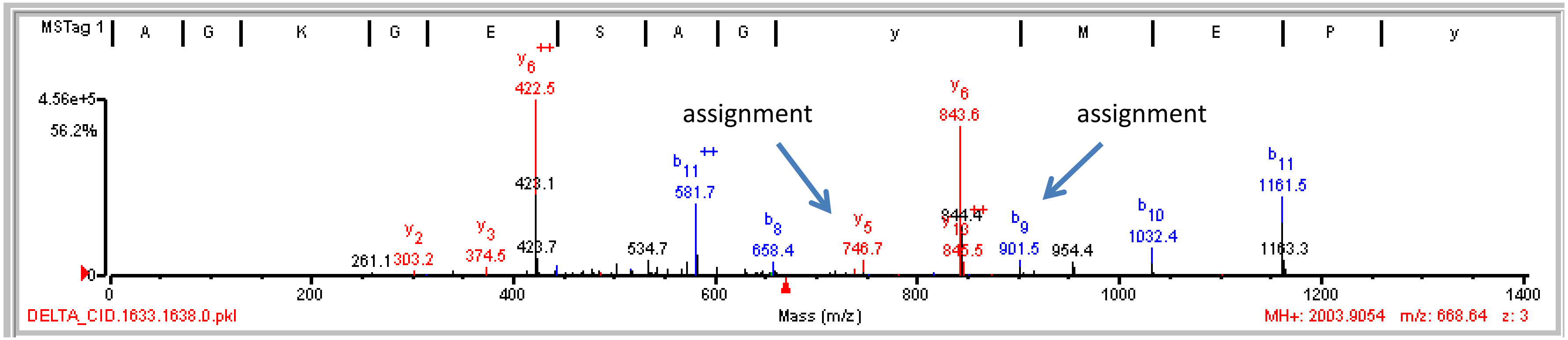
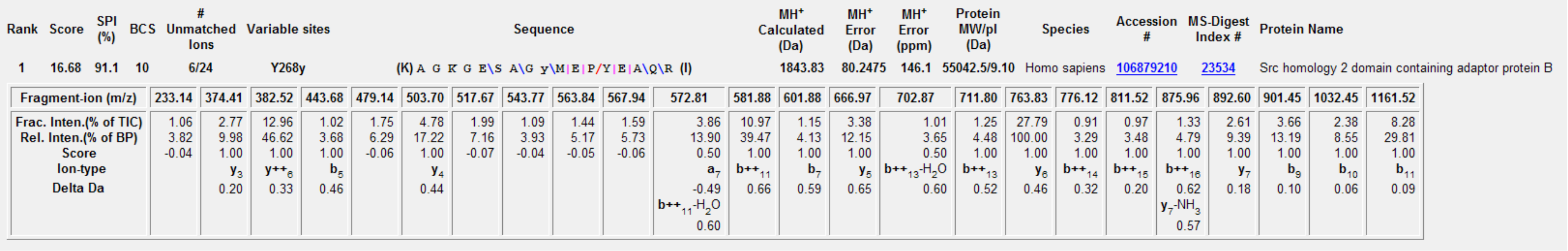
Peak 1



assignment

assignment



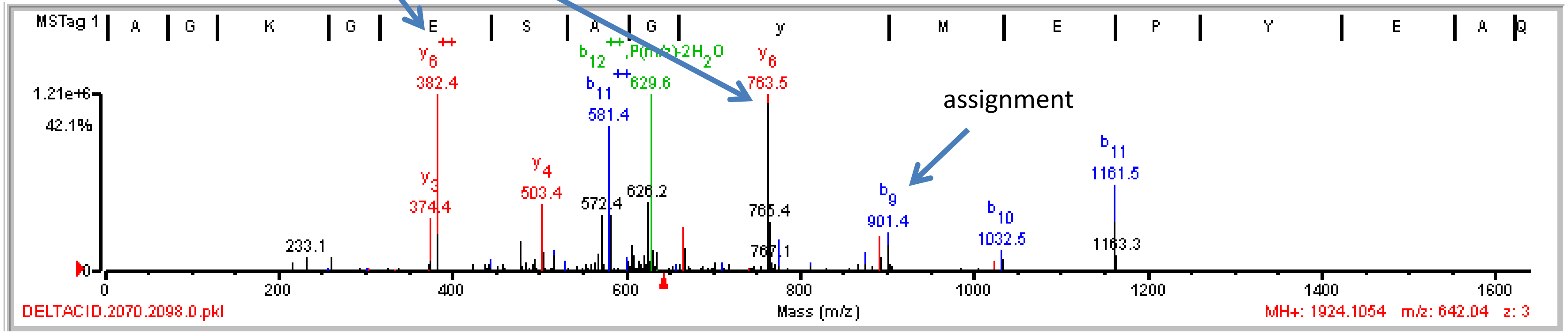
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.68	91.1	10	6/24	Y268y	(K) A G K G E\S A\G y\M|E|P/Y|E|A\Q\R (I)	1843.83	80.2475	146.1	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	233.14	374.41	382.52	443.68	479.14	503.70	517.67	543.77	563.84	567.94	572.81	581.88
Frac. Inten.(% of TIC)	1.06	2.77	12.96	1.02	1.75	4.78	1.99	1.09	1.44	1.59	3.86	10.97
Rel. Inten.(% of BP)	3.82	9.98	46.62	3.68	6.29	17.22	7.16	3.93	5.17	5.73	13.90	39.47
Score	-0.04	1.00	1.00	1.00	-0.06	1.00	-0.07	-0.04	-0.05	-0.06	0.50	1.00
Ion-type		y_3	$y{+}{+}_6$	b_5		y_4					a_7 $b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$
Delta Da		0.20	0.33	0.46		0.44					-0.49 0.60	0.66

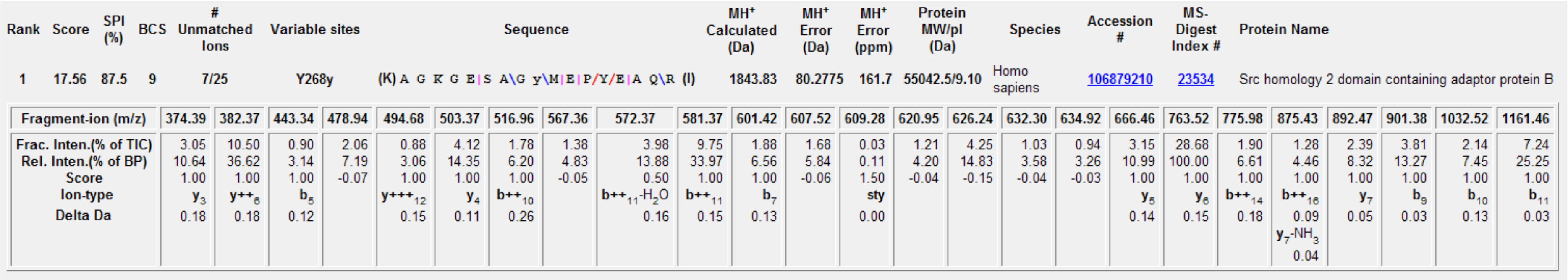
Fragment-ion (m/z)	601.88	666.97	702.87	711.80	763.83	776.12	811.52	875.96	892.60	901.45	1032.45	1161.52
Frac. Inten.(% of TIC)	1.15	3.38	1.01	1.25	27.79	0.91	0.97	1.33	2.61	3.66	2.38	8.28
Rel. Inten.(% of BP)	4.13	12.15	3.65	4.48	100.00	3.29	3.48	4.79	9.39	13.19	8.55	29.81
Score	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b_7	y_5	$b{+}{+}_{13}$-H_2O	$b{+}{+}_{13}$	y_6	$b{+}{+}_{14}$	$b{+}{+}_{15}$	$b{+}{+}_{16}$ y_7-NH_3	y_7	b_9	b_{10}	b_{11}
Delta Da	0.59	0.65	0.60	0.52	0.46	0.32	0.20	0.62 0.57	0.18	0.10	0.06	0.09

Peak 2

Ions that verify assignment



assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.56	87.5	9	7/25	Y268y	(K) A G K G E|S A\G y\M|E|P/Y/E|A Q\R (I)	1843.83	80.2775	161.7	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

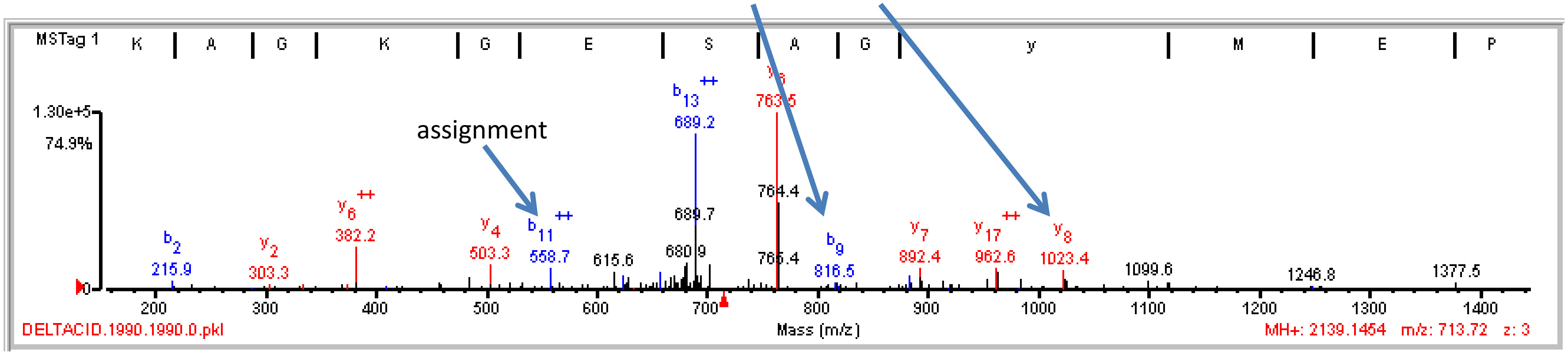
Fragment-ion (m/z)	374.39	382.37	443.34	478.94	494.68	503.37	516.96	567.36	572.37
Frac. Inten.(% of TIC)	3.05	10.50	0.90	2.06	0.88	4.12	1.78	1.38	3.98
Rel. Inten.(% of BP)	10.64	36.62	3.14	7.19	3.06	14.35	6.20	4.83	13.88
Score	1.00	1.00	1.00	-0.07	1.00	1.00	1.00	-0.05	0.50
Ion-type	y_3	y++_6	b_5		y+++_{12}	y_4	b++_{10}		$\text{b++}_{11}\text{-H}_2\text{O}$
Delta Da	0.18	0.18	0.12		0.15	0.11	0.26		0.16

Fragment-ion (m/z)	581.37	601.42	607.52	609.28	620.95	626.24	632.30	634.92
Frac. Inten.(% of TIC)	9.75	1.88	1.68	0.03	1.21	4.25	1.03	0.94
Rel. Inten.(% of BP)	33.97	6.56	5.84	0.11	4.20	14.83	3.58	3.26
Score	1.00	1.00	-0.06	1.50	-0.04	-0.15	-0.04	-0.03
Ion-type	b++_{11}	b_7		sty				
Delta Da	0.15	0.13		0.00				

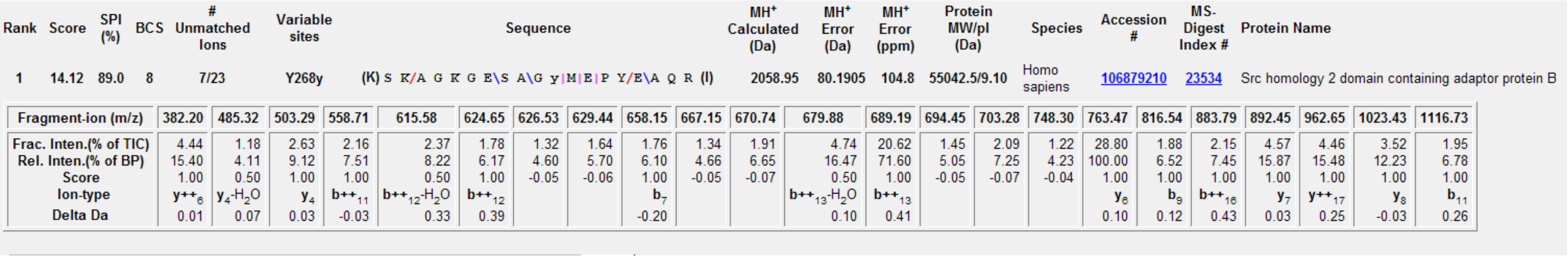
Fragment-ion (m/z)	666.46	763.52	775.98	875.43	892.47	901.38	1032.52	1161.46
Frac. Inten.(% of TIC)	3.15	28.68	1.90	1.28	2.39	3.81	2.14	7.24
Rel. Inten.(% of BP)	10.99	100.00	6.61	4.46	8.32	13.27	7.45	25.25
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y_5	y_6	b++_{14}	b++_{16} $y_7\text{-NH}_3$	y_7	b_9	b_{10}	b_{11}
Delta Da	0.14	0.15	0.18	0.09 0.04	0.05	0.03	0.13	0.03

Peak 3

Ions that verify assignment



assignment

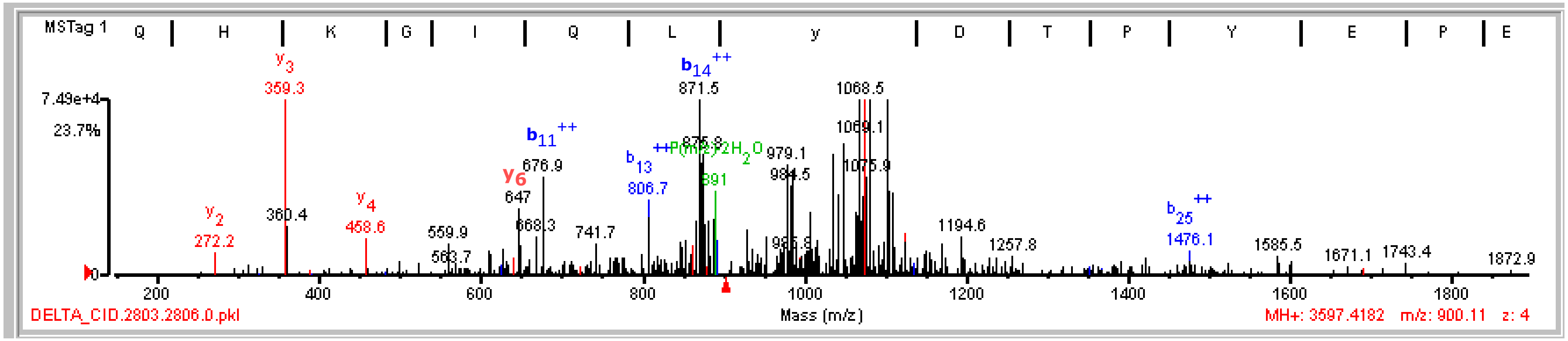


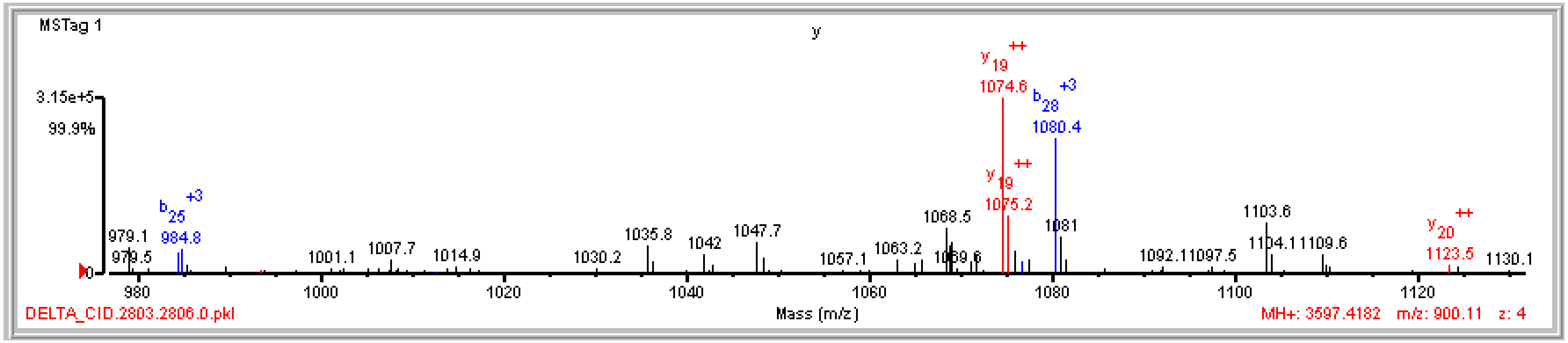
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.12	89.0	8	7/23	Y268y	(K) S K/A G K G E\S A\G y|M|E|P Y/E\A Q R (I)	2058.95	80.1905	104.8	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

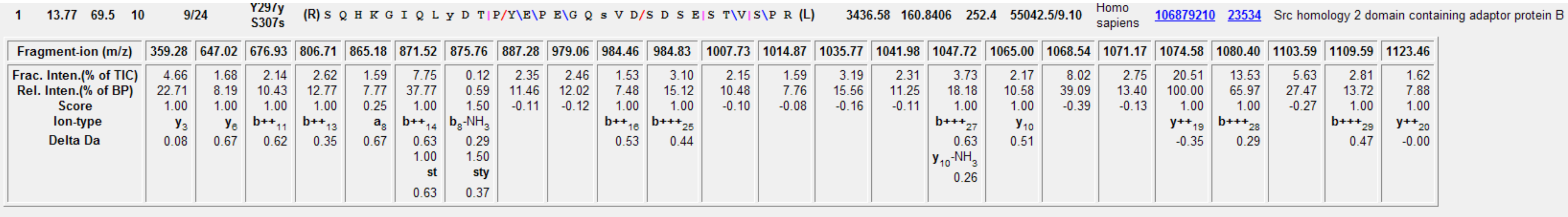
Fragment-ion (m/z)	382.20	485.32	503.29	558.71	615.58	624.65	626.53	629.44	658.15	667.15	670.74	679.88
Frac. Inten.(% of TIC)	4.44	1.18	2.63	2.16	2.37	1.78	1.32	1.64	1.76	1.34	1.91	4.74
Rel. Inten.(% of BP)	15.40	4.11	9.12	7.51	8.22	6.17	4.60	5.70	6.10	4.66	6.65	16.47
Score	1.00	0.50	1.00	1.00	0.50	1.00	-0.05	-0.06	1.00	-0.05	-0.07	0.50
Ion-type	y++$_{6}$	y$_{4}$-H$_{2}$O	y$_{4}$	b++$_{11}$	b++$_{12}$-H$_{2}$O	b++$_{12}$			b$_{7}$			b++$_{13}$-H$_{2}$O
Delta Da	0.01	0.07	0.03	-0.03	0.33	0.39			-0.20			0.10

Fragment-ion (m/z)	689.19	694.45	703.28	748.30	763.47	816.54	883.79	892.45	962.65	1023.43	1116.73
Frac. Inten.(% of TIC)	20.62	1.45	2.09	1.22	28.80	1.88	2.15	4.57	4.46	3.52	1.95
Rel. Inten.(% of BP)	71.60	5.05	7.25	4.23	100.00	6.52	7.45	15.87	15.48	12.23	6.78
Score	1.00	-0.05	-0.07	-0.04	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b++$_{13}$				y$_{6}$	b$_{9}$	b++$_{16}$	y$_{7}$	y++$_{17}$	y$_{8}$	b$_{11}$
Delta Da	0.41				0.10	0.12	0.43	0.03	0.25	-0.03	0.26

Peak 4





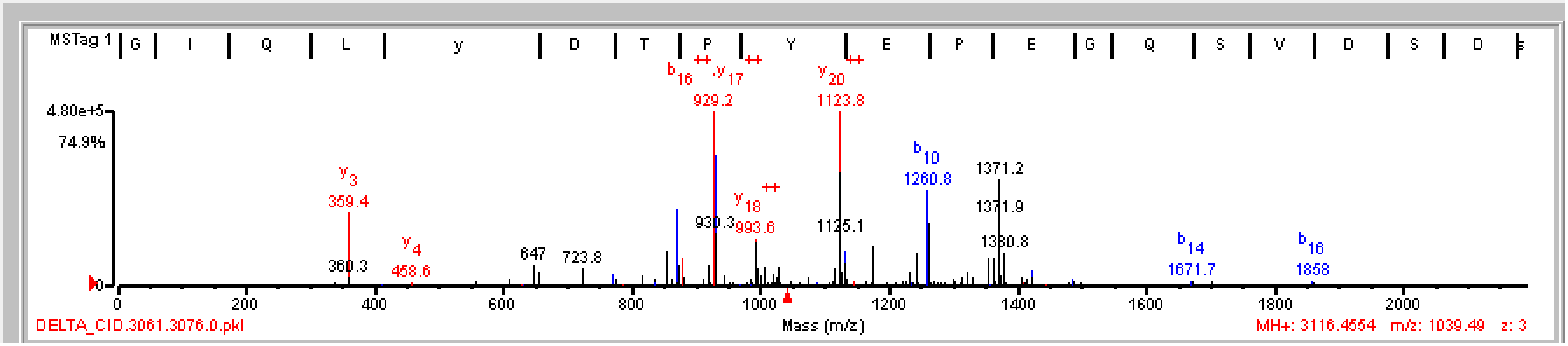


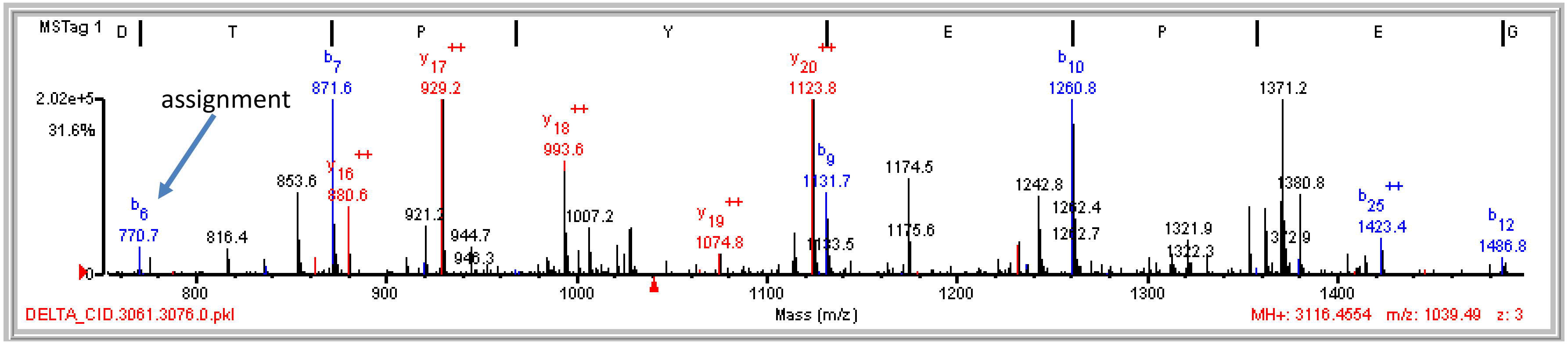
1 13.77 69.5 10 9/24 Y297y S307s (R) S Q H K G I Q L y D T|P/Y\E\P E\G Q s V D/S D S E|S T\V|S\P R (L) 3436.58 160.8406 252.4 55042.5/9.10 Homo sapiens 106879210 23534 Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	359.28	647.02	676.93	806.71	865.18	871.52	875.76	887.28	979.06	984.46	984.83
Frac. Inten.(% of TIC)	4.66	1.68	2.14	2.62	1.59	7.75	0.12	2.35	2.46	1.53	3.10
Rel. Inten.(% of BP)	22.71	8.19	10.43	12.77	7.77	37.77	0.59	11.46	12.02	7.48	15.12
Score	1.00	1.00	1.00	1.00	0.25	1.00	1.50	-0.11	-0.12	1.00	1.00
Ion-type	y_3	y_6	$b{+}{+}_{11}$	$b{+}{+}_{13}$	a_8	$b{+}{+}_{14}$	b_8-NH_3			$b{+}{+}_{16}$	$b{+}{+}{+}_{25}$
Delta Da	0.08	0.67	0.62	0.35	0.67	0.63	0.29			0.53	0.44
						1.00	1.50				
						st	sty				
						0.63	0.37				

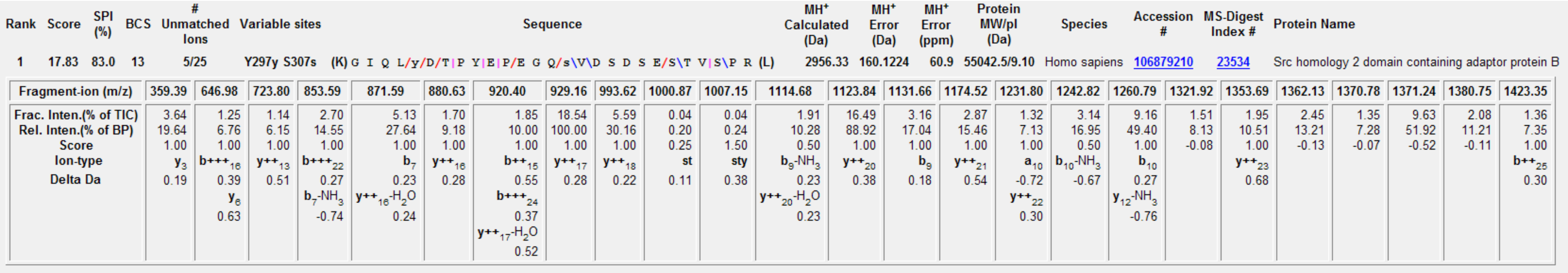
Fragment-ion (m/z)	1007.73	1014.87	1035.77	1041.98	1047.72	1065.00	1068.54	1071.17	1074.58	1080.40	1103.59	1109.59	1123.46
Frac. Inten.(% of TIC)	2.15	1.59	3.19	2.31	3.73	2.17	8.02	2.75	20.51	13.53	5.63	2.81	1.62
Rel. Inten.(% of BP)	10.48	7.76	15.56	11.25	18.18	10.58	39.09	13.40	100.00	65.97	27.47	13.72	7.88
Score	-0.10	-0.08	-0.16	-0.11	1.00	1.00	-0.39	-0.13	1.00	1.00	-0.27	1.00	1.00
Ion-type					$b{+}{+}{+}_{27}$	y_{10}			$y{+}{+}_{19}$	$b{+}{+}{+}_{28}$		$b{+}{+}{+}_{29}$	$y{+}{+}_{20}$
Delta Da					0.63	0.51			-0.35	0.29		0.47	-0.00
					y_{10}-NH_3								
					0.26								

Peak 5





assignment

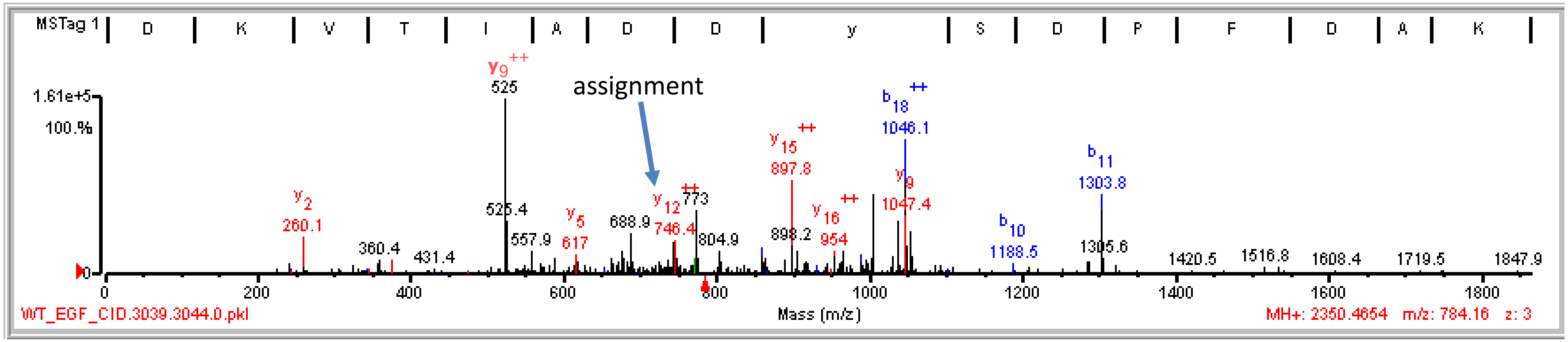


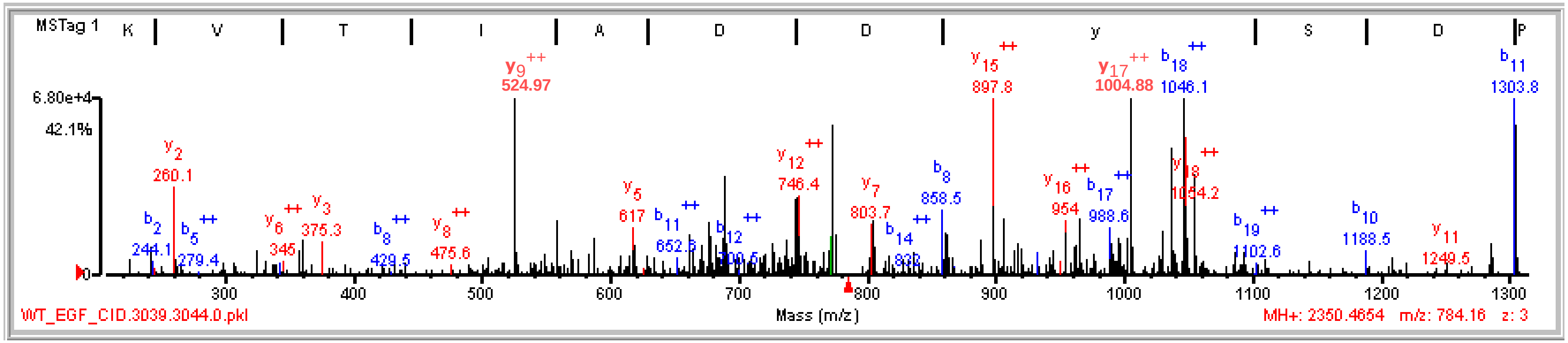
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.83	83.0	13	5/25	Y297y S307s	(K) G I Q L/y/D/T|P Y|E|P/E G Q/s\V\D S D S E/S\T V|S\P R (L)	2956.33	160.1224	60.9	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

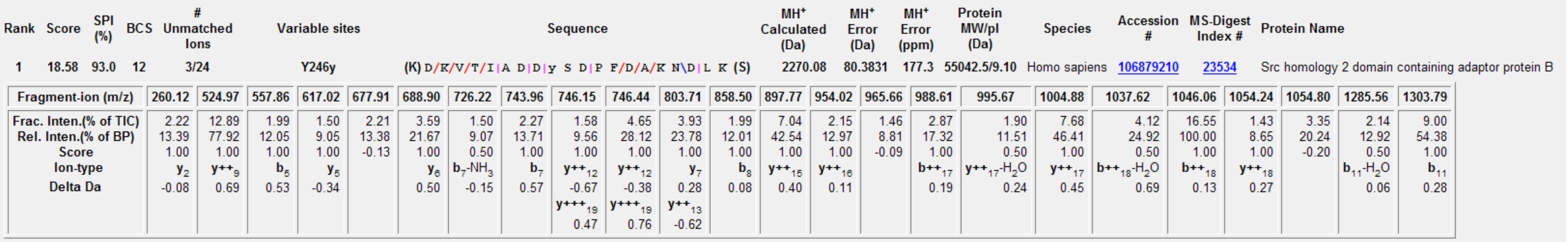
Fragment-ion (m/z)	359.39	646.98	723.80	853.59	871.59	880.63	920.40	929.16	993.62	1000.87	1007.15	1114.68
Frac. Inten.(% of TIC)	3.64	1.25	1.14	2.70	5.13	1.70	1.85	18.54	5.59	0.04	0.04	1.91
Rel. Inten.(% of BP)	19.64	6.76	6.15	14.55	27.64	9.18	10.00	100.00	30.16	0.20	0.24	10.28
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.50	0.50
Ion-type	y_3	$b{+}{+}{+}_{16}$	$y{+}{+}_{13}$	$b{+}{+}{+}_{22}$	b_7	$y{+}{+}_{16}$	$b{+}{+}_{15}$	$y{+}{+}_{17}$	$y{+}{+}_{18}$	st	sty	b_9-NH_3
Delta Da	0.19	0.39	0.51	0.27	0.23	0.28	0.55	0.28	0.22	0.11	0.38	0.23
		y_6		b_7-NH_3	$y{+}{+}_{16}$-H_2O		$b{+}{+}{+}_{24}$					$y{+}{+}_{20}$-H_2O
		0.63		-0.74	0.24		0.37					0.23
							$y{+}{+}_{17}$-H_2O					
							0.52					

Fragment-ion (m/z)	1123.84	1131.66	1174.52	1231.80	1242.82	1260.79	1321.92	1353.69	1362.13	1370.78	1371.24	1380.75	1423.35
Frac. Inten.(% of TIC)	16.49	3.16	2.87	1.32	3.14	9.16	1.51	1.95	2.45	1.35	9.63	2.08	1.36
Rel. Inten.(% of BP)	88.92	17.04	15.46	7.13	16.95	49.40	8.13	10.51	13.21	7.28	51.92	11.21	7.35
Score	1.00	1.00	1.00	1.00	0.50	1.00	-0.08	1.00	-0.13	-0.07	-0.52	-0.11	1.00
Ion-type	$y{+}{+}_{20}$	b_9	$y{+}{+}_{21}$	a_{10}	b_{10}-NH_3	b_{10}		$y{+}{+}_{23}$					$b{+}{+}_{25}$
Delta Da	0.38	0.18	0.54	-0.72	-0.67	0.27		0.68					0.30
				$y{+}{+}_{22}$		y_{12}-NH_3							
				0.30		-0.76							

Peak 6





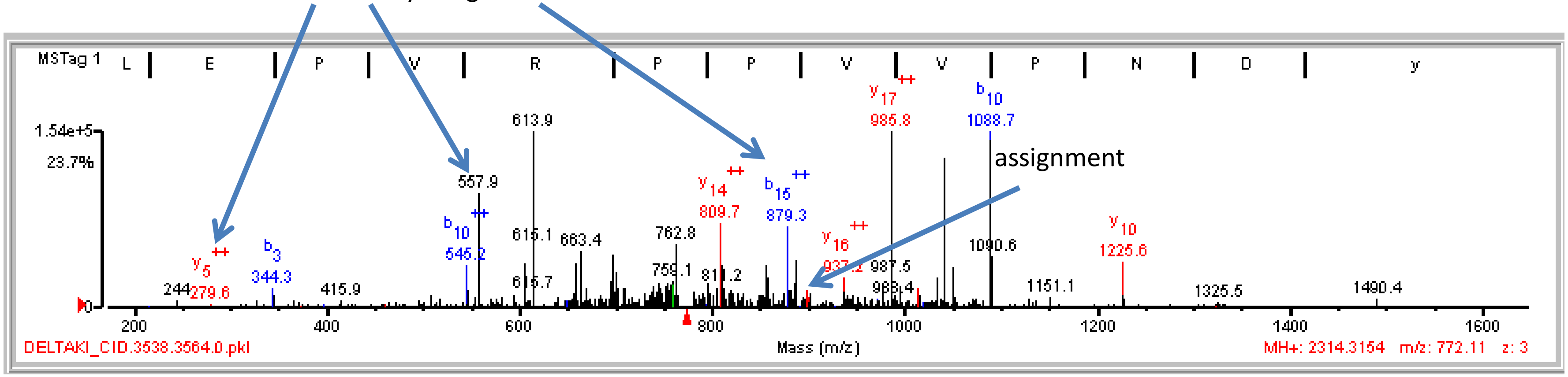


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.58	93.0	12	3/24	Y246y	(K) D/K/V/T/I|A D|D|y S D|P F/D/A/K N\D|L K (S)	2270.08	80.3831	177.3	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

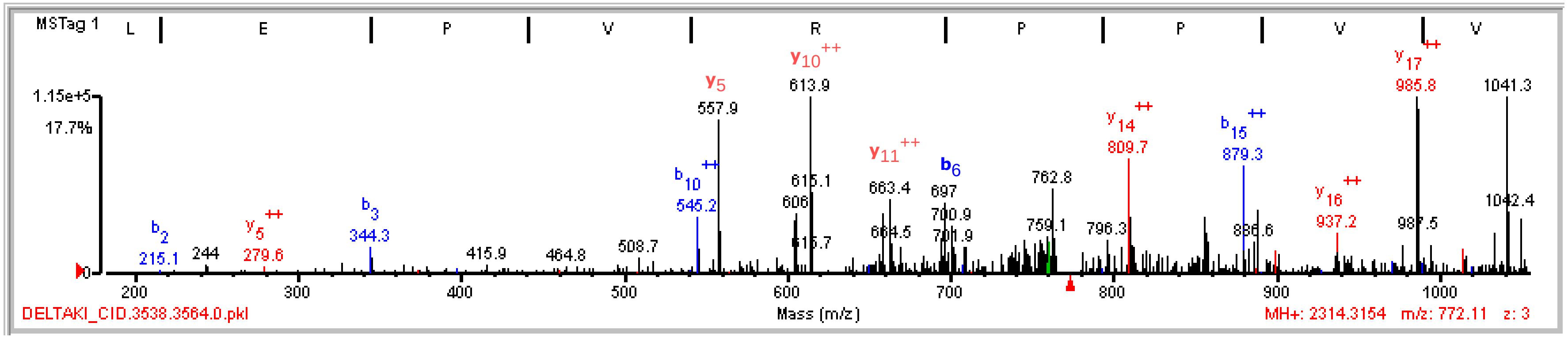
Fragment-ion (m/z)	260.12	524.97	557.86	617.02	677.91	688.90	726.22	743.96	746.15	746.44	803.71	858.50	897.77	954.02	965.66	988.61	995.67	1004.88	1037.62	1046.06	1054.24	1054.80	1285.56	1303.79
Frac. Inten.(% of TIC)	2.22	12.89	1.99	1.50	2.21	3.59	1.50	2.27	1.58	4.65	3.93	1.99	7.04	2.15	1.46	2.87	1.90	7.68	4.12	16.55	1.43	3.35	2.14	9.00
Rel. Inten.(% of BP)	13.39	77.92	12.05	9.05	13.38	21.67	9.07	13.71	9.56	28.12	23.78	12.01	42.54	12.97	8.81	17.32	11.51	46.41	24.92	100.00	8.65	20.24	12.92	54.38
Score	1.00	1.00	1.00	1.00	-0.13	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.09	1.00	0.50	1.00	0.50	1.00	1.00	-0.20	0.50	1.00
Ion-type	y_2	$y{++}_9$	b_5	y_5		y_6	b_7-NH_3	b_7	$y{++}_{12}$ $y{+++}_{19}$	$y{++}_{12}$ $y{+++}_{19}$	y_7 $y{++}_{13}$	b_8	$y{++}_{15}$	$y{++}_{16}$		$b{++}_{17}$	$y{++}_{17}$-H_2O	$y{++}_{17}$	$b{++}_{18}$-H_2O	$b{++}_{18}$	$y{++}_{18}$		b_{11}-H_2O	b_{11}
Delta Da	-0.08	0.69	0.53	-0.34		0.50	-0.15	0.57	-0.67 0.47	-0.38 0.76	0.28 -0.62	0.08	0.40	0.11		0.19	0.24	0.45	0.69	0.13	0.27		0.06	0.28

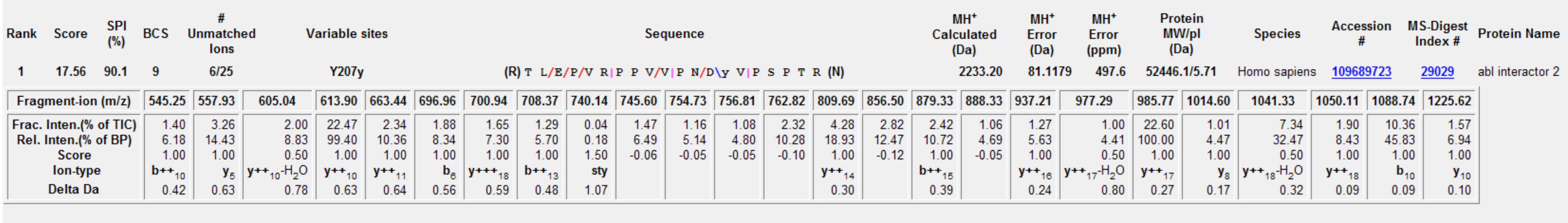
Peak 7

Ions that verify assignment



assignment

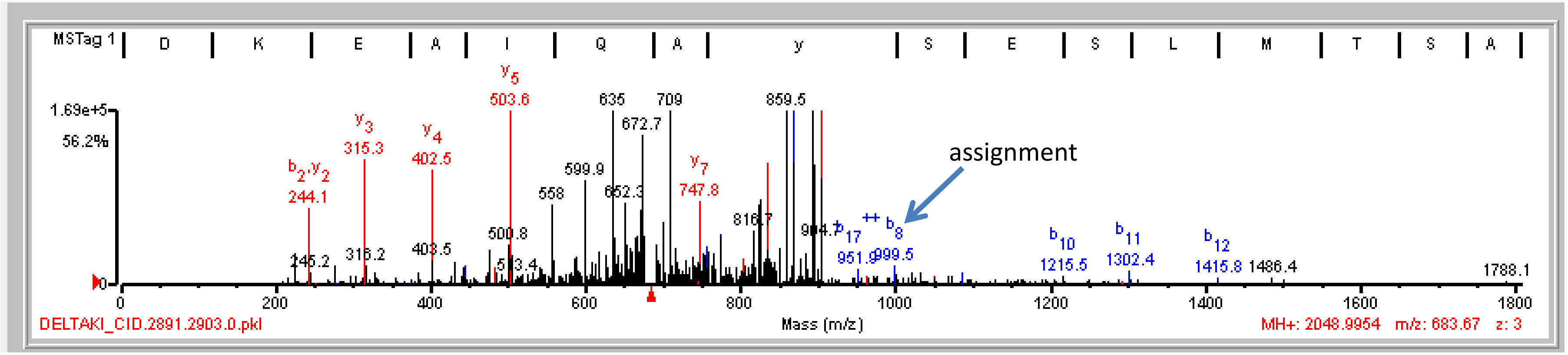




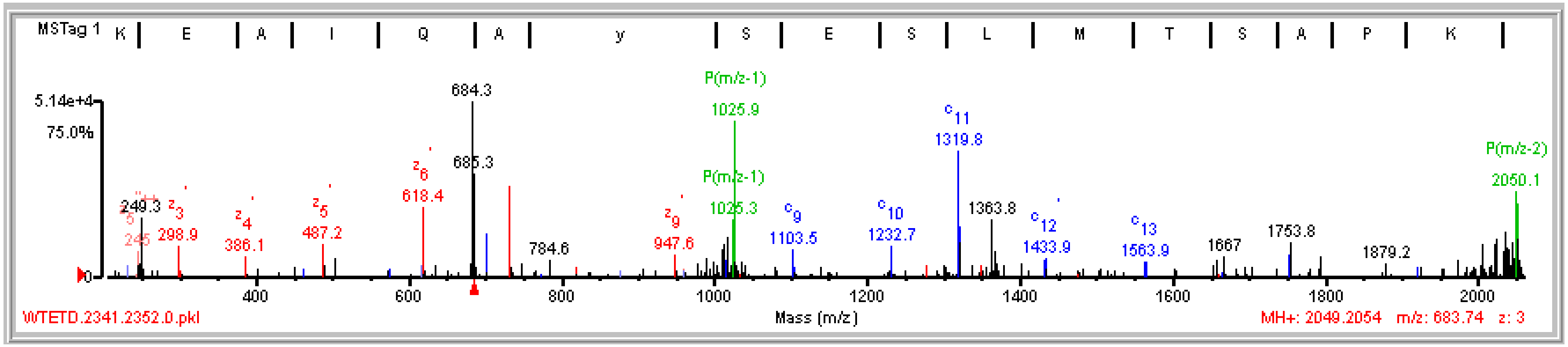
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.56	90.1	9	6/25	Y207y	(R) T L/E/P/V R|P P V/V|P N/D\y V|P S P T R (N)	2233.20	81.1179	497.6	52446.1/5.71	Homo sapiens	109689723	29029	abl interactor 2

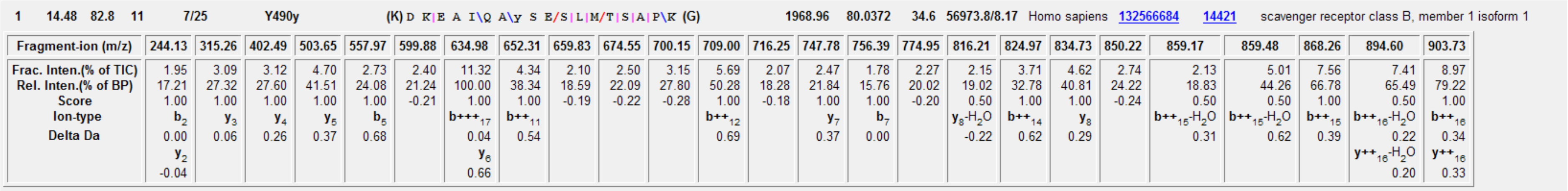
Fragment-ion (m/z)	545.25	557.93	605.04	613.90	663.44	696.96	700.94	708.37	740.14	745.60	754.73	756.81	762.82	809.69	856.50	879.33	888.33	937.21	977.29	985.77	1014.60	1041.33	1050.11	1088.74	1225.62
Frac. Inten.(% of TIC)	1.40	3.26	2.00	22.47	2.34	1.88	1.65	1.29	0.04	1.47	1.16	1.08	2.32	4.28	2.82	2.42	1.06	1.27	1.00	22.60	1.01	7.34	1.90	10.36	1.57
Rel. Inten.(% of BP)	6.18	14.43	8.83	99.40	10.36	8.34	7.30	5.70	0.18	6.49	5.14	4.80	10.28	18.93	12.47	10.72	4.69	5.63	4.41	100.00	4.47	32.47	8.43	45.83	6.94
Score	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.50	-0.06	-0.05	-0.05	-0.10	1.00	-0.12	1.00	-0.05	1.00	0.50	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type	b++$_{10}$	y$_5$	y++$_{10}$-H$_2$O	y++$_{10}$	y++$_{11}$	b$_6$	y+++$_{18}$	b++$_{13}$	sty					y++$_{14}$		b++$_{15}$		y++$_{16}$	y++$_{17}$-H$_2$O	y++$_{17}$	y$_8$	y++$_{18}$-H$_2$O	y++$_{18}$	b$_{10}$	y$_{10}$
Delta Da	0.42	0.63	0.78	0.63	0.64	0.56	0.59	0.48	1.07					0.30		0.39		0.24	0.80	0.27	0.17	0.32	0.09	0.09	0.10

Peak 8



assignment



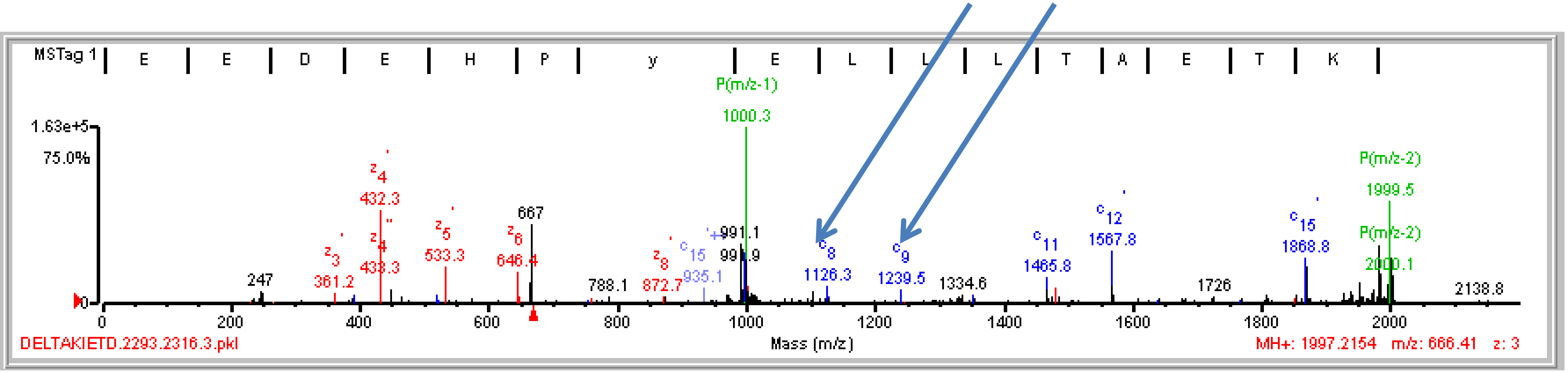


1 14.48 82.8 11 7/25 Y490y (K) D K|E A I\Q A\y S E/S|L|M/T|S|A|P\K (G) 1968.96 80.0372 34.6 56973.8/8.17 Homo sapiens 132566684 14421 scavenger receptor class B, member 1 isoform 1

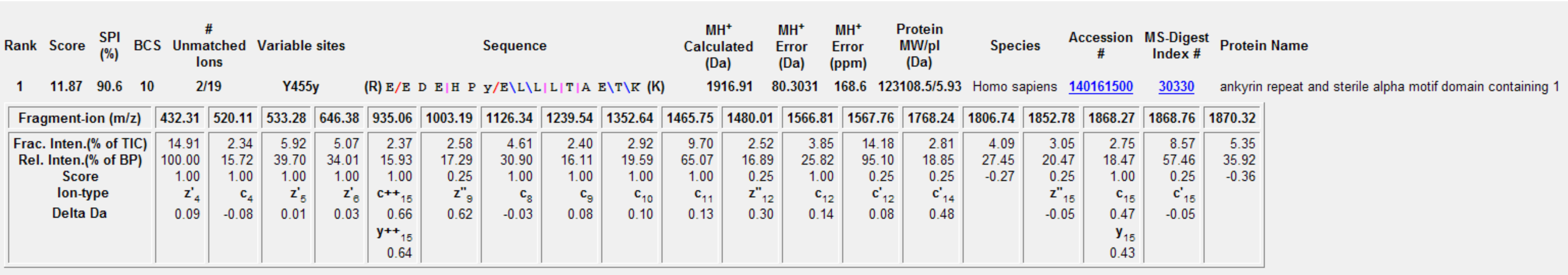
Fragment-ion (m/z)	244.13	315.26	402.49	503.65	557.97	599.88	634.98	652.31	659.83	674.55	700.15	709.00	716.25
Frac. Inten.(% of TIC)	1.95	3.09	3.12	4.70	2.73	2.40	11.32	4.34	2.10	2.50	3.15	5.69	2.07
Rel. Inten.(% of BP)	17.21	27.32	27.60	41.51	24.08	21.24	100.00	38.34	18.59	22.09	27.80	50.28	18.28
Score	1.00	1.00	1.00	1.00	1.00	-0.21	1.00	1.00	-0.19	-0.22	-0.28	1.00	-0.18
Ion-type	b_2	y_3	y_4	y_5	b_5		b+++_{17}	b++_{11}				b++_{12}	
Delta Da	0.00	0.06	0.26	0.37	0.68		0.04	0.54				0.69	
	y_2						y_6						
	-0.04						0.66						

Fragment-ion (m/z)	747.78	756.39	774.95	816.21	824.97	834.73	850.22	859.17	859.48	868.26	894.60	903.73
Frac. Inten.(% of TIC)	2.47	1.78	2.27	2.15	3.71	4.62	2.74	2.13	5.01	7.56	7.41	8.97
Rel. Inten.(% of BP)	21.84	15.76	20.02	19.02	32.78	40.81	24.22	18.83	44.26	66.78	65.49	79.22
Score	1.00	1.00	-0.20	0.50	1.00	1.00	-0.24	0.50	0.50	1.00	0.50	1.00
Ion-type	y_7	b_7		$y_8\text{-}H_2O$	b++_{14}	y_8		$\text{b++}_{15}\text{-}H_2O$	$\text{b++}_{15}\text{-}H_2O$	b++_{15}	$\text{b++}_{16}\text{-}H_2O$	b++_{16}
Delta Da	0.37	0.00		-0.22	0.62	0.29		0.31	0.62	0.39	0.22	0.34
											$\text{y++}_{16}\text{-}H_2O$	y++_{16}
											0.20	0.33

Peak 9



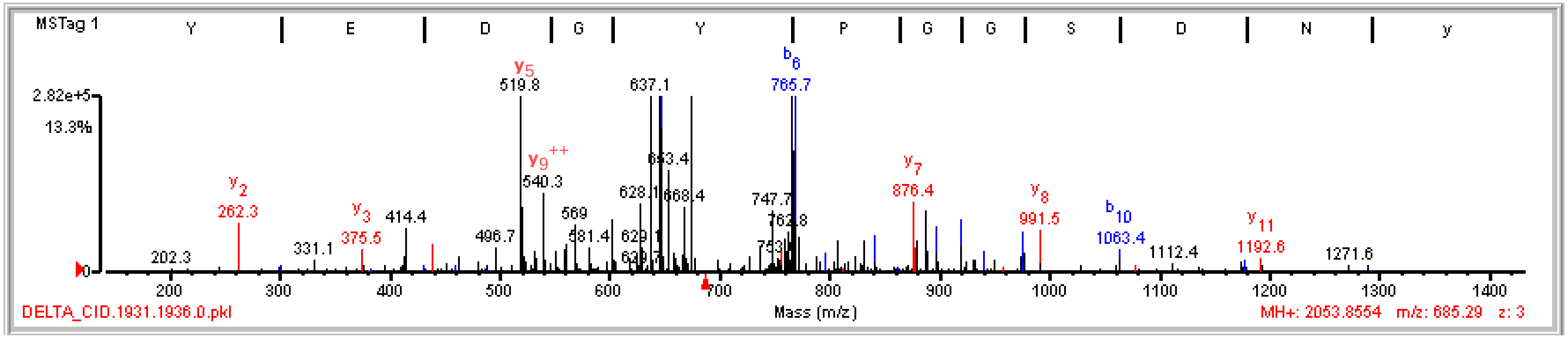
Ions that verify assignment

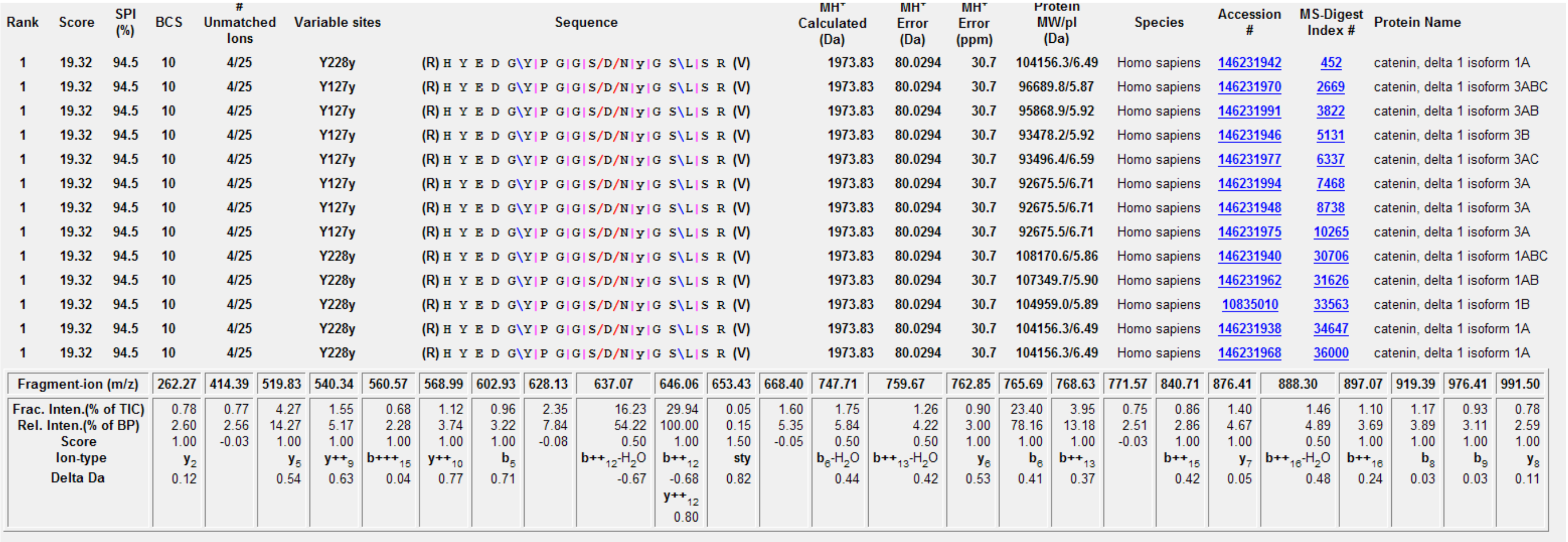


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.87	90.6	10	2/19	Y455y	(R) E/E D E|H P y/E\L\L|L|T|A E\T\K (K)	1916.91	80.3031	168.6	123108.5/5.93	Homo sapiens	140161500	30330	ankyrin repeat and sterile alpha motif domain containing 1

Fragment-ion (m/z)	432.31	520.11	533.28	646.38	935.06	1003.19	1126.34	1239.54	1352.64	1465.75	1480.01	1566.81	1567.76	1768.24	1806.74	1852.78	1868.27	1868.76	1870.32
Frac. Inten.(% of TIC)	14.91	2.34	5.92	5.07	2.37	2.58	4.61	2.40	2.92	9.70	2.52	3.85	14.18	2.81	4.09	3.05	2.75	8.57	5.35
Rel. Inten.(% of BP)	100.00	15.72	39.70	34.01	15.93	17.29	30.90	16.11	19.59	65.07	16.89	25.82	95.10	18.85	27.45	20.47	18.47	57.46	35.92
Score	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	0.25	1.00	0.25	0.25	-0.27	0.25	1.00	0.25	-0.36
Ion-type	z'_{4}	c_{4}	z'_{5}	z'_{6}	c^{++}_{15} 0.66 y^{++}_{15}	z''_{9}	c_{8}	c_{9}	c_{10}	c_{11}	z''_{12}	c_{12}	c'_{12}	c'_{14}		z''_{15}	c_{15} 0.47 y_{15}	c'_{15}	
Delta Da	0.09	-0.08	0.01	0.03	0.64	0.62	-0.03	0.08	0.10	0.13	0.30	0.14	0.08	0.48		-0.05	0.43	-0.05	

Peak 10



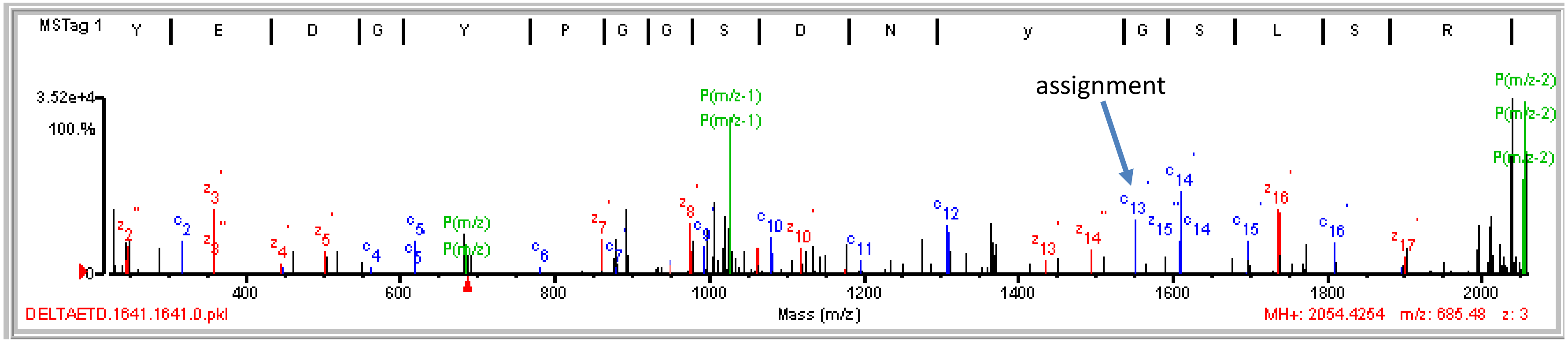


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	104156.3/6.49	Homo sapiens	146231942	452	catenin, delta 1 isoform 1A
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	96689.8/5.87	Homo sapiens	146231970	2669	catenin, delta 1 isoform 3ABC
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	95868.9/5.92	Homo sapiens	146231991	3822	catenin, delta 1 isoform 3AB
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	93478.2/5.92	Homo sapiens	146231946	5131	catenin, delta 1 isoform 3B
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	93496.4/6.59	Homo sapiens	146231977	6337	catenin, delta 1 isoform 3AC
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	92675.5/6.71	Homo sapiens	146231994	7468	catenin, delta 1 isoform 3A
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	92675.5/6.71	Homo sapiens	146231948	8738	catenin, delta 1 isoform 3A
1	19.32	94.5	10	4/25	Y127y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	92675.5/6.71	Homo sapiens	146231975	10265	catenin, delta 1 isoform 3A
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	108170.6/5.86	Homo sapiens	146231940	30706	catenin, delta 1 isoform 1ABC
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	107349.7/5.90	Homo sapiens	146231962	31626	catenin, delta 1 isoform 1AB
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	104959.0/5.89	Homo sapiens	10835010	33563	catenin, delta 1 isoform 1B
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	104156.3/6.49	Homo sapiens	146231938	34647	catenin, delta 1 isoform 1A
1	19.32	94.5	10	4/25	Y228y	(R) H Y E D G\Y|P G|G|S/D/N|y|G S\L|S R (V)	1973.83	80.0294	30.7	104156.3/6.49	Homo sapiens	146231968	36000	catenin, delta 1 isoform 1A

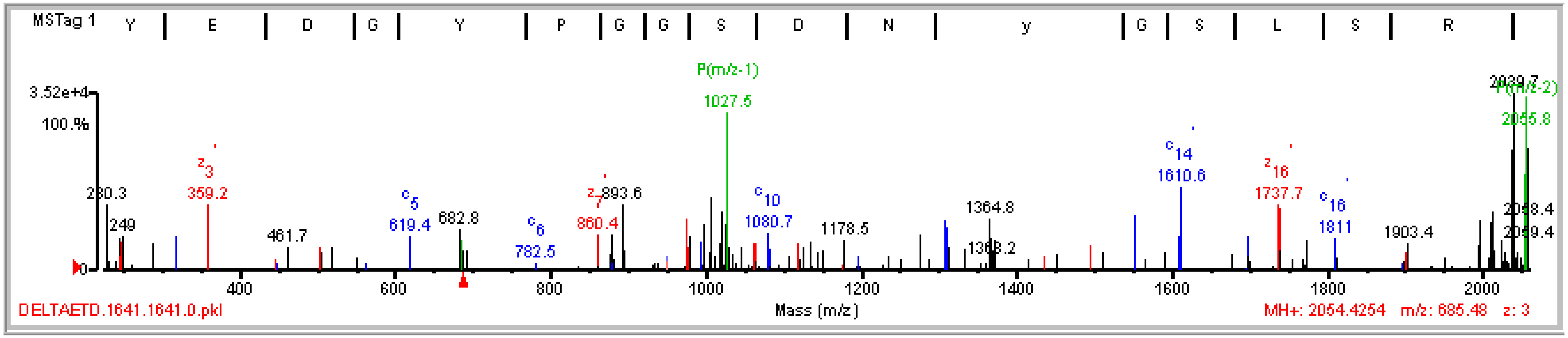
Fragment-ion (m/z)	262.27	414.39	519.83	540.34	560.57	568.99	602.93	628.13	637.07	646.06	653.43	668.40
Frac. Inten.(% of TIC)	0.78	0.77	4.27	1.55	0.68	1.12	0.96	2.35	16.23	29.94	0.05	1.60
Rel. Inten.(% of BP)	2.60	2.56	14.27	5.17	2.28	3.74	3.22	7.84	54.22	100.00	0.15	5.35
Score	1.00	-0.03	1.00	1.00	1.00	1.00	1.00	-0.08	0.50	1.00	1.50	-0.05
Ion-type	y_2		y_5	y^{++}_9	b^{+++}_{15}	y^{++}_{10}	b_5		b^{++}_{12}-H_2O	b^{++}_{12} -0.68 y^{++}_{12}	sty	
Delta Da	0.12		0.54	0.63	0.04	0.77	0.71		-0.67	0.80	0.82	

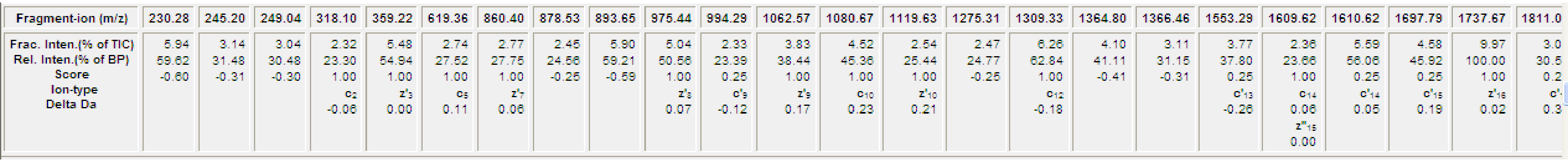
Fragment-ion (m/z)	747.71	759.67	762.85	765.69	768.63	771.57	840.71	876.41	888.30	897.07	919.39	976.41	991.50
Frac. Inten.(% of TIC)	1.75	1.26	0.90	23.40	3.95	0.75	0.86	1.40	1.46	1.10	1.17	0.93	0.78
Rel. Inten.(% of BP)	5.84	4.22	3.00	78.16	13.18	2.51	2.86	4.67	4.89	3.69	3.89	3.11	2.59
Score	0.50	0.50	1.00	1.00	1.00	-0.03	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type	b_6-H_2O	b^{++}_{13}-H_2O	y_6	b_6	b^{++}_{13}		b^{++}_{15}	y_7	b^{++}_{16}-H_2O	b^{++}_{16}	b_8	b_9	y_8
Delta Da	0.44	0.42	0.53	0.41	0.37		0.42	0.05	0.48	0.24	0.03	0.03	0.11

Peak 10



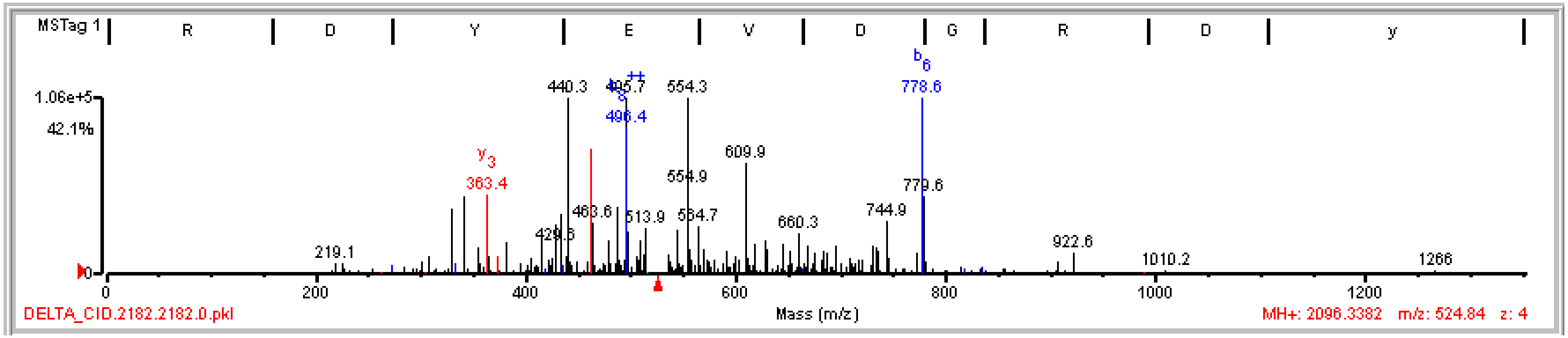
assignment

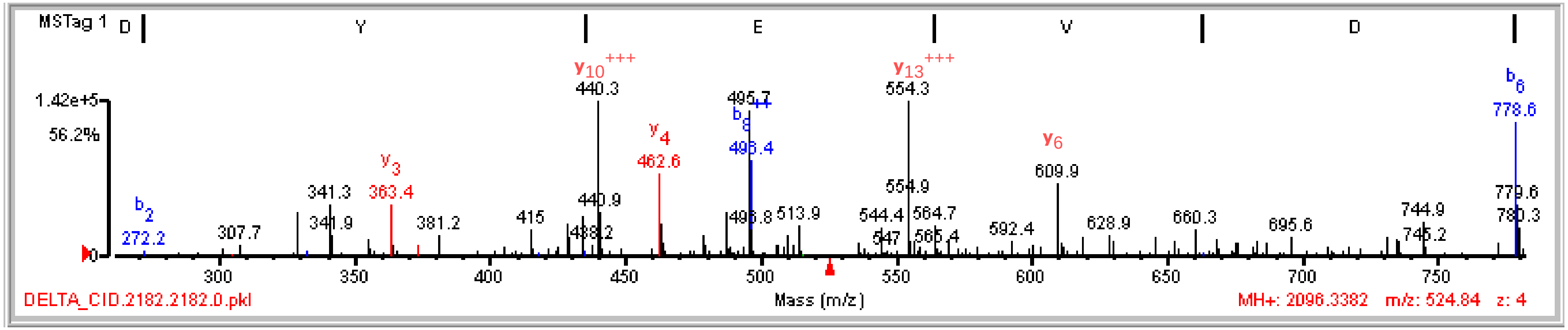


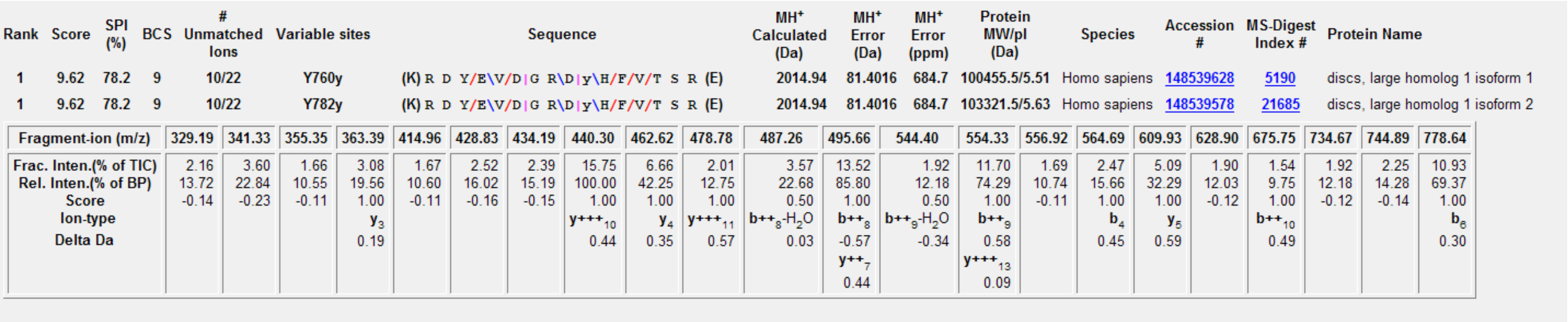


Fragment-ion (m/z)	230.28	245.20	249.04	318.10	359.22	619.36	860.40	878.53	893.65	975.44	994.29	1062.57	1080.67	1119.63	1275.31	1309.33	1364.80	1366.46	1553.29	1609.62	1610.62	1697.79	1737.67	1811.0
Frac. Inten.(% of TIC)	5.94	3.14	3.04	2.32	5.48	2.74	2.77	2.45	5.90	5.04	2.33	3.83	4.52	2.54	2.47	6.26	4.10	3.11	3.77	2.36	5.59	4.58	9.97	3.0
Rel. Inten.(% of BP)	59.62	31.48	30.48	23.30	54.94	27.52	27.75	24.56	59.21	50.56	23.39	38.44	45.36	25.44	24.77	62.84	41.11	31.15	37.80	23.66	56.06	45.92	100.00	30.5
Score	-0.60	-0.31	-0.30	1.00	1.00	1.00	1.00	-0.25	-0.59	1.00	0.25	1.00	1.00	1.00	-0.25	1.00	-0.41	-0.31	0.25	1.00	0.25	0.25	1.00	0.2
Ion-type				c_2	z'_3	c_5	z'_7			z'_8	c'_9	z'_9	c_{10}	z'_{10}		c_{12}			c'_{13}	c_{14} z''_{15}	c'_{14}	c'_{15}	z'_{16}	c'
Delta Da				-0.06	0.00	0.11	0.06			0.07	-0.12	0.17	0.23	0.21		-0.18			-0.26	0.06 0.00	0.05	0.19	0.02	0.3

Peak 11





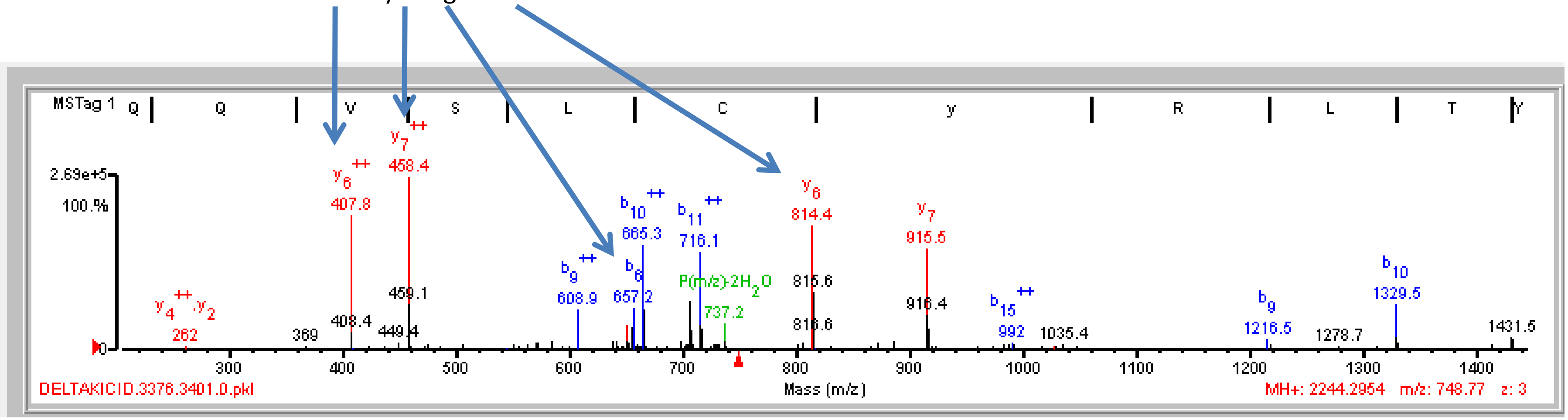


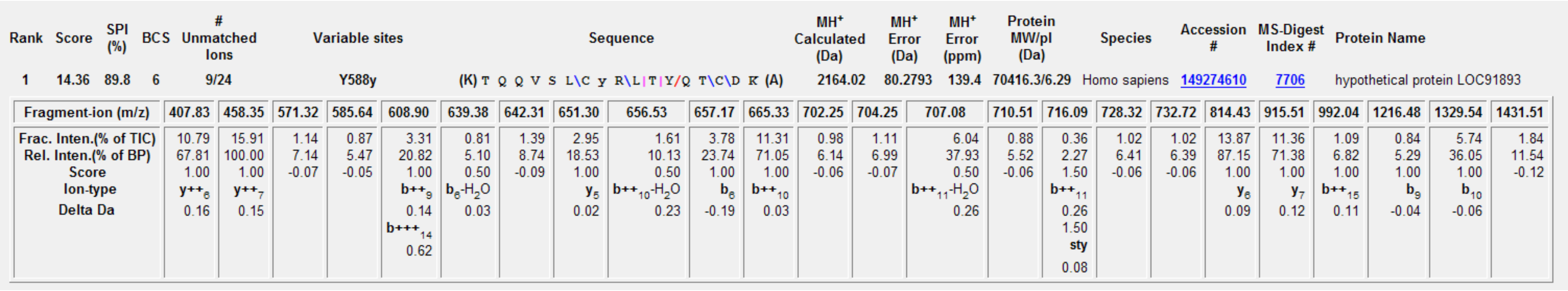
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.62	78.2	9	10/22	Y760y	(K) R D Y/E\V/D|G R\D|y\H/F/V/T S R (E)	2014.94	81.4016	684.7	100455.5/5.51	Homo sapiens	148539628	5190	discs, large homolog 1 isoform 1
1	9.62	78.2	9	10/22	Y782y	(K) R D Y/E\V/D|G R\D|y\H/F/V/T S R (E)	2014.94	81.4016	684.7	103321.5/5.63	Homo sapiens	148539578	21685	discs, large homolog 1 isoform 2

Fragment-ion (m/z)	329.19	341.33	355.35	363.39	414.96	428.83	434.19	440.30	462.62	478.78	487.26	495.66	544.40	554.33	556.92	564.69	609.93	628.90	675.75	734.67	744.89	778.64
Frac. Inten.(% of TIC)	2.16	3.60	1.66	3.08	1.67	2.52	2.39	15.75	6.66	2.01	3.57	13.52	1.92	11.70	1.69	2.47	5.09	1.90	1.54	1.92	2.25	10.93
Rel. Inten.(% of BP)	13.72	22.84	10.55	19.56	10.60	16.02	15.19	100.00	42.25	12.75	22.68	85.80	12.18	74.29	10.74	15.66	32.29	12.03	9.75	12.18	14.28	69.37
Score	-0.14	-0.23	-0.11	1.00	-0.11	-0.16	-0.15	1.00	1.00	1.00	0.50	1.00	0.50	1.00	-0.11	1.00	1.00	-0.12	1.00	-0.12	-0.14	1.00
Ion-type				y_3				$y{+}{+}{+}_{10}$	y_4	$y{+}{+}{+}_{11}$	$b{+}{+}_8\text{-}H_2O$	$b{+}{+}_8$ $y{+}{+}_7$	$b{+}{+}_9\text{-}H_2O$	$b{+}{+}_9$ $y{+}{+}{+}_{13}$		b_4	y_5		$b{+}{+}_{10}$			b_6
Delta Da				0.19				0.44	0.35	0.57	0.03	-0.57 0.44	-0.34	0.58 0.09		0.45	0.59		0.49			0.30

Peak 12

Ions that verify assignment



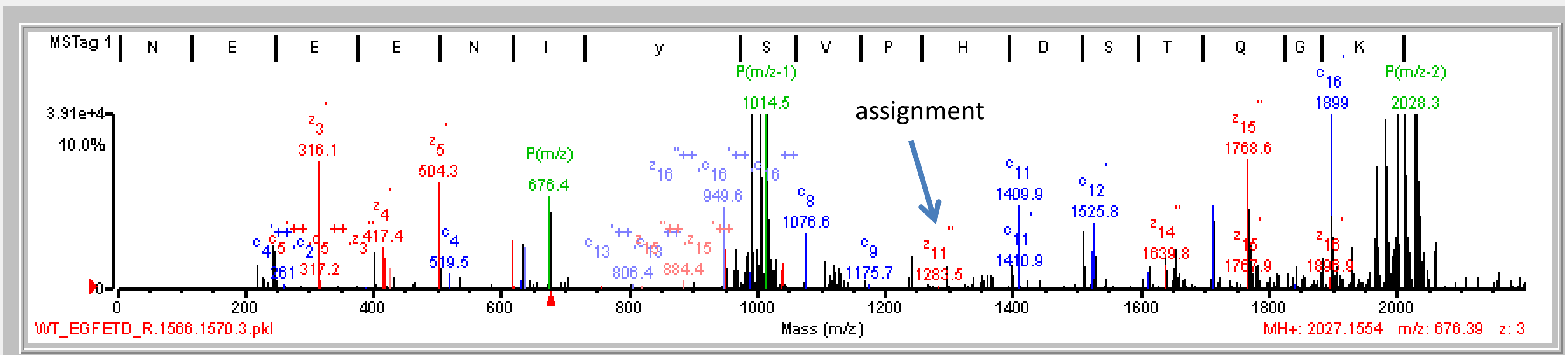


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.36	89.8	6	9/24	Y588y	(K) T Q Q V S L\C y R\L|T|Y/Q T\C\D K (A)	2164.02	80.2793	139.4	70416.3/6.29	Homo sapiens	149274610	7706	hypothetical protein LOC91893

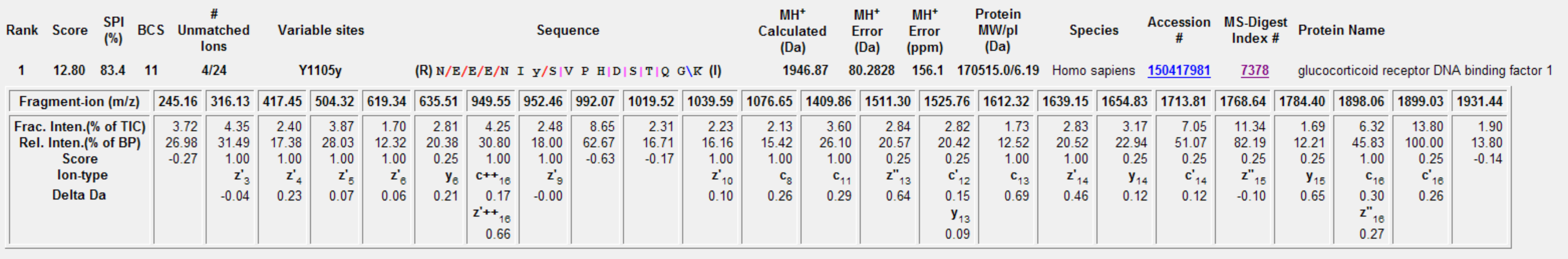
Fragment-ion (m/z)	407.83	458.35	571.32	585.64	608.90	639.38	642.31	651.30	656.53	657.17	665.33
Frac. Inten.(% of TIC)	10.79	15.91	1.14	0.87	3.31	0.81	1.39	2.95	1.61	3.78	11.31
Rel. Inten.(% of BP)	67.81	100.00	7.14	5.47	20.82	5.10	8.74	18.53	10.13	23.74	71.05
Score	1.00	1.00	-0.07	-0.05	1.00	0.50	-0.09	1.00	0.50	1.00	1.00
Ion-type	y^{++}_6	y^{++}_7			b^{++}_9	b_6-H_2O		y_5	b^{++}_{10}-H_2O	b_6	b^{++}_{10}
Delta Da	0.16	0.15			0.14 b^{+++}_{14} 0.62	0.03		0.02	0.23	-0.19	0.03

Fragment-ion (m/z)	702.25	704.25	707.08	710.51	716.09	728.32	732.72	814.43	915.51	992.04	1216.48	1329.54	1431.51
Frac. Inten.(% of TIC)	0.98	1.11	6.04	0.88	0.36	1.02	1.02	13.87	11.36	1.09	0.84	5.74	1.84
Rel. Inten.(% of BP)	6.14	6.99	37.93	5.52	2.27	6.41	6.39	87.15	71.38	6.82	5.29	36.05	11.54
Score	-0.06	-0.07	0.50	-0.06	1.50	-0.06	-0.06	1.00	1.00	1.00	1.00	1.00	-0.12
Ion-type			b^{++}_{11}-H_2O		b^{++}_{11}			y_6	y_7	b^{++}_{15}	b_9	b_{10}	
Delta Da			0.26		0.26 1.50 sty 0.08			0.09	0.12	0.11	-0.04	-0.06	

Peak 13



assignment

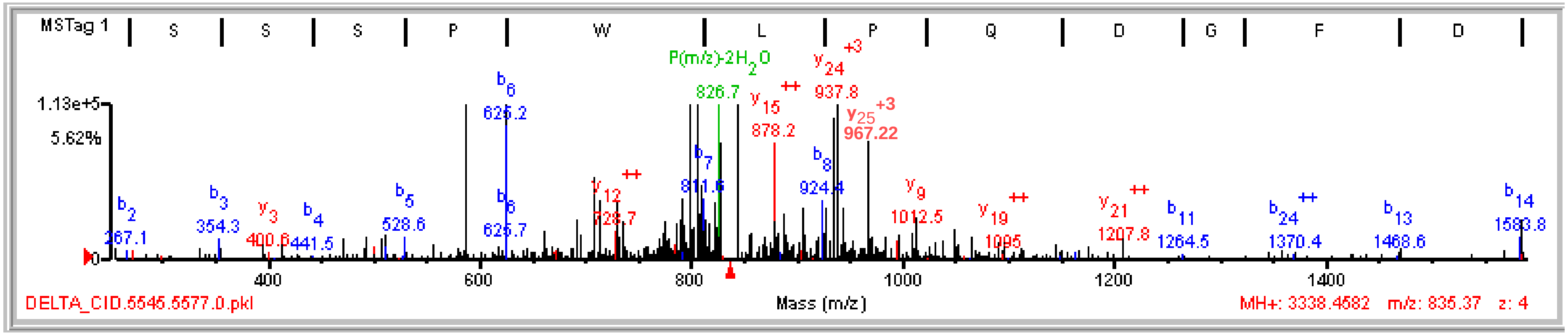


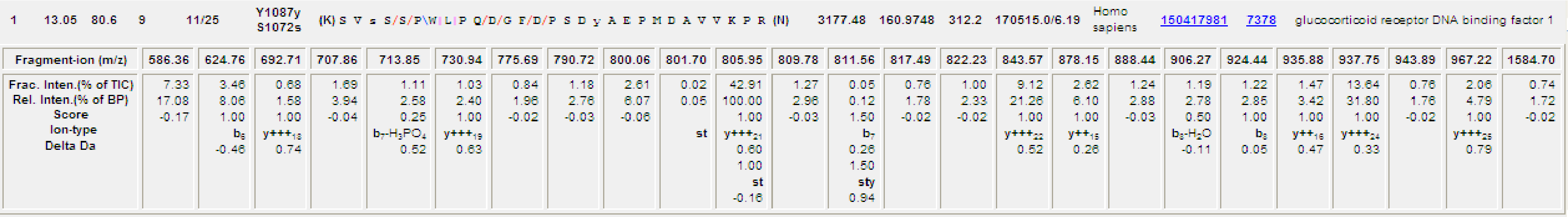
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.80	83.4	11	4/24	Y1105y	(R) N/E/E/E/N I y/S|V P H|D|S|T|Q G\K (I)	1946.87	80.2828	156.1	170515.0/6.19	Homo sapiens	150417981	7378	glucocorticoid receptor DNA binding factor 1

Fragment-ion (m/z)	245.16	316.13	417.45	504.32	619.34	635.51	949.55	952.46	992.07	1019.52	1039.59
Frac. Inten.(% of TIC)	3.72	4.35	2.40	3.87	1.70	2.81	4.25	2.48	8.65	2.31	2.23
Rel. Inten.(% of BP)	26.98	31.49	17.38	28.03	12.32	20.38	30.80	18.00	62.67	16.71	16.16
Score	-0.27	1.00	1.00	1.00	1.00	0.25	1.00	1.00	-0.63	-0.17	1.00
Ion-type		z'_{3}	z'_{4}	z'_{5}	z'_{6}	y_{6}	$c{++}_{16}$ $z'{++}_{16}$	z'_{9}			z'_{10}
Delta Da		-0.04	0.23	0.07	0.06	0.21	0.17 0.66	-0.00			0.10

Fragment-ion (m/z)	1076.65	1409.86	1511.30	1525.76	1612.32	1639.15	1654.83	1713.81	1768.64	1784.40	1898.06	1899.03	1931.44
Frac. Inten.(% of TIC)	2.13	3.60	2.84	2.82	1.73	2.83	3.17	7.05	11.34	1.69	6.32	13.80	1.90
Rel. Inten.(% of BP)	15.42	26.10	20.57	20.42	12.52	20.52	22.94	51.07	82.19	12.21	45.83	100.00	13.80
Score	1.00	1.00	0.25	0.25	1.00	1.00	0.25	0.25	0.25	0.25	1.00	0.25	-0.14
Ion-type	c_{8}	c_{11}	z''_{13}	c'_{12} y_{13}	c_{13}	z'_{14}	y_{14}	c'_{14}	z''_{15}	y_{15}	c_{16} z''_{16}	c'_{16}	
Delta Da	0.26	0.29	0.64	0.15 0.09	0.69	0.46	0.12	0.12	-0.10	0.65	0.30 0.27	0.26	

Peak 14





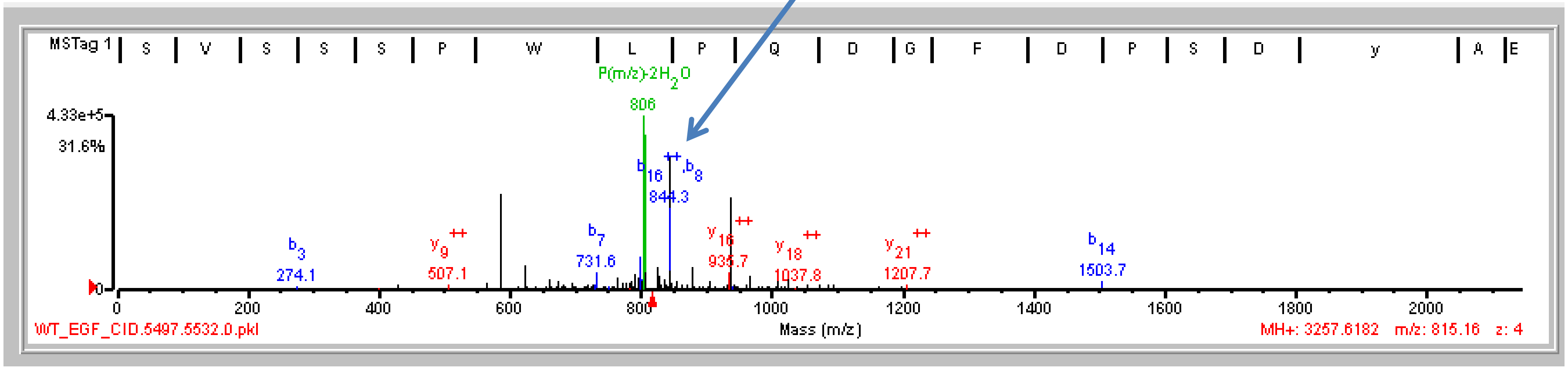
1 13.05 80.6 9 11/25 Y1087y S1072s (K) S V s S/S/P\W|L|P Q/D/G F/D/P S D y A E P M D A V V K P R (N) 3177.48 160.9748 312.2 170515.0/6.19 Homo sapiens 150417981 7378 glucocorticoid receptor DNA binding factor 1

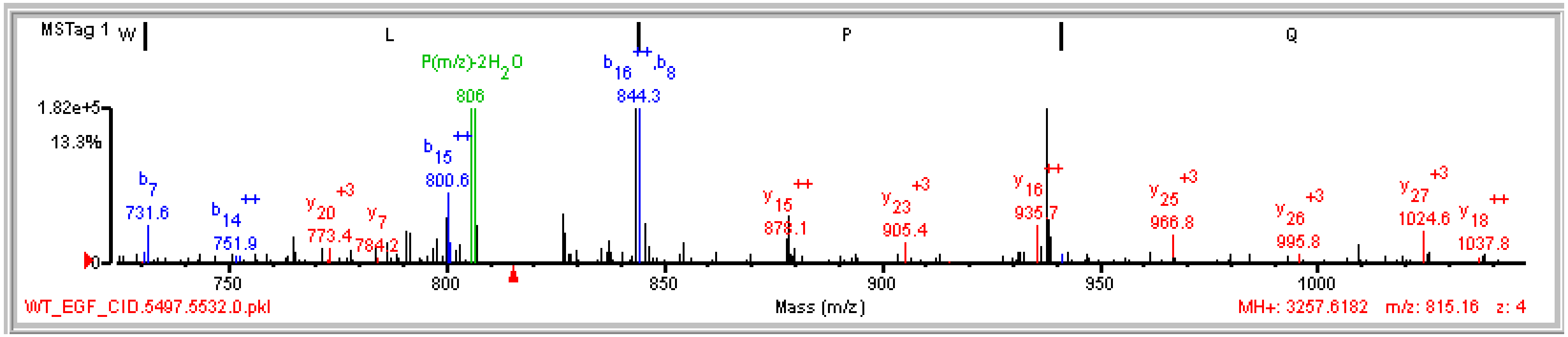
Fragment-ion (m/z)	586.36	624.76	692.71	707.86	713.85	730.94	775.69	790.72	800.06	801.70	805.95
Frac. Inten.(% of TIC)	7.33	3.46	0.68	1.69	1.11	1.03	0.84	1.18	2.61	0.02	42.91
Rel. Inten.(% of BP)	17.08	8.06	1.58	3.94	2.58	2.40	1.96	2.76	6.07	0.05	100.00
Score	-0.17	1.00	1.00	-0.04	0.25	1.00	-0.02	-0.03	-0.06		1.00
Ion-type		b_6	$y{+}{+}{+}_{18}$		b_7-H_3PO_4	$y{+}{+}{+}_{19}$				st	$y{+}{+}{+}_{21}$
Delta Da		-0.46	0.74		0.52	0.63					0.60 1.00 st -0.16

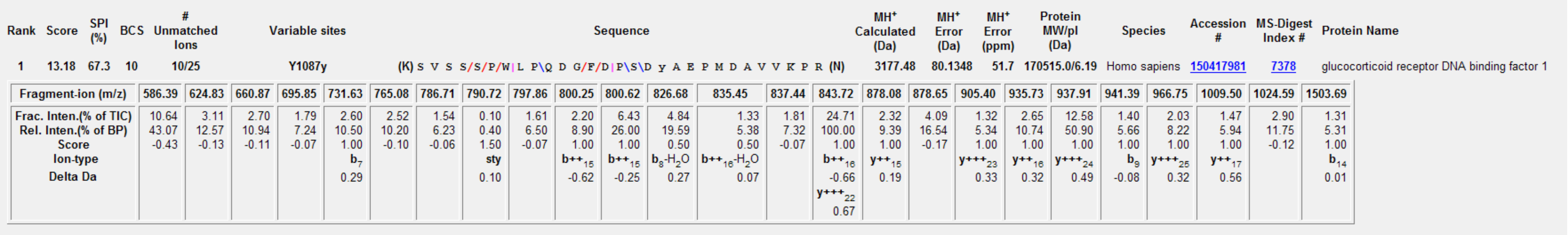
Fragment-ion (m/z)	809.78	811.56	817.49	822.23	843.57	878.15	888.44	906.27	924.44	935.88	937.75	943.89	967.22	1584.70
Frac. Inten.(% of TIC)	1.27	0.05	0.76	1.00	9.12	2.62	1.24	1.19	1.22	1.47	13.64	0.76	2.06	0.74
Rel. Inten.(% of BP)	2.96	0.12	1.78	2.33	21.26	6.10	2.88	2.78	2.85	3.42	31.80	1.76	4.79	1.72
Score	-0.03	1.50	-0.02	-0.02	1.00	1.00	-0.03	0.50	1.00	1.00	1.00	-0.02	1.00	-0.02
Ion-type		b_7			$y{+}{+}{+}_{22}$	$y{+}{+}_{15}$		b_8-H_2O	b_8	$y{+}{+}_{16}$	$y{+}{+}{+}_{24}$		$y{+}{+}{+}_{25}$	
Delta Da		0.26 1.50 sty 0.94			0.52	0.26		-0.11	0.05	0.47	0.33		0.79	

Peak 15

Ions that verify assignment



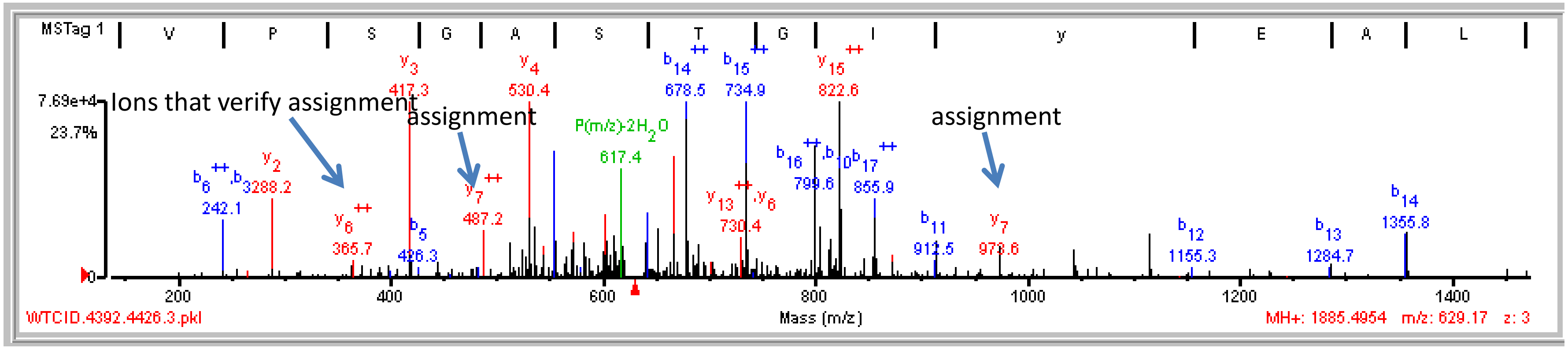




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.18	67.3	10	10/25	Y1087y	(K) S V S S/S/P/W|L P\Q D G/F/D|P\S\D y A E P M D A V V K P R (N)	3177.48	80.1348	51.7	170515.0/6.19	Homo sapiens	150417981	7378	glucocorticoid receptor DNA binding factor 1

Fragment-ion (m/z)	586.39	624.83	660.87	695.85	731.63	765.08	786.71	790.72	797.86	800.25	800.62	826.68	835.45	837.44	843.72	878.08	878.65	905.40	935.73	937.91	941.39	966.75	1009.50	1024.59	1503.69
Frac. Inten.(% of TIC)	10.64	3.11	2.70	1.79	2.60	2.52	1.54	0.10	1.61	2.20	6.43	4.84	1.33	1.81	24.71	2.32	4.09	1.32	2.65	12.58	1.40	2.03	1.47	2.90	1.31
Rel. Inten.(% of BP)	43.07	12.57	10.94	7.24	10.50	10.20	6.23	0.40	6.50	8.90	26.00	19.59	5.38	7.32	100.00	9.39	16.54	5.34	10.74	50.90	5.66	8.22	5.94	11.75	5.31
Score	-0.43	-0.13	-0.11	-0.07	1.00	-0.10	-0.06	1.50	-0.07	1.00	1.00	0.50	0.50	-0.07	1.00	1.00	-0.17	1.00	1.00	1.00	1.00	1.00	1.00	-0.12	1.00
Ion-type					b_7			sty		$b{++}_{15}$	$b{++}_{15}$	b_8-H_2O	$b{++}_{16}$-H_2O		$b{++}_{16}$ $y{+++}_{22}$	$y{++}_{15}$		$y{+++}_{23}$	$y{++}_{16}$	$y{+++}_{24}$	b_9	$y{+++}_{25}$	$y{++}_{17}$		b_{14}
Delta Da					0.29			0.10		-0.62	-0.25	0.27	0.07		-0.66 0.67	0.19		0.33	0.32	0.49	-0.08	0.32	0.56		0.01

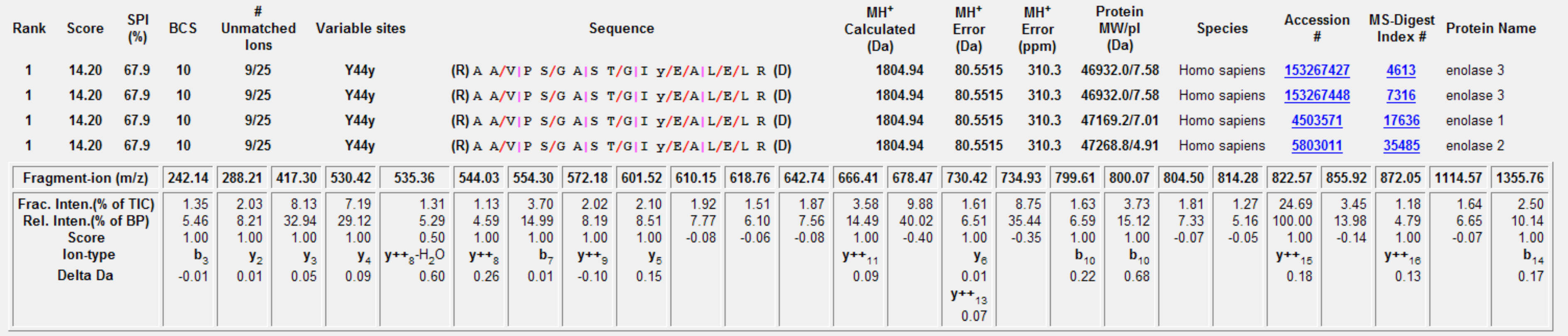
Peak 16



Ions that verify assignment

assignment

assignment



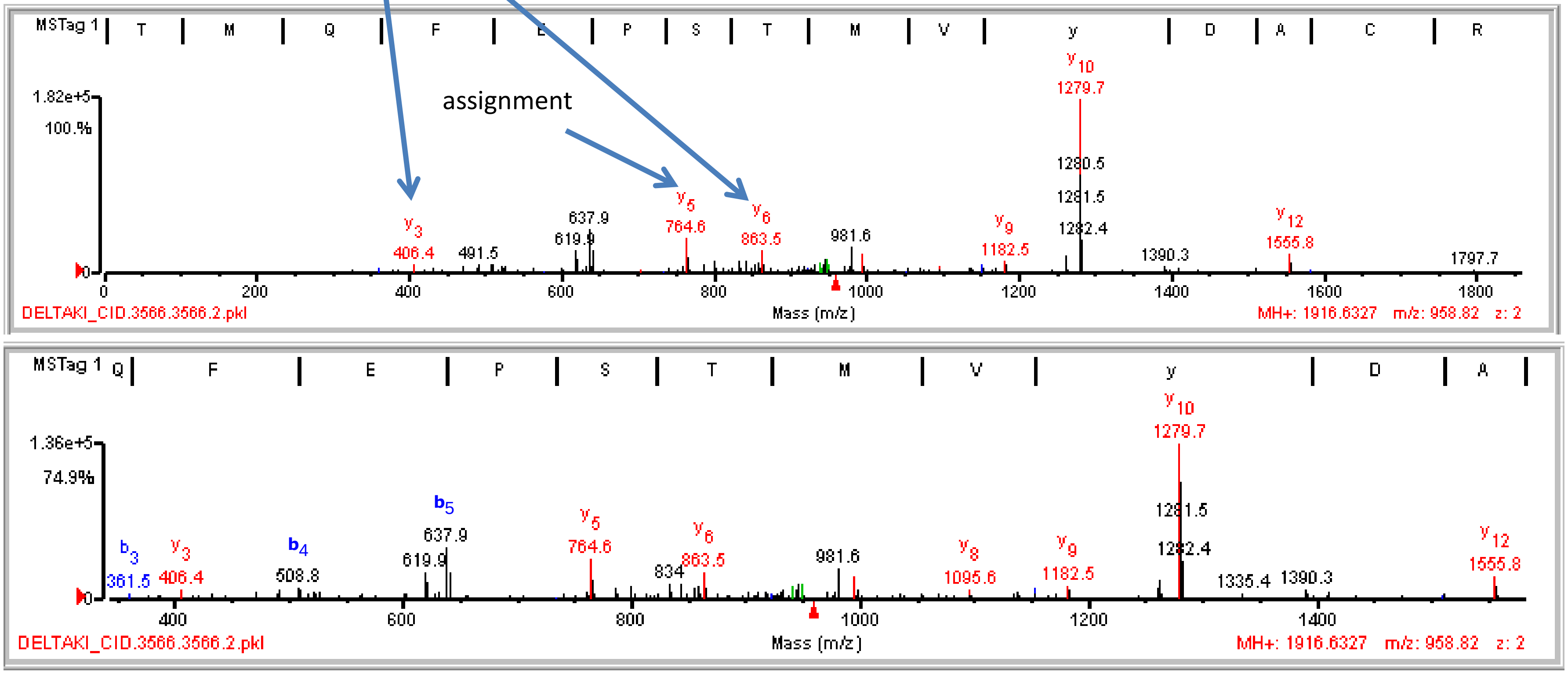
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.20	67.9	10	9/25	Y44y	(R) A A/V|P S/G A|S T/G|I y/E/A|L/E/L R (D)	1804.94	80.5515	310.3	46932.0/7.58	Homo sapiens	153267427	4613	enolase 3
1	14.20	67.9	10	9/25	Y44y	(R) A A/V|P S/G A|S T/G|I y/E/A|L/E/L R (D)	1804.94	80.5515	310.3	46932.0/7.58	Homo sapiens	153267448	7316	enolase 3
1	14.20	67.9	10	9/25	Y44y	(R) A A/V|P S/G A|S T/G|I y/E/A|L/E/L R (D)	1804.94	80.5515	310.3	47169.2/7.01	Homo sapiens	4503571	17636	enolase 1
1	14.20	67.9	10	9/25	Y44y	(R) A A/V|P S/G A|S T/G|I y/E/A|L/E/L R (D)	1804.94	80.5515	310.3	47268.8/4.91	Homo sapiens	5803011	35485	enolase 2

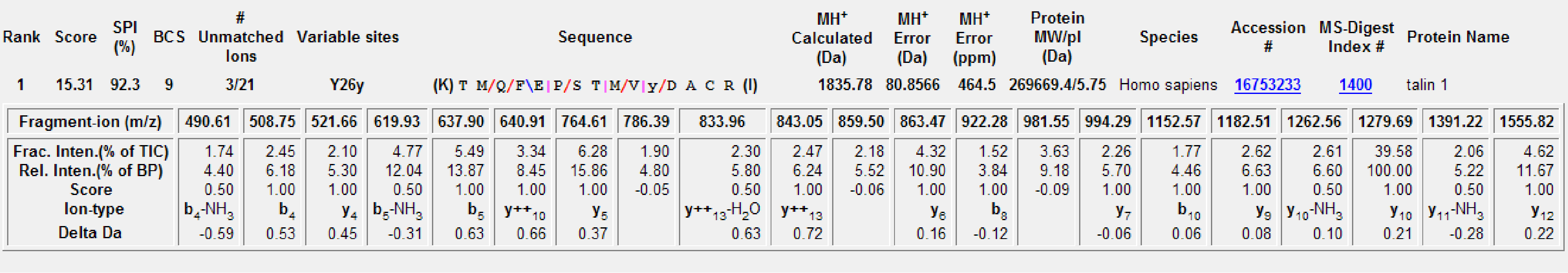
Fragment-ion (m/z)	242.14	288.21	417.30	530.42	535.36	544.03	554.30	572.18	601.52	610.15	618.76	642.74	666.41	678.47	730.42	734.93	799.61	800.07	804.50	814.28	822.57	855.92	872.05	1114.57	1355.76
Frac. Inten.(% of TIC)	1.35	2.03	8.13	7.19	1.31	1.13	3.70	2.02	2.10	1.92	1.51	1.87	3.58	9.88	1.61	8.75	1.63	3.73	1.81	1.27	24.69	3.45	1.18	1.64	2.50
Rel. Inten.(% of BP)	5.46	8.21	32.94	29.12	5.29	4.59	14.99	8.19	8.51	7.77	6.10	7.56	14.49	40.02	6.51	35.44	6.59	15.12	7.33	5.16	100.00	13.98	4.79	6.65	10.14
Score	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00	-0.08	-0.06	-0.08	1.00	-0.40	1.00	-0.35	1.00	1.00	-0.07	-0.05	1.00	-0.14	1.00	-0.07	1.00
Ion-type	b_3	y_2	y_3	y_4	$y{+}{+}_8$-H_2O	$y{+}{+}_8$	b_7	$y{+}{+}_9$	y_5				$y{+}{+}_{11}$		y_6		b_{10}	b_{10}			$y{+}{+}_{15}$		$y{+}{+}_{16}$		b_{14}
Delta Da	-0.01	0.01	0.05	0.09	0.60	0.26	0.01	-0.10	0.15				0.09		0.01		0.22	0.68			0.18		0.13		0.17
															$y{+}{+}_{13}$										
															0.07										

Peak 17

Ions that verify assignment

assignment

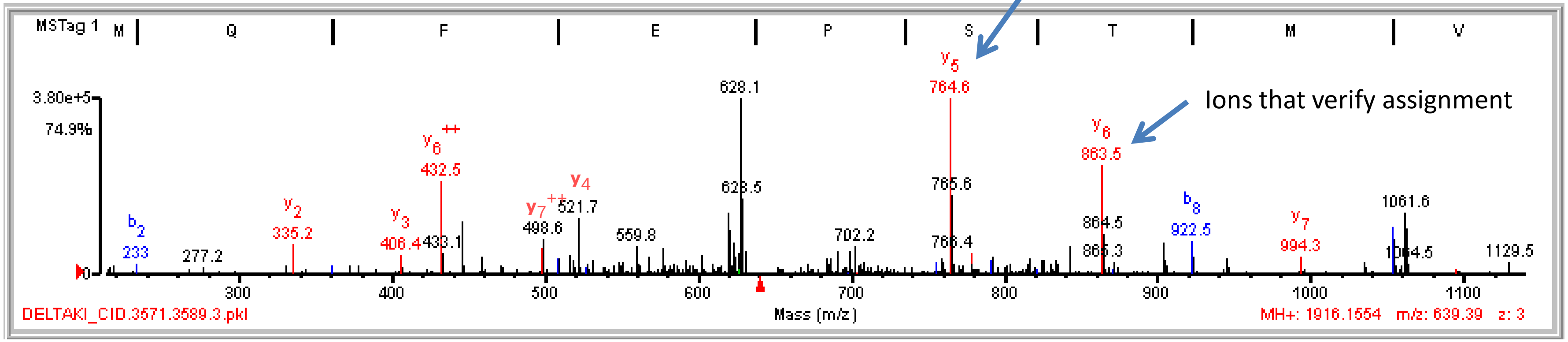




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.31	92.3	9	3/21	Y26y	(K) T M/Q/F\E|P/S T|M/V|y/D A C R (I)	1835.78	80.8566	464.5	269669.4/5.75	Homo sapiens	16753233	1400	talin 1

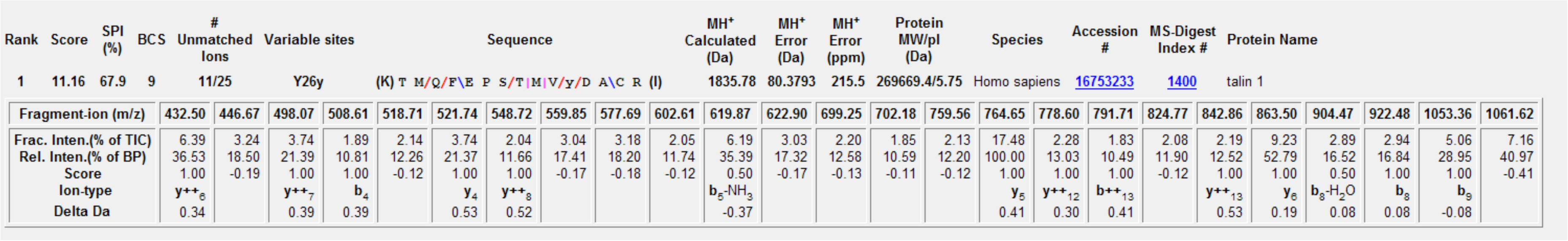
Fragment-ion (m/z)	490.61	508.75	521.66	619.93	637.90	640.91	764.61	786.39	833.96	843.05	859.50	863.47	922.28	981.55	994.29	1152.57	1182.51	1262.56	1279.69	1391.22	1555.82
Frac. Inten.(% of TIC)	1.74	2.45	2.10	4.77	5.49	3.34	6.28	1.90	2.30	2.47	2.18	4.32	1.52	3.63	2.26	1.77	2.62	2.61	39.58	2.06	4.62
Rel. Inten.(% of BP)	4.40	6.18	5.30	12.04	13.87	8.45	15.86	4.80	5.80	6.24	5.52	10.90	3.84	9.18	5.70	4.46	6.63	6.60	100.00	5.22	11.67
Score	0.50	1.00	1.00	0.50	1.00	1.00	1.00	-0.05	0.50	1.00	-0.06	1.00	1.00	-0.09	1.00	1.00	1.00	0.50	1.00	0.50	1.00
Ion-type	b_4-NH_3	b_4	y_4	b_5-NH_3	b_5	$y{+}{+}_{10}$	y_5		$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$		y_6	b_8		y_7	b_{10}	y_9	y_{10}-NH_3	y_{10}	y_{11}-NH_3	y_{12}
Delta Da	-0.59	0.53	0.45	-0.31	0.63	0.66	0.37		0.63	0.72		0.16	-0.12		-0.06	0.06	0.08	0.10	0.21	-0.28	0.22

Peak 18



assignment

Ions that verify assignment

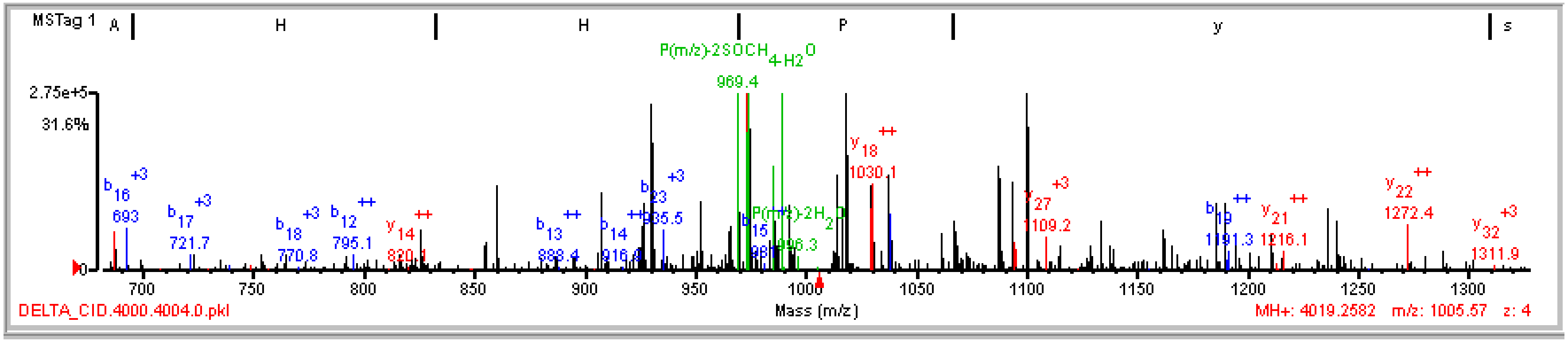


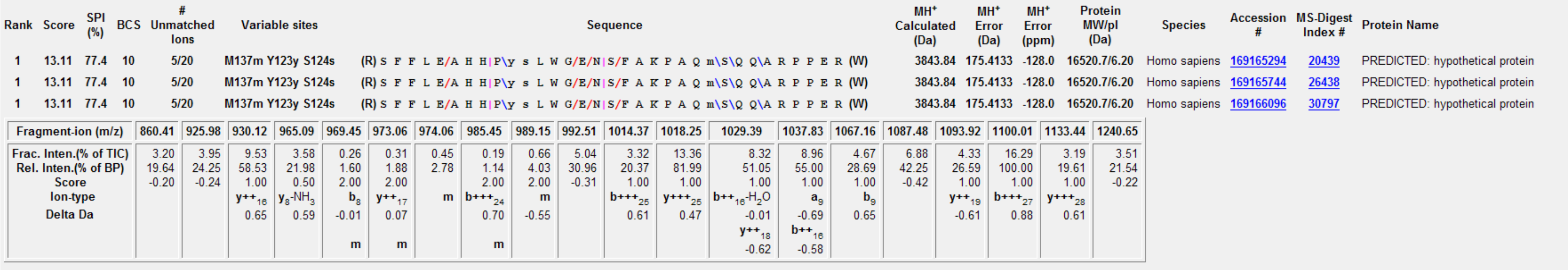
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.16	67.9	9	11/25	Y26y	(K) T M/Q/F\E P S/T|M|V/y/D A\C R (I)	1835.78	80.3793	215.5	269669.4/5.75	Homo sapiens	16753233	1400	talin 1

Fragment-ion (m/z)	432.50	446.67	498.07	508.61	518.71	521.74	548.72	559.85	577.69	602.61	619.87	622.90
Frac. Inten.(% of TIC)	6.39	3.24	3.74	1.89	2.14	3.74	2.04	3.04	3.18	2.05	6.19	3.03
Rel. Inten.(% of BP)	36.53	18.50	21.39	10.81	12.26	21.37	11.66	17.41	18.20	11.74	35.39	17.32
Score	1.00	-0.19	1.00	1.00	-0.12	1.00	1.00	-0.17	-0.18	-0.12	0.50	-0.17
Ion-type	$y{+}{+}_{6}$		$y{+}{+}_{7}$	b_4		y_4	$y{+}{+}_{8}$				b_5-NH_3	
Delta Da	0.34		0.39	0.39		0.53	0.52				-0.37	

Fragment-ion (m/z)	699.25	702.18	759.56	764.65	778.60	791.71	824.77	842.86	863.50	904.47	922.48	1053.36	1061.62
Frac. Inten.(% of TIC)	2.20	1.85	2.13	17.48	2.28	1.83	2.08	2.19	9.23	2.89	2.94	5.06	7.16
Rel. Inten.(% of BP)	12.58	10.59	12.20	100.00	13.03	10.49	11.90	12.52	52.79	16.52	16.84	28.95	40.97
Score	-0.13	-0.11	-0.12	1.00	1.00	1.00	-0.12	1.00	1.00	0.50	1.00	1.00	-0.41
Ion-type				y_5	$y{+}{+}_{12}$	$b{+}{+}_{13}$		$y{+}{+}_{13}$	y_6	b_8-H_2O	b_8	b_9	
Delta Da				0.41	0.30	0.41		0.53	0.19	0.08	0.08	-0.08	

Peak 19

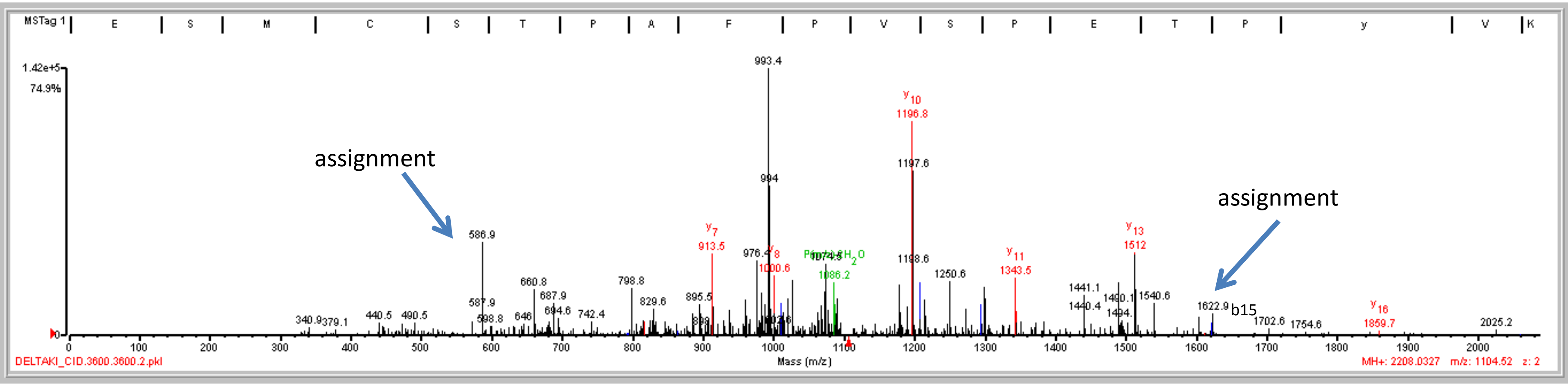


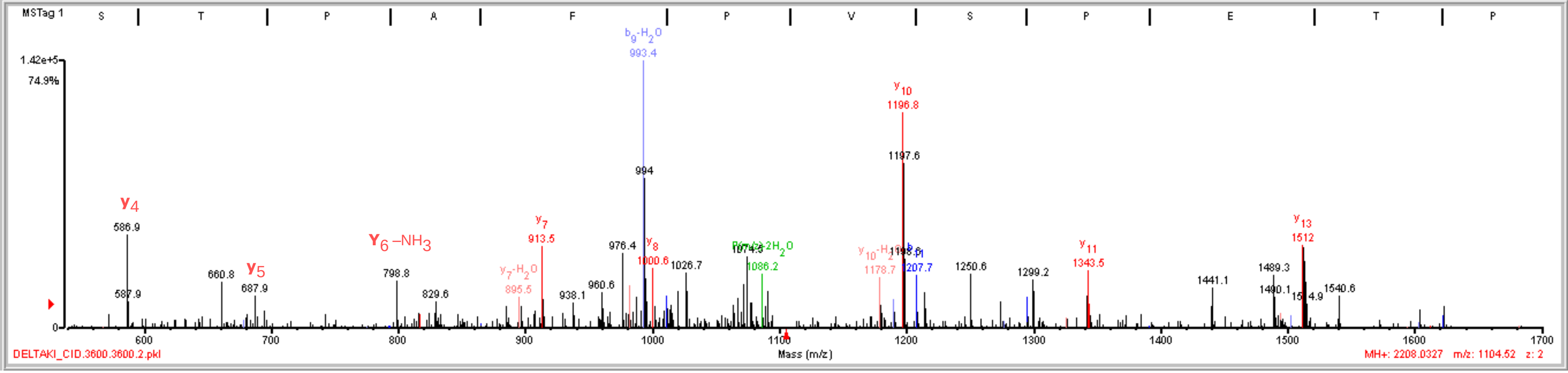


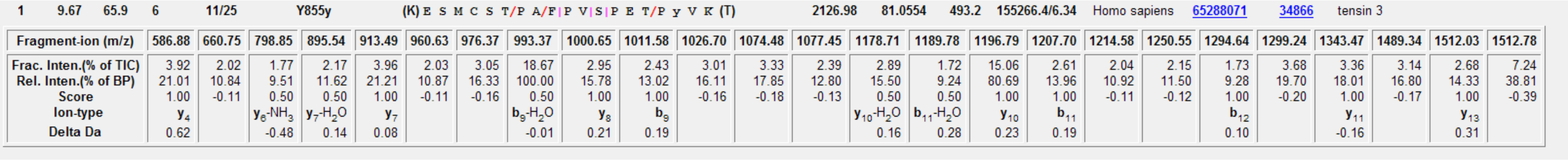
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.11	77.4	10	5/20	M137m Y123y S124s	(R) S F F L E/A H H|P\y s L W G/E/N|S/F A K P A Q m\S\Q Q\A R P P E R (W)	3843.84	175.4133	-128.0	16520.7/6.20	Homo sapiens	169165294	20439	PREDICTED: hypothetical protein
1	13.11	77.4	10	5/20	M137m Y123y S124s	(R) S F F L E/A H H|P\y s L W G/E/N|S/F A K P A Q m\S\Q Q\A R P P E R (W)	3843.84	175.4133	-128.0	16520.7/6.20	Homo sapiens	169165744	26438	PREDICTED: hypothetical protein
1	13.11	77.4	10	5/20	M137m Y123y S124s	(R) S F F L E/A H H|P\y s L W G/E/N|S/F A K P A Q m\S\Q Q\A R P P E R (W)	3843.84	175.4133	-128.0	16520.7/6.20	Homo sapiens	169166096	30797	PREDICTED: hypothetical protein

Fragment-ion (m/z)	860.41	925.98	930.12	965.09	969.45	973.06	974.06	985.45	989.15	992.51	1014.37	1018.25	1029.39	1037.83	1067.16	1087.48	1093.92	1100.01	1133.44	1240.65
Frac. Inten.(% of TIC)	3.20	3.95	9.53	3.58	0.26	0.31	0.45	0.19	0.66	5.04	3.32	13.36	8.32	8.96	4.67	6.88	4.33	16.29	3.19	3.51
Rel. Inten.(% of BP)	19.64	24.25	58.53	21.98	1.60	1.88	2.78	1.14	4.03	30.96	20.37	81.99	51.05	55.00	28.69	42.25	26.59	100.00	19.61	21.54
Score	-0.20	-0.24	1.00	0.50	2.00	2.00		2.00	2.00	-0.31	1.00	1.00	1.00	1.00	1.00	-0.42	1.00	1.00	1.00	-0.22
Ion-type			y++$_{16}$	y_8-NH_3	b_8	y++$_{17}$	m	b+++$_{24}$	m		b+++$_{25}$	y+++$_{25}$	b++$_{16}$-H_2O	a_9	b_9		y++$_{19}$	b+++$_{27}$	y+++$_{28}$	
Delta Da			0.65	0.59	-0.01	0.07		0.70	-0.55		0.61	0.47	-0.01	-0.69	0.65		-0.61	0.88	0.61	
													y++$_{18}$	b++$_{16}$						
													-0.62	-0.58						
					m	m		m												

Peak 20



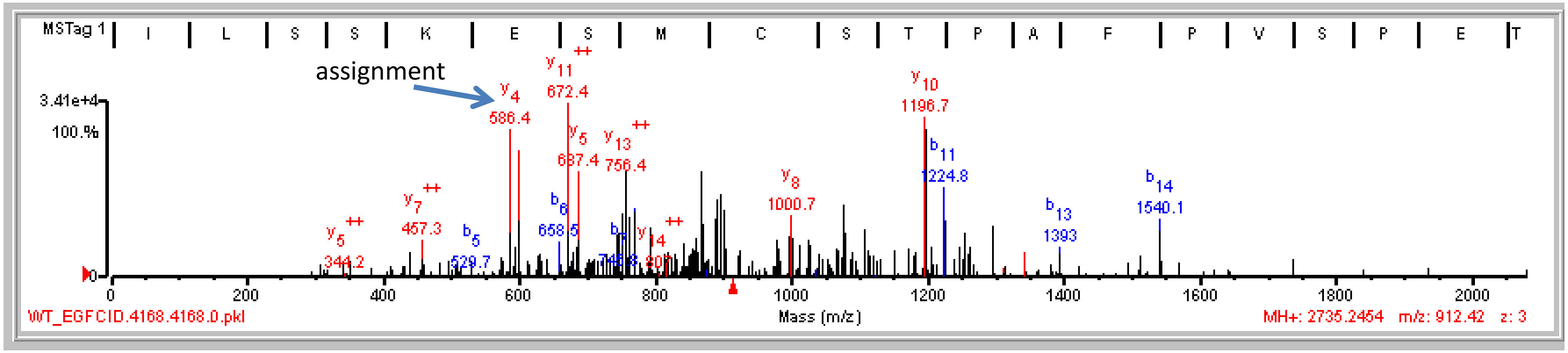




1 9.67 65.9 6 11/25 Y855y (K) E S M C S T/P A/F|P V|S|P E T/P y V K (T) 2126.98 81.0554 493.2 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

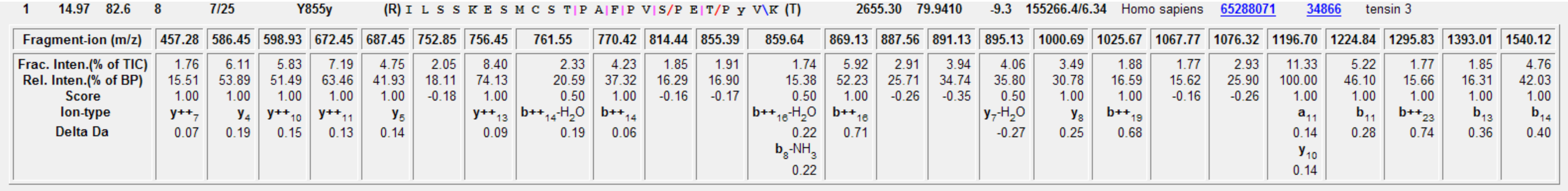
Fragment-ion (m/z)	586.88	660.75	798.85	895.54	913.49	960.63	976.37	993.37	1000.65	1011.58	1026.70	1074.48	1077.45	1178.71	1189.78	1196.79	1207.70	1214.58	1250.55	1294.64	1299.24	1343.47	1489.34	1512.03	1512.78
Frac. Inten.(% of TIC)	3.92	2.02	1.77	2.17	3.96	2.03	3.05	18.67	2.95	2.43	3.01	3.33	2.39	2.89	1.72	15.06	2.61	2.04	2.15	1.73	3.68	3.36	3.14	2.68	7.24
Rel. Inten.(% of BP)	21.01	10.84	9.51	11.62	21.21	10.87	16.33	100.00	15.78	13.02	16.11	17.85	12.80	15.50	9.24	80.69	13.96	10.92	11.50	9.28	19.70	18.01	16.80	14.33	38.81
Score	1.00	-0.11	0.50	0.50	1.00	-0.11	-0.16	0.50	1.00	1.00	-0.16	-0.18	-0.13	0.50	0.50	1.00	1.00	-0.11	-0.12	1.00	-0.20	1.00	-0.17	1.00	-0.39
Ion-type	y_4		y_6-NH_3	y_7-H_2O	y_7			b_9-H_2O	y_8	b_9				$y_{10}-H_2O$	$b_{11}-H_2O$	y_{10}	b_{11}			b_{12}		y_{11}		y_{13}	
Delta Da	0.62		-0.48	0.14	0.08			-0.01	0.21	0.19				0.16	0.28	0.23	0.19			0.10		-0.16		0.31	

Peak 21



WT_EGFCID.4168.4168.0.pkl

MH+: 2735.2454 m/z: 912.42 z: 3



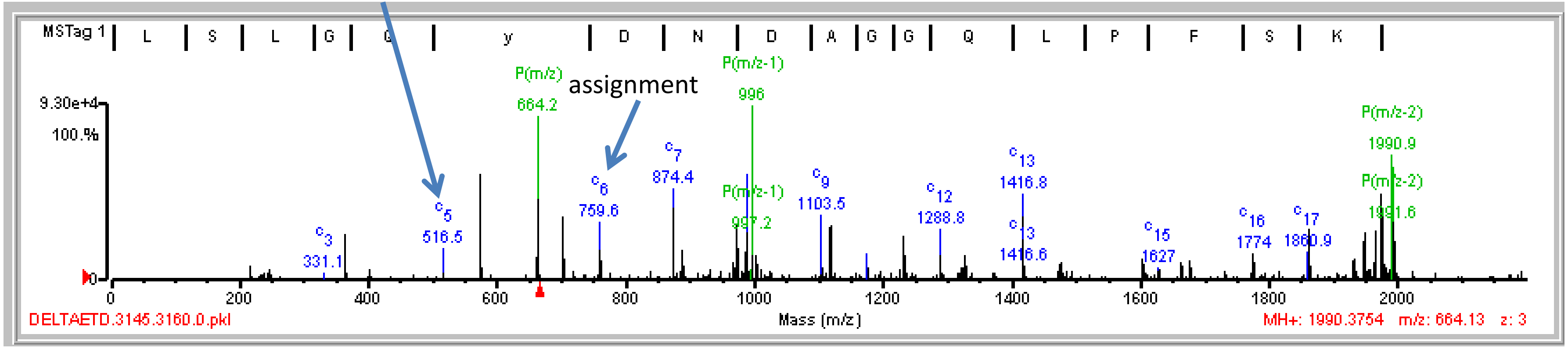
1 14.97 82.6 8 7/25 Y855y (R) I L S S K E S M C S T|P A|F|P V|S/P E|T/P y V\K (T) 2655.30 79.9410 -9.3 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

Fragment-ion (m/z)	457.28	586.45	598.93	672.45	687.45	752.85	756.45	761.55	770.42	814.44	855.39	859.64
Frac. Inten.(% of TIC)	1.76	6.11	5.83	7.19	4.75	2.05	8.40	2.33	4.23	1.85	1.91	1.74
Rel. Inten.(% of BP)	15.51	53.89	51.49	63.46	41.93	18.11	74.13	20.59	37.32	16.29	16.90	15.38
Score	1.00	1.00	1.00	1.00	1.00	-0.18	1.00	0.50	1.00	-0.16	-0.17	0.50
Ion-type	$y{++}_7$	y_4	$y{++}_{10}$	$y{++}_{11}$	y_5		$y{++}_{13}$	$b{++}_{14}$-H_2O	$b{++}_{14}$			$b{++}_{16}$-H_2O b_8-NH_3
Delta Da	0.07	0.19	0.15	0.13	0.14		0.09	0.19	0.06			0.22 0.22

Fragment-ion (m/z)	869.13	887.56	891.13	895.13	1000.69	1025.67	1067.77	1076.32	1196.70	1224.84	1295.83	1393.01	1540.12
Frac. Inten.(% of TIC)	5.92	2.91	3.94	4.06	3.49	1.88	1.77	2.93	11.33	5.22	1.77	1.85	4.76
Rel. Inten.(% of BP)	52.23	25.71	34.74	35.80	30.78	16.59	15.62	25.90	100.00	46.10	15.66	16.31	42.03
Score	1.00	-0.26	-0.35	0.50	1.00	1.00	-0.16	-0.26	1.00	1.00	1.00	1.00	1.00
Ion-type	$b{++}_{16}$			y_7-H_2O	y_8	$b{++}_{19}$			a_{11} y_{10}	b_{11}	$b{++}_{23}$	b_{13}	b_{14}
Delta Da	0.71			-0.27	0.25	0.68			0.14 0.14	0.28	0.74	0.36	0.40

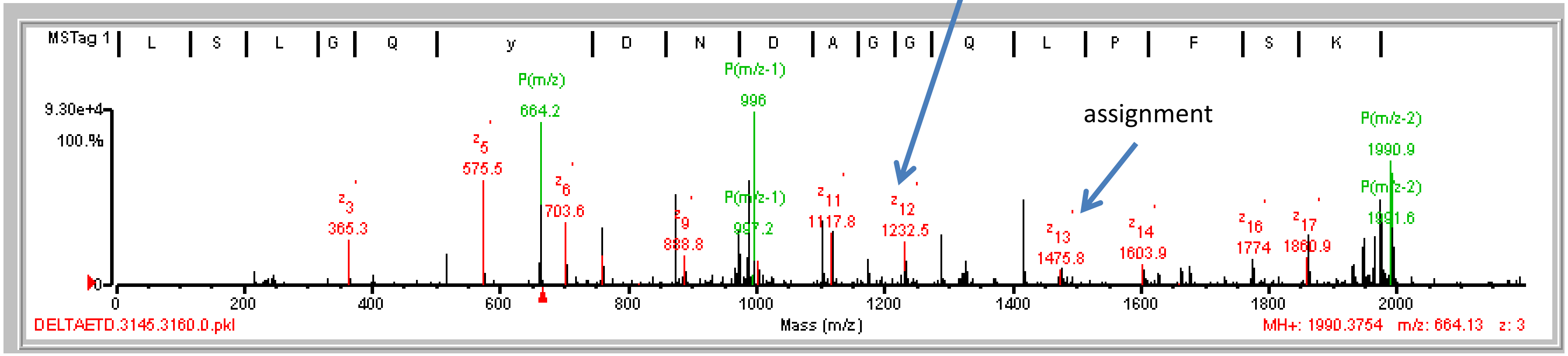
Peak 22

Ions that verify assignment

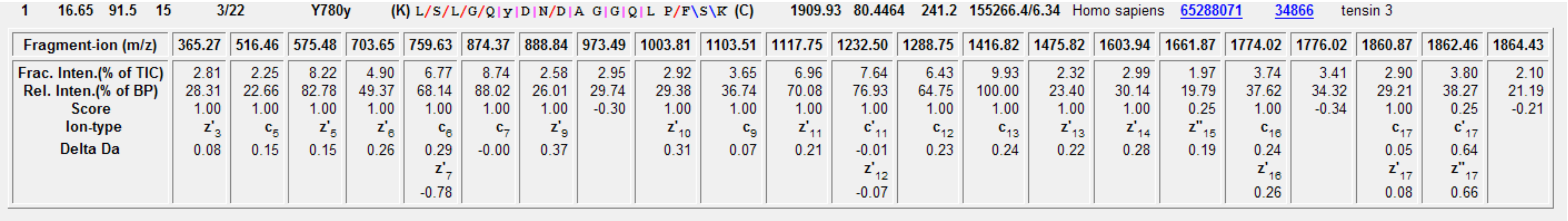


assignment

Ions that verify assignment



assignment

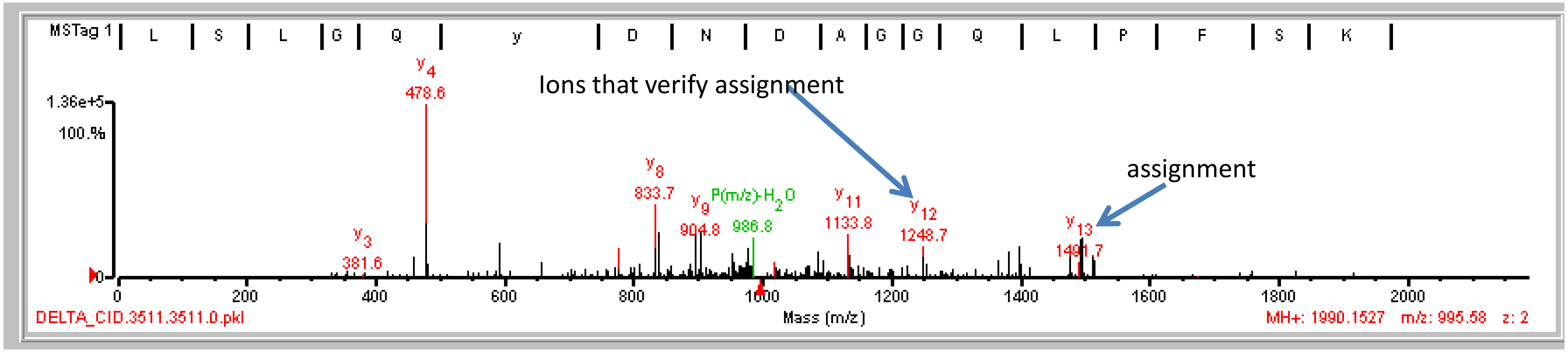


1 16.65 91.5 15 3/22 Y780y (K) L/S/L/G/Q|y|D|N/D|A G|G|Q|L P/F\S\K (C) 1909.93 80.4464 241.2 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

Fragment-ion (m/z)	365.27	516.46	575.48	703.65	759.63	874.37	888.84	973.49	1003.81	1103.51	1117.75
Frac. Inten.(% of TIC)	2.81	2.25	8.22	4.90	6.77	8.74	2.58	2.95	2.92	3.65	6.96
Rel. Inten.(% of BP)	28.31	22.66	82.78	49.37	68.14	88.02	26.01	29.74	29.38	36.74	70.08
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.30	1.00	1.00	1.00
Ion-type	z'_3	c_5	z'_5	z'_6	c_6	c_7	z'_9		z'_{10}	c_9	z'_{11}
Delta Da	0.08	0.15	0.15	0.26	0.29	-0.00	0.37		0.31	0.07	0.21
					z'_7						
					-0.78						

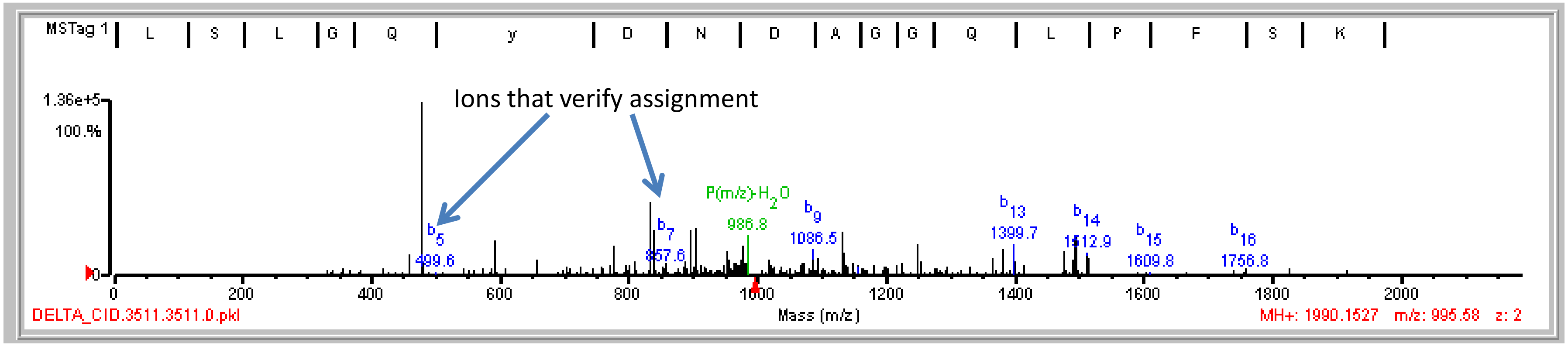
Fragment-ion (m/z)	1232.50	1288.75	1416.82	1475.82	1603.94	1661.87	1774.02	1776.02	1860.87	1862.46	1864.43
Frac. Inten.(% of TIC)	7.64	6.43	9.93	2.32	2.99	1.97	3.74	3.41	2.90	3.80	2.10
Rel. Inten.(% of BP)	76.93	64.75	100.00	23.40	30.14	19.79	37.62	34.32	29.21	38.27	21.19
Score	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.34	1.00	0.25	-0.21
Ion-type	c'_{11}	c_{12}	c_{13}	z'_{13}	z'_{14}	z''_{15}	c_{16}		c_{17}	c'_{17}	
Delta Da	-0.01	0.23	0.24	0.22	0.28	0.19	0.24		0.05	0.64	
	z'_{12}						z'_{16}		z'_{17}	z''_{17}	
	-0.07						0.26		0.08	0.66	

Peak 23

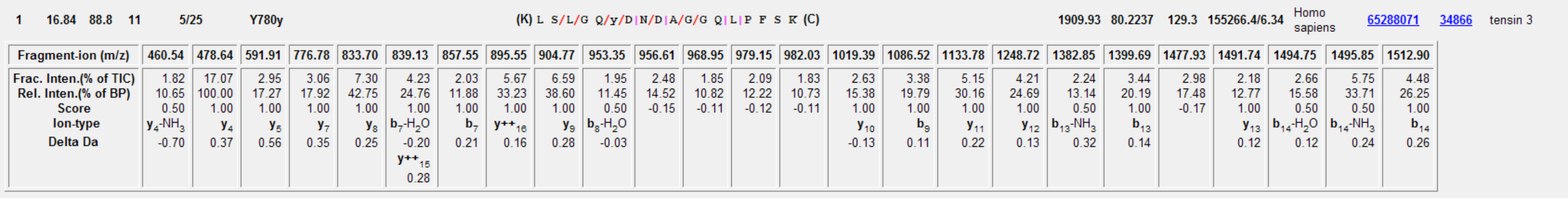


Ions that verify assignment

assignment



Ions that verify assignment

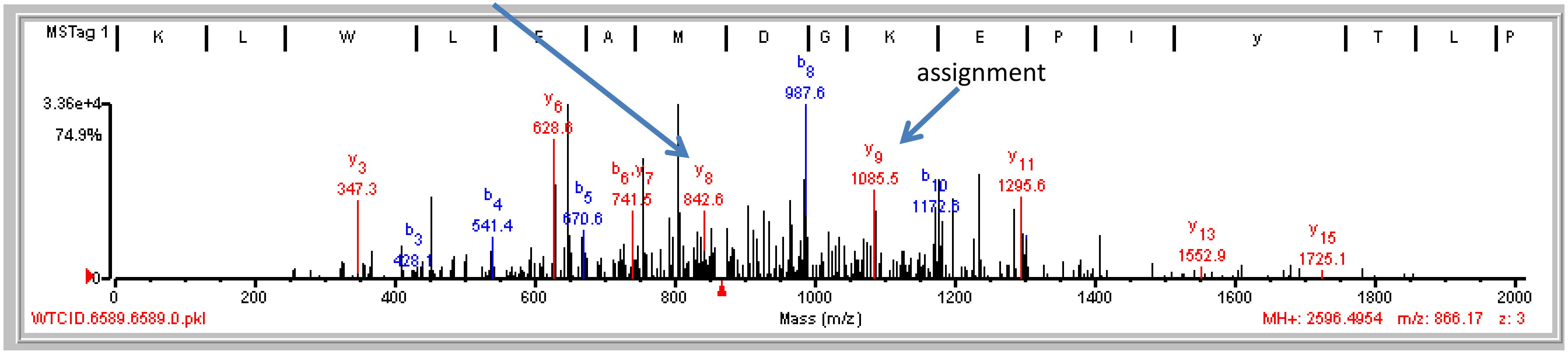


1 16.84 88.8 11 5/25 Y780y (K) L S/L/G Q/y/D|N/D|A/G/G Q|L|P F S K (C) 1909.93 80.2237 129.3 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

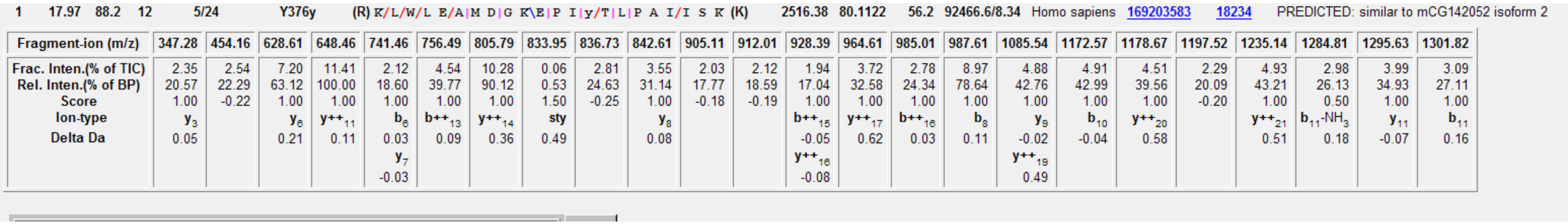
Fragment-ion (m/z)	460.54	478.64	591.91	776.78	833.70	839.13	857.55	895.55	904.77	953.35	956.61	968.95	979.15	982.03	1019.39	1086.52	1133.78	1248.72	1382.85	1399.69	1477.93	1491.74	1494.75	1495.85	1512.90
Frac. Inten.(% of TIC)	1.82	17.07	2.95	3.06	7.30	4.23	2.03	5.67	6.59	1.95	2.48	1.85	2.09	1.83	2.63	3.38	5.15	4.21	2.24	3.44	2.98	2.18	2.66	5.75	4.48
Rel. Inten.(% of BP)	10.65	100.00	17.27	17.92	42.75	24.76	11.88	33.23	38.60	11.45	14.52	10.82	12.22	10.73	15.38	19.79	30.16	24.69	13.14	20.19	17.48	12.77	15.58	33.71	26.25
Score	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	-0.15	-0.11	-0.12	-0.11	1.00	1.00	1.00	1.00	0.50	1.00	-0.17	1.00	0.50	0.50	1.00
Ion-type	y_4-NH_3	y_4	y_5	y_7	y_8	b_7-H_2O	b_7	$y{+}{+}_{16}$	y_9	b_8-H_2O					y_{10}	b_9	y_{11}	y_{12}	b_{13}-NH_3	b_{13}		y_{13}	b_{14}-H_2O	b_{14}-NH_3	b_{14}
Delta Da	-0.70	0.37	0.56	0.35	0.25	-0.20 $y{+}{+}_{15}$ 0.28	0.21	0.16	0.28	-0.03					-0.13	0.11	0.22	0.13	0.32	0.14		0.12	0.12	0.24	0.26

Peak 24

Ions that verify assignment



assignment



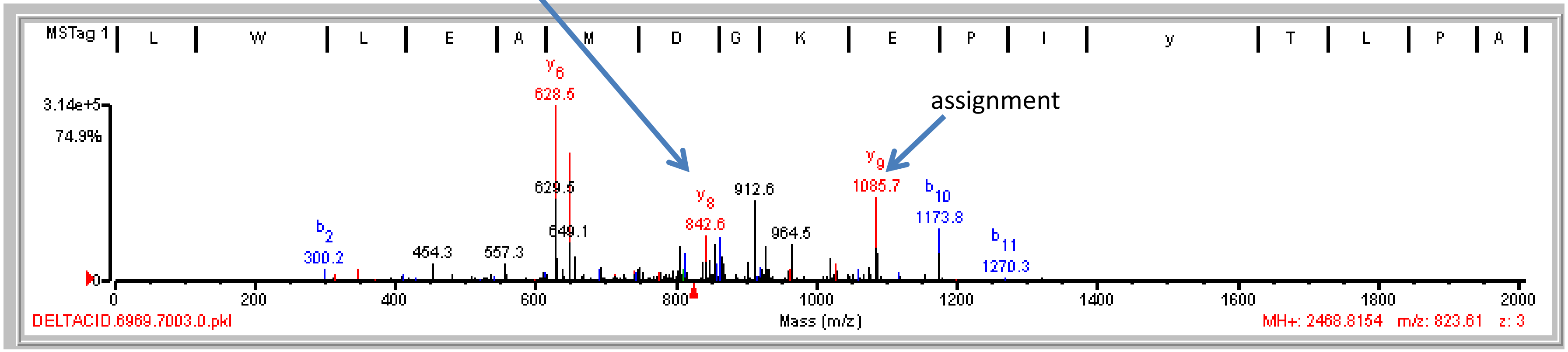
1 17.97 88.2 12 5/24 Y376y (R) K/L/W/L E/A|M D|G K\E|P I|y/T|L|P A I/I S K (K) 2516.38 80.1122 56.2 92466.6/8.34 Homo sapiens 169203583 18234 PREDICTED: similar to mCG142052 isoform 2

Fragment-ion (m/z)	347.28	454.16	628.61	648.46	741.46	756.49	805.79	833.95	836.73	842.61	905.11	912.01
Frac. Inten.(% of TIC)	2.35	2.54	7.20	11.41	2.12	4.54	10.28	0.06	2.81	3.55	2.03	2.12
Rel. Inten.(% of BP)	20.57	22.29	63.12	100.00	18.60	39.77	90.12	0.53	24.63	31.14	17.77	18.59
Score	1.00	-0.22	1.00	1.00	1.00	1.00	1.00	1.50	-0.25	1.00	-0.18	-0.19
Ion-type	y_3		y_6	$y{+}{+}_{11}$	b_6 y_7	$b{+}{+}_{13}$	$y{+}{+}_{14}$	sty		y_8		
Delta Da	0.05		0.21	0.11	0.03 -0.03	0.09	0.36	0.49		0.08		

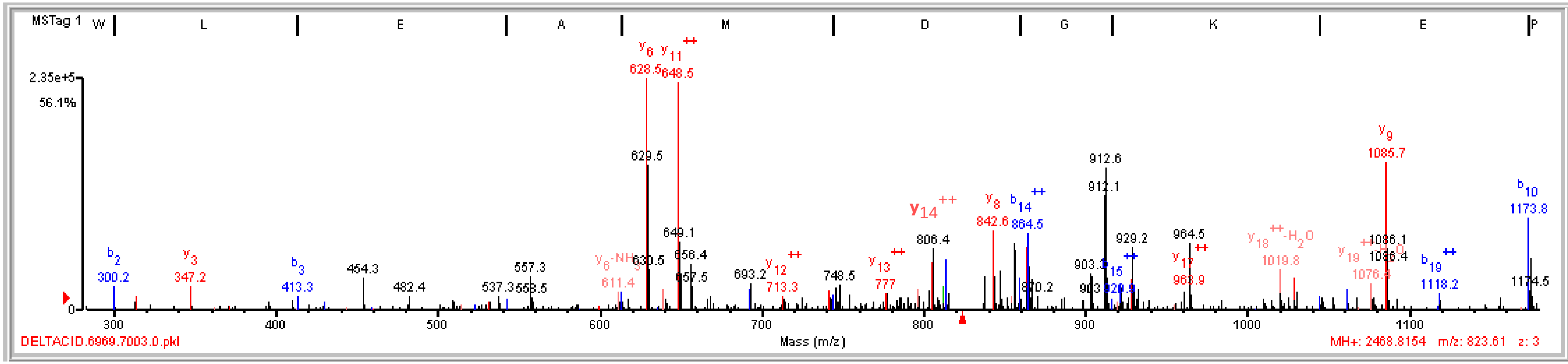
Fragment-ion (m/z)	928.39	964.61	985.01	987.61	1085.54	1172.57	1178.67	1197.52	1235.14	1284.81	1295.63	1301.82
Frac. Inten.(% of TIC)	1.94	3.72	2.78	8.97	4.88	4.91	4.51	2.29	4.93	2.98	3.99	3.09
Rel. Inten.(% of BP)	17.04	32.58	24.34	78.64	42.76	42.99	39.56	20.09	43.21	26.13	34.93	27.11
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.20	1.00	0.50	1.00	1.00
Ion-type	$b{+}{+}_{15}$ $y{+}{+}_{16}$	$y{+}{+}_{17}$	$b{+}{+}_{16}$	b_8	y_9 $y{+}{+}_{19}$	b_{10}	$y{+}{+}_{20}$		$y{+}{+}_{21}$	b_{11}-NH_3	y_{11}	b_{11}
Delta Da	-0.05 -0.08	0.62	0.03	0.11	-0.02 0.49	-0.04	0.58		0.51	0.18	-0.07	0.16

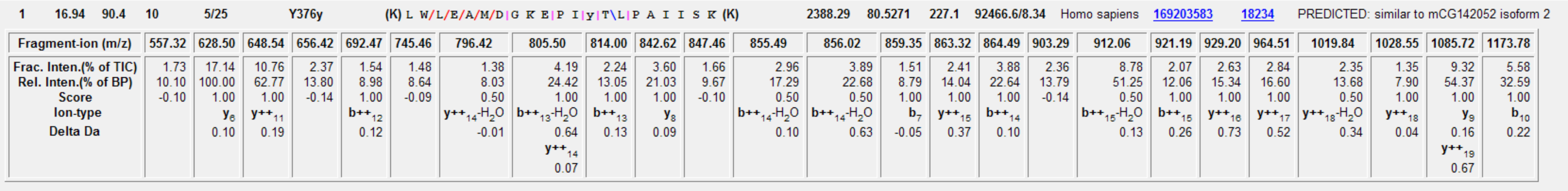
Peak 25

Ions that verify assignment



assignment

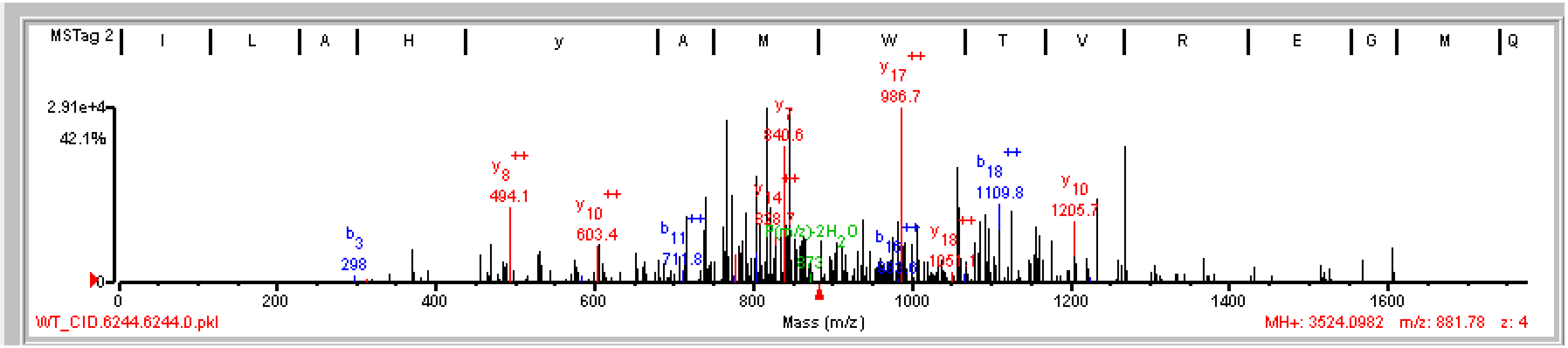


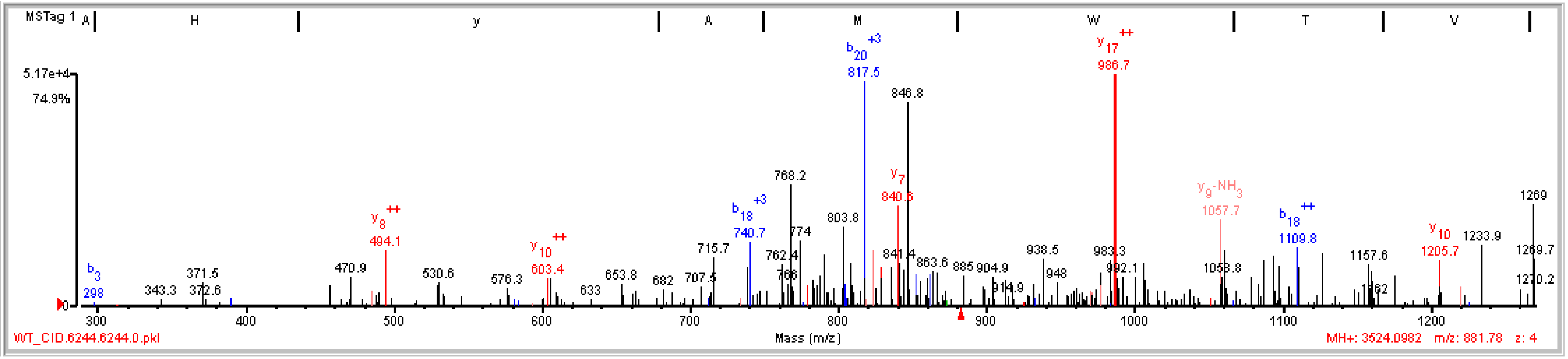


1 16.94 90.4 10 5/25 Y376y (K) L W/L/E/A/M/D|G K E|P I|y|T\L|P A I I S K (K) 2388.29 80.5271 227.1 92466.6/8.34 Homo sapiens 169203583 18234 PREDICTED: similar to mCG142052 isoform 2

Fragment-ion (m/z)	557.32	628.50	648.54	656.42	692.47	745.46	796.42	805.50	814.00	842.62	847.46	855.49	856.02	859.35	863.32	864.49	903.29	912.06	921.19	929.20	964.51	1019.84	1028.55	1085.72	1173.78
Frac. Inten.(% of TIC)	1.73	17.14	10.76	2.37	1.54	1.48	1.38	4.19	2.24	3.60	1.66	2.96	3.89	1.51	2.41	3.88	2.36	8.78	2.07	2.63	2.84	2.35	1.35	9.32	5.58
Rel. Inten.(% of BP)	10.10	100.00	62.77	13.80	8.98	8.64	8.03	24.42	13.05	21.03	9.67	17.29	22.68	8.79	14.04	22.64	13.79	51.25	12.06	15.34	16.60	13.68	7.90	54.37	32.59
Score	-0.10	1.00	1.00	-0.14	1.00	-0.09	0.50	1.00	1.00	1.00	-0.10	0.50	0.50	1.00	1.00	1.00	-0.14	0.50	1.00	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type		y_6	$y{+}{+}_{11}$		$b{+}{+}_{12}$		$y{+}{+}_{14}$-H_2O	$b{+}{+}_{13}$-H_2O $y{+}{+}_{14}$	$b{+}{+}_{13}$	y_8		$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$-H_2O	b_7	$y{+}{+}_{15}$	$b{+}{+}_{14}$		$b{+}{+}_{15}$-H_2O	$b{+}{+}_{15}$	$y{+}{+}_{16}$	$y{+}{+}_{17}$	$y{+}{+}_{18}$-H_2O	$y{+}{+}_{18}$	y_9 $y{+}{+}_{19}$	b_{10}
Delta Da		0.10	0.19		0.12		-0.01	0.64 0.07	0.13	0.09		0.10	0.63	-0.05	0.37	0.10		0.13	0.26	0.73	0.52	0.34	0.04	0.16 0.67	0.22

Peak 26





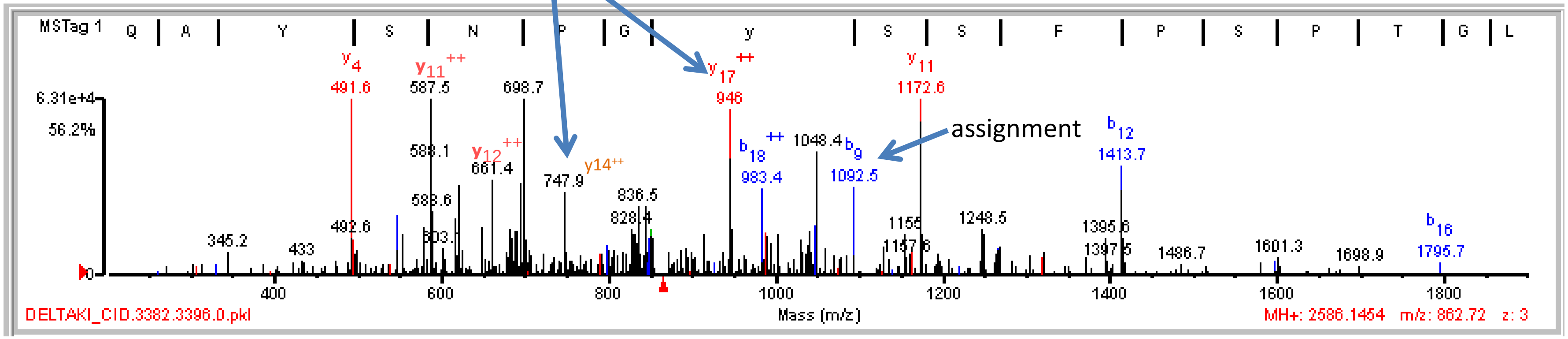
1 12.77 76.2 8 8/23 T201t Y188y (K) I L A H y A M W T V R E/G M Q/V A t\V|M\S|F/L T N P M H\K (I) 3362.67 161.4313 425.2 111896.7/9.58 Homo sapiens 169215032 8292 PREDICTED: similar to hCG40021

Fragment-ion (m/z)	494.14	740.69	768.24	774.02	782.84	790.60	803.78	808.42	817.46	823.21	828.67
Frac. Inten.(% of TIC)	2.46	2.05	5.03	3.23	2.19	2.17	3.82	2.53	8.74	2.05	2.14
Rel. Inten.(% of BP)	12.71	10.62	26.00	16.71	11.31	11.22	19.76	13.06	45.19	10.59	11.04
Score	1.00	1.00	-0.26	1.00	-0.11	-0.11	-0.20	-0.13	1.00	0.50	1.00
Ion-type	$y{++}_{8}$	$b{+++}_{18}$		$b{+++}_{19}$					$b{+++}_{20}$	y_7-NH$_3$	$y{++}_{14}$
Delta Da	-0.12	0.37		0.67					0.43	-0.20	0.28

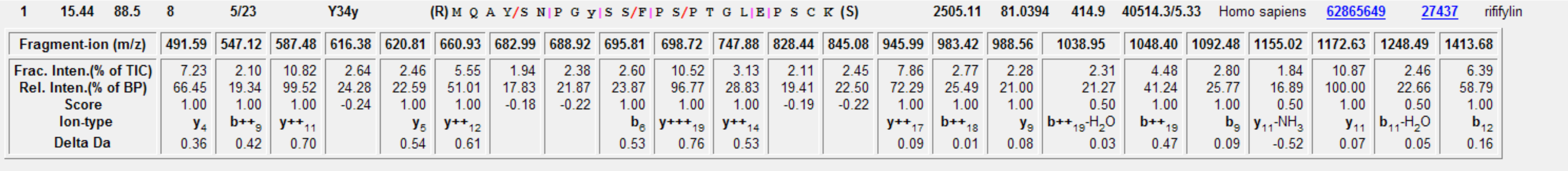
Fragment-ion (m/z)	840.61	846.79	986.68	1006.44	1057.71	1060.71	1093.48	1109.75	1126.40	1160.20	1205.74	1269.01
Frac. Inten.(% of TIC)	4.96	9.25	19.34	2.90	4.50	2.78	2.40	3.14	3.38	2.47	2.70	5.77
Rel. Inten.(% of BP)	25.64	47.84	100.00	14.97	23.28	14.39	12.41	16.23	17.50	12.79	13.94	29.82
Score	1.00	1.00	1.00	-0.15	0.50	-0.14	-0.12	1.00	1.00	1.00	1.00	1.00
Ion-type	y_7	$b{+++}_{21}$	$y{++}_{17}$		y_9-NH$_3$			$b{++}_{18}$	$b{+++}_{28}$	$b{++}_{19}$	y_{10}	$b{++}_{21}$
Delta Da	0.17	0.75	0.23		0.20			-0.23	0.23	0.68	0.16	0.46

Peak 27

Ions that verify assignment



assignment



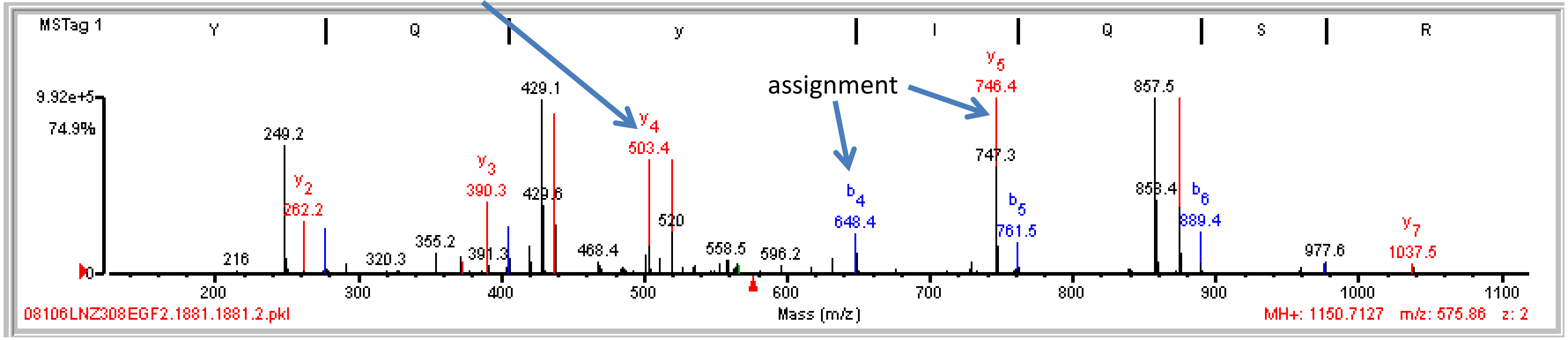
1 15.44 88.5 8 5/23 Y34y (R) M Q A Y/S N|P G y|S S/F|P S/P T G L|E|P S C K (S) 2505.11 81.0394 414.9 40514.3/5.33 Homo sapiens 62865649 27437 rififylin

Fragment-ion (m/z)	491.59	547.12	587.48	616.38	620.81	660.93	682.99	688.92	695.81	698.72	747.88	828.44
Frac. Inten.(% of TIC)	7.23	2.10	10.82	2.64	2.46	5.55	1.94	2.38	2.60	10.52	3.13	2.11
Rel. Inten.(% of BP)	66.45	19.34	99.52	24.28	22.59	51.01	17.83	21.87	23.87	96.77	28.83	19.41
Score	1.00	1.00	1.00	-0.24	1.00	1.00	-0.18	-0.22	1.00	1.00	1.00	-0.19
Ion-type	y_{4}	$b{++}_{9}$	$y{++}_{11}$		y_{5}	$y{++}_{12}$			b_{6}	$y{+++}_{19}$	$y{++}_{14}$	
Delta Da	0.36	0.42	0.70		0.54	0.61			0.53	0.76	0.53	

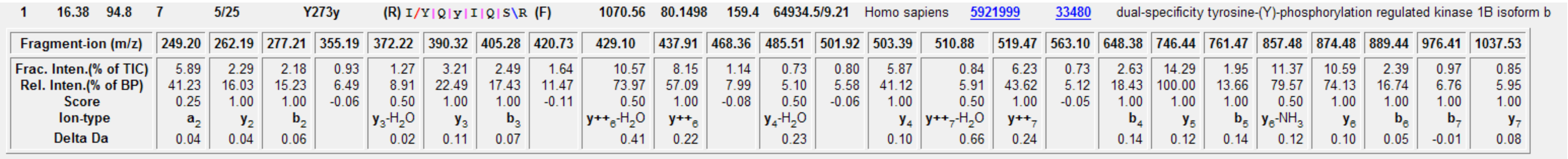
Fragment-ion (m/z)	845.08	945.99	983.42	988.56	1038.95	1048.40	1092.48	1155.02	1172.63	1248.49	1413.68
Frac. Inten.(% of TIC)	2.45	7.86	2.77	2.28	2.31	4.48	2.80	1.84	10.87	2.46	6.39
Rel. Inten.(% of BP)	22.50	72.29	25.49	21.00	21.27	41.24	25.77	16.89	100.00	22.66	58.79
Score	-0.22	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	0.50	1.00
Ion-type		$y{++}_{17}$	$b{++}_{18}$	y_{9}	$b{++}_{19}$-H_2O	$b{++}_{19}$	b_{9}	y_{11}-NH_3	y_{11}	b_{11}-H_2O	b_{12}
Delta Da		0.09	0.01	0.08	0.03	0.47	0.09	-0.52	0.07	0.05	0.16

Peak 28

Ions that verify assignment



assignment



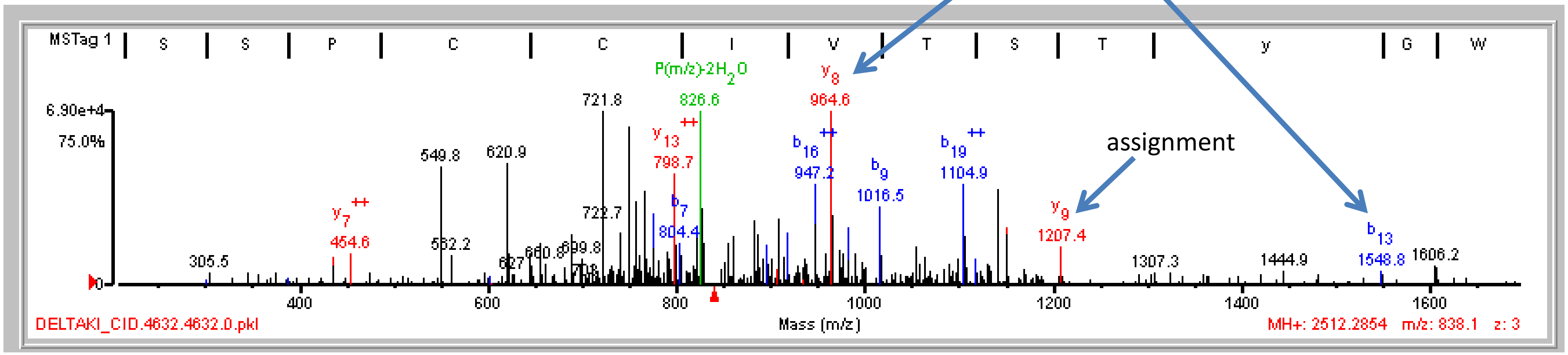
1 16.38 94.8 7 5/25 Y273y (R) I/Y|Q|y|I|Q|S\R (F) 1070.56 80.1498 159.4 64934.5/9.21 Homo sapiens 5921999 33480 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B isoform b

Fragment-ion (m/z)	249.20	262.19	277.21	355.19	372.22	390.32	405.28	420.73	429.10	437.91	468.36	485.51
Frac. Inten.(% of TIC)	5.89	2.29	2.18	0.93	1.27	3.21	2.49	1.64	10.57	8.15	1.14	0.73
Rel. Inten.(% of BP)	41.23	16.03	15.23	6.49	8.91	22.49	17.43	11.47	73.97	57.09	7.99	5.10
Score	0.25	1.00	1.00	-0.06	0.50	1.00	1.00	-0.11	0.50	1.00	-0.08	0.50
Ion-type	a_2	y_2	b_2		y_3-H_2O	y_3	b_3		$y{+}{+}_6$-H_2O	$y{+}{+}_6$		y_4-H_2O
Delta Da	0.04	0.04	0.06		0.02	0.11	0.07		0.41	0.22		0.23

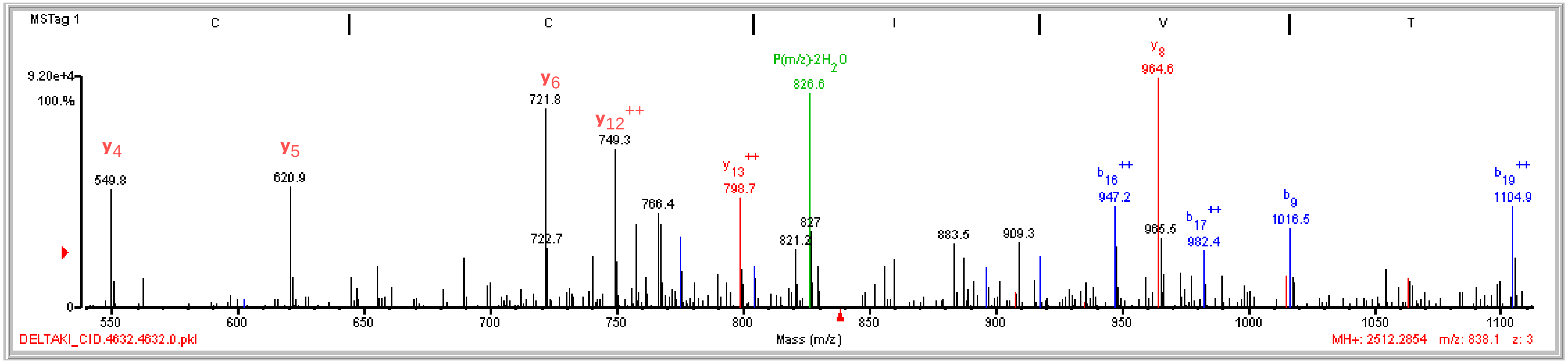
Fragment-ion (m/z)	501.92	503.39	510.88	519.47	563.10	648.38	746.44	761.47	857.48	874.48	889.44	976.41	1037.53
Frac. Inten.(% of TIC)	0.80	5.87	0.84	6.23	0.73	2.63	14.29	1.95	11.37	10.59	2.39	0.97	0.85
Rel. Inten.(% of BP)	5.58	41.12	5.91	43.62	5.12	18.43	100.00	13.66	79.57	74.13	16.74	6.76	5.95
Score	-0.06	1.00	0.50	1.00	-0.05	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type		y_4	$y{+}{+}_7$-H_2O	$y{+}{+}_7$		b_4	y_5	b_5	y_6-NH_3	y_6	b_6	b_7	y_7
Delta Da		0.10	0.66	0.24		0.14	0.12	0.14	0.12	0.10	0.05	-0.01	0.08

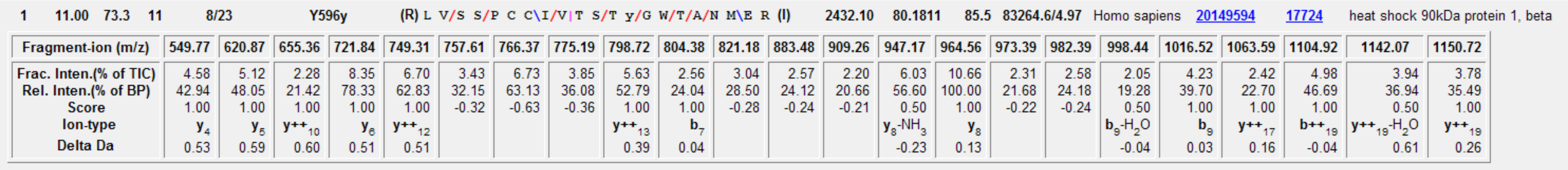
Peak 29

Ions that verify assignment



assignment

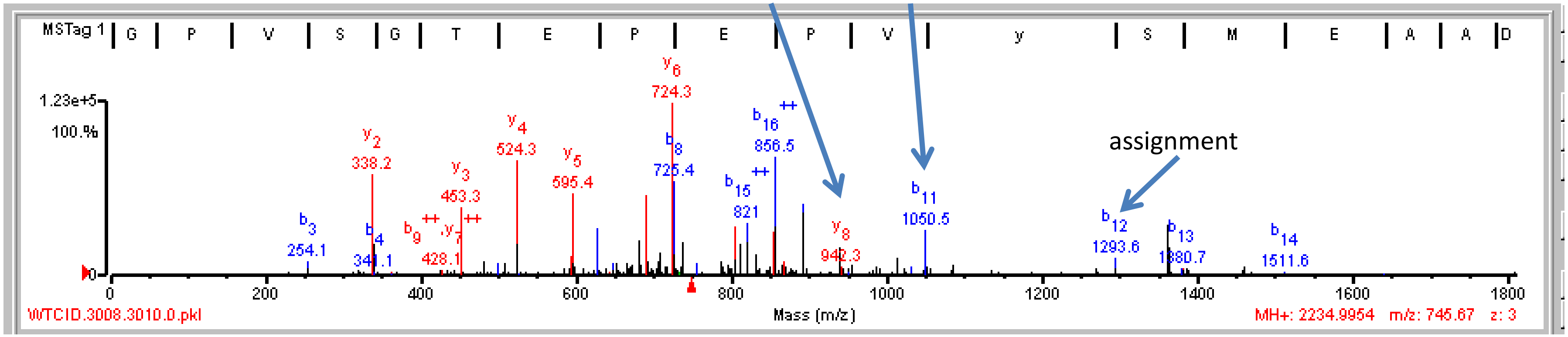




1 11.00 73.3 11 8/23 Y596y (R) L V/S S/P C C\I/V|T S/T y/G W/T/A/N M\E R (I) 2432.10 80.1811 85.5 83264.6/4.97 Homo sapiens 20149594 17724 heat shock 90kDa protein 1, beta

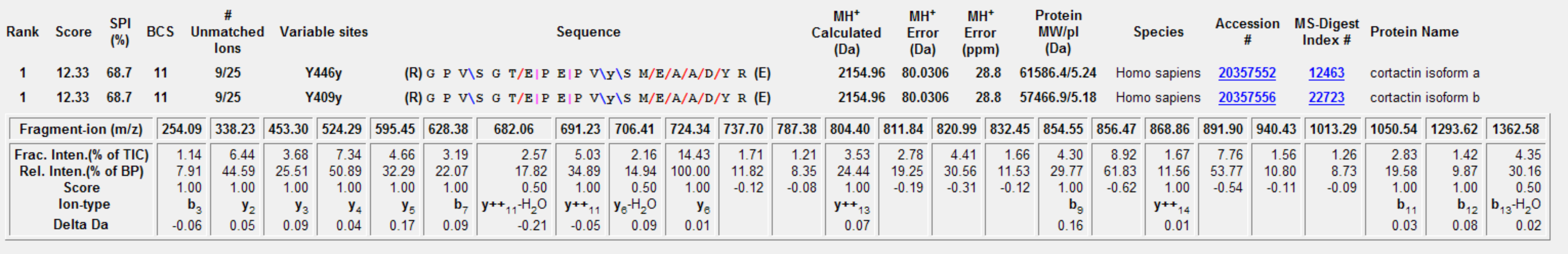
Fragment-ion (m/z)	549.77	620.87	655.36	721.84	749.31	757.61	766.37	775.19	798.72	804.38	821.18	883.48	909.26	947.17	964.56	973.39	982.39	998.44	1016.52	1063.59	1104.92	1142.07	1150.72
Frac. Inten.(% of TIC)	4.58	5.12	2.28	8.35	6.70	3.43	6.73	3.85	5.63	2.56	3.04	2.57	2.20	6.03	10.66	2.31	2.58	2.05	4.23	2.42	4.98	3.94	3.78
Rel. Inten.(% of BP)	42.94	48.05	21.42	78.33	62.83	32.15	63.13	36.08	52.79	24.04	28.50	24.12	20.66	56.60	100.00	21.68	24.18	19.28	39.70	22.70	46.69	36.94	35.49
Score	1.00	1.00	1.00	1.00	1.00	-0.32	-0.63	-0.36	1.00	1.00	-0.28	-0.24	-0.21	0.50	1.00	-0.22	-0.24	0.50	1.00	1.00	1.00	0.50	1.00
Ion-type	y_4	y_5	$y{++}_{10}$	y_6	$y{++}_{12}$				$y{++}_{13}$	b_7				y_8-NH_3	y_8			b_9-H_2O	b_9	$y{++}_{17}$	$b{++}_{19}$	$y{++}_{19}$-H_2O	$y{++}_{19}$
Delta Da	0.53	0.59	0.60	0.51	0.51				0.39	0.04				-0.23	0.13			-0.04	0.03	0.16	-0.04	0.61	0.26

Peak 30



Ions that verify assignment

assignment

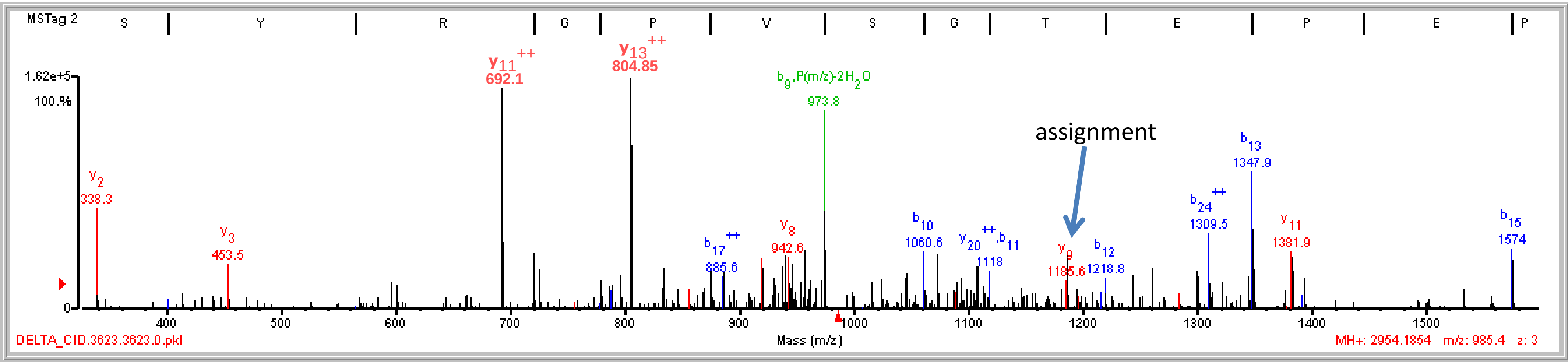


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.33	68.7	11	9/25	Y446y	(R) G P V\S G T/E|P E|P V\y\S M/E/A/A/D/Y R (E)	2154.96	80.0306	28.8	61586.4/5.24	Homo sapiens	20357552	12463	cortactin isoform a
1	12.33	68.7	11	9/25	Y409y	(R) G P V\S G T/E|P E|P V\y\S M/E/A/A/D/Y R (E)	2154.96	80.0306	28.8	57466.9/5.18	Homo sapiens	20357556	22723	cortactin isoform b

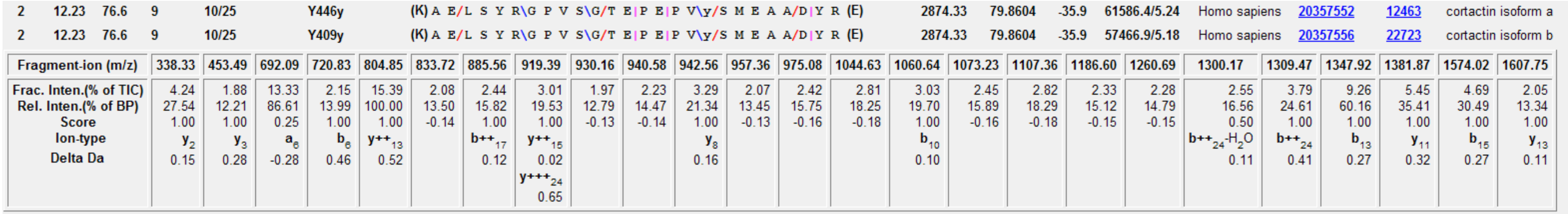
Fragment-ion (m/z)	254.09	338.23	453.30	524.29	595.45	628.38	682.06	691.23	706.41	724.34	737.70	787.38
Frac. Inten.(% of TIC)	1.14	6.44	3.68	7.34	4.66	3.19	2.57	5.03	2.16	14.43	1.71	1.21
Rel. Inten.(% of BP)	7.91	44.59	25.51	50.89	32.29	22.07	17.82	34.89	14.94	100.00	11.82	8.35
Score	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	0.50	1.00	-0.12	-0.08
Ion-type	b_3	y_2	y_3	y_4	y_5	b_7	$y{++}_{11}$-H_2O	$y{++}_{11}$	y_6-H_2O	y_6		
Delta Da	-0.06	0.05	0.09	0.04	0.17	0.09	-0.21	-0.05	0.09	0.01		

Fragment-ion (m/z)	804.40	811.84	820.99	832.45	854.55	856.47	868.86	891.90	940.43	1013.29	1050.54	1293.62	1362.58
Frac. Inten.(% of TIC)	3.53	2.78	4.41	1.66	4.30	8.92	1.67	7.76	1.56	1.26	2.83	1.42	4.35
Rel. Inten.(% of BP)	24.44	19.25	30.56	11.53	29.77	61.83	11.56	53.77	10.80	8.73	19.58	9.87	30.16
Score	1.00	-0.19	-0.31	-0.12	1.00	-0.62	1.00	-0.54	-0.11	-0.09	1.00	1.00	0.50
Ion-type	$y{++}_{13}$				b_9		$y{++}_{14}$				b_{11}	b_{12}	b_{13}-H_2O
Delta Da	0.07				0.16		0.01				0.03	0.08	0.02

Peak 31



assignment

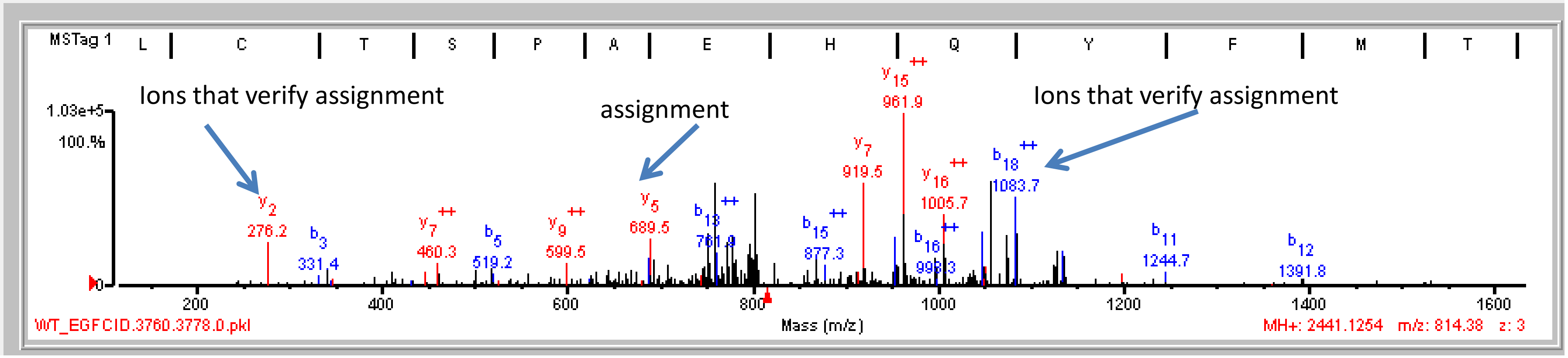


2	12.23	76.6	9	10/25	Y446y	(K) A E/L S Y R\G P V S\G/T E|P E|P V\y/S M E A A/D|Y R (E)	2874.33	79.8604	-35.9	61586.4/5.24	Homo sapiens	20357552	12463	cortactin isoform a
2	12.23	76.6	9	10/25	Y409y	(K) A E/L S Y R\G P V S\G/T E|P E|P V\y/S M E A A/D|Y R (E)	2874.33	79.8604	-35.9	57466.9/5.18	Homo sapiens	20357556	22723	cortactin isoform b

Fragment-ion (m/z)	338.33	453.49	692.09	720.83	804.85	833.72	885.56	919.39	930.16	940.58	942.56	957.36	975.08
Frac. Inten.(% of TIC)	4.24	1.88	13.33	2.15	15.39	2.08	2.44	3.01	1.97	2.23	3.29	2.07	2.42
Rel. Inten.(% of BP)	27.54	12.21	86.61	13.99	100.00	13.50	15.82	19.53	12.79	14.47	21.34	13.45	15.75
Score	1.00	1.00	0.25	1.00	1.00	-0.14	1.00	1.00	-0.13	-0.14	1.00	-0.13	-0.16
Ion-type	y_2	y_3	a_6	b_6	y++$_{13}$		b++$_{17}$	y++$_{15}$ y+++$_{24}$			y_8		
Delta Da	0.15	0.28	-0.28	0.46	0.52		0.12	0.02 0.65			0.16		

Fragment-ion (m/z)	1044.63	1060.64	1073.23	1107.36	1186.60	1260.69	1300.17	1309.47	1347.92	1381.87	1574.02	1607.75
Frac. Inten.(% of TIC)	2.81	3.03	2.45	2.82	2.33	2.28	2.55	3.79	9.26	5.45	4.69	2.05
Rel. Inten.(% of BP)	18.25	19.70	15.89	18.29	15.12	14.79	16.56	24.61	60.16	35.41	30.49	13.34
Score	-0.18	1.00	-0.16	-0.18	-0.15	-0.15	0.50	1.00	1.00	1.00	1.00	1.00
Ion-type		b_{10}					b++$_{24}$-H_2O	b++$_{24}$	b_{13}	y_{11}	b_{15}	y_{13}
Delta Da		0.10					0.11	0.41	0.27	0.32	0.27	0.11

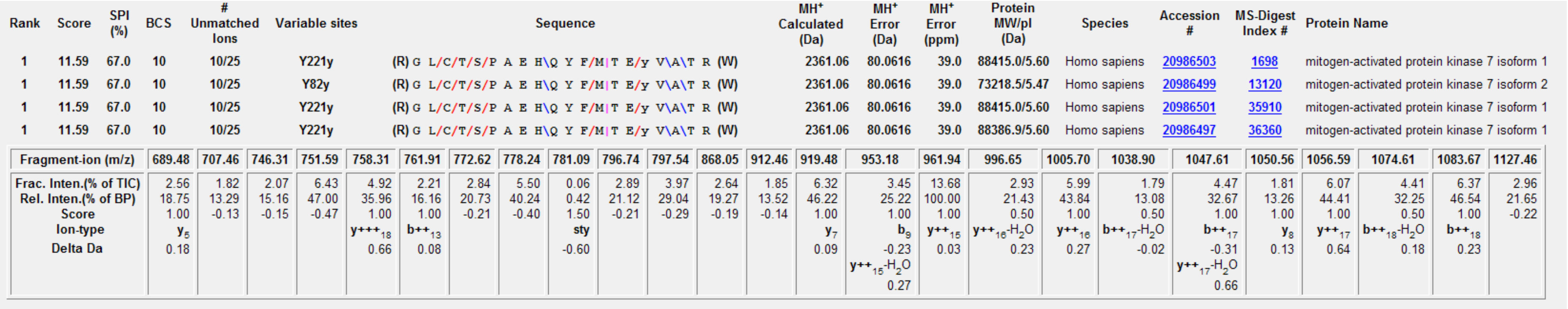
Peak 32



Ions that verify assignment

assignment

Ions that verify assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.59	67.0	10	10/25	Y221y	(R) G L/C/T/S/P A E H\Q Y F/M|T E/y V\A\T R (W)	2361.06	80.0616	39.0	88415.0/5.60	Homo sapiens	20986503	1698	mitogen-activated protein kinase 7 isoform 1
1	11.59	67.0	10	10/25	Y82y	(R) G L/C/T/S/P A E H\Q Y F/M|T E/y V\A\T R (W)	2361.06	80.0616	39.0	73218.5/5.47	Homo sapiens	20986499	13120	mitogen-activated protein kinase 7 isoform 2
1	11.59	67.0	10	10/25	Y221y	(R) G L/C/T/S/P A E H\Q Y F/M|T E/y V\A\T R (W)	2361.06	80.0616	39.0	88415.0/5.60	Homo sapiens	20986501	35910	mitogen-activated protein kinase 7 isoform 1
1	11.59	67.0	10	10/25	Y221y	(R) G L/C/T/S/P A E H\Q Y F/M|T E/y V\A\T R (W)	2361.06	80.0616	39.0	88386.9/5.60	Homo sapiens	20986497	36360	mitogen-activated protein kinase 7 isoform 1

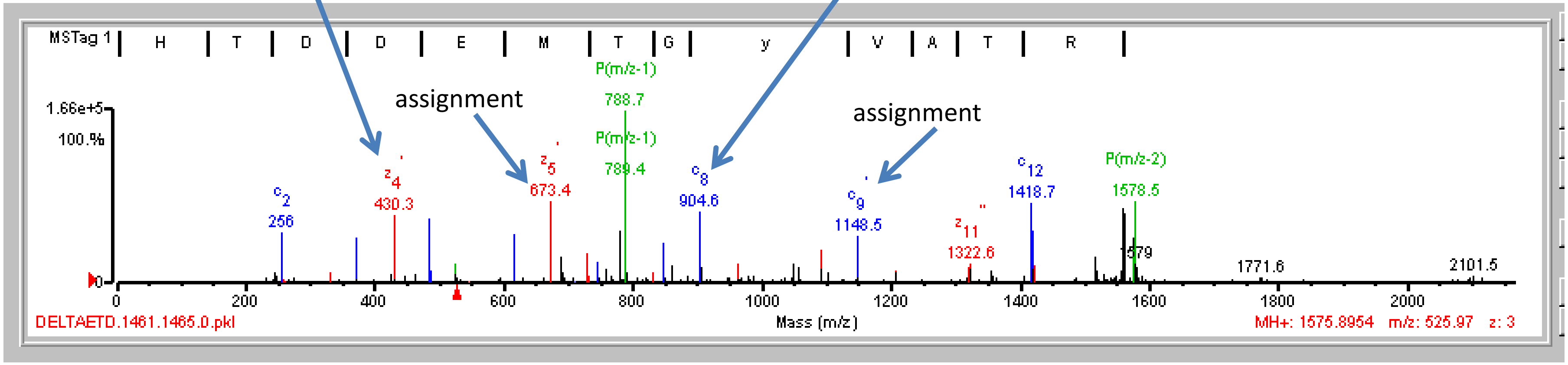
Fragment-ion (m/z)	689.48	707.46	746.31	751.59	758.31	761.91	772.62	778.24	781.09	796.74	797.54	868.05	912.46	919.48
Frac. Inten.(% of TIC)	2.56	1.82	2.07	6.43	4.92	2.21	2.84	5.50	0.06	2.89	3.97	2.64	1.85	6.32
Rel. Inten.(% of BP)	18.75	13.29	15.16	47.00	35.96	16.16	20.73	40.24	0.42	21.12	29.04	19.27	13.52	46.22
Score	1.00	-0.13	-0.15	-0.47	1.00	1.00	-0.21	-0.40	1.50	-0.21	-0.29	-0.19	-0.14	1.00
Ion-type	y_5				y+++$_{18}$	b++$_{13}$			sty					y_7
Delta Da	0.18				0.66	0.08			-0.60					0.09

Fragment-ion (m/z)	953.18	961.94	996.65	1005.70	1038.90	1047.61	1050.56	1056.59	1074.61	1083.67	1127.46
Frac. Inten.(% of TIC)	3.45	13.68	2.93	5.99	1.79	4.47	1.81	6.07	4.41	6.37	2.96
Rel. Inten.(% of BP)	25.22	100.00	21.43	43.84	13.08	32.67	13.26	44.41	32.25	46.54	21.65
Score	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00	0.50	1.00	-0.22
Ion-type	b_9 y++$_{15}$-H_2O	y++$_{15}$	y++$_{16}$-H_2O	y++$_{16}$	b++$_{17}$-H_2O	b++$_{17}$ y++$_{17}$-H_2O	y_8	y++$_{17}$	b++$_{18}$-H_2O	b++$_{18}$	
Delta Da	-0.23 0.27	0.03	0.23	0.27	-0.02	-0.31 0.66	0.13	0.64	0.18	0.23	

Peak 33

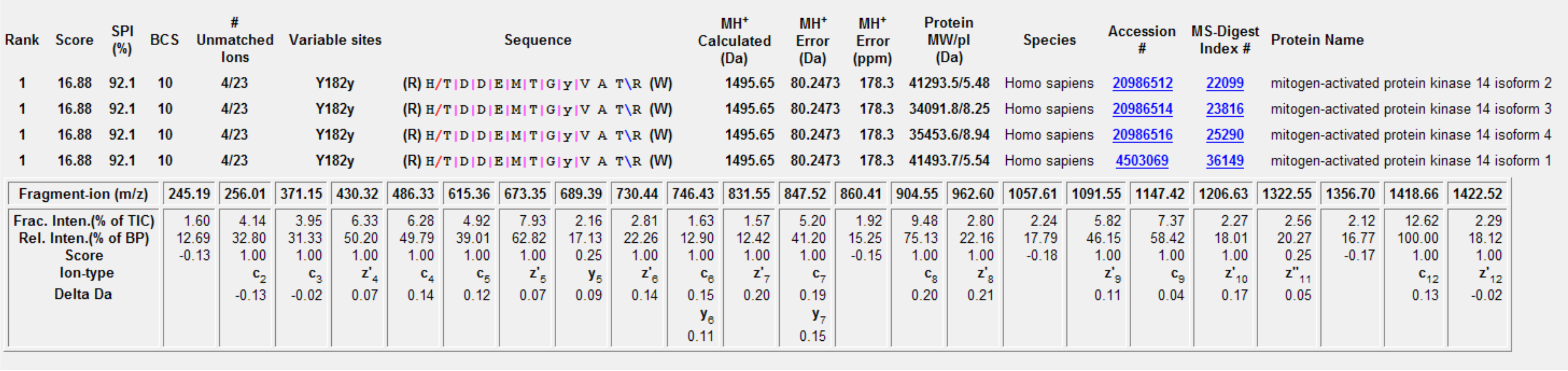
Ions that verify assignment

Ions that verify assignment



assignment

assignment



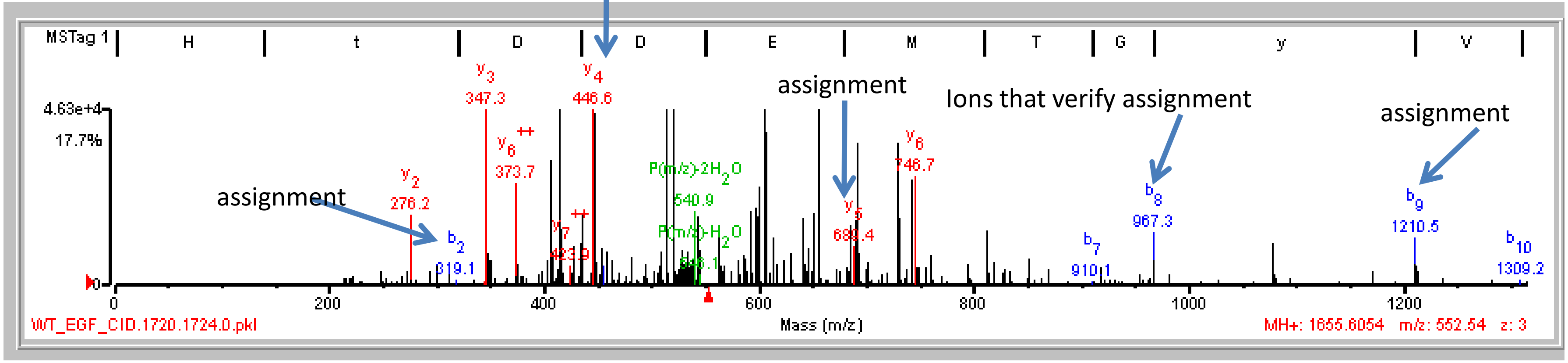
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.88	92.1	10	4/23	Y182y	(R) H/T|D|D|E|M|T|G|y|V A T\R (W)	1495.65	80.2473	178.3	41293.5/5.48	Homo sapiens	20986512	22099	mitogen-activated protein kinase 14 isoform 2
1	16.88	92.1	10	4/23	Y182y	(R) H/T|D|D|E|M|T|G|y|V A T\R (W)	1495.65	80.2473	178.3	34091.8/8.25	Homo sapiens	20986514	23816	mitogen-activated protein kinase 14 isoform 3
1	16.88	92.1	10	4/23	Y182y	(R) H/T|D|D|E|M|T|G|y|V A T\R (W)	1495.65	80.2473	178.3	35453.6/8.94	Homo sapiens	20986516	25290	mitogen-activated protein kinase 14 isoform 4
1	16.88	92.1	10	4/23	Y182y	(R) H/T|D|D|E|M|T|G|y|V A T\R (W)	1495.65	80.2473	178.3	41493.7/5.54	Homo sapiens	4503069	36149	mitogen-activated protein kinase 14 isoform 1

Fragment-ion (m/z)	245.19	256.01	371.15	430.32	486.33	615.36	673.35	689.39	730.44	746.43	831.55	847.52
Frac. Inten.(% of TIC)	1.60	4.14	3.95	6.33	6.28	4.92	7.93	2.16	2.81	1.63	1.57	5.20
Rel. Inten.(% of BP)	12.69	32.80	31.33	50.20	49.79	39.01	62.82	17.13	22.26	12.90	12.42	41.20
Score	-0.13	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00
Ion-type		c_2	c_3	z'_4	c_4	c_5	z'_5	y_5	z'_6	c_6 y_6	z'_7	c_7 y_7
Delta Da		-0.13	-0.02	0.07	0.14	0.12	0.07	0.09	0.14	0.15 0.11	0.20	0.19 0.15

Fragment-ion (m/z)	860.41	904.55	962.60	1057.61	1091.55	1147.42	1206.63	1322.55	1356.70	1418.66	1422.52
Frac. Inten.(% of TIC)	1.92	9.48	2.80	2.24	5.82	7.37	2.27	2.56	2.12	12.62	2.29
Rel. Inten.(% of BP)	15.25	75.13	22.16	17.79	46.15	58.42	18.01	20.27	16.77	100.00	18.12
Score	-0.15	1.00	1.00	-0.18	1.00	1.00	1.00	0.25	-0.17	1.00	1.00
Ion-type		c_8	z'_8		z'_9	c_9	z'_{10}	z''_{11}		c_{12}	z'_{12}
Delta Da		0.20	0.21		0.11	0.04	0.17	0.05		0.13	-0.02

Peak 34

Ions that verify assignment

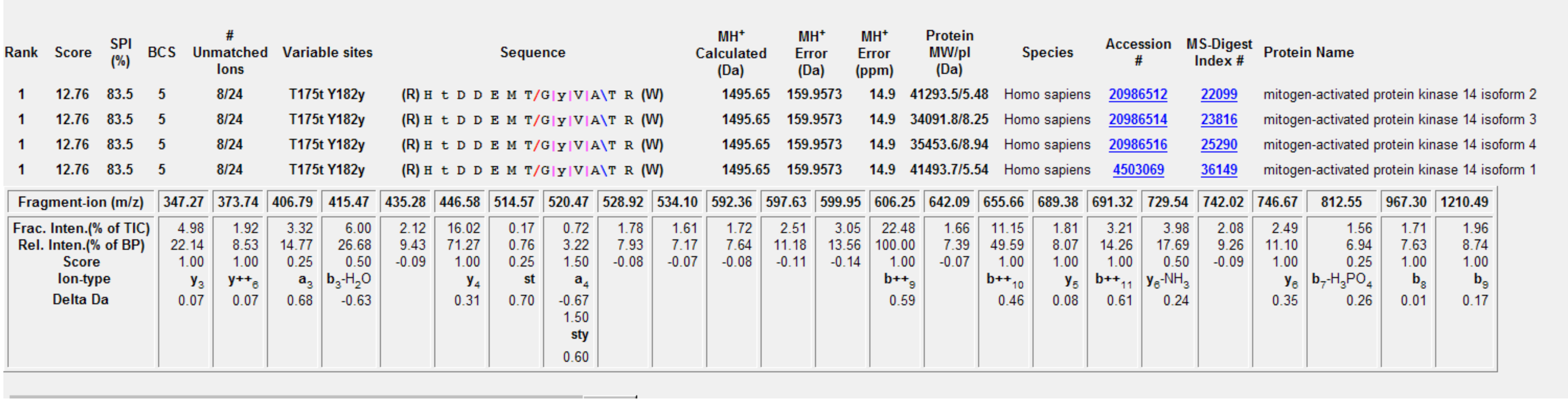


assignment

assignment

Ions that verify assignment

assignment



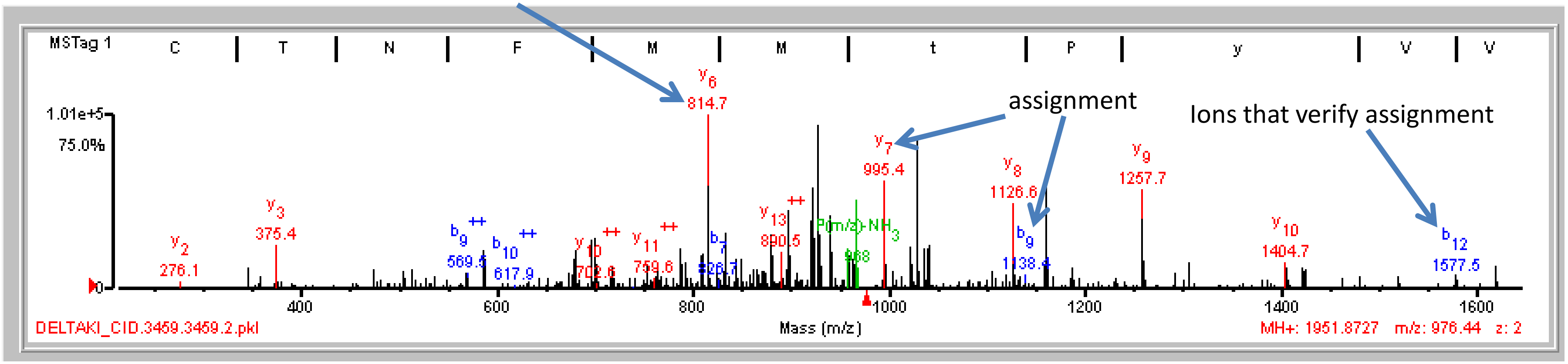
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.76	83.5	5	8/24	T175t Y182y	(R) H t D D E M T/G|y|V|A\T R (W)	1495.65	159.9573	14.9	41293.5/5.48	Homo sapiens	20986512	22099	mitogen-activated protein kinase 14 isoform 2
1	12.76	83.5	5	8/24	T175t Y182y	(R) H t D D E M T/G|y|V|A\T R (W)	1495.65	159.9573	14.9	34091.8/8.25	Homo sapiens	20986514	23816	mitogen-activated protein kinase 14 isoform 3
1	12.76	83.5	5	8/24	T175t Y182y	(R) H t D D E M T/G|y|V|A\T R (W)	1495.65	159.9573	14.9	35453.6/8.94	Homo sapiens	20986516	25290	mitogen-activated protein kinase 14 isoform 4
1	12.76	83.5	5	8/24	T175t Y182y	(R) H t D D E M T/G|y|V|A\T R (W)	1495.65	159.9573	14.9	41493.7/5.54	Homo sapiens	4503069	36149	mitogen-activated protein kinase 14 isoform 1

Fragment-ion (m/z)	347.27	373.74	406.79	415.47	435.28	446.58	514.57	520.47	528.92	534.10	592.36	597.63
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	4.98 22.14 1.00 y_3 0.07	1.92 8.53 1.00 $y{+}{+}_6$ 0.07	3.32 14.77 0.25 a_3 0.68	6.00 26.68 0.50 b_3-H_2O -0.63	2.12 9.43 -0.09	16.02 71.27 1.00 y_4 0.31	0.17 0.76 0.25 st 0.70	0.72 3.22 1.50 a_4 -0.67 1.50 sty 0.60	1.78 7.93 -0.08	1.61 7.17 -0.07	1.72 7.64 -0.08	2.51 11.18 -0.11

Fragment-ion (m/z)	599.95	606.25	642.09	655.66	689.38	691.32	729.54	742.02	746.67	812.55	967.30	1210.49
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	3.05 13.56 -0.14	22.48 100.00 1.00 $b{+}{+}_9$ 0.59	1.66 7.39 -0.07	11.15 49.59 1.00 $b{+}{+}_{10}$ 0.46	1.81 8.07 1.00 y_5 0.08	3.21 14.26 1.00 $b{+}{+}_{11}$ 0.61	3.98 17.69 0.50 y_6-NH_3 0.24	2.08 9.26 -0.09	2.49 11.10 1.00 y_6 0.35	1.56 6.94 0.25 b_7-H_3PO_4 0.26	1.71 7.63 1.00 b_8 0.01	1.96 8.74 1.00 b_9 0.17

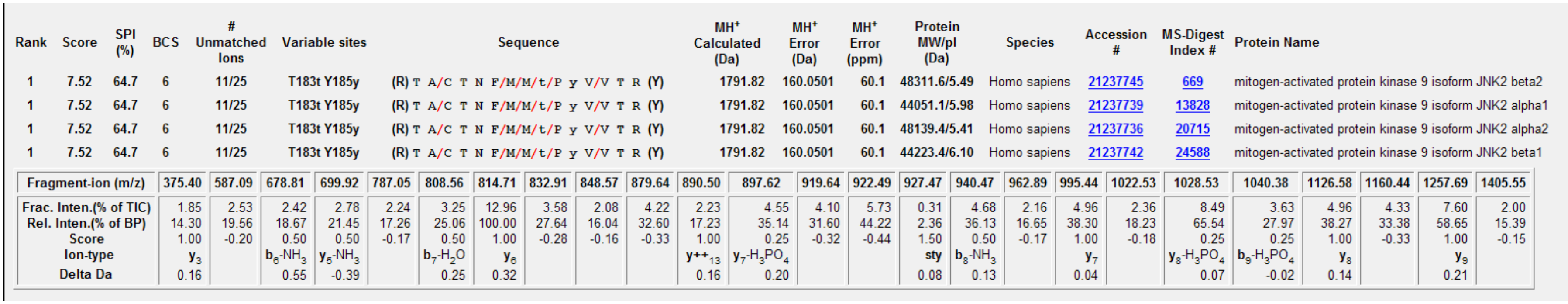
Peak 35

Ions that verify assignment



assignment

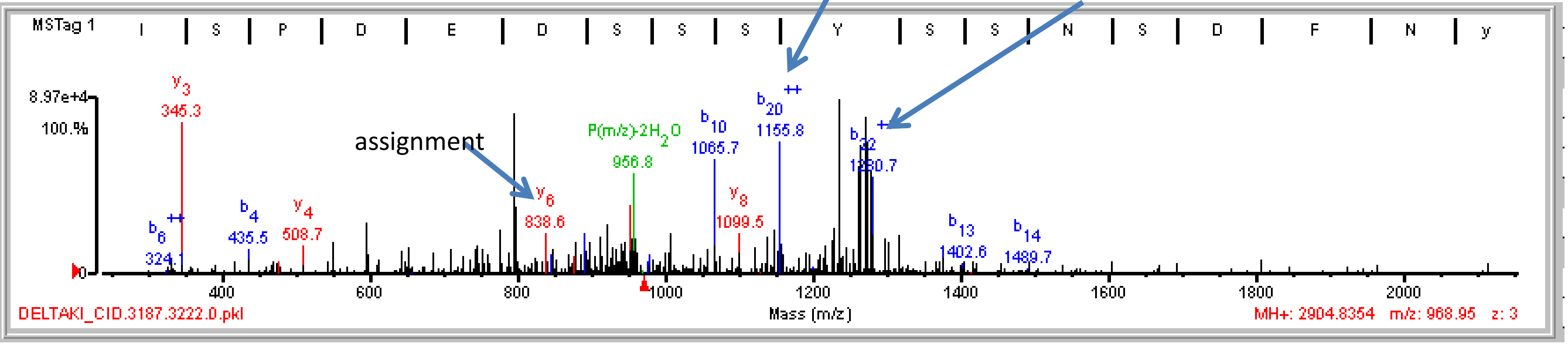
Ions that verify assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.52	64.7	6	11/25	T183t Y185y	(R) T A/C T N F/M/M/t/P y V/V T R (Y)	1791.82	160.0501	60.1	48311.6/5.49	Homo sapiens	21237745	669	mitogen-activated protein kinase 9 isoform JNK2 beta2
1	7.52	64.7	6	11/25	T183t Y185y	(R) T A/C T N F/M/M/t/P y V/V T R (Y)	1791.82	160.0501	60.1	44051.1/5.98	Homo sapiens	21237739	13828	mitogen-activated protein kinase 9 isoform JNK2 alpha1
1	7.52	64.7	6	11/25	T183t Y185y	(R) T A/C T N F/M/M/t/P y V/V T R (Y)	1791.82	160.0501	60.1	48139.4/5.41	Homo sapiens	21237736	20715	mitogen-activated protein kinase 9 isoform JNK2 alpha2
1	7.52	64.7	6	11/25	T183t Y185y	(R) T A/C T N F/M/M/t/P y V/V T R (Y)	1791.82	160.0501	60.1	44223.4/6.10	Homo sapiens	21237742	24588	mitogen-activated protein kinase 9 isoform JNK2 beta1

Fragment-ion (m/z)	375.40	587.09	678.81	699.92	787.05	808.56	814.71	832.91	848.57	879.64	890.50	897.62	919.64	922.49	927.47	940.47	962.89	995.44	1022.53	1028.53	1040.38	1126.58	1160.44	1257.69	1405.55
Frac. Inten.(% of TIC)	1.85	2.53	2.42	2.78	2.24	3.25	12.96	3.58	2.08	4.22	2.23	4.55	4.10	5.73	0.31	4.68	2.16	4.96	2.36	8.49	3.63	4.96	4.33	7.60	2.00
Rel. Inten.(% of BP)	14.30	19.56	18.67	21.45	17.26	25.06	100.00	27.64	16.04	32.60	17.23	35.14	31.60	44.22	2.36	36.13	16.65	38.30	18.23	65.54	27.97	38.27	33.38	58.65	15.39
Score	1.00	-0.20	0.50	0.50	-0.17	0.50	1.00	-0.28	-0.16	-0.33	1.00	0.25	-0.32	-0.44	1.50	0.50	-0.17	1.00	-0.18	0.25	0.25	1.00	-0.33	1.00	-0.15
Ion-type	y_3		b_6-NH_3	y_5-NH_3		b_7-H_2O	y_6				$y{+}{+}_{13}$	y_7-H_3PO_4			sty	b_8-NH_3		y_7		y_8-H_3PO_4	b_9-H_3PO_4	y_8		y_9	
Delta Da	0.16		0.55	-0.39		0.25	0.32				0.16	0.20			0.08	0.13		0.04		0.07	-0.02	0.14		0.21	

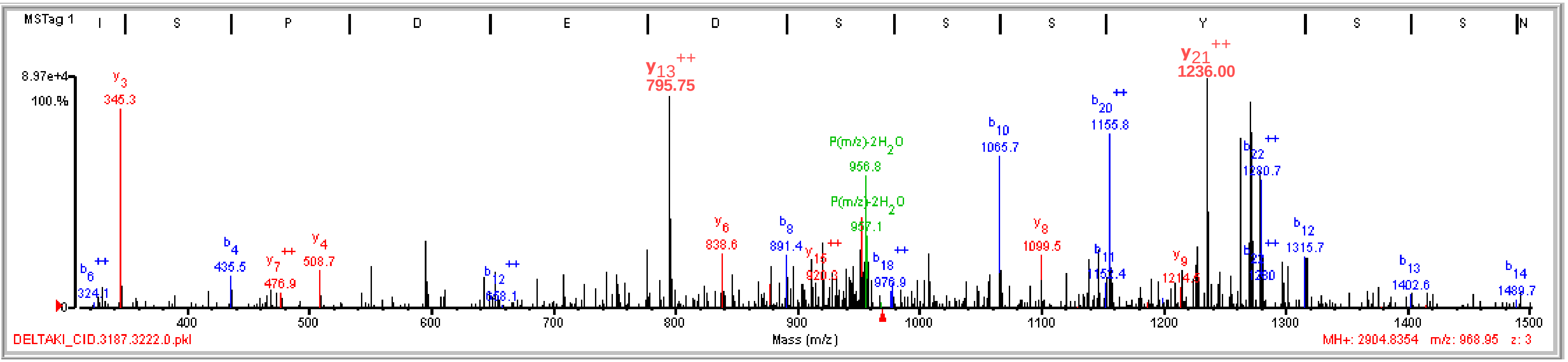
Peak 36

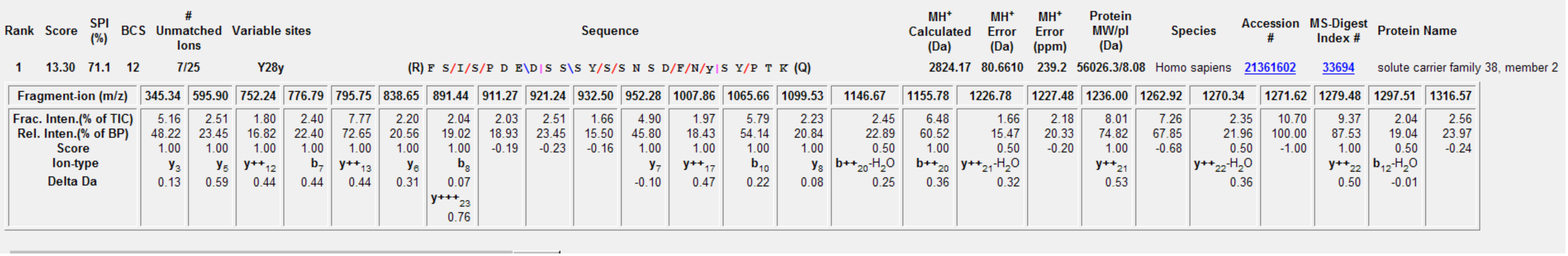


assignment

assignment

Ions that verify assignment

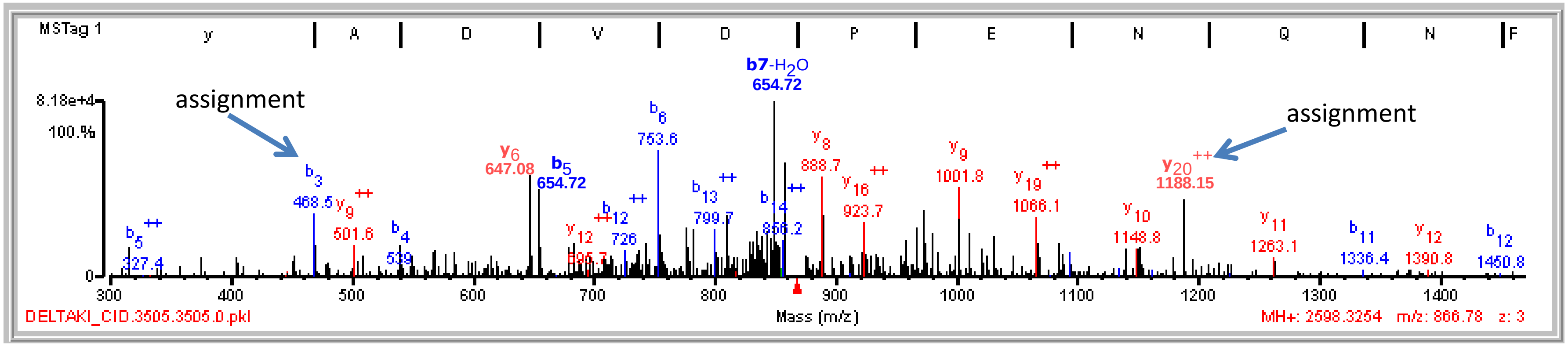


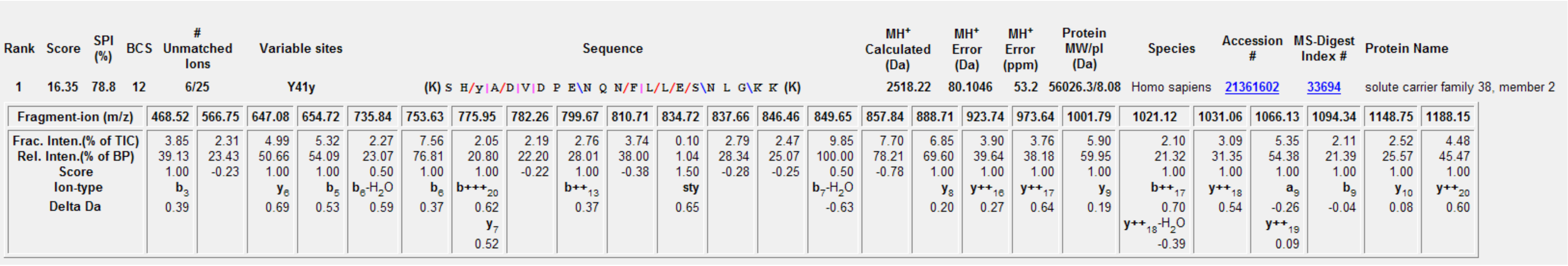


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.30	71.1	12	7/25	Y28y	(R) F S/I/S/P D E\D|S S\S Y/S/S N S D/F/N/y|S Y/P T K (Q)	2824.17	80.6610	239.2	56026.3/8.08	Homo sapiens	21361602	33694	solute carrier family 38, member 2

Fragment-ion (m/z)	345.34	595.90	752.24	776.79	795.75	838.65	891.44	911.27	921.24	932.50	952.28	1007.86	1065.66	1099.53	1146.67	1155.78	1226.78	1227.48	1236.00	1262.92	1270.34	1271.62	1279.48	1297.51	1316.57
Frac. Inten.(% of TIC)	5.16	2.51	1.80	2.40	7.77	2.20	2.04	2.03	2.51	1.66	4.90	1.97	5.79	2.23	2.45	6.48	1.66	2.18	8.01	7.26	2.35	10.70	9.37	2.04	2.56
Rel. Inten.(% of BP)	48.22	23.45	16.82	22.40	72.65	20.56	19.02	18.93	23.45	15.50	45.80	18.43	54.14	20.84	22.89	60.52	15.47	20.33	74.82	67.85	21.96	100.00	87.53	19.04	23.97
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.19	-0.23	-0.16	1.00	1.00	1.00	1.00	0.50	1.00	0.50	-0.20	1.00	-0.68	0.50	-1.00	1.00	0.50	-0.24
Ion-type	y_3	y_5	y^{++}_{12}	b_7	y^{++}_{13}	y_6	b_8 y^{+++}_{23}				y_7	y^{++}_{17}	b_{10}	y_8	b^{++}_{20}-H_2O	b^{++}_{20}	y^{++}_{21}-H_2O		y^{++}_{21}		y^{++}_{22}-H_2O		y^{++}_{22}	b_{12}-H_2O	
Delta Da	0.13	0.59	0.44	0.44	0.44	0.31	0.07 0.76				-0.10	0.47	0.22	0.08	0.25	0.36	0.32		0.53		0.36		0.50	-0.01	

Peak 37



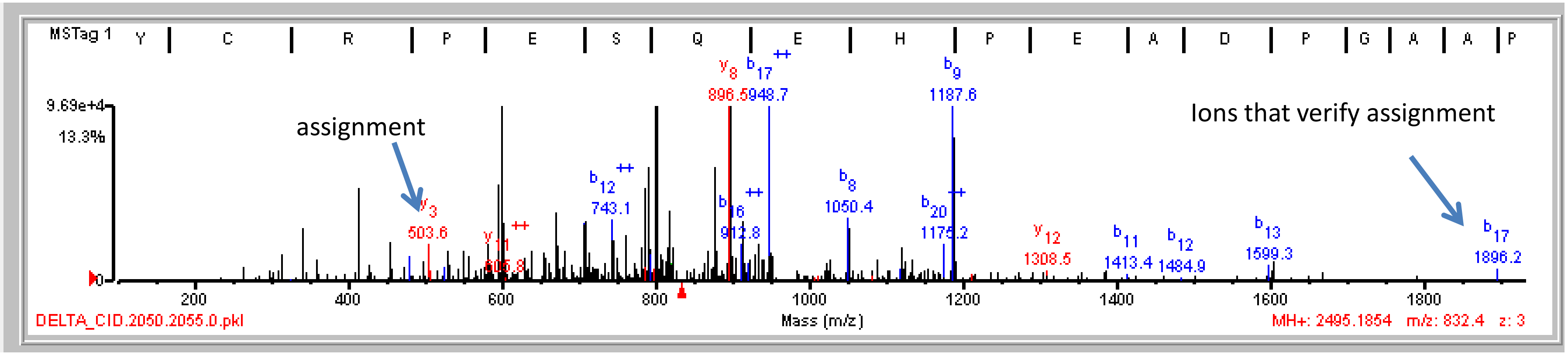


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.35	78.8	12	6/25	Y41y	(K) S H/y|A/D|V|D P E\N Q N/F|L/L/E/S\N L G\K K (K)	2518.22	80.1046	53.2	56026.3/8.08	Homo sapiens	21361602	33694	solute carrier family 38, member 2

Fragment-ion (m/z)	468.52	566.75	647.08	654.72	735.84	753.63	775.95	782.26	799.67	810.71	834.72	837.66	846.46
Frac. Inten.(% of TIC)	3.85	2.31	4.99	5.32	2.27	7.56	2.05	2.19	2.76	3.74	0.10	2.79	2.47
Rel. Inten.(% of BP)	39.13	23.43	50.66	54.09	23.07	76.81	20.80	22.20	28.01	38.00	1.04	28.34	25.07
Score	1.00	-0.23	1.00	1.00	0.50	1.00	1.00	-0.22	1.00	-0.38	1.50	-0.28	-0.25
Ion-type	b_3		y_6	b_5	b_6-H_2O	b_6	$b{+++}_{20}$ y_7		$b{++}_{13}$		sty		
Delta Da	0.39		0.69	0.53	0.59	0.37	0.62 0.52		0.37		0.65		

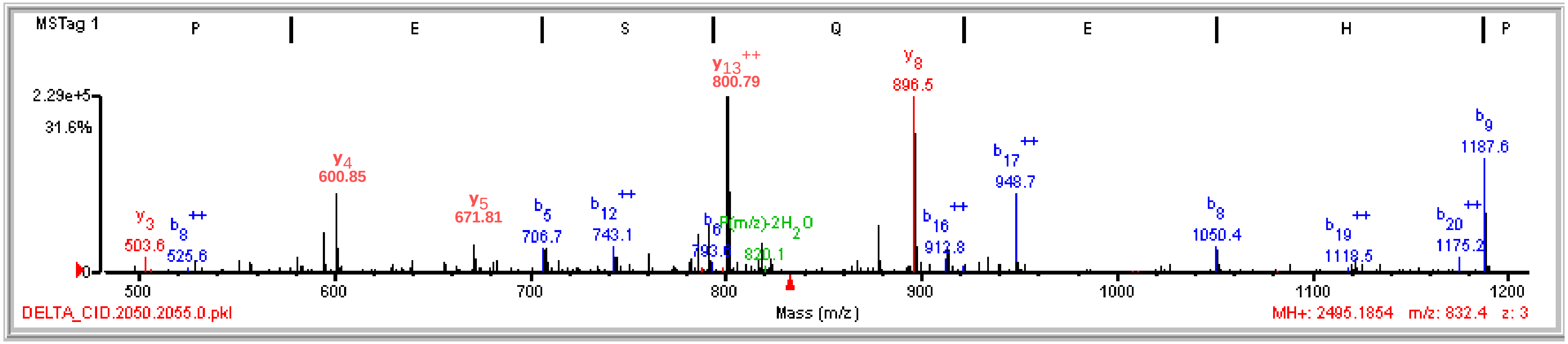
Fragment-ion (m/z)	849.65	857.84	888.71	923.74	973.64	1001.79	1021.12	1031.06	1066.13	1094.34	1148.75	1188.15
Frac. Inten.(% of TIC)	9.85	7.70	6.85	3.90	3.76	5.90	2.10	3.09	5.35	2.11	2.52	4.48
Rel. Inten.(% of BP)	100.00	78.21	69.60	39.64	38.18	59.95	21.32	31.35	54.38	21.39	25.57	45.47
Score	0.50	-0.78	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b_7-H_2O		y_8	$y{++}_{16}$	$y{++}_{17}$	y_9	$b{++}_{17}$ $y{++}_{18}$-H_2O	$y{++}_{18}$	a_9 $y{++}_{19}$	b_9	y_{10}	$y{++}_{20}$
Delta Da	-0.63		0.20	0.27	0.64	0.19	0.70 -0.39	0.54	-0.26 0.09	-0.04	0.08	0.60

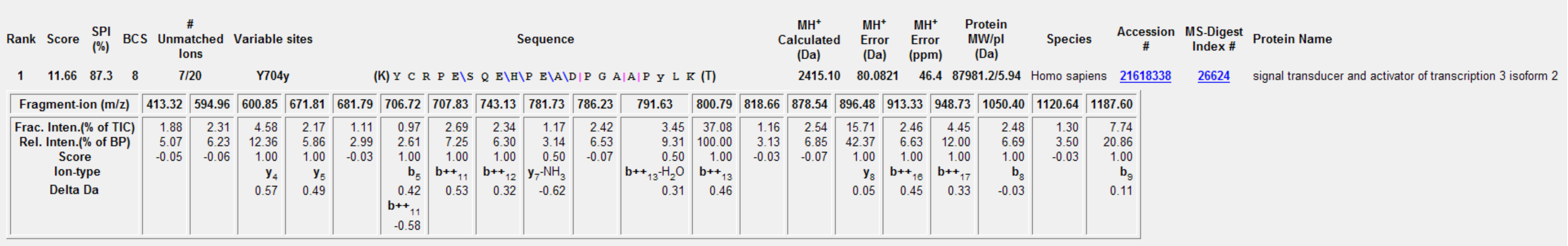
Peak 38



assignment

Ions that verify assignment



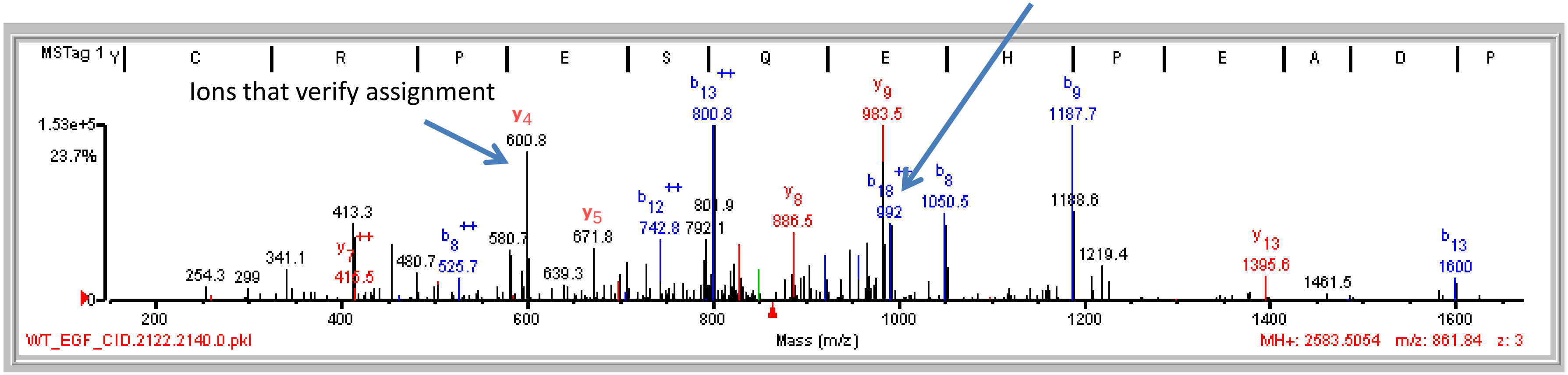


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.66	87.3	8	7/20	Y704y	(K) Y C R P E\S Q E\H\P E\A\D|P G A|A|P y L K (T)	2415.10	80.0821	46.4	87981.2/5.94	Homo sapiens	21618338	26624	signal transducer and activator of transcription 3 isoform 2

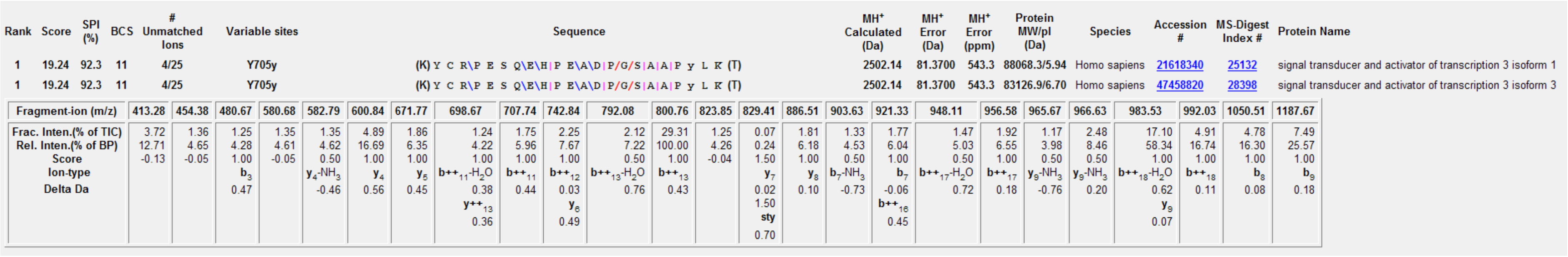
Fragment-ion (m/z)	413.32	594.96	600.85	671.81	681.79	706.72	707.83	743.13	781.73	786.23	791.63	800.79	818.66	878.54	896.48	913.33	948.73	1050.40	1120.64	1187.60
Frac. Inten.(% of TIC)	1.88	2.31	4.58	2.17	1.11	0.97	2.69	2.34	1.17	2.42	3.45	37.08	1.16	2.54	15.71	2.46	4.45	2.48	1.30	7.74
Rel. Inten.(% of BP)	5.07	6.23	12.36	5.86	2.99	2.61	7.25	6.30	3.14	6.53	9.31	100.00	3.13	6.85	42.37	6.63	12.00	6.69	3.50	20.86
Score	-0.05	-0.06	1.00	1.00	-0.03	1.00	1.00	1.00	0.50	-0.07	0.50	1.00	-0.03	-0.07	1.00	1.00	1.00	1.00	-0.03	1.00
Ion-type			y_4	y_5		b_5 $b{+}{+}_{11}$	$b{+}{+}_{11}$	$b{+}{+}_{12}$	y_7-NH_3		$b{+}{+}_{13}$-H_2O	$b{+}{+}_{13}$			y_8	$b{+}{+}_{16}$	$b{+}{+}_{17}$	b_8		b_9
Delta Da			0.57	0.49		0.42 -0.58	0.53	0.32	-0.62		0.31	0.46			0.05	0.45	0.33	-0.03		0.11

Peak 39

Ions that verify assignment



Ions that verify assignment

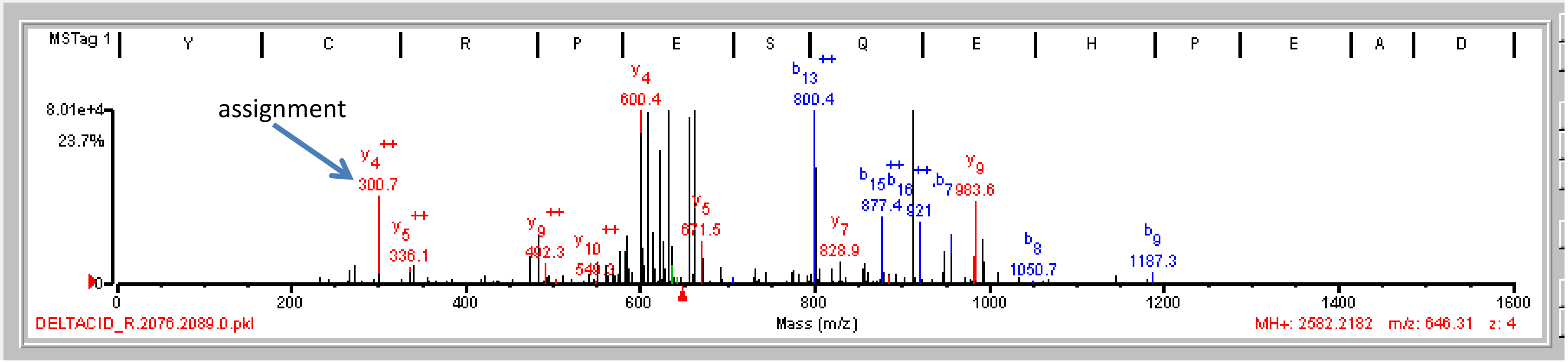


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.24	92.3	11	4/25	Y705y	(K) Y C R\P E S Q\E\H|P E\A\D|P/G/S|A|A|P y L K (T)	2502.14	81.3700	543.3	88068.3/5.94	Homo sapiens	21618340	25132	signal transducer and activator of transcription 3 isoform 1
1	19.24	92.3	11	4/25	Y705y	(K) Y C R\P E S Q\E\H|P E\A\D|P/G/S|A|A|P y L K (T)	2502.14	81.3700	543.3	83126.9/6.70	Homo sapiens	47458820	28398	signal transducer and activator of transcription 3 isoform 3

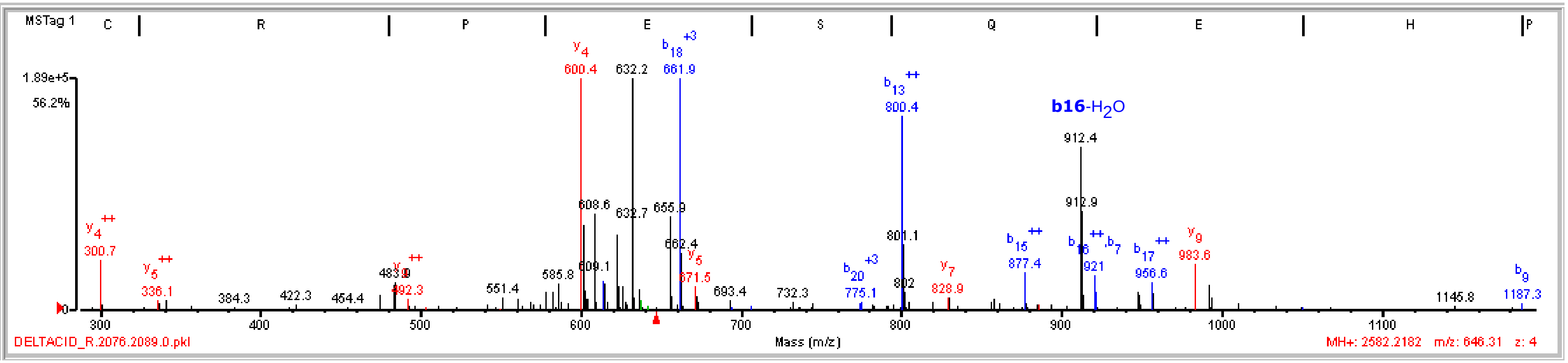
Fragment-ion (m/z)	413.28	454.38	480.67	580.68	582.79	600.84	671.77	698.67	707.74	742.84	792.08	800.76	823.85
Frac. Inten.(% of TIC)	3.72	1.36	1.25	1.35	1.35	4.89	1.86	1.24	1.75	2.25	2.12	29.31	1.25
Rel. Inten.(% of BP)	12.71	4.65	4.28	4.61	4.62	16.69	6.35	4.22	5.96	7.67	7.22	100.00	4.26
Score	-0.13	-0.05	1.00	-0.05	0.50	1.00	1.00	1.00	1.00	1.00	0.50	1.00	-0.04
Ion-type			b_3		y_4-NH_3	y_4	y_5	$b{+}{+}_{11}$-H_2O $y{+}{+}_{13}$	$b{+}{+}_{11}$	$b{+}{+}_{12}$ y_6	$b{+}{+}_{13}$-H_2O	$b{+}{+}_{13}$	
Delta Da			0.47		-0.46	0.56	0.45	0.38 0.36	0.44	0.03 0.49	0.76	0.43	

Fragment-ion (m/z)	829.41	886.51	903.63	921.33	948.11	956.58	965.67	966.63	983.53	992.03	1050.51	1187.67
Frac. Inten.(% of TIC)	0.07	1.81	1.33	1.77	1.47	1.92	1.17	2.48	17.10	4.91	4.78	7.49
Rel. Inten.(% of BP)	0.24	6.18	4.53	6.04	5.03	6.55	3.98	8.46	58.34	16.74	16.30	25.57
Score	1.50 1.50	1.00	0.50	1.00	0.50	1.00	0.50	0.50	1.00	1.00	1.00	1.00
Ion-type	y_7 sty	y_8	b_7-NH_3	b_7 $b{+}{+}_{16}$	$b{+}{+}_{17}$-H_2O	$b{+}{+}_{17}$	y_9-NH_3	y_9-NH_3	$b{+}{+}_{18}$-H_2O y_9	$b{+}{+}_{18}$	b_8	b_9
Delta Da	0.02 0.70	0.10	-0.73	-0.06 0.45	0.72	0.18	-0.76	0.20	0.62 0.07	0.11	0.08	0.18

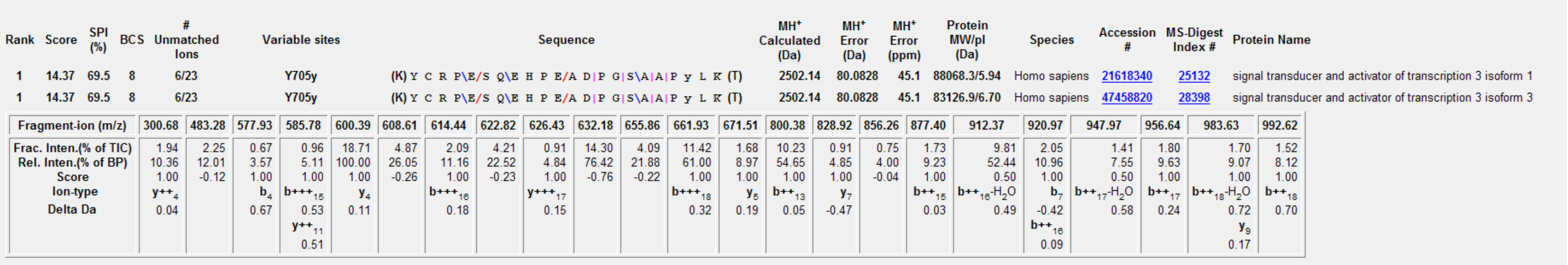
Peak 40



assignment



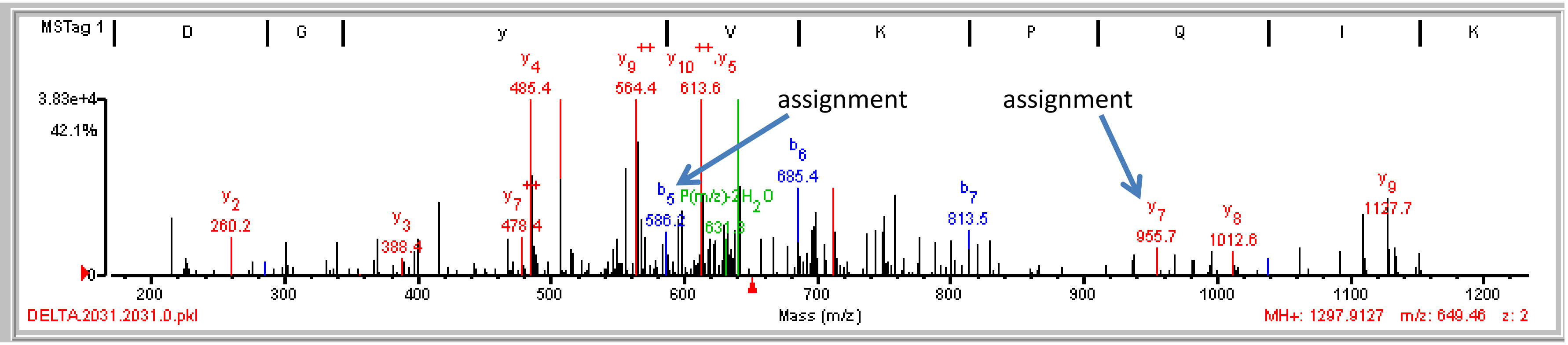
b16-H$_2$O



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.37	69.5	8	6/23	Y705y	(K) Y C R P\E/S Q\E H P E/A D|P G|S\A|A|P y L K (T)	2502.14	80.0828	45.1	88068.3/5.94	Homo sapiens	21618340	25132	signal transducer and activator of transcription 3 isoform 1
1	14.37	69.5	8	6/23	Y705y	(K) Y C R P\E/S Q\E H P E/A D|P G|S\A|A|P y L K (T)	2502.14	80.0828	45.1	83126.9/6.70	Homo sapiens	47458820	28398	signal transducer and activator of transcription 3 isoform 3

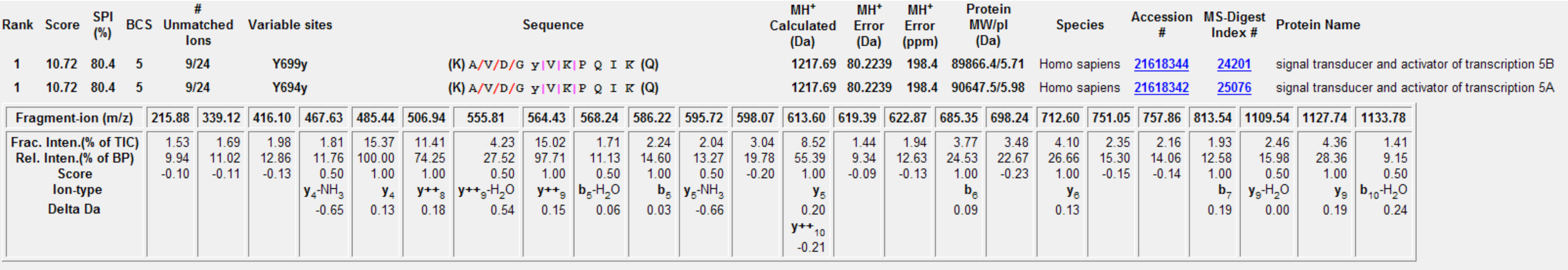
Fragment-ion (m/z)	300.68	483.28	577.93	585.78	600.39	608.61	614.44	622.82	626.43	632.18	655.86	661.93	671.51	800.38	828.92	856.26	877.40	912.37	920.97	947.97	956.64	983.63	992.62
Frac. Inten.(% of TIC)	1.94	2.25	0.67	0.96	18.71	4.87	2.09	4.21	0.91	14.30	4.09	11.42	1.68	10.23	0.91	0.75	1.73	9.81	2.05	1.41	1.80	1.70	1.52
Rel. Inten.(% of BP)	10.36	12.01	3.57	5.11	100.00	26.05	11.16	22.52	4.84	76.42	21.88	61.00	8.97	54.65	4.85	4.00	9.23	52.44	10.96	7.55	9.63	9.07	8.12
Score	1.00	-0.12	1.00	1.00	1.00	-0.26	1.00	-0.23	1.00	-0.76	-0.22	1.00	1.00	1.00	1.00	-0.04	1.00	0.50	1.00	0.50	1.00	1.00	1.00
Ion-type	y++$_4$		b$_4$	b+++$_{15}$ y++$_{11}$	y$_4$		b+++$_{16}$		y+++$_{17}$			b+++$_{18}$	y$_5$	b++$_{13}$	y$_7$		b++$_{15}$	b++$_{16}$-H$_2$O	b$_7$ b++$_{16}$	b++$_{17}$-H$_2$O	b++$_{17}$	b++$_{18}$-H$_2$O y$_9$	b++$_{18}$
Delta Da	0.04		0.67	0.53 0.51	0.11		0.18		0.15			0.32	0.19	0.05	-0.47		0.03	0.49	-0.42 0.09	0.58	0.24	0.72 0.17	0.70

Peak 41



assignment

assignment

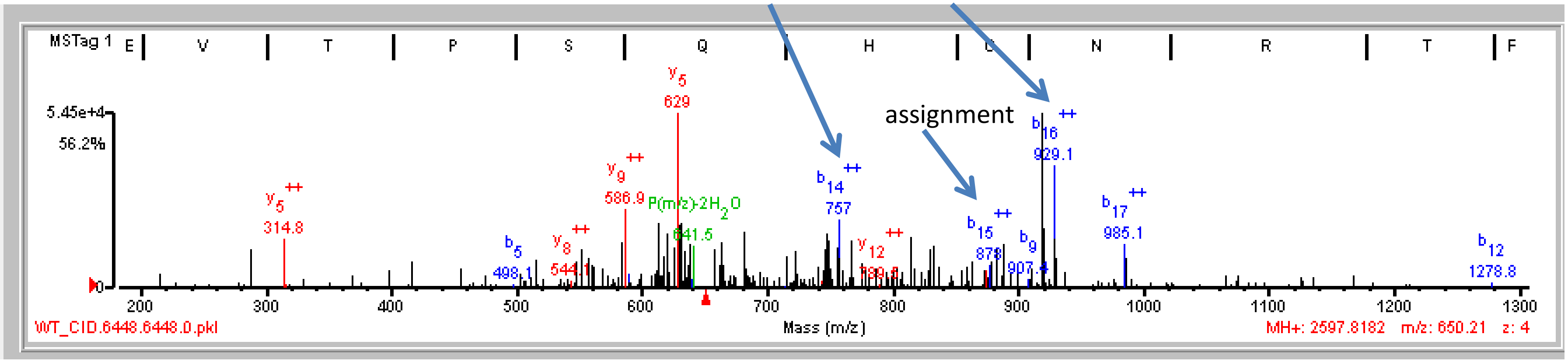


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.72	80.4	5	9/24	Y699y	(K) A/V/D/G y|V|K|P Q I K (Q)	1217.69	80.2239	198.4	89866.4/5.71	Homo sapiens	21618344	24201	signal transducer and activator of transcription 5B
1	10.72	80.4	5	9/24	Y694y	(K) A/V/D/G y|V|K|P Q I K (Q)	1217.69	80.2239	198.4	90647.5/5.98	Homo sapiens	21618342	25076	signal transducer and activator of transcription 5A

Fragment-ion (m/z)	215.88	339.12	416.10	467.63	485.44	506.94	555.81	564.43	568.24	586.22	595.72	598.07
Frac. Inten.(% of TIC)	1.53	1.69	1.98	1.81	15.37	11.41	4.23	15.02	1.71	2.24	2.04	3.04
Rel. Inten.(% of BP)	9.94	11.02	12.86	11.76	100.00	74.25	27.52	97.71	11.13	14.60	13.27	19.78
Score	-0.10	-0.11	-0.13	0.50	1.00	1.00	0.50	1.00	0.50	1.00	0.50	-0.20
Ion-type				y_4-NH_3	y_4	$y{++}_8$	$y{++}_9$-H_2O	$y{++}_9$	b_5-H_2O	b_5	y_5-NH_3	
Delta Da				-0.65	0.13	0.18	0.54	0.15	0.06	0.03	-0.66	

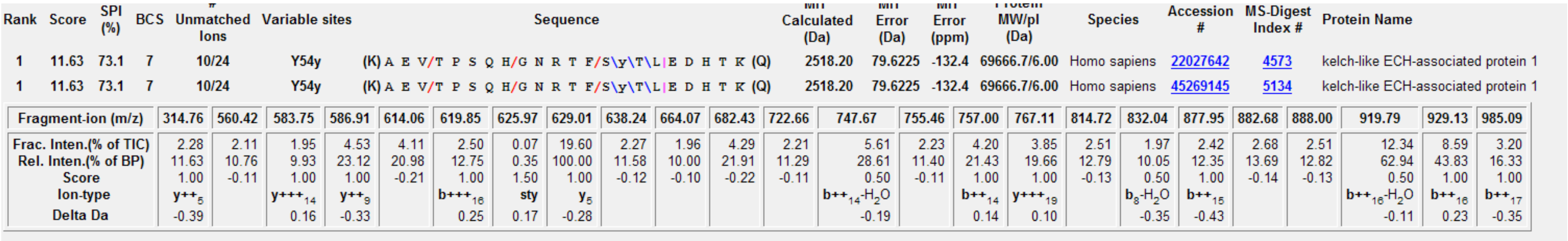
Fragment-ion (m/z)	613.60	619.39	622.87	685.35	698.24	712.60	751.05	757.86	813.54	1109.54	1127.74	1133.78
Frac. Inten.(% of TIC)	8.52	1.44	1.94	3.77	3.48	4.10	2.35	2.16	1.93	2.46	4.36	1.41
Rel. Inten.(% of BP)	55.39	9.34	12.63	24.53	22.67	26.66	15.30	14.06	12.58	15.98	28.36	9.15
Score	1.00	-0.09	-0.13	1.00	-0.23	1.00	-0.15	-0.14	1.00	0.50	1.00	0.50
Ion-type	y_5 $y{++}_{10}$			b_6		y_6			b_7	y_9-H_2O	y_9	b_{10}-H_2O
Delta Da	0.20 -0.21			0.09		0.13			0.19	0.00	0.19	0.24

Peak 42



Ions that verify assignment

assignment

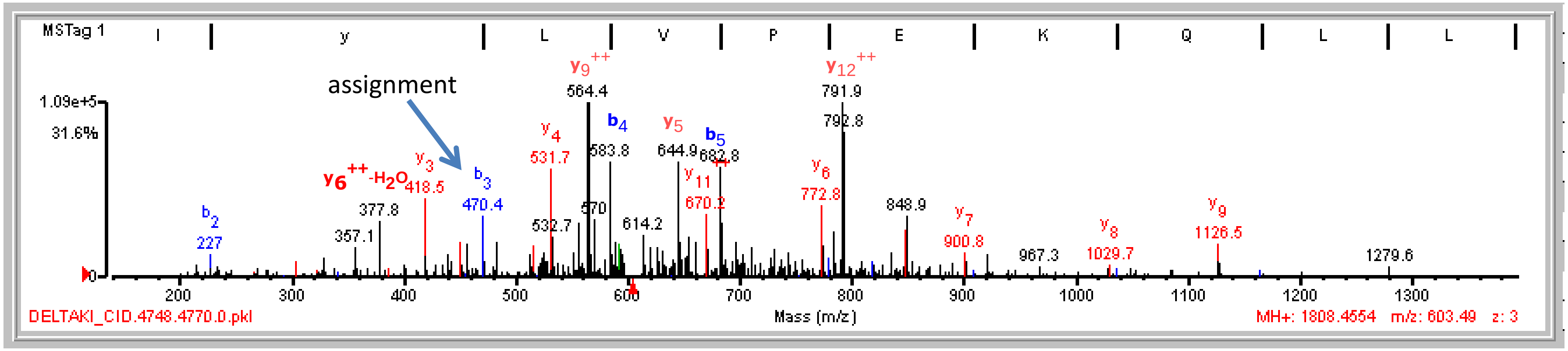


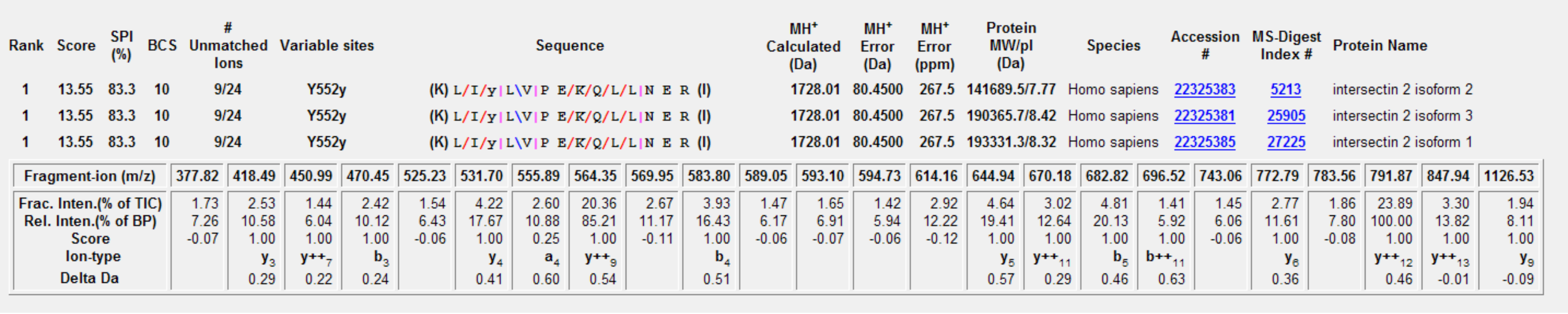
Rank	Score	SPI (%)	BCS	Unmatched Ions	Variable sites	Sequence	Calculated (Da)	Error (Da)	Error (ppm)	MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.63	73.1	7	10/24	Y54y	(K) A E V/T P S Q H/G N R T F/S\y\T\L|E D H T K (Q)	2518.20	79.6225	-132.4	69666.7/6.00	Homo sapiens	22027642	4573	kelch-like ECH-associated protein 1
1	11.63	73.1	7	10/24	Y54y	(K) A E V/T P S Q H/G N R T F/S\y\T\L|E D H T K (Q)	2518.20	79.6225	-132.4	69666.7/6.00	Homo sapiens	45269145	5134	kelch-like ECH-associated protein 1

Fragment-ion (m/z)	314.76	560.42	583.75	586.91	614.06	619.85	625.97	629.01	638.24	664.07	682.43	722.66
Frac. Inten.(% of TIC)	2.28	2.11	1.95	4.53	4.11	2.50	0.07	19.60	2.27	1.96	4.29	2.21
Rel. Inten.(% of BP)	11.63	10.76	9.93	23.12	20.98	12.75	0.35	100.00	11.58	10.00	21.91	11.29
Score	1.00	-0.11	1.00	1.00	-0.21	1.00	1.50	1.00	-0.12	-0.10	-0.22	-0.11
Ion-type	$y{++}_{5}$		$y{+++}_{14}$	$y{++}_{9}$		$b{+++}_{16}$	sty	y_{5}				
Delta Da	-0.39		0.16	-0.33		0.25	0.17	-0.28				

Fragment-ion (m/z)	747.67	755.46	757.00	767.11	814.72	832.04	877.95	882.68	888.00	919.79	929.13	985.09
Frac. Inten.(% of TIC)	5.61	2.23	4.20	3.85	2.51	1.97	2.42	2.68	2.51	12.34	8.59	3.20
Rel. Inten.(% of BP)	28.61	11.40	21.43	19.66	12.79	10.05	12.35	13.69	12.82	62.94	43.83	16.33
Score	0.50	-0.11	1.00	1.00	-0.13	0.50	1.00	-0.14	-0.13	0.50	1.00	1.00
Ion-type	$b{++}_{14}\text{-}H_2O$		$b{++}_{14}$	$y{+++}_{19}$		$b_{8}\text{-}H_2O$	$b{++}_{15}$			$b{++}_{16}\text{-}H_2O$	$b{++}_{16}$	$b{++}_{17}$
Delta Da	-0.19		0.14	0.10		-0.35	-0.43			-0.11	0.23	-0.35

Peak 43



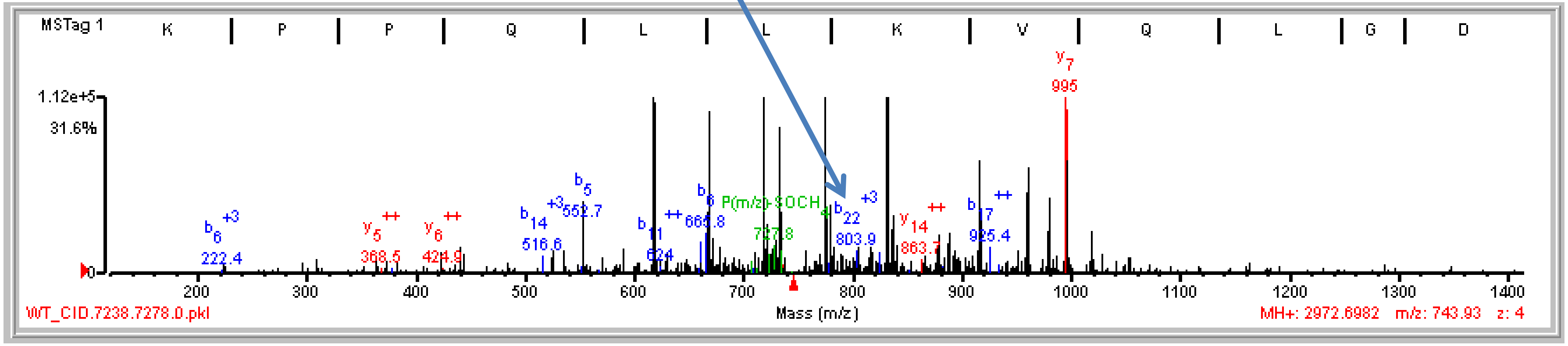


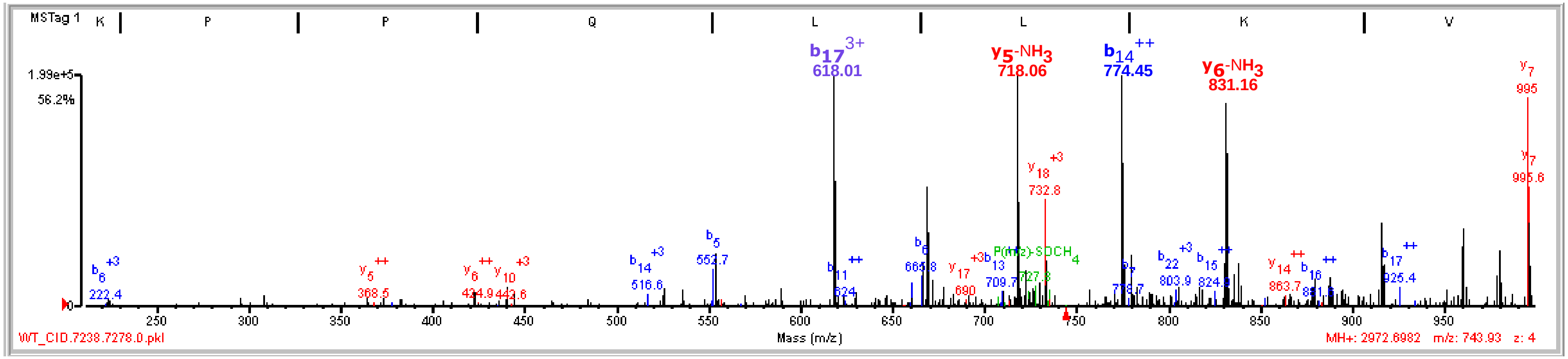
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.55	83.3	10	9/24	Y552y	(K) L/I/y|L\V|P E/K/Q/L/L|N E R (I)	1728.01	80.4500	267.5	141689.5/7.77	Homo sapiens	22325383	5213	intersectin 2 isoform 2
1	13.55	83.3	10	9/24	Y552y	(K) L/I/y|L\V|P E/K/Q/L/L|N E R (I)	1728.01	80.4500	267.5	190365.7/8.42	Homo sapiens	22325381	25905	intersectin 2 isoform 3
1	13.55	83.3	10	9/24	Y552y	(K) L/I/y|L\V|P E/K/Q/L/L|N E R (I)	1728.01	80.4500	267.5	193331.3/8.32	Homo sapiens	22325385	27225	intersectin 2 isoform 1

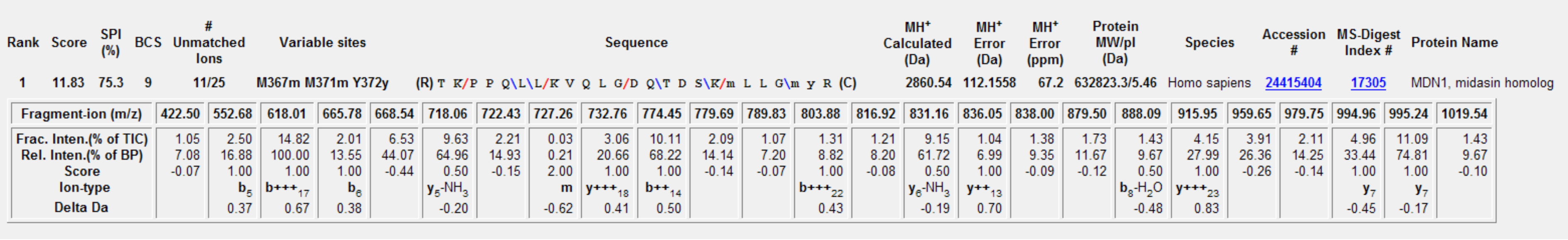
Fragment-ion (m/z)	377.82	418.49	450.99	470.45	525.23	531.70	555.89	564.35	569.95	583.80	589.05	593.10	594.73	614.16	644.94	670.18	682.82	696.52	743.06	772.79	783.56	791.87	847.94	1126.53
Frac. Inten.(% of TIC)	1.73	2.53	1.44	2.42	1.54	4.22	2.60	20.36	2.67	3.93	1.47	1.65	1.42	2.92	4.64	3.02	4.81	1.41	1.45	2.77	1.86	23.89	3.30	1.94
Rel. Inten.(% of BP)	7.26	10.58	6.04	10.12	6.43	17.67	10.88	85.21	11.17	16.43	6.17	6.91	5.94	12.22	19.41	12.64	20.13	5.92	6.06	11.61	7.80	100.00	13.82	8.11
Score	-0.07	1.00	1.00	1.00	-0.06	1.00	0.25	1.00	-0.11	1.00	-0.06	-0.07	-0.06	-0.12	1.00	1.00	1.00	1.00	-0.06	1.00	-0.08	1.00	1.00	1.00
Ion-type		y_3	$y{++}_7$	b_3		y_4	a_4	$y{++}_9$		b_4					y_5	$y{++}_{11}$	b_5	$b{++}_{11}$		y_6		$y{++}_{12}$	$y{++}_{13}$	y_9
Delta Da		0.29	0.22	0.24		0.41	0.60	0.54		0.51					0.57	0.29	0.46	0.63		0.36		0.46	-0.01	-0.09

Peak 44

Ions that verify assignment



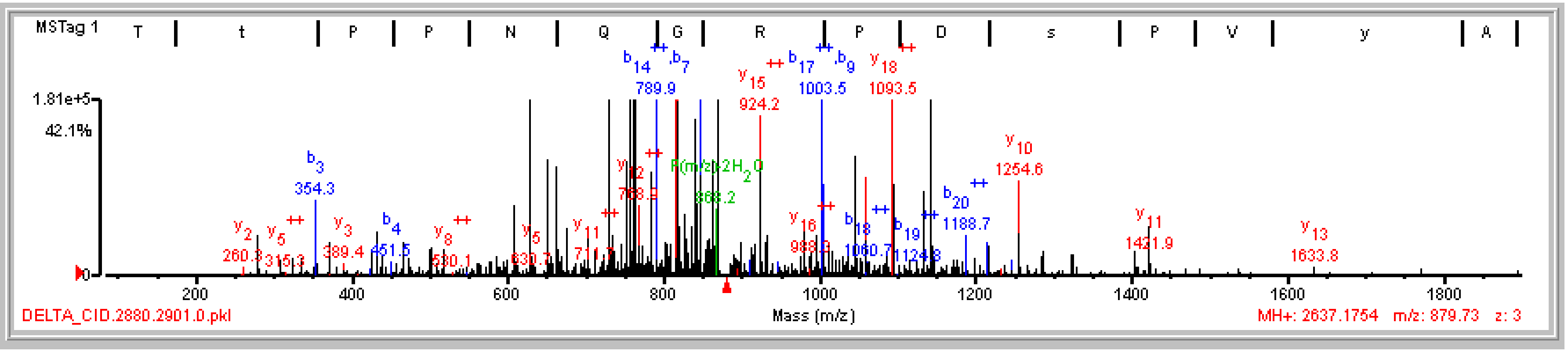


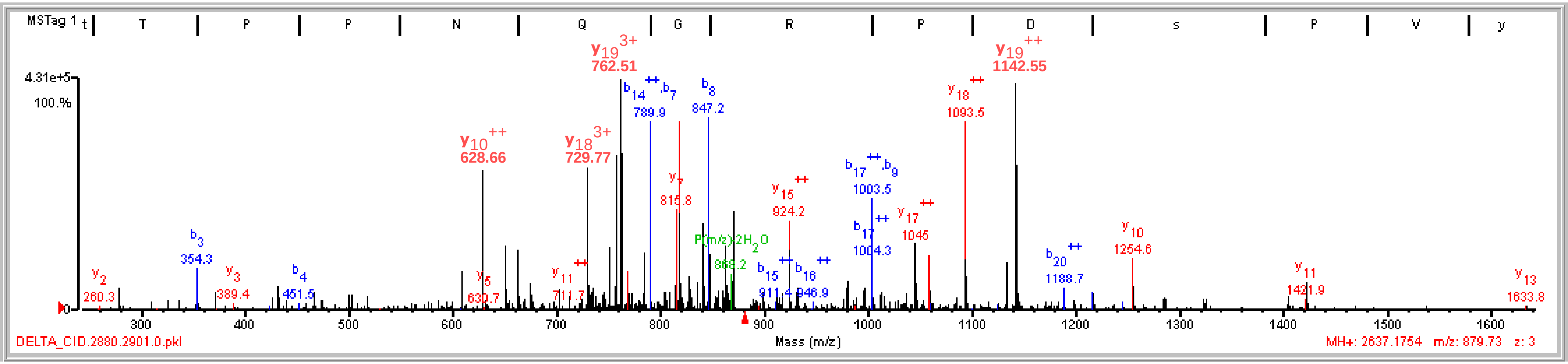


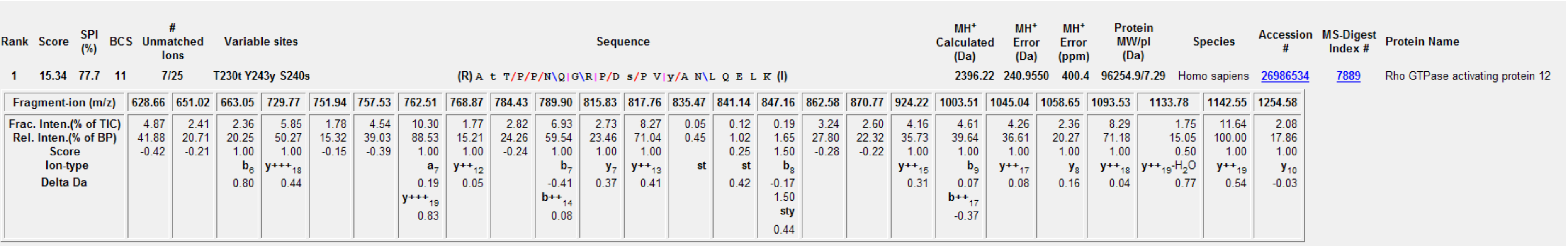
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.83	75.3	9	11/25	M367m M371m Y372y	(R) T K/P P Q\L\L/K V Q L G/D Q\T D S\K/m L L G\m y R (C)	2860.54	112.1558	67.2	632823.3/5.46	Homo sapiens	24415404	17305	MDN1, midasin homolog

Fragment-ion (m/z)	422.50	552.68	618.01	665.78	668.54	718.06	722.43	727.26	732.76	774.45	779.69	789.83	803.88	816.92	831.16	836.05	838.00	879.50	888.09	915.95	959.65	979.75	994.96	995.24	1019.54
Frac. Inten.(% of TIC)	1.05	2.50	14.82	2.01	6.53	9.63	2.21	0.03	3.06	10.11	2.09	1.07	1.31	1.21	9.15	1.04	1.38	1.73	1.43	4.15	3.91	2.11	4.96	11.09	1.43
Rel. Inten.(% of BP)	7.08	16.88	100.00	13.55	44.07	64.96	14.93	0.21	20.66	68.22	14.14	7.20	8.82	8.20	61.72	6.99	9.35	11.67	9.67	27.99	26.36	14.25	33.44	74.81	9.67
Score	-0.07	1.00	1.00	1.00	-0.44	0.50	-0.15	2.00	1.00	1.00	-0.14	-0.07	1.00	-0.08	0.50	1.00	-0.09	-0.12	0.50	1.00	-0.26	-0.14	1.00	1.00	-0.10
Ion-type		b_5	$b{+}{+}{+}_{17}$	b_6		y_5-NH_3		m	$y{+}{+}{+}_{18}$	$b{+}{+}_{14}$			$b{+}{+}{+}_{22}$		y_6-NH_3	$y{+}{+}_{13}$			b_8-H_2O	$y{+}{+}{+}_{23}$			y_7	y_7	
Delta Da		0.37	0.67	0.38		-0.20		-0.62	0.41	0.50			0.43		-0.19	0.70			-0.48	0.83			-0.45	-0.17	

Peak 45





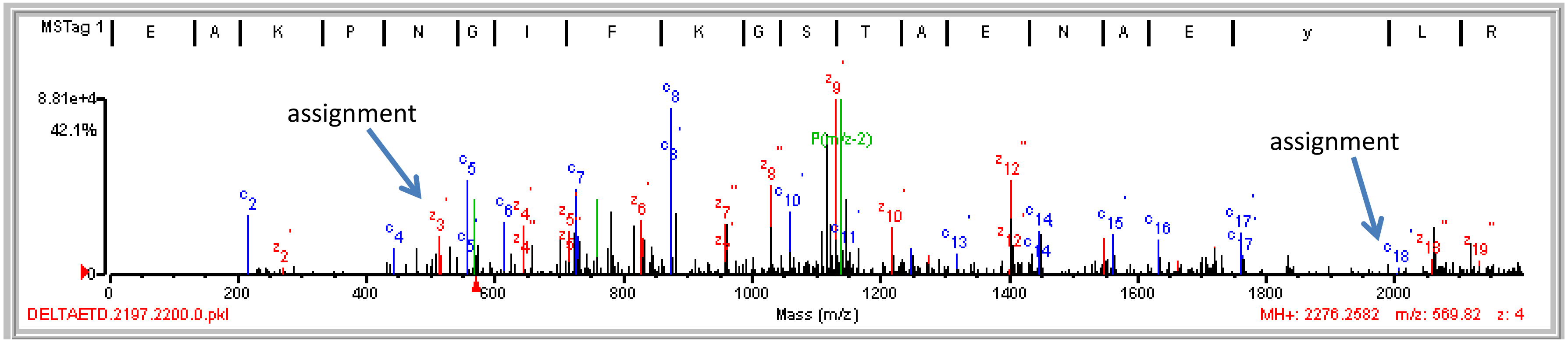


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.34	77.7	11	7/25	T230t Y243y S240s	(R) A t T/P/P/N\Q|G\R|P/D s/P V|y/A N\L Q E L K (I)	2396.22	240.9550	400.4	96254.9/7.29	Homo sapiens	26986534	7889	Rho GTPase activating protein 12

Fragment-ion (m/z)	628.66	651.02	663.05	729.77	751.94	757.53	762.51	768.87	784.43	789.90	815.83
Frac. Inten.(% of TIC)	4.87	2.41	2.36	5.85	1.78	4.54	10.30	1.77	2.82	6.93	2.73
Rel. Inten.(% of BP)	41.88	20.71	20.25	50.27	15.32	39.03	88.53	15.21	24.26	59.54	23.46
Score	-0.42	-0.21	1.00	1.00	-0.15	-0.39	1.00	1.00	-0.24	1.00	1.00
Ion-type			b_6	$y+++_{18}$			a_7 $y+++_{19}$	$y++_{12}$		b_7 $b++_{14}$	y_7
Delta Da			0.80	0.44			0.19 0.83	0.05		-0.41 0.08	0.37

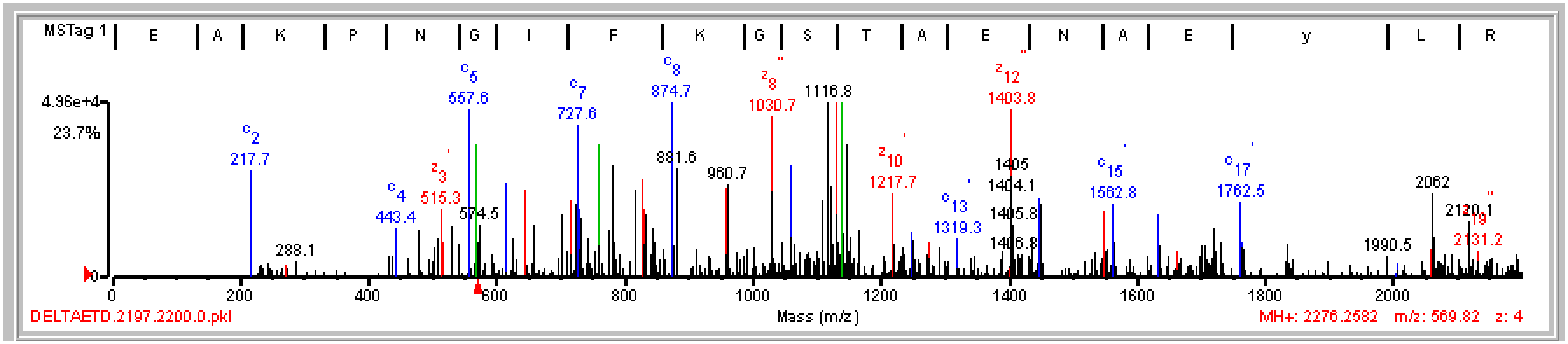
Fragment-ion (m/z)	817.76	835.47	841.14	847.16	862.58	870.77	924.22	1003.51	1045.04	1058.65	1093.53	1133.78	1142.55	1254.58
Frac. Inten.(% of TIC)	8.27	0.05	0.12	0.19	3.24	2.60	4.16	4.61	4.26	2.36	8.29	1.75	11.64	2.08
Rel. Inten.(% of BP)	71.04	0.45	1.02	1.65	27.80	22.32	35.73	39.64	36.61	20.27	71.18	15.05	100.00	17.86
Score	1.00		0.25	1.50 1.50	-0.28	-0.22	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	$y++_{13}$	st	st	b_8 sty			$y++_{15}$	b_9 $b++_{17}$	$y++_{17}$	y_8	$y++_{18}$	$y++_{19}$-H_2O	$y++_{19}$	y_{10}
Delta Da	0.41		0.42	-0.17 0.44			0.31	0.07 -0.37	0.08	0.16	0.04	0.77	0.54	-0.03

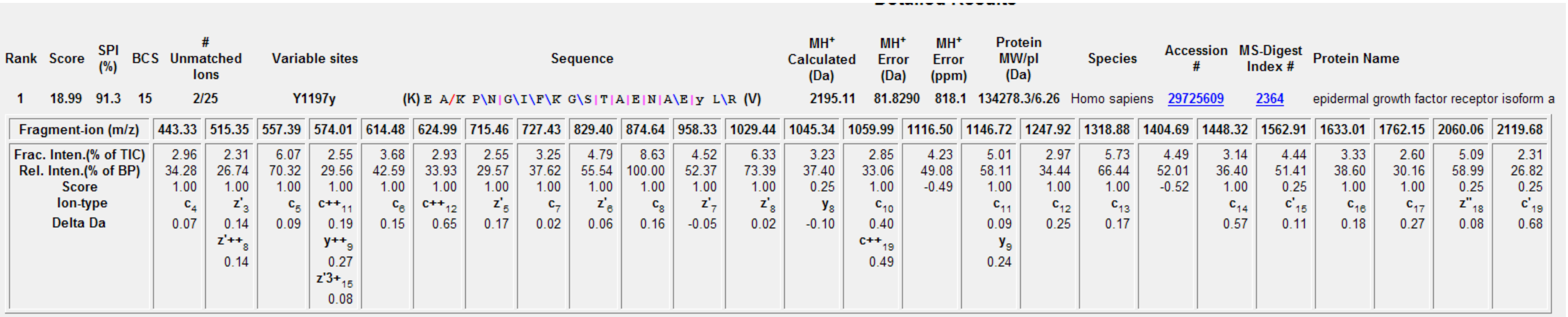
Peak 47



assignment

assignment

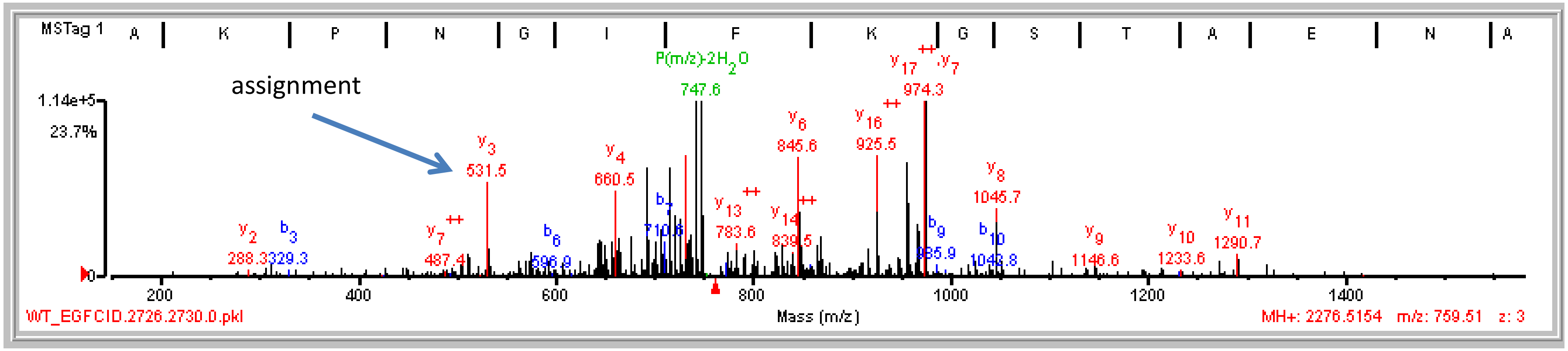




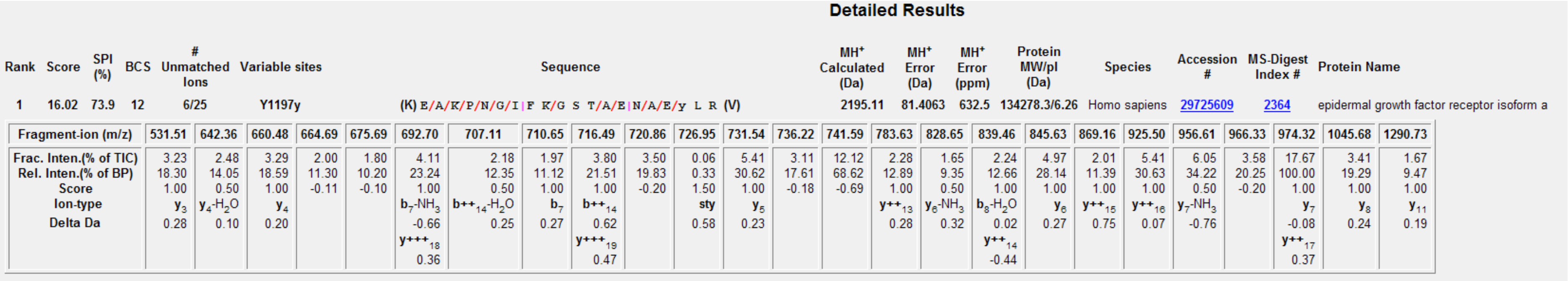
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.99	91.3	15	2/25	Y1197y	(K) E A/K P\N|G\I\F\K G\S|T|A|E|N|A\E|y L\R (V)	2195.11	81.8290	818.1	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

Fragment-ion (m/z)	443.33	515.35	557.39	574.01	614.48	624.99	715.46	727.43	829.40	874.64	958.33	1029.44	1045.34	1059.99	1116.50	1146.72	1247.92	1318.88	1404.69	1448.32	1562.91	1633.01	1762.15	2060.06	2119.68
Frac. Inten.(% of TIC)	2.96	2.31	6.07	2.55	3.68	2.93	2.55	3.25	4.79	8.63	4.52	6.33	3.23	2.85	4.23	5.01	2.97	5.73	4.49	3.14	4.44	3.33	2.60	5.09	2.31
Rel. Inten.(% of BP)	34.28	26.74	70.32	29.56	42.59	33.93	29.57	37.62	55.54	100.00	52.37	73.39	37.40	33.06	49.08	58.11	34.44	66.44	52.01	36.40	51.41	38.60	30.16	58.99	26.82
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.49	1.00	1.00	1.00	-0.52	1.00	0.25	1.00	1.00	0.25	0.25
Ion-type	c_4	z'_3 z'^{++}_8	c_5	c^{++}_{11} y^{++}_9 z'^{3+}_{15}	c_6	c^{++}_{12}	z'_5	c_7	z'_6	c_8	z'_7	z'_8	y_8	c_{10} c^{++}_{19}		c_{11} y_9	c_{12}	c_{13}		c_{14}	c'_{15}	c_{16}	c_{17}	z''_{18}	c'_{19}
Delta Da	0.07	0.14 0.14	0.09	0.19 0.27 0.08	0.15	0.65	0.17	0.02	0.06	0.16	-0.05	0.02	-0.10	0.40 0.49		0.09 0.24	0.25	0.17		0.57	0.11	0.18	0.27	0.08	0.68

Peak 48



assignment



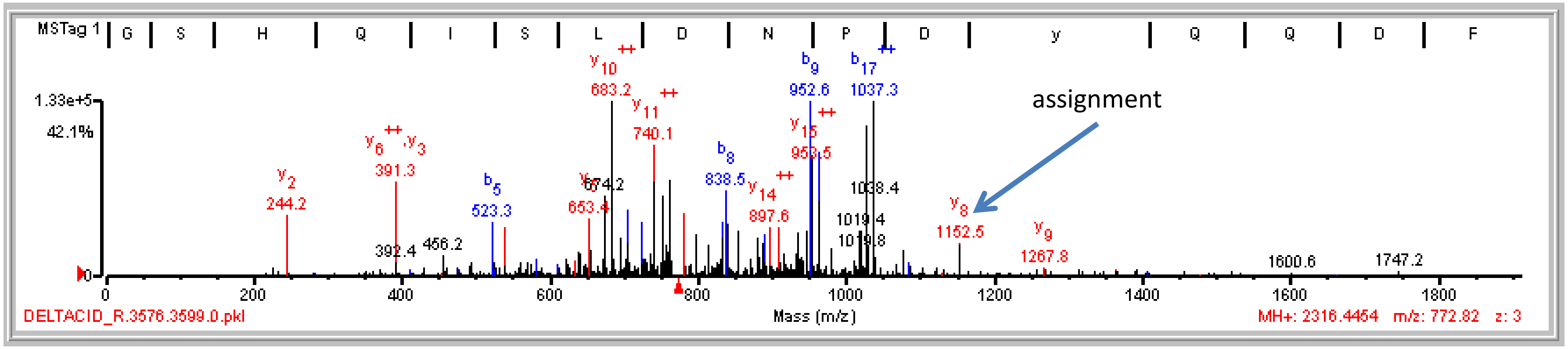
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.02	73.9	12	6/25	Y1197y	(K) E/A/K/P/N/G/I|F K/G S T/A/E|N/A/E/y L R (V)	2195.11	81.4063	632.5	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

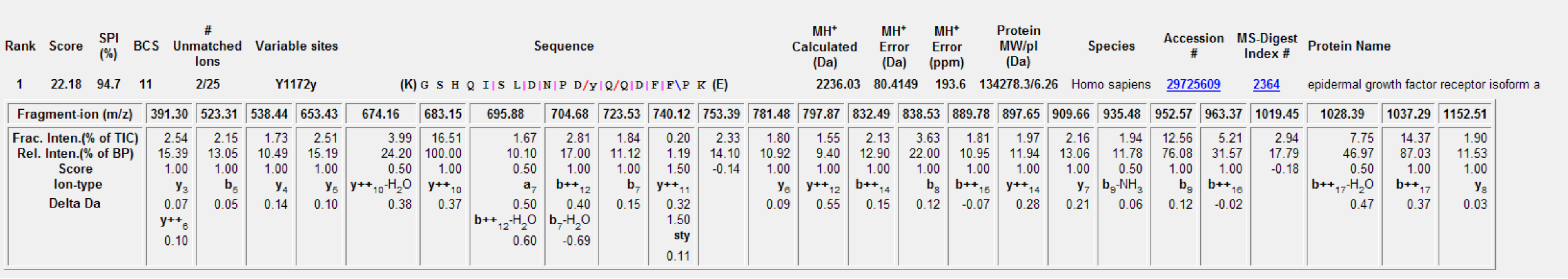
Fragment-ion (m/z)	531.51	642.36	660.48	664.69	675.69	692.70	707.11	710.65	716.49	720.86
Frac. Inten.(% of TIC)	3.23	2.48	3.29	2.00	1.80	4.11	2.18	1.97	3.80	3.50
Rel. Inten.(% of BP)	18.30	14.05	18.59	11.30	10.20	23.24	12.35	11.12	21.51	19.83
Score	1.00	0.50	1.00	-0.11	-0.10	1.00	0.50	1.00	1.00	-0.20
Ion-type	y_3	y_4-H_2O	y_4			b_7-NH_3 $y{+}{+}{+}_{18}$	$b{+}{+}_{14}$-H_2O	b_7	$b{+}{+}_{14}$ $y{+}{+}{+}_{19}$	
Delta Da	0.28	0.10	0.20			-0.66 0.36	0.25	0.27	0.62 0.47	

Fragment-ion (m/z)	726.95	731.54	736.22	741.59	783.63	828.65	839.46	845.63	869.16	925.50	956.61	966.33	974.32	1045.68	1290.73
Frac. Inten.(% of TIC)	0.06	5.41	3.11	12.12	2.28	1.65	2.24	4.97	2.01	5.41	6.05	3.58	17.67	3.41	1.67
Rel. Inten.(% of BP)	0.33	30.62	17.61	68.62	12.89	9.35	12.66	28.14	11.39	30.63	34.22	20.25	100.00	19.29	9.47
Score	1.50	1.00	-0.18	-0.69	1.00	0.50	1.00	1.00	1.00	1.00	0.50	-0.20	1.00	1.00	1.00
Ion-type	sty	y_5			$y{+}{+}_{13}$	y_6-NH_3	b_8-H_2O $y{+}{+}_{14}$	y_6	$y{+}{+}_{15}$	$y{+}{+}_{16}$	y_7-NH_3		y_7 $y{+}{+}_{17}$	y_8	y_{11}
Delta Da	0.58	0.23			0.28	0.32	0.02 -0.44	0.27	0.75	0.07	-0.76		-0.08 0.37	0.24	0.19

Peak 49



assignment

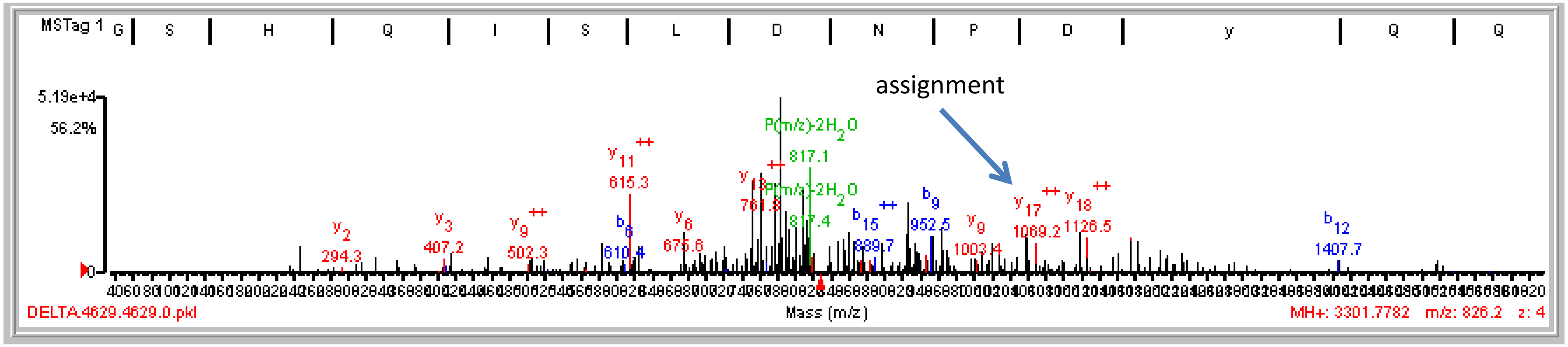


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.18	94.7	11	2/25	Y1172y	(K) G S H Q I|S L|D|N|P D/y|Q/Q|D|F|F\P K (E)	2236.03	80.4149	193.6	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

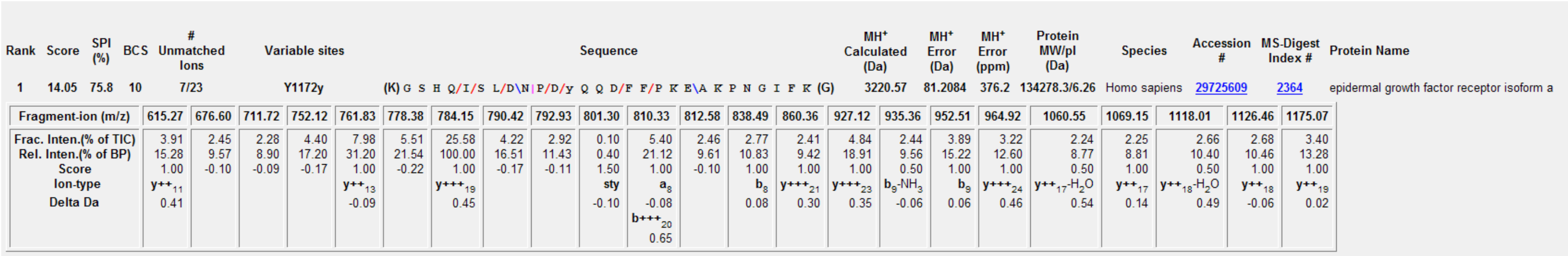
Fragment-ion (m/z)	391.30	523.31	538.44	653.43	674.16	683.15	695.88	704.68	723.53	740.12	753.39	781.48	797.87
Frac. Inten.(% of TIC)	2.54	2.15	1.73	2.51	3.99	16.51	1.67	2.81	1.84	0.20	2.33	1.80	1.55
Rel. Inten.(% of BP)	15.39	13.05	10.49	15.19	24.20	100.00	10.10	17.00	11.12	1.19	14.10	10.92	9.40
Score	1.00	1.00	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.50	-0.14	1.00	1.00
Ion-type	y_3	b_5	y_4	y_5	$y{+}{+}_{10}$-H_2O	$y{+}{+}_{10}$	a_7	$b{+}{+}_{12}$	b_7	$y{+}{+}_{11}$		y_6	$y{+}{+}_{12}$
Delta Da	0.07	0.05	0.14	0.10	0.38	0.37	0.50	0.40	0.15	0.32		0.09	0.55
	$y{+}{+}_6$						$b{+}{+}_{12}$-H_2O	b_7-H_2O		1.50			
	0.10						0.60	-0.69		sty			
										0.11			

Fragment-ion (m/z)	832.49	838.53	889.78	897.65	909.66	935.48	952.57	963.37	1019.45	1028.39	1037.29	1152.51
Frac. Inten.(% of TIC)	2.13	3.63	1.81	1.97	2.16	1.94	12.56	5.21	2.94	7.75	14.37	1.90
Rel. Inten.(% of BP)	12.90	22.00	10.95	11.94	13.06	11.78	76.08	31.57	17.79	46.97	87.03	11.53
Score	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	-0.18	0.50	1.00	1.00
Ion-type	$b{+}{+}_{14}$	b_8	$b{+}{+}_{15}$	$y{+}{+}_{14}$	y_7	b_9-NH_3	b_9	$b{+}{+}_{16}$		$b{+}{+}_{17}$-H_2O	$b{+}{+}_{17}$	y_8
Delta Da	0.15	0.12	-0.07	0.28	0.21	0.06	0.12	-0.02		0.47	0.37	0.03

Peak 50



assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.05	75.8	10	7/23	Y1172y	(K) G S H Q/I/S L/D\N|P/D/y Q Q D/F F/P K E\A K P N G I F K (G)	3220.57	81.2084	376.2	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

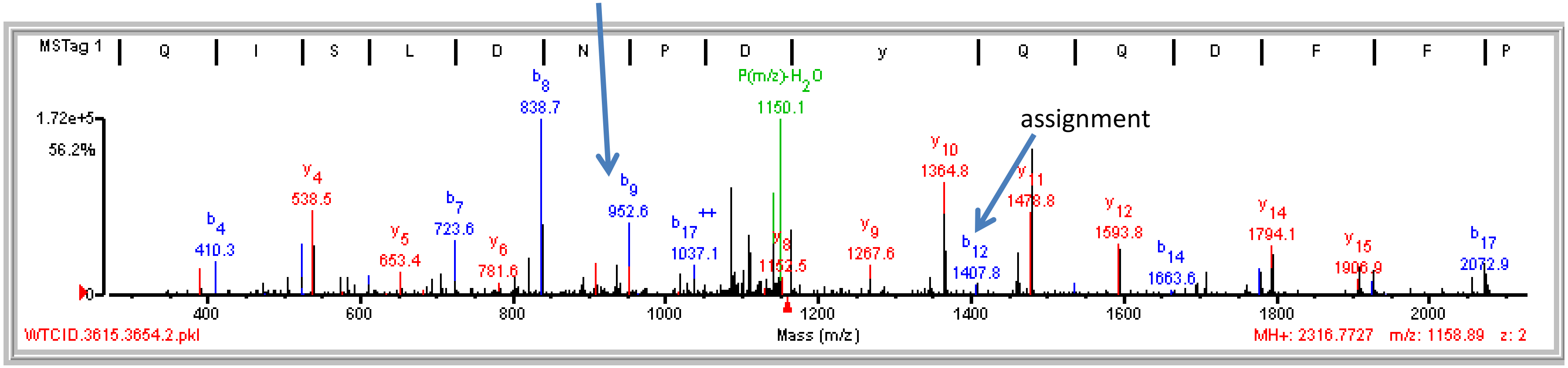
Fragment-ion (m/z)	615.27	676.60	711.72	752.12	761.83	778.38	784.15	790.42	792.93	801.30	810.33
Frac. Inten.(% of TIC)	3.91	2.45	2.28	4.40	7.98	5.51	25.58	4.22	2.92	0.10	5.40
Rel. Inten.(% of BP)	15.28	9.57	8.90	17.20	31.20	21.54	100.00	16.51	11.43	0.40	21.12
Score	1.00	-0.10	-0.09	-0.17	1.00	-0.22	1.00	-0.17	-0.11	1.50	1.00
Ion-type	$\mathrm{y{+}{+}}_{11}$				$\mathrm{y{+}{+}}_{13}$		$\mathrm{y{+}{+}{+}}_{19}$			sty	a_8 $\mathrm{b{+}{+}{+}}_{20}$
Delta Da	0.41				-0.09		0.45			-0.10	-0.08 0.65

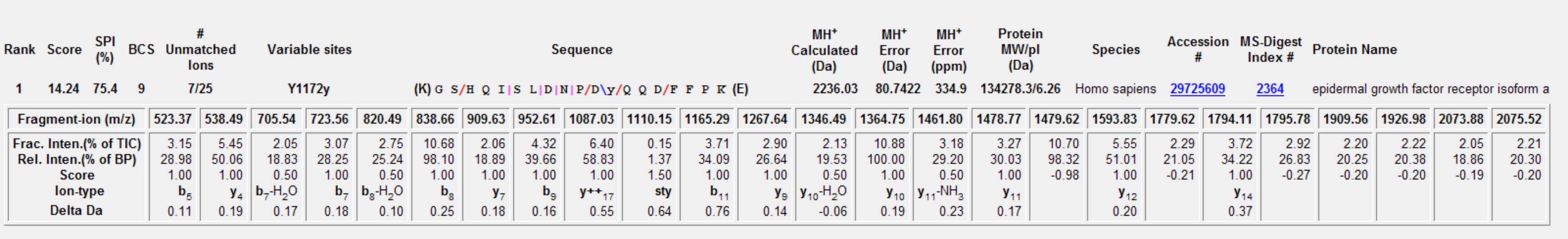
Fragment-ion (m/z)	812.58	838.49	860.36	927.12	935.36	952.51	964.92	1060.55	1069.15	1118.01	1126.46	1175.07
Frac. Inten.(% of TIC)	2.46	2.77	2.41	4.84	2.44	3.89	3.22	2.24	2.25	2.66	2.68	3.40
Rel. Inten.(% of BP)	9.61	10.83	9.42	18.91	9.56	15.22	12.60	8.77	8.81	10.40	10.46	13.28
Score	-0.10	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	0.50	1.00	1.00
Ion-type		b_8	$\mathrm{y{+}{+}{+}}_{21}$	$\mathrm{y{+}{+}{+}}_{23}$	b_9-NH_3	b_9	$\mathrm{y{+}{+}{+}}_{24}$	$\mathrm{y{+}{+}}_{17}$-H_2O	$\mathrm{y{+}{+}}_{17}$	$\mathrm{y{+}{+}}_{18}$-H_2O	$\mathrm{y{+}{+}}_{18}$	$\mathrm{y{+}{+}}_{19}$
Delta Da		0.08	0.30	0.35	-0.06	0.06	0.46	0.54	0.14	0.49	-0.06	0.02

Peak 51

Ions that verify assignment

assignment



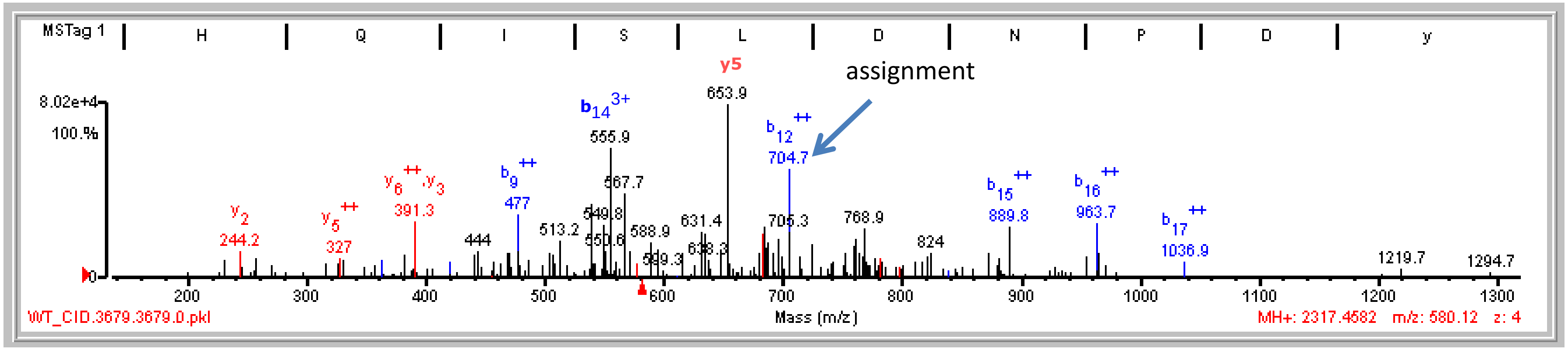


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.24	75.4	9	7/25	Y1172y	(K) G S/H Q I|S L|D|N|P/D\y/Q Q D/F F P K (E)	2236.03	80.7422	334.9	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

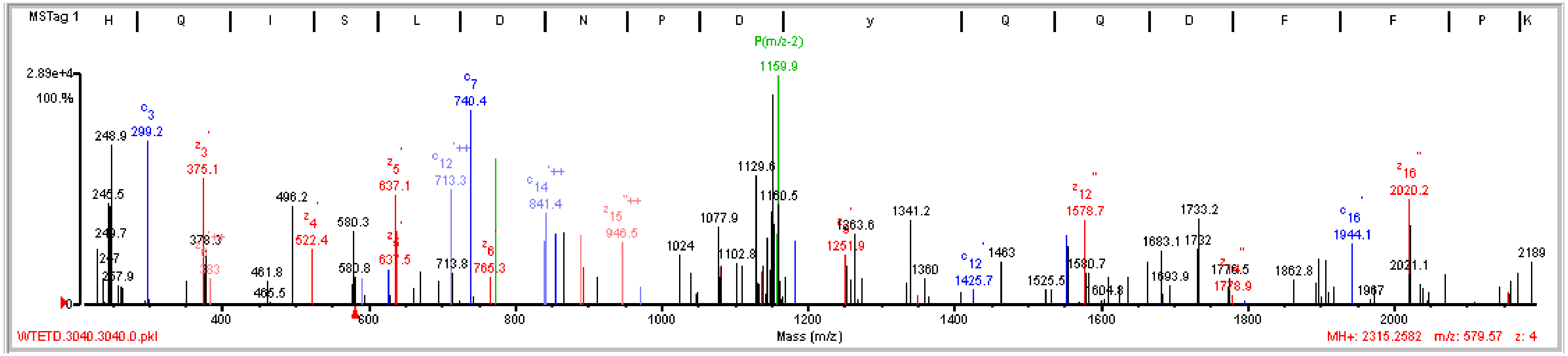
Fragment-ion (m/z)	523.37	538.49	705.54	723.56	820.49	838.66	909.63	952.61	1087.03	1110.15	1165.29	1267.64
Frac. Inten.(% of TIC)	3.15	5.45	2.05	3.07	2.75	10.68	2.06	4.32	6.40	0.15	3.71	2.90
Rel. Inten.(% of BP)	28.98	50.06	18.83	28.25	25.24	98.10	18.89	39.66	58.83	1.37	34.09	26.64
Score	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00	1.00	1.50	1.00	1.00
Ion-type	b_5	y_4	b_7-H_2O	b_7	b_8-H_2O	b_8	y_7	b_9	$y{+}{+}_{17}$	sty	b_{11}	y_9
Delta Da	0.11	0.19	0.17	0.18	0.10	0.25	0.18	0.16	0.55	0.64	0.76	0.14

Fragment-ion (m/z)	1346.49	1364.75	1461.80	1478.77	1479.62	1593.83	1779.62	1794.11	1795.78	1909.56	1926.98	2073.88	2075.52
Frac. Inten.(% of TIC)	2.13	10.88	3.18	3.27	10.70	5.55	2.29	3.72	2.92	2.20	2.22	2.05	2.21
Rel. Inten.(% of BP)	19.53	100.00	29.20	30.03	98.32	51.01	21.05	34.22	26.83	20.25	20.38	18.86	20.30
Score	0.50	1.00	0.50	1.00	-0.98	1.00	-0.21	1.00	-0.27	-0.20	-0.20	-0.19	-0.20
Ion-type	y_{10}-H_2O	y_{10}	y_{11}-NH_3	y_{11}		y_{12}		y_{14}					
Delta Da	-0.06	0.19	0.23	0.17		0.20		0.37					

Peak 52



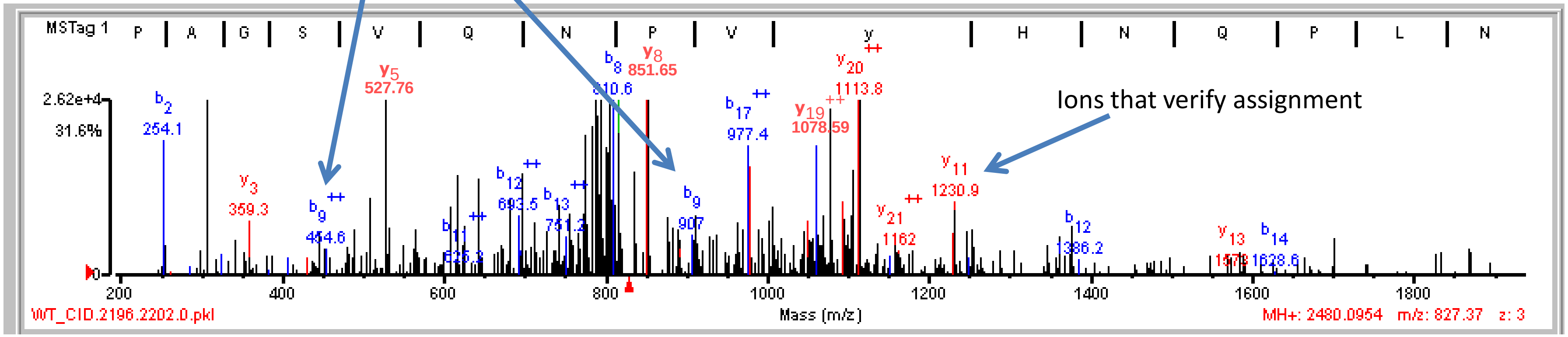
assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.59	77.7	6	3/13	Y1172y	(K) G S H Q I S L D N|P D y\Q\Q|D|F\F P K (E)	2236.03	81.4276	630.6	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

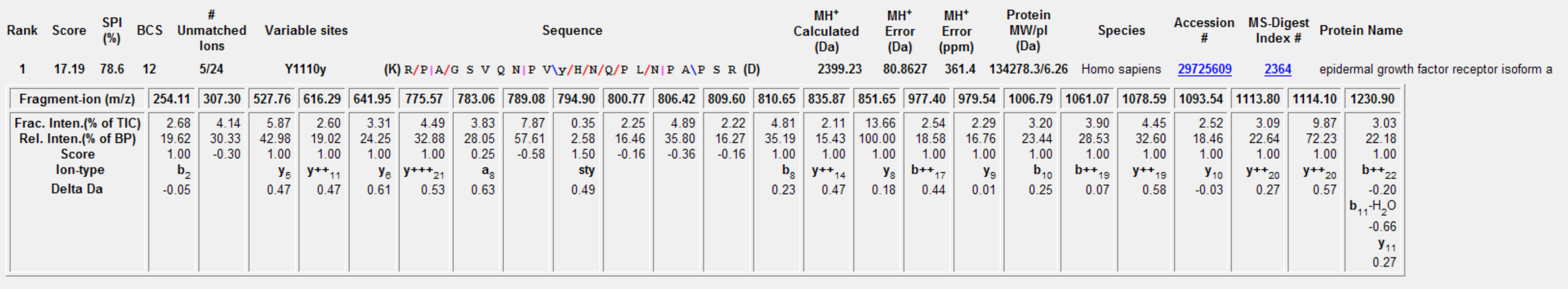
Fragment-ion (m/z)	476.97	538.86	549.83	555.90	567.69	653.87	683.17	685.06	704.68	759.76	768.93	889.78	963.68
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	7.93 50.08 1.00 b^{++}_9 0.24	9.49 59.98 1.00 y_4 0.56	6.68 42.18 -0.42	0.31 1.97 1.50 b^{+++}_{14} 0.67 1.50 sty 0.64	6.51 41.11 -0.41	15.82 100.00 1.00 y_5 0.54	5.30 33.48 1.00 y^{++}_{10} 0.39	9.15 57.81 -0.58	12.55 79.34 1.00 b^{++}_{12} 0.40 b_7-H_2O -0.69	5.99 37.86 0.50 b^{++}_{13}-H_2O 0.45	5.50 34.74 1.00 b^{++}_{13} 0.62	8.05 50.85 1.00 b^{++}_{15} -0.07	6.73 42.53 1.00 b^{++}_{16} 0.29

Peak 53



Ions that verify assignment

Ions that verify assignment

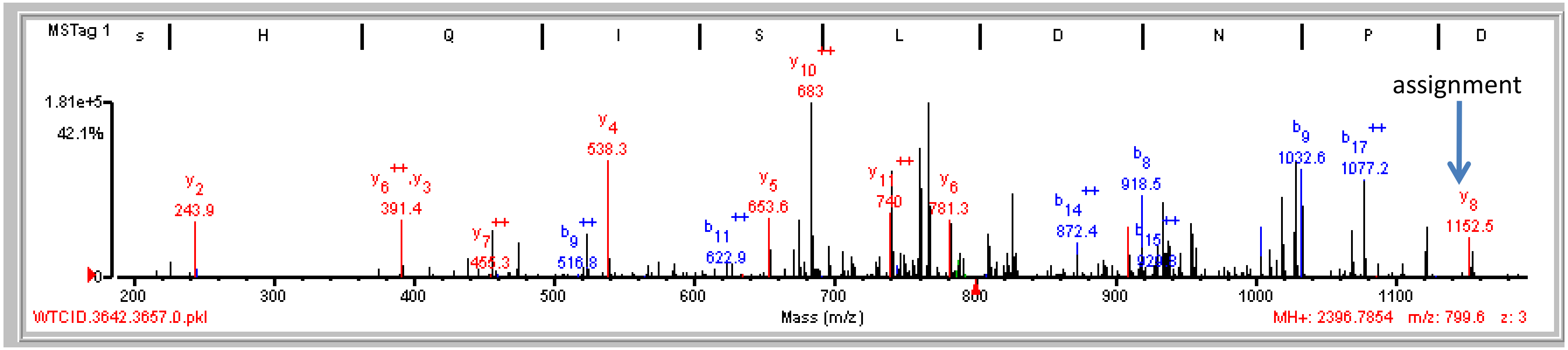


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.19	78.6	12	5/24	Y1110y	(K) R/P|A/G S V Q N|P V\y/H/N/Q/P L/N|P A\P S R (D)	2399.23	80.8627	361.4	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

Fragment-ion (m/z)	254.11	307.30	527.76	616.29	641.95	775.57	783.06	789.08	794.90	800.77	806.42	809.60
Frac. Inten.(% of TIC)	2.68	4.14	5.87	2.60	3.31	4.49	3.83	7.87	0.35	2.25	4.89	2.22
Rel. Inten.(% of BP)	19.62	30.33	42.98	19.02	24.25	32.88	28.05	57.61	2.58	16.46	35.80	16.27
Score	1.00	-0.30	1.00	1.00	1.00	1.00	0.25	-0.58	1.50	-0.16	-0.36	-0.16
Ion-type	b_2		y_5	$y{++}_{11}$	y_6	$y{+++}_{21}$	a_8		sty			
Delta Da	-0.05		0.47	0.47	0.61	0.53	0.63		0.49			

Fragment-ion (m/z)	810.65	835.87	851.65	977.40	979.54	1006.79	1061.07	1078.59	1093.54	1113.80	1114.10	1230.90
Frac. Inten.(% of TIC)	4.81	2.11	13.66	2.54	2.29	3.20	3.90	4.45	2.52	3.09	9.87	3.03
Rel. Inten.(% of BP)	35.19	15.43	100.00	18.58	16.76	23.44	28.53	32.60	18.46	22.64	72.23	22.18
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b_8	$y{++}_{14}$	y_8	$b{++}_{17}$	y_9	b_{10}	$b{++}_{19}$	$y{++}_{19}$	y_{10}	$y{++}_{20}$	$y{++}_{20}$	$b{++}_{22}$
Delta Da	0.23	0.47	0.18	0.44	0.01	0.25	0.07	0.58	-0.03	0.27	0.57	-0.20 b_{11}-H_2O -0.66 y_{11} 0.27

Peak 54



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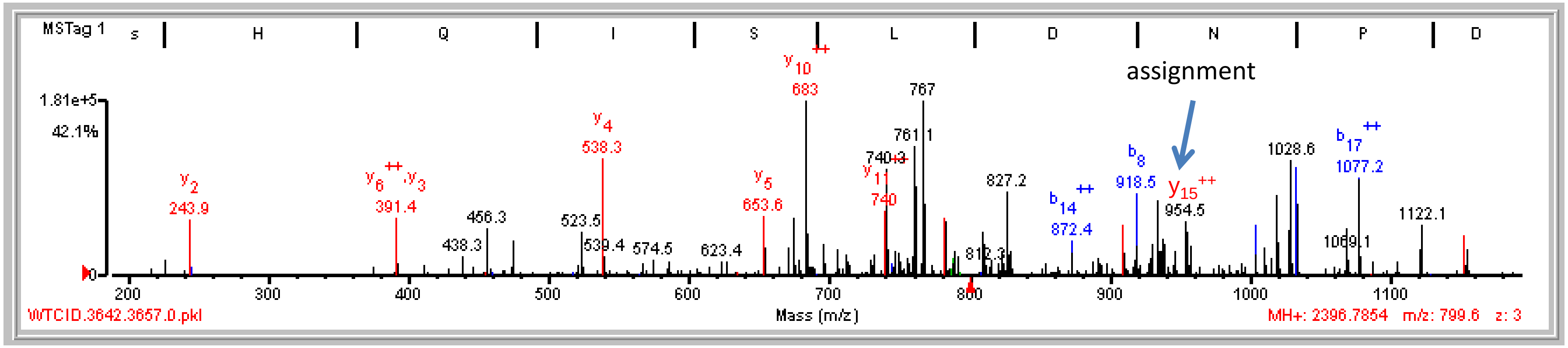

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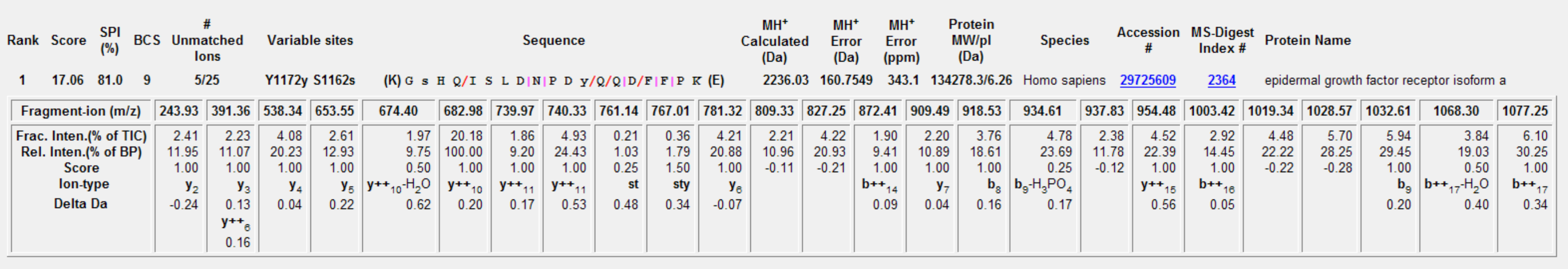


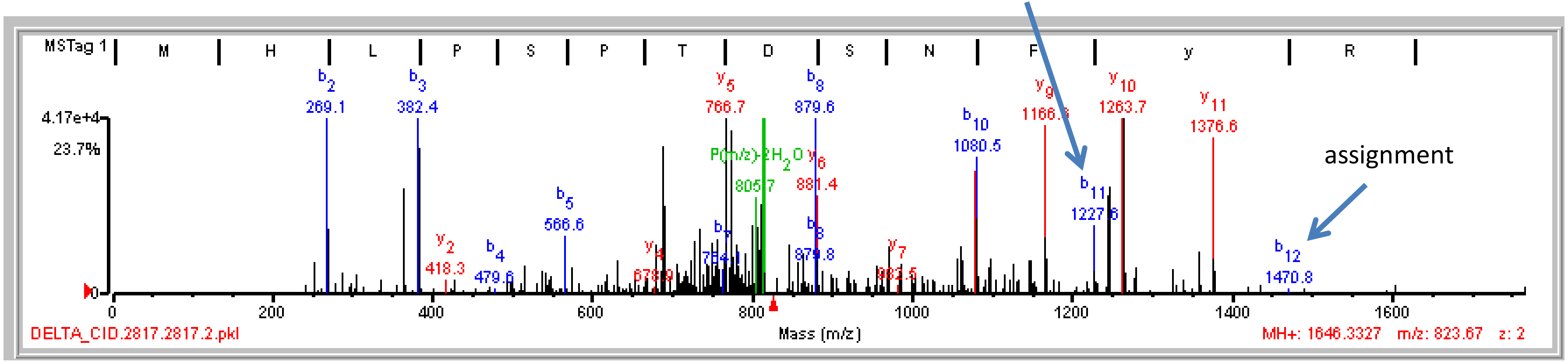
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.06	81.0	9	5/25	Y1172y S1162s	(K) G s H Q/I S L D|N|P D y/Q/Q|D/F|F|P K (E)	2236.03	160.7549	343.1	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

Fragment-ion (m/z)	243.93	391.36	538.34	653.55	674.40	682.98	739.97	740.33	761.14	767.01	781.32	809.33	827.25
Frac. Inten.(% of TIC)	2.41	2.23	4.08	2.61	1.97	20.18	1.86	4.93	0.21	0.36	4.21	2.21	4.22
Rel. Inten.(% of BP)	11.95	11.07	20.23	12.93	9.75	100.00	9.20	24.43	1.03	1.79	20.88	10.96	20.93
Score	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	0.25	1.50	1.00	-0.11	-0.21
Ion-type	y_2	y_3 $y{++}_6$	y_4	y_5	$y{++}_{10}$-H_2O	$y{++}_{10}$	$y{++}_{11}$	$y{++}_{11}$	st	sty	y_6		
Delta Da	-0.24	0.13 0.16	0.04	0.22	0.62	0.20	0.17	0.53	0.48	0.34	-0.07		

Fragment-ion (m/z)	872.41	909.49	918.53	934.61	937.83	954.48	1003.42	1019.34	1028.57	1032.61	1068.30	1077.25
Frac. Inten.(% of TIC)	1.90	2.20	3.76	4.78	2.38	4.52	2.92	4.48	5.70	5.94	3.84	6.10
Rel. Inten.(% of BP)	9.41	10.89	18.61	23.69	11.78	22.39	14.45	22.22	28.25	29.45	19.03	30.25
Score	1.00	1.00	1.00	0.25	-0.12	1.00	1.00	-0.22	-0.28	1.00	0.50	1.00
Ion-type	$b{++}_{14}$	y_7	b_8	b_9-H_3PO_4		$y{++}_{15}$	$b{++}_{16}$			b_9	$b{++}_{17}$-H_2O	$b{++}_{17}$
Delta Da	0.09	0.04	0.16	0.17		0.56	0.05			0.20	0.40	0.34

Peak 55

Ions that verify assignment



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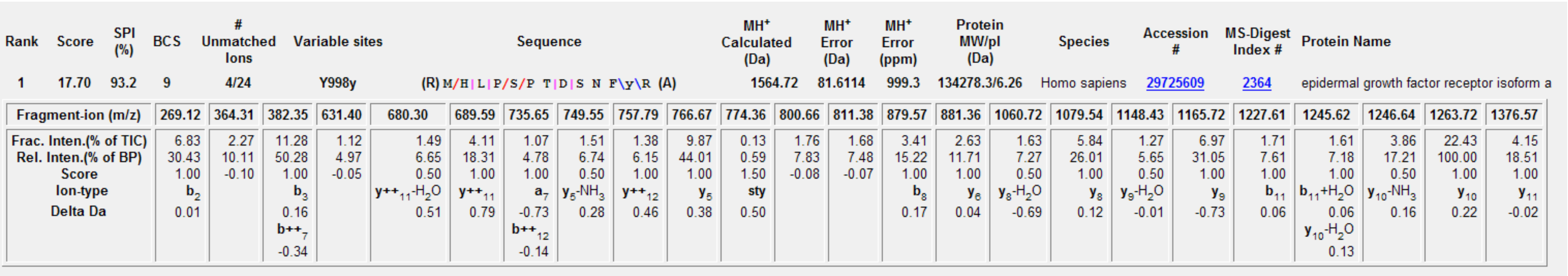


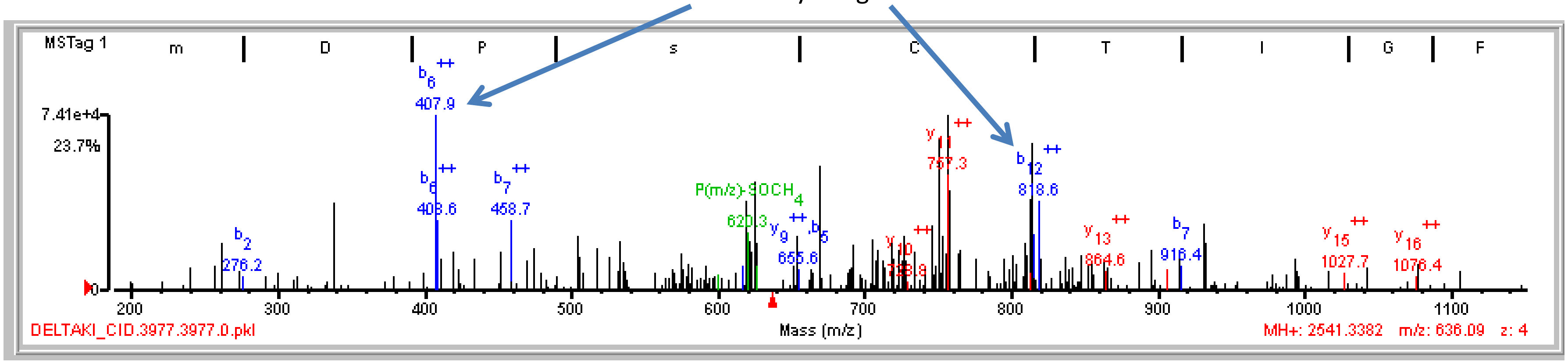
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.70	93.2	9	4/24	Y998y	(R) M/H|L|P/S/P T|D|S N F\y\R (A)	1564.72	81.6114	999.3	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

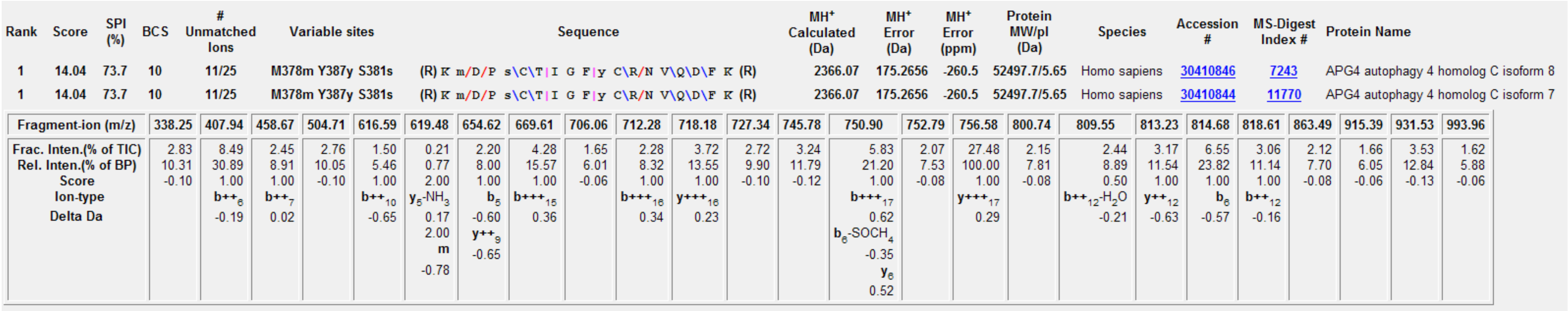
Fragment-ion (m/z)	269.12	364.31	382.35	631.40	680.30	689.59	735.65	749.55	757.79	766.67	774.36	800.66	811.38
Frac. Inten.(% of TIC)	6.83	2.27	11.28	1.12	1.49	4.11	1.07	1.51	1.38	9.87	0.13	1.76	1.68
Rel. Inten.(% of BP)	30.43	10.11	50.28	4.97	6.65	18.31	4.78	6.74	6.15	44.01	0.59	7.83	7.48
Score	1.00	-0.10	1.00	-0.05	0.50	1.00	1.00	0.50	1.00	1.00	1.50	-0.08	-0.07
Ion-type	b_2		b_3		$y{++}_{11}$-H_2O	$y{++}_{11}$	a_7	y_5-NH_3	$y{++}_{12}$	y_5	sty		
Delta Da	0.01		0.16		0.51	0.79	-0.73	0.28	0.46	0.38	0.50		
			$b{++}_7$				$b{++}_{12}$						
			-0.34				-0.14						

Fragment-ion (m/z)	879.57	881.36	1060.72	1079.54	1148.43	1165.72	1227.61	1245.62	1246.64	1263.72	1376.57
Frac. Inten.(% of TIC)	3.41	2.63	1.63	5.84	1.27	6.97	1.71	1.61	3.86	22.43	4.15
Rel. Inten.(% of BP)	15.22	11.71	7.27	26.01	5.65	31.05	7.61	7.18	17.21	100.00	18.51
Score	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	b_8	y_6	y_8-H_2O	y_8	y_9-H_2O	y_9	b_{11}	b_{11}+H_2O	y_{10}-NH_3	y_{10}	y_{11}
Delta Da	0.17	0.04	-0.69	0.12	-0.01	-0.73	0.06	0.06	0.16	0.22	-0.02
								y_{10}-H_2O			
								0.13			

Peak 57

Ions that verify assignment

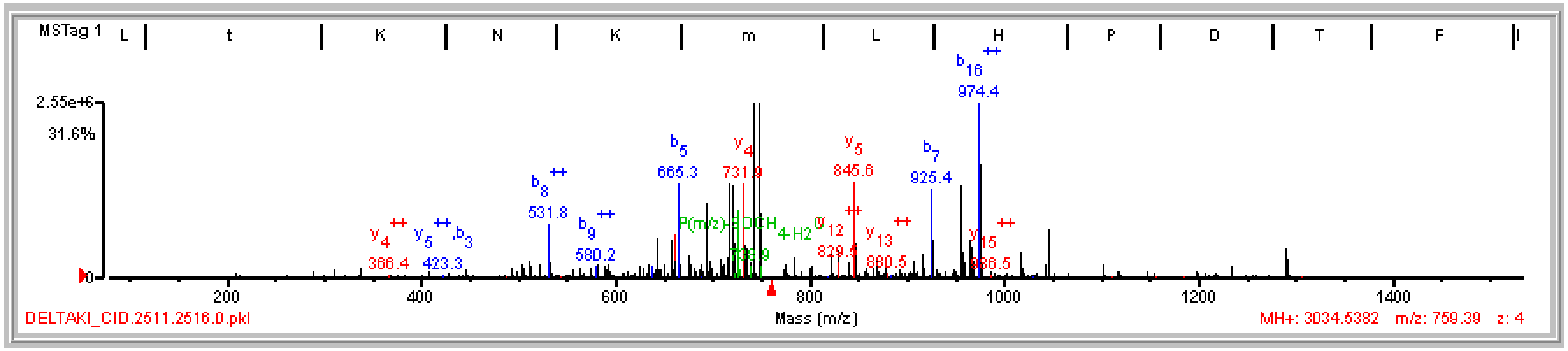


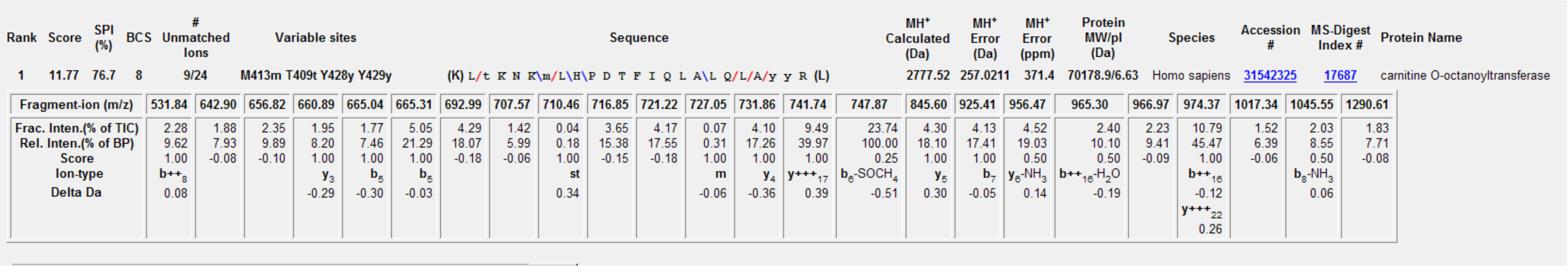


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.04	73.7	10	11/25	M378m Y387y S381s	(R) K m/D/P s\C\T|I G F|y C\R/N V\Q\D\F K (R)	2366.07	175.2656	-260.5	52497.7/5.65	Homo sapiens	30410846	7243	APG4 autophagy 4 homolog C isoform 8
1	14.04	73.7	10	11/25	M378m Y387y S381s	(R) K m/D/P s\C\T|I G F|y C\R/N V\Q\D\F K (R)	2366.07	175.2656	-260.5	52497.7/5.65	Homo sapiens	30410844	11770	APG4 autophagy 4 homolog C isoform 7

Fragment-ion (m/z)	338.25	407.94	458.67	504.71	616.59	619.48	654.62	669.61	706.06	712.28	718.18	727.34	745.78	750.90	752.79	756.58	800.74	809.55	813.23	814.68	818.61	863.49	915.39	931.53	993.96
Frac. Inten.(% of TIC)	2.83	8.49	2.45	2.76	1.50	0.21	2.20	4.28	1.65	2.28	3.72	2.72	3.24	5.83	2.07	27.48	2.15	2.44	3.17	6.55	3.06	2.12	1.66	3.53	1.62
Rel. Inten.(% of BP)	10.31	30.89	8.91	10.05	5.46	0.77	8.00	15.57	6.01	8.32	13.55	9.90	11.79	21.20	7.53	100.00	7.81	8.89	11.54	23.82	11.14	7.70	6.05	12.84	5.88
Score	-0.10	1.00	1.00	-0.10	1.00	2.00 2.00	1.00	1.00	-0.06	1.00	1.00	-0.10	-0.12	1.00	-0.08	1.00	-0.08	0.50	1.00	1.00	1.00	-0.08	-0.06	-0.13	-0.06
Ion-type		$b{++}_6$	$b{++}_7$		$b{++}_{10}$	y_5-NH_3 m	b_5 $y{++}_9$	$b{+++}_{15}$		$b{+++}_{16}$	$y{+++}_{16}$			$b{+++}_{17}$ b_6-$SOCH_4$ y_6		$y{+++}_{17}$		$b{++}_{12}$-H_2O	$y{++}_{12}$	b_6	$b{++}_{12}$				
Delta Da		-0.19	0.02		-0.65	0.17 -0.78	-0.60 -0.65	0.36		0.34	0.23			0.62 -0.35 0.52		0.29		-0.21	-0.63	-0.57	-0.16				

Peak 58

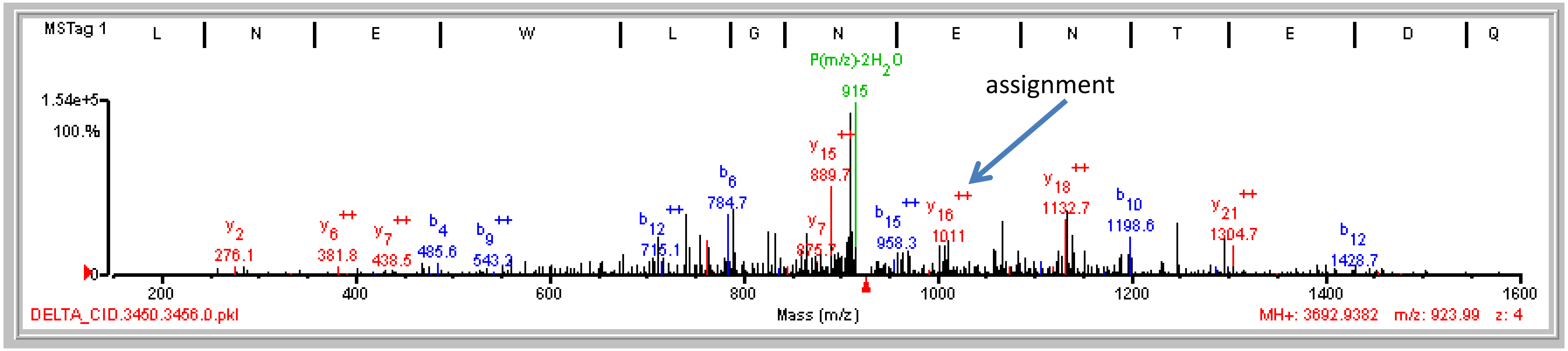




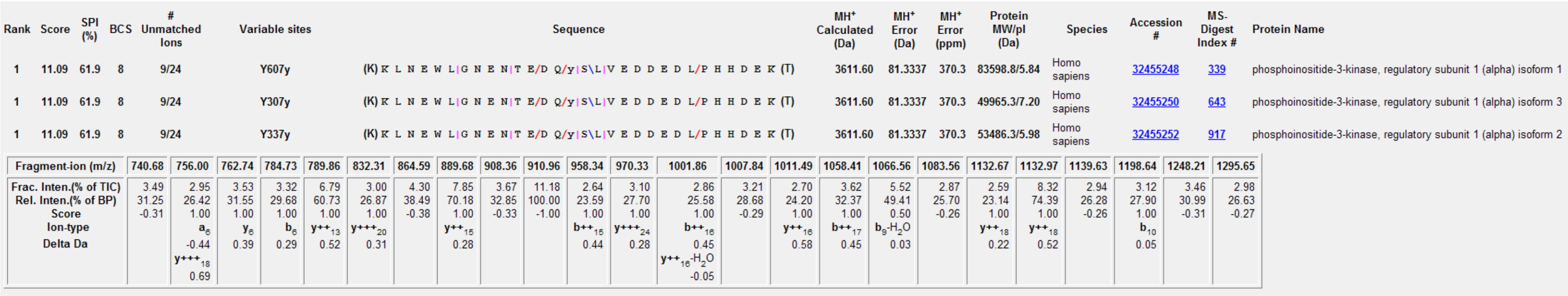
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.77	76.7	8	9/24	M413m T409t Y428y Y429y	(K) L/t K N K\m/L\H\P D T F I Q L A\L Q/L/A/y y R (L)	2777.52	257.0211	371.4	70178.9/6.63	Homo sapiens	31542325	17687	carnitine O-octanoyltransferase

Fragment-ion (m/z)	531.84	642.90	656.82	660.89	665.04	665.31	692.99	707.57	710.46	716.85	721.22	727.05	731.86	741.74	747.87	845.60	925.41	956.47	965.30	966.97	974.37	1017.34	1045.55	1290.61
Frac. Inten.(% of TIC)	2.28	1.88	2.35	1.95	1.77	5.05	4.29	1.42	0.04	3.65	4.17	0.07	4.10	9.49	23.74	4.30	4.13	4.52	2.40	2.23	10.79	1.52	2.03	1.83
Rel. Inten.(% of BP)	9.62	7.93	9.89	8.20	7.46	21.29	18.07	5.99	0.18	15.38	17.55	0.31	17.26	39.97	100.00	18.10	17.41	19.03	10.10	9.41	45.47	6.39	8.55	7.71
Score	1.00	-0.08	-0.10	1.00	1.00	1.00	-0.18	-0.06	1.00	-0.15	-0.18	1.00	1.00	1.00	0.25	1.00	1.00	0.50	0.50	-0.09	1.00	-0.06	0.50	-0.08
Ion-type	$b{+}{+}_8$			y_3	b_5	b_5			st			m	y_4	$y{+}{+}{+}_{17}$	b_6-$SOCH_4$	y_5	b_7	y_6-NH_3	$b{+}{+}_{16}$-H_2O		$b{+}{+}_{16}$ $y{+}{+}{+}_{22}$		b_8-NH_3	
Delta Da	0.08			-0.29	-0.30	-0.03			0.34			-0.06	-0.36	0.39	-0.51	0.30	-0.05	0.14	-0.19		-0.12 0.26		0.06	

Peak 59



assignment

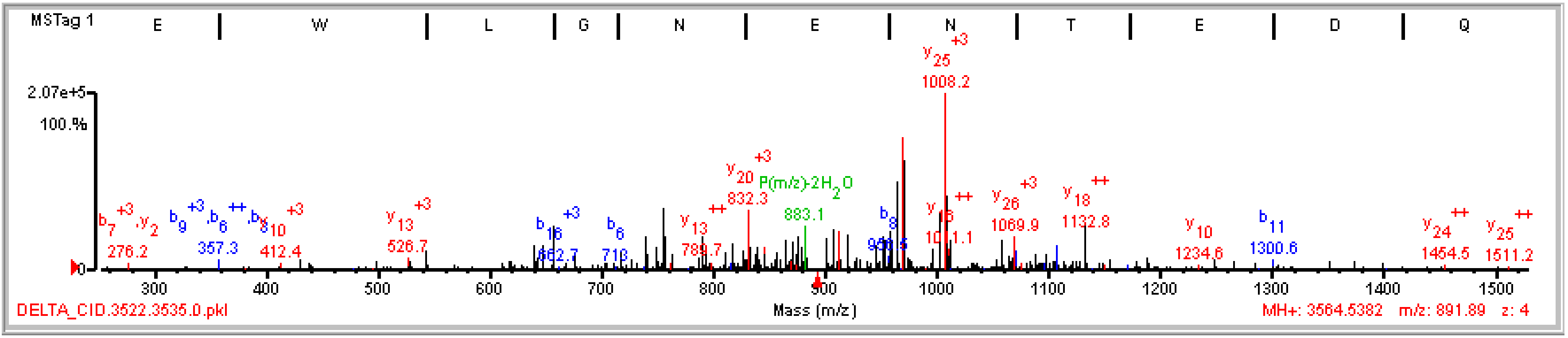


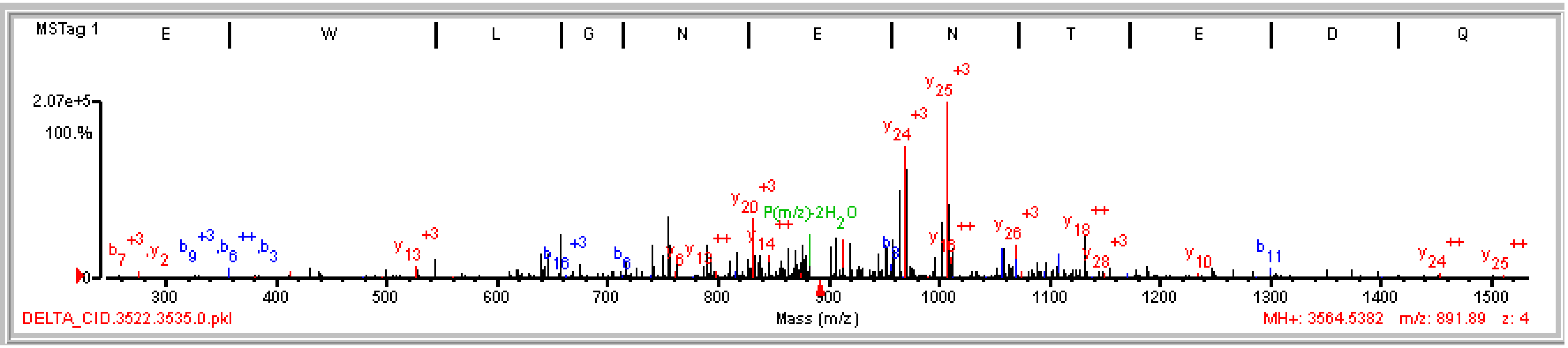
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.09	61.9	8	9/24	Y607y	(K) K L N E W L|G N E N|T E/D Q/y|S\L|V E D D E D L/P H H D E K (T)	3611.60	81.3337	370.3	83598.8/5.84	Homo sapiens	32455248	339	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 1
1	11.09	61.9	8	9/24	Y307y	(K) K L N E W L|G N E N|T E/D Q/y|S\L|V E D D E D L/P H H D E K (T)	3611.60	81.3337	370.3	49965.3/7.20	Homo sapiens	32455250	643	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 3
1	11.09	61.9	8	9/24	Y337y	(K) K L N E W L|G N E N|T E/D Q/y|S\L|V E D D E D L/P H H D E K (T)	3611.60	81.3337	370.3	53486.3/5.98	Homo sapiens	32455252	917	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 2

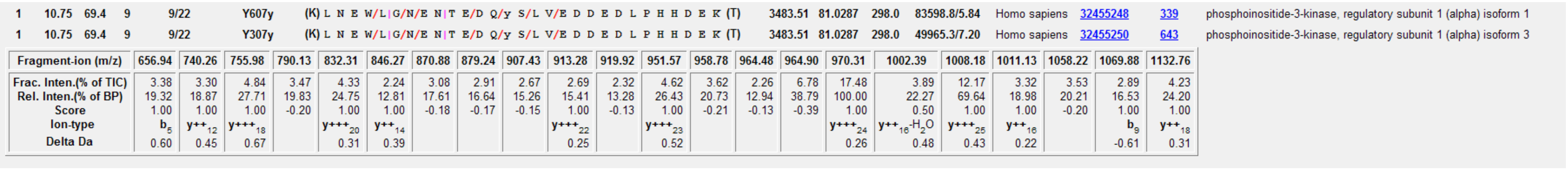
Fragment-ion (m/z)	740.68	756.00	762.74	784.73	789.86	832.31	864.59	889.68	908.36	910.96	958.34	970.33	1001.86
Frac. Inten.(% of TIC)	3.49	2.95	3.53	3.32	6.79	3.00	4.30	7.85	3.67	11.18	2.64	3.10	2.86
Rel. Inten.(% of BP)	31.25	26.42	31.55	29.68	60.73	26.87	38.49	70.18	32.85	100.00	23.59	27.70	25.58
Score	-0.31	1.00	1.00	1.00	1.00	1.00	-0.38	1.00	-0.33	-1.00	1.00	1.00	1.00
Ion-type		a_6	y_6	b_6	$y{+}{+}_{13}$	$y{+}{+}{+}_{20}$		$y{+}{+}_{15}$			$b{+}{+}_{15}$	$y{+}{+}{+}_{24}$	$b{+}{+}_{16}$
Delta Da		-0.44	0.39	0.29	0.52	0.31		0.28			0.44	0.28	0.45
		$y{+}{+}{+}_{18}$ 0.69											$y{+}{+}_{16}$-H_2O -0.05

Fragment-ion (m/z)	1007.84	1011.49	1058.41	1066.56	1083.56	1132.67	1132.97	1139.63	1198.64	1248.21	1295.65
Frac. Inten.(% of TIC)	3.21	2.70	3.62	5.52	2.87	2.59	8.32	2.94	3.12	3.46	2.98
Rel. Inten.(% of BP)	28.68	24.20	32.37	49.41	25.70	23.14	74.39	26.28	27.90	30.99	26.63
Score	-0.29	1.00	1.00	0.50	-0.26	1.00	1.00	-0.26	1.00	-0.31	-0.27
Ion-type		$y{+}{+}_{16}$	$b{+}{+}_{17}$	b_9-H_2O		$y{+}{+}_{18}$	$y{+}{+}_{18}$		b_{10}		
Delta Da		0.58	0.45	0.03		0.22	0.52		0.05		

Peak 60





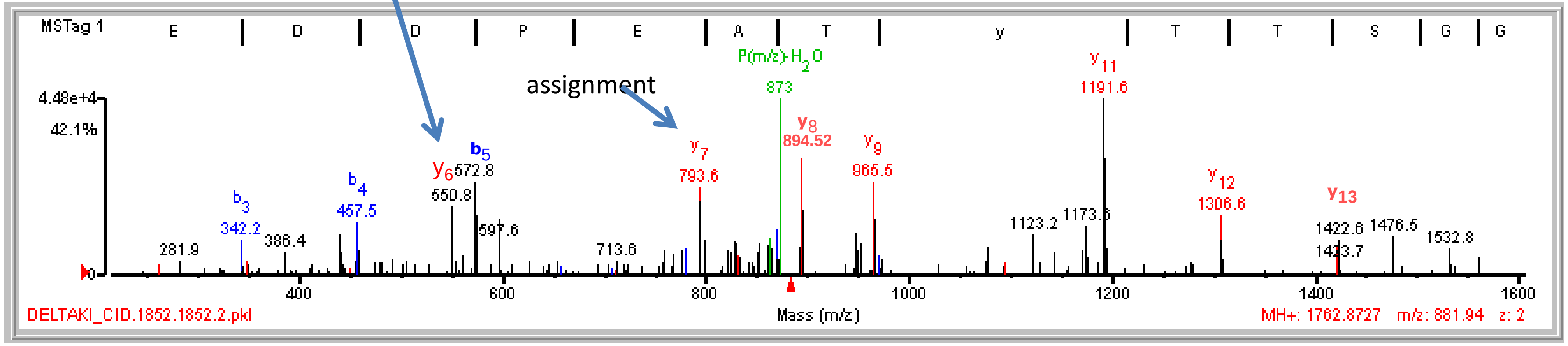


1	10.75	69.4	9	9/22	Y607y	(K) L N E W/L|G/N/E N|T E/D Q/y S/L V/E D D E D L P H H D E K (T)	3483.51	81.0287	298.0	83598.8/5.84	Homo sapiens	32455248	339	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 1
1	10.75	69.4	9	9/22	Y307y	(K) L N E W/L|G/N/E N|T E/D Q/y S/L V/E D D E D L P H H D E K (T)	3483.51	81.0287	298.0	49965.3/7.20	Homo sapiens	32455250	643	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 3

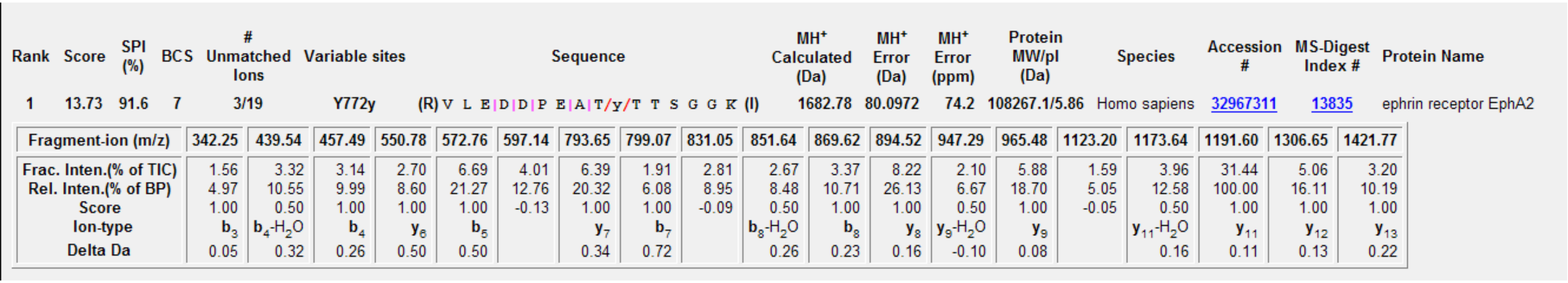
Fragment-ion (m/z)	656.94	740.26	755.98	790.13	832.31	846.27	870.88	879.24	907.43	913.28	919.92	951.57	958.78	964.48	964.90	970.31	1002.39	1008.18	1011.13	1058.22	1069.88	1132.76
Frac. Inten.(% of TIC)	3.38	3.30	4.84	3.47	4.33	2.24	3.08	2.91	2.67	2.69	2.32	4.62	3.62	2.26	6.78	17.48	3.89	12.17	3.32	3.53	2.89	4.23
Rel. Inten.(% of BP)	19.32	18.87	27.71	19.83	24.75	12.81	17.61	16.64	15.26	15.41	13.28	26.43	20.73	12.94	38.79	100.00	22.27	69.64	18.98	20.21	16.53	24.20
Score	1.00	1.00	1.00	-0.20	1.00	1.00	-0.18	-0.17	-0.15	1.00	-0.13	1.00	-0.21	-0.13	-0.39	1.00	0.50	1.00	1.00	-0.20	1.00	1.00
Ion-type	b_5	y++_{12}	y+++_{18}		y+++_{20}	y++_{14}				y+++_{22}		y+++_{23}				y+++_{24}	$\text{y++}_{16}\text{-H}_2\text{O}$	y+++_{25}	y++_{16}		b_9	y++_{18}
Delta Da	0.60	0.45	0.67		0.31	0.39				0.25		0.52				0.26	0.48	0.43	0.22		-0.61	0.31

