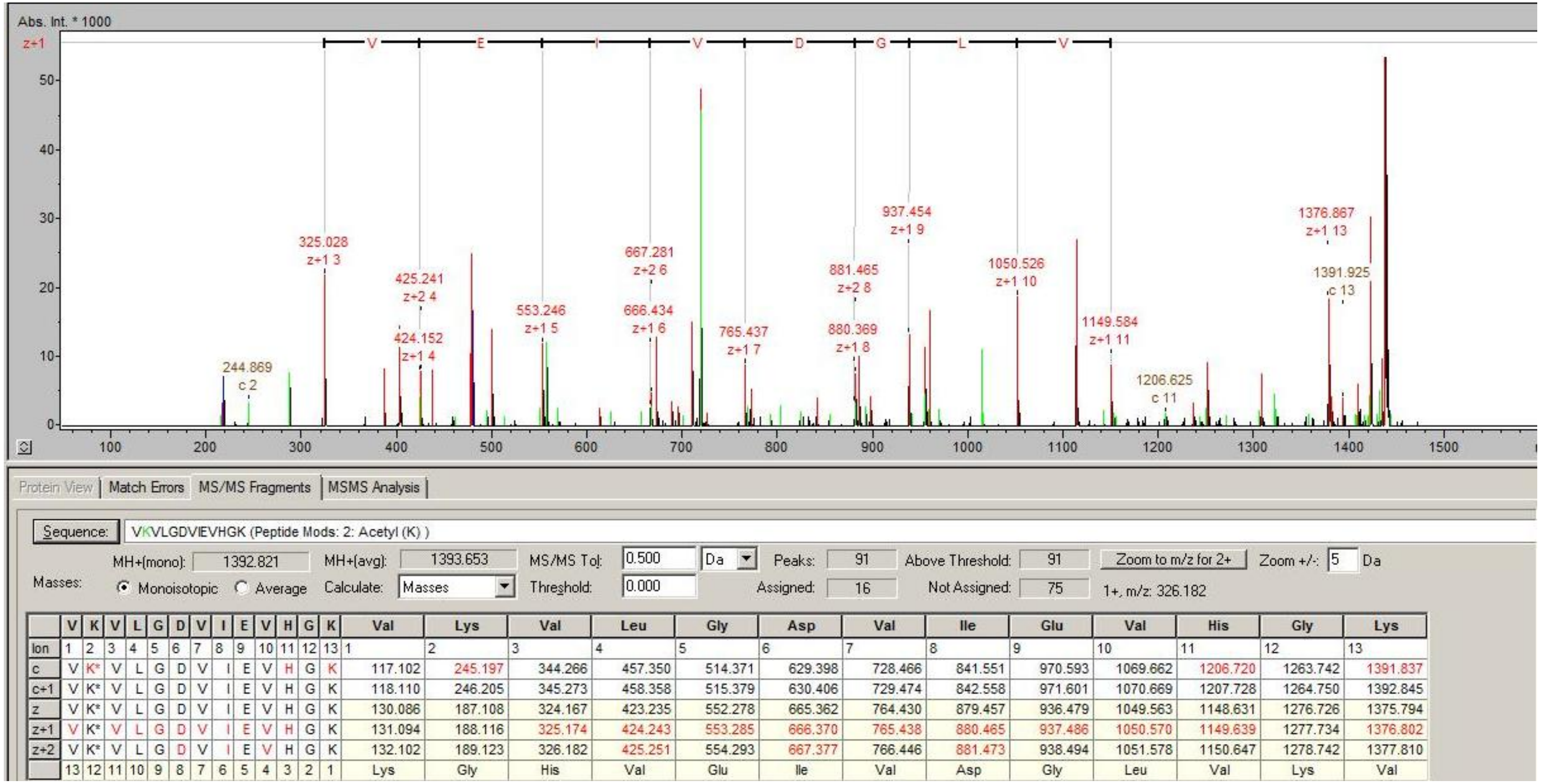
Threshold: 0.000

Assigned: 14

Not Assigned: 74

1+, m/z: 0.000

	H	F	S	P	E	E	L	K	V	K	His	Phe	Ser	Pro	Glu	Glu	Leu	Lys	Val	Lys
Ion	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10
b	H	F	S	P	E	E	L	K*	V	K	138.066	285.135	372.167	469.219	598.262	727.305	840.389	968.484	1067.552	1195.647
b-17	H	F	S	P	E	E	L	K*	V	K	-	-	-	-	-	-	-	951.457	1050.525	1178.620
b-18	H	F	S	P	E	E	L	K*	V	K	-	-	354.156	451.209	580.251	709.294	822.378	950.473	1049.541	1177.636
y	H	F	S	P	E	E	L	K*	V	K	147.113	246.181	374.276	487.360	616.403	745.445	842.498	929.530	1076.599	1213.658
y-17	H	F	S	P	E	E	L	K*	V	K	130.086	229.155	357.250	470.334	599.376	728.419	825.472	912.504	1059.572	1196.631
y-18	H	F	S	P	E	E	L	K*	V	K	-	-	-	-	598.392	727.435	824.488	911.520	1058.588	1195.647
	10	9	8	7	6	5	4	3	2	1	Lys	Val	Lys	Leu	Glu	Glu	Pro	Ser	Phe	His

