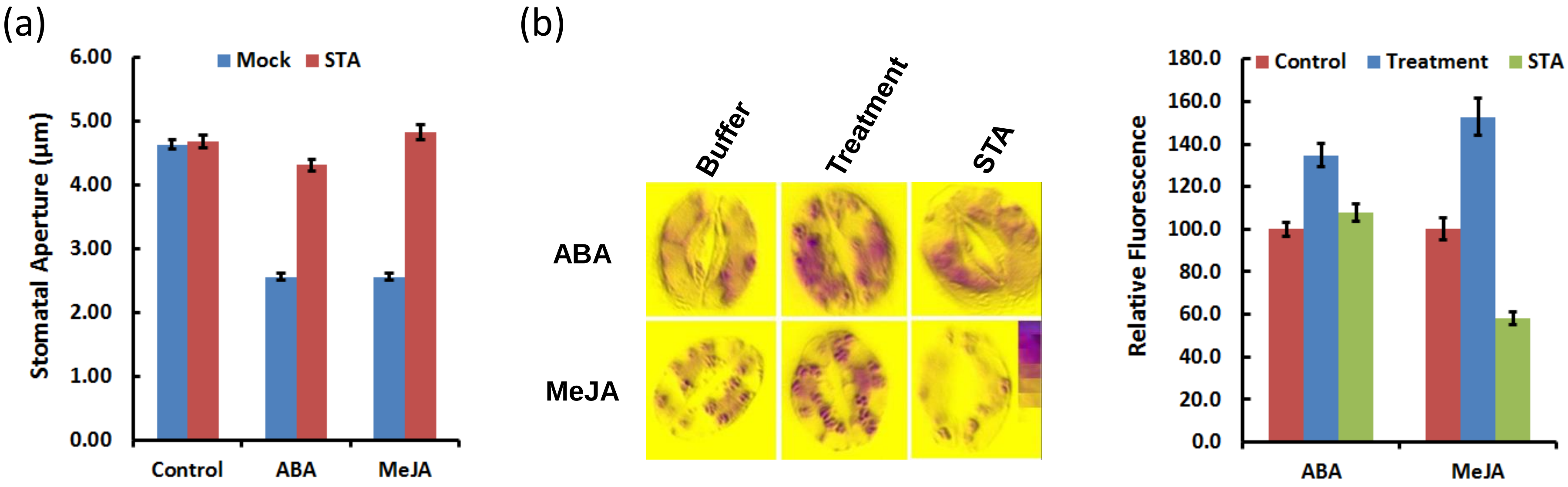


Figure S1. Effect of 2 µM staurosporine (STA) on ABA/MeJA-induced stomatal closure and H_2O_2 production. (a) STA abolishes ABA/MeJA induced closure. (b) STA inhibits ABA/MeJA elevated ROS levels. Left, representative stomatal images; right, quantitative data. The pseudocolor key beside the lower right stomatal image indicates the increase of the fluorescence from bottom to top. At least 60 stomata were analyzed in each experiment and three replicate experiments were conducted. The quantitative data are shown as average ± standard deviation.

Figure S2

MS/MS spectra of ICAT identified ABA responsive cysteines

Twenty seven cysteines were mapped from ABA treated guard cells. The precursor of the cysteine-containing peptide and the fragmented ions were shown as the evidence for mapping.

Ribulose bisphosphate carboxylase large chain precursor
GRPLLGCTIKPK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
5.1.1.1821.4	34.228	1508.9796	504.0005	3	2	GRPLLGCTIKPK	ICAT-C(C)@7	93	1508.8861	3
5.1.1.1822.2	34.280	1517.9985	507.0068	3	2	GRPLLGCTIKPK	ICAT-C:13C(9)(C)@7	76	1517.9163	3
6.1.1.1691.2	30.253	1508.9382	503.9867	3	2	GRPLLGCTIKPK	ICAT-C(C)@7	< 1	1508.8861	3

Peptide ID Hypotheses - 5.1.1.1821.4

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
93	13	2	GRPLLGCTIKPK	ICAT-C(C)@7	1508.8861	503.9693	3	0.0935
< 1	9		EDKEHLQTLLQR		1508.7947	503.9388	3	0.1849
< 1	9		KSTHQGNVKEEPR		1508.7695	503.9305	3	0.2101
< 1	9		RLIQLFTTYLNK		1508.8715	503.9644	3	0.1081
< 1	9		SSNILLTENYRAK	Deamidated(N)@9	1508.7834	503.9351	3	0.1962

Fragmentation Evidence for Peptide

GRPLLGC[C0I]TIKPK

Residue	b	b+2	y
G	58.0287	29.5180	1509.8934
R	**214.1299**	107.5686	1452.8719
P	311.1826	156.0949	1296.7708
L	**424.2667**	212.6370	1199.7180
L	**537.3507**	**269.1790**	1086.6340
G	**594.3722**	**297.6897**	**973.5499**
C[C0I]	**924.5084**	**462.7578**	**916.5284**
T	1025.5561	513.2817	**586.3923**
I	**1138.6401**	569.8237	485.3446
K	1266.7351	633.8712	**372.2605**
P	**1363.7879**	682.3976	**244.1656**
K	1491.8828	**746.4450**	**147.1128**

Ribulose bisphosphate carboxylase large chain precursor
CYHIEPVPGEETQFIAY

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
3.1˙1.15...	40.571	2222.0247	741.6821	3	2	CYHIEPVPGEETQFIAY	ICAT-C(C)@1	99	2222.0354	3
3.1˙1.15...	40.528	2231.0327	744.6848	3	2	CYHIEPVPGEETQFIAY	ICAT-C:13C(9)(C)@1	99	2231.0657	3
10.1˙1.1...	41.428	2221.9971	741.6730	3	2	CYHIEPVPGEETQFIAY	ICAT-C(C)@1	99	2222.0354	3

Peptide ID Hypotheses - 3.1dot;1.1574.2.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	2	CYHIEPVPGEETQFIAY	ICAT-C:13C(9)(C)@1	2231.0657	744.6958	3	-0.0330
< 1	11		GLTITGVPVNMAANTNVVTMGR	Oxidation(M)@20	2231.1401	744.7207	3	-0.1076
< 1	10		HLVWALRDSGINVFKDSFK		2231.1851	744.7357	3	-0.1525
< 1	9		LACRTVGWGVVGGLGPPLPR	ICAT-C(C)@3	2231.2361	744.7526	3	-0.2035

Fragmentation Evidence for Peptide

C[C9I]YHIEPVPGEETQFIAY

Residue	b	b+2	y
C[C9I]	340.1736	170.5905	2232.0729
Y	**503.2370**	**252.1221**	1892.9065
H	**640.2959**	320.6516	1729.8432
I	**753.3800**	**377.1936**	1592.7843
E	**882.4225**	**441.7149**	1479.7002
P	**979.4753**	490.2413	1350.6576
V	**1078.5437**	539.7755	1253.6048
P	**1175.5965**	588.3019	**1154.5364**
G	**1232.6179**	616.8126	1057.4837
E	**1361.6605**	681.3339	1000.4622
E	**1490.7031**	745.8552	871.4196
T	**1591.7508**	**796.3790**	742.3770
Q	**1719.8094**	860.4083	641.3293
F	**1866.8778**	933.9425	**513.2708**
I	1979.9619	990.4846	366.2023
A	2050.9990	1026.0031	**253.1183**
Y	2214.0623	1107.5348	**182.0812**

Ribulose bisphosphate carboxylase large chain precursor
VALEA<u>C</u>VQAR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
3.1˙1.14...	28.250	1285.6472	643.8309	2	2	VALEACVKAR	ICAT-C(C)@6	32	1285.7177	2
3.1˙1.14...	28.164	1294.6741	648.3443	2	2	VALEACVKAR	ICAT-C:13C(9)(C)@6	97	1294.7478	2
9.1˙1.13...	30.087	1285.6302	643.8224	2	2	VALEACVKAR	ICAT-C(C)@6	88	1285.7177	2
9.1˙1.13...	30.044	1294.6531	648.3338	2	2	VALEACVKAR	ICAT-C:13C(9)(C)@6	93	1294.7478	2
10.1˙1.1...	29.917	1285.6475	643.8310	2	2	VALEACVKAR	ICAT-C(C)@6	45	1285.7177	2

Peptide ID Hypotheses - 2.1dot;1.1399.3.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	14	2	VALEACVKAR	ICAT-C:13C(9)(C)@6	1294.7478	648.3812	2	-0.0724
99	14	94, 98,...	VALEACVQAR	ICAT-C:13C(9)(C)@6	1294.7114	648.3630	2	-0.0361
99	14		VAIEACVQAR	ICAT-C:13C(9)(C)@6	1294.7114	648.3630	2	-0.0361
22	14		VALQACVQAR	Deamidated(Q)@4, ICAT-C:...	1294.7114	648.3630	2	-0.0361
21	14		VAPEACVQAR	Oxidation(P)@3, ICAT-C:13...	1294.6750	648.3448	2	0.0003

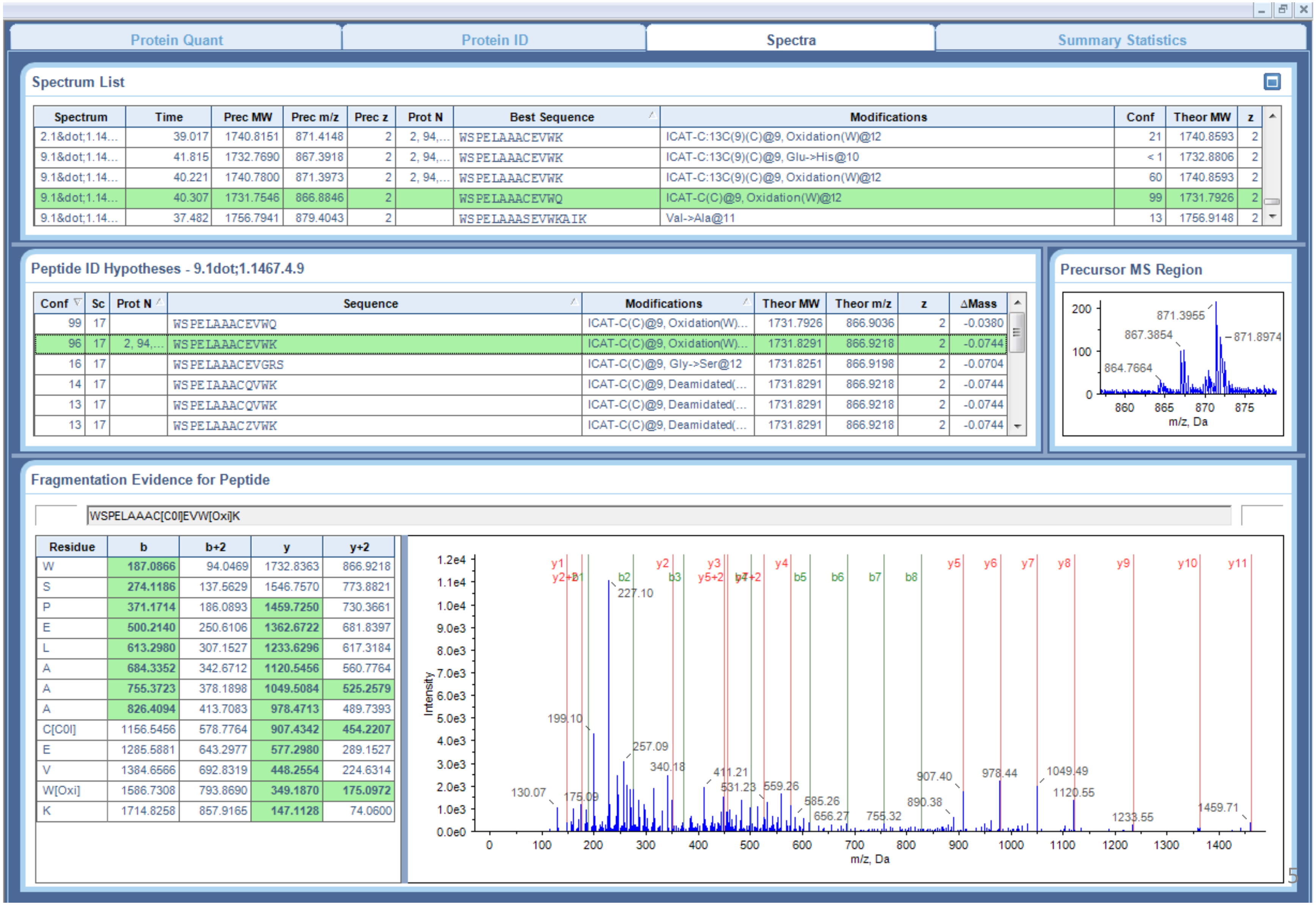
Precursor MS Region

Fragmentation Evidence for Peptide

VALEAC[C9I]VQAR

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1295.7187	**648.3630**
A	**171.1128**	86.0600	**1196.6503**	598.8288
L	**284.1969**	142.6021	**1125.6132**	**563.3102**
E	**413.2395**	207.1234	**1012.5291**	506.7682
A	**484.2766**	242.6419	**883.4865**	442.2469
C[C9I]	823.4429	412.2251	**812.4494**	406.7284
V	922.5114	461.7593	**473.2831**	**237.1452**
Q	**1050.5699**	525.7886	**374.2146**	187.6110
A	1121.6070	561.3072	**246.1561**	123.5817
R	1277.7082	639.3577	**175.1190**	88.0631

Ribulose bisphosphate carboxylase large chain precursor
WSPELAAA<u>C</u>EVWK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
2.1˙1.14...	39.017	1740.8151	871.4148	2	2, 94,...	WSPELAAACEVWK	ICAT-C:13C(9)(C)@9, Oxidation(W)@12	21	1740.8593	2
9.1˙1.14...	41.815	1732.7690	867.3918	2	2, 94,...	WSPELAAACEVWK	ICAT-C:13C(9)(C)@9, Glu->His@10	< 1	1732.8806	2
9.1˙1.14...	40.221	1740.7800	871.3973	2	2, 94,...	WSPELAAACEVWK	ICAT-C:13C(9)(C)@9, Oxidation(W)@12	60	1740.8593	2
9.1˙1.14...	40.307	1731.7546	866.8846	2		WSPELAAACEVWQ	ICAT-C(C)@9, Oxidation(W)@12	99	1731.7926	2
9.1˙1.14...	37.482	1756.7941	879.4043	2		WSPELAAASEVWKAIK	Val->Ala@11	13	1756.9148	2

Peptide ID Hypotheses - 9.1dot;1.1467.4.9

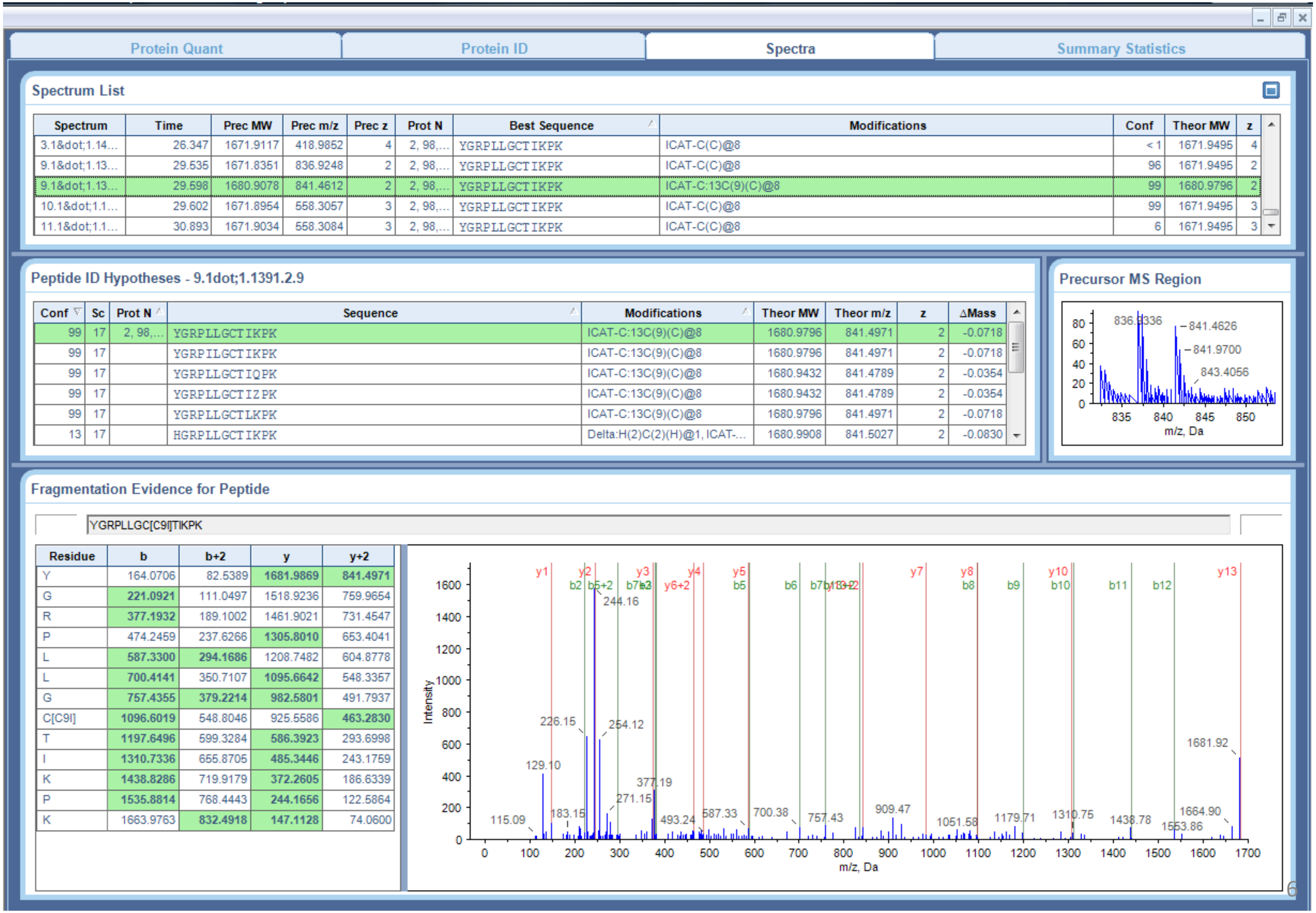
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	17		WSPELAAACEVWQ	ICAT-C(C)@9, Oxidation(W)...	1731.7926	866.9036	2	-0.0380
96	17	2, 94,...	WSPELAAACEVWK	ICAT-C(C)@9, Oxidation(W)...	1731.8291	866.9218	2	-0.0744
16	17		WSPELAAACEVGRS	ICAT-C(C)@9, Gly->Ser@12	1731.8251	866.9198	2	-0.0704
14	17		WSPEIAAACQVWK	ICAT-C(C)@9, Deamidated(...	1731.8291	866.9218	2	-0.0744
13	17		WSPELAAACQVWK	ICAT-C(C)@9, Deamidated(...	1731.8291	866.9218	2	-0.0744
13	17		WSPELAAACZVWK	ICAT-C(C)@9, Deamidated(...	1731.8291	866.9218	2	-0.0744

Fragmentation Evidence for Peptide

WSPELAAAC[C0l]EVW[Oxi]K

Residue	b	b+2	y	y+2
W	**187.0866**	94.0469	1732.8363	866.9218
S	**274.1186**	137.5629	1546.7570	773.8821
P	**371.1714**	186.0893	**1459.7250**	730.3661
E	**500.2140**	250.6106	**1362.6722**	681.8397
L	**613.2980**	307.1527	**1233.6296**	617.3184
A	**684.3352**	342.6712	**1120.5456**	560.7764
A	**755.3723**	378.1898	**1049.5084**	**525.2579**
A	**826.4094**	413.7083	**978.4713**	489.7393
C[C0l]	1156.5456	578.7764	**907.4342**	**454.2207**
E	1285.5881	643.2977	**577.2980**	289.1527
V	1384.6566	692.8319	**448.2554**	224.6314
W[Oxi]	1586.7308	793.8690	**349.1870**	**175.0972**
K	1714.8258	857.9165	**147.1128**	74.0600

Ribulose bisphosphate carboxylase large chain precursor
YGRPLLGCTIKPK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
3.1˙1.14...	26.347	1671.9117	418.9852	4	2, 98,...	YGRPLLGCTIKPK	ICAT-C(C)@8	< 1	1671.9495	4
9.1˙1.13...	29.535	1671.8351	836.9248	2	2, 98,...	YGRPLLGCTIKPK	ICAT-C(C)@8	96	1671.9495	2
9.1˙1.13...	29.598	1680.9078	841.4612	2	2, 98,...	YGRPLLGCTIKPK	ICAT-C:13C(9)(C)@8	99	1680.9796	2
10.1˙1.1...	29.602	1671.8954	558.3057	3	2, 98,...	YGRPLLGCTIKPK	ICAT-C(C)@8	99	1671.9495	3
11.1˙1.1...	30.893	1671.9034	558.3084	3	2, 98,...	YGRPLLGCTIKPK	ICAT-C(C)@8	6	1671.9495	3

Peptide ID Hypotheses - 9.1dot;1.1391.2.9

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	17	2, 98,...	YGRPLLGCTIKPK	ICAT-C:13C(9)(C)@8	1680.9796	841.4971	2	-0.0718
99	17		YGRPILGCTIKPK	ICAT-C:13C(9)(C)@8	1680.9796	841.4971	2	-0.0718
99	17		YGRPLLGCTIQPK	ICAT-C:13C(9)(C)@8	1680.9432	841.4789	2	-0.0354
99	17		YGRPLLGCTIZPK	ICAT-C:13C(9)(C)@8	1680.9432	841.4789	2	-0.0354
99	17		YGRPLLGCTLKPK	ICAT-C:13C(9)(C)@8	1680.9796	841.4971	2	-0.0718
13	17		HGRPLLGCTIKPK	Delta:H(2)C(2)(H)@1, ICAT-...	1680.9908	841.5027	2	-0.0830

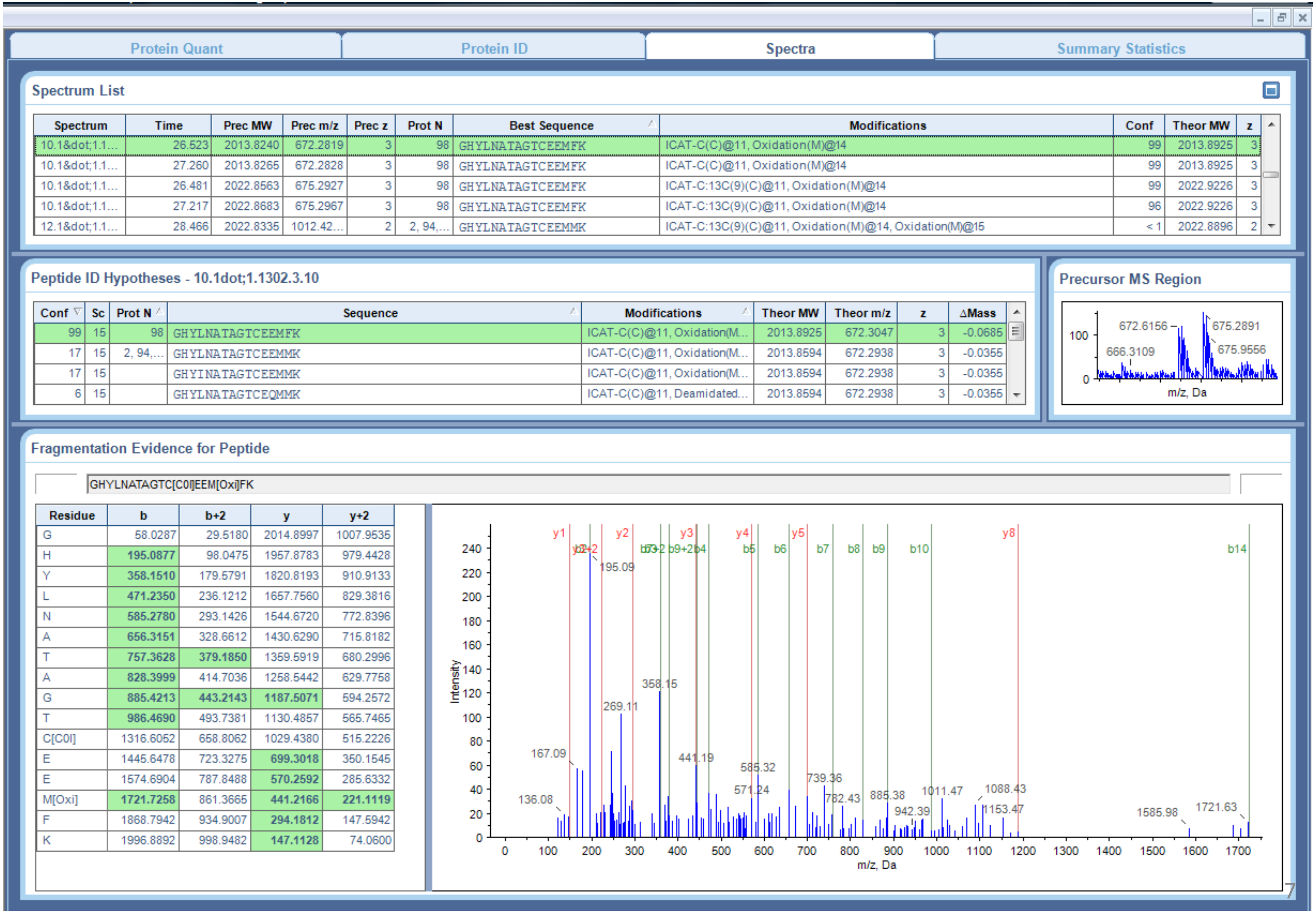
Precursor MS Region

Fragmentation Evidence for Peptide

YGRPLLGC[C9I]TIKPK

Residue	b	b+2	y	y+2
Y	164.0706	82.5389	**1681.9869**	**841.4971**
G	**221.0921**	111.0497	1518.9236	759.9654
R	**377.1932**	189.1002	1461.9021	731.4547
P	474.2459	237.6266	**1305.8010**	653.4041
L	**587.3300**	**294.1686**	1208.7482	604.8778
L	**700.4141**	350.7107	**1095.6642**	548.3357
G	**757.4355**	**379.2214**	**982.5801**	491.7937
C[C9I]	**1096.6019**	548.8046	925.5586	**463.2830**
T	**1197.6496**	599.3284	**586.3923**	293.6998
I	**1310.7336**	655.8705	**485.3446**	243.1759
K	**1438.8286**	719.9179	**372.2605**	186.6339
P	**1535.8814**	768.4443	**244.1656**	122.5864
K	1663.9763	**832.4918**	**147.1128**	74.0600

Ribulose bisphosphate carboxylase large chain precursor
GHYLNATAGTCEEMMK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
10.1˙1.1...	26.523	2013.8240	672.2819	3	98	GHYLNATAGTCEEMFK	ICAT-C(C)@11, Oxidation(M)@14	99	2013.8925	3
10.1˙1.1...	27.260	2013.8265	672.2828	3	98	GHYLNATAGTCEEMFK	ICAT-C(C)@11, Oxidation(M)@14	99	2013.8925	3
10.1˙1.1...	26.481	2022.8563	675.2927	3	98	GHYLNATAGTCEEMFK	ICAT-C:13C(9)(C)@11, Oxidation(M)@14	99	2022.9226	3
10.1˙1.1...	27.217	2022.8683	675.2967	3	98	GHYLNATAGTCEEMFK	ICAT-C:13C(9)(C)@11, Oxidation(M)@14	96	2022.9226	3
12.1˙1.1...	28.466	2022.8335	1012.42...	2	2, 94,...	GHYLNATAGTCEEMMK	ICAT-C:13C(9)(C)@11, Oxidation(M)@14, Oxidation(M)@15	< 1	2022.8896	2

Peptide ID Hypotheses - 10.1dot;1.1302.3.10

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	98	GHYLNATAGTCEEMFK	ICAT-C(C)@11, Oxidation(M...	2013.8925	672.3047	3	-0.0685
17	15	2, 94,...	GHYLNATAGTCEEMMK	ICAT-C(C)@11, Oxidation(M...	2013.8594	672.2938	3	-0.0355
17	15		GHYINATAGTCEEMMK	ICAT-C(C)@11, Oxidation(M...	2013.8594	672.2938	3	-0.0355
6	15		GHYLNATAGTCEQMMK	ICAT-C(C)@11, Deamidated...	2013.8594	672.2938	3	-0.0355

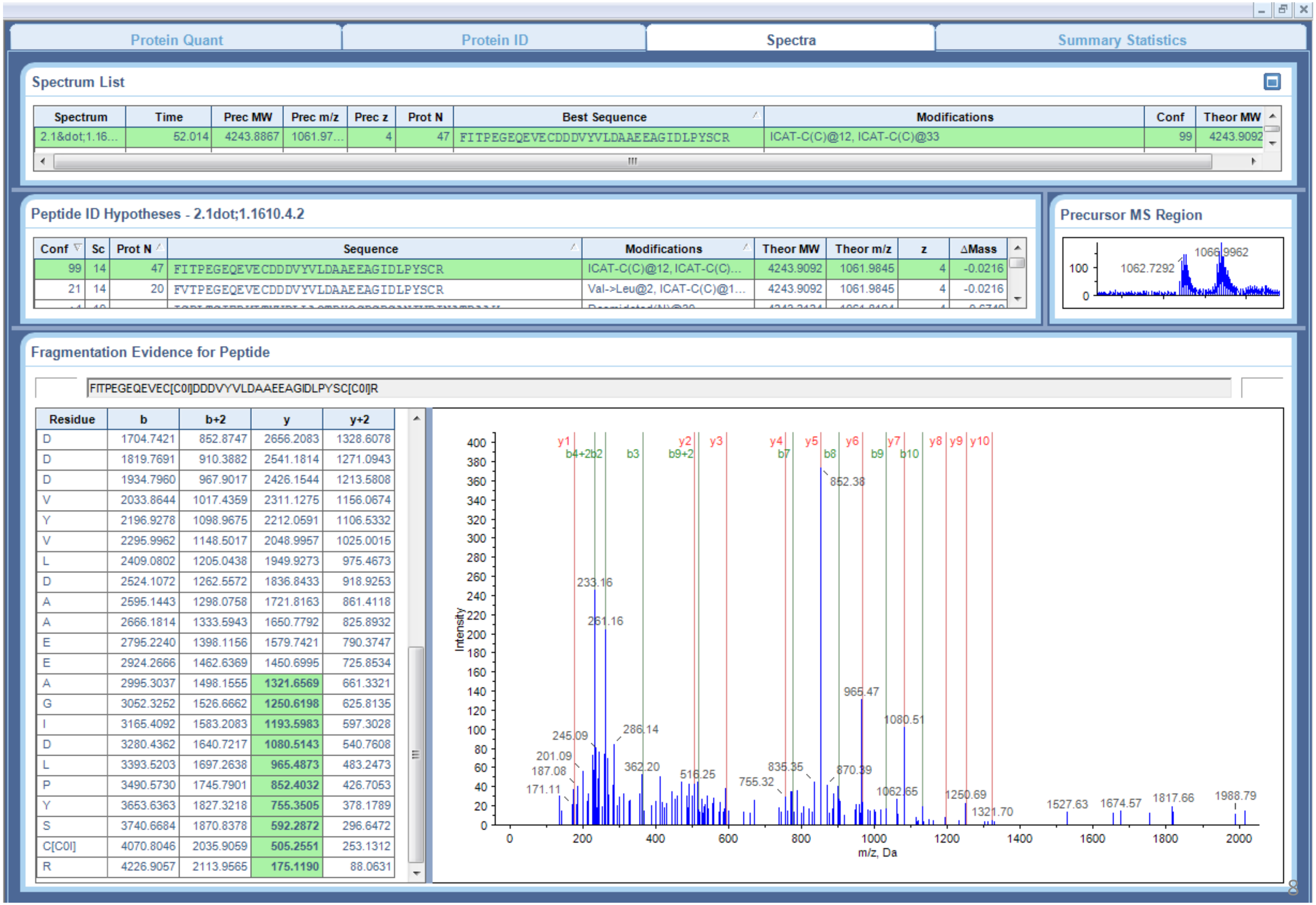
Precursor MS Region

Fragmentation Evidence for Peptide

GHYLNATAGTC[C0I]EEM[Oxi]FK

Residue	b	b+2	y	y+2
G	58.0287	29.5180	2014.8997	1007.9535
H	**195.0877**	98.0475	1957.8783	979.4428
Y	**358.1510**	179.5791	1820.8193	910.9133
L	**471.2350**	236.1212	1657.7560	829.3816
N	**585.2780**	293.1426	1544.6720	772.8396
A	**656.3151**	328.6612	1430.6290	715.8182
T	**757.3628**	**379.1850**	1359.5919	680.2996
A	**828.3999**	414.7036	1258.5442	629.7758
G	**885.4213**	**443.2143**	**1187.5071**	594.2572
T	**986.4690**	493.7381	1130.4857	565.7465
C[C0I]	1316.6052	658.8062	1029.4380	515.2226
E	1445.6478	723.3275	**699.3018**	350.1545
E	1574.6904	787.8488	**570.2592**	285.6332
M[Oxi]	**1721.7258**	861.3665	**441.2166**	**221.1119**
F	1868.7942	934.9007	**294.1812**	147.5942
K	1996.8892	998.9482	**147.1128**	74.0600

Ferredoxin
FITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
2.1˙1.16...	52.014	4243.8867	1061.97...	4	47	FITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCR	ICAT-C(C)@12, ICAT-C(C)@33	99	4243.9092

Peptide ID Hypotheses - 2.1dot;1.1610.4.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	14	47	FITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCR	ICAT-C(C)@12, ICAT-C(C)...	4243.9092	1061.9845	4	-0.0216
21	14	20	FVTPEGEQEVECDDDVYVLDAAEEAGIDLPYSCR	Val->Leu@2, ICAT-C(C)@1...	4243.9092	1061.9845	4	-0.0216

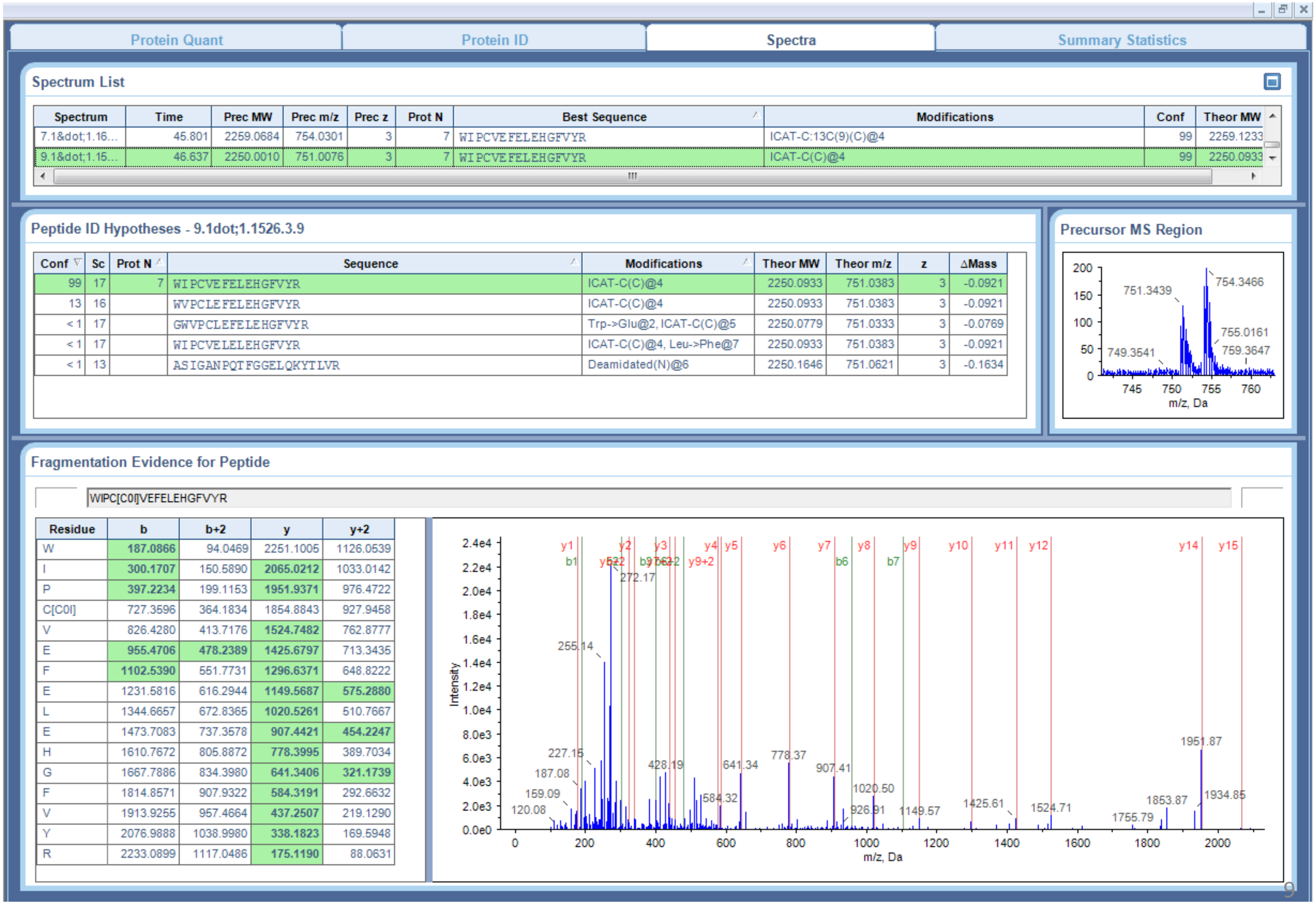
Precursor MS Region

Fragmentation Evidence for Peptide

FITPEGEQEVEC[COI]DDDVYVLDAAEEAGIDLPYSC[COI]R

Residue	b	b+2	y	y+2
D	1704.7421	852.8747	2656.2083	1328.6078
D	1819.7691	910.3882	2541.1814	1271.0943
D	1934.7960	967.9017	2426.1544	1213.5808
V	2033.8644	1017.4359	2311.1275	1156.0674
Y	2196.9278	1098.9675	2212.0591	1106.5332
V	2295.9962	1148.5017	2048.9957	1025.0015
L	2409.0802	1205.0438	1949.9273	975.4673
D	2524.1072	1262.5572	1836.8433	918.9253
A	2595.1443	1298.0758	1721.8163	861.4118
A	2666.1814	1333.5943	1650.7792	825.8932
E	2795.2240	1398.1156	1579.7421	790.3747
E	2924.2666	1462.6369	1450.6995	725.8534
A	2995.3037	1498.1555	1321.6569	661.3321
G	3052.3252	1526.6662	1250.6198	625.8135
I	3165.4092	1583.2083	1193.5983	597.3028
D	3280.4362	1640.7217	1080.5143	540.7608
L	3393.5203	1697.2638	965.4873	483.2473
P	3490.5730	1745.7901	852.4032	426.7053
Y	3653.6363	1827.3218	755.3505	378.1789
S	3740.6684	1870.8378	592.2872	296.6472
C[COI]	4070.8046	2035.9059	505.2551	253.1312
R	4226.9057	2113.9565	175.1190	88.0631

Ribulose bisphosphate carboxylase /oxygenase small subunit WIPCVEFELEHGFVYR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
7.1˙1.16...	45.801	2259.0684	754.0301	3	7	WIPCVEFELEHGFVYR	ICAT-C:13C(9)(C)@4	99	2259.1233
9.1˙1.15...	46.637	2250.0010	751.0076	3	7	WIPCVEFELEHGFVYR	ICAT-C(C)@4	99	2250.0933

Peptide ID Hypotheses - 9.1dot;1.1526.3.9

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	17	7	WIPCVEFELEHGFVYR	ICAT-C(C)@4	2250.0933	751.0383	3	-0.0921
13	16		WVPCLEFELEHGFVYR	ICAT-C(C)@4	2250.0933	751.0383	3	-0.0921
< 1	17		GWVPCLEFELEHGFVYR	Trp->Glu@2, ICAT-C(C)@5	2250.0779	751.0333	3	-0.0769
< 1	17		WIPCVELELEHGFVYR	ICAT-C(C)@4, Leu->Phe@7	2250.0933	751.0383	3	-0.0921
< 1	13		ASIGANPQTFGGELQKYTLVR	Deamidated(N)@6	2250.1646	751.0621	3	-0.1634

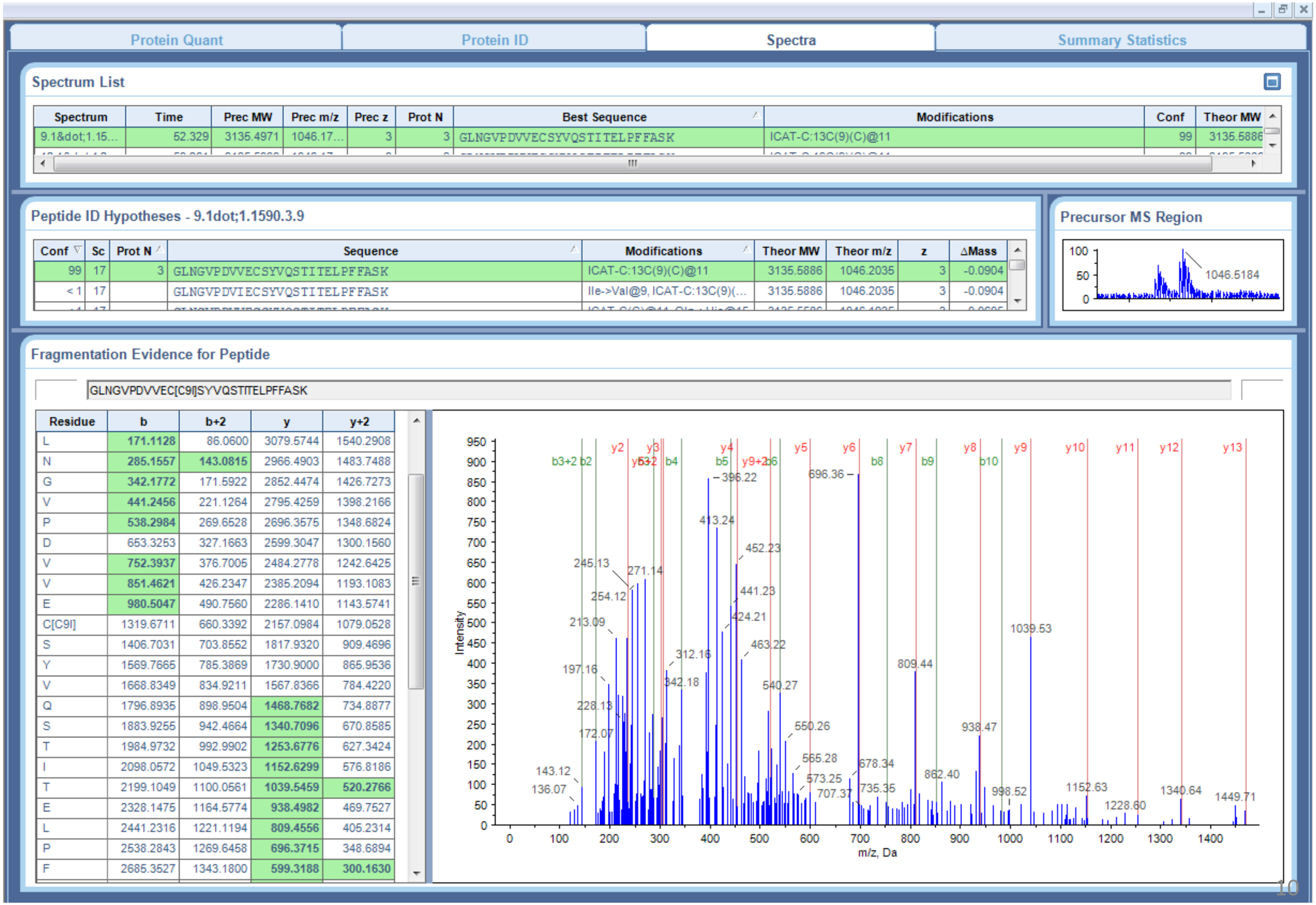
Precursor MS Region

Fragmentation Evidence for Peptide

WIPC[C0I]VEFELEHGFVYR

Residue	b	b+2	y	y+2
W	**187.0866**	94.0469	2251.1005	1126.0539
I	**300.1707**	150.5890	**2065.0212**	1033.0142
P	**397.2234**	199.1153	**1951.9371**	976.4722
C[C0I]	727.3596	364.1834	1854.8843	927.9458
V	826.4280	413.7176	**1524.7482**	762.8777
E	**955.4706**	**478.2389**	**1425.6797**	713.3435
F	**1102.5390**	551.7731	**1296.6371**	648.8222
E	1231.5816	616.2944	**1149.5687**	**575.2880**
L	1344.6657	672.8365	**1020.5261**	510.7667
E	1473.7083	737.3578	**907.4421**	**454.2247**
H	1610.7672	805.8872	**778.3995**	389.7034
G	1667.7886	834.3980	**641.3406**	**321.1739**
F	1814.8571	907.9322	**584.3191**	292.6632
V	1913.9255	957.4664	**437.2507**	219.1290
Y	2076.9888	1038.9980	**338.1823**	169.5948
R	2233.0899	1117.0486	**175.1190**	88.0631

Malate dehydrogenase, mitochondrial precursor
GLNGVPDVVECSYVQSTITELPFFASK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
9.1˙1.15...	52.329	3135.4971	1046.17...	3	3	GLNGVPDVVECSYVQSTITELPFFASK	ICAT-C:13C(9)(C)@11	99	3135.5886

Peptide ID Hypotheses - 9.1dot;1.1590.3.9

Precursor MS Region

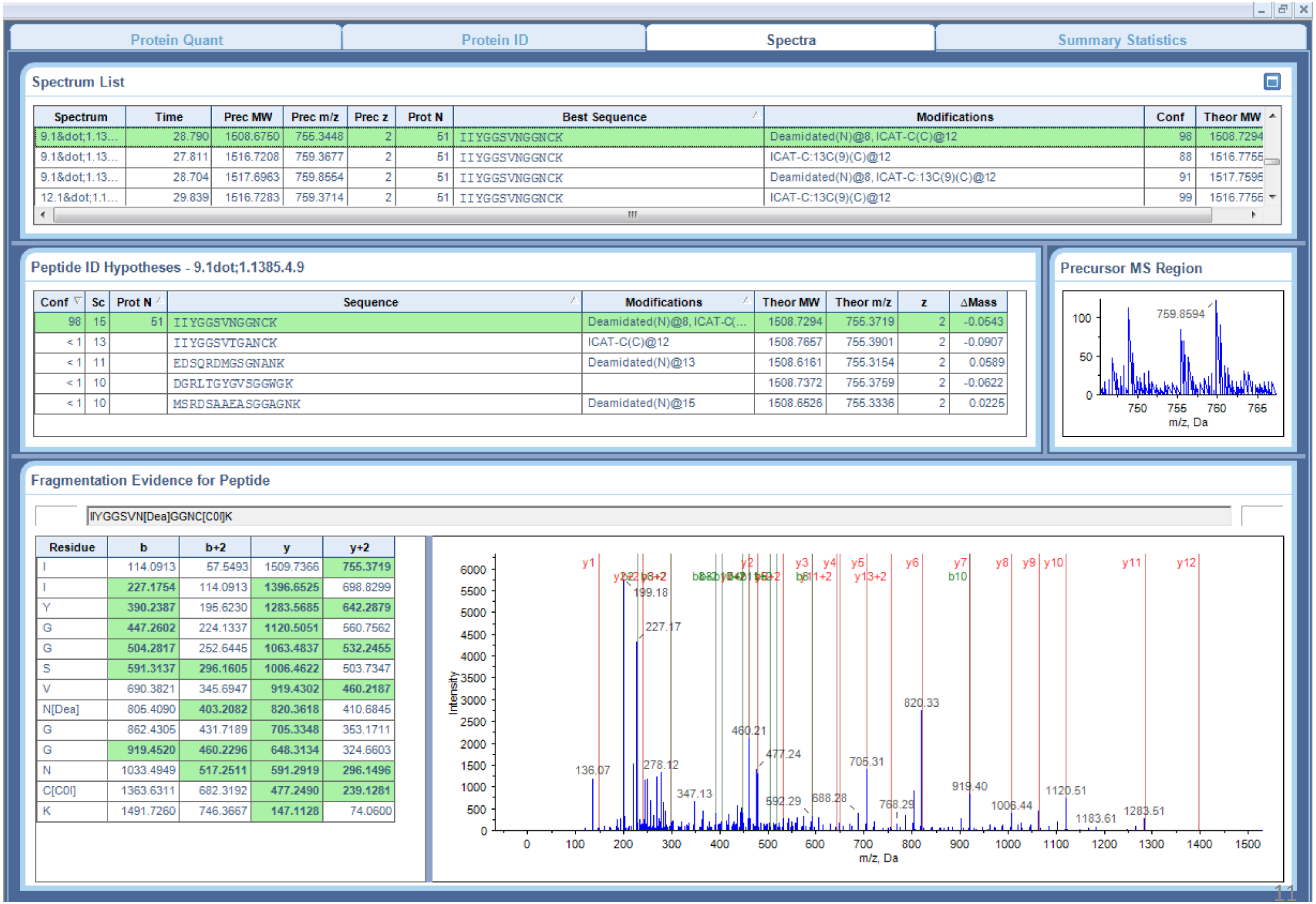
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	17	3	GLNGVPDVVECSYVQSTITELPFFASK	ICAT-C:13C(9)(C)@11	3135.5886	1046.2035	3	-0.0904
< 1	17		GLNGVPDVIECSYVQSTITELPFFASK	Ile->Val@9, ICAT-C:13C(9)(...	3135.5886	1046.2035	3	-0.0904

Fragmentation Evidence for Peptide

GLNGVPDVVEC[C9I]SYVQSTITELPFFASK

Residue	b	b+2	y	y+2
L	**171.1128**	86.0600	3079.5744	1540.2908
N	**285.1557**	**143.0815**	2966.4903	1483.7488
G	**342.1772**	171.5922	2852.4474	1426.7273
V	**441.2456**	221.1264	2795.4259	1398.2166
P	**538.2984**	269.6528	2696.3575	1348.6824
D	653.3253	327.1663	2599.3047	1300.1560
V	**752.3937**	376.7005	2484.2778	1242.6425
V	**851.4621**	426.2347	2385.2094	1193.1083
E	**980.5047**	490.7560	2286.1410	1143.5741
C[C9I]	1319.6711	660.3392	2157.0984	1079.0528
S	1406.7031	703.8552	1817.9320	909.4696
Y	1569.7665	785.3869	1730.9000	865.9536
V	1668.8349	834.9211	1567.8366	784.4220
Q	1796.8935	898.9504	**1468.7682**	734.8877
S	1883.9255	942.4664	**1340.7096**	670.8585
T	1984.9732	992.9902	**1253.6776**	627.3424
I	2098.0572	1049.5323	**1152.6299**	576.8186
T	2199.1049	1100.0561	**1039.5459**	**520.2766**
E	2328.1475	1164.5774	**938.4982**	469.7527
L	2441.2316	1221.1194	**809.4556**	405.2314
P	2538.2843	1269.6458	**696.3715**	348.6894
F	2685.3527	1343.1800	**599.3188**	**300.1630**

Cytosolic triosephosphatisomerase
IIYGGSVNGGNCK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
9.1˙1.13...	28.790	1508.6750	755.3448	2	51	IIYGGSVNGGNCK	Deamidated(N)@8, ICAT-C(C)@12	98	1508.7294
9.1˙1.13...	27.811	1516.7208	759.3677	2	51	IIYGGSVNGGNCK	ICAT-C:13C(9)(C)@12	88	1516.7755
9.1˙1.13...	28.704	1517.6963	759.8554	2	51	IIYGGSVNGGNCK	Deamidated(N)@8, ICAT-C:13C(9)(C)@12	91	1517.7595
12.1˙1.1...	29.839	1516.7283	759.3714	2	51	IIYGGSVNGGNCK	ICAT-C:13C(9)(C)@12	99	1516.7755

Peptide ID Hypotheses - 9.1dot;1.1385.4.9

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98	15	51	IIYGGSVNGGNCK	Deamidated(N)@8, ICAT-C(...	1508.7294	755.3719	2	-0.0543
< 1	13		IIYGGSVTGANCK	ICAT-C(C)@12	1508.7657	755.3901	2	-0.0907
< 1	11		EDSQRDMGSGNANK	Deamidated(N)@13	1508.6161	755.3154	2	0.0589
< 1	10		DGRLTGYGVSGGWGK		1508.7372	755.3759	2	-0.0622
< 1	10		MSRDSAAEASGGAGNK	Deamidated(N)@15	1508.6526	755.3336	2	0.0225

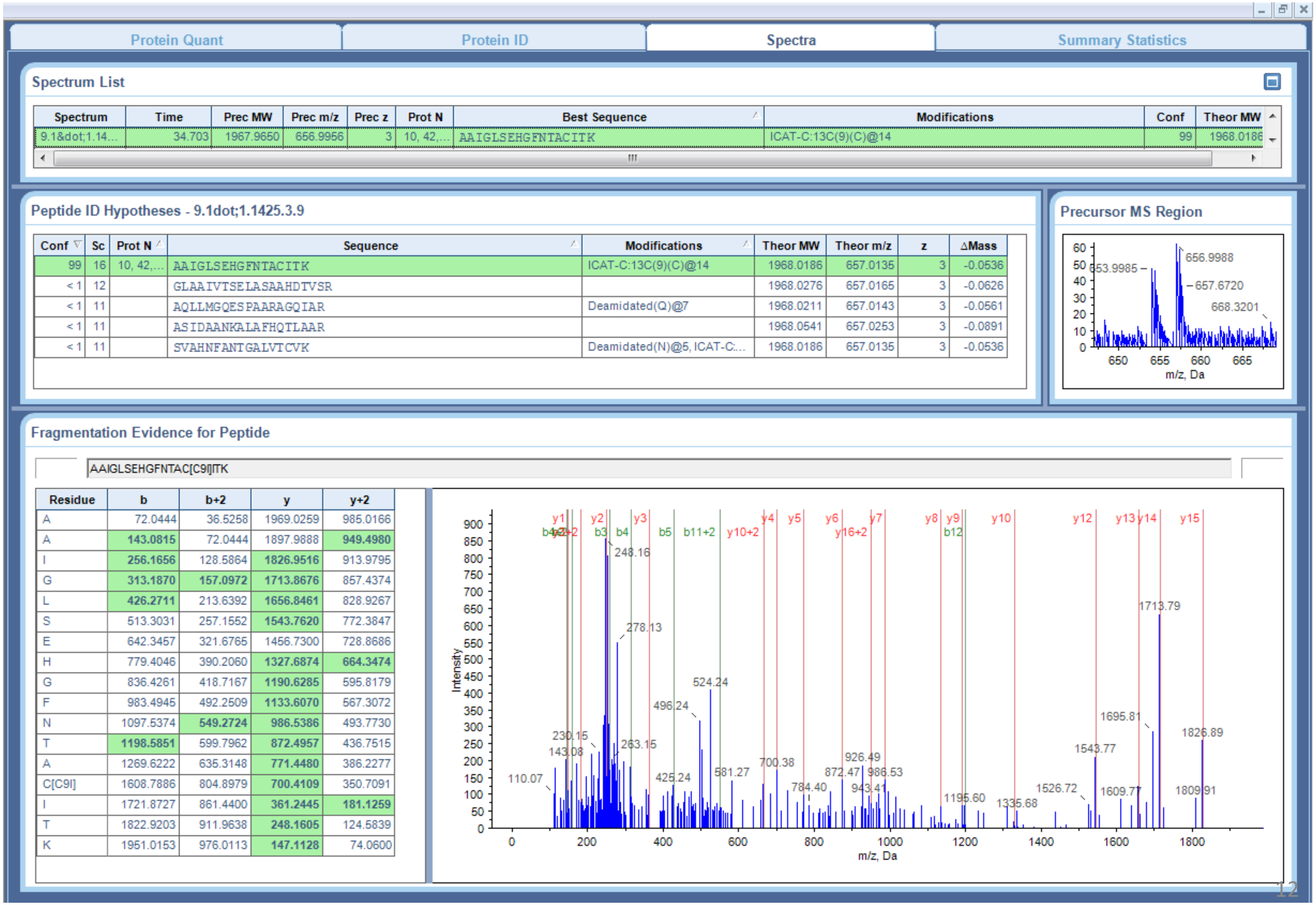
Precursor MS Region

Fragmentation Evidence for Peptide

IIYGGSVN[Dea]GGNC[C0I]K

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1509.7366	**755.3719**
I	**227.1754**	114.0913	**1396.6525**	698.8299
Y	**390.2387**	195.6230	**1283.5685**	**642.2879**
G	**447.2602**	224.1337	**1120.5051**	560.7562
G	**504.2817**	252.6445	**1063.4837**	**532.2455**
S	**591.3137**	**296.1605**	**1006.4622**	503.7347
V	690.3821	345.6947	**919.4302**	**460.2187**
N[Dea]	805.4090	**403.2082**	**820.3618**	410.6845
G	862.4305	431.7189	**705.3348**	353.1711
G	**919.4520**	**460.2296**	**648.3134**	324.6603
N	1033.4949	**517.2511**	**591.2919**	**296.1496**
C[C0I]	1363.6311	682.3192	**477.2490**	**239.1281**
K	1491.7260	746.3667	**147.1128**	74.0600

Succinate dehydrogenase flavoprotein alpha subunit
AAIGLSEHGFNTACITK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
9.1˙1.14...	34.703	1967.9650	656.9956	3	10, 42,...	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14	99	1968.0186

Peptide ID Hypotheses - 9.1dot;1.1425.3.9

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	10, 42,...	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14	1968.0186	657.0135	3	-0.0536
< 1	12		GLAAIVTSELASAAHDTVSR		1968.0276	657.0165	3	-0.0626
< 1	11		AQLLMGQESPAARAGQIAR	Deamidated(Q)@7	1968.0211	657.0143	3	-0.0561
< 1	11		ASIDAANKALAFHQTLAAR		1968.0541	657.0253	3	-0.0891
< 1	11		SVAHNFANTGALVTCVK	Deamidated(N)@5, ICAT-C:...	1968.0186	657.0135	3	-0.0536

Precursor MS Region

Fragmentation Evidence for Peptide

AAIGLSEHGFNTAC[C9I]ITK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1969.0259	985.0166
A	**143.0815**	72.0444	1897.9888	**949.4980**
I	**256.1656**	128.5864	**1826.9516**	913.9795
G	**313.1870**	**157.0972**	**1713.8676**	857.4374
L	**426.2711**	213.6392	**1656.8461**	828.9267
S	513.3031	257.1552	**1543.7620**	772.3847
E	642.3457	321.6765	1456.7300	728.8686
H	779.4046	390.2060	**1327.6874**	**664.3474**
G	836.4261	418.7167	**1190.6285**	595.8179
F	983.4945	492.2509	**1133.6070**	567.3072
N	1097.5374	**549.2724**	**986.5386**	493.7730
T	**1198.5851**	599.7962	**872.4957**	436.7515
A	1269.6222	635.3148	**771.4480**	386.2277
C[C9I]	1608.7886	804.8979	**700.4109**	350.7091
I	1721.8727	861.4400	**361.2445**	**181.1259**
T	1822.9203	911.9638	**248.1605**	124.5839
K	1951.0153	976.0113	**147.1128**	74.0600

Vacuolar ATP synthase subunit A (VHA-A)
YSNSDAVVYVGCGER

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
12.1˙1.1...	27.217	3576.3333	895.0906	4	7	YSMLSSAAVVTSPAQATMVAPFTGLKSSSAFPVTR	Oxidation(M)@3	< 1	3575.8003
2.1˙1.14...	31.976	1844.8093	923.4119	2	8	YSNSDAVVYVGCGER	ICAT-C(C)@12	97	1844.8363
2.1˙1.14...	31.934	1853.8499	927.9322	2	8	YSNSDAVVYVGCGER	ICAT-C:13C(9)(C)@12	99	1853.8665
3.1˙1.15...	31.709	1853.8500	618.9573	3	8	YSNSDAVVYVGCGER	ICAT-C:13C(9)(C)@12	99	1853.8665
10.1˙1.1...	32.321	1844.8029	923.4087	2	8	YSNSDAVVYVGCGER	ICAT-C(C)@12	45	1844.8363

Peptide ID Hypotheses - 3.1dot;1.1508.3.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	8	YSNSDAVVYVGCGER	ICAT-C:13C(9)(C)@12	1853.8665	618.9628	3	-0.0165
65	13		YSNSNAVVYVGCGER	Deamidated(N)@5, ICAT-C:...	1853.8665	618.9628	3	-0.0165
2	12		YSNSDGIVYVGCGER	ICAT-C:13C(9)(C)@12	1853.8665	618.9628	3	-0.0165
< 1	13		YSNSDTVVYVGCGER	Thr->Ala@6, ICAT-C:13C(9)...	1853.8665	618.9628	3	-0.0165

Fragmentation Evidence for Peptide

YSNSDAVVYVGC[C9I]GER

Residue	b	b+2	y	y+2
Y	164.0706	82.5389	1854.8738	927.9405
S	**251.1026**	126.0550	1691.8105	846.4089
N	365.1456	183.0764	1604.7784	802.8929
S	**452.1776**	226.5924	1490.7355	745.8714
D	**567.2045**	284.1059	1403.7035	**702.3554**
A	**638.2416**	319.6245	1288.6765	644.8419
V	**737.3101**	369.1587	1217.6394	609.3233
V	**836.3785**	418.6929	**1118.5710**	559.7891
Y	999.4418	**500.2245**	**1019.5026**	510.2549
V	1098.5102	549.7587	**856.4393**	428.7233
G	1155.5317	578.2695	**757.3708**	379.1891
C[C9I]	1494.6980	747.8527	**700.3494**	350.6783
G	1551.7195	776.3634	**361.1830**	181.0951
E	1680.7621	840.8847	304.1615	152.5844
R	1836.8632	918.9352	**175.1190**	88.0631

Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)
SDLDIVSNASCTTNCLAPLAK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
12.1˙1.1...	40.473	2588.1680	863.7299	3	39	SDLNIVSNASCTTNCLAPLAK	ICAT-C(C)@11, ICAT-C(C)@15	99	2588.2937
12.1˙1.1...	41.156	2589.1445	864.0555	3	39	SDLNIVSNASCTTNCLAPLAK	ICAT-C(C)@11, ICAT-C(C)@15	22	2588.2937

Peptide ID Hypotheses - 12.1dot;1.1622.3.12

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	14	39	SDLNIVSNASCTTNCLAPLAK	ICAT-C(C)@11, ICAT-C(C)...	2588.2937	863.7719	3	-0.1259
99	14		SDINIVSNASCTTNCLAPLAK	ICAT-C(C)@11, ICAT-C(C)...	2588.2937	863.7719	3	-0.1259

Precursor MS Region

Fragmentation Evidence for Peptide

SDLNIVSNASC[C0I]TTNC[C0I]LAPLAK

Residue	b	b+2	y	y+2
S	88.0393	44.5233	2589.3011	1295.1542
D	**203.0662**	102.0368	2502.2691	1251.6382
L	**316.1503**	158.5788	2387.2421	1194.1247
N	**430.1932**	215.6003	2274.1581	1137.5827
I	**543.2773**	**272.1423**	2160.1151	1080.5612
V	**642.3457**	321.6765	2047.0311	1024.0192
S	**729.3777**	365.1925	1947.9627	**974.4850**
N	843.4207	422.2140	1860.9306	930.9690
A	**914.4578**	457.7325	1746.8877	873.9475
S	1001.4898	**501.2485**	1675.8506	838.4289
C[C0I]	1331.6260	666.3166	**1588.8186**	794.9129
T	1432.6737	716.8405	**1258.6824**	629.8448
T	1533.7213	767.3643	**1157.6347**	**579.3210**
N	1647.7643	824.3858	**1056.5870**	528.7972
C[C0I]	1977.9005	**989.4539**	**942.5441**	471.7757
L	2090.9845	1045.9959	**612.4079**	306.7076
A	2162.0216	1081.5145	**499.3239**	250.1656
P	2259.0744	1130.0408	**428.2867**	214.6470
L	2372.1585	1186.5829	**331.2340**	166.1206
A	2443.1956	1222.1014	**218.1499**	109.5786
K	2571.2905	1286.1489	**147.1128**	74.0600

Putative transitional endoplasmic reticulum ATPase
QSAP<u>C</u>VLFFDELDSIATQR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
10.1˙1.1...	57.341	2358.1294	787.0504	3	33	QSAPCVLFFDELDSIATQR	Gln->pyro-Glu@N-term, ICAT-C:13C(9)(C)@5	99	2358.1614
5.1˙1.20...	64.146	0.0000	683.7341	0		QSEMGIFKILQGSLSGEGGK	Gln->pyro-Glu@N-term	< 1	2048.0249

Peptide ID Hypotheses - 10.1dot;1.1661.2.10

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	33	QSAPCVLFFDELDSIATQR	Gln->pyro-Glu@N-term, ICA...	2358.1614	787.0610	3	-0.0319
< 1	16		QSASCVLFFDELDSIATQR	Gln->pyro-Glu@N-term, Ser-...	2358.1614	787.0610	3	-0.0319

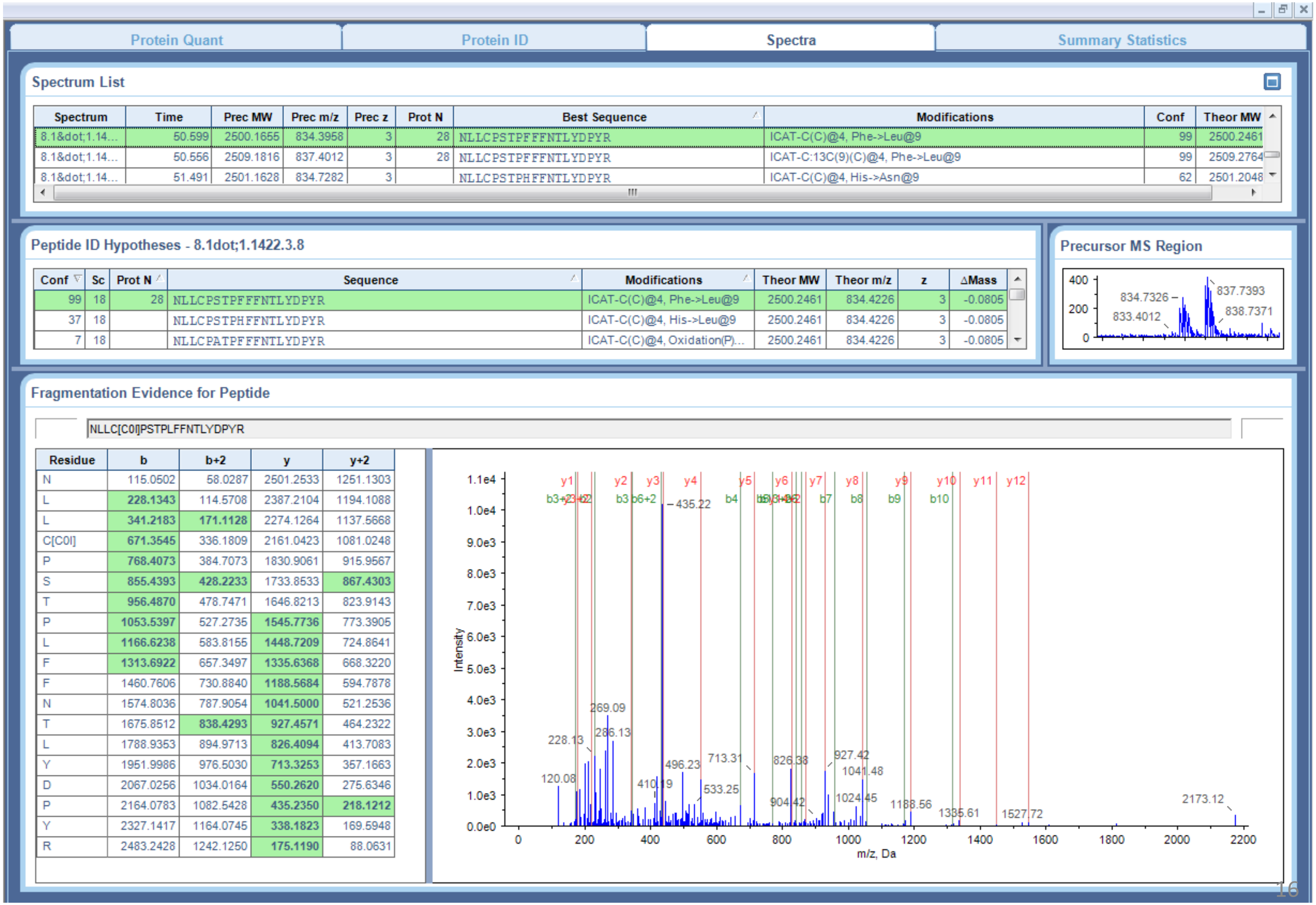
Precursor MS Region

Fragmentation Evidence for Peptide

PGQ QSAPC[C9I]VLFFDELDSIATQR

Residue	b	b+2	y	y+2
Q	112.0393	56.5233	2359.1686	1180.0879
S	199.0713	100.0393	2248.1365	1124.5719
A	270.1084	135.5579	2161.1045	1081.0559
P	367.1612	184.0842	2090.0674	1045.5373
C[C9I]	706.3276	353.6674	1993.0146	997.0110
V	805.3960	403.2016	1653.8483	827.4278
L	918.4801	459.7437	1554.7798	777.8936
F	1065.5485	533.2779	1441.6958	721.3515
F	1212.6169	606.8121	1294.6274	647.8173
D	1327.6438	664.3256	1147.5590	574.2831
E	1456.6864	728.8468	1032.5320	516.7696
L	1569.7705	785.3889	903.4894	452.2483
D	1684.7974	842.9024	790.4054	395.7063
S	1771.8295	886.4184	675.3784	338.1928
I	1884.9135	942.9604	588.3464	294.6768
A	1955.9506	978.4790	475.2623	238.1348
T	2056.9983	1029.0028	404.2252	202.6162
Q	2185.0569	1093.0321	303.1775	152.0924
R	2341.1580	1171.0826	175.1190	88.0631

Reversibly glycosylated polypeptide-1
NLLCPSTPFFFNTLYDPYR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
8.1˙1.14...	50.599	2500.1655	834.3958	3	28	NLLCPSTPFFFNTLYDPYR	ICAT-C(C)@4, Phe->Leu@9	99	2500.2461
8.1˙1.14...	50.556	2509.1816	837.4012	3	28	NLLCPSTPFFFNTLYDPYR	ICAT-C:13C(9)(C)@4, Phe->Leu@9	99	2509.2764
8.1˙1.14...	51.491	2501.1628	834.7282	3		NLLCPSTPHFFNTLYDPYR	ICAT-C(C)@4, His->Asn@9	62	2501.2048

Peptide ID Hypotheses - 8.1dot;1.1422.3.8

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	18	28	NLLCPSTPFFFNTLYDPYR	ICAT-C(C)@4, Phe->Leu@9	2500.2461	834.4226	3	-0.0805
37	18		NLLCPSTPHFFNTLYDPYR	ICAT-C(C)@4, His->Leu@9	2500.2461	834.4226	3	-0.0805
7	18		NLLCPATPFFFNTLYDPYR	ICAT-C(C)@4, Oxidation(P)...	2500.2461	834.4226	3	-0.0805

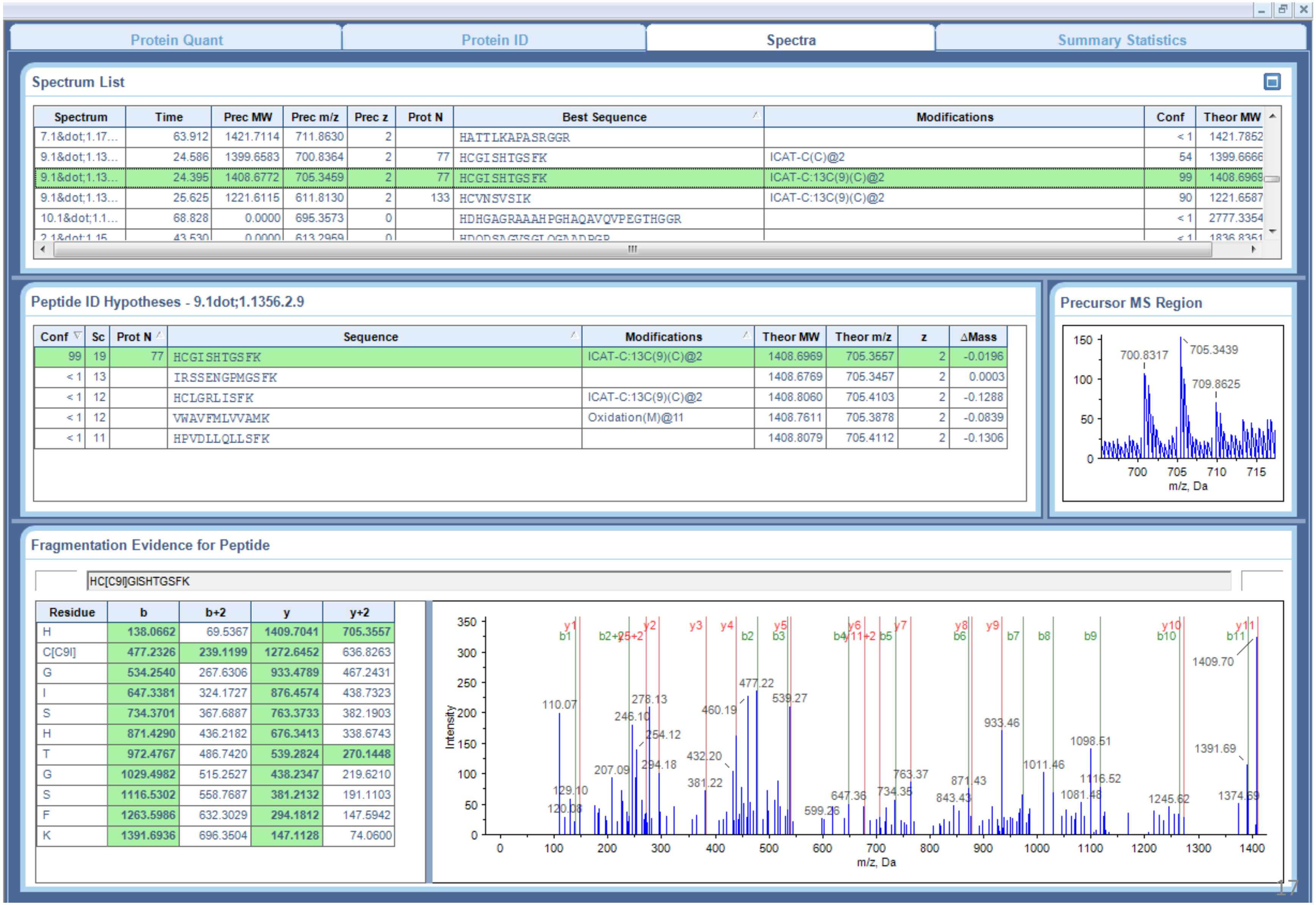
Precursor MS Region

Fragmentation Evidence for Peptide

NLLC[C0I]PSTPLFFNTLYDPYR

Residue	b	b+2	y	y+2
N	115.0502	58.0287	2501.2533	1251.1303
L	**228.1343**	114.5708	2387.2104	1194.1088
L	**341.2183**	**171.1128**	2274.1264	1137.5668
C[C0I]	**671.3545**	336.1809	2161.0423	1081.0248
P	**768.4073**	384.7073	1830.9061	915.9567
S	**855.4393**	**428.2233**	1733.8533	**867.4303**
T	**956.4870**	478.7471	1646.8213	823.9143
P	**1053.5397**	527.2735	**1545.7736**	773.3905
L	**1166.6238**	583.8155	**1448.7209**	724.8641
F	**1313.6922**	657.3497	**1335.6368**	668.3220
F	1460.7606	730.8840	**1188.5684**	594.7878
N	1574.8036	787.9054	**1041.5000**	521.2536
T	1675.8512	**838.4293**	**927.4571**	464.2322
L	1788.9353	894.9713	**826.4094**	413.7083
Y	1951.9986	976.5030	**713.3253**	357.1663
D	2067.0256	1034.0164	**550.2620**	275.6346
P	2164.0783	1082.5428	**435.2350**	**218.1212**
Y	2327.1417	1164.0745	**338.1823**	169.5948
R	2483.2428	1242.1250	**175.1190**	88.0631

Threonine synthase
HCGISHTGSFK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
7.1˙1.17...	63.912	1421.7114	711.8630	2		HATTLKAPASRGGR		< 1	1421.7852
9.1˙1.13...	24.586	1399.6583	700.8364	2	77	HCGISHTGSFK	ICAT-C(C)@2	54	1399.6666
9.1˙1.13...	24.395	1408.6772	705.3459	2	77	HCGISHTGSFK	ICAT-C:13C(9)(C)@2	99	1408.6969
9.1˙1.13...	25.625	1221.6115	611.8130	2	133	HCVNSVSIK	ICAT-C:13C(9)(C)@2	90	1221.6587
10.1˙1.1...	68.828	0.0000	695.3573	0		HDHGAGRAAAHPGHAQAVQVPEGTHGGR		< 1	2777.3354
2.1˙1.15	43.530	0.0000	613.2959	0		[illegible]		< 1	1836.8351

Peptide ID Hypotheses - 9.1dot;1.1356.2.9

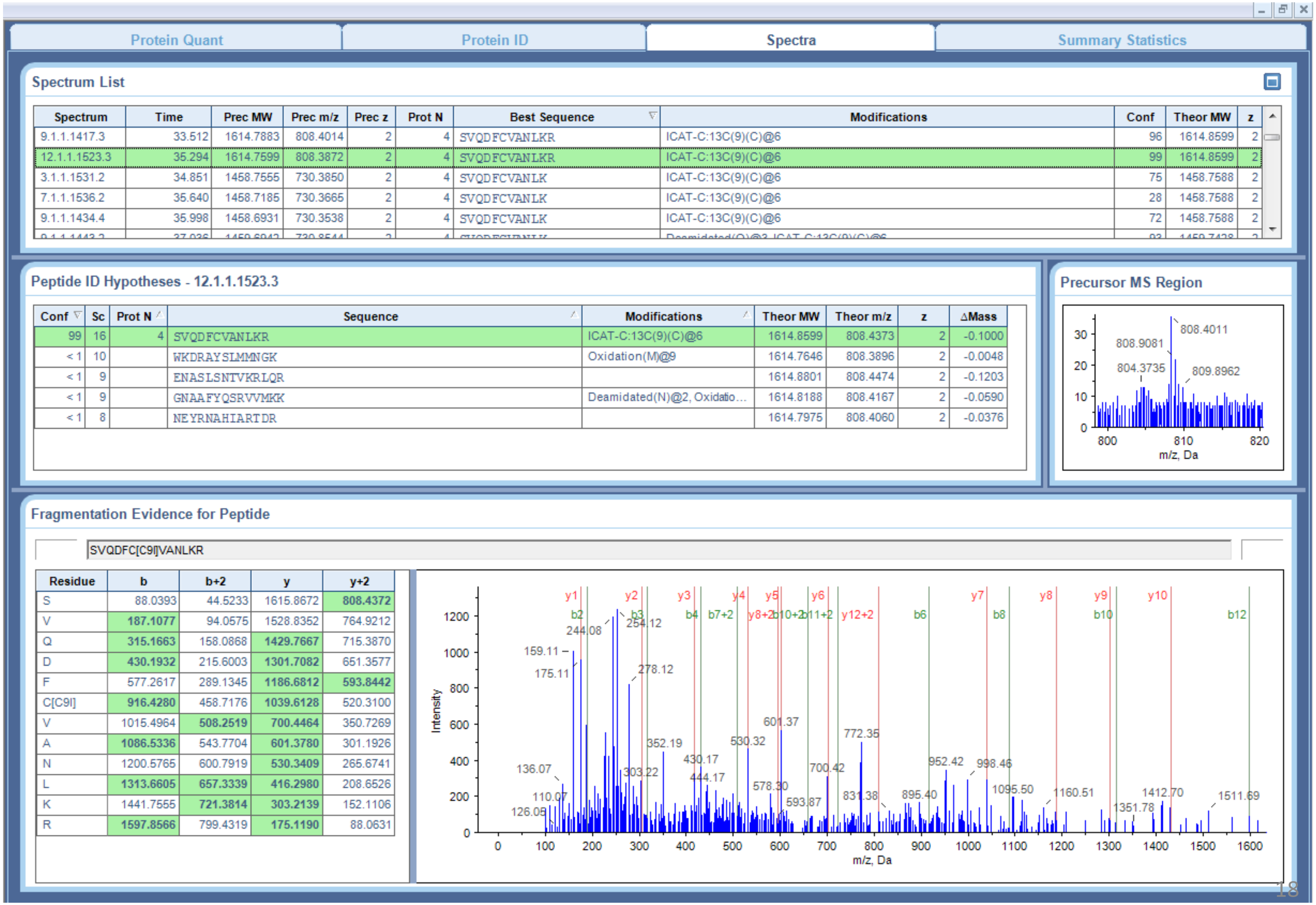
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	19	77	HCGISHTGSFK	ICAT-C:13C(9)(C)@2	1408.6969	705.3557	2	-0.0196
< 1	13		IRSSENGPMGSFK		1408.6769	705.3457	2	0.0003
< 1	12		HCLGRLISFK	ICAT-C:13C(9)(C)@2	1408.8060	705.4103	2	-0.1288
< 1	12		VWAVFMLVVAMK	Oxidation(M)@11	1408.7611	705.3878	2	-0.0839
< 1	11		HPVDLLQLLSFK		1408.8079	705.4112	2	-0.1306