Peak 61

Ions that verify assignment



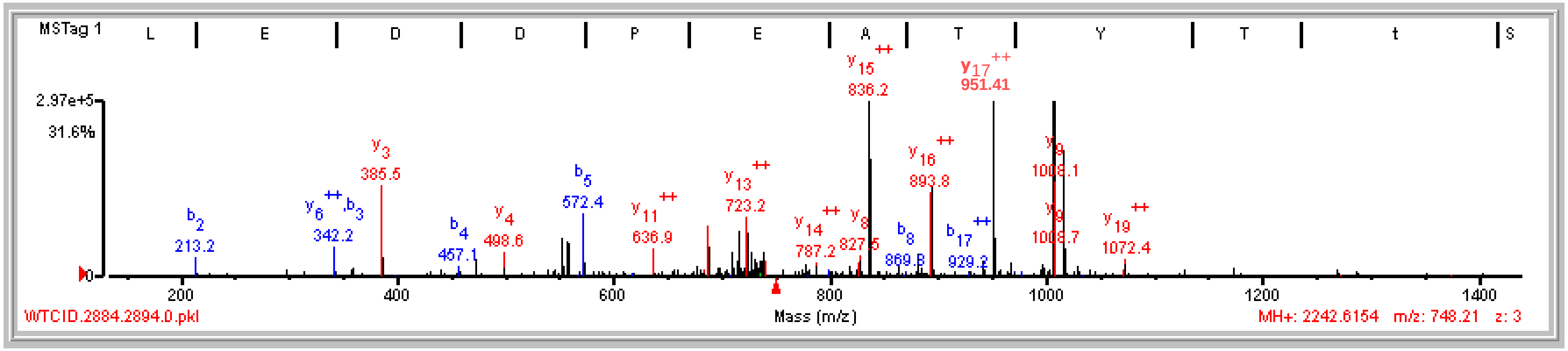
assignment

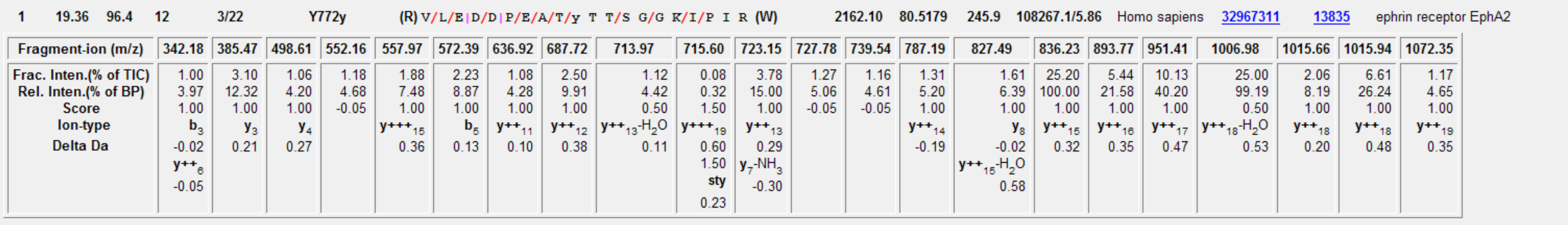


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.73	91.6	7	3/19	Y772y	(R) V L E|D|D|P E|A|T/y/T T S G G K (I)	1682.78	80.0972	74.2	108267.1/5.86	Homo sapiens	32967311	13835	ephrin receptor EphA2

Fragment-ion (m/z)	342.25	439.54	457.49	550.78	572.76	597.14	793.65	799.07	831.05	851.64	869.62	894.52	947.29	965.48	1123.20	1173.64	1191.60	1306.65	1421.77
Frac. Inten.(% of TIC)	1.56	3.32	3.14	2.70	6.69	4.01	6.39	1.91	2.81	2.67	3.37	8.22	2.10	5.88	1.59	3.96	31.44	5.06	3.20
Rel. Inten.(% of BP)	4.97	10.55	9.99	8.60	21.27	12.76	20.32	6.08	8.95	8.48	10.71	26.13	6.67	18.70	5.05	12.58	100.00	16.11	10.19
Score	1.00	0.50	1.00	1.00	1.00	-0.13	1.00	1.00	-0.09	0.50	1.00	1.00	0.50	1.00	-0.05	0.50	1.00	1.00	1.00
Ion-type	b_3	b_4-H_2O	b_4	y_6	b_5		y_7	b_7		b_8-H_2O	b_8	y_8	y_9-H_2O	y_9		y_{11}-H_2O	y_{11}	y_{12}	y_{13}
Delta Da	0.05	0.32	0.26	0.50	0.50		0.34	0.72		0.26	0.23	0.16	-0.10	0.08		0.16	0.11	0.13	0.22

Peak 62

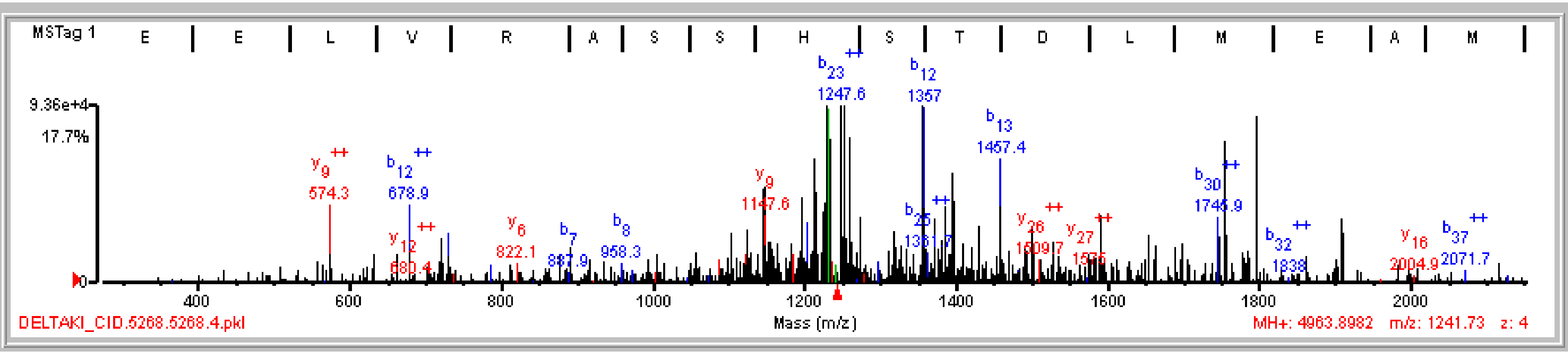


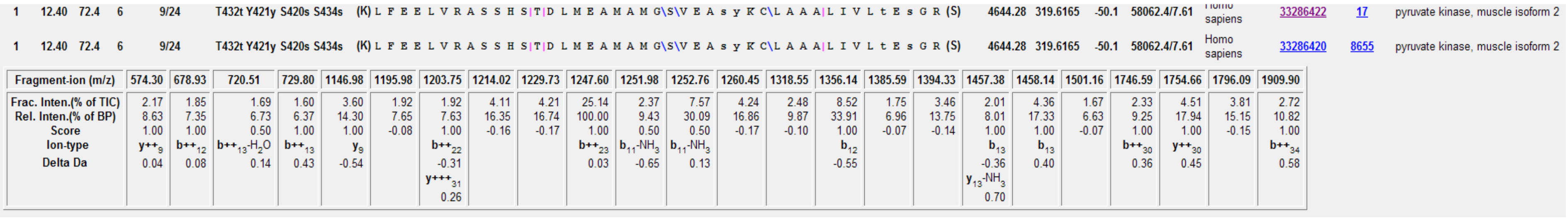


1 19.36 96.4 12 3/22 Y772y (R) V/L/E|D/D|P/E/A/T/y T T/S G/G K/I/P I R (W) 2162.10 80.5179 245.9 108267.1/5.86 Homo sapiens 32967311 13835 ephrin receptor EphA2

Fragment-ion (m/z)	342.18	385.47	498.61	552.16	557.97	572.39	636.92	687.72	713.97	715.60	723.15	727.78	739.54	787.19	827.49	836.23	893.77	951.41	1006.98	1015.66	1015.94	1072.35
Frac. Inten.(% of TIC)	1.00	3.10	1.06	1.18	1.88	2.23	1.08	2.50	1.12	0.08	3.78	1.27	1.16	1.31	1.61	25.20	5.44	10.13	25.00	2.06	6.61	1.17
Rel. Inten.(% of BP)	3.97	12.32	4.20	4.68	7.48	8.87	4.28	9.91	4.42	0.32	15.00	5.06	4.61	5.20	6.39	100.00	21.58	40.20	99.19	8.19	26.24	4.65
Score	1.00	1.00	1.00	-0.05	1.00	1.00	1.00	1.00	0.50	1.50	1.00	-0.05	-0.05	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type	b_3	y_3	y_4		$y+++_{15}$	b_5	$y++_{11}$	$y++_{12}$	$y++_{13}\text{-}H_2O$	$y+++_{19}$	$y++_{13}$			$y++_{14}$	y_8	$y++_{15}$	$y++_{16}$	$y++_{17}$	$y++_{18}\text{-}H_2O$	$y++_{18}$	$y++_{18}$	$y++_{19}$
Delta Da	-0.02	0.21	0.27		0.36	0.13	0.10	0.38	0.11	0.60	0.29			-0.19	-0.02	0.32	0.35	0.47	0.53	0.20	0.48	0.35
	$y++_{6}$									1.50	$y_7\text{-}NH_3$				$y++_{15}\text{-}H_2O$							
	-0.05									sty	-0.30				0.58							
										0.23												

Peak 63



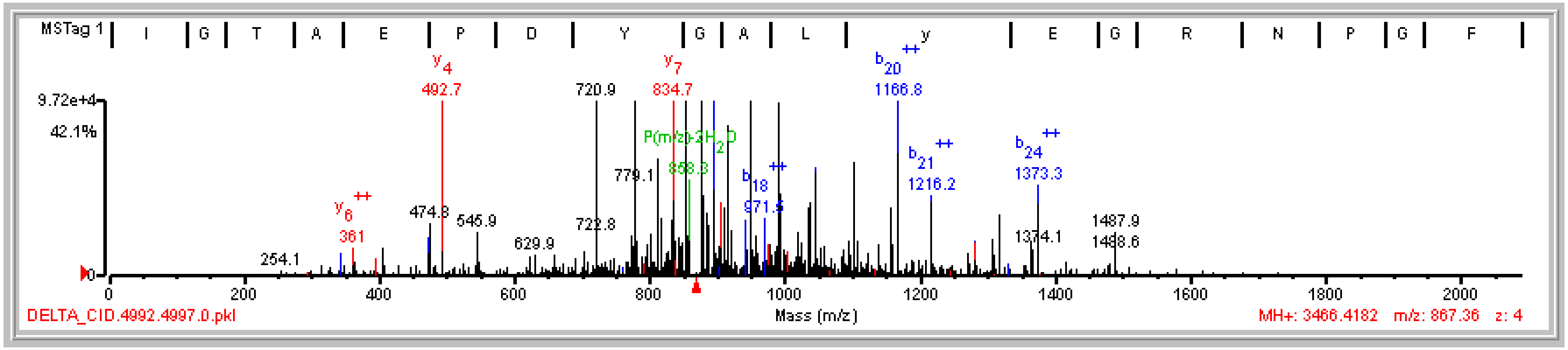


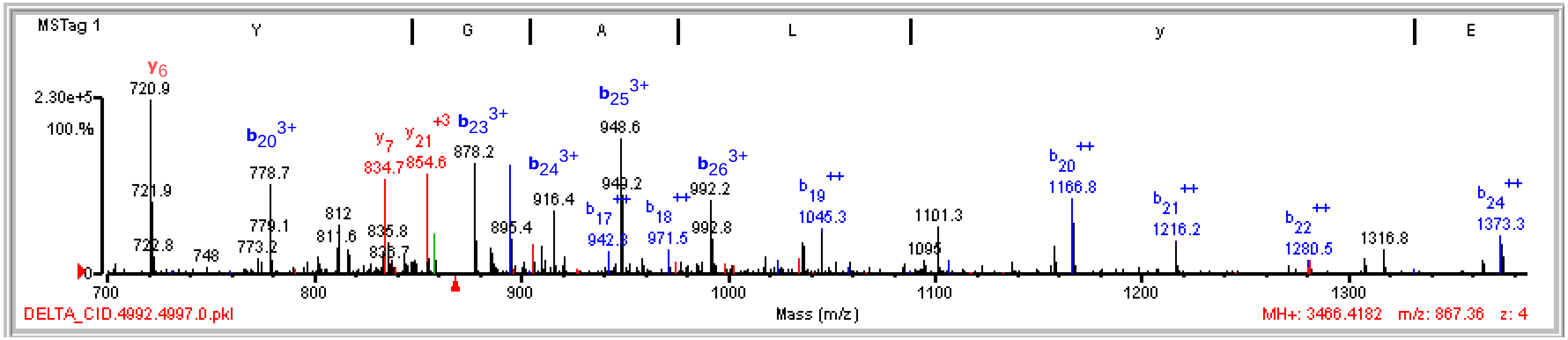
1	12.40	72.4	6	9/24	T432t Y421y S420s S434s	(K) L F E E L V R A S S H S|T|D L M E A M A M G\S\V E A s y K C\L A A A|L I V L t E s G R (S)	4644.28	319.6165	-50.1	58062.4/7.61	Homo sapiens	33286422	17	pyruvate kinase, muscle isoform 2
1	12.40	72.4	6	9/24	T432t Y421y S420s S434s	(K) L F E E L V R A S S H S|T|D L M E A M A M G\S\V E A s y K C\L A A A|L I V L t E s G R (S)	4644.28	319.6165	-50.1	58062.4/7.61	Homo sapiens	33286420	8655	pyruvate kinase, muscle isoform 2

Fragment-ion (m/z)	574.30	678.93	720.51	729.80	1146.98	1195.98	1203.75	1214.02	1229.73	1247.60	1251.98	1252.76
Frac. Inten.(% of TIC)	2.17	1.85	1.69	1.60	3.60	1.92	1.92	4.11	4.21	25.14	2.37	7.57
Rel. Inten.(% of BP)	8.63	7.35	6.73	6.37	14.30	7.65	7.63	16.35	16.74	100.00	9.43	30.09
Score	1.00	1.00	0.50	1.00	1.00	-0.08	1.00	-0.16	-0.17	1.00	0.50	0.50
Ion-type	$y++_{9}$	$b++_{12}$	$b++_{13}\text{-}H_2O$	$b++_{13}$	y_{9}		$b++_{22}$ $y+++_{31}$			$b++_{23}$	$b_{11}\text{-}NH_3$	$b_{11}\text{-}NH_3$
Delta Da	0.04	0.08	0.14	0.43	-0.54		-0.31 0.26			0.03	-0.65	0.13

Fragment-ion (m/z)	1260.45	1318.55	1356.14	1385.59	1394.33	1457.38	1458.14	1501.16	1746.59	1754.66	1796.09	1909.90
Frac. Inten.(% of TIC)	4.24	2.48	8.52	1.75	3.46	2.01	4.36	1.67	2.33	4.51	3.81	2.72
Rel. Inten.(% of BP)	16.86	9.87	33.91	6.96	13.75	8.01	17.33	6.63	9.25	17.94	15.15	10.82
Score	-0.17	-0.10	1.00	-0.07	-0.14	1.00	1.00	-0.07	1.00	1.00	-0.15	1.00
Ion-type			b_{12}			b_{13} $y_{13}\text{-}NH_3$	b_{13}		$b++_{30}$	$y++_{30}$		$b++_{34}$
Delta Da			-0.55			-0.36 0.70	0.40		0.36	0.45		0.58

Peak 64



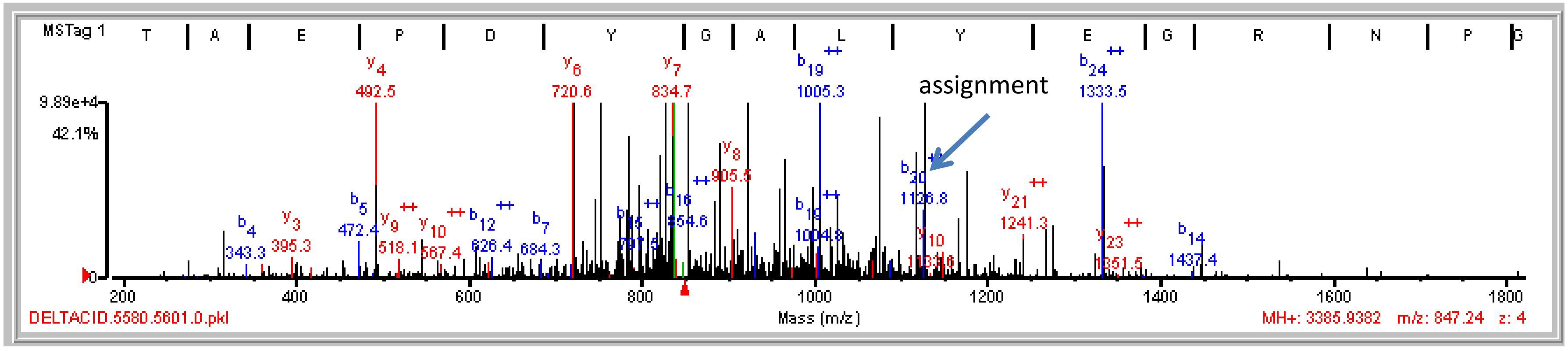


1 19.68 91.7 9 3/25 Y771y Y783y (K) I G T A E P D y G A L Y E G R N\P G F\y\V\E|A|N|P\M|P T F K (C) 3304.56 161.8562 554.9 148532.9/5.73 Homo sapiens 33598946 14027 phospholipase C gamma 1 isoform b

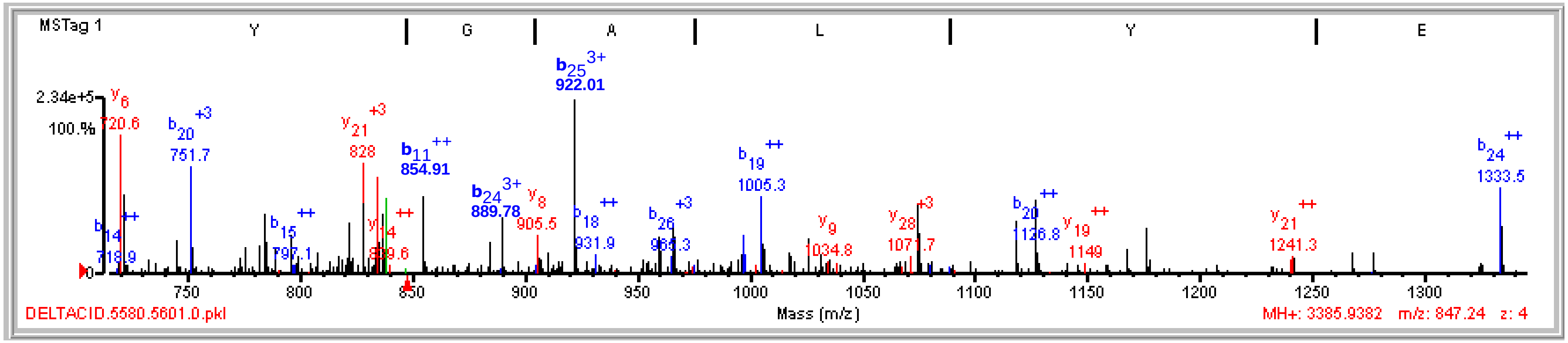
Fragment-ion (m/z)	492.70	720.89	778.71	812.01	816.51	834.74	843.63	854.55	878.16	886.15	894.80	905.55
Frac. Inten.(% of TIC)	4.52	10.14	5.36	2.31	2.60	5.44	0.05	5.44	5.73	2.02	6.57	2.01
Rel. Inten.(% of BP)	44.64	100.00	52.84	22.77	25.67	53.62	0.49	53.63	56.55	19.97	64.80	19.86
Score	1.00	1.00	1.00	-0.23	0.50	1.00	1.50	1.00	1.00	0.50	1.00	1.00
Ion-type	y_4	y_6	$b{+}{+}{+}_{20}$		y_7-H_2O	y_7	sty	$b{+}{+}{+}_{22}$	$b{+}{+}{+}_{23}$	$b{+}{+}_{16}$-H_2O	$b{+}{+}_{16}$	y_8
Delta Da	0.42	0.52	0.73		0.10	0.32	1.25	0.53	0.46	0.77	0.41	0.10

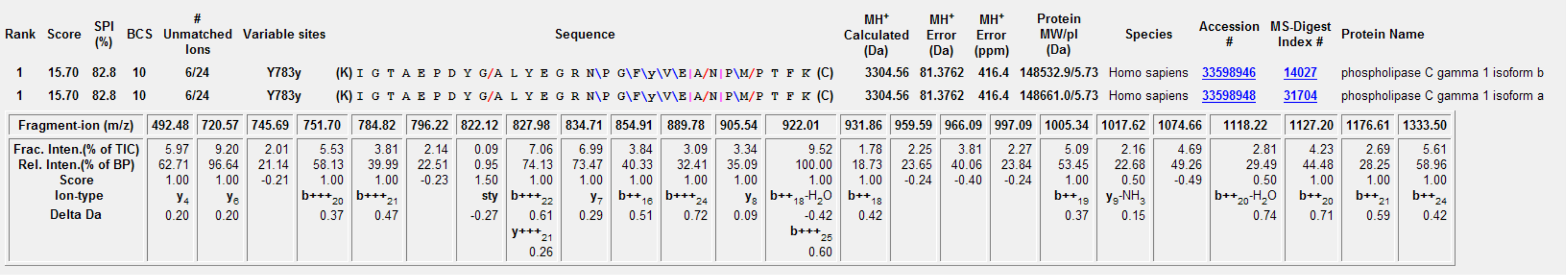
Fragment-ion (m/z)	910.51	916.45	948.64	992.19	1036.52	1045.34	1101.28	1157.78	1166.75	1216.20	1280.53	1316.79	1373.30
Frac. Inten.(% of TIC)	1.93	2.77	9.44	5.22	2.63	3.30	4.08	2.05	5.62	3.19	1.83	1.65	4.10
Rel. Inten.(% of BP)	19.07	27.31	93.15	51.51	25.97	32.61	40.21	20.23	55.41	31.45	18.09	16.30	40.41
Score	-0.19	1.00	1.00	1.00	0.50	1.00	-0.40	0.50	1.00	1.00	1.00	1.00	1.00
Ion-type		$b{+}{+}{+}_{24}$	$b{+}{+}{+}_{25}$	$b{+}{+}{+}_{26}$	$b{+}{+}_{19}$-H_2O	$b{+}{+}_{19}$		$b{+}{+}_{20}$-H_2O	$b{+}{+}_{20}$	$b{+}{+}_{21}$	$b{+}{+}_{22}$	$b{+}{+}_{23}$	$b{+}{+}_{24}$
Delta Da		0.74	0.58	0.45	0.57	0.38		0.31	0.28	0.19	0.00	0.74	0.23

Peak 65



assignment

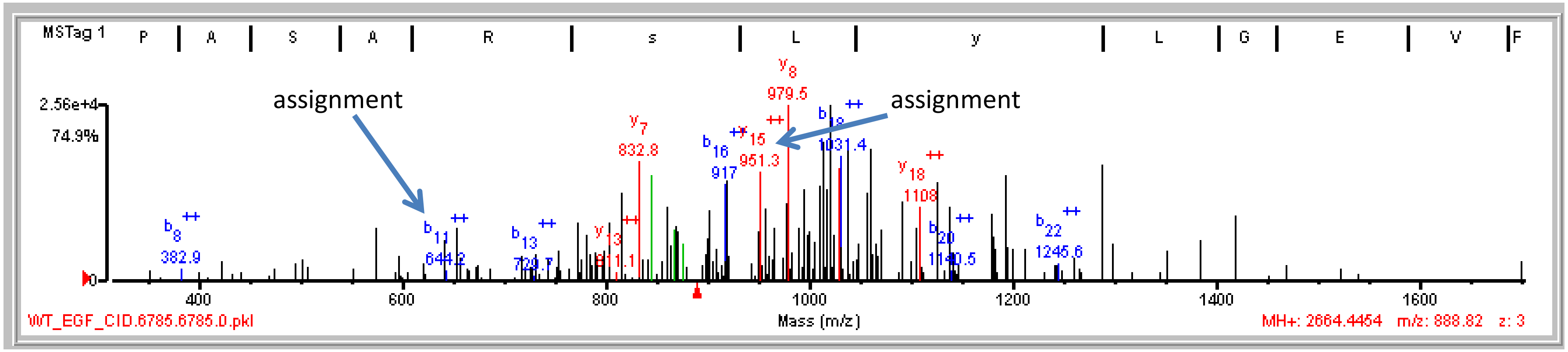




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.70	82.8	10	6/24	Y783y	(K) I G T A E P D Y G/A L Y E G R N\P G\F\y\V\E|A/N|P\M/P T F K (C)	3304.56	81.3762	416.4	148532.9/5.73	Homo sapiens	33598946	14027	phospholipase C gamma 1 isoform b
1	15.70	82.8	10	6/24	Y783y	(K) I G T A E P D Y G/A L Y E G R N\P G\F\y\V\E|A/N|P\M/P T F K (C)	3304.56	81.3762	416.4	148661.0/5.73	Homo sapiens	33598948	31704	phospholipase C gamma 1 isoform a

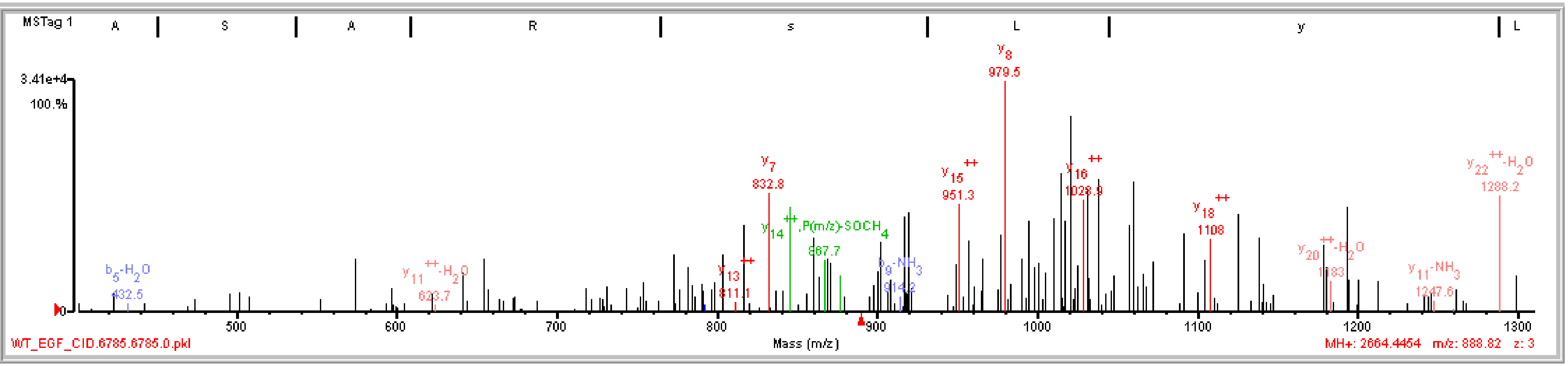
Fragment-ion (m/z)	492.48	720.57	745.69	751.70	784.82	796.22	822.12	827.98	834.71	854.91	889.78	905.54	922.01	931.86	959.59	966.09	997.09	1005.34	1017.62	1074.66	1118.22	1127.20	1176.61	1333.50
Frac. Inten.(% of TIC)	5.97	9.20	2.01	5.53	3.81	2.14	0.09	7.06	6.99	3.84	3.09	3.34	9.52	1.78	2.25	3.81	2.27	5.09	2.16	4.69	2.81	4.23	2.69	5.61
Rel. Inten.(% of BP)	62.71	96.64	21.14	58.13	39.99	22.51	0.95	74.13	73.47	40.33	32.41	35.09	100.00	18.73	23.65	40.06	23.84	53.45	22.68	49.26	29.49	44.48	28.25	58.96
Score	1.00	1.00	-0.21	1.00	1.00	-0.23	1.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.24	-0.40	-0.24	1.00	0.50	-0.49	0.50	1.00	1.00	1.00
Ion-type	y_4	y_6		b+++$_{20}$	b+++$_{21}$		sty	b+++$_{22}$ y+++$_{21}$	y_7	b++$_{16}$	b+++$_{24}$	y_8	b++$_{18}$-H_2O b+++$_{25}$	b++$_{18}$				b++$_{19}$	y_9-NH_3		b++$_{20}$-H_2O	b++$_{20}$	b++$_{21}$	b++$_{24}$
Delta Da	0.20	0.20		0.37	0.47		-0.27	0.61 0.26	0.29	0.51	0.72	0.09	-0.42 0.60	0.42				0.37	0.15		0.74	0.71	0.59	0.42

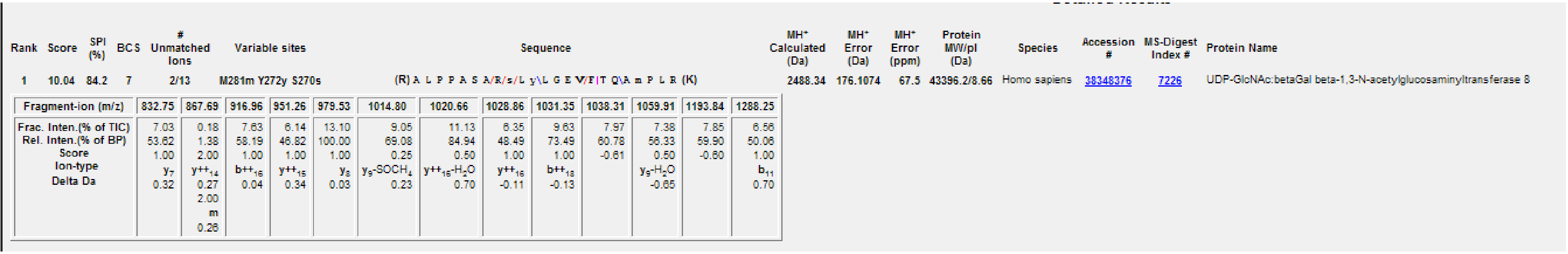
Peak 66



assignment

assignment

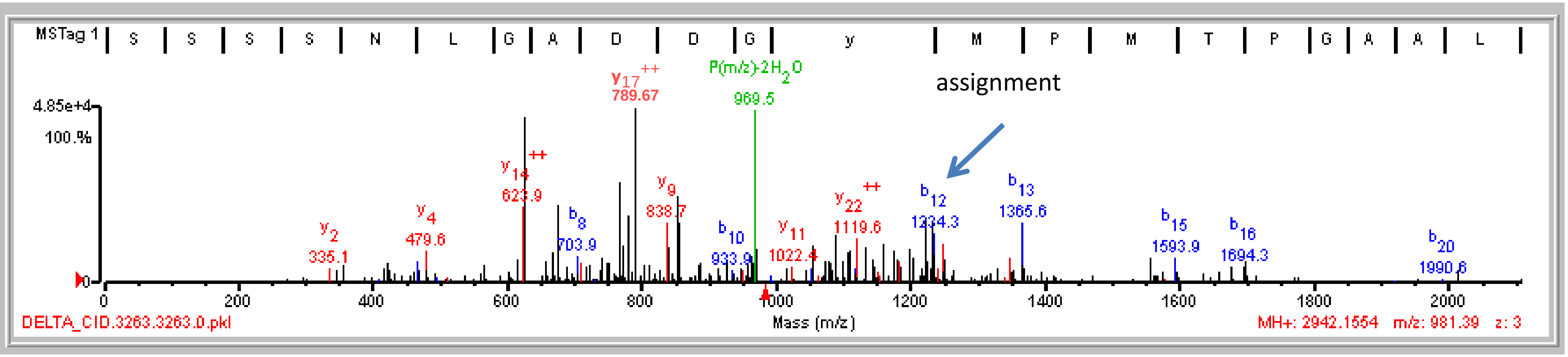




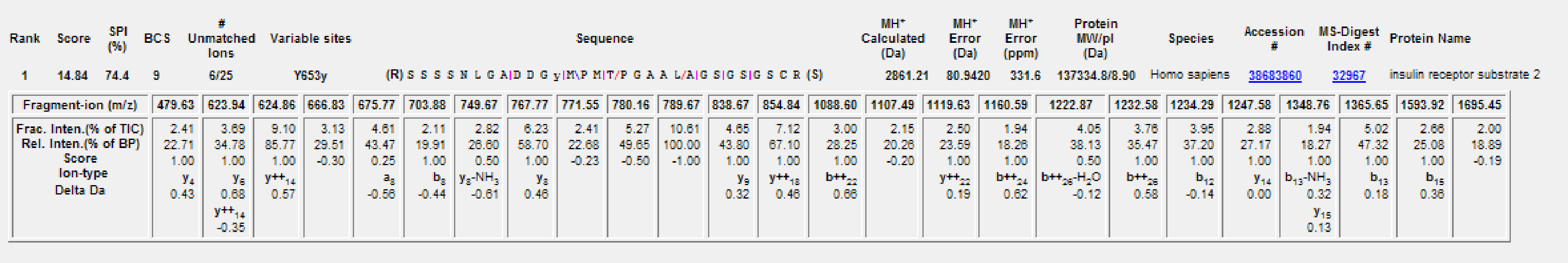
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.04	84.2	7	2/13	M281m Y272y S270s	(R) A L P P A S A/R/s/L y\L G E V/F|T Q\A m P L R (K)	2488.34	176.1074	67.5	43396.2/8.66	Homo sapiens	38348376	7226	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8

Fragment-ion (m/z)	832.75	867.69	916.96	951.26	979.53	1014.80	1020.66	1028.86	1031.35	1038.31	1059.91	1193.84	1288.25
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	7.03 53.62 1.00 y_7 0.32	0.18 1.38 2.00 y^{++}_{14} 0.27 2.00 m 0.26	7.63 58.19 1.00 b^{++}_{16} 0.04	6.14 46.82 1.00 y^{++}_{15} 0.34	13.10 100.00 1.00 y_8 0.03	9.05 69.08 0.25 y_9-$SOCH_4$ 0.23	11.13 84.94 0.50 y^{++}_{16}-H_2O 0.70	6.35 48.49 1.00 y^{++}_{16} -0.11	9.63 73.49 1.00 b^{++}_{18} -0.13	7.97 60.78 -0.61	7.38 56.33 0.50 y_9-H_2O -0.65	7.85 59.90 -0.60	6.56 50.06 1.00 b_{11} 0.70

Peak 67



assignment

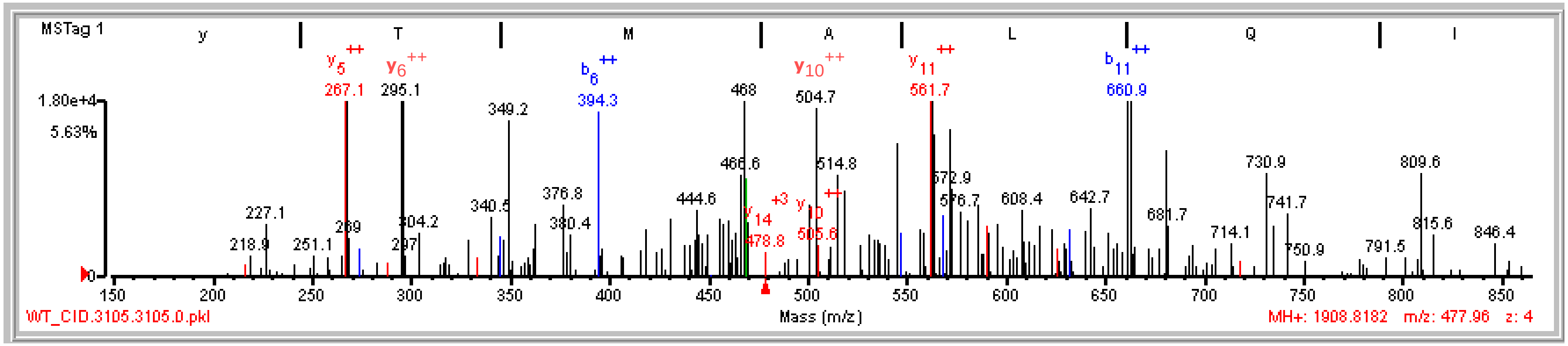


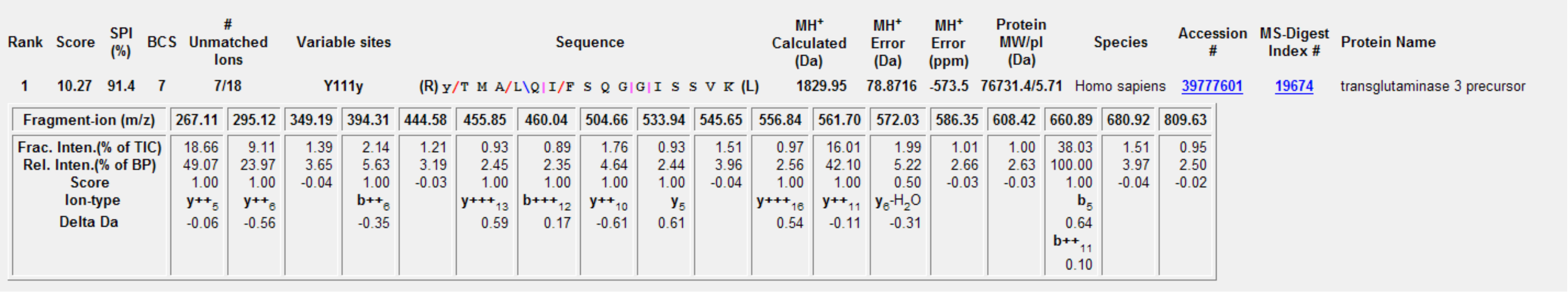
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.84	74.4	9	6/25	Y653y	(R) S S S S N L G A|D D G y|M\P M|T/P G A A L/A|G S|G S|G S C R (S)	2861.21	80.9420	331.6	137334.8/8.90	Homo sapiens	38683860	32967	insulin receptor substrate 2

Fragment-ion (m/z)	479.63	623.94	624.86	666.83	675.77	703.88	749.67	767.77	771.55	780.16	789.67	838.67
Frac. Inten.(% of TIC)	2.41	3.69	9.10	3.13	4.61	2.11	2.82	6.23	2.41	5.27	10.61	4.65
Rel. Inten.(% of BP)	22.71	34.78	85.77	29.51	43.47	19.91	26.60	58.70	22.68	49.65	100.00	43.80
Score	1.00	1.00	1.00	-0.30	0.25	1.00	0.50	1.00	-0.23	-0.50	-1.00	1.00
Ion-type	y_4	y_6 $y{+}{+}_{14}$	$y{+}{+}_{14}$		a_8	b_8	y_8-NH_3	y_8				y_9
Delta Da	0.43	0.68 -0.35	0.57		-0.56	-0.44	-0.61	0.46				0.32

Fragment-ion (m/z)	854.84	1088.60	1107.49	1119.63	1160.59	1222.87	1232.58	1234.29	1247.58	1348.76	1365.65	1593.92	1695.45
Frac. Inten.(% of TIC)	7.12	3.00	2.15	2.50	1.94	4.05	3.76	3.95	2.88	1.94	5.02	2.66	2.00
Rel. Inten.(% of BP)	67.10	28.25	20.26	23.59	18.26	38.13	35.47	37.20	27.17	18.27	47.32	25.08	18.89
Score	1.00	1.00	-0.20	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	-0.19
Ion-type	$y{+}{+}_{18}$	$b{+}{+}_{22}$		$y{+}{+}_{22}$	$b{+}{+}_{24}$	$b{+}{+}_{26}$-H_2O	$b{+}{+}_{26}$	b_{12}	y_{14}	b_{13}-NH_3 y_{15}	b_{13}	b_{15}	
Delta Da	0.46	0.66		0.19	0.62	-0.12	0.58	-0.14	0.00	0.32 0.13	0.18	0.36	

Peak 68



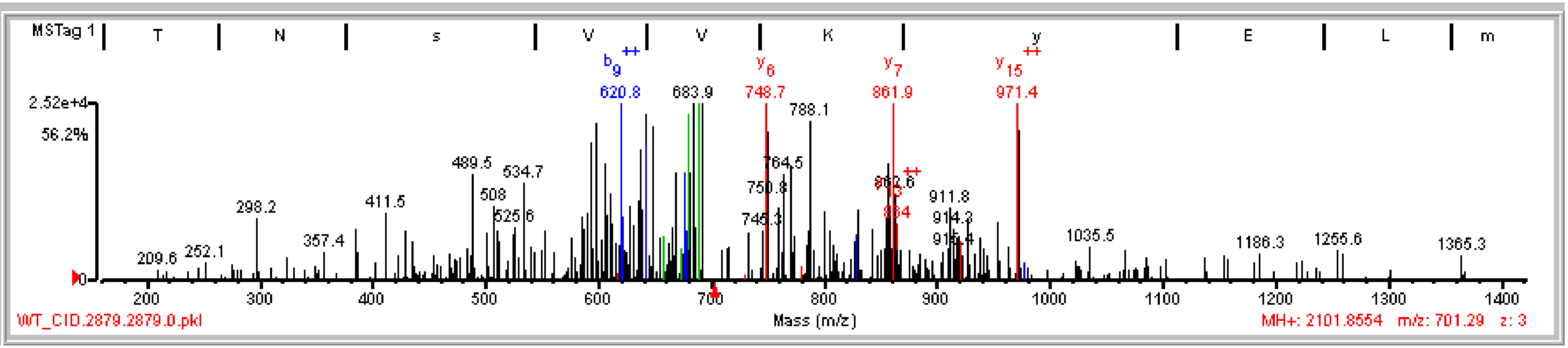


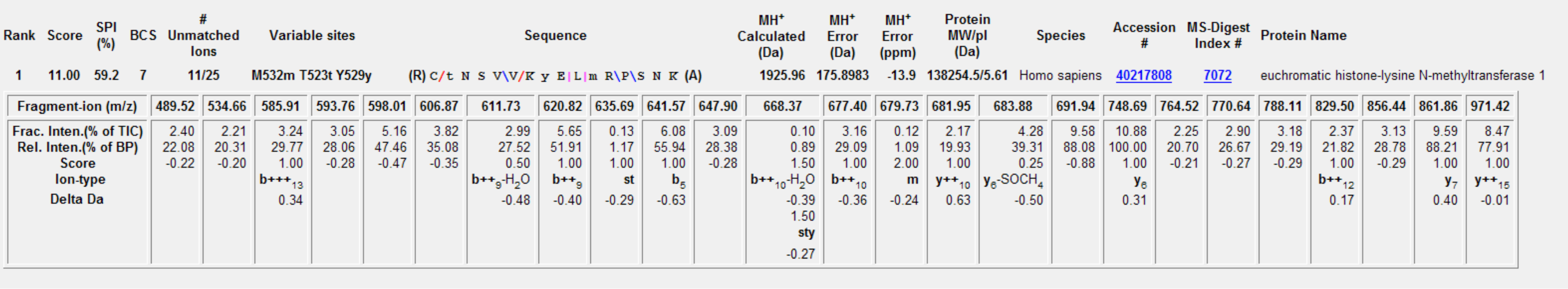
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.27	91.4	7	7/18	Y111y	(R) y/T M A/L\Q|I/F S Q G|G|I S S V K (L)	1829.95	78.8716	-573.5	76731.4/5.71	Homo sapiens	39777601	19674	transglutaminase 3 precursor

Fragment-ion (m/z)	267.11	295.12	349.19	394.31	444.58	455.85	460.04	504.66	533.94
Frac. Inten.(% of TIC)	18.66	9.11	1.39	2.14	1.21	0.93	0.89	1.76	0.93
Rel. Inten.(% of BP)	49.07	23.97	3.65	5.63	3.19	2.45	2.35	4.64	2.44
Score	1.00	1.00	-0.04	1.00	-0.03	1.00	1.00	1.00	1.00
Ion-type	y^{++}_5	y^{++}_6		b^{++}_6		y^{+++}_{13}	b^{+++}_{12}	y^{++}_{10}	y_5
Delta Da	-0.06	-0.56		-0.35		0.59	0.17	-0.61	0.61

Fragment-ion (m/z)	545.65	556.84	561.70	572.03	586.35	608.42	660.89	680.92	809.63
Frac. Inten.(% of TIC)	1.51	0.97	16.01	1.99	1.01	1.00	38.03	1.51	0.95
Rel. Inten.(% of BP)	3.96	2.56	42.10	5.22	2.66	2.63	100.00	3.97	2.50
Score	-0.04	1.00	1.00	0.50	-0.03	-0.03	1.00	-0.04	-0.02
Ion-type		y^{+++}_{16}	y^{++}_{11}	y_6-H_2O			b_5 0.64 b^{++}_{11}		
Delta Da		0.54	-0.11	-0.31			0.10		

Peak 69



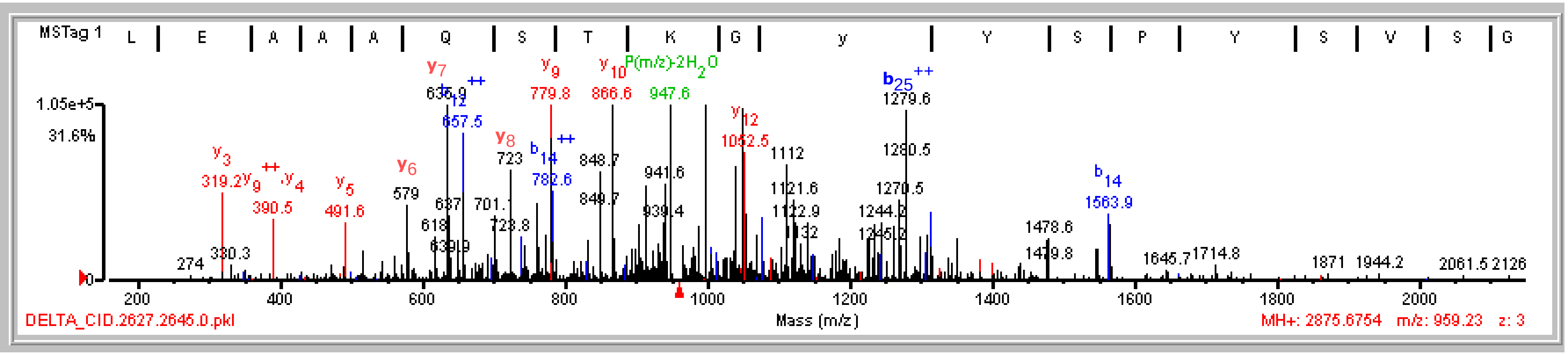


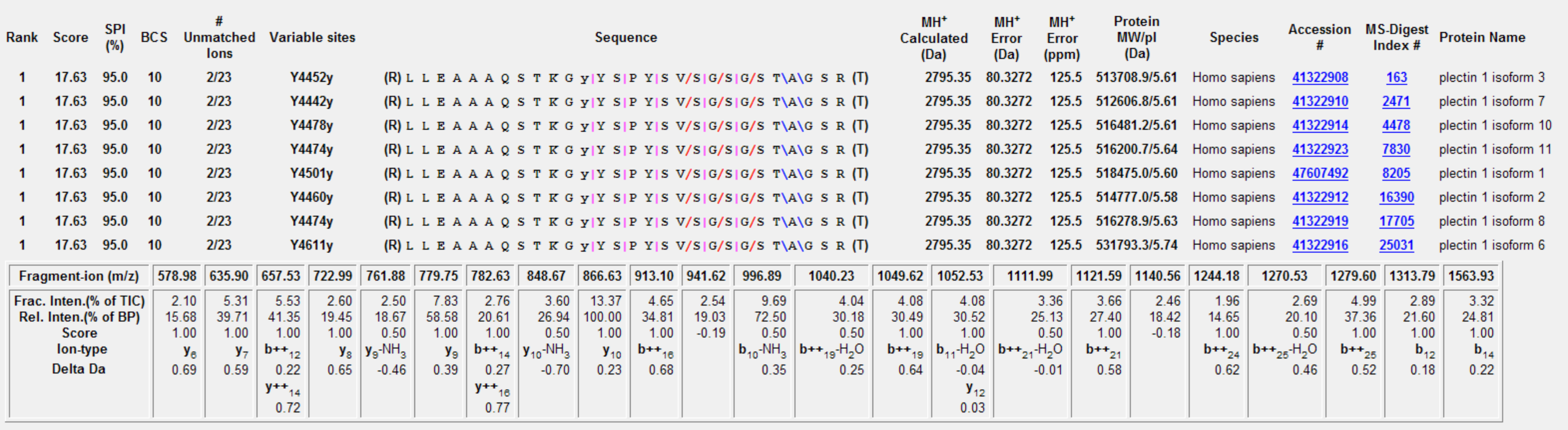
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.00	59.2	7	11/25	M532m T523t Y529y	(R) C/t N S V\V/K y E|L|m R\P\S N K (A)	1925.96	175.8983	-13.9	138254.5/5.61	Homo sapiens	40217808	7072	euchromatic histone-lysine N-methyltransferase 1

Fragment-ion (m/z)	489.52	534.66	585.91	593.76	598.01	606.87	611.73	620.82	635.69	641.57	647.90	668.37
Frac. Inten.(% of TIC)	2.40	2.21	3.24	3.05	5.16	3.82	2.99	5.65	0.13	6.08	3.09	0.10
Rel. Inten.(% of BP)	22.08	20.31	29.77	28.06	47.46	35.08	27.52	51.91	1.17	55.94	28.38	0.89
Score	-0.22	-0.20	1.00	-0.28	-0.47	-0.35	0.50	1.00	1.00	1.00	-0.28	1.50 1.50
Ion-type			b+++$_{13}$				b++$_{9}$-H_2O	b++$_{9}$	st	b_5		b++$_{10}$-H_2O sty
Delta Da			0.34				-0.48	-0.40	-0.29	-0.63		-0.39 -0.27

Fragment-ion (m/z)	677.40	679.73	681.95	683.88	691.94	748.69	764.52	770.64	788.11	829.50	856.44	861.86	971.42
Frac. Inten.(% of TIC)	3.16	0.12	2.17	4.28	9.58	10.88	2.25	2.90	3.18	2.37	3.13	9.59	8.47
Rel. Inten.(% of BP)	29.09	1.09	19.93	39.31	88.08	100.00	20.70	26.67	29.19	21.82	28.78	88.21	77.91
Score	1.00	2.00	1.00	0.25	-0.88	1.00	-0.21	-0.27	-0.29	1.00	-0.29	1.00	1.00
Ion-type	b++$_{10}$	m	y++$_{10}$	y_6-$SOCH_4$		y_6				b++$_{12}$		y_7	y++$_{15}$
Delta Da	-0.36	-0.24	0.63	-0.50		0.31				0.17		0.40	-0.01

Peak 70



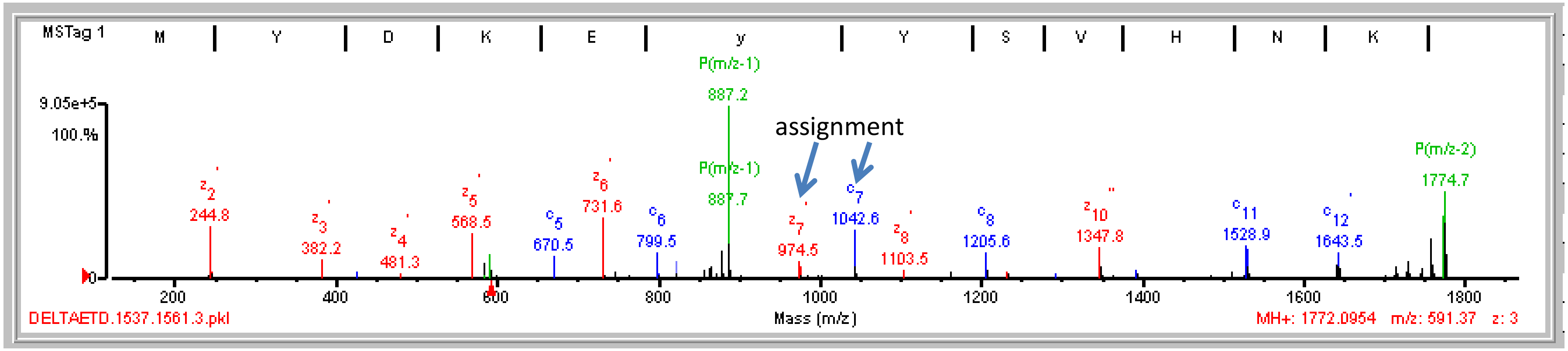


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.63	95.0	10	2/23	Y4452y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	513708.9/5.61	Homo sapiens	41322908	163	plectin 1 isoform 3
1	17.63	95.0	10	2/23	Y4442y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	512606.8/5.61	Homo sapiens	41322910	2471	plectin 1 isoform 7
1	17.63	95.0	10	2/23	Y4478y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	516481.2/5.61	Homo sapiens	41322914	4478	plectin 1 isoform 10
1	17.63	95.0	10	2/23	Y4474y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	516200.7/5.64	Homo sapiens	41322923	7830	plectin 1 isoform 11
1	17.63	95.0	10	2/23	Y4501y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	518475.0/5.60	Homo sapiens	47607492	8205	plectin 1 isoform 1
1	17.63	95.0	10	2/23	Y4460y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	514777.0/5.58	Homo sapiens	41322912	16390	plectin 1 isoform 2
1	17.63	95.0	10	2/23	Y4474y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	516278.9/5.63	Homo sapiens	41322919	17705	plectin 1 isoform 8
1	17.63	95.0	10	2/23	Y4611y	(R) L L E A A A Q S T K G y|Y S|P Y|S V/S|G/S|G/S T\A\G S R (T)	2795.35	80.3272	125.5	531793.3/5.74	Homo sapiens	41322916	25031	plectin 1 isoform 6

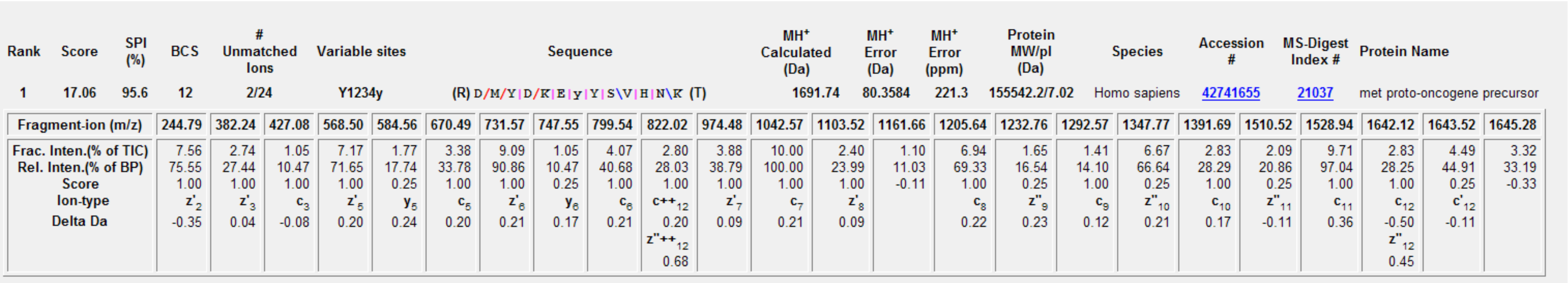
Fragment-ion (m/z)	578.98	635.90	657.53	722.99	761.88	779.75	782.63	848.67	866.63	913.10	941.62	996.89
Frac. Inten.(% of TIC)	2.10	5.31	5.53	2.60	2.50	7.83	2.76	3.60	13.37	4.65	2.54	9.69
Rel. Inten.(% of BP)	15.68	39.71	41.35	19.45	18.67	58.58	20.61	26.94	100.00	34.81	19.03	72.50
Score	1.00	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	1.00	-0.19	0.50
Ion-type	y_6	y_7	b^{++}_{12} y^{++}_{14}	y_8	y_9-NH_3	y_9	b^{++}_{14} y^{++}_{16}	y_{10}-NH_3	y_{10}	b^{++}_{16}		b_{10}-NH_3
Delta Da	0.69	0.59	0.22 0.72	0.65	-0.46	0.39	0.27 0.77	-0.70	0.23	0.68		0.35

Fragment-ion (m/z)	1040.23	1049.62	1052.53	1111.99	1121.59	1140.56	1244.18	1270.53	1279.60	1313.79	1563.93
Frac. Inten.(% of TIC)	4.04	4.08	4.08	3.36	3.66	2.46	1.96	2.69	4.99	2.89	3.32
Rel. Inten.(% of BP)	30.18	30.49	30.52	25.13	27.40	18.42	14.65	20.10	37.36	21.60	24.81
Score	0.50	1.00	1.00	0.50	1.00	-0.18	1.00	0.50	1.00	1.00	1.00
Ion-type	b^{++}_{19}-H_2O	b^{++}_{19}	b_{11}-H_2O y_{12}	b^{++}_{21}-H_2O	b^{++}_{21}		b^{++}_{24}	b^{++}_{25}-H_2O	b^{++}_{25}	b_{12}	b_{14}
Delta Da	0.25	0.64	-0.04 0.03	-0.01	0.58		0.62	0.46	0.52	0.18	0.22

Peak 71



assignment

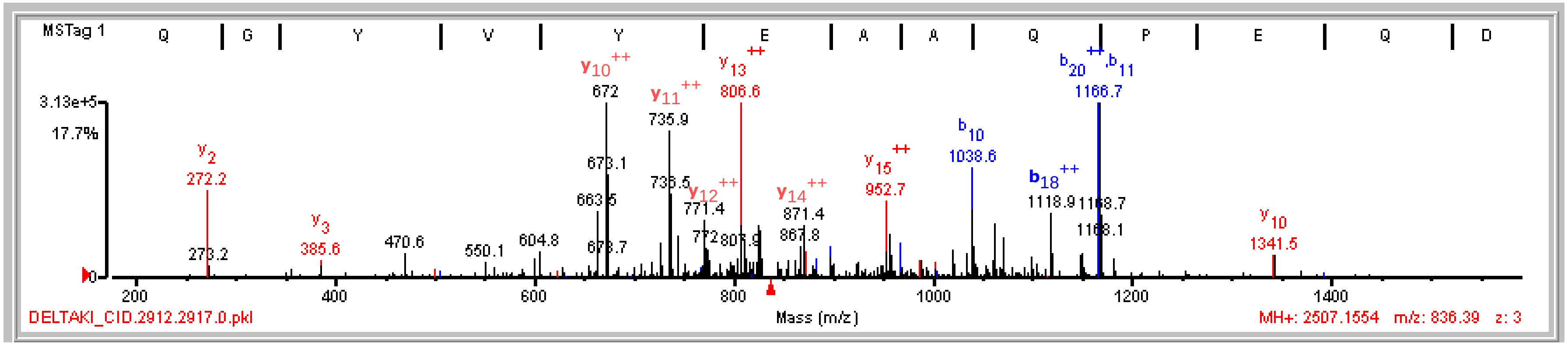


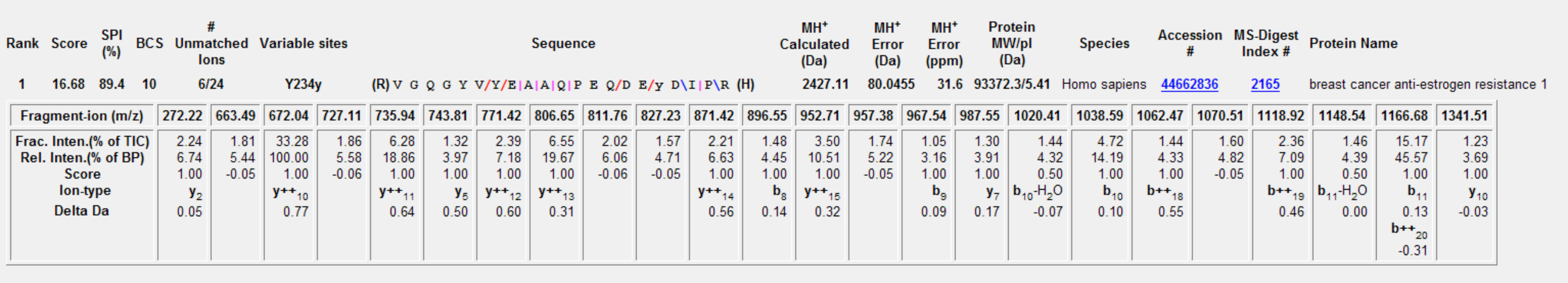
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.06	95.6	12	2/24	Y1234y	(R) D/M/Y|D/K|E|y|Y|S\V|H|N\K (T)	1691.74	80.3584	221.3	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.79	382.24	427.08	568.50	584.56	670.49	731.57	747.55	799.54	822.02	974.48	1042.57
Frac. Inten.(% of TIC)	7.56	2.74	1.05	7.17	1.77	3.38	9.09	1.05	4.07	2.80	3.88	10.00
Rel. Inten.(% of BP)	75.55	27.44	10.47	71.65	17.74	33.78	90.86	10.47	40.68	28.03	38.79	100.00
Score	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00	1.00	1.00	1.00
Ion-type	z'_2	z'_3	c_3	z'_5	y_5	c_5	z'_6	y_6	c_6	$c{++}_{12}$ $z''{++}_{12}$	z'_7	c_7
Delta Da	-0.35	0.04	-0.08	0.20	0.24	0.20	0.21	0.17	0.21	0.20 0.68	0.09	0.21

Fragment-ion (m/z)	1103.52	1161.66	1205.64	1232.76	1292.57	1347.77	1391.69	1510.52	1528.94	1642.12	1643.52	1645.28
Frac. Inten.(% of TIC)	2.40	1.10	6.94	1.65	1.41	6.67	2.83	2.09	9.71	2.83	4.49	3.32
Rel. Inten.(% of BP)	23.99	11.03	69.33	16.54	14.10	66.64	28.29	20.86	97.04	28.25	44.91	33.19
Score	1.00	-0.11	1.00	0.25	1.00	0.25	1.00	0.25	1.00	1.00	0.25	-0.33
Ion-type	z'_8		c_8	z''_9	c_9	z''_{10}	c_{10}	z''_{11}	c_{11}	c_{12} z''_{12}	c'_{12}	
Delta Da	0.09		0.22	0.23	0.12	0.21	0.17	-0.11	0.36	-0.50 0.45	-0.11	

Peak 72



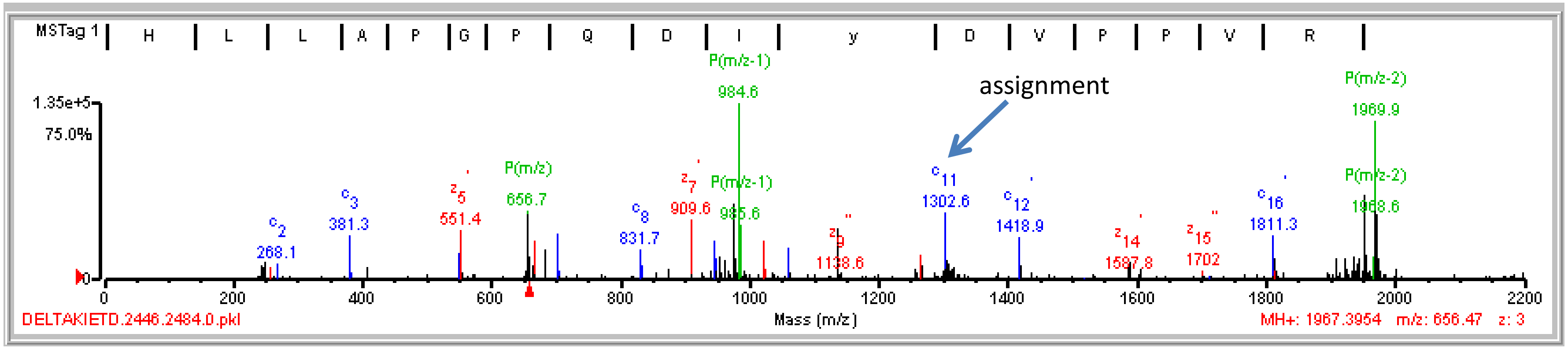


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.68	89.4	10	6/24	Y234y	(R) V G Q G Y V/Y/E|A|A|Q|P E Q/D E/y D\I|P\R (H)	2427.11	80.0455	31.6	93372.3/5.41	Homo sapiens	44662836	2165	breast cancer anti-estrogen resistance 1

Fragment-ion (m/z)	272.22	663.49	672.04	727.11	735.94	743.81	771.42	806.65	811.76	827.23	871.42	896.55
Frac. Inten.(% of TIC)	2.24	1.81	33.28	1.86	6.28	1.32	2.39	6.55	2.02	1.57	2.21	1.48
Rel. Inten.(% of BP)	6.74	5.44	100.00	5.58	18.86	3.97	7.18	19.67	6.06	4.71	6.63	4.45
Score	1.00	-0.05	1.00	-0.06	1.00	1.00	1.00	1.00	-0.06	-0.05	1.00	1.00
Ion-type	y_2		$y{++}_{10}$		$y{++}_{11}$	y_5	$y{++}_{12}$	$y{++}_{13}$			$y{++}_{14}$	b_8
Delta Da	0.05		0.77		0.64	0.50	0.60	0.31			0.56	0.14

Fragment-ion (m/z)	952.71	957.38	967.54	987.55	1020.41	1038.59	1062.47	1070.51	1118.92	1148.54	1166.68	1341.51
Frac. Inten.(% of TIC)	3.50	1.74	1.05	1.30	1.44	4.72	1.44	1.60	2.36	1.46	15.17	1.23
Rel. Inten.(% of BP)	10.51	5.22	3.16	3.91	4.32	14.19	4.33	4.82	7.09	4.39	45.57	3.69
Score	1.00	-0.05	1.00	1.00	0.50	1.00	1.00	-0.05	1.00	0.50	1.00	1.00
Ion-type	$y{++}_{15}$		b_9	y_7	$b_{10}-H_2O$	b_{10}	$b{++}_{18}$		$b{++}_{19}$	$b_{11}-H_2O$	b_{11} $b{++}_{20}$	y_{10}
Delta Da	0.32		0.09	0.17	-0.07	0.10	0.55		0.46	0.00	0.13 -0.31	-0.03

Peak 73



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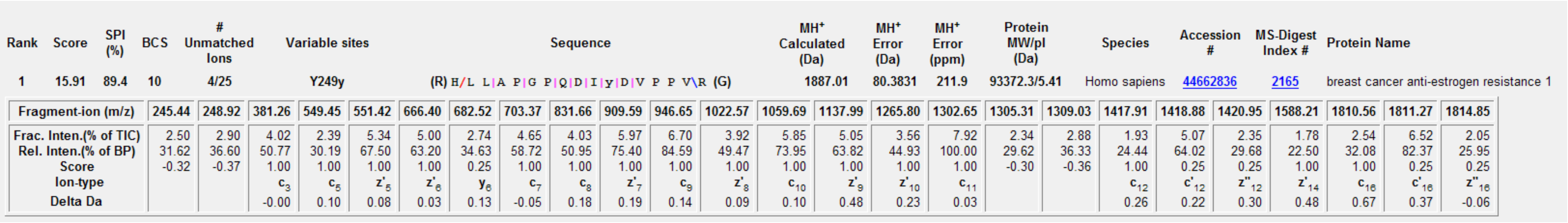
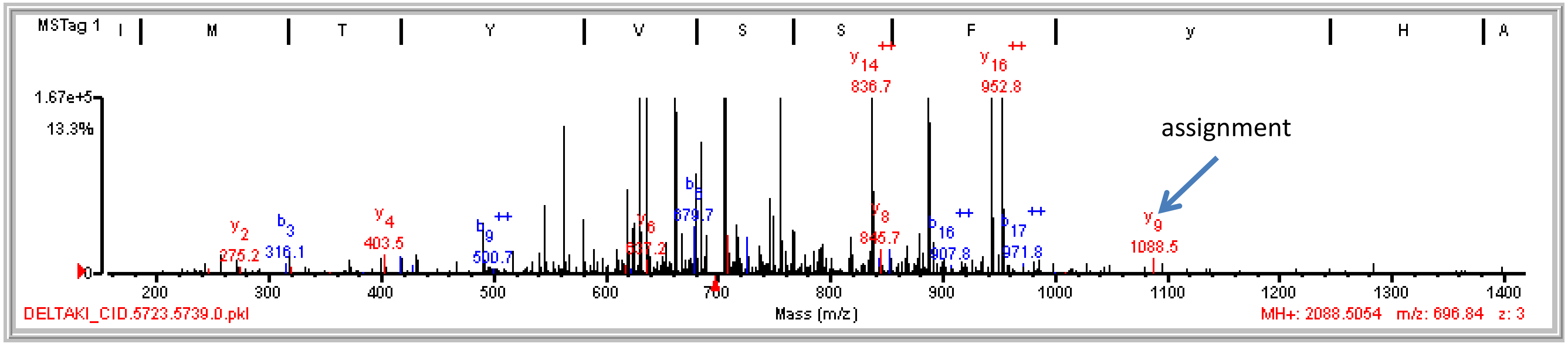


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.91	89.4	10	4/25	Y249y	(R) H/L L|A P|G P|Q|D|I|y|D|V P P V\R (G)	1887.01	80.3831	211.9	93372.3/5.41	Homo sapiens	44662836	2165	breast cancer anti-estrogen resistance 1

Fragment-ion (m/z)	245.44	248.92	381.26	549.45	551.42	666.40	682.52	703.37	831.66	909.59	946.65	1022.57	1059.69	1137.99	1265.80	1302.65	1305.31	1309.03	1417.91	1418.88	1420.95	1588.21	1810.56	1811.27	1814.85
Frac. Inten.(% of TIC)	2.50	2.90	4.02	2.39	5.34	5.00	2.74	4.65	4.03	5.97	6.70	3.92	5.85	5.05	3.56	7.92	2.34	2.88	1.93	5.07	2.35	1.78	2.54	6.52	2.05
Rel. Inten.(% of BP)	31.62	36.60	50.77	30.19	67.50	63.20	34.63	58.72	50.95	75.40	84.59	49.47	73.95	63.82	44.93	100.00	29.62	36.33	24.44	64.02	29.68	22.50	32.08	82.37	25.95
Score	-0.32	-0.37	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.30	-0.36	1.00	0.25	0.25	1.00	1.00	0.25	0.25
Ion-type			c_3	c_5	z'_5	z'_6	y_6	c_7	c_8	z'_7	c_9	z'_8	c_{10}	z'_9	z'_{10}	c_{11}			c_{12}	c'_{12}	z''_{12}	z'_{14}	c_{16}	c'_{16}	z''_{16}
Delta Da			-0.00	0.10	0.08	0.03	0.13	-0.05	0.18	0.19	0.14	0.09	0.10	0.48	0.23	0.03			0.26	0.22	0.30	0.48	0.67	0.37	-0.06

Peak 74



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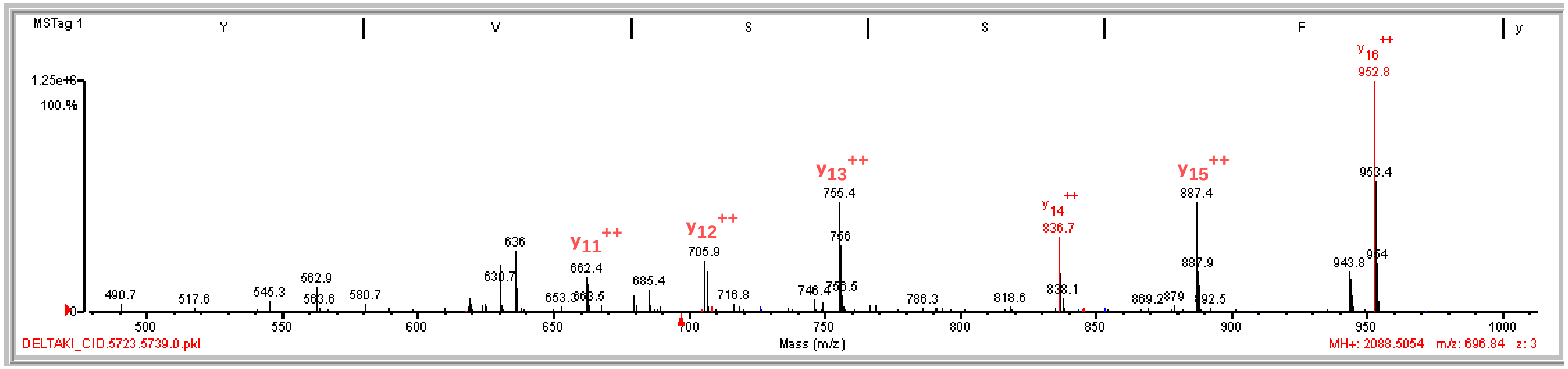
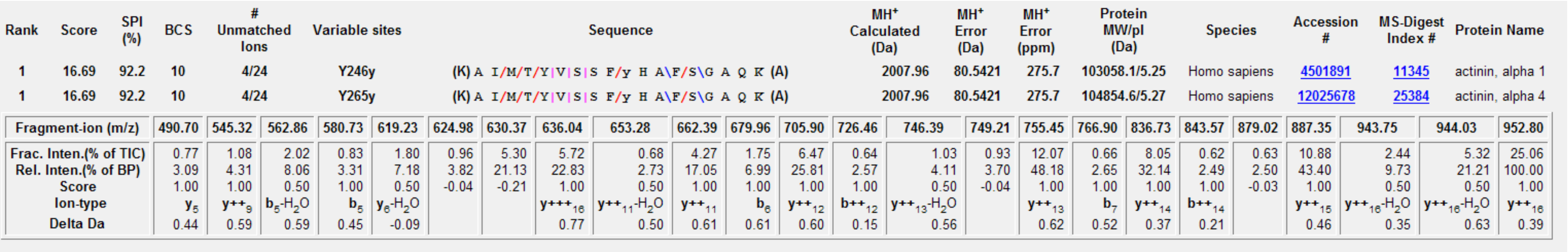


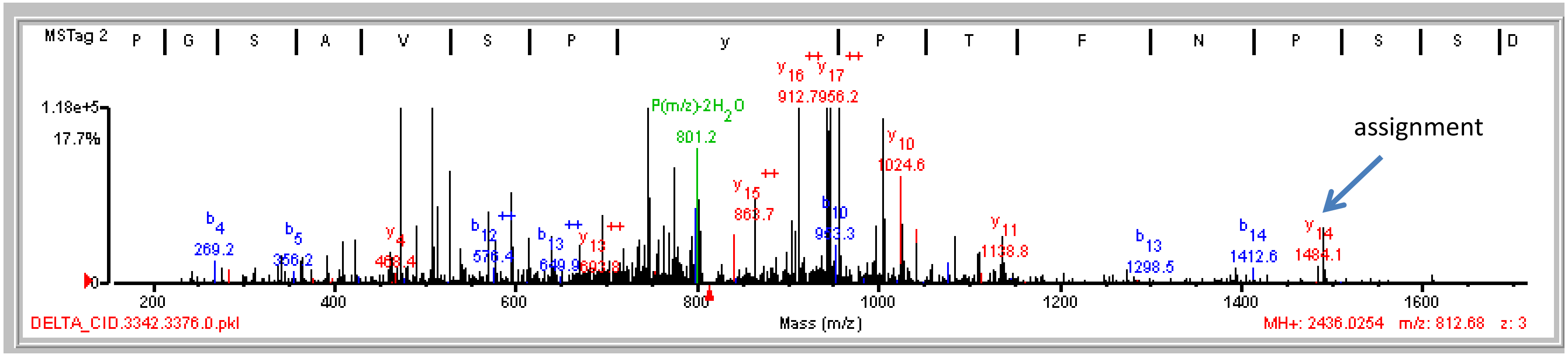


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.69	92.2	10	4/24	Y246y	(K) A I/M/T/Y|V|S|S F/y H A\F/S\G A Q K (A)	2007.96	80.5421	275.7	103058.1/5.25	Homo sapiens	4501891	11345	actinin, alpha 1
1	16.69	92.2	10	4/24	Y265y	(K) A I/M/T/Y|V|S|S F/y H A\F/S\G A Q K (A)	2007.96	80.5421	275.7	104854.6/5.27	Homo sapiens	12025678	25384	actinin, alpha 4

Fragment-ion (m/z)	490.70	545.32	562.86	580.73	619.23	624.98	630.37	636.04	653.28	662.39	679.96	705.90
Frac. Inten.(% of TIC)	0.77	1.08	2.02	0.83	1.80	0.96	5.30	5.72	0.68	4.27	1.75	6.47
Rel. Inten.(% of BP)	3.09	4.31	8.06	3.31	7.18	3.82	21.13	22.83	2.73	17.05	6.99	25.81
Score	1.00	1.00	0.50	1.00	0.50	-0.04	-0.21	1.00	0.50	1.00	1.00	1.00
Ion-type	y_5	$y{++}_9$	$b_5\text{-}H_2O$	b_5	$y_6\text{-}H_2O$			$y{+++}_{16}$	$y{++}_{11}\text{-}H_2O$	$y{++}_{11}$	b_6	$y{++}_{12}$
Delta Da	0.44	0.59	0.59	0.45	-0.09			0.77	0.50	0.61	0.61	0.60

Fragment-ion (m/z)	726.46	746.39	749.21	755.45	766.90	836.73	843.57	879.02	887.35	943.75	944.03	952.80
Frac. Inten.(% of TIC)	0.64	1.03	0.93	12.07	0.66	8.05	0.62	0.63	10.88	2.44	5.32	25.06
Rel. Inten.(% of BP)	2.57	4.11	3.70	48.18	2.65	32.14	2.49	2.50	43.40	9.73	21.21	100.00
Score	1.00	0.50	-0.04	1.00	1.00	1.00	1.00	-0.03	1.00	0.50	0.50	1.00
Ion-type	$b{++}_{12}$	$y{++}_{13}\text{-}H_2O$		$y{++}_{13}$	b_7	$y{++}_{14}$	$b{++}_{14}$		$y{++}_{15}$	$y{++}_{16}\text{-}H_2O$	$y{++}_{16}\text{-}H_2O$	$y{++}_{16}$
Delta Da	0.15	0.56		0.62	0.52	0.37	0.21		0.46	0.35	0.63	0.39

Peak 75



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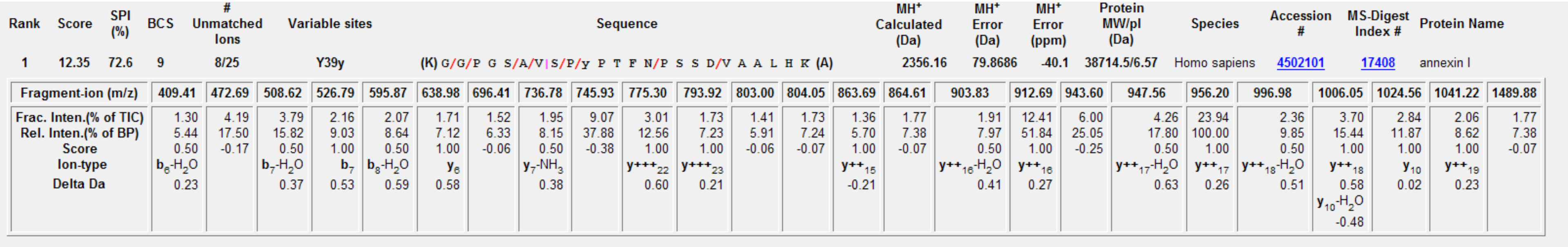
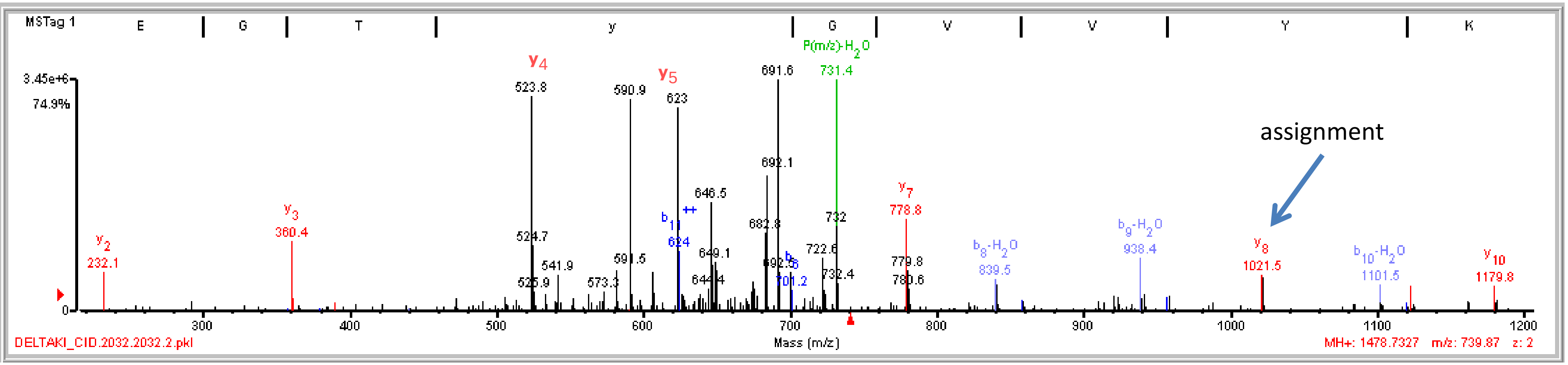


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.35	72.6	9	8/25	Y39y	(K) G/G/P G S/A/V|S/P/y P T F N/P S S D/V A A L H K (A)	2356.16	79.8686	-40.1	38714.5/6.57	Homo sapiens	4502101	17408	annexin I

Fragment-ion (m/z)	409.41	472.69	508.62	526.79	595.87	638.98	696.41	736.78	745.93	775.30	793.92	803.00	804.05	863.69	864.61	903.83	912.69	943.60	947.56	956.20	996.98	1006.05	1024.56	1041.22	1489.88
Frac. Inten.(% of TIC)	1.30	4.19	3.79	2.16	2.07	1.71	1.52	1.95	9.07	3.01	1.73	1.41	1.73	1.36	1.77	1.91	12.41	6.00	4.26	23.94	2.36	3.70	2.84	2.06	1.77
Rel. Inten.(% of BP)	5.44	17.50	15.82	9.03	8.64	7.12	6.33	8.15	37.88	12.56	7.23	5.91	7.24	5.70	7.38	7.97	51.84	25.05	17.80	100.00	9.85	15.44	11.87	8.62	7.38
Score	0.50	-0.17	0.50	1.00	0.50	1.00	-0.06	0.50	-0.38	1.00	1.00	-0.06	-0.07	1.00	-0.07	0.50	1.00	-0.25	0.50	1.00	0.50	1.00	1.00	1.00	-0.07
Ion-type	b_6-H_2O		b_7-H_2O	b_7	b_8-H_2O	y_6		y_7-NH_3		$y{+}{+}{+}_{22}$	$y{+}{+}{+}_{23}$			$y{+}{+}_{15}$		$y{+}{+}_{16}$-H_2O	$y{+}{+}_{16}$		$y{+}{+}_{17}$-H_2O	$y{+}{+}_{17}$	$y{+}{+}_{18}$-H_2O	$y{+}{+}_{18}$ y_{10}-H_2O	y_{10}	$y{+}{+}_{19}$	
Delta Da	0.23		0.37	0.53	0.59	0.58		0.38		0.60	0.21			-0.21		0.41	0.27		0.63	0.26	0.51	0.58 -0.48	0.02	0.23	

Peak 76



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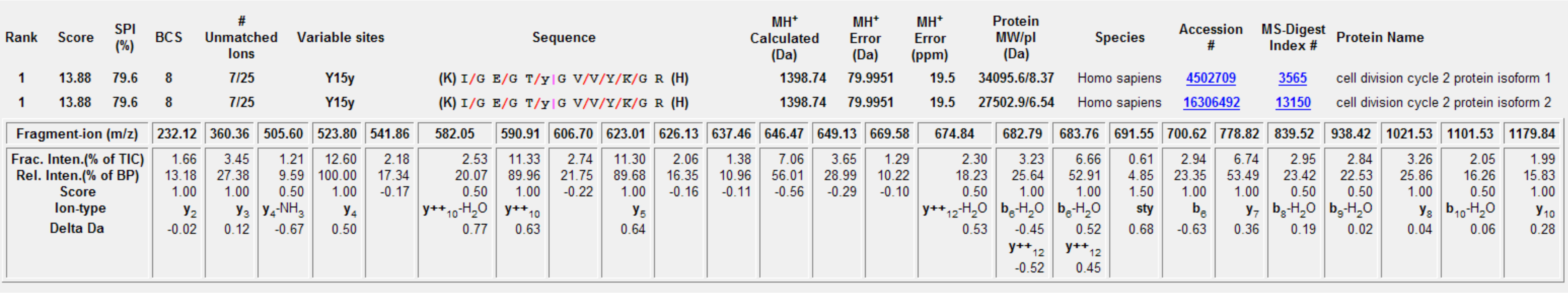
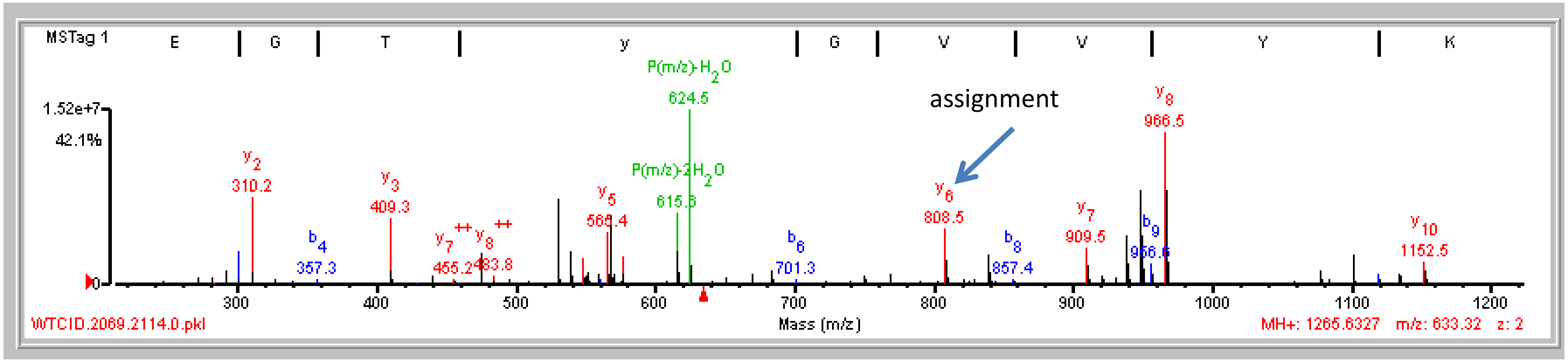


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.88	79.6	8	7/25	Y15y	(K) I/G E/G T/y|G V/V/Y/K/G R (H)	1398.74	79.9951	19.5	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	13.88	79.6	8	7/25	Y15y	(K) I/G E/G T/y|G V/V/Y/K/G R (H)	1398.74	79.9951	19.5	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

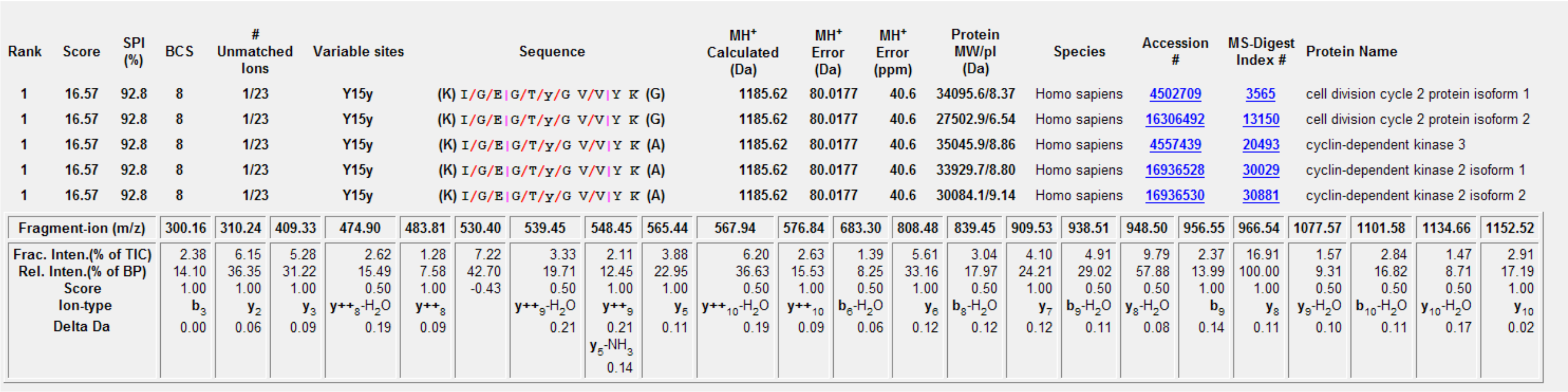
Fragment-ion (m/z)	232.12	360.36	505.60	523.80	541.86	582.05	590.91	606.70	623.01	626.13	637.46
Frac. Inten.(% of TIC)	1.66	3.45	1.21	12.60	2.18	2.53	11.33	2.74	11.30	2.06	1.38
Rel. Inten.(% of BP)	13.18	27.38	9.59	100.00	17.34	20.07	89.96	21.75	89.68	16.35	10.96
Score	1.00	1.00	0.50	1.00	-0.17	0.50	1.00	-0.22	1.00	-0.16	-0.11
Ion-type	y_2	y_3	y_4-NH_3	y_4		$y{++}_{10}$-H_2O	$y{++}_{10}$		y_5		
Delta Da	-0.02	0.12	-0.67	0.50		0.77	0.63		0.64		

Fragment-ion (m/z)	646.47	649.13	669.58	674.84	682.79	683.76	691.55	700.62	778.82	839.52	938.42	1021.53	1101.53	1179.84
Frac. Inten.(% of TIC)	7.06	3.65	1.29	2.30	3.23	6.66	0.61	2.94	6.74	2.95	2.84	3.26	2.05	1.99
Rel. Inten.(% of BP)	56.01	28.99	10.22	18.23	25.64	52.91	4.85	23.35	53.49	23.42	22.53	25.86	16.26	15.83
Score	-0.56	-0.29	-0.10	0.50	1.00	1.00	1.50	1.00	1.00	0.50	0.50	1.00	0.50	1.00
Ion-type				$y{++}_{12}$-H_2O	b_6-H_2O $y{++}_{12}$	b_6-H_2O $y{++}_{12}$	sty	b_6	y_7	b_8-H_2O	b_9-H_2O	y_8	b_{10}-H_2O	y_{10}
Delta Da				0.53	-0.45 -0.52	0.52 0.45	0.68	-0.63	0.36	0.19	0.02	0.04	0.06	0.28

Peak 77



assignment

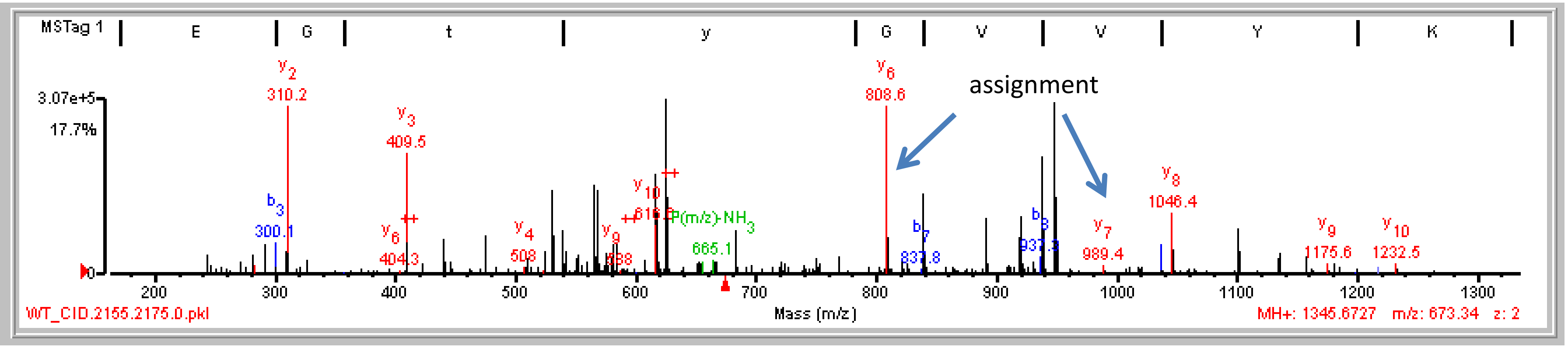


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.57	92.8	8	1/23	Y15y	(K) I/G/E|G/T/y/G V/V|Y K (G)	1185.62	80.0177	40.6	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	16.57	92.8	8	1/23	Y15y	(K) I/G/E|G/T/y/G V/V|Y K (G)	1185.62	80.0177	40.6	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2
1	16.57	92.8	8	1/23	Y15y	(K) I/G/E|G/T/y/G V/V|Y K (A)	1185.62	80.0177	40.6	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
1	16.57	92.8	8	1/23	Y15y	(K) I/G/E|G/T/y/G V/V|Y K (A)	1185.62	80.0177	40.6	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	16.57	92.8	8	1/23	Y15y	(K) I/G/E|G/T/y/G V/V|Y K (A)	1185.62	80.0177	40.6	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

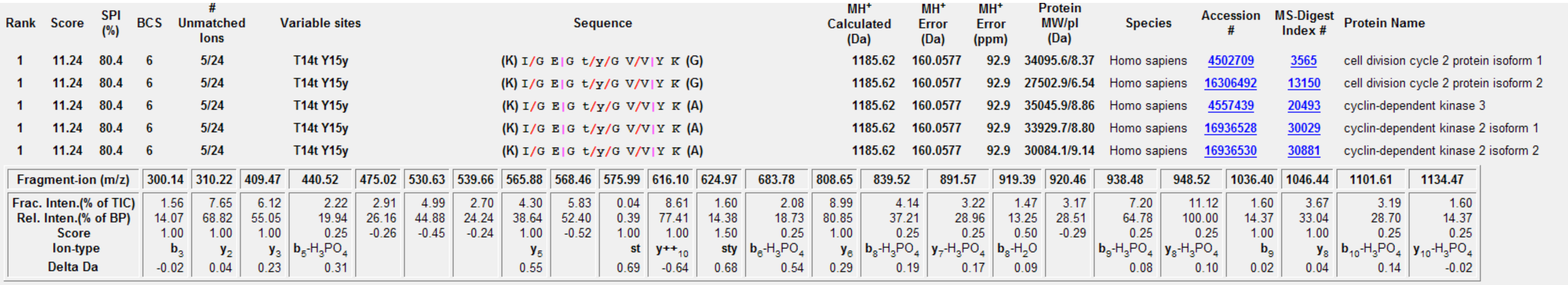
Fragment-ion (m/z)	300.16	310.24	409.33	474.90	483.81	530.40	539.45	548.45	565.44	567.94	576.84	683.30
Frac. Inten.(% of TIC)	2.38	6.15	5.28	2.62	1.28	7.22	3.33	2.11	3.88	6.20	2.63	1.39
Rel. Inten.(% of BP)	14.10	36.35	31.22	15.49	7.58	42.70	19.71	12.45	22.95	36.63	15.53	8.25
Score	1.00	1.00	1.00	0.50	1.00	-0.43	0.50	1.00	1.00	0.50	1.00	0.50
Ion-type	b_3	y_2	y_3	$y{+}{+}_8$-H_2O	$y{+}{+}_8$		$y{+}{+}_9$-H_2O	$y{+}{+}_9$ y_5-NH_3	y_5	$y{+}{+}_{10}$-H_2O	$y{+}{+}_{10}$	b_6-H_2O
Delta Da	0.00	0.06	0.09	0.19	0.09		0.21	0.21 0.14	0.11	0.19	0.09	0.06

Fragment-ion (m/z)	808.48	839.45	909.53	938.51	948.50	956.55	966.54	1077.57	1101.58	1134.66	1152.52
Frac. Inten.(% of TIC)	5.61	3.04	4.10	4.91	9.79	2.37	16.91	1.57	2.84	1.47	2.91
Rel. Inten.(% of BP)	33.16	17.97	24.21	29.02	57.88	13.99	100.00	9.31	16.82	8.71	17.19
Score	1.00	0.50	1.00	0.50	0.50	1.00	1.00	0.50	0.50	0.50	1.00
Ion-type	y_6	b_8-H_2O	y_7	b_9-H_2O	y_8-H_2O	b_9	y_8	y_9-H_2O	b_{10}-H_2O	y_{10}-H_2O	y_{10}
Delta Da	0.12	0.12	0.12	0.11	0.08	0.14	0.11	0.10	0.11	0.17	0.02

Peak 78



assignment

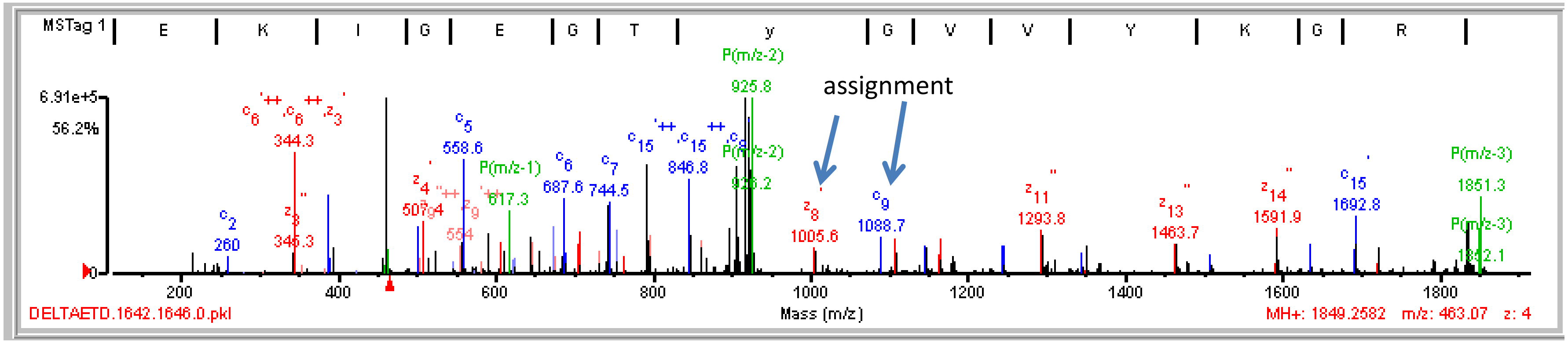


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.24	80.4	6	5/24	T14t Y15y	(K) I/G E|G t/y/G V/V|Y K (G)	1185.62	160.0577	92.9	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	11.24	80.4	6	5/24	T14t Y15y	(K) I/G E|G t/y/G V/V|Y K (G)	1185.62	160.0577	92.9	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2
1	11.24	80.4	6	5/24	T14t Y15y	(K) I/G E|G t/y/G V/V|Y K (A)	1185.62	160.0577	92.9	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
1	11.24	80.4	6	5/24	T14t Y15y	(K) I/G E|G t/y/G V/V|Y K (A)	1185.62	160.0577	92.9	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	11.24	80.4	6	5/24	T14t Y15y	(K) I/G E|G t/y/G V/V|Y K (A)	1185.62	160.0577	92.9	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

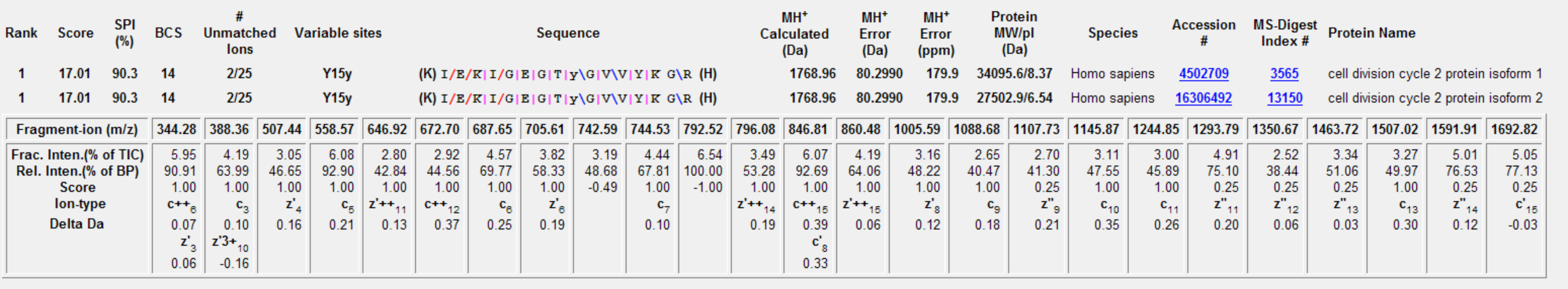
Fragment-ion (m/z)	300.14	310.22	409.47	440.52	475.02	530.63	539.66	565.88	568.46	575.99	616.10	624.97
Frac. Inten.(% of TIC)	1.56	7.65	6.12	2.22	2.91	4.99	2.70	4.30	5.83	0.04	8.61	1.60
Rel. Inten.(% of BP)	14.07	68.82	55.05	19.94	26.16	44.88	24.24	38.64	52.40	0.39	77.41	14.38
Score	1.00	1.00	1.00	0.25	-0.26	-0.45	-0.24	1.00	-0.52	1.00	1.00	1.50
Ion-type	b_3	y_2	y_3	b_5-H_3PO_4				y_5		st	$y{+}{+}_{10}$	sty
Delta Da	-0.02	0.04	0.23	0.31				0.55		0.69	-0.64	0.68

Fragment-ion (m/z)	683.78	808.65	839.52	891.57	919.39	920.46	938.48	948.52	1036.40	1046.44	1101.61	1134.47
Frac. Inten.(% of TIC)	2.08	8.99	4.14	3.22	1.47	3.17	7.20	11.12	1.60	3.67	3.19	1.60
Rel. Inten.(% of BP)	18.73	80.85	37.21	28.96	13.25	28.51	64.78	100.00	14.37	33.04	28.70	14.37
Score	0.25	1.00	0.25	0.25	0.50	-0.29	0.25	0.25	1.00	1.00	0.25	0.25
Ion-type	b_6-H_3PO_4	y_6	b_8-H_3PO_4	y_7-H_3PO_4	b_8-H_2O		b_9-H_3PO_4	y_8-H_3PO_4	b_9	y_8	b_{10}-H_3PO_4	y_{10}-H_3PO_4
Delta Da	0.54	0.29	0.19	0.17	0.09		0.08	0.10	0.02	0.04	0.14	-0.02

Peak 79



assignment

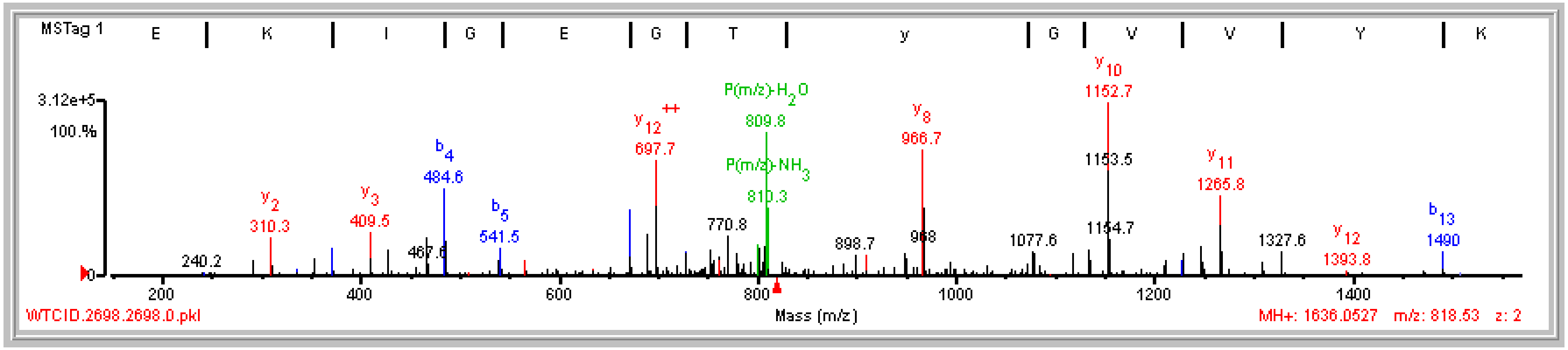


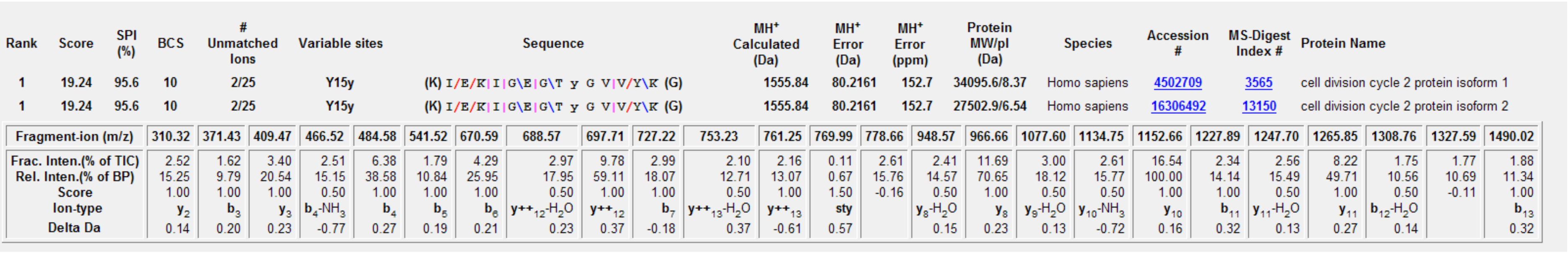
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.01	90.3	14	2/25	Y15y	(K) I/E/K|I/G|E|G|T|y\G|V\V|Y|K G\R (H)	1768.96	80.2990	179.9	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	17.01	90.3	14	2/25	Y15y	(K) I/E/K|I/G|E|G|T|y\G|V\V|Y|K G\R (H)	1768.96	80.2990	179.9	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

Fragment-ion (m/z)	344.28	388.36	507.44	558.57	646.92	672.70	687.65	705.61	742.59	744.53	792.52	796.08	846.81
Frac. Inten.(% of TIC)	5.95	4.19	3.05	6.08	2.80	2.92	4.57	3.82	3.19	4.44	6.54	3.49	6.07
Rel. Inten.(% of BP)	90.91	63.99	46.65	92.90	42.84	44.56	69.77	58.33	48.68	67.81	100.00	53.28	92.69
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.49	1.00	-1.00	1.00	1.00
Ion-type	$c{+}{+}_{6}$ z'_{3}	c_{3} $z'3{+}_{10}$	z'_{4}	c_{5}	$z'{+}{+}_{11}$	$c{+}{+}_{12}$	c_{6}	z'_{6}		c_{7}		$z'{+}{+}_{14}$	$c{+}{+}_{15}$ c'_{8}
Delta Da	0.07 0.06	0.10 -0.16	0.16	0.21	0.13	0.37	0.25	0.19		0.10		0.19	0.39 0.33

Fragment-ion (m/z)	860.48	1005.59	1088.68	1107.73	1145.87	1244.85	1293.79	1350.67	1463.72	1507.02	1591.91	1692.82
Frac. Inten.(% of TIC)	4.19	3.16	2.65	2.70	3.11	3.00	4.91	2.52	3.34	3.27	5.01	5.05
Rel. Inten.(% of BP)	64.06	48.22	40.47	41.30	47.55	45.89	75.10	38.44	51.06	49.97	76.53	77.13
Score	1.00	1.00	1.00	0.25	1.00	1.00	0.25	0.25	0.25	1.00	0.25	0.25
Ion-type	$z'{+}{+}_{15}$	z'_{8}	c_{9}	z''_{9}	c_{10}	c_{11}	z''_{11}	z''_{12}	z''_{13}	c_{13}	z''_{14}	c'_{15}
Delta Da	0.06	0.12	0.18	0.21	0.35	0.26	0.20	0.06	0.03	0.30	0.12	-0.03

Peak 80



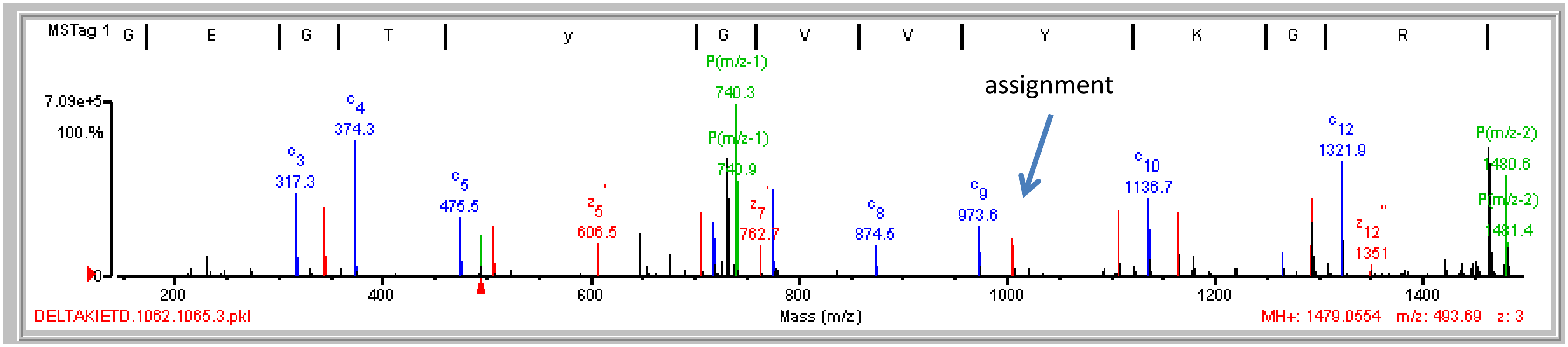


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.24	95.6	10	2/25	Y15y	(K) I/E/K|I|G\E|G\T y G V|V/Y\K (G)	1555.84	80.2161	152.7	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	19.24	95.6	10	2/25	Y15y	(K) I/E/K|I|G\E|G\T y G V|V/Y\K (G)	1555.84	80.2161	152.7	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

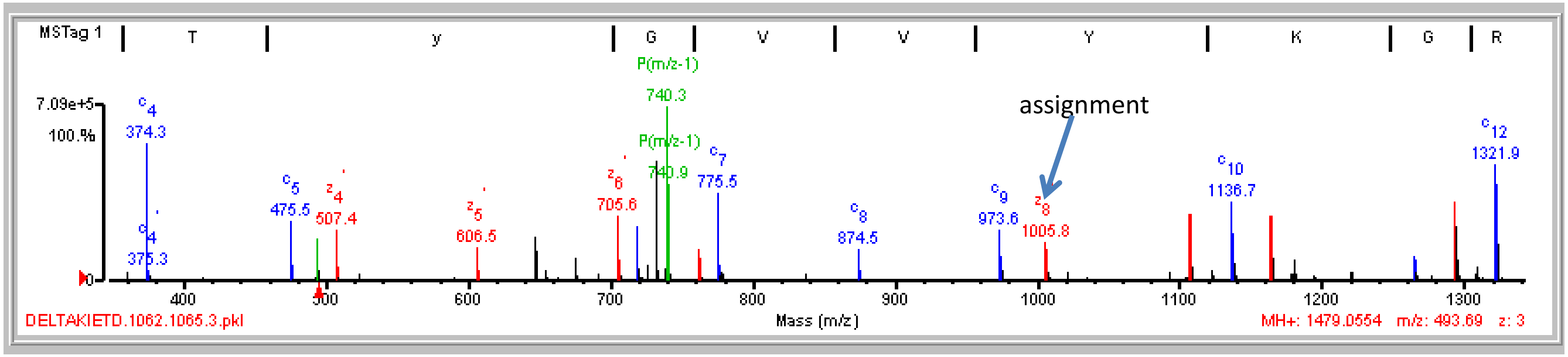
Fragment-ion (m/z)	310.32	371.43	409.47	466.52	484.58	541.52	670.59	688.57	697.71	727.22	753.23	761.25
Frac. Inten.(% of TIC)	2.52	1.62	3.40	2.51	6.38	1.79	4.29	2.97	9.78	2.99	2.10	2.16
Rel. Inten.(% of BP)	15.25	9.79	20.54	15.15	38.58	10.84	25.95	17.95	59.11	18.07	12.71	13.07
Score	1.00	1.00	1.00	0.50	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	y_2	b_3	y_3	b_4-NH_3	b_4	b_5	b_6	$y{+}{+}_{12}$-H_2O	$y{+}{+}_{12}$	b_7	$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$
Delta Da	0.14	0.20	0.23	-0.77	0.27	0.19	0.21	0.23	0.37	-0.18	0.37	-0.61

Fragment-ion (m/z)	769.99	778.66	948.57	966.66	1077.60	1134.75	1152.66	1227.89	1247.70	1265.85	1308.76	1327.59	1490.02
Frac. Inten.(% of TIC)	0.11	2.61	2.41	11.69	3.00	2.61	16.54	2.34	2.56	8.22	1.75	1.77	1.88
Rel. Inten.(% of BP)	0.67	15.76	14.57	70.65	18.12	15.77	100.00	14.14	15.49	49.71	10.56	10.69	11.34
Score	1.50	-0.16	0.50	1.00	0.50	0.50	1.00	1.00	0.50	1.00	0.50	-0.11	1.00
Ion-type	sty		y_8-H_2O	y_8	y_9-H_2O	y_{10}-NH_3	y_{10}	b_{11}	y_{11}-H_2O	y_{11}	b_{12}-H_2O		b_{13}
Delta Da	0.57		0.15	0.23	0.13	-0.72	0.16	0.32	0.13	0.27	0.14		0.32

Peak 81



assignment



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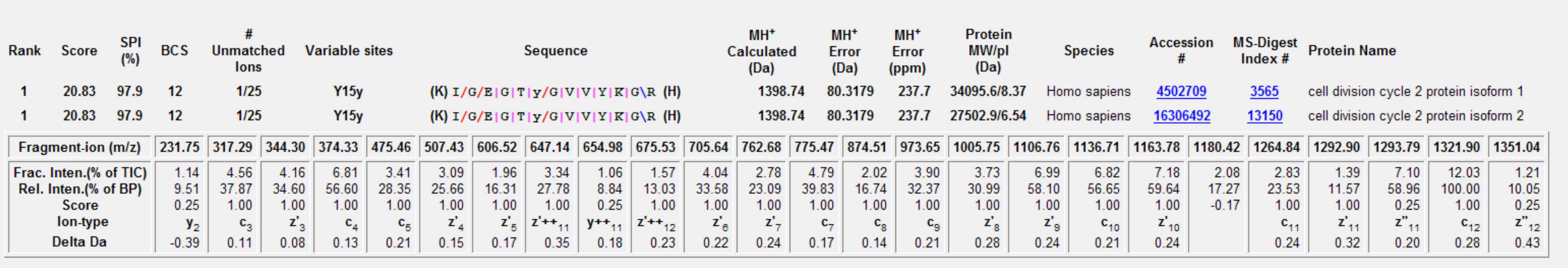
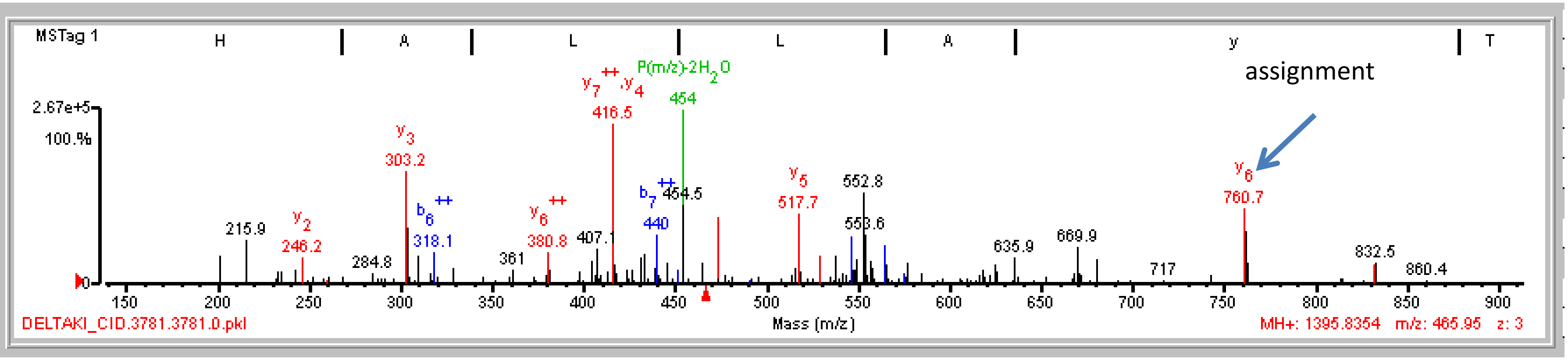


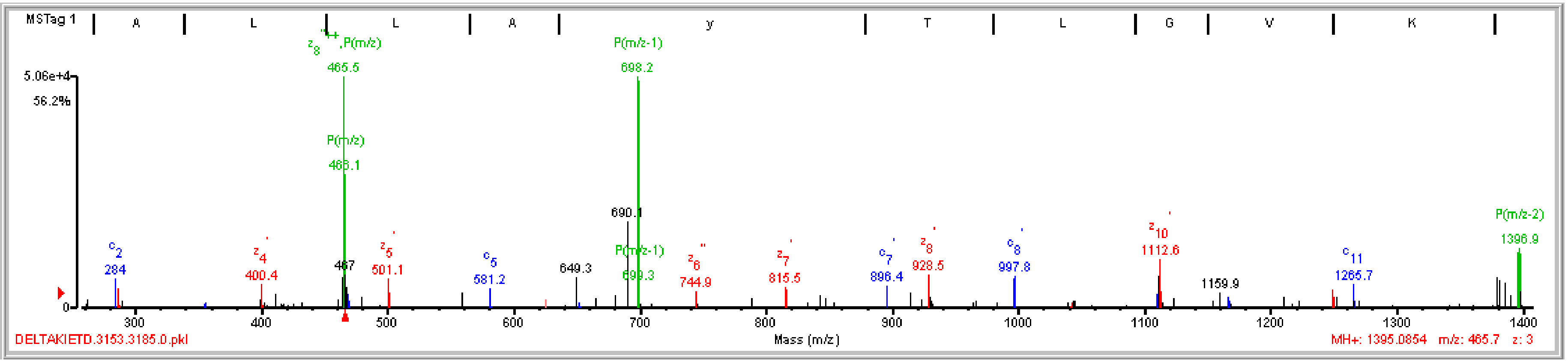
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.83	97.9	12	1/25	Y15y	(K) I/G/E|G|T|y/G|V|V|Y|K|G\R (H)	1398.74	80.3179	237.7	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	20.83	97.9	12	1/25	Y15y	(K) I/G/E|G|T|y/G|V|V|Y|K|G\R (H)	1398.74	80.3179	237.7	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

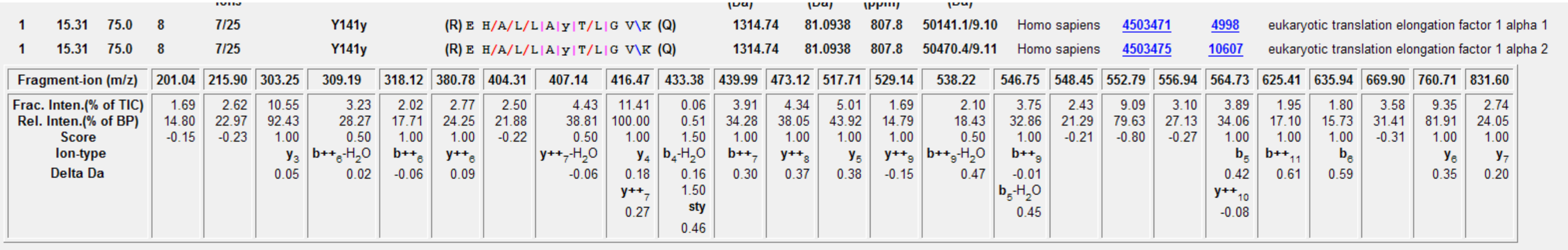
Fragment-ion (m/z)	231.75	317.29	344.30	374.33	475.46	507.43	606.52	647.14	654.98	675.53	705.64	762.68	775.47
Frac. Inten.(% of TIC)	1.14	4.56	4.16	6.81	3.41	3.09	1.96	3.34	1.06	1.57	4.04	2.78	4.79
Rel. Inten.(% of BP)	9.51	37.87	34.60	56.60	28.35	25.66	16.31	27.78	8.84	13.03	33.58	23.09	39.83
Score	0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00
Ion-type	y_2	c_3	z'_3	c_4	c_5	z'_4	z'_5	z'^{++}_{11}	y^{++}_{11}	z'^{++}_{12}	z'_6	z'_7	c_7
Delta Da	-0.39	0.11	0.08	0.13	0.21	0.15	0.17	0.35	0.18	0.23	0.22	0.24	0.17

Fragment-ion (m/z)	874.51	973.65	1005.75	1106.76	1136.71	1163.78	1180.42	1264.84	1292.90	1293.79	1321.90	1351.04
Frac. Inten.(% of TIC)	2.02	3.90	3.73	6.99	6.82	7.18	2.08	2.83	1.39	7.10	12.03	1.21
Rel. Inten.(% of BP)	16.74	32.37	30.99	58.10	56.65	59.64	17.27	23.53	11.57	58.96	100.00	10.05
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.17	1.00	1.00	0.25	1.00	0.25
Ion-type	c_8	c_9	z'_8	z'_9	c_{10}	z'_{10}		c_{11}	z'_{11}	z''_{11}	c_{12}	z''_{12}
Delta Da	0.14	0.21	0.28	0.24	0.21	0.24		0.24	0.32	0.20	0.28	0.43

Peak 82





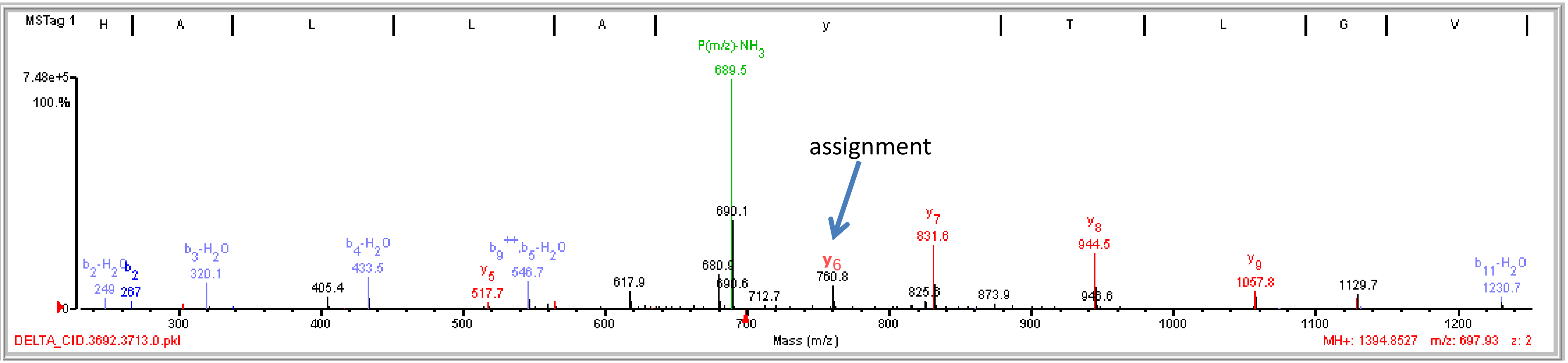


1	15.31	75.0	8	7/25	Y141y	(R) E H/A/L/L|A|y|T/L|G V\K (Q)	1314.74	81.0938	807.8	50141.1/9.10	Homo sapiens	4503471	4998	eukaryotic translation elongation factor 1 alpha 1
1	15.31	75.0	8	7/25	Y141y	(R) E H/A/L/L|A|y|T/L|G V\K (Q)	1314.74	81.0938	807.8	50470.4/9.11	Homo sapiens	4503475	10607	eukaryotic translation elongation factor 1 alpha 2

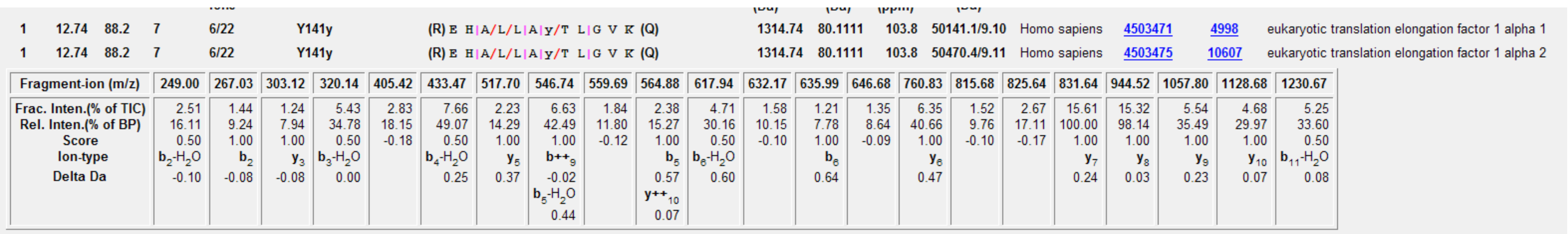
Fragment-ion (m/z)	201.04	215.90	303.25	309.19	318.12	380.78	404.31	407.14	416.47	433.38	439.99	473.12	517.71
Frac. Inten.(% of TIC)	1.69	2.62	10.55	3.23	2.02	2.77	2.50	4.43	11.41	0.06	3.91	4.34	5.01
Rel. Inten.(% of BP)	14.80	22.97	92.43	28.27	17.71	24.25	21.88	38.81	100.00	0.51	34.28	38.05	43.92
Score	-0.15	-0.23	1.00	0.50	1.00	1.00	-0.22	0.50	1.00	1.50 1.50	1.00	1.00	1.00
Ion-type			y_3	$b{+}{+}_6$-H_2O	$b{+}{+}_6$	$y{+}{+}_6$		$y{+}{+}_7$-H_2O	y_4 $y{+}{+}_7$	b_4-H_2O sty	$b{+}{+}_7$	$y{+}{+}_8$	y_5
Delta Da			0.05	0.02	-0.06	0.09		-0.06	0.18 0.27	0.16 0.46	0.30	0.37	0.38

Fragment-ion (m/z)	529.14	538.22	546.75	548.45	552.79	556.94	564.73	625.41	635.94	669.90	760.71	831.60
Frac. Inten.(% of TIC)	1.69	2.10	3.75	2.43	9.09	3.10	3.89	1.95	1.80	3.58	9.35	2.74
Rel. Inten.(% of BP)	14.79	18.43	32.86	21.29	79.63	27.13	34.06	17.10	15.73	31.41	81.91	24.05
Score	1.00	0.50	1.00	-0.21	-0.80	-0.27	1.00	1.00	1.00	-0.31	1.00	1.00
Ion-type	$y{+}{+}_9$	$b{+}{+}_9$-H_2O	$b{+}{+}_9$ b_5-H_2O				b_5 $y{+}{+}_{10}$	$b{+}{+}_{11}$	b_6		y_6	y_7
Delta Da	-0.15	0.47	-0.01 0.45				0.42 -0.08	0.61	0.59		0.35	0.20

Peak 83



assignment

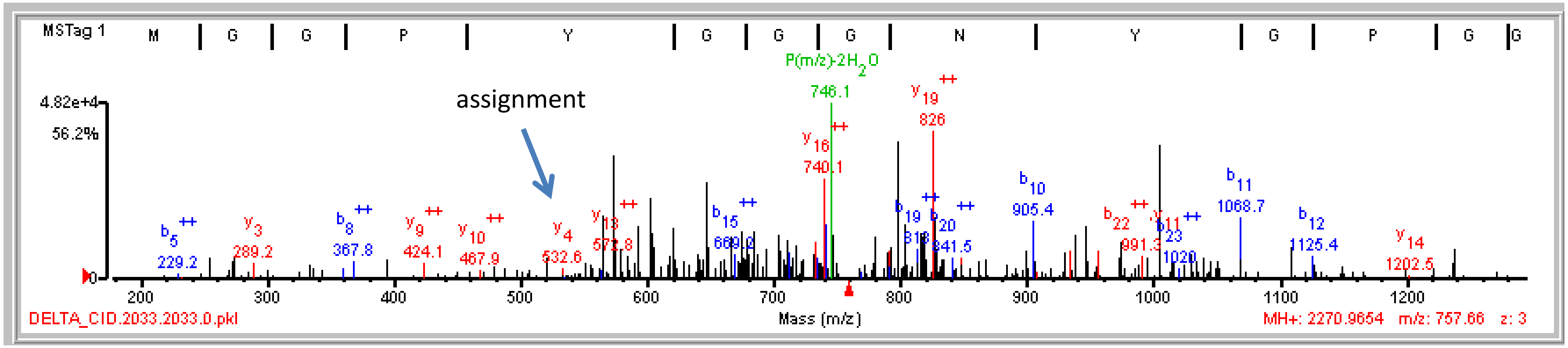


1	12.74	88.2	7	6/22	Y141y	(R) E H|A/L/L|A|y/T L|G V K (Q)	1314.74	80.1111	103.8	50141.1/9.10	Homo sapiens	4503471	4998	eukaryotic translation elongation factor 1 alpha 1
1	12.74	88.2	7	6/22	Y141y	(R) E H|A/L/L|A|y/T L|G V K (Q)	1314.74	80.1111	103.8	50470.4/9.11	Homo sapiens	4503475	10607	eukaryotic translation elongation factor 1 alpha 2

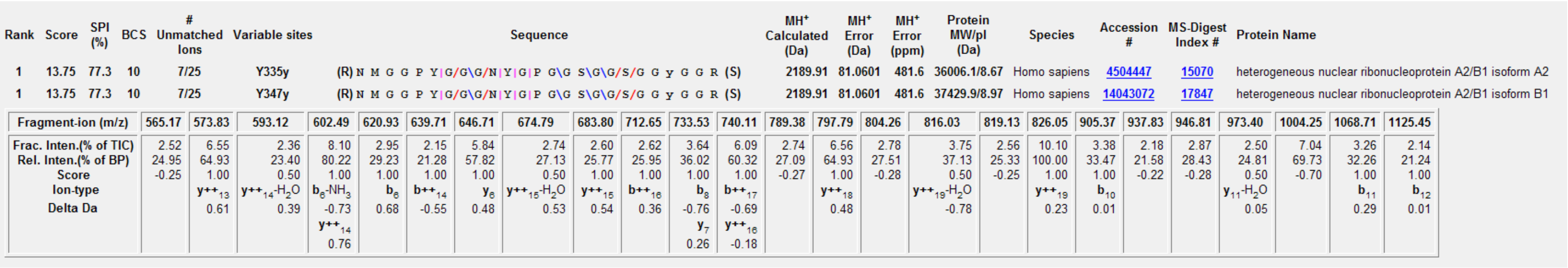
Fragment-ion (m/z)	249.00	267.03	303.12	320.14	405.42	433.47	517.70	546.74	559.69	564.88	617.94	632.17
Frac. Inten.(% of TIC)	2.51	1.44	1.24	5.43	2.83	7.66	2.23	6.63	1.84	2.38	4.71	1.58
Rel. Inten.(% of BP)	16.11	9.24	7.94	34.78	18.15	49.07	14.29	42.49	11.80	15.27	30.16	10.15
Score	0.50	1.00	1.00	0.50	-0.18	0.50	1.00	1.00	-0.12	1.00	0.50	-0.10
Ion-type	b_2-H_2O	b_2	y_3	b_3-H_2O		b_4-H_2O	y_5	$b{+}{+}_9$ -0.02 b_5-H_2O		b_5 0.57 $y{+}{+}_{10}$	b_6-H_2O	
Delta Da	-0.10	-0.08	-0.08	0.00		0.25	0.37	0.44		0.07	0.60	

Fragment-ion (m/z)	635.99	646.68	760.83	815.68	825.64	831.64	944.52	1057.80	1128.68	1230.67
Frac. Inten.(% of TIC)	1.21	1.35	6.35	1.52	2.67	15.61	15.32	5.54	4.68	5.25
Rel. Inten.(% of BP)	7.78	8.64	40.66	9.76	17.11	100.00	98.14	35.49	29.97	33.60
Score	1.00	-0.09	1.00	-0.10	-0.17	1.00	1.00	1.00	1.00	0.50
Ion-type	b_6		y_6			y_7	y_8	y_9	y_{10}	b_{11}-H_2O
Delta Da	0.64		0.47			0.24	0.03	0.23	0.07	0.08

Peak 85



assignment



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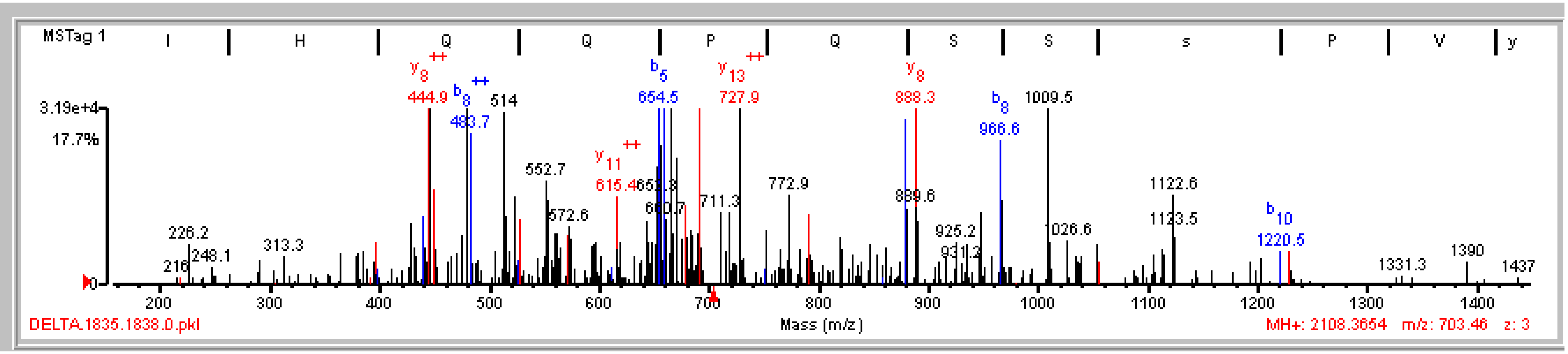
Fragment-ion (m/z)	565.17	573.83	593.12	602.49	620.93	639.71	646.71	674.79	683.80	712.65	733.53	740.11
Frac. Inten.(% of TIC)	2.52	6.55	2.36	8.10	2.95	2.15	5.84	2.74	2.60	2.62	3.64	6.09
Rel. Inten.(% of BP)	24.95	64.93	23.40	80.22	29.23	21.28	57.82	27.13	25.77	25.95	36.02	60.32
Score	-0.25	1.00	0.50	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type		y++$_{13}$	y++$_{14}$-H$_2$O	b$_6$-NH$_3$ y++$_{14}$	b$_6$	b++$_{14}$	y$_6$	y++$_{15}$-H$_2$O	y++$_{15}$	b++$_{16}$	b$_8$ y$_7$	b++$_{17}$ y++$_{16}$
Delta Da		0.61	0.39	-0.73 0.76	0.68	-0.55	0.48	0.53	0.54	0.36	-0.76 0.26	-0.69 -0.18

Fragment-ion (m/z)	789.38	797.79	804.26	816.03	819.13	826.05	905.37	937.83	946.81	973.40	1004.25	1068.71	1125.45
Frac. Inten.(% of TIC)	2.74	6.56	2.78	3.75	2.56	10.10	3.38	2.18	2.87	2.50	7.04	3.26	2.14
Rel. Inten.(% of BP)	27.09	64.93	27.51	37.13	25.33	100.00	33.47	21.58	28.43	24.81	69.73	32.26	21.24
Score	-0.27	1.00	-0.28	0.50	-0.25	1.00	1.00	-0.22	-0.28	0.50	-0.70	1.00	1.00
Ion-type		y++$_{18}$		y++$_{19}$-H$_2$O		y++$_{19}$	b$_{10}$			y$_{11}$-H$_2$O		b$_{11}$	b$_{12}$
Delta Da		0.48		-0.78		0.23	0.01			0.05		0.29	0.01

Peak 86



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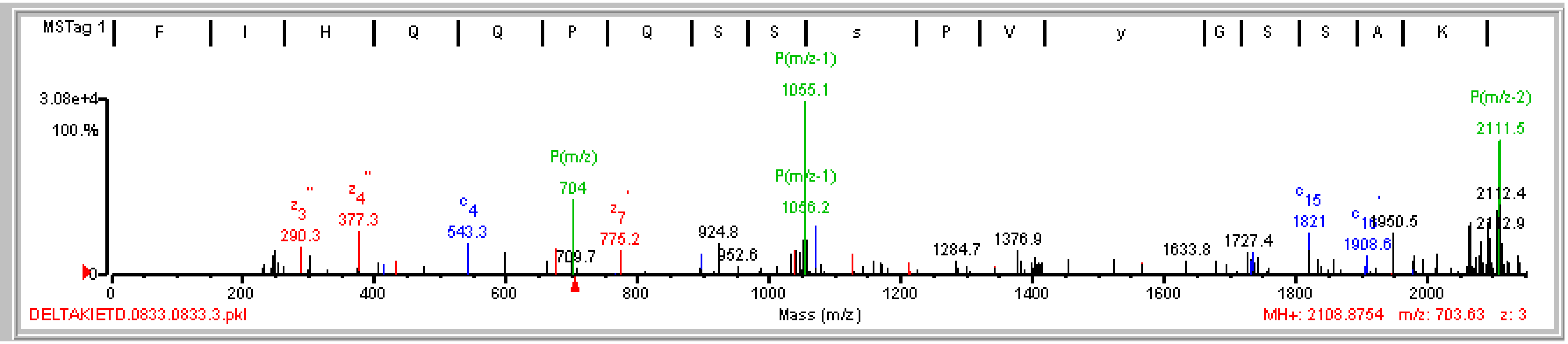


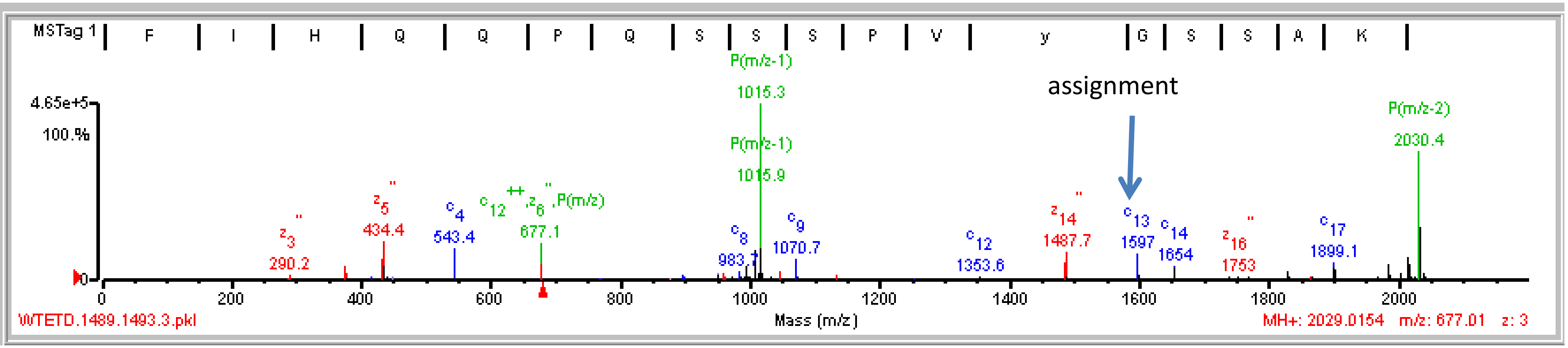
ETD

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.83	79.5	8	5/23	Y88y S85s	(R) F/I H Q Q|P/Q|S|S\s/P\V y/G S S A K (T)	1947.96	160.4095	226.2	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

Fragment-ion (m/z)	444.90	449.30	479.40	483.73	513.99	527.47	552.73	571.70	615.40	652.31
Frac. Inten.(% of TIC)	12.30	2.32	4.13	2.84	4.89	2.19	3.23	2.01	2.15	4.08
Rel. Inten.(% of BP)	100.00	18.88	33.61	23.09	39.73	17.82	26.26	16.38	17.47	33.16
Score	1.00	1.00	-0.34	1.00	-0.40	1.00	-0.26	1.00	1.00	-0.33
Ion-type	$y{++}_{8}$	y_{5}		$b{++}_{8}$		$b{++}_{9}$		$y{++}_{10}$	$y{++}_{11}$	
Delta Da	0.20	0.06		-0.01		0.21		-0.01	0.17	

Fragment-ion (m/z)	654.46	659.32	665.12	670.36	678.95	719.13	727.92	772.89	879.49	888.33	966.60	1009.50	1122.55
Frac. Inten.(% of TIC)	11.98	5.39	0.71	0.13	2.52	2.36	11.85	2.21	4.01	6.33	4.31	4.19	3.86
Rel. Inten.(% of BP)	97.34	43.82	5.77	1.05	20.46	19.20	96.33	17.93	32.58	51.48	35.06	34.03	31.39
Score	1.00	1.00	0.25	1.50	1.00	0.50	1.00	0.50	1.00	1.00	1.00	-0.34	0.25
Ion-type	b_{5}	$b{++}_{11}$	st	$y{++}_{12}$-H_2O	$y{++}_{12}$	$y{++}_{13}$-H_2O	$y{++}_{13}$	y_{7}-H_2O	b_{7}	y_{8}	b_{8}		b_{10}-H_3PO_4
Delta Da	0.12	0.04	0.48	0.11	-0.31	0.35	0.14	-0.43	0.04	-0.06	0.12		0.02
				1.50									
	$y{+++}_{17}$	st		sty									
	0.18			-0.28									

Peak 87



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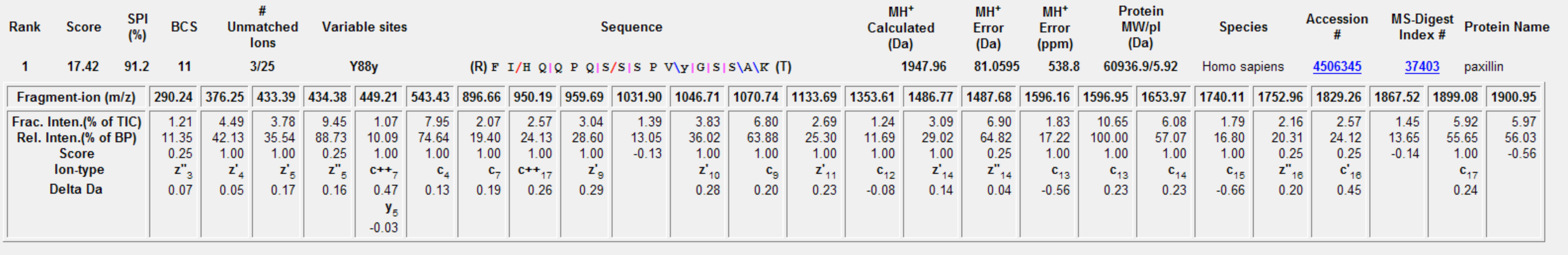
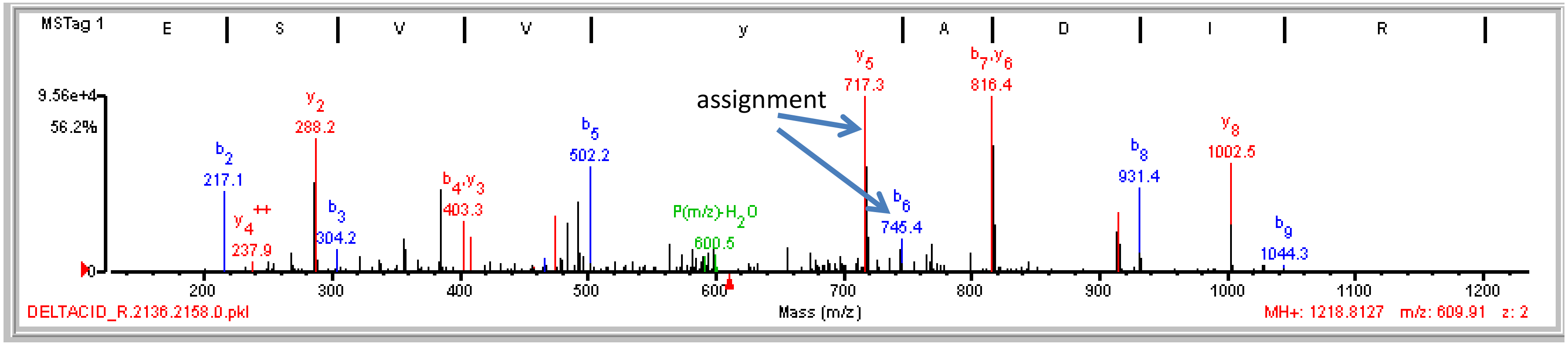


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.42	91.2	11	3/25	Y88y	(R) F I/H Q|Q P Q|S/S|S P V\y|G|S|S\A\K (T)	1947.96	81.0595	538.8	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

Fragment-ion (m/z)	290.24	376.25	433.39	434.38	449.21	543.43	896.66	950.19	959.69	1031.90	1046.71	1070.74
Frac. Inten.(% of TIC)	1.21	4.49	3.78	9.45	1.07	7.95	2.07	2.57	3.04	1.39	3.83	6.80
Rel. Inten.(% of BP)	11.35	42.13	35.54	88.73	10.09	74.64	19.40	24.13	28.60	13.05	36.02	63.88
Score	0.25	1.00	1.00	0.25	1.00	1.00	1.00	1.00	1.00	-0.13	1.00	1.00
Ion-type	z''_{3}	z'_{4}	z'_{5}	z''_{5}	c^{++}_{7}	c_{4}	c_{7}	c^{++}_{17}	z'_{9}		z'_{10}	c_{9}
Delta Da	0.07	0.05	0.17	0.16	0.47 y_{5} -0.03	0.13	0.19	0.26	0.29		0.28	0.20

Fragment-ion (m/z)	1133.69	1353.61	1486.77	1487.68	1596.16	1596.95	1653.97	1740.11	1752.96	1829.26	1867.52	1899.08	1900.95
Frac. Inten.(% of TIC)	2.69	1.24	3.09	6.90	1.83	10.65	6.08	1.79	2.16	2.57	1.45	5.92	5.97
Rel. Inten.(% of BP)	25.30	11.69	29.02	64.82	17.22	100.00	57.07	16.80	20.31	24.12	13.65	55.65	56.03
Score	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	0.25	0.25	-0.14	1.00	-0.56
Ion-type	z'_{11}	c_{12}	z'_{14}	z''_{14}	c_{13}	c_{13}	c_{14}	c_{15}	z''_{16}	c'_{16}		c_{17}	
Delta Da	0.23	-0.08	0.14	0.04	-0.56	0.23	0.23	-0.66	0.20	0.45		0.24	

Peak 88



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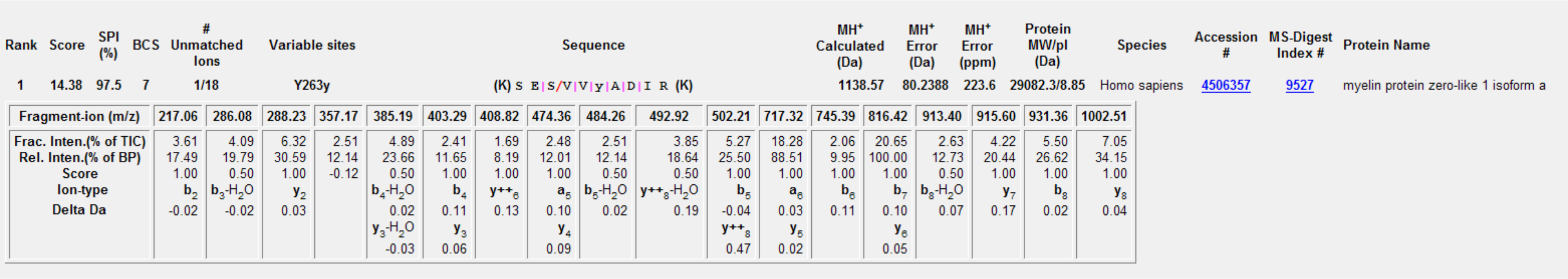
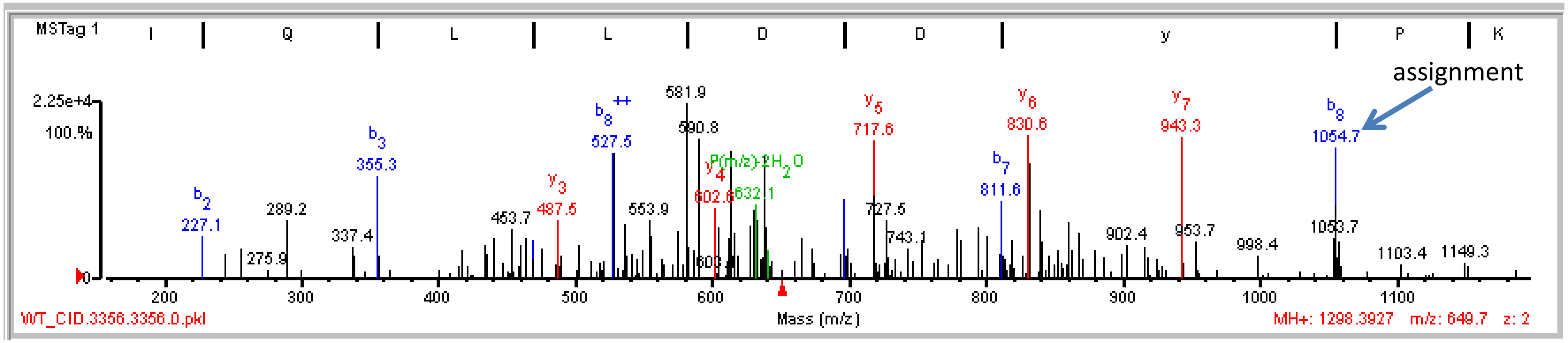
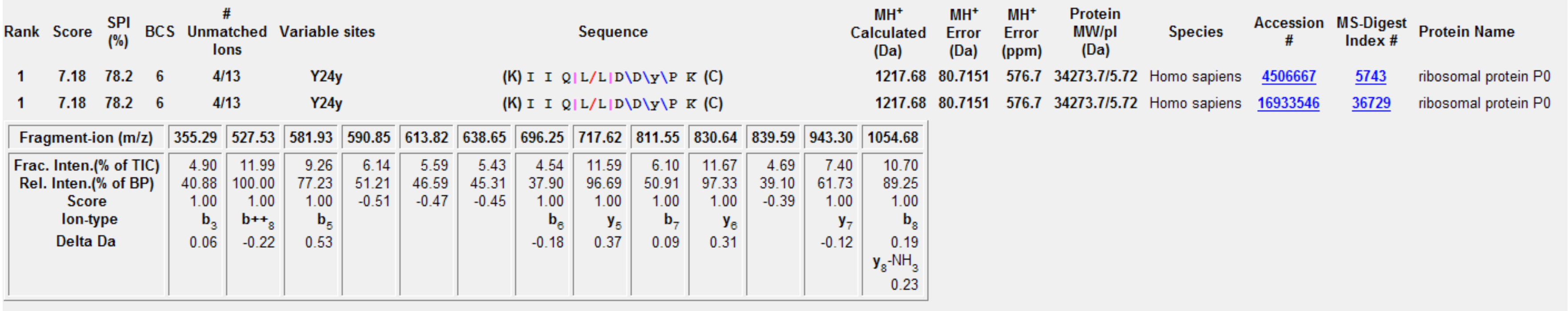


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.38	97.5	7	1/18	Y263y	(K) S E|S/V|V|y|A|D|I R (K)	1138.57	80.2388	223.6	29082.3/8.85	Homo sapiens	4506357	9527	myelin protein zero-like 1 isoform a

Fragment-ion (m/z)	217.06	286.08	288.23	357.17	385.19	403.29	408.82	474.36	484.26	492.92	502.21	717.32	745.39	816.42	913.40	915.60	931.36	1002.51
Frac. Inten.(% of TIC)	3.61	4.09	6.32	2.51	4.89	2.41	1.69	2.48	2.51	3.85	5.27	18.28	2.06	20.65	2.63	4.22	5.50	7.05
Rel. Inten.(% of BP)	17.49	19.79	30.59	12.14	23.66	11.65	8.19	12.01	12.14	18.64	25.50	88.51	9.95	100.00	12.73	20.44	26.62	34.15
Score	1.00	0.50	1.00	-0.12	0.50	1.00	1.00	1.00	0.50	0.50	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type	b_2	b_3-H_2O	y_2		b_4-H_2O	b_4	$y{+}{+}_6$	a_5	b_5-H_2O	$y{+}{+}_8$-H_2O	b_5	a_6	b_6	b_7	b_8-H_2O	y_7	b_8	y_8
Delta Da	-0.02	-0.02	0.03		0.02	0.11	0.13	0.10	0.02	0.19	-0.04	0.03	0.11	0.10	0.07	0.17	0.02	0.04
					y_3-H_2O	y_3		y_4			$y{+}{+}_8$	y_5		y_6				
					-0.03	0.06		0.09			0.47	0.02		0.05				

Peak 89

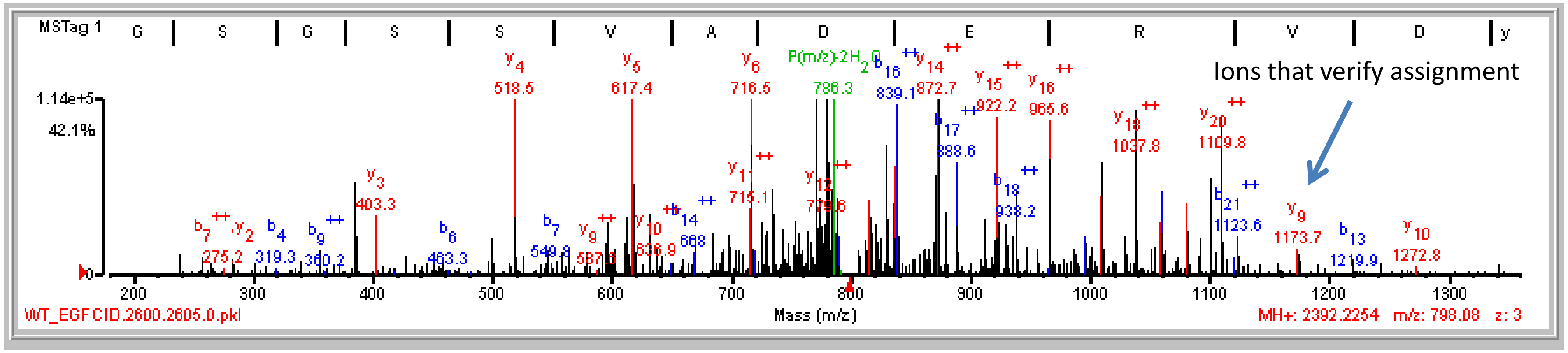




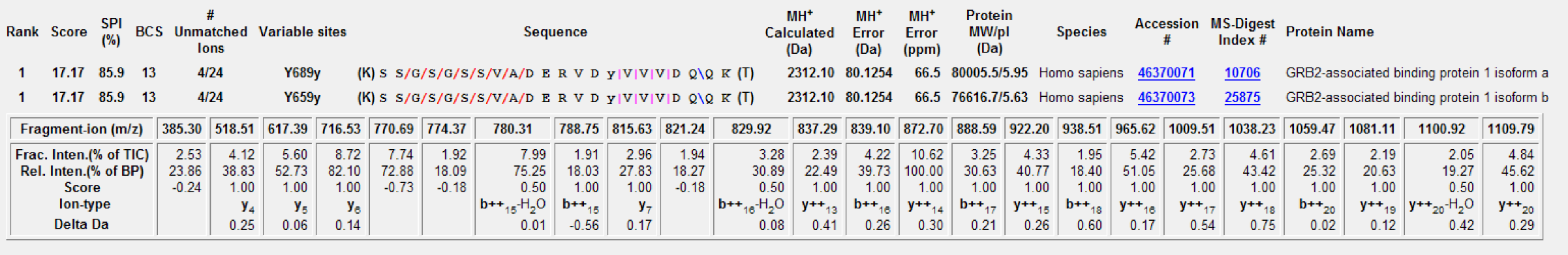
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.18	78.2	6	4/13	Y24y	(K) I I Q|L/L|D\D\y\P K (C)	1217.68	80.7151	576.7	34273.7/5.72	Homo sapiens	4506667	5743	ribosomal protein P0
1	7.18	78.2	6	4/13	Y24y	(K) I I Q|L/L|D\D\y\P K (C)	1217.68	80.7151	576.7	34273.7/5.72	Homo sapiens	16933546	36729	ribosomal protein P0

Fragment-ion (m/z)	355.29	527.53	581.93	590.85	613.82	638.65	696.25	717.62	811.55	830.64	839.59	943.30	1054.68
Frac. Inten.(% of TIC)	4.90	11.99	9.26	6.14	5.59	5.43	4.54	11.59	6.10	11.67	4.69	7.40	10.70
Rel. Inten.(% of BP)	40.88	100.00	77.23	51.21	46.59	45.31	37.90	96.69	50.91	97.33	39.10	61.73	89.25
Score	1.00	1.00	1.00	-0.51	-0.47	-0.45	1.00	1.00	1.00	1.00	-0.39	1.00	1.00
Ion-type	b_3	$b{+}{+}_8$	b_5				b_6	y_5	b_7	y_6		y_7	b_8 y_8-NH_3
Delta Da	0.06	-0.22	0.53				-0.18	0.37	0.09	0.31		-0.12	0.19 0.23

Peak 90



Ions that verify assignment

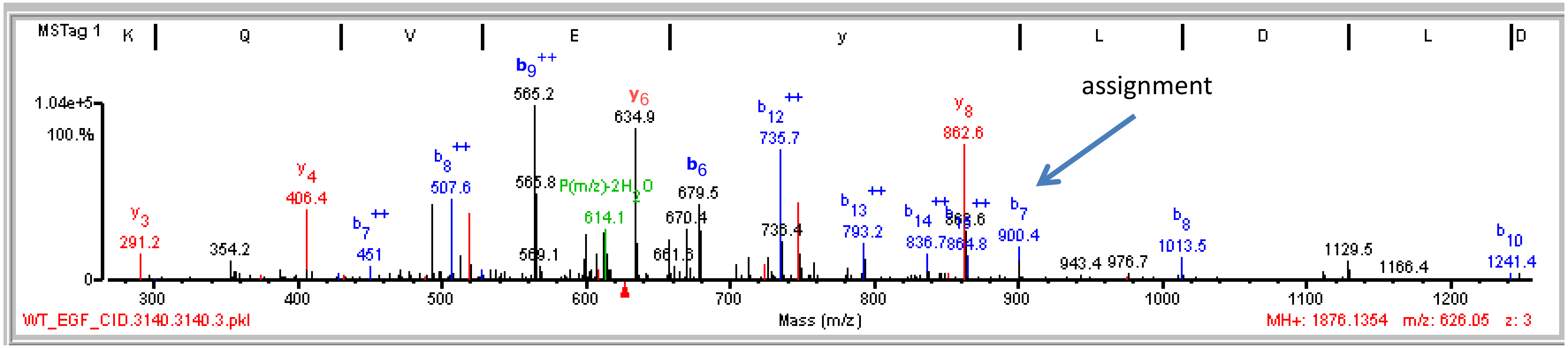


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.17	85.9	13	4/24	Y689y	(K) S S/G/S/G/S/S/V/A/D E R V D y|V|V|V|D Q\Q K (T)	2312.10	80.1254	66.5	80005.5/5.95	Homo sapiens	46370071	10706	GRB2-associated binding protein 1 isoform a
1	17.17	85.9	13	4/24	Y659y	(K) S S/G/S/G/S/S/V/A/D E R V D y|V|V|V|D Q\Q K (T)	2312.10	80.1254	66.5	76616.7/5.63	Homo sapiens	46370073	25875	GRB2-associated binding protein 1 isoform b

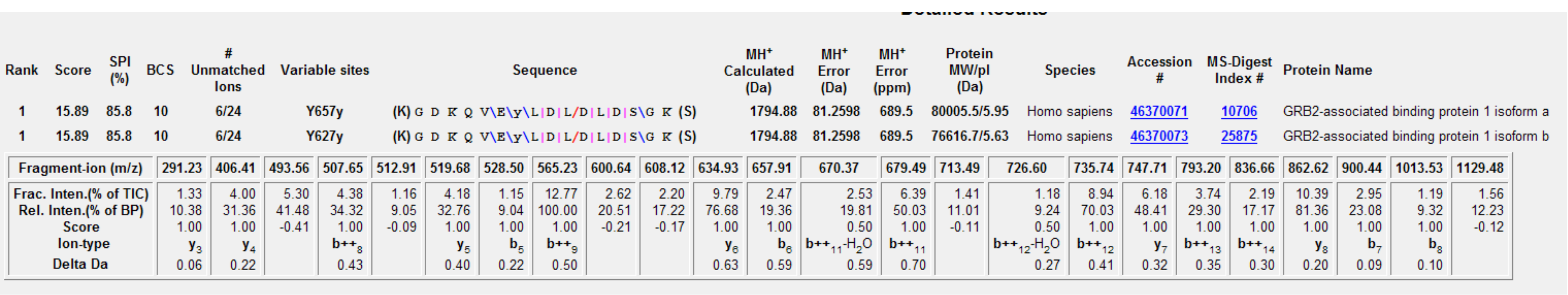
Fragment-ion (m/z)	385.30	518.51	617.39	716.53	770.69	774.37	780.31	788.75	815.63	821.24	829.92
Frac. Inten.(% of TIC)	2.53	4.12	5.60	8.72	7.74	1.92	7.99	1.91	2.96	1.94	3.28
Rel. Inten.(% of BP)	23.86	38.83	52.73	82.10	72.88	18.09	75.25	18.03	27.83	18.27	30.89
Score	-0.24	1.00	1.00	1.00	-0.73	-0.18	0.50	1.00	1.00	-0.18	0.50
Ion-type		y_4	y_5	y_6			$b{+}{+}_{15}$-H_2O	$b{+}{+}_{15}$	y_7		$b{+}{+}_{16}$-H_2O
Delta Da		0.25	0.06	0.14			0.01	-0.56	0.17		0.08

Fragment-ion (m/z)	837.29	839.10	872.70	888.59	922.20	938.51	965.62	1009.51	1038.23	1059.47	1081.11	1100.92	1109.79
Frac. Inten.(% of TIC)	2.39	4.22	10.62	3.25	4.33	1.95	5.42	2.73	4.61	2.69	2.19	2.05	4.84
Rel. Inten.(% of BP)	22.49	39.73	100.00	30.63	40.77	18.40	51.05	25.68	43.42	25.32	20.63	19.27	45.62
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00
Ion-type	$y{+}{+}_{13}$	$b{+}{+}_{16}$	$y{+}{+}_{14}$	$b{+}{+}_{17}$	$y{+}{+}_{15}$	$b{+}{+}_{18}$	$y{+}{+}_{16}$	$y{+}{+}_{17}$	$y{+}{+}_{18}$	$b{+}{+}_{20}$	$y{+}{+}_{19}$	$y{+}{+}_{20}$-H_2O	$y{+}{+}_{20}$
Delta Da	0.41	0.26	0.30	0.21	0.26	0.60	0.17	0.54	0.75	0.02	0.12	0.42	0.29

Peak 91



assignment



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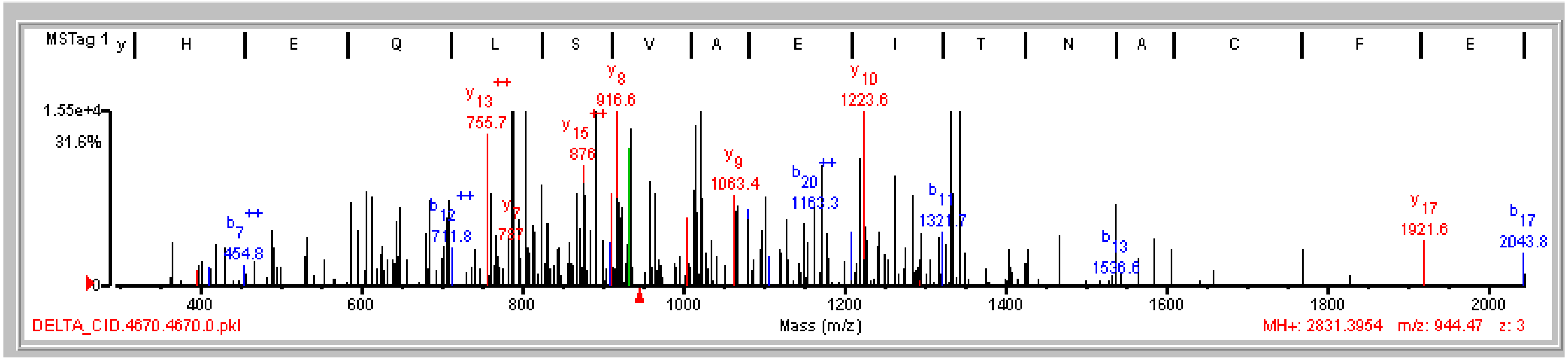
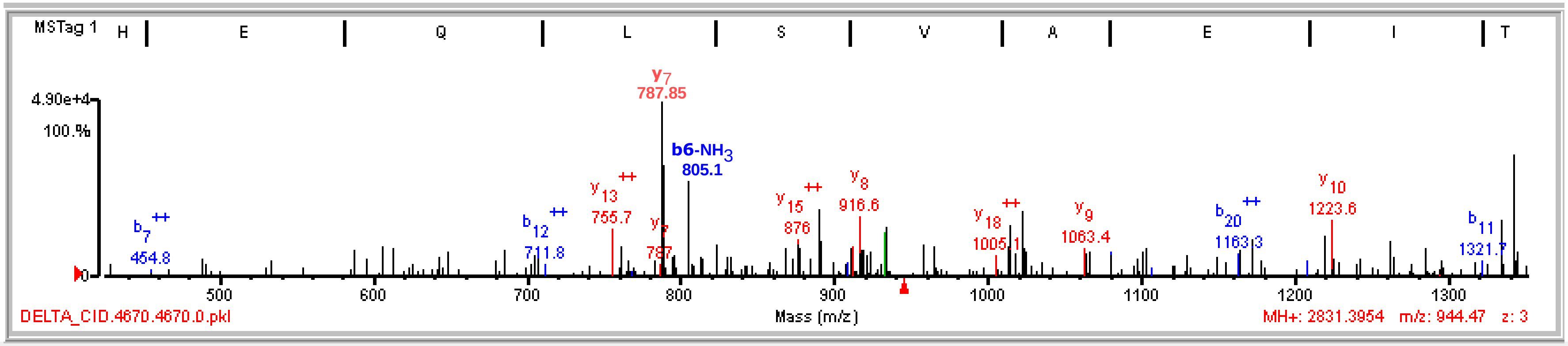
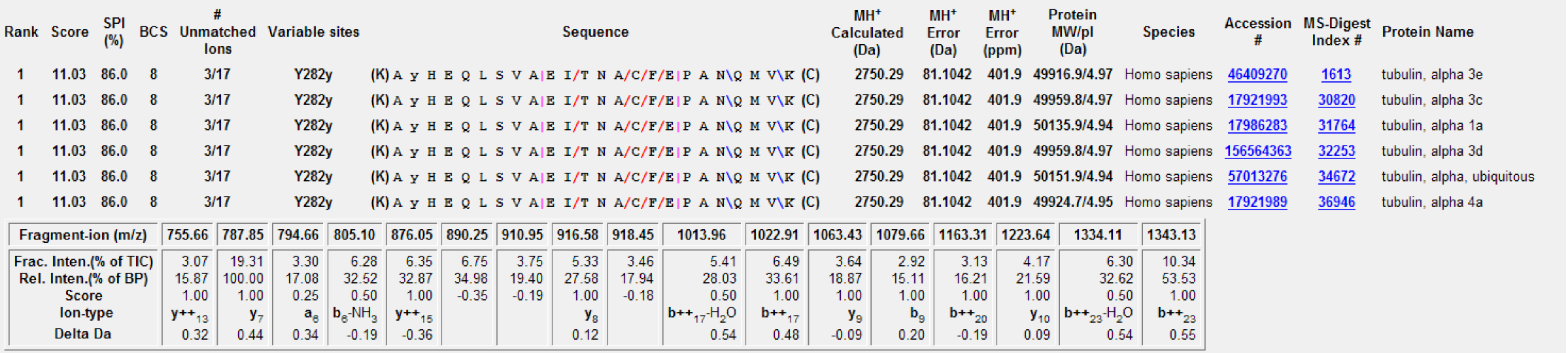
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>15.89</td><td>85.8</td><td>10</td><td>6/24</td><td>Y657y</td><td>(K) G D K Q V\E\y\L|D|L/D|L|D|S\G K (S)</td><td>1794.88</td><td>81.2598</td><td>689.5</td><td>80005.5/5.95</td><td>Homo sapiens</td><td>46370071</td><td>10706</td><td>GRB2-associated binding protein 1 isoform a</td></tr>
<tr><td>1</td><td>15.89</td><td>85.8</td><td>10</td><td>6/24</td><td>Y627y</td><td>(K) G D K Q V\E\y\L|D|L/D|L|D|S\G K (S)</td><td>1794.88</td><td>81.2598</td><td>689.5</td><td>76616.7/5.63</td><td>Homo sapiens</td><td>46370073</td><td>25875</td><td>GRB2-associated binding protein 1 isoform b</td></tr>
</table>

Fragment-ion (m/z)	291.23	406.41	493.56	507.65	512.91	519.68	528.50	565.23	600.64	608.12	634.93	657.91	670.37	679.49	713.49	726.60	735.74	747.71	793.20	836.66	862.62	900.44	1013.53	1129.48
Frac. Inten.(% of TIC)	1.33	4.00	5.30	4.38	1.16	4.18	1.15	12.77	2.62	2.20	9.79	2.47	2.53	6.39	1.41	1.18	8.94	6.18	3.74	2.19	10.39	2.95	1.19	1.56
Rel. Inten.(% of BP)	10.38	31.36	41.48	34.32	9.05	32.76	9.04	100.00	20.51	17.22	76.68	19.36	19.81	50.03	11.01	9.24	70.03	48.41	29.30	17.17	81.36	23.08	9.32	12.23
Score	1.00	1.00	-0.41	1.00	-0.09	1.00	1.00	1.00	-0.21	-0.17	1.00	1.00	0.50	1.00	-0.11	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.12
Ion-type	y_3	y_4		$b{+}{+}_8$		y_5	b_5	$b{+}{+}_9$			y_6	b_6	$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$		$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$	y_7	$b{+}{+}_{13}$	$b{+}{+}_{14}$	y_8	b_7	b_8	
Delta Da	0.06	0.22		0.43		0.40	0.22	0.50			0.63	0.59	0.59	0.70		0.27	0.41	0.32	0.35	0.30	0.20	0.09	0.10	

Peak 92



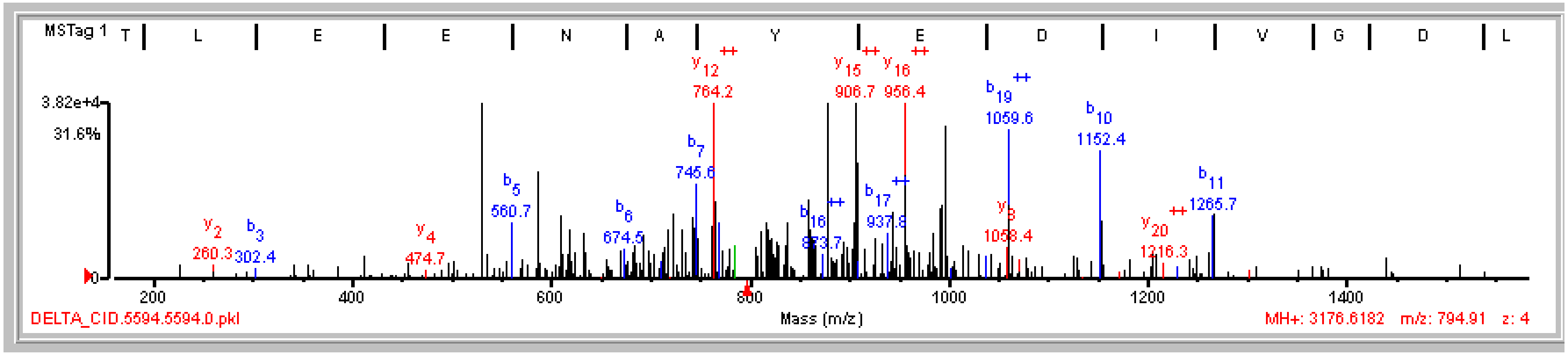


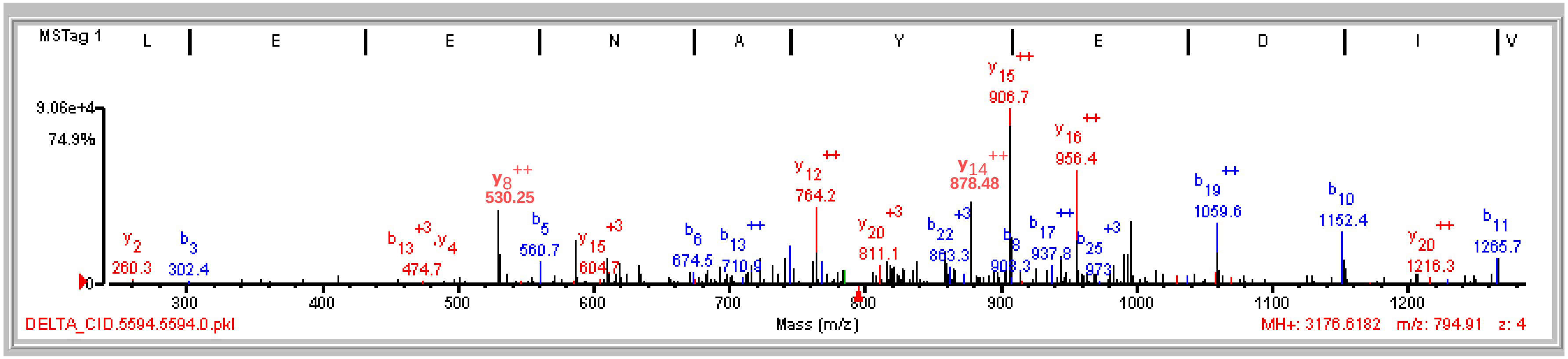


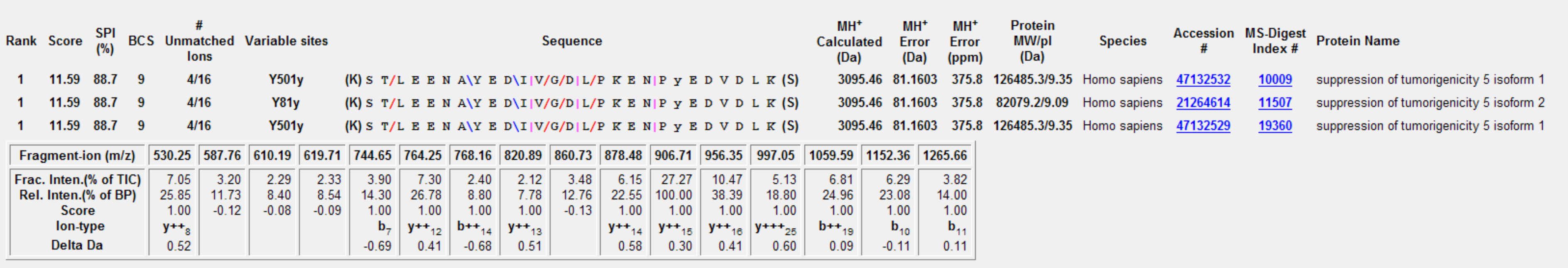
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	49916.9/4.97	Homo sapiens	46409270	1613	tubulin, alpha 3e
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	49959.8/4.97	Homo sapiens	17921993	30820	tubulin, alpha 3c
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	50135.9/4.94	Homo sapiens	17986283	31764	tubulin, alpha 1a
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	49959.8/4.97	Homo sapiens	156564363	32253	tubulin, alpha 3d
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	50151.9/4.94	Homo sapiens	57013276	34672	tubulin, alpha, ubiquitous
1	11.03	86.0	8	3/17	Y282y	(K) A y H E Q L S V A|E I/T N A/C/F/E|P A N\Q M V\K (C)	2750.29	81.1042	401.9	49924.7/4.95	Homo sapiens	17921989	36946	tubulin, alpha 4a

Fragment-ion (m/z)	755.66	787.85	794.66	805.10	876.05	890.25	910.95	916.58	918.45	1013.96	1022.91	1063.43	1079.66	1163.31	1223.64	1334.11	1343.13
Frac. Inten.(% of TIC)	3.07	19.31	3.30	6.28	6.35	6.75	3.75	5.33	3.46	5.41	6.49	3.64	2.92	3.13	4.17	6.30	10.34
Rel. Inten.(% of BP)	15.87	100.00	17.08	32.52	32.87	34.98	19.40	27.58	17.94	28.03	33.61	18.87	15.11	16.21	21.59	32.62	53.53
Score	1.00	1.00	0.25	0.50	1.00	-0.35	-0.19	1.00	-0.18	0.50	1.00	1.00	1.00	1.00	1.00	0.50	1.00
Ion-type	y^{++}_{13}	y_7	a_6	b_6-NH_3	y^{++}_{15}			y_8		b^{++}_{17}-H_2O	b^{++}_{17}	y_9	b_9	b^{++}_{20}	y_{10}	b^{++}_{23}-H_2O	b^{++}_{23}
Delta Da	0.32	0.44	0.34	-0.19	-0.36			0.12		0.54	0.48	-0.09	0.20	-0.19	0.09	0.54	0.55

Peak 93



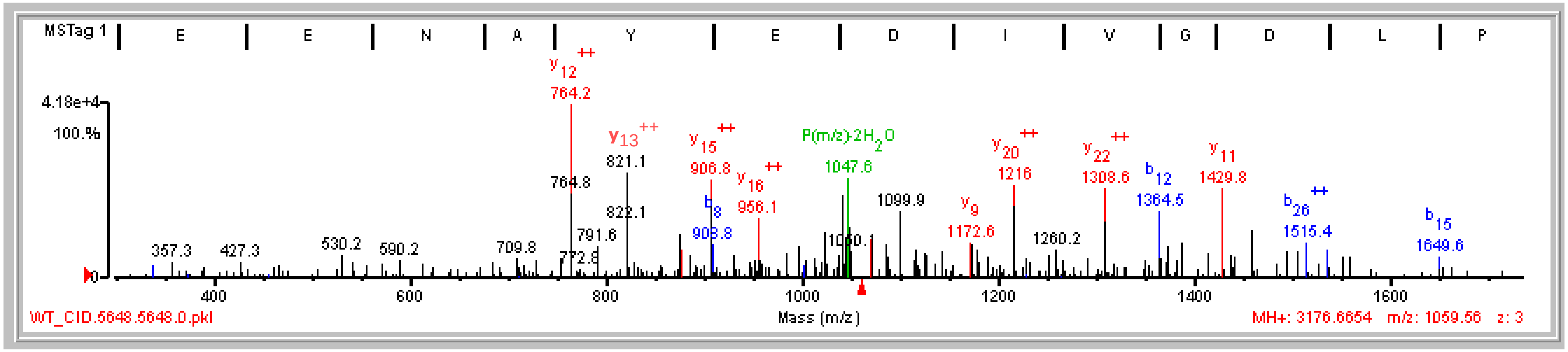


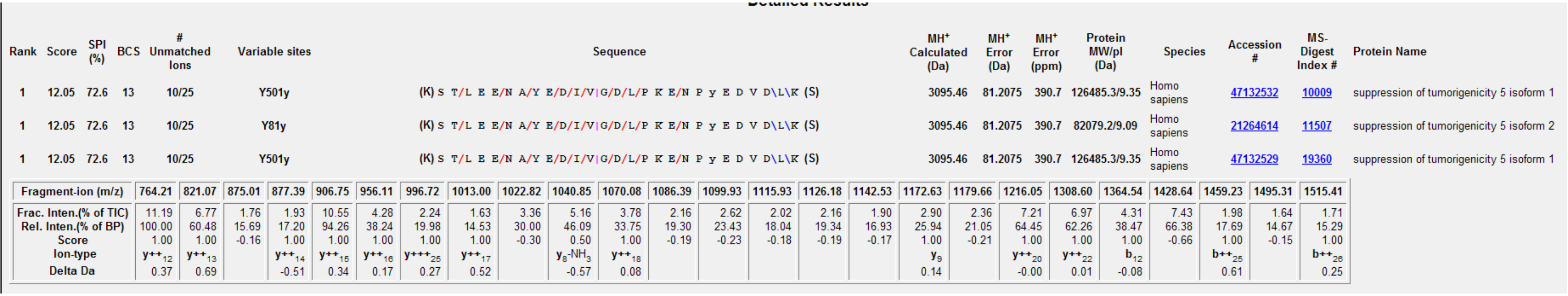


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.59	88.7	9	4/16	Y501y	(K) S T/L E E N A\Y E D\I|V/G/D|L/P K E N|P y E D V D L K (S)	3095.46	81.1603	375.8	126485.3/9.35	Homo sapiens	47132532	10009	suppression of tumorigenicity 5 isoform 1
1	11.59	88.7	9	4/16	Y81y	(K) S T/L E E N A\Y E D\I|V/G/D|L/P K E N|P y E D V D L K (S)	3095.46	81.1603	375.8	82079.2/9.09	Homo sapiens	21264614	11507	suppression of tumorigenicity 5 isoform 2
1	11.59	88.7	9	4/16	Y501y	(K) S T/L E E N A\Y E D\I|V/G/D|L/P K E N|P y E D V D L K (S)	3095.46	81.1603	375.8	126485.3/9.35	Homo sapiens	47132529	19360	suppression of tumorigenicity 5 isoform 1

Fragment-ion (m/z)	530.25	587.76	610.19	619.71	744.65	764.25	768.16	820.89	860.73	878.48	906.71	956.35	997.05	1059.59	1152.36	1265.66
Frac. Inten.(% of TIC)	7.05	3.20	2.29	2.33	3.90	7.30	2.40	2.12	3.48	6.15	27.27	10.47	5.13	6.81	6.29	3.82
Rel. Inten.(% of BP)	25.85	11.73	8.40	8.54	14.30	26.78	8.80	7.78	12.76	22.55	100.00	38.39	18.80	24.96	23.08	14.00
Score	1.00	-0.12	-0.08	-0.09	1.00	1.00	1.00	1.00	-0.13	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y++$_{8}$				b$_{7}$	y++$_{12}$	b++$_{14}$	y++$_{13}$		y++$_{14}$	y++$_{15}$	y++$_{16}$	y+++$_{25}$	b++$_{19}$	b$_{10}$	b$_{11}$
Delta Da	0.52				-0.69	0.41	-0.68	0.51		0.58	0.30	0.41	0.60	0.09	-0.11	0.11

Peak 94



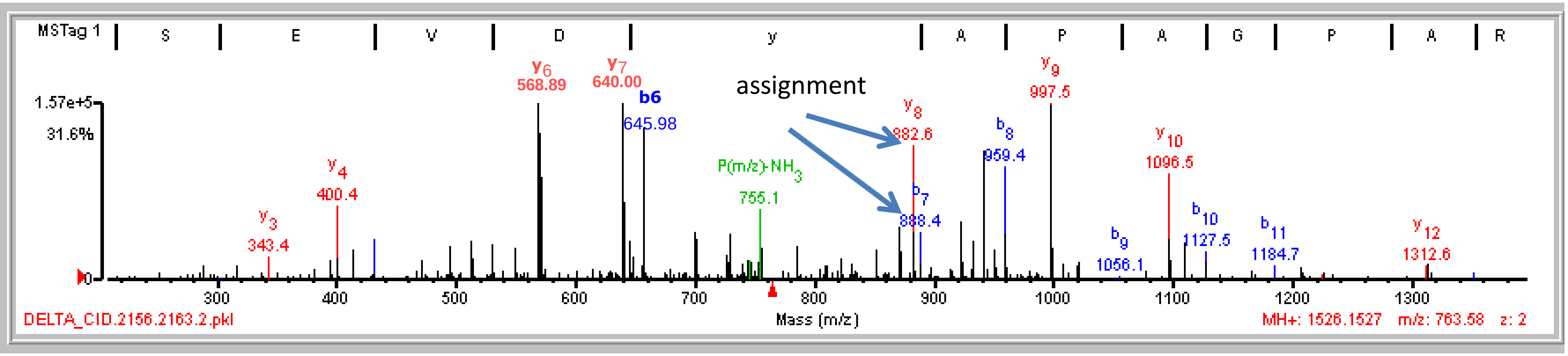


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.05	72.6	13	10/25	Y501y	(K) S T/L E E/N A/Y E/D/I/V|G/D/L/P K E/N P y E D V D\L\K (S)	3095.46	81.2075	390.7	126485.3/9.35	Homo sapiens	47132532	10009	suppression of tumorigenicity 5 isoform 1
1	12.05	72.6	13	10/25	Y81y	(K) S T/L E E/N A/Y E/D/I/V|G/D/L/P K E/N P y E D V D\L\K (S)	3095.46	81.2075	390.7	82079.2/9.09	Homo sapiens	21264614	11507	suppression of tumorigenicity 5 isoform 2
1	12.05	72.6	13	10/25	Y501y	(K) S T/L E E/N A/Y E/D/I/V|G/D/L/P K E/N P y E D V D\L\K (S)	3095.46	81.2075	390.7	126485.3/9.35	Homo sapiens	47132529	19360	suppression of tumorigenicity 5 isoform 1

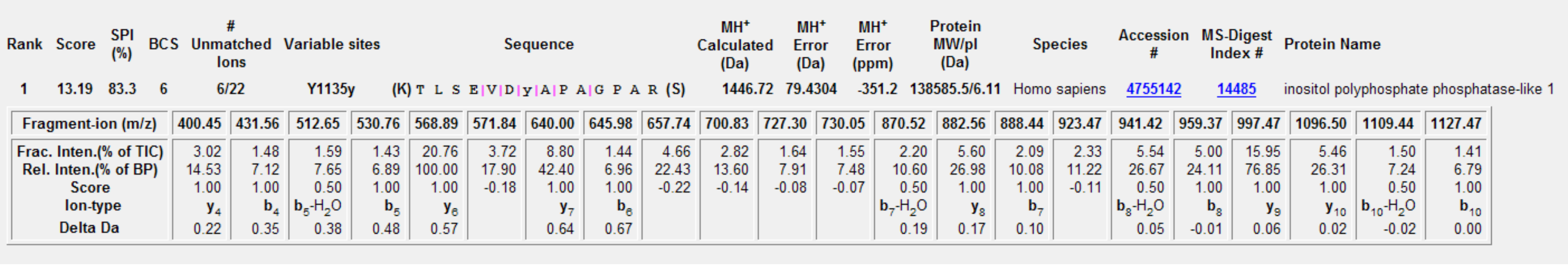
Fragment-ion (m/z)	764.21	821.07	875.01	877.39	906.75	956.11	996.72	1013.00	1022.82	1040.85	1070.08	1086.39	1099.93
Frac. Inten.(% of TIC)	11.19	6.77	1.76	1.93	10.55	4.28	2.24	1.63	3.36	5.16	3.78	2.16	2.62
Rel. Inten.(% of BP)	100.00	60.48	15.69	17.20	94.26	38.24	19.98	14.53	30.00	46.09	33.75	19.30	23.43
Score	1.00	1.00	-0.16	1.00	1.00	1.00	1.00	1.00	-0.30	0.50	1.00	-0.19	-0.23
Ion-type	y^{++}_{12}	y^{++}_{13}		y^{++}_{14}	y^{++}_{15}	y^{++}_{16}	y^{+++}_{25}	y^{++}_{17}		y_8-NH$_3$	y^{++}_{18}		
Delta Da	0.37	0.69		-0.51	0.34	0.17	0.27	0.52		-0.57	0.08		

Fragment-ion (m/z)	1115.93	1126.18	1142.53	1172.63	1179.66	1216.05	1308.60	1364.54	1428.64	1459.23	1495.31	1515.41
Frac. Inten.(% of TIC)	2.02	2.16	1.90	2.90	2.36	7.21	6.97	4.31	7.43	1.98	1.64	1.71
Rel. Inten.(% of BP)	18.04	19.34	16.93	25.94	21.05	64.45	62.26	38.47	66.38	17.69	14.67	15.29
Score	-0.18	-0.19	-0.17	1.00	-0.21	1.00	1.00	1.00	-0.66	1.00	-0.15	1.00
Ion-type				y_9		y^{++}_{20}	y^{++}_{22}	b_{12}		b^{++}_{25}		b^{++}_{26}
Delta Da				0.14		-0.00	0.01	-0.08		0.61		0.25

Peak 95



assignment

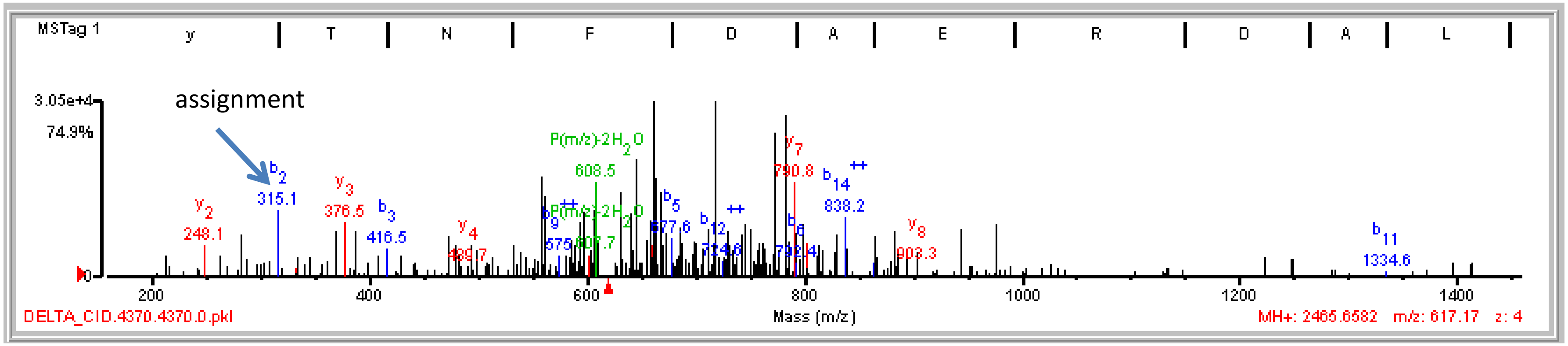


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.19	83.3	6	6/22	Y1135y	(K) T L S E|V|D|y|A|P A|G P A R (S)	1446.72	79.4304	-351.2	138585.5/6.11	Homo sapiens	4755142	14485	inositol polyphosphate phosphatase-like 1

Fragment-ion (m/z)	400.45	431.56	512.65	530.76	568.89	571.84	640.00	645.98	657.74	700.83	727.30
Frac. Inten.(% of TIC)	3.02	1.48	1.59	1.43	20.76	3.72	8.80	1.44	4.66	2.82	1.64
Rel. Inten.(% of BP)	14.53	7.12	7.65	6.89	100.00	17.90	42.40	6.96	22.43	13.60	7.91
Score	1.00	1.00	0.50	1.00	1.00	-0.18	1.00	1.00	-0.22	-0.14	-0.08
Ion-type	y_4	b_4	b_5-H_2O	b_5	y_6		y_7	b_6			
Delta Da	0.22	0.35	0.38	0.48	0.57		0.64	0.67			

Fragment-ion (m/z)	730.05	870.52	882.56	888.44	923.47	941.42	959.37	997.47	1096.50	1109.44	1127.47
Frac. Inten.(% of TIC)	1.55	2.20	5.60	2.09	2.33	5.54	5.00	15.95	5.46	1.50	1.41
Rel. Inten.(% of BP)	7.48	10.60	26.98	10.08	11.22	26.67	24.11	76.85	26.31	7.24	6.79
Score	-0.07	0.50	1.00	1.00	-0.11	0.50	1.00	1.00	1.00	0.50	1.00
Ion-type		b_7-H_2O	y_8	b_7		b_8-H_2O	b_8	y_9	y_{10}	b_{10}-H_2O	b_{10}
Delta Da		0.19	0.17	0.10		0.05	-0.01	0.06	0.02	-0.02	0.00

Peak 96



assignment

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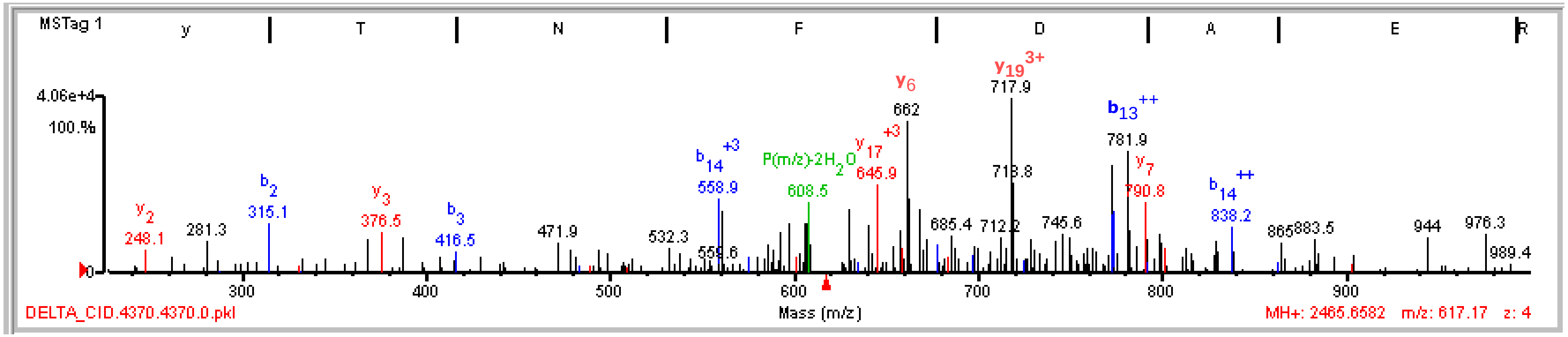

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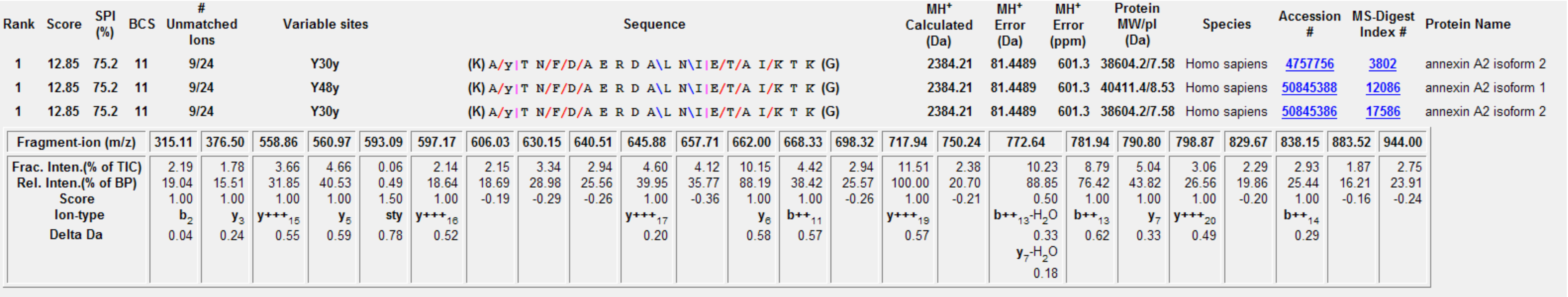
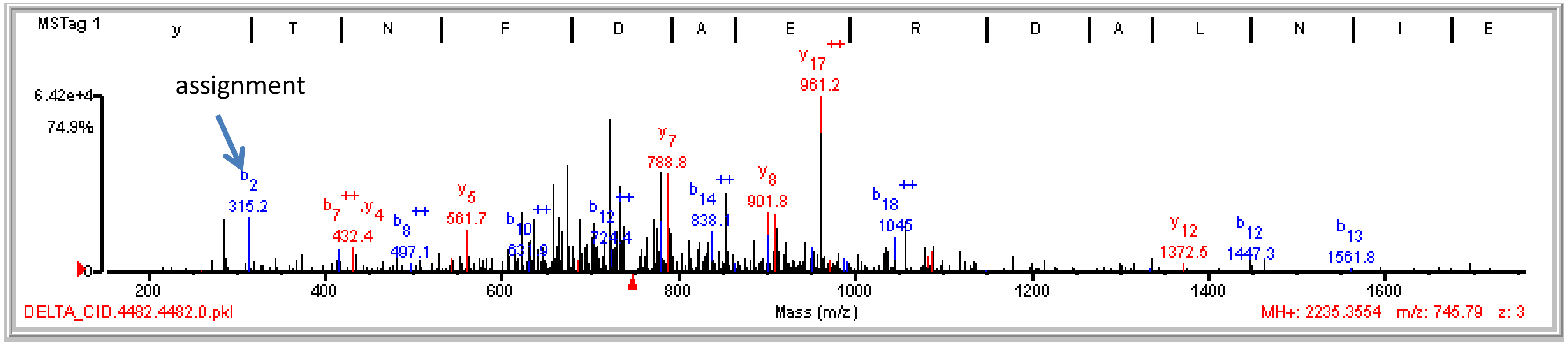


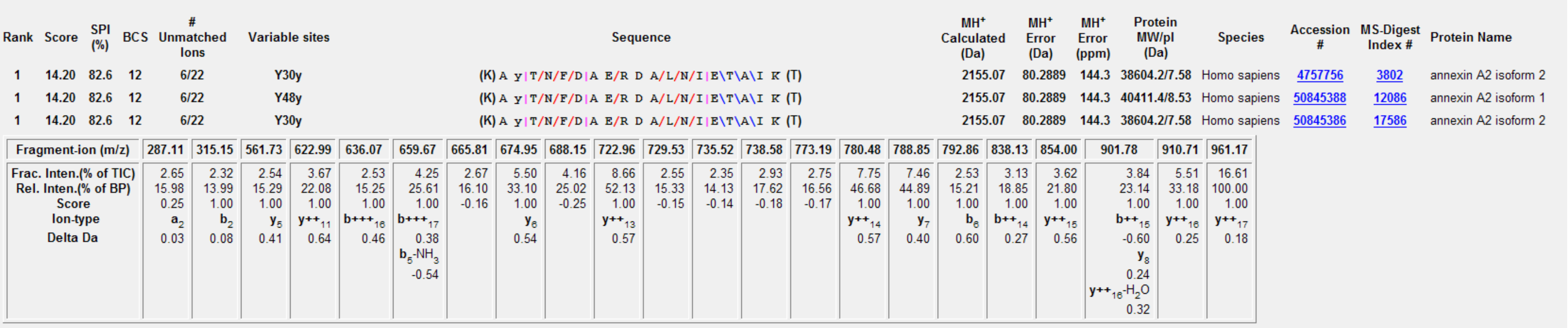
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.85	75.2	11	9/24	Y30y	(K) A/y|T N/F/D/A E R D A\L N\I|E/T/A I/K T K (G)	2384.21	81.4489	601.3	38604.2/7.58	Homo sapiens	4757756	3802	annexin A2 isoform 2
1	12.85	75.2	11	9/24	Y48y	(K) A/y|T N/F/D/A E R D A\L N\I|E/T/A I/K T K (G)	2384.21	81.4489	601.3	40411.4/8.53	Homo sapiens	50845388	12086	annexin A2 isoform 1
1	12.85	75.2	11	9/24	Y30y	(K) A/y|T N/F/D/A E R D A\L N\I|E/T/A I/K T K (G)	2384.21	81.4489	601.3	38604.2/7.58	Homo sapiens	50845386	17586	annexin A2 isoform 2

Fragment-ion (m/z)	315.11	376.50	558.86	560.97	593.09	597.17	606.03	630.15	640.51	645.88	657.71	662.00	668.33	698.32	717.94	750.24	772.64	781.94	790.80	798.87	829.67	838.15	883.52	944.00
Frac. Inten.(% of TIC)	2.19	1.78	3.66	4.66	0.06	2.14	2.15	3.34	2.94	4.60	4.12	10.15	4.42	2.94	11.51	2.38	10.23	8.79	5.04	3.06	2.29	2.93	1.87	2.75
Rel. Inten.(% of BP)	19.04	15.51	31.85	40.53	0.49	18.64	18.69	28.98	25.56	39.95	35.77	88.19	38.42	25.57	100.00	20.70	88.85	76.42	43.82	26.56	19.86	25.44	16.21	23.91
Score	1.00	1.00	1.00	1.00	1.50	1.00	-0.19	-0.29	-0.26	1.00	-0.36	1.00	1.00	-0.26	1.00	-0.21	0.50	1.00	1.00	1.00	-0.20	1.00	-0.16	-0.24
Ion-type	b_2	y_3	$y+++_{15}$	y_5	sty	$y+++_{16}$				$y+++_{17}$		y_6	$b++_{11}$		$y+++_{19}$		$b++_{13}\text{-}H_2O$ $y_7\text{-}H_2O$	$b++_{13}$	y_7	$y+++_{20}$		$b++_{14}$		
Delta Da	0.04	0.24	0.55	0.59	0.78	0.52				0.20		0.58	0.57		0.57		0.33 0.18	0.62	0.33	0.49		0.29		

Peak 97



assignment

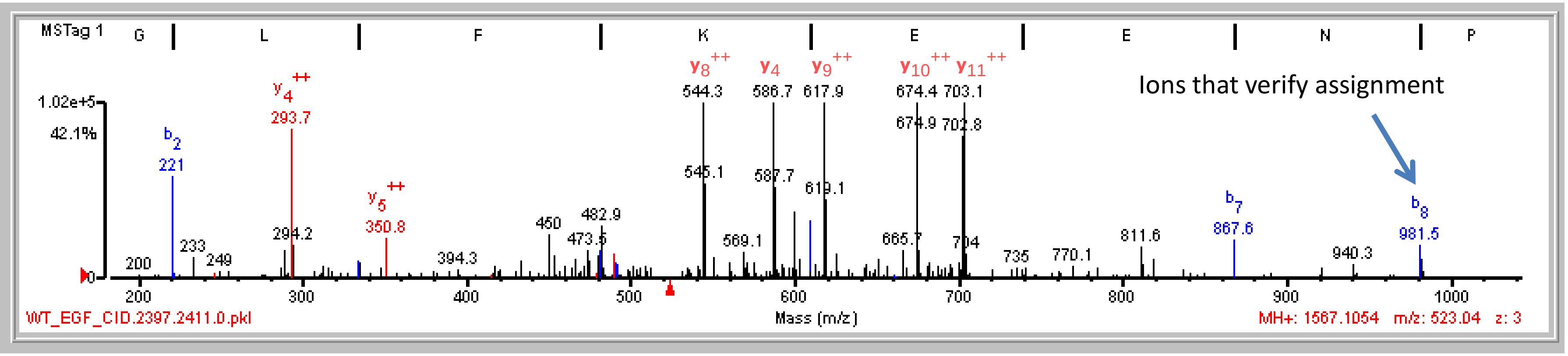


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.20	82.6	12	6/22	Y30y	(K) A y|T/N/F/D|A E/R D A/L/N/I|E\T\A\I K (T)	2155.07	80.2889	144.3	38604.2/7.58	Homo sapiens	4757756	3802	annexin A2 isoform 2
1	14.20	82.6	12	6/22	Y48y	(K) A y|T/N/F/D|A E/R D A/L/N/I|E\T\A\I K (T)	2155.07	80.2889	144.3	40411.4/8.53	Homo sapiens	50845388	12086	annexin A2 isoform 1
1	14.20	82.6	12	6/22	Y30y	(K) A y|T/N/F/D|A E/R D A/L/N/I|E\T\A\I K (T)	2155.07	80.2889	144.3	38604.2/7.58	Homo sapiens	50845386	17586	annexin A2 isoform 2

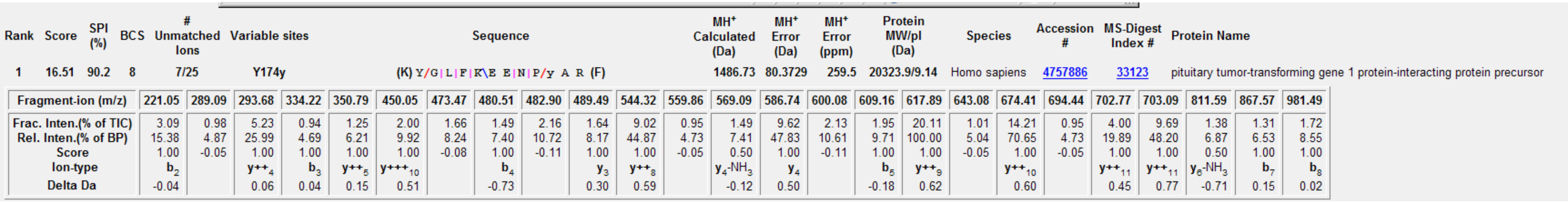
Fragment-ion (m/z)	287.11	315.15	561.73	622.99	636.07	659.67	665.81	674.95	688.15	722.96	729.53
Frac. Inten.(% of TIC)	2.65	2.32	2.54	3.67	2.53	4.25	2.67	5.50	4.16	8.66	2.55
Rel. Inten.(% of BP)	15.98	13.99	15.29	22.08	15.25	25.61	16.10	33.10	25.02	52.13	15.33
Score	0.25	1.00	1.00	1.00	1.00	1.00	-0.16	1.00	-0.25	1.00	-0.15
Ion-type	a_2	b_2	y_5	$y{+}{+}_{11}$	$b{+}{+}{+}_{16}$	$b{+}{+}{+}_{17}$		y_6		$y{+}{+}_{13}$	
Delta Da	0.03	0.08	0.41	0.64	0.46	0.38		0.54		0.57	
						b_5-NH_3					
						-0.54					

Fragment-ion (m/z)	735.52	738.58	773.19	780.48	788.85	792.86	838.13	854.00	901.78	910.71	961.17
Frac. Inten.(% of TIC)	2.35	2.93	2.75	7.75	7.46	2.53	3.13	3.62	3.84	5.51	16.61
Rel. Inten.(% of BP)	14.13	17.62	16.56	46.68	44.89	15.21	18.85	21.80	23.14	33.18	100.00
Score	-0.14	-0.18	-0.17	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type				$y{+}{+}_{14}$	y_7	b_6	$b{+}{+}_{14}$	$y{+}{+}_{15}$	$b{+}{+}_{15}$	$y{+}{+}_{16}$	$y{+}{+}_{17}$
Delta Da				0.57	0.40	0.60	0.27	0.56	-0.60	0.25	0.18
									y_8		
									0.24		
									$y{+}{+}_{16}$-H_2O		
									0.32		

Peak 98



Ions that verify assignment

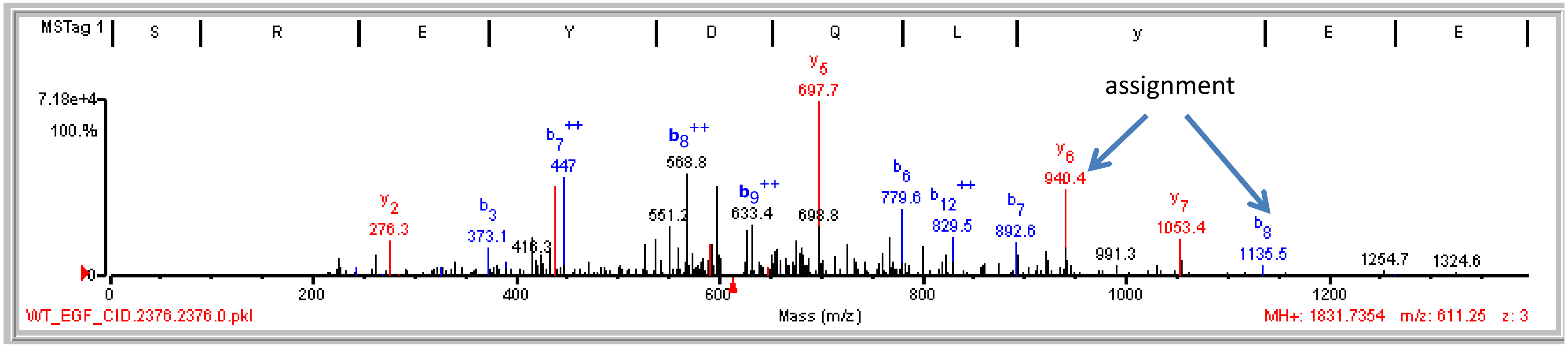


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.51	90.2	8	7/25	Y174y	(K) Y/G|L|F|K\E E|N|P/y A R (F)	1486.73	80.3729	259.5	20323.9/9.14	Homo sapiens	4757886	33123	pituitary tumor-transforming gene 1 protein-interacting protein precursor

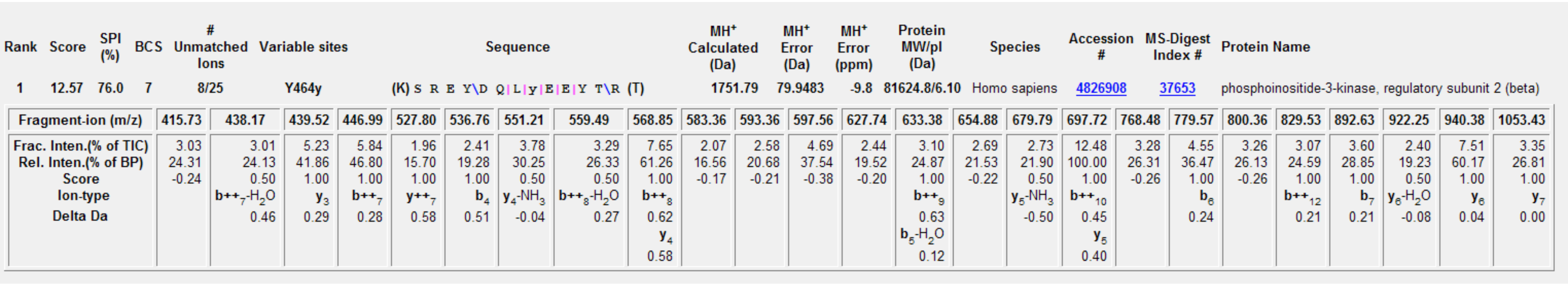
Fragment-ion (m/z)	221.05	289.09	293.68	334.22	350.79	450.05	473.47	480.51	482.90	489.49	544.32	559.86	569.09
Frac. Inten.(% of TIC)	3.09	0.98	5.23	0.94	1.25	2.00	1.66	1.49	2.16	1.64	9.02	0.95	1.49
Rel. Inten.(% of BP)	15.38	4.87	25.99	4.69	6.21	9.92	8.24	7.40	10.72	8.17	44.87	4.73	7.41
Score	1.00	-0.05	1.00	1.00	1.00	1.00	-0.08	1.00	-0.11	1.00	1.00	-0.05	0.50
Ion-type	b_2		$y{+}{+}_4$	b_3	$y{+}{+}_5$	$y{+}{+}{+}_{10}$		b_4		y_3	$y{+}{+}_8$		y_4-NH_3
Delta Da	-0.04		0.06	0.04	0.15	0.51		-0.73		0.30	0.59		-0.12

Fragment-ion (m/z)	586.74	600.08	609.16	617.89	643.08	674.41	694.44	702.77	703.09	811.59	867.57	981.49
Frac. Inten.(% of TIC)	9.62	2.13	1.95	20.11	1.01	14.21	0.95	4.00	9.69	1.38	1.31	1.72
Rel. Inten.(% of BP)	47.83	10.61	9.71	100.00	5.04	70.65	4.73	19.89	48.20	6.87	6.53	8.55
Score	1.00	-0.11	1.00	1.00	-0.05	1.00	-0.05	1.00	1.00	0.50	1.00	1.00
Ion-type	y_4		b_5	$y{+}{+}_9$		$y{+}{+}_{10}$		$y{+}{+}_{11}$	$y{+}{+}_{11}$	y_6-NH_3	b_7	b_8
Delta Da	0.50		-0.18	0.62		0.60		0.45	0.77	-0.71	0.15	0.02

Peak 99



assignment

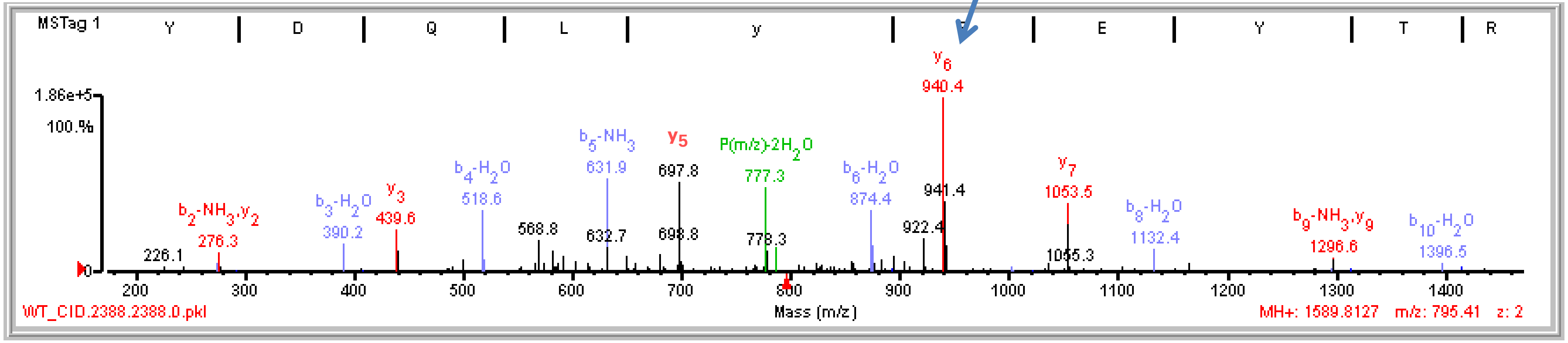


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.57	76.0	7	8/25	Y464y	(K) S R E Y\D Q|L|y|E|E|Y T\R (T)	1751.79	79.9483	-9.8	81624.8/6.10	Homo sapiens	4826908	37653	phosphoinositide-3-kinase, regulatory subunit 2 (beta)

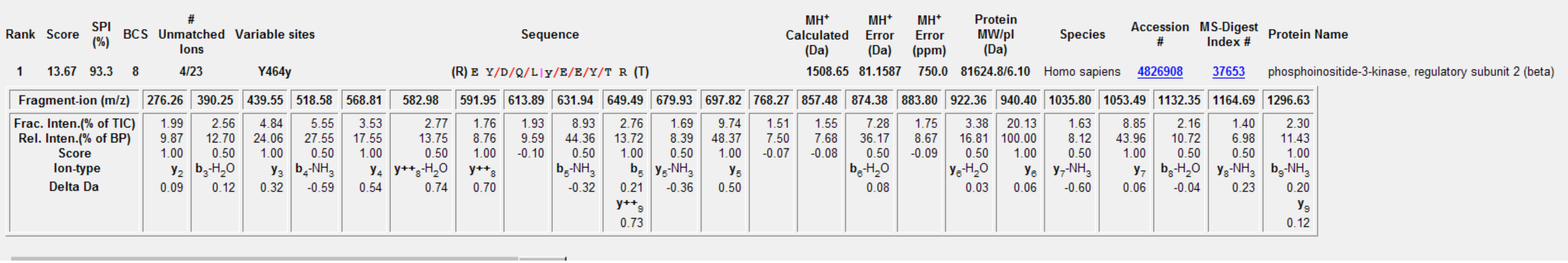
Fragment-ion (m/z)	415.73	438.17	439.52	446.99	527.80	536.76	551.21	559.49	568.85	583.36	593.36
Frac. Inten.(% of TIC)	3.03	3.01	5.23	5.84	1.96	2.41	3.78	3.29	7.65	2.07	2.58
Rel. Inten.(% of BP)	24.31	24.13	41.86	46.80	15.70	19.28	30.25	26.33	61.26	16.56	20.68
Score	-0.24	0.50	1.00	1.00	1.00	1.00	0.50	0.50	1.00	-0.17	-0.21
Ion-type		$b{+}{+}_7$-H_2O	y_3	$b{+}{+}_7$	$y{+}{+}_7$	b_4	y_4-NH_3	$b{+}{+}_8$-H_2O	$b{+}{+}_8$ y_4		
Delta Da		0.46	0.29	0.28	0.58	0.51	-0.04	0.27	0.62 0.58		

Fragment-ion (m/z)	597.56	627.74	633.38	654.88	679.79	697.72	768.48	779.57	800.36	829.53	892.63	922.25	940.38	1053.43
Frac. Inten.(% of TIC)	4.69	2.44	3.10	2.69	2.73	12.48	3.28	4.55	3.26	3.07	3.60	2.40	7.51	3.35
Rel. Inten.(% of BP)	37.54	19.52	24.87	21.53	21.90	100.00	26.31	36.47	26.13	24.59	28.85	19.23	60.17	26.81
Score	-0.38	-0.20	1.00	-0.22	0.50	1.00	-0.26	1.00	-0.26	1.00	1.00	0.50	1.00	1.00
Ion-type			$b{+}{+}_9$ b_5-H_2O		y_5-NH_3	$b{+}{+}_{10}$ y_5		b_6		$b{+}{+}_{12}$	b_7	y_6-H_2O	y_6	y_7
Delta Da			0.63 0.12		-0.50	0.45 0.40		0.24		0.21	0.21	-0.08	0.04	0.00

Peak 100



assignment

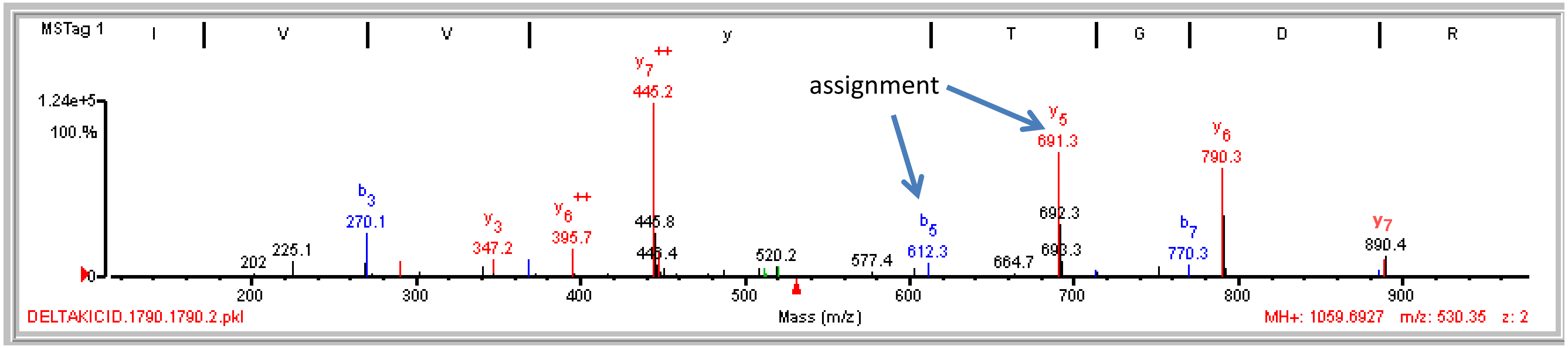


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.67	93.3	8	4/23	Y464y	(R) E Y/D/Q/L|y/E/E/Y/T R (T)	1508.65	81.1587	750.0	81624.8/6.10	Homo sapiens	4826908	37653	phosphoinositide-3-kinase, regulatory subunit 2 (beta)

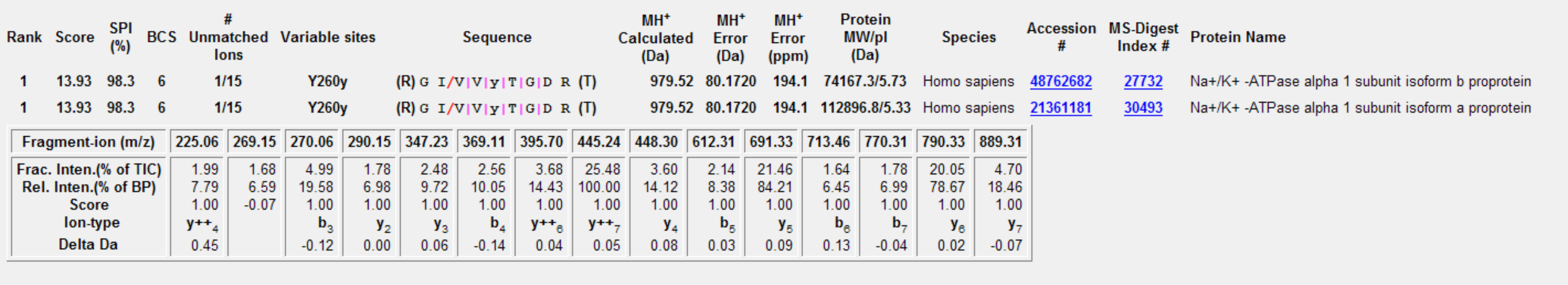
Fragment-ion (m/z)	276.26	390.25	439.55	518.58	568.81	582.98	591.95	613.89	631.94	649.49	679.93
Frac. Inten.(% of TIC)	1.99	2.56	4.84	5.55	3.53	2.77	1.76	1.93	8.93	2.76	1.69
Rel. Inten.(% of BP)	9.87	12.70	24.06	27.55	17.55	13.75	8.76	9.59	44.36	13.72	8.39
Score	1.00	0.50	1.00	0.50	1.00	0.50	1.00	-0.10	0.50	1.00	0.50
Ion-type	y_2	b_3-H_2O	y_3	b_4-NH_3	y_4	y^{++}_8-H_2O	y^{++}_8		b_5-NH_3	b_5 y^{++}_9	y_5-NH_3
Delta Da	0.09	0.12	0.32	-0.59	0.54	0.74	0.70		-0.32	0.21 0.73	-0.36

Fragment-ion (m/z)	697.82	768.27	857.48	874.38	883.80	922.36	940.40	1035.80	1053.49	1132.35	1164.69	1296.63
Frac. Inten.(% of TIC)	9.74	1.51	1.55	7.28	1.75	3.38	20.13	1.63	8.85	2.16	1.40	2.30
Rel. Inten.(% of BP)	48.37	7.50	7.68	36.17	8.67	16.81	100.00	8.12	43.96	10.72	6.98	11.43
Score	1.00	-0.07	-0.08	0.50	-0.09	0.50	1.00	0.50	1.00	0.50	0.50	1.00
Ion-type	y_5			b_6-H_2O		y_6-H_2O	y_6	y_7-NH_3	y_7	b_8-H_2O	y_8-NH_3	b_9-NH_3 y_9
Delta Da	0.50			0.08		0.03	0.06	-0.60	0.06	-0.04	0.23	0.20 0.12

Peak 101



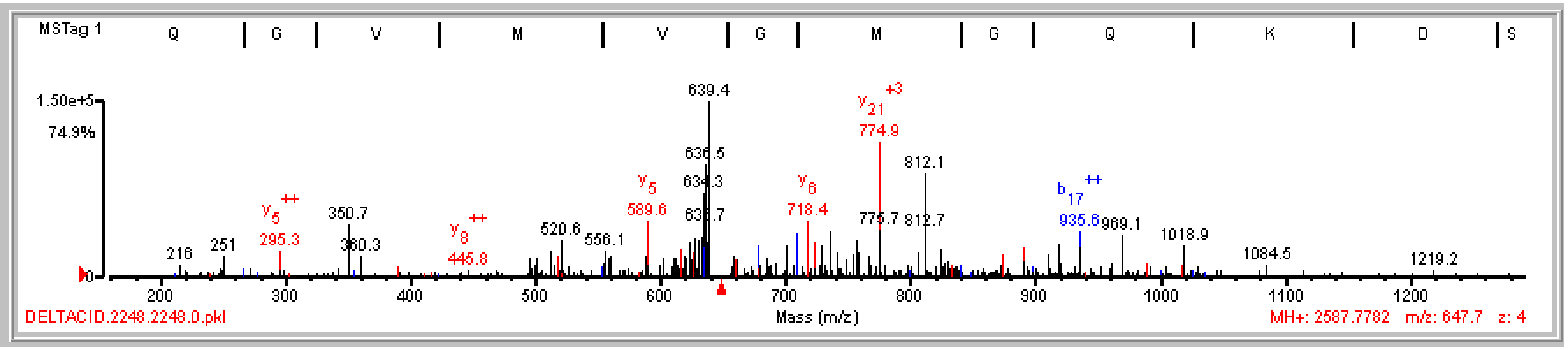
assignment

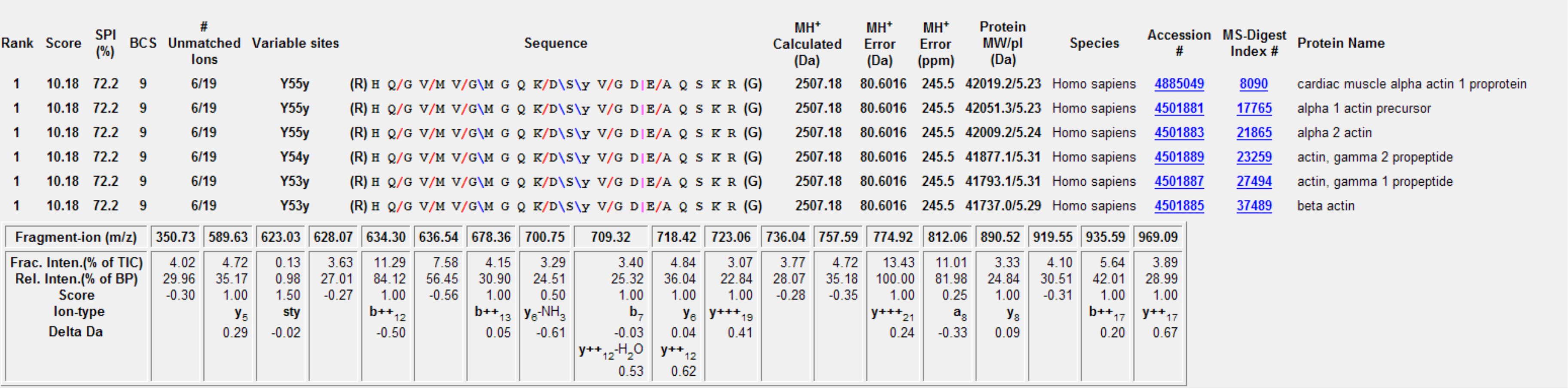


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.93	98.3	6	1/15	Y260y	(R) G I/V|V|y|T|G|D R (T)	979.52	80.1720	194.1	74167.3/5.73	Homo sapiens	48762682	27732	Na+/K+ -ATPase alpha 1 subunit isoform b proprotein
1	13.93	98.3	6	1/15	Y260y	(R) G I/V|V|y|T|G|D R (T)	979.52	80.1720	194.1	112896.8/5.33	Homo sapiens	21361181	30493	Na+/K+ -ATPase alpha 1 subunit isoform a proprotein

Fragment-ion (m/z)	225.06	269.15	270.06	290.15	347.23	369.11	395.70	445.24	448.30	612.31	691.33	713.46	770.31	790.33	889.31
Frac. Inten.(% of TIC)	1.99	1.68	4.99	1.78	2.48	2.56	3.68	25.48	3.60	2.14	21.46	1.64	1.78	20.05	4.70
Rel. Inten.(% of BP)	7.79	6.59	19.58	6.98	9.72	10.05	14.43	100.00	14.12	8.38	84.21	6.45	6.99	78.67	18.46
Score	1.00	-0.07	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{++}_4		b_3	y_2	y_3	b_4	y^{++}_6	y^{++}_7	y_4	b_5	y_5	b_6	b_7	y_6	y_7
Delta Da	0.45		-0.12	0.00	0.06	-0.14	0.04	0.05	0.08	0.03	0.09	0.13	-0.04	0.02	-0.07

Peak 102



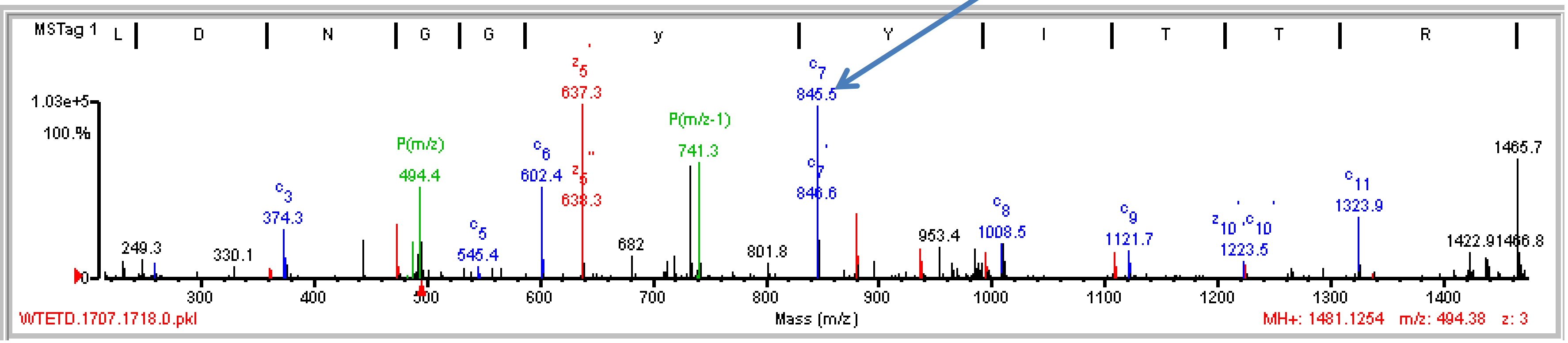


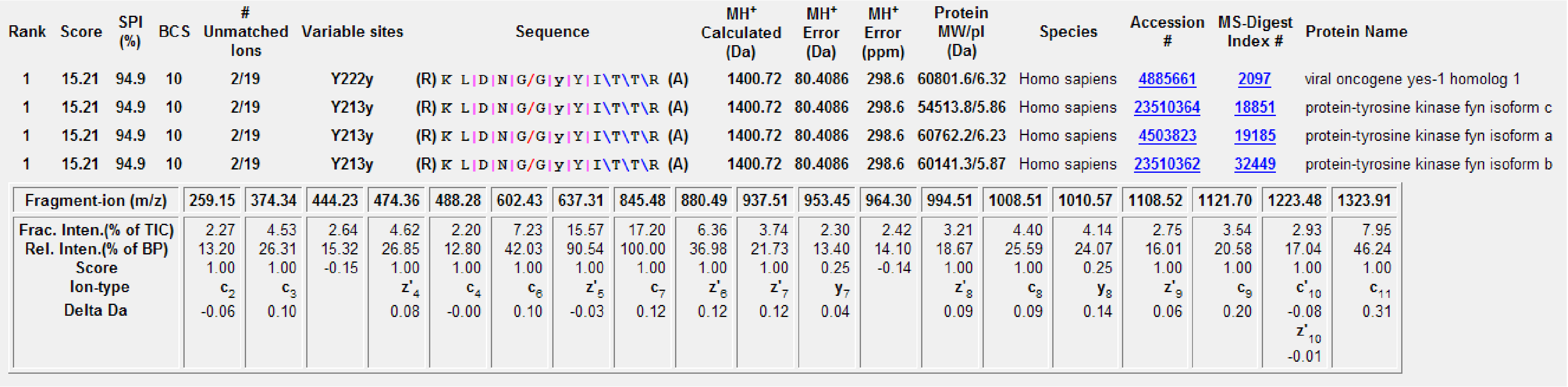
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.18	72.2	9	6/19	Y55y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	42019.2/5.23	Homo sapiens	4885049	8090	cardiac muscle alpha actin 1 proprotein
1	10.18	72.2	9	6/19	Y55y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	42051.3/5.23	Homo sapiens	4501881	17765	alpha 1 actin precursor
1	10.18	72.2	9	6/19	Y55y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	42009.2/5.24	Homo sapiens	4501883	21865	alpha 2 actin
1	10.18	72.2	9	6/19	Y54y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	41877.1/5.31	Homo sapiens	4501889	23259	actin, gamma 2 propeptide
1	10.18	72.2	9	6/19	Y53y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	41793.1/5.31	Homo sapiens	4501887	27494	actin, gamma 1 propeptide
1	10.18	72.2	9	6/19	Y53y	(R) H Q/G V/M V/G\M G Q K/D\S\y V/G D|E/A Q S K R (G)	2507.18	80.6016	245.5	41737.0/5.29	Homo sapiens	4501885	37489	beta actin

Fragment-ion (m/z)	350.73	589.63	623.03	628.07	634.30	636.54	678.36	700.75	709.32	718.42	723.06	736.04	757.59	774.92	812.06	890.52	919.55	935.59	969.09
Frac. Inten.(% of TIC)	4.02	4.72	0.13	3.63	11.29	7.58	4.15	3.29	3.40	4.84	3.07	3.77	4.72	13.43	11.01	3.33	4.10	5.64	3.89
Rel. Inten.(% of BP)	29.96	35.17	0.98	27.01	84.12	56.45	30.90	24.51	25.32	36.04	22.84	28.07	35.18	100.00	81.98	24.84	30.51	42.01	28.99
Score	-0.30	1.00	1.50	-0.27	1.00	-0.56	1.00	0.50	1.00	1.00	1.00	-0.28	-0.35	1.00	0.25	1.00	-0.31	1.00	1.00
Ion-type		y_5	sty		$b{+}{+}_{12}$		$b{+}{+}_{13}$	y_6-NH_3	b_7 $y{+}{+}_{12}$-H_2O	y_6 $y{+}{+}_{12}$	$y{+}{+}{+}_{19}$			$y{+}{+}{+}_{21}$	a_8	y_8		$b{+}{+}_{17}$	$y{+}{+}_{17}$
Delta Da		0.29	-0.02		-0.50		0.05	-0.61	-0.03 0.53	0.04 0.62	0.41			0.24	-0.33	0.09		0.20	0.67

Peak 103

assignment



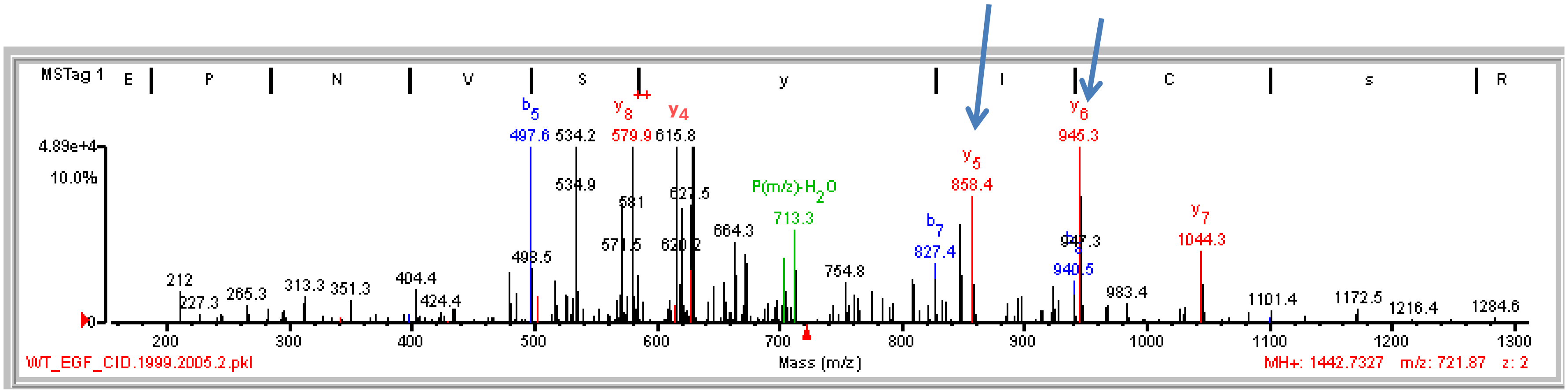


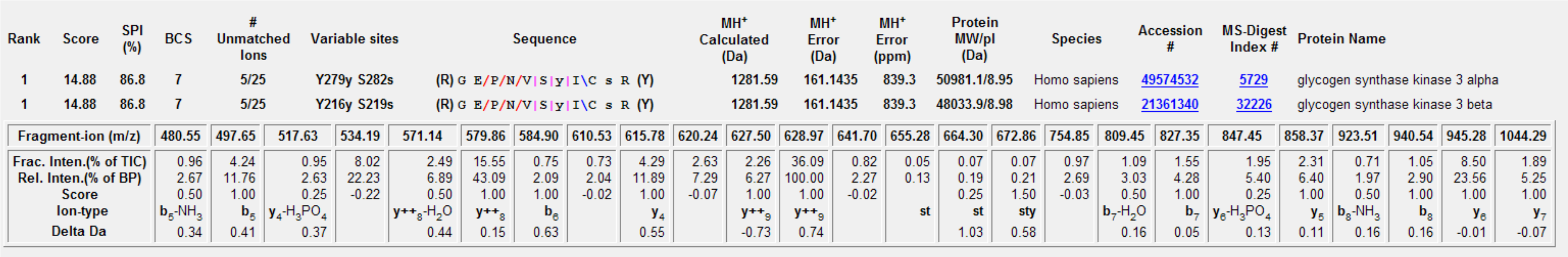
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.21	94.9	10	2/19	Y222y	(R) K L|D|N|G/G|y|Y|I\T\T\R (A)	1400.72	80.4086	298.6	60801.6/6.32	Homo sapiens	4885661	2097	viral oncogene yes-1 homolog 1
1	15.21	94.9	10	2/19	Y213y	(R) K L|D|N|G/G|y|Y|I\T\T\R (A)	1400.72	80.4086	298.6	54513.8/5.86	Homo sapiens	23510364	18851	protein-tyrosine kinase fyn isoform c
1	15.21	94.9	10	2/19	Y213y	(R) K L|D|N|G/G|y|Y|I\T\T\R (A)	1400.72	80.4086	298.6	60762.2/6.23	Homo sapiens	4503823	19185	protein-tyrosine kinase fyn isoform a
1	15.21	94.9	10	2/19	Y213y	(R) K L|D|N|G/G|y|Y|I\T\T\R (A)	1400.72	80.4086	298.6	60141.3/5.87	Homo sapiens	23510362	32449	protein-tyrosine kinase fyn isoform b

Fragment-ion (m/z)	259.15	374.34	444.23	474.36	488.28	602.43	637.31	845.48	880.49	937.51	953.45	964.30	994.51	1008.51	1010.57	1108.52	1121.70	1223.48	1323.91
Frac. Inten.(% of TIC)	2.27	4.53	2.64	4.62	2.20	7.23	15.57	17.20	6.36	3.74	2.30	2.42	3.21	4.40	4.14	2.75	3.54	2.93	7.95
Rel. Inten.(% of BP)	13.20	26.31	15.32	26.85	12.80	42.03	90.54	100.00	36.98	21.73	13.40	14.10	18.67	25.59	24.07	16.01	20.58	17.04	46.24
Score	1.00	1.00	-0.15	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.14	1.00	1.00	0.25	1.00	1.00	1.00	1.00
Ion-type	c_2	c_3		z'_4	c_4	c_6	z'_5	c_7	z'_6	z'_7	y_7		z'_8	c_8	y_8	z'_9	c_9	c'_{10} -0.08 z'_{10}	c_{11}
Delta Da	-0.06	0.10		0.08	-0.00	0.10	-0.03	0.12	0.12	0.12	0.04		0.09	0.09	0.14	0.06	0.20	-0.01	0.31

Peak 104

assignment



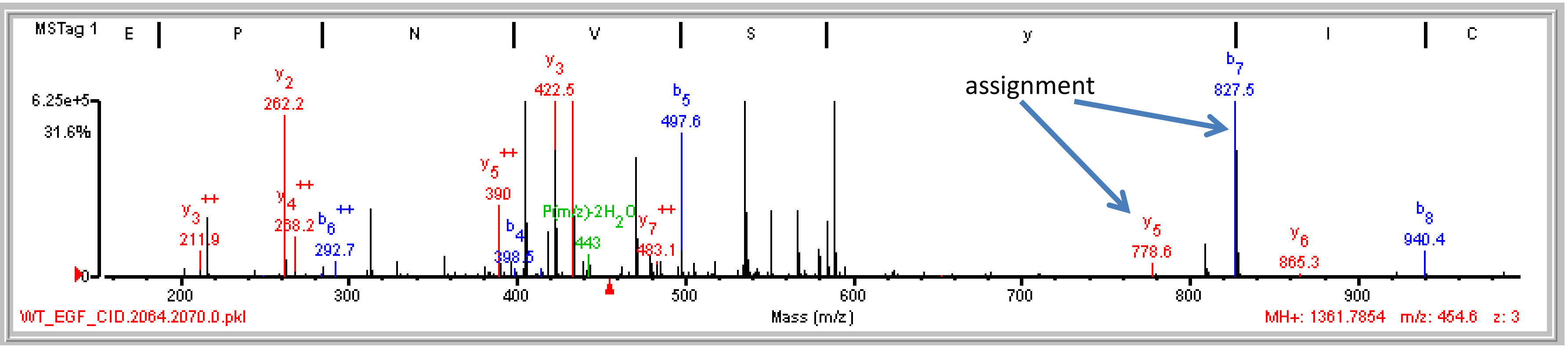


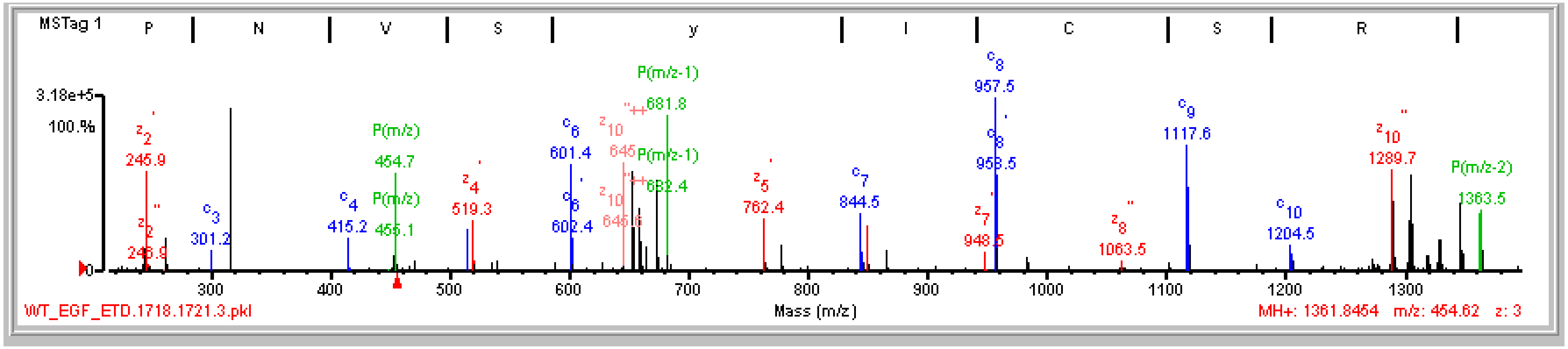
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.88	86.8	7	5/25	Y279y S282s	(R) G E/P/N/V|S|y|I\C s R (Y)	1281.59	161.1435	839.3	50981.1/8.95	Homo sapiens	49574532	5729	glycogen synthase kinase 3 alpha
1	14.88	86.8	7	5/25	Y216y S219s	(R) G E/P/N/V|S|y|I\C s R (Y)	1281.59	161.1435	839.3	48033.9/8.98	Homo sapiens	21361340	32226	glycogen synthase kinase 3 beta

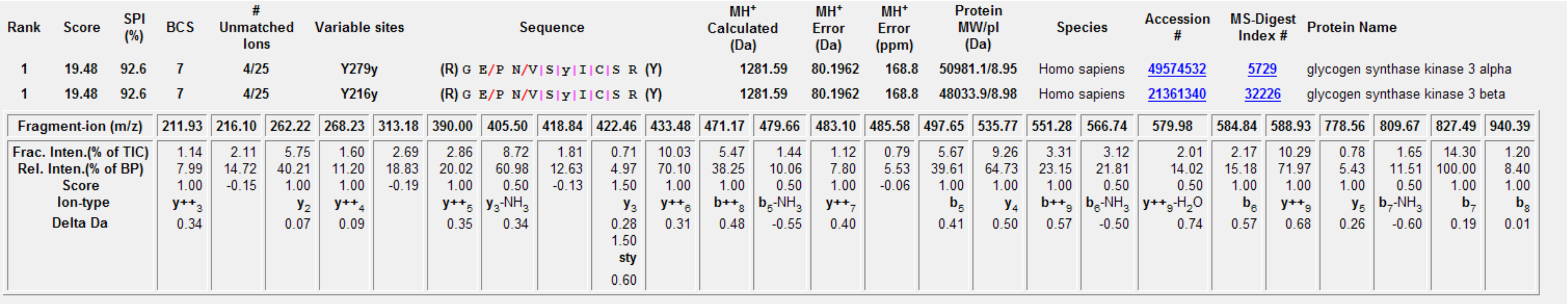
Fragment-ion (m/z)	480.55	497.65	517.63	534.19	571.14	579.86	584.90	610.53	615.78	620.24	627.50	628.97
Frac. Inten.(% of TIC)	0.96	4.24	0.95	8.02	2.49	15.55	0.75	0.73	4.29	2.63	2.26	36.09
Rel. Inten.(% of BP)	2.67	11.76	2.63	22.23	6.89	43.09	2.09	2.04	11.89	7.29	6.27	100.00
Score	0.50	1.00	0.25	-0.22	0.50	1.00	1.00	-0.02	1.00	-0.07	1.00	1.00
Ion-type	$b_5\text{-}NH_3$	b_5	$y_4\text{-}H_3PO_4$		$y{+}{+}_8\text{-}H_2O$	$y{+}{+}_8$	b_6		y_4		$y{+}{+}_9$	$y{+}{+}_9$
Delta Da	0.34	0.41	0.37		0.44	0.15	0.63		0.55		-0.73	0.74

Fragment-ion (m/z)	641.70	655.28	664.30	672.86	754.85	809.45	827.35	847.45	858.37	923.51	940.54	945.28	1044.29
Frac. Inten.(% of TIC)	0.82	0.05	0.07	0.07	0.97	1.09	1.55	1.95	2.31	0.71	1.05	8.50	1.89
Rel. Inten.(% of BP)	2.27	0.13	0.19	0.21	2.69	3.03	4.28	5.40	6.40	1.97	2.90	23.56	5.25
Score	-0.02		0.25	1.50	-0.03	0.50	1.00	0.25	1.00	0.50	1.00	1.00	1.00
Ion-type		st	st	sty		$b_7\text{-}H_2O$	b_7	$y_6\text{-}H_3PO_4$	y_5	$b_8\text{-}NH_3$	b_8	y_6	y_7
Delta Da			1.03	0.58		0.16	0.05	0.13	0.11	0.16	0.16	-0.01	-0.07

Peak 105



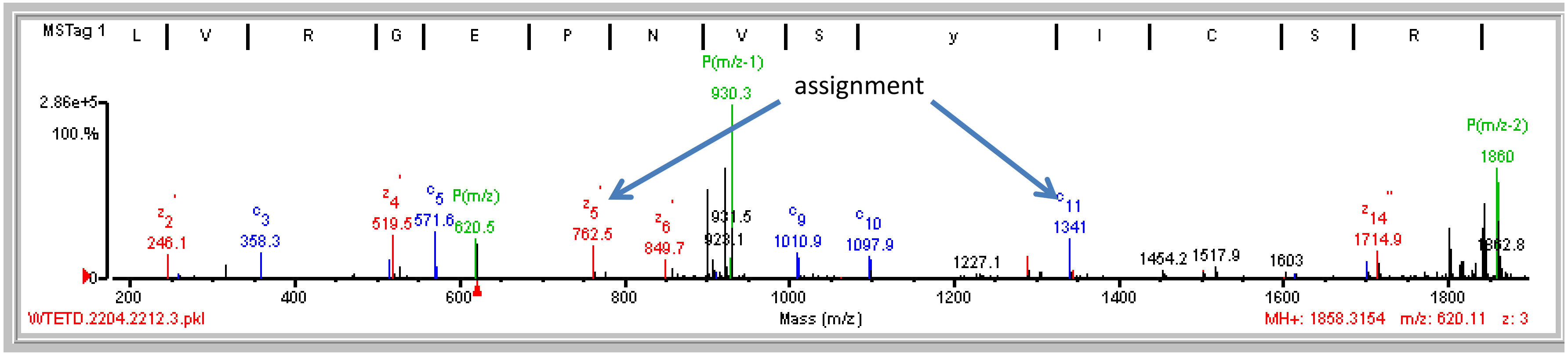




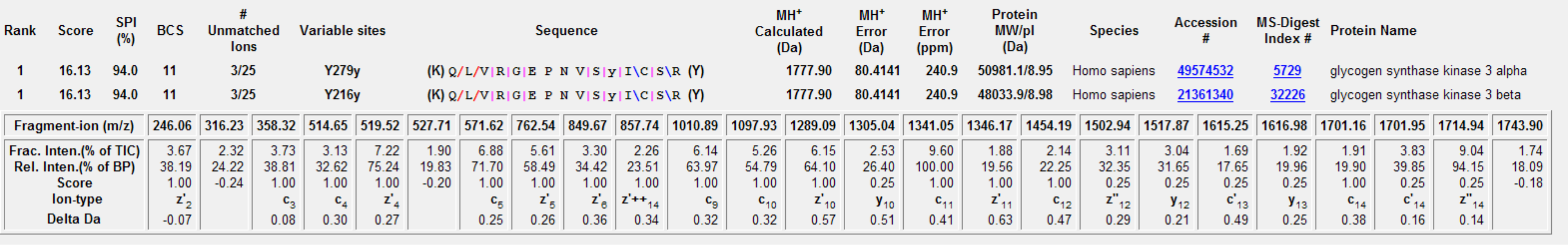
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.48	92.6	7	4/25	Y279y	(R) G E/P N/V|S|y|I|C|S R (Y)	1281.59	80.1962	168.8	50981.1/8.95	Homo sapiens	49574532	5729	glycogen synthase kinase 3 alpha
1	19.48	92.6	7	4/25	Y216y	(R) G E/P N/V|S|y|I|C|S R (Y)	1281.59	80.1962	168.8	48033.9/8.98	Homo sapiens	21361340	32226	glycogen synthase kinase 3 beta

Fragment-ion (m/z)	211.93	216.10	262.22	268.23	313.18	390.00	405.50	418.84	422.46	433.48	471.17	479.66	483.10	485.58	497.65	535.77	551.28	566.74	579.98	584.84	588.93	778.56	809.67	827.49	940.39
Frac. Inten.(% of TIC)	1.14	2.11	5.75	1.60	2.69	2.86	8.72	1.81	0.71	10.03	5.47	1.44	1.12	0.79	5.67	9.26	3.31	3.12	2.01	2.17	10.29	0.78	1.65	14.30	1.20
Rel. Inten.(% of BP)	7.99	14.72	40.21	11.20	18.83	20.02	60.98	12.63	4.97	70.10	38.25	10.06	7.80	5.53	39.61	64.73	23.15	21.81	14.02	15.18	71.97	5.43	11.51	100.00	8.40
Score	1.00	-0.15	1.00	1.00	-0.19	1.00	0.50	-0.13	1.50	1.00	1.00	0.50	1.00	-0.06	1.00	1.00	1.00	0.50	0.50	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	$y{++}_3$		y_2	$y{++}_4$		$y{++}_5$	y_3-NH_3		y_3	$y{++}_6$	$b{++}_8$	b_5-NH_3	$y{++}_7$		b_5	y_4	$b{++}_9$	b_6-NH_3	$y{++}_9$-H_2O	b_6	$y{++}_9$	y_5	b_7-NH_3	b_7	b_8
Delta Da	0.34		0.07	0.09		0.35	0.34		0.28 1.50 sty 0.60	0.31	0.48	-0.55	0.40		0.41	0.50	0.57	-0.50	0.74	0.57	0.68	0.26	-0.60	0.19	0.01

Peak 106



assignment

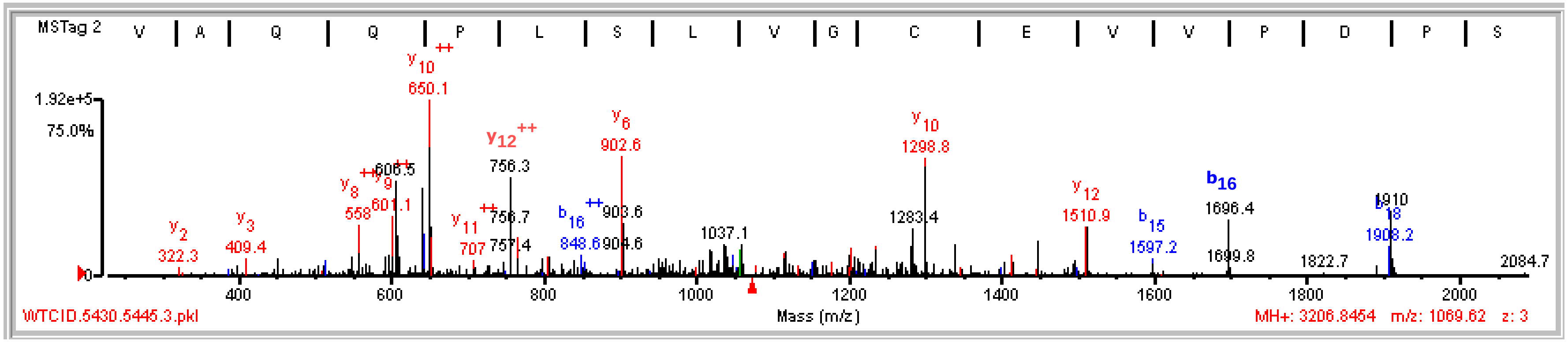


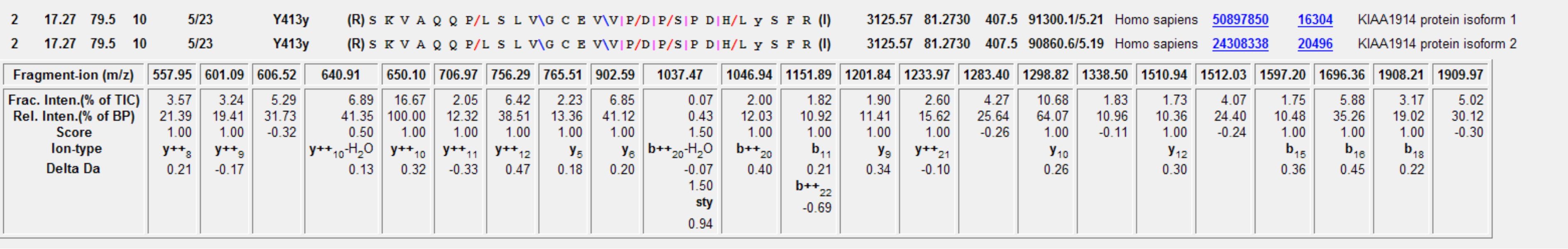
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.13	94.0	11	3/25	Y279y	(K) Q/L/V|R|G|E P N V|S|y|I\C|S\R (Y)	1777.90	80.4141	240.9	50981.1/8.95	Homo sapiens	49574532	5729	glycogen synthase kinase 3 alpha
1	16.13	94.0	11	3/25	Y216y	(K) Q/L/V|R|G|E P N V|S|y|I\C|S\R (Y)	1777.90	80.4141	240.9	48033.9/8.98	Homo sapiens	21361340	32226	glycogen synthase kinase 3 beta

Fragment-ion (m/z)	246.06	316.23	358.32	514.65	519.52	527.71	571.62	762.54	849.67	857.74	1010.89	1097.93
Frac. Inten.(% of TIC)	3.67	2.32	3.73	3.13	7.22	1.90	6.88	5.61	3.30	2.26	6.14	5.26
Rel. Inten.(% of BP)	38.19	24.22	38.81	32.62	75.24	19.83	71.70	58.49	34.42	23.51	63.97	54.79
Score	1.00	-0.24	1.00	1.00	1.00	-0.20	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	z'_2		c_3	c_4	z'_4		c_5	z'_5	z'_6	$z'{++}_{14}$	c_9	c_{10}
Delta Da	-0.07		0.08	0.30	0.27		0.25	0.26	0.36	0.34	0.32	0.32

Fragment-ion (m/z)	1289.09	1305.04	1341.05	1346.17	1454.19	1502.94	1517.87	1615.25	1616.98	1701.16	1701.95	1714.94	1743.90
Frac. Inten.(% of TIC)	6.15	2.53	9.60	1.88	2.14	3.11	3.04	1.69	1.92	1.91	3.83	9.04	1.74
Rel. Inten.(% of BP)	64.10	26.40	100.00	19.56	22.25	32.35	31.65	17.65	19.96	19.90	39.85	94.15	18.09
Score	1.00	0.25	1.00	1.00	1.00	0.25	0.25	0.25	0.25	1.00	0.25	0.25	-0.18
Ion-type	z'_{10}	y_{10}	c_{11}	z'_{11}	c_{12}	z''_{12}	y_{12}	c'_{13}	y_{13}	c_{14}	c'_{14}	z''_{14}	
Delta Da	0.57	0.51	0.41	0.63	0.47	0.29	0.21	0.49	0.25	0.38	0.16	0.14	

Peak 107





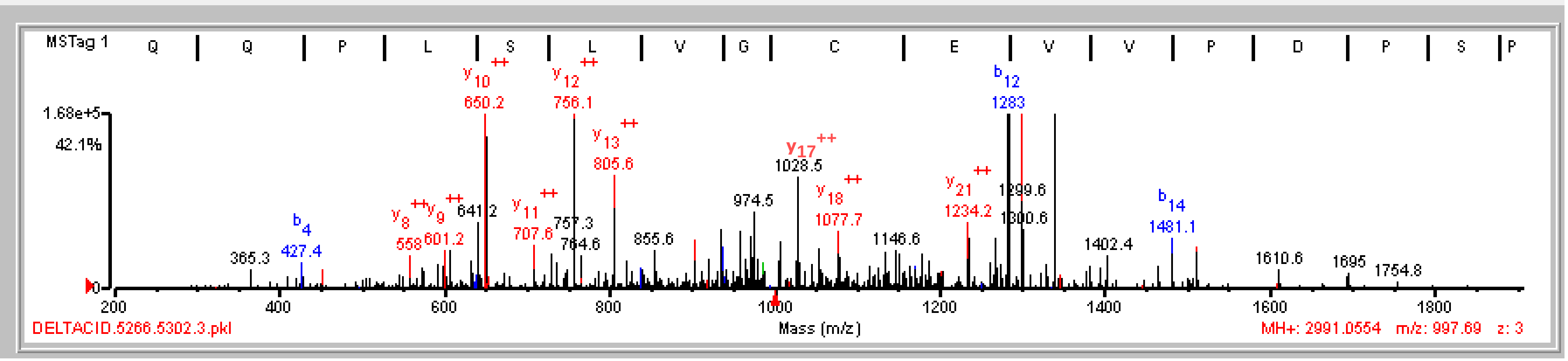
2 17.27 79.5 10 5/23 Y413y (R) S K V A Q Q P/L S L V\G C E V\V|P/D|P/S|P D|H/L y S F R (I) 3125.57 81.2730 407.5 91300.1/5.21 Homo sapiens 50897850 16304 KIAA1914 protein isoform 1

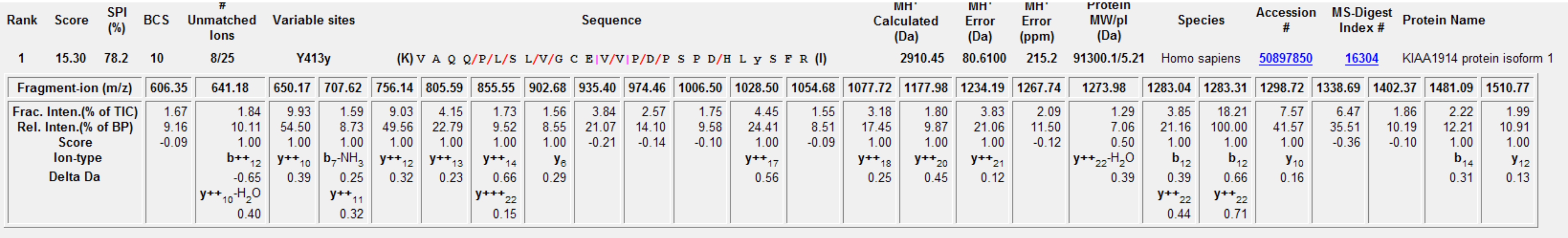
2 17.27 79.5 10 5/23 Y413y (R) S K V A Q Q P/L S L V\G C E V\V|P/D|P/S|P D|H/L y S F R (I) 3125.57 81.2730 407.5 90860.6/5.19 Homo sapiens 24308338 20496 KIAA1914 protein isoform 2

Fragment-ion (m/z)	557.95	601.09	606.52	640.91	650.10	706.97	756.29	765.51	902.59	1037.47
Frac. Inten.(% of TIC)	3.57	3.24	5.29	6.89	16.67	2.05	6.42	2.23	6.85	0.07
Rel. Inten.(% of BP)	21.39	19.41	31.73	41.35	100.00	12.32	38.51	13.36	41.12	0.43
Score	1.00	1.00	-0.32	0.50	1.00	1.00	1.00	1.00	1.00	1.50
Ion-type	y++_{8}	y++_{9}		$\text{y++}_{10}\text{-H}_2\text{O}$	y++_{10}	y++_{11}	y++_{12}	y_{5}	y_{6}	$\text{b++}_{20}\text{-H}_2\text{O}$
Delta Da	0.21	-0.17		0.13	0.32	-0.33	0.47	0.18	0.20	-0.07
										1.50
										sty
										0.94

Fragment-ion (m/z)	1046.94	1151.89	1201.84	1233.97	1283.40	1298.82	1338.50	1510.94	1512.03	1597.20	1696.36	1908.21	1909.97
Frac. Inten.(% of TIC)	2.00	1.82	1.90	2.60	4.27	10.68	1.83	1.73	4.07	1.75	5.88	3.17	5.02
Rel. Inten.(% of BP)	12.03	10.92	11.41	15.62	25.64	64.07	10.96	10.36	24.40	10.48	35.26	19.02	30.12
Score	1.00	1.00	1.00	1.00	-0.26	1.00	-0.11	1.00	-0.24	1.00	1.00	1.00	-0.30
Ion-type	b++_{20}	b_{11}	y_{9}	y++_{21}		y_{10}		y_{12}		b_{15}	b_{16}	b_{18}	
Delta Da	0.40	0.21	0.34	-0.10		0.26		0.30		0.36	0.45	0.22	
		b++_{22}											
		-0.69											

Peak 108



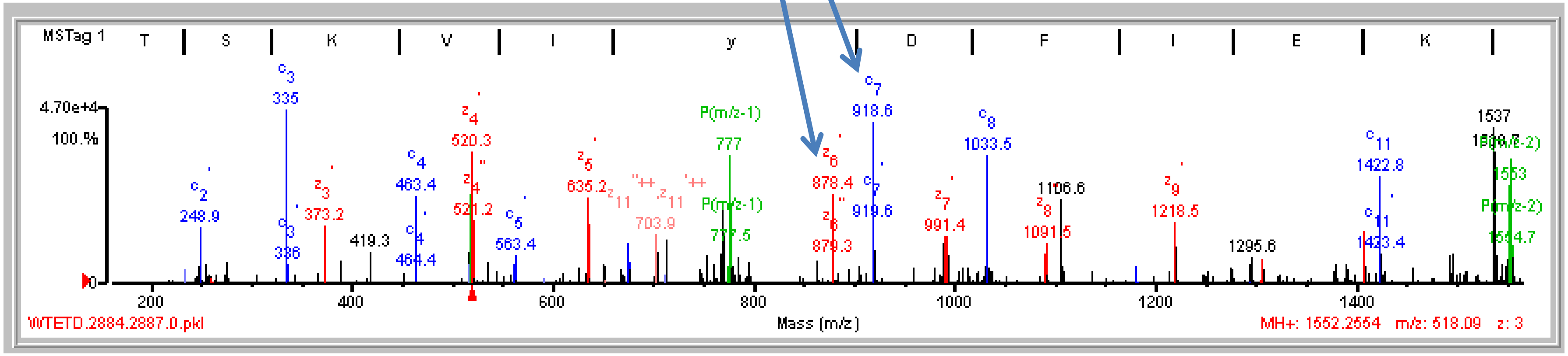


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.30	78.2	10	8/25	Y413y	(K) V A Q Q/P/L/S L/V/G C E|V/V|P/D/P S P D/H L y S F R (I)	2910.45	80.6100	215.2	91300.1/5.21	Homo sapiens	50897850	16304	KIAA1914 protein isoform 1

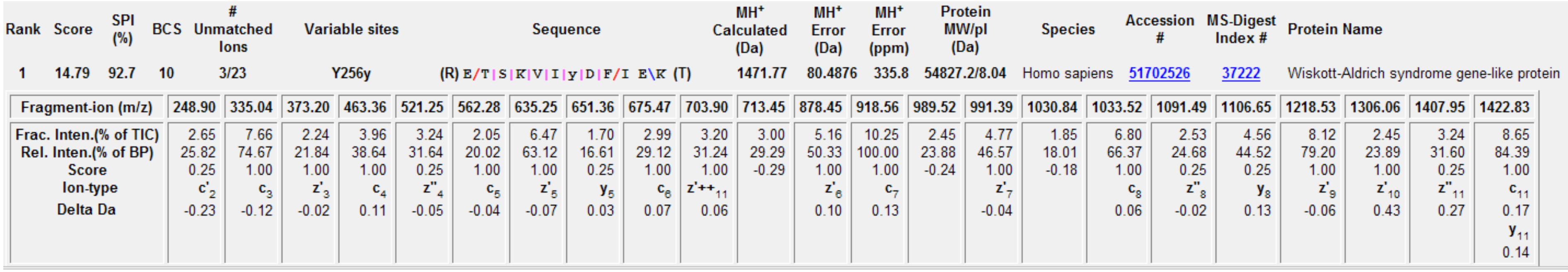
Fragment-ion (m/z)	606.35	641.18	650.17	707.62	756.14	805.59	855.55	902.68	935.40	974.46	1006.50	1028.50
Frac. Inten.(% of TIC)	1.67	1.84	9.93	1.59	9.03	4.15	1.73	1.56	3.84	2.57	1.75	4.45
Rel. Inten.(% of BP)	9.16	10.11	54.50	8.73	49.56	22.79	9.52	8.55	21.07	14.10	9.58	24.41
Score	-0.09	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.21	-0.14	-0.10	1.00
Ion-type		b^{++}_{12}	y^{++}_{10}	b_7-NH_3	y^{++}_{12}	y^{++}_{13}	y^{++}_{14}	y_6				y^{++}_{17}
Delta Da		-0.65	0.39	0.25	0.32	0.23	0.66	0.29				0.56
		y^{++}_{10}-H_2O		y^{++}_{11}			y^{+++}_{22}					
		0.40		0.32			0.15					

Fragment-ion (m/z)	1054.68	1077.72	1177.98	1234.19	1267.74	1273.98	1283.04	1283.31	1298.72	1338.69	1402.37	1481.09	1510.77
Frac. Inten.(% of TIC)	1.55	3.18	1.80	3.83	2.09	1.29	3.85	18.21	7.57	6.47	1.86	2.22	1.99
Rel. Inten.(% of BP)	8.51	17.45	9.87	21.06	11.50	7.06	21.16	100.00	41.57	35.51	10.19	12.21	10.91
Score	-0.09	1.00	1.00	1.00	-0.12	0.50	1.00	1.00	1.00	-0.36	-0.10	1.00	1.00
Ion-type		y^{++}_{18}	y^{++}_{20}	y^{++}_{21}		y^{++}_{22}-H_2O	b_{12}	b_{12}	y_{10}			b_{14}	y_{12}
Delta Da		0.25	0.45	0.12		0.39	0.39	0.66	0.16			0.31	0.13
							y^{++}_{22}	y^{++}_{22}					
							0.44	0.71					

Peak 109



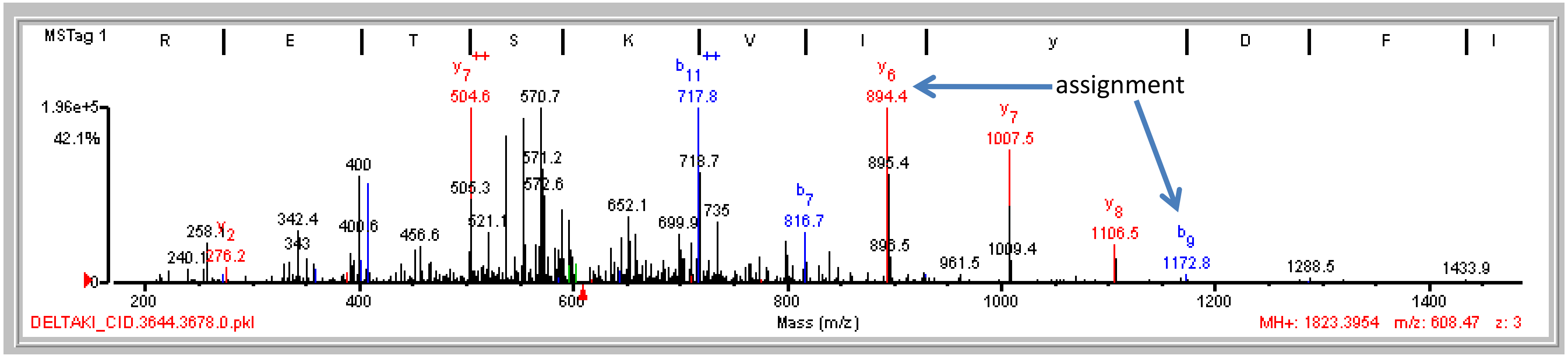
assignment



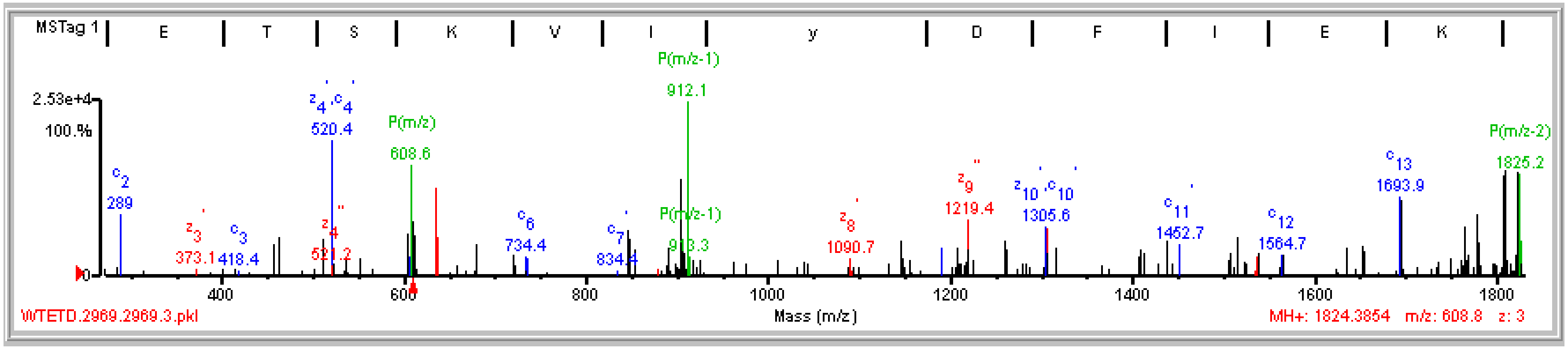
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.79	92.7	10	3/23	Y256y	(R) E/T|S|K|V|I|y|D|F/I E\K (T)	1471.77	80.4876	335.8	54827.2/8.04	Homo sapiens	51702526	37222	Wiskott-Aldrich syndrome gene-like protein

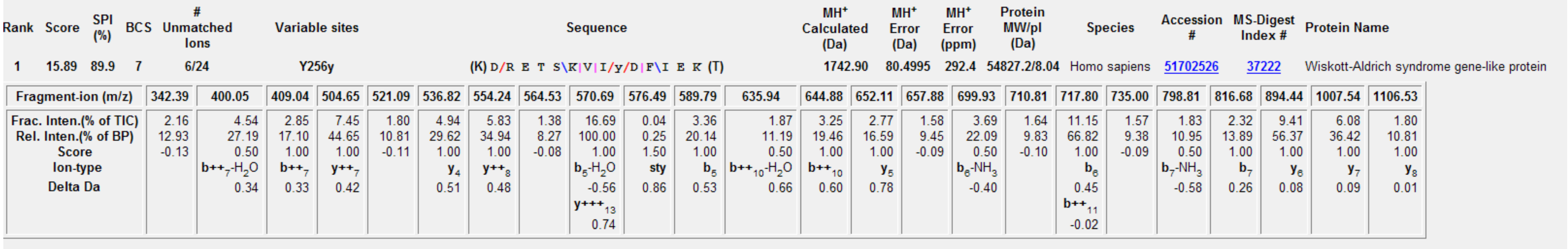
Fragment-ion (m/z)	248.90	335.04	373.20	463.36	521.25	562.28	635.25	651.36	675.47	703.90	713.45	878.45	918.56	989.52	991.39	1030.84	1033.52	1091.49	1106.65	1218.53	1306.06	1407.95	1422.83
Frac. Inten.(% of TIC)	2.65	7.66	2.24	3.96	3.24	2.05	6.47	1.70	2.99	3.20	3.00	5.16	10.25	2.45	4.77	1.85	6.80	2.53	4.56	8.12	2.45	3.24	8.65
Rel. Inten.(% of BP)	25.82	74.67	21.84	38.64	31.64	20.02	63.12	16.61	29.12	31.24	29.29	50.33	100.00	23.88	46.57	18.01	66.37	24.68	44.52	79.20	23.89	31.60	84.39
Score	0.25	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00	1.00	-0.29	1.00	1.00	-0.24	1.00	-0.18	1.00	0.25	0.25	1.00	1.00	0.25	1.00
Ion-type	c'_2	c_3	z'_3	c_4	z''_4	c_5	z'_5	y_5	c_6	$z'{++}_{11}$		z'_6	c_7		z'_7		c_8	z''_8	y_8	z'_9	z'_{10}	z''_{11}	c_{11} y_{11}
Delta Da	-0.23	-0.12	-0.02	0.11	-0.05	-0.04	-0.07	0.03	0.07	0.06		0.10	0.13		-0.04		0.06	-0.02	0.13	-0.06	0.43	0.27	0.17 0.14

Peak 110



assignment



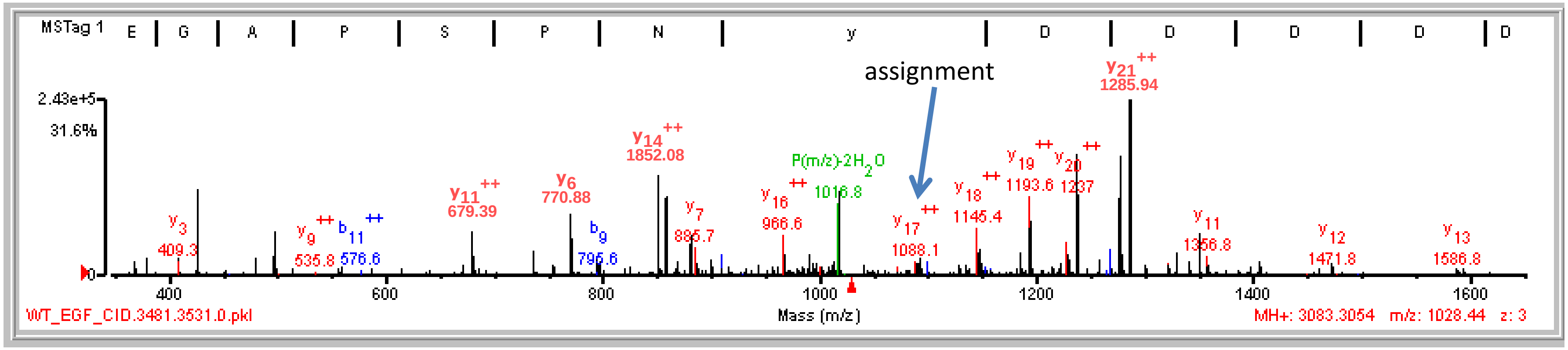


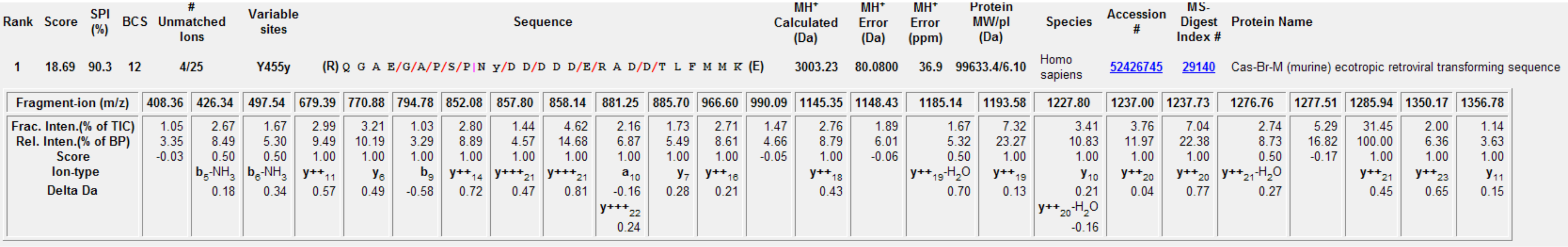
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.89	89.9	7	6/24	Y256y	(K) D/R E T S\K|V|I/y/D|F\I E K (T)	1742.90	80.4995	292.4	54827.2/8.04	Homo sapiens	51702526	37222	Wiskott-Aldrich syndrome gene-like protein

Fragment-ion (m/z)	342.39	400.05	409.04	504.65	521.09	536.82	554.24	564.53	570.69	576.49	589.79	635.94
Frac. Inten.(% of TIC)	2.16	4.54	2.85	7.45	1.80	4.94	5.83	1.38	16.69	0.04	3.36	1.87
Rel. Inten.(% of BP)	12.93	27.19	17.10	44.65	10.81	29.62	34.94	8.27	100.00	0.25	20.14	11.19
Score	-0.13	0.50	1.00	1.00	-0.11	1.00	1.00	-0.08	1.00	1.50	1.00	0.50
Ion-type		$b{++}_7$-H_2O	$b{++}_7$	$y{++}_7$		y_4	$y{++}_8$		b_5-H_2O $y{+++}_{13}$	sty	b_5	$b{++}_{10}$-H_2O
Delta Da		0.34	0.33	0.42		0.51	0.48		-0.56 0.74	0.86	0.53	0.66

Fragment-ion (m/z)	644.88	652.11	657.88	699.93	710.81	717.80	735.00	798.81	816.68	894.44	1007.54	1106.53
Frac. Inten.(% of TIC)	3.25	2.77	1.58	3.69	1.64	11.15	1.57	1.83	2.32	9.41	6.08	1.80
Rel. Inten.(% of BP)	19.46	16.59	9.45	22.09	9.83	66.82	9.38	10.95	13.89	56.37	36.42	10.81
Score	1.00	1.00	-0.09	0.50	-0.10	1.00	-0.09	0.50	1.00	1.00	1.00	1.00
Ion-type	$b{++}_{10}$	y_5		b_6-NH_3		b_6 $b{++}_{11}$		b_7-NH_3	b_7	y_6	y_7	y_8
Delta Da	0.60	0.78		-0.40		0.45 -0.02		-0.58	0.26	0.08	0.09	0.01

Peak 111



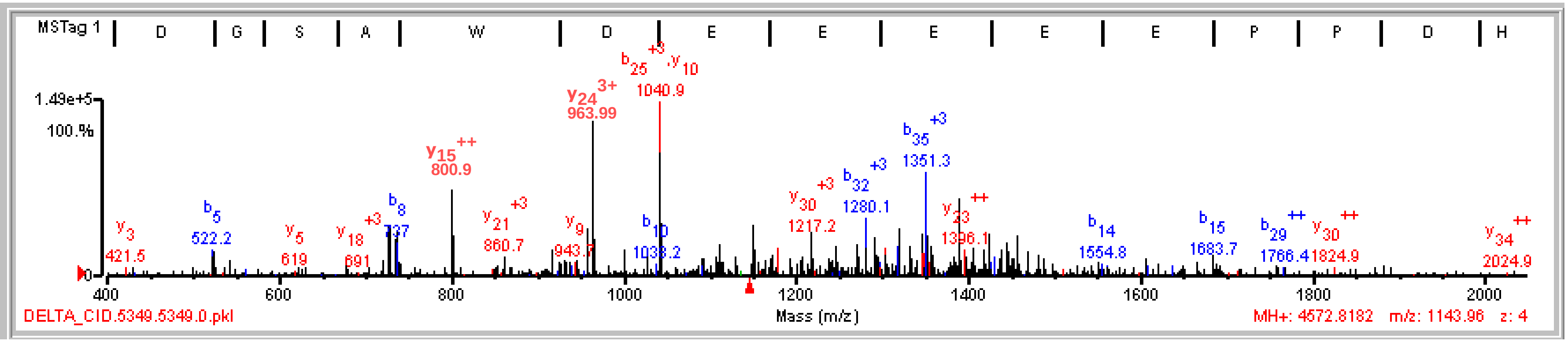


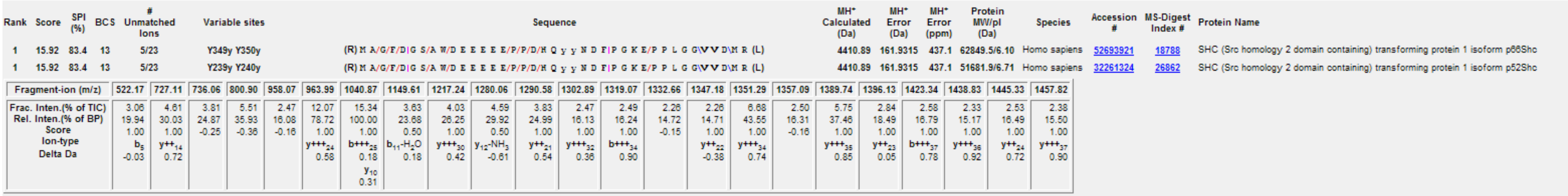
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.69	90.3	12	4/25	Y455y	(R) Q G A E/G/A/P/S/P|N y/D D/D D D/E/R A D/D/T L F M M K (E)	3003.23	80.0800	36.9	99633.4/6.10	Homo sapiens	52426745	29140	Cas-Br-M (murine) ecotropic retroviral transforming sequence

Fragment-ion (m/z)	408.36	426.34	497.54	679.39	770.88	794.78	852.08	857.80	858.14	881.25	885.70	966.60	990.09
Frac. Inten.(% of TIC)	1.05	2.67	1.67	2.99	3.21	1.03	2.80	1.44	4.62	2.16	1.73	2.71	1.47
Rel. Inten.(% of BP)	3.35	8.49	5.30	9.49	10.19	3.29	8.89	4.57	14.68	6.87	5.49	8.61	4.66
Score	-0.03	0.50	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.05
Ion-type		b_5-NH_3	b_6-NH_3	y^{++}_{11}	y_6	b_9	y^{++}_{14}	y^{+++}_{21}	y^{+++}_{21}	a_{10} -0.16 y^{+++}_{22}	y_7	y^{++}_{16}	
Delta Da		0.18	0.34	0.57	0.49	-0.58	0.72	0.47	0.81	0.24	0.28	0.21	

Fragment-ion (m/z)	1145.35	1148.43	1185.14	1193.58	1227.80	1237.00	1237.73	1276.76	1277.51	1285.94	1350.17	1356.78
Frac. Inten.(% of TIC)	2.76	1.89	1.67	7.32	3.41	3.76	7.04	2.74	5.29	31.45	2.00	1.14
Rel. Inten.(% of BP)	8.79	6.01	5.32	23.27	10.83	11.97	22.38	8.73	16.82	100.00	6.36	3.63
Score	1.00	-0.06	0.50	1.00	1.00	1.00	1.00	0.50	-0.17	1.00	1.00	1.00
Ion-type	y^{++}_{18}		y^{++}_{19}-H_2O	y^{++}_{19}	y_{10} 0.21 y^{++}_{20}-H_2O	y^{++}_{20}	y^{++}_{20}	y^{++}_{21}-H_2O		y^{++}_{21}	y^{++}_{23}	y_{11}
Delta Da	0.43		0.70	0.13	-0.16	0.04	0.77	0.27		0.45	0.65	0.15

Peak 112

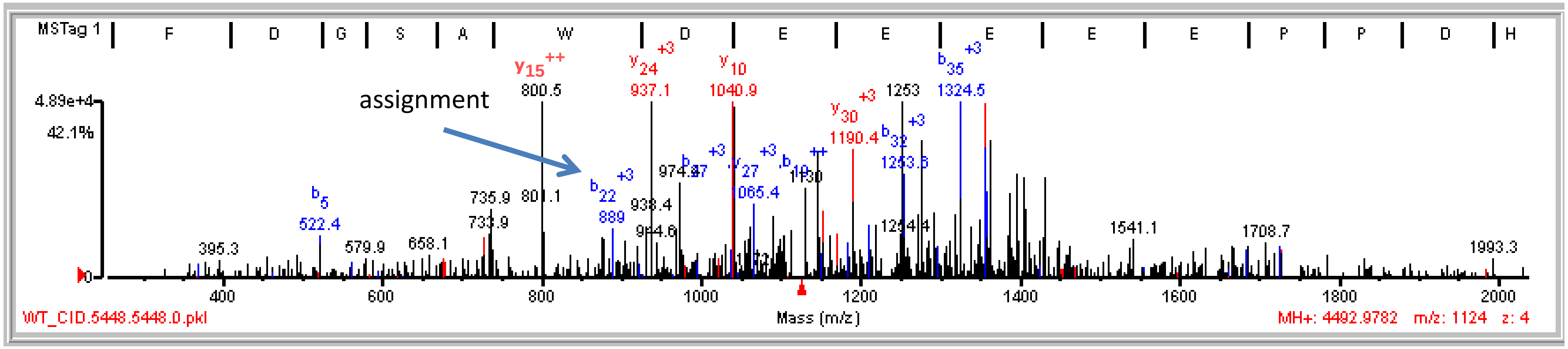




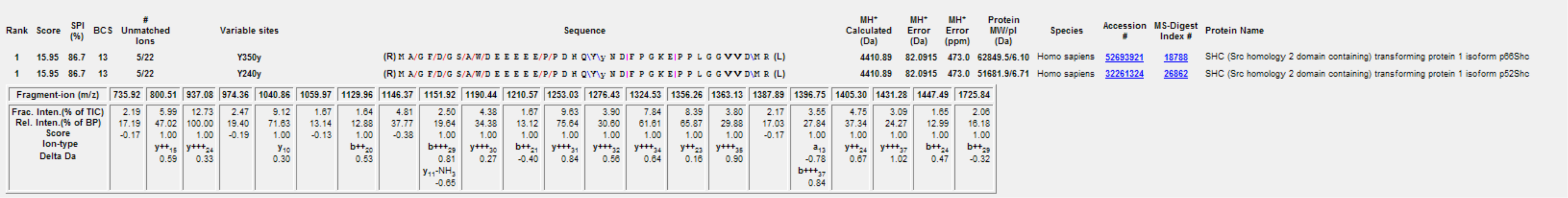
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.92	83.4	13	5/23	Y349y Y350y	(R) M A/G/F/D|G S/A W/D E E E E E/P/P/D/H Q y y N D F|P G K E/P P L G G\V V D\M R (L)	4410.89	161.9315	437.1	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	15.92	83.4	13	5/23	Y239y Y240y	(R) M A/G/F/D|G S/A W/D E E E E E/P/P/D/H Q y y N D F|P G K E/P P L G G\V V D\M R (L)	4410.89	161.9315	437.1	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	522.17	727.11	736.06	800.90	958.07	963.99	1040.87	1149.61	1217.24	1280.06	1290.58	1302.89	1319.07	1332.66	1347.18	1351.29	1357.09	1389.74	1396.13	1423.34	1438.83	1445.33	1457.82
Frac. Inten.(% of TIC)	3.06	4.61	3.81	5.51	2.47	12.07	15.34	3.63	4.03	4.59	3.83	2.47	2.49	2.26	2.26	6.68	2.50	5.75	2.84	2.58	2.33	2.53	2.38
Rel. Inten.(% of BP)	19.94	30.03	24.87	35.93	16.08	78.72	100.00	23.68	26.25	29.92	24.99	16.13	16.24	14.72	14.71	43.55	16.31	37.46	18.49	16.79	15.17	16.49	15.50
Score	1.00	1.00	-0.25	-0.36	-0.16	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00	-0.15	1.00	1.00	-0.16	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b_5	$y{+}{+}_{14}$				$y{+}{+}{+}_{24}$	$b{+}{+}{+}_{25}$ y_{10}	b_{11}-H_2O	$y{+}{+}{+}_{30}$	y_{12}-NH_3	$y{+}{+}_{21}$	$y{+}{+}{+}_{32}$	$b{+}{+}{+}_{34}$		$y{+}{+}_{22}$	$y{+}{+}{+}_{34}$		$y{+}{+}{+}_{35}$	$y{+}{+}_{23}$	$b{+}{+}{+}_{37}$	$y{+}{+}{+}_{36}$	$y{+}{+}_{24}$	$y{+}{+}{+}_{37}$
Delta Da	-0.03	0.72				0.58	0.18 0.31	0.18	0.42	-0.61	0.54	0.36	0.90		-0.38	0.74		0.85	0.05	0.78	0.92	0.72	0.90

Peak 113



assignment

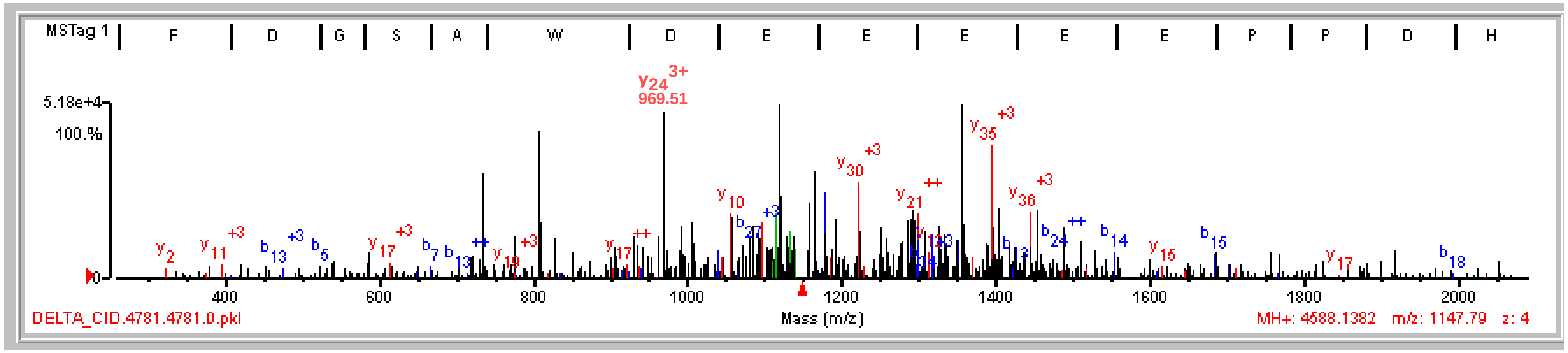


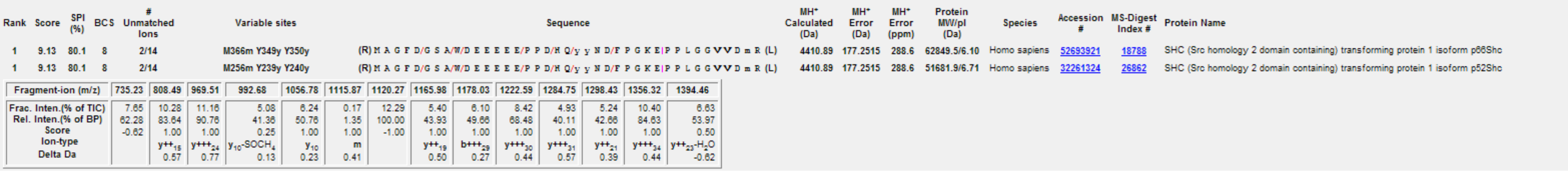
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.95	86.7	13	5/22	Y350y	(R) M A/G F/D/G S/A/W/D E E E E E/P/P D H Q\Y\y N D|F P G K E|P P L G G V V D\M R (L)	4410.89	82.0915	473.0	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	15.95	86.7	13	5/22	Y240y	(R) M A/G F/D/G S/A/W/D E E E E E/P/P D H Q\Y\y N D|F P G K E|P P L G G V V D\M R (L)	4410.89	82.0915	473.0	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	735.92	800.51	937.08	974.36	1040.86	1059.97	1129.96	1146.37	1151.92	1190.44	1210.57
Frac. Inten.(% of TIC)	2.19	5.99	12.73	2.47	9.12	1.67	1.64	4.81	2.50	4.38	1.67
Rel. Inten.(% of BP)	17.19	47.02	100.00	19.40	71.63	13.14	12.88	37.77	19.64	34.38	13.12
Score	-0.17	1.00	1.00	-0.19	1.00	-0.13	1.00	-0.38	1.00	1.00	1.00
Ion-type		y^{++}_{15}	y^{+++}_{24}		y_{10}		b^{++}_{20}		b^{+++}_{29} y_{11}-NH_3	y^{+++}_{30}	b^{++}_{21}
Delta Da		0.59	0.33		0.30		0.53		0.81 -0.65	0.27	-0.40

Fragment-ion (m/z)	1253.03	1276.43	1324.53	1356.26	1363.13	1387.89	1396.75	1405.30	1431.28	1447.49	1725.84
Frac. Inten.(% of TIC)	9.63	3.90	7.84	8.39	3.80	2.17	3.55	4.75	3.09	1.65	2.06
Rel. Inten.(% of BP)	75.64	30.60	61.61	65.87	29.88	17.03	27.84	37.34	24.27	12.99	16.18
Score	1.00	1.00	1.00	1.00	1.00	-0.17	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{+++}_{31}	y^{+++}_{32}	y^{+++}_{34}	y^{++}_{23}	y^{+++}_{35}		a_{13} b^{+++}_{37}	y^{++}_{24}	y^{+++}_{37}	b^{++}_{24}	b^{++}_{29}
Delta Da	0.84	0.56	0.64	0.16	0.90		-0.78 0.84	0.67	1.02	0.47	-0.32

Peak 114

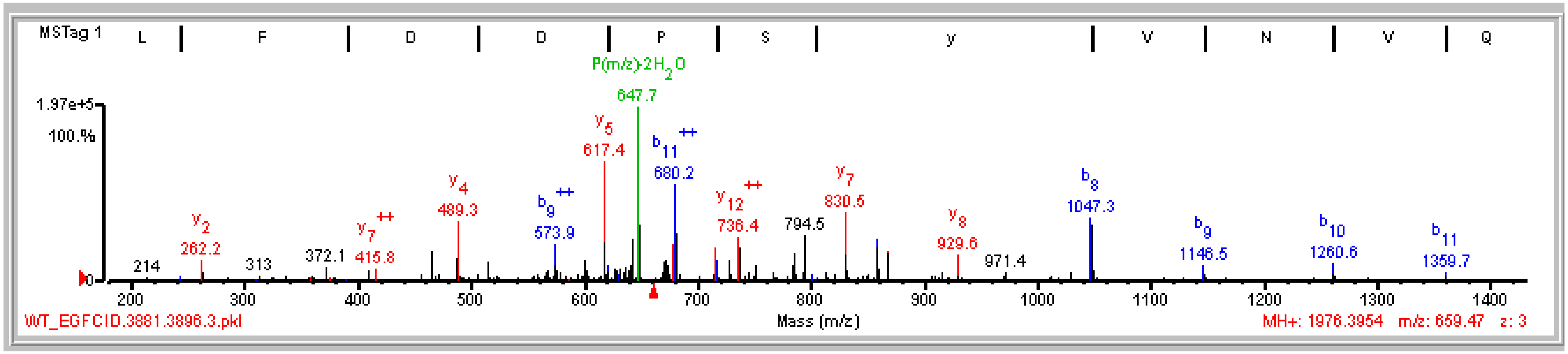


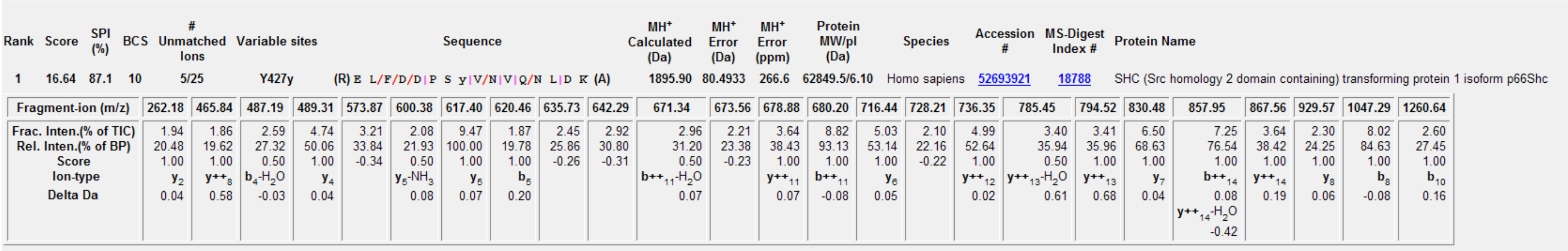


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.13	80.1	8	2/14	M366m Y349y Y350y	(R) M A G F D/G S A/W/D E E E E E/P P D/H Q/y y N D/F P G K E|P P L G G V V D m R (L)	4410.89	177.2515	288.6	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	9.13	80.1	8	2/14	M256m Y239y Y240y	(R) M A G F D/G S A/W/D E E E E E/P P D/H Q/y y N D/F P G K E|P P L G G V V D m R (L)	4410.89	177.2515	288.6	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	735.23	808.49	969.51	992.68	1056.78	1115.87	1120.27	1165.98	1178.03	1222.59	1284.75	1298.43	1356.32	1394.46
Frac. Inten.(% of TIC)	7.65	10.28	11.16	5.08	6.24	0.17	12.29	5.40	6.10	8.42	4.93	5.24	10.40	6.63
Rel. Inten.(% of BP)	62.28	83.64	90.76	41.36	50.76	1.35	100.00	43.93	49.66	68.48	40.11	42.66	84.63	53.97
Score	-0.62	1.00	1.00	0.25	1.00	1.00	-1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50
Ion-type		$y{++}_{15}$	$y{+++}_{24}$	y_{10}-$SOCH_4$	y_{10}	m		$y{++}_{19}$	$b{+++}_{29}$	$y{+++}_{30}$	$y{+++}_{31}$	$y{++}_{21}$	$y{+++}_{34}$	$y{++}_{23}$-H_2O
Delta Da		0.57	0.77	0.13	0.23	0.41		0.50	0.27	0.44	0.57	0.39	0.44	-0.62

Peak 115





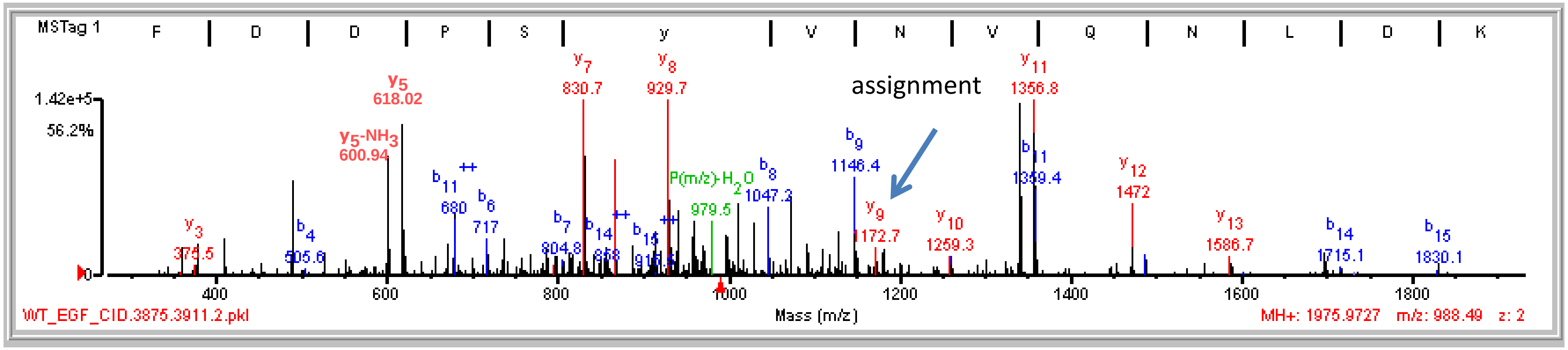
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.64	87.1	10	5/25	Y427y	(R) E L/F/D/D|P S y|V/N|V|Q/N L|D K (A)	1895.90	80.4933	266.6	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc

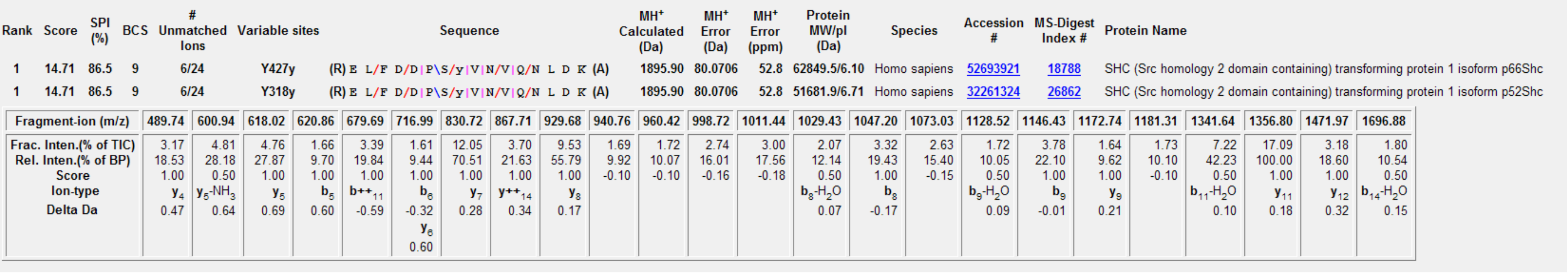
Fragment-ion (m/z)	262.18	465.84	487.19	489.31	573.87	600.38	617.40	620.46	635.73	642.29	671.34	673.56
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	1.94 20.48 1.00 y_2 0.04	1.86 19.62 1.00 $y{+}{+}_8$ 0.58	2.59 27.32 0.50 b_4-H_2O -0.03	4.74 50.06 1.00 y_4 0.04	3.21 33.84 -0.34	2.08 21.93 0.50 y_5-NH_3 0.08	9.47 100.00 1.00 y_5 0.07	1.87 19.78 1.00 b_5 0.20	2.45 25.86 -0.26	2.92 30.80 -0.31	2.96 31.20 0.50 $b{+}{+}_{11}$-H_2O 0.07	2.21 23.38 -0.23

Fragment-ion (m/z)	678.88	680.20	716.44	728.21	736.35	785.45	794.52	830.48	857.95	867.56	929.57	1047.29	1260.64
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	3.64 38.43 1.00 $y{+}{+}_{11}$ 0.07	8.82 93.13 1.00 $b{+}{+}_{11}$ -0.08	5.03 53.14 1.00 y_6 0.05	2.10 22.16 -0.22	4.99 52.64 1.00 $y{+}{+}_{12}$ 0.02	3.40 35.94 0.50 $y{+}{+}_{13}$-H_2O 0.61	3.41 35.96 1.00 $y{+}{+}_{13}$ 0.68	6.50 68.63 1.00 y_7 0.04	7.25 76.54 1.00 $b{+}{+}_{14}$ 0.08 $y{+}{+}_{14}$-H_2O -0.42	3.64 38.42 1.00 $y{+}{+}_{14}$ 0.19	2.30 24.25 1.00 y_8 0.06	8.02 84.63 1.00 b_8 -0.08	2.60 27.45 1.00 b_{10} 0.16

Peak 116

Ions that verify assignment

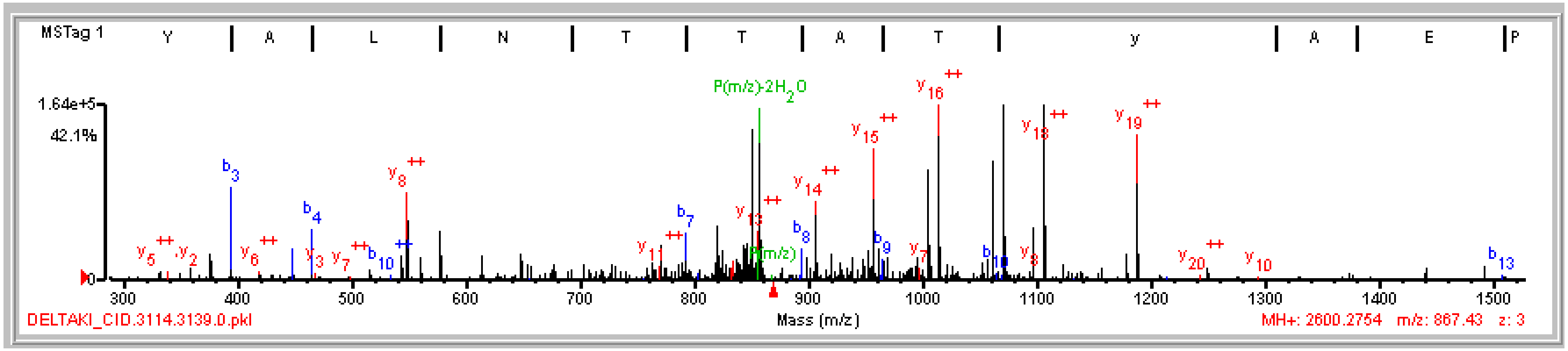


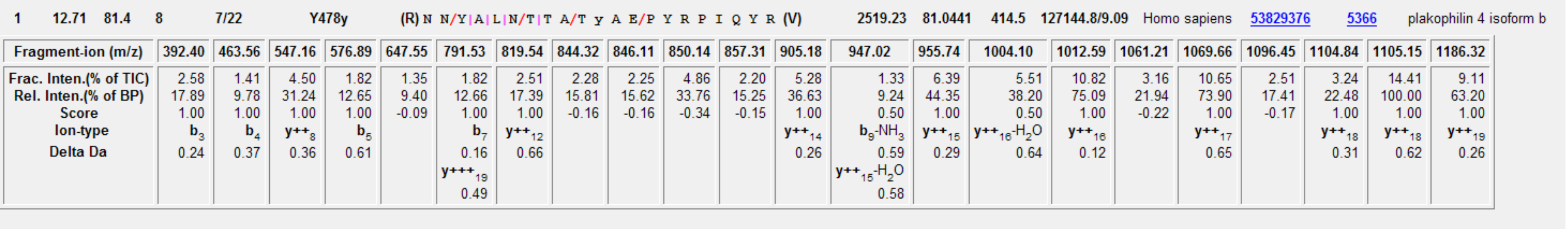


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.71	86.5	9	6/24	Y427y	(R) E L/F D/D|P\S/y|V|N/V|Q/N L D K (A)	1895.90	80.0706	52.8	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	14.71	86.5	9	6/24	Y318y	(R) E L/F D/D|P\S/y|V|N/V|Q/N L D K (A)	1895.90	80.0706	52.8	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	489.74	600.94	618.02	620.86	679.69	716.99	830.72	867.71	929.68	940.76	960.42	998.72	1011.44	1029.43	1047.20	1073.03	1128.52	1146.43	1172.74	1181.31	1341.64	1356.80	1471.97	1696.88
Frac. Inten.(% of TIC)	3.17	4.81	4.76	1.66	3.39	1.61	12.05	3.70	9.53	1.69	1.72	2.74	3.00	2.07	3.32	2.63	1.72	3.78	1.64	1.73	7.22	17.09	3.18	1.80
Rel. Inten.(% of BP)	18.53	28.18	27.87	9.70	19.84	9.44	70.51	21.63	55.79	9.92	10.07	16.01	17.56	12.14	19.43	15.40	10.05	22.10	9.62	10.10	42.23	100.00	18.60	10.54
Score	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.10	-0.10	-0.16	-0.18	0.50	1.00	-0.15	0.50	1.00	1.00	-0.10	0.50	1.00	1.00	0.50
Ion-type	y_4	y_5-NH_3	y_5	b_5	$b++_{11}$	b_6 y_6	y_7	$y++_{14}$	y_8					b_8-H_2O	b_8		b_9-H_2O	b_9	y_9		b_{11}-H_2O	y_{11}	y_{12}	b_{14}-H_2O
Delta Da	0.47	0.64	0.69	0.60	-0.59	-0.32 0.60	0.28	0.34	0.17					0.07	-0.17		0.09	-0.01	0.21		0.10	0.18	0.32	0.15

Peak 117



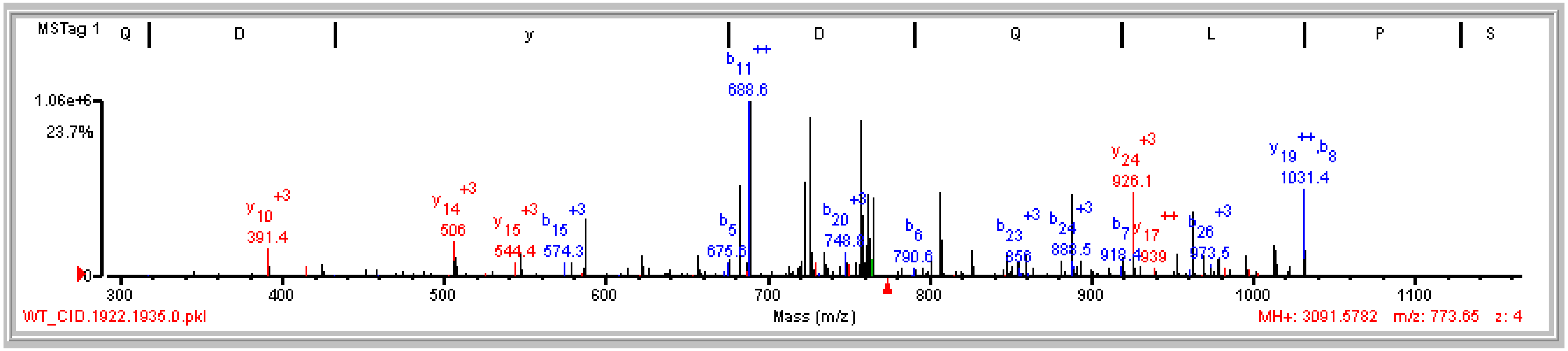


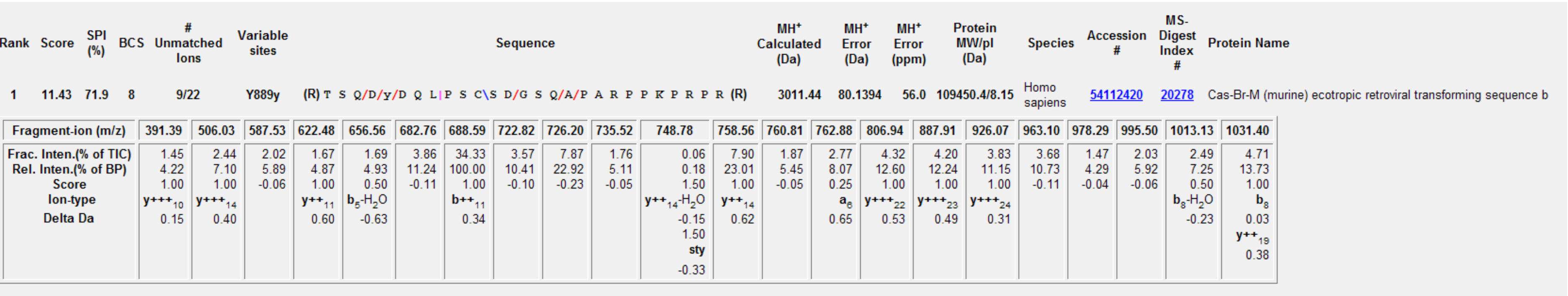
1 12.71 81.4 8 7/22 Y478y (R) N N/Y|A|L|N/T|T A/T y A E/P Y R P I Q Y R (V) 2519.23 81.0441 414.5 127144.8/9.09 Homo sapiens 53829376 5366 plakophilin 4 isoform b

Fragment-ion (m/z)	392.40	463.56	547.16	576.89	647.55	791.53	819.54	844.32	846.11	850.14	857.31
Frac. Inten.(% of TIC)	2.58	1.41	4.50	1.82	1.35	1.82	2.51	2.28	2.25	4.86	2.20
Rel. Inten.(% of BP)	17.89	9.78	31.24	12.65	9.40	12.66	17.39	15.81	15.62	33.76	15.25
Score	1.00	1.00	1.00	1.00	-0.09	1.00	1.00	-0.16	-0.16	-0.34	-0.15
Ion-type	b_3	b_4	$y{++}_{8}$	b_5		b_7 $y{+++}_{19}$	$y{++}_{12}$				
Delta Da	0.24	0.37	0.36	0.61		0.16 0.49	0.66				

Fragment-ion (m/z)	905.18	947.02	955.74	1004.10	1012.59	1061.21	1069.66	1096.45	1104.84	1105.15	1186.32
Frac. Inten.(% of TIC)	5.28	1.33	6.39	5.51	10.82	3.16	10.65	2.51	3.24	14.41	9.11
Rel. Inten.(% of BP)	36.63	9.24	44.35	38.20	75.09	21.94	73.90	17.41	22.48	100.00	63.20
Score	1.00	0.50	1.00	0.50	1.00	-0.22	1.00	-0.17	1.00	1.00	1.00
Ion-type	$y{++}_{14}$	$b_9\text{-}NH_3$ $y{++}_{15}\text{-}H_2O$	$y{++}_{15}$	$y{++}_{16}\text{-}H_2O$	$y{++}_{16}$		$y{++}_{17}$		$y{++}_{18}$	$y{++}_{18}$	$y{++}_{19}$
Delta Da	0.26	0.59 0.58	0.29	0.64	0.12		0.65		0.31	0.62	0.26

Peak 118





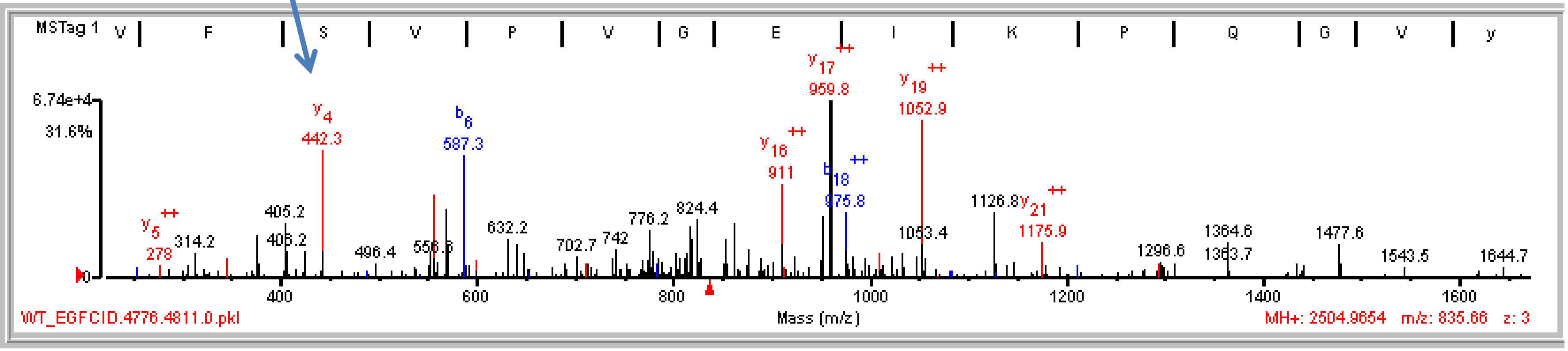
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.43	71.9	8	9/22	Y889y	(R) T S Q/D/y/D Q L|P S C\S D/G S Q/A/P A R P P K P R P R (R)	3011.44	80.1394	56.0	109450.4/8.15	Homo sapiens	54112420	20278	Cas-Br-M (murine) ecotropic retroviral transforming sequence b

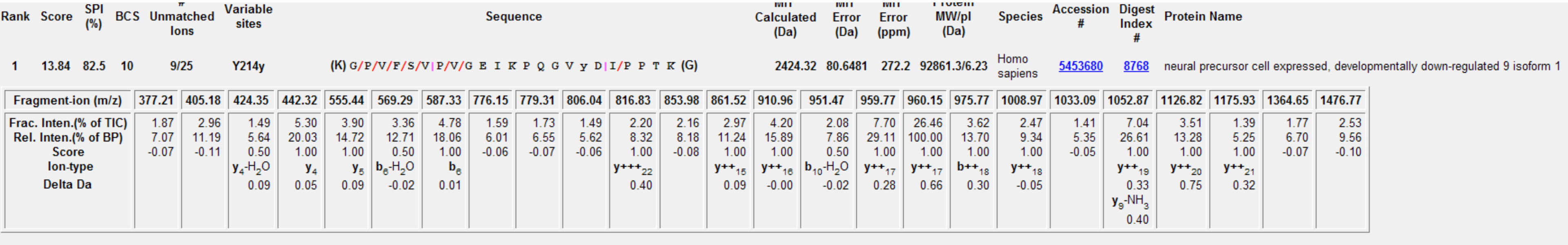
Fragment-ion (m/z)	391.39	506.03	587.53	622.48	656.56	682.76	688.59	722.82	726.20	735.52	748.78
Frac. Inten.(% of TIC)	1.45	2.44	2.02	1.67	1.69	3.86	34.33	3.57	7.87	1.76	0.06
Rel. Inten.(% of BP)	4.22	7.10	5.89	4.87	4.93	11.24	100.00	10.41	22.92	5.11	0.18
Score	1.00	1.00	-0.06	1.00	0.50	-0.11	1.00	-0.10	-0.23	-0.05	1.50
Ion-type	y^{+++}_{10}	y^{+++}_{14}		y^{++}_{11}	b_5-H_2O		b^{++}_{11}				y^{++}_{14}-H_2O
Delta Da	0.15	0.40		0.60	-0.63		0.34				-0.15 1.50 sty -0.33

Fragment-ion (m/z)	758.56	760.81	762.88	806.94	887.91	926.07	963.10	978.29	995.50	1013.13	1031.40
Frac. Inten.(% of TIC)	7.90	1.87	2.77	4.32	4.20	3.83	3.68	1.47	2.03	2.49	4.71
Rel. Inten.(% of BP)	23.01	5.45	8.07	12.60	12.24	11.15	10.73	4.29	5.92	7.25	13.73
Score	1.00	-0.05	0.25	1.00	1.00	1.00	-0.11	-0.04	-0.06	0.50	1.00
Ion-type	y^{++}_{14}		a_6	y^{+++}_{22}	y^{+++}_{23}	y^{+++}_{24}				b_8-H_2O	b_8
Delta Da	0.62		0.65	0.53	0.49	0.31				-0.23	0.03 y^{++}_{19} 0.38

Peak 119

Ions that verify assignment



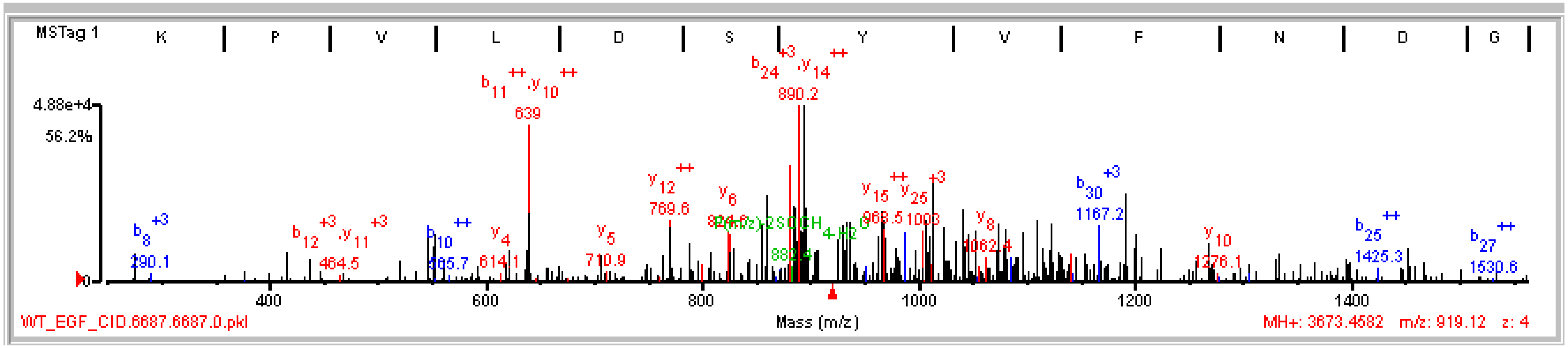


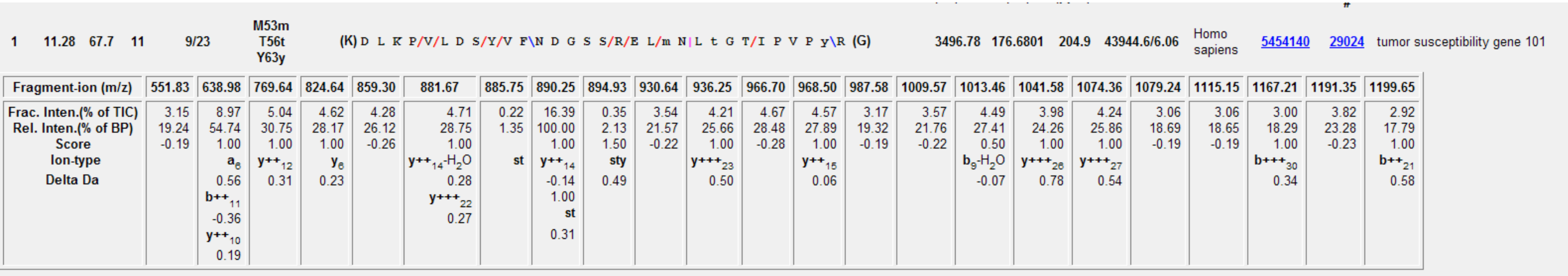
Rank	Score	SPI (%)	BCS	Unmatched Ions	Variable sites	Sequence	Calculated (Da)	Error (Da)	Error (ppm)	MW/pI (Da)	Species	Accession #	Digest Index #	Protein Name
1	13.84	82.5	10	9/25	Y214y	(K) G/P/V/F/S/V|P/V/G E I K P Q G V y D|I/P P T K (G)	2424.32	80.6481	272.2	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

Fragment-ion (m/z)	377.21	405.18	424.35	442.32	555.44	569.29	587.33	776.15	779.31	806.04	816.83	853.98	861.52
Frac. Inten.(% of TIC)	1.87	2.96	1.49	5.30	3.90	3.36	4.78	1.59	1.73	1.49	2.20	2.16	2.97
Rel. Inten.(% of BP)	7.07	11.19	5.64	20.03	14.72	12.71	18.06	6.01	6.55	5.62	8.32	8.18	11.24
Score	-0.07	-0.11	0.50	1.00	1.00	0.50	1.00	-0.06	-0.07	-0.06	1.00	-0.08	1.00
Ion-type			y_4-H_2O	y_4	y_5	b_6-H_2O	b_6				y^{+++}_{22}		y^{++}_{15}
Delta Da			0.09	0.05	0.09	-0.02	0.01				0.40		0.09

Fragment-ion (m/z)	910.96	951.47	959.77	960.15	975.77	1008.97	1033.09	1052.87	1126.82	1175.93	1364.65	1476.77
Frac. Inten.(% of TIC)	4.20	2.08	7.70	26.46	3.62	2.47	1.41	7.04	3.51	1.39	1.77	2.53
Rel. Inten.(% of BP)	15.89	7.86	29.11	100.00	13.70	9.34	5.35	26.61	13.28	5.25	6.70	9.56
Score	1.00	0.50	1.00	1.00	1.00	1.00	-0.05	1.00	1.00	1.00	-0.07	-0.10
Ion-type	y^{++}_{16}	b_{10}-H_2O	y^{++}_{17}	y^{++}_{17}	b^{++}_{18}	y^{++}_{18}		y^{++}_{19} y_9-NH_3	y^{++}_{20}	y^{++}_{21}		
Delta Da	-0.00	-0.02	0.28	0.66	0.30	-0.05		0.33 0.40	0.75	0.32		

Peak 120



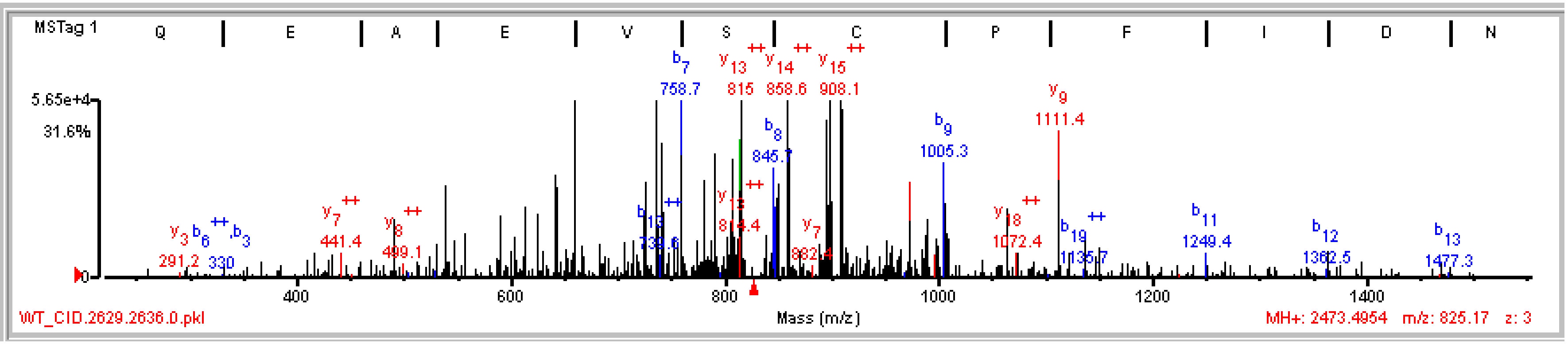


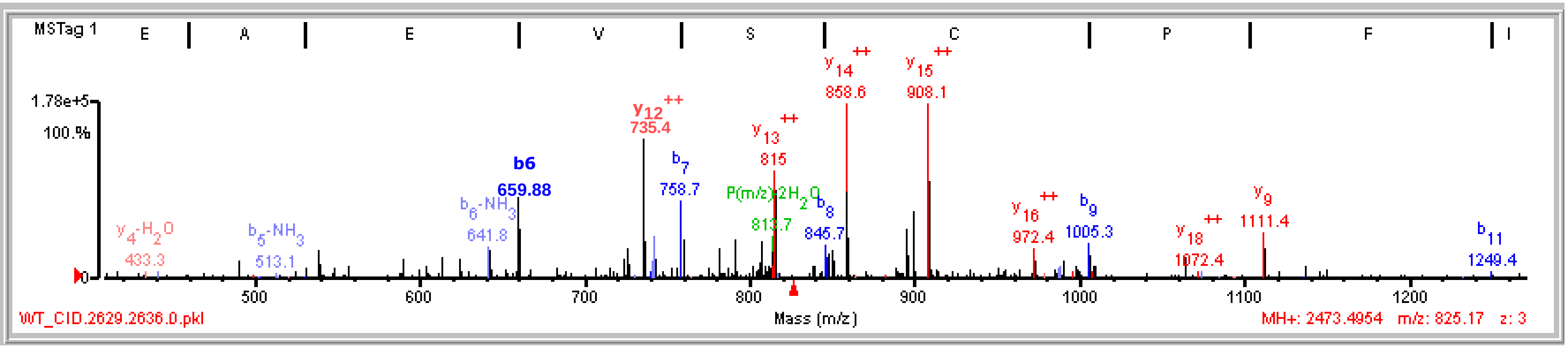
1 11.28 67.7 11 9/23 M53m T56t Y63y (K) D L K P/V/L D S/Y/V F\N D G S S/R/E L/m N|L t G T/I P V P y\R (G) 3496.78 176.6801 204.9 43944.6/6.06 Homo sapiens 5454140 29024 tumor susceptibility gene 101

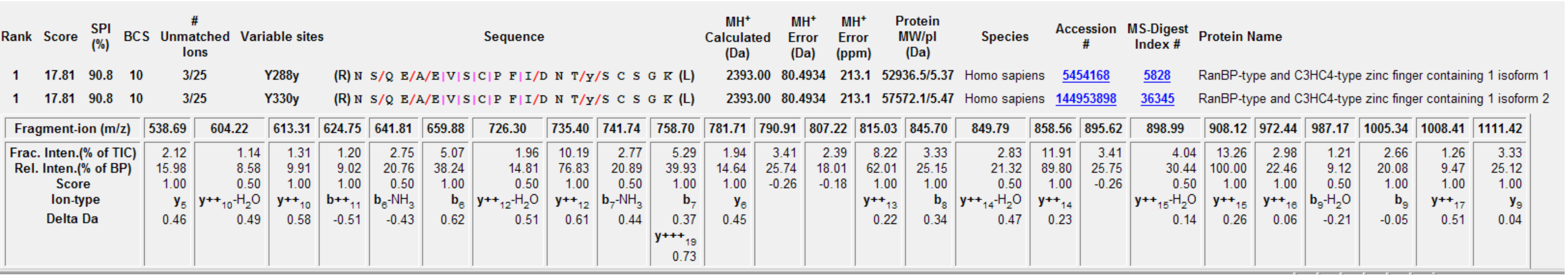
Fragment-ion (m/z)	551.83	638.98	769.64	824.64	859.30	881.67	885.75	890.25	894.93	930.64	936.25
Frac. Inten.(% of TIC)	3.15	8.97	5.04	4.62	4.28	4.71	0.22	16.39	0.35	3.54	4.21
Rel. Inten.(% of BP)	19.24	54.74	30.75	28.17	26.12	28.75	1.35	100.00	2.13	21.57	25.66
Score	-0.19	1.00	1.00	1.00	-0.26	1.00		1.00 1.00	1.50	-0.22	1.00
Ion-type		a_6 $b{+}{+}_{11}$ $y{+}{+}_{10}$	$y{+}{+}_{12}$	y_6		$y{+}{+}_{14}$-H_2O $y{+}{+}{+}_{22}$	st	$y{+}{+}_{14}$ st	sty		$y{+}{+}{+}_{23}$
Delta Da		0.56 -0.36 0.19	0.31	0.23		0.28 0.27		-0.14 0.31	0.49		0.50

Fragment-ion (m/z)	966.70	968.50	987.58	1009.57	1013.46	1041.58	1074.36	1079.24	1115.15	1167.21	1191.35	1199.65
Frac. Inten.(% of TIC)	4.67	4.57	3.17	3.57	4.49	3.98	4.24	3.06	3.06	3.00	3.82	2.92
Rel. Inten.(% of BP)	28.48	27.89	19.32	21.76	27.41	24.26	25.86	18.69	18.65	18.29	23.28	17.79
Score	-0.28	1.00	-0.19	-0.22	0.50	1.00	1.00	-0.19	-0.19	1.00	-0.23	1.00
Ion-type		$y{+}{+}_{15}$			b_9-H_2O	$y{+}{+}{+}_{26}$	$y{+}{+}{+}_{27}$			$b{+}{+}{+}_{30}$		$b{+}{+}_{21}$
Delta Da		0.06			-0.07	0.78	0.54			0.34		0.58

Peak 121





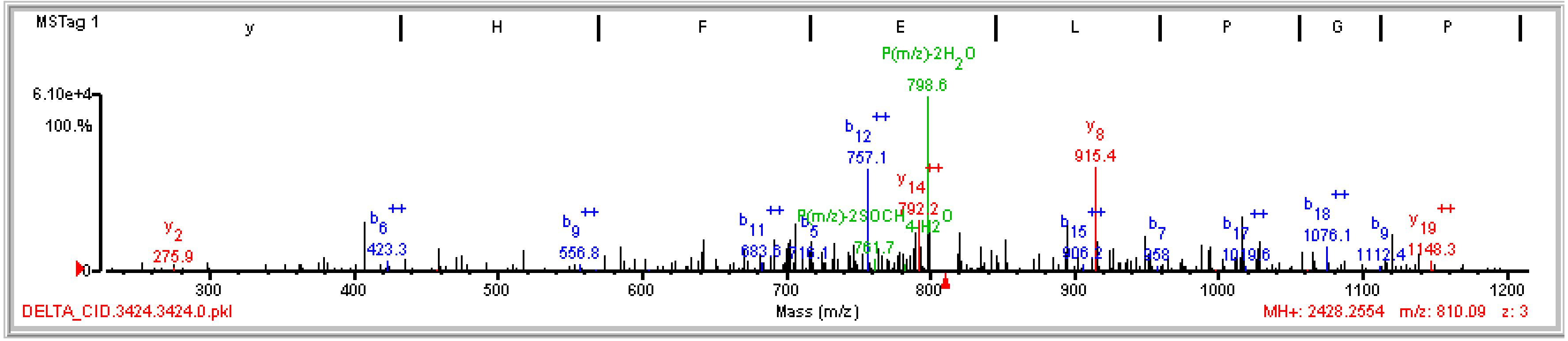


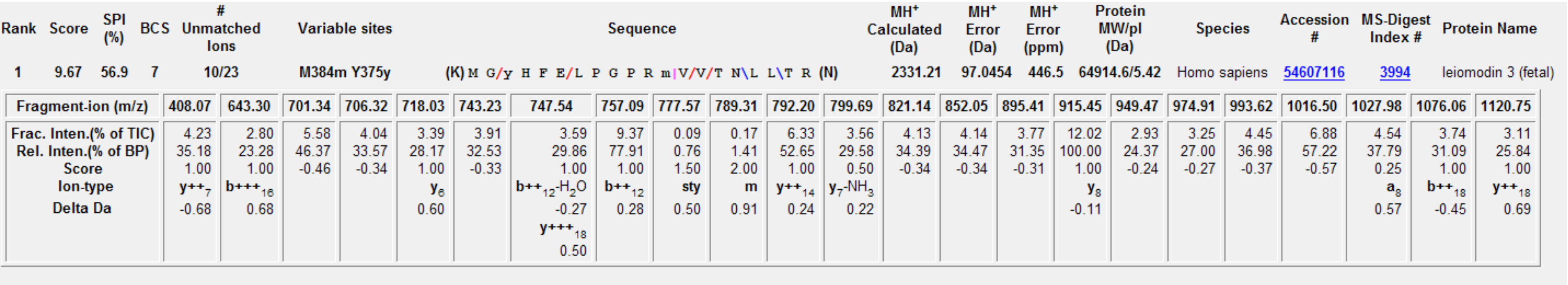
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.81	90.8	10	3/25	Y288y	(R) N S/Q E/A/E|V|S|C|P F|I/D N T/y/S C S G K (L)	2393.00	80.4934	213.1	52936.5/5.37	Homo sapiens	5454168	5828	RanBP-type and C3HC4-type zinc finger containing 1 isoform 1
1	17.81	90.8	10	3/25	Y330y	(R) N S/Q E/A/E|V|S|C|P F|I/D N T/y/S C S G K (L)	2393.00	80.4934	213.1	57572.1/5.47	Homo sapiens	144953898	36345	RanBP-type and C3HC4-type zinc finger containing 1 isoform 2

Fragment-ion (m/z)	538.69	604.22	613.31	624.75	641.81	659.88	726.30	735.40	741.74	758.70	781.71	790.91	807.22
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	2.12 15.98 1.00 y_5 0.46	1.14 8.58 0.50 y++$_{10}$-H$_2$O 0.49	1.31 9.91 1.00 y++$_{10}$ 0.58	1.20 9.02 1.00 b++$_{11}$ -0.51	2.75 20.76 0.50 b_6-NH$_3$ -0.43	5.07 38.24 1.00 b_6 0.62	1.96 14.81 0.50 y++$_{12}$-H$_2$O 0.51	10.19 76.83 1.00 y++$_{12}$ 0.61	2.77 20.89 0.50 b_7-NH$_3$ 0.44	5.29 39.93 1.00 b_7 0.37 y+++$_{19}$ 0.73	1.94 14.64 1.00 y_6 0.45	3.41 25.74 -0.26	2.39 18.01 -0.18

Fragment-ion (m/z)	815.03	845.70	849.79	858.56	895.62	898.99	908.12	972.44	987.17	1005.34	1008.41	1111.42
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	8.22 62.01 1.00 y++$_{13}$ 0.22	3.33 25.15 1.00 b_8 0.34	2.83 21.32 0.50 y++$_{14}$-H$_2$O 0.47	11.91 89.80 1.00 y++$_{14}$ 0.23	3.41 25.75 -0.26	4.04 30.44 0.50 y++$_{15}$-H$_2$O 0.14	13.26 100.00 1.00 y++$_{15}$ 0.26	2.98 22.46 1.00 y++$_{16}$ 0.06	1.21 9.12 0.50 b_9-H$_2$O -0.21	2.66 20.08 1.00 b_9 -0.05	1.26 9.47 1.00 y++$_{17}$ 0.51	3.33 25.12 1.00 y_9 0.04

Peak 122



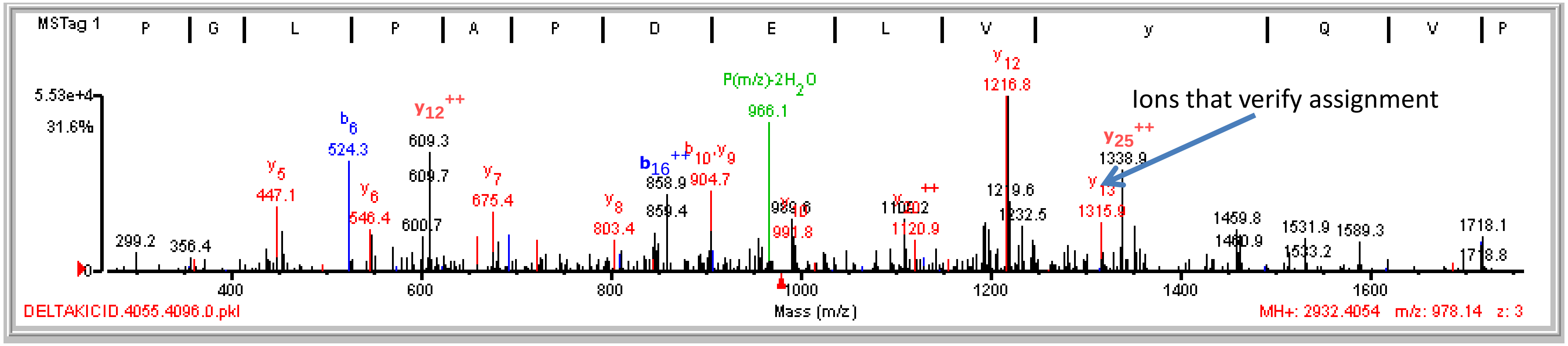


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.67	56.9	7	10/23	M384m Y375y	(K) M G/y H F E/L P G P R m|V/V/T N\L L\T R (N)	2331.21	97.0454	446.5	64914.6/5.42	Homo sapiens	54607116	3994	leiomodin 3 (fetal)

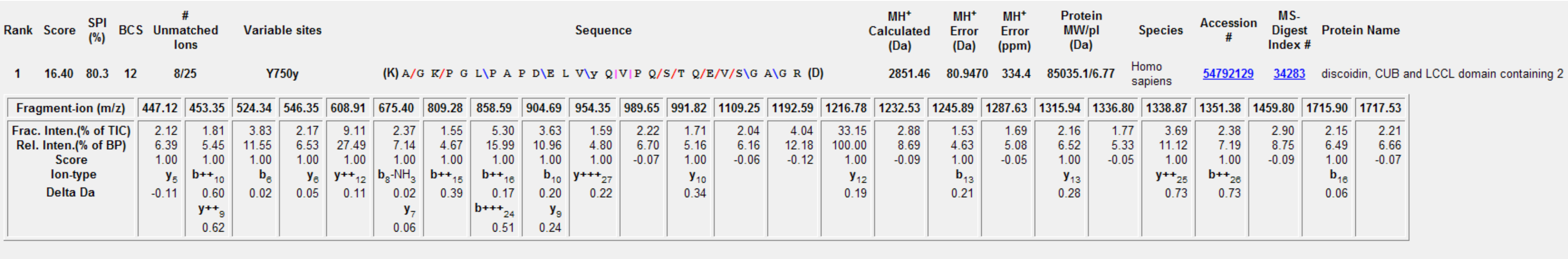
Fragment-ion (m/z)	408.07	643.30	701.34	706.32	718.03	743.23	747.54	757.09	777.57	789.31	792.20	799.69
Frac. Inten.(% of TIC)	4.23	2.80	5.58	4.04	3.39	3.91	3.59	9.37	0.09	0.17	6.33	3.56
Rel. Inten.(% of BP)	35.18	23.28	46.37	33.57	28.17	32.53	29.86	77.91	0.76	1.41	52.65	29.58
Score	1.00	1.00	-0.46	-0.34	1.00	-0.33	1.00	1.00	1.50	2.00	1.00	0.50
Ion-type	$y{+}{+}_{7}$	$b{+}{+}{+}_{16}$			y_{6}		$b{+}{+}_{12}$-H_2O $y{+}{+}{+}_{18}$	$b{+}{+}_{12}$	sty	m	$y{+}{+}_{14}$	y_{7}-NH_3
Delta Da	-0.68	0.68			0.60		-0.27 0.50	0.28	0.50	0.91	0.24	0.22

Fragment-ion (m/z)	821.14	852.05	895.41	915.45	949.47	974.91	993.62	1016.50	1027.98	1076.06	1120.75
Frac. Inten.(% of TIC)	4.13	4.14	3.77	12.02	2.93	3.25	4.45	6.88	4.54	3.74	3.11
Rel. Inten.(% of BP)	34.39	34.47	31.35	100.00	24.37	27.00	36.98	57.22	37.79	31.09	25.84
Score	-0.34	-0.34	-0.31	1.00	-0.24	-0.27	-0.37	-0.57	0.25	1.00	1.00
Ion-type				y_{8}					a_{8}	$b{+}{+}_{18}$	$y{+}{+}_{18}$
Delta Da				-0.11					0.57	-0.45	0.69

Peak 123



Ions that verify assignment

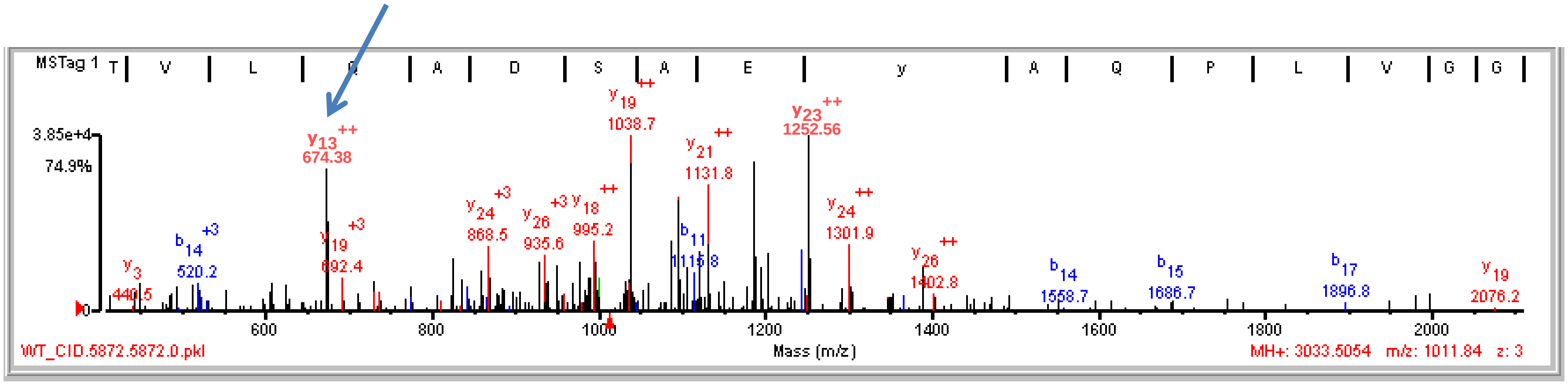


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.40	80.3	12	8/25	Y750y	(K) A/G K/P G L\P A P D\E L V\y Q|V|P Q/S/T Q/E/V/S\G A\G R (D)	2851.46	80.9470	334.4	85035.1/6.77	Homo sapiens	54792129	34283	discoidin, CUB and LCCL domain containing 2

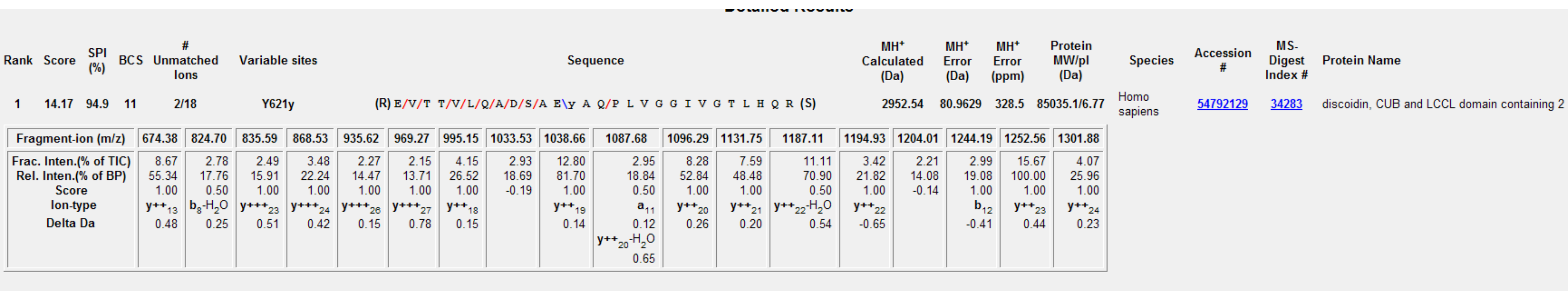
Fragment-ion (m/z)	447.12	453.35	524.34	546.35	608.91	675.40	809.28	858.59	904.69	954.35	989.65	991.82
Frac. Inten.(% of TIC)	2.12	1.81	3.83	2.17	9.11	2.37	1.55	5.30	3.63	1.59	2.22	1.71
Rel. Inten.(% of BP)	6.39	5.45	11.55	6.53	27.49	7.14	4.67	15.99	10.96	4.80	6.70	5.16
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.07	1.00
Ion-type	y_5	b^{++}_{10}	b_6	y_6	y^{++}_{12}	b_8-NH_3	b^{++}_{15}	b^{++}_{16}	b_{10}	y^{+++}_{27}		y_{10}
Delta Da	-0.11	0.60	0.02	0.05	0.11	0.02	0.39	0.17	0.20	0.22		0.34
		y^{++}_9				y_7		b^{+++}_{24}	y_9			
		0.62				0.06		0.51	0.24			

Fragment-ion (m/z)	1109.25	1192.59	1216.78	1232.53	1245.89	1287.63	1315.94	1336.80	1338.87	1351.38	1459.80	1715.90	1717.53
Frac. Inten.(% of TIC)	2.04	4.04	33.15	2.88	1.53	1.69	2.16	1.77	3.69	2.38	2.90	2.15	2.21
Rel. Inten.(% of BP)	6.16	12.18	100.00	8.69	4.63	5.08	6.52	5.33	11.12	7.19	8.75	6.49	6.66
Score	-0.06	-0.12	1.00	-0.09	1.00	-0.05	1.00	-0.05	1.00	1.00	-0.09	1.00	-0.07
Ion-type			y_{12}		b_{13}		y_{13}		y^{++}_{25}	b^{++}_{26}		b_{16}	
Delta Da			0.19		0.21		0.28		0.73	0.73		0.06	