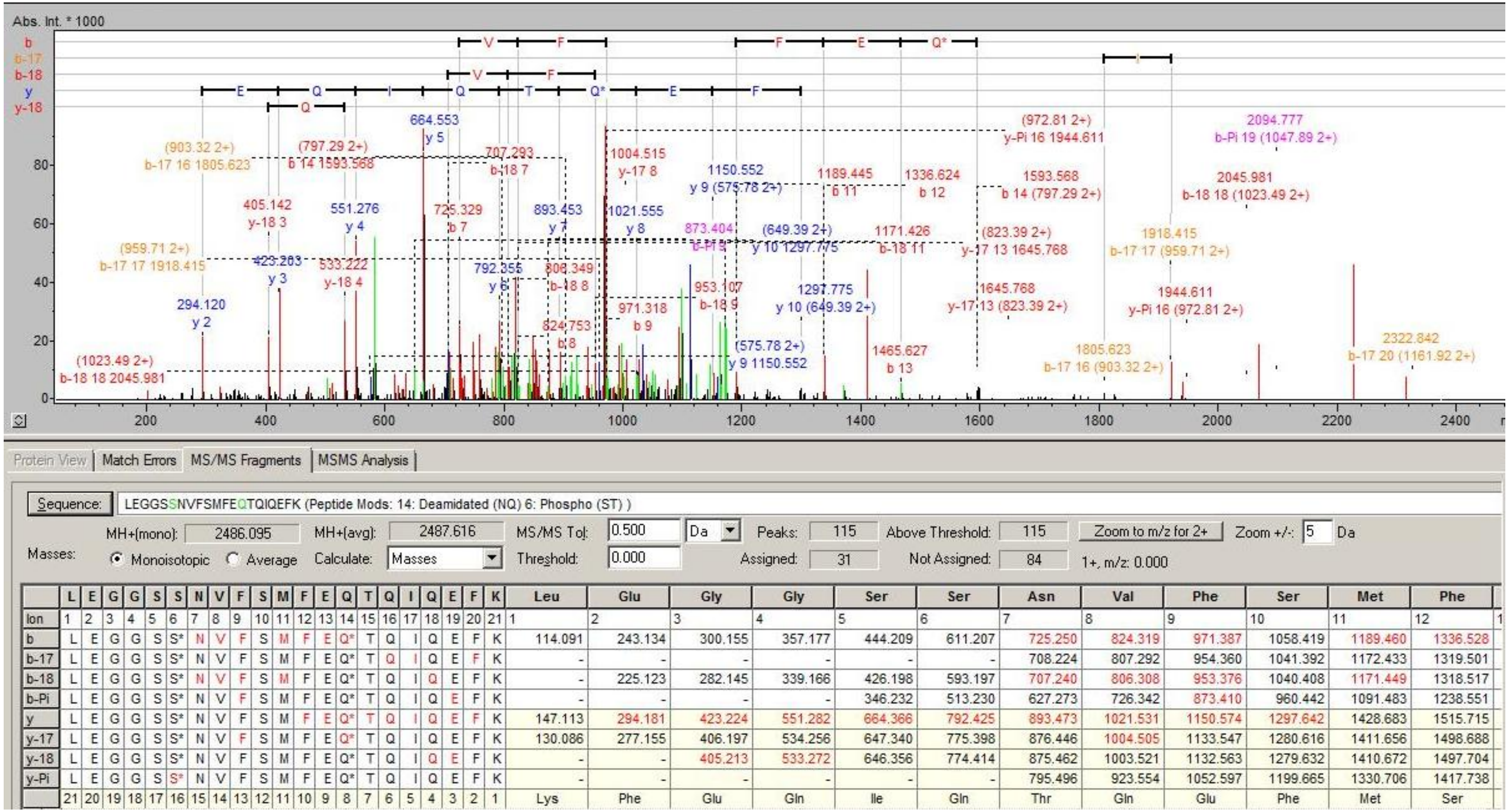


Sequence: VKVLGDVIEVHGK (Peptide Mods: 2: Acetyl (K))

Masses: MH+(mono): 1392.821 MH+(avg): 1393.653 MS/MS Tol: 0.500 Da Peaks: 91 Above Threshold: 91 Zoom +/-: 5 Da

● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 16 Not Assigned: 75 1+, m/z: 326.182

	V	K	V	L	G	D	V	I	E	V	H	G	K	Val	Lys	Val	Leu	Gly	Asp	Val	Ile	Glu	Val	His	Gly	Lys
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	1	2	3	4	5	6	7	8	9	10	11	12	13
c	V	K*	V	L	G	D	V	I	E	V	H	G	K	117.102	245.197	344.266	457.350	514.371	629.398	728.466	841.551	970.593	1069.662	1206.720	1263.742	1391.837
c+1	V	K*	V	L	G	D	V	I	E	V	H	G	K	118.110	246.205	345.273	458.358	515.379	630.406	729.474	842.558	971.601	1070.669	1207.728	1264.750	1392.845
z	V	K*	V	L	G	D	V	I	E	V	H	G	K	130.086	187.108	324.167	423.235	552.278	665.362	764.430	879.457	936.479	1049.563	1148.631	1276.726	1375.794
z+1	V	K*	V	L	G	D	V	I	E	V	H	G	K	131.094	188.116	325.174	424.243	553.285	666.370	765.438	880.465	937.486	1050.570	1149.639	1277.734	1376.802
z+2	V	K*	V	L	G	D	V	I	E	V	H	G	K	132.102	189.123	326.182	425.251	554.293	667.377	766.446	881.473	938.494	1051.578	1150.647	1278.742	1377.810
	13	12	11	10	9	8	7	6	5	4	3	2	1	Lys	Gly	His	Val	Glu	Ile	Val	Asp	Gly	Leu	Val	Lys	Val