Fragmentation Evidence for Peptide

HC[C9I]GISHTGSFK

Residue	b	b+2	y	y+2
H	138.0662	69.5367	1409.7041	705.3557
C[C9I]	477.2326	239.1199	1272.6452	636.8263
G	534.2540	267.6306	933.4789	467.2431
I	647.3381	324.1727	876.4574	438.7323
S	734.3701	367.6887	763.3733	382.1903
H	871.4290	436.2182	676.3413	338.6743
T	972.4767	486.7420	539.2824	270.1448
G	1029.4982	515.2527	438.2347	219.6210
S	1116.5302	558.7687	381.2132	191.1103
F	1263.5986	632.3029	294.1812	147.5942
K	1391.6936	696.3504	147.1128	74.0600

Oxalic acid oxidase
SVQDFCVANLKR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
9.1.1.1417.3	33.512	1614.7883	808.4014	2	4	SVQDFCVANLKR	ICAT-C:13C(9)(C)@6	96	1614.8599	2
12.1.1.1523.3	35.294	1614.7599	808.3872	2	4	SVQDFCVANLKR	ICAT-C:13C(9)(C)@6	99	1614.8599	2
3.1.1.1531.2	34.851	1458.7555	730.3850	2	4	SVQDFCVANLK	ICAT-C:13C(9)(C)@6	75	1458.7588	2
7.1.1.1536.2	35.640	1458.7185	730.3665	2	4	SVQDFCVANLK	ICAT-C:13C(9)(C)@6	28	1458.7588	2
9.1.1.1434.4	35.998	1458.6931	730.3538	2	4	SVQDFCVANLK	ICAT-C:13C(9)(C)@6	72	1458.7588	2

Peptide ID Hypotheses - 12.1.1.1523.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	4	SVQDFCVANLKR	ICAT-C:13C(9)(C)@6	1614.8599	808.4373	2	-0.1000
< 1	10		WKDRAYSLMMNGK	Oxidation(M)@9	1614.7646	808.3896	2	-0.0048
< 1	9		ENASLSNTVKRLQR		1614.8801	808.4474	2	-0.1203
< 1	9		GNAAFYQSRVVMKK	Deamidated(N)@2, Oxidatio...	1614.8188	808.4167	2	-0.0590
< 1	8		NEYRNAHIARTDR		1614.7975	808.4060	2	-0.0376

Precursor MS Region

Fragmentation Evidence for Peptide

SVQDFC[C9I]VANLKR

Residue	b	b+2	y	y+2
S	88.0393	44.5233	1615.8672	**808.4372**
V	**187.1077**	94.0575	1528.8352	764.9212
Q	**315.1663**	158.0868	**1429.7667**	715.3870
D	**430.1932**	215.6003	**1301.7082**	651.3577
F	577.2617	289.1345	**1186.6812**	**593.8442**
C[C9I]	**916.4280**	458.7176	**1039.6128**	520.3100
V	1015.4964	**508.2519**	**700.4464**	350.7269
A	**1086.5336**	543.7704	**601.3780**	301.1926
N	1200.5765	600.7919	**530.3409**	265.6741
L	**1313.6605**	**657.3339**	**416.2980**	208.6526
K	1441.7555	**721.3814**	**303.2139**	152.1106
R	**1597.8566**	799.4319	**175.1190**	88.0631

Oxalic acid oxidase
AETPAGYPCIRPIHVK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
3.1˙1.22...	60.064	1194.6041	598.3093	2		AETFGGEGGTAAK		< 1	1194.5516	2
2.1˙1.15...	28.211	1987.0409	497.7675	4	9	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	1	1987.0760	4
10.1˙1.1...	32.228	1986.9966	663.3395	3	9	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	97	1987.0760	3
12.1˙1.1...	29.203	1987.0282	497.7643	4	9	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	47	1987.0760	4
12.1˙1.2...	74.559	0.0000	717.6059	0		AETRLHSRHESFSAELPSVPSPY...		< 1	2866.4111	4

Peptide ID Hypotheses - 10.1dot;1.1535.3.10

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97	14	9	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	1987.0760	663.3660	3	-0.0794
< 1	11		AFMNEGTIVYIADSNGER	Deamidated(N)@15	1986.8993	663.3071	3	0.0973
< 1	11		SFGMGLFYAVLASPASGNAK		1986.9873	663.3364	3	0.0093
< 1	11		SLTSTLSRGPEGANKEIVK	Deamidated(N)@14	1987.0586	663.3601	3	-0.0620
< 1	11		VAMYNAEIFCETKNK	ICAT-C(C)@10	1986.9543	663.3254	3	0.0423

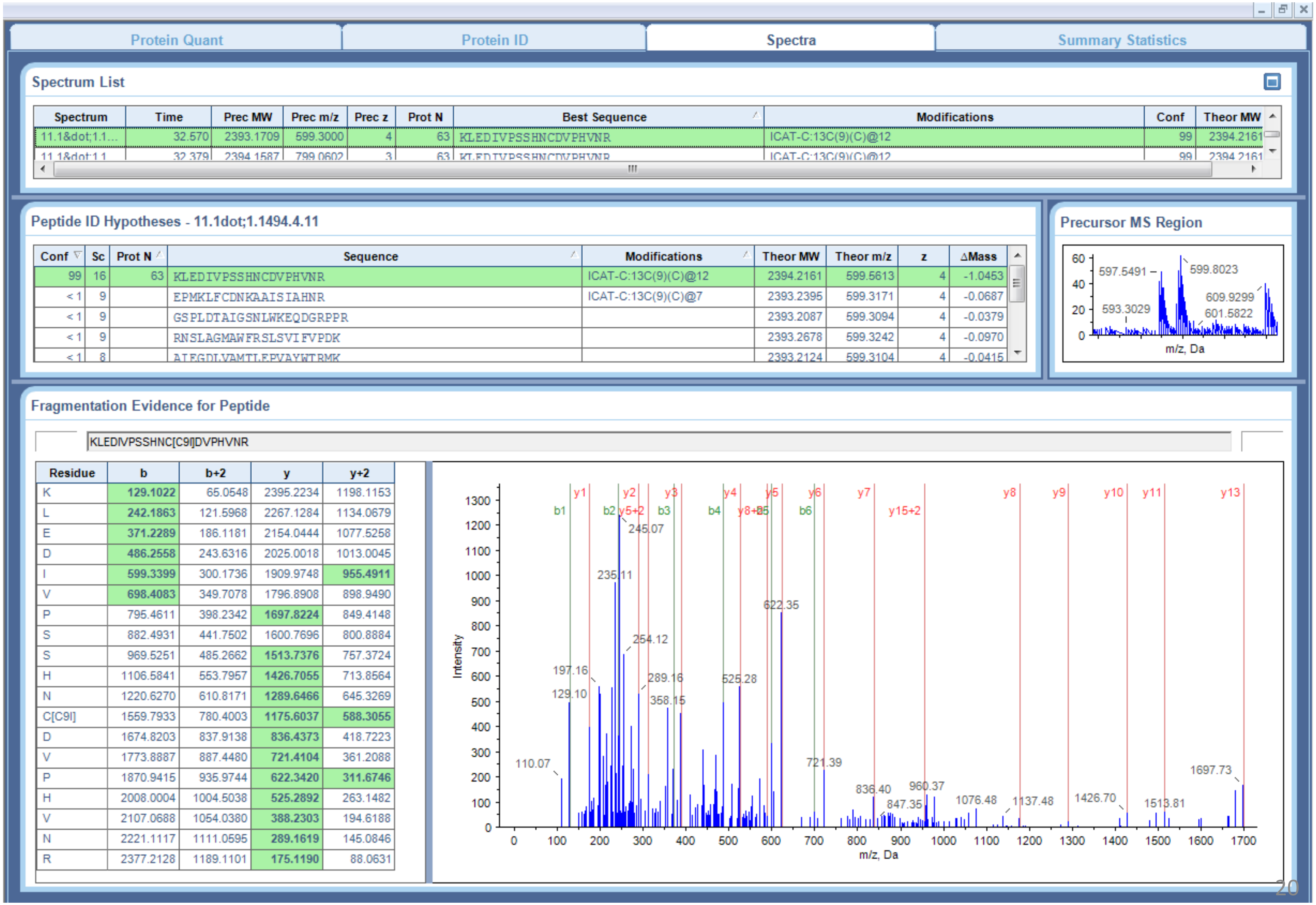
Precursor MS Region

Fragmentation Evidence for Peptide

AETPAGYPC[C9I]IRPIHVK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1988.0833	994.5453
E	**201.0870**	101.0471	1917.0462	959.0267
T	**302.1347**	151.5710	**1788.0036**	894.5054
P	**399.1874**	200.0974	**1686.9559**	843.9816
A	470.2245	235.6159	**1589.9032**	**795.4552**
G	**527.2460**	**264.1266**	**1518.8661**	**759.9367**
Y	690.3093	345.6583	**1461.8446**	**731.4259**
P	787.3621	394.1847	**1298.7813**	649.8943
C[C9I]	1126.5285	563.7679	**1201.7285**	601.3679
I	1239.6125	620.3099	**862.5621**	431.7847
R	1395.7136	698.3605	**749.4781**	375.2427
P	1492.7664	746.8868	**593.3770**	297.1921
I	1605.8505	803.4289	496.3242	248.6657
H	1742.9094	871.9583	**383.2401**	192.1237
V	1841.9778	**921.4925**	**246.1812**	123.5942
K	1970.0728	985.5400	**147.1128**	74.0600

Initiation factor 5A-4, putative
KLEDIVPSSHN<u>C</u>DVPHVNR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
11.1˙1.1...	32.570	2393.1709	599.3000	4	63	KLEDIVPSSHNCDVPHVNR	ICAT-C:13C(9)(C)@12	99	2394.2161
11.1˙1.1	32.379	2394.1587	799.0602	3	63	KLEDIVPSSHNCDVPHVNR	ICAT-C:13C(9)(C)@12	99	2394.2161

Peptide ID Hypotheses - 11.1dot;1.1494.4.11

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	63	KLEDIVPSSHNCDVPHVNR	ICAT-C:13C(9)(C)@12	2394.2161	599.5613	4	-1.0453
< 1	9		EPMKLFCDNKAAISIAHNR	ICAT-C:13C(9)(C)@7	2393.2395	599.3171	4	-0.0687
< 1	9		GSPLDTAIGSNLWKEQDGRPPR		2393.2087	599.3094	4	-0.0379
< 1	9		RNSLAGMAWFRSLSVIFVPDK		2393.2678	599.3242	4	-0.0970
< 1	8		AIEGDLVAMTLEPVAYWTRMK		2393.2124	599.3104	4	-0.0415

Precursor MS Region

Fragmentation Evidence for Peptide

KLEDIVPSSHNC[C9I]DVPHVNR

Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2395.2234	1198.1153
L	**242.1863**	121.5968	2267.1284	1134.0679
E	**371.2289**	186.1181	2154.0444	1077.5258
D	**486.2558**	243.6316	2025.0018	1013.0045
I	**599.3399**	300.1736	1909.9748	**955.4911**
V	**698.4083**	349.7078	1796.8908	898.9490
P	795.4611	398.2342	**1697.8224**	849.4148
S	882.4931	441.7502	1600.7696	800.8884
S	969.5251	485.2662	**1513.7376**	757.3724
H	1106.5841	553.7957	**1426.7055**	713.8564
N	1220.6270	610.8171	**1289.6466**	645.3269
C[C9I]	1559.7933	780.4003	**1175.6037**	**588.3055**
D	1674.8203	837.9138	**836.4373**	418.7223
V	1773.8887	887.4480	**721.4104**	361.2088
P	1870.9415	935.9744	**622.3420**	**311.6746**
H	2008.0004	1004.5038	**525.2892**	263.1482
V	2107.0688	1054.0380	**388.2303**	194.6188
N	2221.1117	1111.0595	**289.1619**	145.0846
R	2377.2128	1189.1101	**175.1190**	88.0631

Mitochondrial elongation factor Tu
QVGVPSLV<u>C</u>FLNK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
7.1˙1.17...	51.281	1612.7650	807.3898	2	75	QVGVPSLVCFLNK	Gln->pyro-Glu@N-term, ICAT-C(C)@9	24	1612.8647	2
7.1˙1.17...	51.174	1621.7965	811.9055	2	75	QVGVPSLVCFLNK	Gln->pyro-Glu@N-term, ICAT-C:13C(9)(C)@9	99	1621.8949	2
7.1˙1.17...	44.684	1629.7897	815.9021	2	75	QVGVPSLVCFLNK	ICAT-C(C)@9	99	1629.8912	2
7.1˙1.17...	44.535	1638.8098	820.4122	2	75	QVGVPSLVCFLNK	ICAT-C:13C(9)(C)@9	99	1638.9214	2
8.1˙1.15...	30.361	1255.5500	628.7823	2	105	QVISSEGQRPR		90	1255.6633	2

Peptide ID Hypotheses - 7.1dot;1.1706.2.7

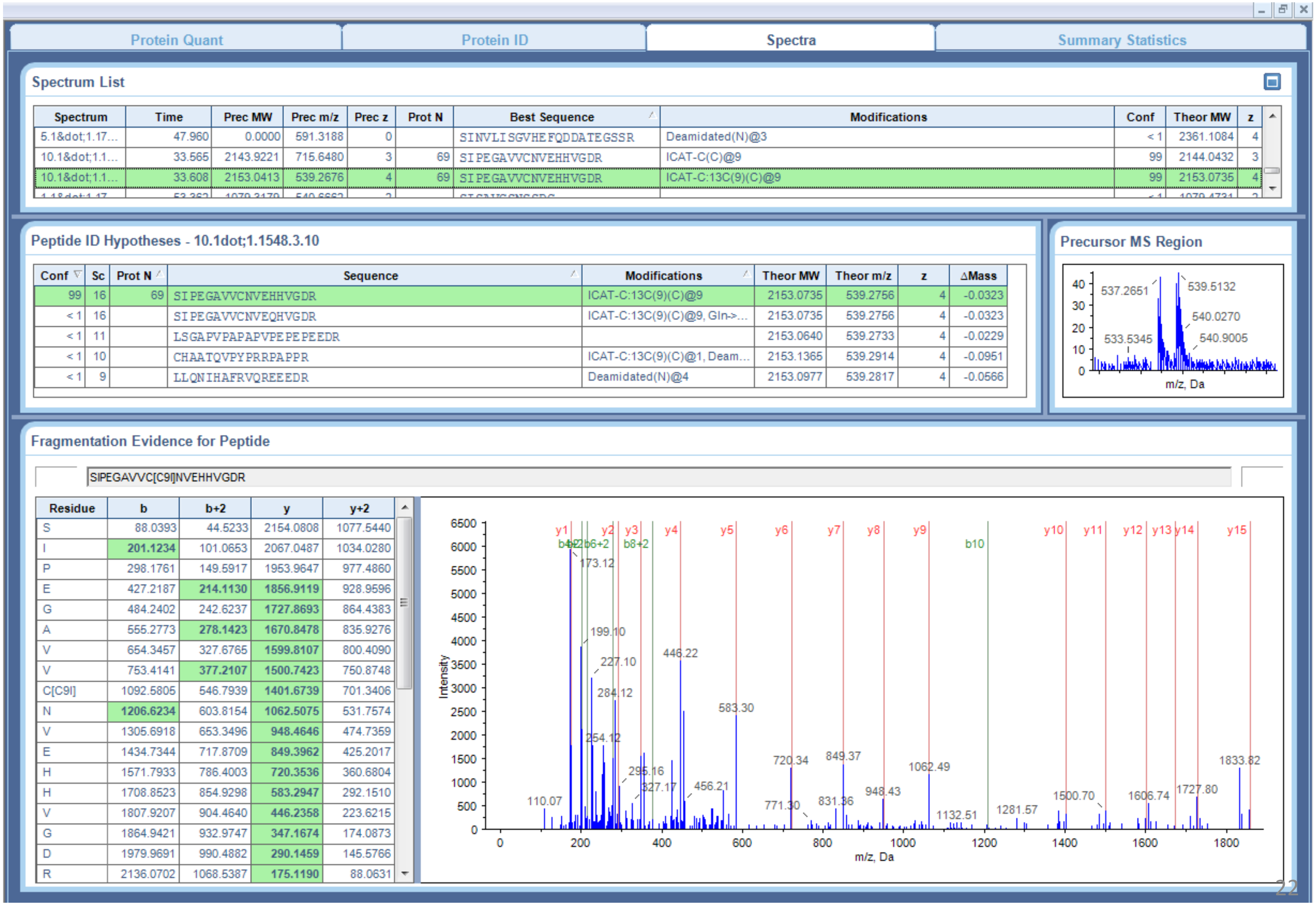
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	75	QVGVPSLVCFLNK	ICAT-C(C)@9	1629.8912	815.9529	2	-0.1016
< 1	11		RKVVMLFQNCR	Deamidated(Q)@8, ICAT-C:...	1629.8894	815.9520	2	-0.0998
< 1	10		GAVGVGSSLGGTSELPDK		1629.8209	815.9178	2	-0.0313
< 1	10		GGLGVVAGGGGGGGGWEMR		1629.7682	815.8914	2	0.0215
< 1	10		INRPTSVFSVRVGAK		1629.9315	815.9730	2	-0.1418

Fragmentation Evidence for Peptide

QVGVPSLVC[C0I]FLNK

Residue	b	b+2	y	y+2
Q	**129.0659**	65.0366	1630.8985	815.9529
V	**228.1343**	114.5708	1502.8399	751.9236
G	**285.1557**	143.0815	**1403.7715**	702.3894
V	**384.2241**	192.6157	**1346.7501**	673.8787
P	**481.2769**	241.1421	**1247.6817**	624.3445
S	568.3089	284.6581	**1150.6289**	575.8181
L	681.3930	341.2001	**1063.5969**	**532.3021**
V	780.4614	390.7343	**950.5128**	475.7600
C[C0I]	1110.5976	555.8024	**851.4444**	**426.2258**
F	1257.6660	629.3366	**521.3082**	**261.1577**
L	1370.7501	685.8787	**374.2398**	187.6235
N	1484.7930	742.9001	**261.1557**	131.0815
K	**1612.8880**	806.9476	**147.1128**	74.0600

60S ribosomal protein L2
SIPEGAVV<u>C</u>NVEHHVGDR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
5.1˙1.17...	47.960	0.0000	591.3188	0		SINVLISGVHEFQDDATEGSSR	Deamidated(N)@3	< 1	2361.1084	4
10.1˙1.1...	33.565	2143.9221	715.6480	3	69	SIPEGAVVCNVEHHVGDR	ICAT-C(C)@9	99	2144.0432	3
10.1˙1.1...	33.608	2153.0413	539.2676	4	69	SIPEGAVVCNVEHHVGDR	ICAT-C:13C(9)(C)@9	99	2153.0735	4

Peptide ID Hypotheses - 10.1dot;1.1548.3.10

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	69	SIPEGAVVCNVEHHVGDR	ICAT-C:13C(9)(C)@9	2153.0735	539.2756	4	-0.0323
< 1	16		SIPEGAVVCNVEQHVGDR	ICAT-C:13C(9)(C)@9, Gln->...	2153.0735	539.2756	4	-0.0323
< 1	11		LSGAPVPAPAPVPEPEPEEDR		2153.0640	539.2733	4	-0.0229
< 1	10		CHAATQVPYPRRPAPPR	ICAT-C:13C(9)(C)@1, Deam...	2153.1365	539.2914	4	-0.0951
< 1	9		LLQNIHAFRVQREEEDR	Deamidated(N)@4	2153.0977	539.2817	4	-0.0566

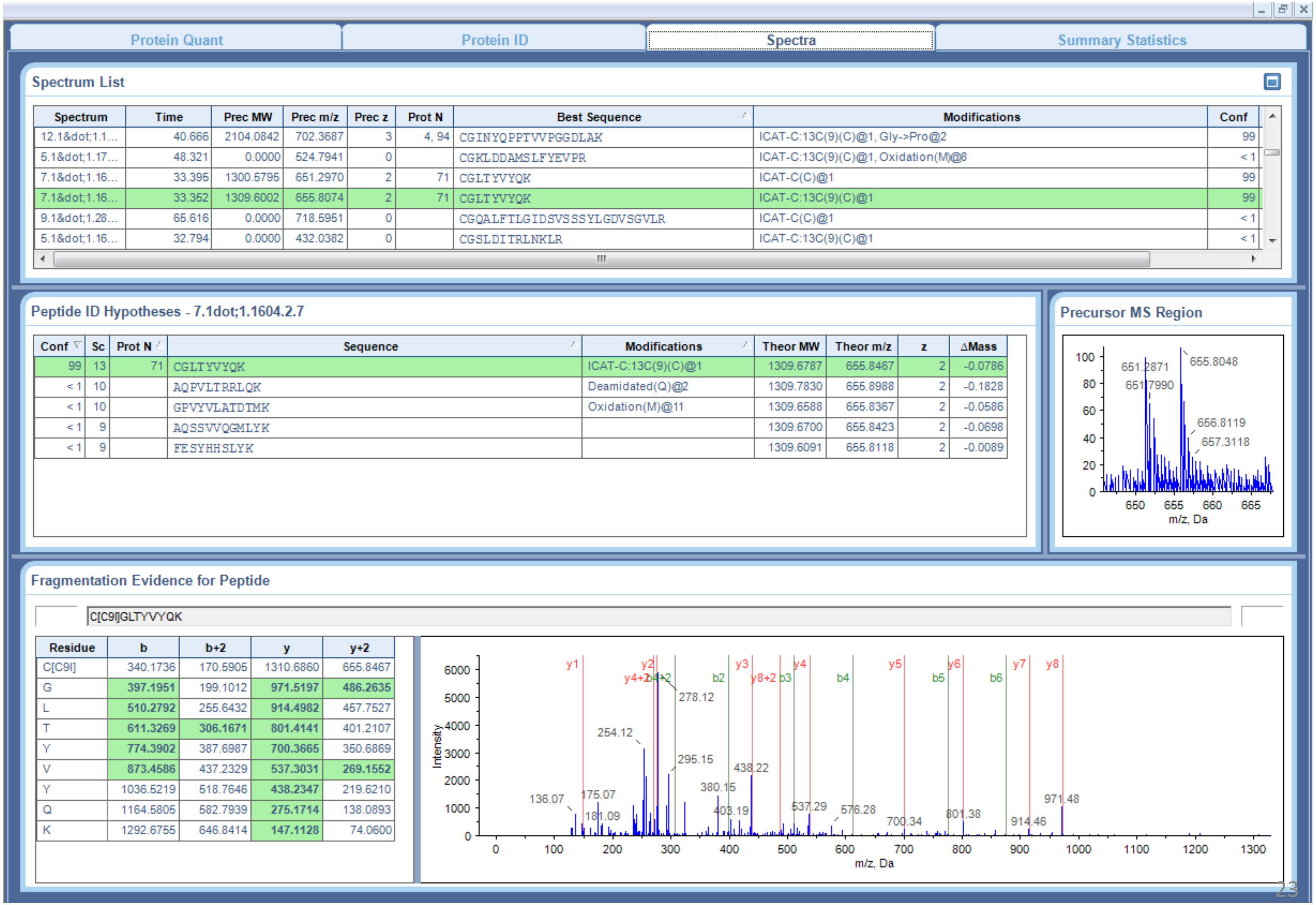
Precursor MS Region

Fragmentation Evidence for Peptide

SIPEGAVVC[C9I]NVEHHVGDR

Residue	b	b+2	y	y+2
S	88.0393	44.5233	2154.0808	1077.5440
I	**201.1234**	101.0653	2067.0487	1034.0280
P	298.1761	149.5917	1953.9647	977.4860
E	427.2187	**214.1130**	**1856.9119**	928.9596
G	484.2402	242.6237	**1727.8693**	864.4383
A	555.2773	**278.1423**	**1670.8478**	835.9276
V	654.3457	327.6765	**1599.8107**	800.4090
V	753.4141	**377.2107**	**1500.7423**	750.8748
C[C9I]	1092.5805	546.7939	**1401.6739**	701.3406
N	**1206.6234**	603.8154	**1062.5075**	531.7574
V	1305.6918	653.3496	**948.4646**	474.7359
E	1434.7344	717.8709	**849.3962**	425.2017
H	1571.7933	786.4003	**720.3536**	360.6804
H	1708.8523	854.9298	**583.2947**	292.1510
V	1807.9207	904.4640	**446.2358**	223.6215
G	1864.9421	932.9747	**347.1674**	174.0873
D	1979.9691	990.4882	**290.1459**	145.5766
R	2136.0702	1068.5387	**175.1190**	88.0631

Ubiquitin extension protein (UBQ5)
CGLTYVYQK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf
12.1˙1.1...	40.666	2104.0842	702.3687	3	4, 94	CGINYQPPTVVPGGDLAK	ICAT-C:13C(9)(C)@1, Gly->Pro@2	99
5.1˙1.17...	48.321	0.0000	524.7941	0		CGKLDDAMSLFYEVPR	ICAT-C:13C(9)(C)@1, Oxidation(M)@8	< 1
7.1˙1.16...	33.395	1300.5795	651.2970	2	71	CGLTYVYQK	ICAT-C(C)@1	99
7.1˙1.16...	33.352	1309.6002	655.8074	2	71	CGLTYVYQK	ICAT-C:13C(9)(C)@1	99
9.1˙1.28...	65.616	0.0000	718.5951	0		CGQALFTLGIDSVSSSYLGDVSGVLR	ICAT-C(C)@1	< 1
5.1˙1.16...	32.794	0.0000	432.0382	0		CGSLDITRLNKLR	ICAT-C:13C(9)(C)@1	< 1

Peptide ID Hypotheses - 7.1dot;1.1604.2.7

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	71	CGLTYVYQK	ICAT-C:13C(9)(C)@1	1309.6787	655.8467	2	-0.0786
< 1	10		AQPVLTRRLQK	Deamidated(Q)@2	1309.7830	655.8988	2	-0.1828
< 1	10		GPVYVLATDTMK	Oxidation(M)@11	1309.6588	655.8367	2	-0.0586
< 1	9		AQSSVVQGMLYK		1309.6700	655.8423	2	-0.0698
< 1	9		FESYHHSLYK		1309.6091	655.8118	2	-0.0089

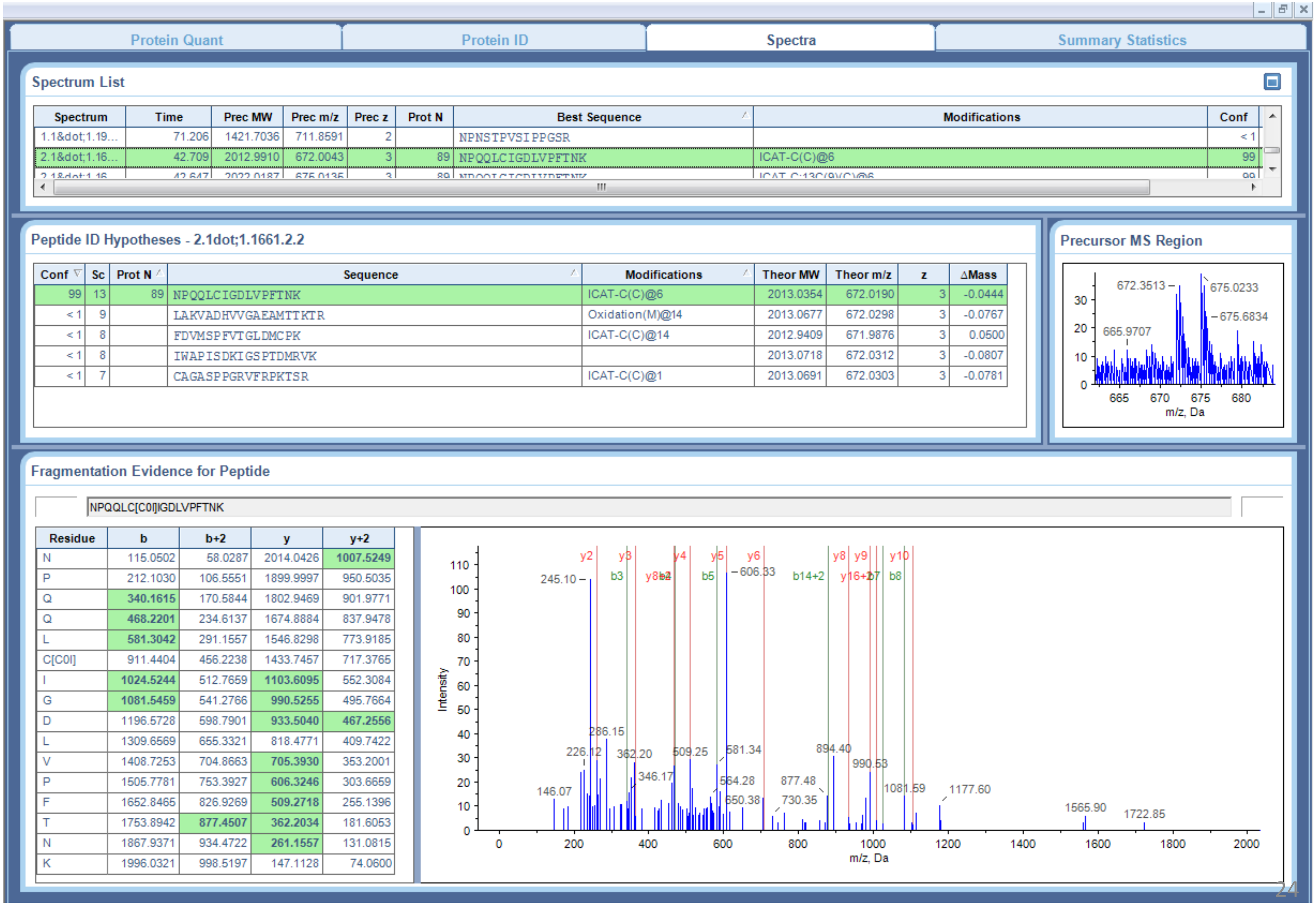
Precursor MS Region

Fragmentation Evidence for Peptide

C[C9I]GLTYVYQK

Residue	b	b+2	y	y+2
C[C9I]	340.1736	170.5905	1310.6860	655.8467
G	**397.1951**	199.1012	**971.5197**	**486.2635**
L	**510.2792**	255.6432	**914.4982**	457.7527
T	**611.3269**	**306.1671**	**801.4141**	401.2107
Y	**774.3902**	387.6987	**700.3665**	350.6869
V	**873.4586**	437.2329	**537.3031**	**269.1552**
Y	1036.5219	518.7646	**438.2347**	219.6210
Q	1164.5805	582.7939	**275.1714**	138.0893
K	1292.6755	646.8414	**147.1128**	74.0600

Early response to dehydration protein (ERD12)
NPQQLCIGDLVPFTNK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf
1.1˙1.19...	71.206	1421.7036	711.8591	2		NPNSTPVSIPPGSR		< 1
2.1˙1.16...	42.709	2012.9910	672.0043	3	89	NPQQLCIGDLVPFTNK	ICAT-C(C)@6	99
2.1˙1.16	42.647	2022.0187	675.0135	3	89	NPQQLCIGDLVPFTNK	ICAT_C:13C(9)(C)@6	99

Peptide ID Hypotheses - 2.1dot;1.1661.2.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	13	89	NPQQLCIGDLVPFTNK	ICAT-C(C)@6	2013.0354	672.0190	3	-0.0444
< 1	9		LAKVADHVVGAEAMTTKTR	Oxidation(M)@14	2013.0677	672.0298	3	-0.0767
< 1	8		FDVMSPFVTGLDMCPK	ICAT-C(C)@14	2012.9409	671.9876	3	0.0500
< 1	8		IWAPISDKIGSPTDMRVK		2013.0718	672.0312	3	-0.0807
< 1	7		CAGASPPGRVFRPKTSR	ICAT-C(C)@1	2013.0691	672.0303	3	-0.0781

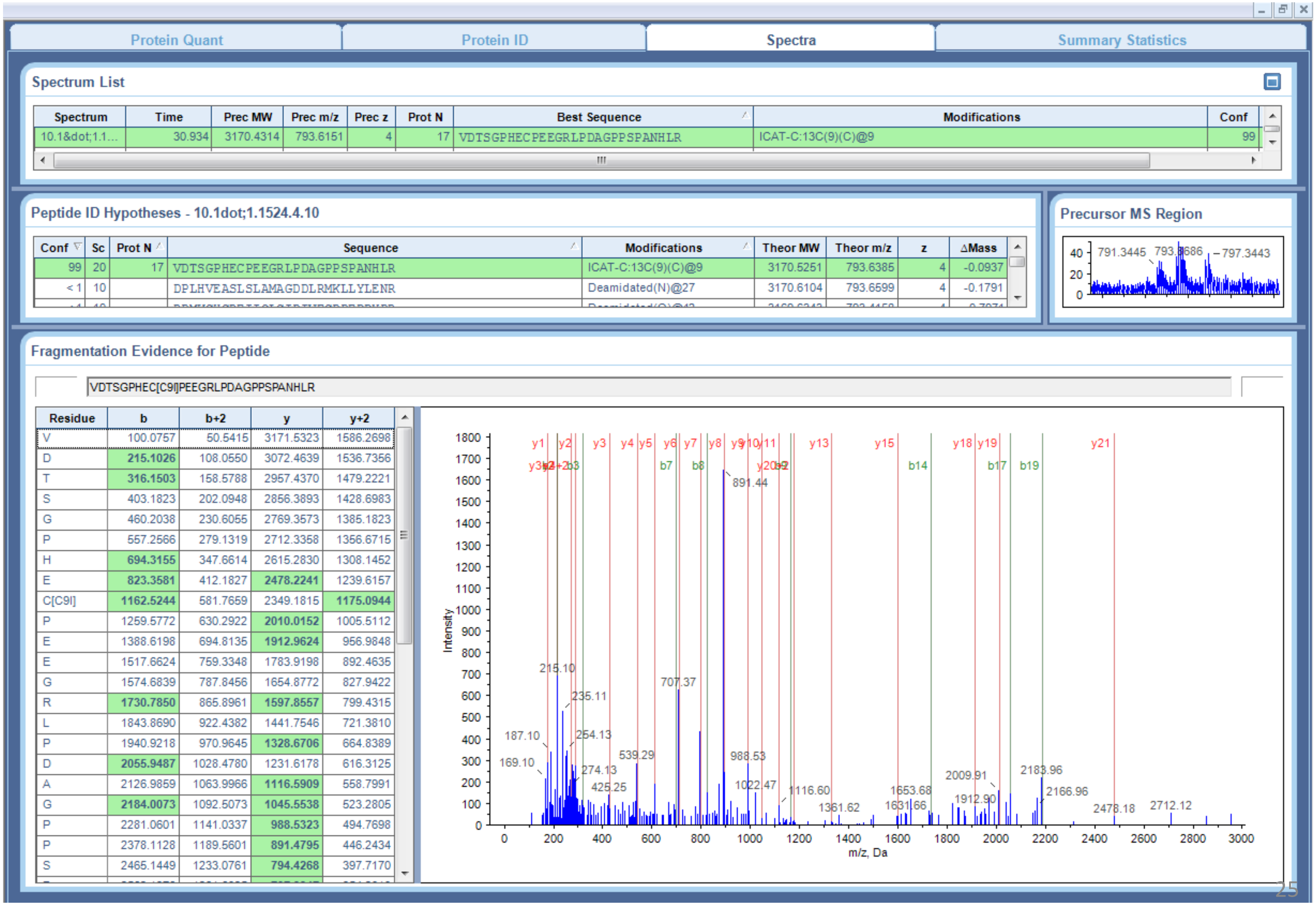
Precursor MS Region

Fragmentation Evidence for Peptide

NPQQLC[C0I]IGDLVPFTNK

Residue	b	b+2	y	y+2
N	115.0502	58.0287	2014.0426	**1007.5249**
P	212.1030	106.5551	1899.9997	950.5035
Q	**340.1615**	170.5844	1802.9469	901.9771
Q	**468.2201**	234.6137	1674.8884	837.9478
L	**581.3042**	291.1557	1546.8298	773.9185
C[C0I]	911.4404	456.2238	1433.7457	717.3765
I	**1024.5244**	512.7659	**1103.6095**	552.3084
G	**1081.5459**	541.2766	**990.5255**	495.7664
D	1196.5728	598.7901	**933.5040**	**467.2556**
L	1309.6569	655.3321	818.4771	409.7422
V	1408.7253	704.8663	**705.3930**	353.2001
P	1505.7781	753.3927	**606.3246**	303.6659
F	1652.8465	826.9269	**509.2718**	255.1396
T	1753.8942	**877.4507**	**362.2034**	181.6053
N	1867.9371	934.4722	**261.1557**	131.0815
K	1996.0321	998.5197	147.1128	74.0600

Stromal ascorbate peroxidase
VDTSGPHECPEEGRLPDAGPPSPANHLR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf
10.1˙1.1...	30.934	3170.4314	793.6151	4	17	VDTSGPHECPEEGRLPDAGPPSPANHLR	ICAT-C:13C(9)(C)@9	99

Peptide ID Hypotheses - 10.1dot;1.1524.4.10

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	20	17	VDTSGPHECPEEGRLPDAGPPSPANHLR	ICAT-C:13C(9)(C)@9	3170.5251	793.6385	4	-0.0937
< 1	10		DPLHVEASLSLAMAGDDLRMKLLYLENR	Deamidated(N)@27	3170.6104	793.6599	4	-0.1791

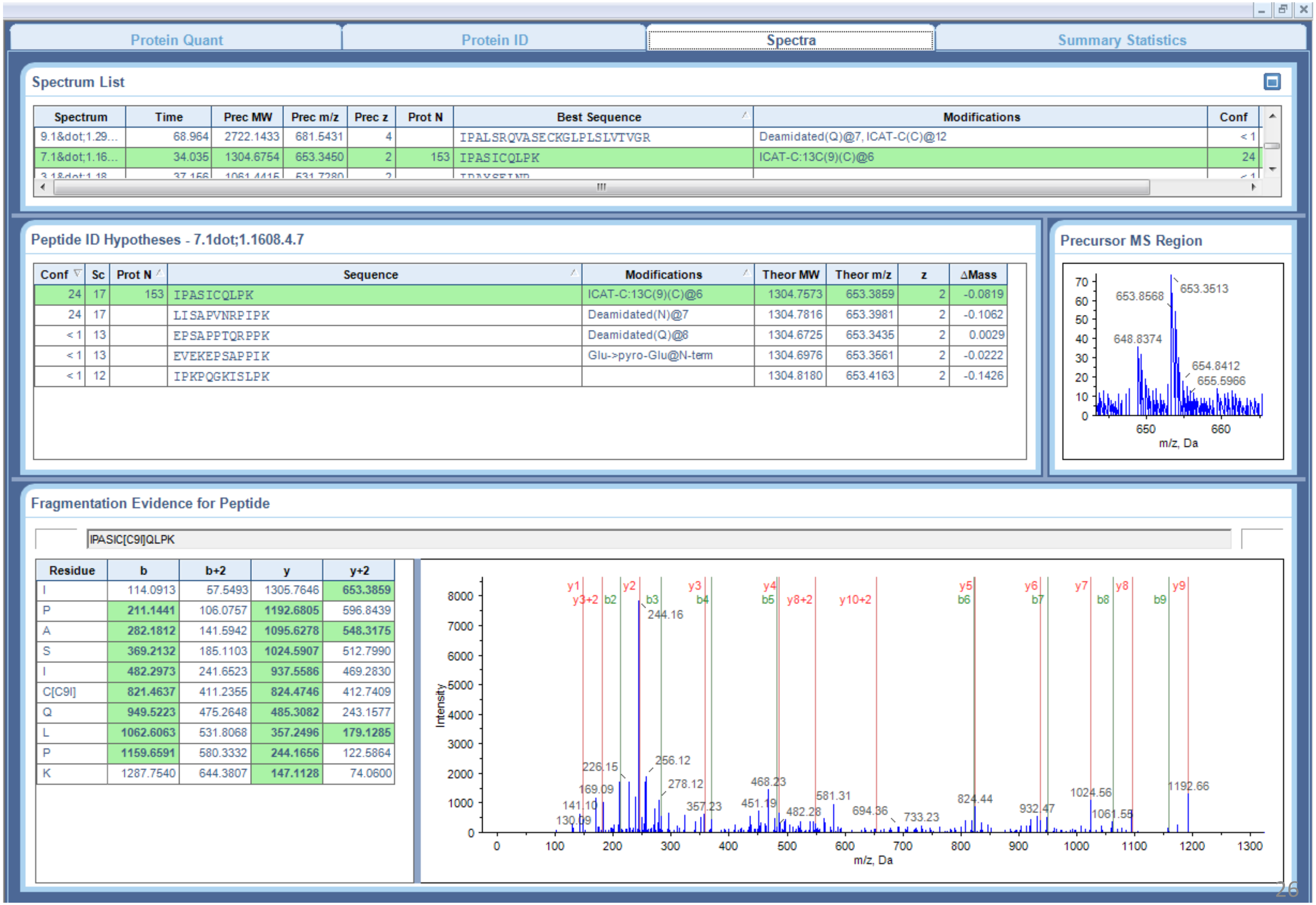
Precursor MS Region

Fragmentation Evidence for Peptide

VDTSGPHEC[C9I]PEEGRLPDAGPPSPANHLR

Residue	b	b+2	y	y+2
V	100.0757	50.5415	3171.5323	1586.2698
D	**215.1026**	108.0550	3072.4639	1536.7356
T	**316.1503**	158.5788	2957.4370	1479.2221
S	403.1823	202.0948	2856.3893	1428.6983
G	460.2038	230.6055	2769.3573	1385.1823
P	557.2566	279.1319	2712.3358	1356.6715
H	**694.3155**	347.6614	2615.2830	1308.1452
E	**823.3581**	412.1827	**2478.2241**	1239.6157
C[C9I]	**1162.5244**	581.7659	2349.1815	**1175.0944**
P	1259.5772	630.2922	**2010.0152**	1005.5112
E	1388.6198	694.8135	**1912.9624**	956.9848
E	1517.6624	759.3348	1783.9198	892.4635
G	1574.6839	787.8456	1654.8772	827.9422
R	**1730.7850**	865.8961	**1597.8557**	799.4315
L	1843.8690	922.4382	1441.7546	721.3810
P	1940.9218	970.9645	**1328.6706**	664.8389
D	**2055.9487**	1028.4780	1231.6178	616.3125
A	2126.9859	1063.9966	**1116.5909**	558.7991
G	**2184.0073**	1092.5073	**1045.5538**	523.2805
P	2281.0601	1141.0337	**988.5323**	494.7698
P	2378.1128	1189.5601	**891.4795**	446.2434
S	2465.1449	1233.0761	**794.4268**	397.7170

Extensin-like protein
IPASICQLPK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf
9.1˙1.29...	68.964	2722.1433	681.5431	4		IPALSRQVASECKGLPLSLVTVGR	Deamidated(Q)@7, ICAT-C(C)@12	< 1
7.1˙1.16...	34.035	1304.6754	653.3450	2	153	IPASICQLPK	ICAT-C:13C(9)(C)@6	24

Peptide ID Hypotheses - 7.1dot;1.1608.4.7

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
24	17	153	IPASICQLPK	ICAT-C:13C(9)(C)@6	1304.7573	653.3859	2	-0.0819
24	17		LISAPVNRPIPK	Deamidated(N)@7	1304.7816	653.3981	2	-0.1062
< 1	13		EPSAPPTQRPPK	Deamidated(Q)@8	1304.6725	653.3435	2	0.0029
< 1	13		EVEKEPSAPPIK	Glu->pyro-Glu@N-term	1304.6976	653.3561	2	-0.0222
< 1	12		IPKPQGKISLPK		1304.8180	653.4163	2	-0.1426

Precursor MS Region

Fragmentation Evidence for Peptide

IPASIC[C9I]QLPK

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1305.7646	**653.3859**
P	**211.1441**	106.0757	**1192.6805**	596.8439
A	**282.1812**	141.5942	**1095.6278**	**548.3175**
S	**369.2132**	185.1103	**1024.5907**	512.7990
I	**482.2973**	241.6523	**937.5586**	469.2830
C[C9I]	**821.4637**	411.2355	**824.4746**	412.7409
Q	**949.5223**	475.2648	**485.3082**	243.1577
L	**1062.6063**	531.8068	**357.2496**	**179.1285**
P	**1159.6591**	580.3332	**244.1656**	122.5864
K	1287.7540	644.3807	**147.1128**	74.0600

Cell division protein FtsH
GCLLVGPPGTGK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
8.1˙1.13...	32.801	1324.6682	663.3414	2	125	GCLLVGPPGTGK	ICAT-C(C)@2	76	1324.7173
8.1˙1.13...	32.758	1333.6885	667.8515	2	125	GCLLVGPPGTGK	ICAT-C:13C(9)(C)@2	93	1333.7476
12.1˙1.2...	74.181	0.0000	685.1399	0		GCSGVKGDTVGPAGYAPVGLGTAFGGSK	ICAT-C(C)@2	< 1	2736.3540
12.1˙1.1...	36.014	3031.2231	1011.41...	3	90	GCVEVNIGANPSAEEGGEDEGVDDSVEK	ICAT-C(C)@2	99	3031.3201
12.1˙1.1...	35.928	3040.2380	1014.42...	3	90	GCVEVNIGANPSAEEGGEDEGVDDSVEK	ICAT-C:13C(9)(C)@2	99	3040.3503
7.1˙1.15...	32.509	0.0000	432.6904	0		GCVNSPEEFIGAIR	ICAT-C:13C(9)(C)@2	< 1	1726.8760
6.1˙1.17...	55.987	0.0000	699.2973	0		GDAAGRPAGLSRGGR		< 1	1396.7284

Peptide ID Hypotheses - 8.1dot;1.1302.2.8

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
93	14	125	GCLLVGPPGTGK	ICAT-C:13C(9)(C)@2	1333.7476	667.8810	2	-0.0591
< 1	11		GASFFNSGGSQFK	Deamidated(N)@6	1333.5939	667.8042	2	0.0946
< 1	11		LGPQLIDNGPGPR	Deamidated(Q)@4	1333.6990	667.8568	2	-0.0106

Precursor MS Region

Fragmentation Evidence for Peptide

GC[C9I]LLVGPPGTGK

Residue	b	b+2	y	y+2
G	58.0287	29.5180	1334.7548	667.8810
C[C9I]	**397.1951**	**199.1012**	1277.7333	639.3703
L	**510.2792**	255.6432	**938.5669**	469.7871
L	**623.3632**	312.1853	**825.4829**	413.2451
V	**722.4317**	361.7195	**712.3988**	356.7030
G	779.4531	390.2302	**613.3304**	307.1688
P	876.5059	438.7566	**556.3089**	278.6581
P	973.5586	487.2830	**459.2562**	230.1317
G	1030.5801	515.7937	**362.2034**	181.6053
T	1131.6278	**566.3175**	**305.1819**	153.0946
G	1188.6492	594.8283	**204.1343**	102.5708
K	1316.7442	658.8757	**147.1128**	74.0600

Unnamed protein product
LLICGGSAYPR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
3.1.1.1960.2	34.430	849.5791	425.7968	2		LLGTRYK		< 1	849.5073	2
2.1.1.1674.4	35.659	1384.8097	693.4121	2		LLICGGSAYPR	ICAT-C:13C(9)(C)@4	62	1384.7584	2
5.1.1.1824.3	34.558	1295.8254	432.9491	3		LLIDNLIKAQR		2	1295.7925	3

Peptide ID Hypotheses - 2.1.1.1674.4

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
62	11		LLICGGSAYPR	ICAT-C:13C(9)(C)@4	1384.7584	693.3865	2	0.0513
< 1	8		ILIQTKKGTDIR		1384.8402	693.4274	2	-0.0305
< 1	8		LLQKAIVDENNK	Deamidated(Q)@3	1384.7562	693.3854	2	0.0535
< 1	8		LLSESPPASIDQK	Deamidated(Q)@12	1384.7086	693.3616	2	0.1011
< 1	8		SYNSPHQVSLPR	Deamidated(N)@3	1384.6736	693.3441	2	0.1361

Fragmentation Evidence for Peptide

LLIC[C9I]GGSAYPR

Residue	b	b+2	y
L	114.0913	57.5493	1385.7657
L	**227.1754**	114.0913	**1272.6816**
I	340.2595	170.6334	**1159.5975**
C[C9I]	679.4258	340.2166	**1046.5135**
G	736.4473	368.7273	**707.3471**
G	793.4688	397.2380	**650.3257**
S	880.5008	440.7540	**593.3042**
A	951.5379	476.2726	**506.2722**
Y	1114.6012	557.8043	**435.2350**
P	1211.6540	606.3306	**272.1717**
R	1367.7551	684.3812	**175.1190**

Figure S3

MS/MS spectra of ICAT identified MeJA responsive cysteines

Twenty one cysteines were mapped from MeJA treated guard cells. The precursor of the cysteine-containing peptide and the fragmented ions were shown as the evidence for mapping.

Ribulose bisphosphate carboxylase large chain precursor
GHYLNATAGTCEEMMKR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
4.1.1.1345.3	24.735	2179.0981	727.3733	3	2	GHYLNATAGTCEEMMKR	ICAT-C:13C(9)(C)@11, Oxidation(M)@14, Oxidation(M)@15	99	2178.9907	3
4.1.1.1344.3	24.588	2179.2559	545.8212	4	2	GHYLNATAGTCEEMMKR	Thr->Lys@10, ICAT-C(C)@11, Methyl(E)@13	33	2179.0337	4
5.1.1.1325.3	25.147	2170.0505	724.3574	3	2	GHYLNATAGTCEEMMKR	ICAT-C:13C(9)(C)@11, Methyl(E)@12, Lys->His@16	99	2169.9805	3
5.1.1.1324.2	24.957	2170.2039	543.5582	4	2	GHYLNATAGTCEEMMKR	ICAT-C(C)@11, Oxidation(M)@14, Oxidation(M)@15	97	2169.9604	4

Peptide ID Hypotheses - 5.1.1.1325.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	17	2	GHYLNATAGTCEEMMKR	ICAT-C:13C(9)(C)@11, Met...	2169.9805	724.3341	3	0.0699
73	15		GHYLNATAGTCEEMMKR	ICAT-C(C)@11, Oxidation(M...	2169.9604	724.3275	3	0.0899
< 1	11		LEDLGIPKRYTHFLTDPR		2170.1536	724.3918	3	-0.1031
< 1	11		MVVKMMKWRPWPPLVTR	Oxidation(M)@5	2170.1731	724.3983	3	-0.1225
< 1	9		ATKLAGDSNGAPLFTVTQSHR		2170.1130	724.3783	3	-0.0626

Fragmentation Evidence for Peptide

GHYLNATAGTC[C9I]E[1Me]EMMHR

Residue	b	b+2	y	y+2
G	58.0287	29.5180	2170.9878	1085.9975
H	**195.0877**	98.0475	2113.9663	**1057.4868**
Y	**358.1510**	179.5791	**1976.9074**	**988.9573**
L	**471.2350**	236.1212	**1813.8441**	**907.4257**
N	**585.2780**	293.1426	1700.7600	850.8836
A	656.3151	328.6612	**1586.7171**	793.8622
T	**757.3628**	**379.1850**	**1515.6800**	**758.3436**
A	**828.3999**	414.7036	**1414.6323**	707.8198
G	**885.4213**	**443.2143**	**1343.5952**	**672.3012**
T	**986.4690**	493.7381	**1286.5737**	643.7905
C[C9I]	1325.6354	663.3213	**1185.5260**	593.2667
E[1Me]	1468.6936	734.8505	846.3597	423.6835
E	1597.7362	799.3718	**703.3014**	352.1544
M	1728.7767	864.8920	574.2588	287.6331
M	1859.8172	930.4122	**443.2183**	222.1128
H	1996.8761	998.9417	312.1779	156.5926
R	2152.9772	1076.9922	**175.1190**	88.0631

Ribulose bisphosphate carboxylase small chain
LPLFGCTDSAQVLK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
4.1.1.1458.2	41.204	1734.0232	579.0150	3	3	LPLFGCTDSAQVLK	ICAT-C(C)@6, Ala->Ser@10	55	1733.902
4.1.1.1457.4	41.142	1743.0562	582.0260	3	3	LPLFGCTDSAQVLK	ICAT-C:13C(9)(C)@6, Ala->Ser@10	99	1742.932
4.1.1.1526.2	51.199	1760.9393	881.4769	2	3	LPLFGCTDSAQVLK	Carbamyl@N-term, ICAT-C(C)@6	96	1760.913

Peptide ID Hypotheses - 4.1.1.1526.2

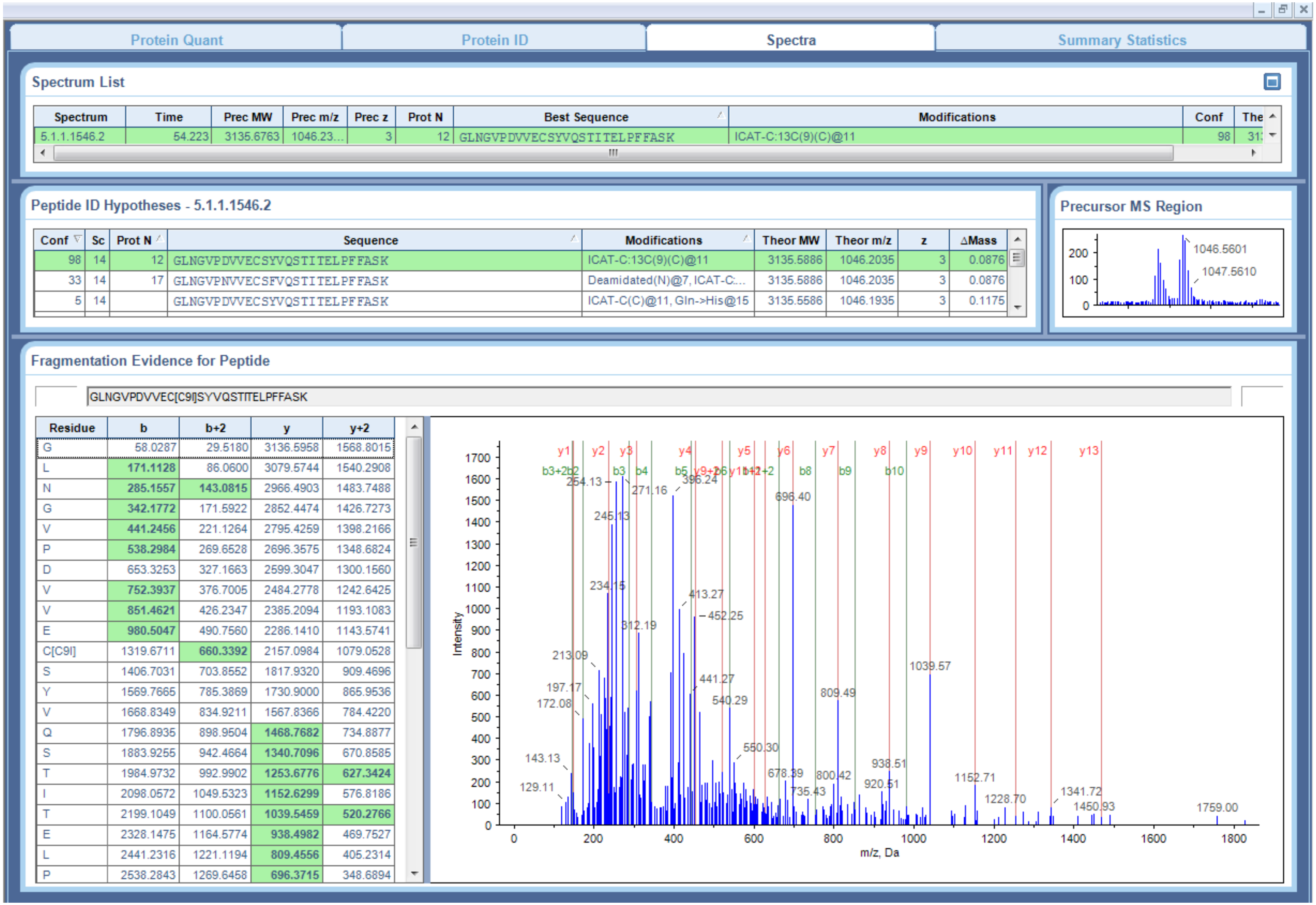
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96	14	3	LPLFGCTDSAQVLK	Carbamyl@N-term, ICAT-C(...	1760.9131	881.4638	2	0.0262
< 1	7	18	GVFQSLQPSDTDLGAKV		1760.8945	881.4545	2	0.0448
< 1	10		LPLFGCTDSAQVLK	Leu->Phe@3, ICAT-C:13C(9...	1760.9219	881.4682	2	0.0175
< 1	8		MIAAGAKSLLGLSMASPK	Oxidation(M)@14	1760.9529	881.4837	2	-0.0136
< 1	8		VSEVSSLLGRAGTMGLGK		1760.9454	881.4800	2	-0.0062
< 1	8		VSSNSLCSLQGLTPK	Deamidated(N)@4, ICAT-C(...	1760.8978	881.4562	2	0.0415

Fragmentation Evidence for Peptide

CRM LPLFGC[C0I]TDSAQVLK

Residue	b	b+2	y	y+2
L	**157.0972**	79.0522	1761.9204	881.4638
P	**254.1499**	127.5786	**1605.8305**	**803.4189**
L	**367.2340**	184.1206	1508.7777	754.8925
F	514.3024	257.6548	**1395.6937**	698.3505
G	**571.3239**	**286.1656**	1248.6253	624.8163
C[C0I]	901.4600	451.2337	**1191.6038**	**596.3055**
T	1002.5077	501.7575	**861.4676**	431.2374
D	1117.5347	559.2710	**760.4199**	380.7136
S	1204.5667	602.7870	**645.3930**	**323.2001**
A	1275.6038	638.3055	**558.3610**	279.6841
Q	1403.6624	702.3348	**487.3239**	244.1656
V	1502.7308	751.8690	**359.2653**	180.1363
L	1615.8149	808.4111	**260.1969**	130.6021
K	1743.9098	872.4585	**147.1128**	74.0600

Malate dehydrogenase, mitochondrial precursor
GLNGVPDVVECSYVQSTITELPFFASK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	The
5.1.1.1546.2	54.223	3135.6763	1046.23...	3	12	GLNGVPDVVECSYVQSTITELPFFASK	ICAT-C:13C(9)(C)@11	98	31

Peptide ID Hypotheses - 5.1.1.1546.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
98	14	12	GLNGVPDVVECSYVQSTITELPFFASK	ICAT-C:13C(9)(C)@11	3135.5886	1046.2035	3	0.0876
33	14	17	GLNGVPNVVECSFVQSTITELPFFASK	Deamidated(N)@7, ICAT-C:...	3135.5886	1046.2035	3	0.0876
5	14		GLNGVPDVVECSYVQSTITELPFFASK	ICAT-C(C)@11, Gln->His@15	3135.5586	1046.1935	3	0.1175

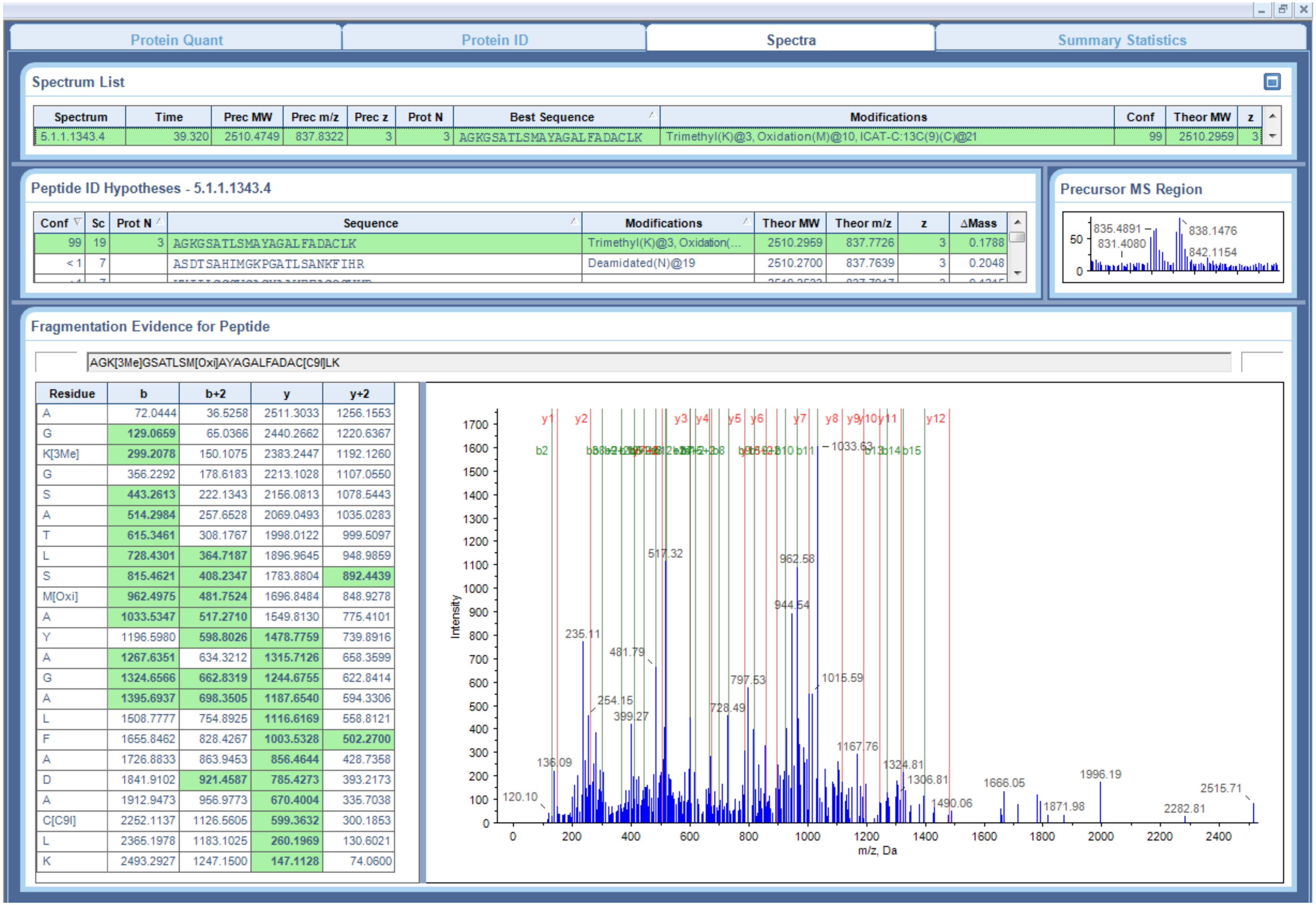
Precursor MS Region

Fragmentation Evidence for Peptide

GLNGVPDVVEC[C9I]SYVQSTITELPFFASK

Residue	b	b+2	y	y+2
G	58.0287	29.5180	3136.5958	1568.8015
L	**171.1128**	86.0600	3079.5744	1540.2908
N	**285.1557**	**143.0815**	2966.4903	1483.7488
G	**342.1772**	171.5922	2852.4474	1426.7273
V	**441.2456**	221.1264	2795.4259	1398.2166
P	**538.2984**	269.6528	2696.3575	1348.6824
D	653.3253	327.1663	2599.3047	1300.1560
V	**752.3937**	376.7005	2484.2778	1242.6425
V	**851.4621**	426.2347	2385.2094	1193.1083
E	**980.5047**	490.7560	2286.1410	1143.5741
C[C9I]	1319.6711	**660.3392**	2157.0984	1079.0528
S	1406.7031	703.8552	1817.9320	909.4696
Y	1569.7665	785.3869	1730.9000	865.9536
V	1668.8349	834.9211	1567.8366	784.4220
Q	1796.8935	898.9504	**1468.7682**	734.8877
S	1883.9255	942.4664	**1340.7096**	670.8585
T	1984.9732	992.9902	**1253.6776**	**627.3424**
I	2098.0572	1049.5323	**1152.6299**	576.8186
T	2199.1049	1100.0561	**1039.5459**	**520.2766**
E	2328.1475	1164.5774	**938.4982**	469.7527
L	2441.2316	1221.1194	**809.4556**	405.2314
P	2538.2843	1269.6458	**696.3715**	348.6894

Malate dehydrogenase, mitochondrial precursor
AGKGSATLSMAYAGALFADACLK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW	z
5.1.1.1343.4	39.320	2510.4749	837.8322	3	3	AGKGSATLSMAYAGALFADACLK	Trimethyl(K)@3, Oxidation(M)@10, ICAT-C:13C(9)(C)@21	99	2510.2959	3

Peptide ID Hypotheses - 5.1.1.1343.4

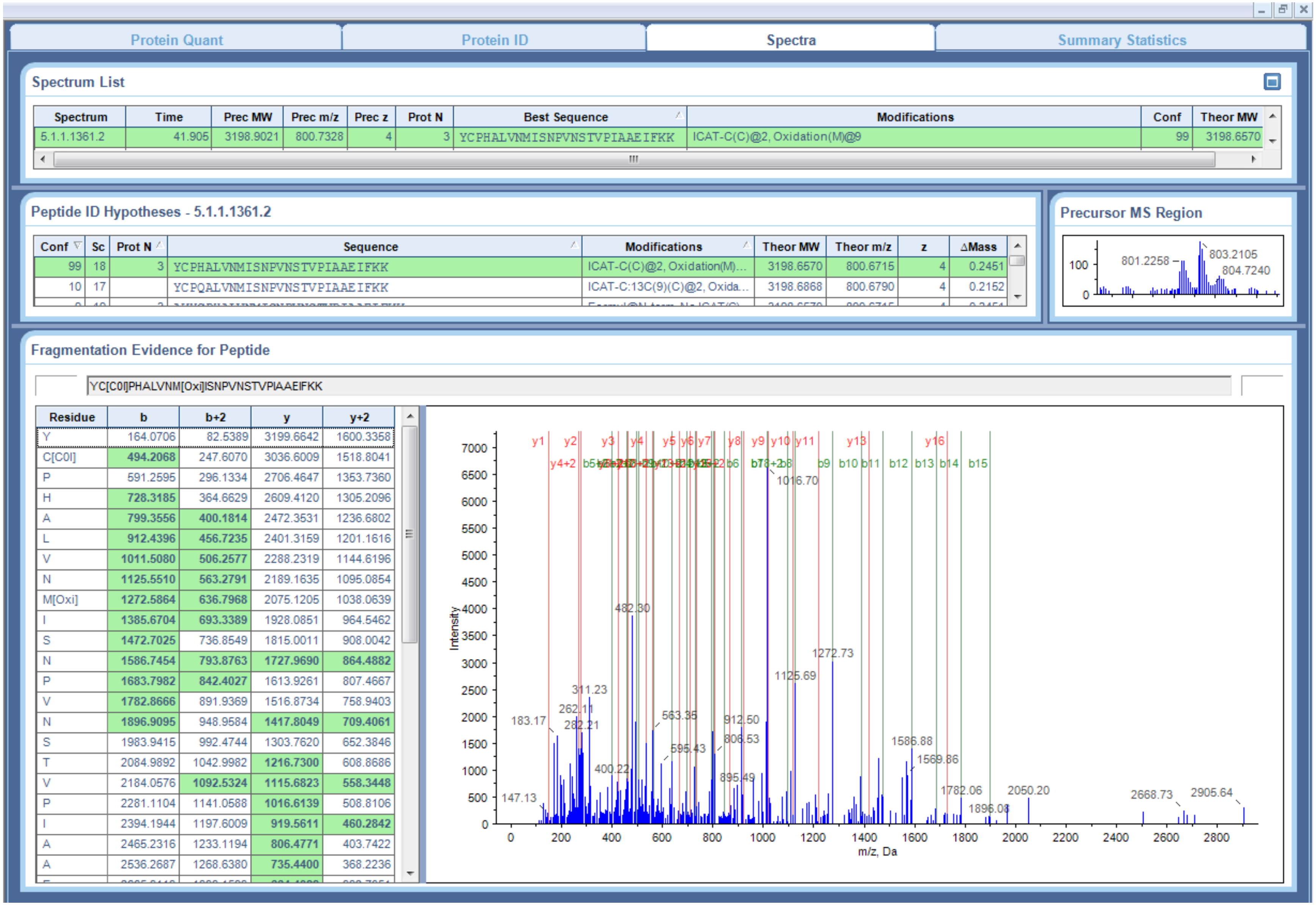
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	19	3	AGKGSATLSMAYAGALFADACLK	Trimethyl(K)@3, Oxidation(...	2510.2959	837.7726	3	0.1788
< 1	7		ASDTSAHIMGKPGATLSANKFIHR	Deamidated(N)@19	2510.2700	837.7639	3	0.2048

Fragmentation Evidence for Peptide

AGK[3Me]GSATLSM[Oxi]AYAGALFADAC[C9I]LK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	2511.3033	1256.1553
G	**129.0659**	65.0366	2440.2662	1220.6367
K[3Me]	**299.2078**	150.1075	2383.2447	1192.1260
G	356.2292	178.6183	2213.1028	1107.0550
S	**443.2613**	222.1343	2156.0813	1078.5443
A	**514.2984**	257.6528	2069.0493	1035.0283
T	**615.3461**	308.1767	1998.0122	999.5097
L	**728.4301**	**364.7187**	1896.9645	948.9859
S	**815.4621**	**408.2347**	1783.8804	**892.4439**
M[Oxi]	**962.4975**	**481.7524**	1696.8484	848.9278
A	**1033.5347**	**517.2710**	1549.8130	775.4101
Y	1196.5980	**598.8026**	**1478.7759**	739.8916
A	**1267.6351**	634.3212	**1315.7126**	658.3599
G	**1324.6566**	**662.8319**	**1244.6755**	622.8414
A	**1395.6937**	**698.3505**	**1187.6540**	594.3306
L	1508.7777	754.8925	**1116.6169**	558.8121
F	1655.8462	828.4267	**1003.5328**	**502.2700**
A	1726.8833	863.9453	**856.4644**	428.7358
D	1841.9102	**921.4587**	**785.4273**	393.2173
A	1912.9473	956.9773	**670.4004**	335.7038
C[C9I]	2252.1137	1126.5605	**599.3632**	300.1853
L	2365.1978	1183.1025	**260.1969**	130.6021
K	2493.2927	1247.1500	**147.1128**	74.0600

Malate dehydrogenase, mitochondrial precursor
YCPHALVNMISNPVNSTVPIAAEIFKK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
5.1.1.1361.2	41.905	3198.9021	800.7328	4	3	YCPHALVNMISNPVNSTVPIAAEIFKK	ICAT-C(C)@2, Oxidation(M)@9	99	3198.6570

Peptide ID Hypotheses - 5.1.1.1361.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	18	3	YCPHALVNMISNPVNSTVPIAAEIFKK	ICAT-C(C)@2, Oxidation(M)...	3198.6570	800.6715	4	0.2451
10	17		YCPQALVNMISNPVNSTVPIAAEIFKK	ICAT-C:13C(9)(C)@2, Oxida...	3198.6868	800.6790	4	0.2152

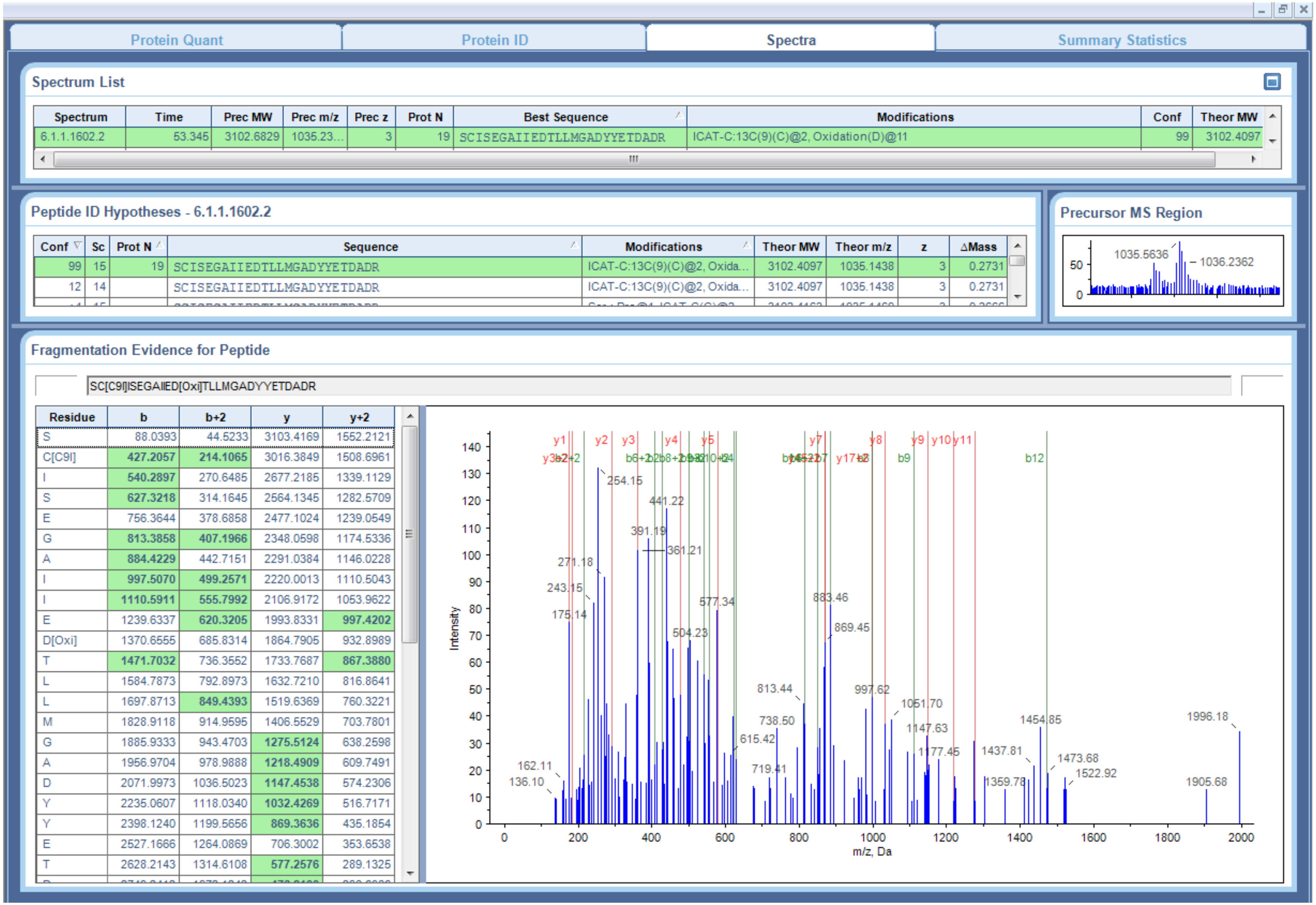
Precursor MS Region

Fragmentation Evidence for Peptide

YC[C0I]PHALVNM[Oxi]ISNPVNSTVPIAAEIFKK

Residue	b	b+2	y	y+2
Y	164.0706	82.5389	3199.6642	1600.3358
C[C0I]	**494.2068**	247.6070	3036.6009	1518.8041
P	591.2595	296.1334	2706.4647	1353.7360
H	**728.3185**	364.6629	2609.4120	1305.2096
A	**799.3556**	**400.1814**	2472.3531	1236.6802
L	**912.4396**	**456.7235**	2401.3159	1201.1616
V	**1011.5080**	**506.2577**	2288.2319	1144.6196
N	**1125.5510**	**563.2791**	2189.1635	1095.0854
M[Oxi]	**1272.5864**	**636.7968**	2075.1205	1038.0639
I	**1385.6704**	**693.3389**	1928.0851	964.5462
S	**1472.7025**	736.8549	1815.0011	908.0042
N	**1586.7454**	**793.8763**	**1727.9690**	**864.4882**
P	**1683.7982**	**842.4027**	1613.9261	807.4667
V	**1782.8666**	891.9369	1516.8734	758.9403
N	**1896.9095**	948.9584	**1417.8049**	**709.4061**
S	1983.9415	992.4744	1303.7620	652.3846
T	2084.9892	1042.9982	**1216.7300**	608.8686
V	2184.0576	**1092.5324**	**1115.6823**	**558.3448**
P	2281.1104	1141.0588	**1016.6139**	508.8106
I	2394.1944	1197.6009	**919.5611**	**460.2842**
A	2465.2316	1233.1194	**806.4771**	403.7422
A	2536.2687	1268.6380	**735.4400**	368.2236

ADP-glucose pyrophosphorylase small subunit
SCISEGAIIEDTLLMGADYYETDADR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
6.1.1.1602.2	53.345	3102.6829	1035.23...	3	19	SCISEGAIIEDTLLMGADYYETDADR	ICAT-C:13C(9)(C)@2, Oxidation(D)@11	99	3102.4097

Peptide ID Hypotheses - 6.1.1.1602.2

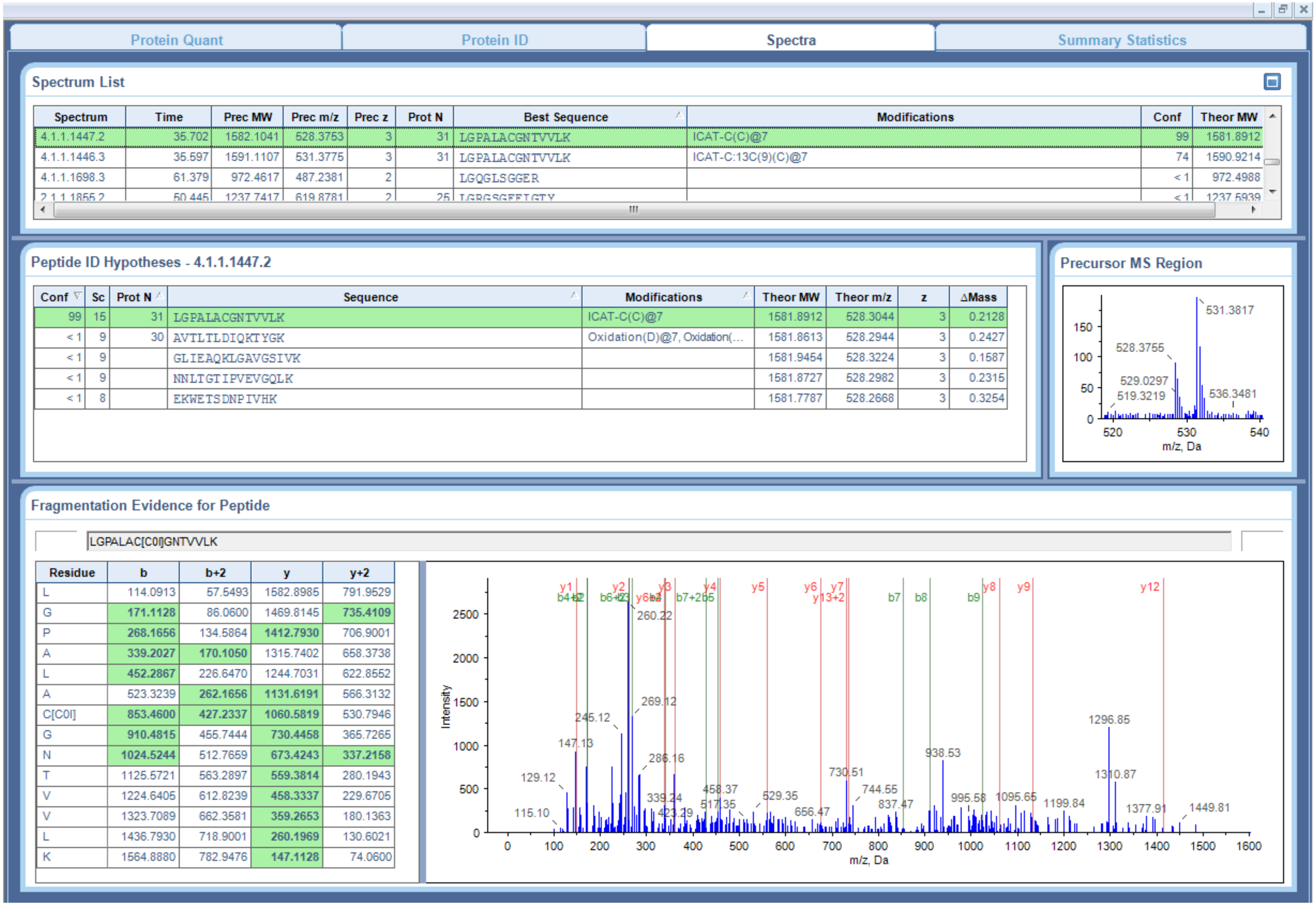
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	19	SCISEGAIIEDTLLMGADYYETDADR	ICAT-C:13C(9)(C)@2, Oxida...	3102.4097	1035.1438	3	0.2731
12	14		SCISEGAIIEDTLLMGADYYETDADR	ICAT-C:13C(9)(C)@2, Oxida...	3102.4097	1035.1438	3	0.2731