Peak 124



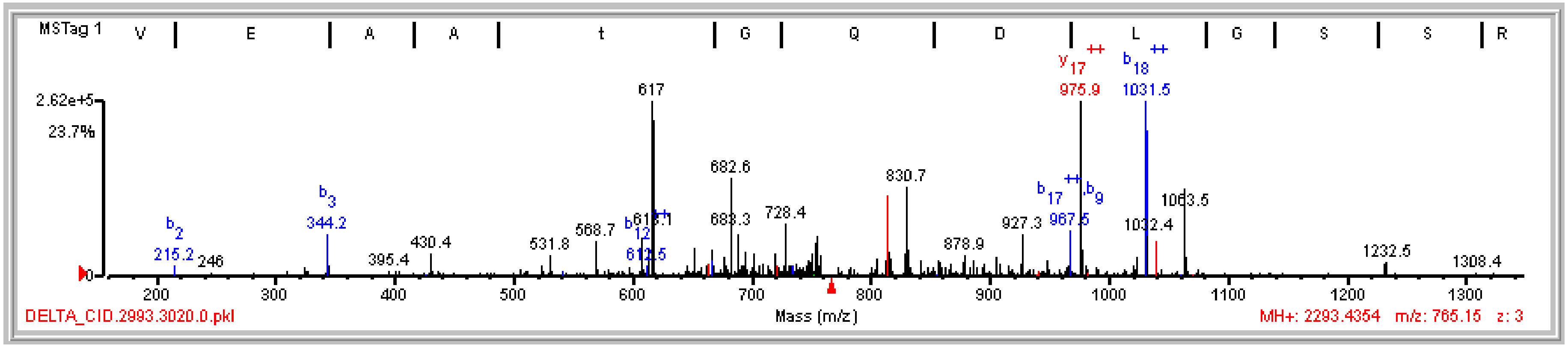
Ions that verify assignment

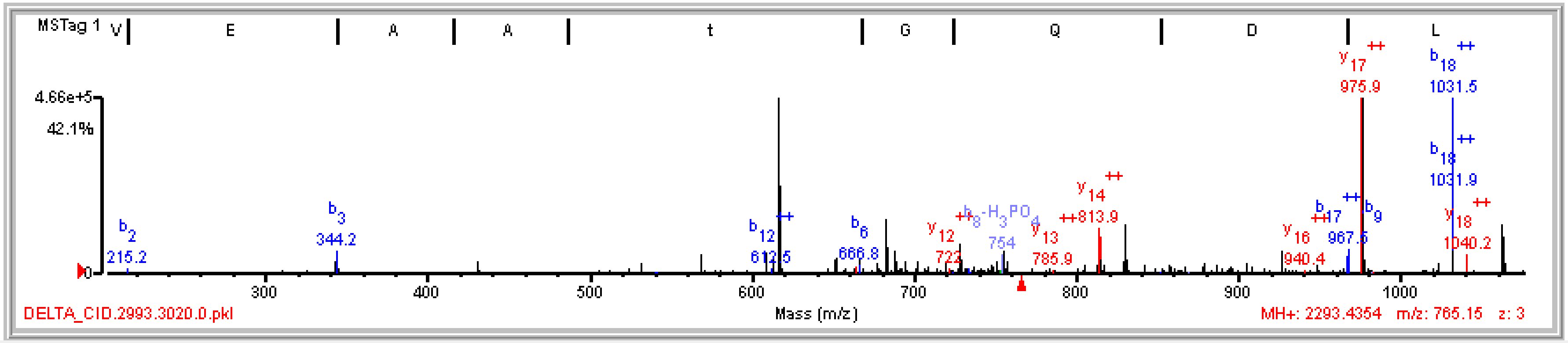


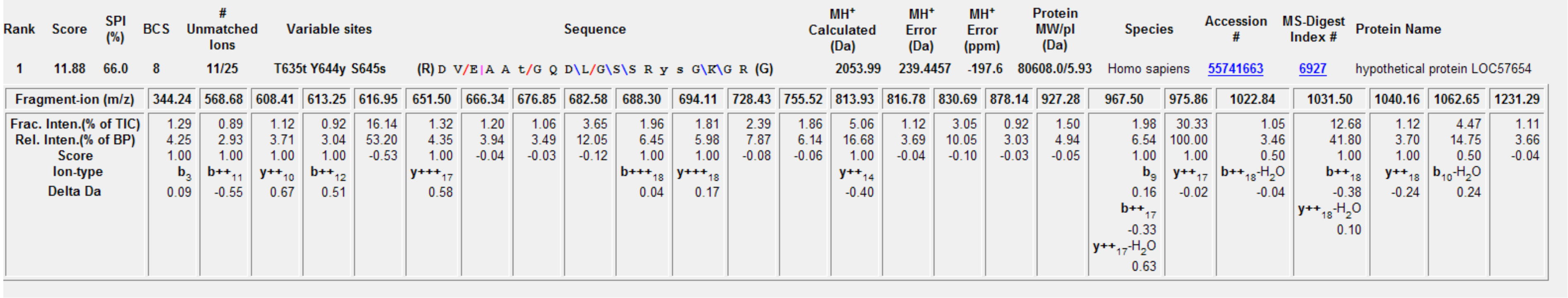
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.17	94.9	11	2/18	Y621y	(R) E/V/T T/V/L/Q/A/D/S/A E\y A Q/P L V G G I V G T L H Q R (S)	2952.54	80.9629	328.5	85035.1/6.77	Homo sapiens	54792129	34283	discoidin, CUB and LCCL domain containing 2

Fragment-ion (m/z)	674.38	824.70	835.59	868.53	935.62	969.27	995.15	1033.53	1038.66	1087.68	1096.29	1131.75	1187.11	1194.93	1204.01	1244.19	1252.56	1301.88
Frac. Inten.(% of TIC)	8.67	2.78	2.49	3.48	2.27	2.15	4.15	2.93	12.80	2.95	8.28	7.59	11.11	3.42	2.21	2.99	15.67	4.07
Rel. Inten.(% of BP)	55.34	17.76	15.91	22.24	14.47	13.71	26.52	18.69	81.70	18.84	52.84	48.48	70.90	21.82	14.08	19.08	100.00	25.96
Score	1.00	0.50	1.00	1.00	1.00	1.00	1.00	-0.19	1.00	0.50	1.00	1.00	0.50	1.00	-0.14	1.00	1.00	1.00
Ion-type	y^{++}_{13}	b_8-H_2O	y^{+++}_{23}	y^{+++}_{24}	y^{+++}_{26}	y^{+++}_{27}	y^{++}_{18}		y^{++}_{19}	a_{11} y^{++}_{20}-H_2O	y^{++}_{20}	y^{++}_{21}	y^{++}_{22}-H_2O	y^{++}_{22}		b_{12}	y^{++}_{23}	y^{++}_{24}
Delta Da	0.48	0.25	0.51	0.42	0.15	0.78	0.15		0.14	0.12 0.65	0.26	0.20	0.54	-0.65		-0.41	0.44	0.23

Peak 125





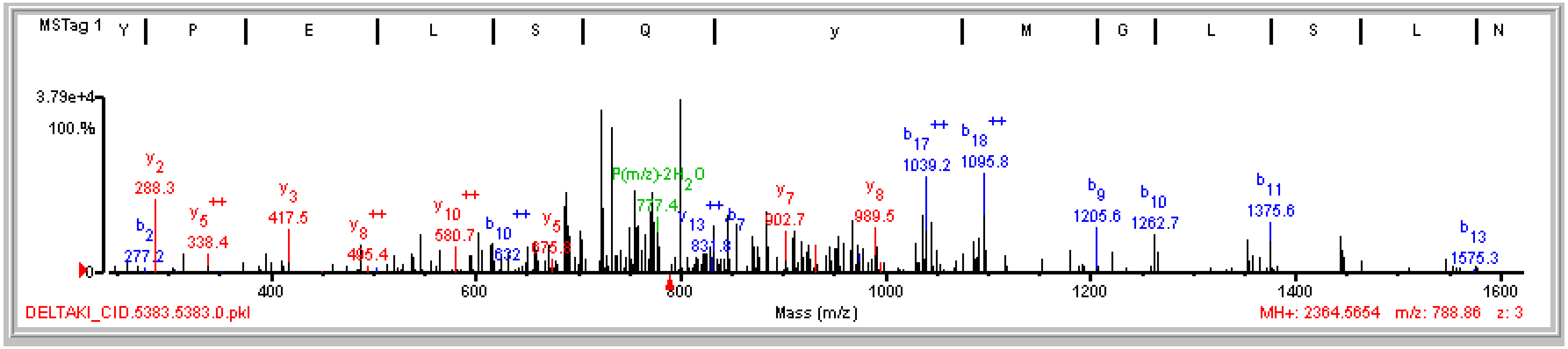


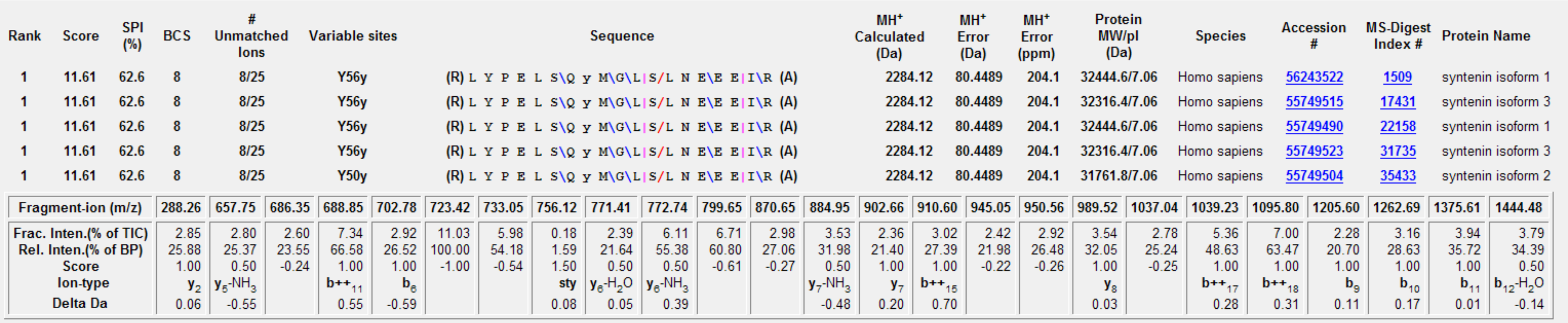
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.88	66.0	8	11/25	T635t Y644y S645s	(R) D V/E|A A t/G Q D\L/G\S\S R y s G\K\G R (G)	2053.99	239.4457	-197.6	80608.0/5.93	Homo sapiens	55741663	6927	hypothetical protein LOC57654

Fragment-ion (m/z)	344.24	568.68	608.41	613.25	616.95	651.50	666.34	676.85	682.58	688.30	694.11	728.43
Frac. Inten.(% of TIC)	1.29	0.89	1.12	0.92	16.14	1.32	1.20	1.06	3.65	1.96	1.81	2.39
Rel. Inten.(% of BP)	4.25	2.93	3.71	3.04	53.20	4.35	3.94	3.49	12.05	6.45	5.98	7.87
Score	1.00	1.00	1.00	1.00	-0.53	1.00	-0.04	-0.03	-0.12	1.00	1.00	-0.08
Ion-type	b_3	$b{++}_{11}$	$y{++}_{10}$	$b{++}_{12}$		$y{+++}_{17}$				$b{+++}_{18}$	$y{+++}_{18}$	
Delta Da	0.09	-0.55	0.67	0.51		0.58				0.04	0.17	

Fragment-ion (m/z)	755.52	813.93	816.78	830.69	878.14	927.28	967.50	975.86	1022.84	1031.50	1040.16	1062.65	1231.29
Frac. Inten.(% of TIC)	1.86	5.06	1.12	3.05	0.92	1.50	1.98	30.33	1.05	12.68	1.12	4.47	1.11
Rel. Inten.(% of BP)	6.14	16.68	3.69	10.05	3.03	4.94	6.54	100.00	3.46	41.80	3.70	14.75	3.66
Score	-0.06	1.00	-0.04	-0.10	-0.03	-0.05	1.00	1.00	0.50	1.00	1.00	0.50	-0.04
Ion-type		$y{++}_{14}$					b_9 $b{++}_{17}$ $y{++}_{17}$-H_2O	$y{++}_{17}$	$b{++}_{18}$-H_2O	$b{++}_{18}$ $y{++}_{18}$-H_2O	$y{++}_{18}$	b_{10}-H_2O	
Delta Da		-0.40					0.16 -0.33 0.63	-0.02	-0.04	-0.38 0.10	-0.24	0.24	

Peak 127



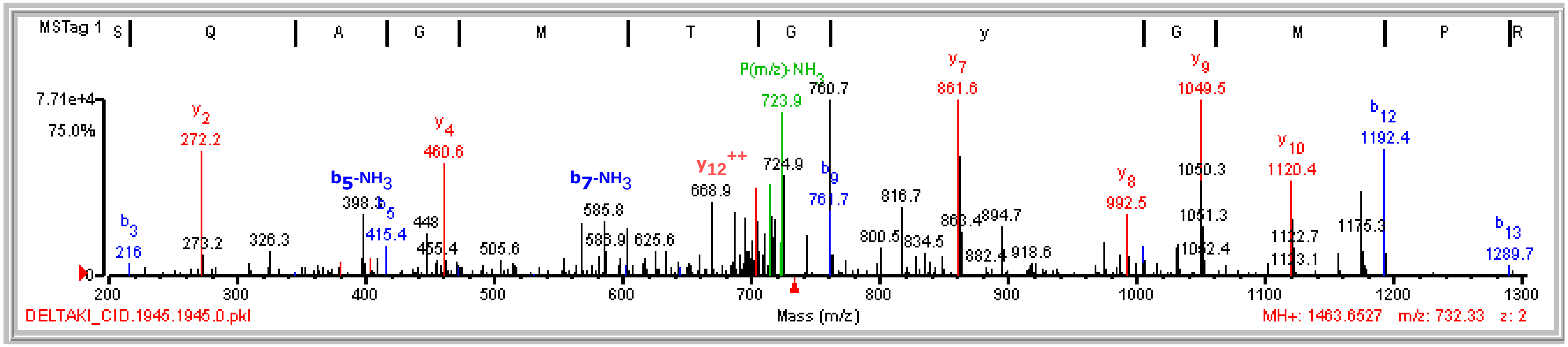


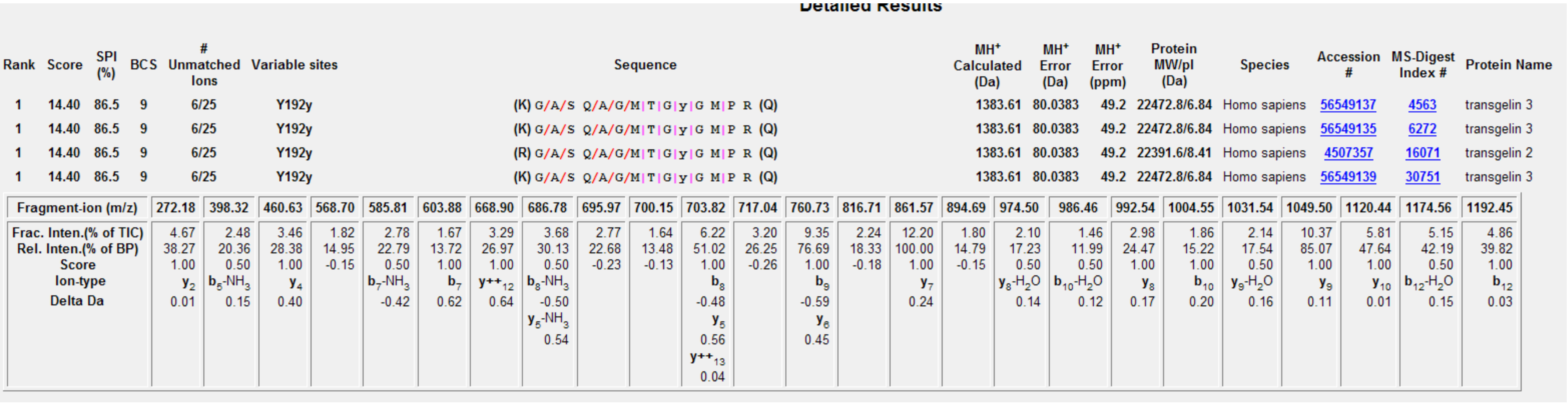
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.61	62.6	8	8/25	Y56y	(R) L Y P E L S\Q y M\G\L|S/L N E\E E|I\R (A)	2284.12	80.4489	204.1	32444.6/7.06	Homo sapiens	56243522	1509	syntenin isoform 1
1	11.61	62.6	8	8/25	Y56y	(R) L Y P E L S\Q y M\G\L|S/L N E\E E|I\R (A)	2284.12	80.4489	204.1	32316.4/7.06	Homo sapiens	55749515	17431	syntenin isoform 3
1	11.61	62.6	8	8/25	Y56y	(R) L Y P E L S\Q y M\G\L|S/L N E\E E|I\R (A)	2284.12	80.4489	204.1	32444.6/7.06	Homo sapiens	55749490	22158	syntenin isoform 1
1	11.61	62.6	8	8/25	Y56y	(R) L Y P E L S\Q y M\G\L|S/L N E\E E|I\R (A)	2284.12	80.4489	204.1	32316.4/7.06	Homo sapiens	55749523	31735	syntenin isoform 3
1	11.61	62.6	8	8/25	Y50y	(R) L Y P E L S\Q y M\G\L|S/L N E\E E|I\R (A)	2284.12	80.4489	204.1	31761.8/7.06	Homo sapiens	55749504	35433	syntenin isoform 2

Fragment-ion (m/z)	288.26	657.75	686.35	688.85	702.78	723.42	733.05	756.12	771.41	772.74	799.65	870.65
Frac. Inten.(% of TIC)	2.85	2.80	2.60	7.34	2.92	11.03	5.98	0.18	2.39	6.11	6.71	2.98
Rel. Inten.(% of BP)	25.88	25.37	23.55	66.58	26.52	100.00	54.18	1.59	21.64	55.38	60.80	27.06
Score	1.00	0.50	-0.24	1.00	1.00	-1.00	-0.54	1.50	0.50	0.50	-0.61	-0.27
Ion-type	y_2	y_5-NH_3		$b{++}_{11}$	b_6			sty	y_6-H_2O	y_6-NH_3		
Delta Da	0.06	-0.55		0.55	-0.59			0.08	0.05	0.39		

Fragment-ion (m/z)	884.95	902.66	910.60	945.05	950.56	989.52	1037.04	1039.23	1095.80	1205.60	1262.69	1375.61	1444.48
Frac. Inten.(% of TIC)	3.53	2.36	3.02	2.42	2.92	3.54	2.78	5.36	7.00	2.28	3.16	3.94	3.79
Rel. Inten.(% of BP)	31.98	21.40	27.39	21.98	26.48	32.05	25.24	48.63	63.47	20.70	28.63	35.72	34.39
Score	0.50	1.00	1.00	-0.22	-0.26	1.00	-0.25	1.00	1.00	1.00	1.00	1.00	0.50
Ion-type	y_7-NH_3	y_7	$b{++}_{15}$			y_8		$b{++}_{17}$	$b{++}_{18}$	b_9	b_{10}	b_{11}	b_{12}-H_2O
Delta Da	-0.48	0.20	0.70			0.03		0.28	0.31	0.11	0.17	0.01	-0.14

Peak 128





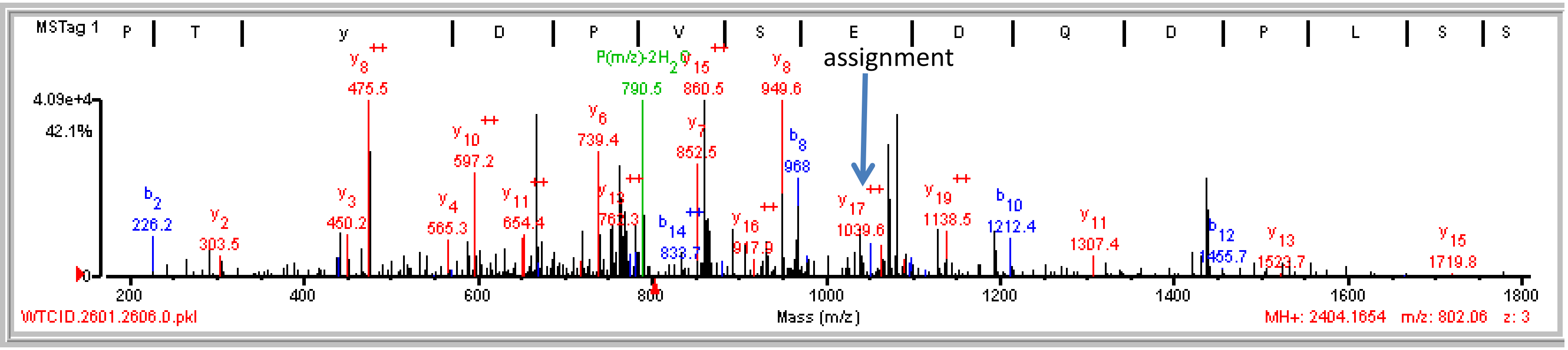
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.40	86.5	9	6/25	Y192y	(K) G/A/S Q/A/G/M|T|G|y|G M|P R (Q)	1383.61	80.0383	49.2	22472.8/6.84	Homo sapiens	56549137	4563	transgelin 3
1	14.40	86.5	9	6/25	Y192y	(K) G/A/S Q/A/G/M|T|G|y|G M|P R (Q)	1383.61	80.0383	49.2	22472.8/6.84	Homo sapiens	56549135	6272	transgelin 3
1	14.40	86.5	9	6/25	Y192y	(R) G/A/S Q/A/G/M|T|G|y|G M|P R (Q)	1383.61	80.0383	49.2	22391.6/8.41	Homo sapiens	4507357	16071	transgelin 2
1	14.40	86.5	9	6/25	Y192y	(K) G/A/S Q/A/G/M|T|G|y|G M|P R (Q)	1383.61	80.0383	49.2	22472.8/6.84	Homo sapiens	56549139	30751	transgelin 3

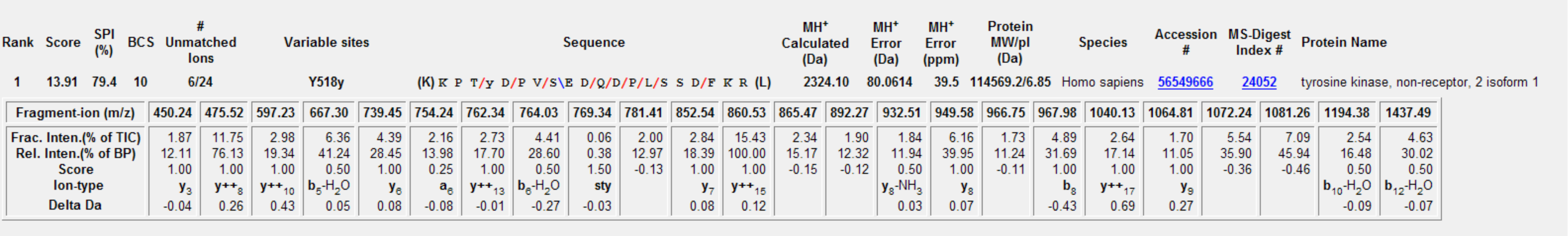
Fragment-ion (m/z)	272.18	398.32	460.63	568.70	585.81	603.88	668.90	686.78	695.97	700.15	703.82	717.04
Frac. Inten.(% of TIC)	4.67	2.48	3.46	1.82	2.78	1.67	3.29	3.68	2.77	1.64	6.22	3.20
Rel. Inten.(% of BP)	38.27	20.36	28.38	14.95	22.79	13.72	26.97	30.13	22.68	13.48	51.02	26.25
Score	1.00	0.50	1.00	-0.15	0.50	1.00	1.00	0.50	-0.23	-0.13	1.00	-0.26
Ion-type	y_2	b_5-NH_3	y_4		b_7-NH_3	b_7	$y{++}_{12}$	b_8-NH_3			b_8	
Delta Da	0.01	0.15	0.40		-0.42	0.62	0.64	-0.50			-0.48	
								y_5-NH_3			y_5	
								0.54			0.56	
											$y{++}_{13}$	
											0.04	

Fragment-ion (m/z)	760.73	816.71	861.57	894.69	974.50	986.46	992.54	1004.55	1031.54	1049.50	1120.44	1174.56	1192.45
Frac. Inten.(% of TIC)	9.35	2.24	12.20	1.80	2.10	1.46	2.98	1.86	2.14	10.37	5.81	5.15	4.86
Rel. Inten.(% of BP)	76.69	18.33	100.00	14.79	17.23	11.99	24.47	15.22	17.54	85.07	47.64	42.19	39.82
Score	1.00	-0.18	1.00	-0.15	0.50	0.50	1.00	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	b_9		y_7		y_8-H_2O	b_{10}-H_2O	y_8	b_{10}	y_9-H_2O	y_9	y_{10}	b_{12}-H_2O	b_{12}
Delta Da	-0.59		0.24		0.14	0.12	0.17	0.20	0.16	0.11	0.01	0.15	0.03
	y_6												
	0.45												

Peak 129



assignment

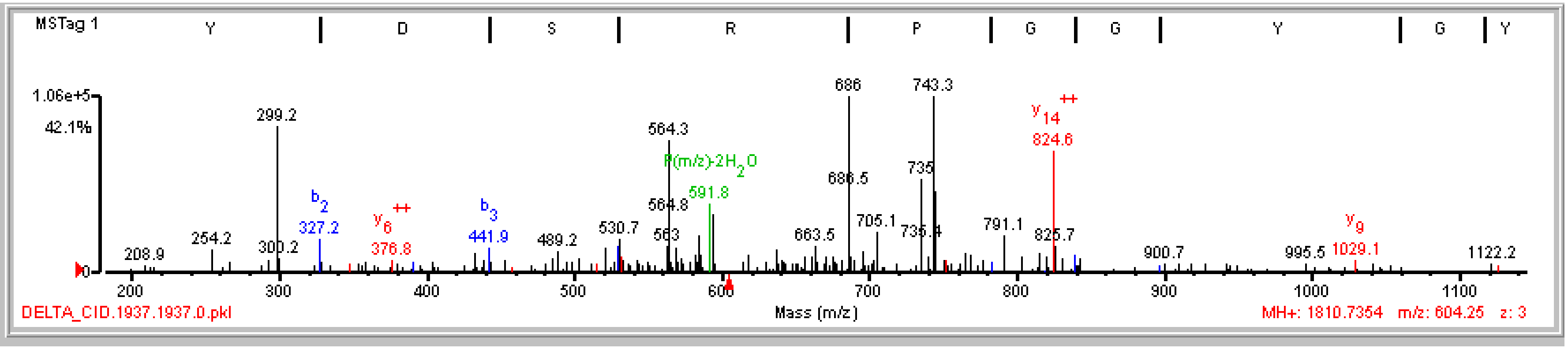


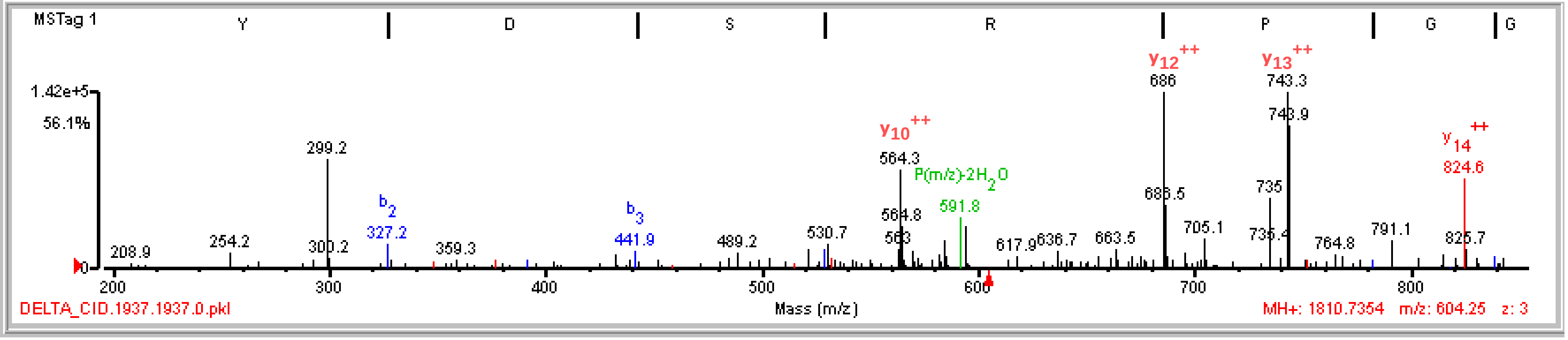
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.91	79.4	10	6/24	Y518y	(K) K P T/y D/P V/S\E D/Q/D/P/L/S S D/F K R (L)	2324.10	80.0614	39.5	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1

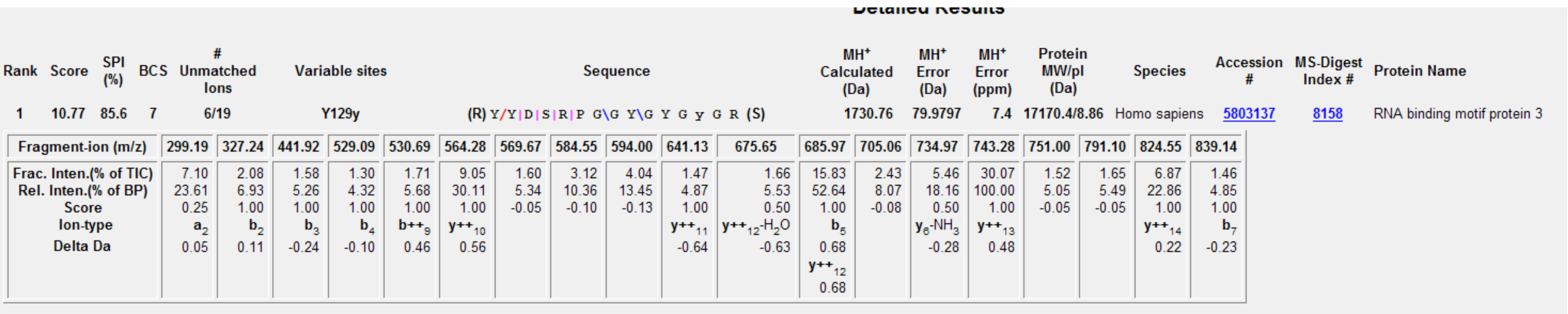
Fragment-ion (m/z)	450.24	475.52	597.23	667.30	739.45	754.24	762.34	764.03	769.34	781.41
Frac. Inten.(% of TIC)	1.87	11.75	2.98	6.36	4.39	2.16	2.73	4.41	0.06	2.00
Rel. Inten.(% of BP)	12.11	76.13	19.34	41.24	28.45	13.98	17.70	28.60	0.38	12.97
Score	1.00	1.00	1.00	0.50	1.00	0.25	1.00	0.50	1.50	-0.13
Ion-type	y_3	$y{++}_8$	$y{++}_{10}$	$b_5\text{-}H_2O$	y_6	a_6	$y{++}_{13}$	$b_6\text{-}H_2O$	sty	
Delta Da	-0.04	0.26	0.43	0.05	0.08	-0.08	-0.01	-0.27	-0.03	

Fragment-ion (m/z)	852.54	860.53	865.47	892.27	932.51	949.58	966.75	967.98	1040.13	1064.81	1072.24	1081.26	1194.38	1437.49
Frac. Inten.(% of TIC)	2.84	15.43	2.34	1.90	1.84	6.16	1.73	4.89	2.64	1.70	5.54	7.09	2.54	4.63
Rel. Inten.(% of BP)	18.39	100.00	15.17	12.32	11.94	39.95	11.24	31.69	17.14	11.05	35.90	45.94	16.48	30.02
Score	1.00	1.00	-0.15	-0.12	0.50	1.00	-0.11	1.00	1.00	1.00	-0.36	-0.46	0.50	0.50
Ion-type	y_7	$y{++}_{15}$			$y_8\text{-}NH_3$	y_8		b_8	$y{++}_{17}$	y_9			$b_{10}\text{-}H_2O$	$b_{12}\text{-}H_2O$
Delta Da	0.08	0.12			0.03	0.07		-0.43	0.69	0.27			-0.09	-0.07

Peak 130





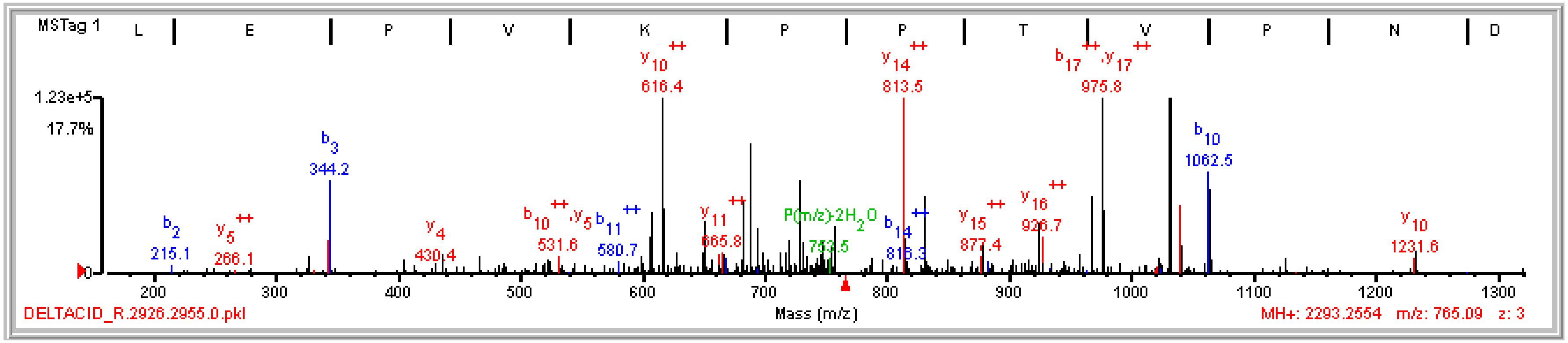


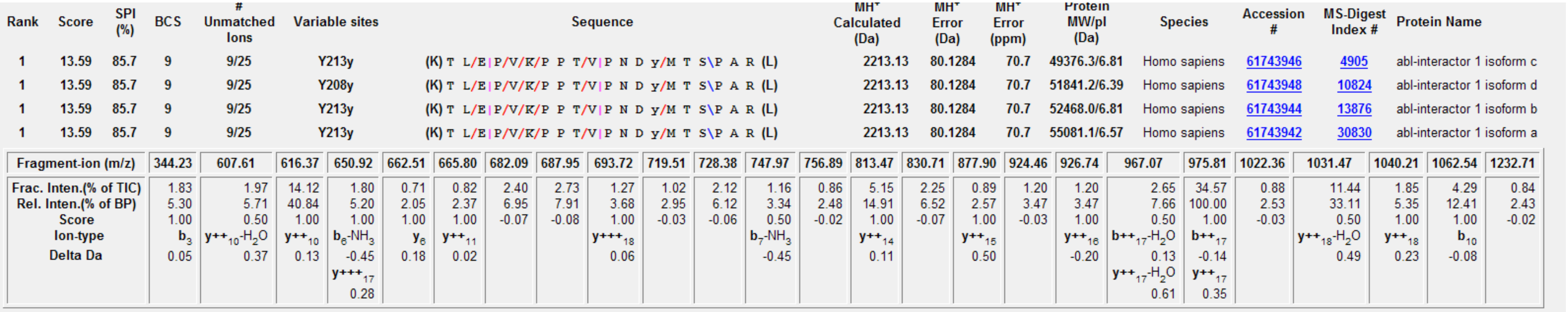
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.77	85.6	7	6/19	Y129y	(R) Y/Y|D|S|R|P G\G Y\G Y G y G R (S)	1730.76	79.9797	7.4	17170.4/8.86	Homo sapiens	5803137	8158	RNA binding motif protein 3

Fragment-ion (m/z)	299.19	327.24	441.92	529.09	530.69	564.28	569.67	584.55	594.00	641.13	675.65	685.97	705.06	734.97	743.28	751.00	791.10	824.55	839.14
Frac. Inten.(% of TIC)	7.10	2.08	1.58	1.30	1.71	9.05	1.60	3.12	4.04	1.47	1.66	15.83	2.43	5.46	30.07	1.52	1.65	6.87	1.46
Rel. Inten.(% of BP)	23.61	6.93	5.26	4.32	5.68	30.11	5.34	10.36	13.45	4.87	5.53	52.64	8.07	18.16	100.00	5.05	5.49	22.86	4.85
Score	0.25	1.00	1.00	1.00	1.00	1.00	-0.05	-0.10	-0.13	1.00	0.50	1.00	-0.08	0.50	1.00	-0.05	-0.05	1.00	1.00
Ion-type	a_2	b_2	b_3	b_4	$b{++}_9$	$y{++}_{10}$				$y{++}_{11}$	$y{++}_{12}\text{-}H_2O$	b_5 0.68 $y{++}_{12}$		$y_6\text{-}NH_3$	$y{++}_{13}$			$y{++}_{14}$	b_7
Delta Da	0.05	0.11	-0.24	-0.10	0.46	0.56				-0.64	-0.63	0.68		-0.28	0.48			0.22	-0.23

Peak 131



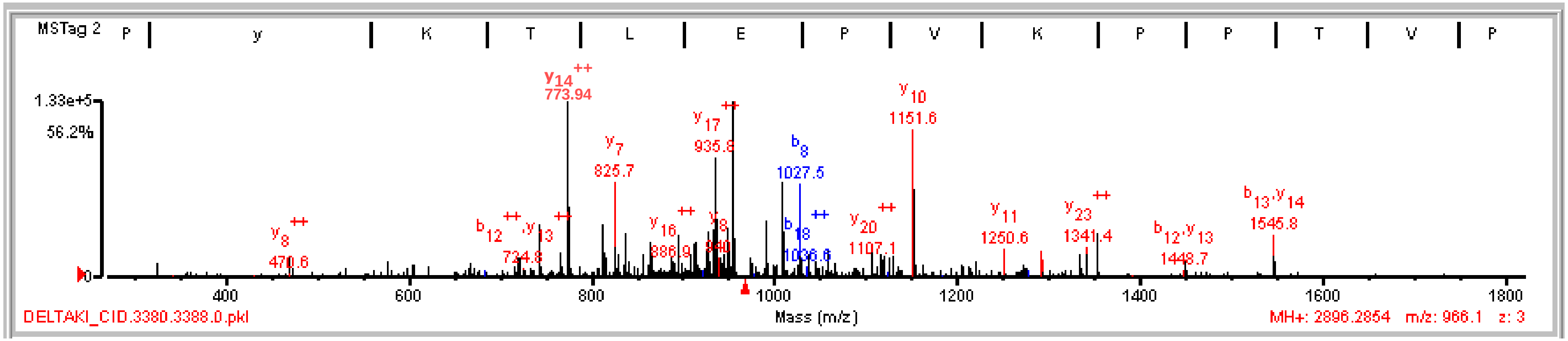


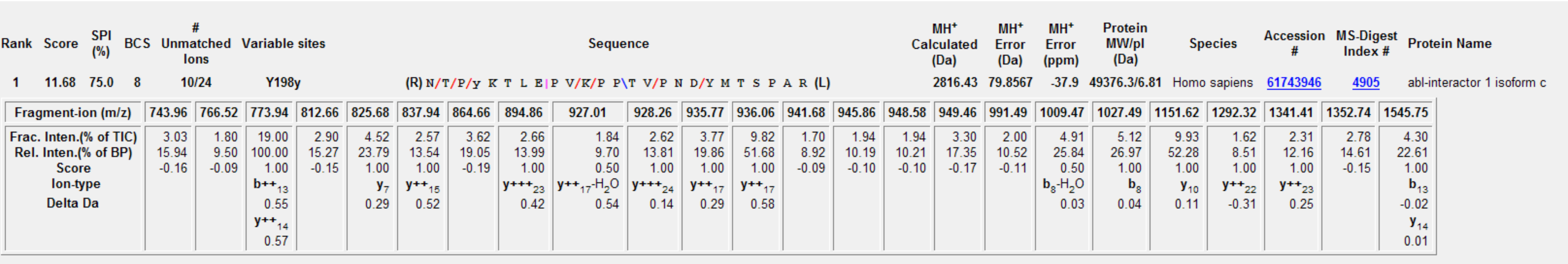
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.59	85.7	9	9/25	Y213y	(K) T L/E|P/V/K/P P T/V|P N D y/M T S\P A R (L)	2213.13	80.1284	70.7	49376.3/6.81	Homo sapiens	61743946	4905	abl-interactor 1 isoform c
1	13.59	85.7	9	9/25	Y208y	(K) T L/E|P/V/K/P P T/V|P N D y/M T S\P A R (L)	2213.13	80.1284	70.7	51841.2/6.39	Homo sapiens	61743948	10824	abl-interactor 1 isoform d
1	13.59	85.7	9	9/25	Y213y	(K) T L/E|P/V/K/P P T/V|P N D y/M T S\P A R (L)	2213.13	80.1284	70.7	52468.0/6.81	Homo sapiens	61743944	13876	abl-interactor 1 isoform b
1	13.59	85.7	9	9/25	Y213y	(K) T L/E|P/V/K/P P T/V|P N D y/M T S\P A R (L)	2213.13	80.1284	70.7	55081.1/6.57	Homo sapiens	61743942	30830	abl-interactor 1 isoform a

Fragment-ion (m/z)	344.23	607.61	616.37	650.92	662.51	665.80	682.09	687.95	693.72	719.51	728.38	747.97	756.89
Frac. Inten.(% of TIC)	1.83	1.97	14.12	1.80	0.71	0.82	2.40	2.73	1.27	1.02	2.12	1.16	0.86
Rel. Inten.(% of BP)	5.30	5.71	40.84	5.20	2.05	2.37	6.95	7.91	3.68	2.95	6.12	3.34	2.48
Score	1.00	0.50	1.00	1.00	1.00	1.00	-0.07	-0.08	1.00	-0.03	-0.06	0.50	-0.02
Ion-type	b_3	y^{++}_{10}-H_2O	y^{++}_{10}	b_6-NH_3 y^{+++}_{17}	y_6	y^{++}_{11}			y^{+++}_{18}			b_7-NH_3	
Delta Da	0.05	0.37	0.13	-0.45 0.28	0.18	0.02			0.06			-0.45	

Fragment-ion (m/z)	813.47	830.71	877.90	924.46	926.74	967.07	975.81	1022.36	1031.47	1040.21	1062.54	1232.71
Frac. Inten.(% of TIC)	5.15	2.25	0.89	1.20	1.20	2.65	34.57	0.88	11.44	1.85	4.29	0.84
Rel. Inten.(% of BP)	14.91	6.52	2.57	3.47	3.47	7.66	100.00	2.53	33.11	5.35	12.41	2.43
Score	1.00	-0.07	1.00	-0.03	1.00	0.50	1.00	-0.03	0.50	1.00	1.00	-0.02
Ion-type	y^{++}_{14}		y^{++}_{15}		y^{++}_{16}	b^{++}_{17}-H_2O y^{++}_{17}-H_2O	b^{++}_{17} y^{++}_{17}		y^{++}_{18}-H_2O	y^{++}_{18}	b_{10}	
Delta Da	0.11		0.50		-0.20	0.13 0.61	-0.14 0.35		0.49	0.23	-0.08	

Peak 132



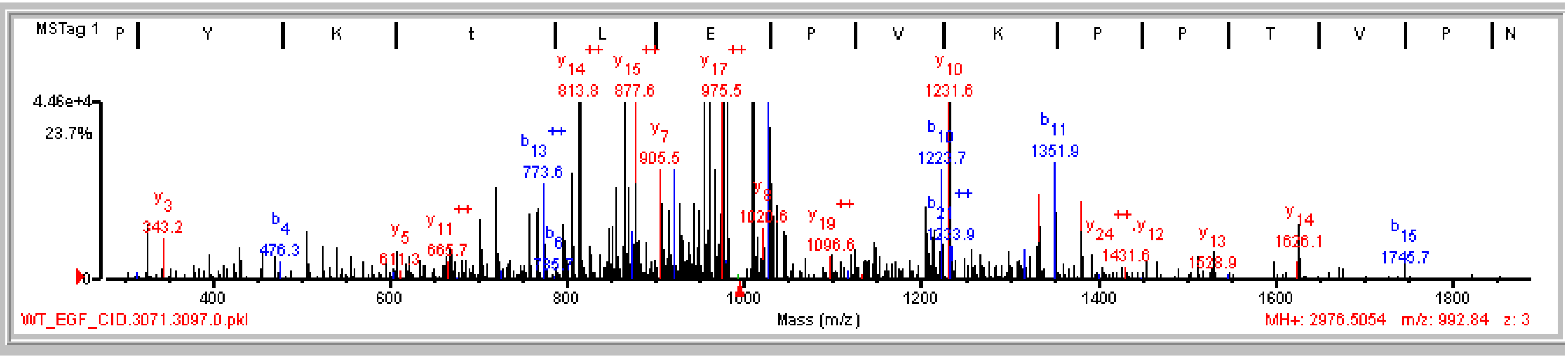


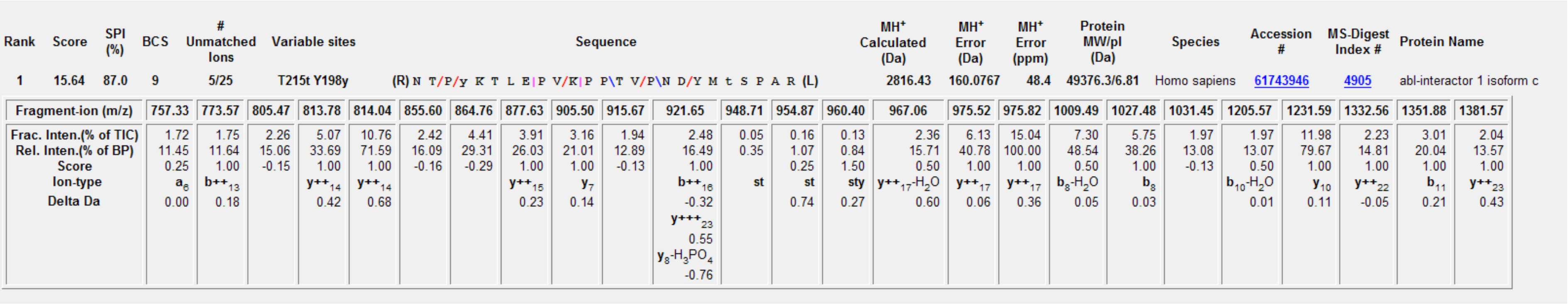
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.68	75.0	8	10/24	Y198y	(R) N/T/P/y K T L E|P V/K/P P\T V/P N D/Y M T S P A R (L)	2816.43	79.8567	-37.9	49376.3/6.81	Homo sapiens	61743946	4905	abl-interactor 1 isoform c

Fragment-ion (m/z)	743.96	766.52	773.94	812.66	825.68	837.94	864.66	894.86	927.01	928.26	935.77	936.06
Frac. Inten.(% of TIC)	3.03	1.80	19.00	2.90	4.52	2.57	3.62	2.66	1.84	2.62	3.77	9.82
Rel. Inten.(% of BP)	15.94	9.50	100.00	15.27	23.79	13.54	19.05	13.99	9.70	13.81	19.86	51.68
Score	-0.16	-0.09	1.00	-0.15	1.00	1.00	-0.19	1.00	0.50	1.00	1.00	1.00
Ion-type			$b{++}_{13}$ $y{++}_{14}$		y_7	$y{++}_{15}$		$y{+++}_{23}$	$y{++}_{17}$-H_2O	$y{+++}_{24}$	$y{++}_{17}$	$y{++}_{17}$
Delta Da			0.55 0.57		0.29	0.52		0.42	0.54	0.14	0.29	0.58

Fragment-ion (m/z)	941.68	945.86	948.58	949.46	991.49	1009.47	1027.49	1151.62	1292.32	1341.41	1352.74	1545.75
Frac. Inten.(% of TIC)	1.70	1.94	1.94	3.30	2.00	4.91	5.12	9.93	1.62	2.31	2.78	4.30
Rel. Inten.(% of BP)	8.92	10.19	10.21	17.35	10.52	25.84	26.97	52.28	8.51	12.16	14.61	22.61
Score	-0.09	-0.10	-0.10	-0.17	-0.11	0.50	1.00	1.00	1.00	1.00	-0.15	1.00
Ion-type						b_8-H_2O	b_8	y_{10}	$y{++}_{22}$	$y{++}_{23}$		b_{13} y_{14}
Delta Da						0.03	0.04	0.11	-0.31	0.25		-0.02 0.01

Peak 133



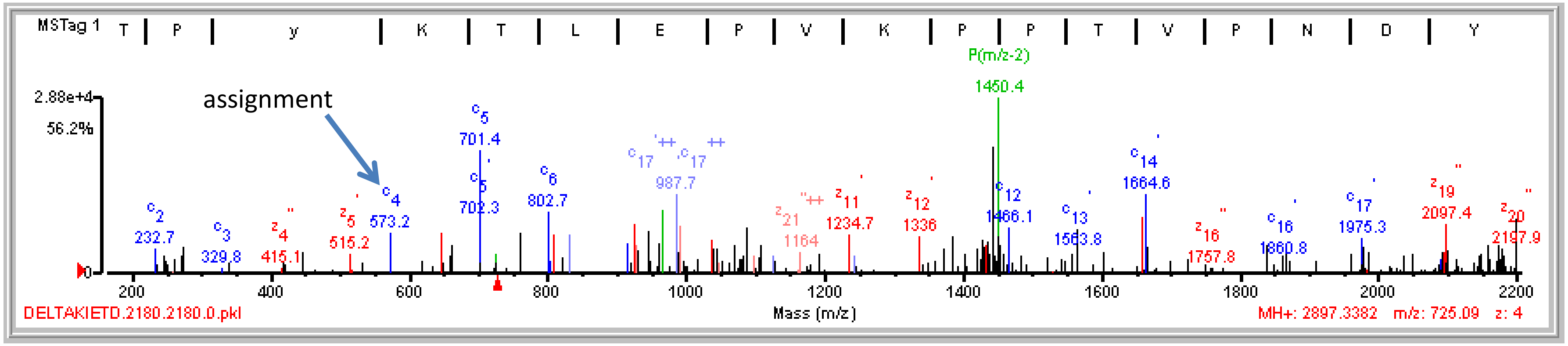


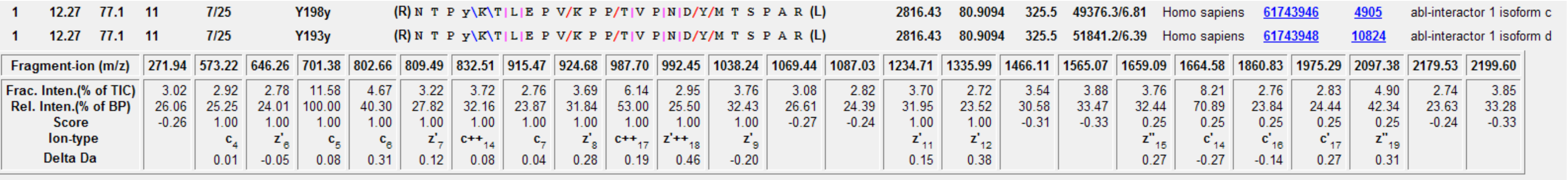
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.64	87.0	9	5/25	T215t Y198y	(R) N T/P/y K T L E|P V/K|P P\T V/P\N D/Y M t S P A R (L)	2816.43	160.0767	48.4	49376.3/6.81	Homo sapiens	61743946	4905	abl-interactor 1 isoform c

Fragment-ion (m/z)	757.33	773.57	805.47	813.78	814.04	855.60	864.76	877.63	905.50	915.67	921.65	948.71
Frac. Inten.(% of TIC)	1.72	1.75	2.26	5.07	10.76	2.42	4.41	3.91	3.16	1.94	2.48	0.05
Rel. Inten.(% of BP)	11.45	11.64	15.06	33.69	71.59	16.09	29.31	26.03	21.01	12.89	16.49	0.35
Score	0.25	1.00	-0.15	1.00	1.00	-0.16	-0.29	1.00	1.00	-0.13	1.00	
Ion-type	a_6	$b{++}_{13}$		$y{++}_{14}$	$y{++}_{14}$			$y{++}_{15}$	y_7		$b{++}_{16}$	st
Delta Da	0.00	0.18		0.42	0.68			0.23	0.14		-0.32 $y{+++}_{23}$ 0.55 y_8-H_3PO_4 -0.76	

Fragment-ion (m/z)	954.87	960.40	967.06	975.52	975.82	1009.49	1027.48	1031.45	1205.57	1231.59	1332.56	1351.88	1381.57
Frac. Inten.(% of TIC)	0.16	0.13	2.36	6.13	15.04	7.30	5.75	1.97	1.97	11.98	2.23	3.01	2.04
Rel. Inten.(% of BP)	1.07	0.84	15.71	40.78	100.00	48.54	38.26	13.08	13.07	79.67	14.81	20.04	13.57
Score	0.25	1.50	0.50	1.00	1.00	0.50	1.00	-0.13	0.50	1.00	1.00	1.00	1.00
Ion-type	st	sty	$y{++}_{17}$-H_2O	$y{++}_{17}$	$y{++}_{17}$	b_8-H_2O	b_8		b_{10}-H_2O	y_{10}	$y{++}_{22}$	b_{11}	$y{++}_{23}$
Delta Da	0.74	0.27	0.60	0.06	0.36	0.05	0.03		0.01	0.11	-0.05	0.21	0.43

Peak 134


assignment



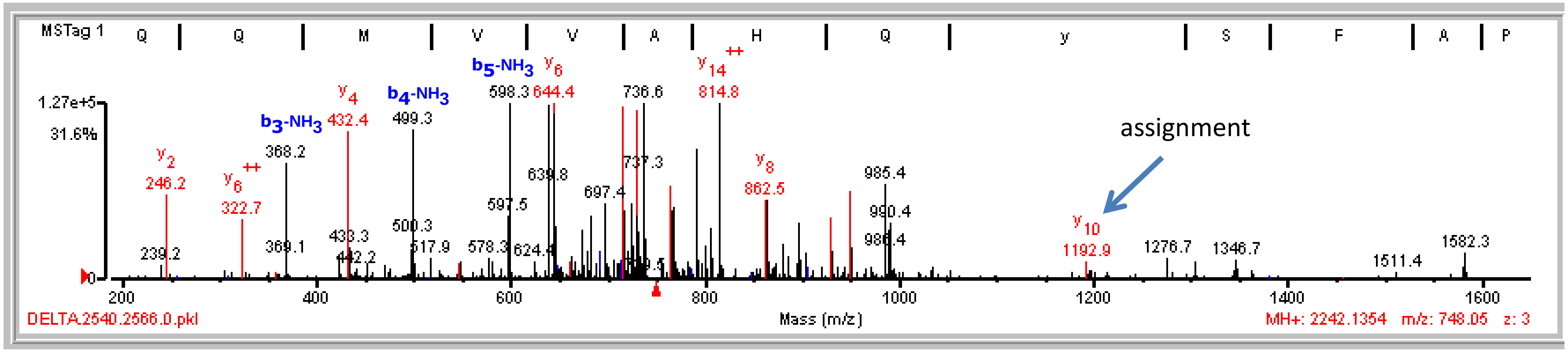
1 12.27 77.1 11 7/25 Y198y (R) N T P y\K\T|L|E P V/K P P/T|V P|N|D/Y/M T S P A R (L) 2816.43 80.9094 325.5 49376.3/6.81 Homo sapiens 61743946 4905 abl-interactor 1 isoform c

1 12.27 77.1 11 7/25 Y193y (R) N T P y\K\T|L|E P V/K P P/T|V P|N|D/Y/M T S P A R (L) 2816.43 80.9094 325.5 51841.2/6.39 Homo sapiens 61743948 10824 abl-interactor 1 isoform d

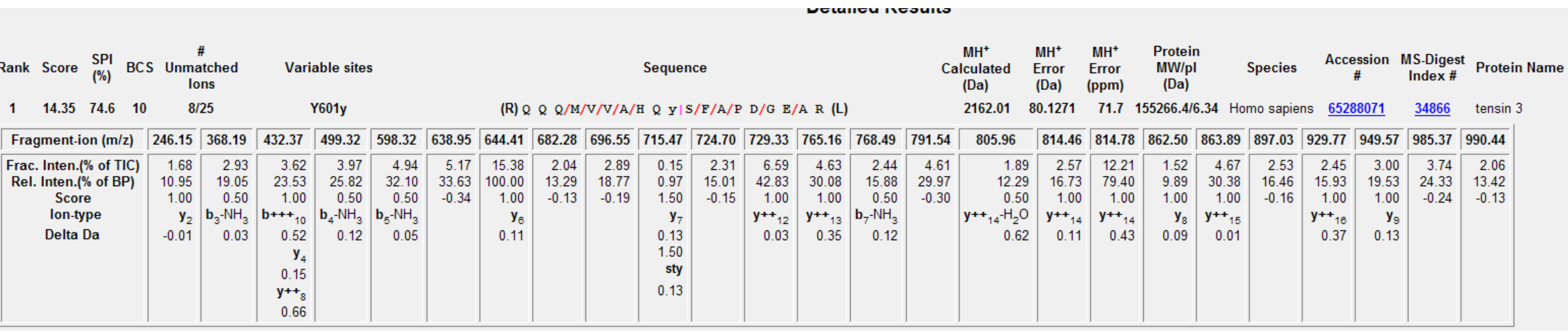
Fragment-ion (m/z)	271.94	573.22	646.26	701.38	802.66	809.49	832.51	915.47	924.68	987.70	992.45	1038.24	1069.44
Frac. Inten.(% of TIC)	3.02	2.92	2.78	11.58	4.67	3.22	3.72	2.76	3.69	6.14	2.95	3.76	3.08
Rel. Inten.(% of BP)	26.06	25.25	24.01	100.00	40.30	27.82	32.16	23.87	31.84	53.00	25.50	32.43	26.61
Score	-0.26	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.27
Ion-type		c_4	z'_6	c_5	c_6	z'_7	$c{+}{+}_{14}$	c_7	z'_8	$c{+}{+}_{17}$	$z'{+}{+}_{18}$	z'_9	
Delta Da		0.01	-0.05	0.08	0.31	0.12	0.08	0.04	0.28	0.19	0.46	-0.20	

Fragment-ion (m/z)	1087.03	1234.71	1335.99	1466.11	1565.07	1659.09	1664.58	1860.83	1975.29	2097.38	2179.53	2199.60
Frac. Inten.(% of TIC)	2.82	3.70	2.72	3.54	3.88	3.76	8.21	2.76	2.83	4.90	2.74	3.85
Rel. Inten.(% of BP)	24.39	31.95	23.52	30.58	33.47	32.44	70.89	23.84	24.44	42.34	23.63	33.28
Score	-0.24	1.00	1.00	-0.31	-0.33	0.25	0.25	0.25	0.25	0.25	-0.24	-0.33
Ion-type		z'_{11}	z'_{12}			z''_{15}	c'_{14}	c'_{16}	c'_{17}	z''_{19}		
Delta Da		0.15	0.38			0.27	-0.27	-0.14	0.27	0.31		

Peak 136



assignment



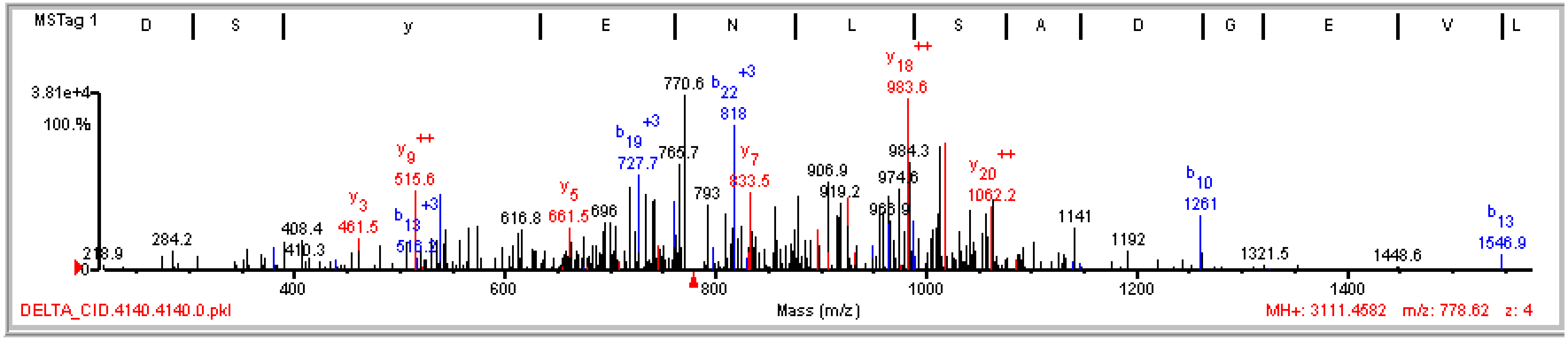
Detailed Results

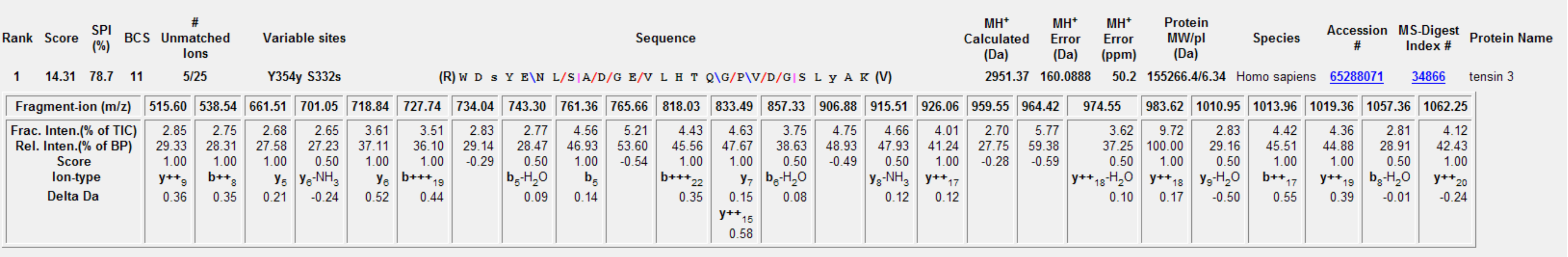
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.35	74.6	10	8/25	Y601y	(R) Q Q Q/M/V/V/A/H Q y|S/F/A/P D/G E/A R (L)	2162.01	80.1271	71.7	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

Fragment-ion (m/z)	246.15	368.19	432.37	499.32	598.32	638.95	644.41	682.28	696.55	715.47	724.70	729.33
Frac. Inten.(% of TIC)	1.68	2.93	3.62	3.97	4.94	5.17	15.38	2.04	2.89	0.15	2.31	6.59
Rel. Inten.(% of BP)	10.95	19.05	23.53	25.82	32.10	33.63	100.00	13.29	18.77	0.97	15.01	42.83
Score	1.00	0.50	1.00	0.50	0.50	-0.34	1.00	-0.13	-0.19	1.50	-0.15	1.00
Ion-type	y_2	b_3-NH$_3$	$b{+++}_{10}$	b_4-NH$_3$	b_5-NH$_3$		y_6			y_7		$y{++}_{12}$
Delta Da	-0.01	0.03	0.52 y_4 0.15 $y{++}_8$ 0.66	0.12	0.05		0.11			0.13 1.50 sty 0.13		0.03

Fragment-ion (m/z)	765.16	768.49	791.54	805.96	814.46	814.78	862.50	863.89	897.03	929.77	949.57	985.37	990.44
Frac. Inten.(% of TIC)	4.63	2.44	4.61	1.89	2.57	12.21	1.52	4.67	2.53	2.45	3.00	3.74	2.06
Rel. Inten.(% of BP)	30.08	15.88	29.97	12.29	16.73	79.40	9.89	30.38	16.46	15.93	19.53	24.33	13.42
Score	1.00	0.50	-0.30	0.50	1.00	1.00	1.00	1.00	-0.16	1.00	1.00	-0.24	-0.13
Ion-type	$y{++}_{13}$	b_7-NH$_3$		$y{++}_{14}$-H$_2$O	$y{++}_{14}$	$y{++}_{14}$	y_8	$y{++}_{15}$		$y{++}_{16}$	y_9		
Delta Da	0.35	0.12		0.62	0.11	0.43	0.09	0.01		0.37	0.13		

Peak 137



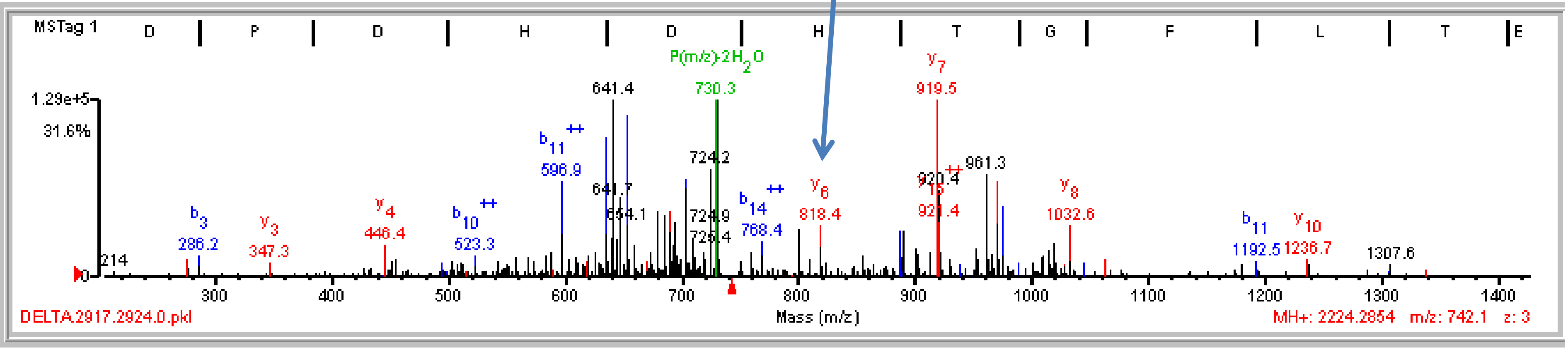


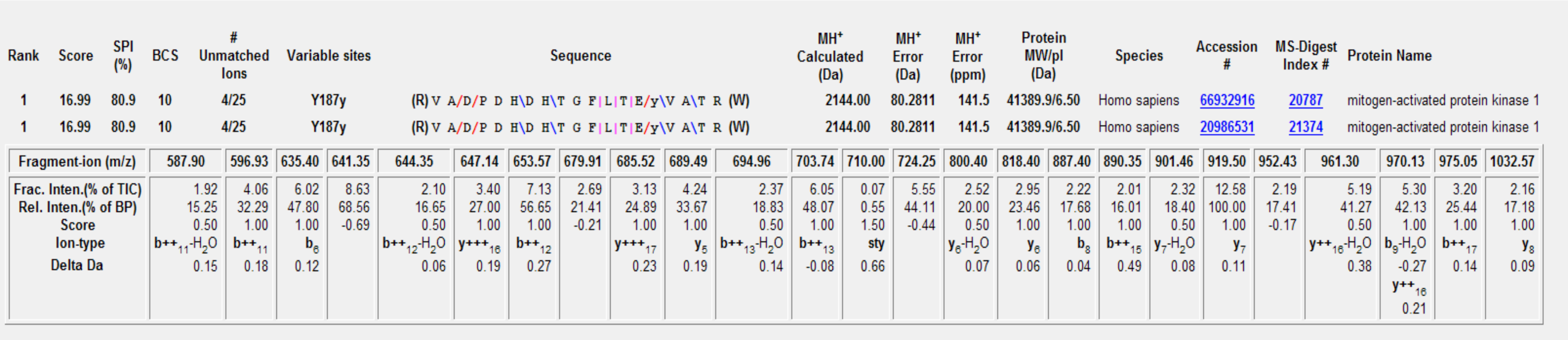
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.31	78.7	11	5/25	Y354y S332s	(R) W D s Y E\N L/S|A/D/G E/V L H T Q\G/P\V/D/G|S L y A K (V)	2951.37	160.0888	50.2	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

Fragment-ion (m/z)	515.60	538.54	661.51	701.05	718.84	727.74	734.04	743.30	761.36	765.66	818.03	833.49	857.33
Frac. Inten.(% of TIC)	2.85	2.75	2.68	2.65	3.61	3.51	2.83	2.77	4.56	5.21	4.43	4.63	3.75
Rel. Inten.(% of BP)	29.33	28.31	27.58	27.23	37.11	36.10	29.14	28.47	46.93	53.60	45.56	47.67	38.63
Score	1.00	1.00	1.00	0.50	1.00	1.00	-0.29	0.50	1.00	-0.54	1.00	1.00	0.50
Ion-type	y^{++}_9	b^{++}_8	y_5	y_6-NH$_3$	y_6	b^{+++}_{19}		b_5-H$_2$O	b_5		b^{+++}_{22}	y_7 y^{++}_{15}	b_6-H$_2$O
Delta Da	0.36	0.35	0.21	-0.24	0.52	0.44		0.09	0.14		0.35	0.15 0.58	0.08

Fragment-ion (m/z)	906.88	915.51	926.06	959.55	964.42	974.55	983.62	1010.95	1013.96	1019.36	1057.36	1062.25
Frac. Inten.(% of TIC)	4.75	4.66	4.01	2.70	5.77	3.62	9.72	2.83	4.42	4.36	2.81	4.12
Rel. Inten.(% of BP)	48.93	47.93	41.24	27.75	59.38	37.25	100.00	29.16	45.51	44.88	28.91	42.43
Score	-0.49	0.50	1.00	-0.28	-0.59	0.50	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type		y_8-NH$_3$	y^{++}_{17}			y^{++}_{18}-H$_2$O	y^{++}_{18}	y_9-H$_2$O	b^{++}_{17}	y^{++}_{19}	b_8-H$_2$O	y^{++}_{20}
Delta Da		0.12	0.12			0.10	0.17	-0.50	0.55	0.39	-0.01	-0.24

Peak 139



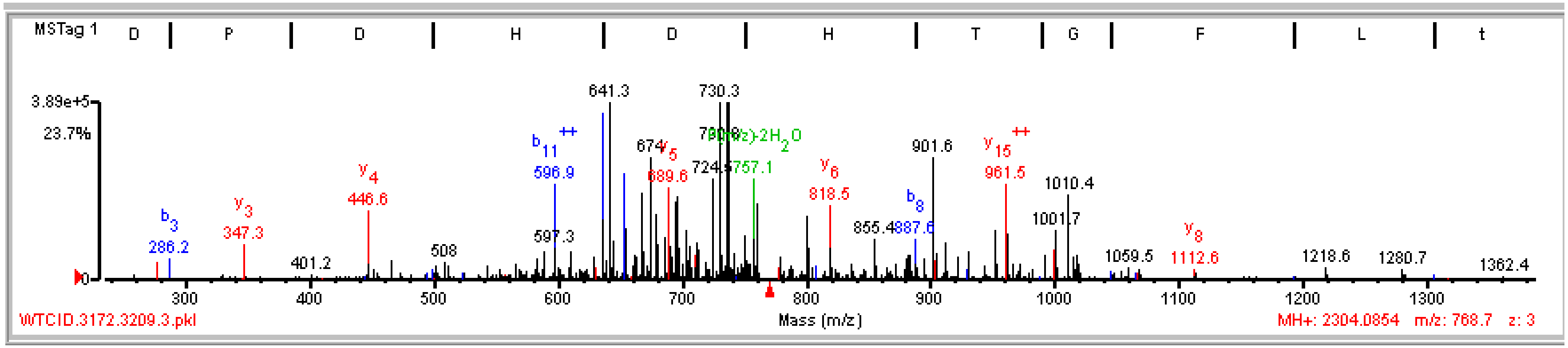


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.99	80.9	10	4/25	Y187y	(R) V A/D/P D H\D H\T G F|L|T|E/y\V A\T R (W)	2144.00	80.2811	141.5	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	16.99	80.9	10	4/25	Y187y	(R) V A/D/P D H\D H\T G F|L|T|E/y\V A\T R (W)	2144.00	80.2811	141.5	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

Fragment-ion (m/z)	587.90	596.93	635.40	641.35	644.35	647.14	653.57	679.91	685.52	689.49	694.96	703.74
Frac. Inten.(% of TIC)	1.92	4.06	6.02	8.63	2.10	3.40	7.13	2.69	3.13	4.24	2.37	6.05
Rel. Inten.(% of BP)	15.25	32.29	47.80	68.56	16.65	27.00	56.65	21.41	24.89	33.67	18.83	48.07
Score	0.50	1.00	1.00	-0.69	0.50	1.00	1.00	-0.21	1.00	1.00	0.50	1.00
Ion-type	$b{++}_{11}$-H_2O	$b{++}_{11}$	b_6		$b{++}_{12}$-H_2O	$y{+++}_{16}$	$b{++}_{12}$		$y{+++}_{17}$	y_5	$b{++}_{13}$-H_2O	$b{++}_{13}$
Delta Da	0.15	0.18	0.12		0.06	0.19	0.27		0.23	0.19	0.14	-0.08

Fragment-ion (m/z)	710.00	724.25	800.40	818.40	887.40	890.35	901.46	919.50	952.43	961.30	970.13	975.05	1032.57
Frac. Inten.(% of TIC)	0.07	5.55	2.52	2.95	2.22	2.01	2.32	12.58	2.19	5.19	5.30	3.20	2.16
Rel. Inten.(% of BP)	0.55	44.11	20.00	23.46	17.68	16.01	18.40	100.00	17.41	41.27	42.13	25.44	17.18
Score	1.50	-0.44	0.50	1.00	1.00	1.00	0.50	1.00	-0.17	0.50	1.00	1.00	1.00
Ion-type	sty		y_6-H_2O	y_6	b_8	$b{++}_{15}$	y_7-H_2O	y_7		$y{++}_{16}$-H_2O	b_9-H_2O $y{++}_{16}$	$b{++}_{17}$	y_8
Delta Da	0.66		0.07	0.06	0.04	0.49	0.08	0.11		0.38	-0.27 0.21	0.14	0.09

Peak 140



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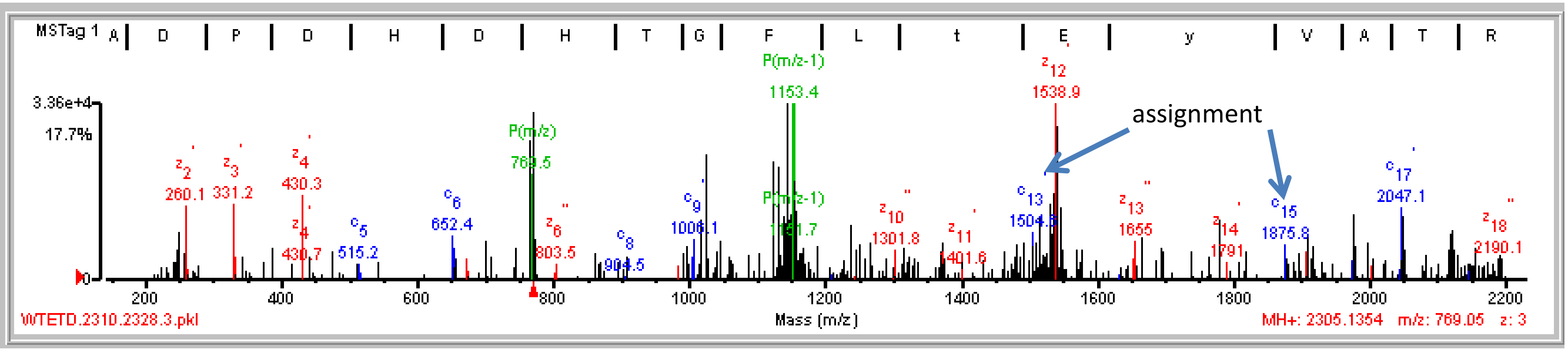

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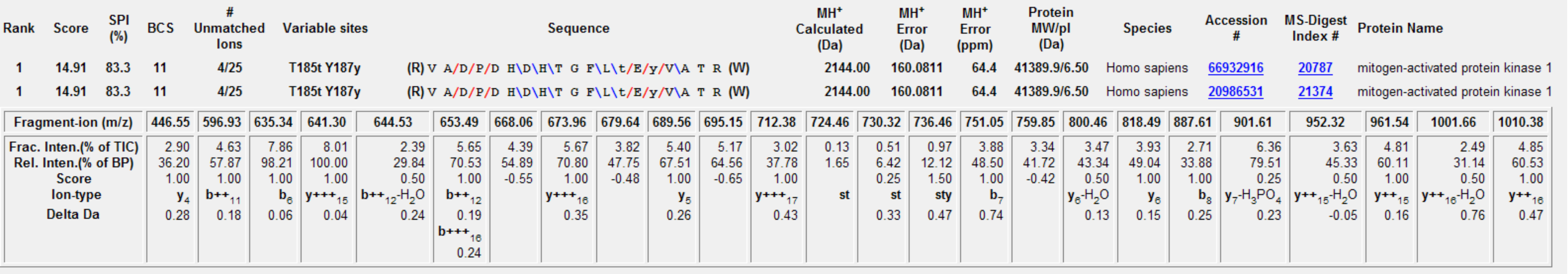
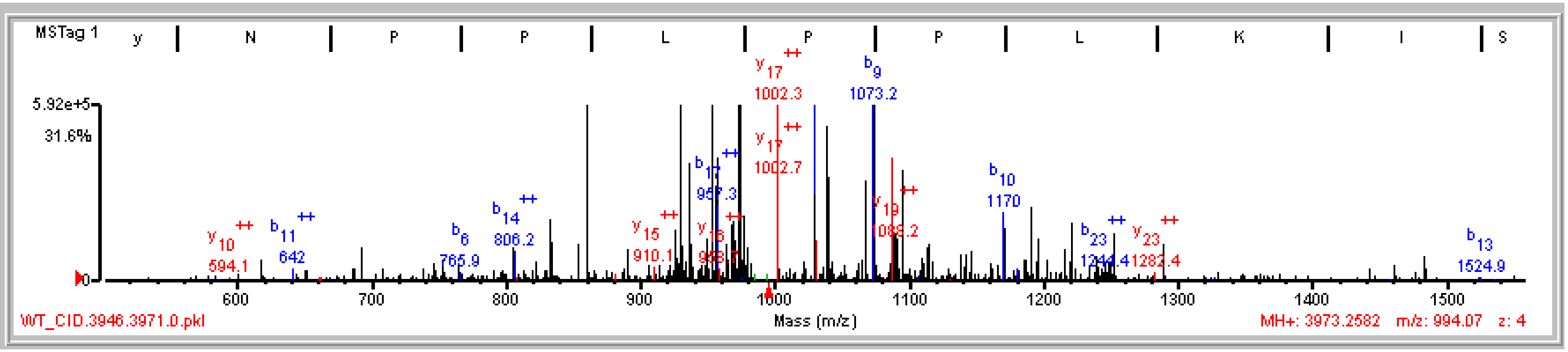


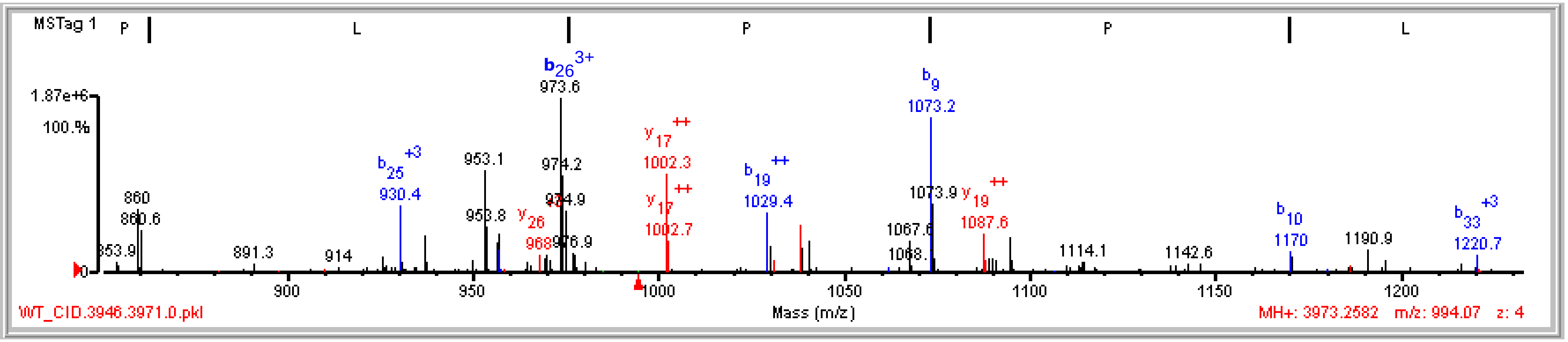
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.91	83.3	11	4/25	T185t Y187y	(R) V A/D/P/D H\D\H\T G F\L\t/E/y/V\A T R (W)	2144.00	160.0811	64.4	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	14.91	83.3	11	4/25	T185t Y187y	(R) V A/D/P/D H\D\H\T G F\L\t/E/y/V\A T R (W)	2144.00	160.0811	64.4	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

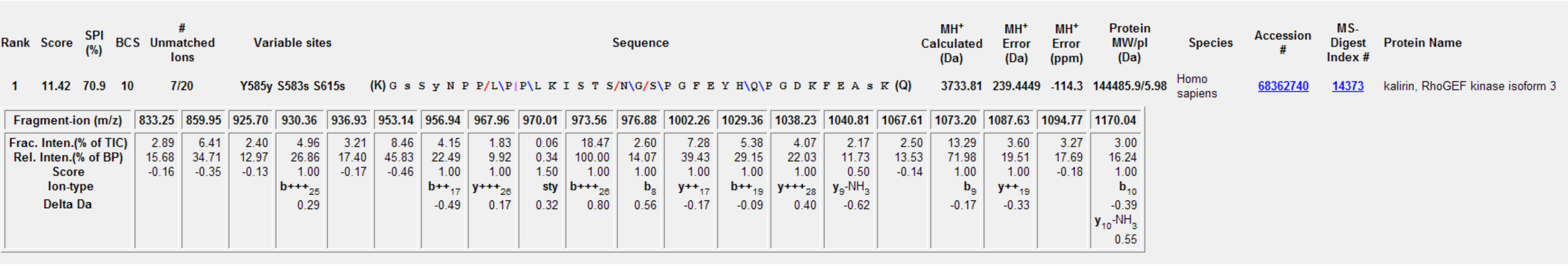
Fragment-ion (m/z)	446.55	596.93	635.34	641.30	644.53	653.49	668.06	673.96	679.64	689.56	695.15	712.38
Frac. Inten.(% of TIC)	2.90	4.63	7.86	8.01	2.39	5.65	4.39	5.67	3.82	5.40	5.17	3.02
Rel. Inten.(% of BP)	36.20	57.87	98.21	100.00	29.84	70.53	54.89	70.80	47.75	67.51	64.56	37.78
Score	1.00	1.00	1.00	1.00	0.50	1.00	-0.55	1.00	-0.48	1.00	-0.65	1.00
Ion-type	y_4	$b{+}{+}_{11}$	b_6	$y{+}{+}{+}_{15}$	$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$ $b{+}{+}{+}_{16}$		$y{+}{+}{+}_{16}$		y_5		$y{+}{+}{+}_{17}$
Delta Da	0.28	0.18	0.06	0.04	0.24	0.19 0.24		0.35		0.26		0.43

Fragment-ion (m/z)	724.46	730.32	736.46	751.05	759.85	800.46	818.49	887.61	901.61	952.32	961.54	1001.66	1010.38
Frac. Inten.(% of TIC)	0.13	0.51	0.97	3.88	3.34	3.47	3.93	2.71	6.36	3.63	4.81	2.49	4.85
Rel. Inten.(% of BP)	1.65	6.42	12.12	48.50	41.72	43.34	49.04	33.88	79.51	45.33	60.11	31.14	60.53
Score		0.25	1.50	1.00	-0.42	0.50	1.00	1.00	0.25	0.50	1.00	0.50	1.00
Ion-type	st	st	sty	b_7		y_6-H_2O	y_6	b_8	y_7-H_3PO_4	$y{+}{+}_{15}$-H_2O	$y{+}{+}_{15}$	$y{+}{+}_{16}$-H_2O	$y{+}{+}_{16}$
Delta Da		0.33	0.47	0.74		0.13	0.15	0.25	0.23	-0.05	0.16	0.76	0.47

Peak 141



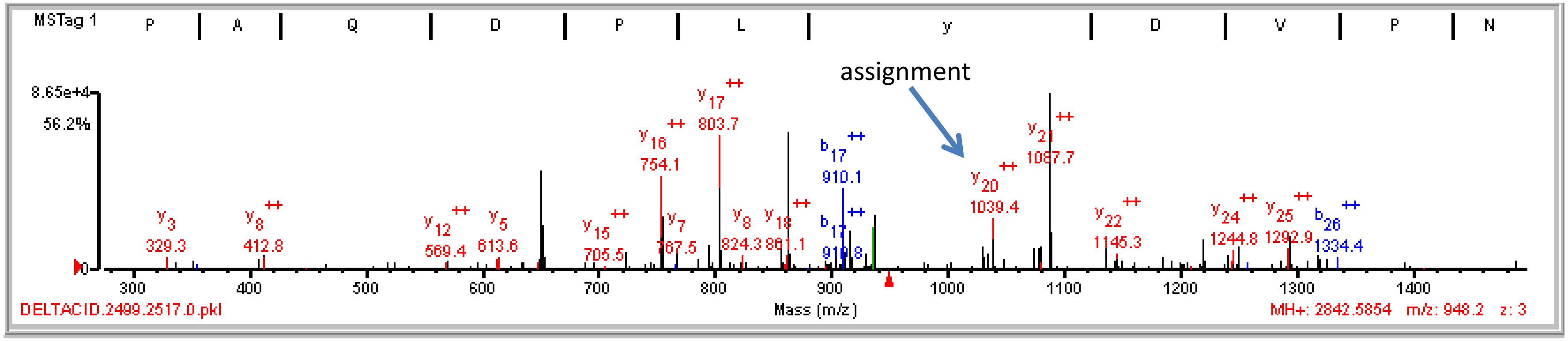




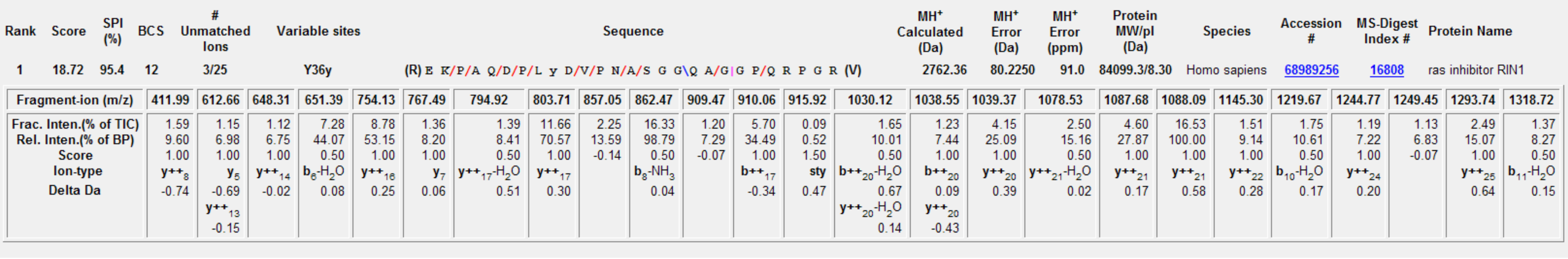
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.42	70.9	10	7/20	Y585y S583s S615s	(K) G s S y N P P/L\P|P\L K I S T S/N\G/S\P G F E Y H\Q\P G D K F E A s K (Q)	3733.81	239.4449	-114.3	144485.9/5.98	Homo sapiens	68362740	14373	kalirin, RhoGEF kinase isoform 3

Fragment-ion (m/z)	833.25	859.95	925.70	930.36	936.93	953.14	956.94	967.96	970.01	973.56	976.88	1002.26	1029.36	1038.23	1040.81	1067.61	1073.20	1087.63	1094.77	1170.04
Frac. Inten.(% of TIC)	2.89	6.41	2.40	4.96	3.21	8.46	4.15	1.83	0.06	18.47	2.60	7.28	5.38	4.07	2.17	2.50	13.29	3.60	3.27	3.00
Rel. Inten.(% of BP)	15.68	34.71	12.97	26.86	17.40	45.83	22.49	9.92	0.34	100.00	14.07	39.43	29.15	22.03	11.73	13.53	71.98	19.51	17.69	16.24
Score	-0.16	-0.35	-0.13	1.00	-0.17	-0.46	1.00	1.00	1.50	1.00	1.00	1.00	1.00	1.00	0.50	-0.14	1.00	1.00	-0.18	1.00
Ion-type				b+++_{25}			b++_{17}	y+++_{26}	sty	b+++_{26}	b_{8}	y++_{17}	b++_{19}	y+++_{28}	$\text{y}_{9}\text{-NH}_{3}$		b_{9}	y++_{19}		b_{10} -0.39 $\text{y}_{10}\text{-NH}_{3}$
Delta Da				0.29			-0.49	0.17	0.32	0.80	0.56	-0.17	-0.09	0.40	-0.62		-0.17	-0.33		0.55

Peak 143



assignment

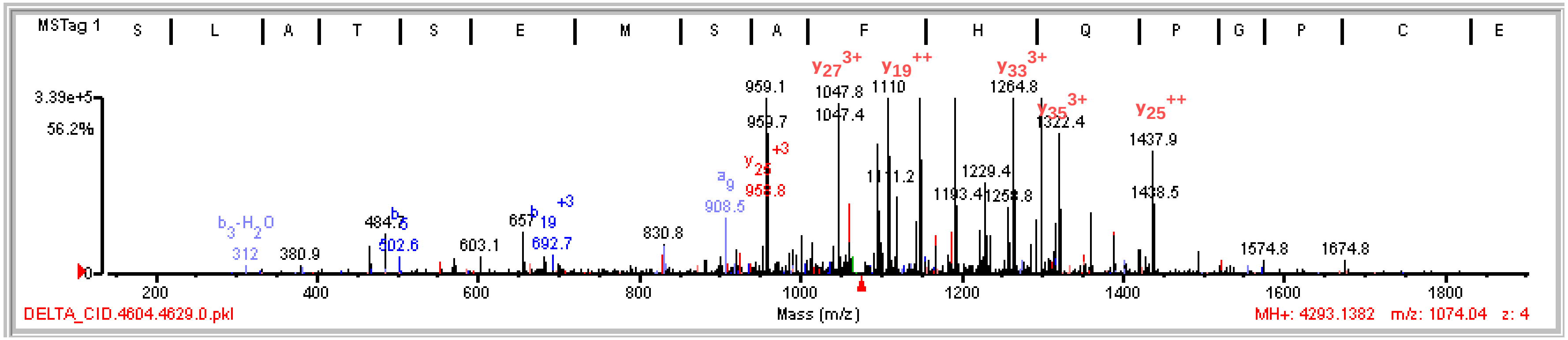


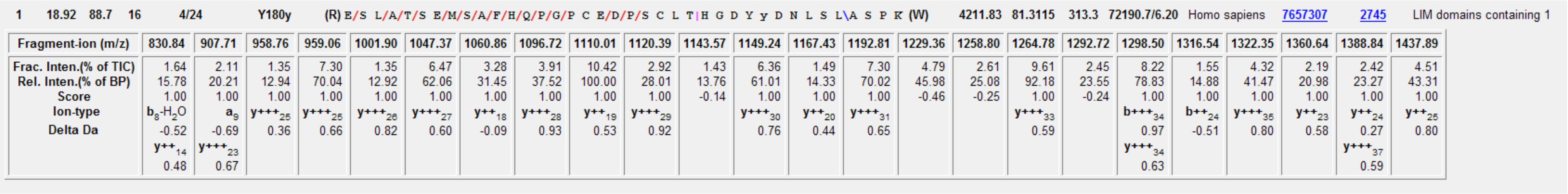
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.72	95.4	12	3/25	Y36y	(R) E K/P/A Q/D/P/L y D/V/P N/A/S G G\Q A/G|G P/Q R P G R (V)	2762.36	80.2250	91.0	84099.3/8.30	Homo sapiens	68989256	16808	ras inhibitor RIN1

Fragment-ion (m/z)	411.99	612.66	648.31	651.39	754.13	767.49	794.92	803.71	857.05	862.47	909.47	910.06	915.92
Frac. Inten.(% of TIC)	1.59	1.15	1.12	7.28	8.78	1.36	1.39	11.66	2.25	16.33	1.20	5.70	0.09
Rel. Inten.(% of BP)	9.60	6.98	6.75	44.07	53.15	8.20	8.41	70.57	13.59	98.79	7.29	34.49	0.52
Score	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	-0.14	0.50	-0.07	1.00	1.50
Ion-type	$y{+}{+}_{8}$	y_{5} $y{+}{+}_{13}$	$y{+}{+}_{14}$	b_{6}-H_2O	$y{+}{+}_{16}$	y_{7}	$y{+}{+}_{17}$-H_2O	$y{+}{+}_{17}$		b_{8}-NH_3		$b{+}{+}_{17}$	sty
Delta Da	-0.74	-0.69 -0.15	-0.02	0.08	0.25	0.06	0.51	0.30		0.04		-0.34	0.47

Fragment-ion (m/z)	1030.12	1038.55	1039.37	1078.53	1087.68	1088.09	1145.30	1219.67	1244.77	1249.45	1293.74	1318.72
Frac. Inten.(% of TIC)	1.65	1.23	4.15	2.50	4.60	16.53	1.51	1.75	1.19	1.13	2.49	1.37
Rel. Inten.(% of BP)	10.01	7.44	25.09	15.16	27.87	100.00	9.14	10.61	7.22	6.83	15.07	8.27
Score	0.50	1.00	1.00	0.50	1.00	1.00	1.00	0.50	1.00	-0.07	1.00	0.50
Ion-type	$b{+}{+}_{20}$-H_2O $y{+}{+}_{20}$-H_2O	$b{+}{+}_{20}$ $y{+}{+}_{20}$	$y{+}{+}_{20}$	$y{+}{+}_{21}$-H_2O	$y{+}{+}_{21}$	$y{+}{+}_{21}$	$y{+}{+}_{22}$	b_{10}-H_2O	$y{+}{+}_{24}$		$y{+}{+}_{25}$	b_{11}-H_2O
Delta Da	0.67 0.14	0.09 -0.43	0.39	0.02	0.17	0.58	0.28	0.17	0.20		0.64	0.15

Peak 144



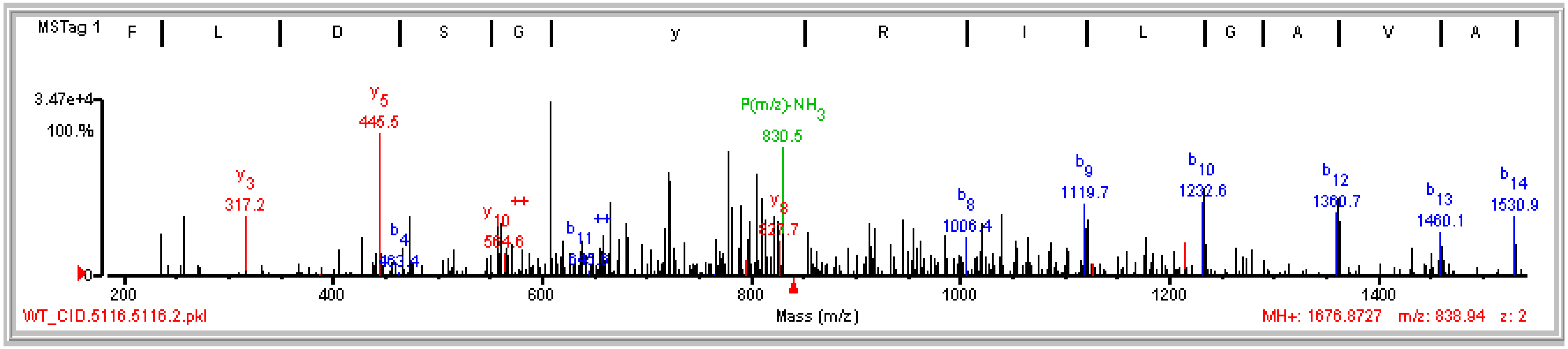


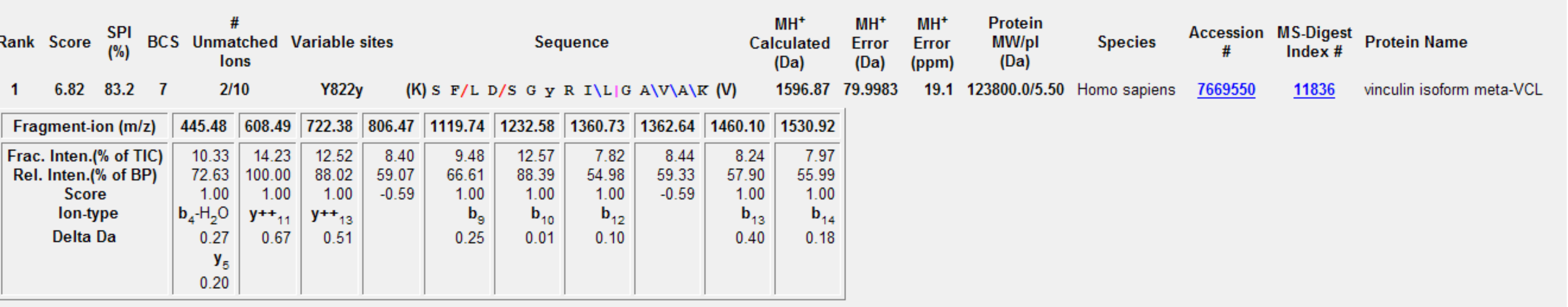
1 18.92 88.7 16 4/24 Y180y (R) E/S L/A/T/S E/M/S/A/F/H/Q/P/G/P C E/D/P/S C L T|H G D Y y D N L S L\A S P K (W) 4211.83 81.3115 313.3 72190.7/6.20 Homo sapiens 7657307 2745 LIM domains containing 1

Fragment-ion (m/z)	830.84	907.71	958.76	959.06	1001.90	1047.37	1060.86	1096.72	1110.01	1120.39	1143.57	1149.24
Frac. Inten.(% of TIC)	1.64	2.11	1.35	7.30	1.35	6.47	3.28	3.91	10.42	2.92	1.43	6.36
Rel. Inten.(% of BP)	15.78	20.21	12.94	70.04	12.92	62.06	31.45	37.52	100.00	28.01	13.76	61.01
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.14	1.00
Ion-type	b_8-H_2O	a_9	$y{+}{+}{+}_{25}$	$y{+}{+}{+}_{25}$	$y{+}{+}{+}_{26}$	$y{+}{+}{+}_{27}$	$y{+}{+}_{18}$	$y{+}{+}{+}_{28}$	$y{+}{+}_{19}$	$y{+}{+}{+}_{29}$		$y{+}{+}{+}_{30}$
Delta Da	-0.52	-0.69	0.36	0.66	0.82	0.60	-0.09	0.93	0.53	0.92		0.76
	$y{+}{+}_{14}$	$y{+}{+}{+}_{23}$										
	0.48	0.67										

Fragment-ion (m/z)	1167.43	1192.81	1229.36	1258.80	1264.78	1292.72	1298.50	1316.54	1322.35	1360.64	1388.84	1437.89
Frac. Inten.(% of TIC)	1.49	7.30	4.79	2.61	9.61	2.45	8.22	1.55	4.32	2.19	2.42	4.51
Rel. Inten.(% of BP)	14.33	70.02	45.98	25.08	92.18	23.55	78.83	14.88	41.47	20.98	23.27	43.31
Score	1.00	1.00	-0.46	-0.25	1.00	-0.24	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	$y{+}{+}_{20}$	$y{+}{+}{+}_{31}$			$y{+}{+}{+}_{33}$		$b{+}{+}{+}_{34}$	$b{+}{+}_{24}$	$y{+}{+}{+}_{35}$	$y{+}{+}_{23}$	$y{+}{+}_{24}$	$y{+}{+}_{25}$
Delta Da	0.44	0.65			0.59		0.97	-0.51	0.80	0.58	0.27	0.80
							$y{+}{+}{+}_{34}$				$y{+}{+}{+}_{37}$	
							0.63				0.59	

Peak 145

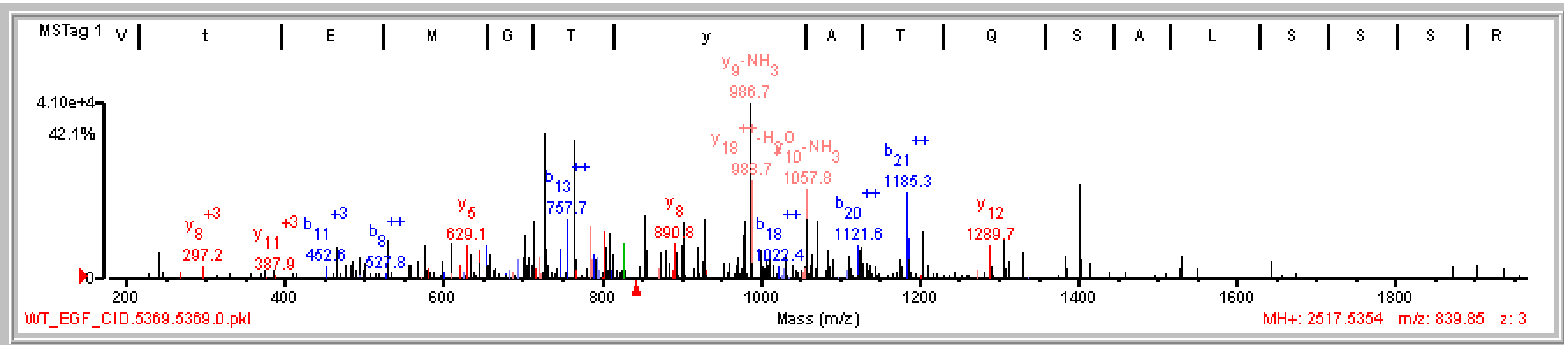


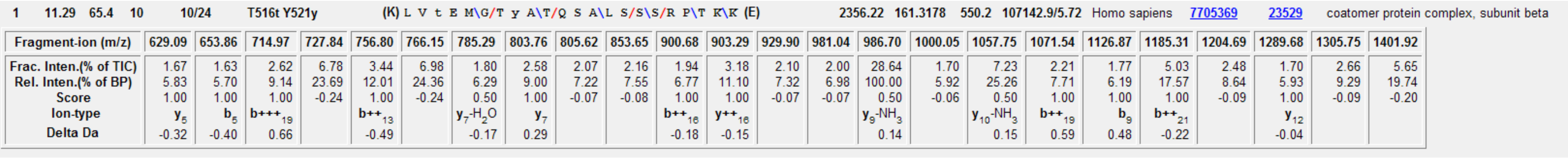


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.82	83.2	7	2/10	Y822y	(K) S F/L D/S G y R I\L|G A\V\A\K (V)	1596.87	79.9983	19.1	123800.0/5.50	Homo sapiens	7669550	11836	vinculin isoform meta-VCL

Fragment-ion (m/z)	445.48	608.49	722.38	806.47	1119.74	1232.58	1360.73	1362.64	1460.10	1530.92
Frac. Inten.(% of TIC)	10.33	14.23	12.52	8.40	9.48	12.57	7.82	8.44	8.24	7.97
Rel. Inten.(% of BP)	72.63	100.00	88.02	59.07	66.61	88.39	54.98	59.33	57.90	55.99
Score	1.00	1.00	1.00	-0.59	1.00	1.00	1.00	-0.59	1.00	1.00
Ion-type	b_4-H_2O y_5	$y{+}{+}_{11}$	$y{+}{+}_{13}$		b_9	b_{10}	b_{12}		b_{13}	b_{14}
Delta Da	0.27 0.20	0.67	0.51		0.25	0.01	0.10		0.40	0.18

Peak 146



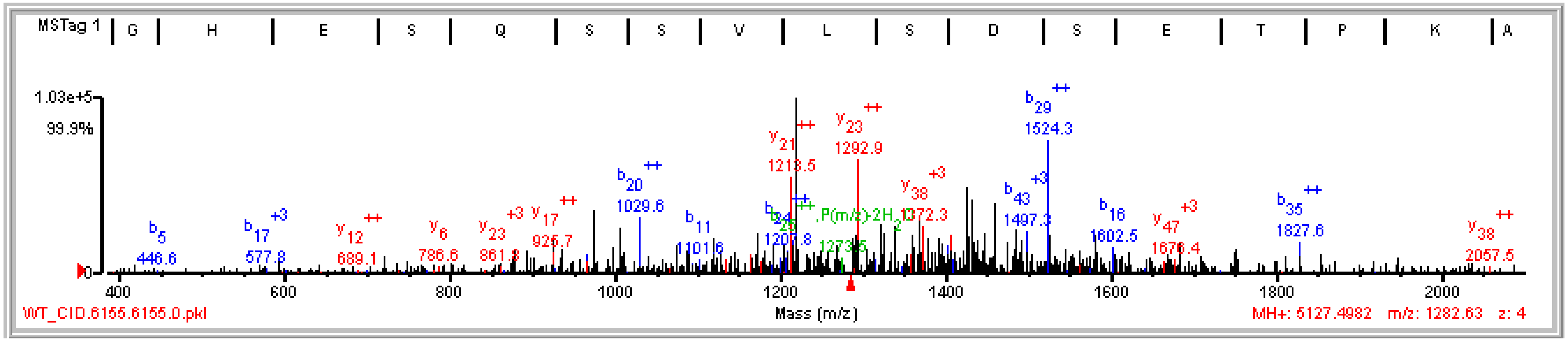


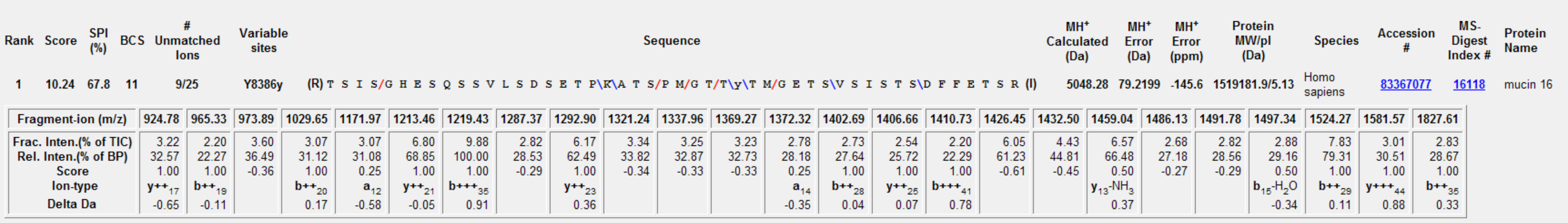
1 11.29 65.4 10 10/24 T516t Y521y (K) L V t E M\G/T y A\T/Q S A\L S/S\S/R P\T K\K (E) 2356.22 161.3178 550.2 107142.9/5.72 Homo sapiens 7705369 23529 coatomer protein complex, subunit beta

Fragment-ion (m/z)	629.09	653.86	714.97	727.84	756.80	766.15	785.29	803.76	805.62	853.65	900.68	903.29
Frac. Inten.(% of TIC)	1.67	1.63	2.62	6.78	3.44	6.98	1.80	2.58	2.07	2.16	1.94	3.18
Rel. Inten.(% of BP)	5.83	5.70	9.14	23.69	12.01	24.36	6.29	9.00	7.22	7.55	6.77	11.10
Score	1.00	1.00	1.00	-0.24	1.00	-0.24	0.50	1.00	-0.07	-0.08	1.00	1.00
Ion-type	y_5	b_5	$b{+}{+}{+}_{19}$		$b{+}{+}_{13}$		y_7-H_2O	y_7			$b{+}{+}_{16}$	$y{+}{+}_{16}$
Delta Da	-0.32	-0.40	0.66		-0.49		-0.17	0.29			-0.18	-0.15

Fragment-ion (m/z)	929.90	981.04	986.70	1000.05	1057.75	1071.54	1126.87	1185.31	1204.69	1289.68	1305.75	1401.92
Frac. Inten.(% of TIC)	2.10	2.00	28.64	1.70	7.23	2.21	1.77	5.03	2.48	1.70	2.66	5.65
Rel. Inten.(% of BP)	7.32	6.98	100.00	5.92	25.26	7.71	6.19	17.57	8.64	5.93	9.29	19.74
Score	-0.07	-0.07	0.50	-0.06	0.50	1.00	1.00	1.00	-0.09	1.00	-0.09	-0.20
Ion-type			y_9-NH_3		y_{10}-NH_3	$b{+}{+}_{19}$	b_9	$b{+}{+}_{21}$		y_{12}		
Delta Da			0.14		0.15	0.59	0.48	-0.22		-0.04		

Peak 147



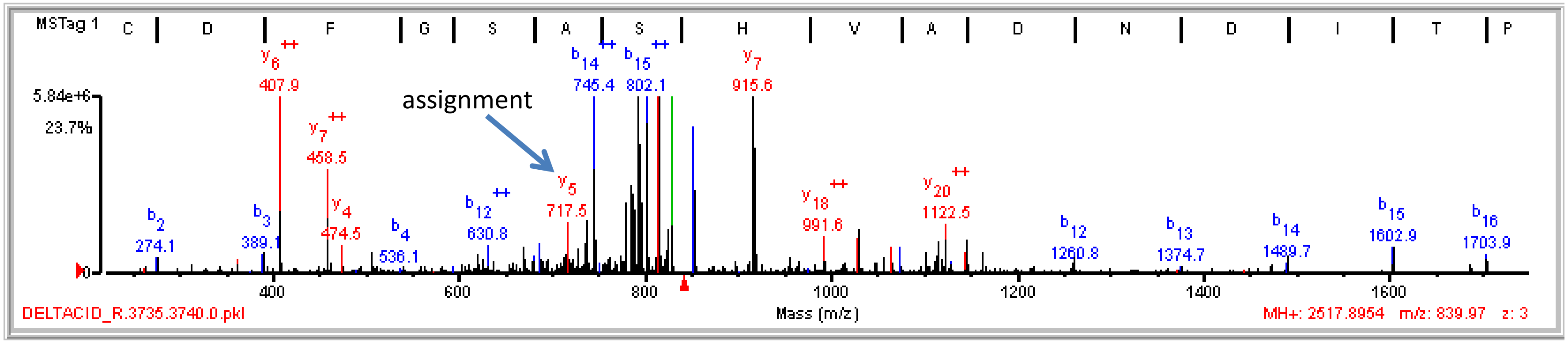


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.24	67.8	11	9/25	Y8386y	(R) T S I S/G H E S Q S S V L S D S E T P\K\A T S/P M/G T/T\y\T M/G E T S\V S I S T S\D F F E T S R (I)	5048.28	79.2199	-145.6	1519181.9/5.13	Homo sapiens	83367077	16118	mucin 16

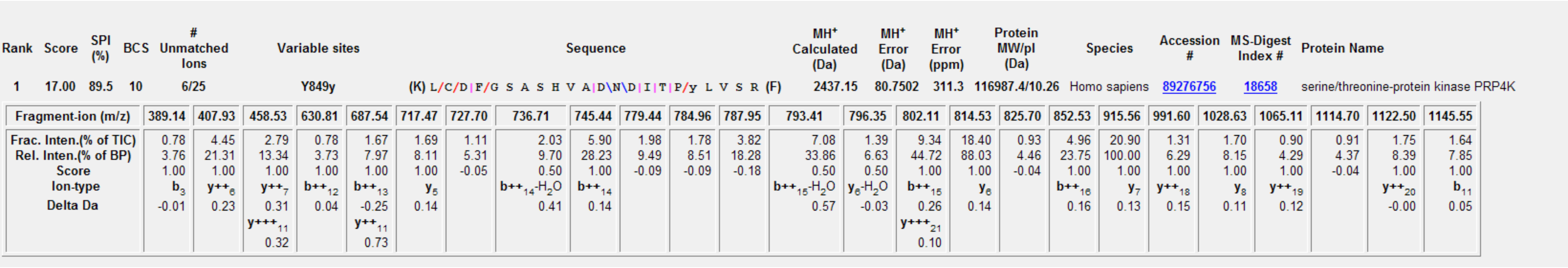
Fragment-ion (m/z)	924.78	965.33	973.89	1029.65	1171.97	1213.46	1219.43	1287.37	1292.90	1321.24	1337.96	1369.27
Frac. Inten.(% of TIC)	3.22	2.20	3.60	3.07	3.07	6.80	9.88	2.82	6.17	3.34	3.25	3.23
Rel. Inten.(% of BP)	32.57	22.27	36.49	31.12	31.08	68.85	100.00	28.53	62.49	33.82	32.87	32.73
Score	1.00	1.00	-0.36	1.00	0.25	1.00	1.00	-0.29	1.00	-0.34	-0.33	-0.33
Ion-type	$y{+}{+}_{17}$	$b{+}{+}_{19}$		$b{+}{+}_{20}$	a_{12}	$y{+}{+}_{21}$	$b{+}{+}{+}_{35}$		$y{+}{+}_{23}$			
Delta Da	-0.65	-0.11		0.17	-0.58	-0.05	0.91		0.36			

Fragment-ion (m/z)	1372.32	1402.69	1406.66	1410.73	1426.45	1432.50	1459.04	1486.13	1491.78	1497.34	1524.27	1581.57	1827.61
Frac. Inten.(% of TIC)	2.78	2.73	2.54	2.20	6.05	4.43	6.57	2.68	2.82	2.88	7.83	3.01	2.83
Rel. Inten.(% of BP)	28.18	27.64	25.72	22.29	61.23	44.81	66.48	27.18	28.56	29.16	79.31	30.51	28.67
Score	0.25	1.00	1.00	1.00	-0.61	-0.45	0.50	-0.27	-0.29	0.50	1.00	1.00	1.00
Ion-type	a_{14}	$b{+}{+}_{28}$	$y{+}{+}_{25}$	$b{+}{+}{+}_{41}$			y_{13}-NH_3			b_{15}-H_2O	$b{+}{+}_{29}$	$y{+}{+}{+}_{44}$	$b{+}{+}_{35}$
Delta Da	-0.35	0.04	0.07	0.78			0.37			-0.34	0.11	0.88	0.33

Peak 148



assignment



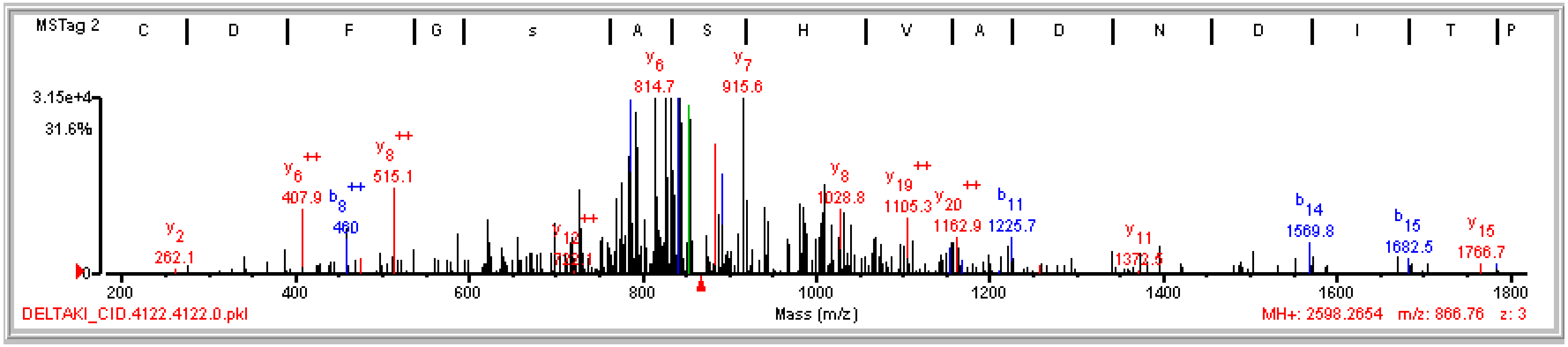
<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>17.00</td><td>89.5</td><td>10</td><td>6/25</td><td>Y849y</td><td>(K) L/C/D|F/G S A S H V A|D\N\D|I|T|P/y L V S R (F)</td><td>2437.15</td><td>80.7502</td><td>311.3</td><td>116987.4/10.26</td><td>Homo sapiens</td><td>89276756</td><td>18658</td><td>serine/threonine-protein kinase PRP4K</td></tr>
</table>

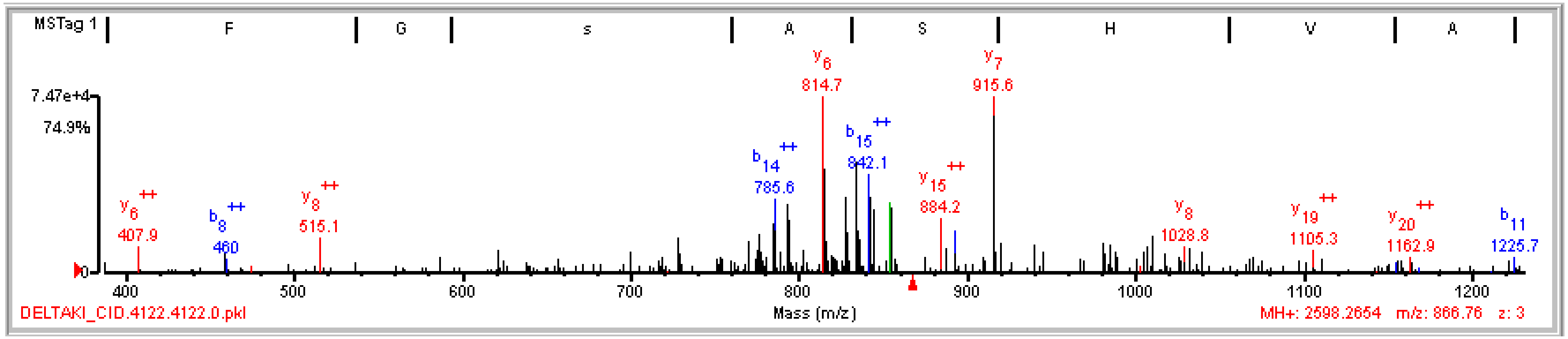
Fragment-ion (m/z)	389.14	407.93	458.53	630.81	687.54	717.47	727.70	736.71	745.44	779.44	784.96	787.95
Frac. Inten.(% of TIC)	0.78	4.45	2.79	0.78	1.67	1.69	1.11	2.03	5.90	1.98	1.78	3.82
Rel. Inten.(% of BP)	3.76	21.31	13.34	3.73	7.97	8.11	5.31	9.70	28.23	9.49	8.51	18.28
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.05	0.50	1.00	-0.09	-0.09	-0.18
Ion-type	b_3	$y{+}{+}_6$	$y{+}{+}_7$	$b{+}{+}_{12}$	$b{+}{+}_{13}$	y_5		$b{+}{+}_{14}\text{-}H_2O$	$b{+}{+}_{14}$			
Delta Da	-0.01	0.23	0.31	0.04	-0.25	0.14		0.41	0.14			
			$y{+}{+}{+}_{11}$		$y{+}{+}_{11}$							
			0.32		0.73							

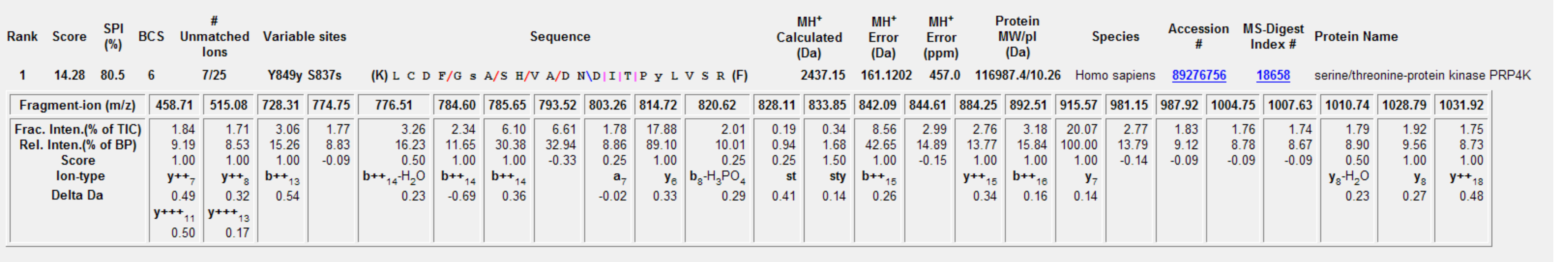
Fragment-ion (m/z)	793.41	796.35	802.11	814.53	825.70	852.53	915.56	991.60	1028.63	1065.11	1114.70	1122.50	1145.55
Frac. Inten.(% of TIC)	7.08	1.39	9.34	18.40	0.93	4.96	20.90	1.31	1.70	0.90	0.91	1.75	1.64
Rel. Inten.(% of BP)	33.86	6.63	44.72	88.03	4.46	23.75	100.00	6.29	8.15	4.29	4.37	8.39	7.85
Score	0.50	0.50	1.00	1.00	-0.04	1.00	1.00	1.00	1.00	1.00	-0.04	1.00	1.00
Ion-type	$b{+}{+}_{15}\text{-}H_2O$	$y_6\text{-}H_2O$	$b{+}{+}_{15}$	y_6		$b{+}{+}_{16}$	y_7	$y{+}{+}_{18}$	y_8	$y{+}{+}_{19}$		$y{+}{+}_{20}$	b_{11}
Delta Da	0.57	-0.03	0.26	0.14		0.16	0.13	0.15	0.11	0.12		-0.00	0.05
			$y{+}{+}{+}_{21}$										
			0.10										

assignment

Peak 149





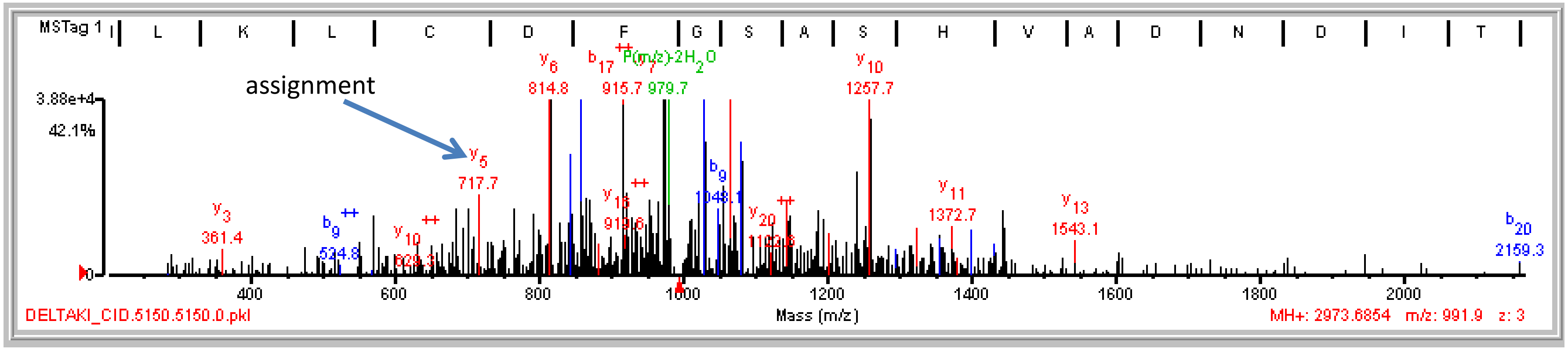


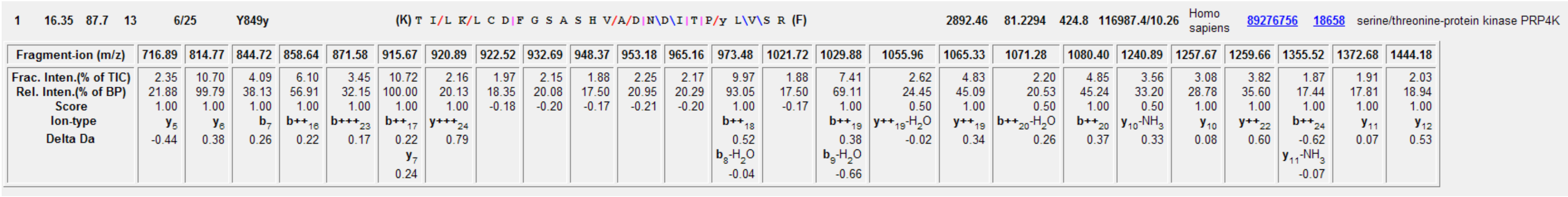
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.28	80.5	6	7/25	Y849y S837s	(K) L C D F/G s A/S H/V A/D N\D|I|T|P y L V S R (F)	2437.15	161.1202	457.0	116987.4/10.26	Homo sapiens	89276756	18658	serine/threonine-protein kinase PRP4K

Fragment-ion (m/z)	458.71	515.08	728.31	774.75	776.51	784.60	785.65	793.52	803.26	814.72	820.62
Frac. Inten.(% of TIC)	1.84	1.71	3.06	1.77	3.26	2.34	6.10	6.61	1.78	17.88	2.01
Rel. Inten.(% of BP)	9.19	8.53	15.26	8.83	16.23	11.65	30.38	32.94	8.86	89.10	10.01
Score	1.00	1.00	1.00	-0.09	0.50	1.00	1.00	-0.33	0.25	1.00	0.25
Ion-type	y^{++}_{7}	y^{++}_{8}	b^{++}_{13}		b^{++}_{14}-H_2O	b^{++}_{14}	b^{++}_{14}		a_7	y_6	b_8-H_3PO_4
Delta Da	0.49	0.32	0.54		0.23	-0.69	0.36		-0.02	0.33	0.29
	y^{+++}_{11}	y^{+++}_{13}									
	0.50	0.17									

Fragment-ion (m/z)	828.11	833.85	842.09	844.61	884.25	892.51	915.57	981.15	987.92	1004.75	1007.63	1010.74	1028.79	1031.92
Frac. Inten.(% of TIC)	0.19	0.34	8.56	2.99	2.76	3.18	20.07	2.77	1.83	1.76	1.74	1.79	1.92	1.75
Rel. Inten.(% of BP)	0.94	1.68	42.65	14.89	13.77	15.84	100.00	13.79	9.12	8.78	8.67	8.90	9.56	8.73
Score	0.25	1.50	1.00	-0.15	1.00	1.00	1.00	-0.14	-0.09	-0.09	-0.09	0.50	1.00	1.00
Ion-type	st	sty	b^{++}_{15}		y^{++}_{15}	b^{++}_{16}	y_7					y_8-H_2O	y_8	y^{++}_{18}
Delta Da	0.41	0.14	0.26		0.34	0.16	0.14					0.23	0.27	0.48

Peak 150



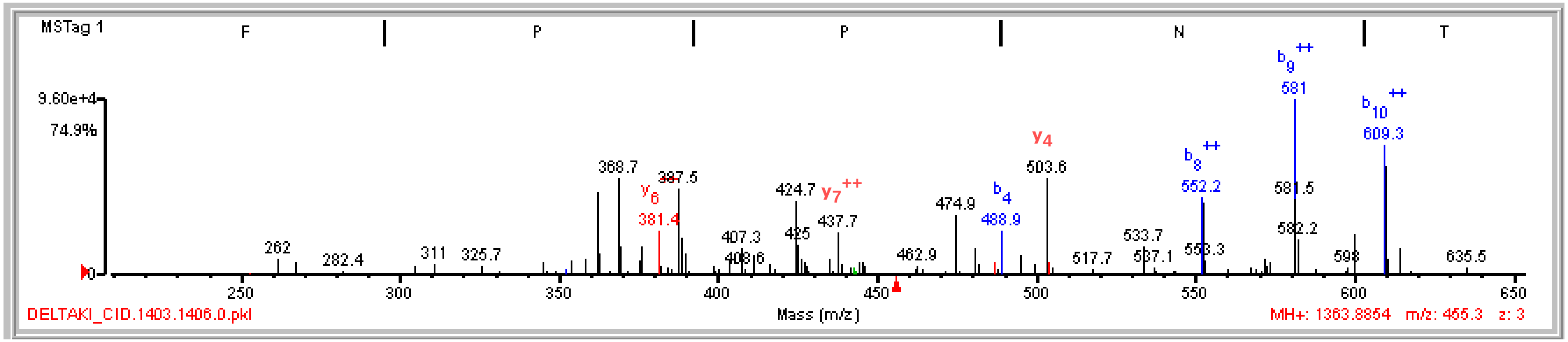


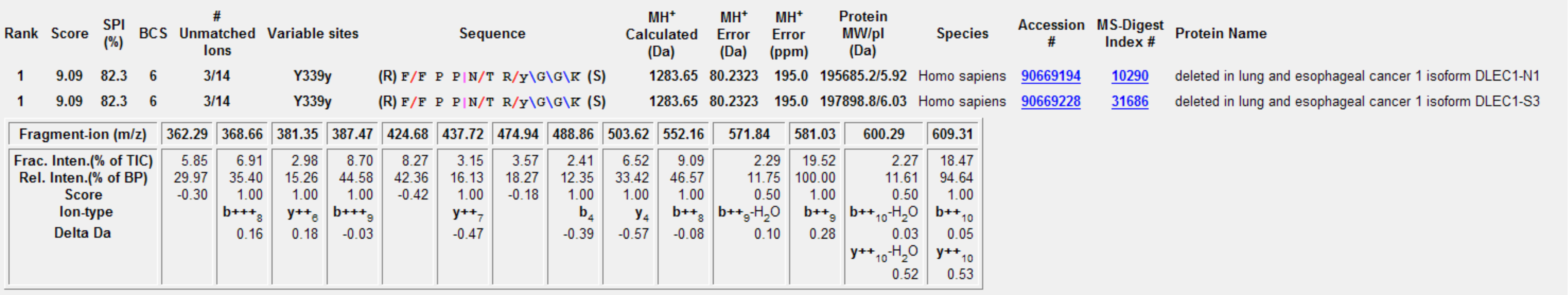
1 16.35 87.7 13 6/25 Y849y (K) T I/L K/L C D|F G S A S H V/A/D|N\D\I|T|P/y L\V\S R (F) 2892.46 81.2294 424.8 116987.4/10.26 Homo sapiens 89276756 18658 serine/threonine-protein kinase PRP4K

Fragment-ion (m/z)	716.89	814.77	844.72	858.64	871.58	915.67	920.89	922.52	932.69	948.37	953.18	965.16	973.48	1021.72
Frac. Inten.(% of TIC)	2.35	10.70	4.09	6.10	3.45	10.72	2.16	1.97	2.15	1.88	2.25	2.17	9.97	1.88
Rel. Inten.(% of BP)	21.88	99.79	38.13	56.91	32.15	100.00	20.13	18.35	20.08	17.50	20.95	20.29	93.05	17.50
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.18	-0.20	-0.17	-0.21	-0.20	1.00	-0.17
Ion-type	y_5	y_6	b_7	$b{++}_{16}$	$b{+++}_{23}$	$b{++}_{17}$ y_7	$y{+++}_{24}$						$b{++}_{18}$ b_8-H_2O	
Delta Da	-0.44	0.38	0.26	0.22	0.17	0.22 0.24	0.79						0.52 -0.04	

Fragment-ion (m/z)	1029.88	1055.96	1065.33	1071.28	1080.40	1240.89	1257.67	1259.66	1355.52	1372.68	1444.18
Frac. Inten.(% of TIC)	7.41	2.62	4.83	2.20	4.85	3.56	3.08	3.82	1.87	1.91	2.03
Rel. Inten.(% of BP)	69.11	24.45	45.09	20.53	45.24	33.20	28.78	35.60	17.44	17.81	18.94
Score	1.00	0.50	1.00	0.50	1.00	0.50	1.00	1.00	1.00	1.00	1.00
Ion-type	$b{++}_{19}$ b_9-H_2O	$y{++}_{19}$-H_2O	$y{++}_{19}$	$b{++}_{20}$-H_2O	$b{++}_{20}$	y_{10}-NH_3	y_{10}	$y{++}_{22}$	$b{++}_{24}$ y_{11}-NH_3	y_{11}	y_{12}
Delta Da	0.38 -0.66	-0.02	0.34	0.26	0.37	0.33	0.08	0.60	-0.62 -0.07	0.07	0.53

Peak 151

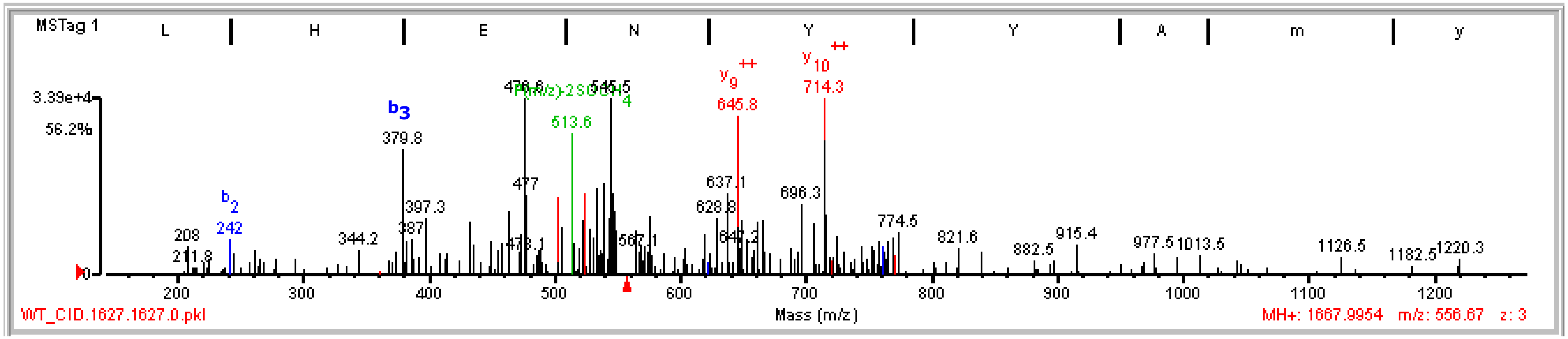


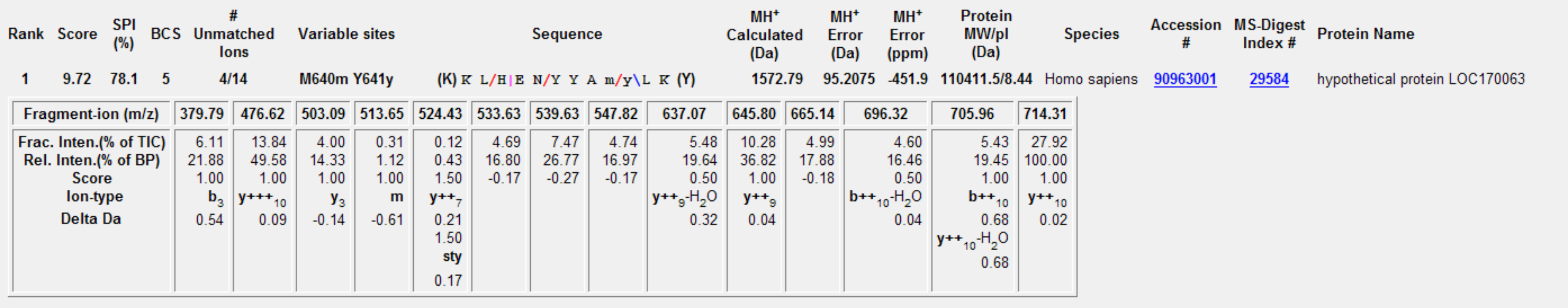


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.09	82.3	6	3/14	Y339y	(R) F/F P P|N/T R/y\G\G\K (S)	1283.65	80.2323	195.0	195685.2/5.92	Homo sapiens	90669194	10290	deleted in lung and esophageal cancer 1 isoform DLEC1-N1
1	9.09	82.3	6	3/14	Y339y	(R) F/F P P|N/T R/y\G\G\K (S)	1283.65	80.2323	195.0	197898.8/6.03	Homo sapiens	90669228	31686	deleted in lung and esophageal cancer 1 isoform DLEC1-S3

Fragment-ion (m/z)	362.29	368.66	381.35	387.47	424.68	437.72	474.94	488.86	503.62	552.16	571.84	581.03	600.29	609.31
Frac. Inten.(% of TIC)	5.85	6.91	2.98	8.70	8.27	3.15	3.57	2.41	6.52	9.09	2.29	19.52	2.27	18.47
Rel. Inten.(% of BP)	29.97	35.40	15.26	44.58	42.36	16.13	18.27	12.35	33.42	46.57	11.75	100.00	11.61	94.64
Score	-0.30	1.00	1.00	1.00	-0.42	1.00	-0.18	1.00	1.00	1.00	0.50	1.00	0.50	1.00
Ion-type		$b{+}{+}{+}_8$	$y{+}{+}_6$	$b{+}{+}{+}_9$		$y{+}{+}_7$		b_4	y_4	$b{+}{+}_8$	$b{+}{+}_9$-H_2O	$b{+}{+}_9$	$b{+}{+}_{10}$-H_2O	$b{+}{+}_{10}$
Delta Da		0.16	0.18	-0.03		-0.47		-0.39	-0.57	-0.08	0.10	0.28	0.03	0.05
													$y{+}{+}_{10}$-H_2O	$y{+}{+}_{10}$
													0.52	0.53

Peak 152

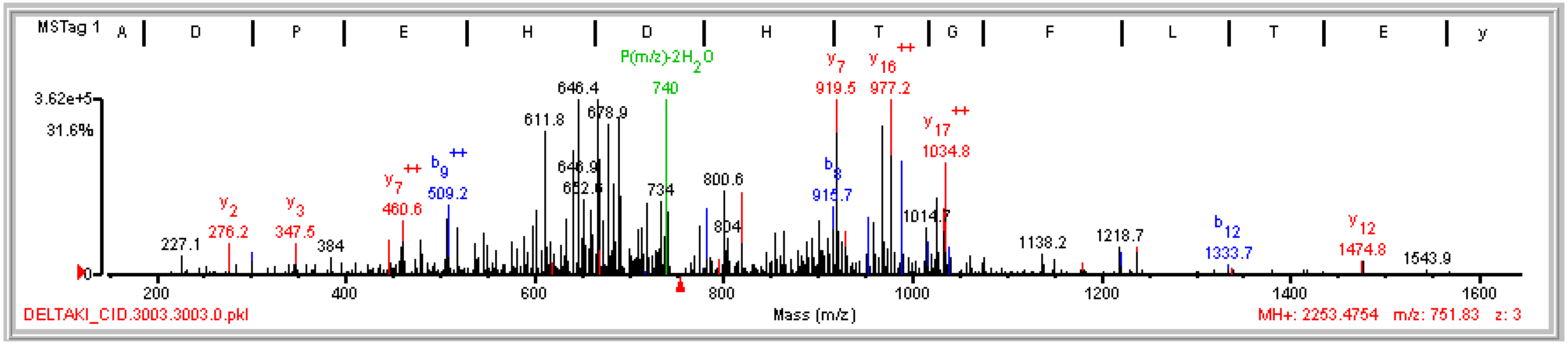


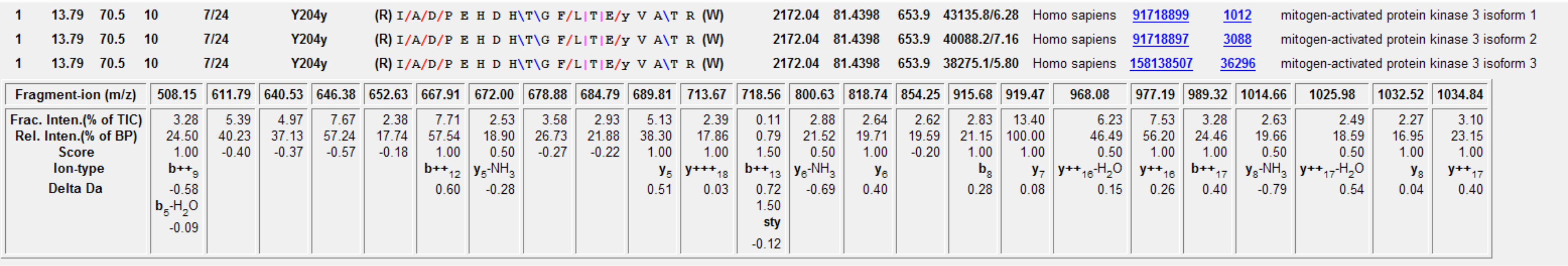


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.72	78.1	5	4/14	M640m Y641y	(K) K L/H|E N/Y Y A m/y\L K (Y)	1572.79	95.2075	-451.9	110411.5/8.44	Homo sapiens	90963001	29584	hypothetical protein LOC170063

Fragment-ion (m/z)	379.79	476.62	503.09	513.65	524.43	533.63	539.63	547.82	637.07	645.80	665.14	696.32	705.96	714.31
Frac. Inten.(% of TIC)	6.11	13.84	4.00	0.31	0.12	4.69	7.47	4.74	5.48	10.28	4.99	4.60	5.43	27.92
Rel. Inten.(% of BP)	21.88	49.58	14.33	1.12	0.43	16.80	26.77	16.97	19.64	36.82	17.88	16.46	19.45	100.00
Score	1.00	1.00	1.00	1.00	1.50	-0.17	-0.27	-0.17	0.50	1.00	-0.18	0.50	1.00	1.00
Ion-type	b_3	$y{+}{+}{+}_{10}$	y_3	m	$y{+}{+}_7$				$y{+}{+}_9$-H_2O	$y{+}{+}_9$		$b{+}{+}_{10}$-H_2O	$b{+}{+}_{10}$	$y{+}{+}_{10}$
Delta Da	0.54	0.09	-0.14	-0.61	0.21				0.32	0.04		0.04	0.68	0.02
					1.50								$y{+}{+}_{10}$-H_2O	
					sty								0.68	
					0.17									

Peak 153



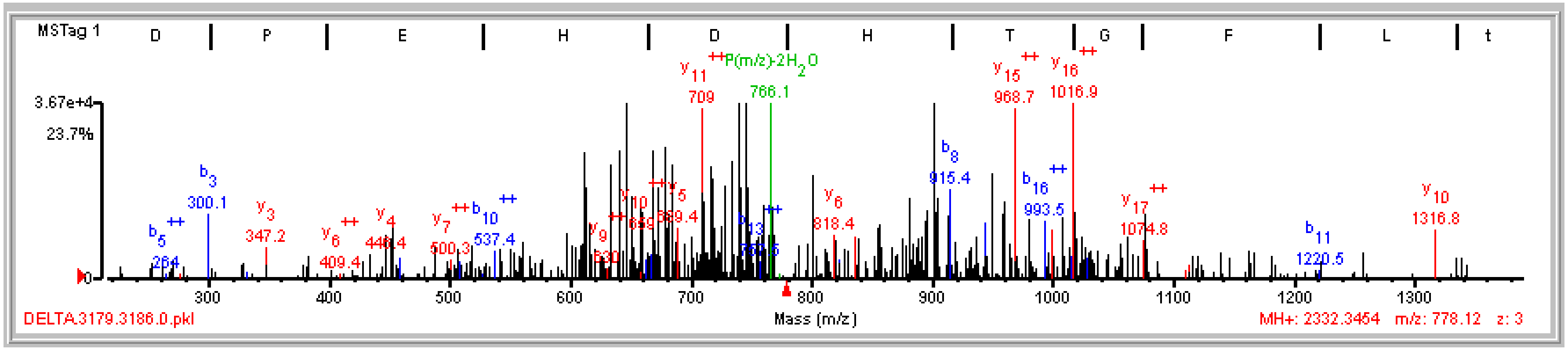


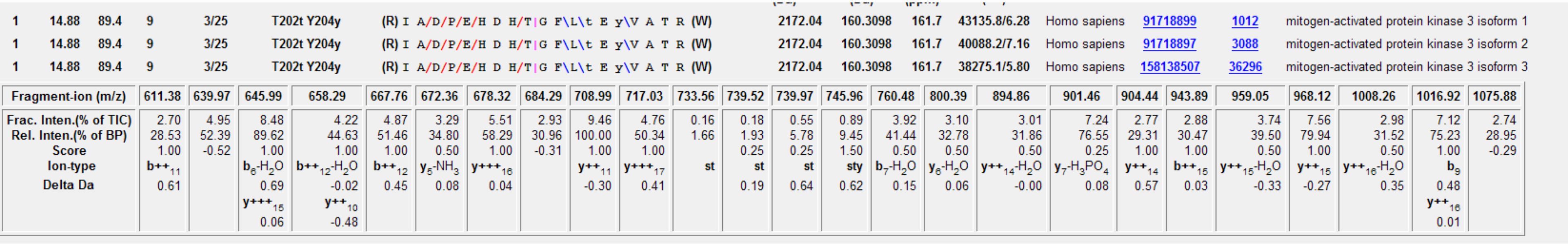
1	13.79	70.5	10	7/24	Y204y	(R) I/A/D/P E H D H\T\G F/L|T|E/y V A\T R (W)	2172.04	81.4398	653.9	43135.8/6.28	Homo sapiens	91718899	1012	mitogen-activated protein kinase 3 isoform 1
1	13.79	70.5	10	7/24	Y204y	(R) I/A/D/P E H D H\T\G F/L|T|E/y V A\T R (W)	2172.04	81.4398	653.9	40088.2/7.16	Homo sapiens	91718897	3088	mitogen-activated protein kinase 3 isoform 2
1	13.79	70.5	10	7/24	Y204y	(R) I/A/D/P E H D H\T\G F/L|T|E/y V A\T R (W)	2172.04	81.4398	653.9	38275.1/5.80	Homo sapiens	158138507	36296	mitogen-activated protein kinase 3 isoform 3

Fragment-ion (m/z)	508.15	611.79	640.53	646.38	652.63	667.91	672.00	678.88	684.79	689.81	713.67	718.56
Frac. Inten.(% of TIC)	3.28	5.39	4.97	7.67	2.38	7.71	2.53	3.58	2.93	5.13	2.39	0.11
Rel. Inten.(% of BP)	24.50	40.23	37.13	57.24	17.74	57.54	18.90	26.73	21.88	38.30	17.86	0.79
Score	1.00	-0.40	-0.37	-0.57	-0.18	1.00	0.50	-0.27	-0.22	1.00	1.00	1.50 1.50
Ion-type	b^{++}_{9} b_5-H_2O					b^{++}_{12}	y_5-NH_3			y_5	y^{+++}_{18}	b^{++}_{13} sty
Delta Da	-0.58 -0.09					0.60	-0.28			0.51	0.03	0.72 -0.12

Fragment-ion (m/z)	800.63	818.74	854.25	915.68	919.47	968.08	977.19	989.32	1014.66	1025.98	1032.52	1034.84
Frac. Inten.(% of TIC)	2.88	2.64	2.62	2.83	13.40	6.23	7.53	3.28	2.63	2.49	2.27	3.10
Rel. Inten.(% of BP)	21.52	19.71	19.59	21.15	100.00	46.49	56.20	24.46	19.66	18.59	16.95	23.15
Score	0.50	1.00	-0.20	1.00	1.00	0.50	1.00	1.00	0.50	0.50	1.00	1.00
Ion-type	y_6-NH_3	y_6		b_8	y_7	$y^{++}_{16}-H_2O$	y^{++}_{16}	b^{++}_{17}	y_8-NH_3	$y^{++}_{17}-H_2O$	y_8	y^{++}_{17}
Delta Da	-0.69	0.40		0.28	0.08	0.15	0.26	0.40	-0.79	0.54	0.04	0.40

Peak 154



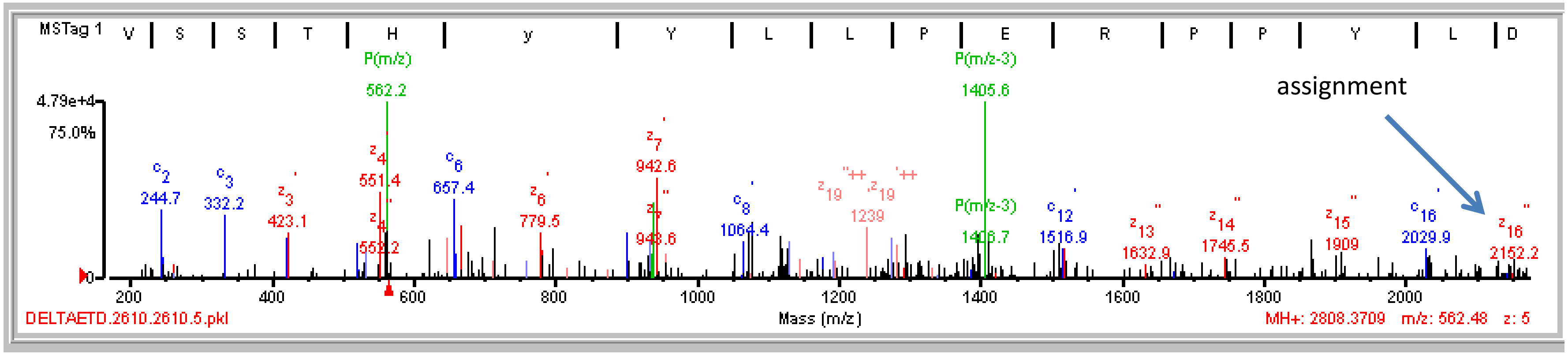


1	14.88	89.4	9	3/25	T202t Y204y	(R) I A/D/P/E/H D H/T|G F\L\t E y\V A T R (W)	2172.04	160.3098	161.7	43135.8/6.28	Homo sapiens	91718899	1012	mitogen-activated protein kinase 3 isoform 1
1	14.88	89.4	9	3/25	T202t Y204y	(R) I A/D/P/E/H D H/T|G F\L\t E y\V A T R (W)	2172.04	160.3098	161.7	40088.2/7.16	Homo sapiens	91718897	3088	mitogen-activated protein kinase 3 isoform 2
1	14.88	89.4	9	3/25	T202t Y204y	(R) I A/D/P/E/H D H/T|G F\L\t E y\V A T R (W)	2172.04	160.3098	161.7	38275.1/5.80	Homo sapiens	158138507	36296	mitogen-activated protein kinase 3 isoform 3

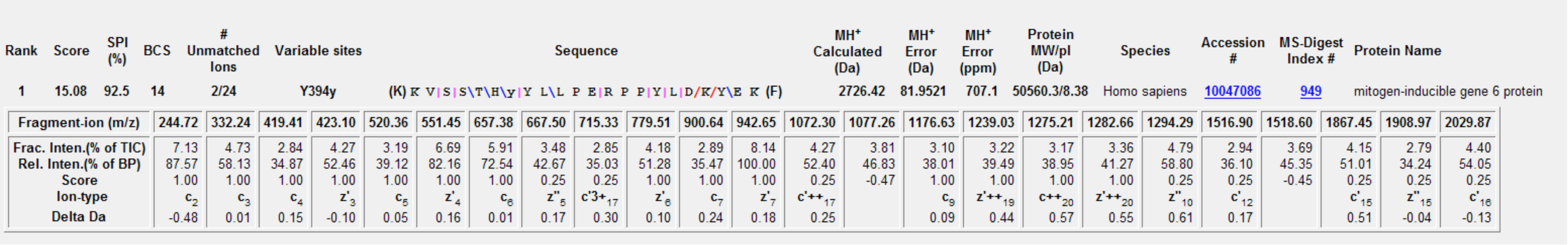
Fragment-ion (m/z)	611.38	639.97	645.99	658.29	667.76	672.36	678.32	684.29	708.99	717.03	733.56	739.52
Frac. Inten.(% of TIC)	2.70	4.95	8.48	4.22	4.87	3.29	5.51	2.93	9.46	4.76	0.16	0.18
Rel. Inten.(% of BP)	28.53	52.39	89.62	44.63	51.46	34.80	58.29	30.96	100.00	50.34	1.66	1.93
Score	1.00	-0.52	1.00	1.00	1.00	0.50	1.00	-0.31	1.00	1.00		0.25
Ion-type	$b{+}{+}_{11}$		b_6-H_2O $y{+}{+}{+}_{15}$	$b{+}{+}_{12}$-H_2O $y{+}{+}_{10}$	$b{+}{+}_{12}$	y_5-NH_3	$y{+}{+}{+}_{16}$		$y{+}{+}_{11}$	$y{+}{+}{+}_{17}$	st	st
Delta Da	0.61		0.69 0.06	-0.02 -0.48	0.45	0.08	0.04		-0.30	0.41		0.19

Fragment-ion (m/z)	739.97	745.96	760.48	800.39	894.86	901.46	904.44	943.89	959.05	968.12	1008.26	1016.92	1075.88
Frac. Inten.(% of TIC)	0.55	0.89	3.92	3.10	3.01	7.24	2.77	2.88	3.74	7.56	2.98	7.12	2.74
Rel. Inten.(% of BP)	5.78	9.45	41.44	32.78	31.86	76.55	29.31	30.47	39.50	79.94	31.52	75.23	28.95
Score	0.25	1.50	0.50	0.50	0.50	0.25	1.00	1.00	0.50	1.00	0.50	1.00	-0.29
Ion-type	st	sty	b_7-H_2O	y_6-H_2O	$y{+}{+}_{14}$-H_2O	y_7-H_3PO_4	$y{+}{+}_{14}$	$b{+}{+}_{15}$	$y{+}{+}_{15}$-H_2O	$y{+}{+}_{15}$	$y{+}{+}_{16}$-H_2O	b_9 $y{+}{+}_{16}$	
Delta Da	0.64	0.62	0.15	0.06	-0.00	0.08	0.57	0.03	-0.33	-0.27	0.35	0.48 0.01	

Peak 156



assignment

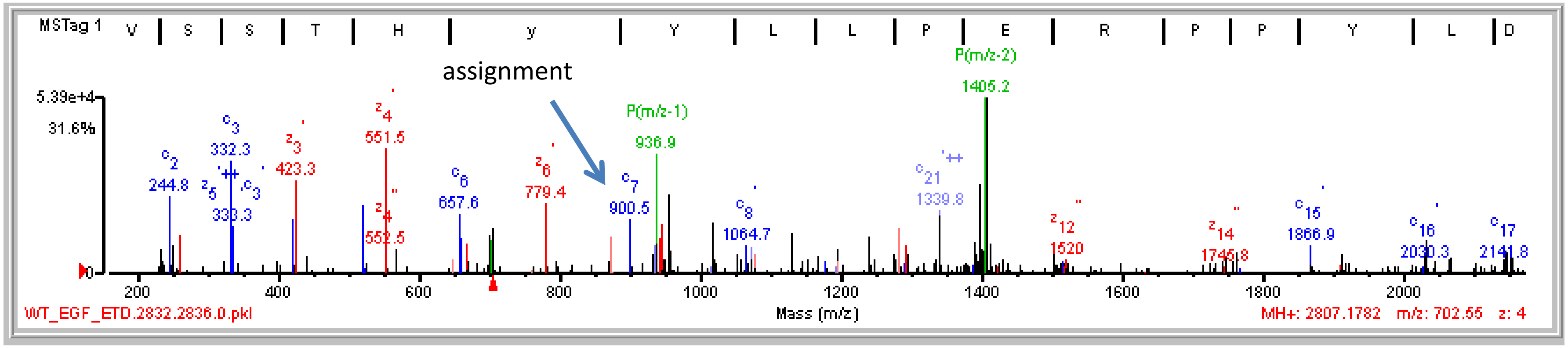


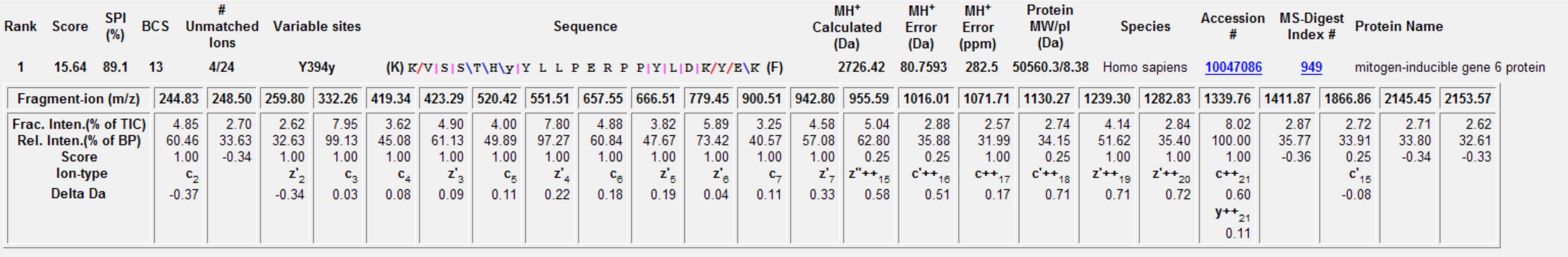
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.08	92.5	14	2/24	Y394y	(K) K V|S|S\T\H\y|Y L\L P E|R P P|Y|L|D/K/Y\E K (F)	2726.42	81.9521	707.1	50560.3/8.38	Homo sapiens	10047086	949	mitogen-inducible gene 6 protein

Fragment-ion (m/z)	244.72	332.24	419.41	423.10	520.36	551.45	657.38	667.50	715.33	779.51	900.64	942.65
Frac. Inten.(% of TIC)	7.13	4.73	2.84	4.27	3.19	6.69	5.91	3.48	2.85	4.18	2.89	8.14
Rel. Inten.(% of BP)	87.57	58.13	34.87	52.46	39.12	82.16	72.54	42.67	35.03	51.28	35.47	100.00
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	0.25	1.00	1.00	1.00
Ion-type	c_2	c_3	c_4	z'_3	c_5	z'_4	c_6	z''_5	$c'3+_{17}$	z'_6	c_7	z'_7
Delta Da	-0.48	0.01	0.15	-0.10	0.05	0.16	0.01	0.17	0.30	0.10	0.24	0.18

Fragment-ion (m/z)	1072.30	1077.26	1176.63	1239.03	1275.21	1282.66	1294.29	1516.90	1518.60	1867.45	1908.97	2029.87
Frac. Inten.(% of TIC)	4.27	3.81	3.10	3.22	3.17	3.36	4.79	2.94	3.69	4.15	2.79	4.40
Rel. Inten.(% of BP)	52.40	46.83	38.01	39.49	38.95	41.27	58.80	36.10	45.35	51.01	34.24	54.05
Score	0.25	-0.47	1.00	1.00	1.00	1.00	0.25	0.25	-0.45	0.25	0.25	0.25
Ion-type	$c'{+}{+}_{17}$		c_9	$z'{+}{+}_{19}$	$c{+}{+}_{20}$	$z'{+}{+}_{20}$	z''_{10}	c'_{12}		c'_{15}	z''_{15}	c'_{16}
Delta Da	0.25		0.09	0.44	0.57	0.55	0.61	0.17		0.51	-0.04	-0.13

Peak 157





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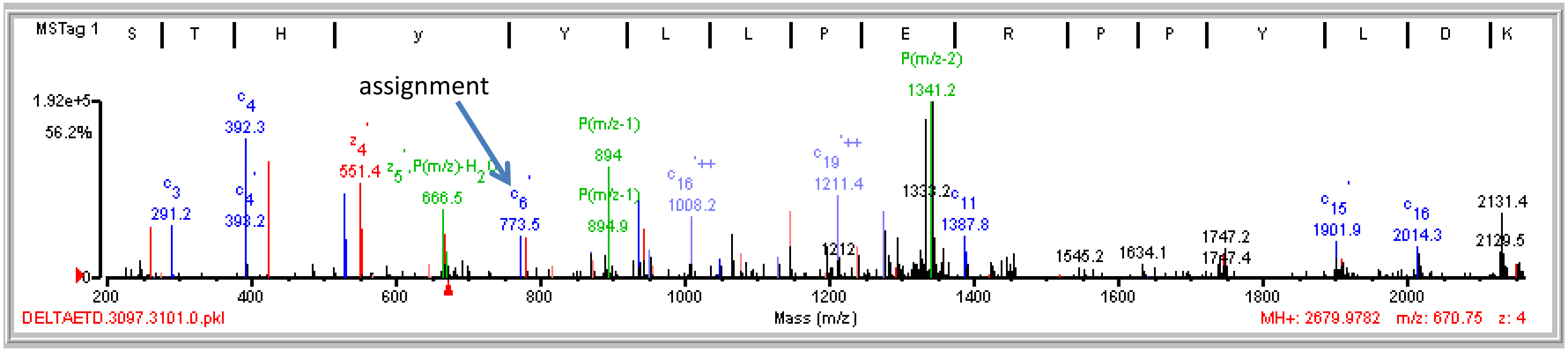
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>15.64</td><td>89.1</td><td>13</td><td>4/24</td><td>Y394y</td><td>(K) K/V|S|S\T\H\y|Y L L P E R P P|Y|L|D|K/Y/E\K (F)</td><td>2726.42</td><td>80.7593</td><td>282.5</td><td>50560.3/8.38</td><td>Homo sapiens</td><td>10047086</td><td>949</td><td>mitogen-inducible gene 6 protein</td></tr>
</table>

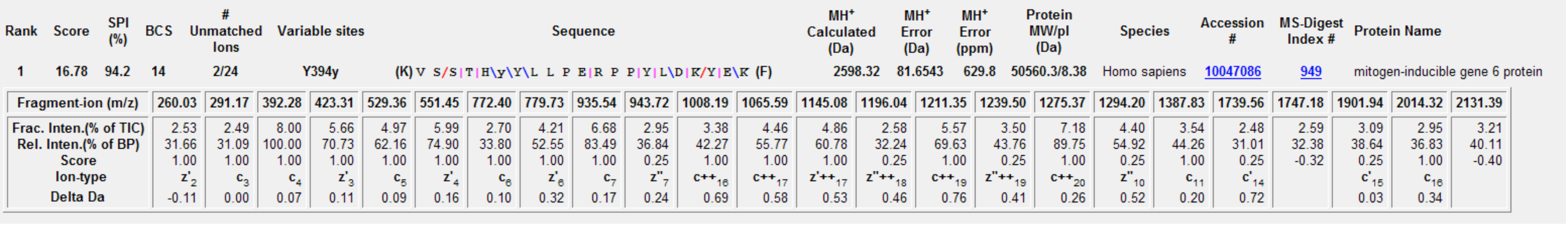
Fragment-ion (m/z)	244.83	248.50	259.80	332.26	419.34	423.29	520.42	551.51	657.55	666.51	779.45	900.51
Frac. Inten.(% of TIC)	4.85	2.70	2.62	7.95	3.62	4.90	4.00	7.80	4.88	3.82	5.89	3.25
Rel. Inten.(% of BP)	60.46	33.63	32.63	99.13	45.08	61.13	49.89	97.27	60.84	47.67	73.42	40.57
Score	1.00	-0.34	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	c_2		z'_2	c_3	c_4	z'_3	c_5	z'_4	c_6	z'_5	z'_6	c_7
Delta Da	-0.37		-0.34	0.03	0.08	0.09	0.11	0.22	0.18	0.19	0.04	0.11

Fragment-ion (m/z)	942.80	955.59	1016.01	1071.71	1130.27	1239.30	1282.83	1339.76	1411.87	1866.86	2145.45	2153.57
Frac. Inten.(% of TIC)	4.58	5.04	2.88	2.57	2.74	4.14	2.84	8.02	2.87	2.72	2.71	2.62
Rel. Inten.(% of BP)	57.08	62.80	35.88	31.99	34.15	51.62	35.40	100.00	35.77	33.91	33.80	32.61
Score	1.00	0.25	0.25	1.00	0.25	1.00	1.00	1.00	-0.36	0.25	-0.34	-0.33
Ion-type	z'_7	$z''{++}_{15}$	$c'{++}_{16}$	$c{++}_{17}$	$c'{++}_{18}$	$z'{++}_{19}$	$z'{++}_{20}$	$c{++}_{21}$ $y{++}_{21}$		c'_{15}		
Delta Da	0.33	0.58	0.51	0.17	0.71	0.71	0.72	0.60 0.11		-0.08		

Peak 158



assignment

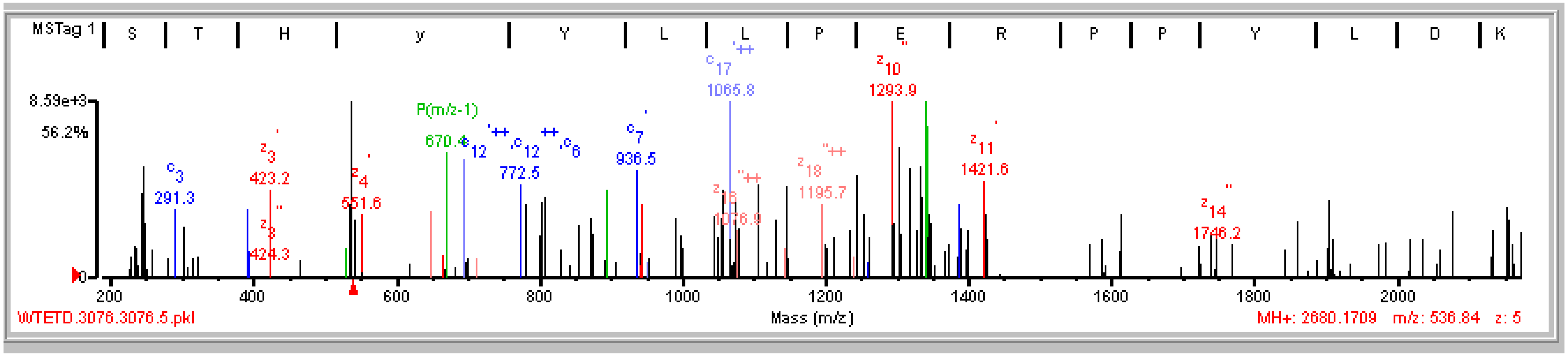


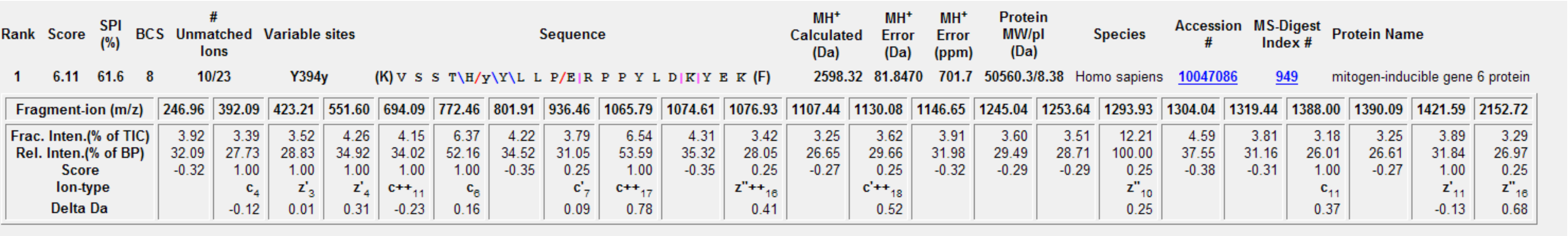
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.78	94.2	14	2/24	Y394y	(K) V S/S|T|H\y\Y\L L P E|R P P|Y|L\D|K/Y|E\K (F)	2598.32	81.6543	629.8	50560.3/8.38	Homo sapiens	10047086	949	mitogen-inducible gene 6 protein

Fragment-ion (m/z)	260.03	291.17	392.28	423.31	529.36	551.45	772.40	779.73	935.54	943.72	1008.19	1065.59
Frac. Inten.(% of TIC)	2.53	2.49	8.00	5.66	4.97	5.99	2.70	4.21	6.68	2.95	3.38	4.46
Rel. Inten.(% of BP)	31.66	31.09	100.00	70.73	62.16	74.90	33.80	52.55	83.49	36.84	42.27	55.77
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type	z'_2	c_3	c_4	z'_3	c_5	z'_4	c_6	z'_6	c_7	z''_7	$c{++}_{16}$	$c{++}_{17}$
Delta Da	-0.11	0.00	0.07	0.11	0.09	0.16	0.10	0.32	0.17	0.24	0.69	0.58

Fragment-ion (m/z)	1145.08	1196.04	1211.35	1239.50	1275.37	1294.20	1387.83	1739.56	1747.18	1901.94	2014.32	2131.39
Frac. Inten.(% of TIC)	4.86	2.58	5.57	3.50	7.18	4.40	3.54	2.48	2.59	3.09	2.95	3.21
Rel. Inten.(% of BP)	60.78	32.24	69.63	43.76	89.75	54.92	44.26	31.01	32.38	38.64	36.83	40.11
Score	1.00	0.25	1.00	0.25	1.00	0.25	1.00	0.25	-0.32	0.25	1.00	-0.40
Ion-type	$z'{++}_{17}$	$z''{++}_{18}$	$c{++}_{19}$	$z''{++}_{19}$	$c{++}_{20}$	z''_{10}	c_{11}	c'_{14}		c'_{15}	c_{16}	
Delta Da	0.53	0.46	0.76	0.41	0.26	0.52	0.20	0.72		0.03	0.34	

Peak 159



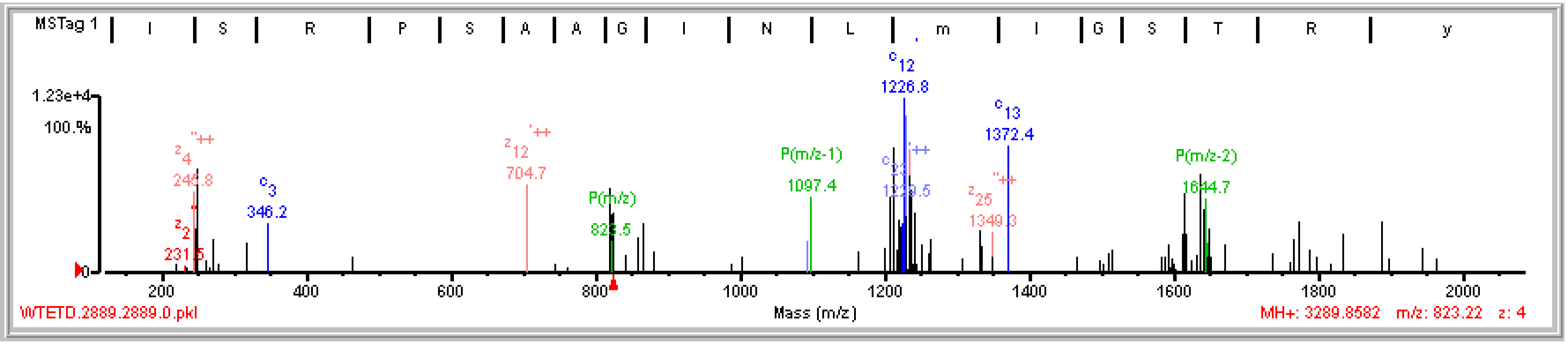


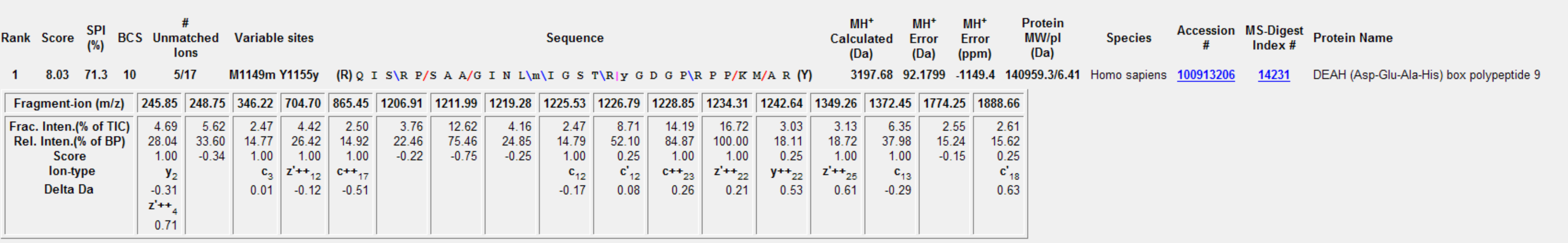
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.11	61.6	8	10/23	Y394y	(K) V S S T\H/y\Y\L L P/E|R P P Y L D|K|Y E K (F)	2598.32	81.8470	701.7	50560.3/8.38	Homo sapiens	10047086	949	mitogen-inducible gene 6 protein

Fragment-ion (m/z)	246.96	392.09	423.21	551.60	694.09	772.46	801.91	936.46	1065.79	1074.61	1076.93
Frac. Inten.(% of TIC)	3.92	3.39	3.52	4.26	4.15	6.37	4.22	3.79	6.54	4.31	3.42
Rel. Inten.(% of BP)	32.09	27.73	28.83	34.92	34.02	52.16	34.52	31.05	53.59	35.32	28.05
Score	-0.32	1.00	1.00	1.00	1.00	1.00	-0.35	0.25	1.00	-0.35	0.25
Ion-type		c_4	z'_3	z'_4	$c{++}_{11}$	c_6		c'_7	$c{++}_{17}$		$z''{++}_{16}$
Delta Da		-0.12	0.01	0.31	-0.23	0.16		0.09	0.78		0.41

Fragment-ion (m/z)	1107.44	1130.08	1146.65	1245.04	1253.64	1293.93	1304.04	1319.44	1388.00	1390.09	1421.59	2152.72
Frac. Inten.(% of TIC)	3.25	3.62	3.91	3.60	3.51	12.21	4.59	3.81	3.18	3.25	3.89	3.29
Rel. Inten.(% of BP)	26.65	29.66	31.98	29.49	28.71	100.00	37.55	31.16	26.01	26.61	31.84	26.97
Score	-0.27	0.25	-0.32	-0.29	-0.29	0.25	-0.38	-0.31	1.00	-0.27	1.00	0.25
Ion-type		$c'{++}_{18}$				z''_{10}			c_{11}		z'_{11}	z''_{16}
Delta Da		0.52				0.25			0.37		-0.13	0.68

Peak 160

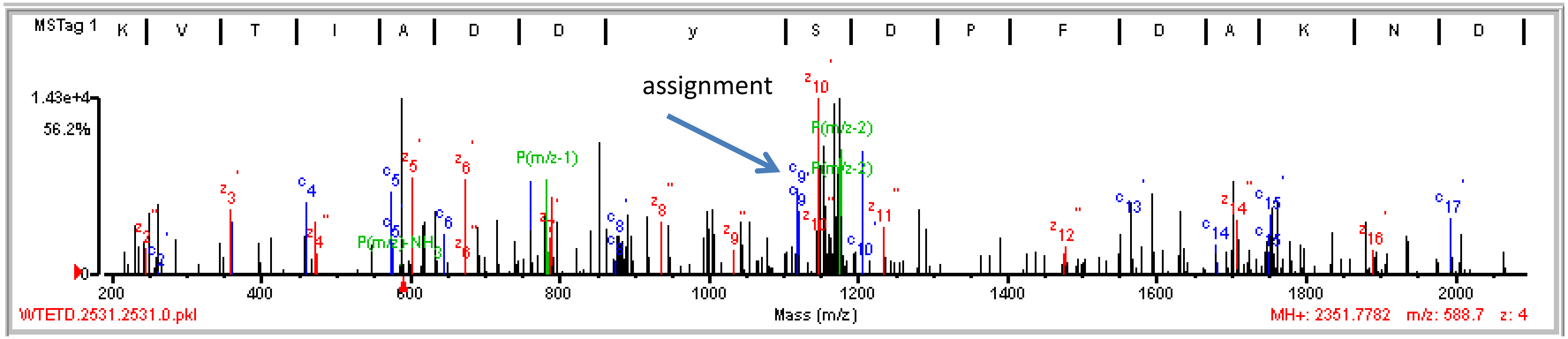




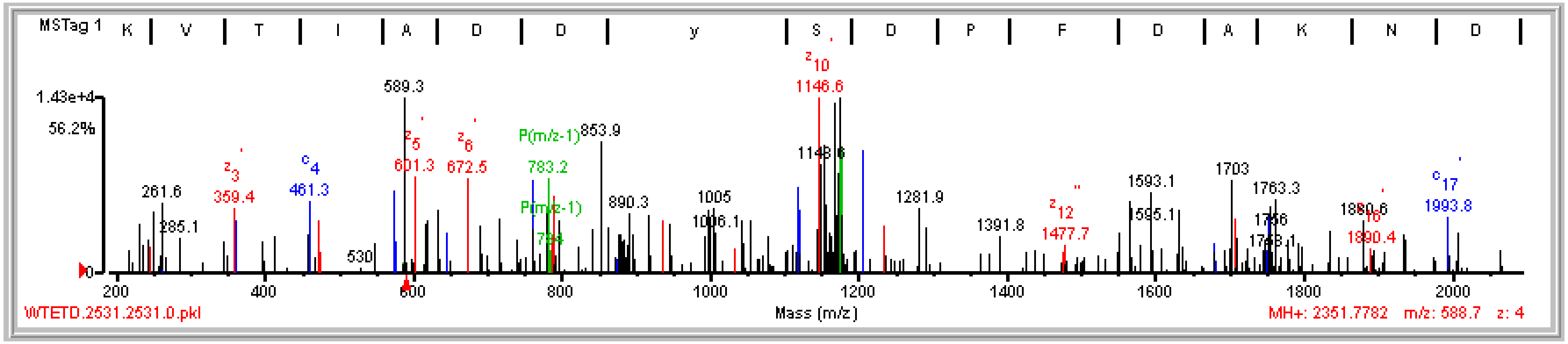
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.03	71.3	10	5/17	M1149m Y1155y	(R) Q I S\R P/S A A/G I N L\m\I G S T\R|y G D G P\R P P/K M/A R (Y)	3197.68	92.1799	-1149.4	140959.3/6.41	Homo sapiens	100913206	14231	DEAH (Asp-Glu-Ala-His) box polypeptide 9

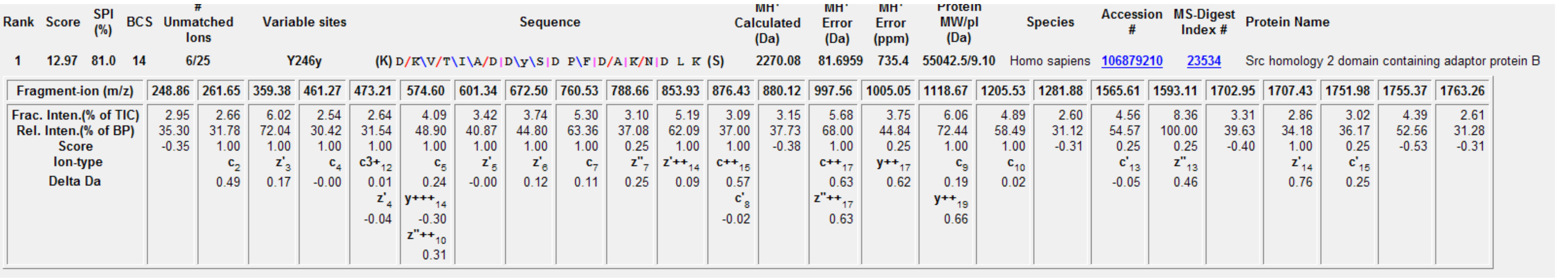
Fragment-ion (m/z)	245.85	248.75	346.22	704.70	865.45	1206.91	1211.99	1219.28	1225.53	1226.79	1228.85	1234.31	1242.64	1349.26	1372.45	1774.25	1888.66
Frac. Inten.(% of TIC)	4.69	5.62	2.47	4.42	2.50	3.76	12.62	4.16	2.47	8.71	14.19	16.72	3.03	3.13	6.35	2.55	2.61
Rel. Inten.(% of BP)	28.04	33.60	14.77	26.42	14.92	22.46	75.46	24.85	14.79	52.10	84.87	100.00	18.11	18.72	37.98	15.24	15.62
Score	1.00	-0.34	1.00	1.00	1.00	-0.22	-0.75	-0.25	1.00	0.25	1.00	1.00	0.25	1.00	1.00	-0.15	0.25
Ion-type	y_2		c_3	$z'{++}_{12}$	$c{++}_{17}$				c_{12}	c'_{12}	$c{++}_{23}$	$z'{++}_{22}$	$y{++}_{22}$	$z'{++}_{25}$	c_{13}		c'_{18}
Delta Da	-0.31		0.01	-0.12	-0.51				-0.17	0.08	0.26	0.21	0.53	0.61	-0.29		0.63
	$z'{++}_4$																
	0.71																

Peak 161



assignment



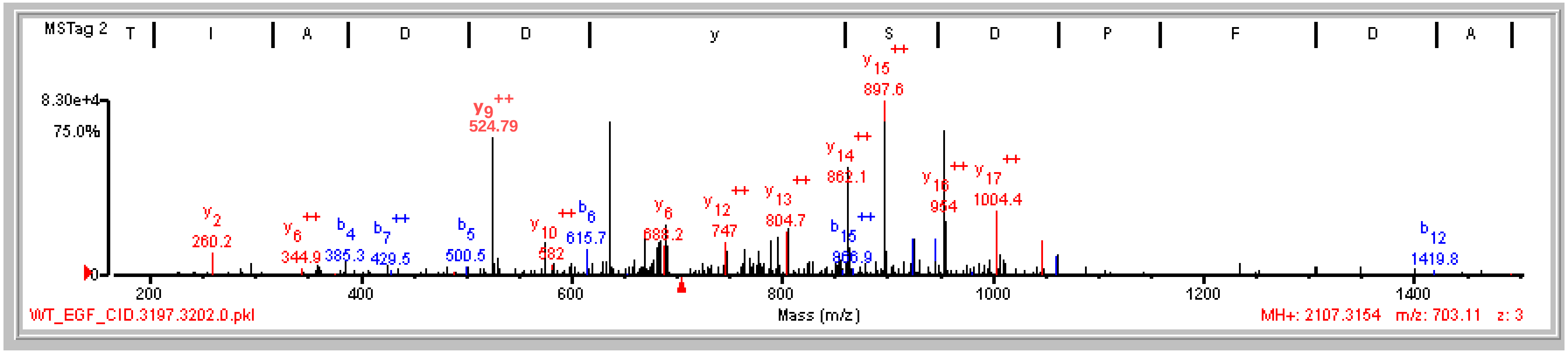


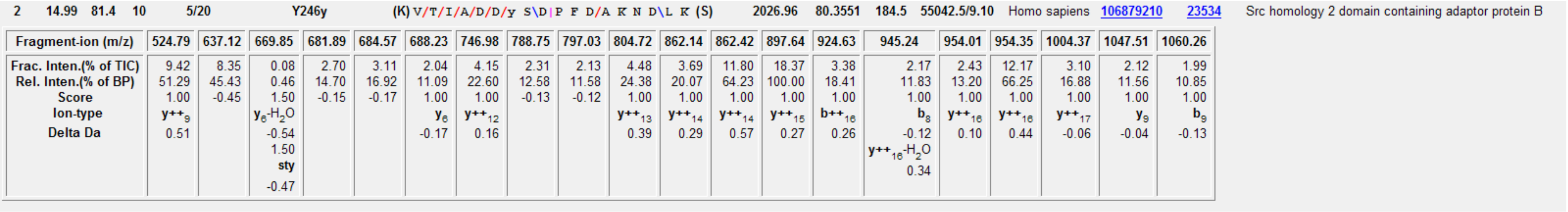
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.97	81.0	14	6/25	Y246y	(K) D/K\V/T\I\A/D|D\y\S|D P\F|D/A|K/N|D L K (S)	2270.08	81.6959	735.4	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	248.86	261.65	359.38	461.27	473.21	574.60	601.34	672.50	760.53	788.66	853.93	876.43
Frac. Inten.(% of TIC)	2.95	2.66	6.02	2.54	2.64	4.09	3.42	3.74	5.30	3.10	5.19	3.09
Rel. Inten.(% of BP)	35.30	31.78	72.04	30.42	31.54	48.90	40.87	44.80	63.36	37.08	62.09	37.00
Score	-0.35	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type		c_2	z'_3	c_4	$c3+_{12}$ z'_4	c_5 $y{+}{+}{+}_{14}$ $z''{+}{+}_{10}$	z'_5	z'_6	c_7	z''_7	$z'{+}{+}_{14}$	$c{+}{+}_{15}$ c'_8
Delta Da		0.49	0.17	-0.00	0.01 -0.04	0.24 -0.30 0.31	-0.00	0.12	0.11	0.25	0.09	0.57 -0.02

Fragment-ion (m/z)	880.12	997.56	1005.05	1118.67	1205.53	1281.88	1565.61	1593.11	1702.95	1707.43	1751.98	1755.37	1763.26
Frac. Inten.(% of TIC)	3.15	5.68	3.75	6.06	4.89	2.60	4.56	8.36	3.31	2.86	3.02	4.39	2.61
Rel. Inten.(% of BP)	37.73	68.00	44.84	72.44	58.49	31.12	54.57	100.00	39.63	34.18	36.17	52.56	31.28
Score	-0.38	1.00	0.25	1.00	1.00	-0.31	0.25	0.25	-0.40	1.00	0.25	-0.53	-0.31
Ion-type		$c{+}{+}_{17}$ $z''{+}{+}_{17}$	$y{+}{+}_{17}$	c_9 $y{+}{+}_{19}$	c_{10}		c'_{13}	z''_{13}		z'_{14}	c'_{15}		
Delta Da		0.63 0.63	0.62	0.19 0.66	0.02		-0.05	0.46		0.76	0.25		

Peak 162



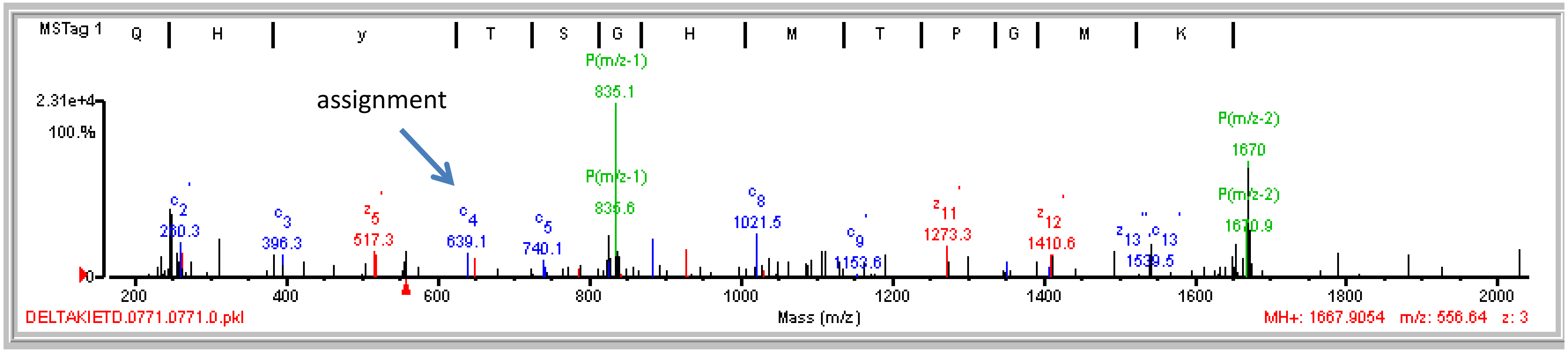


2 14.99 81.4 10 5/20 Y246y (K) V/T/I/A/D/D/y S\D|P F D/A K N D\L K (S) 2026.96 80.3551 184.5 55042.5/9.10 Homo sapiens 106879210 23534 Src homology 2 domain containing adaptor protein B

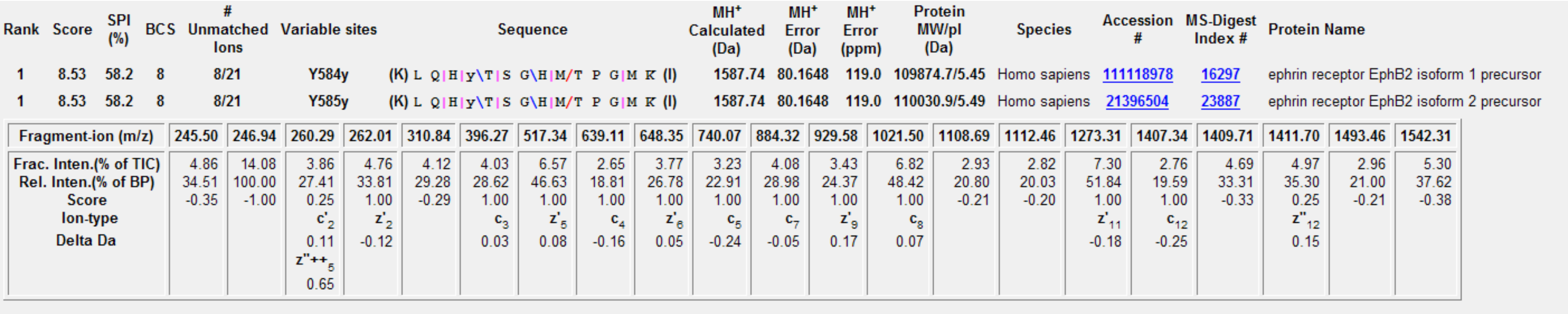
Fragment-ion (m/z)	524.79	637.12	669.85	681.89	684.57	688.23	746.98	788.75	797.03	804.72
Frac. Inten.(% of TIC)	9.42	8.35	0.08	2.70	3.11	2.04	4.15	2.31	2.13	4.48
Rel. Inten.(% of BP)	51.29	45.43	0.46	14.70	16.92	11.09	22.60	12.58	11.58	24.38
Score	1.00	-0.45	1.50	-0.15	-0.17	1.00	1.00	-0.13	-0.12	1.00
Ion-type	y++_{9}		$\text{y}_{6}\text{-H}_2\text{O}$			y_{6}	y++_{12}			y++_{13}
Delta Da	0.51		-0.54			-0.17	0.16			0.39
			1.50							
			sty							
			-0.47							

Fragment-ion (m/z)	862.14	862.42	897.64	924.63	945.24	954.01	954.35	1004.37	1047.51	1060.26
Frac. Inten.(% of TIC)	3.69	11.80	18.37	3.38	2.17	2.43	12.17	3.10	2.12	1.99
Rel. Inten.(% of BP)	20.07	64.23	100.00	18.41	11.83	13.20	66.25	16.88	11.56	10.85
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y++_{14}	y++_{14}	y++_{15}	b++_{16}	b_{8}	y++_{16}	y++_{16}	y++_{17}	y_{9}	b_{9}
Delta Da	0.29	0.57	0.27	0.26	-0.12	0.10	0.44	-0.06	-0.04	-0.13
					$\text{y++}_{16}\text{-H}_2\text{O}$					
					0.34					

Peak 163



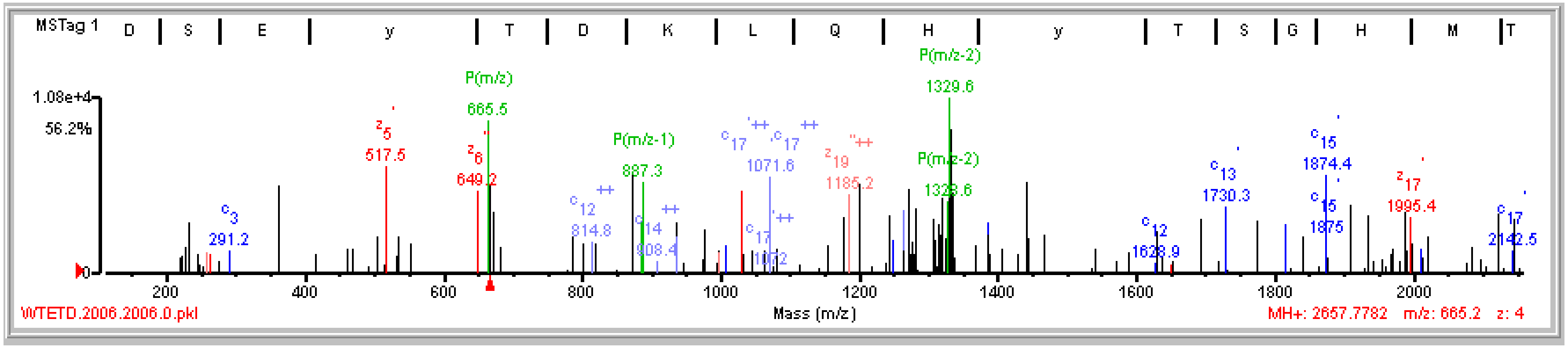
assignment

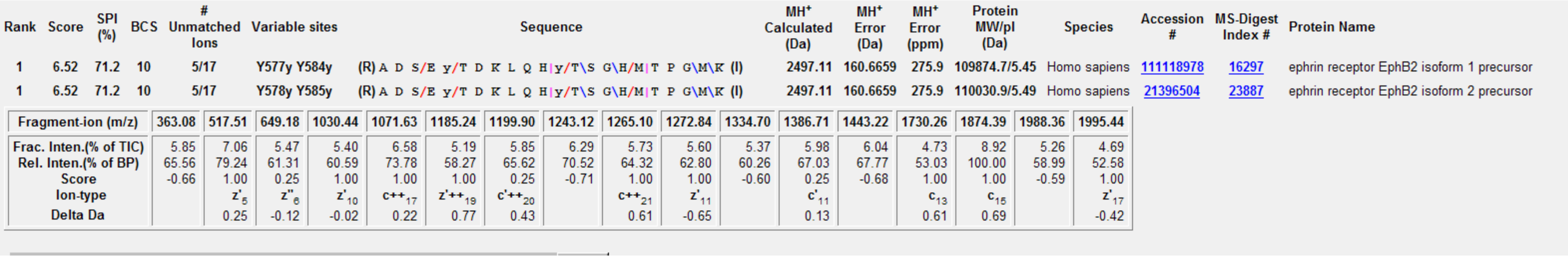


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.53	58.2	8	8/21	Y584y	(K) L Q|H|y\T|S G\H|M/T P G|M K (I)	1587.74	80.1648	119.0	109874.7/5.45	Homo sapiens	111118978	16297	ephrin receptor EphB2 isoform 1 precursor
1	8.53	58.2	8	8/21	Y585y	(K) L Q|H|y\T|S G\H|M/T P G|M K (I)	1587.74	80.1648	119.0	110030.9/5.49	Homo sapiens	21396504	23887	ephrin receptor EphB2 isoform 2 precursor

Fragment-ion (m/z)	245.50	246.94	260.29	262.01	310.84	396.27	517.34	639.11	648.35	740.07	884.32	929.58	1021.50	1108.69	1112.46	1273.31	1407.34	1409.71	1411.70	1493.46	1542.31
Frac. Inten.(% of TIC)	4.86	14.08	3.86	4.76	4.12	4.03	6.57	2.65	3.77	3.23	4.08	3.43	6.82	2.93	2.82	7.30	2.76	4.69	4.97	2.96	5.30
Rel. Inten.(% of BP)	34.51	100.00	27.41	33.81	29.28	28.62	46.63	18.81	26.78	22.91	28.98	24.37	48.42	20.80	20.03	51.84	19.59	33.31	35.30	21.00	37.62
Score	-0.35	-1.00	0.25	1.00	-0.29	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.21	-0.20	1.00	1.00	-0.33	0.25	-0.21	-0.38
Ion-type			c'_2	z'_2		c_3	z'_5	c_4	z'_6	c_5	c_7	z'_9	c_8			z'_{11}	c_{12}		z''_{12}		
Delta Da			0.11 $z''++_5$ 0.65	-0.12		0.03	0.08	-0.16	0.05	-0.24	-0.05	0.17	0.07			-0.18	-0.25		0.15		

Peak 164

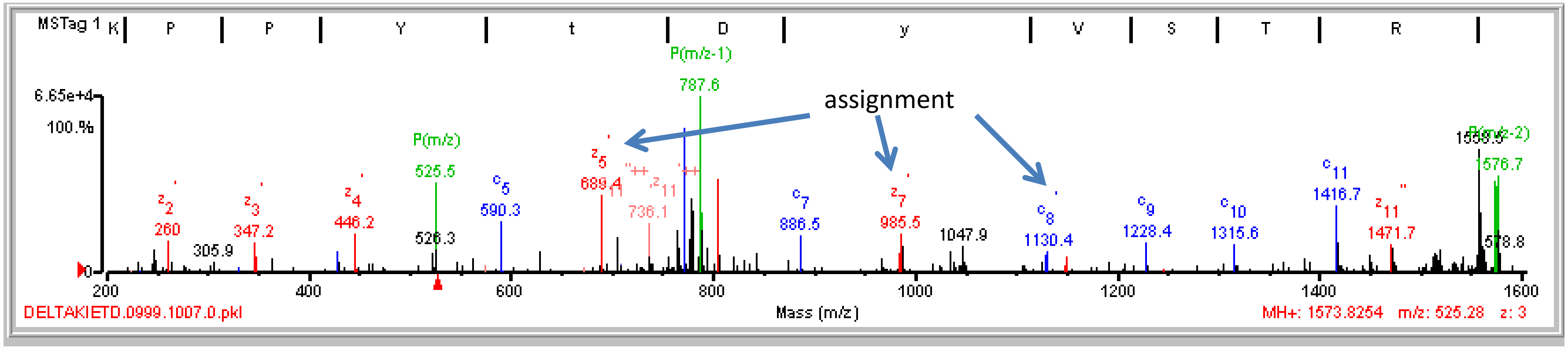




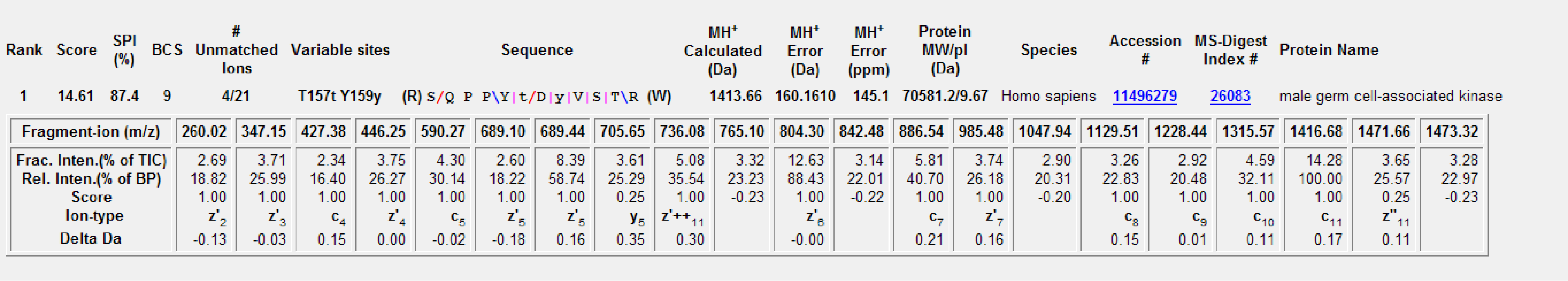
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.52	71.2	10	5/17	Y577y Y584y	(R) A D S/E y/T D K L Q H|y/T\S G\H/M|T P G\M\K (I)	2497.11	160.6659	275.9	109874.7/5.45	Homo sapiens	111118978	16297	ephrin receptor EphB2 isoform 1 precursor
1	6.52	71.2	10	5/17	Y578y Y585y	(R) A D S/E y/T D K L Q H|y/T\S G\H/M|T P G\M\K (I)	2497.11	160.6659	275.9	110030.9/5.49	Homo sapiens	21396504	23887	ephrin receptor EphB2 isoform 2 precursor

Fragment-ion (m/z)	363.08	517.51	649.18	1030.44	1071.63	1185.24	1199.90	1243.12	1265.10	1272.84	1334.70	1386.71	1443.22	1730.26	1874.39	1988.36	1995.44
Frac. Inten.(% of TIC)	5.85	7.06	5.47	5.40	6.58	5.19	5.85	6.29	5.73	5.60	5.37	5.98	6.04	4.73	8.92	5.26	4.69
Rel. Inten.(% of BP)	65.56	79.24	61.31	60.59	73.78	58.27	65.62	70.52	64.32	62.80	60.26	67.03	67.77	53.03	100.00	58.99	52.58
Score	-0.66	1.00	0.25	1.00	1.00	1.00	0.25	-0.71	1.00	1.00	-0.60	0.25	-0.68	1.00	1.00	-0.59	1.00
Ion-type		z'_{5}	z''_{6}	z'_{10}	$c{++}_{17}$	$z'{++}_{19}$	$c'{++}_{20}$		$c{++}_{21}$	z'_{11}		c'_{11}		c_{13}	c_{15}		z'_{17}
Delta Da		0.25	-0.12	-0.02	0.22	0.77	0.43		0.61	-0.65		0.13		0.61	0.69		-0.42

Peak 165



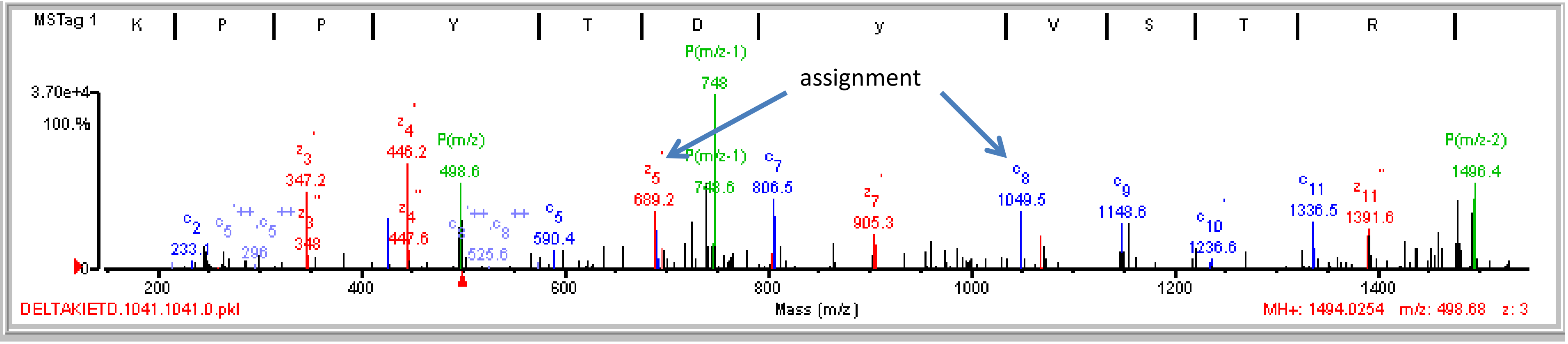
assignment



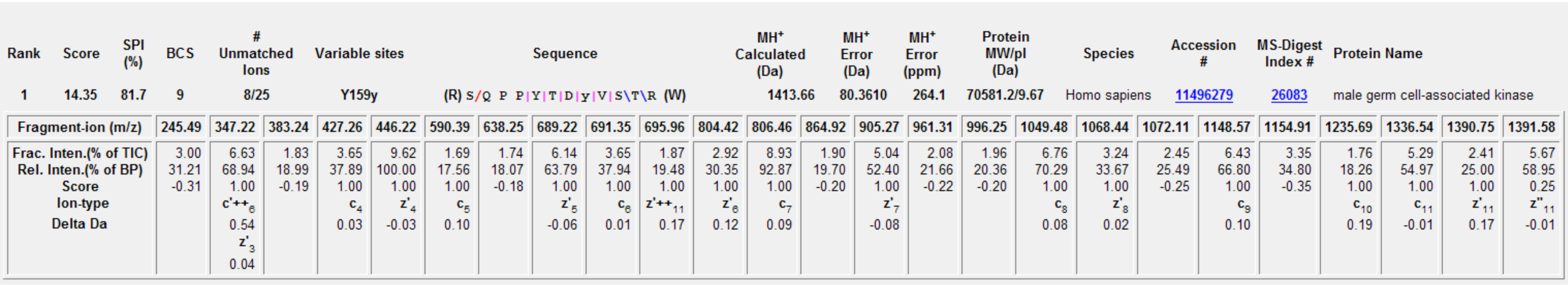
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.61	87.4	9	4/21	T157t Y159y	(R) S/Q P P\Y|t/D|y|V|S|T\R (W)	1413.66	160.1610	145.1	70581.2/9.67	Homo sapiens	11496279	26083	male germ cell-associated kinase

Fragment-ion (m/z)	260.02	347.15	427.38	446.25	590.27	689.10	689.44	705.65	736.08	765.10	804.30	842.48	886.54	985.48	1047.94	1129.51	1228.44	1315.57	1416.68	1471.66	1473.32
Frac. Inten.(% of TIC)	2.69	3.71	2.34	3.75	4.30	2.60	8.39	3.61	5.08	3.32	12.63	3.14	5.81	3.74	2.90	3.26	2.92	4.59	14.28	3.65	3.28
Rel. Inten.(% of BP)	18.82	25.99	16.40	26.27	30.14	18.22	58.74	25.29	35.54	23.23	88.43	22.01	40.70	26.18	20.31	22.83	20.48	32.11	100.00	25.57	22.97
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.23	1.00	-0.22	1.00	1.00	-0.20	1.00	1.00	1.00	1.00	0.25	-0.23
Ion-type	z'_2	z'_3	c_4	z'_4	c_5	z'_5	z'_5	y_5	$z'{++}_{11}$		z'_6		c_7	z'_7		c_8	c_9	c_{10}	c_{11}	z''_{11}	
Delta Da	-0.13	-0.03	0.15	0.00	-0.02	-0.18	0.16	0.35	0.30		-0.00		0.21	0.16		0.15	0.01	0.11	0.17	0.11	

Peak 166



assignment

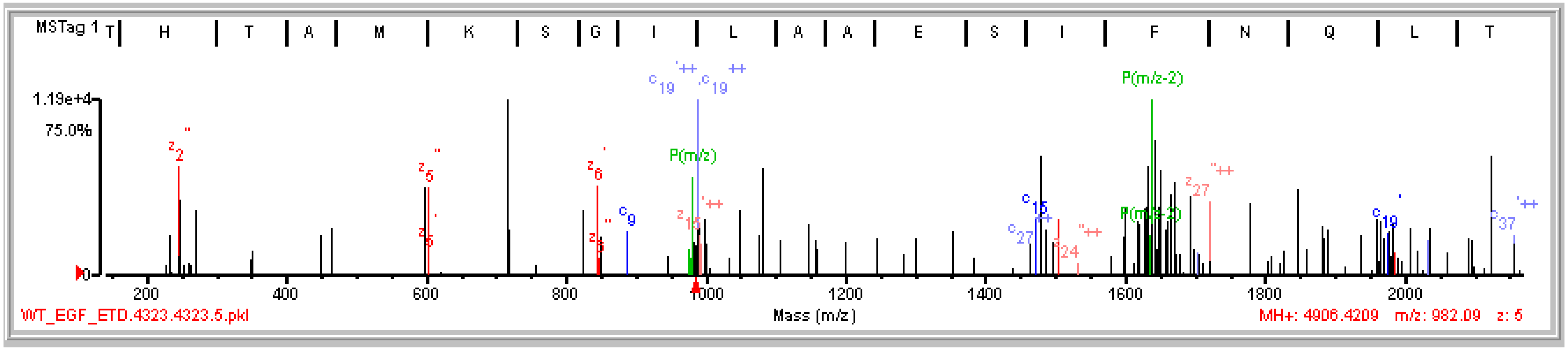


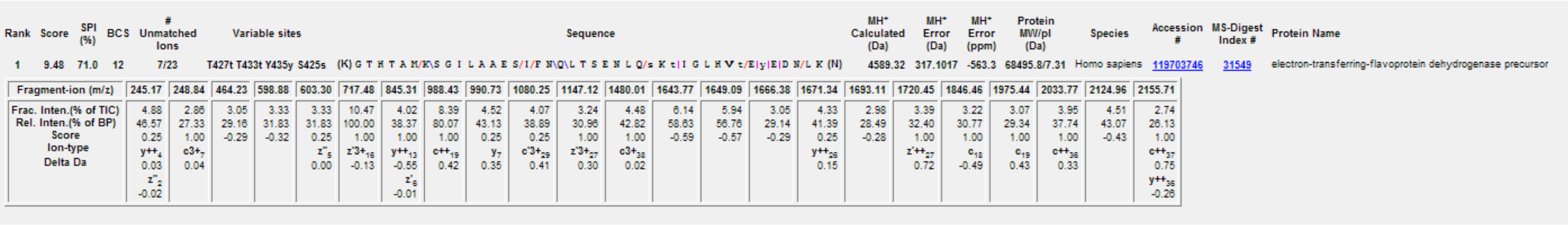
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.35	81.7	9	8/25	Y159y	(R) S/Q P P|Y|T|D|y|V|S\T\R (W)	1413.66	80.3610	264.1	70581.2/9.67	Homo sapiens	11496279	26083	male germ cell-associated kinase

Fragment-ion (m/z)	245.49	347.22	383.24	427.26	446.22	590.39	638.25	689.22	691.35	695.96	804.42	806.46
Frac. Inten.(% of TIC)	3.00	6.63	1.83	3.65	9.62	1.69	1.74	6.14	3.65	1.87	2.92	8.93
Rel. Inten.(% of BP)	31.21	68.94	18.99	37.89	100.00	17.56	18.07	63.79	37.94	19.48	30.35	92.87
Score	-0.31	1.00	-0.19	1.00	1.00	1.00	-0.18	1.00	1.00	1.00	1.00	1.00
Ion-type		$c'{++}_6$		c_4	z'_4	c_5		z'_5	c_6	$z'{++}_{11}$	z'_6	c_7
Delta Da		0.54 z'_3 0.04		0.03	-0.03	0.10		-0.06	0.01	0.17	0.12	0.09

Fragment-ion (m/z)	864.92	905.27	961.31	996.25	1049.48	1068.44	1072.11	1148.57	1154.91	1235.69	1336.54	1390.75	1391.58
Frac. Inten.(% of TIC)	1.90	5.04	2.08	1.96	6.76	3.24	2.45	6.43	3.35	1.76	5.29	2.41	5.67
Rel. Inten.(% of BP)	19.70	52.40	21.66	20.36	70.29	33.67	25.49	66.80	34.80	18.26	54.97	25.00	58.95
Score	-0.20	1.00	-0.22	-0.20	1.00	1.00	-0.25	1.00	-0.35	1.00	1.00	1.00	0.25
Ion-type		z'_7			c_8	z'_8		c_9		c_{10}	c_{11}	z'_{11}	z''_{11}
Delta Da		-0.08			0.08	0.02		0.10		0.19	-0.01	0.17	-0.01

Peak 167



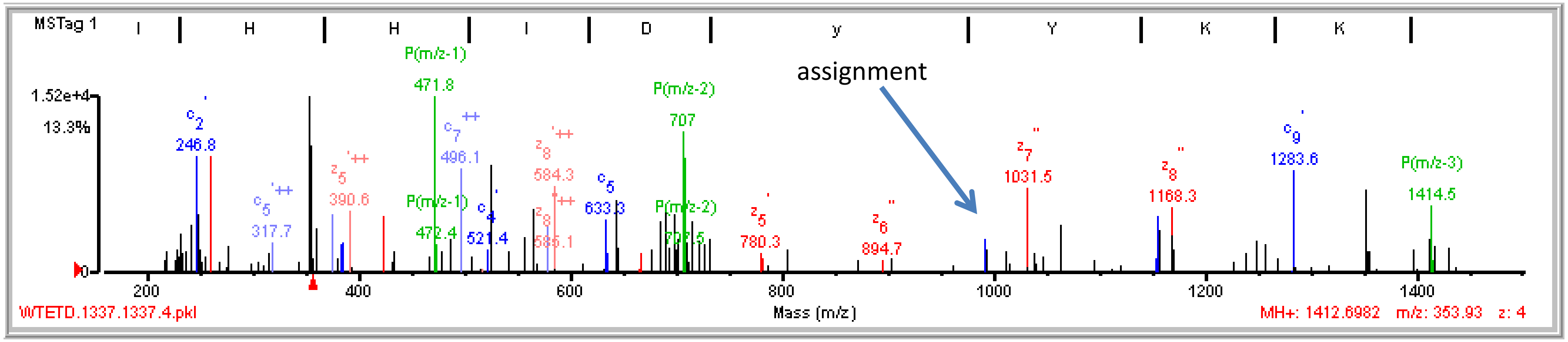


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.48	71.0	12	7/23	T427t T433t Y435y S425s	(K) G T H T A M/K\S G I L A A E S/I/F N\Q\L T S E N L Q/s K t|I G L H V t/E|y|E|D N/L K (N)	4589.32	317.1017	-563.3	68495.8/7.31	Homo sapiens	119703746	31549	electron-transferring-flavoprotein dehydrogenase precursor

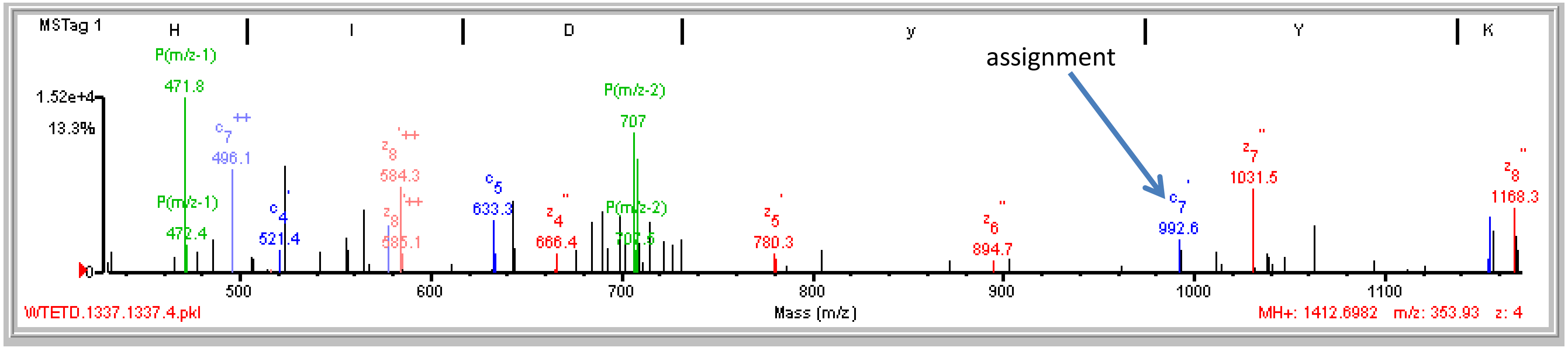
Fragment-ion (m/z)	245.17	248.84	464.23	598.88	603.30	717.48	845.31	988.43	990.73	1080.25	1147.12	1480.01
Frac. Inten.(% of TIC)	4.88	2.86	3.05	3.33	3.33	10.47	4.02	8.39	4.52	4.07	3.24	4.48
Rel. Inten.(% of BP)	46.57	27.33	29.16	31.83	31.83	100.00	38.37	80.07	43.13	38.89	30.96	42.82
Score	0.25	1.00	-0.29	-0.32	0.25	1.00	1.00	1.00	0.25	0.25	1.00	1.00
Ion-type	$y{++}_4$ z''_2	$c3+_7$			z''_5	$z'3+_{16}$	$y{++}_{13}$ z'_6	$c{++}_{19}$	y_7	$c'3+_{29}$	$z'3+_{27}$	$c3+_{38}$
Delta Da	0.03 -0.02	0.04			0.00	-0.13	-0.55 -0.01	0.42	0.35	0.41	0.30	0.02

Fragment-ion (m/z)	1643.77	1649.09	1666.38	1671.34	1693.11	1720.45	1846.46	1975.44	2033.77	2124.96	2155.71
Frac. Inten.(% of TIC)	6.14	5.94	3.05	4.33	2.98	3.39	3.22	3.07	3.95	4.51	2.74
Rel. Inten.(% of BP)	58.63	56.76	29.14	41.39	28.49	32.40	30.77	29.34	37.74	43.07	26.13
Score	-0.59	-0.57	-0.29	0.25	-0.28	1.00	1.00	1.00	1.00	-0.43	1.00
Ion-type				$y{++}_{26}$		$z'{++}_{27}$	c_{18}	c_{19}	$c{++}_{36}$		$c{++}_{37}$ $y{++}_{36}$
Delta Da				0.15		0.72	-0.49	0.43	0.33		0.75 -0.26

Peak 168



assignment



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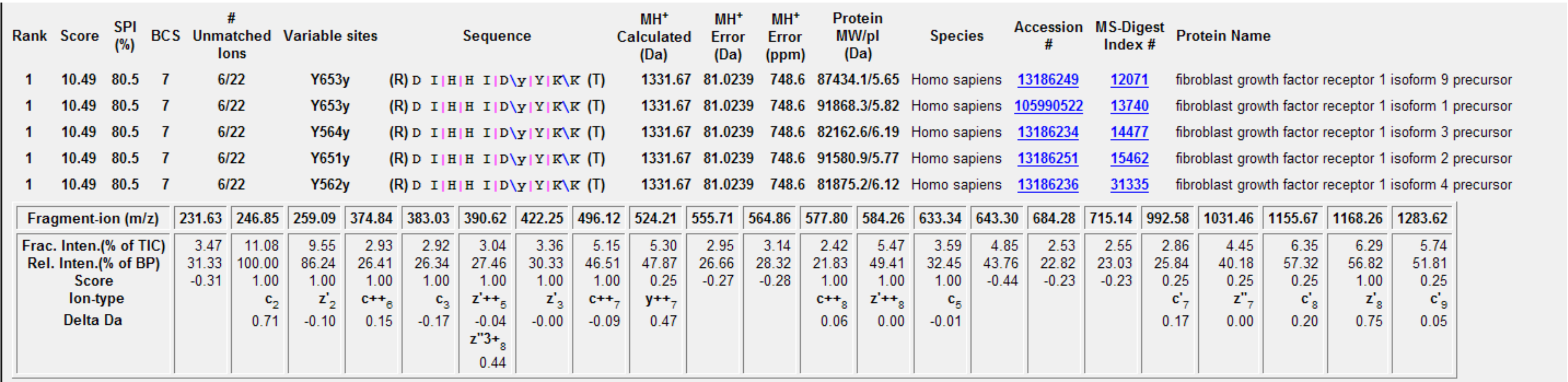
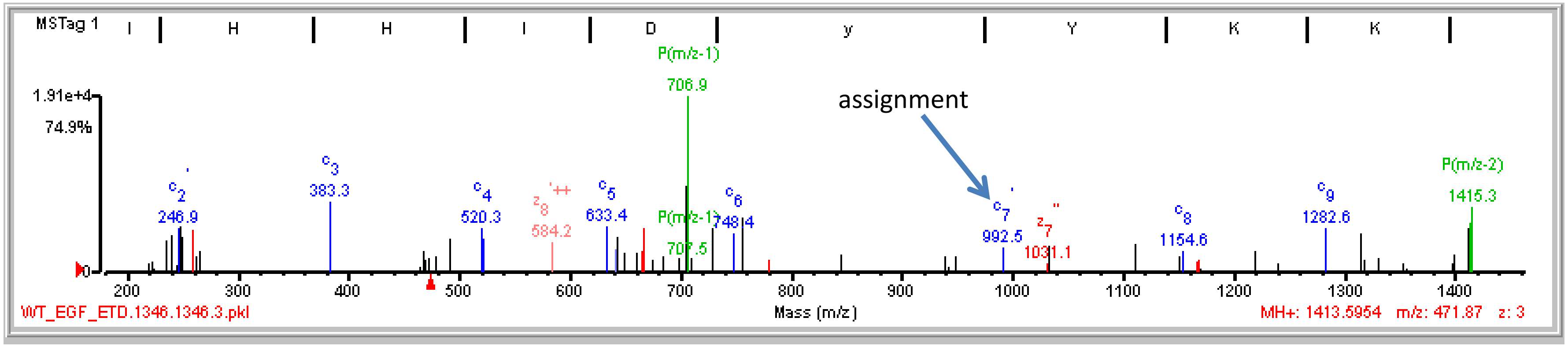


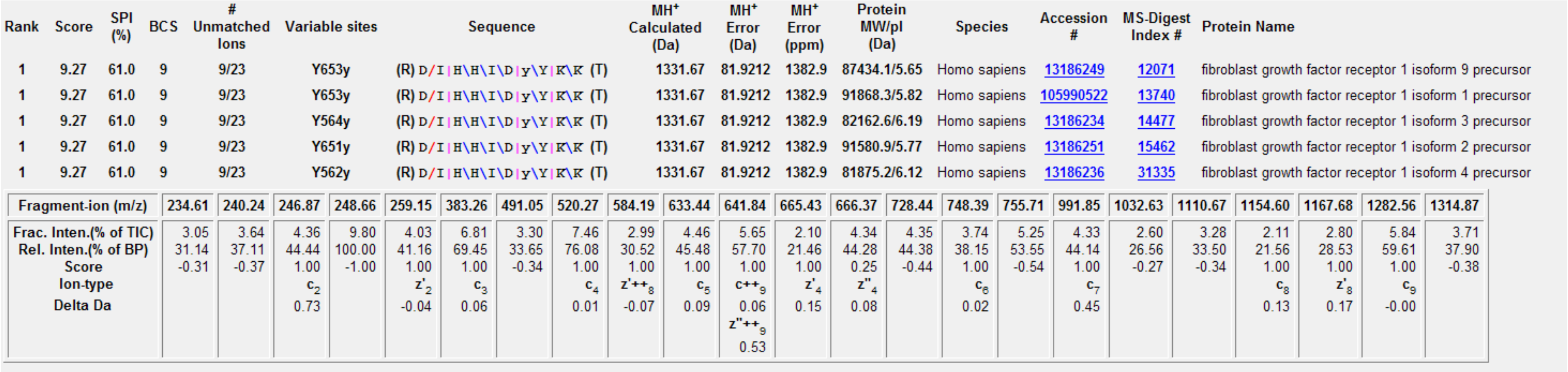
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.49	80.5	7	6/22	Y653y	(R) D I|H|H I|D\y|Y|K\K (T)	1331.67	81.0239	748.6	87434.1/5.65	Homo sapiens	13186249	12071	fibroblast growth factor receptor 1 isoform 9 precursor
1	10.49	80.5	7	6/22	Y653y	(R) D I|H|H I|D\y|Y|K\K (T)	1331.67	81.0239	748.6	91868.3/5.82	Homo sapiens	105990522	13740	fibroblast growth factor receptor 1 isoform 1 precursor
1	10.49	80.5	7	6/22	Y564y	(R) D I|H|H I|D\y|Y|K\K (T)	1331.67	81.0239	748.6	82162.6/6.19	Homo sapiens	13186234	14477	fibroblast growth factor receptor 1 isoform 3 precursor
1	10.49	80.5	7	6/22	Y651y	(R) D I|H|H I|D\y|Y|K\K (T)	1331.67	81.0239	748.6	91580.9/5.77	Homo sapiens	13186251	15462	fibroblast growth factor receptor 1 isoform 2 precursor
1	10.49	80.5	7	6/22	Y562y	(R) D I|H|H I|D\y|Y|K\K (T)	1331.67	81.0239	748.6	81875.2/6.12	Homo sapiens	13186236	31335	fibroblast growth factor receptor 1 isoform 4 precursor

Fragment-ion (m/z)	231.63	246.85	259.09	374.84	383.03	390.62	422.25	496.12	524.21	555.71	564.86	577.80	584.26	633.34	643.30	684.28	715.14	992.58	1031.46	1155.67	1168.26	1283.62
Frac. Inten.(% of TIC)	3.47	11.08	9.55	2.93	2.92	3.04	3.36	5.15	5.30	2.95	3.14	2.42	5.47	3.59	4.85	2.53	2.55	2.86	4.45	6.35	6.29	5.74
Rel. Inten.(% of BP)	31.33	100.00	86.24	26.41	26.34	27.46	30.33	46.51	47.87	26.66	28.32	21.83	49.41	32.45	43.76	22.82	23.03	25.84	40.18	57.32	56.82	51.81
Score	-0.31	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.27	-0.28	1.00	1.00	1.00	-0.44	-0.23	-0.23	0.25	0.25	0.25	1.00	0.25
Ion-type		c_2	z'_2	c++_6	c_3	z'++_5 z''3+_8	z'_3	c++_7	y++_7			c++_8	z'++_8	c_5				c'_7	z''_7	c'_8	z'_8	c'_9
Delta Da		0.71	-0.10	0.15	-0.17	-0.04 0.44	-0.00	-0.09	0.47			0.06	0.00	-0.01				0.17	0.00	0.20	0.75	0.05

Peak 170



assignment

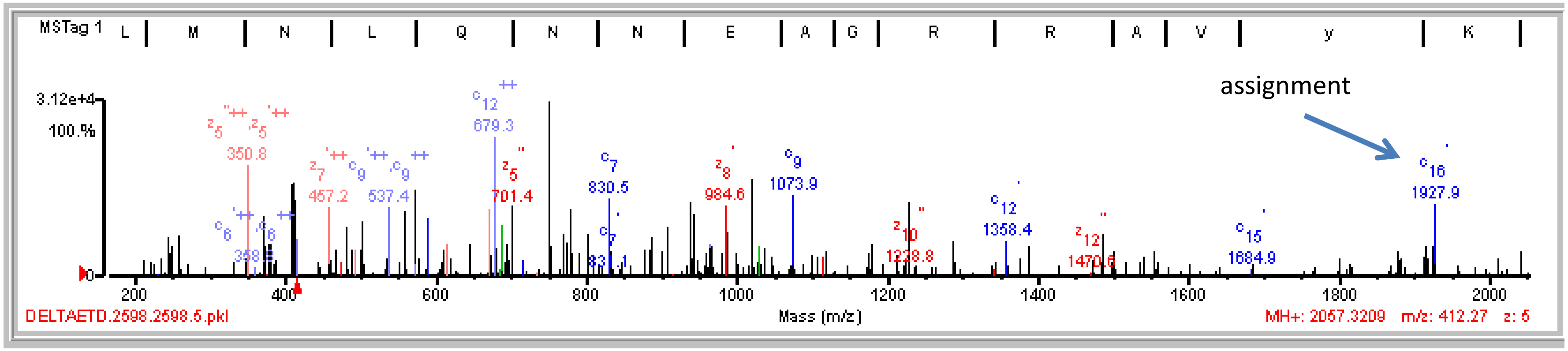


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.27	61.0	9	9/23	Y653y	(R) D/I|H\H\I\D|y\Y|K\K (T)	1331.67	81.9212	1382.9	87434.1/5.65	Homo sapiens	13186249	12071	fibroblast growth factor receptor 1 isoform 9 precursor
1	9.27	61.0	9	9/23	Y653y	(R) D/I|H\H\I\D|y\Y|K\K (T)	1331.67	81.9212	1382.9	91868.3/5.82	Homo sapiens	105990522	13740	fibroblast growth factor receptor 1 isoform 1 precursor
1	9.27	61.0	9	9/23	Y564y	(R) D/I|H\H\I\D|y\Y|K\K (T)	1331.67	81.9212	1382.9	82162.6/6.19	Homo sapiens	13186234	14477	fibroblast growth factor receptor 1 isoform 3 precursor
1	9.27	61.0	9	9/23	Y651y	(R) D/I|H\H\I\D|y\Y|K\K (T)	1331.67	81.9212	1382.9	91580.9/5.77	Homo sapiens	13186251	15462	fibroblast growth factor receptor 1 isoform 2 precursor
1	9.27	61.0	9	9/23	Y562y	(R) D/I|H\H\I\D|y\Y|K\K (T)	1331.67	81.9212	1382.9	81875.2/6.12	Homo sapiens	13186236	31335	fibroblast growth factor receptor 1 isoform 4 precursor

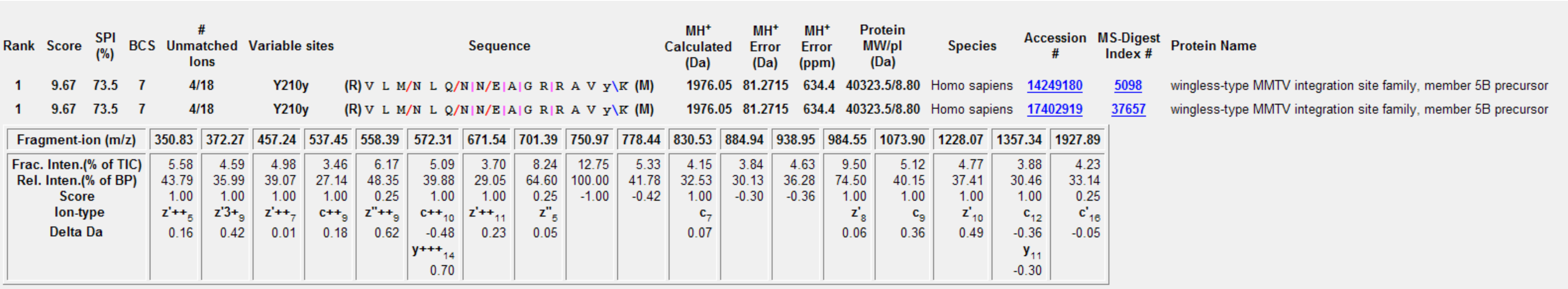
Fragment-ion (m/z)	234.61	240.24	246.87	248.66	259.15	383.26	491.05	520.27	584.19	633.44	641.84
Frac. Inten.(% of TIC)	3.05	3.64	4.36	9.80	4.03	6.81	3.30	7.46	2.99	4.46	5.65
Rel. Inten.(% of BP)	31.14	37.11	44.44	100.00	41.16	69.45	33.65	76.08	30.52	45.48	57.70
Score	-0.31	-0.37	1.00	-1.00	1.00	1.00	-0.34	1.00	1.00	1.00	1.00
Ion-type			c_2		z'_2	c_3		c_4	$z'{++}_8$	c_5	$c{++}_9$ $z''{++}_9$
Delta Da			0.73		-0.04	0.06		0.01	-0.07	0.09	0.06 0.53

Fragment-ion (m/z)	665.43	666.37	728.44	748.39	755.71	991.85	1032.63	1110.67	1154.60	1167.68	1282.56	1314.87
Frac. Inten.(% of TIC)	2.10	4.34	4.35	3.74	5.25	4.33	2.60	3.28	2.11	2.80	5.84	3.71
Rel. Inten.(% of BP)	21.46	44.28	44.38	38.15	53.55	44.14	26.56	33.50	21.56	28.53	59.61	37.90
Score	1.00	0.25	-0.44	1.00	-0.54	1.00	-0.27	-0.34	1.00	1.00	1.00	-0.38
Ion-type	z'_4	z''_4		c_6		c_7			c_8	z'_8	c_9	
Delta Da	0.15	0.08		0.02		0.45			0.13	0.17	-0.00	

Peak 171



assignment

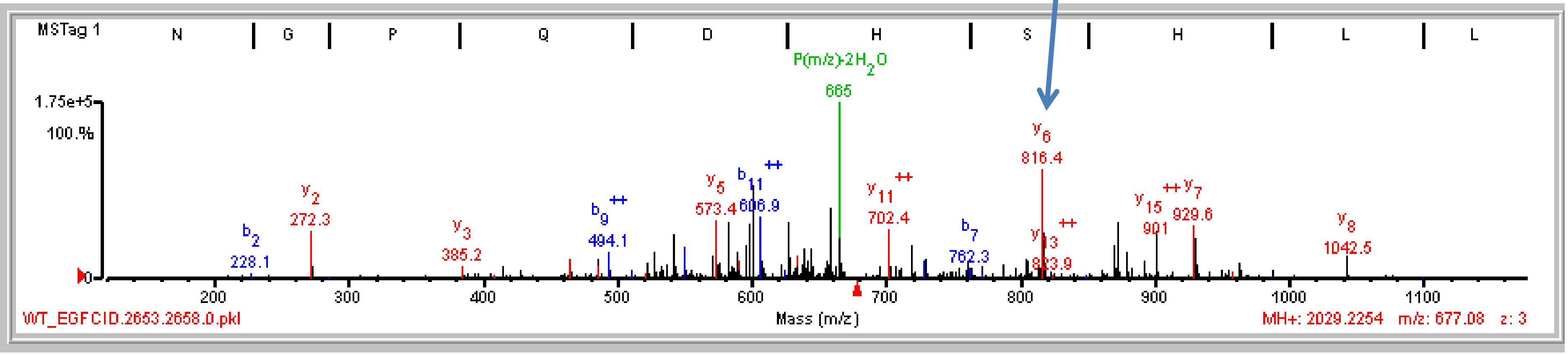


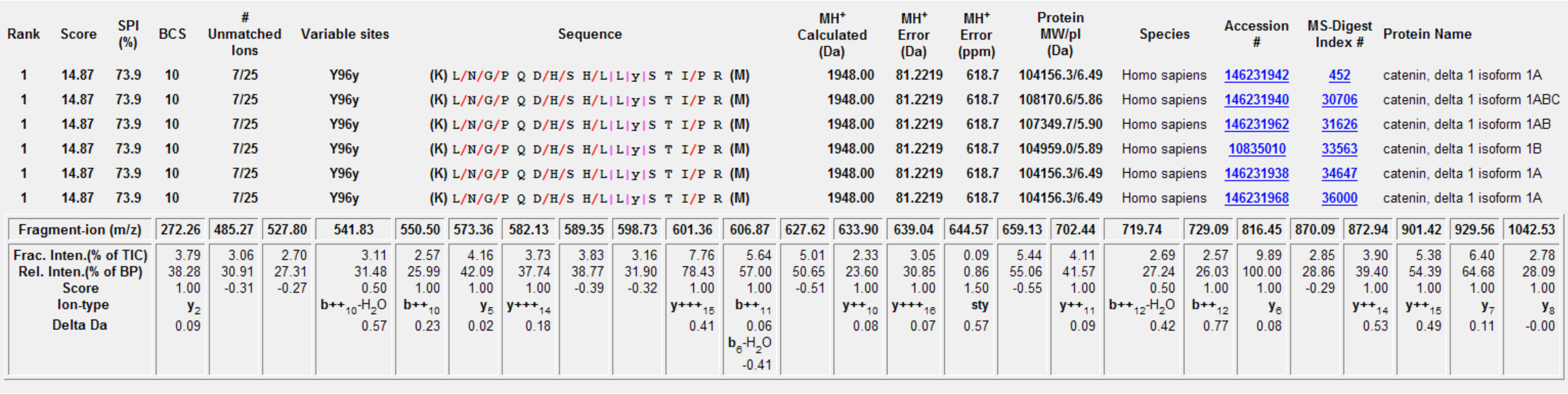
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.67	73.5	7	4/18	Y210y	(R) V L M/N L Q/N|N/E|A|G R|R A V y\K (M)	1976.05	81.2715	634.4	40323.5/8.80	Homo sapiens	14249180	5098	wingless-type MMTV integration site family, member 5B precursor
1	9.67	73.5	7	4/18	Y210y	(R) V L M/N L Q/N|N/E|A|G R|R A V y\K (M)	1976.05	81.2715	634.4	40323.5/8.80	Homo sapiens	17402919	37657	wingless-type MMTV integration site family, member 5B precursor

Fragment-ion (m/z)	350.83	372.27	457.24	537.45	558.39	572.31	671.54	701.39	750.97	778.44	830.53	884.94	938.95	984.55	1073.90	1228.07	1357.34	1927.89
Frac. Inten.(% of TIC)	5.58	4.59	4.98	3.46	6.17	5.09	3.70	8.24	12.75	5.33	4.15	3.84	4.63	9.50	5.12	4.77	3.88	4.23
Rel. Inten.(% of BP)	43.79	35.99	39.07	27.14	48.35	39.88	29.05	64.60	100.00	41.78	32.53	30.13	36.28	74.50	40.15	37.41	30.46	33.14
Score	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	-1.00	-0.42	1.00	-0.30	-0.36	1.00	1.00	1.00	1.00	0.25
Ion-type	$z'{++}_{5}$	$z'3{+}_{9}$	$z'{++}_{7}$	$c{++}_{9}$	$z''{++}_{9}$	$c{++}_{10}$	$z'{++}_{11}$	z''_{5}			c_{7}			z'_{8}	c_{9}	z'_{10}	c_{12}	c'_{16}
Delta Da	0.16	0.42	0.01	0.18	0.62	-0.48	0.23	0.05			0.07			0.06	0.36	0.49	-0.36	-0.05
						$y{+++}_{14}$											y_{11}	
						0.70											-0.30	

Peak 172

assignment



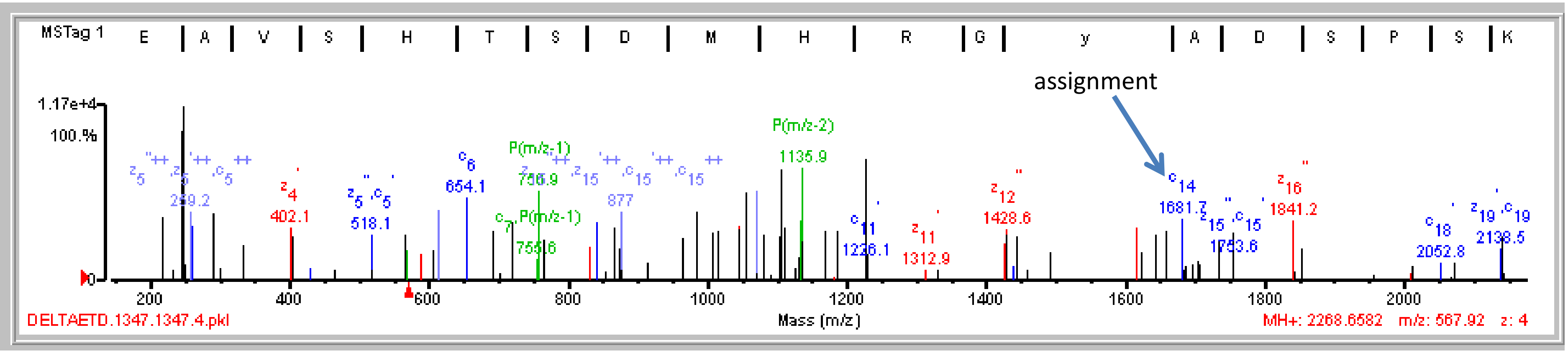


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	104156.3/6.49	Homo sapiens	146231942	452	catenin, delta 1 isoform 1A
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	108170.6/5.86	Homo sapiens	146231940	30706	catenin, delta 1 isoform 1ABC
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	107349.7/5.90	Homo sapiens	146231962	31626	catenin, delta 1 isoform 1AB
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	104959.0/5.89	Homo sapiens	10835010	33563	catenin, delta 1 isoform 1B
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	104156.3/6.49	Homo sapiens	146231938	34647	catenin, delta 1 isoform 1A
1	14.87	73.9	10	7/25	Y96y	(K) L/N/G/P Q D/H/S H/L|L|y|S T I/P R (M)	1948.00	81.2219	618.7	104156.3/6.49	Homo sapiens	146231968	36000	catenin, delta 1 isoform 1A

Fragment-ion (m/z)	272.26	485.27	527.80	541.83	550.50	573.36	582.13	589.35	598.73	601.36	606.87	627.62	633.90
Frac. Inten.(% of TIC)	3.79	3.06	2.70	3.11	2.57	4.16	3.73	3.83	3.16	7.76	5.64	5.01	2.33
Rel. Inten.(% of BP)	38.28	30.91	27.31	31.48	25.99	42.09	37.74	38.77	31.90	78.43	57.00	50.65	23.60
Score	1.00	-0.31	-0.27	0.50	1.00	1.00	1.00	-0.39	-0.32	1.00	1.00	-0.51	1.00
Ion-type	y_2			$b{++}_{10}$-H_2O	$b{++}_{10}$	y_5	$y{+}{+}{+}_{14}$			$y{+}{+}{+}_{15}$	$b{++}_{11}$ b_6-H_2O		$y{++}_{10}$
Delta Da	0.09			0.57	0.23	0.02	0.18			0.41	0.06 -0.41		0.08

Fragment-ion (m/z)	639.04	644.57	659.13	702.44	719.74	729.09	816.45	870.09	872.94	901.42	929.56	1042.53
Frac. Inten.(% of TIC)	3.05	0.09	5.44	4.11	2.69	2.57	9.89	2.85	3.90	5.38	6.40	2.78
Rel. Inten.(% of BP)	30.85	0.86	55.06	41.57	27.24	26.03	100.00	28.86	39.40	54.39	64.68	28.09
Score	1.00	1.50	-0.55	1.00	0.50	1.00	1.00	-0.29	1.00	1.00	1.00	1.00
Ion-type	$y{+}{+}{+}_{16}$	sty		$y{++}_{11}$	$b{++}_{12}$-H_2O	$b{++}_{12}$	y_6		$y{++}_{14}$	$y{++}_{15}$	y_7	y_8
Delta Da	0.07	0.57		0.09	0.42	0.77	0.08		0.53	0.49	0.11	-0.00

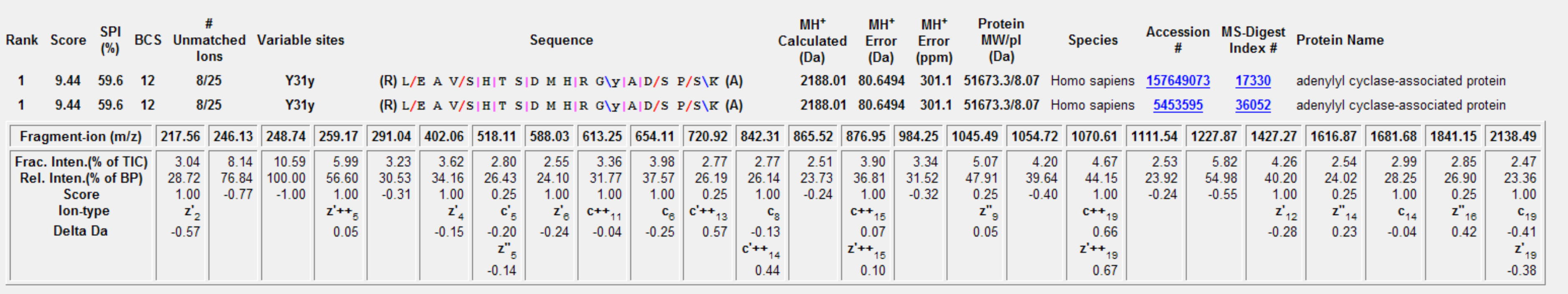
Peak 173



DELTAETD.1347.1347.4.pkl

MH+: 2268.6582 m/z: 567.92 z: 4

assignment

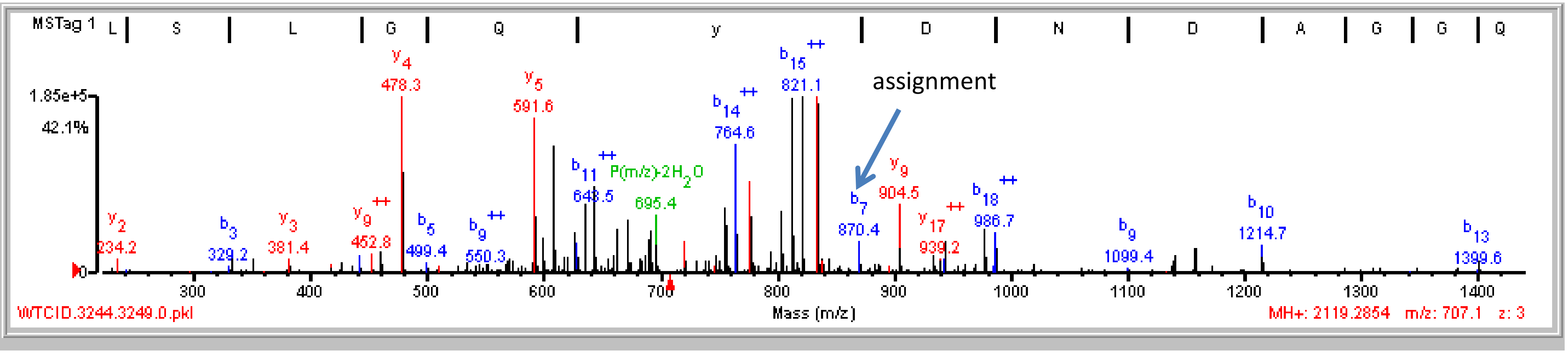


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.44	59.6	12	8/25	Y31y	(R) L/E A V/S|H|T S|D M H|R G\y|A|D/S P/S\K (A)	2188.01	80.6494	301.1	51673.3/8.07	Homo sapiens	157649073	17330	adenylyl cyclase-associated protein
1	9.44	59.6	12	8/25	Y31y	(R) L/E A V/S|H|T S|D M H|R G\y|A|D/S P/S\K (A)	2188.01	80.6494	301.1	51673.3/8.07	Homo sapiens	5453595	36052	adenylyl cyclase-associated protein

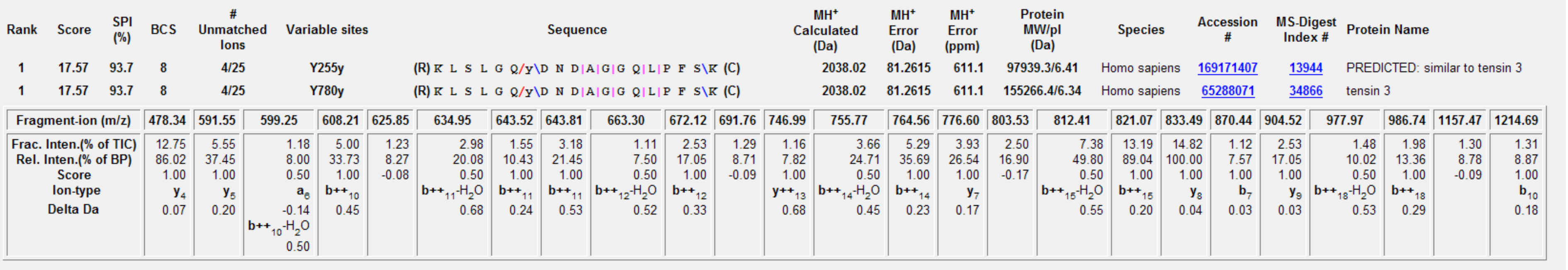
Fragment-ion (m/z)	217.56	246.13	248.74	259.17	291.04	402.06	518.11	588.03	613.25	654.11	720.92	842.31	865.52
Frac. Inten.(% of TIC)	3.04	8.14	10.59	5.99	3.23	3.62	2.80	2.55	3.36	3.98	2.77	2.77	2.51
Rel. Inten.(% of BP)	28.72	76.84	100.00	56.60	30.53	34.16	26.43	24.10	31.77	37.57	26.19	26.14	23.73
Score	1.00	-0.77	-1.00	1.00	-0.31	1.00	0.25	1.00	1.00	1.00	0.25	1.00	-0.24
Ion-type	z'_2			$z'{++}_5$		z'_4	c'_5	z'_6	$c{++}_{11}$	c_6	$c'{++}_{13}$	c_8	
Delta Da	-0.57			0.05		-0.15	-0.20	-0.24	-0.04	-0.25	0.57	-0.13	
							z''_5					$c'{++}_{14}$	
							-0.14					0.44	

Fragment-ion (m/z)	876.95	984.25	1045.49	1054.72	1070.61	1111.54	1227.87	1427.27	1616.87	1681.68	1841.15	2138.49
Frac. Inten.(% of TIC)	3.90	3.34	5.07	4.20	4.67	2.53	5.82	4.26	2.54	2.99	2.85	2.47
Rel. Inten.(% of BP)	36.81	31.52	47.91	39.64	44.15	23.92	54.98	40.20	24.02	28.25	26.90	23.36
Score	1.00	-0.32	0.25	-0.40	1.00	-0.24	-0.55	1.00	0.25	1.00	0.25	1.00
Ion-type	$c{++}_{15}$		z''_9		$c{++}_{19}$			z'_{12}	z''_{14}	c_{14}	z''_{16}	c_{19}
Delta Da	0.07		0.05		0.66			-0.28	0.23	-0.04	0.42	-0.41
	$z'{++}_{15}$				$z'{++}_{19}$							z'_{19}
	0.10				0.67							-0.38

Peak 174



assignment

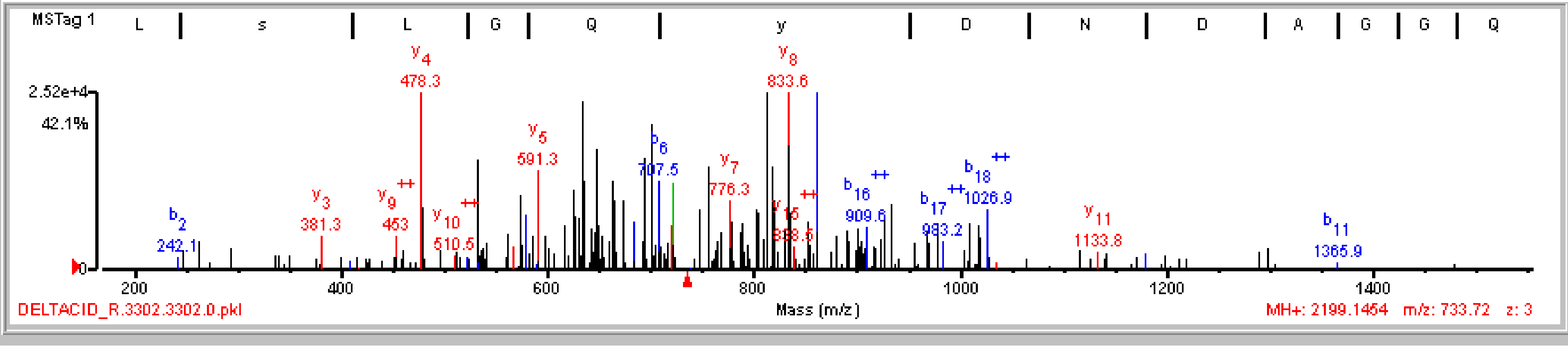


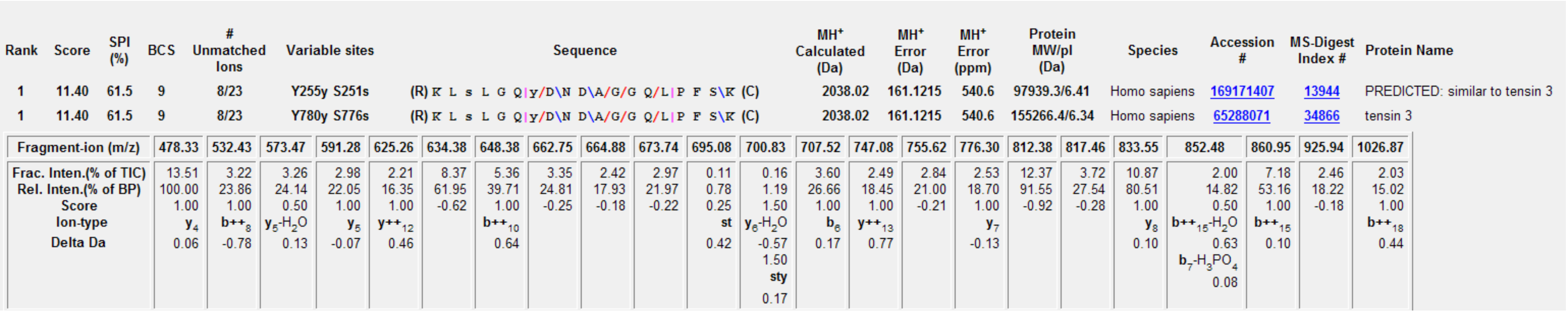
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.57	93.7	8	4/25	Y255y	(R) K L S L G Q/y\D N D|A|G|G Q|L|P F S\K (C)	2038.02	81.2615	611.1	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	17.57	93.7	8	4/25	Y780y	(R) K L S L G Q/y\D N D|A|G|G Q|L|P F S\K (C)	2038.02	81.2615	611.1	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

Fragment-ion (m/z)	478.34	591.55	599.25	608.21	625.85	634.95	643.52	643.81	663.30	672.12	691.76	746.99
Frac. Inten.(% of TIC)	12.75	5.55	1.18	5.00	1.23	2.98	1.55	3.18	1.11	2.53	1.29	1.16
Rel. Inten.(% of BP)	86.02	37.45	8.00	33.73	8.27	20.08	10.43	21.45	7.50	17.05	8.71	7.82
Score	1.00	1.00	0.50	1.00	-0.08	0.50	1.00	1.00	0.50	1.00	-0.09	1.00
Ion-type	y_4	y_5	a_6 $b{+}{+}_{10}$-H_2O	$b{+}{+}_{10}$		$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$	$b{+}{+}_{11}$	$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$		$y{+}{+}_{13}$
Delta Da	0.07	0.20	-0.14 0.50	0.45		0.68	0.24	0.53	0.52	0.33		0.68

Fragment-ion (m/z)	755.77	764.56	776.60	803.53	812.41	821.07	833.49	870.44	904.52	977.97	986.74	1157.47	1214.69
Frac. Inten.(% of TIC)	3.66	5.29	3.93	2.50	7.38	13.19	14.82	1.12	2.53	1.48	1.98	1.30	1.31
Rel. Inten.(% of BP)	24.71	35.69	26.54	16.90	49.80	89.04	100.00	7.57	17.05	10.02	13.36	8.78	8.87
Score	0.50	1.00	1.00	-0.17	0.50	1.00	1.00	1.00	1.00	0.50	1.00	-0.09	1.00
Ion-type	$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$	y_7		$b{+}{+}_{15}$-H_2O	$b{+}{+}_{15}$	y_8	b_7	y_9	$b{+}{+}_{18}$-H_2O	$b{+}{+}_{18}$		b_{10}
Delta Da	0.45	0.23	0.17		0.55	0.20	0.04	0.03	0.03	0.53	0.29		0.18

Peak 175



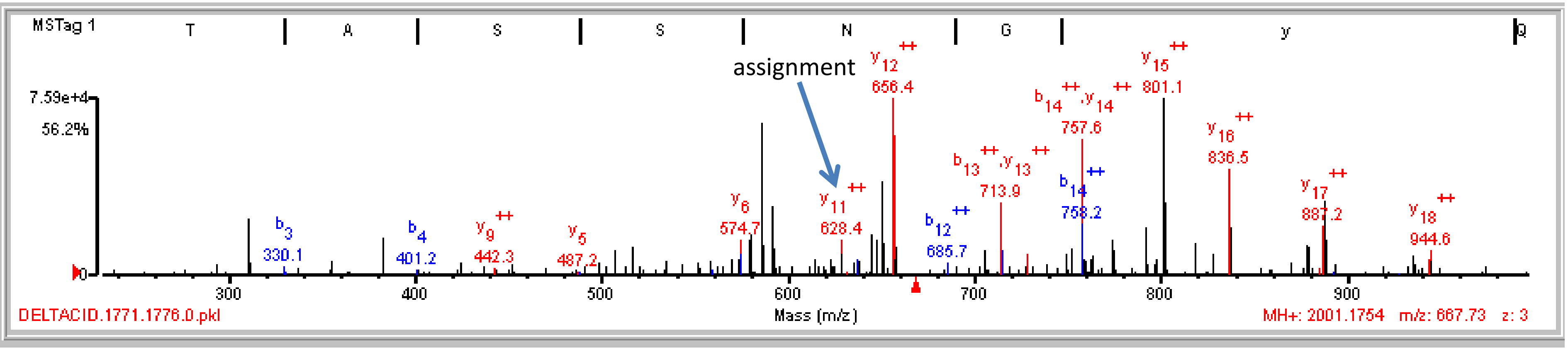


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.40	61.5	9	8/23	Y255y S251s	(R) K L s L G Q|y/D\N D\A/G/G Q/L|P F S\K (C)	2038.02	161.1215	540.6	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	11.40	61.5	9	8/23	Y780y S776s	(R) K L s L G Q|y/D\N D\A/G/G Q/L|P F S\K (C)	2038.02	161.1215	540.6	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

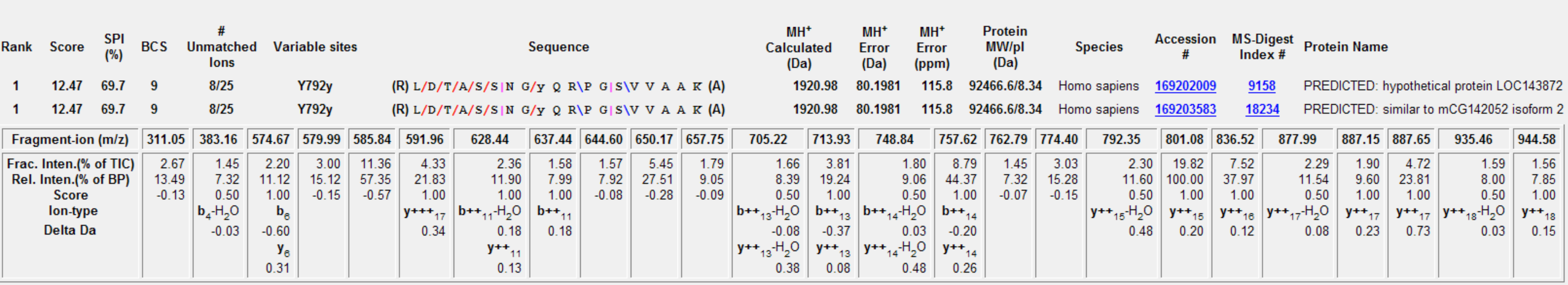
Fragment-ion (m/z)	478.33	532.43	573.47	591.28	625.26	634.38	648.38	662.75	664.88	673.74	695.08
Frac. Inten.(% of TIC)	13.51	3.22	3.26	2.98	2.21	8.37	5.36	3.35	2.42	2.97	0.11
Rel. Inten.(% of BP)	100.00	23.86	24.14	22.05	16.35	61.95	39.71	24.81	17.93	21.97	0.78
Score	1.00	1.00	0.50	1.00	1.00	-0.62	1.00	-0.25	-0.18	-0.22	0.25
Ion-type	y_4	$b{++}_8$	y_5-H_2O	y_5	$y{++}_{12}$		$b{++}_{10}$				st
Delta Da	0.06	-0.78	0.13	-0.07	0.46		0.64				0.42

Fragment-ion (m/z)	700.83	707.52	747.08	755.62	776.30	812.38	817.46	833.55	852.48	860.95	925.94	1026.87
Frac. Inten.(% of TIC)	0.16	3.60	2.49	2.84	2.53	12.37	3.72	10.87	2.00	7.18	2.46	2.03
Rel. Inten.(% of BP)	1.19	26.66	18.45	21.00	18.70	91.55	27.54	80.51	14.82	53.16	18.22	15.02
Score	1.50	1.00	1.00	-0.21	1.00	-0.92	-0.28	1.00	0.50	1.00	-0.18	1.00
Ion-type	y_6-H_2O	b_6	$y{++}_{13}$		y_7			y_8	$b{++}_{15}$-H_2O	$b{++}_{15}$		$b{++}_{18}$
Delta Da	-0.57 1.50 sty 0.17	0.17	0.77		-0.13			0.10	0.63 b_7-H_3PO_4 0.08	0.10		0.44

Peak 176



assignment

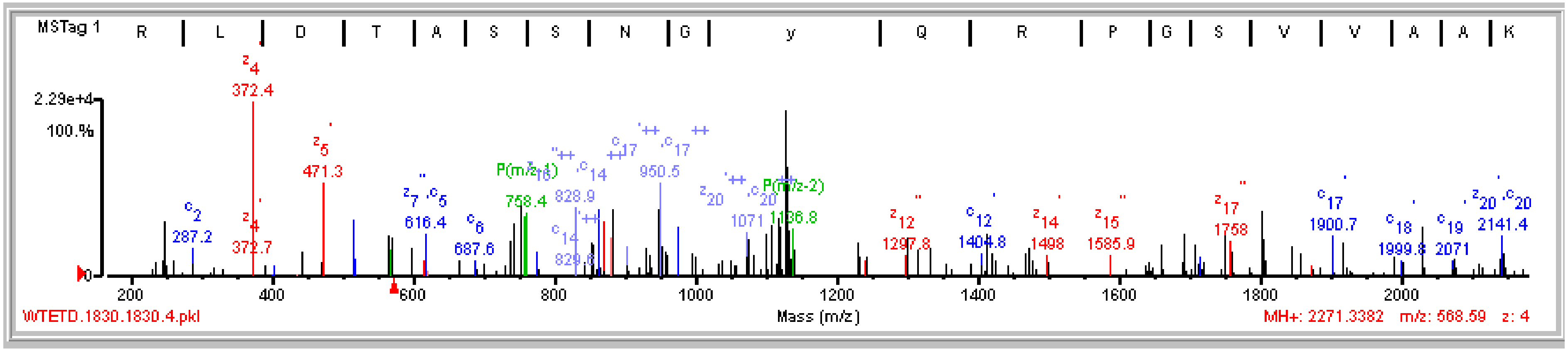


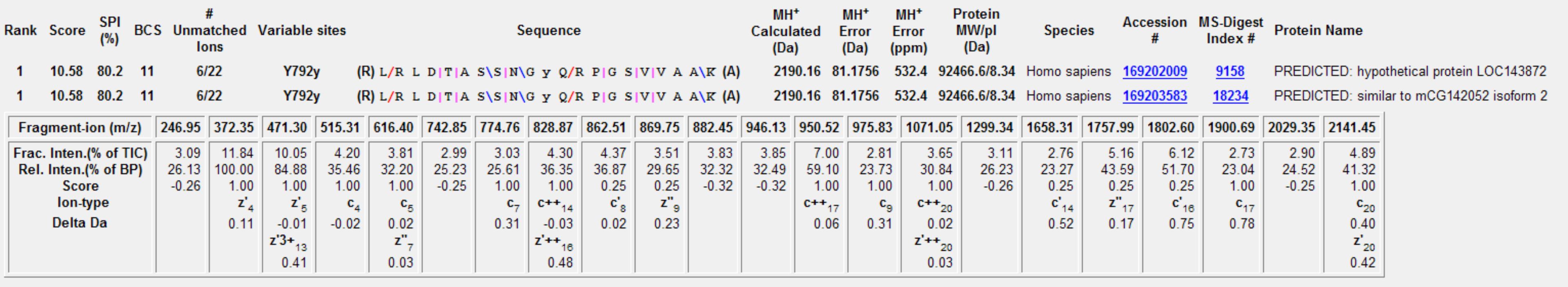
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.47	69.7	9	8/25	Y792y	(R) L/D/T/A/S/S|N G/y Q R\P G|S\V V A A K (A)	1920.98	80.1981	115.8	92466.6/8.34	Homo sapiens	169202009	9158	PREDICTED: hypothetical protein LOC143872
1	12.47	69.7	9	8/25	Y792y	(R) L/D/T/A/S/S|N G/y Q R\P G|S\V V A A K (A)	1920.98	80.1981	115.8	92466.6/8.34	Homo sapiens	169203583	18234	PREDICTED: similar to mCG142052 isoform 2

Fragment-ion (m/z)	311.05	383.16	574.67	579.99	585.84	591.96	628.44	637.44	644.60	650.17	657.75	705.22	713.93
Frac. Inten.(% of TIC)	2.67	1.45	2.20	3.00	11.36	4.33	2.36	1.58	1.57	5.45	1.79	1.66	3.81
Rel. Inten.(% of BP)	13.49	7.32	11.12	15.12	57.35	21.83	11.90	7.99	7.92	27.51	9.05	8.39	19.24
Score	-0.13	0.50	1.00	-0.15	-0.57	1.00	1.00	1.00	-0.08	-0.28	-0.09	0.50	1.00
Ion-type		b_4-H_2O	b_6 y_6			$y{+}{+}{+}_{17}$	$b{+}{+}_{11}-H_2O$ $y{+}{+}_{11}$	$b{+}{+}_{11}$				$b{+}{+}_{13}-H_2O$ $y{+}{+}_{13}-H_2O$	$b{+}{+}_{13}$ $y{+}{+}_{13}$
Delta Da		-0.03	-0.60 0.31			0.34	0.18 0.13	0.18				-0.08 0.38	-0.37 0.08

Fragment-ion (m/z)	748.84	757.62	762.79	774.40	792.35	801.08	836.52	877.99	887.15	887.65	935.46	944.58
Frac. Inten.(% of TIC)	1.80	8.79	1.45	3.03	2.30	19.82	7.52	2.29	1.90	4.72	1.59	1.56
Rel. Inten.(% of BP)	9.06	44.37	7.32	15.28	11.60	100.00	37.97	11.54	9.60	23.81	8.00	7.85
Score	0.50	1.00	-0.07	-0.15	0.50	1.00	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	$b{+}{+}_{14}-H_2O$ $y{+}{+}_{14}-H_2O$	$b{+}{+}_{14}$ $y{+}{+}_{14}$			$y{+}{+}_{15}-H_2O$	$y{+}{+}_{15}$	$y{+}{+}_{16}$	$y{+}{+}_{17}-H_2O$	$y{+}{+}_{17}$	$y{+}{+}_{17}$	$y{+}{+}_{18}-H_2O$	$y{+}{+}_{18}$
Delta Da	0.03 0.48	-0.20 0.26			0.48	0.20	0.12	0.08	0.23	0.73	0.03	0.15

Peak 177



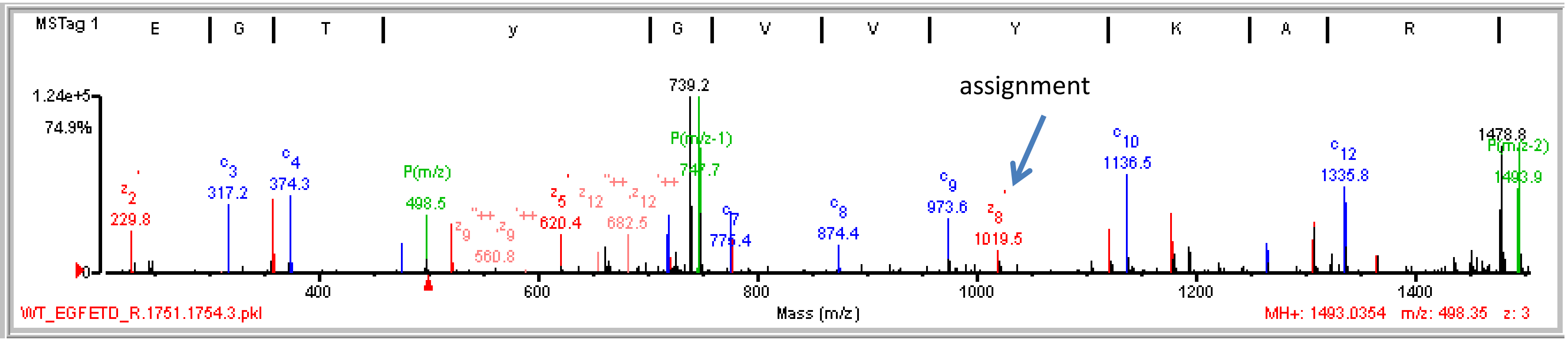


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.58	80.2	11	6/22	Y792y	(R) L/R L D|T|A S\S|N\G y Q/R P|G S|V|V A A\K (A)	2190.16	81.1756	532.4	92466.6/8.34	Homo sapiens	169202009	9158	PREDICTED: hypothetical protein LOC143872
1	10.58	80.2	11	6/22	Y792y	(R) L/R L D|T|A S\S|N\G y Q/R P|G S|V|V A A\K (A)	2190.16	81.1756	532.4	92466.6/8.34	Homo sapiens	169203583	18234	PREDICTED: similar to mCG142052 isoform 2

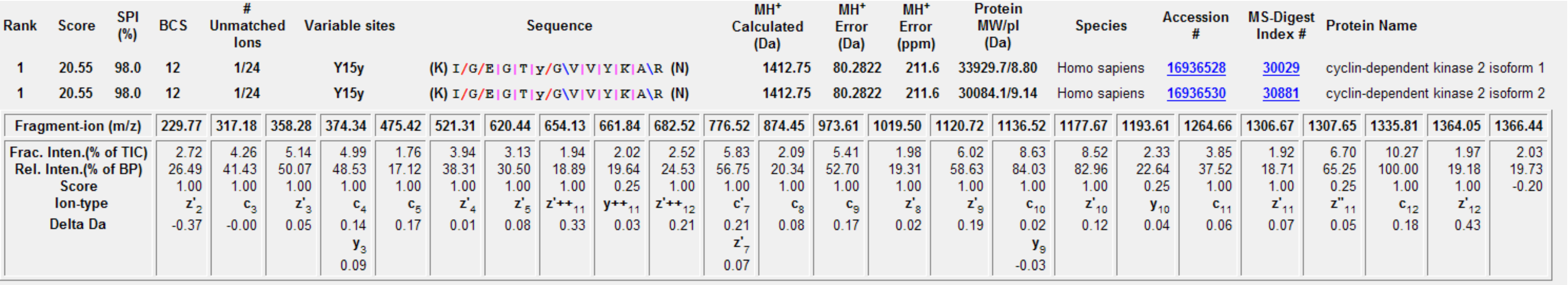
Fragment-ion (m/z)	246.95	372.35	471.30	515.31	616.40	742.85	774.76	828.87	862.51	869.75	882.45
Frac. Inten.(% of TIC)	3.09	11.84	10.05	4.20	3.81	2.99	3.03	4.30	4.37	3.51	3.83
Rel. Inten.(% of BP)	26.13	100.00	84.88	35.46	32.20	25.23	25.61	36.35	36.87	29.65	32.32
Score	-0.26	1.00	1.00	1.00	1.00	-0.25	1.00	1.00	0.25	0.25	-0.32
Ion-type		z'_4	z'_5	c_4	c_5		c_7	$c{++}_{14}$	c'_8	z''_9	
Delta Da		0.11	-0.01	-0.02	0.02		0.31	-0.03	0.02	0.23	
			$z'3{+}_{13}$		z''_7			$z'{++}_{16}$			
			0.41		0.03			0.48			

Fragment-ion (m/z)	946.13	950.52	975.83	1071.05	1299.34	1658.31	1757.99	1802.60	1900.69	2029.35	2141.45
Frac. Inten.(% of TIC)	3.85	7.00	2.81	3.65	3.11	2.76	5.16	6.12	2.73	2.90	4.89
Rel. Inten.(% of BP)	32.49	59.10	23.73	30.84	26.23	23.27	43.59	51.70	23.04	24.52	41.32
Score	-0.32	1.00	1.00	1.00	-0.26	0.25	0.25	0.25	1.00	-0.25	1.00
Ion-type		$c{++}_{17}$	c_9	$c{++}_{20}$		c'_{14}	z''_{17}	c'_{16}	c_{17}		c_{20}
Delta Da		0.06	0.31	0.02		0.52	0.17	0.75	0.78		0.40
				$z'{++}_{20}$							z'_{20}
				0.03							0.42

Peak 178



assignment

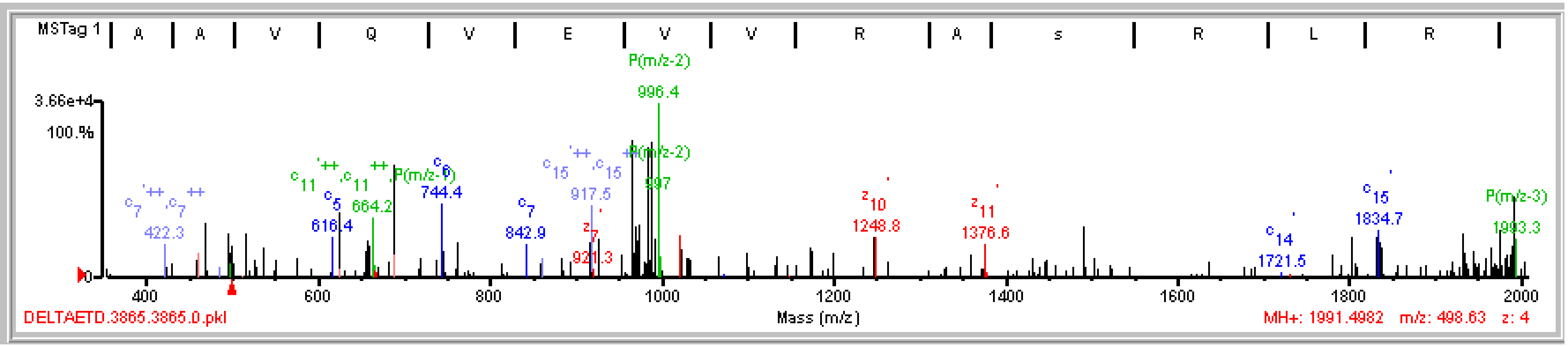


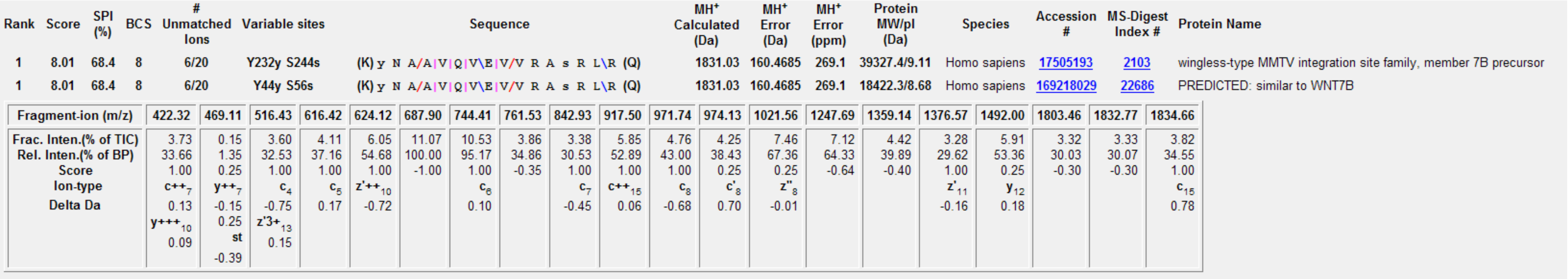
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.55	98.0	12	1/24	Y15y	(K) I/G/E|G|T|y/G\V|V|Y|K|A\R (N)	1412.75	80.2822	211.6	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	20.55	98.0	12	1/24	Y15y	(K) I/G/E|G|T|y/G\V|V|Y|K|A\R (N)	1412.75	80.2822	211.6	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

Fragment-ion (m/z)	229.77	317.18	358.28	374.34	475.42	521.31	620.44	654.13	661.84	682.52	776.52	874.45
Frac. Inten.(% of TIC)	2.72	4.26	5.14	4.99	1.76	3.94	3.13	1.94	2.02	2.52	5.83	2.09
Rel. Inten.(% of BP)	26.49	41.43	50.07	48.53	17.12	38.31	30.50	18.89	19.64	24.53	56.75	20.34
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00
Ion-type	z'_{2}	c_{3}	z'_{3}	c_{4}	c_{5}	z'_{4}	z'_{5}	z'^{++}_{11}	y^{++}_{11}	z'^{++}_{12}	c'_{7}	c_{8}
Delta Da	-0.37	-0.00	0.05	0.14	0.17	0.01	0.08	0.33	0.03	0.21	0.21	0.08
				y_{3}							z'_{7}	
				0.09							0.07	

Fragment-ion (m/z)	973.61	1019.50	1120.72	1136.52	1177.67	1193.61	1264.66	1306.67	1307.65	1335.81	1364.05	1366.44
Frac. Inten.(% of TIC)	5.41	1.98	6.02	8.63	8.52	2.33	3.85	1.92	6.70	10.27	1.97	2.03
Rel. Inten.(% of BP)	52.70	19.31	58.63	84.03	82.96	22.64	37.52	18.71	65.25	100.00	19.18	19.73
Score	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00	1.00	-0.20
Ion-type	c_{9}	z'_{8}	z'_{9}	c_{10}	z'_{10}	y_{10}	c_{11}	z'_{11}	z''_{11}	c_{12}	z'_{12}	
Delta Da	0.17	0.02	0.19	0.02	0.12	0.04	0.06	0.07	0.05	0.18	0.43	
				y_{9}								
				-0.03								

Peak 179

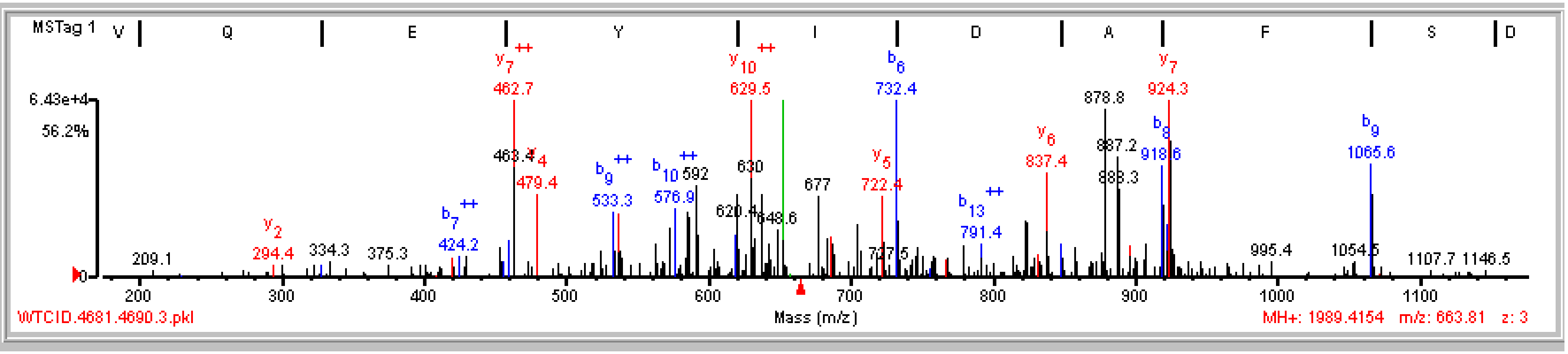




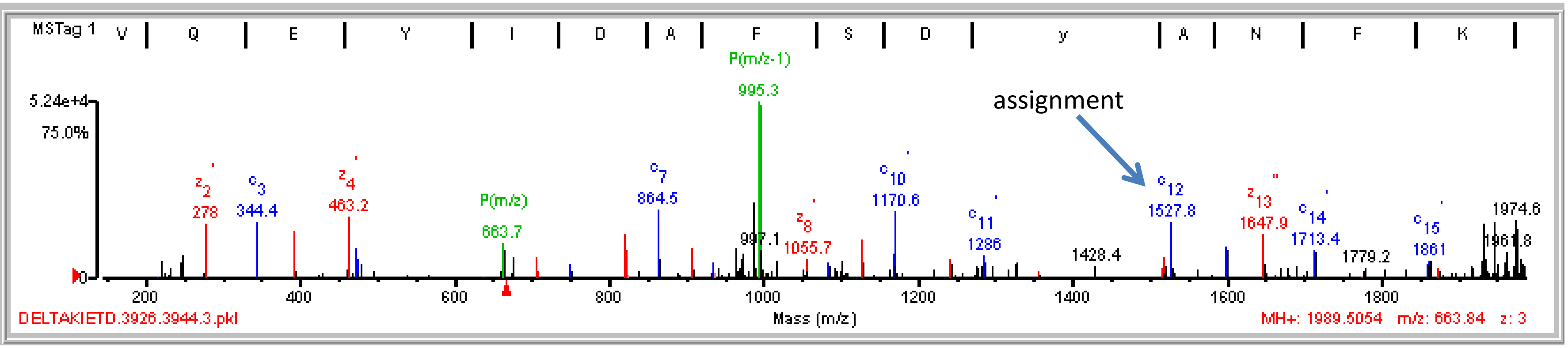
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.01	68.4	8	6/20	Y232y S244s	(K) y N A/A|V|Q|V\E|V/V R A s R L\R (Q)	1831.03	160.4685	269.1	39327.4/9.11	Homo sapiens	17505193	2103	wingless-type MMTV integration site family, member 7B precursor
1	8.01	68.4	8	6/20	Y44y S56s	(K) y N A/A|V|Q|V\E|V/V R A s R L\R (Q)	1831.03	160.4685	269.1	18422.3/8.68	Homo sapiens	169218029	22686	PREDICTED: similar to WNT7B

Fragment-ion (m/z)	422.32	469.11	516.43	616.42	624.12	687.90	744.41	761.53	842.93	917.50	971.74	974.13	1021.56	1247.69	1359.14	1376.57	1492.00	1803.46	1832.77	1834.66
Frac. Inten.(% of TIC)	3.73	0.15	3.60	4.11	6.05	11.07	10.53	3.86	3.38	5.85	4.76	4.25	7.46	7.12	4.42	3.28	5.91	3.32	3.33	3.82
Rel. Inten.(% of BP)	33.66	1.35	32.53	37.16	54.68	100.00	95.17	34.86	30.53	52.89	43.00	38.43	67.36	64.33	39.89	29.62	53.36	30.03	30.07	34.55
Score	1.00	0.25	1.00	1.00	1.00	-1.00	1.00	-0.35	1.00	1.00	1.00	0.25	0.25	-0.64	-0.40	1.00	0.25	-0.30	-0.30	1.00
Ion-type	c++_{7}	y++_{7}	c_{4}	c_{5}	z'++_{10}		c_{6}		c_{7}	c++_{15}	c_{8}	c'_{8}	z''_{8}			z'_{11}	y_{12}			c_{15}
Delta Da	0.13	-0.15	-0.75	0.17	-0.72		0.10		-0.45	0.06	-0.68	0.70	-0.01			-0.16	0.18			0.78
	y+++_{10}	0.25	z'3+_{13}																	
	0.09	st	0.15																	
		-0.39																		

Peak 180

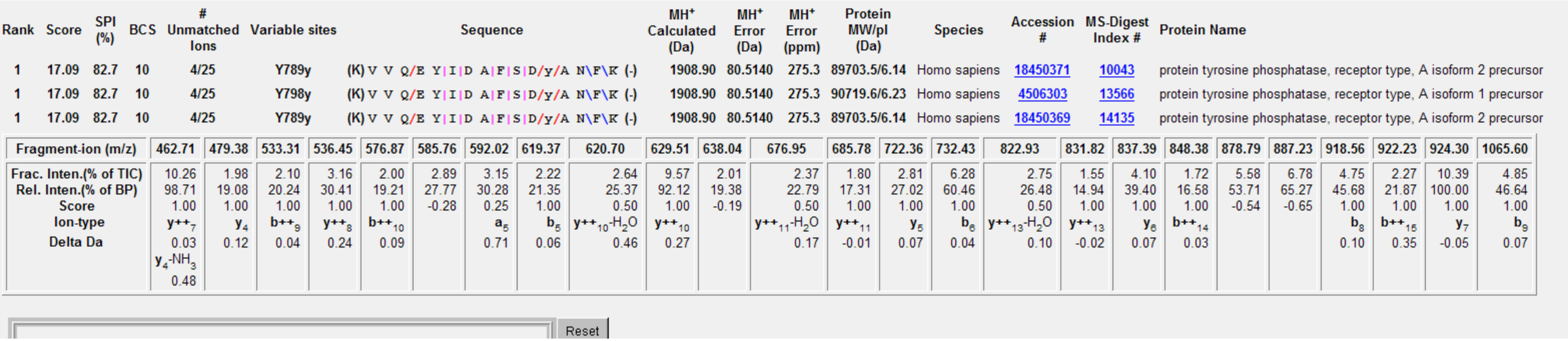


CID



assignment

ETD

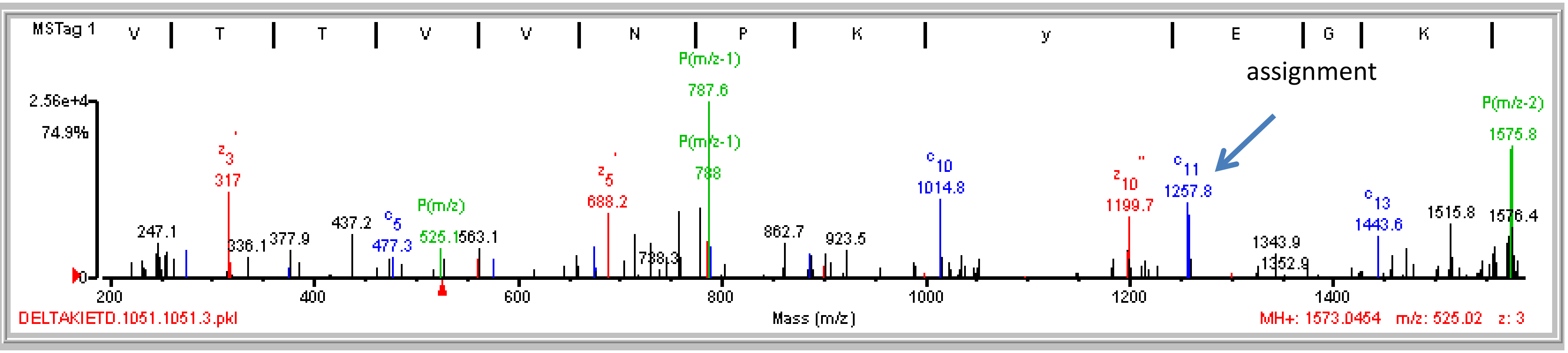


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.09	82.7	10	4/25	Y789y	(K) V V Q/E Y|I|D A|F|S|D/y/A N\F\K (-)	1908.90	80.5140	275.3	89703.5/6.14	Homo sapiens	18450371	10043	protein tyrosine phosphatase, receptor type, A isoform 2 precursor
1	17.09	82.7	10	4/25	Y798y	(K) V V Q/E Y|I|D A|F|S|D/y/A N\F\K (-)	1908.90	80.5140	275.3	90719.6/6.23	Homo sapiens	4506303	13566	protein tyrosine phosphatase, receptor type, A isoform 1 precursor
1	17.09	82.7	10	4/25	Y789y	(K) V V Q/E Y|I|D A|F|S|D/y/A N\F\K (-)	1908.90	80.5140	275.3	89703.5/6.14	Homo sapiens	18450369	14135	protein tyrosine phosphatase, receptor type, A isoform 2 precursor

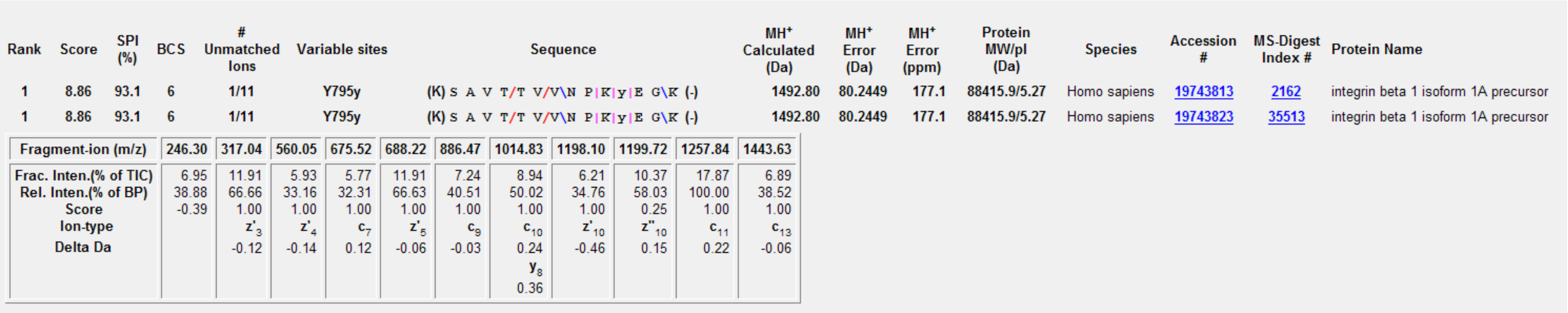
Fragment-ion (m/z)	462.71	479.38	533.31	536.45	576.87	585.76	592.02	619.37	620.70	629.51	638.04	676.95
Frac. Inten.(% of TIC)	10.26	1.98	2.10	3.16	2.00	2.89	3.15	2.22	2.64	9.57	2.01	2.37
Rel. Inten.(% of BP)	98.71	19.08	20.24	30.41	19.21	27.77	30.28	21.35	25.37	92.12	19.38	22.79
Score	1.00	1.00	1.00	1.00	1.00	-0.28	0.25	1.00	0.50	1.00	-0.19	0.50
Ion-type	$y{+}{+}_{7}$ y_{4}-NH_{3}	y_{4}	$b{+}{+}_{9}$	$y{+}{+}_{8}$	$b{+}{+}_{10}$		a_{5}	b_{5}	$y{+}{+}_{10}$-$H_{2}O$	$y{+}{+}_{10}$		$y{+}{+}_{11}$-$H_{2}O$
Delta Da	0.03 0.48	0.12	0.04	0.24	0.09		0.71	0.06	0.46	0.27		0.17

Fragment-ion (m/z)	685.78	722.36	732.43	822.93	831.82	837.39	848.38	878.79	887.23	918.56	922.23	924.30	1065.60
Frac. Inten.(% of TIC)	1.80	2.81	6.28	2.75	1.55	4.10	1.72	5.58	6.78	4.75	2.27	10.39	4.85
Rel. Inten.(% of BP)	17.31	27.02	60.46	26.48	14.94	39.40	16.58	53.71	65.27	45.68	21.87	100.00	46.64
Score	1.00	1.00	1.00	0.50	1.00	1.00	1.00	-0.54	-0.65	1.00	1.00	1.00	1.00
Ion-type	$y{+}{+}_{11}$	y_{5}	b_{6}	$y{+}{+}_{13}$-$H_{2}O$	$y{+}{+}_{13}$	y_{6}	$b{+}{+}_{14}$			b_{8}	$b{+}{+}_{15}$	y_{7}	b_{9}
Delta Da	-0.01	0.07	0.04	0.10	-0.02	0.07	0.03			0.10	0.35	-0.05	0.07

Peak 181



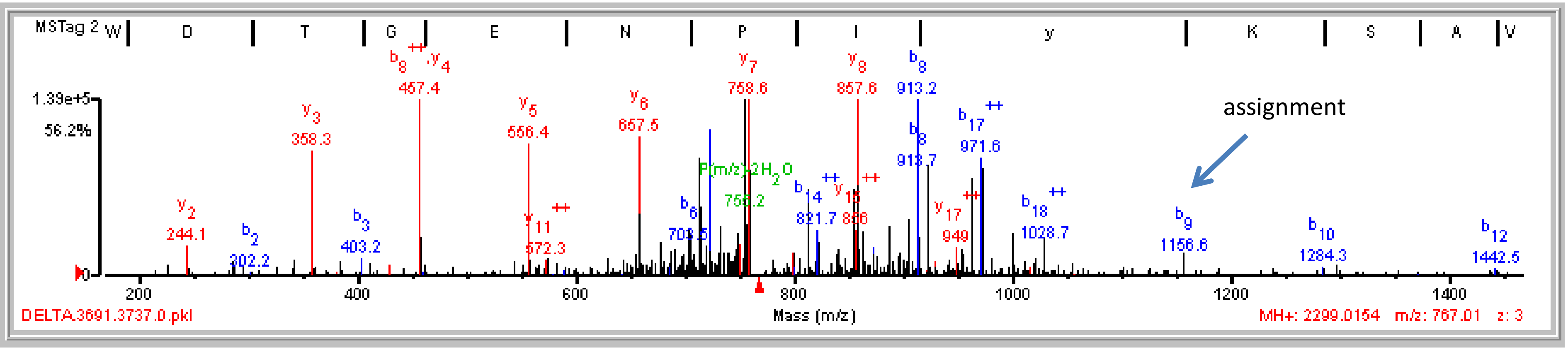
assignment



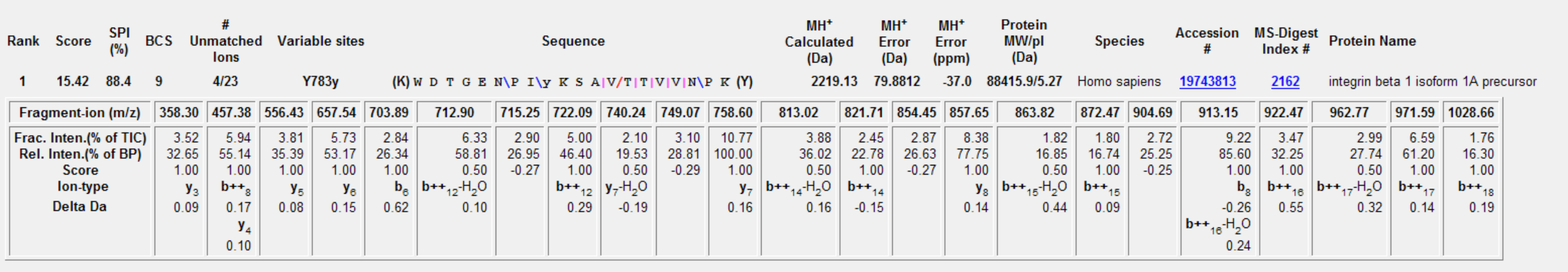
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.86	93.1	6	1/11	Y795y	(K) S A V T/T V/V\N P|K|y|E G\K (-)	1492.80	80.2449	177.1	88415.9/5.27	Homo sapiens	19743813	2162	integrin beta 1 isoform 1A precursor
1	8.86	93.1	6	1/11	Y795y	(K) S A V T/T V/V\N P|K|y|E G\K (-)	1492.80	80.2449	177.1	88415.9/5.27	Homo sapiens	19743823	35513	integrin beta 1 isoform 1A precursor

Fragment-ion (m/z)	246.30	317.04	560.05	675.52	688.22	886.47	1014.83	1198.10	1199.72	1257.84	1443.63
Frac. Inten.(% of TIC)	6.95	11.91	5.93	5.77	11.91	7.24	8.94	6.21	10.37	17.87	6.89
Rel. Inten.(% of BP)	38.88	66.66	33.16	32.31	66.63	40.51	50.02	34.76	58.03	100.00	38.52
Score	-0.39	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type		z'_3	z'_4	c_7	z'_5	c_9	c_{10}	z'_{10}	z''_{10}	c_{11}	c_{13}
Delta Da		-0.12	-0.14	0.12	-0.06	-0.03	0.24	-0.46	0.15	0.22	-0.06
							y_8 0.36				

Peak 182



assignment

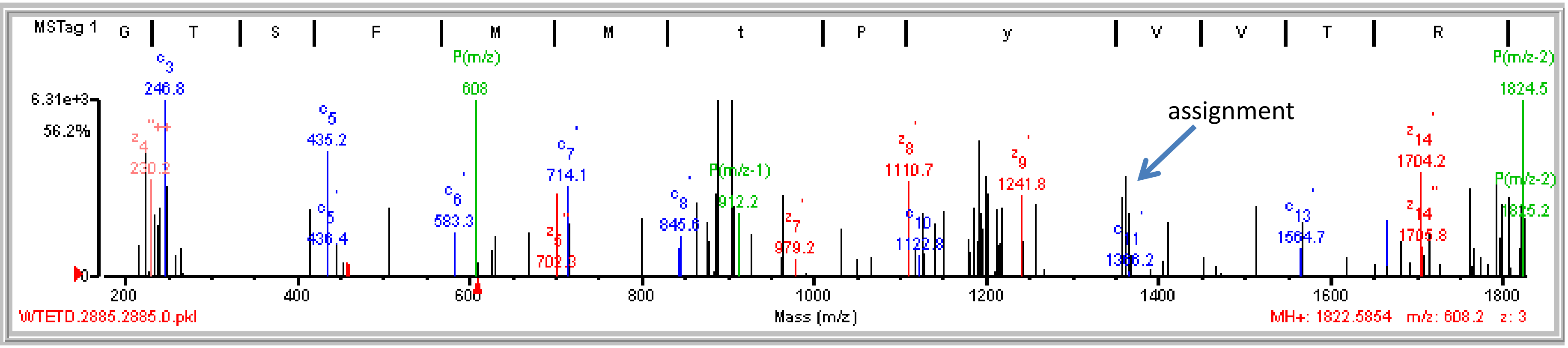


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.42	88.4	9	4/23	Y783y	(K) W D T G E N\P I\y K S A|V/T|T|V|V|N\P K (Y)	2219.13	79.8812	-37.0	88415.9/5.27	Homo sapiens	19743813	2162	integrin beta 1 isoform 1A precursor

Fragment-ion (m/z)	358.30	457.38	556.43	657.54	703.89	712.90	715.25	722.09	740.24	749.07	758.60
Frac. Inten.(% of TIC)	3.52	5.94	3.81	5.73	2.84	6.33	2.90	5.00	2.10	3.10	10.77
Rel. Inten.(% of BP)	32.65	55.14	35.39	53.17	26.34	58.81	26.95	46.40	19.53	28.81	100.00
Score	1.00	1.00	1.00	1.00	1.00	0.50	-0.27	1.00	0.50	-0.29	1.00
Ion-type	y_3	b++$_8$ y_4	y_5	y_6	b_6	b++$_{12}$-H$_2$O		b++$_{12}$	y_7-H$_2$O		y_7
Delta Da	0.09	0.17 0.10	0.08	0.15	0.62	0.10		0.29	-0.19		0.16

Fragment-ion (m/z)	813.02	821.71	854.45	857.65	863.82	872.47	904.69	913.15	922.47	962.77	971.59	1028.66
Frac. Inten.(% of TIC)	3.88	2.45	2.87	8.38	1.82	1.80	2.72	9.22	3.47	2.99	6.59	1.76
Rel. Inten.(% of BP)	36.02	22.78	26.63	77.75	16.85	16.74	25.25	85.60	32.25	27.74	61.20	16.30
Score	0.50	1.00	-0.27	1.00	0.50	1.00	-0.25	1.00	1.00	0.50	1.00	1.00
Ion-type	b++$_{14}$-H$_2$O	b++$_{14}$		y_8	b++$_{15}$-H$_2$O	b++$_{15}$		b_8 b++$_{16}$-H$_2$O	b++$_{16}$	b++$_{17}$-H$_2$O	b++$_{17}$	b++$_{18}$
Delta Da	0.16	-0.15		0.14	0.44	0.09		-0.26 0.24	0.55	0.32	0.14	0.19

Peak 183



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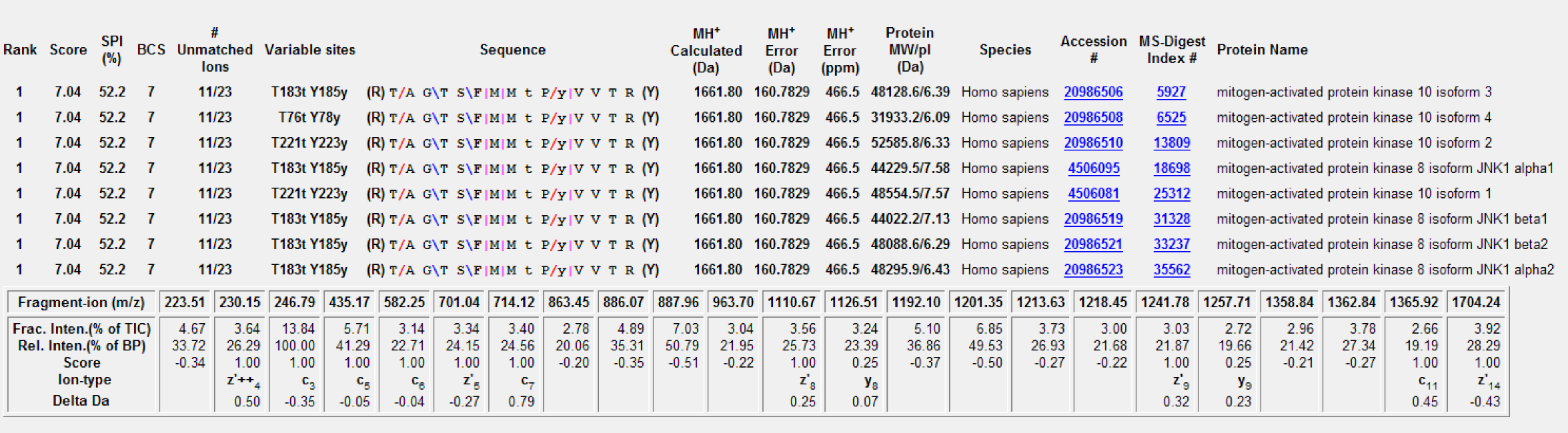
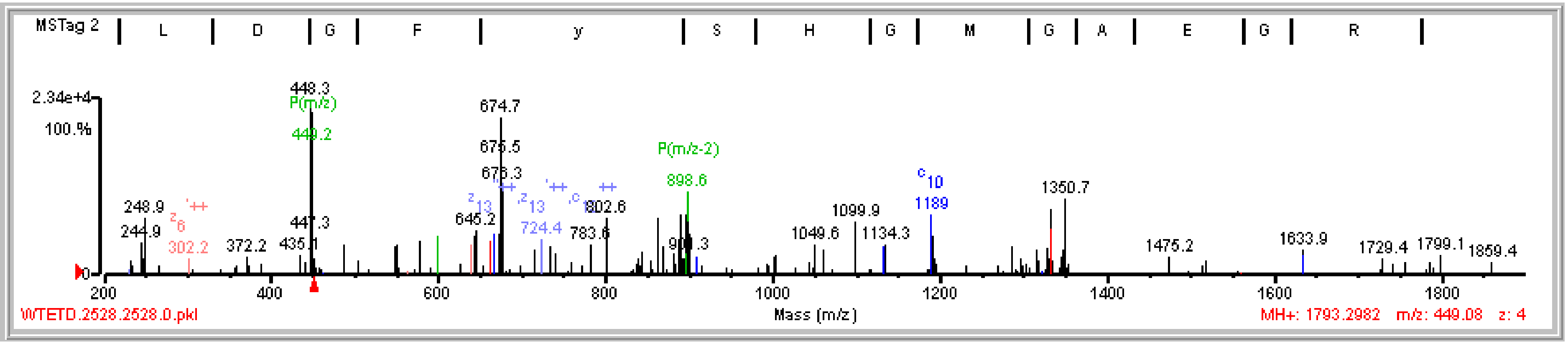


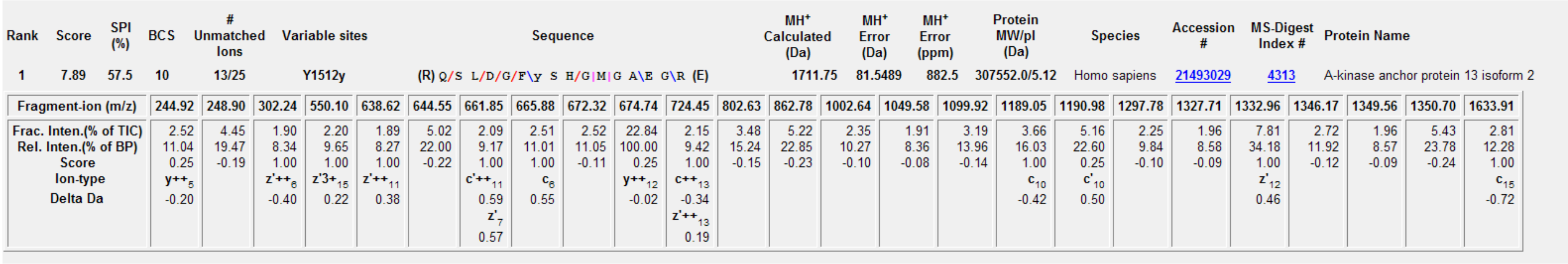
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.04	52.2	7	11/23	T183t Y185y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	48128.6/6.39	Homo sapiens	20986506	5927	mitogen-activated protein kinase 10 isoform 3
1	7.04	52.2	7	11/23	T76t Y78y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	31933.2/6.09	Homo sapiens	20986508	6525	mitogen-activated protein kinase 10 isoform 4
1	7.04	52.2	7	11/23	T221t Y223y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	52585.8/6.33	Homo sapiens	20986510	13809	mitogen-activated protein kinase 10 isoform 2
1	7.04	52.2	7	11/23	T183t Y185y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	44229.5/7.58	Homo sapiens	4506095	18698	mitogen-activated protein kinase 8 isoform JNK1 alpha1
1	7.04	52.2	7	11/23	T221t Y223y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	48554.5/7.57	Homo sapiens	4506081	25312	mitogen-activated protein kinase 10 isoform 1
1	7.04	52.2	7	11/23	T183t Y185y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	44022.2/7.13	Homo sapiens	20986519	31328	mitogen-activated protein kinase 8 isoform JNK1 beta1
1	7.04	52.2	7	11/23	T183t Y185y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	48088.6/6.29	Homo sapiens	20986521	33237	mitogen-activated protein kinase 8 isoform JNK1 beta2
1	7.04	52.2	7	11/23	T183t Y185y	(R) T/A G\T S\F|M|M t P/y|V V T R (Y)	1661.80	160.7829	466.5	48295.9/6.43	Homo sapiens	20986523	35562	mitogen-activated protein kinase 8 isoform JNK1 alpha2

Fragment-ion (m/z)	223.51	230.15	246.79	435.17	582.25	701.04	714.12	863.45	886.07	887.96	963.70
Frac. Inten.(% of TIC)	4.67	3.64	13.84	5.71	3.14	3.34	3.40	2.78	4.89	7.03	3.04
Rel. Inten.(% of BP)	33.72	26.29	100.00	41.29	22.71	24.15	24.56	20.06	35.31	50.79	21.95
Score	-0.34	1.00	1.00	1.00	1.00	1.00	1.00	-0.20	-0.35	-0.51	-0.22
Ion-type		z'^{++}_4	c_3	c_5	c_6	z'_5	c_7				
Delta Da		0.50	-0.35	-0.05	-0.04	-0.27	0.79				

Fragment-ion (m/z)	1110.67	1126.51	1192.10	1201.35	1213.63	1218.45	1241.78	1257.71	1358.84	1362.84	1365.92	1704.24
Frac. Inten.(% of TIC)	3.56	3.24	5.10	6.85	3.73	3.00	3.03	2.72	2.96	3.78	2.66	3.92
Rel. Inten.(% of BP)	25.73	23.39	36.86	49.53	26.93	21.68	21.87	19.66	21.42	27.34	19.19	28.29
Score	1.00	0.25	-0.37	-0.50	-0.27	-0.22	1.00	0.25	-0.21	-0.27	1.00	1.00
Ion-type	z'_8	y_8					z'_9	y_9			c_{11}	z'_{14}
Delta Da	0.25	0.07					0.32	0.23			0.45	-0.43

Peak 185



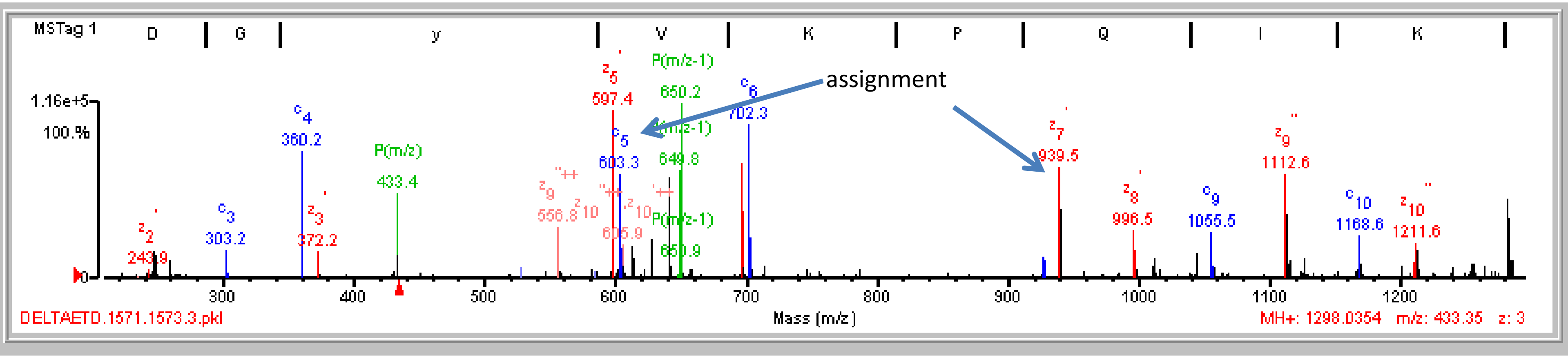


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.89	57.5	10	13/25	Y1512y	(R) Q/S L/D/G/F\y S H/G|M|G A\E G\R (E)	1711.75	81.5489	882.5	307552.0/5.12	Homo sapiens	21493029	4313	A-kinase anchor protein 13 isoform 2

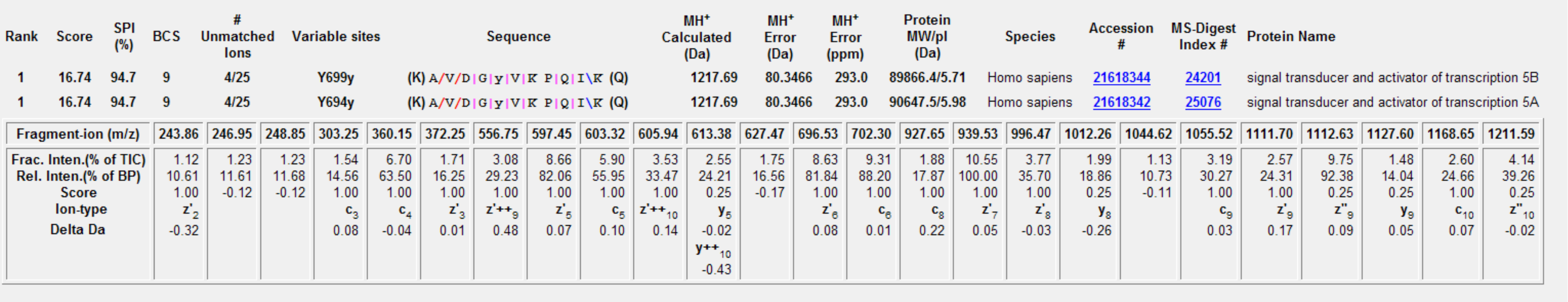
Fragment-ion (m/z)	244.92	248.90	302.24	550.10	638.62	644.55	661.85	665.88	672.32	674.74	724.45	802.63
Frac. Inten.(% of TIC)	2.52	4.45	1.90	2.20	1.89	5.02	2.09	2.51	2.52	22.84	2.15	3.48
Rel. Inten.(% of BP)	11.04	19.47	8.34	9.65	8.27	22.00	9.17	11.01	11.05	100.00	9.42	15.24
Score	0.25	-0.19	1.00	1.00	1.00	-0.22	1.00	1.00	-0.11	0.25	1.00	-0.15
Ion-type	y^{++}_{5}		z'^{++}_{6}	z'^{3+}_{15}	z'^{++}_{11}		c'^{++}_{11} z'_{7}	c_{6}		y^{++}_{12}	c^{++}_{13} z'^{++}_{13}	
Delta Da	-0.20		-0.40	0.22	0.38		0.59 0.57	0.55		-0.02	-0.34 0.19	

Fragment-ion (m/z)	862.78	1002.64	1049.58	1099.92	1189.05	1190.98	1297.78	1327.71	1332.96	1346.17	1349.56	1350.70	1633.91
Frac. Inten.(% of TIC)	5.22	2.35	1.91	3.19	3.66	5.16	2.25	1.96	7.81	2.72	1.96	5.43	2.81
Rel. Inten.(% of BP)	22.85	10.27	8.36	13.96	16.03	22.60	9.84	8.58	34.18	11.92	8.57	23.78	12.28
Score	-0.23	-0.10	-0.08	-0.14	1.00	0.25	-0.10	-0.09	1.00	-0.12	-0.09	-0.24	1.00
Ion-type					c_{10}	c'_{10}			z'_{12}				c_{15}
Delta Da					-0.42	0.50			0.46				-0.72

Peak 186



assignment

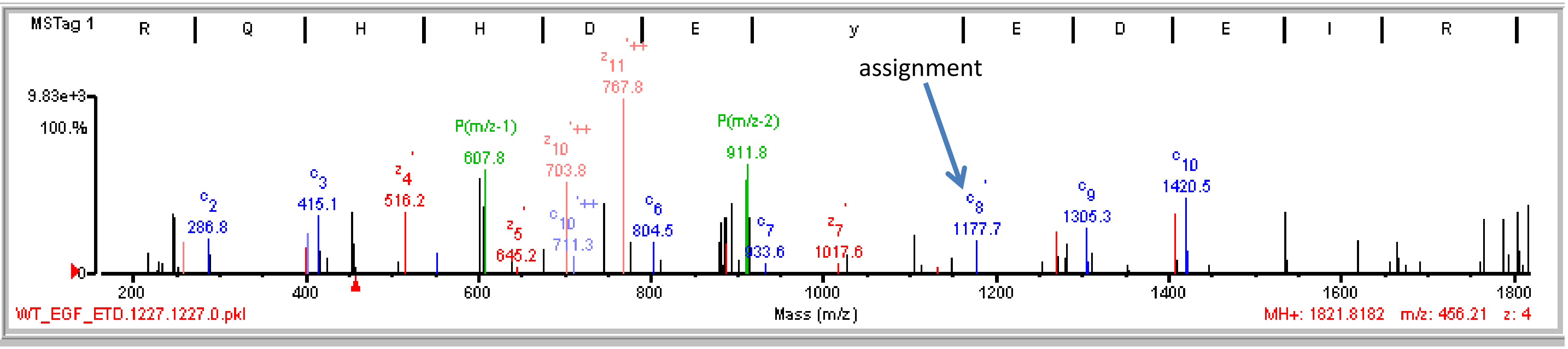


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.74	94.7	9	4/25	Y699y	(K) A/V/D|G|y|V|K P|Q|I\K (Q)	1217.69	80.3466	293.0	89866.4/5.71	Homo sapiens	21618344	24201	signal transducer and activator of transcription 5B
1	16.74	94.7	9	4/25	Y694y	(K) A/V/D|G|y|V|K P|Q|I\K (Q)	1217.69	80.3466	293.0	90647.5/5.98	Homo sapiens	21618342	25076	signal transducer and activator of transcription 5A

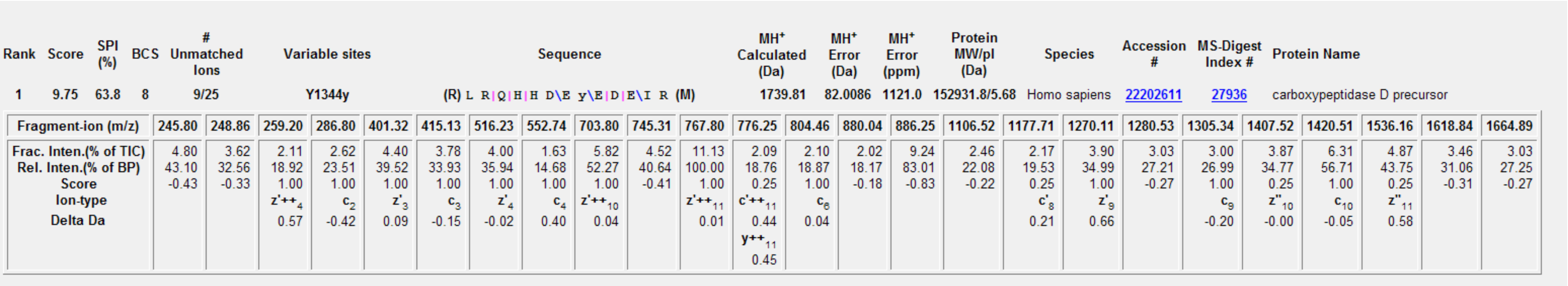
Fragment-ion (m/z)	243.86	246.95	248.85	303.25	360.15	372.25	556.75	597.45	603.32	605.94	613.38	627.47
Frac. Inten.(% of TIC)	1.12	1.23	1.23	1.54	6.70	1.71	3.08	8.66	5.90	3.53	2.55	1.75
Rel. Inten.(% of BP)	10.61	11.61	11.68	14.56	63.50	16.25	29.23	82.06	55.95	33.47	24.21	16.56
Score	1.00	-0.12	-0.12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.17
Ion-type	z'_2			c_3	c_4	z'_3	$z'{++}_9$	z'_5	c_5	$z'{++}_{10}$	y_5 $y{++}_{10}$	
Delta Da	-0.32			0.08	-0.04	0.01	0.48	0.07	0.10	0.14	-0.02 -0.43	

Fragment-ion (m/z)	696.53	702.30	927.65	939.53	996.47	1012.26	1044.62	1055.52	1111.70	1112.63	1127.60	1168.65	1211.59
Frac. Inten.(% of TIC)	8.63	9.31	1.88	10.55	3.77	1.99	1.13	3.19	2.57	9.75	1.48	2.60	4.14
Rel. Inten.(% of BP)	81.84	88.20	17.87	100.00	35.70	18.86	10.73	30.27	24.31	92.38	14.04	24.66	39.26
Score	1.00	1.00	1.00	1.00	1.00	0.25	-0.11	1.00	1.00	0.25	0.25	1.00	0.25
Ion-type	z'_6	c_6	c_8	z'_7	z'_8	y_8		c_9	z'_9	z''_9	y_9	c_{10}	z''_{10}
Delta Da	0.08	0.01	0.22	0.05	-0.03	-0.26		0.03	0.17	0.09	0.05	0.07	-0.02

Peak 187



assignment

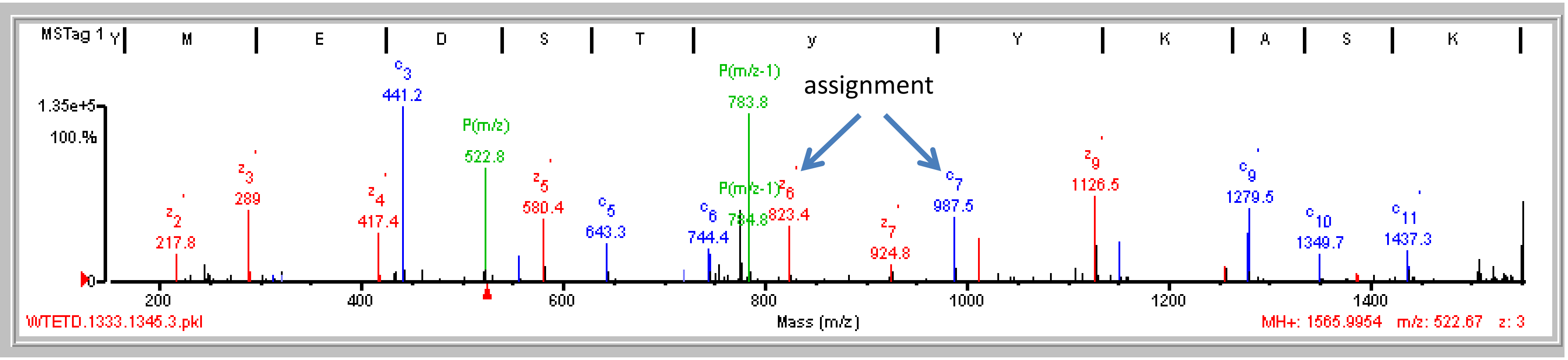


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.75	63.8	8	9/25	Y1344y	(R) L R|Q|H|H D\E y\E|D|E\I R (M)	1739.81	82.0086	1121.0	152931.8/5.68	Homo sapiens	22202611	27936	carboxypeptidase D precursor

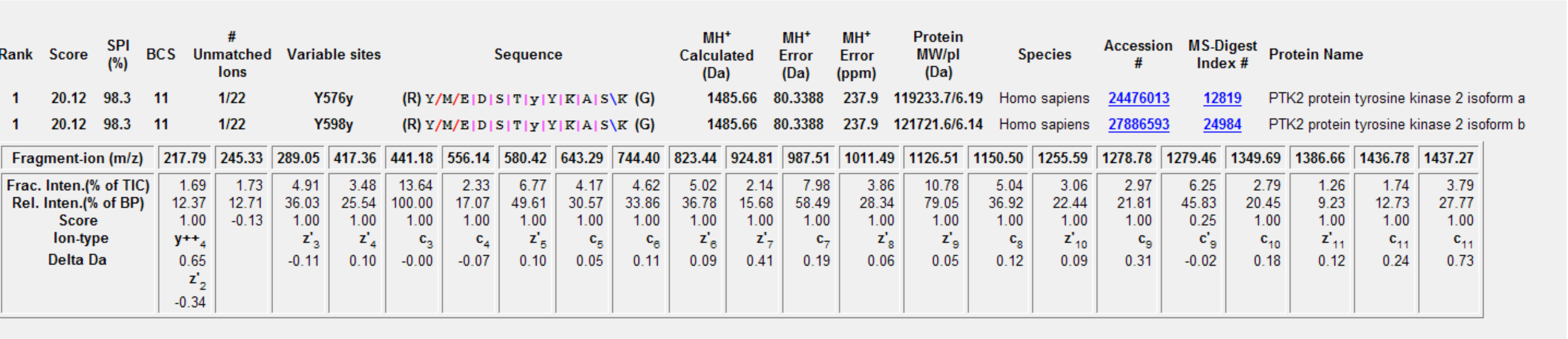
Fragment-ion (m/z)	245.80	248.86	259.20	286.80	401.32	415.13	516.23	552.74	703.80	745.31	767.80	776.25	804.46
Frac. Inten.(% of TIC)	4.80	3.62	2.11	2.62	4.40	3.78	4.00	1.63	5.82	4.52	11.13	2.09	2.10
Rel. Inten.(% of BP)	43.10	32.56	18.92	23.51	39.52	33.93	35.94	14.68	52.27	40.64	100.00	18.76	18.87
Score	-0.43	-0.33	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.41	1.00	0.25	1.00
Ion-type			z'^{++}_{4}	c_2	z'_3	c_3	z'_4	c_4	z'^{++}_{10}		z'^{++}_{11}	c'^{++}_{11} y^{++}_{11}	c_6
Delta Da			0.57	-0.42	0.09	-0.15	-0.02	0.40	0.04		0.01	0.44 0.45	0.04

Fragment-ion (m/z)	880.04	886.25	1106.52	1177.71	1270.11	1280.53	1305.34	1407.52	1420.51	1536.16	1618.84	1664.89
Frac. Inten.(% of TIC)	2.02	9.24	2.46	2.17	3.90	3.03	3.00	3.87	6.31	4.87	3.46	3.03
Rel. Inten.(% of BP)	18.17	83.01	22.08	19.53	34.99	27.21	26.99	34.77	56.71	43.75	31.06	27.25
Score	-0.18	-0.83	-0.22	0.25	1.00	-0.27	1.00	0.25	1.00	0.25	-0.31	-0.27
Ion-type				c'_8	z'_9		c_9	z''_{10}	c_{10}	z''_{11}		
Delta Da				0.21	0.66		-0.20	-0.00	-0.05	0.58		

Peak 188



assignment

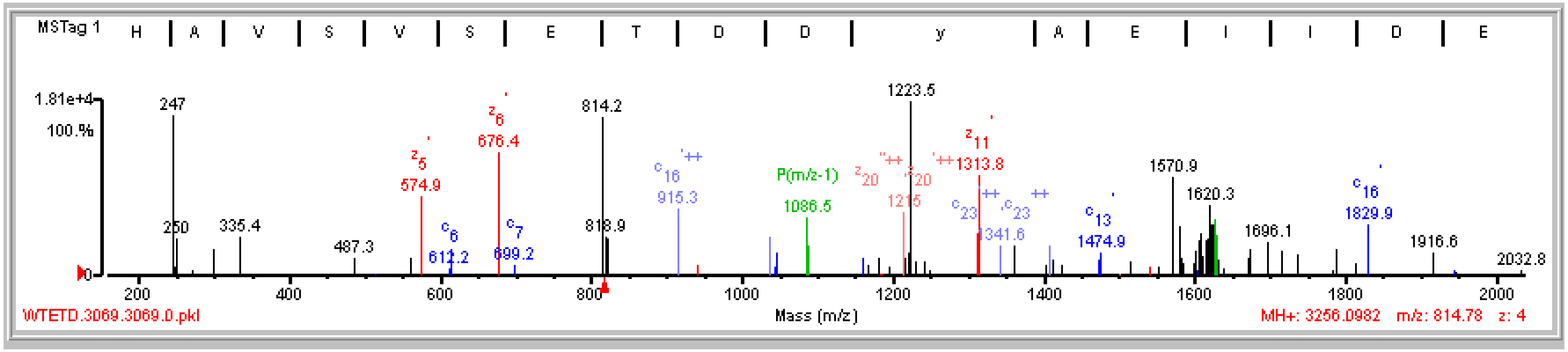


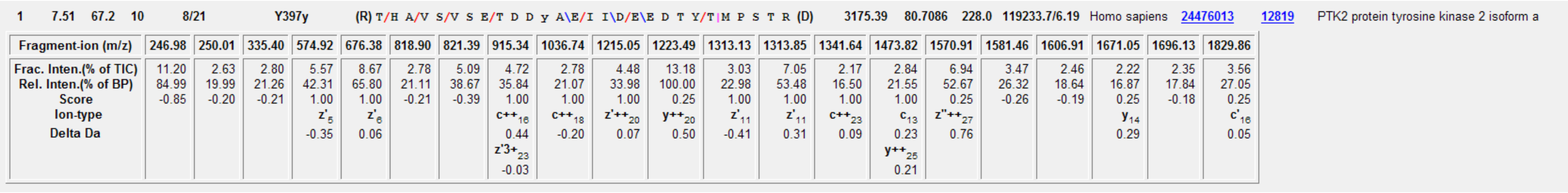
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.12	98.3	11	1/22	Y576y	(R) Y/M/E|D|S|T|y|Y|K|A|S\K (G)	1485.66	80.3388	237.9	119233.7/6.19	Homo sapiens	24476013	12819	PTK2 protein tyrosine kinase 2 isoform a
1	20.12	98.3	11	1/22	Y598y	(R) Y/M/E|D|S|T|y|Y|K|A|S\K (G)	1485.66	80.3388	237.9	121721.6/6.14	Homo sapiens	27886593	24984	PTK2 protein tyrosine kinase 2 isoform b

Fragment-ion (m/z)	217.79	245.33	289.05	417.36	441.18	556.14	580.42	643.29	744.40	823.44	924.81
Frac. Inten.(% of TIC)	1.69	1.73	4.91	3.48	13.64	2.33	6.77	4.17	4.62	5.02	2.14
Rel. Inten.(% of BP)	12.37	12.71	36.03	25.54	100.00	17.07	49.61	30.57	33.86	36.78	15.68
Score	1.00	-0.13	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{++}_4 z'_2		z'_3	z'_4	c_3	c_4	z'_5	c_5	c_6	z'_6	z'_7
Delta Da	0.65 -0.34		-0.11	0.10	-0.00	-0.07	0.10	0.05	0.11	0.09	0.41

Fragment-ion (m/z)	987.51	1011.49	1126.51	1150.50	1255.59	1278.78	1279.46	1349.69	1386.66	1436.78	1437.27
Frac. Inten.(% of TIC)	7.98	3.86	10.78	5.04	3.06	2.97	6.25	2.79	1.26	1.74	3.79
Rel. Inten.(% of BP)	58.49	28.34	79.05	36.92	22.44	21.81	45.83	20.45	9.23	12.73	27.77
Score	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00
Ion-type	c_7	z'_8	z'_9	c_8	z'_{10}	c_9	c'_9	c_{10}	z'_{11}	c_{11}	c_{11}
Delta Da	0.19	0.06	0.05	0.12	0.09	0.31	-0.02	0.18	0.12	0.24	0.73

Peak 189



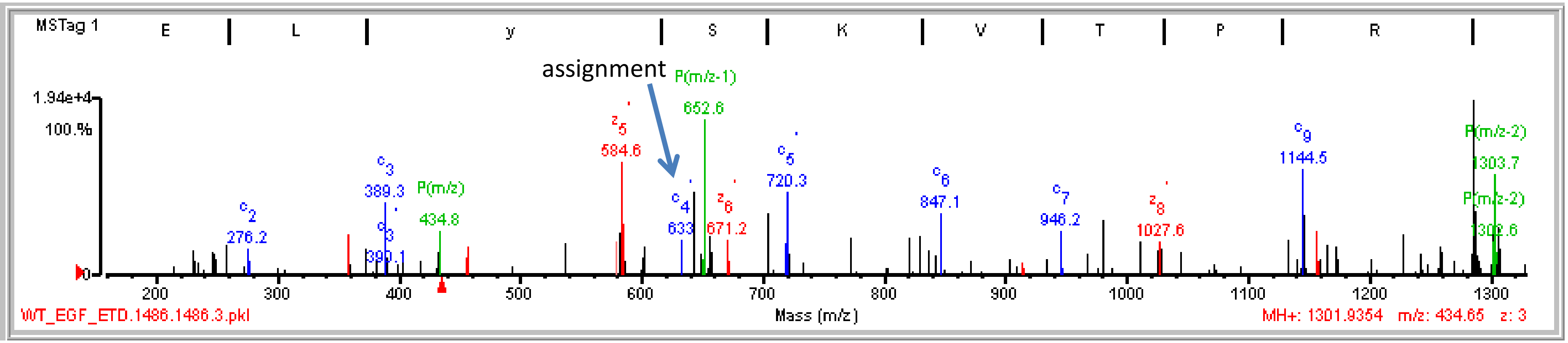


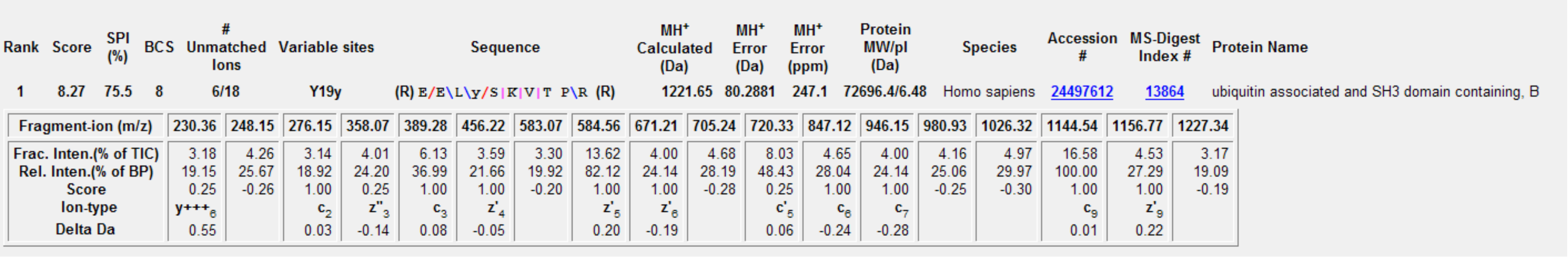
1 7.51 67.2 10 8/21 Y397y (R) T/H A/V S/V S E/T D D y A\E/I I\D/E\E D T Y/T|M P S T R (D) 3175.39 80.7086 228.0 119233.7/6.19 Homo sapiens 24476013 12819 PTK2 protein tyrosine kinase 2 isoform a

Fragment-ion (m/z)	246.98	250.01	335.40	574.92	676.38	818.90	821.39	915.34	1036.74	1215.05
Frac. Inten.(% of TIC)	11.20	2.63	2.80	5.57	8.67	2.78	5.09	4.72	2.78	4.48
Rel. Inten.(% of BP)	84.99	19.99	21.26	42.31	65.80	21.11	38.67	35.84	21.07	33.98
Score	-0.85	-0.20	-0.21	1.00	1.00	-0.21	-0.39	1.00	1.00	1.00
Ion-type				z'_5	z'_6			$c{+}{+}_{16}$	$c{+}{+}_{18}$	$z'{+}{+}_{20}$
Delta Da				-0.35	0.06			0.44 $z'3{+}_{23}$ -0.03	-0.20	0.07

Fragment-ion (m/z)	1223.49	1313.13	1313.85	1341.64	1473.82	1570.91	1581.46	1606.91	1671.05	1696.13	1829.86
Frac. Inten.(% of TIC)	13.18	3.03	7.05	2.17	2.84	6.94	3.47	2.46	2.22	2.35	3.56
Rel. Inten.(% of BP)	100.00	22.98	53.48	16.50	21.55	52.67	26.32	18.64	16.87	17.84	27.05
Score	0.25	1.00	1.00	1.00	1.00	0.25	-0.26	-0.19	0.25	-0.18	0.25
Ion-type	$y{+}{+}_{20}$	z'_{11}	z'_{11}	$c{+}{+}_{23}$	c_{13}	$z''{+}{+}_{27}$			y_{14}		c'_{16}
Delta Da	0.50	-0.41	0.31	0.09	0.23 $y{+}{+}_{25}$ 0.21	0.76			0.29		0.05

Peak 190



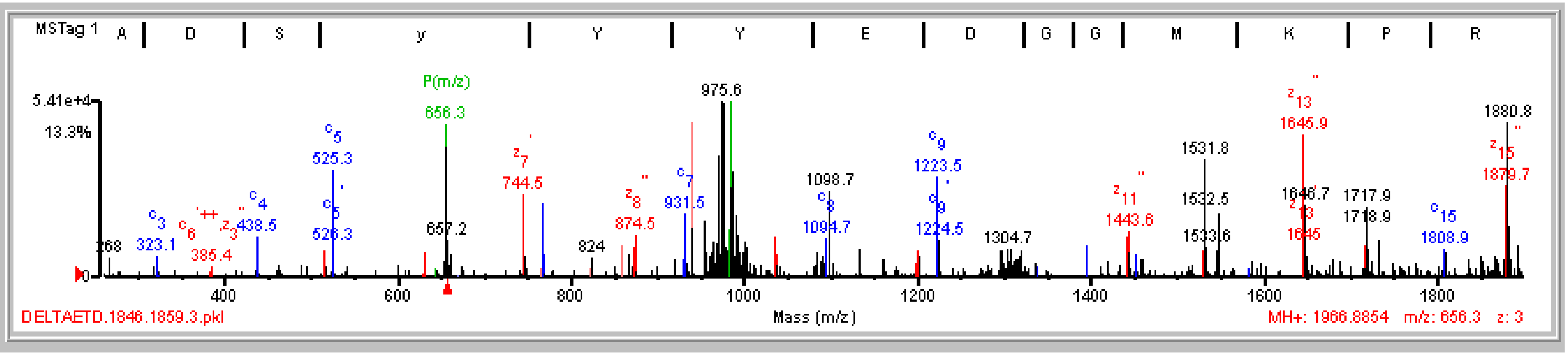


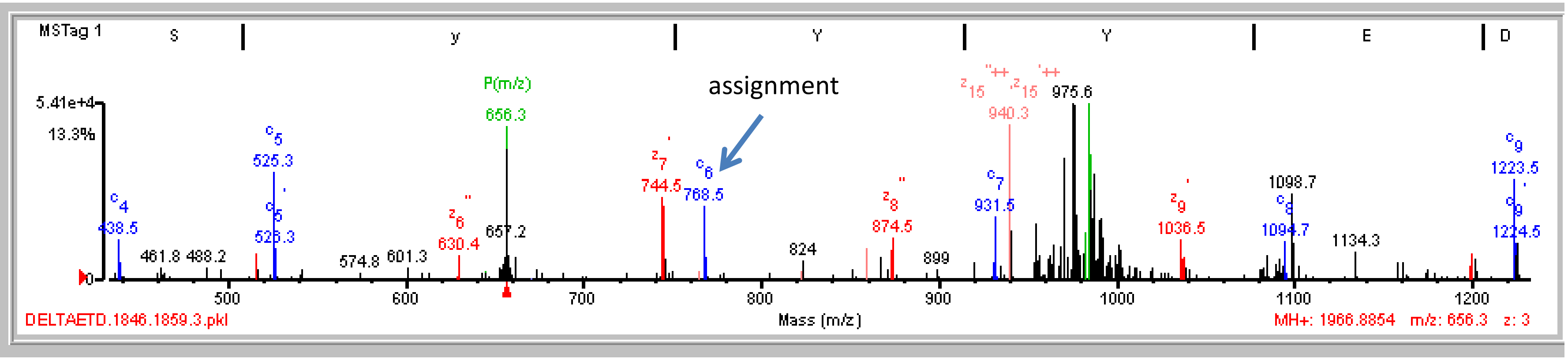
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.27	75.5	8	6/18	Y19y	(R) E/E\L\y/S|K|V|T P\R (R)	1221.65	80.2881	247.1	72696.4/6.48	Homo sapiens	24497612	13864	ubiquitin associated and SH3 domain containing, B

Fragment-ion (m/z)	230.36	248.15	276.15	358.07	389.28	456.22	583.07	584.56	671.21
Frac. Inten.(% of TIC)	3.18	4.26	3.14	4.01	6.13	3.59	3.30	13.62	4.00
Rel. Inten.(% of BP)	19.15	25.67	18.92	24.20	36.99	21.66	19.92	82.12	24.14
Score	0.25	-0.26	1.00	0.25	1.00	1.00	-0.20	1.00	1.00
Ion-type	$y+++_6$		c_2	z''_3	c_3	z'_4		z'_5	z'_6
Delta Da	0.55		0.03	-0.14	0.08	-0.05		0.20	-0.19

Fragment-ion (m/z)	705.24	720.33	847.12	946.15	980.93	1026.32	1144.54	1156.77	1227.34
Frac. Inten.(% of TIC)	4.68	8.03	4.65	4.00	4.16	4.97	16.58	4.53	3.17
Rel. Inten.(% of BP)	28.19	48.43	28.04	24.14	25.06	29.97	100.00	27.29	19.09
Score	-0.28	0.25	1.00	1.00	-0.25	-0.30	1.00	1.00	-0.19
Ion-type		c'_5	c_6	c_7			c_9	z'_9	
Delta Da		0.06	-0.24	-0.28			0.01	0.22	

Peak 191

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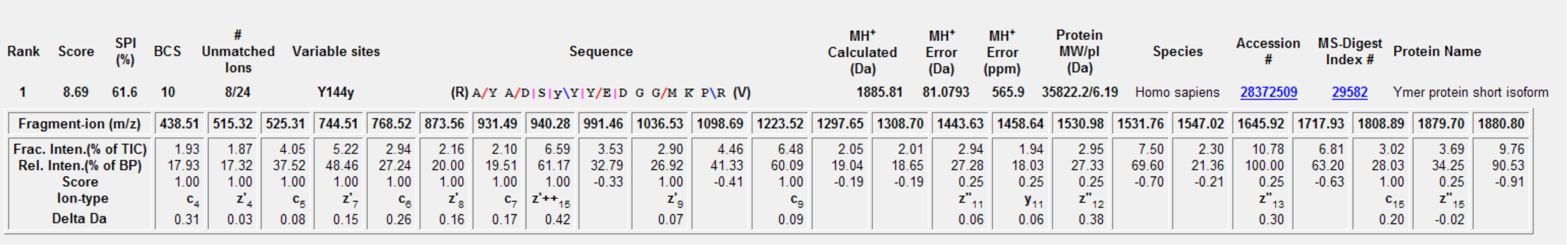
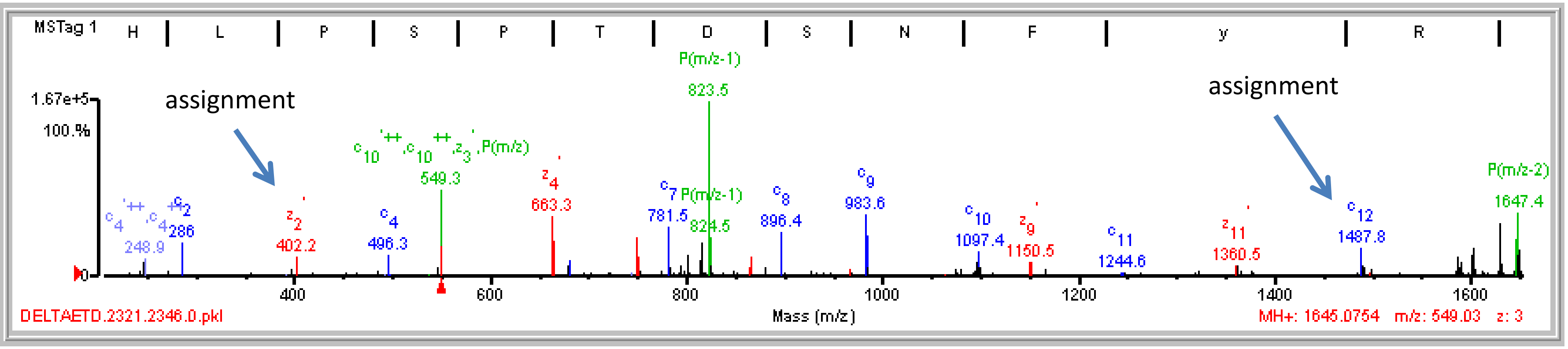


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.69	61.6	10	8/24	Y144y	(R) A/Y A/D|S|y\Y|Y/E|D G G/M K P\R (V)	1885.81	81.0793	565.9	35822.2/6.19	Homo sapiens	28372509	29582	Ymer protein short isoform

Fragment-ion (m/z)	438.51	515.32	525.31	744.51	768.52	873.56	931.49	940.28	991.46	1036.53	1098.69
Frac. Inten.(% of TIC)	1.93	1.87	4.05	5.22	2.94	2.16	2.10	6.59	3.53	2.90	4.46
Rel. Inten.(% of BP)	17.93	17.32	37.52	48.46	27.24	20.00	19.51	61.17	32.79	26.92	41.33
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.33	1.00	-0.41
Ion-type	c_4	z'_4	c_5	z'_7	c_6	z'_8	c_7	$z'{++}_{15}$		z'_9	
Delta Da	0.31	0.03	0.08	0.15	0.26	0.16	0.17	0.42		0.07	

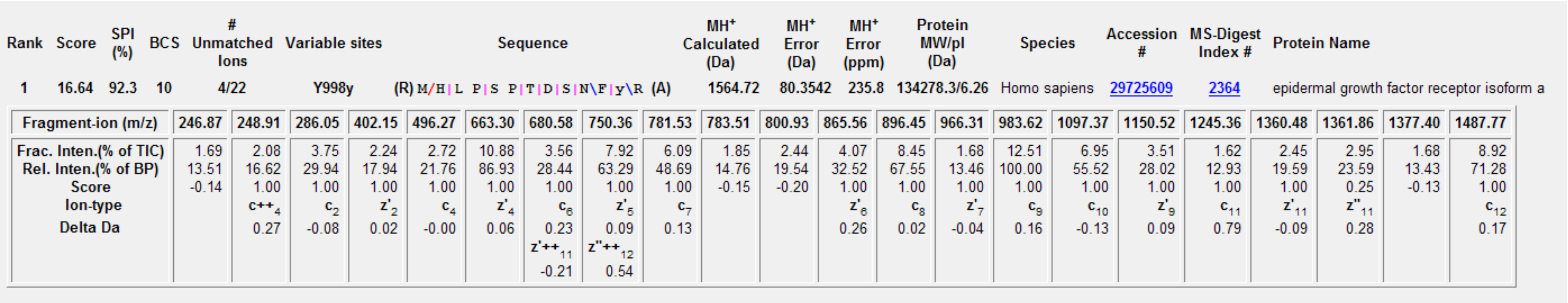
Fragment-ion (m/z)	1223.52	1297.65	1308.70	1443.63	1458.64	1530.98	1531.76	1547.02	1645.92	1717.93	1808.89	1879.70	1880.80
Frac. Inten.(% of TIC)	6.48	2.05	2.01	2.94	1.94	2.95	7.50	2.30	10.78	6.81	3.02	3.69	9.76
Rel. Inten.(% of BP)	60.09	19.04	18.65	27.28	18.03	27.33	69.60	21.36	100.00	63.20	28.03	34.25	90.53
Score	1.00	-0.19	-0.19	0.25	0.25	0.25	-0.70	-0.21	0.25	-0.63	1.00	0.25	-0.91
Ion-type	c_9			z''_{11}	y_{11}	z''_{12}			z''_{13}		c_{15}	z''_{15}	
Delta Da	0.09			0.06	0.06	0.38			0.30		0.20	-0.02	

Peak 192



assignment

assignment

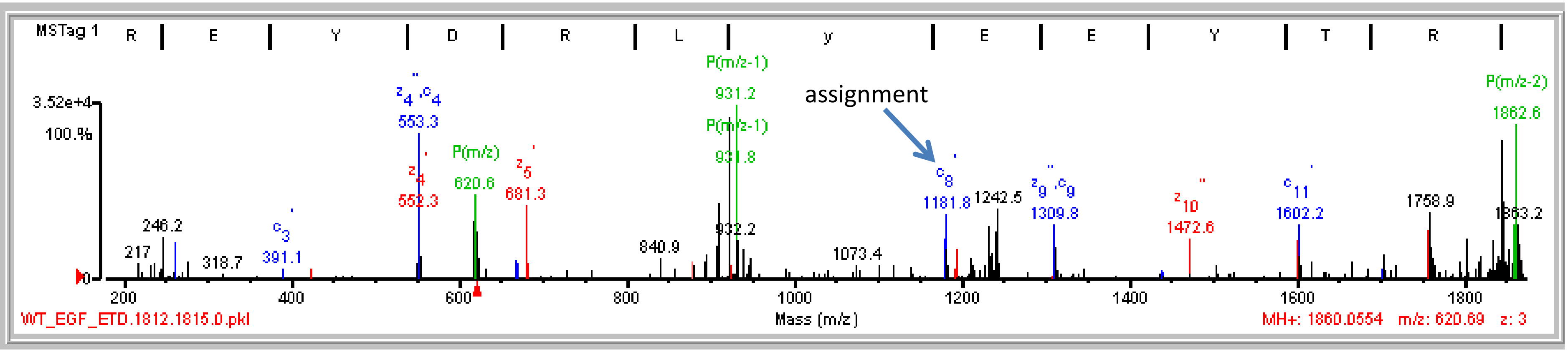


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.64	92.3	10	4/22	Y998y	(R) M/H|L P|S P|T|D|S|N\F|y\R (A)	1564.72	80.3542	235.8	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

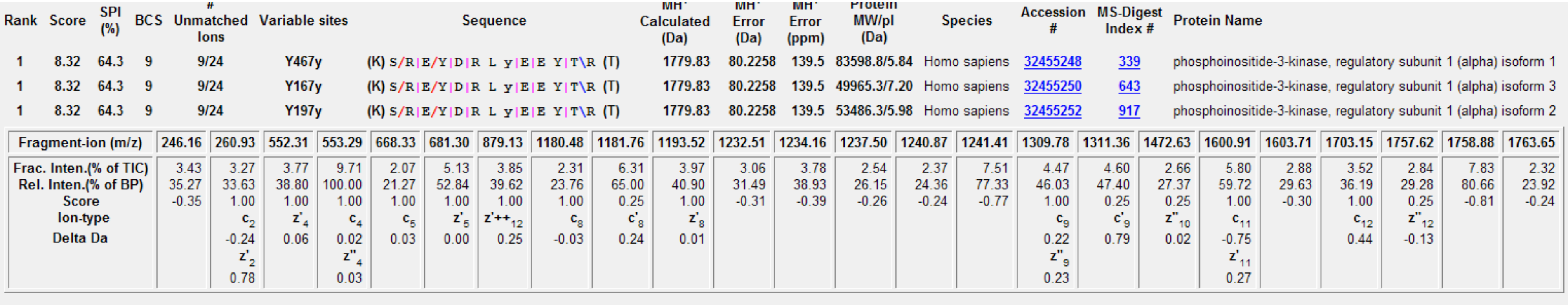
Fragment-ion (m/z)	246.87	248.91	286.05	402.15	496.27	663.30	680.58	750.36	781.53	783.51	800.93
Frac. Inten.(% of TIC)	1.69	2.08	3.75	2.24	2.72	10.88	3.56	7.92	6.09	1.85	2.44
Rel. Inten.(% of BP)	13.51	16.62	29.94	17.94	21.76	86.93	28.44	63.29	48.69	14.76	19.54
Score	-0.14	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.15	-0.20
Ion-type		$c{++}_4$	c_2	z'_2	c_4	z'_4	c_6	z'_5	c_7		
Delta Da		0.27	-0.08	0.02	-0.00	0.06	0.23	0.09	0.13		
							$z'{++}_{11}$	$z''{++}_{12}$			
							-0.21	0.54			

Fragment-ion (m/z)	865.56	896.45	966.31	983.62	1097.37	1150.52	1245.36	1360.48	1361.86	1377.40	1487.77
Frac. Inten.(% of TIC)	4.07	8.45	1.68	12.51	6.95	3.51	1.62	2.45	2.95	1.68	8.92
Rel. Inten.(% of BP)	32.52	67.55	13.46	100.00	55.52	28.02	12.93	19.59	23.59	13.43	71.28
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.13	1.00
Ion-type	z'_6	c_8	z'_7	c_9	c_{10}	z'_9	c_{11}	z'_{11}	z''_{11}		c_{12}
Delta Da	0.26	0.02	-0.04	0.16	-0.13	0.09	0.79	-0.09	0.28		0.17

Peak 193



assignment

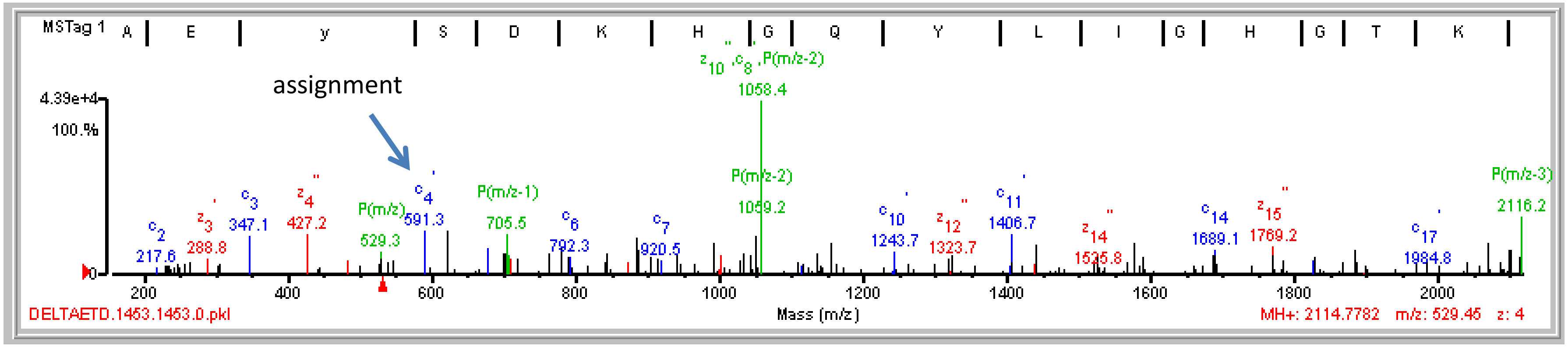


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.32	64.3	9	9/24	Y467y	(K) S/R|E/Y|D|R L y|E|E Y|T\R (T)	1779.83	80.2258	139.5	83598.8/5.84	Homo sapiens	32455248	339	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 1
1	8.32	64.3	9	9/24	Y167y	(K) S/R|E/Y|D|R L y|E|E Y|T\R (T)	1779.83	80.2258	139.5	49965.3/7.20	Homo sapiens	32455250	643	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 3
1	8.32	64.3	9	9/24	Y197y	(K) S/R|E/Y|D|R L y|E|E Y|T\R (T)	1779.83	80.2258	139.5	53486.3/5.98	Homo sapiens	32455252	917	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) isoform 2