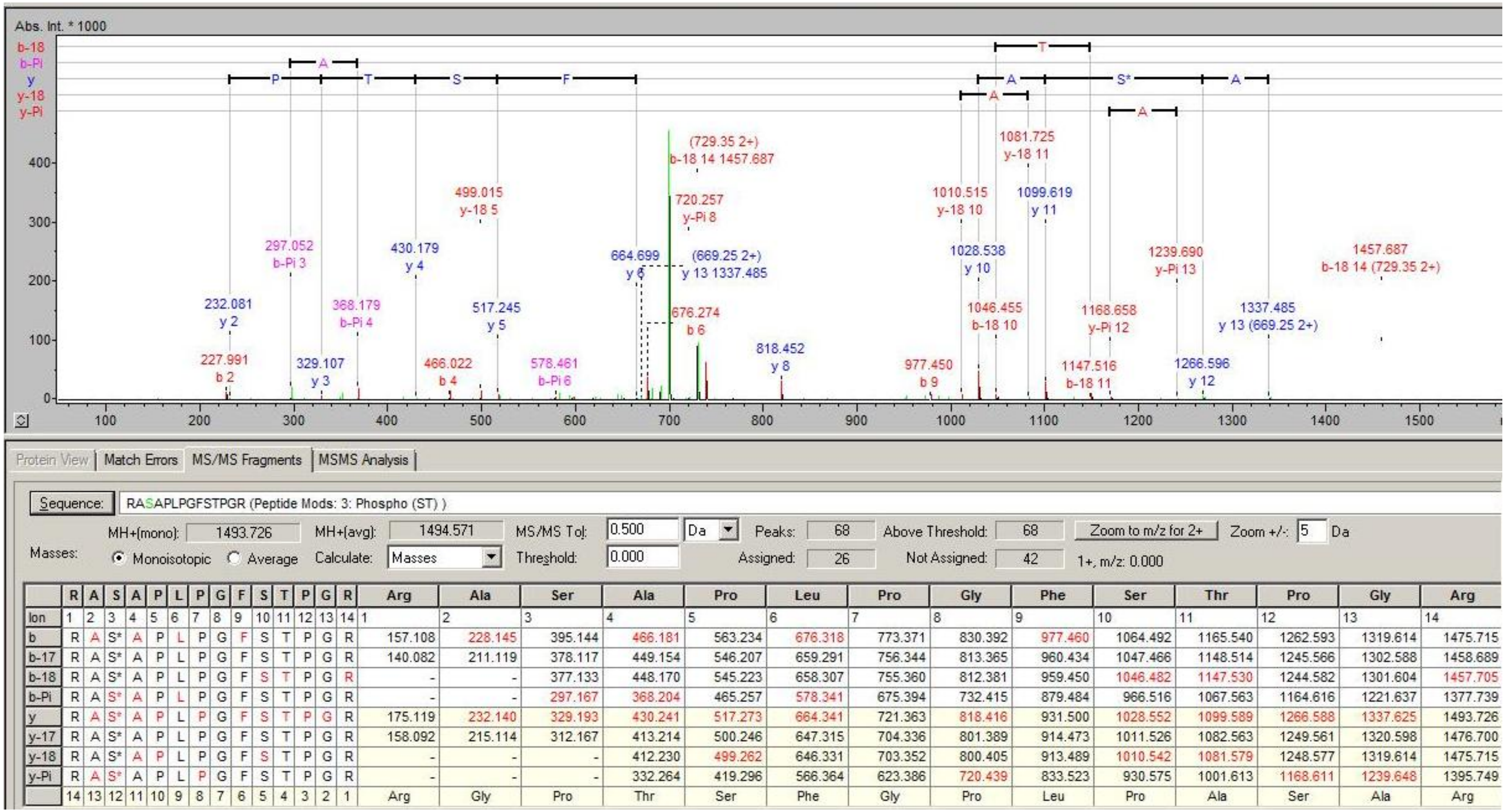


Sequence: LEGGSSNVFSMFEQTQIQEFK (Peptide Mods: 14: Deamidated (NQ) 6: Phospho (ST))

Masses:
MH+(mono): 2486.095
MH+(avg): 2487.616
● Monoisotopic ○ Average
Calculate: Masses
MS/MS Tol: 0.500 Da
Threshold: 0.000
Peaks: 115
Above Threshold: 115
Assigned: 31
Not Assigned: 84
Zoom +/-: 5 Da
1+, m/z: 0.000