Fragmentation Evidence for Peptide

SC[C9I]ISEGAIIED[Oxi]TLLMGADYYETDADR

Residue	b	b+2	y	y+2
S	88.0393	44.5233	3103.4169	1552.2121
C[C9I]	**427.2057**	**214.1065**	3016.3849	1508.6961
I	**540.2897**	270.6485	2677.2185	1339.1129
S	**627.3218**	314.1645	2564.1345	1282.5709
E	756.3644	378.6858	2477.1024	1239.0549
G	**813.3858**	**407.1966**	2348.0598	1174.5336
A	**884.4229**	442.7151	2291.0384	1146.0228
I	**997.5070**	**499.2571**	2220.0013	1110.5043
I	**1110.5911**	**555.7992**	2106.9172	1053.9622
E	1239.6337	**620.3205**	1993.8331	**997.4202**
D[Oxi]	1370.6555	685.8314	1864.7905	932.8989
T	**1471.7032**	736.3552	1733.7687	**867.3880**
L	1584.7873	792.8973	1632.7210	816.8641
L	1697.8713	**849.4393**	1519.6369	760.3221
M	1828.9118	914.9595	1406.5529	703.7801
G	1885.9333	943.4703	**1275.5124**	638.2598
A	1956.9704	978.9888	**1218.4909**	609.7491
D	2071.9973	1036.5023	**1147.4538**	574.2306
Y	2235.0607	1118.0340	**1032.4269**	516.7171
Y	2398.1240	1199.5656	**869.3636**	435.1854
E	2527.1666	1264.0869	706.3002	353.6538
T	2628.2143	1314.6108	**577.2576**	289.1325

Putative aldehyde dehydrogenase
LGPALACGNTVVLK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
4.1.1.1447.2	35.702	1582.1041	528.3753	3	31	LGPALACGNTVVLK	ICAT-C(C)@7	99	1581.8912
4.1.1.1446.3	35.597	1591.1107	531.3775	3	31	LGPALACGNTVVLK	ICAT-C:13C(9)(C)@7	74	1590.9214
4.1.1.1698.3	61.379	972.4617	487.2381	2		LGQGLSGGER		< 1	972.4988
2.1.1.1855.2	50.445	1237.7417	619.8781	2	25	LGRGSGFEIGTY		< 1	1237.5939

Peptide ID Hypotheses - 4.1.1.1447.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	31	LGPALACGNTVVLK	ICAT-C(C)@7	1581.8912	528.3044	3	0.2128
< 1	9	30	AVTLTLDIQKTYGK	Oxidation(D)@7, Oxidation(...	1581.8613	528.2944	3	0.2427
< 1	9		GLIEAQKLGAVGSIVK		1581.9454	528.3224	3	0.1587
< 1	9		NNLTGTIPVEVGQLK		1581.8727	528.2982	3	0.2315
< 1	8		EKWETSDNPIVHK		1581.7787	528.2668	3	0.3254

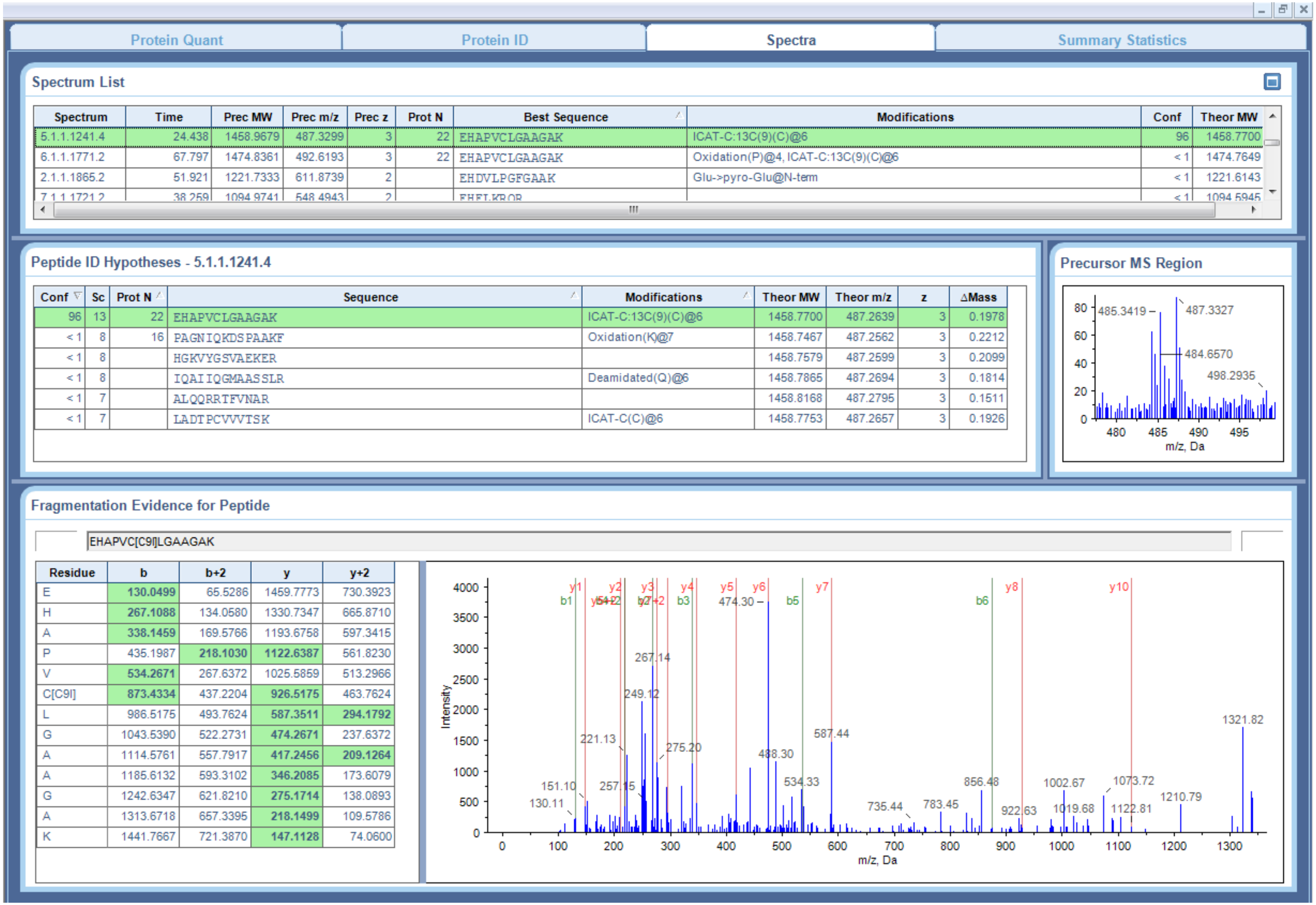
Precursor MS Region

Fragmentation Evidence for Peptide

LGPALAC[C0I]GNTVVLK

Residue	b	b+2	y	y+2
L	114.0913	57.5493	1582.8985	791.9529
G	**171.1128**	86.0600	1469.8145	**735.4109**
P	**268.1656**	134.5864	**1412.7930**	706.9001
A	**339.2027**	**170.1050**	1315.7402	658.3738
L	**452.2867**	226.6470	1244.7031	622.8552
A	523.3239	**262.1656**	**1131.6191**	566.3132
C[C0I]	**853.4600**	**427.2337**	**1060.5819**	530.7946
G	**910.4815**	455.7444	**730.4458**	365.7265
N	**1024.5244**	512.7659	**673.4243**	**337.2158**
T	1125.5721	563.2897	**559.3814**	280.1943
V	1224.6405	612.8239	**458.3337**	229.6705
V	1323.7089	662.3581	**359.2653**	180.1363
L	1436.7930	718.9001	**260.1969**	130.6021
K	1564.8880	782.9476	**147.1128**	74.0600

3-isopropylmalate dehydratase-like protein (small subunit)
EHAPVCLGAAGAK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
5.1.1.1241.4	24.438	1458.9679	487.3299	3	22	EHAPVCLGAAGAK	ICAT-C:13C(9)(C)@6	96	1458.7700
6.1.1.1771.2	67.797	1474.8361	492.6193	3	22	EHAPVCLGAAGAK	Oxidation(P)@4, ICAT-C:13C(9)(C)@6	< 1	1474.7649
2.1.1.1865.2	51.921	1221.7333	611.8739	2		EHDVLPGFGAAK	Glu->pyro-Glu@N-term	< 1	1221.6143
7.1.1.1721.2	38.259	1094.9741	548.4943	2		[illegible]		< 1	1094.5945

Peptide ID Hypotheses - 5.1.1.1241.4

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
96	13	22	EHAPVCLGAAGAK	ICAT-C:13C(9)(C)@6	1458.7700	487.2639	3	0.1978
< 1	8	16	PAGNIQKDSPAAKF	Oxidation(K)@7	1458.7467	487.2562	3	0.2212
< 1	8		HGKVYGSVAEKER		1458.7579	487.2599	3	0.2099
< 1	8		IQAIIQGMAASSLR	Deamidated(Q)@6	1458.7865	487.2694	3	0.1814
< 1	7		ALQQRRTFVNAR		1458.8168	487.2795	3	0.1511
< 1	7		LADTPCVVVTSK	ICAT-C(C)@6	1458.7753	487.2657	3	0.1926

Fragmentation Evidence for Peptide

EHAPVC[C9I]LGAAGAK

Residue	b	b+2	y	y+2
E	**130.0499**	65.5286	1459.7773	730.3923
H	**267.1088**	134.0580	1330.7347	665.8710
A	**338.1459**	169.5766	1193.6758	597.3415
P	435.1987	**218.1030**	**1122.6387**	561.8230
V	**534.2671**	267.6372	1025.5859	513.2966
C[C9I]	**873.4334**	437.2204	**926.5175**	463.7624
L	986.5175	493.7624	**587.3511**	**294.1792**
G	1043.5390	522.2731	**474.2671**	237.6372
A	1114.5761	557.7917	**417.2456**	**209.1264**
A	1185.6132	593.3102	**346.2085**	173.6079
G	1242.6347	621.8210	**275.1714**	138.0893
A	1313.6718	657.3395	**218.1499**	109.5786
K	1441.7667	721.3870	**147.1128**	74.0600

Aspartate aminotransferase Asp2
VGALSIV<u>C</u>K

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
7.1.1.2046.2	63.491	0.0000	595.2124	0		VFNDTARYVDQGGGKR	Deamidated(Q)@11	< 1	1782.8649
4.1.1.1450.3	36.188	1117.7579	559.8862	2		VGALKFSPNGK	Deamidated(N)@9	61	1117.6132
4.1.1.1427.2	32.747	1115.7665	558.8905	2	53	VGALSIVCK	ICAT-C(C)@8	97	1115.6372
7.1.1.1720.4	38.197	1088.7499	545.3822	2		VGAVFASGLLR		< 1	1088.6343

Peptide ID Hypotheses - 4.1.1.1427.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
97	13	53	VGALSIVCK	ICAT-C(C)@8	1115.6372	558.8259	2	0.1292
< 1	10		GVRDIVNTNK	Deamidated(N)@9	1115.5935	558.8040	2	0.1730
< 1	10		INLLSKGMIK		1115.6737	558.8441	2	0.0928
< 1	9		RRDSDGVVGR		1115.5796	558.7971	2	0.1869
< 1	9		RVGDLGRSIK	Oxidation(R)@7	1115.6411	558.8278	2	0.1253
< 1	9		VSKIIVDKSK		1115.6914	558.8530	2	0.0750

Fragmentation Evidence for Peptide

VGALSIVC[C0I]K

Residue	b	b+2	y	y+2
V	**100.0757**	50.5415	1116.6445	558.8259
G	**157.0972**	79.0522	**1017.5761**	**509.2917**
A	**228.1343**	114.5708	**960.5547**	480.7810
L	**341.2183**	**171.1128**	**889.5176**	445.2624
S	**428.2504**	214.6288	**776.4335**	388.7204
I	**541.3344**	**271.1709**	**689.4015**	345.2044
V	640.4028	320.7051	**576.3174**	288.6623
C[C0I]	970.5390	485.7731	**477.2490**	**239.1281**
K	1098.6340	549.8206	**147.1128**	74.0600

Oxalic acid oxidase
AETPAGYPCIRPIHVK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
8.1.1.1747.3	31.470	1698.8354	850.4250	2		AETAANSCLFSGHR	ICAT-C:13C(9)(C)@8	< 1	1698.8195
5.1.1.1278.3	29.864	1978.2782	495.5768	4	6	AETPAGYPCIRPIHVK	ICAT-C(C)@9	6	1978.0459
5.1.1.1278.2	29.821	1987.2930	497.8305	4	6	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	99	1987.0760
6.1.1.1418.4	31.173	1978.1763	990.0954	2	6	AETPAGYPCIRPIHVK	ICAT-C(C)@9	99	1978.0459

Peptide ID Hypotheses - 5.1.1.1278.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	14	6	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9	1987.0760	497.7763	4	0.2169
< 1	8		DDHLVGHFVKAVALSDHK		1987.0276	497.7642	4	0.2654
< 1	8		IVEGQQIEPAPSVILHMK		1988.0765	498.0264	4	-0.7836
< 1	7		AHWLTLGTKKPNNDPAPK		1987.0640	497.7733	4	0.2290
< 1	7		TRQTLTHTTLIPNYTVK	Deamidated(N)@13	1987.0739	497.7757	4	0.2191

Precursor MS Region

Fragmentation Evidence for Peptide

AETPAGYPC[C9I]IRPIHVK

Residue	b	b+2	y	y+2
A	72.0444	36.5258	1988.0833	994.5453
E	**201.0870**	101.0471	1917.0462	959.0267
T	**302.1347**	151.5710	1788.0036	894.5054
P	**399.1874**	200.0974	**1686.9559**	843.9816
A	**470.2245**	235.6159	**1589.9032**	**795.4552**
G	**527.2460**	**264.1266**	**1518.8661**	**759.9367**
Y	690.3093	345.6583	**1461.8446**	731.4259
P	787.3621	394.1847	**1298.7813**	**649.8943**
C[C9I]	1126.5285	563.7679	**1201.7285**	**601.3679**
I	1239.6125	620.3099	**862.5621**	**431.7847**
R	1395.7136	698.3605	**749.4781**	375.2427
P	1492.7664	746.8868	**593.3770**	**297.1921**
I	1605.8505	**803.4289**	**496.3242**	248.6657
H	1742.9094	871.9583	**383.2401**	192.1237
V	1841.9778	921.4925	**246.1812**	123.5942
K	1970.0728	985.5400	**147.1128**	74.0600

homocysteine S-methyltransferase
CVKPPVIYGDVSRPK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
3.1.1.1812.3	56.476	2011.3837	671.4685	3		CVCFIICKHHK	ICAT-C(C)@1, ICAT-C(C)@3, ICAT-C(C)@7	< 1	2011.0317
5.1.1.1270.4	28.724	1884.2605	472.0724	4	8	CVKPPVIYGDVSRPK	ICAT-C(C)@1	95	1884.0292
5.1.1.1269.4	28.576	1893.3053	474.3336	4	8	CVKPPVIYGDVSRPK	ICAT-C:13C(9)(C)@1	99	1893.0593
8.1.1.2272.3	60.954	0.0000	742.7405	0	25	CVRFASFVAGVQDLGILGR	ICAT-C:13C(9)(C)@1	< 1	2225.2039

Peptide ID Hypotheses - 5.1.1.1269.4

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	8	CVKPPVIYGDVSRPK	ICAT-C:13C(9)(C)@1	1893.0593	474.2721	4	0.2459
< 1	8		EFPSRASVLVLQQQQY	Deamidated(Q)@15	1892.9633	474.2481	4	0.3420
< 1	7		ARGNSLIIPYSASNRFK		1893.0221	474.2628	4	0.2832
< 1	7		DPLLQFAFLGKVSRFR		1893.0625	474.2729	4	0.2428
< 1	7		YVKLGYHYLITHLFK		1894.0505	474.5199	4	-0.7453

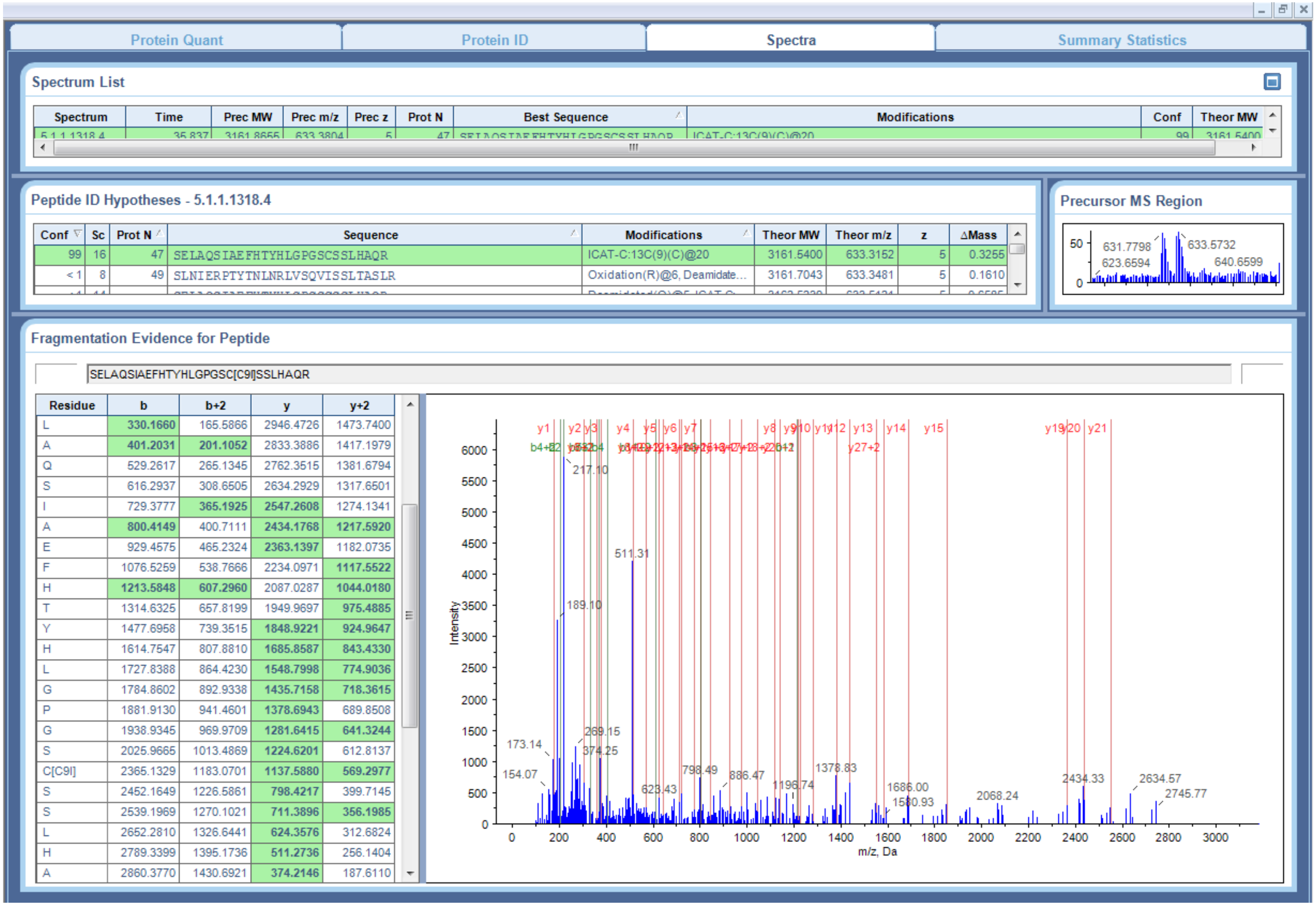
Precursor MS Region

Fragmentation Evidence for Peptide

C[C9I]VKPPVIYGDVSRPK

Residue	b	b+2	y	y+2
C[C9I]	340.1736	170.5905	1894.0666	947.5369
V	**439.2421**	**220.1247**	1554.9002	777.9538
K	**567.3370**	284.1721	**1455.8318**	**728.4196**
P	**664.3898**	332.6985	**1327.7369**	**664.3721**
P	761.4426	381.2249	**1230.6841**	**615.8457**
V	**860.5110**	430.7591	**1133.6313**	**567.3193**
I	973.5950	**487.3012**	**1034.5629**	**517.7851**
Y	1136.6584	568.8328	**921.4789**	**461.2431**
G	1193.6798	597.3435	**758.4155**	**379.7114**
D	1308.7068	654.8570	**701.3941**	**351.2007**
V	1407.7752	704.3912	**586.3671**	**293.6872**
S	1494.8072	747.9072	**487.2987**	**244.1530**
R	1650.9083	825.9578	**400.2667**	200.6370
P	1747.9611	874.4842	**244.1656**	122.5864
K	1876.0560	938.5317	**147.1128**	74.0600

Streptomyces cyclase/dehydrase family protein
SELAQSIAEFHTYHLGPGSCSSLHAQR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
5.1.1.1318.4	35.837	3161.8655	633.3804	5	47	SELAQSIAEFHTYHLGPGSCSSLHAQR	ICAT-C:13C(9)(C)@20	99	3161.5400

Peptide ID Hypotheses - 5.1.1.1318.4

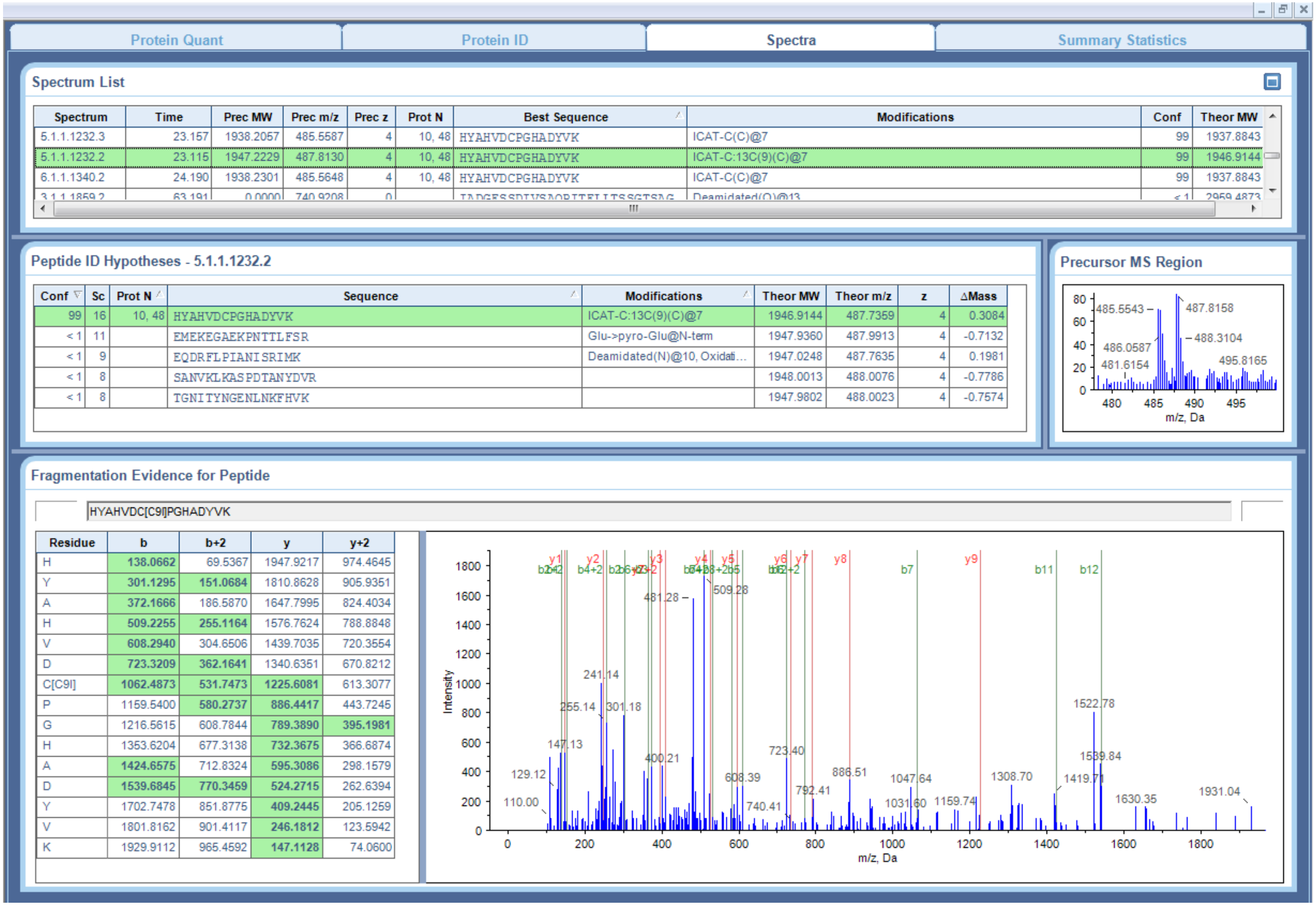
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	47	SELAQSIAEFHTYHLGPGSCSSLHAQR	ICAT-C:13C(9)(C)@20	3161.5400	633.3152	5	0.3255
< 1	8	49	SLNIERPTYTNLNRLVSQVISSLTASLR	Oxidation(R)@6, Deamidate...	3161.7043	633.3481	5	0.1610

Fragmentation Evidence for Peptide

SELAQSIAEFHTYHLGPGSC[C9I]SSLHAQR

Residue	b	b+2	y	y+2
L	**330.1660**	165.5866	2946.4726	1473.7400
A	**401.2031**	**201.1052**	2833.3886	1417.1979
Q	529.2617	265.1345	2762.3515	1381.6794
S	616.2937	308.6505	2634.2929	1317.6501
I	729.3777	**365.1925**	**2547.2608**	1274.1341
A	**800.4149**	400.7111	**2434.1768**	**1217.5920**
E	929.4575	465.2324	**2363.1397**	1182.0735
F	1076.5259	538.7666	2234.0971	**1117.5522**
H	**1213.5848**	**607.2960**	2087.0287	**1044.0180**
T	1314.6325	657.8199	1949.9697	**975.4885**
Y	1477.6958	739.3515	**1848.9221**	**924.9647**
H	1614.7547	807.8810	**1685.8587**	**843.4330**
L	1727.8388	864.4230	**1548.7998**	**774.9036**
G	1784.8602	892.9338	**1435.7158**	**718.3615**
P	1881.9130	941.4601	**1378.6943**	689.8508
G	1938.9345	969.9709	**1281.6415**	**641.3244**
S	2025.9665	1013.4869	**1224.6201**	612.8137
C[C9I]	2365.1329	1183.0701	**1137.5880**	**569.2977**
S	2452.1649	1226.5861	**798.4217**	399.7145
S	2539.1969	1270.1021	**711.3896**	**356.1985**
L	2652.2810	1326.6441	**624.3576**	312.6824
H	2789.3399	1395.1736	**511.2736**	256.1404
A	2860.3770	1430.6921	**374.2146**	187.6110

Arabidopsis Rab GTPase homolog E1b
HYAHVDCPGHADYVK



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
5.1.1.1232.3	23.157	1938.2057	485.5587	4	10, 48	HYAHVDCPGHADYVK	ICAT-C(C)@7	99	1937.8843
5.1.1.1232.2	23.115	1947.2229	487.8130	4	10, 48	HYAHVDCPGHADYVK	ICAT-C:13C(9)(C)@7	99	1946.9144
6.1.1.1340.2	24.190	1938.2301	485.5648	4	10, 48	HYAHVDCPGHADYVK	ICAT-C(C)@7	99	1937.8843
3.1.1.1859.2	63.191	0.0000	740.9208	0		TADGESSDIVSAQRITEILTSSGTSAG	Deamidated(Q)@13	< 1	2959.4873

Peptide ID Hypotheses - 5.1.1.1232.2

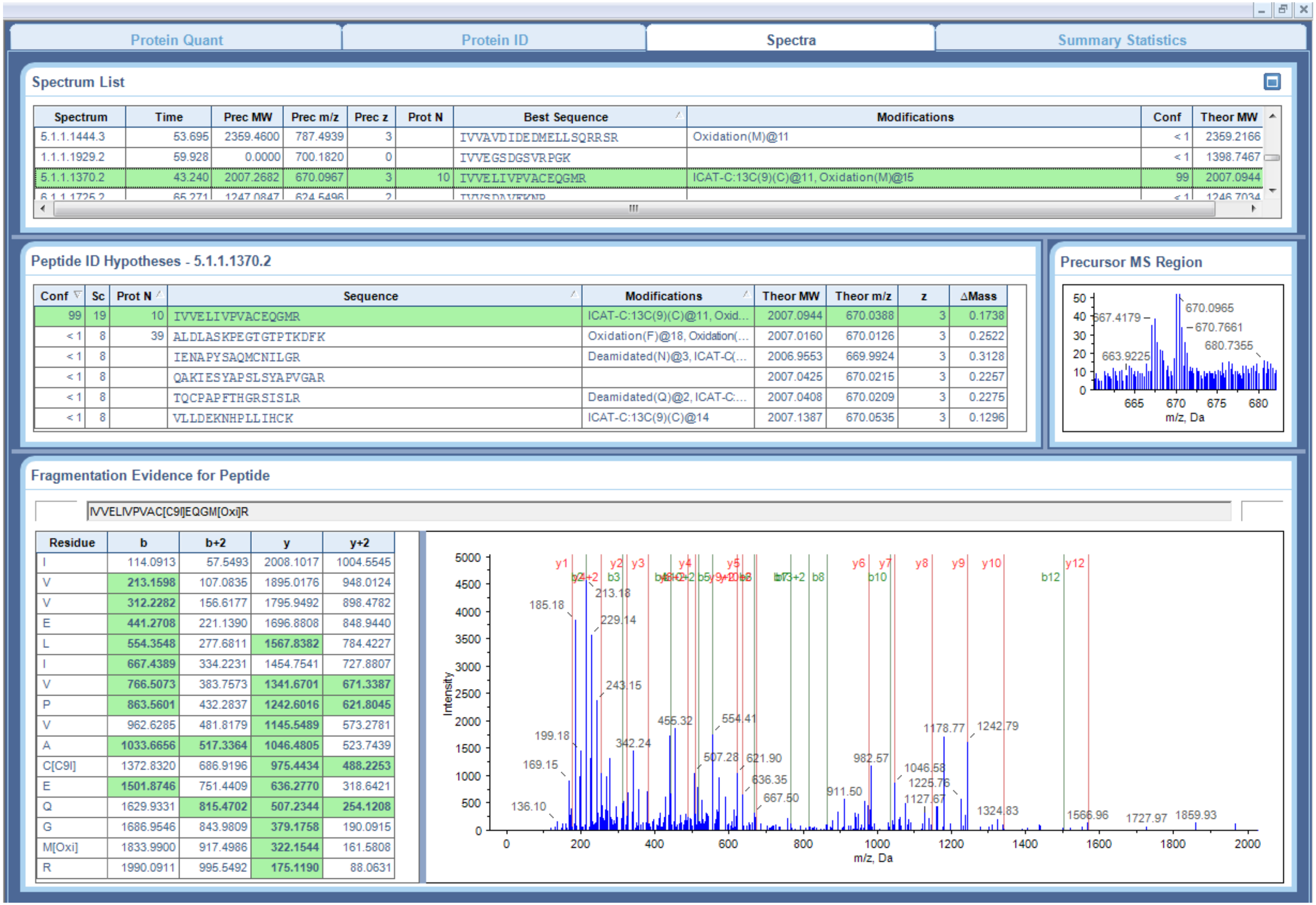
Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	16	10, 48	HYAHVDCPGHADYVK	ICAT-C:13C(9)(C)@7	1946.9144	487.7359	4	0.3084
< 1	11		EMEKEGAEKPNTTLFSR	Glu->pyro-Glu@N-term	1947.9360	487.9913	4	-0.7132
< 1	9		EQDRFLPIANISRIMK	Deamidated(N)@10, Oxidati...	1947.0248	487.7635	4	0.1981
< 1	8		SANVKLKASPDTANYDVR		1948.0013	488.0076	4	-0.7786
< 1	8		TGNITYNGENLNKFHVK		1947.9802	488.0023	4	-0.7574

Fragmentation Evidence for Peptide

HYAHVDC[C9I]PGHADYVK

Residue	b	b+2	y	y+2
H	**138.0662**	69.5367	1947.9217	974.4645
Y	**301.1295**	**151.0684**	1810.8628	905.9351
A	**372.1666**	186.5870	1647.7995	824.4034
H	**509.2255**	**255.1164**	1576.7624	788.8848
V	**608.2940**	304.6506	1439.7035	720.3554
D	**723.3209**	**362.1641**	1340.6351	670.8212
C[C9I]	**1062.4873**	**531.7473**	**1225.6081**	613.3077
P	1159.5400	**580.2737**	**886.4417**	443.7245
G	1216.5615	608.7844	**789.3890**	**395.1981**
H	1353.6204	677.3138	**732.3675**	366.6874
A	**1424.6575**	712.8324	**595.3086**	298.1579
D	**1539.6845**	**770.3459**	**524.2715**	262.6394
Y	1702.7478	851.8775	**409.2445**	205.1259
V	1801.8162	901.4117	**246.1812**	123.5942
K	1929.9112	965.4592	**147.1128**	74.0600

Arabidopsis Rab GTPase homolog E1b
IVVELIVPVACEQGMR



Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
5.1.1.1444.3	53.695	2359.4600	787.4939	3		IVVAVDIDEDMELLSQRRSR	Oxidation(M)@11	< 1	2359.2166
1.1.1.1929.2	59.928	0.0000	700.1820	0		IVVEGSDGSVRPGK		< 1	1398.7467
5.1.1.1370.2	43.240	2007.2682	670.0967	3	10	IVVELIVPVACEQGMR	ICAT-C:13C(9)(C)@11, Oxidation(M)@15	99	2007.0944
6.1.1.1725.2	65.271	1247.0847	624.5496	2		[illegible]		< 1	1246.7034

Peptide ID Hypotheses - 5.1.1.1370.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	19	10	IVVELIVPVACEQGMR	ICAT-C:13C(9)(C)@11, Oxid...	2007.0944	670.0388	3	0.1738
< 1	8	39	ALDLASKPEGTGTPTKDFK	Oxidation(F)@18, Oxidation(...	2007.0160	670.0126	3	0.2522
< 1	8		IENAPYSAQMCNILGR	Deamidated(N)@3, ICAT-C(...	2006.9553	669.9924	3	0.3128
< 1	8		QAKIESYAPSLSYAPVGAR		2007.0425	670.0215	3	0.2257
< 1	8		TQCPAPFTHGRSISLR	Deamidated(Q)@2, ICAT-C:...	2007.0408	670.0209	3	0.2275
< 1	8		VLLDEKNHPLLIHCK	ICAT-C:13C(9)(C)@14	2007.1387	670.0535	3	0.1296

Precursor MS Region

Fragmentation Evidence for Peptide

IVVELIVPVAC[C9I]EQGM[Oxi]R

Residue	b	b+2	y	y+2
I	114.0913	57.5493	2008.1017	1004.5545
V	**213.1598**	107.0835	1895.0176	948.0124
V	**312.2282**	156.6177	1795.9492	898.4782
E	**441.2708**	221.1390	1696.8808	848.9440
L	**554.3548**	277.6811	**1567.8382**	784.4227
I	**667.4389**	334.2231	1454.7541	727.8807
V	**766.5073**	383.7573	**1341.6701**	**671.3387**
P	**863.5601**	432.2837	**1242.6016**	**621.8045**
V	962.6285	481.8179	**1145.5489**	573.2781
A	**1033.6656**	**517.3364**	**1046.4805**	523.7439
C[C9I]	1372.8320	686.9196	**975.4434**	**488.2253**
E	**1501.8746**	751.4409	**636.2770**	318.6421
Q	1629.9331	**815.4702**	**507.2344**	**254.1208**
G	1686.9546	843.9809	**379.1758**	190.0915
M[Oxi]	1833.9900	917.4986	**322.1544**	161.5808
R	1990.0911	995.5492	**175.1190**	88.0631

Multicatalytic endopeptidase complex
ITQLTDNVYVCR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
3.1.1.1568.2	27.616	1015.5605	508.7875	2		ITPVLGSSNK	Deamidated(N)@9	< 1	1015.5550
4.1.1.1441.4	34.900	1651.0510	551.3576	3	27	ITQLTDNVYVCR	ICAT-C(C)@11	33	1650.8400
4.1.1.1441.3	34.857	1660.0840	554.3686	3	27	ITQLTDNVYVCR	ICAT-C:13C(9)(C)@11	99	1659.8701
1.1.1.1565.2	27.045	1803.0051	602.0090	3	38	ITVDPSLNEENPRLR	Oxidation(P)@5, Deamidated(N)@8, Oxidation(P)@12	< 1	1802.9163

Peptide ID Hypotheses - 4.1.1.1441.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	27	ITQLTDNVYVCR	ICAT-C:13C(9)(C)@11	1659.8701	554.2973	3	0.2138
< 1	9		FTSNLPPKSMGARVR		1659.8879	554.3032	3	0.1961
< 1	8		MVEISSLAEKVVAIR	Oxidation(M)@1	1659.9230	554.3149	3	0.1610
< 1	8		QHIEVRLIEGDVPR		1659.9056	554.3091	3	0.1783
< 1	8		QLVWNKNYNVKPR	Deamidated(N)@5, Deamid...	1659.8733	554.2984	3	0.2107

Precursor MS Region

Fragmentation Evidence for Peptide

ITQLTDNVYVC[C9I]R

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1660.8774	830.9423
T	**215.1390**	108.0731	1547.7933	774.4003
Q	**343.1976**	**172.1024**	1446.7457	723.8765
L	**456.2817**	228.6445	1318.6871	659.8472
T	**557.3293**	279.1683	**1205.6030**	**603.3052**
D	672.3563	336.6818	**1104.5553**	552.7813
N	**786.3992**	393.7032	**989.5284**	495.2678
V	**885.4676**	443.2374	**875.4855**	**438.2464**
Y	**1048.5310**	524.7691	**776.4171**	388.7122
V	1147.5994	574.3033	**613.3537**	**307.1805**
C[C9I]	1486.7657	743.8865	**514.2853**	257.6463
R	1642.8668	821.9371	**175.1190**	88.0631

Myrosinase
QIIQDFKDYADLCFK

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
6.1.1.1579.2	51.049	2056.1816	686.4011	3	1	QIIQDFKDYADLCFK	Gln->pyro-Glu@N-term, ICAT-C(C)@13	99	2055.9976
6.1.1.1511.4	43.712	2082.2493	695.0904	3	1	QIIQDFKDYADLCFK	Deamidated(Q)@4, ICAT-C:13C(9)(C)@13	56	2083.0383
5.1.1.1423.2	51.011	2574.3772	859.1330	3	1	QIIQDFKDYADLCFKEFGGK	Gln->pyro-Glu@N-term, ICAT-C(C)@13	99	2574.2466
5.1.1.1423.3	51.054	2583.4109	862.1442	3	1	QIIQDFKDYADLCFKEFGGK	Gln->pyro-Glu@N-term, ICAT-C:13C(9)(C)@13	99	2583.2766

Peptide ID Hypotheses - 6.1.1.1579.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z	ΔMass
99	15	1	QIIQDFKDYADLCFK	Gln->pyro-Glu@N-term, ICA...	2055.9976	686.3398	3	0.1840
< 1	10		FPPQERFASMIADAGFEK	Oxidation(M)@10	2055.9724	686.3314	3	0.2091
< 1	10		QVIEDFRDLADLCFK	Deamidated(Q)@1, Oxidatio...	2055.9824	686.3347	3	0.1992
< 1	9		MRPTMQEVLDNLNAIAQI		2056.0444	686.3555	3	0.1370
< 1	9		TNFDAVVEPLDICKQK	ICAT-C:13C(9)(C)@13, Dea...	2056.0598	686.3605	3	0.1218

Precursor MS Region

Fragmentation Evidence for Peptide

PGQ QIIQDFKDYADLC[C0I]FK

Residue	b	b+2	y	y+2
Q	112.0393	56.5233	2057.0048	1029.0061
I	**225.1234**	113.0653	1945.9728	973.4900
I	**338.2074**	169.6074	1832.8887	916.9480
Q	**466.2660**	233.6366	1719.8047	860.4060
D	**581.2930**	291.1501	1591.7461	**796.3767**
F	728.3614	364.6843	**1476.7192**	**738.8632**
K	**856.4563**	428.7318	**1329.6507**	**665.3290**
D	**971.4833**	486.2453	1201.5558	601.2815
Y	**1134.5466**	567.7769	**1086.5288**	543.7681
A	1205.5837	603.2955	**923.4655**	462.2364
D	**1320.6107**	660.8090	**852.4284**	426.7178
L	1433.6947	717.3510	**737.4015**	**369.2044**
C[C0I]	1763.8309	882.4191	**624.3174**	312.6623
F	1910.8993	955.9533	**294.1812**	147.5942
K	2038.9943	1020.0008	**147.1128**	74.0600

Myrosinase
CSPMVDTKHRCYGGNSSTEPYIVAHNQLLAHATVVDLYR

Spectrum List

Spectrum	Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications
8.1.1.1887.2	40.952	4613.3354	923.6744	5	1	CSPMVDTKHRCYGGNSSTEPYIVAHNQLLAHATVVDLYR	Cys->Thr@1, Dioxidation(K)@8, ICAT-C:13C(9)(C)@11

Peptide ID Hypotheses - 8.1.1.1887.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z
99	18	1	CSPMVDTKHRCYGGNSSTEPYIVAHNQLLAHATVVDLYR	Cys->Thr@1, Dioxidation(K)@8, ICAT-C:13C(9)(C)@11	4611.2686	923.2610	

Precursor MS Region

Fragmentation Evidence for Peptide

TSPMVDTK[2Ox]HRC[C9I]YGGNSSTEPYIVAHNQLLAHATVVDLYR

Residue	b	b+2	y	y+2
T	102.0550	51.5311	4612.2758	2306.6416
S	189.0870	95.0471	4511.2282	2256.1177
P	**286.1397**	143.5735	4424.1961	2212.6017
M	**417.1802**	**209.0938**	4327.1434	2164.0753
V	**516.2486**	258.6280	4196.1029	2098.5551
D	631.2756	316.1414	4097.0345	2049.0209
T	732.3233	366.6653	3982.0075	1991.5074
K[2Ox]	892.4081	446.7077	3880.9599	1940.9836
H	**1029.4670**	515.2371	3720.8751	1860.9412
R	1185.5681	**593.2877**	3583.8162	1792.4117
C[C9I]	1524.7345	762.8709	3427.7150	1714.3612
Y	1687.7978	844.4025	3088.5487	1544.7780
G	1744.8192	872.9133	2925.4853	1463.2463
G	1801.8407	901.4240	2868.4639	**1434.7356**
N	1915.8836	958.4455	2811.4424	1406.2248
S	2002.9157	1001.9615	2697.3995	1349.2034
S	2089.9477	1045.4775	2610.3675	1305.6874
T	2190.9954	1096.0013	2523.3354	1262.1714
E	2320.0380	1160.5226	2422.2878	1211.6475
P	2417.0907	1209.0490	2293.2452	1147.1262
Y	2580.1541	1290.5807	2196.1924	**1098.5998**
I	2693.2381	1347.1227	2033.1291	1017.0682

Extensin-like protein
IPASICQLPK

Spectrum List

Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
32.537	1304.8840	653.4493	2	38	IPASICQLPK	ICAT-C:13C(9)(C)@6	99	1304.7573
42.205	695.4387	696.4459	1	48	IPDPVR		< 1	695.3966
65.934	1557.9241	779.9693	2		IPGNISGYTAGHSQR	Deamidated(N)@4	< 1	1557.7535

Peptide ID Hypotheses - 4.1.1.1425.4

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z
99	14	38	IPASICQLPK	ICAT-C:13C(9)(C)@6	1304.7573	653.3859	2
< 1	9		ASPTASLSSLEDK		1304.6460	653.3303	2
< 1	9		EGGLKKSVDMNK		1304.6758	653.3452	2
< 1	9		IENVLRVGYDK		1304.7089	653.3617	2
< 1	9		KDLEDMGIRTK		1304.6758	653.3452	2

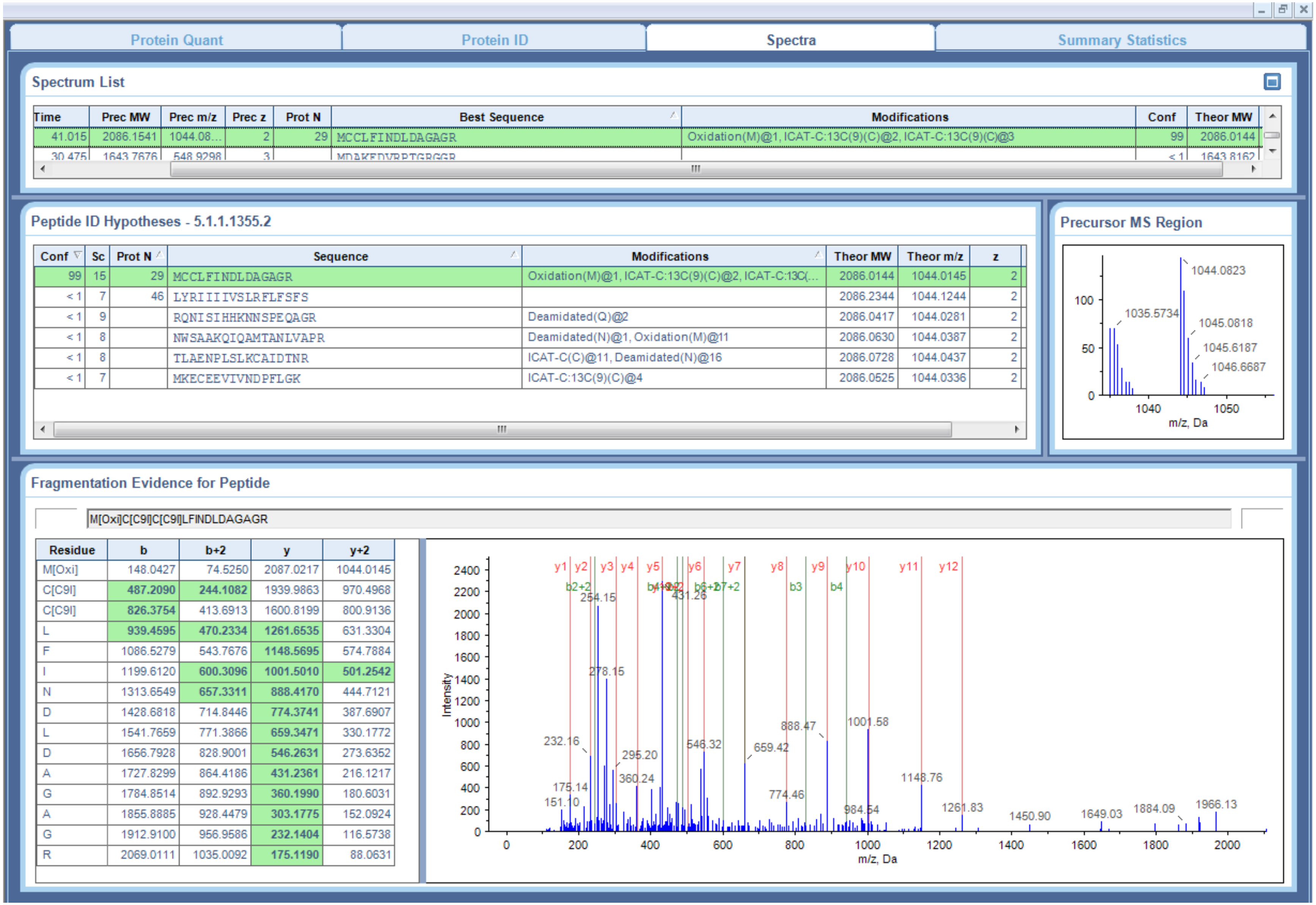
Precursor MS Region

Fragmentation Evidence for Peptide

IPASIC[C9I]QLPK

Residue	b	b+2	y	y+2
I	114.0913	57.5493	**1305.7646**	**653.3859**
P	**211.1441**	106.0757	**1192.6805**	596.8439
A	**282.1812**	141.5942	**1095.6278**	**548.3175**
S	**369.2132**	**185.1103**	**1024.5907**	**512.7990**
I	**482.2973**	241.6523	**937.5586**	469.2830
C[C9I]	821.4637	411.2355	**824.4746**	412.7409
Q	**949.5223**	**475.2648**	**485.3082**	**243.1577**
L	**1062.6063**	**531.8068**	**357.2496**	179.1285
P	1159.6591	580.3332	**244.1656**	122.5864
K	1287.7540	644.3807	**147.1128**	74.0600

Hypothetical protein
MCCLFINDLDAGAGR



Spectrum List

Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
41.015	2086.1541	1044.08...	2	29	MCCLFINDLDAGAGR	Oxidation(M)@1, ICAT-C:13C(9)(C)@2, ICAT-C:13C(9)(C)@3	99	2086.0144
30.475	1643.7676	548.9298	3		MDAKEDVRPTGRGGR		< 1	1643.8162

Peptide ID Hypotheses - 5.1.1.1355.2

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z
99	15	29	MCCLFINDLDAGAGR	Oxidation(M)@1, ICAT-C:13C(9)(C)@2, ICAT-C:13C(...	2086.0144	1044.0145	2
< 1	7	46	LYRIIIIVSLRFLFSFS		2086.2344	1044.1244	2
< 1	9		RQNISIHHKNNSPEQAGR	Deamidated(Q)@2	2086.0417	1044.0281	2
< 1	8		NWSAAKQIQAMTANLVAPR	Deamidated(N)@1, Oxidation(M)@11	2086.0630	1044.0387	2
< 1	8		TLAENPLSLKCAIDTNR	ICAT-C(C)@11, Deamidated(N)@16	2086.0728	1044.0437	2
< 1	7		MKECEEVIVNDPFLGK	ICAT-C:13C(9)(C)@4	2086.0525	1044.0336	2

Fragmentation Evidence for Peptide

M[Oxi]C[C9I]C[C9I]LFINDLDAGAGR

Residue	b	b+2	y	y+2
M[Oxi]	148.0427	74.5250	2087.0217	1044.0145
C[C9I]	**487.2090**	**244.1082**	1939.9863	970.4968
C[C9I]	**826.3754**	413.6913	1600.8199	800.9136
L	**939.4595**	**470.2334**	**1261.6535**	631.3304
F	1086.5279	543.7676	**1148.5695**	574.7884
I	1199.6120	**600.3096**	**1001.5010**	**501.2542**
N	1313.6549	**657.3311**	**888.4170**	444.7121
D	1428.6818	714.8446	**774.3741**	387.6907
L	1541.7659	771.3866	**659.3471**	330.1772
D	1656.7928	828.9001	**546.2631**	273.6352
A	1727.8299	864.4186	**431.2361**	216.1217
G	1784.8514	892.9293	**360.1990**	180.6031
A	1855.8885	928.4479	**303.1775**	152.0924
G	1912.9100	956.9586	**232.1404**	116.5738
R	2069.0111	1035.0092	**175.1190**	88.0631

Unknown protein
LGACVDLLGGLVK

Spectrum List

Time	Prec MW	Prec m/z	Prec z	Prot N	Best Sequence	Modifications	Conf	Theor MW
36.614	0.0000	459.1318	0		LFPTEQIGINSR	Deamidated(N)@10	< 1	1374.7144
63.764	1458.8007	730.4076	2		LFTGGGDPVIITGGR		< 1	1458.7831
44.721	1483.9393	742.9769	2	43	LGACVDLLGGLVK	ICAT-C(C)@4	99	1483.8433
44.764	1492.9680	747.4913	2	43	LGACVDLLGGLVK	ICAT-C:13C(9)(C)@4	99	1492.8734

Peptide ID Hypotheses - 4.1.1.1508.3

Conf	Sc	Prot N	Sequence	Modifications	Theor MW	Theor m/z	z
99	16	43	LGACVDLLGGLVK	ICAT-C:13C(9)(C)@4	1492.8734	747.4440	2
< 1	8		AGRIEDGLTMFRK		1492.7820	747.3983	2
< 1	8		MKYLLVINLSGNK	Deamidated(N)@12	1492.8323	747.4235	2
< 1	8		SLDFSKGKYLAHK		1492.8038	747.4092	2
< 1	8		SLKEQLENAFSVK	Deamidated(N)@8	1492.7773	747.3959	2

Precursor MS Region

Fragmentation Evidence for Peptide

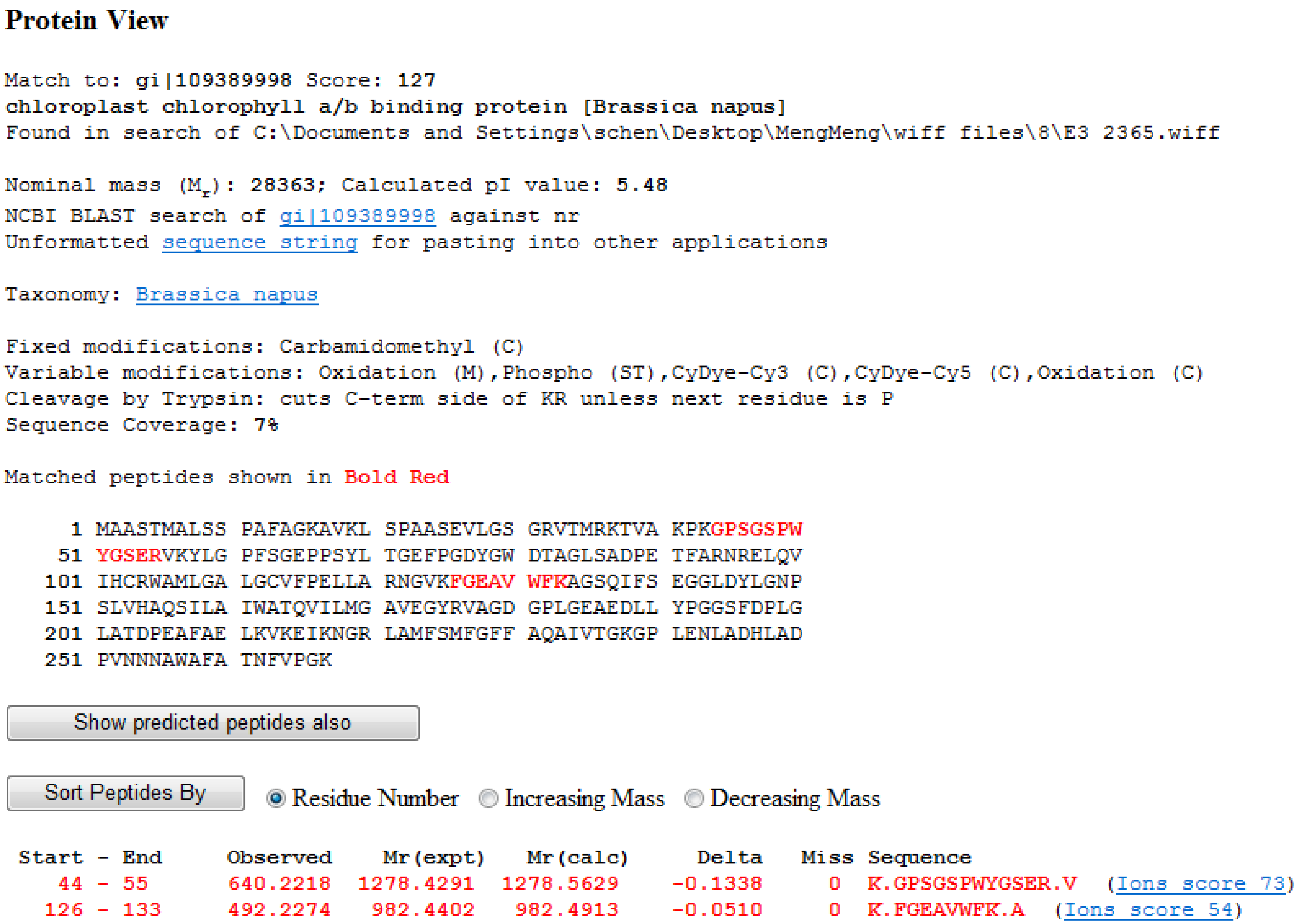
LGAC[C9I]VDLLGGLVK

Residue	b	b+2	y	y+2
L	114.0913	57.5493	1493.8807	**747.4440**
G	**171.1128**	86.0600	1380.7966	690.9020
A	**242.1499**	121.5786	1323.7752	**662.3912**
C[C9I]	**581.3163**	**291.1618**	**1252.7381**	626.8727
V	680.3847	340.6960	**913.5717**	457.2895
D	**795.4116**	398.2095	**814.5033**	407.7553
L	**908.4957**	454.7515	**699.4763**	350.2418
L	**1021.5798**	511.2935	**586.3923**	293.6998
G	1078.6012	539.8043	**473.3082**	**237.1577**
G	1135.6227	568.3150	**416.2867**	208.6470
L	1248.7068	624.8570	**359.2653**	180.1363
V	**1347.7752**	674.3912	**246.1812**	123.5942
K	1475.8701	738.4387	**147.1128**	74.0600

Figure S4

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to ABA treatment in guard cells by redox DIGE.

gi|109389998 Chloroplast chlorophyll a/b binding protein



Protein View

```
Match to: gi|109389998 Score: 127
chloroplast chlorophyll a/b binding protein [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\8\E3 2365.wiff

Nominal mass (Mr): 28363; Calculated pI value: 5.48
NCBI BLAST search of gi|109389998 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

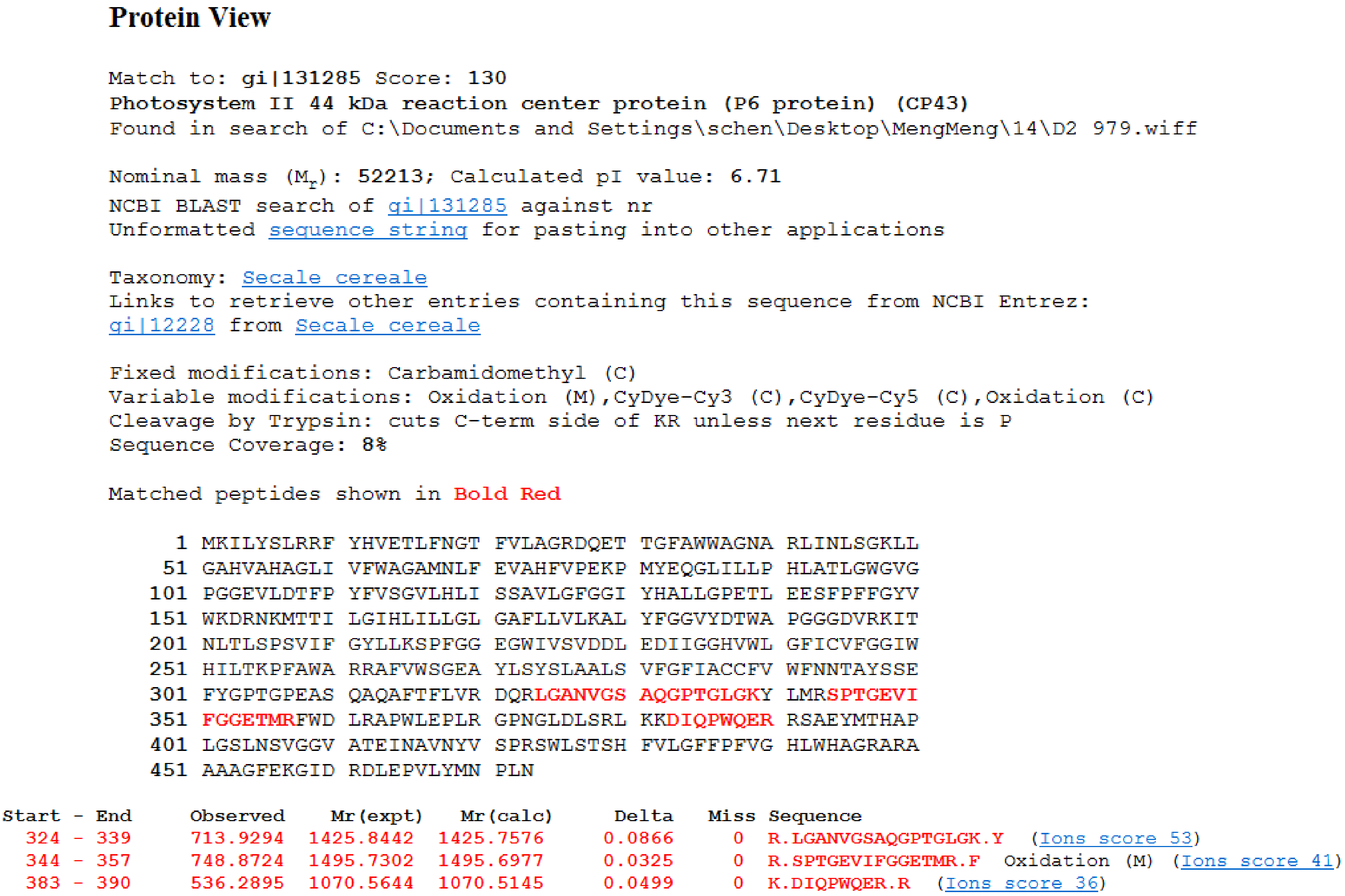
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in Bold Red

    1 MAASTMALSS PAFAGKAVKL SPAASEVLGS GRVTMRKTVA KPKGPSGSPW
   51 YGSERVKYLG PFSGEPPSYL TGEFPGDYGW DTAGLSADPE TFARNRELQV
  101 IHCRWAMLGA LGCVFPELLA RNGVKFGEAV WFKAGSQIFS EGGLDYLGNP
  151 SLVHAQSILA IWATQVILMG AVEGYRVAGD GPLGEAEDLL YPGGSFDPLG
  201 LATDPEAFAE LKVKEIKNGR LAMFSMFGFF AQAIVTGKGP LENLADHLAD
  251 PVNNNAWAFA TNFVPGK
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   44 - 55     640.2218  1278.4291  1278.5629   -0.1338     0  K.GPSGSPWYGSER.V   (Ions score 73)
  126 - 133    492.2274   982.4402   982.4913   -0.0510     0  K.FGEAVWFK.A   (Ions score 54)
```

gi|131285 Photosystem II 44 kDa reaction center protein



Protein View

Match to: **gi|131285** Score: **130**
Photosystem II 44 kDa reaction center protein (P6 protein) (CP43)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff

Nominal mass (M_r): **52213**; Calculated pI value: **6.71**
NCBI BLAST search of gi|131285 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Secale cereale
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12228 from Secale cereale

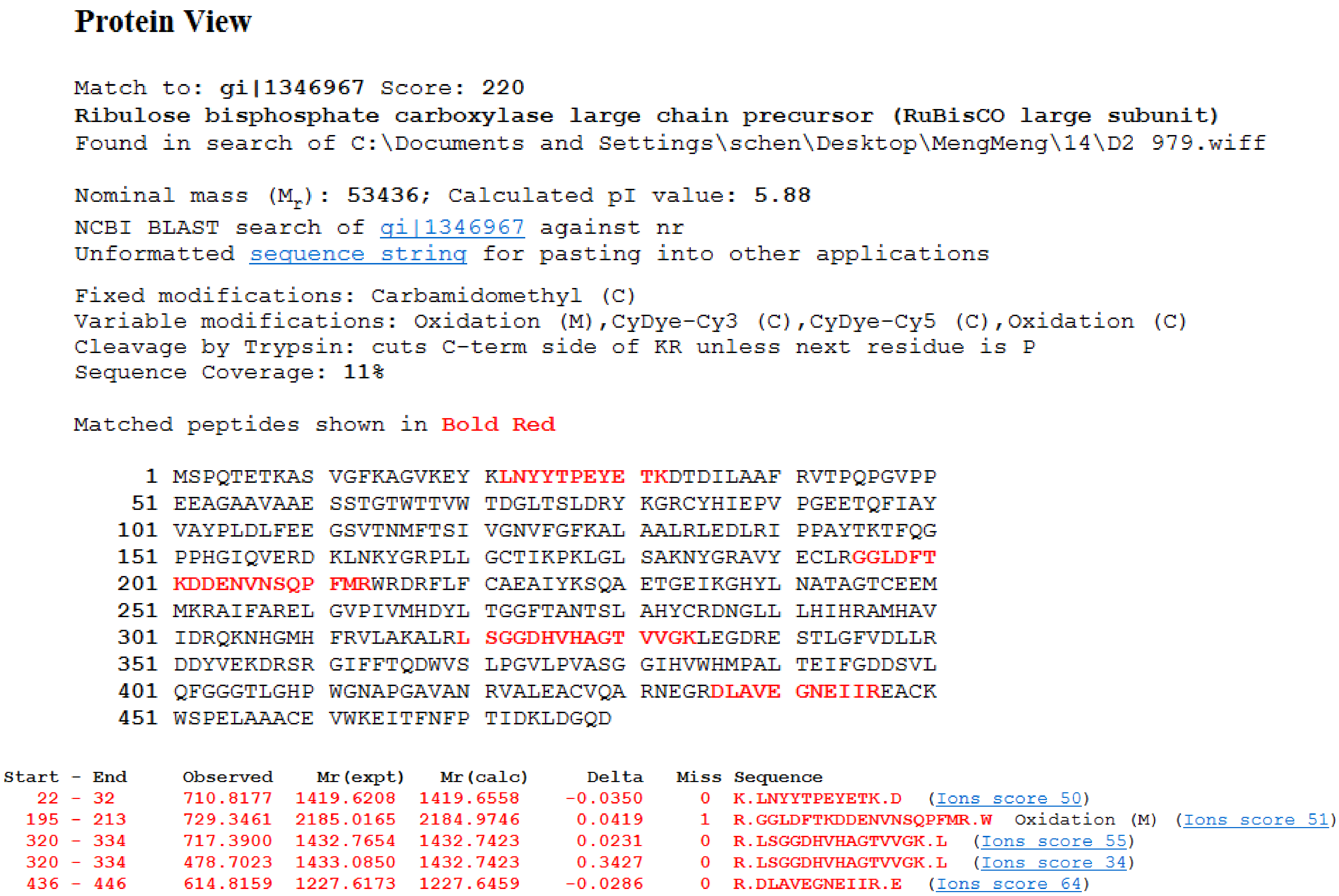
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```
  1 MKILYSLRRF YHVETLFNGT FVLAGRDQET TGFAWWAGNA RLINLSGKLL
 51 GAHVAHAGLI VFWAGAMNLF EVAHFVPEKP MYEQGLILLP HLATLGWGVG
101 PGGEVLDTFP YFVSGVLHLI SSAVLGFGGI YHALLGPETL EESFPFFGYV
151 WKDRNKMTTI LGIHLILLGL GAFLLVLKAL YFGGVYDTWA PGGGDVRKIT
201 NLTLSPSVIF GYLLKSPFGG EGWIVSVDDL EDIIGGHVWL GFICVFGGIW
251 HILTKPFAWA RRAFVWSGEA YLSYSLAALS VFGFIACCFV WFNNTAYSSE
301 FYGPTGPEAS QAQAFTFLVR DQRLGANVGS AQGPTGLGKY LMRSPTGEVI
351 FGGETMRFWD LRAPWLEPLR GPNGLDLSRL KKDIQPWQER RSAEYMTHAP
401 LGSLNSVGGV ATEINAVNYV SPRSWLSTSH FVLGFFPFVG HLWHAGRARA
451 AAAGFEKGID RDLEPVLYMN PLN
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  324 - 339    713.9294  1425.8442  1425.7576    0.0866     0   R.LGANVGSAQGPTGLGK.Y   (Ions score 53)
  344 - 357    748.8724  1495.7302  1495.6977    0.0325     0   R.SPTGEVIFGGETMR.F  Oxidation (M)  (Ions score 41)
  383 - 390    536.2895  1070.5644  1070.5145    0.0499     0   K.DIQPWQER.R   (Ions score 36)
```

gi|8745521 Ribulose bisphosphate carboxylase large chain precursor



Protein View

```
Match to: gi|1346967 Score: 220
Ribulose bisphosphate carboxylase large chain precursor (RuBisCO large subunit)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff

Nominal mass (Mr): 53436; Calculated pI value: 5.88
NCBI BLAST search of gi|1346967 against nr
Unformatted sequence string for pasting into other applications

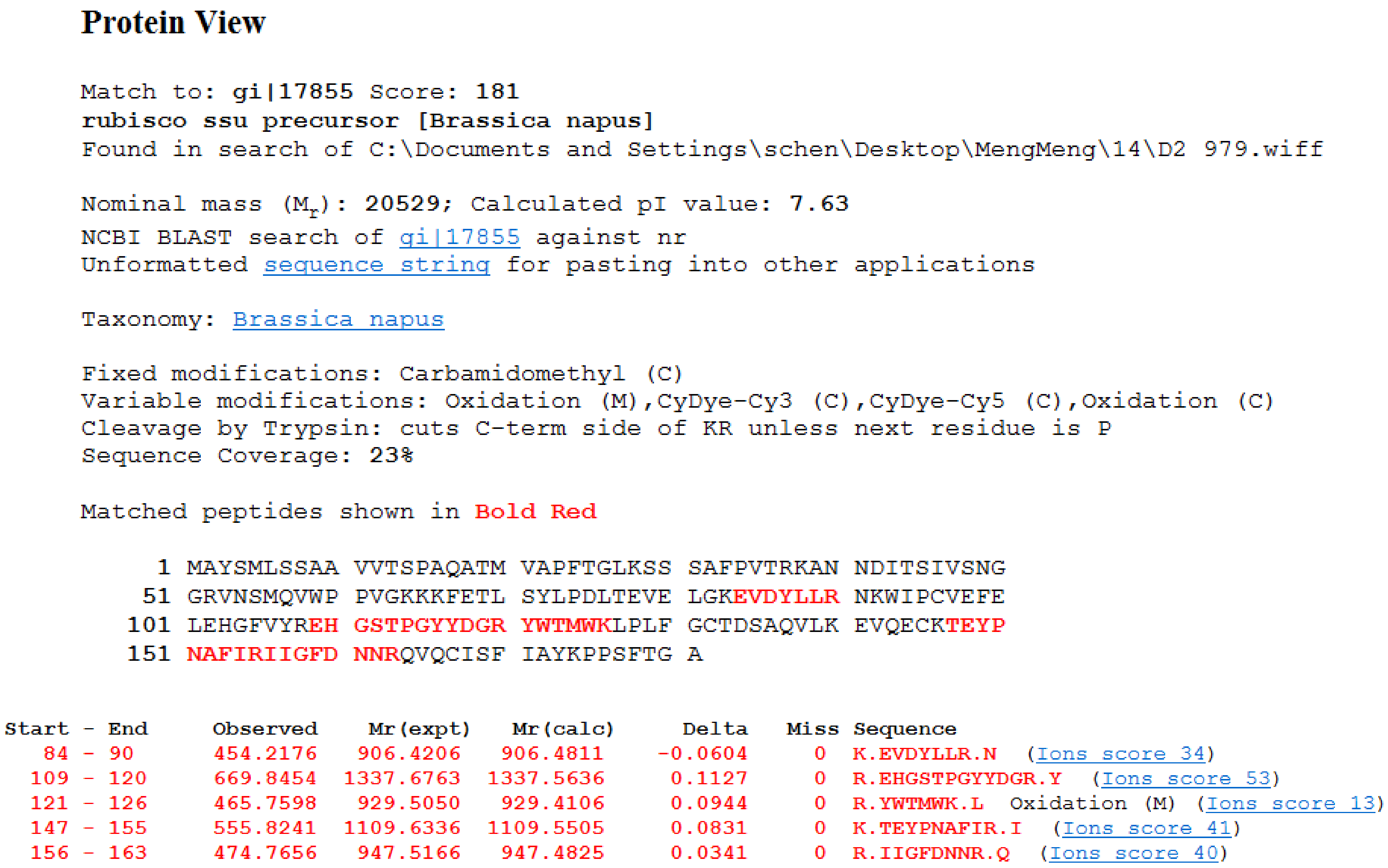
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%

Matched peptides shown in Bold Red

      1 MSPQTETKAS VGFKAGVKEY KLNYYTPEYE TKDTDILAAF RVTPQPGVPP
     51 EEAGAAVAAE SSTGTWTTVW TDGLTSLDRY KGRCYHIEPV PGEETQFIAY
    101 VAYPLDLFEE GSVTNMFTSI VGNVFGFKAL AALRLEDLRI PPAYTKTFQG
    151 PPHGIQVERD KLNKYGRPLL GCTIKPKLGL SAKNYGRAVY ECLRGGLDFT
    201 KDDENVNSQP FMRWRDRFLF CAEAIYKSQA ETGEIKGHYL NATAGTCEEM
    251 MKRAIFAREL GVPIVMHDYL TGGFTANTSL AHYCRDNGLL LHIHRAMHAV
    301 IDRQKNHGMH FRVLAKALRL SGGDHVHAGT VVGKLEGDRE STLGFVDLLR
    351 DDYVEKDRSR GIFFTQDWVS LPGVLPVASG GIHVWHMPAL TEIFGDDSVL
    401 QFGGGTLGHP WGNAPGAVAN RVALEACVQA RNEGRDLAVE GNEIIREACK
    451 WSPELAAACE VWKEITFNFP TIDKLDGQD

Start - End      Observed    Mr(expt)    Mr(calc)      Delta    Miss  Sequence
   22 - 32       710.8177   1419.6208   1419.6558    -0.0350      0  K.LNYYTPEYETK.D  (Ions score 50)
  195 - 213      729.3461   2185.0165   2184.9746     0.0419      1  R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)  (Ions score 51)
  320 - 334      717.3900   1432.7654   1432.7423     0.0231      0  R.LSGGDHVHAGTVVGK.L  (Ions score 55)
  320 - 334      478.7023   1433.0850   1432.7423     0.3427      0  R.LSGGDHVHAGTVVGK.L  (Ions score 34)
  436 - 446      614.8159   1227.6173   1227.6459    -0.0286      0  R.DLAVEGNEIIR.E  (Ions score 64)
```

gi|17855 Rubisco small subunit precursor



Protein View

Match to: **gi|17855** Score: **181**
rubisco ssu precursor [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff

Nominal mass (M_r): **20529**; Calculated pI value: **7.63**
NCBI BLAST search of gi|17855 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

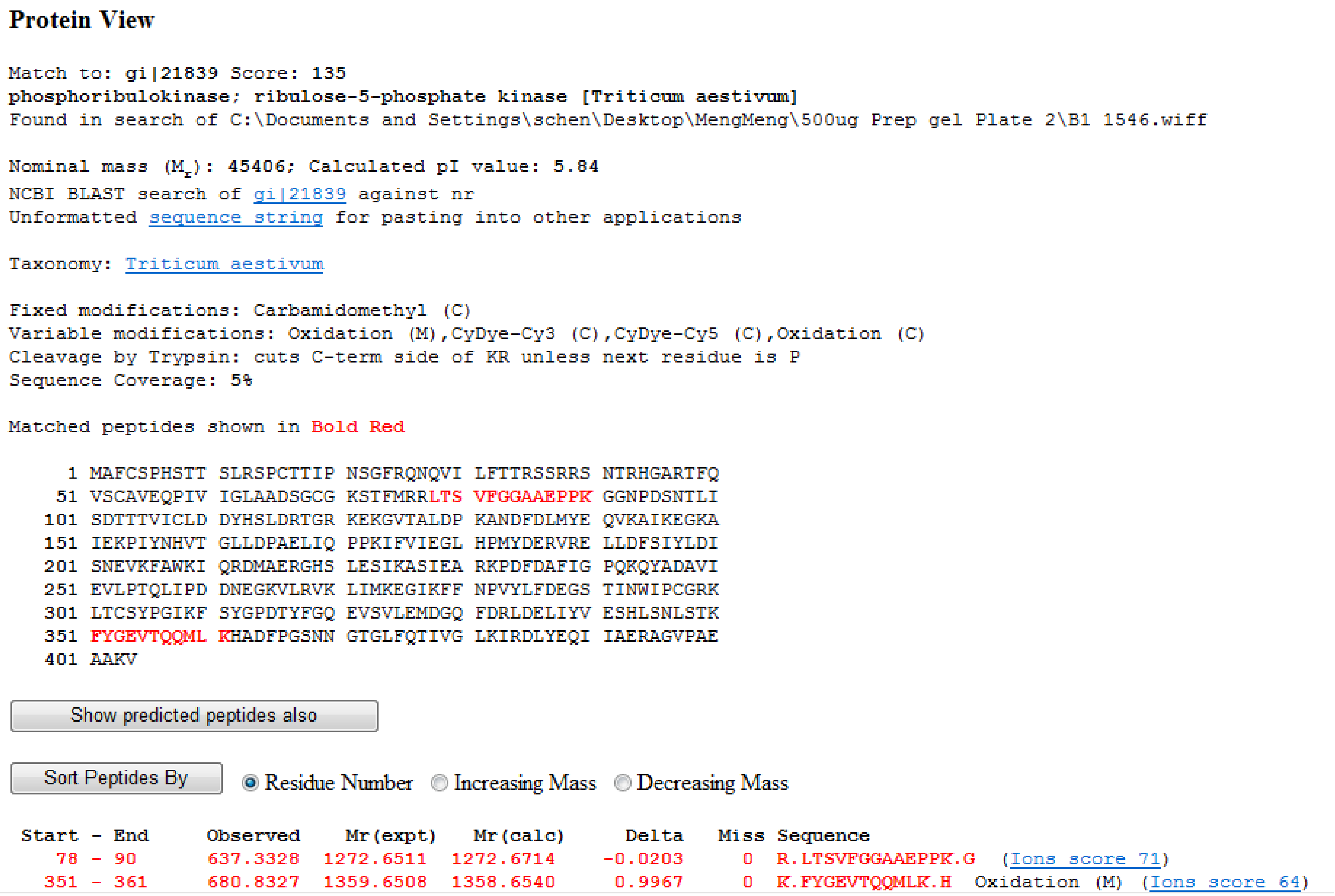
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 23%

Matched peptides shown in **Bold Red**

1 MAYSMLSSAA VVTSPAQATM VAPFTGLKSS SAFPVTRKAN NDITSIVSNG
51 GRVNSMQVWP PVGKKKFETL SYLPDLTEVE LGK**EVDYLLR** NKWIPCVEFE
101 LEHGFVYR**EH GSTPGYYDGR YWTMWK**LPLF GCTDSAQVLK EVQECK**TEYP**
151 **NAFIRIIGFD NNR**QVQCISF IAYKPPSFTG A

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss Sequence
  84 - 90       454.2176    906.4206   906.4811   -0.0604     0  K.EVDYLLR.N   (Ions score 34)
 109 - 120      669.8454   1337.6763  1337.5636    0.1127     0  R.EHGSTPGYYDGR.Y   (Ions score 53)
 121 - 126      465.7598    929.5050   929.4106    0.0944     0  R.YWTMWK.L  Oxidation (M)  (Ions score 13)
 147 - 155      555.8241   1109.6336  1109.5505    0.0831     0  K.TEYPNAFIR.I   (Ions score 41)
 156 - 163      474.7656    947.5166   947.4825    0.0341     0  R.IIGFDNNR.Q   (Ions score 40)
```

gi|21839 Phosphoribulokinase; ribulose-5-phosphate kinase



Protein View

```
Match to: gi|21839 Score: 135
phosphoribulokinase; ribulose-5-phosphate kinase [Triticum aestivum]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff

Nominal mass (Mr): 45406; Calculated pI value: 5.84
NCBI BLAST search of gi|21839 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

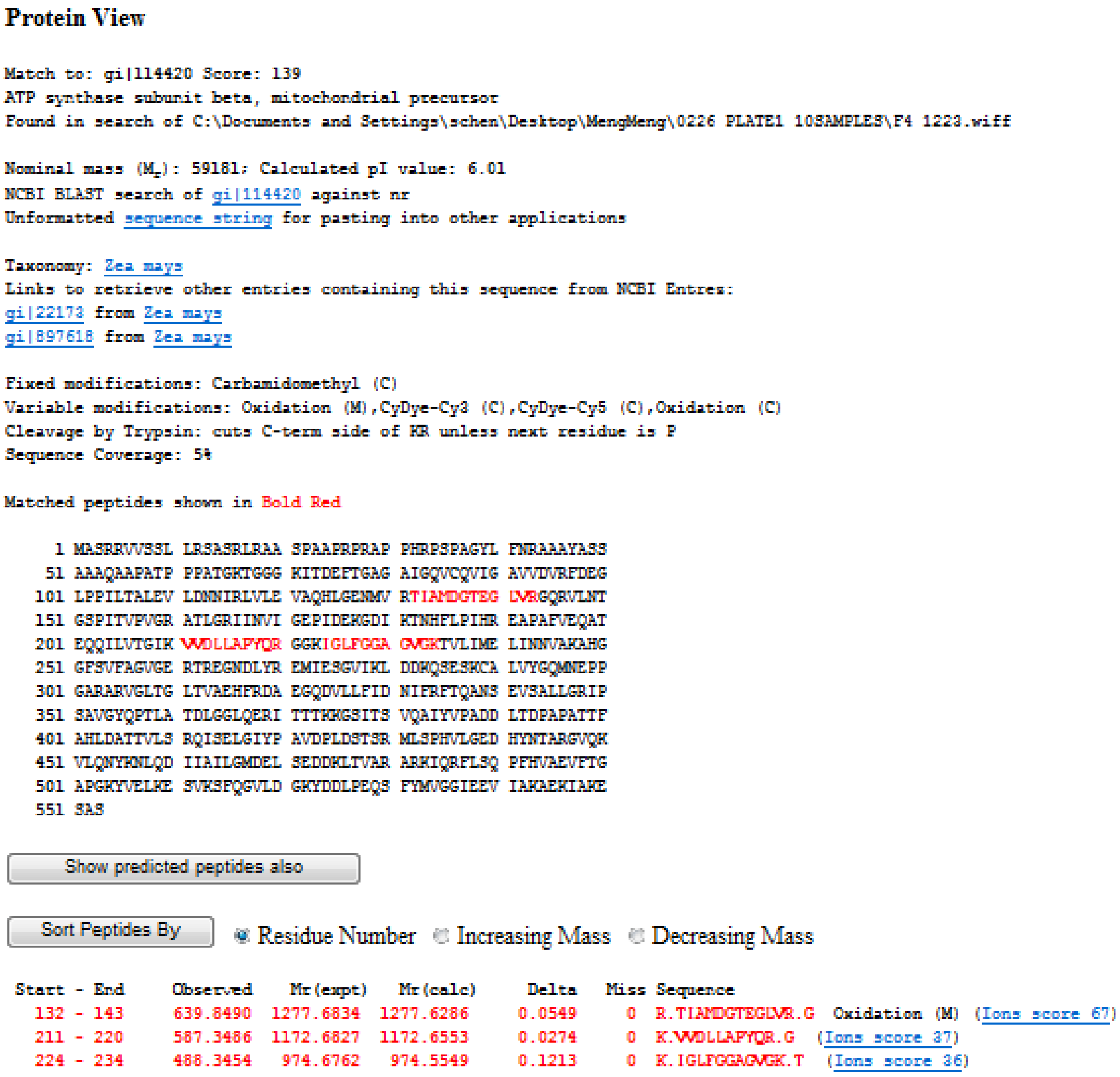
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

     1 MAFCSPHSTT SLRSPCTTIP NSGFRQNQVI LFTTRSSRRS NTRHGARTFQ
    51 VSCAVEQPIV IGLAADSGCG KSTFMRRLTS VFGGAAEPPK GGNPDSNTLI
   101 SDTTTVICLD DYHSLDRTGR KEKGVTALDP KANDFDLMYE QVKAIKEGKA
   151 IEKPIYNHVT GLLDPAELIQ PPKIFVIEGL HPMYDERVRE LLDFSIYLDI
   201 SNEVKFAWKI QRDMAERGHS LESIKASIEA RKPDFDAFIG PQKQYADAVI
   251 EVLPTQLIPD DNEGKVLRVK LIMKEGIKFF NPVYLFDEGS TINWIPCGRK
   301 LTCSYPGIKF SYGPDTYFGQ EVSVLEMDGQ FDRLDELIYV ESHLSNLSTK
   351 FYGEVTQQML KHADFPGSNN GTGLFQTIVG LKIRDLYEQI IAERAGVPAE
   401 AAKV
```