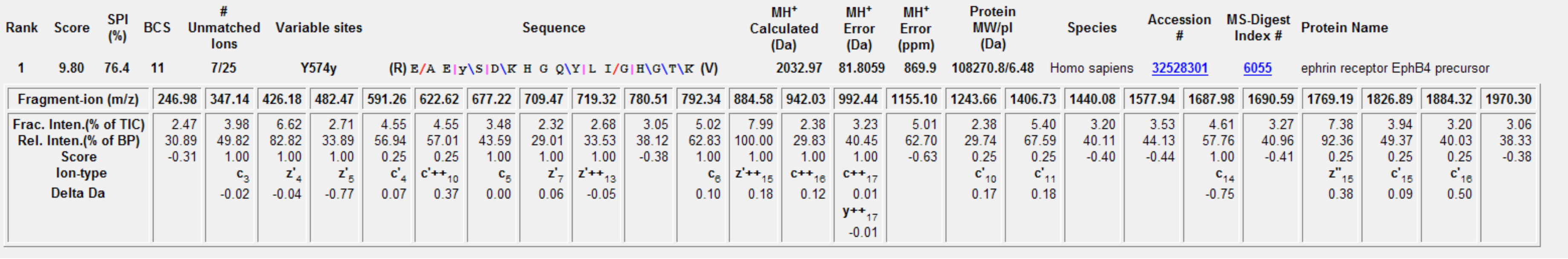
Fragment-ion (m/z)	246.16	260.93	552.31	553.29	668.33	681.30	879.13	1180.48	1181.76	1193.52	1232.51	1234.16
Frac. Inten.(% of TIC)	3.43	3.27	3.77	9.71	2.07	5.13	3.85	2.31	6.31	3.97	3.06	3.78
Rel. Inten.(% of BP)	35.27	33.63	38.80	100.00	21.27	52.84	39.62	23.76	65.00	40.90	31.49	38.93
Score	-0.35	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.31	-0.39
Ion-type		c_2 z'_2	z'_4	c_4 z''_4	c_5	z'_5	$z'{++}_{12}$	c_8	c'_8	z'_8		
Delta Da		-0.24 0.78	0.06	0.02 0.03	0.03	0.00	0.25	-0.03	0.24	0.01		

Fragment-ion (m/z)	1237.50	1240.87	1241.41	1309.78	1311.36	1472.63	1600.91	1603.71	1703.15	1757.62	1758.88	1763.65
Frac. Inten.(% of TIC)	2.54	2.37	7.51	4.47	4.60	2.66	5.80	2.88	3.52	2.84	7.83	2.32
Rel. Inten.(% of BP)	26.15	24.36	77.33	46.03	47.40	27.37	59.72	29.63	36.19	29.28	80.66	23.92
Score	-0.26	-0.24	-0.77	1.00	0.25	0.25	1.00	-0.30	1.00	0.25	-0.81	-0.24
Ion-type				c_9 z''_9	c'_9	z''_{10}	c_{11} z'_{11}		c_{12}	z''_{12}		
Delta Da				0.22 0.23	0.79	0.02	-0.75 0.27		0.44	-0.13		

Peak 194



assignment

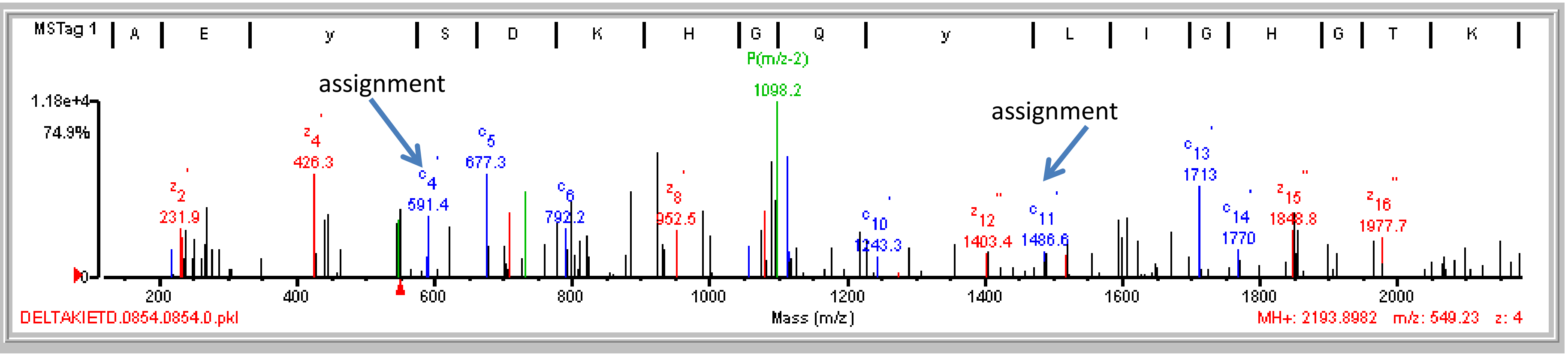


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.80	76.4	11	7/25	Y574y	(R) E/A E|y\S|D\K H G Q\Y|L I/G|H\G\T\K (V)	2032.97	81.8059	869.9	108270.8/6.48	Homo sapiens	32528301	6055	ephrin receptor EphB4 precursor

Fragment-ion (m/z)	246.98	347.14	426.18	482.47	591.26	622.62	677.22	709.47	719.32	780.51	792.34	884.58
Frac. Inten.(% of TIC)	2.47	3.98	6.62	2.71	4.55	4.55	3.48	2.32	2.68	3.05	5.02	7.99
Rel. Inten.(% of BP)	30.89	49.82	82.82	33.89	56.94	57.01	43.59	29.01	33.53	38.12	62.83	100.00
Score	-0.31	1.00	1.00	1.00	0.25	0.25	1.00	1.00	1.00	-0.38	1.00	1.00
Ion-type		c_3	z'_4	z'_5	c'_4	$c'++_{10}$	c_5	z'_7	$z'++_{13}$		c_6	$z'++_{15}$
Delta Da		-0.02	-0.04	-0.77	0.07	0.37	0.00	0.06	-0.05		0.10	0.18

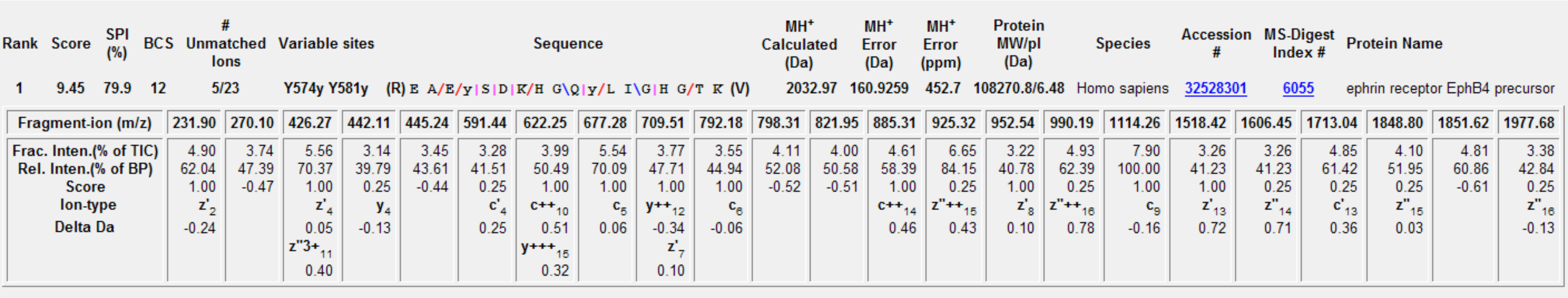
Fragment-ion (m/z)	942.03	992.44	1155.10	1243.66	1406.73	1440.08	1577.94	1687.98	1690.59	1769.19	1826.89	1884.32	1970.30
Frac. Inten.(% of TIC)	2.38	3.23	5.01	2.38	5.40	3.20	3.53	4.61	3.27	7.38	3.94	3.20	3.06
Rel. Inten.(% of BP)	29.83	40.45	62.70	29.74	67.59	40.11	44.13	57.76	40.96	92.36	49.37	40.03	38.33
Score	1.00	1.00	-0.63	0.25	0.25	-0.40	-0.44	1.00	-0.41	0.25	0.25	0.25	-0.38
Ion-type	$c++_{16}$	$c++_{17}$ $y++_{17}$		c'_{10}	c'_{11}			c_{14}		z''_{15}	c'_{15}	c'_{16}	
Delta Da	0.12	0.01 -0.01		0.17	0.18			-0.75		0.38	0.09	0.50	

Peak 195



assignment

assignment

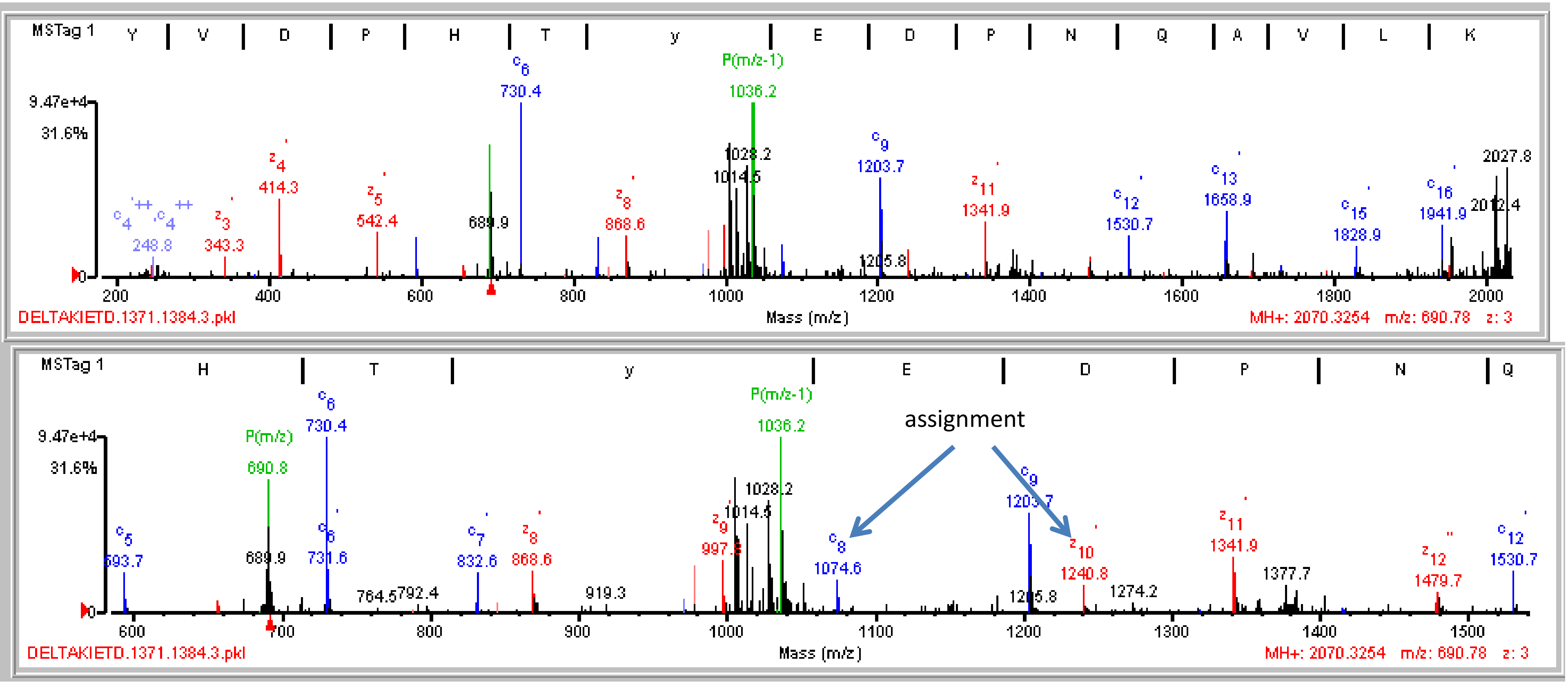


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.45	79.9	12	5/23	Y574y Y581y	(R) E A/E/y|S|D|K/H G\Q|y/L I\G|H G/T K (V)	2032.97	160.9259	452.7	108270.8/6.48	Homo sapiens	32528301	6055	ephrin receptor EphB4 precursor

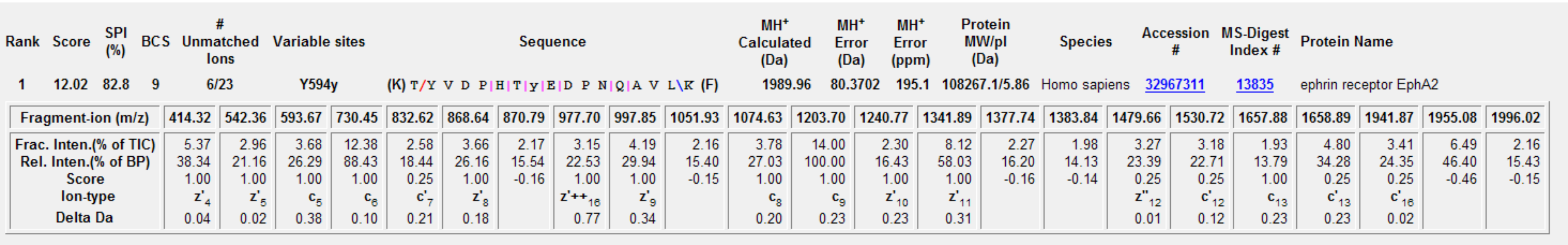
Fragment-ion (m/z)	231.90	270.10	426.27	442.11	445.24	591.44	622.25	677.28	709.51	792.18	798.31
Frac. Inten.(% of TIC)	4.90	3.74	5.56	3.14	3.45	3.28	3.99	5.54	3.77	3.55	4.11
Rel. Inten.(% of BP)	62.04	47.39	70.37	39.79	43.61	41.51	50.49	70.09	47.71	44.94	52.08
Score	1.00	-0.47	1.00	0.25	-0.44	0.25	1.00	1.00	1.00	1.00	-0.52
Ion-type	z'_2		z'_4 $z''3+_{11}$	y_4		c'_4	$c{+}{+}_{10}$ $y{+}{+}{+}_{15}$	c_5	$y{+}{+}_{12}$ z'_7	c_6	
Delta Da	-0.24		0.05 0.40	-0.13		0.25	0.51 0.32	0.06	-0.34 0.10	-0.06	

Fragment-ion (m/z)	821.95	885.31	925.32	952.54	990.19	1114.26	1518.42	1606.45	1713.04	1848.80	1851.62	1977.68
Frac. Inten.(% of TIC)	4.00	4.61	6.65	3.22	4.93	7.90	3.26	3.26	4.85	4.10	4.81	3.38
Rel. Inten.(% of BP)	50.58	58.39	84.15	40.78	62.39	100.00	41.23	41.23	61.42	51.95	60.86	42.84
Score	-0.51	1.00	0.25	1.00	0.25	1.00	1.00	0.25	0.25	0.25	-0.61	0.25
Ion-type		$c{+}{+}_{14}$	$z''{+}{+}_{15}$	z'_8	$z''{+}{+}_{16}$	c_9	z'_{13}	z''_{14}	c'_{13}	z''_{15}		z''_{16}
Delta Da		0.46	0.43	0.10	0.78	-0.16	0.72	0.71	0.36	0.03		-0.13

Peak 196



assignment

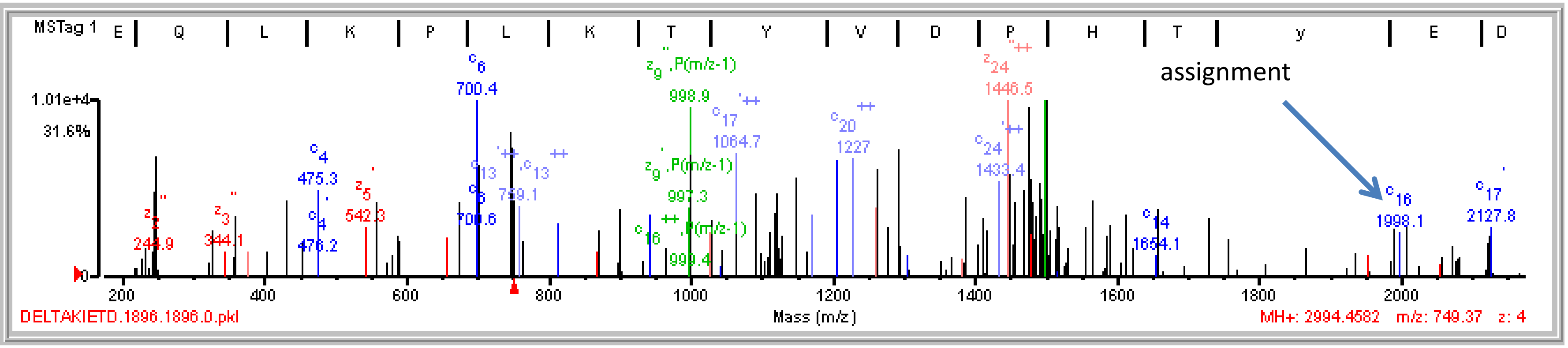


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.02	82.8	9	6/23	Y594y	(K) T/Y V D P|H|T|y|E|D P N|Q|A V L\K (F)	1989.96	80.3702	195.1	108267.1/5.86	Homo sapiens	32967311	13835	ephrin receptor EphA2

Fragment-ion (m/z)	414.32	542.36	593.67	730.45	832.62	868.64	870.79	977.70	997.85	1051.93	1074.63
Frac. Inten.(% of TIC)	5.37	2.96	3.68	12.38	2.58	3.66	2.17	3.15	4.19	2.16	3.78
Rel. Inten.(% of BP)	38.34	21.16	26.29	88.43	18.44	26.16	15.54	22.53	29.94	15.40	27.03
Score	1.00	1.00	1.00	1.00	0.25	1.00	-0.16	1.00	1.00	-0.15	1.00
Ion-type	z'_4	z'_5	c_5	c_6	c'_7	z'_8		$z'{++}_{16}$	z'_9		c_8
Delta Da	0.04	0.02	0.38	0.10	0.21	0.18		0.77	0.34		0.20

Fragment-ion (m/z)	1203.70	1240.77	1341.89	1377.74	1383.84	1479.66	1530.72	1657.88	1658.89	1941.87	1955.08	1996.02
Frac. Inten.(% of TIC)	14.00	2.30	8.12	2.27	1.98	3.27	3.18	1.93	4.80	3.41	6.49	2.16
Rel. Inten.(% of BP)	100.00	16.43	58.03	16.20	14.13	23.39	22.71	13.79	34.28	24.35	46.40	15.43
Score	1.00	1.00	1.00	-0.16	-0.14	0.25	0.25	1.00	0.25	0.25	-0.46	-0.15
Ion-type	c_9	z'_{10}	z'_{11}			z''_{12}	c'_{12}	c_{13}	c'_{13}	c'_{16}		
Delta Da	0.23	0.23	0.31			0.01	0.12	0.23	0.23	0.02		

Peak 197



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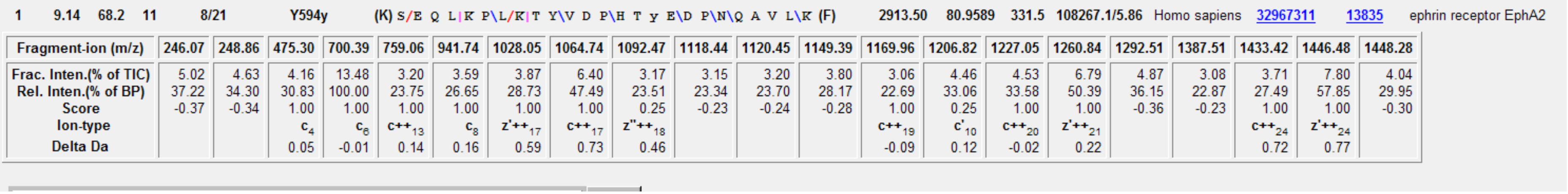
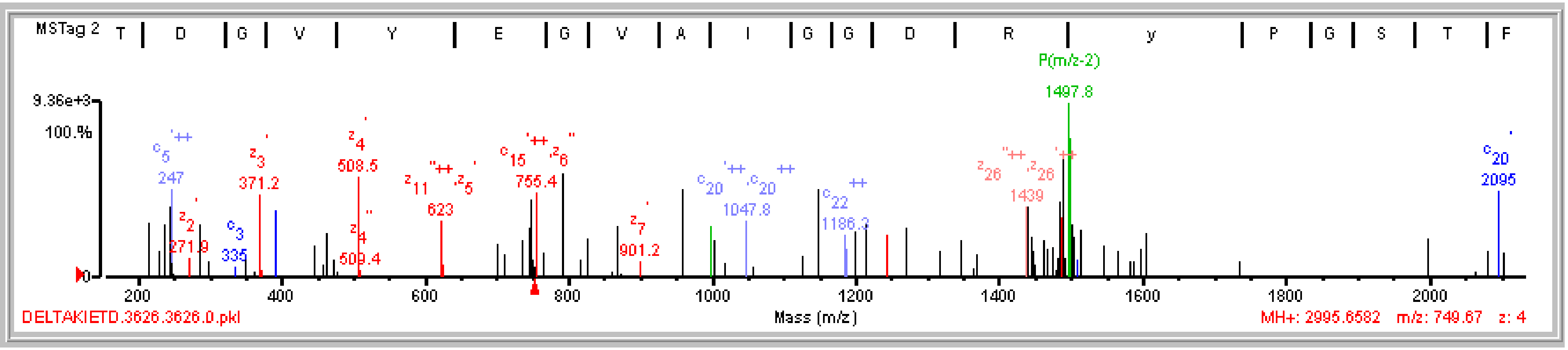


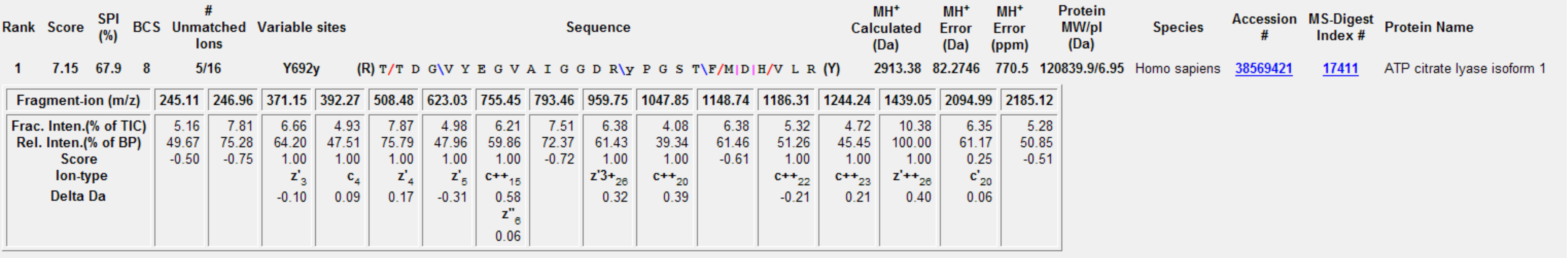
1 9.14 68.2 11 8/21 Y594y (K) S/E Q L|K P\L/K|T Y\V D P\H T y E\D P\N\Q A V L\K (F) 2913.50 80.9589 331.5 108267.1/5.86 Homo sapiens 32967311 13835 ephrin receptor EphA2

Fragment-ion (m/z)	246.07	248.86	475.30	700.39	759.06	941.74	1028.05	1064.74	1092.47	1118.44	1120.45
Frac. Inten.(% of TIC)	5.02	4.63	4.16	13.48	3.20	3.59	3.87	6.40	3.17	3.15	3.20
Rel. Inten.(% of BP)	37.22	34.30	30.83	100.00	23.75	26.65	28.73	47.49	23.51	23.34	23.70
Score	-0.37	-0.34	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.23	-0.24
Ion-type			c_4	c_6	c^{++}_{13}	c_8	z'^{++}_{17}	c^{++}_{17}	z''^{++}_{18}		
Delta Da			0.05	-0.01	0.14	0.16	0.59	0.73	0.46		

Fragment-ion (m/z)	1149.39	1169.96	1206.82	1227.05	1260.84	1292.51	1387.51	1433.42	1446.48	1448.28
Frac. Inten.(% of TIC)	3.80	3.06	4.46	4.53	6.79	4.87	3.08	3.71	7.80	4.04
Rel. Inten.(% of BP)	28.17	22.69	33.06	33.58	50.39	36.15	22.87	27.49	57.85	29.95
Score	-0.28	1.00	0.25	1.00	1.00	-0.36	-0.23	1.00	1.00	-0.30
Ion-type		c^{++}_{19}	c'_{10}	c^{++}_{20}	z'^{++}_{21}			c^{++}_{24}	z'^{++}_{24}	
Delta Da		-0.09	0.12	-0.02	0.22			0.72	0.77	

Peak 198





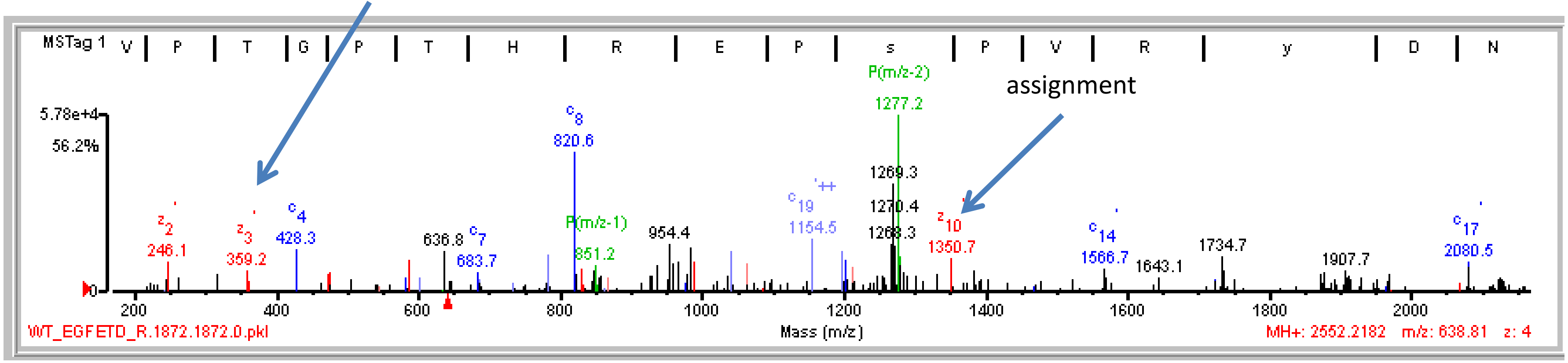
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.15	67.9	8	5/16	Y692y	(R) T/T D G\V Y E G V A I G G D R\y P G S T\F/M|D|H/V L R (Y)	2913.38	82.2746	770.5	120839.9/6.95	Homo sapiens	38569421	17411	ATP citrate lyase isoform 1

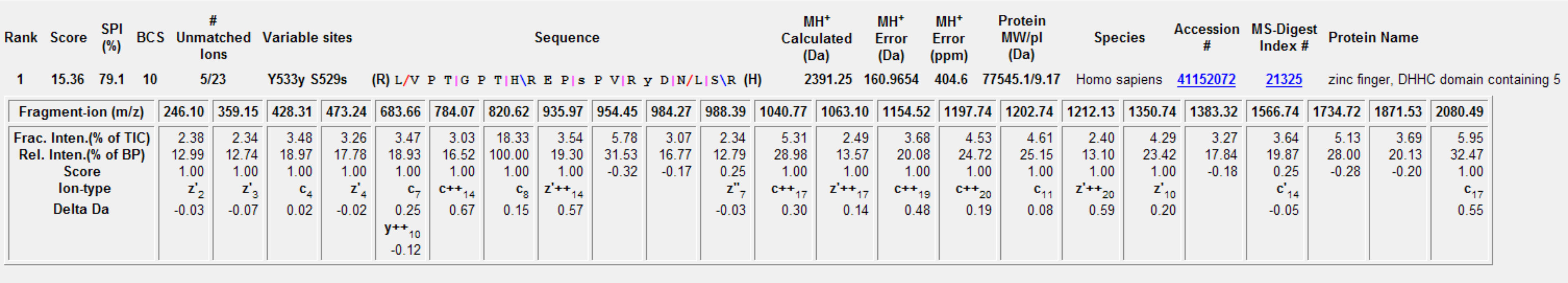
Fragment-ion (m/z)	245.11	246.96	371.15	392.27	508.48	623.03	755.45	793.46	959.75	1047.85	1148.74	1186.31	1244.24	1439.05	2094.99	2185.12
Frac. Inten.(% of TIC)	5.16	7.81	6.66	4.93	7.87	4.98	6.21	7.51	6.38	4.08	6.38	5.32	4.72	10.38	6.35	5.28
Rel. Inten.(% of BP)	49.67	75.28	64.20	47.51	75.79	47.96	59.86	72.37	61.43	39.34	61.46	51.26	45.45	100.00	61.17	50.85
Score	-0.50	-0.75	1.00	1.00	1.00	1.00	1.00	-0.72	1.00	1.00	-0.61	1.00	1.00	1.00	0.25	-0.51
Ion-type			z'_3	c_4	z'_4	z'_5	$c{+}{+}_{15}$ z''_6		$z'3{+}_{26}$	$c{+}{+}_{20}$		$c{+}{+}_{22}$	$c{+}{+}_{23}$	$z'{+}{+}_{26}$	c'_{20}	
Delta Da			-0.10	0.09	0.17	-0.31	0.58 0.06		0.32	0.39		-0.21	0.21	0.40	0.06	

Peak 199

Ions that verify assignment

assignment



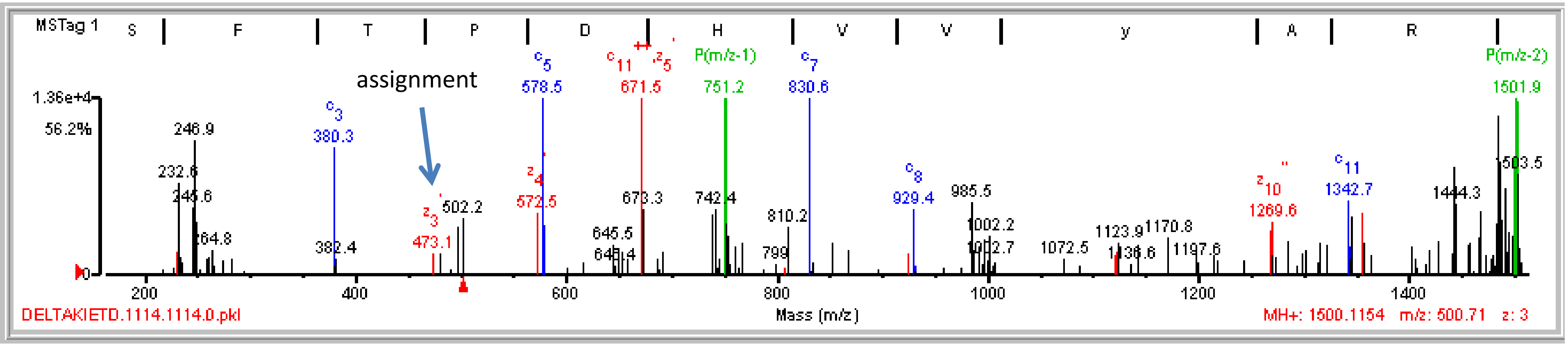


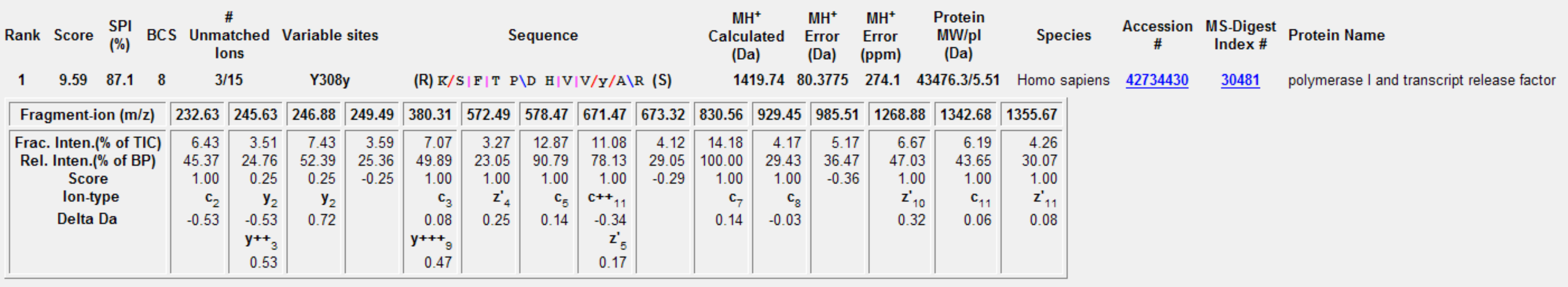
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.36	79.1	10	5/23	Y533y S529s	(R) L/V P T|G P T|H\R E P|s P V|R y D|N/L|S\R (H)	2391.25	160.9654	404.6	77545.1/9.17	Homo sapiens	41152072	21325	zinc finger, DHHC domain containing 5

Fragment-ion (m/z)	246.10	359.15	428.31	473.24	683.66	784.07	820.62	935.97	954.45	984.27	988.39
Frac. Inten.(% of TIC)	2.38	2.34	3.48	3.26	3.47	3.03	18.33	3.54	5.78	3.07	2.34
Rel. Inten.(% of BP)	12.99	12.74	18.97	17.78	18.93	16.52	100.00	19.30	31.53	16.77	12.79
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.32	-0.17	0.25
Ion-type	z'_2	z'_3	c_4	z'_4	c_7 $y++_{10}$	$c++_{14}$	c_8	$z'++_{14}$			z''_7
Delta Da	-0.03	-0.07	0.02	-0.02	0.25 -0.12	0.67	0.15	0.57			-0.03

Fragment-ion (m/z)	1040.77	1063.10	1154.52	1197.74	1202.74	1212.13	1350.74	1383.32	1566.74	1734.72	1871.53	2080.49
Frac. Inten.(% of TIC)	5.31	2.49	3.68	4.53	4.61	2.40	4.29	3.27	3.64	5.13	3.69	5.95
Rel. Inten.(% of BP)	28.98	13.57	20.08	24.72	25.15	13.10	23.42	17.84	19.87	28.00	20.13	32.47
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.18	0.25	-0.28	-0.20	1.00
Ion-type	$c++_{17}$	$z'++_{17}$	$c++_{19}$	$c++_{20}$	c_{11}	$z'++_{20}$	z'_{10}		c'_{14}			c_{17}
Delta Da	0.30	0.14	0.48	0.19	0.08	0.59	0.20		-0.05			0.55

Peak 200

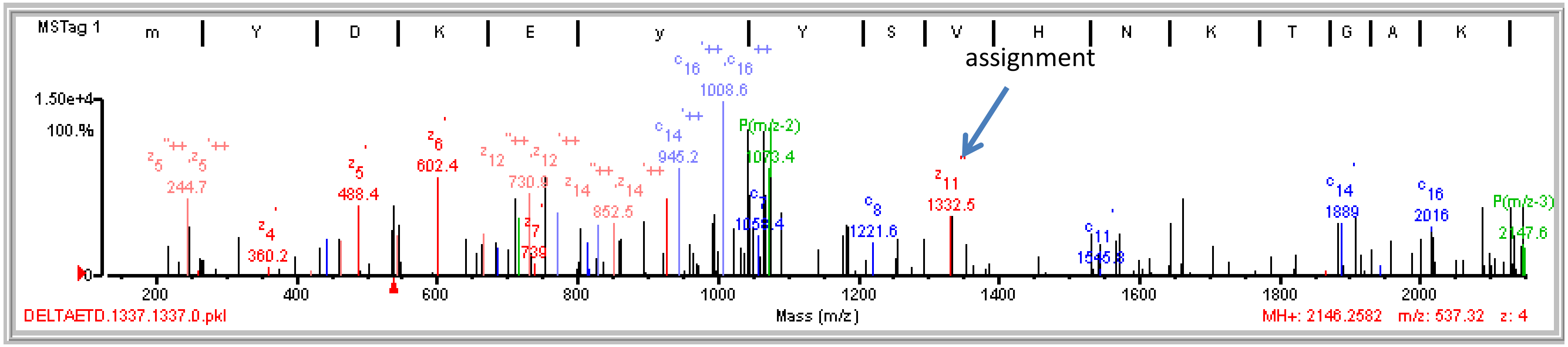




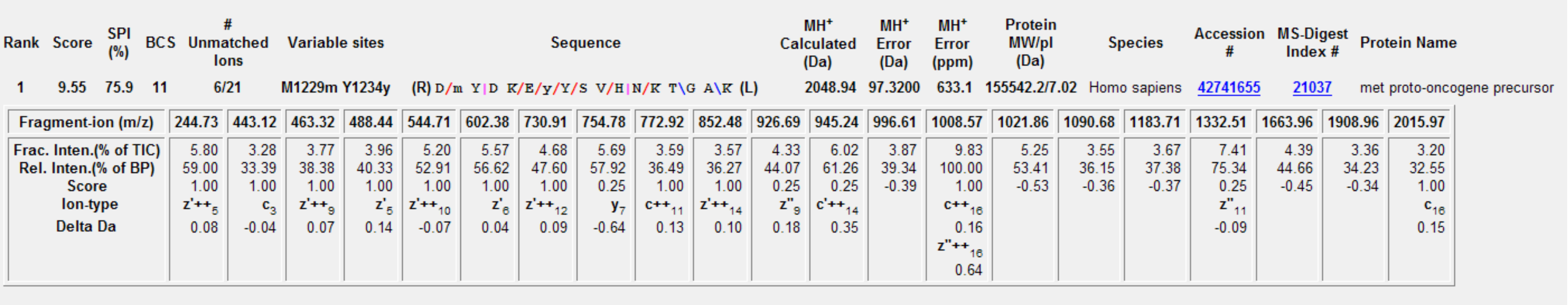
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.59	87.1	8	3/15	Y308y	(R) K/S|F|T P\D H|V|V/y/A\R (S)	1419.74	80.3775	274.1	43476.3/5.51	Homo sapiens	42734430	30481	polymerase I and transcript release factor

Fragment-ion (m/z)	232.63	245.63	246.88	249.49	380.31	572.49	578.47	671.47	673.32	830.56	929.45	985.51	1268.88	1342.68	1355.67
Frac. Inten.(% of TIC)	6.43	3.51	7.43	3.59	7.07	3.27	12.87	11.08	4.12	14.18	4.17	5.17	6.67	6.19	4.26
Rel. Inten.(% of BP)	45.37	24.76	52.39	25.36	49.89	23.05	90.79	78.13	29.05	100.00	29.43	36.47	47.03	43.65	30.07
Score	1.00	0.25	0.25	-0.25	1.00	1.00	1.00	1.00	-0.29	1.00	1.00	-0.36	1.00	1.00	1.00
Ion-type	c_2	y_2	y_2		c_3	z'_4	c_5	c^{++}_{11}		c_7	c_8		z'_{10}	c_{11}	z'_{11}
Delta Da	-0.53	-0.53	0.72		0.08	0.25	0.14	-0.34		0.14	-0.03		0.32	0.06	0.08
		y^{++}_3			y^{+++}_9			z'_5							
		0.53			0.47			0.17							

Peak 201



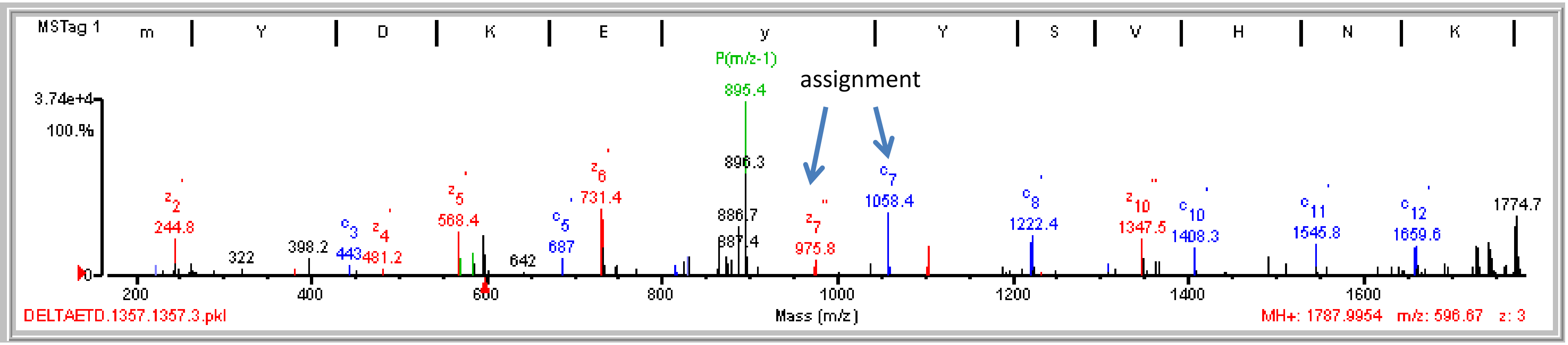
assignment

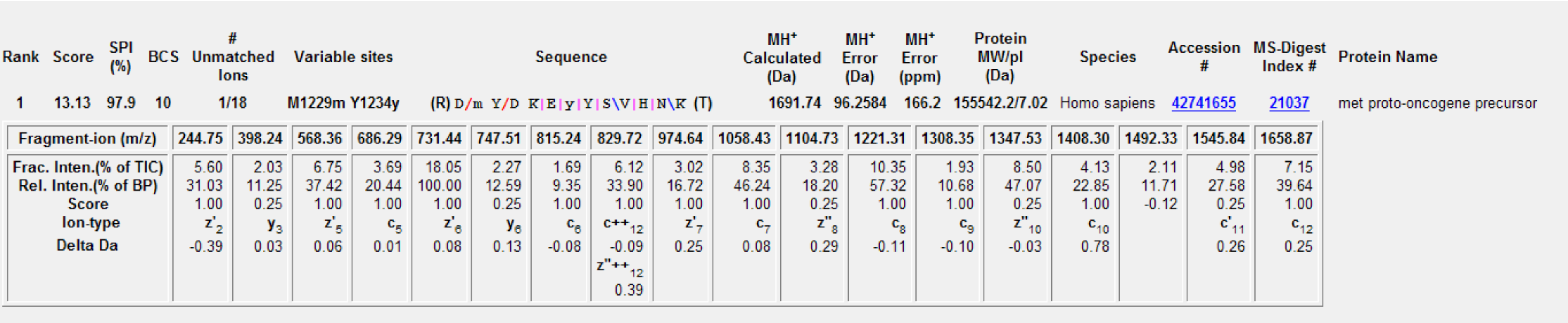


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.55	75.9	11	6/21	M1229m Y1234y	(R) D/m Y|D K/E/y/Y/S V/H|N/K T\G A\K (L)	2048.94	97.3200	633.1	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.73	443.12	463.32	488.44	544.71	602.38	730.91	754.78	772.92	852.48	926.69	945.24	996.61	1008.57	1021.86	1090.68	1183.71	1332.51	1663.96	1908.96	2015.97
Frac. Inten.(% of TIC)	5.80	3.28	3.77	3.96	5.20	5.57	4.68	5.69	3.59	3.57	4.33	6.02	3.87	9.83	5.25	3.55	3.67	7.41	4.39	3.36	3.20
Rel. Inten.(% of BP)	59.00	33.39	38.38	40.33	52.91	56.62	47.60	57.92	36.49	36.27	44.07	61.26	39.34	100.00	53.41	36.15	37.38	75.34	44.66	34.23	32.55
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	0.25	-0.39	1.00	-0.53	-0.36	-0.37	0.25	-0.45	-0.34	1.00
Ion-type	z'++_{5}	c_{3}	z'++_{9}	z'_{5}	z'++_{10}	z'_{6}	z'++_{12}	y_{7}	c++_{11}	z'++_{14}	z''_{9}	c'++_{14}		c++_{16} z''++_{16}				z''_{11}			c_{16}
Delta Da	0.08	-0.04	0.07	0.14	-0.07	0.04	0.09	-0.64	0.13	0.10	0.18	0.35		0.16 0.64				-0.09			0.15

Peak 202

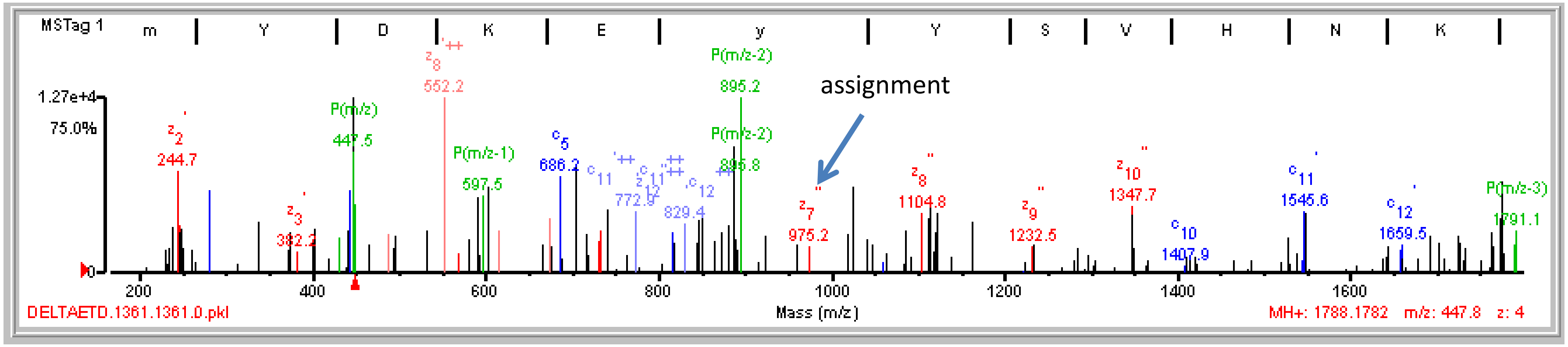




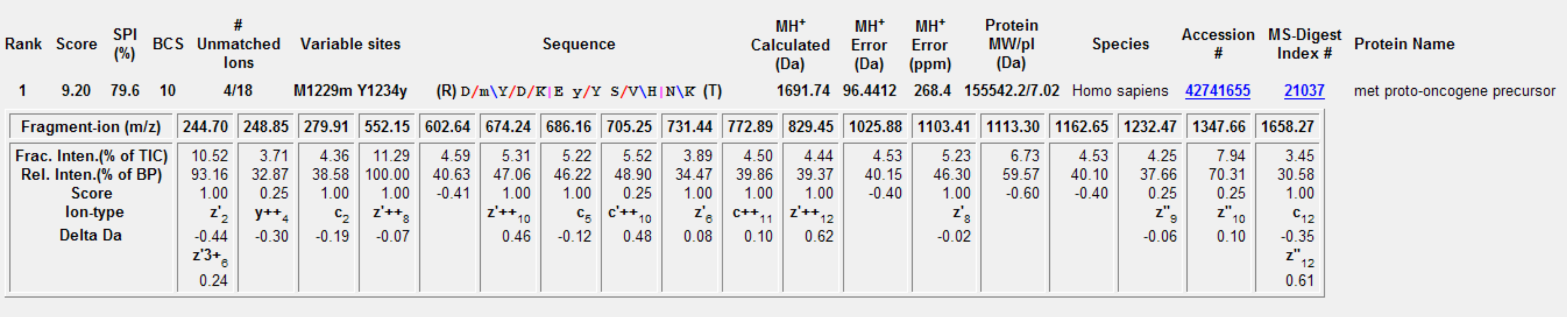
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.13	97.9	10	1/18	M1229m Y1234y	(R) D/m Y/D K|E|y|Y|S\V|H|N\K (T)	1691.74	96.2584	166.2	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.75	398.24	568.36	686.29	731.44	747.51	815.24	829.72	974.64	1058.43	1104.73	1221.31	1308.35	1347.53	1408.30	1492.33	1545.84	1658.87
Frac. Inten.(% of TIC)	5.60	2.03	6.75	3.69	18.05	2.27	1.69	6.12	3.02	8.35	3.28	10.35	1.93	8.50	4.13	2.11	4.98	7.15
Rel. Inten.(% of BP)	31.03	11.25	37.42	20.44	100.00	12.59	9.35	33.90	16.72	46.24	18.20	57.32	10.68	47.07	22.85	11.71	27.58	39.64
Score	1.00	0.25	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00	-0.12	0.25	1.00
Ion-type	z'_2	y_3	z'_5	c_5	z'_6	y_6	c_6	$c{+}{+}_{12}$ $z''{+}{+}_{12}$	z'_7	c_7	z''_8	c_8	c_9	z''_{10}	c_{10}		c'_{11}	c_{12}
Delta Da	-0.39	0.03	0.06	0.01	0.08	0.13	-0.08	-0.09 0.39	0.25	0.08	0.29	-0.11	-0.10	-0.03	0.78		0.26	0.25

Peak 203



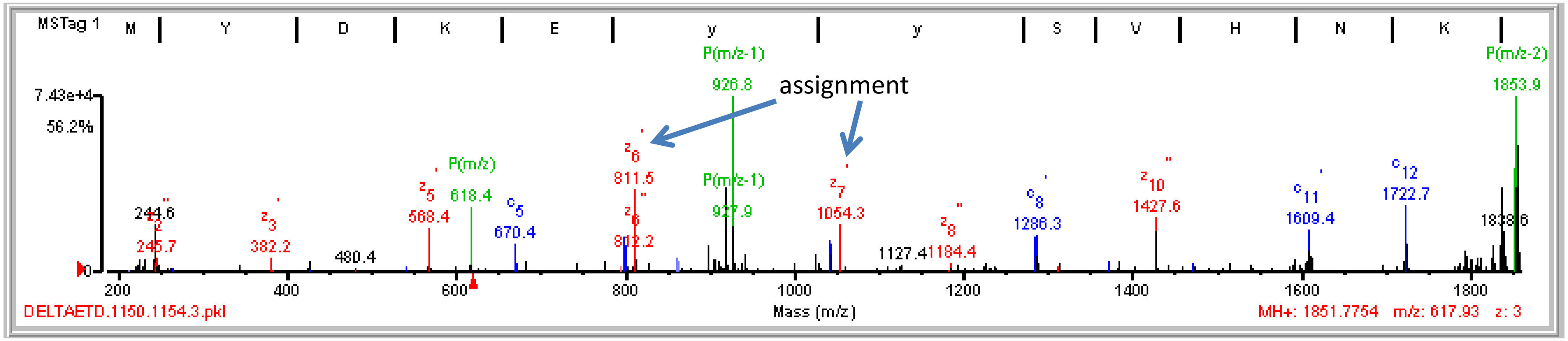
assignment

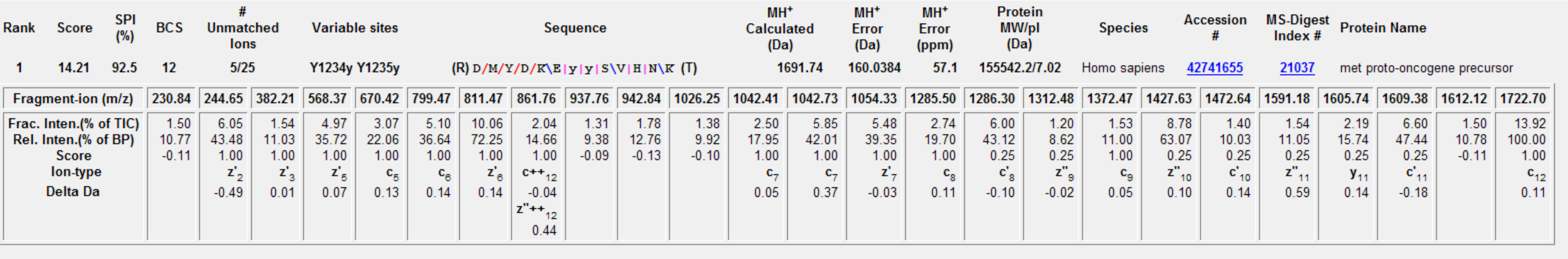


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.20	79.6	10	4/18	M1229m Y1234y	(R) D/m\Y/D/K|E y/Y S/V\H|N\K (T)	1691.74	96.4412	268.4	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.70	248.85	279.91	552.15	602.64	674.24	686.16	705.25	731.44	772.89	829.45	1025.88	1103.41	1113.30	1162.65	1232.47	1347.66	1658.27
Frac. Inten.(% of TIC)	10.52	3.71	4.36	11.29	4.59	5.31	5.22	5.52	3.89	4.50	4.44	4.53	5.23	6.73	4.53	4.25	7.94	3.45
Rel. Inten.(% of BP)	93.16	32.87	38.58	100.00	40.63	47.06	46.22	48.90	34.47	39.86	39.37	40.15	46.30	59.57	40.10	37.66	70.31	30.58
Score	1.00	0.25	1.00	1.00	-0.41	1.00	1.00	0.25	1.00	1.00	1.00	-0.40	1.00	-0.60	-0.40	0.25	0.25	1.00
Ion-type	z'_2	$y{++}_4$	c_2	$z'{++}_8$		$z'{++}_{10}$	c_5	$c'{++}_{10}$	z'_6	$c{++}_{11}$	$z'{++}_{12}$		z'_8			z''_9	z''_{10}	c_{12}
Delta Da	-0.44	-0.30	-0.19	-0.07		0.46	-0.12	0.48	0.08	0.10	0.62		-0.02			-0.06	0.10	-0.35
	$z'3{+}_6$																	z''_{12}
	0.24																	0.61

Peak 204



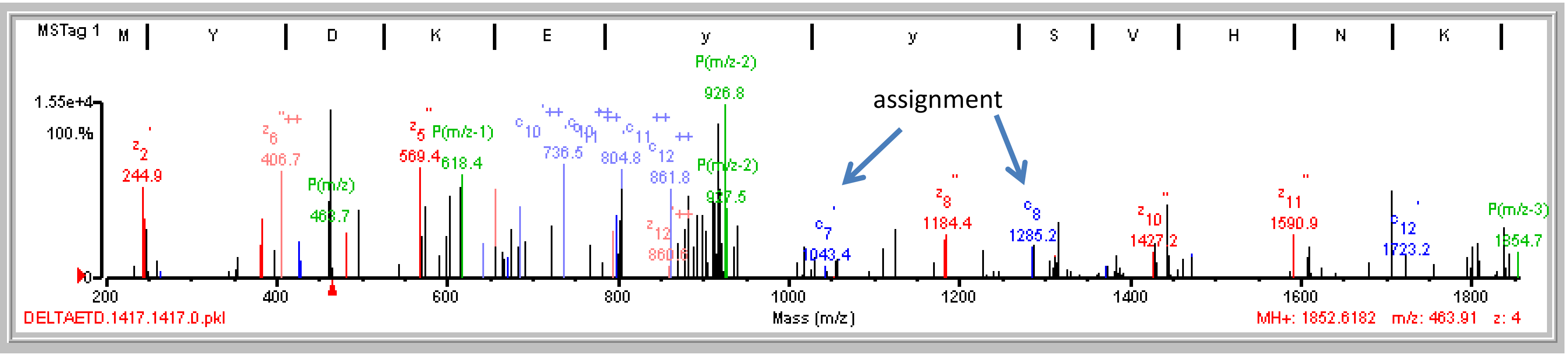


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.21	92.5	12	5/25	Y1234y Y1235y	(R) D/M/Y/D/K\E|y|y|S\V|H|N\K (T)	1691.74	160.0384	57.1	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

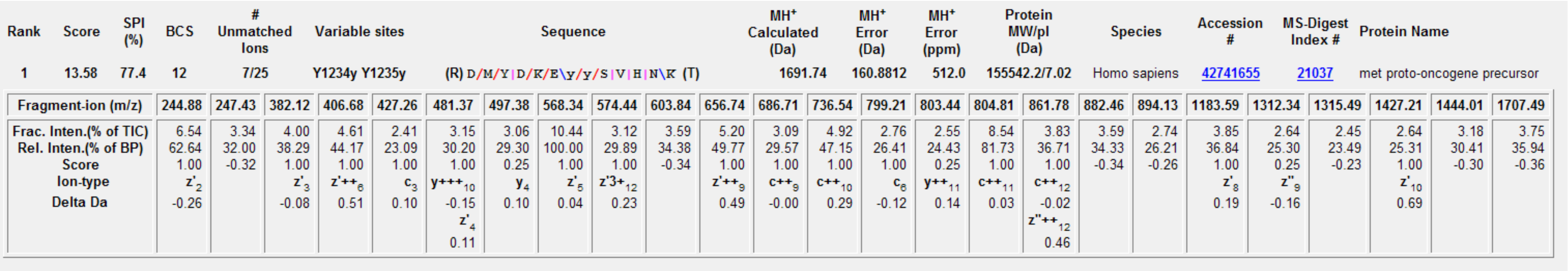
Fragment-ion (m/z)	230.84	244.65	382.21	568.37	670.42	799.47	811.47	861.76	937.76	942.84	1026.25	1042.41
Frac. Inten.(% of TIC)	1.50	6.05	1.54	4.97	3.07	5.10	10.06	2.04	1.31	1.78	1.38	2.50
Rel. Inten.(% of BP)	10.77	43.48	11.03	35.72	22.06	36.64	72.25	14.66	9.38	12.76	9.92	17.95
Score	-0.11	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.09	-0.13	-0.10	1.00
Ion-type		z'_2	z'_3	z'_5	c_5	c_6	z'_6	$c{++}_{12}$ $z''{++}_{12}$				c_7
Delta Da		-0.49	0.01	0.07	0.13	0.14	0.14	-0.04 0.44				0.05

Fragment-ion (m/z)	1042.73	1054.33	1285.50	1286.30	1312.48	1372.47	1427.63	1472.64	1591.18	1605.74	1609.38	1612.12	1722.70
Frac. Inten.(% of TIC)	5.85	5.48	2.74	6.00	1.20	1.53	8.78	1.40	1.54	2.19	6.60	1.50	13.92
Rel. Inten.(% of BP)	42.01	39.35	19.70	43.12	8.62	11.00	63.07	10.03	11.05	15.74	47.44	10.78	100.00
Score	1.00	1.00	1.00	0.25	0.25	1.00	0.25	0.25	0.25	0.25	0.25	-0.11	1.00
Ion-type	c_7	z'_7	c_8	c'_8	z''_9	c_9	z''_{10}	c'_{10}	z''_{11}	y_{11}	c'_{11}		c_{12}
Delta Da	0.37	-0.03	0.11	-0.10	-0.02	0.05	0.10	0.14	0.59	0.14	-0.18		0.11

Peak 205



assignment



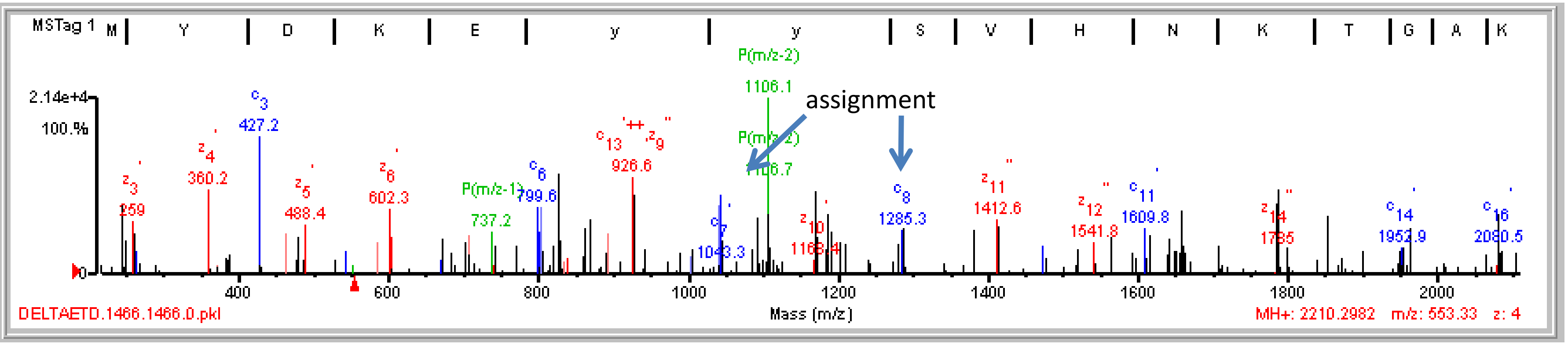
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.58	77.4	12	7/25	Y1234y Y1235y	(R) D/M/Y|D/K/E\y/y/S|V|H|N\K (T)	1691.74	160.8812	512.0	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.88	247.43	382.12	406.68	427.26	481.37	497.38	568.34
Frac. Inten.(% of TIC)	6.54	3.34	4.00	4.61	2.41	3.15	3.06	10.44
Rel. Inten.(% of BP)	62.64	32.00	38.29	44.17	23.09	30.20	29.30	100.00
Score	1.00	-0.32	1.00	1.00	1.00	1.00	0.25	1.00
Ion-type	z'_2		z'_3	$z'{++}_6$	c_3	$y{+++}_{10}$ z'_4	y_4	z'_5
Delta Da	-0.26		-0.08	0.51	0.10	-0.15 0.11	0.10	0.04

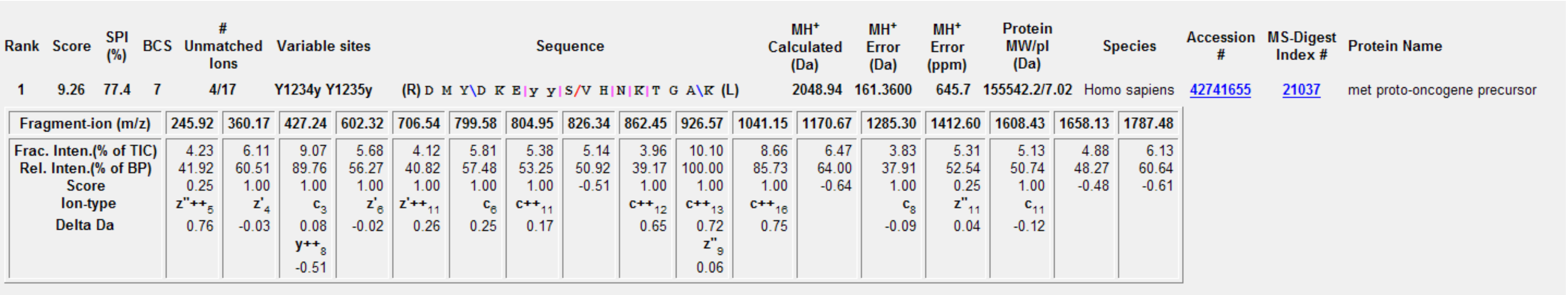
Fragment-ion (m/z)	574.44	603.84	656.74	686.71	736.54	799.21	803.44	804.81
Frac. Inten.(% of TIC)	3.12	3.59	5.20	3.09	4.92	2.76	2.55	8.54
Rel. Inten.(% of BP)	29.89	34.38	49.77	29.57	47.15	26.41	24.43	81.73
Score	1.00	-0.34	1.00	1.00	1.00	1.00	0.25	1.00
Ion-type	$z'3{+}_{12}$		$z'{++}_9$	$c{++}_9$	$c{++}_{10}$	c_6	$y{++}_{11}$	$c{++}_{11}$
Delta Da	0.23		0.49	-0.00	0.29	-0.12	0.14	0.03

Fragment-ion (m/z)	861.78	882.46	894.13	1183.59	1312.34	1315.49	1427.21	1444.01	1707.49
Frac. Inten.(% of TIC)	3.83	3.59	2.74	3.85	2.64	2.45	2.64	3.18	3.75
Rel. Inten.(% of BP)	36.71	34.33	26.21	36.84	25.30	23.49	25.31	30.41	35.94
Score	1.00	-0.34	-0.26	1.00	0.25	-0.23	1.00	-0.30	-0.36
Ion-type	$c{++}_{12}$ $z''{++}_{12}$			z'_8	z''_9		z'_{10}		
Delta Da	-0.02 0.46			0.19	-0.16		0.69		

Peak 206



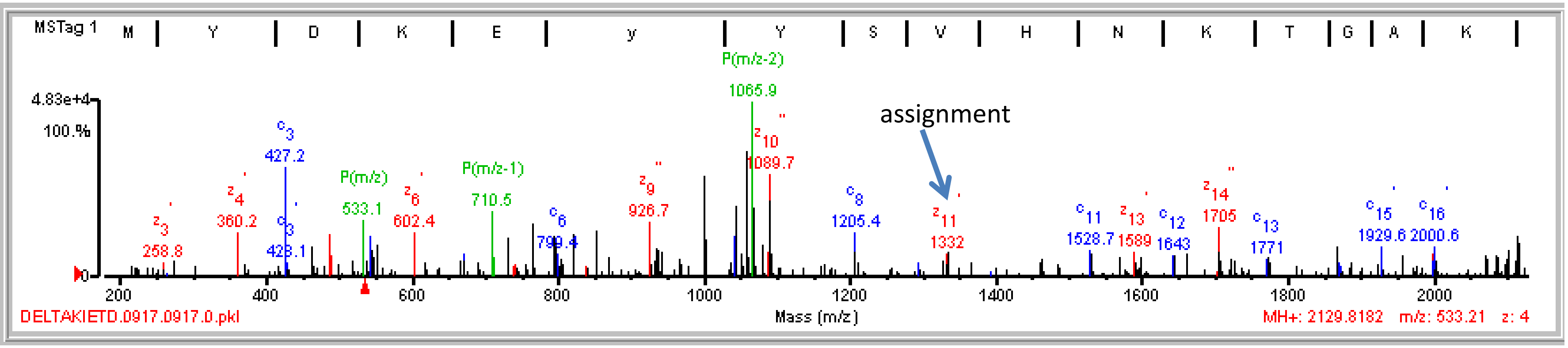
assignment



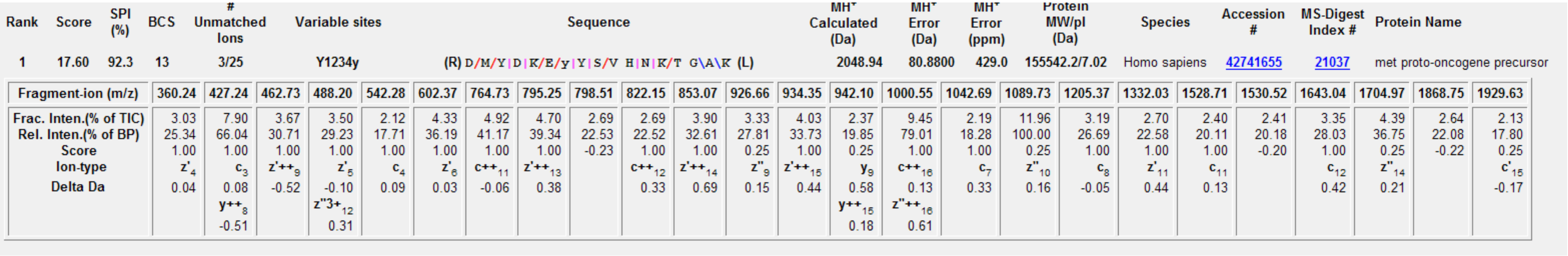
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.26	77.4	7	4/17	Y1234y Y1235y	(R) D M Y\D K E|y y|S/V H|N|K|T G A\K (L)	2048.94	161.3600	645.7	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	245.92	360.17	427.24	602.32	706.54	799.58	804.95	826.34	862.45	926.57	1041.15	1170.67	1285.30	1412.60	1608.43	1658.13	1787.48
Frac. Inten.(% of TIC)	4.23	6.11	9.07	5.68	4.12	5.81	5.38	5.14	3.96	10.10	8.66	6.47	3.83	5.31	5.13	4.88	6.13
Rel. Inten.(% of BP)	41.92	60.51	89.76	56.27	40.82	57.48	53.25	50.92	39.17	100.00	85.73	64.00	37.91	52.54	50.74	48.27	60.64
Score	0.25	1.00	1.00	1.00	1.00	1.00	1.00	-0.51	1.00	1.00	1.00	-0.64	1.00	0.25	1.00	-0.48	-0.61
Ion-type	z''^{++}_{5}	z'_{4}	c_{3} y^{++}_{8}	z'_{6}	z'^{++}_{11}	c_{6}	c^{++}_{11}		c^{++}_{12}	c^{++}_{13} z''_{9}	c^{++}_{16}		c_{8}	z''_{11}	c_{11}		
Delta Da	0.76	-0.03	0.08 -0.51	-0.02	0.26	0.25	0.17		0.65	0.72 0.06	0.75		-0.09	0.04	-0.12		

Peak 207



assignment

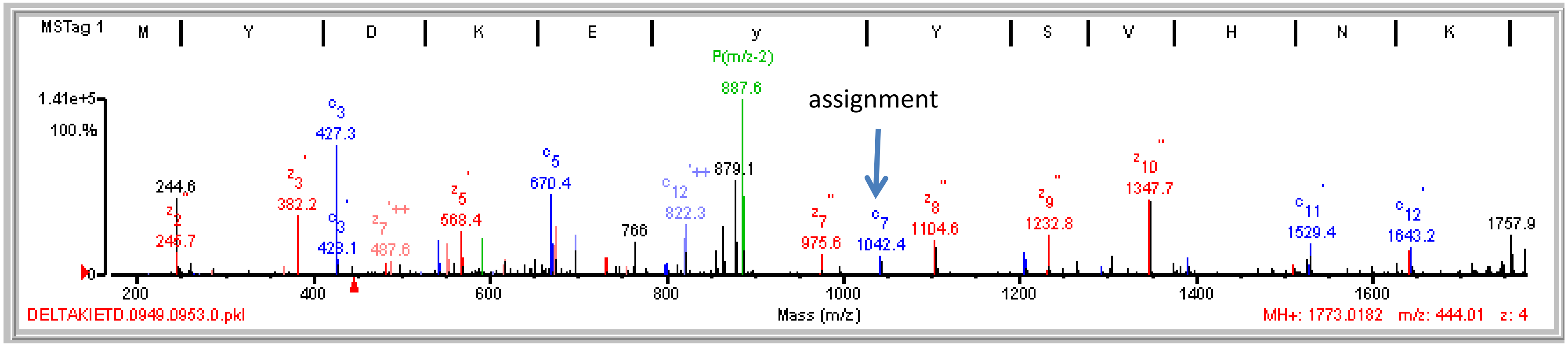


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.60	92.3	13	3/25	Y1234y	(R) D/M/Y|D|K/E/y|Y|S/V H|N|K/T G\A\K (L)	2048.94	80.8800	429.0	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

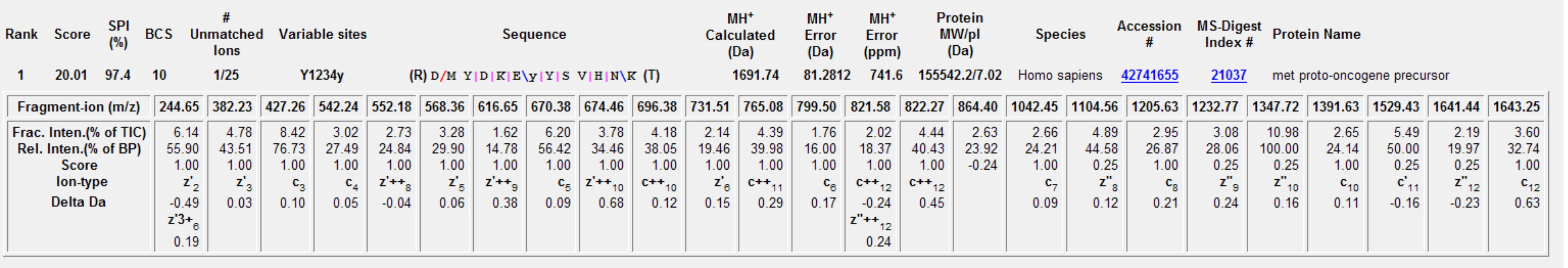
Fragment-ion (m/z)	360.24	427.24	462.73	488.20	542.28	602.37	764.73	795.25	798.51	822.15	853.07	926.66
Frac. Inten.(% of TIC)	3.03	7.90	3.67	3.50	2.12	4.33	4.92	4.70	2.69	2.69	3.90	3.33
Rel. Inten.(% of BP)	25.34	66.04	30.71	29.23	17.71	36.19	41.17	39.34	22.53	22.52	32.61	27.81
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.23	1.00	1.00	0.25
Ion-type	z'_4	c_3	$z'{++}_9$	z'_5	c_4	z'_6	$c{++}_{11}$	$z'{++}_{13}$		$c{++}_{12}$	$z'{++}_{14}$	z''_9
Delta Da	0.04	0.08	-0.52	-0.10	0.09	0.03	-0.06	0.38		0.33	0.69	0.15
		$y{++}_8$		$z''3{+}_{12}$								
		-0.51		0.31								

Fragment-ion (m/z)	934.35	942.10	1000.55	1042.69	1089.73	1205.37	1332.03	1528.71	1530.52	1643.04	1704.97	1868.75	1929.63
Frac. Inten.(% of TIC)	4.03	2.37	9.45	2.19	11.96	3.19	2.70	2.40	2.41	3.35	4.39	2.64	2.13
Rel. Inten.(% of BP)	33.73	19.85	79.01	18.28	100.00	26.69	22.58	20.11	20.18	28.03	36.75	22.08	17.80
Score	1.00	0.25	1.00	1.00	0.25	1.00	1.00	1.00	-0.20	1.00	0.25	-0.22	0.25
Ion-type	$z'{++}_{15}$	y_9	$c{++}_{16}$	c_7	z''_{10}	c_8	z'_{11}	c_{11}		c_{12}	z''_{14}		c'_{15}
Delta Da	0.44	0.58	0.13	0.33	0.16	-0.05	0.44	0.13		0.42	0.21		-0.17
		$y{++}_{15}$	$z''{++}_{16}$										
		0.18	0.61										

Peak 208



assignment

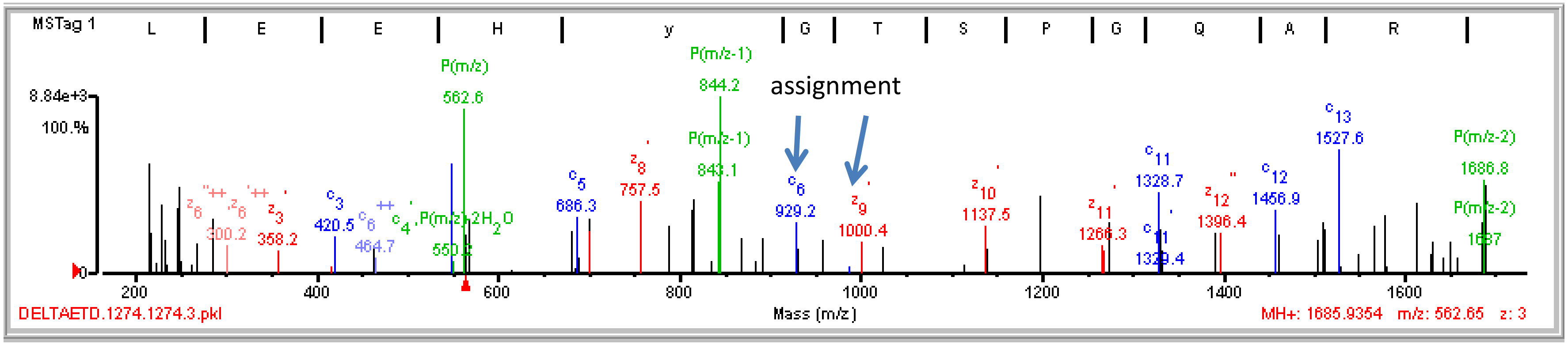


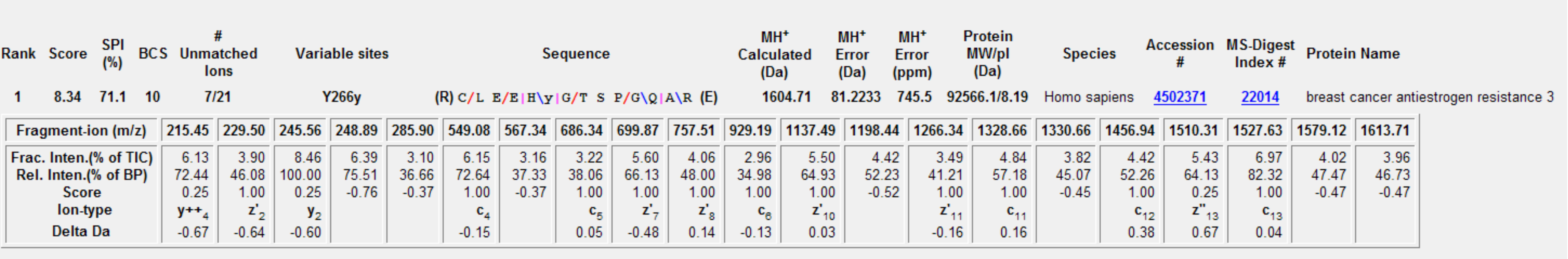
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.01	97.4	10	1/25	Y1234y	(R) D/M Y|D|K|E\y|Y|S V|H|N\K (T)	1691.74	81.2812	741.6	155542.2/7.02	Homo sapiens	42741655	21037	met proto-oncogene precursor

Fragment-ion (m/z)	244.65	382.23	427.26	542.24	552.18	568.36	616.65	670.38	674.46	696.38	731.51	765.08
Frac. Inten.(% of TIC)	6.14	4.78	8.42	3.02	2.73	3.28	1.62	6.20	3.78	4.18	2.14	4.39
Rel. Inten.(% of BP)	55.90	43.51	76.73	27.49	24.84	29.90	14.78	56.42	34.46	38.05	19.46	39.98
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	z'_2 $z'3+_6$	z'_3	c_3	c_4	$z'++_8$	z'_5	$z'++_9$	c_5	$z'++_{10}$	$c++_{10}$	z'_6	$c++_{11}$
Delta Da	-0.49 0.19	0.03	0.10	0.05	-0.04	0.06	0.38	0.09	0.68	0.12	0.15	0.29

Fragment-ion (m/z)	799.50	821.58	822.27	864.40	1042.45	1104.56	1205.63	1232.77	1347.72	1391.63	1529.43	1641.44	1643.25
Frac. Inten.(% of TIC)	1.76	2.02	4.44	2.63	2.66	4.89	2.95	3.08	10.98	2.65	5.49	2.19	3.60
Rel. Inten.(% of BP)	16.00	18.37	40.43	23.92	24.21	44.58	26.87	28.06	100.00	24.14	50.00	19.97	32.74
Score	1.00	1.00	1.00	-0.24	1.00	0.25	1.00	0.25	0.25	1.00	0.25	0.25	1.00
Ion-type	c_6	$c++_{12}$ $z''++_{12}$	$c++_{12}$		c_7	z''_8	c_8	z''_9	z''_{10}	c_{10}	c'_{11}	z''_{12}	c_{12}
Delta Da	0.17	-0.24 0.24	0.45		0.09	0.12	0.21	0.24	0.16	0.11	-0.16	-0.23	0.63

Peak 210



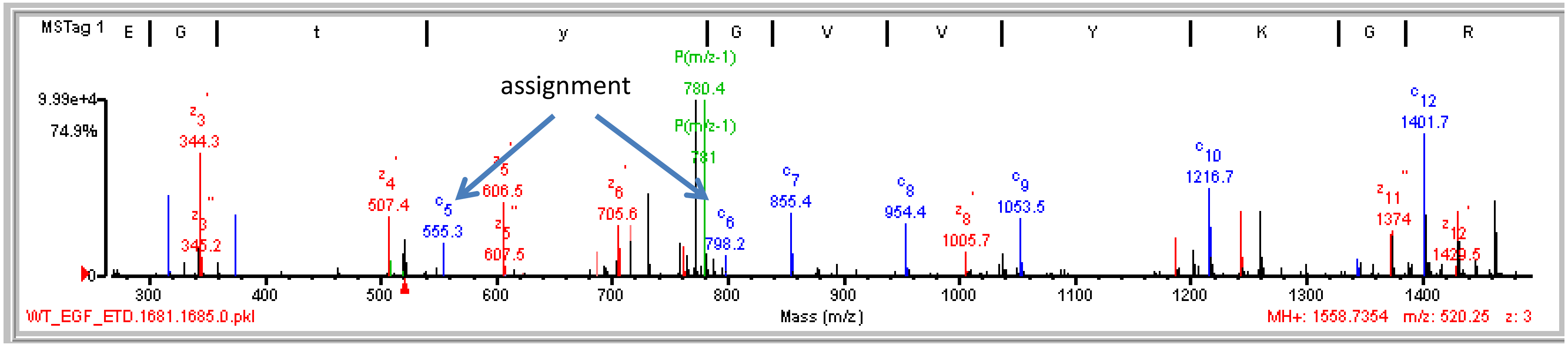


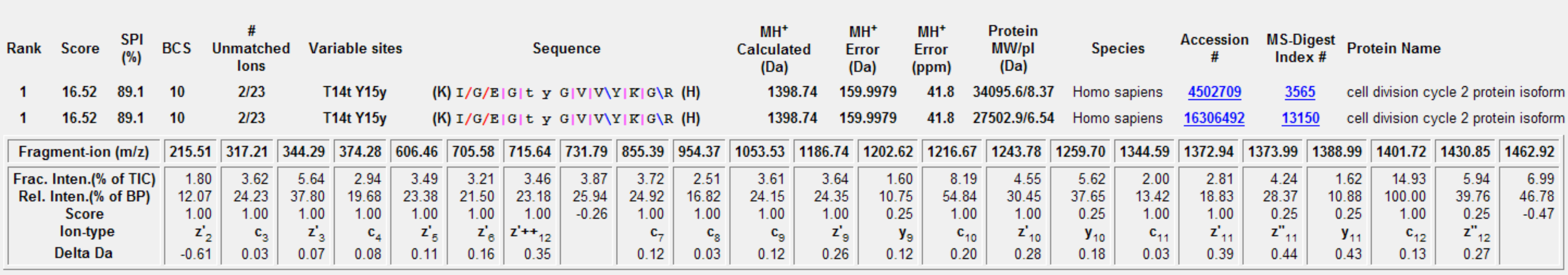
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.34	71.1	10	7/21	Y266y	(R) C/L E/E|H\y|G/T S P/G\Q|A\R (E)	1604.71	81.2233	745.5	92566.1/8.19	Homo sapiens	4502371	22014	breast cancer antiestrogen resistance 3

Fragment-ion (m/z)	215.45	229.50	245.56	248.89	285.90	549.08	567.34	686.34	699.87	757.51
Frac. Inten.(% of TIC)	6.13	3.90	8.46	6.39	3.10	6.15	3.16	3.22	5.60	4.06
Rel. Inten.(% of BP)	72.44	46.08	100.00	75.51	36.66	72.64	37.33	38.06	66.13	48.00
Score	0.25	1.00	0.25	-0.76	-0.37	1.00	-0.37	1.00	1.00	1.00
Ion-type	$y{++}_4$	z'_2	y_2			c_4		c_5	z'_7	z'_8
Delta Da	-0.67	-0.64	-0.60			-0.15		0.05	-0.48	0.14

Fragment-ion (m/z)	929.19	1137.49	1198.44	1266.34	1328.66	1330.66	1456.94	1510.31	1527.63	1579.12	1613.71
Frac. Inten.(% of TIC)	2.96	5.50	4.42	3.49	4.84	3.82	4.42	5.43	6.97	4.02	3.96
Rel. Inten.(% of BP)	34.98	64.93	52.23	41.21	57.18	45.07	52.26	64.13	82.32	47.47	46.73
Score	1.00	1.00	-0.52	1.00	1.00	-0.45	1.00	0.25	1.00	-0.47	-0.47
Ion-type	c_6	z'_{10}		z'_{11}	c_{11}		c_{12}	z''_{13}	c_{13}		
Delta Da	-0.13	0.03		-0.16	0.16		0.38	0.67	0.04		

Peak 211



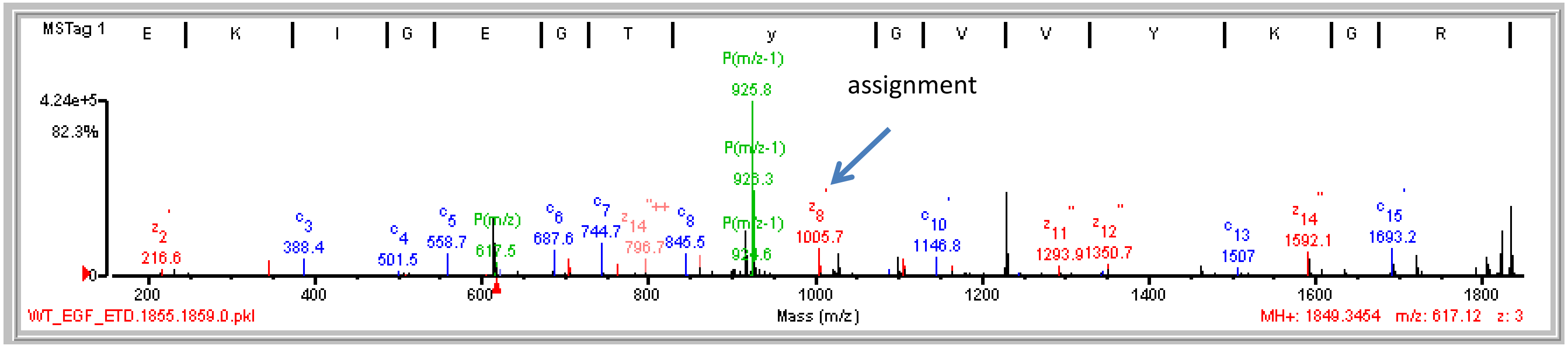


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.52	89.1	10	2/23	T14t Y15y	(K) I/G/E|G|t y G|V|V\Y|K|G\R (H)	1398.74	159.9979	41.8	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	16.52	89.1	10	2/23	T14t Y15y	(K) I/G/E|G|t y G|V|V\Y|K|G\R (H)	1398.74	159.9979	41.8	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

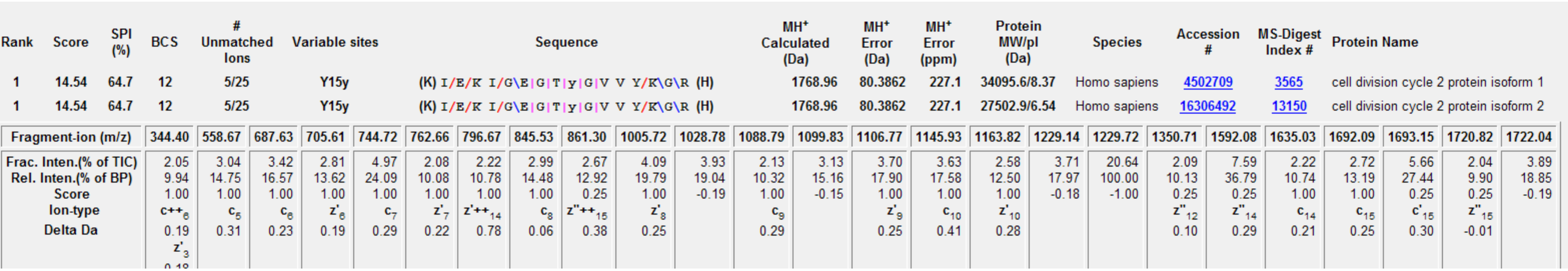
Fragment-ion (m/z)	215.51	317.21	344.29	374.28	606.46	705.58	715.64	731.79	855.39	954.37	1053.53	1186.74
Frac. Inten.(% of TIC)	1.80	3.62	5.64	2.94	3.49	3.21	3.46	3.87	3.72	2.51	3.61	3.64
Rel. Inten.(% of BP)	12.07	24.23	37.80	19.68	23.38	21.50	23.18	25.94	24.92	16.82	24.15	24.35
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.26	1.00	1.00	1.00	1.00
Ion-type	z'_2	c_3	z'_3	c_4	z'_5	z'_6	$z'{++}_{12}$		c_7	c_8	c_9	z'_9
Delta Da	-0.61	0.03	0.07	0.08	0.11	0.16	0.35		0.12	0.03	0.12	0.26

Fragment-ion (m/z)	1202.62	1216.67	1243.78	1259.70	1344.59	1372.94	1373.99	1388.99	1401.72	1430.85	1462.92
Frac. Inten.(% of TIC)	1.60	8.19	4.55	5.62	2.00	2.81	4.24	1.62	14.93	5.94	6.99
Rel. Inten.(% of BP)	10.75	54.84	30.45	37.65	13.42	18.83	28.37	10.88	100.00	39.76	46.78
Score	0.25	1.00	1.00	0.25	1.00	1.00	0.25	0.25	1.00	0.25	-0.47
Ion-type	y_9	c_{10}	z'_{10}	y_{10}	c_{11}	z'_{11}	z''_{11}	y_{11}	c_{12}	z''_{12}	
Delta Da	0.12	0.20	0.28	0.18	0.03	0.39	0.44	0.43	0.13	0.27	

Peak 212



assignment

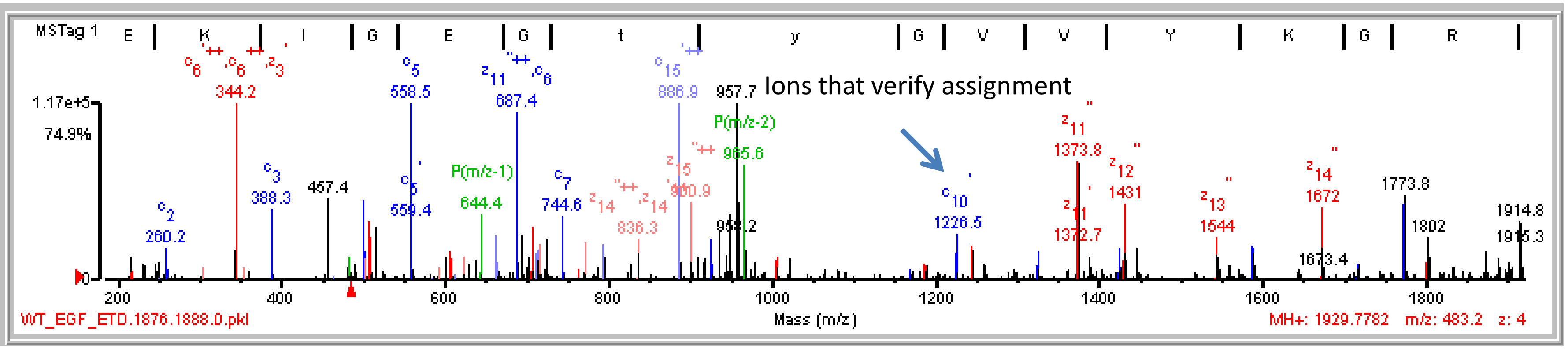


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.54	64.7	12	5/25	Y15y	(K) I/E/K I/G\E|G|T|y|G|V V Y/K\G\R (H)	1768.96	80.3862	227.1	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	14.54	64.7	12	5/25	Y15y	(K) I/E/K I/G\E|G|T|y|G|V V Y/K\G\R (H)	1768.96	80.3862	227.1	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

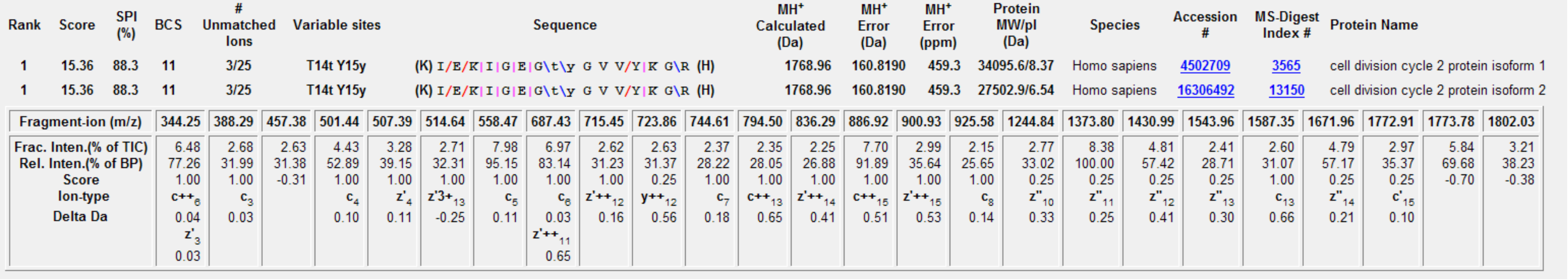
Fragment-ion (m/z)	344.40	558.67	687.63	705.61	744.72	762.66	796.67	845.53	861.30	1005.72	1028.78
Frac. Inten.(% of TIC)	2.05	3.04	3.42	2.81	4.97	2.08	2.22	2.99	2.67	4.09	3.93
Rel. Inten.(% of BP)	9.94	14.75	16.57	13.62	24.09	10.08	10.78	14.48	12.92	19.79	19.04
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.19
Ion-type	c^{++}_{6} z'_{3}	c_{5}	c_{6}	z'_{6}	c_{7}	z'_{7}	z'^{++}_{14}	c_{8}	z''^{++}_{15}	z'_{8}	
Delta Da	0.19 0.18	0.31	0.23	0.19	0.29	0.22	0.78	0.06	0.38	0.25	

Fragment-ion (m/z)	1088.79	1099.83	1106.77	1145.93	1163.82	1229.14	1229.72	1350.71	1592.08	1635.03	1692.09	1693.15	1720.82	1722.04
Frac. Inten.(% of TIC)	2.13	3.13	3.70	3.63	2.58	3.71	20.64	2.09	7.59	2.22	2.72	5.66	2.04	3.89
Rel. Inten.(% of BP)	10.32	15.16	17.90	17.58	12.50	17.97	100.00	10.13	36.79	10.74	13.19	27.44	9.90	18.85
Score	1.00	-0.15	1.00	1.00	1.00	-0.18	-1.00	0.25	0.25	1.00	1.00	0.25	0.25	-0.19
Ion-type	c_{9}		z'_{9}	c_{10}	z'_{10}			z''_{12}	z''_{14}	c_{14}	c_{15}	c'_{15}	z''_{15}	
Delta Da	0.29		0.25	0.41	0.28			0.10	0.29	0.21	0.25	0.30	-0.01	

Peak 214



Ions that verify assignment

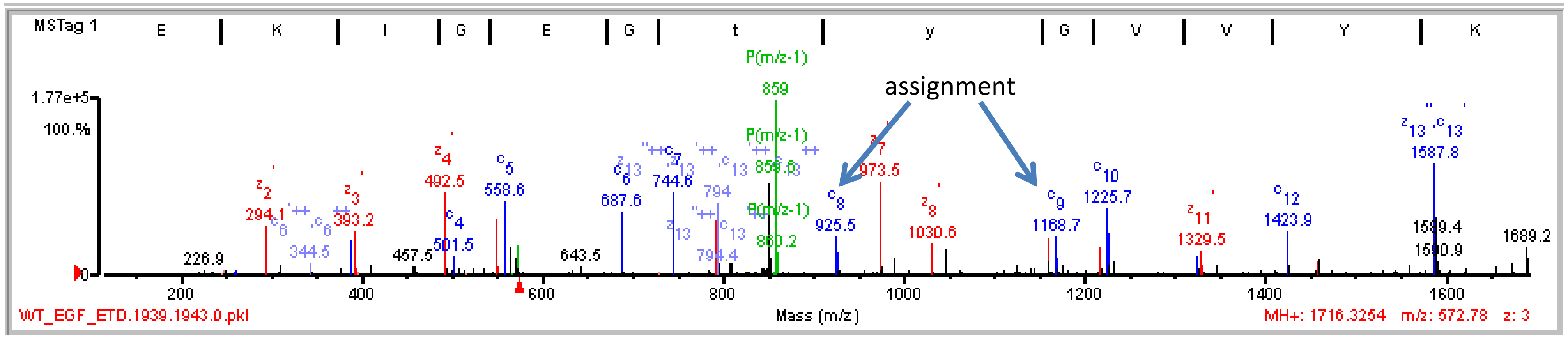


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.36	88.3	11	3/25	T14t Y15y	(K) I/E/K|I|G|E|G\t\y G V V/Y|K G\R (H)	1768.96	160.8190	459.3	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	15.36	88.3	11	3/25	T14t Y15y	(K) I/E/K|I|G|E|G\t\y G V V/Y|K G\R (H)	1768.96	160.8190	459.3	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

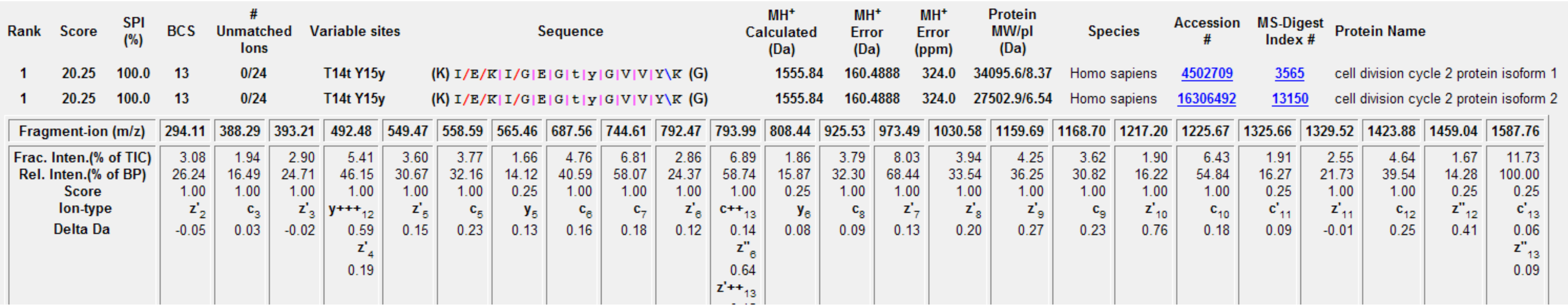
Fragment-ion (m/z)	344.25	388.29	457.38	501.44	507.39	514.64	558.47	687.43	715.45	723.86	744.61	794.50	836.29
Frac. Inten.(% of TIC)	6.48	2.68	2.63	4.43	3.28	2.71	7.98	6.97	2.62	2.63	2.37	2.35	2.25
Rel. Inten.(% of BP)	77.26	31.99	31.38	52.89	39.15	32.31	95.15	83.14	31.23	31.37	28.22	28.05	26.88
Score	1.00	1.00	-0.31	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00
Ion-type	c++$_{6}$ z'$_{3}$	c$_{3}$		c$_{4}$	z'$_{4}$	z'3+$_{13}$	c$_{5}$	c$_{6}$ z'++$_{11}$	z'++$_{12}$	y++$_{12}$	c$_{7}$	c++$_{13}$	z'++$_{14}$
Delta Da	0.04 0.03	0.03		0.10	0.11	-0.25	0.11	0.03 0.65	0.16	0.56	0.18	0.65	0.41

Fragment-ion (m/z)	886.92	900.93	925.58	1244.84	1373.80	1430.99	1543.96	1587.35	1671.96	1772.91	1773.78	1802.03
Frac. Inten.(% of TIC)	7.70	2.99	2.15	2.77	8.38	4.81	2.41	2.60	4.79	2.97	5.84	3.21
Rel. Inten.(% of BP)	91.89	35.64	25.65	33.02	100.00	57.42	28.71	31.07	57.17	35.37	69.68	38.23
Score	1.00	1.00	1.00	0.25	0.25	0.25	0.25	1.00	0.25	0.25	-0.70	-0.38
Ion-type	c++$_{15}$	z'++$_{15}$	c$_{8}$	z"$_{10}$	z"$_{11}$	z"$_{12}$	z"$_{13}$	c$_{13}$	z"$_{14}$	c'$_{15}$		
Delta Da	0.51	0.53	0.14	0.33	0.25	0.41	0.30	0.66	0.21	0.10		

Peak 215



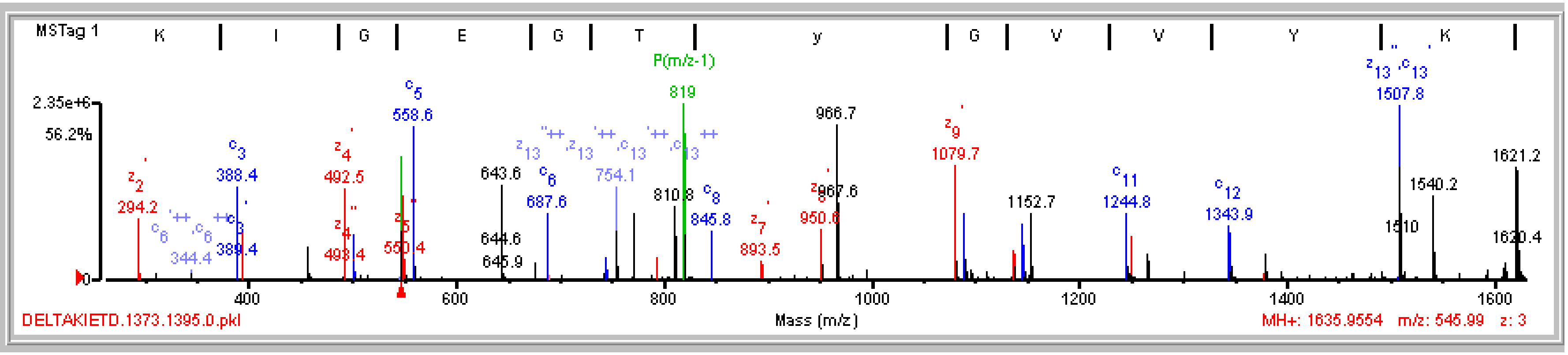
assignment

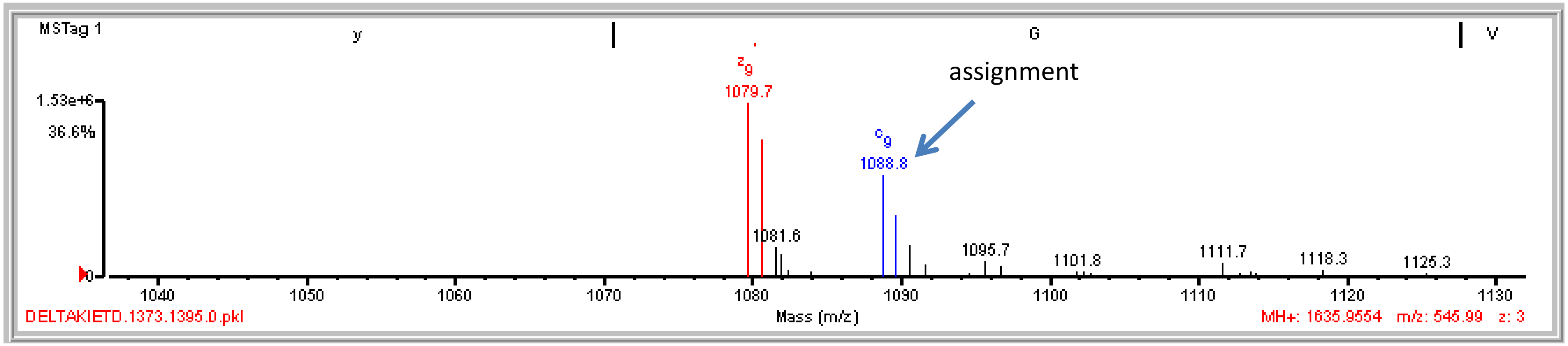


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.25	100.0	13	0/24	T14t Y15y	(K) I/E/K|I/G|E|G|t|y|G|V|V|Y\K (G)	1555.84	160.4888	324.0	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	20.25	100.0	13	0/24	T14t Y15y	(K) I/E/K|I/G|E|G|t|y|G|V|V|Y\K (G)	1555.84	160.4888	324.0	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

Fragment-ion (m/z)	294.11	388.29	393.21	492.48	549.47	558.59	565.46	687.56	744.61	792.47	793.99	808.44	925.53	973.49	1030.58	1159.69	1168.70	1217.20	1225.67	1325.66	1329.52	1423.88	1459.04	1587.76
Frac. Inten.(% of TIC)	3.08	1.94	2.90	5.41	3.60	3.77	1.66	4.76	6.81	2.86	6.89	1.86	3.79	8.03	3.94	4.25	3.62	1.90	6.43	1.91	2.55	4.64	1.67	11.73
Rel. Inten.(% of BP)	26.24	16.49	24.71	46.15	30.67	32.16	14.12	40.59	58.07	24.37	58.74	15.87	32.30	68.44	33.54	36.25	30.82	16.22	54.84	16.27	21.73	39.54	14.28	100.00
Score	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	0.25
Ion-type	z'_2	c_3	z'_3	y^{+++}_{12} z'_4	z'_5	c_5	y_5	c_6	c_7	z'_6	c^{++}_{13} z''_6 z'^{++}_{13}	y_6	c_8	z'_7	z'_8	z'_9	c_9	z'_{10}	c_{10}	c'_{11}	z'_{11}	c_{12}	z''_{12}	c'_{13} z''_{13}
Delta Da	-0.05	0.03	-0.02	0.59 0.19	0.15	0.23	0.13	0.16	0.18	0.12	0.14 0.64	0.08	0.09	0.13	0.20	0.27	0.23	0.76	0.18	0.09	-0.01	0.25	0.41	0.06 0.09

Peak 216





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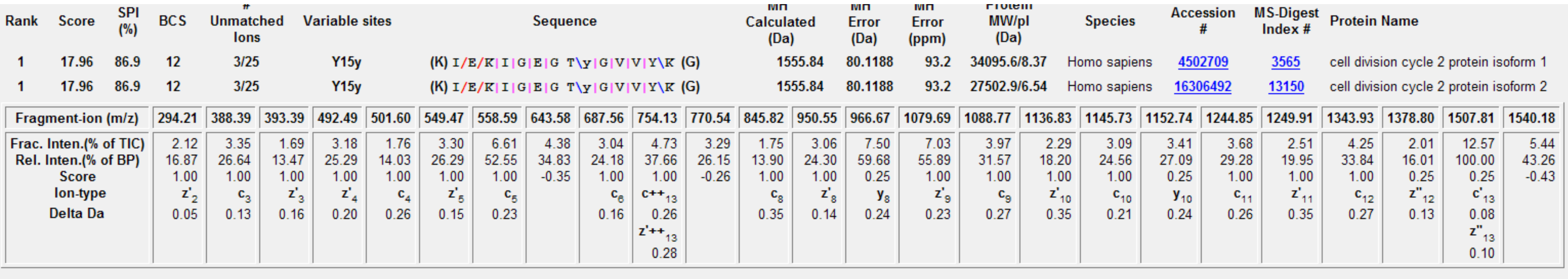
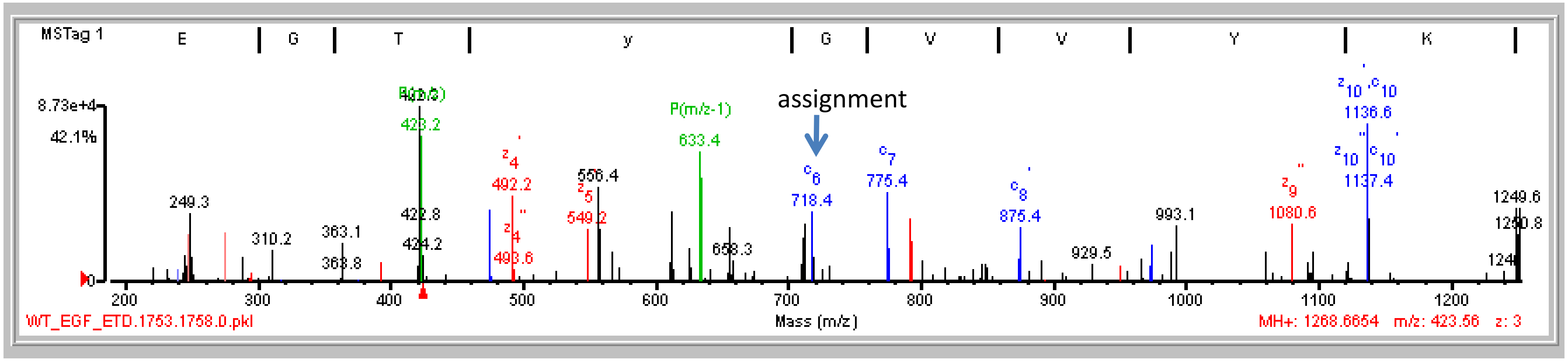


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH Calculated (Da)	MH Error (Da)	MH Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.96	86.9	12	3/25	Y15y	(K) I/E/K|I|G|E|G T\y|G|V|V|Y\K (G)	1555.84	80.1188	93.2	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	17.96	86.9	12	3/25	Y15y	(K) I/E/K|I|G|E|G T\y|G|V|V|Y\K (G)	1555.84	80.1188	93.2	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

Fragment-ion (m/z)	294.21	388.39	393.39	492.49	501.60	549.47	558.59	643.58	687.56	754.13	770.54	845.82	950.55
Frac. Inten.(% of TIC)	2.12	3.35	1.69	3.18	1.76	3.30	6.61	4.38	3.04	4.73	3.29	1.75	3.06
Rel. Inten.(% of BP)	16.87	26.64	13.47	25.29	14.03	26.29	52.55	34.83	24.18	37.66	26.15	13.90	24.30
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.35	1.00	1.00	-0.26	1.00	1.00
Ion-type	z'_2	c_3	z'_3	z'_4	c_4	z'_5	c_5		c_6	$c{+}{+}_{13}$ 0.26 $z'{+}{+}_{13}$		c_8	z'_8
Delta Da	0.05	0.13	0.16	0.20	0.26	0.15	0.23		0.16	0.28		0.35	0.14

Fragment-ion (m/z)	966.67	1079.69	1088.77	1136.83	1145.73	1152.74	1244.85	1249.91	1343.93	1378.80	1507.81	1540.18
Frac. Inten.(% of TIC)	7.50	7.03	3.97	2.29	3.09	3.41	3.68	2.51	4.25	2.01	12.57	5.44
Rel. Inten.(% of BP)	59.68	55.89	31.57	18.20	24.56	27.09	29.28	19.95	33.84	16.01	100.00	43.26
Score	0.25	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	0.25	0.25	-0.43
Ion-type	y_8	z'_9	c_9	z'_{10}	c_{10}	y_{10}	c_{11}	z'_{11}	c_{12}	z''_{12}	c'_{13} 0.08 z''_{13}	
Delta Da	0.24	0.23	0.27	0.35	0.21	0.24	0.26	0.35	0.27	0.13	0.10	

Peak 217



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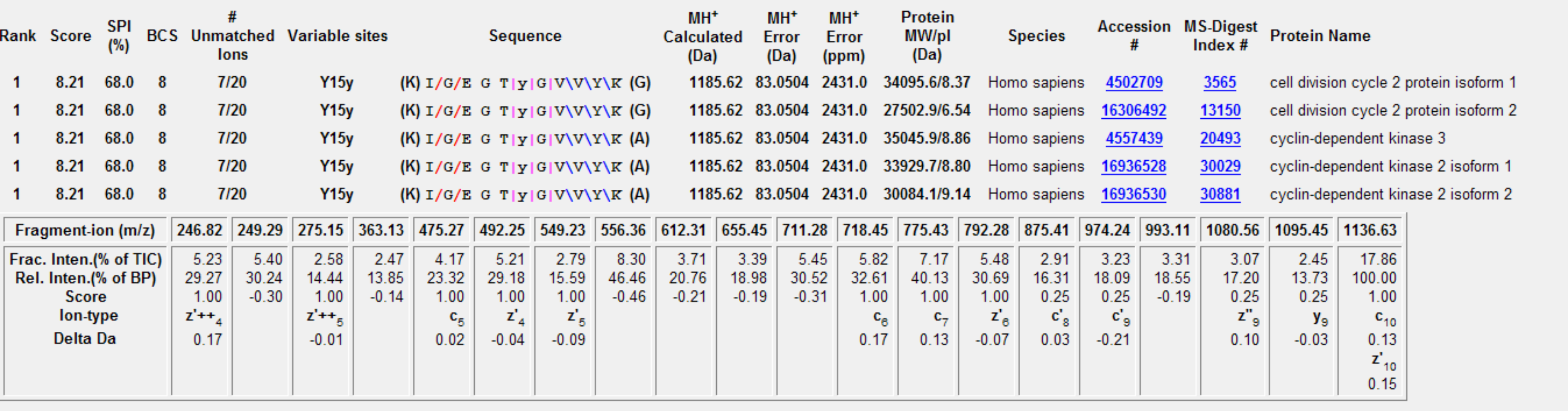
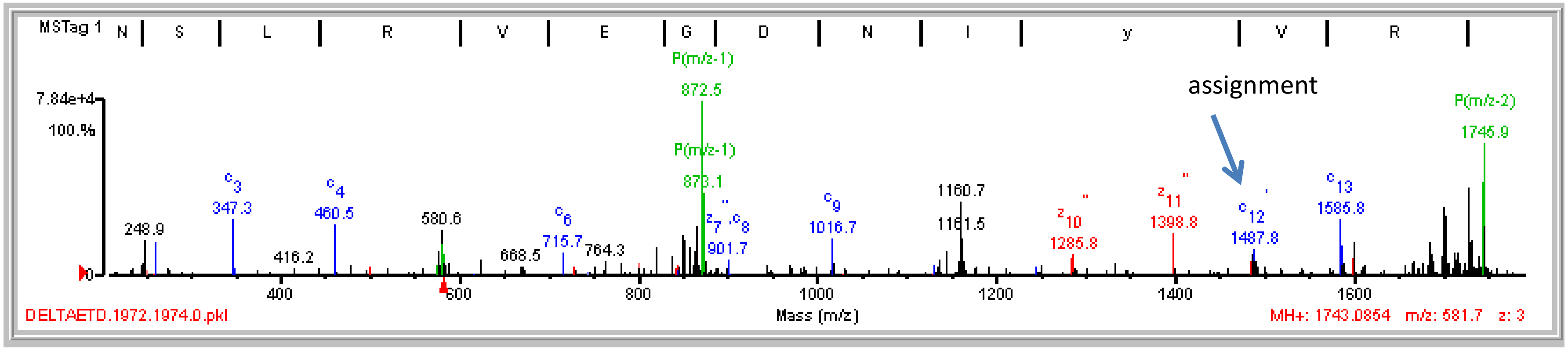


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.21	68.0	8	7/20	Y15y	(K) I/G/E G T|y|G|V\V\Y\K (G)	1185.62	83.0504	2431.0	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	8.21	68.0	8	7/20	Y15y	(K) I/G/E G T|y|G|V\V\Y\K (G)	1185.62	83.0504	2431.0	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2
1	8.21	68.0	8	7/20	Y15y	(K) I/G/E G T|y|G|V\V\Y\K (A)	1185.62	83.0504	2431.0	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
1	8.21	68.0	8	7/20	Y15y	(K) I/G/E G T|y|G|V\V\Y\K (A)	1185.62	83.0504	2431.0	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	8.21	68.0	8	7/20	Y15y	(K) I/G/E G T|y|G|V\V\Y\K (A)	1185.62	83.0504	2431.0	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

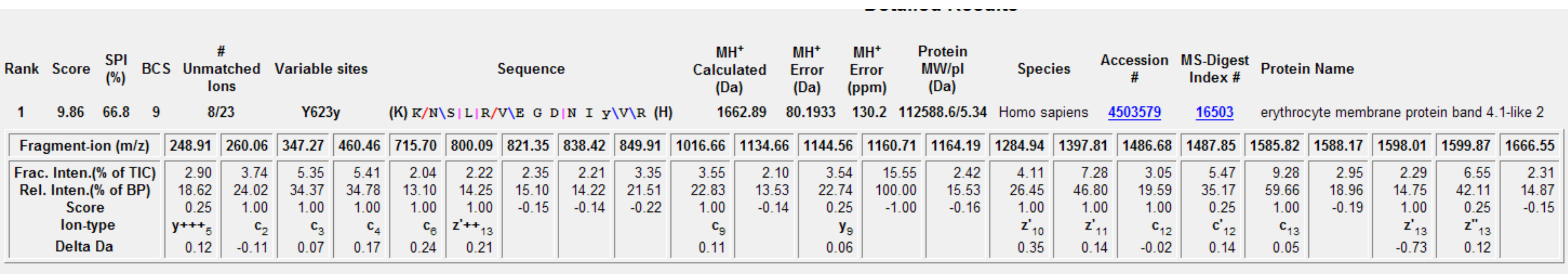
Fragment-ion (m/z)	246.82	249.29	275.15	363.13	475.27	492.25	549.23	556.36	612.31	655.45
Frac. Inten.(% of TIC)	5.23	5.40	2.58	2.47	4.17	5.21	2.79	8.30	3.71	3.39
Rel. Inten.(% of BP)	29.27	30.24	14.44	13.85	23.32	29.18	15.59	46.46	20.76	18.98
Score	1.00	-0.30	1.00	-0.14	1.00	1.00	1.00	-0.46	-0.21	-0.19
Ion-type	$z'{++}_4$		$z'{++}_5$		c_5	z'_4	z'_5			
Delta Da	0.17		-0.01		0.02	-0.04	-0.09			

Fragment-ion (m/z)	711.28	718.45	775.43	792.28	875.41	974.24	993.11	1080.56	1095.45	1136.63
Frac. Inten.(% of TIC)	5.45	5.82	7.17	5.48	2.91	3.23	3.31	3.07	2.45	17.86
Rel. Inten.(% of BP)	30.52	32.61	40.13	30.69	16.31	18.09	18.55	17.20	13.73	100.00
Score	-0.31	1.00	1.00	1.00	0.25	0.25	-0.19	0.25	0.25	1.00
Ion-type		c_6	c_7	z'_6	c'_8	c'_9		z''_9	y_9	c_{10}
Delta Da		0.17	0.13	-0.07	0.03	-0.21		0.10	-0.03	0.13
										z'_{10}
										0.15

Peak 218



assignment

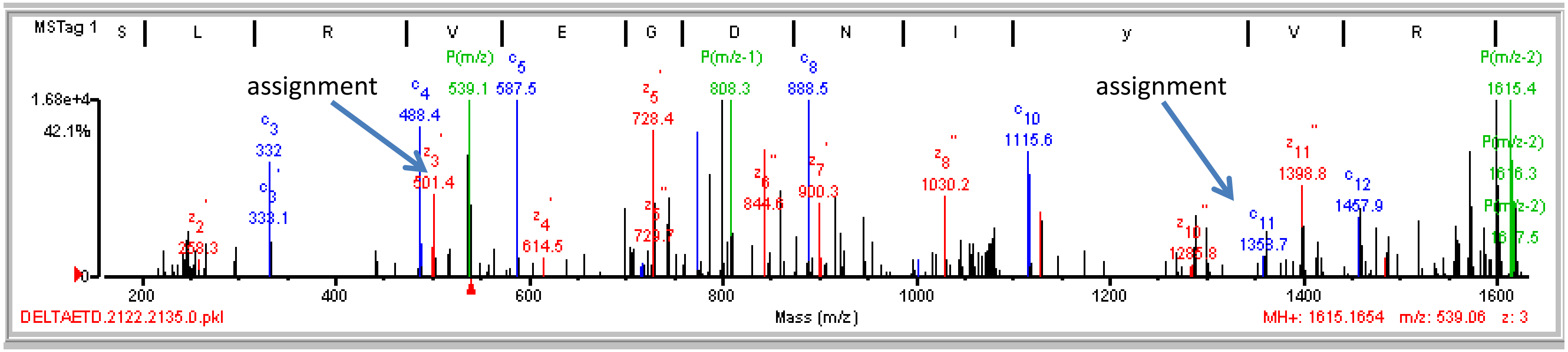


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.86	66.8	9	8/23	Y623y	(K) K/N\S|L|R/V\E G D|N I y\V\R (H)	1662.89	80.1933	130.2	112588.6/5.34	Homo sapiens	4503579	16503	erythrocyte membrane protein band 4.1-like 2

Fragment-ion (m/z)	248.91	260.06	347.27	460.46	715.70	800.09	821.35	838.42	849.91	1016.66
Frac. Inten.(% of TIC)	2.90	3.74	5.35	5.41	2.04	2.22	2.35	2.21	3.35	3.55
Rel. Inten.(% of BP)	18.62	24.02	34.37	34.78	13.10	14.25	15.10	14.22	21.51	22.83
Score	0.25	1.00	1.00	1.00	1.00	1.00	-0.15	-0.14	-0.22	1.00
Ion-type	$y{+}{+}{+}_5$	c_2	c_3	c_4	c_6	$z'{+}{+}_{13}$				c_9
Delta Da	0.12	-0.11	0.07	0.17	0.24	0.21				0.11

Fragment-ion (m/z)	1134.66	1144.56	1160.71	1164.19	1284.94	1397.81	1486.68	1487.85	1585.82	1588.17	1598.01	1599.87	1666.55
Frac. Inten.(% of TIC)	2.10	3.54	15.55	2.42	4.11	7.28	3.05	5.47	9.28	2.95	2.29	6.55	2.31
Rel. Inten.(% of BP)	13.53	22.74	100.00	15.53	26.45	46.80	19.59	35.17	59.66	18.96	14.75	42.11	14.87
Score	-0.14	0.25	-1.00	-0.16	1.00	1.00	1.00	0.25	1.00	-0.19	1.00	0.25	-0.15
Ion-type		y_9			z'_{10}	z'_{11}	c_{12}	c'_{12}	c_{13}		z'_{13}	z''_{13}	
Delta Da		0.06			0.35	0.14	-0.02	0.14	0.05		-0.73	0.12	

Peak 219



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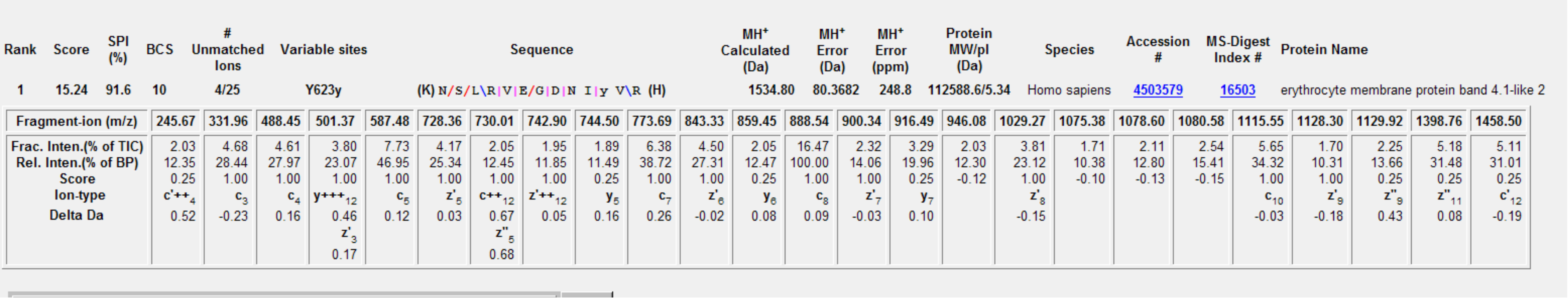
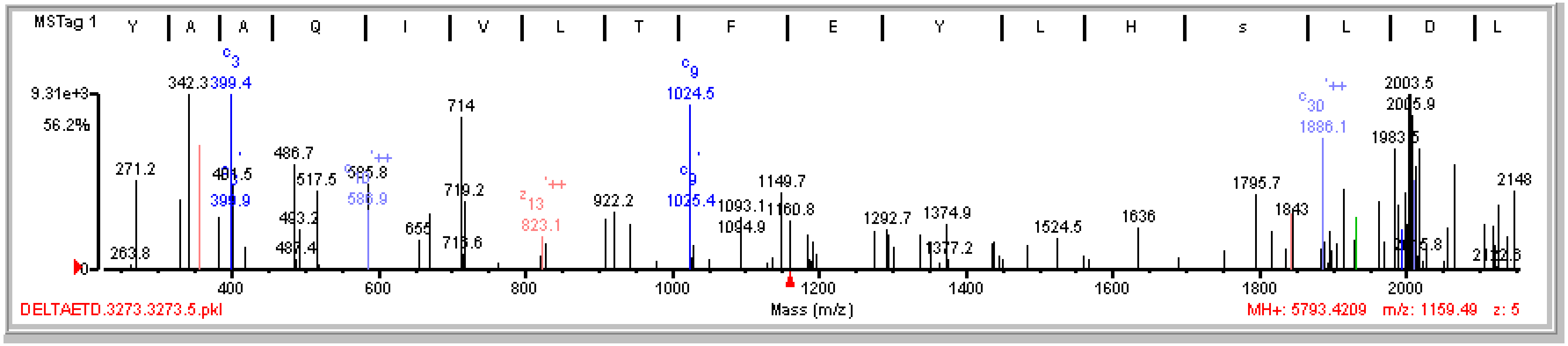
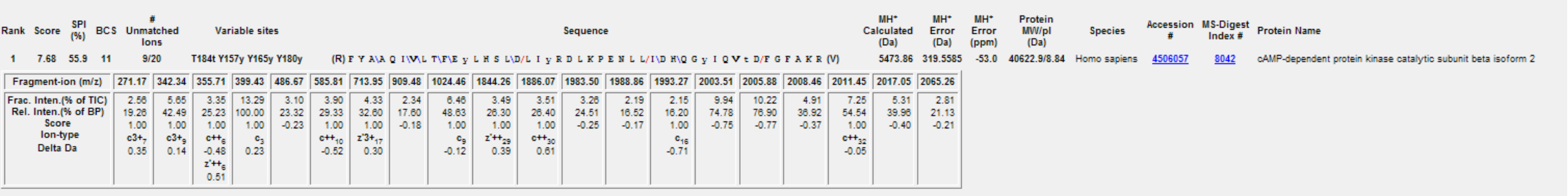


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.24	91.6	10	4/25	Y623y	(K) N/S/L\R|V|E/G|D|N I|y V\R (H)	1534.80	80.3682	248.8	112588.6/5.34	Homo sapiens	4503579	16503	erythrocyte membrane protein band 4.1-like 2

Fragment-ion (m/z)	245.67	331.96	488.45	501.37	587.48	728.36	730.01	742.90	744.50	773.69	843.33	859.45	888.54	900.34	916.49	946.08	1029.27	1075.38	1078.60	1080.58	1115.55	1128.30	1129.92	1398.76	1458.50
Frac. Inten.(% of TIC)	2.03	4.68	4.61	3.80	7.73	4.17	2.05	1.95	1.89	6.38	4.50	2.05	16.47	2.32	3.29	2.03	3.81	1.71	2.11	2.54	5.65	1.70	2.25	5.18	5.11
Rel. Inten.(% of BP)	12.35	28.44	27.97	23.07	46.95	25.34	12.45	11.85	11.49	38.72	27.31	12.47	100.00	14.06	19.96	12.30	23.12	10.38	12.80	15.41	34.32	10.31	13.66	31.48	31.01
Score	0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00	1.00	0.25	-0.12	1.00	-0.10	-0.13	-0.15	1.00	1.00	0.25	0.25	0.25
Ion-type	c'^{++}_{4}	c_3	c_4	y^{+++}_{12} z'_3	c_5	z'_5	c^{++}_{12} z''_5	z'^{++}_{12}	y_5	c_7	z'_6	y_6	c_8	z'_7	y_7		z'_8				c_{10}	z'_9	z''_9	z''_{11}	c'_{12}
Delta Da	0.52	-0.23	0.16	0.46 0.17	0.12	0.03	0.67 0.68	0.05	0.16	0.26	-0.02	0.08	0.09	-0.03	0.10		-0.15				-0.03	-0.18	0.43	0.08	-0.19

Peak 220

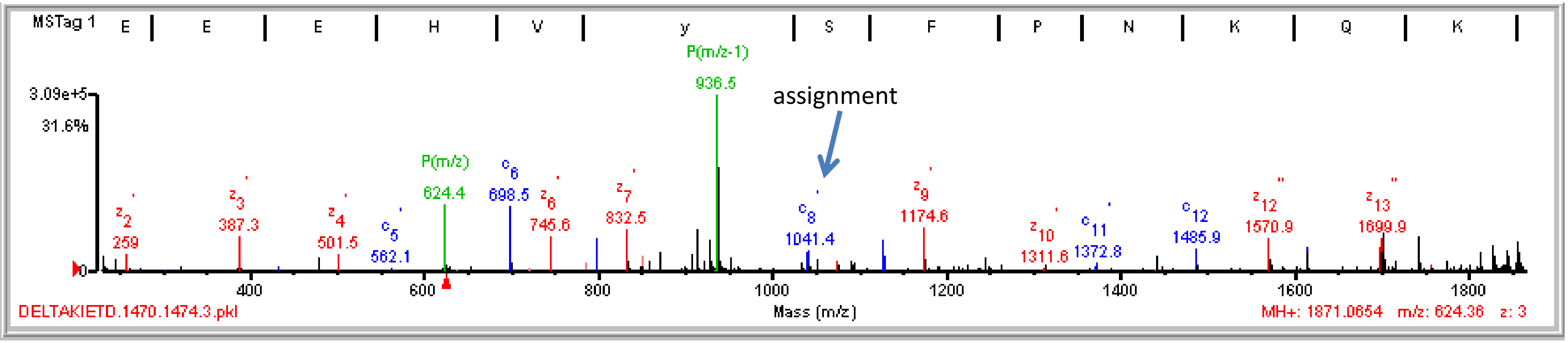




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.68	55.9	11	9/20	T184t Y157y Y165y Y180y	(R) F Y A\A Q I\V\L T\F\E y L H S L\D/L I y R D L K P E N L L/I\D H\Q G y I Q V t D/F G F A K R (V)	5473.86	319.5585	-53.0	40622.9/8.84	Homo sapiens	4506057	8042	cAMP-dependent protein kinase catalytic subunit beta isoform 2

Fragment-ion (m/z)	271.17	342.34	355.71	399.43	486.67	585.81	713.95	909.48	1024.46	1844.26	1886.07	1983.50	1988.86	1993.27	2003.51	2005.88	2008.46	2011.45	2017.05	2065.26
Frac. Inten.(% of TIC)	2.56	5.65	3.35	13.29	3.10	3.90	4.33	2.34	6.46	3.49	3.51	3.26	2.19	2.15	9.94	10.22	4.91	7.25	5.31	2.81
Rel. Inten.(% of BP)	19.26	42.49	25.23	100.00	23.32	29.33	32.60	17.60	48.63	26.30	26.40	24.51	16.52	16.20	74.78	76.90	36.92	54.54	39.96	21.13
Score	1.00	1.00	1.00	1.00	-0.23	1.00	1.00	-0.18	1.00	1.00	1.00	-0.25	-0.17	1.00	-0.75	-0.77	-0.37	1.00	-0.40	-0.21
Ion-type	c3+$_{7}$	c3+$_{9}$	c++$_{6}$ z'++$_{6}$	c$_{3}$		c++$_{10}$	z'3+$_{17}$		c$_{9}$	z'++$_{29}$	c++$_{30}$			c$_{16}$				c++$_{32}$		
Delta Da	0.35	0.14	-0.48 0.51	0.23		-0.52	0.30		-0.12	0.39	0.61			-0.71				-0.05		

Peak 221



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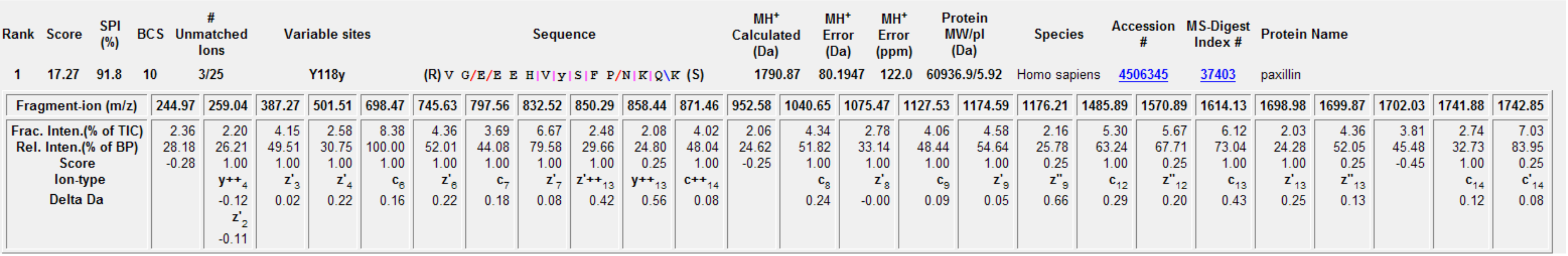
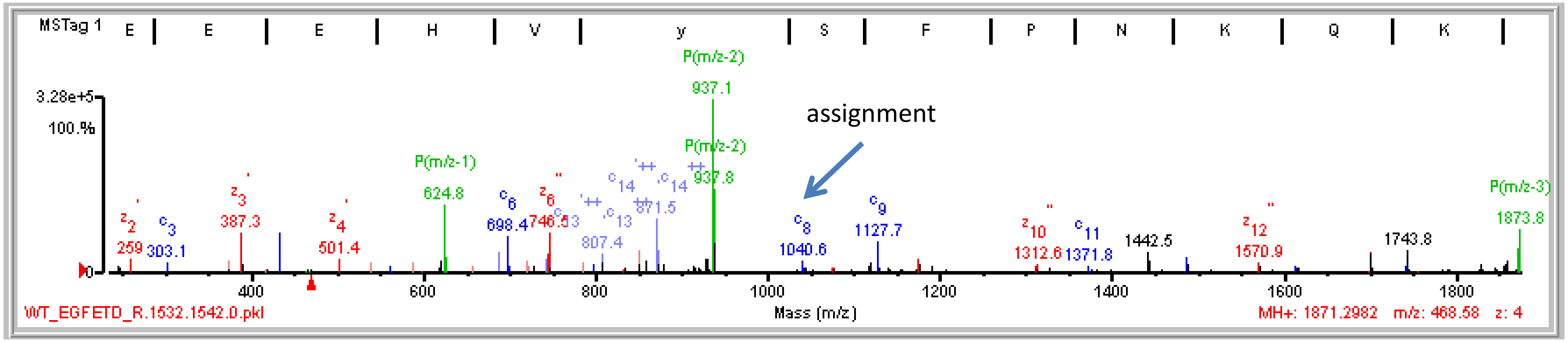


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.27	91.8	10	3/25	Y118y	(R) V G/E/E E H|V|y|S|F P/N|K|Q\K (S)	1790.87	80.1947	122.0	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

Fragment-ion (m/z)	244.97	259.04	387.27	501.51	698.47	745.63	797.56	832.52	850.29	858.44	871.46	952.58	1040.65	1075.47	1127.53	1174.59	1176.21	1485.89	1570.89	1614.13	1698.98	1699.87	1702.03	1741.88	1742.85
Frac. Inten.(% of TIC)	2.36	2.20	4.15	2.58	8.38	4.36	3.69	6.67	2.48	2.08	4.02	2.06	4.34	2.78	4.06	4.58	2.16	5.30	5.67	6.12	2.03	4.36	3.81	2.74	7.03
Rel. Inten.(% of BP)	28.18	26.21	49.51	30.75	100.00	52.01	44.08	79.58	29.66	24.80	48.04	24.62	51.82	33.14	48.44	54.64	25.78	63.24	67.71	73.04	24.28	52.05	45.48	32.73	83.95
Score	-0.28	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.25	1.00	1.00	1.00	1.00	0.25	1.00	0.25	1.00	1.00	0.25	-0.45	1.00	0.25
Ion-type		y^{++}_4 z'_2	z'_3	z'_4	c_6	z'_6	c_7	z'_7	z'^{++}_{13}	y^{++}_{13}	c^{++}_{14}		c_8	z'_8	c_9	z'_9	z''_9	c_{12}	z''_{12}	c_{13}	z'_{13}	z''_{13}		c_{14}	c'_{14}
Delta Da		-0.12 -0.11	0.02	0.22	0.16	0.22	0.18	0.08	0.42	0.56	0.08		0.24	-0.00	0.09	0.05	0.66	0.29	0.20	0.43	0.25	0.13		0.12	0.08

Peak 222



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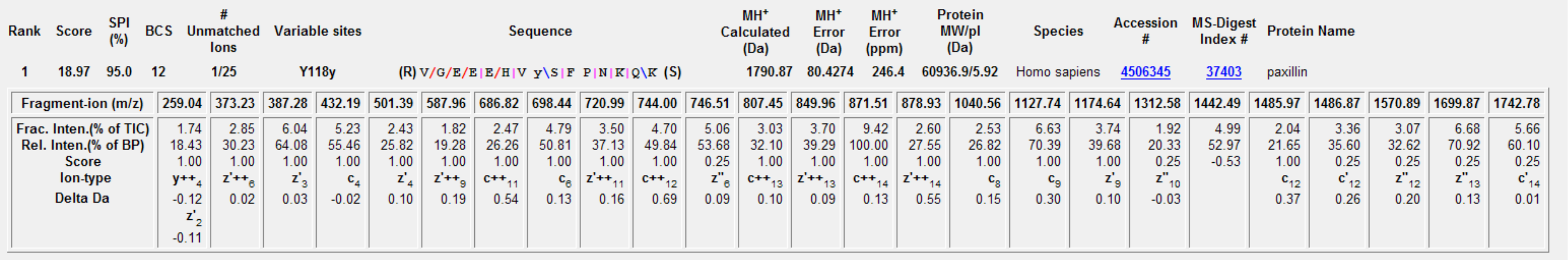
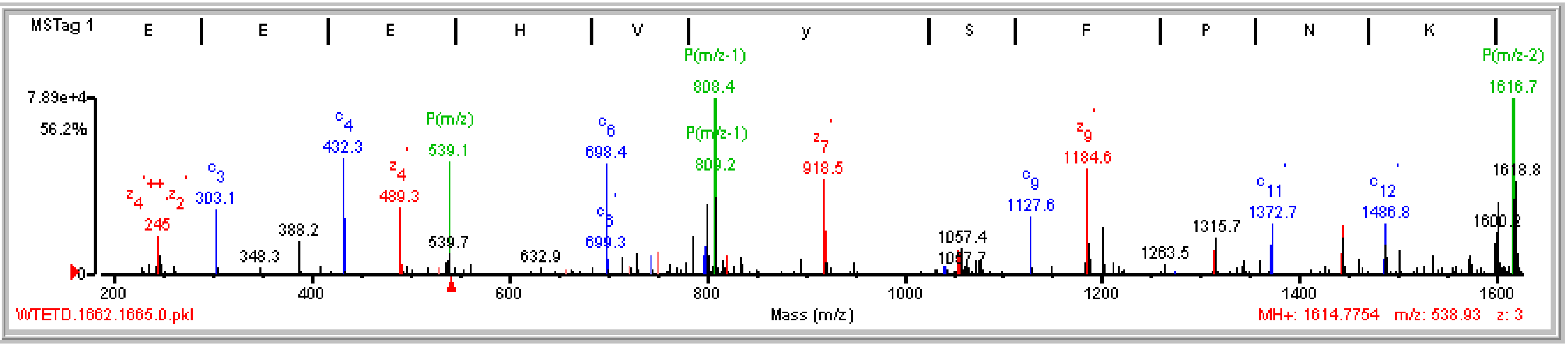


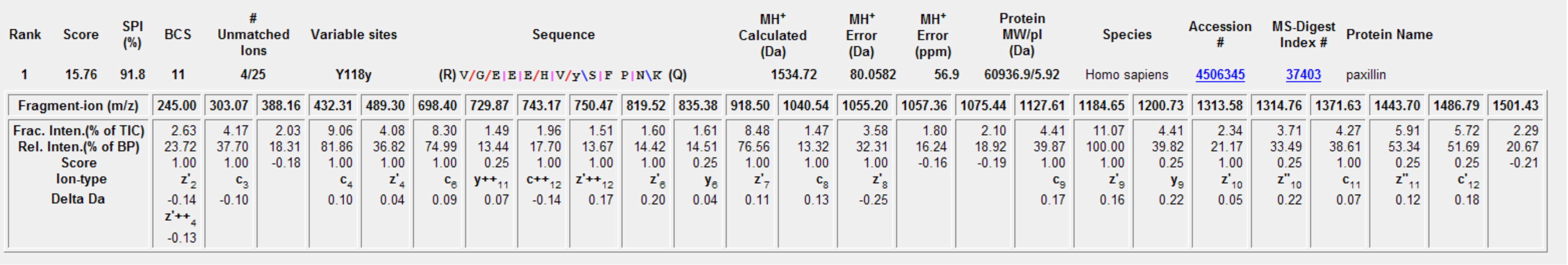
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.97	95.0	12	1/25	Y118y	(R) V/G/E/E|E/H|V y\S|F P|N|K|Q\K (S)	1790.87	80.4274	246.4	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

Fragment-ion (m/z)	259.04	373.23	387.28	432.19	501.39	587.96	686.82	698.44	720.99	744.00	746.51	807.45	849.96
Frac. Inten.(% of TIC)	1.74	2.85	6.04	5.23	2.43	1.82	2.47	4.79	3.50	4.70	5.06	3.03	3.70
Rel. Inten.(% of BP)	18.43	30.23	64.08	55.46	25.82	19.28	26.26	50.81	37.13	49.84	53.68	32.10	39.29
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type	y^{++}_4 z'_2	z'^{++}_6	z'_3	c_4	z'_4	z'^{++}_9	c^{++}_{11}	c_6	z'^{++}_{11}	c^{++}_{12}	z''_6	c^{++}_{13}	z'^{++}_{13}
Delta Da	-0.12 -0.11	0.02	0.03	-0.02	0.10	0.19	0.54	0.13	0.16	0.69	0.09	0.10	0.09

Fragment-ion (m/z)	871.51	878.93	1040.56	1127.74	1174.64	1312.58	1442.49	1485.97	1486.87	1570.89	1699.87	1742.78
Frac. Inten.(% of TIC)	9.42	2.60	2.53	6.63	3.74	1.92	4.99	2.04	3.36	3.07	6.68	5.66
Rel. Inten.(% of BP)	100.00	27.55	26.82	70.39	39.68	20.33	52.97	21.65	35.60	32.62	70.92	60.10
Score	1.00	1.00	1.00	1.00	1.00	0.25	-0.53	1.00	0.25	0.25	0.25	0.25
Ion-type	c^{++}_{14}	z'^{++}_{14}	c_8	c_9	z'_9	z''_{10}		c_{12}	c'_{12}	z''_{12}	z''_{13}	c'_{14}
Delta Da	0.13	0.55	0.15	0.30	0.10	-0.03		0.37	0.26	0.20	0.13	0.01

Peak 223



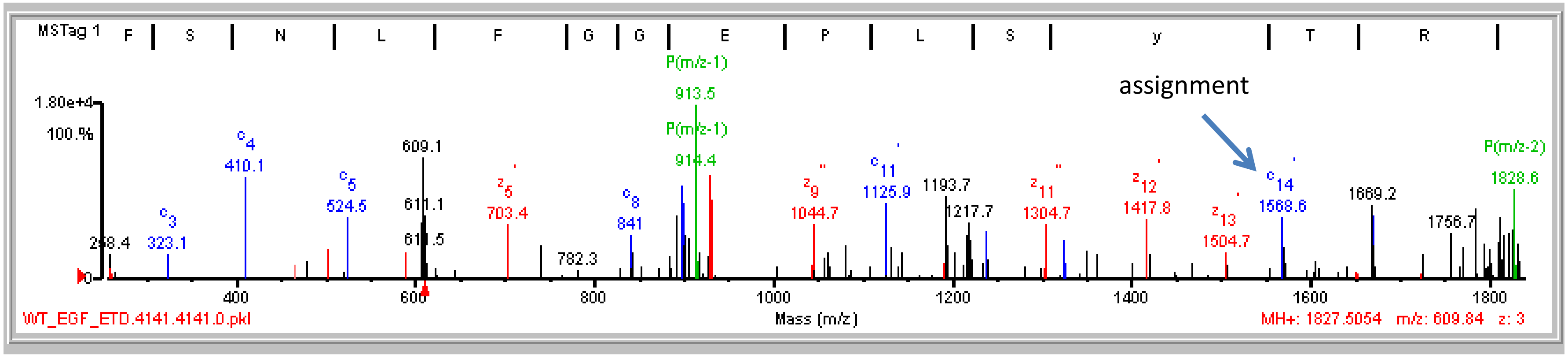


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.76	91.8	11	4/25	Y118y	(R) V/G/E|E|E/H|V/y\S|F P|N\K (Q)	1534.72	80.0582	56.9	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

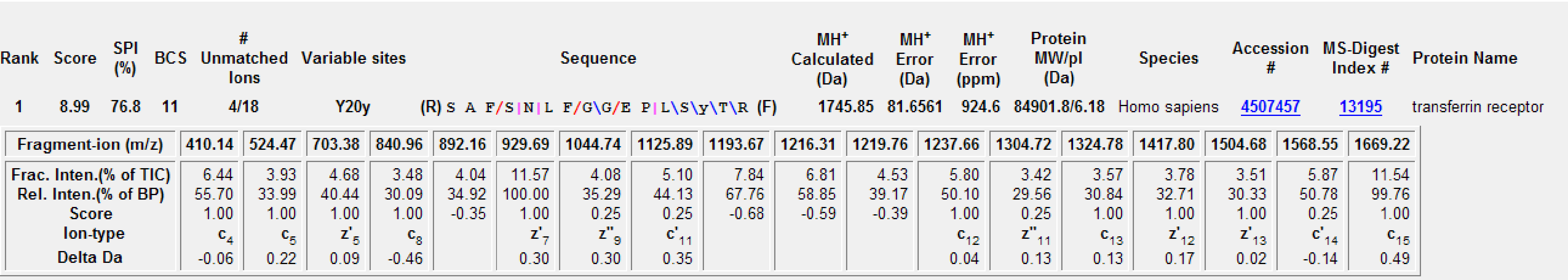
Fragment-ion (m/z)	245.00	303.07	388.16	432.31	489.30	698.40	729.87	743.17	750.47	819.52	835.38	918.50
Frac. Inten.(% of TIC)	2.63	4.17	2.03	9.06	4.08	8.30	1.49	1.96	1.51	1.60	1.61	8.48
Rel. Inten.(% of BP)	23.72	37.70	18.31	81.86	36.82	74.99	13.44	17.70	13.67	14.42	14.51	76.56
Score	1.00	1.00	-0.18	1.00	1.00	1.00	0.25	1.00	1.00	1.00	0.25	1.00
Ion-type	z'_{2} z'^{++}_{4}	c_{3}		c_{4}	z'_{4}	c_{6}	y^{++}_{11}	c^{++}_{12}	z'^{++}_{12}	z'_{6}	y_{6}	z'_{7}
Delta Da	-0.14 -0.13	-0.10		0.10	0.04	0.09	0.07	-0.14	0.17	0.20	0.04	0.11

Fragment-ion (m/z)	1040.54	1055.20	1057.36	1075.44	1127.61	1184.65	1200.73	1313.58	1314.76	1371.63	1443.70	1486.79	1501.43
Frac. Inten.(% of TIC)	1.47	3.58	1.80	2.10	4.41	11.07	4.41	2.34	3.71	4.27	5.91	5.72	2.29
Rel. Inten.(% of BP)	13.32	32.31	16.24	18.92	39.87	100.00	39.82	21.17	33.49	38.61	53.34	51.69	20.67
Score	1.00	1.00	-0.16	-0.19	1.00	1.00	0.25	1.00	0.25	1.00	0.25	0.25	-0.21
Ion-type	c_{8}	z'_{8}			c_{9}	z'_{9}	y_{9}	z'_{10}	z''_{10}	c_{11}	z''_{11}	c'_{12}	
Delta Da	0.13	-0.25			0.17	0.16	0.22	0.05	0.22	0.07	0.12	0.18	

Peak 225



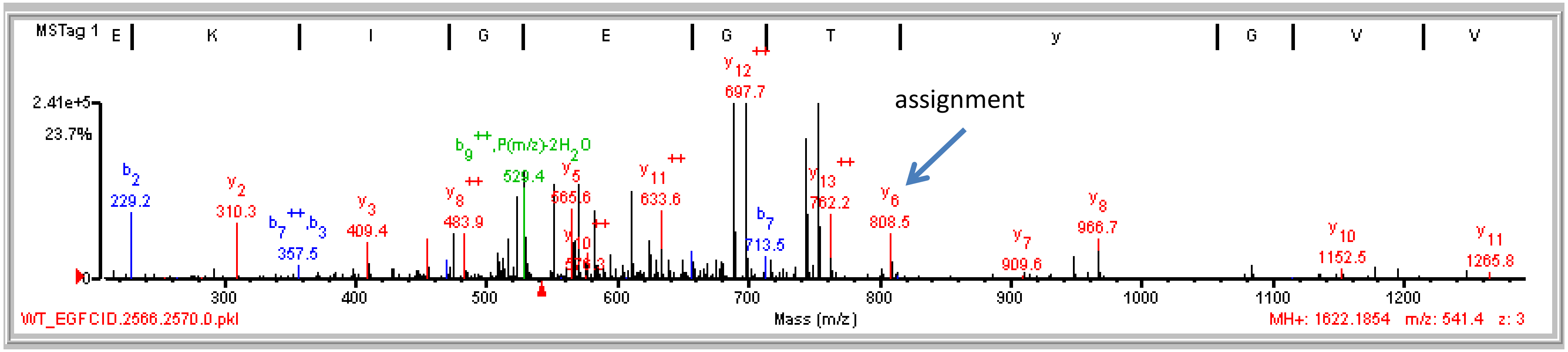
assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.99	76.8	11	4/18	Y20y	(R) S A F/S|N|L F/G\G/E P|L\S\y\T\R (F)	1745.85	81.6561	924.6	84901.8/6.18	Homo sapiens	4507457	13195	transferrin receptor

Fragment-ion (m/z)	410.14	524.47	703.38	840.96	892.16	929.69	1044.74	1125.89	1193.67	1216.31	1219.76	1237.66	1304.72	1324.78	1417.80	1504.68	1568.55	1669.22
Frac. Inten.(% of TIC)	6.44	3.93	4.68	3.48	4.04	11.57	4.08	5.10	7.84	6.81	4.53	5.80	3.42	3.57	3.78	3.51	5.87	11.54
Rel. Inten.(% of BP)	55.70	33.99	40.44	30.09	34.92	100.00	35.29	44.13	67.76	58.85	39.17	50.10	29.56	30.84	32.71	30.33	50.78	99.76
Score	1.00	1.00	1.00	1.00	-0.35	1.00	0.25	0.25	-0.68	-0.59	-0.39	1.00	0.25	1.00	1.00	1.00	0.25	1.00
Ion-type	c_4	c_5	z'_5	c_8		z'_7	z''_9	c'_{11}				c_{12}	z''_{11}	c_{13}	z'_{12}	z'_{13}	c'_{14}	c_{15}
Delta Da	-0.06	0.22	0.09	-0.46		0.30	0.30	0.35				0.04	0.13	0.13	0.17	0.02	-0.14	0.49

Peak 226



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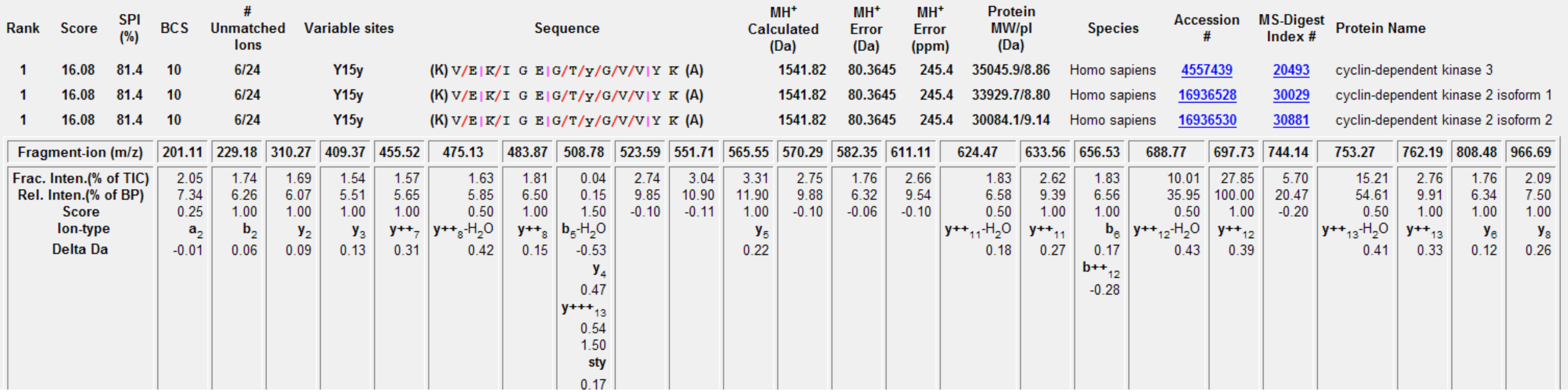
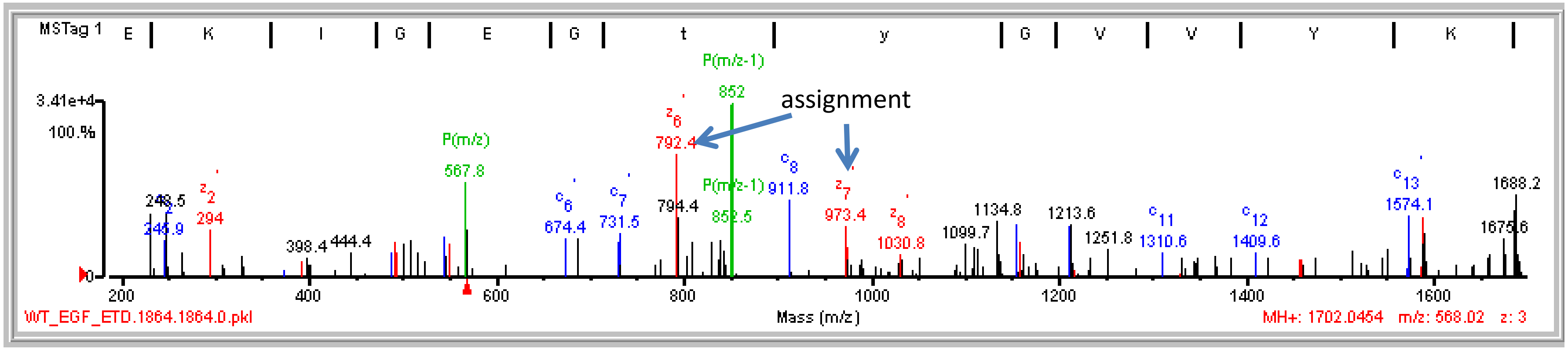


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.08	81.4	10	6/24	Y15y	(K) V/E|K/I G E|G/T/y/G/V/V|Y K (A)	1541.82	80.3645	245.4	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
1	16.08	81.4	10	6/24	Y15y	(K) V/E|K/I G E|G/T/y/G/V/V|Y K (A)	1541.82	80.3645	245.4	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	16.08	81.4	10	6/24	Y15y	(K) V/E|K/I G E|G/T/y/G/V/V|Y K (A)	1541.82	80.3645	245.4	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

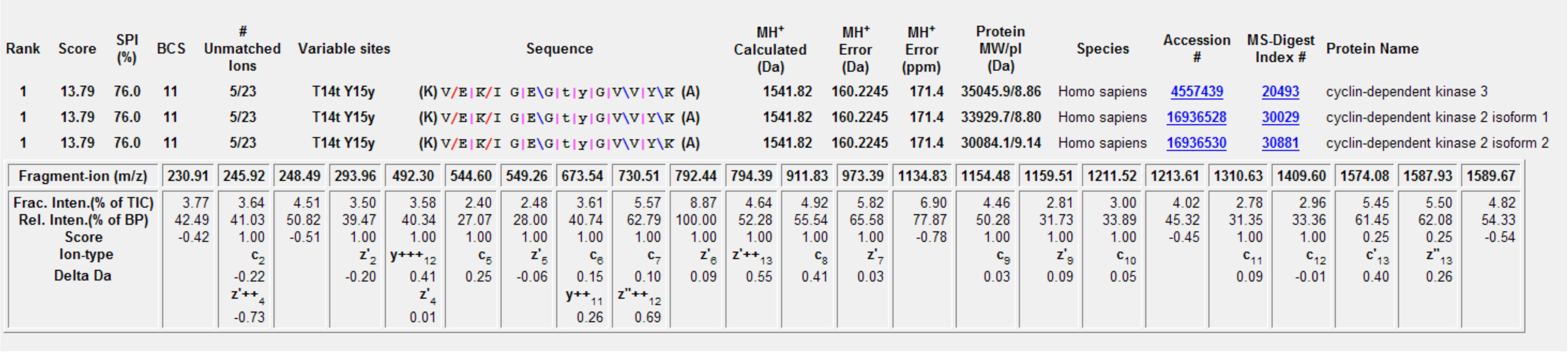
Fragment-ion (m/z)	201.11	229.18	310.27	409.37	455.52	475.13	483.87	508.78	523.59	551.71	565.55
Frac. Inten.(% of TIC)	2.05	1.74	1.69	1.54	1.57	1.63	1.81	0.04	2.74	3.04	3.31
Rel. Inten.(% of BP)	7.34	6.26	6.07	5.51	5.65	5.85	6.50	0.15	9.85	10.90	11.90
Score	0.25	1.00	1.00	1.00	1.00	0.50	1.00	1.50	-0.10	-0.11	1.00
Ion-type	a_2	b_2	y_2	y_3	y^{++}_7	y^{++}_8-H_2O	y^{++}_8	b_5-H_2O			y_5
Delta Da	-0.01	0.06	0.09	0.13	0.31	0.42	0.15	-0.53 y_4 0.47 y^{+++}_{13} 0.54 1.50 sty 0.17			0.22

Fragment-ion (m/z)	570.29	582.35	611.11	624.47	633.56	656.53	688.77	697.73	744.14	753.27	762.19	808.48	966.69
Frac. Inten.(% of TIC)	2.75	1.76	2.66	1.83	2.62	1.83	10.01	27.85	5.70	15.21	2.76	1.76	2.09
Rel. Inten.(% of BP)	9.88	6.32	9.54	6.58	9.39	6.56	35.95	100.00	20.47	54.61	9.91	6.34	7.50
Score	-0.10	-0.06	-0.10	0.50	1.00	1.00	0.50	1.00	-0.20	0.50	1.00	1.00	1.00
Ion-type				y^{++}_{11}-H_2O	y^{++}_{11}	b_6	y^{++}_{12}-H_2O	y^{++}_{12}		y^{++}_{13}-H_2O	y^{++}_{13}	y_6	y_8
Delta Da				0.18	0.27	0.17 b^{++}_{12} -0.28	0.43	0.39		0.41	0.33	0.12	0.26

Peak 227



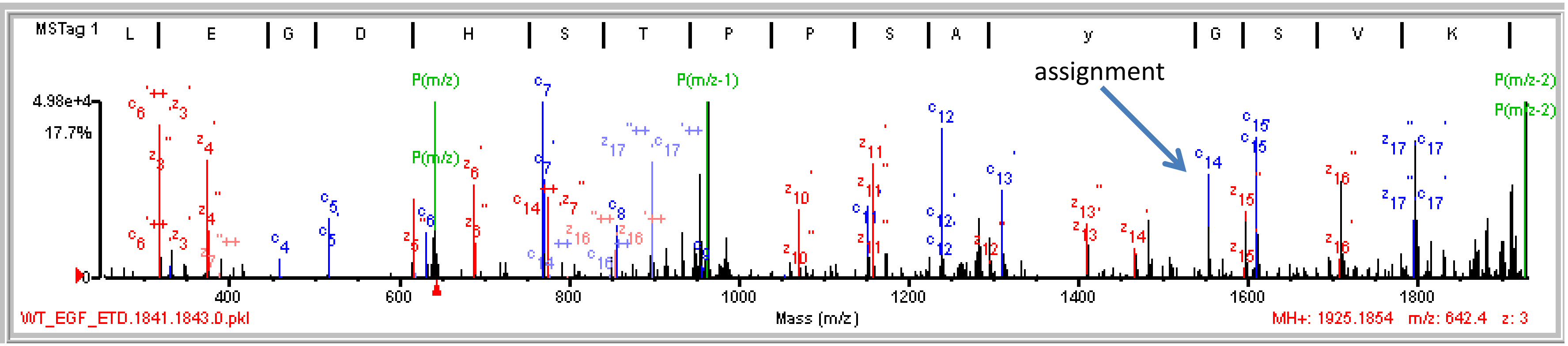
assignment



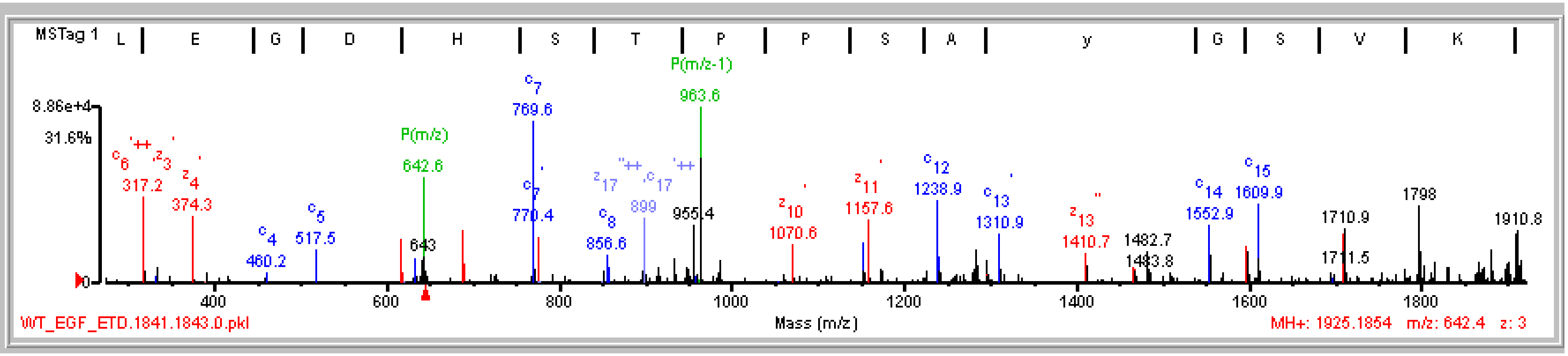
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.79	76.0	11	5/23	T14t Y15y	(K) V/E|K/I G|E\G|t|y|G|V\V|Y\K (A)	1541.82	160.2245	171.4	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
1	13.79	76.0	11	5/23	T14t Y15y	(K) V/E|K/I G|E\G|t|y|G|V\V|Y\K (A)	1541.82	160.2245	171.4	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	13.79	76.0	11	5/23	T14t Y15y	(K) V/E|K/I G|E\G|t|y|G|V\V|Y\K (A)	1541.82	160.2245	171.4	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

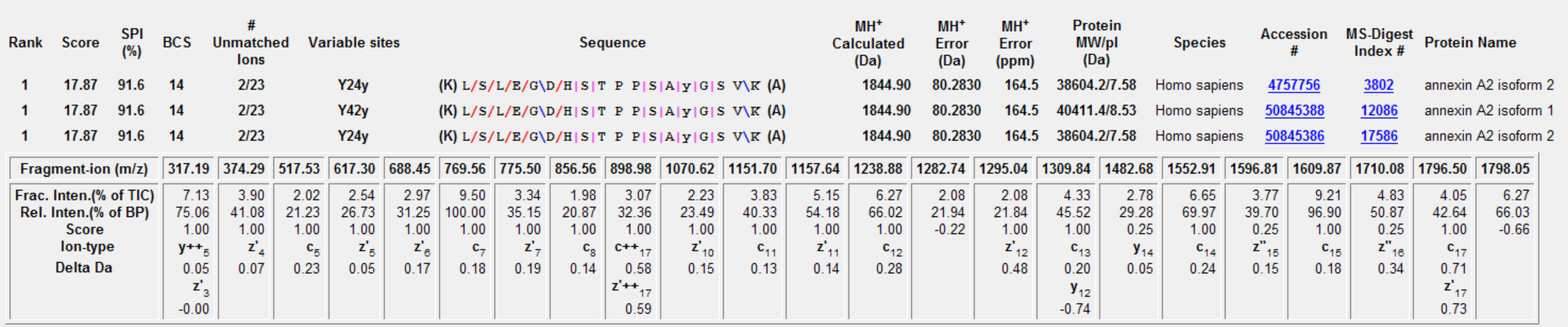
Fragment-ion (m/z)	230.91	245.92	248.49	293.96	492.30	544.60	549.26	673.54	730.51	792.44	794.39	911.83	973.39	1134.83	1154.48	1159.51	1211.52	1213.61	1310.63	1409.60	1574.08	1587.93	1589.67
Frac. Inten.(% of TIC)	3.77	3.64	4.51	3.50	3.58	2.40	2.48	3.61	5.57	8.87	4.64	4.92	5.82	6.90	4.46	2.81	3.00	4.02	2.78	2.96	5.45	5.50	4.82
Rel. Inten.(% of BP)	42.49	41.03	50.82	39.47	40.34	27.07	28.00	40.74	62.79	100.00	52.28	55.54	65.58	77.87	50.28	31.73	33.89	45.32	31.35	33.36	61.45	62.08	54.33
Score	-0.42	1.00	-0.51	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.78	1.00	1.00	1.00	-0.45	1.00	1.00	0.25	0.25	-0.54
Ion-type		c_2		z'_2	$y+++_{12}$	c_5	z'_5	c_6	c_7	z'_6	$z'{++}_{13}$	c_8	z'_7		c_9	z'_9	c_{10}		c_{11}	c_{12}	c'_{13}	z''_{13}	
Delta Da		-0.22 $z'{++}_4$ -0.73		-0.20	0.41 z'_4 0.01	0.25	-0.06	0.15 $y{++}_{11}$ 0.26	0.10 $z''{++}_{12}$ 0.69	0.09	0.55	0.41	0.03		0.03	0.09	0.05		0.09	-0.01	0.40	0.26	

Peak 228



assignment

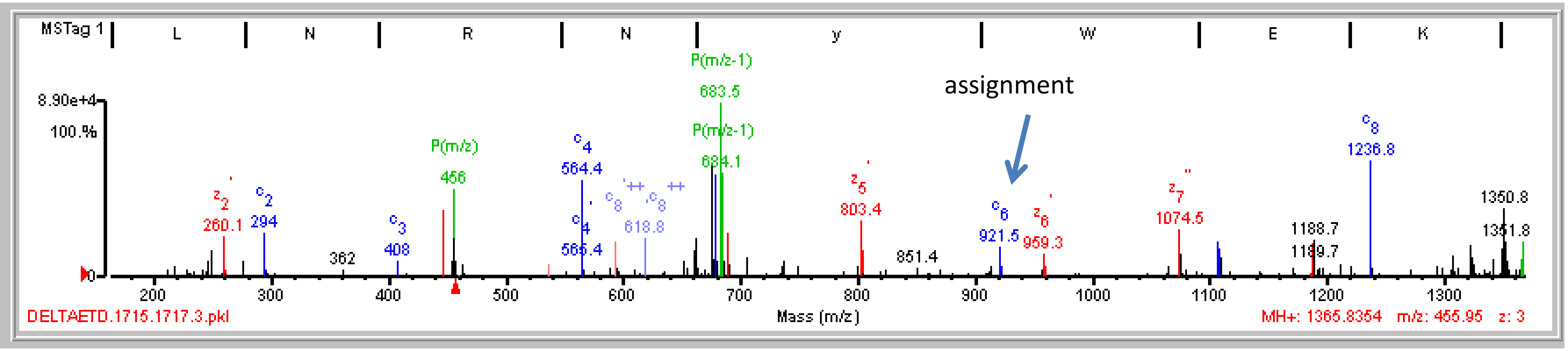




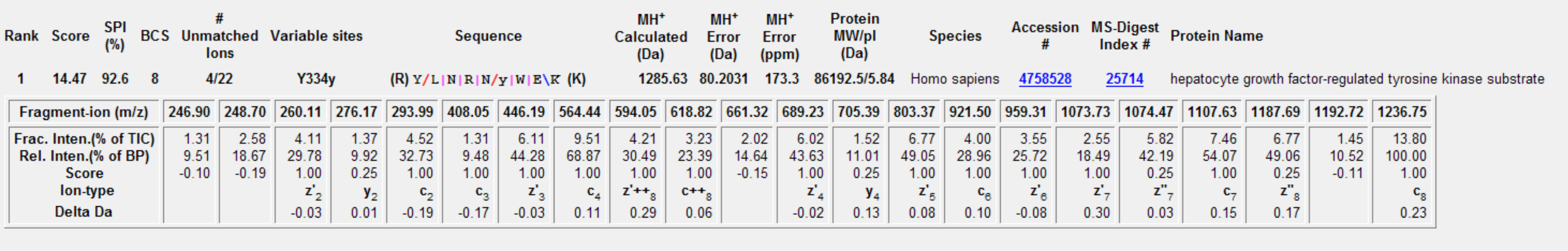
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.87	91.6	14	2/23	Y24y	(K) L/S/L/E/G\D/H|S|T P P|S|A|y|G|S V\K (A)	1844.90	80.2830	164.5	38604.2/7.58	Homo sapiens	4757756	3802	annexin A2 isoform 2
1	17.87	91.6	14	2/23	Y42y	(K) L/S/L/E/G\D/H|S|T P P|S|A|y|G|S V\K (A)	1844.90	80.2830	164.5	40411.4/8.53	Homo sapiens	50845388	12086	annexin A2 isoform 1
1	17.87	91.6	14	2/23	Y24y	(K) L/S/L/E/G\D/H|S|T P P|S|A|y|G|S V\K (A)	1844.90	80.2830	164.5	38604.2/7.58	Homo sapiens	50845386	17586	annexin A2 isoform 2

Fragment-ion (m/z)	317.19	374.29	517.53	617.30	688.45	769.56	775.50	856.56	898.98	1070.62	1151.70	1157.64	1238.88	1282.74	1295.04	1309.84	1482.68	1552.91	1596.81	1609.87	1710.08	1796.50	1798.05
Frac. Inten.(% of TIC)	7.13	3.90	2.02	2.54	2.97	9.50	3.34	1.98	3.07	2.23	3.83	5.15	6.27	2.08	2.08	4.33	2.78	6.65	3.77	9.21	4.83	4.05	6.27
Rel. Inten.(% of BP)	75.06	41.08	21.23	26.73	31.25	100.00	35.15	20.87	32.36	23.49	40.33	54.18	66.02	21.94	21.84	45.52	29.28	69.97	39.70	96.90	50.87	42.64	66.03
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.22	1.00	1.00	0.25	1.00	0.25	1.00	0.25	1.00	-0.66
Ion-type	y^{++}_5 z'_3	z'_4	c_5	z'_5	z'_6	c_7	z'_7	c_8	c^{++}_{17} z'^{++}_{17}	z'_{10}	c_{11}	z'_{11}	c_{12}		z'_{12}	c_{13} y_{12}	y_{14}	c_{14}	z''_{15}	c_{15}	z''_{16}	c_{17} z'_{17}	
Delta Da	0.05 -0.00	0.07	0.23	0.05	0.17	0.18	0.19	0.14	0.58 0.59	0.15	0.13	0.14	0.28		0.48	0.20 -0.74	0.05	0.24	0.15	0.18	0.34	0.71 0.73	

Peak 229



assignment

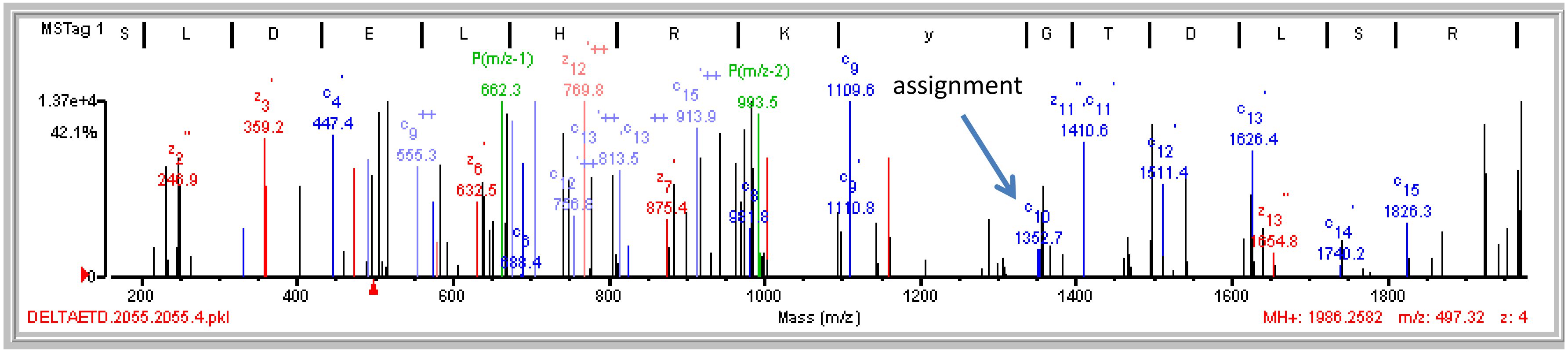


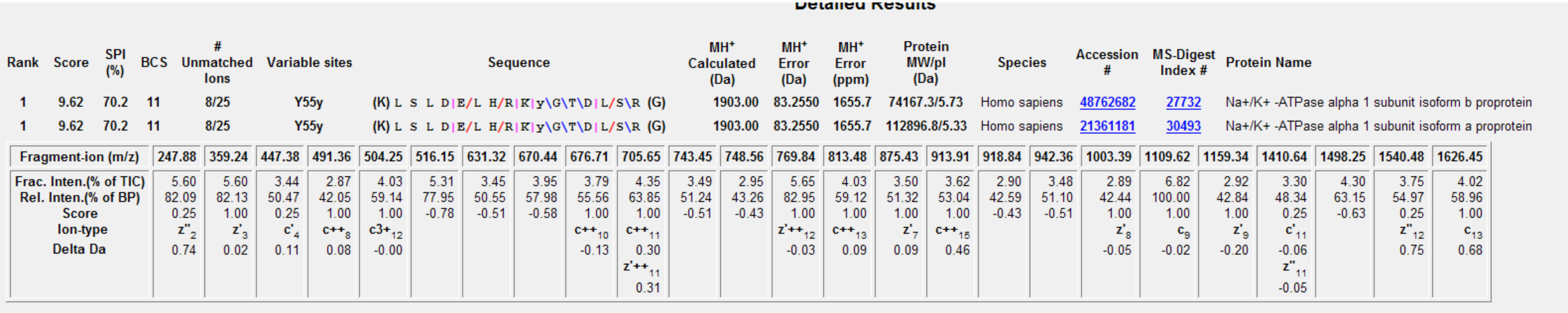
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.47	92.6	8	4/22	Y334y	(R) Y/L|N|R|N/y|W|E\K (K)	1285.63	80.2031	173.3	86192.5/5.84	Homo sapiens	4758528	25714	hepatocyte growth factor-regulated tyrosine kinase substrate

Fragment-ion (m/z)	246.90	248.70	260.11	276.17	293.99	408.05	446.19	564.44	594.05	618.82	661.32	689.23
Frac. Inten.(% of TIC)	1.31	2.58	4.11	1.37	4.52	1.31	6.11	9.51	4.21	3.23	2.02	6.02
Rel. Inten.(% of BP)	9.51	18.67	29.78	9.92	32.73	9.48	44.28	68.87	30.49	23.39	14.64	43.63
Score	-0.10	-0.19	1.00	0.25	1.00	1.00	1.00	1.00	1.00	1.00	-0.15	1.00
Ion-type			z'_2	y_2	c_2	c_3	z'_3	c_4	$z'{++}_8$	$c{++}_8$		z'_4
Delta Da			-0.03	0.01	-0.19	-0.17	-0.03	0.11	0.29	0.06		-0.02

Fragment-ion (m/z)	705.39	803.37	921.50	959.31	1073.73	1074.47	1107.63	1187.69	1192.72	1236.75
Frac. Inten.(% of TIC)	1.52	6.77	4.00	3.55	2.55	5.82	7.46	6.77	1.45	13.80
Rel. Inten.(% of BP)	11.01	49.05	28.96	25.72	18.49	42.19	54.07	49.06	10.52	100.00
Score	0.25	1.00	1.00	1.00	1.00	0.25	1.00	0.25	-0.11	1.00
Ion-type	y_4	z'_5	c_6	z'_6	z'_7	z''_7	c_7	z''_8		c_8
Delta Da	0.13	0.08	0.10	-0.08	0.30	0.03	0.15	0.17		0.23

Peak 230





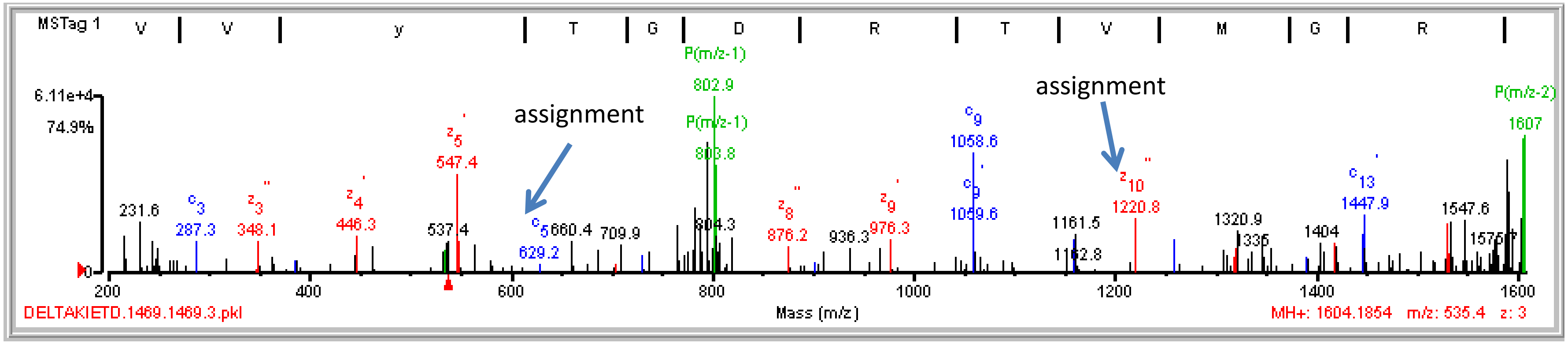
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.62	70.2	11	8/25	Y55y	(K) L S L D|E/L H/R|K|y\G\T\D|L/S\R (G)	1903.00	83.2550	1655.7	74167.3/5.73	Homo sapiens	48762682	27732	Na+/K+ -ATPase alpha 1 subunit isoform b proprotein
1	9.62	70.2	11	8/25	Y55y	(K) L S L D|E/L H/R|K|y\G\T\D|L/S\R (G)	1903.00	83.2550	1655.7	112896.8/5.33	Homo sapiens	21361181	30493	Na+/K+ -ATPase alpha 1 subunit isoform a proprotein

Fragment-ion (m/z)	247.88	359.24	447.38	491.36	504.25	516.15	631.32	670.44	676.71	705.65	743.45	748.56	769.84
Frac. Inten.(% of TIC)	5.60	5.60	3.44	2.87	4.03	5.31	3.45	3.95	3.79	4.35	3.49	2.95	5.65
Rel. Inten.(% of BP)	82.09	82.13	50.47	42.05	59.14	77.95	50.55	57.98	55.56	63.85	51.24	43.26	82.95
Score	0.25	1.00	0.25	1.00	1.00	-0.78	-0.51	-0.58	1.00	1.00	-0.51	-0.43	1.00
Ion-type	z''_2	z'_3	c'_4	$c{+}{+}_8$	$c3{+}_{12}$				$c{+}{+}_{10}$	$c{+}{+}_{11}$ $z'{+}{+}_{11}$			$z'{+}{+}_{12}$
Delta Da	0.74	0.02	0.11	0.08	-0.00				-0.13	0.30 0.31			-0.03

Fragment-ion (m/z)	813.48	875.43	913.91	918.84	942.36	1003.39	1109.62	1159.34	1410.64	1498.25	1540.48	1626.45
Frac. Inten.(% of TIC)	4.03	3.50	3.62	2.90	3.48	2.89	6.82	2.92	3.30	4.30	3.75	4.02
Rel. Inten.(% of BP)	59.12	51.32	53.04	42.59	51.10	42.44	100.00	42.84	48.34	63.15	54.97	58.96
Score	1.00	1.00	1.00	-0.43	-0.51	1.00	1.00	1.00	0.25	-0.63	0.25	1.00
Ion-type	$c{+}{+}_{13}$	z'_7	$c{+}{+}_{15}$			z'_8	c_9	z'_9	c'_{11} z''_{11}		z''_{12}	c_{13}
Delta Da	0.09	0.09	0.46			-0.05	-0.02	-0.20	-0.06 -0.05		0.75	0.68

Peak 231



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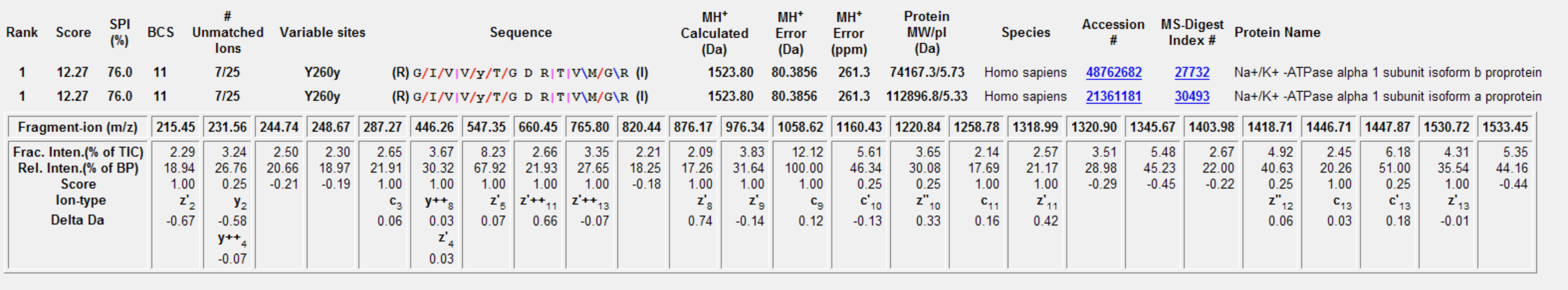
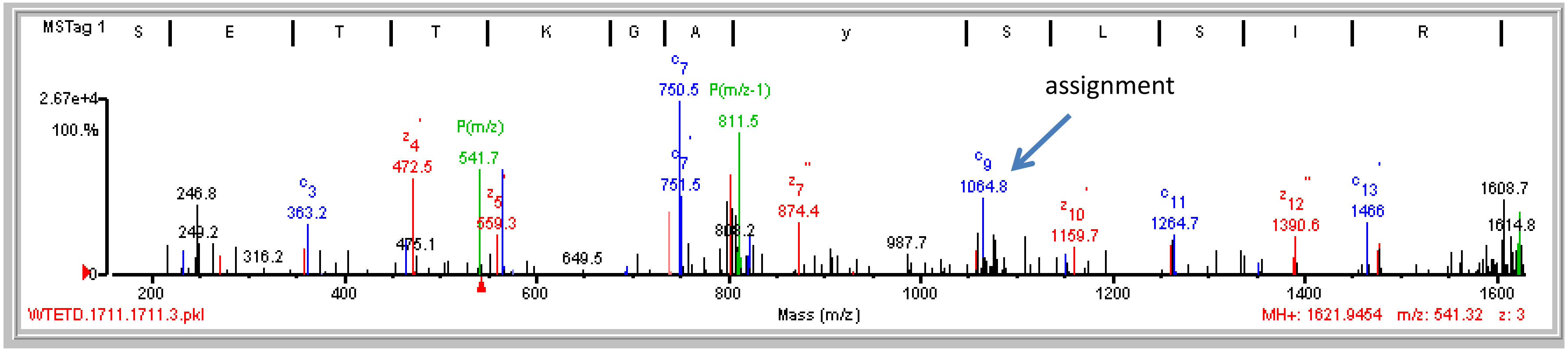


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.27	76.0	11	7/25	Y260y	(R) G/I/V|V/y/T/G D R|T|V\M/G\R (I)	1523.80	80.3856	261.3	74167.3/5.73	Homo sapiens	48762682	27732	Na+/K+ -ATPase alpha 1 subunit isoform b proprotein
1	12.27	76.0	11	7/25	Y260y	(R) G/I/V|V/y/T/G D R|T|V\M/G\R (I)	1523.80	80.3856	261.3	112896.8/5.33	Homo sapiens	21361181	30493	Na+/K+ -ATPase alpha 1 subunit isoform a proprotein

Fragment-ion (m/z)	215.45	231.56	244.74	248.67	287.27	446.26	547.35	660.45	765.80	820.44	876.17	976.34	1058.62
Frac. Inten.(% of TIC)	2.29	3.24	2.50	2.30	2.65	3.67	8.23	2.66	3.35	2.21	2.09	3.83	12.12
Rel. Inten.(% of BP)	18.94	26.76	20.66	18.97	21.91	30.32	67.92	21.93	27.65	18.25	17.26	31.64	100.00
Score	1.00	0.25	-0.21	-0.19	1.00	1.00	1.00	1.00	1.00	-0.18	1.00	1.00	1.00
Ion-type	z'_2	y_2 y^{++}_4			c_3	y^{++}_8 z'_4	z'_5	z'^{++}_{11}	z'^{++}_{13}		z'_8	z'_9	c_9
Delta Da	-0.67	-0.58 -0.07			0.06	0.03 0.03	0.07	0.66	-0.07		0.74	-0.14	0.12

Fragment-ion (m/z)	1160.43	1220.84	1258.78	1318.99	1320.90	1345.67	1403.98	1418.71	1446.71	1447.87	1530.72	1533.45
Frac. Inten.(% of TIC)	5.61	3.65	2.14	2.57	3.51	5.48	2.67	4.92	2.45	6.18	4.31	5.35
Rel. Inten.(% of BP)	46.34	30.08	17.69	21.17	28.98	45.23	22.00	40.63	20.26	51.00	35.54	44.16
Score	0.25	0.25	1.00	1.00	-0.29	-0.45	-0.22	0.25	1.00	0.25	1.00	-0.44
Ion-type	c'_{10}	z''_{10}	c_{11}	z'_{11}				z''_{12}	c_{13}	c'_{13}	z'_{13}	
Delta Da	-0.13	0.33	0.16	0.42				0.06	0.03	0.18	-0.01	

Peak 232



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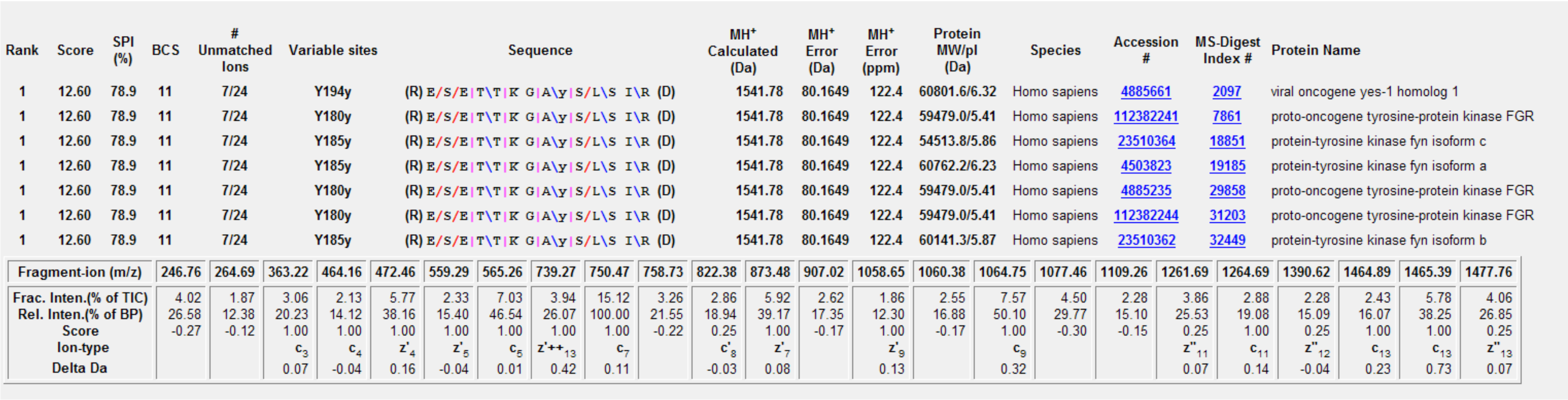
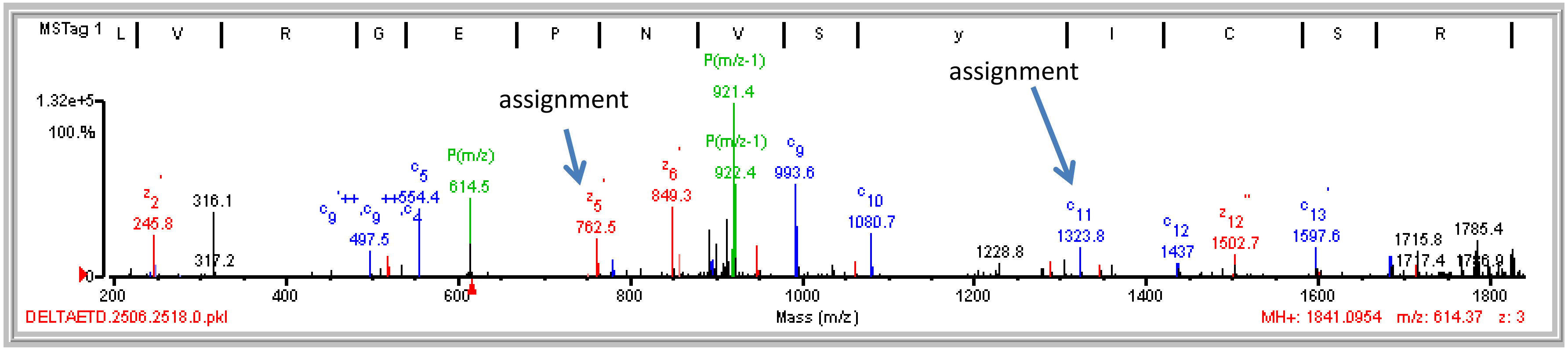


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.60	78.9	11	7/24	Y194y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	60801.6/6.32	Homo sapiens	4885661	2097	viral oncogene yes-1 homolog 1
1	12.60	78.9	11	7/24	Y180y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	59479.0/5.41	Homo sapiens	112382241	7861	proto-oncogene tyrosine-protein kinase FGR
1	12.60	78.9	11	7/24	Y185y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	54513.8/5.86	Homo sapiens	23510364	18851	protein-tyrosine kinase fyn isoform c
1	12.60	78.9	11	7/24	Y185y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	60762.2/6.23	Homo sapiens	4503823	19185	protein-tyrosine kinase fyn isoform a
1	12.60	78.9	11	7/24	Y180y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	59479.0/5.41	Homo sapiens	4885235	29858	proto-oncogene tyrosine-protein kinase FGR
1	12.60	78.9	11	7/24	Y180y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	59479.0/5.41	Homo sapiens	112382244	31203	proto-oncogene tyrosine-protein kinase FGR
1	12.60	78.9	11	7/24	Y185y	(R) E/S/E|T\T|K G|A\y|S/L\S I\R (D)	1541.78	80.1649	122.4	60141.3/5.87	Homo sapiens	23510362	32449	protein-tyrosine kinase fyn isoform b

Fragment-ion (m/z)	246.76	264.69	363.22	464.16	472.46	559.29	565.26	739.27	750.47	758.73	822.38	873.48	907.02	1058.65	1060.38	1064.75	1077.46	1109.26	1261.69	1264.69	1390.62	1464.89	1465.39	1477.76
Frac. Inten.(% of TIC)	4.02	1.87	3.06	2.13	5.77	2.33	7.03	3.94	15.12	3.26	2.86	5.92	2.62	1.86	2.55	7.57	4.50	2.28	3.86	2.88	2.28	2.43	5.78	4.06
Rel. Inten.(% of BP)	26.58	12.38	20.23	14.12	38.16	15.40	46.54	26.07	100.00	21.55	18.94	39.17	17.35	12.30	16.88	50.10	29.77	15.10	25.53	19.08	15.09	16.07	38.25	26.85
Score	-0.27	-0.12	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.22	0.25	1.00	-0.17	1.00	-0.17	1.00	-0.30	-0.15	0.25	1.00	0.25	1.00	1.00	0.25
Ion-type			c_3	c_4	z'_4	z'_5	c_5	$z'{++}_{13}$	c_7		c'_8	z'_7		z'_9		c_9			z''_{11}	c_{11}	z''_{12}	c_{13}	c_{13}	z''_{13}
Delta Da			0.07	-0.04	0.16	-0.04	0.01	0.42	0.11		-0.03	0.08		0.13		0.32			0.07	0.14	-0.04	0.23	0.73	0.07

Peak 233



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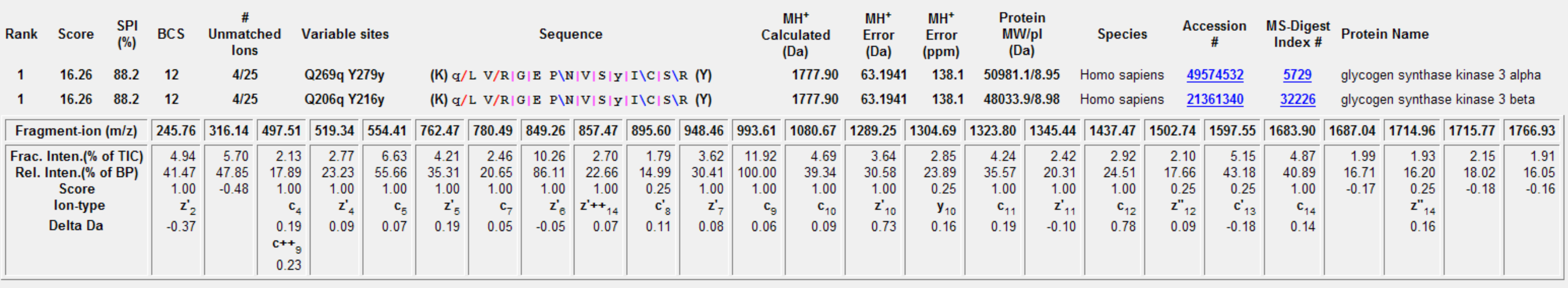
assignment



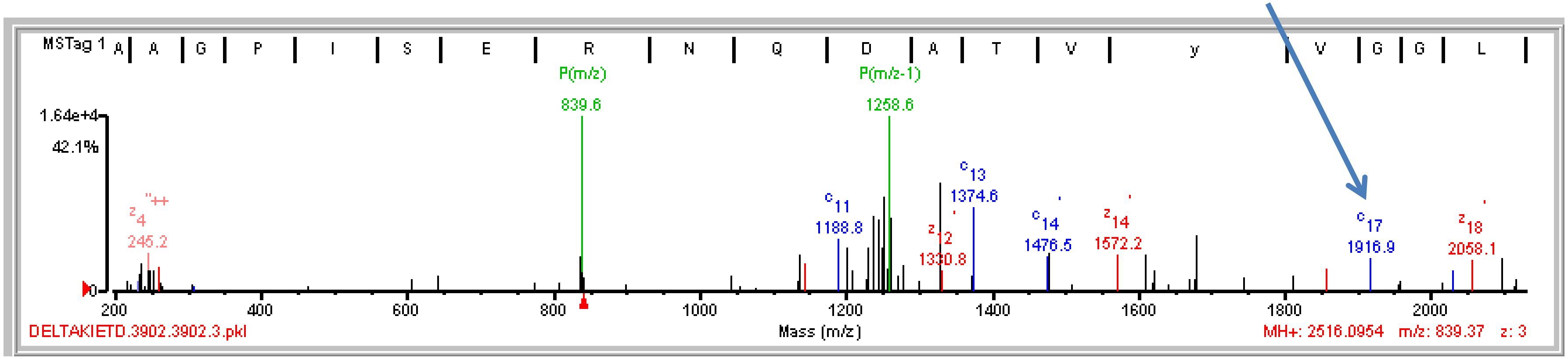
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.26	88.2	12	4/25	Q269q Y279y	(K) q/L V/R|G|E P\N|V|S|y|I\C|S\R (Y)	1777.90	63.1941	138.1	50981.1/8.95	Homo sapiens	49574532	5729	glycogen synthase kinase 3 alpha
1	16.26	88.2	12	4/25	Q206q Y216y	(K) q/L V/R|G|E P\N|V|S|y|I\C|S\R (Y)	1777.90	63.1941	138.1	48033.9/8.98	Homo sapiens	21361340	32226	glycogen synthase kinase 3 beta

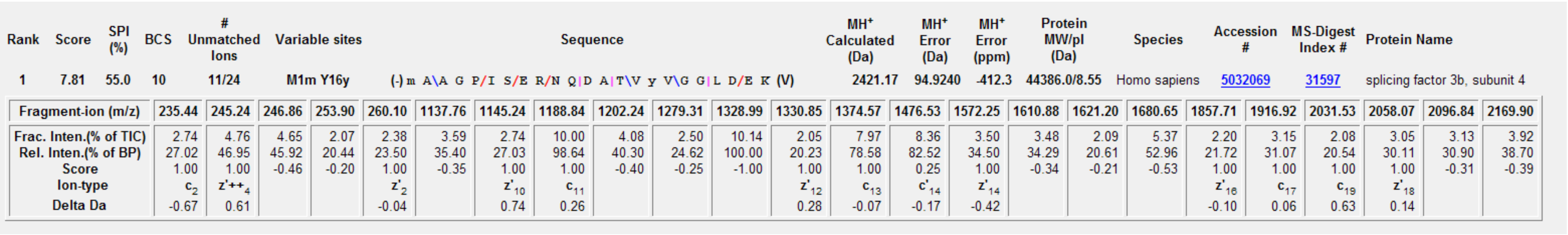
Fragment-ion (m/z)	245.76	316.14	497.51	519.34	554.41	762.47	780.49	849.26	857.47	895.60	948.46	993.61
Frac. Inten.(% of TIC)	4.94	5.70	2.13	2.77	6.63	4.21	2.46	10.26	2.70	1.79	3.62	11.92
Rel. Inten.(% of BP)	41.47	47.85	17.89	23.23	55.66	35.31	20.65	86.11	22.66	14.99	30.41	100.00
Score	1.00	-0.48	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type	z'_2		c_4 $c{++}_9$	z'_4	c_5	z'_5	c_7	z'_6	$z'{++}_{14}$	c'_8	z'_7	c_9
Delta Da	-0.37		0.19 0.23	0.09	0.07	0.19	0.05	-0.05	0.07	0.11	0.08	0.06

Fragment-ion (m/z)	1080.67	1289.25	1304.69	1323.80	1345.44	1437.47	1502.74	1597.55	1683.90	1687.04	1714.96	1715.77	1766.93
Frac. Inten.(% of TIC)	4.69	3.64	2.85	4.24	2.42	2.92	2.10	5.15	4.87	1.99	1.93	2.15	1.91
Rel. Inten.(% of BP)	39.34	30.58	23.89	35.57	20.31	24.51	17.66	43.18	40.89	16.71	16.20	18.02	16.05
Score	1.00	1.00	0.25	1.00	1.00	1.00	0.25	0.25	1.00	-0.17	0.25	-0.18	-0.16
Ion-type	c_{10}	z'_{10}	y_{10}	c_{11}	z'_{11}	c_{12}	z''_{12}	c'_{13}	c_{14}		z''_{14}		
Delta Da	0.09	0.73	0.16	0.19	-0.10	0.78	0.09	-0.18	0.14		0.16		

Peak 234

Ions that verify assignment



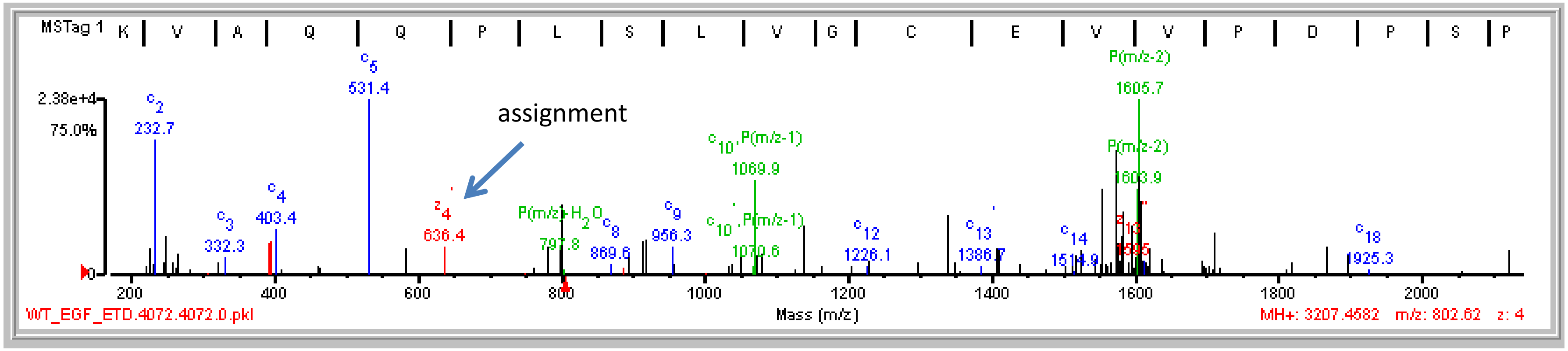


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.81	55.0	10	11/24	M1m Y16y	(-) m A\A G P/I S/E R/N Q|D A|T\V y V\G G|L D/E K (V)	2421.17	94.9240	-412.3	44386.0/8.55	Homo sapiens	5032069	31597	splicing factor 3b, subunit 4

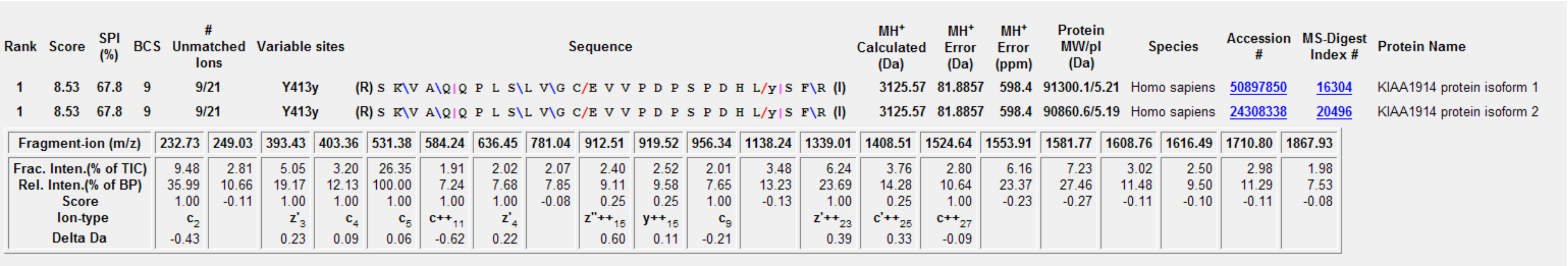
Fragment-ion (m/z)	235.44	245.24	246.86	253.90	260.10	1137.76	1145.24	1188.84	1202.24	1279.31	1328.99	1330.85
Frac. Inten.(% of TIC)	2.74	4.76	4.65	2.07	2.38	3.59	2.74	10.00	4.08	2.50	10.14	2.05
Rel. Inten.(% of BP)	27.02	46.95	45.92	20.44	23.50	35.40	27.03	98.64	40.30	24.62	100.00	20.23
Score	1.00	1.00	-0.46	-0.20	1.00	-0.35	1.00	1.00	-0.40	-0.25	-1.00	1.00
Ion-type	c_2	z'^{++}_4			z'_2		z'_{10}	c_{11}				z'_{12}
Delta Da	-0.67	0.61			-0.04		0.74	0.26				0.28

Fragment-ion (m/z)	1374.57	1476.53	1572.25	1610.88	1621.20	1680.65	1857.71	1916.92	2031.53	2058.07	2096.84	2169.90
Frac. Inten.(% of TIC)	7.97	8.36	3.50	3.48	2.09	5.37	2.20	3.15	2.08	3.05	3.13	3.92
Rel. Inten.(% of BP)	78.58	82.52	34.50	34.29	20.61	52.96	21.72	31.07	20.54	30.11	30.90	38.70
Score	1.00	0.25	1.00	-0.34	-0.21	-0.53	1.00	1.00	1.00	1.00	-0.31	-0.39
Ion-type	c_{13}	c'_{14}	z'_{14}				z'_{16}	c_{17}	c_{19}	z'_{18}		
Delta Da	-0.07	-0.17	-0.42				-0.10	0.06	0.63	0.14		

Peak 235



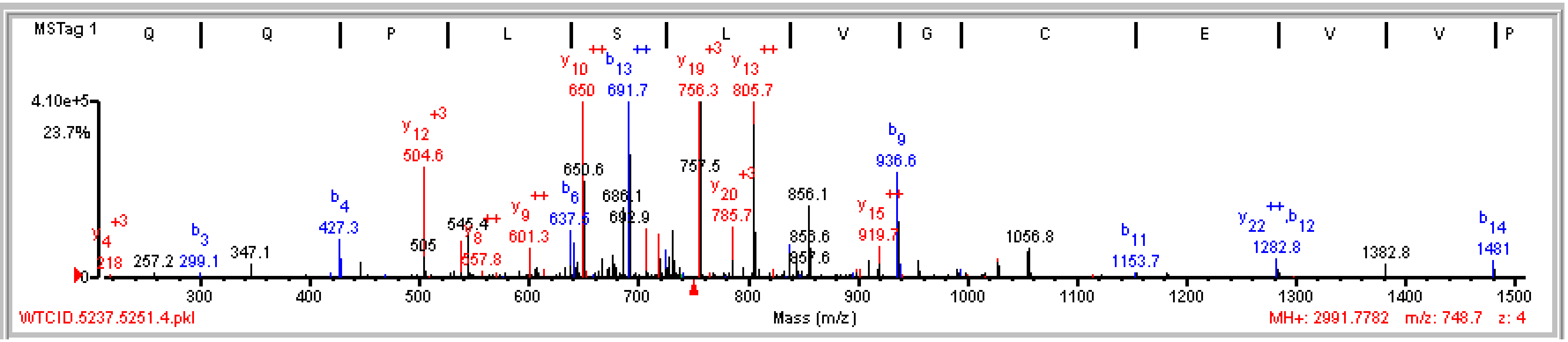
assignment



Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.53	67.8	9	9/21	Y413y	(R) S K\V A\Q|Q P L S\L V\G C/E V V P D P S P D H L/y|S F\R (I)	3125.57	81.8857	598.4	91300.1/5.21	Homo sapiens	50897850	16304	KIAA1914 protein isoform 1
1	8.53	67.8	9	9/21	Y413y	(R) S K\V A\Q|Q P L S\L V\G C/E V V P D P S P D H L/y|S F\R (I)	3125.57	81.8857	598.4	90860.6/5.19	Homo sapiens	24308338	20496	KIAA1914 protein isoform 2

Fragment-ion (m/z)	232.73	249.03	393.43	403.36	531.38	584.24	636.45	781.04	912.51	919.52	956.34	1138.24	1339.01	1408.51	1524.64	1553.91	1581.77	1608.76	1616.49	1710.80	1867.93
Frac. Inten.(% of TIC)	9.48	2.81	5.05	3.20	26.35	1.91	2.02	2.07	2.40	2.52	2.01	3.48	6.24	3.76	2.80	6.16	7.23	3.02	2.50	2.98	1.98
Rel. Inten.(% of BP)	35.99	10.66	19.17	12.13	100.00	7.24	7.68	7.85	9.11	9.58	7.65	13.23	23.69	14.28	10.64	23.37	27.46	11.48	9.50	11.29	7.53
Score	1.00	-0.11	1.00	1.00	1.00	1.00	1.00	-0.08	0.25	0.25	1.00	-0.13	1.00	0.25	1.00	-0.23	-0.27	-0.11	-0.10	-0.11	-0.08
Ion-type	c_2		z'_3	c_4	c_5	$c{++}_{11}$	z'_4		$z''{++}_{15}$	$y{++}_{15}$	c_9		$z'{++}_{23}$	$c'{++}_{25}$	$c{++}_{27}$						
Delta Da	-0.43		0.23	0.09	0.06	-0.62	0.22		0.60	0.11	-0.21		0.39	0.33	-0.09						

Peak 236



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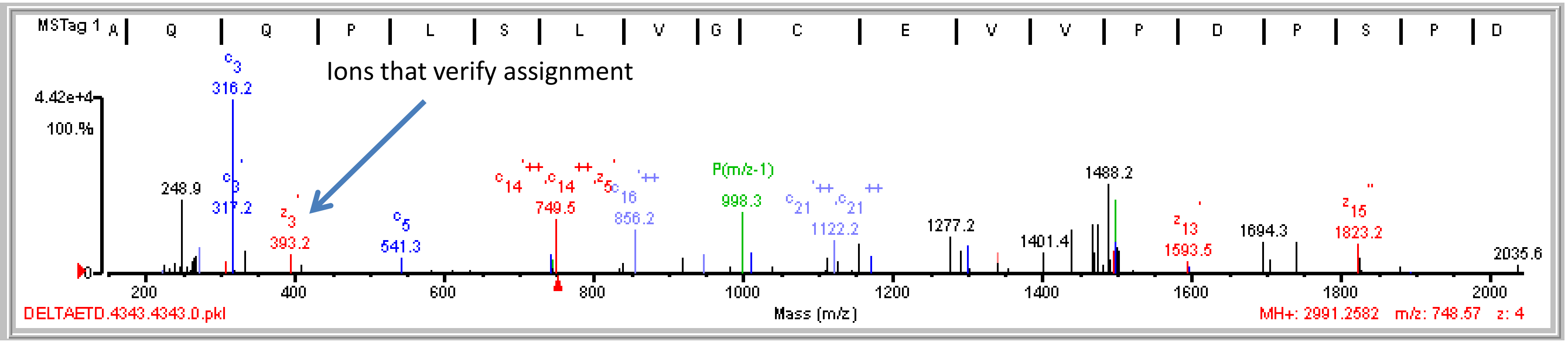
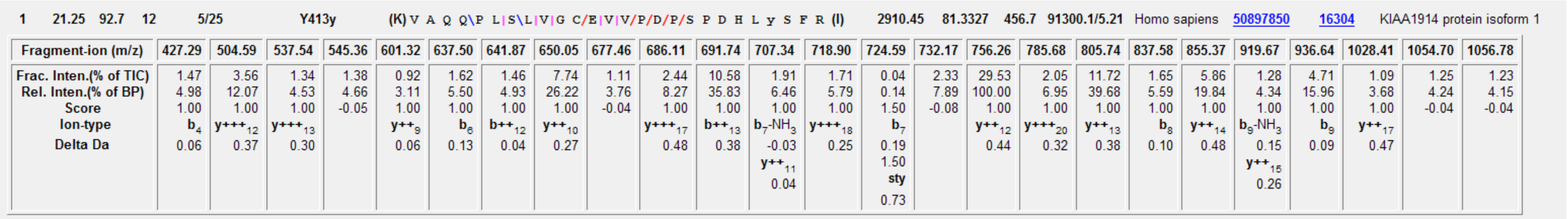


Ions that verify assignment

ETD

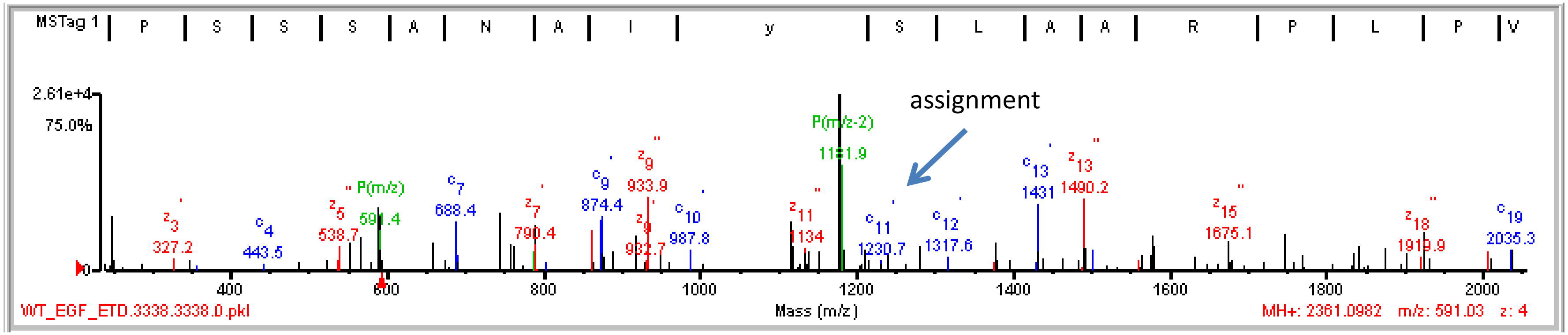


1 21.25 92.7 12 5/25 Y413y (K) V A Q Q\P L|S\L|V|G C/E|V|V/P/D/P/S P D H L y S F R (I) 2910.45 81.3327 456.7 91300.1/5.21 Homo sapiens 50897850 16304 KIAA1914 protein isoform 1

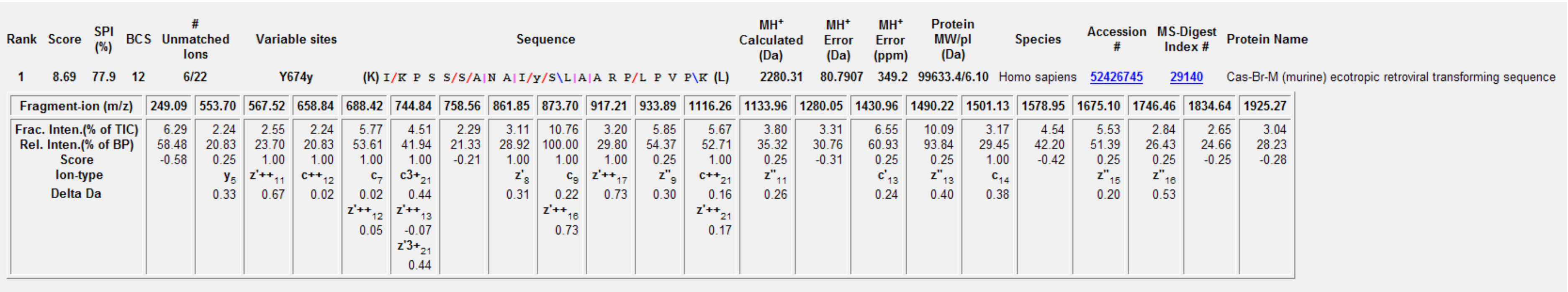
Fragment-ion (m/z)	427.29	504.59	537.54	545.36	601.32	637.50	641.87	650.05	677.46	686.11	691.74	707.34
Frac. Inten.(% of TIC)	1.47	3.56	1.34	1.38	0.92	1.62	1.46	7.74	1.11	2.44	10.58	1.91
Rel. Inten.(% of BP)	4.98	12.07	4.53	4.66	3.11	5.50	4.93	26.22	3.76	8.27	35.83	6.46
Score	1.00	1.00	1.00	-0.05	1.00	1.00	1.00	1.00	-0.04	1.00	1.00	1.00
Ion-type	b_4	y+++$_{12}$	y+++$_{13}$		y++$_9$	b_6	b++$_{12}$	y++$_{10}$		y+++$_{17}$	b++$_{13}$	b_7-NH_3 y++$_{11}$
Delta Da	0.06	0.37	0.30		0.06	0.13	0.04	0.27		0.48	0.38	-0.03 0.04

Fragment-ion (m/z)	718.90	724.59	732.17	756.26	785.68	805.74	837.58	855.37	919.67	936.64	1028.41	1054.70	1056.78
Frac. Inten.(% of TIC)	1.71	0.04	2.33	29.53	2.05	11.72	1.65	5.86	1.28	4.71	1.09	1.25	1.23
Rel. Inten.(% of BP)	5.79	0.14	7.89	100.00	6.95	39.68	5.59	19.84	4.34	15.96	3.68	4.24	4.15
Score	1.00	1.50	-0.08	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.04	-0.04
Ion-type	y+++$_{18}$	b_7 1.50 sty		y++$_{12}$	y+++$_{20}$	y++$_{13}$	b_8	y++$_{14}$	b_9-NH_3 y++$_{15}$	b_9	y++$_{17}$		
Delta Da	0.25	0.19 0.73		0.44	0.32	0.38	0.10	0.48	0.15 0.26	0.09	0.47		

Peak 237



assignment

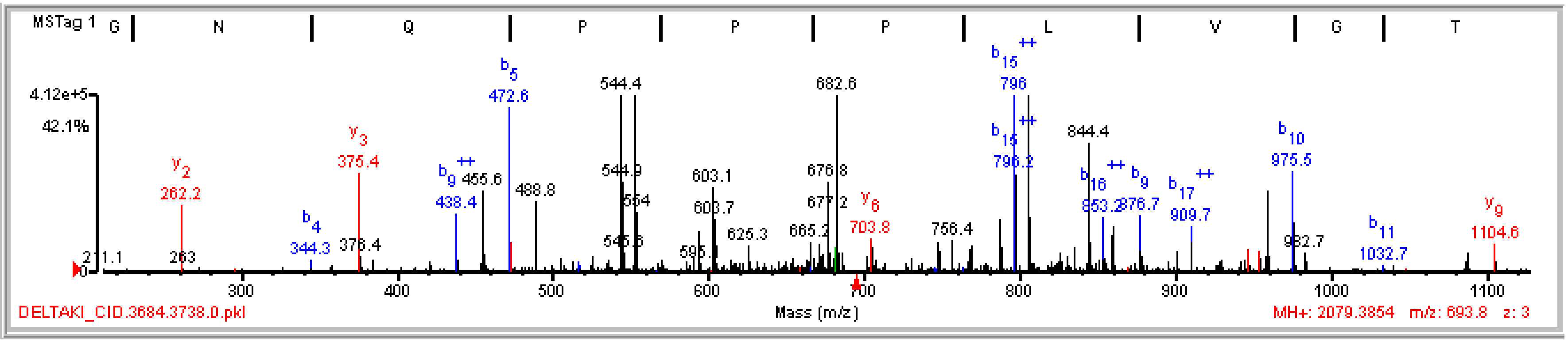


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.69	77.9	12	6/22	Y674y	(K) I/K P S S/S/A|N A|I/y/S\L|A|A R P/L P V P\K (L)	2280.31	80.7907	349.2	99633.4/6.10	Homo sapiens	52426745	29140	Cas-Br-M (murine) ecotropic retroviral transforming sequence

Fragment-ion (m/z)	249.09	553.70	567.52	658.84	688.42	744.84	758.56	861.85	873.70	917.21	933.89
Frac. Inten.(% of TIC)	6.29	2.24	2.55	2.24	5.77	4.51	2.29	3.11	10.76	3.20	5.85
Rel. Inten.(% of BP)	58.48	20.83	23.70	20.83	53.61	41.94	21.33	28.92	100.00	29.80	54.37
Score	-0.58	0.25	1.00	1.00	1.00	1.00	-0.21	1.00	1.00	1.00	0.25
Ion-type		y_5	$z'{++}_{11}$	$c{++}_{12}$	c_7 $z'{++}_{12}$	$c3{+}_{21}$ $z'{++}_{13}$ $z'3{+}_{21}$		z'_8	c_9 $z'{++}_{16}$	$z'{++}_{17}$	z''_9
Delta Da		0.33	0.67	0.02	0.02 0.05	0.44 -0.07 0.44		0.31	0.22 0.73	0.73	0.30

Fragment-ion (m/z)	1116.26	1133.96	1280.05	1430.96	1490.22	1501.13	1578.95	1675.10	1746.46	1834.64	1925.27
Frac. Inten.(% of TIC)	5.67	3.80	3.31	6.55	10.09	3.17	4.54	5.53	2.84	2.65	3.04
Rel. Inten.(% of BP)	52.71	35.32	30.76	60.93	93.84	29.45	42.20	51.39	26.43	24.66	28.23
Score	1.00	0.25	-0.31	0.25	0.25	1.00	-0.42	0.25	0.25	-0.25	-0.28
Ion-type	$c{++}_{21}$ $z'{++}_{21}$	z''_{11}		c'_{13}	z''_{13}	c_{14}		z''_{15}	z''_{16}		
Delta Da	0.16 0.17	0.26		0.24	0.40	0.38		0.20	0.53		

Peak 238



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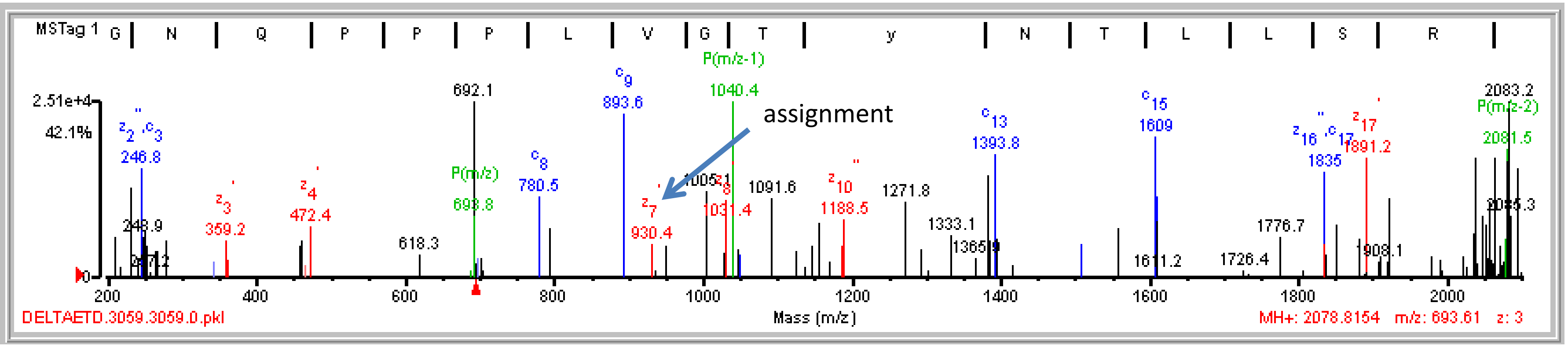
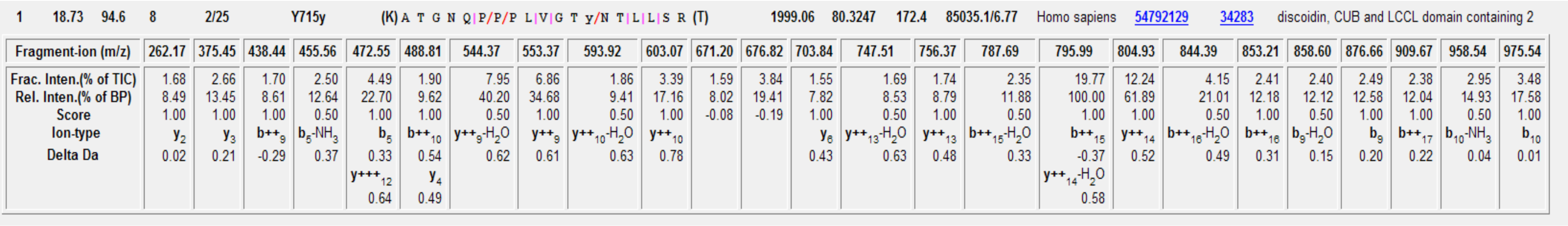


assignment

ETD

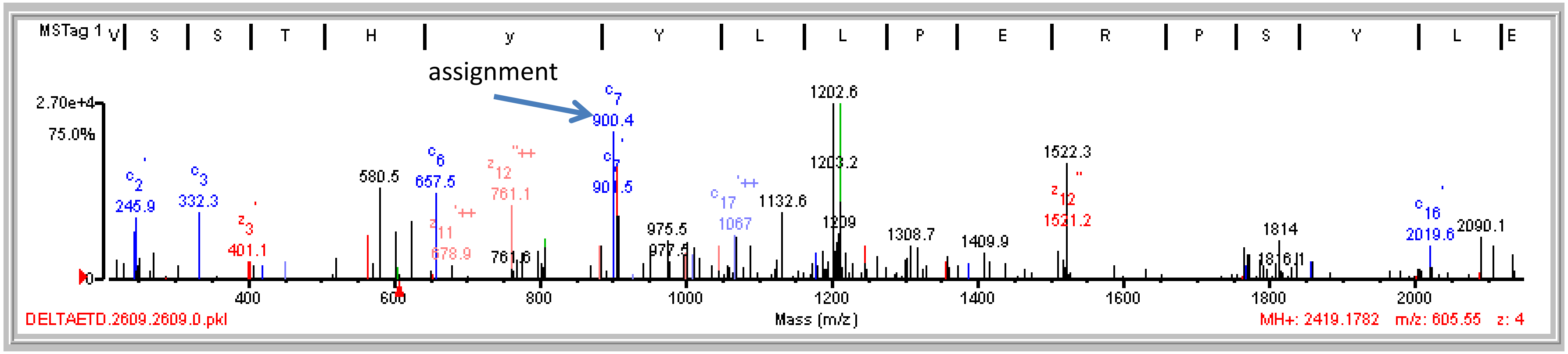


1 18.73 94.6 8 2/25 Y715y (K) A T G N Q|P/P/P L|V|G T y/N T|L|L|S R (T) 1999.06 80.3247 172.4 85035.1/6.77 Homo sapiens 54792129 34283 discoidin, CUB and LCCL domain containing 2

Fragment-ion (m/z)	262.17	375.45	438.44	455.56	472.55	488.81	544.37	553.37	593.92	603.07	671.20	676.82
Frac. Inten.(% of TIC)	1.68	2.66	1.70	2.50	4.49	1.90	7.95	6.86	1.86	3.39	1.59	3.84
Rel. Inten.(% of BP)	8.49	13.45	8.61	12.64	22.70	9.62	40.20	34.68	9.41	17.16	8.02	19.41
Score	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	0.50	1.00	-0.08	-0.19
Ion-type	y_2	y_3	b^{++}_9	b_5-NH_3	b_5 y^{+++}_{12}	b^{++}_{10} y_4	y^{++}_9-H_2O	y^{++}_9	y^{++}_{10}-H_2O	y^{++}_{10}		
Delta Da	0.02	0.21	-0.29	0.37	0.33 0.64	0.54 0.49	0.62	0.61	0.63	0.78		

Fragment-ion (m/z)	703.84	747.51	756.37	787.69	795.99	804.93	844.39	853.21	858.60	876.66	909.67	958.54	975.54
Frac. Inten.(% of TIC)	1.55	1.69	1.74	2.35	19.77	12.24	4.15	2.41	2.40	2.49	2.38	2.95	3.48
Rel. Inten.(% of BP)	7.82	8.53	8.79	11.88	100.00	61.89	21.01	12.18	12.12	12.58	12.04	14.93	17.58
Score	1.00	0.50	1.00	0.50	1.00	1.00	0.50	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	y_6	y^{++}_{13}-H_2O	y^{++}_{13}	b^{++}_{15}-H_2O	b^{++}_{15} y^{++}_{14}-H_2O	y^{++}_{14}	b^{++}_{16}-H_2O	b^{++}_{16}	b_9-H_2O	b_9	b^{++}_{17}	b_{10}-NH_3	b_{10}
Delta Da	0.43	0.63	0.48	0.33	-0.37 0.58	0.52	0.49	0.31	0.15	0.20	0.22	0.04	0.01

Peak 239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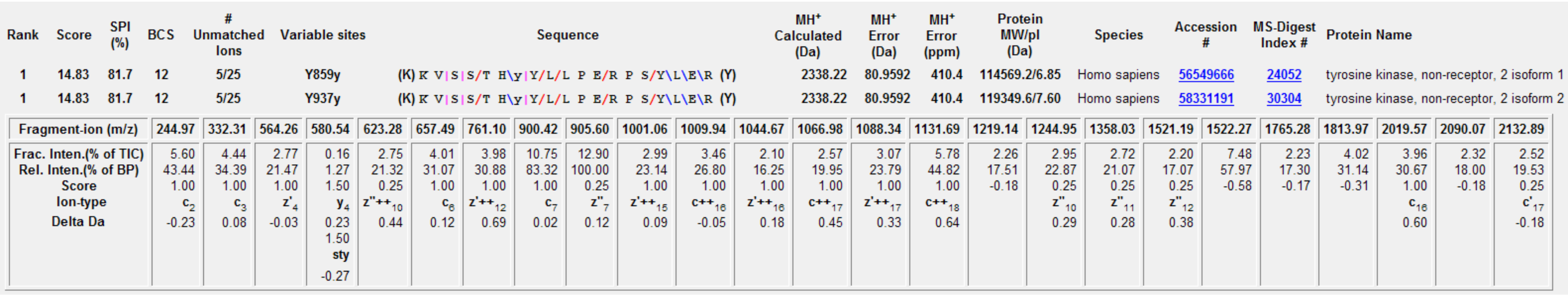
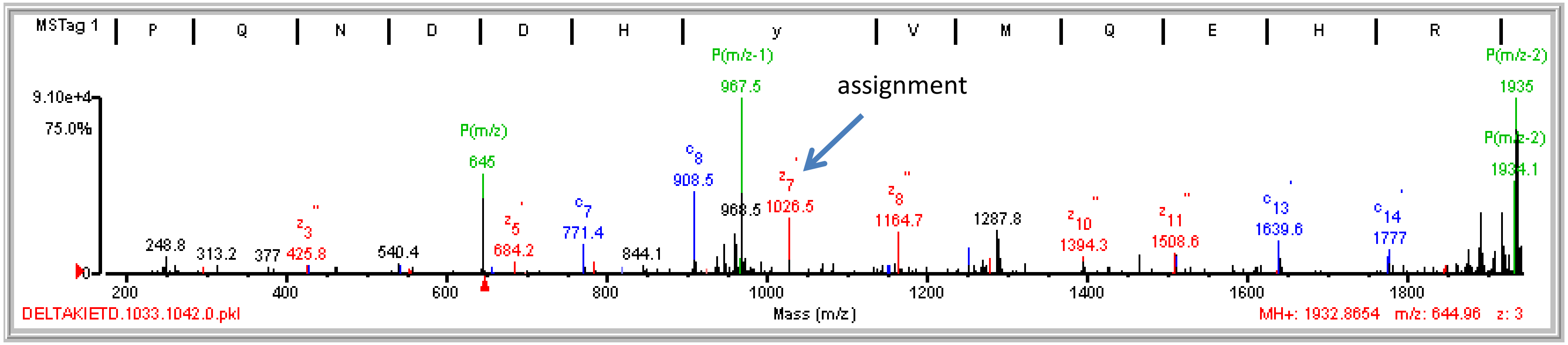


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.83	81.7	12	5/25	Y859y	(K) K V|S|S/T H\y|Y/L/L P E/R P S/Y\L\E\R (Y)	2338.22	80.9592	410.4	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1
1	14.83	81.7	12	5/25	Y937y	(K) K V|S|S/T H\y|Y/L/L P E/R P S/Y\L\E\R (Y)	2338.22	80.9592	410.4	119349.6/7.60	Homo sapiens	58331191	30304	tyrosine kinase, non-receptor, 2 isoform 2

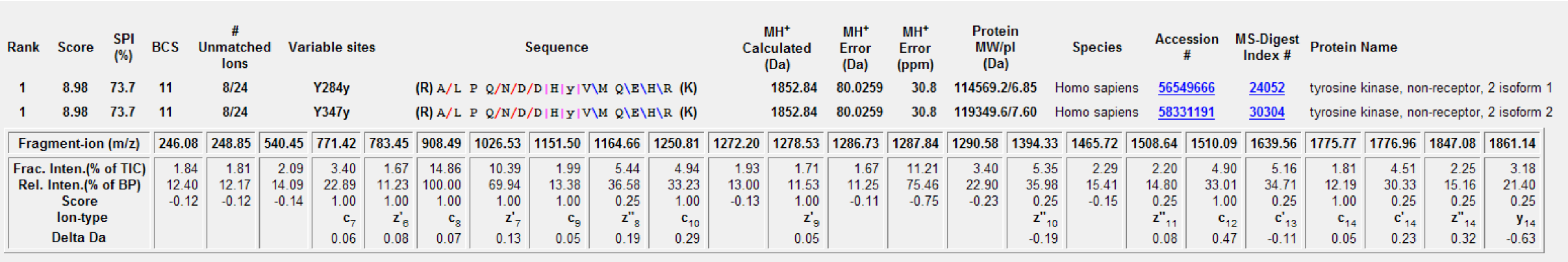
Fragment-ion (m/z)	244.97	332.31	564.26	580.54	623.28	657.49	761.10	900.42	905.60	1001.06	1009.94	1044.67
Frac. Inten.(% of TIC)	5.60	4.44	2.77	0.16	2.75	4.01	3.98	10.75	12.90	2.99	3.46	2.10
Rel. Inten.(% of BP)	43.44	34.39	21.47	1.27	21.32	31.07	30.88	83.32	100.00	23.14	26.80	16.25
Score	1.00	1.00	1.00	1.50	0.25	1.00	1.00	1.00	0.25	1.00	1.00	1.00
Ion-type	c_2	c_3	z'_4	y_4	$z''{++}_{10}$	c_6	$z'{++}_{12}$	c_7	z''_7	$z'{++}_{15}$	$c{++}_{16}$	$z'{++}_{16}$
Delta Da	-0.23	0.08	-0.03	0.23 1.50 sty -0.27	0.44	0.12	0.69	0.02	0.12	0.09	-0.05	0.18

Fragment-ion (m/z)	1066.98	1088.34	1131.69	1219.14	1244.95	1358.03	1521.19	1522.27	1765.28	1813.97	2019.57	2090.07	2132.89
Frac. Inten.(% of TIC)	2.57	3.07	5.78	2.26	2.95	2.72	2.20	7.48	2.23	4.02	3.96	2.32	2.52
Rel. Inten.(% of BP)	19.95	23.79	44.82	17.51	22.87	21.07	17.07	57.97	17.30	31.14	30.67	18.00	19.53
Score	1.00	1.00	1.00	-0.18	0.25	0.25	0.25	-0.58	-0.17	-0.31	1.00	-0.18	0.25
Ion-type	$c{++}_{17}$	$z'{++}_{17}$	$c{++}_{18}$		z''_{10}	z''_{11}	z''_{12}				c_{16}		c'_{17}
Delta Da	0.45	0.33	0.64		0.29	0.28	0.38				0.60		-0.18

Peak 240



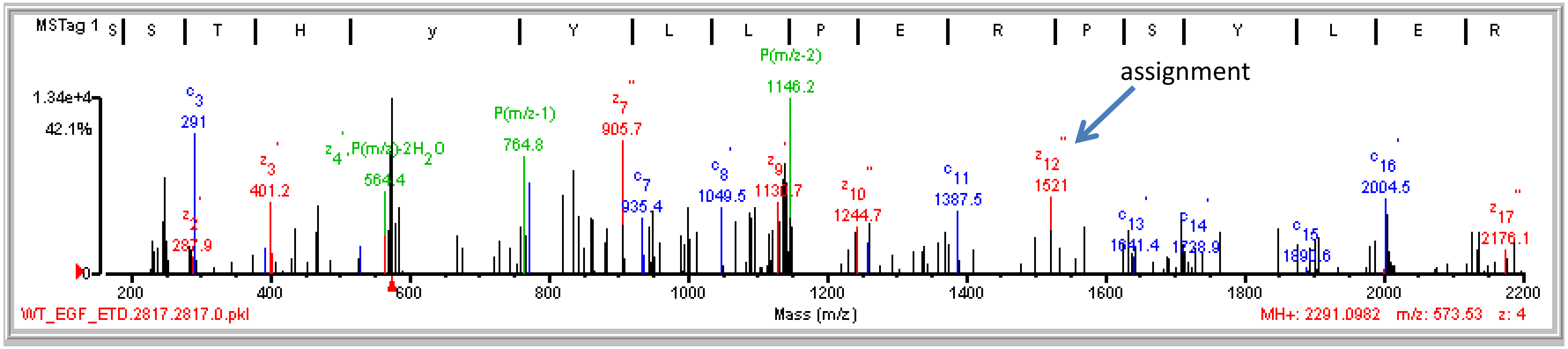
assignment



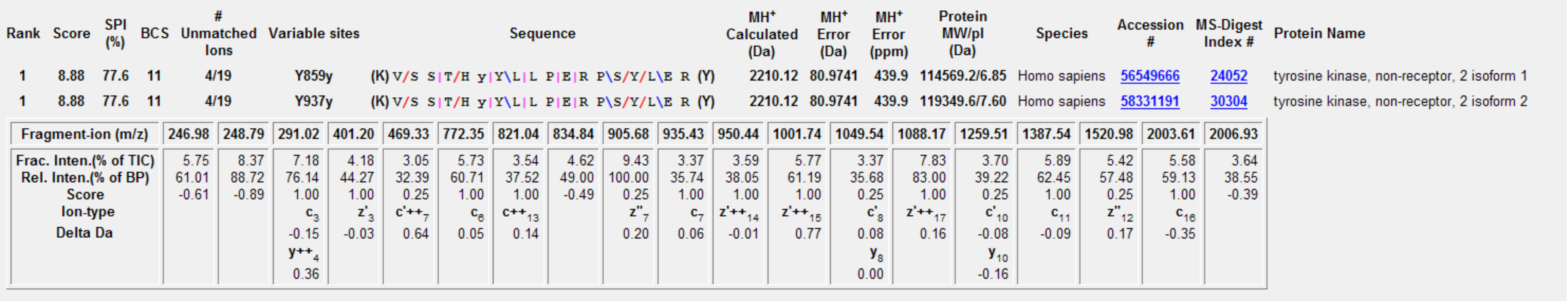
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.98	73.7	11	8/24	Y284y	(R) A/L P Q/N/D/D|H|y|V\M Q\E\H\R (K)	1852.84	80.0259	30.8	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1
1	8.98	73.7	11	8/24	Y347y	(R) A/L P Q/N/D/D|H|y|V\M Q\E\H\R (K)	1852.84	80.0259	30.8	119349.6/7.60	Homo sapiens	58331191	30304	tyrosine kinase, non-receptor, 2 isoform 2

Fragment-ion (m/z)	246.08	248.85	540.45	771.42	783.45	908.49	1026.53	1151.50	1164.66	1250.81	1272.20	1278.53	1286.73	1287.84	1290.58	1394.33	1465.72	1508.64	1510.09	1639.56	1775.77	1776.96	1847.08	1861.14
Frac. Inten.(% of TIC)	1.84	1.81	2.09	3.40	1.67	14.86	10.39	1.99	5.44	4.94	1.93	1.71	1.67	11.21	3.40	5.35	2.29	2.20	4.90	5.16	1.81	4.51	2.25	3.18
Rel. Inten.(% of BP)	12.40	12.17	14.09	22.89	11.23	100.00	69.94	13.38	36.58	33.23	13.00	11.53	11.25	75.46	22.90	35.98	15.41	14.80	33.01	34.71	12.19	30.33	15.16	21.40
Score	-0.12	-0.12	-0.14	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.13	1.00	-0.11	-0.75	-0.23	0.25	-0.15	0.25	1.00	0.25	1.00	0.25	0.25	0.25
Ion-type				c_7	z'_6	c_8	z'_7	c_9	z''_8	c_{10}		z'_9				z''_{10}		z''_{11}	c_{12}	c'_{13}	c_{14}	c'_{14}	z''_{14}	y_{14}
Delta Da				0.06	0.08	0.07	0.13	0.05	0.19	0.29		0.05				-0.19		0.08	0.47	-0.11	0.05	0.23	0.32	-0.63

Peak 241



assignment

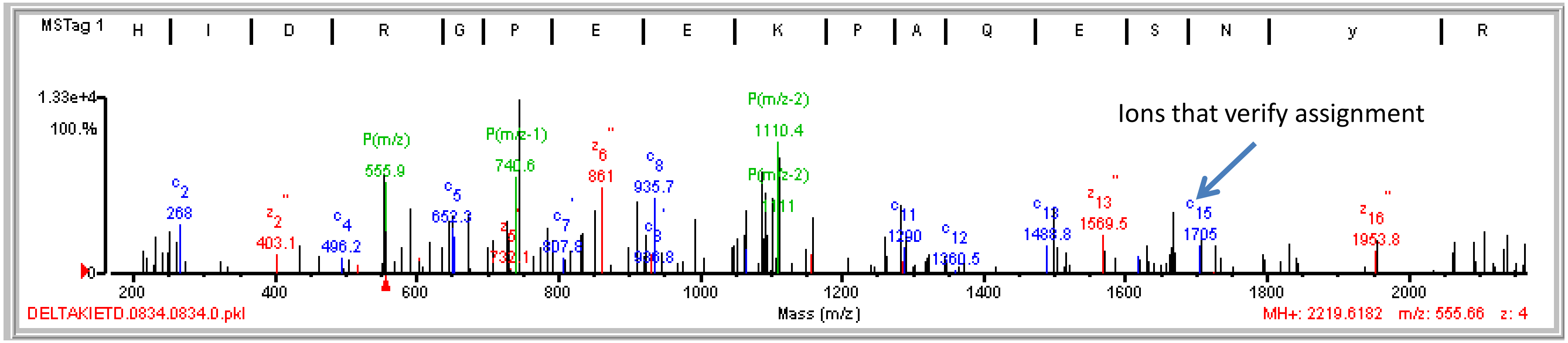


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.88	77.6	11	4/19	Y859y	(K) V/S S|T/H y|Y\L|L P|E|R P\S/Y/L\E R (Y)	2210.12	80.9741	439.9	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1
1	8.88	77.6	11	4/19	Y937y	(K) V/S S|T/H y|Y\L|L P|E|R P\S/Y/L\E R (Y)	2210.12	80.9741	439.9	119349.6/7.60	Homo sapiens	58331191	30304	tyrosine kinase, non-receptor, 2 isoform 2

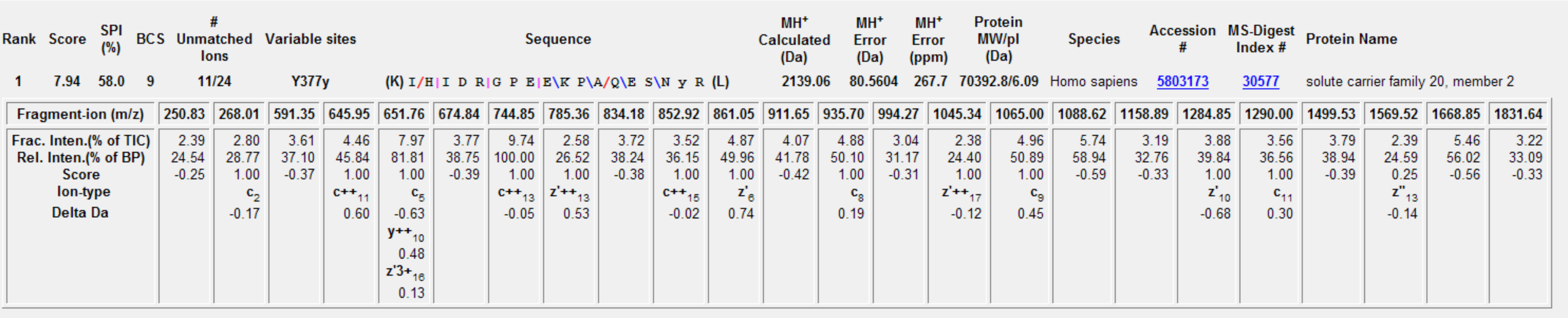
Fragment-ion (m/z)	246.98	248.79	291.02	401.20	469.33	772.35	821.04	834.84	905.68
Frac. Inten.(% of TIC)	5.75	8.37	7.18	4.18	3.05	5.73	3.54	4.62	9.43
Rel. Inten.(% of BP)	61.01	88.72	76.14	44.27	32.39	60.71	37.52	49.00	100.00
Score	-0.61	-0.89	1.00	1.00	0.25	1.00	1.00	-0.49	0.25
Ion-type			c_3	z'_3	$c'{++}_7$	c_6	$c{++}_{13}$		z''_7
Delta Da			-0.15	-0.03	0.64	0.05	0.14		0.20
			$y{++}_4$						
			0.36						

Fragment-ion (m/z)	935.43	950.44	1001.74	1049.54	1088.17	1259.51	1387.54	1520.98	2003.61	2006.93
Frac. Inten.(% of TIC)	3.37	3.59	5.77	3.37	7.83	3.70	5.89	5.42	5.58	3.64
Rel. Inten.(% of BP)	35.74	38.05	61.19	35.68	83.00	39.22	62.45	57.48	59.13	38.55
Score	1.00	1.00	1.00	0.25	1.00	0.25	1.00	0.25	1.00	-0.39
Ion-type	c_7	$z'{++}_{14}$	$z'{++}_{15}$	c'_8	$z'{++}_{17}$	c'_{10}	c_{11}	z''_{12}	c_{16}	
Delta Da	0.06	-0.01	0.77	0.08	0.16	-0.08	-0.09	0.17	-0.35	
				y_8		y_{10}				
				0.00		-0.16				

Peak 243



Ions that verify assignment

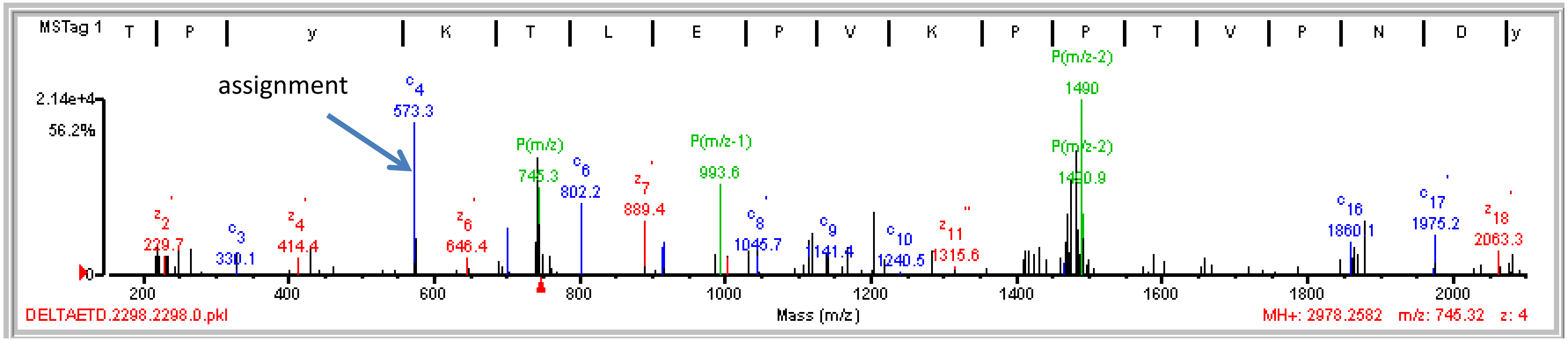


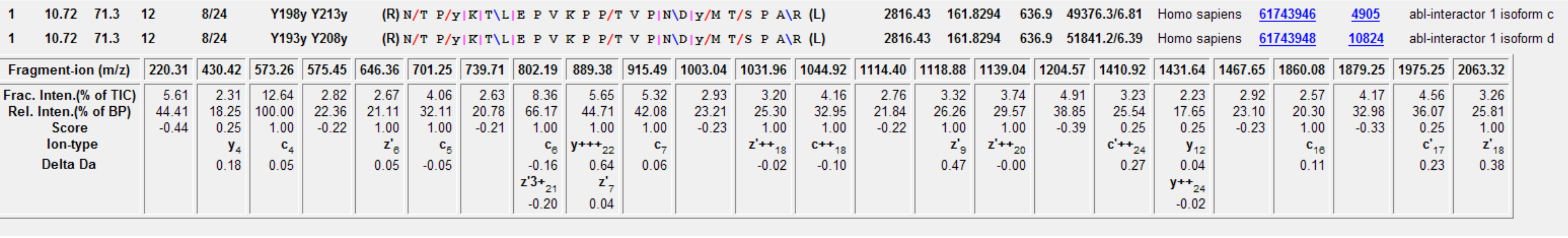
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.94	58.0	9	11/24	Y377y	(K) I/H|I D R|G P E|E\K P\A/Q\E S\N y R (L)	2139.06	80.5604	267.7	70392.8/6.09	Homo sapiens	5803173	30577	solute carrier family 20, member 2

Fragment-ion (m/z)	250.83	268.01	591.35	645.95	651.76	674.84	744.85	785.36	834.18	852.92	861.05
Frac. Inten.(% of TIC)	2.39	2.80	3.61	4.46	7.97	3.77	9.74	2.58	3.72	3.52	4.87
Rel. Inten.(% of BP)	24.54	28.77	37.10	45.84	81.81	38.75	100.00	26.52	38.24	36.15	49.96
Score	-0.25	1.00	-0.37	1.00	1.00	-0.39	1.00	1.00	-0.38	1.00	1.00
Ion-type		c_2		$c{++}_{11}$	c_5 $y{++}_{10}$ $z'3{+}_{16}$		$c{++}_{13}$	$z'{++}_{13}$		$c{++}_{15}$	z'_6
Delta Da		-0.17		0.60	-0.63 0.48 0.13		-0.05	0.53		-0.02	0.74

Fragment-ion (m/z)	911.65	935.70	994.27	1045.34	1065.00	1088.62	1158.89	1284.85	1290.00	1499.53	1569.52	1668.85	1831.64
Frac. Inten.(% of TIC)	4.07	4.88	3.04	2.38	4.96	5.74	3.19	3.88	3.56	3.79	2.39	5.46	3.22
Rel. Inten.(% of BP)	41.78	50.10	31.17	24.40	50.89	58.94	32.76	39.84	36.56	38.94	24.59	56.02	33.09
Score	-0.42	1.00	-0.31	1.00	1.00	-0.59	-0.33	1.00	1.00	-0.39	0.25	-0.56	-0.33
Ion-type		c_8		$z'{++}_{17}$	c_9			z'_{10}	c_{11}		z''_{13}		
Delta Da		0.19		-0.12	0.45			-0.68	0.30		-0.14		

Peak 244





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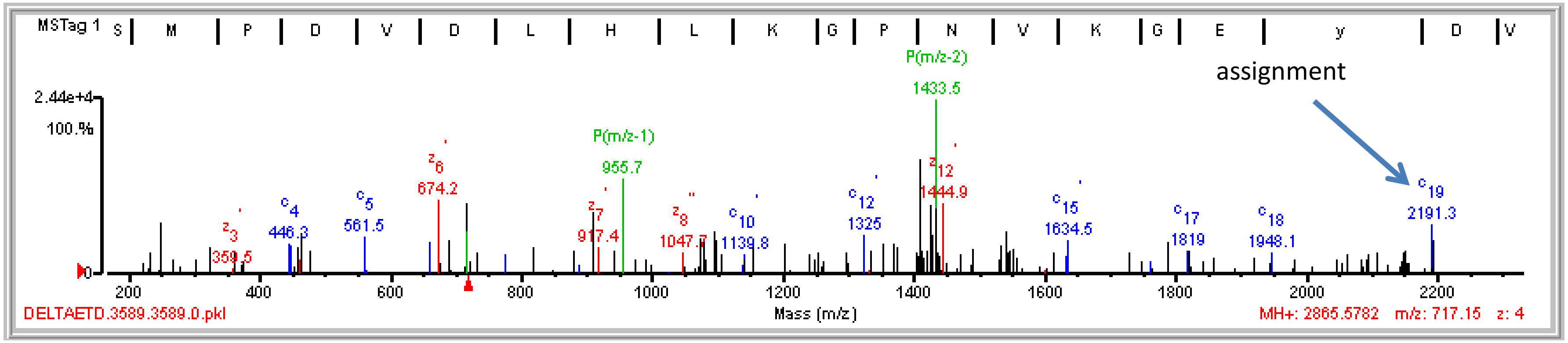
<tr><td>1</td><td>10.72</td><td>71.3</td><td>12</td><td>8/24</td><td>Y198y Y213y</td><td>(R) N/T P/y|K|T\L|E P V K P P/T V P|N\D|y/M T/S P A\R (L)</td><td>2816.43</td><td>161.8294</td><td>636.9</td><td>49376.3/6.81</td><td>Homo sapiens</td><td>61743946</td><td>4905</td><td>abl-interactor 1 isoform c</td></tr>
<tr><td>1</td><td>10.72</td><td>71.3</td><td>12</td><td>8/24</td><td>Y193y Y208y</td><td>(R) N/T P/y|K|T\L|E P V K P P/T V P|N\D|y/M T/S P A\R (L)</td><td>2816.43</td><td>161.8294</td><td>636.9</td><td>51841.2/6.39</td><td>Homo sapiens</td><td>61743948</td><td>10824</td><td>abl-interactor 1 isoform d</td></tr>
</table>

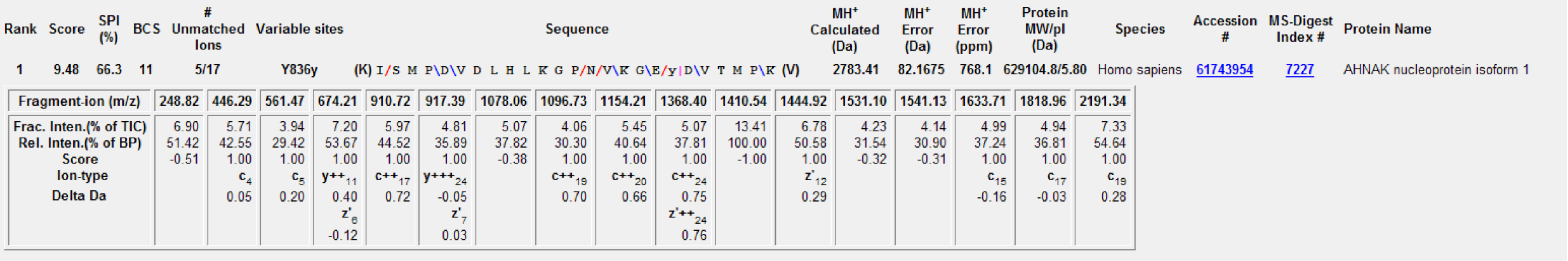
Fragment-ion (m/z)	220.31	430.42	573.26	575.45	646.36	701.25	739.71	802.19	889.38	915.49	1003.04	1031.96
Frac. Inten.(% of TIC)	5.61	2.31	12.64	2.82	2.67	4.06	2.63	8.36	5.65	5.32	2.93	3.20
Rel. Inten.(% of BP)	44.41	18.25	100.00	22.36	21.11	32.11	20.78	66.17	44.71	42.08	23.21	25.30
Score	-0.44	0.25	1.00	-0.22	1.00	1.00	-0.21	1.00	1.00	1.00	-0.23	1.00
Ion-type		y_4	c_4		z'_6	c_5		c_6 $z'3+_{21}$	$y+++_{22}$ z'_7	c_7		$z'++_{18}$
Delta Da		0.18	0.05		0.05	-0.05		-0.16 -0.20	0.64 0.04	0.06		-0.02

Fragment-ion (m/z)	1044.92	1114.40	1118.88	1139.04	1204.57	1410.92	1431.64	1467.65	1860.08	1879.25	1975.25	2063.32
Frac. Inten.(% of TIC)	4.16	2.76	3.32	3.74	4.91	3.23	2.23	2.92	2.57	4.17	4.56	3.26
Rel. Inten.(% of BP)	32.95	21.84	26.26	29.57	38.85	25.54	17.65	23.10	20.30	32.98	36.07	25.81
Score	1.00	-0.22	1.00	1.00	-0.39	0.25	0.25	-0.23	1.00	-0.33	0.25	1.00
Ion-type	$c++_{18}$		z'_9	$z'++_{20}$		$c'++_{24}$	y_{12} $y++_{24}$		c_{16}		c'_{17}	z'_{18}
Delta Da	-0.10		0.47	-0.00		0.27	0.04 -0.02		0.11		0.23	0.38

Peak 246



assignment

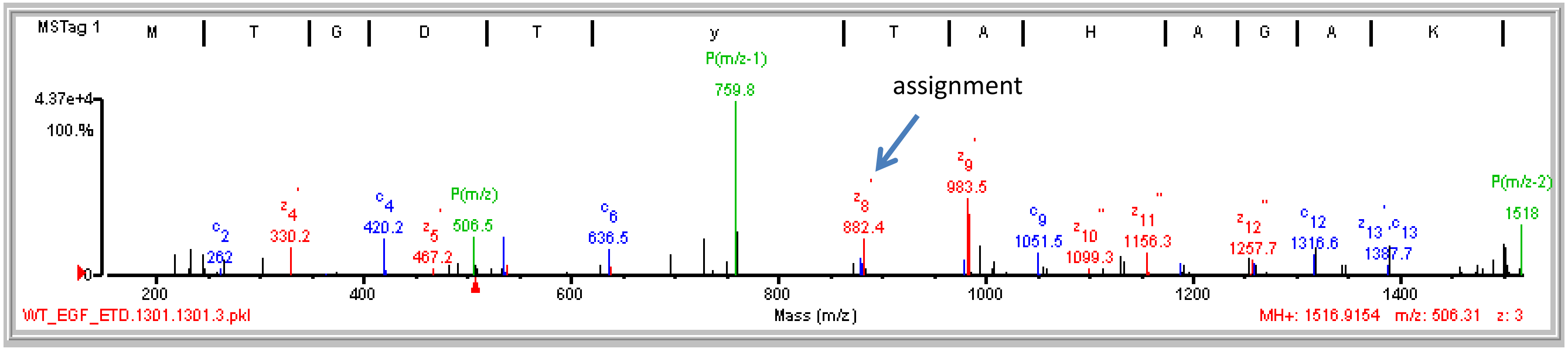


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.48	66.3	11	5/17	Y836y	(K) I/S M P\D\V D L H L K G P/N/V\K G\E/y|D\V T M P\K (V)	2783.41	82.1675	768.1	629104.8/5.80	Homo sapiens	61743954	7227	AHNAK nucleoprotein isoform 1

Fragment-ion (m/z)	248.82	446.29	561.47	674.21	910.72	917.39	1078.06	1096.73	1154.21
Frac. Inten.(% of TIC)	6.90	5.71	3.94	7.20	5.97	4.81	5.07	4.06	5.45
Rel. Inten.(% of BP)	51.42	42.55	29.42	53.67	44.52	35.89	37.82	30.30	40.64
Score	-0.51	1.00	1.00	1.00	1.00	1.00	-0.38	1.00	1.00
Ion-type		c_{4}	c_{5}	y^{++}_{11} z'_{6}	c^{++}_{17}	y^{+++}_{24} z'_{7}		c^{++}_{19}	c^{++}_{20}
Delta Da		0.05	0.20	0.40 -0.12	0.72	-0.05 0.03		0.70	0.66

Fragment-ion (m/z)	1368.40	1410.54	1444.92	1531.10	1541.13	1633.71	1818.96	2191.34
Frac. Inten.(% of TIC)	5.07	13.41	6.78	4.23	4.14	4.99	4.94	7.33
Rel. Inten.(% of BP)	37.81	100.00	50.58	31.54	30.90	37.24	36.81	54.64
Score	1.00	-1.00	1.00	-0.32	-0.31	1.00	1.00	1.00
Ion-type	c^{++}_{24} z'^{++}_{24}		z'_{12}			c_{15}	c_{17}	c_{19}
Delta Da	0.75 0.76		0.29			-0.16	-0.03	0.28

Peak 247



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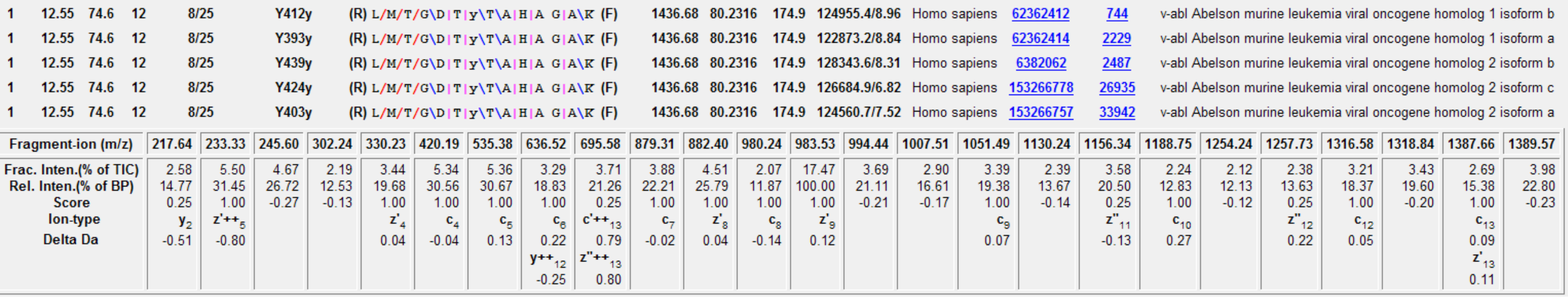
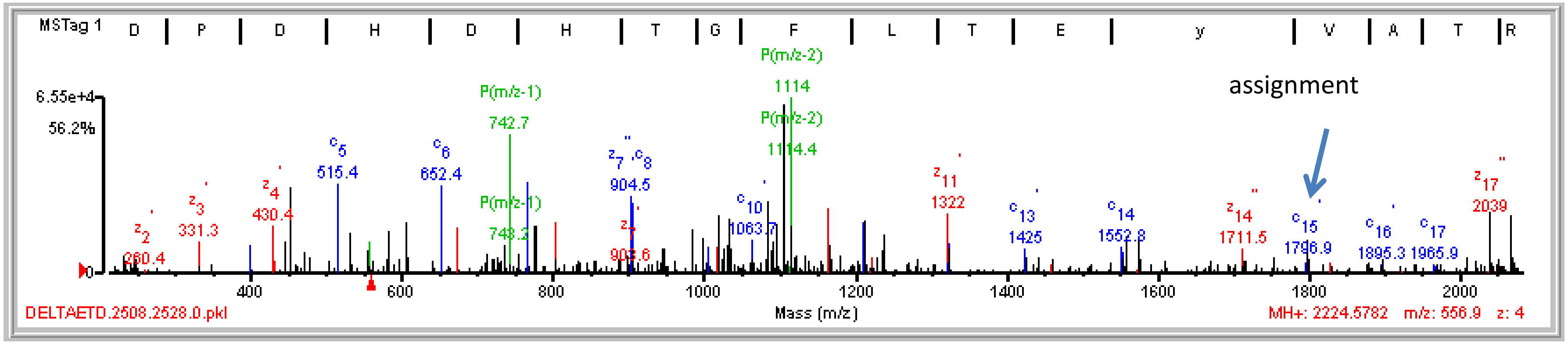


1	12.55	74.6	12	8/25	Y412y	(R) L/M/T/G\D|T|y\T\A|H|A G|A\K (F)	1436.68	80.2316	174.9	124955.4/8.96	Homo sapiens	62362412	744	v-abl Abelson murine leukemia viral oncogene homolog 1 isoform b
1	12.55	74.6	12	8/25	Y393y	(R) L/M/T/G\D|T|y\T\A|H|A G|A\K (F)	1436.68	80.2316	174.9	122873.2/8.84	Homo sapiens	62362414	2229	v-abl Abelson murine leukemia viral oncogene homolog 1 isoform a
1	12.55	74.6	12	8/25	Y439y	(R) L/M/T/G\D|T|y\T\A|H|A G|A\K (F)	1436.68	80.2316	174.9	128343.6/8.31	Homo sapiens	6382062	2487	v-abl Abelson murine leukemia viral oncogene homolog 2 isoform b
1	12.55	74.6	12	8/25	Y424y	(R) L/M/T/G\D|T|y\T\A|H|A G|A\K (F)	1436.68	80.2316	174.9	126684.9/6.82	Homo sapiens	153266778	26935	v-abl Abelson murine leukemia viral oncogene homolog 2 isoform c
1	12.55	74.6	12	8/25	Y403y	(R) L/M/T/G\D|T|y\T\A|H|A G|A\K (F)	1436.68	80.2316	174.9	124560.7/7.52	Homo sapiens	153266757	33942	v-abl Abelson murine leukemia viral oncogene homolog 2 isoform a

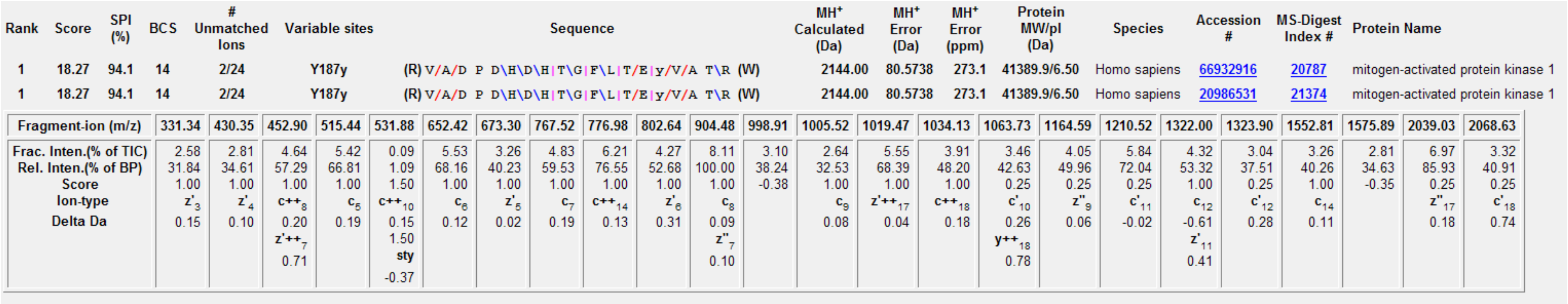
Fragment-ion (m/z)	217.64	233.33	245.60	302.24	330.23	420.19	535.38	636.52	695.58	879.31	882.40	980.24
Frac. Inten.(% of TIC)	2.58	5.50	4.67	2.19	3.44	5.34	5.36	3.29	3.71	3.88	4.51	2.07
Rel. Inten.(% of BP)	14.77	31.45	26.72	12.53	19.68	30.56	30.67	18.83	21.26	22.21	25.79	11.87
Score	0.25	1.00	-0.27	-0.13	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00
Ion-type	y_2	$z'{++}_5$			z'_4	c_4	c_5	c_6 $y{++}_{12}$	$c'{++}_{13}$ $z''{++}_{13}$	c_7	z'_8	c_8
Delta Da	-0.51	-0.80			0.04	-0.04	0.13	0.22 -0.25	0.79 0.80	-0.02	0.04	-0.14

Fragment-ion (m/z)	983.53	994.44	1007.51	1051.49	1130.24	1156.34	1188.75	1254.24	1257.73	1316.58	1318.84	1387.66	1389.57
Frac. Inten.(% of TIC)	17.47	3.69	2.90	3.39	2.39	3.58	2.24	2.12	2.38	3.21	3.43	2.69	3.98
Rel. Inten.(% of BP)	100.00	21.11	16.61	19.38	13.67	20.50	12.83	12.13	13.63	18.37	19.60	15.38	22.80
Score	1.00	-0.21	-0.17	1.00	-0.14	0.25	1.00	-0.12	0.25	1.00	-0.20	1.00	-0.23
Ion-type	z'_9			c_9		z''_{11}	c_{10}		z''_{12}	c_{12}		c_{13} z'_{13}	
Delta Da	0.12			0.07		-0.13	0.27		0.22	0.05		0.09 0.11	

Peak 248



assignment

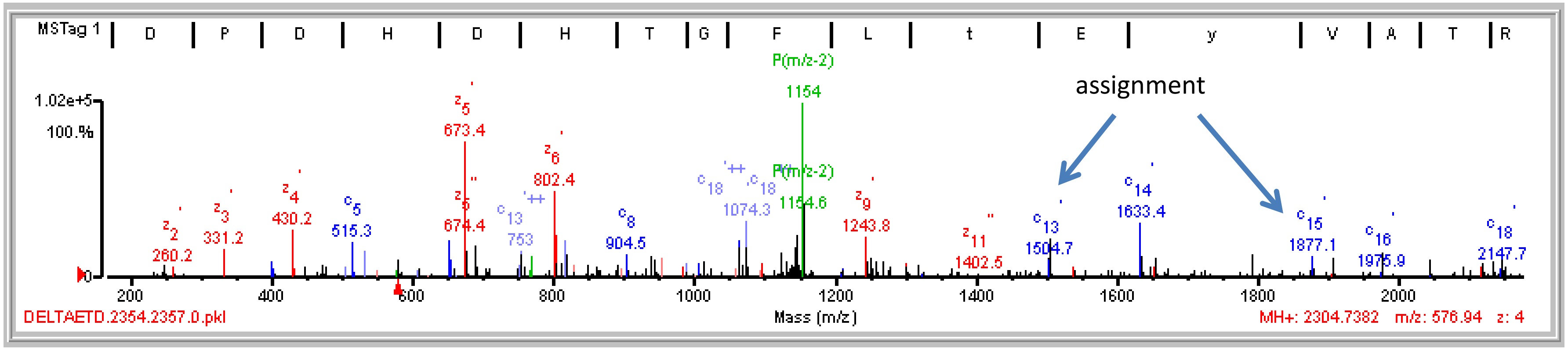


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.27	94.1	14	2/24	Y187y	(R) V/A/D P D\H\D\H|T\G|F\L|T/E|y/V/A T\R (W)	2144.00	80.5738	273.1	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	18.27	94.1	14	2/24	Y187y	(R) V/A/D P D\H\D\H|T\G|F\L|T/E|y/V/A T\R (W)	2144.00	80.5738	273.1	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

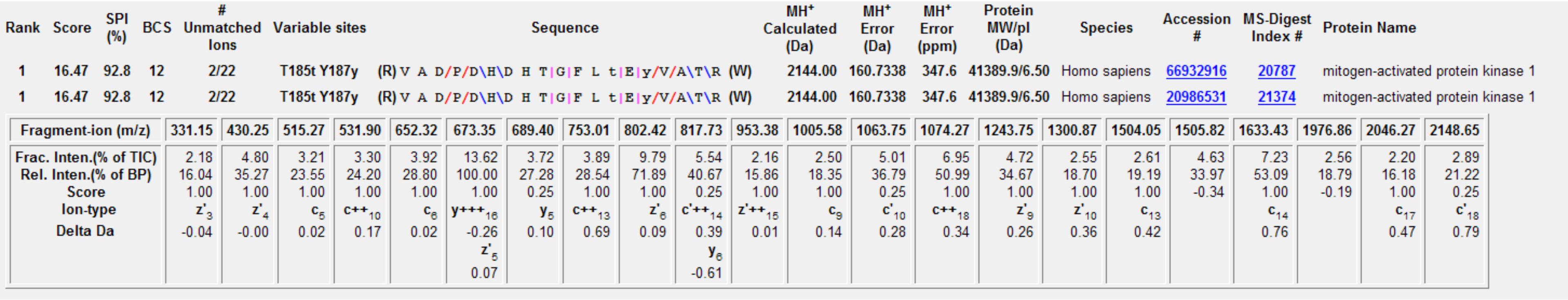
Fragment-ion (m/z)	331.34	430.35	452.90	515.44	531.88	652.42	673.30	767.52	776.98	802.64	904.48	998.91
Frac. Inten.(% of TIC)	2.58	2.81	4.64	5.42	0.09	5.53	3.26	4.83	6.21	4.27	8.11	3.10
Rel. Inten.(% of BP)	31.84	34.61	57.29	66.81	1.09	68.16	40.23	59.53	76.55	52.68	100.00	38.24
Score	1.00	1.00	1.00	1.00	1.50	1.00	1.00	1.00	1.00	1.00	1.00	-0.38
Ion-type	z'_3	z'_4	$c{++}_8$	c_5	$c{++}_{10}$	c_6	z'_5	c_7	$c{++}_{14}$	z'_6	c_8	
Delta Da	0.15	0.10	0.20	0.19	0.15	0.12	0.02	0.19	0.13	0.31	0.09	
			$z'{++}_7$		1.50						z''_7	
			0.71		sty						0.10	
					-0.37							

Fragment-ion (m/z)	1005.52	1019.47	1034.13	1063.73	1164.59	1210.52	1322.00	1323.90	1552.81	1575.89	2039.03	2068.63
Frac. Inten.(% of TIC)	2.64	5.55	3.91	3.46	4.05	5.84	4.32	3.04	3.26	2.81	6.97	3.32
Rel. Inten.(% of BP)	32.53	68.39	48.20	42.63	49.96	72.04	53.32	37.51	40.26	34.63	85.93	40.91
Score	1.00	1.00	1.00	0.25	0.25	0.25	1.00	0.25	1.00	-0.35	0.25	0.25
Ion-type	c_9	$z'{++}_{17}$	$c{++}_{18}$	c'_{10}	z''_9	c'_{11}	c_{12}	c'_{12}	c_{14}		z''_{17}	c'_{18}
Delta Da	0.08	0.04	0.18	0.26	0.06	-0.02	-0.61	0.28	0.11		0.18	0.74
				$y{++}_{18}$			z'_{11}					
				0.78			0.41					

Peak 249



assignment

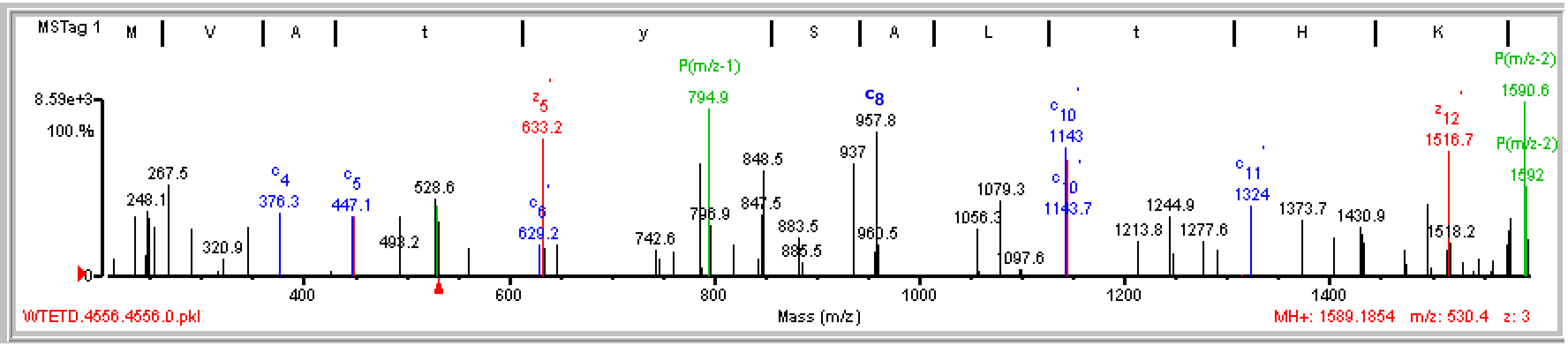


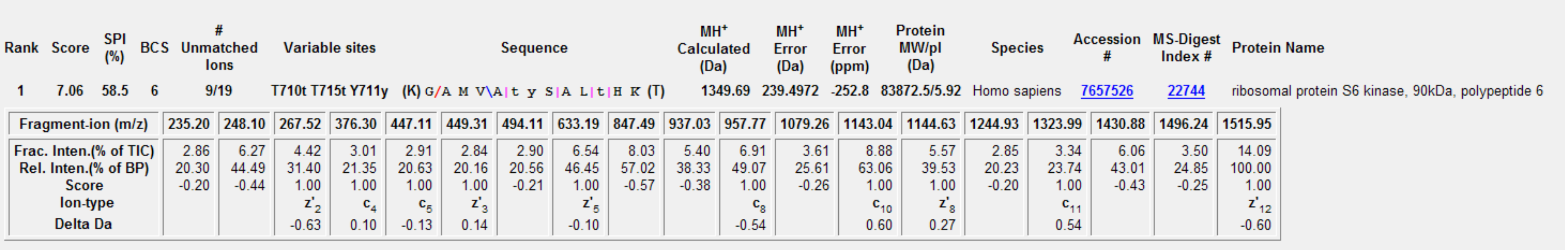
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.47	92.8	12	2/22	T185t Y187y	(R) V A D/P/D\H\D H T|G|F L t|E|y/V/A\T\R (W)	2144.00	160.7338	347.6	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	16.47	92.8	12	2/22	T185t Y187y	(R) V A D/P/D\H\D H T|G|F L t|E|y/V/A\T\R (W)	2144.00	160.7338	347.6	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

Fragment-ion (m/z)	331.15	430.25	515.27	531.90	652.32	673.35	689.40	753.01	802.42	817.73	953.38
Frac. Inten.(% of TIC)	2.18	4.80	3.21	3.30	3.92	13.62	3.72	3.89	9.79	5.54	2.16
Rel. Inten.(% of BP)	16.04	35.27	23.55	24.20	28.80	100.00	27.28	28.54	71.89	40.67	15.86
Score	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	1.00
Ion-type	z'_3	z'_4	c_5	c++_{10}	c_6	y+++_{16} z'_5	y_5	c++_{13}	z'_6	c'++_{14} y_6	z'++_{15}
Delta Da	-0.04	-0.00	0.02	0.17	0.02	-0.26 0.07	0.10	0.69	0.09	0.39 -0.61	0.01

Fragment-ion (m/z)	1005.58	1063.75	1074.27	1243.75	1300.87	1504.05	1505.82	1633.43	1976.86	2046.27	2148.65
Frac. Inten.(% of TIC)	2.50	5.01	6.95	4.72	2.55	2.61	4.63	7.23	2.56	2.20	2.89
Rel. Inten.(% of BP)	18.35	36.79	50.99	34.67	18.70	19.19	33.97	53.09	18.79	16.18	21.22
Score	1.00	0.25	1.00	1.00	1.00	1.00	-0.34	1.00	-0.19	1.00	0.25
Ion-type	c_9	c'_{10}	c++_{18}	z'_9	z'_{10}	c_{13}		c_{14}		c_{17}	c'_{18}
Delta Da	0.14	0.28	0.34	0.26	0.36	0.42		0.76		0.47	0.79

Peak 251

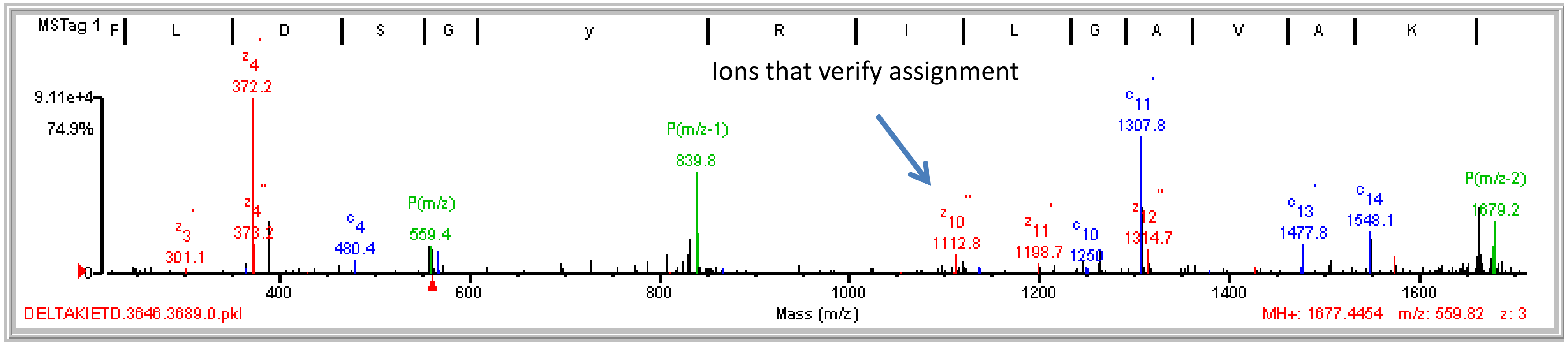




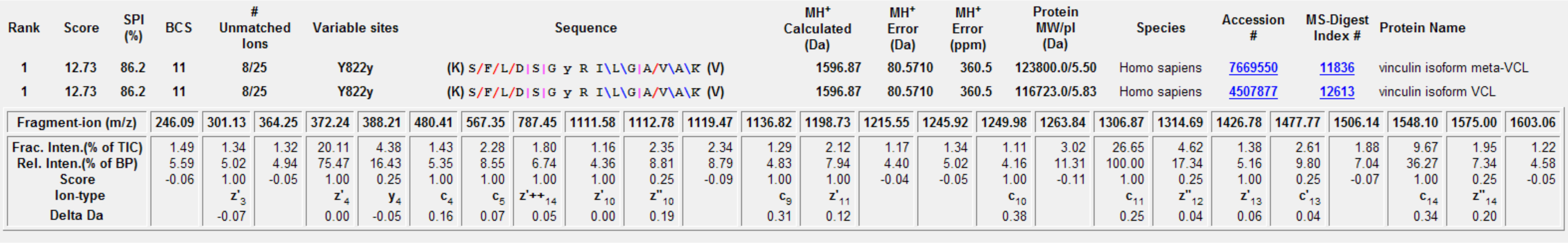
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.06	58.5	6	9/19	T710t T715t Y711y	(K) G/A M V\A|t y S|A L|t|H K (T)	1349.69	239.4972	-252.8	83872.5/5.92	Homo sapiens	7657526	22744	ribosomal protein S6 kinase, 90kDa, polypeptide 6

Fragment-ion (m/z)	235.20	248.10	267.52	376.30	447.11	449.31	494.11	633.19	847.49	937.03	957.77	1079.26	1143.04	1144.63	1244.93	1323.99	1430.88	1496.24	1515.95
Frac. Inten.(% of TIC)	2.86	6.27	4.42	3.01	2.91	2.84	2.90	6.54	8.03	5.40	6.91	3.61	8.88	5.57	2.85	3.34	6.06	3.50	14.09
Rel. Inten.(% of BP)	20.30	44.49	31.40	21.35	20.63	20.16	20.56	46.45	57.02	38.33	49.07	25.61	63.06	39.53	20.23	23.74	43.01	24.85	100.00
Score	-0.20	-0.44	1.00	1.00	1.00	1.00	-0.21	1.00	-0.57	-0.38	1.00	-0.26	1.00	1.00	-0.20	1.00	-0.43	-0.25	1.00
Ion-type			z'_2	c_4	c_5	z'_3		z'_5			c_8		c_{10}	z'_8		c_{11}			z'_{12}
Delta Da			-0.63	0.10	-0.13	0.14		-0.10			-0.54		0.60	0.27		0.54			-0.60

Peak 252



Ions that verify assignment



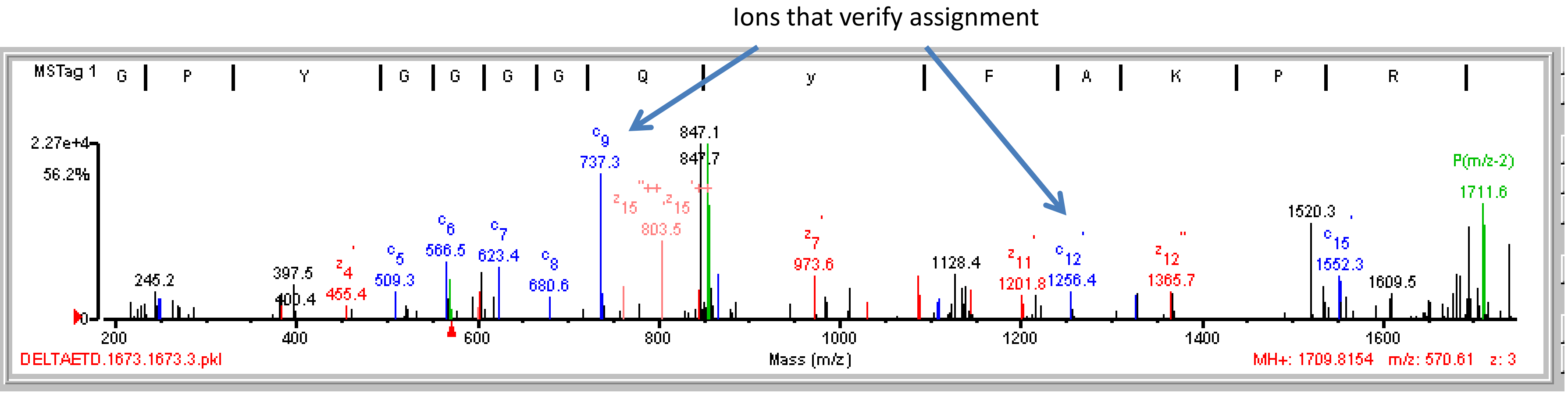
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.73	86.2	11	8/25	Y822y	(K) S/F/L/D|S|G y R I\L\G|A/V\A\K (V)	1596.87	80.5710	360.5	123800.0/5.50	Homo sapiens	7669550	11836	vinculin isoform meta-VCL
1	12.73	86.2	11	8/25	Y822y	(K) S/F/L/D|S|G y R I\L\G|A/V\A\K (V)	1596.87	80.5710	360.5	116723.0/5.83	Homo sapiens	4507877	12613	vinculin isoform VCL

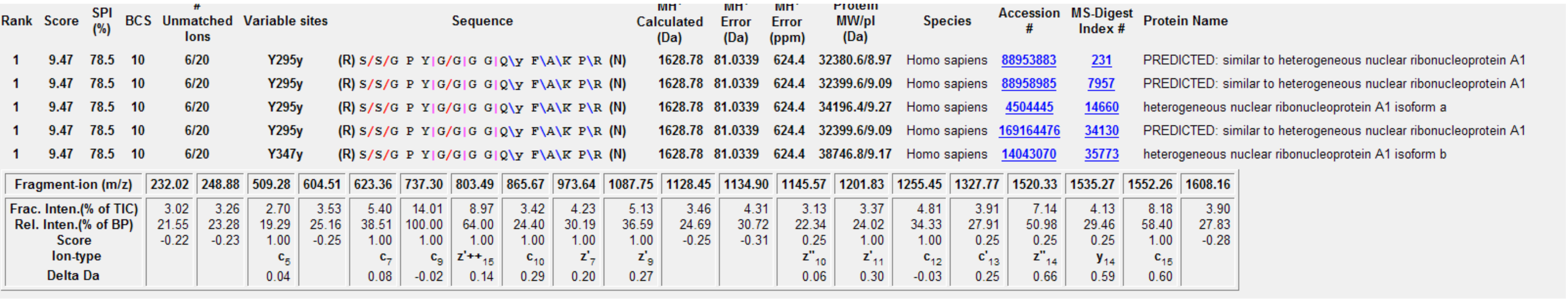
Fragment-ion (m/z)	246.09	301.13	364.25	372.24	388.21	480.41	567.35	787.45	1111.58	1112.78	1119.47	1136.82
Frac. Inten.(% of TIC)	1.49	1.34	1.32	20.11	4.38	1.43	2.28	1.80	1.16	2.35	2.34	1.29
Rel. Inten.(% of BP)	5.59	5.02	4.94	75.47	16.43	5.35	8.55	6.74	4.36	8.81	8.79	4.83
Score	-0.06	1.00	-0.05	1.00	0.25	1.00	1.00	1.00	1.00	0.25	-0.09	1.00
Ion-type		z'_3		z'_4	y_4	c_4	c_5	$z'{++}_{14}$	z'_{10}	z''_{10}		c_9
Delta Da		-0.07		0.00	-0.05	0.16	0.07	0.05	0.00	0.19		0.31

Fragment-ion (m/z)	1198.73	1215.55	1245.92	1249.98	1263.84	1306.87	1314.69	1426.78	1477.77	1506.14	1548.10	1575.00	1603.06
Frac. Inten.(% of TIC)	2.12	1.17	1.34	1.11	3.02	26.65	4.62	1.38	2.61	1.88	9.67	1.95	1.22
Rel. Inten.(% of BP)	7.94	4.40	5.02	4.16	11.31	100.00	17.34	5.16	9.80	7.04	36.27	7.34	4.58
Score	1.00	-0.04	-0.05	1.00	-0.11	1.00	0.25	1.00	0.25	-0.07	1.00	0.25	-0.05
Ion-type	z'_{11}			c_{10}		c_{11}	z''_{12}	z'_{13}	c'_{13}		c_{14}	z''_{14}	
Delta Da	0.12			0.38		0.25	0.04	0.06	0.04		0.34	0.20	

Peak 253

Ions that verify assignment

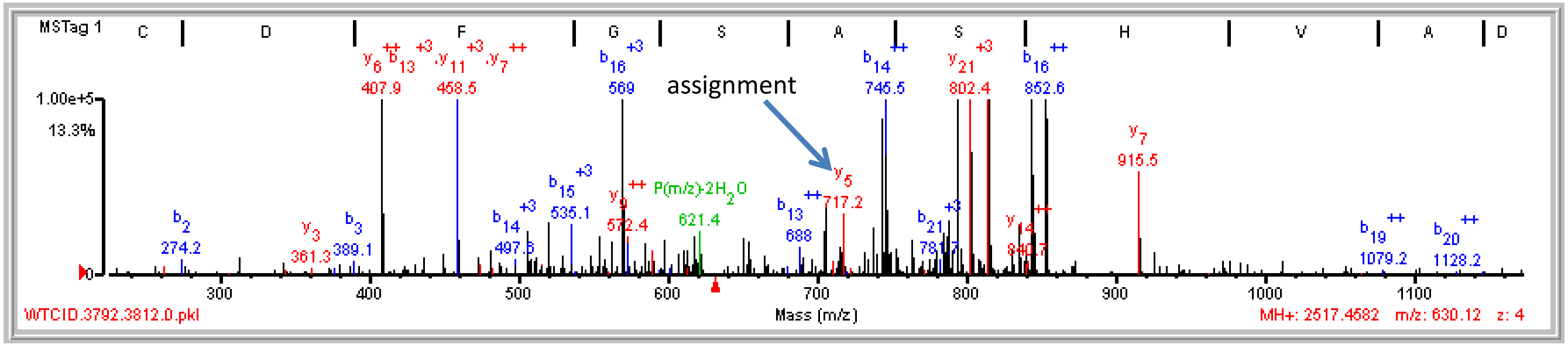


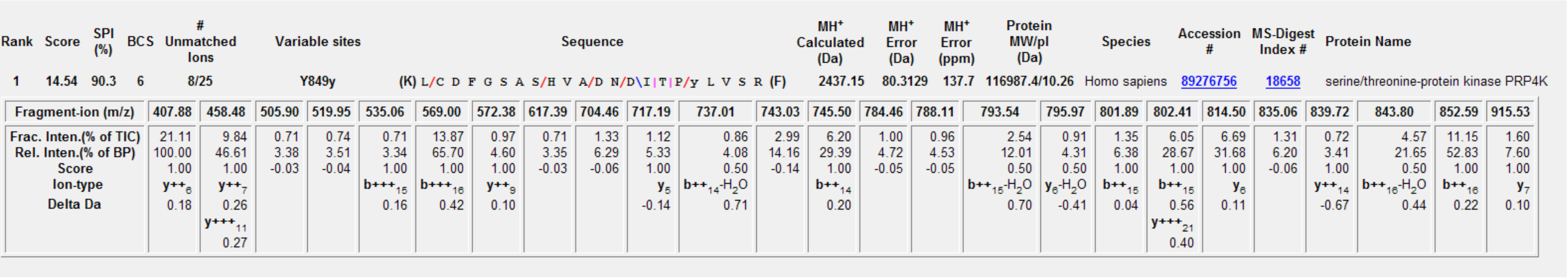


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.47	78.5	10	6/20	Y295y	(R) S/S/G P Y|G/G|G G|Q\y F\A\K P\R (N)	1628.78	81.0339	624.4	32380.6/8.97	Homo sapiens	88953883	231	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A1
1	9.47	78.5	10	6/20	Y295y	(R) S/S/G P Y|G/G|G G|Q\y F\A\K P\R (N)	1628.78	81.0339	624.4	32399.6/9.09	Homo sapiens	88958985	7957	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A1
1	9.47	78.5	10	6/20	Y295y	(R) S/S/G P Y|G/G|G G|Q\y F\A\K P\R (N)	1628.78	81.0339	624.4	34196.4/9.27	Homo sapiens	4504445	14660	heterogeneous nuclear ribonucleoprotein A1 isoform a
1	9.47	78.5	10	6/20	Y295y	(R) S/S/G P Y|G/G|G G|Q\y F\A\K P\R (N)	1628.78	81.0339	624.4	32399.6/9.09	Homo sapiens	169164476	34130	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A1
1	9.47	78.5	10	6/20	Y347y	(R) S/S/G P Y|G/G|G G|Q\y F\A\K P\R (N)	1628.78	81.0339	624.4	38746.8/9.17	Homo sapiens	14043070	35773	heterogeneous nuclear ribonucleoprotein A1 isoform b

Fragment-ion (m/z)	232.02	248.88	509.28	604.51	623.36	737.30	803.49	865.67	973.64	1087.75	1128.45	1134.90	1145.57	1201.83	1255.45	1327.77	1520.33	1535.27	1552.26	1608.16
Frac. Inten.(% of TIC)	3.02	3.26	2.70	3.53	5.40	14.01	8.97	3.42	4.23	5.13	3.46	4.31	3.13	3.37	4.81	3.91	7.14	4.13	8.18	3.90
Rel. Inten.(% of BP)	21.55	23.28	19.29	25.16	38.51	100.00	64.00	24.40	30.19	36.59	24.69	30.72	22.34	24.02	34.33	27.91	50.98	29.46	58.40	27.83
Score	-0.22	-0.23	1.00	-0.25	1.00	1.00	1.00	1.00	1.00	1.00	-0.25	-0.31	0.25	1.00	1.00	0.25	0.25	0.25	1.00	-0.28
Ion-type			c_5		c_7	c_9	z'^{++}_{15}	c_{10}	z'_7	z'_9			z''_{10}	z'_{11}	c_{12}	c'_{13}	z''_{14}	y_{14}	c_{15}	
Delta Da			0.04		0.08	-0.02	0.14	0.29	0.20	0.27			0.06	0.30	-0.03	0.25	0.66	0.59	0.60	

Peak 254



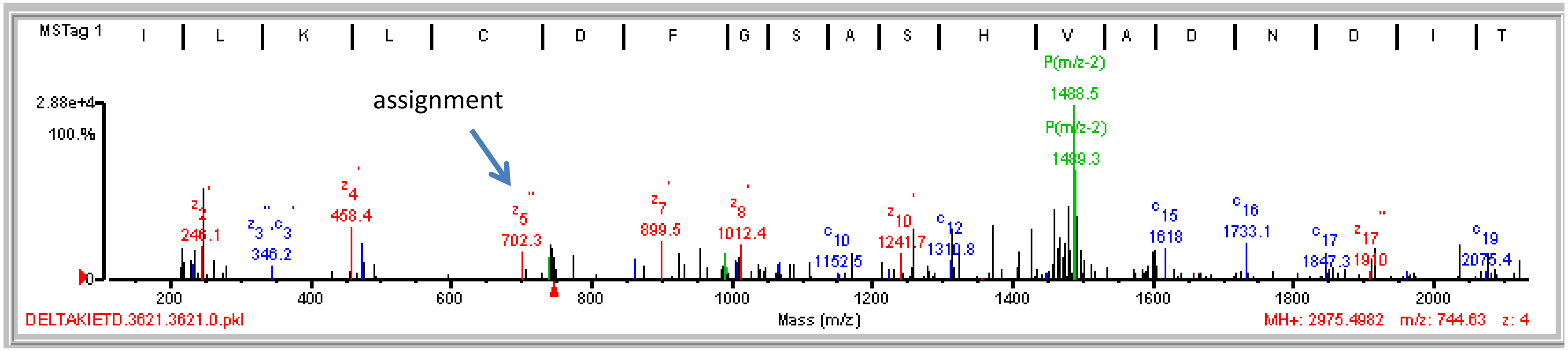


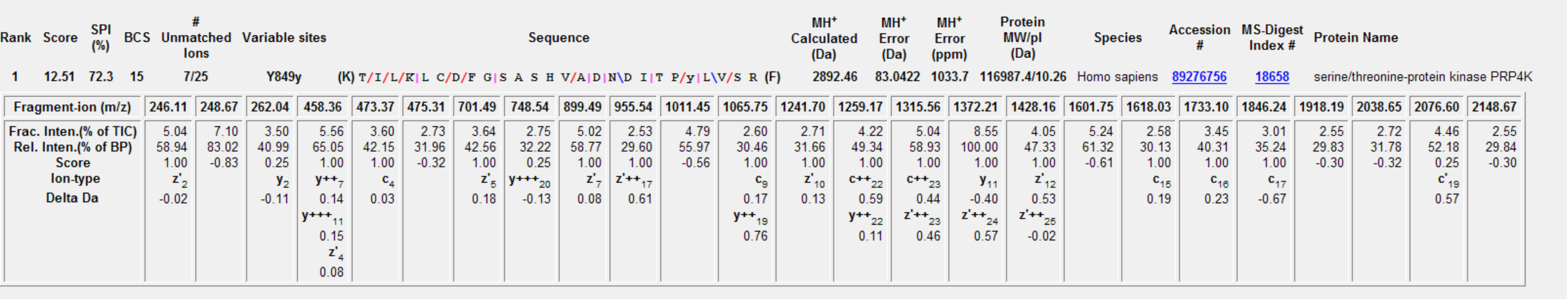
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.54	90.3	6	8/25	Y849y	(K) L/C D F G S A S/H V A/D N/D\I|T|P/y L V S R (F)	2437.15	80.3129	137.7	116987.4/10.26	Homo sapiens	89276756	18658	serine/threonine-protein kinase PRP4K

Fragment-ion (m/z)	407.88	458.48	505.90	519.95	535.06	569.00	572.38	617.39	704.46	717.19	737.01	743.03
Frac. Inten.(% of TIC)	21.11	9.84	0.71	0.74	0.71	13.87	0.97	0.71	1.33	1.12	0.86	2.99
Rel. Inten.(% of BP)	100.00	46.61	3.38	3.51	3.34	65.70	4.60	3.35	6.29	5.33	4.08	14.16
Score	1.00	1.00	-0.03	-0.04	1.00	1.00	1.00	-0.03	-0.06	1.00	0.50	-0.14
Ion-type	$y{+}{+}_{6}$	$y{+}{+}_{7}$ $y{+}{+}{+}_{11}$			$b{+}{+}{+}_{15}$	$b{+}{+}{+}_{16}$	$y{+}{+}_{9}$			y_5	$b{+}{+}_{14}$-H_2O	
Delta Da	0.18	0.26 0.27			0.16	0.42	0.10			-0.14	0.71	

Fragment-ion (m/z)	745.50	784.46	788.11	793.54	795.97	801.89	802.41	814.50	835.06	839.72	843.80	852.59	915.53
Frac. Inten.(% of TIC)	6.20	1.00	0.96	2.54	0.91	1.35	6.05	6.69	1.31	0.72	4.57	11.15	1.60
Rel. Inten.(% of BP)	29.39	4.72	4.53	12.01	4.31	6.38	28.67	31.68	6.20	3.41	21.65	52.83	7.60
Score	1.00	-0.05	-0.05	0.50	0.50	1.00	1.00	1.00	-0.06	1.00	0.50	1.00	1.00
Ion-type	$b{+}{+}_{14}$			$b{+}{+}_{15}$-H_2O	y_6-H_2O	$b{+}{+}_{15}$	$b{+}{+}_{15}$ $y{+}{+}{+}_{21}$	y_6		$y{+}{+}_{14}$	$b{+}{+}_{16}$-H_2O	$b{+}{+}_{16}$	y_7
Delta Da	0.20			0.70	-0.41	0.04	0.56 0.40	0.11		-0.67	0.44	0.22	0.10

Peak 255



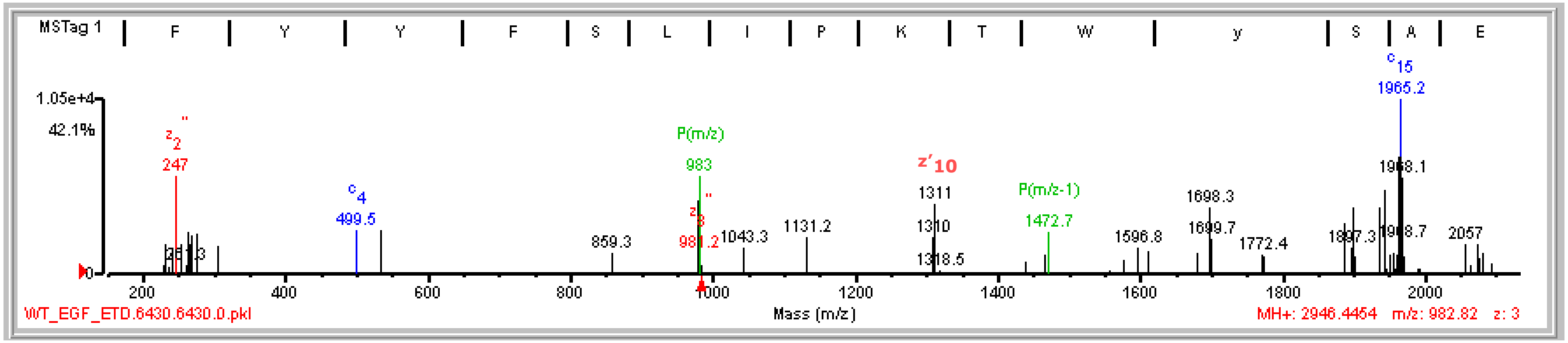


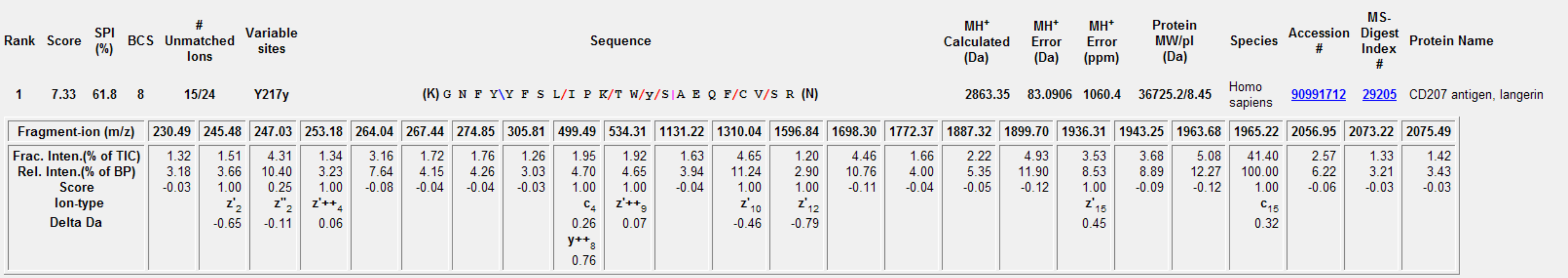
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.51	72.3	15	7/25	Y849y	(K) T/I/L/K|L C/D/F G|S A S H V/A|D|N\D I|T P/y|L\V/S R (F)	2892.46	83.0422	1033.7	116987.4/10.26	Homo sapiens	89276756	18658	serine/threonine-protein kinase PRP4K

Fragment-ion (m/z)	246.11	248.67	262.04	458.36	473.37	475.31	701.49	748.54	899.49	955.54	1011.45	1065.75	1241.70
Frac. Inten.(% of TIC)	5.04	7.10	3.50	5.56	3.60	2.73	3.64	2.75	5.02	2.53	4.79	2.60	2.71
Rel. Inten.(% of BP)	58.94	83.02	40.99	65.05	42.15	31.96	42.56	32.22	58.77	29.60	55.97	30.46	31.66
Score	1.00	-0.83	0.25	1.00	1.00	-0.32	1.00	0.25	1.00	1.00	-0.56	1.00	1.00
Ion-type	z'_{2}		y_{2}	y^{++}_{7} y^{+++}_{11} z'_{4}	c_{4}		z'_{5}	y^{+++}_{20}	z'_{7}	z'^{++}_{17}		c_{9} y^{++}_{19}	z'_{10}
Delta Da	-0.02		-0.11	0.14 0.15 0.08	0.03		0.18	-0.13	0.08	0.61		0.17 0.76	0.13

Fragment-ion (m/z)	1259.17	1315.56	1372.21	1428.16	1601.75	1618.03	1733.10	1846.24	1918.19	2038.65	2076.60	2148.67
Frac. Inten.(% of TIC)	4.22	5.04	8.55	4.05	5.24	2.58	3.45	3.01	2.55	2.72	4.46	2.55
Rel. Inten.(% of BP)	49.34	58.93	100.00	47.33	61.32	30.13	40.31	35.24	29.83	31.78	52.18	29.84
Score	1.00	1.00	1.00	1.00	-0.61	1.00	1.00	1.00	-0.30	-0.32	0.25	-0.30
Ion-type	c^{++}_{22} y^{++}_{22}	c^{++}_{23} z'^{++}_{23}	y_{11} z'^{++}_{24}	z'_{12} z'^{++}_{25}		c_{15}	c_{16}	c_{17}			c'_{19}	
Delta Da	0.59 0.11	0.44 0.46	-0.40 0.57	0.53 -0.02		0.19	0.23	-0.67			0.57	

Peak 256

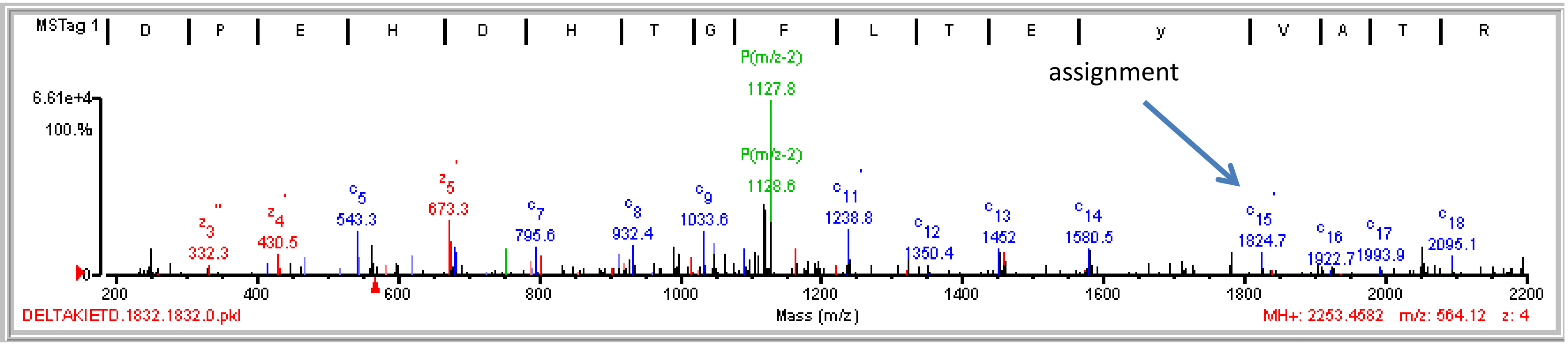




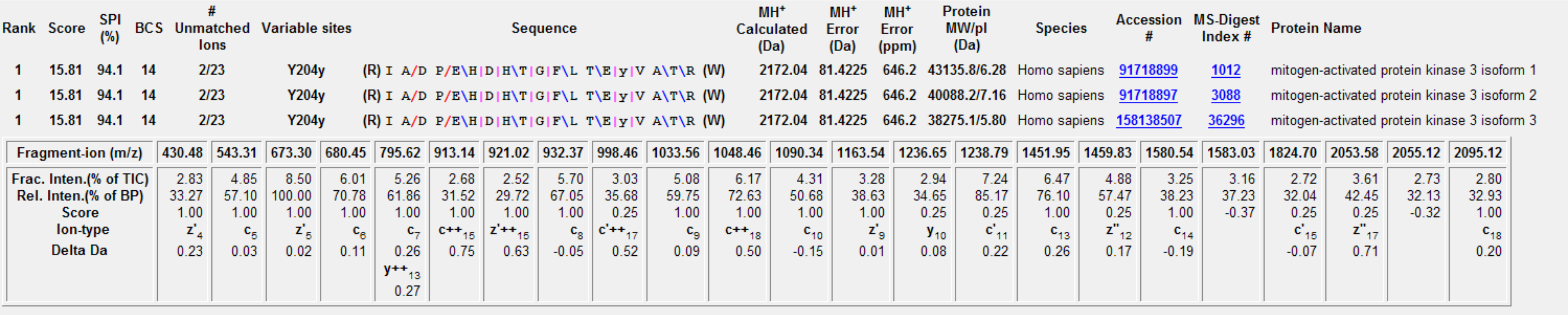
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.33	61.8	8	15/24	Y217y	(K) G N F Y\Y F S L/I P K/T W/y/S|A E Q F/C V/S R (N)	2863.35	83.0906	1060.4	36725.2/8.45	Homo sapiens	90991712	29205	CD207 antigen, langerin

Fragment-ion (m/z)	230.49	245.48	247.03	253.18	264.04	267.44	274.85	305.81	499.49	534.31	1131.22	1310.04	1596.84	1698.30	1772.37	1887.32	1899.70	1936.31	1943.25	1963.68	1965.22	2056.95	2073.22	2075.49
Frac. Inten.(% of TIC)	1.32	1.51	4.31	1.34	3.16	1.72	1.76	1.26	1.95	1.92	1.63	4.65	1.20	4.46	1.66	2.22	4.93	3.53	3.68	5.08	41.40	2.57	1.33	1.42
Rel. Inten.(% of BP)	3.18	3.66	10.40	3.23	7.64	4.15	4.26	3.03	4.70	4.65	3.94	11.24	2.90	10.76	4.00	5.35	11.90	8.53	8.89	12.27	100.00	6.22	3.21	3.43
Score	-0.03	1.00	0.25	1.00	-0.08	-0.04	-0.04	-0.03	1.00	1.00	-0.04	1.00	1.00	-0.11	-0.04	-0.05	-0.12	1.00	-0.09	-0.12	1.00	-0.06	-0.03	-0.03
Ion-type		z'_2	z''_2	$z'{++}_4$					c_4 $y{++}_8$	$z'{++}_9$		z'_{10}	z'_{12}					z'_{15}			c_{15}			
Delta Da		-0.65	-0.11	0.06					0.26 0.76	0.07		-0.46	-0.79					0.45			0.32			

Peak 257



assignment

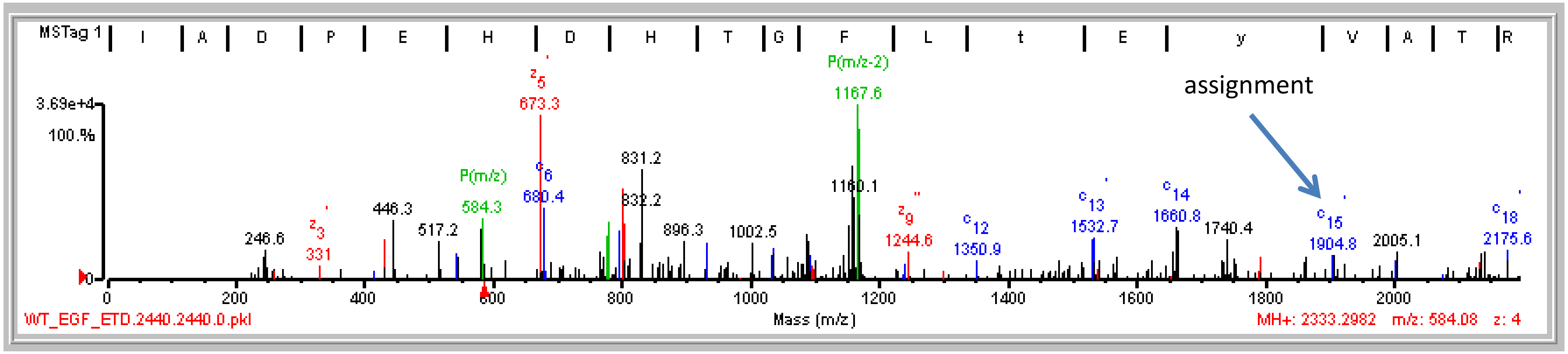


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.81	94.1	14	2/23	Y204y	(R) I A/D P/E\H|D|H\T|G|F\L T\E|y|V A\T\R (W)	2172.04	81.4225	646.2	43135.8/6.28	Homo sapiens	91718899	1012	mitogen-activated protein kinase 3 isoform 1
1	15.81	94.1	14	2/23	Y204y	(R) I A/D P/E\H|D|H\T|G|F\L T\E|y|V A\T\R (W)	2172.04	81.4225	646.2	40088.2/7.16	Homo sapiens	91718897	3088	mitogen-activated protein kinase 3 isoform 2
1	15.81	94.1	14	2/23	Y204y	(R) I A/D P/E\H|D|H\T|G|F\L T\E|y|V A\T\R (W)	2172.04	81.4225	646.2	38275.1/5.80	Homo sapiens	158138507	36296	mitogen-activated protein kinase 3 isoform 3

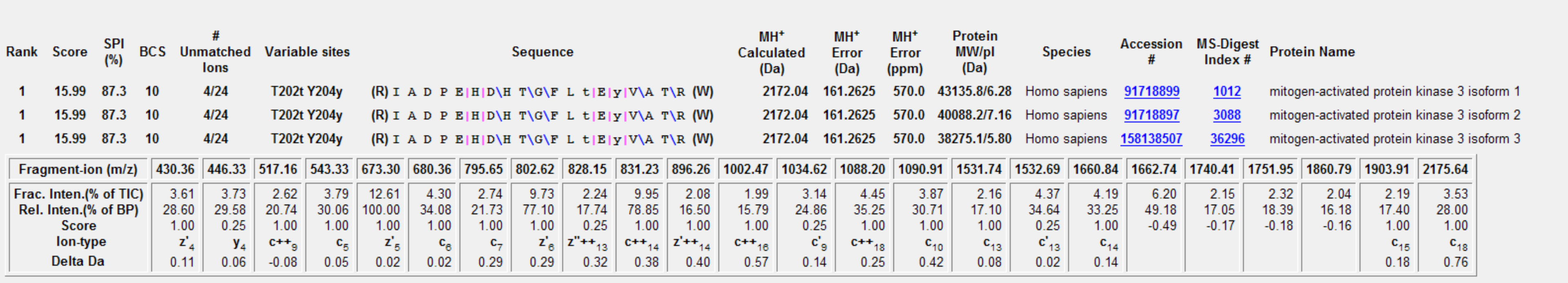
Fragment-ion (m/z)	430.48	543.31	673.30	680.45	795.62	913.14	921.02	932.37	998.46	1033.56	1048.46
Frac. Inten.(% of TIC)	2.83	4.85	8.50	6.01	5.26	2.68	2.52	5.70	3.03	5.08	6.17
Rel. Inten.(% of BP)	33.27	57.10	100.00	70.78	61.86	31.52	29.72	67.05	35.68	59.75	72.63
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type	z'_4	c_5	z'_5	c_6	c_7 y^{++}_{13}	c^{++}_{15}	z'^{++}_{15}	c_8	c'^{++}_{17}	c_9	c^{++}_{18}
Delta Da	0.23	0.03	0.02	0.11	0.26 0.27	0.75	0.63	-0.05	0.52	0.09	0.50

Fragment-ion (m/z)	1090.34	1163.54	1236.65	1238.79	1451.95	1459.83	1580.54	1583.03	1824.70	2053.58	2055.12	2095.12
Frac. Inten.(% of TIC)	4.31	3.28	2.94	7.24	6.47	4.88	3.25	3.16	2.72	3.61	2.73	2.80
Rel. Inten.(% of BP)	50.68	38.63	34.65	85.17	76.10	57.47	38.23	37.23	32.04	42.45	32.13	32.93
Score	1.00	1.00	0.25	0.25	1.00	0.25	1.00	-0.37	0.25	0.25	-0.32	1.00
Ion-type	c_{10}	z'_9	y_{10}	c'_{11}	c_{13}	z''_{12}	c_{14}		c'_{15}	z''_{17}		c_{18}
Delta Da	-0.15	0.01	0.08	0.22	0.26	0.17	-0.19		-0.07	0.71		0.20

Peak 258



assignment



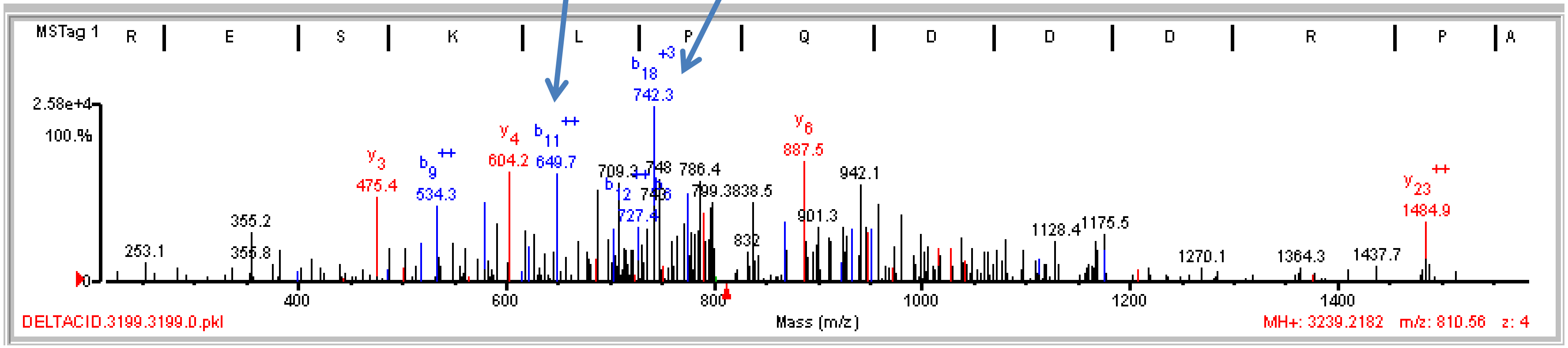
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.99	87.3	10	4/24	T202t Y204y	(R) I A D P E|H|D\H T\G\F L t|E|y|V\A T\R (W)	2172.04	161.2625	570.0	43135.8/6.28	Homo sapiens	91718899	1012	mitogen-activated protein kinase 3 isoform 1
1	15.99	87.3	10	4/24	T202t Y204y	(R) I A D P E|H|D\H T\G\F L t|E|y|V\A T\R (W)	2172.04	161.2625	570.0	40088.2/7.16	Homo sapiens	91718897	3088	mitogen-activated protein kinase 3 isoform 2
1	15.99	87.3	10	4/24	T202t Y204y	(R) I A D P E|H|D\H T\G\F L t|E|y|V\A T\R (W)	2172.04	161.2625	570.0	38275.1/5.80	Homo sapiens	158138507	36296	mitogen-activated protein kinase 3 isoform 3

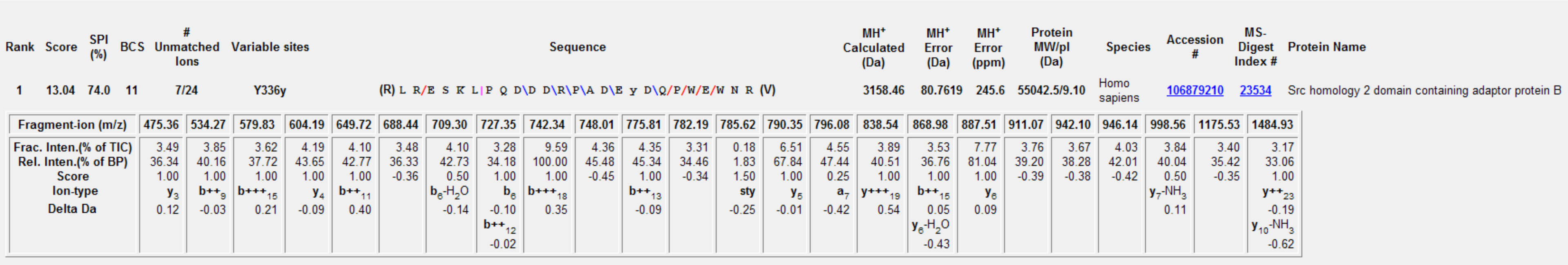
Fragment-ion (m/z)	430.36	446.33	517.16	543.33	673.30	680.36	795.65	802.62	828.15	831.23	896.26
Frac. Inten.(% of TIC)	3.61	3.73	2.62	3.79	12.61	4.30	2.74	9.73	2.24	9.95	2.08
Rel. Inten.(% of BP)	28.60	29.58	20.74	30.06	100.00	34.08	21.73	77.10	17.74	78.85	16.50
Score	1.00	0.25	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00
Ion-type	z'_4	y_4	$c{+}{+}_9$	c_5	z'_5	c_6	c_7	z'_6	$z''{+}{+}_{13}$	$c{+}{+}_{14}$	$z'{+}{+}_{14}$
Delta Da	0.11	0.06	-0.08	0.05	0.02	0.02	0.29	0.29	0.32	0.38	0.40

Fragment-ion (m/z)	1002.47	1034.62	1088.20	1090.91	1531.74	1532.69	1660.84	1662.74	1740.41	1751.95	1860.79	1903.91	2175.64
Frac. Inten.(% of TIC)	1.99	3.14	4.45	3.87	2.16	4.37	4.19	6.20	2.15	2.32	2.04	2.19	3.53
Rel. Inten.(% of BP)	15.79	24.86	35.25	30.71	17.10	34.64	33.25	49.18	17.05	18.39	16.18	17.40	28.00
Score	1.00	0.25	1.00	1.00	1.00	0.25	1.00	-0.49	-0.17	-0.18	-0.16	1.00	1.00
Ion-type	$c{+}{+}_{16}$	c'_9	$c{+}{+}_{18}$	c_{10}	c_{13}	c'_{13}	c_{14}					c_{15}	c_{18}
Delta Da	0.57	0.14	0.25	0.42	0.08	0.02	0.14					0.18	0.76

Peak 259

Ions that verify assignment



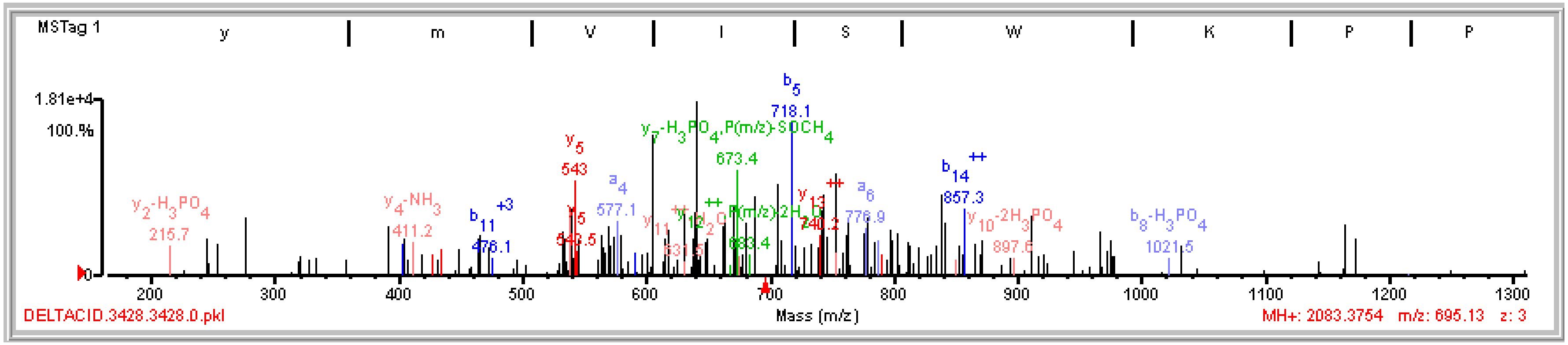


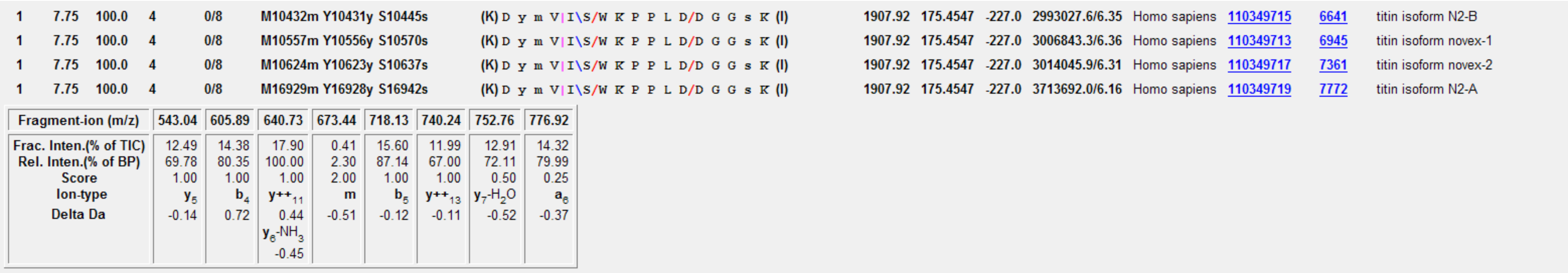
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.04	74.0	11	7/24	Y336y	(R) L R/E S K L|P Q D\D D\R\P\A D\E y D\Q/P/W/E/W N R (V)	3158.46	80.7619	245.6	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	475.36	534.27	579.83	604.19	649.72	688.44	709.30	727.35	742.34	748.01	775.81	782.19
Frac. Inten.(% of TIC)	3.49	3.85	3.62	4.19	4.10	3.48	4.10	3.28	9.59	4.36	4.35	3.31
Rel. Inten.(% of BP)	36.34	40.16	37.72	43.65	42.77	36.33	42.73	34.18	100.00	45.48	45.34	34.46
Score	1.00	1.00	1.00	1.00	1.00	-0.36	0.50	1.00	1.00	-0.45	1.00	-0.34
Ion-type	y_{3}	$b{++}_{9}$	$b{+++}_{15}$	y_{4}	$b{++}_{11}$		b_{6}-H_2O	b_{6} $b{++}_{12}$	$b{+++}_{18}$		$b{++}_{13}$	
Delta Da	0.12	-0.03	0.21	-0.09	0.40		-0.14	-0.10 -0.02	0.35		-0.09	

Fragment-ion (m/z)	785.62	790.35	796.08	838.54	868.98	887.51	911.07	942.10	946.14	998.56	1175.53	1484.93
Frac. Inten.(% of TIC)	0.18	6.51	4.55	3.89	3.53	7.77	3.76	3.67	4.03	3.84	3.40	3.17
Rel. Inten.(% of BP)	1.83	67.84	47.44	40.51	36.76	81.04	39.20	38.28	42.01	40.04	35.42	33.06
Score	1.50	1.00	0.25	1.00	1.00	1.00	-0.39	-0.38	-0.42	0.50	-0.35	1.00
Ion-type	sty	y_{5}	a_{7}	$y{+++}_{19}$	$b{++}_{15}$ y_{6}-H_2O	y_{6}				y_{7}-NH_3		$y{++}_{23}$ y_{10}-NH_3
Delta Da	-0.25	-0.01	-0.42	0.54	0.05 -0.43	0.09				0.11		-0.19 -0.62

Peak 260

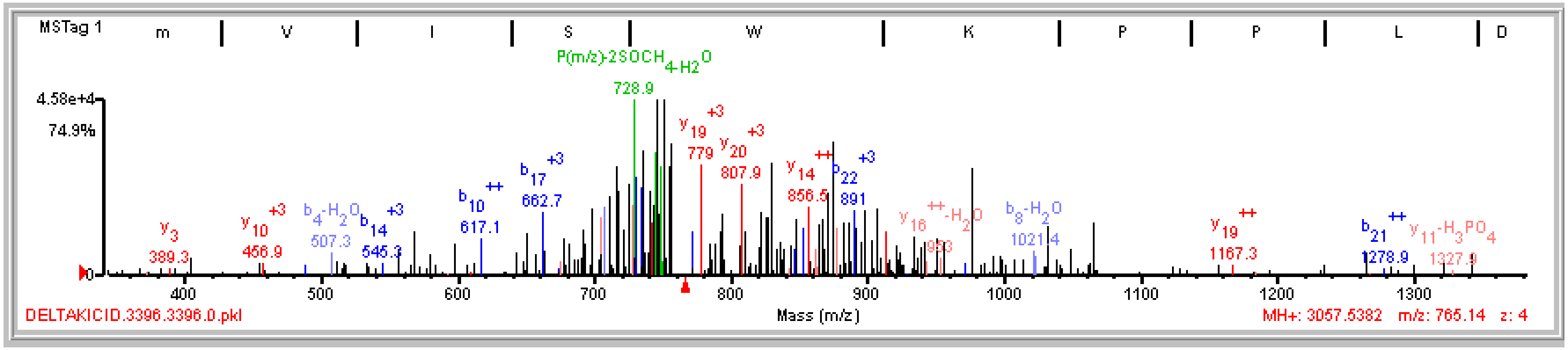


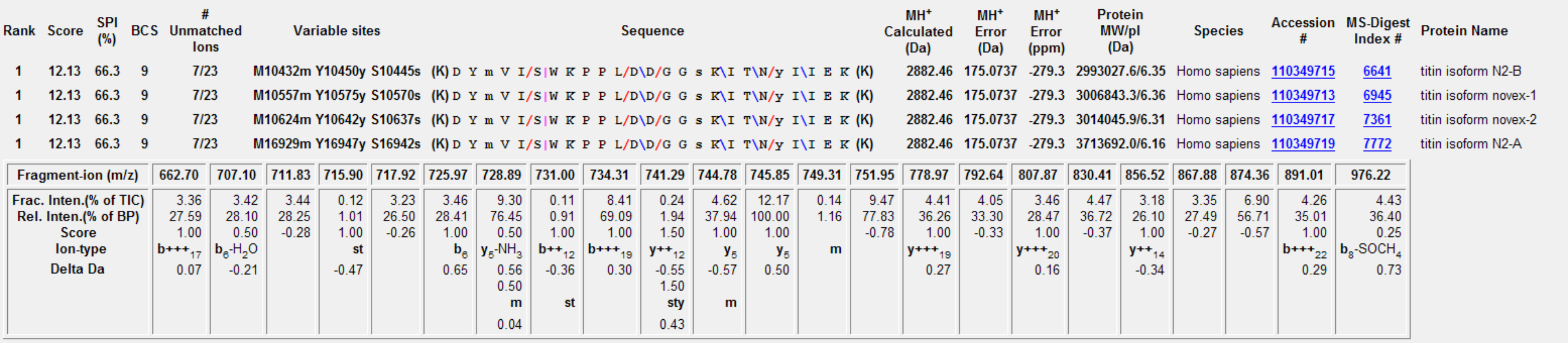


1	7.75	100.0	4	0/8	M10432m Y10431y S10445s	(K) D y m V|I\S/W K P P L D/D G G s K (I)	1907.92	175.4547	-227.0	2993027.6/6.35	Homo sapiens	110349715	6641	titin isoform N2-B
1	7.75	100.0	4	0/8	M10557m Y10556y S10570s	(K) D y m V|I\S/W K P P L D/D G G s K (I)	1907.92	175.4547	-227.0	3006843.3/6.36	Homo sapiens	110349713	6945	titin isoform novex-1
1	7.75	100.0	4	0/8	M10624m Y10623y S10637s	(K) D y m V|I\S/W K P P L D/D G G s K (I)	1907.92	175.4547	-227.0	3014045.9/6.31	Homo sapiens	110349717	7361	titin isoform novex-2
1	7.75	100.0	4	0/8	M16929m Y16928y S16942s	(K) D y m V|I\S/W K P P L D/D G G s K (I)	1907.92	175.4547	-227.0	3713692.0/6.16	Homo sapiens	110349719	7772	titin isoform N2-A

Fragment-ion (m/z)	543.04	605.89	640.73	673.44	718.13	740.24	752.76	776.92
Frac. Inten.(% of TIC)	12.49	14.38	17.90	0.41	15.60	11.99	12.91	14.32
Rel. Inten.(% of BP)	69.78	80.35	100.00	2.30	87.14	67.00	72.11	79.99
Score	1.00	1.00	1.00	2.00	1.00	1.00	0.50	0.25
Ion-type	y_5	b_4	$y{+}{+}_{11}$ y_6-NH_3	m	b_5	$y{+}{+}_{13}$	y_7-H_2O	a_6
Delta Da	-0.14	0.72	0.44 -0.45	-0.51	-0.12	-0.11	-0.52	-0.37

Peak 261

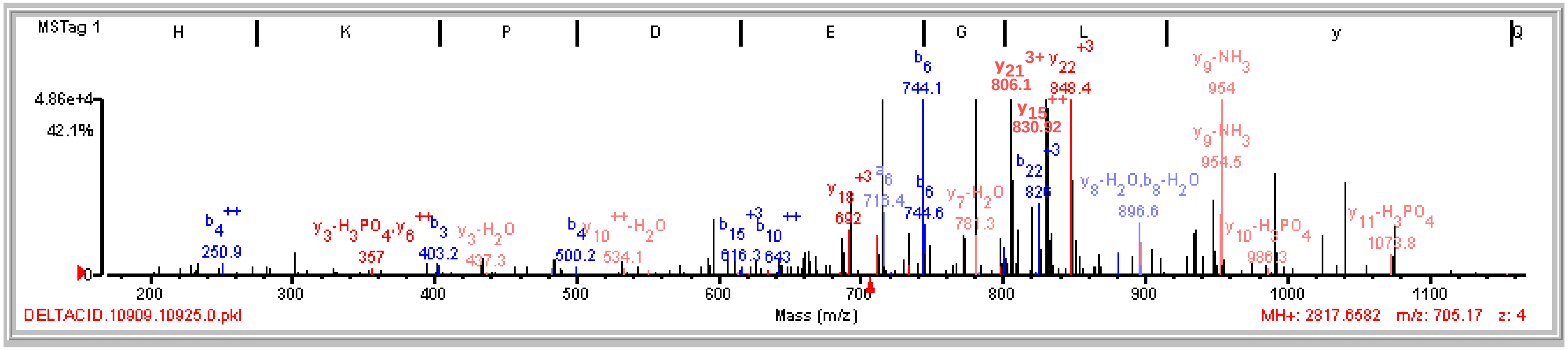


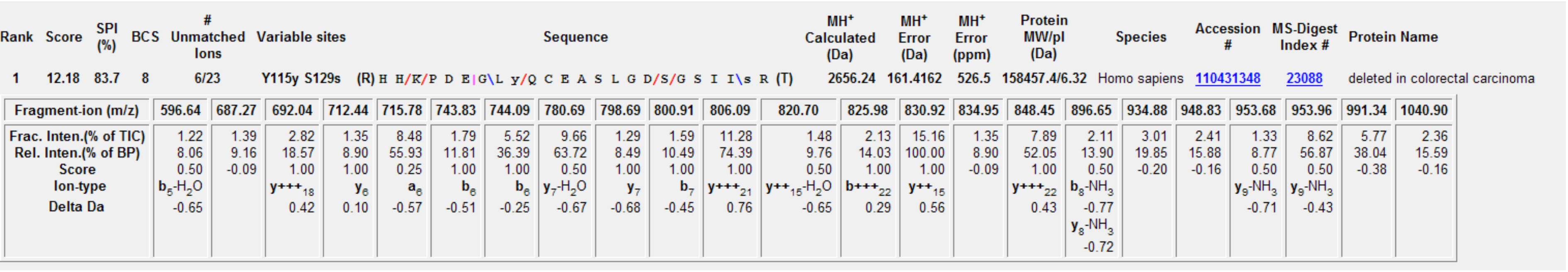


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.13	66.3	9	7/23	M10432m Y10450y S10445s	(K) D Y m V I/S|W K P P L/D\D/G G s K\I T\N/y I\I E K (K)	2882.46	175.0737	-279.3	2993027.6/6.35	Homo sapiens	110349715	6641	titin isoform N2-B
1	12.13	66.3	9	7/23	M10557m Y10575y S10570s	(K) D Y m V I/S|W K P P L/D\D/G G s K\I T\N/y I\I E K (K)	2882.46	175.0737	-279.3	3006843.3/6.36	Homo sapiens	110349713	6945	titin isoform novex-1
1	12.13	66.3	9	7/23	M10624m Y10642y S10637s	(K) D Y m V I/S|W K P P L/D\D/G G s K\I T\N/y I\I E K (K)	2882.46	175.0737	-279.3	3014045.9/6.31	Homo sapiens	110349717	7361	titin isoform novex-2
1	12.13	66.3	9	7/23	M16929m Y16947y S16942s	(K) D Y m V I/S|W K P P L/D\D/G G s K\I T\N/y I\I E K (K)	2882.46	175.0737	-279.3	3713692.0/6.16	Homo sapiens	110349719	7772	titin isoform N2-A

Fragment-ion (m/z)	662.70	707.10	711.83	715.90	717.92	725.97	728.89	731.00	734.31	741.29	744.78	745.85	749.31	751.95	778.97	792.64	807.87	830.41	856.52	867.88	874.36	891.01	976.22
Frac. Inten.(% of TIC)	3.36	3.42	3.44	0.12	3.23	3.46	9.30	0.11	8.41	0.24	4.62	12.17	0.14	9.47	4.41	4.05	3.46	4.47	3.18	3.35	6.90	4.26	4.43
Rel. Inten.(% of BP)	27.59	28.10	28.25	1.01	26.50	28.41	76.45	0.91	69.09	1.94	37.94	100.00	1.16	77.83	36.26	33.30	28.47	36.72	26.10	27.49	56.71	35.01	36.40
Score	1.00	0.50	-0.28	1.00	-0.26	1.00	0.50	1.00	1.00	1.50	1.00	1.00		-0.78	1.00	-0.33	1.00	-0.37	1.00	-0.27	-0.57	1.00	0.25
Ion-type	b+++$_{17}$	b_6-H_2O		st		b_6	y_5-NH_3	b++$_{12}$	b+++$_{19}$	y++$_{12}$	y_5	y_5	m		y+++$_{19}$		y+++$_{20}$		y++$_{14}$			b+++$_{22}$	b_8-$SOCH_4$
Delta Da	0.07	-0.21		-0.47		0.65	0.56	-0.36	0.30	-0.55	-0.57	0.50			0.27		0.16		-0.34			0.29	0.73
							0.50			1.50													
							m	st		sty	m												
							0.04			0.43													

Peak 262



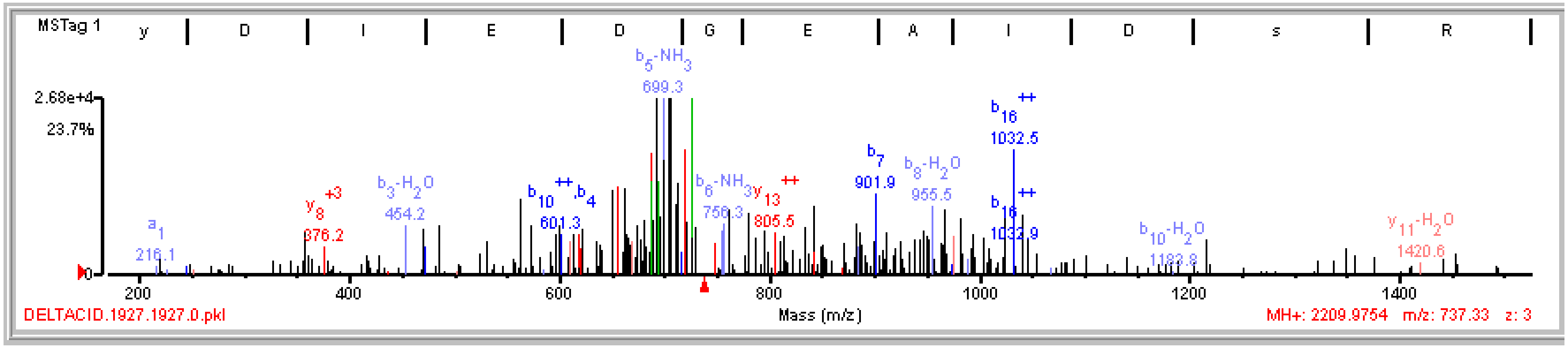


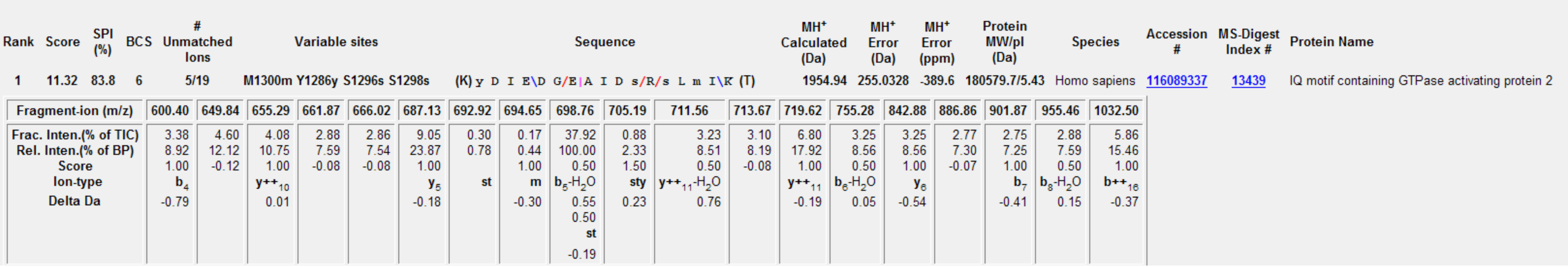
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.18	83.7	8	6/23	Y115y S129s	(R) H H/K/P D E|G\L y/Q C E A S L G D/S/G S I I\s R (T)	2656.24	161.4162	526.5	158457.4/6.32	Homo sapiens	110431348	23088	deleted in colorectal carcinoma

Fragment-ion (m/z)	596.64	687.27	692.04	712.44	715.78	743.83	744.09	780.69	798.69	800.91	806.09	820.70
Frac. Inten.(% of TIC)	1.22	1.39	2.82	1.35	8.48	1.79	5.52	9.66	1.29	1.59	11.28	1.48
Rel. Inten.(% of BP)	8.06	9.16	18.57	8.90	55.93	11.81	36.39	63.72	8.49	10.49	74.39	9.76
Score	0.50	-0.09	1.00	1.00	0.25	1.00	1.00	0.50	1.00	1.00	1.00	0.50
Ion-type	b_5-H_2O		$y{+}{+}{+}_{18}$	y_6	a_6	b_6	b_6	y_7-H_2O	y_7	b_7	$y{+}{+}{+}_{21}$	$y{+}{+}_{15}-H_2O$
Delta Da	-0.65		0.42	0.10	-0.57	-0.51	-0.25	-0.67	-0.68	-0.45	0.76	-0.65

Fragment-ion (m/z)	825.98	830.92	834.95	848.45	896.65	934.88	948.83	953.68	953.96	991.34	1040.90
Frac. Inten.(% of TIC)	2.13	15.16	1.35	7.89	2.11	3.01	2.41	1.33	8.62	5.77	2.36
Rel. Inten.(% of BP)	14.03	100.00	8.90	52.05	13.90	19.85	15.88	8.77	56.87	38.04	15.59
Score	1.00	1.00	-0.09	1.00	0.50	-0.20	-0.16	0.50	0.50	-0.38	-0.16
Ion-type	$b{+}{+}{+}_{22}$	$y{+}{+}_{15}$		$y{+}{+}{+}_{22}$	b_8-NH_3 y_8-NH_3			y_9-NH_3	y_9-NH_3		
Delta Da	0.29	0.56		0.43	-0.77 -0.72			-0.71	-0.43		

Peak 263



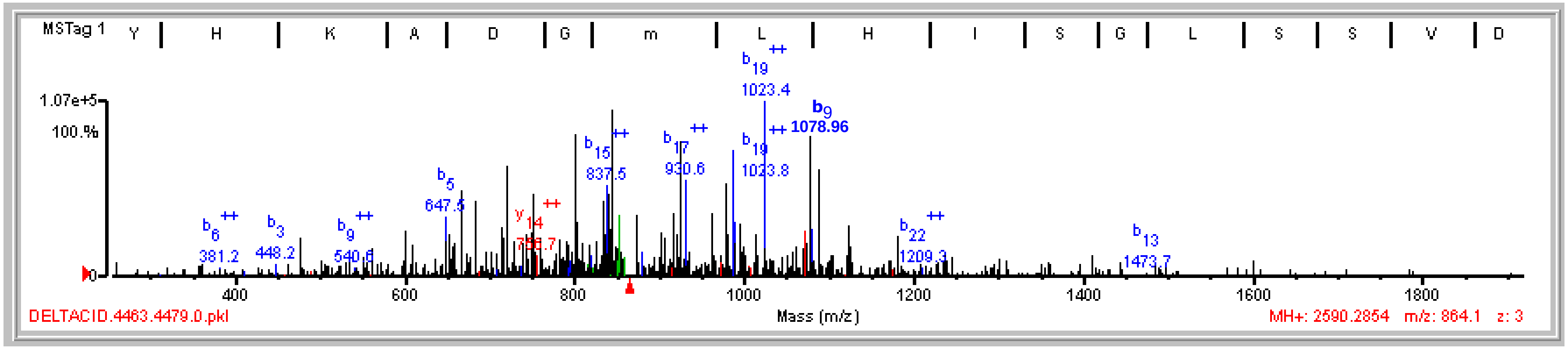


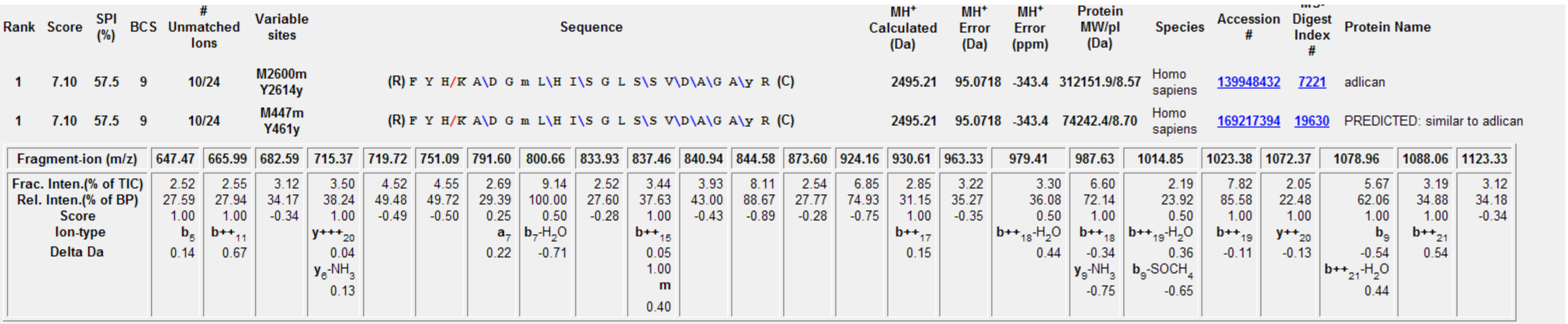
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.32	83.8	6	5/19	M1300m Y1286y S1296s S1298s	(K) y D I E\D G/E|A I D s/R/s L m I\K (T)	1954.94	255.0328	-389.6	180579.7/5.43	Homo sapiens	116089337	13439	IQ motif containing GTPase activating protein 2

Fragment-ion (m/z)	600.40	649.84	655.29	661.87	666.02	687.13	692.92	694.65	698.76	705.19
Frac. Inten.(% of TIC)	3.38	4.60	4.08	2.88	2.86	9.05	0.30	0.17	37.92	0.88
Rel. Inten.(% of BP)	8.92	12.12	10.75	7.59	7.54	23.87	0.78	0.44	100.00	2.33
Score	1.00	-0.12	1.00	-0.08	-0.08	1.00		1.00	0.50	1.50
Ion-type	b_4		$y{+}{+}_{10}$			y_5	st	m	b_5-H_2O	sty
Delta Da	-0.79		0.01			-0.18		-0.30	0.55	0.23
									0.50	
									st	
									-0.19	

Fragment-ion (m/z)	711.56	713.67	719.62	755.28	842.88	886.86	901.87	955.46	1032.50
Frac. Inten.(% of TIC)	3.23	3.10	6.80	3.25	3.25	2.77	2.75	2.88	5.86
Rel. Inten.(% of BP)	8.51	8.19	17.92	8.56	8.56	7.30	7.25	7.59	15.46
Score	0.50	-0.08	1.00	0.50	1.00	-0.07	1.00	0.50	1.00
Ion-type	$y{+}{+}_{11}$-H_2O		$y{+}{+}_{11}$	b_6-H_2O	y_6		b_7	b_8-H_2O	$b{+}{+}_{16}$
Delta Da	0.76		-0.19	0.05	-0.54		-0.41	0.15	-0.37

Peak 264





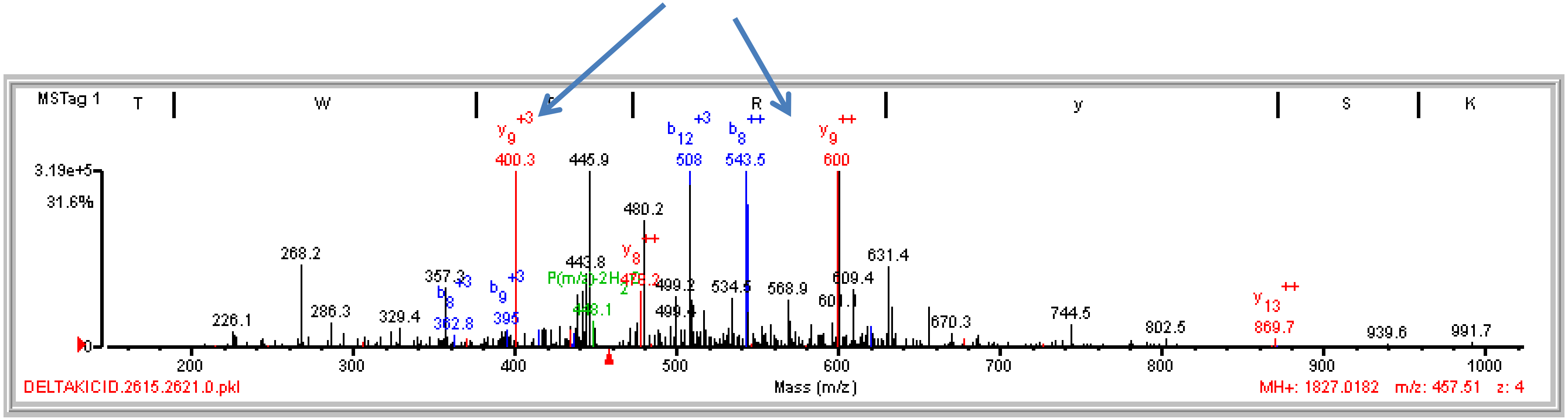
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.10	57.5	9	10/24	M2600m Y2614y	(R) F Y H/K A\D G m L\H I\S G L S\S V\D\A\G A\y R (C)	2495.21	95.0718	-343.4	312151.9/8.57	Homo sapiens	139948432	7221	adlican
1	7.10	57.5	9	10/24	M447m Y461y	(R) F Y H/K A\D G m L\H I\S G L S\S V\D\A\G A\y R (C)	2495.21	95.0718	-343.4	74242.4/8.70	Homo sapiens	169217394	19630	PREDICTED: similar to adlican