	L	E	G	G	S	S	N	V	F	S	M	F	E	Q	T	Q	I	Q	E	F	K
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
b	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
b-17	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
b-18	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
b-Pi	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
y	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
y-17	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
y-18	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
y-Pi	L	E	G	G	S	S*	N	V	F	S	M	F	E	Q*	T	Q	I	Q	E	F	K
	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1

	Leu	Glu	Gly	Gly	Ser	Ser	Asn	Val	Phe	Ser	Met	Phe
Ion	1	2	3	4	5	6	7	8	9	10	11	12
b	114.091	243.134	300.155	357.177	444.209	611.207	725.250	824.319	971.387	1058.419	1189.460	1336.528
b-17	-	-	-	-	-	-	708.224	807.292	954.360	1041.392	1172.433	1319.501
b-18	-	225.123	282.145	339.166	426.198	593.197	707.240	806.308	953.376	1040.408	1171.449	1318.517
b-Pi	-	-	-	-	346.232	513.230	627.273	726.342	873.410	960.442	1091.483	1238.551
y	147.113	294.181	423.224	551.282	664.366	792.425	893.473	1021.531	1150.574	1297.642	1428.683	1515.715
y-17	130.086	277.155	406.197	534.256	647.340	775.398	876.446	1004.505	1133.547	1280.616	1411.656	1498.688
y-18	-	-	405.213	533.272	646.356	774.414	875.462	1003.521	1132.563	1279.632	1410.672	1497.704
y-Pi	-	-	-	-	-	-	795.496	923.554	1052.597	1199.665	1330.706	1417.738
	Lys	Phe	Glu	Gln	Ile	Gln	Thr	Gln	Glu	Phe	Met	Ser



Sequence: RASAPLPGFSTPGR (Peptide Mods: 3: Phospho (ST))

MH+(mono): 1493.726 MH+(avg): 1494.571 MS/MS Tol: 0.500 Da Peaks: 68 Above Threshold: 68 Zoom +/-: 5 Da

Masses: ● Monoisotopic ○ Average Calculate: Masses Threshold: 0.000 Assigned: 26 Not Assigned: 42 1+, m/z: 0.000

	R	A	S	A	P	L	P	G	F	S	T	P	G	R	Arg	Ala	Ser	Ala	Pro	Leu	Pro	Gly	Phe	Ser	Thr	Pro	Gly	Arg
Ion	1	2	3	4	5	6	7	8	9	10	11	12	13	14	1	2	3	4	5	6	7	8	9	10	11	12	13	14
b	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	157.108	228.145	395.144	466.181	563.234	676.318	773.371	830.392	977.460	1064.492	1165.540	1262.593	1319.614	1475.715
b-17	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	140.082	211.119	378.117	449.154	546.207	659.291	756.344	813.365	960.434	1047.466	1148.514	1245.566	1302.588	1458.689
b-18	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	-	-	377.133	448.170	545.223	658.307	755.360	812.381	959.450	1046.482	1147.530	1244.582	1301.604	1457.705
b-Pi	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	-	-	297.167	368.204	465.257	578.341	675.394	732.415	879.484	966.516	1067.563	1164.616	1221.637	1377.739
y	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	175.119	232.140	329.193	430.241	517.273	664.341	721.363	818.416	931.500	1028.552	1099.589	1266.588	1337.625	1493.726
y-17	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	158.092	215.114	312.167	413.214	500.246	647.315	704.336	801.389	914.473	1011.526	1082.563	1249.561	1320.598	1476.700
y-18	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	-	-	-	412.230	499.262	646.331	703.352	800.405	913.489	1010.542	1081.579	1248.577	1319.614	1475.715
y-Pi	R	A	S*	A	P	L	P	G	F	S	T	P	G	R	-	-	-	332.264	419.296	566.364	623.386	720.439	833.523	930.575	1001.613	1168.611	1239.648	1395.749
	14	13	12	11	10	9	8	7	6	5	4	3	2	1	Arg	Gly	Pro	Thr	Ser	Phe	Gly	Pro	Leu	Pro	Ala	Ser	Ala	Arg