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta  Miss Sequence
    78 - 90      637.3328   1272.6511  1272.6714   -0.0203     0 R.LTSVFGGAAEPPK.G  (Ions score 71)
   351 - 361     680.8327   1359.6508  1358.6540    0.9967     0 K.FYGEVTQQMLK.H  Oxidation (M) (Ions score 64)
```

gi|114420 ATP synthase subunit beta, mitochondrial precursor



Protein View

```
Match to: gi|114420 Score: 139
ATP synthase subunit beta, mitochondrial precursor
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\F4 1223.wiff

Nominal mass (Mr): 59181; Calculated pI value: 6.01
NCBI BLAST search of gi|114420 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|22173 from Zea mays
gi|897618 from Zea mays

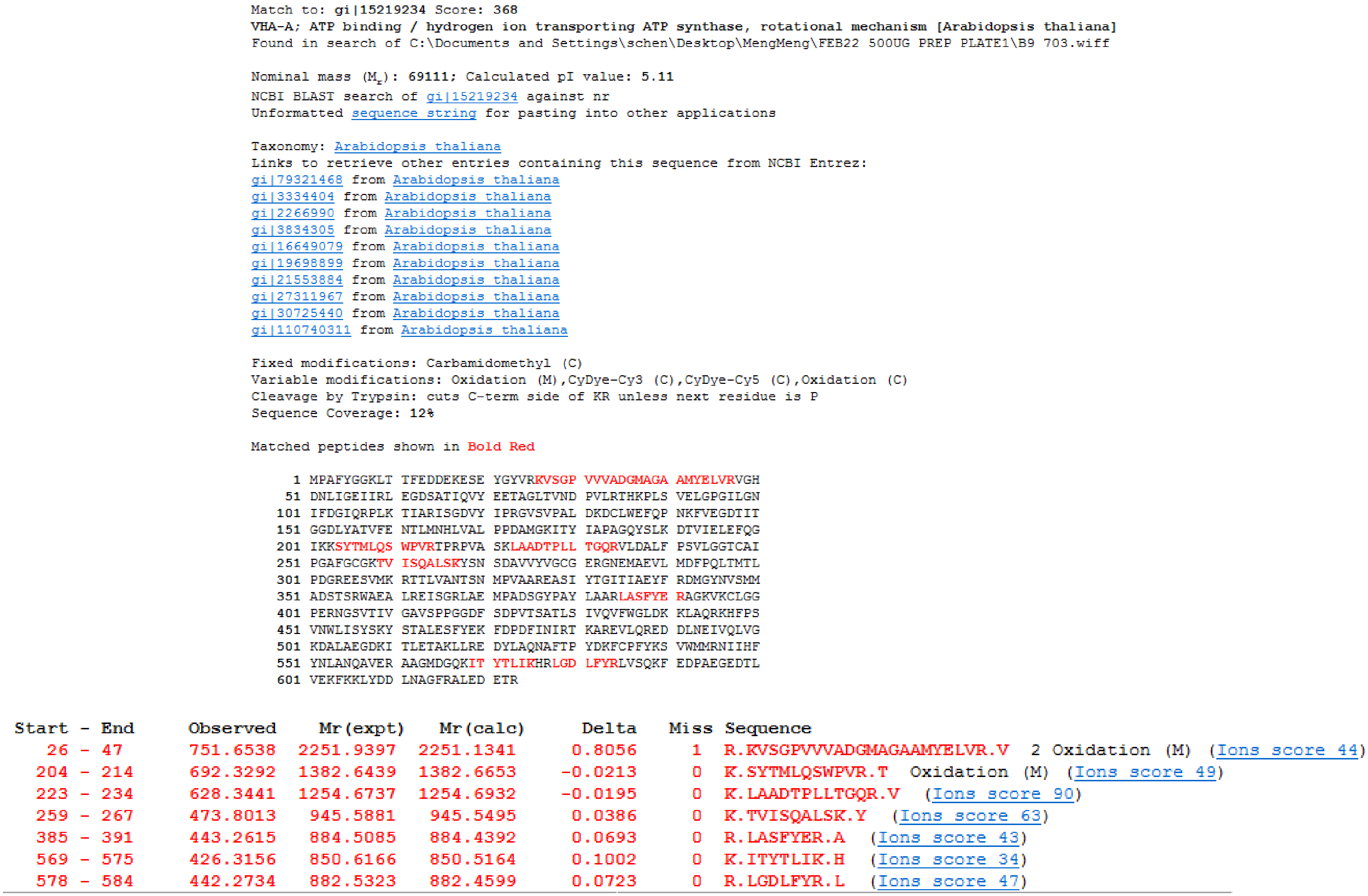
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

     1 MASRRVVSSL LRSASRLRAA SPAAPRPRAP PHRPSPAGYL FNRAAAYASS
    51 AAAQAAPATP PPATGKTGGG KITDEFTGAG AIGQVCQVIG AVVDVRFDEG
   101 LPPILTALEV LDNNIRLVLE VAQHLGENMV RTIAMDGTEG LVRGQRVLNT
   151 GSPITVPVGR ATLGRIINVI GEPIDEKGDI KTNHFLPIHR EAPAFVEQAT
   201 EQQILVTGIK VVDLLAPYQR GGKIGLFGGA GVGKTVLIME LINNVAKAHG
   251 GFSVFAGVGE RTREGNDLYR EMIESGVIKL DDKQSESKCA LVYGQMNEPP
   301 GARARVGLTG LTVAEHFRDA EGQDVLLFID NIFRFTQANS EVSALLGRIP
   351 SAVGYQPTLA TDLGGLQERI TTTKKGSITS VQAIYVPADD LTDPAPATTF
   401 AHLDATTVLS RQISELGIYP AVDPLDSTSR MLSPHVLGED HYNTARGVQK
   451 VLQNYKNLQD IIAILGMDEL SEDDKLTVAR ARKIQRFLSQ PFHVAEVFTG
   501 APGKYVELKE SVKSFQGVLD GKYDDLPEQS FYMVGGIEEV IAKAEKIAKE
   551 SAS
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   132 - 143     639.8490  1277.6834  1277.6286    0.0549     0  R.TIAMDGTEGLVR.G  Oxidation (M)  (Ions score 67)
   211 - 220     587.3486  1172.6827  1172.6553    0.0274     0  K.VVDLLAPYQR.G  (Ions score 37)
   224 - 234     488.3454   974.6762   974.5549    0.1213     0  K.IGLFGGAGVGK.T  (Ions score 36)
```

gi|15219234 Vacuolar ATP synthase subunit A (VHA-A)



```
Match to: gi|15219234 Score: 368
VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\B9 703.wiff

Nominal mass (Mr): 69111; Calculated pI value: 5.11
NCBI BLAST search of gi|15219234 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|79321468 from Arabidopsis thaliana
gi|3334404 from Arabidopsis thaliana
gi|2266990 from Arabidopsis thaliana
gi|3834305 from Arabidopsis thaliana
gi|16649079 from Arabidopsis thaliana
gi|19698899 from Arabidopsis thaliana
gi|21553884 from Arabidopsis thaliana
gi|27311967 from Arabidopsis thaliana
gi|30725440 from Arabidopsis thaliana
gi|110740311 from Arabidopsis thaliana

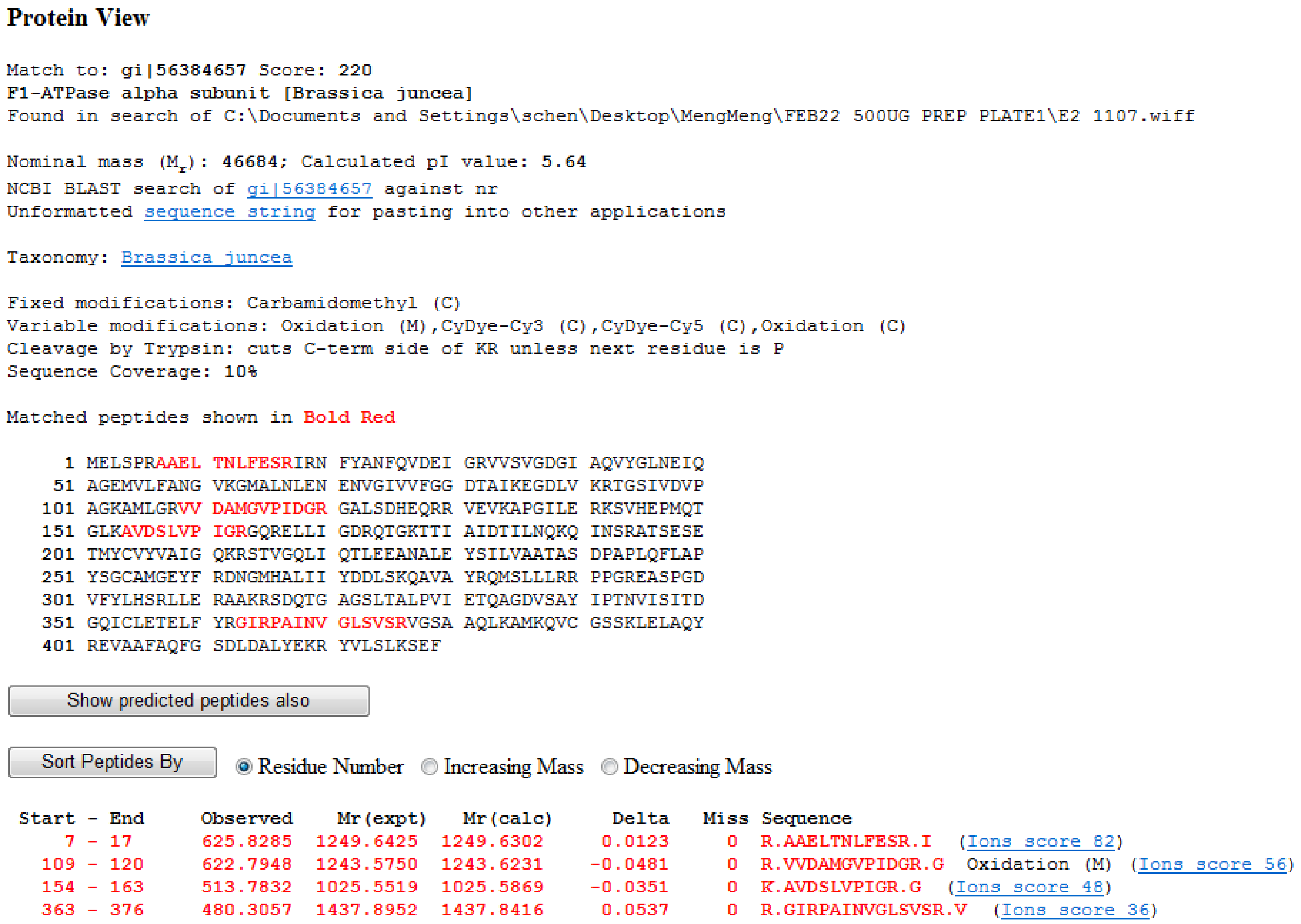
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%

Matched peptides shown in Bold Red

    1 MPAFYGGKLT TFEDDEKESE YGYVRKVSGP VVVADGMAGA AMYELVRVGH
   51 DNLIGEIIRL EGDSATIQVY EETAGLTVND PVLRTHKPLS VELGPGILGN
  101 IFDGIQRPLK TIARISGDVY IPRGVSVPAL DKDCLWEFQP NKFVEGDTIT
  151 GGDLYATVFE NTLMNHLVAL PPDAMGKITY IAPAGQYSLK DTVIELEFQG
  201 IKKSYTMLQS WPVRTPRPVA SKLAADTPLL TGQRVLDALF PSVLGGTCAI
  251 PGAFGCGKTV ISQALSKYSN SDAVVYVGCG ERGNEMAEVL MDFPQLTMTL
  301 PDGREESVMK RTTLVANTSN MPVAAREASI YTGITIAEYF RDMGYNVSMM
  351 ADSTSRWAEA LREISGRLAE MPADSGYPAY LAARLASFYE RAGKVKCLGG
  401 PERNGSVTIV GAVSPPGGDF SDPVTSATLS IVQVFWGLDK KLAQRKHFPS
  451 VNWLISYSKY STALESFYEK FDPDFINIRT KAREVLQRED DLNEIVQLVG
  501 KDALAEGDKI TLETAKLLRE DYLAQNAFTP YDKFCPFYKS VWMMRNIIHF
  551 YNLANQAVER AAGMDGQKIT YTLIKHRLGD LFYRLVSQKF EDPAEGEDTL
  601 VEKFKKLYDD LNAGFRALED ETR

Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss  Sequence
  26 - 47      751.6538  2251.9397  2251.1341    0.8056     1  R.KVSGPVVVADGMAGAAMYELVR.V  2 Oxidation (M)  (Ions score 44)
 204 - 214     692.3292  1382.6439  1382.6653   -0.0213     0  K.SYTMLQSWPVR.T  Oxidation (M)  (Ions score 49)
 223 - 234     628.3441  1254.6737  1254.6932   -0.0195     0  K.LAADTPLLTGQR.V  (Ions score 90)
 259 - 267     473.8013   945.5881   945.5495    0.0386     0  K.TVISQALSK.Y  (Ions score 63)
 385 - 391     443.2615   884.5085   884.4392    0.0693     0  R.LASFYER.A  (Ions score 43)
 569 - 575     426.3156   850.6166   850.5164    0.1002     0  K.ITYTLIK.H  (Ions score 34)
 578 - 584     442.2734   882.5323   882.4599    0.0723     0  R.LGDLFYR.L  (Ions score 47)
```

gi|56384657 F1-ATPase alpha subunit



Protein View

Match to: gi|56384657 Score: 220
F1-ATPase alpha subunit [Brassica juncea]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\E2 1107.wiff

Nominal mass (M_r): **46684**; Calculated pI value: **5.64**
NCBI BLAST search of gi|56384657 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica juncea

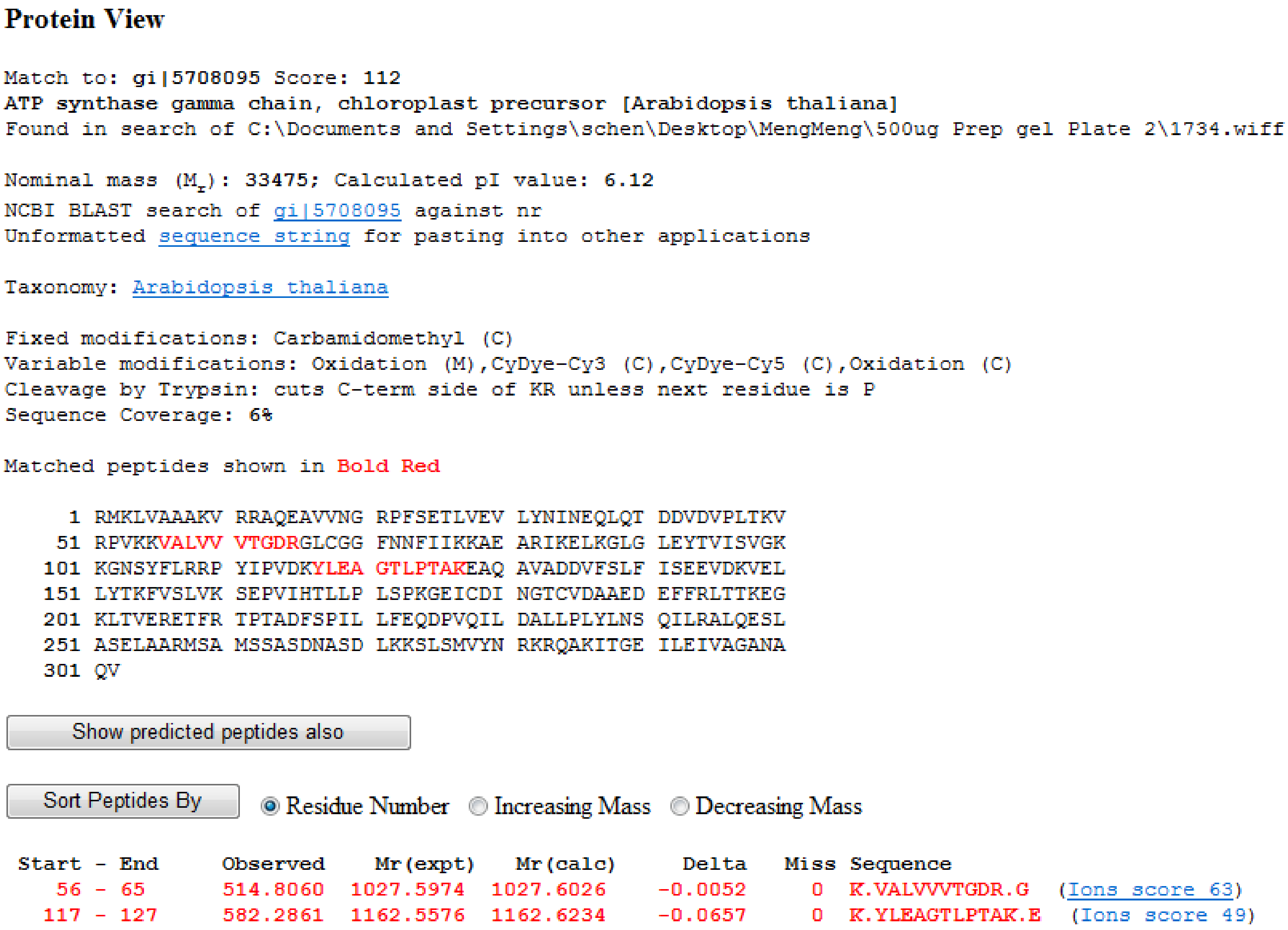
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
  1 MELSPRAAEL TNLFESRIRN FYANFQVDEI GRVVSVGDGI AQVYGLNEIQ
 51 AGEMVLFANG VKGMALNLEN ENVGIVVFGG DTAIKEGDLV KRTGSIVDVP
101 AGKAMLGRVV DAMGVPIDGR GALSDHEQRR VEVKAPGILE RKSVHEPMQT
151 GLKAVDSLVP IGRGQRELLI GDRQTGKTTI AIDTILNQKQ INSRATSESE
201 TMYCVYVAIG QKRSTVGQLI QTLEEANALE YSILVAATAS DPAPLQFLAP
251 YSGCAMGEYF RDNGMHALII YDDLSKQAVA YRQMSLLLRR PPGREASPGD
301 VFYLHSRLLE RAAKRSDQTG AGSLTALPVI ETQAGDVSAY IPTNVISITD
351 GQICLETELF YRGIRPAINV GLSVSRVGSA AQLKAMKQVC GSSKLELAQY
401 REVAAFAQFG SDLDALYEKR YVLSLKSEF
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
    7 - 17     625.8285  1249.6425  1249.6302    0.0123     0  R.AAELTNLFESR.I   (Ions score 82)
  109 - 120    622.7948  1243.5750  1243.6231   -0.0481     0  R.VVDAMGVPIDGR.G  Oxidation (M)  (Ions score 56)
  154 - 163    513.7832  1025.5519  1025.5869   -0.0351     0  K.AVDSLVPIGR.G  (Ions score 48)
  363 - 376    480.3057  1437.8952  1437.8416    0.0537     0  R.GIRPAINVGLSVSR.V   (Ions score 36)
```

gi|5708095 ATP synthase gamma chain, chloroplast precursor



Protein View

Match to: gi|5708095 Score: 112
ATP synthase gamma chain, chloroplast precursor [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1734.wiff

Nominal mass (M_r): 33475; Calculated pI value: 6.12
NCBI BLAST search of gi|5708095 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

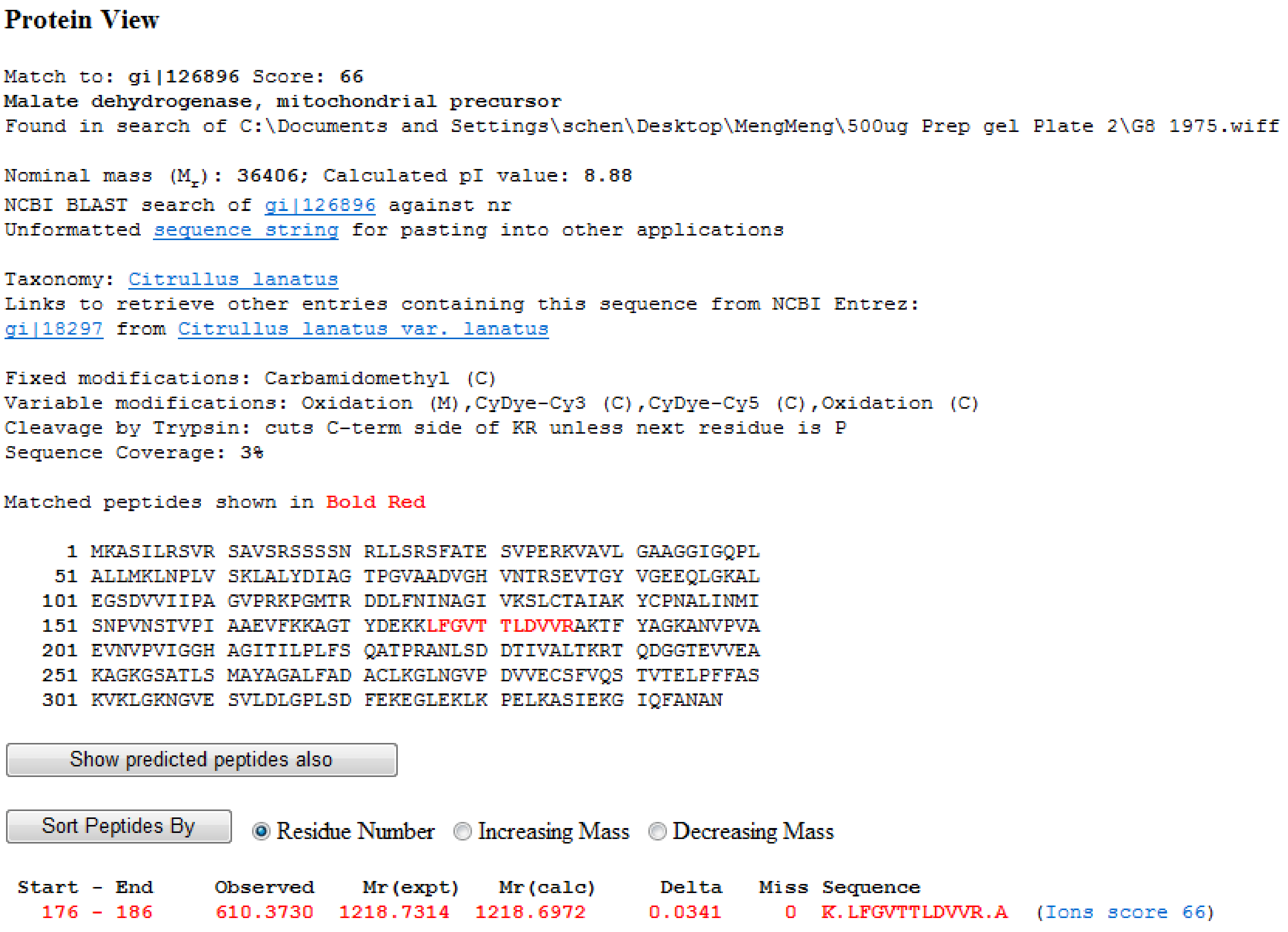
Matched peptides shown in **Bold Red**

```
  1 RMKLVAAAKV RRAQEAVVNG RPFSETLVEV LYNINEQLQT DDVDVPLTKV
 51 RPVKKVALVV VTGDRGLCGG FNNFIIKKAE ARIKELKGLG LEYTVISVGK
101 KGNSYFLRRP YIPVDKYLEA GTLPTAKEAQ AVADDVFSLF ISEEVDKVEL
151 LYTKFVSLVK SEPVIHTLLP LSPKGEICDI NGTCVDAAED EFFRLTTKEG
201 KLTVERETFR TPTADFSPIL LFEQDPVQIL DALLPLYLNS QILRALQESL
251 ASELAARMSA MSSASDNASD LKKSLSMVYN RKRQAKITGE ILEIVAGANA
301 QV
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
    56 - 65      514.8060  1027.5974  1027.6026   -0.0052    0  K.VALVVVTGDR.G   (Ions score 63)
   117 - 127     582.2861  1162.5576  1162.6234   -0.0657    0  K.YLEAGTLPTAK.E   (Ions score 49)
```

gi|126896 Malate dehydrogenase, mitochondrial precursor



Protein View

Match to: gi|126896 Score: 66
Malate dehydrogenase, mitochondrial precursor
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\G8 1975.wiff

Nominal mass (M_r): 36406; Calculated pI value: 8.88
NCBI BLAST search of gi|126896 against nr
Unformatted sequence string for pasting into other applications

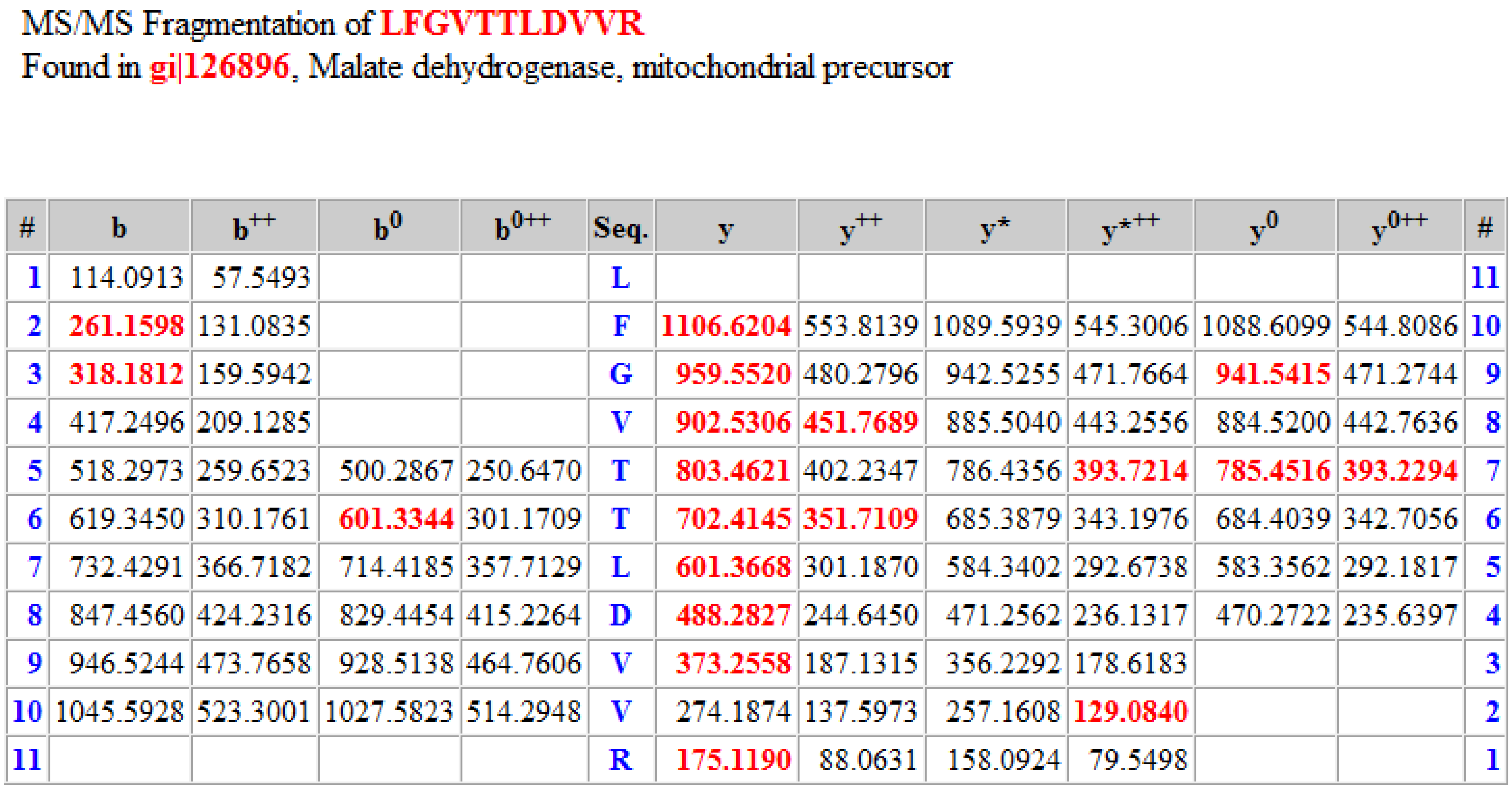
Taxonomy: Citrullus lanatus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|18297 from Citrullus lanatus var. lanatus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

```
  1 MKASILRSVR SAVSRSSSSN RLLSRSFATE SVPERKVAVL GAAGGIGQPL
 51 ALLMKLNPLV SKLALYDIAG TPGVAADVGH VNTRSEVTGY VGEEQLGKAL
101 EGSDVVIIPA GVPRKPGMTR DDLFNINAGI VKSLCTAIAK YCPNALINMI
151 SNPVNSTVPI AAEVFKKAGT YDEKKLFGVT TLDVVRAKTF YAGKANVPVA
201 EVNVPVIGGH AGITILPLFS QATPRANLSD DTIVALTKRT QDGGTEVVEA
251 KAGKGSATLS MAYAGALFAD ACLKGLNGVP DVVECSFVQS TVTELPFFAS
301 KVKLGKNGVE SVLDLGPLSD FEKEGLEKLK PELKASIEKG IQFANAN
```

```
Start - End      Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  176 - 186      610.3730   1218.7314  1218.6972    0.0341     0  K.LFGVTTLDVVR.A    (Ions score 66)
```

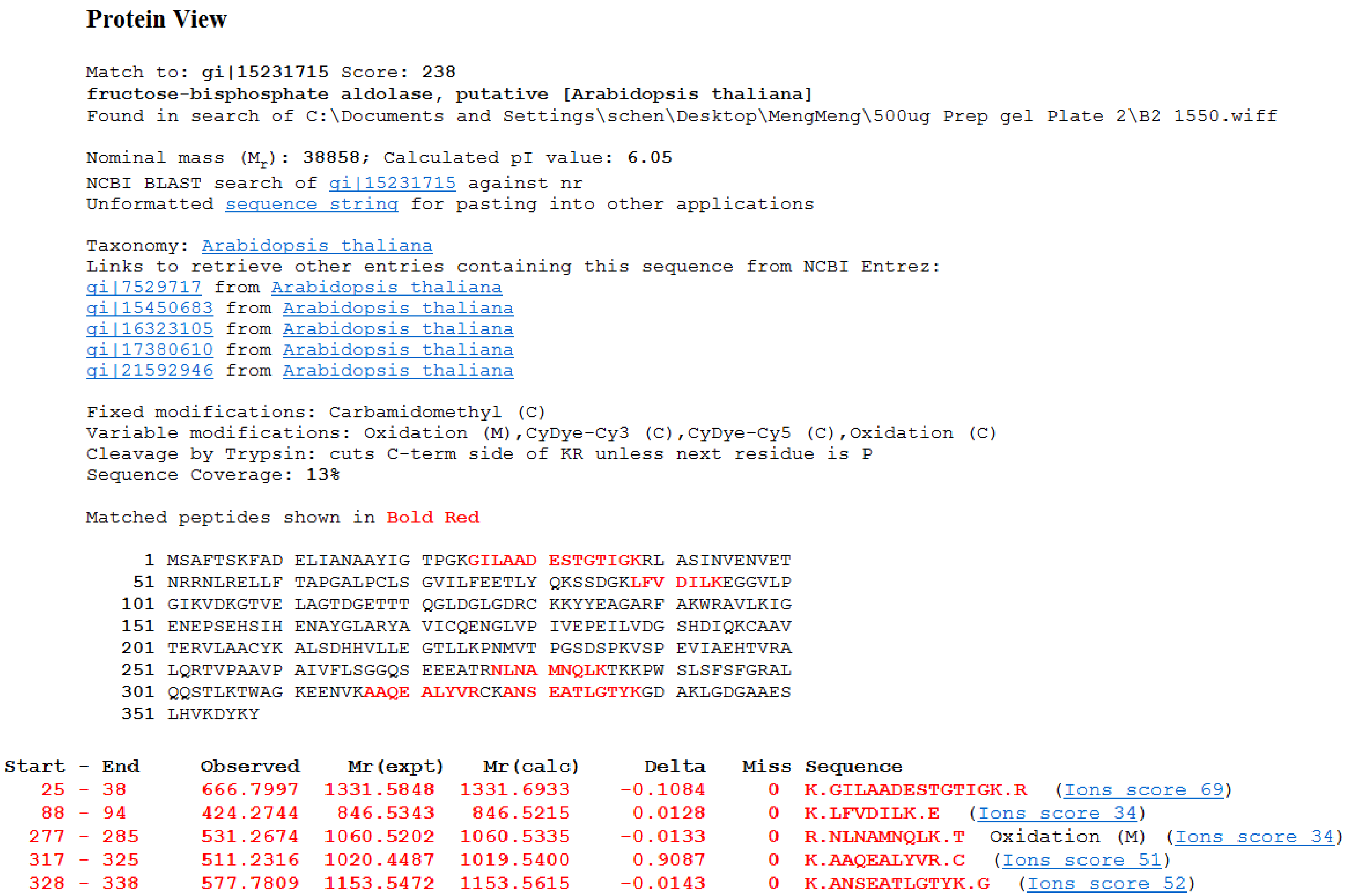


MS/MS Fragmentation of **LFGVTTLDVVR**

Found in **gi|126896**, Malate dehydrogenase, mitochondrial precursor

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							11
2	**261.1598**	131.0835			F	**1106.6204**	553.8139	1089.5939	545.3006	1088.6099	544.8086	10
3	**318.1812**	159.5942			G	**959.5520**	480.2796	942.5255	471.7664	**941.5415**	471.2744	9
4	417.2496	209.1285			V	**902.5306**	**451.7689**	885.5040	443.2556	884.5200	442.7636	8
5	518.2973	259.6523	500.2867	250.6470	T	**803.4621**	402.2347	786.4356	**393.7214**	**785.4516**	**393.2294**	7
6	619.3450	310.1761	**601.3344**	301.1709	T	**702.4145**	**351.7109**	685.3879	343.1976	684.4039	342.7056	6
7	732.4291	366.7182	714.4185	357.7129	L	**601.3668**	301.1870	584.3402	292.6738	583.3562	292.1817	5
8	847.4560	424.2316	829.4454	415.2264	D	**488.2827**	244.6450	471.2562	236.1317	470.2722	235.6397	4
9	946.5244	473.7658	928.5138	464.7606	V	**373.2558**	187.1315	356.2292	178.6183			3
10	1045.5928	523.3001	1027.5823	514.2948	V	274.1874	137.5973	257.1608	**129.0840**			2
11					R	**175.1190**	88.0631	158.0924	79.5498			1

gi|15231715 Fructose-bisphosphate aldolase, putative



Protein View

Match to: **gi|15231715** Score: **238**
fructose-bisphosphate aldolase, putative [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B2 1550.wiff

Nominal mass (M_r): **38858**; Calculated pI value: **6.05**
NCBI BLAST search of gi|15231715 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|7529717 from Arabidopsis thaliana
gi|15450683 from Arabidopsis thaliana
gi|16323105 from Arabidopsis thaliana
gi|17380610 from Arabidopsis thaliana
gi|21592946 from Arabidopsis thaliana

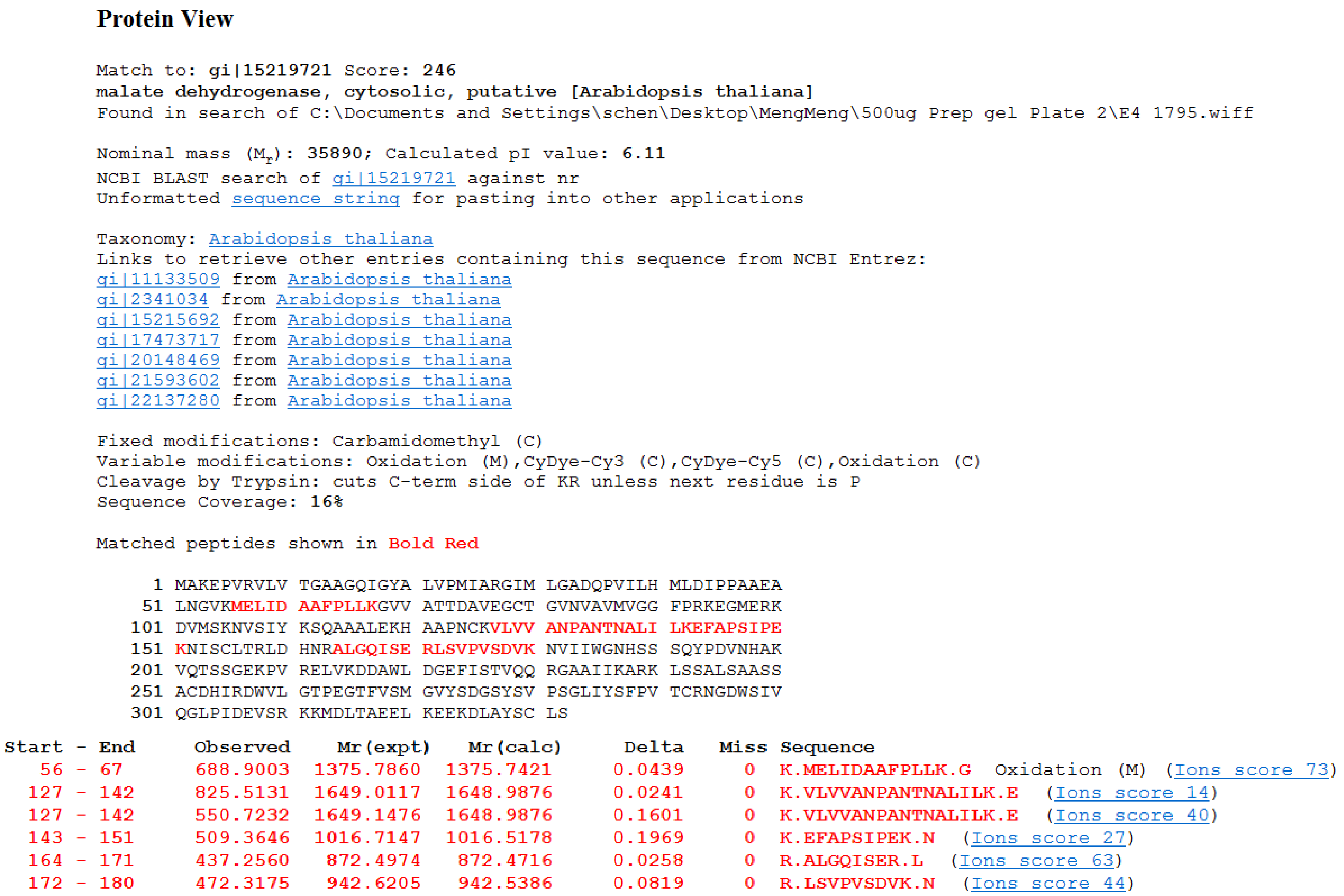
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **13%**

Matched peptides shown in **Bold Red**

```
  1 MSAFTSKFAD ELIANAAYIG TPGKGILAAD ESTGTIGKRL ASINVENVET
 51 NRRNLRELLF TAPGALPCLS GVILFEETLY QKSSDGKLFV DILKEGGVLP
101 GIKVDKGTVE LAGTDGETTT QGLDGLGDRC KKYYEAGARF AKWRAVLKIG
151 ENEPSEHSIH ENAYGLARYA VICQENGLVP IVEPEILVDG SHDIQKCAAV
201 TERVLAACYK ALSDHHVLLE GTLLKPNMVT PGSDSPKVSP EVIAEHTVRA
251 LQRTVPAAVP AIVFLSGGQS EEEATRNLNA MNQLKTKKPW SLSFSFGRAL
301 QQSTLKTWAG KEENVKAAQE ALYVRCKANS EATLGTYKGD AKLGDGAAES
351 LHVKDYKY
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   25 - 38      666.7997  1331.5848  1331.6933   -0.1084     0  K.GILAADESTGTIGK.R   (Ions score 69)
   88 - 94      424.2744   846.5343   846.5215    0.0128     0  K.LFVDILK.E   (Ions score 34)
  277 - 285     531.2674  1060.5202  1060.5335   -0.0133     0  R.NLNAMNQLK.T   Oxidation (M)  (Ions score 34)
  317 - 325     511.2316  1020.4487  1019.5400    0.9087     0  K.AAQEALYVR.C   (Ions score 51)
  328 - 338     577.7809  1153.5472  1153.5615   -0.0143     0  K.ANSEATLGTYK.G   (Ions score 52)
```

gi|15219721 Malate dehydrogenase, cytosolic, putative



Protein View

```
Match to: gi|15219721 Score: 246
malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\E4 1795.wiff

Nominal mass (Mr): 35890; Calculated pI value: 6.11
NCBI BLAST search of gi|15219721 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|11133509 from Arabidopsis thaliana
gi|2341034 from Arabidopsis thaliana
gi|15215692 from Arabidopsis thaliana
gi|17473717 from Arabidopsis thaliana
gi|20148469 from Arabidopsis thaliana
gi|21593602 from Arabidopsis thaliana
gi|22137280 from Arabidopsis thaliana

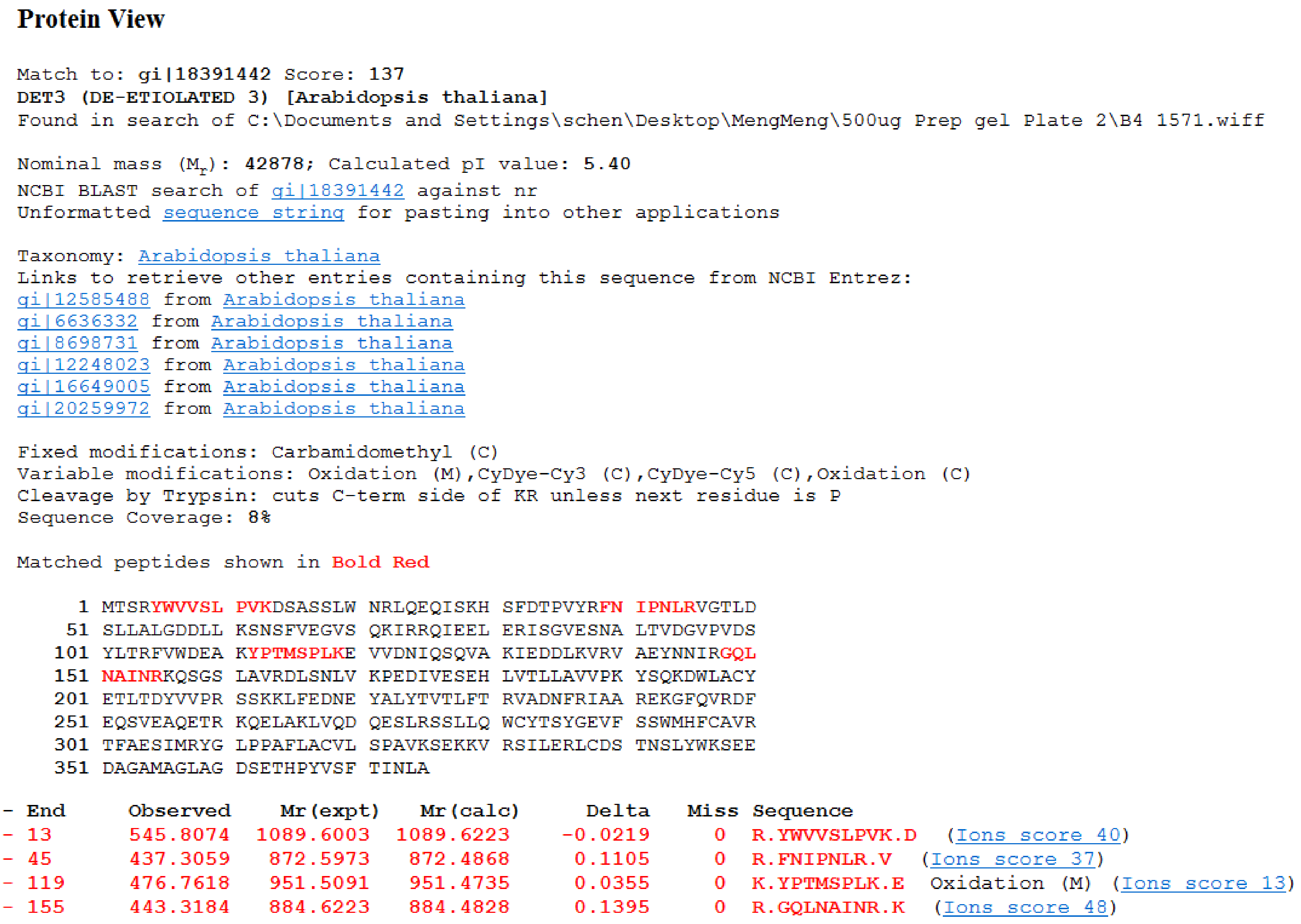
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%

Matched peptides shown in Bold Red

      1 MAKEPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH MLDIPPAAEA
     51 LNGVKMELID AAFPLLKGVV ATTDAVEGCT GVNVAVMVGG FPRKEGMERK
    101 DVMSKNVSIY KSQAAALEKH AAPNCKVLVV ANPANTNALI LKEFAPSIPE
    151 KNISCLTRLD HNRALGQISE RLSVPVSDVK NVIIWGNHSS SQYPDVNHAK
    201 VQTSSGEKPV RELVKDDAWL DGEFISTVQQ RGAAIIKARK LSSALSAASS
    251 ACDHIRDWVL GTPEGTFVSM GVYSDGSYSV PSGLIYSFPV TCRNGDWSIV
    301 QGLPIDEVSR KKMDLTAEEL KEEKDLAYSC LS
```

```
Start - End      Observed    Mr(expt)   Mr(calc)      Delta    Miss  Sequence
   56 - 67       688.9003   1375.7860  1375.7421     0.0439     0   K.MELIDAAFPLLK.G  Oxidation (M)  (Ions score 73)
  127 - 142      825.5131   1649.0117  1648.9876     0.0241     0   K.VLVVANPANTNALILK.E  (Ions score 14)
  127 - 142      550.7232   1649.1476  1648.9876     0.1601     0   K.VLVVANPANTNALILK.E  (Ions score 40)
  143 - 151      509.3646   1016.7147  1016.5178     0.1969     0   K.EFAPSIPEK.N  (Ions score 27)
  164 - 171      437.2560    872.4974   872.4716     0.0258     0   R.ALGQISER.L  (Ions score 63)
  172 - 180      472.3175    942.6205   942.5386     0.0819     0   R.LSVPVSDVK.N  (Ions score 44)
```

gi|18391442 De-etiolated 3 (DET3)



Protein View

Match to: **gi|18391442** Score: **137**
DET3 (DE-ETIOLATED 3) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B4 1571.wiff

Nominal mass (M_r): **42878**; Calculated pI value: **5.40**
NCBI BLAST search of gi|18391442 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12585488 from Arabidopsis thaliana
gi|6636332 from Arabidopsis thaliana
gi|8698731 from Arabidopsis thaliana
gi|12248023 from Arabidopsis thaliana
gi|16649005 from Arabidopsis thaliana
gi|20259972 from Arabidopsis thaliana

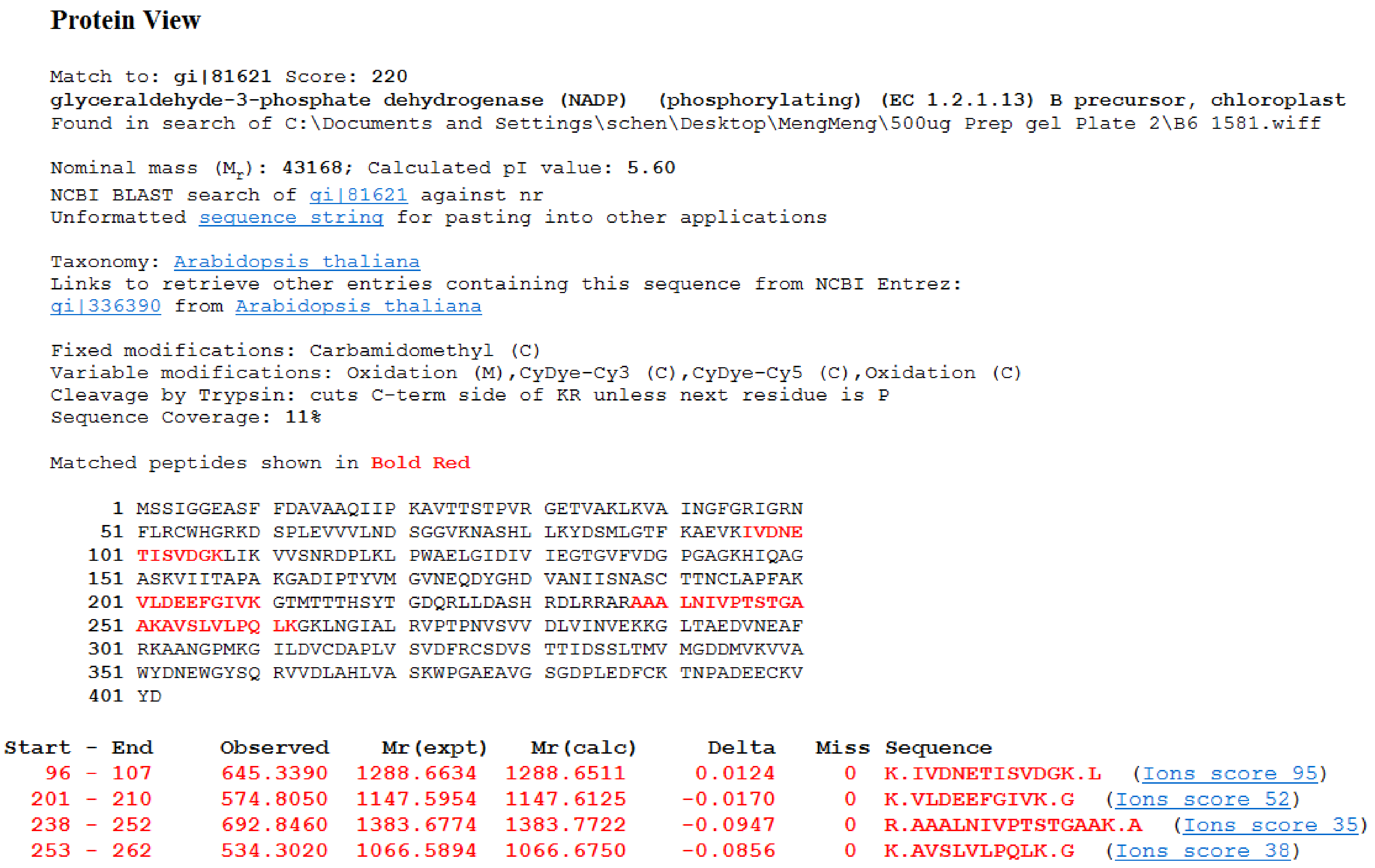
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

```
  1 MTSRYWVVSL PVKDSASSLW NRLQEQISKH SFDTPVYRFN IPNLRVGTLD
 51 SLLALGDDLL KSNSFVEGVS QKIRRQIEEL ERISGVESNA LTVDGVPVDS
101 YLTRFVWDEA KYPTMSPLKE VVDNIQSQVA KIEDDLKVRV AEYNNIRGQL
151 NAINRKQSGS LAVRDLSNLV KPEDIVESEH LVTLLAVVPK YSQKDWLACY
201 ETLTDYVVPR SSKKLFEDNE YALYTVTLFT RVADNFRIAA REKGFQVRDF
251 EQSVEAQETR KQELAKLVQD QESLRSSLLQ WCYTSYGEVF SSWMHFCAVR
301 TFAESIMRYG LPPAFLACVL SPAVKSEKKV RSILERLCDS TNSLYWKSEE
351 DAGAMAGLAG DSETHPYVSF TINLA
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
    5 - 13      545.8074  1089.6003  1089.6223   -0.0219     0   R.YWVVSLPVK.D  (Ions score 40)
   39 - 45      437.3059   872.5973   872.4868    0.1105     0   R.FNIPNLR.V  (Ions score 37)
  112 - 119     476.7618   951.5091   951.4735    0.0355     0   K.YPTMSPLK.E  Oxidation (M)  (Ions score 13)
  148 - 155     443.3184   884.6223   884.4828    0.1395     0   R.GQLNAINR.K  (Ions score 48)
```

gi|81621 Glyceraldehyde-3-phosphate dehydrogenase (NADP) B precursor



Protein View

Match to: **gi|81621** Score: **220**
glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B6 1581.wiff

Nominal mass (M_r): **43168**; Calculated pI value: **5.60**
NCBI BLAST search of gi|81621 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|336390 from Arabidopsis thaliana

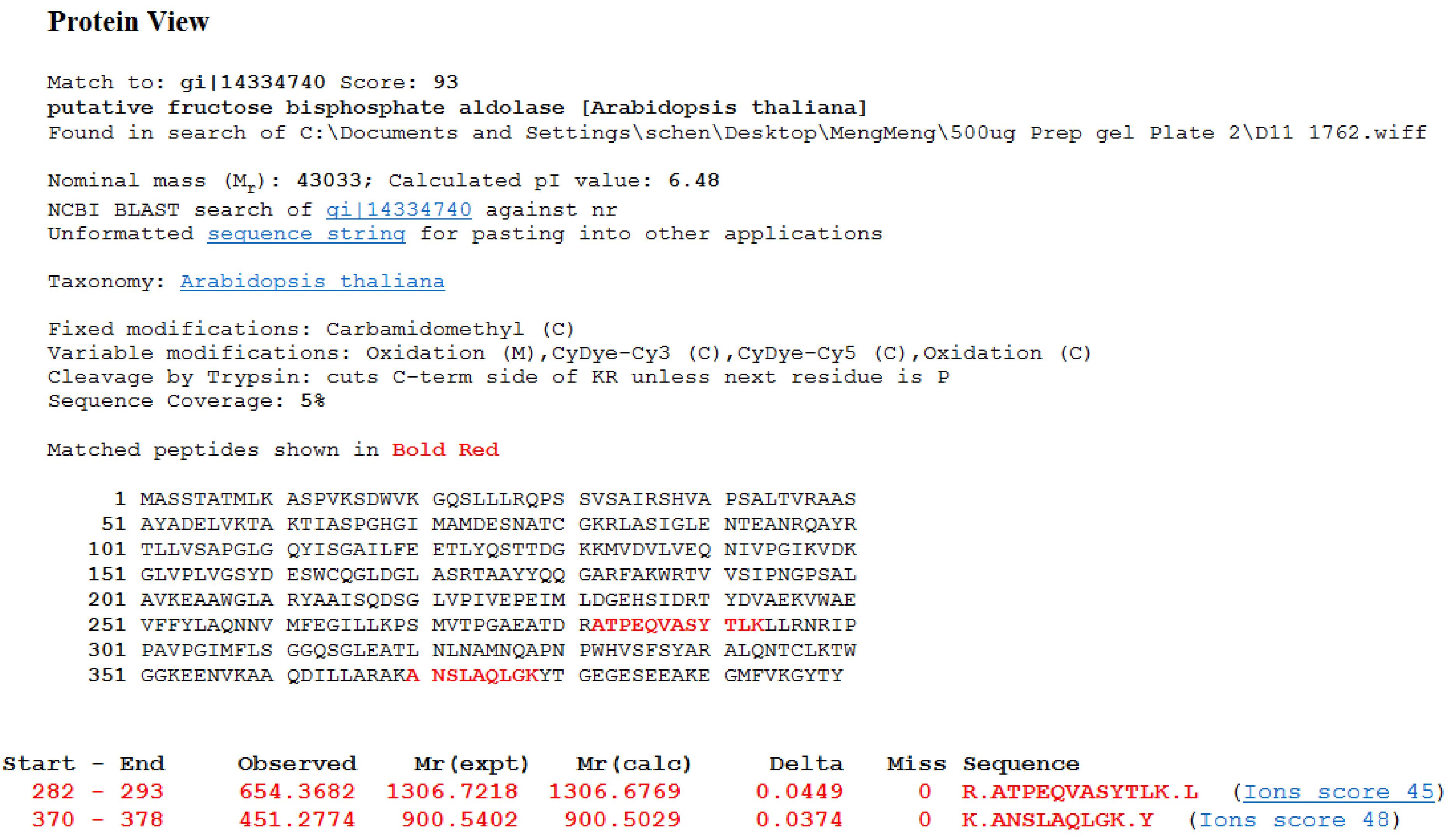
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
  1 MSSIGGEASF FDAVAAQIIP KAVTTSTPVR GETVAKLKVA INGFGRIGRN
 51 FLRCWHGRKD SPLEVVVLND SGGVKNASHL LKYDSMLGTF KAEVKIVDNE
101 TISVDGKLIK VVSNRDPLKL PWAELGIDIV IEGTGVFVDG PGAGKHIQAG
151 ASKVIITAPA KGADIPTYVM GVNEQDYGHD VANIISNASC TTNCLAPFAK
201 VLDEEFGIVK GTMTTTHSYT GDQRLLDASH RDLRRARAAA LNIVPTSTGA
251 AKAVSLVLPQ LKGKLNGIAL RVPTPNVSVV DLVINVEKKG LTAEDVNEAF
301 RKAANGPMKG ILDVCDAPLV SVDFRCSDVS TTIDSSLTMV MGDDMVKVVA
351 WYDNEWGYSQ RVVDLAHLVA SKWPGAEAVG SGDPLEDFCK TNPADEECKV
401 YD
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   96 - 107    645.3390  1288.6634  1288.6511    0.0124     0  K.IVDNETISVDGK.L   (Ions score 95)
  201 - 210    574.8050  1147.5954  1147.6125   -0.0170     0  K.VLDEEFGIVK.G   (Ions score 52)
  238 - 252    692.8460  1383.6774  1383.7722   -0.0947     0  R.AAALNIVPTSTGAAK.A   (Ions score 35)
  253 - 262    534.3020  1066.5894  1066.6750   -0.0856     0  K.AVSLVLPQLK.G   (Ions score 38)
```

gi|14334740 Putative fructose bisphosphate aldolase



Protein View

```
Match to: gi|14334740 Score: 93
putative fructose bisphosphate aldolase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (Mr): 43033; Calculated pI value: 6.48
NCBI BLAST search of gi|14334740 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

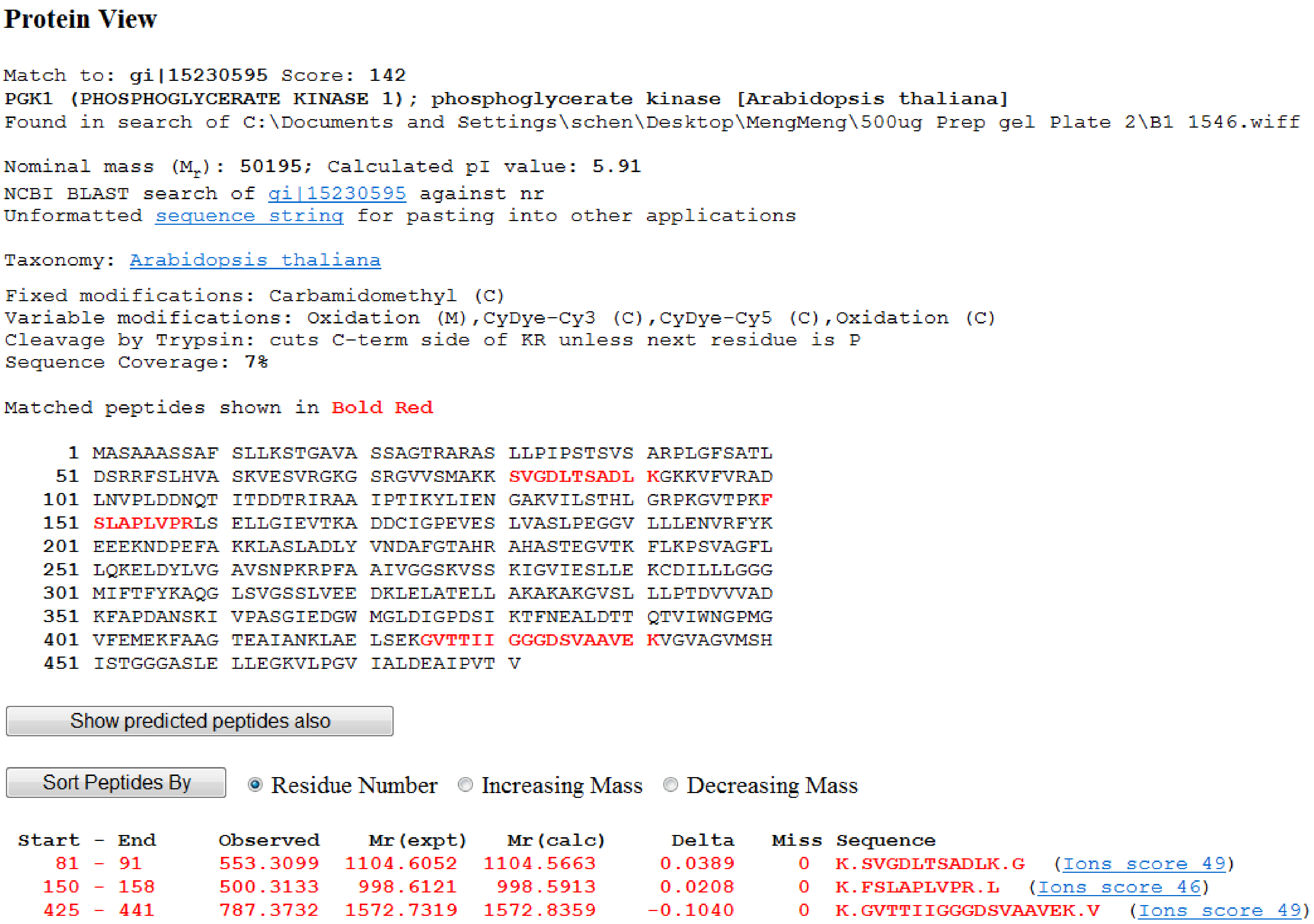
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

      1 MASSTATMLK ASPVKSDWVK GQSLLLRQPS SVSAIRSHVA PSALTVRAAS
     51 AYADELVKTA KTIASPGHGI MAMDESNATC GKRLASIGLE NTEANRQAYR
    101 TLLVSAPGLG QYISGAILFE ETLYQSTTDG KKMVDVLVEQ NIVPGIKVDK
    151 GLVPLVGSYD ESWCQGLDGL ASRTAAYYQQ GARFAKWRTV VSIPNGPSAL
    201 AVKEAAWGLA RYAAISQDSG LVPIVEPEIM LDGEHSIDRT YDVAEKVWAE
    251 VFFYLAQNNV MFEGILLKPS MVTPGAEATD RATPEQVASY TLKLLRNRIP
    301 PAVPGIMFLS GGQSGLEATL NLNAMNQAPN PWHVSFSYAR ALQNTCLKTW
    351 GGKEENVKAA QDILLARAKA NSLAQLGKYT GEGESEEAKE GMFVKGYTY
```

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  282 - 293     654.3682   1306.7218  1306.6769    0.0449     0  R.ATPEQVASYTLK.L   (Ions score 45)
  370 - 378     451.2774    900.5402   900.5029    0.0374     0  K.ANSLAQLGK.Y   (Ions score 48)
```

gi|15230595 Phosphoglycerate kinase 1 (PGK1)



Protein View

```
Match to: gi|15230595 Score: 142
PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff
```

Nominal mass (M_r): 50195; Calculated pI value: 5.91

NCBI BLAST search of gi|15230595 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

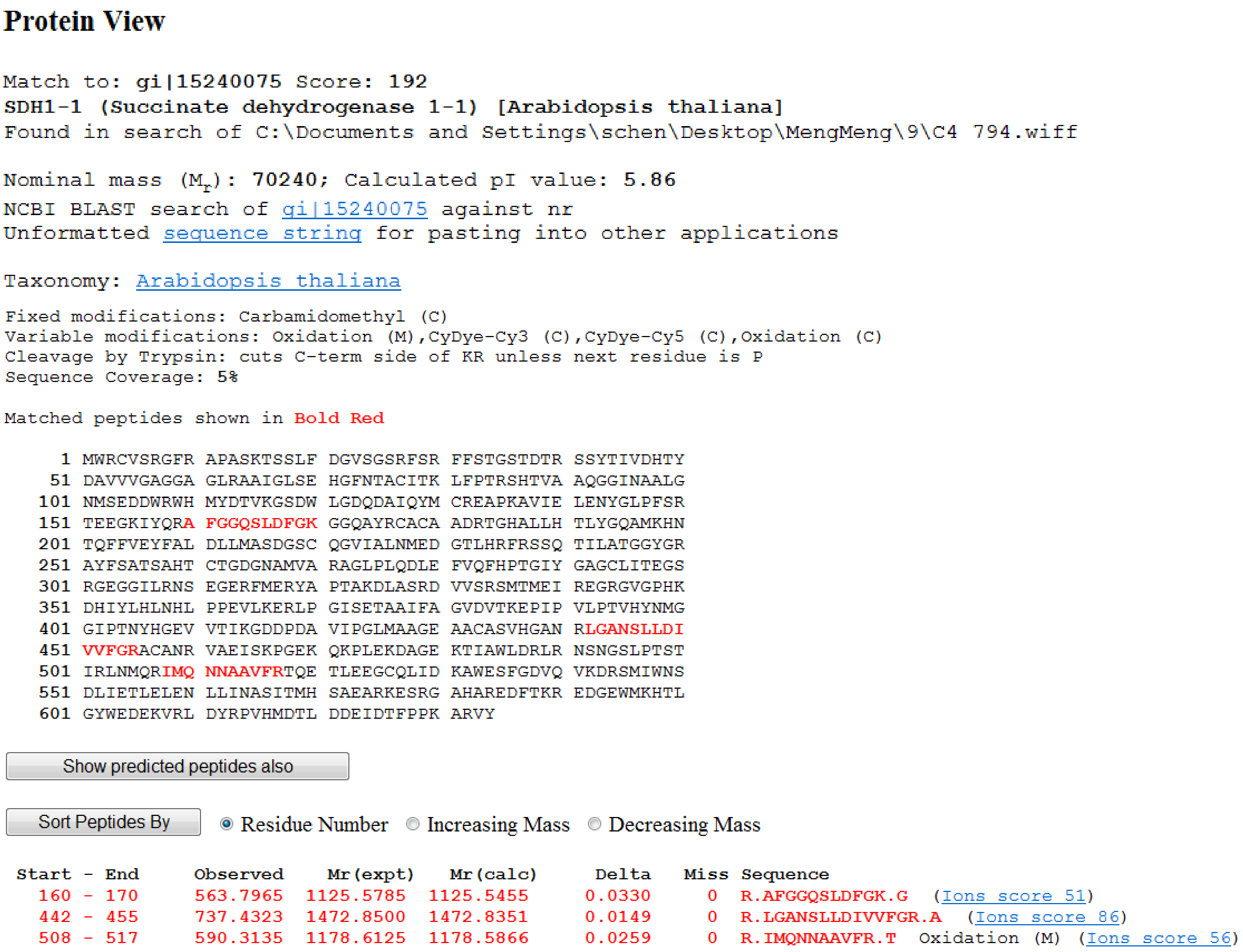
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

```
      1 MASAAASSAF SLLKSTGAVA SSAGTRARAS LLPIPSTSVS ARPLGFSATL
     51 DSRRFSLHVA SKVESVRGKG SRGVVSMAKK SVGDLTSADL KGKKVFVRAD
    101 LNVPLDDNQT ITDDTRIRAA IPTIKYLIEN GAKVILSTHL GRPKGVTPKF
    151 SLAPLVPRLS ELLGIEVTKA DDCIGPEVES LVASLPEGGV LLLENVRFYK
    201 EEEKNDPEFA KKLASLADLY VNDAFGTAHR AHASTEGVTK FLKPSVAGFL
    251 LQKELDYLVG AVSNPKRPFA AIVGGSKVSS KIGVIESLLE KCDILLLGGG
    301 MIFTFYKAQG LSVGSSLVEE DKLELATELL AKAKAKGVSL LLPTDVVVAD
    351 KFAPDANSKI VPASGIEDGW MGLDIGPDSI KTFNEALDTT QTVIWNGPMG
    401 VFEMEKFAAG TEAIANKLAE LSEKGVTTII GGGDSVAAVE KVGVAGVMSH
    451 ISTGGGASLE LLEGKVLPGV IALDEAIPVT V
```

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   81 - 91      553.3099   1104.6052  1104.5663    0.0389     0   K.SVGDLTSADLK.G   (Ions score 49)
  150 - 158     500.3133    998.6121   998.5913    0.0208     0   K.FSLAPLVPR.L   (Ions score 46)
  425 - 441     787.3732   1572.7319  1572.8359   -0.1040     0   K.GVTTIIGGGDSVAAVEK.V   (Ions score 49)
```

gi|15240075 Succinate dehydrogenase 1-1 (SDH1-1)



Protein View

```
Match to: gi|15240075 Score: 192
SDH1-1 (Succinate dehydrogenase 1-1) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\C4 794.wiff

Nominal mass (Mr): 70240; Calculated pI value: 5.86
NCBI BLAST search of gi|15240075 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

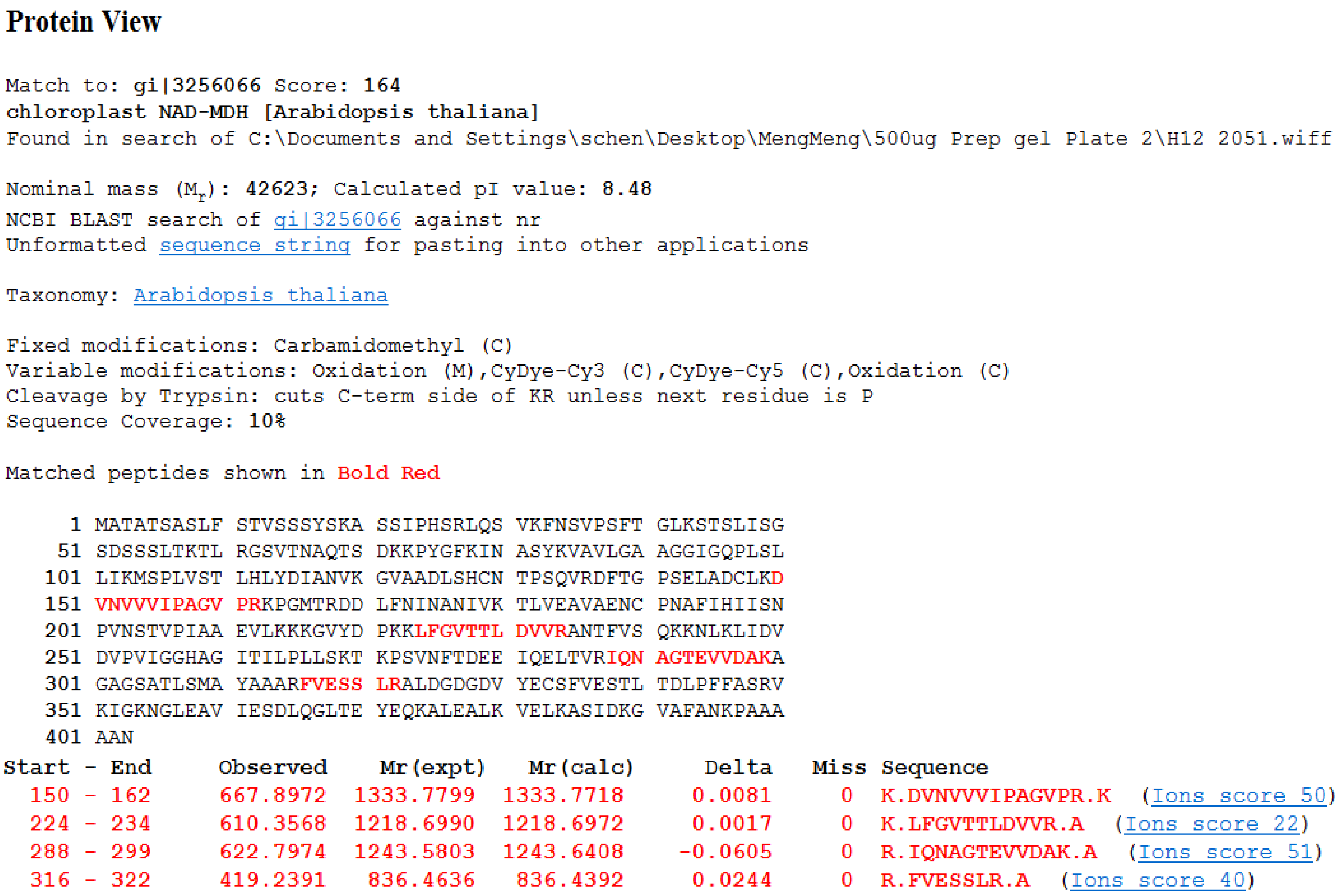
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

  1 MWRCVSRGFR APASKTSSLF DGVSGSRFSR FFSTGSTDTR SSYTIVDHTY
 51 DAVVVGAGGA GLRAAIGLSE HGFNTACITK LFPTRSHTVA AQGGINAALG
101 NMSEDDWRWH MYDTVKGSDW LGDQDAIQYM CREAPKAVIE LENYGLPFSR
151 TEEGKIYQRA FGGQSLDFGK GGQAYRCACA ADRTGHALLH TLYGQAMKHN
201 TQFFVEYFAL DLLMASDGSC QGVIALNMED GTLHRFRSSQ TILATGGYGR
251 AYFSATSAHT CTGDGNAMVA RAGLPLQDLE FVQFHPTGIY GAGCLITEGS
301 RGEGGILRNS EGERFMERYA PTAKDLASRD VVSRSMTMEI REGRGVGPHK
351 DHIYLHLNHL PPEVLKERLP GISETAAIFA GVDVTKEPIP VLPTVHYNMG
401 GIPTNYHGEV VTIKGDDPDA VIPGLMAAGE AACASVHGAN RLGANSLLDI
451 VVFGRACANR VAEISKPGEK QKPLEKDAGE KTIAWLDRLR NSNGSLPTST
501 IRLNMQRIMQ NNAAVFRTQE TLEEGCQLID KAWESFGDVQ VKDRSMIWNS
551 DLIETLELEN LLINASITMH SAEARKESRG AHAREDFTKR EDGEWMKHTL
601 GYWEDEKVRL DYRPVHMDTL DDEIDTFPPK ARVY
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   160 - 170     563.7965  1125.5785  1125.5455   0.0330     0 R.AFGGQSLDFGK.G  (Ions score 51)
   442 - 455     737.4323  1472.8500  1472.8351   0.0149     0 R.LGANSLLDIVVFGR.A  (Ions score 86)
   508 - 517     590.3135  1178.6125  1178.5866   0.0259     0 R.IMQNNAAVFR.T  Oxidation (M)  (Ions score 56)
```

gi|3256066 Chloroplast NAD-dependent malate dehydrogenase



Protein View

Match to: **gi|3256066** Score: **164**
chloroplast NAD-MDH [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r): **42623**; Calculated pI value: **8.48**
NCBI BLAST search of gi|3256066 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

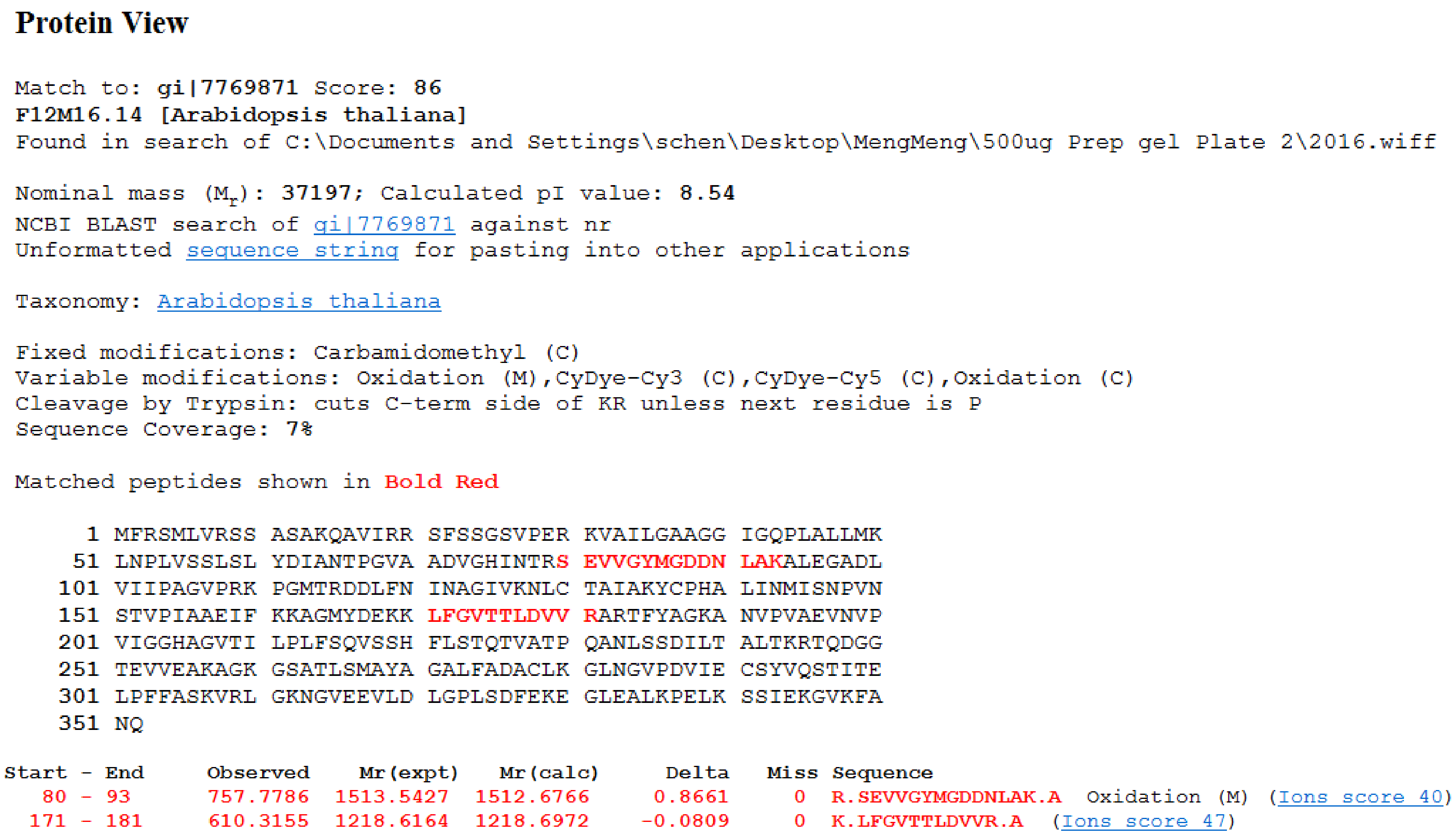
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
  1 MATATSASLF STVSSSYSKA SSIPHSRLQS VKFNSVPSFT GLKSTSLISG
 51 SDSSSLTKTL RGSVTNAQTS DKKPYGFKIN ASYKVAVLGA AGGIGQPLSL
101 LIKMSPLVST LHLYDIANVK GVAADLSHCN TPSQVRDFTG PSELADCLKD
151 VNVVVIPAGV PRKPGMTRDD LFNINANIVK TLVEAVAENC PNAFIHIISN
201 PVNSTVPIAA EVLKKKGVYD PKKLFGVTTL DVVRANTFVS QKKNLKLIDV
251 DVPVIGGHAG ITILPLLSKT KPSVNFTDEE IQELTVRIQN AGTEVVDAKA
301 GAGSATLSMA YAAARFVESS LRALDGDGDV YECSFVESTL TDLPFFASRV
351 KIGKNGLEAV IESDLQGLTE YEQKALEALK VELKASIDKG VAFANKPAAA
401 AAN
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  150 - 162     667.8972  1333.7799  1333.7718    0.0081     0  K.DVNVVVIPAGVPR.K   (Ions score 50)
  224 - 234     610.3568  1218.6990  1218.6972    0.0017     0  K.LFGVTTLDVVR.A  (Ions score 22)
  288 - 299     622.7974  1243.5803  1243.6408   -0.0605     0  R.IQNAGTEVVDAK.A   (Ions score 51)
  316 - 322     419.2391   836.4636   836.4392    0.0244     0  R.FVESSLR.A  (Ions score 40)
```

gi|7769871 F12M16.14



Protein View

Match to: **gi|7769871** Score: **86**
F12M16.14 [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\2016.wiff