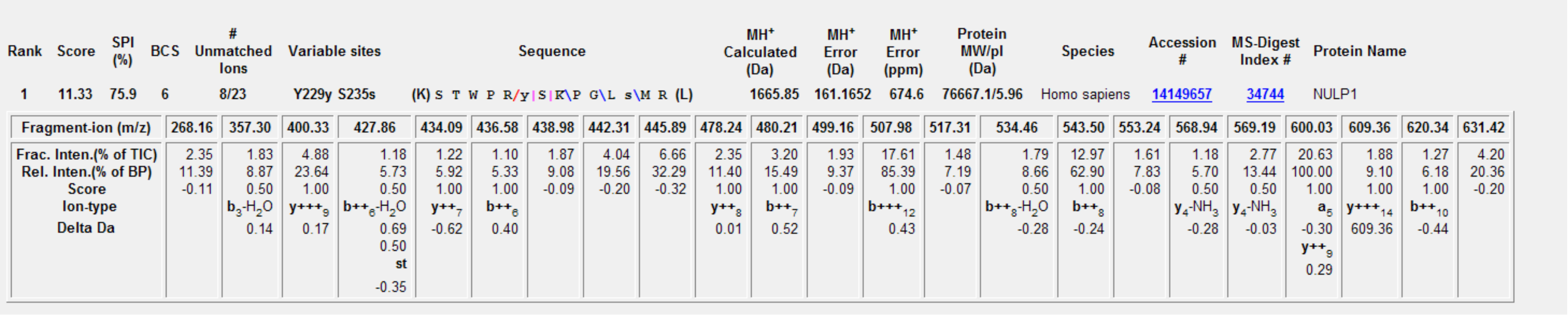
Fragment-ion (m/z)	647.47	665.99	682.59	715.37	719.72	751.09	791.60	800.66	833.93	837.46	840.94	844.58	873.60
Frac. Inten.(% of TIC)	2.52	2.55	3.12	3.50	4.52	4.55	2.69	9.14	2.52	3.44	3.93	8.11	2.54
Rel. Inten.(% of BP)	27.59	27.94	34.17	38.24	49.48	49.72	29.39	100.00	27.60	37.63	43.00	88.67	27.77
Score	1.00	1.00	-0.34	1.00	-0.49	-0.50	0.25	0.50	-0.28	1.00 1.00	-0.43	-0.89	-0.28
Ion-type	b_5	$b{++}_{11}$		$y{+++}_{20}$ y_6-NH_3			a_7	b_7-H_2O		$b{++}_{15}$ m			
Delta Da	0.14	0.67		0.04 0.13			0.22	-0.71		0.05 0.40			

Fragment-ion (m/z)	924.16	930.61	963.33	979.41	987.63	1014.85	1023.38	1072.37	1078.96	1088.06	1123.33
Frac. Inten.(% of TIC)	6.85	2.85	3.22	3.30	6.60	2.19	7.82	2.05	5.67	3.19	3.12
Rel. Inten.(% of BP)	74.93	31.15	35.27	36.08	72.14	23.92	85.58	22.48	62.06	34.88	34.18
Score	-0.75	1.00	-0.35	0.50	1.00	0.50	1.00	1.00	1.00	1.00	-0.34
Ion-type		$b{++}_{17}$		$b{++}_{18}$-H_2O	$b{++}_{18}$ y_9-NH_3	$b{++}_{19}$-H_2O b_9-$SOCH_4$	$b{++}_{19}$	$y{++}_{20}$	b_9 $b{++}_{21}$-H_2O	$b{++}_{21}$	
Delta Da		0.15		0.44	-0.34 -0.75	0.36 -0.65	-0.11	-0.13	-0.54 0.44	0.54	

Peak 265

assignment

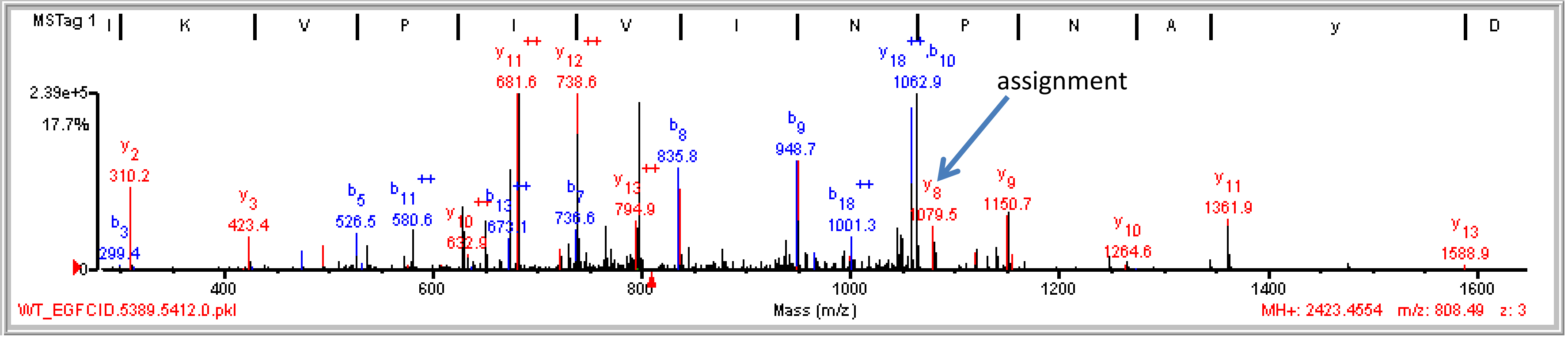




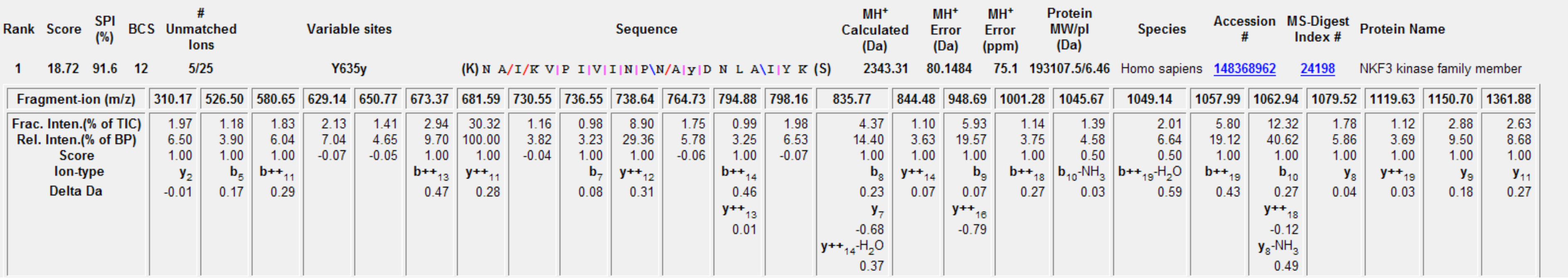
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.33	75.9	6	8/23	Y229y S235s	(K) S T W P R/y|S|K\P G\L s\M R (L)	1665.85	161.1652	674.6	76667.1/5.96	Homo sapiens	14149657	34744	NULP1

Fragment-ion (m/z)	268.16	357.30	400.33	427.86	434.09	436.58	438.98	442.31	445.89	478.24	480.21	499.16	507.98	517.31	534.46	543.50	553.24	568.94	569.19	600.03	609.36	620.34	631.42
Frac. Inten.(% of TIC)	2.35	1.83	4.88	1.18	1.22	1.10	1.87	4.04	6.66	2.35	3.20	1.93	17.61	1.48	1.79	12.97	1.61	1.18	2.77	20.63	1.88	1.27	4.20
Rel. Inten.(% of BP)	11.39	8.87	23.64	5.73	5.92	5.33	9.08	19.56	32.29	11.40	15.49	9.37	85.39	7.19	8.66	62.90	7.83	5.70	13.44	100.00	9.10	6.18	20.36
Score	-0.11	0.50	1.00	0.50 0.50	1.00	1.00	-0.09	-0.20	-0.32	1.00	1.00	-0.09	1.00	-0.07	0.50	1.00	-0.08	0.50	0.50	1.00	1.00	1.00	-0.20
Ion-type		b_3-H_2O	$y{+}{+}{+}_9$	$b{+}{+}_6$-H_2O st	$y{+}{+}_7$	$b{+}{+}_6$				$y{+}{+}_8$	$b{+}{+}_7$		$b{+}{+}{+}_{12}$		$b{+}{+}_8$-H_2O	$b{+}{+}_8$		y_4-NH_3	y_4-NH_3	a_5 $y{+}{+}_9$	$y{+}{+}{+}_{14}$	$b{+}{+}_{10}$	
Delta Da		0.14	0.17	0.69 -0.35	-0.62	0.40				0.01	0.52		0.43		-0.28	-0.24		-0.28	-0.03	-0.30 0.29	609.36	-0.44	

Peak 266



assignment

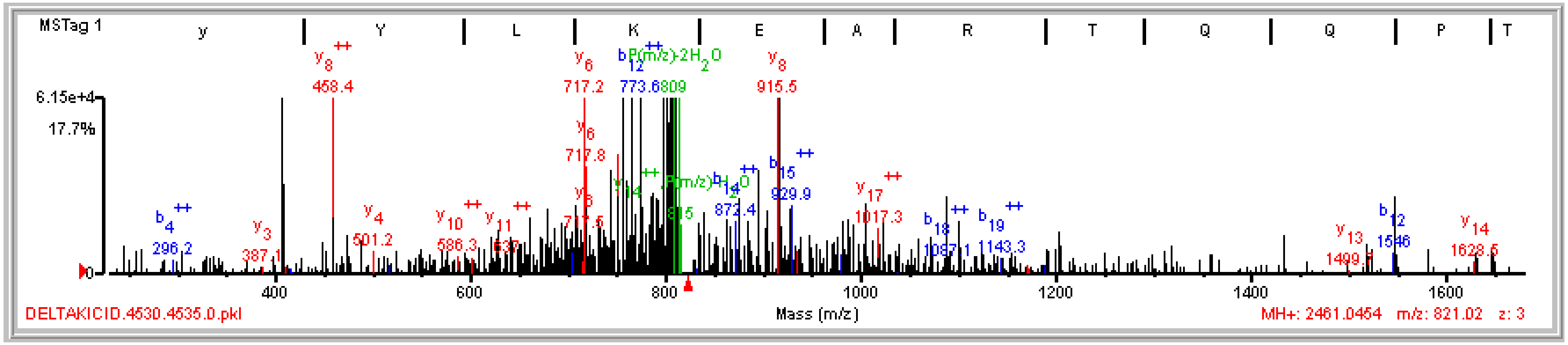


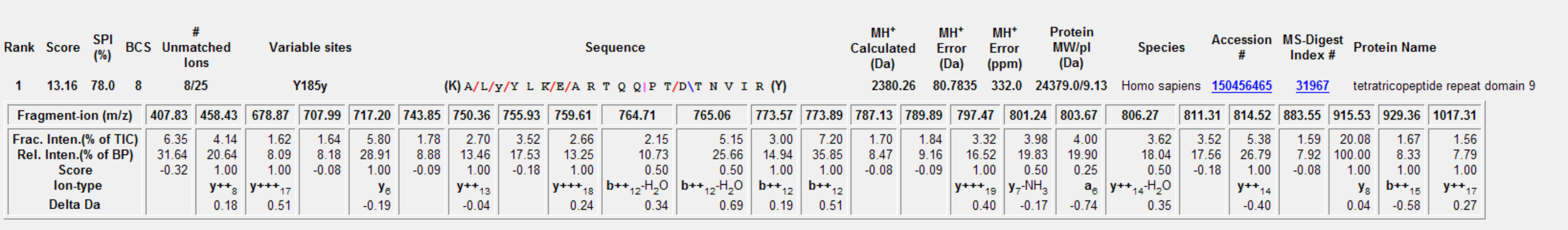
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.72	91.6	12	5/25	Y635y	(K) N A/I/K V|P I|V|I|N|P\N/A|y|D N L A\I|Y K (S)	2343.31	80.1484	75.1	193107.5/6.46	Homo sapiens	148368962	24198	NKF3 kinase family member

Fragment-ion (m/z)	310.17	526.50	580.65	629.14	650.77	673.37	681.59	730.55	736.55	738.64	764.73	794.88
Frac. Inten.(% of TIC)	1.97	1.18	1.83	2.13	1.41	2.94	30.32	1.16	0.98	8.90	1.75	0.99
Rel. Inten.(% of BP)	6.50	3.90	6.04	7.04	4.65	9.70	100.00	3.82	3.23	29.36	5.78	3.25
Score	1.00	1.00	1.00	-0.07	-0.05	1.00	1.00	-0.04	1.00	1.00	-0.06	1.00
Ion-type	y_2	b_5	b++_{11}			b++_{13}	y++_{11}		b_7	y++_{12}		b++_{14} y++_{13}
Delta Da	-0.01	0.17	0.29			0.47	0.28		0.08	0.31		0.46 0.01

Fragment-ion (m/z)	798.16	835.77	844.48	948.69	1001.28	1045.67	1049.14	1057.99	1062.94	1079.52	1119.63	1150.70	1361.88
Frac. Inten.(% of TIC)	1.98	4.37	1.10	5.93	1.14	1.39	2.01	5.80	12.32	1.78	1.12	2.88	2.63
Rel. Inten.(% of BP)	6.53	14.40	3.63	19.57	3.75	4.58	6.64	19.12	40.62	5.86	3.69	9.50	8.68
Score	-0.07	1.00	1.00	1.00	1.00	0.50	0.50	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type		b_8 y_7 $\text{y++}_{14}\text{-H}_2\text{O}$	y++_{14}	b_9 y++_{16}	b++_{18}	$b_{10}\text{-NH}_3$	$\text{b++}_{19}\text{-H}_2\text{O}$	b++_{19}	b_{10} y++_{18} $y_8\text{-NH}_3$	y_8	y++_{19}	y_9	y_{11}
Delta Da		0.23 -0.68 0.37	0.07	0.07 -0.79	0.27	0.03	0.59	0.43	0.27 -0.12 0.49	0.04	0.03	0.18	0.27

Peak 267





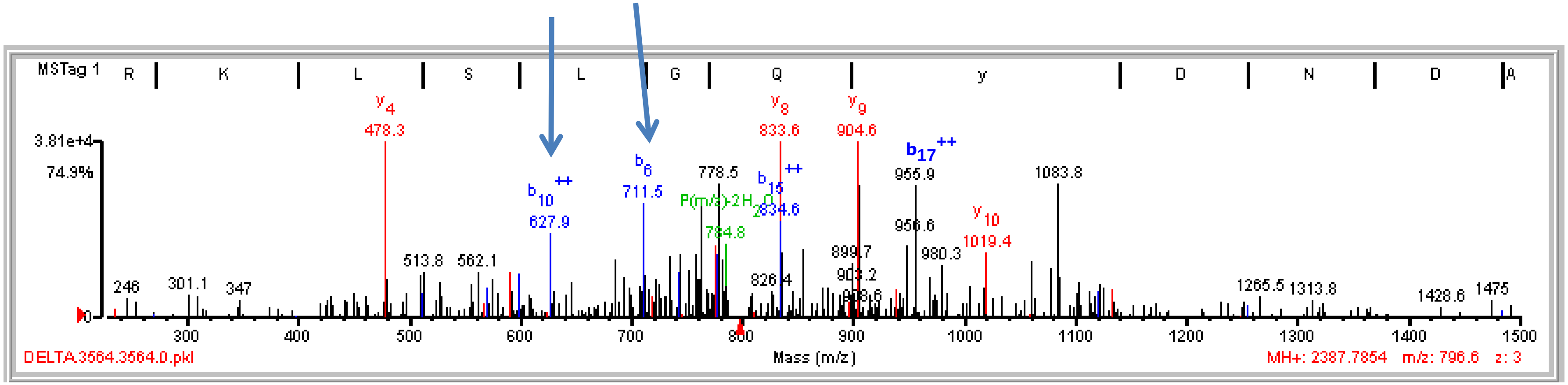
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.16	78.0	8	8/25	Y185y	(K) A/L/y/Y L K/E/A R T Q Q|P T/D\T N V I R (Y)	2380.26	80.7835	332.0	24379.0/9.13	Homo sapiens	150456465	31967	tetratricopeptide repeat domain 9

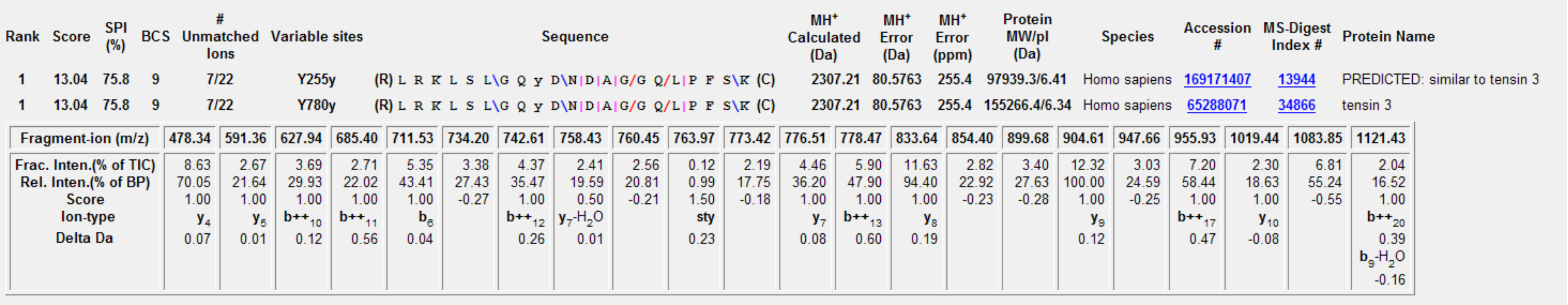
Fragment-ion (m/z)	407.83	458.43	678.87	707.99	717.20	743.85	750.36	755.93	759.61	764.71	765.06	773.57
Frac. Inten.(% of TIC)	6.35	4.14	1.62	1.64	5.80	1.78	2.70	3.52	2.66	2.15	5.15	3.00
Rel. Inten.(% of BP)	31.64	20.64	8.09	8.18	28.91	8.88	13.46	17.53	13.25	10.73	25.66	14.94
Score	-0.32	1.00	1.00	-0.08	1.00	-0.09	1.00	-0.18	1.00	0.50	0.50	1.00
Ion-type		$y{+}{+}_{8}$	$y{+}{+}{+}_{17}$		y_{6}		$y{+}{+}_{13}$		$y{+}{+}{+}_{18}$	$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$
Delta Da		0.18	0.51		-0.19		-0.04		0.24	0.34	0.69	0.19

Fragment-ion (m/z)	773.89	787.13	789.89	797.47	801.24	803.67	806.27	811.31	814.52	883.55	915.53	929.36	1017.31
Frac. Inten.(% of TIC)	7.20	1.70	1.84	3.32	3.98	4.00	3.62	3.52	5.38	1.59	20.08	1.67	1.56
Rel. Inten.(% of BP)	35.85	8.47	9.16	16.52	19.83	19.90	18.04	17.56	26.79	7.92	100.00	8.33	7.79
Score	1.00	-0.08	-0.09	1.00	0.50	0.25	0.50	-0.18	1.00	-0.08	1.00	1.00	1.00
Ion-type	$b{+}{+}_{12}$			$y{+}{+}{+}_{19}$	y_{7}-NH_3	a_{6}	$y{+}{+}_{14}$-H_2O		$y{+}{+}_{14}$		y_{8}	$b{+}{+}_{15}$	$y{+}{+}_{17}$
Delta Da	0.51			0.40	-0.17	-0.74	0.35		-0.40		0.04	-0.58	0.27

Peak 268

Ions that verify assignment





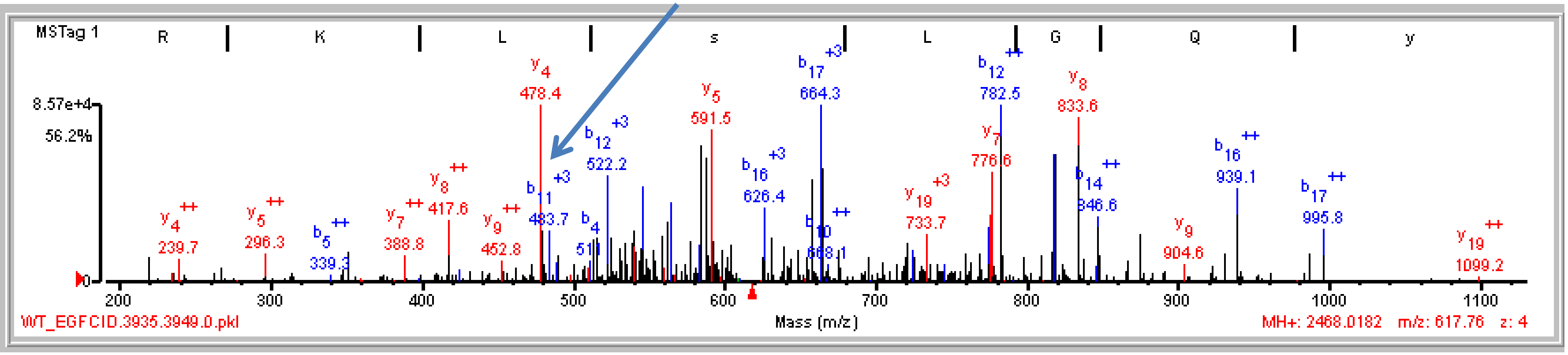
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.04	75.8	9	7/22	Y255y	(R) L R K L S L\G Q y D\N|D|A|G/G Q/L|P F S\K (C)	2307.21	80.5763	255.4	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	13.04	75.8	9	7/22	Y780y	(R) L R K L S L\G Q y D\N|D|A|G/G Q/L|P F S\K (C)	2307.21	80.5763	255.4	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

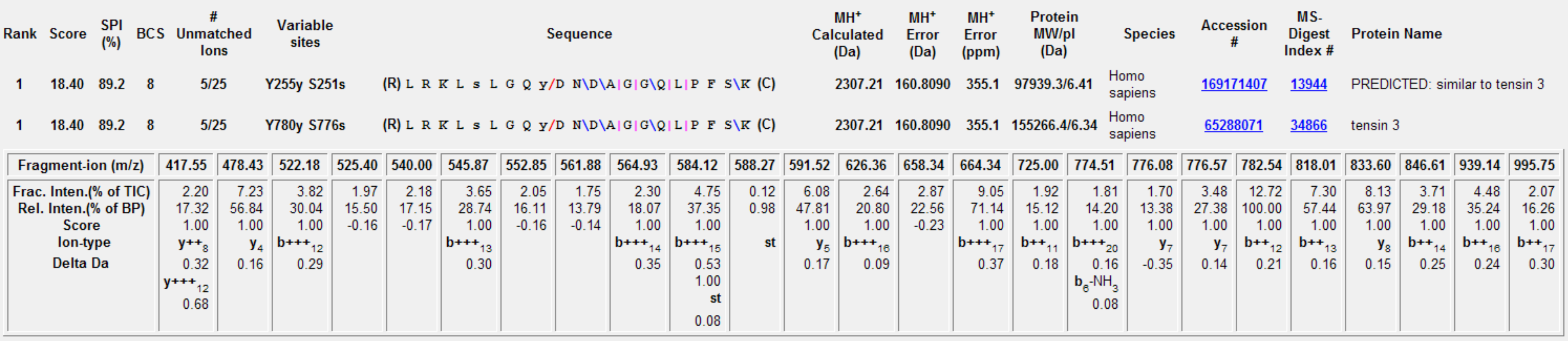
Fragment-ion (m/z)	478.34	591.36	627.94	685.40	711.53	734.20	742.61	758.43	760.45	763.97
Frac. Inten.(% of TIC)	8.63	2.67	3.69	2.71	5.35	3.38	4.37	2.41	2.56	0.12
Rel. Inten.(% of BP)	70.05	21.64	29.93	22.02	43.41	27.43	35.47	19.59	20.81	0.99
Score	1.00	1.00	1.00	1.00	1.00	-0.27	1.00	0.50	-0.21	1.50
Ion-type	y_4	y_5	$b{++}_{10}$	$b{++}_{11}$	b_6		$b{++}_{12}$	$y_7\text{-}H_2O$		sty
Delta Da	0.07	0.01	0.12	0.56	0.04		0.26	0.01		0.23

Fragment-ion (m/z)	773.42	776.51	778.47	833.64	854.40	899.68	904.61	947.66	955.93	1019.44	1083.85	1121.43
Frac. Inten.(% of TIC)	2.19	4.46	5.90	11.63	2.82	3.40	12.32	3.03	7.20	2.30	6.81	2.04
Rel. Inten.(% of BP)	17.75	36.20	47.90	94.40	22.92	27.63	100.00	24.59	58.44	18.63	55.24	16.52
Score	-0.18	1.00	1.00	1.00	-0.23	-0.28	1.00	-0.25	1.00	1.00	-0.55	1.00
Ion-type		y_7	$b{++}_{13}$	y_8			y_9		$b{++}_{17}$	y_{10}		$b{++}_{20}$
Delta Da		0.08	0.60	0.19			0.12		0.47	-0.08		0.39
												$b_9\text{-}H_2O$
												-0.16

Peak 269

Ions that verify assignment



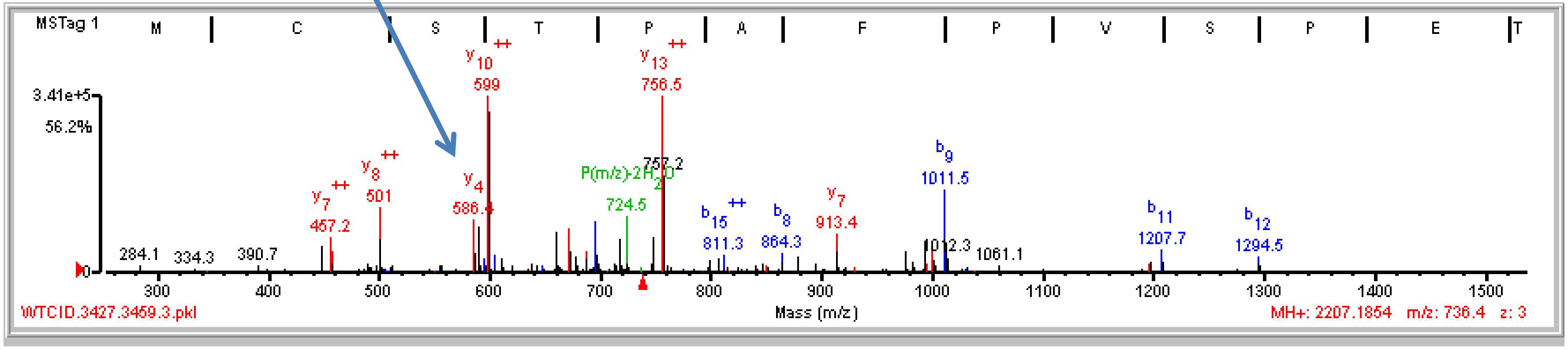


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.40	89.2	8	5/25	Y255y S251s	(R) L R K L s L G Q y/D N\D\A|G|G\Q|L|P F S\K (C)	2307.21	160.8090	355.1	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	18.40	89.2	8	5/25	Y780y S776s	(R) L R K L s L G Q y/D N\D\A|G|G\Q|L|P F S\K (C)	2307.21	160.8090	355.1	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

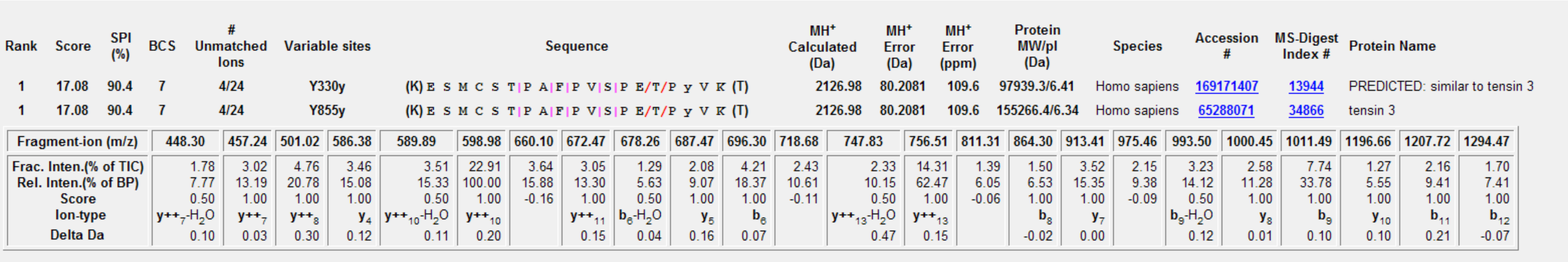
Fragment-ion (m/z)	417.55	478.43	522.18	525.40	540.00	545.87	552.85	561.88	564.93	584.12	588.27	591.52	626.36
Frac. Inten.(% of TIC)	2.20	7.23	3.82	1.97	2.18	3.65	2.05	1.75	2.30	4.75	0.12	6.08	2.64
Rel. Inten.(% of BP)	17.32	56.84	30.04	15.50	17.15	28.74	16.11	13.79	18.07	37.35	0.98	47.81	20.80
Score	1.00	1.00	1.00	-0.16	-0.17	1.00	-0.16	-0.14	1.00	1.00		1.00	1.00
Ion-type	$y{++}_{8}$	y_{4}	$b{+++}_{12}$			$b{+++}_{13}$			$b{+++}_{14}$	$b{+++}_{15}$	st	y_{5}	$b{+++}_{16}$
Delta Da	0.32	0.16	0.29			0.30			0.35	0.53		0.17	0.09
										1.00			
	$y{+++}_{12}$									st			
	0.68									0.08			

Fragment-ion (m/z)	658.34	664.34	725.00	774.51	776.08	776.57	782.54	818.01	833.60	846.61	939.14	995.75
Frac. Inten.(% of TIC)	2.87	9.05	1.92	1.81	1.70	3.48	12.72	7.30	8.13	3.71	4.48	2.07
Rel. Inten.(% of BP)	22.56	71.14	15.12	14.20	13.38	27.38	100.00	57.44	63.97	29.18	35.24	16.26
Score	-0.23	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type		$b{+++}_{17}$	$b{++}_{11}$	$b{+++}_{20}$	y_{7}	y_{7}	$b{++}_{12}$	$b{++}_{13}$	y_{8}	$b{++}_{14}$	$b{++}_{16}$	$b{++}_{17}$
Delta Da		0.37	0.18	0.16	-0.35	0.14	0.21	0.16	0.15	0.25	0.24	0.30
				b_{6}-NH_{3}								
				0.08								

Peak 270



Ions that verify assignment

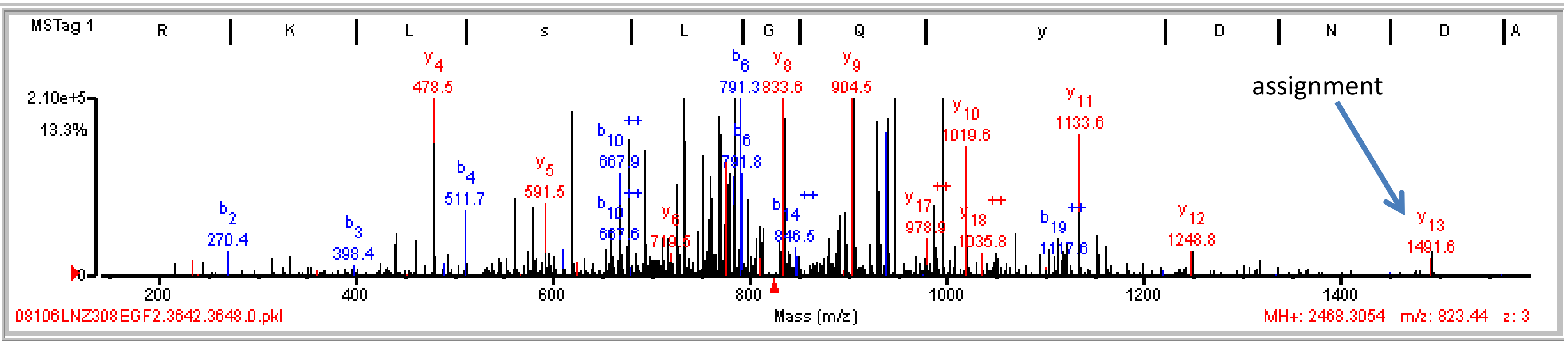


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.08	90.4	7	4/24	Y330y	(K) E S M C S T|P A|F|P V|S|P E/T/P y V K (T)	2126.98	80.2081	109.6	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	17.08	90.4	7	4/24	Y855y	(K) E S M C S T|P A|F|P V|S|P E/T/P y V K (T)	2126.98	80.2081	109.6	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

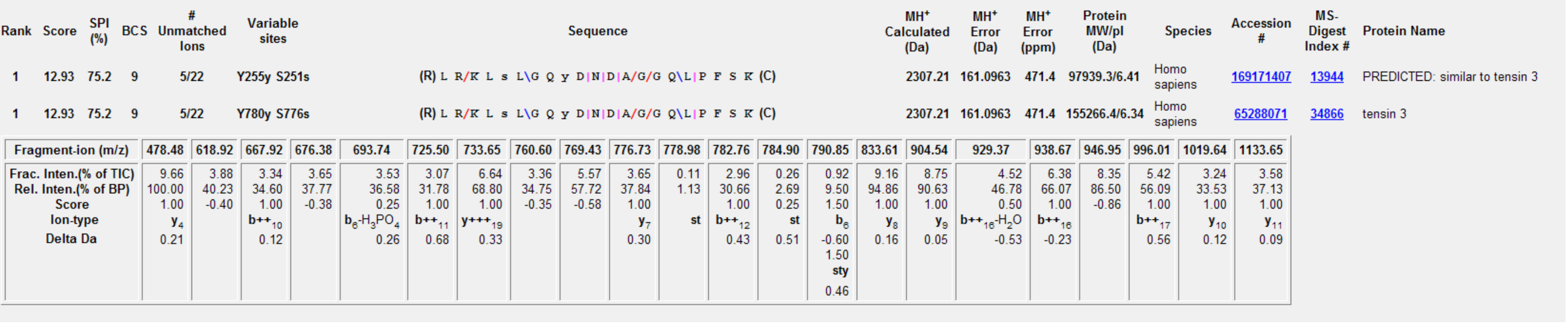
Fragment-ion (m/z)	448.30	457.24	501.02	586.38	589.89	598.98	660.10	672.47	678.26	687.47	696.30
Frac. Inten.(% of TIC)	1.78	3.02	4.76	3.46	3.51	22.91	3.64	3.05	1.29	2.08	4.21
Rel. Inten.(% of BP)	7.77	13.19	20.78	15.08	15.33	100.00	15.88	13.30	5.63	9.07	18.37
Score	0.50	1.00	1.00	1.00	0.50	1.00	-0.16	1.00	0.50	1.00	1.00
Ion-type	$y{+}{+}_7$-H_2O	$y{+}{+}_7$	$y{+}{+}_8$	y_4	$y{+}{+}_{10}$-H_2O	$y{+}{+}_{10}$		$y{+}{+}_{11}$	b_6-H_2O	y_5	b_6
Delta Da	0.10	0.03	0.30	0.12	0.11	0.20		0.15	0.04	0.16	0.07

Fragment-ion (m/z)	718.68	747.83	756.51	811.31	864.30	913.41	975.46	993.50	1000.45	1011.49	1196.66	1207.72	1294.47
Frac. Inten.(% of TIC)	2.43	2.33	14.31	1.39	1.50	3.52	2.15	3.23	2.58	7.74	1.27	2.16	1.70
Rel. Inten.(% of BP)	10.61	10.15	62.47	6.05	6.53	15.35	9.38	14.12	11.28	33.78	5.55	9.41	7.41
Score	-0.11	0.50	1.00	-0.06	1.00	1.00	-0.09	0.50	1.00	1.00	1.00	1.00	1.00
Ion-type		$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$		b_8	y_7		b_9-H_2O	y_8	b_9	y_{10}	b_{11}	b_{12}
Delta Da		0.47	0.15		-0.02	0.00		0.12	0.01	0.10	0.10	0.21	-0.07

Peak 271



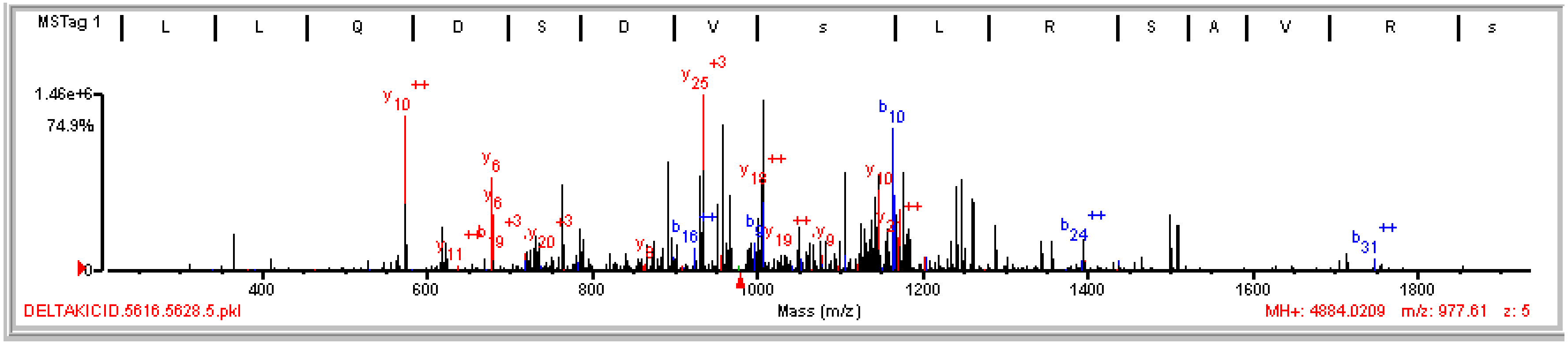
assignment

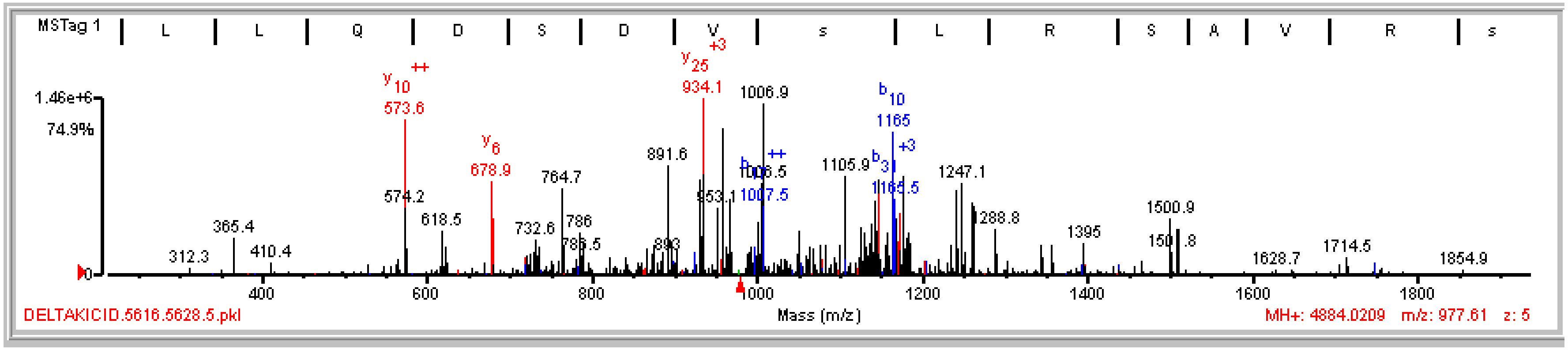


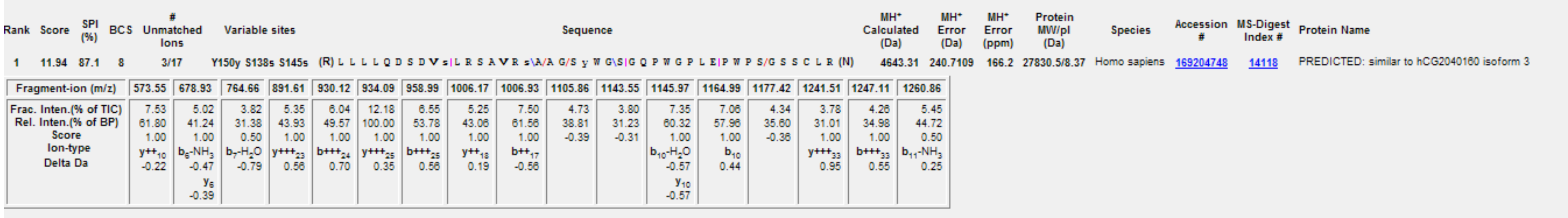
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.93	75.2	9	5/22	Y255y S251s	(R) L R/K L s L\G Q y D|N|D|A/G/G Q\L|P F S K (C)	2307.21	161.0963	471.4	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	12.93	75.2	9	5/22	Y780y S776s	(R) L R/K L s L\G Q y D|N|D|A/G/G Q\L|P F S K (C)	2307.21	161.0963	471.4	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

Fragment-ion (m/z)	478.48	618.92	667.92	676.38	693.74	725.50	733.65	760.60	769.43	776.73	778.98	782.76	784.90	790.85	833.61	904.54	929.37	938.67	946.95	996.01	1019.64	1133.65
Frac. Inten.(% of TIC)	9.66	3.88	3.34	3.65	3.53	3.07	6.64	3.36	5.57	3.65	0.11	2.96	0.26	0.92	9.16	8.75	4.52	6.38	8.35	5.42	3.24	3.58
Rel. Inten.(% of BP)	100.00	40.23	34.60	37.77	36.58	31.78	68.80	34.75	57.72	37.84	1.13	30.66	2.69	9.50	94.86	90.63	46.78	66.07	86.50	56.09	33.53	37.13
Score	1.00	-0.40	1.00	-0.38	0.25	1.00	1.00	-0.35	-0.58	1.00		1.00	0.25	1.50 1.50	1.00	1.00	0.50	1.00	-0.86	1.00	1.00	1.00
Ion-type	y_4		b^{++}_{10}		b_6-H_3PO_4	b^{++}_{11}	y^{+++}_{19}			y_7	st	b^{++}_{12}	st	b_6 sty	y_8	y_9	b^{++}_{16}-H_2O	b^{++}_{16}		b^{++}_{17}	y_{10}	y_{11}
Delta Da	0.21		0.12		0.26	0.68	0.33			0.30		0.43	0.51	-0.60 0.46	0.16	0.05	-0.53	-0.23		0.56	0.12	0.09

Peak 272



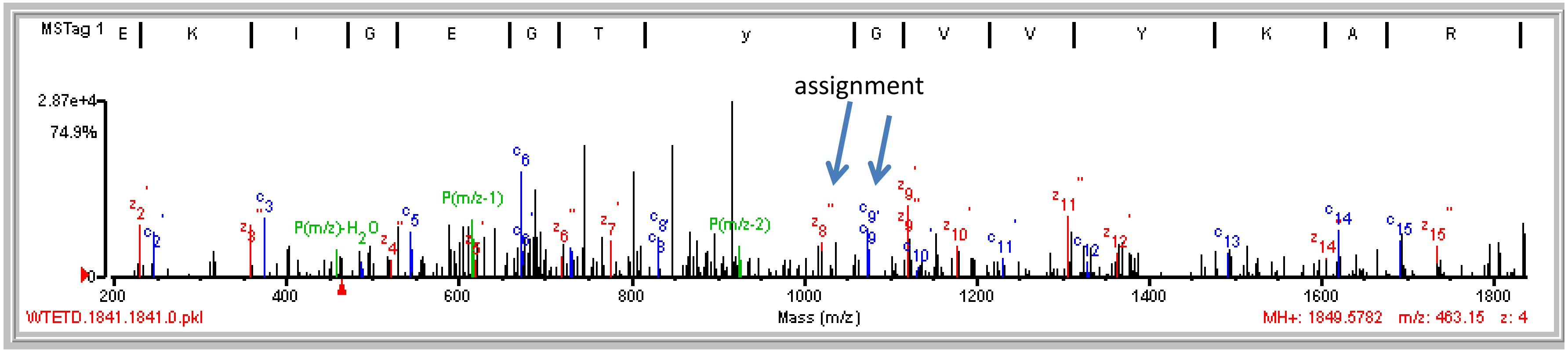


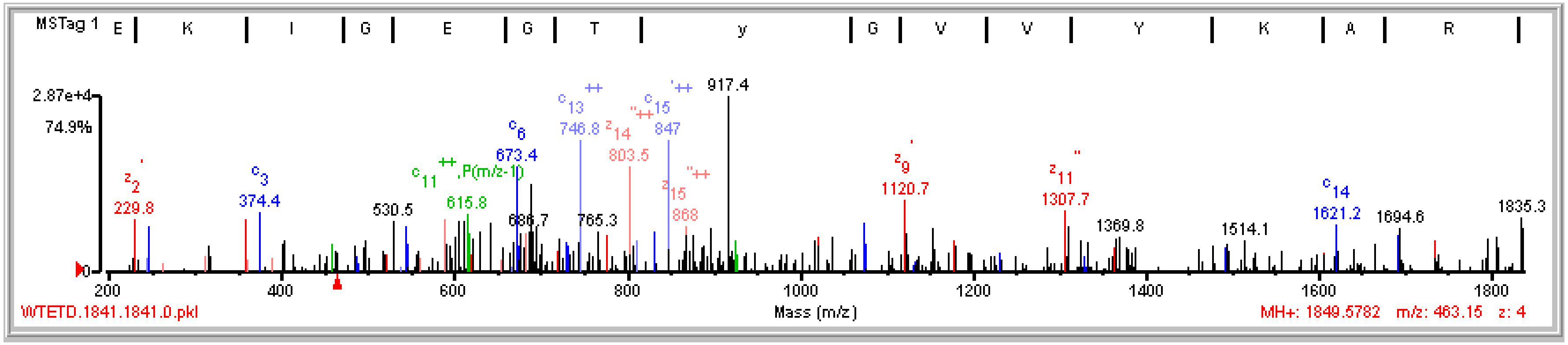


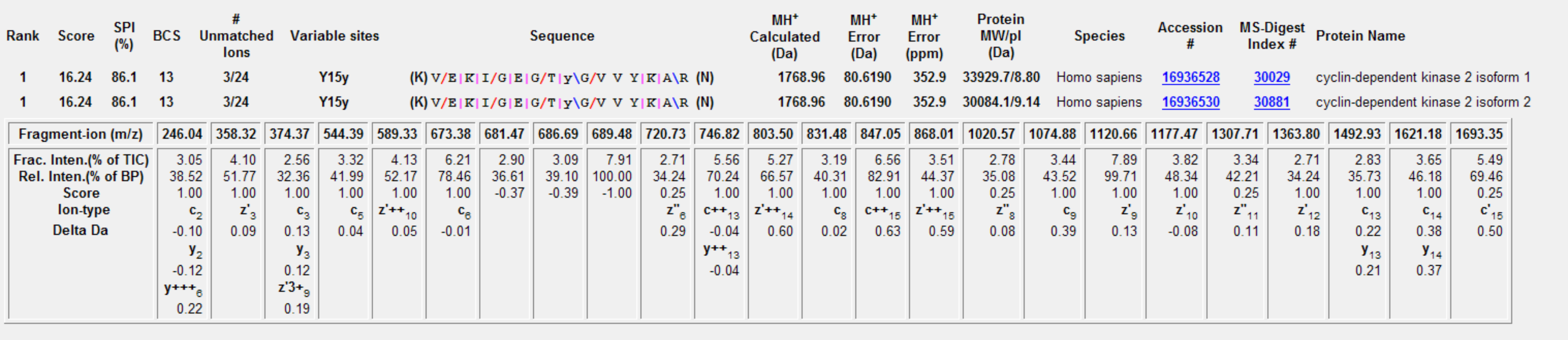
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.94	87.1	8	3/17	Y150y S138s S145s	(R) L L L L Q D S D V s|L R S A V R s\A/A G/S y W G\S|G Q P W G P L E|P W P S/G S S C L R (N)	4643.31	240.7109	166.2	27830.5/8.37	Homo sapiens	169204748	14118	PREDICTED: similar to hCG2040160 isoform 3

Fragment-ion (m/z)	573.55	678.93	764.66	891.61	930.12	934.09	958.99	1006.17	1006.93	1105.86	1143.55	1145.97	1164.99	1177.42	1241.51	1247.11	1260.86
Frac. Inten.(% of TIC)	7.53	5.02	3.82	5.35	6.04	12.18	6.55	5.25	7.50	4.73	3.80	7.35	7.06	4.34	3.78	4.26	5.45
Rel. Inten.(% of BP)	61.80	41.24	31.38	43.93	49.57	100.00	53.78	43.06	61.56	38.81	31.23	60.32	57.96	35.60	31.01	34.98	44.72
Score	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	-0.39	-0.31	1.00	1.00	-0.36	1.00	1.00	0.50
Ion-type	$y{+}{+}_{10}$	b_6-NH_3 y_6	b_7-H_2O	$y{+}{+}{+}_{23}$	$b{+}{+}{+}_{24}$	$y{+}{+}{+}_{25}$	$b{+}{+}{+}_{25}$	$y{+}{+}_{18}$	$b{+}{+}_{17}$			b_{10}-H_2O y_{10}	b_{10}		$y{+}{+}{+}_{33}$	$b{+}{+}{+}_{33}$	b_{11}-NH_3
Delta Da	-0.22	-0.47 -0.39	-0.79	0.56	0.70	0.35	0.56	0.19	-0.56			-0.57 -0.57	0.44		0.95	0.55	0.25

Peak 274





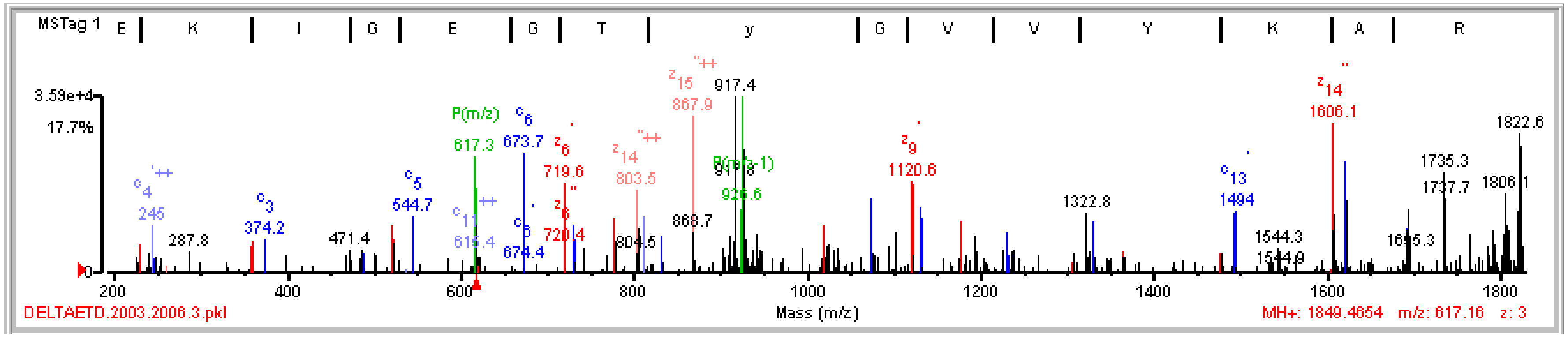


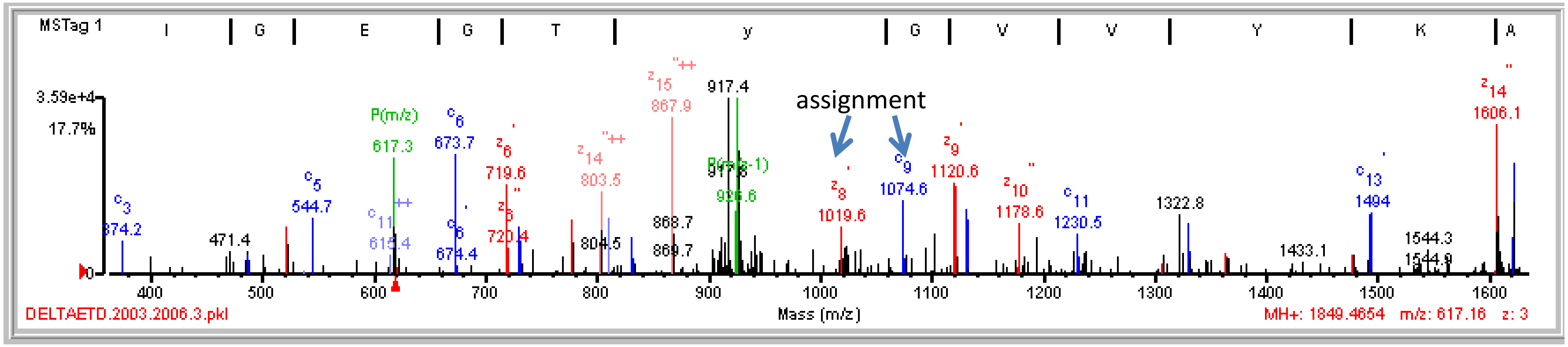
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.24	86.1	13	3/24	Y15y	(K) V/E|K|I/G|E|G/T|y\G/V V Y|K|A\R (N)	1768.96	80.6190	352.9	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	16.24	86.1	13	3/24	Y15y	(K) V/E|K|I/G|E|G/T|y\G/V V Y|K|A\R (N)	1768.96	80.6190	352.9	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

Fragment-ion (m/z)	246.04	358.32	374.37	544.39	589.33	673.38	681.47	686.69	689.48	720.73	746.82	803.50
Frac. Inten.(% of TIC)	3.05	4.10	2.56	3.32	4.13	6.21	2.90	3.09	7.91	2.71	5.56	5.27
Rel. Inten.(% of BP)	38.52	51.77	32.36	41.99	52.17	78.46	36.61	39.10	100.00	34.24	70.24	66.57
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.37	-0.39	-1.00	0.25	1.00	1.00
Ion-type	c_2	z'_3	c_3	c_5	$z'++_{10}$	c_6				z''_6	$c++_{13}$	$z'++_{14}$
Delta Da	-0.10	0.09	0.13	0.04	0.05	-0.01				0.29	-0.04	0.60
	y_2		y_3								$y++_{13}$	
	-0.12		0.12								-0.04	
	$y+++_6$		$z'3+_9$									
	0.22		0.19									

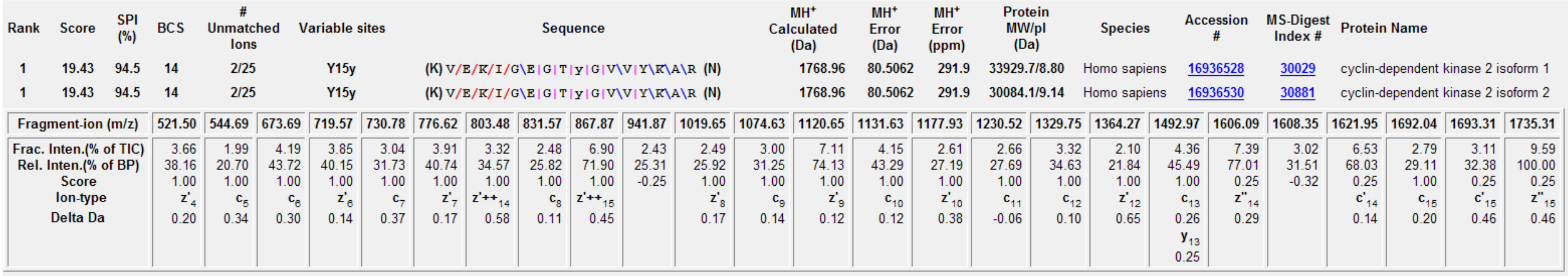
Fragment-ion (m/z)	831.48	847.05	868.01	1020.57	1074.88	1120.66	1177.47	1307.71	1363.80	1492.93	1621.18	1693.35
Frac. Inten.(% of TIC)	3.19	6.56	3.51	2.78	3.44	7.89	3.82	3.34	2.71	2.83	3.65	5.49
Rel. Inten.(% of BP)	40.31	82.91	44.37	35.08	43.52	99.71	48.34	42.21	34.24	35.73	46.18	69.46
Score	1.00	1.00	1.00	0.25	1.00	1.00	1.00	0.25	1.00	1.00	1.00	0.25
Ion-type	c_8	$c++_{15}$	$z'++_{15}$	z''_8	c_9	z'_9	z'_{10}	z''_{11}	z'_{12}	c_{13}	c_{14}	c'_{15}
Delta Da	0.02	0.63	0.59	0.08	0.39	0.13	-0.08	0.11	0.18	0.22	0.38	0.50
										y_{13}	y_{14}	
										0.21	0.37	

Peak 275





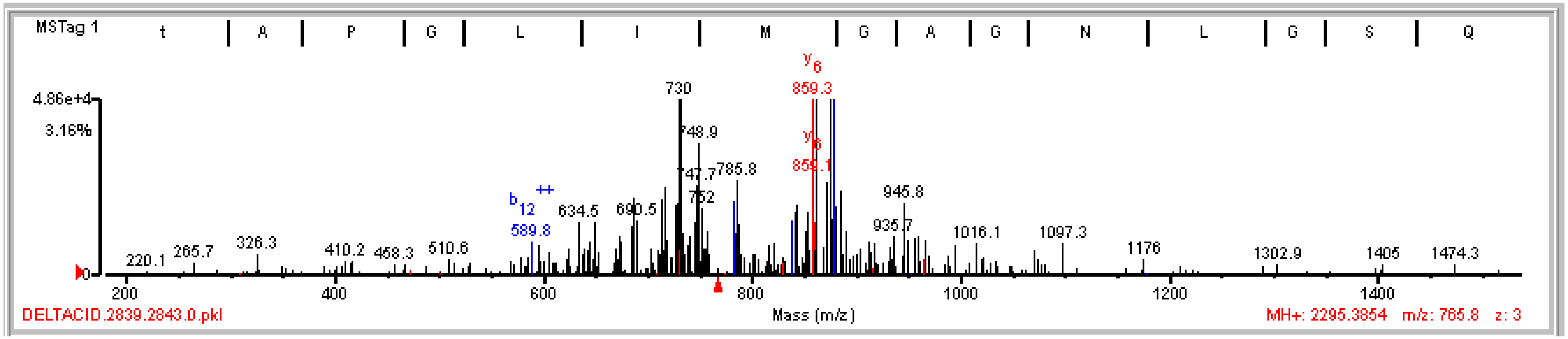
assignment

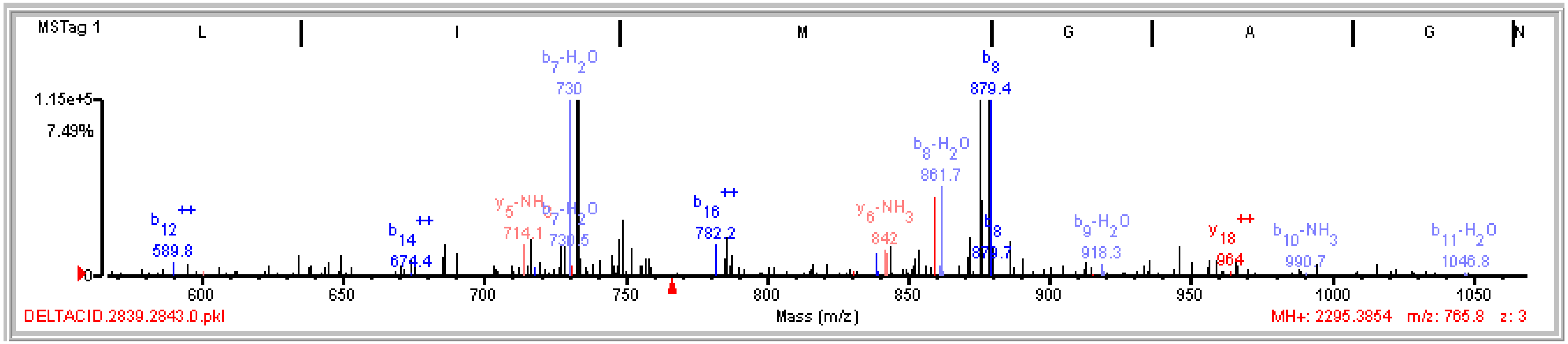


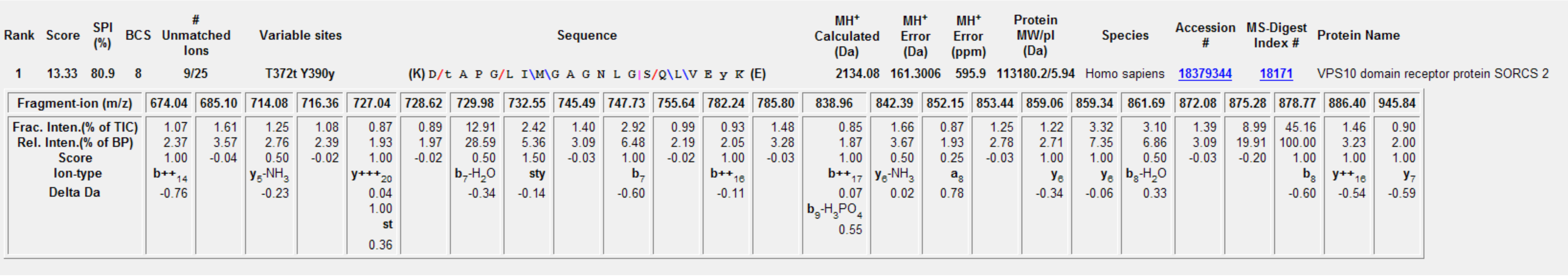
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.43	94.5	14	2/25	Y15y	(K) V/E/K/I/G\E|G|T|y|G|V\V|Y\K\A\R (N)	1768.96	80.5062	291.9	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1
1	19.43	94.5	14	2/25	Y15y	(K) V/E/K/I/G\E|G|T|y|G|V\V|Y\K\A\R (N)	1768.96	80.5062	291.9	30084.1/9.14	Homo sapiens	16936530	30881	cyclin-dependent kinase 2 isoform 2

Fragment-ion (m/z)	521.50	544.69	673.69	719.57	730.78	776.62	803.48	831.57	867.87	941.87	1019.65	1074.63	1120.65	1131.63	1177.93	1230.52	1329.75	1364.27	1492.97	1606.09	1608.35	1621.95	1692.04	1693.31	1735.31
Frac. Inten.(% of TIC)	3.66	1.99	4.19	3.85	3.04	3.91	3.32	2.48	6.90	2.43	2.49	3.00	7.11	4.15	2.61	2.66	3.32	2.10	4.36	7.39	3.02	6.53	2.79	3.11	9.59
Rel. Inten.(% of BP)	38.16	20.70	43.72	40.15	31.73	40.74	34.57	25.82	71.90	25.31	25.92	31.25	74.13	43.29	27.19	27.69	34.63	21.84	45.49	77.01	31.51	68.03	29.11	32.38	100.00
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.25	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.32	0.25	1.00	0.25	0.25
Ion-type	z'_4	c_5	c_6	z'_6	c_7	z'_7	z'^{++}_{14}	c_8	z'^{++}_{15}		z'_8	c_9	z'_9	c_{10}	z'_{10}	c_{11}	c_{12}	z'_{12}	c_{13} y_{13}	z''_{14}		c'_{14}	c_{15}	c'_{15}	z''_{15}
Delta Da	0.20	0.34	0.30	0.14	0.37	0.17	0.58	0.11	0.45		0.17	0.14	0.12	0.12	0.38	-0.06	0.10	0.65	0.26 0.25	0.29		0.14	0.20	0.46	0.46

Peak 276





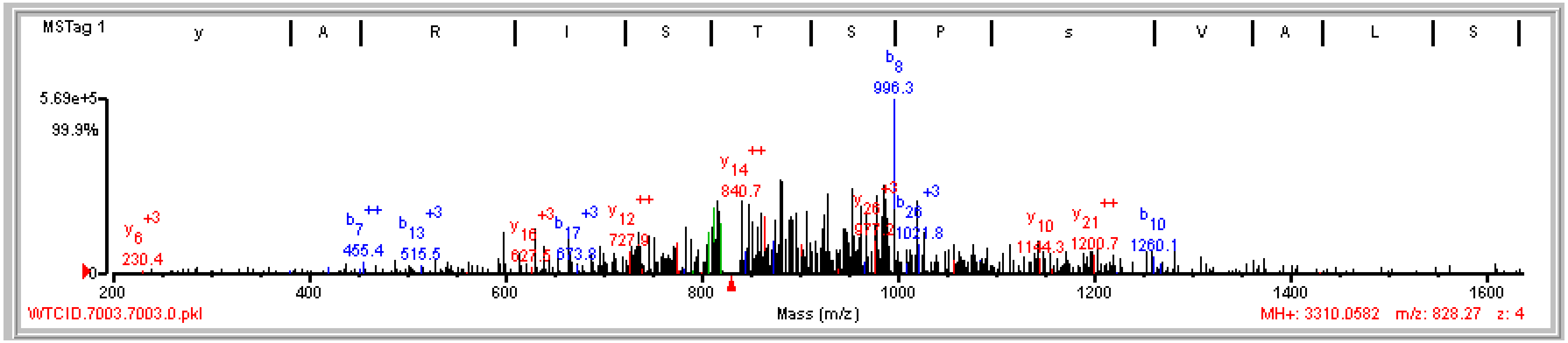


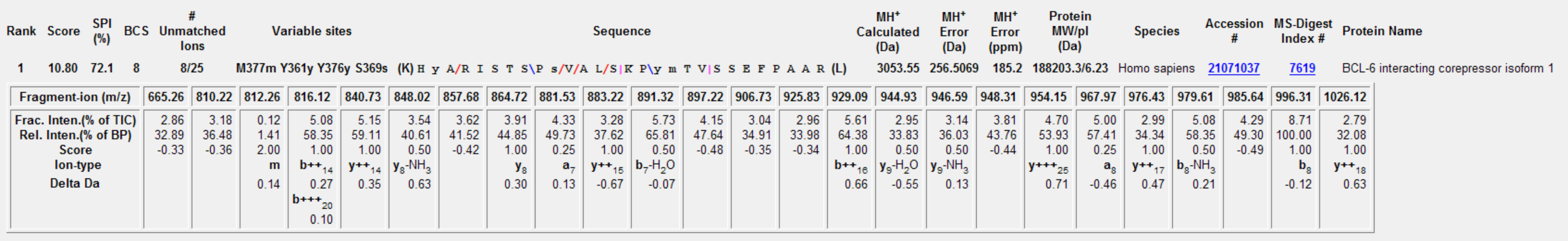
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.33	80.9	8	9/25	T372t Y390y	(K) D/t A P G/L I\M\G A G N L G|S/Q\L\V E y K (E)	2134.08	161.3006	595.9	113180.2/5.94	Homo sapiens	18379344	18171	VPS10 domain receptor protein SORCS 2

Fragment-ion (m/z)	674.04	685.10	714.08	716.36	727.04	728.62	729.98	732.55	745.49	747.73	755.64	782.24	785.80
Frac. Inten.(% of TIC)	1.07	1.61	1.25	1.08	0.87	0.89	12.91	2.42	1.40	2.92	0.99	0.93	1.48
Rel. Inten.(% of BP)	2.37	3.57	2.76	2.39	1.93	1.97	28.59	5.36	3.09	6.48	2.19	2.05	3.28
Score	1.00	-0.04	0.50	-0.02	1.00	-0.02	0.50	1.50	-0.03	1.00	-0.02	1.00	-0.03
Ion-type	b^{++}_{14}		y_5-NH_3		y^{+++}_{20}		b_7-H_2O	sty		b_7		b^{++}_{16}	
Delta Da	-0.76		-0.23		0.04		-0.34	-0.14		-0.60		-0.11	
					1.00								
					st								
					0.36								

Fragment-ion (m/z)	838.96	842.39	852.15	853.44	859.06	859.34	861.69	872.08	875.28	878.77	886.40	945.84
Frac. Inten.(% of TIC)	0.85	1.66	0.87	1.25	1.22	3.32	3.10	1.39	8.99	45.16	1.46	0.90
Rel. Inten.(% of BP)	1.87	3.67	1.93	2.78	2.71	7.35	6.86	3.09	19.91	100.00	3.23	2.00
Score	1.00	0.50	0.25	-0.03	1.00	1.00	0.50	-0.03	-0.20	1.00	1.00	1.00
Ion-type	b^{++}_{17}	y_6-NH_3	a_8		y_6	y_6	b_8-H_2O			b_8	y^{++}_{16}	y_7
Delta Da	0.07	0.02	0.78		-0.34	-0.06	0.33			-0.60	-0.54	-0.59
	b_9-H_3PO_4											
	0.55											

Peak 277



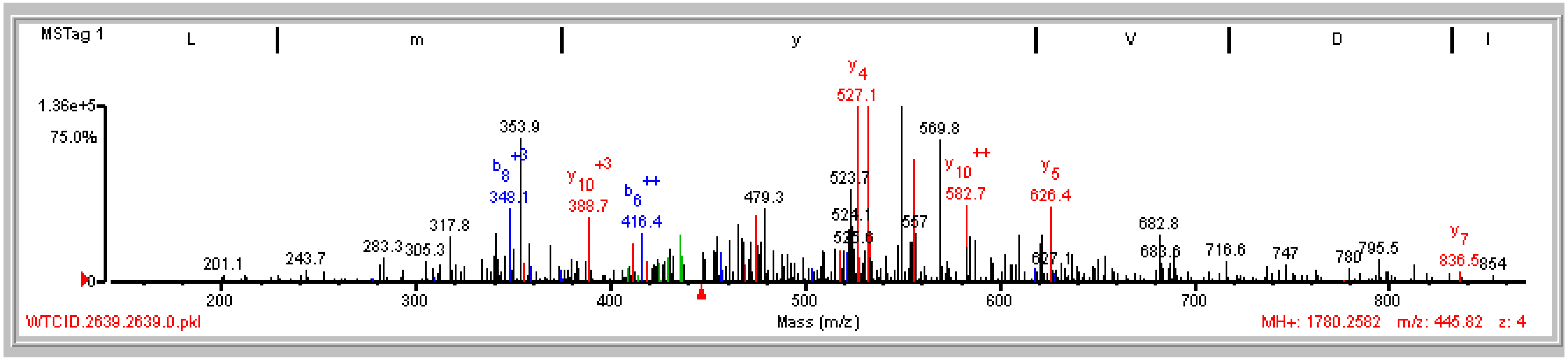


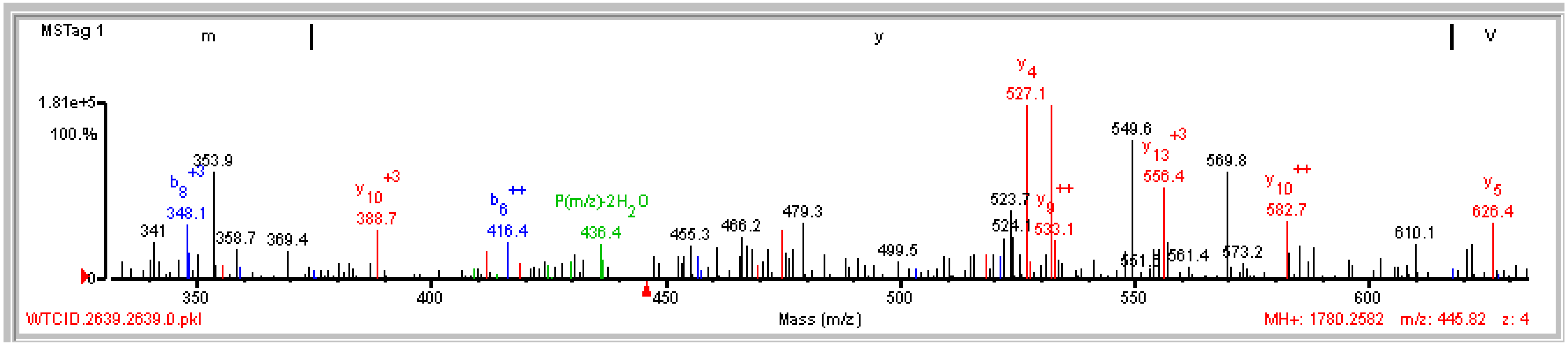
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.80	72.1	8	8/25	M377m Y361y Y376y S369s	(K) H y A/R I S T S\P s/V/A L/S|K P\y m T V|S S E F P A A R (L)	3053.55	256.5069	185.2	188203.3/6.23	Homo sapiens	21071037	7619	BCL-6 interacting corepressor isoform 1

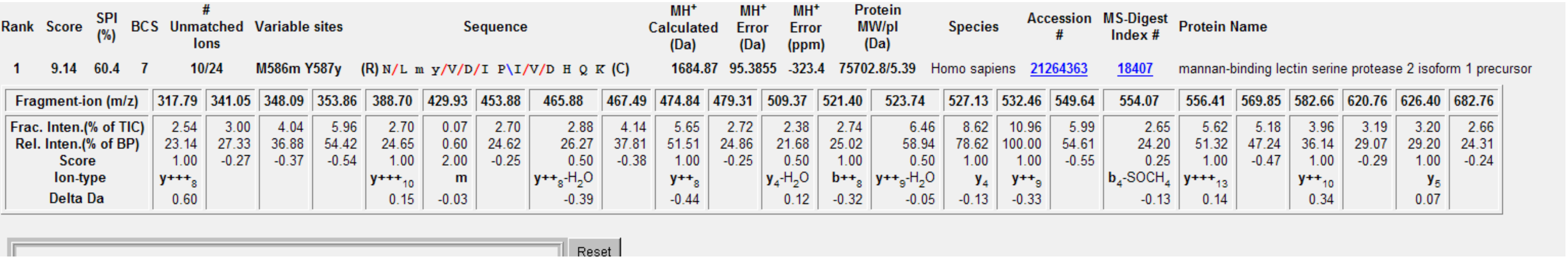
Fragment-ion (m/z)	665.26	810.22	812.26	816.12	840.73	848.02	857.68	864.72	881.53	883.22	891.32	897.22	906.73	925.83
Frac. Inten.(% of TIC)	2.86	3.18	0.12	5.08	5.15	3.54	3.62	3.91	4.33	3.28	5.73	4.15	3.04	2.96
Rel. Inten.(% of BP)	32.89	36.48	1.41	58.35	59.11	40.61	41.52	44.85	49.73	37.62	65.81	47.64	34.91	33.98
Score	-0.33	-0.36	2.00	1.00	1.00	0.50	-0.42	1.00	0.25	1.00	0.50	-0.48	-0.35	-0.34
Ion-type			m	$b{++}_{14}$ $b{+++}_{20}$	$y{++}_{14}$	y_8-NH_3		y_8	a_7	$y{++}_{15}$	b_7-H_2O			
Delta Da			0.14	0.27 0.10	0.35	0.63		0.30	0.13	-0.67	-0.07			

Fragment-ion (m/z)	929.09	944.93	946.59	948.31	954.15	967.97	976.43	979.61	985.64	996.31	1026.12
Frac. Inten.(% of TIC)	5.61	2.95	3.14	3.81	4.70	5.00	2.99	5.08	4.29	8.71	2.79
Rel. Inten.(% of BP)	64.38	33.83	36.03	43.76	53.93	57.41	34.34	58.35	49.30	100.00	32.08
Score	1.00	0.50	0.50	-0.44	1.00	0.25	1.00	0.50	-0.49	1.00	1.00
Ion-type	$b{++}_{16}$	y_9-H_2O	y_9-NH_3		$y{+++}_{25}$	a_8	$y{++}_{17}$	b_8-NH_3		b_8	$y{++}_{18}$
Delta Da	0.66	-0.55	0.13		0.71	-0.46	0.47	0.21		-0.12	0.63

Peak 278





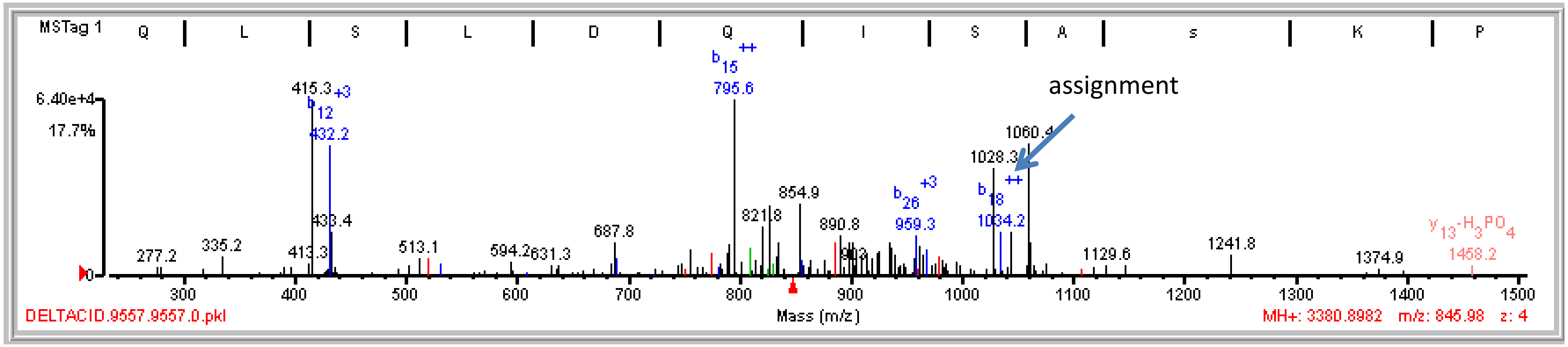


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.14	60.4	7	10/24	M586m Y587y	(R) N/L m y/V/D/I P\I/V/D H Q K (C)	1684.87	95.3855	-323.4	75702.8/5.39	Homo sapiens	21264363	18407	mannan-binding lectin serine protease 2 isoform 1 precursor

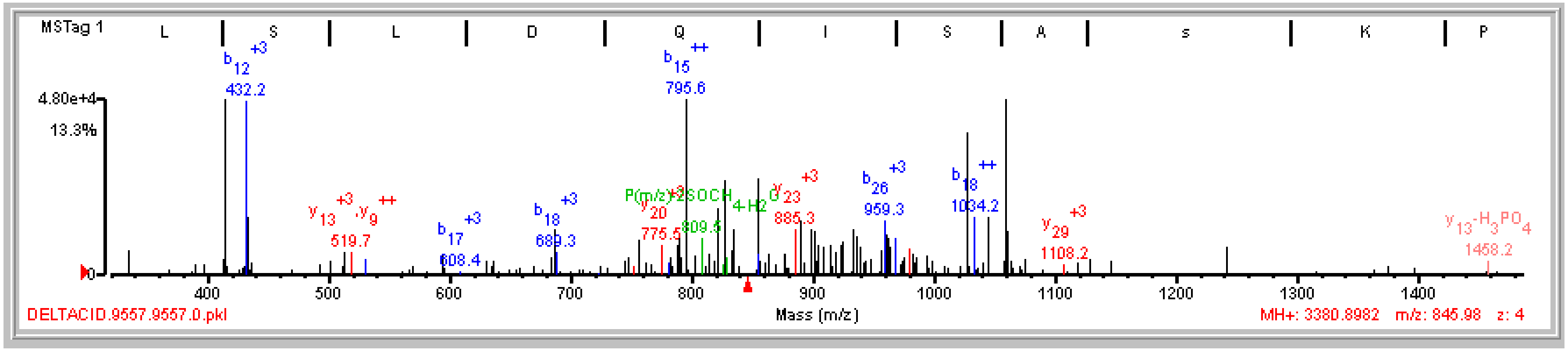
Fragment-ion (m/z)	317.79	341.05	348.09	353.86	388.70	429.93	453.88	465.88	467.49	474.84	479.31
Frac. Inten.(% of TIC)	2.54	3.00	4.04	5.96	2.70	0.07	2.70	2.88	4.14	5.65	2.72
Rel. Inten.(% of BP)	23.14	27.33	36.88	54.42	24.65	0.60	24.62	26.27	37.81	51.51	24.86
Score	1.00	-0.27	-0.37	-0.54	1.00	2.00	-0.25	0.50	-0.38	1.00	-0.25
Ion-type	$y{+++}_{8}$				$y{+++}_{10}$	m		$y{++}_{8}$-H_2O		$y{++}_{8}$	
Delta Da	0.60				0.15	-0.03		-0.39		-0.44	

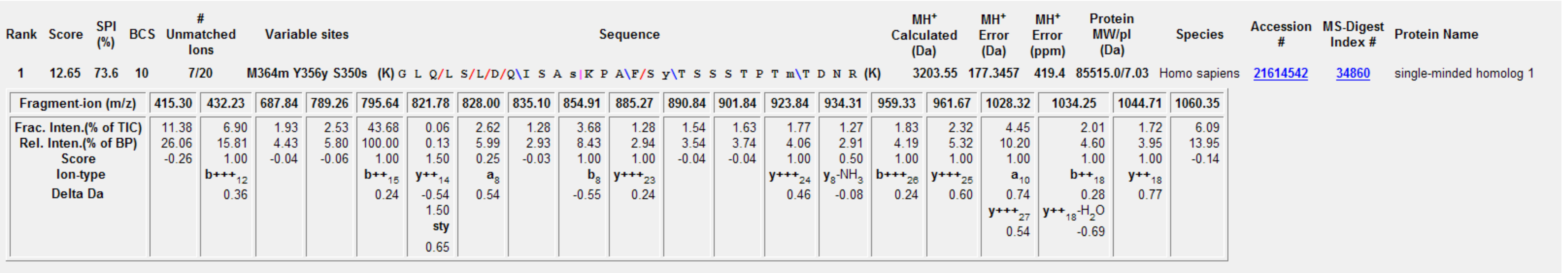
Fragment-ion (m/z)	509.37	521.40	523.74	527.13	532.46	549.64	554.07	556.41	569.85	582.66	620.76	626.40	682.76
Frac. Inten.(% of TIC)	2.38	2.74	6.46	8.62	10.96	5.99	2.65	5.62	5.18	3.96	3.19	3.20	2.66
Rel. Inten.(% of BP)	21.68	25.02	58.94	78.62	100.00	54.61	24.20	51.32	47.24	36.14	29.07	29.20	24.31
Score	0.50	1.00	0.50	1.00	1.00	-0.55	0.25	1.00	-0.47	1.00	-0.29	1.00	-0.24
Ion-type	y_4-H_2O	$b{++}_{8}$	$y{++}_{9}$-H_2O	y_4	$y{++}_{9}$		b_4-$SOCH_4$	$y{+++}_{13}$		$y{++}_{10}$		y_5	
Delta Da	0.12	-0.32	-0.05	-0.13	-0.33		-0.13	0.14		0.34		0.07	

Peak 279



assignment

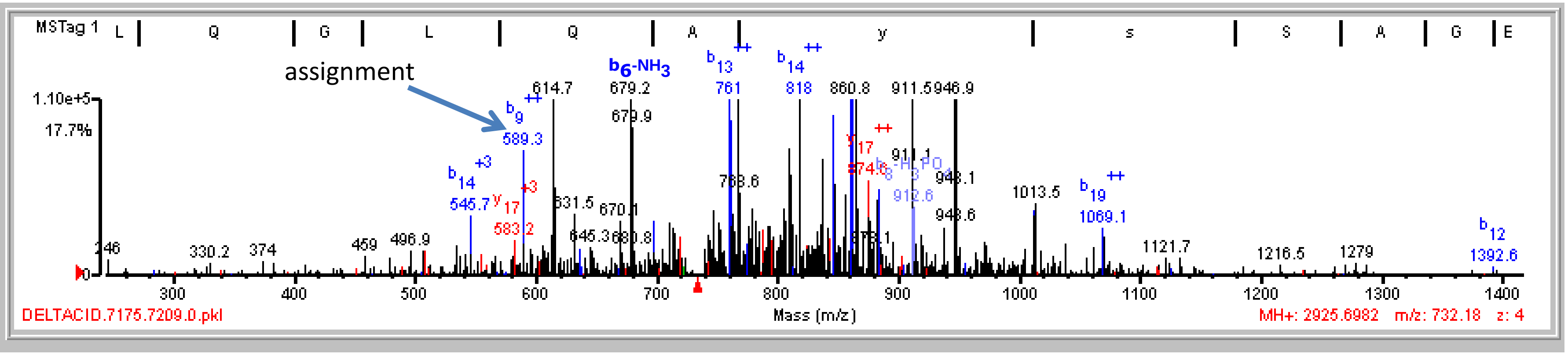


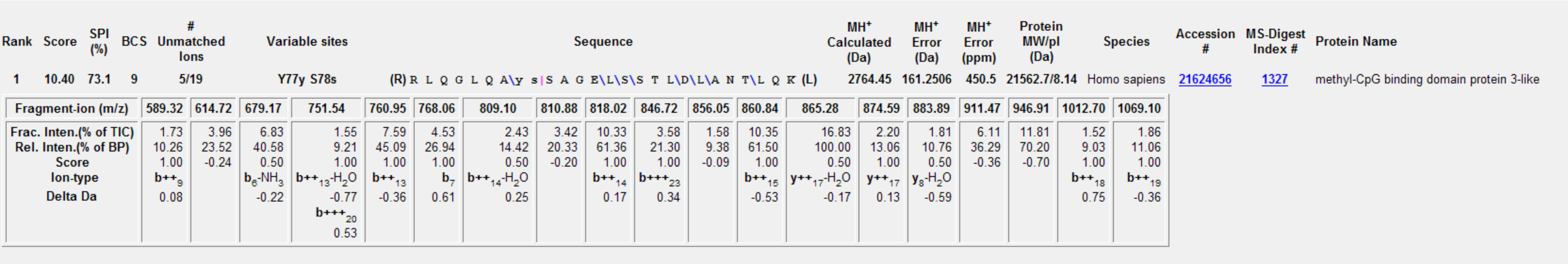


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.65	73.6	10	7/20	M364m Y356y S350s	(K) G L Q/L S/L/D/Q\I S A s|K P A\F/S y\T S S S T P T m\T D N R (K)	3203.55	177.3457	419.4	85515.0/7.03	Homo sapiens	21614542	34860	single-minded homolog 1

Fragment-ion (m/z)	415.30	432.23	687.84	789.26	795.64	821.78	828.00	835.10	854.91	885.27	890.84	901.84	923.84	934.31	959.33	961.67	1028.32	1034.25	1044.71	1060.35
Frac. Inten.(% of TIC)	11.38	6.90	1.93	2.53	43.68	0.06	2.62	1.28	3.68	1.28	1.54	1.63	1.77	1.27	1.83	2.32	4.45	2.01	1.72	6.09
Rel. Inten.(% of BP)	26.06	15.81	4.43	5.80	100.00	0.13	5.99	2.93	8.43	2.94	3.54	3.74	4.06	2.91	4.19	5.32	10.20	4.60	3.95	13.95
Score	-0.26	1.00	-0.04	-0.06	1.00	1.50	0.25	-0.03	1.00	1.00	-0.04	-0.04	1.00	0.50	1.00	1.00	1.00	1.00	1.00	-0.14
Ion-type		$b{+}{+}{+}_{12}$			$b{+}{+}_{15}$	$y{+}{+}_{14}$	a_{8}		b_{8}	$y{+}{+}{+}_{23}$			$y{+}{+}{+}_{24}$	$y_{8}\text{-}NH_{3}$	$b{+}{+}{+}_{26}$	$y{+}{+}{+}_{25}$	a_{10}	$b{+}{+}_{18}$	$y{+}{+}_{18}$	
Delta Da		0.36			0.24	-0.54	0.54		-0.55	0.24			0.46	-0.08	0.24	0.60	0.74	0.28	0.77	
						1.50														
						sty											$y{+}{+}{+}_{27}$	$y{+}{+}_{18}\text{-}H_{2}O$		
						0.65											0.54	-0.69		

Peak 280


assignment

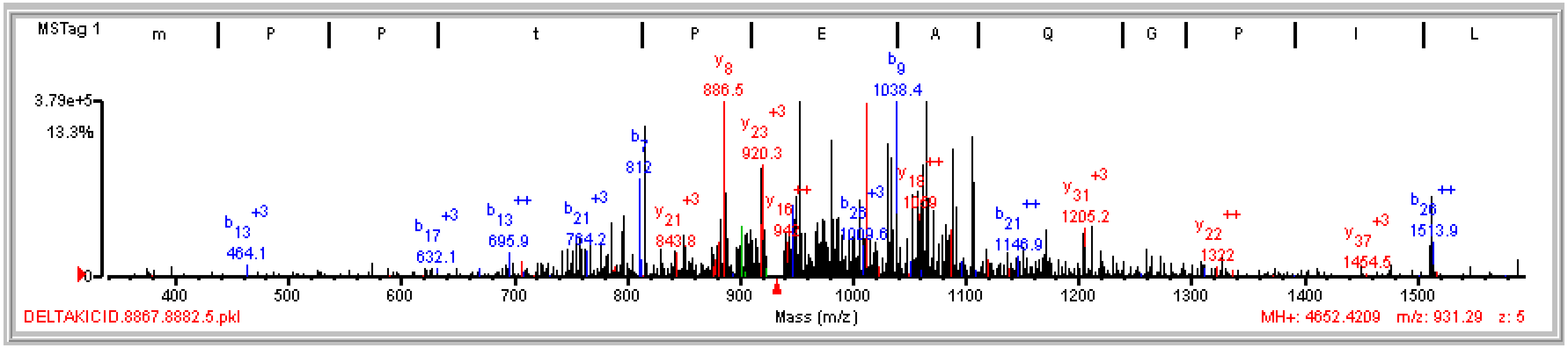


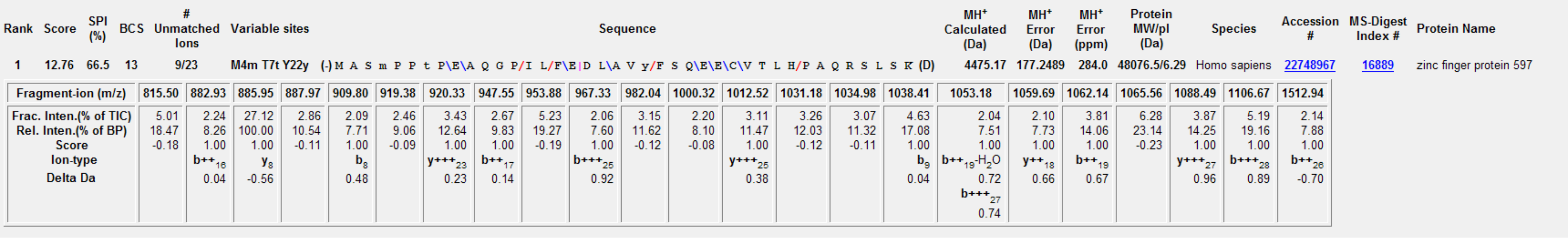
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.40	73.1	9	5/19	Y77y S78s	(R) R L Q G L Q A\y s|S A G E\L\S\S T L\D\L\A N T\L Q K (L)	2764.45	161.2506	450.5	21562.7/8.14	Homo sapiens	21624656	1327	methyl-CpG binding domain protein 3-like

Fragment-ion (m/z)	589.32	614.72	679.17	751.54	760.95	768.06	809.10	810.88	818.02	846.72
Frac. Inten.(% of TIC)	1.73	3.96	6.83	1.55	7.59	4.53	2.43	3.42	10.33	3.58
Rel. Inten.(% of BP)	10.26	23.52	40.58	9.21	45.09	26.94	14.42	20.33	61.36	21.30
Score	1.00	-0.24	0.50	1.00	1.00	1.00	0.50	-0.20	1.00	1.00
Ion-type	b++$_{9}$		b$_{6}$-NH$_{3}$	b++$_{13}$-H$_{2}$O -0.77 b+++$_{20}$	b++$_{13}$	b$_{7}$	b++$_{14}$-H$_{2}$O		b++$_{14}$	b+++$_{23}$
Delta Da	0.08		-0.22	0.53	-0.36	0.61	0.25		0.17	0.34

Fragment-ion (m/z)	856.05	860.84	865.28	874.59	883.89	911.47	946.91	1012.70	1069.10
Frac. Inten.(% of TIC)	1.58	10.35	16.83	2.20	1.81	6.11	11.81	1.52	1.86
Rel. Inten.(% of BP)	9.38	61.50	100.00	13.06	10.76	36.29	70.20	9.03	11.06
Score	-0.09	1.00	0.50	1.00	0.50	-0.36	-0.70	1.00	1.00
Ion-type		b++$_{15}$	y++$_{17}$-H$_{2}$O	y++$_{17}$	y$_{8}$-H$_{2}$O			b++$_{18}$	b++$_{19}$
Delta Da		-0.53	-0.17	0.13	-0.59			0.75	-0.36

Peak 281



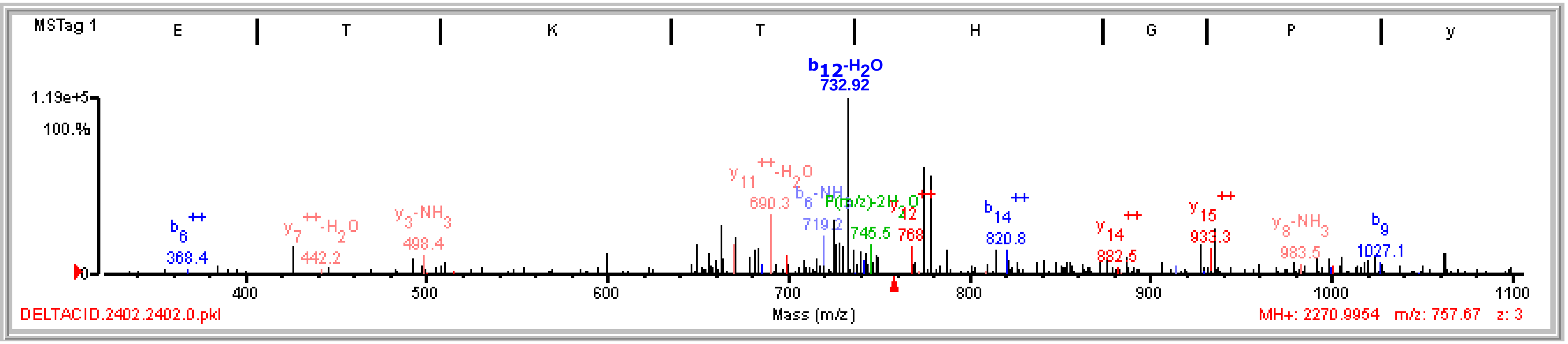


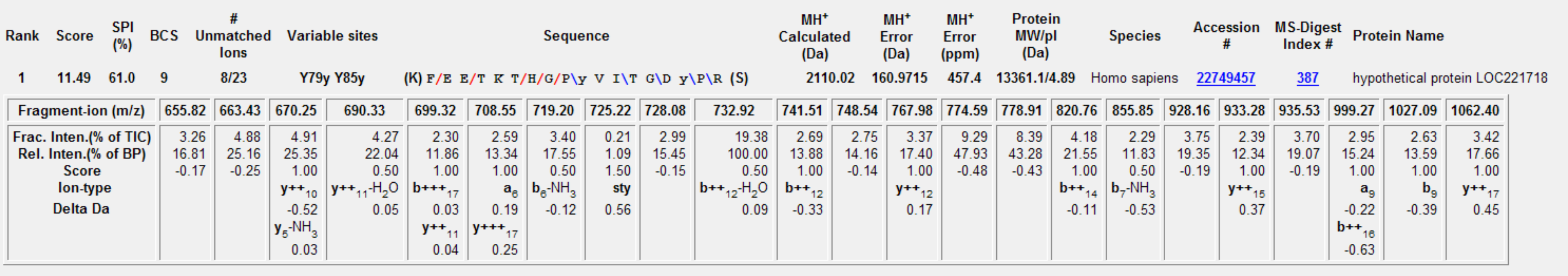
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.76	66.5	13	9/23	M4m T7t Y22y	(-) M A S m P P t P\E\A Q G P/I L/F\E|D L\A V y/F S Q\E\E\C\V T L H/P A Q R S L S K (D)	4475.17	177.2489	284.0	48076.5/6.29	Homo sapiens	22748967	16889	zinc finger protein 597

Fragment-ion (m/z)	815.50	882.93	885.95	887.97	909.80	919.38	920.33	947.55	953.88	967.33	982.04	1000.32
Frac. Inten.(% of TIC)	5.01	2.24	27.12	2.86	2.09	2.46	3.43	2.67	5.23	2.06	3.15	2.20
Rel. Inten.(% of BP)	18.47	8.26	100.00	10.54	7.71	9.06	12.64	9.83	19.27	7.60	11.62	8.10
Score	-0.18	1.00	1.00	-0.11	1.00	-0.09	1.00	1.00	-0.19	1.00	-0.12	-0.08
Ion-type		b++_{16}	y_{8}		b_{8}		y+++_{23}	b++_{17}		b+++_{25}		
Delta Da		0.04	-0.56		0.48		0.23	0.14		0.92		

Fragment-ion (m/z)	1012.52	1031.18	1034.98	1038.41	1053.18	1059.69	1062.14	1065.56	1088.49	1106.67	1512.94
Frac. Inten.(% of TIC)	3.11	3.26	3.07	4.63	2.04	2.10	3.81	6.28	3.87	5.19	2.14
Rel. Inten.(% of BP)	11.47	12.03	11.32	17.08	7.51	7.73	14.06	23.14	14.25	19.16	7.88
Score	1.00	-0.12	-0.11	1.00	1.00	1.00	1.00	-0.23	1.00	1.00	1.00
Ion-type	y+++_{25}			b_{9}	$\text{b++}_{19}\text{-H}_2\text{O}$ b+++_{27}	y++_{18}	b++_{19}		y+++_{27}	b+++_{28}	b++_{26}
Delta Da	0.38			0.04	0.72 0.74	0.66	0.67		0.96	0.89	-0.70

Peak 282

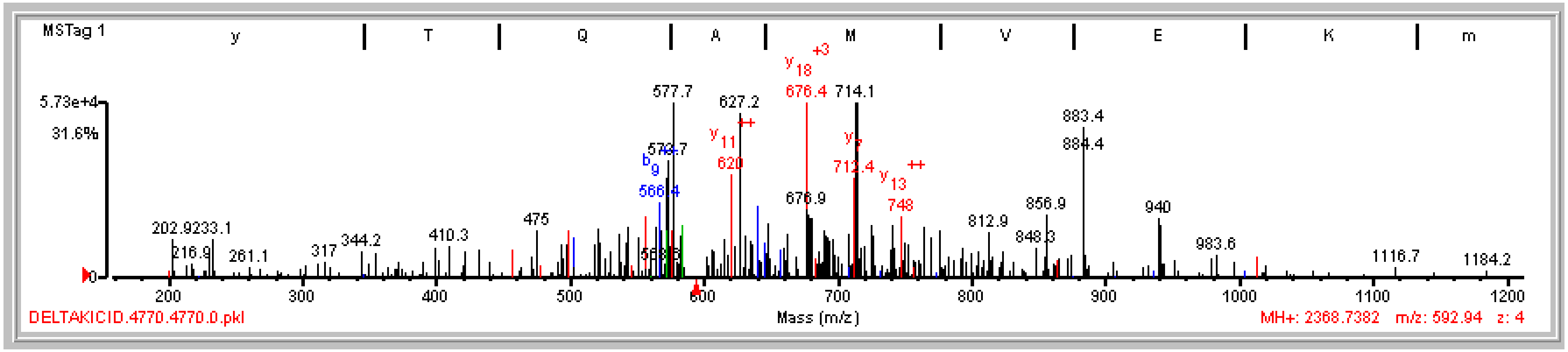


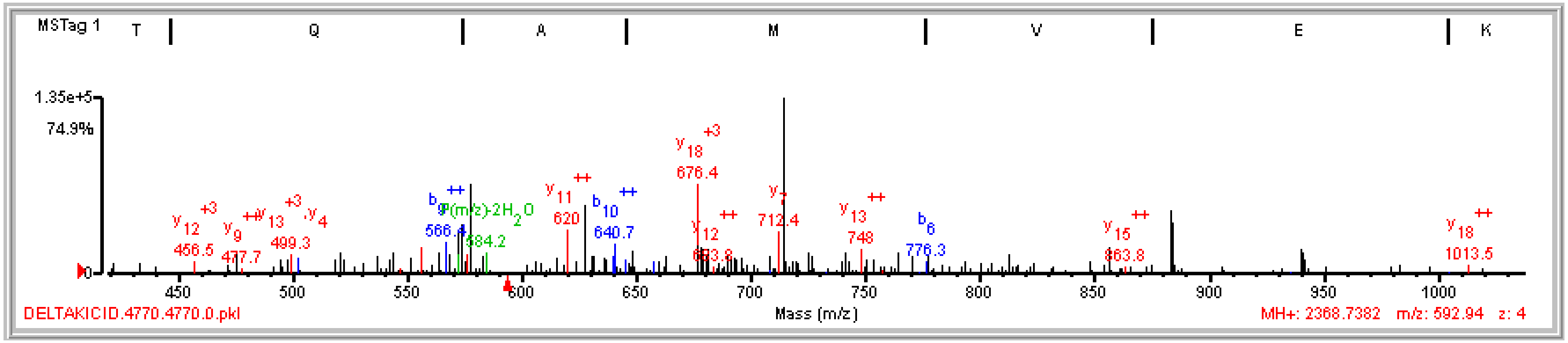


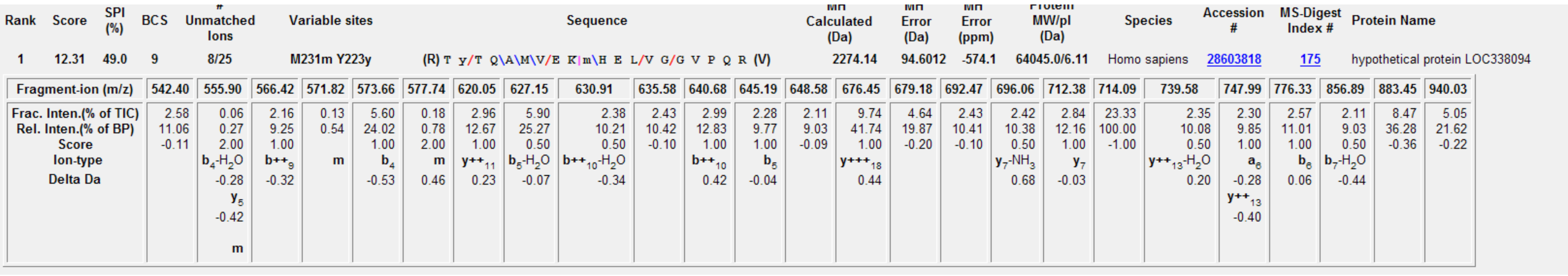
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.49	61.0	9	8/23	Y79y Y85y	(K) F/E E/T K T/H/G/P\y V I\T G\D y\P\R (S)	2110.02	160.9715	457.4	13361.1/4.89	Homo sapiens	22749457	387	hypothetical protein LOC221718

Fragment-ion (m/z)	655.82	663.43	670.25	690.33	699.32	708.55	719.20	725.22	728.08	732.92	741.51	748.54	767.98	774.59	778.91	820.76	855.85	928.16	933.28	935.53	999.27	1027.09	1062.40
Frac. Inten.(% of TIC)	3.26	4.88	4.91	4.27	2.30	2.59	3.40	0.21	2.99	19.38	2.69	2.75	3.37	9.29	8.39	4.18	2.29	3.75	2.39	3.70	2.95	2.63	3.42
Rel. Inten.(% of BP)	16.81	25.16	25.35	22.04	11.86	13.34	17.55	1.09	15.45	100.00	13.88	14.16	17.40	47.93	43.28	21.55	11.83	19.35	12.34	19.07	15.24	13.59	17.66
Score	-0.17	-0.25	1.00	0.50	1.00	1.00	0.50	1.50	-0.15	0.50	1.00	-0.14	1.00	-0.48	-0.43	1.00	0.50	-0.19	1.00	-0.19	1.00	1.00	1.00
Ion-type			y++$_{10}$	y++$_{11}$-H$_2$O	b+++$_{17}$	a$_6$	b$_6$-NH$_3$	sty		b++$_{12}$-H$_2$O	b++$_{12}$		y++$_{12}$			b++$_{14}$	b$_7$-NH$_3$		y++$_{15}$		a$_9$	b$_9$	y++$_{17}$
Delta Da			-0.52	0.05	0.03	0.19	-0.12	0.56		0.09	-0.33		0.17			-0.11	-0.53		0.37		-0.22	-0.39	0.45
			y$_5$-NH$_3$		y++$_{11}$	y+++$_{17}$															b++$_{16}$		
			0.03		0.04	0.25															-0.63		

Peak 283





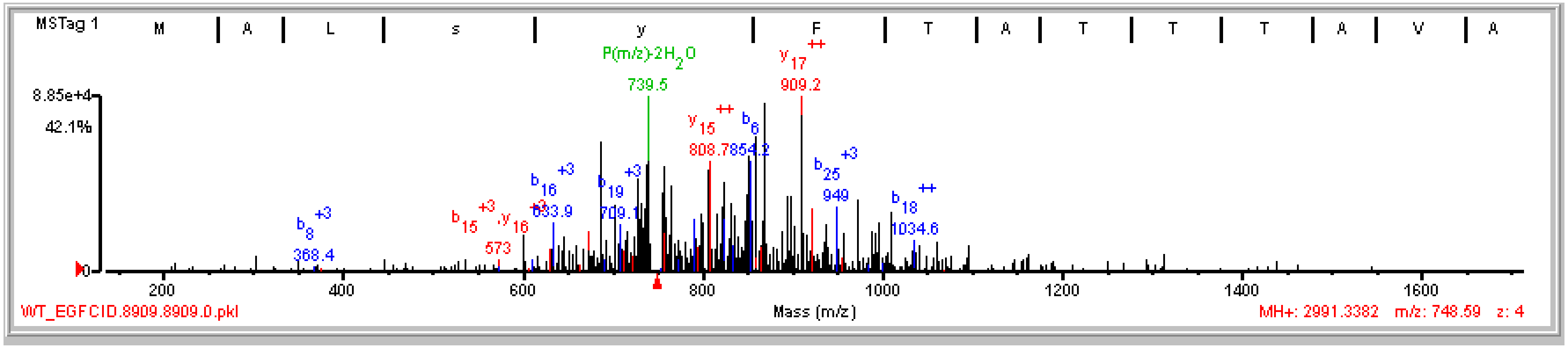


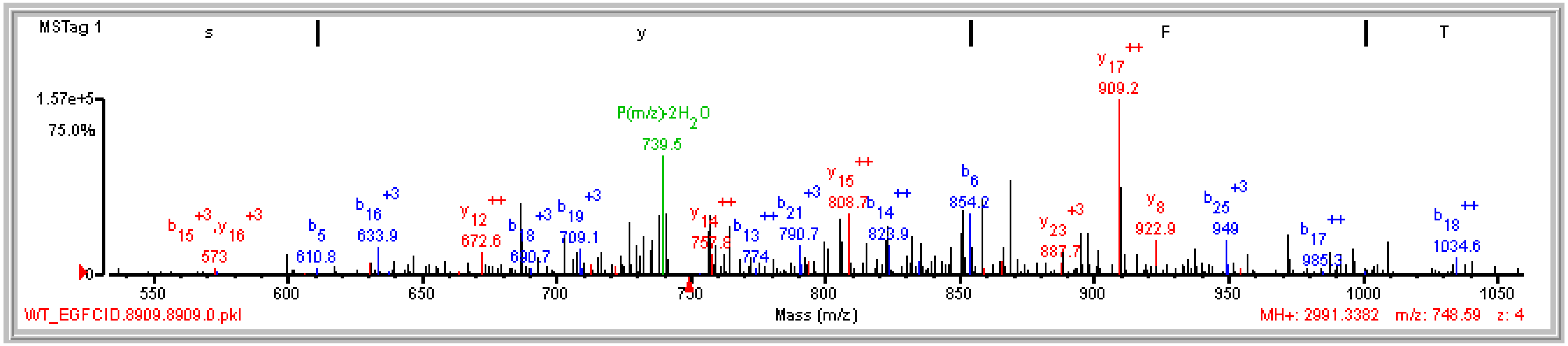
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH Calculated (Da)	MH Error (Da)	MH Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.31	49.0	9	8/25	M231m Y223y	(R) T y/T Q\A\M\V/E K|m\H E L/V G/G V P Q R (V)	2274.14	94.6012	-574.1	64045.0/6.11	Homo sapiens	28603818	175	hypothetical protein LOC338094

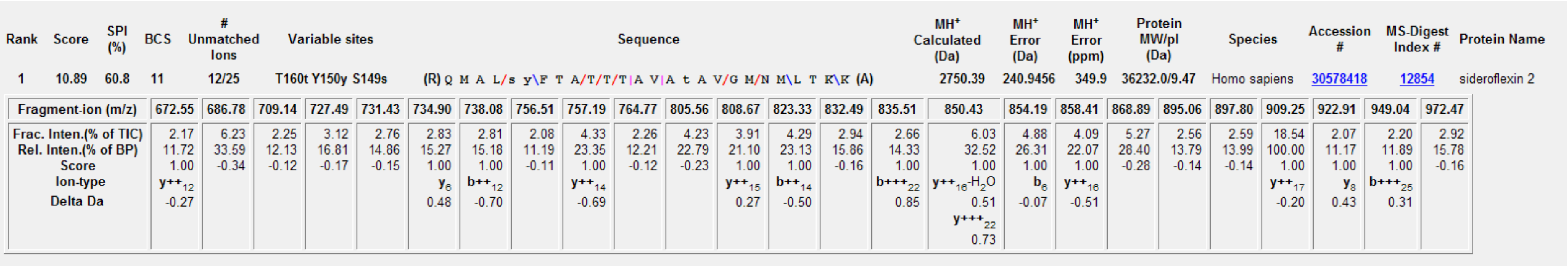
Fragment-ion (m/z)	542.40	555.90	566.42	571.82	573.66	577.74	620.05	627.15	630.91	635.58	640.68	645.19	648.58
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	2.58 11.06 -0.11	0.06 0.27 2.00 b_4-H_2O -0.28 y_5 -0.42 m	2.16 9.25 1.00 $b{+}{+}_9$ -0.32	0.13 0.54 m	5.60 24.02 1.00 b_4 -0.53	0.18 0.78 2.00 m 0.46	2.96 12.67 1.00 $y{+}{+}_{11}$ 0.23	5.90 25.27 0.50 b_5-H_2O -0.07	2.38 10.21 0.50 $b{+}{+}_{10}$-H_2O -0.34	2.43 10.42 -0.10	2.99 12.83 1.00 $b{+}{+}_{10}$ 0.42	2.28 9.77 1.00 b_5 -0.04	2.11 9.03 -0.09

Fragment-ion (m/z)	676.45	679.18	692.47	696.06	712.38	714.09	739.58	747.99	776.33	856.89	883.45	940.03
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	9.74 41.74 1.00 $y{+}{+}{+}_{18}$ 0.44	4.64 19.87 -0.20	2.43 10.41 -0.10	2.42 10.38 0.50 y_7-NH_3 0.68	2.84 12.16 1.00 y_7 -0.03	23.33 100.00 -1.00	2.35 10.08 0.50 $y{+}{+}_{13}$-H_2O 0.20	2.30 9.85 1.00 a_6 -0.28 $y{+}{+}_{13}$ -0.40	2.57 11.01 1.00 b_6 0.06	2.11 9.03 0.50 b_7-H_2O -0.44	8.47 36.28 -0.36	5.05 21.62 -0.22

Peak 284





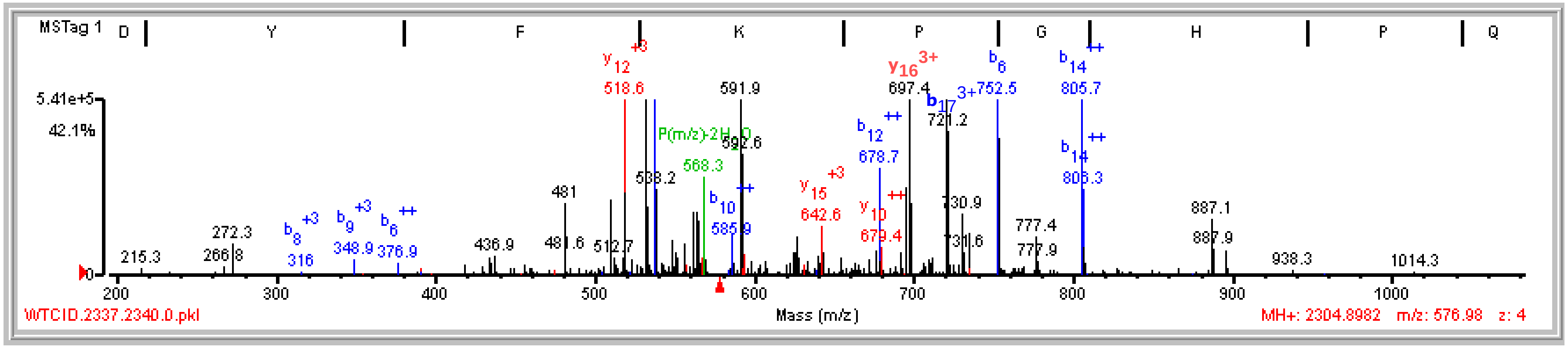


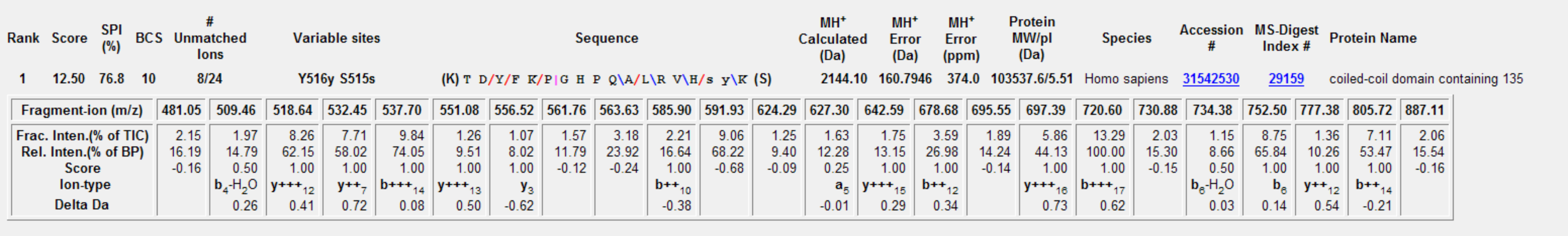
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.89	60.8	11	12/25	T160t Y150y S149s	(R) Q M A L/s y\F T A/T/T/T|A V|A t A V/G M/N M\L T K\K (A)	2750.39	240.9456	349.9	36232.0/9.47	Homo sapiens	30578418	12854	sideroflexin 2

Fragment-ion (m/z)	672.55	686.78	709.14	727.49	731.43	734.90	738.08	756.51	757.19	764.77	805.56	808.67
Frac. Inten.(% of TIC)	2.17	6.23	2.25	3.12	2.76	2.83	2.81	2.08	4.33	2.26	4.23	3.91
Rel. Inten.(% of BP)	11.72	33.59	12.13	16.81	14.86	15.27	15.18	11.19	23.35	12.21	22.79	21.10
Score	1.00	-0.34	-0.12	-0.17	-0.15	1.00	1.00	-0.11	1.00	-0.12	-0.23	1.00
Ion-type	y^{++}_{12}					y_6	b^{++}_{12}		y^{++}_{14}			y^{++}_{15}
Delta Da	-0.27					0.48	-0.70		-0.69			0.27

Fragment-ion (m/z)	823.33	832.49	835.51	850.43	854.19	858.41	868.89	895.06	897.80	909.25	922.91	949.04	972.47
Frac. Inten.(% of TIC)	4.29	2.94	2.66	6.03	4.88	4.09	5.27	2.56	2.59	18.54	2.07	2.20	2.92
Rel. Inten.(% of BP)	23.13	15.86	14.33	32.52	26.31	22.07	28.40	13.79	13.99	100.00	11.17	11.89	15.78
Score	1.00	-0.16	1.00	1.00	1.00	1.00	-0.28	-0.14	-0.14	1.00	1.00	1.00	-0.16
Ion-type	b^{++}_{14}		b^{+++}_{22}	y^{++}_{16}-H_2O y^{+++}_{22}	b_6	y^{++}_{16}				y^{++}_{17}	y_8	b^{+++}_{25}	
Delta Da	-0.50		0.85	0.51 0.73	-0.07	-0.51				-0.20	0.43	0.31	

Peak 285





Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.50	76.8	10	8/24	Y516y S515s	(K) T D/Y/F K/P|G H P Q\A/L\R V\H/s y\K (S)	2144.10	160.7946	374.0	103537.6/5.51	Homo sapiens	31542530	29159	coiled-coil domain containing 135

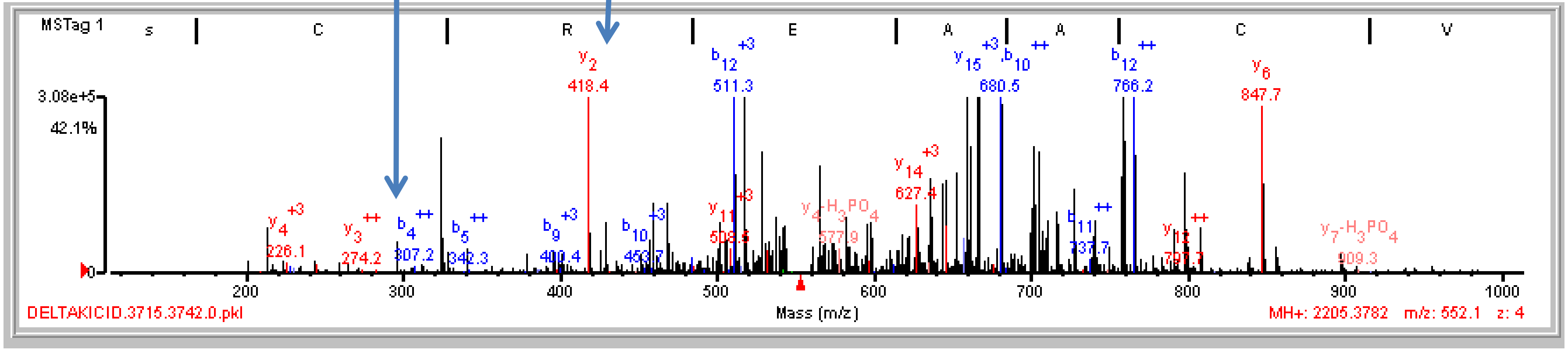
Fragment-ion (m/z)	481.05	509.46	518.64	532.45	537.70	551.08	556.52	561.76	563.63	585.90	591.93	624.29
Frac. Inten.(% of TIC)	2.15	1.97	8.26	7.71	9.84	1.26	1.07	1.57	3.18	2.21	9.06	1.25
Rel. Inten.(% of BP)	16.19	14.79	62.15	58.02	74.05	9.51	8.02	11.79	23.92	16.64	68.22	9.40
Score	-0.16	0.50	1.00	1.00	1.00	1.00	1.00	-0.12	-0.24	1.00	-0.68	-0.09
Ion-type		b_4-H_2O	y+++$_{12}$	y++$_7$	b+++$_{14}$	y+++$_{13}$	y_3			b++$_{10}$		
Delta Da		0.26	0.41	0.72	0.08	0.50	-0.62			-0.38		

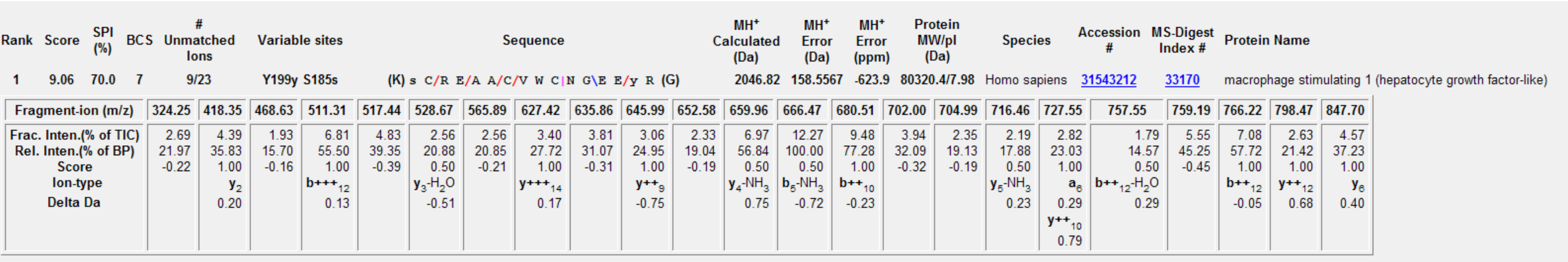
Fragment-ion (m/z)	627.30	642.59	678.68	695.55	697.39	720.60	730.88	734.38	752.50	777.38	805.72	887.11
Frac. Inten.(% of TIC)	1.63	1.75	3.59	1.89	5.86	13.29	2.03	1.15	8.75	1.36	7.11	2.06
Rel. Inten.(% of BP)	12.28	13.15	26.98	14.24	44.13	100.00	15.30	8.66	65.84	10.26	53.47	15.54
Score	0.25	1.00	1.00	-0.14	1.00	1.00	-0.15	0.50	1.00	1.00	1.00	-0.16
Ion-type	a_5	y+++$_{15}$	b++$_{12}$		y+++$_{16}$	b+++$_{17}$		b_6-H_2O	b_6	y++$_{12}$	b++$_{14}$	
Delta Da	-0.01	0.29	0.34		0.73	0.62		0.03	0.14	0.54	-0.21	

Peak 286

Ions that verify assignment

assignment



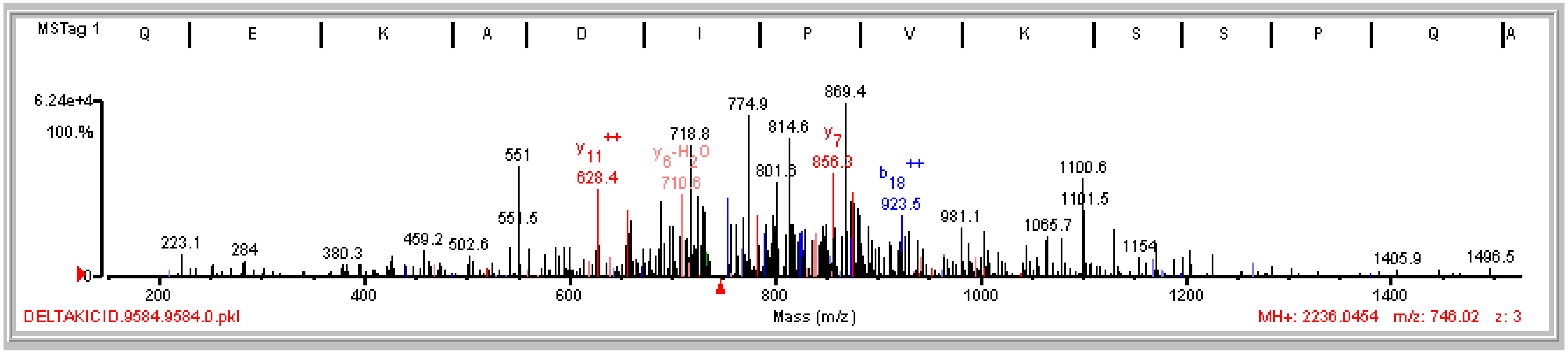


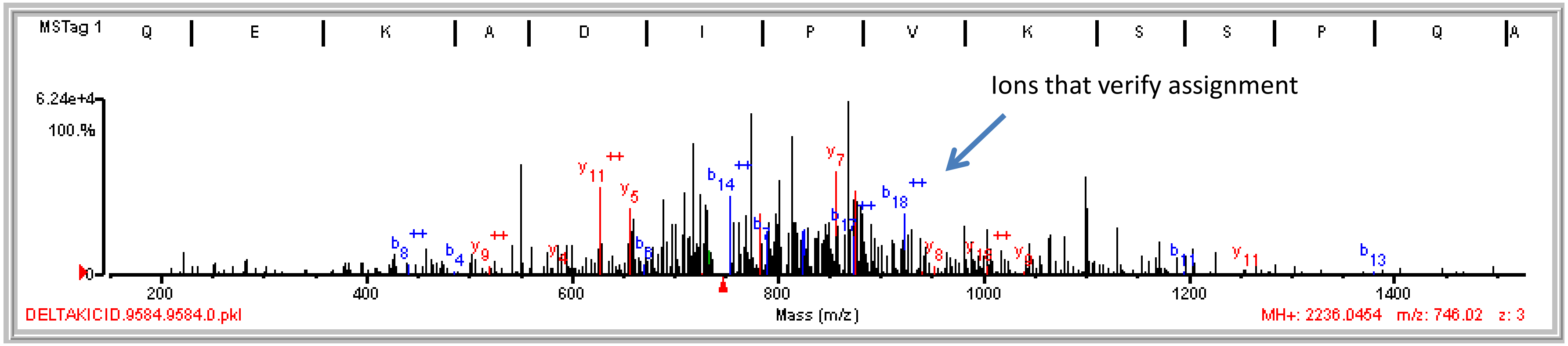
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.06	70.0	7	9/23	Y199y S185s	(K) s C/R E/A A/C/V W C|N G\E E/y R (G)	2046.82	158.5567	-623.9	80320.4/7.98	Homo sapiens	31543212	33170	macrophage stimulating 1 (hepatocyte growth factor-like)

Fragment-ion (m/z)	324.25	418.35	468.63	511.31	517.44	528.67	565.89	627.42	635.86	645.99	652.58
Frac. Inten.(% of TIC)	2.69	4.39	1.93	6.81	4.83	2.56	2.56	3.40	3.81	3.06	2.33
Rel. Inten.(% of BP)	21.97	35.83	15.70	55.50	39.35	20.88	20.85	27.72	31.07	24.95	19.04
Score	-0.22	1.00	-0.16	1.00	-0.39	0.50	-0.21	1.00	-0.31	1.00	-0.19
Ion-type		y_2		$b{+}{+}{+}_{12}$		y_3-H_2O		$y{+}{+}{+}_{14}$		$y{+}{+}_9$	
Delta Da		0.20		0.13		-0.51		0.17		-0.75	

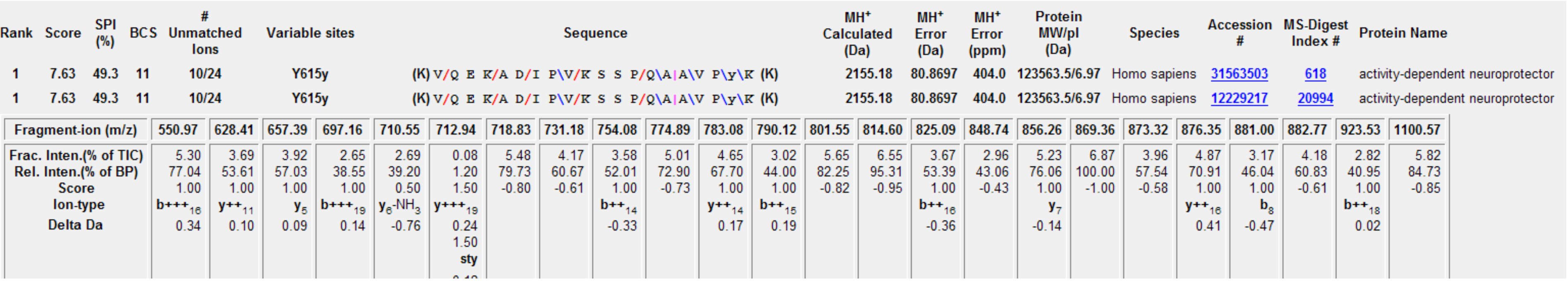
Fragment-ion (m/z)	659.96	666.47	680.51	702.00	704.99	716.46	727.55	757.55	759.19	766.22	798.47	847.70
Frac. Inten.(% of TIC)	6.97	12.27	9.48	3.94	2.35	2.19	2.82	1.79	5.55	7.08	2.63	4.57
Rel. Inten.(% of BP)	56.84	100.00	77.28	32.09	19.13	17.88	23.03	14.57	45.25	57.72	21.42	37.23
Score	0.50	0.50	1.00	-0.32	-0.19	0.50	1.00	0.50	-0.45	1.00	1.00	1.00
Ion-type	y_4-NH_3	b_5-NH_3	$b{+}{+}_{10}$			y_5-NH_3	a_6 $y{+}{+}_{10}$	$b{+}{+}_{12}$-H_2O		$b{+}{+}_{12}$	$y{+}{+}_{12}$	y_6
Delta Da	0.75	-0.72	-0.23			0.23	0.29 0.79	0.29		-0.05	0.68	0.40

Peak 287





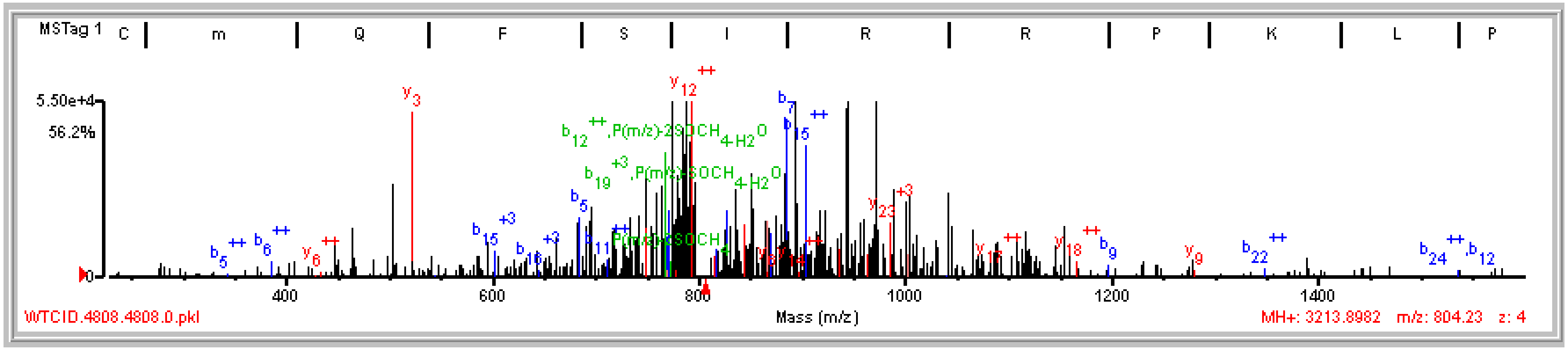
Ions that verify assignment

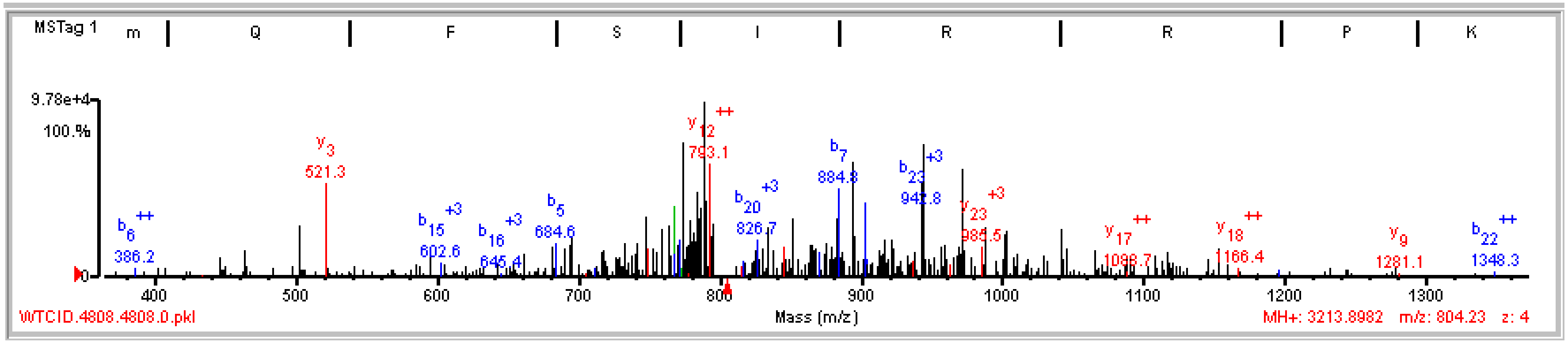


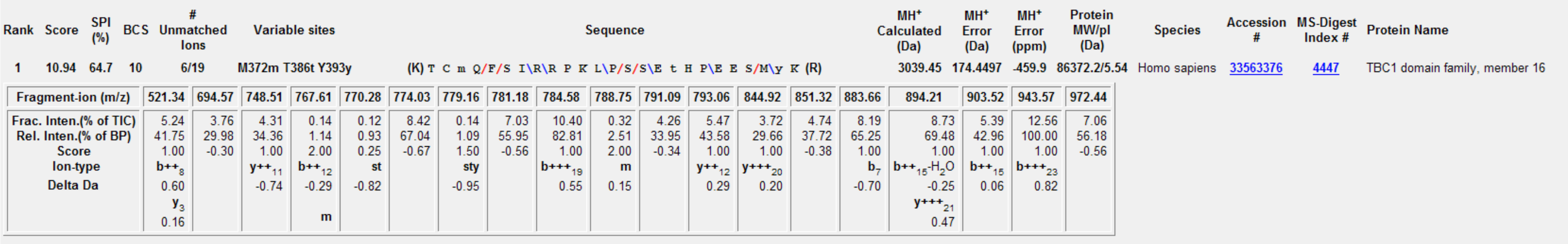
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.63	49.3	11	10/24	Y615y	(K) V/Q E K/A D/I P\V/K S S P/Q\A|A\V P\y\K (K)	2155.18	80.8697	404.0	123563.5/6.97	Homo sapiens	31563503	618	activity-dependent neuroprotector
1	7.63	49.3	11	10/24	Y615y	(K) V/Q E K/A D/I P\V/K S S P/Q\A|A\V P\y\K (K)	2155.18	80.8697	404.0	123563.5/6.97	Homo sapiens	12229217	20994	activity-dependent neuroprotector

Fragment-ion (m/z)	550.97	628.41	657.39	697.16	710.55	712.94	718.83	731.18	754.08	774.89	783.08	790.12	801.55	814.60	825.09	848.74	856.26	869.36	873.32	876.35	881.00	882.77	923.53	1100.57
Frac. Inten.(% of TIC)	5.30	3.69	3.92	2.65	2.69	0.08	5.48	4.17	3.58	5.01	4.65	3.02	5.65	6.55	3.67	2.96	5.23	6.87	3.96	4.87	3.17	4.18	2.82	5.82
Rel. Inten.(% of BP)	77.04	53.61	57.03	38.55	39.20	1.20	79.73	60.67	52.01	72.90	67.70	44.00	82.25	95.31	53.39	43.06	76.06	100.00	57.54	70.91	46.04	60.83	40.95	84.73
Score	1.00	1.00	1.00	1.00	0.50	1.50	-0.80	-0.61	1.00	-0.73	1.00	1.00	-0.82	-0.95	1.00	-0.43	1.00	-1.00	-0.58	1.00	1.00	-0.61	1.00	-0.85
Ion-type	$b{+}{+}{+}_{16}$	$y{+}{+}_{11}$	y_5	$b{+}{+}{+}_{19}$	y_6-NH_3	$y{+}{+}{+}_{19}$			$b{+}{+}_{14}$		$y{+}{+}_{14}$	$b{+}{+}_{15}$			$b{+}{+}_{16}$		y_7			$y{+}{+}_{16}$	b_8		$b{+}{+}_{18}$	
Delta Da	0.34	0.10	0.09	0.14	-0.76	0.24 1.50 sty			-0.33		0.17	0.19			-0.36		-0.14			0.41	-0.47		0.02	

Peak 289



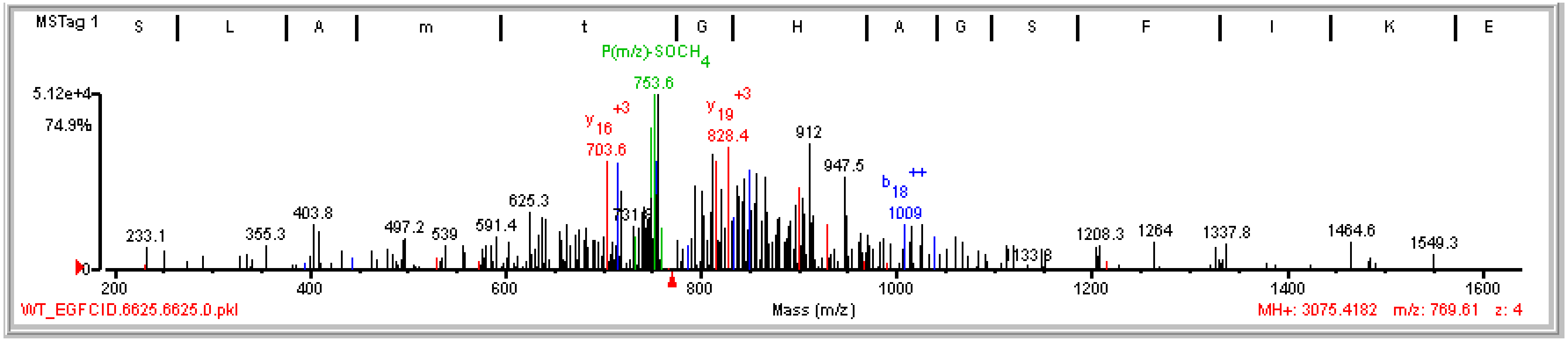


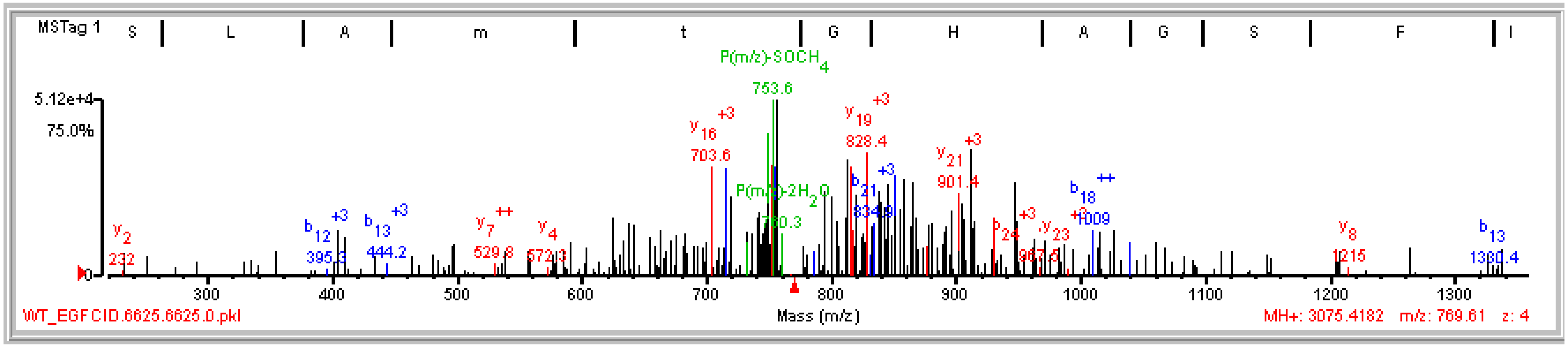


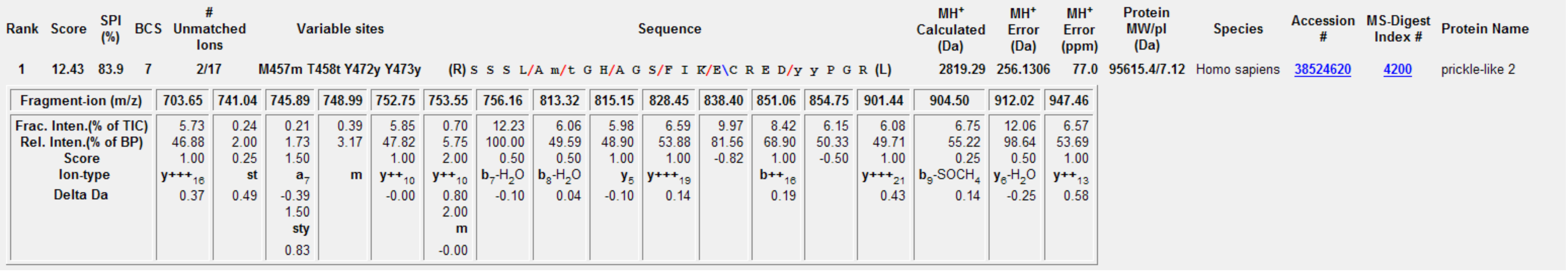
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.94	64.7	10	6/19	M372m T386t Y393y	(K) T C m Q/F/S I\R\R P K L\P/S/S\E t H P\E E S/M\y K (R)	3039.45	174.4497	-459.9	86372.2/5.54	Homo sapiens	33563376	4447	TBC1 domain family, member 16

Fragment-ion (m/z)	521.34	694.57	748.51	767.61	770.28	774.03	779.16	781.18	784.58	788.75	791.09	793.06	844.92	851.32	883.66	894.21	903.52	943.57	972.44
Frac. Inten.(% of TIC)	5.24	3.76	4.31	0.14	0.12	8.42	0.14	7.03	10.40	0.32	4.26	5.47	3.72	4.74	8.19	8.73	5.39	12.56	7.06
Rel. Inten.(% of BP)	41.75	29.98	34.36	1.14	0.93	67.04	1.09	55.95	82.81	2.51	33.95	43.58	29.66	37.72	65.25	69.48	42.96	100.00	56.18
Score	1.00	-0.30	1.00	2.00	0.25	-0.67	1.50	-0.56	1.00	2.00	-0.34	1.00	1.00	-0.38	1.00	1.00	1.00	1.00	-0.56
Ion-type	b++$_{8}$ y$_{3}$		y++$_{11}$	b++$_{12}$ m	st		sty		b+++$_{19}$	m		y++$_{12}$	y+++$_{20}$		b$_{7}$	b++$_{15}$-H_2O y+++$_{21}$	b++$_{15}$	b+++$_{23}$	
Delta Da	0.60 0.16		-0.74	-0.29	-0.82		-0.95		0.55	0.15		0.29	0.20		-0.70	-0.25 0.47	0.06	0.82	

Peak 290





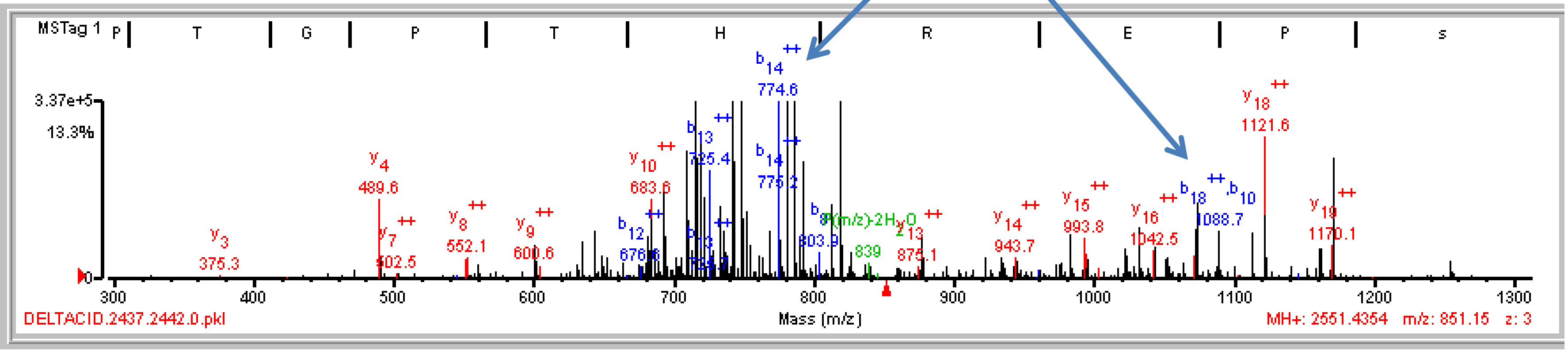


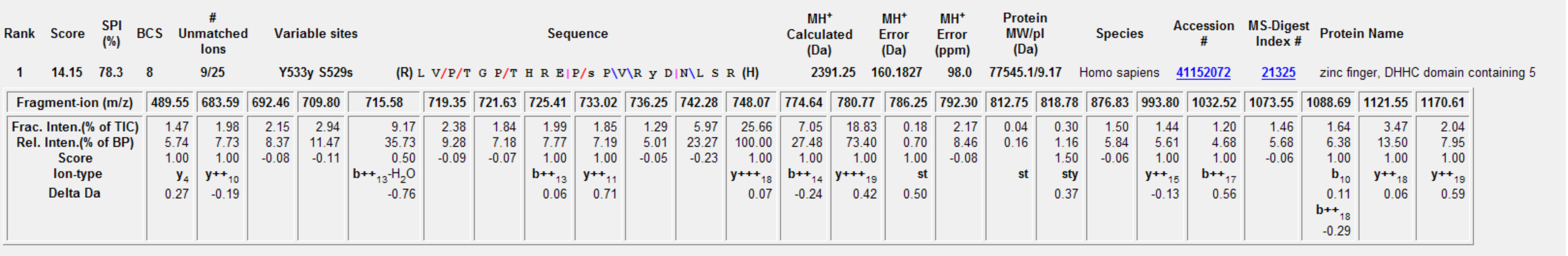
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.43	83.9	7	2/17	M457m T458t Y472y Y473y	(R) S S S L/A m/t G H/A G S/F I K/E\C R E D/y y P G R (L)	2819.29	256.1306	77.0	95615.4/7.12	Homo sapiens	38524620	4200	prickle-like 2

Fragment-ion (m/z)	703.65	741.04	745.89	748.99	752.75	753.55	756.16	813.32	815.15	828.45	838.40	851.06	854.75	901.44	904.50	912.02	947.46
Frac. Inten.(% of TIC)	5.73	0.24	0.21	0.39	5.85	0.70	12.23	6.06	5.98	6.59	9.97	8.42	6.15	6.08	6.75	12.06	6.57
Rel. Inten.(% of BP)	46.88	2.00	1.73	3.17	47.82	5.75	100.00	49.59	48.90	53.88	81.56	68.90	50.33	49.71	55.22	98.64	53.69
Score	1.00	0.25	1.50		1.00	2.00	0.50	0.50	1.00	1.00	-0.82	1.00	-0.50	1.00	0.25	0.50	1.00
Ion-type	$y+++_{16}$	st	a_7	m	$y++_{10}$	$y++_{10}$	b_7-H_2O	b_8-H_2O	y_5	$y+++_{19}$		$b++_{16}$		$y+++_{21}$	b_9-$SOCH_4$	y_6-H_2O	$y++_{13}$
Delta Da	0.37	0.49	-0.39		-0.00	0.80	-0.10	0.04	-0.10	0.14		0.19		0.43	0.14	-0.25	0.58
			1.50			2.00											
			sty			m											
			0.83			-0.00											

Peak 291

Ions that verify assignment



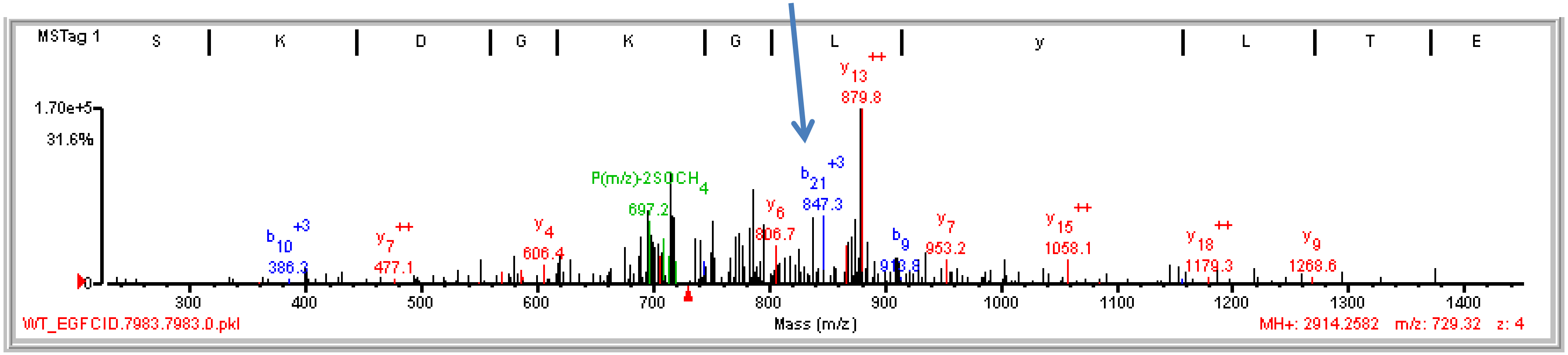


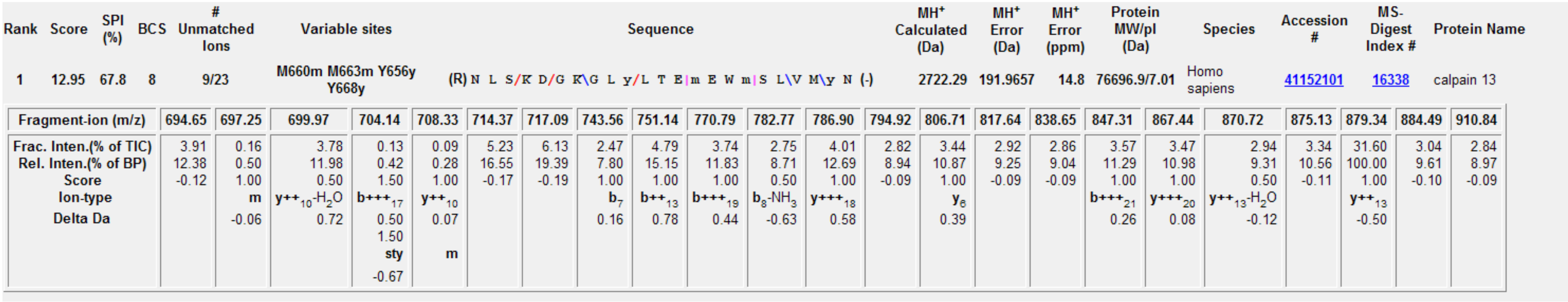
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.15	78.3	8	9/25	Y533y S529s	(R) L V/P/T G P/T H R E|P/s P\V\R y D|N\L S R (H)	2391.25	160.1827	98.0	77545.1/9.17	Homo sapiens	41152072	21325	zinc finger, DHHC domain containing 5

Fragment-ion (m/z)	489.55	683.59	692.46	709.80	715.58	719.35	721.63	725.41	733.02	736.25	742.28	748.07
Frac. Inten.(% of TIC)	1.47	1.98	2.15	2.94	9.17	2.38	1.84	1.99	1.85	1.29	5.97	25.66
Rel. Inten.(% of BP)	5.74	7.73	8.37	11.47	35.73	9.28	7.18	7.77	7.19	5.01	23.27	100.00
Score	1.00	1.00	-0.08	-0.11	0.50	-0.09	-0.07	1.00	1.00	-0.05	-0.23	1.00
Ion-type	y_4	$y{+}{+}_{10}$			$b{+}{+}_{13}$-H_2O			$b{+}{+}_{13}$	$y{+}{+}_{11}$			$y{+}{+}{+}_{18}$
Delta Da	0.27	-0.19			-0.76			0.06	0.71			0.07

Fragment-ion (m/z)	774.64	780.77	786.25	792.30	812.75	818.78	876.83	993.80	1032.52	1073.55	1088.69	1121.55	1170.61
Frac. Inten.(% of TIC)	7.05	18.83	0.18	2.17	0.04	0.30	1.50	1.44	1.20	1.46	1.64	3.47	2.04
Rel. Inten.(% of BP)	27.48	73.40	0.70	8.46	0.16	1.16	5.84	5.61	4.68	5.68	6.38	13.50	7.95
Score	1.00	1.00	1.00	-0.08		1.50	-0.06	1.00	1.00	-0.06	1.00	1.00	1.00
Ion-type	$b{+}{+}_{14}$	$y{+}{+}{+}_{19}$	st		st	sty		$y{+}{+}_{15}$	$b{+}{+}_{17}$		b_{10} $b{+}{+}_{18}$	$y{+}{+}_{18}$	$y{+}{+}_{19}$
Delta Da	-0.24	0.42	0.50			0.37		-0.13	0.56		0.11 -0.29	0.06	0.59

Peak 293


Ions that verify assignment

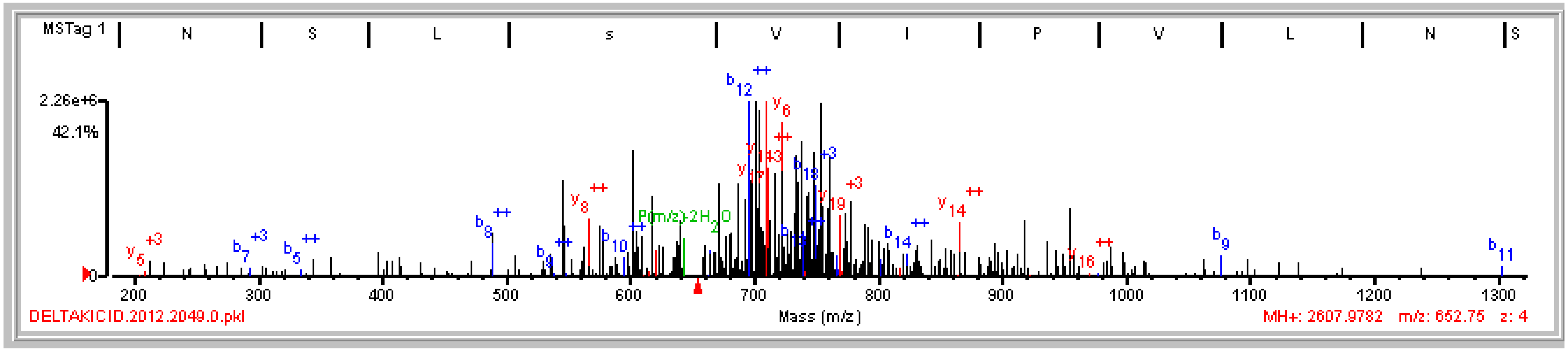


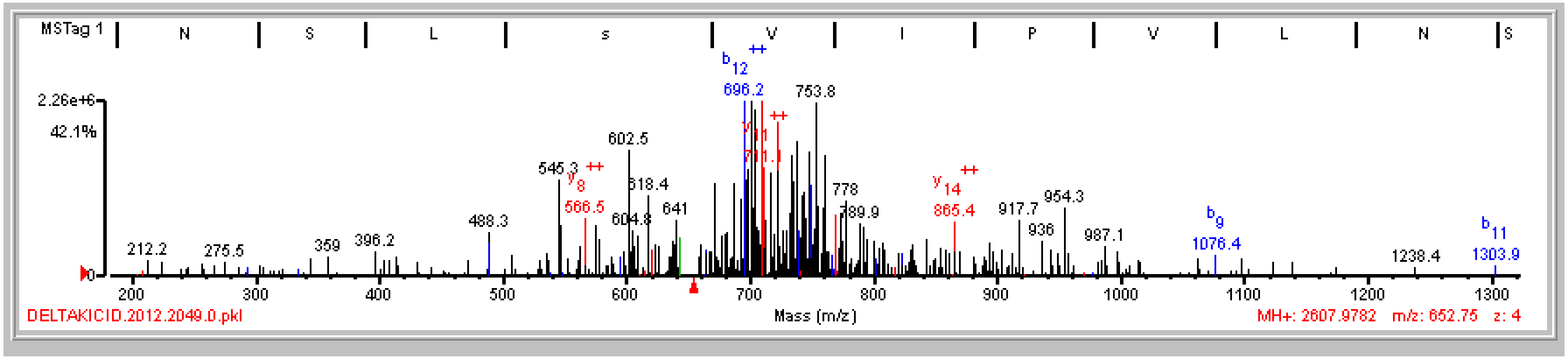
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.95	67.8	8	9/23	M660m M663m Y656y Y668y	(R) N L S/K D/G K\G L y/L T E|m E W m|S L\V M\y N (-)	2722.29	191.9657	14.8	76696.9/7.01	Homo sapiens	41152101	16338	calpain 13

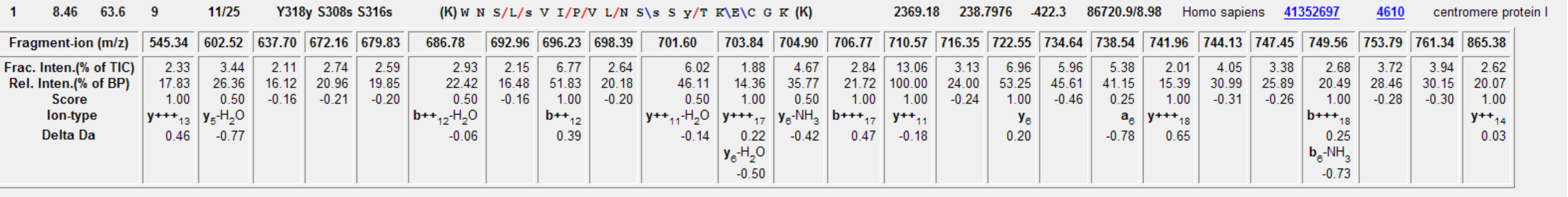
Fragment-ion (m/z)	694.65	697.25	699.97	704.14	708.33	714.37	717.09	743.56	751.14	770.79	782.77	786.90
Frac. Inten.(% of TIC)	3.91	0.16	3.78	0.13	0.09	5.23	6.13	2.47	4.79	3.74	2.75	4.01
Rel. Inten.(% of BP)	12.38	0.50	11.98	0.42	0.28	16.55	19.39	7.80	15.15	11.83	8.71	12.69
Score	-0.12	1.00	0.50	1.50 1.50	1.00	-0.17	-0.19	1.00	1.00	1.00	0.50	1.00
Ion-type		m	y++_{10}-H_2O	b+++_{17} sty	y++_{10} m			b_7	b++_{13}	b+++_{19}	b_8-NH_3	y+++_{18}
Delta Da		-0.06	0.72	0.50 -0.67	0.07			0.16	0.78	0.44	-0.63	0.58

Fragment-ion (m/z)	794.92	806.71	817.64	838.65	847.31	867.44	870.72	875.13	879.34	884.49	910.84
Frac. Inten.(% of TIC)	2.82	3.44	2.92	2.86	3.57	3.47	2.94	3.34	31.60	3.04	2.84
Rel. Inten.(% of BP)	8.94	10.87	9.25	9.04	11.29	10.98	9.31	10.56	100.00	9.61	8.97
Score	-0.09	1.00	-0.09	-0.09	1.00	1.00	0.50	-0.11	1.00	-0.10	-0.09
Ion-type		y_6			b+++_{21}	y+++_{20}	y++_{13}-H_2O		y++_{13}		
Delta Da		0.39			0.26	0.08	-0.12		-0.50		

Peak 294



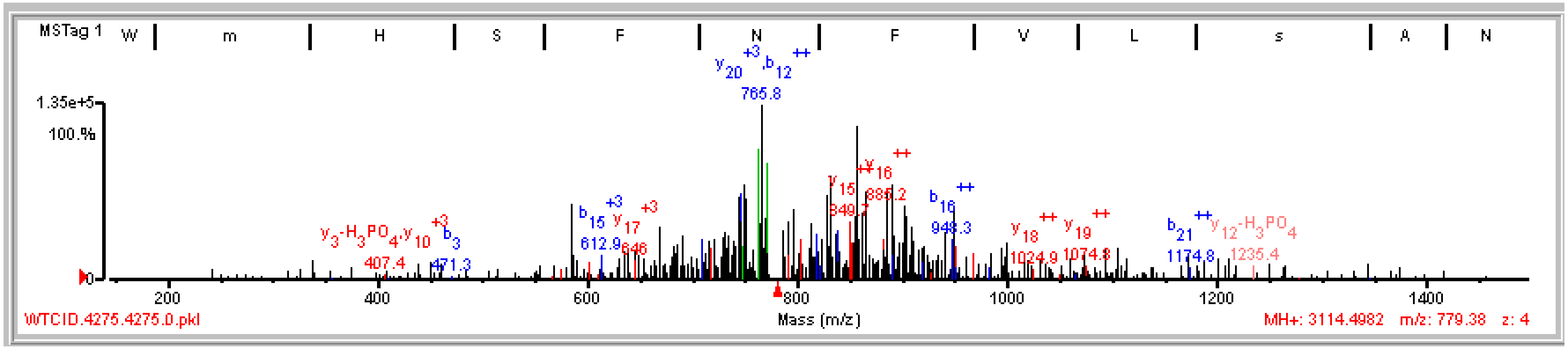


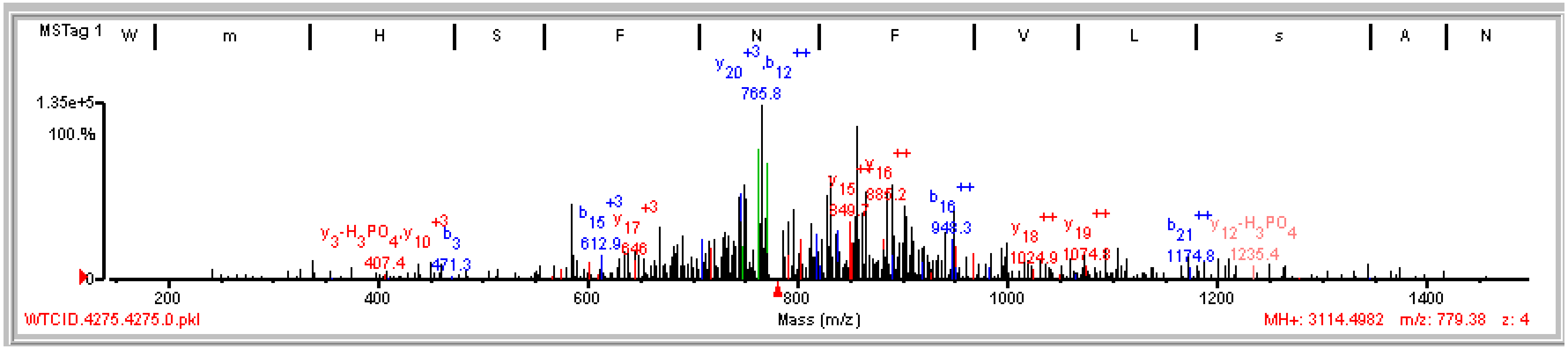


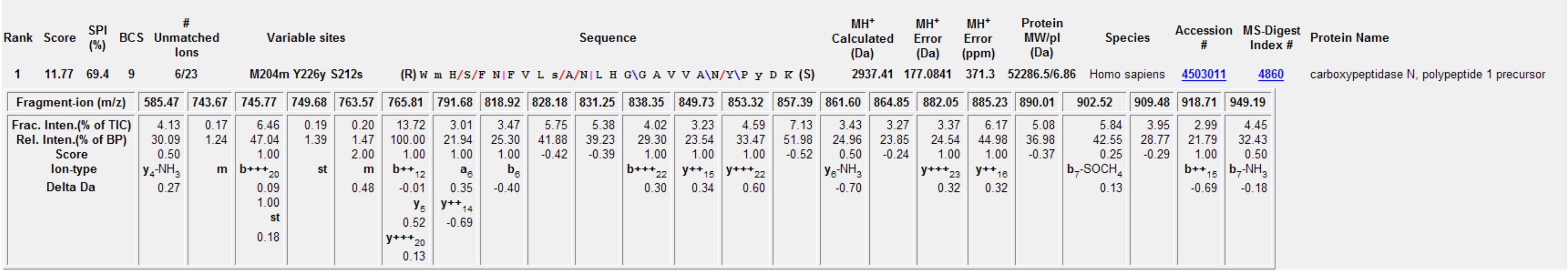
1 8.46 63.6 9 11/25 Y318y S308s S316s (K) W N S/L/s V I/P/V L/N S\s S y/T K\E\C G K (K) 2369.18 238.7976 -422.3 86720.9/8.98 Homo sapiens 41352697 4610 centromere protein I

Fragment-ion (m/z)	545.34	602.52	637.70	672.16	679.83	686.78	692.96	696.23	698.39	701.60	703.84	704.90	706.77	710.57	716.35	722.55	734.64	738.54	741.96	744.13	747.45	749.56	753.79	761.34	865.38
Frac. Inten.(% of TIC)	2.33	3.44	2.11	2.74	2.59	2.93	2.15	6.77	2.64	6.02	1.88	4.67	2.84	13.06	3.13	6.96	5.96	5.38	2.01	4.05	3.38	2.68	3.72	3.94	2.62
Rel. Inten.(% of BP)	17.83	26.36	16.12	20.96	19.85	22.42	16.48	51.83	20.18	46.11	14.36	35.77	21.72	100.00	24.00	53.25	45.61	41.15	15.39	30.99	25.89	20.49	28.46	30.15	20.07
Score	1.00	0.50	-0.16	-0.21	-0.20	0.50	-0.16	1.00	-0.20	0.50	1.00	0.50	1.00	1.00	-0.24	1.00	-0.46	0.25	1.00	-0.31	-0.26	1.00	-0.28	-0.30	1.00
Ion-type	$y+++_{13}$	y_5-H_2O				$b++_{12}$-H_2O		$b++_{12}$		$y++_{11}$-H_2O	$y+++_{17}$ y_6-H_2O	y_6-NH_3	$b+++_{17}$	$y++_{11}$		y_6		a_6	$y+++_{18}$			$b+++_{18}$ b_6-NH_3			$y++_{14}$
Delta Da	0.46	-0.77				-0.06		0.39		-0.14	0.22 -0.50	-0.42	0.47	-0.18		0.20		-0.78	0.65			0.25 -0.73			0.03

Peak 296



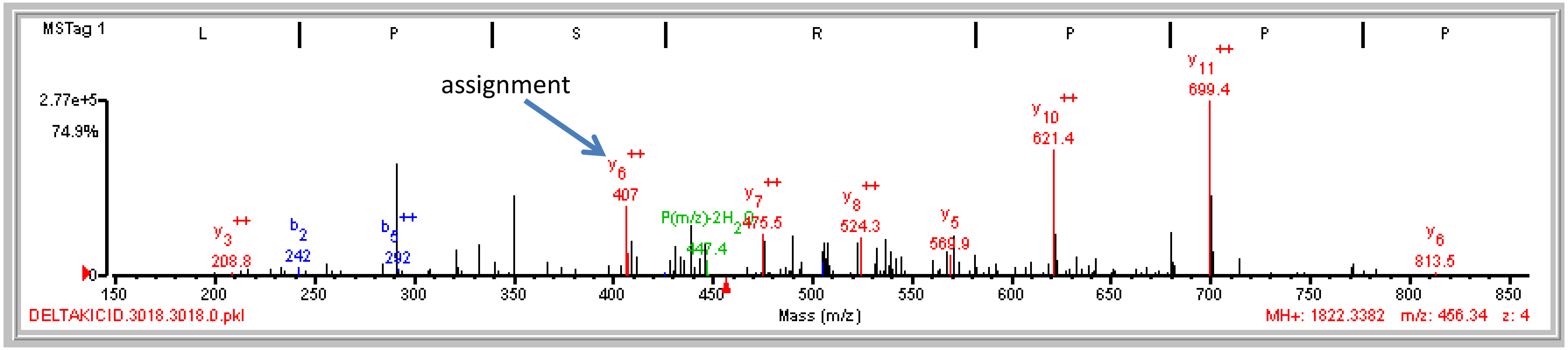




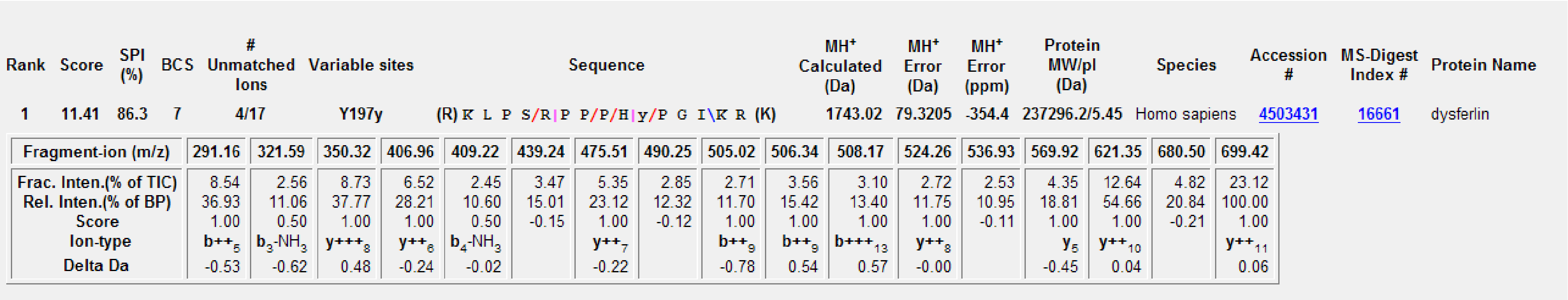
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.77	69.4	9	6/23	M204m Y226y S212s	(R) W m H/S/F N|F V L s/A/N|L H G\G A V V A\N/Y\P y D K (S)	2937.41	177.0841	371.3	52286.5/6.86	Homo sapiens	4503011	4860	carboxypeptidase N, polypeptide 1 precursor

Fragment-ion (m/z)	585.47	743.67	745.77	749.68	763.57	765.81	791.68	818.92	828.18	831.25	838.35	849.73	853.32	857.39	861.60	864.85	882.05	885.23	890.01	902.52	909.48	918.71	949.19
Frac. Inten.(% of TIC)	4.13	0.17	6.46	0.19	0.20	13.72	3.01	3.47	5.75	5.38	4.02	3.23	4.59	7.13	3.43	3.27	3.37	6.17	5.08	5.84	3.95	2.99	4.45
Rel. Inten.(% of BP)	30.09	1.24	47.04	1.39	1.47	100.00	21.94	25.30	41.88	39.23	29.30	23.54	33.47	51.98	24.96	23.85	24.54	44.98	36.98	42.55	28.77	21.79	32.43
Score	0.50		1.00		2.00	1.00	1.00	1.00	-0.42	-0.39	1.00	1.00	1.00	-0.52	0.50	-0.24	1.00	1.00	-0.37	0.25	-0.29	1.00	0.50
Ion-type	y_4-NH$_3$	m	b+++$_{20}$	st	m	b++$_{12}$	a_6	b_6			b+++$_{22}$	y++$_{15}$	y+++$_{22}$		y_6-NH$_3$		y+++$_{23}$	y++$_{16}$		b_7-SOCH$_4$		b++$_{15}$	b_7-NH$_3$
Delta Da	0.27		0.09		0.48	-0.01	0.35	-0.40			0.30	0.34	0.60		-0.70		0.32	0.32		0.13		-0.69	-0.18
			1.00																				
			st			y_5	y++$_{14}$																
			0.18			0.52	-0.69																
						y+++$_{20}$																	
						0.13																	

Peak 297



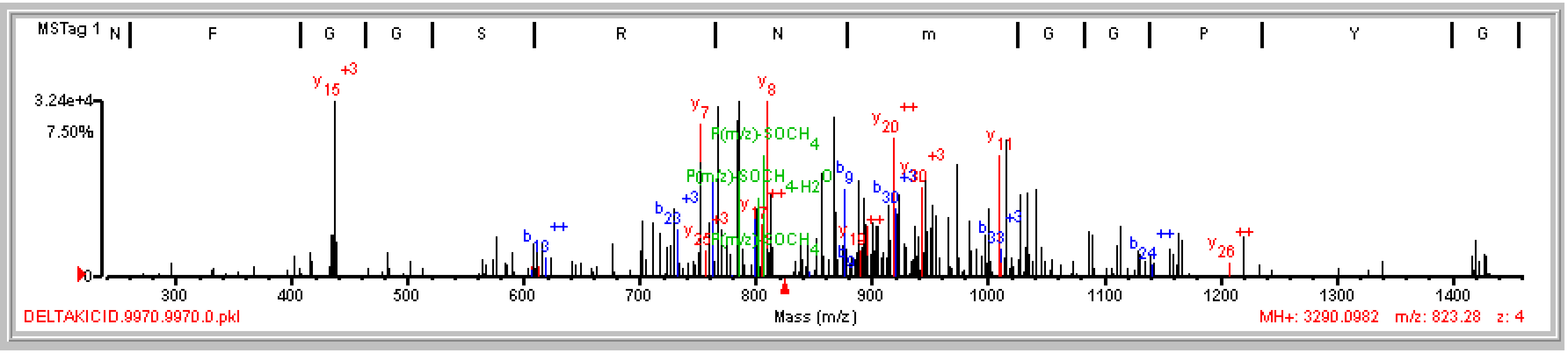
assignment

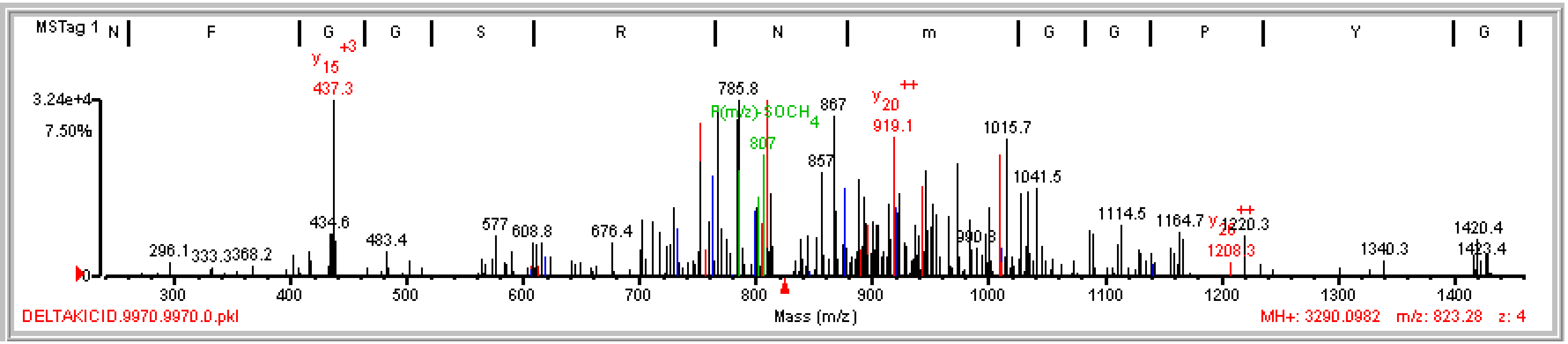


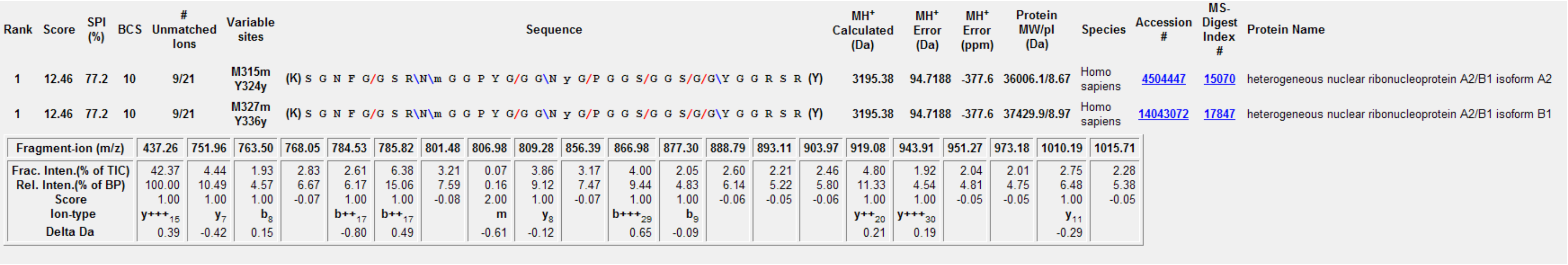
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.41	86.3	7	4/17	Y197y	(R) K L P S/R|P P/P/H|y/P G I\K R (K)	1743.02	79.3205	-354.4	237296.2/5.45	Homo sapiens	4503431	16661	dysferlin

Fragment-ion (m/z)	291.16	321.59	350.32	406.96	409.22	439.24	475.51	490.25	505.02	506.34	508.17	524.26	536.93	569.92	621.35	680.50	699.42
Frac. Inten.(% of TIC)	8.54	2.56	8.73	6.52	2.45	3.47	5.35	2.85	2.71	3.56	3.10	2.72	2.53	4.35	12.64	4.82	23.12
Rel. Inten.(% of BP)	36.93	11.06	37.77	28.21	10.60	15.01	23.12	12.32	11.70	15.42	13.40	11.75	10.95	18.81	54.66	20.84	100.00
Score	1.00	0.50	1.00	1.00	0.50	-0.15	1.00	-0.12	1.00	1.00	1.00	1.00	-0.11	1.00	1.00	-0.21	1.00
Ion-type	$b{++}_5$	b_3-NH_3	$y{+++}_8$	$y{++}_6$	b_4-NH_3		$y{++}_7$		$b{++}_9$	$b{++}_9$	$b{+++}_{13}$	$y{++}_8$		y_5	$y{++}_{10}$		$y{++}_{11}$
Delta Da	-0.53	-0.62	0.48	-0.24	-0.02		-0.22		-0.78	0.54	0.57	-0.00		-0.45	0.04		0.06

Peak 298



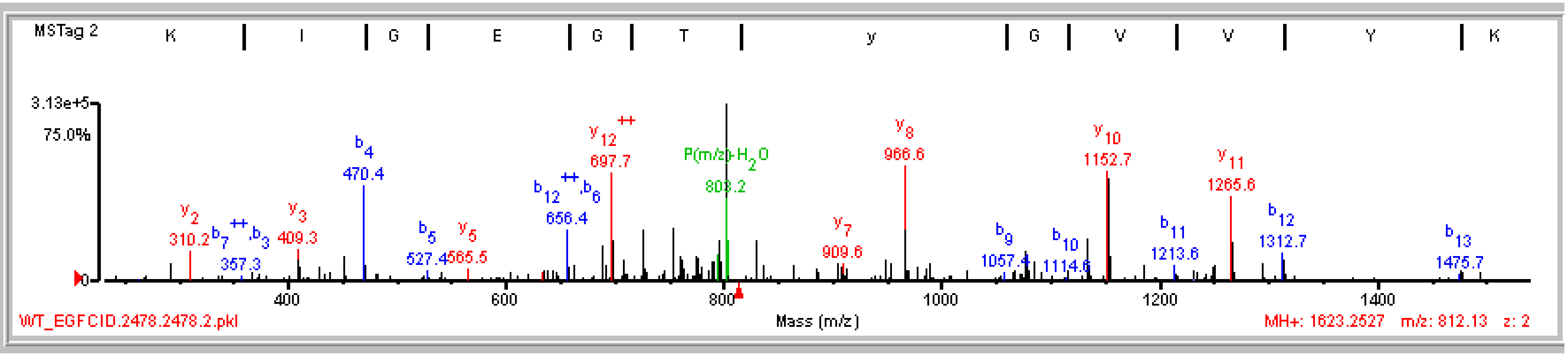


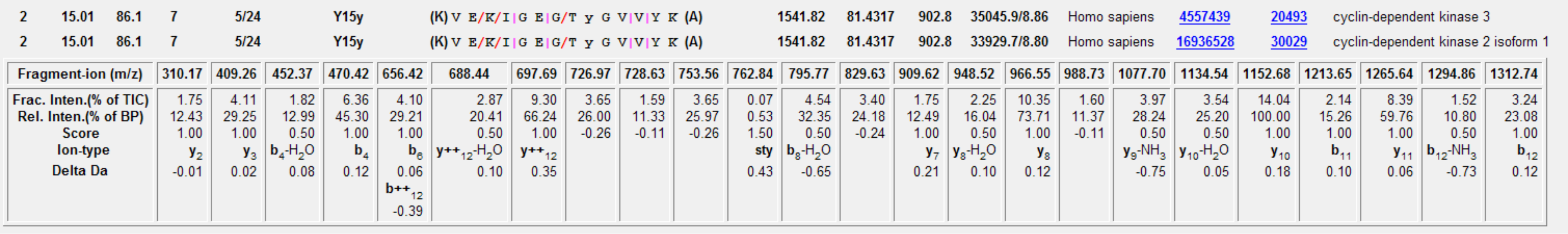


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.46	77.2	10	9/21	M315m Y324y	(K) S G N F G/G S R\N\m G G P Y G/G G\N y G/P G G S/G G S/G/G\Y G G R S R (Y)	3195.38	94.7188	-377.6	36006.1/8.67	Homo sapiens	4504447	15070	heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2
1	12.46	77.2	10	9/21	M327m Y336y	(K) S G N F G/G S R\N\m G G P Y G/G G\N y G/P G G S/G G S/G/G\Y G G R S R (Y)	3195.38	94.7188	-377.6	37429.9/8.97	Homo sapiens	14043072	17847	heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1

Fragment-ion (m/z)	437.26	751.96	763.50	768.05	784.53	785.82	801.48	806.98	809.28	856.39	866.98	877.30	888.79	893.11	903.97	919.08	943.91	951.27	973.18	1010.19	1015.71
Frac. Inten.(% of TIC)	42.37	4.44	1.93	2.83	2.61	6.38	3.21	0.07	3.86	3.17	4.00	2.05	2.60	2.21	2.46	4.80	1.92	2.04	2.01	2.75	2.28
Rel. Inten.(% of BP)	100.00	10.49	4.57	6.67	6.17	15.06	7.59	0.16	9.12	7.47	9.44	4.83	6.14	5.22	5.80	11.33	4.54	4.81	4.75	6.48	5.38
Score	1.00	1.00	1.00	-0.07	1.00	1.00	-0.08	2.00	1.00	-0.07	1.00	1.00	-0.06	-0.05	-0.06	1.00	1.00	-0.05	-0.05	1.00	-0.05
Ion-type	$y+++_{15}$	y_7	b_8		$b++_{17}$	$b++_{17}$		m	y_8		$b+++_{29}$	b_9				$y++_{20}$	$y+++_{30}$			y_{11}	
Delta Da	0.39	-0.42	0.15		-0.80	0.49		-0.61	-0.12		0.65	-0.09				0.21	0.19			-0.29	

Peak 299



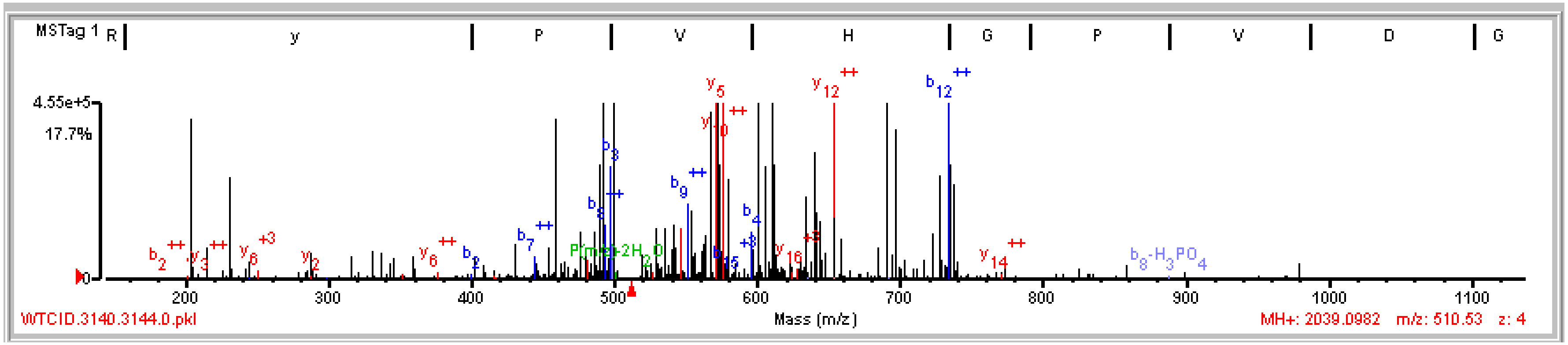


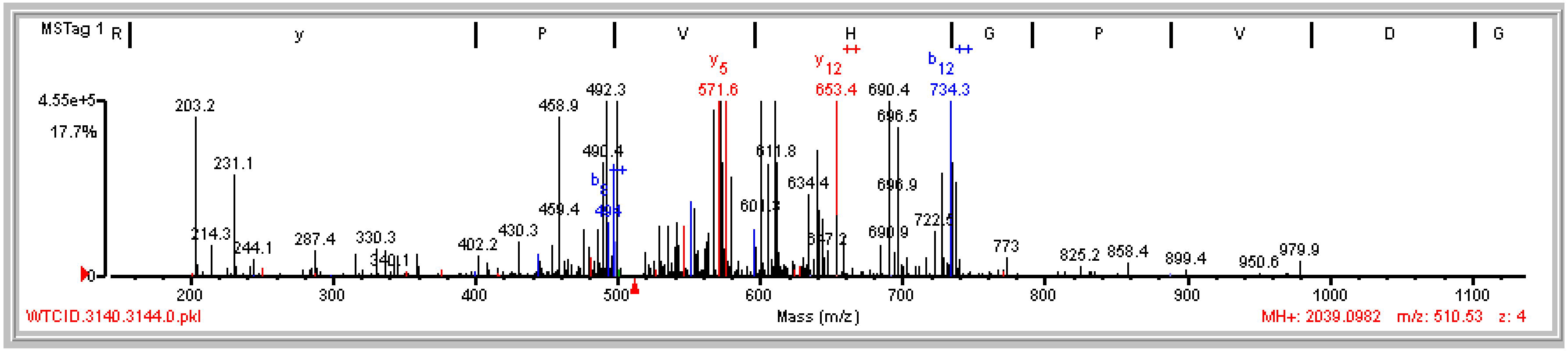
2	15.01	86.1	7	5/24	Y15y	(K) V E/K/I|G E|G/T y G V|V|Y K (A)	1541.82	81.4317	902.8	35045.9/8.86	Homo sapiens	4557439	20493	cyclin-dependent kinase 3
2	15.01	86.1	7	5/24	Y15y	(K) V E/K/I|G E|G/T y G V|V|Y K (A)	1541.82	81.4317	902.8	33929.7/8.80	Homo sapiens	16936528	30029	cyclin-dependent kinase 2 isoform 1

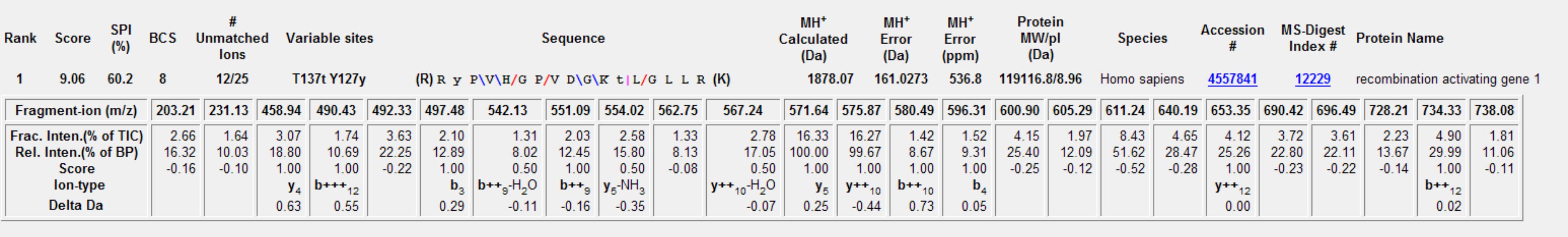
Fragment-ion (m/z)	310.17	409.26	452.37	470.42	656.42	688.44	697.69	726.97	728.63	753.56	762.84	795.77
Frac. Inten.(% of TIC)	1.75	4.11	1.82	6.36	4.10	2.87	9.30	3.65	1.59	3.65	0.07	4.54
Rel. Inten.(% of BP)	12.43	29.25	12.99	45.30	29.21	20.41	66.24	26.00	11.33	25.97	0.53	32.35
Score	1.00	1.00	0.50	1.00	1.00	0.50	1.00	-0.26	-0.11	-0.26	1.50	0.50
Ion-type	y_2	y_3	b_4-H_2O	b_4	b_6 $b{++}_{12}$	$y{++}_{12}$-H_2O	$y{++}_{12}$				sty	b_8-H_2O
Delta Da	-0.01	0.02	0.08	0.12	0.06 -0.39	0.10	0.35				0.43	-0.65

Fragment-ion (m/z)	829.63	909.62	948.52	966.55	988.73	1077.70	1134.54	1152.68	1213.65	1265.64	1294.86	1312.74
Frac. Inten.(% of TIC)	3.40	1.75	2.25	10.35	1.60	3.97	3.54	14.04	2.14	8.39	1.52	3.24
Rel. Inten.(% of BP)	24.18	12.49	16.04	73.71	11.37	28.24	25.20	100.00	15.26	59.76	10.80	23.08
Score	-0.24	1.00	0.50	1.00	-0.11	0.50	0.50	1.00	1.00	1.00	0.50	1.00
Ion-type		y_7	y_8-H_2O	y_8		y_9-NH_3	y_{10}-H_2O	y_{10}	b_{11}	y_{11}	b_{12}-NH_3	b_{12}
Delta Da		0.21	0.10	0.12		-0.75	0.05	0.18	0.10	0.06	-0.73	0.12

Peak 300



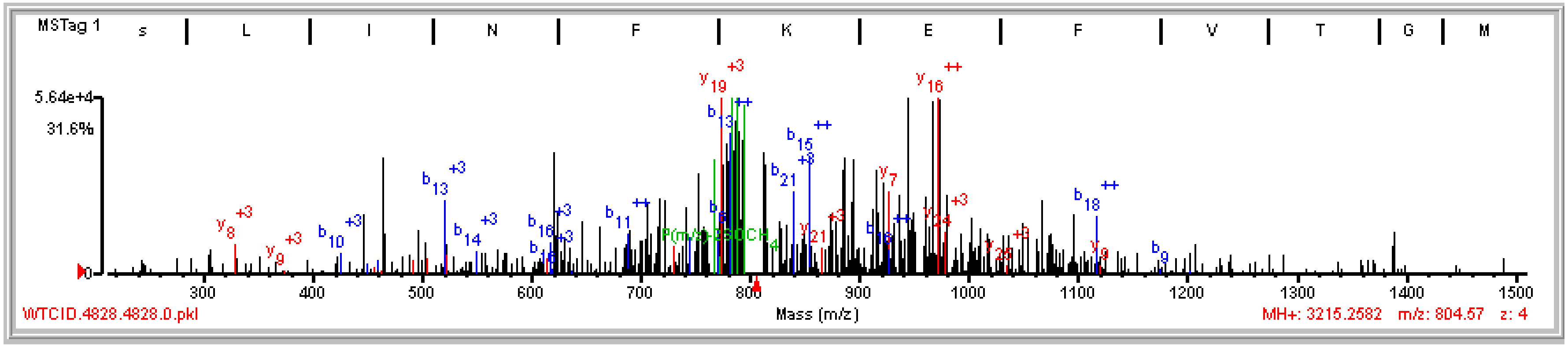


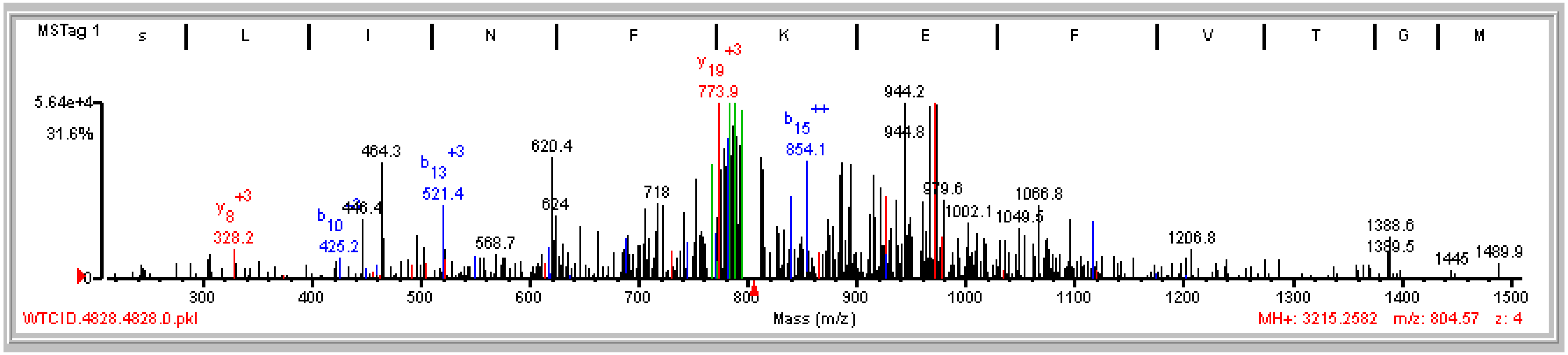


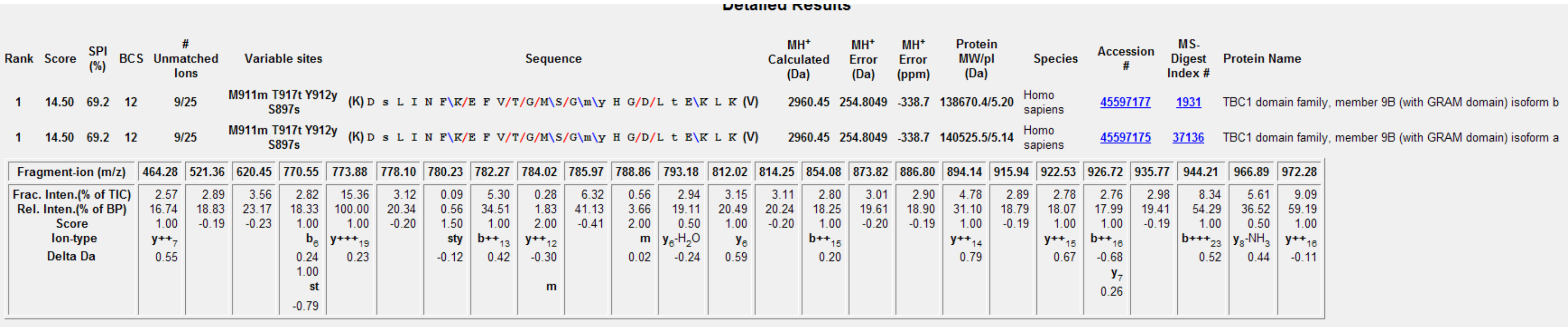
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.06	60.2	8	12/25	T137t Y127y	(R) R y P\V\H/G P/V D\G\K t|L/G L L R (K)	1878.07	161.0273	536.8	119116.8/8.96	Homo sapiens	4557841	12229	recombination activating gene 1

Fragment-ion (m/z)	203.21	231.13	458.94	490.43	492.33	497.48	542.13	551.09	554.02	562.75	567.24	571.64	575.87	580.49	596.31	600.90	605.29	611.24	640.19	653.35	690.42	696.49	728.21	734.33	738.08
Frac. Inten.(% of TIC)	2.66	1.64	3.07	1.74	3.63	2.10	1.31	2.03	2.58	1.33	2.78	16.33	16.27	1.42	1.52	4.15	1.97	8.43	4.65	4.12	3.72	3.61	2.23	4.90	1.81
Rel. Inten.(% of BP)	16.32	10.03	18.80	10.69	22.25	12.89	8.02	12.45	15.80	8.13	17.05	100.00	99.67	8.67	9.31	25.40	12.09	51.62	28.47	25.26	22.80	22.11	13.67	29.99	11.06
Score	-0.16	-0.10	1.00	1.00	-0.22	1.00	0.50	1.00	0.50	-0.08	0.50	1.00	1.00	1.00	1.00	-0.25	-0.12	-0.52	-0.28	1.00	-0.23	-0.22	-0.14	1.00	-0.11
Ion-type			y_4	$b{+}{+}{+}_{12}$		b_3	$b{+}{+}_9$-H_2O	$b{+}{+}_9$	y_5-NH_3		$y{+}{+}_{10}$-H_2O	y_5	$y{+}{+}_{10}$	$b{+}{+}_{10}$	b_4					$y{+}{+}_{12}$				$b{+}{+}_{12}$	
Delta Da			0.63	0.55		0.29	-0.11	-0.16	-0.35		-0.07	0.25	-0.44	0.73	0.05					0.00				0.02	

Peak 301





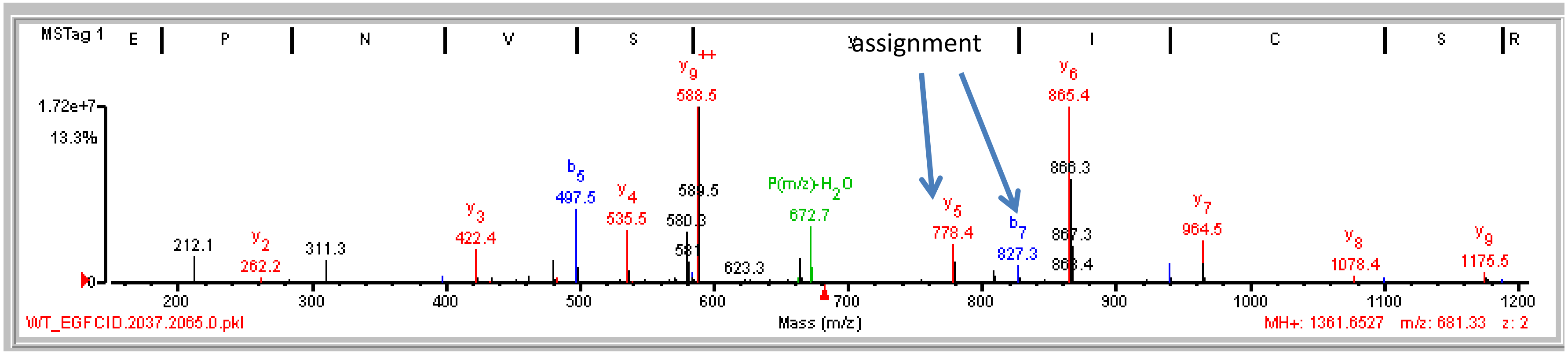


Detailed Results

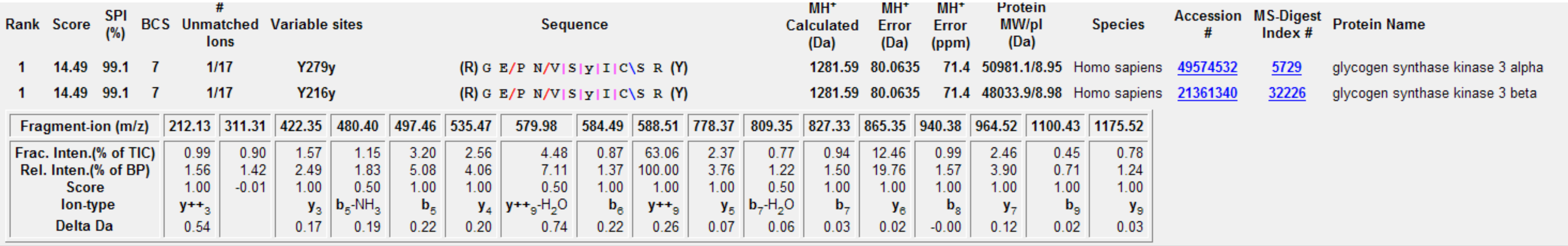
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.50	69.2	12	9/25	M911m T917t Y912y S897s	(K) D s L I N F\K/E F V/T/G/M\S/G\m\y H G/D/L t E\K L K (V)	2960.45	254.8049	-338.7	138670.4/5.20	Homo sapiens	45597177	1931	TBC1 domain family, member 9B (with GRAM domain) isoform b
1	14.50	69.2	12	9/25	M911m T917t Y912y S897s	(K) D s L I N F\K/E F V/T/G/M\S/G\m\y H G/D/L t E\K L K (V)	2960.45	254.8049	-338.7	140525.5/5.14	Homo sapiens	45597175	37136	TBC1 domain family, member 9B (with GRAM domain) isoform a

Fragment-ion (m/z)	464.28	521.36	620.45	770.55	773.88	778.10	780.23	782.27	784.02	785.97	788.86	793.18	812.02	814.25	854.08	873.82	886.80	894.14	915.94	922.53	926.72	935.77	944.21	966.89	972.28
Frac. Inten.(% of TIC)	2.57	2.89	3.56	2.82	15.36	3.12	0.09	5.30	0.28	6.32	0.56	2.94	3.15	3.11	2.80	3.01	2.90	4.78	2.89	2.78	2.76	2.98	8.34	5.61	9.09
Rel. Inten.(% of BP)	16.74	18.83	23.17	18.33	100.00	20.34	0.56	34.51	1.83	41.13	3.66	19.11	20.49	20.24	18.25	19.61	18.90	31.10	18.79	18.07	17.99	19.41	54.29	36.52	59.19
Score	1.00	-0.19	-0.23	1.00	1.00	-0.20	1.50	1.00	2.00	-0.41	2.00	0.50	1.00	-0.20	1.00	-0.20	-0.19	1.00	-0.19	1.00	1.00	-0.19	1.00	0.50	1.00
Ion-type	y^{++}_7			b_6	y^{+++}_{19}		sty	b^{++}_{13}	y^{++}_{12}		m	y_6-H_2O	y_6		b^{++}_{15}			y^{++}_{14}		y^{++}_{15}	b^{++}_{16}		b^{+++}_{23}	y_8-NH_3	y^{++}_{16}
Delta Da	0.55			0.24	0.23		-0.12	0.42	-0.30		0.02	-0.24	0.59		0.20			0.79		0.67	-0.68		0.52	0.44	-0.11
				1.00																					
				st					m												y_7				
				-0.79																	0.26				

Peak 302



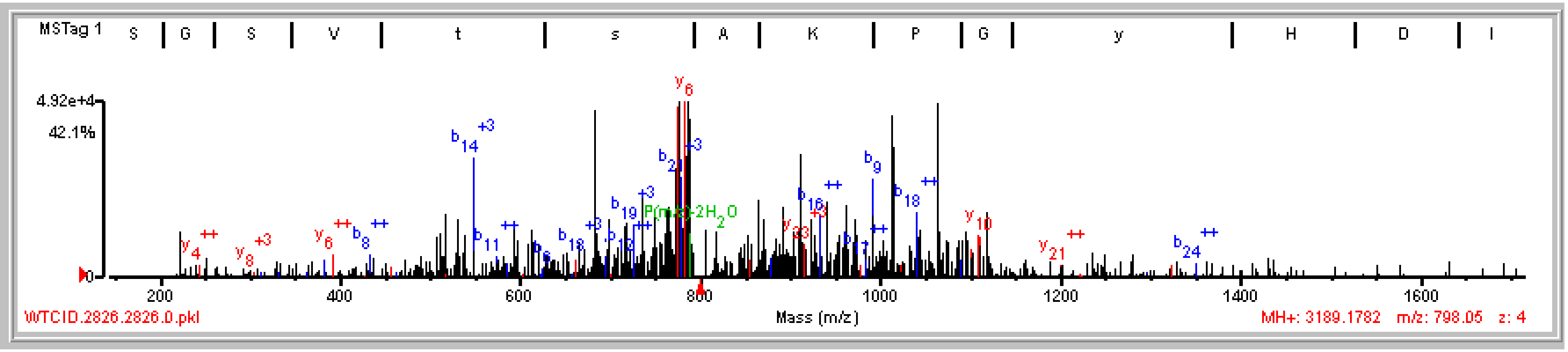
assignment

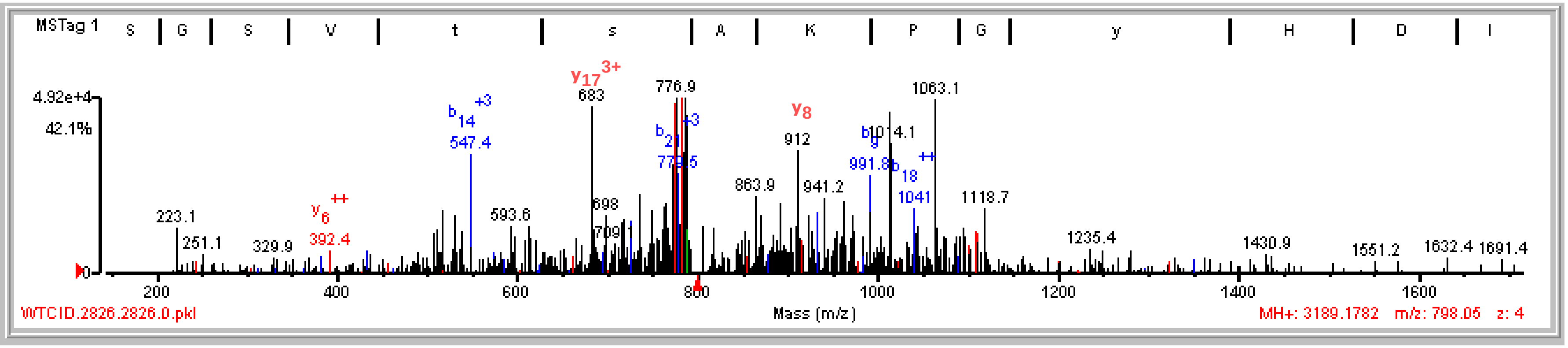


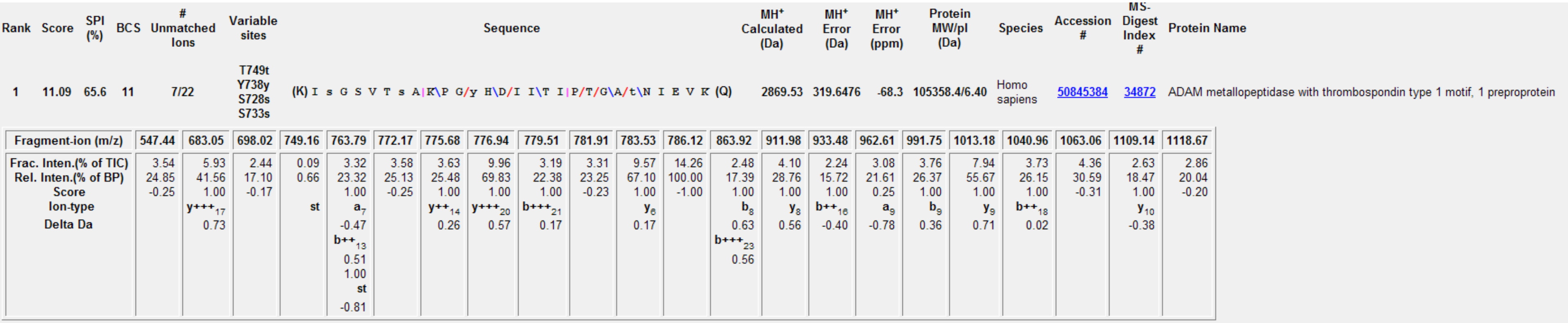
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.49	99.1	7	1/17	Y279y	(R) G E/P N/V|S|y|I|C\S R (Y)	1281.59	80.0635	71.4	50981.1/8.95	Homo sapiens	49574532	5729	glycogen synthase kinase 3 alpha
1	14.49	99.1	7	1/17	Y216y	(R) G E/P N/V|S|y|I|C\S R (Y)	1281.59	80.0635	71.4	48033.9/8.98	Homo sapiens	21361340	32226	glycogen synthase kinase 3 beta

Fragment-ion (m/z)	212.13	311.31	422.35	480.40	497.46	535.47	579.98	584.49	588.51	778.37	809.35	827.33	865.35	940.38	964.52	1100.43	1175.52
Frac. Inten.(% of TIC)	0.99	0.90	1.57	1.15	3.20	2.56	4.48	0.87	63.06	2.37	0.77	0.94	12.46	0.99	2.46	0.45	0.78
Rel. Inten.(% of BP)	1.56	1.42	2.49	1.83	5.08	4.06	7.11	1.37	100.00	3.76	1.22	1.50	19.76	1.57	3.90	0.71	1.24
Score	1.00	-0.01	1.00	0.50	1.00	1.00	0.50	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	$y{++}_3$		y_3	b_5-NH_3	b_5	y_4	$y{++}_9$-H_2O	b_6	$y{++}_9$	y_5	b_7-H_2O	b_7	y_6	b_8	y_7	b_9	y_9
Delta Da	0.54		0.17	0.19	0.22	0.20	0.74	0.22	0.26	0.07	0.06	0.03	0.02	-0.00	0.12	0.02	0.03

Peak 303





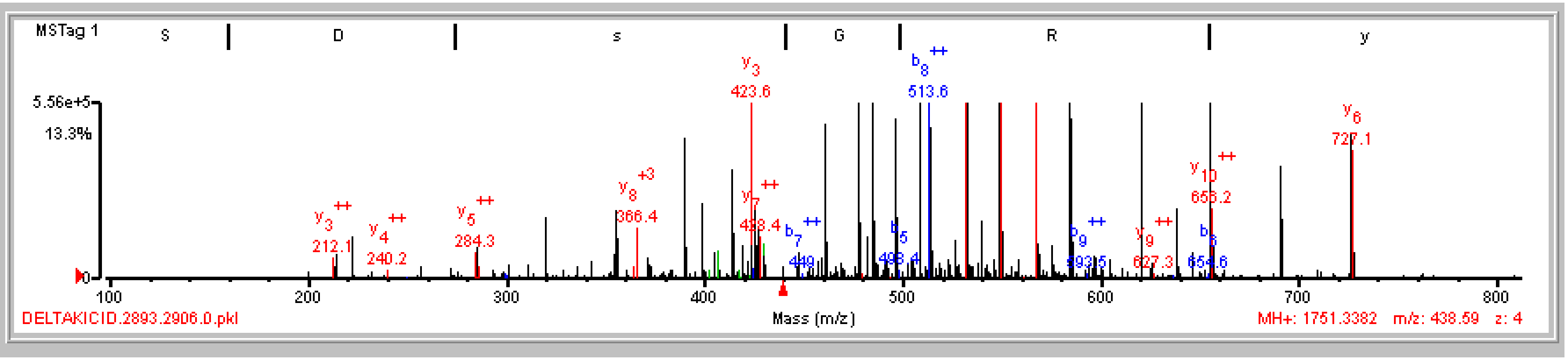


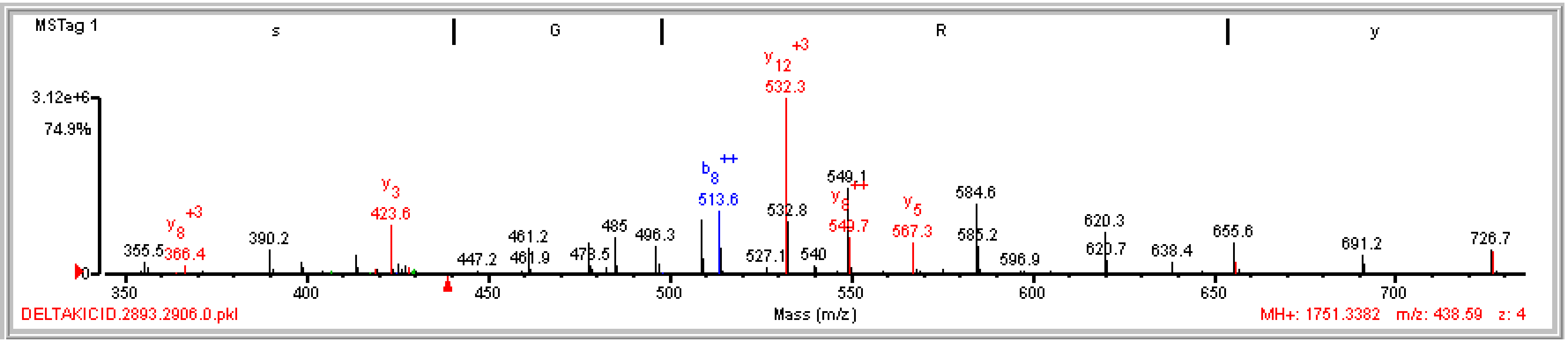
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.09	65.6	11	7/22	T749t Y738y S728s S733s	(K) I s G S V T s A|K\P G/y H\D/I I\T I|P/T/G\A/t\N I E V K (Q)	2869.53	319.6476	-68.3	105358.4/6.40	Homo sapiens	50845384	34872	ADAM metallopeptidase with thrombospondin type 1 motif, 1 preproprotein

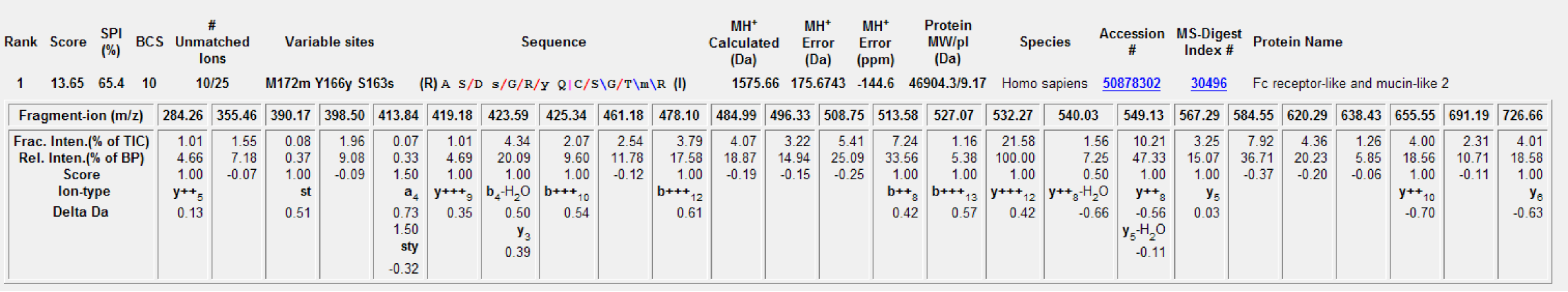
Fragment-ion (m/z)	547.44	683.05	698.02	749.16	763.79	772.17	775.68	776.94	779.51	781.91	783.53	786.12
Frac. Inten.(% of TIC)	3.54	5.93	2.44	0.09	3.32	3.58	3.63	9.96	3.19	3.31	9.57	14.26
Rel. Inten.(% of BP)	24.85	41.56	17.10	0.66	23.32	25.13	25.48	69.83	22.38	23.25	67.10	100.00
Score	-0.25	1.00	-0.17		1.00	-0.25	1.00	1.00	1.00	-0.23	1.00	-1.00
Ion-type		y+++$_{17}$		st	a$_{7}$		y++$_{14}$	y+++$_{20}$	b+++$_{21}$		y$_{6}$	
Delta Da		0.73			-0.47		0.26	0.57	0.17		0.17	
					b++$_{13}$							
					0.51							
					1.00							
					st							
					-0.81							

Fragment-ion (m/z)	863.92	911.98	933.48	962.61	991.75	1013.18	1040.96	1063.06	1109.14	1118.67
Frac. Inten.(% of TIC)	2.48	4.10	2.24	3.08	3.76	7.94	3.73	4.36	2.63	2.86
Rel. Inten.(% of BP)	17.39	28.76	15.72	21.61	26.37	55.67	26.15	30.59	18.47	20.04
Score	1.00	1.00	1.00	0.25	1.00	1.00	1.00	-0.31	1.00	-0.20
Ion-type	b$_{8}$	y$_{8}$	b++$_{16}$	a$_{9}$	b$_{9}$	y$_{9}$	b++$_{18}$		y$_{10}$	
Delta Da	0.63	0.56	-0.40	-0.78	0.36	0.71	0.02		-0.38	
	b+++$_{23}$									
	0.56									

Peak 304





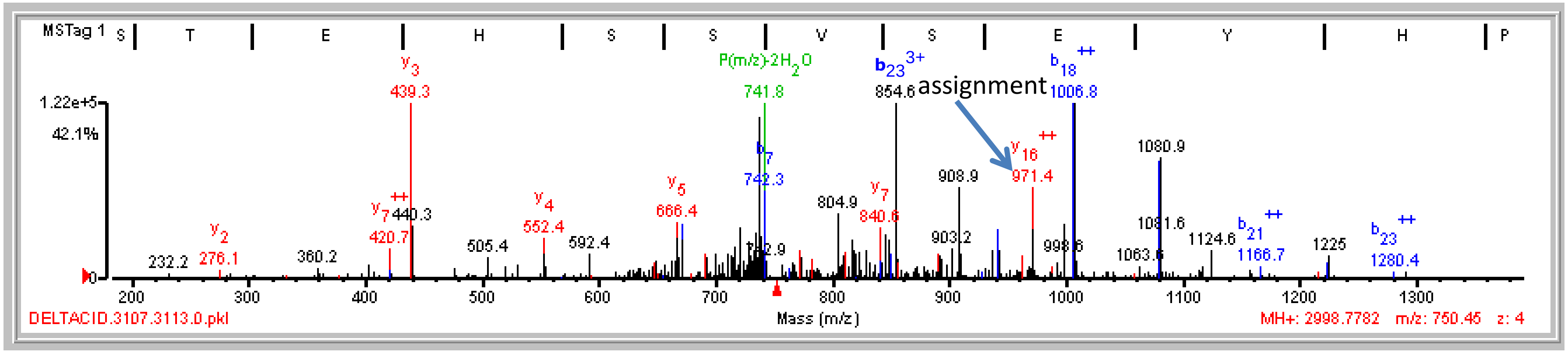


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.65	65.4	10	10/25	M172m Y166y S163s	(R) A S/D s/G/R/y Q|C/S\G/T\m\R (I)	1575.66	175.6743	-144.6	46904.3/9.17	Homo sapiens	50878302	30496	Fc receptor-like and mucin-like 2

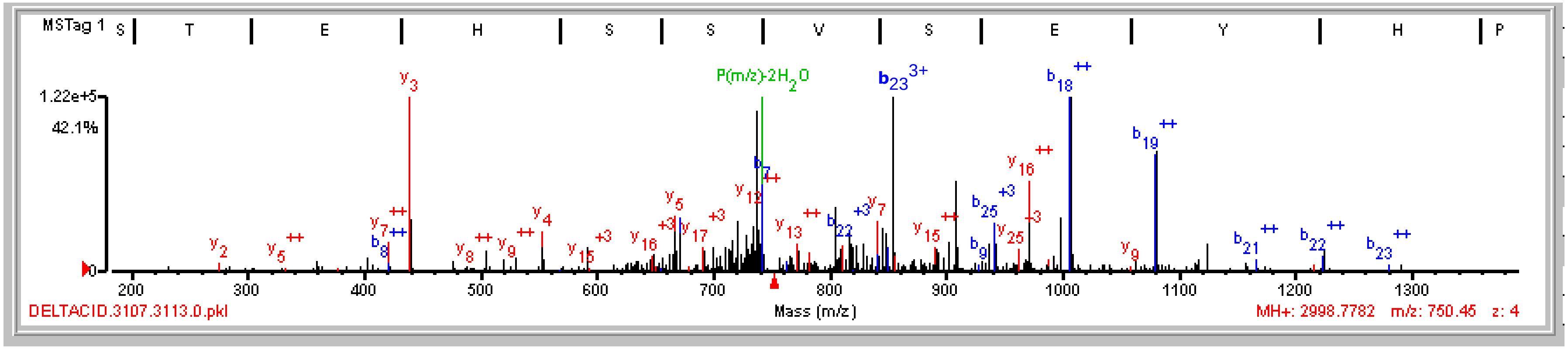
Fragment-ion (m/z)	284.26	355.46	390.17	398.50	413.84	419.18	423.59	425.34	461.18	478.10	484.99	496.33
Frac. Inten.(% of TIC)	1.01	1.55	0.08	1.96	0.07	1.01	4.34	2.07	2.54	3.79	4.07	3.22
Rel. Inten.(% of BP)	4.66	7.18	0.37	9.08	0.33	4.69	20.09	9.60	11.78	17.58	18.87	14.94
Score	1.00	-0.07	1.00	-0.09	1.50	1.00	1.00	1.00	-0.12	1.00	-0.19	-0.15
Ion-type	y++$_5$		st		a$_4$	y+++$_9$	b$_4$-H$_2$O	b+++$_{10}$		b+++$_{12}$		
Delta Da	0.13		0.51		0.73 1.50 sty -0.32	0.35	0.50 y$_3$ 0.39	0.54		0.61		

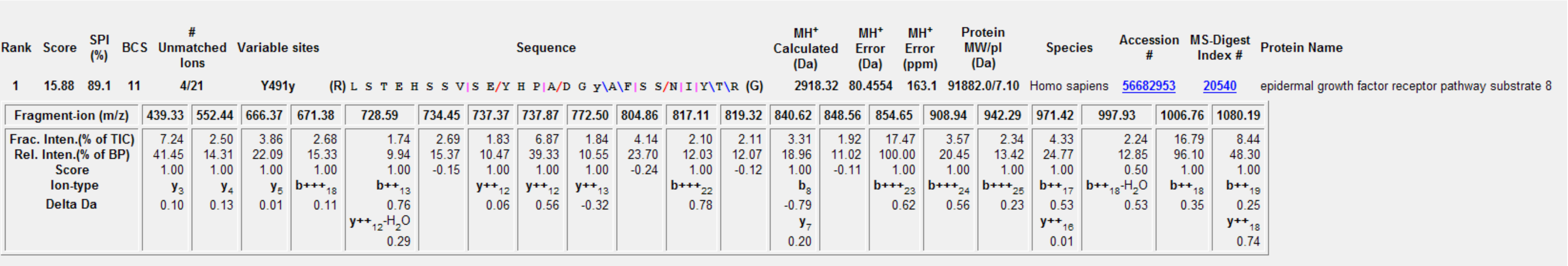
Fragment-ion (m/z)	508.75	513.58	527.07	532.27	540.03	549.13	567.29	584.55	620.29	638.43	655.55	691.19	726.66
Frac. Inten.(% of TIC)	5.41	7.24	1.16	21.58	1.56	10.21	3.25	7.92	4.36	1.26	4.00	2.31	4.01
Rel. Inten.(% of BP)	25.09	33.56	5.38	100.00	7.25	47.33	15.07	36.71	20.23	5.85	18.56	10.71	18.58
Score	-0.25	1.00	1.00	1.00	0.50	1.00	1.00	-0.37	-0.20	-0.06	1.00	-0.11	1.00
Ion-type		b++$_8$	b+++$_{13}$	y+++$_{12}$	y++$_8$-H$_2$O	y++$_8$	y$_5$				y++$_{10}$		y$_6$
Delta Da		0.42	0.57	0.42	-0.66	-0.56 y$_5$-H$_2$O -0.11	0.03				-0.70		-0.63

Peak 305



assignment

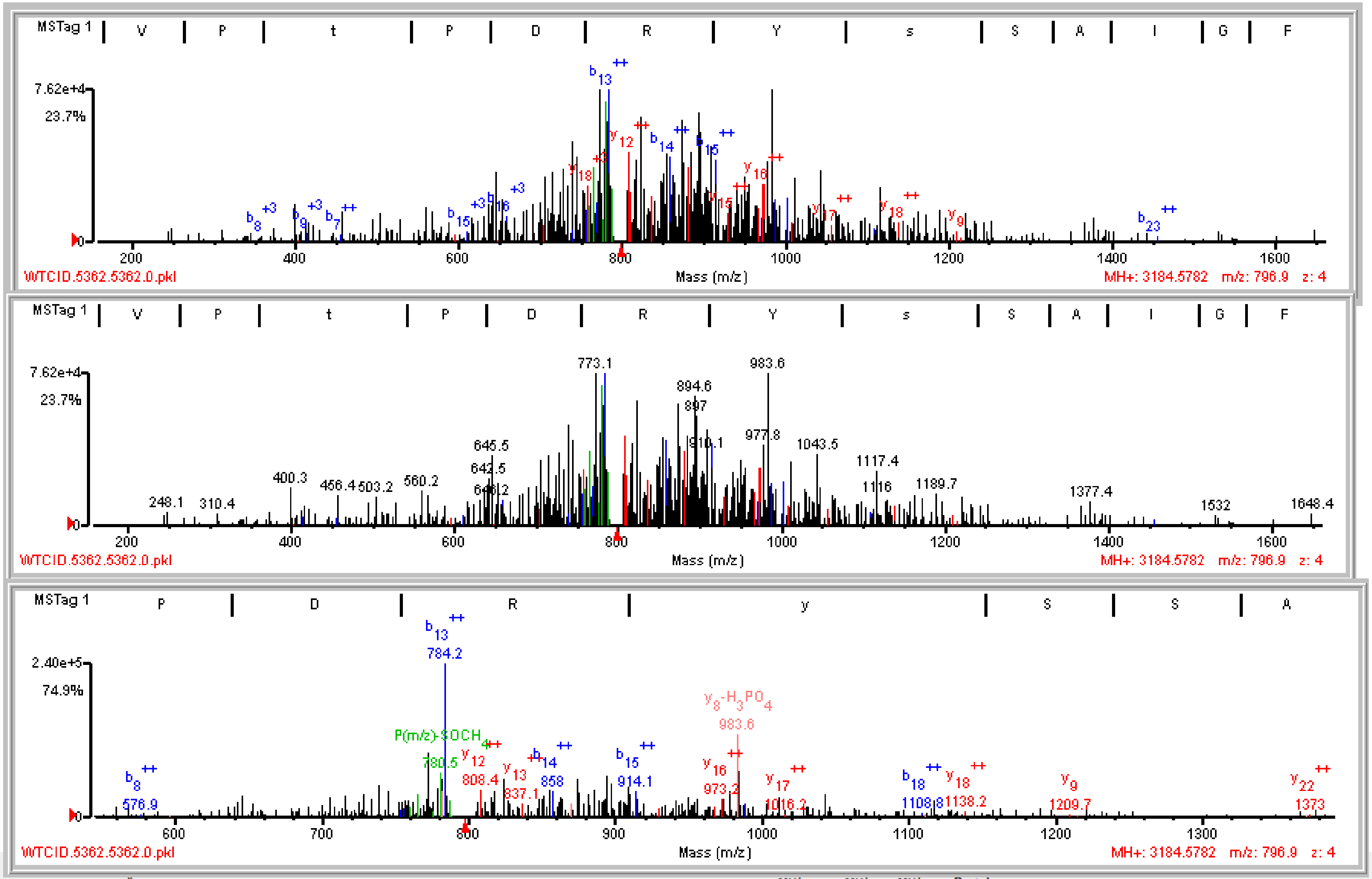




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.88	89.1	11	4/21	Y491y	(R) L S T E H S S V|S E/Y H P|A/D G y\A\F|S S/N|I|Y\T\R (G)	2918.32	80.4554	163.1	91882.0/7.10	Homo sapiens	56682953	20540	epidermal growth factor receptor pathway substrate 8

Fragment-ion (m/z)	439.33	552.44	666.37	671.38	728.59	734.45	737.37	737.87	772.50	804.86	817.11	819.32	840.62	848.56	854.65	908.94	942.29	971.42	997.93	1006.76	1080.19
Frac. Inten.(% of TIC)	7.24	2.50	3.86	2.68	1.74	2.69	1.83	6.87	1.84	4.14	2.10	2.11	3.31	1.92	17.47	3.57	2.34	4.33	2.24	16.79	8.44
Rel. Inten.(% of BP)	41.45	14.31	22.09	15.33	9.94	15.37	10.47	39.33	10.55	23.70	12.03	12.07	18.96	11.02	100.00	20.45	13.42	24.77	12.85	96.10	48.30
Score	1.00	1.00	1.00	1.00	1.00	-0.15	1.00	1.00	1.00	-0.24	1.00	-0.12	1.00	-0.11	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	y_3	y_4	y_5	$b{+}{+}{+}_{18}$	$b{+}{+}_{13}$		$y{+}{+}_{12}$	$y{+}{+}_{12}$	$y{+}{+}_{13}$		$b{+}{+}{+}_{22}$		b_8		$b{+}{+}{+}_{23}$	$b{+}{+}{+}_{24}$	$b{+}{+}{+}_{25}$	$b{+}{+}_{17}$	$b{+}{+}_{18}$-H_2O	$b{+}{+}_{18}$	$b{+}{+}_{19}$
Delta Da	0.10	0.13	0.01	0.11	0.76		0.06	0.56	-0.32		0.78		-0.79		0.62	0.56	0.23	0.53	0.53	0.35	0.25
Ion-type					$y{+}{+}_{12}$-H_2O								y_7					$y{+}{+}_{16}$			$y{+}{+}_{18}$
Delta Da					0.29								0.20					0.01			0.74

Peak 306

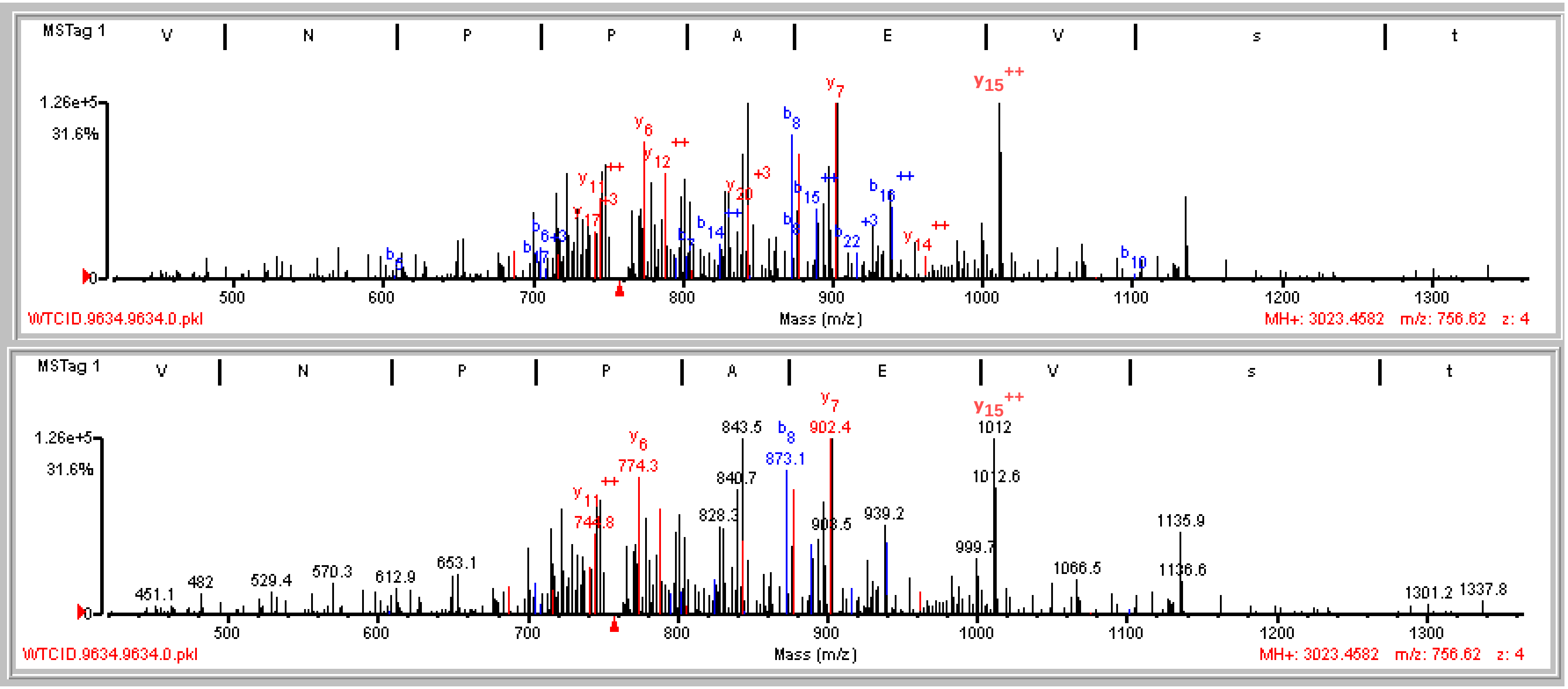


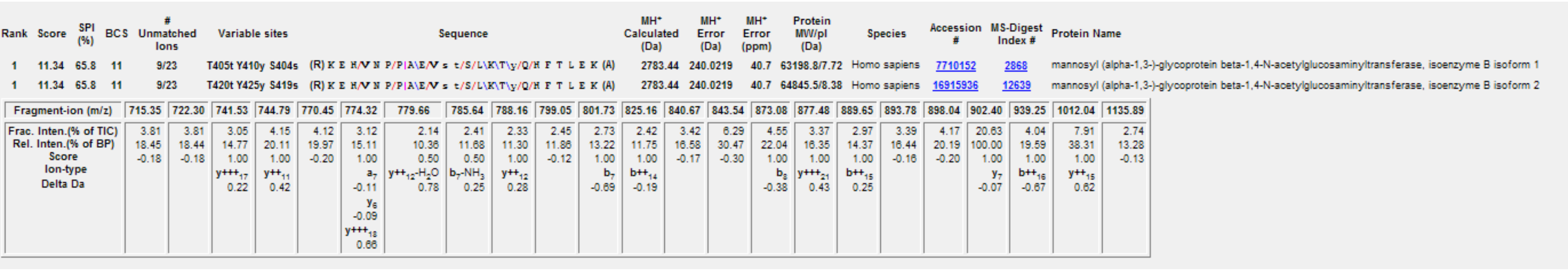
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.15	74.3	8	7/23	M903m T910t Y888y Y895y	(K) y V P T P/D R\y S/S A/I G|F\L\m K N S W Q\I t P R (N)	2927.49	257.0909	375.9	154374.5/8.41	Homo sapiens	7019555	24268	transmembrane protein 2

Fragment-ion (m/z)	738.64	773.08	780.54	784.18	808.43	816.51	823.69	849.87	858.05	862.31	873.94	881.77	885.51
Frac. Inten.(% of TIC)	4.06	0.21	0.26	19.01	4.35	3.25	3.54	3.49	2.64	3.48	5.76	2.85	3.04
Rel. Inten.(% of BP)	21.36	1.11	1.35	100.00	22.88	17.11	18.60	18.38	13.91	18.31	30.28	15.01	15.97
Score	-0.21	1.50	2.00	1.00	1.00	-0.17	-0.19	1.00	1.00	-0.18	1.00	0.25	0.50
Ion-type		sty	m	$b{++}_{13}$	$y{++}_{12}$			$y{+++}_{20}$	$b{++}_{14}$		$b{+++}_{21}$	a_7	$y{++}_{14}$-H_2O
Delta Da		0.97	-0.06	-0.14	-0.46			0.49	0.20		0.56	0.38	0.58

Fragment-ion (m/z)	892.31	894.64	897.05	902.73	905.57	908.66	914.10	973.24	977.80	983.55
Frac. Inten.(% of TIC)	2.86	3.62	5.17	3.13	3.45	4.22	2.74	3.93	3.10	11.85
Rel. Inten.(% of BP)	15.03	19.07	27.19	16.44	18.15	22.22	14.40	20.67	16.29	62.31
Score	0.50	1.00	-0.27	-0.16	0.50	1.00	1.00	1.00	-0.16	0.25
Ion-type	b_7-NH_3	$y{++}_{14}$			$b{++}_{15}$-H_2O	b_7	$b{++}_{15}$	$y{++}_{16}$		y_8-H_3PO_4
Delta Da	-0.05	0.70			0.18	-0.73	-0.29	0.27		0.04

Peak 307

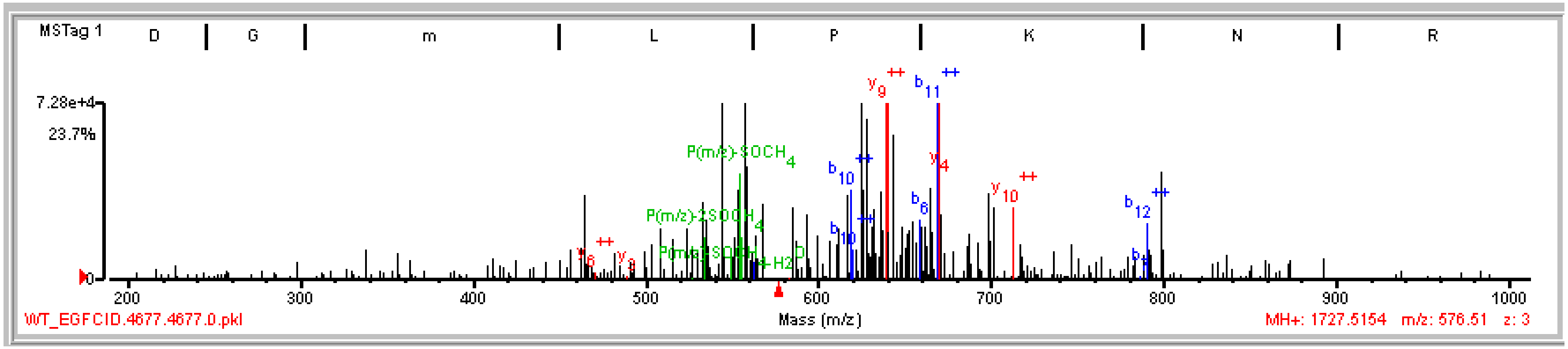


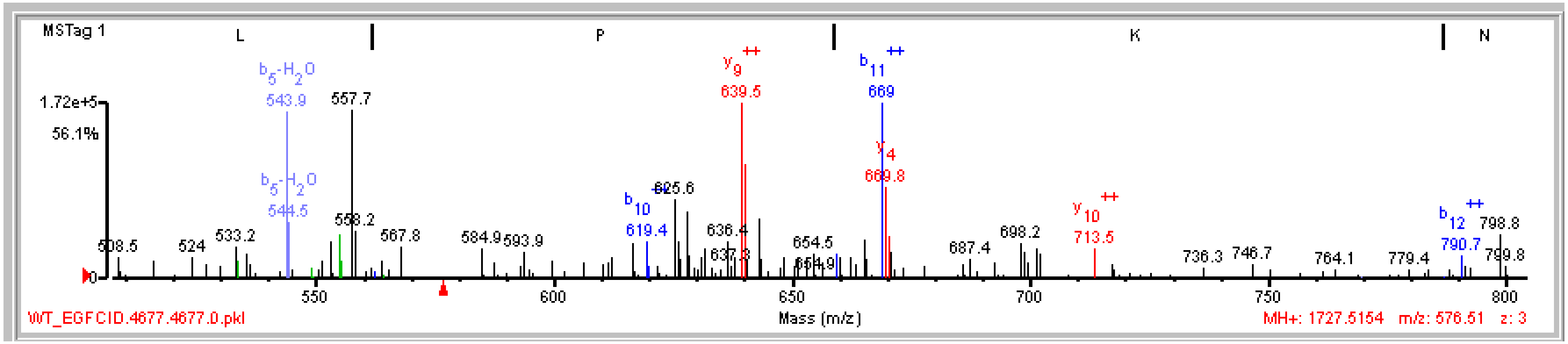


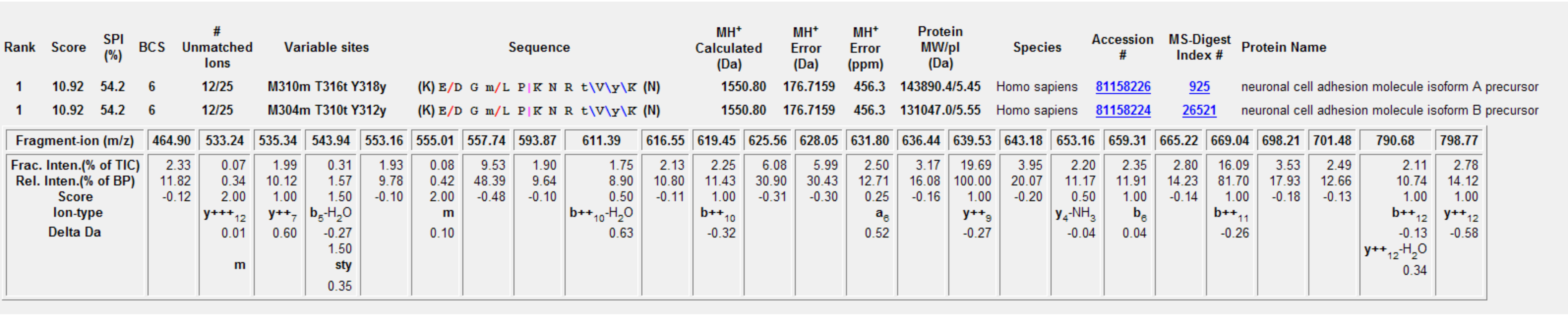
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.34	65.8	11	9/23	T405t Y410y S404s	(R) K E H/V N P/P|A\E/V s t/S/L\K\T\y/Q/H F T L E K (A)	2783.44	240.0219	40.7	63198.8/7.72	Homo sapiens	7710152	2868	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B isoform 1
1	11.34	65.8	11	9/23	T420t Y425y S419s	(R) K E H/V N P/P|A\E/V s t/S/L\K\T\y/Q/H F T L E K (A)	2783.44	240.0219	40.7	64845.5/8.38	Homo sapiens	16915936	12639	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B isoform 2

Fragment-ion (m/z)	715.35	722.30	741.53	744.79	770.45	774.32	779.66	785.64	788.16	799.05	801.73	825.16	840.67	843.54	873.08	877.48	889.65	893.78	898.04	902.40	939.25	1012.04	1135.89
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	3.81 18.45 -0.18	3.81 18.44 -0.18	3.05 14.77 1.00 $y{+}{+}{+}_{17}$ 0.22	4.15 20.11 1.00 $y{+}{+}_{11}$ 0.42	4.12 19.97 -0.20	3.12 15.11 1.00 a_7 -0.11 y_6 -0.09 $y{+}{+}{+}_{18}$ 0.66	2.14 10.36 0.50 $y{+}{+}_{12}\text{-}H_2O$ 0.78	2.41 11.68 0.50 $b_7\text{-}NH_3$ 0.25	2.33 11.30 1.00 $y{+}{+}_{12}$ 0.28	2.45 11.86 -0.12	2.73 13.22 1.00 b_7 -0.69	2.42 11.75 1.00 $b{+}{+}_{14}$ -0.19	3.42 16.58 -0.17	6.29 30.47 -0.30	4.55 22.04 1.00 b_8 -0.38	3.37 16.35 1.00 $y{+}{+}{+}_{21}$ 0.43	2.97 14.37 1.00 $b{+}{+}_{15}$ 0.25	3.39 16.44 -0.16	4.17 20.19 -0.20	20.63 100.00 1.00 y_7 -0.07	4.04 19.59 1.00 $b{+}{+}_{16}$ -0.67	7.91 38.31 1.00 $y{+}{+}_{15}$ 0.62	2.74 13.28 -0.13

Peak 308



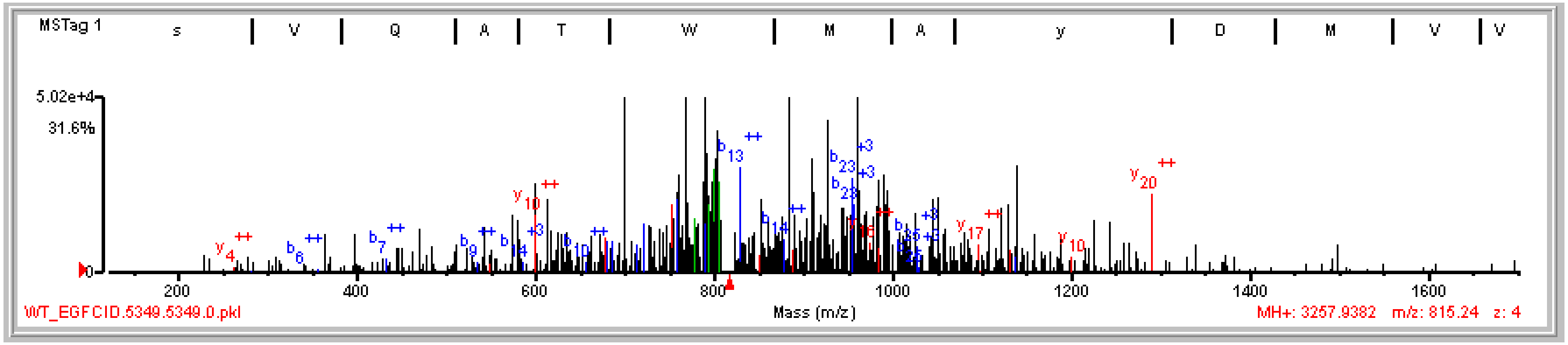


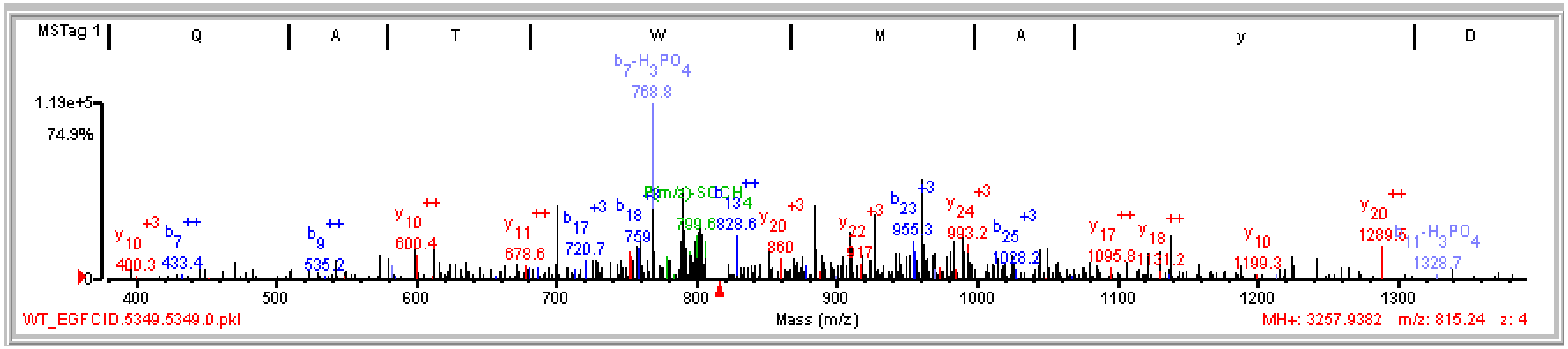


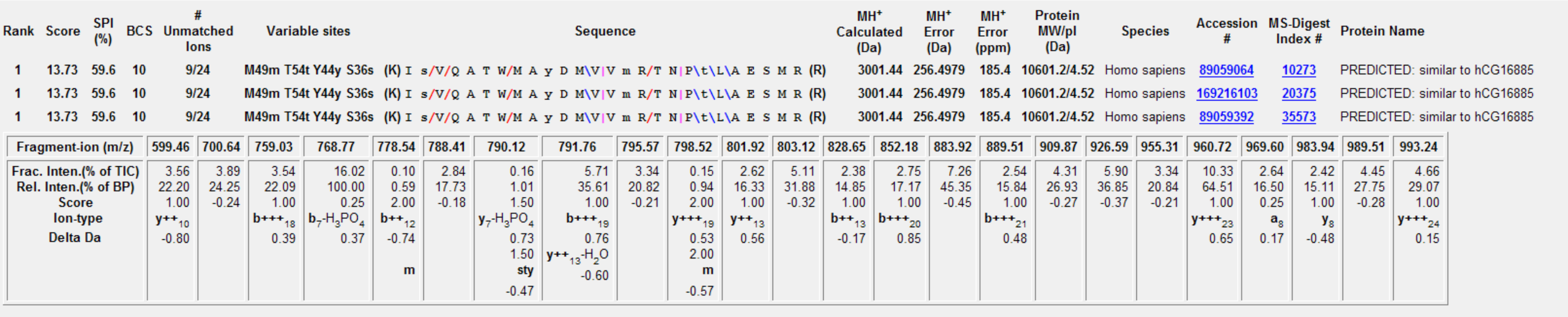
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.92	54.2	6	12/25	M310m T316t Y318y	(K) E/D G m/L P|K N R t\V\y\K (N)	1550.80	176.7159	456.3	143890.4/5.45	Homo sapiens	81158226	925	neuronal cell adhesion molecule isoform A precursor
1	10.92	54.2	6	12/25	M304m T310t Y312y	(K) E/D G m/L P|K N R t\V\y\K (N)	1550.80	176.7159	456.3	131047.0/5.55	Homo sapiens	81158224	26521	neuronal cell adhesion molecule isoform B precursor

Fragment-ion (m/z)	464.90	533.24	535.34	543.94	553.16	555.01	557.74	593.87	611.39	616.55	619.45	625.56	628.05	631.80	636.44	639.53	643.18	653.16	659.31	665.22	669.04	698.21	701.48	790.68	798.77
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	2.33 11.82 -0.12	0.07 0.34 2.00 $y+++_{12}$ 0.01 m	1.99 10.12 1.00 $y++_{7}$ 0.60	0.31 1.57 1.50 b_5-H_2O -0.27 1.50 sty 0.35	1.93 9.78 -0.10	0.08 0.42 2.00 m 0.10	9.53 48.39 -0.48	1.90 9.64 -0.10	1.75 8.90 0.50 $b++_{10}$-H_2O 0.63	2.13 10.80 -0.11	2.25 11.43 1.00 $b++_{10}$ -0.32	6.08 30.90 -0.31	5.99 30.43 -0.30	2.50 12.71 0.25 a_6 0.52	3.17 16.08 -0.16	19.69 100.00 1.00 $y++_{9}$ -0.27	3.95 20.07 -0.20	2.20 11.17 0.50 y_4-NH_3 -0.04	2.35 11.91 1.00 b_6 0.04	2.80 14.23 -0.14	16.09 81.70 1.00 $b++_{11}$ -0.26	3.53 17.93 -0.18	2.49 12.66 -0.13	2.11 10.74 1.00 $b++_{12}$ -0.13 $y++_{12}$-H_2O 0.34	2.78 14.12 1.00 $y++_{12}$ -0.58

Peak 309





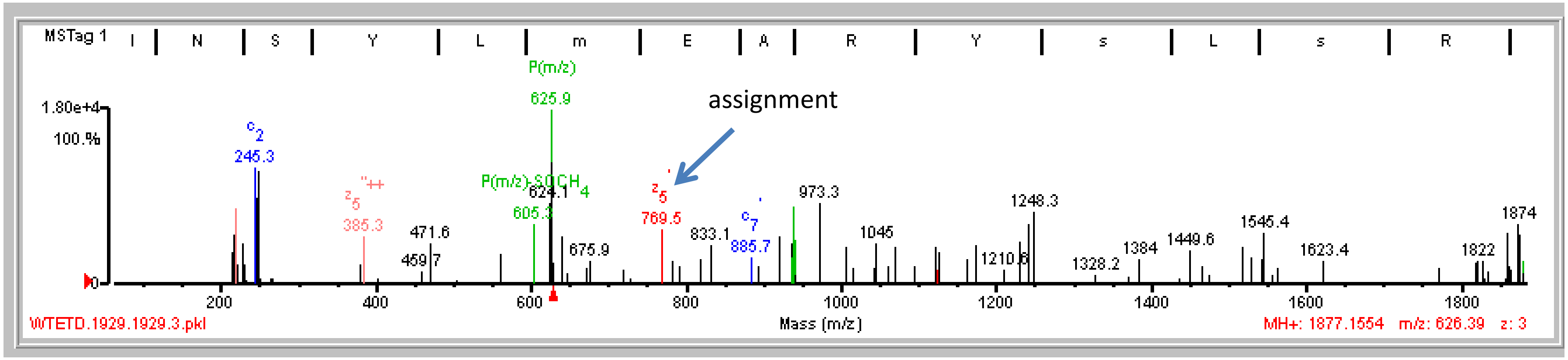


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.73	59.6	10	9/24	M49m T54t Y44y S36s	(K) I s/V/Q A T W/M A y D M\V|V m R/T N|P\t\L\A E S M R (R)	3001.44	256.4979	185.4	10601.2/4.52	Homo sapiens	89059064	10273	PREDICTED: similar to hCG16885
1	13.73	59.6	10	9/24	M49m T54t Y44y S36s	(K) I s/V/Q A T W/M A y D M\V|V m R/T N|P\t\L\A E S M R (R)	3001.44	256.4979	185.4	10601.2/4.52	Homo sapiens	169216103	20375	PREDICTED: similar to hCG16885
1	13.73	59.6	10	9/24	M49m T54t Y44y S36s	(K) I s/V/Q A T W/M A y D M\V|V m R/T N|P\t\L\A E S M R (R)	3001.44	256.4979	185.4	10601.2/4.52	Homo sapiens	89059392	35573	PREDICTED: similar to hCG16885

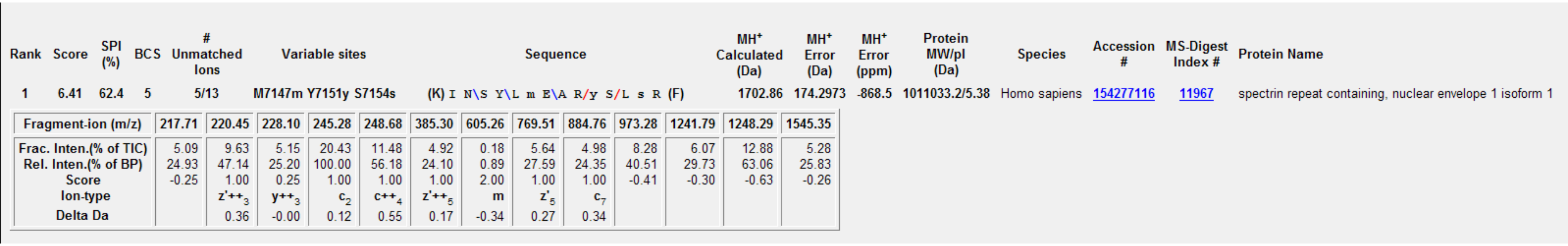
Fragment-ion (m/z)	599.46	700.64	759.03	768.77	778.54	788.41	790.12	791.76	795.57	798.52	801.92
Frac. Inten.(% of TIC)	3.56	3.89	3.54	16.02	0.10	2.84	0.16	5.71	3.34	0.15	2.62
Rel. Inten.(% of BP)	22.20	24.25	22.09	100.00	0.59	17.73	1.01	35.61	20.82	0.94	16.33
Score	1.00	-0.24	1.00	0.25	2.00	-0.18	1.50	1.00	-0.21	2.00	1.00
Ion-type	y^{++}_{10}		b^{+++}_{18}	$b_7\text{-}H_3PO_4$	b^{++}_{12}		$y_7\text{-}H_3PO_4$	b^{+++}_{19}		y^{+++}_{19}	y^{++}_{13}
Delta Da	-0.80		0.39	0.37	-0.74		0.73	0.76		0.53	0.56
							1.50	$y^{++}_{13}\text{-}H_2O$		2.00	
					m		sty	-0.60		m	
							-0.47			-0.57	

Fragment-ion (m/z)	803.12	828.65	852.18	883.92	889.51	909.87	926.59	955.31	960.72	969.60	983.94	989.51	993.24
Frac. Inten.(% of TIC)	5.11	2.38	2.75	7.26	2.54	4.31	5.90	3.34	10.33	2.64	2.42	4.45	4.66
Rel. Inten.(% of BP)	31.88	14.85	17.17	45.35	15.84	26.93	36.85	20.84	64.51	16.50	15.11	27.75	29.07
Score	-0.32	1.00	1.00	-0.45	1.00	-0.27	-0.37	-0.21	1.00	0.25	1.00	-0.28	1.00
Ion-type		b^{++}_{13}	b^{+++}_{20}		b^{+++}_{21}				y^{+++}_{23}	a_8	y_8		y^{+++}_{24}
Delta Da		-0.17	0.85		0.48				0.65	0.17	-0.48		0.15

Peak 310



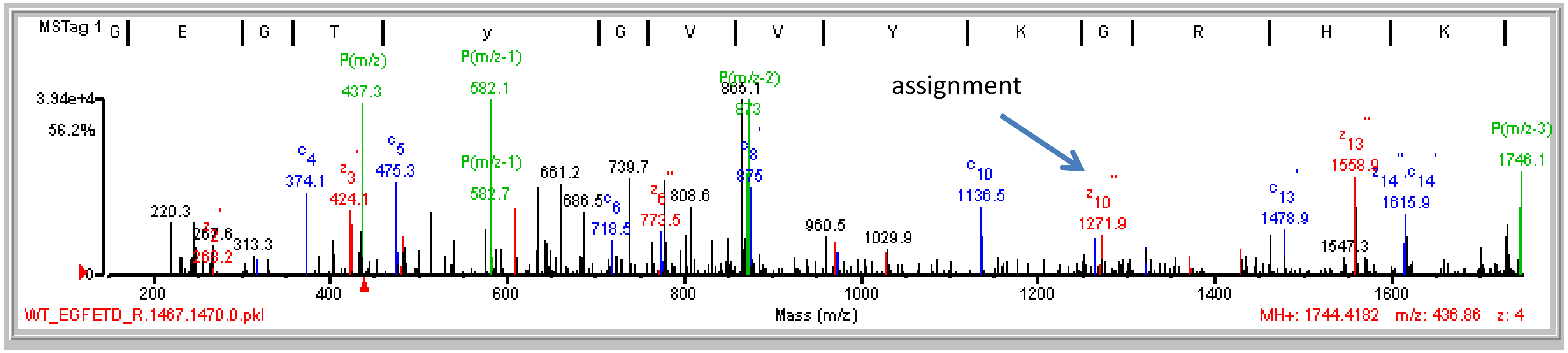
assignment



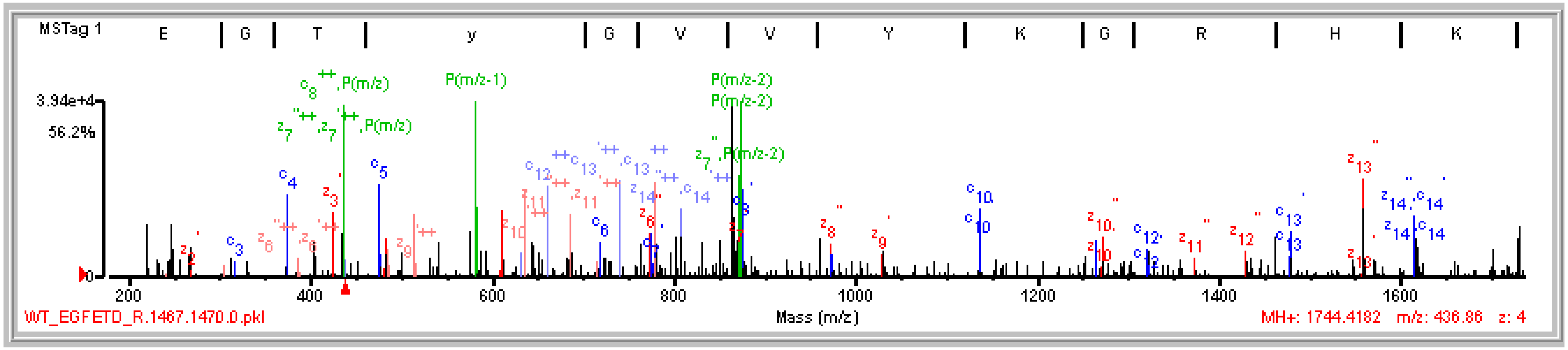
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.41	62.4	5	5/13	M7147m Y7151y S7154s	(K) I N\S Y\L m E\A R/y S/L s R (F)	1702.86	174.2973	-868.5	1011033.2/5.38	Homo sapiens	154277116	11967	spectrin repeat containing, nuclear envelope 1 isoform 1

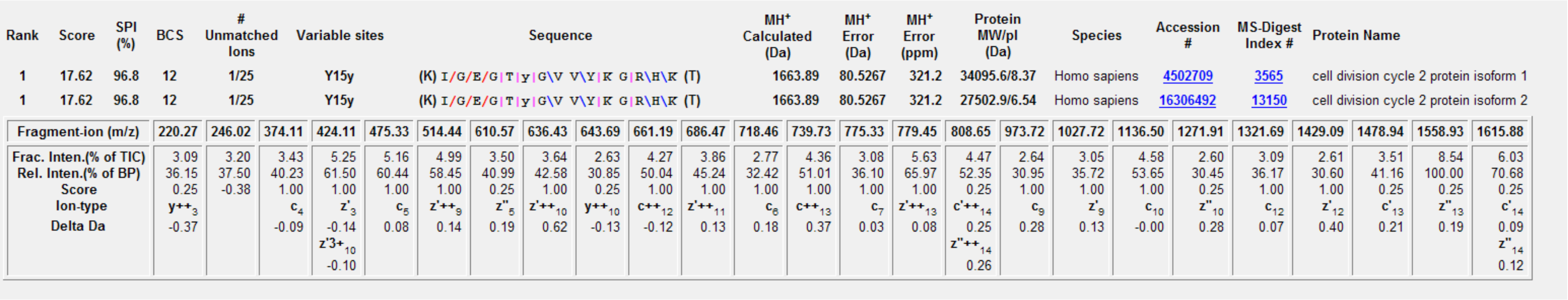
Fragment-ion (m/z)	217.71	220.45	228.10	245.28	248.68	385.30	605.26	769.51	884.76	973.28	1241.79	1248.29	1545.35
Frac. Inten.(% of TIC)	5.09	9.63	5.15	20.43	11.48	4.92	0.18	5.64	4.98	8.28	6.07	12.88	5.28
Rel. Inten.(% of BP)	24.93	47.14	25.20	100.00	56.18	24.10	0.89	27.59	24.35	40.51	29.73	63.06	25.83
Score	-0.25	1.00	0.25	1.00	1.00	1.00	2.00	1.00	1.00	-0.41	-0.30	-0.63	-0.26
Ion-type		z'^{++}_{3}	y^{++}_{3}	c_2	c^{++}_{4}	z'^{++}_{5}	m	z'_5	c_7				
Delta Da		0.36	-0.00	0.12	0.55	0.17	-0.34	0.27	0.34				

Peak 311



assignment





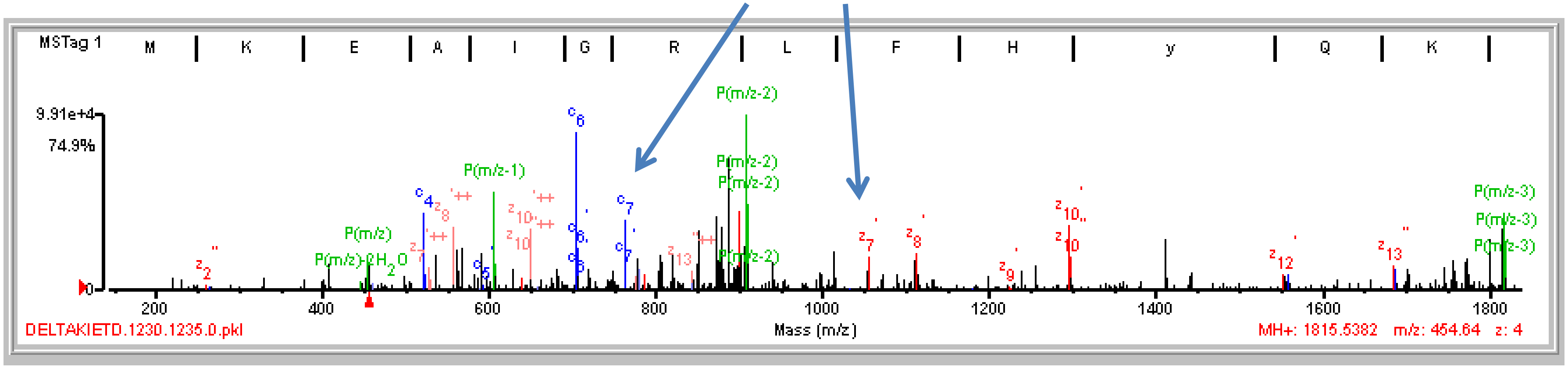
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.62	96.8	12	1/25	Y15y	(K) I/G/E/G|T|y|G\V V\Y|K G|R\H\K (T)	1663.89	80.5267	321.2	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	17.62	96.8	12	1/25	Y15y	(K) I/G/E/G|T|y|G\V V\Y|K G|R\H\K (T)	1663.89	80.5267	321.2	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

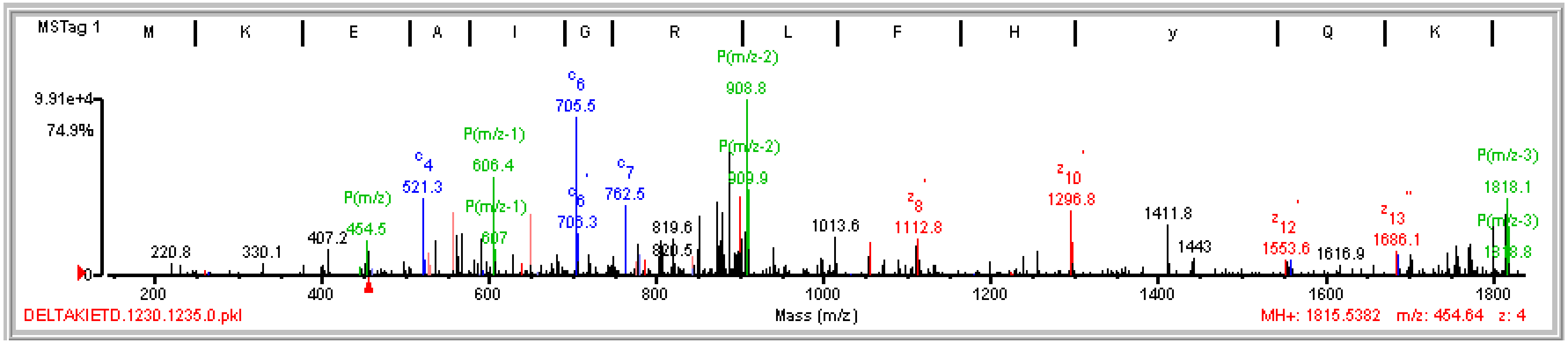
Fragment-ion (m/z)	220.27	246.02	374.11	424.11	475.33	514.44	610.57	636.43	643.69	661.19	686.47	718.46
Frac. Inten.(% of TIC)	3.09	3.20	3.43	5.25	5.16	4.99	3.50	3.64	2.63	4.27	3.86	2.77
Rel. Inten.(% of BP)	36.15	37.50	40.23	61.50	60.44	58.45	40.99	42.58	30.85	50.04	45.24	32.42
Score	0.25	-0.38	1.00	1.00	1.00	1.00	0.25	1.00	0.25	1.00	1.00	1.00
Ion-type	$y{++}_3$		c_4	z'_3 $z'3{+}_{10}$	c_5	$z'{++}_9$	z''_5	$z'{++}_{10}$	$y{++}_{10}$	$c{++}_{12}$	$z'{++}_{11}$	c_6
Delta Da	-0.37		-0.09	-0.14 -0.10	0.08	0.14	0.19	0.62	-0.13	-0.12	0.13	0.18

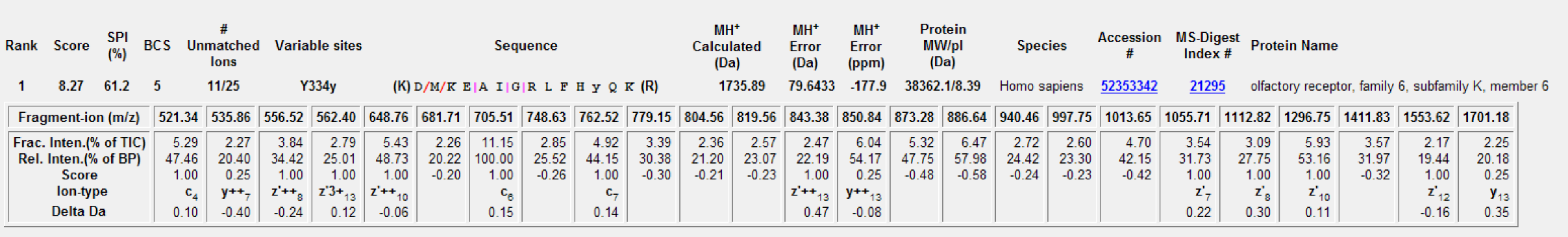
Fragment-ion (m/z)	739.73	775.33	779.45	808.65	973.72	1027.72	1136.50	1271.91	1321.69	1429.09	1478.94	1558.93	1615.88
Frac. Inten.(% of TIC)	4.36	3.08	5.63	4.47	2.64	3.05	4.58	2.60	3.09	2.61	3.51	8.54	6.03
Rel. Inten.(% of BP)	51.01	36.10	65.97	52.35	30.95	35.72	53.65	30.45	36.17	30.60	41.16	100.00	70.68
Score	1.00	1.00	1.00	0.25	1.00	1.00	1.00	0.25	1.00	1.00	0.25	0.25	0.25
Ion-type	$c{++}_{13}$	c_7	$z'{++}_{13}$	$c'{++}_{14}$ $z''{++}_{14}$	c_9	z'_9	c_{10}	z''_{10}	c_{12}	z'_{12}	c'_{13}	z''_{13}	c'_{14} z''_{14}
Delta Da	0.37	0.03	0.08	0.25 0.26	0.28	0.13	-0.00	0.28	0.07	0.40	0.21	0.19	0.09 0.12

Peak 312

Ions that verify assignment







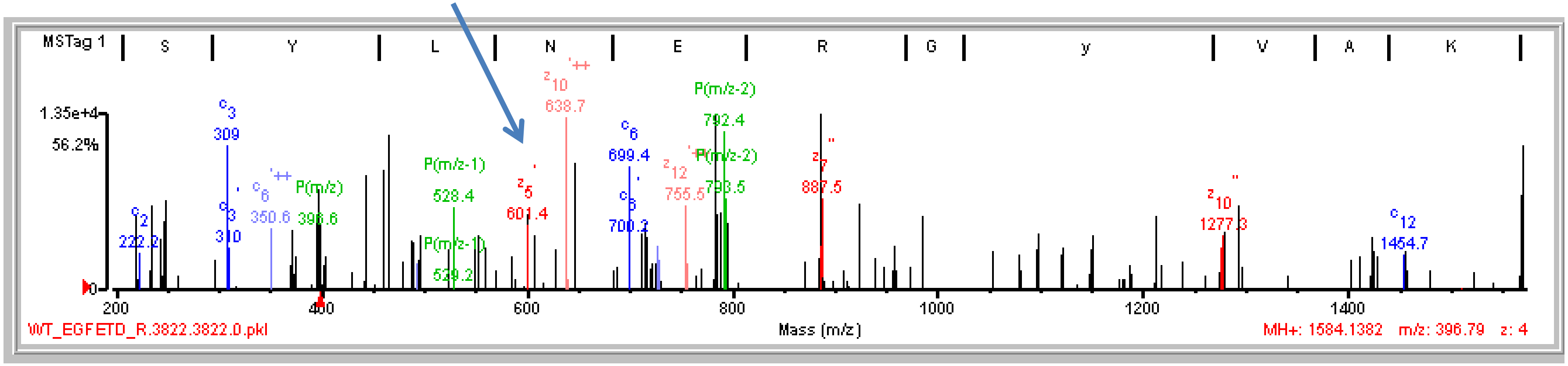
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.27	61.2	5	11/25	Y334y	(K) D/M/K E|A I|G|R L F H y Q K (R)	1735.89	79.6433	-177.9	38362.1/8.39	Homo sapiens	52353342	21295	olfactory receptor, family 6, subfamily K, member 6

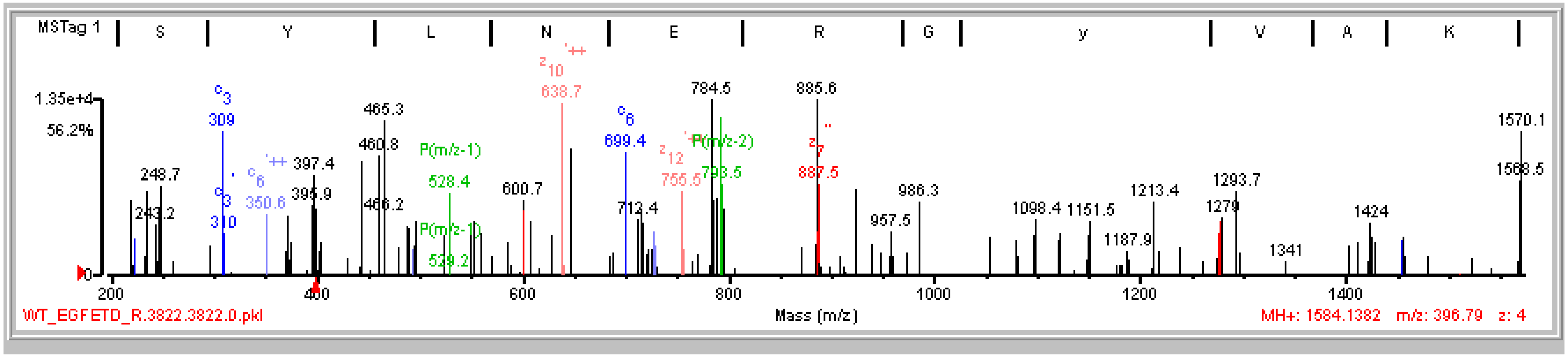
Fragment-ion (m/z)	521.34	535.86	556.52	562.40	648.76	681.71	705.51	748.63	762.52	779.15	804.56	819.56	843.38
Frac. Inten.(% of TIC)	5.29	2.27	3.84	2.79	5.43	2.26	11.15	2.85	4.92	3.39	2.36	2.57	2.47
Rel. Inten.(% of BP)	47.46	20.40	34.42	25.01	48.73	20.22	100.00	25.52	44.15	30.38	21.20	23.07	22.19
Score	1.00	0.25	1.00	1.00	1.00	-0.20	1.00	-0.26	1.00	-0.30	-0.21	-0.23	1.00
Ion-type	c_4	$y++_7$	$z'++_8$	$z'3+_{13}$	$z'++_{10}$		c_6		c_7				$z'++_{13}$
Delta Da	0.10	-0.40	-0.24	0.12	-0.06		0.15		0.14				0.47

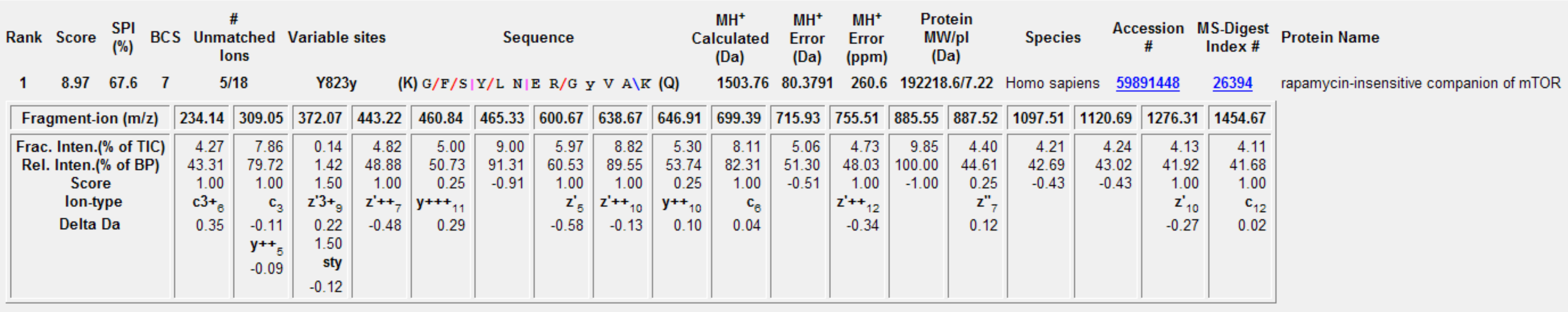
Fragment-ion (m/z)	850.84	873.28	886.64	940.46	997.75	1013.65	1055.71	1112.82	1296.75	1411.83	1553.62	1701.18
Frac. Inten.(% of TIC)	6.04	5.32	6.47	2.72	2.60	4.70	3.54	3.09	5.93	3.57	2.17	2.25
Rel. Inten.(% of BP)	54.17	47.75	57.98	24.42	23.30	42.15	31.73	27.75	53.16	31.97	19.44	20.18
Score	0.25	-0.48	-0.58	-0.24	-0.23	-0.42	1.00	1.00	1.00	-0.32	1.00	0.25
Ion-type	$y++_{13}$						z'_7	z'_8	z'_{10}		z'_{12}	y_{13}
Delta Da	-0.08						0.22	0.30	0.11		-0.16	0.35

Peak 314

Ions that verify assignment



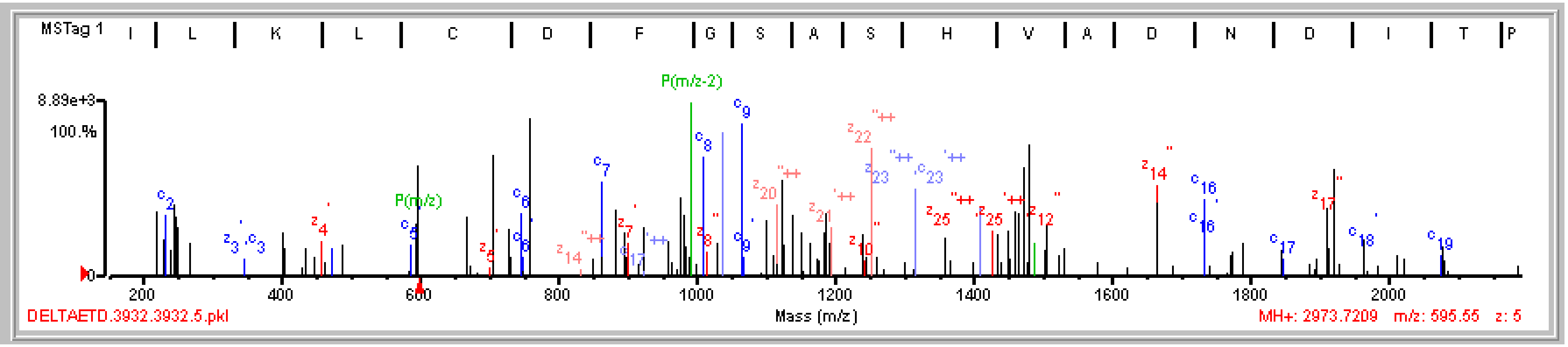


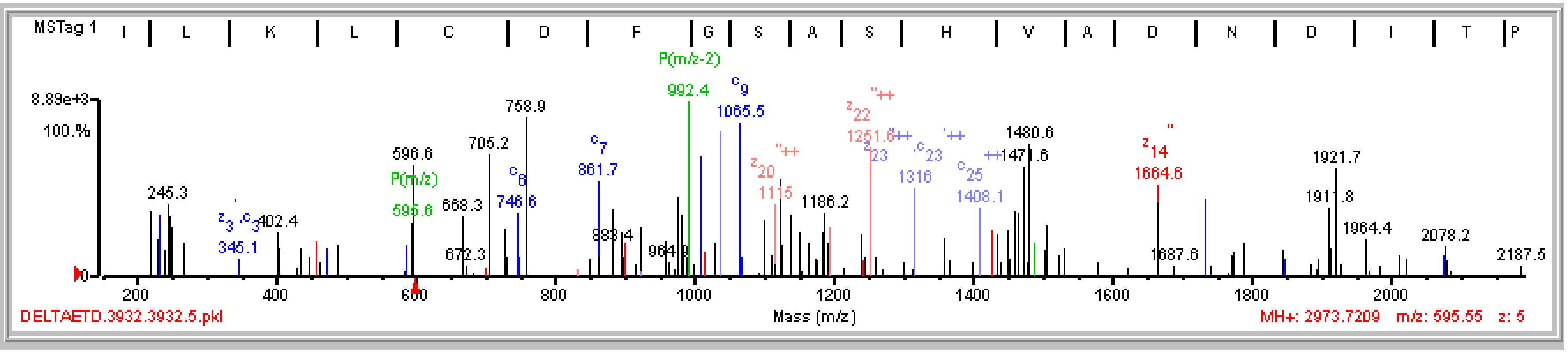


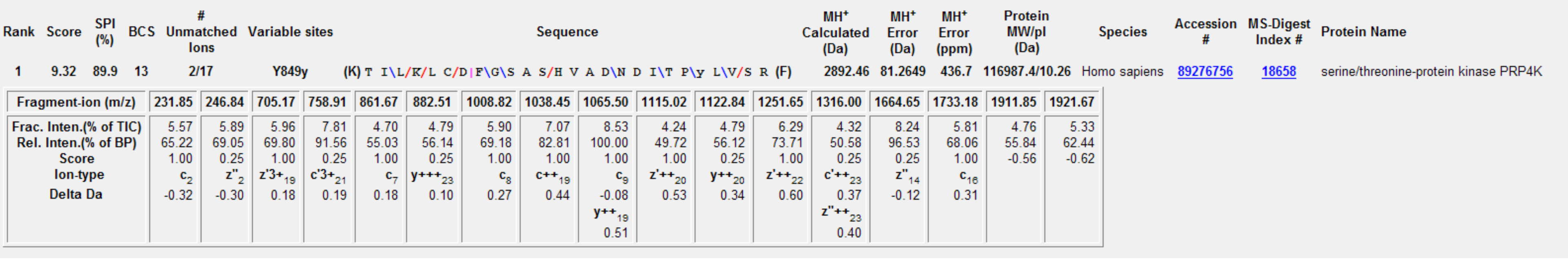
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.97	67.6	7	5/18	Y823y	(K) G/F/S|Y/L N|E R/G y V A\K (Q)	1503.76	80.3791	260.6	192218.6/7.22	Homo sapiens	59891448	26394	rapamycin-insensitive companion of mTOR

Fragment-ion (m/z)	234.14	309.05	372.07	443.22	460.84	465.33	600.67	638.67	646.91	699.39	715.93	755.51	885.55	887.52	1097.51	1120.69	1276.31	1454.67
Frac. Inten.(% of TIC)	4.27	7.86	0.14	4.82	5.00	9.00	5.97	8.82	5.30	8.11	5.06	4.73	9.85	4.40	4.21	4.24	4.13	4.11
Rel. Inten.(% of BP)	43.31	79.72	1.42	48.88	50.73	91.31	60.53	89.55	53.74	82.31	51.30	48.03	100.00	44.61	42.69	43.02	41.92	41.68
Score	1.00	1.00	1.50	1.00	0.25	-0.91	1.00	1.00	0.25	1.00	-0.51	1.00	-1.00	0.25	-0.43	-0.43	1.00	1.00
Ion-type	$c3+_6$	c_3	$z'3+_9$	$z'{++}_7$	$y{+++}_{11}$		z'_5	$z'{++}_{10}$	$y{++}_{10}$	c_6		$z'{++}_{12}$		z''_7			z'_{10}	c_{12}
Delta Da	0.35	-0.11 $y{++}_5$ -0.09	0.22 1.50 sty -0.12	-0.48	0.29		-0.58	-0.13	0.10	0.04		-0.34		0.12			-0.27	0.02

Peak 315



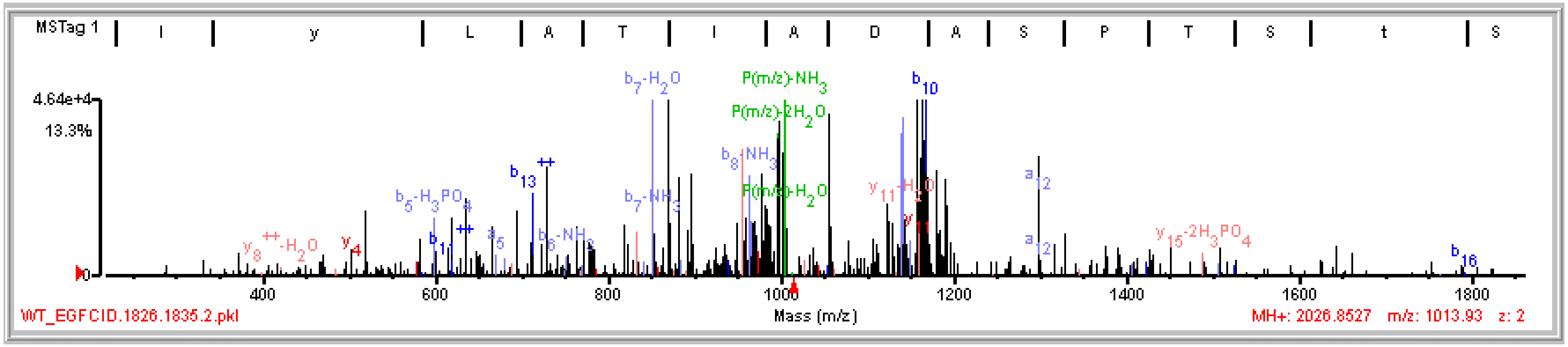


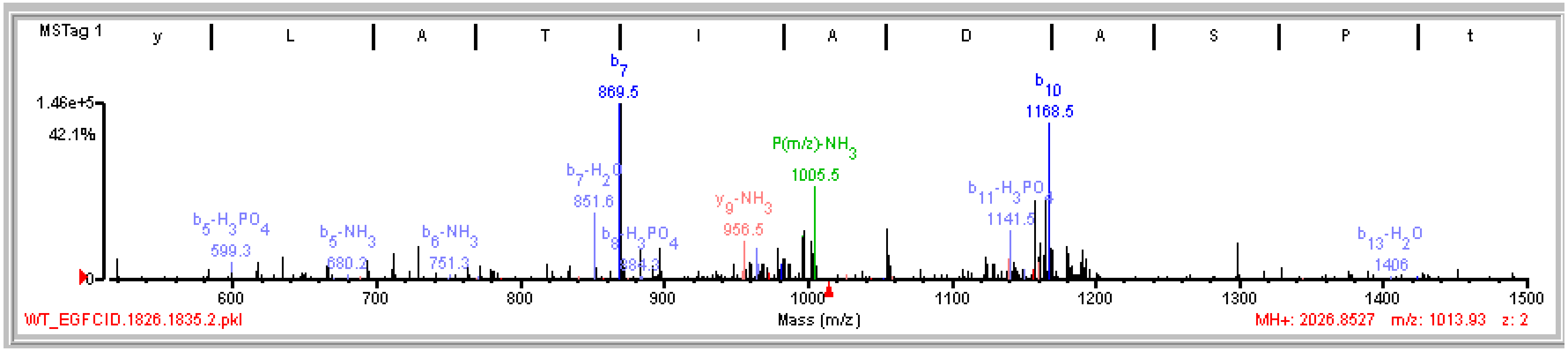


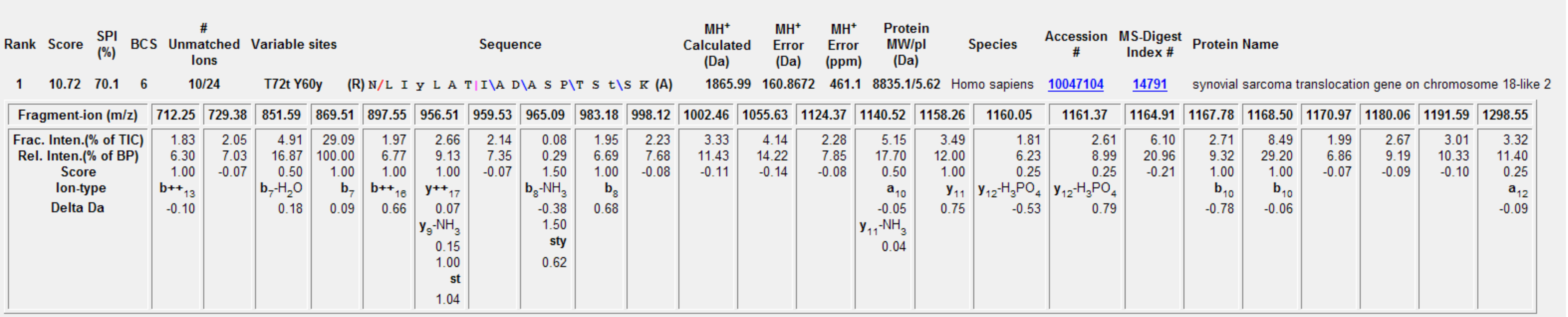
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.32	89.9	13	2/17	Y849y	(K) T I\L/K/L C/D|F\G\S A S/H V A D\N D I\T P\y L\V/S R (F)	2892.46	81.2649	436.7	116987.4/10.26	Homo sapiens	89276756	18658	serine/threonine-protein kinase PRP4K

Fragment-ion (m/z)	231.85	246.84	705.17	758.91	861.67	882.51	1008.82	1038.45	1065.50	1115.02	1122.84	1251.65	1316.00	1664.65	1733.18	1911.85	1921.67
Frac. Inten.(% of TIC)	5.57	5.89	5.96	7.81	4.70	4.79	5.90	7.07	8.53	4.24	4.79	6.29	4.32	8.24	5.81	4.76	5.33
Rel. Inten.(% of BP)	65.22	69.05	69.80	91.56	55.03	56.14	69.18	82.81	100.00	49.72	56.12	73.71	50.58	96.53	68.06	55.84	62.44
Score	1.00	0.25	1.00	0.25	1.00	0.25	1.00	1.00	1.00	1.00	0.25	1.00	0.25	0.25	1.00	-0.56	-0.62
Ion-type	c_2	z''_2	$z'3+_{19}$	$c'3+_{21}$	c_7	$y{+}{+}{+}_{23}$	c_8	$c{+}{+}_{19}$	c_9 $y{+}{+}_{19}$	$z'{+}{+}_{20}$	$y{+}{+}_{20}$	$z'{+}{+}_{22}$	$c'{+}{+}_{23}$ $z''{+}{+}_{23}$	z''_{14}	c_{16}		
Delta Da	-0.32	-0.30	0.18	0.19	0.18	0.10	0.27	0.44	-0.08 0.51	0.53	0.34	0.60	0.37 0.40	-0.12	0.31		

Peak 317





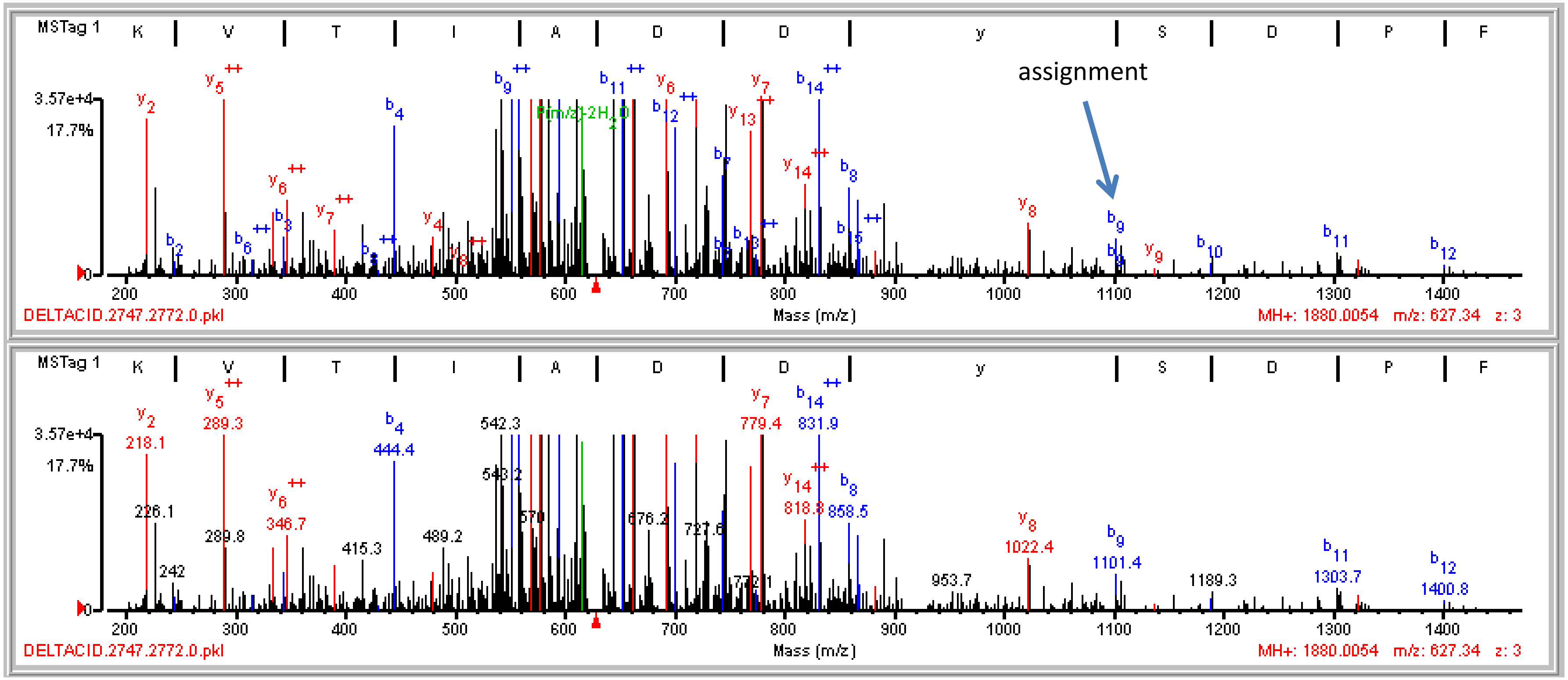


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.72	70.1	6	10/24	T72t Y60y	(R) N/L I y L A T|I\A D\A S P\T S t\S K (A)	1865.99	160.8672	461.1	8835.1/5.62	Homo sapiens	10047104	14791	synovial sarcoma translocation gene on chromosome 18-like 2

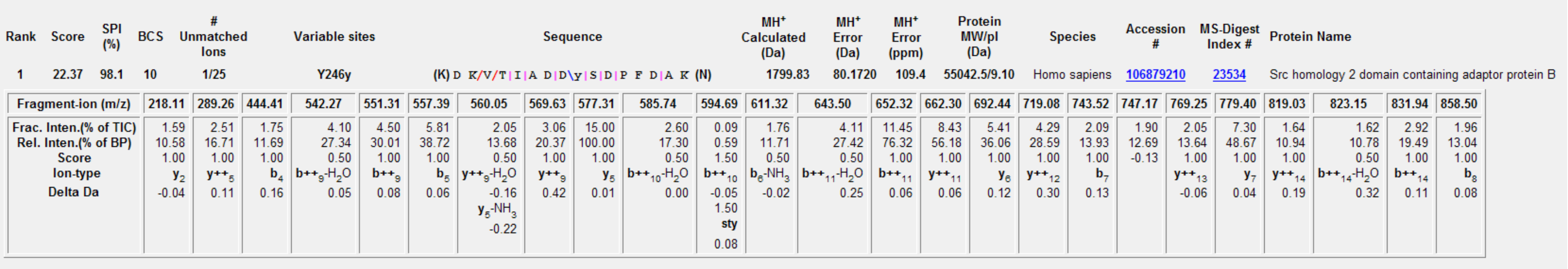
Fragment-ion (m/z)	712.25	729.38	851.59	869.51	897.55	956.51	959.53	965.09	983.18	998.12	1002.46
Frac. Inten.(% of TIC)	1.83	2.05	4.91	29.09	1.97	2.66	2.14	0.08	1.95	2.23	3.33
Rel. Inten.(% of BP)	6.30	7.03	16.87	100.00	6.77	9.13	7.35	0.29	6.69	7.68	11.43
Score	1.00	-0.07	0.50	1.00	1.00	1.00	-0.07	1.50	1.00	-0.08	-0.11
Ion-type	$b{+}{+}_{13}$		b_7-H_2O	b_7	$b{+}{+}_{16}$	$y{+}{+}_{17}$		b_8-NH_3	b_8		
Delta Da	-0.10		0.18	0.09	0.66	0.07 y_9-NH_3 0.15 1.00 st 1.04		-0.38 1.50 sty 0.62	0.68		

Fragment-ion (m/z)	1055.63	1124.37	1140.52	1158.26	1160.05	1161.37	1164.91	1167.78	1168.50	1170.97	1180.06	1191.59	1298.55
Frac. Inten.(% of TIC)	4.14	2.28	5.15	3.49	1.81	2.61	6.10	2.71	8.49	1.99	2.67	3.01	3.32
Rel. Inten.(% of BP)	14.22	7.85	17.70	12.00	6.23	8.99	20.96	9.32	29.20	6.86	9.19	10.33	11.40
Score	-0.14	-0.08	0.50	1.00	0.25	0.25	-0.21	1.00	1.00	-0.07	-0.09	-0.10	0.25
Ion-type			a_{10}	y_{11}	y_{12}-H_3PO_4	y_{12}-H_3PO_4		b_{10}	b_{10}				a_{12}
Delta Da			-0.05 y_{11}-NH_3 0.04	0.75	-0.53	0.79		-0.78	-0.06				-0.09

Peak 318



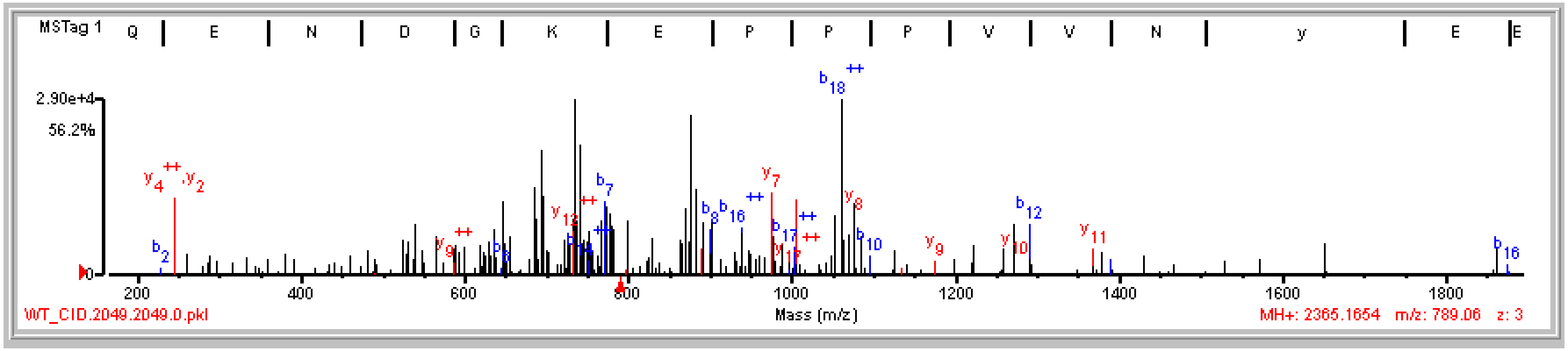
assignment

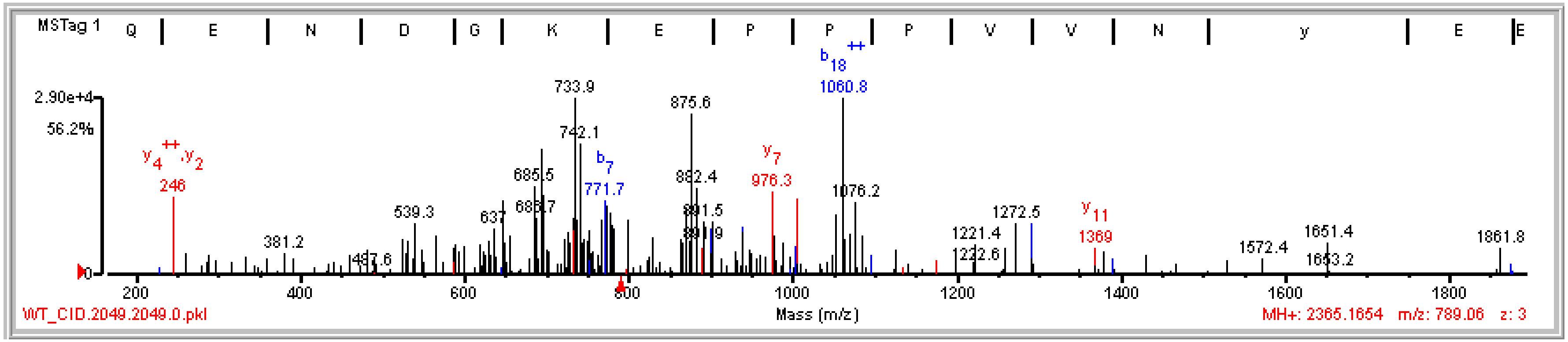


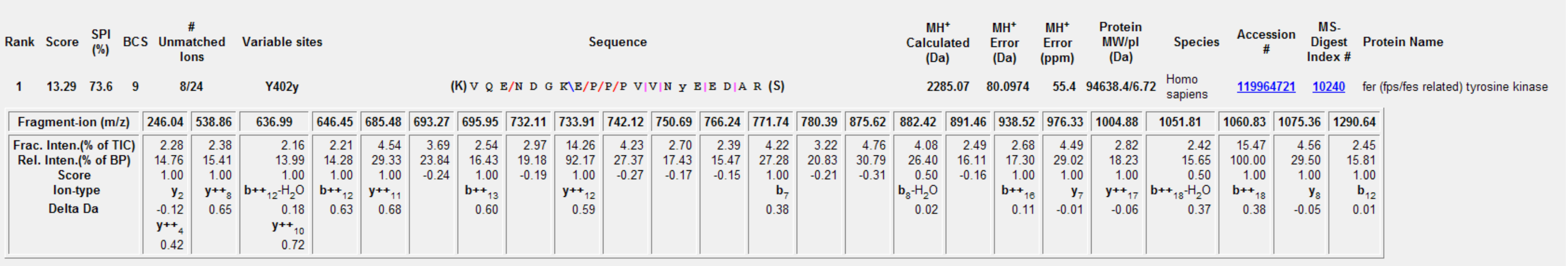
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	22.37	98.1	10	1/25	Y246y	(K) D K/V/T|I|A D|D\y|S|D|P F D|A K (N)	1799.83	80.1720	109.4	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	218.11	289.26	444.41	542.27	551.31	557.39	560.05	569.63	577.31	585.74	594.69	611.32	643.50	652.32	662.30	692.44	719.08	743.52	747.17	769.25	779.40	819.03	823.15	831.94	858.50
Frac. Inten.(% of TIC)	1.59	2.51	1.75	4.10	4.50	5.81	2.05	3.06	15.00	2.60	0.09	1.76	4.11	11.45	8.43	5.41	4.29	2.09	1.90	2.05	7.30	1.64	1.62	2.92	1.96
Rel. Inten.(% of BP)	10.58	16.71	11.69	27.34	30.01	38.72	13.68	20.37	100.00	17.30	0.59	11.71	27.42	76.32	56.18	36.06	28.59	13.93	12.69	13.64	48.67	10.94	10.78	19.49	13.04
Score	1.00	1.00	1.00	0.50	1.00	1.00	0.50	1.00	1.00	0.50	1.50	0.50	0.50	1.00	1.00	1.00	1.00	1.00	-0.13	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	y_2	$y{+}{+}_5$	b_4	$b{+}{+}_9$-H_2O	$b{+}{+}_9$	b_5	$y{+}{+}_9$-H_2O	$y{+}{+}_9$	y_5	$b{+}{+}_{10}$-H_2O	$b{+}{+}_{10}$	b_6-NH_3	$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$	$y{+}{+}_{11}$	y_6	$y{+}{+}_{12}$	b_7		$y{+}{+}_{13}$	y_7	$y{+}{+}_{14}$	$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$	b_8
Delta Da	-0.04	0.11	0.16	0.05	0.08	0.06	-0.16 y_5-NH_3 -0.22	0.42	0.01	0.00	-0.05 1.50 sty 0.08	-0.02	0.25	0.06	0.06	0.12	0.30	0.13		-0.06	0.04	0.19	0.32	0.11	0.08

Peak 319



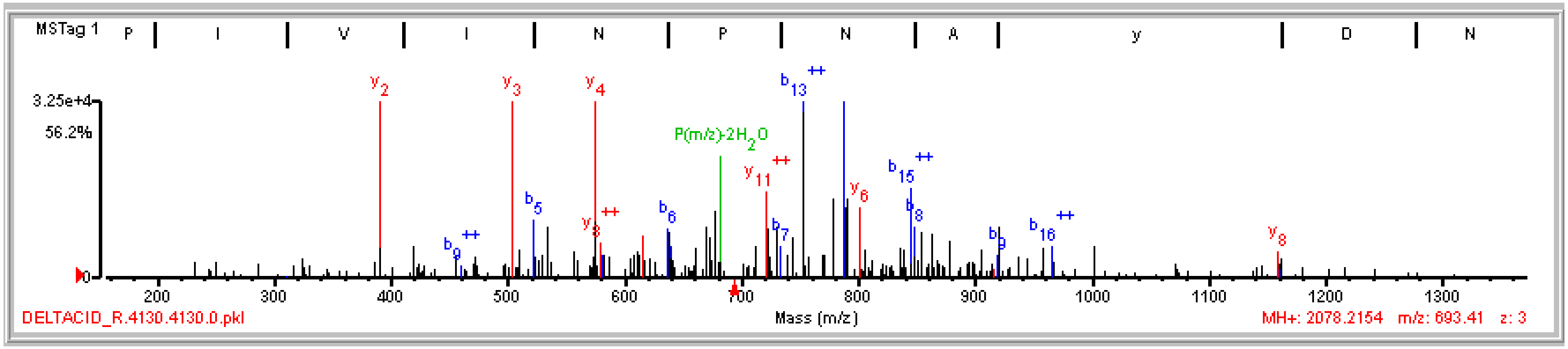


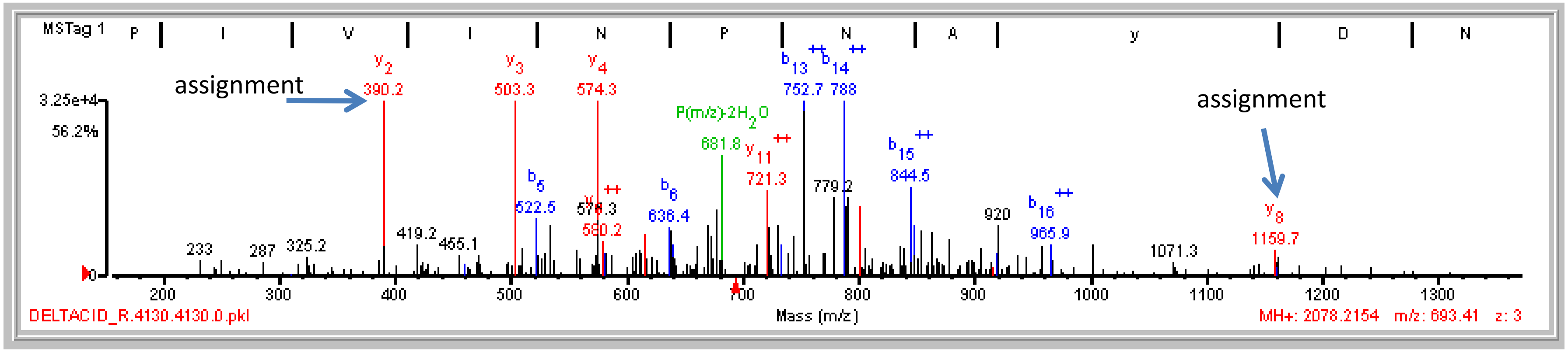


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.29	73.6	9	8/24	Y402y	(K) V Q E/N D G K\E/P/P/P V|V|N y E|E D|A R (S)	2285.07	80.0974	55.4	94638.4/6.72	Homo sapiens	119964721	10240	fer (fps/fes related) tyrosine kinase

Fragment-ion (m/z)	246.04	538.86	636.99	646.45	685.48	693.27	695.95	732.11	733.91	742.12	750.69	766.24	771.74	780.39	875.62	882.42	891.46	938.52	976.33	1004.88	1051.81	1060.83	1075.36	1290.64
Frac. Inten.(% of TIC)	2.28	2.38	2.16	2.21	4.54	3.69	2.54	2.97	14.26	4.23	2.70	2.39	4.22	3.22	4.76	4.08	2.49	2.68	4.49	2.82	2.42	15.47	4.56	2.45
Rel. Inten.(% of BP)	14.76	15.41	13.99	14.28	29.33	23.84	16.43	19.18	92.17	27.37	17.43	15.47	27.28	20.83	30.79	26.40	16.11	17.30	29.02	18.23	15.65	100.00	29.50	15.81
Score	1.00	1.00	1.00	1.00	1.00	-0.24	1.00	-0.19	1.00	-0.27	-0.17	-0.15	1.00	-0.21	-0.31	0.50	-0.16	1.00	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type	y_2 y^{++}_4	y^{++}_8	b^{++}_{12}-H_2O y^{++}_{10}	b^{++}_{12}	y^{++}_{11}		b^{++}_{13}		y^{++}_{12}				b_7			b_8-H_2O		b^{++}_{16}	y_7	y^{++}_{17}	b^{++}_{18}-H_2O	b^{++}_{18}	y_8	b_{12}
Delta Da	-0.12 0.42	0.65	0.18 0.72	0.63	0.68		0.60		0.59				0.38			0.02		0.11	-0.01	-0.06	0.37	0.38	-0.05	0.01

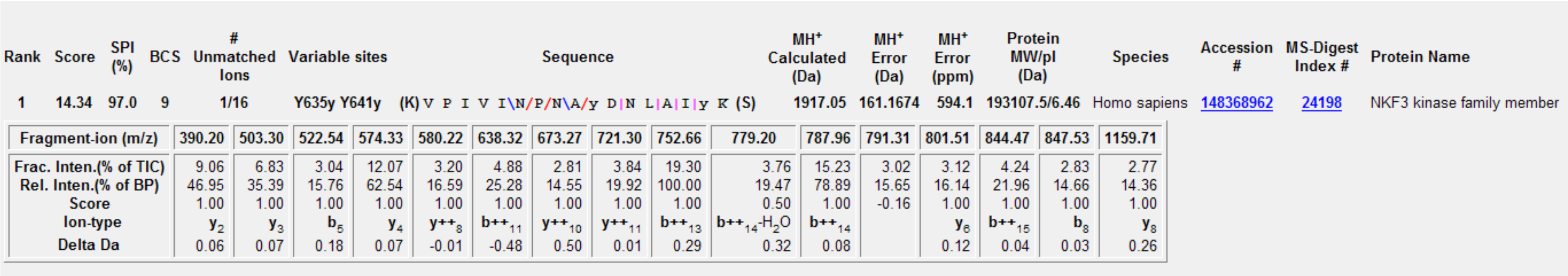
Peak 320





assignment

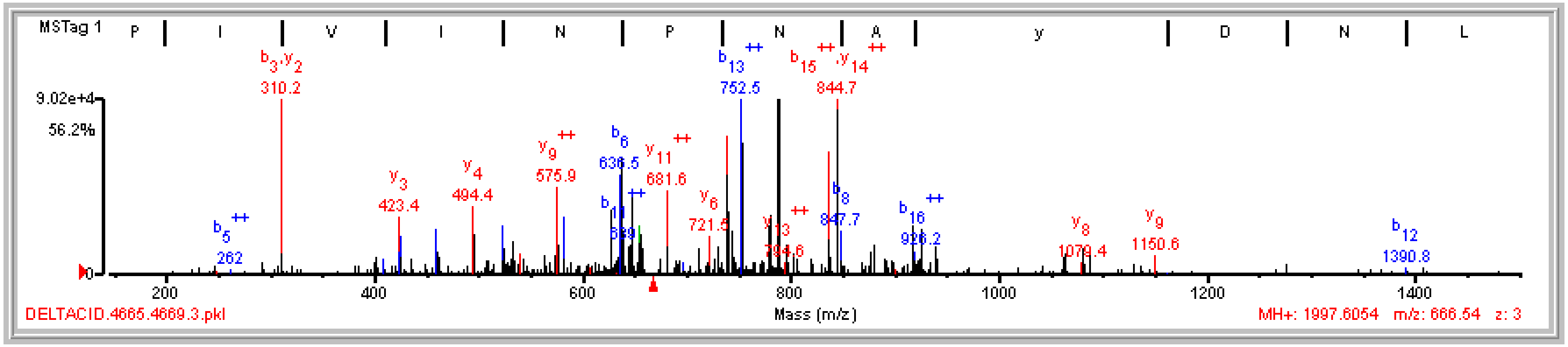
assignment

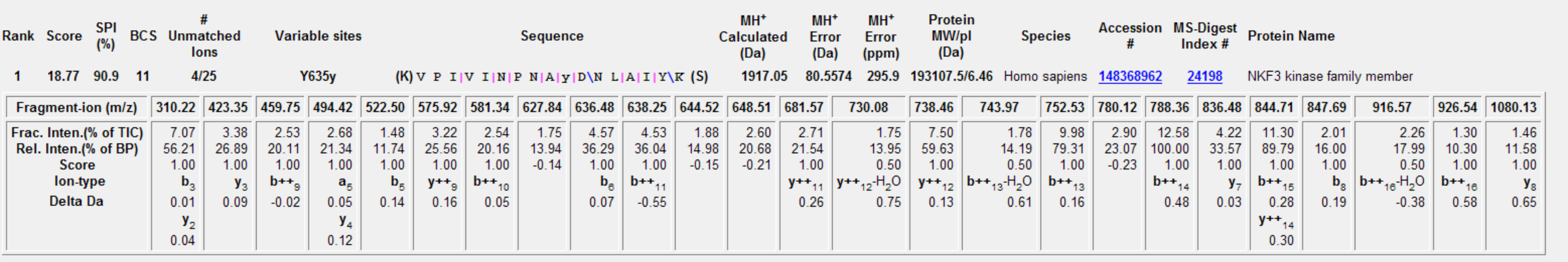


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.34	97.0	9	1/16	Y635y Y641y	(K) V P I V I\N/P/N\A/y D|N L|A|I|y K (S)	1917.05	161.1674	594.1	193107.5/6.46	Homo sapiens	148368962	24198	NKF3 kinase family member

Fragment-ion (m/z)	390.20	503.30	522.54	574.33	580.22	638.32	673.27	721.30	752.66	779.20	787.96	791.31	801.51	844.47	847.53	1159.71
Frac. Inten.(% of TIC)	9.06	6.83	3.04	12.07	3.20	4.88	2.81	3.84	19.30	3.76	15.23	3.02	3.12	4.24	2.83	2.77
Rel. Inten.(% of BP)	46.95	35.39	15.76	62.54	16.59	25.28	14.55	19.92	100.00	19.47	78.89	15.65	16.14	21.96	14.66	14.36
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	-0.16	1.00	1.00	1.00	1.00
Ion-type	y_2	y_3	b_5	y_4	$y{++}_8$	$b{++}_{11}$	$y{++}_{10}$	$y{++}_{11}$	$b{++}_{13}$	$b{++}_{14}$-H_2O	$b{++}_{14}$		y_6	$b{++}_{15}$	b_8	y_8
Delta Da	0.06	0.07	0.18	0.07	-0.01	-0.48	0.50	0.01	0.29	0.32	0.08		0.12	0.04	0.03	0.26

Peak 321



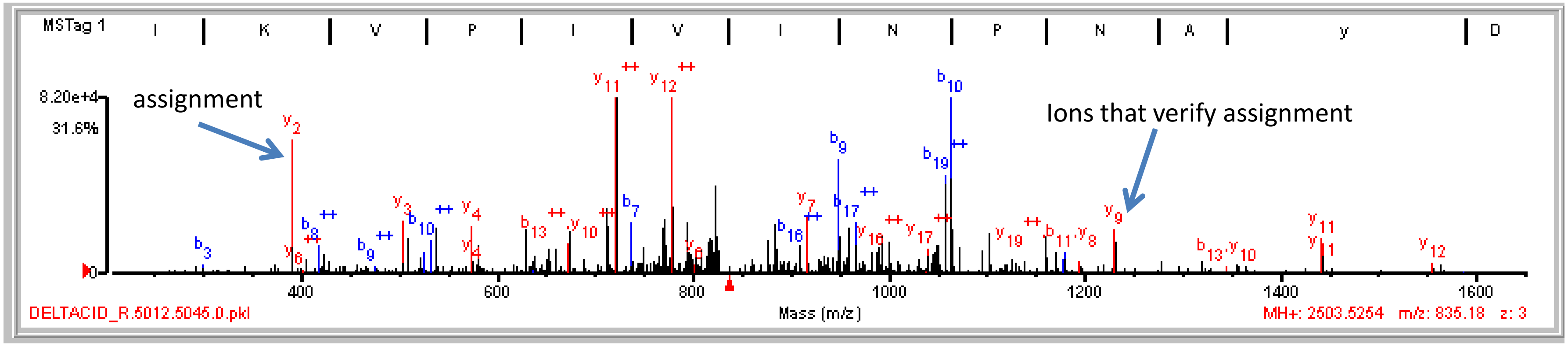


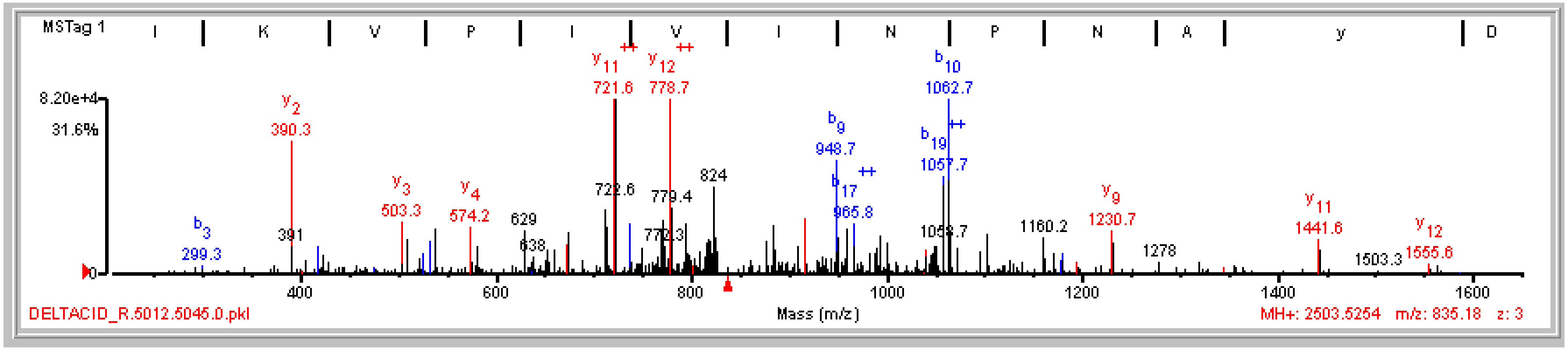
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.77	90.9	11	4/25	Y635y	(K) V P I|V I|N|P N|A|y|D\N L|A|I|Y\K (S)	1917.05	80.5574	295.9	193107.5/6.46	Homo sapiens	148368962	24198	NKF3 kinase family member

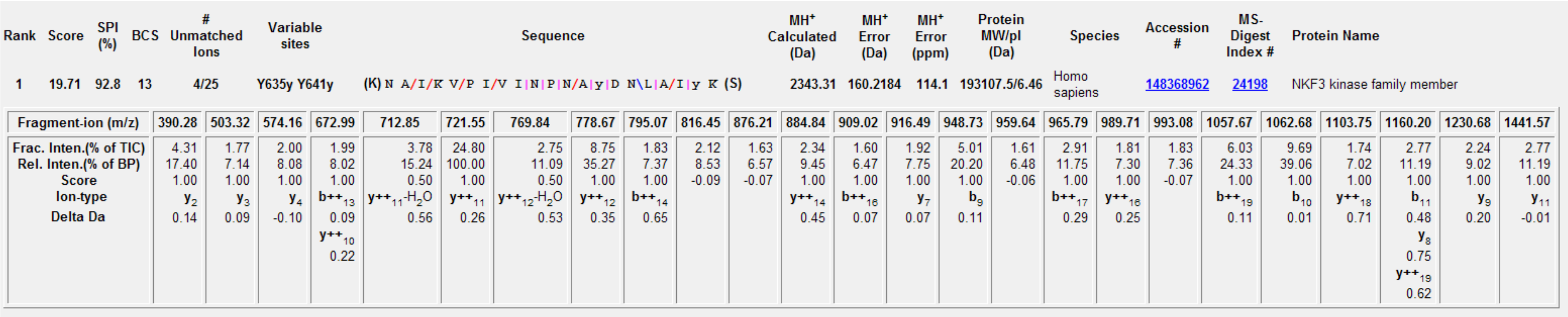
Fragment-ion (m/z)	310.22	423.35	459.75	494.42	522.50	575.92	581.34	627.84	636.48	638.25	644.52	648.51	681.57
Frac. Inten.(% of TIC)	7.07	3.38	2.53	2.68	1.48	3.22	2.54	1.75	4.57	4.53	1.88	2.60	2.71
Rel. Inten.(% of BP)	56.21	26.89	20.11	21.34	11.74	25.56	20.16	13.94	36.29	36.04	14.98	20.68	21.54
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.14	1.00	1.00	-0.15	-0.21	1.00
Ion-type	b_3 y_2	y_3	$b{++}_9$	a_5 y_4	b_5	$y{++}_9$	$b{++}_{10}$		b_6	$b{++}_{11}$			$y{++}_{11}$
Delta Da	0.01 0.04	0.09	-0.02	0.05 0.12	0.14	0.16	0.05		0.07	-0.55			0.26

Fragment-ion (m/z)	730.08	738.46	743.97	752.53	780.12	788.36	836.48	844.71	847.69	916.57	926.54	1080.13
Frac. Inten.(% of TIC)	1.75	7.50	1.78	9.98	2.90	12.58	4.22	11.30	2.01	2.26	1.30	1.46
Rel. Inten.(% of BP)	13.95	59.63	14.19	79.31	23.07	100.00	33.57	89.79	16.00	17.99	10.30	11.58
Score	0.50	1.00	0.50	1.00	-0.23	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	$y{++}_{12}$-H_2O	$y{++}_{12}$	$b{++}_{13}$-H_2O	$b{++}_{13}$		$b{++}_{14}$	y_7	$b{++}_{15}$ $y{++}_{14}$	b_8	$b{++}_{16}$-H_2O	$b{++}_{16}$	y_8
Delta Da	0.75	0.13	0.61	0.16		0.48	0.03	0.28 0.30	0.19	-0.38	0.58	0.65

Peak 322





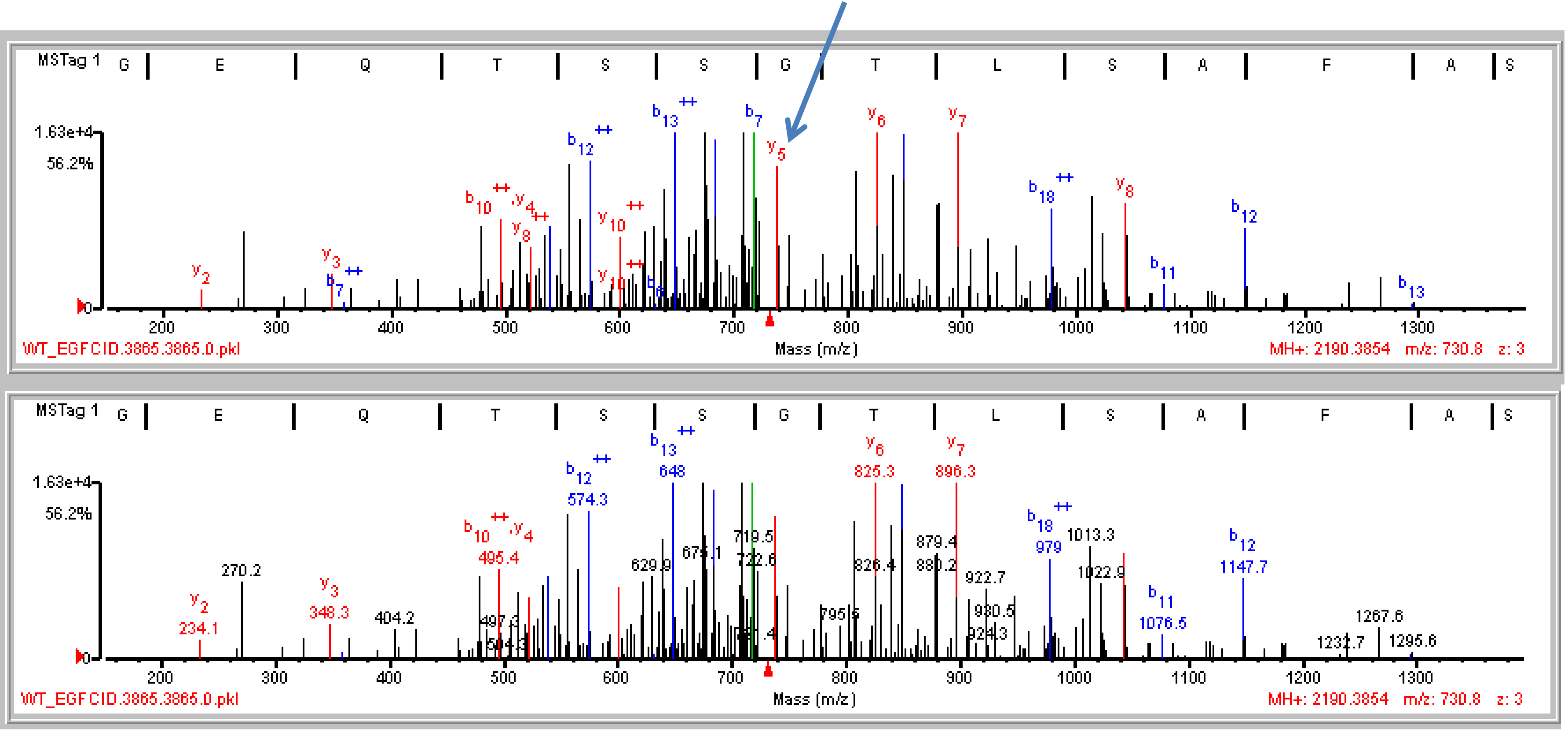


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.71	92.8	13	4/25	Y635y Y641y	(K) N A/I/K V/P I/V I|N|P|N/A|y|D N\L|A/I|y K (S)	2343.31	160.2184	114.1	193107.5/6.46	Homo sapiens	148368962	24198	NKF3 kinase family member

Fragment-ion (m/z)	390.28	503.32	574.16	672.99	712.85	721.55	769.84	778.67	795.07	816.45	876.21
Frac. Inten.(% of TIC)	4.31	1.77	2.00	1.99	3.78	24.80	2.75	8.75	1.83	2.12	1.63
Rel. Inten.(% of BP)	17.40	7.14	8.08	8.02	15.24	100.00	11.09	35.27	7.37	8.53	6.57
Score	1.00	1.00	1.00	1.00	0.50	1.00	0.50	1.00	1.00	-0.09	-0.07
Ion-type	y_2	y_3	y_4	$b{++}_{13}$ $y{++}_{10}$	$y{++}_{11}$-H_2O	$y{++}_{11}$	$y{++}_{12}$-H_2O	$y{++}_{12}$	$b{++}_{14}$		
Delta Da	0.14	0.09	-0.10	0.09 0.22	0.56	0.26	0.53	0.35	0.65		

Fragment-ion (m/z)	884.84	909.02	916.49	948.73	959.64	965.79	989.71	993.08	1057.67	1062.68	1103.75	1160.20	1230.68	1441.57
Frac. Inten.(% of TIC)	2.34	1.60	1.92	5.01	1.61	2.91	1.81	1.83	6.03	9.69	1.74	2.77	2.24	2.77
Rel. Inten.(% of BP)	9.45	6.47	7.75	20.20	6.48	11.75	7.30	7.36	24.33	39.06	7.02	11.19	9.02	11.19
Score	1.00	1.00	1.00	1.00	-0.06	1.00	1.00	-0.07	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	$y{++}_{14}$	$b{++}_{16}$	y_7	b_9		$b{++}_{17}$	$y{++}_{16}$		$b{++}_{19}$	b_{10}	$y{++}_{18}$	b_{11} y_8 $y{++}_{19}$	y_9	y_{11}
Delta Da	0.45	0.07	0.07	0.11		0.29	0.25		0.11	0.01	0.71	0.48 0.75 0.62	0.20	-0.01

Peak 323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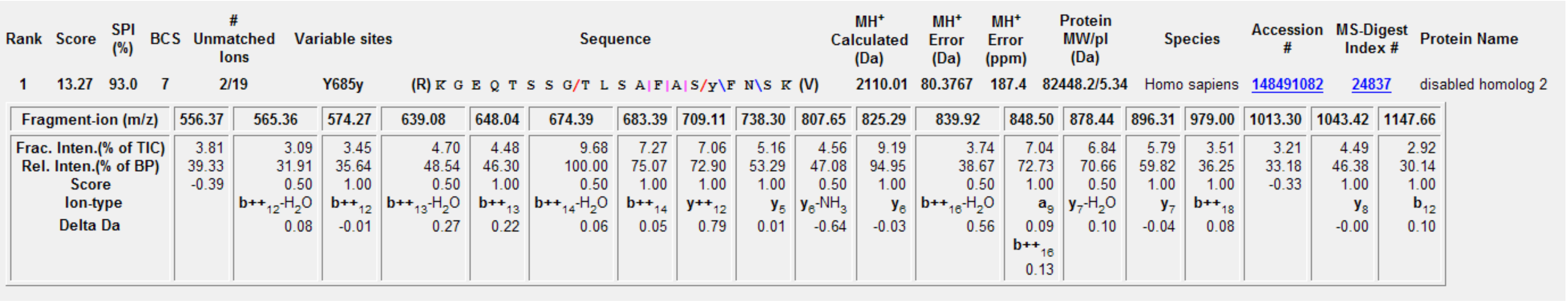
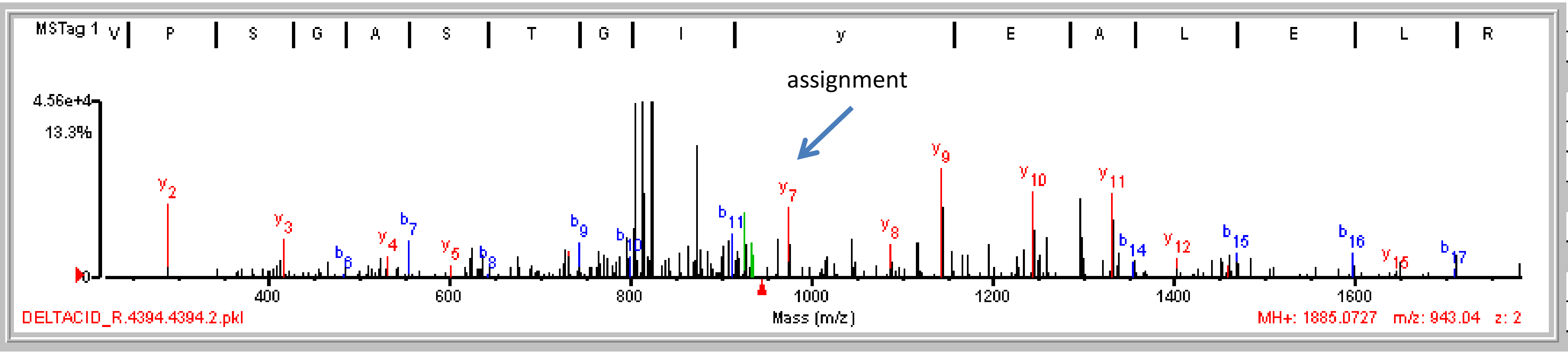


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.27	93.0	7	2/19	Y685y	(R) K G E Q T S S G/T L S A|F|A|S/y\F N\S K (V)	2110.01	80.3767	187.4	82448.2/5.34	Homo sapiens	148491082	24837	disabled homolog 2

Fragment-ion (m/z)	556.37	565.36	574.27	639.08	648.04	674.39	683.39	709.11	738.30	807.65
Frac. Inten.(% of TIC)	3.81	3.09	3.45	4.70	4.48	9.68	7.27	7.06	5.16	4.56
Rel. Inten.(% of BP)	39.33	31.91	35.64	48.54	46.30	100.00	75.07	72.90	53.29	47.08
Score	-0.39	0.50	1.00	0.50	1.00	0.50	1.00	1.00	1.00	0.50
Ion-type		b++$_{12}$-H$_2$O	b++$_{12}$	b++$_{13}$-H$_2$O	b++$_{13}$	b++$_{14}$-H$_2$O	b++$_{14}$	y++$_{12}$	y$_5$	y$_6$-NH$_3$
Delta Da		0.08	-0.01	0.27	0.22	0.06	0.05	0.79	0.01	-0.64

Fragment-ion (m/z)	825.29	839.92	848.50	878.44	896.31	979.00	1013.30	1043.42	1147.66
Frac. Inten.(% of TIC)	9.19	3.74	7.04	6.84	5.79	3.51	3.21	4.49	2.92
Rel. Inten.(% of BP)	94.95	38.67	72.73	70.66	59.82	36.25	33.18	46.38	30.14
Score	1.00	0.50	1.00	0.50	1.00	1.00	-0.33	1.00	1.00
Ion-type	y$_6$	b++$_{16}$-H$_2$O	a$_9$ b++$_{16}$	y$_7$-H$_2$O	y$_7$	b++$_{18}$		y$_8$	b$_{12}$
Delta Da	-0.03	0.56	0.09 0.13	0.10	-0.04	0.08		-0.00	0.10

Peak 324



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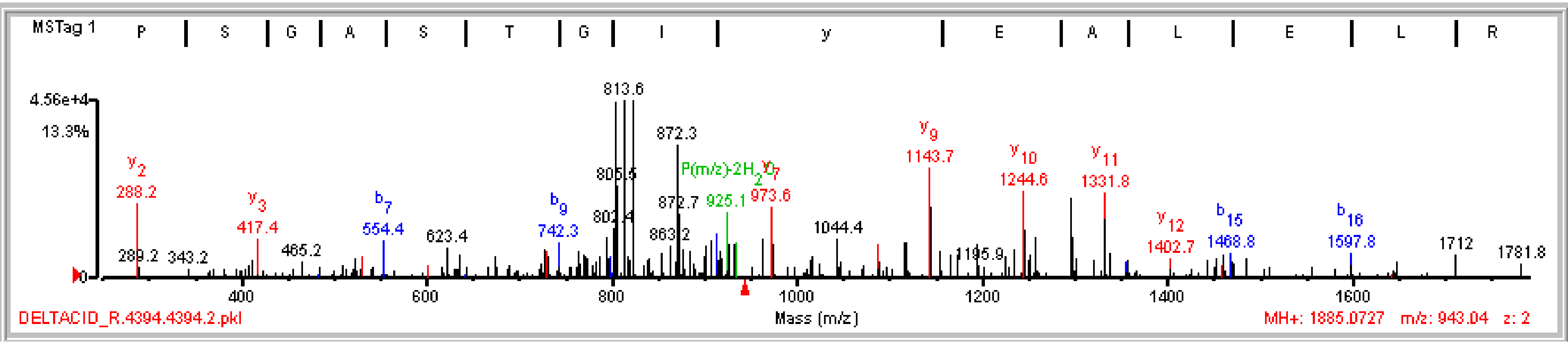
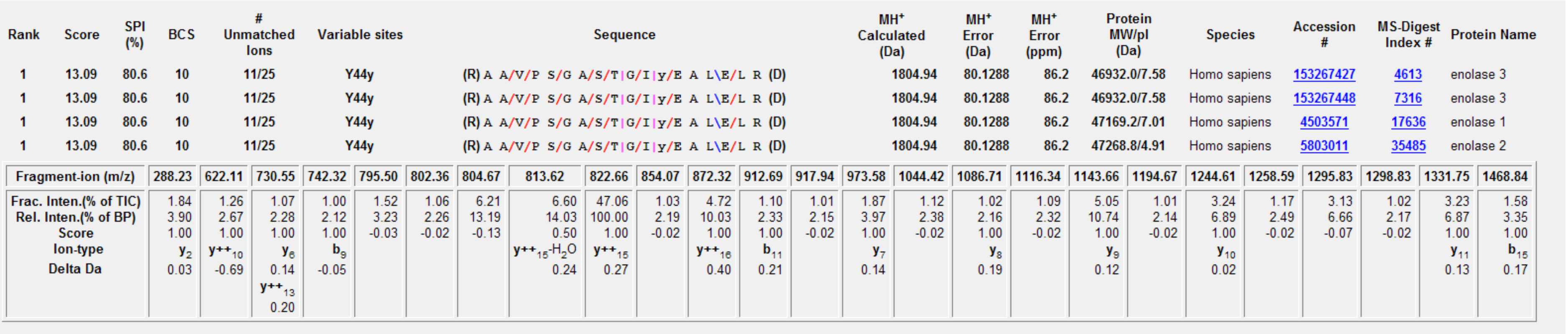


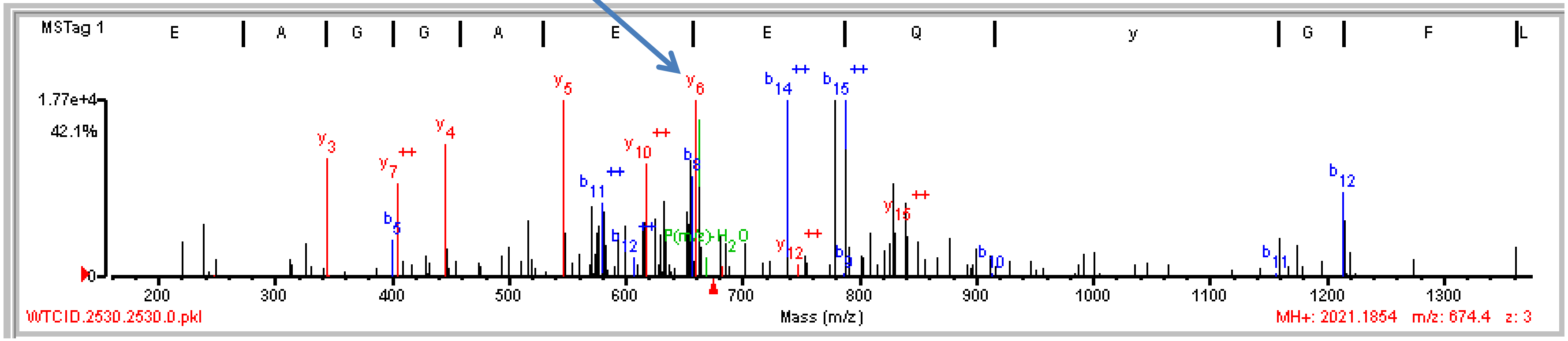


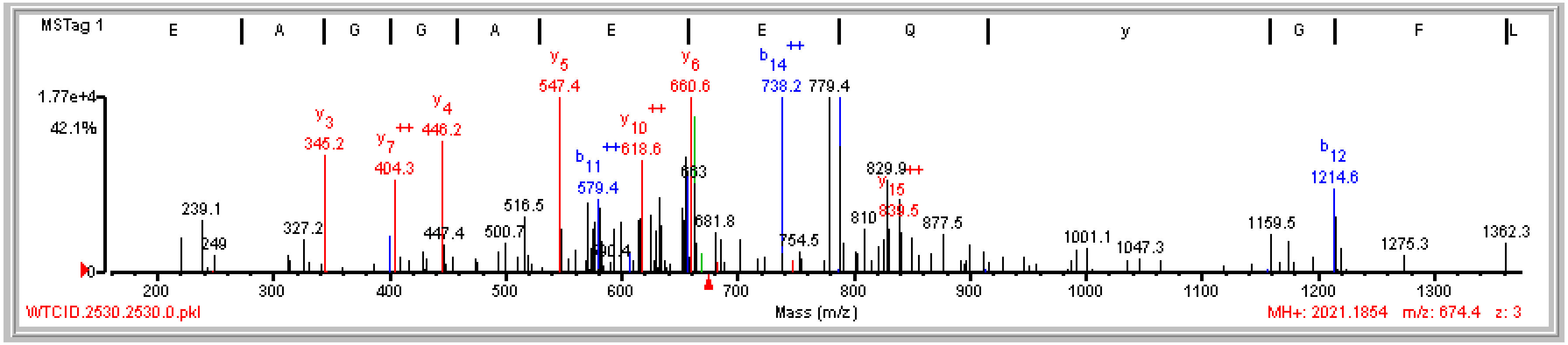
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.09	80.6	10	11/25	Y44y	(R) A A/V/P S/G A/S/T|G/I|y/E A L\E/L R (D)	1804.94	80.1288	86.2	46932.0/7.58	Homo sapiens	153267427	4613	enolase 3
1	13.09	80.6	10	11/25	Y44y	(R) A A/V/P S/G A/S/T|G/I|y/E A L\E/L R (D)	1804.94	80.1288	86.2	46932.0/7.58	Homo sapiens	153267448	7316	enolase 3
1	13.09	80.6	10	11/25	Y44y	(R) A A/V/P S/G A/S/T|G/I|y/E A L\E/L R (D)	1804.94	80.1288	86.2	47169.2/7.01	Homo sapiens	4503571	17636	enolase 1
1	13.09	80.6	10	11/25	Y44y	(R) A A/V/P S/G A/S/T|G/I|y/E A L\E/L R (D)	1804.94	80.1288	86.2	47268.8/4.91	Homo sapiens	5803011	35485	enolase 2

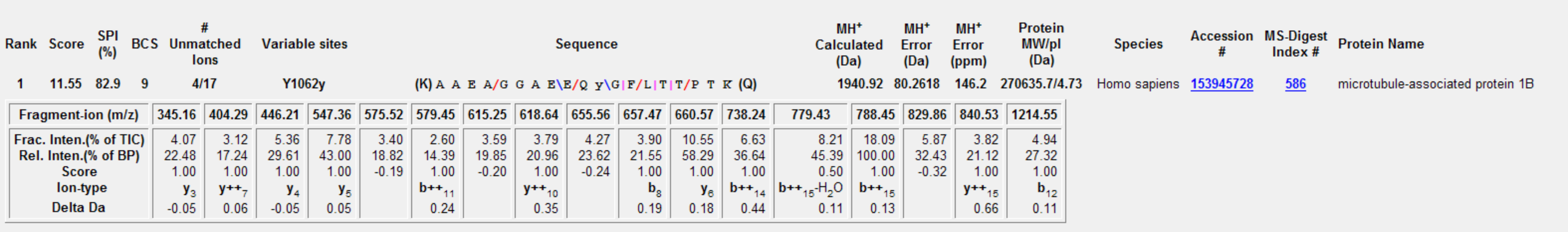
Fragment-ion (m/z)	288.23	622.11	730.55	742.32	795.50	802.36	804.67	813.62	822.66	854.07	872.32	912.69	917.94	973.58	1044.42	1086.71	1116.34	1143.66	1194.67	1244.61	1258.59	1295.83	1298.83	1331.75	1468.84
Frac. Inten.(% of TIC)	1.84	1.26	1.07	1.00	1.52	1.06	6.21	6.60	47.06	1.03	4.72	1.10	1.01	1.87	1.12	1.02	1.09	5.05	1.01	3.24	1.17	3.13	1.02	3.23	1.58
Rel. Inten.(% of BP)	3.90	2.67	2.28	2.12	3.23	2.26	13.19	14.03	100.00	2.19	10.03	2.33	2.15	3.97	2.38	2.16	2.32	10.74	2.14	6.89	2.49	6.66	2.17	6.87	3.35
Score	1.00	1.00	1.00	1.00	-0.03	-0.02	-0.13	0.50	1.00	-0.02	1.00	1.00	-0.02	1.00	-0.02	1.00	-0.02	1.00	-0.02	1.00	-0.02	-0.07	-0.02	1.00	1.00
Ion-type	y_2	$y{+}{+}_{10}$	y_6 $y{+}{+}_{13}$	b_9				$y{+}{+}_{15}$-H_2O	$y{+}{+}_{15}$		$y{+}{+}_{16}$	b_{11}		y_7		y_8		y_9		y_{10}				y_{11}	b_{15}
Delta Da	0.03	-0.69	0.14 0.20	-0.05				0.24	0.27		0.40	0.21		0.14		0.19		0.12		0.02				0.13	0.17

Peak 325

Ions that verify assignment



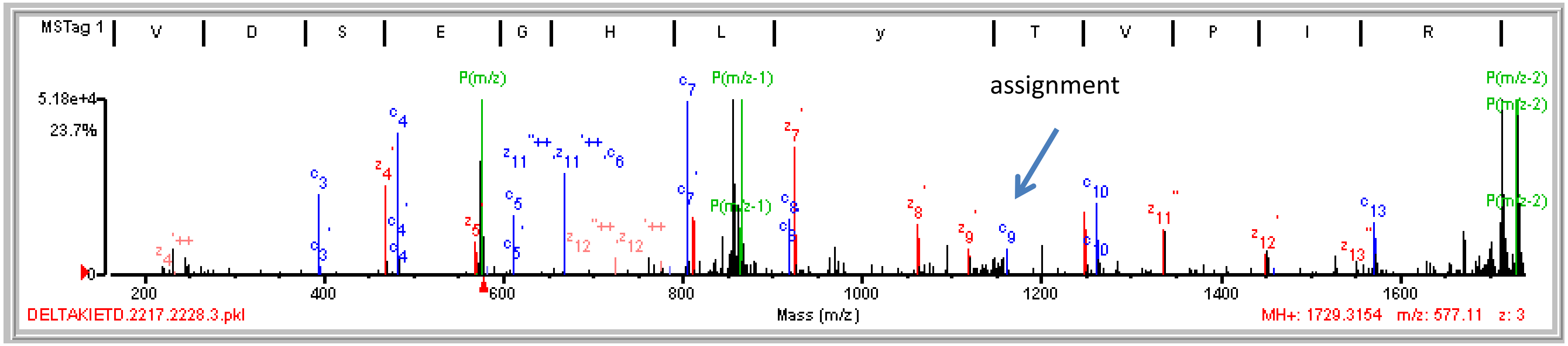




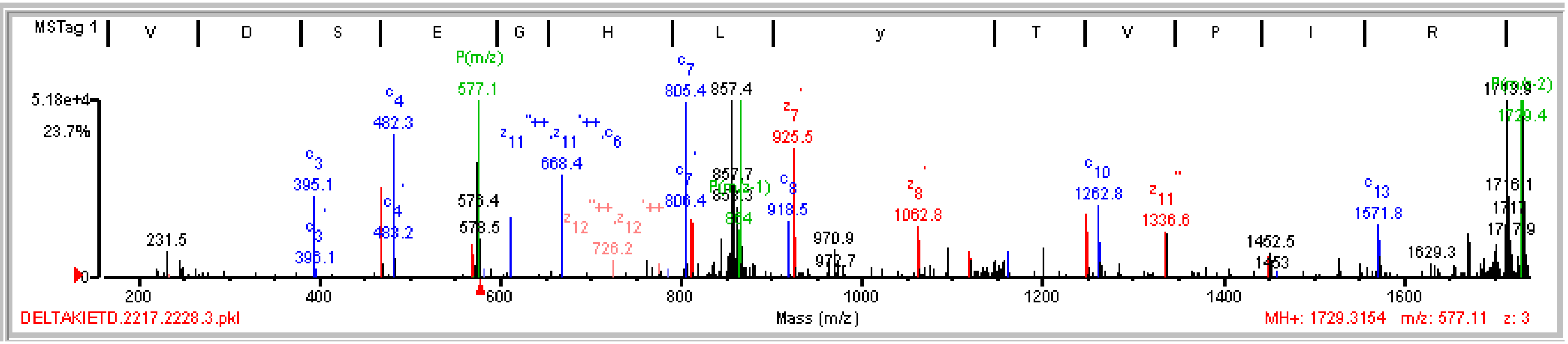
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.55	82.9	9	4/17	Y1062y	(K) A A E A/G G A E\E/Q y\G|F/L|T|T/P T K (Q)	1940.92	80.2618	146.2	270635.7/4.73	Homo sapiens	153945728	586	microtubule-associated protein 1B

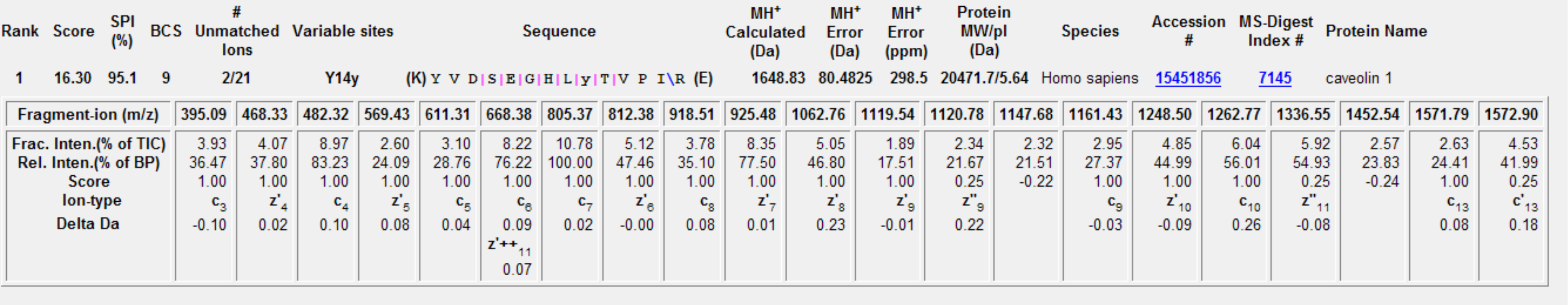
Fragment-ion (m/z)	345.16	404.29	446.21	547.36	575.52	579.45	615.25	618.64	655.56	657.47	660.57	738.24	779.43	788.45	829.86	840.53	1214.55
Frac. Inten.(% of TIC)	4.07	3.12	5.36	7.78	3.40	2.60	3.59	3.79	4.27	3.90	10.55	6.63	8.21	18.09	5.87	3.82	4.94
Rel. Inten.(% of BP)	22.48	17.24	29.61	43.00	18.82	14.39	19.85	20.96	23.62	21.55	58.29	36.64	45.39	100.00	32.43	21.12	27.32
Score	1.00	1.00	1.00	1.00	-0.19	1.00	-0.20	1.00	-0.24	1.00	1.00	1.00	0.50	1.00	-0.32	1.00	1.00
Ion-type	y_3	$y{++}_7$	y_4	y_5		$b{++}_{11}$		$y{++}_{10}$		b_8	y_6	$b{++}_{14}$	$b{++}_{15}\text{-}H_2O$	$b{++}_{15}$		$y{++}_{15}$	b_{12}
Delta Da	-0.05	0.06	-0.05	0.05		0.24		0.35		0.19	0.18	0.44	0.11	0.13		0.66	0.11