Nominal mass (M_r): **37197**; Calculated pI value: **8.54**
NCBI BLAST search of gi|7769871 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

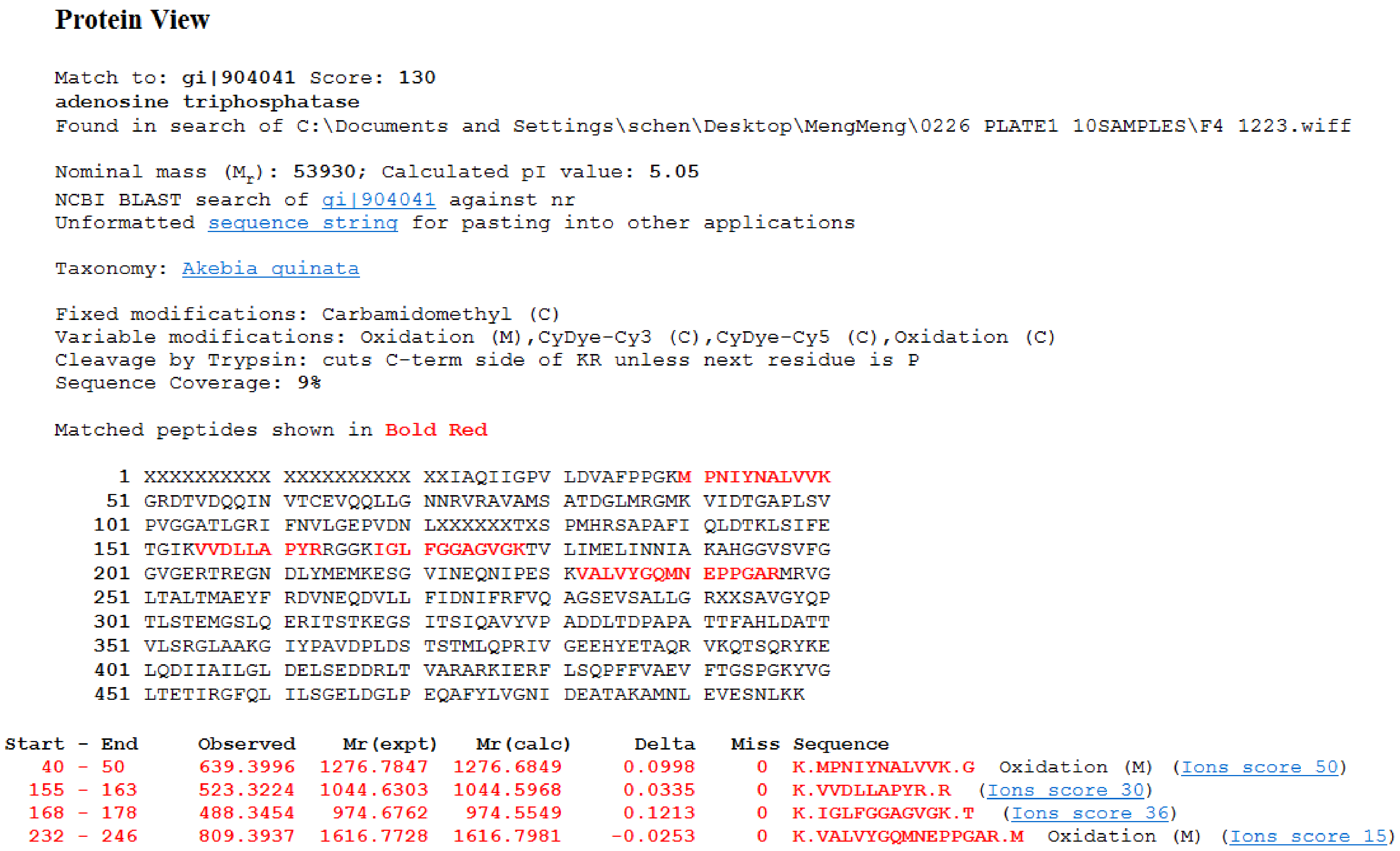
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

```
  1 MFRSMLVRSS ASAKQAVIRR SFSSGSVPER KVAILGAAGG IGQPLALLMK
 51 LNPLVSSLSL YDIANTPGVA ADVGHINTRS EVVGYMGDDN LAKALEGADL
101 VIIPAGVPRK PGMTRDDLFN INAGIVKNLC TAIAKYCPHA LINMISNPVN
151 STVPIAAEIF KKAGMYDEKK LFGVTTLDVV RARTFYAGKA NVPVAEVNVP
201 VIGGHAGVTI LPLFSQVSSH FLSTQTVATP QANLSSDILT ALTKRTQDGG
251 TEVVEAKAGK GSATLSMAYA GALFADACLK GLNGVPDVIE CSYVQSTITE
301 LPFFASKVRL GKNGVEEVLD LGPLSDFEKE GLEALKPELK SSIEKGVKFA
351 NQ
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   80 - 93      757.7786   1513.5427   1512.6766     0.8661      0  R.SEVVGYMGDDNLAK.A  Oxidation (M)  (Ions score 40)
  171 - 181     610.3155   1218.6164   1218.6972    -0.0809      0  K.LFGVTTLDVVR.A  (Ions score 47)
```

gi|904041 Adenosine triphosphatase



Protein View

Match to: **gi|904041** Score: **130**
adenosine triphosphatase
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\F4 1223.wiff

Nominal mass (M_r): **53930**; Calculated pI value: **5.05**
NCBI BLAST search of gi|904041 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Akebia quinata

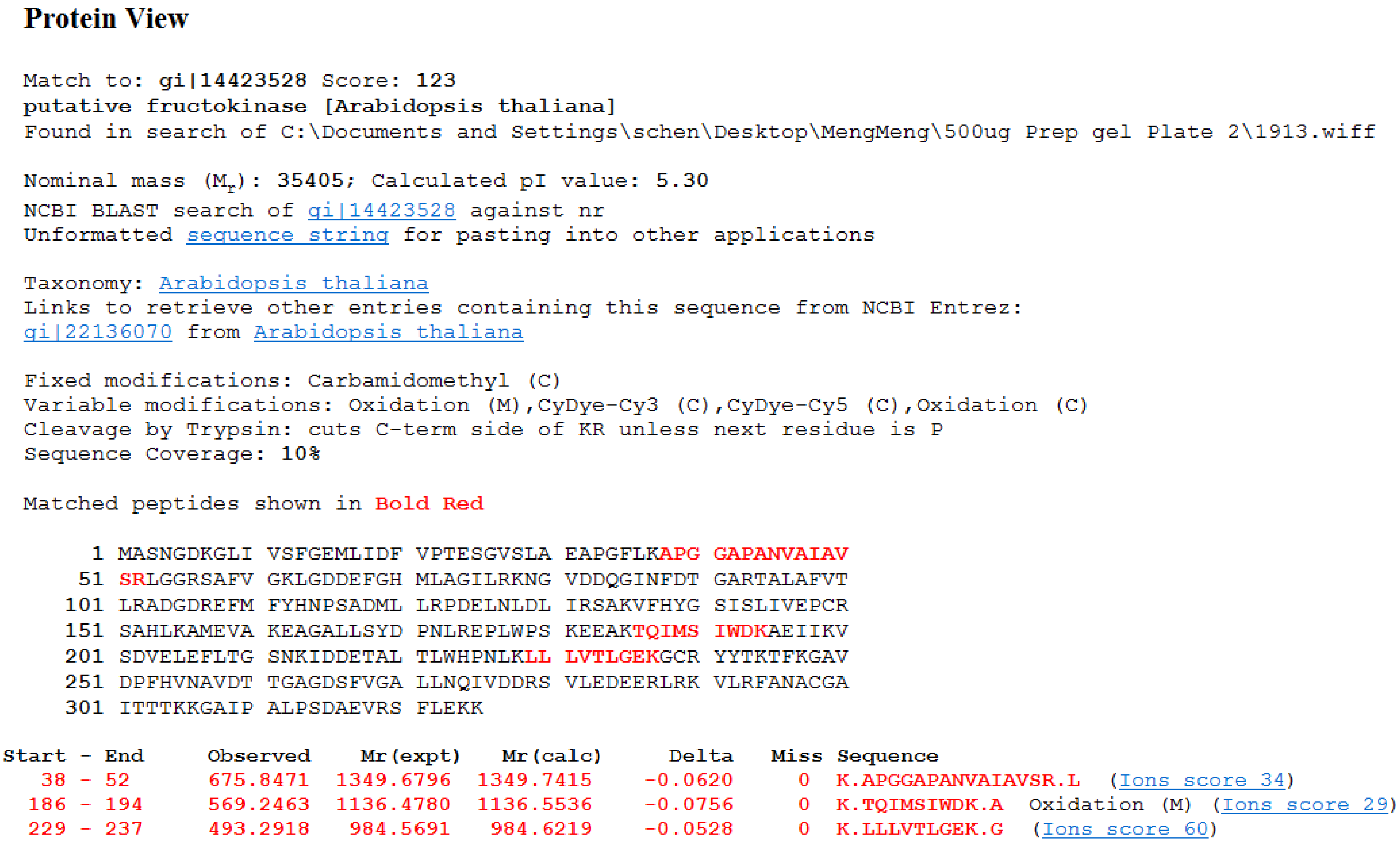
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

```
  1 XXXXXXXXXX XXXXXXXXXX XXIAQIIGPV LDVAFPPGKM PNIYNALVVK
 51 GRDTVDQQIN VTCEVQQLLG NNRVRAVAMS ATDGLMRGMK VIDTGAPLSV
101 PVGGATLGRI FNVLGEPVDN LXXXXXXTXS PMHRSAPAFI QLDTKLSIFE
151 TGIKVVDLLA PYRRGGKIGL FGGAGVGKTV LIMELINNIA KAHGGVSVFG
201 GVGERTREGN DLYMEMKESG VINEQNIPES KVALVYGQMN EPPGARMRVG
251 LTALTMAEYF RDVNEQDVLL FIDNIFRFVQ AGSEVSALLG RXXSAVGYQP
301 TLSTEMGSLQ ERITSTKEGS ITSIQAVYVP ADDLTDPAPA TTFAHLDATT
351 VLSRGLAAKG IYPAVDPLDS TSTMLQPRIV GEEHYETAQR VKQTSQRYKE
401 LQDIIAILGL DELSEDDRLT VARARKIERF LSQPFFVAEV FTGSPGKYVG
451 LTETIRGFQL ILSGELDGLP EQAFYLVGNI DEATAKAMNL EVESNLKK
```

```
Start - End     Observed    Mr(expt)   Mr(calc)      Delta    Miss  Sequence
  40 - 50       639.3996   1276.7847  1276.6849     0.0998      0   K.MPNIYNALVVK.G  Oxidation (M)  (Ions score 50)
 155 - 163      523.3224   1044.6303  1044.5968     0.0335      0   K.VVDLLAPYR.R  (Ions score 30)
 168 - 178      488.3454    974.6762   974.5549     0.1213      0   K.IGLFGGAGVGK.T  (Ions score 36)
 232 - 246      809.3937   1616.7728  1616.7981    -0.0253      0   K.VALVYGQMNEPPGAR.M  Oxidation (M)  (Ions score 15)
```

gi|14423528 Putative fructokinase



Protein View

Match to: **gi|14423528** Score: **123**
putative fructokinase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1913.wiff

Nominal mass (M_r): **35405**; Calculated pI value: **5.30**
NCBI BLAST search of gi|14423528 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|22136070 from Arabidopsis thaliana

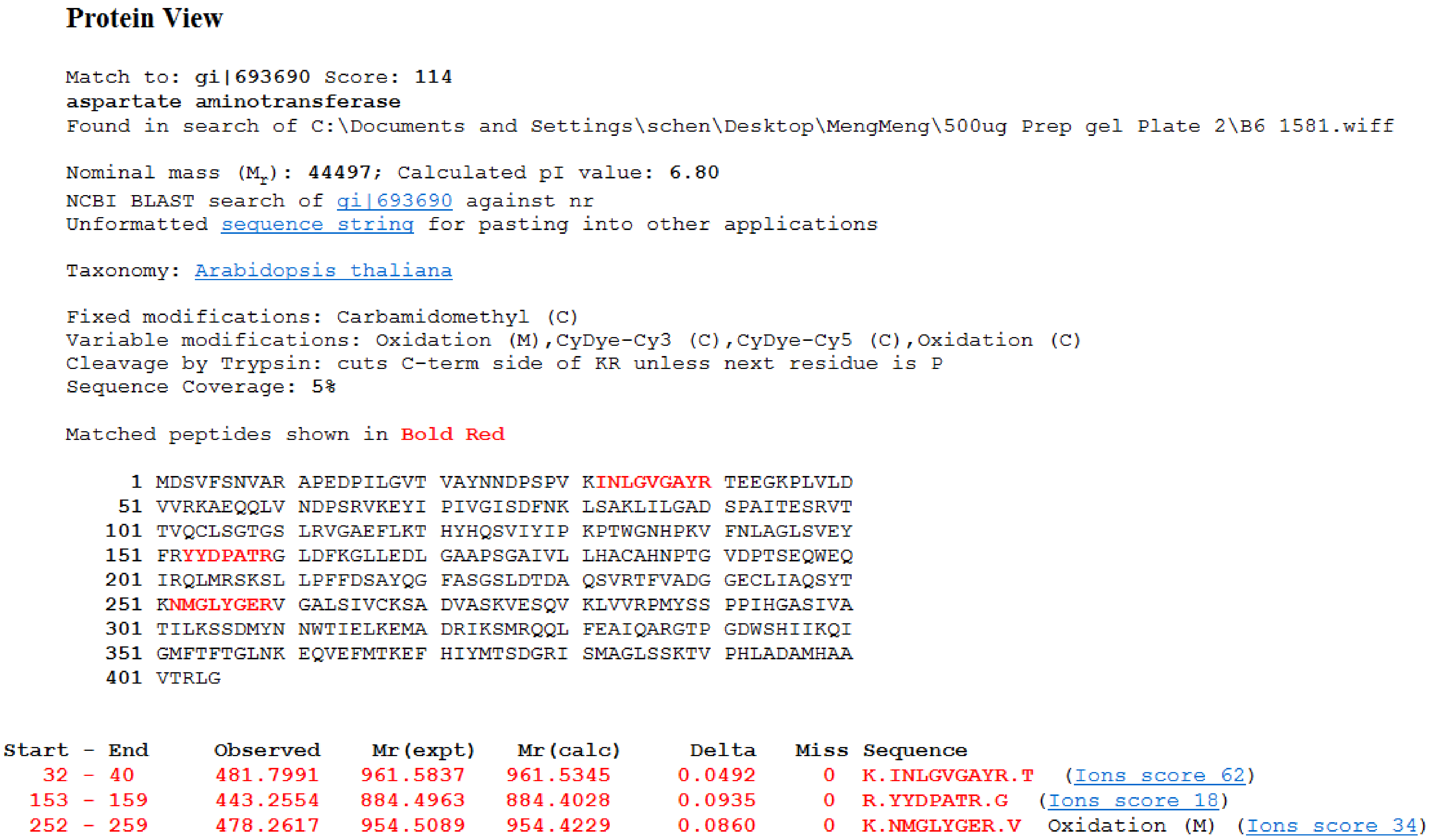
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
  1 MASNGDKGLI VSFGEMLIDF VPTESGVSLA EAPGFLKAPG GAPANVAIAV
 51 SRLGGRSAFV GKLGDDEFGH MLAGILRKNG VDDQGINFDT GARTALAFVT
101 LRADGDREFM FYHNPSADML LRPDELNLDL IRSAKVFHYG SISLIVEPCR
151 SAHLKAMEVA KEAGALLSYD PNLREPLWPS KEEAKTQIMS IWDKAEIIKV
201 SDVELEFLTG SNKIDDETAL TLWHPNLKLL LVTLGEKGCR YYTKTFKGAV
251 DPFHVNAVDT TGAGDSFVGA LLNQIVDDRS VLEDEERLRK VLRFANACGA
301 ITTTKKGAIP ALPSDAEVRS FLEKK
```

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
  38 - 52      675.8471  1349.6796  1349.7415  -0.0620    0   K.APGGAPANVAIAVSR.L  (Ions score 34)
 186 - 194     569.2463  1136.4780  1136.5536  -0.0756    0   K.TQIMSIWDK.A  Oxidation (M)  (Ions score 29)
 229 - 237     493.2918   984.5691   984.6219  -0.0528    0   K.LLLVTLGEK.G  (Ions score 60)
```

gi|693690 Aspartate aminotransferase



Protein View

Match to: **gi|693690** Score: **114**
aspartate aminotransferase
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B6 1581.wiff

Nominal mass (M_r): **44497**; Calculated pI value: **6.80**
NCBI BLAST search of gi|693690 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

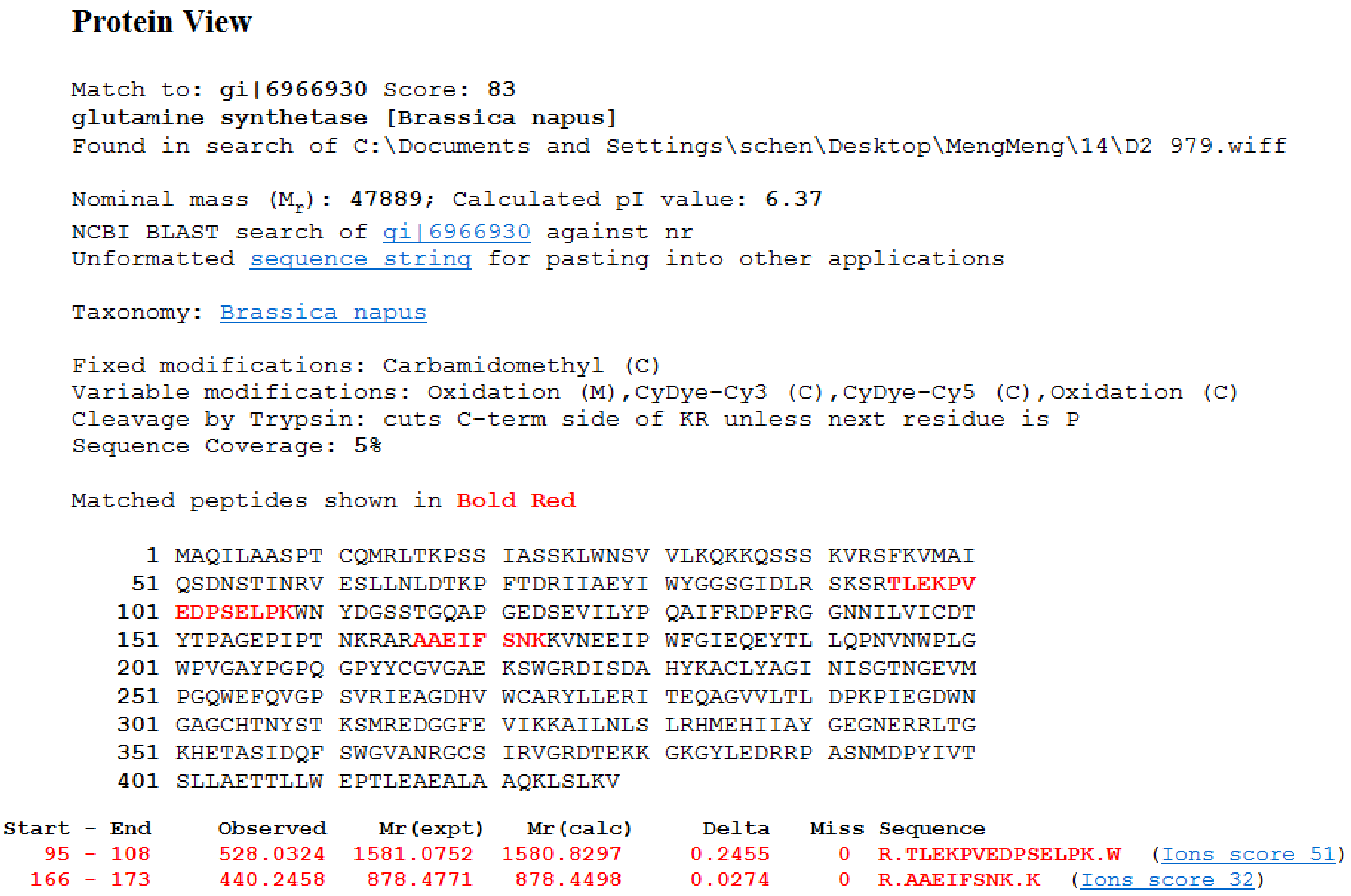
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in **Bold Red**

```
  1 MDSVFSNVAR APEDPILGVT VAYNNDPSPV KINLGVGAYR TEEGKPLVLD
 51 VVRKAEQQLV NDPSRVKEYI PIVGISDFNK LSAKLILGAD SPAITESRVT
101 TVQCLSGTGS LRVGAEFLKT HYHQSVIYIP KPTWGNHPKV FNLAGLSVEY
151 FRYYDPATRG LDFKGLLEDL GAAPSGAIVL LHACAHNPTG VDPTSEQWEQ
201 IRQLMRSKSL LPFFDSAYQG FASGSLDTDA QSVRTFVADG GECLIAQSYT
251 KNMGLYGERV GALSIVCKSA DVASKVESQV KLVVRPMYSS PPIHGASIVA
301 TILKSSDMYN NWTIELKEMA DRIKSMRQQL FEAIQARGTP GDWSHIIKQI
351 GMFTFTGLNK EQVEFMTKEF HIYMTSDGRI SMAGLSSKTV PHLADAMHAA
401 VTRLG
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
32 - 40	481.7991	961.5837	961.5345	0.0492	0	K.INLGVGAYR.T (Ions score 62)
153 - 159	443.2554	884.4963	884.4028	0.0935	0	R.YYDPATR.G (Ions score 18)
252 - 259	478.2617	954.5089	954.4229	0.0860	0	K.NMGLYGER.V Oxidation (M) (Ions score 34)

gi|6966930 Glutamine synthetase



Protein View

Match to: **gi|6966930** Score: **83**
glutamine synthetase [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\14\D2 979.wiff

Nominal mass (M_r): **47889**; Calculated pI value: **6.37**
NCBI BLAST search of gi|6966930 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

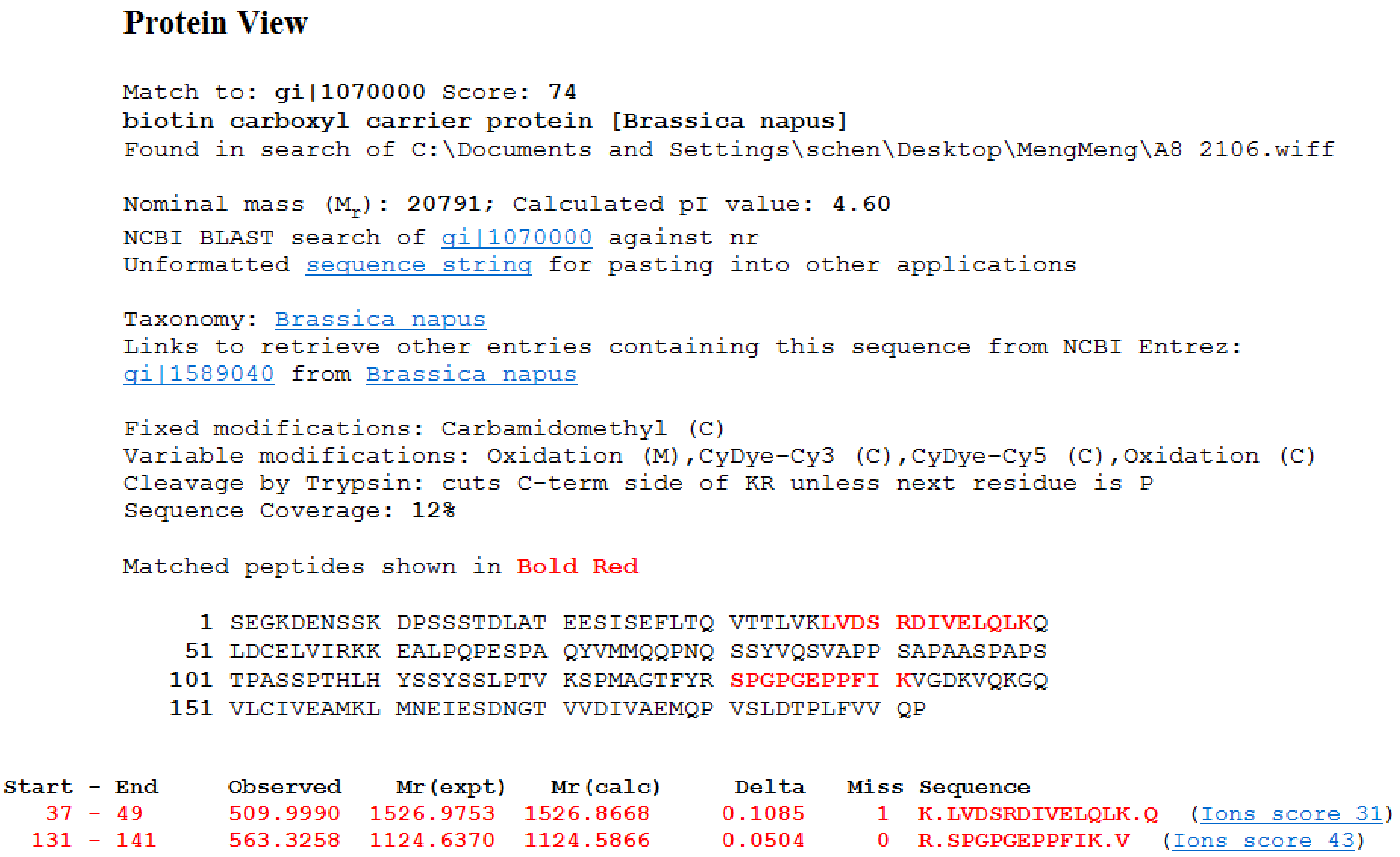
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```
  1 MAQILAASPT CQMRLTKPSS IASSKLWNSV VLKQKKQSSS KVRSFKVMAI
 51 QSDNSTINRV ESLLNLDTKP FTDRIIAEYI WYGGSGIDLR SKSRTLEKPV
101 EDPSELPKWN YDGSSTGQAP GEDSEVILYP QAIFRDPFRG GNNILVICDT
151 YTPAGEPIPT NKRARAAEIF SNKKVNEEIP WFGIEQEYTL LQPNVNWPLG
201 WPVGAYPGPQ GPYYCGVGAE KSWGRDISDA HYKACLYAGI NISGTNGEVM
251 PGQWEFQVGP SVRIEAGDHV WCARYLLERI TEQAGVVLTL DPKPIEGDWN
301 GAGCHTNYST KSMREDGGFE VIKKAILNLS LRHMEHIIAY GEGNERRLTG
351 KHETASIDQF SWGVANRGCS IRVGRDTEKK GKGYLEDRRP ASNMDPYIVT
401 SLLAETTLLW EPTLEAEALA AQKLSLKV
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta    Miss  Sequence
   95 - 108    528.0324   1581.0752   1580.8297     0.2455     0    R.TLEKPVEDPSELPK.W   (Ions score 51)
  166 - 173    440.2458    878.4771    878.4498     0.0274     0    R.AAEIFSNK.K   (Ions score 32)
```

gi|1070000 Biotin carboxyl carrier protein



Protein View

Match to: **gi|1070000** Score: **74**
biotin carboxyl carrier protein [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\A8 2106.wiff

Nominal mass (M_r): **20791**; Calculated pI value: **4.60**
NCBI BLAST search of gi|1070000 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1589040 from Brassica napus

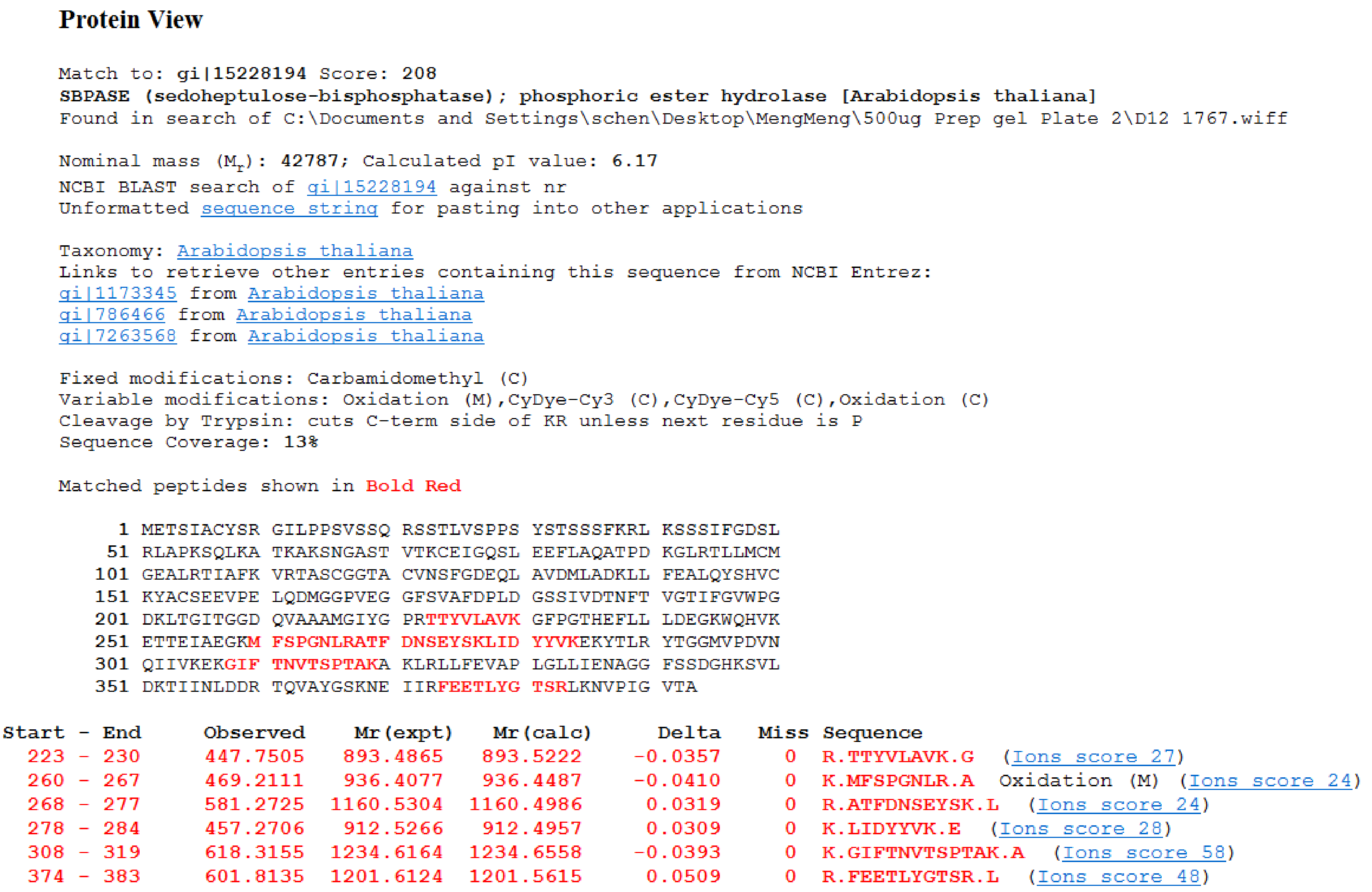
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
  1 SEGKDENSSK DPSSSTDLAT EESISEFLTQ VTTLVKLVDS RDIVELQLKQ
 51 LDCELVIRKK EALPQPESPA QYVMMQQPNQ SSYVQSVAPP SAPAASPAPS
101 TPASSPTHLH YSSYSSLPTV KSPMAGTFYR SPGPGEPPFI KVGDKVQKGQ
151 VLCIVEAMKL MNEIESDNGT VVDIVAEMQP VSLDTPLFVV QP
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  37 - 49      509.9990  1526.9753  1526.8668    0.1085     1  K.LVDSRDIVELQLK.Q  (Ions score 31)
 131 - 141     563.3258  1124.6370  1124.5866    0.0504     0  R.SPGPGEPPFIK.V  (Ions score 43)
```

gi|15228194 Sedoheptulose bisphosphatase (SBPASE)



Protein View

Match to: **gi|15228194** Score: **208**
SBPASE (sedoheptulose-bisphosphatase); phosphoric ester hydrolase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D12 1767.wiff

Nominal mass (M_r): **42787**; Calculated pI value: **6.17**
NCBI BLAST search of gi|15228194 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1173345 from Arabidopsis thaliana
gi|786466 from Arabidopsis thaliana
gi|7263568 from Arabidopsis thaliana

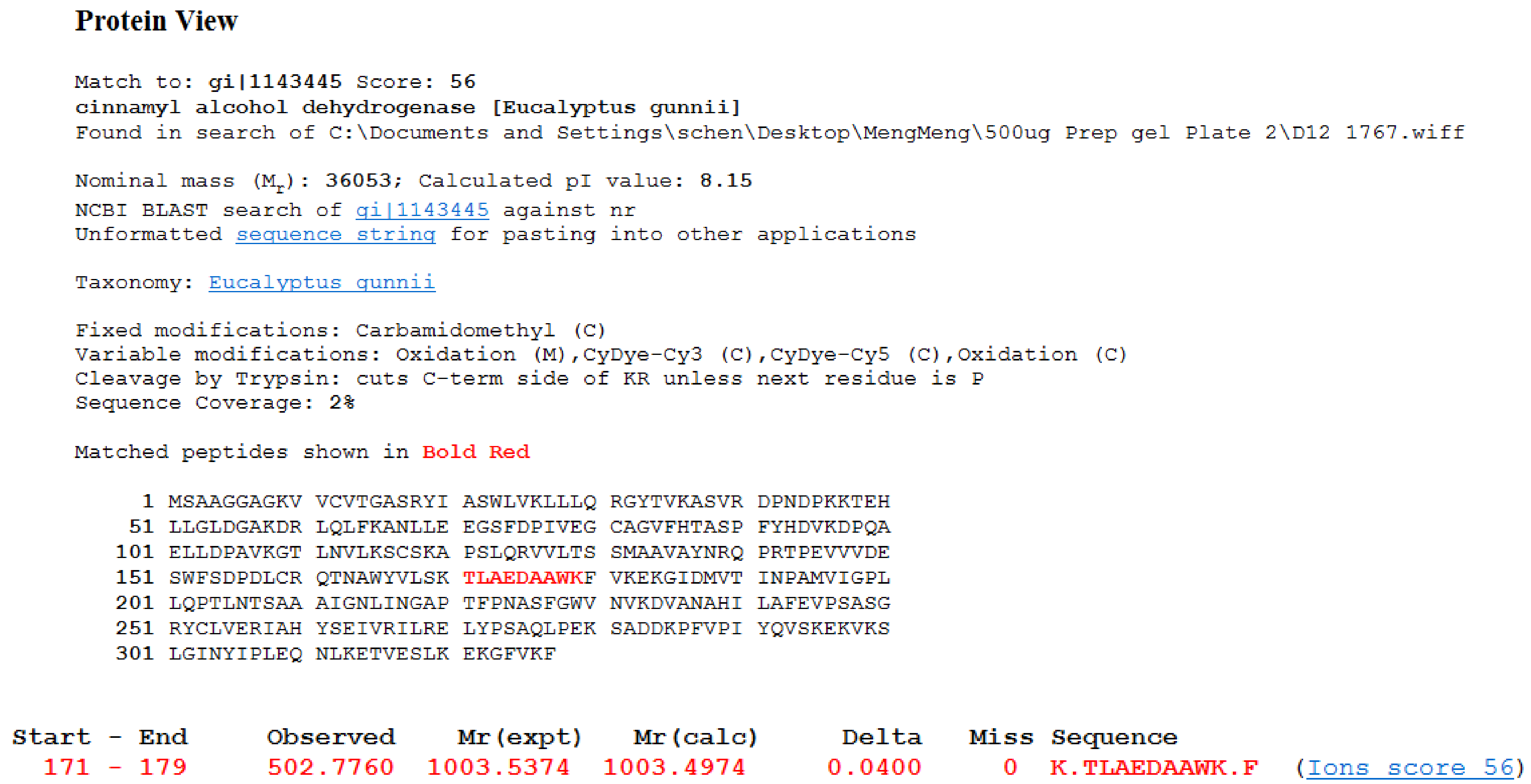
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
51 RLAPKSQLKA TKAKSNGAST VTKCEIGQSL EEFLAQATPD KGLRTLLMCM
101 GEALRTIAFK VRTASCGGTA CVNSFGDEQL AVDMLADKLL FEALQYSHVC
151 KYACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
201 DKLTGITGGD QVAAAMGIYG PR**TTYVLAVK** GFPGTHEFLL LDEGKWQHVK
251 ETTEIAEGK**M** **FSPGNLRATF** **DNSEYSKLID** **YYVK**EKYTLR YTGGMVPDVN
301 QIIVKEK**GIF** **TNVTSPTAK**A KLRLLFEVAP LGLLIENAGG FSSDGHKSVL
351 DKTIINLDDR TQVAYGSKNE IIR**FEETLYG** **TSR**LKNVPIG VTA

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
223 - 230	447.7505	893.4865	893.5222	-0.0357	0	**R.TTYVLAVK.G** (Ions score 27)
260 - 267	469.2111	936.4077	936.4487	-0.0410	0	**K.MFSPGNLR.A** Oxidation (M) (Ions score 24)
268 - 277	581.2725	1160.5304	1160.4986	0.0319	0	**R.ATFDNSEYSK.L** (Ions score 24)
278 - 284	457.2706	912.5266	912.4957	0.0309	0	**K.LIDYYVK.E** (Ions score 28)
308 - 319	618.3155	1234.6164	1234.6558	-0.0393	0	**K.GIFTNVTSPTAK.A** (Ions score 58)
374 - 383	601.8135	1201.6124	1201.5615	0.0509	0	**R.FEETLYGTSR.L** (Ions score 48)

gi|1143445 Cinnamyl alcohol dehydrogenase



Protein View

Match to: gi|1143445 Score: **56**
cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D12 1767.wiff

Nominal mass (M_r): **36053**; Calculated pI value: **8.15**
NCBI BLAST search of gi|1143445 against nr
Unformatted sequence string for pasting into other applications

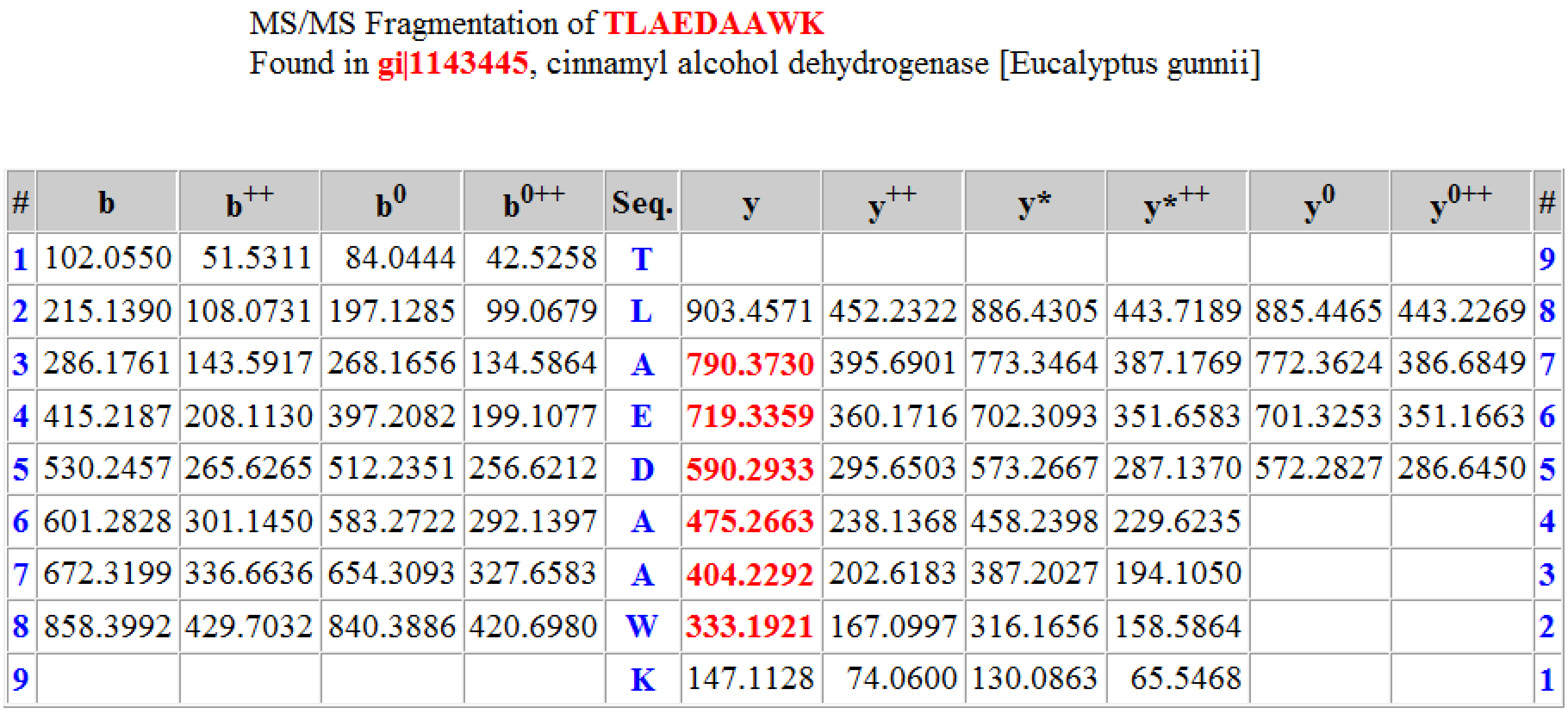
Taxonomy: Eucalyptus gunnii

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 MSAAGGAGKV VCVTGASRYI ASWLVKLLLQ RGYTVKASVR DPNDPKKTEH
 51 LLGLDGAKDR LQLFKANLLE EGSFDPIVEG CAGVFHTASP FYHDVKDPQA
101 ELLDPAVKGT LNVLKSCSKA PSLQRVVLTS SMAAVAYNRQ PRTPEVVVDE
151 SWFSDPDLCR QTNAWYVLSK TLAEDAAWKF VKEKGIDMVT INPAMVIGPL
201 LQPTLNTSAA AIGNLINGAP TFPNASFGWV NVKDVANAHI LAFEVPSASG
251 RYCLVERIAH YSEIVRILRE LYPSAQLPEK SADDKPFVPI YQVSKEKVKS
301 LGINYIPLEQ NLKETVESLK EKGFVKF
```

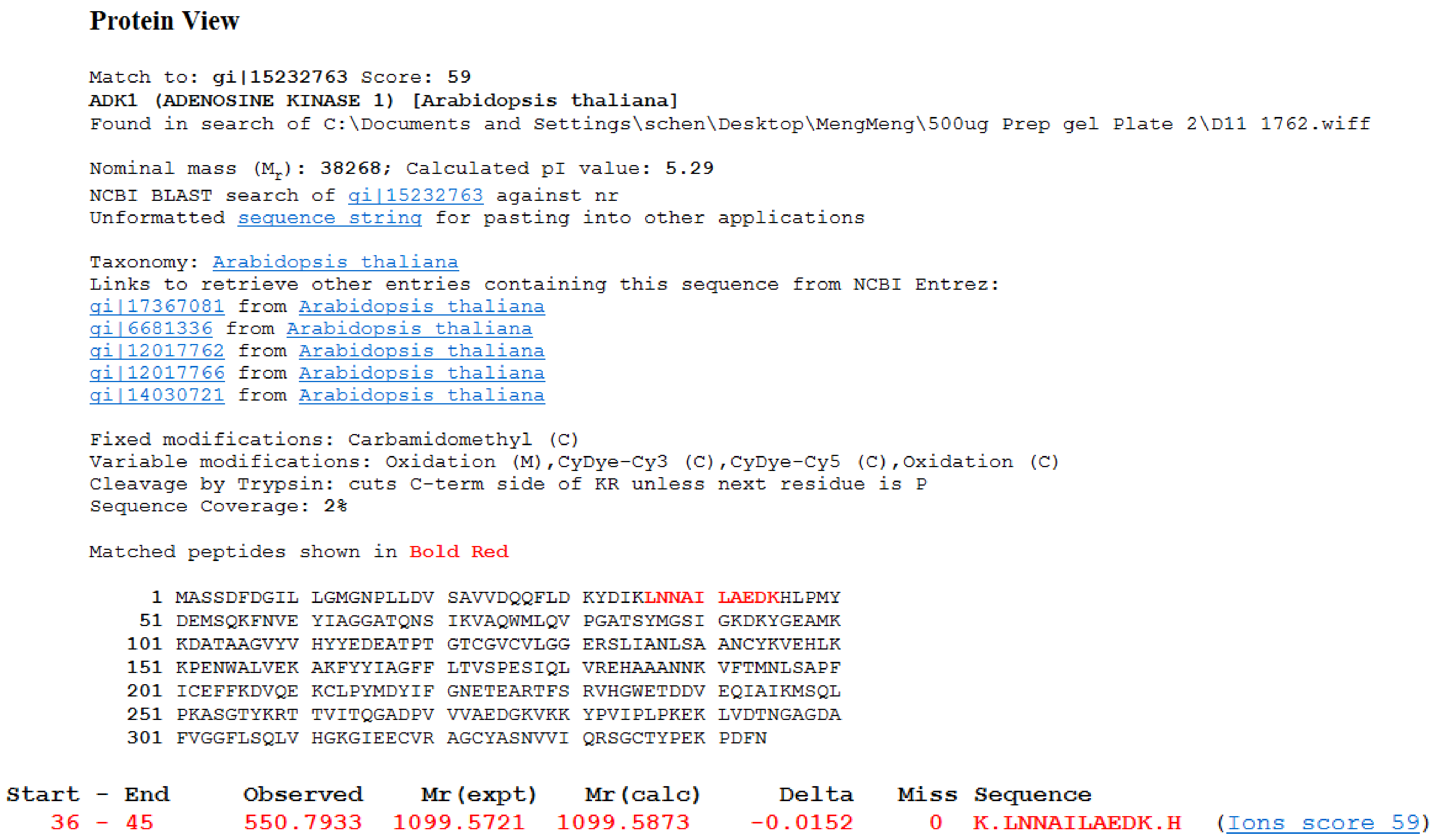
```
Start - End      Observed    Mr(expt)   Mr(calc)      Delta   Miss  Sequence
  171 - 179      502.7760   1003.5374  1003.4974     0.0400     0  K.TLAEDAAWK.F    (Ions score 56)
```



MS/MS Fragmentation of **TLAEDAAWK**
Found in **gi|1143445**, cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							9
2	215.1390	108.0731	197.1285	99.0679	L	903.4571	452.2322	886.4305	443.7189	885.4465	443.2269	8
3	286.1761	143.5917	268.1656	134.5864	A	**790.3730**	395.6901	773.3464	387.1769	772.3624	386.6849	7
4	415.2187	208.1130	397.2082	199.1077	E	**719.3359**	360.1716	702.3093	351.6583	701.3253	351.1663	6
5	530.2457	265.6265	512.2351	256.6212	D	**590.2933**	295.6503	573.2667	287.1370	572.2827	286.6450	5
6	601.2828	301.1450	583.2722	292.1397	A	**475.2663**	238.1368	458.2398	229.6235			4
7	672.3199	336.6636	654.3093	327.6583	A	**404.2292**	202.6183	387.2027	194.1050			3
8	858.3992	429.7032	840.3886	420.6980	W	**333.1921**	167.0997	316.1656	158.5864			2
9					K	147.1128	74.0600	130.0863	65.5468			1

gi|15232763 Adenosine kinase 1 (ADK1)



Protein View

Match to: gi|15232763 Score: 59
ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (M_r): **38268**; Calculated pI value: **5.29**
NCBI BLAST search of gi|15232763 against nr
Unformatted sequence string for pasting into other applications

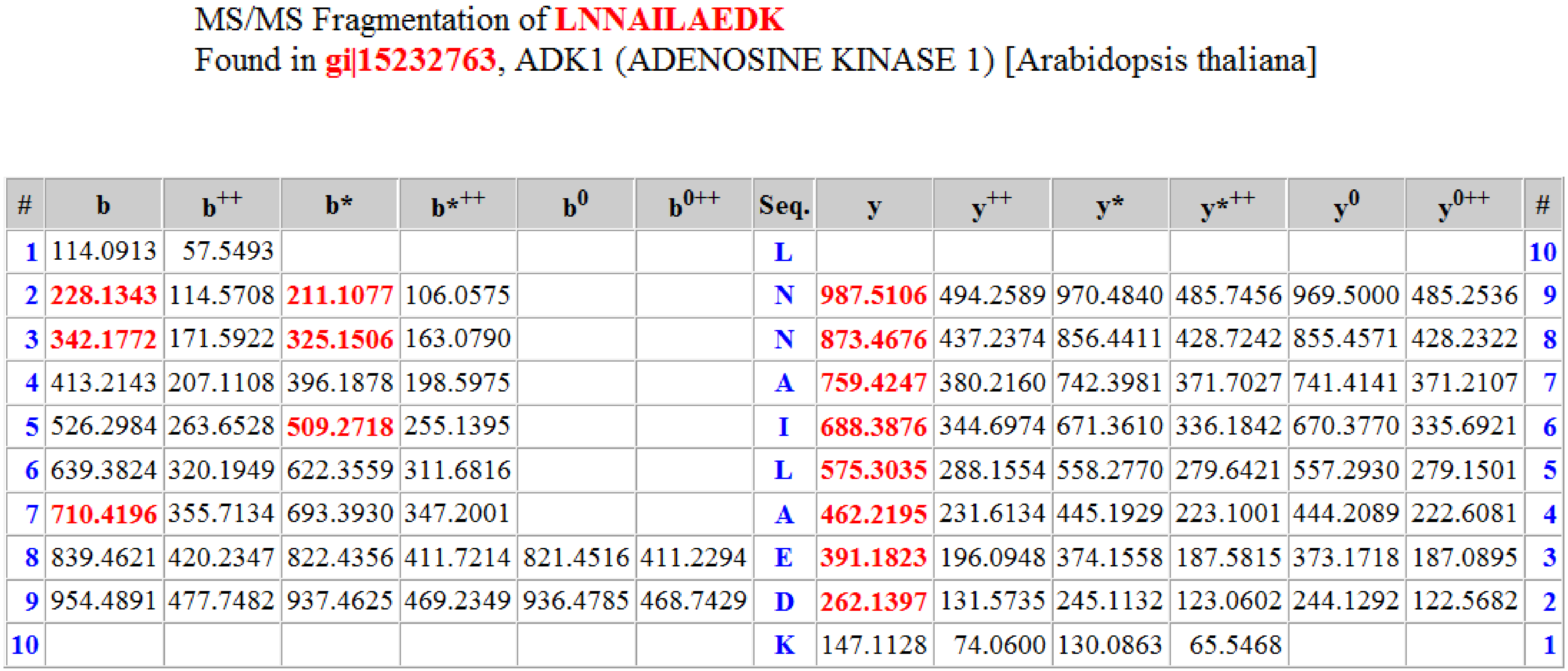
Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|17367081 from Arabidopsis thaliana
gi|6681336 from Arabidopsis thaliana
gi|12017762 from Arabidopsis thaliana
gi|12017766 from Arabidopsis thaliana
gi|14030721 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 MASSDFDGIL LGMGNPLLDV SAVVDQQFLD KYDIKLNNAI LAEDKHLPMY
 51 DEMSQKFNVE YIAGGATQNS IKVAQWMLQV PGATSYMGSI GKDKYGEAMK
101 KDATAAGVYV HYYEDEATPT GTCGVCVLGG ERSLIANLSA ANCYKVEHLK
151 KPENWALVEK AKFYYIAGFF LTVSPESIQL VREHAAANNK VFTMNLSAPF
201 ICEFFKDVQE KCLPYMDYIF GNETEARTFS RVHGWETDDV EQIAIKMSQL
251 PKASGTYKRT TVITQGADPV VVAEDGKVKK YPVIPLPKEK LVDTNGAGDA
301 FVGGFLSQLV HGKGIEECVR AGCYASNVVI QRSGCTYPEK PDFN
```

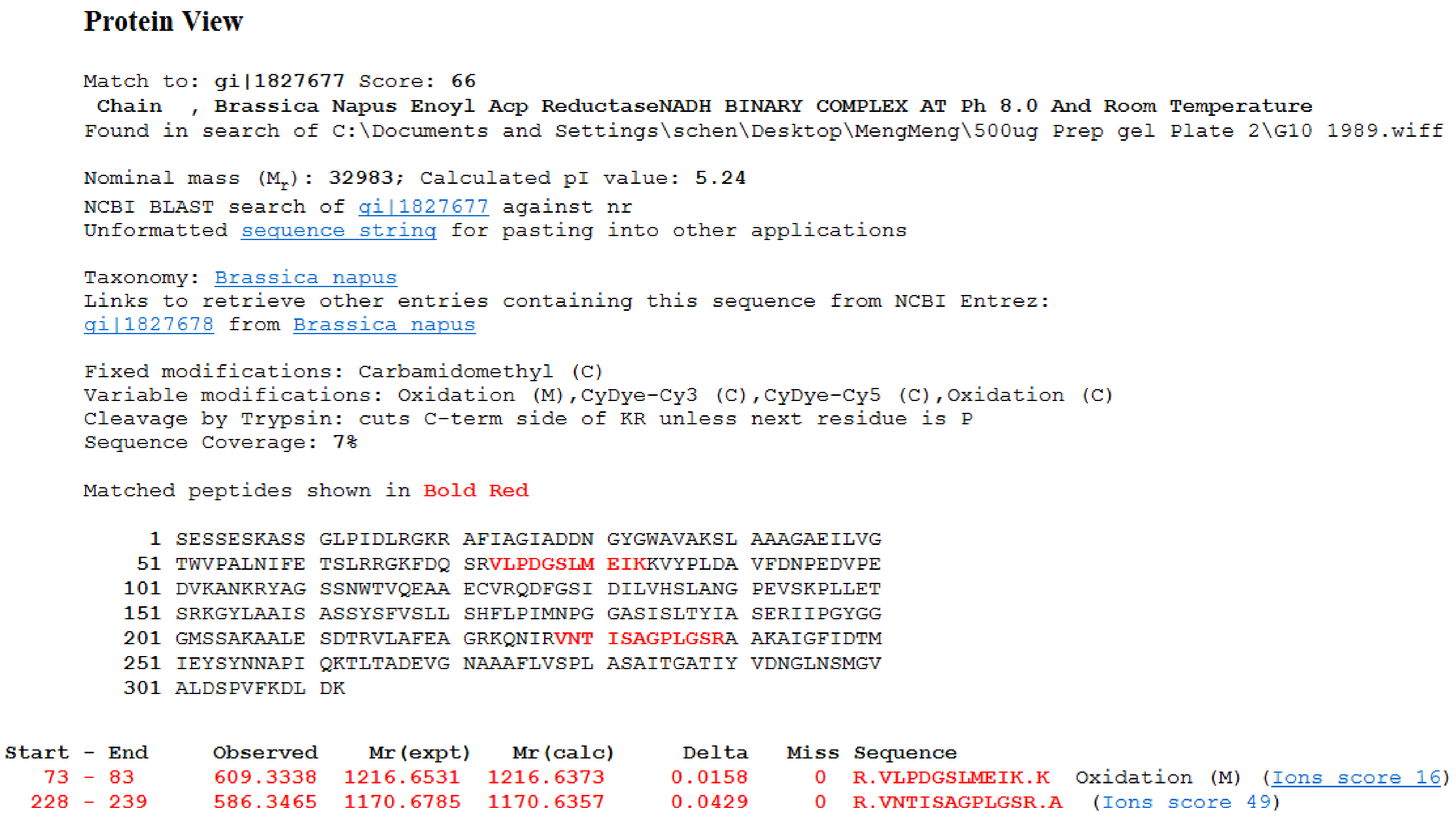
```
Start - End     Observed   Mr(expt)   Mr(calc)      Delta   Miss  Sequence
  36 - 45       550.7933  1099.5721  1099.5873    -0.0152     0  K.LNNAILAEDK.H    (Ions score 59)
```



MS/MS Fragmentation of **LNNAILAEDK**
Found in **gi|15232763**, ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana]

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					**L**							**10**
2	**228.1343**	114.5708	**211.1077**	106.0575			**N**	**987.5106**	494.2589	970.4840	485.7456	969.5000	485.2536	**9**
3	**342.1772**	171.5922	**325.1506**	163.0790			**N**	**873.4676**	437.2374	856.4411	428.7242	855.4571	428.2322	**8**
4	413.2143	207.1108	396.1878	198.5975			**A**	**759.4247**	380.2160	742.3981	371.7027	741.4141	371.2107	**7**
5	526.2984	263.6528	**509.2718**	255.1395			**I**	**688.3876**	344.6974	671.3610	336.1842	670.3770	335.6921	**6**
6	639.3824	320.1949	622.3559	311.6816			**L**	**575.3035**	288.1554	558.2770	279.6421	557.2930	279.1501	**5**
7	**710.4196**	355.7134	693.3930	347.2001			**A**	**462.2195**	231.6134	445.1929	223.1001	444.2089	222.6081	**4**
8	839.4621	420.2347	822.4356	411.7214	821.4516	411.2294	**E**	**391.1823**	196.0948	374.1558	187.5815	373.1718	187.0895	**3**
9	954.4891	477.7482	937.4625	469.2349	936.4785	468.7429	**D**	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
10							**K**	147.1128	74.0600	130.0863	65.5468			**1**

gi|1827677 Enoyl reductase



Protein View

Match to: gi|1827677 Score: 66
Chain , Brassica Napus Enoyl Acp ReductaseNADH BINARY COMPLEX AT Ph 8.0 And Room Temperature
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\G10 1989.wiff

Nominal mass (M_r): **32983**; Calculated pI value: **5.24**
NCBI BLAST search of gi|1827677 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1827678 from Brassica napus

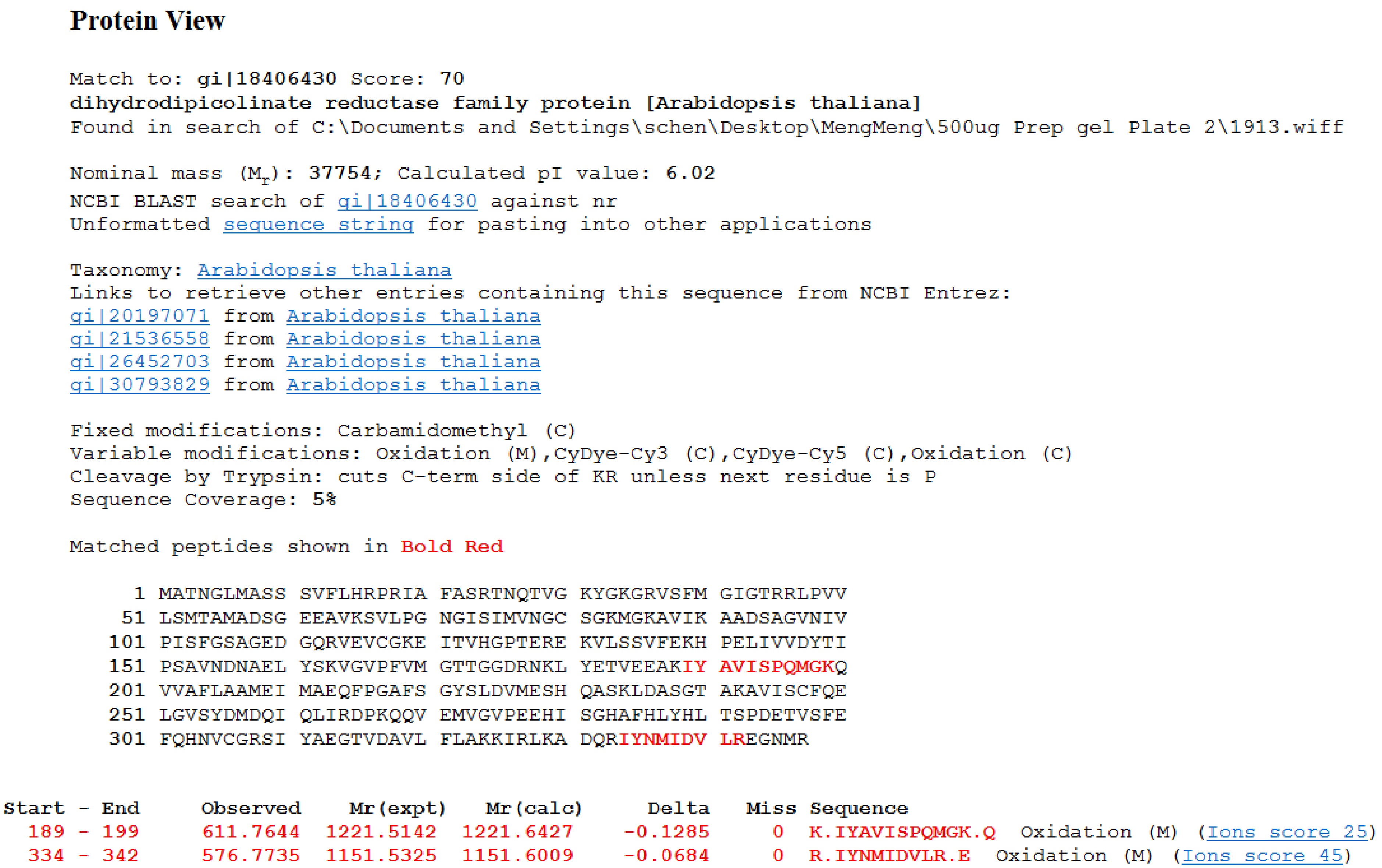
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

Matched peptides shown in **Bold Red**

1 SESSESKASS GLPIDLRGKR AFIAGIADDN GYGWAVAKSL AAAGAEILVG
51 TWVPALNIFE TSLRRGKFDQ SR**VLPDGSLM** **EIK**KVYPLDA VFDNPEDVPE
101 DVKANKRYAG SSNWTVQEAA ECVRQDFGSI DILVHSLANG PEVSKPLLET
151 SRKGYLAAIS ASSYSFVSLL SHFLPIMNPG GASISLTYIA SERIIPGYGG
201 GMSSAKAALE SDTRVLAFEA GRKQNIR**VNT** **ISAGPLGSR**A AKAIGFIDTM
251 IEYSYNNAPI QKTLTADEVG NAAAFLVSPL ASAITGATIY VDNGLNSMGV
301 ALDSPVFKDL DK

```
Start - End     Observed     Mr(expt)    Mr(calc)      Delta    Miss  Sequence
   73 - 83      609.3338    1216.6531   1216.6373    0.0158      0  R.VLPDGSLMEIK.K  Oxidation (M)  (Ions score 16)
  228 - 239     586.3465    1170.6785   1170.6357    0.0429      0  R.VNTISAGPLGSR.A  (Ions score 49)
```

gi|18406430 Dihydrodipicolinate reductase family protein



Protein View

Match to: **gi|18406430** Score: **70**
dihydrodipicolinate reductase family protein [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1913.wiff

Nominal mass (M_r): **37754**; Calculated pI value: **6.02**
NCBI BLAST search of gi|18406430 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|20197071 from Arabidopsis thaliana
gi|21536558 from Arabidopsis thaliana
gi|26452703 from Arabidopsis thaliana
gi|30793829 from Arabidopsis thaliana

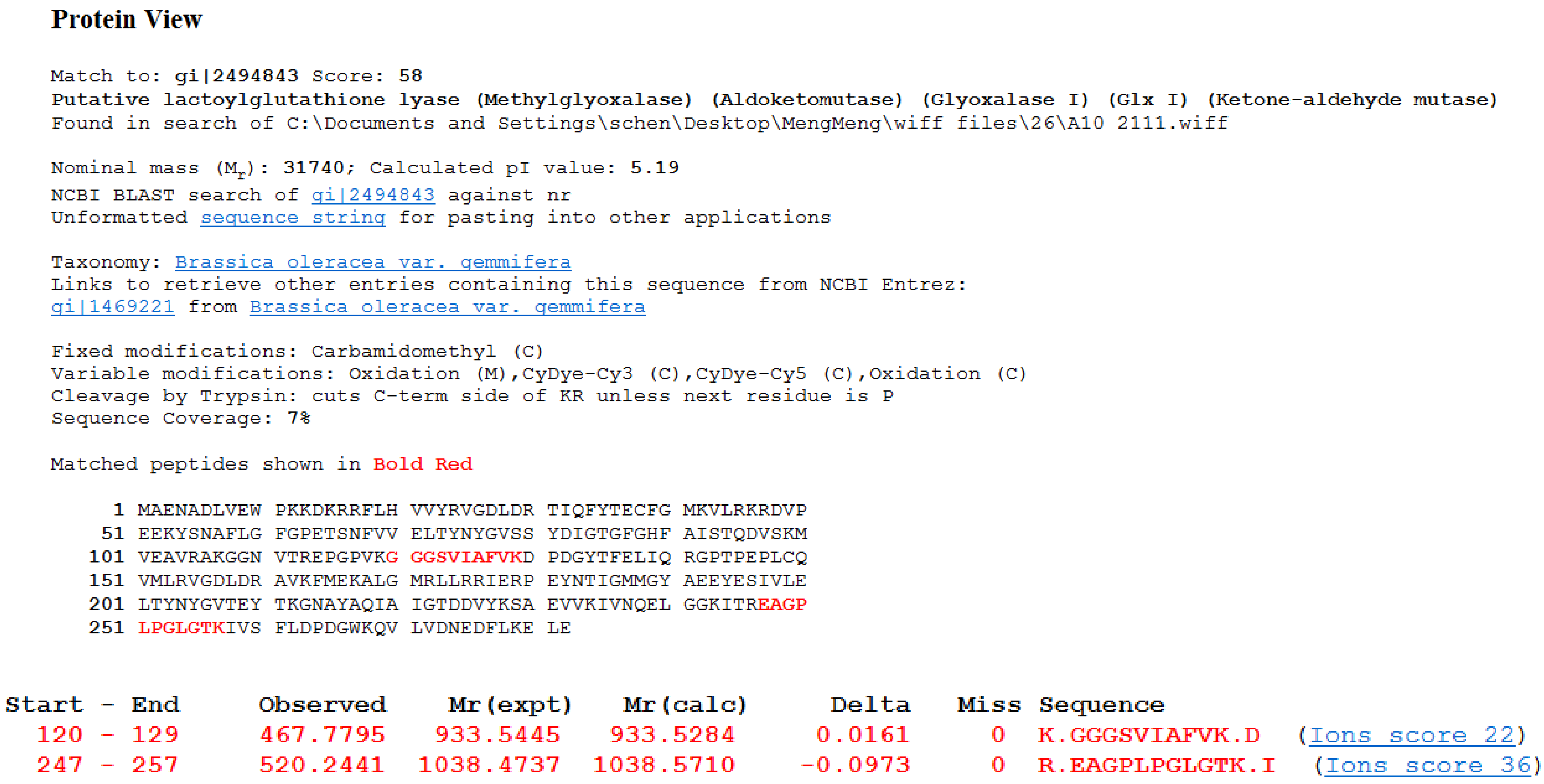
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```
  1 MATNGLMASS SVFLHRPRIA FASRTNQTVG KYGKGRVSFM GIGTRRLPVV
 51 LSMTAMADSG EEAVKSVLPG NGISIMVNGC SGKMGKAVIK AADSAGVNIV
101 PISFGSAGED GQRVEVCGKE ITVHGPTERE KVLSSVFEKH PELIVVDYTI
151 PSAVNDNAEL YSKVGVPFVM GTTGGDRNKL YETVEEAKIY AVISPQMGKQ
201 VVAFLAAMEI MAEQFPGAFS GYSLDVMESH QASKLDASGT AKAVISCFQE
251 LGVSYDMDQI QLIRDPKQQV EMVGVPEEHI SGHAFHLYHL TSPDETVSFE
301 FQHNVCGRSI YAEGTVDAVL FLAKKIRLKA DQRIYNMIDV LREGNMR
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  189 - 199    611.7644  1221.5142  1221.6427   -0.1285     0  K.IYAVISPQMGK.Q  Oxidation (M)  (Ions score 25)
  334 - 342    576.7735  1151.5325  1151.6009   -0.0684     0  R.IYNMIDVLR.E  Oxidation (M)  (Ions score 45)
```

gi|2494843 Putative lactoylglutathione lyase (Methylglyoxalase)



Protein View

Match to: gi|2494843 Score: 58
Putative lactoylglutathione lyase (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff

Nominal mass (M_r): 31740; Calculated pI value: 5.19
NCBI BLAST search of gi|2494843 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica oleracea var. gemmifera
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1469221 from Brassica oleracea var. gemmifera

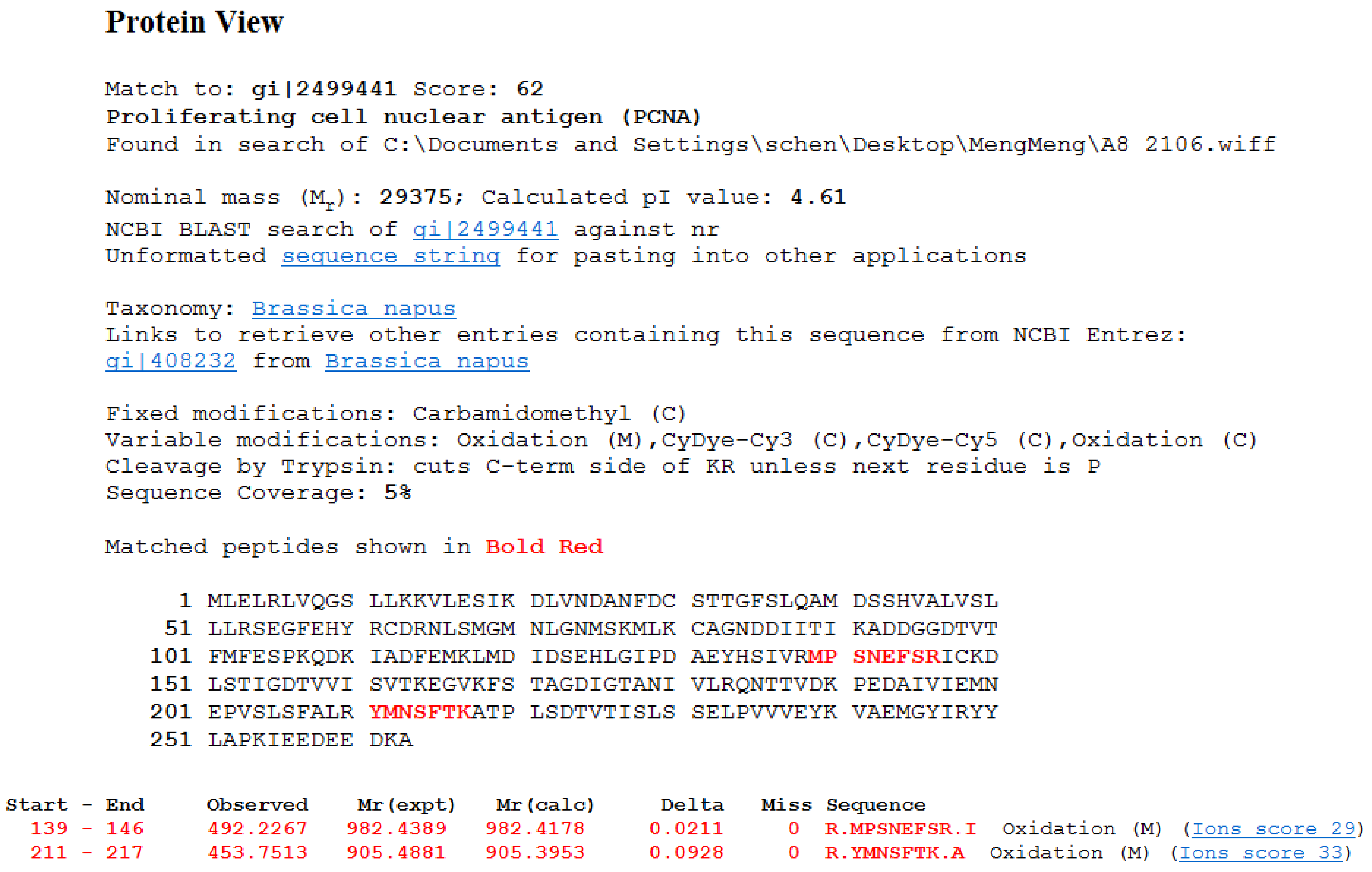
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

```
  1 MAENADLVEW PKKDKRRFLH VVYRVGDLDR TIQFYTECFG MKVLRKRDVP
 51 EEKYSNAFLG FGPETSNFVV ELTYNYGVSS YDIGTGFGHF AISTQDVSKM
101 VEAVRAKGGN VTREPGPVKG GGSVIAFVKD PDGYTFELIQ RGPTPEPLCQ
151 VMLRVGDLDR AVKFMEKALG MRLLRRIERP EYNTIGMMGY AEEYESIVLE
201 LTYNYGVTEY TKGNAYAQIA IGTDDVYKSA EVVKIVNQEL GGKITREAGP
251 LPGLGTKIVS FLDPDGWKQV LVDNEDFLKE LE
```

```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
  120 - 129     467.7795    933.5445    933.5284    0.0161     0   K.GGGSVIAFVK.D   (Ions score 22)
  247 - 257     520.2441   1038.4737   1038.5710   -0.0973     0   R.EAGPLPGLGTK.I   (Ions score 36)
```

gi|2499441 Proliferating cell nuclear antigen (PCNA)



Protein View

Match to: **gi|2499441** Score: **62**
Proliferating cell nuclear antigen (PCNA)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\A8 2106.wiff

Nominal mass (M_r): **29375**; Calculated pI value: **4.61**
NCBI BLAST search of gi|2499441 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|408232 from Brassica napus

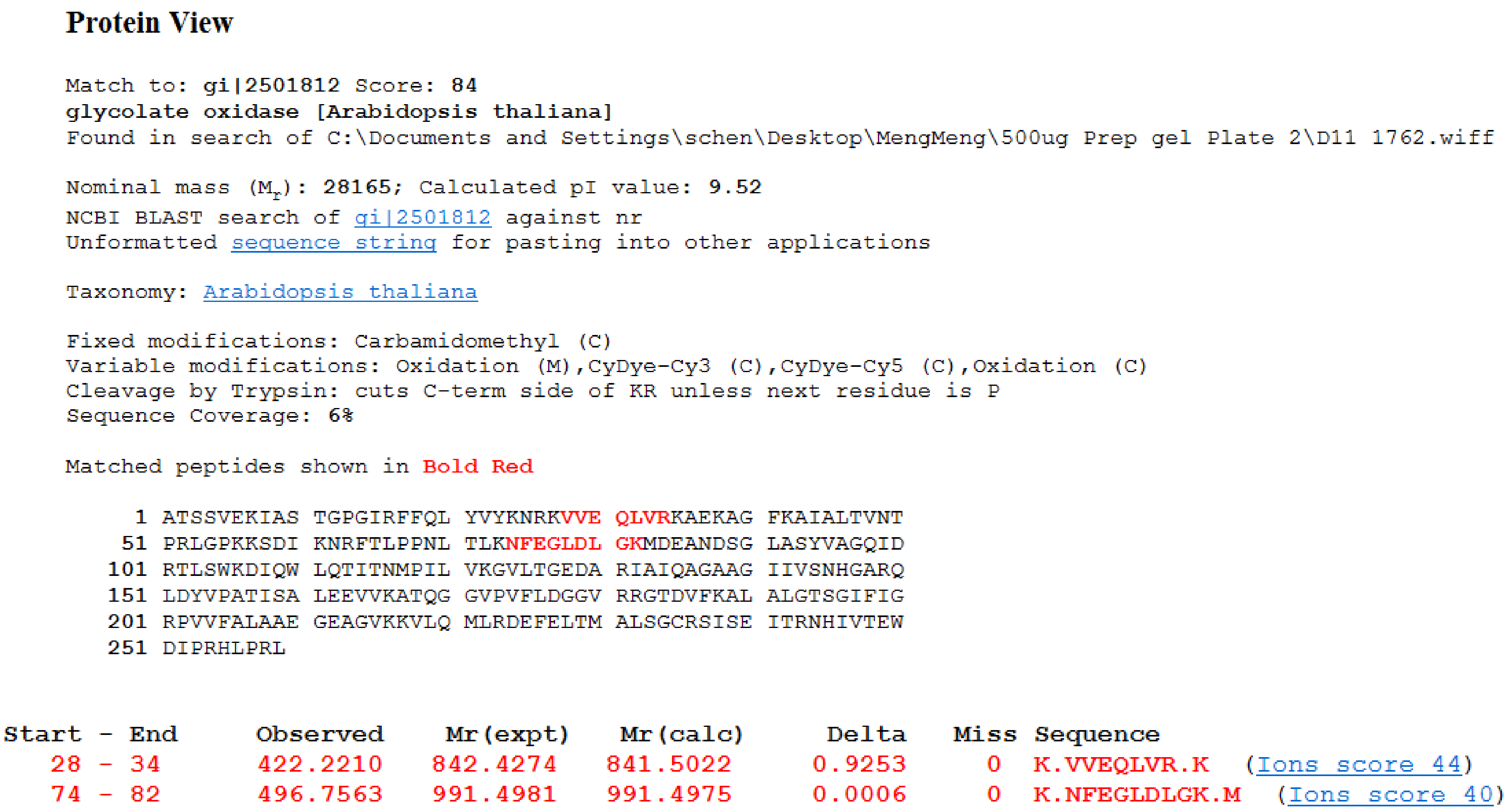
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in **Bold Red**

1 MLELRLVQGS LLKKVLESIK DLVNDANFDC STTGFSLQAM DSSHVALVSL
51 LLRSEGFEHY RCDRNLSMGM NLGNMSKMLK CAGNDDIITI KADDGGDTVT
101 FMFESPKQDK IADFEMKLMD IDSEHLGIPD AEYHSIVR**MP** **SNEFSR**ICKD
151 LSTIGDTVVI SVTKEGVKFS TAGDIGTANI VLRQNTTVDK PEDAIVIEMN
201 EPVSLSFALR **YMNSFTK**ATP LSDTVTISLS SELPVVVEYK VAEMGYIRYY
251 LAPKIEEDEE DKA