Peak 326



assignment

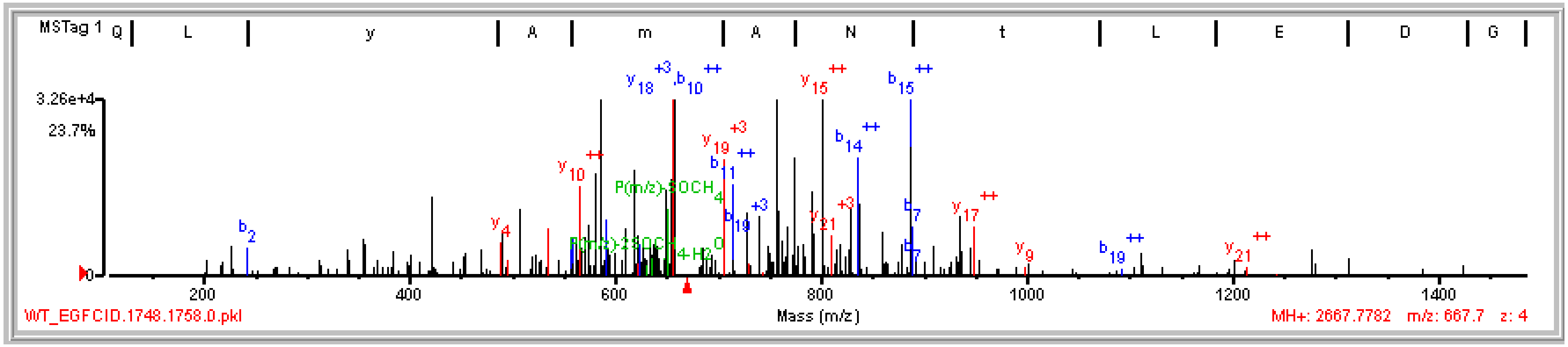


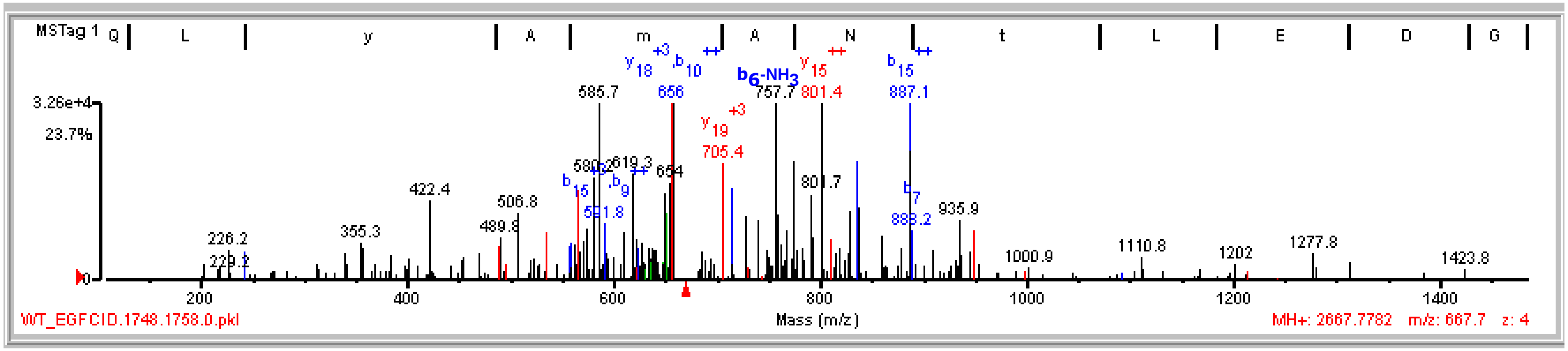


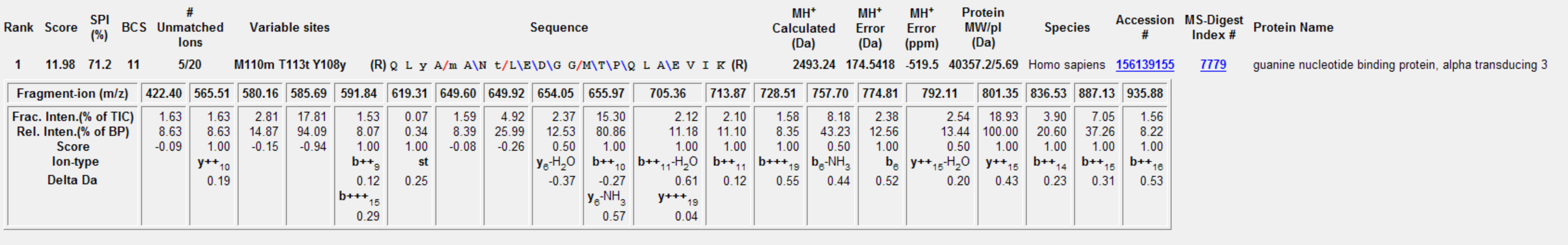
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.30	95.1	9	2/21	Y14y	(K) Y V D|S|E|G|H|L|y|T|V P I\R (E)	1648.83	80.4825	298.5	20471.7/5.64	Homo sapiens	15451856	7145	caveolin 1

Fragment-ion (m/z)	395.09	468.33	482.32	569.43	611.31	668.38	805.37	812.38	918.51	925.48	1062.76	1119.54	1120.78	1147.68	1161.43	1248.50	1262.77	1336.55	1452.54	1571.79	1572.90
Frac. Inten.(% of TIC)	3.93	4.07	8.97	2.60	3.10	8.22	10.78	5.12	3.78	8.35	5.05	1.89	2.34	2.32	2.95	4.85	6.04	5.92	2.57	2.63	4.53
Rel. Inten.(% of BP)	36.47	37.80	83.23	24.09	28.76	76.22	100.00	47.46	35.10	77.50	46.80	17.51	21.67	21.51	27.37	44.99	56.01	54.93	23.83	24.41	41.99
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.25	-0.22	1.00	1.00	1.00	0.25	-0.24	1.00	0.25
Ion-type	c_3	z'_4	c_4	z'_5	c_5	c_6 z'^{++}_{11}	c_7	z'_6	c_8	z'_7	z'_8	z'_9	z''_9		c_9	z'_{10}	c_{10}	z''_{11}		c_{13}	c'_{13}
Delta Da	-0.10	0.02	0.10	0.08	0.04	0.09 0.07	0.02	-0.00	0.08	0.01	0.23	-0.01	0.22		-0.03	-0.09	0.26	-0.08		0.08	0.18

Peak 327





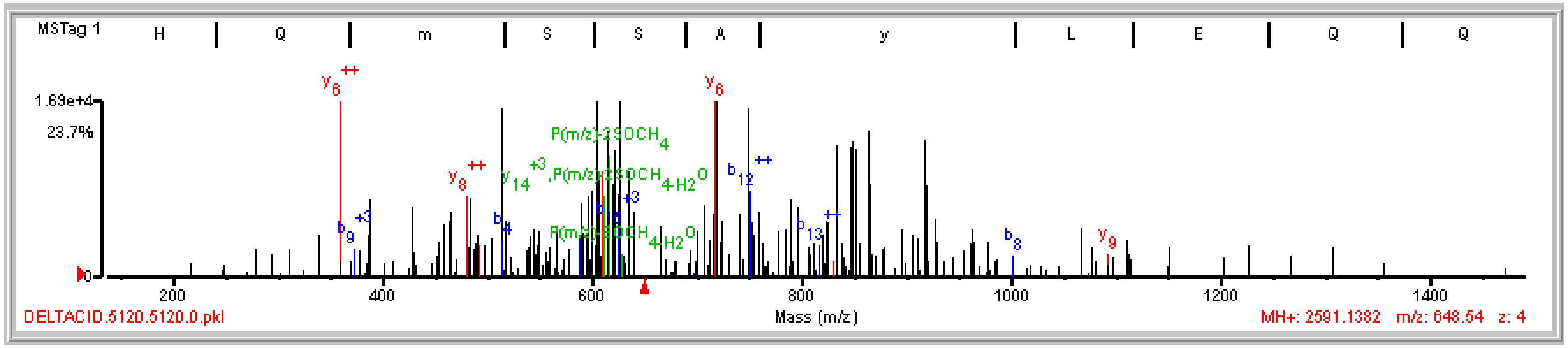


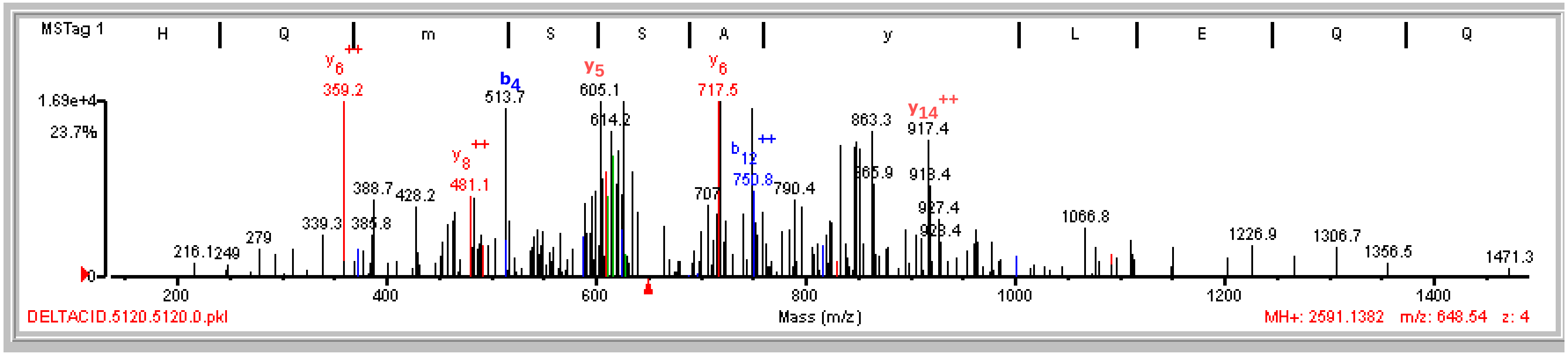
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.98	71.2	11	5/20	M110m T113t Y108y	(R) Q L y A/m A\N t/L\E\D\G G/M\T\P\Q L A\E V I K (R)	2493.24	174.5418	-519.5	40357.2/5.69	Homo sapiens	156139155	7779	guanine nucleotide binding protein, alpha transducing 3

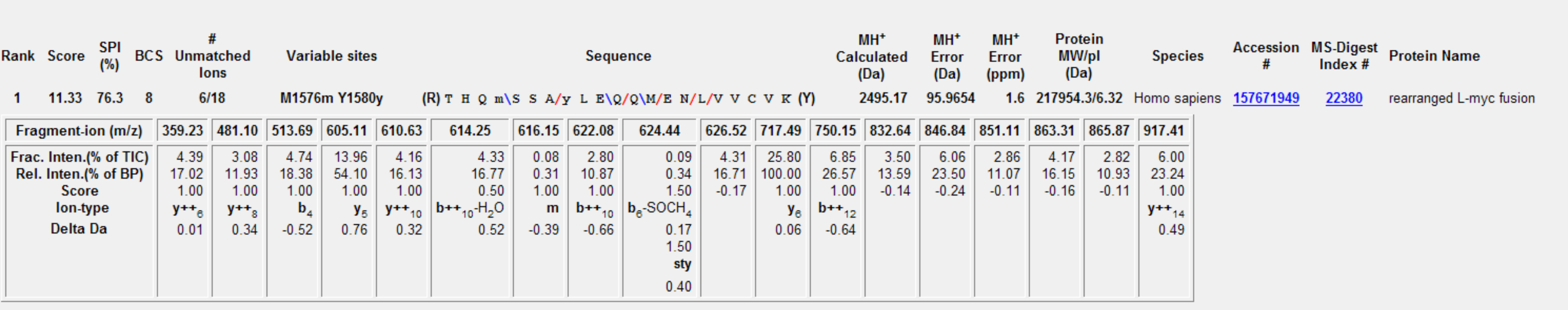
Fragment-ion (m/z)	422.40	565.51	580.16	585.69	591.84	619.31	649.60	649.92	654.05	655.97
Frac. Inten.(% of TIC)	1.63	1.63	2.81	17.81	1.53	0.07	1.59	4.92	2.37	15.30
Rel. Inten.(% of BP)	8.63	8.63	14.87	94.09	8.07	0.34	8.39	25.99	12.53	80.86
Score	-0.09	1.00	-0.15	-0.94	1.00	1.00	-0.08	-0.26	0.50	1.00
Ion-type		y^{++}_{10}			b^{++}_{9} b^{+++}_{15}	st			y_6-H_2O	b^{++}_{10} y_6-NH_3
Delta Da		0.19			0.12 0.29	0.25			-0.37	-0.27 0.57

Fragment-ion (m/z)	705.36	713.87	728.51	757.70	774.81	792.11	801.35	836.53	887.13	935.88
Frac. Inten.(% of TIC)	2.12	2.10	1.58	8.18	2.38	2.54	18.93	3.90	7.05	1.56
Rel. Inten.(% of BP)	11.18	11.10	8.35	43.23	12.56	13.44	100.00	20.60	37.26	8.22
Score	1.00	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type	b^{++}_{11}-H_2O y^{+++}_{19}	b^{++}_{11}	b^{+++}_{19}	b_6-NH_3	b_6	y^{++}_{15}-H_2O	y^{++}_{15}	b^{++}_{14}	b^{++}_{15}	b^{++}_{16}
Delta Da	0.61 0.04	0.12	0.55	0.44	0.52	0.20	0.43	0.23	0.31	0.53

Peak 328



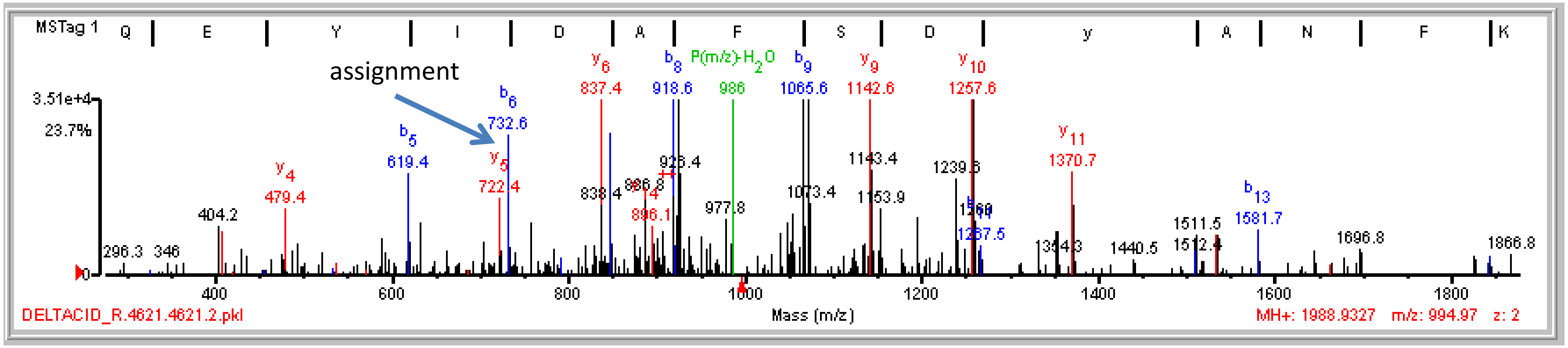




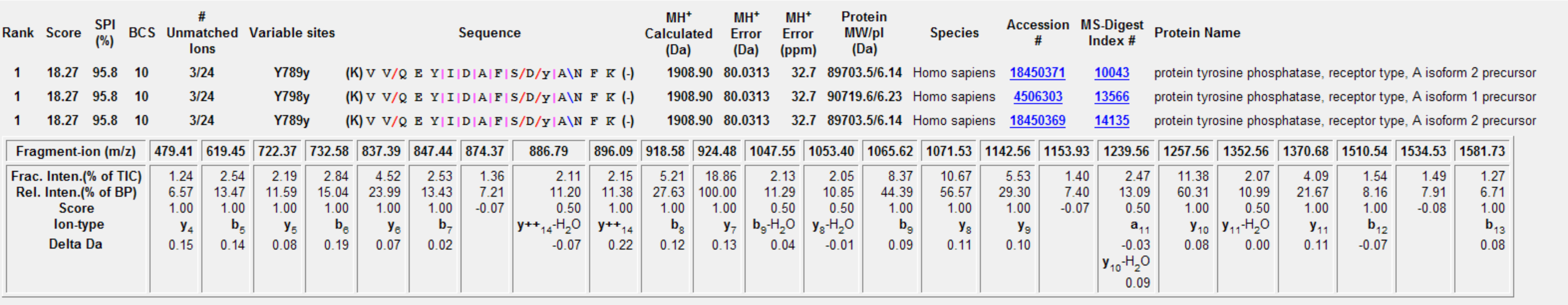
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.33	76.3	8	6/18	M1576m Y1580y	(R) T H Q m\S S A/y L E\Q/Q\M/E N/L/V V C V K (Y)	2495.17	95.9654	1.6	217954.3/6.32	Homo sapiens	157671949	22380	rearranged L-myc fusion

Fragment-ion (m/z)	359.23	481.10	513.69	605.11	610.63	614.25	616.15	622.08	624.44	626.52	717.49	750.15	832.64	846.84	851.11	863.31	865.87	917.41
Frac. Inten.(% of TIC)	4.39	3.08	4.74	13.96	4.16	4.33	0.08	2.80	0.09	4.31	25.80	6.85	3.50	6.06	2.86	4.17	2.82	6.00
Rel. Inten.(% of BP)	17.02	11.93	18.38	54.10	16.13	16.77	0.31	10.87	0.34	16.71	100.00	26.57	13.59	23.50	11.07	16.15	10.93	23.24
Score	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.50	-0.17	1.00	1.00	-0.14	-0.24	-0.11	-0.16	-0.11	1.00
Ion-type	$y{+}{+}_6$	$y{+}{+}_8$	b_4	y_5	$y{+}{+}_{10}$	$b{+}{+}_{10}$-H_2O	m	$b{+}{+}_{10}$	b_6-$SOCH_4$		y_6	$b{+}{+}_{12}$						$y{+}{+}_{14}$
Delta Da	0.01	0.34	-0.52	0.76	0.32	0.52	-0.39	-0.66	0.17 1.50 sty 0.40		0.06	-0.64						0.49

Peak 329



assignment

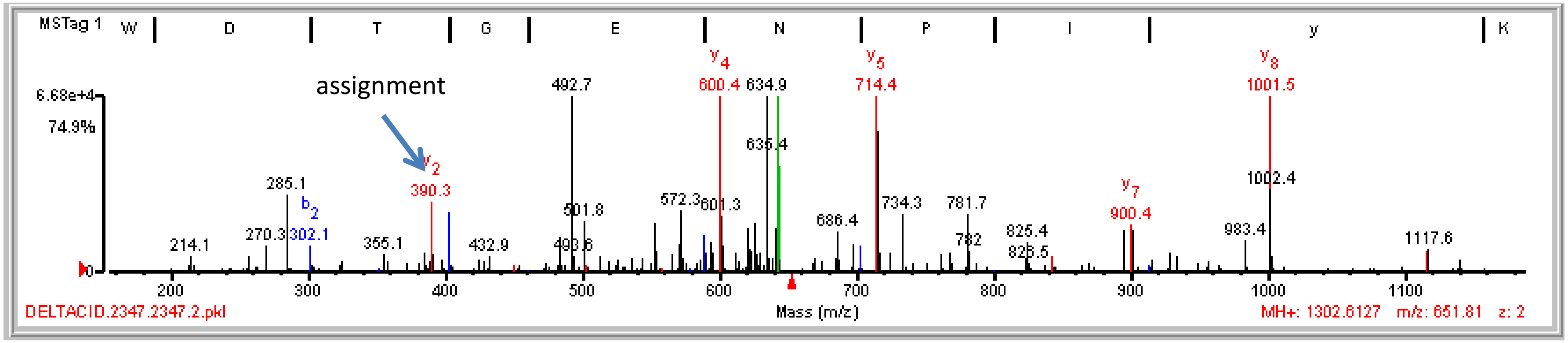


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.27	95.8	10	3/24	Y789y	(K) V V/Q E Y|I|D|A|F|S/D/y|A\N F K (-)	1908.90	80.0313	32.7	89703.5/6.14	Homo sapiens	18450371	10043	protein tyrosine phosphatase, receptor type, A isoform 2 precursor
1	18.27	95.8	10	3/24	Y798y	(K) V V/Q E Y|I|D|A|F|S/D/y|A\N F K (-)	1908.90	80.0313	32.7	90719.6/6.23	Homo sapiens	4506303	13566	protein tyrosine phosphatase, receptor type, A isoform 1 precursor
1	18.27	95.8	10	3/24	Y789y	(K) V V/Q E Y|I|D|A|F|S/D/y|A\N F K (-)	1908.90	80.0313	32.7	89703.5/6.14	Homo sapiens	18450369	14135	protein tyrosine phosphatase, receptor type, A isoform 2 precursor

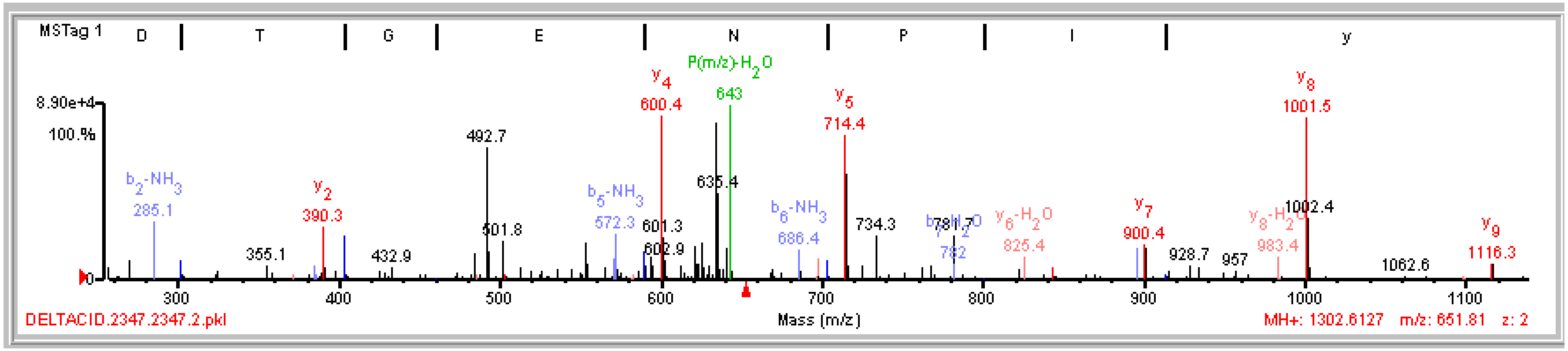
Fragment-ion (m/z)	479.41	619.45	722.37	732.58	837.39	847.44	874.37	886.79	896.09	918.58	924.48	1047.55
Frac. Inten.(% of TIC)	1.24	2.54	2.19	2.84	4.52	2.53	1.36	2.11	2.15	5.21	18.86	2.13
Rel. Inten.(% of BP)	6.57	13.47	11.59	15.04	23.99	13.43	7.21	11.20	11.38	27.63	100.00	11.29
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.07	0.50	1.00	1.00	1.00	0.50
Ion-type	y_4	b_5	y_5	b_6	y_6	b_7		$y{+}{+}_{14}-H_2O$	$y{+}{+}_{14}$	b_8	y_7	b_9-H_2O
Delta Da	0.15	0.14	0.08	0.19	0.07	0.02		-0.07	0.22	0.12	0.13	0.04

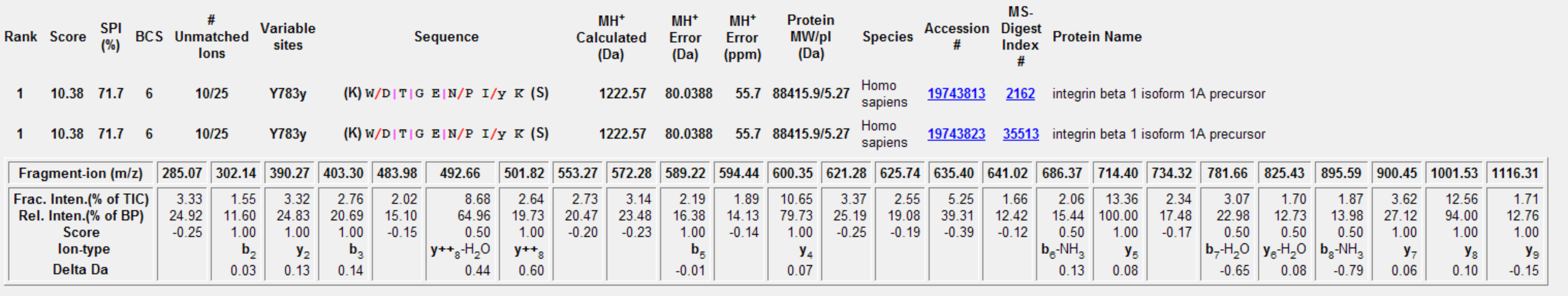
Fragment-ion (m/z)	1053.40	1065.62	1071.53	1142.56	1153.93	1239.56	1257.56	1352.56	1370.68	1510.54	1534.53	1581.73
Frac. Inten.(% of TIC)	2.05	8.37	10.67	5.53	1.40	2.47	11.38	2.07	4.09	1.54	1.49	1.27
Rel. Inten.(% of BP)	10.85	44.39	56.57	29.30	7.40	13.09	60.31	10.99	21.67	8.16	7.91	6.71
Score	0.50	1.00	1.00	1.00	-0.07	0.50	1.00	0.50	1.00	1.00	-0.08	1.00
Ion-type	y_8-H_2O	b_9	y_8	y_9		a_{11} $y_{10}-H_2O$	y_{10}	$y_{11}-H_2O$	y_{11}	b_{12}		b_{13}
Delta Da	-0.01	0.09	0.11	0.10		-0.03 0.09	0.08	0.00	0.11	-0.07		0.08

Peak 330



assignment

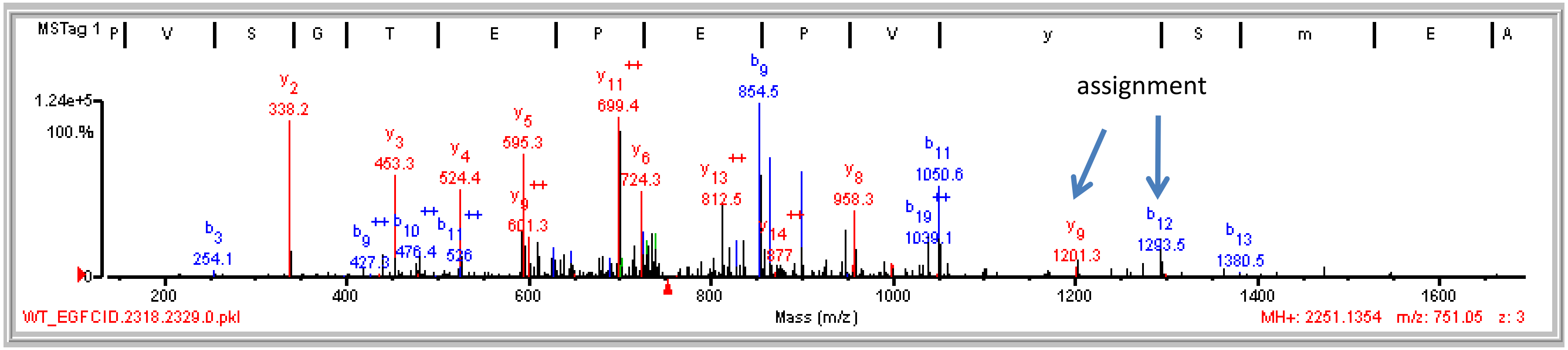




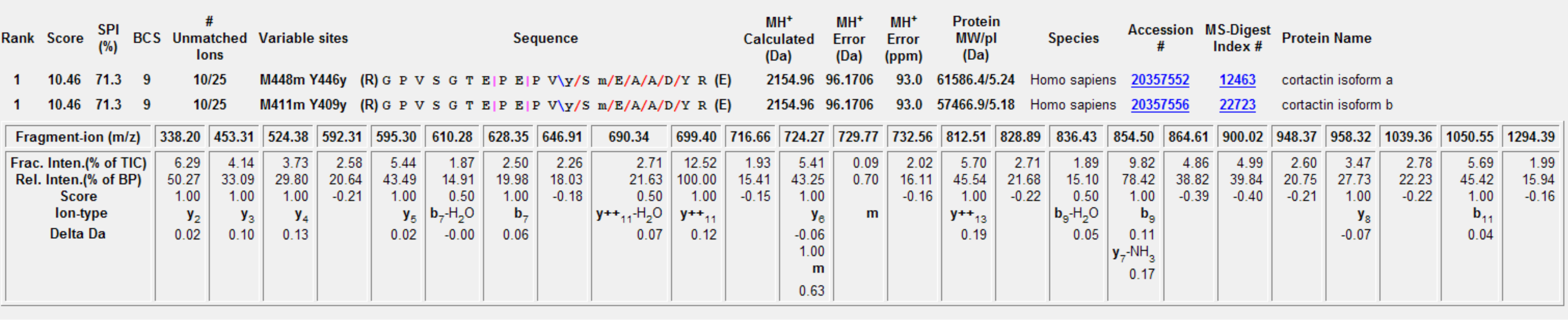
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.38	71.7	6	10/25	Y783y	(K) W/D|T|G E|N/P I/y K (S)	1222.57	80.0388	55.7	88415.9/5.27	Homo sapiens	19743813	2162	integrin beta 1 isoform 1A precursor
1	10.38	71.7	6	10/25	Y783y	(K) W/D|T|G E|N/P I/y K (S)	1222.57	80.0388	55.7	88415.9/5.27	Homo sapiens	19743823	35513	integrin beta 1 isoform 1A precursor

Fragment-ion (m/z)	285.07	302.14	390.27	403.30	483.98	492.66	501.82	553.27	572.28	589.22	594.44	600.35	621.28	625.74	635.40	641.02	686.37	714.40	734.32	781.66	825.43	895.59	900.45	1001.53	1116.31
Frac. Inten.(% of TIC)	3.33	1.55	3.32	2.76	2.02	8.68	2.64	2.73	3.14	2.19	1.89	10.65	3.37	2.55	5.25	1.66	2.06	13.36	2.34	3.07	1.70	1.87	3.62	12.56	1.71
Rel. Inten.(% of BP)	24.92	11.60	24.83	20.69	15.10	64.96	19.73	20.47	23.48	16.38	14.13	79.73	25.19	19.08	39.31	12.42	15.44	100.00	17.48	22.98	12.73	13.98	27.12	94.00	12.76
Score	-0.25	1.00	1.00	1.00	-0.15	0.50	1.00	-0.20	-0.23	1.00	-0.14	1.00	-0.25	-0.19	-0.39	-0.12	0.50	1.00	-0.17	0.50	0.50	0.50	1.00	1.00	1.00
Ion-type		b_2	y_2	b_3		$y{+}{+}_8$-H_2O	$y{+}{+}_8$			b_5		y_4					b_6-NH_3	y_5		b_7-H_2O	y_6-H_2O	b_8-NH_3	y_7	y_8	y_9
Delta Da		0.03	0.13	0.14		0.44	0.60			-0.01		0.07					0.13	0.08		-0.65	0.08	-0.79	0.06	0.10	-0.15

Peak 331



assignment



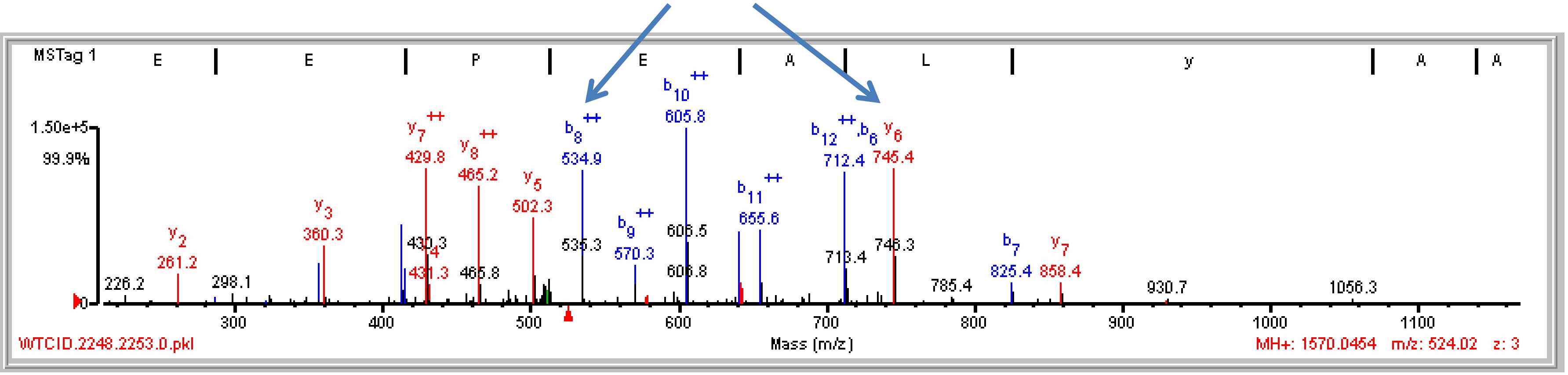
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.46	71.3	9	10/25	M448m Y446y	(R) G P V S G T E|P E|P V\y/S m/E/A/A/D/Y R (E)	2154.96	96.1706	93.0	61586.4/5.24	Homo sapiens	20357552	12463	cortactin isoform a
1	10.46	71.3	9	10/25	M411m Y409y	(R) G P V S G T E|P E|P V\y/S m/E/A/A/D/Y R (E)	2154.96	96.1706	93.0	57466.9/5.18	Homo sapiens	20357556	22723	cortactin isoform b

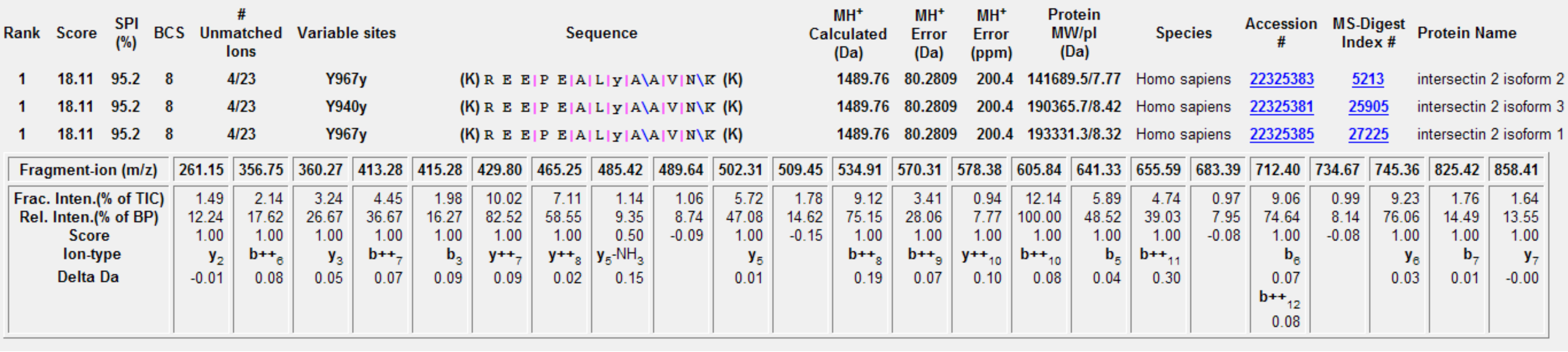
Fragment-ion (m/z)	338.20	453.31	524.38	592.31	595.30	610.28	628.35	646.91	690.34	699.40
Frac. Inten.(% of TIC)	6.29	4.14	3.73	2.58	5.44	1.87	2.50	2.26	2.71	12.52
Rel. Inten.(% of BP)	50.27	33.09	29.80	20.64	43.49	14.91	19.98	18.03	21.63	100.00
Score	1.00	1.00	1.00	-0.21	1.00	0.50	1.00	-0.18	0.50	1.00
Ion-type	y_2	y_3	y_4		y_5	b_7-H_2O	b_7		$y++_{11}$-H_2O	$y++_{11}$
Delta Da	0.02	0.10	0.13		0.02	-0.00	0.06		0.07	0.12

Fragment-ion (m/z)	716.66	724.27	729.77	732.56	812.51	828.89	836.43	854.50	864.61	900.02	948.37	958.32	1039.36	1050.55	1294.39
Frac. Inten.(% of TIC)	1.93	5.41	0.09	2.02	5.70	2.71	1.89	9.82	4.86	4.99	2.60	3.47	2.78	5.69	1.99
Rel. Inten.(% of BP)	15.41	43.25	0.70	16.11	45.54	21.68	15.10	78.42	38.82	39.84	20.75	27.73	22.23	45.42	15.94
Score	-0.15	1.00		-0.16	1.00	-0.22	0.50	1.00	-0.39	-0.40	-0.21	1.00	-0.22	1.00	-0.16
Ion-type		y_6	m		$y++_{13}$		b_9-H_2O	b_9				y_8		b_{11}	
Delta Da		-0.06			0.19		0.05	0.11				-0.07		0.04	
		1.00						y_7-NH_3							
		m						0.17							
		0.63													

Peak 332

assignment





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<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH+ Calculated (Da)</th><th>MH+ Error (Da)</th><th>MH+ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>18.11</td><td>95.2</td><td>8</td><td>4/23</td><td>Y967y</td><td>(K) R E E|P E|A|L|y|A\A|V|N\K (K)</td><td>1489.76</td><td>80.2809</td><td>200.4</td><td>141689.5/7.77</td><td>Homo sapiens</td><td>22325383</td><td>5213</td><td>intersectin 2 isoform 2</td></tr>
<tr><td>1</td><td>18.11</td><td>95.2</td><td>8</td><td>4/23</td><td>Y940y</td><td>(K) R E E|P E|A|L|y|A\A|V|N\K (K)</td><td>1489.76</td><td>80.2809</td><td>200.4</td><td>190365.7/8.42</td><td>Homo sapiens</td><td>22325381</td><td>25905</td><td>intersectin 2 isoform 3</td></tr>
<tr><td>1</td><td>18.11</td><td>95.2</td><td>8</td><td>4/23</td><td>Y967y</td><td>(K) R E E|P E|A|L|y|A\A|V|N\K (K)</td><td>1489.76</td><td>80.2809</td><td>200.4</td><td>193331.3/8.32</td><td>Homo sapiens</td><td>22325385</td><td>27225</td><td>intersectin 2 isoform 1</td></tr>
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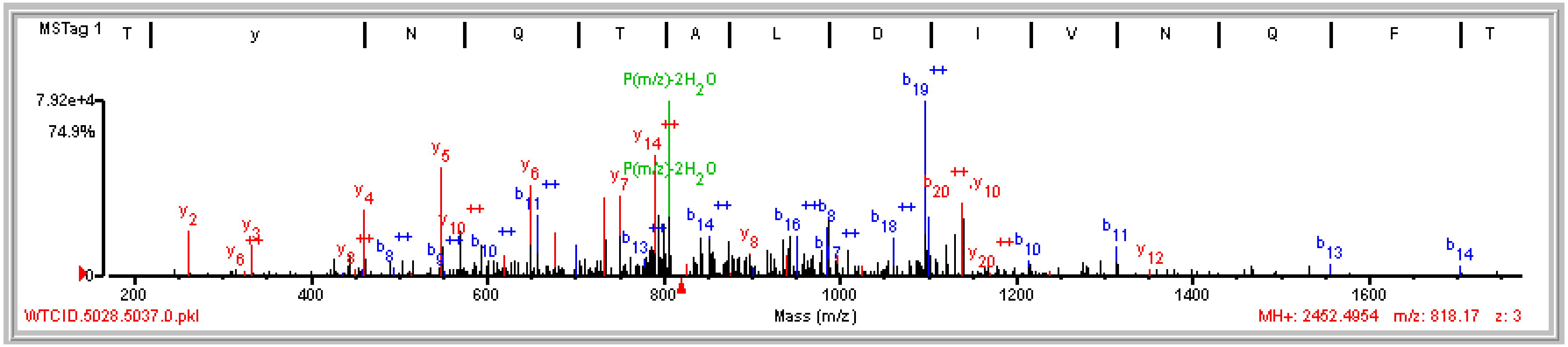
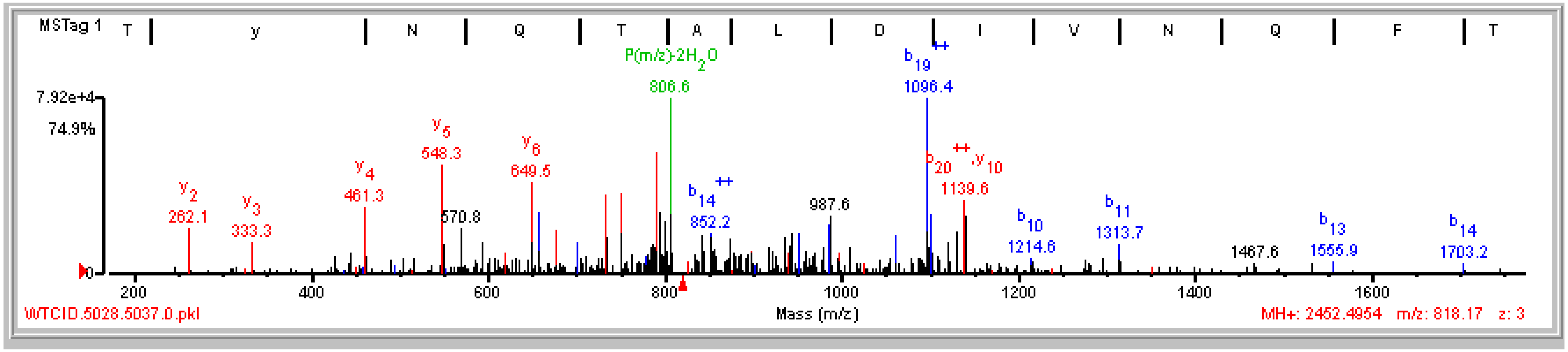
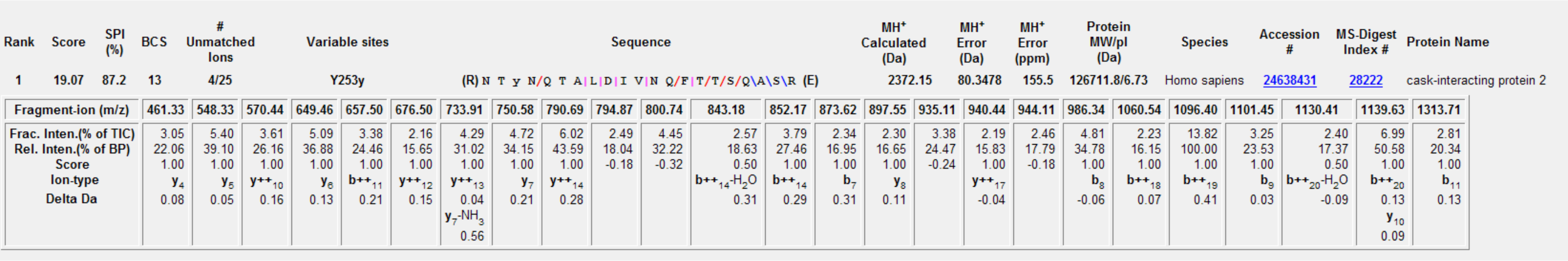
Fragment-ion (m/z)	261.15	356.75	360.27	413.28	415.28	429.80	465.25	485.42	489.64	502.31	509.45	534.91	570.31	578.38	605.84	641.33	655.59	683.39	712.40	734.67	745.36	825.42	858.41
Frac. Inten.(% of TIC)	1.49	2.14	3.24	4.45	1.98	10.02	7.11	1.14	1.06	5.72	1.78	9.12	3.41	0.94	12.14	5.89	4.74	0.97	9.06	0.99	9.23	1.76	1.64
Rel. Inten.(% of BP)	12.24	17.62	26.67	36.67	16.27	82.52	58.55	9.35	8.74	47.08	14.62	75.15	28.06	7.77	100.00	48.52	39.03	7.95	74.64	8.14	76.06	14.49	13.55
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	-0.09	1.00	-0.15	1.00	1.00	1.00	1.00	1.00	1.00	-0.08	1.00	-0.08	1.00	1.00	1.00
Ion-type	y_2	$b{+}{+}_6$	y_3	$b{+}{+}_7$	b_3	$y{+}{+}_7$	$y{+}{+}_8$	$y_5\text{-}NH_3$		y_5		$b{+}{+}_8$	$b{+}{+}_9$	$y{+}{+}_{10}$	$b{+}{+}_{10}$	b_5	$b{+}{+}_{11}$		b_6 $b{+}{+}_{12}$		y_6	b_7	y_7
Delta Da	-0.01	0.08	0.05	0.07	0.09	0.09	0.02	0.15		0.01		0.19	0.07	0.10	0.08	0.04	0.30		0.07 0.08		0.03	0.01	-0.00

Peak 333





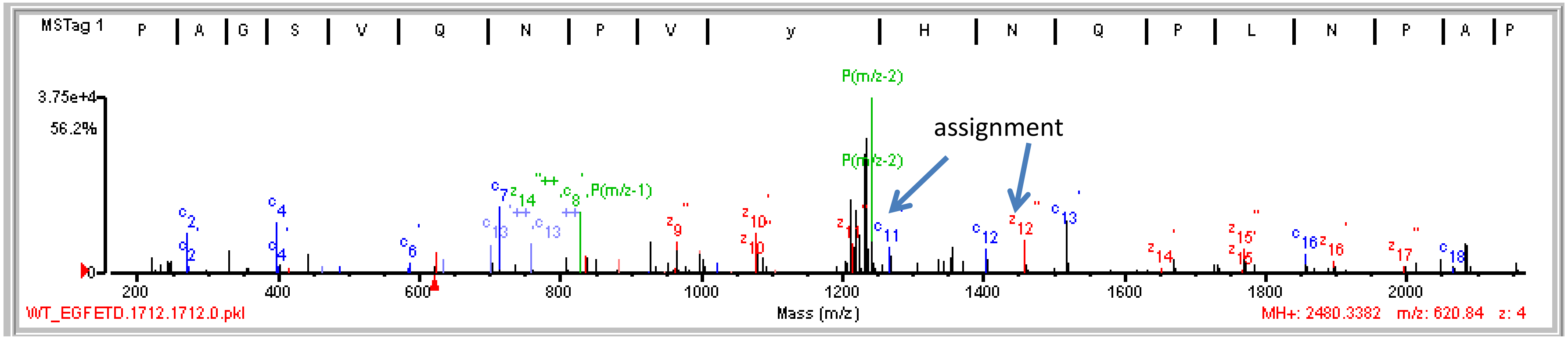


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.07	87.2	13	4/25	Y253y	(R) N T y N/Q T A|L|D|I V|N Q/F|T/T/S/Q\A\S\R (E)	2372.15	80.3478	155.5	126711.8/6.73	Homo sapiens	24638431	28222	cask-interacting protein 2

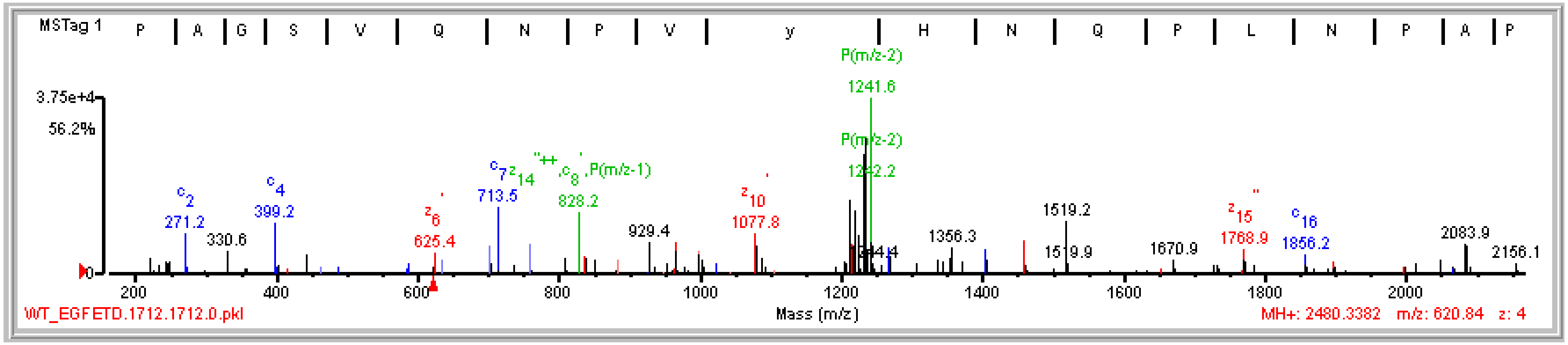
Fragment-ion (m/z)	461.33	548.33	570.44	649.46	657.50	676.50	733.91	750.58	790.69	794.87	800.74	843.18	852.17
Frac. Inten.(% of TIC)	3.05	5.40	3.61	5.09	3.38	2.16	4.29	4.72	6.02	2.49	4.45	2.57	3.79
Rel. Inten.(% of BP)	22.06	39.10	26.16	36.88	24.46	15.65	31.02	34.15	43.59	18.04	32.22	18.63	27.46
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.18	-0.32	0.50	1.00
Ion-type	y_4	y_5	y++_{10}	y_6	b++_{11}	y++_{12}	y++_{13}	y_7	y++_{14}			$\text{b++}_{14}\text{-}H_2O$	b++_{14}
Delta Da	0.08	0.05	0.16	0.13	0.21	0.15	0.04 $y_7\text{-}NH_3$ 0.56	0.21	0.28			0.31	0.29

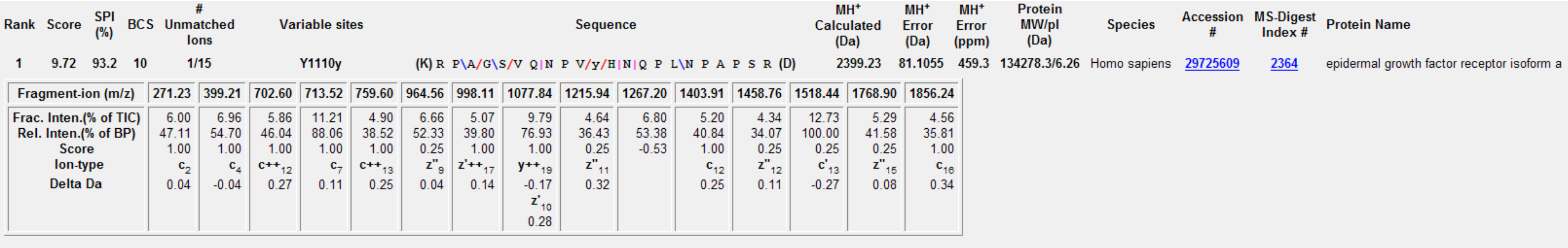
Fragment-ion (m/z)	873.62	897.55	935.11	940.44	944.11	986.34	1060.54	1096.40	1101.45	1130.41	1139.63	1313.71
Frac. Inten.(% of TIC)	2.34	2.30	3.38	2.19	2.46	4.81	2.23	13.82	3.25	2.40	6.99	2.81
Rel. Inten.(% of BP)	16.95	16.65	24.47	15.83	17.79	34.78	16.15	100.00	23.53	17.37	50.58	20.34
Score	1.00	1.00	-0.24	1.00	-0.18	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	b_7	y_8		y++_{17}		b_8	b++_{18}	b++_{19}	b_9	$\text{b++}_{20}\text{-}H_2O$	b++_{20}	b_{11}
Delta Da	0.31	0.11		-0.04		-0.06	0.07	0.41	0.03	-0.09	0.13 y_{10} 0.09	0.13

Peak 334



assignment

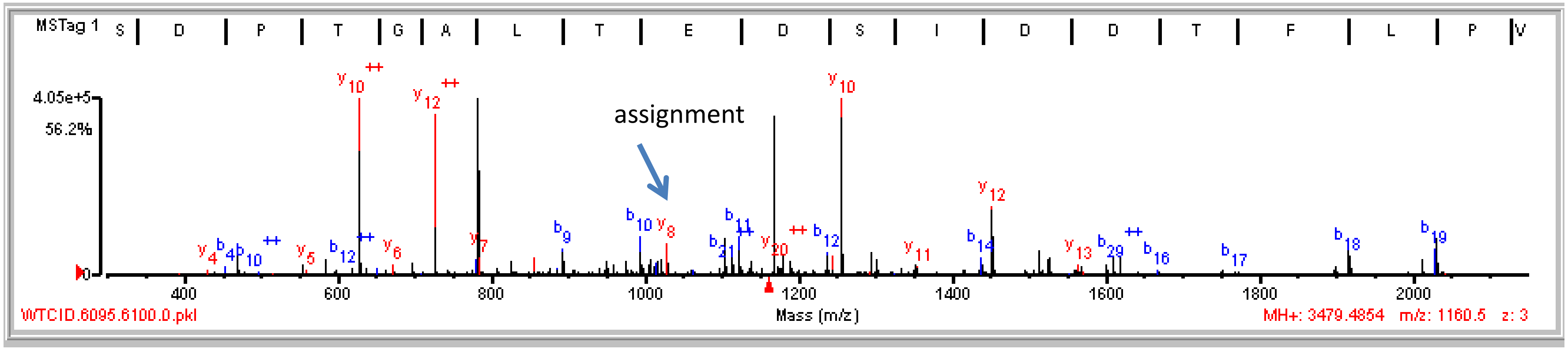




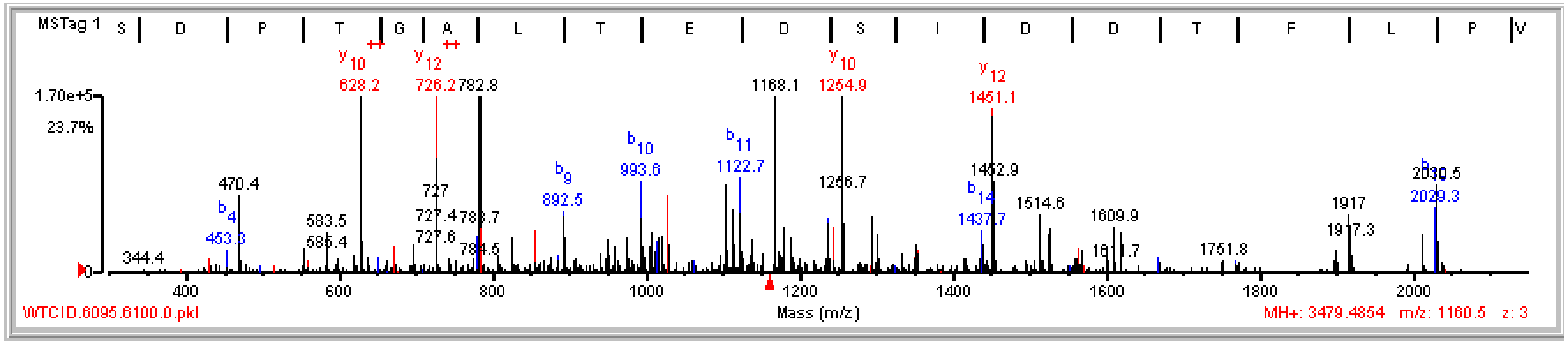
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.72	93.2	10	1/15	Y1110y	(K) R P\A/G\S/V Q|N P V/y/H|N|Q P L\N P A P S R (D)	2399.23	81.1055	459.3	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

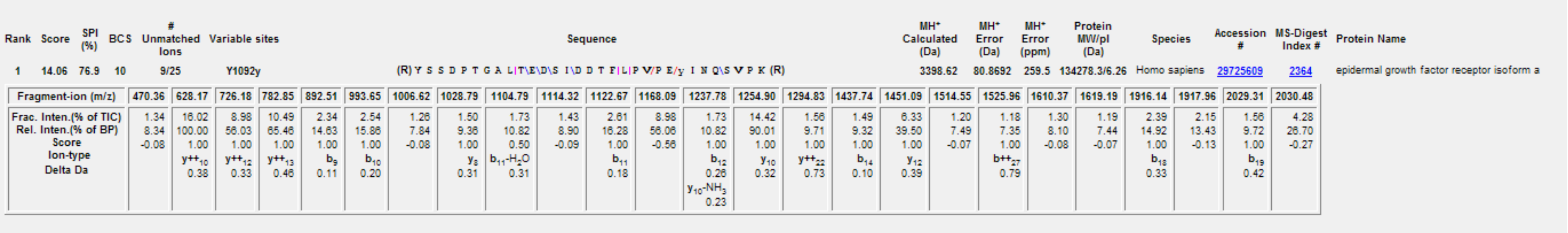
Fragment-ion (m/z)	271.23	399.21	702.60	713.52	759.60	964.56	998.11	1077.84	1215.94	1267.20	1403.91	1458.76	1518.44	1768.90	1856.24
Frac. Inten.(% of TIC)	6.00	6.96	5.86	11.21	4.90	6.66	5.07	9.79	4.64	6.80	5.20	4.34	12.73	5.29	4.56
Rel. Inten.(% of BP)	47.11	54.70	46.04	88.06	38.52	52.33	39.80	76.93	36.43	53.38	40.84	34.07	100.00	41.58	35.81
Score	1.00	1.00	1.00	1.00	1.00	0.25	1.00	1.00	0.25	-0.53	1.00	0.25	0.25	0.25	1.00
Ion-type	c_2	c_4	c^{++}_{12}	c_7	c^{++}_{13}	z''_9	z'^{++}_{17}	y^{++}_{19}	z''_{11}		c_{12}	z''_{12}	c'_{13}	z''_{15}	c_{16}
Delta Da	0.04	-0.04	0.27	0.11	0.25	0.04	0.14	-0.17 z'_{10} 0.28	0.32		0.25	0.11	-0.27	0.08	0.34

Peak 335



assignment



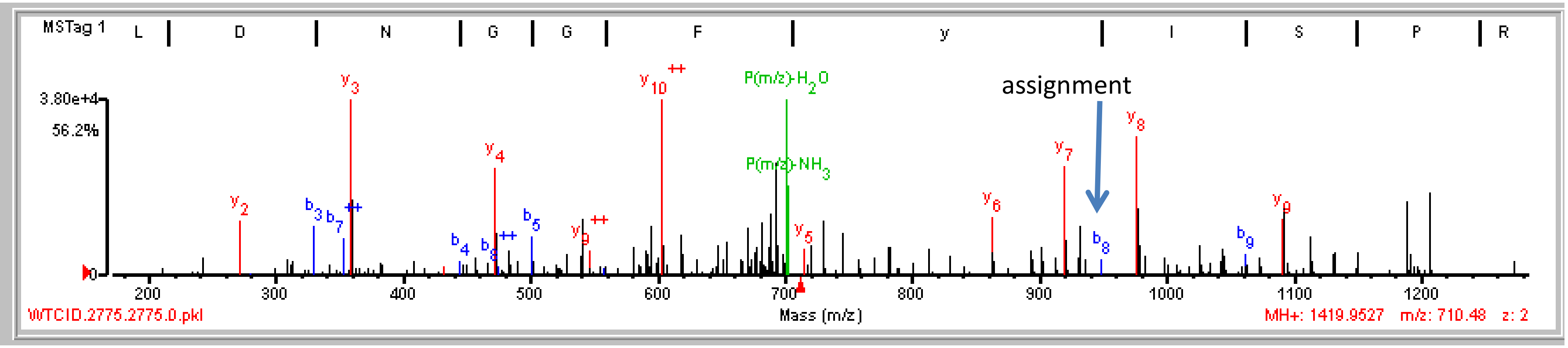


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.06	76.9	10	9/25	Y1092y	(R) Y S S D P T G A L|T\E\D\S I\D D T F|L|P V/P E/y I N Q\S V P K (R)	3398.62	80.8692	259.5	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

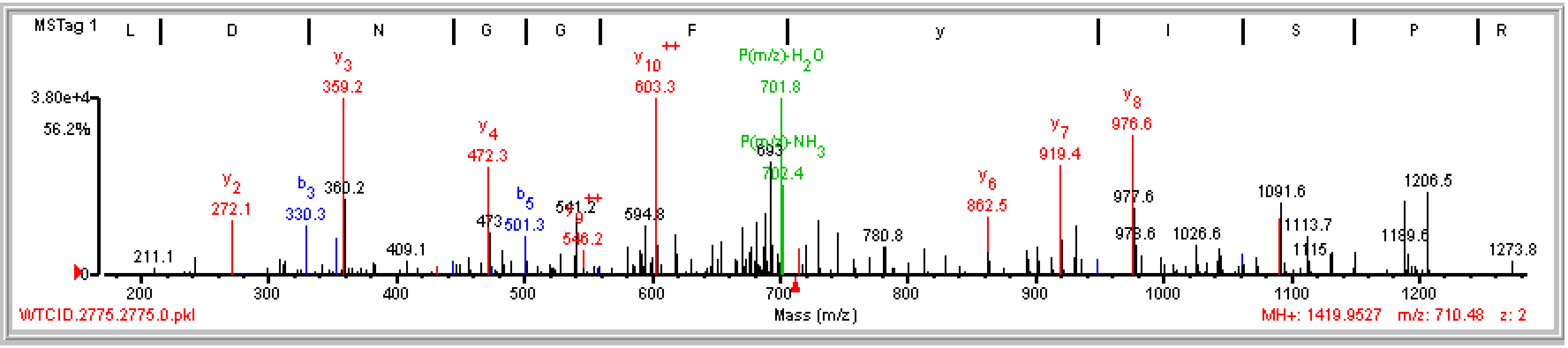
Fragment-ion (m/z)	470.36	628.17	726.18	782.85	892.51	993.65	1006.62	1028.79	1104.79	1114.32	1122.67	1168.09
Frac. Inten.(% of TIC)	1.34	16.02	8.98	10.49	2.34	2.54	1.26	1.50	1.73	1.43	2.61	8.98
Rel. Inten.(% of BP)	8.34	100.00	56.03	65.46	14.63	15.86	7.84	9.36	10.82	8.90	16.28	56.06
Score	-0.08	1.00	1.00	1.00	1.00	1.00	-0.08	1.00	0.50	-0.09	1.00	-0.56
Ion-type		y^{++}_{10}	y^{++}_{12}	y^{++}_{13}	b_9	b_{10}		y_8	b_{11}-H_2O		b_{11}	
Delta Da		0.38	0.33	0.46	0.11	0.20		0.31	0.31		0.18	

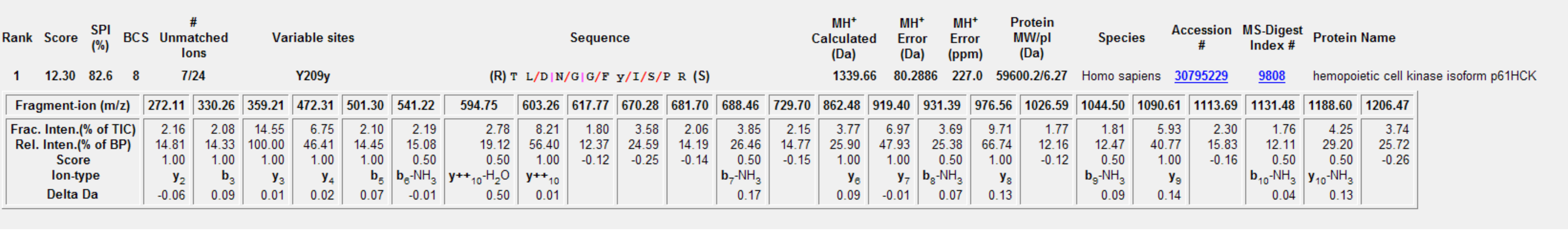
Fragment-ion (m/z)	1237.78	1254.90	1294.83	1437.74	1451.09	1514.55	1525.96	1610.37	1619.19	1916.14	1917.96	2029.31	2030.48
Frac. Inten.(% of TIC)	1.73	14.42	1.56	1.49	6.33	1.20	1.18	1.30	1.19	2.39	2.15	1.56	4.28
Rel. Inten.(% of BP)	10.82	90.01	9.71	9.32	39.50	7.49	7.35	8.10	7.44	14.92	13.43	9.72	26.70
Score	1.00	1.00	1.00	1.00	1.00	-0.07	1.00	-0.08	-0.07	1.00	-0.13	1.00	-0.27
Ion-type	b_{12} y_{10}-NH_3	y_{10}	y^{++}_{22}	b_{14}	y_{12}		b^{++}_{27}			b_{18}		b_{19}	
Delta Da	0.26 0.23	0.32	0.73	0.10	0.39		0.79			0.33		0.42	

Peak 336



assignment





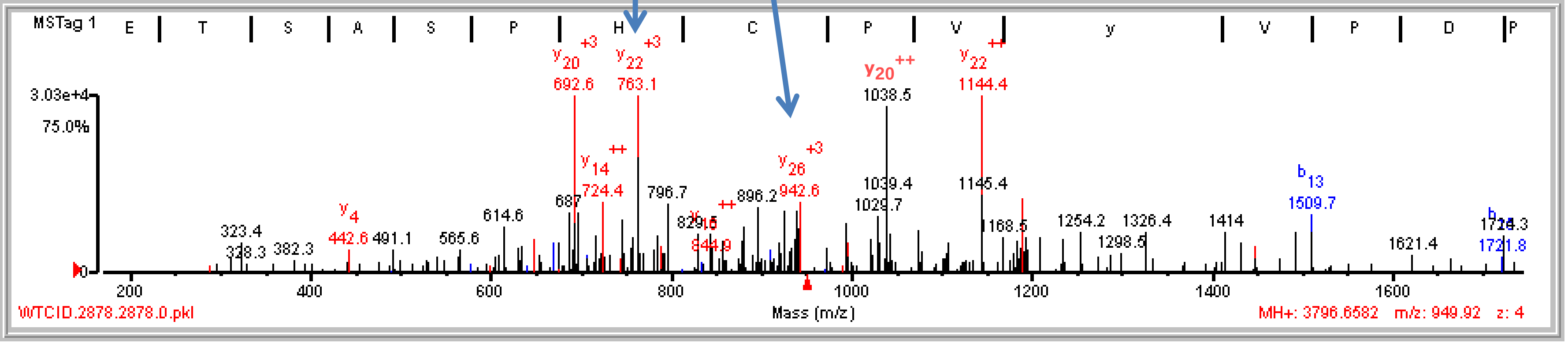
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.30	82.6	8	7/24	Y209y	(R) T L/D|N/G|G/F y/I/S/P R (S)	1339.66	80.2886	227.0	59600.2/6.27	Homo sapiens	30795229	9808	hemopoietic cell kinase isoform p61HCK

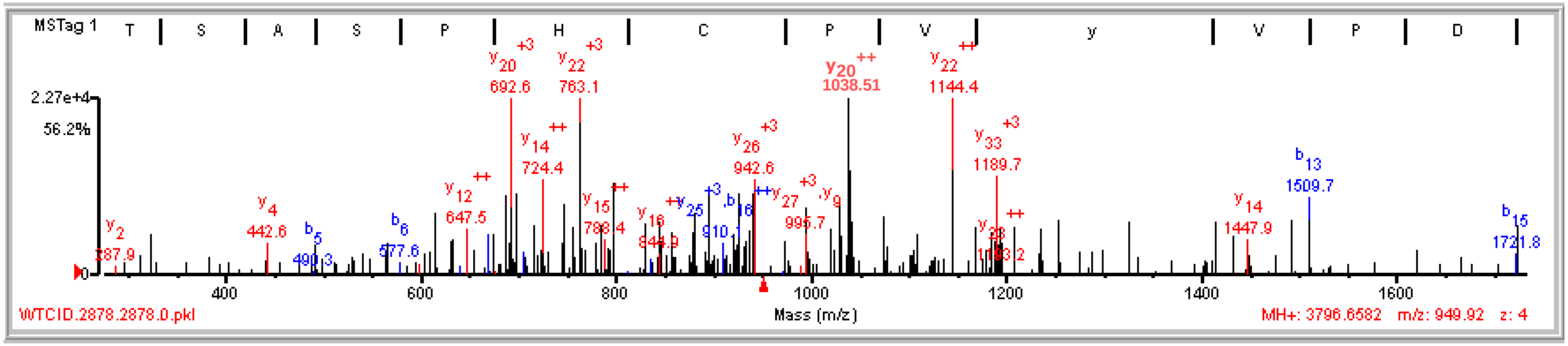
Fragment-ion (m/z)	272.11	330.26	359.21	472.31	501.30	541.22	594.75	603.26	617.77	670.28	681.70	688.46
Frac. Inten.(% of TIC)	2.16	2.08	14.55	6.75	2.10	2.19	2.78	8.21	1.80	3.58	2.06	3.85
Rel. Inten.(% of BP)	14.81	14.33	100.00	46.41	14.45	15.08	19.12	56.40	12.37	24.59	14.19	26.46
Score	1.00	1.00	1.00	1.00	1.00	0.50	0.50	1.00	-0.12	-0.25	-0.14	0.50
Ion-type	y_2	b_3	y_3	y_4	b_5	b_6-NH_3	$y{++}_{10}$-H_2O	$y{++}_{10}$				b_7-NH_3
Delta Da	-0.06	0.09	0.01	0.02	0.07	-0.01	0.50	0.01				0.17

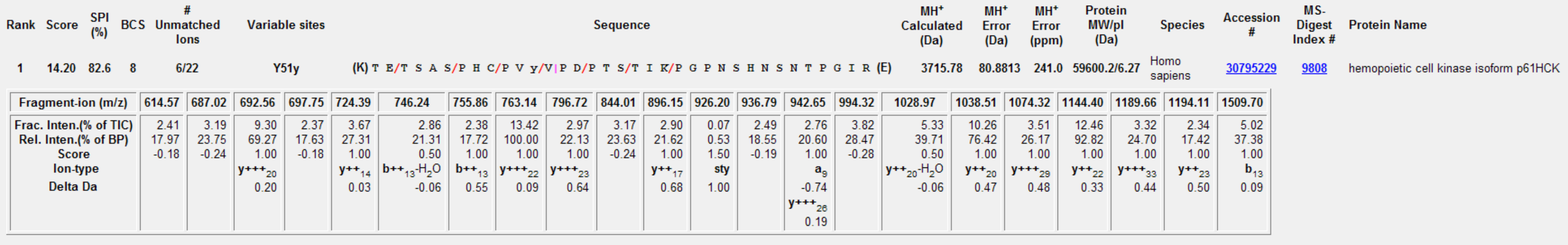
Fragment-ion (m/z)	729.70	862.48	919.40	931.39	976.56	1026.59	1044.50	1090.61	1113.69	1131.48	1188.60	1206.47
Frac. Inten.(% of TIC)	2.15	3.77	6.97	3.69	9.71	1.77	1.81	5.93	2.30	1.76	4.25	3.74
Rel. Inten.(% of BP)	14.77	25.90	47.93	25.38	66.74	12.16	12.47	40.77	15.83	12.11	29.20	25.72
Score	-0.15	1.00	1.00	0.50	1.00	-0.12	0.50	1.00	-0.16	0.50	0.50	-0.26
Ion-type		y_6	y_7	b_8-NH_3	y_8		b_9-NH_3	y_9		b_{10}-NH_3	y_{10}-NH_3	
Delta Da		0.09	-0.01	0.07	0.13		0.09	0.14		0.04	0.13	

Peak 337

Ions that verify assignment





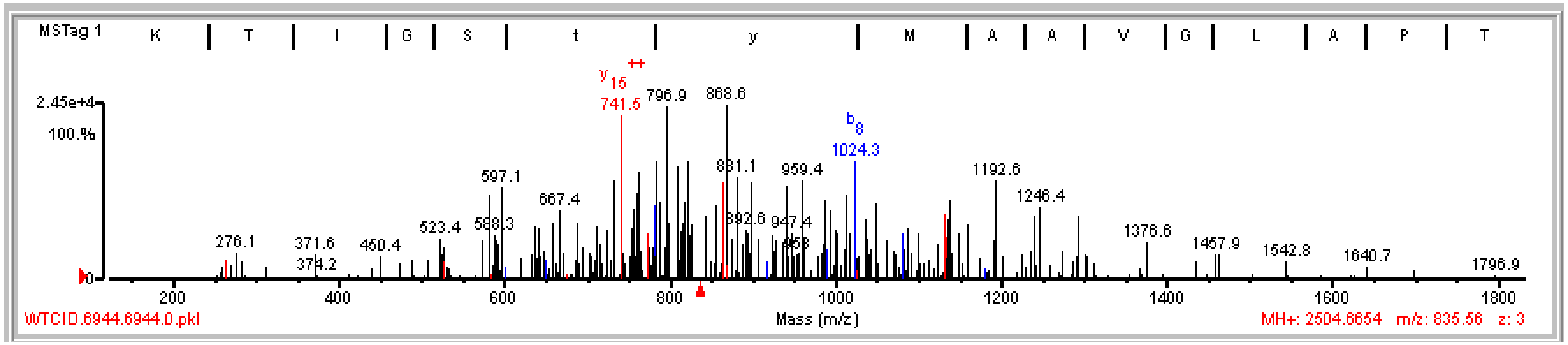


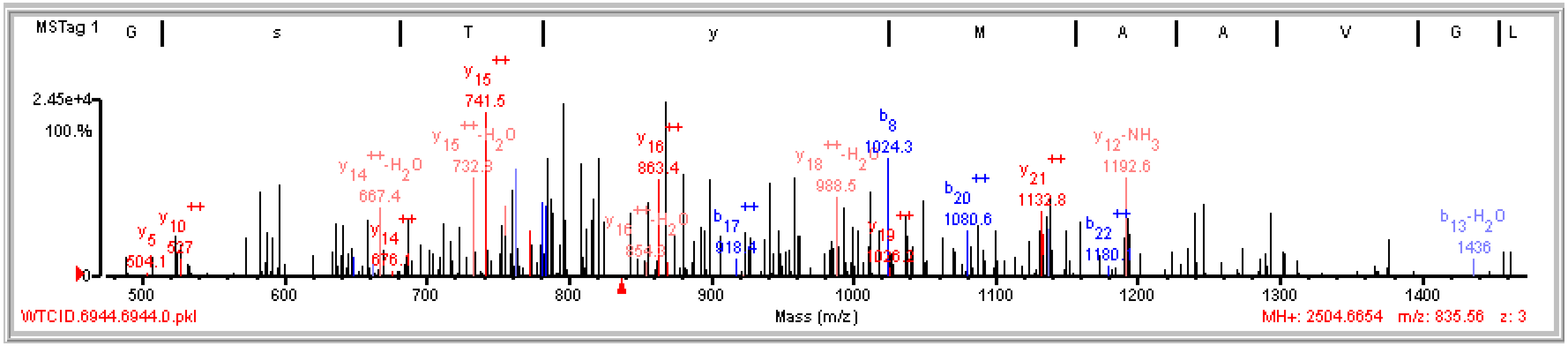
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.20	82.6	8	6/22	Y51y	(K) T E/T S A S/P H C/P V y/V|P D/P T S/T I K/P G P N S H N S N T P G I R (E)	3715.78	80.8813	241.0	59600.2/6.27	Homo sapiens	30795229	9808	hemopoietic cell kinase isoform p61HCK

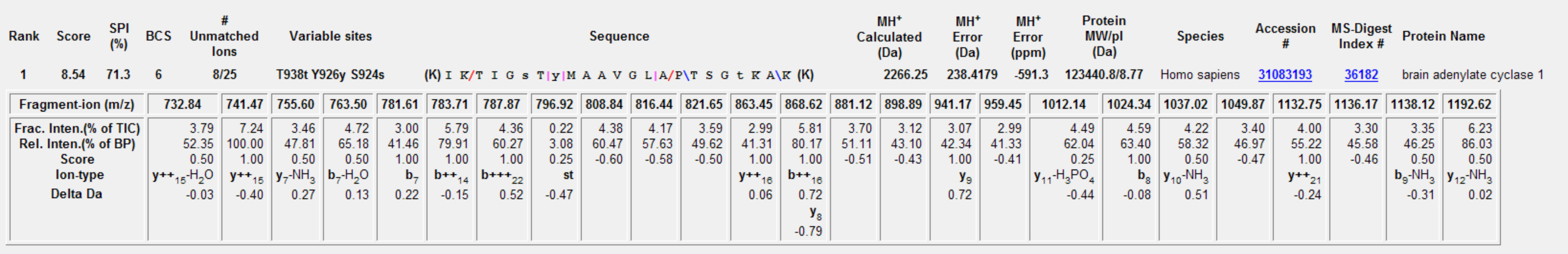
Fragment-ion (m/z)	614.57	687.02	692.56	697.75	724.39	746.24	755.86	763.14	796.72	844.01	896.15
Frac. Inten.(% of TIC)	2.41	3.19	9.30	2.37	3.67	2.86	2.38	13.42	2.97	3.17	2.90
Rel. Inten.(% of BP)	17.97	23.75	69.27	17.63	27.31	21.31	17.72	100.00	22.13	23.63	21.62
Score	-0.18	-0.24	1.00	-0.18	1.00	0.50	1.00	1.00	1.00	-0.24	1.00
Ion-type			$y{+}{+}{+}_{20}$		$y{+}{+}_{14}$	$b{+}{+}_{13}$-H_2O	$b{+}{+}_{13}$	$y{+}{+}{+}_{22}$	$y{+}{+}{+}_{23}$		$y{+}{+}_{17}$
Delta Da			0.20		0.03	-0.06	0.55	0.09	0.64		0.68

Fragment-ion (m/z)	926.20	936.79	942.65	994.32	1028.97	1038.51	1074.32	1144.40	1189.66	1194.11	1509.70
Frac. Inten.(% of TIC)	0.07	2.49	2.76	3.82	5.33	10.26	3.51	12.46	3.32	2.34	5.02
Rel. Inten.(% of BP)	0.53	18.55	20.60	28.47	39.71	76.42	26.17	92.82	24.70	17.42	37.38
Score	1.50	-0.19	1.00	-0.28	0.50	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	sty		a_9 $y{+}{+}{+}_{26}$		$y{+}{+}_{20}$-H_2O	$y{+}{+}_{20}$	$y{+}{+}{+}_{29}$	$y{+}{+}_{22}$	$y{+}{+}{+}_{33}$	$y{+}{+}_{23}$	b_{13}
Delta Da	1.00		-0.74 0.19		-0.06	0.47	0.48	0.33	0.44	0.50	0.09

Peak 338







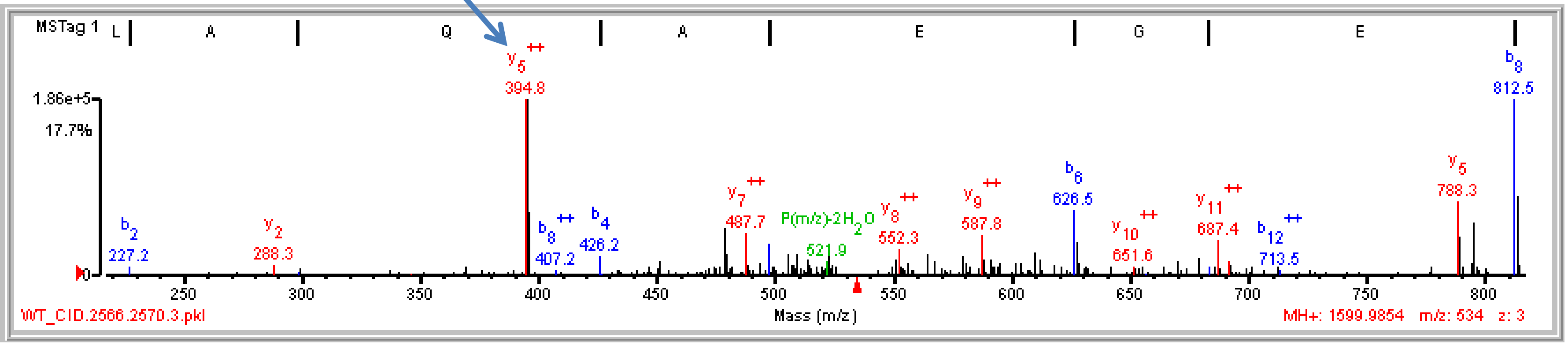
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.54	71.3	6	8/25	T938t Y926y S924s	(K) I K/T I G s T|y|M A A V G L|A/P\T S G t K A\K (K)	2266.25	238.4179	-591.3	123440.8/8.77	Homo sapiens	31083193	36182	brain adenylate cyclase 1

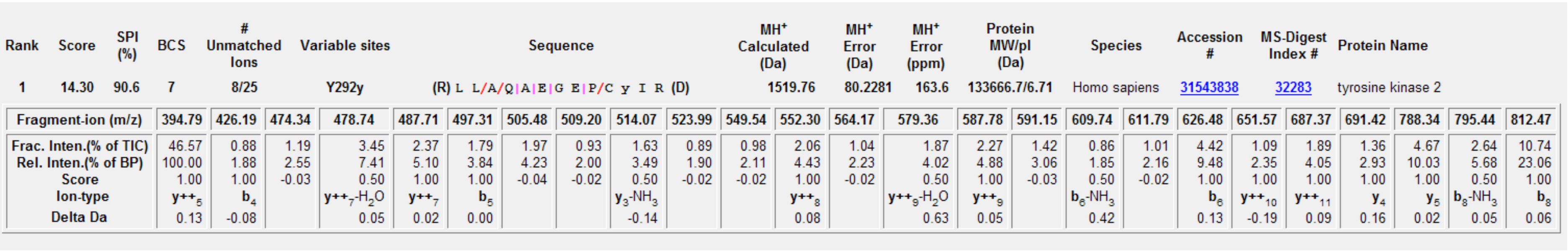
Fragment-ion (m/z)	732.84	741.47	755.60	763.50	781.61	783.71	787.87	796.92	808.84	816.44	821.65	863.45
Frac. Inten.(% of TIC)	3.79	7.24	3.46	4.72	3.00	5.79	4.36	0.22	4.38	4.17	3.59	2.99
Rel. Inten.(% of BP)	52.35	100.00	47.81	65.18	41.46	79.91	60.27	3.08	60.47	57.63	49.62	41.31
Score	0.50	1.00	0.50	0.50	1.00	1.00	1.00	0.25	-0.60	-0.58	-0.50	1.00
Ion-type	y++$_{15}$-H_2O	y++$_{15}$	y_7-NH_3	b_7-H_2O	b_7	b++$_{14}$	b+++$_{22}$	st				y++$_{16}$
Delta Da	-0.03	-0.40	0.27	0.13	0.22	-0.15	0.52	-0.47				0.06

Fragment-ion (m/z)	868.62	881.12	898.89	941.17	959.45	1012.14	1024.34	1037.02	1049.87	1132.75	1136.17	1138.12	1192.62
Frac. Inten.(% of TIC)	5.81	3.70	3.12	3.07	2.99	4.49	4.59	4.22	3.40	4.00	3.30	3.35	6.23
Rel. Inten.(% of BP)	80.17	51.11	43.10	42.34	41.33	62.04	63.40	58.32	46.97	55.22	45.58	46.25	86.03
Score	1.00	-0.51	-0.43	1.00	-0.41	0.25	1.00	0.50	-0.47	1.00	-0.46	0.50	0.50
Ion-type	b++$_{16}$ y_8			y_9		y_{11}-H_3PO_4	b_8	y_{10}-NH_3		y++$_{21}$		b_9-NH_3	y_{12}-NH_3
Delta Da	0.72 -0.79			0.72		-0.44	-0.08	0.51		-0.24		-0.31	0.02

Peak 339

Ions that verify assignment



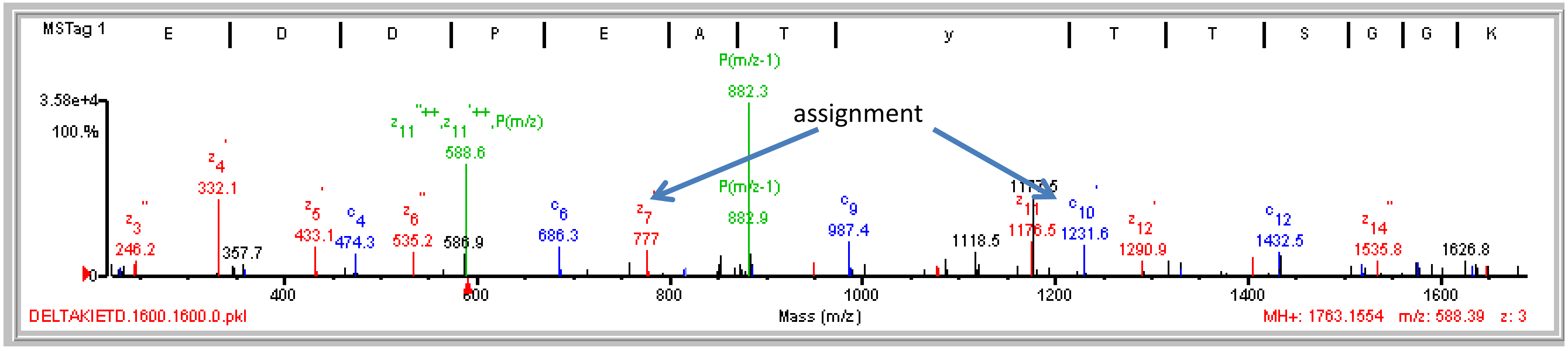


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.30	90.6	7	8/25	Y292y	(R) L L/A/Q|A|E|G E|P/C y I R (D)	1519.76	80.2281	163.6	133666.7/6.71	Homo sapiens	31543838	32283	tyrosine kinase 2

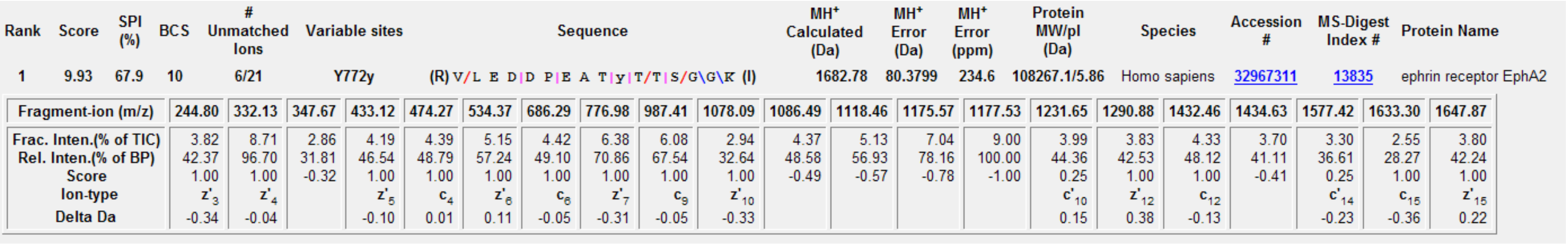
Fragment-ion (m/z)	394.79	426.19	474.34	478.74	487.71	497.31	505.48	509.20	514.07	523.99	549.54	552.30	564.17
Frac. Inten.(% of TIC)	46.57	0.88	1.19	3.45	2.37	1.79	1.97	0.93	1.63	0.89	0.98	2.06	1.04
Rel. Inten.(% of BP)	100.00	1.88	2.55	7.41	5.10	3.84	4.23	2.00	3.49	1.90	2.11	4.43	2.23
Score	1.00	1.00	-0.03	0.50	1.00	1.00	-0.04	-0.02	0.50	-0.02	-0.02	1.00	-0.02
Ion-type	$y{+}{+}_5$	b_4		$y{+}{+}_7$-H_2O	$y{+}{+}_7$	b_5			y_3-NH_3			$y{+}{+}_8$	
Delta Da	0.13	-0.08		0.05	0.02	0.00			-0.14			0.08	

Fragment-ion (m/z)	579.36	587.78	591.15	609.74	611.79	626.48	651.57	687.37	691.42	788.34	795.44	812.47
Frac. Inten.(% of TIC)	1.87	2.27	1.42	0.86	1.01	4.42	1.09	1.89	1.36	4.67	2.64	10.74
Rel. Inten.(% of BP)	4.02	4.88	3.06	1.85	2.16	9.48	2.35	4.05	2.93	10.03	5.68	23.06
Score	0.50	1.00	-0.03	0.50	-0.02	1.00	1.00	1.00	1.00	1.00	0.50	1.00
Ion-type	$y{+}{+}_9$-H_2O	$y{+}{+}_9$		b_6-NH_3		b_6	$y{+}{+}_{10}$	$y{+}{+}_{11}$	y_4	y_5	b_8-NH_3	b_8
Delta Da	0.63	0.05		0.42		0.13	-0.19	0.09	0.16	0.02	0.05	0.06

Peak 340



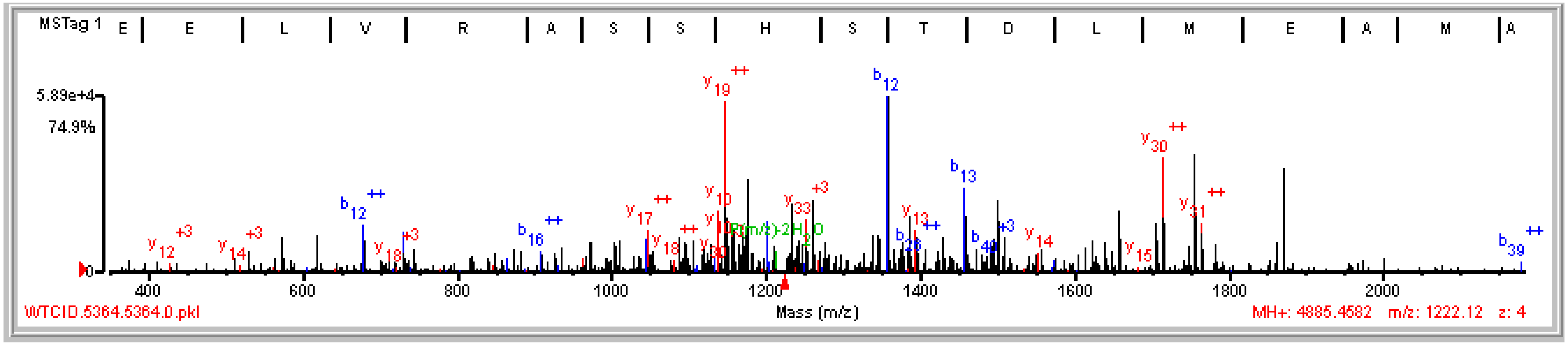
assignment

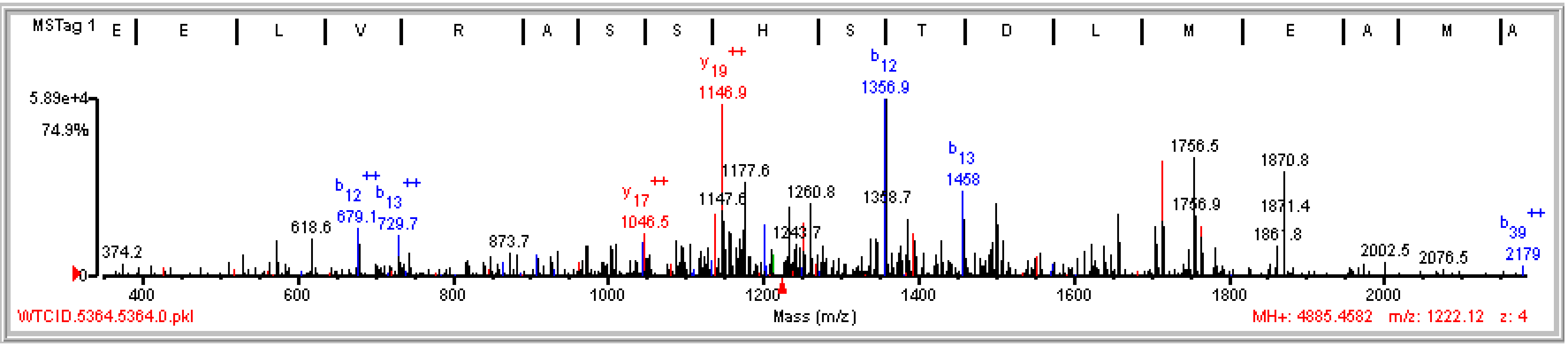


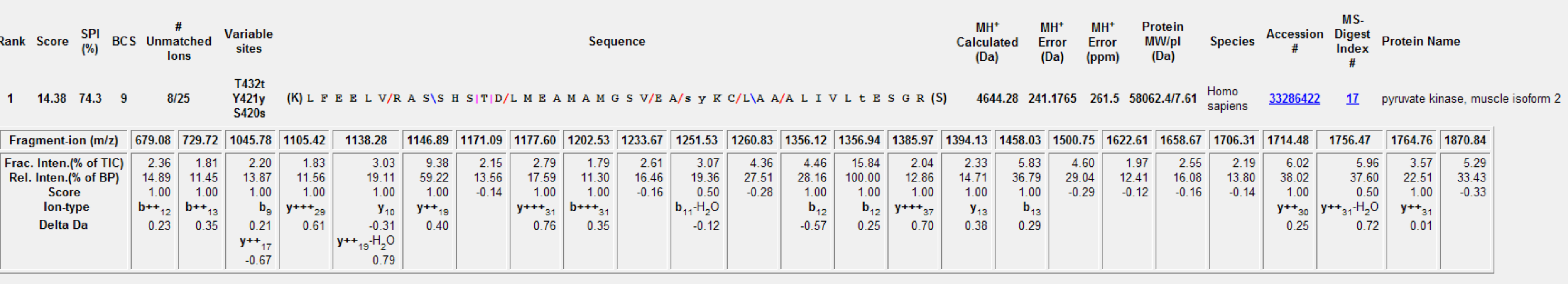
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.93	67.9	10	6/21	Y772y	(R) V/L E D|D P|E A T|y|T/T|S/G\G\K (I)	1682.78	80.3799	234.6	108267.1/5.86	Homo sapiens	32967311	13835	ephrin receptor EphA2

Fragment-ion (m/z)	244.80	332.13	347.67	433.12	474.27	534.37	686.29	776.98	987.41	1078.09	1086.49	1118.46	1175.57	1177.53	1231.65	1290.88	1432.46	1434.63	1577.42	1633.30	1647.87
Frac. Inten.(% of TIC)	3.82	8.71	2.86	4.19	4.39	5.15	4.42	6.38	6.08	2.94	4.37	5.13	7.04	9.00	3.99	3.83	4.33	3.70	3.30	2.55	3.80
Rel. Inten.(% of BP)	42.37	96.70	31.81	46.54	48.79	57.24	49.10	70.86	67.54	32.64	48.58	56.93	78.16	100.00	44.36	42.53	48.12	41.11	36.61	28.27	42.24
Score	1.00	1.00	-0.32	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.49	-0.57	-0.78	-1.00	0.25	1.00	1.00	-0.41	0.25	1.00	1.00
Ion-type	z'_3	z'_4		z'_5	c_4	z'_6	c_6	z'_7	c_9	z'_{10}					c'_{10}	z'_{12}	c_{12}		c'_{14}	c_{15}	z'_{15}
Delta Da	-0.34	-0.04		-0.10	0.01	0.11	-0.05	-0.31	-0.05	-0.33					0.15	0.38	-0.13		-0.23	-0.36	0.22

Peak 341





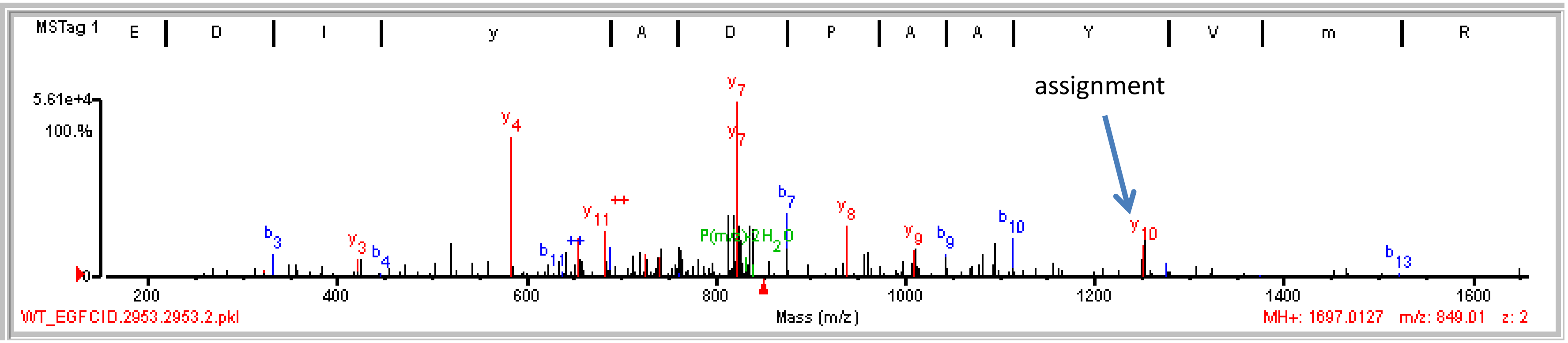


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.38	74.3	9	8/25	T432t Y421y S420s	(K) L F E E L V/R A S\S H S|T|D/L M E A M A M G S V/E A/s y K C/L\A A/A L I V L t E S G R (S)	4644.28	241.1765	261.5	58062.4/7.61	Homo sapiens	33286422	17	pyruvate kinase, muscle isoform 2

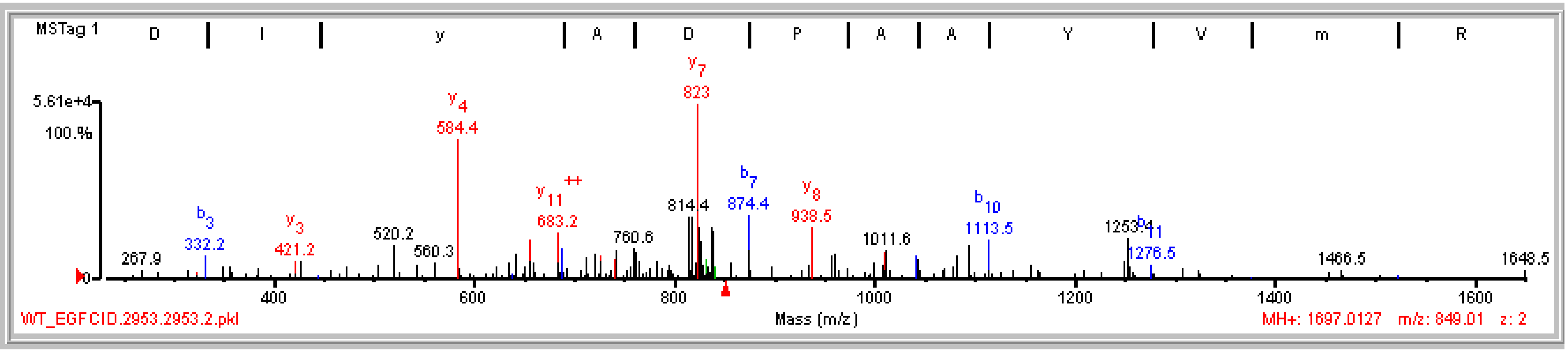
Fragment-ion (m/z)	679.08	729.72	1045.78	1105.42	1138.28	1146.89	1171.09	1177.60	1202.53	1233.67	1251.53	1260.83
Frac. Inten.(% of TIC)	2.36	1.81	2.20	1.83	3.03	9.38	2.15	2.79	1.79	2.61	3.07	4.36
Rel. Inten.(% of BP)	14.89	11.45	13.87	11.56	19.11	59.22	13.56	17.59	11.30	16.46	19.36	27.51
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.14	1.00	1.00	-0.16	0.50	-0.28
Ion-type	b^{++}_{12}	b^{++}_{13}	b_9 0.21 y^{++}_{17}	y^{+++}_{29}	y_{10} -0.31 y^{++}_{19}-H_2O	y^{++}_{19}		y^{+++}_{31}	b^{+++}_{31}		b_{11}-H_2O	
Delta Da	0.23	0.35	-0.67	0.61	0.79	0.40		0.76	0.35		-0.12	

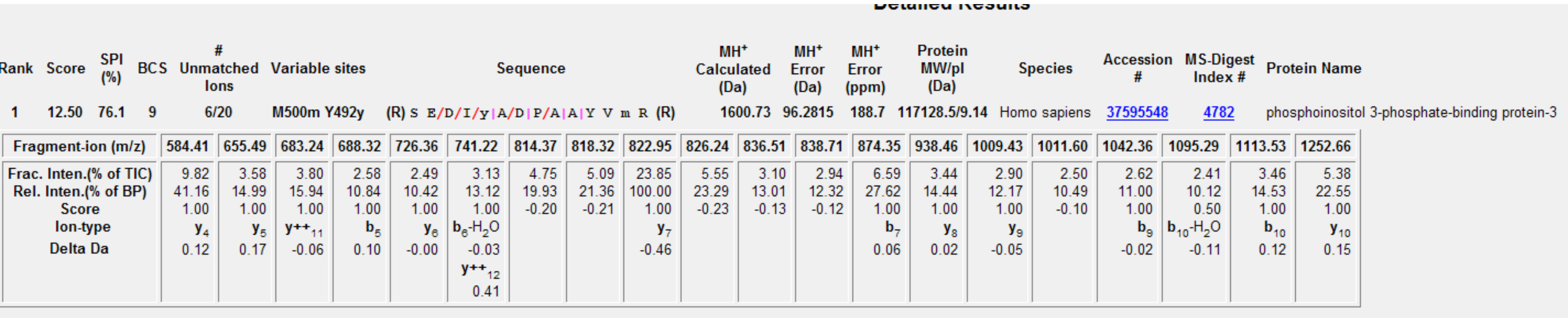
Fragment-ion (m/z)	1356.12	1356.94	1385.97	1394.13	1458.03	1500.75	1622.61	1658.67	1706.31	1714.48	1756.47	1764.76	1870.84
Frac. Inten.(% of TIC)	4.46	15.84	2.04	2.33	5.83	4.60	1.97	2.55	2.19	6.02	5.96	3.57	5.29
Rel. Inten.(% of BP)	28.16	100.00	12.86	14.71	36.79	29.04	12.41	16.08	13.80	38.02	37.60	22.51	33.43
Score	1.00	1.00	1.00	1.00	1.00	-0.29	-0.12	-0.16	-0.14	1.00	0.50	1.00	-0.33
Ion-type	b_{12}	b_{12}	y^{+++}_{37}	y_{13}	b_{13}					y^{++}_{30}	y^{++}_{31}-H_2O	y^{++}_{31}	
Delta Da	-0.57	0.25	0.70	0.38	0.29					0.25	0.72	0.01	

Peak 342



assignment



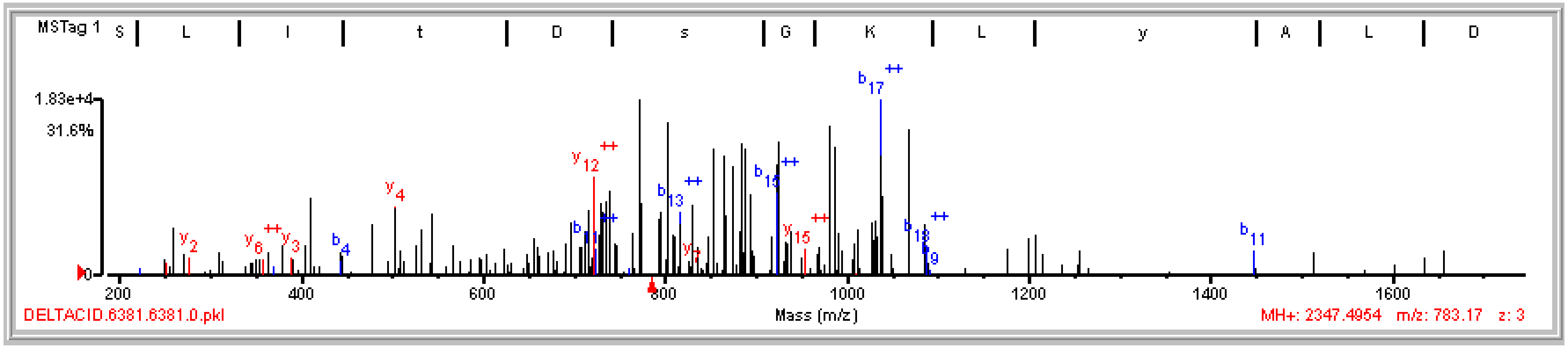


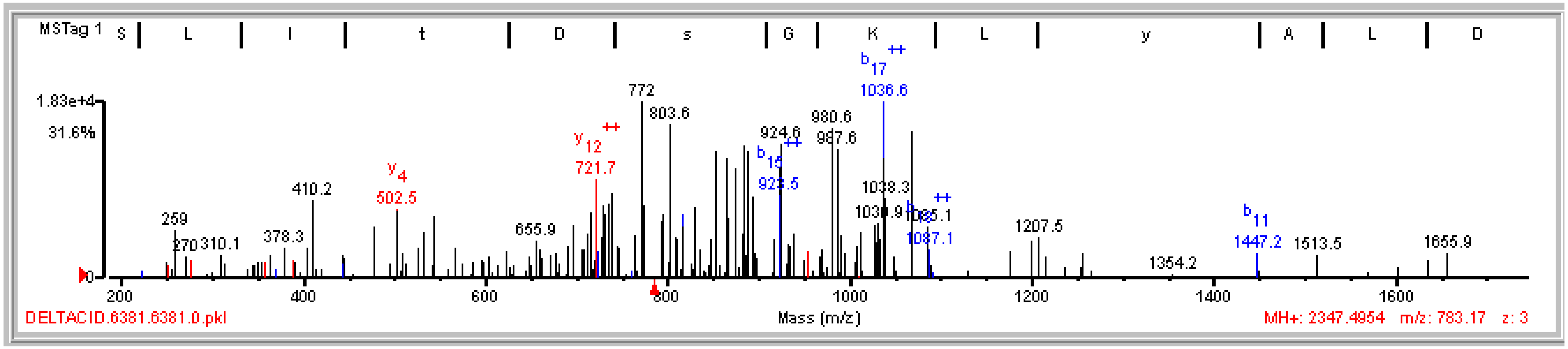
Detailed Results

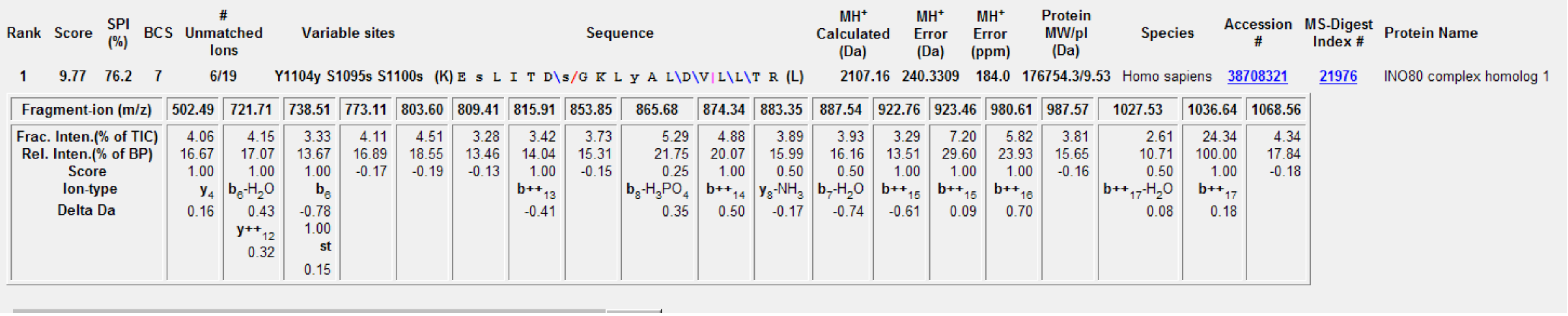
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.50	76.1	9	6/20	M500m Y492y	(R) S E/D/I/y|A/D|P/A|A|Y V m R (R)	1600.73	96.2815	188.7	117128.5/9.14	Homo sapiens	37595548	4782	phosphoinositol 3-phosphate-binding protein-3

Fragment-ion (m/z)	584.41	655.49	683.24	688.32	726.36	741.22	814.37	818.32	822.95	826.24	836.51	838.71	874.35	938.46	1009.43	1011.60	1042.36	1095.29	1113.53	1252.66
Frac. Inten.(% of TIC)	9.82	3.58	3.80	2.58	2.49	3.13	4.75	5.09	23.85	5.55	3.10	2.94	6.59	3.44	2.90	2.50	2.62	2.41	3.46	5.38
Rel. Inten.(% of BP)	41.16	14.99	15.94	10.84	10.42	13.12	19.93	21.36	100.00	23.29	13.01	12.32	27.62	14.44	12.17	10.49	11.00	10.12	14.53	22.55
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.20	-0.21	1.00	-0.23	-0.13	-0.12	1.00	1.00	1.00	-0.10	1.00	0.50	1.00	1.00
Ion-type	y_4	y_5	y^{++}_{11}	b_5	y_6	b_6-H_2O y^{++}_{12}			y_7				b_7	y_8	y_9		b_9	b_{10}-H_2O	b_{10}	y_{10}
Delta Da	0.12	0.17	-0.06	0.10	-0.00	-0.03 0.41			-0.46				0.06	0.02	-0.05		-0.02	-0.11	0.12	0.15

Peak 343





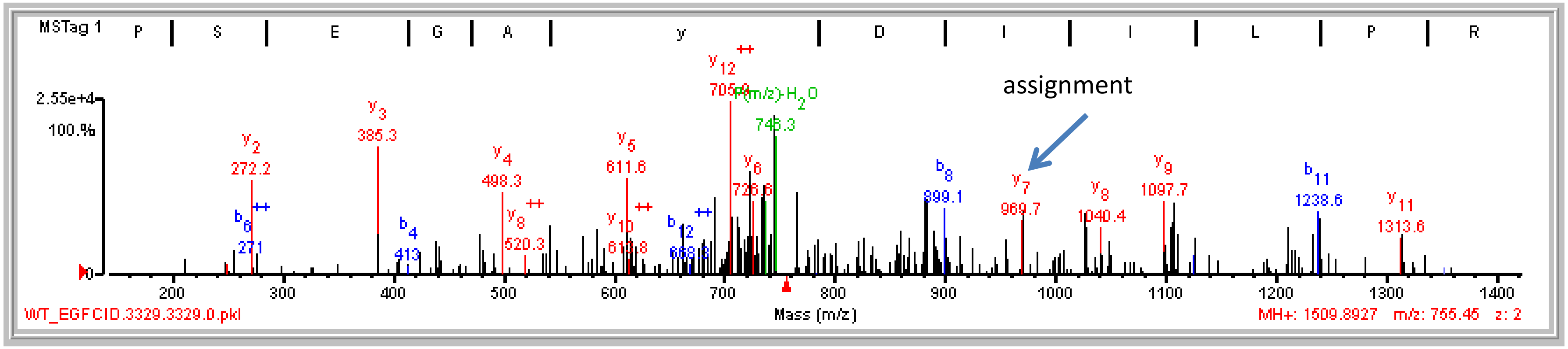


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.77	76.2	7	6/19	Y1104y S1095s S1100s	(K) E s L I T D\s/G K L y A L\D\V|L\L\T R (L)	2107.16	240.3309	184.0	176754.3/9.53	Homo sapiens	38708321	21976	INO80 complex homolog 1

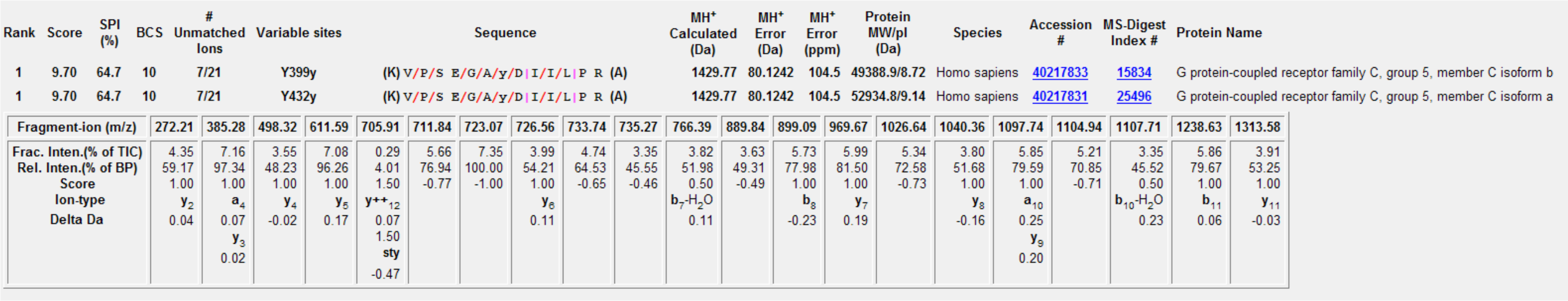
Fragment-ion (m/z)	502.49	721.71	738.51	773.11	803.60	809.41	815.91	853.85	865.68	874.34
Frac. Inten.(% of TIC)	4.06	4.15	3.33	4.11	4.51	3.28	3.42	3.73	5.29	4.88
Rel. Inten.(% of BP)	16.67	17.07	13.67	16.89	18.55	13.46	14.04	15.31	21.75	20.07
Score	1.00	1.00	1.00	-0.17	-0.19	-0.13	1.00	-0.15	0.25	1.00
Ion-type	y_4	b_6-H_2O	b_6				$b{+}{+}_{13}$		b_8-H_3PO_4	$b{+}{+}_{14}$
Delta Da	0.16	0.43	-0.78				-0.41		0.35	0.50
			1.00							
		$y{+}{+}_{12}$	st							
		0.32	0.15							

Fragment-ion (m/z)	883.35	887.54	922.76	923.46	980.61	987.57	1027.53	1036.64	1068.56
Frac. Inten.(% of TIC)	3.89	3.93	3.29	7.20	5.82	3.81	2.61	24.34	4.34
Rel. Inten.(% of BP)	15.99	16.16	13.51	29.60	23.93	15.65	10.71	100.00	17.84
Score	0.50	0.50	1.00	1.00	1.00	-0.16	0.50	1.00	-0.18
Ion-type	y_8-NH_3	b_7-H_2O	$b{+}{+}_{15}$	$b{+}{+}_{15}$	$b{+}{+}_{16}$		$b{+}{+}_{17}$-H_2O	$b{+}{+}_{17}$	
Delta Da	-0.17	-0.74	-0.61	0.09	0.70		0.08	0.18	

Peak 344



assignment

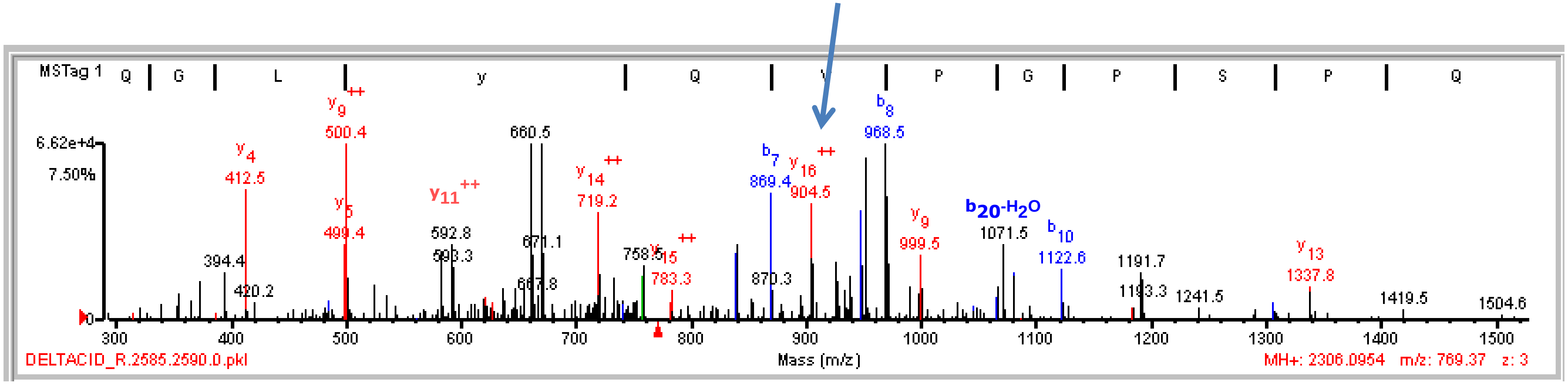


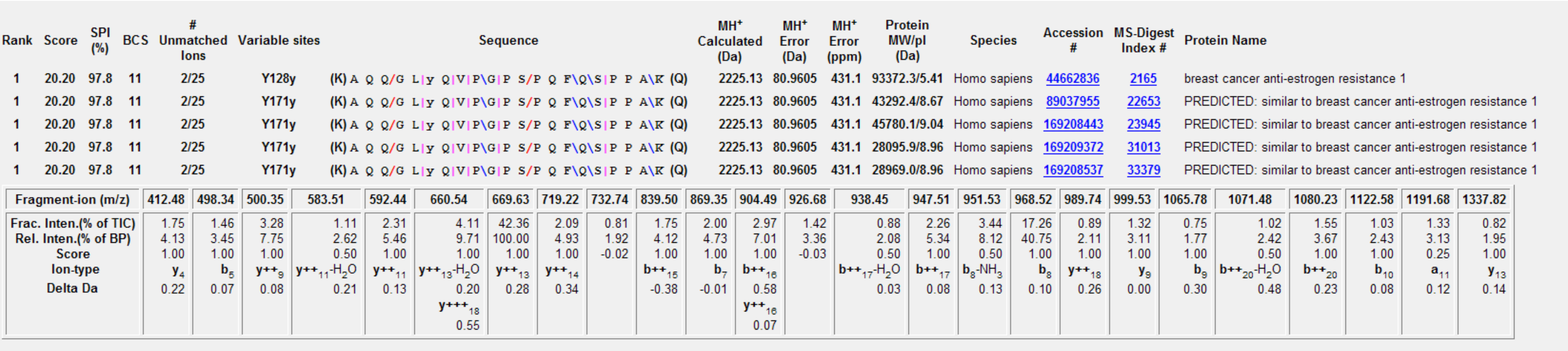
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.70	64.7	10	7/21	Y399y	(K) V/P/S E/G/A/y/D|I/I/L|P R (A)	1429.77	80.1242	104.5	49388.9/8.72	Homo sapiens	40217833	15834	G protein-coupled receptor family C, group 5, member C isoform b
1	9.70	64.7	10	7/21	Y432y	(K) V/P/S E/G/A/y/D|I/I/L|P R (A)	1429.77	80.1242	104.5	52934.8/9.14	Homo sapiens	40217831	25496	G protein-coupled receptor family C, group 5, member C isoform a

Fragment-ion (m/z)	272.21	385.28	498.32	611.59	705.91	711.84	723.07	726.56	733.74	735.27	766.39	889.84	899.09	969.67	1026.64	1040.36	1097.74	1104.94	1107.71	1238.63	1313.58
Frac. Inten.(% of TIC)	4.35	7.16	3.55	7.08	0.29	5.66	7.35	3.99	4.74	3.35	3.82	3.63	5.73	5.99	5.34	3.80	5.85	5.21	3.35	5.86	3.91
Rel. Inten.(% of BP)	59.17	97.34	48.23	96.26	4.01	76.94	100.00	54.21	64.53	45.55	51.98	49.31	77.98	81.50	72.58	51.68	79.59	70.85	45.52	79.67	53.25
Score	1.00	1.00	1.00	1.00	1.50	-0.77	-1.00	1.00	-0.65	-0.46	0.50	-0.49	1.00	1.00	-0.73	1.00	1.00	-0.71	0.50	1.00	1.00
Ion-type	y_2	a_4	y_4	y_5	$y{++}_{12}$			y_6			b_7-H_2O		b_8	y_7		y_8	a_{10}		b_{10}-H_2O	b_{11}	y_{11}
Delta Da	0.04	0.07	-0.02	0.17	0.07			0.11			0.11		-0.23	0.19		-0.16	0.25		0.23	0.06	-0.03
		y_3			1.50												y_9				
		0.02			sty												0.20				
					-0.47																

Peak 345

assignment





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<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>20.20</td><td>97.8</td><td>11</td><td>2/25</td><td>Y128y</td><td>(K) A Q Q/G L|y Q|V|P\G|P S/P Q F\Q\S|P P A\K (Q)</td><td>2225.13</td><td>80.9605</td><td>431.1</td><td>93372.3/5.41</td><td>Homo sapiens</td><td>44662836</td><td>2165</td><td>breast cancer anti-estrogen resistance 1</td></tr>
<tr><td>1</td><td>20.20</td><td>97.8</td><td>11</td><td>2/25</td><td>Y171y</td><td>(K) A Q Q/G L|y Q|V|P\G|P S/P Q F\Q\S|P P A\K (Q)</td><td>2225.13</td><td>80.9605</td><td>431.1</td><td>43292.4/8.67</td><td>Homo sapiens</td><td>89037955</td><td>22653</td><td>PREDICTED: similar to breast cancer anti-estrogen resistance 1</td></tr>
<tr><td>1</td><td>20.20</td><td>97.8</td><td>11</td><td>2/25</td><td>Y171y</td><td>(K) A Q Q/G L|y Q|V|P\G|P S/P Q F\Q\S|P P A\K (Q)</td><td>2225.13</td><td>80.9605</td><td>431.1</td><td>45780.1/9.04</td><td>Homo sapiens</td><td>169208443</td><td>23945</td><td>PREDICTED: similar to breast cancer anti-estrogen resistance 1</td></tr>
<tr><td>1</td><td>20.20</td><td>97.8</td><td>11</td><td>2/25</td><td>Y171y</td><td>(K) A Q Q/G L|y Q|V|P\G|P S/P Q F\Q\S|P P A\K (Q)</td><td>2225.13</td><td>80.9605</td><td>431.1</td><td>28095.9/8.96</td><td>Homo sapiens</td><td>169209372</td><td>31013</td><td>PREDICTED: similar to breast cancer anti-estrogen resistance 1</td></tr>
<tr><td>1</td><td>20.20</td><td>97.8</td><td>11</td><td>2/25</td><td>Y171y</td><td>(K) A Q Q/G L|y Q|V|P\G|P S/P Q F\Q\S|P P A\K (Q)</td><td>2225.13</td><td>80.9605</td><td>431.1</td><td>28969.0/8.96</td><td>Homo sapiens</td><td>169208537</td><td>33379</td><td>PREDICTED: similar to breast cancer anti-estrogen resistance 1</td></tr>
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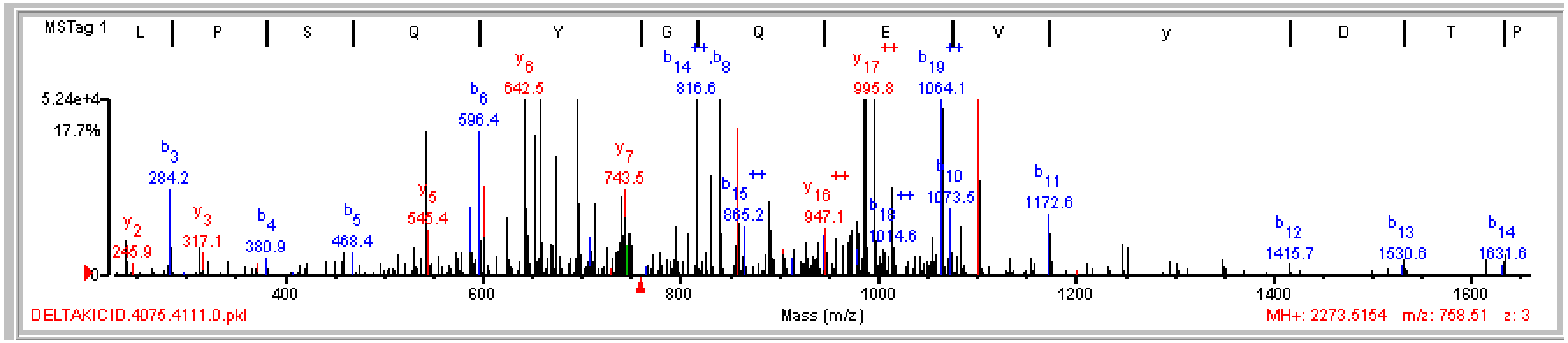
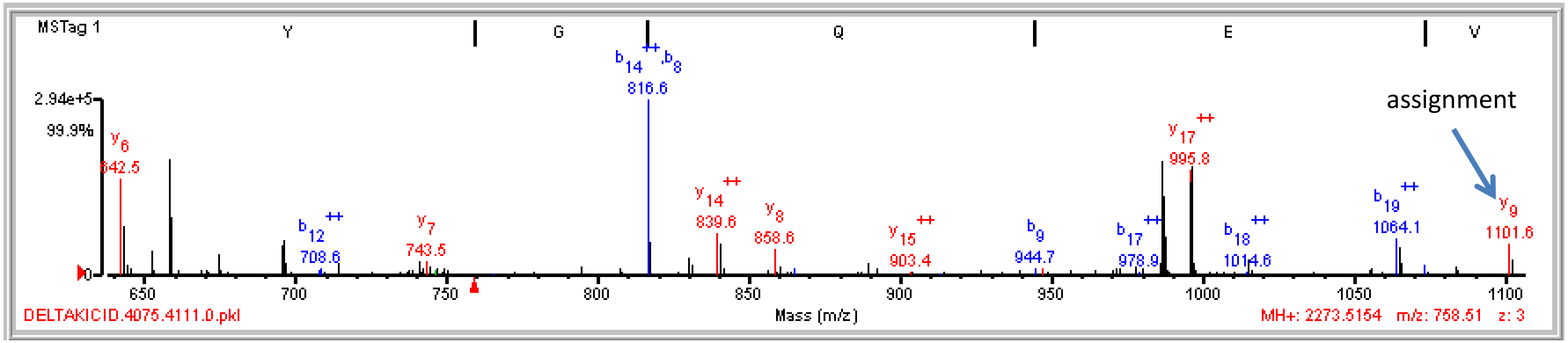
Fragment-ion (m/z)	412.48	498.34	500.35	583.51	592.44	660.54	669.63	719.22	732.74	839.50	869.35	904.49
Frac. Inten.(% of TIC)	1.75	1.46	3.28	1.11	2.31	4.11	42.36	2.09	0.81	1.75	2.00	2.97
Rel. Inten.(% of BP)	4.13	3.45	7.75	2.62	5.46	9.71	100.00	4.93	1.92	4.12	4.73	7.01
Score	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00	-0.02	1.00	1.00	1.00
Ion-type	y$_{4}$	b$_{5}$	y++$_{9}$	y++$_{11}$-H$_2$O	y++$_{11}$	y++$_{13}$-H$_2$O y+++$_{18}$	y++$_{13}$	y++$_{14}$		b++$_{15}$	b$_{7}$	b++$_{16}$ y++$_{16}$
Delta Da	0.22	0.07	0.08	0.21	0.13	0.20 0.55	0.28	0.34		-0.38	-0.01	0.58 0.07

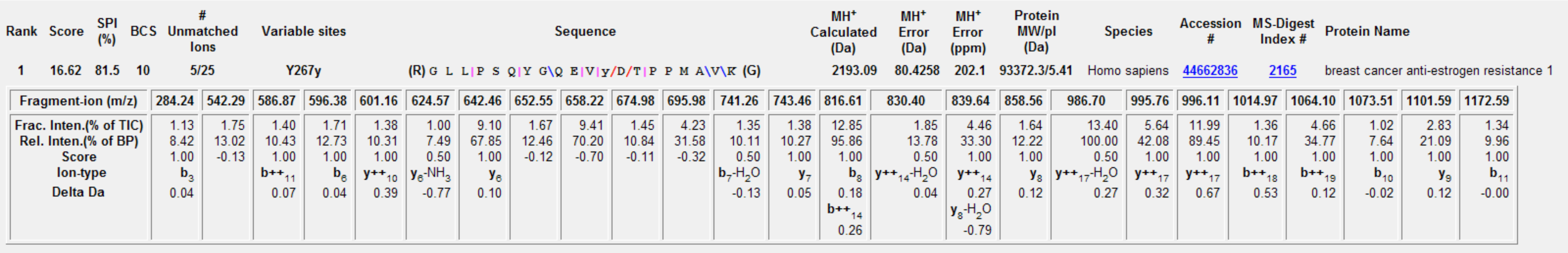
Fragment-ion (m/z)	926.68	938.45	947.51	951.53	968.52	989.74	999.53	1065.78	1071.48	1080.23	1122.58	1191.68	1337.82
Frac. Inten.(% of TIC)	1.42	0.88	2.26	3.44	17.26	0.89	1.32	0.75	1.02	1.55	1.03	1.33	0.82
Rel. Inten.(% of BP)	3.36	2.08	5.34	8.12	40.75	2.11	3.11	1.77	2.42	3.67	2.43	3.13	1.95
Score	-0.03	0.50	1.00	0.50	1.00	1.00	1.00	1.00	0.50	1.00	1.00	0.25	1.00
Ion-type		b++$_{17}$-H$_2$O	b++$_{17}$	b$_{8}$-NH$_3$	b$_{8}$	y++$_{18}$	y$_{9}$	b$_{9}$	b++$_{20}$-H$_2$O	b++$_{20}$	b$_{10}$	a$_{11}$	y$_{13}$
Delta Da		0.03	0.08	0.13	0.10	0.26	0.00	0.30	0.48	0.23	0.08	0.12	0.14

Peak 346





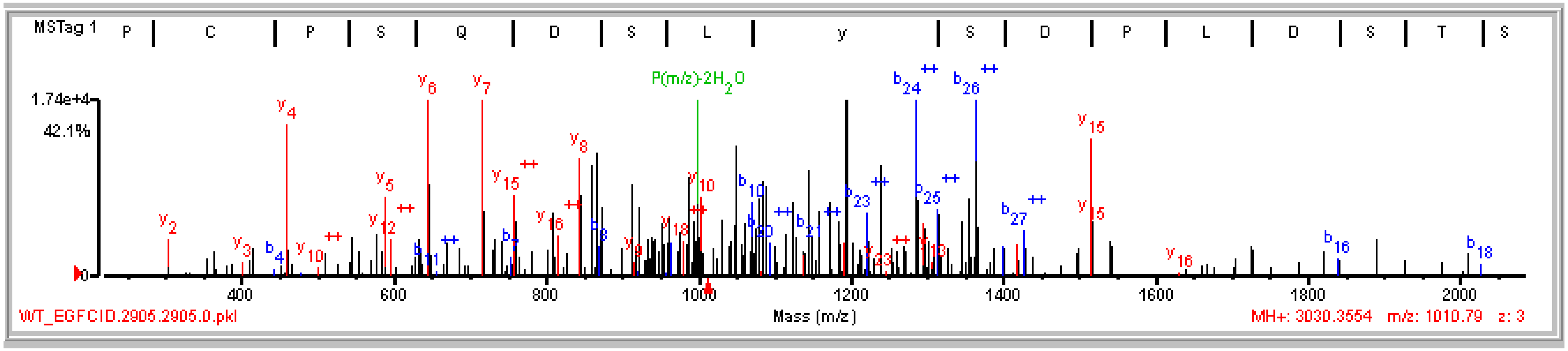
assignment

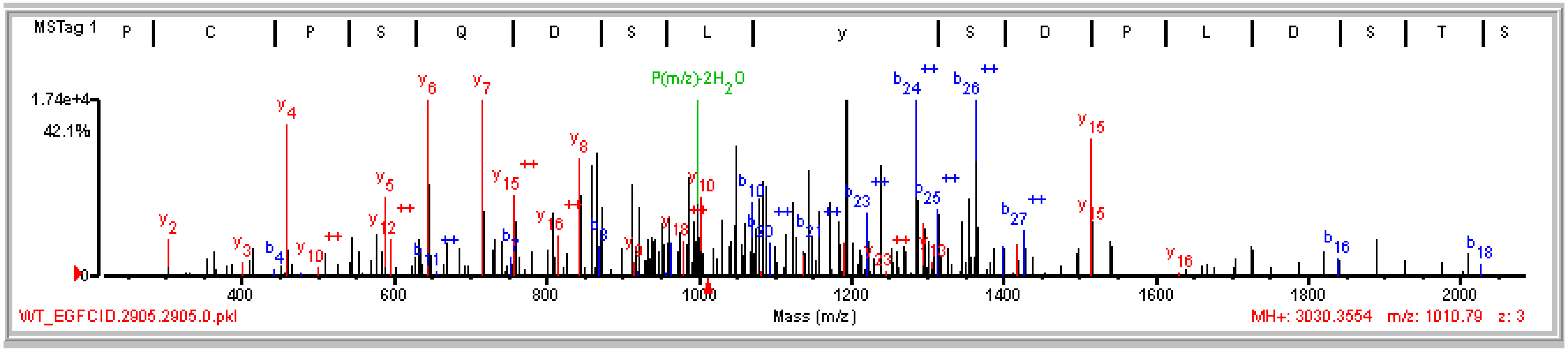


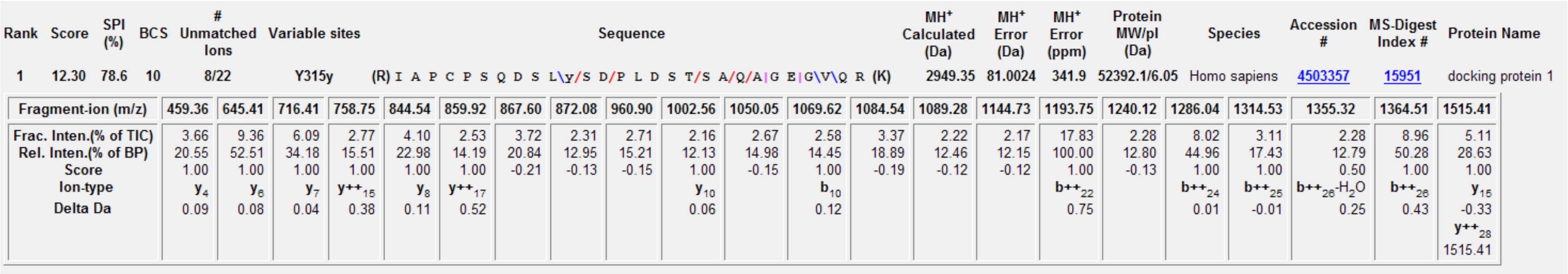
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.62	81.5	10	5/25	Y267y	(R) G L L|P S Q|Y G\Q E|V|y/D/T|P P M A\V\K (G)	2193.09	80.4258	202.1	93372.3/5.41	Homo sapiens	44662836	2165	breast cancer anti-estrogen resistance 1

Fragment-ion (m/z)	284.24	542.29	586.87	596.38	601.16	624.57	642.46	652.55	658.22	674.98	695.98	741.26	743.46	816.61	830.40	839.64	858.56	986.70	995.76	996.11	1014.97	1064.10	1073.51	1101.59	1172.59
Frac. Inten.(% of TIC)	1.13	1.75	1.40	1.71	1.38	1.00	9.10	1.67	9.41	1.45	4.23	1.35	1.38	12.85	1.85	4.46	1.64	13.40	5.64	11.99	1.36	4.66	1.02	2.83	1.34
Rel. Inten.(% of BP)	8.42	13.02	10.43	12.73	10.31	7.49	67.85	12.46	70.20	10.84	31.58	10.11	10.27	95.86	13.78	33.30	12.22	100.00	42.08	89.45	10.17	34.77	7.64	21.09	9.96
Score	1.00	-0.13	1.00	1.00	1.00	0.50	1.00	-0.12	-0.70	-0.11	-0.32	0.50	1.00	1.00	0.50	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	b_3		$b{+}{+}_{11}$	b_6	$y{+}{+}_{10}$	y_6-NH_3	y_6					b_7-H_2O	y_7	b_8 $b{+}{+}_{14}$	$y{+}{+}_{14}$-H_2O	$y{+}{+}_{14}$ y_8-H_2O	y_8	$y{+}{+}_{17}$-H_2O	$y{+}{+}_{17}$	$y{+}{+}_{17}$	$b{+}{+}_{18}$	$b{+}{+}_{19}$	b_{10}	y_9	b_{11}
Delta Da	0.04		0.07	0.04	0.39	-0.77	0.10					-0.13	0.05	0.18 0.26	0.04	0.27 -0.79	0.12	0.27	0.32	0.67	0.53	0.12	-0.02	0.12	-0.00

Peak 347



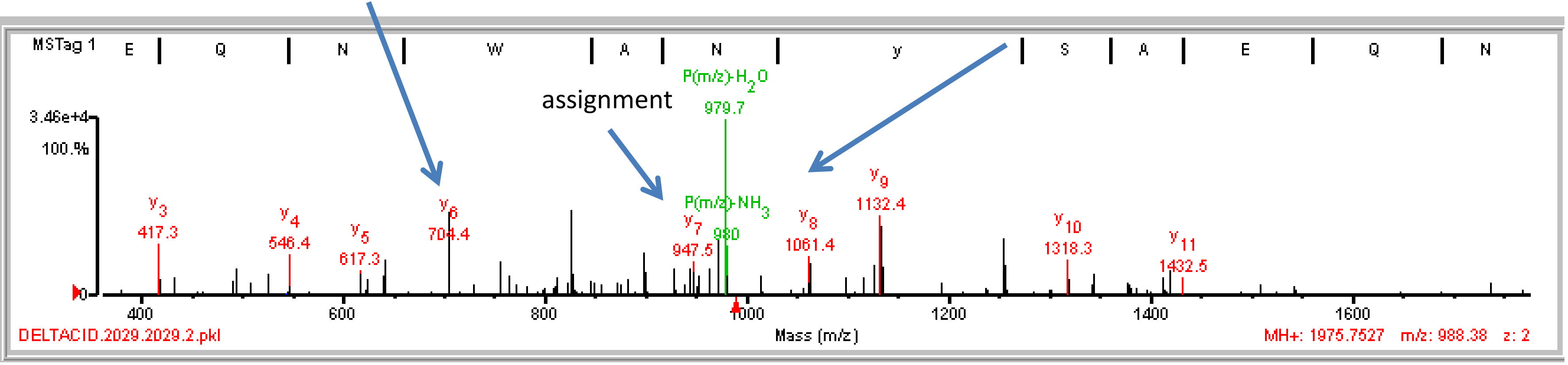




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.30	78.6	10	8/22	Y315y	(R) I A P C P S Q D S L\y/S D/P L D S T/S A/Q/A|G E|G\V\Q R (K)	2949.35	81.0024	341.9	52392.1/6.05	Homo sapiens	4503357	15951	docking protein 1

Fragment-ion (m/z)	459.36	645.41	716.41	758.75	844.54	859.92	867.60	872.08	960.90	1002.56	1050.05	1069.62	1084.54	1089.28	1144.73	1193.75	1240.12	1286.04	1314.53	1355.32	1364.51	1515.41
Frac. Inten.(% of TIC)	3.66	9.36	6.09	2.77	4.10	2.53	3.72	2.31	2.71	2.16	2.67	2.58	3.37	2.22	2.17	17.83	2.28	8.02	3.11	2.28	8.96	5.11
Rel. Inten.(% of BP)	20.55	52.51	34.18	15.51	22.98	14.19	20.84	12.95	15.21	12.13	14.98	14.45	18.89	12.46	12.15	100.00	12.80	44.96	17.43	12.79	50.28	28.63
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.21	-0.13	-0.15	1.00	-0.15	1.00	-0.19	-0.12	-0.12	1.00	-0.13	1.00	1.00	0.50	1.00	1.00
Ion-type	y_4	y_6	y_7	y++_{15}	y_8	y++_{17}				y_{10}		b_{10}				b++_{22}		b++_{24}	b++_{25}	$\text{b++}_{26}\text{-}H_2O$	b++_{26}	y_{15}
Delta Da	0.09	0.08	0.04	0.38	0.11	0.52				0.06		0.12				0.75		0.01	-0.01	0.25	0.43	-0.33
																						y++_{28}
																						1515.41

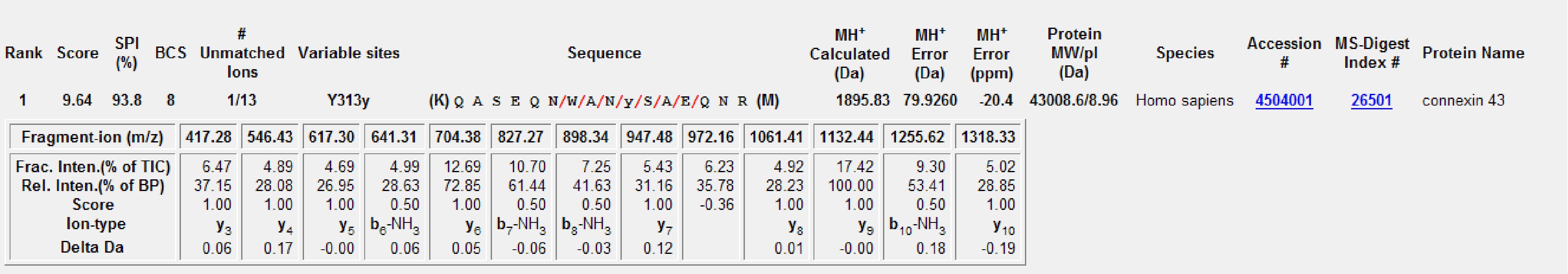
Peak 348



Ions that verify assignment

assignment

Ions that verify assignment

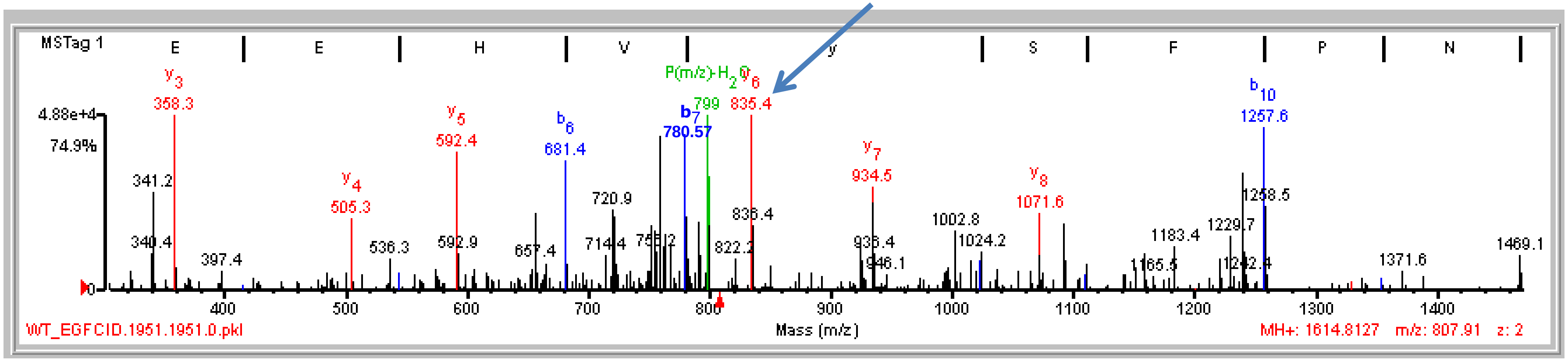


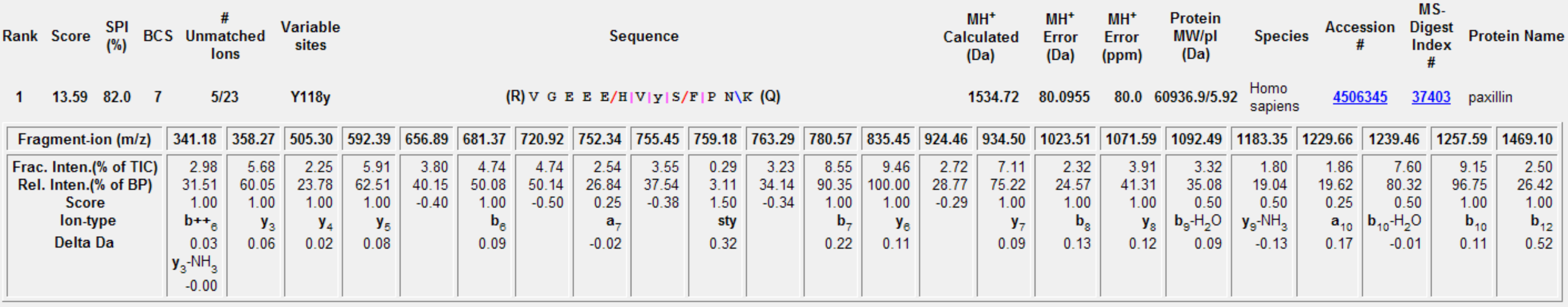
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.64	93.8	8	1/13	Y313y	(K) Q A S E Q N/W/A/N/y/S/A/E/Q N R (M)	1895.83	79.9260	-20.4	43008.6/8.96	Homo sapiens	4504001	26501	connexin 43

Fragment-ion (m/z)	417.28	546.43	617.30	641.31	704.38	827.27	898.34	947.48	972.16	1061.41	1132.44	1255.62	1318.33
Frac. Inten.(% of TIC)	6.47	4.89	4.69	4.99	12.69	10.70	7.25	5.43	6.23	4.92	17.42	9.30	5.02
Rel. Inten.(% of BP)	37.15	28.08	26.95	28.63	72.85	61.44	41.63	31.16	35.78	28.23	100.00	53.41	28.85
Score	1.00	1.00	1.00	0.50	1.00	0.50	0.50	1.00	-0.36	1.00	1.00	0.50	1.00
Ion-type	y_3	y_4	y_5	b_6-NH_3	y_6	b_7-NH_3	b_8-NH_3	y_7		y_8	y_9	b_{10}-NH_3	y_{10}
Delta Da	0.06	0.17	-0.00	0.06	0.05	-0.06	-0.03	0.12		0.01	-0.00	0.18	-0.19

Peak 349

assignment

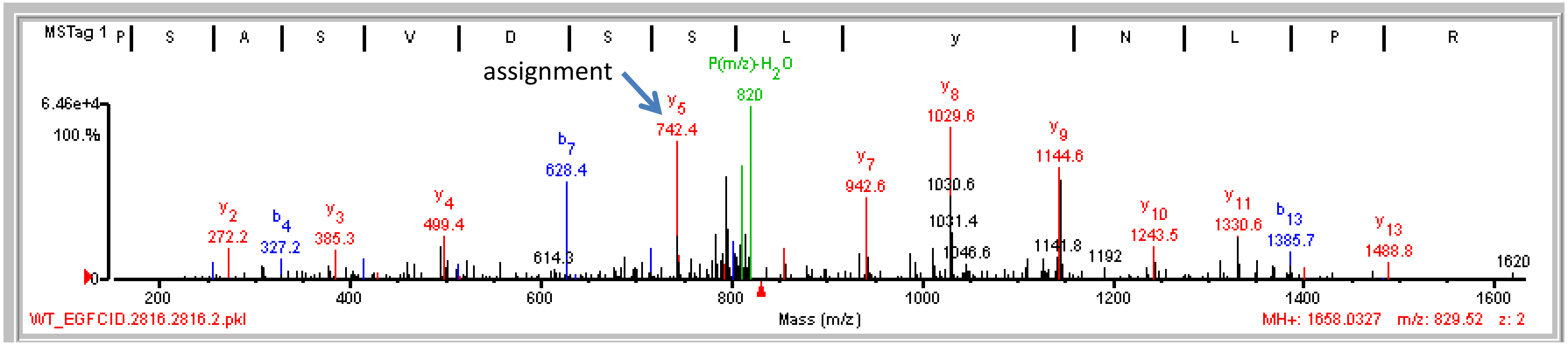


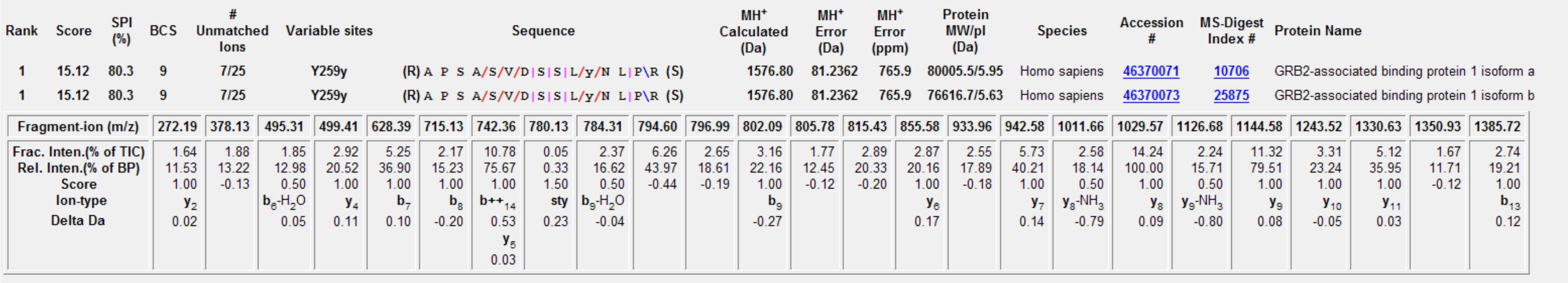


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.59	82.0	7	5/23	Y118y	(R) V G E E E/H|V|y|S/F|P N\K (Q)	1534.72	80.0955	80.0	60936.9/5.92	Homo sapiens	4506345	37403	paxillin

Fragment-ion (m/z)	341.18	358.27	505.30	592.39	656.89	681.37	720.92	752.34	755.45	759.18	763.29	780.57	835.45	924.46	934.50	1023.51	1071.59	1092.49	1183.35	1229.66	1239.46	1257.59	1469.10
Frac. Inten.(% of TIC)	2.98	5.68	2.25	5.91	3.80	4.74	4.74	2.54	3.55	0.29	3.23	8.55	9.46	2.72	7.11	2.32	3.91	3.32	1.80	1.86	7.60	9.15	2.50
Rel. Inten.(% of BP)	31.51	60.05	23.78	62.51	40.15	50.08	50.14	26.84	37.54	3.11	34.14	90.35	100.00	28.77	75.22	24.57	41.31	35.08	19.04	19.62	80.32	96.75	26.42
Score	1.00	1.00	1.00	1.00	-0.40	1.00	-0.50	0.25	-0.38	1.50	-0.34	1.00	1.00	-0.29	1.00	1.00	1.00	0.50	0.50	0.25	0.50	1.00	1.00
Ion-type	$b{++}_6$ y_3-NH_3	y_3	y_4	y_5		b_6		a_7		sty		b_7	y_6		y_7	b_8	y_8	b_9-H_2O	y_9-NH_3	a_{10}	b_{10}-H_2O	b_{10}	b_{12}
Delta Da	0.03 -0.00	0.06	0.02	0.08		0.09		-0.02		0.32		0.22	0.11		0.09	0.13	0.12	0.09	-0.13	0.17	-0.01	0.11	0.52

Peak 350



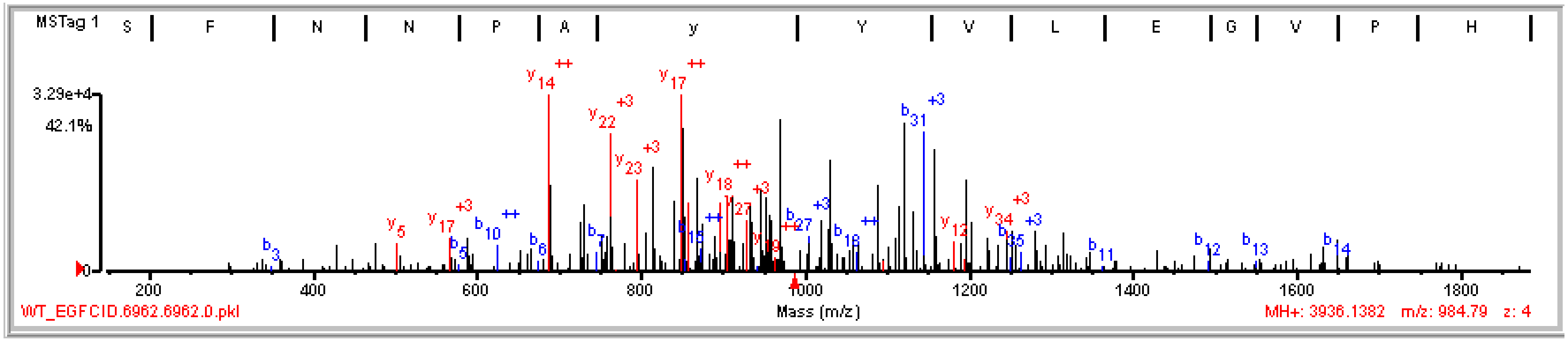


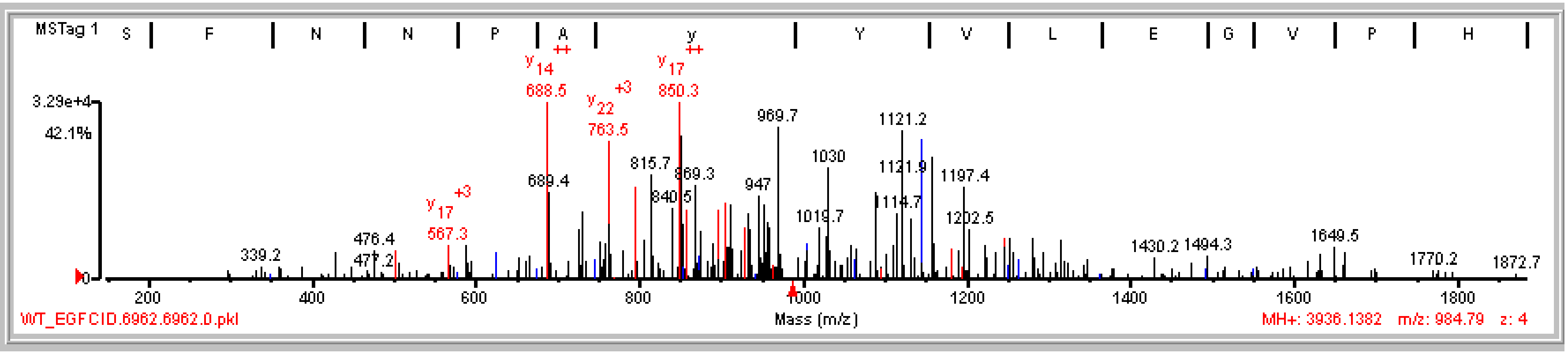
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.12	80.3	9	7/25	Y259y	(R) A P S A/S/V/D|S|S|L/y/N L|P\R (S)	1576.80	81.2362	765.9	80005.5/5.95	Homo sapiens	46370071	10706	GRB2-associated binding protein 1 isoform a
1	15.12	80.3	9	7/25	Y259y	(R) A P S A/S/V/D|S|S|L/y/N L|P\R (S)	1576.80	81.2362	765.9	76616.7/5.63	Homo sapiens	46370073	25875	GRB2-associated binding protein 1 isoform b

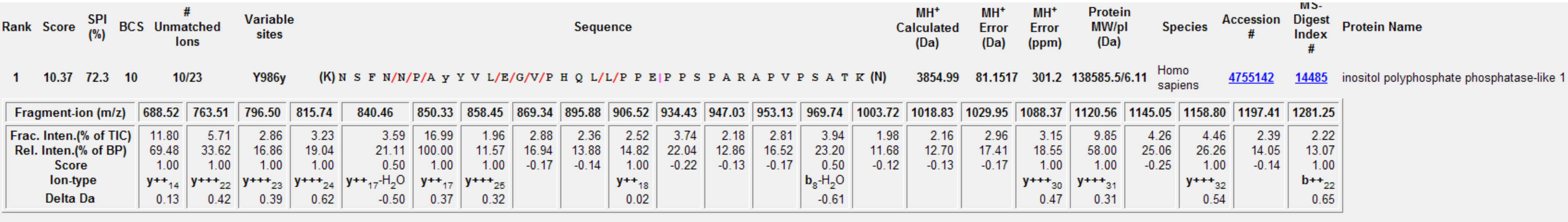
Fragment-ion (m/z)	272.19	378.13	495.31	499.41	628.39	715.13	742.36	780.13	784.31	794.60	796.99	802.09
Frac. Inten.(% of TIC)	1.64	1.88	1.85	2.92	5.25	2.17	10.78	0.05	2.37	6.26	2.65	3.16
Rel. Inten.(% of BP)	11.53	13.22	12.98	20.52	36.90	15.23	75.67	0.33	16.62	43.97	18.61	22.16
Score	1.00	-0.13	0.50	1.00	1.00	1.00	1.00	1.50	0.50	-0.44	-0.19	1.00
Ion-type	y_2		b_6-H_2O	y_4	b_7	b_8	$b{++}_{14}$ y_5	sty	b_9-H_2O			b_9
Delta Da	0.02		0.05	0.11	0.10	-0.20	0.53 0.03	0.23	-0.04			-0.27

Fragment-ion (m/z)	805.78	815.43	855.58	933.96	942.58	1011.66	1029.57	1126.68	1144.58	1243.52	1330.63	1350.93	1385.72
Frac. Inten.(% of TIC)	1.77	2.89	2.87	2.55	5.73	2.58	14.24	2.24	11.32	3.31	5.12	1.67	2.74
Rel. Inten.(% of BP)	12.45	20.33	20.16	17.89	40.21	18.14	100.00	15.71	79.51	23.24	35.95	11.71	19.21
Score	-0.12	-0.20	1.00	-0.18	1.00	0.50	1.00	0.50	1.00	1.00	1.00	-0.12	1.00
Ion-type			y_6		y_7	y_8-NH_3	y_8	y_9-NH_3	y_9	y_{10}	y_{11}		b_{13}
Delta Da			0.17		0.14	-0.79	0.09	-0.80	0.08	-0.05	0.03		0.12

Peak 351



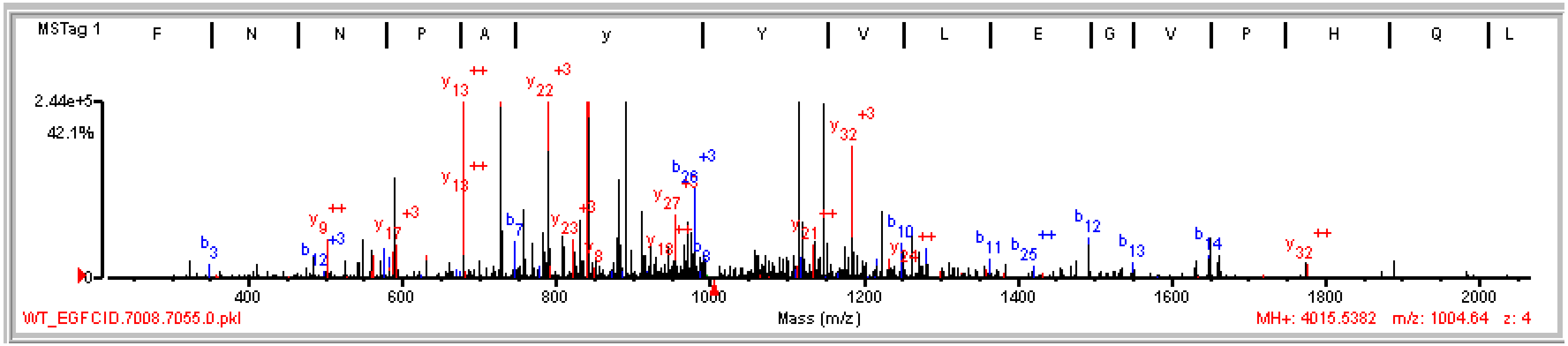


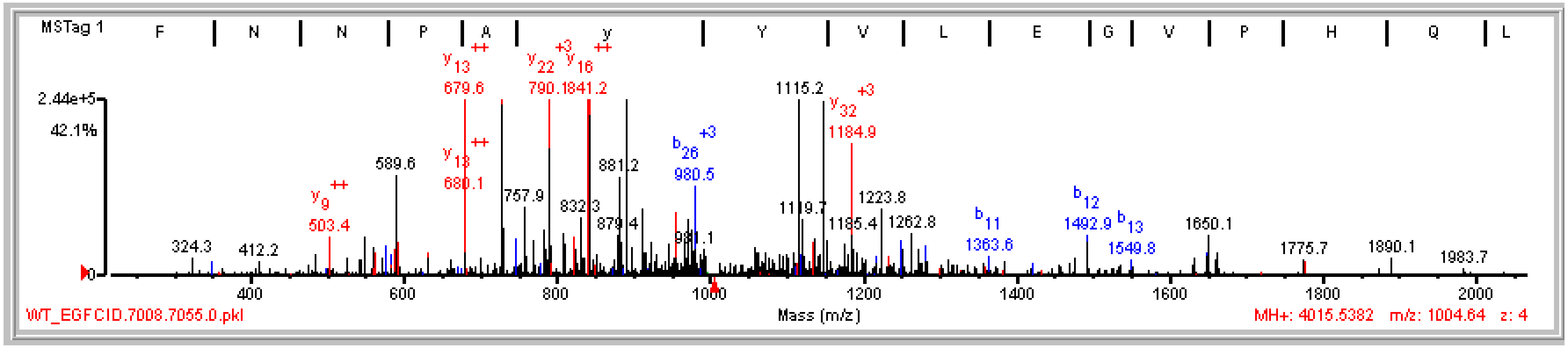


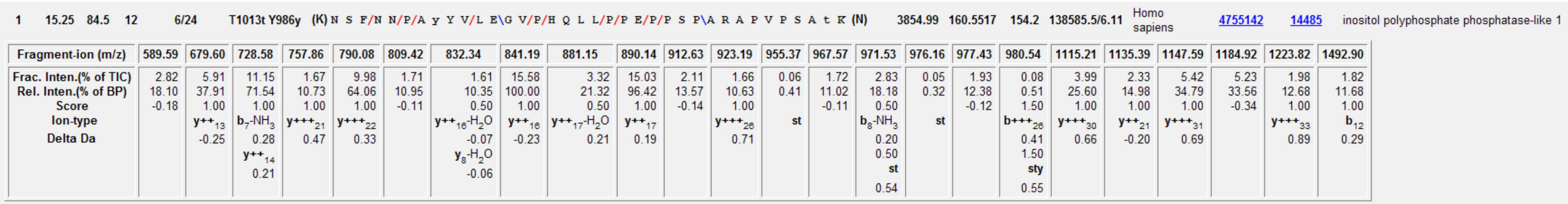
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.37	72.3	10	10/23	Y986y	(K) N S F N/N/P/A y Y V L/E/G/V/P H Q L/L/P P E|P P S P A R A P V P S A T K (N)	3854.99	81.1517	301.2	138585.5/6.11	Homo sapiens	4755142	14485	inositol polyphosphate phosphatase-like 1

Fragment-ion (m/z)	688.52	763.51	796.50	815.74	840.46	850.33	858.45	869.34	895.88	906.52	934.43	947.03	953.13	969.74	1003.72	1018.83	1029.95	1088.37	1120.56	1145.05	1158.80	1197.41	1281.25
Frac. Inten.(% of TIC)	11.80	5.71	2.86	3.23	3.59	16.99	1.96	2.88	2.36	2.52	3.74	2.18	2.81	3.94	1.98	2.16	2.96	3.15	9.85	4.26	4.46	2.39	2.22
Rel. Inten.(% of BP)	69.48	33.62	16.86	19.04	21.11	100.00	11.57	16.94	13.88	14.82	22.04	12.86	16.52	23.20	11.68	12.70	17.41	18.55	58.00	25.06	26.26	14.05	13.07
Score	1.00	1.00	1.00	1.00	0.50	1.00	1.00	-0.17	-0.14	1.00	-0.22	-0.13	-0.17	0.50	-0.12	-0.13	-0.17	1.00	1.00	-0.25	1.00	-0.14	1.00
Ion-type	y++_{14}	y+++_{22}	y+++_{23}	y+++_{24}	$\text{y++}_{17}\text{-H}_2\text{O}$	y++_{17}	y+++_{25}			y++_{18}				$\text{b}_8\text{-H}_2\text{O}$				y+++_{30}	y+++_{31}		y+++_{32}		b++_{22}
Delta Da	0.13	0.42	0.39	0.62	-0.50	0.37	0.32			0.02				-0.61				0.47	0.31		0.54		0.65

Peak 352







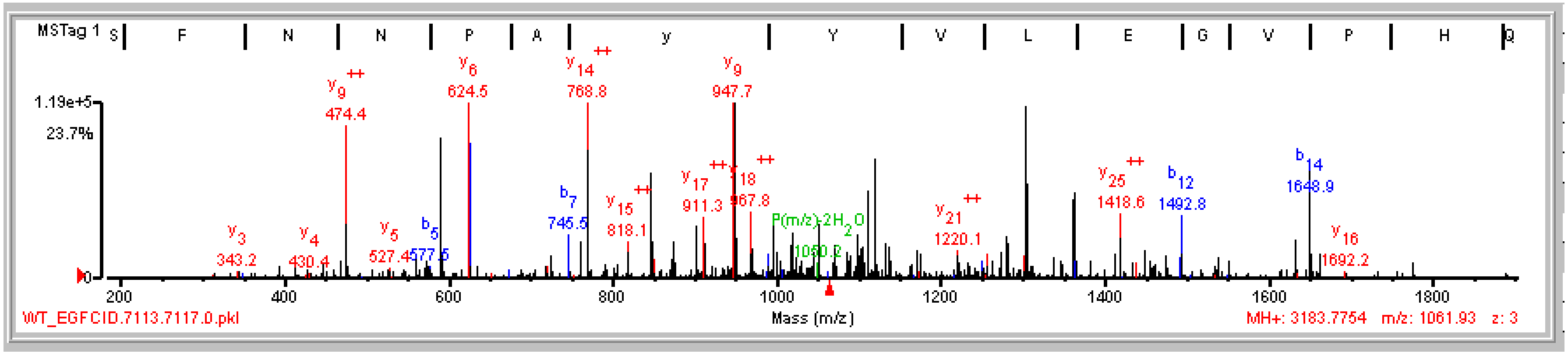
1 15.25 84.5 12 6/24 T1013t Y986y (K) N S F/N N/P/A y Y V/L E\G V/P/H Q L L/P/P E/P/P S P\A R A P V P S A t K (N) 3854.99 160.5517 154.2 138585.5/6.11 Homo sapiens 4755142 14485 inositol polyphosphate phosphatase-like 1

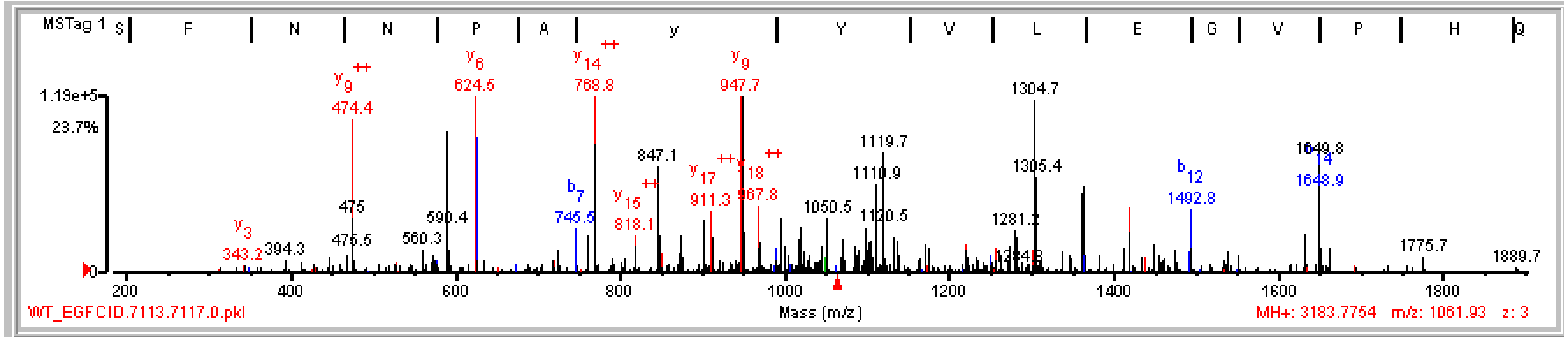
Fragment-ion (m/z)	589.59	679.60	728.58	757.86	790.08	809.42	832.34	841.19	881.15	890.14	912.63	923.19
Frac. Inten.(% of TIC)	2.82	5.91	11.15	1.67	9.98	1.71	1.61	15.58	3.32	15.03	2.11	1.66
Rel. Inten.(% of BP)	18.10	37.91	71.54	10.73	64.06	10.95	10.35	100.00	21.32	96.42	13.57	10.63
Score	-0.18	1.00	1.00	1.00	1.00	-0.11	0.50	1.00	0.50	1.00	-0.14	1.00
Ion-type		$y{+}{+}_{13}$	b_7-NH_3	$y{+}{+}{+}_{21}$	$y{+}{+}{+}_{22}$		$y{+}{+}_{16}$-H_2O	$y{+}{+}_{16}$	$y{+}{+}_{17}$-H_2O	$y{+}{+}_{17}$		$y{+}{+}{+}_{26}$
Delta Da		-0.25	0.28	0.47	0.33		-0.07	-0.23	0.21	0.19		0.71
			$y{+}{+}_{14}$				y_8-H_2O					
			0.21				-0.06					

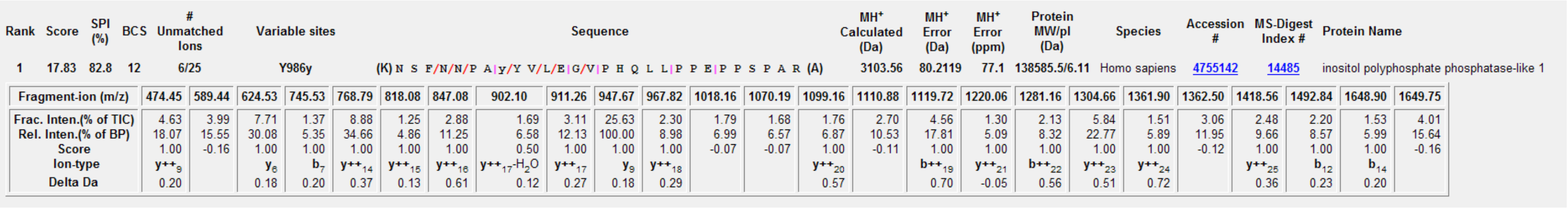
Fragment-ion (m/z)	955.37	967.57	971.53	976.16	977.43	980.54	1115.21	1135.39	1147.59	1184.92	1223.82	1492.90
Frac. Inten.(% of TIC)	0.06	1.72	2.83	0.05	1.93	0.08	3.99	2.33	5.42	5.23	1.98	1.82
Rel. Inten.(% of BP)	0.41	11.02	18.18	0.32	12.38	0.51	25.60	14.98	34.79	33.56	12.68	11.68
Score		-0.11	0.50		-0.12	1.50	1.00	1.00	1.00	-0.34	1.00	1.00
Ion-type	st		b_8-NH_3	st		$b{+}{+}{+}_{26}$	$y{+}{+}{+}_{30}$	$y{+}{+}_{21}$	$y{+}{+}{+}_{31}$		$y{+}{+}{+}_{33}$	b_{12}
Delta Da			0.20			0.41	0.66	-0.20	0.69		0.89	0.29
			0.50			1.50						
			st			sty						
			0.54			0.55						

Peak 353

Ions that verify assignment





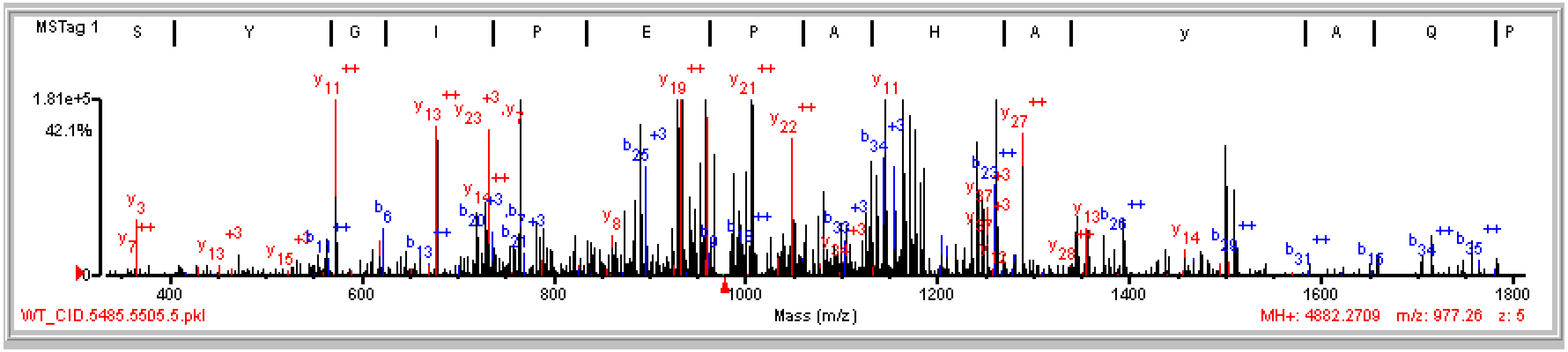


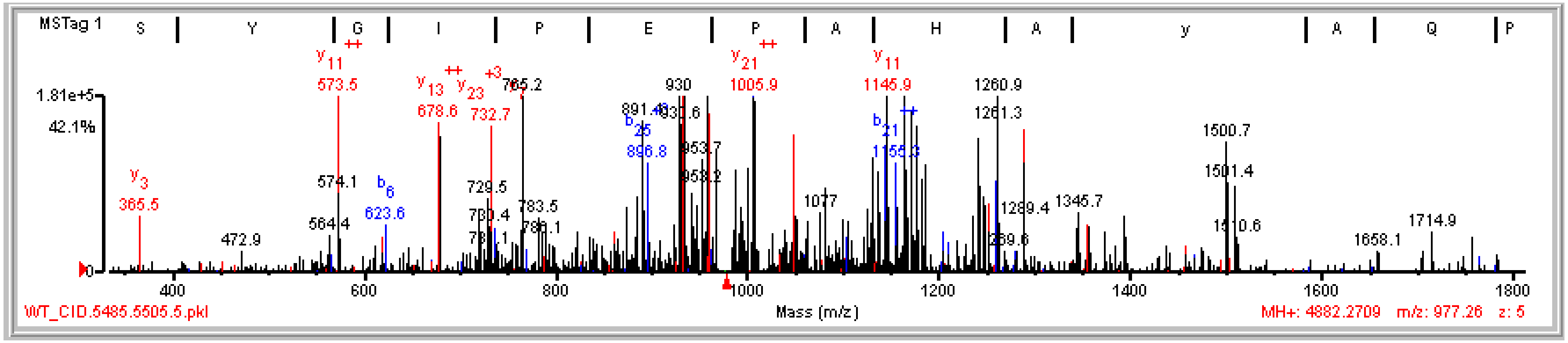
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.83	82.8	12	6/25	Y986y	(K) N S F/N/N/P A|y/Y V/L/E|G/V|P H Q L L|P P E|P P S P A R (A)	3103.56	80.2119	77.1	138585.5/6.11	Homo sapiens	4755142	14485	inositol polyphosphate phosphatase-like 1

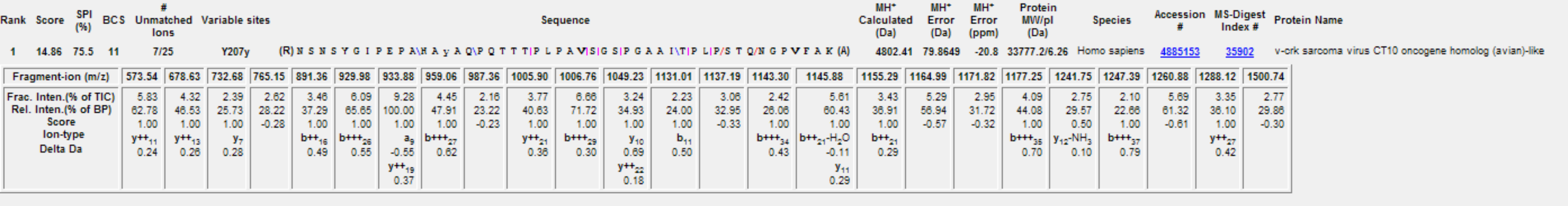
Fragment-ion (m/z)	474.45	589.44	624.53	745.53	768.79	818.08	847.08	902.10	911.26	947.67	967.82	1018.16	1070.19
Frac. Inten.(% of TIC)	4.63	3.99	7.71	1.37	8.88	1.25	2.88	1.69	3.11	25.63	2.30	1.79	1.68
Rel. Inten.(% of BP)	18.07	15.55	30.08	5.35	34.66	4.86	11.25	6.58	12.13	100.00	8.98	6.99	6.57
Score	1.00	-0.16	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	-0.07	-0.07
Ion-type	$y{++}_9$		y_6	b_7	$y{++}_{14}$	$y{++}_{15}$	$y{++}_{16}$	$y{++}_{17}$-H_2O	$y{++}_{17}$	y_9	$y{++}_{18}$		
Delta Da	0.20		0.18	0.20	0.37	0.13	0.61	0.12	0.27	0.18	0.29		

Fragment-ion (m/z)	1099.16	1110.88	1119.72	1220.06	1281.16	1304.66	1361.90	1362.50	1418.56	1492.84	1648.90	1649.75
Frac. Inten.(% of TIC)	1.76	2.70	4.56	1.30	2.13	5.84	1.51	3.06	2.48	2.20	1.53	4.01
Rel. Inten.(% of BP)	6.87	10.53	17.81	5.09	8.32	22.77	5.89	11.95	9.66	8.57	5.99	15.64
Score	1.00	-0.11	1.00	1.00	1.00	1.00	1.00	-0.12	1.00	1.00	1.00	-0.16
Ion-type	$y{++}_{20}$		$b{++}_{19}$	$y{++}_{21}$	$b{++}_{22}$	$y{++}_{23}$	$y{++}_{24}$		$y{++}_{25}$	b_{12}	b_{14}	
Delta Da	0.57		0.70	-0.05	0.56	0.51	0.72		0.36	0.23	0.20	

Peak 354





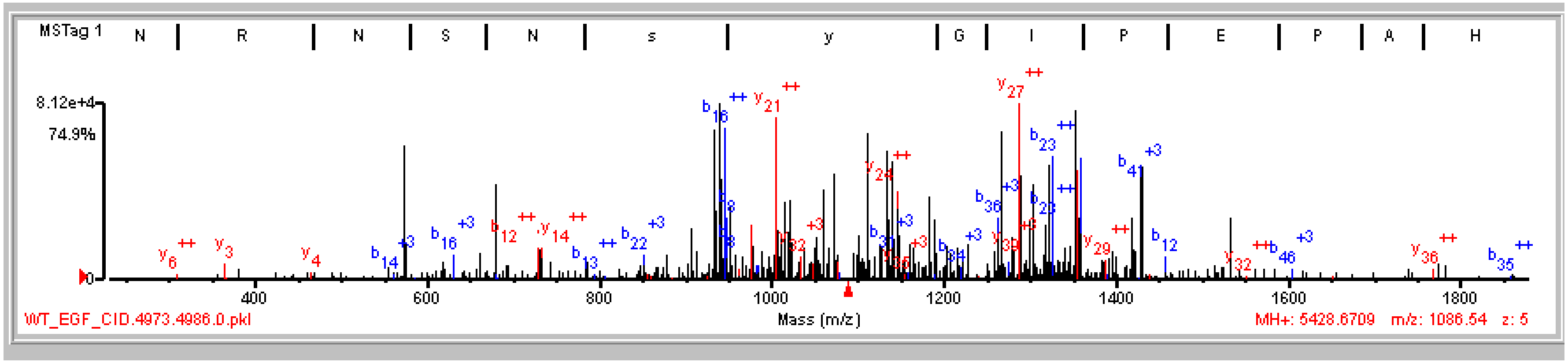


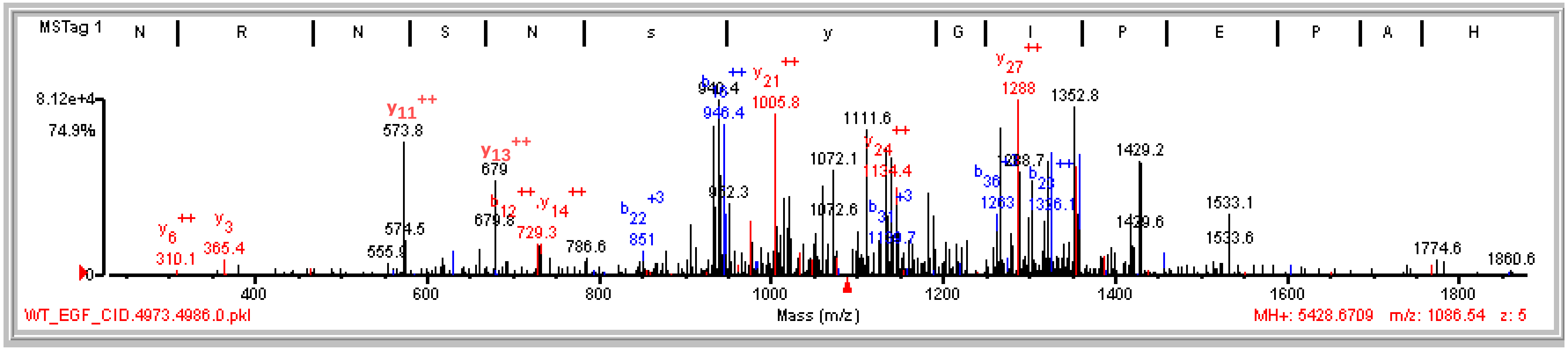
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.86	75.5	11	7/25	Y207y	(R) N S N S Y G I P E P A\H A y A Q\P Q T T T|P L P A V|S|G S|P G A A I\T|P L|P/S T Q/N G P V F A K (A)	4802.41	79.8649	-20.8	33777.2/6.26	Homo sapiens	4885153	35902	v-crk sarcoma virus CT10 oncogene homolog (avian)-like

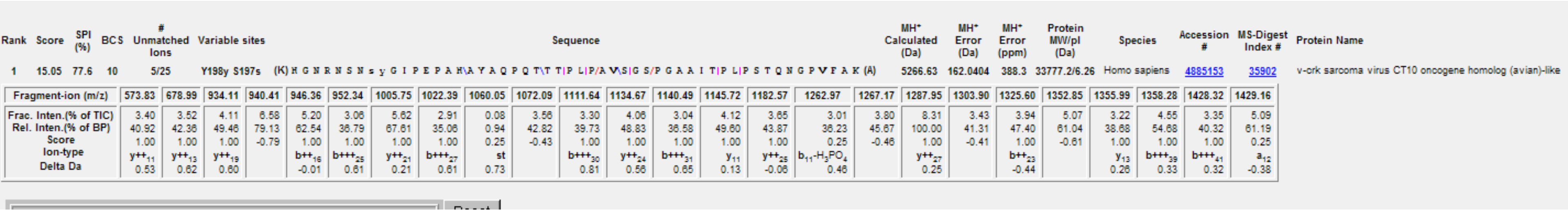
Fragment-ion (m/z)	573.54	678.63	732.68	765.15	891.36	929.98	933.88	959.06	987.36	1005.90	1006.76	1049.23	1131.01
Frac. Inten.(% of TIC)	5.83	4.32	2.39	2.62	3.46	6.09	9.28	4.45	2.16	3.77	6.66	3.24	2.23
Rel. Inten.(% of BP)	62.78	46.53	25.73	28.22	37.29	65.65	100.00	47.91	23.22	40.63	71.72	34.93	24.00
Score	1.00	1.00	1.00	-0.28	1.00	1.00	1.00	1.00	-0.23	1.00	1.00	1.00	1.00
Ion-type	y^{++}_{11}	y^{++}_{13}	y_7		b^{++}_{16}	b^{+++}_{26}	a_9 y^{++}_{19}	b^{+++}_{27}		y^{++}_{21}	b^{+++}_{29}	y_{10} y^{++}_{22}	b_{11}
Delta Da	0.24	0.26	0.28		0.49	0.55	-0.55 0.37	0.62		0.36	0.30	0.69 0.18	0.50

Fragment-ion (m/z)	1137.19	1143.30	1145.88	1155.29	1164.99	1171.82	1177.25	1241.75	1247.39	1260.88	1288.12	1500.74
Frac. Inten.(% of TIC)	3.06	2.42	5.61	3.43	5.29	2.95	4.09	2.75	2.10	5.69	3.35	2.77
Rel. Inten.(% of BP)	32.95	26.06	60.43	36.91	56.94	31.72	44.08	29.57	22.66	61.32	36.10	29.86
Score	-0.33	1.00	1.00	1.00	-0.57	-0.32	1.00	0.50	1.00	-0.61	1.00	-0.30
Ion-type		b^{+++}_{34}	$b^{++}_{21}-H_2O$ y_{11}	b^{++}_{21}			b^{+++}_{35}	$y_{12}-NH_3$	b^{+++}_{37}		y^{++}_{27}	
Delta Da		0.43	-0.11 0.29	0.29			0.70	0.10	0.79		0.42	

Peak 355



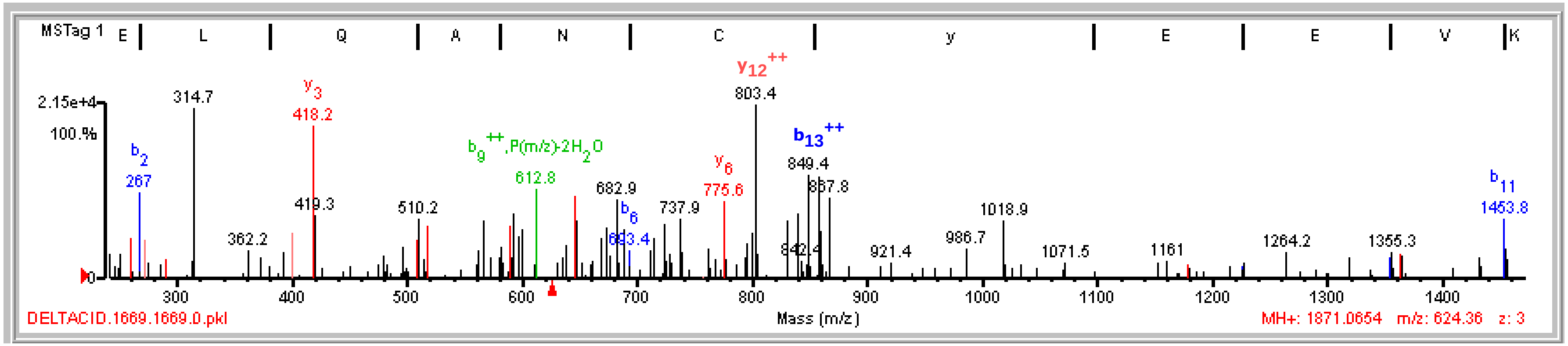


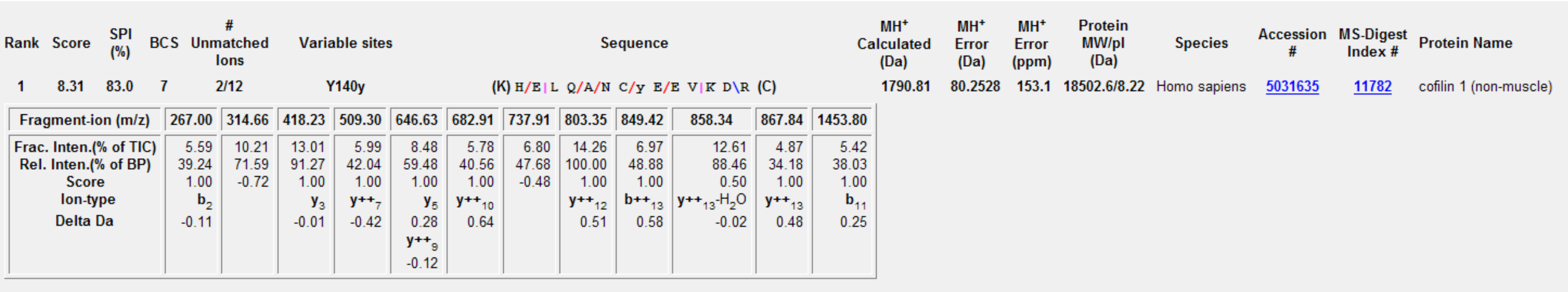


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.05	77.6	10	5/25	Y198y S197s	(K) H G N R N S N s y G I P E P A H\A Y A Q P Q T\T T|P L|P/A V\S|G S/P G A A I T|P L|P S T Q N G P V F A K (A)	5266.63	162.0404	388.3	33777.2/6.26	Homo sapiens	4885153	35902	v-crk sarcoma virus CT10 oncogene homolog (avian)-like

Fragment-ion (m/z)	573.83	678.99	934.11	940.41	946.36	952.34	1005.75	1022.39	1060.05	1072.09	1111.64	1134.67	1140.49	1145.72	1182.57	1262.97	1267.17	1287.95	1303.90	1325.60	1352.85	1355.99	1358.28	1428.32	1429.16
Frac. Inten.(% of TIC)	3.40	3.52	4.11	6.58	5.20	3.06	5.62	2.91	0.08	3.56	3.30	4.06	3.04	4.12	3.65	3.01	3.80	8.31	3.43	3.94	5.07	3.22	4.55	3.35	5.09
Rel. Inten.(% of BP)	40.92	42.36	49.46	79.13	62.54	36.79	67.61	35.06	0.94	42.82	39.73	48.83	36.58	49.60	43.87	36.23	45.67	100.00	41.31	47.40	61.04	38.68	54.68	40.32	61.19
Score	1.00	1.00	1.00	-0.79	1.00	1.00	1.00	1.00	0.25	-0.43	1.00	1.00	1.00	1.00	1.00	0.25	-0.46	1.00	-0.41	1.00	-0.61	1.00	1.00	1.00	0.25
Ion-type	y^{++}_{11}	y^{++}_{13}	y^{++}_{19}		b^{++}_{16}	b^{+++}_{25}	y^{++}_{21}	b^{+++}_{27}	st		b^{+++}_{30}	y^{++}_{24}	b^{+++}_{31}	y_{11}	y^{++}_{25}	b_{11}-H_3PO_4		y^{++}_{27}		b^{++}_{23}		y_{13}	b^{+++}_{39}	b^{+++}_{41}	a_{12}
Delta Da	0.53	0.62	0.60		-0.01	0.61	0.21	0.61	0.73		0.81	0.56	0.65	0.13	-0.06	0.46		0.25		-0.44		0.26	0.33	0.32	-0.38

Peak 356



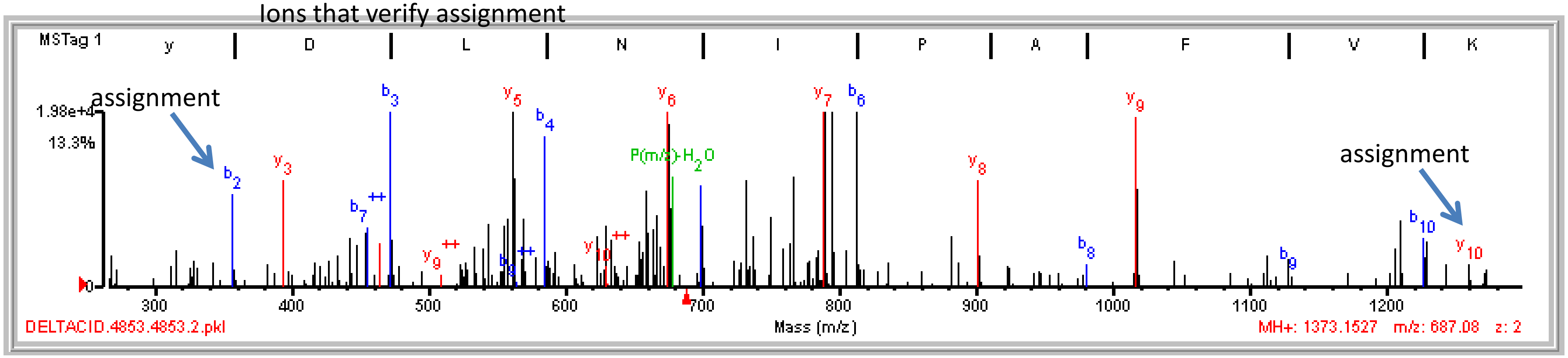


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.31	83.0	7	2/12	Y140y	(K) H/E|L Q/A/N C/y E/E V|K D\R (C)	1790.81	80.2528	153.1	18502.6/8.22	Homo sapiens	5031635	11782	cofilin 1 (non-muscle)

Fragment-ion (m/z)	267.00	314.66	418.23	509.30	646.63	682.91	737.91	803.35	849.42	858.34	867.84	1453.80
Frac. Inten.(% of TIC)	5.59	10.21	13.01	5.99	8.48	5.78	6.80	14.26	6.97	12.61	4.87	5.42
Rel. Inten.(% of BP)	39.24	71.59	91.27	42.04	59.48	40.56	47.68	100.00	48.88	88.46	34.18	38.03
Score	1.00	-0.72	1.00	1.00	1.00	1.00	-0.48	1.00	1.00	0.50	1.00	1.00
Ion-type	b_2		y_3	$y++_7$	y_5 $y++_9$	$y++_{10}$		$y++_{12}$	$b++_{13}$	$y++_{13}$-H_2O	$y++_{13}$	b_{11}
Delta Da	-0.11		-0.01	-0.42	0.28 -0.12	0.64		0.51	0.58	-0.02	0.48	0.25

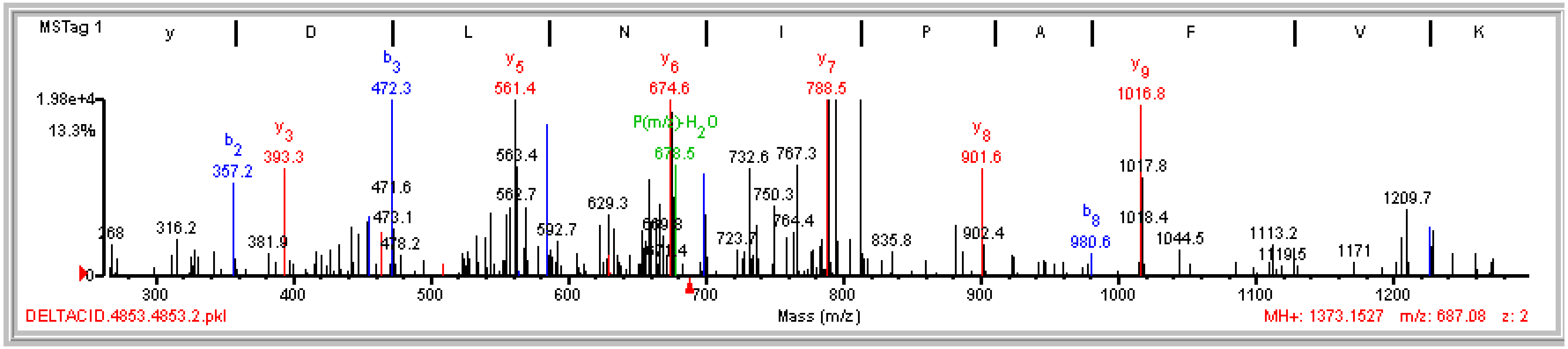
Peak 357

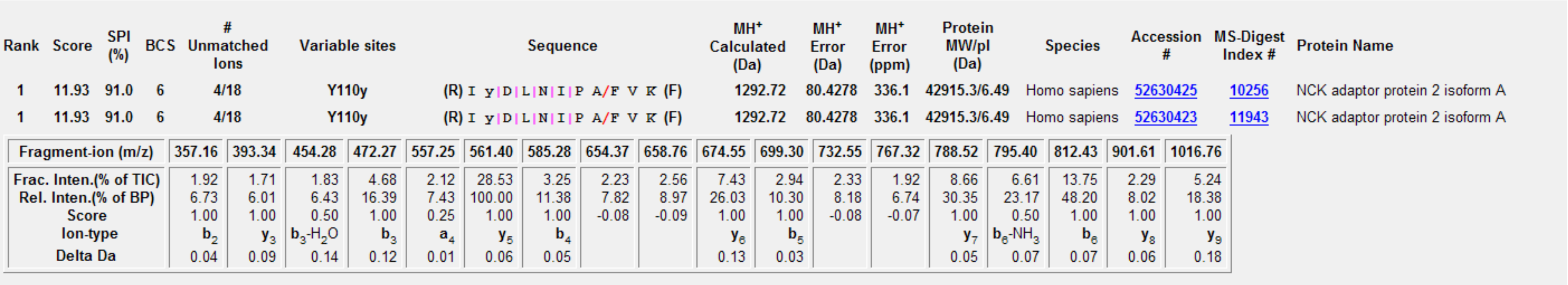
Ions that verify assignment



assignment

assignment

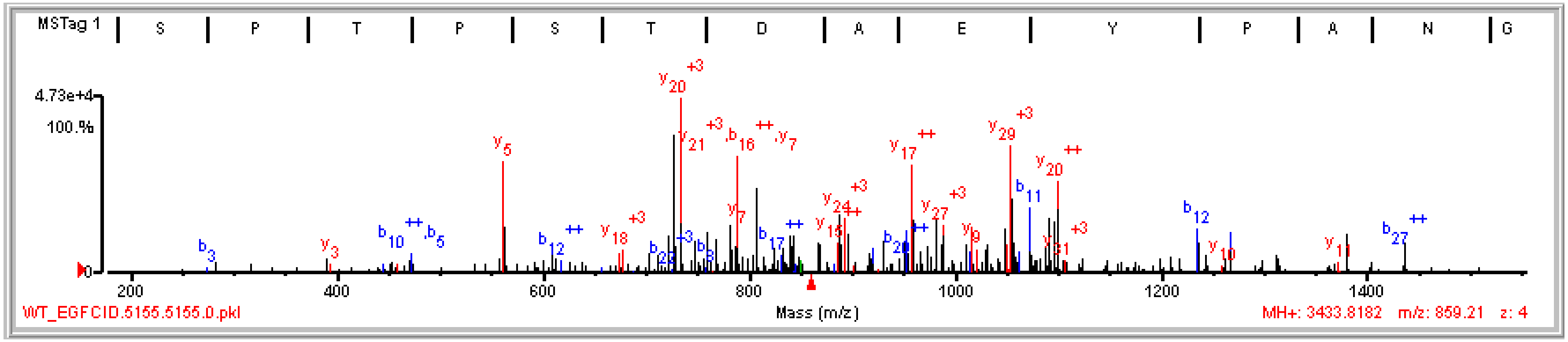


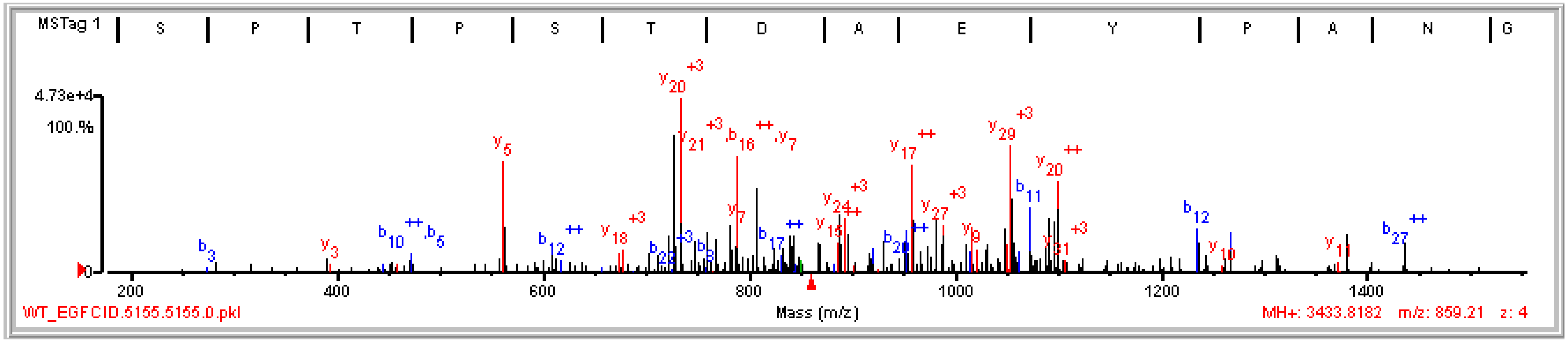


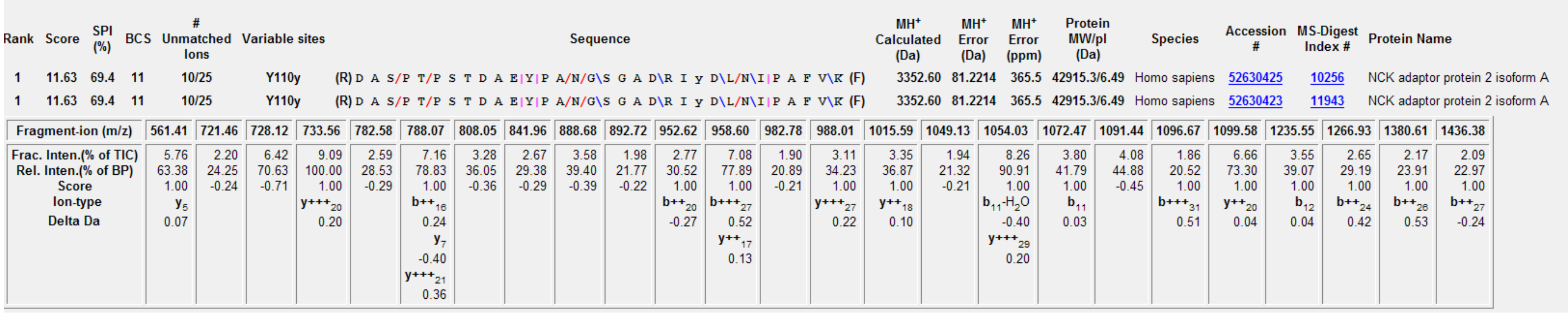
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.93	91.0	6	4/18	Y110y	(R) I y|D|L|N|I|P A/F V K (F)	1292.72	80.4278	336.1	42915.3/6.49	Homo sapiens	52630425	10256	NCK adaptor protein 2 isoform A
1	11.93	91.0	6	4/18	Y110y	(R) I y|D|L|N|I|P A/F V K (F)	1292.72	80.4278	336.1	42915.3/6.49	Homo sapiens	52630423	11943	NCK adaptor protein 2 isoform A

Fragment-ion (m/z)	357.16	393.34	454.28	472.27	557.25	561.40	585.28	654.37	658.76	674.55	699.30	732.55	767.32	788.52	795.40	812.43	901.61	1016.76
Frac. Inten.(% of TIC)	1.92	1.71	1.83	4.68	2.12	28.53	3.25	2.23	2.56	7.43	2.94	2.33	1.92	8.66	6.61	13.75	2.29	5.24
Rel. Inten.(% of BP)	6.73	6.01	6.43	16.39	7.43	100.00	11.38	7.82	8.97	26.03	10.30	8.18	6.74	30.35	23.17	48.20	8.02	18.38
Score	1.00	1.00	0.50	1.00	0.25	1.00	1.00	-0.08	-0.09	1.00	1.00	-0.08	-0.07	1.00	0.50	1.00	1.00	1.00
Ion-type	b_2	y_3	b_3-H_2O	b_3	a_4	y_5	b_4			y_6	b_5			y_7	b_6-NH_3	b_6	y_8	y_9
Delta Da	0.04	0.09	0.14	0.12	0.01	0.06	0.05			0.13	0.03			0.05	0.07	0.07	0.06	0.18

Peak 358







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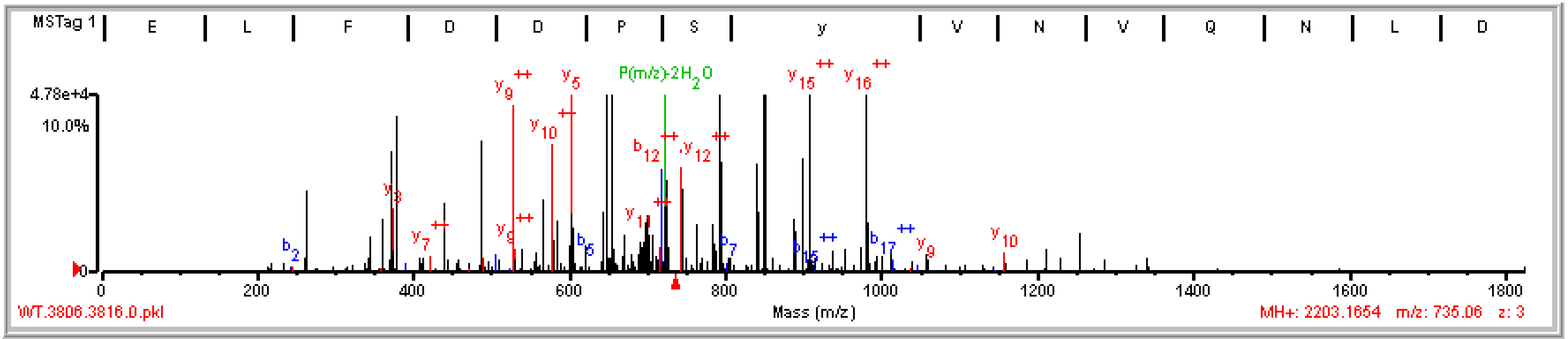
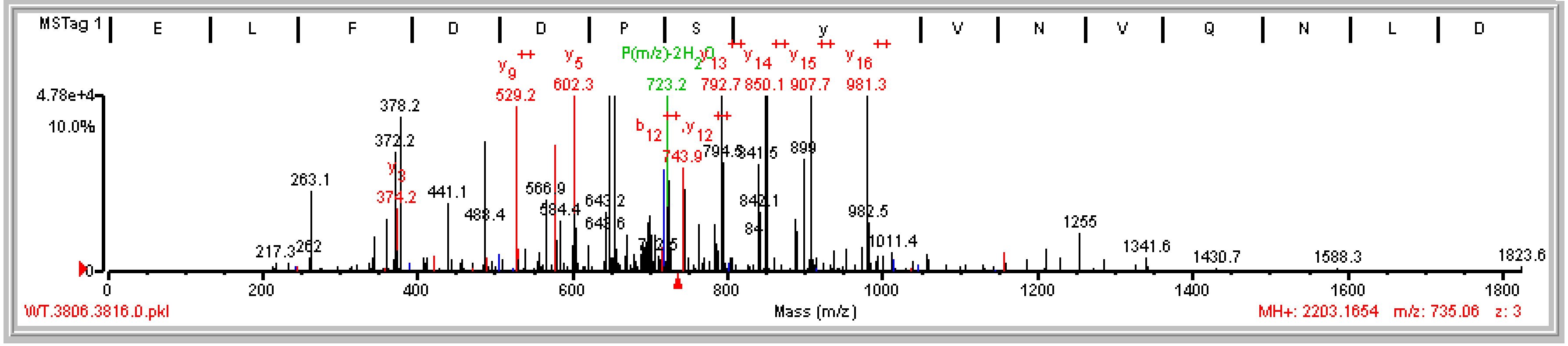
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>11.63</td><td>69.4</td><td>11</td><td>10/25</td><td>Y110y</td><td>(R) D A S/P T/P S T D A E|Y|P A/N/G\S G A D\R I y D\L/N\I|P A F V\K (F)</td><td>3352.60</td><td>81.2214</td><td>365.5</td><td>42915.3/6.49</td><td>Homo sapiens</td><td>52630425</td><td>10256</td><td>NCK adaptor protein 2 isoform A</td></tr>
<tr><td>1</td><td>11.63</td><td>69.4</td><td>11</td><td>10/25</td><td>Y110y</td><td>(R) D A S/P T/P S T D A E|Y|P A/N/G\S G A D\R I y D\L/N\I|P A F V\K (F)</td><td>3352.60</td><td>81.2214</td><td>365.5</td><td>42915.3/6.49</td><td>Homo sapiens</td><td>52630423</td><td>11943</td><td>NCK adaptor protein 2 isoform A</td></tr>
</table>

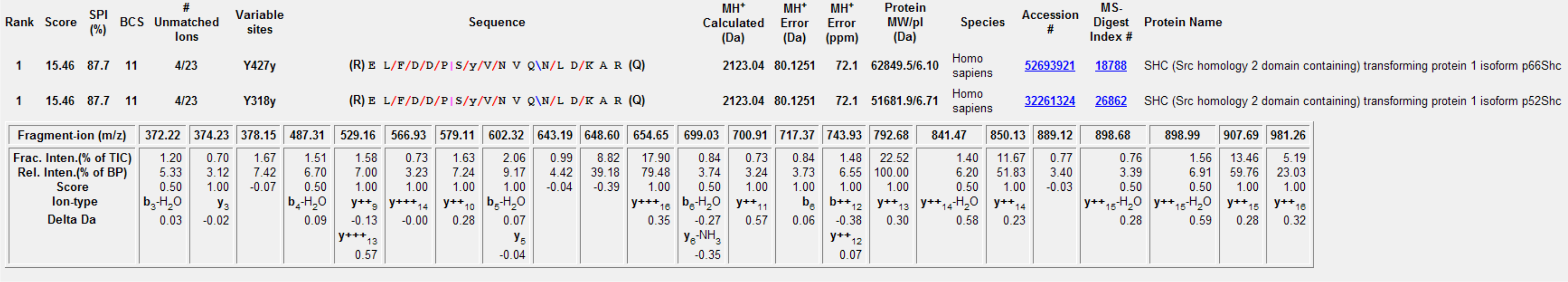
Fragment-ion (m/z)	561.41	721.46	728.12	733.56	782.58	788.07	808.05	841.96	888.68	892.72	952.62	958.60
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	5.76 63.38 1.00 y_5 0.07	2.20 24.25 -0.24	6.42 70.63 -0.71	9.09 100.00 1.00 $y{+}{+}{+}_{20}$ 0.20	2.59 28.53 -0.29	7.16 78.83 1.00 $b{+}{+}_{16}$ 0.24 y_7 -0.40 $y{+}{+}{+}_{21}$ 0.36	3.28 36.05 -0.36	2.67 29.38 -0.29	3.58 39.40 -0.39	1.98 21.77 -0.22	2.77 30.52 1.00 $b{+}{+}_{20}$ -0.27	7.08 77.89 1.00 $b{+}{+}{+}_{27}$ 0.52 $y{+}{+}_{17}$ 0.13

Fragment-ion (m/z)	982.78	988.01	1015.59	1049.13	1054.03	1072.47	1091.44	1096.67	1099.58	1235.55	1266.93	1380.61	1436.38
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	1.90 20.89 -0.21	3.11 34.23 1.00 $y{+}{+}{+}_{27}$ 0.22	3.35 36.87 1.00 $y{+}{+}_{18}$ 0.10	1.94 21.32 -0.21	8.26 90.91 1.00 b_{11}-H_2O -0.40 $y{+}{+}{+}_{29}$ 0.20	3.80 41.79 1.00 b_{11} 0.03	4.08 44.88 -0.45	1.86 20.52 1.00 $b{+}{+}{+}_{31}$ 0.51	6.66 73.30 1.00 $y{+}{+}_{20}$ 0.04	3.55 39.07 1.00 b_{12} 0.04	2.65 29.19 1.00 $b{+}{+}_{24}$ 0.42	2.17 23.91 1.00 $b{+}{+}_{26}$ 0.53	2.09 22.97 1.00 $b{+}{+}_{27}$ -0.24

Peak 359



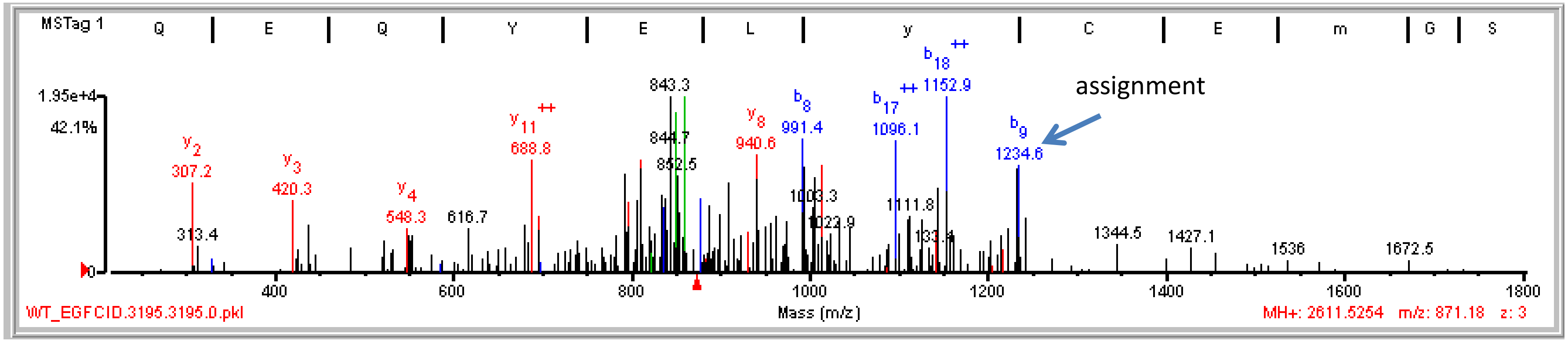




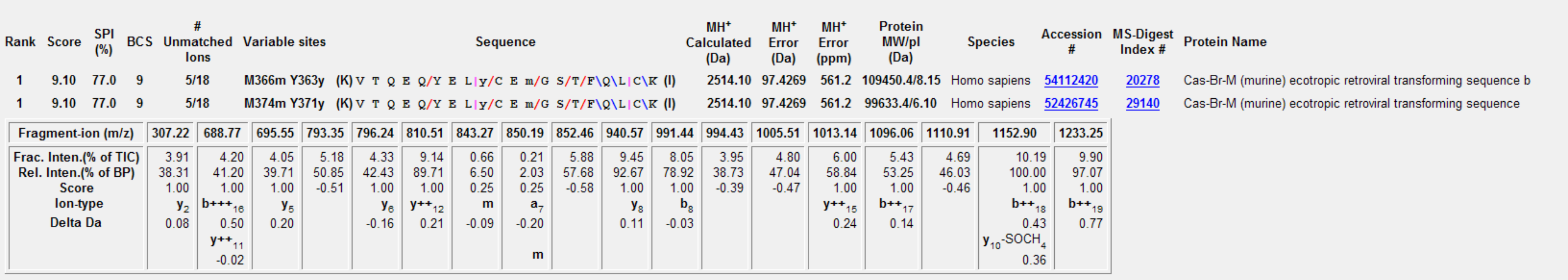
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.46	87.7	11	4/23	Y427y	(R) E L/F/D/D/P|S/y/V/N V Q\N/L D/K A R (Q)	2123.04	80.1251	72.1	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	15.46	87.7	11	4/23	Y318y	(R) E L/F/D/D/P|S/y/V/N V Q\N/L D/K A R (Q)	2123.04	80.1251	72.1	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	372.22	374.23	378.15	487.31	529.16	566.93	579.11	602.32	643.19	648.60	654.65	699.03	700.91	717.37	743.93	792.68	841.47	850.13	889.12	898.68	898.99	907.69	981.26
Frac. Inten.(% of TIC)	1.20	0.70	1.67	1.51	1.58	0.73	1.63	2.06	0.99	8.82	17.90	0.84	0.73	0.84	1.48	22.52	1.40	11.67	0.77	0.76	1.56	13.46	5.19
Rel. Inten.(% of BP)	5.33	3.12	7.42	6.70	7.00	3.23	7.24	9.17	4.42	39.18	79.48	3.74	3.24	3.73	6.55	100.00	6.20	51.83	3.40	3.39	6.91	59.76	23.03
Score	0.50	1.00	-0.07	0.50	1.00	1.00	1.00	1.00	-0.04	-0.39	1.00	0.50	1.00	1.00	1.00	1.00	0.50	1.00	-0.03	0.50	0.50	1.00	1.00
Ion-type	b_3-H_2O	y_3		b_4-H_2O	y++_{9}	y+++_{14}	y++_{10}	b_5-H_2O			y+++_{16}	b_6-H_2O	y++_{11}	b_6	b++_{12}	y++_{13}	y++_{14}-H_2O	y++_{14}		y++_{15}-H_2O	y++_{15}-H_2O	y++_{15}	y++_{16}
Delta Da	0.03	-0.02		0.09	-0.13	-0.00	0.28	0.07			0.35	-0.27	0.57	0.06	-0.38	0.30	0.58	0.23		0.28	0.59	0.28	0.32
					y+++_{13}			y_5				y_6-NH_3			y++_{12}								
					0.57			-0.04				-0.35			0.07								

Peak 361



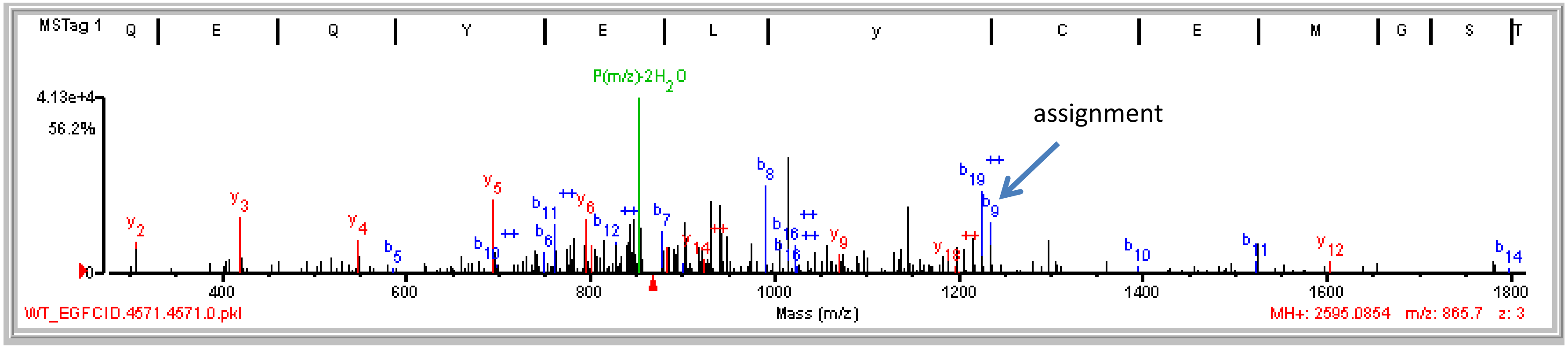
assignment



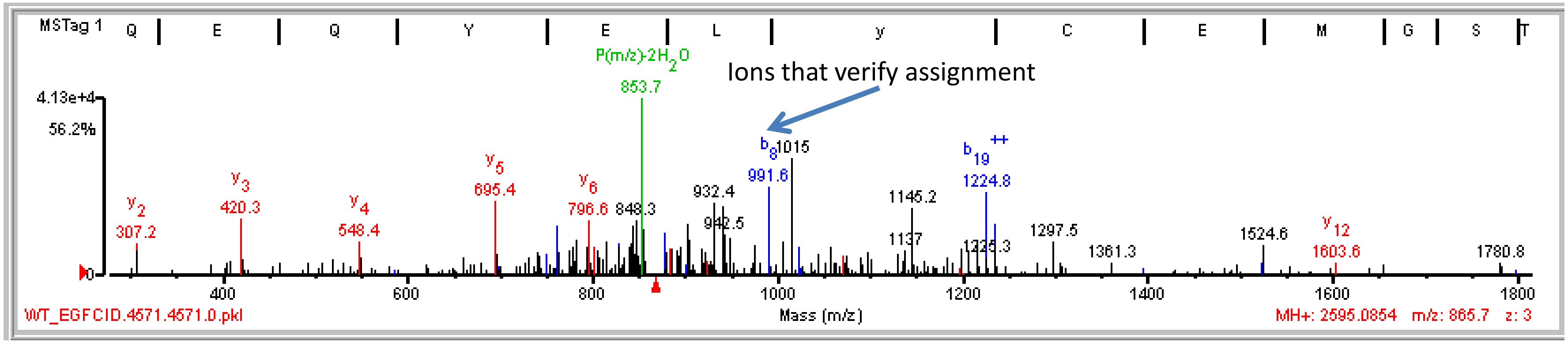
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.10	77.0	9	5/18	M366m Y363y	(K) V T Q E Q/Y E L|y/C E m/G S/T/F\Q\L|C\K (I)	2514.10	97.4269	561.2	109450.4/8.15	Homo sapiens	54112420	20278	Cas-Br-M (murine) ecotropic retroviral transforming sequence b
1	9.10	77.0	9	5/18	M374m Y371y	(K) V T Q E Q/Y E L|y/C E m/G S/T/F\Q\L|C\K (I)	2514.10	97.4269	561.2	99633.4/6.10	Homo sapiens	52426745	29140	Cas-Br-M (murine) ecotropic retroviral transforming sequence

Fragment-ion (m/z)	307.22	688.77	695.55	793.35	796.24	810.51	843.27	850.19	852.46	940.57	991.44	994.43	1005.51	1013.14	1096.06	1110.91	1152.90	1233.25
Frac. Inten.(% of TIC)	3.91	4.20	4.05	5.18	4.33	9.14	0.66	0.21	5.88	9.45	8.05	3.95	4.80	6.00	5.43	4.69	10.19	9.90
Rel. Inten.(% of BP)	38.31	41.20	39.71	50.85	42.43	89.71	6.50	2.03	57.68	92.67	78.92	38.73	47.04	58.84	53.25	46.03	100.00	97.07
Score	1.00	1.00	1.00	-0.51	1.00	1.00	0.25	0.25	-0.58	1.00	1.00	-0.39	-0.47	1.00	1.00	-0.46	1.00	1.00
Ion-type	y_2	$b{+}{+}{+}_{16}$	y_5		y_6	$y{+}{+}_{12}$	m	a_7		y_8	b_8			$y{+}{+}_{15}$	$b{+}{+}_{17}$		$b{+}{+}_{18}$	$b{+}{+}_{19}$
Delta Da	0.08	0.50	0.20		-0.16	0.21	-0.09	-0.20		0.11	-0.03			0.24	0.14		0.43	0.77
		$y{+}{+}_{11}$															y_{10}-$SOCH_4$	
		-0.02						m									0.36	

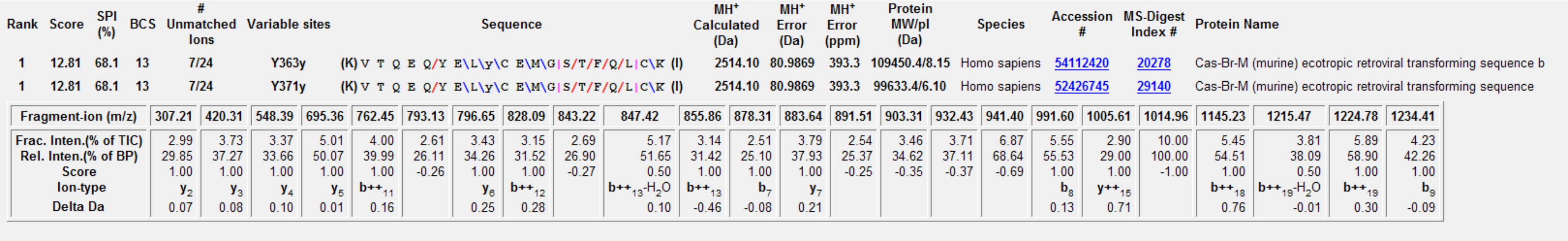
Peak 362



assignment



Ions that verify assignment

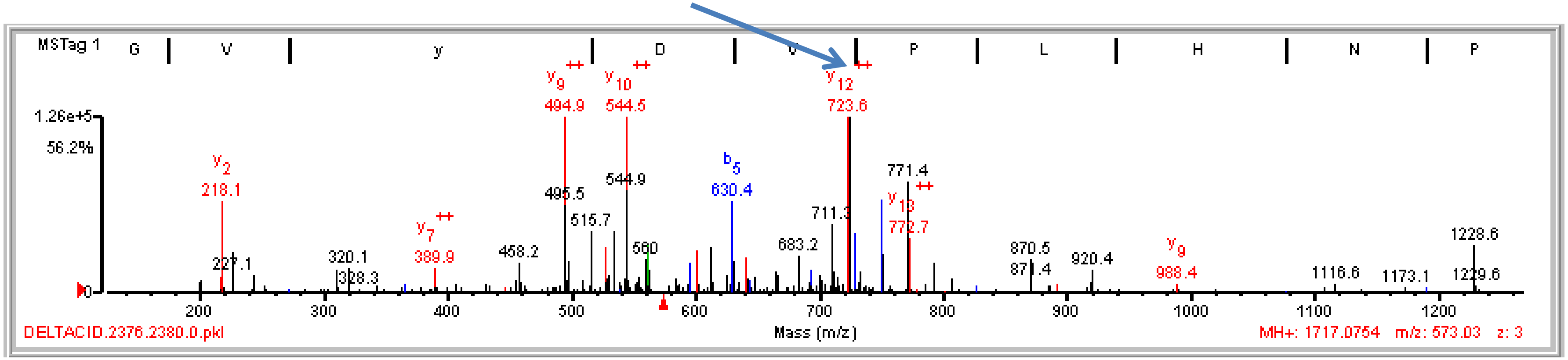


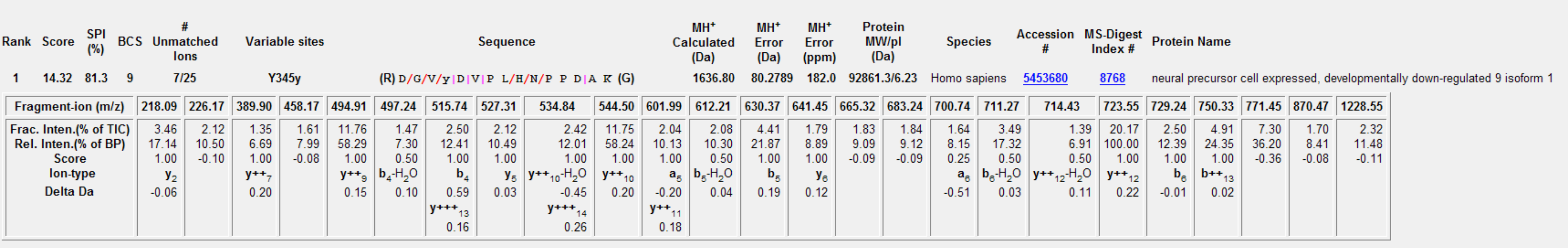
<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH$^+$ Calculated (Da)</th><th>MH$^+$ Error (Da)</th><th>MH$^+$ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>12.81</td><td>68.1</td><td>13</td><td>7/24</td><td>Y363y</td><td>(K) V T Q E Q/Y E\L\y\C E\M\G|S/T/F/Q/L|C\K (I)</td><td>2514.10</td><td>80.9869</td><td>393.3</td><td>109450.4/8.15</td><td>Homo sapiens</td><td>54112420</td><td>20278</td><td>Cas-Br-M (murine) ecotropic retroviral transforming sequence b</td></tr>
<tr><td>1</td><td>12.81</td><td>68.1</td><td>13</td><td>7/24</td><td>Y371y</td><td>(K) V T Q E Q/Y E\L\y\C E\M\G|S/T/F/Q/L|C\K (I)</td><td>2514.10</td><td>80.9869</td><td>393.3</td><td>99633.4/6.10</td><td>Homo sapiens</td><td>52426745</td><td>29140</td><td>Cas-Br-M (murine) ecotropic retroviral transforming sequence</td></tr>
</table>

Fragment-ion (m/z)	307.21	420.31	548.39	695.36	762.45	793.13	796.65	828.09	843.22	847.42
Frac. Inten.(% of TIC)	2.99	3.73	3.37	5.01	4.00	2.61	3.43	3.15	2.69	5.17
Rel. Inten.(% of BP)	29.85	37.27	33.66	50.07	39.99	26.11	34.26	31.52	26.90	51.65
Score	1.00	1.00	1.00	1.00	1.00	-0.26	1.00	1.00	-0.27	0.50
Ion-type	y_2	y_3	y_4	y_5	b++$_{11}$		y_6	b++$_{12}$		b++$_{13}$-H$_2$O
Delta Da	0.07	0.08	0.10	0.01	0.16		0.25	0.28		0.10

Fragment-ion (m/z)	855.86	878.31	883.64	891.51	903.31	932.43	941.40	991.60	1005.61	1014.96	1145.23	1215.47	1224.78	1234.41
Frac. Inten.(% of TIC)	3.14	2.51	3.79	2.54	3.46	3.71	6.87	5.55	2.90	10.00	5.45	3.81	5.89	4.23
Rel. Inten.(% of BP)	31.42	25.10	37.93	25.37	34.62	37.11	68.64	55.53	29.00	100.00	54.51	38.09	58.90	42.26
Score	1.00	1.00	1.00	-0.25	-0.35	-0.37	-0.69	1.00	1.00	-1.00	1.00	0.50	1.00	1.00
Ion-type	b++$_{13}$	b_7	y_7					b_8	y++$_{15}$		b++$_{18}$	b++$_{19}$-H$_2$O	b++$_{19}$	b_9
Delta Da	-0.46	-0.08	0.21					0.13	0.71		0.76	-0.01	0.30	-0.09

Peak 363


assignment

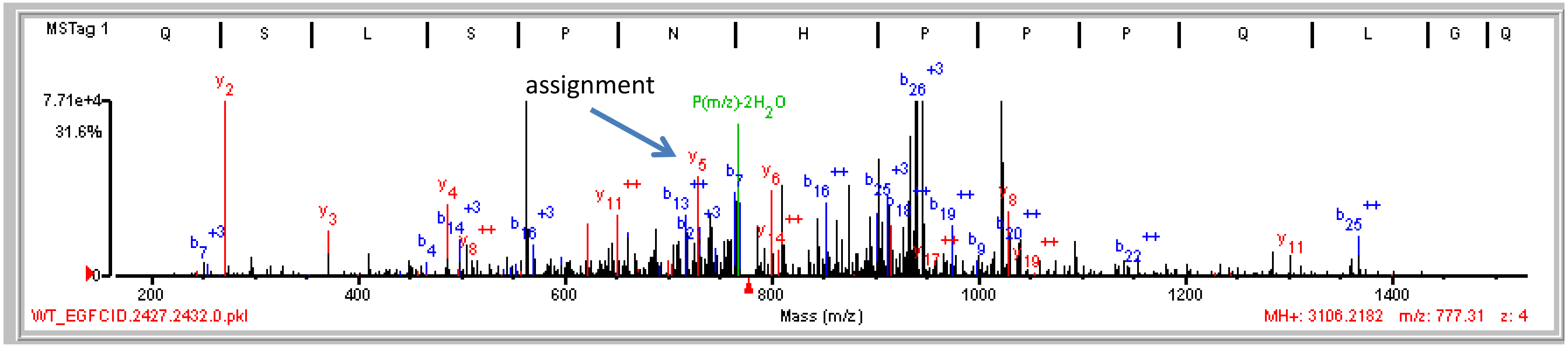


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.32	81.3	9	7/25	Y345y	(R) D/G/V/y|D|V|P L/H/N/P P D|A K (G)	1636.80	80.2789	182.0	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

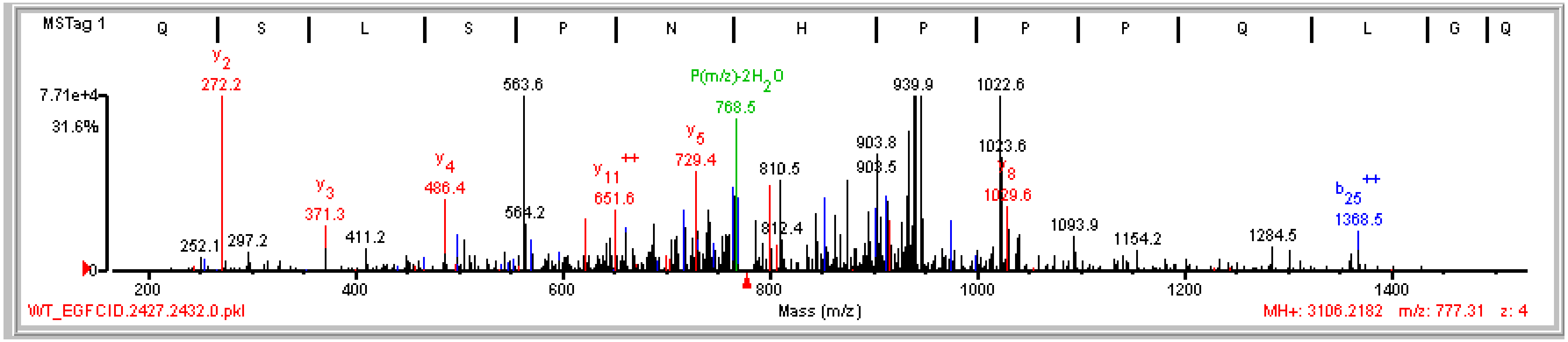
Fragment-ion (m/z)	218.09	226.17	389.90	458.17	494.91	497.24	515.74	527.31	534.84	544.50	601.99	612.21
Frac. Inten.(% of TIC)	3.46	2.12	1.35	1.61	11.76	1.47	2.50	2.12	2.42	11.75	2.04	2.08
Rel. Inten.(% of BP)	17.14	10.50	6.69	7.99	58.29	7.30	12.41	10.49	12.01	58.24	10.13	10.30
Score	1.00	-0.10	1.00	-0.08	1.00	0.50	1.00	1.00	1.00	1.00	1.00	0.50
Ion-type	y_2		$y{++}_7$		$y{++}_9$	$b_4\text{-}H_2O$	b_4	y_5	$y{++}_{10}\text{-}H_2O$	$y{++}_{10}$	a_5	$b_5\text{-}H_2O$
Delta Da	-0.06		0.20		0.15	0.10	0.59	0.03	-0.45	0.20	-0.20	0.04
							$y{+++}_{13}$		$y{+++}_{14}$		$y{++}_{11}$	
							0.16		0.26		0.18	

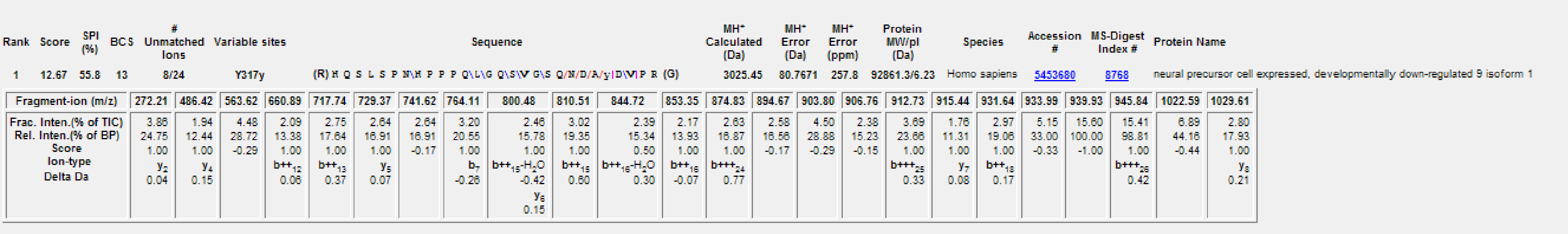
Fragment-ion (m/z)	630.37	641.45	665.32	683.24	700.74	711.27	714.43	723.55	729.24	750.33	771.45	870.47	1228.55
Frac. Inten.(% of TIC)	4.41	1.79	1.83	1.84	1.64	3.49	1.39	20.17	2.50	4.91	7.30	1.70	2.32
Rel. Inten.(% of BP)	21.87	8.89	9.09	9.12	8.15	17.32	6.91	100.00	12.39	24.35	36.20	8.41	11.48
Score	1.00	1.00	-0.09	-0.09	0.25	0.50	0.50	1.00	1.00	1.00	-0.36	-0.08	-0.11
Ion-type	b_5	y_6			a_6	$b_6\text{-}H_2O$	$y{++}_{12}\text{-}H_2O$	$y{++}_{12}$	b_6	$b{++}_{13}$			
Delta Da	0.19	0.12			-0.51	0.03	0.11	0.22	-0.01	0.02			

Peak 364



assignment



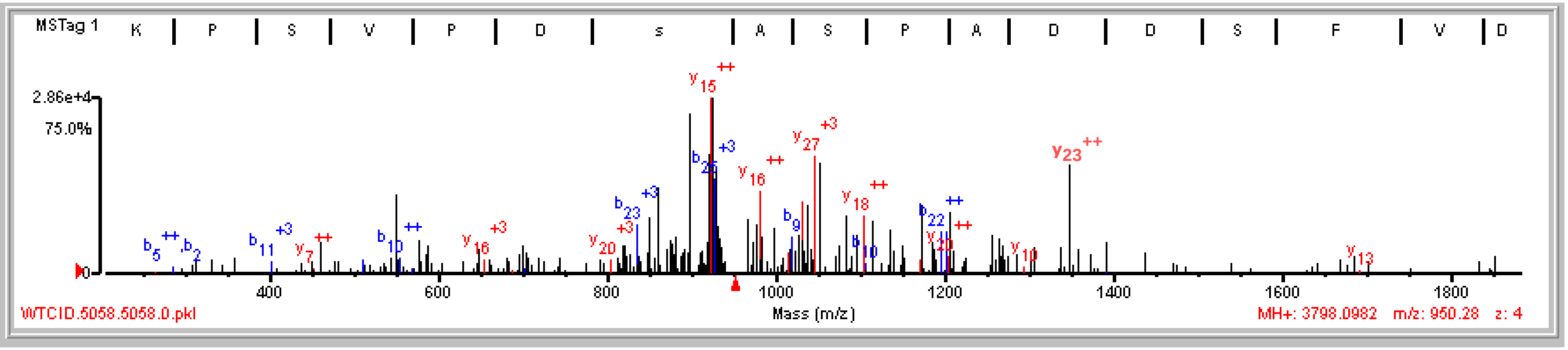


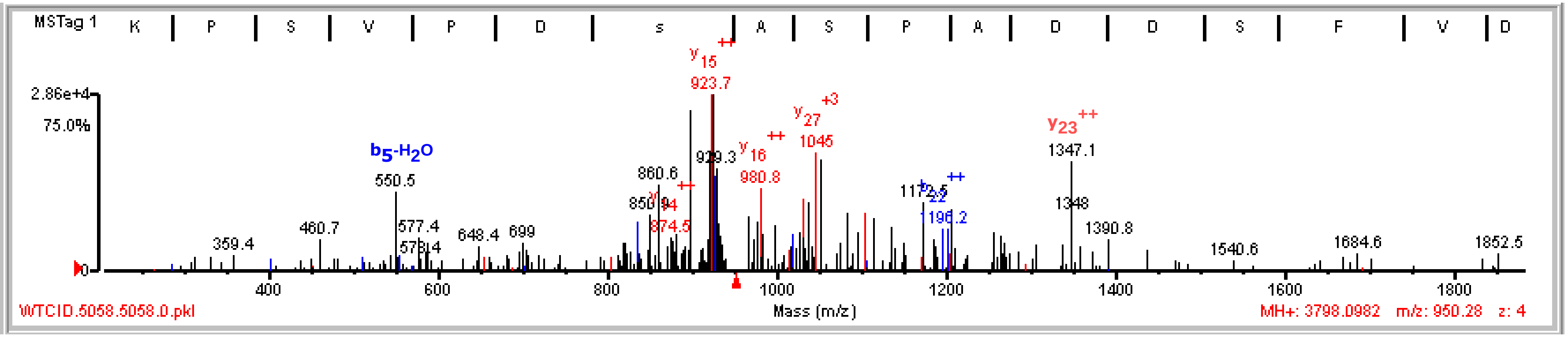
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.67	55.8	13	8/24	Y317y	(R) H Q S L S P N\H P P P Q\L\G Q\S\V G\S Q/N/D/A/y|D\V|P R (G)	3025.45	80.7671	257.8	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

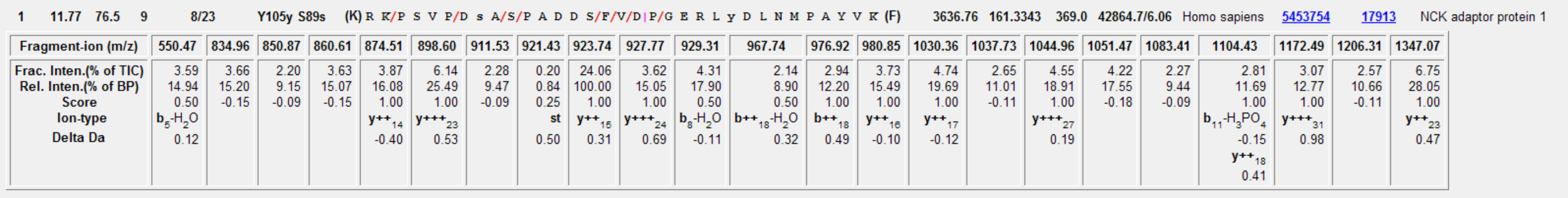
Fragment-ion (m/z)	272.21	486.42	563.62	660.89	717.74	729.37	741.62	764.11	800.48	810.51	844.72
Frac. Inten.(% of TIC)	3.86	1.94	4.48	2.09	2.75	2.64	2.64	3.20	2.46	3.02	2.39
Rel. Inten.(% of BP)	24.75	12.44	28.72	13.38	17.64	16.91	16.91	20.55	15.78	19.35	15.34
Score	1.00	1.00	-0.29	1.00	1.00	1.00	-0.17	1.00	1.00	1.00	0.50
Ion-type	y_2	y_4		b++$_{12}$	b++$_{13}$	y_5		b_7	b++$_{15}$-H_2O y_6	b++$_{15}$	b++$_{16}$-H_2O
Delta Da	0.04	0.15		0.06	0.37	0.07		-0.26	-0.42 0.15	0.60	0.30

Fragment-ion (m/z)	853.35	874.83	894.67	903.80	906.76	912.73	915.44	931.64	933.99	939.93	945.84	1022.59	1029.61
Frac. Inten.(% of TIC)	2.17	2.63	2.58	4.50	2.38	3.69	1.76	2.97	5.15	15.60	15.41	6.89	2.80
Rel. Inten.(% of BP)	13.93	16.87	16.56	28.88	15.23	23.66	11.31	19.06	33.00	100.00	98.81	44.16	17.93
Score	1.00	1.00	-0.17	-0.29	-0.15	1.00	1.00	1.00	-0.33	-1.00	1.00	-0.44	1.00
Ion-type	b++$_{16}$	b+++$_{24}$				b+++$_{25}$	y_7	b++$_{18}$			b+++$_{26}$		y_8
Delta Da	-0.07	0.77				0.33	0.08	0.17			0.42		0.21

Peak 365





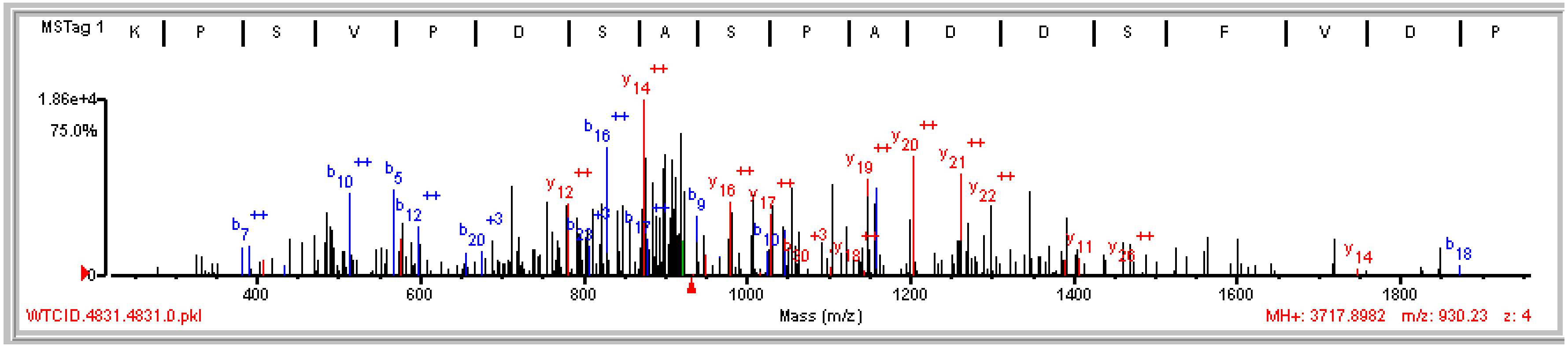


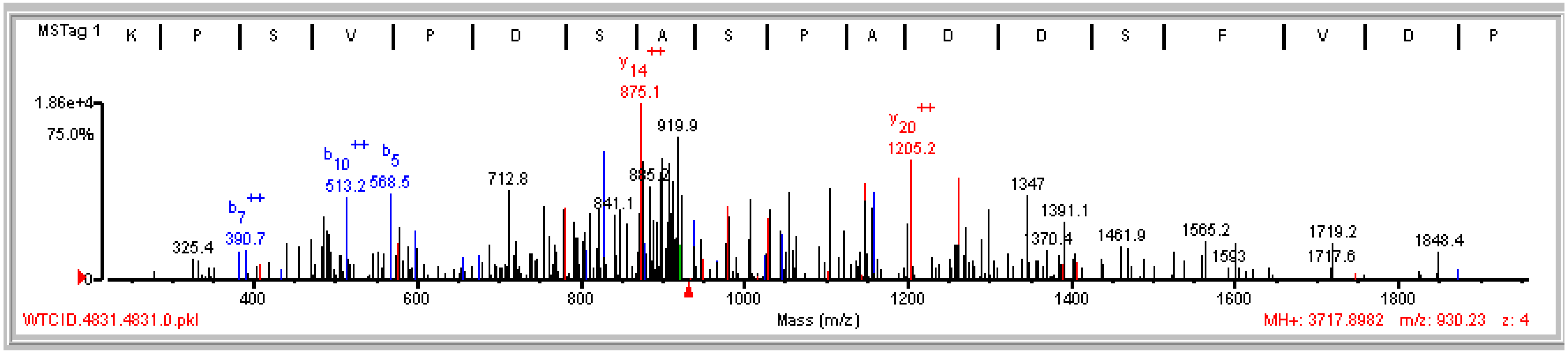
1 11.77 76.5 9 8/23 Y105y S89s (K) R K/P S V P/D s A/S/P A D D S/F/V/D|P/G E R L y D L N M P A Y V K (F) 3636.76 161.3343 369.0 42864.7/6.06 Homo sapiens 5453754 17913 NCK adaptor protein 1

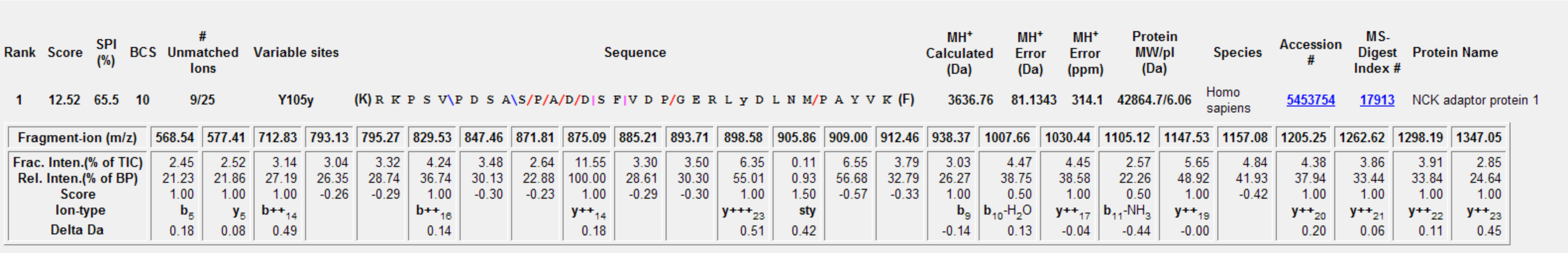
Fragment-ion (m/z)	550.47	834.96	850.87	860.61	874.51	898.60	911.53	921.43	923.74	927.77	929.31
Frac. Inten.(% of TIC)	3.59	3.66	2.20	3.63	3.87	6.14	2.28	0.20	24.06	3.62	4.31
Rel. Inten.(% of BP)	14.94	15.20	9.15	15.07	16.08	25.49	9.47	0.84	100.00	15.05	17.90
Score	0.50	-0.15	-0.09	-0.15	1.00	1.00	-0.09	0.25	1.00	1.00	0.50
Ion-type	b_5-H_2O				y^{++}_{14}	y^{+++}_{23}		st	y^{++}_{15}	y^{+++}_{24}	b_8-H_2O
Delta Da	0.12				-0.40	0.53		0.50	0.31	0.69	-0.11

Fragment-ion (m/z)	967.74	976.92	980.85	1030.36	1037.73	1044.96	1051.47	1083.41	1104.43	1172.49	1206.31	1347.07
Frac. Inten.(% of TIC)	2.14	2.94	3.73	4.74	2.65	4.55	4.22	2.27	2.81	3.07	2.57	6.75
Rel. Inten.(% of BP)	8.90	12.20	15.49	19.69	11.01	18.91	17.55	9.44	11.69	12.77	10.66	28.05
Score	0.50	1.00	1.00	1.00	-0.11	1.00	-0.18	-0.09	1.00	1.00	-0.11	1.00
Ion-type	$b^{++}_{18}-H_2O$	b^{++}_{18}	y^{++}_{16}	y^{++}_{17}		y^{+++}_{27}			$b_{11}-H_3PO_4$ -0.15 y^{++}_{18}	y^{+++}_{31}		y^{++}_{23}
Delta Da	0.32	0.49	-0.10	-0.12		0.19			0.41	0.98		0.47

Peak 366





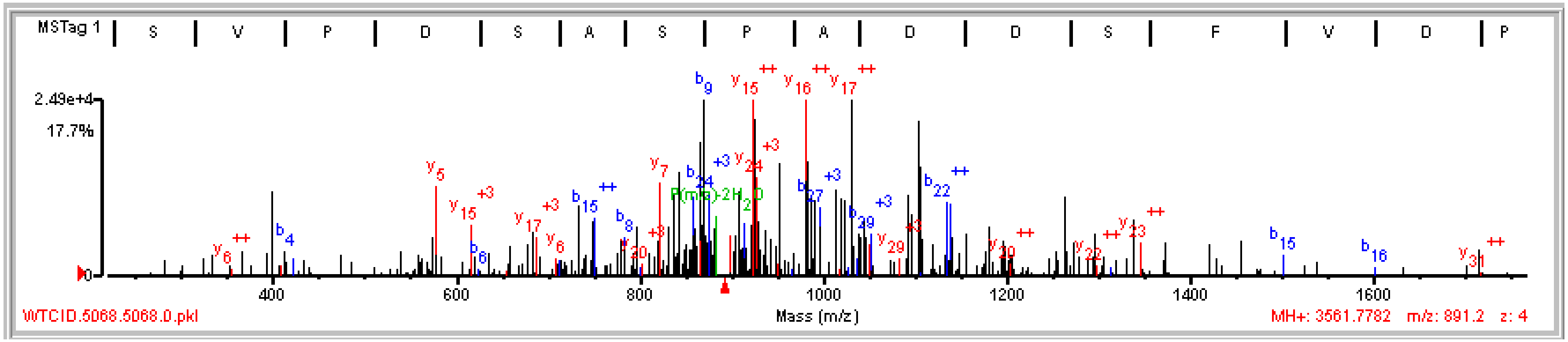


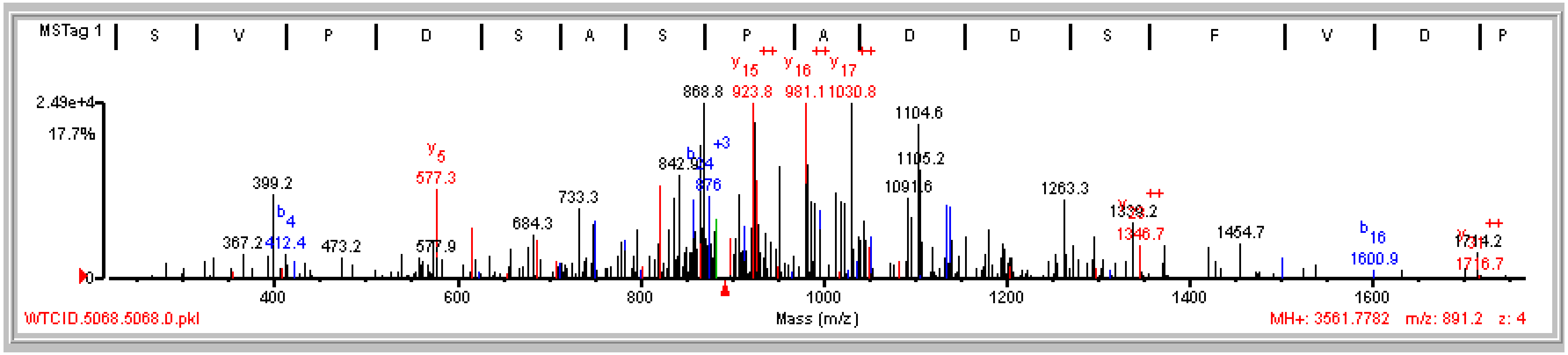
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.52	65.5	10	9/25	Y105y	(K) R K P S V\P D S A\S/P/A/D/D|S F|V D P/G E R L y D L N M/P A Y V K (F)	3636.76	81.1343	314.1	42864.7/6.06	Homo sapiens	5453754	17913	NCK adaptor protein 1

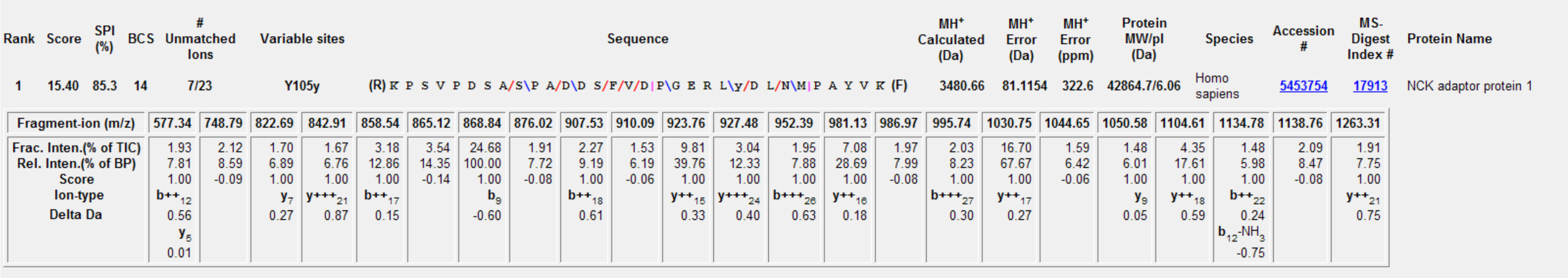
Fragment-ion (m/z)	568.54	577.41	712.83	793.13	795.27	829.53	847.46	871.81	875.09	885.21	893.71	898.58	905.86
Frac. Inten.(% of TIC)	2.45	2.52	3.14	3.04	3.32	4.24	3.48	2.64	11.55	3.30	3.50	6.35	0.11
Rel. Inten.(% of BP)	21.23	21.86	27.19	26.35	28.74	36.74	30.13	22.88	100.00	28.61	30.30	55.01	0.93
Score	1.00	1.00	1.00	-0.26	-0.29	1.00	-0.30	-0.23	1.00	-0.29	-0.30	1.00	1.50
Ion-type	b_5	y_5	$\mathrm{b++}_{14}$			$\mathrm{b++}_{16}$			$\mathrm{y++}_{14}$			$\mathrm{y+++}_{23}$	sty
Delta Da	0.18	0.08	0.49			0.14			0.18			0.51	0.42

Fragment-ion (m/z)	909.00	912.46	938.37	1007.66	1030.44	1105.12	1147.53	1157.08	1205.25	1262.62	1298.19	1347.05
Frac. Inten.(% of TIC)	6.55	3.79	3.03	4.47	4.45	2.57	5.65	4.84	4.38	3.86	3.91	2.85
Rel. Inten.(% of BP)	56.68	32.79	26.27	38.75	38.58	22.26	48.92	41.93	37.94	33.44	33.84	24.64
Score	-0.57	-0.33	1.00	0.50	1.00	0.50	1.00	-0.42	1.00	1.00	1.00	1.00
Ion-type			b_9	b_{10}-H_2O	$\mathrm{y++}_{17}$	b_{11}-NH_3	$\mathrm{y++}_{19}$		$\mathrm{y++}_{20}$	$\mathrm{y++}_{21}$	$\mathrm{y++}_{22}$	$\mathrm{y++}_{23}$
Delta Da			-0.14	0.13	-0.04	-0.44	-0.00		0.20	0.06	0.11	0.45

Peak 368



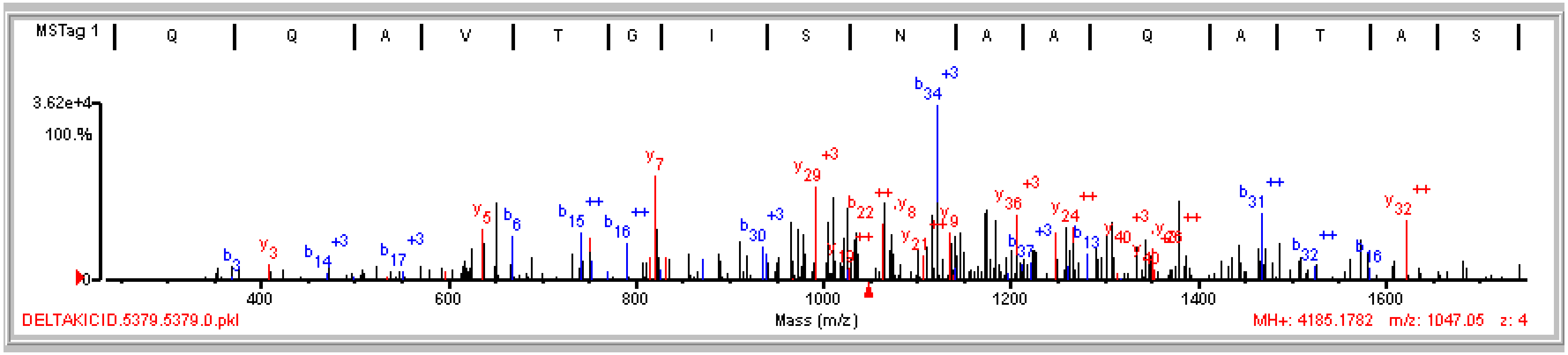




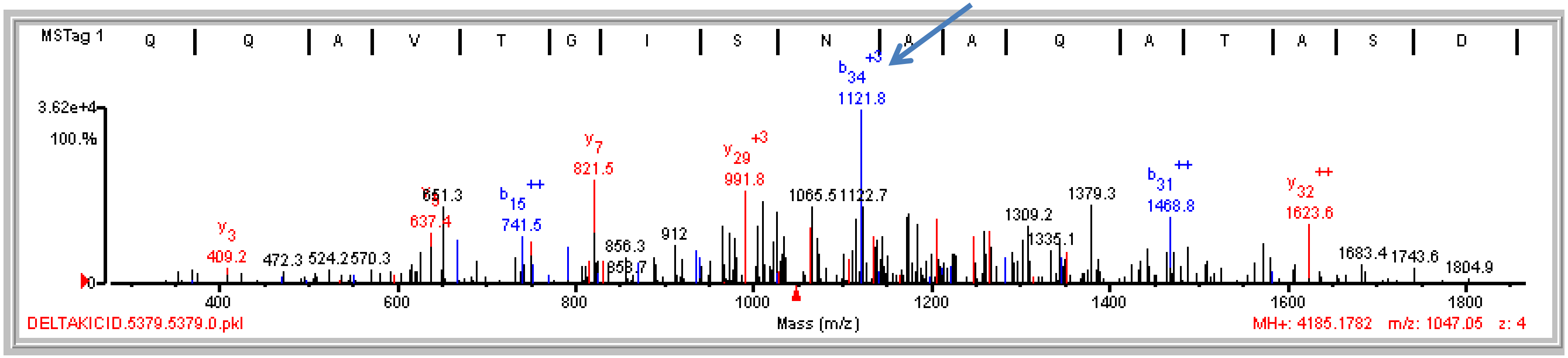
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.40	85.3	14	7/23	Y105y	(R) K P S V P D S A/S\P A/D\D S/F/V/D|P\G E R L\y/D L/N\M|P A Y V K (F)	3480.66	81.1154	322.6	42864.7/6.06	Homo sapiens	5453754	17913	NCK adaptor protein 1

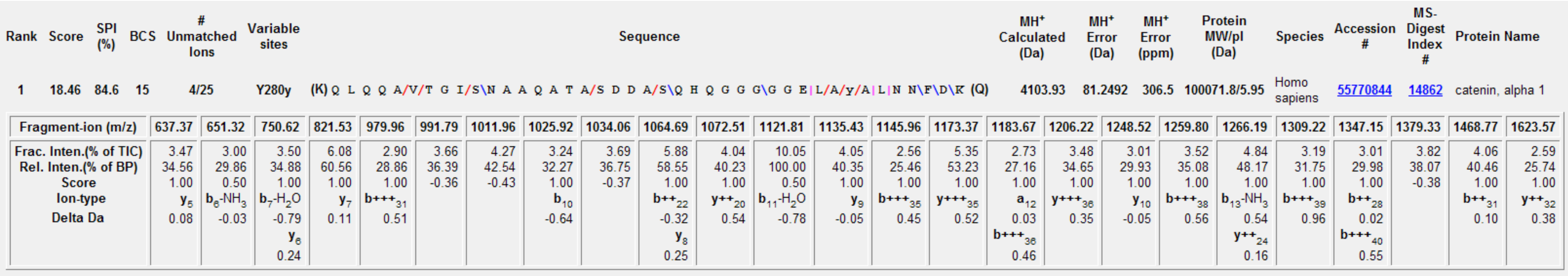
Fragment-ion (m/z)	577.34	748.79	822.69	842.91	858.54	865.12	868.84	876.02	907.53	910.09	923.76	927.48	952.39	981.13	986.97	995.74	1030.75	1044.65	1050.58	1104.61	1134.78	1138.76	1263.31
Frac. Inten.(% of TIC)	1.93	2.12	1.70	1.67	3.18	3.54	24.68	1.91	2.27	1.53	9.81	3.04	1.95	7.08	1.97	2.03	16.70	1.59	1.48	4.35	1.48	2.09	1.91
Rel. Inten.(% of BP)	7.81	8.59	6.89	6.76	12.86	14.35	100.00	7.72	9.19	6.19	39.76	12.33	7.88	28.69	7.99	8.23	67.67	6.42	6.01	17.61	5.98	8.47	7.75
Score	1.00	-0.09	1.00	1.00	1.00	-0.14	1.00	-0.08	1.00	-0.06	1.00	1.00	1.00	1.00	-0.08	1.00	1.00	-0.06	1.00	1.00	1.00	-0.08	1.00
Ion-type	$b{++}_{12}$ y_5		y_7	$y{+++}_{21}$	$b{++}_{17}$		b_9		$b{++}_{18}$		$y{++}_{15}$	$y{+++}_{24}$	$b{+++}_{26}$	$y{++}_{16}$		$b{+++}_{27}$	$y{++}_{17}$		y_9	$y{++}_{18}$	$b{++}_{22}$ b_{12}-NH_3		$y{++}_{21}$
Delta Da	0.56 0.01		0.27	0.87	0.15		-0.60		0.61		0.33	0.40	0.63	0.18		0.30	0.27		0.05	0.59	0.24 -0.75		0.75

Peak 369



assignment

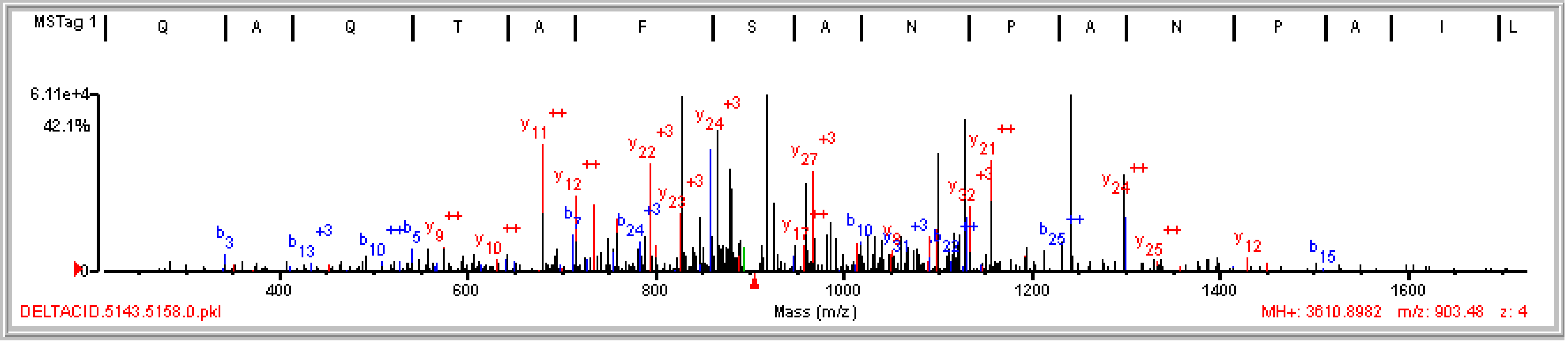


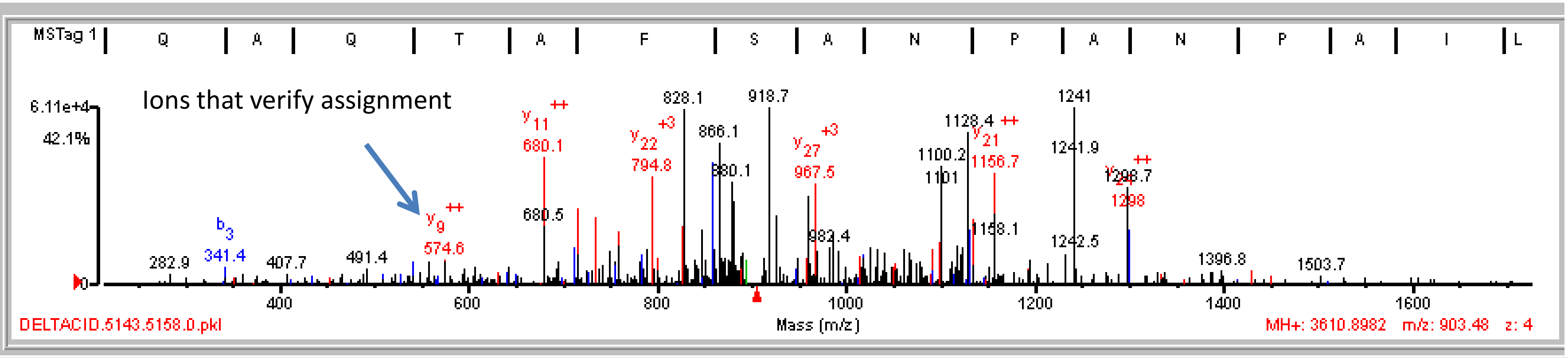


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.46	84.6	15	4/25	Y280y	(K) Q L Q Q A/V/T G I/S\N A A Q A T A/S D D A/S\Q H Q G G G\G G E|L/A/y/A|L|N N\F\D\K (Q)	4103.93	81.2492	306.5	100071.8/5.95	Homo sapiens	55770844	14862	catenin, alpha 1

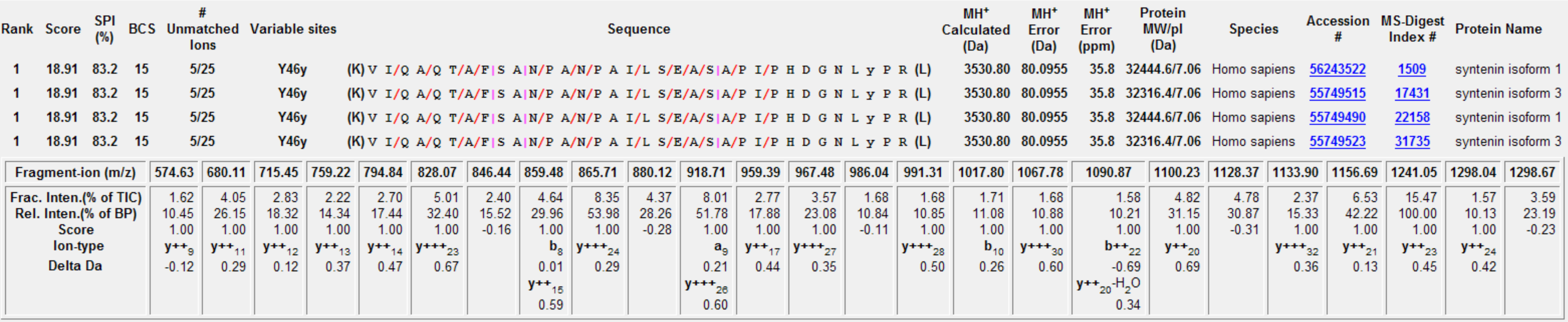
Fragment-ion (m/z)	637.37	651.32	750.62	821.53	979.96	991.79	1011.96	1025.92	1034.06	1064.69	1072.51	1121.81	1135.43	1145.96	1173.37	1183.67	1206.22	1248.52	1259.80	1266.19	1309.22	1347.15	1379.33	1468.77	1623.57
Frac. Inten.(% of TIC)	3.47	3.00	3.50	6.08	2.90	3.66	4.27	3.24	3.69	5.88	4.04	10.05	4.05	2.56	5.35	2.73	3.48	3.01	3.52	4.84	3.19	3.01	3.82	4.06	2.59
Rel. Inten.(% of BP)	34.56	29.86	34.88	60.56	28.86	36.39	42.54	32.27	36.75	58.55	40.23	100.00	40.35	25.46	53.23	27.16	34.65	29.93	35.08	48.17	31.75	29.98	38.07	40.46	25.74
Score	1.00	0.50	1.00	1.00	1.00	-0.36	-0.43	1.00	-0.37	1.00	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.38	1.00	1.00
Ion-type	y_5	b_6-NH_3	b_7-H_2O	y_7	$b{+}{+}{+}_{31}$			b_{10}		$b{+}{+}_{22}$	$y{+}{+}_{20}$	b_{11}-H_2O	y_9	$b{+}{+}{+}_{35}$	$y{+}{+}{+}_{35}$	a_{12}	$y{+}{+}{+}_{36}$	y_{10}	$b{+}{+}{+}_{38}$	b_{13}-NH_3	$b{+}{+}{+}_{39}$	$b{+}{+}_{28}$		$b{+}{+}_{31}$	$y{+}{+}_{32}$
Delta Da	0.08	-0.03	-0.79	0.11	0.51			-0.64		-0.32	0.54	-0.78	-0.05	0.45	0.52	0.03	0.35	-0.05	0.56	0.54	0.96	0.02		0.10	0.38
			y_6							y_8						$b{+}{+}{+}_{36}$				$y{+}{+}_{24}$		$b{+}{+}{+}_{40}$			
			0.24							0.25						0.46				0.16		0.55			

Peak 370





Ions that verify assignment

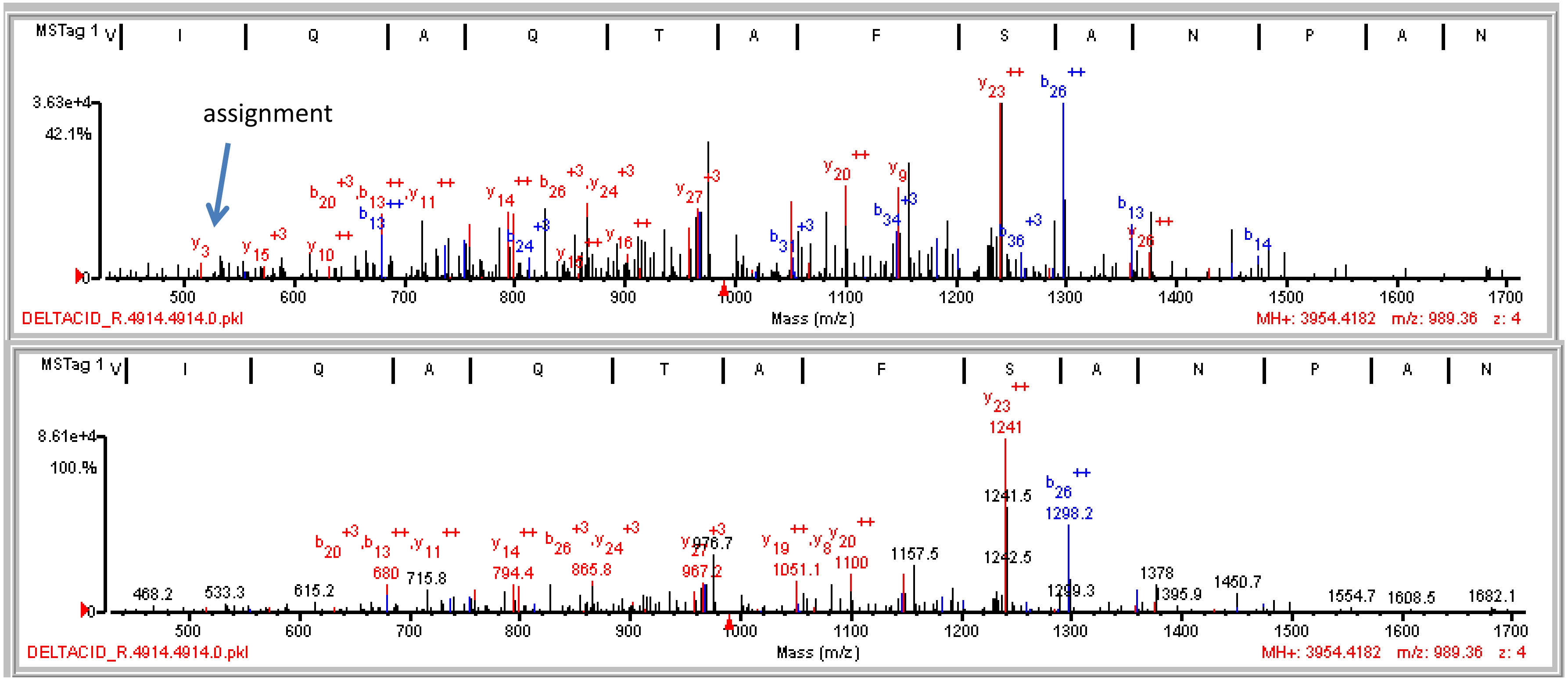


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.91	83.2	15	5/25	Y46y	(K) V I/Q A/Q T/A/F|S A|N/P A/N/P A I/L S/E/A/S|A/P I/P H D G N L y P R (L)	3530.80	80.0955	35.8	32444.6/7.06	Homo sapiens	56243522	1509	syntenin isoform 1
1	18.91	83.2	15	5/25	Y46y	(K) V I/Q A/Q T/A/F|S A|N/P A/N/P A I/L S/E/A/S|A/P I/P H D G N L y P R (L)	3530.80	80.0955	35.8	32316.4/7.06	Homo sapiens	55749515	17431	syntenin isoform 3
1	18.91	83.2	15	5/25	Y46y	(K) V I/Q A/Q T/A/F|S A|N/P A/N/P A I/L S/E/A/S|A/P I/P H D G N L y P R (L)	3530.80	80.0955	35.8	32444.6/7.06	Homo sapiens	55749490	22158	syntenin isoform 1
1	18.91	83.2	15	5/25	Y46y	(K) V I/Q A/Q T/A/F|S A|N/P A/N/P A I/L S/E/A/S|A/P I/P H D G N L y P R (L)	3530.80	80.0955	35.8	32316.4/7.06	Homo sapiens	55749523	31735	syntenin isoform 3

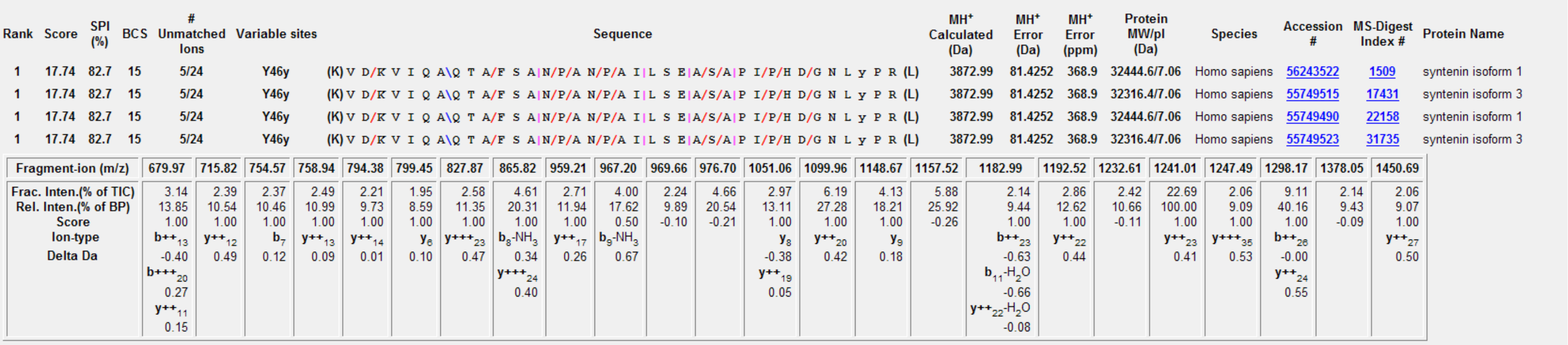
Fragment-ion (m/z)	574.63	680.11	715.45	759.22	794.84	828.07	846.44	859.48	865.71	880.12	918.71	959.39
Frac. Inten.(% of TIC)	1.62	4.05	2.83	2.22	2.70	5.01	2.40	4.64	8.35	4.37	8.01	2.77
Rel. Inten.(% of BP)	10.45	26.15	18.32	14.34	17.44	32.40	15.52	29.96	53.98	28.26	51.78	17.88
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.16	1.00	1.00	-0.28	1.00	1.00
Ion-type	y++_{9}	y++_{11}	y++_{12}	y++_{13}	y++_{14}	y+++_{23}		b_{8}	y+++_{24}		a_{9}	y++_{17}
Delta Da	-0.12	0.29	0.12	0.37	0.47	0.67		0.01 y++_{15} 0.59	0.29		0.21 y+++_{26} 0.60	0.44

Fragment-ion (m/z)	967.48	986.04	991.31	1017.80	1067.78	1090.87	1100.23	1128.37	1133.90	1156.69	1241.05	1298.04	1298.67
Frac. Inten.(% of TIC)	3.57	1.68	1.68	1.71	1.68	1.58	4.82	4.78	2.37	6.53	15.47	1.57	3.59
Rel. Inten.(% of BP)	23.08	10.84	10.85	11.08	10.88	10.21	31.15	30.87	15.33	42.22	100.00	10.13	23.19
Score	1.00	-0.11	1.00	1.00	1.00	1.00	1.00	-0.31	1.00	1.00	1.00	1.00	-0.23
Ion-type	y+++_{27}		y+++_{28}	b_{10}	y+++_{30}	b++_{22}	y++_{20}		y+++_{32}	y++_{21}	y++_{23}	y++_{24}	
Delta Da	0.35		0.50	0.26	0.60	-0.69 $\text{y++}_{20}\text{-H}_2\text{O}$ 0.34	0.69		0.36	0.13	0.45	0.42	

Peak 371



assignment



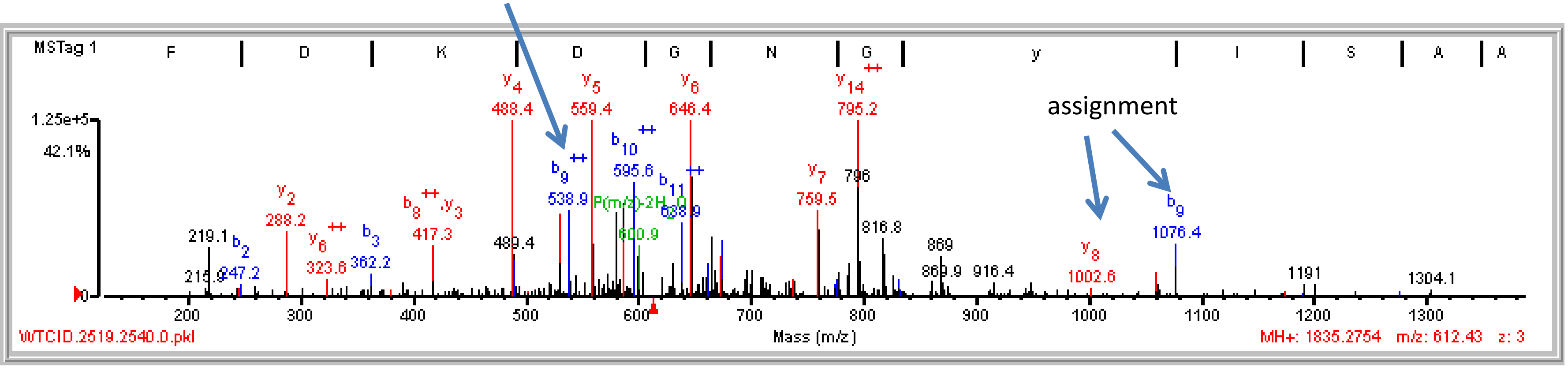
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.74	82.7	15	5/24	Y46y	(K) V D/K V I Q A\Q T A/F S A|N/P/A N/P/A I|L S E|A/S/A|P I/P/H D/G N L y P R (L)	3872.99	81.4252	368.9	32444.6/7.06	Homo sapiens	56243522	1509	syntenin isoform 1
1	17.74	82.7	15	5/24	Y46y	(K) V D/K V I Q A\Q T A/F S A|N/P/A N/P/A I|L S E|A/S/A|P I/P/H D/G N L y P R (L)	3872.99	81.4252	368.9	32316.4/7.06	Homo sapiens	55749515	17431	syntenin isoform 3
1	17.74	82.7	15	5/24	Y46y	(K) V D/K V I Q A\Q T A/F S A|N/P/A N/P/A I|L S E|A/S/A|P I/P/H D/G N L y P R (L)	3872.99	81.4252	368.9	32444.6/7.06	Homo sapiens	55749490	22158	syntenin isoform 1
1	17.74	82.7	15	5/24	Y46y	(K) V D/K V I Q A\Q T A/F S A|N/P/A N/P/A I|L S E|A/S/A|P I/P/H D/G N L y P R (L)	3872.99	81.4252	368.9	32316.4/7.06	Homo sapiens	55749523	31735	syntenin isoform 3

Fragment-ion (m/z)	679.97	715.82	754.57	758.94	794.38	799.45	827.87	865.82	959.21	967.20	969.66	976.70
Frac. Inten.(% of TIC)	3.14	2.39	2.37	2.49	2.21	1.95	2.58	4.61	2.71	4.00	2.24	4.66
Rel. Inten.(% of BP)	13.85	10.54	10.46	10.99	9.73	8.59	11.35	20.31	11.94	17.62	9.89	20.54
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	-0.10	-0.21
Ion-type	b++$_{13}$ b+++$_{20}$ y++$_{11}$	y++$_{12}$	b$_{7}$	y++$_{13}$	y++$_{14}$	y$_{6}$	y+++$_{23}$	b$_{8}$-NH$_{3}$ y+++$_{24}$	y++$_{17}$	b$_{9}$-NH$_{3}$		
Delta Da	-0.40 0.27 0.15	0.49	0.12	0.09	0.01	0.10	0.47	0.34 0.40	0.26	0.67		

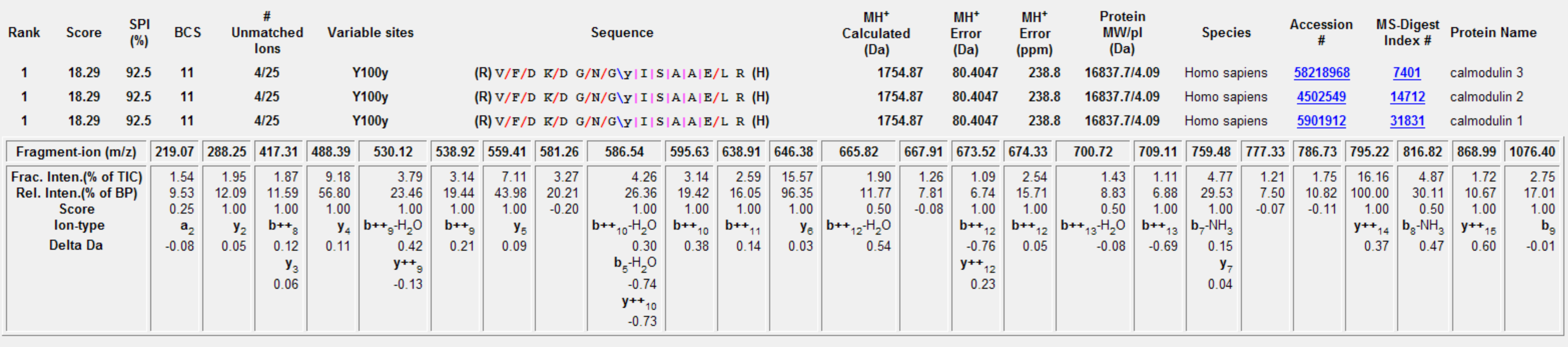
Fragment-ion (m/z)	1051.06	1099.96	1148.67	1157.52	1182.99	1192.52	1232.61	1241.01	1247.49	1298.17	1378.05	1450.69
Frac. Inten.(% of TIC)	2.97	6.19	4.13	5.88	2.14	2.86	2.42	22.69	2.06	9.11	2.14	2.06
Rel. Inten.(% of BP)	13.11	27.28	18.21	25.92	9.44	12.62	10.66	100.00	9.09	40.16	9.43	9.07
Score	1.00	1.00	1.00	-0.26	1.00	1.00	-0.11	1.00	1.00	1.00	-0.09	1.00
Ion-type	y$_{8}$ y++$_{19}$	y++$_{20}$	y$_{9}$		b++$_{23}$ b$_{11}$-H$_{2}$O y++$_{22}$-H$_{2}$O	y++$_{22}$		y++$_{23}$	y+++$_{35}$	b++$_{26}$ y++$_{24}$		y++$_{27}$
Delta Da	-0.38 0.05	0.42	0.18		-0.63 -0.66 -0.08	0.44		0.41	0.53	-0.00 0.55		0.50

Peak 372

assignment



assignment

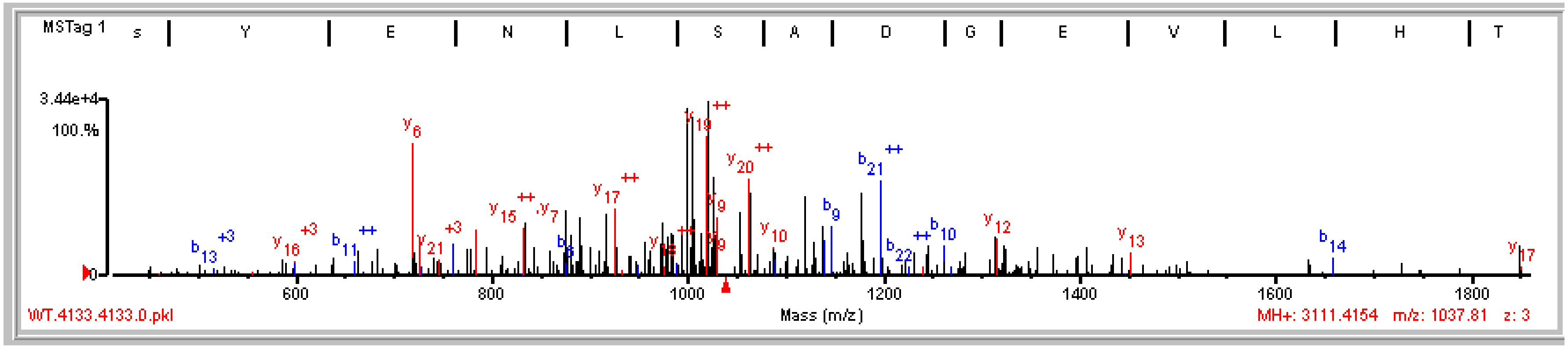


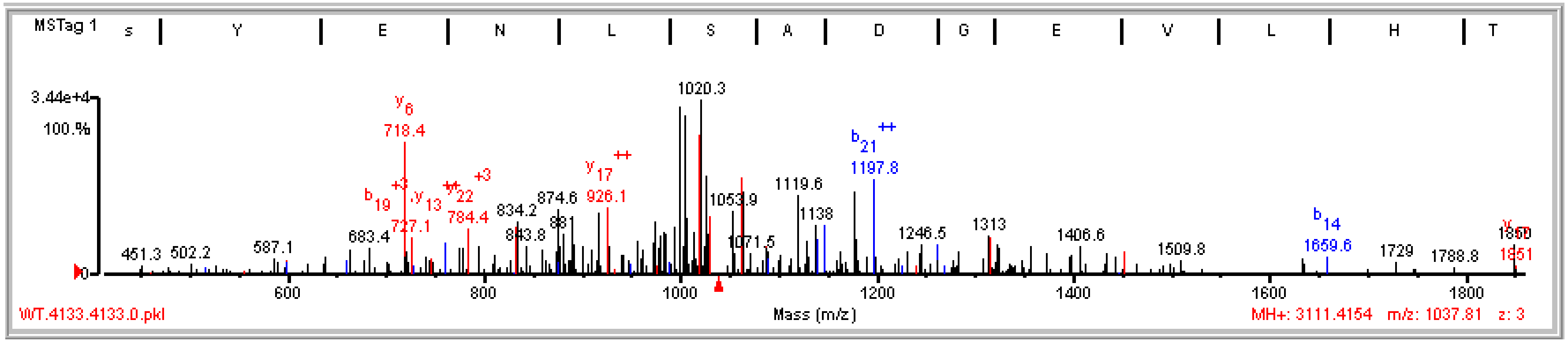
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.29	92.5	11	4/25	Y100y	(R) V/F/D K/D G/N/G\y|I|S|A|A|E/L R (H)	1754.87	80.4047	238.8	16837.7/4.09	Homo sapiens	58218968	7401	calmodulin 3
1	18.29	92.5	11	4/25	Y100y	(R) V/F/D K/D G/N/G\y|I|S|A|A|E/L R (H)	1754.87	80.4047	238.8	16837.7/4.09	Homo sapiens	4502549	14712	calmodulin 2
1	18.29	92.5	11	4/25	Y100y	(R) V/F/D K/D G/N/G\y|I|S|A|A|E/L R (H)	1754.87	80.4047	238.8	16837.7/4.09	Homo sapiens	5901912	31831	calmodulin 1

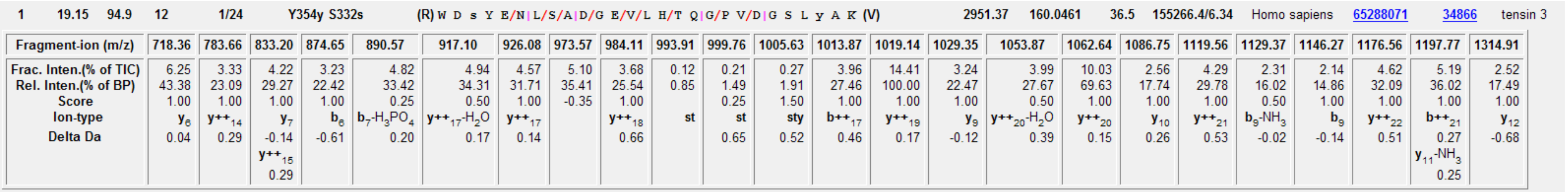
Fragment-ion (m/z)	219.07	288.25	417.31	488.39	530.12	538.92	559.41	581.26	586.54	595.63	638.91	646.38
Frac. Inten.(% of TIC)	1.54	1.95	1.87	9.18	3.79	3.14	7.11	3.27	4.26	3.14	2.59	15.57
Rel. Inten.(% of BP)	9.53	12.09	11.59	56.80	23.46	19.44	43.98	20.21	26.36	19.42	16.05	96.35
Score	0.25	1.00	1.00	1.00	1.00	1.00	1.00	-0.20	1.00	1.00	1.00	1.00
Ion-type	a_2	y_2	$b{+}{+}_{8}$ y_3	y_4	$b{+}{+}_{9}$-H_2O $y{+}{+}_{9}$	$b{+}{+}_{9}$	y_5		$b{+}{+}_{10}$-H_2O b_5-H_2O $y{+}{+}_{10}$	$b{+}{+}_{10}$	$b{+}{+}_{11}$	y_6
Delta Da	-0.08	0.05	0.12 0.06	0.11	0.42 -0.13	0.21	0.09		0.30 -0.74 -0.73	0.38	0.14	0.03

Fragment-ion (m/z)	665.82	667.91	673.52	674.33	700.72	709.11	759.48	777.33	786.73	795.22	816.82	868.99	1076.40
Frac. Inten.(% of TIC)	1.90	1.26	1.09	2.54	1.43	1.11	4.77	1.21	1.75	16.16	4.87	1.72	2.75
Rel. Inten.(% of BP)	11.77	7.81	6.74	15.71	8.83	6.88	29.53	7.50	10.82	100.00	30.11	10.67	17.01
Score	0.50	-0.08	1.00	1.00	0.50	1.00	1.00	-0.07	-0.11	1.00	0.50	1.00	1.00
Ion-type	$b{+}{+}_{12}$-H_2O		$b{+}{+}_{12}$ $y{+}{+}_{12}$	$b{+}{+}_{12}$	$b{+}{+}_{13}$-H_2O	$b{+}{+}_{13}$	b_7-NH_3 y_7			$y{+}{+}_{14}$	b_8-NH_3	$y{+}{+}_{15}$	b_9
Delta Da	0.54		-0.76 0.23	0.05	-0.08	-0.69	0.15 0.04			0.37	0.47	0.60	-0.01

Peak 373





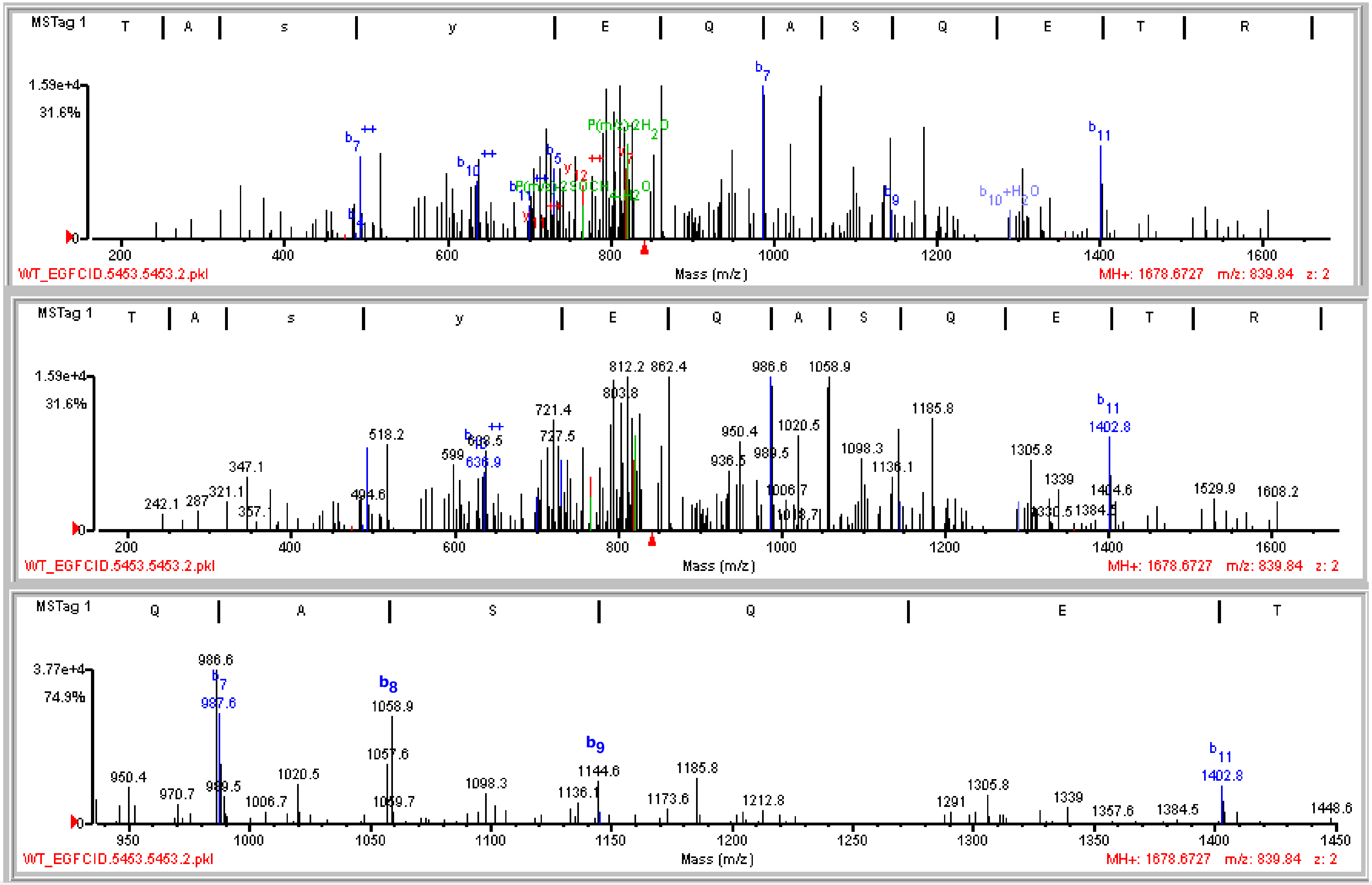


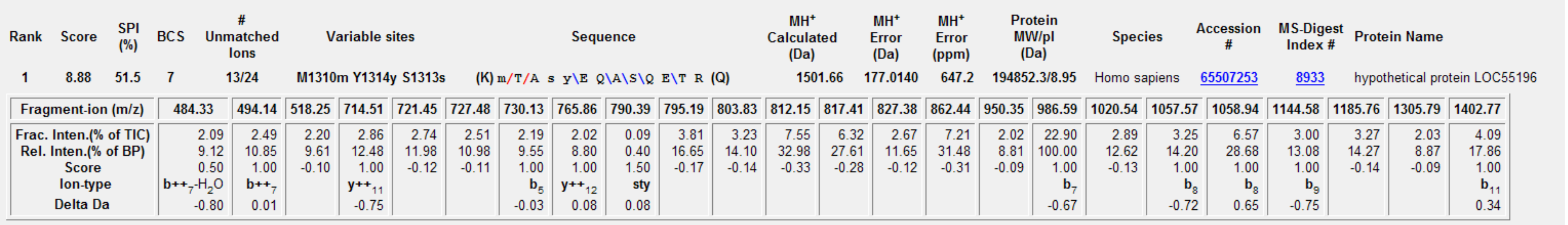
1 19.15 94.9 12 1/24 Y354y S332s (R) W D s Y E/N|L/S/A|D/G E/V/L H/T Q|G/P V/D|G S L y A K (V) 2951.37 160.0461 36.5 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

Fragment-ion (m/z)	718.36	783.66	833.20	874.65	890.57	917.10	926.08	973.57	984.11	993.91	999.76	1005.63	1013.87
Frac. Inten.(% of TIC)	6.25	3.33	4.22	3.23	4.82	4.94	4.57	5.10	3.68	0.12	0.21	0.27	3.96
Rel. Inten.(% of BP)	43.38	23.09	29.27	22.42	33.42	34.31	31.71	35.41	25.54	0.85	1.49	1.91	27.46
Score	1.00	1.00	1.00	1.00	0.25	0.50	1.00	-0.35	1.00		0.25	1.50	1.00
Ion-type	y_6	$y{++}_{14}$	y_7 $y{++}_{15}$	b_6	b_7-H_3PO_4	$y{++}_{17}$-H_2O	$y{++}_{17}$		$y{++}_{18}$	st	st	sty	$b{++}_{17}$
Delta Da	0.04	0.29	-0.14 0.29	-0.61	0.20	0.17	0.14		0.66		0.65	0.52	0.46

Fragment-ion (m/z)	1019.14	1029.35	1053.87	1062.64	1086.75	1119.56	1129.37	1146.27	1176.56	1197.77	1314.91
Frac. Inten.(% of TIC)	14.41	3.24	3.99	10.03	2.56	4.29	2.31	2.14	4.62	5.19	2.52
Rel. Inten.(% of BP)	100.00	22.47	27.67	69.63	17.74	29.78	16.02	14.86	32.09	36.02	17.49
Score	1.00	1.00	0.50	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type	$y{++}_{19}$	y_9	$y{++}_{20}$-H_2O	$y{++}_{20}$	y_{10}	$y{++}_{21}$	b_9-NH_3	b_9	$y{++}_{22}$	$b{++}_{21}$ y_{11}-NH_3	y_{12}
Delta Da	0.17	-0.12	0.39	0.15	0.26	0.53	-0.02	-0.14	0.51	0.27 0.25	-0.68

Peak 375

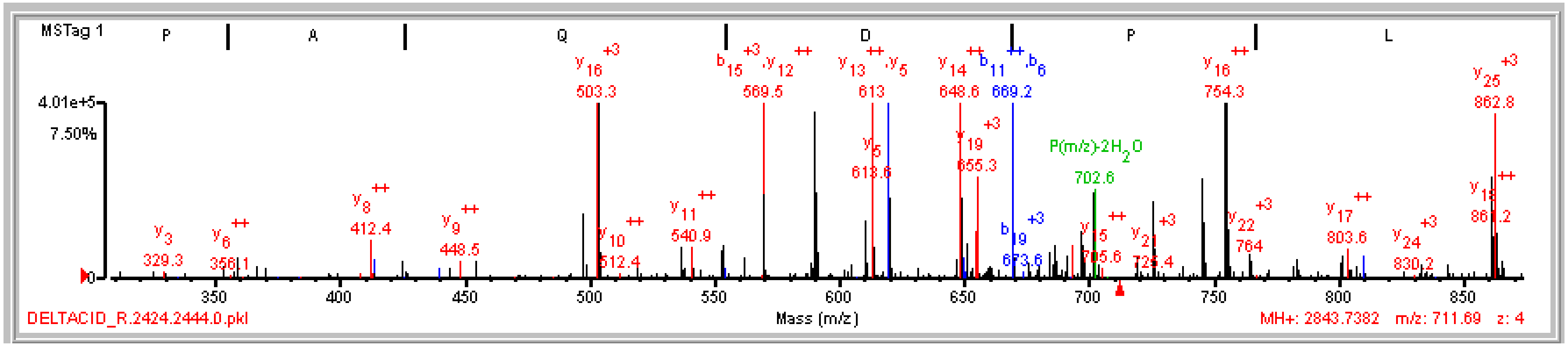


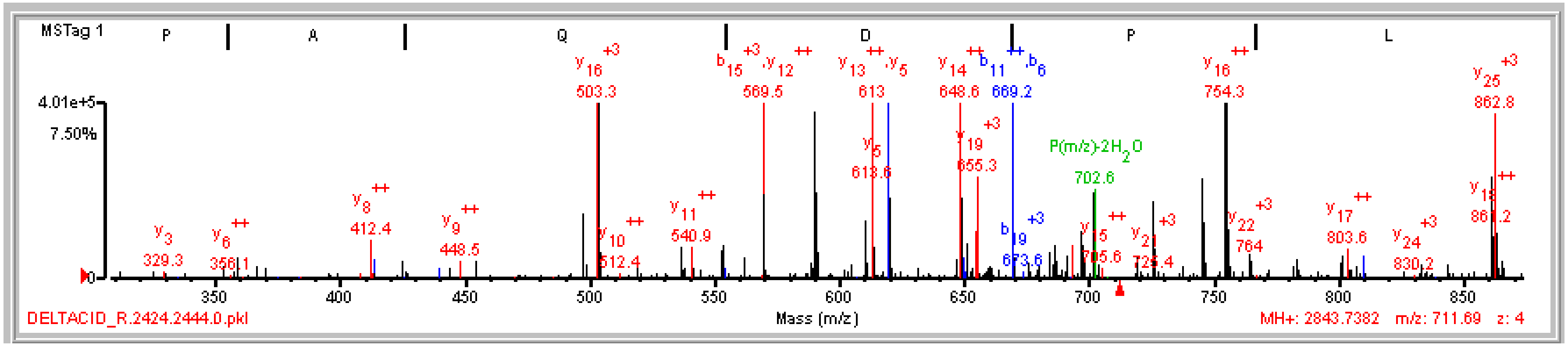


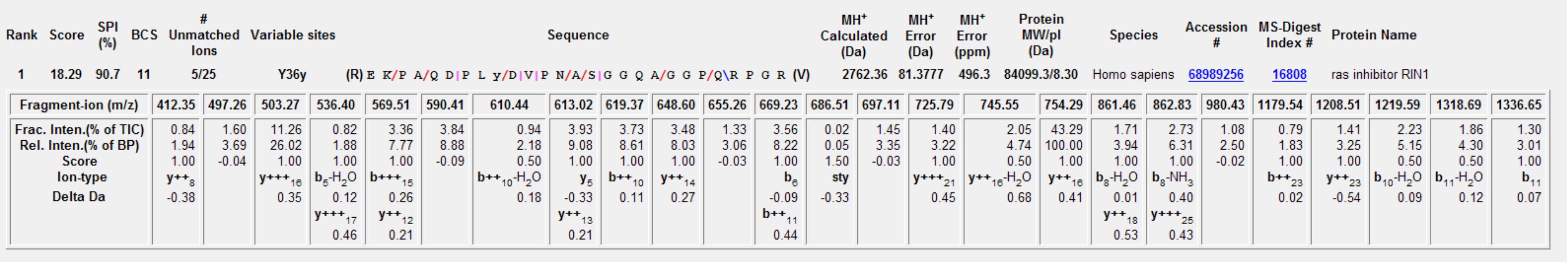
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.88	51.5	7	13/24	M1310m Y1314y S1313s	(K) m/T/A s y\E Q\A\S\Q E\T R (Q)	1501.66	177.0140	647.2	194852.3/8.95	Homo sapiens	65507253	8933	hypothetical protein LOC55196

Fragment-ion (m/z)	484.33	494.14	518.25	714.51	721.45	727.48	730.13	765.86	790.39	795.19	803.83	812.15	817.41	827.38	862.44	950.35	986.59	1020.54	1057.57	1058.94	1144.58	1185.76	1305.79	1402.77
Frac. Inten.(% of TIC)	2.09	2.49	2.20	2.86	2.74	2.51	2.19	2.02	0.09	3.81	3.23	7.55	6.32	2.67	7.21	2.02	22.90	2.89	3.25	6.57	3.00	3.27	2.03	4.09
Rel. Inten.(% of BP)	9.12	10.85	9.61	12.48	11.98	10.98	9.55	8.80	0.40	16.65	14.10	32.98	27.61	11.65	31.48	8.81	100.00	12.62	14.20	28.68	13.08	14.27	8.87	17.86
Score	0.50	1.00	-0.10	1.00	-0.12	-0.11	1.00	1.00	1.50	-0.17	-0.14	-0.33	-0.28	-0.12	-0.31	-0.09	1.00	-0.13	1.00	1.00	1.00	-0.14	-0.09	1.00
Ion-type	$b{+}{+}_7$-H_2O	$b{+}{+}_7$		$y{+}{+}_{11}$			b_5	$y{+}{+}_{12}$	sty								b_7		b_8	b_8	b_9			b_{11}
Delta Da	-0.80	0.01		-0.75			-0.03	0.08	0.08								-0.67		-0.72	0.65	-0.75			0.34

Peak 376





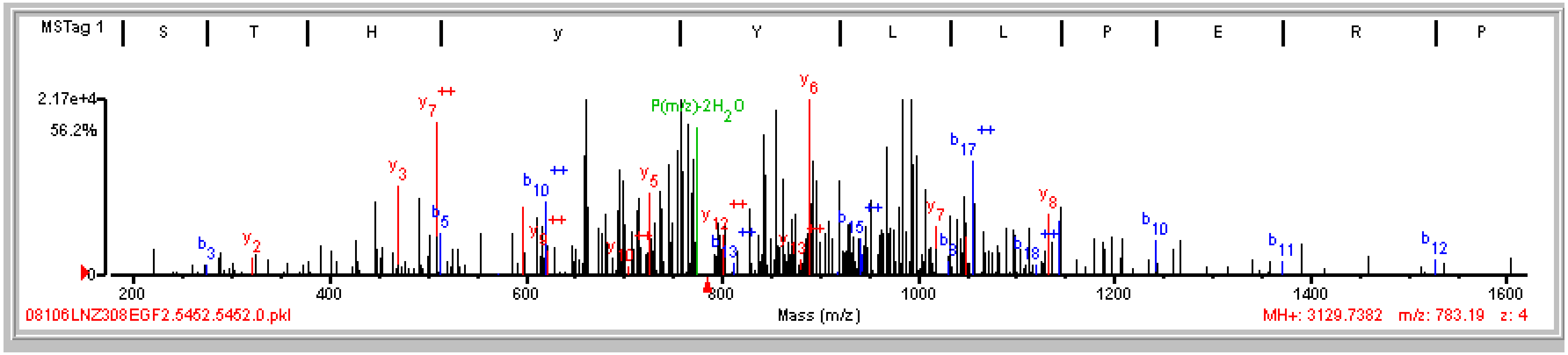


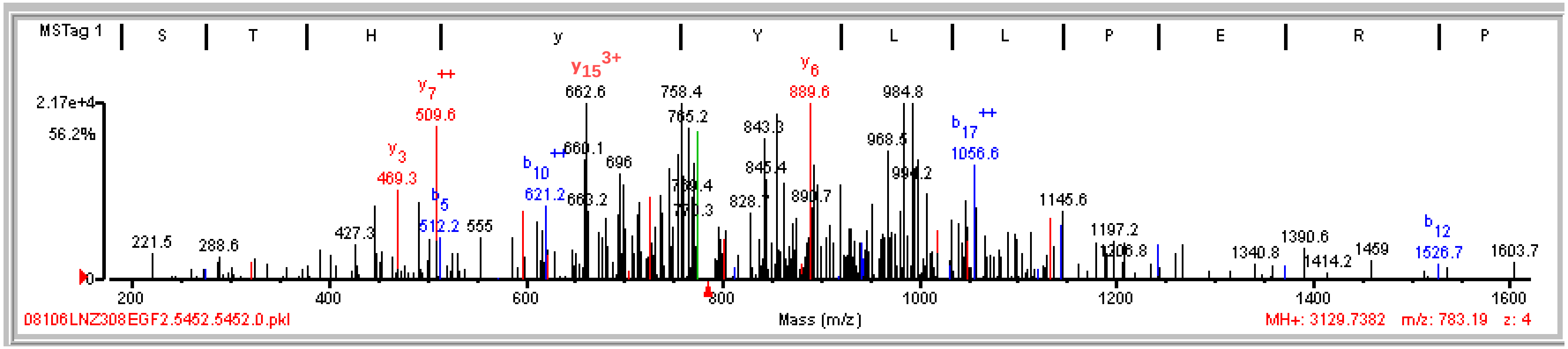
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.29	90.7	11	5/25	Y36y	(R) E K/P A/Q D|P L y/D|V|P N/A/S|G G Q A/G G P/Q\R P G R (V)	2762.36	81.3777	496.3	84099.3/8.30	Homo sapiens	68989256	16808	ras inhibitor RIN1

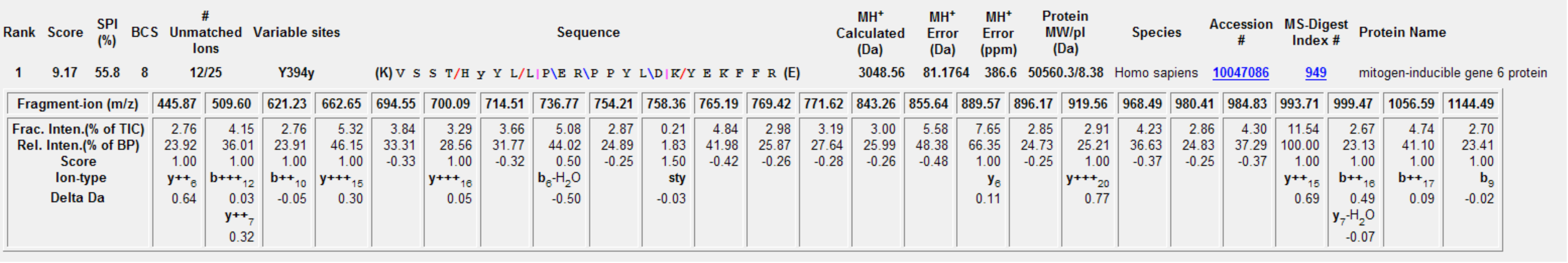
Fragment-ion (m/z)	412.35	497.26	503.27	536.40	569.51	590.41	610.44	613.02	619.37	648.60	655.26	669.23	686.51
Frac. Inten.(% of TIC)	0.84	1.60	11.26	0.82	3.36	3.84	0.94	3.93	3.73	3.48	1.33	3.56	0.02
Rel. Inten.(% of BP)	1.94	3.69	26.02	1.88	7.77	8.88	2.18	9.08	8.61	8.03	3.06	8.22	0.05
Score	1.00	-0.04	1.00	1.00	1.00	-0.09	0.50	1.00	1.00	1.00	-0.03	1.00	1.50
Ion-type	y++$_{8}$		y+++$_{16}$	b$_{5}$-H$_2$O y+++$_{17}$	b+++$_{15}$ y++$_{12}$		b++$_{10}$-H$_2$O	y$_{5}$ y++$_{13}$	b++$_{10}$	y++$_{14}$		b$_{6}$ b++$_{11}$	sty
Delta Da	-0.38		0.35	0.12 0.46	0.26 0.21		0.18	-0.33 0.21	0.11	0.27		-0.09 0.44	-0.33

Fragment-ion (m/z)	697.11	725.79	745.55	754.29	861.46	862.83	980.43	1179.54	1208.51	1219.59	1318.69	1336.65
Frac. Inten.(% of TIC)	1.45	1.40	2.05	43.29	1.71	2.73	1.08	0.79	1.41	2.23	1.86	1.30
Rel. Inten.(% of BP)	3.35	3.22	4.74	100.00	3.94	6.31	2.50	1.83	3.25	5.15	4.30	3.01
Score	-0.03	1.00	0.50	1.00	1.00	1.00	-0.02	1.00	1.00	0.50	0.50	1.00
Ion-type		y+++$_{21}$	y++$_{16}$-H$_2$O	y++$_{16}$	b$_{8}$-H$_2$O y++$_{18}$	b$_{8}$-NH$_3$ y+++$_{25}$		b++$_{23}$	y++$_{23}$	b$_{10}$-H$_2$O	b$_{11}$-H$_2$O	b$_{11}$
Delta Da		0.45	0.68	0.41	0.01 0.53	0.40 0.43		0.02	-0.54	0.09	0.12	0.07

Peak 377





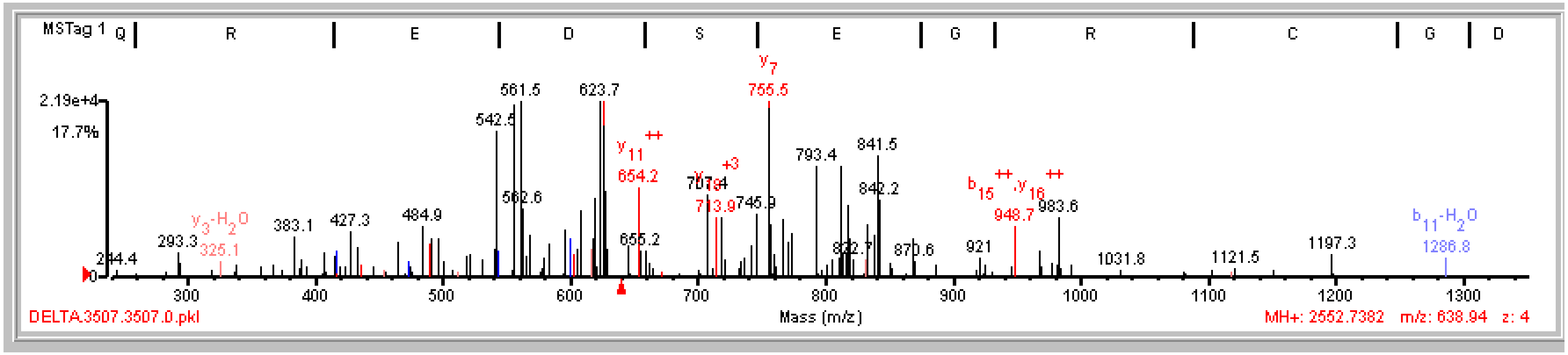


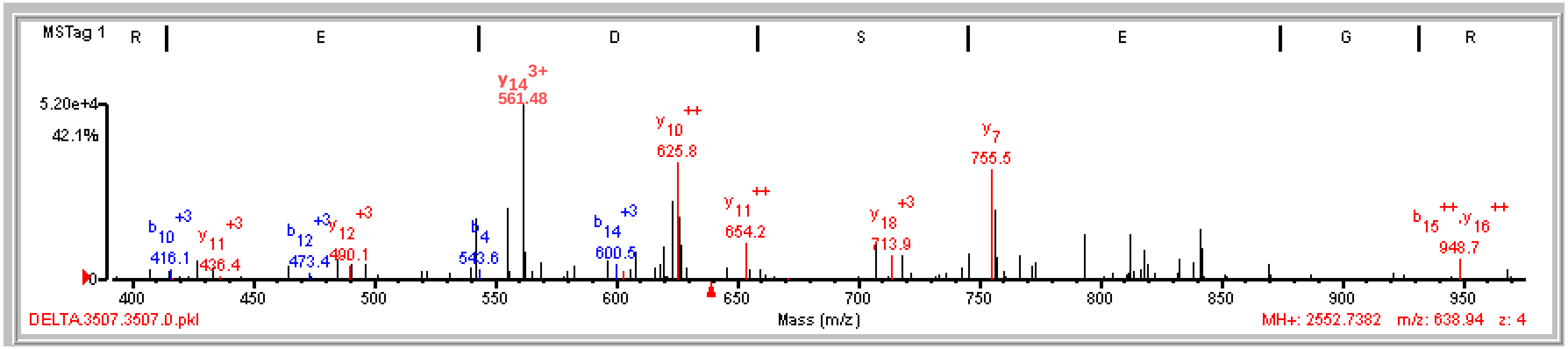
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.17	55.8	8	12/25	Y394y	(K) V S S T/H y Y L/L|P\E R\P P Y L\D|K/Y E K F F R (E)	3048.56	81.1764	386.6	50560.3/8.38	Homo sapiens	10047086	949	mitogen-inducible gene 6 protein

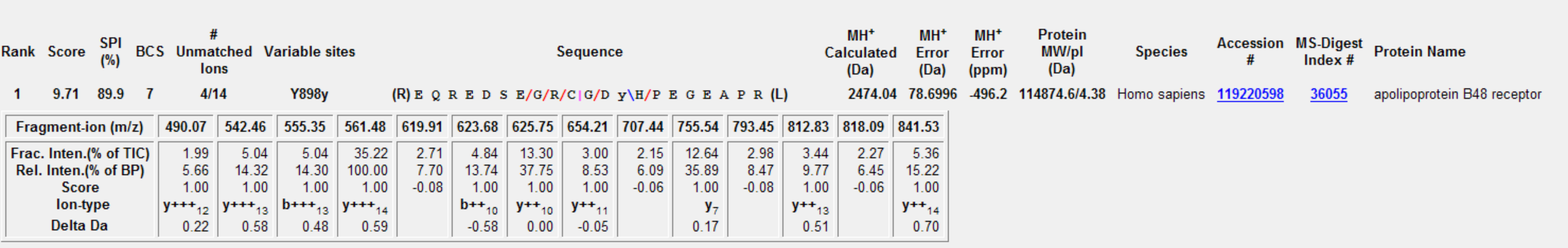
Fragment-ion (m/z)	445.87	509.60	621.23	662.65	694.55	700.09	714.51	736.77	754.21	758.36
Frac. Inten.(% of TIC)	2.76	4.15	2.76	5.32	3.84	3.29	3.66	5.08	2.87	0.21
Rel. Inten.(% of BP)	23.92	36.01	23.91	46.15	33.31	28.56	31.77	44.02	24.89	1.83
Score	1.00	1.00	1.00	1.00	-0.33	1.00	-0.32	0.50	-0.25	1.50
Ion-type	y^{++}_{6}	b^{+++}_{12} y^{++}_{7}	b^{++}_{10}	y^{+++}_{15}		y^{+++}_{16}		b_6-H_2O		sty
Delta Da	0.64	0.03 0.32	-0.05	0.30		0.05		-0.50		-0.03

Fragment-ion (m/z)	765.19	769.42	771.62	843.26	855.64	889.57	896.17	919.56	968.49	980.41	984.83	993.71	999.47	1056.59	1144.49
Frac. Inten.(% of TIC)	4.84	2.98	3.19	3.00	5.58	7.65	2.85	2.91	4.23	2.86	4.30	11.54	2.67	4.74	2.70
Rel. Inten.(% of BP)	41.98	25.87	27.64	25.99	48.38	66.35	24.73	25.21	36.63	24.83	37.29	100.00	23.13	41.10	23.41
Score	-0.42	-0.26	-0.28	-0.26	-0.48	1.00	-0.25	1.00	-0.37	-0.25	-0.37	1.00	1.00	1.00	1.00
Ion-type						y_6		y^{+++}_{20}				y^{++}_{15}	b^{++}_{16} y_7-H_2O	b^{++}_{17}	b_9
Delta Da						0.11		0.77				0.69	0.49 -0.07	0.09	-0.02

Peak 379



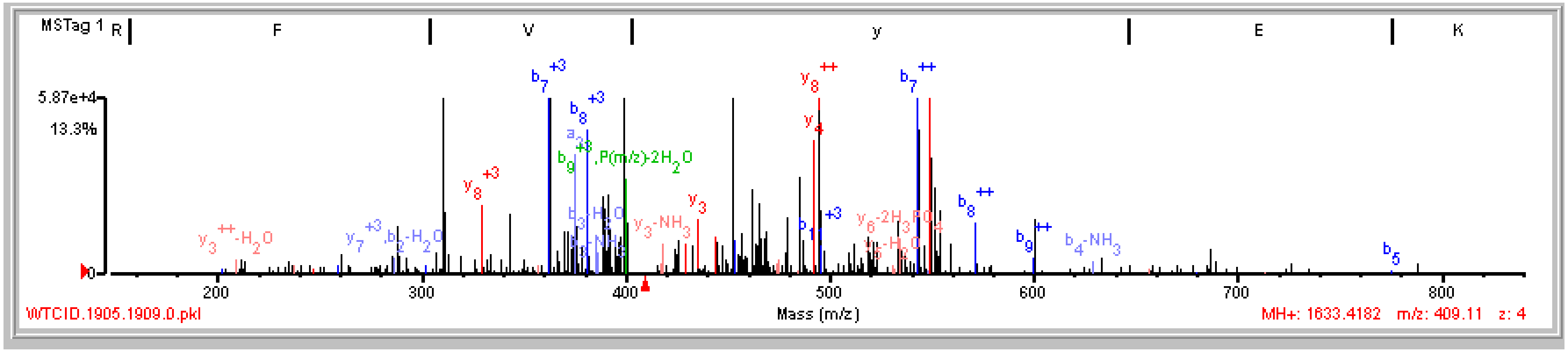


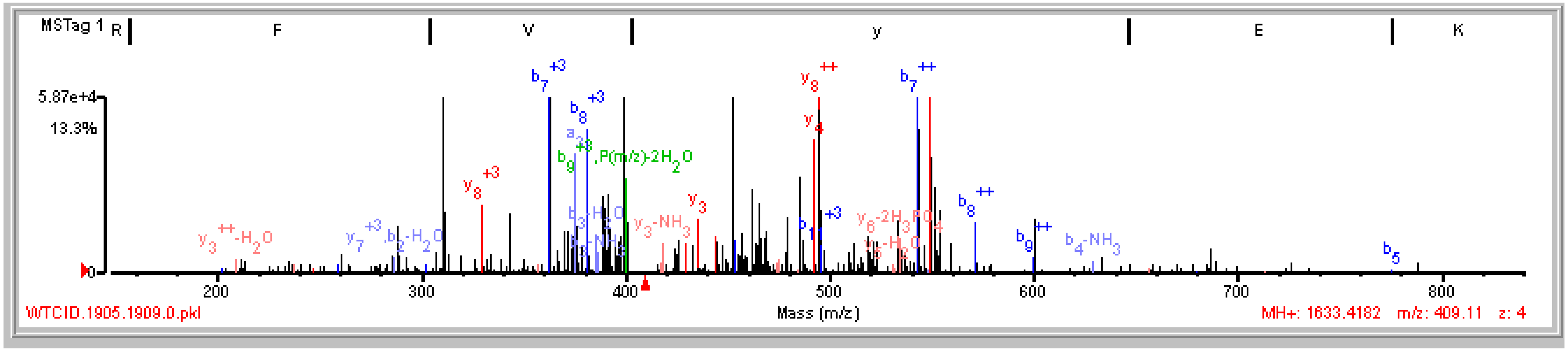


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.71	89.9	7	4/14	Y898y	(R) E Q R E D S E/G/R/C|G/D y\H/P E G E A P R (L)	2474.04	78.6996	-496.2	114874.6/4.38	Homo sapiens	119220598	36055	apolipoprotein B48 receptor

Fragment-ion (m/z)	490.07	542.46	555.35	561.48	619.91	623.68	625.75	654.21	707.44	755.54	793.45	812.83	818.09	841.53
Frac. Inten.(% of TIC)	1.99	5.04	5.04	35.22	2.71	4.84	13.30	3.00	2.15	12.64	2.98	3.44	2.27	5.36
Rel. Inten.(% of BP)	5.66	14.32	14.30	100.00	7.70	13.74	37.75	8.53	6.09	35.89	8.47	9.77	6.45	15.22
Score	1.00	1.00	1.00	1.00	-0.08	1.00	1.00	1.00	-0.06	1.00	-0.08	1.00	-0.06	1.00
Ion-type	$y+++_{12}$	$y+++_{13}$	$b+++_{13}$	$y+++_{14}$		$b++_{10}$	$y++_{10}$	$y++_{11}$		y_7		$y++_{13}$		$y++_{14}$
Delta Da	0.22	0.58	0.48	0.59		-0.58	0.00	-0.05		0.17		0.51		0.70

Peak 380



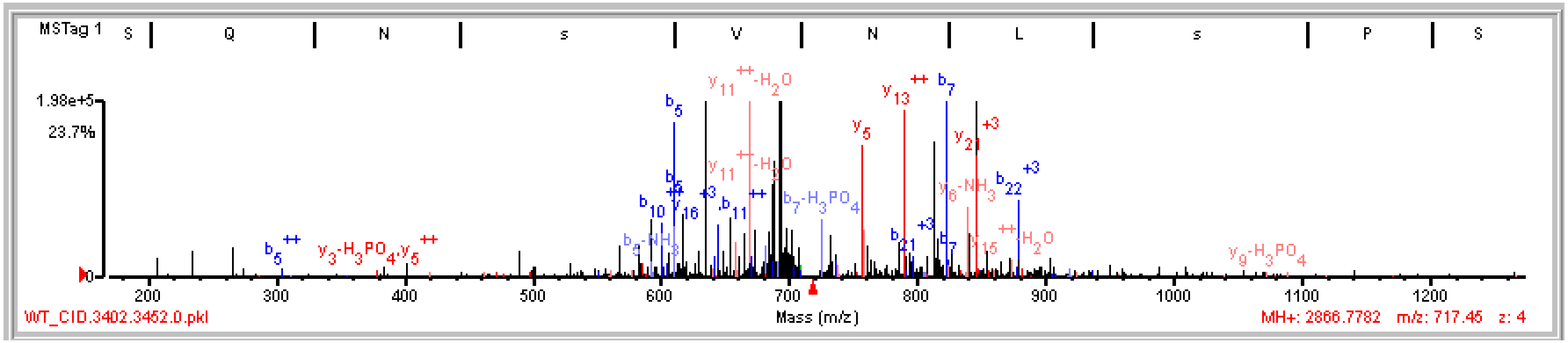


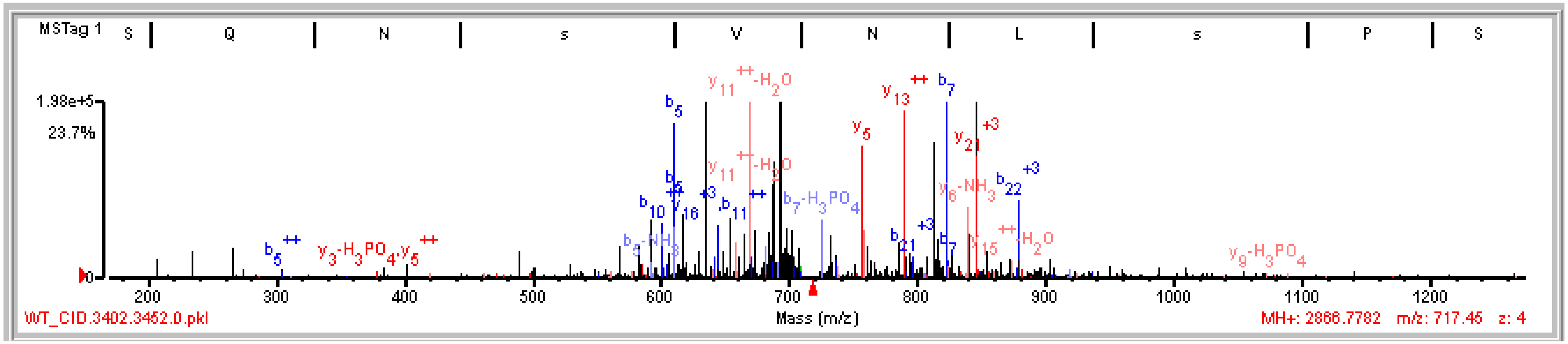
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.03	81.0	7	10/25	T694t Y691y	(K) R F/V y/E\K\t|G|G/C Q K (L)	1472.73	160.6867	461.6	87134.2/5.19	Homo sapiens	119220605	17324	ubiquitin specific protease 10

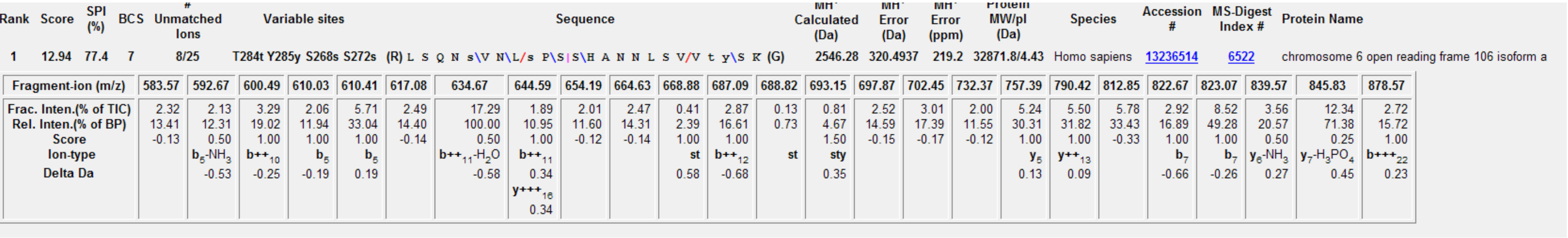
Fragment-ion (m/z)	311.06	329.97	362.44	369.92	375.50	381.35	385.48	388.77	391.21	394.84	396.52	435.35
Frac. Inten.(% of TIC)	4.32	1.33	26.94	2.02	0.09	2.84	1.21	2.84	2.37	1.32	1.55	1.19
Rel. Inten.(% of BP)	16.03	4.95	100.00	7.51	0.33	10.55	4.50	10.52	8.78	4.88	5.75	4.43
Score	-0.16	1.00	1.00	-0.08	0.25	1.00	0.50	1.00	-0.09	-0.05	-0.06	1.00
Ion-type		$y{+}{+}{+}_8$	$b{+}{+}{+}_7$		a_3	$b{+}{+}{+}_8$	b_3-NH_3	$b{+}{+}_5$				y_3
Delta Da		0.17	0.29		0.25	0.20	-0.74	0.61				0.15
					0.25							
					st							
					0.08							

Fragment-ion (m/z)	443.98	452.74	461.90	463.84	465.98	468.13	485.76	492.32	494.42	519.32	533.40	543.03	549.35
Frac. Inten.(% of TIC)	1.31	4.78	1.58	1.35	1.93	1.83	1.62	2.38	12.73	1.23	2.05	7.53	11.66
Rel. Inten.(% of BP)	4.88	17.73	5.88	4.99	7.17	6.81	6.01	8.83	47.24	4.56	7.60	27.95	43.28
Score	1.00	1.00	-0.06	-0.05	-0.07	-0.07	0.50	1.00	1.00	-0.05	0.50	1.00	1.00
Ion-type	$b{+}{+}_6$-H_2O	$b{+}{+}_6$					$y{+}{+}_8$-H_2O	y_4	$y{+}{+}_8$		$b{+}{+}_7$-H_2O	$b{+}{+}_7$	y_5
Delta Da	0.78	0.53					0.56	0.10	0.22		-0.31	0.31	0.11
	$y{+}{+}{+}_{10}$												
	0.14												

Peak 381





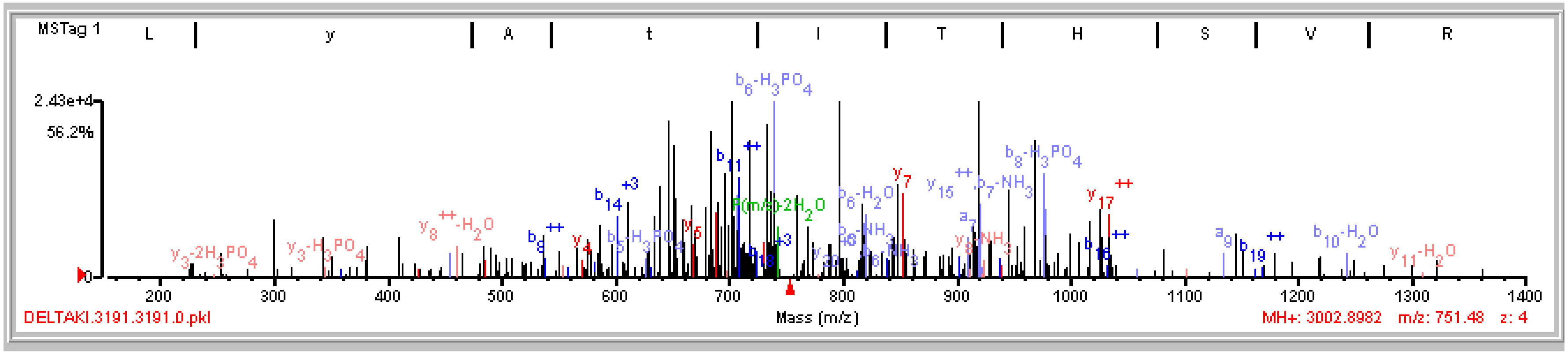


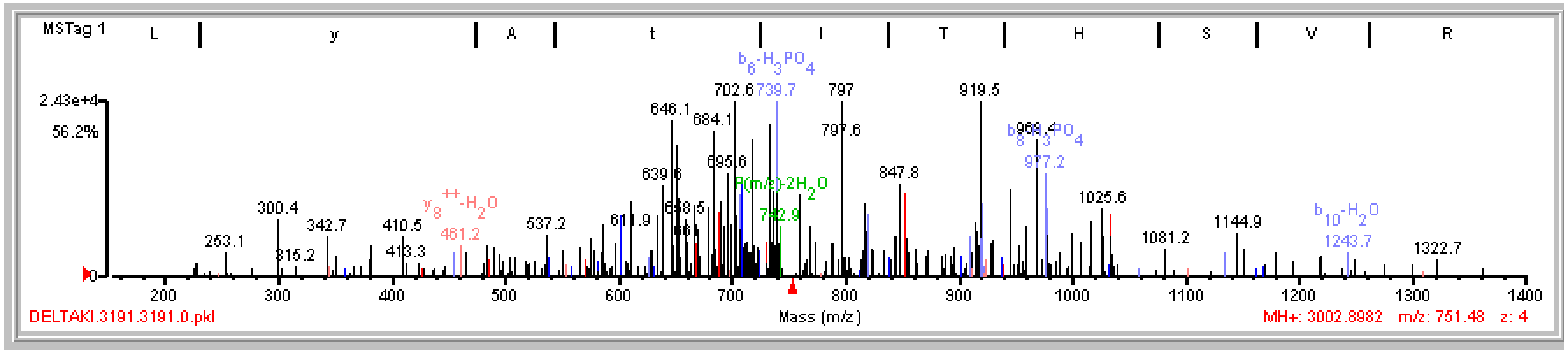
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.94	77.4	7	8/25	T284t Y285y S268s S272s	(R) L S Q N s\V N\L/s P\S|S\H A N N L S V/V t y\S K (G)	2546.28	320.4937	219.2	32871.8/4.43	Homo sapiens	13236514	6522	chromosome 6 open reading frame 106 isoform a

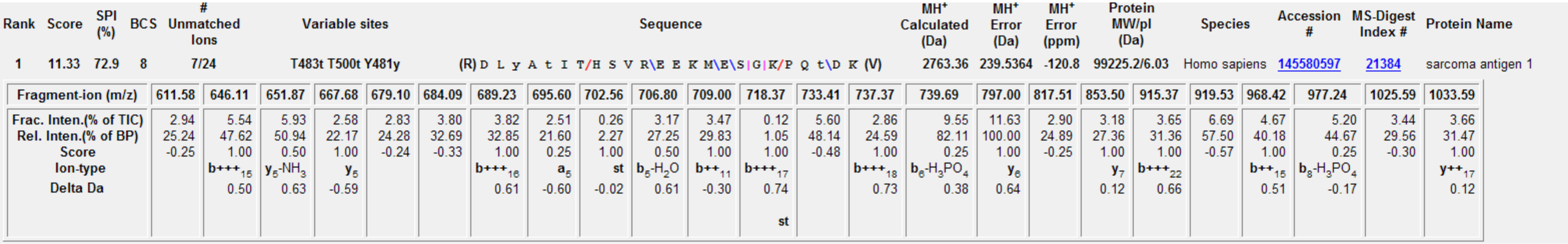
Fragment-ion (m/z)	583.57	592.67	600.49	610.03	610.41	617.08	634.67	644.59	654.19	664.63	668.88	687.09	688.82
Frac. Inten.(% of TIC)	2.32	2.13	3.29	2.06	5.71	2.49	17.29	1.89	2.01	2.47	0.41	2.87	0.13
Rel. Inten.(% of BP)	13.41	12.31	19.02	11.94	33.04	14.40	100.00	10.95	11.60	14.31	2.39	16.61	0.73
Score	-0.13	0.50	1.00	1.00	1.00	-0.14	0.50	1.00	-0.12	-0.14	1.00	1.00	
Ion-type		b_5-NH_3	$b{+}{+}_{10}$	b_5	b_5		$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$ $y{+}{+}{+}_{16}$			st	$b{+}{+}_{12}$	st
Delta Da		-0.53	-0.25	-0.19	0.19		-0.58	0.34 0.34			0.58	-0.68	

Fragment-ion (m/z)	693.15	697.87	702.45	732.37	757.39	790.42	812.85	822.67	823.07	839.57	845.83	878.57
Frac. Inten.(% of TIC)	0.81	2.52	3.01	2.00	5.24	5.50	5.78	2.92	8.52	3.56	12.34	2.72
Rel. Inten.(% of BP)	4.67	14.59	17.39	11.55	30.31	31.82	33.43	16.89	49.28	20.57	71.38	15.72
Score	1.50	-0.15	-0.17	-0.12	1.00	1.00	-0.33	1.00	1.00	0.50	0.25	1.00
Ion-type	sty				y_5	$y{+}{+}_{13}$		b_7	b_7	y_6-NH_3	y_7-H_3PO_4	$b{+}{+}{+}_{22}$
Delta Da	0.35				0.13	0.09		-0.66	-0.26	0.27	0.45	0.23

Peak 382





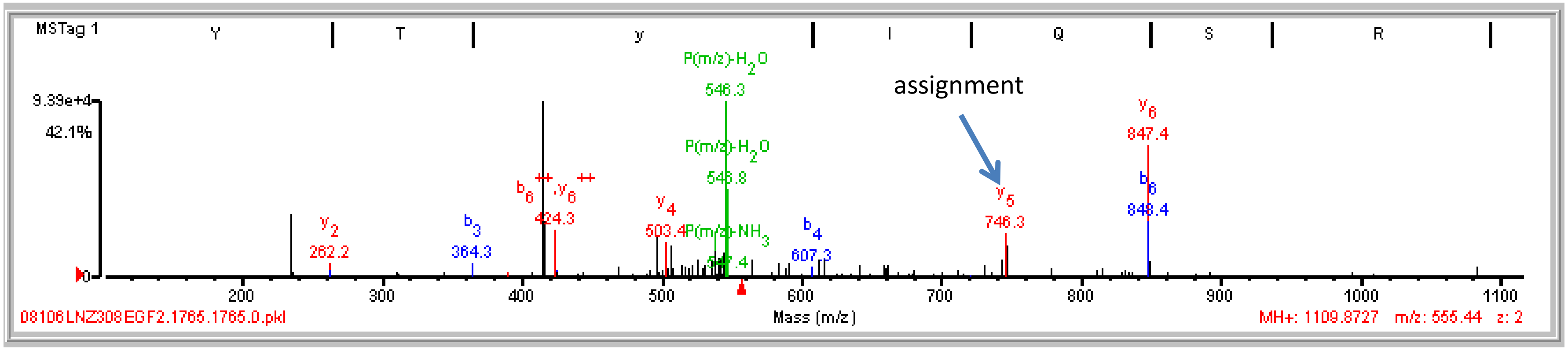


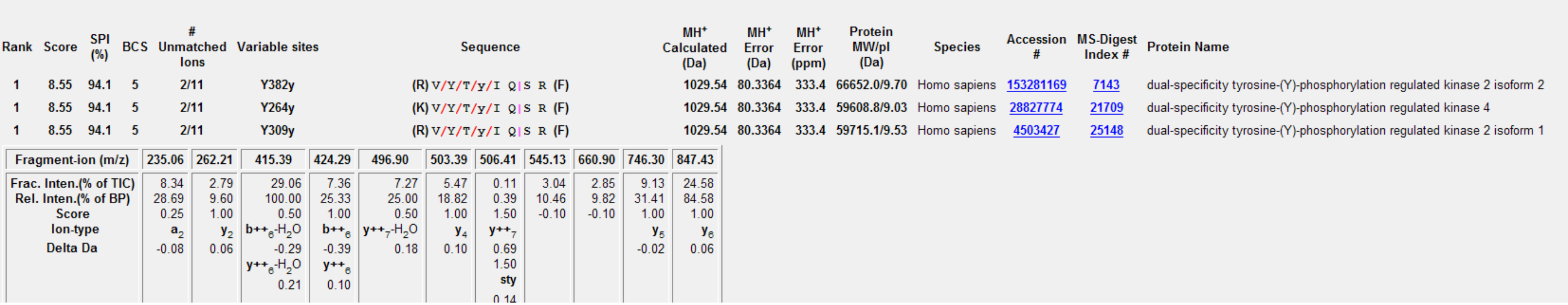
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.33	72.9	8	7/24	T483t T500t Y481y	(R) D L y A t I T/H S V R\E E K M\E\S|G|K/P Q t\D K (V)	2763.36	239.5364	-120.8	99225.2/6.03	Homo sapiens	145580597	21384	sarcoma antigen 1

Fragment-ion (m/z)	611.58	646.11	651.87	667.68	679.10	684.09	689.23	695.60	702.56	706.80	709.00	718.37
Frac. Inten.(% of TIC)	2.94	5.54	5.93	2.58	2.83	3.80	3.82	2.51	0.26	3.17	3.47	0.12
Rel. Inten.(% of BP)	25.24	47.62	50.94	22.17	24.28	32.69	32.85	21.60	2.27	27.25	29.83	1.05
Score	-0.25	1.00	0.50	1.00	-0.24	-0.33	1.00	0.25	1.00	0.50	1.00	1.00
Ion-type		b+++$_{15}$	y_5-NH_3	y_5			b+++$_{16}$	a_5	st	b_5-H_2O	b++$_{11}$	b+++$_{17}$
Delta Da		0.50	0.63	-0.59			0.61	-0.60	-0.02	0.61	-0.30	0.74
												st

Fragment-ion (m/z)	733.41	737.37	739.69	797.00	817.51	853.50	915.37	919.53	968.42	977.24	1025.59	1033.59
Frac. Inten.(% of TIC)	5.60	2.86	9.55	11.63	2.90	3.18	3.65	6.69	4.67	5.20	3.44	3.66
Rel. Inten.(% of BP)	48.14	24.59	82.11	100.00	24.89	27.36	31.36	57.50	40.18	44.67	29.56	31.47
Score	-0.48	1.00	0.25	1.00	-0.25	1.00	1.00	-0.57	1.00	0.25	-0.30	1.00
Ion-type		b+++$_{18}$	b_6-H_3PO_4	y_6		y_7	b+++$_{22}$		b++$_{15}$	b_8-H_3PO_4		y++$_{17}$
Delta Da		0.73	0.38	0.64		0.12	0.66		0.51	-0.17		0.12

Peak 383

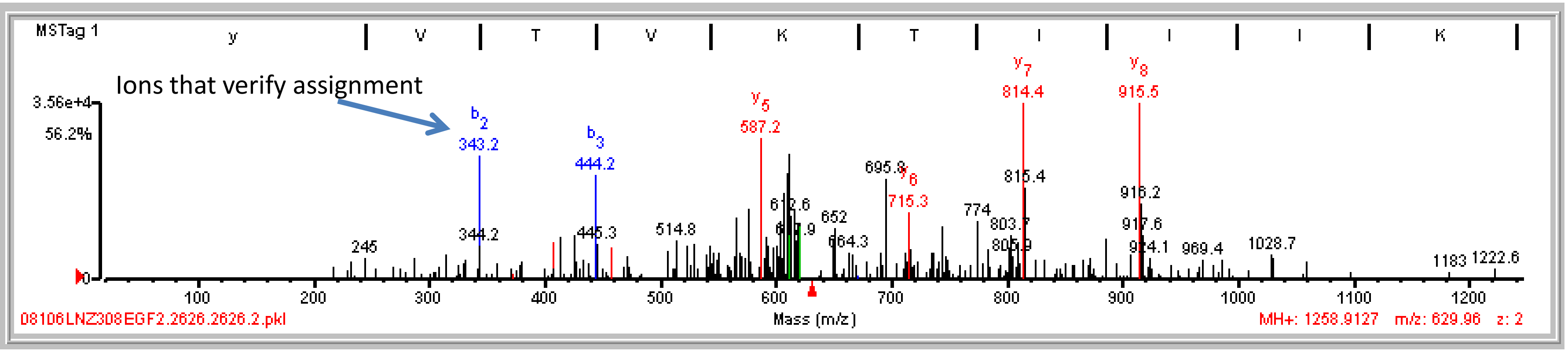


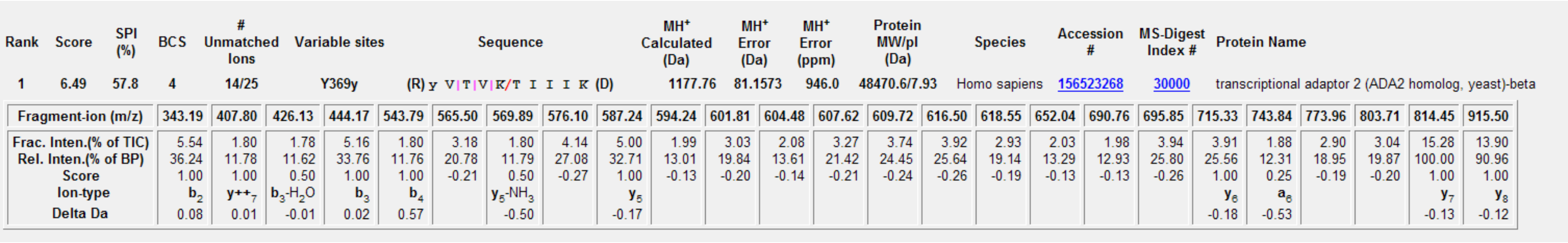


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.55	94.1	5	2/11	Y382y	(R) V/Y/T/y/I Q|S R (F)	1029.54	80.3364	333.4	66652.0/9.70	Homo sapiens	153281169	7143	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 2
1	8.55	94.1	5	2/11	Y264y	(K) V/Y/T/y/I Q|S R (F)	1029.54	80.3364	333.4	59608.8/9.03	Homo sapiens	28827774	21709	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
1	8.55	94.1	5	2/11	Y309y	(R) V/Y/T/y/I Q|S R (F)	1029.54	80.3364	333.4	59715.1/9.53	Homo sapiens	4503427	25148	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1

Fragment-ion (m/z)	235.06	262.21	415.39	424.29	496.90	503.39	506.41	545.13	660.90	746.30	847.43
Frac. Inten.(% of TIC)	8.34	2.79	29.06	7.36	7.27	5.47	0.11	3.04	2.85	9.13	24.58
Rel. Inten.(% of BP)	28.69	9.60	100.00	25.33	25.00	18.82	0.39	10.46	9.82	31.41	84.58
Score	0.25	1.00	0.50	1.00	0.50	1.00	1.50	-0.10	-0.10	1.00	1.00
Ion-type	a_2	y_2	$b{++}_6$-H_2O	$b{++}_6$	$y{++}_7$-H_2O	y_4	$y{++}_7$			y_5	y_6
Delta Da	-0.08	0.06	-0.29	-0.39	0.18	0.10	0.69			-0.02	0.06
			$y{++}_6$-H_2O	$y{++}_6$			1.50				
			0.21	0.10			sty				
							0.14				

Peak 384


Ions that verify assignment

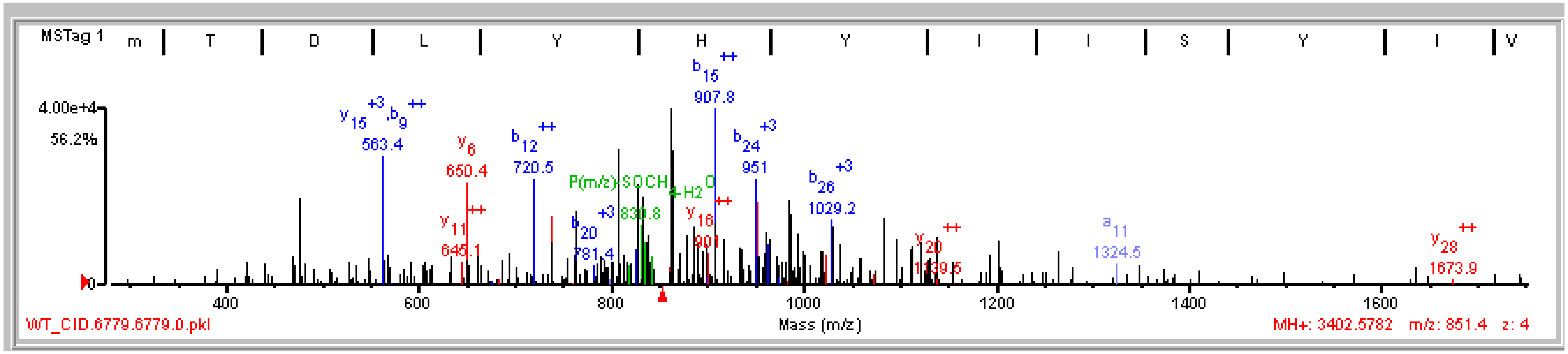


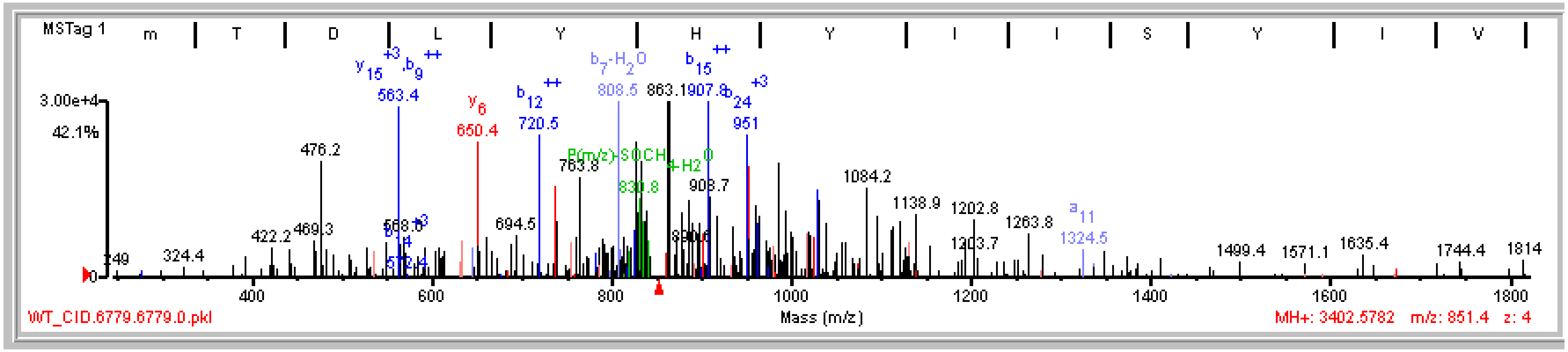
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.49	57.8	4	14/25	Y369y	(R) y V|T|V|K/T I I I K (D)	1177.76	81.1573	946.0	48470.6/7.93	Homo sapiens	156523268	30000	transcriptional adaptor 2 (ADA2 homolog, yeast)-beta

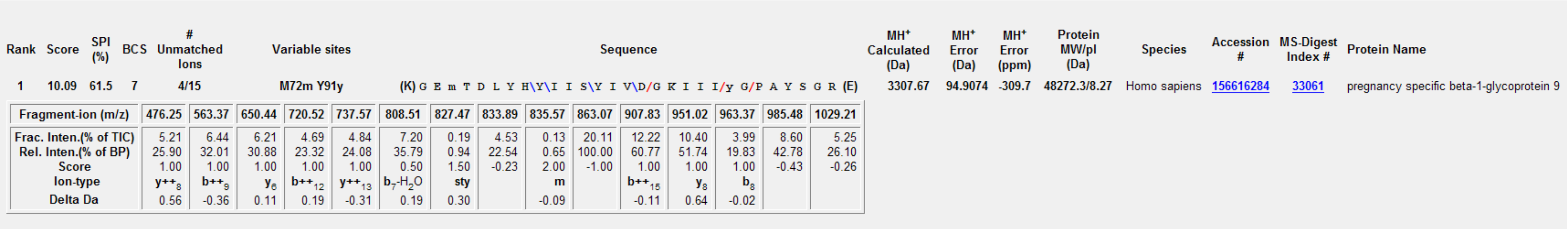
Fragment-ion (m/z)	343.19	407.80	426.13	444.17	543.79	565.50	569.89	576.10	587.24	594.24	601.81	604.48
Frac. Inten.(% of TIC)	5.54	1.80	1.78	5.16	1.80	3.18	1.80	4.14	5.00	1.99	3.03	2.08
Rel. Inten.(% of BP)	36.24	11.78	11.62	33.76	11.76	20.78	11.79	27.08	32.71	13.01	19.84	13.61
Score	1.00	1.00	0.50	1.00	1.00	-0.21	0.50	-0.27	1.00	-0.13	-0.20	-0.14
Ion-type	b_2	$y{+}{+}_7$	b_3-H_2O	b_3	b_4		y_5-NH_3		y_5			
Delta Da	0.08	0.01	-0.01	0.02	0.57		-0.50		-0.17			

Fragment-ion (m/z)	607.62	609.72	616.50	618.55	652.04	690.76	695.85	715.33	743.84	773.96	803.71	814.45	915.50
Frac. Inten.(% of TIC)	3.27	3.74	3.92	2.93	2.03	1.98	3.94	3.91	1.88	2.90	3.04	15.28	13.90
Rel. Inten.(% of BP)	21.42	24.45	25.64	19.14	13.29	12.93	25.80	25.56	12.31	18.95	19.87	100.00	90.96
Score	-0.21	-0.24	-0.26	-0.19	-0.13	-0.13	-0.26	1.00	0.25	-0.19	-0.20	1.00	1.00
Ion-type								y_6	a_6			y_7	y_8
Delta Da								-0.18	-0.53			-0.13	-0.12

Peak 385



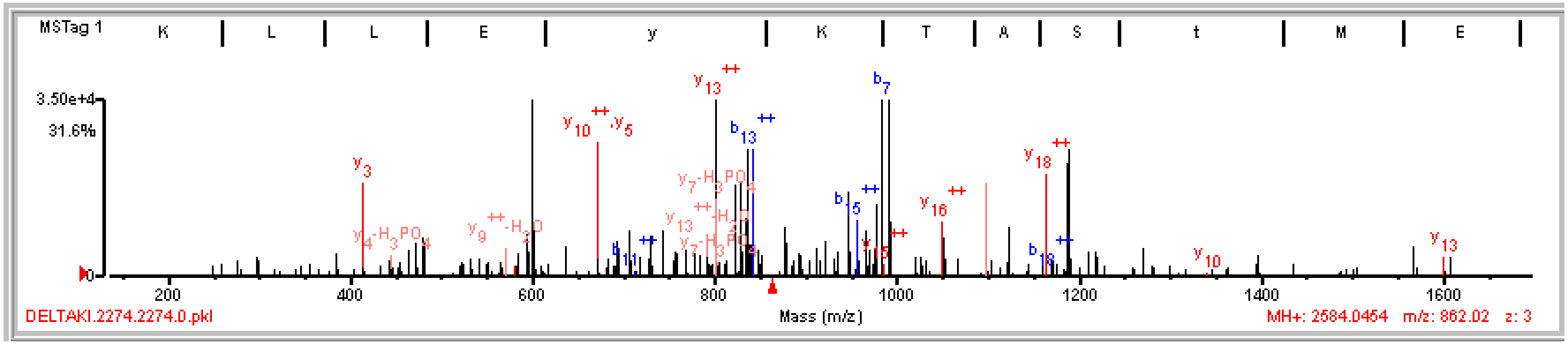


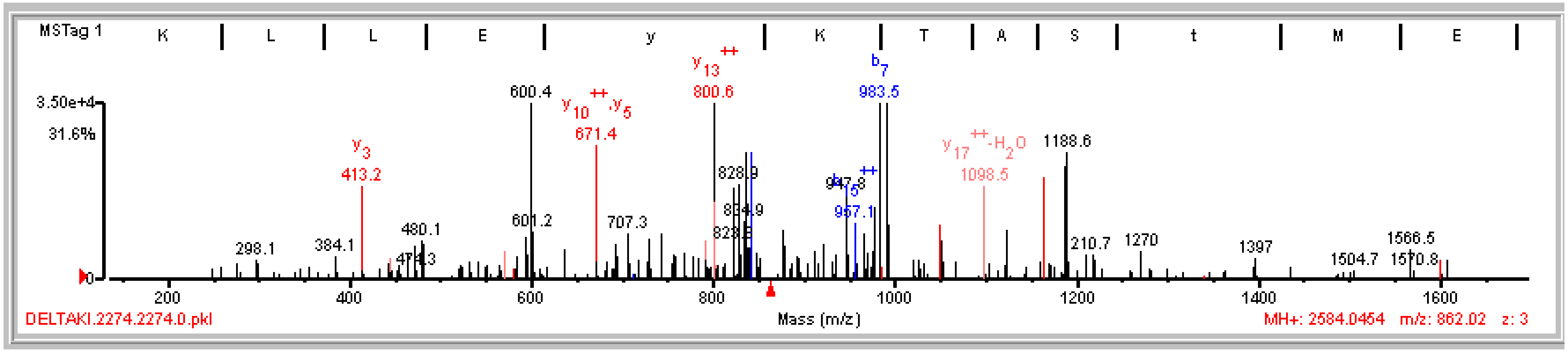


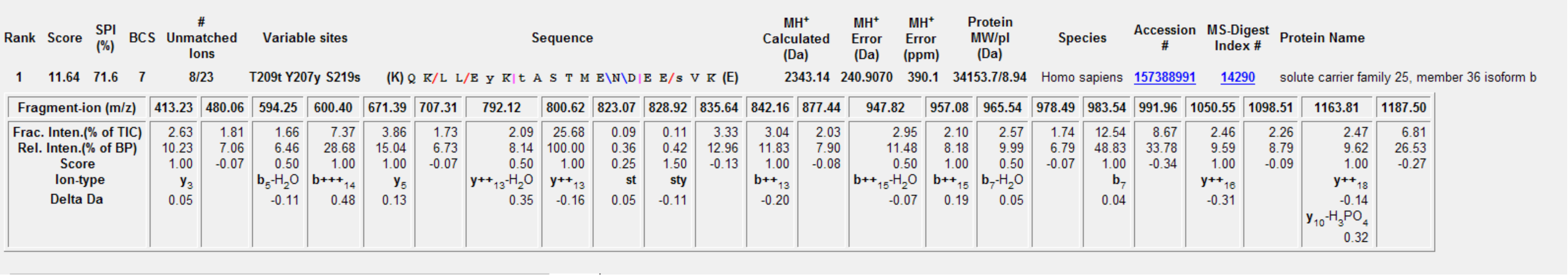
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.09	61.5	7	4/15	M72m Y91y	(K) G E m T D L Y H\Y\I I S\Y I V\D/G K I I I/y G/P A Y S G R (E)	3307.67	94.9074	-309.7	48272.3/8.27	Homo sapiens	156616284	33061	pregnancy specific beta-1-glycoprotein 9

Fragment-ion (m/z)	476.25	563.37	650.44	720.52	737.57	808.51	827.47	833.89	835.57	863.07	907.83	951.02	963.37	985.48	1029.21
Frac. Inten.(% of TIC)	5.21	6.44	6.21	4.69	4.84	7.20	0.19	4.53	0.13	20.11	12.22	10.40	3.99	8.60	5.25
Rel. Inten.(% of BP)	25.90	32.01	30.88	23.32	24.08	35.79	0.94	22.54	0.65	100.00	60.77	51.74	19.83	42.78	26.10
Score	1.00	1.00	1.00	1.00	1.00	0.50	1.50	-0.23	2.00	-1.00	1.00	1.00	1.00	-0.43	-0.26
Ion-type	y++_{8}	b++_{9}	y_6	b++_{12}	y++_{13}	b_7-H_2O	sty		m		b++_{15}	y_8	b_8		
Delta Da	0.56	-0.36	0.11	0.19	-0.31	0.19	0.30		-0.09		-0.11	0.64	-0.02		

Peak 386



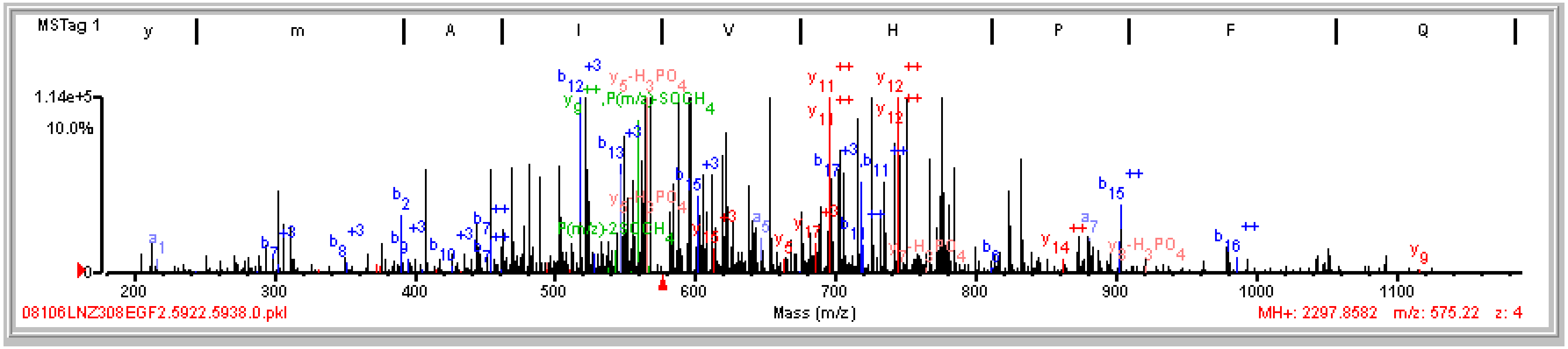


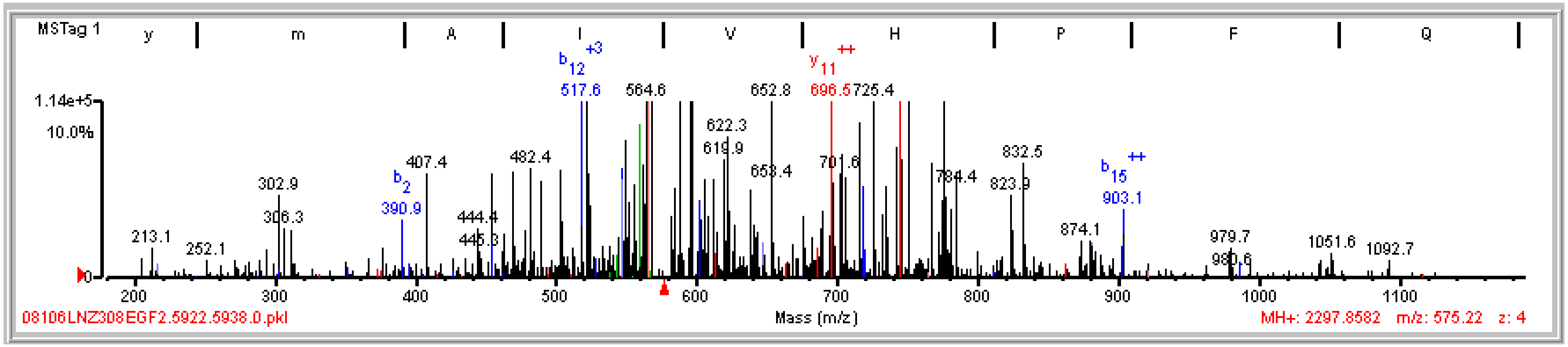


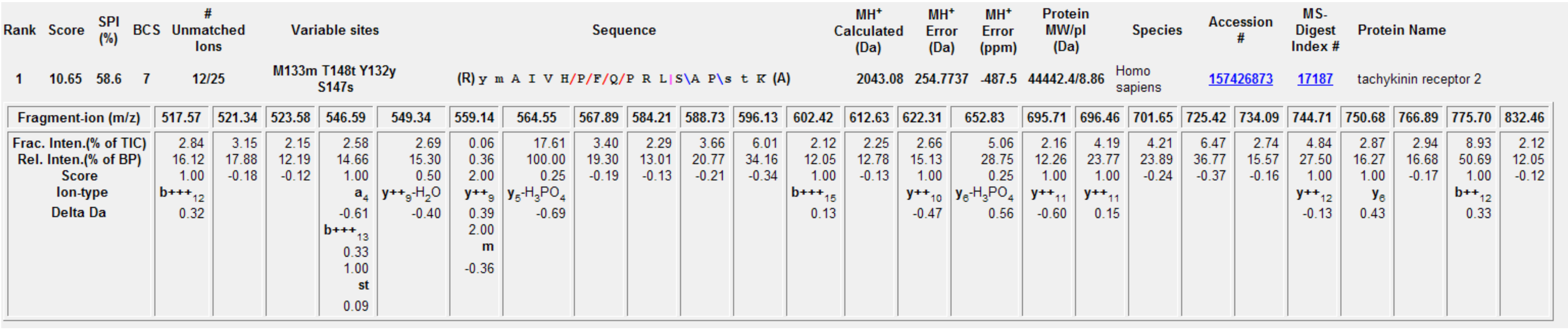
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.64	71.6	7	8/23	T209t Y207y S219s	(K) Q K/L L/E y K|t A S T M E\N\D|E E/s V K (E)	2343.14	240.9070	390.1	34153.7/8.94	Homo sapiens	157388991	14290	solute carrier family 25, member 36 isoform b

Fragment-ion (m/z)	413.23	480.06	594.25	600.40	671.39	707.31	792.12	800.62	823.07	828.92	835.64	842.16	877.44	947.82	957.08	965.54	978.49	983.54	991.96	1050.55	1098.51	1163.81	1187.50
Frac. Inten.(% of TIC)	2.63	1.81	1.66	7.37	3.86	1.73	2.09	25.68	0.09	0.11	3.33	3.04	2.03	2.95	2.10	2.57	1.74	12.54	8.67	2.46	2.26	2.47	6.81
Rel. Inten.(% of BP)	10.23	7.06	6.46	28.68	15.04	6.73	8.14	100.00	0.36	0.42	12.96	11.83	7.90	11.48	8.18	9.99	6.79	48.83	33.78	9.59	8.79	9.62	26.53
Score	1.00	-0.07	0.50	1.00	1.00	-0.07	0.50	1.00	0.25	1.50	-0.13	1.00	-0.08	0.50	1.00	0.50	-0.07	1.00	-0.34	1.00	-0.09	1.00	-0.27
Ion-type	y_3		b_5-H_2O	$b{+}{+}{+}_{14}$	y_5		$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$	st	sty		$b{+}{+}_{13}$		$b{+}{+}_{15}$-H_2O	$b{+}{+}_{15}$	b_7-H_2O		b_7		$y{+}{+}_{16}$		$y{+}{+}_{18}$ -0.14 y_{10}-H_3PO_4	
Delta Da	0.05		-0.11	0.48	0.13		0.35	-0.16	0.05	-0.11		-0.20		-0.07	0.19	0.05		0.04		-0.31		0.32	

Peak 387





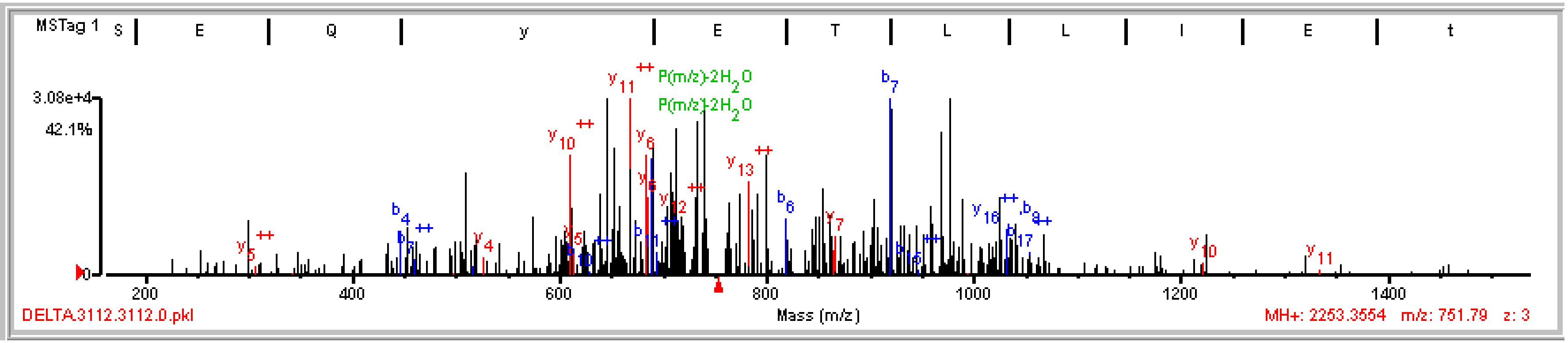


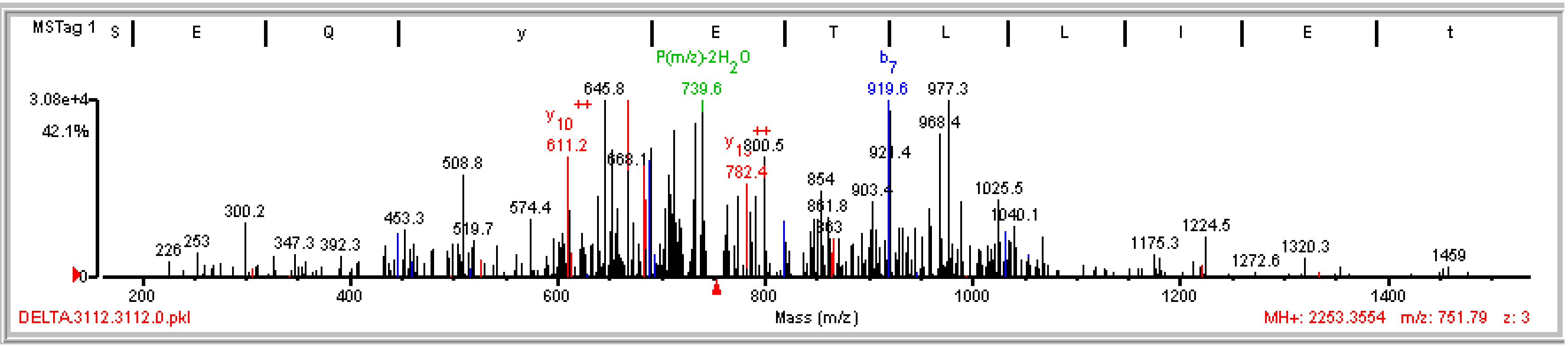
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.65	58.6	7	12/25	M133m T148t Y132y S147s	(R) y m A I V H/P/F/Q/P R L|S\A P\s t K (A)	2043.08	254.7737	-487.5	44442.4/8.86	Homo sapiens	157426873	17187	tachykinin receptor 2

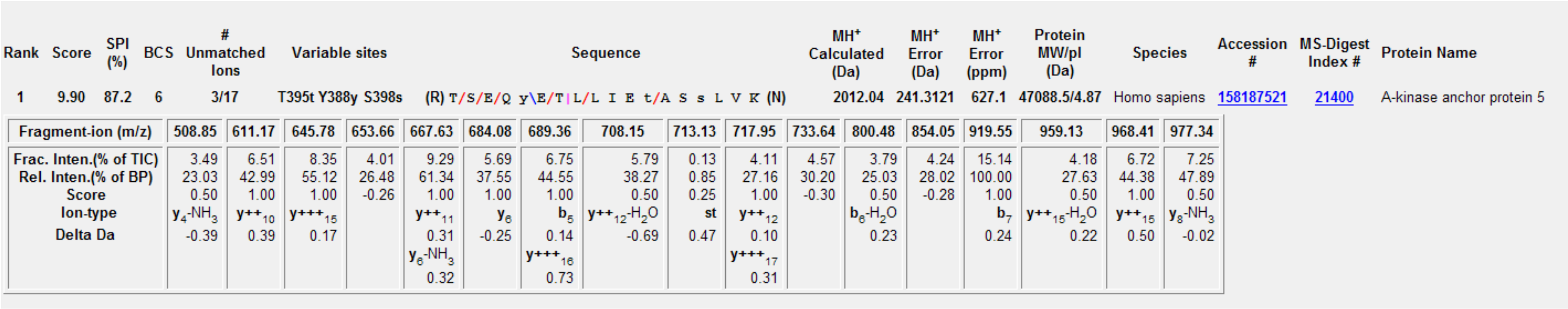
Fragment-ion (m/z)	517.57	521.34	523.58	546.59	549.34	559.14	564.55	567.89	584.21	588.73	596.13	602.42
Frac. Inten.(% of TIC)	2.84	3.15	2.15	2.58	2.69	0.06	17.61	3.40	2.29	3.66	6.01	2.12
Rel. Inten.(% of BP)	16.12	17.88	12.19	14.66	15.30	0.36	100.00	19.30	13.01	20.77	34.16	12.05
Score	1.00	-0.18	-0.12	1.00	0.50	2.00	0.25	-0.19	-0.13	-0.21	-0.34	1.00
Ion-type	b+++$_{12}$			a$_4$	y++$_9$-H$_2$O	y++$_9$	y$_5$-H$_3$PO$_4$					b+++$_{15}$
Delta Da	0.32			-0.61 b+++$_{13}$ 0.33 1.00 st 0.09	-0.40	0.39 2.00 m -0.36	-0.69					0.13

Fragment-ion (m/z)	612.63	622.31	652.83	695.71	696.46	701.65	725.42	734.09	744.71	750.68	766.89	775.70	832.46
Frac. Inten.(% of TIC)	2.25	2.66	5.06	2.16	4.19	4.21	6.47	2.74	4.84	2.87	2.94	8.93	2.12
Rel. Inten.(% of BP)	12.78	15.13	28.75	12.26	23.77	23.89	36.77	15.57	27.50	16.27	16.68	50.69	12.05
Score	-0.13	1.00	0.25	1.00	1.00	-0.24	-0.37	-0.16	1.00	1.00	-0.17	1.00	-0.12
Ion-type		y++$_{10}$	y$_6$-H$_3$PO$_4$	y++$_{11}$	y++$_{11}$				y++$_{12}$	y$_6$		b++$_{12}$	
Delta Da		-0.47	0.56	-0.60	0.15				-0.13	0.43		0.33	

Peak 388



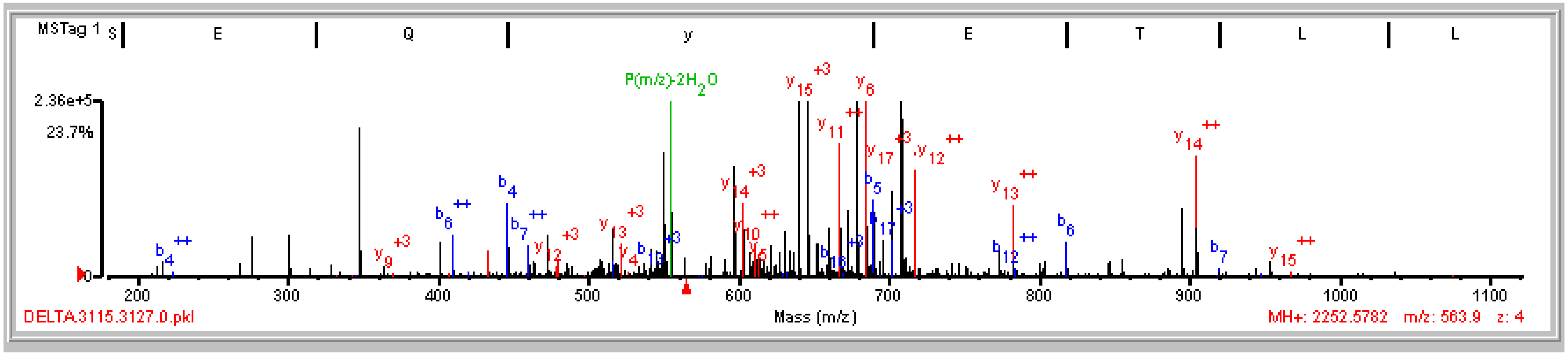


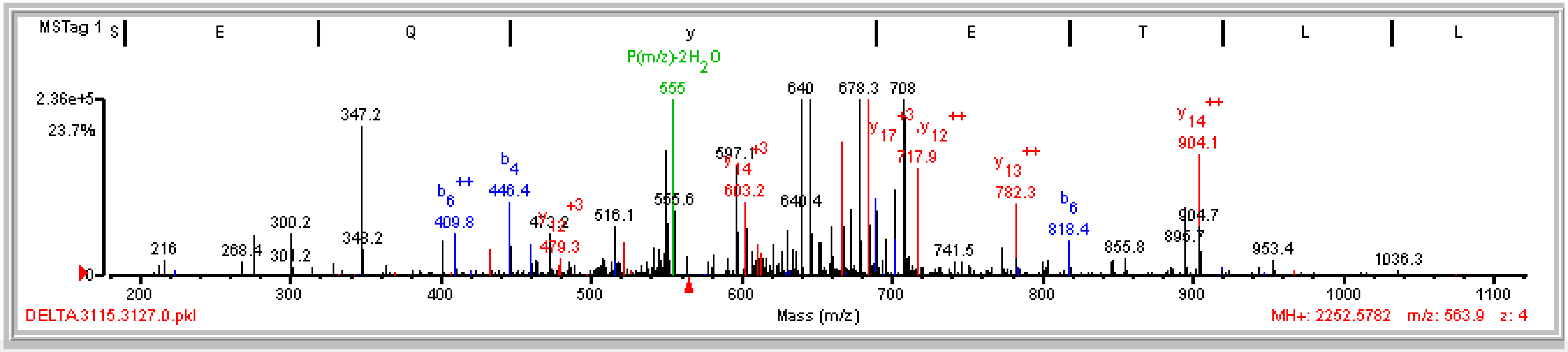


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.90	87.2	6	3/17	T395t Y388y S398s	(R) T/S/E/Q y\E/T|L/L I E t/A S s L V K (N)	2012.04	241.3121	627.1	47088.5/4.87	Homo sapiens	158187521	21400	A-kinase anchor protein 5

Fragment-ion (m/z)	508.85	611.17	645.78	653.66	667.63	684.08	689.36	708.15	713.13	717.95	733.64	800.48	854.05	919.55	959.13	968.41	977.34
Frac. Inten.(% of TIC) Rel. Inten.(% of BP) Score Ion-type Delta Da	3.49 23.03 0.50 y_4-NH_3 -0.39	6.51 42.99 1.00 $y{+}{+}_{10}$ 0.39	8.35 55.12 1.00 $y{+}{+}{+}_{15}$ 0.17	4.01 26.48 -0.26	9.29 61.34 1.00 $y{+}{+}_{11}$ 0.31 y_6-NH_3 0.32	5.69 37.55 1.00 y_6 -0.25	6.75 44.55 1.00 b_5 0.14 $y{+}{+}{+}_{16}$ 0.73	5.79 38.27 0.50 $y{+}{+}_{12}$-H_2O -0.69	0.13 0.85 0.25 st 0.47	4.11 27.16 1.00 $y{+}{+}_{12}$ 0.10 $y{+}{+}{+}_{17}$ 0.31	4.57 30.20 -0.30	3.79 25.03 0.50 b_6-H_2O 0.23	4.24 28.02 -0.28	15.14 100.00 1.00 b_7 0.24	4.18 27.63 0.50 $y{+}{+}_{15}$-H_2O 0.22	6.72 44.38 1.00 $y{+}{+}_{15}$ 0.50	7.25 47.89 0.50 y_8-NH_3 -0.02

Peak 389



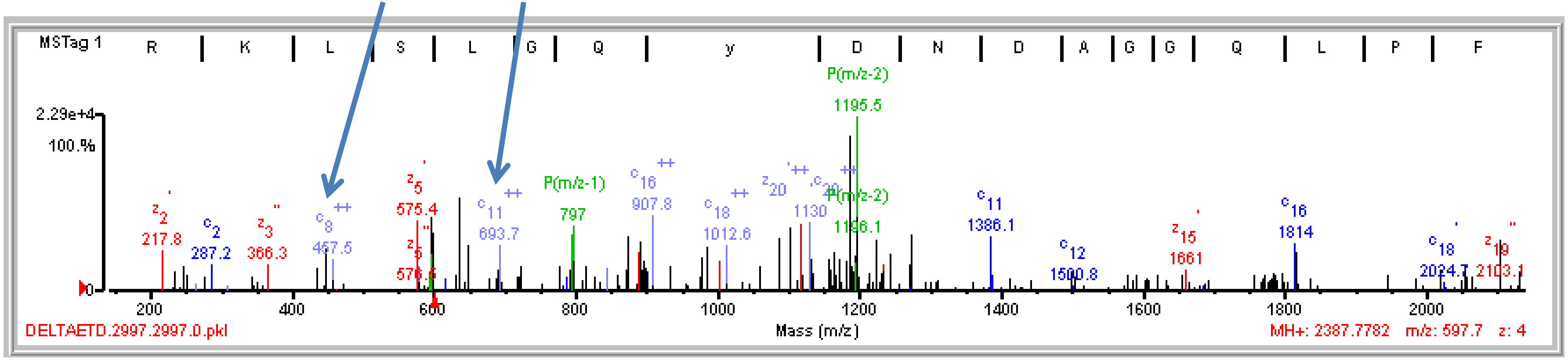


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.06	60.3	9	9/22	T395t Y388y S397s	(R) T/S E/Q|y|E/T/L|L I E t/A/s|S L V K (N)	2012.04	240.5348	282.2	47088.5/4.87	Homo sapiens	158187521	21400	A-kinase anchor protein 5

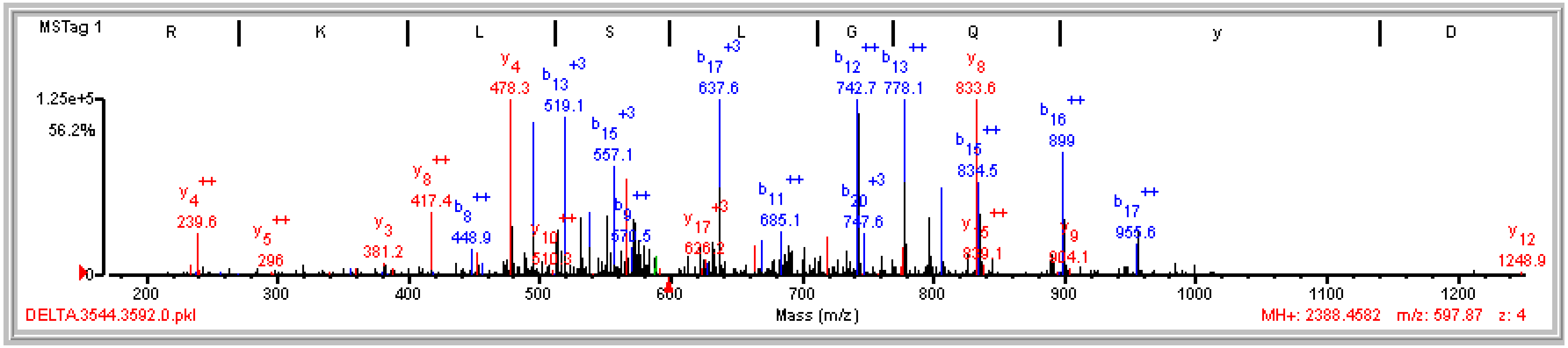
Fragment-ion (m/z)	347.21	446.39	516.09	550.52	597.09	603.17	610.76	613.31	640.02	646.00	659.82	667.57	672.71	678.34	684.33	689.41	701.95	707.98	717.90	782.34	895.16	904.12
Frac. Inten.(% of TIC)	3.38	2.07	1.60	3.95	3.06	2.67	1.47	1.23	5.24	13.68	2.38	4.26	1.55	6.88	20.48	3.00	2.36	9.84	2.16	2.60	2.38	3.74
Rel. Inten.(% of BP)	16.51	10.12	7.82	19.27	14.93	13.01	7.20	6.00	25.56	66.80	11.62	20.81	7.58	33.57	100.00	14.67	11.51	48.04	10.54	12.71	11.64	18.28
Score	-0.17	1.00	1.00	-0.19	-0.15	-0.13	1.00	1.00	-0.26	1.00	-0.12	1.00	0.50	-0.34	1.00	1.00	-0.12	-0.48	1.00	1.00	0.50	1.00
Ion-type		b_4 y_4	$b{+}{+}_8$				$y{+}{+}_{10}$	y_5		$y{+}{+}{+}_{15}$		$y{+}{+}_{11}$ y_6-NH_3	b_5-NH_3		y_6	b_5			$y{+}{+}_{12}$ $y{+}{+}{+}_{17}$	$y{+}{+}_{13}$	$b{+}{+}_{14}$-H_2O $y{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$ $y{+}{+}_{14}$
Delta Da		0.20 0.09	-0.61				-0.02	0.01		0.39		0.25 0.26	0.52		-0.00	0.19			0.05 0.26	-0.03	0.34 0.28	0.29 0.24

Peak 390

Ions that verify assignment



ETD



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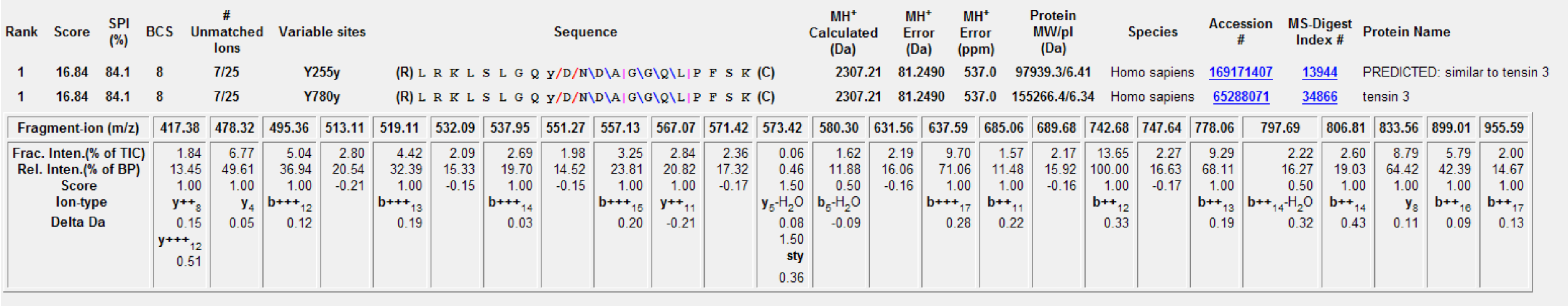
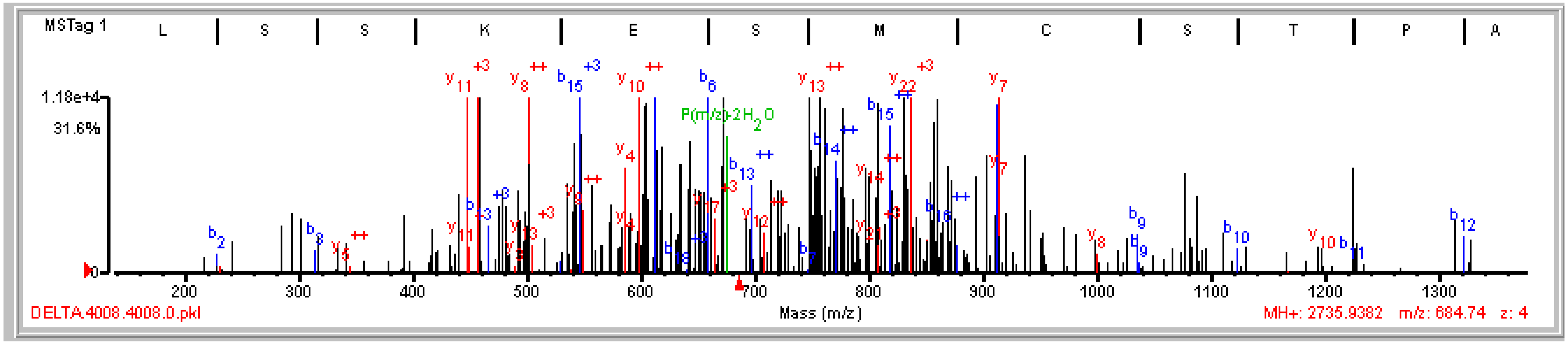


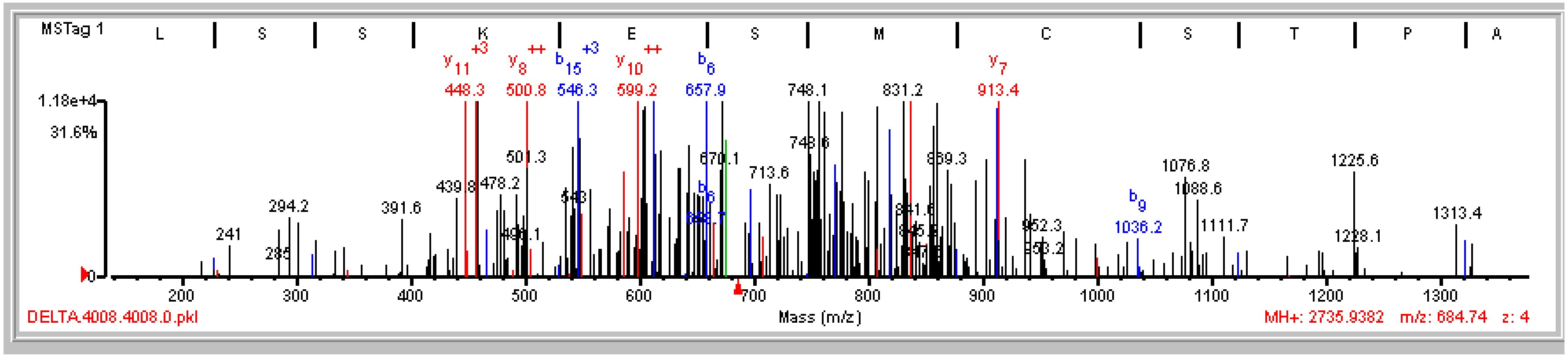
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.84	84.1	8	7/25	Y255y	(R) L R K L S L G Q y/D/N\D\A|G\G\Q\L|P F S K (C)	2307.21	81.2490	537.0	97939.3/6.41	Homo sapiens	169171407	13944	PREDICTED: similar to tensin 3
1	16.84	84.1	8	7/25	Y780y	(R) L R K L S L G Q y/D/N\D\A|G\G\Q\L|P F S K (C)	2307.21	81.2490	537.0	155266.4/6.34	Homo sapiens	65288071	34866	tensin 3

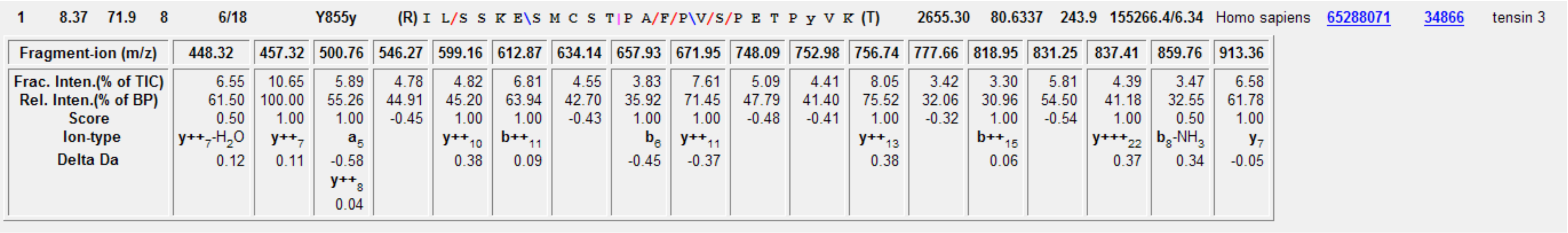
Fragment-ion (m/z)	417.38	478.32	495.36	513.11	519.11	532.09	537.95	551.27	557.13	567.07	571.42	573.42
Frac. Inten.(% of TIC)	1.84	6.77	5.04	2.80	4.42	2.09	2.69	1.98	3.25	2.84	2.36	0.06
Rel. Inten.(% of BP)	13.45	49.61	36.94	20.54	32.39	15.33	19.70	14.52	23.81	20.82	17.32	0.46
Score	1.00	1.00	1.00	-0.21	1.00	-0.15	1.00	-0.15	1.00	1.00	-0.17	1.50 1.50
Ion-type	$y{+}{+}_{8}$ $y{+}{+}{+}_{12}$	y_{4}	$b{+}{+}{+}_{12}$		$b{+}{+}{+}_{13}$		$b{+}{+}{+}_{14}$		$b{+}{+}{+}_{15}$	$y{+}{+}_{11}$		y_{5}-H_2O sty
Delta Da	0.15 0.51	0.05	0.12		0.19		0.03		0.20	-0.21		0.08 0.36

Fragment-ion (m/z)	580.30	631.56	637.59	685.06	689.68	742.68	747.64	778.06	797.69	806.81	833.56	899.01	955.59
Frac. Inten.(% of TIC)	1.62	2.19	9.70	1.57	2.17	13.65	2.27	9.29	2.22	2.60	8.79	5.79	2.00
Rel. Inten.(% of BP)	11.88	16.06	71.06	11.48	15.92	100.00	16.63	68.11	16.27	19.03	64.42	42.39	14.67
Score	0.50	-0.16	1.00	1.00	-0.16	1.00	-0.17	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type	b_{5}-H_2O		$b{+}{+}{+}_{17}$	$b{+}{+}_{11}$		$b{+}{+}_{12}$		$b{+}{+}_{13}$	$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$	y_{8}	$b{+}{+}_{16}$	$b{+}{+}_{17}$
Delta Da	-0.09		0.28	0.22		0.33		0.19	0.32	0.43	0.11	0.09	0.13

Peak 391



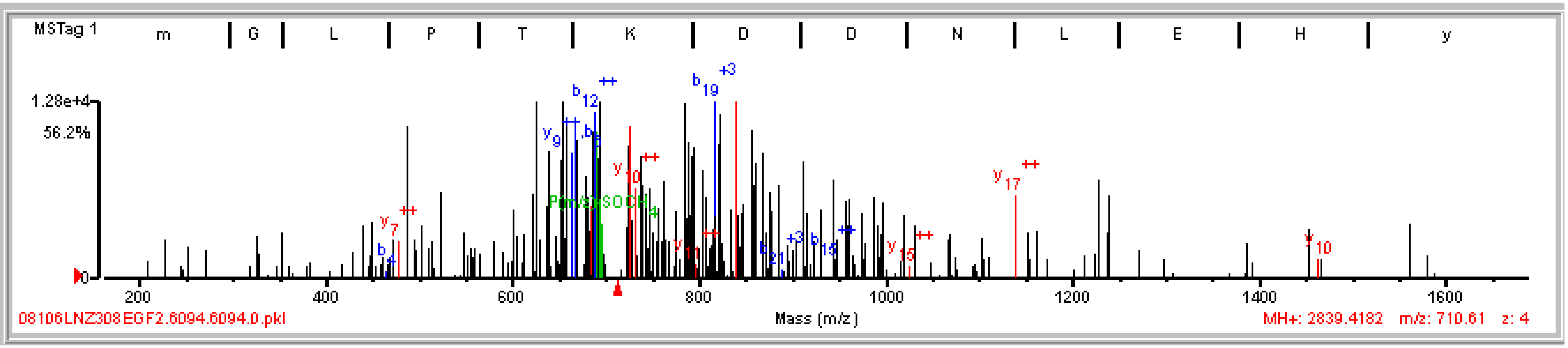


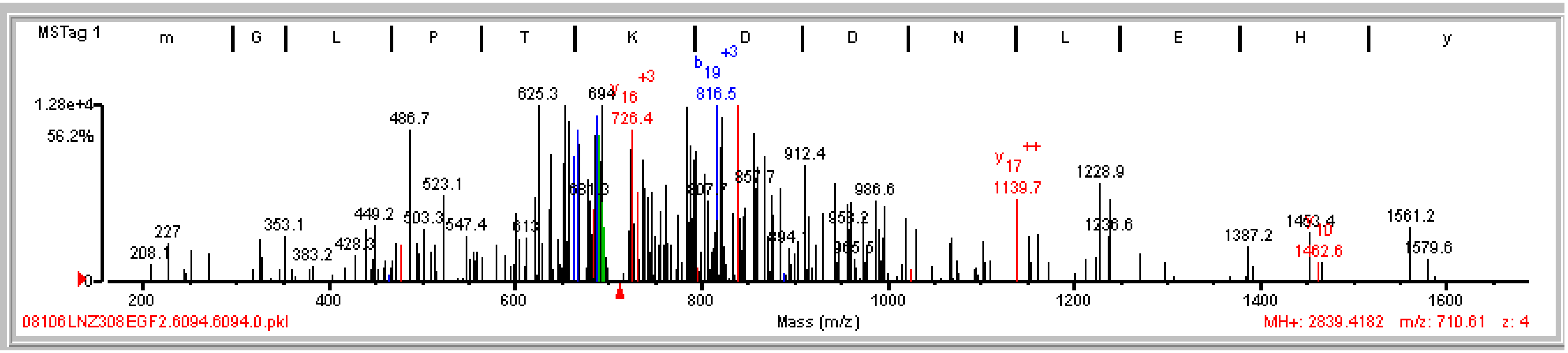


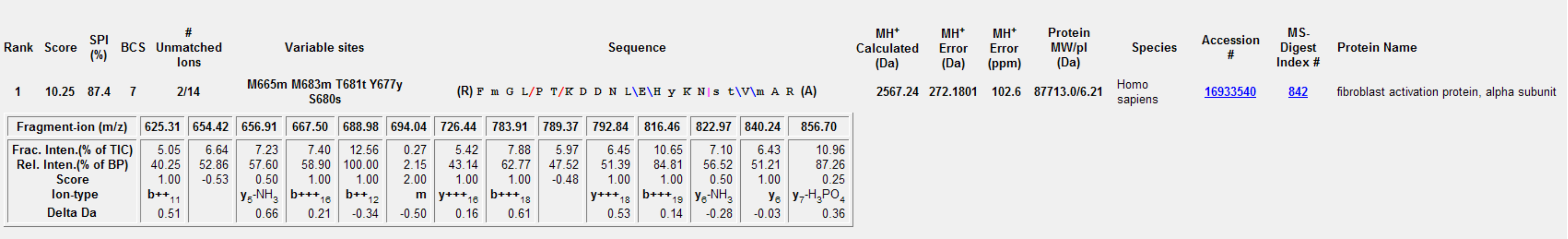
1 8.37 71.9 8 6/18 Y855y (R) I L/S S K E\S M C S T|P A/F/P\V/S/P E T P y V K (T) 2655.30 80.6337 243.9 155266.4/6.34 Homo sapiens 65288071 34866 tensin 3

Fragment-ion (m/z)	448.32	457.32	500.76	546.27	599.16	612.87	634.14	657.93	671.95	748.09	752.98	756.74	777.66	818.95	831.25	837.41	859.76	913.36
Frac. Inten.(% of TIC)	6.55	10.65	5.89	4.78	4.82	6.81	4.55	3.83	7.61	5.09	4.41	8.05	3.42	3.30	5.81	4.39	3.47	6.58
Rel. Inten.(% of BP)	61.50	100.00	55.26	44.91	45.20	63.94	42.70	35.92	71.45	47.79	41.40	75.52	32.06	30.96	54.50	41.18	32.55	61.78
Score	0.50	1.00	1.00	-0.45	1.00	1.00	-0.43	1.00	1.00	-0.48	-0.41	1.00	-0.32	1.00	-0.54	1.00	0.50	1.00
Ion-type	y++$_7$-H$_2$O	y++$_7$	a$_5$ y++$_8$		y++$_{10}$	b++$_{11}$		b$_6$	y++$_{11}$			y++$_{13}$		b++$_{15}$		y+++$_{22}$	b$_8$-NH$_3$	y$_7$
Delta Da	0.12	0.11	-0.58 0.04		0.38	0.09		-0.45	-0.37			0.38		0.06		0.37	0.34	-0.05

Peak 392



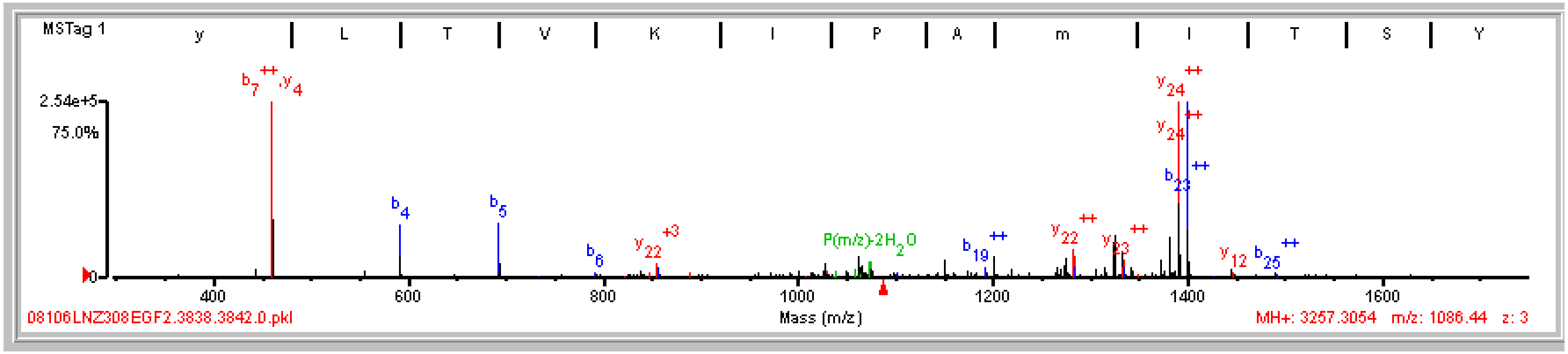


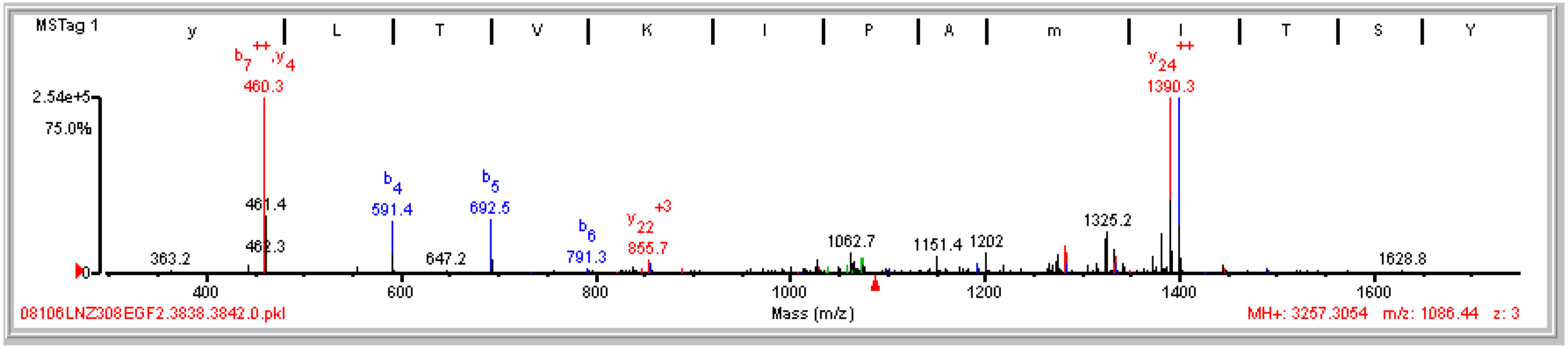


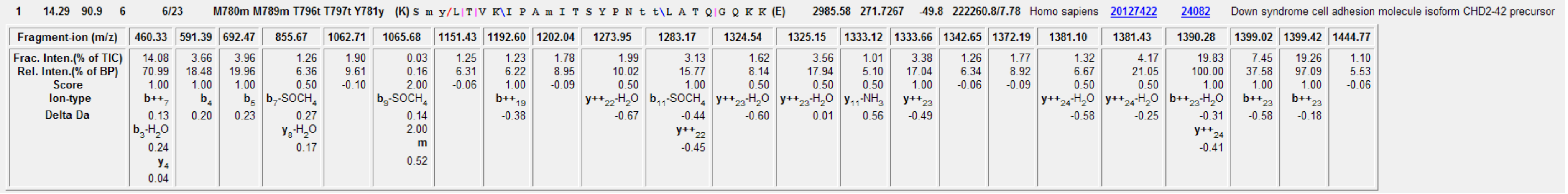
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.25	87.4	7	2/14	M665m M683m T681t Y677y S680s	(R) F m G L/P T/K D D N L\E\H y K N|s t\V\m A R (A)	2567.24	272.1801	102.6	87713.0/6.21	Homo sapiens	16933540	842	fibroblast activation protein, alpha subunit

Fragment-ion (m/z)	625.31	654.42	656.91	667.50	688.98	694.04	726.44	783.91	789.37	792.84	816.46	822.97	840.24	856.70
Frac. Inten.(% of TIC)	5.05	6.64	7.23	7.40	12.56	0.27	5.42	7.88	5.97	6.45	10.65	7.10	6.43	10.96
Rel. Inten.(% of BP)	40.25	52.86	57.60	58.90	100.00	2.15	43.14	62.77	47.52	51.39	84.81	56.52	51.21	87.26
Score	1.00	-0.53	0.50	1.00	1.00	2.00	1.00	1.00	-0.48	1.00	1.00	0.50	1.00	0.25
Ion-type	b^{++}_{11}		y_5-NH_3	b^{+++}_{16}	b^{++}_{12}	m	y^{+++}_{16}	b^{+++}_{18}		y^{+++}_{18}	b^{+++}_{19}	y_6-NH_3	y_6	y_7-H_3PO_4
Delta Da	0.51		0.66	0.21	-0.34	-0.50	0.16	0.61		0.53	0.14	-0.28	-0.03	0.36

Peak 393



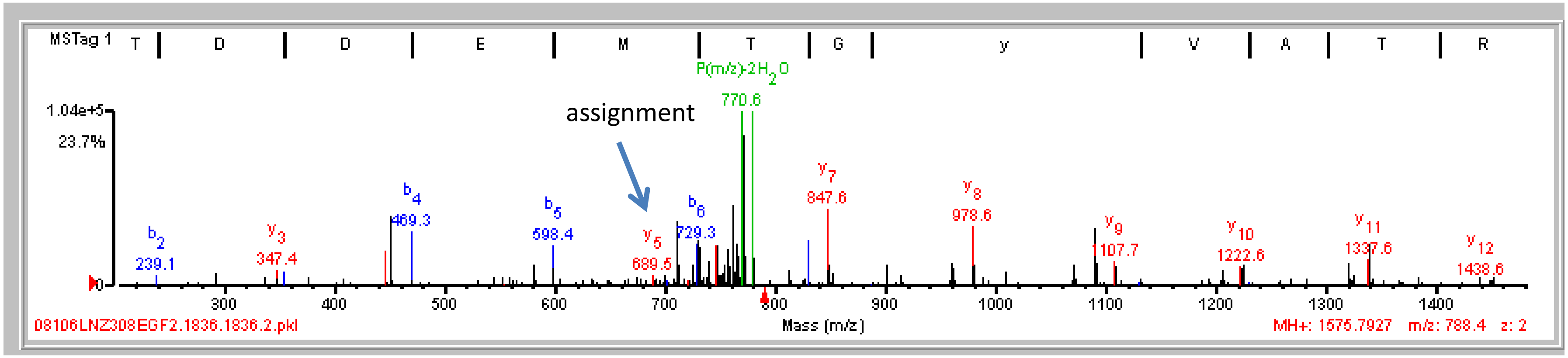


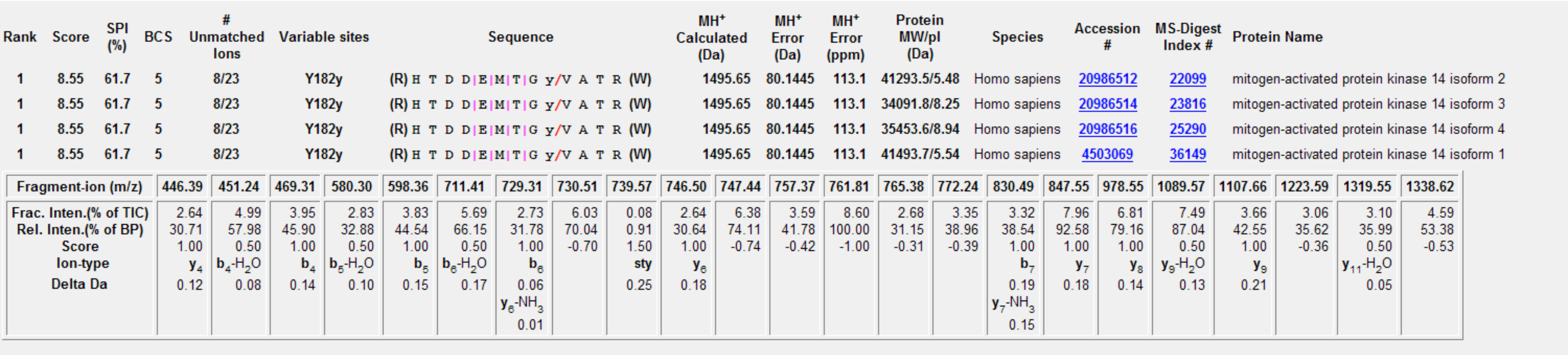


1 14.29 90.9 6 6/23 M780m M789m T796t T797t Y781y (K) S m y/L|T|V K\I P A m I T S Y P N t t\L A T Q|G Q K K (E) 2985.58 271.7267 -49.8 222260.8/7.78 Homo sapiens 20127422 24082 Down syndrome cell adhesion molecule isoform CHD2-42 precursor

Fragment-ion (m/z)	460.33	591.39	692.47	855.67	1062.71	1065.68	1151.43	1192.60	1202.04	1273.95	1283.17	1324.54	1325.15	1333.12	1333.66	1342.65	1372.19	1381.10	1381.43	1390.28	1399.02	1399.42	1444.77
Frac. Inten.(% of TIC)	14.08	3.66	3.96	1.26	1.90	0.03	1.25	1.23	1.78	1.99	3.13	1.62	3.56	1.01	3.38	1.26	1.77	1.32	4.17	19.83	7.45	19.26	1.10
Rel. Inten.(% of BP)	70.99	18.48	19.96	6.36	9.61	0.16	6.31	6.22	8.95	10.02	15.77	8.14	17.94	5.10	17.04	6.34	8.92	6.67	21.05	100.00	37.58	97.09	5.53
Score	1.00	1.00	1.00	0.50	-0.10	2.00	-0.06	1.00	-0.09	0.50	1.00	0.50	0.50	0.50	1.00	-0.06	-0.09	0.50	0.50	1.00	1.00	1.00	-0.06
Ion-type	$b{+}{+}_{7}$	b_4	b_5	$b_7\text{-SOCH}_4$		$b_9\text{-SOCH}_4$		$b{+}{+}_{19}$		$y{+}{+}_{22}\text{-H}_2\text{O}$	$b_{11}\text{-SOCH}_4$	$y{+}{+}_{23}\text{-H}_2\text{O}$	$y{+}{+}_{23}\text{-H}_2\text{O}$	$y_{11}\text{-NH}_3$	$y{+}{+}_{23}$			$y{+}{+}_{24}\text{-H}_2\text{O}$	$y{+}{+}_{24}\text{-H}_2\text{O}$	$b{+}{+}_{23}\text{-H}_2\text{O}$	$b{+}{+}_{23}$	$b{+}{+}_{23}$	
Delta Da	0.13 $b_3\text{-H}_2\text{O}$ 0.24 y_4 0.04	0.20	0.23	0.27 $y_8\text{-H}_2\text{O}$ 0.17		0.14 2.00 m 0.52		-0.38		-0.67	-0.44 $y{+}{+}_{22}$ -0.45	-0.60	0.01	0.56	-0.49			-0.58	-0.25	-0.31 $y{+}{+}_{24}$ -0.41	-0.58	-0.18	

Peak 394

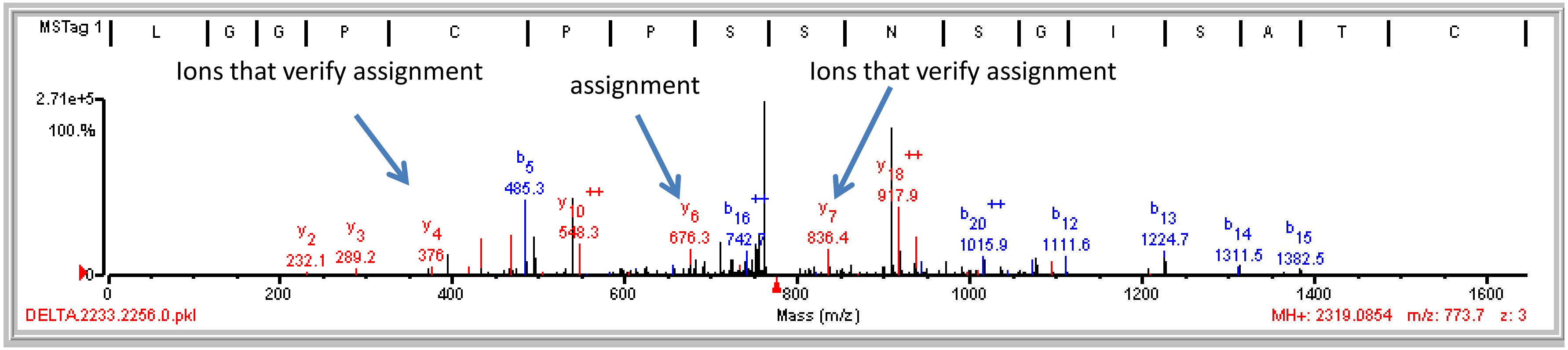




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.55	61.7	5	8/23	Y182y	(R) H T D D|E|M|T|G y/V A T R (W)	1495.65	80.1445	113.1	41293.5/5.48	Homo sapiens	20986512	22099	mitogen-activated protein kinase 14 isoform 2
1	8.55	61.7	5	8/23	Y182y	(R) H T D D|E|M|T|G y/V A T R (W)	1495.65	80.1445	113.1	34091.8/8.25	Homo sapiens	20986514	23816	mitogen-activated protein kinase 14 isoform 3
1	8.55	61.7	5	8/23	Y182y	(R) H T D D|E|M|T|G y/V A T R (W)	1495.65	80.1445	113.1	35453.6/8.94	Homo sapiens	20986516	25290	mitogen-activated protein kinase 14 isoform 4
1	8.55	61.7	5	8/23	Y182y	(R) H T D D|E|M|T|G y/V A T R (W)	1495.65	80.1445	113.1	41493.7/5.54	Homo sapiens	4503069	36149	mitogen-activated protein kinase 14 isoform 1

Fragment-ion (m/z)	446.39	451.24	469.31	580.30	598.36	711.41	729.31	730.51	739.57	746.50	747.44	757.37	761.81	765.38	772.24	830.49	847.55	978.55	1089.57	1107.66	1223.59	1319.55	1338.62
Frac. Inten.(% of TIC)	2.64	4.99	3.95	2.83	3.83	5.69	2.73	6.03	0.08	2.64	6.38	3.59	8.60	2.68	3.35	3.32	7.96	6.81	7.49	3.66	3.06	3.10	4.59
Rel. Inten.(% of BP)	30.71	57.98	45.90	32.88	44.54	66.15	31.78	70.04	0.91	30.64	74.11	41.78	100.00	31.15	38.96	38.54	92.58	79.16	87.04	42.55	35.62	35.99	53.38
Score	1.00	0.50	1.00	0.50	1.00	0.50	1.00	-0.70	1.50	1.00	-0.74	-0.42	-1.00	-0.31	-0.39	1.00	1.00	1.00	0.50	1.00	-0.36	0.50	-0.53
Ion-type	y_4	b_4-H_2O	b_4	b_5-H_2O	b_5	b_6-H_2O	b_6 y_6-NH_3		sty	y_6						b_7 y_7-NH_3	y_7	y_8	y_9-H_2O	y_9		y_{11}-H_2O	
Delta Da	0.12	0.08	0.14	0.10	0.15	0.17	0.06 0.01		0.25	0.18						0.19 0.15	0.18	0.14	0.13	0.21		0.05	

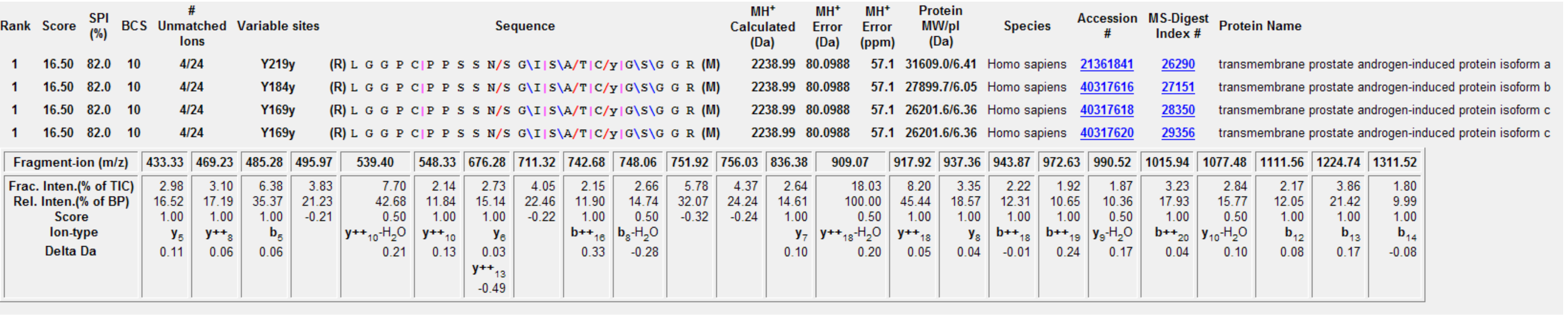
Peak 395



Ions that verify assignment

assignment

Ions that verify assignment

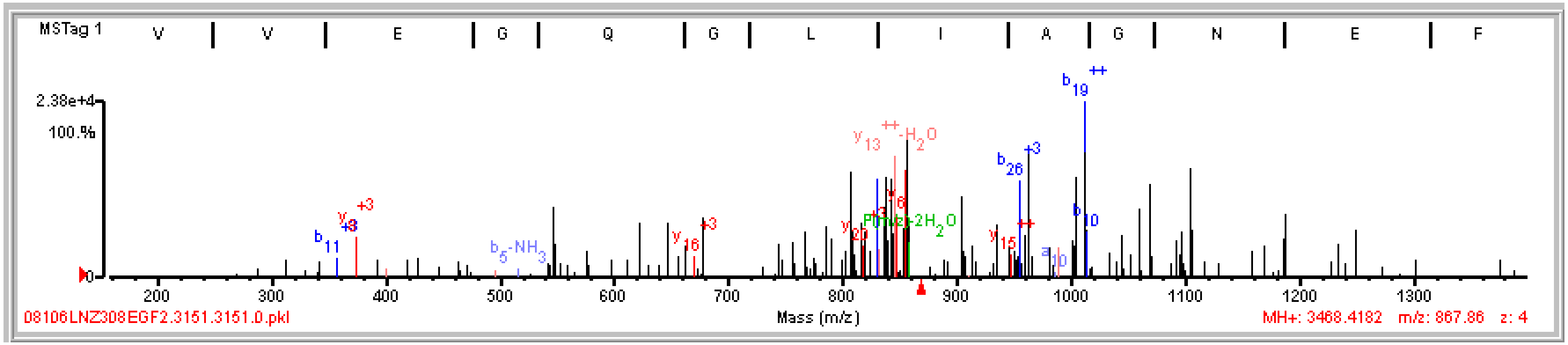


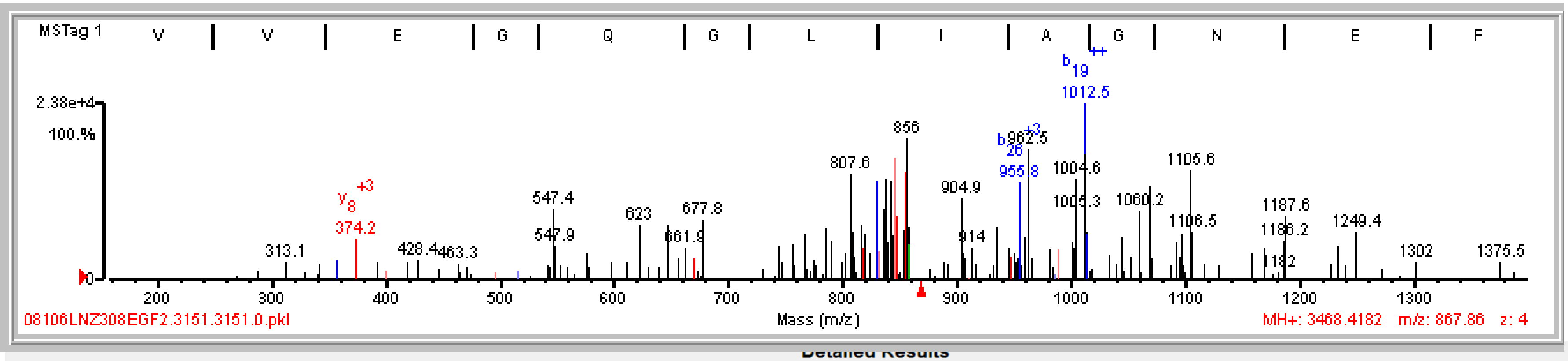
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.50	82.0	10	4/24	Y219y	(R) L G G P C|P P S S N/S G\I|S\A/T|C/y|G\S\G G R (M)	2238.99	80.0988	57.1	31609.0/6.41	Homo sapiens	21361841	26290	transmembrane prostate androgen-induced protein isoform a
1	16.50	82.0	10	4/24	Y184y	(R) L G G P C|P P S S N/S G\I|S\A/T|C/y|G\S\G G R (M)	2238.99	80.0988	57.1	27899.7/6.05	Homo sapiens	40317616	27151	transmembrane prostate androgen-induced protein isoform b
1	16.50	82.0	10	4/24	Y169y	(R) L G G P C|P P S S N/S G\I|S\A/T|C/y|G\S\G G R (M)	2238.99	80.0988	57.1	26201.6/6.36	Homo sapiens	40317618	28350	transmembrane prostate androgen-induced protein isoform c
1	16.50	82.0	10	4/24	Y169y	(R) L G G P C|P P S S N/S G\I|S\A/T|C/y|G\S\G G R (M)	2238.99	80.0988	57.1	26201.6/6.36	Homo sapiens	40317620	29356	transmembrane prostate androgen-induced protein isoform c

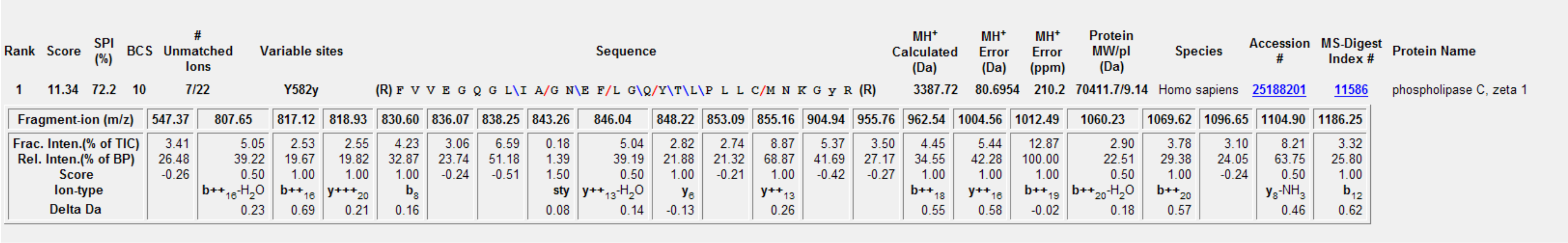
Fragment-ion (m/z)	433.33	469.23	485.28	495.97	539.40	548.33	676.28	711.32	742.68	748.06	751.92	756.03
Frac. Inten.(% of TIC)	2.98	3.10	6.38	3.83	7.70	2.14	2.73	4.05	2.15	2.66	5.78	4.37
Rel. Inten.(% of BP)	16.52	17.19	35.37	21.23	42.68	11.84	15.14	22.46	11.90	14.74	32.07	24.24
Score	1.00	1.00	1.00	-0.21	0.50	1.00	1.00	-0.22	1.00	0.50	-0.32	-0.24
Ion-type	y_5	$y{++}_8$	b_5		$y{++}_{10}$-H_2O	$y{++}_{10}$	y_6		$b{++}_{16}$	b_8-H_2O		
Delta Da	0.11	0.06	0.06		0.21	0.13	0.03 $y{++}_{13}$ -0.49		0.33	-0.28		

Fragment-ion (m/z)	836.38	909.07	917.92	937.36	943.87	972.63	990.52	1015.94	1077.48	1111.56	1224.74	1311.52
Frac. Inten.(% of TIC)	2.64	18.03	8.20	3.35	2.22	1.92	1.87	3.23	2.84	2.17	3.86	1.80
Rel. Inten.(% of BP)	14.61	100.00	45.44	18.57	12.31	10.65	10.36	17.93	15.77	12.05	21.42	9.99
Score	1.00	0.50	1.00	1.00	1.00	1.00	0.50	1.00	0.50	1.00	1.00	1.00
Ion-type	y_7	$y{++}_{18}$-H_2O	$y{++}_{18}$	y_8	$b{++}_{18}$	$b{++}_{19}$	y_9-H_2O	$b{++}_{20}$	y_{10}-H_2O	b_{12}	b_{13}	b_{14}
Delta Da	0.10	0.20	0.05	0.04	-0.01	0.24	0.17	0.04	0.10	0.08	0.17	-0.08

Peak 396





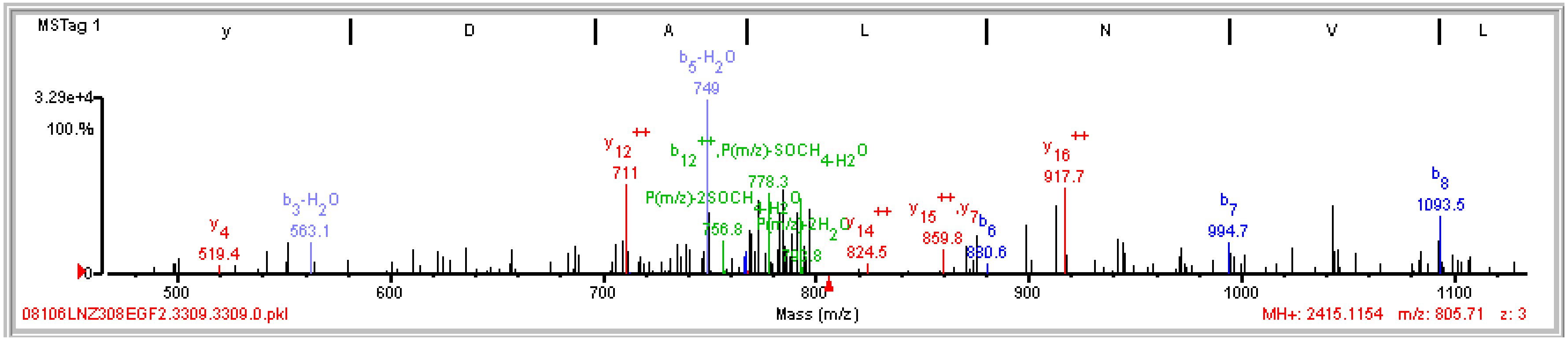


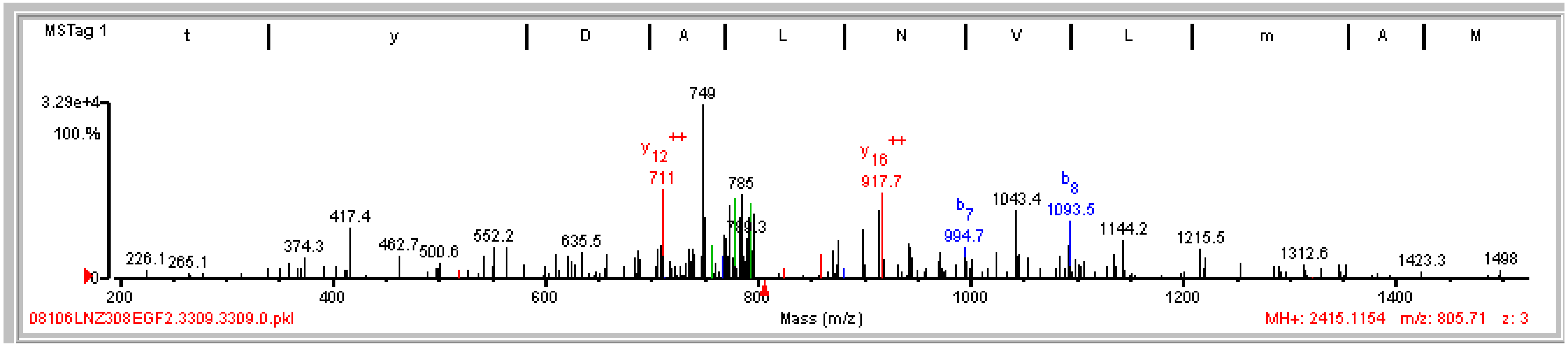
Detailed Results

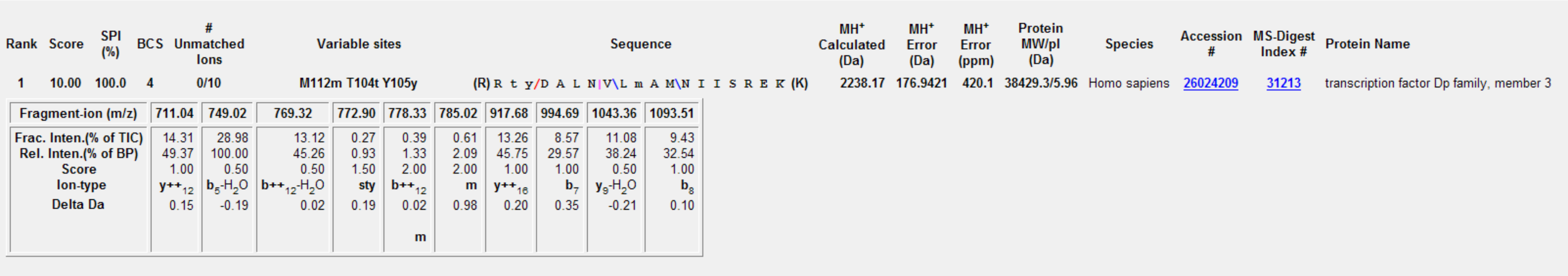
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.34	72.2	10	7/22	Y582y	(R) F V V E G Q G L\I A/G N\E F/L G\Q/Y\T\L\P L L C/M N K G y R (R)	3387.72	80.6954	210.2	70411.7/9.14	Homo sapiens	25188201	11586	phospholipase C, zeta 1

Fragment-ion (m/z)	547.37	807.65	817.12	818.93	830.60	836.07	838.25	843.26	846.04	848.22	853.09	855.16	904.94	955.76	962.54	1004.56	1012.49	1060.23	1069.62	1096.65	1104.90	1186.25
Frac. Inten.(% of TIC)	3.41	5.05	2.53	2.55	4.23	3.06	6.59	0.18	5.04	2.82	2.74	8.87	5.37	3.50	4.45	5.44	12.87	2.90	3.78	3.10	8.21	3.32
Rel. Inten.(% of BP)	26.48	39.22	19.67	19.82	32.87	23.74	51.18	1.39	39.19	21.88	21.32	68.87	41.69	27.17	34.55	42.28	100.00	22.51	29.38	24.05	63.75	25.80
Score	-0.26	0.50	1.00	1.00	1.00	-0.24	-0.51	1.50	0.50	1.00	-0.21	1.00	-0.42	-0.27	1.00	1.00	1.00	0.50	1.00	-0.24	0.50	1.00
Ion-type		$b{+}{+}_{16}$-H_2O	$b{+}{+}_{16}$	$y{+}{+}{+}_{20}$	b_8			sty	$y{+}{+}_{13}$-H_2O	y_6		$y{+}{+}_{13}$			$b{+}{+}_{18}$	$y{+}{+}_{16}$	$b{+}{+}_{19}$	$b{+}{+}_{20}$-H_2O	$b{+}{+}_{20}$		y_8-NH_3	b_{12}
Delta Da		0.23	0.69	0.21	0.16			0.08	0.14	-0.13		0.26			0.55	0.58	-0.02	0.18	0.57		0.46	0.62

Peak 397



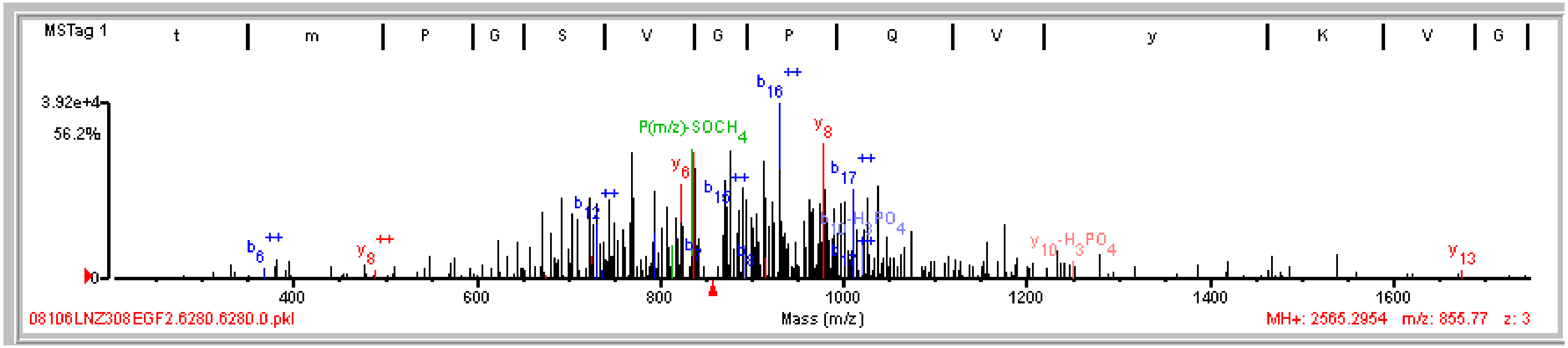


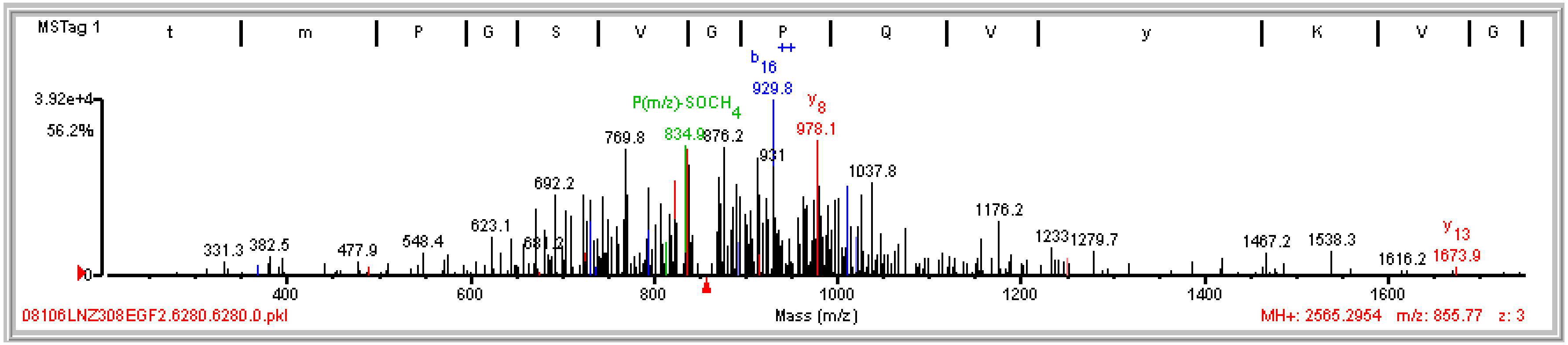


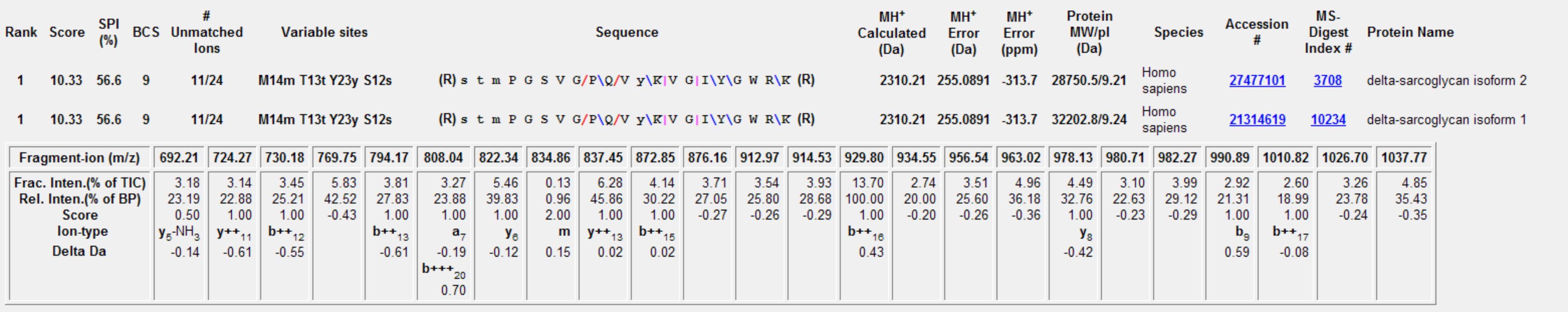
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.00	100.0	4	0/10	M112m T104t Y105y	(R) R t y/D A L N|V\L m A M\N I I S R E K (K)	2238.17	176.9421	420.1	38429.3/5.96	Homo sapiens	26024209	31213	transcription factor Dp family, member 3

Fragment-ion (m/z)	711.04	749.02	769.32	772.90	778.33	785.02	917.68	994.69	1043.36	1093.51
Frac. Inten.(% of TIC)	14.31	28.98	13.12	0.27	0.39	0.61	13.26	8.57	11.08	9.43
Rel. Inten.(% of BP)	49.37	100.00	45.26	0.93	1.33	2.09	45.75	29.57	38.24	32.54
Score	1.00	0.50	0.50	1.50	2.00	2.00	1.00	1.00	0.50	1.00
Ion-type	y^{++}_{12}	b_5-H_2O	b^{++}_{12}-H_2O	sty	b^{++}_{12}	m	y^{++}_{16}	b_7	y_9-H_2O	b_8
Delta Da	0.15	-0.19	0.02	0.19	0.02	0.98	0.20	0.35	-0.21	0.10
					m					

Peak 398





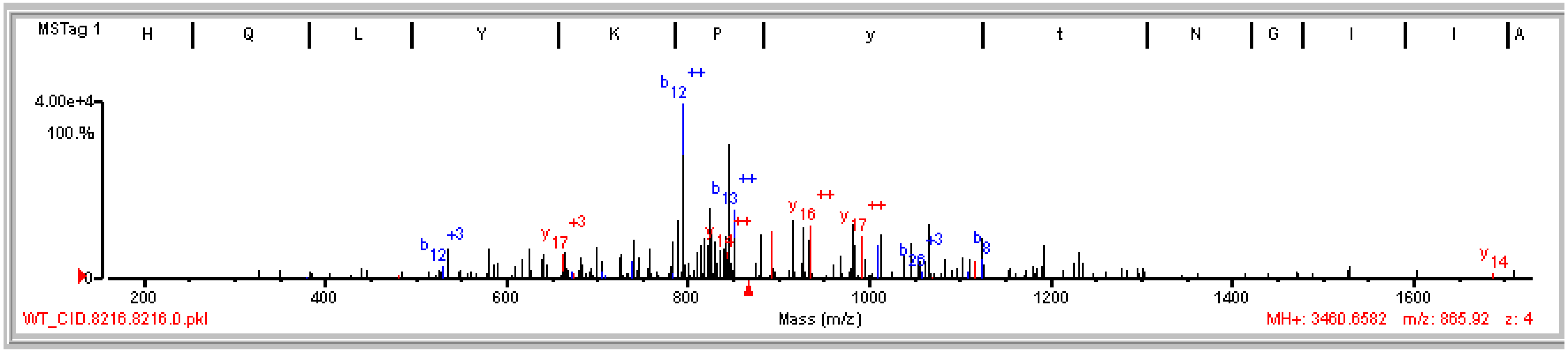


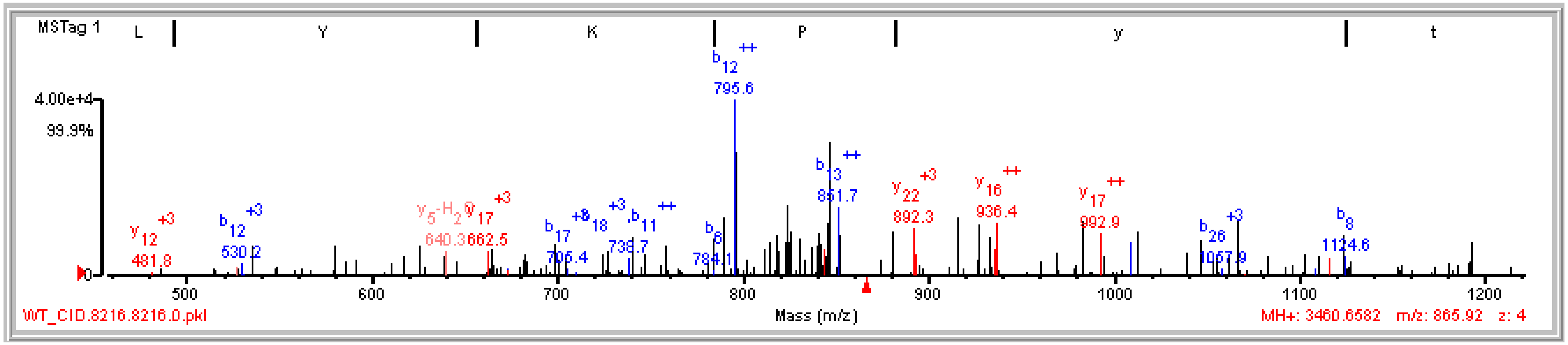
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.33	56.6	9	11/24	M14m T13t Y23y S12s	(R) s t m P G S V G/P\Q/V y\K|V G|I\Y\G W R\K (R)	2310.21	255.0891	-313.7	28750.5/9.21	Homo sapiens	27477101	3708	delta-sarcoglycan isoform 2
1	10.33	56.6	9	11/24	M14m T13t Y23y S12s	(R) s t m P G S V G/P\Q/V y\K|V G|I\Y\G W R\K (R)	2310.21	255.0891	-313.7	32202.8/9.24	Homo sapiens	21314619	10234	delta-sarcoglycan isoform 1

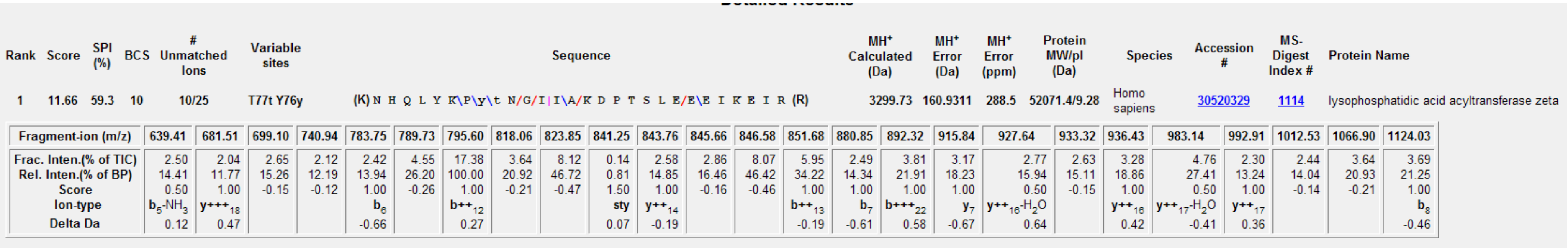
Fragment-ion (m/z)	692.21	724.27	730.18	769.75	794.17	808.04	822.34	834.86	837.45	872.85	876.16	912.97
Frac. Inten.(% of TIC)	3.18	3.14	3.45	5.83	3.81	3.27	5.46	0.13	6.28	4.14	3.71	3.54
Rel. Inten.(% of BP)	23.19	22.88	25.21	42.52	27.83	23.88	39.83	0.96	45.86	30.22	27.05	25.80
Score	0.50	1.00	1.00	-0.43	1.00	1.00	1.00	2.00	1.00	1.00	-0.27	-0.26
Ion-type	$y_5\text{-}NH_3$	$y{+}{+}_{11}$	$b{+}{+}_{12}$		$b{+}{+}_{13}$	a_7 $b{+}{+}{+}_{20}$	y_6	m	$y{+}{+}_{13}$	$b{+}{+}_{15}$		
Delta Da	-0.14	-0.61	-0.55		-0.61	-0.19 0.70	-0.12	0.15	0.02	0.02		

Fragment-ion (m/z)	914.53	929.80	934.55	956.54	963.02	978.13	980.71	982.27	990.89	1010.82	1026.70	1037.77
Frac. Inten.(% of TIC)	3.93	13.70	2.74	3.51	4.96	4.49	3.10	3.99	2.92	2.60	3.26	4.85
Rel. Inten.(% of BP)	28.68	100.00	20.00	25.60	36.18	32.76	22.63	29.12	21.31	18.99	23.78	35.43
Score	-0.29	1.00	-0.20	-0.26	-0.36	1.00	-0.23	-0.29	1.00	1.00	-0.24	-0.35
Ion-type		$b{+}{+}_{16}$				y_8			b_9	$b{+}{+}_{17}$		
Delta Da		0.43				-0.42			0.59	-0.08		

Peak 400





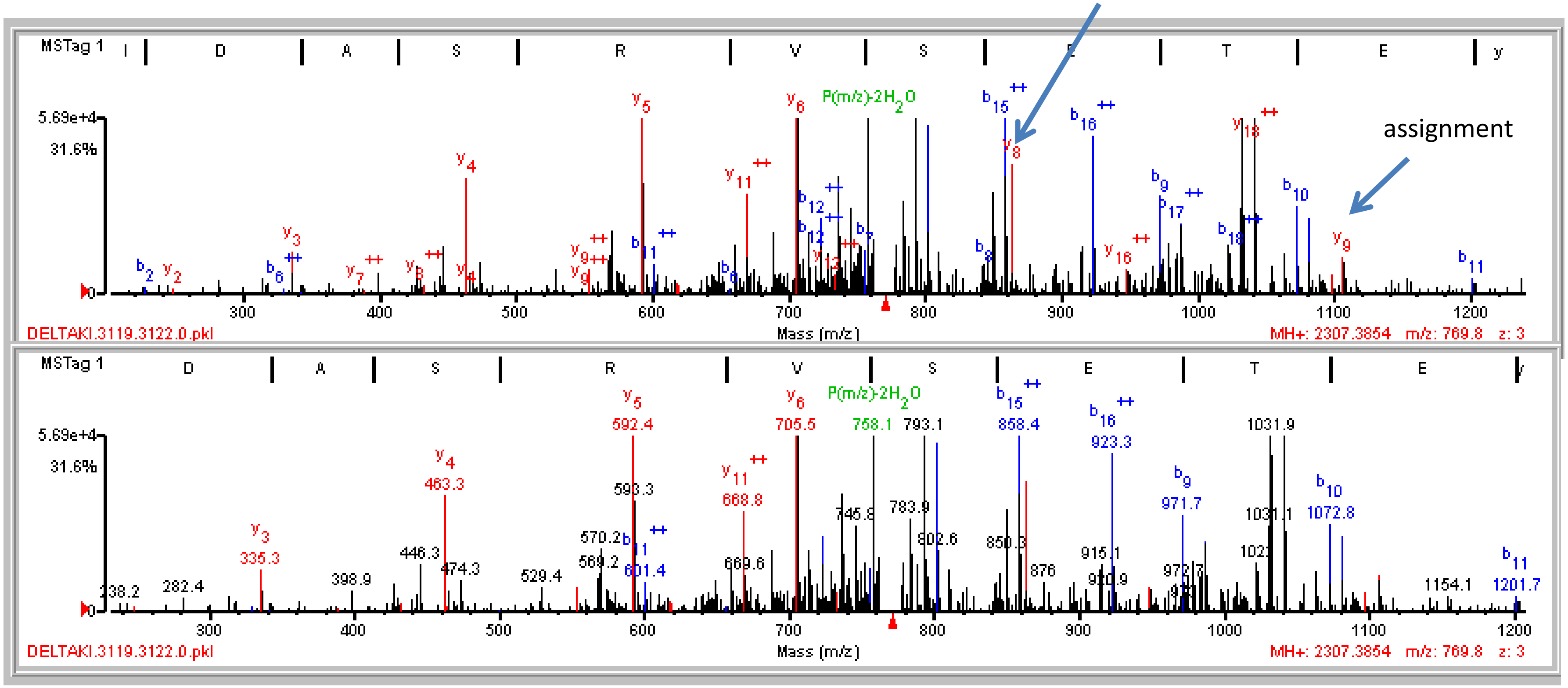


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.66	59.3	10	10/25	T77t Y76y	(K) N H Q L Y K\P\y\t N/G/I|I\A/K D P T S L E/E\E I K E I R (R)	3299.73	160.9311	288.5	52071.4/9.28	Homo sapiens	30520329	1114	lysophosphatidic acid acyltransferase zeta

Fragment-ion (m/z)	639.41	681.51	699.10	740.94	783.75	789.73	795.60	818.06	823.85	841.25	843.76	845.66	846.58
Frac. Inten.(% of TIC)	2.50	2.04	2.65	2.12	2.42	4.55	17.38	3.64	8.12	0.14	2.58	2.86	8.07
Rel. Inten.(% of BP)	14.41	11.77	15.26	12.19	13.94	26.20	100.00	20.92	46.72	0.81	14.85	16.46	46.42
Score	0.50	1.00	-0.15	-0.12	1.00	-0.26	1.00	-0.21	-0.47	1.50	1.00	-0.16	-0.46
Ion-type	b_5-NH_3	$y{+}{+}{+}_{18}$			b_6		$b{+}{+}_{12}$			sty	$y{+}{+}_{14}$		
Delta Da	0.12	0.47			-0.66		0.27			0.07	-0.19		

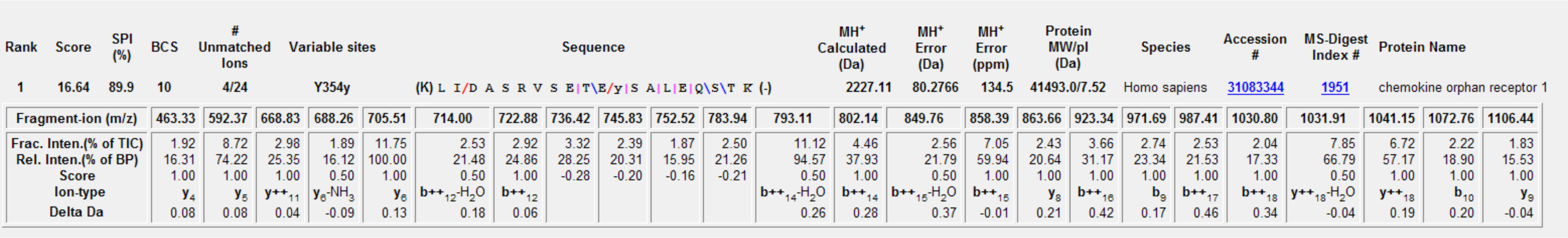
Fragment-ion (m/z)	851.68	880.85	892.32	915.84	927.64	933.32	936.43	983.14	992.91	1012.53	1066.90	1124.03
Frac. Inten.(% of TIC)	5.95	2.49	3.81	3.17	2.77	2.63	3.28	4.76	2.30	2.44	3.64	3.69
Rel. Inten.(% of BP)	34.22	14.34	21.91	18.23	15.94	15.11	18.86	27.41	13.24	14.04	20.93	21.25
Score	1.00	1.00	1.00	1.00	0.50	-0.15	1.00	0.50	1.00	-0.14	-0.21	1.00
Ion-type	$b{+}{+}_{13}$	b_7	$b{+}{+}{+}_{22}$	y_7	$y{+}{+}_{16}$-H_2O		$y{+}{+}_{16}$	$y{+}{+}_{17}$-H_2O	$y{+}{+}_{17}$			b_8
Delta Da	-0.19	-0.61	0.58	-0.67	0.64		0.42	-0.41	0.36			-0.46

Peak 401



Ions that verify assignment

assignment

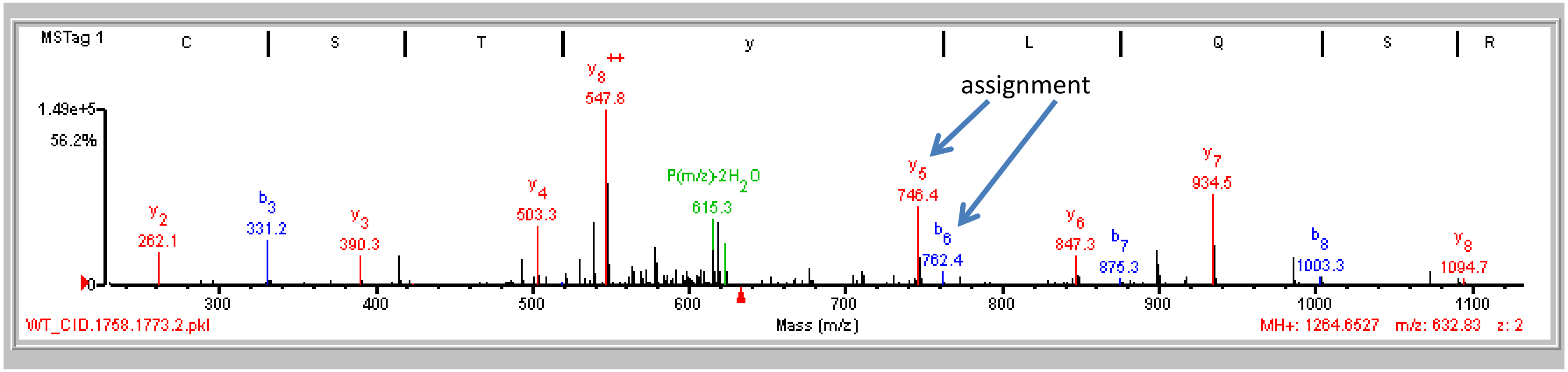


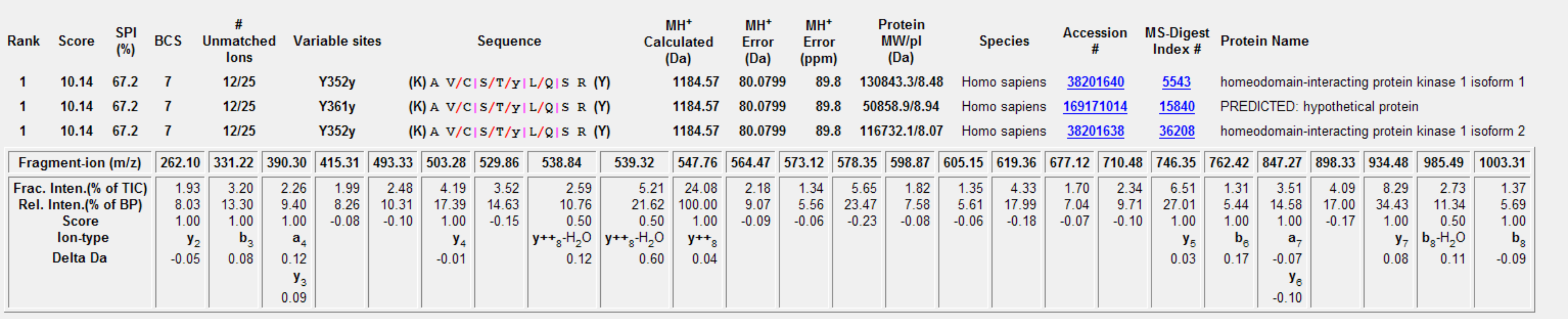
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	16.64	89.9	10	4/24	Y354y	(K) L I/D A S R V S E|T\E/y|S A|L|E|Q\S\T K (-)	2227.11	80.2766	134.5	41493.0/7.52	Homo sapiens	31083344	1951	chemokine orphan receptor 1

Fragment-ion (m/z)	463.33	592.37	668.83	688.26	705.51	714.00	722.88	736.42	745.83	752.52	783.94
Frac. Inten.(% of TIC)	1.92	8.72	2.98	1.89	11.75	2.53	2.92	3.32	2.39	1.87	2.50
Rel. Inten.(% of BP)	16.31	74.22	25.35	16.12	100.00	21.48	24.86	28.25	20.31	15.95	21.26
Score	1.00	1.00	1.00	0.50	1.00	0.50	1.00	-0.28	-0.20	-0.16	-0.21
Ion-type	y_4	y_5	$y{++}_{11}$	y_6-NH_3	y_6	$b{++}_{12}$-H_2O	$b{++}_{12}$				
Delta Da	0.08	0.08	0.04	-0.09	0.13	0.18	0.06				

Fragment-ion (m/z)	793.11	802.14	849.76	858.39	863.66	923.34	971.69	987.41	1030.80	1031.91	1041.15	1072.76	1106.44
Frac. Inten.(% of TIC)	11.12	4.46	2.56	7.05	2.43	3.66	2.74	2.53	2.04	7.85	6.72	2.22	1.83
Rel. Inten.(% of BP)	94.57	37.93	21.79	59.94	20.64	31.17	23.34	21.53	17.33	66.79	57.17	18.90	15.53
Score	0.50	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00
Ion-type	$b{++}_{14}$-H_2O	$b{++}_{14}$	$b{++}_{15}$-H_2O	$b{++}_{15}$	y_8	$b{++}_{16}$	b_9	$b{++}_{17}$	$b{++}_{18}$	$y{++}_{18}$-H_2O	$y{++}_{18}$	b_{10}	y_9
Delta Da	0.26	0.28	0.37	-0.01	0.21	0.42	0.17	0.46	0.34	-0.04	0.19	0.20	-0.04

Peak 403



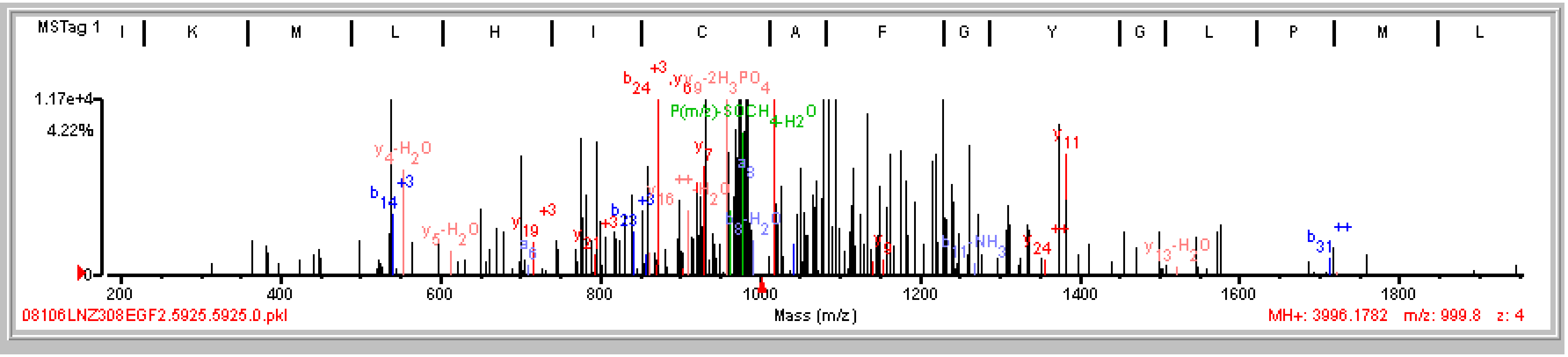


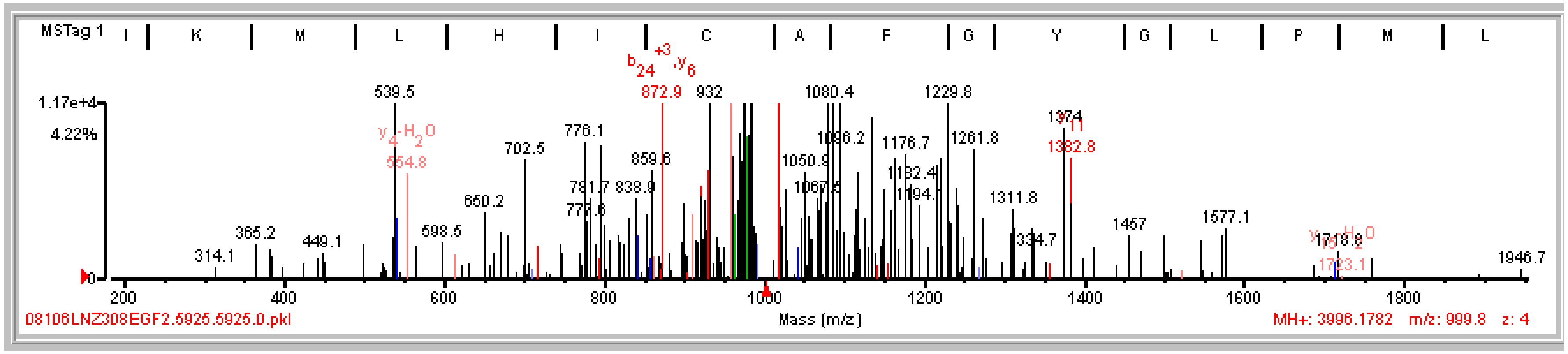
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.14	67.2	7	12/25	Y352y	(K) A V/C|S/T/y|L/Q|S R (Y)	1184.57	80.0799	89.8	130843.3/8.48	Homo sapiens	38201640	5543	homeodomain-interacting protein kinase 1 isoform 1
1	10.14	67.2	7	12/25	Y361y	(K) A V/C|S/T/y|L/Q|S R (Y)	1184.57	80.0799	89.8	50858.9/8.94	Homo sapiens	169171014	15840	PREDICTED: hypothetical protein
1	10.14	67.2	7	12/25	Y352y	(K) A V/C|S/T/y|L/Q|S R (Y)	1184.57	80.0799	89.8	116732.1/8.07	Homo sapiens	38201638	36208	homeodomain-interacting protein kinase 1 isoform 2

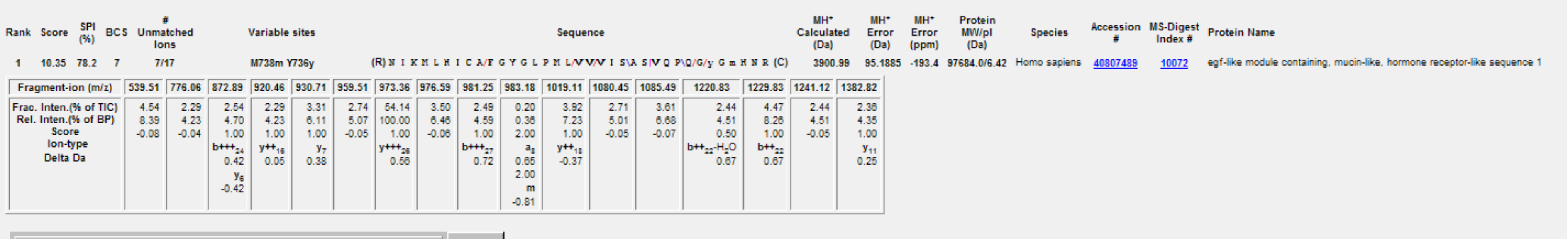
Fragment-ion (m/z)	262.10	331.22	390.30	415.31	493.33	503.28	529.86	538.84	539.32	547.76	564.47	573.12	578.35
Frac. Inten.(% of TIC)	1.93	3.20	2.26	1.99	2.48	4.19	3.52	2.59	5.21	24.08	2.18	1.34	5.65
Rel. Inten.(% of BP)	8.03	13.30	9.40	8.26	10.31	17.39	14.63	10.76	21.62	100.00	9.07	5.56	23.47
Score	1.00	1.00	1.00	-0.08	-0.10	1.00	-0.15	0.50	0.50	1.00	-0.09	-0.06	-0.23
Ion-type	y_2	b_3	a_4 y_3			y_4		$y{+}{+}_8$-H_2O	$y{+}{+}_8$-H_2O	$y{+}{+}_8$			
Delta Da	-0.05	0.08	0.12 0.09			-0.01		0.12	0.60	0.04			

Fragment-ion (m/z)	598.87	605.15	619.36	677.12	710.48	746.35	762.42	847.27	898.33	934.48	985.49	1003.31
Frac. Inten.(% of TIC)	1.82	1.35	4.33	1.70	2.34	6.51	1.31	3.51	4.09	8.29	2.73	1.37
Rel. Inten.(% of BP)	7.58	5.61	17.99	7.04	9.71	27.01	5.44	14.58	17.00	34.43	11.34	5.69
Score	-0.08	-0.06	-0.18	-0.07	-0.10	1.00	1.00	1.00	-0.17	1.00	0.50	1.00
Ion-type						y_5	b_6	a_7 y_6		y_7	b_8-H_2O	b_8
Delta Da						0.03	0.17	-0.07 -0.10		0.08	0.11	-0.09

Peak 404



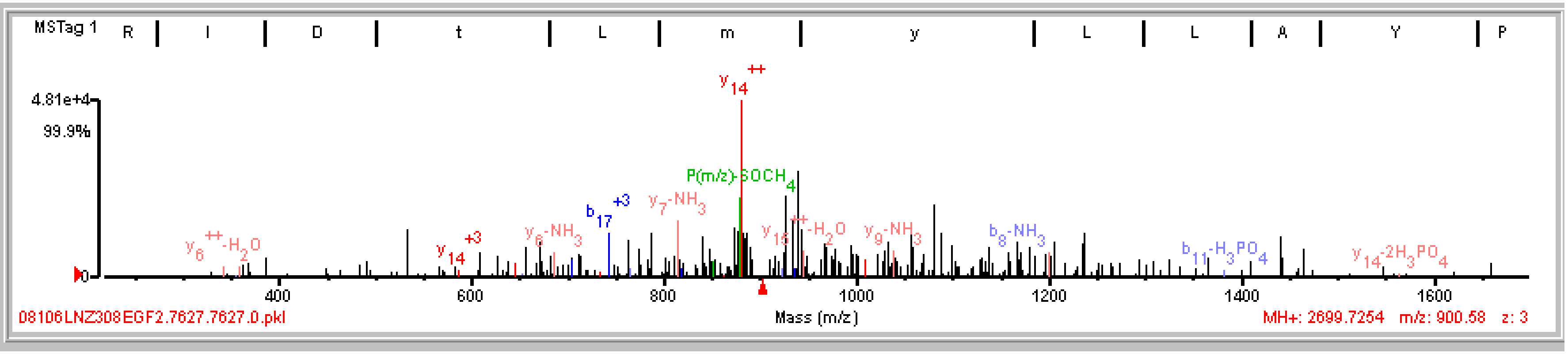


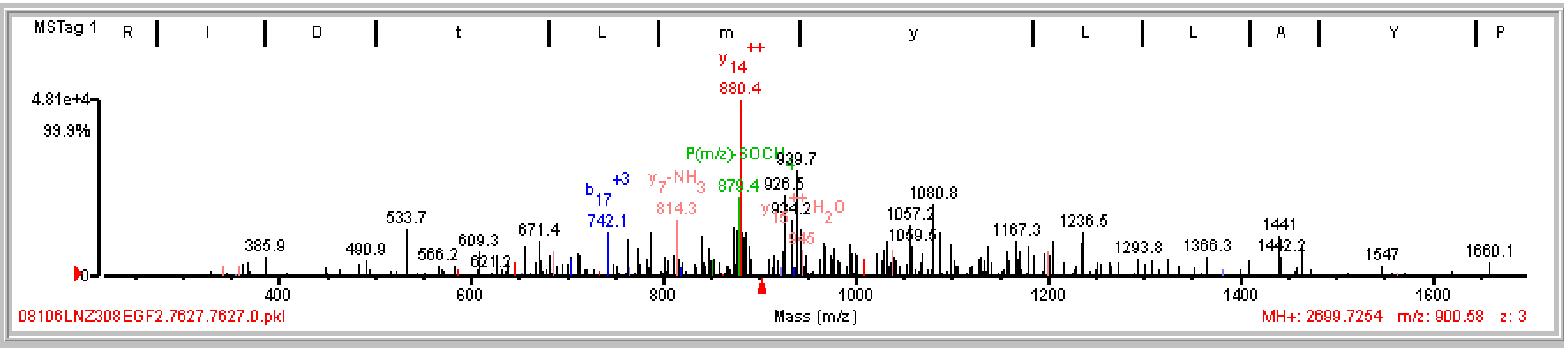


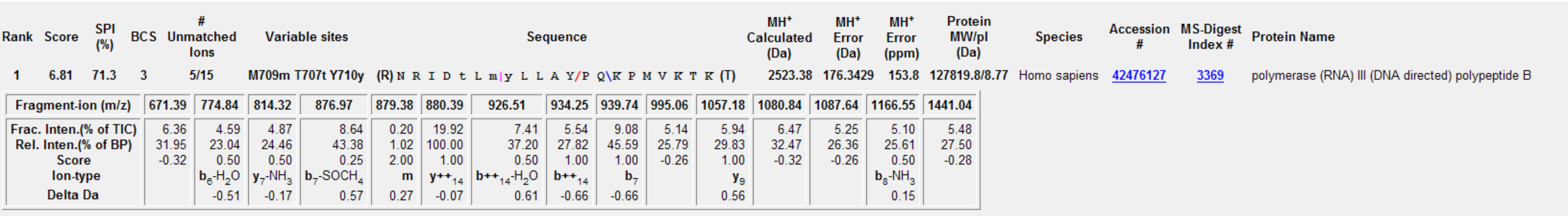
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.35	78.2	7	7/17	M738m Y736y	(R) N I K M L H I C A/F G Y G L P M L/V V/V I S\A S|V Q P\Q/G/y G m H N R (C)	3900.99	95.1885	-193.4	97684.0/6.42	Homo sapiens	40807489	10072	egf-like module containing, mucin-like, hormone receptor-like sequence 1

Fragment-ion (m/z)	539.51	776.06	872.89	920.46	930.71	959.51	973.36	976.59	981.25	983.18	1019.11	1080.45	1085.49	1220.83	1229.83	1241.12	1382.82
Frac. Inten.(% of TIC)	4.54	2.29	2.54	2.29	3.31	2.74	54.14	3.50	2.49	0.20	3.92	2.71	3.61	2.44	4.47	2.44	2.36
Rel. Inten.(% of BP)	8.39	4.23	4.70	4.23	6.11	5.07	100.00	6.46	4.59	0.36	7.23	5.01	6.68	4.51	8.26	4.51	4.35
Score	-0.08	-0.04	1.00	1.00	1.00	-0.05	1.00	-0.06	1.00	2.00 2.00	1.00	-0.05	-0.07	0.50	1.00	-0.05	1.00
Ion-type			b^{+++}_{24} y_6	y^{++}_{16}	y_7		y^{+++}_{26}		b^{+++}_{27}	a_8 m	y^{++}_{18}			b^{++}_{22}-H_2O	b^{++}_{22}		y_{11}
Delta Da			0.42 -0.42	0.05	0.38		0.56		0.72	0.65 -0.81	-0.37			0.67	0.67		0.25

Peak 405



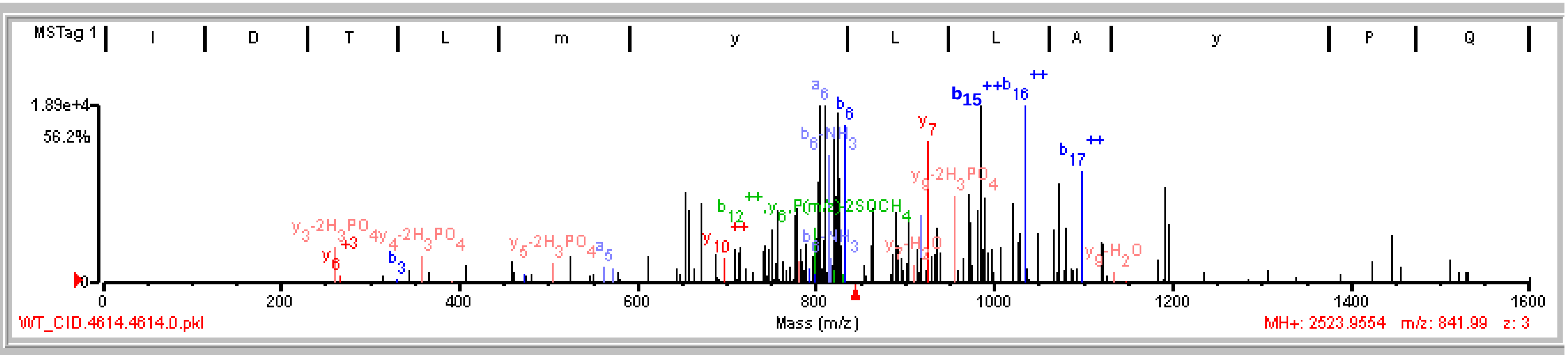


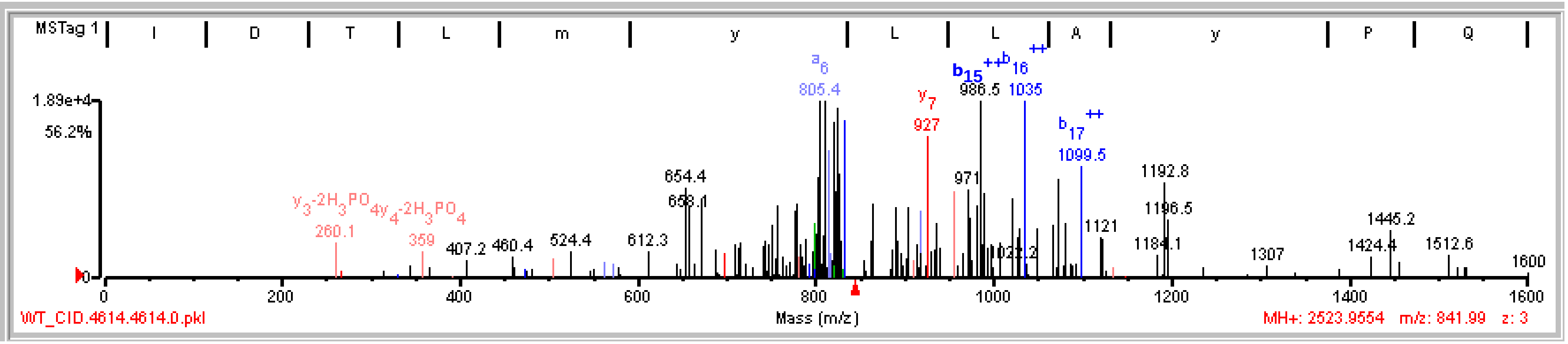


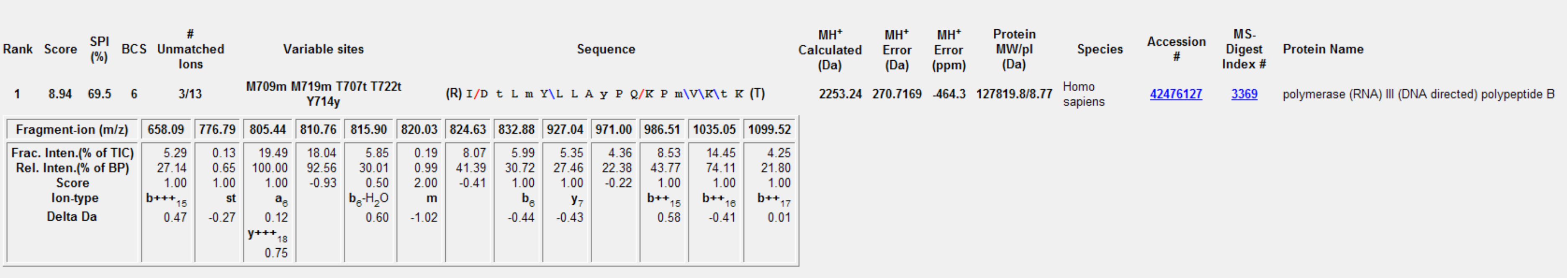
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.81	71.3	3	5/15	M709m T707t Y710y	(R) N R I D t L m|y L L A Y/P Q\K P M V K T K (T)	2523.38	176.3429	153.8	127819.8/8.77	Homo sapiens	42476127	3369	polymerase (RNA) III (DNA directed) polypeptide B

Fragment-ion (m/z)	671.39	774.84	814.32	876.97	879.38	880.39	926.51	934.25	939.74	995.06	1057.18	1080.84	1087.64	1166.55	1441.04
Frac. Inten.(% of TIC)	6.36	4.59	4.87	8.64	0.20	19.92	7.41	5.54	9.08	5.14	5.94	6.47	5.25	5.10	5.48
Rel. Inten.(% of BP)	31.95	23.04	24.46	43.38	1.02	100.00	37.20	27.82	45.59	25.79	29.83	32.47	26.36	25.61	27.50
Score	-0.32	0.50	0.50	0.25	2.00	1.00	0.50	1.00	1.00	-0.26	1.00	-0.32	-0.26	0.50	-0.28
Ion-type		b_6-H$_2$O	y_7-NH$_3$	b_7-SOCH$_4$	m	$y{+}{+}_{14}$	$b{+}{+}_{14}$-H$_2$O	$b{+}{+}_{14}$	b_7		y_9			b_8-NH$_3$	
Delta Da		-0.51	-0.17	0.57	0.27	-0.07	0.61	-0.66	-0.66		0.56			0.15	

Peak 406



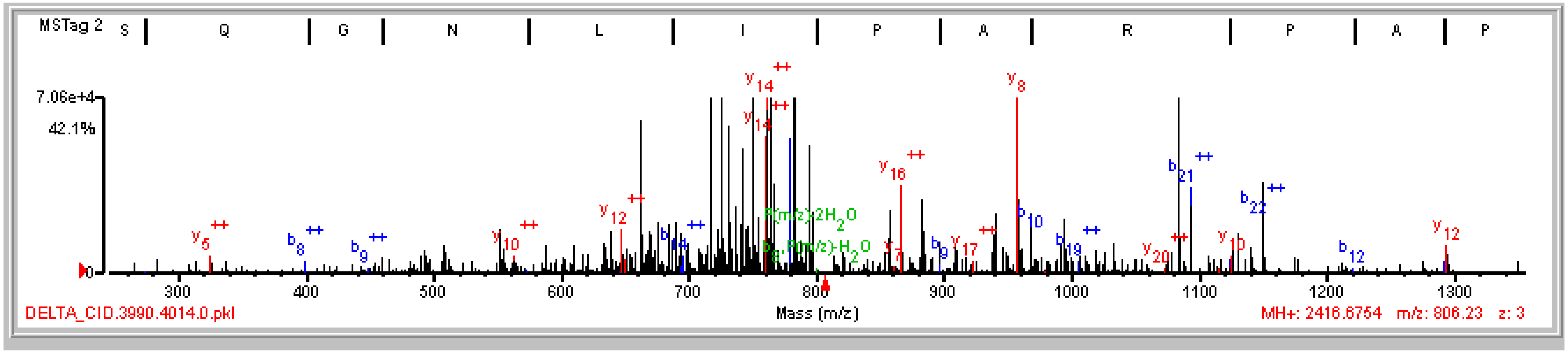


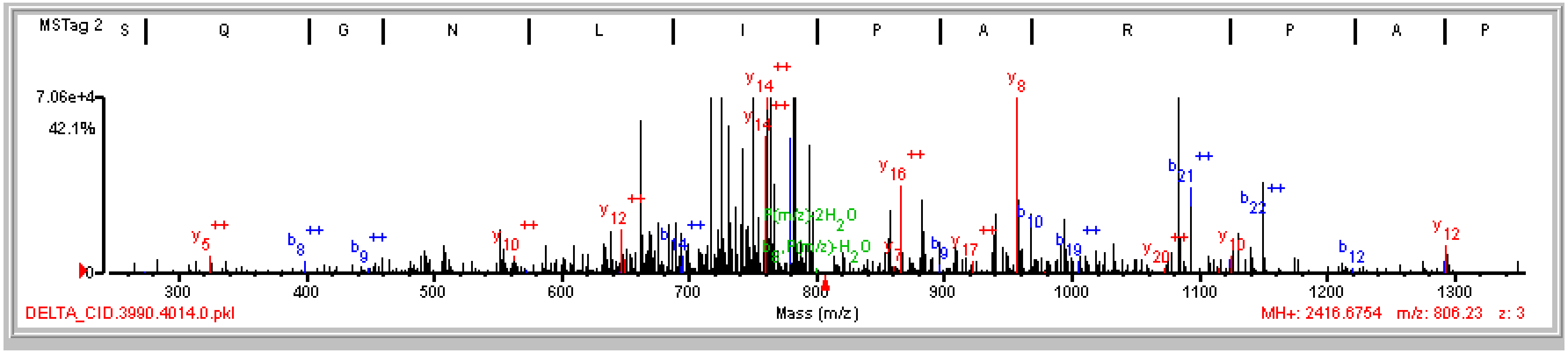


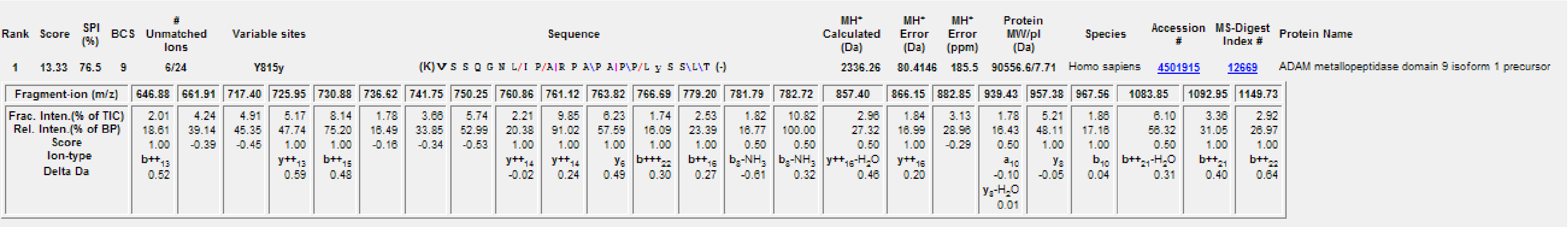
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.94	69.5	6	3/13	M709m M719m T707t T722t Y714y	(R) I/D t L m Y\L L A y P Q/K P m\V\K\t K (T)	2253.24	270.7169	-464.3	127819.8/8.77	Homo sapiens	42476127	3369	polymerase (RNA) III (DNA directed) polypeptide B

Fragment-ion (m/z)	658.09	776.79	805.44	810.76	815.90	820.03	824.63	832.88	927.04	971.00	986.51	1035.05	1099.52
Frac. Inten.(% of TIC)	5.29	0.13	19.49	18.04	5.85	0.19	8.07	5.99	5.35	4.36	8.53	14.45	4.25
Rel. Inten.(% of BP)	27.14	0.65	100.00	92.56	30.01	0.99	41.39	30.72	27.46	22.38	43.77	74.11	21.80
Score	1.00	1.00	1.00	-0.93	0.50	2.00	-0.41	1.00	1.00	-0.22	1.00	1.00	1.00
Ion-type	$b{+}{+}{+}_{15}$	st	a_6		b_6-H_2O	m		b_6	y_7		$b{+}{+}_{15}$	$b{+}{+}_{16}$	$b{+}{+}_{17}$
Delta Da	0.47	-0.27	0.12 $y{+}{+}{+}_{18}$ 0.75		0.60	-1.02		-0.44	-0.43		0.58	-0.41	0.01

Peak 407





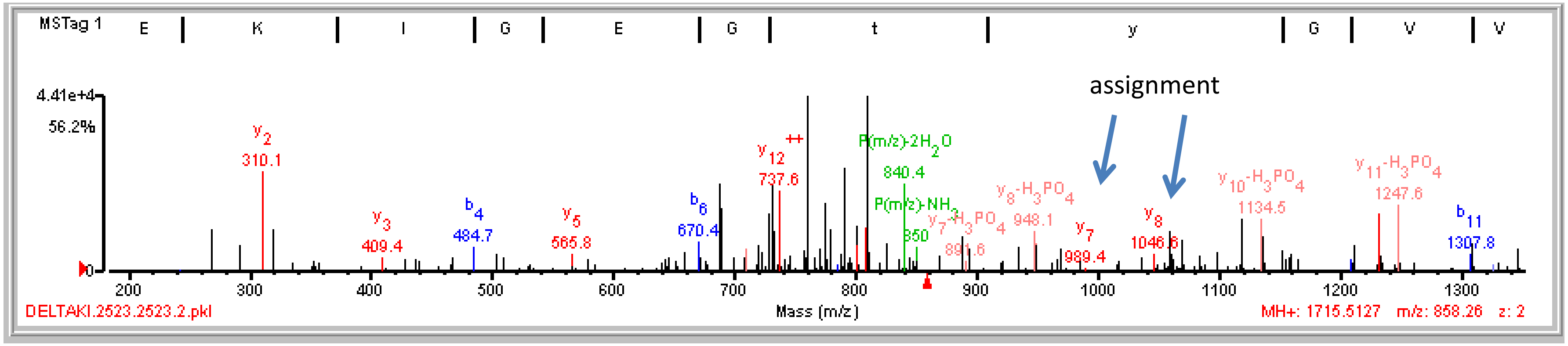


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.33	76.5	9	6/24	Y815y	(K)V S S Q G N L/I P/A|R P A\P A|P\P/L y S S\L\T (-)	2336.26	80.4146	185.5	90556.6/7.71	Homo sapiens	4501915	12669	ADAM metallopeptidase domain 9 isoform 1 precursor

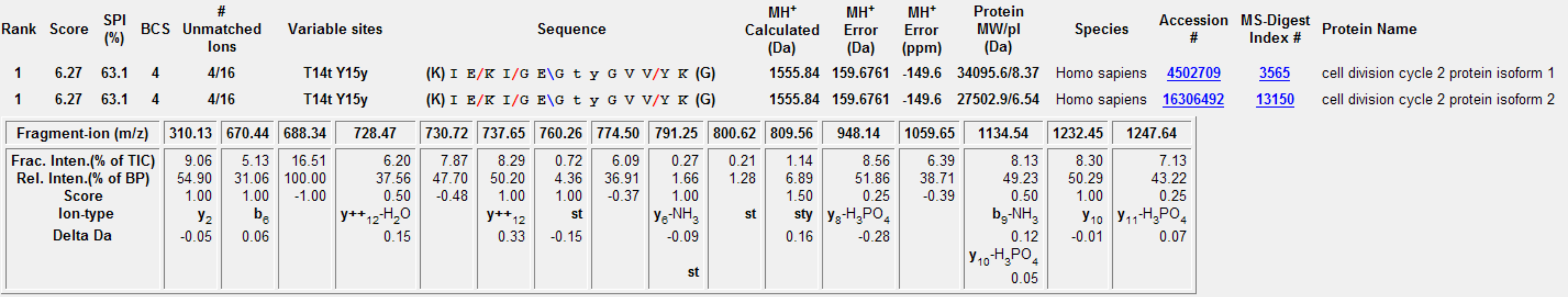
Fragment-ion (m/z)	646.88	661.91	717.40	725.95	730.88	736.62	741.75	750.25	760.86	761.12	763.82
Frac. Inten.(% of TIC)	2.01	4.24	4.91	5.17	8.14	1.78	3.66	5.74	2.21	9.85	6.23
Rel. Inten.(% of BP)	18.61	39.14	45.35	47.74	75.20	16.49	33.85	52.99	20.38	91.02	57.59
Score	1.00	-0.39	-0.45	1.00	1.00	-0.16	-0.34	-0.53	1.00	1.00	1.00
Ion-type	b^{++}_{13}			y^{++}_{13}	b^{++}_{15}				y^{++}_{14}	y^{++}_{14}	y_6
Delta Da	0.52			0.59	0.48				-0.02	0.24	0.49

Fragment-ion (m/z)	766.69	779.20	781.79	782.72	857.40	866.15	882.85	939.43	957.38	967.56	1083.85	1092.95	1149.73
Frac. Inten.(% of TIC)	1.74	2.53	1.82	10.82	2.96	1.84	3.13	1.78	5.21	1.86	6.10	3.36	2.92
Rel. Inten.(% of BP)	16.09	23.39	16.77	100.00	27.32	16.99	28.96	16.43	48.11	17.16	56.32	31.05	26.97
Score	1.00	1.00	0.50	0.50	0.50	1.00	-0.29	0.50	1.00	1.00	0.50	1.00	1.00
Ion-type	b^{+++}_{22}	b^{++}_{16}	b_8-NH_3	b_8-NH_3	y^{++}_{16}-H_2O	y^{++}_{16}		a_{10} y_8-H_2O	y_8	b_{10}	b^{++}_{21}-H_2O	b^{++}_{21}	b^{++}_{22}
Delta Da	0.30	0.27	-0.61	0.32	0.46	0.20		-0.10 0.01	-0.05	0.04	0.31	0.40	0.64

Peak 408



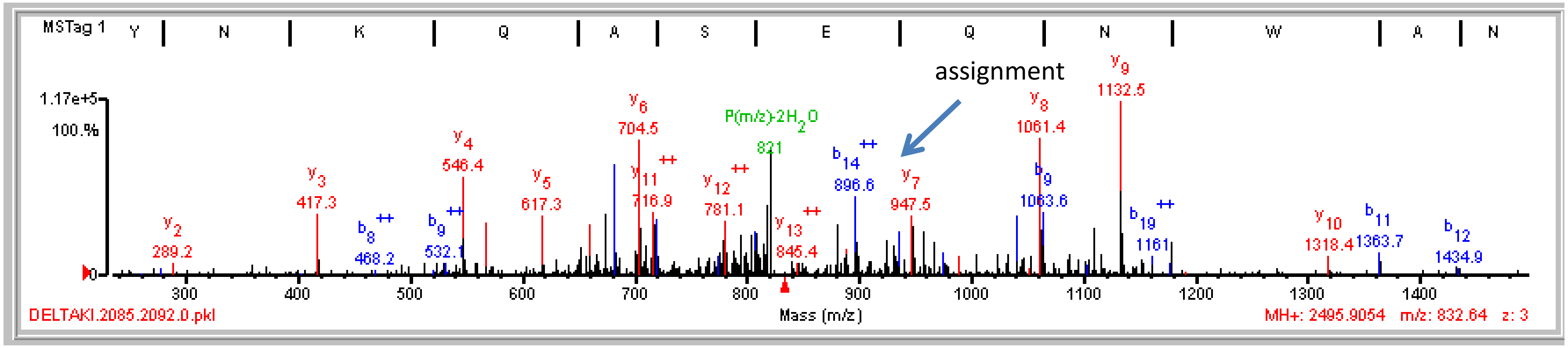
assignment

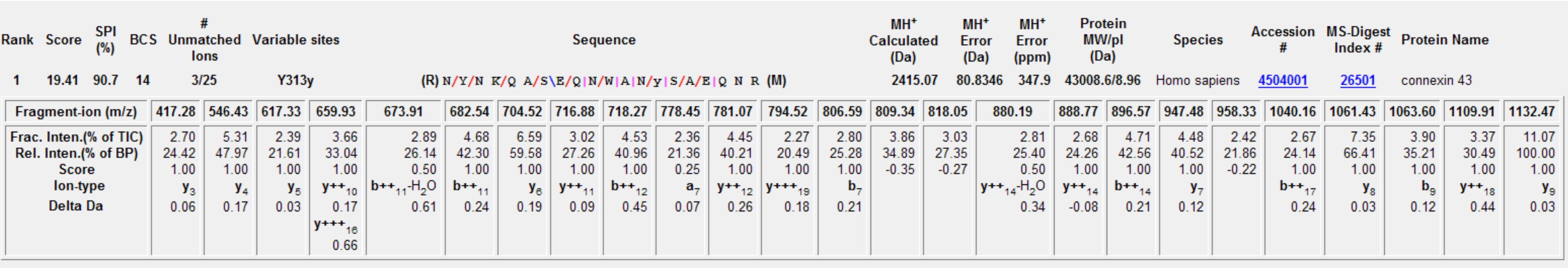


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.27	63.1	4	4/16	T14t Y15y	(K) I E/K I/G E\G t y G V V/Y K (G)	1555.84	159.6761	-149.6	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	6.27	63.1	4	4/16	T14t Y15y	(K) I E/K I/G E\G t y G V V/Y K (G)	1555.84	159.6761	-149.6	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

Fragment-ion (m/z)	310.13	670.44	688.34	728.47	730.72	737.65	760.26	774.50	791.25	800.62	809.56	948.14	1059.65	1134.54	1232.45	1247.64
Frac. Inten.(% of TIC)	9.06	5.13	16.51	6.20	7.87	8.29	0.72	6.09	0.27	0.21	1.14	8.56	6.39	8.13	8.30	7.13
Rel. Inten.(% of BP)	54.90	31.06	100.00	37.56	47.70	50.20	4.36	36.91	1.66	1.28	6.89	51.86	38.71	49.23	50.29	43.22
Score	1.00	1.00	-1.00	0.50	-0.48	1.00	1.00	-0.37	1.00		1.50	0.25	-0.39	0.50	1.00	0.25
Ion-type	y_2	b_6		$y++_{12}$-H_2O		$y++_{12}$	st		y_6-NH_3	st	sty	y_8-H_3PO_4		b_9-NH_3	y_{10}	y_{11}-H_3PO_4
Delta Da	-0.05	0.06		0.15		0.33	-0.15		-0.09		0.16	-0.28		0.12	-0.01	0.07
									st					y_{10}-H_3PO_4		
														0.05		

Peak 409



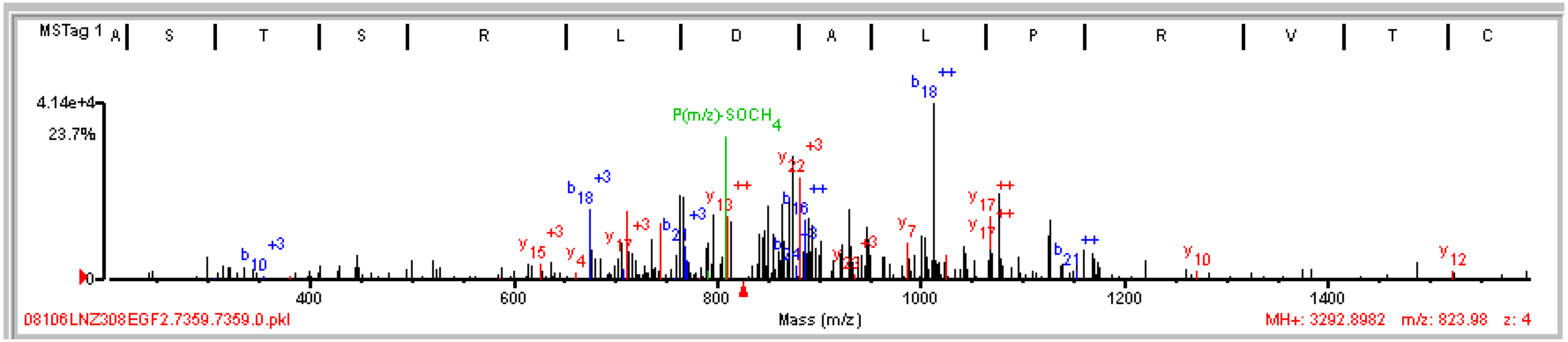


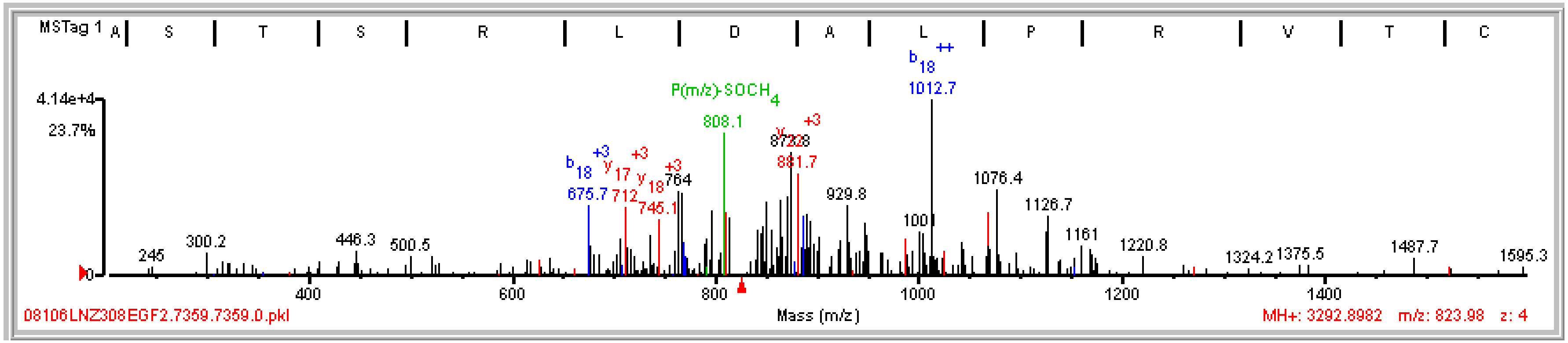
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	19.41	90.7	14	3/25	Y313y	(R) N/Y/N K/Q A/S\E/Q|N/W|A|N/y|S/A/E|Q N R (M)	2415.07	80.8346	347.9	43008.6/8.96	Homo sapiens	4504001	26501	connexin 43

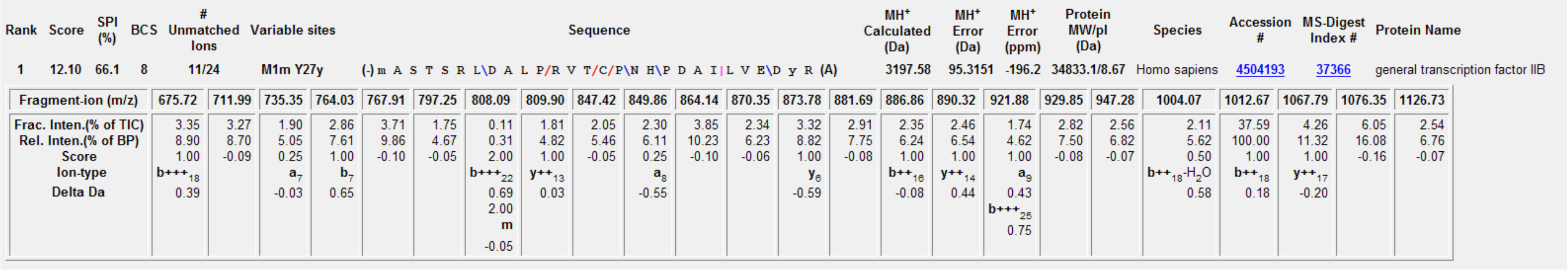
Fragment-ion (m/z)	417.28	546.43	617.33	659.93	673.91	682.54	704.52	716.88	718.27	778.45	781.07	794.52	806.59
Frac. Inten.(% of TIC)	2.70	5.31	2.39	3.66	2.89	4.68	6.59	3.02	4.53	2.36	4.45	2.27	2.80
Rel. Inten.(% of BP)	24.42	47.97	21.61	33.04	26.14	42.30	59.58	27.26	40.96	21.36	40.21	20.49	25.28
Score	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00
Ion-type	y_3	y_4	y_5	$y{+}{+}_{10}$	$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$	y_6	$y{+}{+}_{11}$	$b{+}{+}_{12}$	a_7	$y{+}{+}_{12}$	$y{+}{+}{+}_{19}$	b_7
Delta Da	0.06	0.17	0.03	0.17 $y{+}{+}{+}_{16}$ 0.66	0.61	0.24	0.19	0.09	0.45	0.07	0.26	0.18	0.21

Fragment-ion (m/z)	809.34	818.05	880.19	888.77	896.57	947.48	958.33	1040.16	1061.43	1063.60	1109.91	1132.47
Frac. Inten.(% of TIC)	3.86	3.03	2.81	2.68	4.71	4.48	2.42	2.67	7.35	3.90	3.37	11.07
Rel. Inten.(% of BP)	34.89	27.35	25.40	24.26	42.56	40.52	21.86	24.14	66.41	35.21	30.49	100.00
Score	-0.35	-0.27	0.50	1.00	1.00	1.00	-0.22	1.00	1.00	1.00	1.00	1.00
Ion-type			$y{+}{+}_{14}$-H_2O	$y{+}{+}_{14}$	$b{+}{+}_{14}$	y_7		$b{+}{+}_{17}$	y_8	b_9	$y{+}{+}_{18}$	y_9
Delta Da			0.34	-0.08	0.21	0.12		0.24	0.03	0.12	0.44	0.03

Peak 410





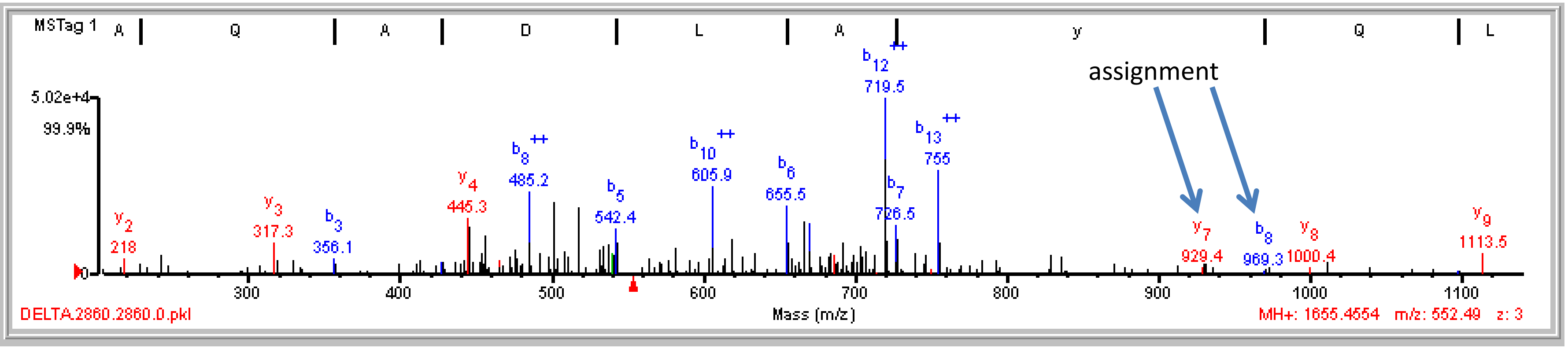


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.10	66.1	8	11/24	M1m Y27y	(-) m A S T S R L\D A L P/R V T/C/P\N H\P D A I|L V E\D y R (A)	3197.58	95.3151	-196.2	34833.1/8.67	Homo sapiens	4504193	37366	general transcription factor IIB

Fragment-ion (m/z)	675.72	711.99	735.35	764.03	767.91	797.25	808.09	809.90	847.42	849.86	864.14	870.35	873.78
Frac. Inten.(% of TIC)	3.35	3.27	1.90	2.86	3.71	1.75	0.11	1.81	2.05	2.30	3.85	2.34	3.32
Rel. Inten.(% of BP)	8.90	8.70	5.05	7.61	9.86	4.67	0.31	4.82	5.46	6.11	10.23	6.23	8.82
Score	1.00	-0.09	0.25	1.00	-0.10	-0.05	2.00 2.00	1.00	-0.05	0.25	-0.10	-0.06	1.00
Ion-type	b^{+++}_{18}		a_7	b_7			b^{+++}_{22} m	y^{++}_{13}		a_8			y_6
Delta Da	0.39		-0.03	0.65			0.69 -0.05	0.03		-0.55			-0.59

Fragment-ion (m/z)	881.69	886.86	890.32	921.88	929.85	947.28	1004.07	1012.67	1067.79	1076.35	1126.73
Frac. Inten.(% of TIC)	2.91	2.35	2.46	1.74	2.82	2.56	2.11	37.59	4.26	6.05	2.54
Rel. Inten.(% of BP)	7.75	6.24	6.54	4.62	7.50	6.82	5.62	100.00	11.32	16.08	6.76
Score	-0.08	1.00	1.00	1.00	-0.08	-0.07	0.50	1.00	1.00	-0.16	-0.07
Ion-type		b^{++}_{16}	y^{++}_{14}	a_9 b^{+++}_{25}			$b^{++}_{18}-H_2O$	b^{++}_{18}	y^{++}_{17}		
Delta Da		-0.08	0.44	0.43 0.75			0.58	0.18	-0.20		

Peak 413



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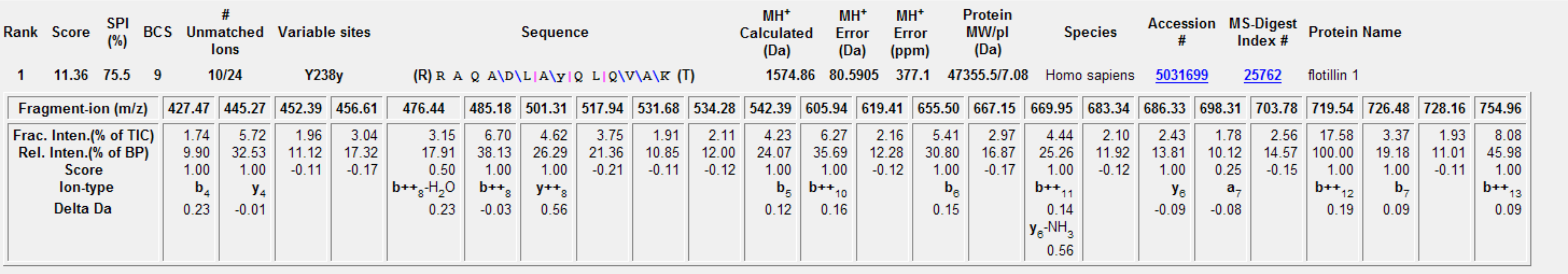
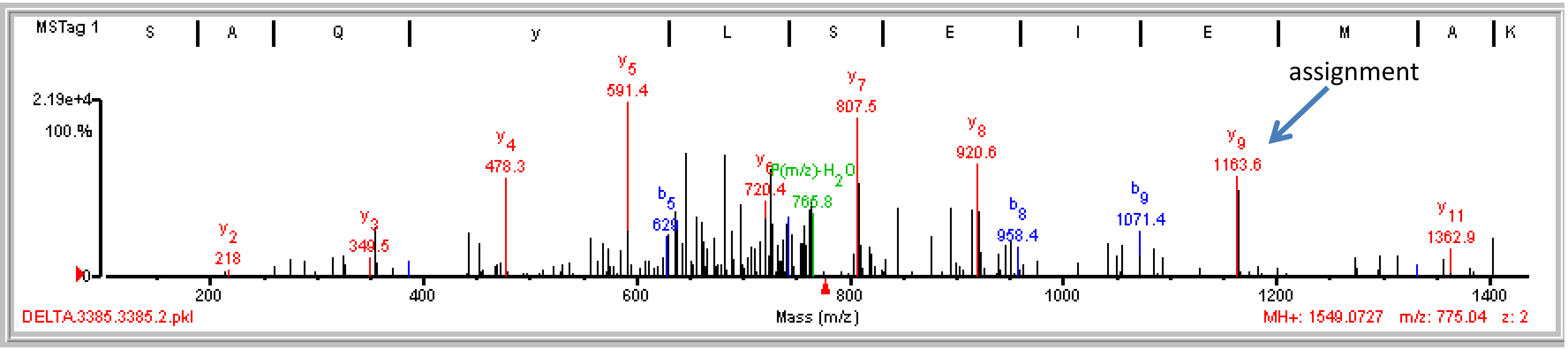


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.36	75.5	9	10/24	Y238y	(R) R A Q A\D\L|A\y|Q L|Q\V\A\K (T)	1574.86	80.5905	377.1	47355.5/7.08	Homo sapiens	5031699	25762	flotillin 1

Fragment-ion (m/z)	427.47	445.27	452.39	456.61	476.44	485.18	501.31	517.94	531.68	534.28	542.39	605.94
Frac. Inten.(% of TIC)	1.74	5.72	1.96	3.04	3.15	6.70	4.62	3.75	1.91	2.11	4.23	6.27
Rel. Inten.(% of BP)	9.90	32.53	11.12	17.32	17.91	38.13	26.29	21.36	10.85	12.00	24.07	35.69
Score	1.00	1.00	-0.11	-0.17	0.50	1.00	1.00	-0.21	-0.11	-0.12	1.00	1.00
Ion-type	b_4	y_4			$b{+}{+}_8$-H_2O	$b{+}{+}_8$	$y{+}{+}_8$				b_5	$b{+}{+}_{10}$
Delta Da	0.23	-0.01			0.23	-0.03	0.56				0.12	0.16

Fragment-ion (m/z)	619.41	655.50	667.15	669.95	683.34	686.33	698.31	703.78	719.54	726.48	728.16	754.96
Frac. Inten.(% of TIC)	2.16	5.41	2.97	4.44	2.10	2.43	1.78	2.56	17.58	3.37	1.93	8.08
Rel. Inten.(% of BP)	12.28	30.80	16.87	25.26	11.92	13.81	10.12	14.57	100.00	19.18	11.01	45.98
Score	-0.12	1.00	-0.17	1.00	-0.12	1.00	0.25	-0.15	1.00	1.00	-0.11	1.00
Ion-type		b_6		$b{+}{+}_{11}$ 0.14 y_6-NH_3		y_6	a_7		$b{+}{+}_{12}$	b_7		$b{+}{+}_{13}$
Delta Da		0.15		0.56		-0.09	-0.08		0.19	0.09		0.09

Peak 414



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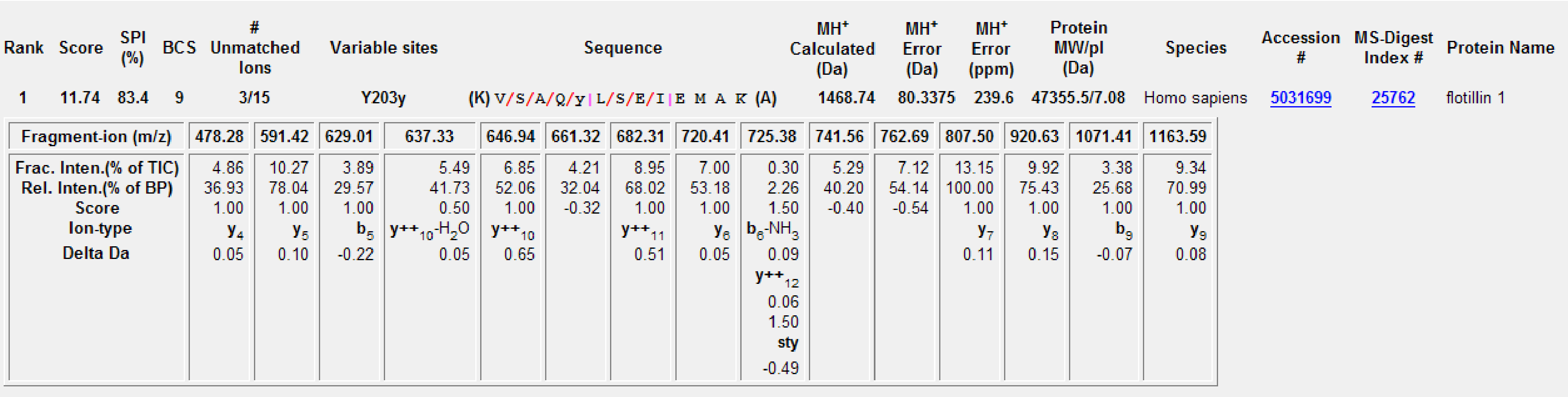
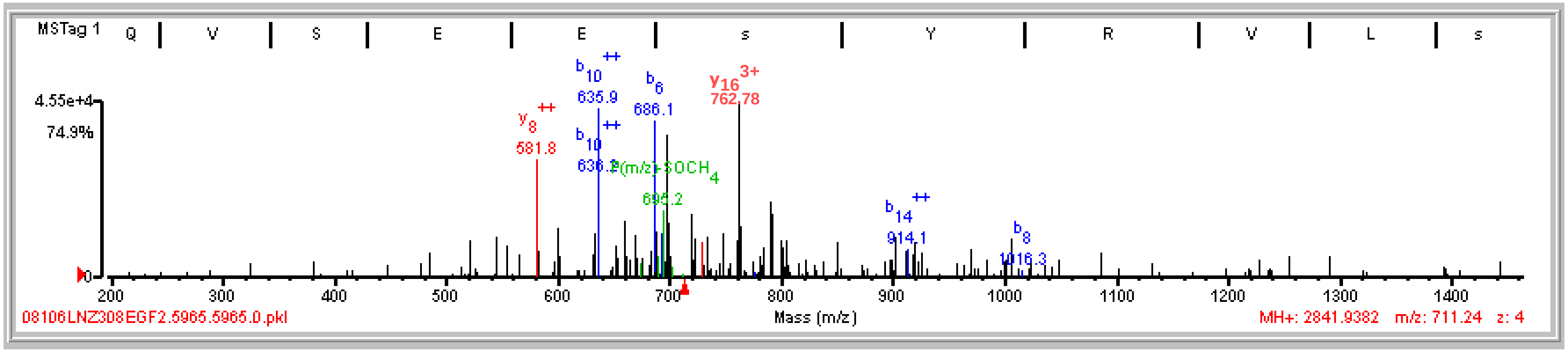
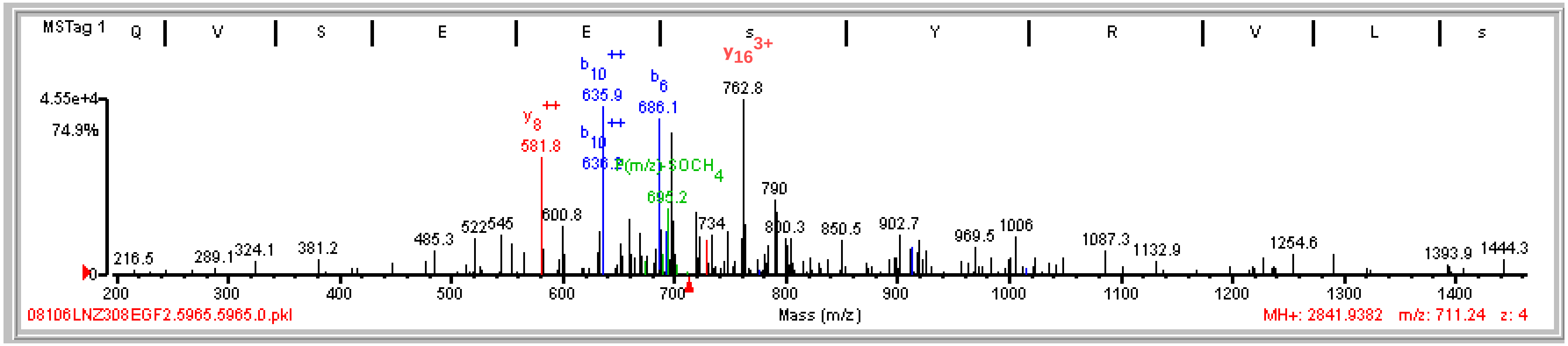


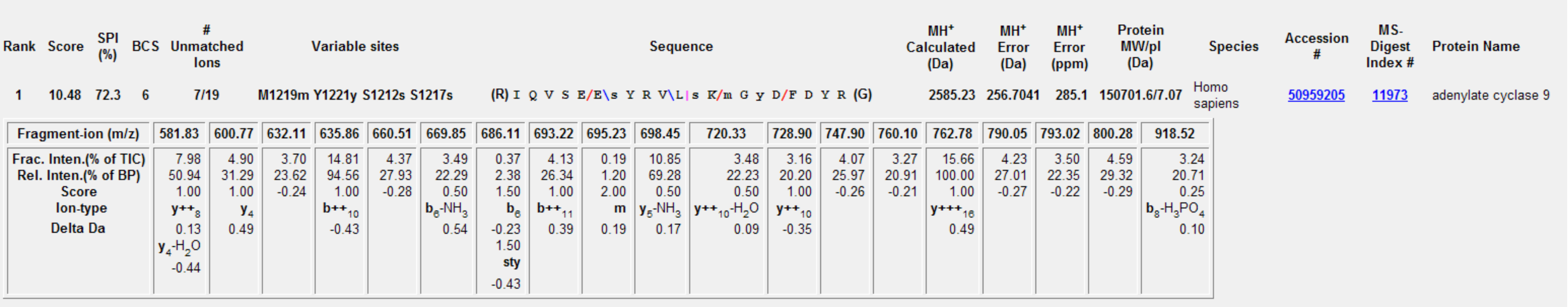
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.74	83.4	9	3/15	Y203y	(K) V/S/A/Q/y|L/S/E/I|E M A K (A)	1468.74	80.3375	239.6	47355.5/7.08	Homo sapiens	5031699	25762	flotillin 1

Fragment-ion (m/z)	478.28	591.42	629.01	637.33	646.94	661.32	682.31	720.41	725.38	741.56	762.69	807.50	920.63	1071.41	1163.59
Frac. Inten.(% of TIC)	4.86	10.27	3.89	5.49	6.85	4.21	8.95	7.00	0.30	5.29	7.12	13.15	9.92	3.38	9.34
Rel. Inten.(% of BP)	36.93	78.04	29.57	41.73	52.06	32.04	68.02	53.18	2.26	40.20	54.14	100.00	75.43	25.68	70.99
Score	1.00	1.00	1.00	0.50	1.00	-0.32	1.00	1.00	1.50	-0.40	-0.54	1.00	1.00	1.00	1.00
Ion-type	y_4	y_5	b_5	y^{++}_{10}-H$_2$O	y^{++}_{10}		y^{++}_{11}	y_6	b_6-NH$_3$			y_7	y_8	b_9	y_9
Delta Da	0.05	0.10	-0.22	0.05	0.65		0.51	0.05	0.09 y^{++}_{12} 0.06 1.50 sty -0.49			0.11	0.15	-0.07	0.08

Peak 415



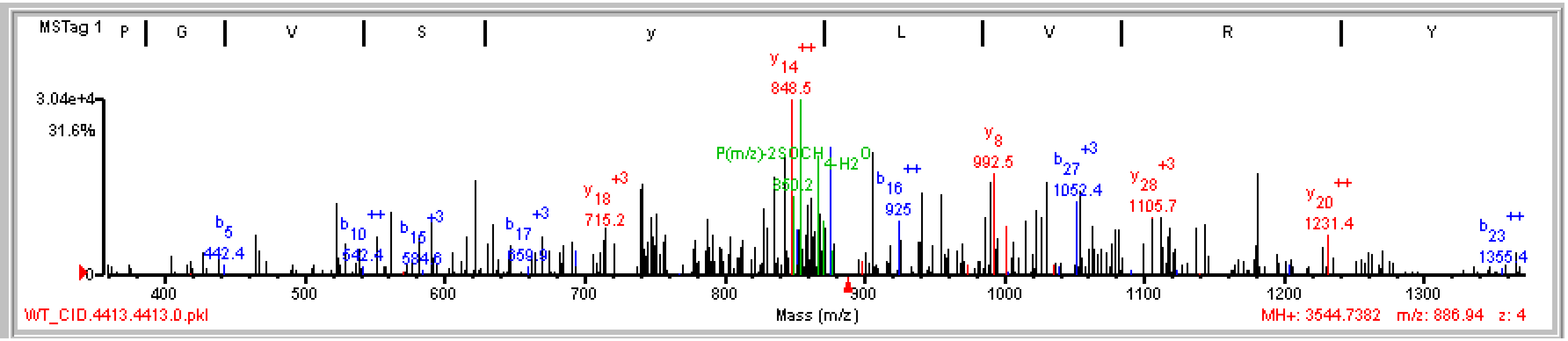


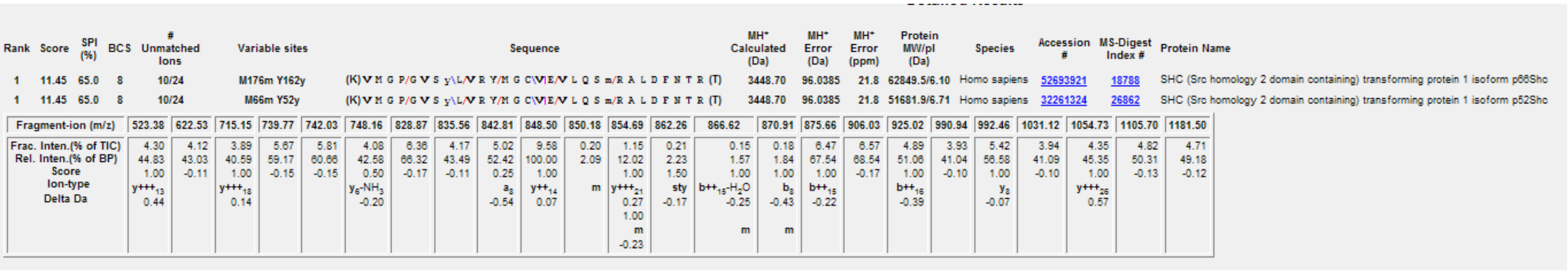


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.48	72.3	6	7/19	M1219m Y1221y S1212s S1217s	(R) I Q V S E/E\s Y R V\L|s K/m G y D/F D Y R (G)	2585.23	256.7041	285.1	150701.6/7.07	Homo sapiens	50959205	11973	adenylate cyclase 9

Fragment-ion (m/z)	581.83	600.77	632.11	635.86	660.51	669.85	686.11	693.22	695.23	698.45	720.33	728.90	747.90	760.10	762.78	790.05	793.02	800.28	918.52
Frac. Inten.(% of TIC)	7.98	4.90	3.70	14.81	4.37	3.49	0.37	4.13	0.19	10.85	3.48	3.16	4.07	3.27	15.66	4.23	3.50	4.59	3.24
Rel. Inten.(% of BP)	50.94	31.29	23.62	94.56	27.93	22.29	2.38	26.34	1.20	69.28	22.23	20.20	25.97	20.91	100.00	27.01	22.35	29.32	20.71
Score	1.00	1.00	-0.24	1.00	-0.28	0.50	1.50	1.00	2.00	0.50	0.50	1.00	-0.26	-0.21	1.00	-0.27	-0.22	-0.29	0.25
Ion-type	y++$_{8}$	y$_{4}$		b++$_{10}$		b$_{6}$-NH$_{3}$	b$_{6}$	b++$_{11}$	m	y$_{5}$-NH$_{3}$	y++$_{10}$-H$_{2}$O	y++$_{10}$			y+++$_{16}$				b$_{8}$-H$_{3}$PO$_{4}$
Delta Da	0.13	0.49		-0.43		0.54	-0.23	0.39	0.19	0.17	0.09	-0.35			0.49				0.10
	y$_{4}$-H$_{2}$O						1.50												
	-0.44						sty												
							-0.43												

Peak 417

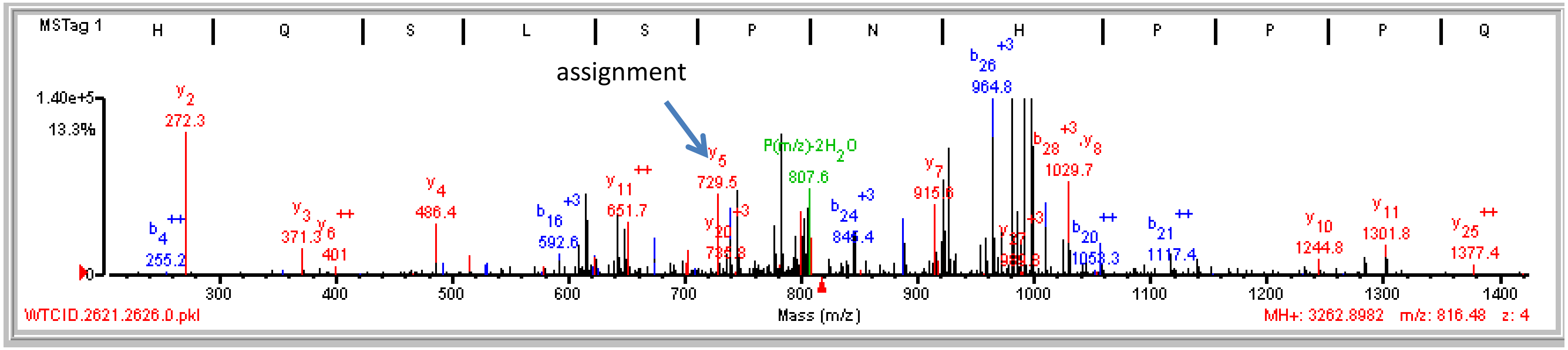




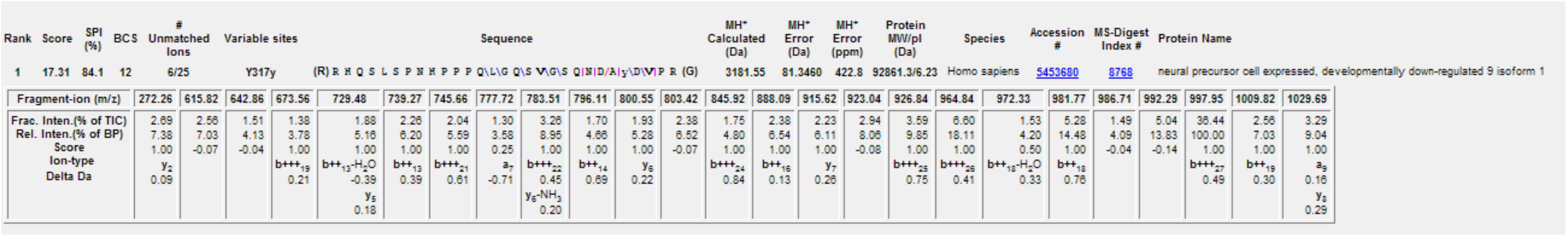
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.45	65.0	8	10/24	M176m Y162y	(K) V M G P/G V S y\L/V R Y/M G C\V|E/V L Q S m/R A L D F N T R (T)	3448.70	96.0385	21.8	62849.5/6.10	Homo sapiens	52693921	18788	SHC (Src homology 2 domain containing) transforming protein 1 isoform p66Shc
1	11.45	65.0	8	10/24	M66m Y52y	(K) V M G P/G V S y\L/V R Y/M G C\V|E/V L Q S m/R A L D F N T R (T)	3448.70	96.0385	21.8	51681.9/6.71	Homo sapiens	32261324	26862	SHC (Src homology 2 domain containing) transforming protein 1 isoform p52Shc

Fragment-ion (m/z)	523.38	622.53	715.15	739.77	742.03	748.16	828.87	835.56	842.81	848.50	850.18	854.69	862.26	866.62	870.91	875.66	906.03	925.02	990.94	992.46	1031.12	1054.73	1105.70	1181.50
Frac. Inten.(% of TIC)	4.30	4.12	3.89	5.67	5.81	4.08	6.36	4.17	5.02	9.58	0.20	1.15	0.21	0.15	0.18	6.47	6.57	4.89	3.93	5.42	3.94	4.35	4.82	4.71
Rel. Inten.(% of BP)	44.83	43.03	40.59	59.17	60.66	42.58	66.32	43.49	52.42	100.00	2.09	12.02	2.23	1.57	1.84	67.54	68.54	51.06	41.04	56.58	41.09	45.35	50.31	49.18
Score	1.00	-0.11	1.00	-0.15	-0.15	0.50	-0.17	-0.11	0.25	1.00		1.00	1.50	1.00	1.00	1.00	-0.17	1.00	-0.10	1.00	-0.10	1.00	-0.13	-0.12
Ion-type	y+++_{13}		y+++_{18}			$\text{y}_6\text{-NH}_3$			a_8	y++_{14}	m	y+++_{21}	sty	$\text{b++}_{15}\text{-H}_2\text{O}$	b_8	b++_{15}		b++_{16}		y_8		y+++_{26}		
Delta Da	0.44		0.14			-0.20			-0.54	0.07		0.27	-0.17	-0.25	-0.43	-0.22		-0.39		-0.07		0.57		
												1.00												
												m		m	m									
												-0.23												

Peak 418



assignment

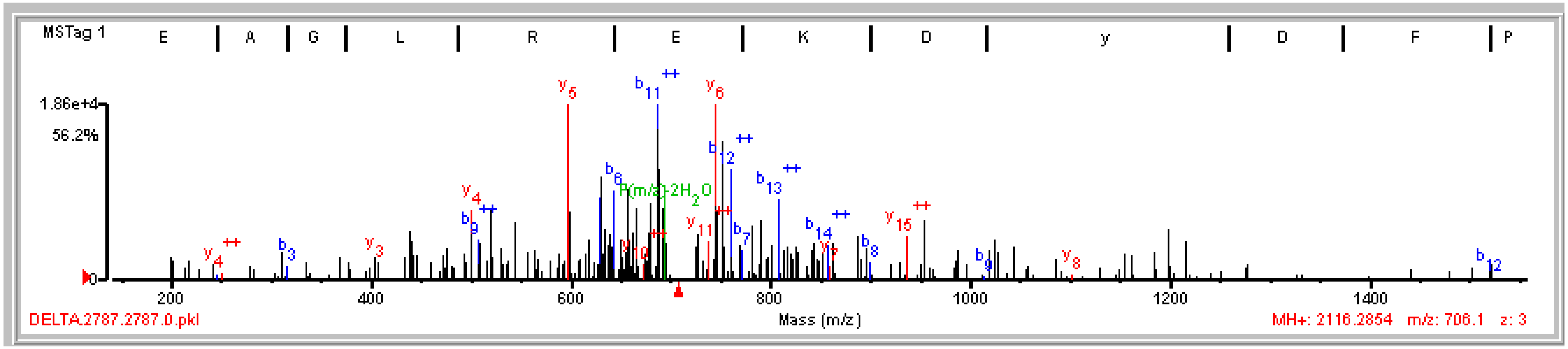


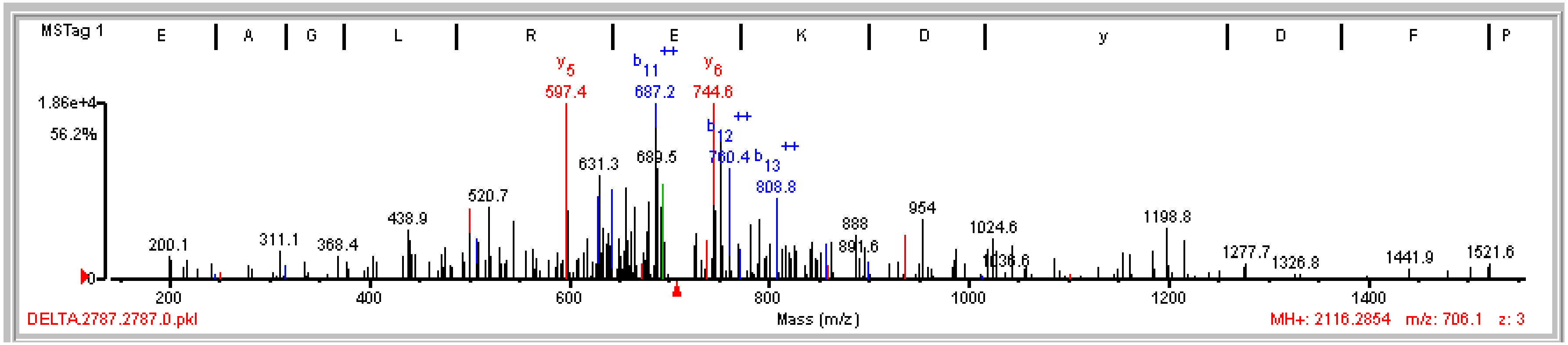
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	17.31	84.1	12	6/25	Y317y	(R) R H Q S L S P N H P P P Q\L\G Q\S V\G\S Q|N|D/A|y\D\V|P R (G)	3181.55	81.3460	422.8	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

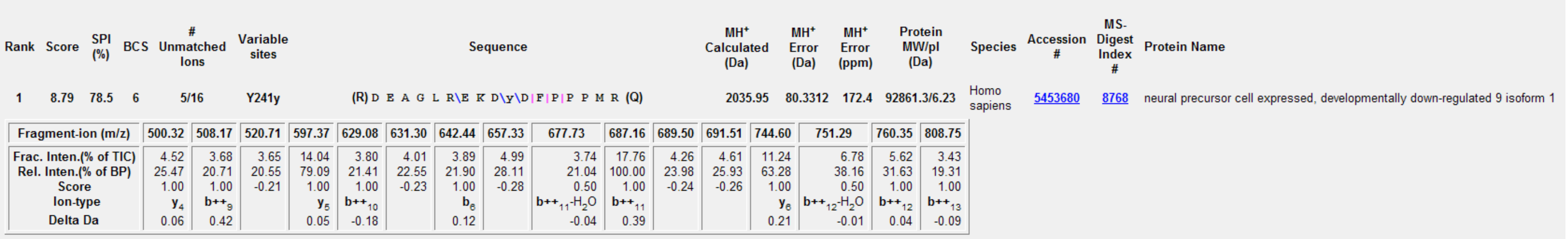
Fragment-ion (m/z)	272.26	615.82	642.86	673.56	729.48	739.27	745.66	777.72	783.51	796.11	800.55	803.42
Frac. Inten.(% of TIC)	2.69	2.56	1.51	1.38	1.88	2.26	2.04	1.30	3.26	1.70	1.93	2.38
Rel. Inten.(% of BP)	7.38	7.03	4.13	3.78	5.16	6.20	5.59	3.58	8.95	4.66	5.28	6.52
Score	1.00	-0.07	-0.04	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	-0.07
Ion-type	y_2			b+++$_{19}$	b++$_{13}$-H_2O y_5	b++$_{13}$	b+++$_{21}$	a_7	b+++$_{22}$ y_6-NH_3	b++$_{14}$	y_6	
Delta Da	0.09			0.21	-0.39 0.18	0.39	0.61	-0.71	0.45 0.20	0.69	0.22	

Fragment-ion (m/z)	845.92	888.09	915.62	923.04	926.84	964.84	972.33	981.77	986.71	992.29	997.95	1009.82	1029.69
Frac. Inten.(% of TIC)	1.75	2.38	2.23	2.94	3.59	6.60	1.53	5.28	1.49	5.04	36.44	2.56	3.29
Rel. Inten.(% of BP)	4.80	6.54	6.11	8.06	9.85	18.11	4.20	14.48	4.09	13.83	100.00	7.03	9.04
Score	1.00	1.00	1.00	-0.08	1.00	1.00	0.50	1.00	-0.04	-0.14	1.00	1.00	1.00
Ion-type	b+++$_{24}$	b++$_{16}$	y_7		b+++$_{25}$	b+++$_{26}$	b++$_{18}$-H_2O	b++$_{18}$			b+++$_{27}$	b++$_{19}$	a_9 y_8
Delta Da	0.84	0.13	0.26		0.75	0.41	0.33	0.76			0.49	0.30	0.16 0.29

Peak 419



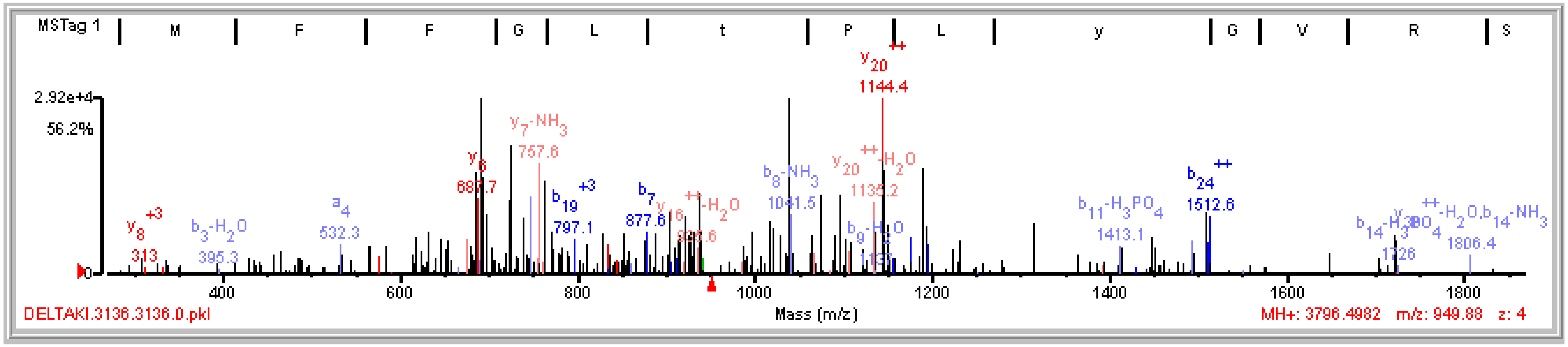


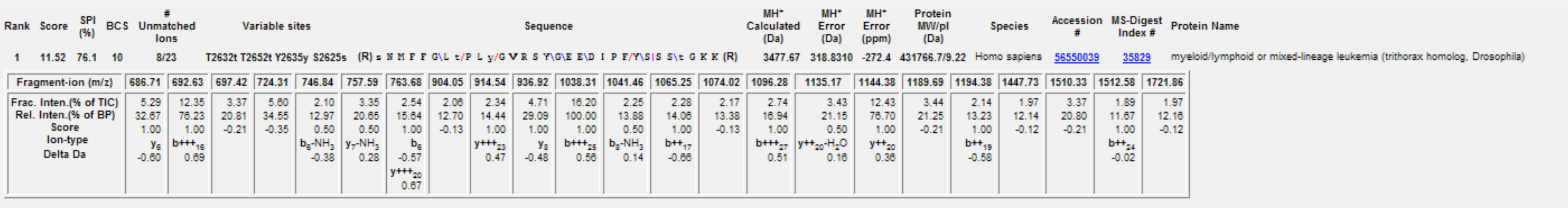


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.79	78.5	6	5/16	Y241y	(R) D E A G L R\E K D\y\D|F|P|P P M R (Q)	2035.95	80.3312	172.4	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

Fragment-ion (m/z)	500.32	508.17	520.71	597.37	629.08	631.30	642.44	657.33	677.73	687.16	689.50	691.51	744.60	751.29	760.35	808.75
Frac. Inten.(% of TIC)	4.52	3.68	3.65	14.04	3.80	4.01	3.89	4.99	3.74	17.76	4.26	4.61	11.24	6.78	5.62	3.43
Rel. Inten.(% of BP)	25.47	20.71	20.55	79.09	21.41	22.55	21.90	28.11	21.04	100.00	23.98	25.93	63.28	38.16	31.63	19.31
Score	1.00	1.00	-0.21	1.00	1.00	-0.23	1.00	-0.28	0.50	1.00	-0.24	-0.26	1.00	0.50	1.00	1.00
Ion-type	y_4	$b{+}{+}_9$		y_5	$b{+}{+}_{10}$		b_6		$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$			y_6	$b{+}{+}_{12}$-H_2O	$b{+}{+}_{12}$	$b{+}{+}_{13}$
Delta Da	0.06	0.42		0.05	-0.18		0.12		-0.04	0.39			0.21	-0.01	0.04	-0.09

Peak 420



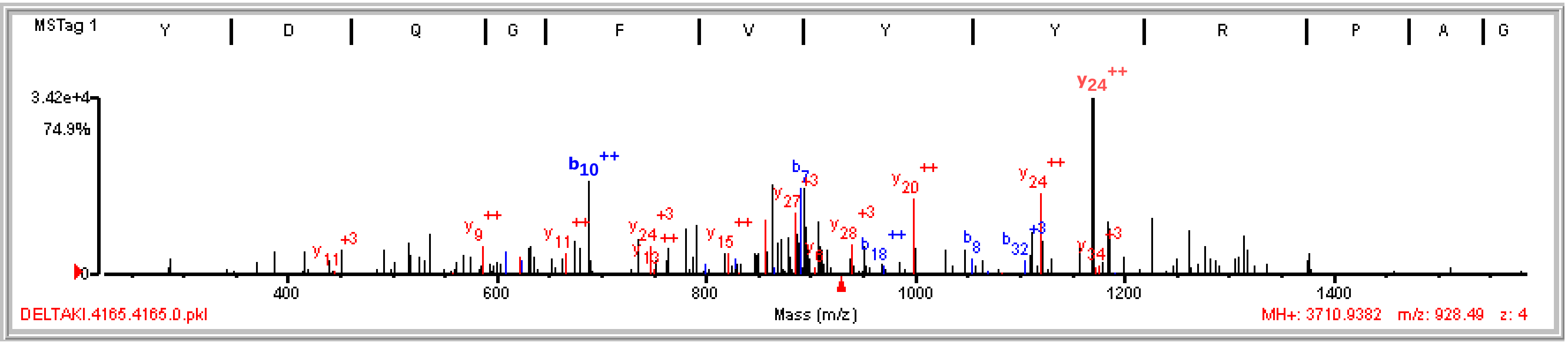


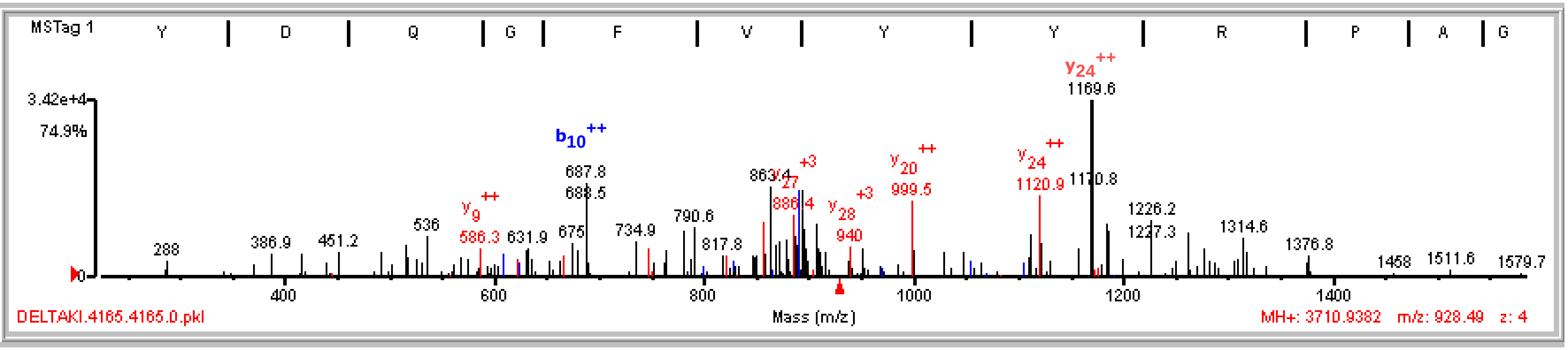
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.52	76.1	10	8/23	T2632t T2652t Y2635y S2625s	(R) s N M F F G\L t/P L y/G V R S Y\G\E E\D I P F/Y\S|S S\t G K K (R)	3477.67	318.8310	-272.4	431766.7/9.22	Homo sapiens	56550039	35829	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)

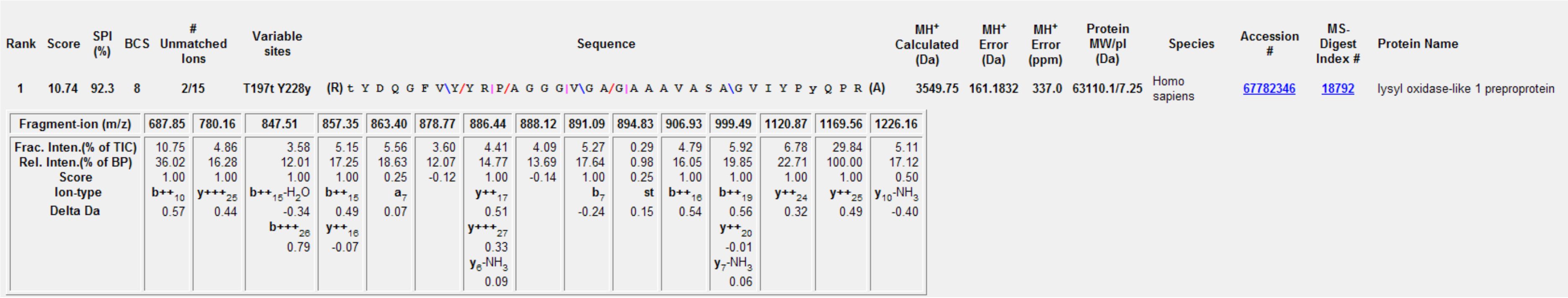
Fragment-ion (m/z)	686.71	692.63	697.42	724.31	746.84	757.59	763.68	904.05	914.54	936.92	1038.31	1041.46
Frac. Inten.(% of TIC)	5.29	12.35	3.37	5.60	2.10	3.35	2.54	2.06	2.34	4.71	16.20	2.25
Rel. Inten.(% of BP)	32.67	76.23	20.81	34.55	12.97	20.65	15.64	12.70	14.44	29.09	100.00	13.88
Score	1.00	1.00	-0.21	-0.35	0.50	0.50	1.00	-0.13	1.00	1.00	1.00	0.50
Ion-type	y_6	$b{+}{+}{+}_{16}$			b_6-NH_3	y_7-NH_3	b_6 $y{+}{+}{+}_{20}$		$y{+}{+}{+}_{23}$	y_8	$b{+}{+}{+}_{25}$	b_8-NH_3
Delta Da	-0.60	0.69			-0.38	0.28	-0.57 0.67		0.47	-0.48	0.56	0.14

Fragment-ion (m/z)	1065.25	1074.02	1096.28	1135.17	1144.38	1189.69	1194.38	1447.73	1510.33	1512.58	1721.86
Frac. Inten.(% of TIC)	2.28	2.17	2.74	3.43	12.43	3.44	2.14	1.97	3.37	1.89	1.97
Rel. Inten.(% of BP)	14.06	13.38	16.94	21.15	76.70	21.25	13.23	12.14	20.80	11.67	12.16
Score	1.00	-0.13	1.00	0.50	1.00	-0.21	1.00	-0.12	-0.21	1.00	-0.12
Ion-type	$b{+}{+}_{17}$		$b{+}{+}{+}_{27}$	$y{+}{+}_{20}$-H_2O	$y{+}{+}_{20}$		$b{+}{+}_{19}$			$b{+}{+}_{24}$	
Delta Da	-0.66		0.51	0.16	0.36		-0.58			-0.02	

Peak 422



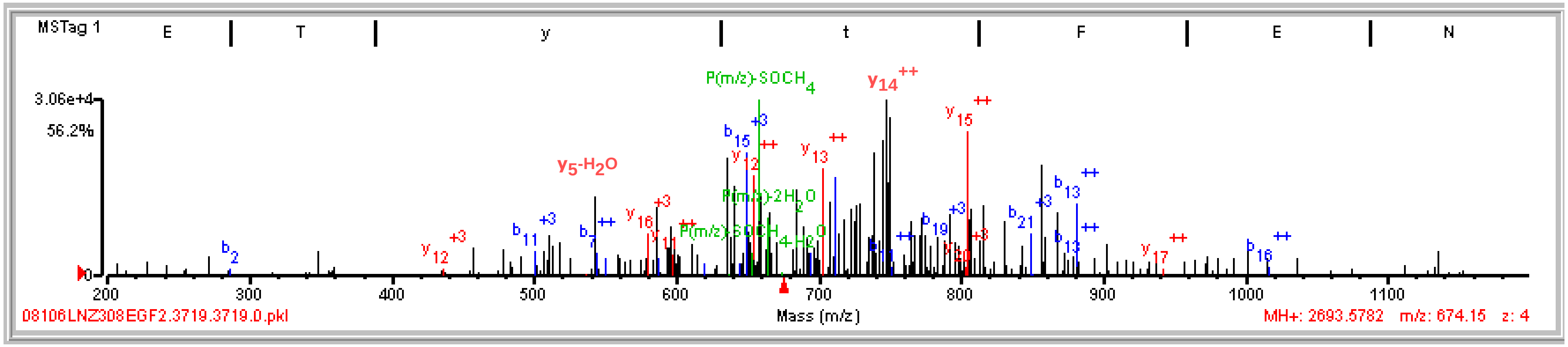


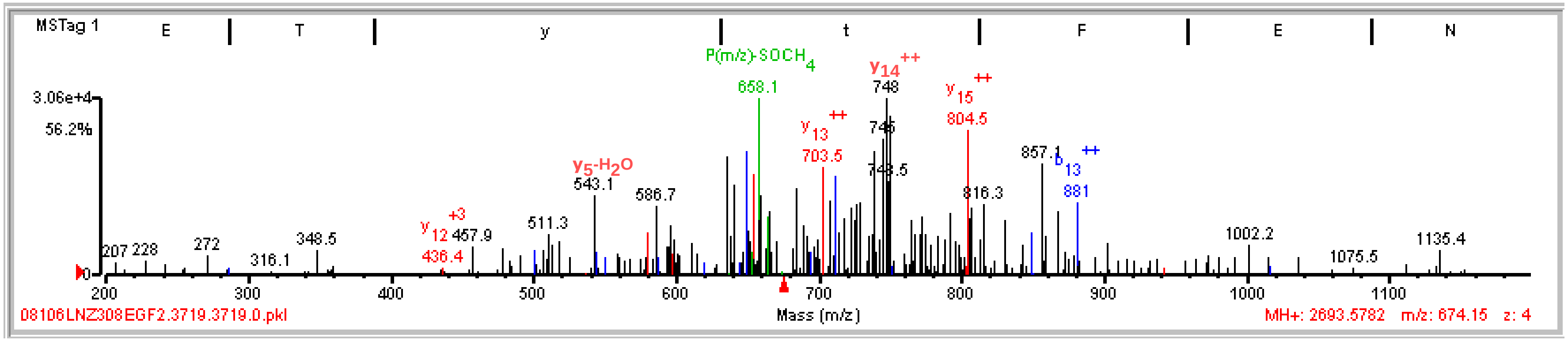


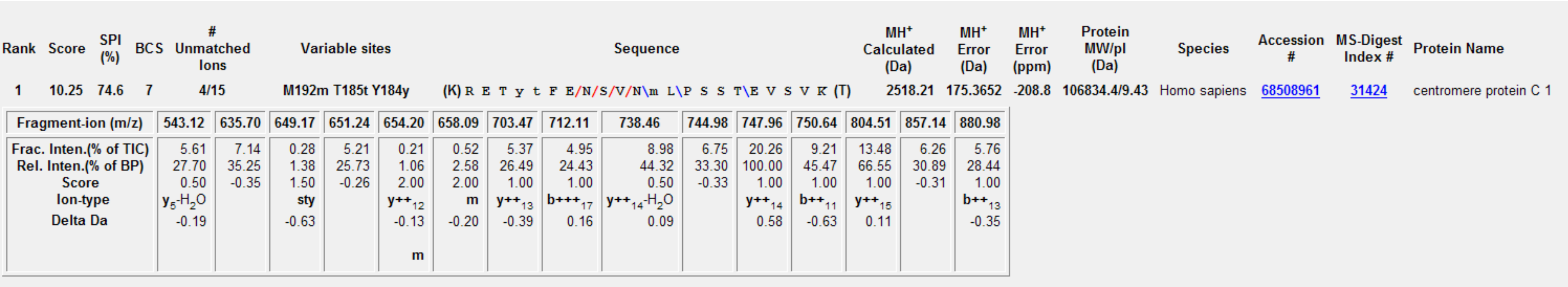
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.74	92.3	8	2/15	T197t Y228y	(R) t Y D Q G F V\Y/Y R|P/A G G G|V\G A/G|A A A V A S A\G V I Y P y Q P R (A)	3549.75	161.1832	337.0	63110.1/7.25	Homo sapiens	67782346	18792	lysyl oxidase-like 1 preproprotein

Fragment-ion (m/z)	687.85	780.16	847.51	857.35	863.40	878.77	886.44	888.12	891.09	894.83	906.93	999.49	1120.87	1169.56	1226.16
Frac. Inten.(% of TIC)	10.75	4.86	3.58	5.15	5.56	3.60	4.41	4.09	5.27	0.29	4.79	5.92	6.78	29.84	5.11
Rel. Inten.(% of BP)	36.02	16.28	12.01	17.25	18.63	12.07	14.77	13.69	17.64	0.98	16.05	19.85	22.71	100.00	17.12
Score	1.00	1.00	1.00	1.00	0.25	-0.12	1.00	-0.14	1.00	0.25	1.00	1.00	1.00	1.00	0.50
Ion-type	b^{++}_{10}	y^{+++}_{25}	b^{++}_{15}-H_2O	b^{++}_{15}	a_7		y^{++}_{17}		b_7	st	b^{++}_{16}	b^{++}_{19}	y^{++}_{24}	y^{++}_{25}	y_{10}-NH_3
Delta Da	0.57	0.44	-0.34	0.49	0.07		0.51		-0.24	0.15	0.54	0.56	0.32	0.49	-0.40
			b^{+++}_{26}	y^{++}_{16}			y^{+++}_{27}					y^{++}_{20}			
			0.79	-0.07			0.33					-0.01			
							y_6-NH_3					y_7-NH_3			
							0.09					0.06			

Peak 423



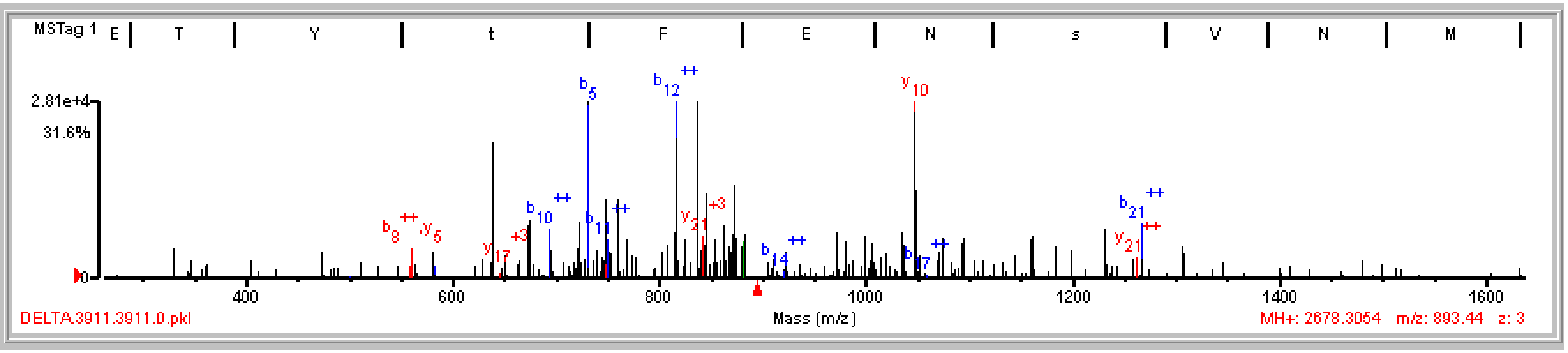


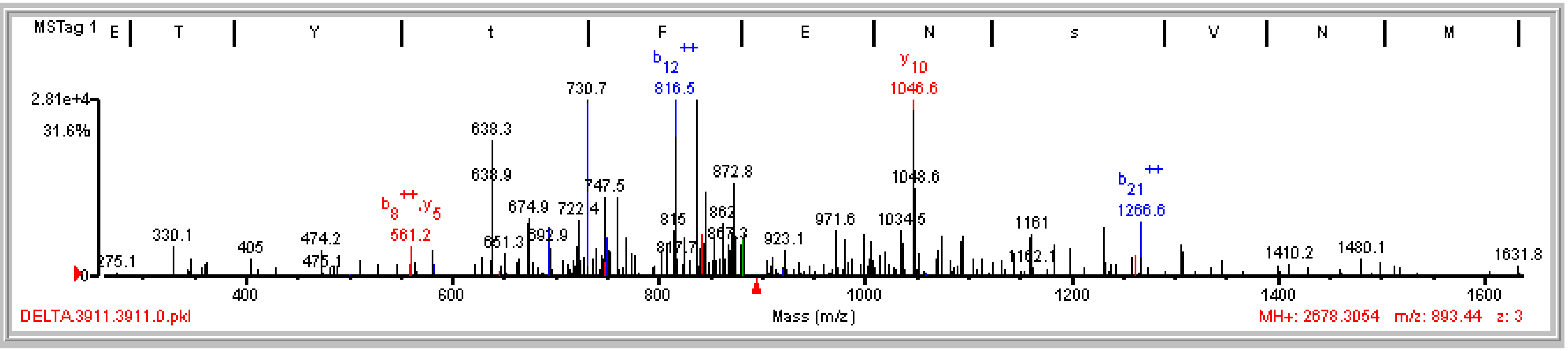


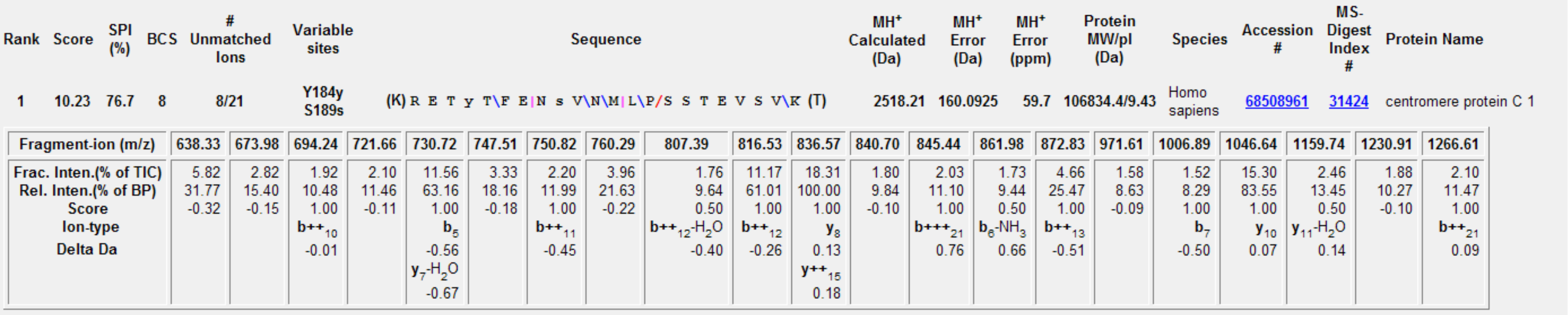
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.25	74.6	7	4/15	M192m T185t Y184y	(K) R E T y t F E/N/S/V/N\m L\P S S T\E V S V K (T)	2518.21	175.3652	-208.8	106834.4/9.43	Homo sapiens	68508961	31424	centromere protein C 1

Fragment-ion (m/z)	543.12	635.70	649.17	651.24	654.20	658.09	703.47	712.11	738.46	744.98	747.96	750.64	804.51	857.14	880.98
Frac. Inten.(% of TIC)	5.61	7.14	0.28	5.21	0.21	0.52	5.37	4.95	8.98	6.75	20.26	9.21	13.48	6.26	5.76
Rel. Inten.(% of BP)	27.70	35.25	1.38	25.73	1.06	2.58	26.49	24.43	44.32	33.30	100.00	45.47	66.55	30.89	28.44
Score	0.50	-0.35	1.50	-0.26	2.00	2.00	1.00	1.00	0.50	-0.33	1.00	1.00	1.00	-0.31	1.00
Ion-type	y_5-H_2O		sty		$y{++}_{12}$ m	m	$y{++}_{13}$	$b{+++}_{17}$	$y{++}_{14}$-H_2O		$y{++}_{14}$	$b{++}_{11}$	$y{++}_{15}$		$b{++}_{13}$
Delta Da	-0.19		-0.63		-0.13	-0.20	-0.39	0.16	0.09		0.58	-0.63	0.11		-0.35

Peak 424





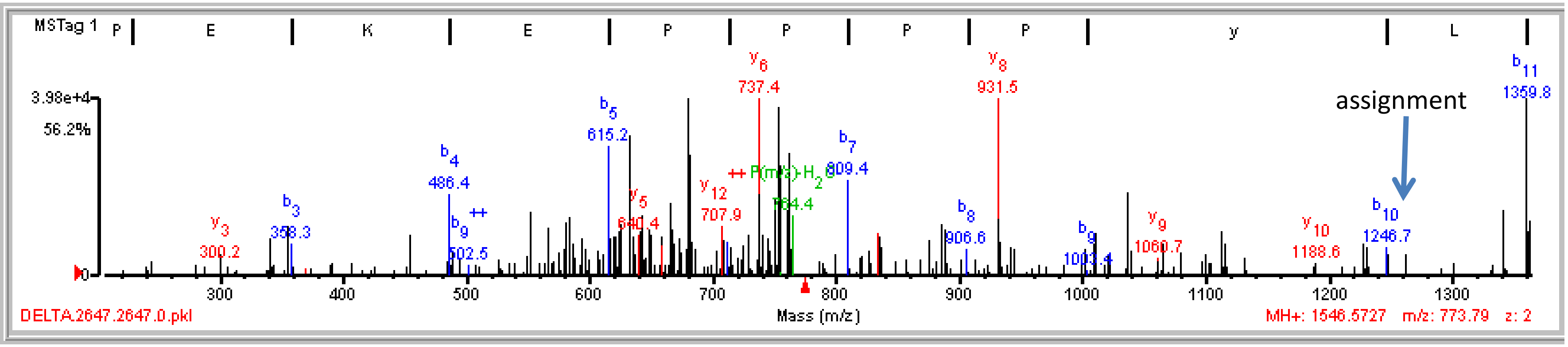


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.23	76.7	8	8/21	Y184y S189s	(K) R E T y T\F E|N s V\N\M|L\P/S S T E V S V\K (T)	2518.21	160.0925	59.7	106834.4/9.43	Homo sapiens	68508961	31424	centromere protein C 1

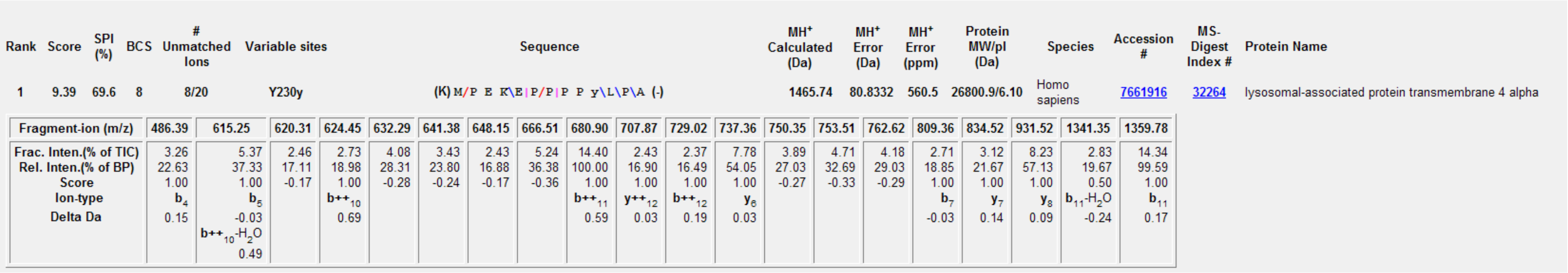
Fragment-ion (m/z)	638.33	673.98	694.24	721.66	730.72	747.51	750.82	760.29	807.39	816.53	836.57
Frac. Inten.(% of TIC)	5.82	2.82	1.92	2.10	11.56	3.33	2.20	3.96	1.76	11.17	18.31
Rel. Inten.(% of BP)	31.77	15.40	10.48	11.46	63.16	18.16	11.99	21.63	9.64	61.01	100.00
Score	-0.32	-0.15	1.00	-0.11	1.00	-0.18	1.00	-0.22	0.50	1.00	1.00
Ion-type			b++$_{10}$		b$_5$ y$_7$-H$_2$O		b++$_{11}$		b++$_{12}$-H$_2$O	b++$_{12}$	y$_8$ y++$_{15}$
Delta Da			-0.01		-0.56 -0.67		-0.45		-0.40	-0.26	0.13 0.18

Fragment-ion (m/z)	840.70	845.44	861.98	872.83	971.61	1006.89	1046.64	1159.74	1230.91	1266.61
Frac. Inten.(% of TIC)	1.80	2.03	1.73	4.66	1.58	1.52	15.30	2.46	1.88	2.10
Rel. Inten.(% of BP)	9.84	11.10	9.44	25.47	8.63	8.29	83.55	13.45	10.27	11.47
Score	-0.10	1.00	0.50	1.00	-0.09	1.00	1.00	0.50	-0.10	1.00
Ion-type		b+++$_{21}$	b$_6$-NH$_3$	b++$_{13}$		b$_7$	y$_{10}$	y$_{11}$-H$_2$O		b++$_{21}$
Delta Da		0.76	0.66	-0.51		-0.50	0.07	0.14		0.09

Peak 425



assignment

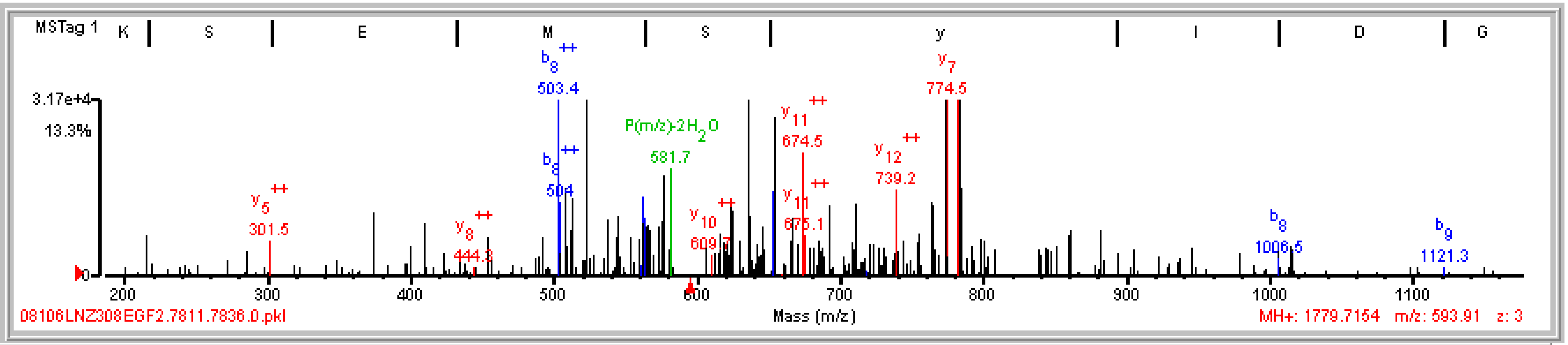


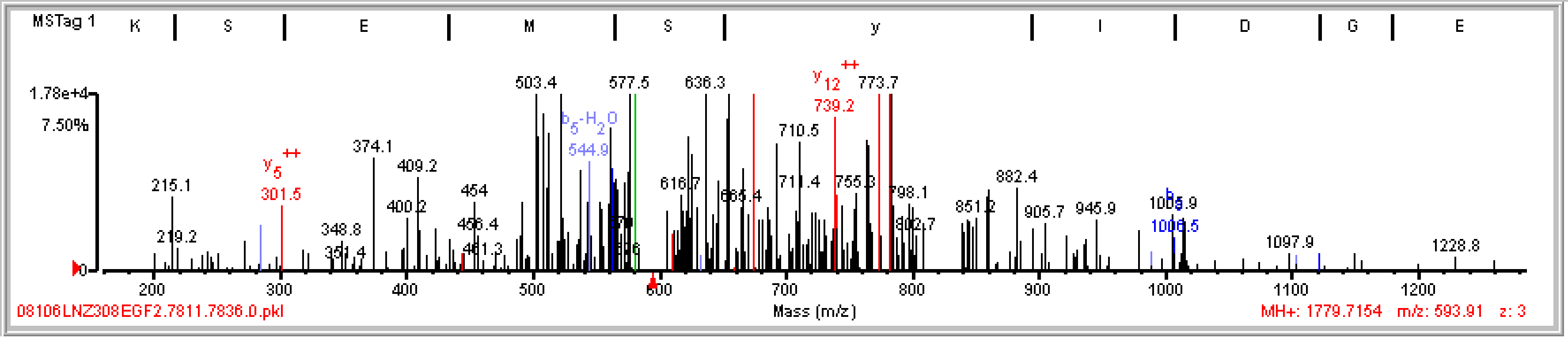
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.39	69.6	8	8/20	Y230y	(K) M/P E K\E|P/P|P P y\L\P\A (-)	1465.74	80.8332	560.5	26800.9/6.10	Homo sapiens	7661916	32264	lysosomal-associated protein transmembrane 4 alpha

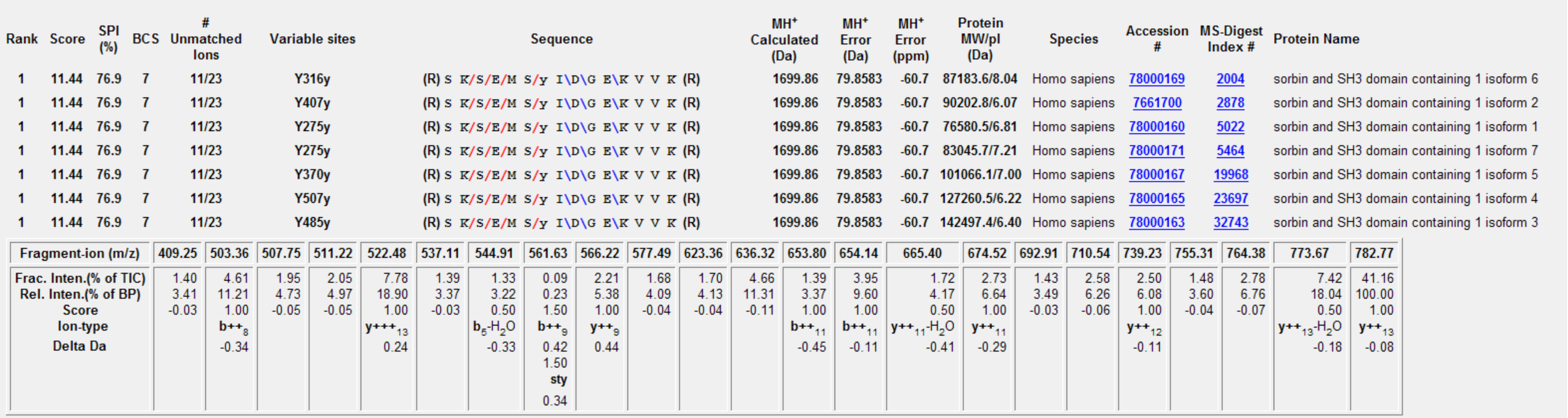
Fragment-ion (m/z)	486.39	615.25	620.31	624.45	632.29	641.38	648.15	666.51	680.90	707.87
Frac. Inten.(% of TIC)	3.26	5.37	2.46	2.73	4.08	3.43	2.43	5.24	14.40	2.43
Rel. Inten.(% of BP)	22.63	37.33	17.11	18.98	28.31	23.80	16.88	36.38	100.00	16.90
Score	1.00	1.00	-0.17	1.00	-0.28	-0.24	-0.17	-0.36	1.00	1.00
Ion-type	b_4	b_5 $b{+}{+}_{10}-H_2O$		$b{+}{+}_{10}$					$b{+}{+}_{11}$	$y{+}{+}_{12}$
Delta Da	0.15	-0.03 0.49		0.69					0.59	0.03

Fragment-ion (m/z)	729.02	737.36	750.35	753.51	762.62	809.36	834.52	931.52	1341.35	1359.78
Frac. Inten.(% of TIC)	2.37	7.78	3.89	4.71	4.18	2.71	3.12	8.23	2.83	14.34
Rel. Inten.(% of BP)	16.49	54.05	27.03	32.69	29.03	18.85	21.67	57.13	19.67	99.59
Score	1.00	1.00	-0.27	-0.33	-0.29	1.00	1.00	1.00	0.50	1.00
Ion-type	$b{+}{+}_{12}$	y_6				b_7	y_7	y_8	$b_{11}-H_2O$	b_{11}
Delta Da	0.19	0.03				-0.03	0.14	0.09	-0.24	0.17

Peak 426





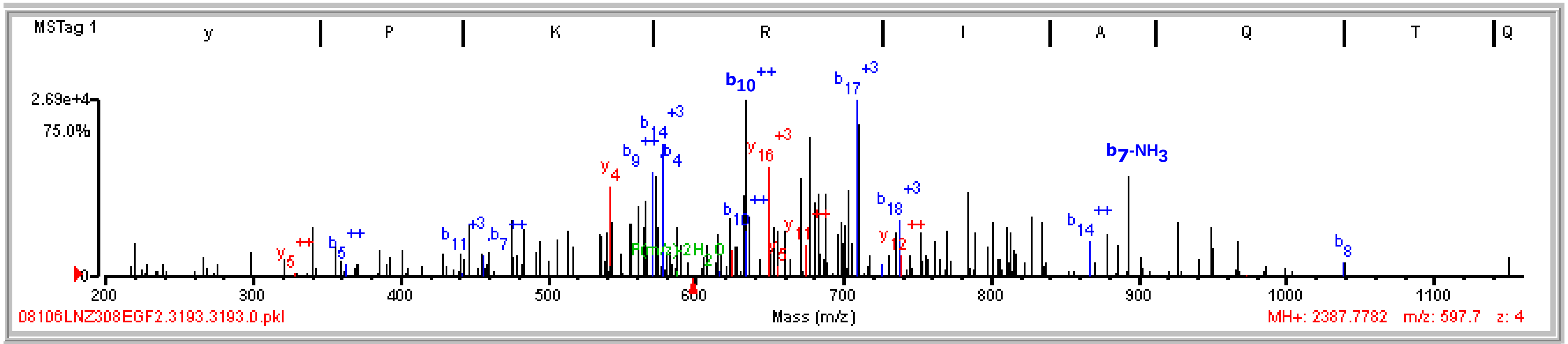


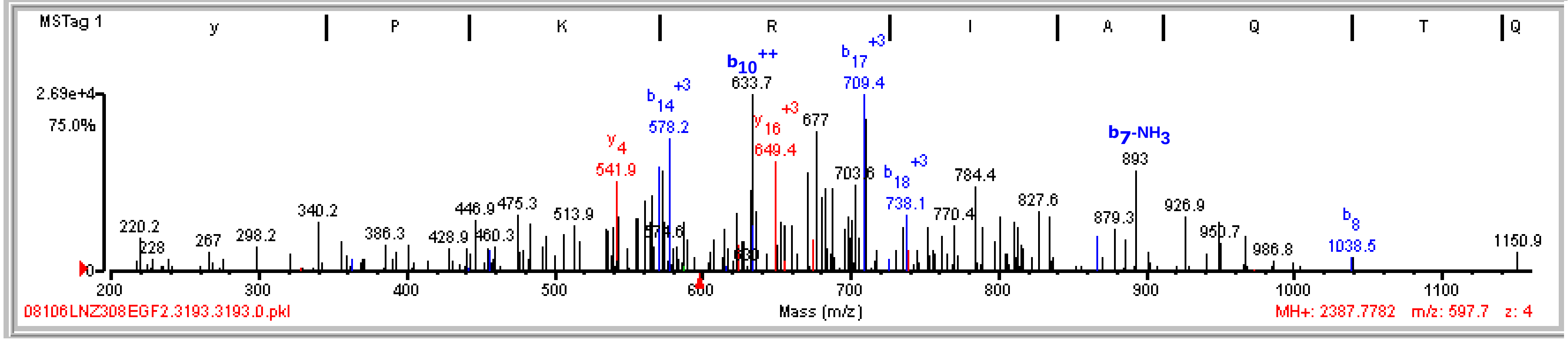
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.44	76.9	7	11/23	Y316y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	87183.6/8.04	Homo sapiens	78000169	2004	sorbin and SH3 domain containing 1 isoform 6
1	11.44	76.9	7	11/23	Y407y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	90202.8/6.07	Homo sapiens	7661700	2878	sorbin and SH3 domain containing 1 isoform 2
1	11.44	76.9	7	11/23	Y275y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	76580.5/6.81	Homo sapiens	78000160	5022	sorbin and SH3 domain containing 1 isoform 1
1	11.44	76.9	7	11/23	Y275y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	83045.7/7.21	Homo sapiens	78000171	5464	sorbin and SH3 domain containing 1 isoform 7
1	11.44	76.9	7	11/23	Y370y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	101066.1/7.00	Homo sapiens	78000167	19968	sorbin and SH3 domain containing 1 isoform 5
1	11.44	76.9	7	11/23	Y507y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	127260.5/6.22	Homo sapiens	78000165	23697	sorbin and SH3 domain containing 1 isoform 4
1	11.44	76.9	7	11/23	Y485y	(R) S K/S/E/M S/y I\D\G E\K V V K (R)	1699.86	79.8583	-60.7	142497.4/6.40	Homo sapiens	78000163	32743	sorbin and SH3 domain containing 1 isoform 3

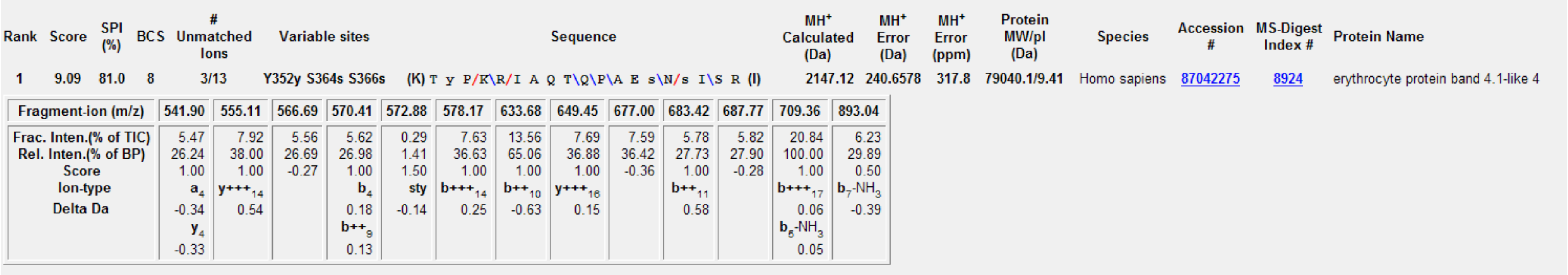
Fragment-ion (m/z)	409.25	503.36	507.75	511.22	522.48	537.11	544.91	561.63	566.22	577.49	623.36
Frac. Inten.(% of TIC)	1.40	4.61	1.95	2.05	7.78	1.39	1.33	0.09	2.21	1.68	1.70
Rel. Inten.(% of BP)	3.41	11.21	4.73	4.97	18.90	3.37	3.22	0.23	5.38	4.09	4.13
Score	-0.03	1.00	-0.05	-0.05	1.00	-0.03	0.50	1.50	1.00	-0.04	-0.04
Ion-type		b^{++}_8			y^{+++}_{13}		b_5-H_2O	b^{++}_9	y^{++}_9		
Delta Da		-0.34			0.24		-0.33	0.42 1.50 sty 0.34	0.44		

Fragment-ion (m/z)	636.32	653.80	654.14	665.40	674.52	692.91	710.54	739.23	755.31	764.38	773.67	782.77
Frac. Inten.(% of TIC)	4.66	1.39	3.95	1.72	2.73	1.43	2.58	2.50	1.48	2.78	7.42	41.16
Rel. Inten.(% of BP)	11.31	3.37	9.60	4.17	6.64	3.49	6.26	6.08	3.60	6.76	18.04	100.00
Score	-0.11	1.00	1.00	0.50	1.00	-0.03	-0.06	1.00	-0.04	-0.07	0.50	1.00
Ion-type		b^{++}_{11}	b^{++}_{11}	$y^{++}_{11}-H_2O$	y^{++}_{11}			y^{++}_{12}			$y^{++}_{13}-H_2O$	y^{++}_{13}
Delta Da		-0.45	-0.11	-0.41	-0.29			-0.11			-0.18	-0.08

Peak 427



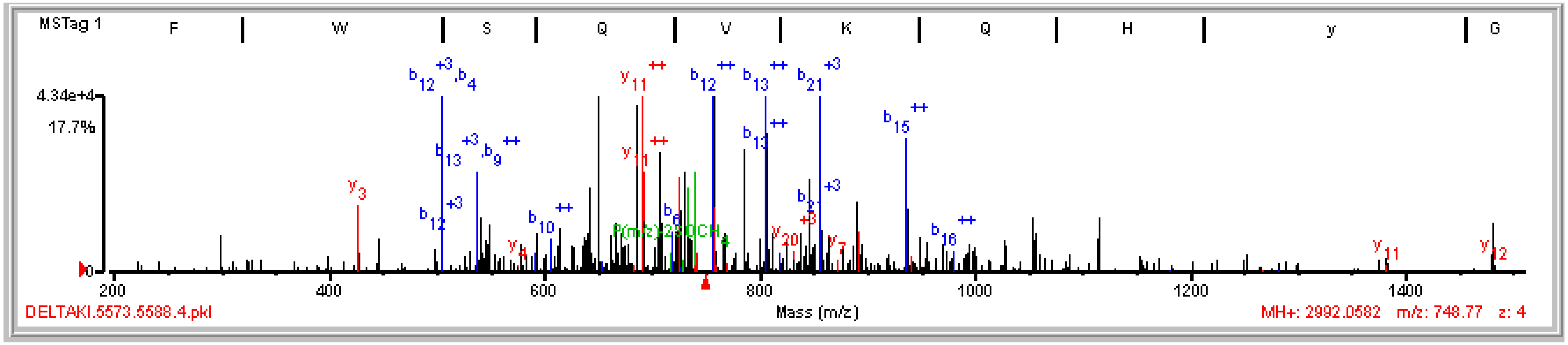


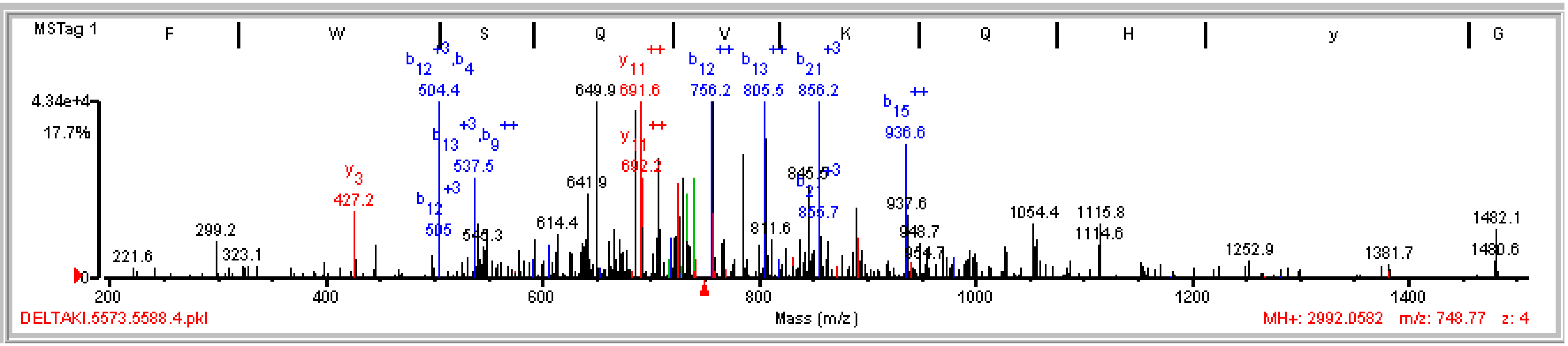


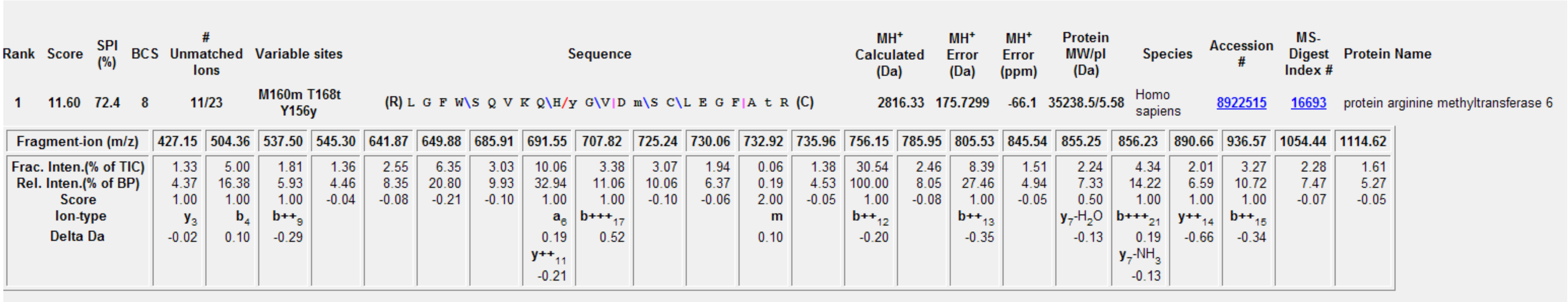
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.09	81.0	8	3/13	Y352y S364s S366s	(K) T y P/K\R/I A Q T\Q\P\A E s\N/s I\S R (I)	2147.12	240.6578	317.8	79040.1/9.41	Homo sapiens	87042275	8924	erythrocyte protein band 4.1-like 4

Fragment-ion (m/z)	541.90	555.11	566.69	570.41	572.88	578.17	633.68	649.45	677.00	683.42	687.77	709.36	893.04
Frac. Inten.(% of TIC)	5.47	7.92	5.56	5.62	0.29	7.63	13.56	7.69	7.59	5.78	5.82	20.84	6.23
Rel. Inten.(% of BP)	26.24	38.00	26.69	26.98	1.41	36.63	65.06	36.88	36.42	27.73	27.90	100.00	29.89
Score	1.00	1.00	-0.27	1.00	1.50	1.00	1.00	1.00	-0.36	1.00	-0.28	1.00	0.50
Ion-type	a_4	$y{+}{+}{+}_{14}$		b_4	sty	$b{+}{+}{+}_{14}$	$b{+}{+}_{10}$	$y{+}{+}{+}_{16}$		$b{+}{+}_{11}$		$b{+}{+}{+}_{17}$	b_7-NH_3
Delta Da	-0.34	0.54		0.18	-0.14	0.25	-0.63	0.15		0.58		0.06	-0.39
	y_4			$b{+}{+}_9$								b_5-NH_3	
	-0.33			0.13								0.05	

Peak 428





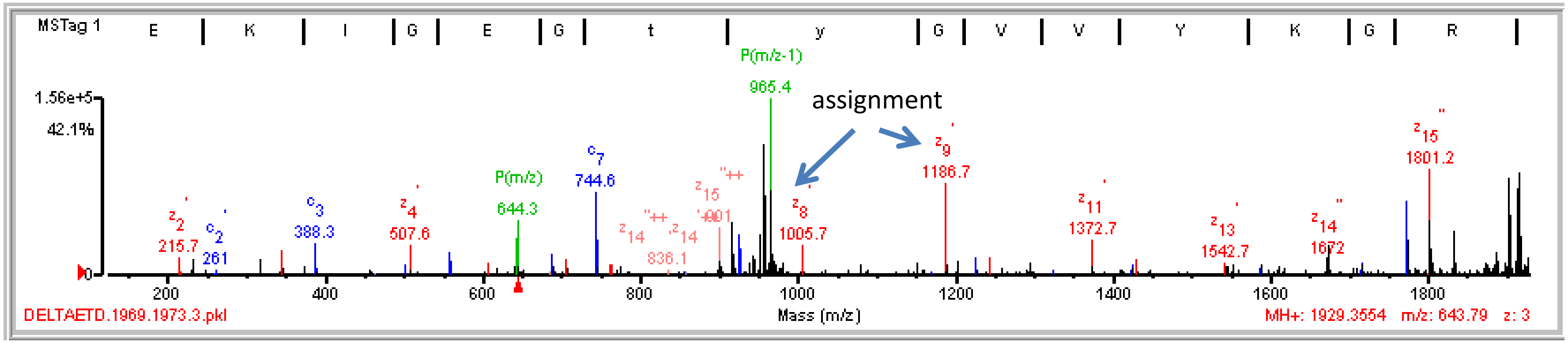


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.60	72.4	8	11/23	M160m T168t Y156y	(R) L G F W\S Q V K Q\H/y G\V|D m\S C\L E G F|A t R (C)	2816.33	175.7299	-66.1	35238.5/5.58	Homo sapiens	8922515	16693	protein arginine methyltransferase 6

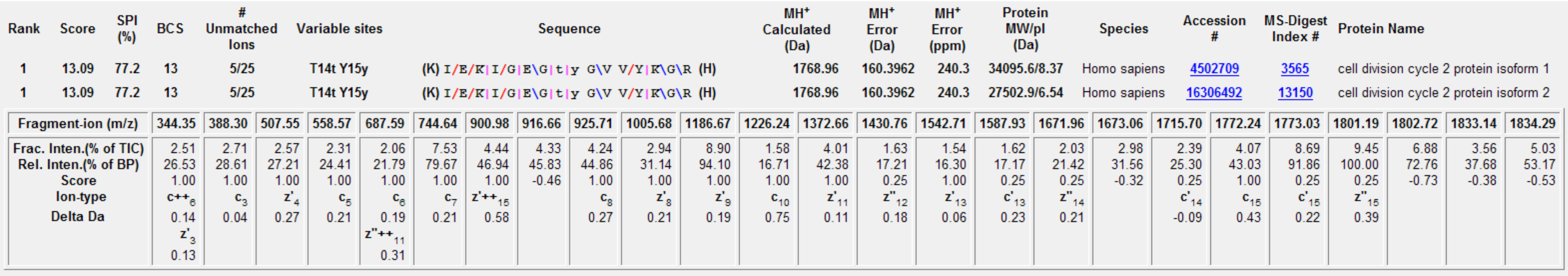
Fragment-ion (m/z)	427.15	504.36	537.50	545.30	641.87	649.88	685.91	691.55	707.82	725.24	730.06	732.92
Frac. Inten.(% of TIC)	1.33	5.00	1.81	1.36	2.55	6.35	3.03	10.06	3.38	3.07	1.94	0.06
Rel. Inten.(% of BP)	4.37	16.38	5.93	4.46	8.35	20.80	9.93	32.94	11.06	10.06	6.37	0.19
Score	1.00	1.00	1.00	-0.04	-0.08	-0.21	-0.10	1.00	1.00	-0.10	-0.06	2.00
Ion-type	y_3	b_4	$b{+}{+}_9$					a_6 $y{+}{+}_{11}$	$b{+}{+}{+}_{17}$			m
Delta Da	-0.02	0.10	-0.29					0.19 -0.21	0.52			0.10

Fragment-ion (m/z)	735.96	756.15	785.95	805.53	845.54	855.25	856.23	890.66	936.57	1054.44	1114.62
Frac. Inten.(% of TIC)	1.38	30.54	2.46	8.39	1.51	2.24	4.34	2.01	3.27	2.28	1.61
Rel. Inten.(% of BP)	4.53	100.00	8.05	27.46	4.94	7.33	14.22	6.59	10.72	7.47	5.27
Score	-0.05	1.00	-0.08	1.00	-0.05	0.50	1.00	1.00	1.00	-0.07	-0.05
Ion-type		$b{+}{+}_{12}$		$b{+}{+}_{13}$		y_7-H_2O	$b{+}{+}{+}_{21}$ y_7-NH_3	$y{+}{+}_{14}$	$b{+}{+}_{15}$		
Delta Da		-0.20		-0.35		-0.13	0.19 -0.13	-0.66	-0.34		

Peak 429



assignment

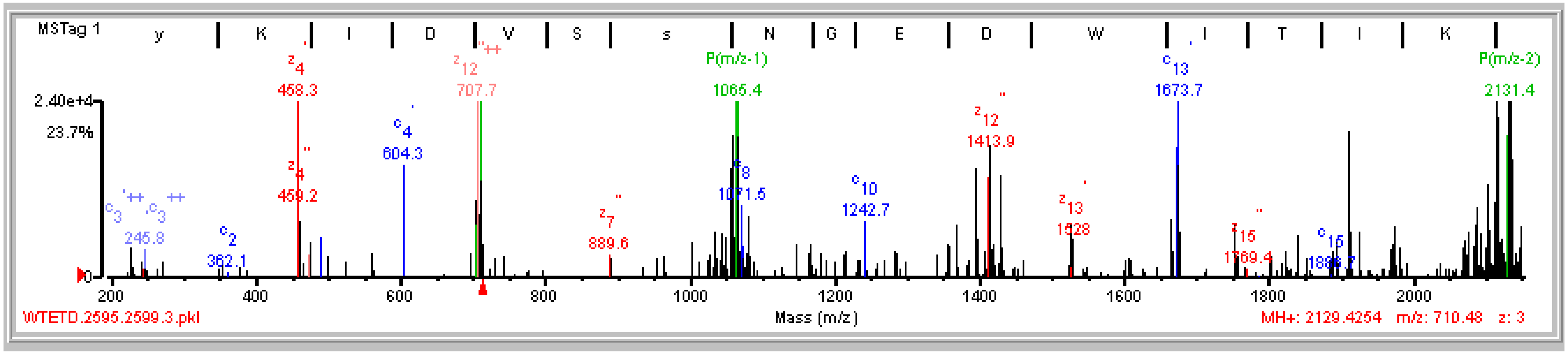


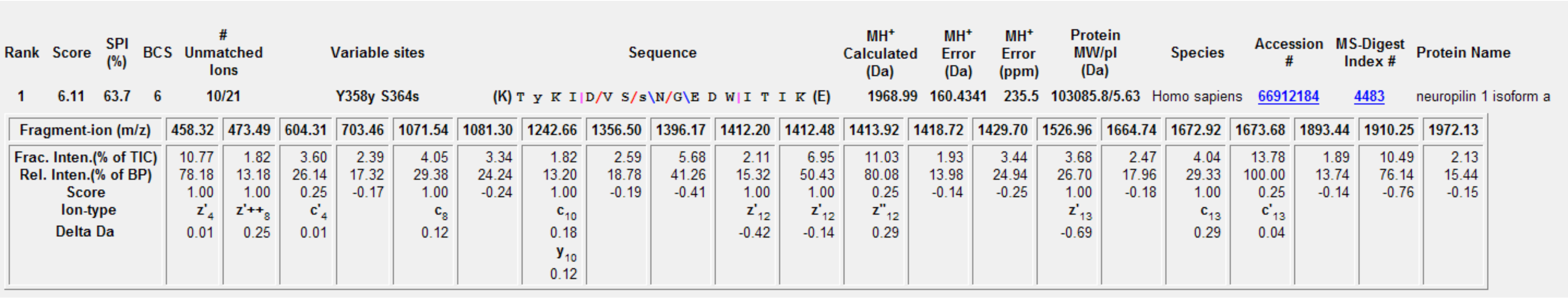
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.09	77.2	13	5/25	T14t Y15y	(K) I/E/K|I/G|E\G|t|y G\V V/Y|K\G\R (H)	1768.96	160.3962	240.3	34095.6/8.37	Homo sapiens	4502709	3565	cell division cycle 2 protein isoform 1
1	13.09	77.2	13	5/25	T14t Y15y	(K) I/E/K|I/G|E\G|t|y G\V V/Y|K\G\R (H)	1768.96	160.3962	240.3	27502.9/6.54	Homo sapiens	16306492	13150	cell division cycle 2 protein isoform 2

Fragment-ion (m/z)	344.35	388.30	507.55	558.57	687.59	744.64	900.98	916.66	925.71	1005.68	1186.67	1226.24
Frac. Inten.(% of TIC)	2.51	2.71	2.57	2.31	2.06	7.53	4.44	4.33	4.24	2.94	8.90	1.58
Rel. Inten.(% of BP)	26.53	28.61	27.21	24.41	21.79	79.67	46.94	45.83	44.86	31.14	94.10	16.71
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.46	1.00	1.00	1.00	1.00
Ion-type	$\mathrm{c{+}{+}}_{6}$ $\mathrm{z'}_{3}$	c_{3}	$\mathrm{z'}_{4}$	c_{5}	c_{6} $\mathrm{z''{+}{+}}_{11}$	c_{7}	$\mathrm{z'{+}{+}}_{15}$		c_{8}	$\mathrm{z'}_{8}$	$\mathrm{z'}_{9}$	c_{10}
Delta Da	0.14 0.13	0.04	0.27	0.21	0.19 0.31	0.21	0.58		0.27	0.21	0.19	0.75

Fragment-ion (m/z)	1372.66	1430.76	1542.71	1587.93	1671.96	1673.06	1715.70	1772.24	1773.03	1801.19	1802.72	1833.14	1834.29
Frac. Inten.(% of TIC)	4.01	1.63	1.54	1.62	2.03	2.98	2.39	4.07	8.69	9.45	6.88	3.56	5.03
Rel. Inten.(% of BP)	42.38	17.21	16.30	17.17	21.42	31.56	25.30	43.03	91.86	100.00	72.76	37.68	53.17
Score	1.00	0.25	1.00	0.25	0.25	-0.32	0.25	1.00	0.25	0.25	-0.73	-0.38	-0.53
Ion-type	$\mathrm{z'}_{11}$	$\mathrm{z''}_{12}$	$\mathrm{z'}_{13}$	$\mathrm{c'}_{13}$	$\mathrm{z''}_{14}$		$\mathrm{c'}_{14}$	c_{15}	$\mathrm{c'}_{15}$	$\mathrm{z''}_{15}$			
Delta Da	0.11	0.18	0.06	0.23	0.21		-0.09	0.43	0.22	0.39			

Peak 430



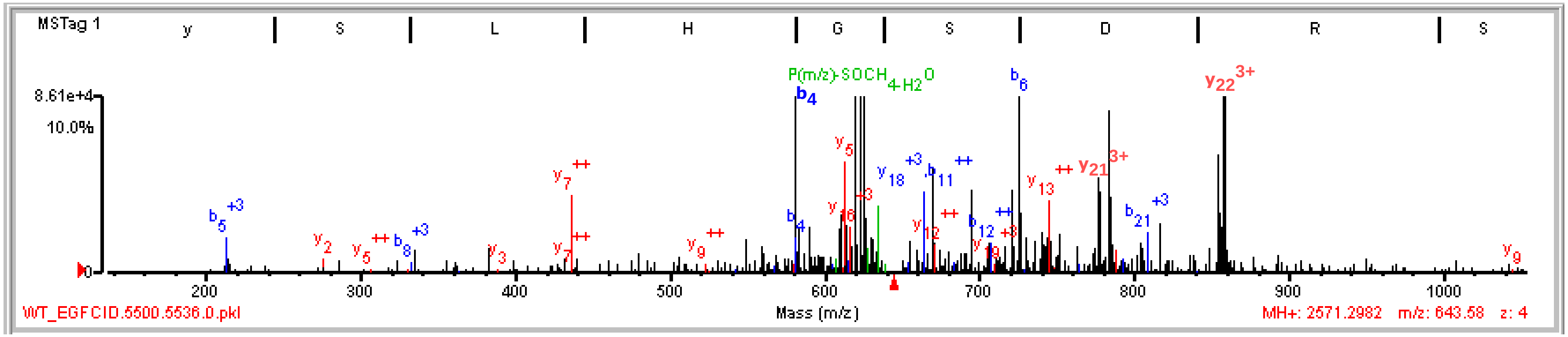


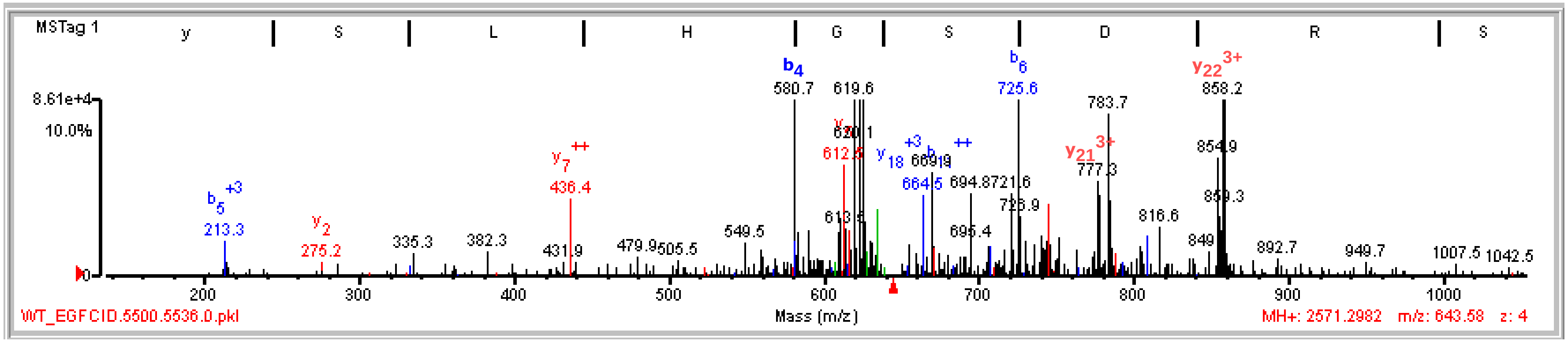
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.11	63.7	6	10/21	Y358y S364s	(K) T y K I|D/V S/s\N/G\E D W|I T I K (E)	1968.99	160.4341	235.5	103085.8/5.63	Homo sapiens	66912184	4483	neuropilin 1 isoform a

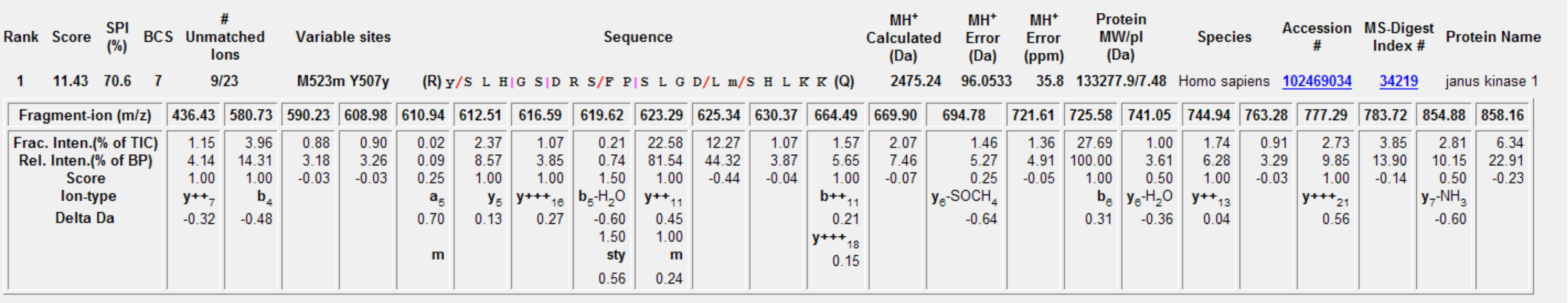
Fragment-ion (m/z)	458.32	473.49	604.31	703.46	1071.54	1081.30	1242.66	1356.50	1396.17	1412.20
Frac. Inten.(% of TIC)	10.77	1.82	3.60	2.39	4.05	3.34	1.82	2.59	5.68	2.11
Rel. Inten.(% of BP)	78.18	13.18	26.14	17.32	29.38	24.24	13.20	18.78	41.26	15.32
Score	1.00	1.00	0.25	-0.17	1.00	-0.24	1.00	-0.19	-0.41	1.00
Ion-type	z'_{4}	z'^{++}_{8}	c'_{4}		c_{8}		c_{10} y_{10}			z'_{12}
Delta Da	0.01	0.25	0.01		0.12		0.18 0.12			-0.42

Fragment-ion (m/z)	1412.48	1413.92	1418.72	1429.70	1526.96	1664.74	1672.92	1673.68	1893.44	1910.25	1972.13
Frac. Inten.(% of TIC)	6.95	11.03	1.93	3.44	3.68	2.47	4.04	13.78	1.89	10.49	2.13
Rel. Inten.(% of BP)	50.43	80.08	13.98	24.94	26.70	17.96	29.33	100.00	13.74	76.14	15.44
Score	1.00	0.25	-0.14	-0.25	1.00	-0.18	1.00	0.25	-0.14	-0.76	-0.15
Ion-type	z'_{12}	z''_{12}			z'_{13}		c_{13}	c'_{13}			
Delta Da	-0.14	0.29			-0.69		0.29	0.04			

Peak 431



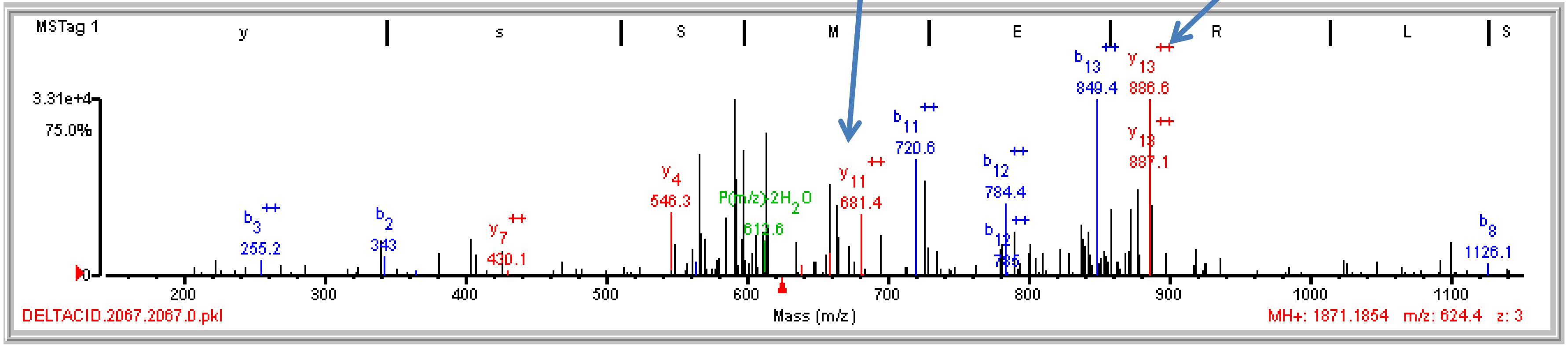




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.43	70.6	7	9/23	M523m Y507y	(R) y/S L H|G S|D R S/F P|S L G D/L m/S H L K K (Q)	2475.24	96.0533	35.8	133277.9/7.48	Homo sapiens	102469034	34219	janus kinase 1

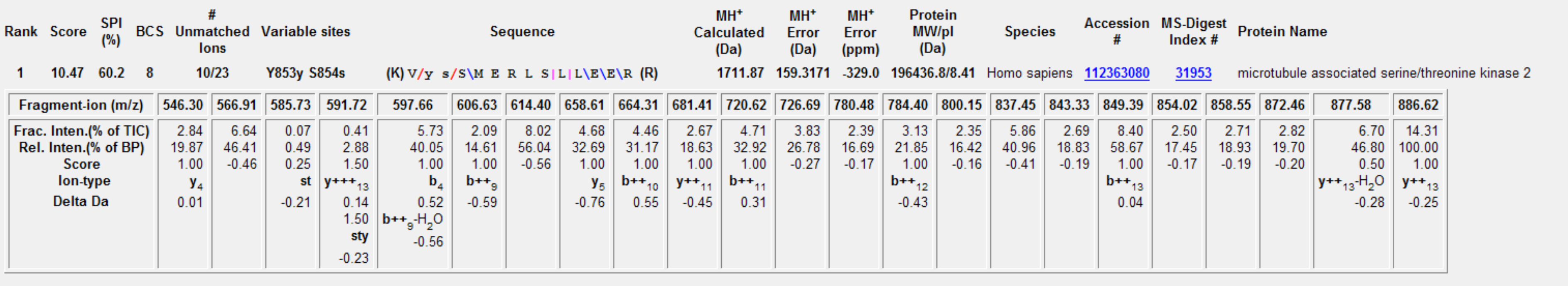
Fragment-ion (m/z)	436.43	580.73	590.23	608.98	610.94	612.51	616.59	619.62	623.29	625.34	630.37	664.49	669.90	694.78	721.61	725.58	741.05	744.94	763.28	777.29	783.72	854.88	858.16
Frac. Inten.(% of TIC)	1.15	3.96	0.88	0.90	0.02	2.37	1.07	0.21	22.58	12.27	1.07	1.57	2.07	1.46	1.36	27.69	1.00	1.74	0.91	2.73	3.85	2.81	6.34
Rel. Inten.(% of BP)	4.14	14.31	3.18	3.26	0.09	8.57	3.85	0.74	81.54	44.32	3.87	5.65	7.46	5.27	4.91	100.00	3.61	6.28	3.29	9.85	13.90	10.15	22.91
Score	1.00	1.00	-0.03	-0.03	0.25	1.00	1.00	1.50	1.00	-0.44	-0.04	1.00	-0.07	0.25	-0.05	1.00	0.50	1.00	-0.03	1.00	-0.14	0.50	-0.23
Ion-type	$y++_7$	b_4			a_5	y_5	$y+++_{16}$	b_5-H_2O	$y++_{11}$			$b++_{11}$		y_6-$SOCH_4$		b_6	y_6-H_2O	$y++_{13}$		$y+++_{21}$		y_7-NH_3	
Delta Da	-0.32	-0.48			0.70	0.13	0.27	-0.60	0.45			0.21		-0.64		0.31	-0.36	0.04		0.56		-0.60	
								1.50	1.00			$y+++_{18}$											
					m			sty	m			0.15											
								0.56	0.24														

Peak 432



Ions that verify assignment

assignment

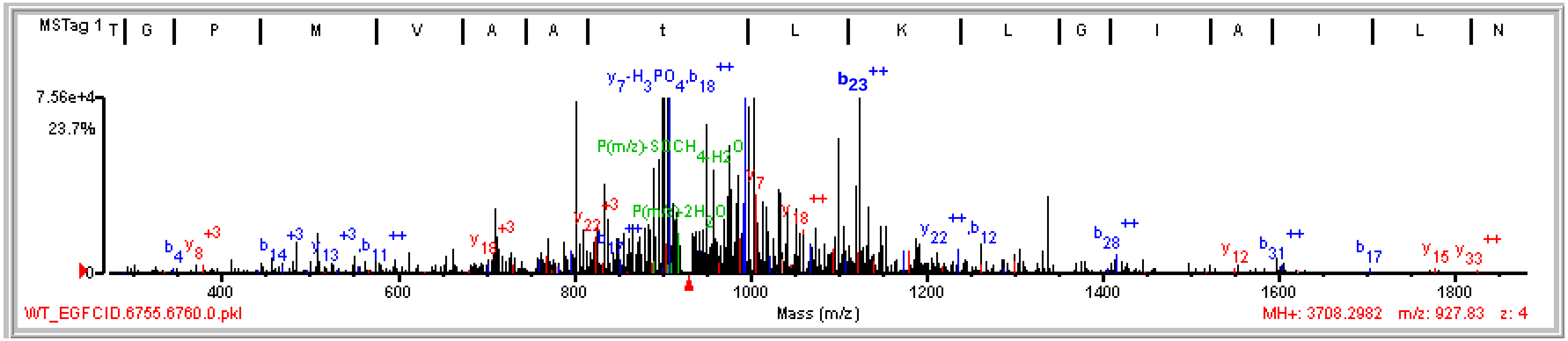


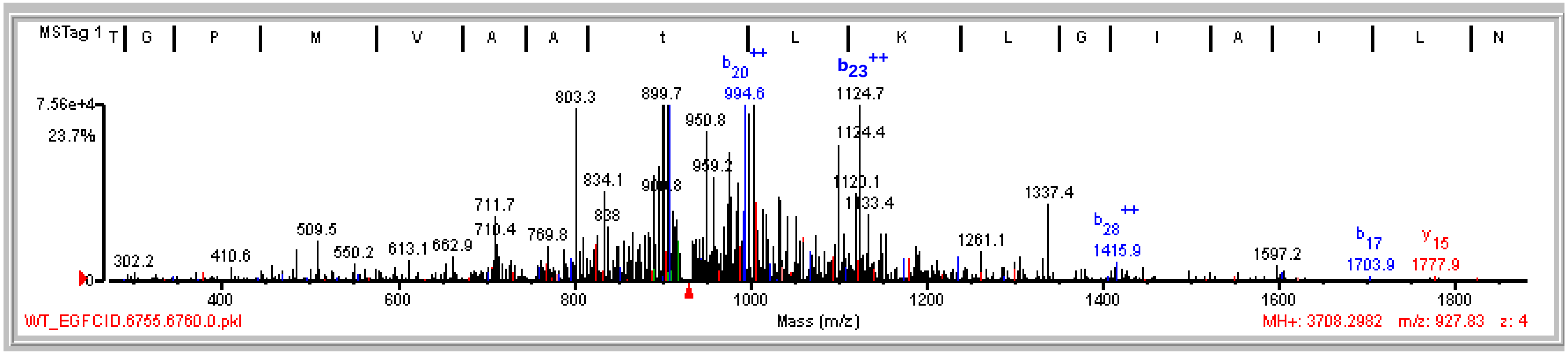
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.47	60.2	8	10/23	Y853y S854s	(K) V/y s/S\M E R L S|L|L\E\E\R (R)	1711.87	159.3171	-329.0	196436.8/8.41	Homo sapiens	112363080	31953	microtubule associated serine/threonine kinase 2

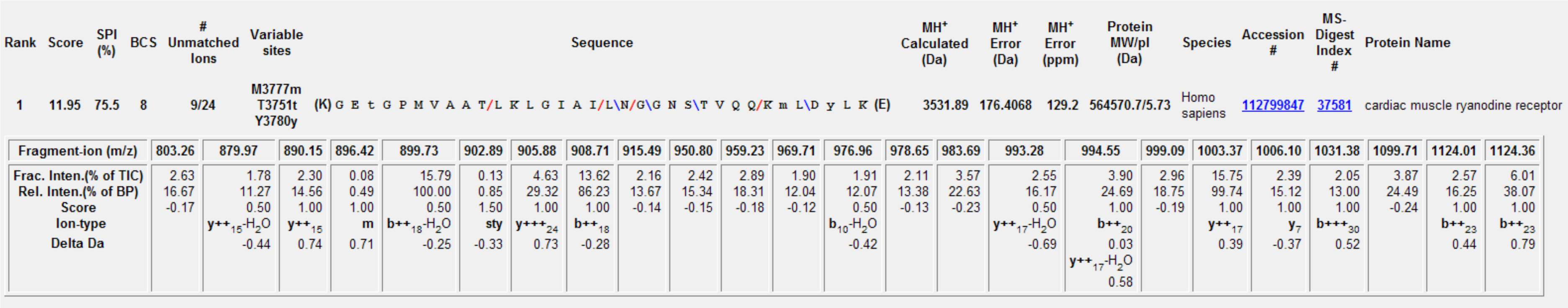
Fragment-ion (m/z)	546.30	566.91	585.73	591.72	597.66	606.63	614.40	658.61	664.31	681.41	720.62
Frac. Inten.(% of TIC)	2.84	6.64	0.07	0.41	5.73	2.09	8.02	4.68	4.46	2.67	4.71
Rel. Inten.(% of BP)	19.87	46.41	0.49	2.88	40.05	14.61	56.04	32.69	31.17	18.63	32.92
Score	1.00	-0.46	0.25	1.50 1.50	1.00	1.00	-0.56	1.00	1.00	1.00	1.00
Ion-type	y_4		st	$y{+}{+}{+}_{13}$ sty	b_4 $b{+}{+}_9\text{-}H_2O$	$b{+}{+}_9$		y_5	$b{+}{+}_{10}$	$y{+}{+}_{11}$	$b{+}{+}_{11}$
Delta Da	0.01		-0.21	0.14 -0.23	0.52 -0.56	-0.59		-0.76	0.55	-0.45	0.31

Fragment-ion (m/z)	726.69	780.48	784.40	800.15	837.45	843.33	849.39	854.02	858.55	872.46	877.58	886.62
Frac. Inten.(% of TIC)	3.83	2.39	3.13	2.35	5.86	2.69	8.40	2.50	2.71	2.82	6.70	14.31
Rel. Inten.(% of BP)	26.78	16.69	21.85	16.42	40.96	18.83	58.67	17.45	18.93	19.70	46.80	100.00
Score	-0.27	-0.17	1.00	-0.16	-0.41	-0.19	1.00	-0.17	-0.19	-0.20	0.50	1.00
Ion-type			$b{+}{+}_{12}$				$b{+}{+}_{13}$				$y{+}{+}_{13}\text{-}H_2O$	$y{+}{+}_{13}$
Delta Da			-0.43				0.04				-0.28	-0.25

Peak 433





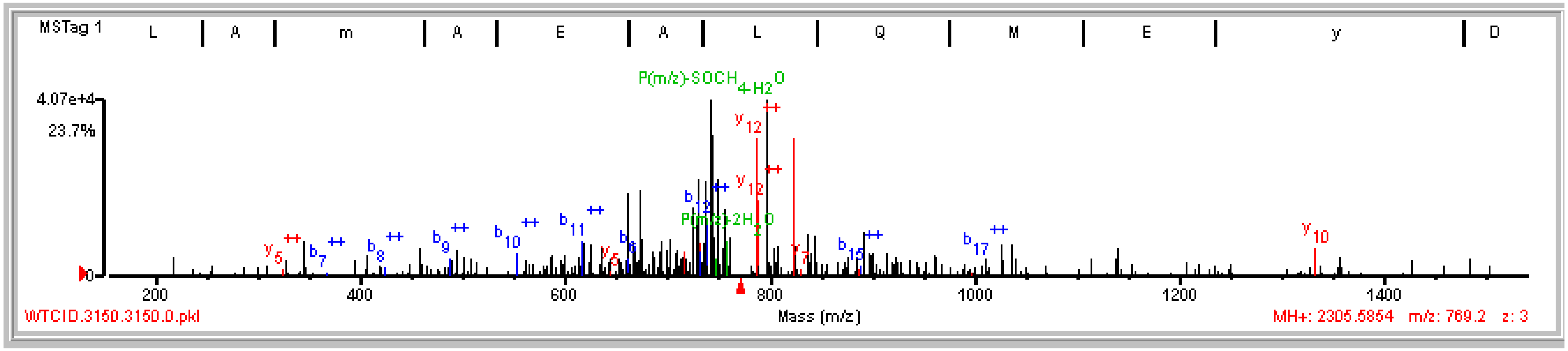


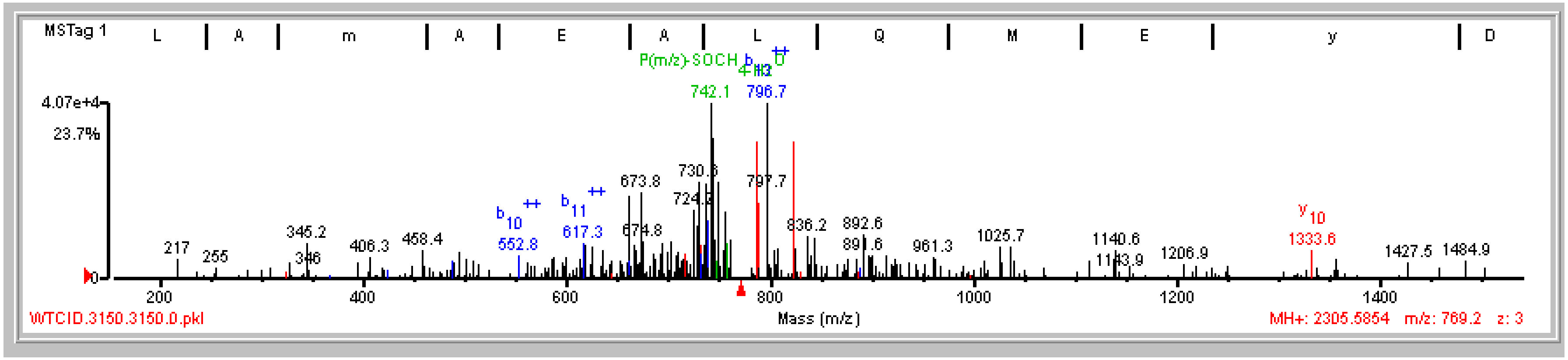
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.95	75.5	8	9/24	M3777m T3751t Y3780y	(K) G E t G P M V A A T/L K L G I A I/L\N/G\G N S\T V Q Q/K m L\D y L K (E)	3531.89	176.4068	129.2	564570.7/5.73	Homo sapiens	112799847	37581	cardiac muscle ryanodine receptor

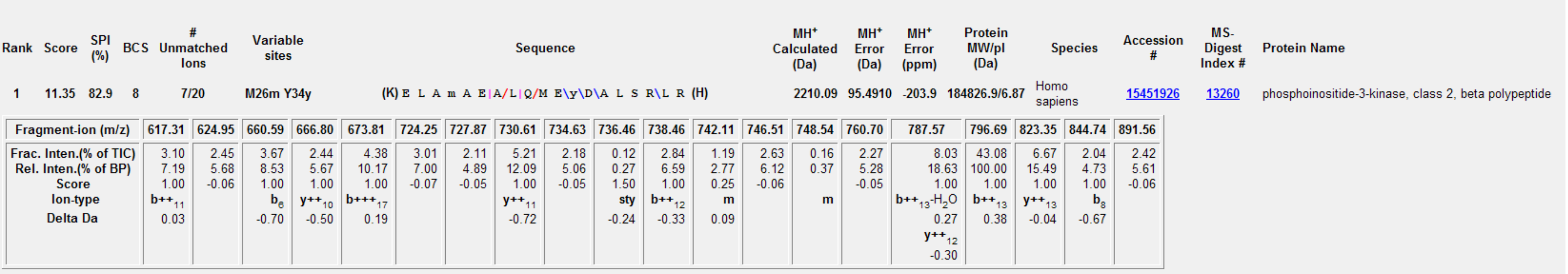
Fragment-ion (m/z)	803.26	879.97	890.15	896.42	899.73	902.89	905.88	908.71	915.49	950.80	959.23
Frac. Inten.(% of TIC)	2.63	1.78	2.30	0.08	15.79	0.13	4.63	13.62	2.16	2.42	2.89
Rel. Inten.(% of BP)	16.67	11.27	14.56	0.49	100.00	0.85	29.32	86.23	13.67	15.34	18.31
Score	-0.17	0.50	1.00	1.00	0.50	1.50	1.00	1.00	-0.14	-0.15	-0.18
Ion-type		$y{+}{+}_{15}$-H_2O	$y{+}{+}_{15}$	m	$b{+}{+}_{18}$-H_2O	sty	$y{+}{+}{+}_{24}$	$b{+}{+}_{18}$			
Delta Da		-0.44	0.74	0.71	-0.25	-0.33	0.73	-0.28			

Fragment-ion (m/z)	969.71	976.96	978.65	983.69	993.28	994.55	999.09	1003.37	1006.10	1031.38	1099.71	1124.01	1124.36
Frac. Inten.(% of TIC)	1.90	1.91	2.11	3.57	2.55	3.90	2.96	15.75	2.39	2.05	3.87	2.57	6.01
Rel. Inten.(% of BP)	12.04	12.07	13.38	22.63	16.17	24.69	18.75	99.74	15.12	13.00	24.49	16.25	38.07
Score	-0.12	0.50	-0.13	-0.23	0.50	1.00	-0.19	1.00	1.00	1.00	-0.24	1.00	1.00
Ion-type		b_{10}-H_2O			$y{+}{+}_{17}$-H_2O	$b{+}{+}_{20}$ 0.03 $y{+}{+}_{17}$-H_2O		$y{+}{+}_{17}$	y_7	$b{+}{+}{+}_{30}$		$b{+}{+}_{23}$	$b{+}{+}_{23}$
Delta Da		-0.42			-0.69	0.58		0.39	-0.37	0.52		0.44	0.79

Peak 434







<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH^+ Calculated (Da)</th><th>MH^+ Error (Da)</th><th>MH^+ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>11.35</td><td>82.9</td><td>8</td><td>7/20</td><td>M26m Y34y</td><td>(K) E L A m A E|A/L|Q/M E\y\D\A L S R\L R (H)</td><td>2210.09</td><td>95.4910</td><td>-203.9</td><td>184826.9/6.87</td><td>Homo sapiens</td><td>15451926</td><td>13260</td><td>phosphoinositide-3-kinase, class 2, beta polypeptide</td></tr>
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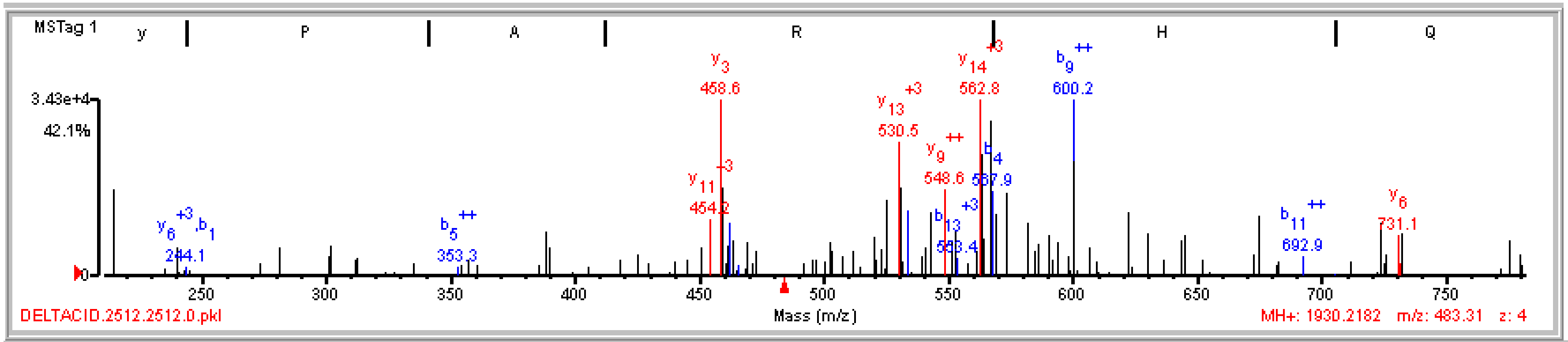
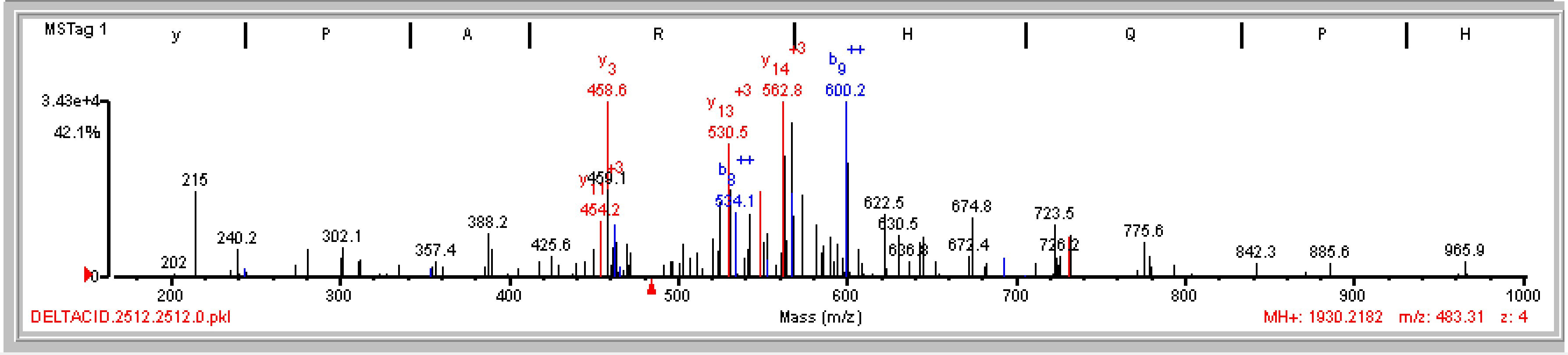
Fragment-ion (m/z)	617.31	624.95	660.59	666.80	673.81	724.25	727.87	730.61	734.63	736.46	738.46	742.11	746.51	748.54	760.70	787.57	796.69	823.35	844.74	891.56
Frac. Inten.(% of TIC)	3.10	2.45	3.67	2.44	4.38	3.01	2.11	5.21	2.18	0.12	2.84	1.19	2.63	0.16	2.27	8.03	43.08	6.67	2.04	2.42
Rel. Inten.(% of BP)	7.19	5.68	8.53	5.67	10.17	7.00	4.89	12.09	5.06	0.27	6.59	2.77	6.12	0.37	5.28	18.63	100.00	15.49	4.73	5.61
Score	1.00	-0.06	1.00	1.00	1.00	-0.07	-0.05	1.00	-0.05	1.50	1.00	0.25	-0.06		-0.05	1.00	1.00	1.00	1.00	-0.06
Ion-type	$b{+}{+}_{11}$		b_6	$y{+}{+}_{10}$	$b{+}{+}{+}_{17}$			$y{+}{+}_{11}$		sty	$b{+}{+}_{12}$	m		m		$b{+}{+}_{13}\text{-}H_2O$ $y{+}{+}_{12}$	$b{+}{+}_{13}$	$y{+}{+}_{13}$	b_8	
Delta Da	0.03		-0.70	-0.50	0.19			-0.72		-0.24	-0.33	0.09				0.27 -0.30	0.38	-0.04	-0.67	

Peak 435

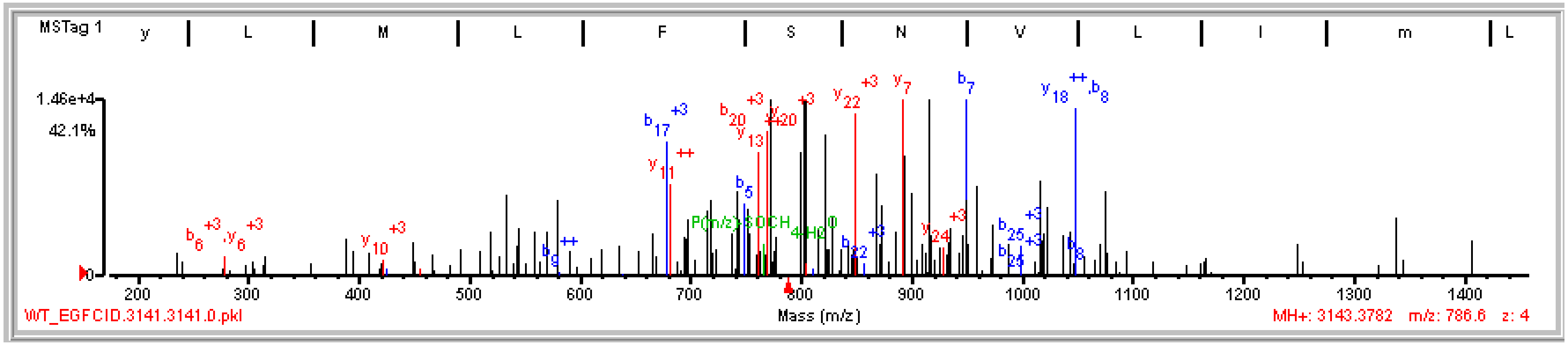


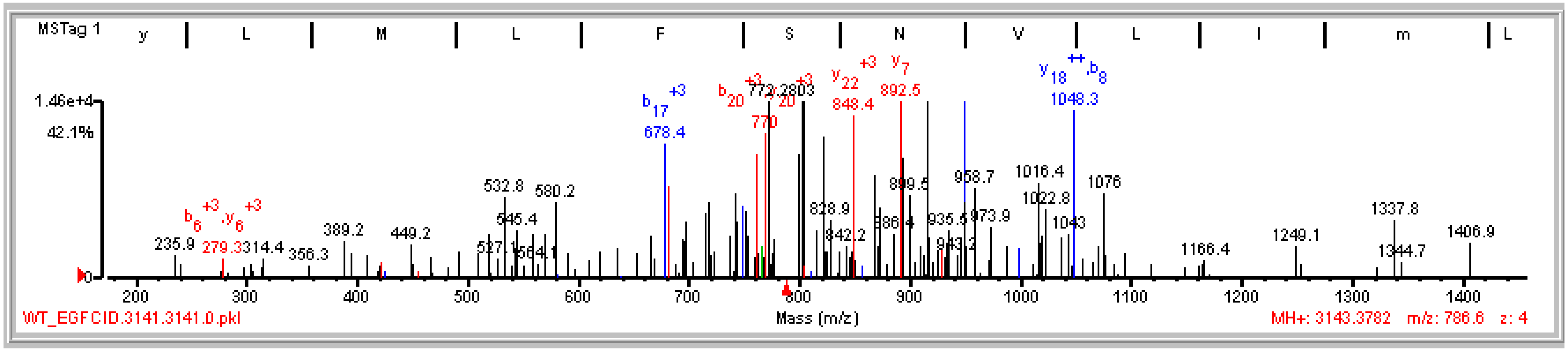


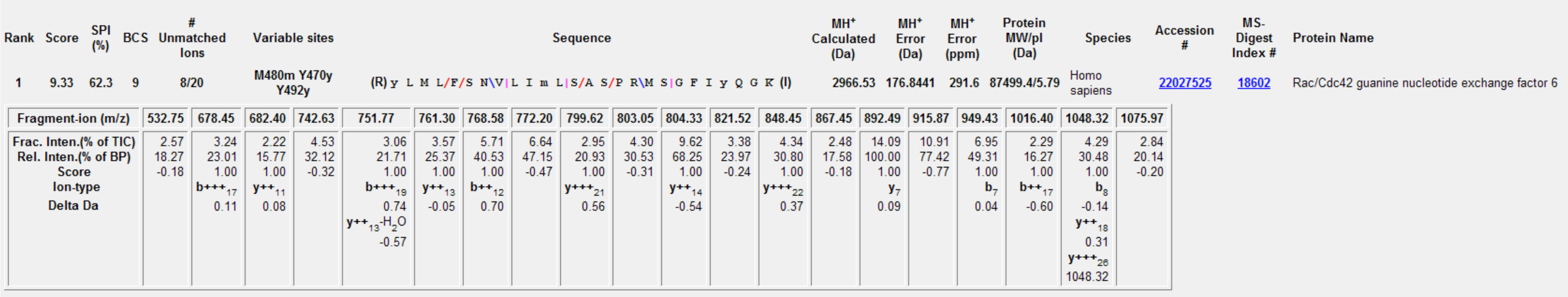
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.19	82.1	8	5/16	Y297y	(R) y/P/A R\H Q/P H\M|A D\S/W P R (S)	1848.87	81.3471	715.3	36774.1/6.59	Homo sapiens	157951718	21704	GSG1-like isoform 1
1	11.19	82.1	8	5/16	Y142y	(R) y/P/A R\H Q/P H\M|A D\S/W P R (S)	1848.87	81.3471	715.3	20586.5/6.12	Homo sapiens	21389571	22136	GSG1-like isoform 2

Fragment-ion (m/z)	215.02	458.64	462.49	525.50	530.52	534.08	548.63	551.41	562.83	567.46	573.31	600.18	622.51	643.69	723.52	731.10
Frac. Inten.(% of TIC)	3.54	0.36	4.47	3.10	9.74	2.88	3.60	4.08	15.36	12.43	3.59	22.04	3.03	3.21	4.60	3.97
Rel. Inten.(% of BP)	16.08	1.63	20.29	14.07	44.21	13.05	16.34	18.50	69.73	56.40	16.28	100.00	13.76	14.58	20.88	18.01
Score	-0.16	1.50	1.00	-0.14	1.00	1.00	1.00	0.50	1.00	1.00	-0.16	1.00	-0.14	1.00	-0.21	1.00
Ion-type		y_3	$b{+}{+}{+}_{11}$		$y{+}{+}{+}_{13}$	$b{+}{+}_8$	$y{+}{+}_9$	b_4-NH_3	$y{+}{+}{+}_{14}$	b_4		$b{+}{+}_9$		$y{+}{+}{+}_{15}$		y_6
Delta Da		0.39 1.50 sty 0.17	0.30		0.26	-0.15	-0.12	0.21	0.22	-0.77		0.43		643.69 y_5-NH_3 0.41		-0.25

Peak 437





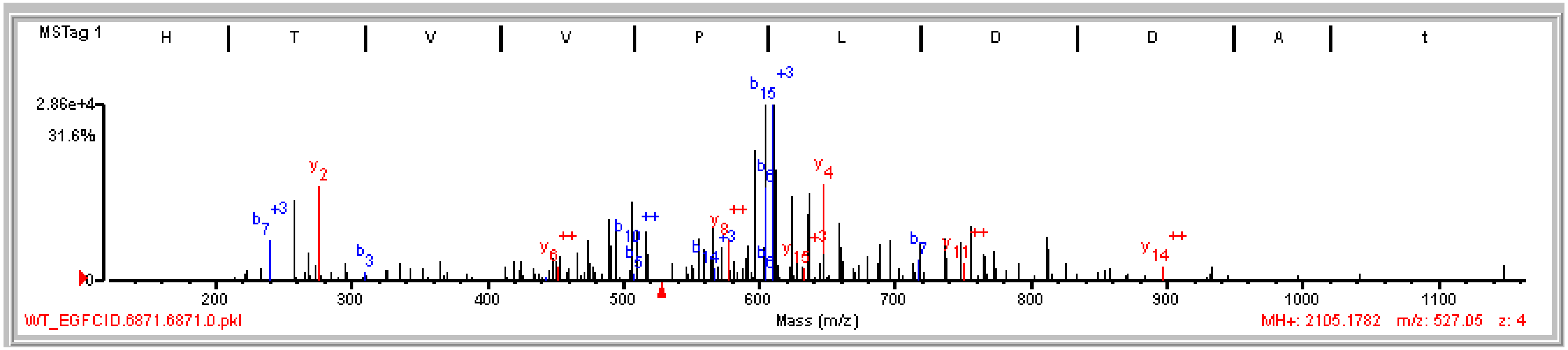


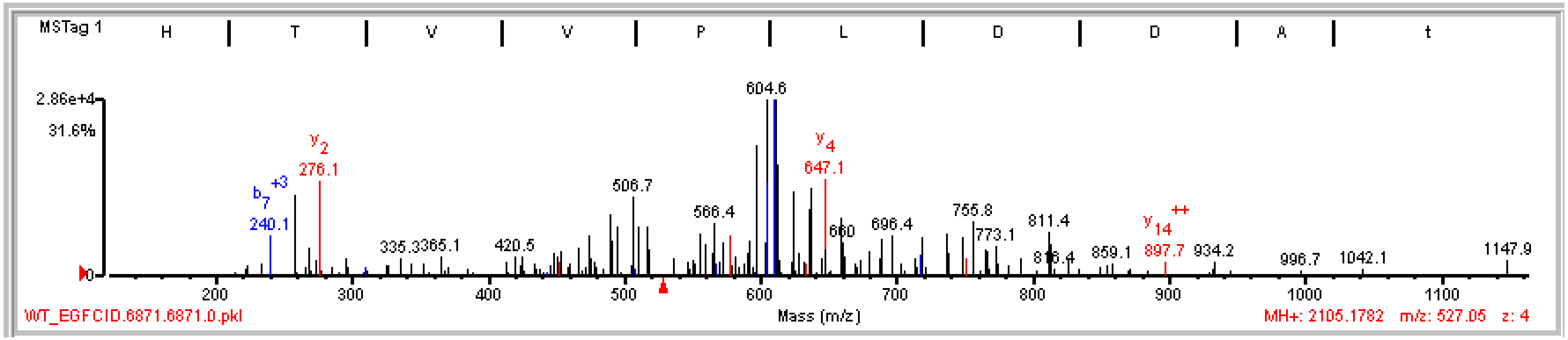
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.33	62.3	9	8/20	M480m Y470y Y492y	(R) y L M L/F/S N\V|L I m L|S/A S/P R\M S|G F I y Q G K (I)	2966.53	176.8441	291.6	87499.4/5.79	Homo sapiens	22027525	18602	Rac/Cdc42 guanine nucleotide exchange factor 6

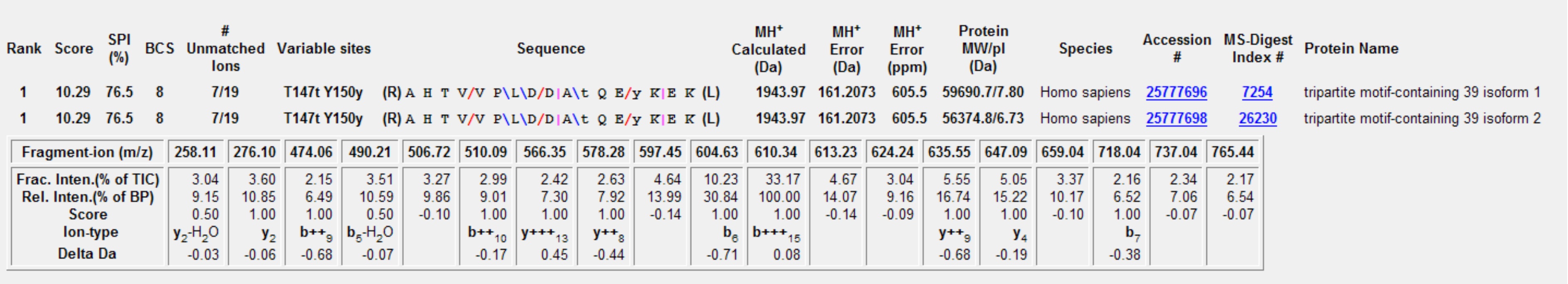
Fragment-ion (m/z)	532.75	678.45	682.40	742.63	751.77	761.30	768.58	772.20	799.62	803.05
Frac. Inten.(% of TIC)	2.57	3.24	2.22	4.53	3.06	3.57	5.71	6.64	2.95	4.30
Rel. Inten.(% of BP)	18.27	23.01	15.77	32.12	21.71	25.37	40.53	47.15	20.93	30.53
Score	-0.18	1.00	1.00	-0.32	1.00	1.00	1.00	-0.47	1.00	-0.31
Ion-type		b+++_{17}	y++_{11}		b+++_{19} $\text{y++}_{13}\text{-}H_2O$	y++_{13}	b++_{12}		y+++_{21}	
Delta Da		0.11	0.08		0.74 -0.57	-0.05	0.70		0.56	

Fragment-ion (m/z)	804.33	821.52	848.45	867.45	892.49	915.87	949.43	1016.40	1048.32	1075.97
Frac. Inten.(% of TIC)	9.62	3.38	4.34	2.48	14.09	10.91	6.95	2.29	4.29	2.84
Rel. Inten.(% of BP)	68.25	23.97	30.80	17.58	100.00	77.42	49.31	16.27	30.48	20.14
Score	1.00	-0.24	1.00	-0.18	1.00	-0.77	1.00	1.00	1.00	-0.20
Ion-type	y++_{14}		y+++_{22}		y_7		b_7	b++_{17}	b_8 y++_{18} y+++_{26}	
Delta Da	-0.54		0.37		0.09		0.04	-0.60	-0.14 0.31 1048.32	

Peak 438



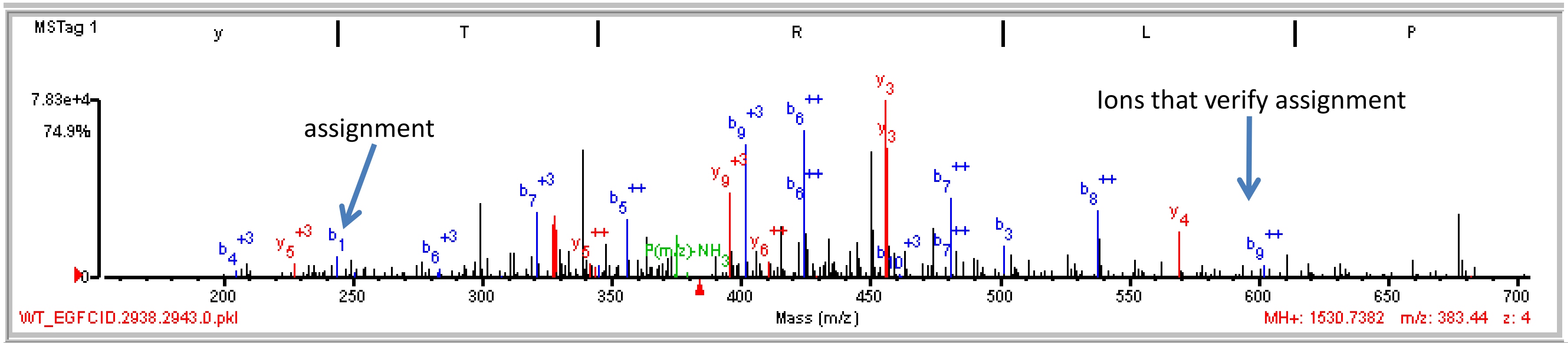




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.29	76.5	8	7/19	T147t Y150y	(R) A H T V/V P\L\D/D|A\t Q E/y K|E K (L)	1943.97	161.2073	605.5	59690.7/7.80	Homo sapiens	25777696	7254	tripartite motif-containing 39 isoform 1
1	10.29	76.5	8	7/19	T147t Y150y	(R) A H T V/V P\L\D/D|A\t Q E/y K|E K (L)	1943.97	161.2073	605.5	56374.8/6.73	Homo sapiens	25777698	26230	tripartite motif-containing 39 isoform 2

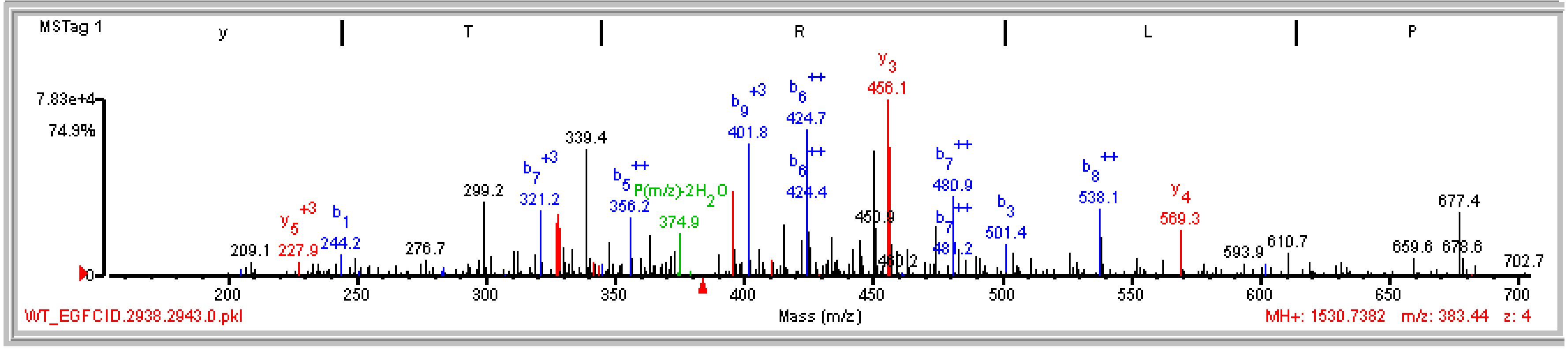
Fragment-ion (m/z)	258.11	276.10	474.06	490.21	506.72	510.09	566.35	578.28	597.45	604.63	610.34	613.23	624.24	635.55	647.09	659.04	718.04	737.04	765.44
Frac. Inten.(% of TIC)	3.04	3.60	2.15	3.51	3.27	2.99	2.42	2.63	4.64	10.23	33.17	4.67	3.04	5.55	5.05	3.37	2.16	2.34	2.17
Rel. Inten.(% of BP)	9.15	10.85	6.49	10.59	9.86	9.01	7.30	7.92	13.99	30.84	100.00	14.07	9.16	16.74	15.22	10.17	6.52	7.06	6.54
Score	0.50	1.00	1.00	0.50	-0.10	1.00	1.00	1.00	-0.14	1.00	1.00	-0.14	-0.09	1.00	1.00	-0.10	1.00	-0.07	-0.07
Ion-type	y_2-H_2O	y_2	$b{+}{+}_9$	b_5-H_2O		$b{+}{+}_{10}$	$y{+}{+}{+}_{13}$	$y{+}{+}_8$		b_6	$b{+}{+}{+}_{15}$			$y{+}{+}_9$	y_4		b_7		
Delta Da	-0.03	-0.06	-0.68	-0.07		-0.17	0.45	-0.44		-0.71	0.08			-0.68	-0.19		-0.38		

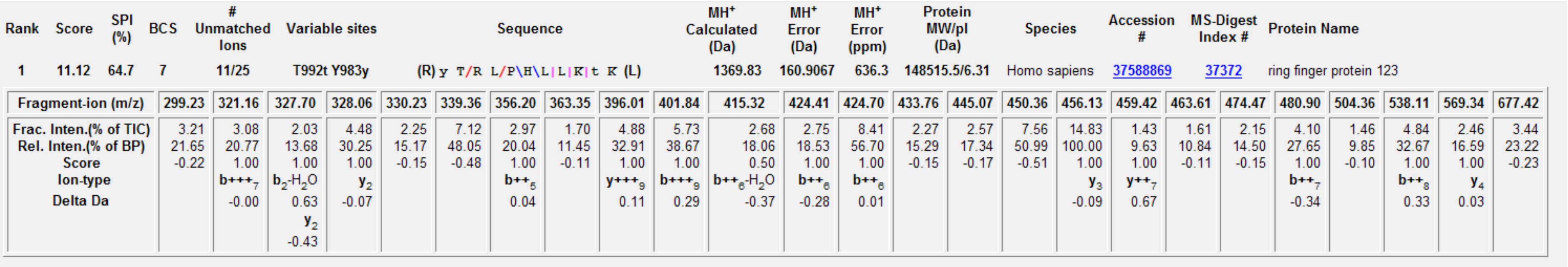
Peak 439



assignment

Ions that verify assignment



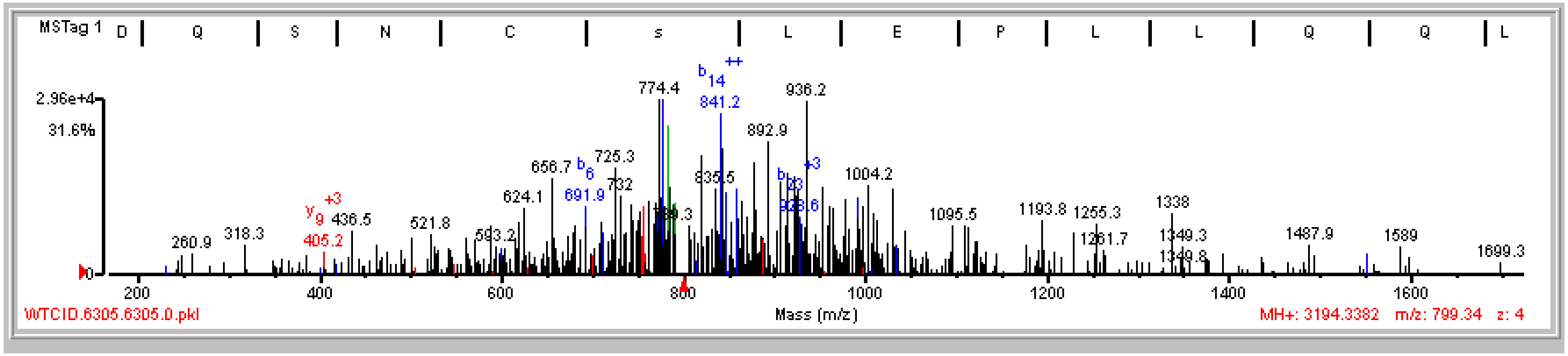


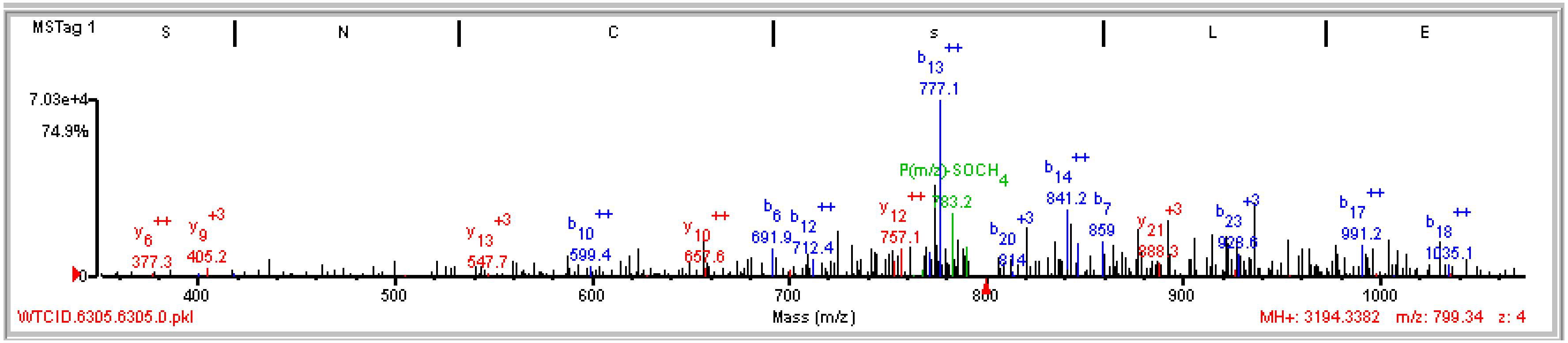
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.12	64.7	7	11/25	T992t Y983y	(R) y T/R L/P\H\L|L|K|t K (L)	1369.83	160.9067	636.3	148515.5/6.31	Homo sapiens	37588869	37372	ring finger protein 123

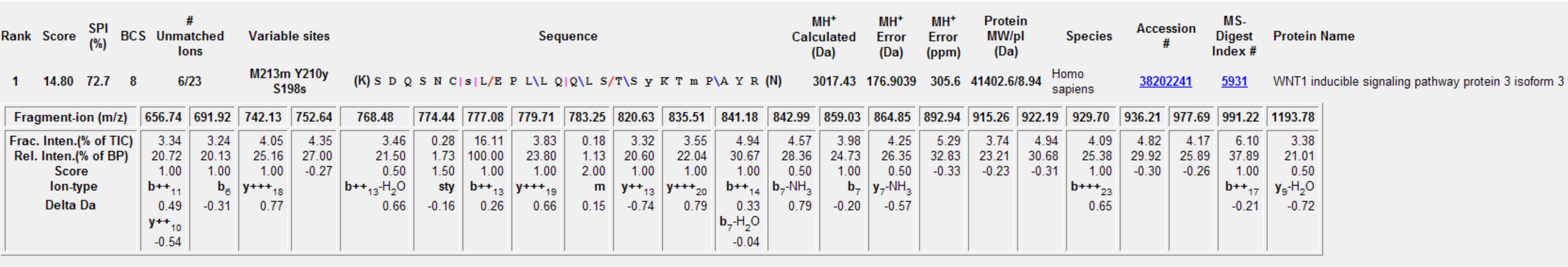
Fragment-ion (m/z)	299.23	321.16	327.70	328.06	330.23	339.36	356.20	363.35	396.01	401.84	415.32	424.41	424.70
Frac. Inten.(% of TIC)	3.21	3.08	2.03	4.48	2.25	7.12	2.97	1.70	4.88	5.73	2.68	2.75	8.41
Rel. Inten.(% of BP)	21.65	20.77	13.68	30.25	15.17	48.05	20.04	11.45	32.91	38.67	18.06	18.53	56.70
Score	-0.22	1.00	1.00	1.00	-0.15	-0.48	1.00	-0.11	1.00	1.00	0.50	1.00	1.00
Ion-type		b+++$_7$	b$_2$-H$_2$O y$_2$	y$_2$			b++$_5$		y+++$_9$	b+++$_9$	b++$_6$-H$_2$O	b++$_6$	b++$_6$
Delta Da		-0.00	0.63 -0.43	-0.07			0.04		0.11	0.29	-0.37	-0.28	0.01

Fragment-ion (m/z)	433.76	445.07	450.36	456.13	459.42	463.61	474.47	480.90	504.36	538.11	569.34	677.42
Frac. Inten.(% of TIC)	2.27	2.57	7.56	14.83	1.43	1.61	2.15	4.10	1.46	4.84	2.46	3.44
Rel. Inten.(% of BP)	15.29	17.34	50.99	100.00	9.63	10.84	14.50	27.65	9.85	32.67	16.59	23.22
Score	-0.15	-0.17	-0.51	1.00	1.00	-0.11	-0.15	1.00	-0.10	1.00	1.00	-0.23
Ion-type				y$_3$	y++$_7$			b++$_7$		b++$_8$	y$_4$	
Delta Da				-0.09	0.67			-0.34		0.33	0.03	

Peak 440



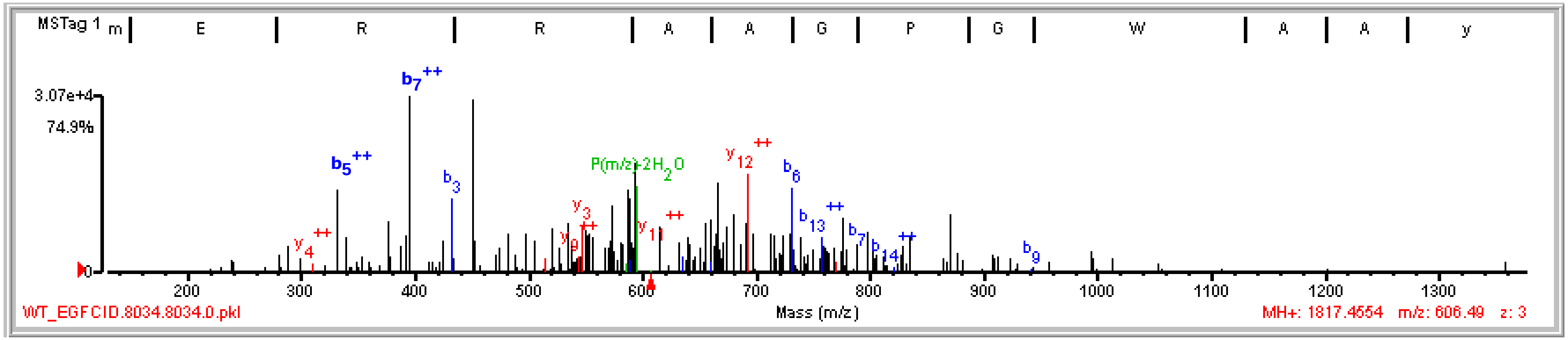


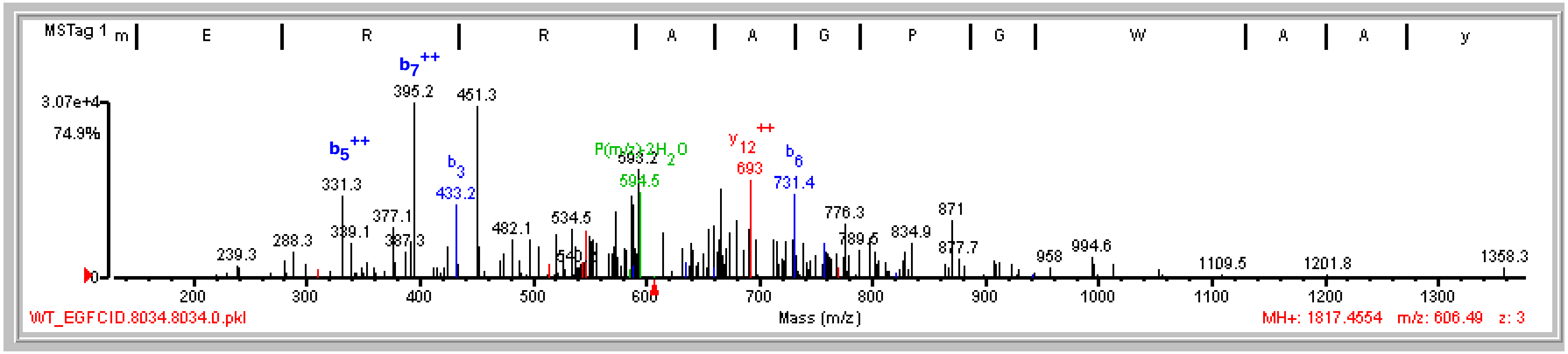


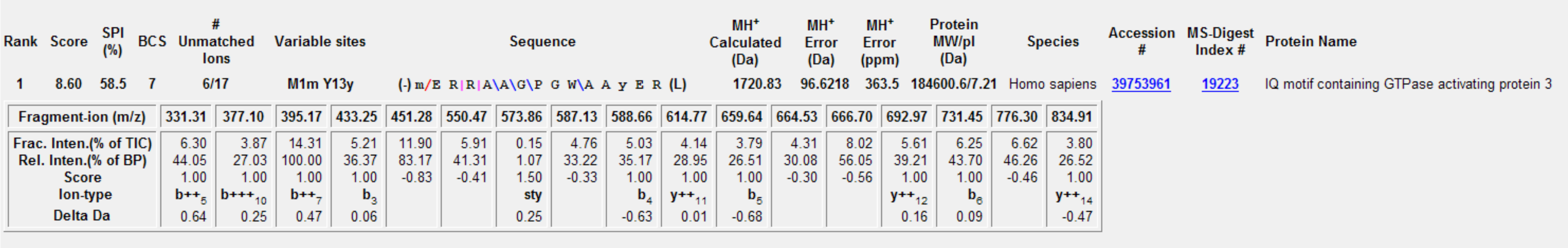
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.80	72.7	8	6/23	M213m Y210y S198s	(K) S D Q S N C|s|L/E P L\L Q|Q\L S/T\S y K T m P\A Y R (N)	3017.43	176.9039	305.6	41402.6/8.94	Homo sapiens	38202241	5931	WNT1 inducible signaling pathway protein 3 isoform 3

Fragment-ion (m/z)	656.74	691.92	742.13	752.64	768.48	774.44	777.08	779.71	783.25	820.63	835.51	841.18	842.99	859.03	864.85	892.94	915.26	922.19	929.70	936.21	977.69	991.22	1193.78
Frac. Inten.(% of TIC)	3.34	3.24	4.05	4.35	3.46	0.28	16.11	3.83	0.18	3.32	3.55	4.94	4.57	3.98	4.25	5.29	3.74	4.94	4.09	4.82	4.17	6.10	3.38
Rel. Inten.(% of BP)	20.72	20.13	25.16	27.00	21.50	1.73	100.00	23.80	1.13	20.60	22.04	30.67	28.36	24.73	26.35	32.83	23.21	30.68	25.38	29.92	25.89	37.89	21.01
Score	1.00	1.00	1.00	-0.27	0.50	1.50	1.00	1.00	2.00	1.00	1.00	1.00	0.50	1.00	0.50	-0.33	-0.23	-0.31	1.00	-0.30	-0.26	1.00	0.50
Ion-type	b++$_{11}$ y++$_{10}$	b_6	y+++$_{18}$		b++$_{13}$-H_2O	sty	b++$_{13}$	y+++$_{19}$	m	y++$_{13}$	y+++$_{20}$	b++$_{14}$ b_7-H_2O	b_7-NH_3	b_7	y_7-NH_3				b+++$_{23}$			b++$_{17}$	y_9-H_2O
Delta Da	0.49 -0.54	-0.31	0.77		0.66	-0.16	0.26	0.66	0.15	-0.74	0.79	0.33 -0.04	0.79	-0.20	-0.57				0.65			-0.21	-0.72

Peak 441



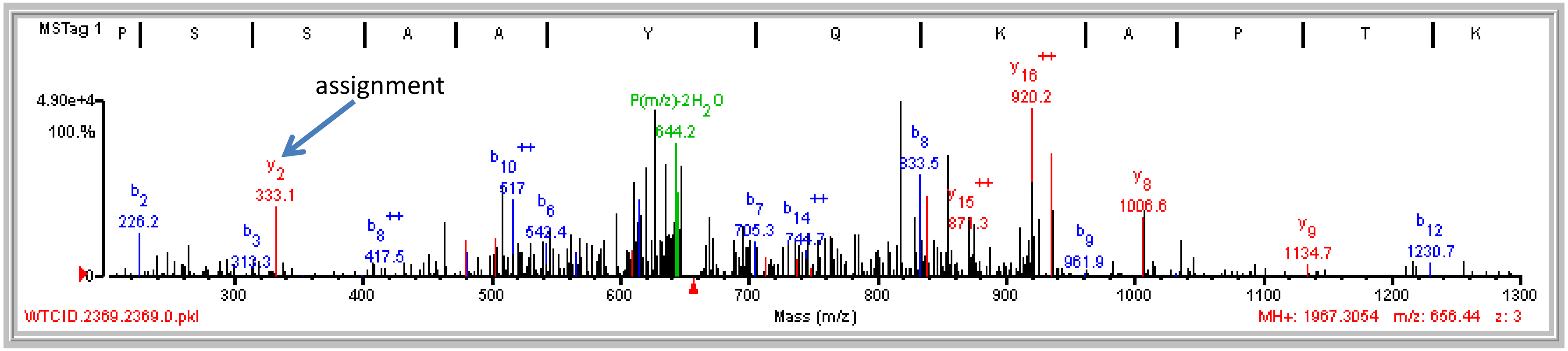


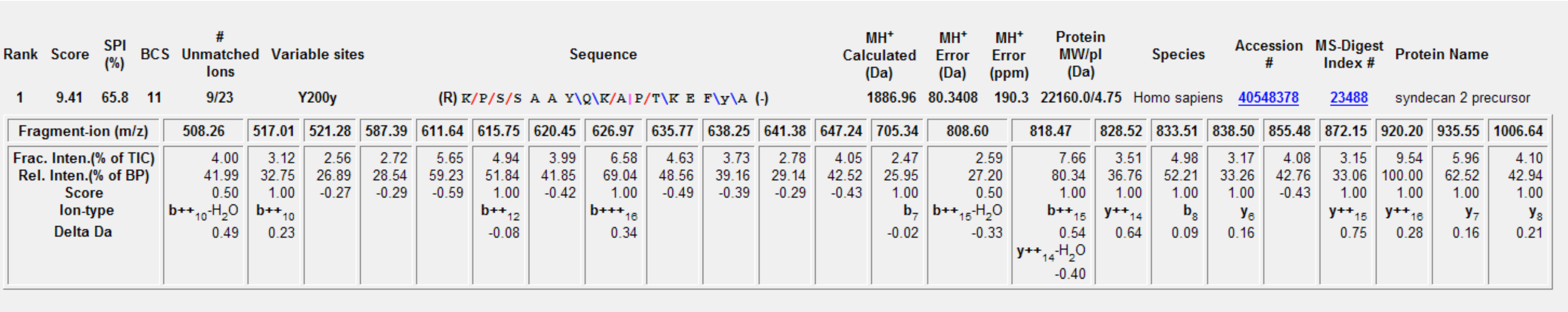


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.60	58.5	7	6/17	M1m Y13y	(-) m/E R|R|A\A\G\P G W\A A y E R (L)	1720.83	96.6218	363.5	184600.6/7.21	Homo sapiens	39753961	19223	IQ motif containing GTPase activating protein 3

Fragment-ion (m/z)	331.31	377.10	395.17	433.25	451.28	550.47	573.86	587.13	588.66	614.77	659.64	664.53	666.70	692.97	731.45	776.30	834.91
Frac. Inten.(% of TIC)	6.30	3.87	14.31	5.21	11.90	5.91	0.15	4.76	5.03	4.14	3.79	4.31	8.02	5.61	6.25	6.62	3.80
Rel. Inten.(% of BP)	44.05	27.03	100.00	36.37	83.17	41.31	1.07	33.22	35.17	28.95	26.51	30.08	56.05	39.21	43.70	46.26	26.52
Score	1.00	1.00	1.00	1.00	-0.83	-0.41	1.50	-0.33	1.00	1.00	1.00	-0.30	-0.56	1.00	1.00	-0.46	1.00
Ion-type	b++_5	b+++_{10}	b++_7	b_3			sty		b_4	y++_{11}	b_5			y++_{12}	b_6		y++_{14}
Delta Da	0.64	0.25	0.47	0.06			0.25		-0.63	0.01	-0.68			0.16	0.09		-0.47

Peak 442


assignment

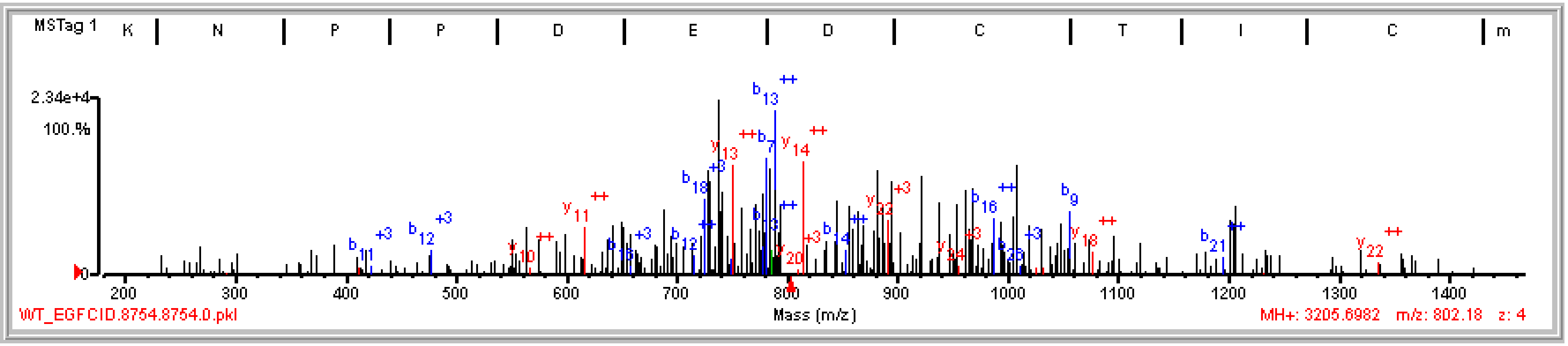


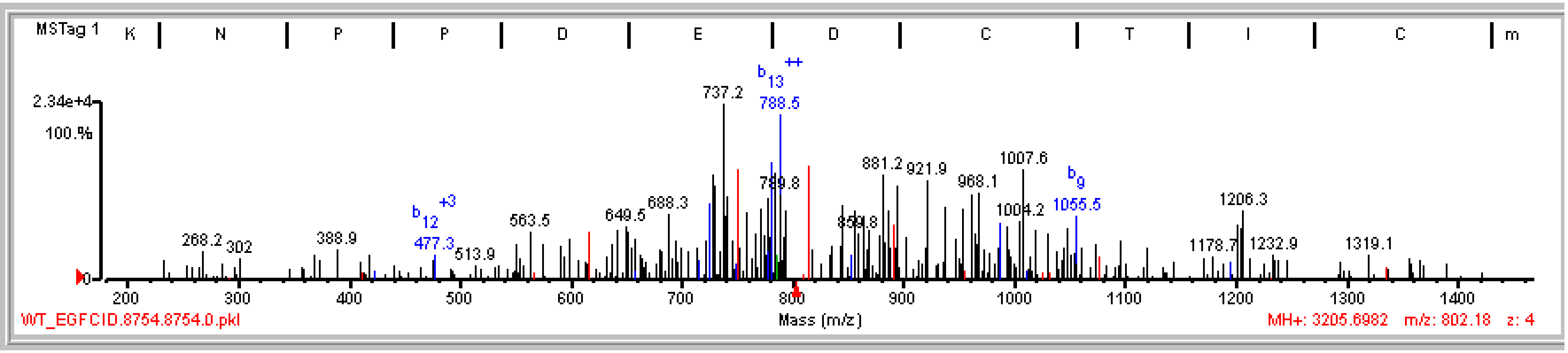
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.41	65.8	11	9/23	Y200y	(R) K/P/S/S A A Y\Q\K/A|P/T\K E F\y\A (-)	1886.96	80.3408	190.3	22160.0/4.75	Homo sapiens	40548378	23488	syndecan 2 precursor

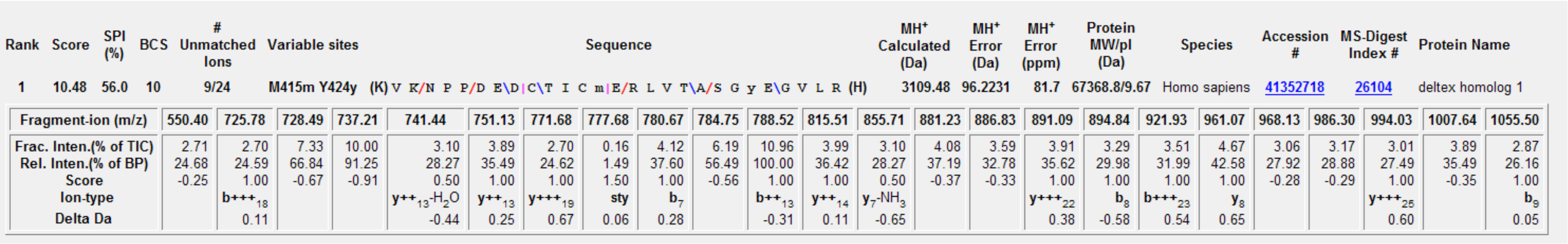
Fragment-ion (m/z)	508.26	517.01	521.28	587.39	611.64	615.75	620.45	626.97	635.77	638.25	641.38
Frac. Inten.(% of TIC)	4.00	3.12	2.56	2.72	5.65	4.94	3.99	6.58	4.63	3.73	2.78
Rel. Inten.(% of BP)	41.99	32.75	26.89	28.54	59.23	51.84	41.85	69.04	48.56	39.16	29.14
Score	0.50	1.00	-0.27	-0.29	-0.59	1.00	-0.42	1.00	-0.49	-0.39	-0.29
Ion-type	b^{++}_{10}-H_2O	b^{++}_{10}				b^{++}_{12}		b^{+++}_{16}			
Delta Da	0.49	0.23				-0.08		0.34			

Fragment-ion (m/z)	647.24	705.34	808.60	818.47	828.52	833.51	838.50	855.48	872.15	920.20	935.55	1006.64
Frac. Inten.(% of TIC)	4.05	2.47	2.59	7.66	3.51	4.98	3.17	4.08	3.15	9.54	5.96	4.10
Rel. Inten.(% of BP)	42.52	25.95	27.20	80.34	36.76	52.21	33.26	42.76	33.06	100.00	62.52	42.94
Score	-0.43	1.00	0.50	1.00	1.00	1.00	1.00	-0.43	1.00	1.00	1.00	1.00
Ion-type		b_7	b^{++}_{15}-H_2O	b^{++}_{15} y^{++}_{14}-H_2O	y^{++}_{14}	b_8	y_6		y^{++}_{15}	y^{++}_{16}	y_7	y_8
Delta Da		-0.02	-0.33	0.54 -0.40	0.64	0.09	0.16		0.75	0.28	0.16	0.21

Peak 443





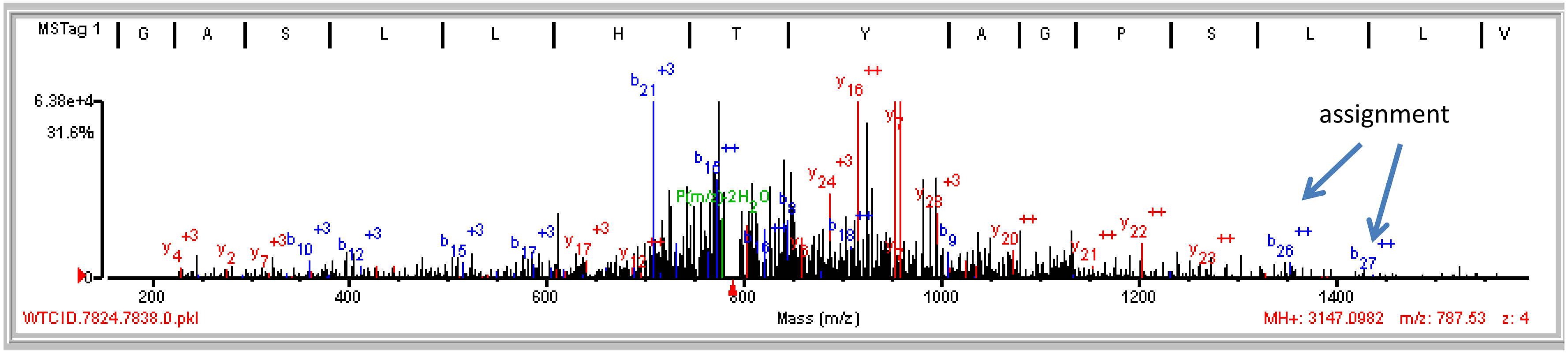


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.48	56.0	10	9/24	M415m Y424y	(K) V K/N P P/D E\D|C\T I C m|E/R L V T\A/S G y E\G V L R (H)	3109.48	96.2231	81.7	67368.8/9.67	Homo sapiens	41352718	26104	deltex homolog 1

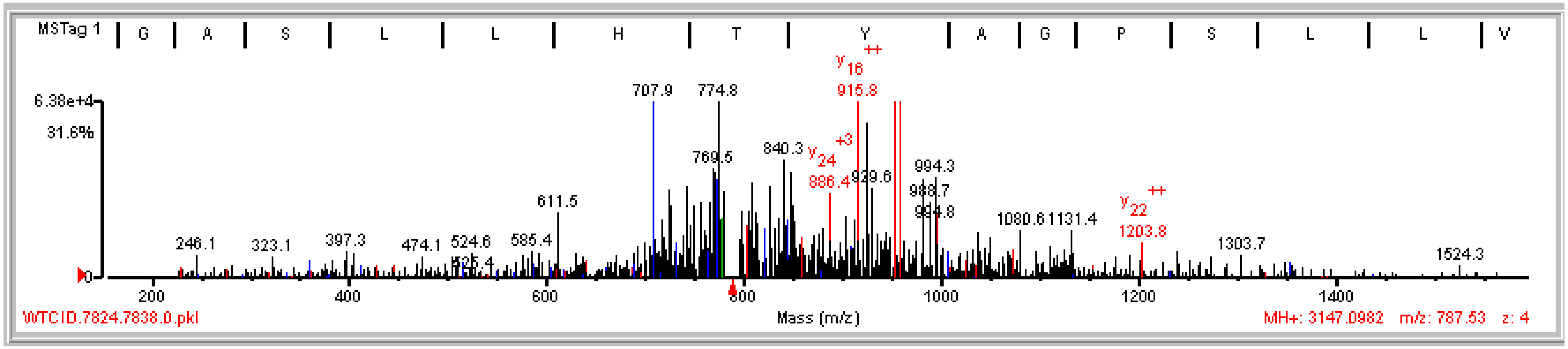
Fragment-ion (m/z)	550.40	725.78	728.49	737.21	741.44	751.13	771.68	777.68	780.67	784.75	788.52
Frac. Inten.(% of TIC)	2.71	2.70	7.33	10.00	3.10	3.89	2.70	0.16	4.12	6.19	10.96
Rel. Inten.(% of BP)	24.68	24.59	66.84	91.25	28.27	35.49	24.62	1.49	37.60	56.49	100.00
Score	-0.25	1.00	-0.67	-0.91	0.50	1.00	1.00	1.50	1.00	-0.56	1.00
Ion-type		$b{+}{+}{+}_{18}$			$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$	$y{+}{+}{+}_{19}$	sty	b_7		$b{+}{+}_{13}$
Delta Da		0.11			-0.44	0.25	0.67	0.06	0.28		-0.31

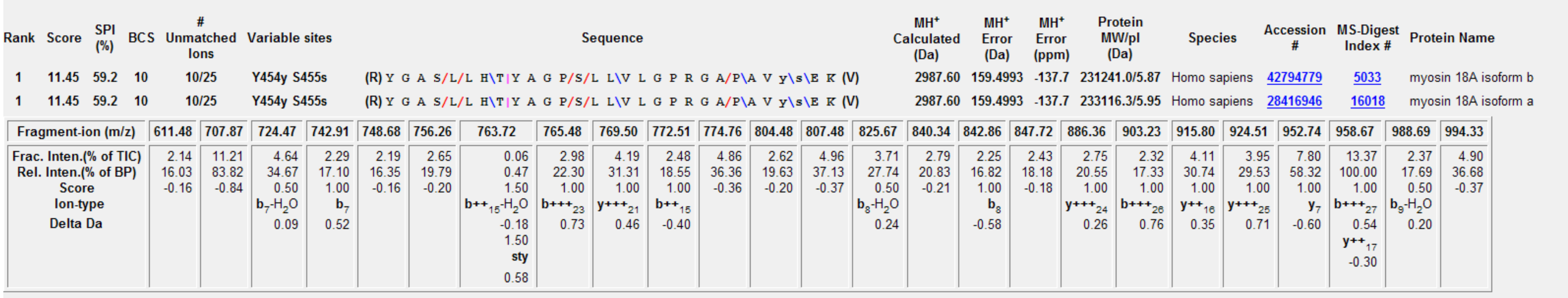
Fragment-ion (m/z)	815.51	855.71	881.23	886.83	891.09	894.84	921.93	961.07	968.13	986.30	994.03	1007.64	1055.50
Frac. Inten.(% of TIC)	3.99	3.10	4.08	3.59	3.91	3.29	3.51	4.67	3.06	3.17	3.01	3.89	2.87
Rel. Inten.(% of BP)	36.42	28.27	37.19	32.78	35.62	29.98	31.99	42.58	27.92	28.88	27.49	35.49	26.16
Score	1.00	0.50	-0.37	-0.33	1.00	1.00	1.00	1.00	-0.28	-0.29	1.00	-0.35	1.00
Ion-type	$y{+}{+}_{14}$	y_7-NH_3			$y{+}{+}{+}_{22}$	b_8	$b{+}{+}{+}_{23}$	y_8			$y{+}{+}{+}_{25}$		b_9
Delta Da	0.11	-0.65			0.38	-0.58	0.54	0.65			0.60		0.05

Peak 444



assignment





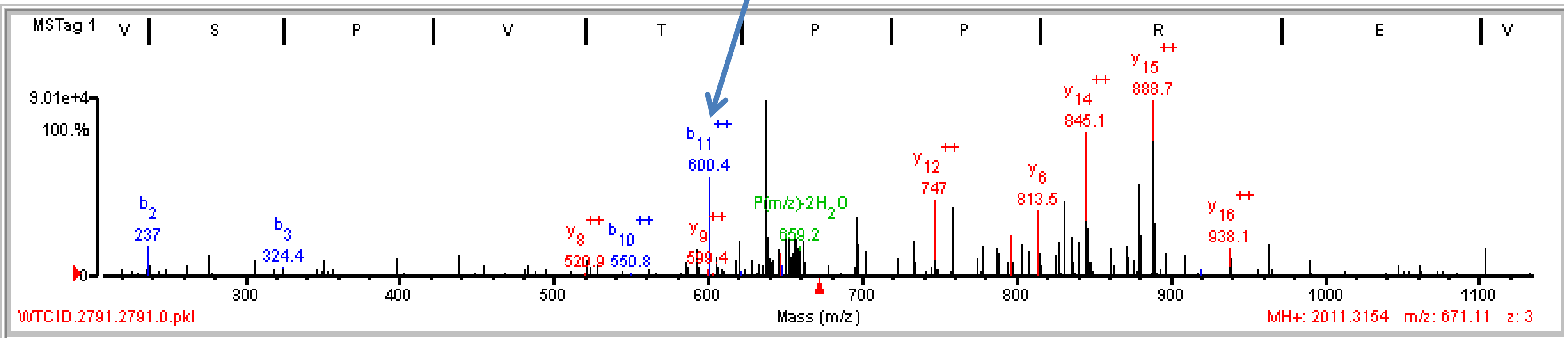
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.45	59.2	10	10/25	Y454y S455s	(R) Y G A S/L/L H\T|Y A G P/S/L L\V L G P R G A/P\A V y\s\E K (V)	2987.60	159.4993	-137.7	231241.0/5.87	Homo sapiens	42794779	5033	myosin 18A isoform b
1	11.45	59.2	10	10/25	Y454y S455s	(R) Y G A S/L/L H\T|Y A G P/S/L L\V L G P R G A/P\A V y\s\E K (V)	2987.60	159.4993	-137.7	233116.3/5.95	Homo sapiens	28416946	16018	myosin 18A isoform a

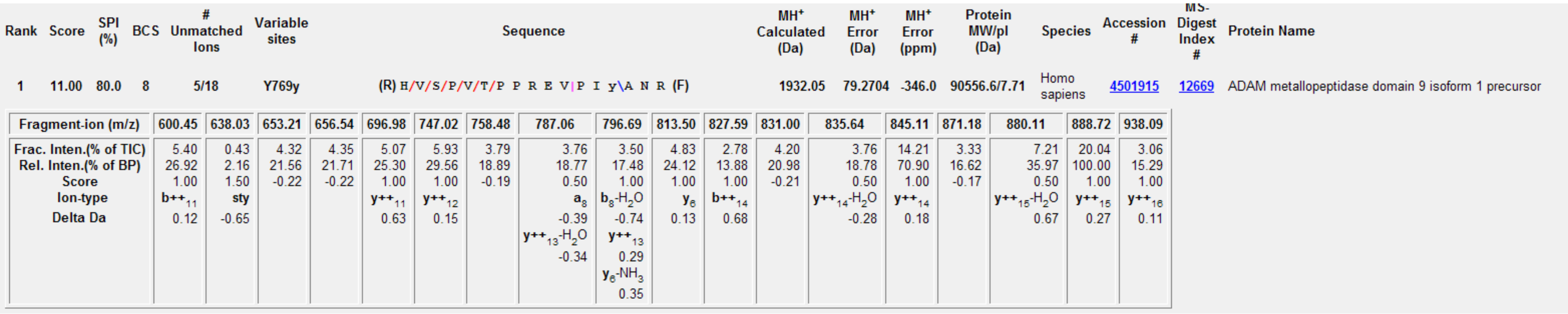
Fragment-ion (m/z)	611.48	707.87	724.47	742.91	748.68	756.26	763.72	765.48	769.50	772.51	774.76	804.48	807.48
Frac. Inten.(% of TIC)	2.14	11.21	4.64	2.29	2.19	2.65	0.06	2.98	4.19	2.48	4.86	2.62	4.96
Rel. Inten.(% of BP)	16.03	83.82	34.67	17.10	16.35	19.79	0.47	22.30	31.31	18.55	36.36	19.63	37.13
Score	-0.16	-0.84	0.50	1.00	-0.16	-0.20	1.50	1.00	1.00	1.00	-0.36	-0.20	-0.37
Ion-type			b_7-H_2O	b_7			$b{++}_{15}$-H_2O	$b{+++}_{23}$	$y{+++}_{21}$	$b{++}_{15}$			
Delta Da			0.09	0.52			-0.18 1.50 sty 0.58	0.73	0.46	-0.40			

Fragment-ion (m/z)	825.67	840.34	842.86	847.72	886.36	903.23	915.80	924.51	952.74	958.67	988.69	994.33
Frac. Inten.(% of TIC)	3.71	2.79	2.25	2.43	2.75	2.32	4.11	3.95	7.80	13.37	2.37	4.90
Rel. Inten.(% of BP)	27.74	20.83	16.82	18.18	20.55	17.33	30.74	29.53	58.32	100.00	17.69	36.68
Score	0.50	-0.21	1.00	-0.18	1.00	1.00	1.00	1.00	1.00	1.00	0.50	-0.37
Ion-type	b_8-H_2O		b_8		$y{+++}_{24}$	$b{+++}_{26}$	$y{++}_{16}$	$y{+++}_{25}$	y_7	$b{+++}_{27}$	b_9-H_2O	
Delta Da	0.24		-0.58		0.26	0.76	0.35	0.71	-0.60	0.54 $y{++}_{17}$ -0.30	0.20	

Peak 445

Ions that verify assignment

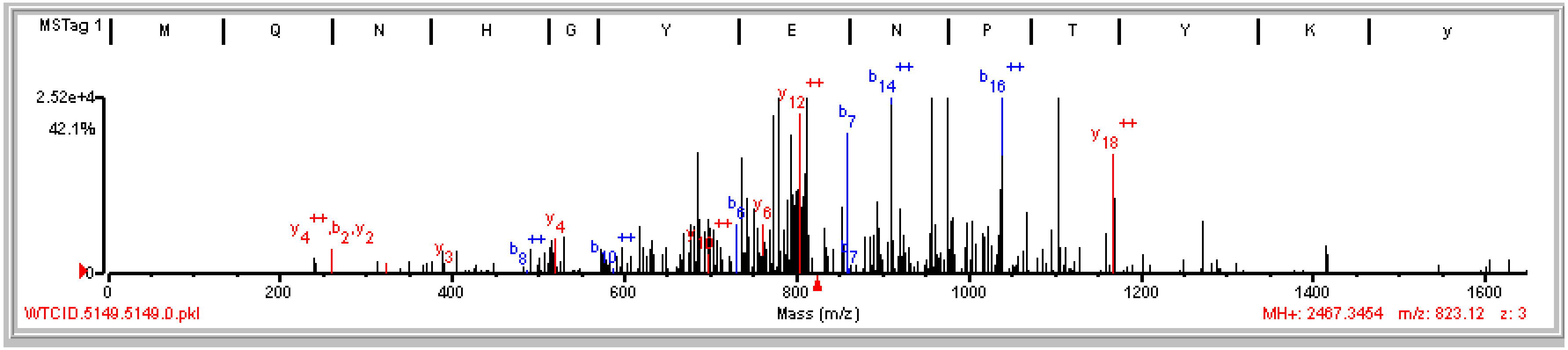


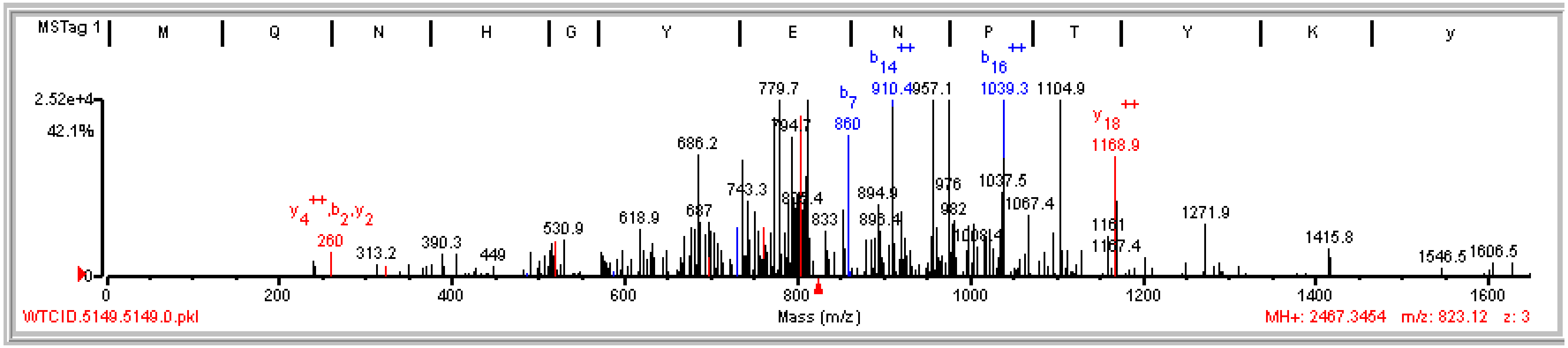


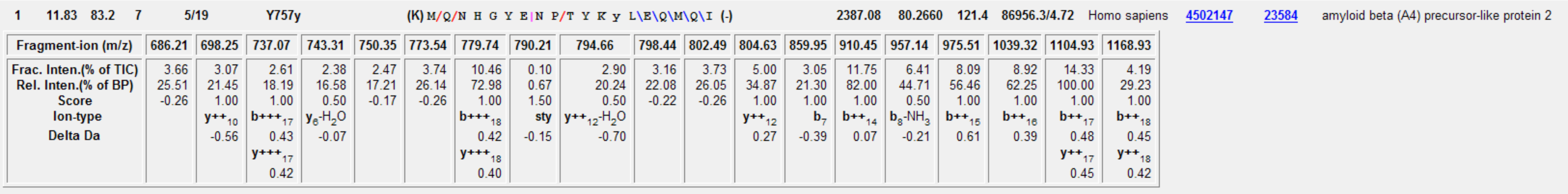
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.00	80.0	8	5/18	Y769y	(R) H/V/S/P/V/T/P P R E V|P I y\A N R (F)	1932.05	79.2704	-346.0	90556.6/7.71	Homo sapiens	4501915	12669	ADAM metallopeptidase domain 9 isoform 1 precursor

Fragment-ion (m/z)	600.45	638.03	653.21	656.54	696.98	747.02	758.48	787.06	796.69	813.50	827.59	831.00	835.64	845.11	871.18	880.11	888.72	938.09
Frac. Inten.(% of TIC)	5.40	0.43	4.32	4.35	5.07	5.93	3.79	3.76	3.50	4.83	2.78	4.20	3.76	14.21	3.33	7.21	20.04	3.06
Rel. Inten.(% of BP)	26.92	2.16	21.56	21.71	25.30	29.56	18.89	18.77	17.48	24.12	13.88	20.98	18.78	70.90	16.62	35.97	100.00	15.29
Score	1.00	1.50	-0.22	-0.22	1.00	1.00	-0.19	0.50	1.00	1.00	1.00	-0.21	0.50	1.00	-0.17	0.50	1.00	1.00
Ion-type	$b{++}_{11}$	sty			$y{++}_{11}$	$y{++}_{12}$		a_8 $y{++}_{13}$-H_2O	b_8-H_2O $y{++}_{13}$ y_6-NH_3	y_6	$b{++}_{14}$		$y{++}_{14}$-H_2O	$y{++}_{14}$		$y{++}_{15}$-H_2O	$y{++}_{15}$	$y{++}_{16}$
Delta Da	0.12	-0.65			0.63	0.15		-0.39 -0.34	-0.74 0.29 0.35	0.13	0.68		-0.28	0.18		0.67	0.27	0.11

Peak 446





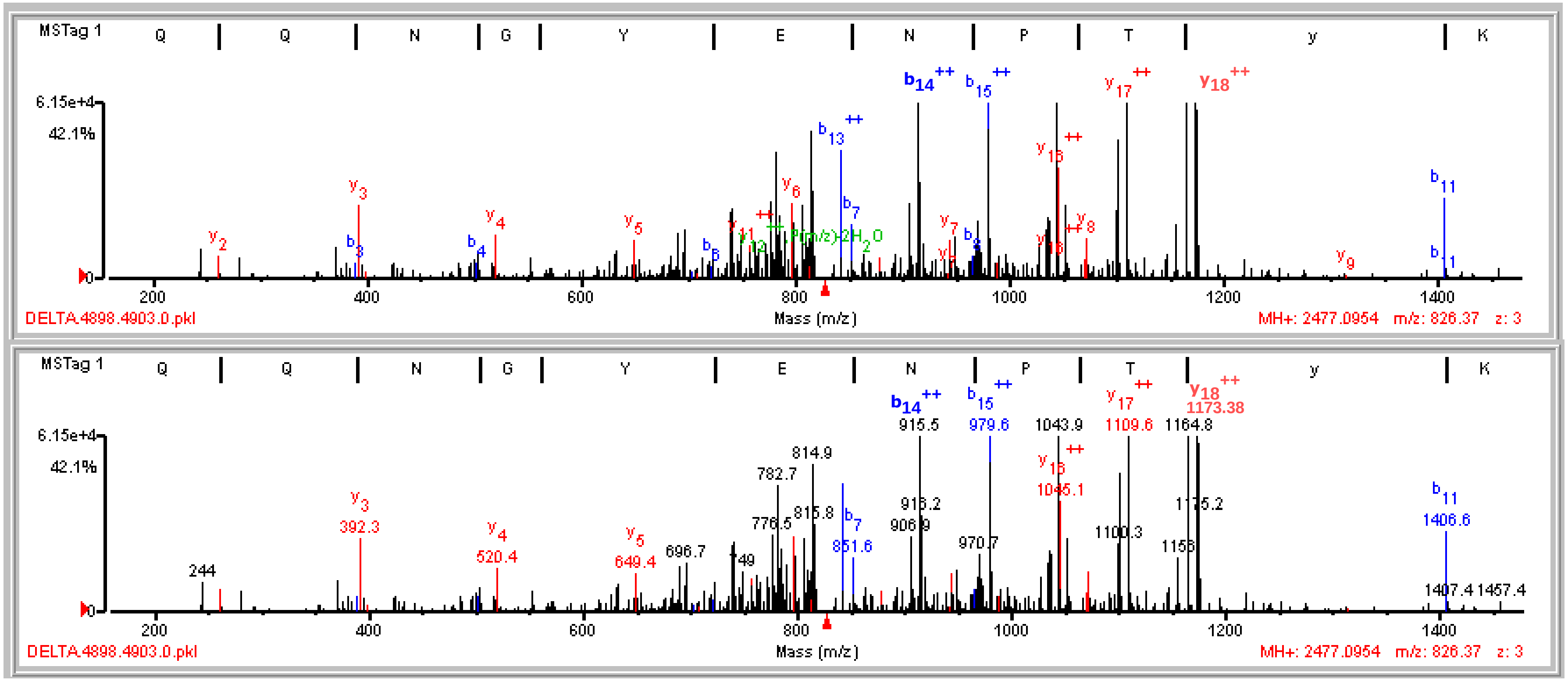


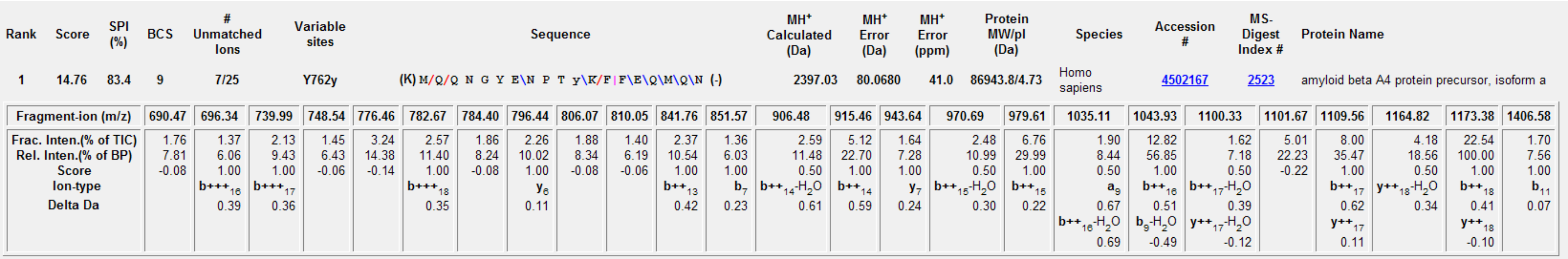
1 11.83 83.2 7 5/19 Y757y (K) M/Q/N H G Y E|N P/T Y K y L\E\Q\M\Q\I (-) 2387.08 80.2660 121.4 86956.3/4.72 Homo sapiens 4502147 23584 amyloid beta (A4) precursor-like protein 2

Fragment-ion (m/z)	686.21	698.25	737.07	743.31	750.35	773.54	779.74	790.21	794.66
Frac. Inten.(% of TIC)	3.66	3.07	2.61	2.38	2.47	3.74	10.46	0.10	2.90
Rel. Inten.(% of BP)	25.51	21.45	18.19	16.58	17.21	26.14	72.98	0.67	20.24
Score	-0.26	1.00	1.00	0.50	-0.17	-0.26	1.00	1.50	0.50
Ion-type		$y{++}_{10}$	$b{+++}_{17}$ $y{+++}_{17}$	y_6-H_2O			$b{+++}_{18}$ $y{+++}_{18}$	sty	$y{++}_{12}$-H_2O
Delta Da		-0.56	0.43 0.42	-0.07			0.42 0.40	-0.15	-0.70