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
  139 - 146     492.2267   982.4389   982.4178    0.0211     0  R.MPSNEFSR.I  Oxidation (M)  (Ions score 29)
  211 - 217     453.7513   905.4881   905.3953    0.0928     0  R.YMNSFTK.A  Oxidation (M)  (Ions score 33)
```

gi|2501812 Glycolate oxidase



Protein View

Match to: **gi|2501812** Score: **84**
glycolate oxidase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\D11 1762.wiff

Nominal mass (M_r): **28165**; Calculated pI value: **9.52**
NCBI BLAST search of gi|2501812 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

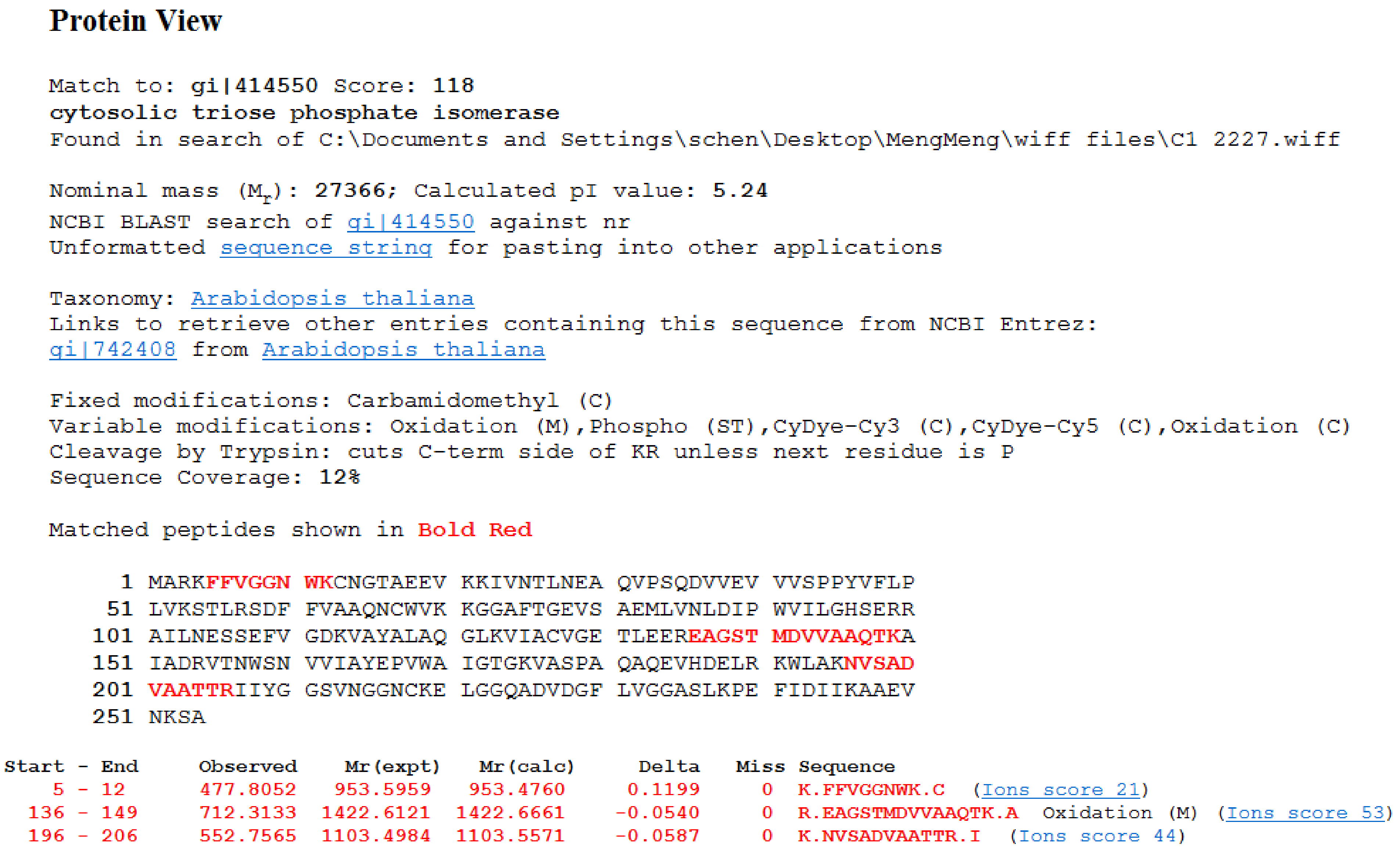
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
     1 ATSSVEKIAS TGPGIRFFQL YVYKNRKVVE QLVRKAEKAG FKAIALTVNT
    51 PRLGPKKSDI KNRFTLPPNL TLKNFEGLDL GKMDEANDSG LASYVAGQID
   101 RTLSWKDIQW LQTITNMPIL VKGVLTGEDA RIAIQAGAAG IIVSNHGARQ
   151 LDYVPATISA LEEVVKATQG GVPVFLDGGV RRGTDVFKAL ALGTSGIFIG
   201 RPVVFALAAE GEAGVKKVLQ MLRDEFELTM ALSGCRSISE ITRNHIVTEW
   251 DIPRHLPRL
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   28 - 34      422.2210    842.4274    841.5022     0.9253     0   K.VVEQLVR.K   (Ions score 44)
   74 - 82      496.7563    991.4981    991.4975     0.0006     0   K.NFEGLDLGK.M   (Ions score 40)
```

gi|414550 Cytosolic triose phosphate isomerase



Protein View

Match to: gi|414550 Score: 118
cytosolic triose phosphate isomerase
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\C1 2227.wiff

Nominal mass (M_r): **27366**; Calculated pI value: **5.24**
NCBI BLAST search of gi|414550 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|742408 from Arabidopsis thaliana

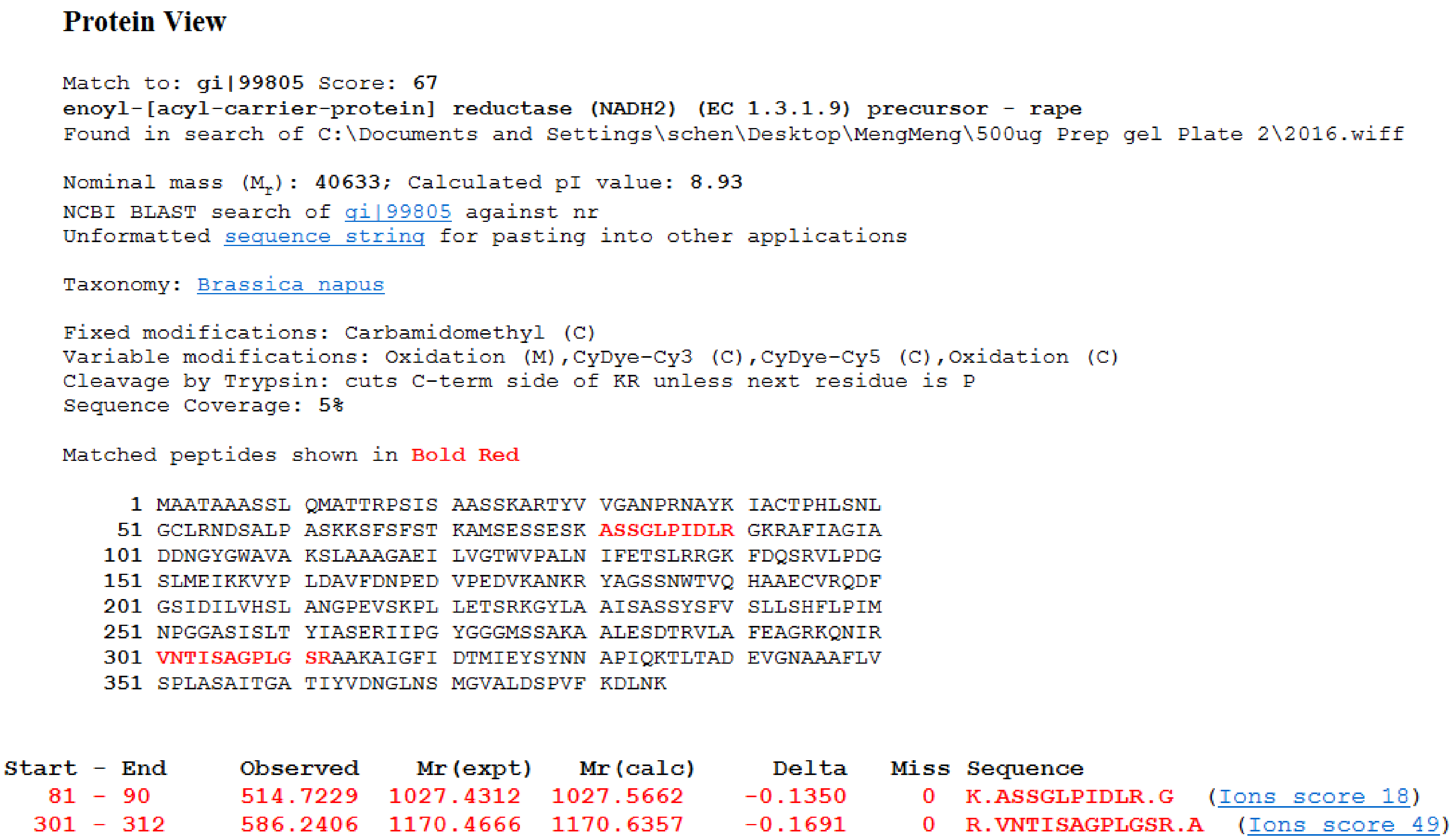
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

```
  1 MARKFFVGGN WKCNGTAEEV KKIVNTLNEA QVPSQDVVEV VVSPPYVFLP
 51 LVKSTLRSDF FVAAQNCWVK KGGAFTGEVS AEMLVNLDIP WVILGHSERR
101 AILNESSEFV GDKVAYALAQ GLKVIACVGE TLEEREAGST MDVVAAQTKA
151 IADRVTNWSN VVIAYEPVWA IGTGKVASPA QAQEVHDELR KWLAKNVSAD
201 VAATTRIIYG GSVNGGNCKE LGGQADVDGF LVGGASLKPE FIDIIKAAEV
251 NKSA
```

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss Sequence
   5 - 12       477.8052    953.5959   953.4760    0.1199     0  K.FFVGGNWK.C   (Ions score 21)
 136 - 149      712.3133   1422.6121  1422.6661   -0.0540     0  R.EAGSTMDVVAAQTK.A  Oxidation (M)  (Ions score 53)
 196 - 206      552.7565   1103.4984  1103.5571   -0.0587     0  K.NVSADVAATTR.I   (Ions score 44)
```

gi|99805 Enoyl-[acyl-carrier-protein] reductase (NADH2) precursor



Protein View

Match to: **gi|99805** Score: **67**
enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) precursor - rape
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\2016.wiff

Nominal mass (M_r): **40633**; Calculated pI value: **8.93**
NCBI BLAST search of gi|99805 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

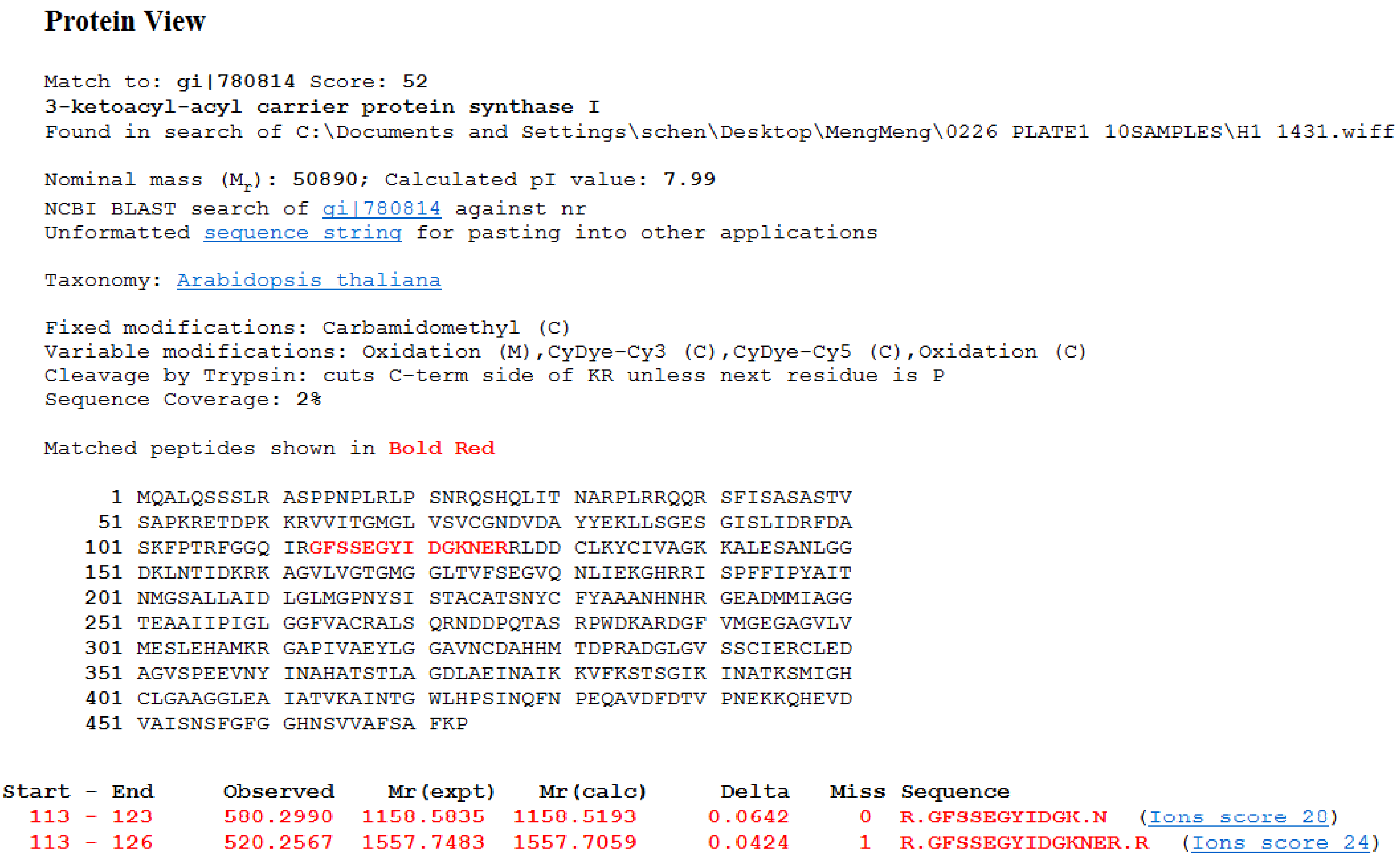
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```
  1 MAATAAASSL QMATTRPSIS AASSKARTYV VGANPRNAYK IACTPHLSNL
 51 GCLRNDSALP ASKKSFSFST KAMSESSESK ASSGLPIDLR GKRAFIAGIA
101 DDNGYGWAVA KSLAAAGAEI LVGTWVPALN IFETSLRRGK FDQSRVLPDG
151 SLMEIKKVYP LDAVFDNPED VPEDVKANKR YAGSSNWTVQ HAAECVRQDF
201 GSIDILVHSL ANGPEVSKPL LETSRKGYLA AISASSYSFV SLLSHFLPIM
251 NPGGASISLT YIASERIIPG YGGGMSSAKA ALESDTRVLA FEAGRKQNIR
301 VNTISAGPLG SRAAKAIGFI DTMIEYSYNN APIQKTLTAD EVGNAAAFLV
351 SPLASAITGA TIYVDNGLNS MGVALDSPVF KDLNK
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  81 - 90      514.7229  1027.4312  1027.5662   -0.1350     0   K.ASSGLPIDLR.G   (Ions score 18)
 301 - 312     586.2406  1170.4666  1170.6357   -0.1691     0   R.VNTISAGPLGSR.A   (Ions score 49)
```

gi|780814 3-ketoacyl-acyl carrier protein synthase I



Protein View

Match to: **gi|780814** Score: **52**
3-ketoacyl-acyl carrier protein synthase I
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\H1 1431.wiff

Nominal mass (M_r): **50890**; Calculated pI value: **7.99**
NCBI BLAST search of gi|780814 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

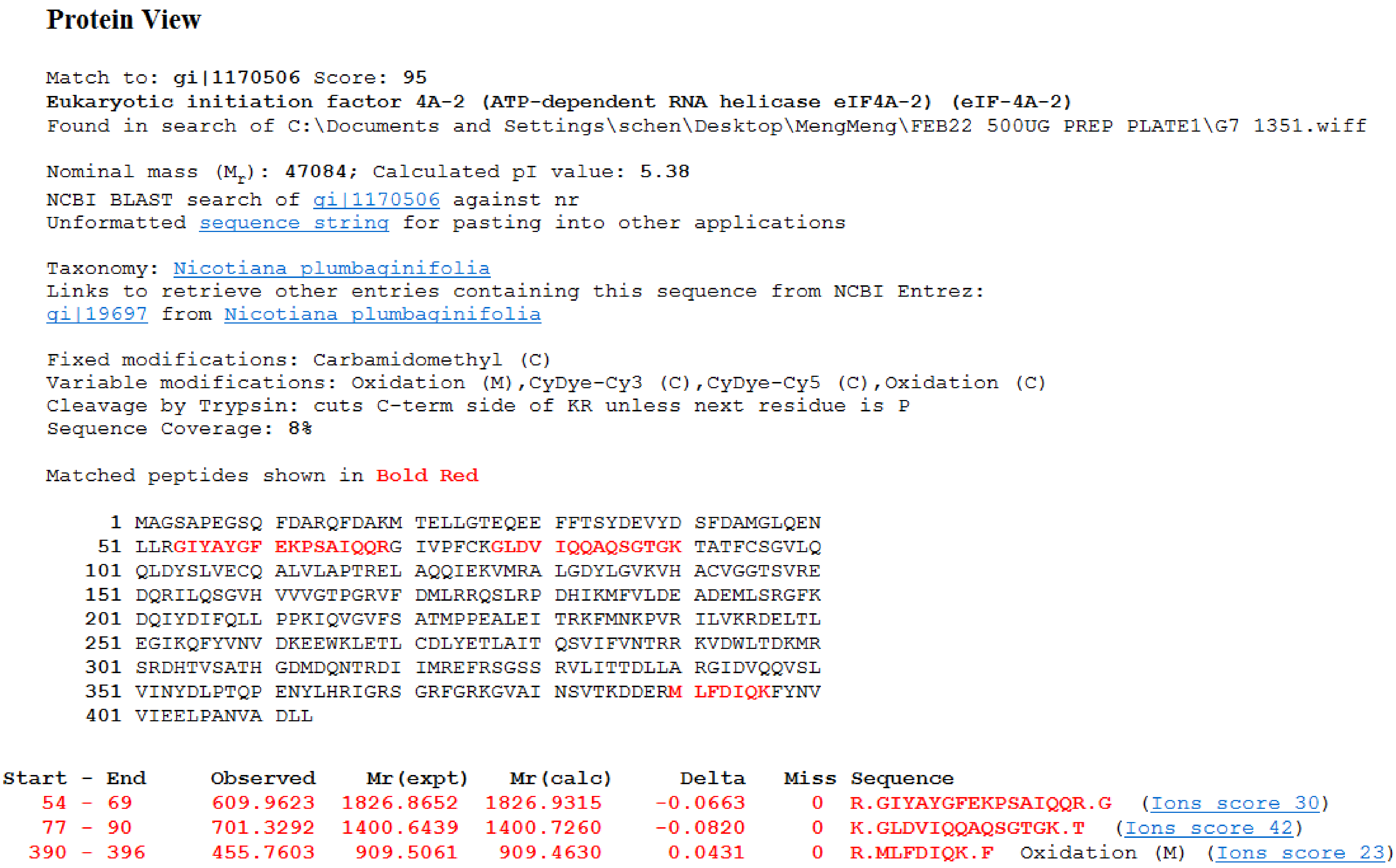
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 MQALQSSSLR ASPPNPLRLP SNRQSHQLIT NARPLRRQQR SFISASASTV
 51 SAPKRETDPK KRVVITGMGL VSVCGNDVDA YYEKLLSGES GISLIDRFDA
101 SKFPTRFGGQ IRGFSSEGYI DGKNERRLDD CLKYCIVAGK KALESANLGG
151 DKLNTIDKRK AGVLVGTGMG GLTVFSEGVQ NLIEKGHRRI SPFFIPYAIT
201 NMGSALLAID LGLMGPNYSI STACATSNYC FYAAANHNHR GEADMMIAGG
251 TEAAIIPIGL GGFVACRALS QRNDDPQTAS RPWDKARDGF VMGEGAGVLV
301 MESLEHAMKR GAPIVAEYLG GAVNCDAHHM TDPRADGLGV SSCIERCLED
351 AGVSPEEVNY INAHATSTLA GDLAEINAIK KVFKSTSGIK INATKSMIGH
401 CLGAAGGLEA IATVKAINTG WLHPSINQFN PEQAVDFDTV PNEKKQHEVD
451 VAISNSFGFG GHNSVVAFSA FKP
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  113 - 123     580.2990  1158.5835  1158.5193    0.0642     0 R.GFSSEGYIDGK.N      (Ions score 20)
  113 - 126     520.2567  1557.7483  1557.7059    0.0424     1 R.GFSSEGYIDGKNER.R   (Ions score 24)
```

gi|1170506 Eukaryotic initiation factor 4A-2



Protein View

Match to: **gi|1170506** Score: **95**
Eukaryotic initiation factor 4A-2 (ATP-dependent RNA helicase eIF4A-2) (eIF-4A-2)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\G7 1351.wiff

Nominal mass (M_r): **47084**; Calculated pI value: **5.38**
NCBI BLAST search of gi|1170506 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Nicotiana plumbaginifolia
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|19697 from Nicotiana plumbaginifolia

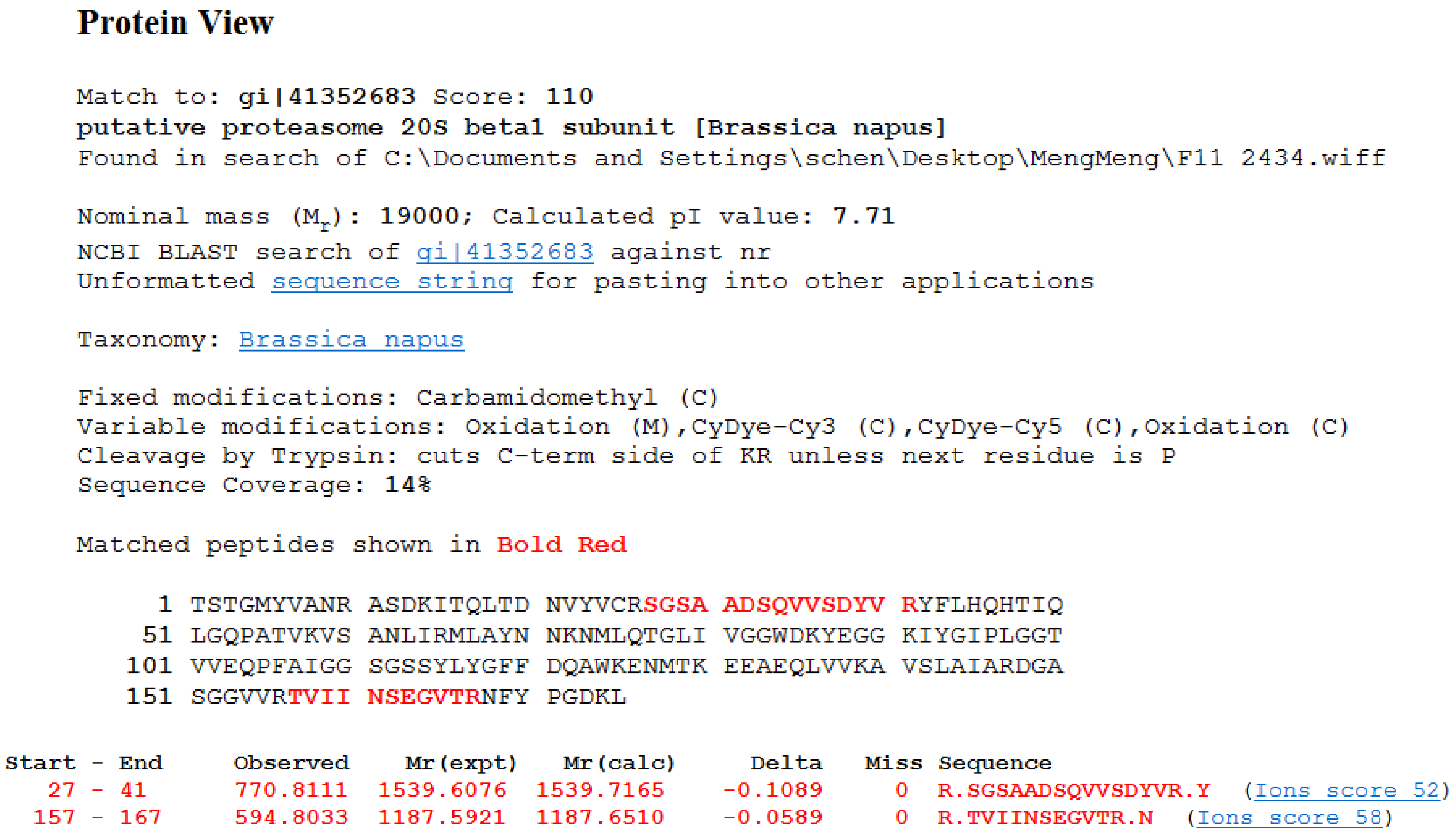
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```
  1 MAGSAPEGSQ FDARQFDAKM TELLGTEQEE FFTSYDEVYD SFDAMGLQEN
 51 LLRGIYAYGF EKPSAIQQRG IVPFCKGLDV IQQAQSGTGK TATFCSGVLQ
101 QLDYSLVECQ ALVLAPTREL AQQIEKVMRA LGDYLGVKVH ACVGGTSVRE
151 DQRILQSGVH VVVGTPGRVF DMLRRQSLRP DHIKMFVLDE ADEMLSRGFK
201 DQIYDIFQLL PPKIQVGVFS ATMPPEALEI TRKFMNKPVR ILVKRDELTL
251 EGIKQFYVNV DKEEWKLETL CDLYETLAIT QSVIFVNTRR KVDWLTDKMR
301 SRDHTVSATH GDMDQNTRDI IMREFRSGSS RVLITTDLLA RGIDVQQVSL
351 VINYDLPTQP ENYLHRIGRS GRFGRKGVAI NSVTKDDERM LFDIQKFYNV
401 VIEELPANVA DLL
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
54 - 69	609.9623	1826.8652	1826.9315	-0.0663	0	**R.GIYAYGFEKPSAIQQR.G** (Ions score 30)
77 - 90	701.3292	1400.6439	1400.7260	-0.0820	0	**K.GLDVIQQAQSGTGK.T** (Ions score 42)
390 - 396	455.7603	909.5061	909.4630	0.0431	0	**R.MLFDIQK.F** Oxidation (M) (Ions score 23)

gi|41352683 Putative proteasome 20S beta1 subunit



Protein View

Match to: **gi|41352683** Score: **110**
putative proteasome 20S beta1 subunit [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\F11 2434.wiff

Nominal mass (M_r): **19000**; Calculated pI value: **7.71**
NCBI BLAST search of gi|41352683 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
  1 TSTGMYVANR ASDKITQLTD NVYVCRSGSA ADSQVVSDYV RYFLHQHTIQ
 51 LGQPATVKVS ANLIRMLAYN NKNMLQTGLI VGGWDKYEGG KIYGIPLGGT
101 VVEQPFAIGG SGSSYLYGFF DQAWKENMTK EEAEQLVVKA VSLAIARDGA
151 SGGVVRTVII NSEGVTRNFY PGDKL
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  27 - 41       770.8111  1539.6076  1539.7165   -0.1089     0   R.SGSAADSQVVSDYVR.Y   (Ions score 52)
 157 - 167      594.8033  1187.5921  1187.6510   -0.0589     0   R.TVIINSEGVTR.N   (Ions score 58)
```

gi|147801436 Hypothetical protein, containing elongation factor 1 domain

Protein View

Match to: **gi|147801436** Score: **74**
hypothetical protein [Vitis vinifera]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\H10 1421.wiff

Nominal mass (M_r): **59829**; Calculated pI value: **6.66**
NCBI BLAST search of gi|147801436 against nr
Unformatted sequence string for pasting into other applications

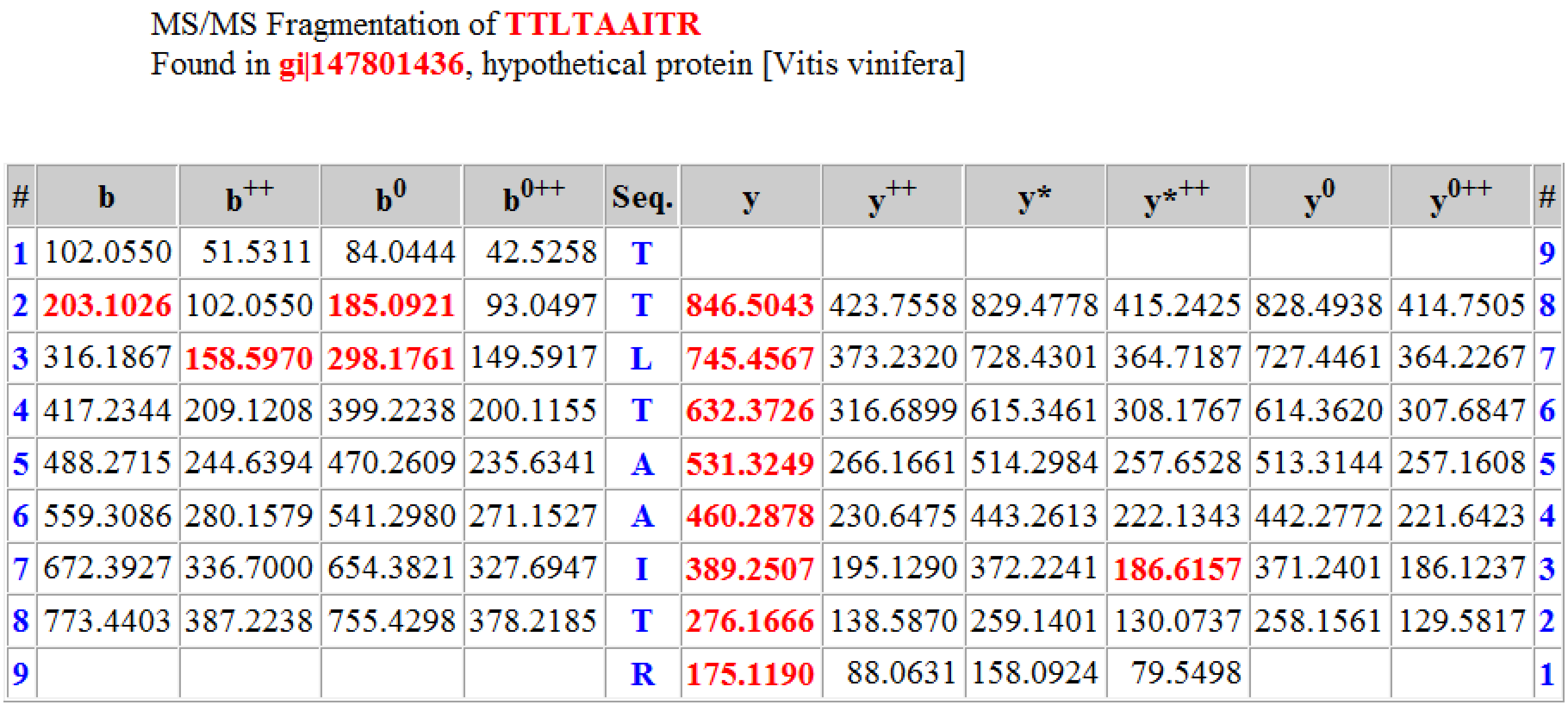
Taxonomy: Vitis vinifera

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **1%**

Matched peptides shown in **Bold Red**

```
  1 MEDCRPPFGA PSFLSFFAAH LPAGRLFESQ VLPPGWLLWN QLSGIDGRMR
 51 KRHQVGGYAE DSESVMEGAL AAGTFEDKRD FQMSMNLGGC VGHMGIKSTQ
101 QEIIVGQAST SPGISGQIIQ KSMCLSLLVK GLLGKWPYES QVGPSKTVWA
151 EEDEHRVTRA HMGVASEGND DYGTPPFNVE QLVSLHGKTT LTAAITRVLA
201 EEGKAKVVAL DEIDKAPKEK KRGITIATTH IEYETAKRHC DHVDCPGHAD
251 YVKNMITGAA QMDGSIQETH SSCVPEMEFR ELLSFYEFPG DEIPVIRGSA
301 ICVLQGTHEE MRKQGCGTVA IGRAEQGTIE VGEDLRIWRG TSALAEHMRW
351 KIAARRNQTV IWVKPLTSDC CIKKGTLVLN LHSTDLMMVR MLCGMLPNGT
401 LAQLLHDSTK ISEYEPDWLT RLTIATGVAE GLAFLHHADY DMVLGVLYRH
451 LSCLQDIVTA VGRLRPIEPL RQVTIRLRPP FDQLDKRSGK ERKSFCTLRL
501 VELNRLVGSS SGSIGWAVFG STTILFNLKP FKQQV
```

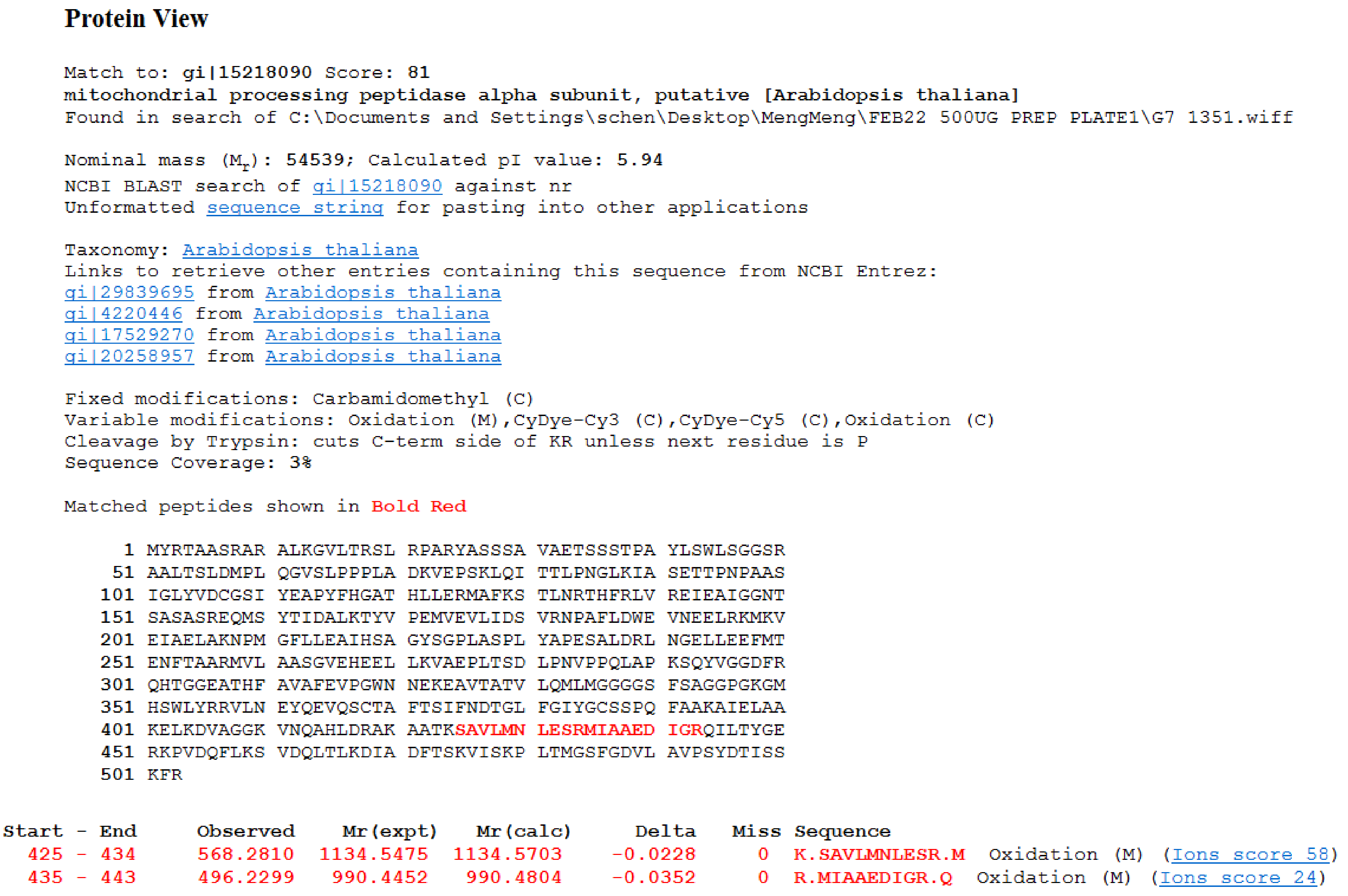
```
Start - End     Observed     Mr(expt)     Mr(calc)      Delta    Miss  Sequence
  189 - 197     474.2925     946.5704     946.5447     0.0257      0   K.TTLTAAITR.V     (Ions score 74)
```



MS/MS Fragmentation of **TTLTAAITR**
Found in **gi|147801436**, hypothetical protein [Vitis vinifera]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	**T**							**9**
2	**203.1026**	102.0550	**185.0921**	93.0497	**T**	**846.5043**	423.7558	829.4778	415.2425	828.4938	414.7505	**8**
3	316.1867	**158.5970**	**298.1761**	149.5917	**L**	**745.4567**	373.2320	728.4301	364.7187	727.4461	364.2267	**7**
4	417.2344	209.1208	399.2238	200.1155	**T**	**632.3726**	316.6899	615.3461	308.1767	614.3620	307.6847	**6**
5	488.2715	244.6394	470.2609	235.6341	**A**	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	**5**
6	559.3086	280.1579	541.2980	271.1527	**A**	**460.2878**	230.6475	443.2613	222.1343	442.2772	221.6423	**4**
7	672.3927	336.7000	654.3821	327.6947	**I**	**389.2507**	195.1290	372.2241	**186.6157**	371.2401	186.1237	**3**
8	773.4403	387.2238	755.4298	378.2185	**T**	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
9					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

gi|15218090 Mitochondrial processing peptidase alpha subunit



Protein View

Match to: **gi|15218090** Score: **81**
mitochondrial processing peptidase alpha subunit, putative [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\G7 1351.wiff

Nominal mass (M_r): **54539**; Calculated pI value: **5.94**
NCBI BLAST search of gi|15218090 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|29839695 from Arabidopsis thaliana
gi|4220446 from Arabidopsis thaliana
gi|17529270 from Arabidopsis thaliana
gi|20258957 from Arabidopsis thaliana

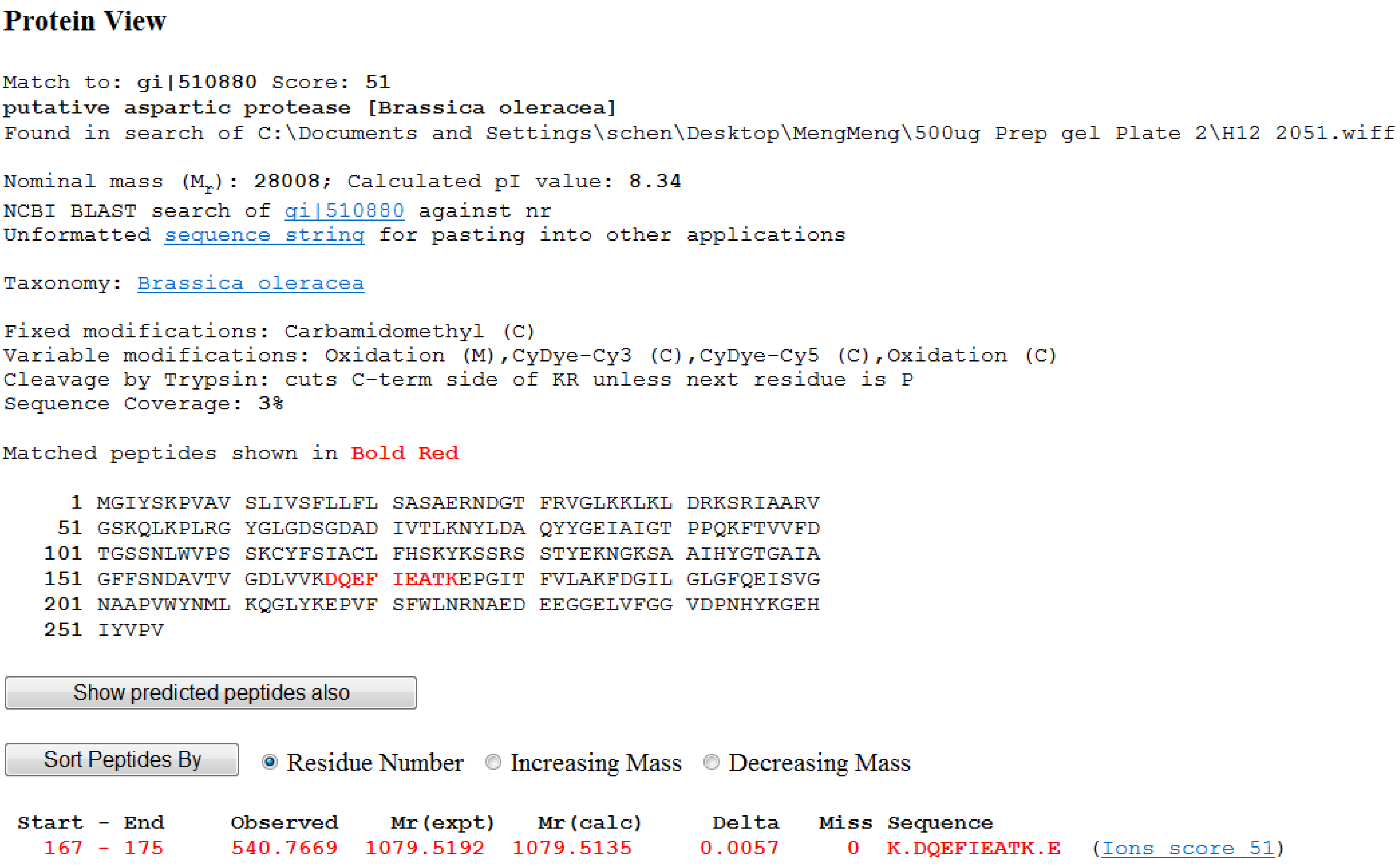
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **3%**

Matched peptides shown in **Bold Red**

```
  1 MYRTAASRAR ALKGVLTRSL RPARYASSSA VAETSSSTPA YLSWLSGGSR
 51 AALTSLDMPL QGVSLPPPLA DKVEPSKLQI TTLPNGLKIA SETTPNPAAS
101 IGLYVDCGSI YEAPYFHGAT HLLERMAFKS TLNRTHFRLV REIEAIGGNT
151 SASASREQMS YTIDALKTYV PEMVEVLIDS VRNPAFLDWE VNEELRKMKV
201 EIAELAKNPM GFLLEAIHSA GYSGPLASPL YAPESALDRL NGELLEEFMT
251 ENFTAARMVL AASGVEHEEL LKVAEPLTSD LPNVPPQLAP KSQYVGGDFR
301 QHTGGEATHF AVAFEVPGWN NEKEAVTATV LQMLMGGGGS FSAGGPGKGM
351 HSWLYRRVLN EYQEVQSCTA FTSIFNDTGL FGIYGCSSPQ FAAKAIELAA
401 KELKDVAGGK VNQAHLDRAK AATKSAVLMN LESRMIAAED IGRQILTYGE
451 RKPVDQFLKS VDQLTLKDIA DFTSKVISKP LTMGSFGDVL AVPSYDTISS
501 KFR
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
  425 - 434     568.2810   1134.5475   1134.5703    -0.0228      0  K.SAVLMNLESR.M  Oxidation (M)  (Ions score 58)
  435 - 443     496.2299    990.4452    990.4804    -0.0352      0  R.MIAAEDIGR.Q  Oxidation (M)  (Ions score 24)
```

gi|510880 Putative aspartic protease



Protein View

Match to: **gi|510880** Score: **51**
putative aspartic protease [Brassica oleracea]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r): **28008**; Calculated pI value: **8.34**
NCBI BLAST search of gi|510880 against nr
Unformatted sequence string for pasting into other applications

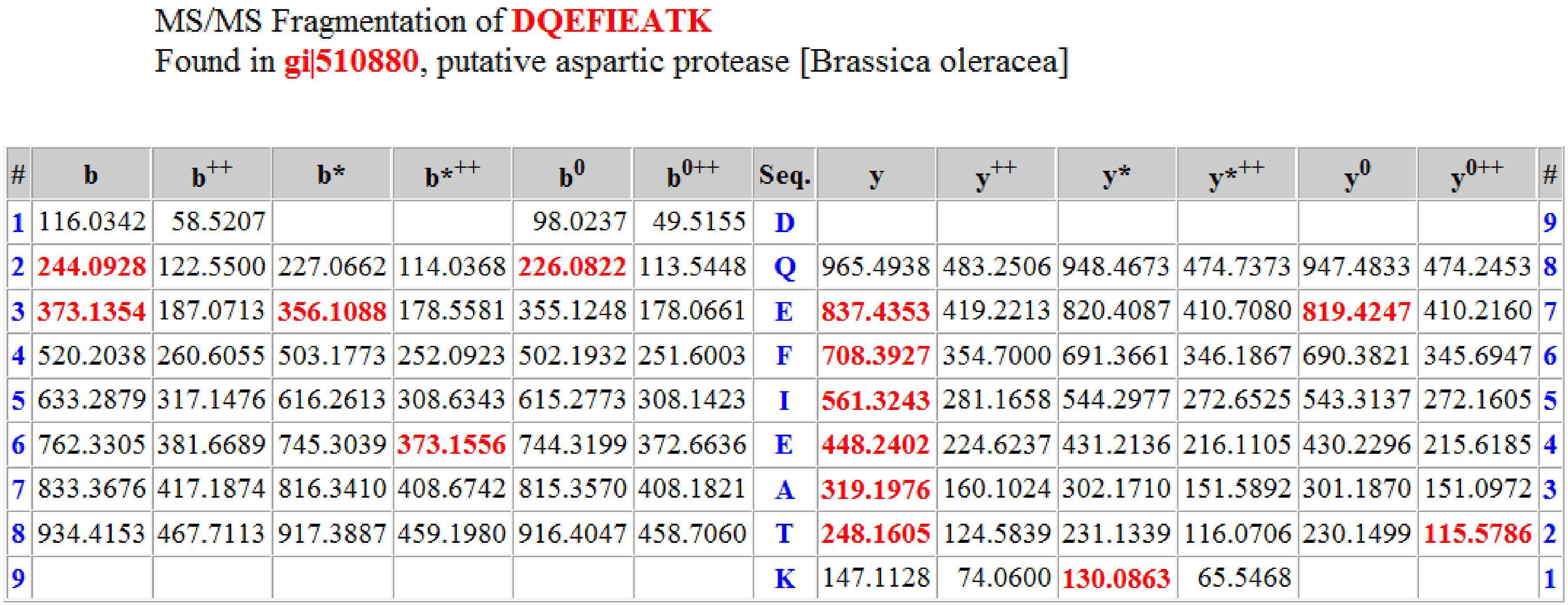
Taxonomy: Brassica oleracea

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **3%**

Matched peptides shown in **Bold Red**

```
     1 MGIYSKPVAV SLIVSFLLFL SASAERNDGT FRVGLKKLKL DRKSRIAARV
    51 GSKQLKPLRG YGLGDSGDAD IVTLKNYLDA QYYGEIAIGT PPQKFTVVFD
   101 TGSSNLWVPS SKCYFSIACL FHSKYKSSRS STYEKNGKSA AIHYGTGAIA
   151 GFFSNDAVTV GDLVVKDQEF IEATKEPGIT FVLAKFDGIL GLGFQEISVG
   201 NAAPVWYNML KQGLYKEPVF SFWLNRNAED EEGGELVFGG VDPNHYKGEH
   251 IYVPV
```

```
 Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   167 - 175     540.7669   1079.5192   1079.5135     0.0057     0  K.DQEFIEATK.E   (Ions score 51)
```

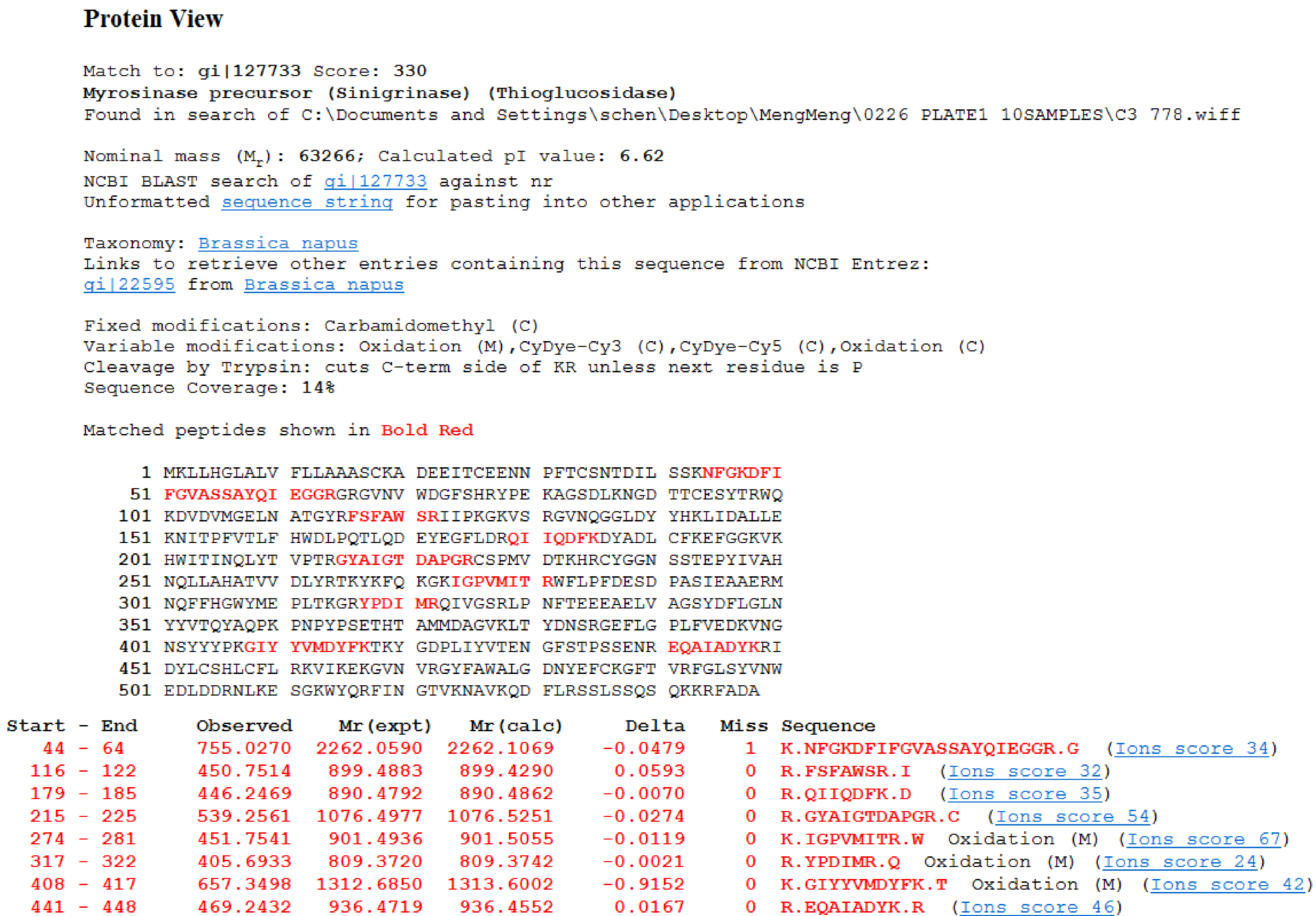


MS/MS Fragmentation of **DQEFIEATK**

Found in **gi|510880**, putative aspartic protease [Brassica oleracea]

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							9
2	**244.0928**	122.5500	227.0662	114.0368	**226.0822**	113.5448	Q	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	8
3	**373.1354**	187.0713	**356.1088**	178.5581	355.1248	178.0661	E	**837.4353**	419.2213	820.4087	410.7080	**819.4247**	410.2160	7
4	520.2038	260.6055	503.1773	252.0923	502.1932	251.6003	F	**708.3927**	354.7000	691.3661	346.1867	690.3821	345.6947	6
5	633.2879	317.1476	616.2613	308.6343	615.2773	308.1423	I	**561.3243**	281.1658	544.2977	272.6525	543.3137	272.1605	5
6	762.3305	381.6689	745.3039	**373.1556**	744.3199	372.6636	E	**448.2402**	224.6237	431.2136	216.1105	430.2296	215.6185	4
7	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	A	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3
8	934.4153	467.7113	917.3887	459.1980	916.4047	458.7060	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	**115.5786**	2
9							K	147.1128	74.0600	**130.0863**	65.5468			1

gi|127733 Myrosinase precursor



Protein View

```
Match to: gi|127733 Score: 330
Myrosinase precursor (Sinigrinase) (Thioglucosidase)
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\C3 778.wiff

Nominal mass (Mr): 63266; Calculated pI value: 6.62
NCBI BLAST search of gi|127733 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|22595 from Brassica napus

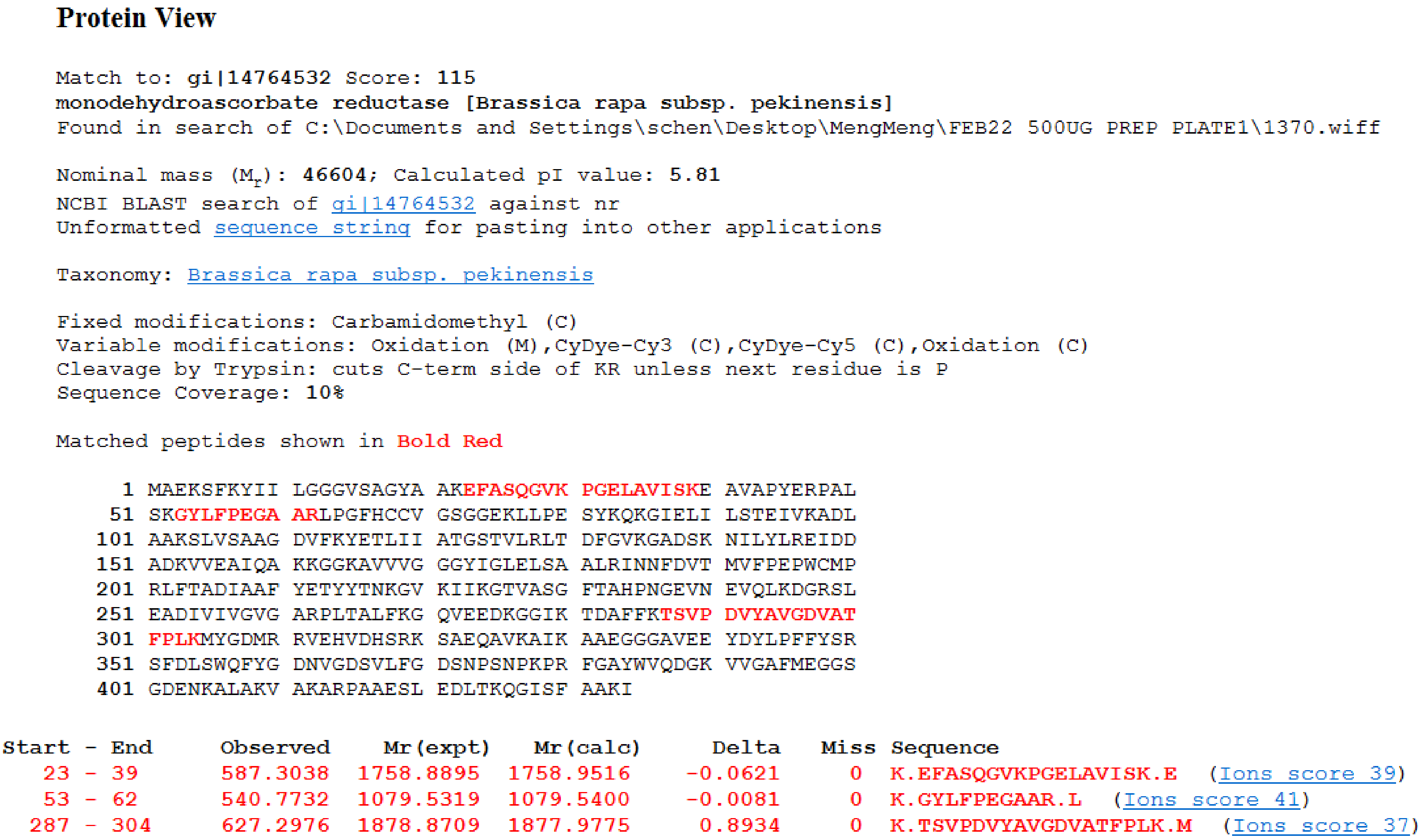
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 14%

Matched peptides shown in Bold Red

  1 MKLLHGLALV FLLAAASCKA DEEITCEENN PFTCSNTDIL SSKNFGKDFI
 51 FGVASSAYQI EGGRGRGVNV WDGFSHRYPE KAGSDLKNGD TTCESYTRWQ
101 KDVDVMGELN ATGYRFSFAW SRIIPKGKVS RGVNQGGLDY YHKLIDALLE
151 KNITPFVTLF HWDLPQTLQD EYEGFLDRQI IQDFKDYADL CFKEFGGKVK
201 HWITINQLYT VPTRGYAIGT DAPGRCSPMV DTKHRCYGGN SSTEPYIVAH
251 NQLLAHATVV DLYRTKYKFQ KGKIGPVMIT RWFLPFDESD PASIEAAERM
301 NQFFHGWYME PLTKGRYPDI MRQIVGSRLP NFTEEEAELV AGSYDFLGLN
351 YYVTQYAQPK PNPYPSETHT AMMDAGVKLT YDNSRGEFLG PLFVEDKVNG
401 NSYYYPKGIY YVMDYFKTKY GDPLIYVTEN GFSTPSSENR EQAIADYKRI
451 DYLCSHLCFL RKVIKEKGVN VRGYFAWALG DNYEFCKGFT VRFGLSYVNW
501 EDLDDRNLKE SGKWYQRFIN GTVKNAVKQD FLRSSLSSQS QKKRFADA

Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  44 -  64     755.0270  2262.0590  2262.1069   -0.0479    1  K.NFGKDFIFGVASSAYQIEGGR.G  (Ions score 34)
 116 - 122     450.7514   899.4883   899.4290    0.0593    0  R.FSFAWSR.I  (Ions score 32)
 179 - 185     446.2469   890.4792   890.4862   -0.0070    0  R.QIIQDFK.D  (Ions score 35)
 215 - 225     539.2561  1076.4977  1076.5251   -0.0274    0  R.GYAIGTDAPGR.C  (Ions score 54)
 274 - 281     451.7541   901.4936   901.5055   -0.0119    0  K.IGPVMITR.W  Oxidation (M)  (Ions score 67)
 317 - 322     405.6933   809.3720   809.3742   -0.0021    0  R.YPDIMR.Q  Oxidation (M)  (Ions score 24)
 408 - 417     657.3498  1312.6850  1313.6002   -0.9152    0  K.GIYYVMDYFK.T  Oxidation (M)  (Ions score 42)
 441 - 448     469.2432   936.4719   936.4552    0.0167    0  R.EQAIADYK.R  (Ions score 46)
```

gi|14764532 Monodehydroascorbate reductase



Protein View

Match to: **gi|14764532** Score: **115**
monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\FEB22 500UG PREP PLATE1\1370.wiff

Nominal mass (M_r): **46604**; Calculated pI value: **5.81**
NCBI BLAST search of gi|14764532 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

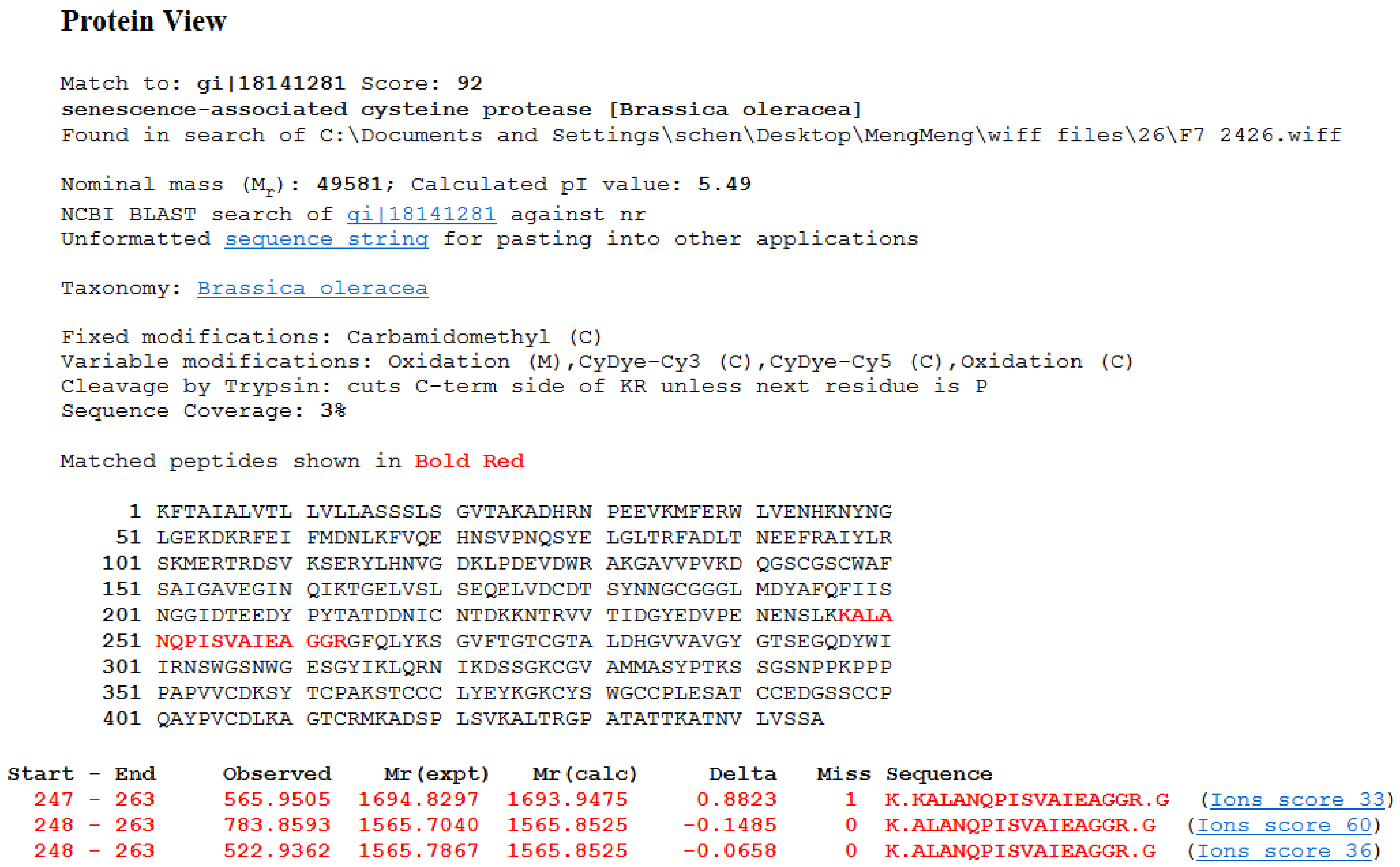
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
  1 MAEKSFKYII LGGGVSAGYA AKEFASQGVK PGELAVISKE AVAPYERPAL
 51 SKGYLFPEGA ARLPGFHCCV GSGGEKLLPE SYKQKGIELI LSTEIVKADL
101 AAKSLVSAAG DVFKYETLII ATGSTVLRLT DFGVKGADSK NILYLREIDD
151 ADKVVEAIQA KKGGKAVVVG GGYIGLELSA ALRINNFDVT MVFPEPWCMP
201 RLFTADIAAF YETYYTNKGV KIIKGTVASG FTAHPNGEVN EVQLKDGRSL
251 EADIVIVGVG ARPLTALFKG QVEEDKGGIK TDAFFKTSVP DVYAVGDVAT
301 FPLKMYGDMR RVEHVDHSRK SAEQAVKAIK AAEGGAVEE YDYLPFFYSR
351 SFDLSWQFYG DNVGDSVLFG DSNPSNPKPR FGAYWVQDGK VVGAFMEGGS
401 GDENKALAKV AKARPAAESL EDLTKQGISF AAKI
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  23 - 39      587.3038  1758.8895  1758.9516   -0.0621     0   K.EFASQGVKPGELAVISK.E   (Ions score 39)
  53 - 62      540.7732  1079.5319  1079.5400   -0.0081     0   K.GYLFPEGAAR.L   (Ions score 41)
 287 - 304     627.2976  1878.8709  1877.9775    0.8934     0   K.TSVPDVYAVGDVATFPLK.M   (Ions score 37)
```

gi|18141281 Senescence-associated cysteine protease



Protein View

Match to: **gi|18141281** **Score:** **92**
senescence-associated cysteine protease [Brassica oleracea]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\F7 2426.wiff

Nominal mass (M_r): **49581**; Calculated pI value: **5.49**
NCBI BLAST search of gi|18141281 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica oleracea

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

```
  1 KFTAIALVTL LVLLASSSLS GVTAKADHRN PEEVKMFERW LVENHKNYNG
 51 LGEKDKRFEI FMDNLKFVQE HNSVPNQSYE LGLTRFADLT NEEFRAIYLR
101 SKMERTRDSV KSERYLHNVG DKLPDEVDWR AKGAVVPVKD QGSCGSCWAF
151 SAIGAVEGIN QIKTGELVSL SEQELVDCDT SYNNGCGGGL MDYAFQFIIS
201 NGGIDTEEDY PYTATDDNIC NTDKKNTRVV TIDGYEDVPE NENSLKKALA
251 NQPISVAIEA GGRGFQLYKS GVFTGTCGTA LDHGVVAVGY GTSEGQDYWI
301 IRNSWGSNWG ESGYIKLQRN IKDSSGKCGV AMMASYPTKS SGSNPPKPPP
351 PAPVVCDKSY TCPAKSTCCC LYEYKGKCYS WGCCPLESAT CCEDGSSCCP
401 QAYPVCDLKA GTCRMKADSP LSVKALTRGP ATATTKATNV LVSSA

Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  247 - 263     565.9505  1694.8297  1693.9475    0.8823     1  K.KALANQPISVAIEAGGR.G   (Ions score 33)
  248 - 263     783.8593  1565.7040  1565.8525   -0.1485     0  K.ALANQPISVAIEAGGR.G   (Ions score 60)
  248 - 263     522.9362  1565.7867  1565.8525   -0.0658     0  K.ALANQPISVAIEAGGR.G   (Ions score 36)
```

gi|15227987 Low expression of osmotically responsive genes 1 (LOS2)

Protein View

Match to: **gi|15227987** Score: **127**
LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\0226 PLATE1 10SAMPLES\F4 1223.wiff

Nominal mass (M_r): **47974**; Calculated pI value: **5.54**
NCBI BLAST search of gi|15227987 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|119350 from Arabidopsis thaliana
gi|15983458 from Arabidopsis thaliana
gi|16271 from Arabidopsis thaliana
gi|4581151 from Arabidopsis thaliana
gi|23297411 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

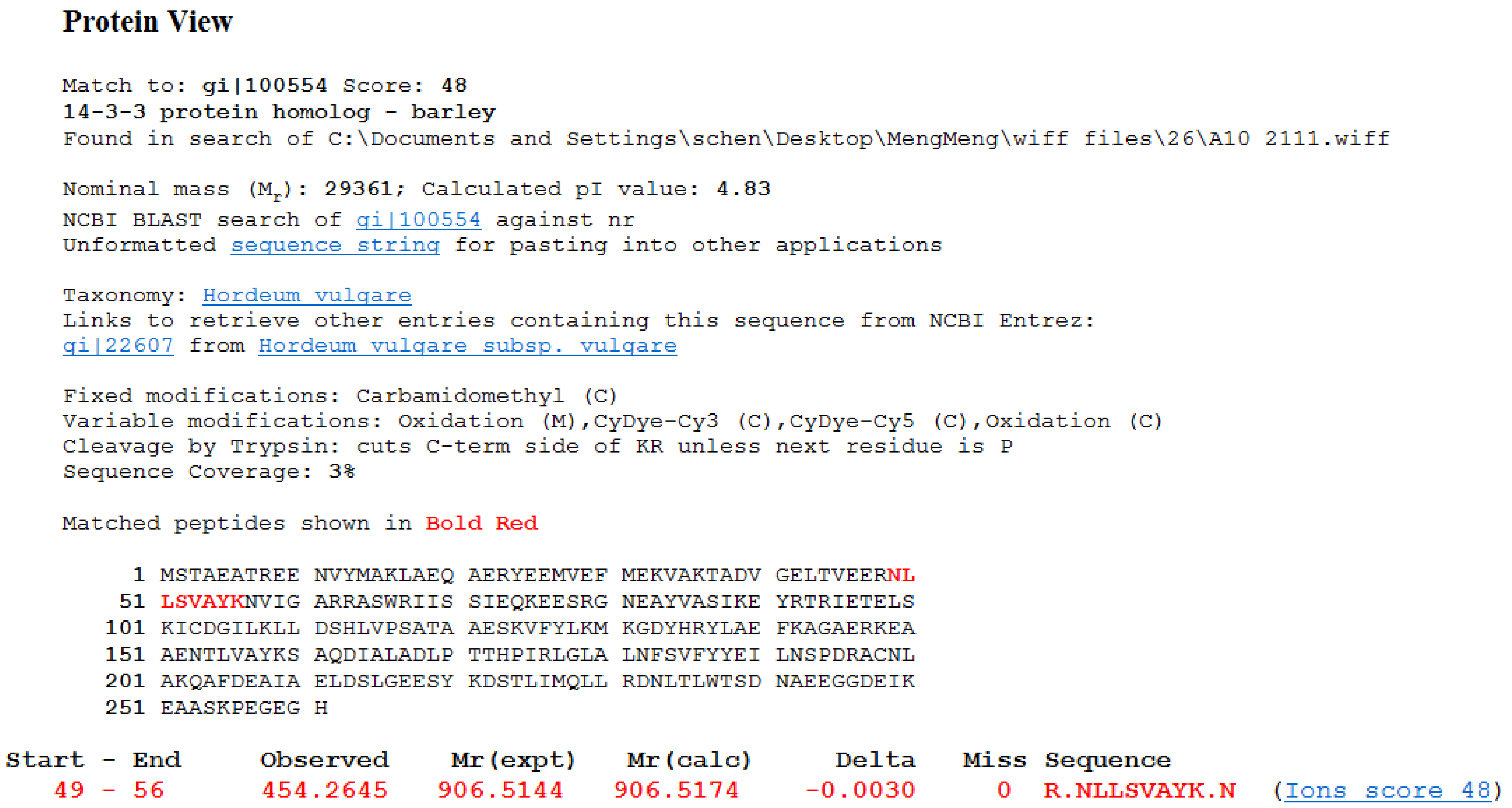
1 MATITVVKAR QIFDSRGNPT VEVDIHTSNG IKVTAAVPSG ASTGIYEALE
51 LRDGGSDYLG KGVSKAVGNV NNIIGPALIG KDPTQQTAID NFMVHELDGT
101 QNEWGWCKQK LGANAILAVS LAVCK**AGAVV SGIPLYK**HIA NLAGNPKIVL
151 PVPAFNVING GSHAGNKLAM QEFMILPVGA ASFKEAMKMG VEVYHHLKSV
201 IKKKYGQDAT NVGDEGGFAP NIQENKEGLE LLKTAIEKAG YTGKVVIGMD
251 VAASEFYSED KTYDLNFKEE NNNGSQKISG DALKDLYKSF VAEYPIVSIE
301 DPFDQDDWEH YAKMTTECGT EVQIVGDDLL VTNPKRVAKA IAEKSCNALL
351 LK**VNQIGSVT ESIEAVK**MSK KAGWGVMTSH RSGETEDTFI ADLAVGLSTG
401 QIKTGAPCRS ERLAK**YNQLL R**IEEELGSEA IYAGVNFRKP VEPY

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
126 - 137	587.9131	1173.8116	1173.6758	0.1358	0	K.AGAVVSGIPLYK.H (Ions score 34)
353 - 367	525.3462	1573.0169	1572.8359	0.1810	0	K.VNQIGSVTESIEAVK.M (Ions score 53)
416 - 421	403.7902	805.5658	805.4446	0.1212	0	K.YNQLLR.I (Ions score 41)

gi|100554 14-3-3 protein homolog



Protein View

Match to: gi|100554 Score: 48
14-3-3 protein homolog - barley
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff

Nominal mass (M_r): **29361**; Calculated pI value: **4.83**
NCBI BLAST search of gi|100554 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|22607 from Hordeum vulgare subsp. vulgare

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

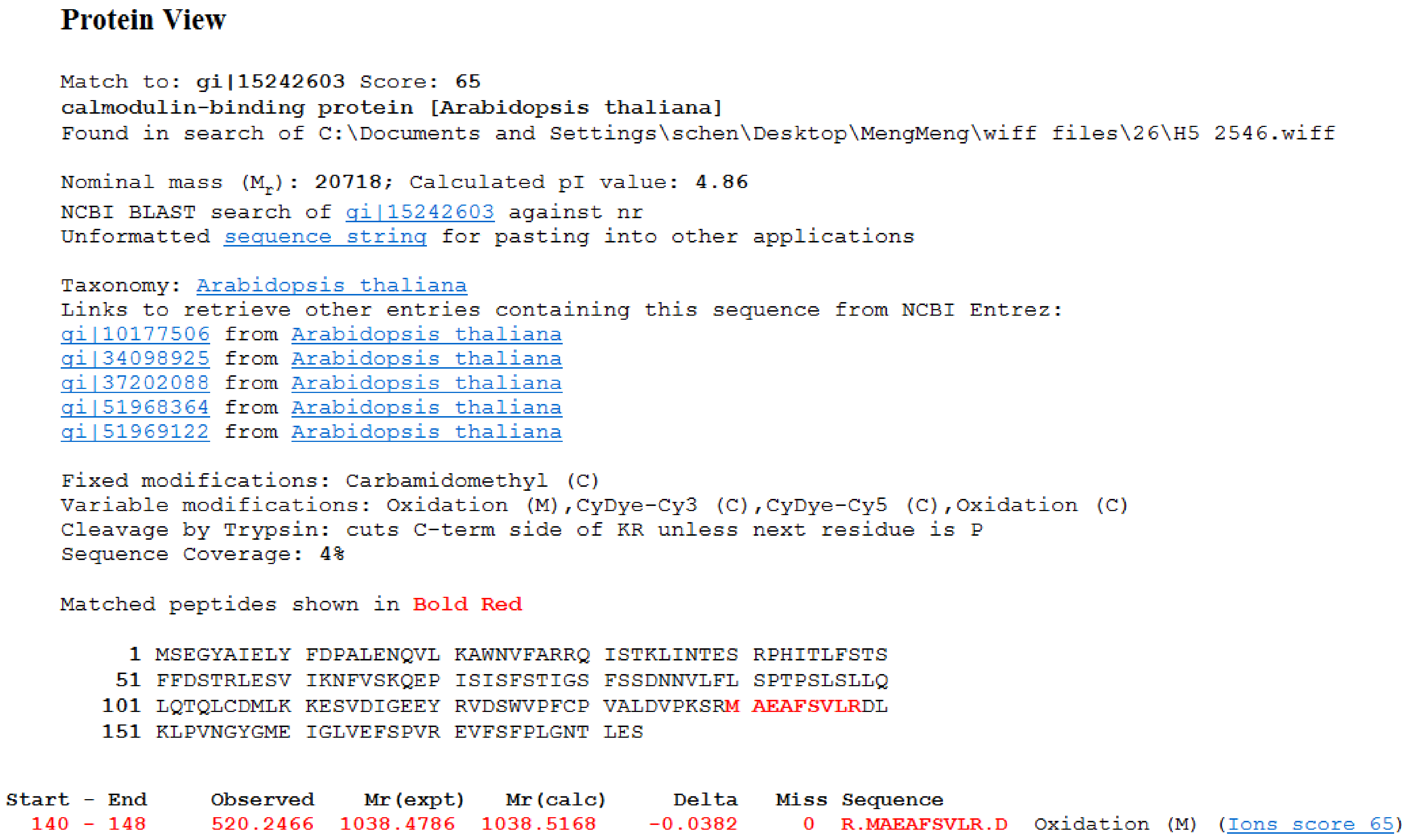
```
  1 MSTAEATREE NVYMAKLAEQ AERYEEMVEF MEKVAKTADV GELTVEERNL
 51 LSVAYKNVIG ARRASWRIIS SIEQKEESRG NEAYVASIKE YRTRIETELS
101 KICDGILKLL DSHLVPSATA AESKVFYLKM KGDYHRYLAE FKAGAERKEA
151 AENTLVAYKS AQDIALADLP TTHPIRLGLA LNFSVFYYEI LNSPDRACNL
201 AKQAFDEAIA ELDSLGEESY KDSTLIMQLL RDNLTLWTSD NAEEGGDEIK
251 EAASKPEGEG H
```

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss Sequence
   49 - 56      454.2645    906.5144   906.5174   -0.0030     0  R.NLLSVAYK.N   (Ions score 48)
```

MS/MS Fragmentation of **NLLSVAYK**
Found in **gi|100554**, 14-3-3 protein homolog - barley

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							8
2	228.1343	114.5708	211.1077	106.0575			L	**793.4818**	397.2445	776.4553	388.7313	775.4713	388.2393	7
3	341.2183	171.1128	**324.1918**	162.5995			L	**680.3978**	340.7025	663.3712	332.1892	662.3872	331.6972	6
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	**567.3137**	284.1605	550.2871	275.6472	549.3031	275.1552	5
5	527.3188	264.1630	510.2922	255.6497	509.3082	255.1577	V	**480.2817**	240.6445	463.2551	232.1312			4
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	A	**381.2132**	191.1103	364.1867	**182.5970**			3
7	761.4192	**381.2132**	744.3927	372.7000	743.4087	372.2080	Y	**310.1761**	155.5917	293.1496	147.0784			2
8							K	147.1128	74.0600	130.0863	65.5468			1

gi|15242603 Calmodulin-binding protein



Protein View

Match to: **gi|15242603** Score: **65**
calmodulin-binding protein [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\H5 2546.wiff

Nominal mass (M_r): **20718**; Calculated pI value: **4.86**
NCBI BLAST search of gi|15242603 against nr
Unformatted sequence string for pasting into other applications

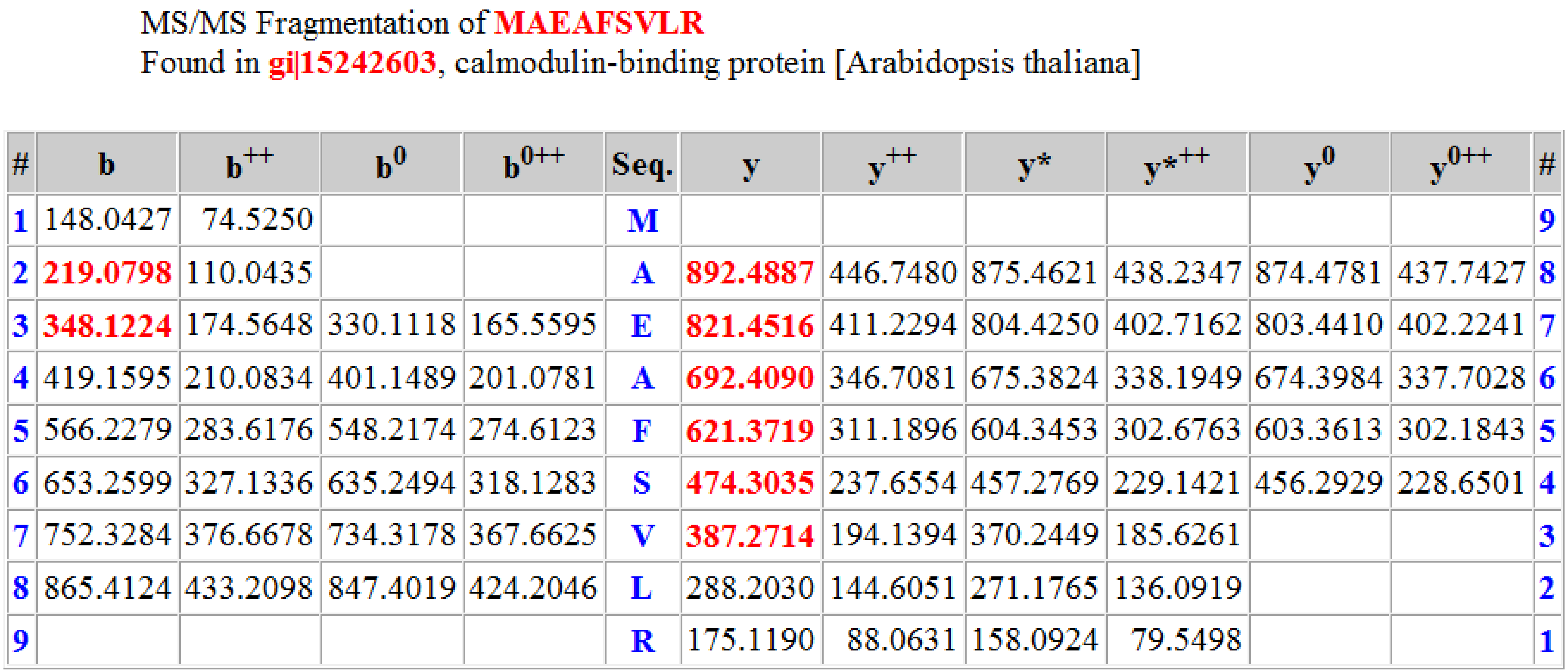
Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|10177506 from Arabidopsis thaliana
gi|34098925 from Arabidopsis thaliana
gi|37202088 from Arabidopsis thaliana
gi|51968364 from Arabidopsis thaliana
gi|51969122 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%

Matched peptides shown in **Bold Red**

```
  1 MSEGYAIELY FDPALENQVL KAWNVFARRQ ISTKLINTES RPHITLFSTS
 51 FFDSTRLESV IKNFVSKQEP ISISFSTIGS FSSDNNVLFL SPTPSLSLLQ
101 LQTQLCDMLK KESVDIGEEY RVDSWVPFCP VALDVPKSRM AEAFSVLRDL
151 KLPVNGYGME IGLVEFSPVR EVFSFPLGNT LES
```

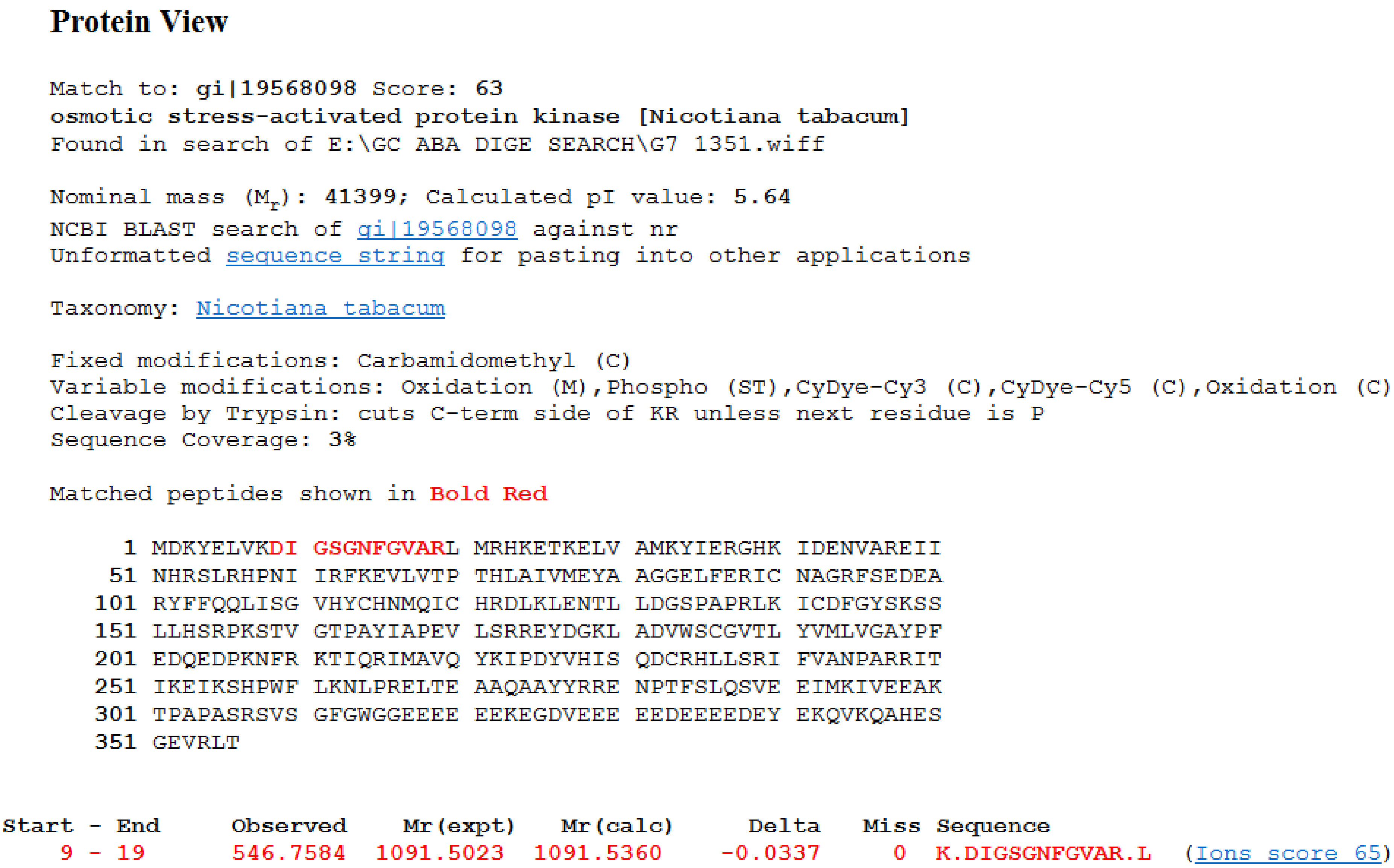
```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
 140 - 148      520.2466   1038.4786   1038.5168   -0.0382     0   R.MAEAFSVLR.D  Oxidation (M)  (Ions score 65)
```



MS/MS Fragmentation of **MAEAFSVLR**
Found in **gi|15242603**, calmodulin-binding protein [Arabidopsis thaliana]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250			**M**							**9**
2	**219.0798**	110.0435			**A**	**892.4887**	446.7480	875.4621	438.2347	874.4781	437.7427	**8**
3	**348.1224**	174.5648	330.1118	165.5595	**E**	**821.4516**	411.2294	804.4250	402.7162	803.4410	402.2241	**7**
4	419.1595	210.0834	401.1489	201.0781	**A**	**692.4090**	346.7081	675.3824	338.1949	674.3984	337.7028	**6**
5	566.2279	283.6176	548.2174	274.6123	**F**	**621.3719**	311.1896	604.3453	302.6763	603.3613	302.1843	**5**
6	653.2599	327.1336	635.2494	318.1283	**S**	**474.3035**	237.6554	457.2769	229.1421	456.2929	228.6501	**4**
7	752.3284	376.6678	734.3178	367.6625	**V**	**387.2714**	194.1394	370.2449	185.6261			**3**
8	865.4124	433.2098	847.4019	424.2046	**L**	288.2030	144.6051	271.1765	136.0919			**2**
9					**R**	175.1190	88.0631	158.0924	79.5498			**1**

gi|19568098 Osmotic stress-activated protein kinase (OST1)



Protein View

Match to: **gi|19568098** Score: **63**
osmotic stress-activated protein kinase [Nicotiana tabacum]
Found in search of E:\GC ABA DIGE SEARCH\G7 1351.wiff

Nominal mass (M_r): **41399**; Calculated pI value: **5.64**
NCBI BLAST search of gi|19568098 against nr
Unformatted sequence string for pasting into other applications

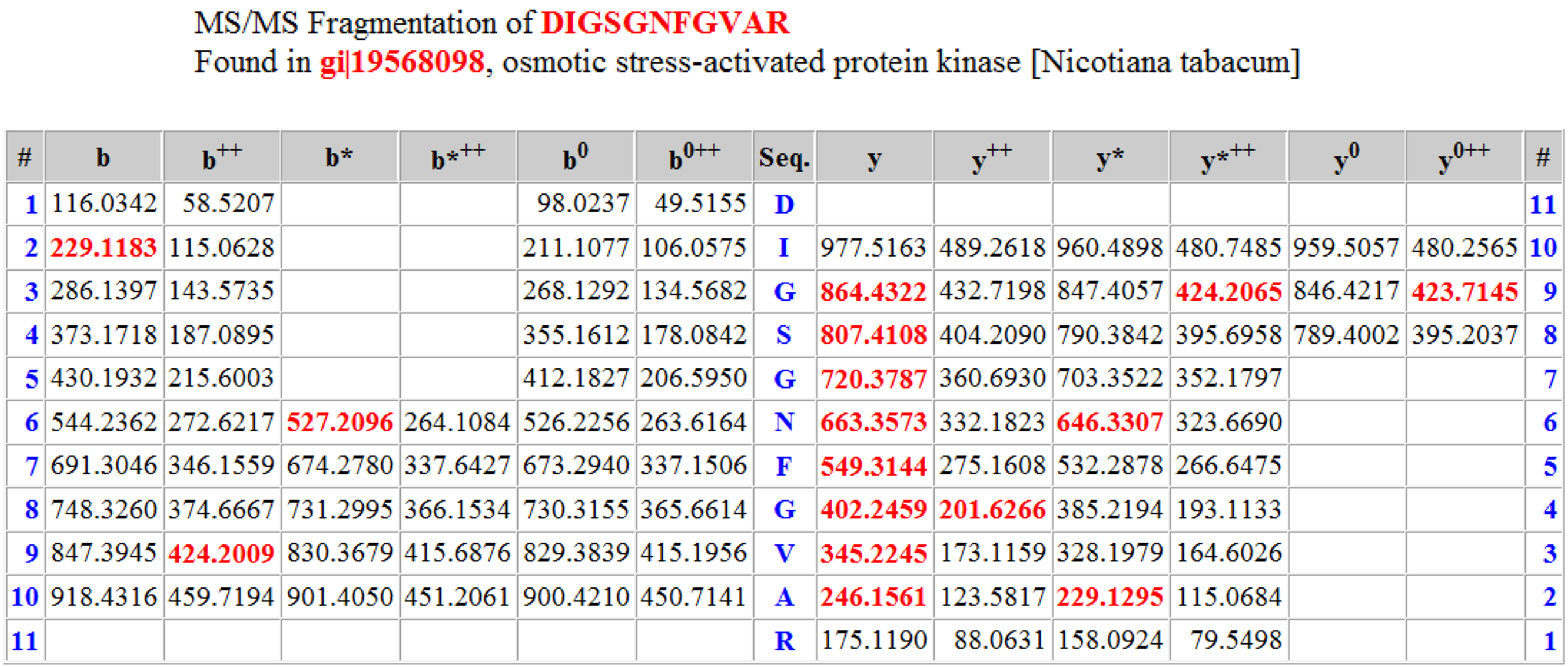
Taxonomy: Nicotiana tabacum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

```
  1 MDKYELVKDI GSGNFGVARL MRHKETKELV AMKYIERGHK IDENVAREII
 51 NHRSLRHPNI IRFKEVLVTP THLAIVMEYA AGGELFERIC NAGRFSEDEA
101 RYFFQQLISG VHYCHNMQIC HRDLKLENTL LDGSPAPRLK ICDFGYSKSS
151 LLHSRPKSTV GTPAYIAPEV LSRREYDGKL ADVWSCGVTL YVMLVGAYPF
201 EDQEDPKNFR KTIQRIMAVQ YKIPDYVHIS QDCRHLLSRI FVANPARRIT
251 IKEIKSHPWF LKNLPRELTE AAQAAYYRRE NPTFSLQSVE EIMKIVEEAK
301 TPAPASRSVS GFGWGGEEEE EEKEGDVEEE EEDEEEEDEY EKQVKQAHES
351 GEVRLT
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   9 - 19       546.7584   1091.5023   1091.5360    -0.0337     0   K.DIGSGNFGVAR.L    (Ions score 65)
```

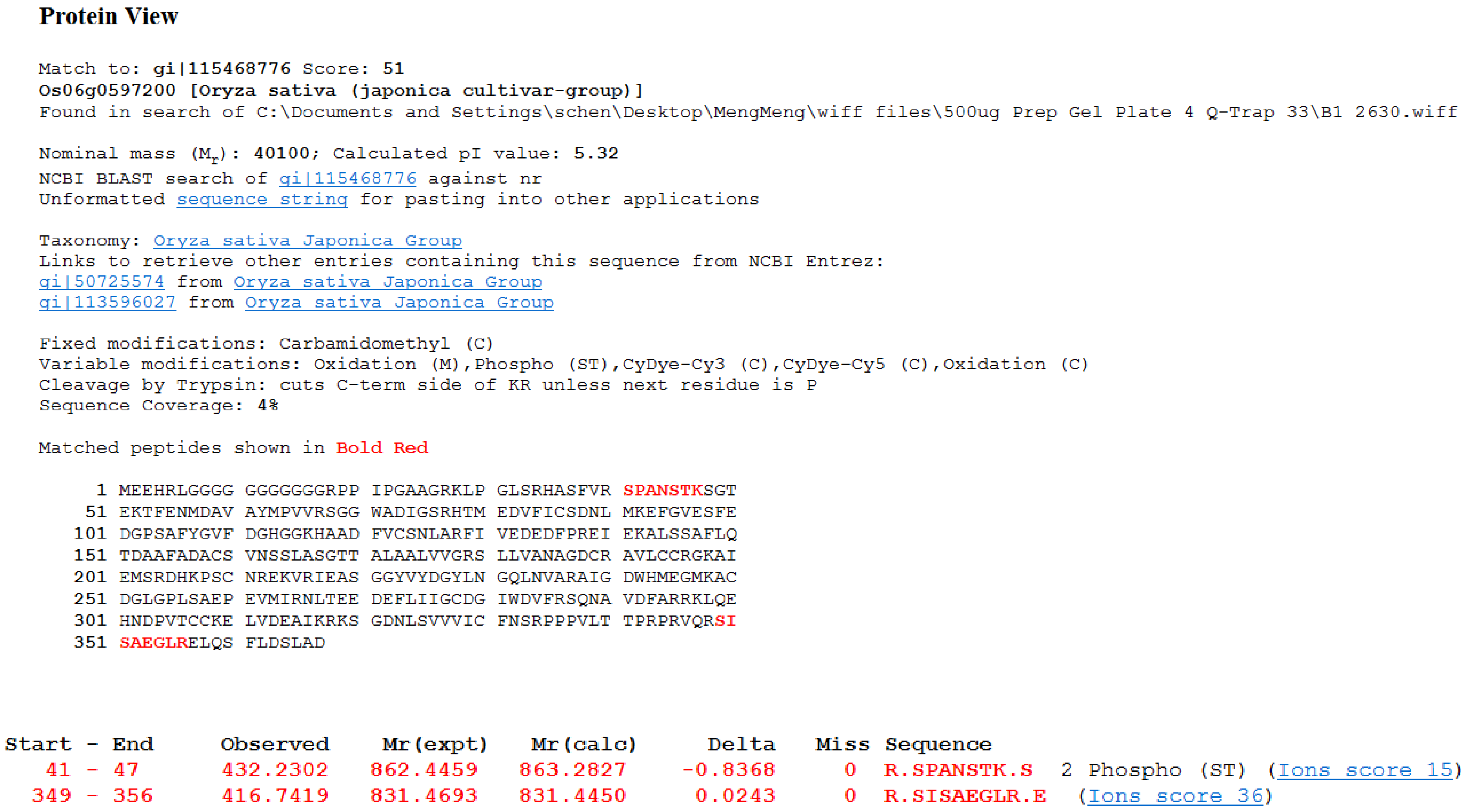


MS/MS Fragmentation of **DIGSGNFGVAR**

Found in **gi|19568098**, osmotic stress-activated protein kinase [Nicotiana tabacum]

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	**229.1183**	115.0628			211.1077	106.0575	I	977.5163	489.2618	960.4898	480.7485	959.5057	480.2565	10
3	286.1397	143.5735			268.1292	134.5682	G	**864.4322**	432.7198	847.4057	**424.2065**	846.4217	**423.7145**	9
4	373.1718	187.0895			355.1612	178.0842	S	**807.4108**	404.2090	790.3842	395.6958	789.4002	395.2037	8
5	430.1932	215.6003			412.1827	206.5950	G	**720.3787**	360.6930	703.3522	352.1797			7
6	544.2362	272.6217	**527.2096**	264.1084	526.2256	263.6164	N	**663.3573**	332.1823	**646.3307**	323.6690			6
7	691.3046	346.1559	674.2780	337.6427	673.2940	337.1506	F	**549.3144**	275.1608	532.2878	266.6475			5
8	748.3260	374.6667	731.2995	366.1534	730.3155	365.6614	G	**402.2459**	**201.6266**	385.2194	193.1133			4
9	847.3945	**424.2009**	830.3679	415.6876	829.3839	415.1956	V	**345.2245**	173.1159	328.1979	164.6026			3
10	918.4316	459.7194	901.4050	451.2061	900.4210	450.7141	A	**246.1561**	123.5817	**229.1295**	115.0684			2
11							R	175.1190	88.0631	158.0924	79.5498			1

gi|115468776 Os06g0597200, Serine/threonine phosphatases 2C (PP2C) family



Protein View

Match to: **gi|115468776** Score: **51**
Os06g0597200 [Oryza sativa (japonica cultivar-group)]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\500ug Prep Gel Plate 4 Q-Trap 33\B1 2630.wiff

Nominal mass (M_r): **40100**; Calculated pI value: **5.32**
NCBI BLAST search of gi|115468776 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|50725574 from Oryza sativa Japonica Group
gi|113596027 from Oryza sativa Japonica Group

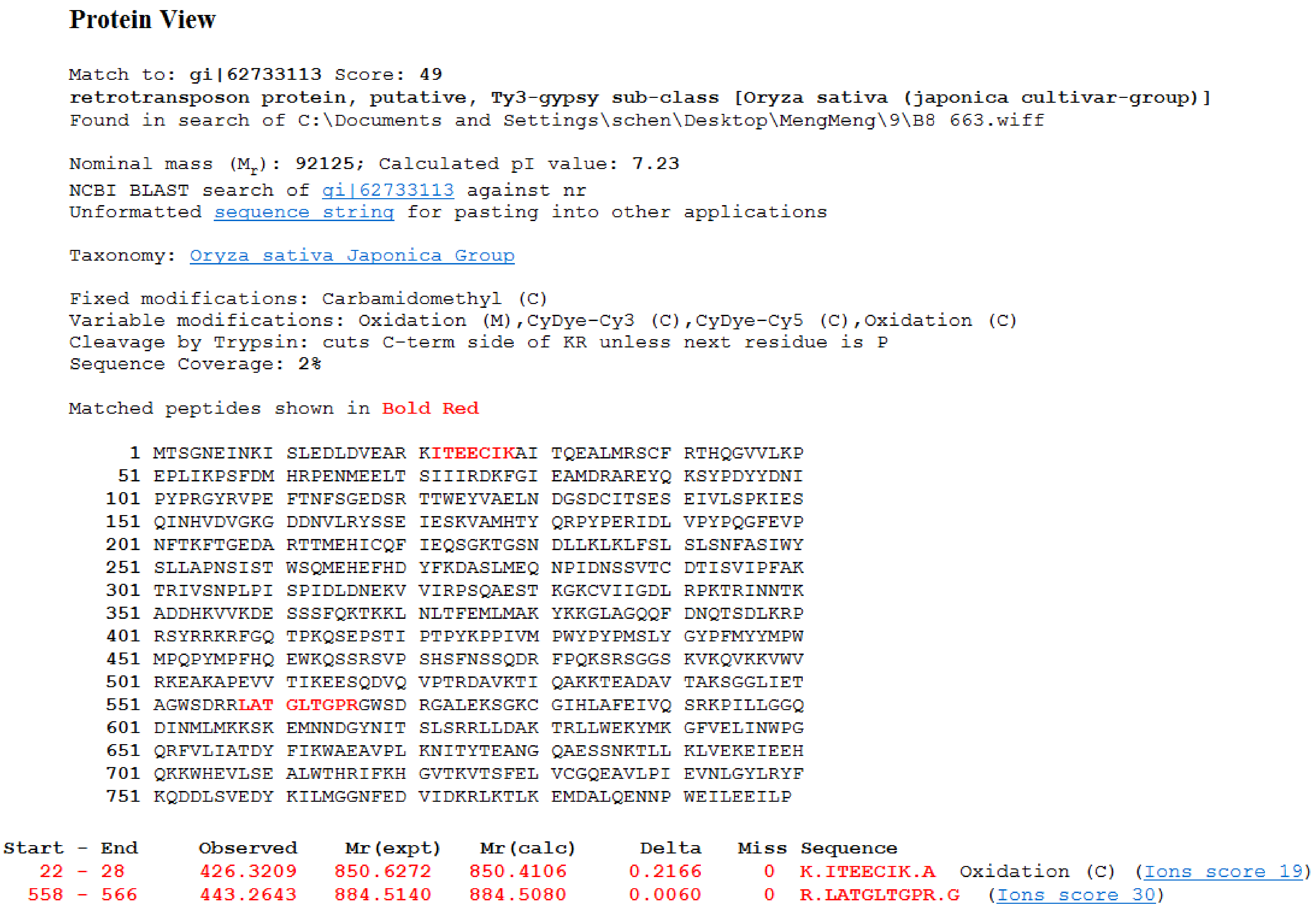
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**

```
    1 MEEHRLGGGG GGGGGGGRPP IPGAAGRKLP GLSRHASFVR SPANSTKSGT
   51 EKTFENMDAV AYMPVVRSGG WADIGSRHTM EDVFICSDNL MKEFGVESFE
  101 DGPSAFYGVF DGHGGKHAAD FVCSNLARFI VEDEDFPREI EKALSSAFLQ
  151 TDAAFADACS VNSSLASGTT ALAALVVGRS LLVANAGDCR AVLCCRGKAI
  201 EMSRDHKPSC NREKVRIEAS GGYVYDGYLN GQLNVARAIG DWHMEGMKAC
  251 DGLGPLSAEP EVMIRNLTEE DEFLIIGCDG IWDVFRSQNA VDFARRKLQE
  301 HNDPVTCCKE LVDEAIKRKS GDNLSVVVIC FNSRPPPVLT TPRPRVQRSI
  351 SAEGLRELQS FLDSLAD
```

```
Start - End      Observed    Mr(expt)    Mr(calc)      Delta    Miss  Sequence
   41 - 47       432.2302    862.4459    863.2827    -0.8368      0   R.SPANSTK.S   2 Phospho (ST)  (Ions score 15)
  349 - 356      416.7419    831.4693    831.4450     0.0243      0   R.SISAEGLR.E   (Ions score 36)
```

gi|62733113 Retrotransposon protein, putative



Protein View

Match to: gi|62733113 Score: 49
retrotransposon protein, putative, Ty3-gypsy sub-class [Oryza sativa (japonica cultivar-group)]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\B8 663.wiff

Nominal mass (M_r): **92125**; Calculated pI value: **7.23**
NCBI BLAST search of gi|62733113 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

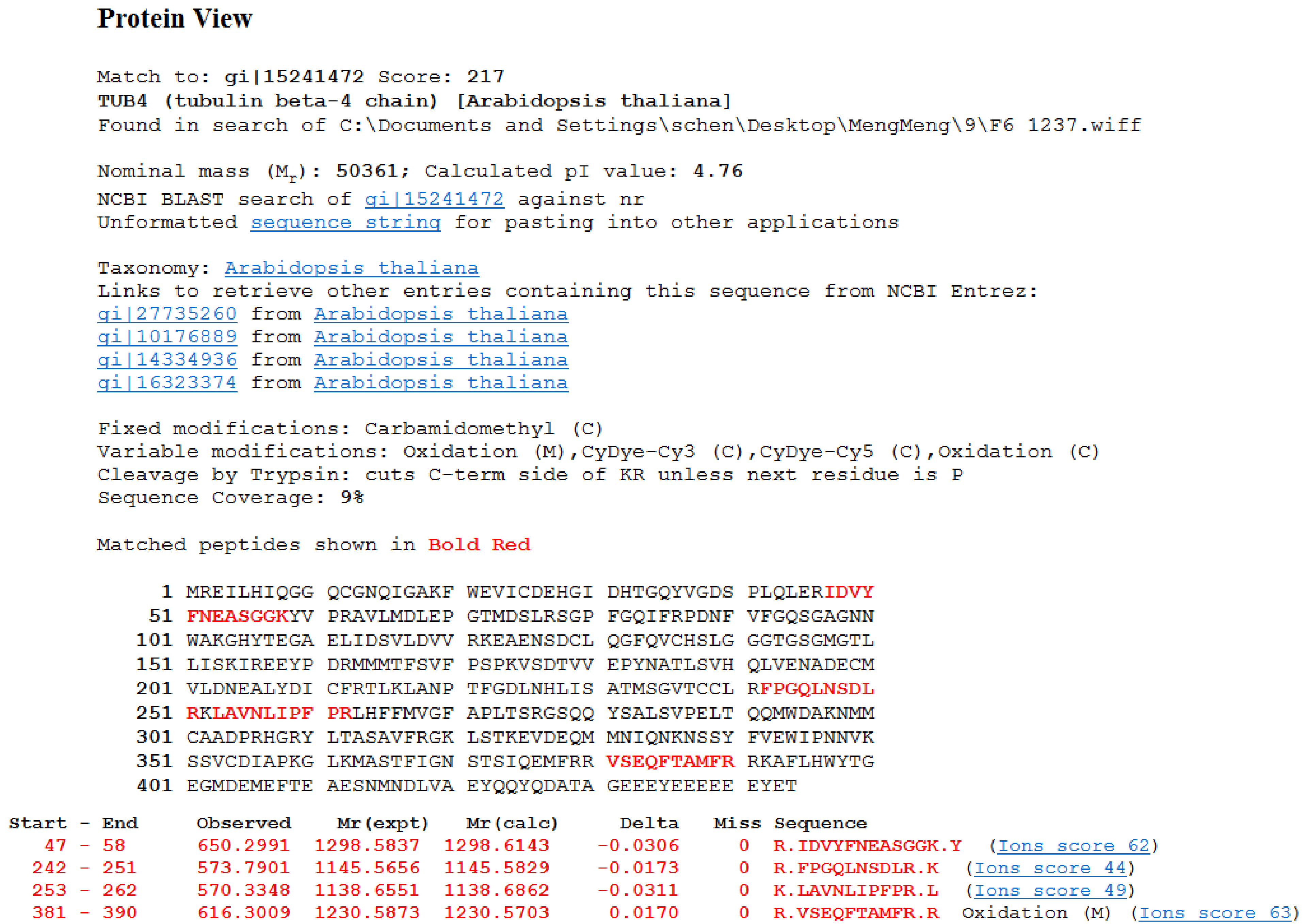
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 MTSGNEINKI SLEDLDVEAR KITEECIKAI TQEALMRSCF RTHQGVVLKP
 51 EPLIKPSFDM HRPENMEELT SIIIRDKFGI EAMDRAREYQ KSYPDYYDNI
101 PYPRGYRVPE FTNFSGEDSR TTWEYVAELN DGSDCITSES EIVLSPKIES
151 QINHVDVGKG DDNVLRYSSE IESKVAMHTY QRPYPERIDL VPYPQGFEVP
201 NFTKFTGEDA RTTMEHICQF IEQSGKTGSN DLLKLKLFSL SLSNFASIWY
251 SLLAPNSIST WSQMEHEFHD YFKDASLMEQ NPIDNSSVTC DTISVIPFAK
301 TRIVSNPLPI SPIDLDNEKV VIRPSQAEST KGKCVIIGDL RPKTRINNTK
351 ADDHKVVKDE SSSFQKTKKL NLTFEMLMAK YKKGLAGQQF DNQTSDLKRP
401 RSYRRKRFGQ TPKQSEPSTI PTPYKPPIVM PWYPYPMSLY GYPFMYYMPW
451 MPQPYMPFHQ EWKQSSRSVP SHSFNSSQDR FPQKSRSGGS KVKQVKKVWV
501 RKEAKAPEVV TIKEESQDVQ VPTRDAVKTI QAKKTEADAV TAKSGGLIET
551 AGWSDRRLAT GLTGPRGWSD RGALEKSGKC GIHLAFEIVQ SRKPILLGGQ
601 DINMLMKKSK EMNNDGYNIT SLSRRLLDAK TRLLWEKYMK GFVELINWPG
651 QRFVLIATDY FIKWAEAVPL KNITYTEANG QAESSNKTLL KLVEKEIEEH
701 QKKWHEVLSE ALWTHRIFKH GVTKVTSFEL VCGQEAVLPI EVNLGYLRYF
751 KQDDLSVEDY KILMGGNFED VIDKRLKTLK EMDALQENNP WEILEEILP
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   22 - 28      426.3209    850.6272    850.4106     0.2166     0  K.ITEECIK.A  Oxidation (C) (Ions score 19)
  558 - 566     443.2643    884.5140    884.5080     0.0060     0  R.LATGLTGPR.G  (Ions score 30)
```

gi|15241472 Tubulin beta-4 chain(TUB4)



Protein View

```
Match to: gi|15241472 Score: 217
TUB4 (tubulin beta-4 chain) [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\9\F6 1237.wiff

Nominal mass (Mr): 50361; Calculated pI value: 4.76
NCBI BLAST search of gi|15241472 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|27735260 from Arabidopsis thaliana
gi|10176889 from Arabidopsis thaliana
gi|14334936 from Arabidopsis thaliana
gi|16323374 from Arabidopsis thaliana

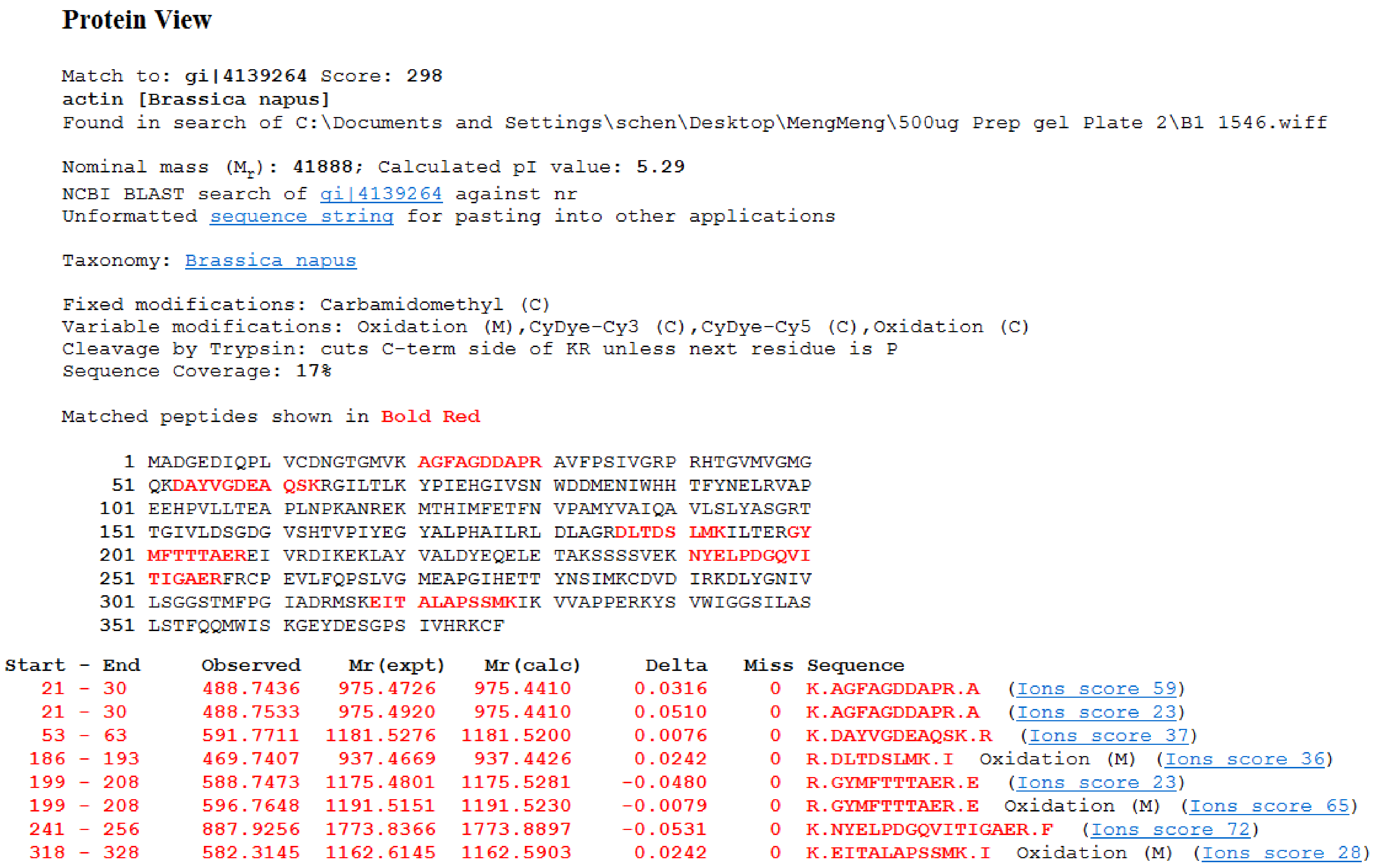
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

Matched peptides shown in Bold Red

      1 MREILHIQGG QCGNQIGAKF WEVICDEHGI DHTGQYVGDS PLQLERIDVY
     51 FNEASGGKYV PRAVLMDLEP GTMDSLRSGP FGQIFRPDNF VFGQSGAGNN
    101 WAKGHYTEGA ELIDSVLDVV RKEAENSDCL QGFQVCHSLG GGTGSGMGTL
    151 LISKIREEYP DRMMMTFSVF PSPKVSDTVV EPYNATLSVH QLVENADECM
    201 VLDNEALYDI CFRTLKLANP TFGDLNHLIS ATMSGVTCCL RFPGQLNSDL
    251 RKLAVNLIPF PRLHFFMVGF APLTSRGSQQ YSALSVPELT QQMWDAKNMM
    301 CAADPRHGRY LTASAVFRGK LSTKEVDEQM MNIQNKNSSY FVEWIPNNVK
    351 SSVCDIAPKG LKMASTFIGN STSIQEMFRR VSEQFTAMFR RKAFLHWYTG
    401 EGMDEMEFTE AESNMNDLVA EYQQYQDATA GEEEYEEEEE EYET

Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   47 - 58     650.2991  1298.5837  1298.6143   -0.0306     0 R.IDVYFNEASGGK.Y   (Ions score 62)
  242 - 251    573.7901  1145.5656  1145.5829   -0.0173     0 R.FPGQLNSDLR.K   (Ions score 44)
  253 - 262    570.3348  1138.6551  1138.6862   -0.0311     0 K.LAVNLIPFPR.L   (Ions score 49)
  381 - 390    616.3009  1230.5873  1230.5703    0.0170     0 R.VSEQFTAMFR.R  Oxidation (M)  (Ions score 63)
```

gi|4139264 Actin



Protein View

Match to: **gi|4139264** Score: **298**
actin [Brassica napus]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\B1 1546.wiff

Nominal mass (M_r): **41888**; Calculated pI value: **5.29**
NCBI BLAST search of gi|4139264 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

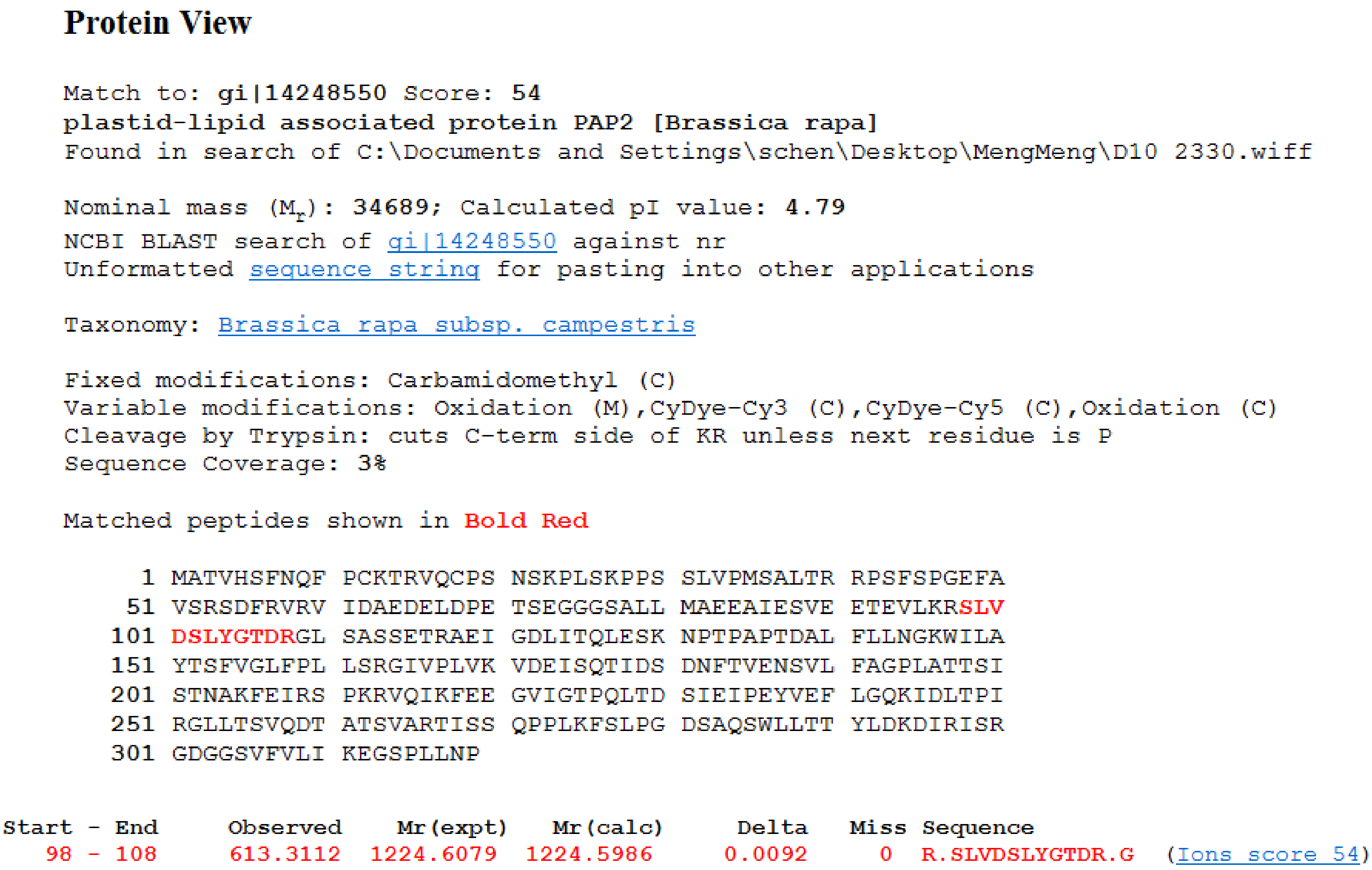
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
      1 MADGEDIQPL VCDNGTGMVK AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG
     51 QKDAYVGDEA QSKRGILTLK YPIEHGIVSN WDDMENIWHH TFYNELRVAP
    101 EEHPVLLTEA PLNPKANREK MTHIMFETFN VPAMYVAIQA VLSLYASGRT
    151 TGIVLDSGDG VSHTVPIYEG YALPHAILRL DLAGRDLTDS LMKILTERGY
    201 MFTTTAEREI VRDIKEKLAY VALDYEQELE TAKSSSSVEK NYELPDGQVI
    251 TIGAERFRCP EVLFQPSLVG MEAPGIHETT YNSIMKCDVD IRKDLYGNIV
    301 LSGGSTMFPG IADRMSKEIT ALAPSSMKIK VVAPPERKYS VWIGGSILAS
    351 LSTFQQMWIS KGEYDESGPS IVHRKCF
```

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   21 - 30     488.7436   975.4726   975.4410   0.0316     0  K.AGFAGDDAPR.A  (Ions score 59)
   21 - 30     488.7533   975.4920   975.4410   0.0510     0  K.AGFAGDDAPR.A  (Ions score 23)
   53 - 63     591.7711  1181.5276  1181.5200   0.0076     0  K.DAYVGDEAQSK.R  (Ions score 37)
  186 - 193    469.7407   937.4669   937.4426   0.0242     0  R.DLTDSLMK.I  Oxidation (M)  (Ions score 36)
  199 - 208    588.7473  1175.4801  1175.5281  -0.0480     0  R.GYMFTTTAER.E  (Ions score 23)
  199 - 208    596.7648  1191.5151  1191.5230  -0.0079     0  R.GYMFTTTAER.E  Oxidation (M)  (Ions score 65)
  241 - 256    887.9256  1773.8366  1773.8897  -0.0531     0  K.NYELPDGQVITIGAER.F  (Ions score 72)
  318 - 328    582.3145  1162.6145  1162.5903   0.0242     0  K.EITALAPSSMK.I  Oxidation (M)  (Ions score 28)
```

gi|14248550 Plastid-lipid associated protein PAP2



Protein View

Match to: **gi|14248550** Score: **54**
plastid-lipid associated protein PAP2 [Brassica rapa]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\D10 2330.wiff

Nominal mass (M_r): **34689**; Calculated pI value: **4.79**
NCBI BLAST search of gi|14248550 against nr
Unformatted sequence string for pasting into other applications

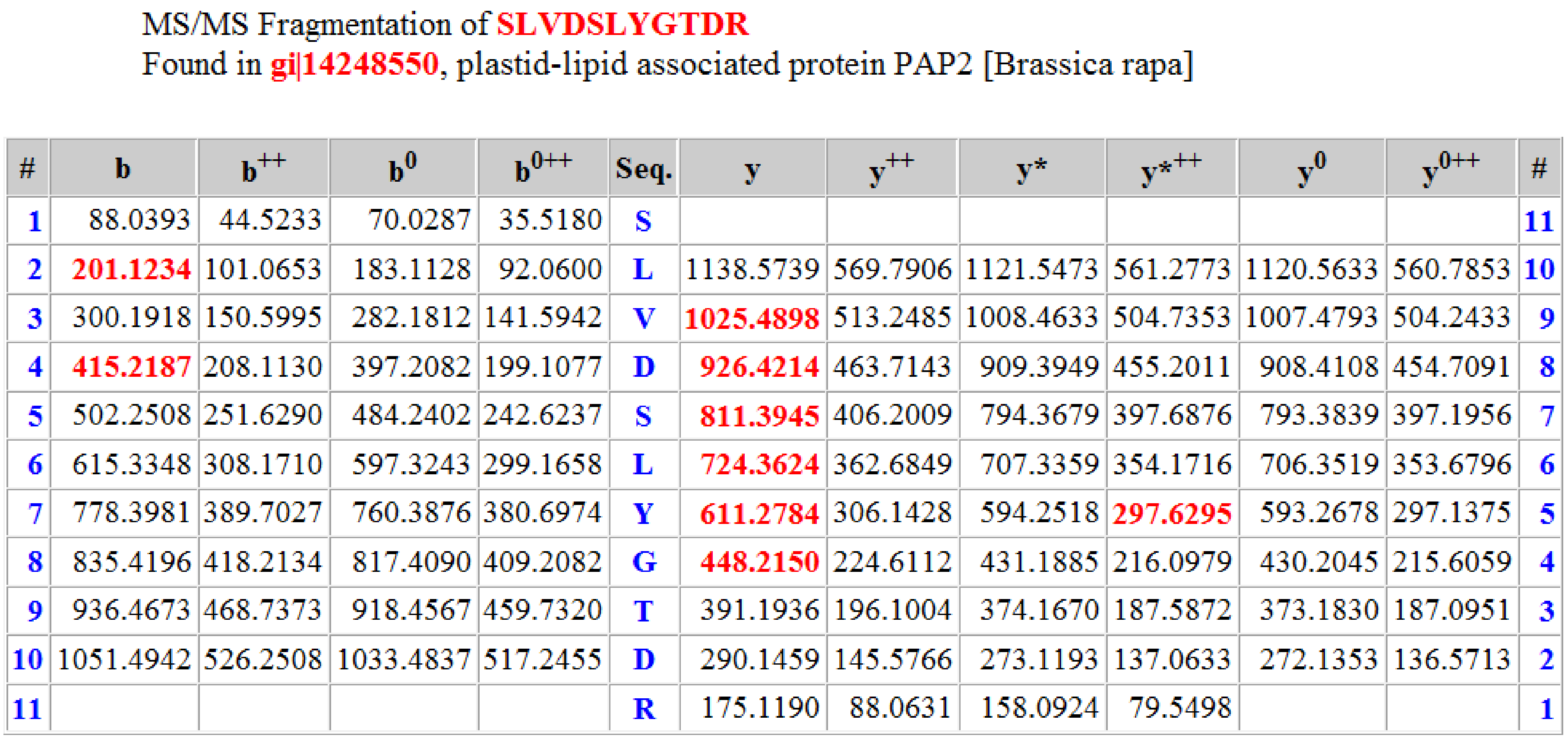
Taxonomy: Brassica rapa subsp. campestris

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

1 MATVHSFNQF PCKTRVQCPS NSKPLSKPPS SLVPMSALTR RPSFSPGEFA
51 VSRSDFRVRV IDAEDELDPE TSEGGGSALL MAEEAIESVE ETEVLKR**SLV**
101 **DSLYGTDR**GL SASSETRAEI GDLITQLESK NPTPAPTDAL FLLNGKWILA
151 YTSFVGLFPL LSRGIVPLVK VDEISQTIDS DNFTVENSVL FAGPLATTSI
201 STNAKFEIRS PKRVQIKFEE GVIGTPQLTD SIEIPEYVEF LGQKIDLTPI
251 RGLLTSVQDT ATSVARTISS QPPLKFSLPG DSAQSWLLTT YLDKDIRISR
301 GDGGSVFVLI KEGSPLLNP

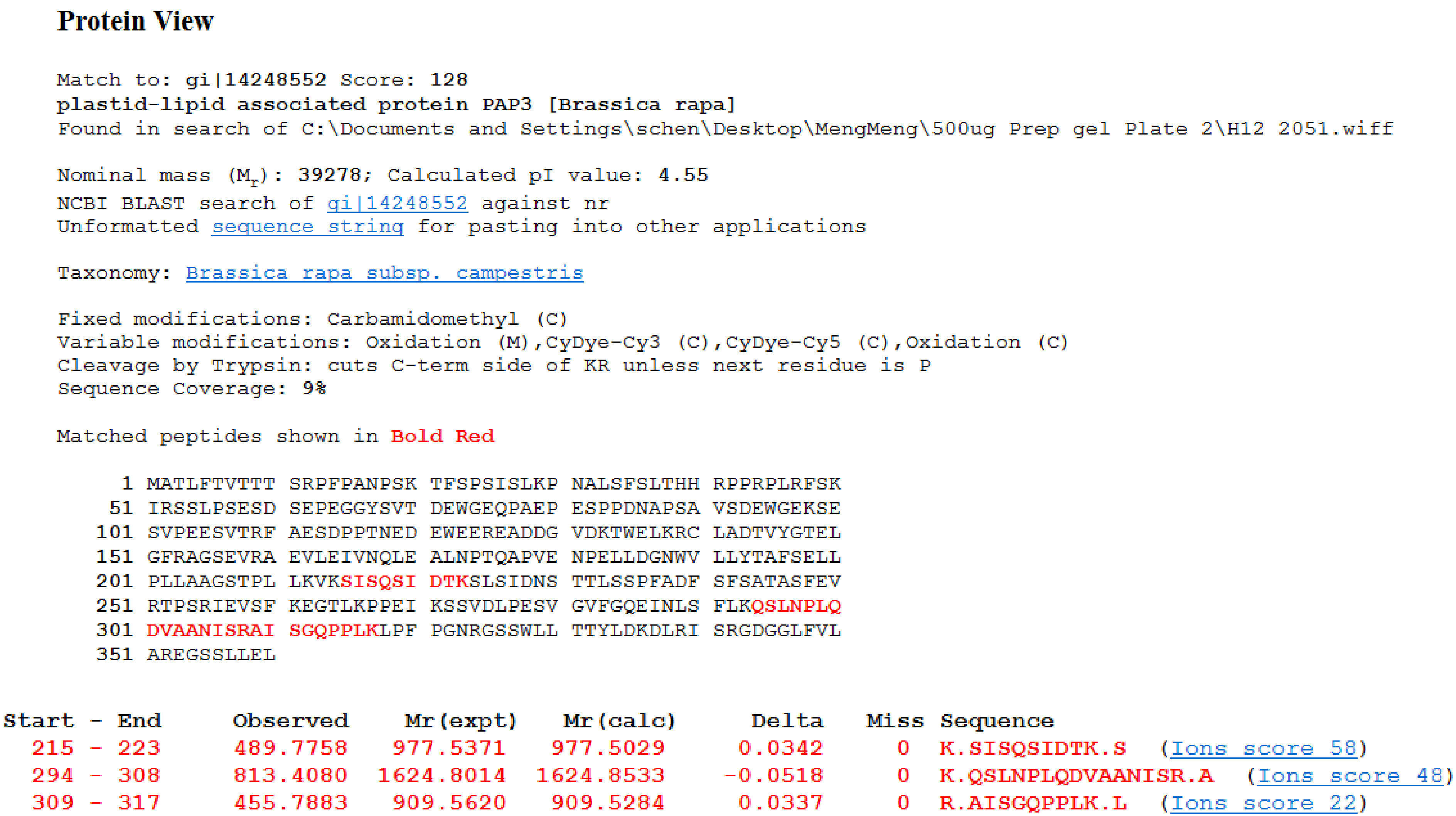
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
98 - 108	613.3112	1224.6079	1224.5986	0.0092	0	R.SLVDSLYGTDR.G	(Ions score 54)



MS/MS Fragmentation of **SLVDSLYGTDR**
Found in **gi|14248550**, plastid-lipid associated protein PAP2 [Brassica rapa]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	S							11
2	**201.1234**	101.0653	183.1128	92.0600	L	1138.5739	569.7906	1121.5473	561.2773	1120.5633	560.7853	10
3	300.1918	150.5995	282.1812	141.5942	V	**1025.4898**	513.2485	1008.4633	504.7353	1007.4793	504.2433	9
4	**415.2187**	208.1130	397.2082	199.1077	D	**926.4214**	463.7143	909.3949	455.2011	908.4108	454.7091	8
5	502.2508	251.6290	484.2402	242.6237	S	**811.3945**	406.2009	794.3679	397.6876	793.3839	397.1956	7
6	615.3348	308.1710	597.3243	299.1658	L	**724.3624**	362.6849	707.3359	354.1716	706.3519	353.6796	6
7	778.3981	389.7027	760.3876	380.6974	Y	**611.2784**	306.1428	594.2518	**297.6295**	593.2678	297.1375	5
8	835.4196	418.2134	817.4090	409.2082	G	**448.2150**	224.6112	431.1885	216.0979	430.2045	215.6059	4
9	936.4673	468.7373	918.4567	459.7320	T	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
10	1051.4942	526.2508	1033.4837	517.2455	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11					R	175.1190	88.0631	158.0924	79.5498			1

gi|14248552 Plastid-lipid associated protein PAP3



Protein View

Match to: **gi|14248552** Score: **128**
plastid-lipid associated protein PAP3 [Brassica rapa]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\H12 2051.wiff

Nominal mass (M_r): **39278**; Calculated pI value: **4.55**
NCBI BLAST search of gi|14248552 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

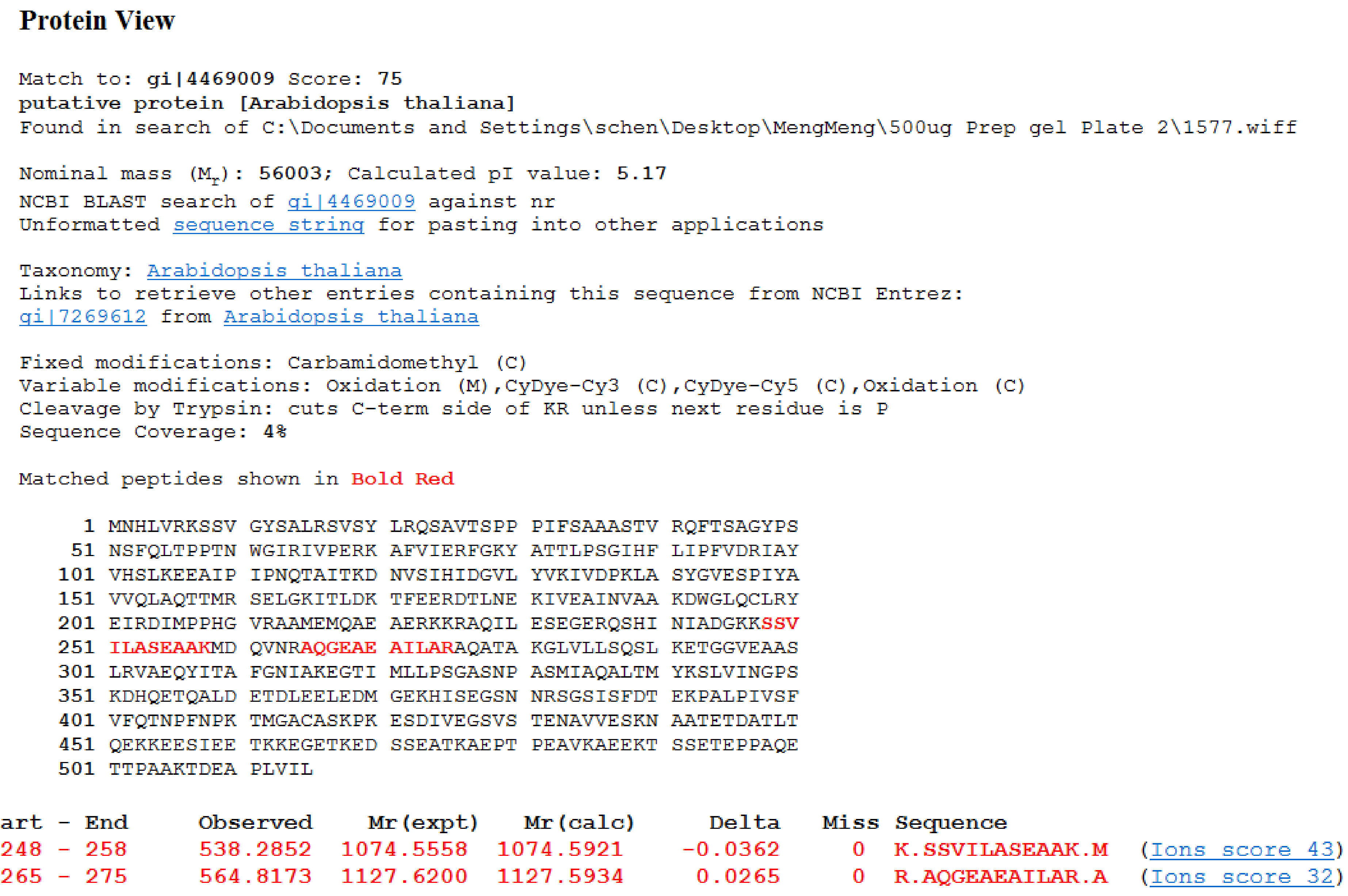
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```
  1 MATLFTVTTT SRPFPANPSK TFSPSISLKP NALSFSLTHH RPPRPLRFSK
 51 IRSSLPSESD SEPEGGYSVT DEWGEQPAEP ESPPDNAPSA VSDEWGEKSE
101 SVPEESVTRF AESDPPTNED EWEEREADDG VDKTWELKRC LADTVYGTEL
151 GFRAGSEVRA EVLEIVNQLE ALNPTQAPVE NPELLDGNWV LLYTAFSELL
201 PLLAAGSTPL LKVKSISQSI DTKSLSIDNS TTLSSPFADF SFSATASFEV
251 RTPSRIEVSF KEGTLKPPEI KSSVDLPESV GVFGQEINLS FLKQSLNPLQ
301 DVAANISRAI SGQPPLKLPF PGNRGSSWLL TTYLDKDLRI SRGDGGLFVL
351 AREGSSLLEL
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
215 - 223	489.7758	977.5371	977.5029	0.0342	0	K.SISQSIDTK.S	(Ions score 58)
294 - 308	813.4080	1624.8014	1624.8533	-0.0518	0	K.QSLNPLQDVAANISR.A	(Ions score 48)
309 - 317	455.7883	909.5620	909.5284	0.0337	0	R.AISGQPPLK.L	(Ions score 22)

gi|4469009 Putative protein, containing band 7 stomatin domain



Protein View

Match to: **gi|4469009** Score: **75**
putative protein [Arabidopsis thaliana]
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\500ug Prep gel Plate 2\1577.wiff

Nominal mass (M_r): **56003**; Calculated pI value: **5.17**
NCBI BLAST search of gi|4469009 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|7269612 from Arabidopsis thaliana

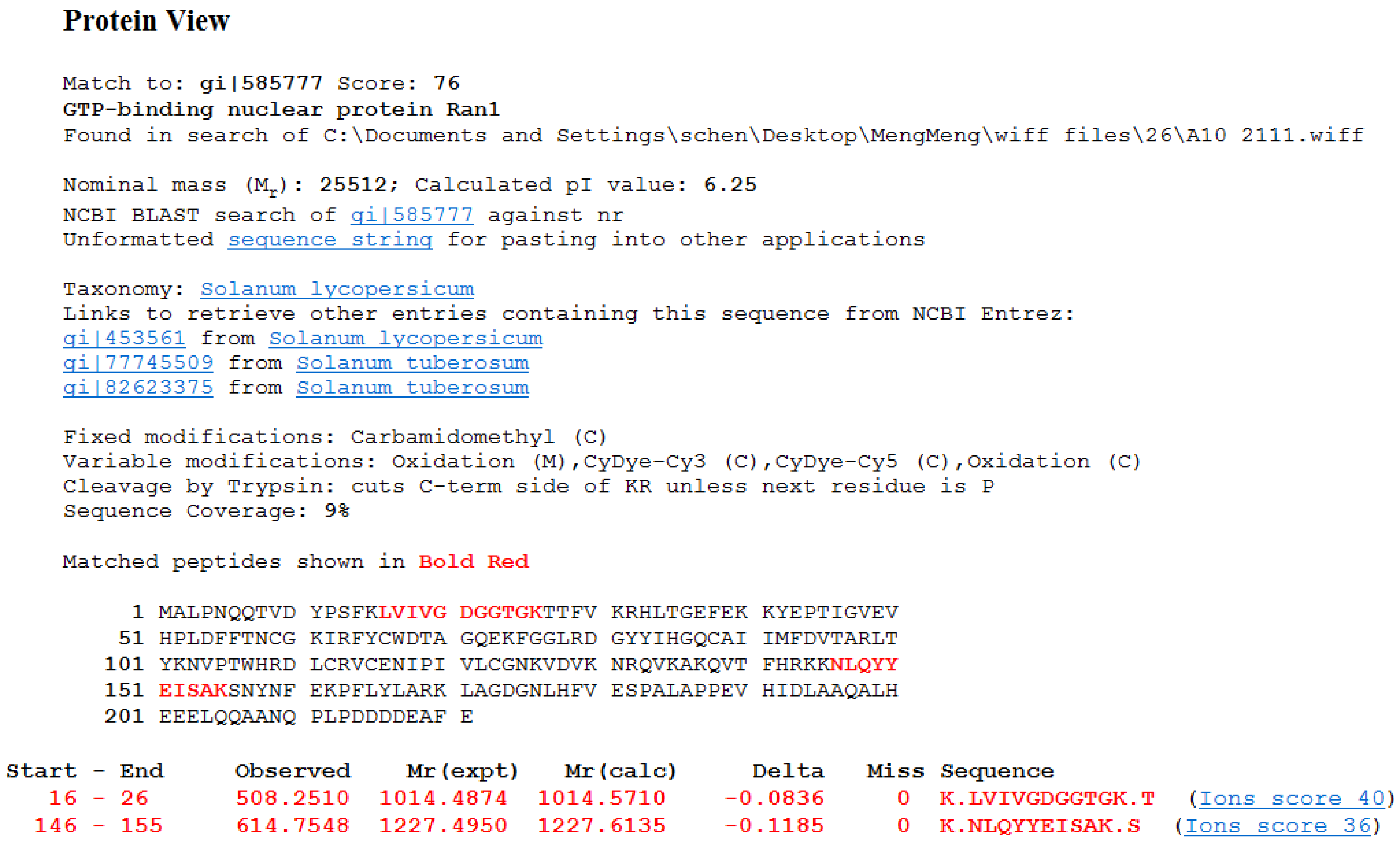
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**

```
  1 MNHLVRKSSV GYSALRSVSY LRQSAVTSPP PIFSAAASTV RQFTSAGYPS
 51 NSFQLTPPTN WGIRIVPERK AFVIERFGKY ATTLPSGIHF LIPFVDRIAY
101 VHSLKEEAIP IPNQTAITKD NVSIHIDGVL YVKIVDPKLA SYGVESPIYA
151 VVQLAQTTMR SELGKITLDK TFEERDTLNE KIVEAINVAA KDWGLQCLRY
201 EIRDIMPPHG VRAAMEMQAE AERKKRAQIL ESEGERQSHI NIADGKKSSV
251 ILASEAAKMD QVNRAQGEAE AILARAQATA KGLVLLSQSL KETGGVEAAS
301 LRVAEQYITA FGNIAKEGTI MLLPSGASNP ASMIAQALTM YKSLVINGPS
351 KDHQETQALD ETDLEELEDM GEKHISEGSN NRSGSISFDT EKPALPIVSF
401 VFQTNPFNPK TMGACASKPK ESDIVEGSVS TENAVVESKN AATETDATLT
451 QEKKEESIEE TKKEGETKED SSEATKAEPT PEAVKAEEKT SSETEPPAQE
501 TTPAAKTDEA PLVIL
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  248 - 258     538.2852  1074.5558  1074.5921   -0.0362      0  K.SSVILASEAAK.M   (Ions score 43)
  265 - 275     564.8173  1127.6200  1127.5934    0.0265      0  R.AQGEAEAILAR.A   (Ions score 32)
```

gi|585777 GTP-binding nuclear protein RAN1



Protein View

Match to: **gi|585777** Score: **76**
GTP-binding nuclear protein Ran1
Found in search of C:\Documents and Settings\schen\Desktop\MengMeng\wiff files\26\A10 2111.wiff

Nominal mass (M_r): **25512**; Calculated pI value: **6.25**
NCBI BLAST search of gi|585777 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Solanum lycopersicum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|453561 from Solanum lycopersicum
gi|77745509 from Solanum tuberosum
gi|82623375 from Solanum tuberosum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),CyDye-Cy3 (C),CyDye-Cy5 (C),Oxidation (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

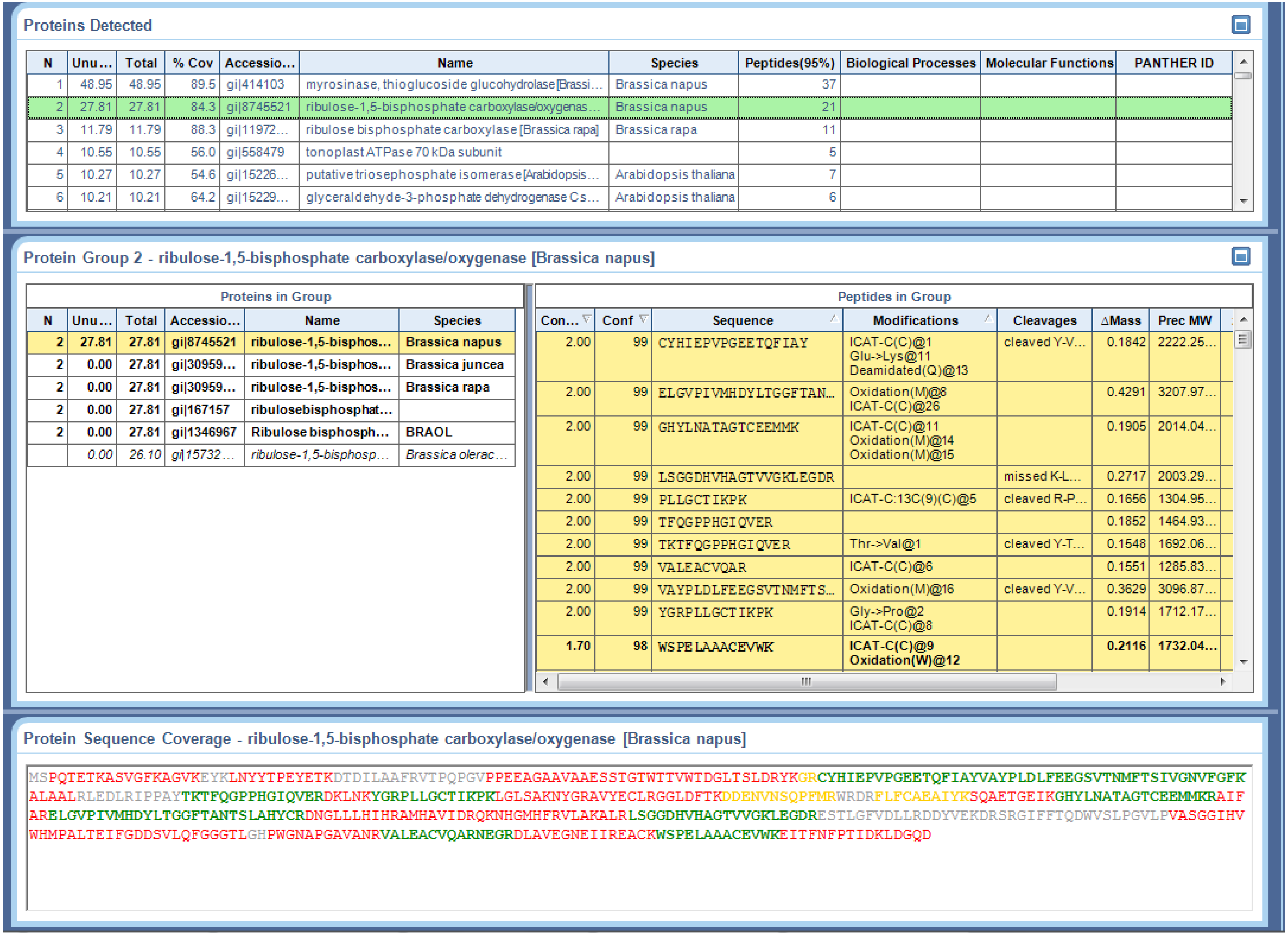
```
  1 MALPNQQTVD YPSFKLVIVG DGGTGKTTFV KRHLTGEFEK KYEPTIGVEV
 51 HPLDFFTNCG KIRFYCWDTA GQEKFGGLRD GYYIHGQCAI IMFDVTARLT
101 YKNVPTWHRD LCRVCENIPI VLCGNKVDVK NRQVKAKQVT FHRKKNLQYY
151 EISAKSNYNF EKPFLYLARK LAGDGNLHFV ESPALAPPEV HIDLAAQALH
201 EEELQQAANQ PLPDDDDEAF E
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  16 - 26      508.2510  1014.4874  1014.5710   -0.0836     0  K.LVIVGDGGTGK.T   (Ions score 40)
 146 - 155     614.7548  1227.4950  1227.6135   -0.1185     0  K.NLQYYEISAK.S   (Ions score 36)
```

Figure S5

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to ABA treatment in guard cells by ICAT.

gi|8745521 Ribulose-1,5-bisphosphate carboxylase / oxygenase large subunit



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
1	48.95	48.95	89.5	gi|414103	myrosinase, thioglucoside glucohydrolase [Brassi...	Brassica napus	37			
2	27.81	27.81	84.3	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas...	Brassica napus	21			
3	11.79	11.79	88.3	gi|11972...	ribulose bisphosphate carboxylase [Brassica rapa]	Brassica rapa	11			
4	10.55	10.55	56.0	gi|558479	tonoplast ATPase 70 kDa subunit		5			
5	10.27	10.27	54.6	gi|15226...	putative triosephosphate isomerase [Arabidopsis...	Arabidopsis thaliana	7			
6	10.21	10.21	64.2	gi|15229...	glyceraldehyde-3-phosphate dehydrogenase Cs...	Arabidopsis thaliana	6			

Protein Group 2 - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

Proteins in Group

N	Unu...	Total	Accessio...	Name	Species
2	**27.81**	**27.81**	**gi|8745521**	**ribulose-1,5-bisphos...**	**Brassica napus**
2	**0.00**	**27.81**	**gi|30959...**	**ribulose-1,5-bisphos...**	**Brassica juncea**
2	**0.00**	**27.81**	**gi|30959...**	**ribulose-1,5-bisphos...**	**Brassica rapa**
2	**0.00**	**27.81**	**gi|167157**	**ribulosebisphosphat...**	
2	**0.00**	**27.81**	**gi|1346967**	**Ribulose bisphosph...**	**BRAOL**
	0.00	*26.10*	*gi|15732...*	*ribulose-1,5-bisphosp...*	*Brassica olerac...*

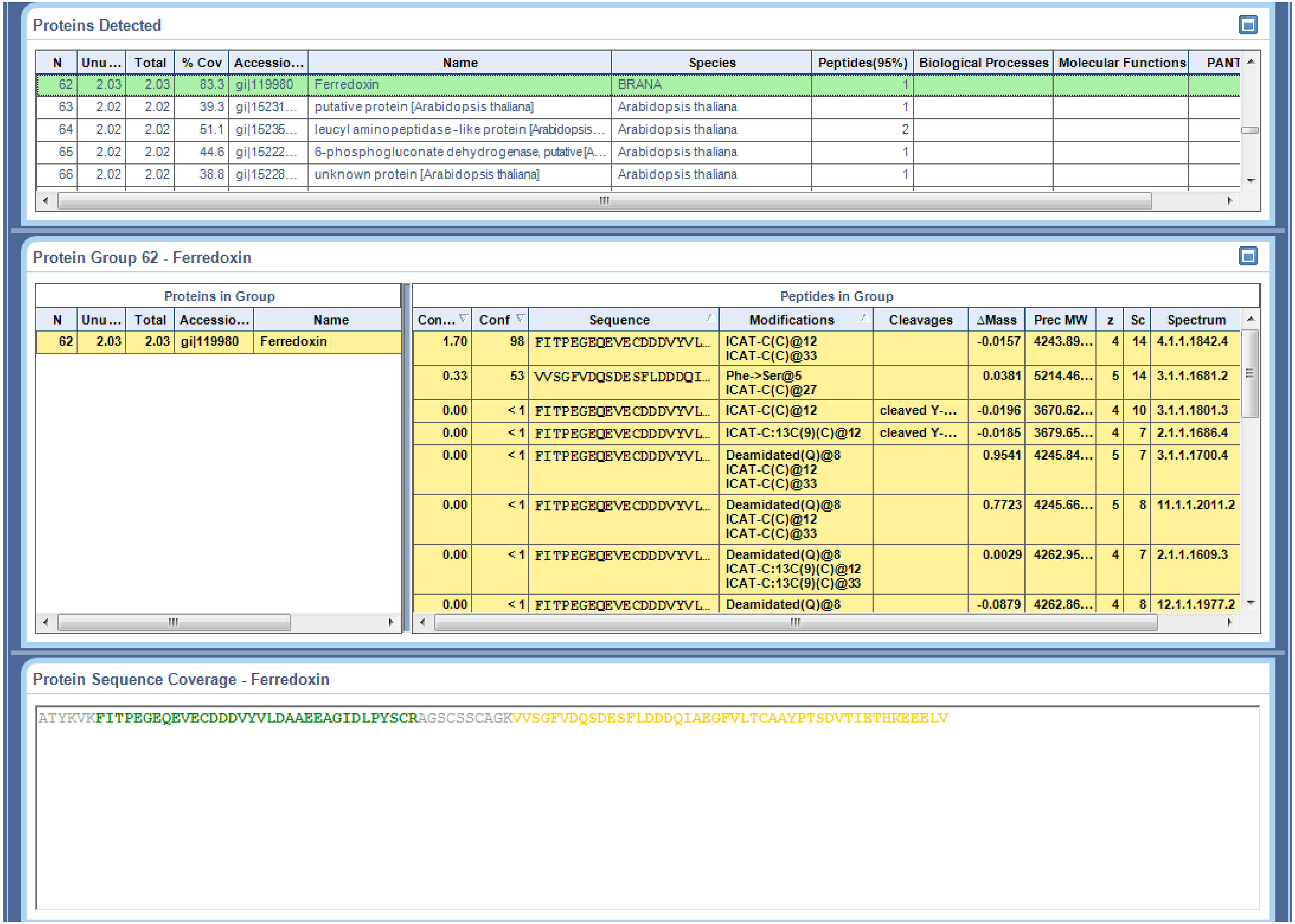
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	CYHIEPVPGEETQFIAY	ICAT-C(C)@1 Glu->Lys@11 Deamidated(Q)@13	cleaved Y-V...	0.1842	2222.25...
2.00	99	ELGVPIVMHDYLTGGFTAN...	Oxidation(M)@8 ICAT-C(C)@26		0.4291	3207.97...
2.00	99	GHYLNATAGTCEEMMK	ICAT-C(C)@11 Oxidation(M)@14 Oxidation(M)@15		0.1905	2014.04...
2.00	99	LSGGDHVHAGTVVGKLEGDR		missed K-L...	0.2717	2003.29...
2.00	99	PLLGCTIKPK	ICAT-C:13C(9)(C)@5	cleaved R-P...	0.1656	1304.95...
2.00	99	TFQGPPHGIQVER			0.1852	1464.93...
2.00	99	TKTFQGPPHGIQVER	Thr->Val@1	cleaved Y-T...	0.1548	1692.06...
2.00	99	VALEACVQAR	ICAT-C(C)@6		0.1551	1285.83...
2.00	99	VAYPLDLFEEGSVTNMFTS...	Oxidation(M)@16	cleaved Y-V...	0.3629	3096.87...
2.00	99	YGRPLLGCTIKPK	Gly->Pro@2 ICAT-C(C)@8		0.1914	1712.17...
1.70	**98**	**WSPELAAACEVWK**	**ICAT-C(C)@9 Oxidation(W)@12**		**0.2116**	**1732.04...**

Protein Sequence Coverage - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

```
MSPQTETKASVGFKAGVKEYKLNYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVPGEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFK
ALAALRLEDLRIPPAYTKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKSQAETGEIKGHYLNATAGTCEEMMKRAIF
ARELGVPIVMHDYLTGGFTANTSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHVHAGTVVGKLEGDRESTLGFVDLLRDDYVEKDRSRGIFFTQDWVSLPGVLPVASGGIHV
WHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAVEGNEIIREACKWSPELAAACEVWKEITFNFPTIDKLDGQD
```

gi|119980 Ferredoxin



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
62	2.03	2.03	83.3	gi|119980	Ferredoxin	BRANA	1			
63	2.02	2.02	39.3	gi|15231...	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
64	2.02	2.02	51.1	gi|15235...	leucyl aminopeptidase-like protein [Arabidopsis...	Arabidopsis thaliana	2			
65	2.02	2.02	44.6	gi|15222...	6-phosphogluconate dehydrogenase, putative [A...	Arabidopsis thaliana	1			
66	2.02	2.02	38.8	gi|15228...	unknown protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			

Protein Group 62 - Ferredoxin

Proteins in Group

N	Unu...	Total	Accessio...	Name
62	2.03	2.03	gi|119980	Ferredoxin

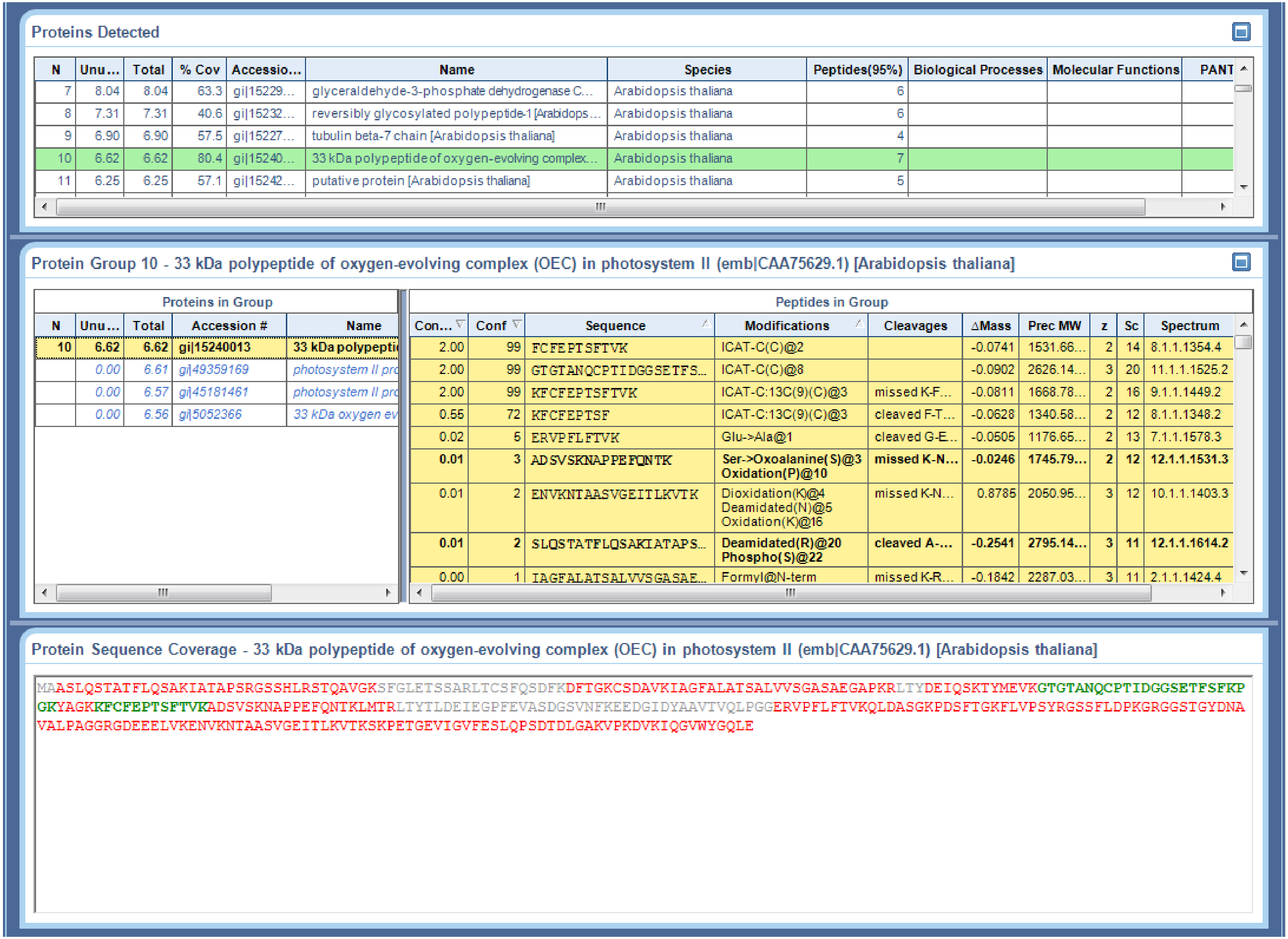
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
1.70	98	FITPEGEQEVECDDDVYVL...	ICAT-C(C)@12 ICAT-C(C)@33		-0.0157	4243.89...	4	14	4.1.1.1842.4
0.33	53	VVSGFVDQSDESFLDDDQI...	Phe->Ser@5 ICAT-C(C)@27		0.0381	5214.46...	5	14	3.1.1.1681.2
0.00	< 1	FITPEGEQEVECDDDVYVL...	ICAT-C(C)@12	cleaved Y-...	-0.0196	3670.62...	4	10	3.1.1.1801.3
0.00	< 1	FITPEGEQEVECDDDVYVL...	ICAT-C:13C(9)(C)@12	cleaved Y-...	-0.0185	3679.65...	4	7	2.1.1.1686.4
0.00	< 1	FITPEGEQEVECDDDVYVL...	Deamidated(Q)@8 ICAT-C(C)@12 ICAT-C(C)@33		0.9541	4245.84...	5	7	3.1.1.1700.4
0.00	< 1	FITPEGEQEVECDDDVYVL...	Deamidated(Q)@8 ICAT-C(C)@12 ICAT-C(C)@33		0.7723	4245.66...	5	8	11.1.1.2011.2
0.00	< 1	FITPEGEQEVECDDDVYVL...	Deamidated(Q)@8 ICAT-C:13C(9)(C)@12 ICAT-C:13C(9)(C)@33		0.0029	4262.95...	4	7	2.1.1.1609.3
0.00	< 1	FITPEGEQEVECDDDVYVL...	Deamidated(Q)@8		-0.0879	4262.86...	4	8	12.1.1.1977.2

Protein Sequence Coverage - Ferredoxin

ATYKVKFITPEGEQEVECDDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGFVDQSDESFLDDDQIAEGFVLTCAAYPTSDVTIETHKEEELV

gi|15240013 33 kDa polypeptide of oxygen-evolving complex in photosystem II



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
7	8.04	8.04	63.3	gi|15229...	glyceraldehyde-3-phosphate dehydrogenase C...	Arabidopsis thaliana	6			
8	7.31	7.31	40.6	gi|15232...	reversibly glycosylated polypeptide-1 [Arabidops...	Arabidopsis thaliana	6			
9	6.90	6.90	57.5	gi|15227...	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4			
10	6.62	6.62	80.4	gi|15240...	33 kDa polypeptide of oxygen-evolving complex...	Arabidopsis thaliana	7			
11	6.25	6.25	57.1	gi|15242...	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5			

Protein Group 10 - 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb|CAA75629.1) [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name
10	**6.62**	**6.62**	**gi|15240013**	**33 kDa polypepti**
	0.00	*6.61*	*gi|49359169*	*photosystem II pro*
	0.00	*6.57*	*gi|45181461*	*photosystem II pro*
	0.00	*6.56*	*gi|5052366*	*33 kDa oxygen ev*

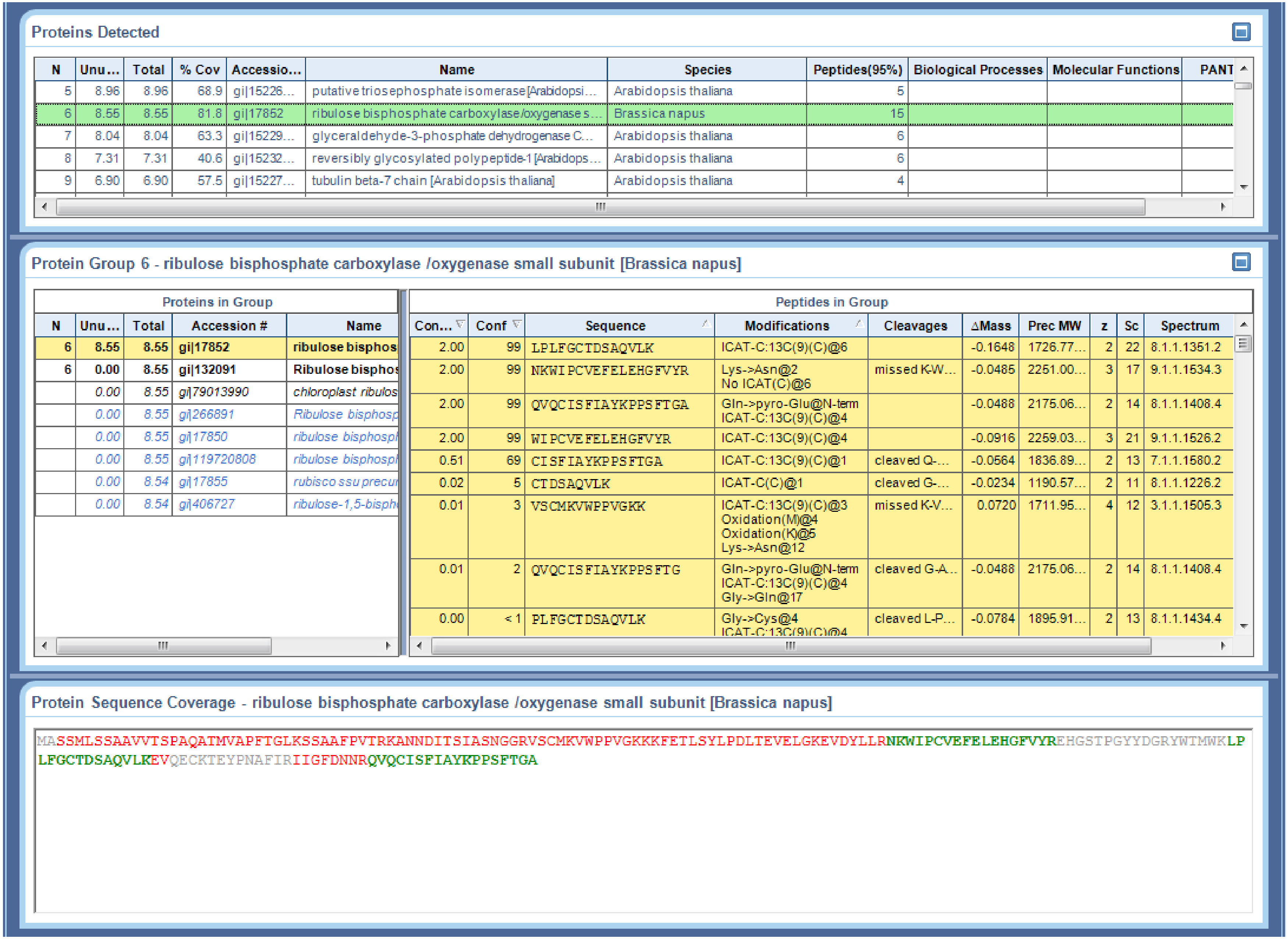
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	FCFEPTSFTVK	ICAT-C(C)@2		-0.0741	1531.66...	2	14	8.1.1.1354.4
2.00	99	GTGTANQCPTIDGGSETFS...	ICAT-C(C)@8		-0.0902	2626.14...	3	20	11.1.1.1525.2
2.00	99	KFCFEPTSFTVK	ICAT-C:13C(9)(C)@3	missed K-F...	-0.0811	1668.78...	2	16	9.1.1.1449.2
0.55	72	KFCFEPTSF	ICAT-C:13C(9)(C)@3	cleaved F-T...	-0.0628	1340.58...	2	12	8.1.1.1348.2
0.02	5	ERVPFLFTVK	Glu->Ala@1	cleaved G-E...	-0.0505	1176.65...	2	13	7.1.1.1578.3
0.01	**3**	**ADSVSKNAPPEFQNTK**	**Ser->Oxoalanine(S)@3 Oxidation(P)@10**	**missed K-N...**	**-0.0246**	**1745.79...**	**2**	**12**	**12.1.1.1531.3**
0.01	2	ENVKNTAASVGEITLKVTK	Dioxidation(K)@4 Deamidated(N)@5 Oxidation(K)@16	missed K-N...	0.8785	2050.95...	3	12	10.1.1.1403.3
0.01	**2**	**SLQSTATFLQSAKIATAPS...**	**Deamidated(R)@20 Phospho(S)@22**	**cleaved A-...**	**-0.2541**	**2795.14...**	**3**	**11**	**12.1.1.1614.2**
0.00	1	IAGFALATSALVVSGASAE...	Formyl@N-term	missed K-R...	-0.1842	2287.03...	3	11	2.1.1.1424.4

Protein Sequence Coverage - 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb|CAA75629.1) [Arabidopsis thaliana]