Fragment-ion (m/z)	798.44	802.49	804.63	859.95	910.45	957.14	975.51	1039.32	1104.93	1168.93
Frac. Inten.(% of TIC)	3.16	3.73	5.00	3.05	11.75	6.41	8.09	8.92	14.33	4.19
Rel. Inten.(% of BP)	22.08	26.05	34.87	21.30	82.00	44.71	56.46	62.25	100.00	29.23
Score	-0.22	-0.26	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type			$y{++}_{12}$	b_7	$b{++}_{14}$	b_8-NH_3	$b{++}_{15}$	$b{++}_{16}$	$b{++}_{17}$ $y{++}_{17}$	$b{++}_{18}$ $y{++}_{18}$
Delta Da			0.27	-0.39	0.07	-0.21	0.61	0.39	0.48 0.45	0.45 0.42

Peak 447





<table>
<tr><th>Rank</th><th>Score</th><th>SPI (%)</th><th>BCS</th><th># Unmatched Ions</th><th>Variable sites</th><th>Sequence</th><th>MH⁺ Calculated (Da)</th><th>MH⁺ Error (Da)</th><th>MH⁺ Error (ppm)</th><th>Protein MW/pI (Da)</th><th>Species</th><th>Accession #</th><th>MS-Digest Index #</th><th>Protein Name</th></tr>
<tr><td>1</td><td>14.76</td><td>83.4</td><td>9</td><td>7/25</td><td>Y762y</td><td>(K) M/Q/Q N G Y E\N P T y\K/F|F\E\Q\M\Q\N (-)</td><td>2397.03</td><td>80.0680</td><td>41.0</td><td>86943.8/4.73</td><td>Homo sapiens</td><td>4502167</td><td>2523</td><td>amyloid beta A4 protein precursor, isoform a</td></tr>
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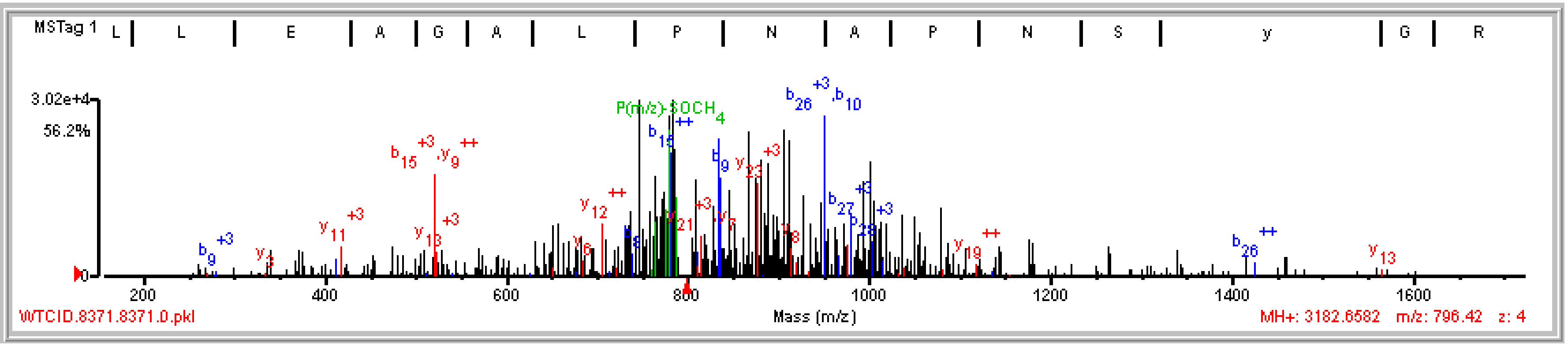
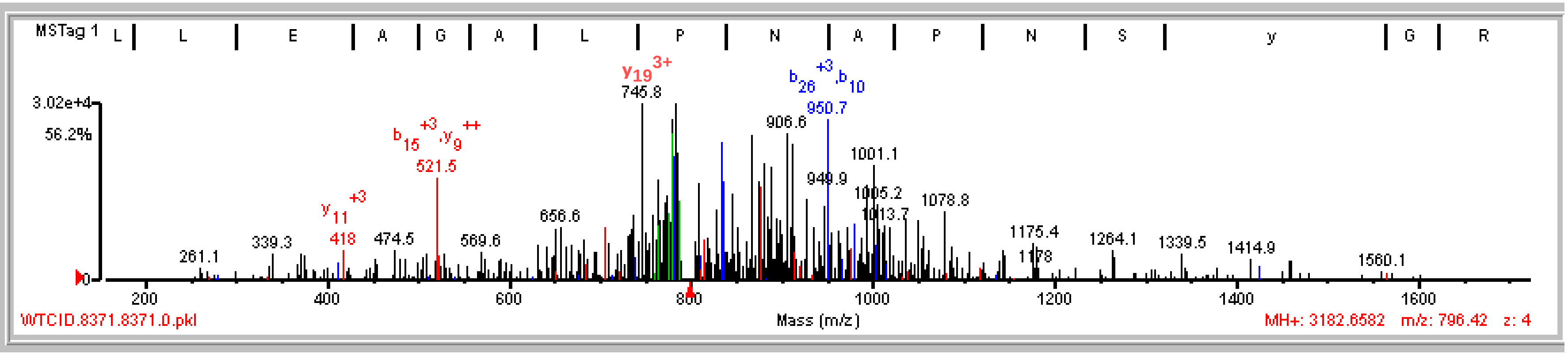
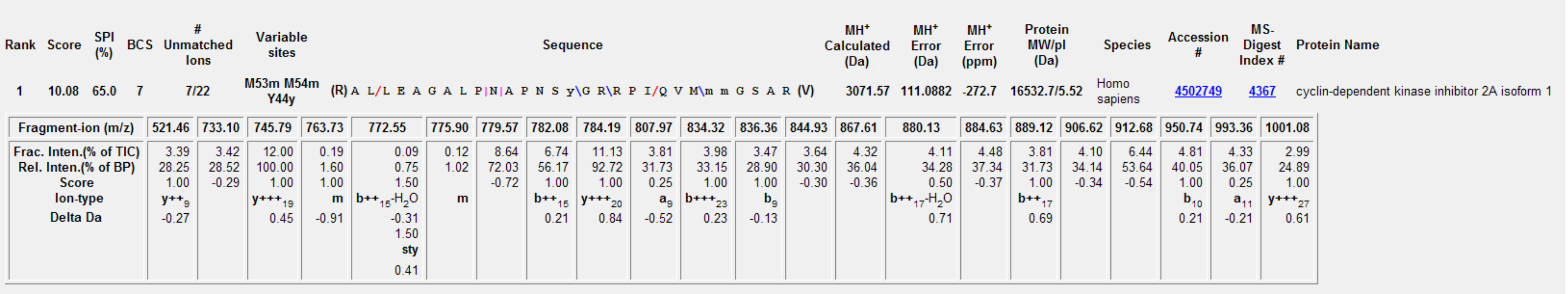
Fragment-ion (m/z)	690.47	696.34	739.99	748.54	776.46	782.67	784.40	796.44	806.07	810.05	841.76	851.57
Frac. Inten.(% of TIC)	1.76	1.37	2.13	1.45	3.24	2.57	1.86	2.26	1.88	1.40	2.37	1.36
Rel. Inten.(% of BP)	7.81	6.06	9.43	6.43	14.38	11.40	8.24	10.02	8.34	6.19	10.54	6.03
Score	-0.08	1.00	1.00	-0.06	-0.14	1.00	-0.08	1.00	-0.08	-0.06	1.00	1.00
Ion-type		$b{+}{+}{+}_{16}$	$b{+}{+}{+}_{17}$			$b{+}{+}{+}_{18}$		y_6			$b{+}{+}_{13}$	b_7
Delta Da		0.39	0.36			0.35		0.11			0.42	0.23

Fragment-ion (m/z)	906.48	915.46	943.64	970.69	979.61	1035.11	1043.93	1100.33	1101.67	1109.56	1164.82	1173.38	1406.58
Frac. Inten.(% of TIC)	2.59	5.12	1.64	2.48	6.76	1.90	12.82	1.62	5.01	8.00	4.18	22.54	1.70
Rel. Inten.(% of BP)	11.48	22.70	7.28	10.99	29.99	8.44	56.85	7.18	22.23	35.47	18.56	100.00	7.56
Score	0.50	1.00	1.00	0.50	1.00	0.50	1.00	0.50	-0.22	1.00	0.50	1.00	1.00
Ion-type	$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$	y_7	$b{+}{+}_{15}$-H_2O	$b{+}{+}_{15}$	a_9 $b{+}{+}_{16}$-H_2O	$b{+}{+}_{16}$ b_9-H_2O	$b{+}{+}_{17}$-H_2O $y{+}{+}_{17}$-H_2O		$b{+}{+}_{17}$ $y{+}{+}_{17}$	$y{+}{+}_{18}$-H_2O	$b{+}{+}_{18}$ $y{+}{+}_{18}$	b_{11}
Delta Da	0.61	0.59	0.24	0.30	0.22	0.67 0.69	0.51 -0.49	0.39 -0.12		0.62 0.11	0.34	0.41 -0.10	0.07

Peak 448





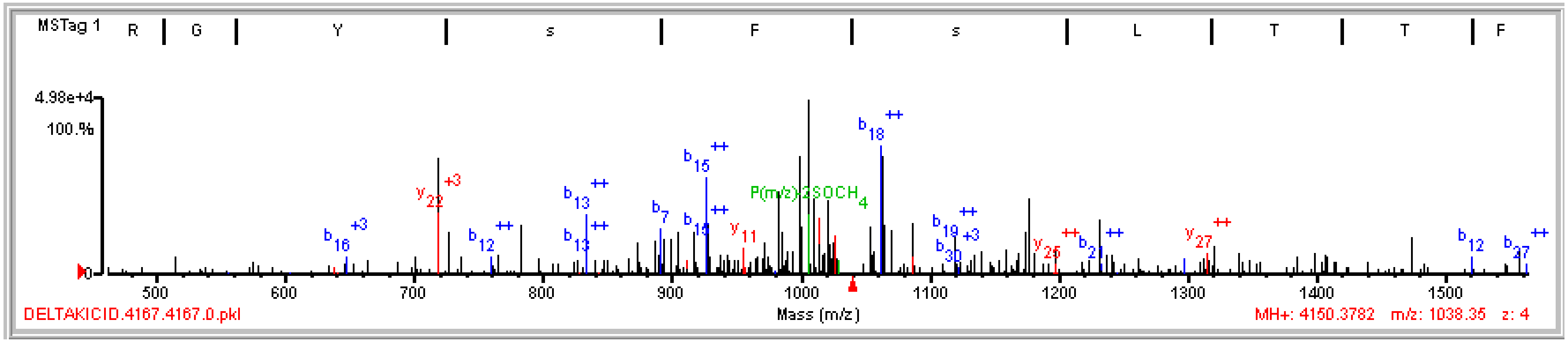


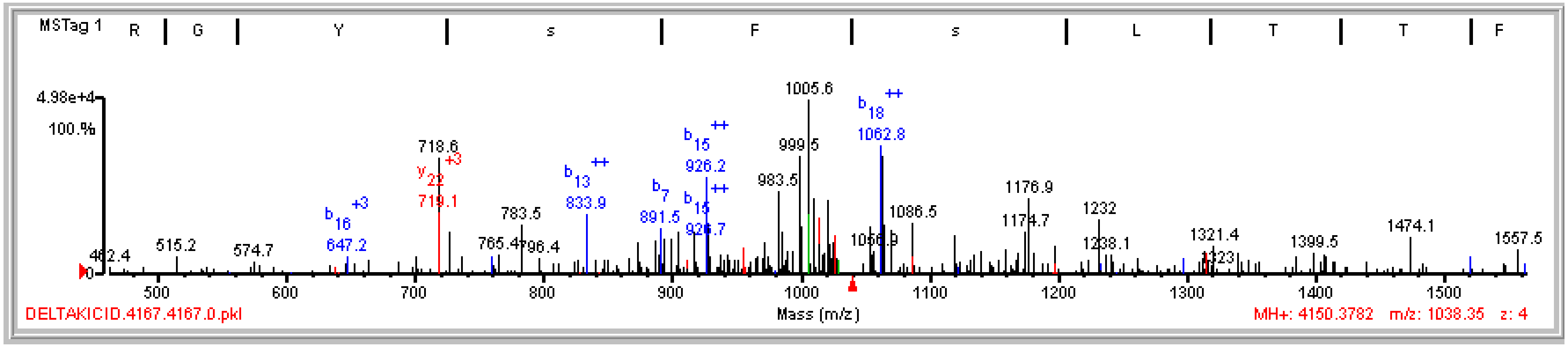
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.08	65.0	7	7/22	M53m M54m Y44y	(R) A L/L E A G A L P|N|A P N S y\G R\R P I/Q V M\m m G S A R (V)	3071.57	111.0882	-272.7	16532.7/5.52	Homo sapiens	4502749	4367	cyclin-dependent kinase inhibitor 2A isoform 1

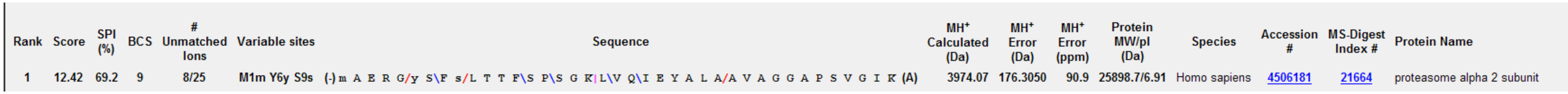
Fragment-ion (m/z)	521.46	733.10	745.79	763.73	772.55	775.90	779.57	782.08	784.19	807.97	834.32
Frac. Inten.(% of TIC)	3.39	3.42	12.00	0.19	0.09	0.12	8.64	6.74	11.13	3.81	3.98
Rel. Inten.(% of BP)	28.25	28.52	100.00	1.60	0.75	1.02	72.03	56.17	92.72	31.73	33.15
Score	1.00	-0.29	1.00	1.00	1.50		-0.72	1.00	1.00	0.25	1.00
Ion-type	y++$_{9}$		y+++$_{19}$	m	b++$_{15}$-H_2O	m		b++$_{15}$	y+++$_{20}$	a$_{9}$	b+++$_{23}$
Delta Da	-0.27		0.45	-0.91	-0.31			0.21	0.84	-0.52	0.23
					1.50						
					sty						
					0.41						

Fragment-ion (m/z)	836.36	844.93	867.61	880.13	884.63	889.12	906.62	912.68	950.74	993.36	1001.08
Frac. Inten.(% of TIC)	3.47	3.64	4.32	4.11	4.48	3.81	4.10	6.44	4.81	4.33	2.99
Rel. Inten.(% of BP)	28.90	30.30	36.04	34.28	37.34	31.73	34.14	53.64	40.05	36.07	24.89
Score	1.00	-0.30	-0.36	0.50	-0.37	1.00	-0.34	-0.54	1.00	0.25	1.00
Ion-type	b$_{9}$			b++$_{17}$-H_2O		b++$_{17}$			b$_{10}$	a$_{11}$	y+++$_{27}$
Delta Da	-0.13			0.71		0.69			0.21	-0.21	0.61

Peak 450

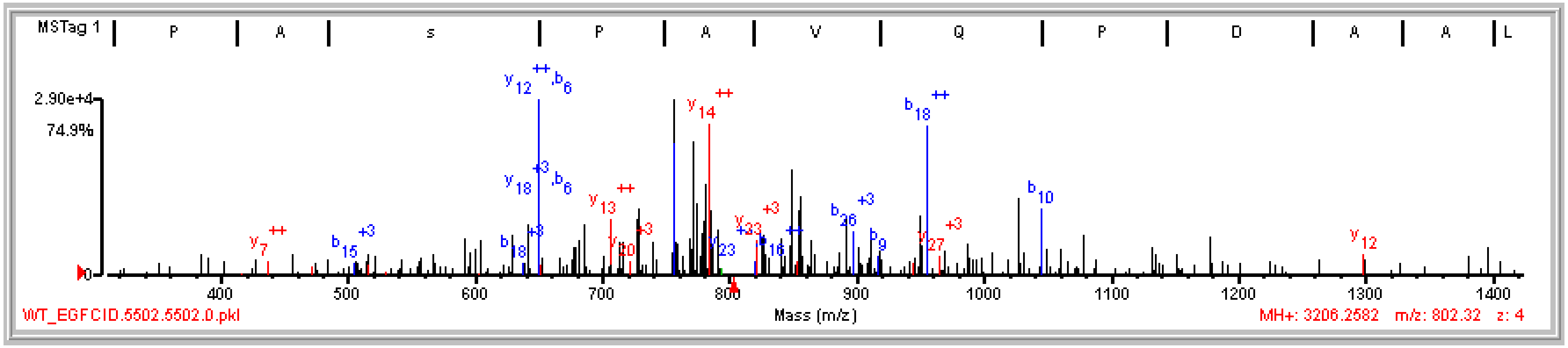


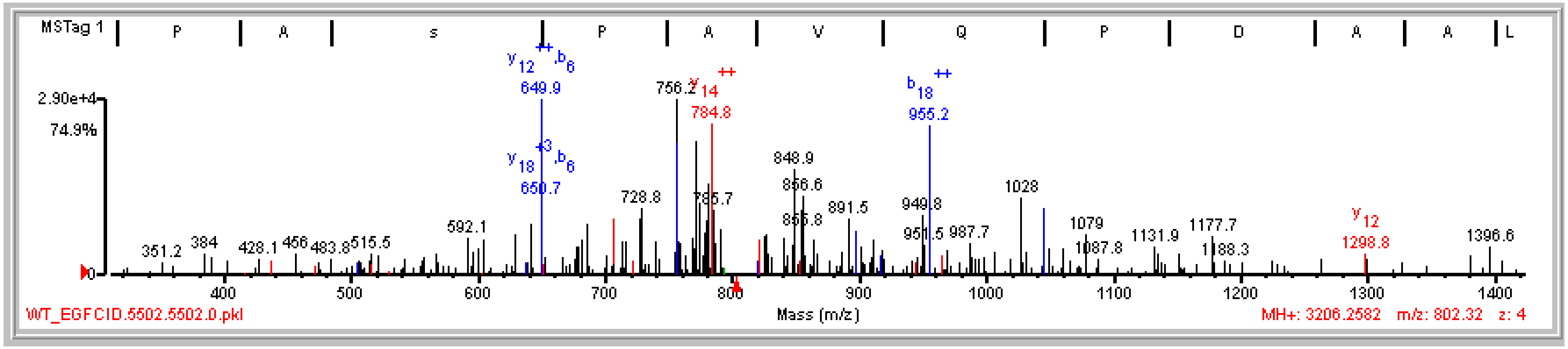


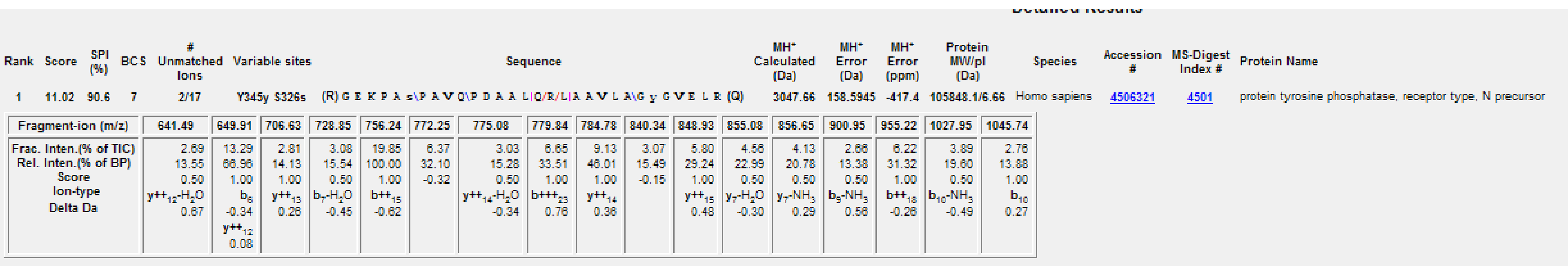


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.42	69.2	9	8/25	M1m Y6y S9s	(-) m A E R G/y S\F s/L T T F\S P\S G K|L\V Q\I E Y A L A/A V A G G A P S V G I K (A)	3974.07	176.3050	90.9	25898.7/6.91	Homo sapiens	4506181	21664	proteasome alpha 2 subunit

Peak 451





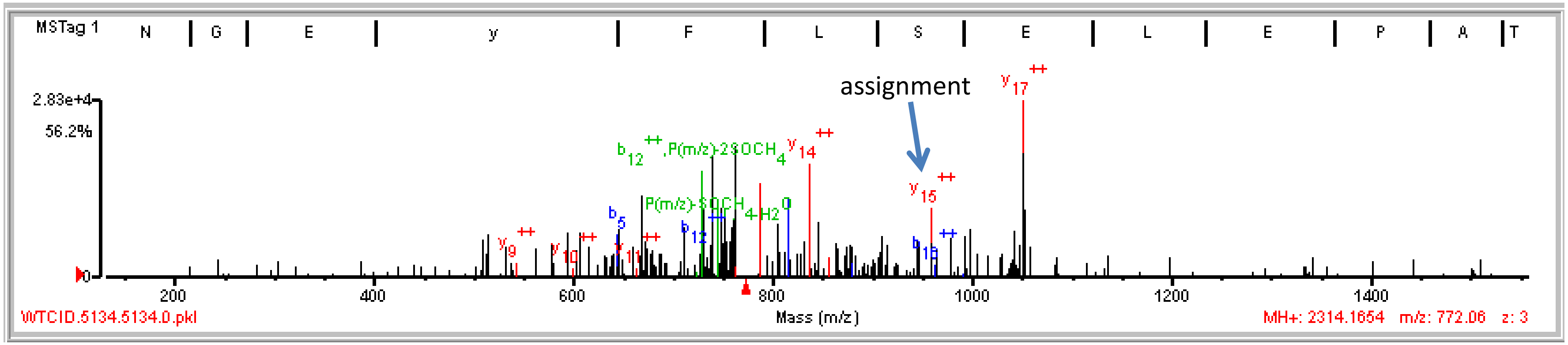


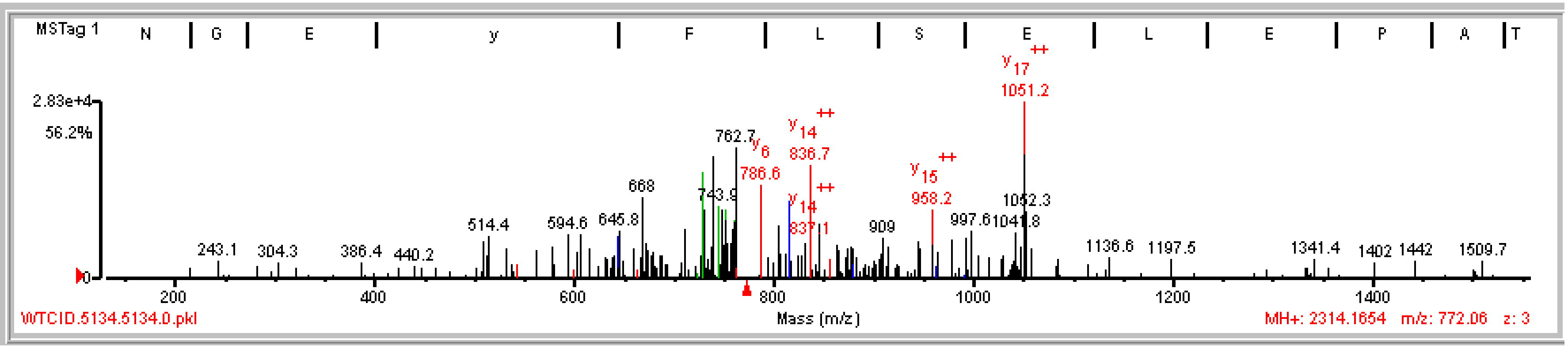
Detailed Results

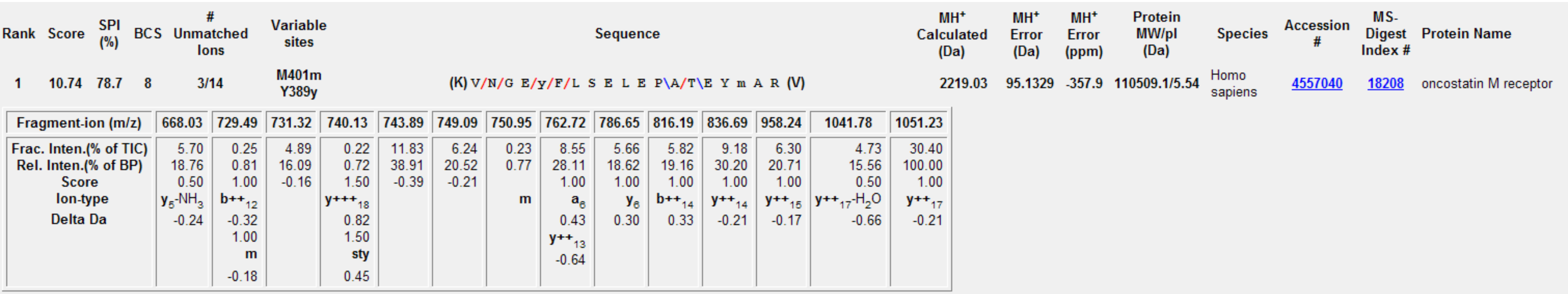
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.02	90.6	7	2/17	Y345y S326s	(R) G E K P A s\P A V Q\P D A A L|Q/R/L|A A V L A\G y G V E L R (Q)	3047.66	158.5945	-417.4	105848.1/6.66	Homo sapiens	4506321	4501	protein tyrosine phosphatase, receptor type, N precursor

Fragment-ion (m/z)	641.49	649.91	706.63	728.85	756.24	772.25	775.08	779.84	784.78	840.34	848.93	855.08	856.65	900.95	955.22	1027.95	1045.74
Frac. Inten.(% of TIC)	2.69	13.29	2.81	3.08	19.85	6.37	3.03	6.65	9.13	3.07	5.80	4.56	4.13	2.66	6.22	3.89	2.76
Rel. Inten.(% of BP)	13.55	66.96	14.13	15.54	100.00	32.10	15.28	33.51	46.01	15.49	29.24	22.99	20.78	13.38	31.32	19.60	13.88
Score	0.50	1.00	1.00	0.50	1.00	-0.32	0.50	1.00	1.00	-0.15	1.00	0.50	0.50	0.50	1.00	0.50	1.00
Ion-type	y++$_{12}$-H$_2$O	b$_6$ y++$_{12}$	y++$_{13}$	b$_7$-H$_2$O	b++$_{15}$		y++$_{14}$-H$_2$O	b+++$_{23}$	y++$_{14}$		y++$_{15}$	y$_7$-H$_2$O	y$_7$-NH$_3$	b$_9$-NH$_3$	b++$_{18}$	b$_{10}$-NH$_3$	b$_{10}$
Delta Da	0.67	-0.34 0.08	0.26	-0.45	-0.62		-0.34	0.76	0.36		0.48	-0.30	0.29	0.56	-0.26	-0.49	0.27

Peak 452


assignment

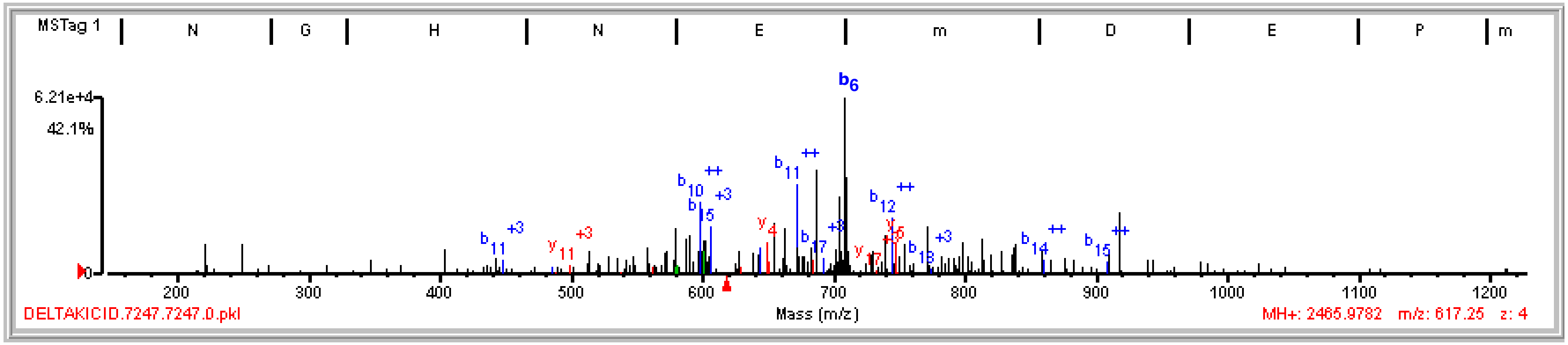


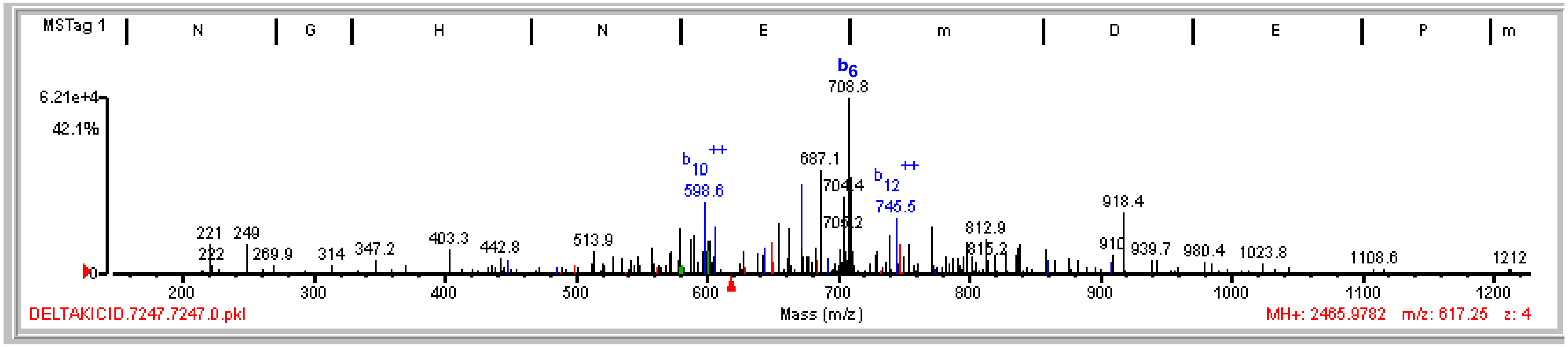


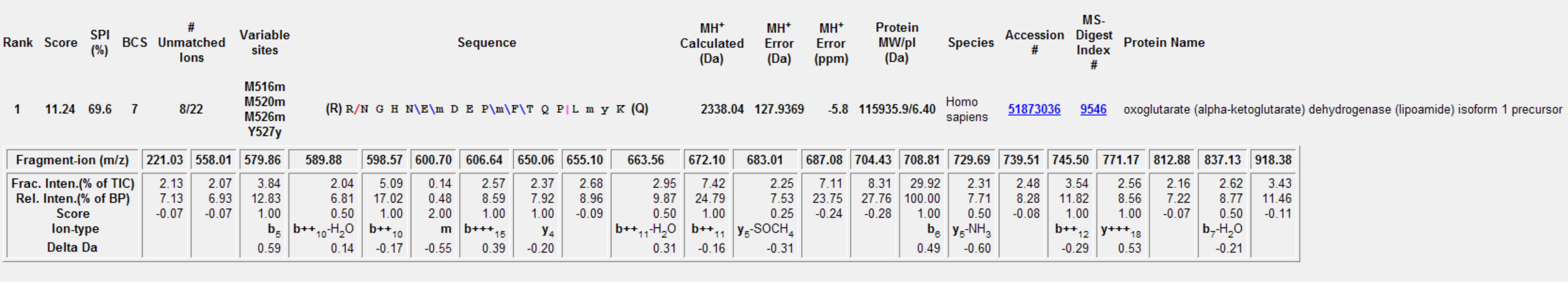
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.74	78.7	8	3/14	M401m Y389y	(K) V/N/G E/y/F/L S E L E P\A/T\E Y m A R (V)	2219.03	95.1329	-357.9	110509.1/5.54	Homo sapiens	4557040	18208	oncostatin M receptor

Fragment-ion (m/z)	668.03	729.49	731.32	740.13	743.89	749.09	750.95	762.72	786.65	816.19	836.69	958.24	1041.78	1051.23
Frac. Inten.(% of TIC)	5.70	0.25	4.89	0.22	11.83	6.24	0.23	8.55	5.66	5.82	9.18	6.30	4.73	30.40
Rel. Inten.(% of BP)	18.76	0.81	16.09	0.72	38.91	20.52	0.77	28.11	18.62	19.16	30.20	20.71	15.56	100.00
Score	0.50	1.00	-0.16	1.50	-0.39	-0.21		1.00	1.00	1.00	1.00	1.00	0.50	1.00
Ion-type	y_5-NH_3	$b++_{12}$		$y+++_{18}$			m	a_6	y_6	$b++_{14}$	$y++_{14}$	$y++_{15}$	$y++_{17}$-H_2O	$y++_{17}$
Delta Da	-0.24	-0.32		0.82				0.43	0.30	0.33	-0.21	-0.17	-0.66	-0.21
		1.00		1.50				$y++_{13}$						
		m		sty				-0.64						
		-0.18		0.45										

Peak 453







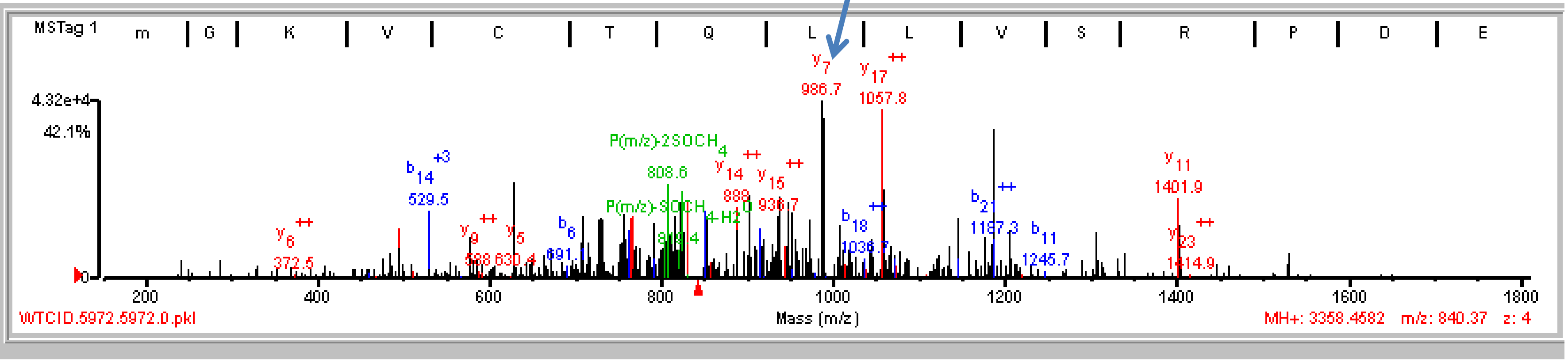
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.24	69.6	7	8/22	M516m M520m M526m Y527y	(R) R/N G H N\E\m D E P\m\F\T Q P|L m y K (Q)	2338.04	127.9369	-5.8	115935.9/6.40	Homo sapiens	51873036	9546	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor

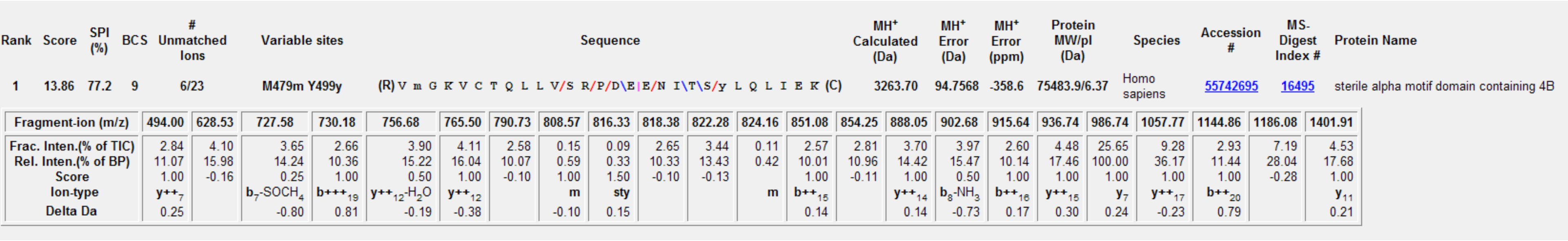
Fragment-ion (m/z)	221.03	558.01	579.86	589.88	598.57	600.70	606.64	650.06	655.10	663.56	672.10
Frac. Inten.(% of TIC)	2.13	2.07	3.84	2.04	5.09	0.14	2.57	2.37	2.68	2.95	7.42
Rel. Inten.(% of BP)	7.13	6.93	12.83	6.81	17.02	0.48	8.59	7.92	8.96	9.87	24.79
Score	-0.07	-0.07	1.00	0.50	1.00	2.00	1.00	1.00	-0.09	0.50	1.00
Ion-type			b_5	$b{+}{+}_{10}$-H_2O	$b{+}{+}_{10}$	m	$b{+}{+}{+}_{15}$	y_4		$b{+}{+}_{11}$-H_2O	$b{+}{+}_{11}$
Delta Da			0.59	0.14	-0.17	-0.55	0.39	-0.20		0.31	-0.16

Fragment-ion (m/z)	683.01	687.08	704.43	708.81	729.69	739.51	745.50	771.17	812.88	837.13	918.38
Frac. Inten.(% of TIC)	2.25	7.11	8.31	29.92	2.31	2.48	3.54	2.56	2.16	2.62	3.43
Rel. Inten.(% of BP)	7.53	23.75	27.76	100.00	7.71	8.28	11.82	8.56	7.22	8.77	11.46
Score	0.25	-0.24	-0.28	1.00	0.50	-0.08	1.00	1.00	-0.07	0.50	-0.11
Ion-type	y_5-$SOCH_4$			b_6	y_5-NH_3		$b{+}{+}_{12}$	$y{+}{+}{+}_{18}$		b_7-H_2O	
Delta Da	-0.31			0.49	-0.60		-0.29	0.53		-0.21	

Peak 454

assignment

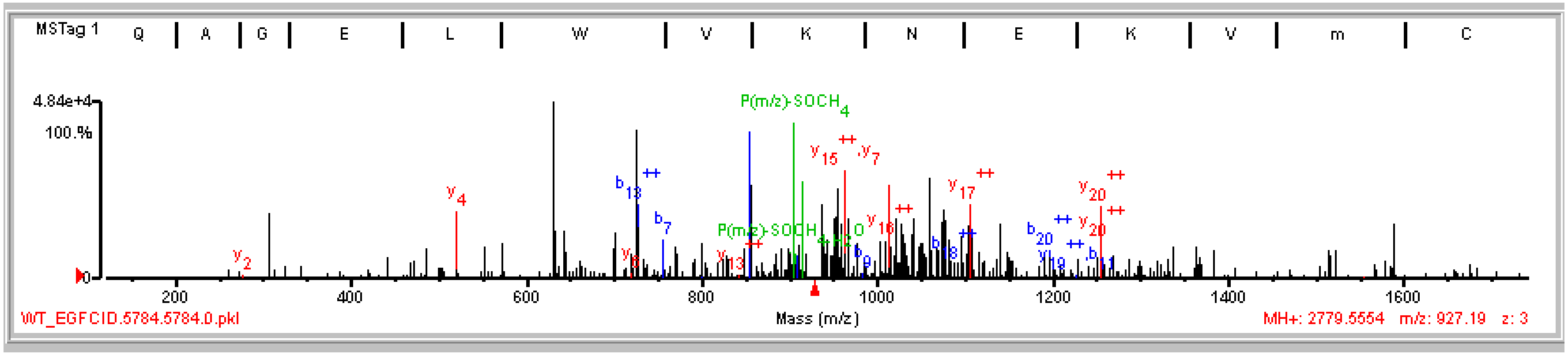


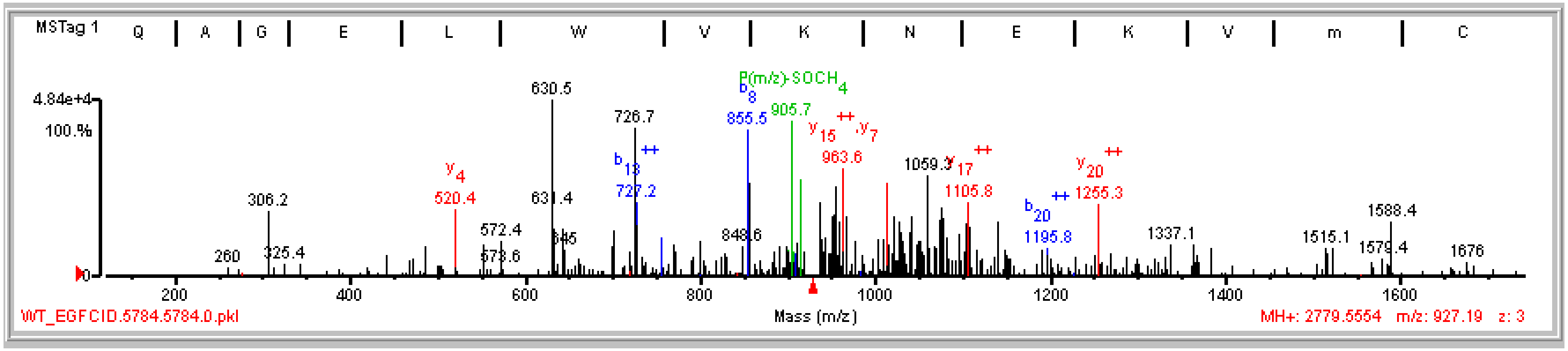


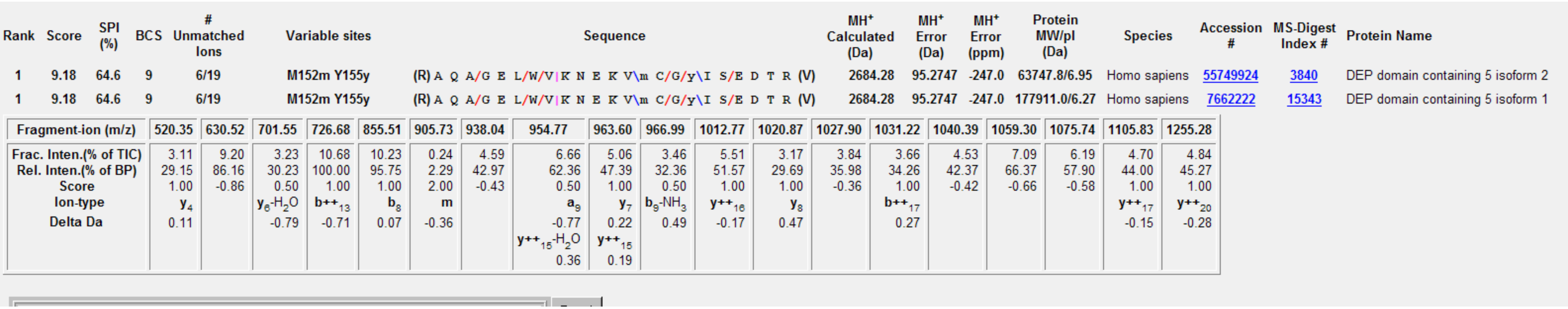
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.86	77.2	9	6/23	M479m Y499y	(R) V m G K V C T Q L L V/S R/P/D\E|E/N I\T\S/y L Q L I E K (C)	3263.70	94.7568	-358.6	75483.9/6.37	Homo sapiens	55742695	16495	sterile alpha motif domain containing 4B

Fragment-ion (m/z)	494.00	628.53	727.58	730.18	756.68	765.50	790.73	808.57	816.33	818.38	822.28	824.16	851.08	854.25	888.05	902.68	915.64	936.74	986.74	1057.77	1144.86	1186.08	1401.91
Frac. Inten.(% of TIC)	2.84	4.10	3.65	2.66	3.90	4.11	2.58	0.15	0.09	2.65	3.44	0.11	2.57	2.81	3.70	3.97	2.60	4.48	25.65	9.28	2.93	7.19	4.53
Rel. Inten.(% of BP)	11.07	15.98	14.24	10.36	15.22	16.04	10.07	0.59	0.33	10.33	13.43	0.42	10.01	10.96	14.42	15.47	10.14	17.46	100.00	36.17	11.44	28.04	17.68
Score	1.00	-0.16	0.25	1.00	0.50	1.00	-0.10	1.00	1.50	-0.10	-0.13		1.00	-0.11	1.00	0.50	1.00	1.00	1.00	1.00	1.00	-0.28	1.00
Ion-type	$y{+}{+}_{7}$		b_{7}-SOCH$_4$	$b{+}{+}{+}_{19}$	$y{+}{+}_{12}$-H$_2$O	$y{+}{+}_{12}$		m	sty			m	$b{+}{+}_{15}$		$y{+}{+}_{14}$	b_{8}-NH$_3$	$b{+}{+}_{16}$	$y{+}{+}_{15}$	y_{7}	$y{+}{+}_{17}$	$b{+}{+}_{20}$		y_{11}
Delta Da	0.25		-0.80	0.81	-0.19	-0.38		-0.10	0.15				0.14		0.14	-0.73	0.17	0.30	0.24	-0.23	0.79		0.21

Peak 455



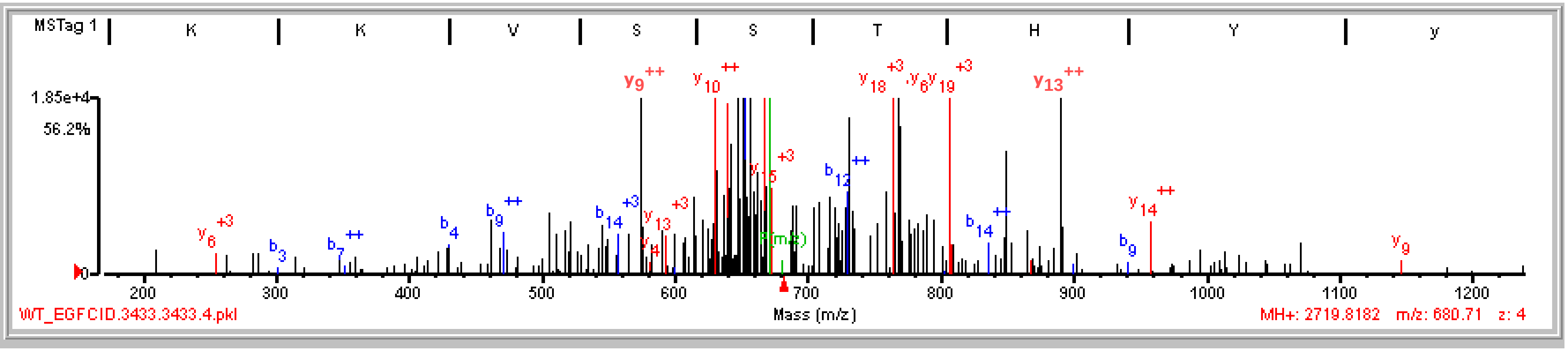


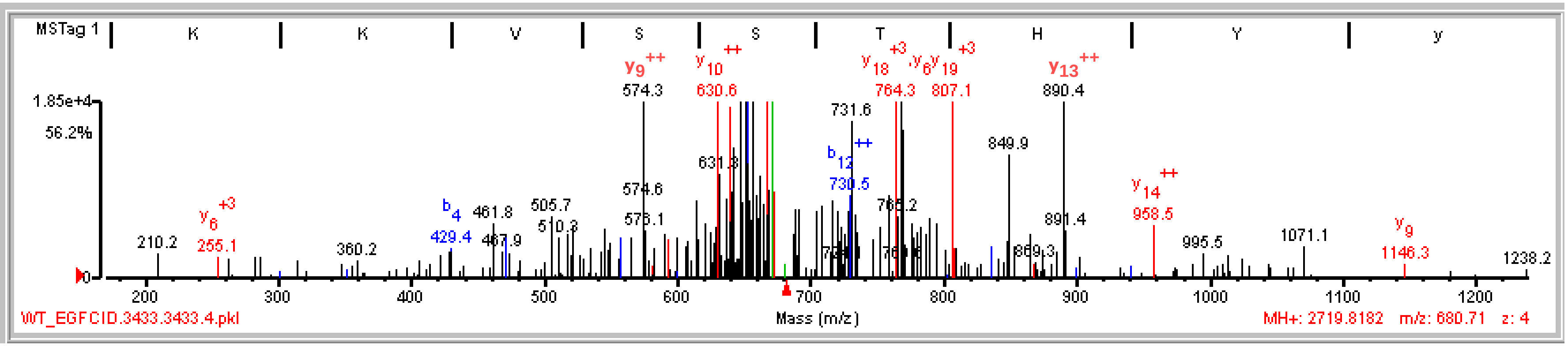


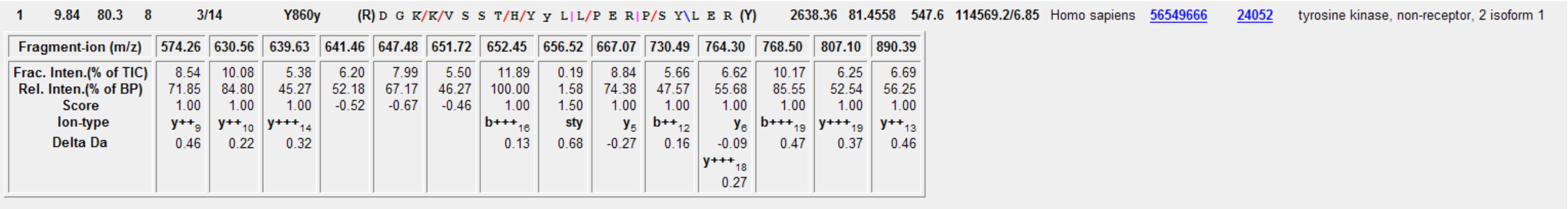
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.18	64.6	9	6/19	M152m Y155y	(R) A Q A/G E L/W/V|K N E K V\m C/G/y\I S/E D T R (V)	2684.28	95.2747	-247.0	63747.8/6.95	Homo sapiens	55749924	3840	DEP domain containing 5 isoform 2
1	9.18	64.6	9	6/19	M152m Y155y	(R) A Q A/G E L/W/V|K N E K V\m C/G/y\I S/E D T R (V)	2684.28	95.2747	-247.0	177911.0/6.27	Homo sapiens	7662222	15343	DEP domain containing 5 isoform 1

Fragment-ion (m/z)	520.35	630.52	701.55	726.68	855.51	905.73	938.04	954.77	963.60	966.99	1012.77	1020.87	1027.90	1031.22	1040.39	1059.30	1075.74	1105.83	1255.28
Frac. Inten.(% of TIC)	3.11	9.20	3.23	10.68	10.23	0.24	4.59	6.66	5.06	3.46	5.51	3.17	3.84	3.66	4.53	7.09	6.19	4.70	4.84
Rel. Inten.(% of BP)	29.15	86.16	30.23	100.00	95.75	2.29	42.97	62.36	47.39	32.36	51.57	29.69	35.98	34.26	42.37	66.37	57.90	44.00	45.27
Score	1.00	-0.86	0.50	1.00	1.00	2.00	-0.43	0.50	1.00	0.50	1.00	1.00	-0.36	1.00	-0.42	-0.66	-0.58	1.00	1.00
Ion-type	y_4		y_6-H_2O	$b{+}{+}_{13}$	b_8	m		a_9 $y{+}{+}_{15}$-H_2O	y_7 $y{+}{+}_{15}$	b_9-NH_3	$y{+}{+}_{16}$	y_8		$b{+}{+}_{17}$				$y{+}{+}_{17}$	$y{+}{+}_{20}$
Delta Da	0.11		-0.79	-0.71	0.07	-0.36		-0.77 0.36	0.22 0.19	0.49	-0.17	0.47		0.27				-0.15	-0.28

Peak 456



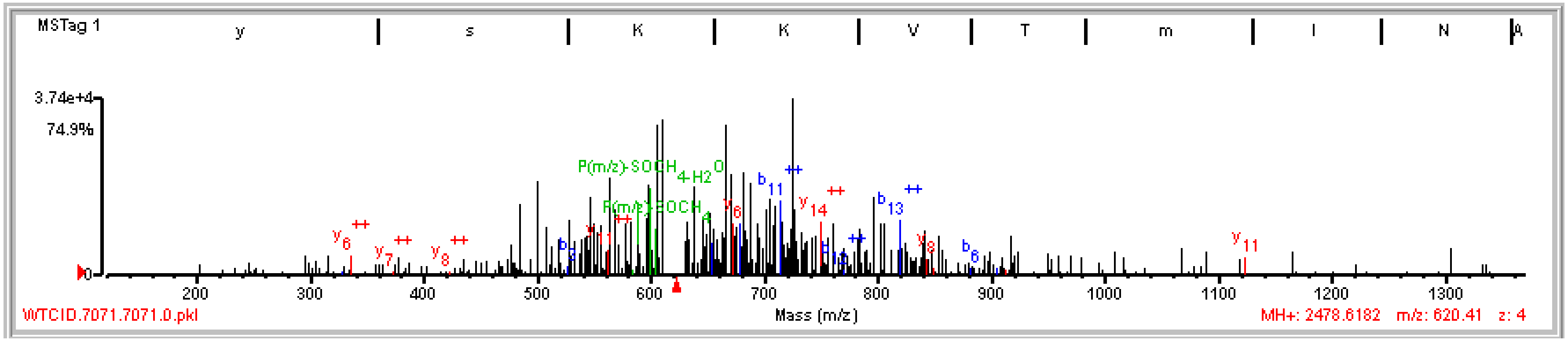


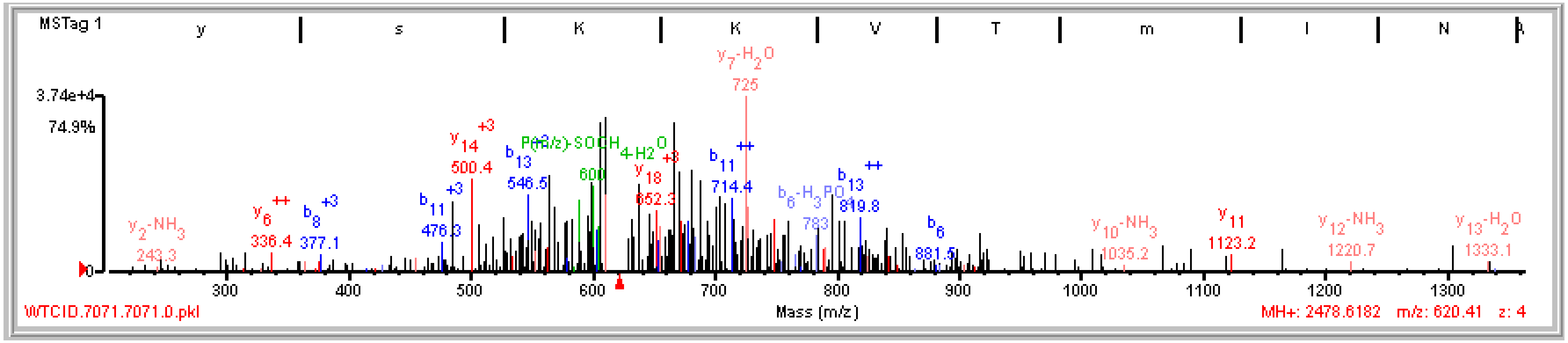


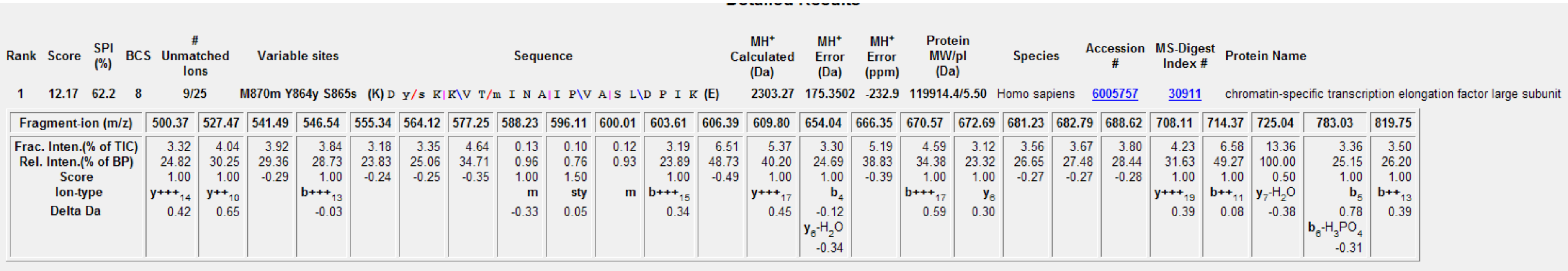
1 9.84 80.3 8 3/14 Y860y (R) D G K/K/V S S T/H/Y y L|L/P E R|P/S Y\L E R (Y) 2638.36 81.4558 547.6 114569.2/6.85 Homo sapiens 56549666 24052 tyrosine kinase, non-receptor, 2 isoform 1

Fragment-ion (m/z)	574.26	630.56	639.63	641.46	647.48	651.72	652.45	656.52	667.07	730.49	764.30	768.50	807.10	890.39
Frac. Inten.(% of TIC)	8.54	10.08	5.38	6.20	7.99	5.50	11.89	0.19	8.84	5.66	6.62	10.17	6.25	6.69
Rel. Inten.(% of BP)	71.85	84.80	45.27	52.18	67.17	46.27	100.00	1.58	74.38	47.57	55.68	85.55	52.54	56.25
Score	1.00	1.00	1.00	-0.52	-0.67	-0.46	1.00	1.50	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{++}_{9}	y^{++}_{10}	y^{+++}_{14}				b^{+++}_{16}	sty	y_{5}	b^{++}_{12}	y_{6} -0.09 y^{+++}_{18}	b^{+++}_{19}	y^{+++}_{19}	y^{++}_{13}
Delta Da	0.46	0.22	0.32				0.13	0.68	-0.27	0.16	0.27	0.47	0.37	0.46

Peak 457





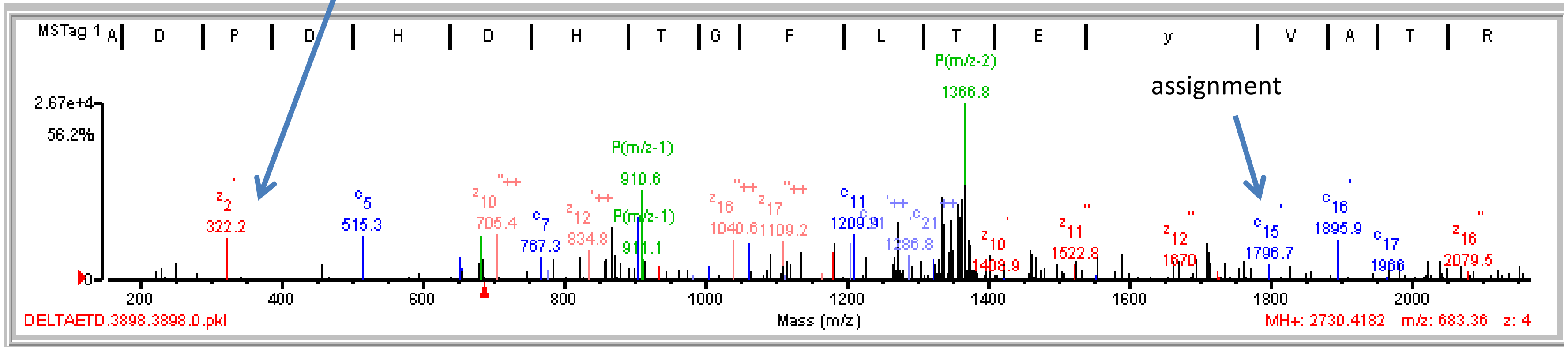


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.17	62.2	8	9/25	M870m Y864y S865s	(K) D y/s K|K\V T/m I N A|I P\V A|S L\D P I K (E)	2303.27	175.3502	-232.9	119914.4/5.50	Homo sapiens	6005757	30911	chromatin-specific transcription elongation factor large subunit

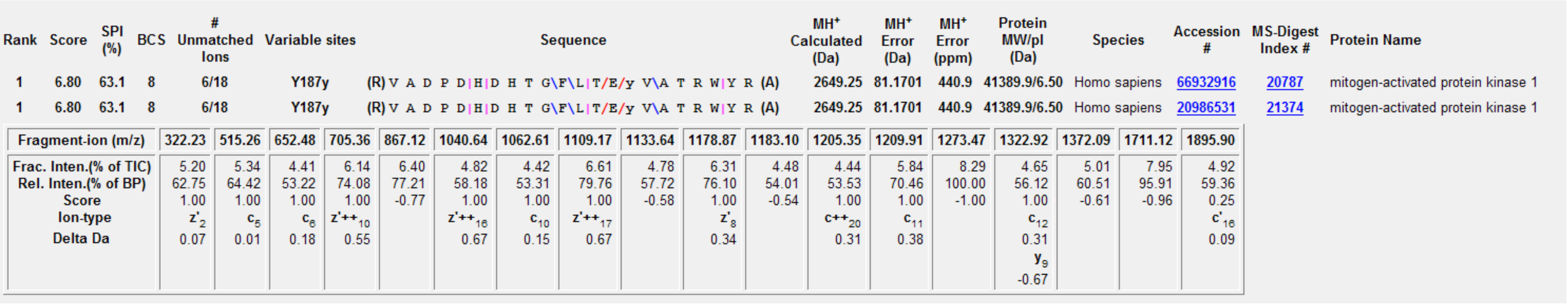
Fragment-ion (m/z)	500.37	527.47	541.49	546.54	555.34	564.12	577.25	588.23	596.11	600.01	603.61	606.39	609.80	654.04	666.35	670.57	672.69	681.23	682.79	688.62	708.11	714.37	725.04	783.03	819.75
Frac. Inten.(% of TIC)	3.32	4.04	3.92	3.84	3.18	3.35	4.64	0.13	0.10	0.12	3.19	6.51	5.37	3.30	5.19	4.59	3.12	3.56	3.67	3.80	4.23	6.58	13.36	3.36	3.50
Rel. Inten.(% of BP)	24.82	30.25	29.36	28.73	23.83	25.06	34.71	0.96	0.76	0.93	23.89	48.73	40.20	24.69	38.83	34.38	23.32	26.65	27.48	28.44	31.63	49.27	100.00	25.15	26.20
Score	1.00	1.00	-0.29	1.00	-0.24	-0.25	-0.35	1.00	1.50		1.00	-0.49	1.00	1.00	-0.39	1.00	1.00	-0.27	-0.27	-0.28	1.00	1.00	0.50	1.00	1.00
Ion-type	$y+++_{14}$	$y++_{10}$		$b+++_{13}$				m	sty	m	$b+++_{15}$		$y+++_{17}$	b_4 y_6-H_2O		$b+++_{17}$	y_6				$y+++_{19}$	$b++_{11}$	y_7-H_2O	b_5 b_6-H_3PO_4	$b++_{13}$
Delta Da	0.42	0.65		-0.03				-0.33	0.05		0.34		0.45	-0.12 -0.34		0.59	0.30				0.39	0.08	-0.38	0.78 -0.31	0.39

Peak 458

Ions that verify assignment



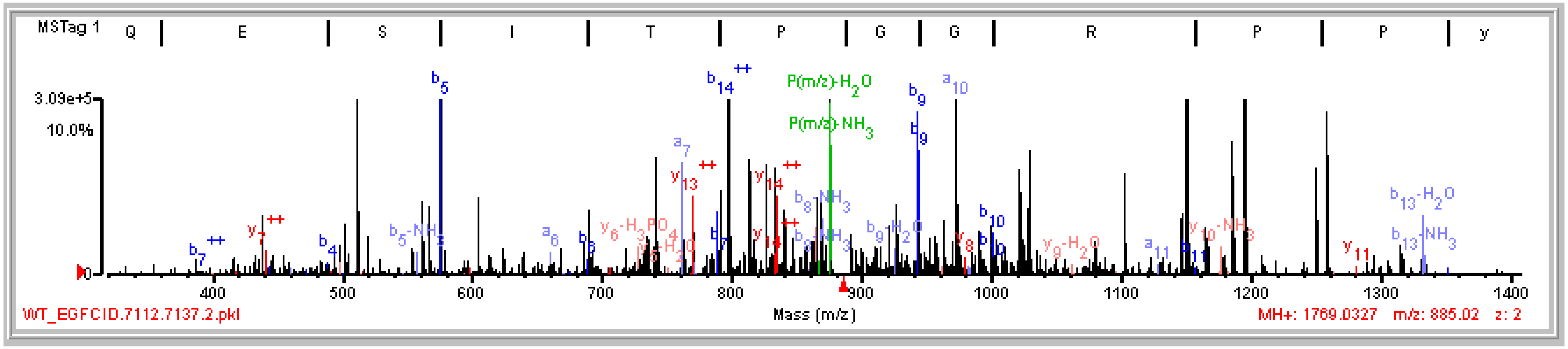
assignment

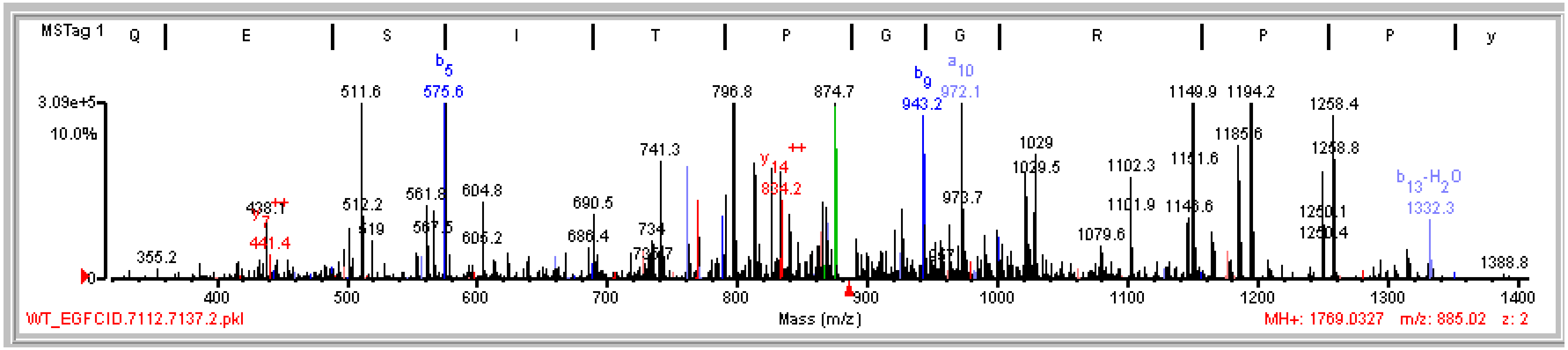


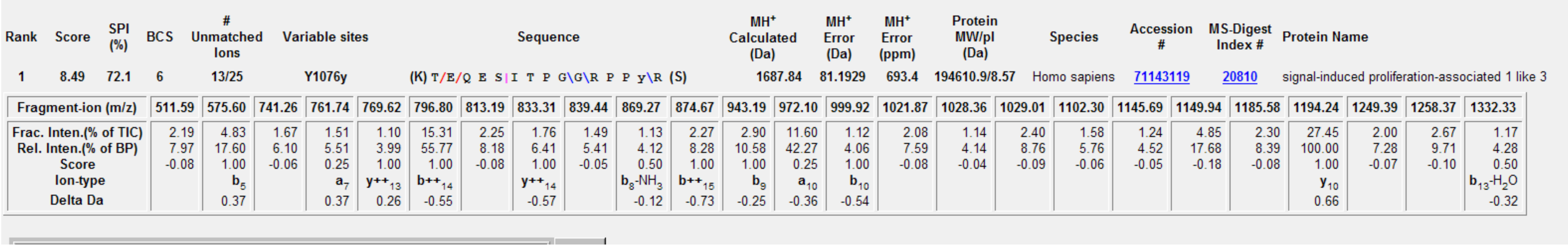
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.80	63.1	8	6/18	Y187y	(R) V A D P D|H|D H T G\F\L|T/E/y V\A T R W|Y R (A)	2649.25	81.1701	440.9	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	6.80	63.1	8	6/18	Y187y	(R) V A D P D|H|D H T G\F\L|T/E/y V\A T R W|Y R (A)	2649.25	81.1701	440.9	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

Fragment-ion (m/z)	322.23	515.26	652.48	705.36	867.12	1040.64	1062.61	1109.17	1133.64	1178.87	1183.10	1205.35	1209.91	1273.47	1322.92	1372.09	1711.12	1895.90
Frac. Inten.(% of TIC)	5.20	5.34	4.41	6.14	6.40	4.82	4.42	6.61	4.78	6.31	4.48	4.44	5.84	8.29	4.65	5.01	7.95	4.92
Rel. Inten.(% of BP)	62.75	64.42	53.22	74.08	77.21	58.18	53.31	79.76	57.72	76.10	54.01	53.53	70.46	100.00	56.12	60.51	95.91	59.36
Score	1.00	1.00	1.00	1.00	-0.77	1.00	1.00	1.00	-0.58	1.00	-0.54	1.00	1.00	-1.00	1.00	-0.61	-0.96	0.25
Ion-type	z'_2	c_5	c_6	$z'{++}_{10}$		$z'{++}_{16}$	c_{10}	$z'{++}_{17}$		z'_8		$c{++}_{20}$	c_{11}		c_{12} y_9			c'_{16}
Delta Da	0.07	0.01	0.18	0.55		0.67	0.15	0.67		0.34		0.31	0.38		0.31 -0.67			0.09

Peak 459





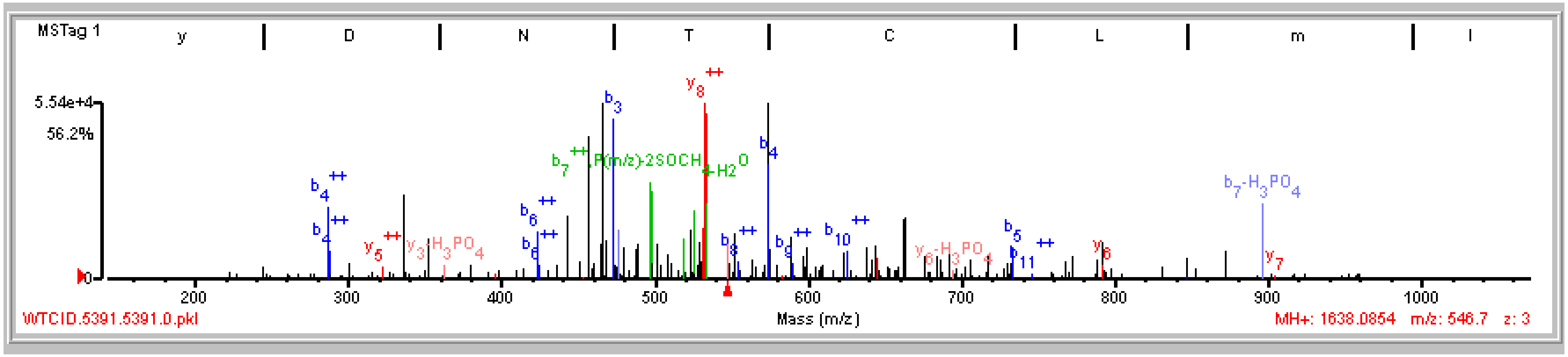


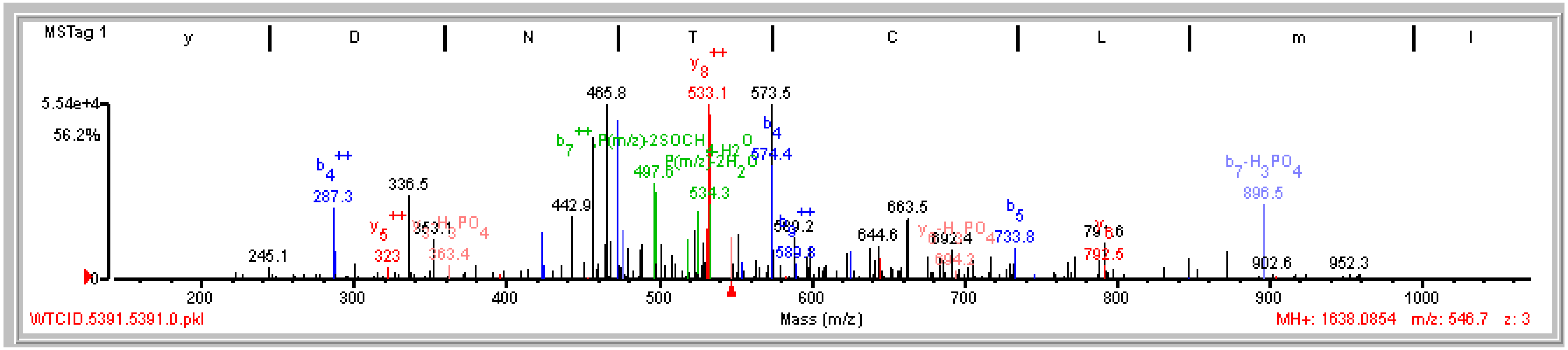
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.49	72.1	6	13/25	Y1076y	(K) T/E/Q E S|I T P G\G\R P P y\R (S)	1687.84	81.1929	693.4	194610.9/8.57	Homo sapiens	71143119	20810	signal-induced proliferation-associated 1 like 3

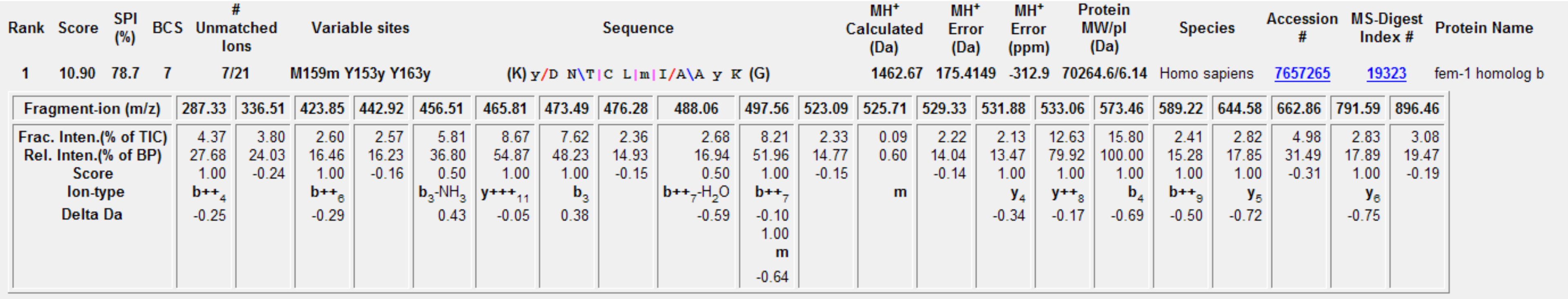
Fragment-ion (m/z)	511.59	575.60	741.26	761.74	769.62	796.80	813.19	833.31	839.44	869.27	874.67
Frac. Inten.(% of TIC)	2.19	4.83	1.67	1.51	1.10	15.31	2.25	1.76	1.49	1.13	2.27
Rel. Inten.(% of BP)	7.97	17.60	6.10	5.51	3.99	55.77	8.18	6.41	5.41	4.12	8.28
Score	-0.08	1.00	-0.06	0.25	1.00	1.00	-0.08	1.00	-0.05	0.50	1.00
Ion-type		b_5		a_7	$y{+}{+}_{13}$	$b{+}{+}_{14}$		$y{+}{+}_{14}$		b_8-NH_3	$b{+}{+}_{15}$
Delta Da		0.37		0.37	0.26	-0.55		-0.57		-0.12	-0.73

Fragment-ion (m/z)	943.19	972.10	999.92	1021.87	1028.36	1029.01	1102.30	1145.69	1149.94	1185.58	1194.24	1249.39	1258.37	1332.33
Frac. Inten.(% of TIC)	2.90	11.60	1.12	2.08	1.14	2.40	1.58	1.24	4.85	2.30	27.45	2.00	2.67	1.17
Rel. Inten.(% of BP)	10.58	42.27	4.06	7.59	4.14	8.76	5.76	4.52	17.68	8.39	100.00	7.28	9.71	4.28
Score	1.00	0.25	1.00	-0.08	-0.04	-0.09	-0.06	-0.05	-0.18	-0.08	1.00	-0.07	-0.10	0.50
Ion-type	b_9	a_{10}	b_{10}								y_{10}			b_{13}-H_2O
Delta Da	-0.25	-0.36	-0.54								0.66			-0.32

Peak 460



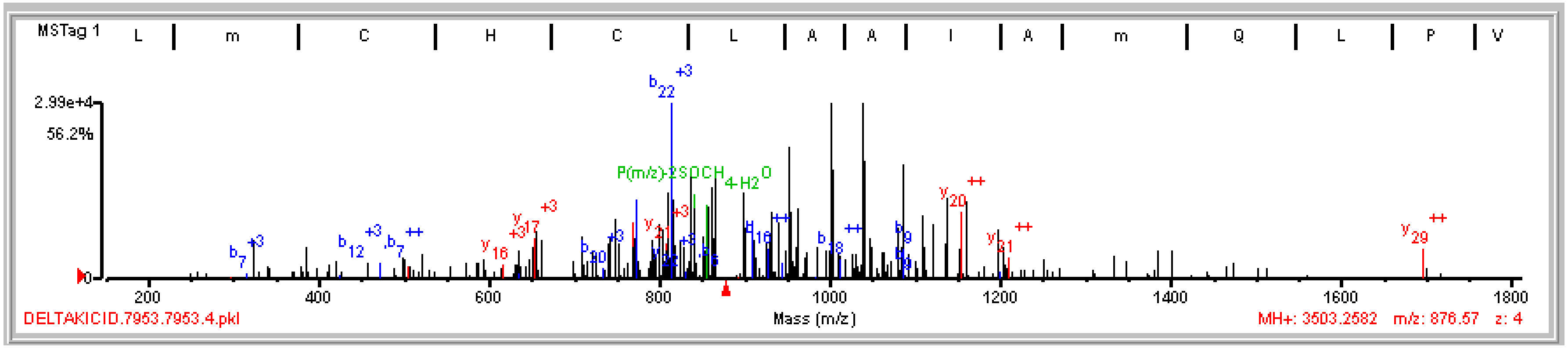


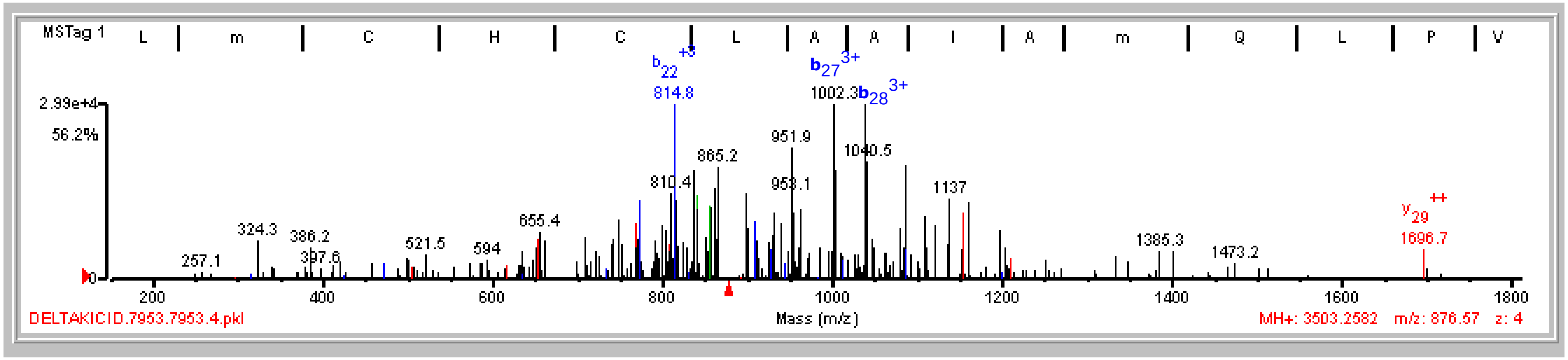


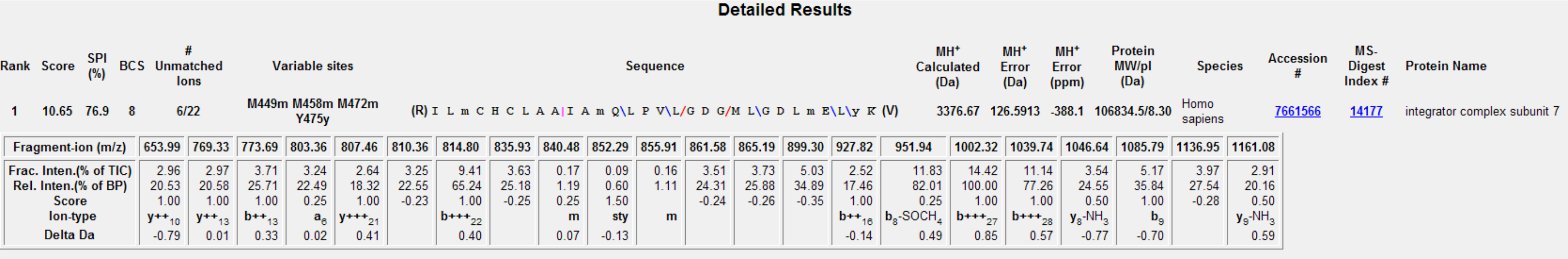
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.90	78.7	7	7/21	M159m Y153y Y163y	(K) y/D N\T|C L|m|I/A\A y K (G)	1462.67	175.4149	-312.9	70264.6/6.14	Homo sapiens	7657265	19323	fem-1 homolog b

Fragment-ion (m/z)	287.33	336.51	423.85	442.92	456.51	465.81	473.49	476.28	488.06	497.56	523.09	525.71	529.33	531.88	533.06	573.46	589.22	644.58	662.86	791.59	896.46
Frac. Inten.(% of TIC)	4.37	3.80	2.60	2.57	5.81	8.67	7.62	2.36	2.68	8.21	2.33	0.09	2.22	2.13	12.63	15.80	2.41	2.82	4.98	2.83	3.08
Rel. Inten.(% of BP)	27.68	24.03	16.46	16.23	36.80	54.87	48.23	14.93	16.94	51.96	14.77	0.60	14.04	13.47	79.92	100.00	15.28	17.85	31.49	17.89	19.47
Score	1.00	-0.24	1.00	-0.16	0.50	1.00	1.00	-0.15	0.50	1.00	-0.15		-0.14	1.00	1.00	1.00	1.00	1.00	-0.31	1.00	-0.19
Ion-type	$b{++}_4$		$b{++}_6$		b_3-NH$_3$	$y{+++}_{11}$	b_3		$b{++}_7$-H$_2$O	$b{++}_7$		m		y_4	$y{++}_8$	b_4	$b{++}_9$	y_5		y_6	
Delta Da	-0.25		-0.29		0.43	-0.05	0.38		-0.59	-0.10				-0.34	-0.17	-0.69	-0.50	-0.72		-0.75	
										1.00											
										m											
										-0.64											

Peak 461







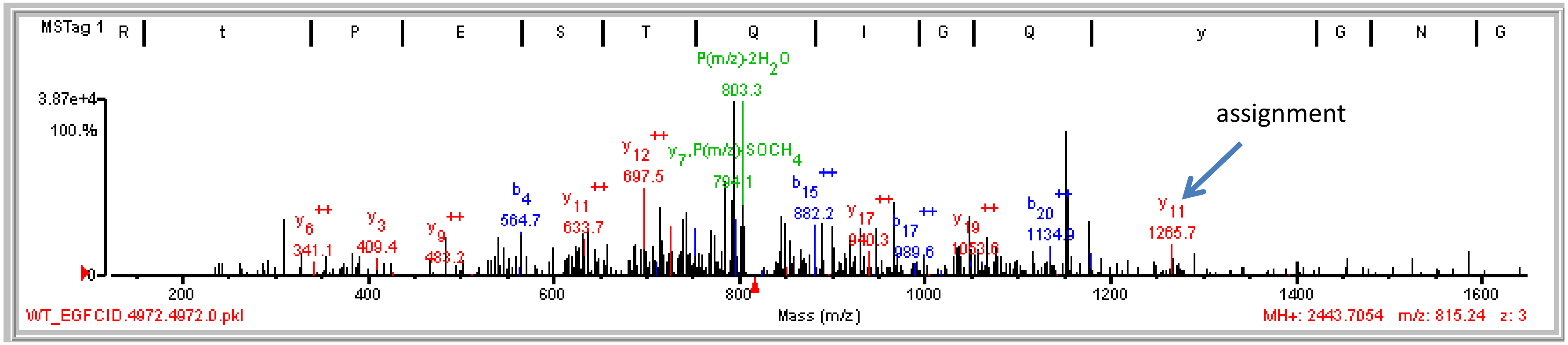
Detailed Results

Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.65	76.9	8	6/22	M449m M458m M472m Y475y	(R) I L m C H C L A A|I A m Q\L P V\L/G D G/M L\G D L m E\L\y K (V)	3376.67	126.5913	-388.1	106834.5/8.30	Homo sapiens	7661566	14177	integrator complex subunit 7

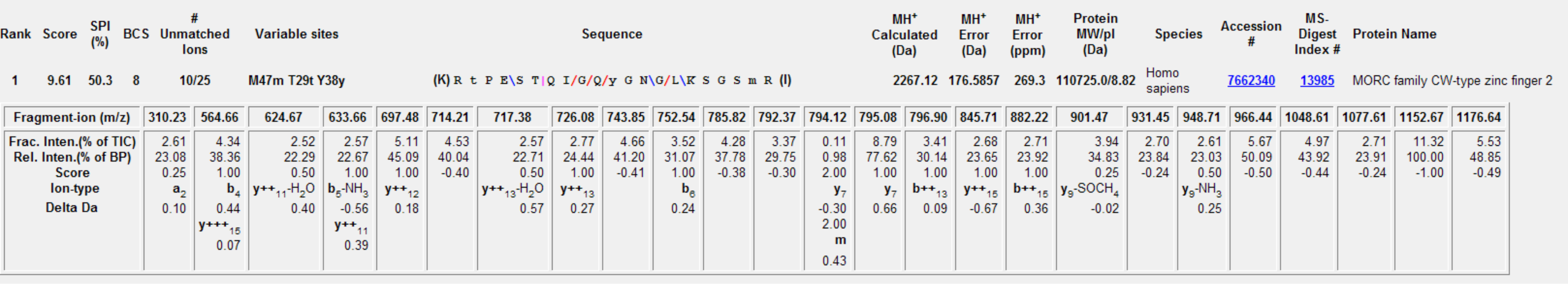
Fragment-ion (m/z)	653.99	769.33	773.69	803.36	807.46	810.36	814.80	835.93	840.48	852.29	855.91
Frac. Inten.(% of TIC)	2.96	2.97	3.71	3.24	2.64	3.25	9.41	3.63	0.17	0.09	0.16
Rel. Inten.(% of BP)	20.53	20.58	25.71	22.49	18.32	22.55	65.24	25.18	1.19	0.60	1.11
Score	1.00	1.00	1.00	0.25	1.00	-0.23	1.00	-0.25	0.25	1.50	
Ion-type	$y{++}_{10}$	$y{++}_{13}$	$b{++}_{13}$	a_6	$y{+++}_{21}$		$b{+++}_{22}$		m	sty	m
Delta Da	-0.79	0.01	0.33	0.02	0.41		0.40		0.07	-0.13	

Fragment-ion (m/z)	861.58	865.19	899.30	927.82	951.94	1002.32	1039.74	1046.64	1085.79	1136.95	1161.08
Frac. Inten.(% of TIC)	3.51	3.73	5.03	2.52	11.83	14.42	11.14	3.54	5.17	3.97	2.91
Rel. Inten.(% of BP)	24.31	25.88	34.89	17.46	82.01	100.00	77.26	24.55	35.84	27.54	20.16
Score	-0.24	-0.26	-0.35	1.00	0.25	1.00	1.00	0.50	1.00	-0.28	0.50
Ion-type				$b{++}_{16}$	b_8-$SOCH_4$	$b{+++}_{27}$	$b{+++}_{28}$	y_8-NH_3	b_9		y_9-NH_3
Delta Da				-0.14	0.49	0.85	0.57	-0.77	-0.70		0.59

Peak 462



assignment

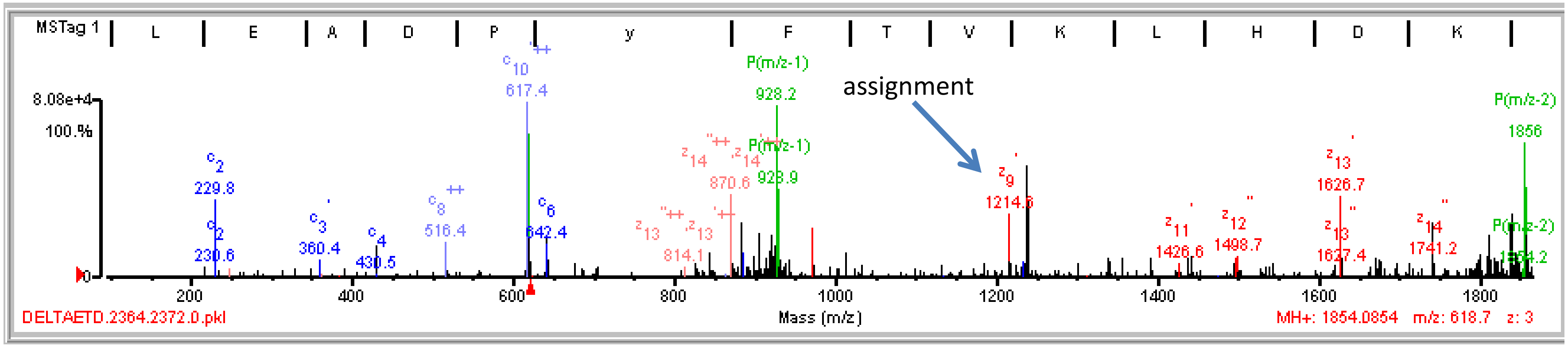


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.61	50.3	8	10/25	M47m T29t Y38y	(K) R t P E\S T|Q I/G/Q/y G N\G/L\K S G S m R (I)	2267.12	176.5857	269.3	110725.0/8.82	Homo sapiens	7662340	13985	MORC family CW-type zinc finger 2

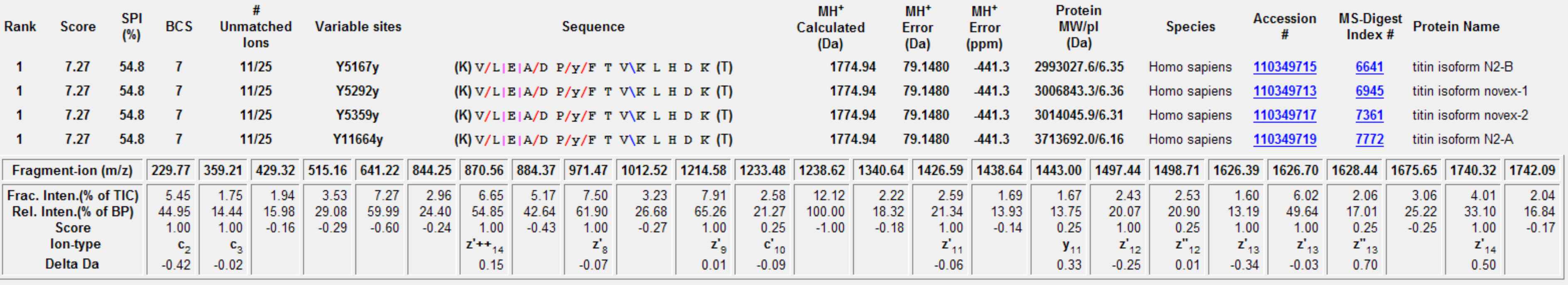
Fragment-ion (m/z)	310.23	564.66	624.67	633.66	697.48	714.21	717.38	726.08	743.85	752.54	785.82	792.37
Frac. Inten.(% of TIC)	2.61	4.34	2.52	2.57	5.11	4.53	2.57	2.77	4.66	3.52	4.28	3.37
Rel. Inten.(% of BP)	23.08	38.36	22.29	22.67	45.09	40.04	22.71	24.44	41.20	31.07	37.78	29.75
Score	0.25	1.00	0.50	1.00	1.00	-0.40	0.50	1.00	-0.41	1.00	-0.38	-0.30
Ion-type	a_2	b_4 y^{+++}_{15}	y^{++}_{11}-H_2O	b_5-NH_3 y^{++}_{11}	y^{++}_{12}		y^{++}_{13}-H_2O	y^{++}_{13}		b_6		
Delta Da	0.10	0.44 0.07	0.40	-0.56 0.39	0.18		0.57	0.27		0.24		

Fragment-ion (m/z)	794.12	795.08	796.90	845.71	882.22	901.47	931.45	948.71	966.44	1048.61	1077.61	1152.67	1176.64
Frac. Inten.(% of TIC)	0.11	8.79	3.41	2.68	2.71	3.94	2.70	2.61	5.67	4.97	2.71	11.32	5.53
Rel. Inten.(% of BP)	0.98	77.62	30.14	23.65	23.92	34.83	23.84	23.03	50.09	43.92	23.91	100.00	48.85
Score	2.00	1.00	1.00	1.00	1.00	0.25	-0.24	0.50	-0.50	-0.44	-0.24	-1.00	-0.49
Ion-type	y_7	y_7	b^{++}_{13}	y^{++}_{15}	b^{++}_{15}	y_9-$SOCH_4$		y_9-NH_3					
Delta Da	-0.30 2.00 m 0.43	0.66	0.09	-0.67	0.36	-0.02		0.25					

Peak 463



assignment

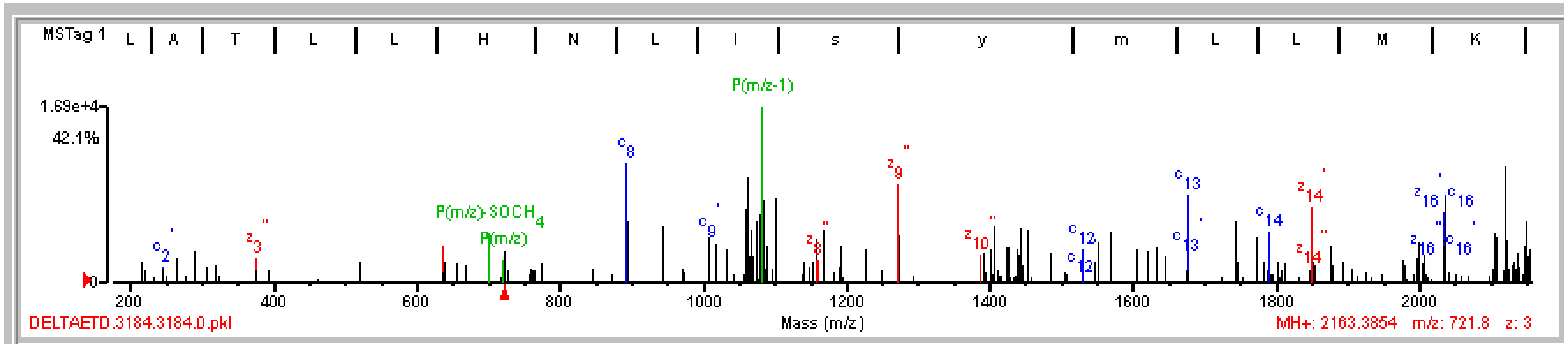


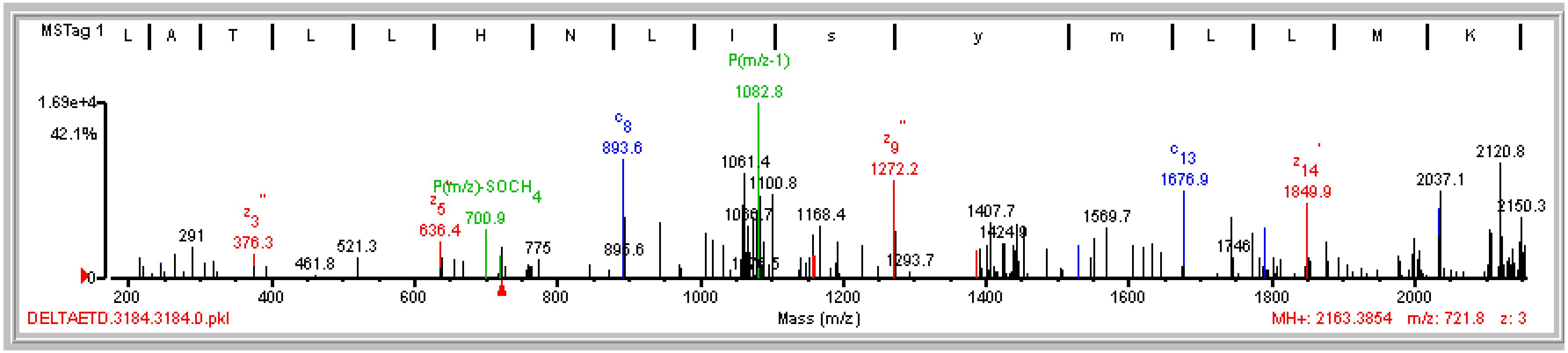
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.27	54.8	7	11/25	Y5167y	(K) V/L|E|A/D P/y/F T V\K L H D K (T)	1774.94	79.1480	-441.3	2993027.6/6.35	Homo sapiens	110349715	6641	titin isoform N2-B
1	7.27	54.8	7	11/25	Y5292y	(K) V/L|E|A/D P/y/F T V\K L H D K (T)	1774.94	79.1480	-441.3	3006843.3/6.36	Homo sapiens	110349713	6945	titin isoform novex-1
1	7.27	54.8	7	11/25	Y5359y	(K) V/L|E|A/D P/y/F T V\K L H D K (T)	1774.94	79.1480	-441.3	3014045.9/6.31	Homo sapiens	110349717	7361	titin isoform novex-2
1	7.27	54.8	7	11/25	Y11664y	(K) V/L|E|A/D P/y/F T V\K L H D K (T)	1774.94	79.1480	-441.3	3713692.0/6.16	Homo sapiens	110349719	7772	titin isoform N2-A

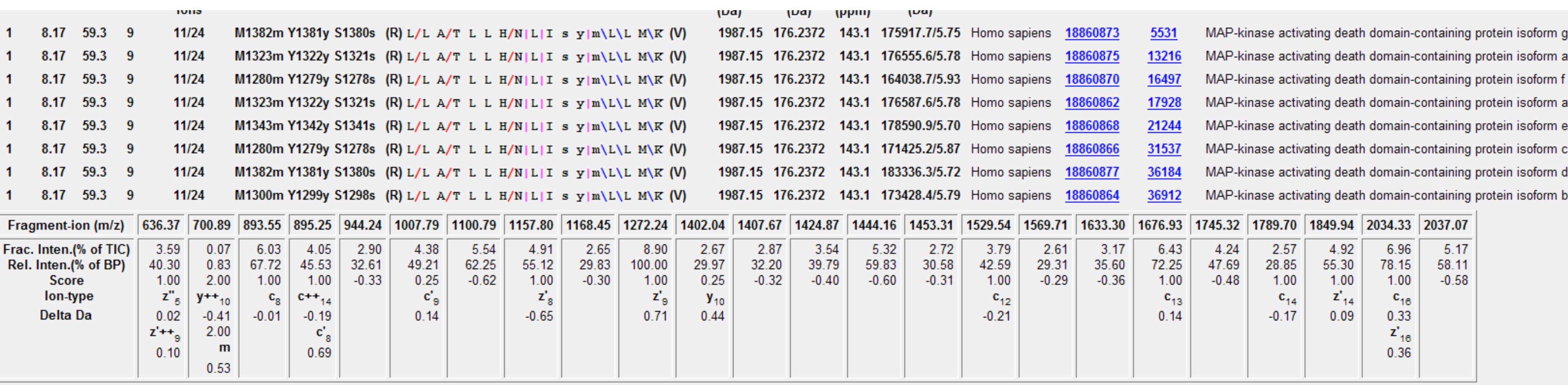
Fragment-ion (m/z)	229.77	359.21	429.32	515.16	641.22	844.25	870.56	884.37	971.47	1012.52	1214.58	1233.48
Frac. Inten.(% of TIC)	5.45	1.75	1.94	3.53	7.27	2.96	6.65	5.17	7.50	3.23	7.91	2.58
Rel. Inten.(% of BP)	44.95	14.44	15.98	29.08	59.99	24.40	54.85	42.64	61.90	26.68	65.26	21.27
Score	1.00	1.00	-0.16	-0.29	-0.60	-0.24	1.00	-0.43	1.00	-0.27	1.00	0.25
Ion-type	c_2	c_3					$z'{++}_{14}$		z'_8		z'_9	c'_{10}
Delta Da	-0.42	-0.02					0.15		-0.07		0.01	-0.09

Fragment-ion (m/z)	1238.62	1340.64	1426.59	1438.64	1443.00	1497.44	1498.71	1626.39	1626.70	1628.44	1675.65	1740.32	1742.09
Frac. Inten.(% of TIC)	12.12	2.22	2.59	1.69	1.67	2.43	2.53	1.60	6.02	2.06	3.06	4.01	2.04
Rel. Inten.(% of BP)	100.00	18.32	21.34	13.93	13.75	20.07	20.90	13.19	49.64	17.01	25.22	33.10	16.84
Score	-1.00	-0.18	1.00	-0.14	0.25	1.00	0.25	1.00	1.00	0.25	-0.25	1.00	-0.17
Ion-type			z'_{11}		y_{11}	z'_{12}	z''_{12}	z'_{13}	z'_{13}	z''_{13}		z'_{14}	
Delta Da			-0.06		0.33	-0.25	0.01	-0.34	-0.03	0.70		0.50	

Peak 464



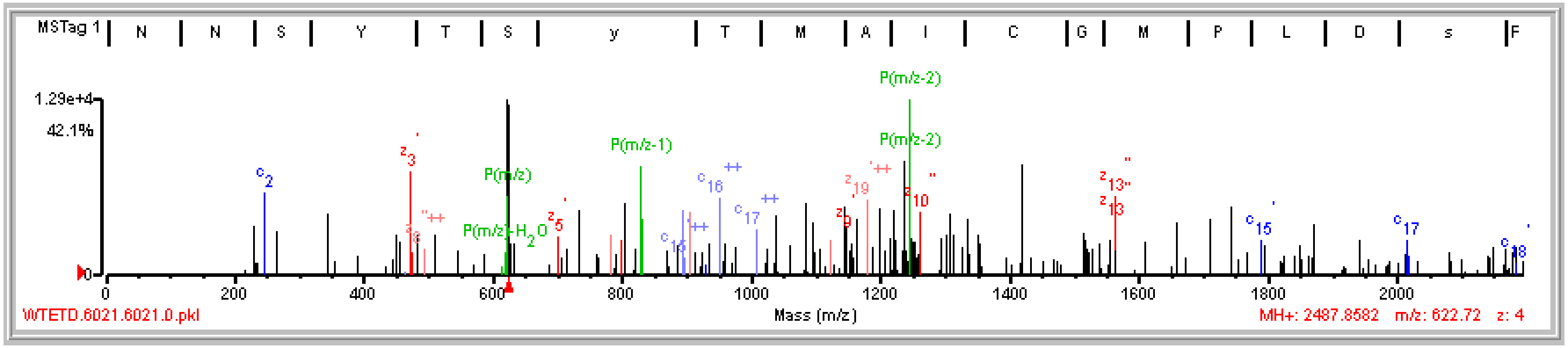


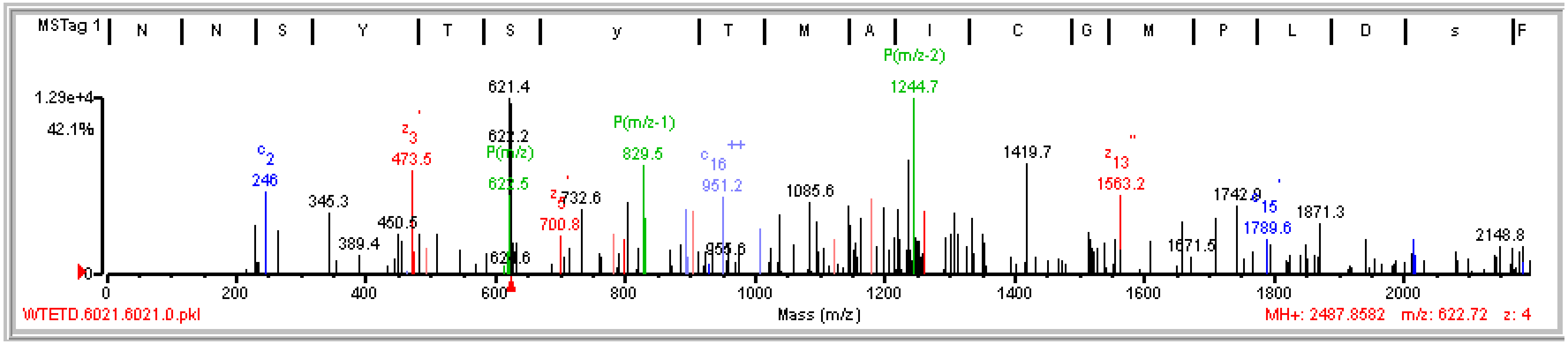


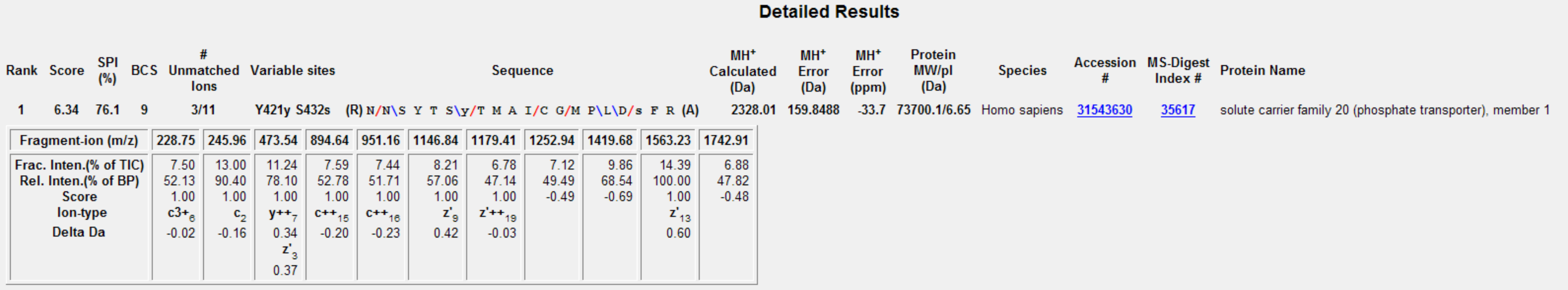
				Ions			(Da)	(Da)	(ppm)	(Da)				
1	8.17	59.3	9	11/24	M1382m Y1381y S1380s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	175917.7/5.75	Homo sapiens	18860873	5531	MAP-kinase activating death domain-containing protein isoform g
1	8.17	59.3	9	11/24	M1323m Y1322y S1321s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	176555.6/5.78	Homo sapiens	18860875	13216	MAP-kinase activating death domain-containing protein isoform a
1	8.17	59.3	9	11/24	M1280m Y1279y S1278s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	164038.7/5.93	Homo sapiens	18860870	16497	MAP-kinase activating death domain-containing protein isoform f
1	8.17	59.3	9	11/24	M1323m Y1322y S1321s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	176587.6/5.78	Homo sapiens	18860862	17928	MAP-kinase activating death domain-containing protein isoform a
1	8.17	59.3	9	11/24	M1343m Y1342y S1341s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	178590.9/5.70	Homo sapiens	18860868	21244	MAP-kinase activating death domain-containing protein isoform e
1	8.17	59.3	9	11/24	M1280m Y1279y S1278s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	171425.2/5.87	Homo sapiens	18860866	31537	MAP-kinase activating death domain-containing protein isoform c
1	8.17	59.3	9	11/24	M1382m Y1381y S1380s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	183336.3/5.72	Homo sapiens	18860877	36184	MAP-kinase activating death domain-containing protein isoform d
1	8.17	59.3	9	11/24	M1300m Y1299y S1298s	(R) L/L A/T L L H/N|L|I s y|m\L\L M\K (V)	1987.15	176.2372	143.1	173428.4/5.79	Homo sapiens	18860864	36912	MAP-kinase activating death domain-containing protein isoform b

Fragment-ion (m/z)	636.37	700.89	893.55	895.25	944.24	1007.79	1100.79	1157.80	1168.45	1272.24	1402.04	1407.67	1424.87	1444.16	1453.31	1529.54	1569.71	1633.30	1676.93	1745.32	1789.70	1849.94	2034.33	2037.07
Frac. Inten.(% of TIC)	3.59	0.07	6.03	4.05	2.90	4.38	5.54	4.91	2.65	8.90	2.67	2.87	3.54	5.32	2.72	3.79	2.61	3.17	6.43	4.24	2.57	4.92	6.96	5.17
Rel. Inten.(% of BP)	40.30	0.83	67.72	45.53	32.61	49.21	62.25	55.12	29.83	100.00	29.97	32.20	39.79	59.83	30.58	42.59	29.31	35.60	72.25	47.69	28.85	55.30	78.15	58.11
Score	1.00	2.00	1.00	1.00	-0.33	0.25	-0.62	1.00	-0.30	1.00	0.25	-0.32	-0.40	-0.60	-0.31	1.00	-0.29	-0.36	1.00	-0.48	1.00	1.00	1.00	-0.58
Ion-type	z''_{5}	$y{++}_{10}$	c_{8}	$c{++}_{14}$		c'_{9}		z'_{8}		z'_{9}	y_{10}					c_{12}			c_{13}		c_{14}	z'_{14}	c_{16}	
Delta Da	0.02	-0.41	-0.01	-0.19		0.14		-0.65		0.71	0.44					-0.21			0.14		-0.17	0.09	0.33	
	$z'{++}_{9}$	2.00		c'_{8}																			z'_{16}	
	0.10	m		0.69																			0.36	
		0.53																						

Peak 465





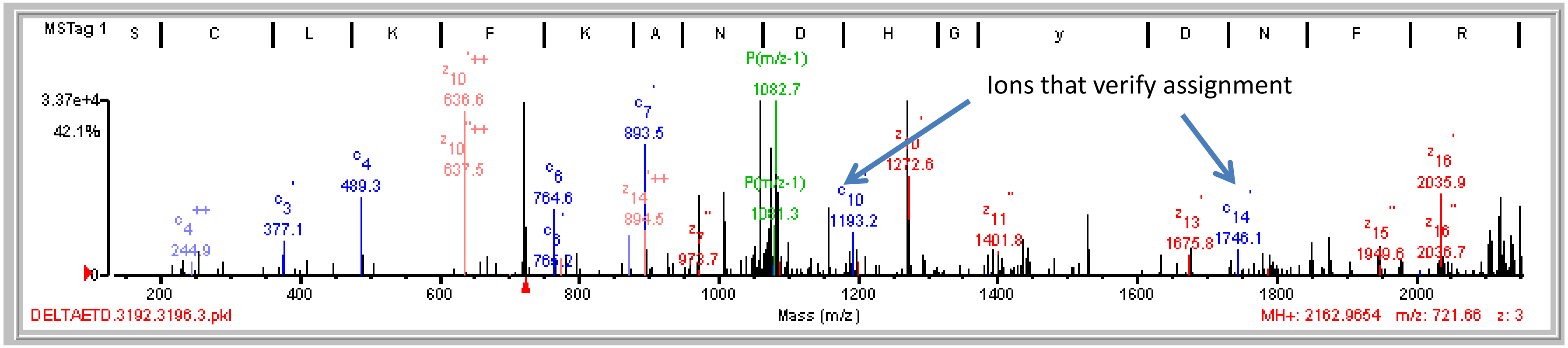


Detailed Results

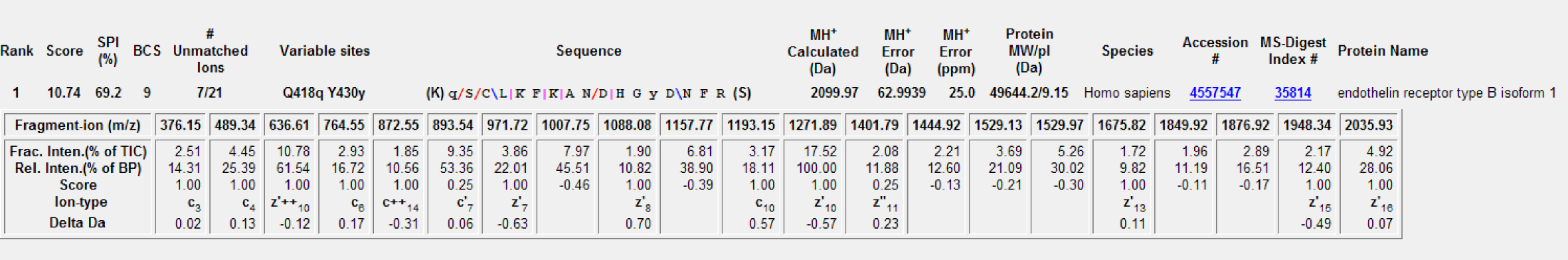
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.34	76.1	9	3/11	Y421y S432s	(R) N/N\S Y T S\y/T M A I/C G/M P\L\D/s F R (A)	2328.01	159.8488	-33.7	73700.1/6.65	Homo sapiens	31543630	35617	solute carrier family 20 (phosphate transporter), member 1

Fragment-ion (m/z)	228.75	245.96	473.54	894.64	951.16	1146.84	1179.41	1252.94	1419.68	1563.23	1742.91
Frac. Inten.(% of TIC)	7.50	13.00	11.24	7.59	7.44	8.21	6.78	7.12	9.86	14.39	6.88
Rel. Inten.(% of BP)	52.13	90.40	78.10	52.78	51.71	57.06	47.14	49.49	68.54	100.00	47.82
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	-0.49	-0.69	1.00	-0.48
Ion-type	$c3+_6$	c_2	$y{++}_7$ z'_3	$c{++}_{15}$	$c{++}_{16}$	z'_9	$z'{++}_{19}$			z'_{13}	
Delta Da	-0.02	-0.16	0.34 0.37	-0.20	-0.23	0.42	-0.03			0.60	

Peak 467



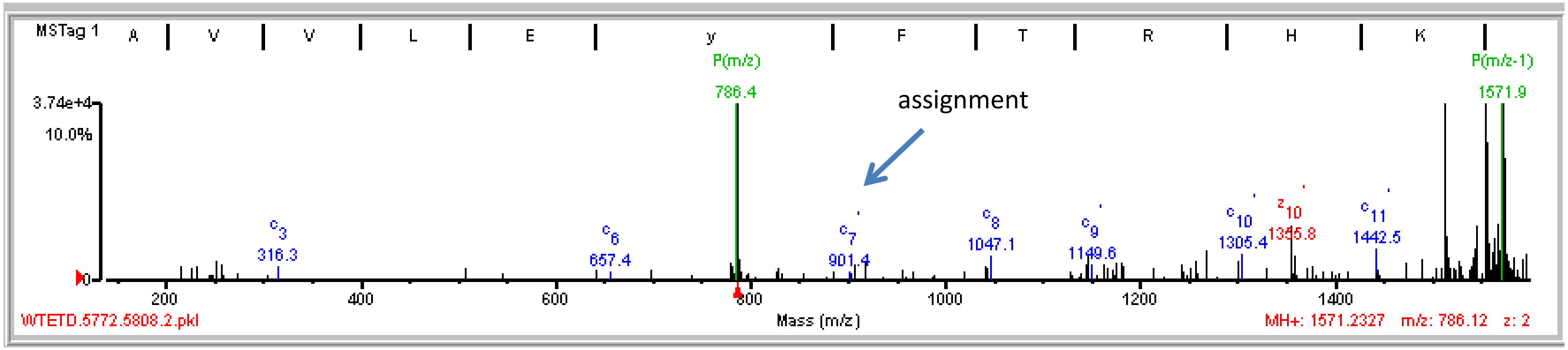
Ions that verify assignment



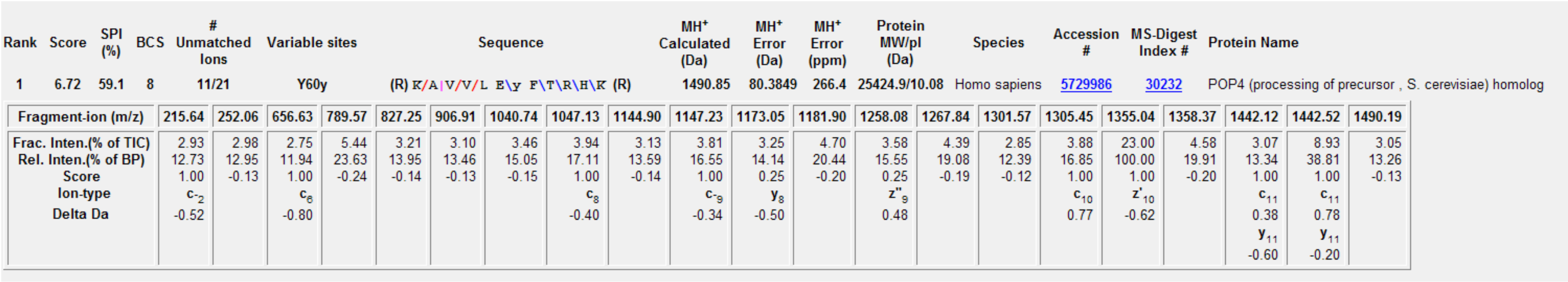
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.74	69.2	9	7/21	Q418q Y430y	(K) q/S/C\L|K F|K|A N/D|H G y D\N F R (S)	2099.97	62.9939	25.0	49644.2/9.15	Homo sapiens	4557547	35814	endothelin receptor type B isoform 1

Fragment-ion (m/z)	376.15	489.34	636.61	764.55	872.55	893.54	971.72	1007.75	1088.08	1157.77	1193.15	1271.89	1401.79	1444.92	1529.13	1529.97	1675.82	1849.92	1876.92	1948.34	2035.93
Frac. Inten.(% of TIC)	2.51	4.45	10.78	2.93	1.85	9.35	3.86	7.97	1.90	6.81	3.17	17.52	2.08	2.21	3.69	5.26	1.72	1.96	2.89	2.17	4.92
Rel. Inten.(% of BP)	14.31	25.39	61.54	16.72	10.56	53.36	22.01	45.51	10.82	38.90	18.11	100.00	11.88	12.60	21.09	30.02	9.82	11.19	16.51	12.40	28.06
Score	1.00	1.00	1.00	1.00	1.00	0.25	1.00	-0.46	1.00	-0.39	1.00	1.00	0.25	-0.13	-0.21	-0.30	1.00	-0.11	-0.17	1.00	1.00
Ion-type	c_3	c_4	z'^{++}_{10}	c_6	c^{++}_{14}	c'_7	z'_7		z'_8		c_{10}	z'_{10}	z''_{11}				z'_{13}			z'_{15}	z'_{16}
Delta Da	0.02	0.13	-0.12	0.17	-0.31	0.06	-0.63		0.70		0.57	-0.57	0.23				0.11			-0.49	0.07

Peak 469



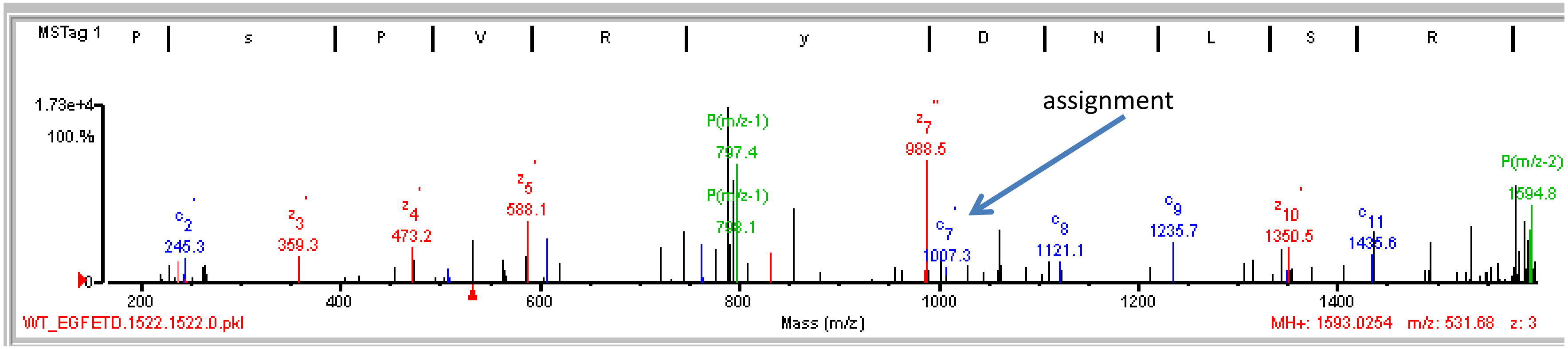
assignment



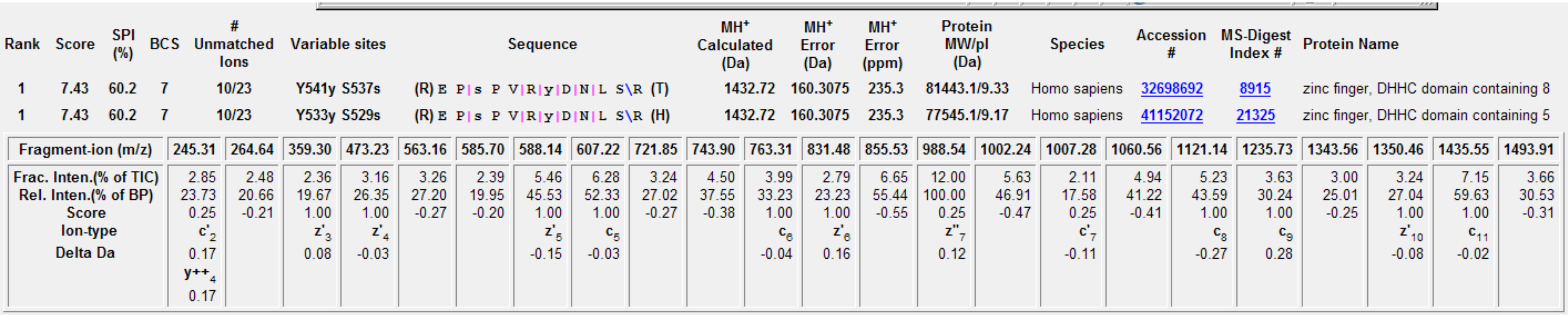
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.72	59.1	8	11/21	Y60y	(R) K/A|V/V/L E\y F\T\R\H\K (R)	1490.85	80.3849	266.4	25424.9/10.08	Homo sapiens	5729986	30232	POP4 (processing of precursor , S. cerevisiae) homolog

Fragment-ion (m/z)	215.64	252.06	656.63	789.57	827.25	906.91	1040.74	1047.13	1144.90	1147.23	1173.05	1181.90	1258.08	1267.84	1301.57	1305.45	1355.04	1358.37	1442.12	1442.52	1490.19
Frac. Inten.(% of TIC)	2.93	2.98	2.75	5.44	3.21	3.10	3.46	3.94	3.13	3.81	3.25	4.70	3.58	4.39	2.85	3.88	23.00	4.58	3.07	8.93	3.05
Rel. Inten.(% of BP)	12.73	12.95	11.94	23.63	13.95	13.46	15.05	17.11	13.59	16.55	14.14	20.44	15.55	19.08	12.39	16.85	100.00	19.91	13.34	38.81	13.26
Score	1.00	-0.13	1.00	-0.24	-0.14	-0.13	-0.15	1.00	-0.14	1.00	0.25	-0.20	0.25	-0.19	-0.12	1.00	1.00	-0.20	1.00	1.00	-0.13
Ion-type	$c\text{-}_2$		c_6					c_8		$c\text{-}_9$	y_8		z''_9			c_{10}	z'_{10}		c_{11}	c_{11}	
Delta Da	-0.52		-0.80					-0.40		-0.34	-0.50		0.48			0.77	-0.62		0.38	0.78	
																			y_{11}	y_{11}	
																			-0.60	-0.20	

Peak 471



assignment

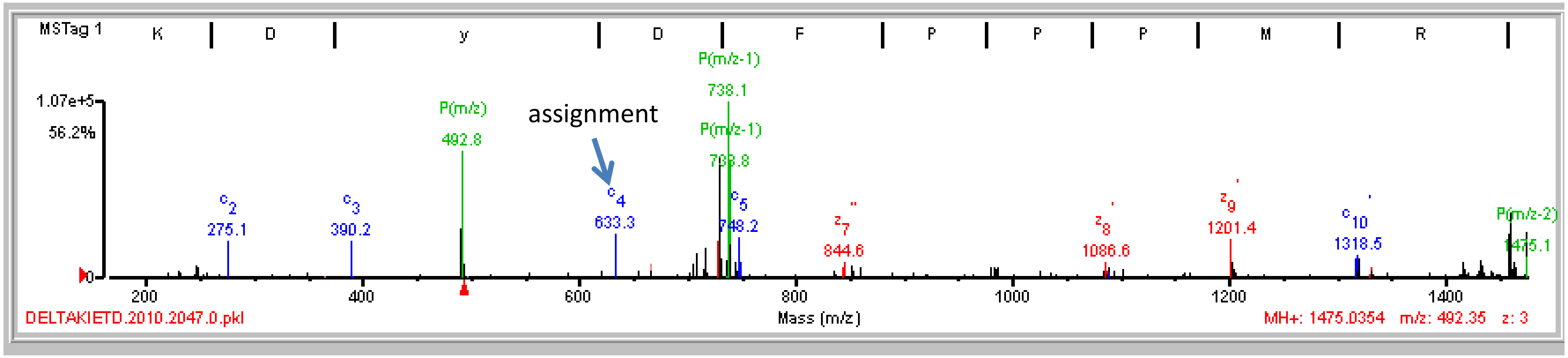


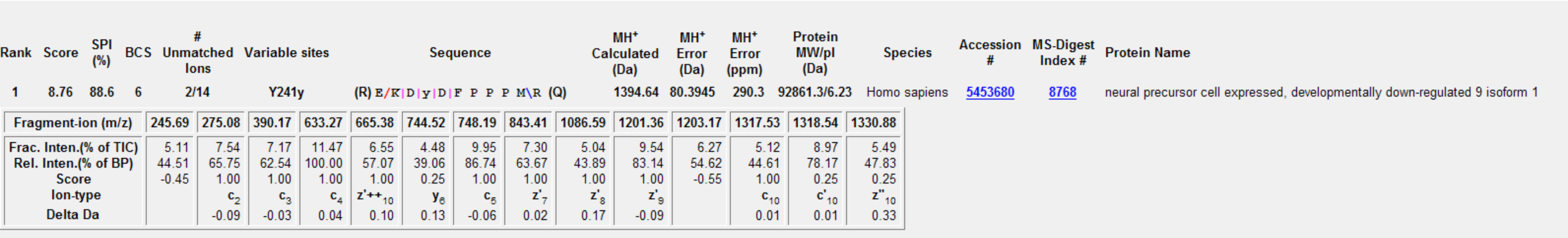
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	7.43	60.2	7	10/23	Y541y S537s	(R) E P|s P V|R|y|D|N|L S\R (T)	1432.72	160.3075	235.3	81443.1/9.33	Homo sapiens	32698692	8915	zinc finger, DHHC domain containing 8
1	7.43	60.2	7	10/23	Y533y S529s	(R) E P|s P V|R|y|D|N|L S\R (H)	1432.72	160.3075	235.3	77545.1/9.17	Homo sapiens	41152072	21325	zinc finger, DHHC domain containing 5

Fragment-ion (m/z)	245.31	264.64	359.30	473.23	563.16	585.70	588.14	607.22	721.85	743.90	763.31	831.48
Frac. Inten.(% of TIC)	2.85	2.48	2.36	3.16	3.26	2.39	5.46	6.28	3.24	4.50	3.99	2.79
Rel. Inten.(% of BP)	23.73	20.66	19.67	26.35	27.20	19.95	45.53	52.33	27.02	37.55	33.23	23.23
Score	0.25	-0.21	1.00	1.00	-0.27	-0.20	1.00	1.00	-0.27	-0.38	1.00	1.00
Ion-type	c'_2 y^{++}_4		z'_3	z'_4			z'_5	c_5			c_6	z'_6
Delta Da	0.17 0.17		0.08	-0.03			-0.15	-0.03			-0.04	0.16

Fragment-ion (m/z)	855.53	988.54	1002.24	1007.28	1060.56	1121.14	1235.73	1343.56	1350.46	1435.55	1493.91
Frac. Inten.(% of TIC)	6.65	12.00	5.63	2.11	4.94	5.23	3.63	3.00	3.24	7.15	3.66
Rel. Inten.(% of BP)	55.44	100.00	46.91	17.58	41.22	43.59	30.24	25.01	27.04	59.63	30.53
Score	-0.55	0.25	-0.47	0.25	-0.41	1.00	1.00	-0.25	1.00	1.00	-0.31
Ion-type		z''_7		c'_7		c_8	c_9		z'_{10}	c_{11}	
Delta Da		0.12		-0.11		-0.27	0.28		-0.08	-0.02	

Peak 473

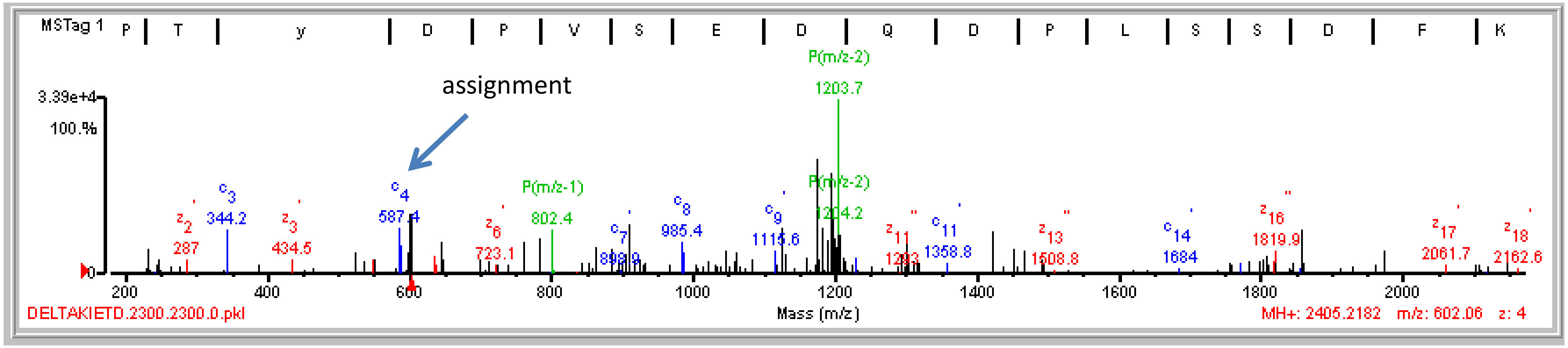




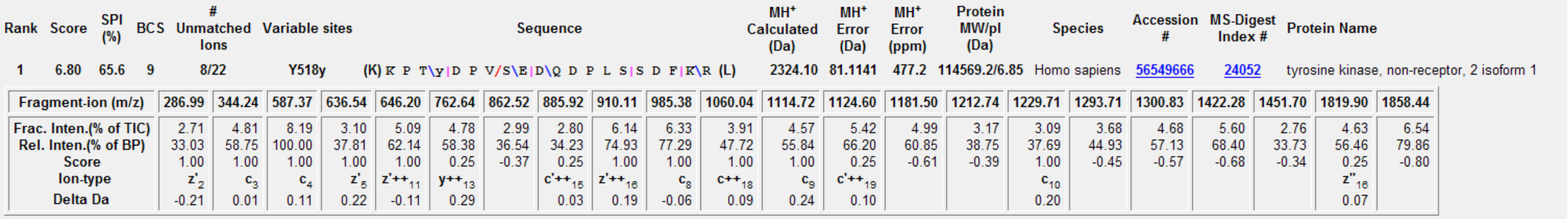
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.76	88.6	6	2/14	Y241y	(R) E/K|D|y|D|F P P P M\R (Q)	1394.64	80.3945	290.3	92861.3/6.23	Homo sapiens	5453680	8768	neural precursor cell expressed, developmentally down-regulated 9 isoform 1

Fragment-ion (m/z)	245.69	275.08	390.17	633.27	665.38	744.52	748.19	843.41	1086.59	1201.36	1203.17	1317.53	1318.54	1330.88
Frac. Inten.(% of TIC)	5.11	7.54	7.17	11.47	6.55	4.48	9.95	7.30	5.04	9.54	6.27	5.12	8.97	5.49
Rel. Inten.(% of BP)	44.51	65.75	62.54	100.00	57.07	39.06	86.74	63.67	43.89	83.14	54.62	44.61	78.17	47.83
Score	-0.45	1.00	1.00	1.00	1.00	0.25	1.00	1.00	1.00	1.00	-0.55	1.00	0.25	0.25
Ion-type		c_2	c_3	c_4	z'^{++}_{10}	y_6	c_5	z'_7	z'_8	z'_9		c_{10}	c'_{10}	z''_{10}
Delta Da		-0.09	-0.03	0.04	0.10	0.13	-0.06	0.02	0.17	-0.09		0.01	0.01	0.33

Peak 474



assignment

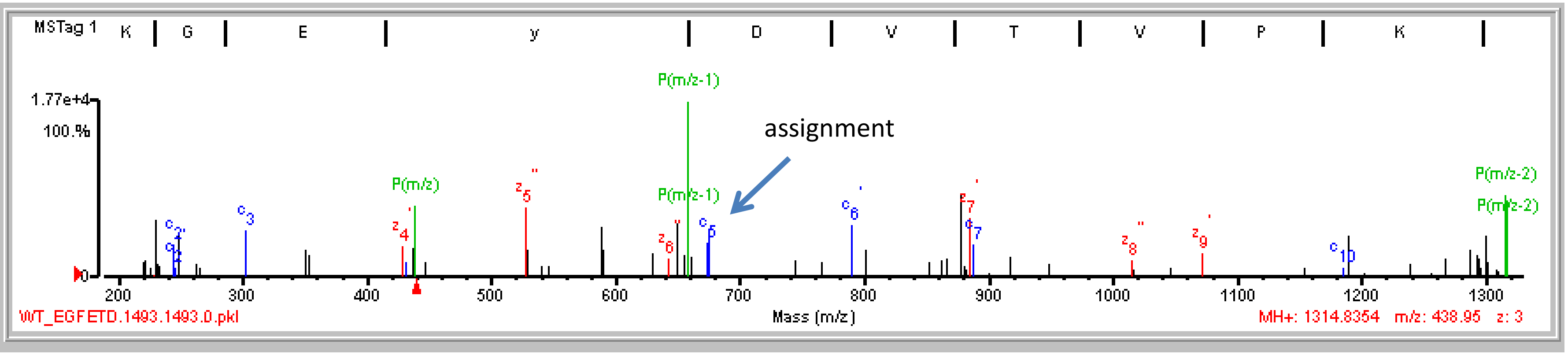


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.80	65.6	9	8/22	Y518y	(K) K P T\y|D P V/S\E|D\Q D P L S|S D F|K\R (L)	2324.10	81.1141	477.2	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1

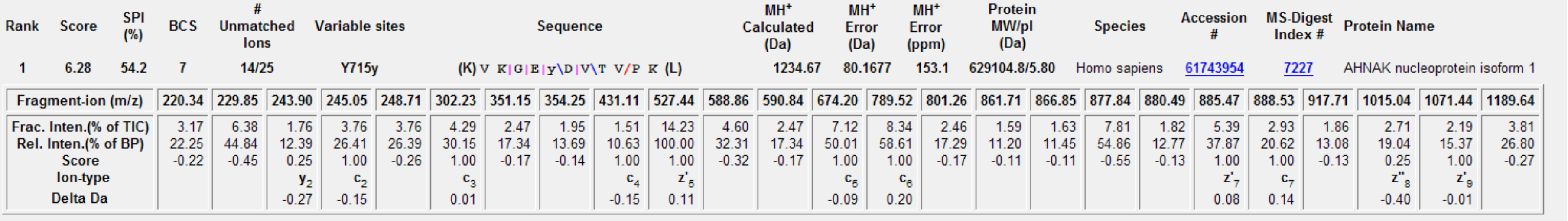
Fragment-ion (m/z)	286.99	344.24	587.37	636.54	646.20	762.64	862.52	885.92	910.11	985.38	1060.04
Frac. Inten.(% of TIC)	2.71	4.81	8.19	3.10	5.09	4.78	2.99	2.80	6.14	6.33	3.91
Rel. Inten.(% of BP)	33.03	58.75	100.00	37.81	62.14	58.38	36.54	34.23	74.93	77.29	47.72
Score	1.00	1.00	1.00	1.00	1.00	0.25	-0.37	0.25	1.00	1.00	1.00
Ion-type	z'_2	c_3	c_4	z'_5	$z'{++}_{11}$	$y{++}_{13}$		$c'{++}_{15}$	$z'{++}_{16}$	c_8	$c{++}_{18}$
Delta Da	-0.21	0.01	0.11	0.22	-0.11	0.29		0.03	0.19	-0.06	0.09

Fragment-ion (m/z)	1114.72	1124.60	1181.50	1212.74	1229.71	1293.71	1300.83	1422.28	1451.70	1819.90	1858.44
Frac. Inten.(% of TIC)	4.57	5.42	4.99	3.17	3.09	3.68	4.68	5.60	2.76	4.63	6.54
Rel. Inten.(% of BP)	55.84	66.20	60.85	38.75	37.69	44.93	57.13	68.40	33.73	56.46	79.86
Score	1.00	0.25	-0.61	-0.39	1.00	-0.45	-0.57	-0.68	-0.34	0.25	-0.80
Ion-type	c_9	$c'{++}_{19}$			c_{10}					z''_{16}	
Delta Da	0.24	0.10			0.20					0.07	

Peak 475



assignment

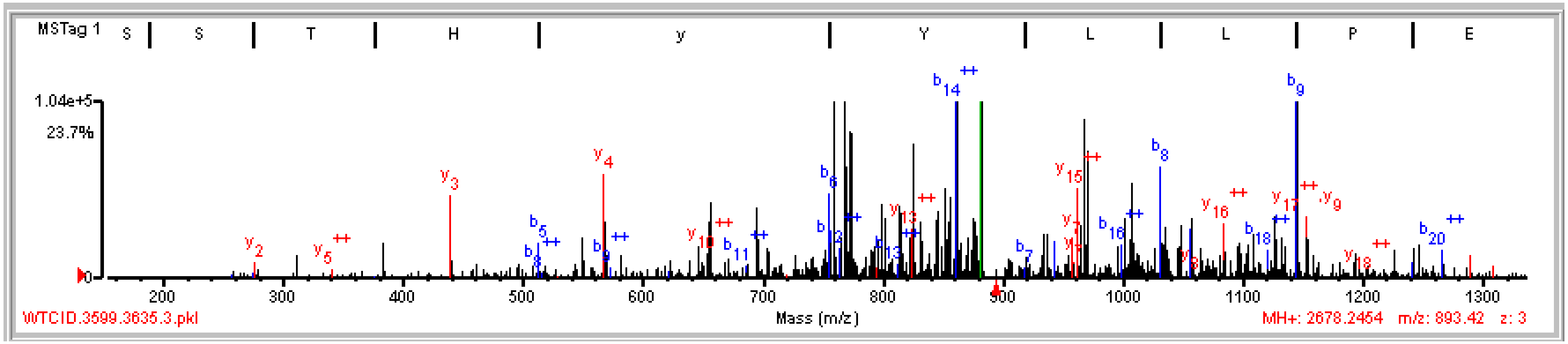


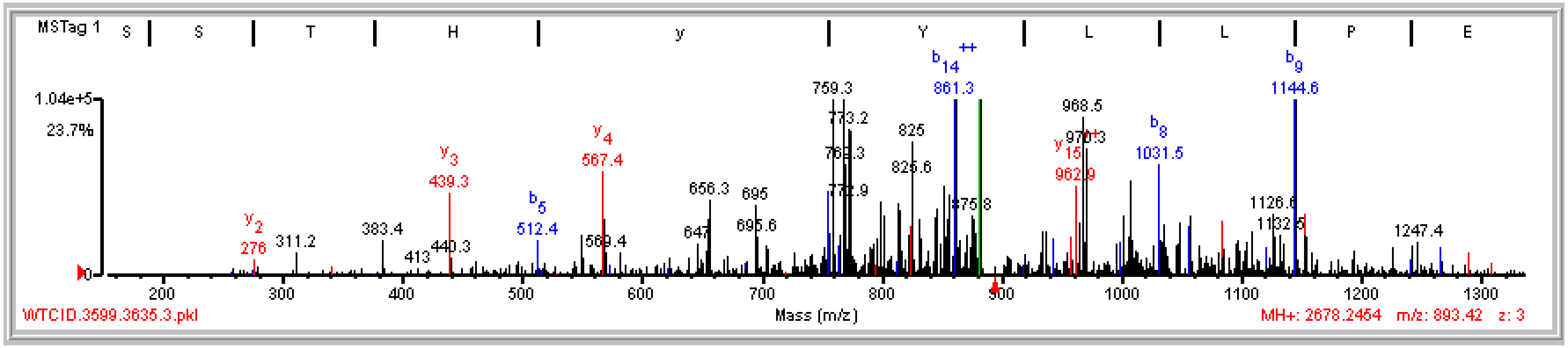
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.28	54.2	7	14/25	Y715y	(K) V K|G|E|y\D|V\T V/P K (L)	1234.67	80.1677	153.1	629104.8/5.80	Homo sapiens	61743954	7227	AHNAK nucleoprotein isoform 1

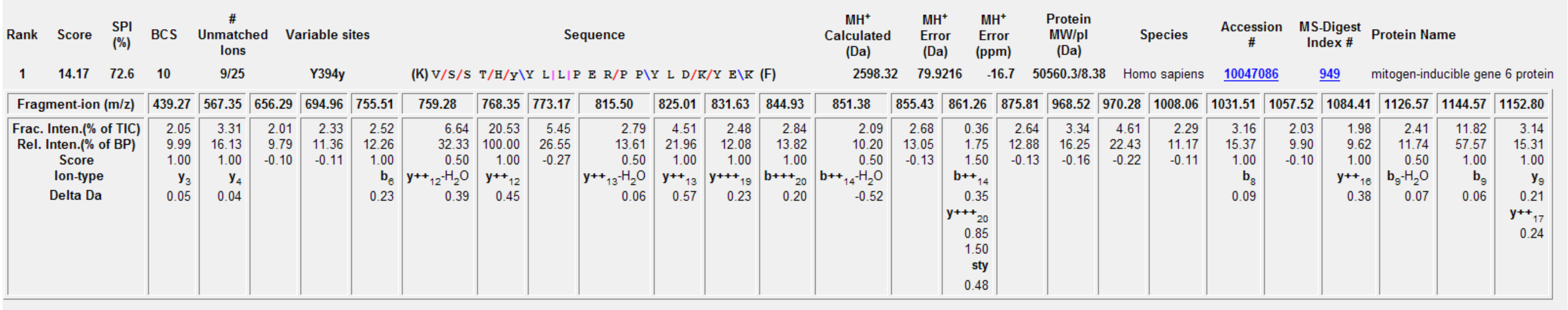
Fragment-ion (m/z)	220.34	229.85	243.90	245.05	248.71	302.23	351.15	354.25	431.11	527.44	588.86	590.84
Frac. Inten.(% of TIC)	3.17	6.38	1.76	3.76	3.76	4.29	2.47	1.95	1.51	14.23	4.60	2.47
Rel. Inten.(% of BP)	22.25	44.84	12.39	26.41	26.39	30.15	17.34	13.69	10.63	100.00	32.31	17.34
Score	-0.22	-0.45	0.25	1.00	-0.26	1.00	-0.17	-0.14	1.00	1.00	-0.32	-0.17
Ion-type			y_2	c_2		c_3			c_4	z'_5		
Delta Da			-0.27	-0.15		0.01			-0.15	0.11		

Fragment-ion (m/z)	674.20	789.52	801.26	861.71	866.85	877.84	880.49	885.47	888.53	917.71	1015.04	1071.44	1189.64
Frac. Inten.(% of TIC)	7.12	8.34	2.46	1.59	1.63	7.81	1.82	5.39	2.93	1.86	2.71	2.19	3.81
Rel. Inten.(% of BP)	50.01	58.61	17.29	11.20	11.45	54.86	12.77	37.87	20.62	13.08	19.04	15.37	26.80
Score	1.00	1.00	-0.17	-0.11	-0.11	-0.55	-0.13	1.00	1.00	-0.13	0.25	1.00	-0.27
Ion-type	c_5	c_6						z'_7	c_7		z''_8	z'_9	
Delta Da	-0.09	0.20						0.08	0.14		-0.40	-0.01	

Peak 476



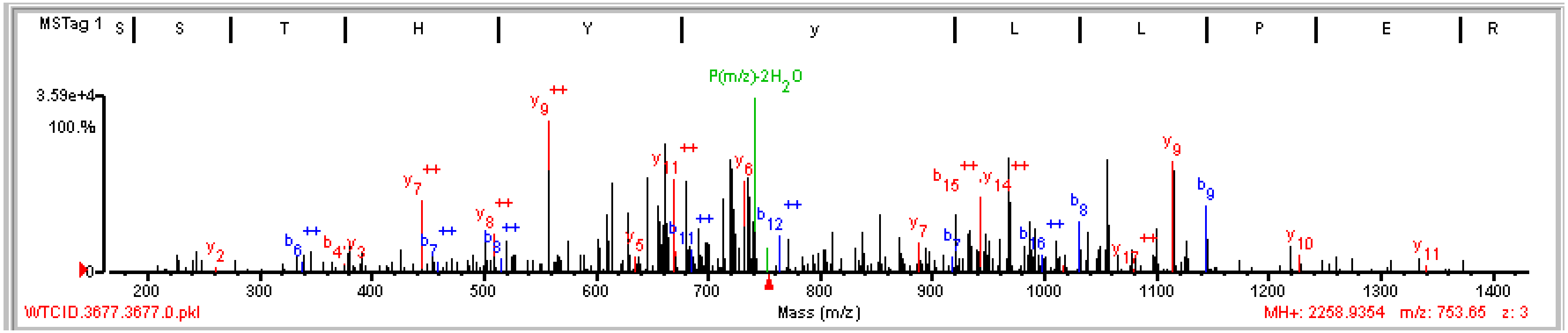


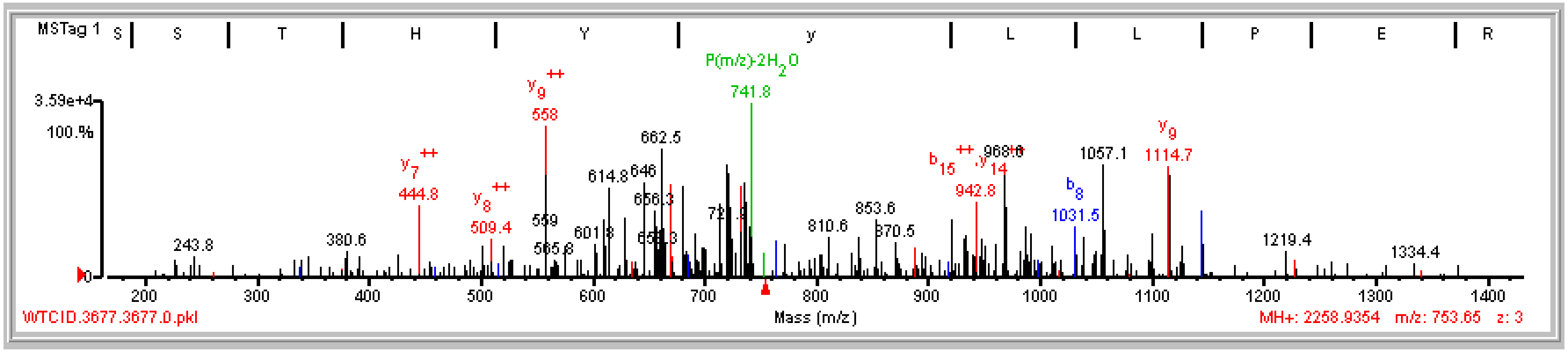


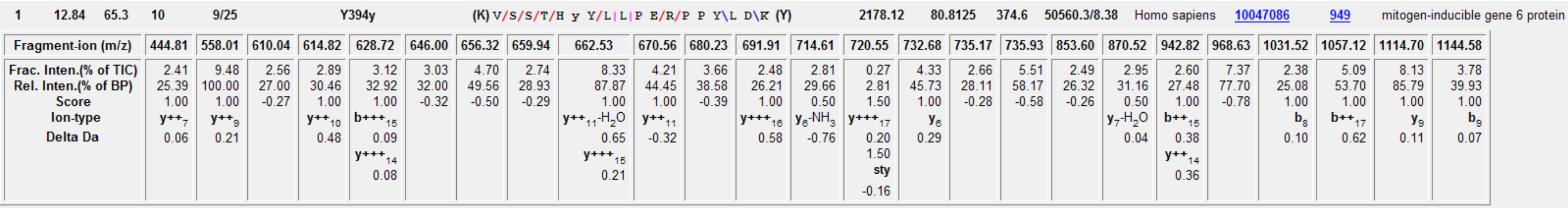
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.17	72.6	10	9/25	Y394y	(K) V/S/S T/H/y\Y L|L|P E R/P P\Y L D/K/Y E\K (F)	2598.32	79.9216	-16.7	50560.3/8.38	Homo sapiens	10047086	949	mitogen-inducible gene 6 protein

Fragment-ion (m/z)	439.27	567.35	656.29	694.96	755.51	759.28	768.35	773.17	815.50	825.01	831.63	844.93	851.38	855.43	861.26	875.81	968.52	970.28	1008.06	1031.51	1057.52	1084.41	1126.57	1144.57	1152.80
Frac. Inten.(% of TIC)	2.05	3.31	2.01	2.33	2.52	6.64	20.53	5.45	2.79	4.51	2.48	2.84	2.09	2.68	0.36	2.64	3.34	4.61	2.29	3.16	2.03	1.98	2.41	11.82	3.14
Rel. Inten.(% of BP)	9.99	16.13	9.79	11.36	12.26	32.33	100.00	26.55	13.61	21.96	12.08	13.82	10.20	13.05	1.75	12.88	16.25	22.43	11.17	15.37	9.90	9.62	11.74	57.57	15.31
Score	1.00	1.00	-0.10	-0.11	1.00	0.50	1.00	-0.27	0.50	1.00	1.00	1.00	0.50	-0.13	1.50	-0.13	-0.16	-0.22	-0.11	1.00	-0.10	1.00	0.50	1.00	1.00
Ion-type	y_3	y_4			b_6	$y{+}{+}_{12}$-H_2O	$y{+}{+}_{12}$		$y{+}{+}_{13}$-H_2O	$y{+}{+}_{13}$	$y{+}{+}{+}_{19}$	$b{+}{+}{+}_{20}$	$b{+}{+}_{14}$-H_2O		$b{+}{+}_{14}$					b_8		$y{+}{+}_{16}$	b_9-H_2O	b_9	y_9
Delta Da	0.05	0.04			0.23	0.39	0.45		0.06	0.57	0.23	0.20	-0.52		0.35					0.09		0.38	0.07	0.06	0.21
															$y{+}{+}{+}_{20}$ 0.85 1.50 sty 0.48										$y{+}{+}_{17}$ 0.24

Peak 477





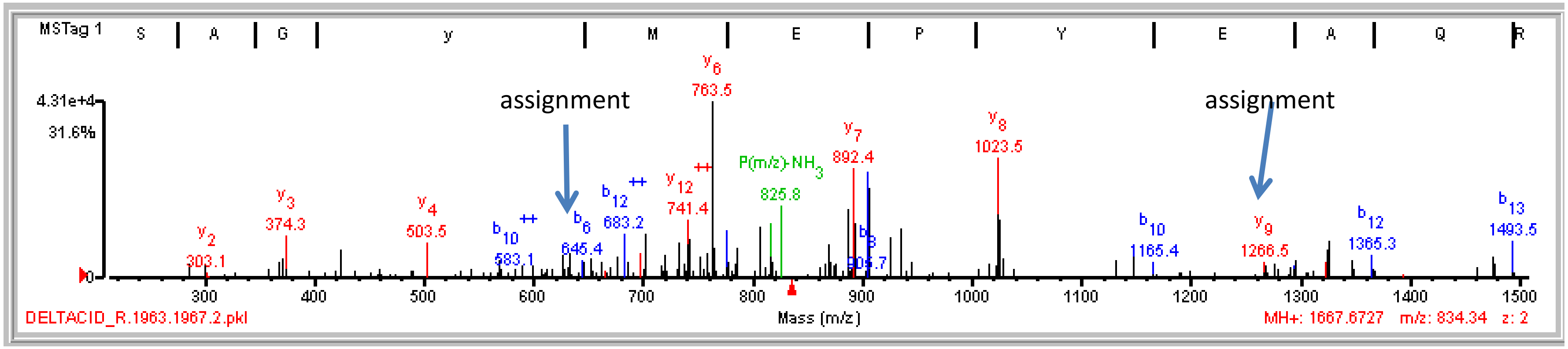


1 12.84 65.3 10 9/25 Y394y (K) V/S/S/T/H y Y/L|L|P E/R/P P Y\L D\K (Y) 2178.12 80.8125 374.6 50560.3/8.38 Homo sapiens 10047086 949 mitogen-inducible gene 6 protein

Fragment-ion (m/z)	444.81	558.01	610.04	614.82	628.72	646.00	656.32	659.94	662.53	670.56	680.23	691.91	714.61
Frac. Inten.(% of TIC)	2.41	9.48	2.56	2.89	3.12	3.03	4.70	2.74	8.33	4.21	3.66	2.48	2.81
Rel. Inten.(% of BP)	25.39	100.00	27.00	30.46	32.92	32.00	49.56	28.93	87.87	44.45	38.58	26.21	29.66
Score	1.00	1.00	-0.27	1.00	1.00	-0.32	-0.50	-0.29	1.00	1.00	-0.39	1.00	0.50
Ion-type	$y{++}_7$	$y{++}_9$		$y{++}_{10}$	$b{+++}_{15}$ $y{+++}_{14}$				$y{++}_{11}$-H_2O $y{+++}_{15}$	$y{++}_{11}$		$y{+++}_{16}$	y_6-NH_3
Delta Da	0.06	0.21		0.48	0.09 0.08				0.65 0.21	-0.32		0.58	-0.76

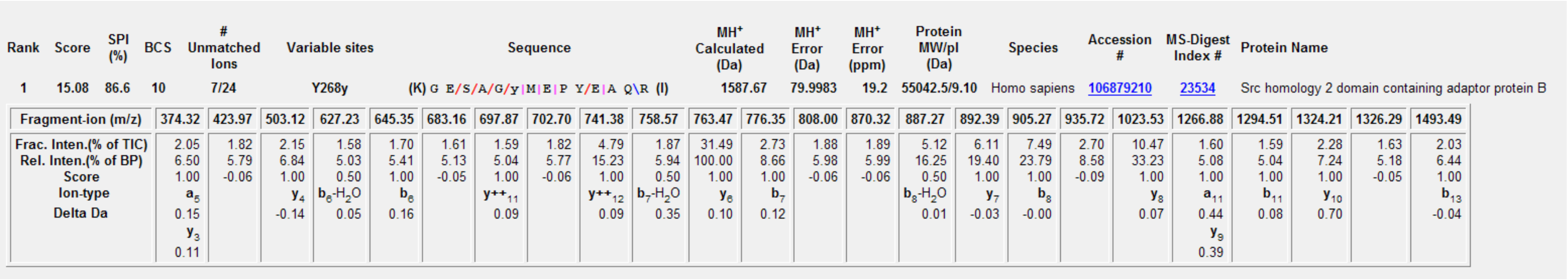
Fragment-ion (m/z)	720.55	732.68	735.17	735.93	853.60	870.52	942.82	968.63	1031.52	1057.12	1114.70	1144.58
Frac. Inten.(% of TIC)	0.27	4.33	2.66	5.51	2.49	2.95	2.60	7.37	2.38	5.09	8.13	3.78
Rel. Inten.(% of BP)	2.81	45.73	28.11	58.17	26.32	31.16	27.48	77.70	25.08	53.70	85.79	39.93
Score	1.50	1.00	-0.28	-0.58	-0.26	0.50	1.00	-0.78	1.00	1.00	1.00	1.00
Ion-type	$y{+++}_{17}$	y_6				y_7-H_2O	$b{++}_{15}$ $y{++}_{14}$		b_8	$b{++}_{17}$	y_9	b_9
Delta Da	0.20 1.50 sty -0.16	0.29				0.04	0.38 0.36		0.10	0.62	0.11	0.07

Peak 478



assignment

assignment

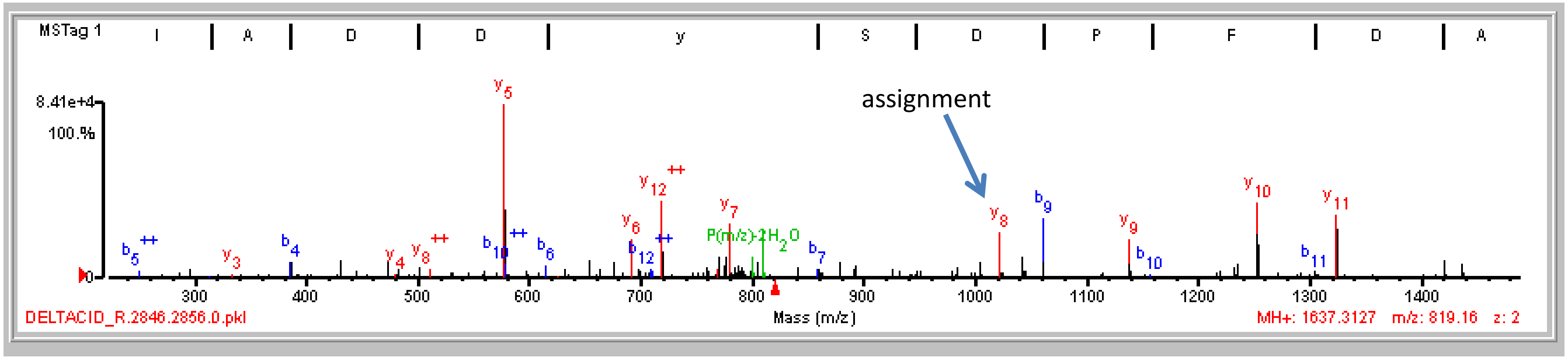


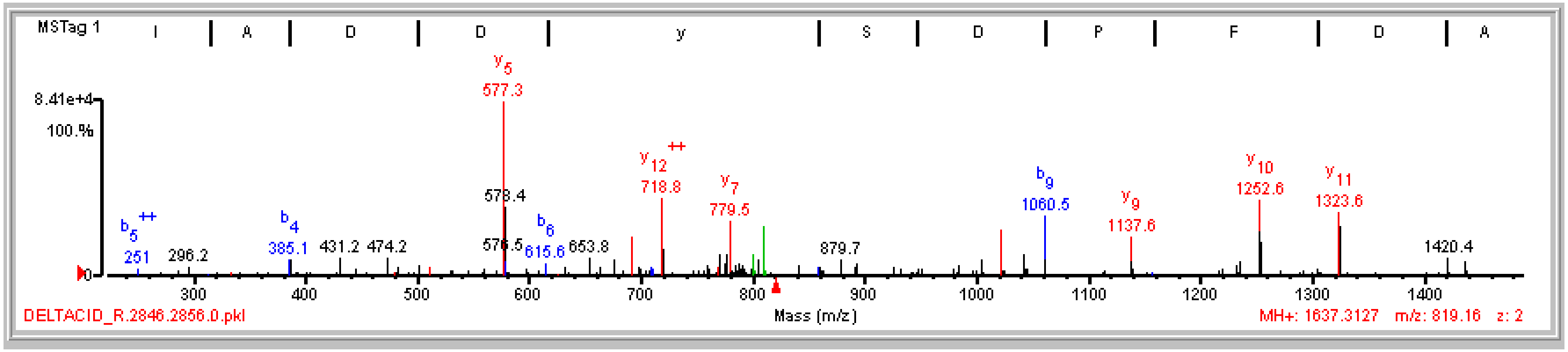
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	15.08	86.6	10	7/24	Y268y	(K) G E/S/A/G/y|M|E|P Y/E|A Q\R (I)	1587.67	79.9983	19.2	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

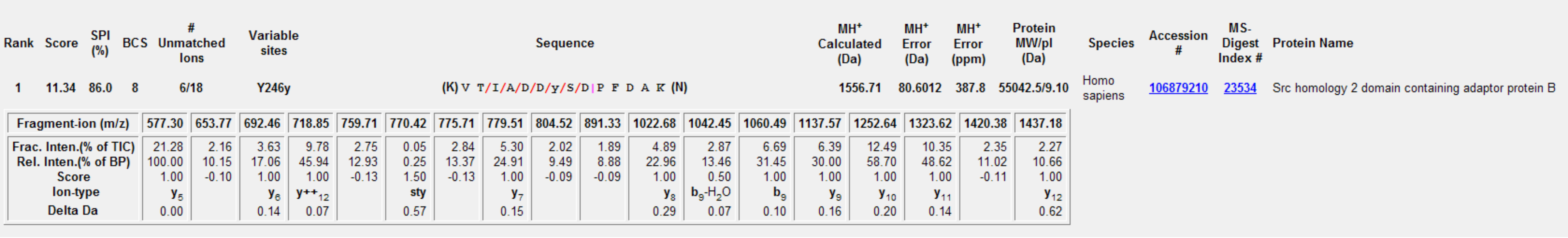
Fragment-ion (m/z)	374.32	423.97	503.12	627.23	645.35	683.16	697.87	702.70	741.38	758.57	763.47	776.35
Frac. Inten.(% of TIC)	2.05	1.82	2.15	1.58	1.70	1.61	1.59	1.82	4.79	1.87	31.49	2.73
Rel. Inten.(% of BP)	6.50	5.79	6.84	5.03	5.41	5.13	5.04	5.77	15.23	5.94	100.00	8.66
Score	1.00	-0.06	1.00	0.50	1.00	-0.05	1.00	-0.06	1.00	0.50	1.00	1.00
Ion-type	a_5		y_4	b_6-H_2O	b_6		$y{++}_{11}$		$y{++}_{12}$	b_7-H_2O	y_6	b_7
Delta Da	0.15		-0.14	0.05	0.16		0.09		0.09	0.35	0.10	0.12
	y_3											
	0.11											

Fragment-ion (m/z)	808.00	870.32	887.27	892.39	905.27	935.72	1023.53	1266.88	1294.51	1324.21	1326.29	1493.49
Frac. Inten.(% of TIC)	1.88	1.89	5.12	6.11	7.49	2.70	10.47	1.60	1.59	2.28	1.63	2.03
Rel. Inten.(% of BP)	5.98	5.99	16.25	19.40	23.79	8.58	33.23	5.08	5.04	7.24	5.18	6.44
Score	-0.06	-0.06	0.50	1.00	1.00	-0.09	1.00	1.00	1.00	1.00	-0.05	1.00
Ion-type			b_8-H_2O	y_7	b_8		y_8	a_{11}	b_{11}	y_{10}		b_{13}
Delta Da			0.01	-0.03	-0.00		0.07	0.44	0.08	0.70		-0.04
								y_9				
								0.39				

Peak 479



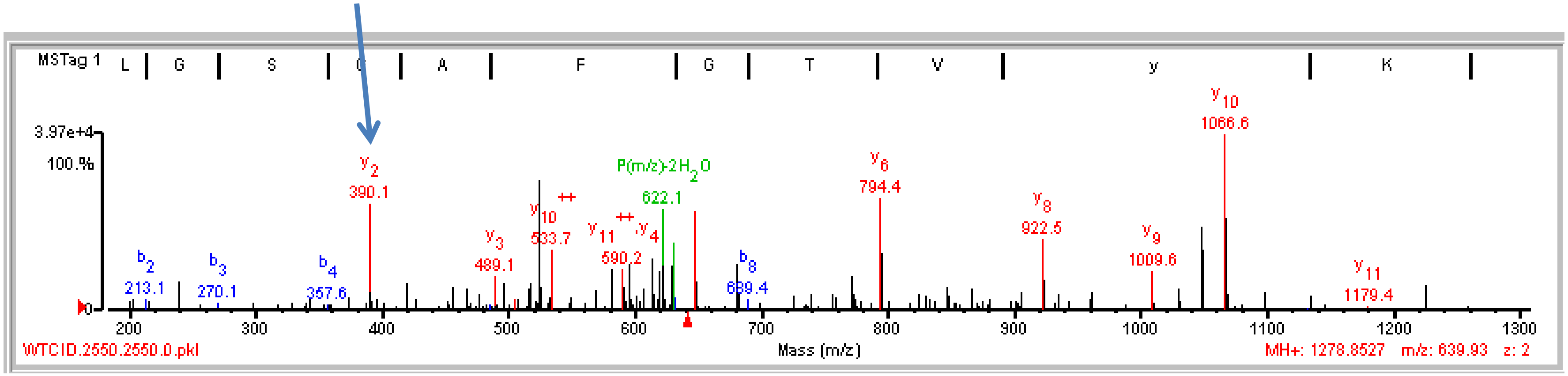


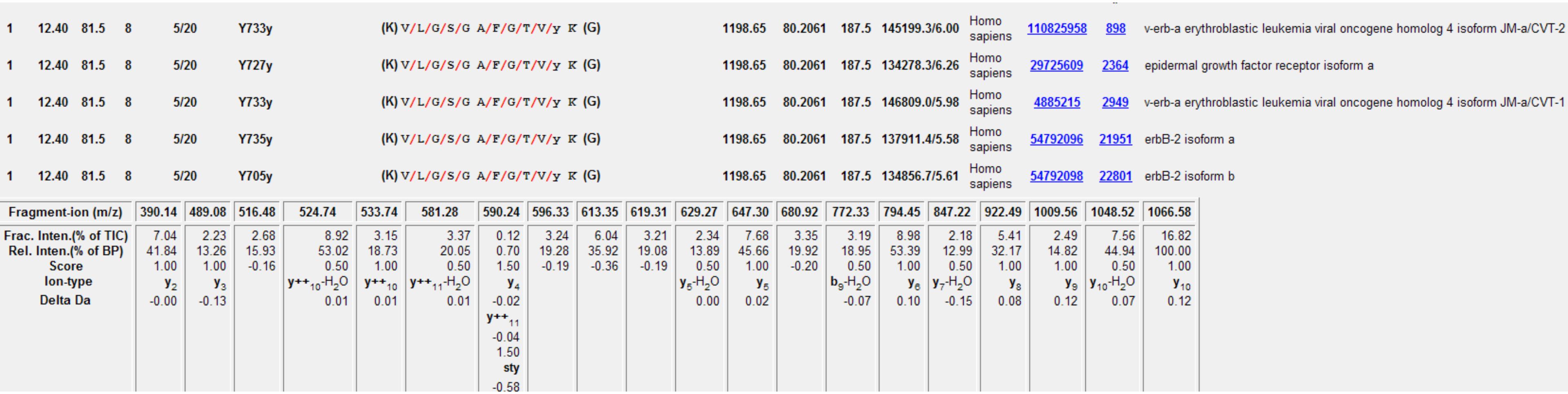


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.34	86.0	8	6/18	Y246y	(K) V T/I/A/D/D/y/S/D|P F D A K (N)	1556.71	80.6012	387.8	55042.5/9.10	Homo sapiens	106879210	23534	Src homology 2 domain containing adaptor protein B

Fragment-ion (m/z)	577.30	653.77	692.46	718.85	759.71	770.42	775.71	779.51	804.52	891.33	1022.68	1042.45	1060.49	1137.57	1252.64	1323.62	1420.38	1437.18
Frac. Inten.(% of TIC)	21.28	2.16	3.63	9.78	2.75	0.05	2.84	5.30	2.02	1.89	4.89	2.87	6.69	6.39	12.49	10.35	2.35	2.27
Rel. Inten.(% of BP)	100.00	10.15	17.06	45.94	12.93	0.25	13.37	24.91	9.49	8.88	22.96	13.46	31.45	30.00	58.70	48.62	11.02	10.66
Score	1.00	-0.10	1.00	1.00	-0.13	1.50	-0.13	1.00	-0.09	-0.09	1.00	0.50	1.00	1.00	1.00	1.00	-0.11	1.00
Ion-type	y_5		y_6	y^{++}_{12}		sty		y_7			y_8	b_9-H_2O	b_9	y_9	y_{10}	y_{11}		y_{12}
Delta Da	0.00		0.14	0.07		0.57		0.15			0.29	0.07	0.10	0.16	0.20	0.14		0.62

Peak 480

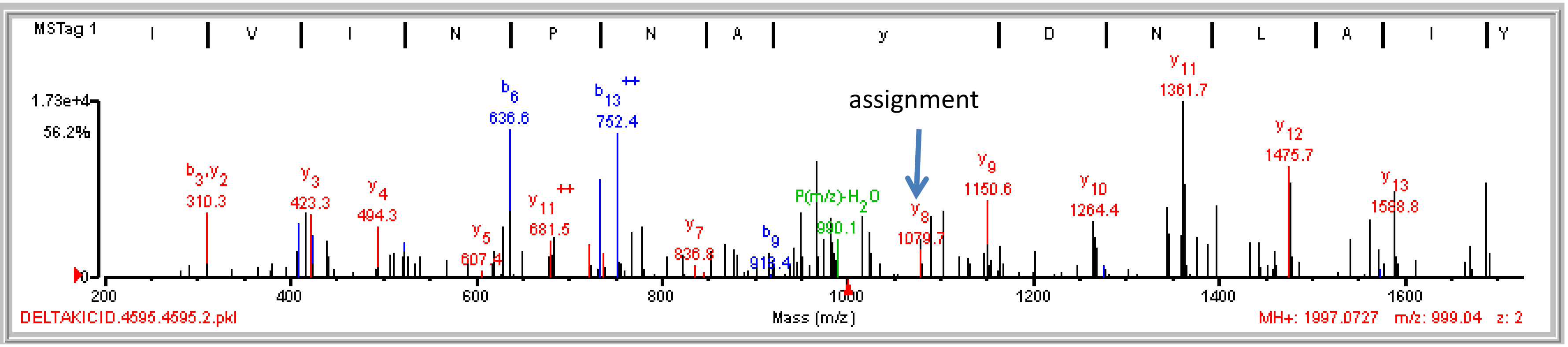

assignment



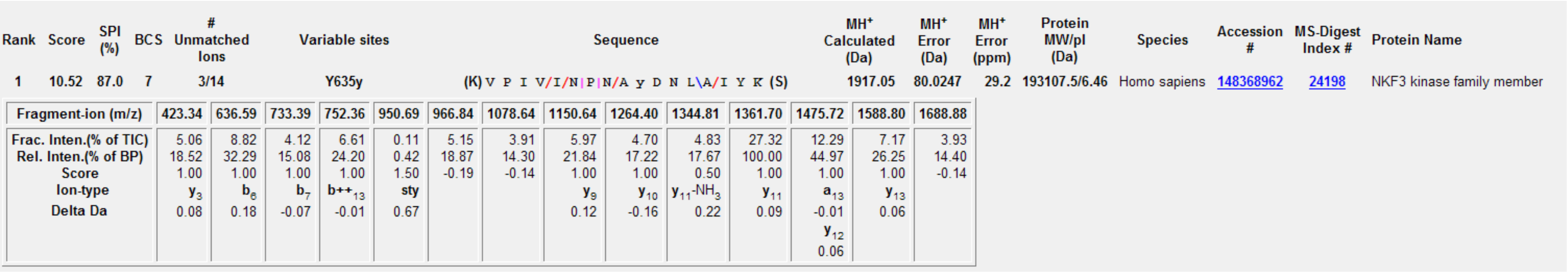
1	12.40	81.5	8	5/20	Y733y	(K) V/L/G/S/G A/F/G/T/V/y K (G)	1198.65	80.2061	187.5	145199.3/6.00	Homo sapiens	110825958	898	v-erb-a erythroblastic leukemia viral oncogene homolog 4 isoform JM-a/CVT-2
1	12.40	81.5	8	5/20	Y727y	(K) V/L/G/S/G A/F/G/T/V/y K (G)	1198.65	80.2061	187.5	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a
1	12.40	81.5	8	5/20	Y733y	(K) V/L/G/S/G A/F/G/T/V/y K (G)	1198.65	80.2061	187.5	146809.0/5.98	Homo sapiens	4885215	2949	v-erb-a erythroblastic leukemia viral oncogene homolog 4 isoform JM-a/CVT-1
1	12.40	81.5	8	5/20	Y735y	(K) V/L/G/S/G A/F/G/T/V/y K (G)	1198.65	80.2061	187.5	137911.4/5.58	Homo sapiens	54792096	21951	erbB-2 isoform a
1	12.40	81.5	8	5/20	Y705y	(K) V/L/G/S/G A/F/G/T/V/y K (G)	1198.65	80.2061	187.5	134856.7/5.61	Homo sapiens	54792098	22801	erbB-2 isoform b

Fragment-ion (m/z)	390.14	489.08	516.48	524.74	533.74	581.28	590.24	596.33	613.35	619.31	629.27	647.30	680.92	772.33	794.45	847.22	922.49	1009.56	1048.52	1066.58
Frac. Inten.(% of TIC)	7.04	2.23	2.68	8.92	3.15	3.37	0.12	3.24	6.04	3.21	2.34	7.68	3.35	3.19	8.98	2.18	5.41	2.49	7.56	16.82
Rel. Inten.(% of BP)	41.84	13.26	15.93	53.02	18.73	20.05	0.70	19.28	35.92	19.08	13.89	45.66	19.92	18.95	53.39	12.99	32.17	14.82	44.94	100.00
Score	1.00	1.00	-0.16	0.50	1.00	0.50	1.50	-0.19	-0.36	-0.19	0.50	1.00	-0.20	0.50	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	y_2	y_3		$y{++}_{10}$-H_2O	$y{++}_{10}$	$y{++}_{11}$-H_2O	y_4				y_5-H_2O	y_5		b_9-H_2O	y_6	y_7-H_2O	y_8	y_9	y_{10}-H_2O	y_{10}
Delta Da	-0.00	-0.13		0.01	0.01	0.01	-0.02 $y{++}_{11}$ -0.04 1.50 sty -0.58				0.00	0.02		-0.07	0.10	-0.15	0.08	0.12	0.07	0.12

Peak 481



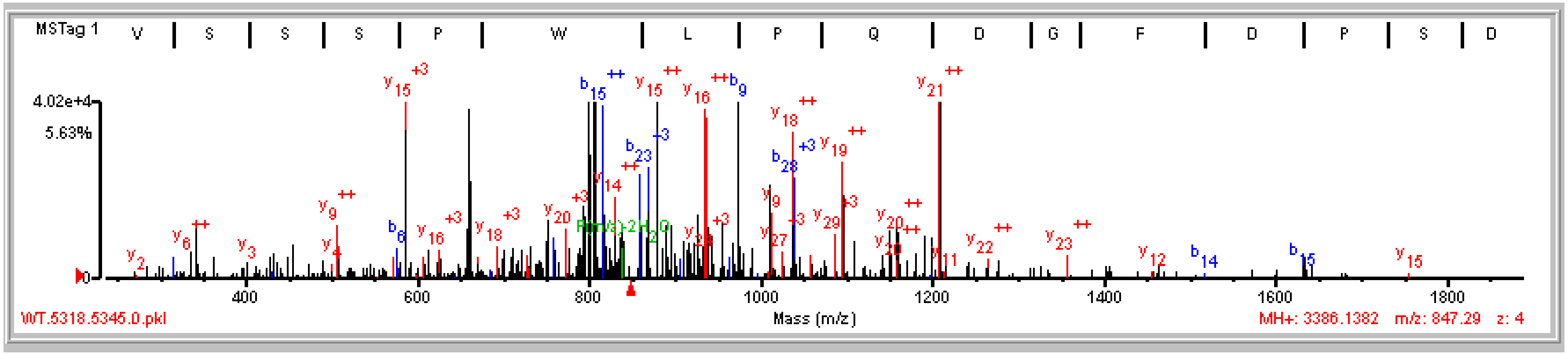
assignment

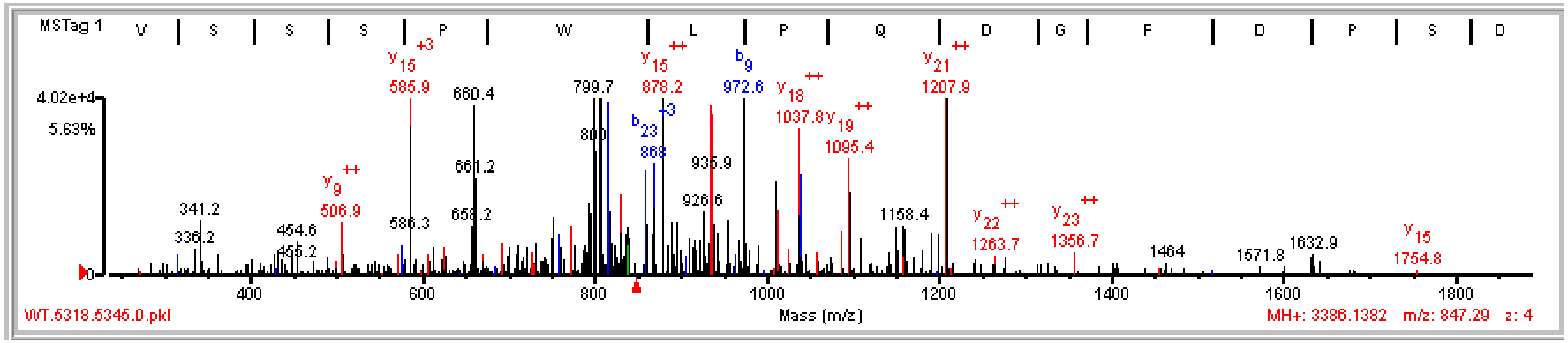


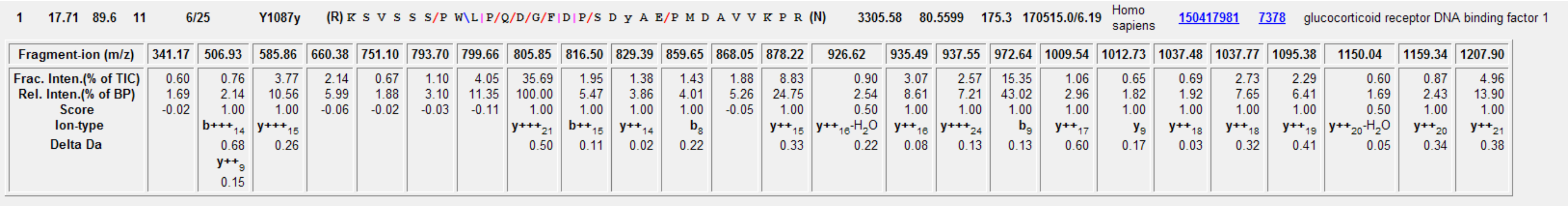
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.52	87.0	7	3/14	Y635y	(K) V P I V/I/N|P|N/A y D N L\A/I Y K (S)	1917.05	80.0247	29.2	193107.5/6.46	Homo sapiens	148368962	24198	NKF3 kinase family member

Fragment-ion (m/z)	423.34	636.59	733.39	752.36	950.69	966.84	1078.64	1150.64	1264.40	1344.81	1361.70	1475.72	1588.80	1688.88
Frac. Inten.(% of TIC)	5.06	8.82	4.12	6.61	0.11	5.15	3.91	5.97	4.70	4.83	27.32	12.29	7.17	3.93
Rel. Inten.(% of BP)	18.52	32.29	15.08	24.20	0.42	18.87	14.30	21.84	17.22	17.67	100.00	44.97	26.25	14.40
Score	1.00	1.00	1.00	1.00	1.50	-0.19	-0.14	1.00	1.00	0.50	1.00	1.00	1.00	-0.14
Ion-type	y_3	b_6	b_7	$b{++}_{13}$	sty			y_9	y_{10}	y_{11}-NH_3	y_{11}	a_{13} y_{12}	y_{13}	
Delta Da	0.08	0.18	-0.07	-0.01	0.67			0.12	-0.16	0.22	0.09	-0.01 0.06	0.06	

Peak 482



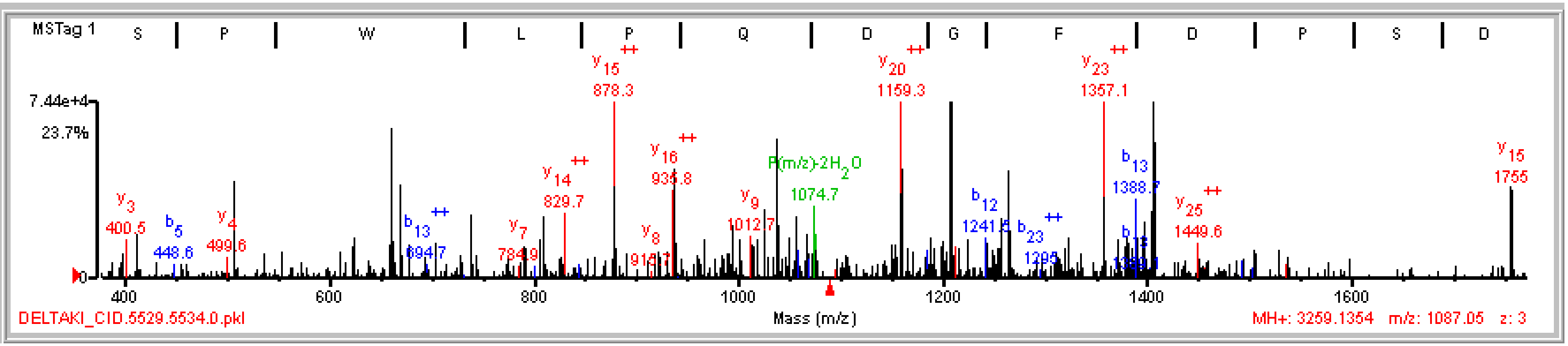


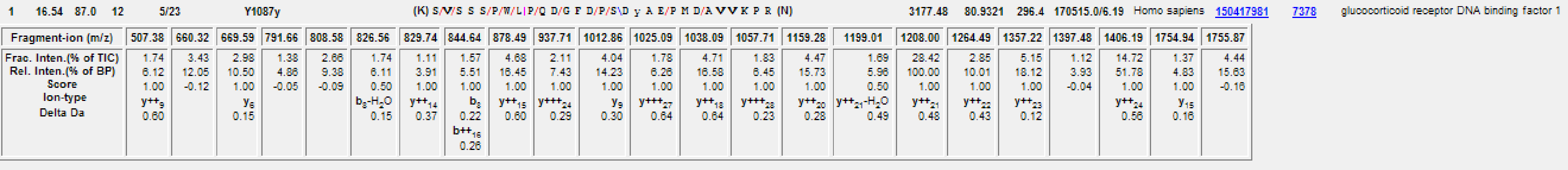


1 17.71 89.6 11 6/25 Y1087y (R) K S V S S S/P W\L|P/Q/D/G/F|D|P/S D y A E/P M D A V V K P R (N) 3305.58 80.5599 175.3 170515.0/6.19 Homo sapiens 150417981 7378 glucocorticoid receptor DNA binding factor 1

Fragment-ion (m/z)	341.17	506.93	585.86	660.38	751.10	793.70	799.66	805.85	816.50	829.39	859.65	868.05	878.22	926.62	935.49	937.55	972.64	1009.54	1012.73	1037.48	1037.77	1095.38	1150.04	1159.34	1207.90
Frac. Inten.(% of TIC)	0.60	0.76	3.77	2.14	0.67	1.10	4.05	35.69	1.95	1.38	1.43	1.88	8.83	0.90	3.07	2.57	15.35	1.06	0.65	0.69	2.73	2.29	0.60	0.87	4.96
Rel. Inten.(% of BP)	1.69	2.14	10.56	5.99	1.88	3.10	11.35	100.00	5.47	3.86	4.01	5.26	24.75	2.54	8.61	7.21	43.02	2.96	1.82	1.92	7.65	6.41	1.69	2.43	13.90
Score	-0.02	1.00	1.00	-0.06	-0.02	-0.03	-0.11	1.00	1.00	1.00	1.00	-0.05	1.00	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type		b+++$_{14}$ y++$_{9}$	y+++$_{15}$					y+++$_{21}$	b++$_{15}$	y++$_{14}$	b$_{8}$		y++$_{15}$	y++$_{16}$-H_2O	y++$_{16}$	y+++$_{24}$	b$_{9}$	y++$_{17}$	y$_{9}$	y++$_{18}$	y++$_{18}$	y++$_{19}$	y++$_{20}$-H_2O	y++$_{20}$	y++$_{21}$
Delta Da		0.68 0.15	0.26					0.50	0.11	0.02	0.22		0.33	0.22	0.08	0.13	0.13	0.60	0.17	0.03	0.32	0.41	0.05	0.34	0.38

Peak 483

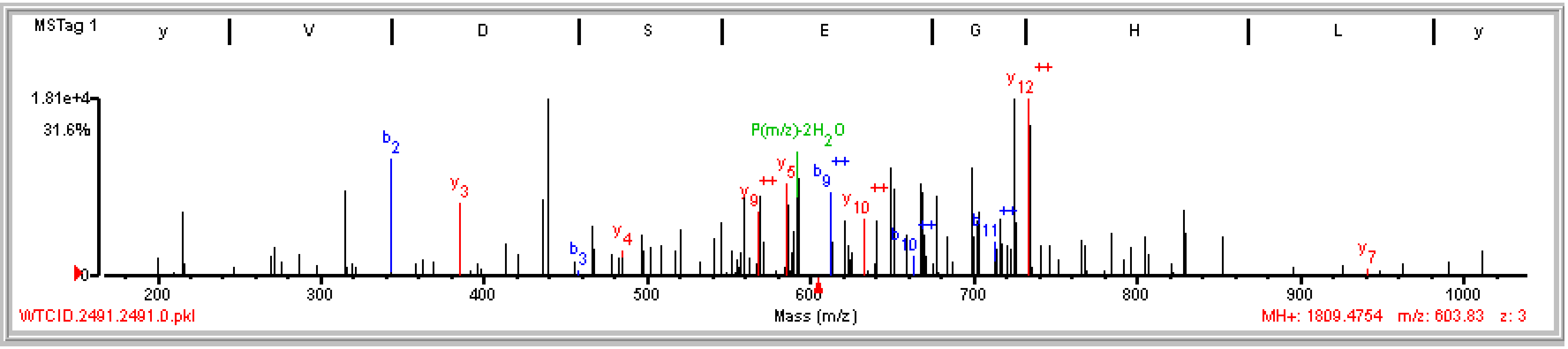


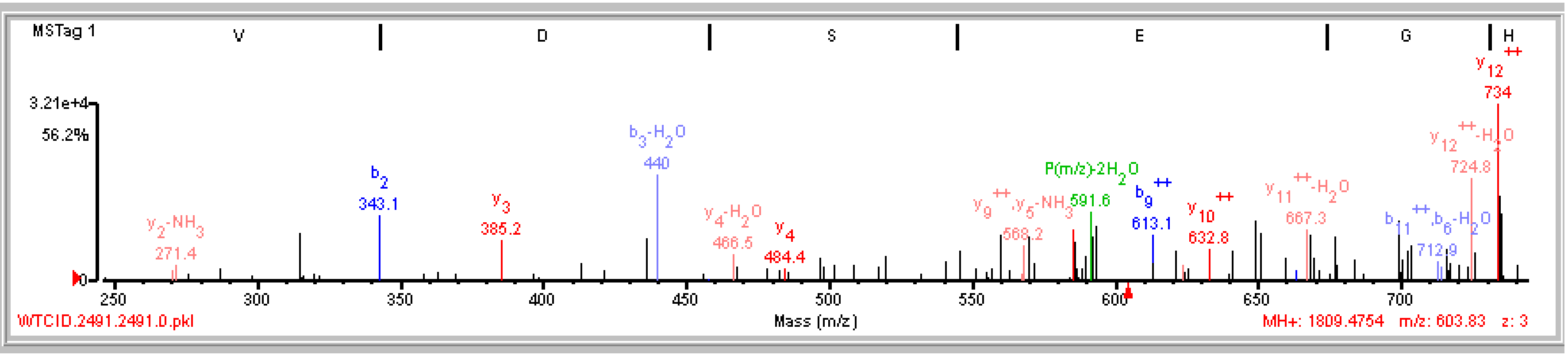


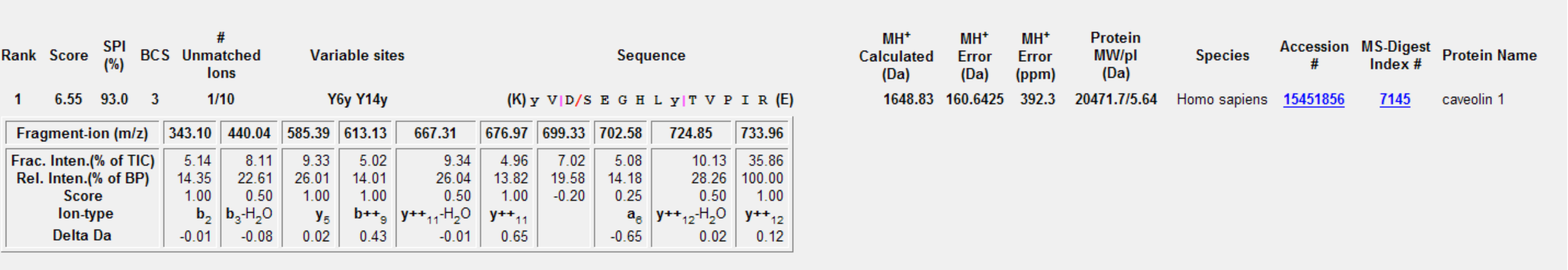
1 16.54 87.0 12 5/23 Y1087y (K) S/V/S S S/P/W/L|P/Q D/G F D/P/S\D y A E/P M D/A V V K P R (N) 3177.48 80.9321 296.4 170515.0/6.19 Homo sapiens 150417981 7378 glucocorticoid receptor DNA binding factor 1

Fragment-ion (m/z)	507.38	660.32	669.59	791.66	808.58	826.56	829.74	844.64	878.49	937.71	1012.86	1025.09	1038.09	1057.71	1159.28	1199.01	1208.00	1264.49	1357.22	1397.48	1406.19	1754.94	1755.87
Frac. Inten.(% of TIC)	1.74	3.43	2.98	1.38	2.66	1.74	1.11	1.57	4.68	2.11	4.04	1.78	4.71	1.83	4.47	1.69	28.42	2.85	5.15	1.12	14.72	1.37	4.44
Rel. Inten.(% of BP)	6.12	12.05	10.50	4.86	9.38	6.11	3.91	5.51	16.45	7.43	14.23	6.26	16.58	6.45	15.73	5.96	100.00	10.01	18.12	3.93	51.78	4.83	15.63
Score	1.00	-0.12	1.00	-0.05	-0.09	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	-0.04	1.00	1.00	-0.16
Ion-type	y^{++}_{9}		y_6			b_8-H_2O	y^{++}_{14}	b_8 b^{++}_{16}	y^{++}_{15}	y^{+++}_{24}	y_9	y^{+++}_{27}	y^{++}_{18}	y^{+++}_{28}	y^{++}_{20}	y^{++}_{21}-H_2O	y^{++}_{21}	y^{++}_{22}	y^{++}_{23}		y^{++}_{24}	y_{15}	
Delta Da	0.60		0.15			0.15	0.37	0.22 0.26	0.60	0.29	0.30	0.64	0.64	0.23	0.28	0.49	0.48	0.43	0.12		0.56	0.16	

Peak 484



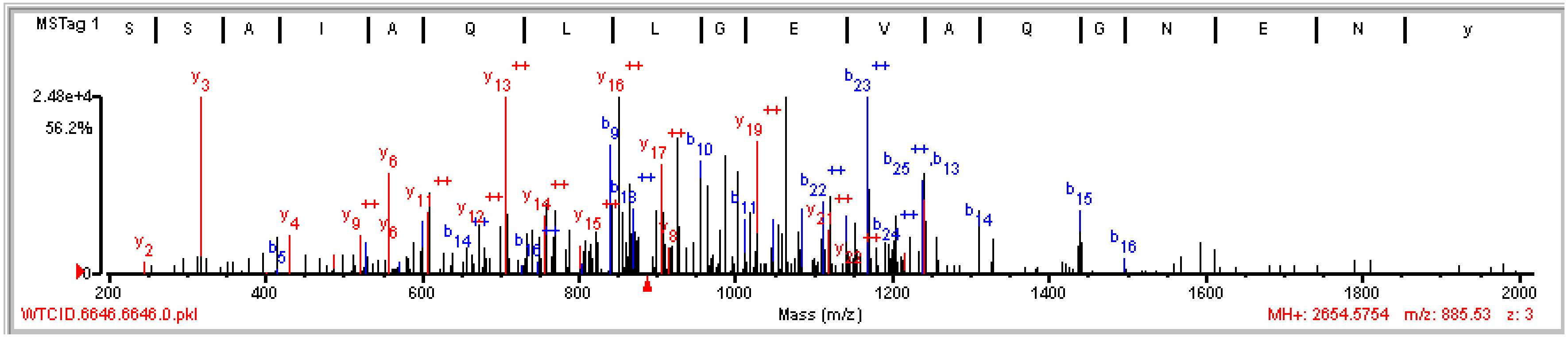


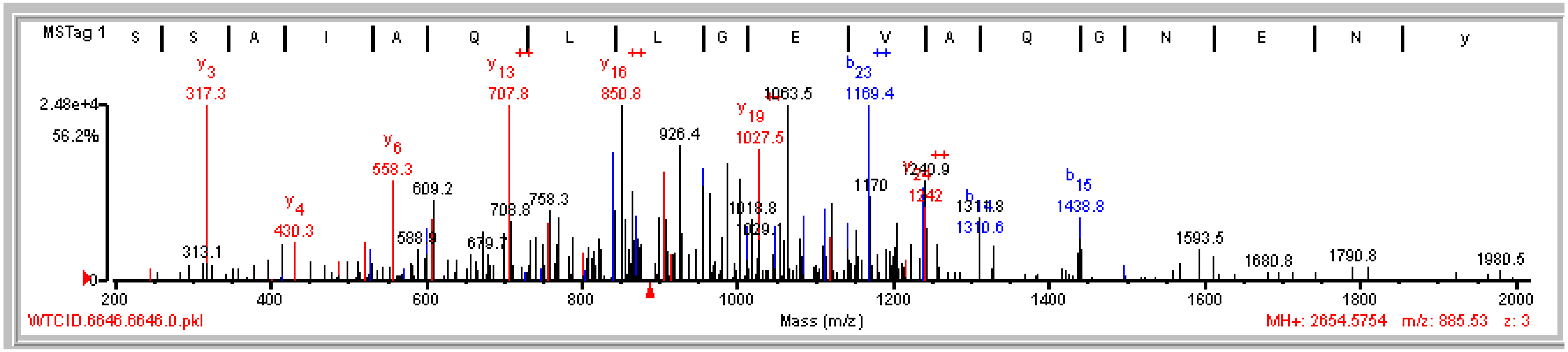


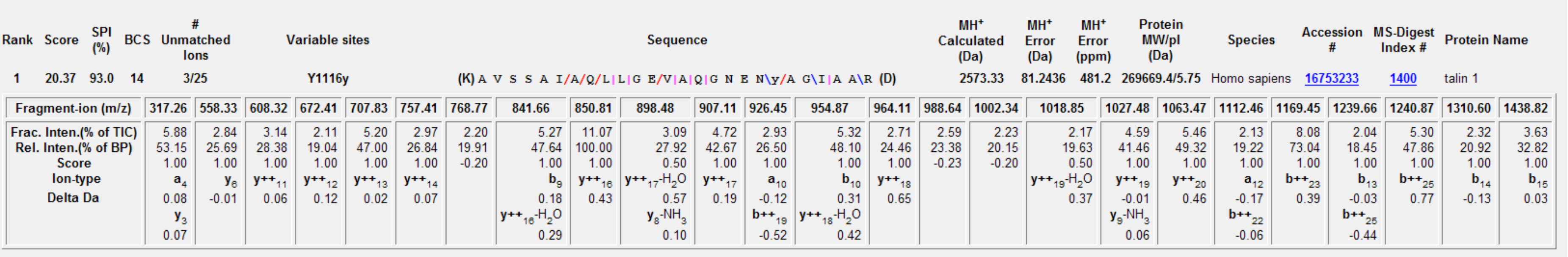
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.55	93.0	3	1/10	Y6y Y14y	(K) y V|D/S E G H L y|T V P I R (E)	1648.83	160.6425	392.3	20471.7/5.64	Homo sapiens	15451856	7145	caveolin 1

Fragment-ion (m/z)	343.10	440.04	585.39	613.13	667.31	676.97	699.33	702.58	724.85	733.96
Frac. Inten.(% of TIC)	5.14	8.11	9.33	5.02	9.34	4.96	7.02	5.08	10.13	35.86
Rel. Inten.(% of BP)	14.35	22.61	26.01	14.01	26.04	13.82	19.58	14.18	28.26	100.00
Score	1.00	0.50	1.00	1.00	0.50	1.00	-0.20	0.25	0.50	1.00
Ion-type	b_2	b_3-H_2O	y_5	$b{+}{+}_9$	$y{+}{+}_{11}$-H_2O	$y{+}{+}_{11}$		a_6	$y{+}{+}_{12}$-H_2O	$y{+}{+}_{12}$
Delta Da	-0.01	-0.08	0.02	0.43	-0.01	0.65		-0.65	0.02	0.12

Peak 485





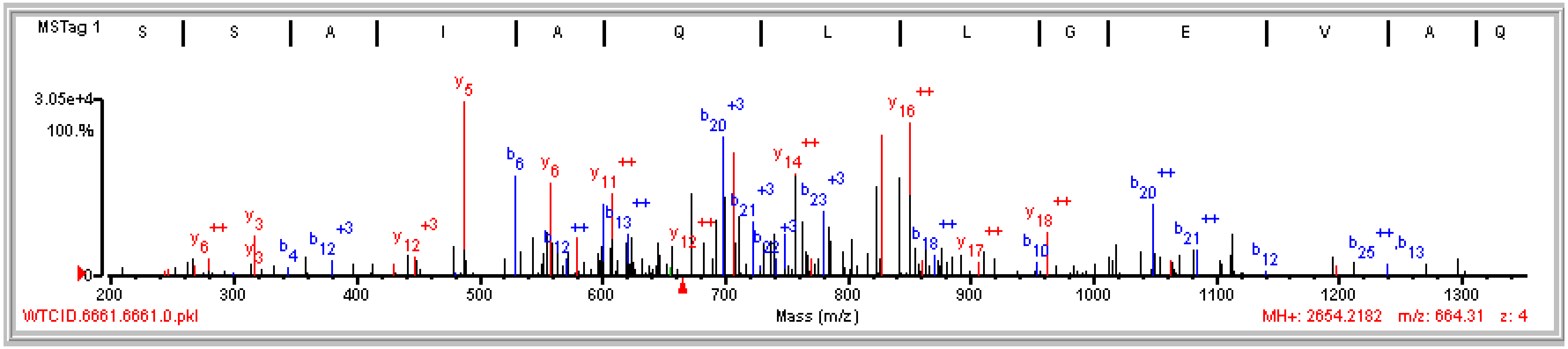


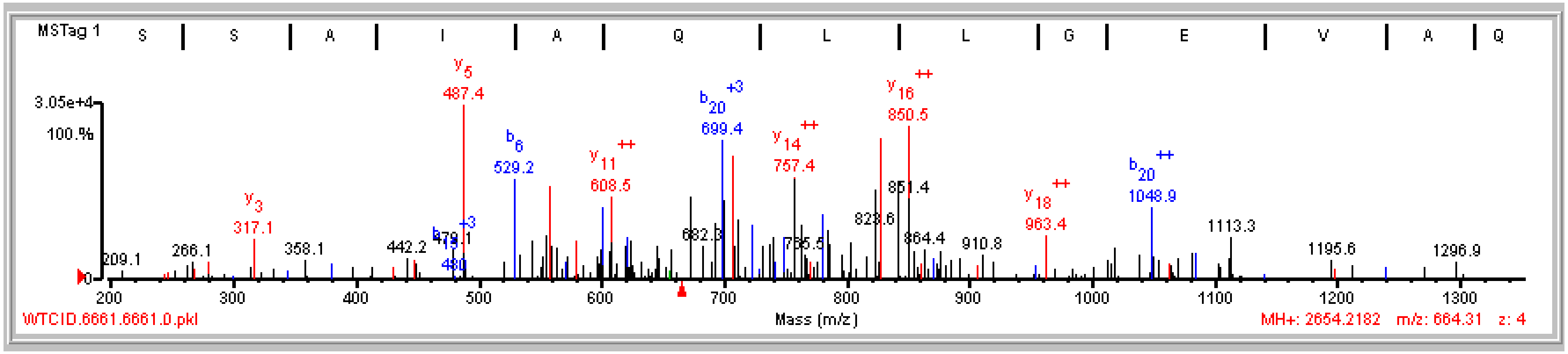
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	20.37	93.0	14	3/25	Y1116y	(K) A V S S A I/A/Q/L|L|G E/V|A|Q|G N E N\y/A G\I|A A\R (D)	2573.33	81.2436	481.2	269669.4/5.75	Homo sapiens	16753233	1400	talin 1

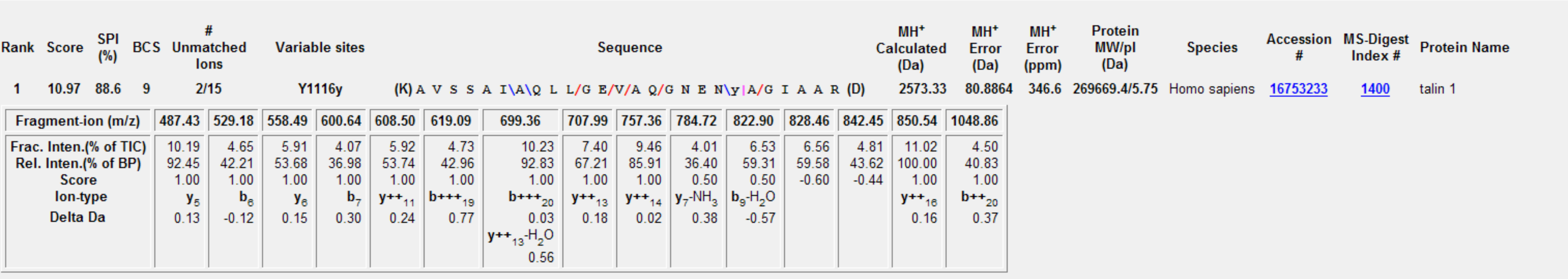
Fragment-ion (m/z)	317.26	558.33	608.32	672.41	707.83	757.41	768.77	841.66	850.81	898.48	907.11
Frac. Inten.(% of TIC)	5.88	2.84	3.14	2.11	5.20	2.97	2.20	5.27	11.07	3.09	4.72
Rel. Inten.(% of BP)	53.15	25.69	28.38	19.04	47.00	26.84	19.91	47.64	100.00	27.92	42.67
Score	1.00	1.00	1.00	1.00	1.00	1.00	-0.20	1.00	1.00	0.50	1.00
Ion-type	a_4 y_3	y_6	$y{+}{+}_{11}$	$y{+}{+}_{12}$	$y{+}{+}_{13}$	$y{+}{+}_{14}$		b_9 $y{+}{+}_{16}\text{-}H_2O$	$y{+}{+}_{16}$	$y{+}{+}_{17}\text{-}H_2O$ $y_8\text{-}NH_3$	$y{+}{+}_{17}$
Delta Da	0.08 0.07	-0.01	0.06	0.12	0.02	0.07		0.18 0.29	0.43	0.57 0.10	0.19

Fragment-ion (m/z)	926.45	954.87	964.11	988.64	1002.34	1018.85	1027.48	1063.47	1112.46	1169.45	1239.66	1240.87	1310.60	1438.82
Frac. Inten.(% of TIC)	2.93	5.32	2.71	2.59	2.23	2.17	4.59	5.46	2.13	8.08	2.04	5.30	2.32	3.63
Rel. Inten.(% of BP)	26.50	48.10	24.46	23.38	20.15	19.63	41.46	49.32	19.22	73.04	18.45	47.86	20.92	32.82
Score	1.00	1.00	1.00	-0.23	-0.20	0.50	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	a_{10} $b{+}{+}_{19}$	b_{10} $y{+}{+}_{18}\text{-}H_2O$	$y{+}{+}_{18}$			$y{+}{+}_{19}\text{-}H_2O$	$y{+}{+}_{19}$ $y_9\text{-}NH_3$	$y{+}{+}_{20}$	a_{12} $b{+}{+}_{22}$	$b{+}{+}_{23}$	b_{13} $b{+}{+}_{25}$	$b{+}{+}_{25}$	b_{14}	b_{15}
Delta Da	-0.12 -0.52	0.31 0.42	0.65			0.37	-0.01 0.06	0.46	-0.17 -0.06	0.39	-0.03 -0.44	0.77	-0.13	0.03

Peak 486





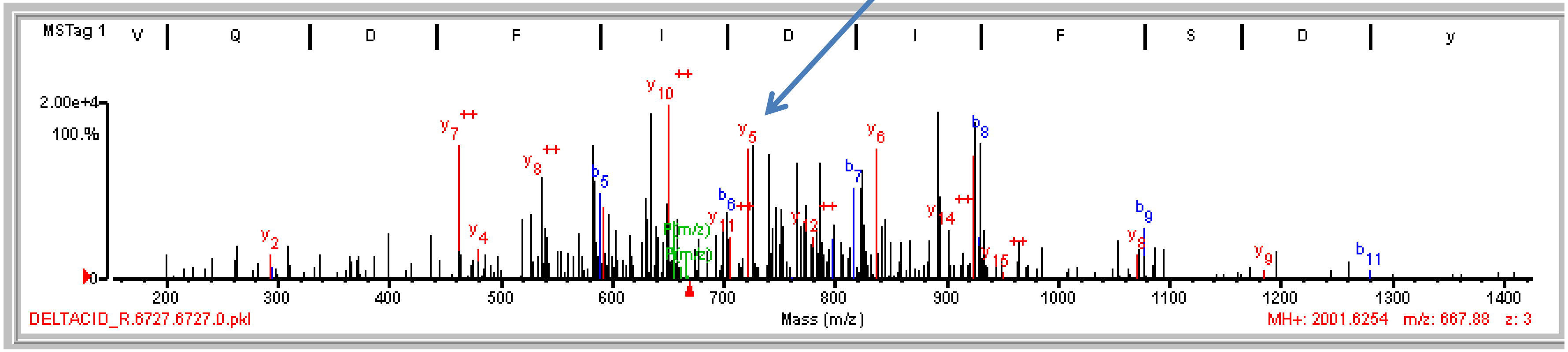


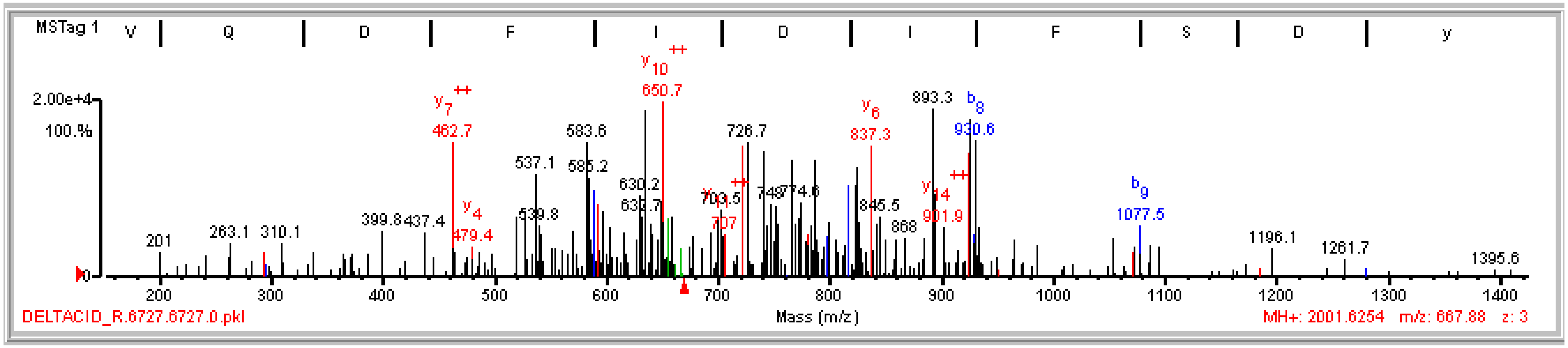
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.97	88.6	9	2/15	Y1116y	(K) A V S S A I\A\Q L L/G E/V/A Q/G N E N\y|A/G I A A R (D)	2573.33	80.8864	346.6	269669.4/5.75	Homo sapiens	16753233	1400	talin 1

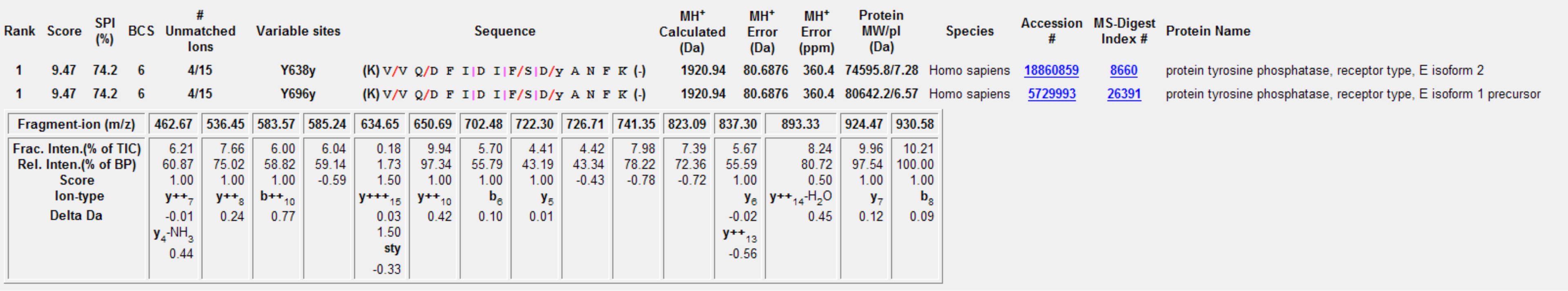
Fragment-ion (m/z)	487.43	529.18	558.49	600.64	608.50	619.09	699.36	707.99	757.36	784.72	822.90	828.46	842.45	850.54	1048.86
Frac. Inten.(% of TIC)	10.19	4.65	5.91	4.07	5.92	4.73	10.23	7.40	9.46	4.01	6.53	6.56	4.81	11.02	4.50
Rel. Inten.(% of BP)	92.45	42.21	53.68	36.98	53.74	42.96	92.83	67.21	85.91	36.40	59.31	59.58	43.62	100.00	40.83
Score	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50	0.50	-0.60	-0.44	1.00	1.00
Ion-type	y_5	b_6	y_6	b_7	$y{+}{+}_{11}$	$b{+}{+}{+}_{19}$	$b{+}{+}{+}_{20}$ $y{+}{+}_{13}\text{-}H_2O$	$y{+}{+}_{13}$	$y{+}{+}_{14}$	$y_7\text{-}NH_3$	$b_9\text{-}H_2O$			$y{+}{+}_{16}$	$b{+}{+}_{20}$
Delta Da	0.13	-0.12	0.15	0.30	0.24	0.77	0.03 0.56	0.18	0.02	0.38	-0.57			0.16	0.37

Peak 487

assignment



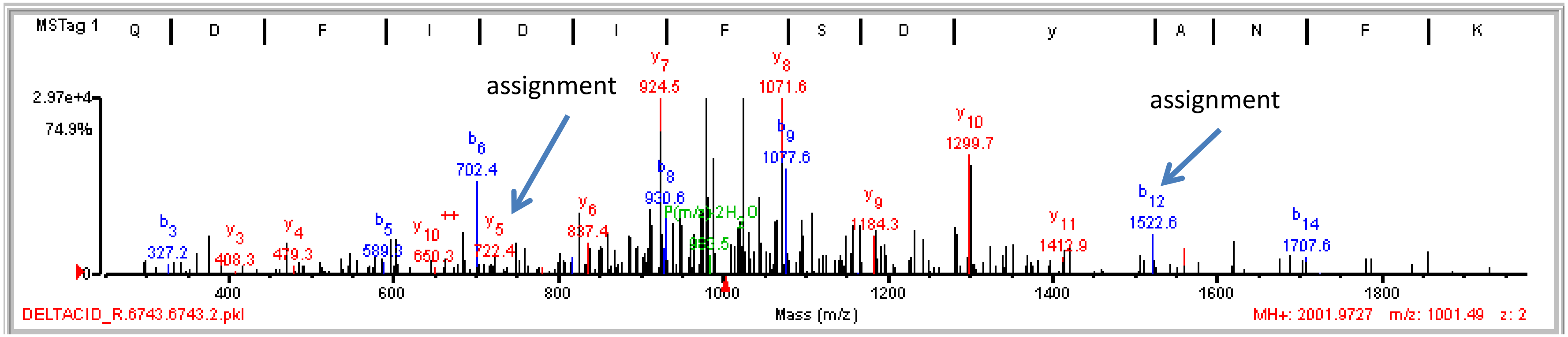




Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	9.47	74.2	6	4/15	Y638y	(K) V/V Q/D F I|D I|F/S|D/y A N F K (-)	1920.94	80.6876	360.4	74595.8/7.28	Homo sapiens	18860859	8660	protein tyrosine phosphatase, receptor type, E isoform 2
1	9.47	74.2	6	4/15	Y696y	(K) V/V Q/D F I|D I|F/S|D/y A N F K (-)	1920.94	80.6876	360.4	80642.2/6.57	Homo sapiens	5729993	26391	protein tyrosine phosphatase, receptor type, E isoform 1 precursor

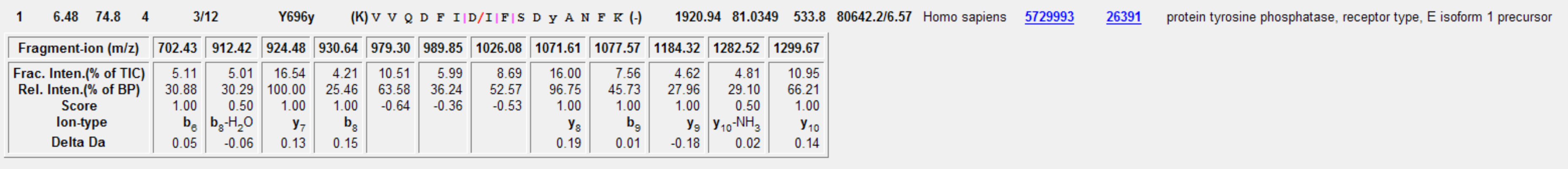
Fragment-ion (m/z)	462.67	536.45	583.57	585.24	634.65	650.69	702.48	722.30	726.71	741.35	823.09	837.30	893.33	924.47	930.58
Frac. Inten.(% of TIC)	6.21	7.66	6.00	6.04	0.18	9.94	5.70	4.41	4.42	7.98	7.39	5.67	8.24	9.96	10.21
Rel. Inten.(% of BP)	60.87	75.02	58.82	59.14	1.73	97.34	55.79	43.19	43.34	78.22	72.36	55.59	80.72	97.54	100.00
Score	1.00	1.00	1.00	-0.59	1.50	1.00	1.00	1.00	-0.43	-0.78	-0.72	1.00	0.50	1.00	1.00
Ion-type	y++$_7$	y++$_8$	b++$_{10}$		y+++$_{15}$	y++$_{10}$	b$_6$	y$_5$				y$_6$	y++$_{14}$-H$_2$O	y$_7$	b$_8$
Delta Da	-0.01	0.24	0.77		0.03	0.42	0.10	0.01				-0.02	0.45	0.12	0.09
	y$_4$-NH$_3$				1.50							y++$_{13}$			
	0.44				sty							-0.56			
					-0.33										

Peak 488



assignment

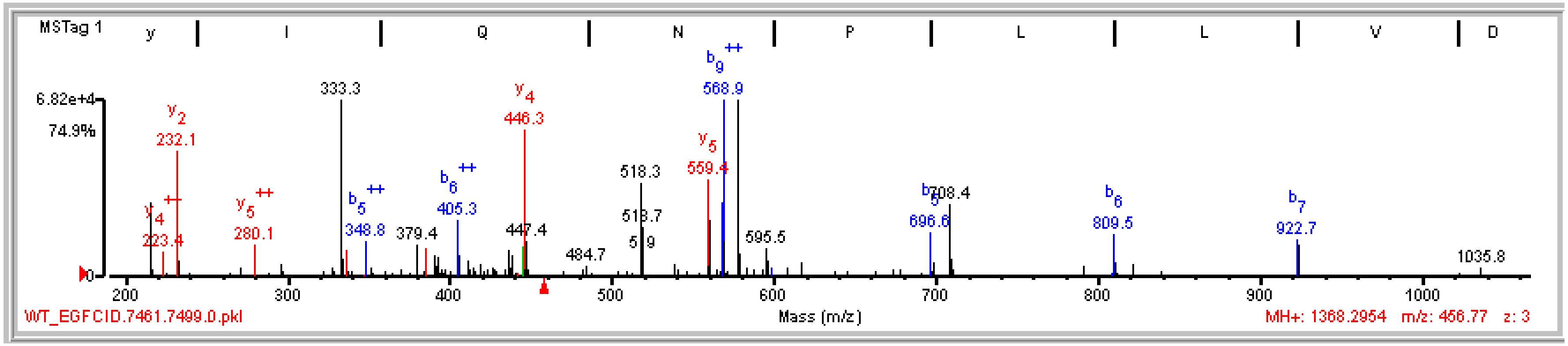
assignment

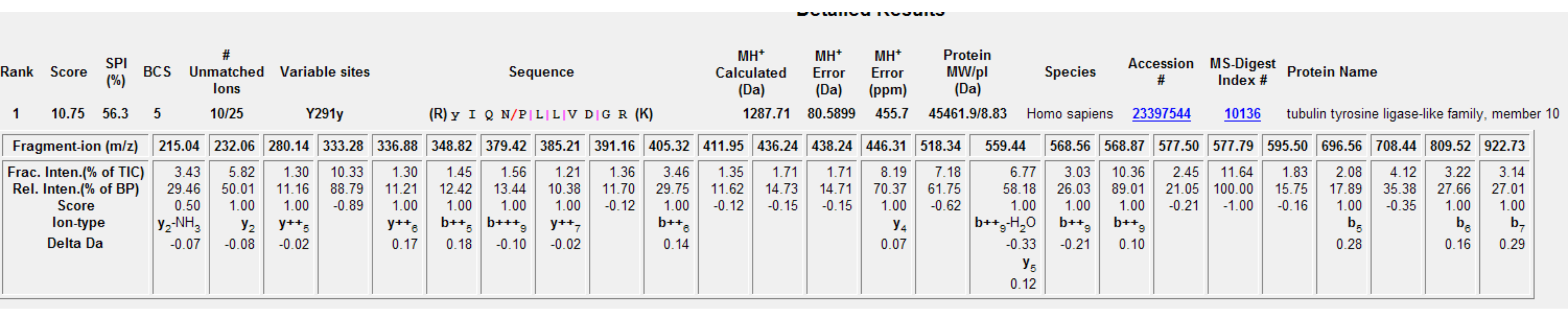


1 6.48 74.8 4 3/12 Y696y (K) V V Q D F I|D/I|F|S D y A N F K (-) 1920.94 81.0349 533.8 80642.2/6.57 Homo sapiens 5729993 26391 protein tyrosine phosphatase, receptor type, E isoform 1 precursor

Fragment-ion (m/z)	702.43	912.42	924.48	930.64	979.30	989.85	1026.08	1071.61	1077.57	1184.32	1282.52	1299.67
Frac. Inten.(% of TIC)	5.11	5.01	16.54	4.21	10.51	5.99	8.69	16.00	7.56	4.62	4.81	10.95
Rel. Inten.(% of BP)	30.88	30.29	100.00	25.46	63.58	36.24	52.57	96.75	45.73	27.96	29.10	66.21
Score	1.00	0.50	1.00	1.00	-0.64	-0.36	-0.53	1.00	1.00	1.00	0.50	1.00
Ion-type	b_6	b_8-H_2O	y_7	b_8				y_8	b_9	y_9	y_{10}-NH_3	y_{10}
Delta Da	0.05	-0.06	0.13	0.15				0.19	0.01	-0.18	0.02	0.14

Peak 489





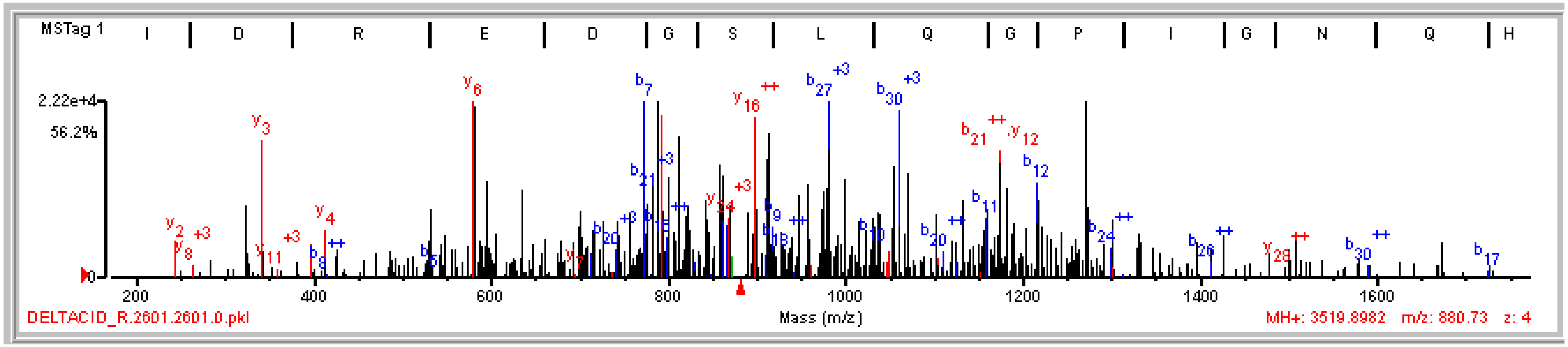
Detailed Results

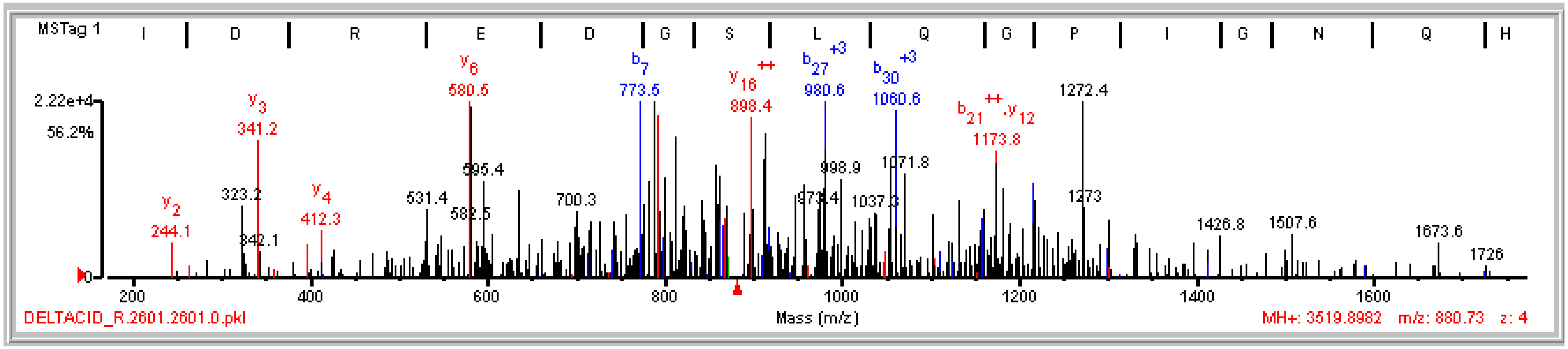
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	10.75	56.3	5	10/25	Y291y	(R) y I Q N/P|L|L|V D|G R (K)	1287.71	80.5899	455.7	45461.9/8.83	Homo sapiens	23397544	10136	tubulin tyrosine ligase-like family, member 10

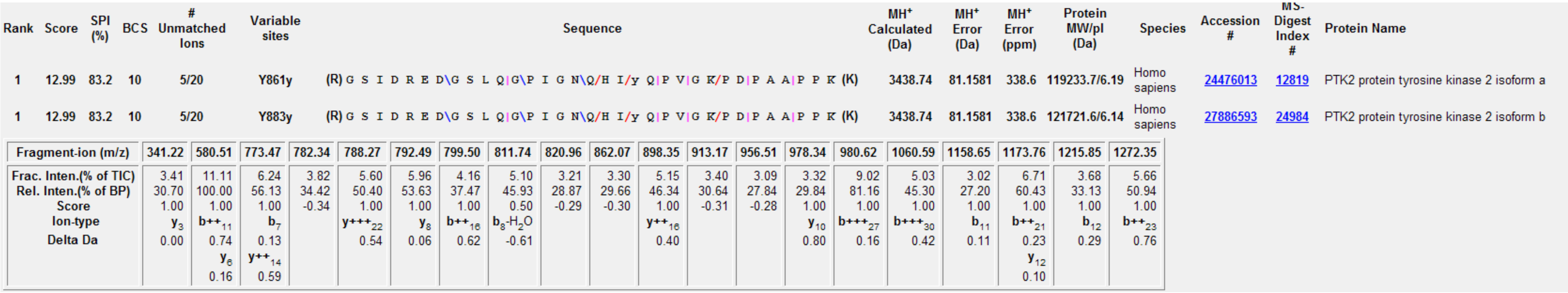
Fragment-ion (m/z)	215.04	232.06	280.14	333.28	336.88	348.82	379.42	385.21	391.16	405.32
Frac. Inten.(% of TIC)	3.43	5.82	1.30	10.33	1.30	1.45	1.56	1.21	1.36	3.46
Rel. Inten.(% of BP)	29.46	50.01	11.16	88.79	11.21	12.42	13.44	10.38	11.70	29.75
Score	0.50	1.00	1.00	-0.89	1.00	1.00	1.00	1.00	-0.12	1.00
Ion-type	y_2-NH_3	y_2	$y{+}{+}_5$		$y{+}{+}_6$	$b{+}{+}_5$	$b{+}{+}{+}_9$	$y{+}{+}_7$		$b{+}{+}_6$
Delta Da	-0.07	-0.08	-0.02		0.17	0.18	-0.10	-0.02		0.14

Fragment-ion (m/z)	411.95	436.24	438.24	446.31	518.34	559.44	568.56	568.87	577.50	577.79	595.50	696.56	708.44	809.52	922.73
Frac. Inten.(% of TIC)	1.35	1.71	1.71	8.19	7.18	6.77	3.03	10.36	2.45	11.64	1.83	2.08	4.12	3.22	3.14
Rel. Inten.(% of BP)	11.62	14.73	14.71	70.37	61.75	58.18	26.03	89.01	21.05	100.00	15.75	17.89	35.38	27.66	27.01
Score	-0.12	-0.15	-0.15	1.00	-0.62	1.00	1.00	1.00	-0.21	-1.00	-0.16	1.00	-0.35	1.00	1.00
Ion-type				y_4		$b{+}{+}_9$-H_2O -0.33 y_5	$b{+}{+}_9$	$b{+}{+}_9$				b_5		b_6	b_7
Delta Da				0.07		0.12	-0.21	0.10				0.28		0.16	0.29

Peak 490



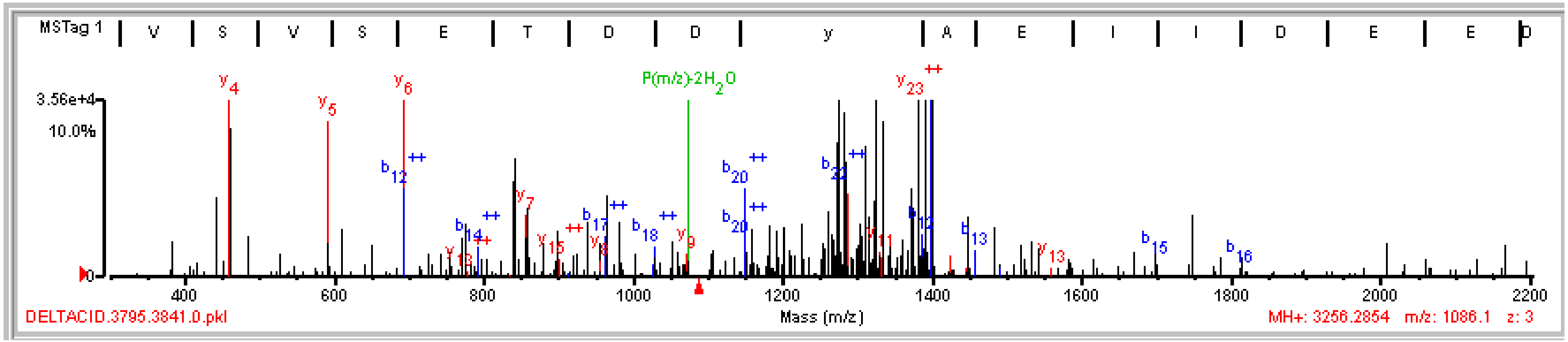


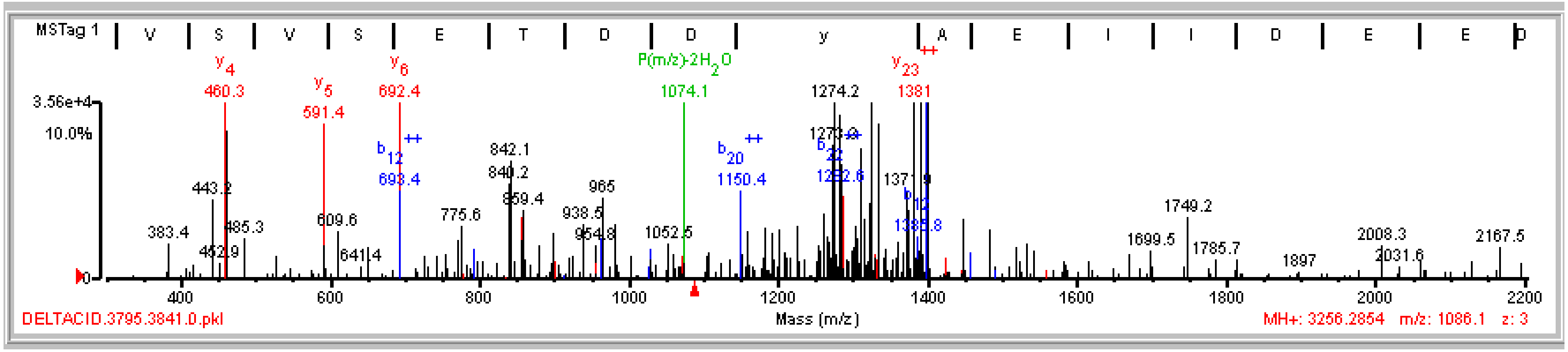


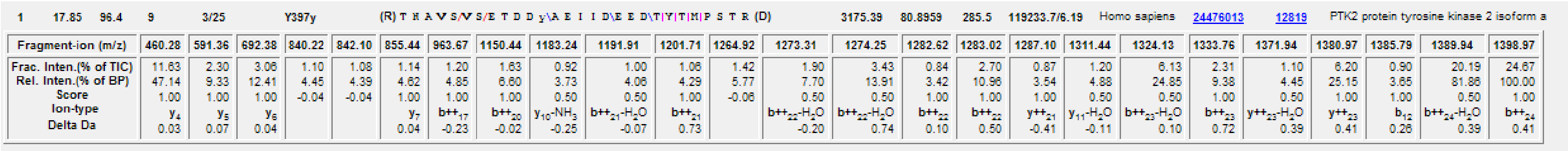
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.99	83.2	10	5/20	Y861y	(R) G S I D R E D\G S L Q|G\P I G N\Q/H I/y Q|P V|G K/P D|P A A|P P K (K)	3438.74	81.1581	338.6	119233.7/6.19	Homo sapiens	24476013	12819	PTK2 protein tyrosine kinase 2 isoform a
1	12.99	83.2	10	5/20	Y883y	(R) G S I D R E D\G S L Q|G\P I G N\Q/H I/y Q|P V|G K/P D|P A A|P P K (K)	3438.74	81.1581	338.6	121721.6/6.14	Homo sapiens	27886593	24984	PTK2 protein tyrosine kinase 2 isoform b

Fragment-ion (m/z)	341.22	580.51	773.47	782.34	788.27	792.49	799.50	811.74	820.96	862.07	898.35	913.17	956.51	978.34	980.62	1060.59	1158.65	1173.76	1215.85	1272.35
Frac. Inten.(% of TIC)	3.41	11.11	6.24	3.82	5.60	5.96	4.16	5.10	3.21	3.30	5.15	3.40	3.09	3.32	9.02	5.03	3.02	6.71	3.68	5.66
Rel. Inten.(% of BP)	30.70	100.00	56.13	34.42	50.40	53.63	37.47	45.93	28.87	29.66	46.34	30.64	27.84	29.84	81.16	45.30	27.20	60.43	33.13	50.94
Score	1.00	1.00	1.00	-0.34	1.00	1.00	1.00	0.50	-0.29	-0.30	1.00	-0.31	-0.28	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y_{3}	$b{++}_{11}$	b_{7}		$y{+++}_{22}$	y_{8}	$b{++}_{16}$	$b_{8}\text{-}H_{2}O$			$y{++}_{16}$			y_{10}	$b{+++}_{27}$	$b{+++}_{30}$	b_{11}	$b{++}_{21}$	b_{12}	$b{++}_{23}$
Delta Da	0.00	0.74	0.13		0.54	0.06	0.62	-0.61			0.40			0.80	0.16	0.42	0.11	0.23	0.29	0.76
		y_{6}	$y{++}_{14}$															y_{12}		
		0.16	0.59															0.10		

Peak 491





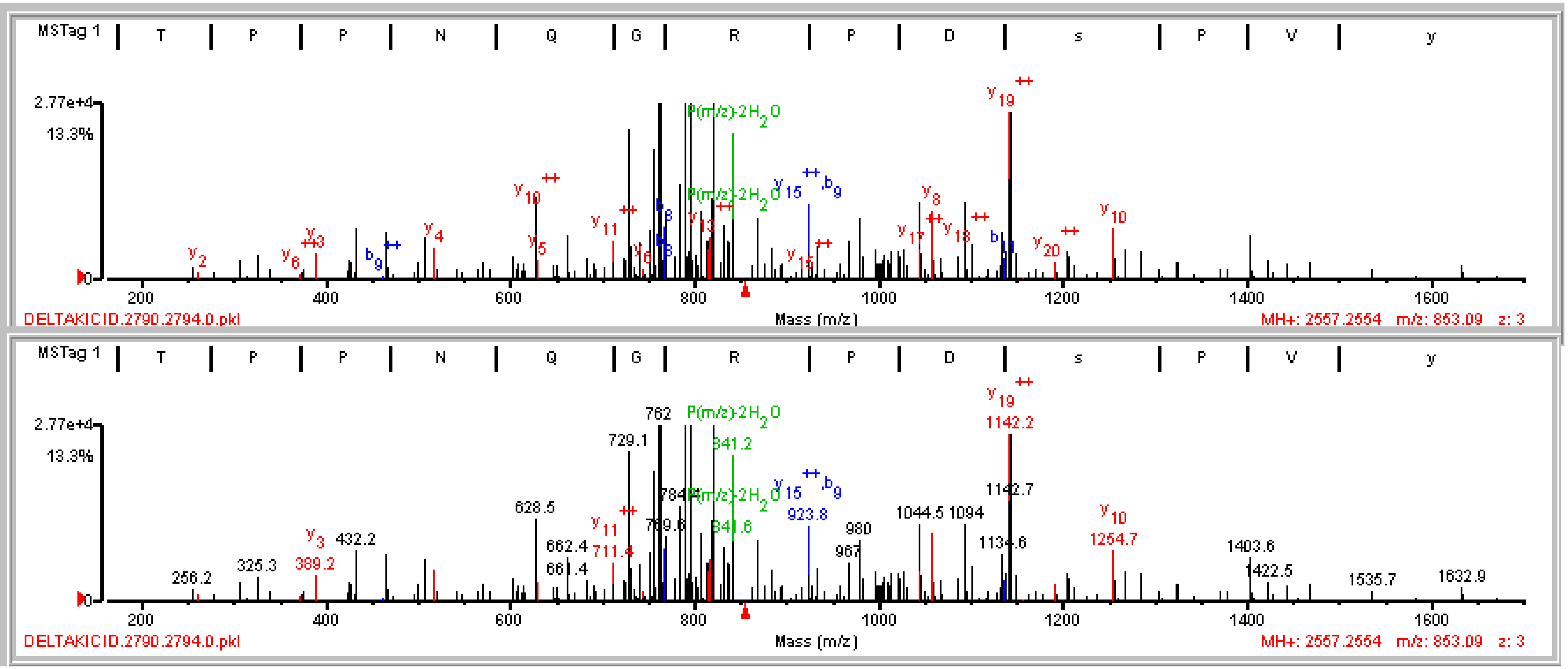


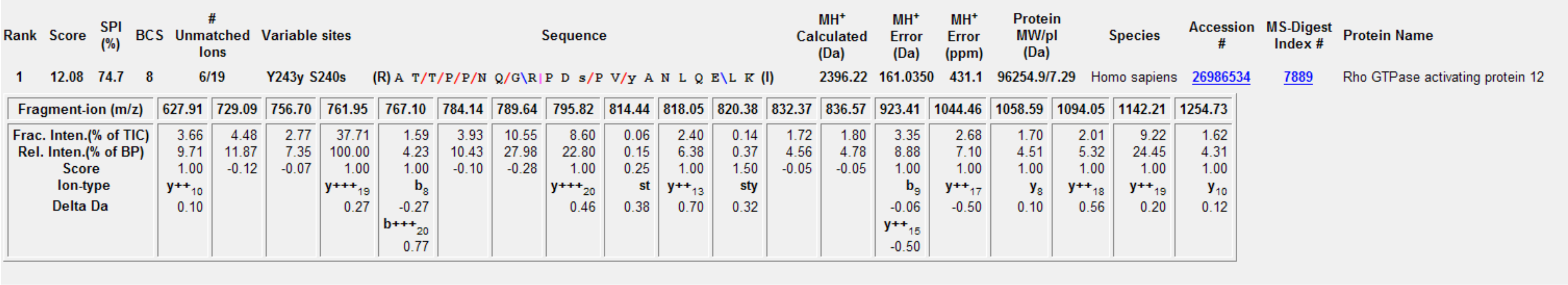
1 17.85 96.4 9 3/25 Y397y (R) T H A V S/V S/E T D D y\A E I I D\E E D\T|Y|T|M|P S T R (D) 3175.39 80.8959 285.5 119233.7/6.19 Homo sapiens 24476013 12819 PTK2 protein tyrosine kinase 2 isoform a

Fragment-ion (m/z)	460.28	591.36	692.38	840.22	842.10	855.44	963.67	1150.44	1183.24	1191.91	1201.71	1264.92
Frac. Inten.(% of TIC)	11.63	2.30	3.06	1.10	1.08	1.14	1.20	1.63	0.92	1.00	1.06	1.42
Rel. Inten.(% of BP)	47.14	9.33	12.41	4.45	4.39	4.62	4.85	6.60	3.73	4.06	4.29	5.77
Score	1.00	1.00	1.00	-0.04	-0.04	1.00	1.00	1.00	0.50	0.50	1.00	-0.06
Ion-type	y_4	y_5	y_6			y_7	$b{+}{+}_{17}$	$b{+}{+}_{20}$	y_{10}-NH_3	$b{+}{+}_{21}$-H_2O	$b{+}{+}_{21}$	
Delta Da	0.03	0.07	0.04			0.04	-0.23	-0.02	-0.25	-0.07	0.73	

Fragment-ion (m/z)	1273.31	1274.25	1282.62	1283.02	1287.10	1311.44	1324.13	1333.76	1371.94	1380.97	1385.79	1389.94	1398.97
Frac. Inten.(% of TIC)	1.90	3.43	0.84	2.70	0.87	1.20	6.13	2.31	1.10	6.20	0.90	20.19	24.67
Rel. Inten.(% of BP)	7.70	13.91	3.42	10.96	3.54	4.88	24.85	9.38	4.45	25.15	3.65	81.86	100.00
Score	0.50	0.50	1.00	1.00	1.00	0.50	0.50	1.00	0.50	1.00	1.00	0.50	1.00
Ion-type	$b{+}{+}_{22}$-H_2O	$b{+}{+}_{22}$-H_2O	$b{+}{+}_{22}$	$b{+}{+}_{22}$	$y{+}{+}_{21}$	y_{11}-H_2O	$b{+}{+}_{23}$-H_2O	$b{+}{+}_{23}$	$y{+}{+}_{23}$-H_2O	$y{+}{+}_{23}$	b_{12}	$b{+}{+}_{24}$-H_2O	$b{+}{+}_{24}$
Delta Da	-0.20	0.74	0.10	0.50	-0.41	-0.11	0.10	0.72	0.39	0.41	0.26	0.39	0.41

Peak 492

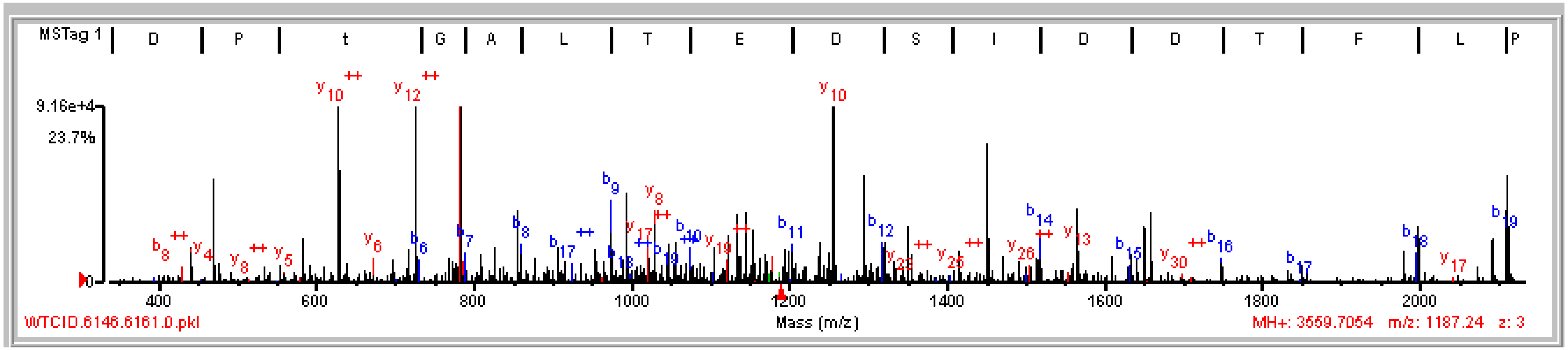


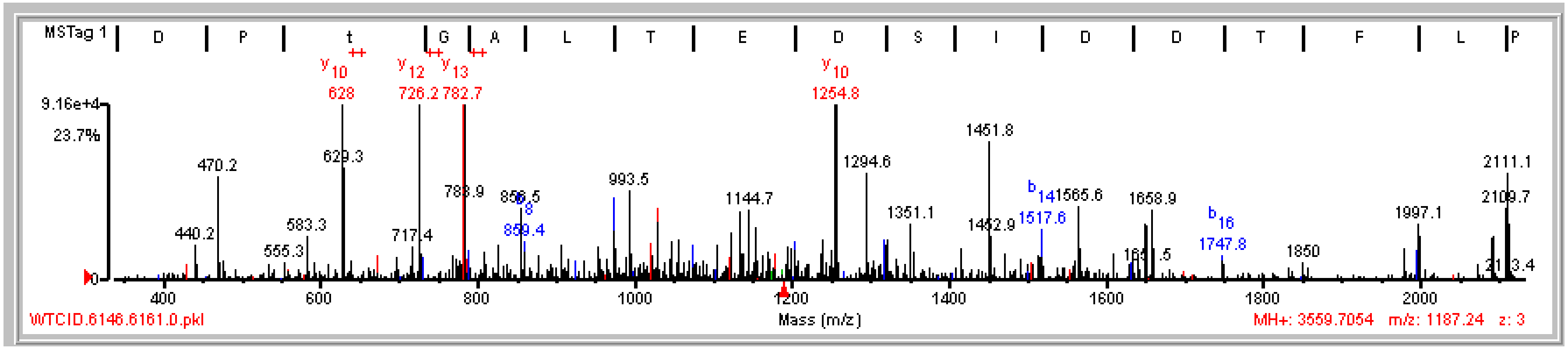


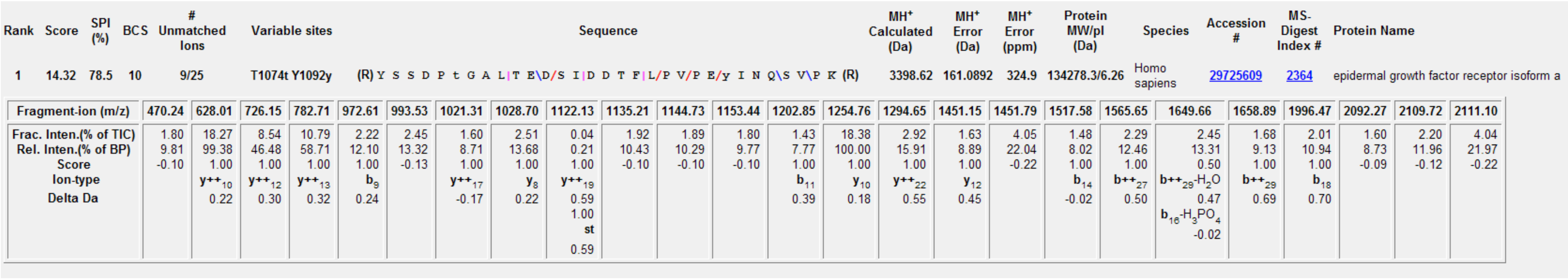
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.08	74.7	8	6/19	Y243y S240s	(R) A T/T/P/P/N Q/G\R|P D s/P V/y A N L Q E\L K (I)	2396.22	161.0350	431.1	96254.9/7.29	Homo sapiens	26986534	7889	Rho GTPase activating protein 12

Fragment-ion (m/z)	627.91	729.09	756.70	761.95	767.10	784.14	789.64	795.82	814.44	818.05	820.38	832.37	836.57	923.41	1044.46	1058.59	1094.05	1142.21	1254.73
Frac. Inten.(% of TIC)	3.66	4.48	2.77	37.71	1.59	3.93	10.55	8.60	0.06	2.40	0.14	1.72	1.80	3.35	2.68	1.70	2.01	9.22	1.62
Rel. Inten.(% of BP)	9.71	11.87	7.35	100.00	4.23	10.43	27.98	22.80	0.15	6.38	0.37	4.56	4.78	8.88	7.10	4.51	5.32	24.45	4.31
Score	1.00	-0.12	-0.07	1.00	1.00	-0.10	-0.28	1.00	0.25	1.00	1.50	-0.05	-0.05	1.00	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{++}_{10}			y^{+++}_{19}	b_8 b^{+++}_{20}			y^{+++}_{20}	st	y^{++}_{13}	sty			b_9 y^{++}_{15}	y^{++}_{17}	y_8	y^{++}_{18}	y^{++}_{19}	y_{10}
Delta Da	0.10			0.27	-0.27 0.77			0.46	0.38	0.70	0.32			-0.06 -0.50	-0.50	0.10	0.56	0.20	0.12

Peak 493





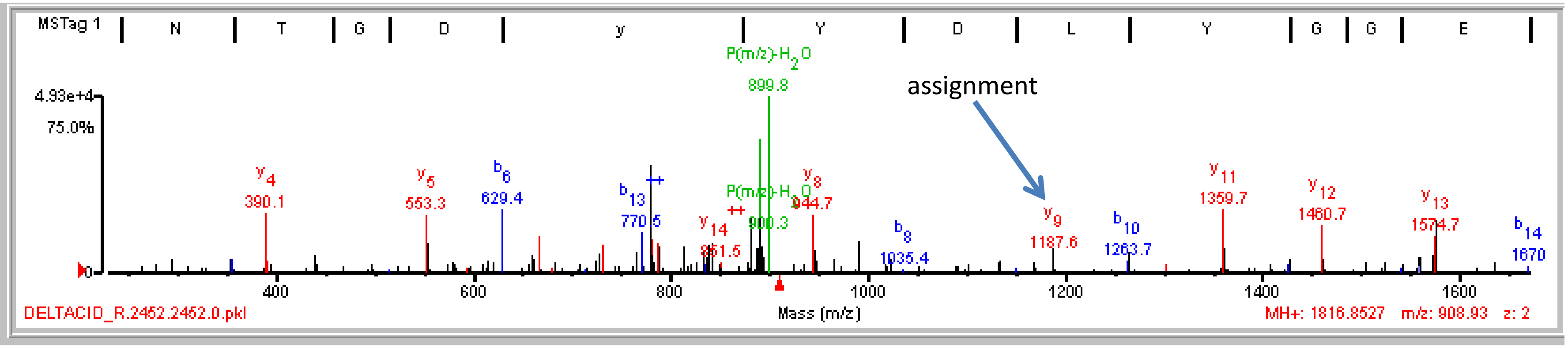


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.32	78.5	10	9/25	T1074t Y1092y	(R) Y S S D P t G A L|T E\D/S I|D D T F|L/P V/P E/y I N Q\S V\P K (R)	3398.62	161.0892	324.9	134278.3/6.26	Homo sapiens	29725609	2364	epidermal growth factor receptor isoform a

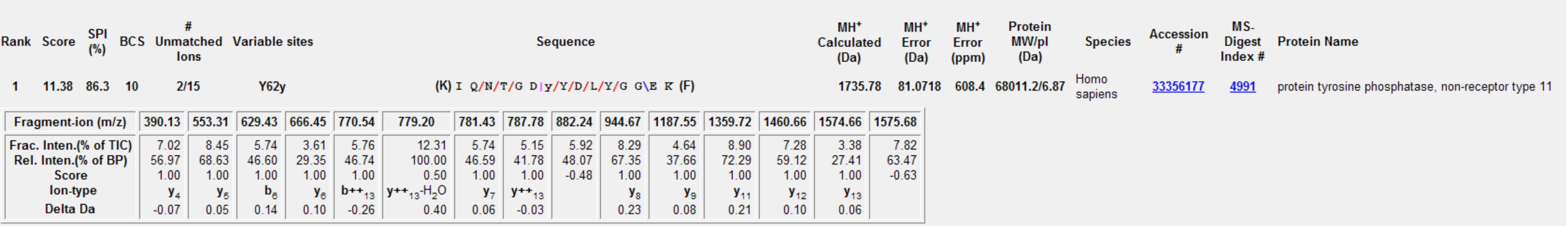
Fragment-ion (m/z)	470.24	628.01	726.15	782.71	972.61	993.53	1021.31	1028.70	1122.13	1135.21	1144.73	1153.44
Frac. Inten.(% of TIC)	1.80	18.27	8.54	10.79	2.22	2.45	1.60	2.51	0.04	1.92	1.89	1.80
Rel. Inten.(% of BP)	9.81	99.38	46.48	58.71	12.10	13.32	8.71	13.68	0.21	10.43	10.29	9.77
Score	-0.10	1.00	1.00	1.00	1.00	-0.13	1.00	1.00	1.00 1.00	-0.10	-0.10	-0.10
Ion-type		y^{++}_{10}	y^{++}_{12}	y^{++}_{13}	b_9		y^{++}_{17}	y_8	y^{++}_{19} st			
Delta Da		0.22	0.30	0.32	0.24		-0.17	0.22	0.59 0.59			

Fragment-ion (m/z)	1202.85	1254.76	1294.65	1451.15	1451.79	1517.58	1565.65	1649.66	1658.89	1996.47	2092.27	2109.72	2111.10
Frac. Inten.(% of TIC)	1.43	18.38	2.92	1.63	4.05	1.48	2.29	2.45	1.68	2.01	1.60	2.20	4.04
Rel. Inten.(% of BP)	7.77	100.00	15.91	8.89	22.04	8.02	12.46	13.31	9.13	10.94	8.73	11.96	21.97
Score	1.00	1.00	1.00	1.00	-0.22	1.00	1.00	0.50	1.00	1.00	-0.09	-0.12	-0.22
Ion-type	b_{11}	y_{10}	y^{++}_{22}	y_{12}		b_{14}	b^{++}_{27}	b^{++}_{29}-H_2O b_{16}-H_3PO_4	b^{++}_{29}	b_{18}			
Delta Da	0.39	0.18	0.55	0.45		-0.02	0.50	0.47 -0.02	0.69	0.70			

Peak 495



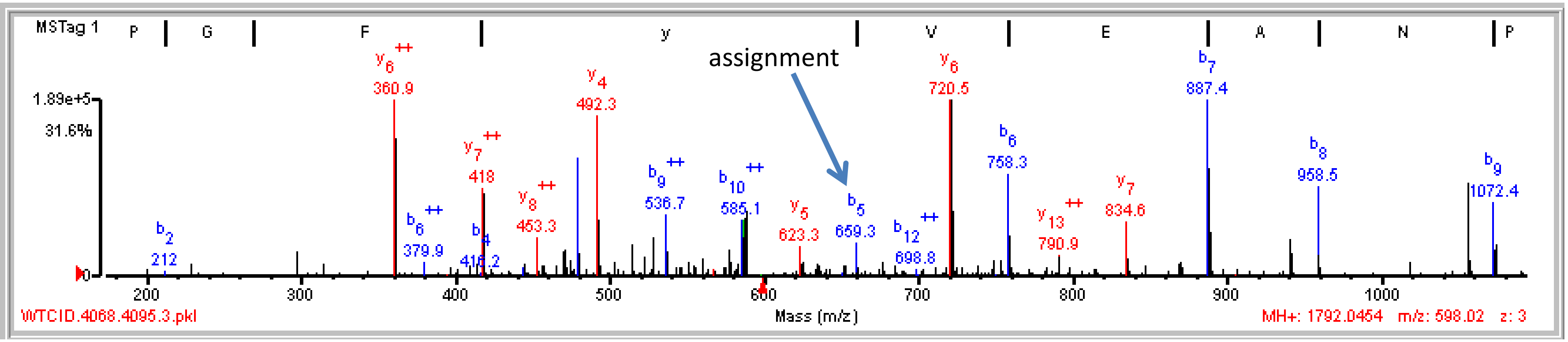
assignment

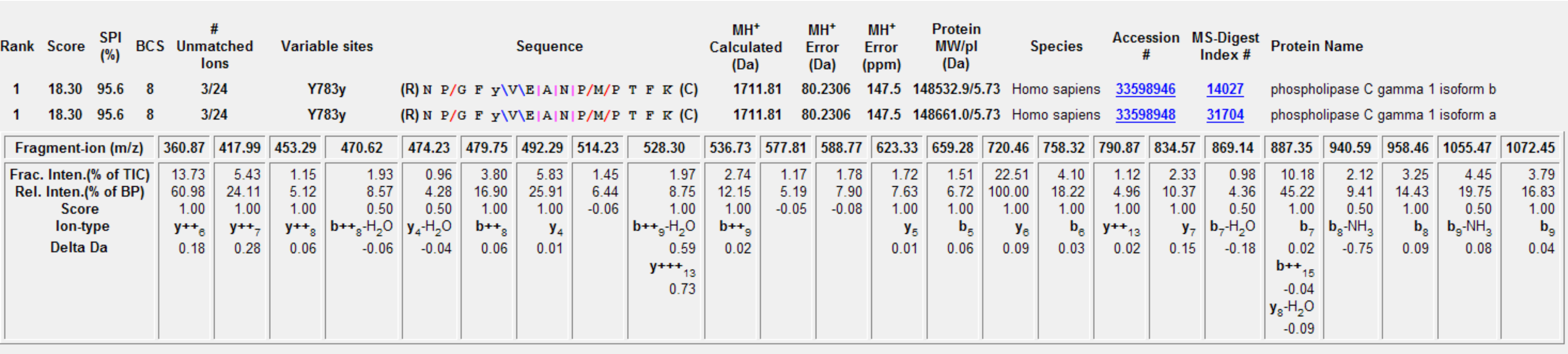


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.38	86.3	10	2/15	Y62y	(K) I Q/N/T/G D|y/Y/D/L/Y/G G\E K (F)	1735.78	81.0718	608.4	68011.2/6.87	Homo sapiens	33356177	4991	protein tyrosine phosphatase, non-receptor type 11

Fragment-ion (m/z)	390.13	553.31	629.43	666.45	770.54	779.20	781.43	787.78	882.24	944.67	1187.55	1359.72	1460.66	1574.66	1575.68
Frac. Inten.(% of TIC)	7.02	8.45	5.74	3.61	5.76	12.31	5.74	5.15	5.92	8.29	4.64	8.90	7.28	3.38	7.82
Rel. Inten.(% of BP)	56.97	68.63	46.60	29.35	46.74	100.00	46.59	41.78	48.07	67.35	37.66	72.29	59.12	27.41	63.47
Score	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00	-0.48	1.00	1.00	1.00	1.00	1.00	-0.63
Ion-type	y_4	y_5	b_6	y_6	$b{++}_{13}$	$y{++}_{13}$-H_2O	y_7	$y{++}_{13}$		y_8	y_9	y_{11}	y_{12}	y_{13}	
Delta Da	-0.07	0.05	0.14	0.10	-0.26	0.40	0.06	-0.03		0.23	0.08	0.21	0.10	0.06	

Peak 496



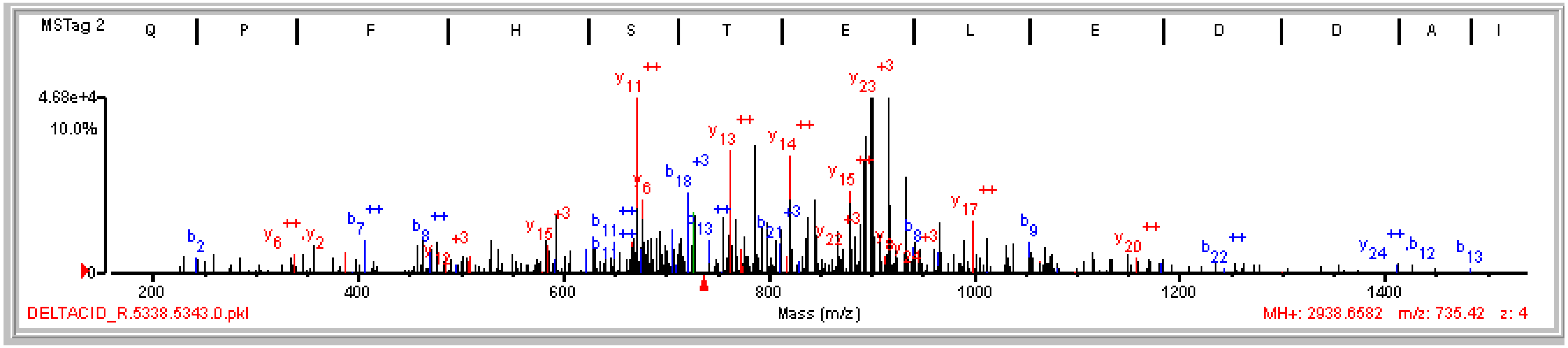


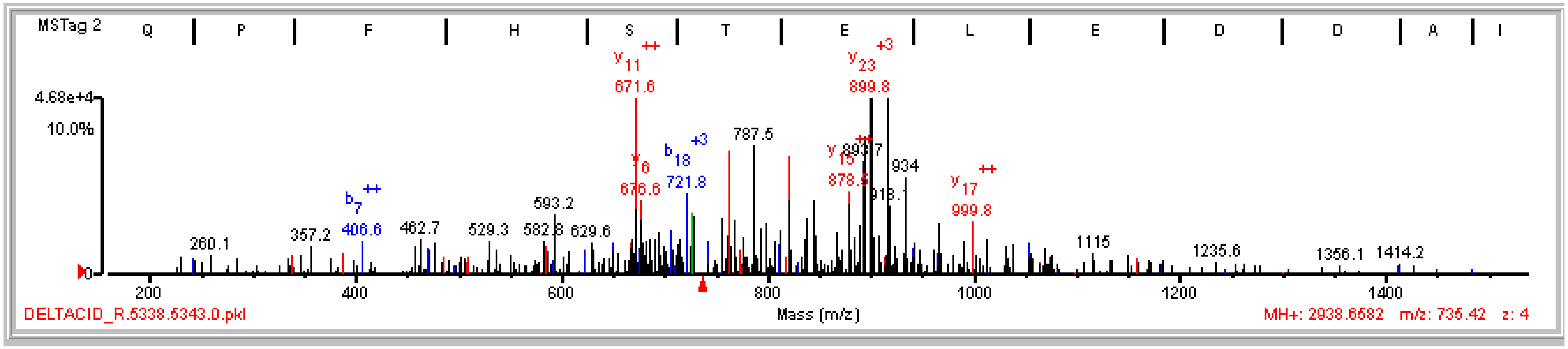
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	18.30	95.6	8	3/24	Y783y	(R) N P/G F y\V\E|A|N|P/M/P T F K (C)	1711.81	80.2306	147.5	148532.9/5.73	Homo sapiens	33598946	14027	phospholipase C gamma 1 isoform b
1	18.30	95.6	8	3/24	Y783y	(R) N P/G F y\V\E|A|N|P/M/P T F K (C)	1711.81	80.2306	147.5	148661.0/5.73	Homo sapiens	33598948	31704	phospholipase C gamma 1 isoform a

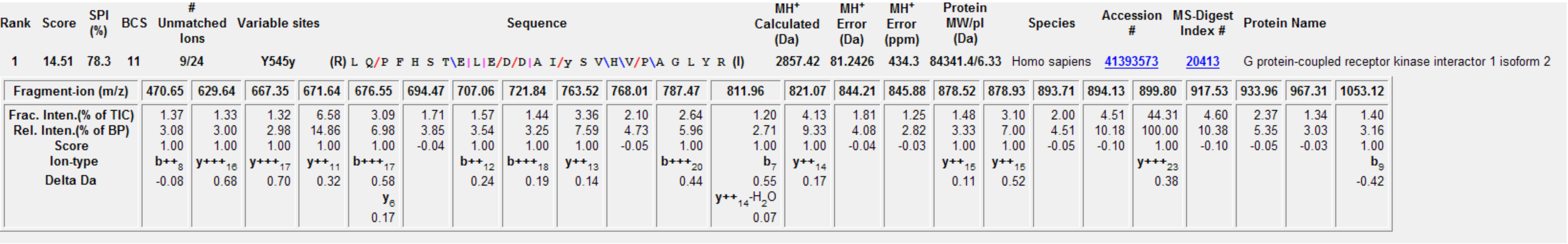
Fragment-ion (m/z)	360.87	417.99	453.29	470.62	474.23	479.75	492.29	514.23	528.30	536.73	577.81	588.77
Frac. Inten.(% of TIC)	13.73	5.43	1.15	1.93	0.96	3.80	5.83	1.45	1.97	2.74	1.17	1.78
Rel. Inten.(% of BP)	60.98	24.11	5.12	8.57	4.28	16.90	25.91	6.44	8.75	12.15	5.19	7.90
Score	1.00	1.00	1.00	0.50	0.50	1.00	1.00	-0.06	1.00	1.00	-0.05	-0.08
Ion-type	y++$_6$	y++$_7$	y++$_8$	b++$_8$-H$_2$O	y$_4$-H$_2$O	b++$_8$	y$_4$		b++$_9$-H$_2$O y+++$_{13}$	b++$_9$		
Delta Da	0.18	0.28	0.06	-0.06	-0.04	0.06	0.01		0.59 0.73	0.02		

Fragment-ion (m/z)	623.33	659.28	720.46	758.32	790.87	834.57	869.14	887.35	940.59	958.46	1055.47	1072.45
Frac. Inten.(% of TIC)	1.72	1.51	22.51	4.10	1.12	2.33	0.98	10.18	2.12	3.25	4.45	3.79
Rel. Inten.(% of BP)	7.63	6.72	100.00	18.22	4.96	10.37	4.36	45.22	9.41	14.43	19.75	16.83
Score	1.00	1.00	1.00	1.00	1.00	1.00	0.50	1.00	0.50	1.00	0.50	1.00
Ion-type	y$_5$	b$_5$	y$_6$	b$_6$	y++$_{13}$	y$_7$	b$_7$-H$_2$O	b$_7$ b++$_{15}$ y$_8$-H$_2$O	b$_8$-NH$_3$	b$_8$	b$_9$-NH$_3$	b$_9$
Delta Da	0.01	0.06	0.09	0.03	0.02	0.15	-0.18	0.02 -0.04 -0.09	-0.75	0.09	0.08	0.04

Peak 497





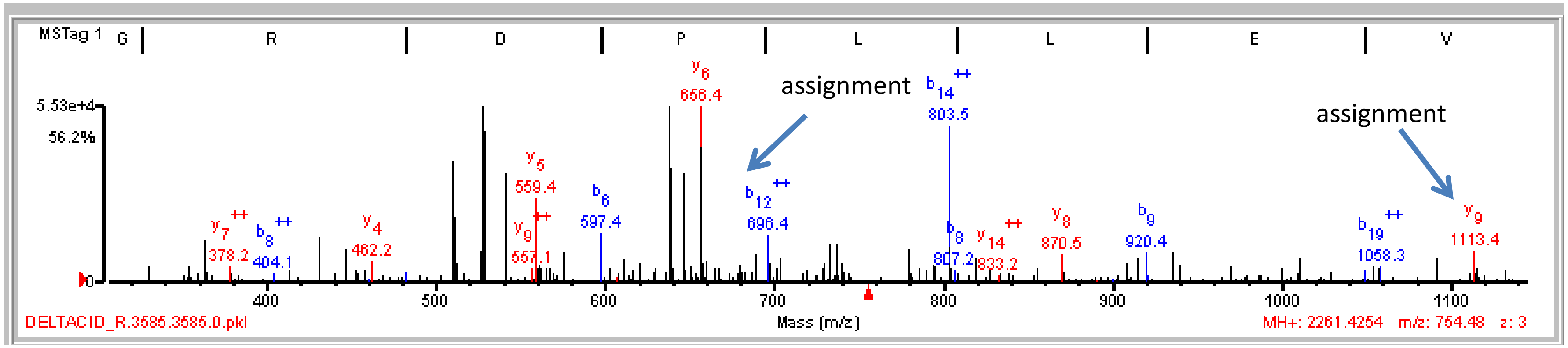


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.51	78.3	11	9/24	Y545y	(R) L Q/P F H S T\E|L|E/D/D|A I/y S V\H\V/P\A G L Y R (I)	2857.42	81.2426	434.3	84341.4/6.33	Homo sapiens	41393573	20413	G protein-coupled receptor kinase interactor 1 isoform 2

Fragment-ion (m/z)	470.65	629.64	667.35	671.64	676.55	694.47	707.06	721.84	763.52	768.01	787.47	811.96
Frac. Inten.(% of TIC)	1.37	1.33	1.32	6.58	3.09	1.71	1.57	1.44	3.36	2.10	2.64	1.20
Rel. Inten.(% of BP)	3.08	3.00	2.98	14.86	6.98	3.85	3.54	3.25	7.59	4.73	5.96	2.71
Score	1.00	1.00	1.00	1.00	1.00	-0.04	1.00	1.00	1.00	-0.05	1.00	1.00
Ion-type	$b{++}_{8}$	$y{+++}_{16}$	$y{+++}_{17}$	$y{++}_{11}$	$b{+++}_{17}$		$b{++}_{12}$	$b{+++}_{18}$	$y{++}_{13}$		$b{+++}_{20}$	b_{7}
Delta Da	-0.08	0.68	0.70	0.32	0.58		0.24	0.19	0.14		0.44	0.55
					y_{6}							$y{++}_{14}\text{-}H_2O$
					0.17							0.07

Fragment-ion (m/z)	821.07	844.21	845.88	878.52	878.93	893.71	894.13	899.80	917.53	933.96	967.31	1053.12
Frac. Inten.(% of TIC)	4.13	1.81	1.25	1.48	3.10	2.00	4.51	44.31	4.60	2.37	1.34	1.40
Rel. Inten.(% of BP)	9.33	4.08	2.82	3.33	7.00	4.51	10.18	100.00	10.38	5.35	3.03	3.16
Score	1.00	-0.04	-0.03	1.00	1.00	-0.05	-0.10	1.00	-0.10	-0.05	-0.03	1.00
Ion-type	$y{++}_{14}$			$y{++}_{15}$	$y{++}_{15}$			$y{+++}_{23}$				b_{9}
Delta Da	0.17			0.11	0.52			0.38				-0.42

Peak 498



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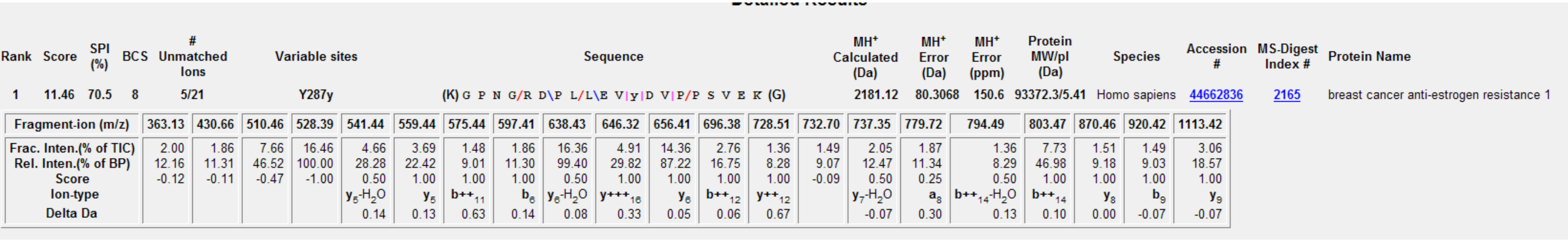
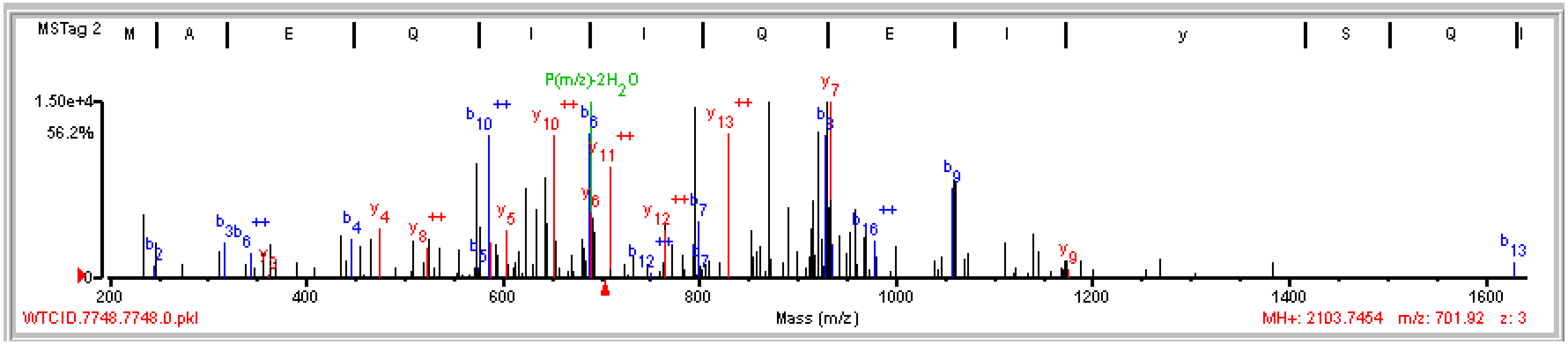
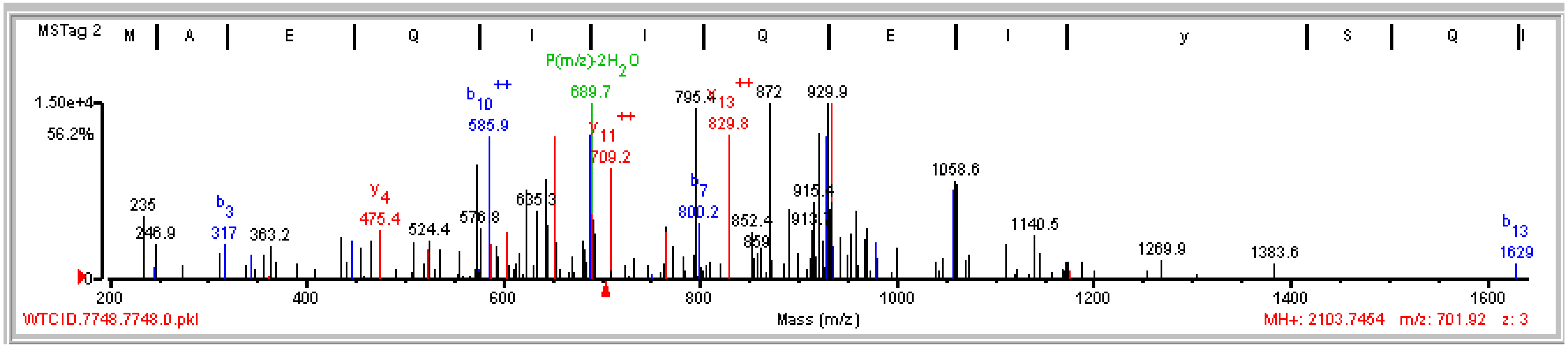


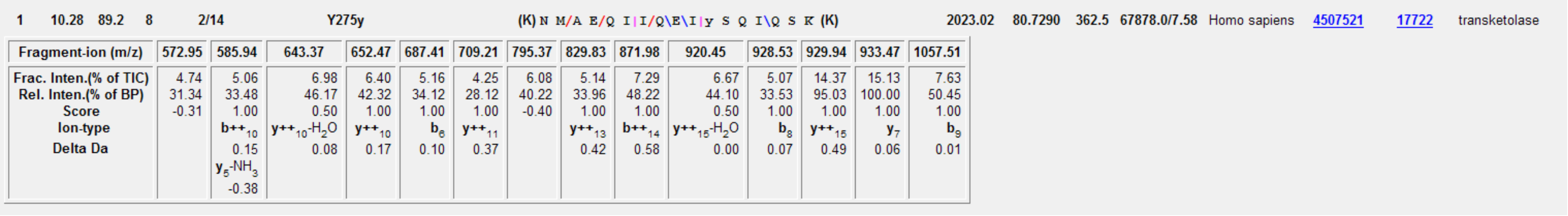
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.46	70.5	8	5/21	Y287y	(K) G P N G/R D\P L/L\E V|y|D V|P/P S V E K (G)	2181.12	80.3068	150.6	93372.3/5.41	Homo sapiens	44662836	2165	breast cancer anti-estrogen resistance 1

Fragment-ion (m/z)	363.13	430.66	510.46	528.39	541.44	559.44	575.44	597.41	638.43	646.32	656.41	696.38	728.51	732.70	737.35	779.72	794.49	803.47	870.46	920.42	1113.42
Frac. Inten.(% of TIC)	2.00	1.86	7.66	16.46	4.66	3.69	1.48	1.86	16.36	4.91	14.36	2.76	1.36	1.49	2.05	1.87	1.36	7.73	1.51	1.49	3.06
Rel. Inten.(% of BP)	12.16	11.31	46.52	100.00	28.28	22.42	9.01	11.30	99.40	29.82	87.22	16.75	8.28	9.07	12.47	11.34	8.29	46.98	9.18	9.03	18.57
Score	-0.12	-0.11	-0.47	-1.00	0.50	1.00	1.00	1.00	0.50	1.00	1.00	1.00	1.00	-0.09	0.50	0.25	0.50	1.00	1.00	1.00	1.00
Ion-type					y_5-H_2O	y_5	$b{+}{+}_{11}$	b_6	y_6-H_2O	$y{+}{+}{+}_{16}$	y_6	$b{+}{+}_{12}$	$y{+}{+}_{12}$		y_7-H_2O	a_8	$b{+}{+}_{14}$-H_2O	$b{+}{+}_{14}$	y_8	b_9	y_9
Delta Da					0.14	0.13	0.63	0.14	0.08	0.33	0.05	0.06	0.67		-0.07	0.30	0.13	0.10	0.00	-0.07	-0.07

Peak 499



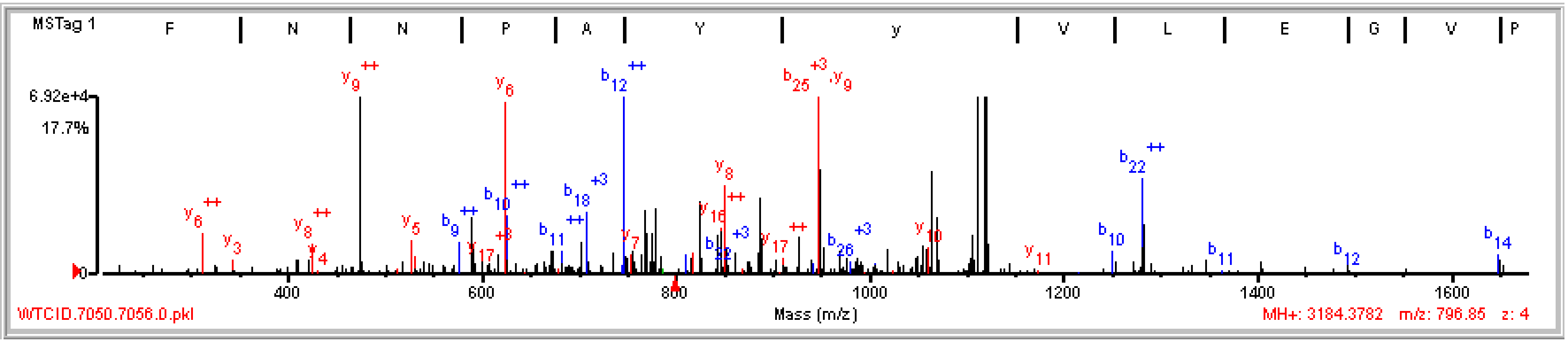


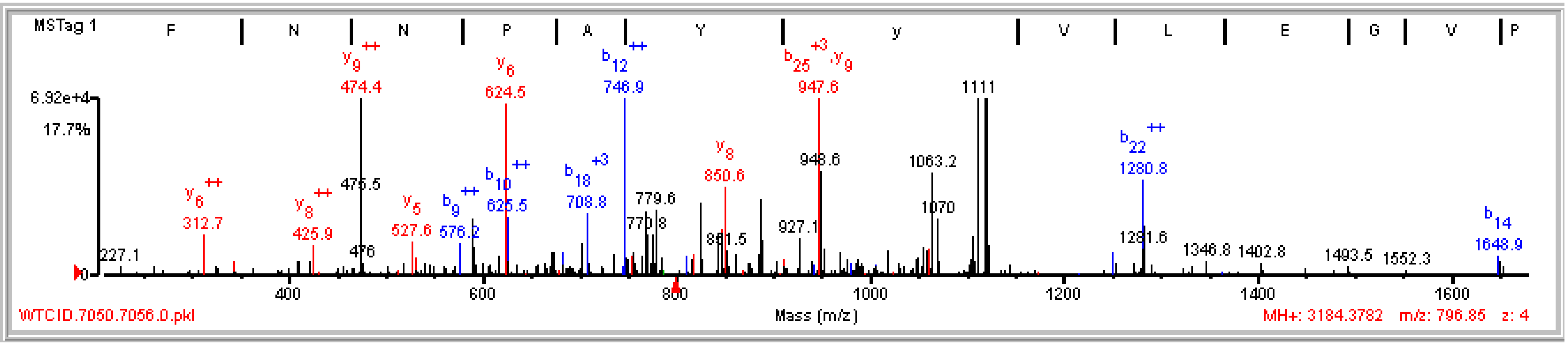


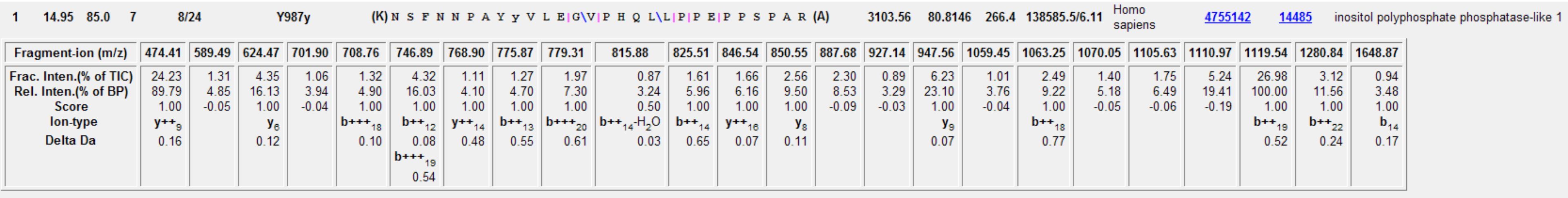
1 10.28 89.2 8 2/14 Y275y (K) N M/A E/Q I|I/Q\E\I|y S Q I\Q S K (K) 2023.02 80.7290 362.5 67878.0/7.58 Homo sapiens 4507521 17722 transketolase

Fragment-ion (m/z)	572.95	585.94	643.37	652.47	687.41	709.21	795.37	829.83	871.98	920.45	928.53	929.94	933.47	1057.51
Frac. Inten.(% of TIC)	4.74	5.06	6.98	6.40	5.16	4.25	6.08	5.14	7.29	6.67	5.07	14.37	15.13	7.63
Rel. Inten.(% of BP)	31.34	33.48	46.17	42.32	34.12	28.12	40.22	33.96	48.22	44.10	33.53	95.03	100.00	50.45
Score	-0.31	1.00	0.50	1.00	1.00	1.00	-0.40	1.00	1.00	0.50	1.00	1.00	1.00	1.00
Ion-type		b++$_{10}$ y$_5$-NH$_3$	y++$_{10}$-H$_2$O	y++$_{10}$	b$_6$	y++$_{11}$		y++$_{13}$	b++$_{14}$	y++$_{15}$-H$_2$O	b$_8$	y++$_{15}$	y$_7$	b$_9$
Delta Da		0.15 -0.38	0.08	0.17	0.10	0.37		0.42	0.58	0.00	0.07	0.49	0.06	0.01

Peak 500





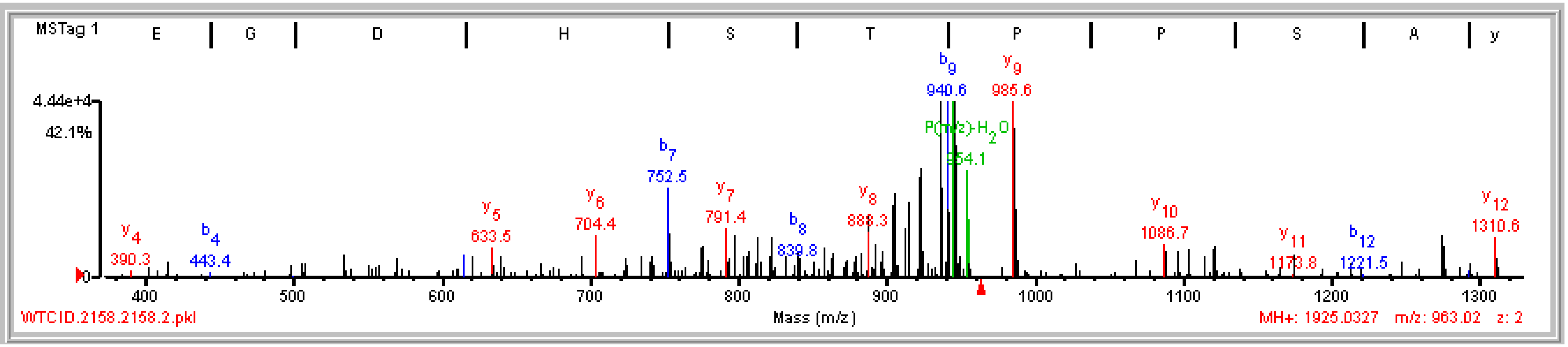


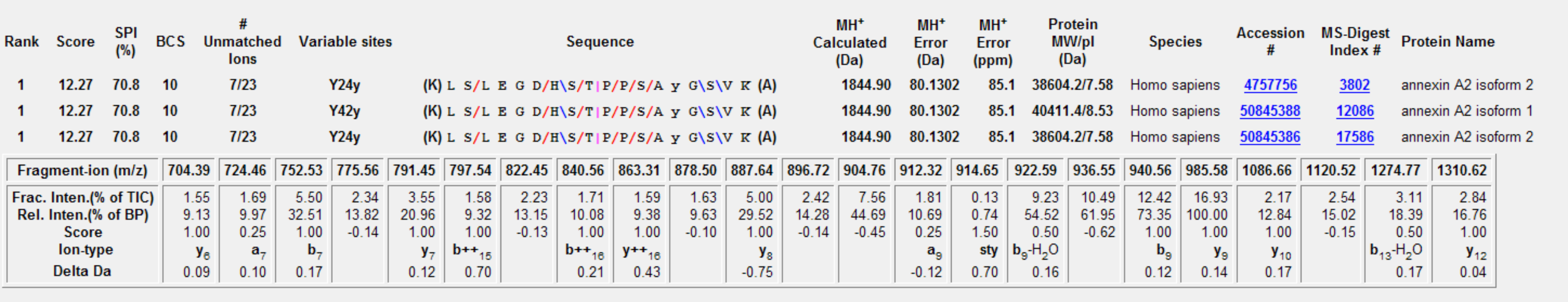
1 14.95 85.0 7 8/24 Y987y (K) N S F N N P A Y y V L E|G\V|P H Q L\L|P|P E|P P S P A R (A) 3103.56 80.8146 266.4 138585.5/6.11 Homo sapiens 4755142 14485 inositol polyphosphate phosphatase-like 1

Fragment-ion (m/z)	474.41	589.49	624.47	701.90	708.76	746.89	768.90	775.87	779.31	815.88	825.51	846.54
Frac. Inten.(% of TIC)	24.23	1.31	4.35	1.06	1.32	4.32	1.11	1.27	1.97	0.87	1.61	1.66
Rel. Inten.(% of BP)	89.79	4.85	16.13	3.94	4.90	16.03	4.10	4.70	7.30	3.24	5.96	6.16
Score	1.00	-0.05	1.00	-0.04	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ion-type	y++$_{9}$		y$_{6}$		b+++$_{18}$	b++$_{12}$ b+++$_{19}$	y++$_{14}$	b++$_{13}$	b+++$_{20}$	b++$_{14}$-H_2O	b++$_{14}$	y++$_{16}$
Delta Da	0.16		0.12		0.10	0.08 0.54	0.48	0.55	0.61	0.03	0.65	0.07

Fragment-ion (m/z)	850.55	887.68	927.14	947.56	1059.45	1063.25	1070.05	1105.63	1110.97	1119.54	1280.84	1648.87
Frac. Inten.(% of TIC)	2.56	2.30	0.89	6.23	1.01	2.49	1.40	1.75	5.24	26.98	3.12	0.94
Rel. Inten.(% of BP)	9.50	8.53	3.29	23.10	3.76	9.22	5.18	6.49	19.41	100.00	11.56	3.48
Score	1.00	-0.09	-0.03	1.00	-0.04	1.00	-0.05	-0.06	-0.19	1.00	1.00	1.00
Ion-type	y$_{8}$			y$_{9}$		b++$_{18}$				b++$_{19}$	b++$_{22}$	b$_{14}$
Delta Da	0.11			0.07		0.77				0.52	0.24	0.17

Peak 503

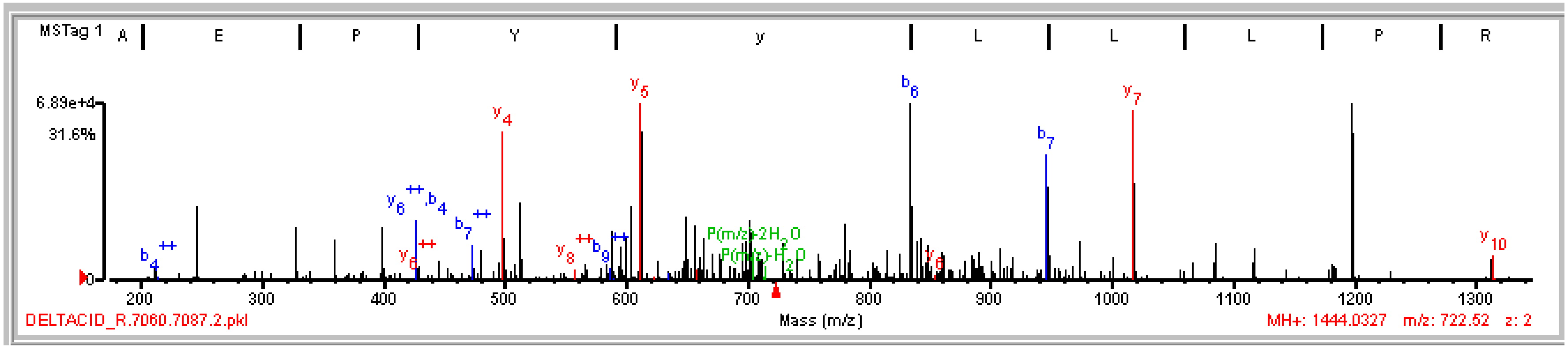


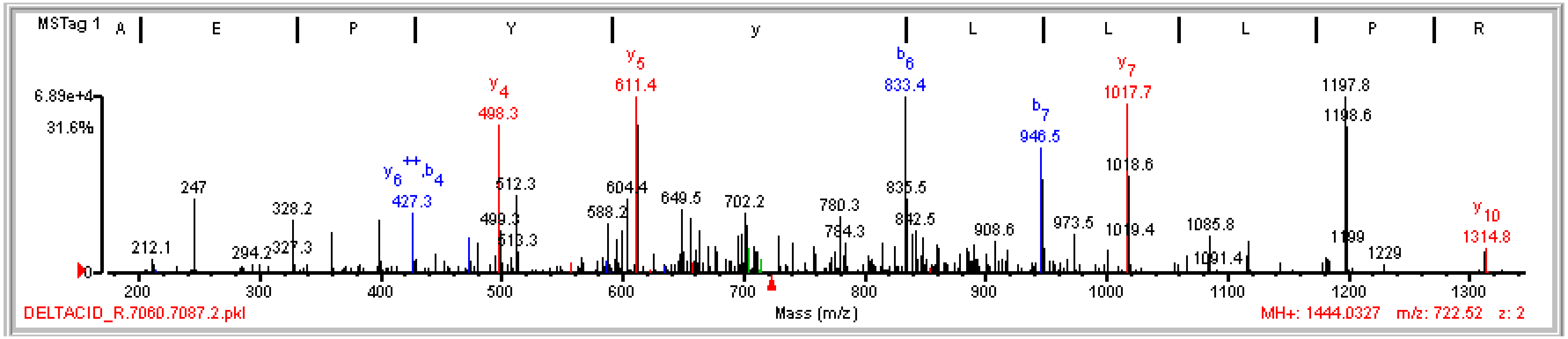


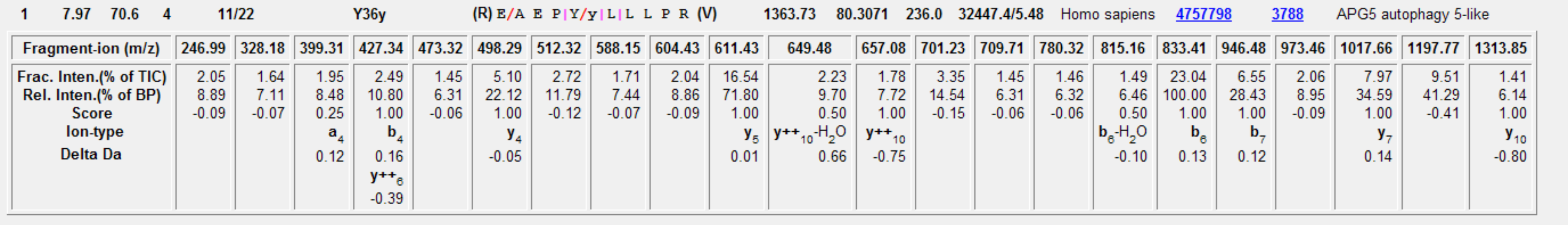
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.27	70.8	10	7/23	Y24y	(K) L S/L E G D/H\S/T|P/P/S/A y G\S\V K (A)	1844.90	80.1302	85.1	38604.2/7.58	Homo sapiens	4757756	3802	annexin A2 isoform 2
1	12.27	70.8	10	7/23	Y42y	(K) L S/L E G D/H\S/T|P/P/S/A y G\S\V K (A)	1844.90	80.1302	85.1	40411.4/8.53	Homo sapiens	50845388	12086	annexin A2 isoform 1
1	12.27	70.8	10	7/23	Y24y	(K) L S/L E G D/H\S/T|P/P/S/A y G\S\V K (A)	1844.90	80.1302	85.1	38604.2/7.58	Homo sapiens	50845386	17586	annexin A2 isoform 2

Fragment-ion (m/z)	704.39	724.46	752.53	775.56	791.45	797.54	822.45	840.56	863.31	878.50	887.64	896.72	904.76	912.32	914.65	922.59	936.55	940.56	985.58	1086.66	1120.52	1274.77	1310.62
Frac. Inten.(% of TIC)	1.55	1.69	5.50	2.34	3.55	1.58	2.23	1.71	1.59	1.63	5.00	2.42	7.56	1.81	0.13	9.23	10.49	12.42	16.93	2.17	2.54	3.11	2.84
Rel. Inten.(% of BP)	9.13	9.97	32.51	13.82	20.96	9.32	13.15	10.08	9.38	9.63	29.52	14.28	44.69	10.69	0.74	54.52	61.95	73.35	100.00	12.84	15.02	18.39	16.76
Score	1.00	0.25	1.00	-0.14	1.00	1.00	-0.13	1.00	1.00	-0.10	1.00	-0.14	-0.45	0.25	1.50	0.50	-0.62	1.00	1.00	1.00	-0.15	0.50	1.00
Ion-type	y_6	a_7	b_7		y_7	$b{++}_{15}$		$b{++}_{16}$	$y{++}_{16}$		y_8			a_9	sty	b_9-H_2O		b_9	y_9	y_{10}		b_{13}-H_2O	y_{12}
Delta Da	0.09	0.10	0.17		0.12	0.70		0.21	0.43		-0.75			-0.12	0.70	0.16		0.12	0.14	0.17		0.17	0.04

Peak 504





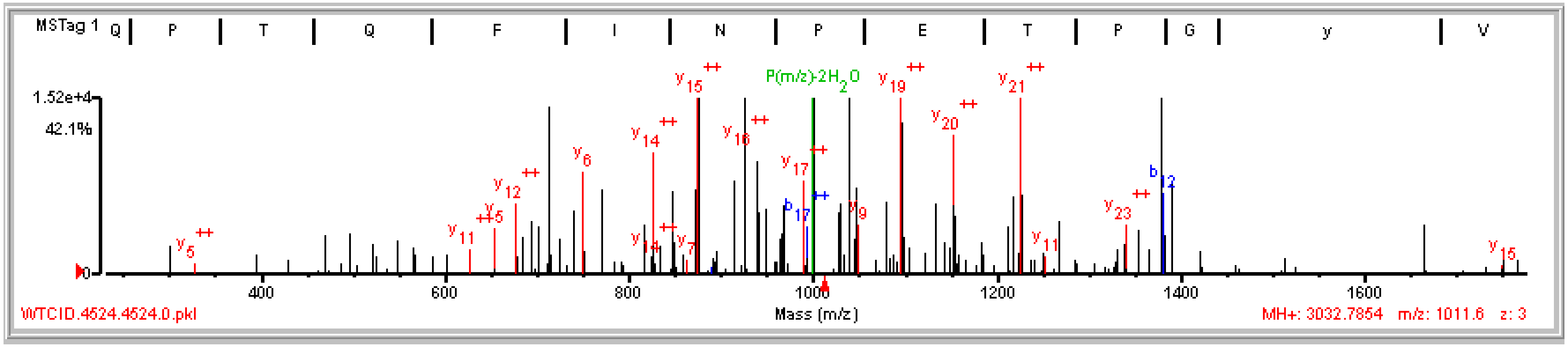


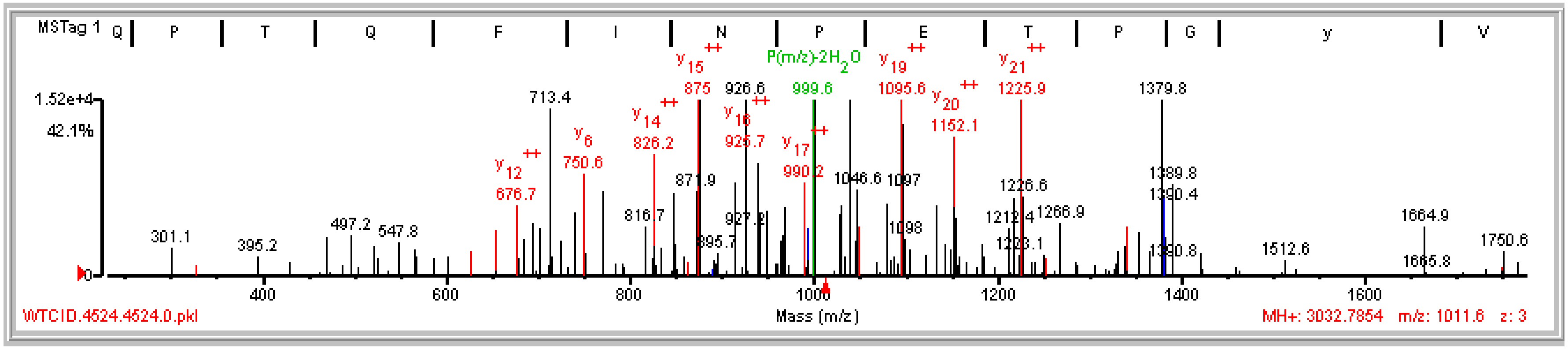
1 7.97 70.6 4 11/22 Y36y (R) E/A E P|Y/y|L|L L P R (V) 1363.73 80.3071 236.0 32447.4/5.48 Homo sapiens 4757798 3788 APG5 autophagy 5-like

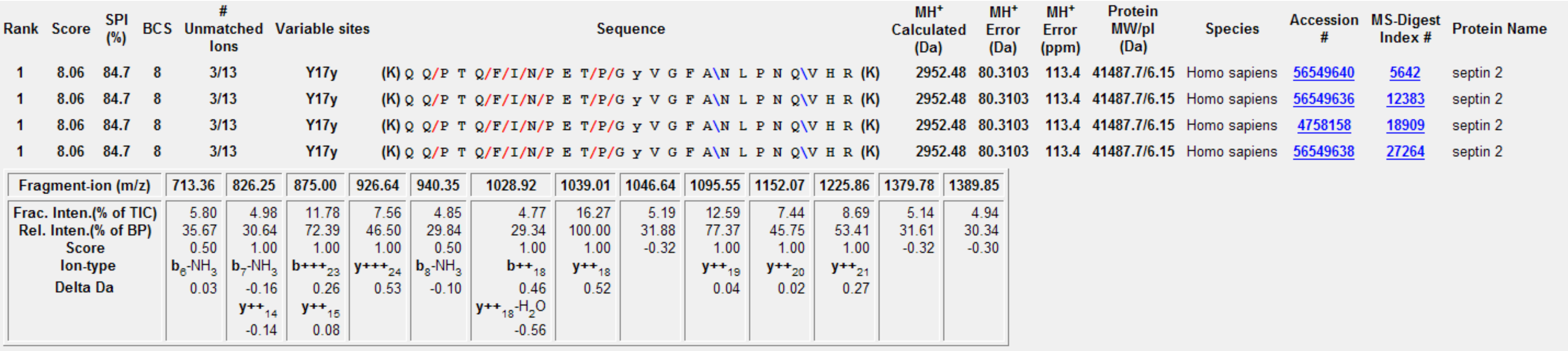
Fragment-ion (m/z)	246.99	328.18	399.31	427.34	473.32	498.29	512.32	588.15	604.43	611.43	649.48
Frac. Inten.(% of TIC)	2.05	1.64	1.95	2.49	1.45	5.10	2.72	1.71	2.04	16.54	2.23
Rel. Inten.(% of BP)	8.89	7.11	8.48	10.80	6.31	22.12	11.79	7.44	8.86	71.80	9.70
Score	-0.09	-0.07	0.25	1.00	-0.06	1.00	-0.12	-0.07	-0.09	1.00	0.50
Ion-type			a_4	b_4		y_4				y_5	y^{++}_{10}-H_2O
Delta Da			0.12	0.16		-0.05				0.01	0.66
				y^{++}_6							
				-0.39							

Fragment-ion (m/z)	657.08	701.23	709.71	780.32	815.16	833.41	946.48	973.46	1017.66	1197.77	1313.85
Frac. Inten.(% of TIC)	1.78	3.35	1.45	1.46	1.49	23.04	6.55	2.06	7.97	9.51	1.41
Rel. Inten.(% of BP)	7.72	14.54	6.31	6.32	6.46	100.00	28.43	8.95	34.59	41.29	6.14
Score	1.00	-0.15	-0.06	-0.06	0.50	1.00	1.00	-0.09	1.00	-0.41	1.00
Ion-type	y^{++}_{10}				b_6-H_2O	b_6	b_7		y_7		y_{10}
Delta Da	-0.75				-0.10	0.13	0.12		0.14		-0.80

Peak 505



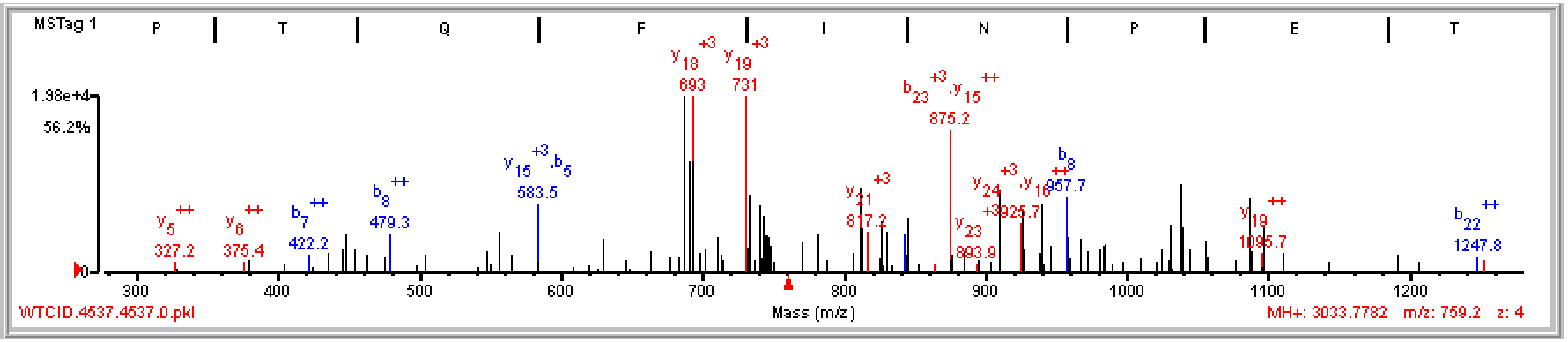


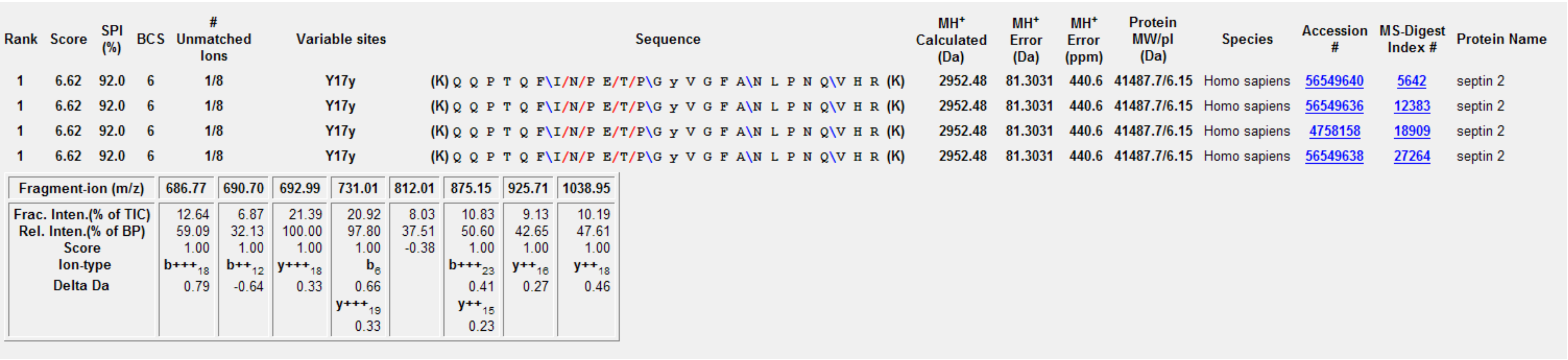


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH^+ Calculated (Da)	MH^+ Error (Da)	MH^+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	8.06	84.7	8	3/13	Y17y	(K) Q Q/P T Q/F/I/N/P E T/P/G y V G F A\N L P N Q\V H R (K)	2952.48	80.3103	113.4	41487.7/6.15	Homo sapiens	56549640	5642	septin 2
1	8.06	84.7	8	3/13	Y17y	(K) Q Q/P T Q/F/I/N/P E T/P/G y V G F A\N L P N Q\V H R (K)	2952.48	80.3103	113.4	41487.7/6.15	Homo sapiens	56549636	12383	septin 2
1	8.06	84.7	8	3/13	Y17y	(K) Q Q/P T Q/F/I/N/P E T/P/G y V G F A\N L P N Q\V H R (K)	2952.48	80.3103	113.4	41487.7/6.15	Homo sapiens	4758158	18909	septin 2
1	8.06	84.7	8	3/13	Y17y	(K) Q Q/P T Q/F/I/N/P E T/P/G y V G F A\N L P N Q\V H R (K)	2952.48	80.3103	113.4	41487.7/6.15	Homo sapiens	56549638	27264	septin 2

Fragment-ion (m/z)	713.36	826.25	875.00	926.64	940.35	1028.92	1039.01	1046.64	1095.55	1152.07	1225.86	1379.78	1389.85
Frac. Inten.(% of TIC)	5.80	4.98	11.78	7.56	4.85	4.77	16.27	5.19	12.59	7.44	8.69	5.14	4.94
Rel. Inten.(% of BP)	35.67	30.64	72.39	46.50	29.84	29.34	100.00	31.88	77.37	45.75	53.41	31.61	30.34
Score	0.50	1.00	1.00	1.00	0.50	1.00	1.00	-0.32	1.00	1.00	1.00	-0.32	-0.30
Ion-type	b_6-NH_3	b_7-NH_3	$b{+}{+}{+}_{23}$	$y{+}{+}{+}_{24}$	b_8-NH_3	$b{+}{+}_{18}$	$y{+}{+}_{18}$		$y{+}{+}_{19}$	$y{+}{+}_{20}$	$y{+}{+}_{21}$		
Delta Da	0.03	-0.16	0.26	0.53	-0.10	0.46	0.52		0.04	0.02	0.27		
		$y{+}{+}_{14}$	$y{+}{+}_{15}$			$y{+}{+}_{18}$-H_2O							
		-0.14	0.08			-0.56							

Peak 506

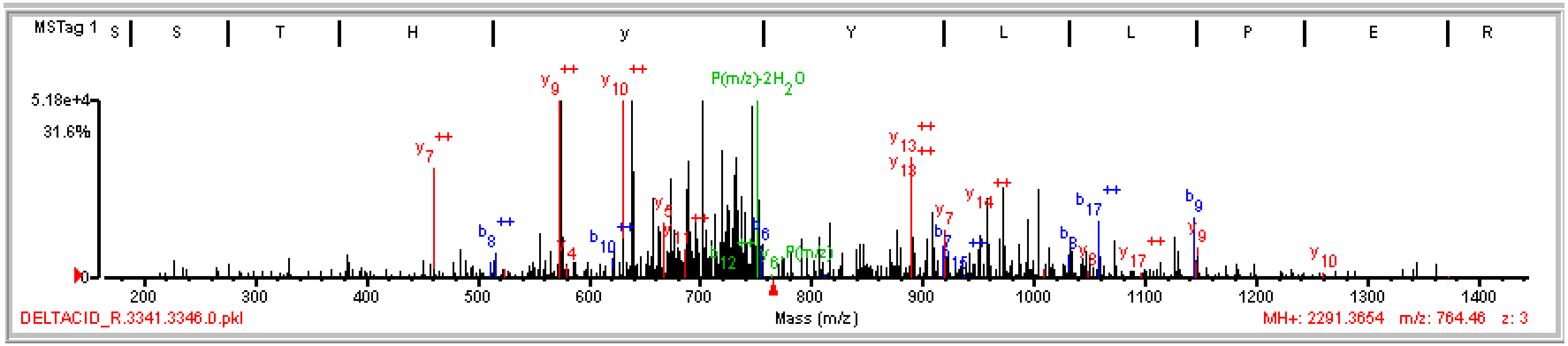


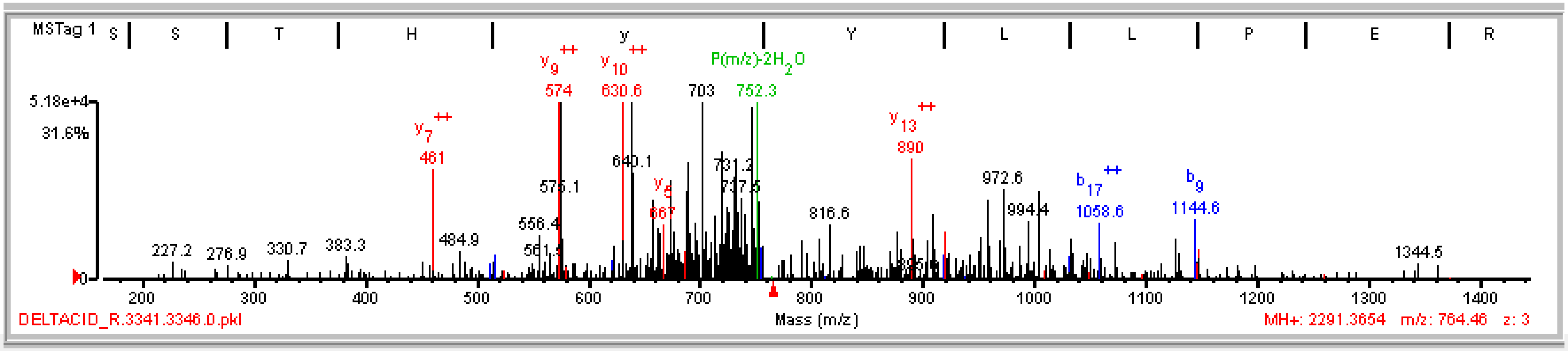


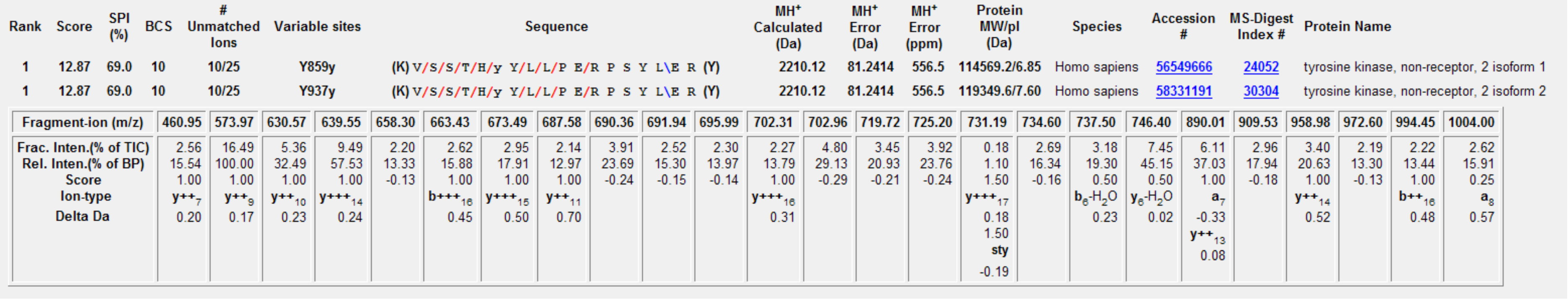
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	6.62	92.0	6	1/8	Y17y	(K) Q Q P T Q F\I/N/P E/T/P\G y V G F A\N L P N Q\V H R (K)	2952.48	81.3031	440.6	41487.7/6.15	Homo sapiens	56549640	5642	septin 2
1	6.62	92.0	6	1/8	Y17y	(K) Q Q P T Q F\I/N/P E/T/P\G y V G F A\N L P N Q\V H R (K)	2952.48	81.3031	440.6	41487.7/6.15	Homo sapiens	56549636	12383	septin 2
1	6.62	92.0	6	1/8	Y17y	(K) Q Q P T Q F\I/N/P E/T/P\G y V G F A\N L P N Q\V H R (K)	2952.48	81.3031	440.6	41487.7/6.15	Homo sapiens	4758158	18909	septin 2
1	6.62	92.0	6	1/8	Y17y	(K) Q Q P T Q F\I/N/P E/T/P\G y V G F A\N L P N Q\V H R (K)	2952.48	81.3031	440.6	41487.7/6.15	Homo sapiens	56549638	27264	septin 2

Fragment-ion (m/z)	686.77	690.70	692.99	731.01	812.01	875.15	925.71	1038.95
Frac. Inten.(% of TIC)	12.64	6.87	21.39	20.92	8.03	10.83	9.13	10.19
Rel. Inten.(% of BP)	59.09	32.13	100.00	97.80	37.51	50.60	42.65	47.61
Score	1.00	1.00	1.00	1.00	-0.38	1.00	1.00	1.00
Ion-type	b^{+++}_{18}	b^{++}_{12}	y^{+++}_{18}	b_{6}		b^{+++}_{23}	y^{++}_{16}	y^{++}_{18}
Delta Da	0.79	-0.64	0.33	0.66		0.41	0.27	0.46
				y^{+++}_{19}		y^{++}_{15}		
				0.33		0.23		

Peak 507





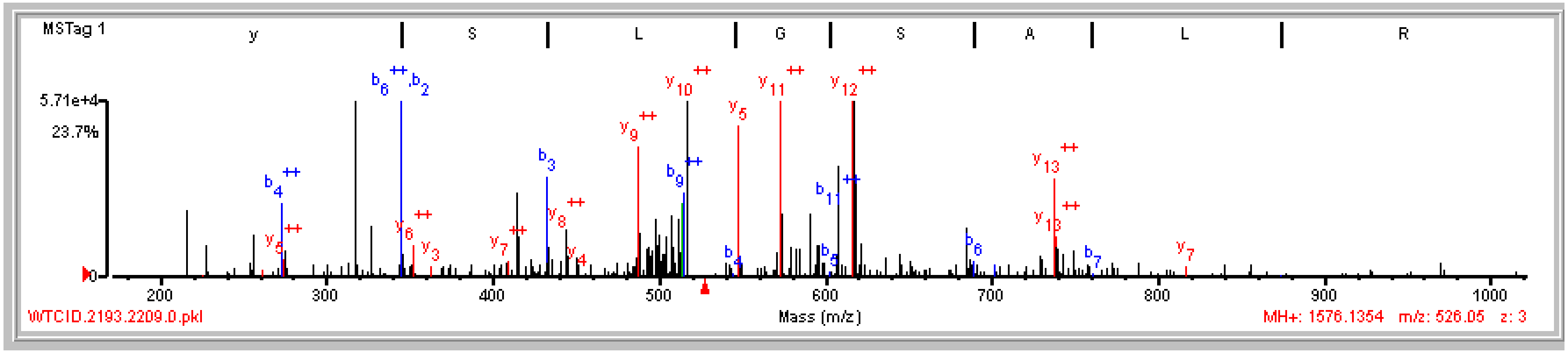


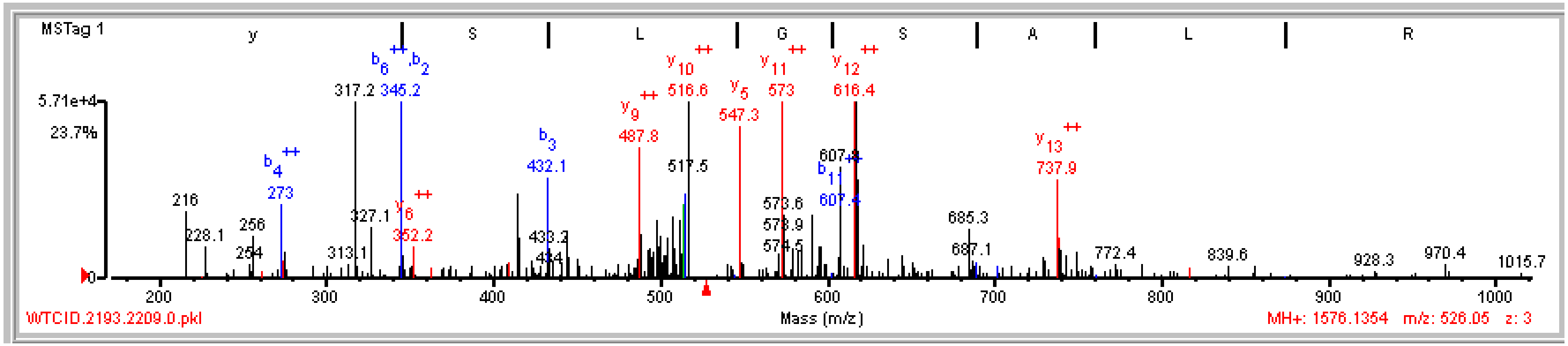
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH$^+$ Calculated (Da)	MH$^+$ Error (Da)	MH$^+$ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	12.87	69.0	10	10/25	Y859y	(K) V/S/S/T/H/y Y/L/L/P E/R P S Y L\E R (Y)	2210.12	81.2414	556.5	114569.2/6.85	Homo sapiens	56549666	24052	tyrosine kinase, non-receptor, 2 isoform 1
1	12.87	69.0	10	10/25	Y937y	(K) V/S/S/T/H/y Y/L/L/P E/R P S Y L\E R (Y)	2210.12	81.2414	556.5	119349.6/7.60	Homo sapiens	58331191	30304	tyrosine kinase, non-receptor, 2 isoform 2

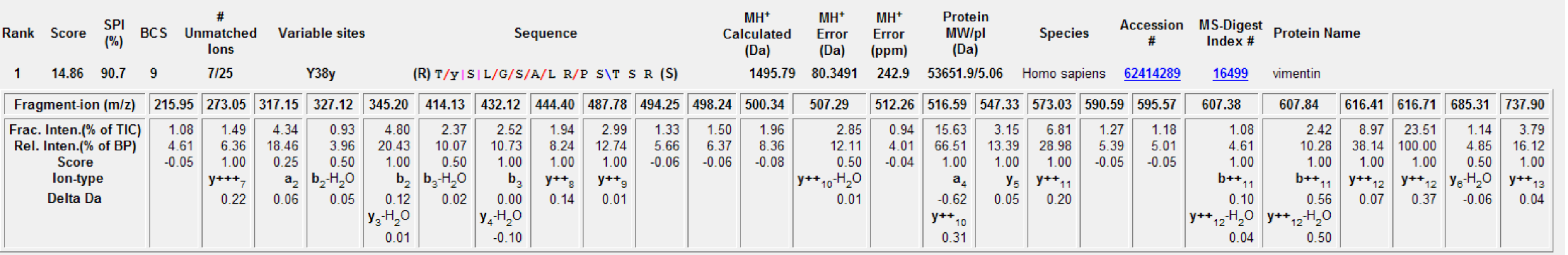
Fragment-ion (m/z)	460.95	573.97	630.57	639.55	658.30	663.43	673.49	687.58	690.36	691.94	695.99	702.31
Frac. Inten.(% of TIC)	2.56	16.49	5.36	9.49	2.20	2.62	2.95	2.14	3.91	2.52	2.30	2.27
Rel. Inten.(% of BP)	15.54	100.00	32.49	57.53	13.33	15.88	17.91	12.97	23.69	15.30	13.97	13.79
Score	1.00	1.00	1.00	1.00	-0.13	1.00	1.00	1.00	-0.24	-0.15	-0.14	1.00
Ion-type	y++_{7}	y++_{9}	y++_{10}	y+++_{14}		b+++_{16}	y+++_{15}	y++_{11}				y+++_{16}
Delta Da	0.20	0.17	0.23	0.24		0.45	0.50	0.70				0.31

Fragment-ion (m/z)	702.96	719.72	725.20	731.19	734.60	737.50	746.40	890.01	909.53	958.98	972.60	994.45	1004.00
Frac. Inten.(% of TIC)	4.80	3.45	3.92	0.18	2.69	3.18	7.45	6.11	2.96	3.40	2.19	2.22	2.62
Rel. Inten.(% of BP)	29.13	20.93	23.76	1.10	16.34	19.30	45.15	37.03	17.94	20.63	13.30	13.44	15.91
Score	-0.29	-0.21	-0.24	1.50	-0.16	0.50	0.50	1.00	-0.18	1.00	-0.13	1.00	0.25
Ion-type				y+++_{17}		b_6-H_2O	y_6-H_2O	a_7		y++_{14}		b++_{16}	a_8
Delta Da				0.18 1.50 sty -0.19		0.23	0.02	-0.33 y++_{13} 0.08		0.52		0.48	0.57

Peak 509



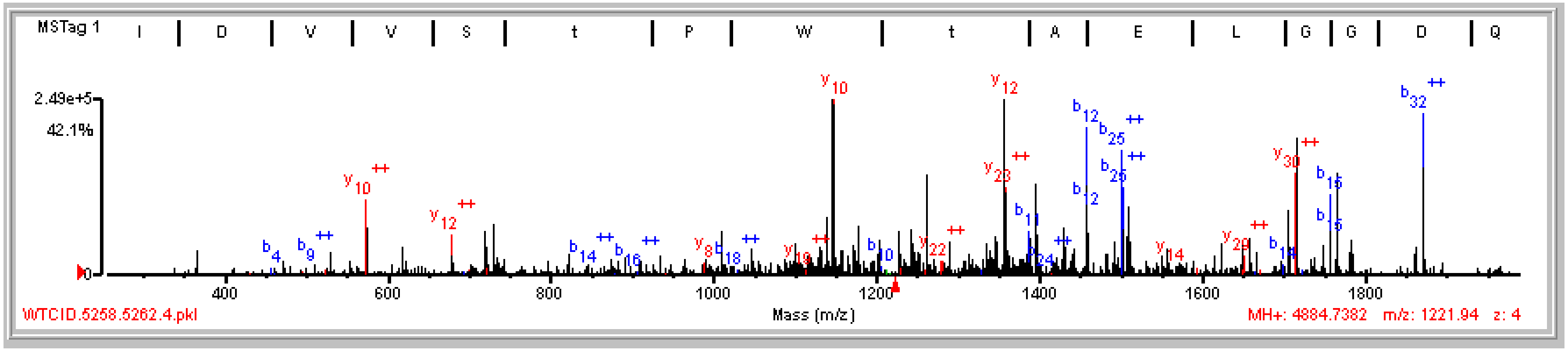


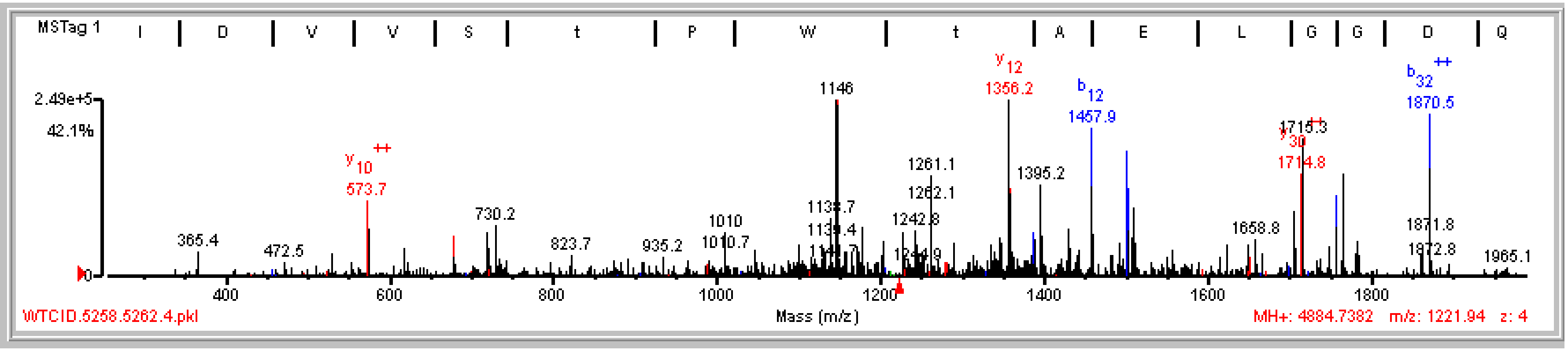


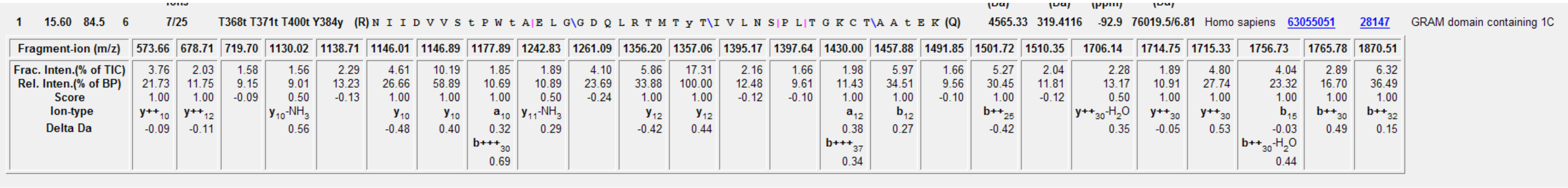
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	14.86	90.7	9	7/25	Y38y	(R) T/y|S|L/G/S/A/L R/P S\T S R (S)	1495.79	80.3491	242.9	53651.9/5.06	Homo sapiens	62414289	16499	vimentin

Fragment-ion (m/z)	215.95	273.05	317.15	327.12	345.20	414.13	432.12	444.40	487.78	494.25	498.24	500.34	507.29	512.26	516.59	547.33	573.03	590.59	595.57	607.38	607.84	616.41	616.71	685.31	737.90
Frac. Inten.(% of TIC)	1.08	1.49	4.34	0.93	4.80	2.37	2.52	1.94	2.99	1.33	1.50	1.96	2.85	0.94	15.63	3.15	6.81	1.27	1.18	1.08	2.42	8.97	23.51	1.14	3.79
Rel. Inten.(% of BP)	4.61	6.36	18.46	3.96	20.43	10.07	10.73	8.24	12.74	5.66	6.37	8.36	12.11	4.01	66.51	13.39	28.98	5.39	5.01	4.61	10.28	38.14	100.00	4.85	16.12
Score	-0.05	1.00	0.25	0.50	1.00	0.50	1.00	1.00	1.00	-0.06	-0.06	-0.08	0.50	-0.04	1.00	1.00	1.00	-0.05	-0.05	1.00	1.00	1.00	1.00	0.50	1.00
Ion-type		y+++$_7$	a$_2$	b$_2$-H$_2$O	b$_2$ y$_3$-H$_2$O	b$_3$-H$_2$O	b$_3$ y$_4$-H$_2$O	y++$_8$	y++$_9$				y++$_{10}$-H$_2$O		a$_4$ y++$_{10}$	y$_5$	y++$_{11}$			b++$_{11}$ y++$_{12}$-H$_2$O	b++$_{11}$ y++$_{12}$-H$_2$O	y++$_{12}$	y++$_{12}$	y$_6$-H$_2$O	y++$_{13}$
Delta Da		0.22	0.06	0.05	0.12 0.01	0.02	0.00 -0.10	0.14	0.01				0.01		-0.62 0.31	0.05	0.20			0.10 0.04	0.56 0.50	0.07	0.37	-0.06	0.04

Peak 510



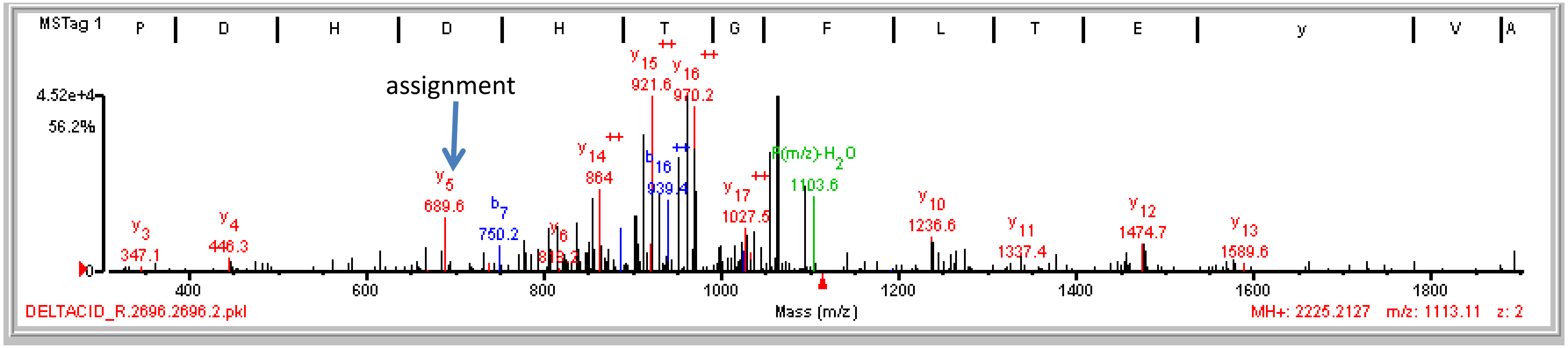


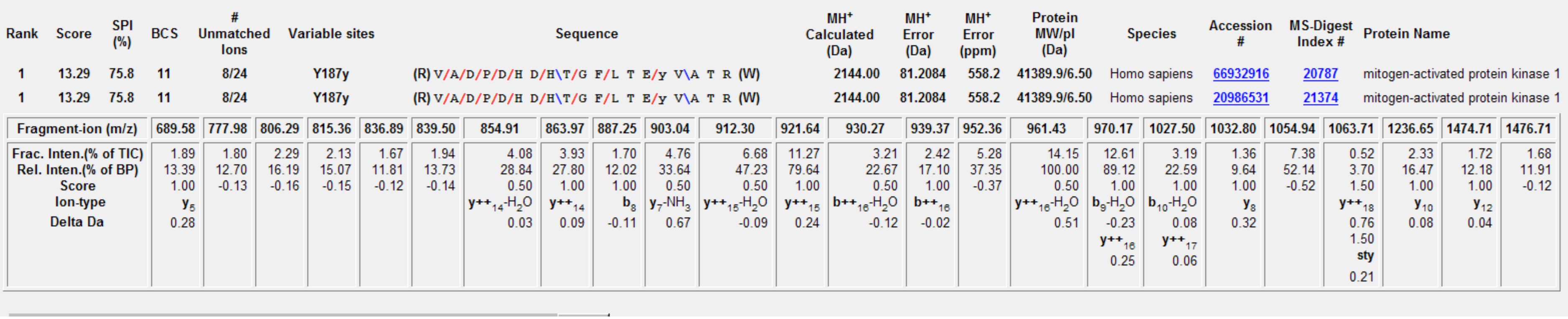


1 15.60 84.5 6 7/25 T368t T371t T400t Y384y (R) N I I D V V S t P W t A|E L G\G D Q L R T M T y T\I V L N S|P L|T G K C T\A A t E K (Q) 4565.33 319.4116 -92.9 76019.5/6.81 Homo sapiens 63055051 28147 GRAM domain containing 1C

Fragment-ion (m/z)	573.66	678.71	719.70	1130.02	1138.71	1146.01	1146.89	1177.89	1242.83	1261.09	1356.20	1357.06	1395.17	1397.64	1430.00	1457.88	1491.85	1501.72	1510.35	1706.14	1714.75	1715.33	1756.73	1765.78	1870.51
Frac. Inten.(% of TIC)	3.76	2.03	1.58	1.56	2.29	4.61	10.19	1.85	1.89	4.10	5.86	17.31	2.16	1.66	1.98	5.97	1.66	5.27	2.04	2.28	1.89	4.80	4.04	2.89	6.32
Rel. Inten.(% of BP)	21.73	11.75	9.15	9.01	13.23	26.66	58.89	10.69	10.89	23.69	33.88	100.00	12.48	9.61	11.43	34.51	9.56	30.45	11.81	13.17	10.91	27.74	23.32	16.70	36.49
Score	1.00	1.00	-0.09	0.50	-0.13	1.00	1.00	1.00	0.50	-0.24	1.00	1.00	-0.12	-0.10	1.00	1.00	-0.10	1.00	-0.12	0.50	1.00	1.00	1.00	1.00	1.00
Ion-type	y^{++}_{10}	y^{++}_{12}		y_{10}-NH_3		y_{10}	y_{10}	a_{10} b^{+++}_{30}	y_{11}-NH_3		y_{12}	y_{12}			a_{12} b^{+++}_{37}	b_{12}		b^{++}_{25}		y^{++}_{30}-H_2O	y^{++}_{30}	y^{++}_{30}	b_{15} b^{++}_{30}-H_2O	b^{++}_{30}	b^{++}_{32}
Delta Da	-0.09	-0.11		0.56		-0.48	0.40	0.32 0.69	0.29		-0.42	0.44			0.38 0.34	0.27		-0.42		0.35	-0.05	0.53	-0.03 0.44	0.49	0.15

Peak 511



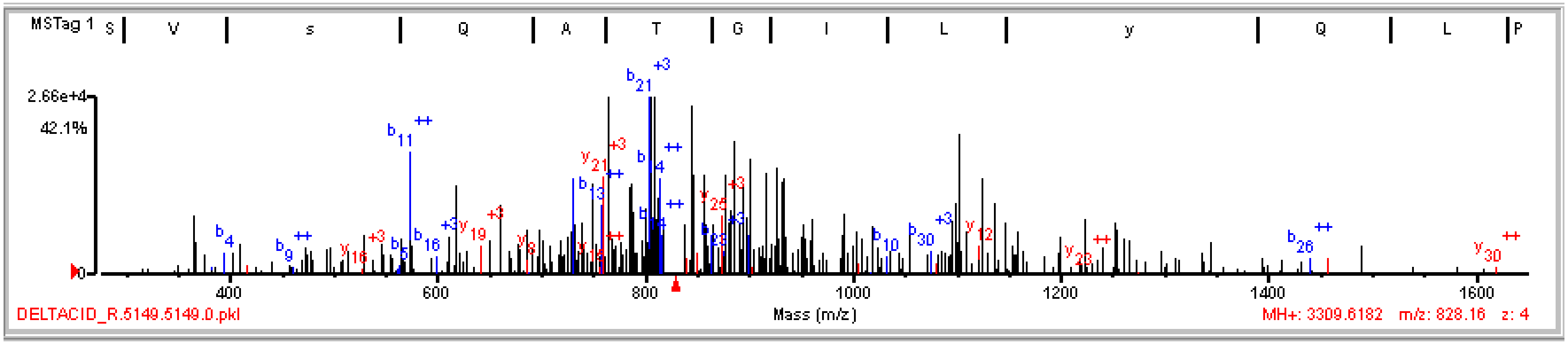


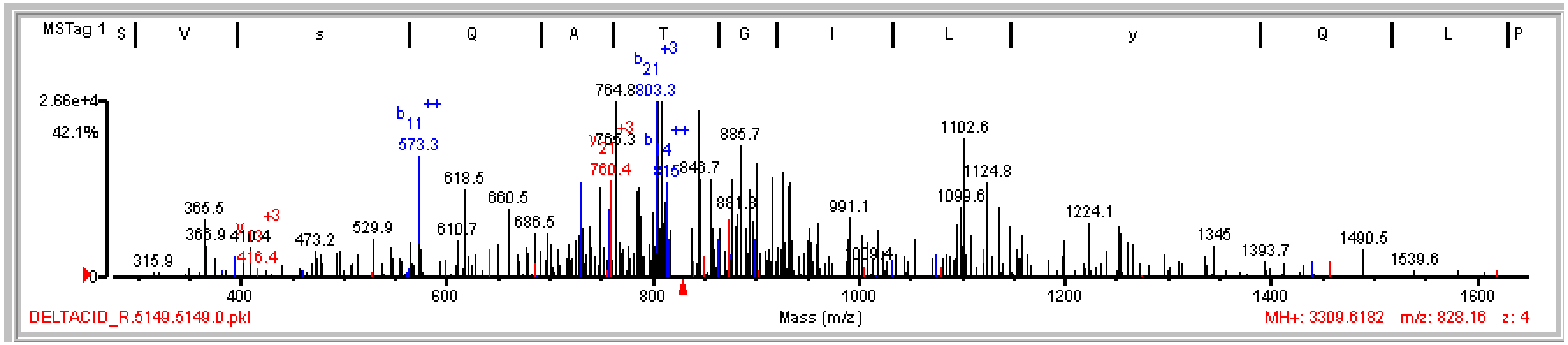
Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH⁺ Calculated (Da)	MH⁺ Error (Da)	MH⁺ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	13.29	75.8	11	8/24	Y187y	(R) V/A/D/P/D/H D/H\T/G F/L T E/y V\A T R (W)	2144.00	81.2084	558.2	41389.9/6.50	Homo sapiens	66932916	20787	mitogen-activated protein kinase 1
1	13.29	75.8	11	8/24	Y187y	(R) V/A/D/P/D/H D/H\T/G F/L T E/y V\A T R (W)	2144.00	81.2084	558.2	41389.9/6.50	Homo sapiens	20986531	21374	mitogen-activated protein kinase 1

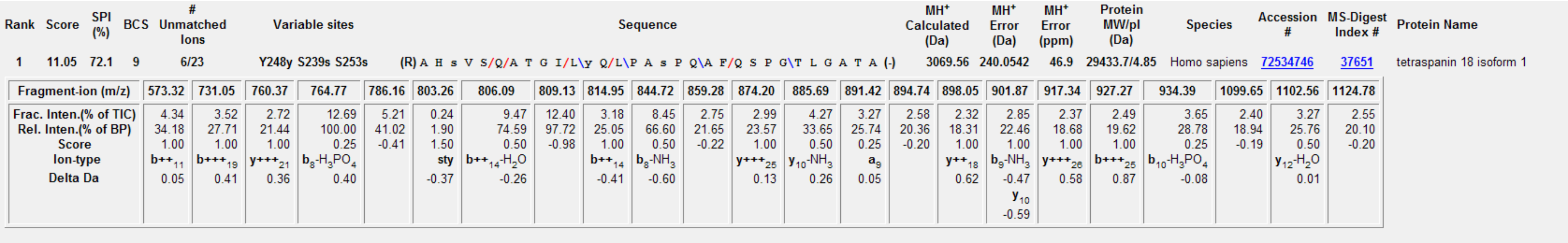
Fragment-ion (m/z)	689.58	777.98	806.29	815.36	836.89	839.50	854.91	863.97	887.25	903.04	912.30	921.64
Frac. Inten.(% of TIC)	1.89	1.80	2.29	2.13	1.67	1.94	4.08	3.93	1.70	4.76	6.68	11.27
Rel. Inten.(% of BP)	13.39	12.70	16.19	15.07	11.81	13.73	28.84	27.80	12.02	33.64	47.23	79.64
Score	1.00	-0.13	-0.16	-0.15	-0.12	-0.14	0.50	1.00	1.00	0.50	0.50	1.00
Ion-type	y_5						$y{+}{+}_{14}$-H_2O	$y{+}{+}_{14}$	b_8	y_7-NH_3	$y{+}{+}_{15}$-H_2O	$y{+}{+}_{15}$
Delta Da	0.28						0.03	0.09	-0.11	0.67	-0.09	0.24

Fragment-ion (m/z)	930.27	939.37	952.36	961.43	970.17	1027.50	1032.80	1054.94	1063.71	1236.65	1474.71	1476.71
Frac. Inten.(% of TIC)	3.21	2.42	5.28	14.15	12.61	3.19	1.36	7.38	0.52	2.33	1.72	1.68
Rel. Inten.(% of BP)	22.67	17.10	37.35	100.00	89.12	22.59	9.64	52.14	3.70	16.47	12.18	11.91
Score	0.50	1.00	-0.37	0.50	1.00	1.00	1.00	-0.52	1.50	1.00	1.00	-0.12
Ion-type	$b{+}{+}_{16}$-H_2O	$b{+}{+}_{16}$		$y{+}{+}_{16}$-H_2O	b_9-H_2O	b_{10}-H_2O	y_8		$y{+}{+}_{18}$	y_{10}	y_{12}	
Delta Da	-0.12	-0.02		0.51	-0.23	0.08	0.32		0.76	0.08	0.04	
									1.50			
					$y{+}{+}_{16}$	$y{+}{+}_{17}$			sty			
					0.25	0.06			0.21			

Peak 512



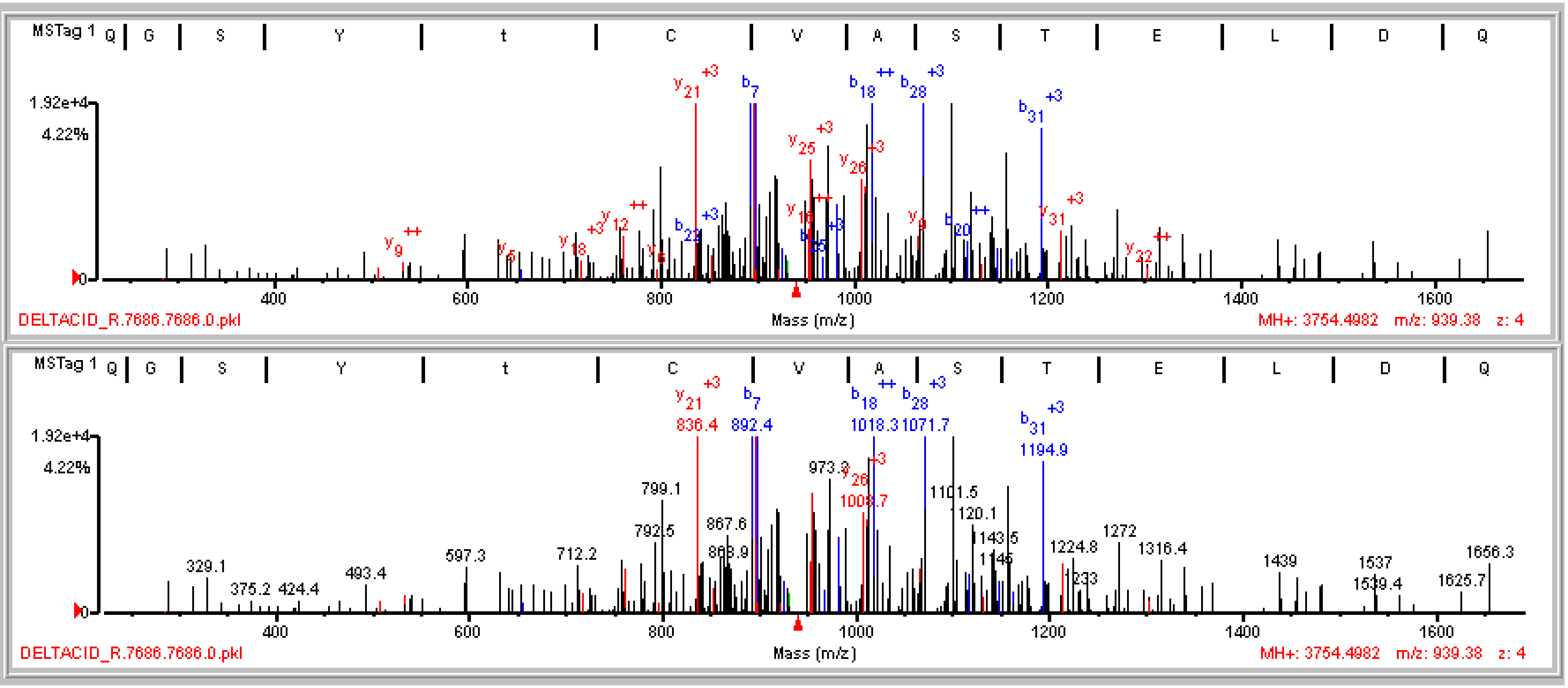


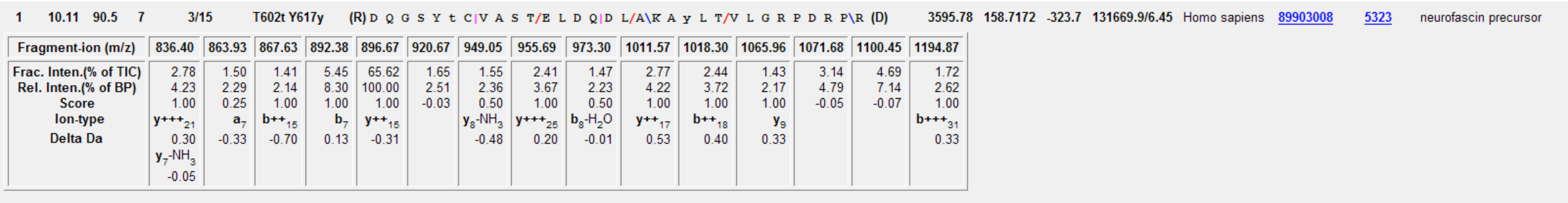


Rank	Score	SPI (%)	BCS	# Unmatched Ions	Variable sites	Sequence	MH+ Calculated (Da)	MH+ Error (Da)	MH+ Error (ppm)	Protein MW/pI (Da)	Species	Accession #	MS-Digest Index #	Protein Name
1	11.05	72.1	9	6/23	Y248y S239s S253s	(R) A H s V S/Q/A T G I/L\y Q/L\P A s P Q\A F/Q S P G\T L G A T A (-)	3069.56	240.0542	46.9	29433.7/4.85	Homo sapiens	72534746	37651	tetraspanin 18 isoform 1

Fragment-ion (m/z)	573.32	731.05	760.37	764.77	786.16	803.26	806.09	809.13	814.95	844.72	859.28	874.20	885.69	891.42	894.74	898.05	901.87	917.34	927.27	934.39	1099.65	1102.56	1124.78
Frac. Inten.(% of TIC)	4.34	3.52	2.72	12.69	5.21	0.24	9.47	12.40	3.18	8.45	2.75	2.99	4.27	3.27	2.58	2.32	2.85	2.37	2.49	3.65	2.40	3.27	2.55
Rel. Inten.(% of BP)	34.18	27.71	21.44	100.00	41.02	1.90	74.59	97.72	25.05	66.60	21.65	23.57	33.65	25.74	20.36	18.31	22.46	18.68	19.62	28.78	18.94	25.76	20.10
Score	1.00	1.00	1.00	0.25	-0.41	1.50	0.50	-0.98	1.00	0.50	-0.22	1.00	0.50	0.25	-0.20	1.00	1.00	1.00	1.00	0.25	-0.19	0.50	-0.20
Ion-type	$b{++}_{11}$	$b{+++}_{19}$	$y{+++}_{21}$	b_8-H_3PO_4		sty	$b{++}_{14}$-H_2O		$b{++}_{14}$	b_8-NH_3		$y{+++}_{25}$	y_{10}-NH_3	a_9		$y{++}_{18}$	b_9-NH_3 y_{10}	$y{+++}_{26}$	$b{+++}_{25}$	b_{10}-H_3PO_4		y_{12}-H_2O	
Delta Da	0.05	0.41	0.36	0.40		-0.37	-0.26		-0.41	-0.60		0.13	0.26	0.05		0.62	-0.47 -0.59	0.58	0.87	-0.08		0.01	

Peak 514





1 10.11 90.5 7 3/15 T602t Y617y (R) D Q G S Y t C|V A S T/E L D Q|D L/A\K A y L T/V L G R P D R P\R (D) 3595.78 158.7172 -323.7 131669.9/6.45 Homo sapiens 89903008 5323 neurofascin precursor

Fragment-ion (m/z)	836.40	863.93	867.63	892.38	896.67	920.67	949.05	955.69	973.30	1011.57	1018.30	1065.96	1071.68	1100.45	1194.87
Frac. Inten.(% of TIC)	2.78	1.50	1.41	5.45	65.62	1.65	1.55	2.41	1.47	2.77	2.44	1.43	3.14	4.69	1.72
Rel. Inten.(% of BP)	4.23	2.29	2.14	8.30	100.00	2.51	2.36	3.67	2.23	4.22	3.72	2.17	4.79	7.14	2.62
Score	1.00	0.25	1.00	1.00	1.00	-0.03	0.50	1.00	0.50	1.00	1.00	1.00	-0.05	-0.07	1.00
Ion-type	$y{+}{+}{+}_{21}$ y_7-NH_3	a_7	$b{+}{+}_{15}$	b_7	$y{+}{+}_{15}$		y_8-NH_3	$y{+}{+}{+}_{25}$	b_8-H_2O	$y{+}{+}_{17}$	$b{+}{+}_{18}$	y_9			$b{+}{+}{+}_{31}$
Delta Da	0.30 -0.05	-0.33	-0.70	0.13	-0.31		-0.48	0.20	-0.01	0.53	0.40	0.33			0.33