```
MAASLQSTATFLQSAKIATAPSRGSSHLRSTQAVGKSFGLETSSARLTCSFQSDFKDFTGKCSDAVKIAGFALATSALVVSGASAEGAPKRLTYDEIQSKTYMEVKGTGTANQCPTIDGGSETFSFKP
GKYAGKKFCFEPTSFTVKADSVSKNAPPEFQNTKLMTRLTYTLDEIEGPFEVASDGSVNFKEEDGIDYAAVTVQLPGGERVPFLFTVKQLDASGKPDSFTGKFLVPSYRGSSFLDPKGRGGSTGYDNA
VALPAGGRGDEEELVKENVKNTAASVGEITLKVTKSKPETGEVIGVFESLQPSDTDLGAKVPKDVKIQGVWYGQLE
```

gi|17852 Ribulose bisphosphate carboxylase /oxygenase small subunit



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
5	8.96	8.96	68.9	gi|15226...	putative triosephosphate isomerase [Arabidopsi...	Arabidopsis thaliana	5			
6	8.55	8.55	81.8	gi|17852	ribulose bisphosphate carboxylase /oxygenase s...	Brassica napus	15			
7	8.04	8.04	63.3	gi|15229...	glyceraldehyde-3-phosphate dehydrogenase C...	Arabidopsis thaliana	6			
8	7.31	7.31	40.6	gi|15232...	reversibly glycosylated polypeptide-1 [Arabidops...	Arabidopsis thaliana	6			
9	6.90	6.90	57.5	gi|15227...	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4			

Protein Group 6 - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

Proteins in Group

N	Unu...	Total	Accession #	Name
6	**8.55**	**8.55**	**gi|17852**	**ribulose bisphos**
6	**0.00**	**8.55**	**gi|132091**	**Ribulose bisphos**
	0.00	*8.55*	*gi|79013990*	*chloroplast ribulos*
	0.00	*8.55*	*gi|266891*	*Ribulose bisphosp*
	0.00	*8.55*	*gi|17850*	*ribulose bisphosph*
	0.00	*8.55*	*gi|119720808*	*ribulose bisphosph*
	0.00	*8.54*	*gi|17855*	*rubisco ssu precur*
	0.00	*8.54*	*gi|406727*	*ribulose-1,5-bisph*

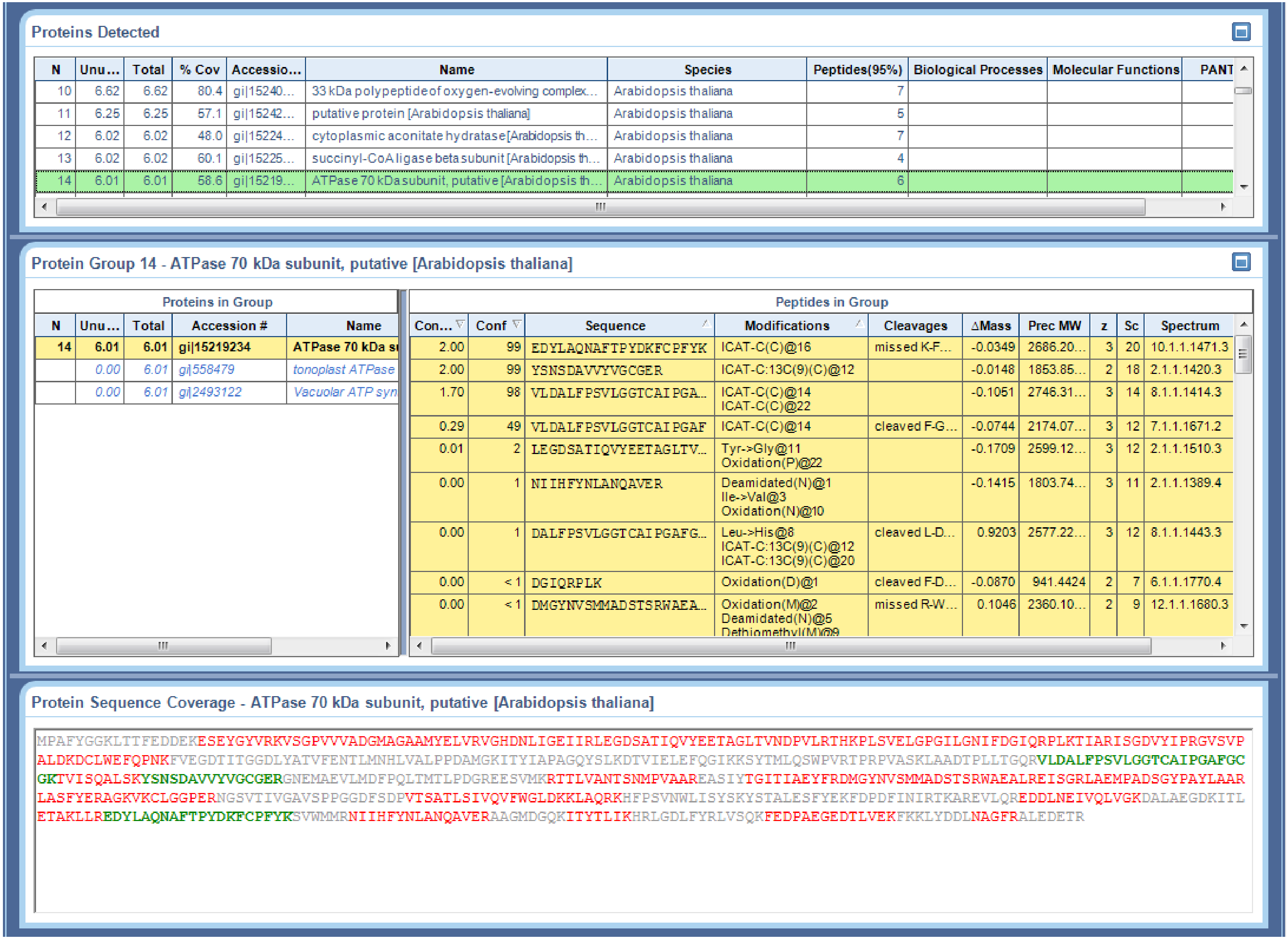
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	LPLFGCTDSAQVLK	ICAT-C:13C(9)(C)@6		-0.1648	1726.77...	2	22	8.1.1.1351.2
2.00	99	NKWIPCVEFELEHGFVYR	Lys->Asn@2 No ICAT(C)@6	missed K-W...	-0.0485	2251.00...	3	17	9.1.1.1534.3
2.00	99	QVQCISFIAYKPPSFTGA	Gln->pyro-Glu@N-term ICAT-C:13C(9)(C)@4		-0.0488	2175.06...	2	14	8.1.1.1408.4
2.00	99	WIPCVEFELEHGFVYR	ICAT-C:13C(9)(C)@4		-0.0916	2259.03...	3	21	9.1.1.1526.2
0.51	69	CISFIAYKPPSFTGA	ICAT-C:13C(9)(C)@1	cleaved Q-...	-0.0564	1836.89...	2	13	7.1.1.1580.2
0.02	5	CTDSAQVLK	ICAT-C(C)@1	cleaved G-...	-0.0234	1190.57...	2	11	8.1.1.1226.2
0.01	3	VSCMKVWPPVGKK	ICAT-C:13C(9)(C)@3 Oxidation(M)@4 Oxidation(K)@5 Lys->Asn@12	missed K-V...	0.0720	1711.95...	4	12	3.1.1.1505.3
0.01	2	QVQCISFIAYKPPSFTG	Gln->pyro-Glu@N-term ICAT-C:13C(9)(C)@4 Gly->Gln@17	cleaved G-A...	-0.0488	2175.06...	2	14	8.1.1.1408.4
0.00	< 1	PLFGCTDSAQVLK	Gly->Cys@4 ICAT-C:13C(9)(C)@4	cleaved L-P...	-0.0784	1895.91...	2	13	8.1.1.1434.4

Protein Sequence Coverage - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

MASSMLSSAAVVTSPAQATMVAPFTGLKSSAAFPVTRKANNDITSIASNGGRVSCMKVWPPVGKKKFETLSYLPDLTEVELGKEVDYLLRNKWIPCVEFELEHGFVYREHGSTPGYYDGRYWTMWKLP
LFGCTDSAQVLKEVQECKTEYPNAFIRIIGFDNNRQVQCISFIAYKPPSFTGA

gi|15219234 ATPase 70 kDa subunit, putative



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
10	6.62	6.62	80.4	gi|15240...	33 kDa polypeptide of oxygen-evolving complex...	Arabidopsis thaliana	7			
11	6.25	6.25	57.1	gi|15242...	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5			
12	6.02	6.02	48.0	gi|15224...	cytoplasmic aconitate hydratase [Arabidopsis th...	Arabidopsis thaliana	7			
13	6.02	6.02	60.1	gi|15225...	succinyl-CoA ligase beta subunit [Arabidopsis th...	Arabidopsis thaliana	4			
14	6.01	6.01	58.6	gi|15219...	ATPase 70 kDa subunit, putative [Arabidopsis th...	Arabidopsis thaliana	6			

Protein Group 14 - ATPase 70 kDa subunit, putative [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name
14	**6.01**	**6.01**	**gi|15219234**	**ATPase 70 kDa su**
	0.00	*6.01*	*gi|558479*	*tonoplast ATPase*
	0.00	*6.01*	*gi|2493122*	*Vacuolar ATP syn*

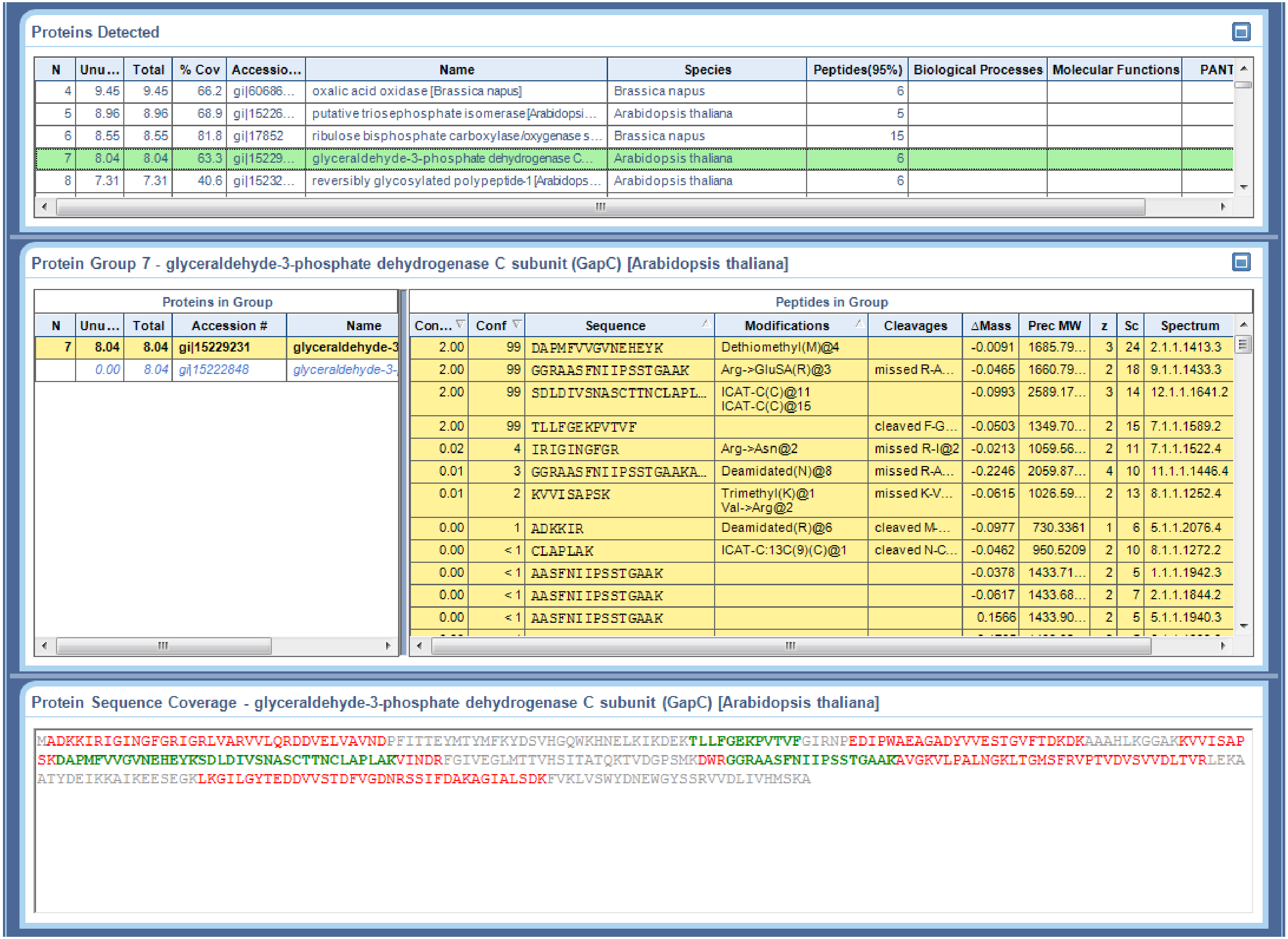
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	EDYLAQNAFTPYDKFCPFYK	ICAT-C(C)@16	missed K-F...	-0.0349	2686.20...	3	20	10.1.1.1471.3
2.00	99	YSNSDAVVYVGCGER	ICAT-C:13C(9)(C)@12		-0.0148	1853.85...	2	18	2.1.1.1420.3
1.70	98	VLDALFPSVLGGTCAIPGA...	ICAT-C(C)@14 ICAT-C(C)@22		-0.1051	2746.31...	3	14	8.1.1.1414.3
0.29	49	VLDALFPSVLGGTCAIPGAF	ICAT-C(C)@14	cleaved F-G...	-0.0744	2174.07...	3	12	7.1.1.1671.2
0.01	2	LEGDSATIQVYEETAGLTV...	Tyr->Gly@11 Oxidation(P)@22		-0.1709	2599.12...	3	12	2.1.1.1510.3
0.00	1	NIIHFYNLANQAVER	Deamidated(N)@1 Ile->Val@3 Oxidation(N)@10		-0.1415	1803.74...	3	11	2.1.1.1389.4
0.00	1	DALFPSVLGGTCAIPGAFG...	Leu->His@8 ICAT-C:13C(9)(C)@12 ICAT-C:13C(9)(C)@20	cleaved L-D...	0.9203	2577.22...	3	12	8.1.1.1443.3
0.00	< 1	DGIQRPLK	Oxidation(D)@1	cleaved F-D...	-0.0870	941.4424	2	7	6.1.1.1770.4
0.00	< 1	DMGYNVSMMADSTSRWAEA...	Oxidation(M)@2 Deamidated(N)@5 Dethiomethyl(M)@9	missed R-W...	0.1046	2360.10...	2	9	12.1.1.1680.3

Protein Sequence Coverage - ATPase 70 kDa subunit, putative [Arabidopsis thaliana]

```
MPAFYGGKLTTFEDDEKESEYGYVRKVSGPVVVADGMAGAAMYELVRVGHDNLIGEIIRLEGDSATIQVYEETAGLTVNDPVLRTHKPLSVELGPGILGNIFDGIQRPLKTIARISGDVYIPRGVSVP
ALDKDCLWEFQPNKFVEGDTITGGDLYATVFENTLMNHLVALPPDAMGKITYIAPAGQYSLKDTVIELEFQGIKKSYTMLQSWPVRTPRPVASKLAADTPLLTGQRVLDALFPSVLGGTCAIPGAFGC
GKTVISQALSKYSNSDAVVYVGCGERGNEMAEVLMDFPQLTMTLPDGREESVMKRTTLVANTSNMPVAAREASIYTGITIAEYFRDMGYNVSMMADSTSRWAEALREISGRLAEMPADSGYPAYLAAR
LASFYERAGKVKCLGGPERNGSVTIVGAVSPPGGDFSDPVTSATLSIVQVFWGLDKKLAQRKHFPSVNWLISYSKYSTALESFYEKFDPDFINIRTKAREVLQREDDLNEIVQLVGKDALAEGDKITL
ETAKLLREDYLAQNAFTPYDKFCPFYKSVWMMRNIIHFYNLANQAVERAAGMDGQKITYTLIKHRLGDLFYRLVSQKFEDPAEGEDTLVEKFKKLYDDLNAGFRALEDETR
```

gi|15229231 Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
4	9.45	9.45	66.2	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	6			
5	8.96	8.96	68.9	gi|15226…	putative triosephosphate isomerase [Arabidopsi…	Arabidopsis thaliana	5			
6	8.55	8.55	81.8	gi|17852	ribulose bisphosphate carboxylase/oxygenase s…	Brassica napus	15			
7	8.04	8.04	63.3	gi|15229…	glyceraldehyde-3-phosphate dehydrogenase C…	Arabidopsis thaliana	6			
8	7.31	7.31	40.6	gi|15232…	reversibly glycosylated polypeptide-1 [Arabidops…	Arabidopsis thaliana	6			

Protein Group 7 - glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
7	**8.04**	**8.04**	**gi|15229231**	**glyceraldehyde-3**
	0.00	*8.04*	*gi|15222848*	*glyceraldehyde-3-*

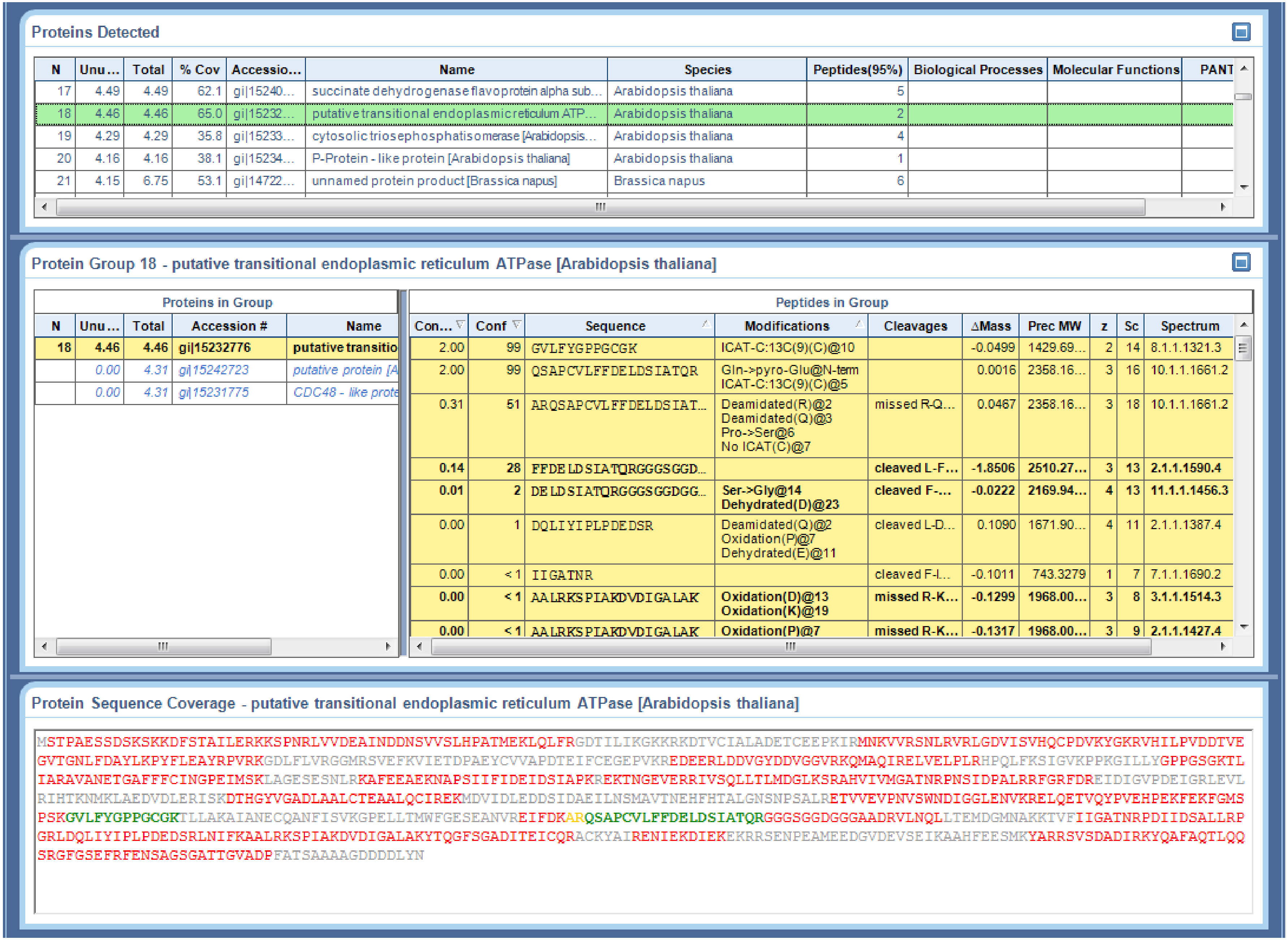
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	DAPMFVVGVNEHEYK	Dethiomethyl(M)@4		-0.0091	1685.79…	3	24	2.1.1.1413.3
2.00	99	GGRAASFNIIPSSTGAAK	Arg->GluSA(R)@3	missed R-A…	-0.0465	1660.79…	2	18	9.1.1.1433.3
2.00	99	SDLDIVSNASCTTNCLAPL…	ICAT-C(C)@11 ICAT-C(C)@15		-0.0993	2589.17…	3	14	12.1.1.1641.2
2.00	99	TLLFGEKPVTVF		cleaved F-G…	-0.0503	1349.70…	2	15	7.1.1.1589.2
0.02	4	IRIGINGFGR	Arg->Asn@2	missed R-I@2	-0.0213	1059.56…	2	11	7.1.1.1522.4
0.01	3	GGRAASFNIIPSSTGAAKA…	Deamidated(N)@8	missed R-A…	-0.2246	2059.87…	4	10	11.1.1.1446.4
0.01	2	KVVISAPSK	Trimethyl(K)@1 Val->Arg@2	missed K-V…	-0.0615	1026.59…	2	13	8.1.1.1252.4
0.00	1	ADKKIR	Deamidated(R)@6	cleaved M-…	-0.0977	730.3361	1	6	5.1.1.2076.4
0.00	< 1	CLAPLAK	ICAT-C:13C(9)(C)@1	cleaved N-C…	-0.0462	950.5209	2	10	8.1.1.1272.2
0.00	< 1	AASFNIIPSSTGAAK			-0.0378	1433.71…	2	5	1.1.1.1942.3
0.00	< 1	AASFNIIPSSTGAAK			-0.0617	1433.68…	2	7	2.1.1.1844.2
0.00	< 1	AASFNIIPSSTGAAK			0.1566	1433.90…	2	5	5.1.1.1940.3

Protein Sequence Coverage - glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [Arabidopsis thaliana]

```
MADKKIRIGINGFGRIGRLVARVVLQRDDVELVAVNDPFITTEYMTYMFKYDSVHGQWKHNELKIKDEKTLLFGEKPVTVFGIRNPEDIPWAEAGADYVVESTGVFTDKDKAAAHLKGGAKKVVISAP
SKDAPMFVVGVNEHEYKSDLDIVSNASCTTNCLAPLAKVINDRFGIVEGLMTTVHSITATQKTVDGPSMKDWRGGRAASFNIIPSSTGAAKAVGKVLPALNGKLTGMSFRVPTVDVSVVDLTVRLEKA
ATYDEIKKAIKEESEGKLKGILGYTEDDVVSTDFVGDNRSSIFDAKAGIALSDKFVKLVSWYDNEWGYSSRVVDLIVHMSKA
```

gi|15232776 Putative transitional endoplasmic reticulum ATPase



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
17	4.49	4.49	62.1	gi|15240...	succinate dehydrogenase flavoprotein alpha sub...	Arabidopsis thaliana	5			
18	4.46	4.46	65.0	gi|15232...	putative transitional endoplasmic reticulum ATP...	Arabidopsis thaliana	2			
19	4.29	4.29	35.8	gi|15233...	cytosolic triosephosphatisomerase [Arabidopsis...	Arabidopsis thaliana	4			
20	4.16	4.16	38.1	gi|15234...	P-Protein - like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
21	4.15	6.75	53.1	gi|14722...	unnamed protein product [Brassica napus]	Brassica napus	6			

Protein Group 18 - putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name
18	**4.46**	**4.46**	**gi|15232776**	**putative transitio**
	0.00	*4.31*	*gi|15242723*	*putative protein [A*
	0.00	*4.31*	*gi|15231775*	*CDC48 - like prote*

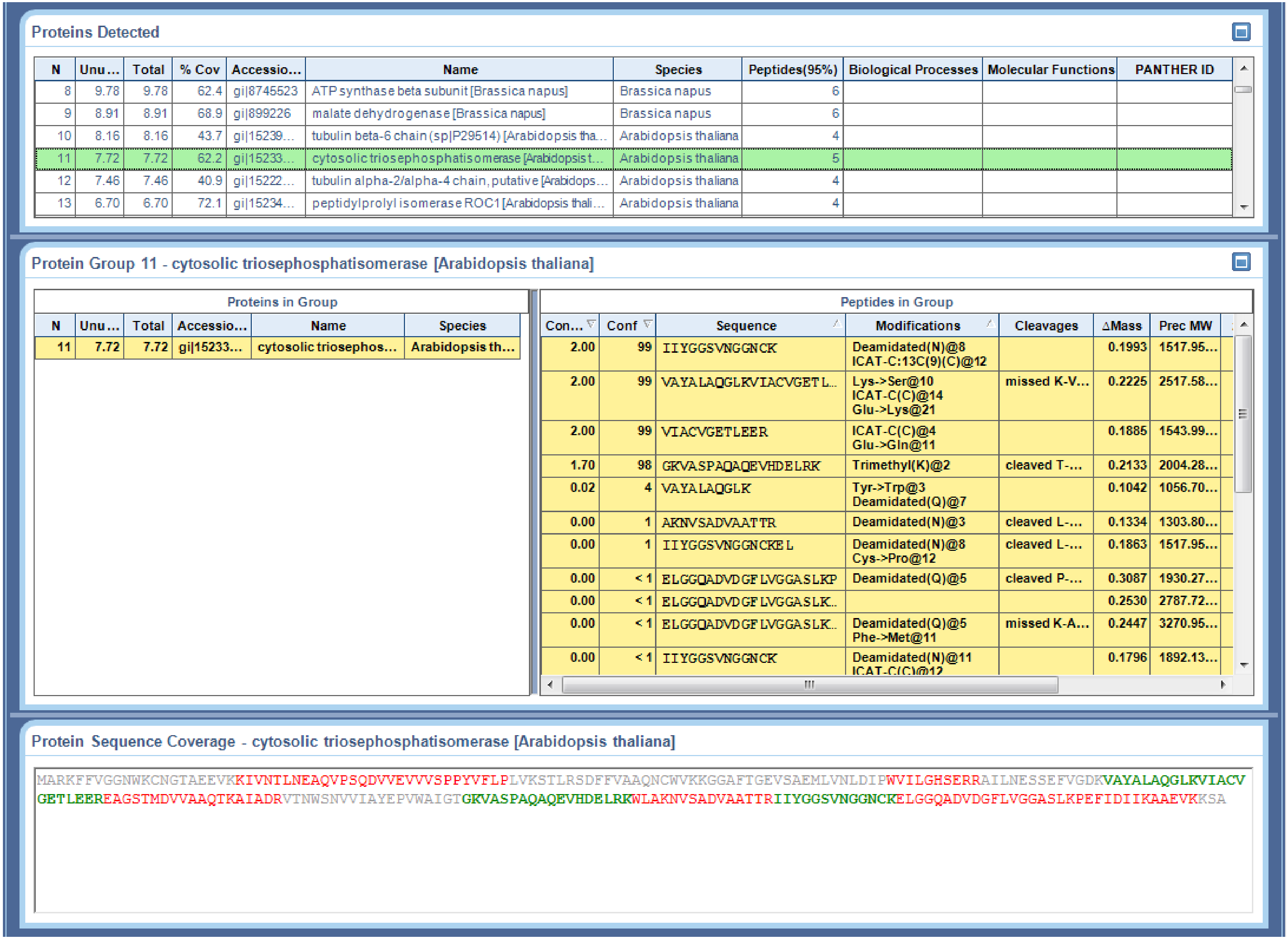
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	GVLFYGPPGCGK	ICAT-C:13C(9)(C)@10		-0.0499	1429.69...	2	14	8.1.1.1321.3
2.00	99	QSAPCVLFFDELDSIATQR	Gln->pyro-Glu@N-term ICAT-C:13C(9)(C)@5		0.0016	2358.16...	3	16	10.1.1.1661.2
0.31	51	ARQSAPCVLFFDELDSIAT...	Deamidated(R)@2 Deamidated(Q)@3 Pro->Ser@6 No ICAT(C)@7	missed R-Q...	0.0467	2358.16...	3	18	10.1.1.1661.2
0.14	**28**	**FFDELDSIATQRGGGSGGD...**		**cleaved L-F...**	**-1.8506**	**2510.27...**	**3**	**13**	**2.1.1.1590.4**
0.01	**2**	**DELDSIATQRGGGSGGDGG...**	**Ser->Gly@14 Dehydrated(D)@23**	**cleaved F-...**	**-0.0222**	**2169.94...**	**4**	**13**	**11.1.1.1456.3**
0.00	1	DQLIYIPLPDEDSR	Deamidated(Q)@2 Oxidation(P)@7 Dehydrated(E)@11	cleaved L-D...	0.1090	1671.90...	4	11	2.1.1.1387.4
0.00	< 1	IIGATNR		cleaved F-I...	-0.1011	743.3279	1	7	7.1.1.1690.2
0.00	**< 1**	**AALRKSPIAKDVDIGALAK**	**Oxidation(D)@13 Oxidation(K)@19**	**missed R-K...**	**-0.1299**	**1968.00...**	**3**	**8**	**3.1.1.1514.3**
0.00	**< 1**	**AALRKSPIAKDVDIGALAK**	**Oxidation(P)@7**	**missed R-K...**	**-0.1317**	**1968.00...**	**3**	**9**	**2.1.1.1427.4**

Protein Sequence Coverage - putative transitional endoplasmic reticulum ATPase [Arabidopsis thaliana]

```
MSTPAESSDSKSKKDFSTAILERKKSPNRLVVDEAINDDNSVVSLHPATMEKLQLFRGDTILIKGKKRKDTVCIALADETCEEPKIRMNKVVRSNLRVRLGDVISVHQCPDVKYGKRVHILPVDDTVE
GVTGNLFDAYLKPYFLEAYRPVRKGDLFLVRGGMRSVEFKVIETDPAEYCVVAPDTEIFCEGEPVKREDEERLDDVGYDDVGGVRKQMAQIRELVELPLRHPQLFKSIGVKPPKGILLYGPPGSGKTL
IARAVANETGAFFFCINGPEIMSKLAGESESNLRKAFEEAEKNAPSIIFIDEIDSIAPKREKTNGEVERRIVSQLLTLMDGLKSRAHVIVMGATNRPNSIDPALRRFGRFDREIDIGVPDEIGRLEVL
RIHTKNMKLAEDVDLERISKDTHGYVGADLAALCTEAALQCIREKMDVIDLEDDSIDAEILNSMAVTNEHFHTALGNSNPSALRETVVEVPNVSWNDIGGLENVKRELQETVQYPVEHPEKFEKFGMS
PSKGVLFYGPPGCGKTLLAKAIANECQANFISVKGPELLTMWFGESEANVREIFDKARQSAPCVLFFDELDSIATQRGGGSGGDGGGAADRVLNQLLTEMDGMNAKKTVFIIGATNRPDIIDSALLRP
GRLDQLIYIPLPDEDSRLNIFKAALRKSPIAKDVDIGALAKYTQGFSGADITEICQRACKYAIRENIEKDIEKEKRRSENPEAMEEDGVDEVSEIKAAHFEESMKYARRSVSDADIRKYQAFAQTLQQ
SRGFGSEFRFENSAGSGATTGVADPFATSAAAAGDDDDLYN
```

gi|15233272 Cytosolic triosephosphatisomerase



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
8	9.78	9.78	62.4	gi|8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	6			
9	8.91	8.91	68.9	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	6			
10	8.16	8.16	43.7	gi|15239...	tubulin beta-6 chain (sp|P29514) [Arabidopsis tha...	Arabidopsis thaliana	4			
11	7.72	7.72	62.2	gi|15233...	cytosolic triosephosphatisomerase [Arabidopsis t...	Arabidopsis thaliana	5			
12	7.46	7.46	40.9	gi|15222...	tubulin alpha-2/alpha-4 chain, putative [Arabidops...	Arabidopsis thaliana	4			
13	6.70	6.70	72.1	gi|15234...	peptidylprolyl isomerase ROC1 [Arabidopsis thali...	Arabidopsis thaliana	4			

Protein Group 11 - cytosolic triosephosphatisomerase [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accessio...	Name	Species
11	7.72	7.72	gi|15233...	cytosolic triosephos...	Arabidopsis th...

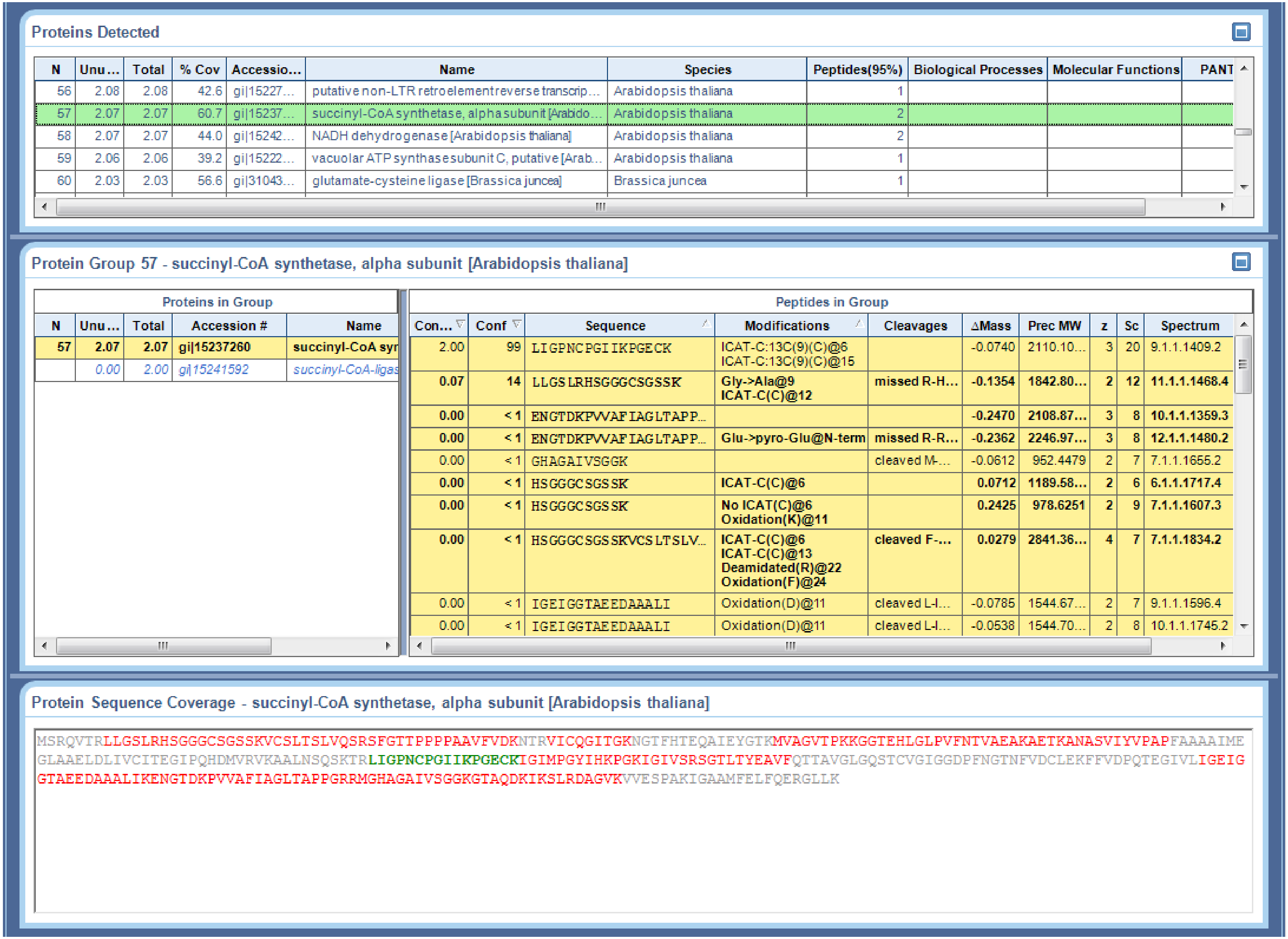
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	IIYGGSVNGGNCK	Deamidated(N)@8 ICAT-C:13C(9)(C)@12		0.1993	1517.95...
2.00	99	VAYALAQGLKVIACVGETL...	Lys->Ser@10 ICAT-C(C)@14 Glu->Lys@21	missed K-V...	0.2225	2517.58...
2.00	99	VIACVGETLEER	ICAT-C(C)@4 Glu->Gln@11		0.1885	1543.99...
1.70	98	GKVASPAQAQEVHDELRK	Trimethyl(K)@2	cleaved T-...	0.2133	2004.28...
0.02	4	VAYALAQGLK	Tyr->Trp@3 Deamidated(Q)@7		0.1042	1056.70...
0.00	1	AKNVSADVAATTR	Deamidated(N)@3	cleaved L-...	0.1334	1303.80...
0.00	1	IIYGGSVNGGNCKEL	Deamidated(N)@8 Cys->Pro@12	cleaved L-...	0.1863	1517.95...
0.00	< 1	ELGGQADVDGFLVGGASLKP	Deamidated(Q)@5	cleaved P-...	0.3087	1930.27...
0.00	< 1	ELGGQADVDGFLVGGASLK..			0.2530	2787.72...
0.00	< 1	ELGGQADVDGFLVGGASLK..	Deamidated(Q)@5 Phe->Met@11	missed K-A...	0.2447	3270.95...
0.00	< 1	IIYGGSVNGGNCK	Deamidated(N)@11 ICAT-C(C)@12		0.1796	1892.13...

Protein Sequence Coverage - cytosolic triosephosphatisomerase [Arabidopsis thaliana]

```
MARKFFVGGNWKCNGTAEEVKKIVNTLNEAQVPSQDVVEVVVSPPYVFLPLVKSTLRSDFFVAAQNCWVKKGGAFTGEVSAEMLVNLDIPWVILGHSERRAILNESSEFVGDKVAYALAQGLKVIACV
GETLEEREAGSTMDVVAAQTKAIADRVTNWSNVVIAYEPVWAIGTGKVASPAQAQEVHDELRKWLAKNVSADVAATTRIIYGGSVNGGNCKELGGQADVDGFLVGGASLKPEFIDIIKAAEVKKSA
```

gi|15237260 Succinyl-CoA synthetase, alpha subunit



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
56	2.08	2.08	42.6	gi|15227…	putative non-LTR retroelement reverse transcrip…	Arabidopsis thaliana	1			
57	2.07	2.07	60.7	gi|15237…	succinyl-CoA synthetase, alpha subunit [Arabido…	Arabidopsis thaliana	2			
58	2.07	2.07	44.0	gi|15242…	NADH dehydrogenase [Arabidopsis thaliana]	Arabidopsis thaliana	2			
59	2.06	2.06	39.2	gi|15222…	vacuolar ATP synthase subunit C, putative [Arab…	Arabidopsis thaliana	1			
60	2.03	2.03	56.6	gi|31043…	glutamate-cysteine ligase [Brassica juncea]	Brassica juncea	1			

Protein Group 57 - succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
57	**2.07**	**2.07**	**gi|15237260**	**succinyl-CoA syr**
	0.00	*2.00*	*gi|15241592*	*succinyl-CoA-ligas*

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	LIGPNCPGIIKPGECK	ICAT-C:13C(9)(C)@6 ICAT-C:13C(9)(C)@15		-0.0740	2110.10…	3	20	9.1.1.1409.2
0.07	**14**	LLGSLRHSGGGCSGSSK	**Gly->Ala@9** **ICAT-C(C)@12**	**missed R-H…**	**-0.1354**	**1842.80…**	**2**	**12**	**11.1.1.1468.4**
0.00	**< 1**	ENGTDKPVVAFIAGLTAPP…			**-0.2470**	**2108.87…**	**3**	**8**	**10.1.1.1359.3**
0.00	**< 1**	ENGTDKPVVAFIAGLTAPP…	**Glu->pyro-Glu@N-term**	**missed R-R…**	**-0.2362**	**2246.97…**	**3**	**8**	**12.1.1.1480.2**
0.00	< 1	GHAGAIVSGGK		cleaved M-…	-0.0612	952.4479	2	7	7.1.1.1655.2
0.00	**< 1**	HSGGGCSGSSK	**ICAT-C(C)@6**		**0.0712**	**1189.58…**	**2**	**6**	**6.1.1.1717.4**
0.00	**< 1**	HSGGGCSGSSK	**No ICAT(C)@6** **Oxidation(K)@11**		**0.2425**	**978.6251**	**2**	**9**	**7.1.1.1607.3**
0.00	**< 1**	HSGGGCSGSSKVCSLTSLV…	**ICAT-C(C)@6** **ICAT-C(C)@13** **Deamidated(R)@22** **Oxidation(F)@24**	**cleaved F-…**	**0.0279**	**2841.36…**	**4**	**7**	**7.1.1.1834.2**
0.00	< 1	IGEIGGTAEEDAAALI	Oxidation(D)@11	cleaved L-I…	-0.0785	1544.67…	2	7	9.1.1.1596.4
0.00	< 1	IGEIGGTAEEDAAALI	Oxidation(D)@11	cleaved L-I…	-0.0538	1544.70…	2	8	10.1.1.1745.2

Protein Sequence Coverage - succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]

```
MSRQVTRLLGSLRHSGGGCSGSSKVCSLTSLVQSRSFGTTPPPPAAVFVDKNTRVICQGITGKNGTFHTEQAIEYGTKMVAGVTPKKGGTEHLGLPVFNTVAEAKAETKANASVIYVPAPFAAAAIME
GLAAELDLIVCITEGIPQHDMVRVKAALNSQSKTRLIGPNCPGIIKPGECKIGIMPGYIHKPGKIGIVSRSGTLTYEAVFQTTAVGLGQSTCVGIGGDPFNGTNFVDCLEKFFVDPQTEGIVLIGEIG
GTAEEDAAALIKENGTDKPVVAFIAGLTAPPGRRMGHAGAIVSGGKGTAQDKIKSLRDAGVKVVESPAKIGAAMFELFQERGLLK
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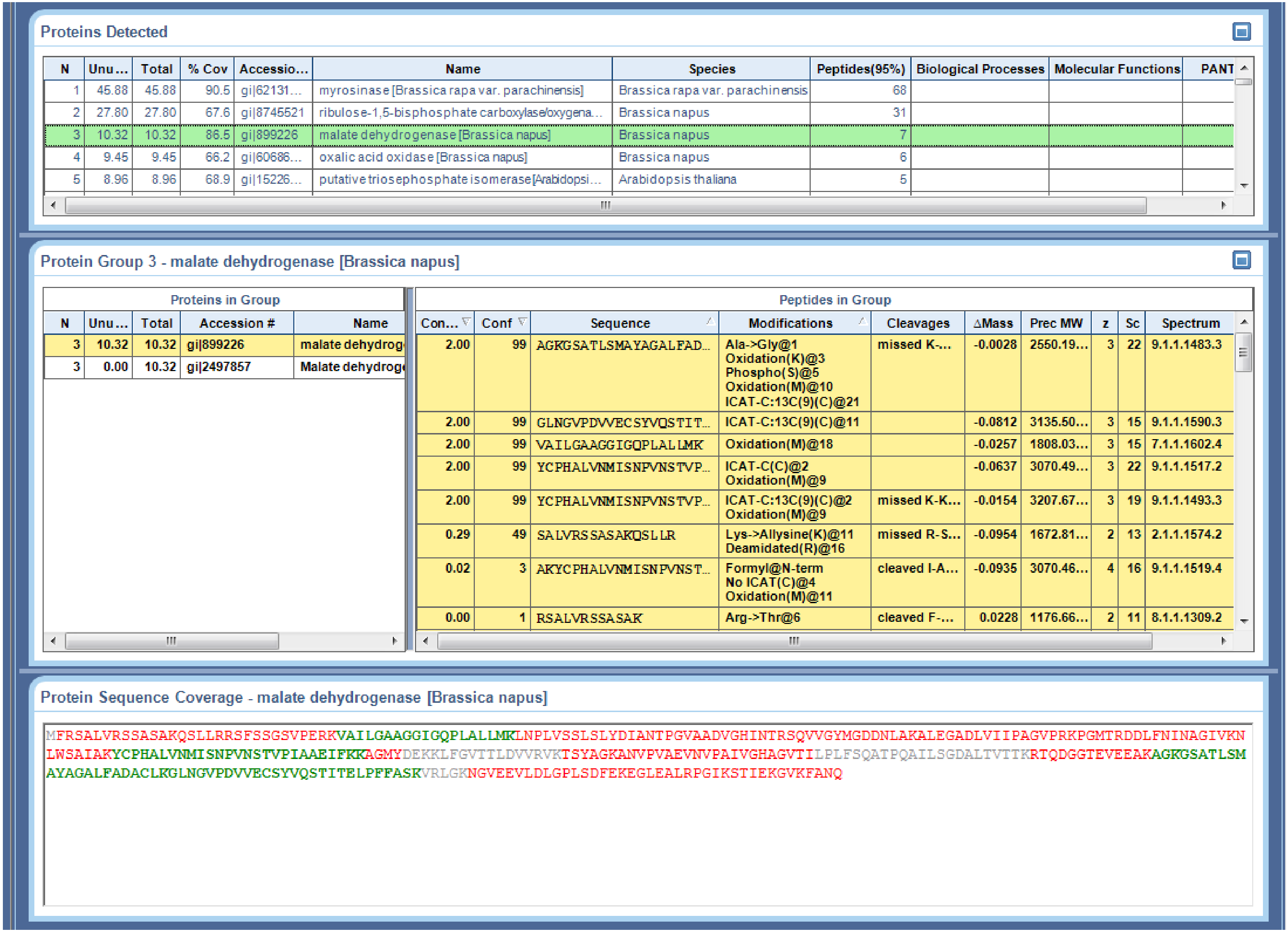
gi|899226 Malate dehydrogenase, mitochondrial precursor



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
1	45.88	45.88	90.5	gi|62131…	myrosinase [Brassica rapa var. parachinensis]	Brassica rapa var. parachinensis	68			
2	27.80	27.80	67.6	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygena…	Brassica napus	31			
3	10.32	10.32	86.5	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	7			
4	9.45	9.45	66.2	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	6			
5	8.96	8.96	68.9	gi|15226…	putative triosephosphate isomerase [Arabidopsi…	Arabidopsis thaliana	5			

Protein Group 3 - malate dehydrogenase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accession #	Name
3	10.32	10.32	gi|899226	malate dehydrog
3	0.00	10.32	gi|2497857	Malate dehydrog

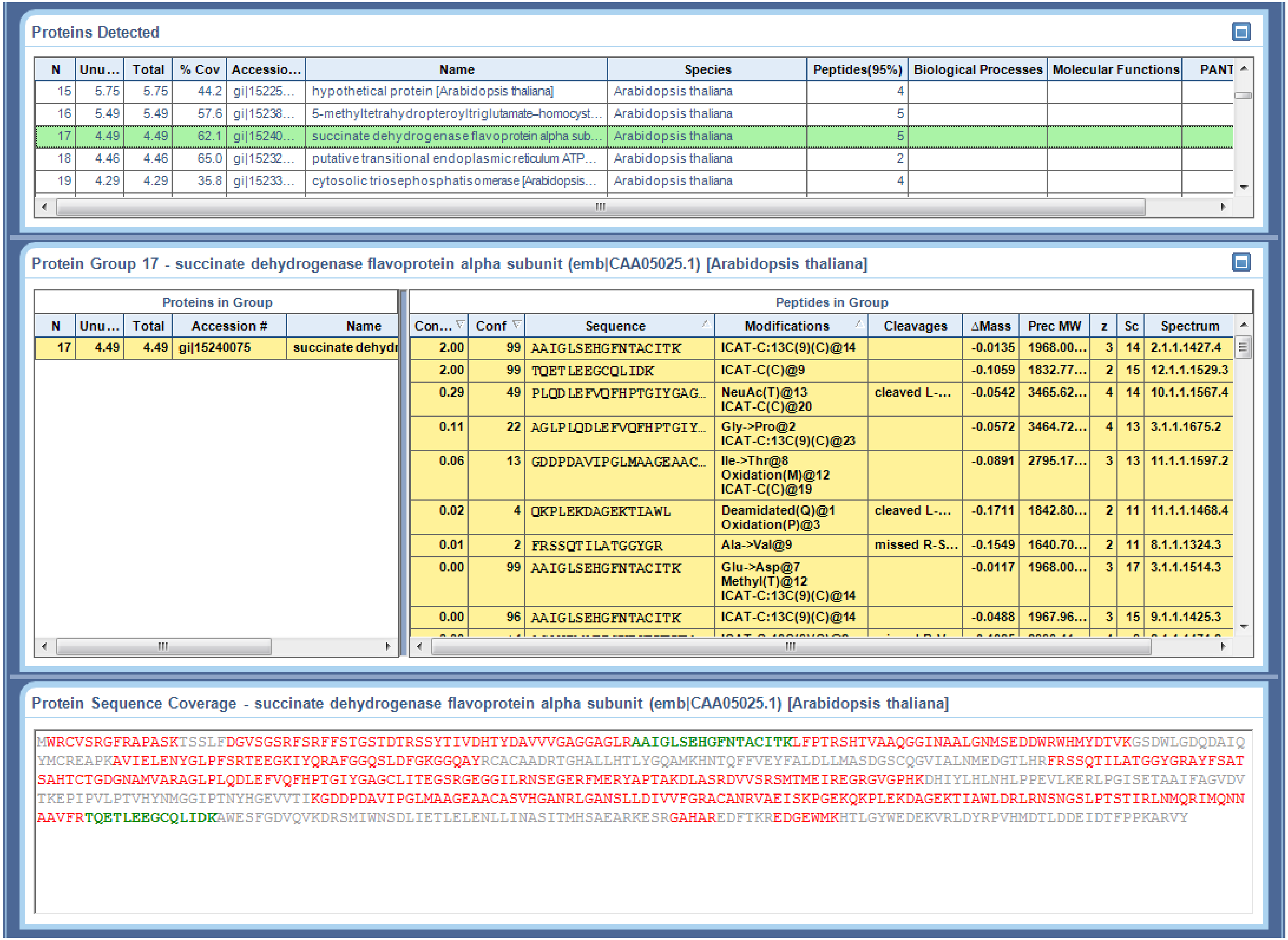
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	AGKGSATLSMAYAGALFAD…	Ala->Gly@1 Oxidation(K)@3 Phospho(S)@5 Oxidation(M)@10 ICAT-C:13C(9)(C)@21	missed K-…	-0.0028	2550.19…	3	22	9.1.1.1483.3
2.00	99	GLNGVPDVVECSYVQSTIT…	ICAT-C:13C(9)(C)@11		-0.0812	3135.50…	3	15	9.1.1.1590.3
2.00	99	VAILGAAGGIGQPLALLMK	Oxidation(M)@18		-0.0257	1808.03…	3	15	7.1.1.1602.4
2.00	99	YCPHALVNMISNPVNSTVP…	ICAT-C(C)@2 Oxidation(M)@9		-0.0637	3070.49…	3	22	9.1.1.1517.2
2.00	99	YCPHALVNMISNPVNSTVP…	ICAT-C:13C(9)(C)@2 Oxidation(M)@9	missed K-K…	-0.0154	3207.67…	3	19	9.1.1.1493.3
0.29	49	SALVRSSASAKQSLLR	Lys->Allysine(K)@11 Deamidated(R)@16	missed R-S…	-0.0954	1672.81…	2	13	2.1.1.1574.2
0.02	3	AKYCPHALVNMISNPVNST…	Formyl@N-term No ICAT(C)@4 Oxidation(M)@11	cleaved I-A…	-0.0935	3070.46…	4	16	9.1.1.1519.4
0.00	1	RSALVRSSASAK	Arg->Thr@6	cleaved F-…	0.0228	1176.66…	2	11	8.1.1.1309.2

Protein Sequence Coverage - malate dehydrogenase [Brassica napus]

```
MFRSALVRSSASAKQSLLRRSFSSGSVPERKVAILGAAGGIGQPLALLMKLNPLVSSLSLYDIANTPGVAADVGHINTRSQVVGYMGDDNLAKALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKN
LWSAIAKYCPHALVNMISNPVNSTVPIAAEIFKKAGMYDEKKLFGVTTLDVVRVKTSYAGKANVPVAEVNVPAIVGHAGVTILPLFSQATPQAILSGDALTVTTKRTQDGGTEVEEAKAGKGSATLSM
AYAGALFADACLKGLNGVPDVVECSYVQSTITELPFFASKVRLGKNGVEEVLDLGPLSDFEKEGLEALRPGIKSTIEKGVKFANQ
```

gi|15240075 Succinate dehydrogenase flavoprotein alpha subunit



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
15	5.75	5.75	44.2	gi|15225…	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	4			
16	5.49	5.49	57.6	gi|15238…	5-methyltetrahydropteroyltriglutamate–homocyst…	Arabidopsis thaliana	5			
17	4.49	4.49	62.1	gi|15240…	succinate dehydrogenase flavoprotein alpha sub…	Arabidopsis thaliana	5			
18	4.46	4.46	65.0	gi|15232…	putative transitional endoplasmic reticulum ATP…	Arabidopsis thaliana	2			
19	4.29	4.29	35.8	gi|15233…	cytosolic triosephosphatisomerase [Arabidopsis…	Arabidopsis thaliana	4			

Protein Group 17 - succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
17	4.49	4.49	gi|15240075	succinate dehydr

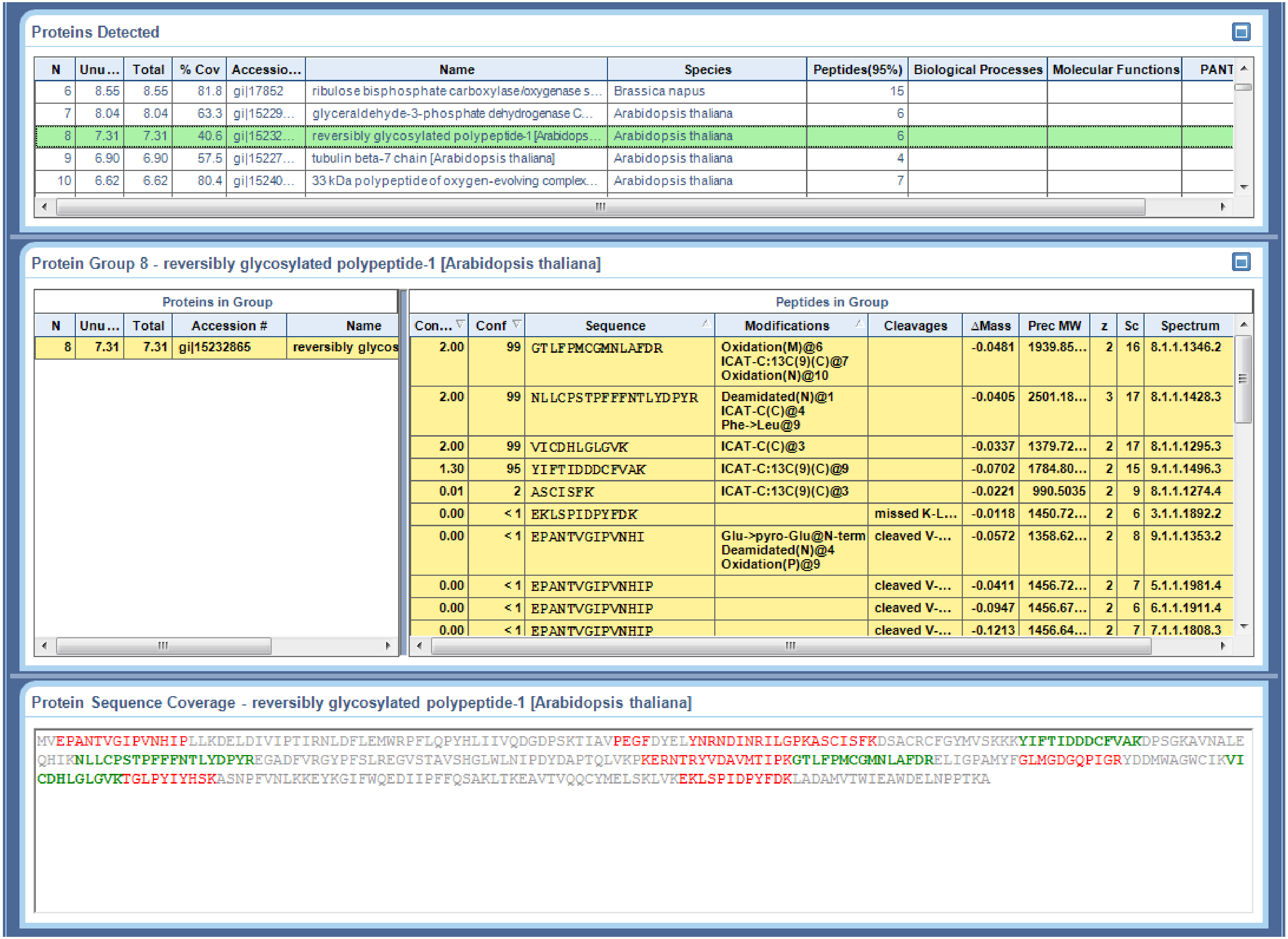
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14		-0.0135	1968.00…	3	14	2.1.1.1427.4
2.00	99	TQETLEEGCQLIDK	ICAT-C(C)@9		-0.1059	1832.77…	2	15	12.1.1.1529.3
0.29	49	PLQDLEFVQFHPTGIYGAG…	NeuAc(T)@13 ICAT-C(C)@20	cleaved L-…	-0.0542	3465.62…	4	14	10.1.1.1567.4
0.11	22	AGLPLQDLEFVQFHPTGIY…	Gly->Pro@2 ICAT-C:13C(9)(C)@23		-0.0572	3464.72…	4	13	3.1.1.1675.2
0.06	13	GDDPDAVIPGLMAAGEAAC…	Ile->Thr@8 Oxidation(M)@12 ICAT-C(C)@19		-0.0891	2795.17…	3	13	11.1.1.1597.2
0.02	4	QKPLEKDAGEKTIAWL	Deamidated(Q)@1 Oxidation(P)@3	cleaved L-…	-0.1711	1842.80…	2	11	11.1.1.1468.4
0.01	2	FRSSQTILATGGYGR	Ala->Val@9	missed R-S…	-0.1549	1640.70…	2	11	8.1.1.1324.3
0.00	99	AAIGLSEHGFNTACITK	Glu->Asp@7 Methyl(T)@12 ICAT-C:13C(9)(C)@14		-0.0117	1968.00…	3	17	3.1.1.1514.3
0.00	96	AAIGLSEHGFNTACITK	ICAT-C:13C(9)(C)@14		-0.0488	1967.96…	3	15	9.1.1.1425.3

Protein Sequence Coverage - succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) [Arabidopsis thaliana]

```
MWRCVSRGFRAPASKTSSLFDGVSGSRFSRFFSTGSTDTRSSYTIVDHTYDAVVVGAGGAGLRAAIGLSEHGFNTACITKLFPTRSHTVAAQGGINAALGNMSEDDWRWHMYDTVKGSDWLGDQDAIQ
YMCREAPKAVIELENYGLPFSRTEEGKIYQRAFGGQSLDFGKGGQAYRCACAADRTGHALLHTLYGQAMKHNTQFFVEYFALDLLMASDGSCQGVIALNMEDGTLHRFRSSQTILATGGYGRAYFSAT
SAHTCTGDGNAMVARAGLPLQDLEFVQFHPTGIYGAGCLITEGSRGEGGILRNSEGERFMERYAPTAKDLASRDVVSRSMTMEIREGRGVGPHKDHIYLHLNHLPPEVLKERLPGISETAAIFAGVDV
TKEPIPVLPTVHYNMGGIPTNYHGEVVTIKGDDPDAVIPGLMAAGEAACASVHGANRLGANSLLDIVVFGRACANRVAEISKPGEKQKPLEKDAGEKTIAWLDRLRNSNGSLPTSTIRLNMQRIMQNN
AAVFRTQETLEEGCQLIDKAWESFGDVQVKDRSMIWNSDLIETLELENLLINASITMHSAEARKESRGAHAREDFTKREDGEWMKHTLGYWEDEKVRLDYRPVHMDTLDDEIDTFPPKARVY
```

gi|15232865 Reversibly glycosylated polypeptide-1



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
6	8.55	8.55	81.8	gi|17852	ribulose bisphosphate carboxylase/oxygenase s…	Brassica napus	15			
7	8.04	8.04	63.3	gi|15229…	glyceraldehyde-3-phosphate dehydrogenase C…	Arabidopsis thaliana	6			
8	7.31	7.31	40.6	gi|15232…	reversibly glycosylated polypeptide-1 [Arabidops…	Arabidopsis thaliana	6			
9	6.90	6.90	57.5	gi|15227…	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4			
10	6.62	6.62	80.4	gi|15240…	33 kDa polypeptide of oxygen-evolving complex…	Arabidopsis thaliana	7			

Protein Group 8 - reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
8	7.31	7.31	gi|15232865	reversibly glycos

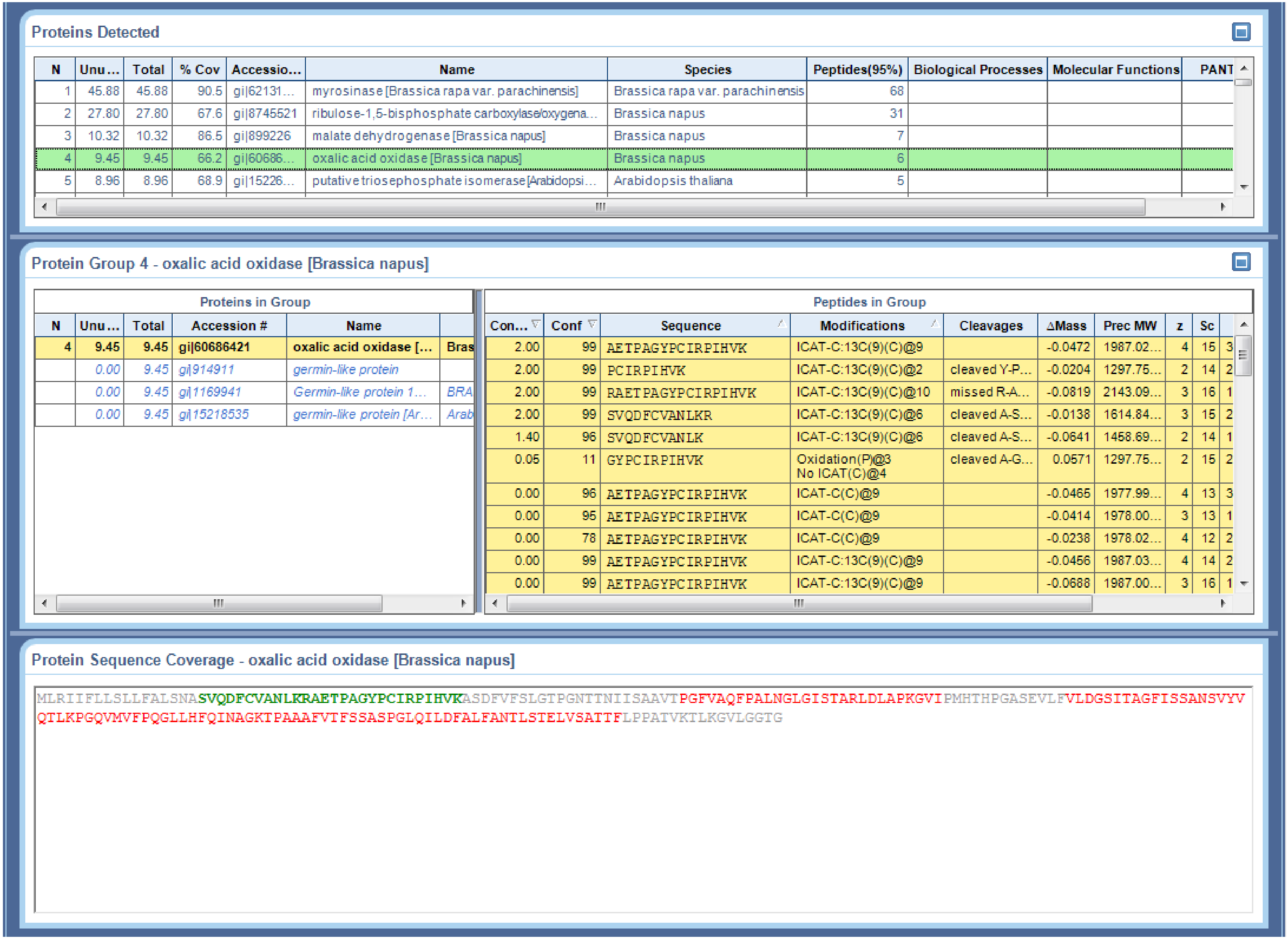
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	GTLFPMCGMNLAFDR	Oxidation(M)@6 ICAT-C:13C(9)(C)@7 Oxidation(N)@10		-0.0481	1939.85…	2	16	8.1.1.1346.2
2.00	99	NLLCPSTPFFFNTLYDPYR	Deamidated(N)@1 ICAT-C(C)@4 Phe->Leu@9		-0.0405	2501.18…	3	17	8.1.1.1428.3
2.00	99	VICDHLGLGVK	ICAT-C(C)@3		-0.0337	1379.72…	2	17	8.1.1.1295.3
1.30	95	YIFTIDDDCFVAK	ICAT-C:13C(9)(C)@9		-0.0702	1784.80…	2	15	9.1.1.1496.3
0.01	2	ASCISFK	ICAT-C:13C(9)(C)@3		-0.0221	990.5035	2	9	8.1.1.1274.4
0.00	< 1	EKLSPIDPYFDK		missed K-L…	-0.0118	1450.72…	2	6	3.1.1.1892.2
0.00	< 1	EPANTVGIPVNHI	Glu->pyro-Glu@N-term Deamidated(N)@4 Oxidation(P)@9	cleaved V-…	-0.0572	1358.62…	2	8	9.1.1.1353.2
0.00	< 1	EPANTVGIPVNHIP		cleaved V-…	-0.0411	1456.72…	2	7	5.1.1.1981.4
0.00	< 1	EPANTVGIPVNHIP		cleaved V-…	-0.0947	1456.67…	2	6	6.1.1.1911.4
0.00	< 1	EPANTVGIPVNHIP		cleaved V-…	-0.1213	1456.64…	2	7	7.1.1.1808.3

Protein Sequence Coverage - reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

MVEPANTVGIPVNHIPLLKDELDIVIPTIRNLDFLEMWRPFLQPYHLIIVQDGDPSKTIAVPEGFDYELYNRNDINRILGPKASCISFKDSACRCFGYMVSKKKYIFTIDDDCFVAKDPSGKAVNALE
QHIKNLLCPSTPFFFNTLYDPYREGADFVRGYPFSLREGVSTAVSHGLWLNIPDYDAPTQLVKPKERNTRYVDAVMTIPKGTLFPMCGMNLAFDRELIGPAMYFGLMGDGQPIGRYDDMWAGWCIKVI
CDHLGLGVKTGLPYIYHSKASNPFVNLKKEYKGIFWQEDIIPFFQSAKLTKEAVTVQQCYMELSKLVKEKLSPIDPYFDKLADAMVTWIEAWDELNPPTKA

gi|60686421 Oxalic acid oxidase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
1	45.88	45.88	90.5	gi|62131…	myrosinase [Brassica rapa var. parachinensis]	Brassica rapa var. parachinensis	68			
2	27.80	27.80	67.6	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygena…	Brassica napus	31			
3	10.32	10.32	86.5	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	7			
4	9.45	9.45	66.2	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	6			
5	8.96	8.96	68.9	gi|15226…	putative triosephosphate isomerase [Arabidopsi…	Arabidopsis thaliana	5			

Protein Group 4 - oxalic acid oxidase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accession #	Name	
4	**9.45**	**9.45**	**gi|60686421**	**oxalic acid oxidase […**	**Bras**
	0.00	*9.45*	*gi|914911*	*germin-like protein*	
	0.00	*9.45*	*gi|1169941*	*Germin-like protein 1…*	*BRA*
	0.00	*9.45*	*gi|15218535*	*germin-like protein [Ar…*	*Arab*

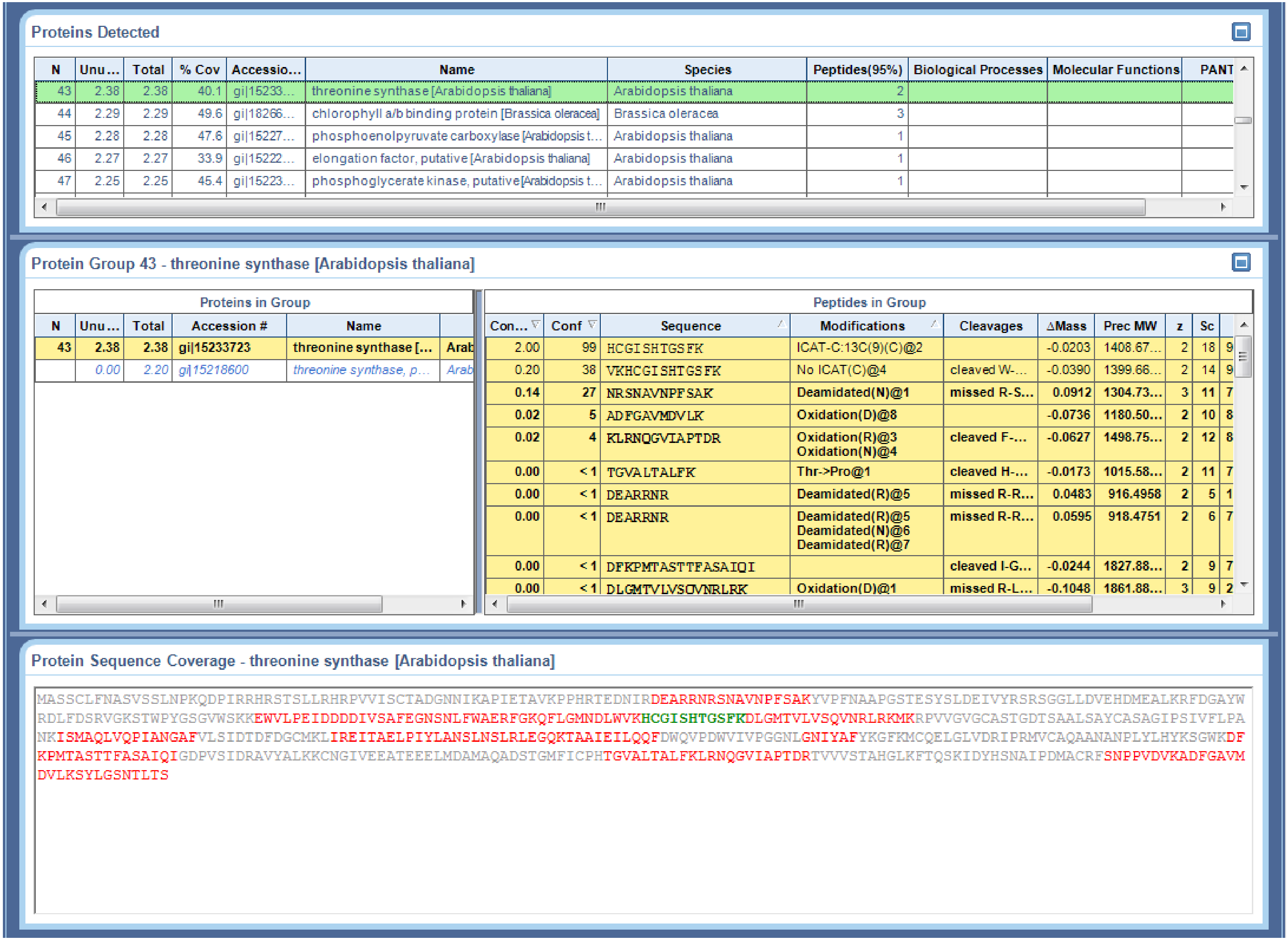
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0472	1987.02…	4	15	3
2.00	99	PCIRPIHVK	ICAT-C:13C(9)(C)@2	cleaved Y-P…	-0.0204	1297.75…	2	14	2
2.00	99	RAETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@10	missed R-A…	-0.0819	2143.09…	3	16	1
2.00	99	SVQDFCVANLKR	ICAT-C:13C(9)(C)@6	cleaved A-S…	-0.0138	1614.84…	3	15	2
1.40	96	SVQDFCVANLK	ICAT-C:13C(9)(C)@6	cleaved A-S…	-0.0641	1458.69…	2	14	1
0.05	11	GYPCIRPIHVK	Oxidation(P)@3 No ICAT(C)@4	cleaved A-G…	0.0571	1297.75…	2	15	2
0.00	96	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0465	1977.99…	4	13	3
0.00	95	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0414	1978.00…	3	13	1
0.00	78	AETPAGYPCIRPIHVK	ICAT-C(C)@9		-0.0238	1978.02…	4	12	2
0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0456	1987.03…	4	14	2
0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		-0.0688	1987.00…	3	16	1

Protein Sequence Coverage - oxalic acid oxidase [Brassica napus]

```
MLRIIFLLSLLFALSNASVQDFCVANLKRAETPAGYPCIRPIHVKASDFVFSLGTPGNTTNIISAAVTPGFVAQFPALNGLGISTARLDLAPKGVIPMHTHPGASEVLFVLDGSITAGFISSANSVYV
QTLKPGQVMVFPQGLLHFQINAGKTPAAAFVTFSSASPGLQILDFALFANTLSTELVSATTFLPPATVKTLKGVLGGTG
```

gi|15233723 Threonine synthase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
43	2.38	2.38	40.1	gi|15233…	threonine synthase [Arabidopsis thaliana]	Arabidopsis thaliana	2			
44	2.29	2.29	49.6	gi|18266…	chlorophyll a/b binding protein [Brassica oleracea]	Brassica oleracea	3			
45	2.28	2.28	47.6	gi|15227…	phosphoenolpyruvate carboxylase [Arabidopsis t…	Arabidopsis thaliana	1			
46	2.27	2.27	33.9	gi|15222…	elongation factor, putative [Arabidopsis thaliana]	Arabidopsis thaliana	1			
47	2.25	2.25	45.4	gi|15223…	phosphoglycerate kinase, putative [Arabidopsis t…	Arabidopsis thaliana	1			

Protein Group 43 - threonine synthase [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
43	**2.38**	**2.38**	**gi|15233723**	**threonine synthase [...**	**Arab**
	0.00	*2.20*	*gi|15218600*	*threonine synthase, p…*	*Arab*

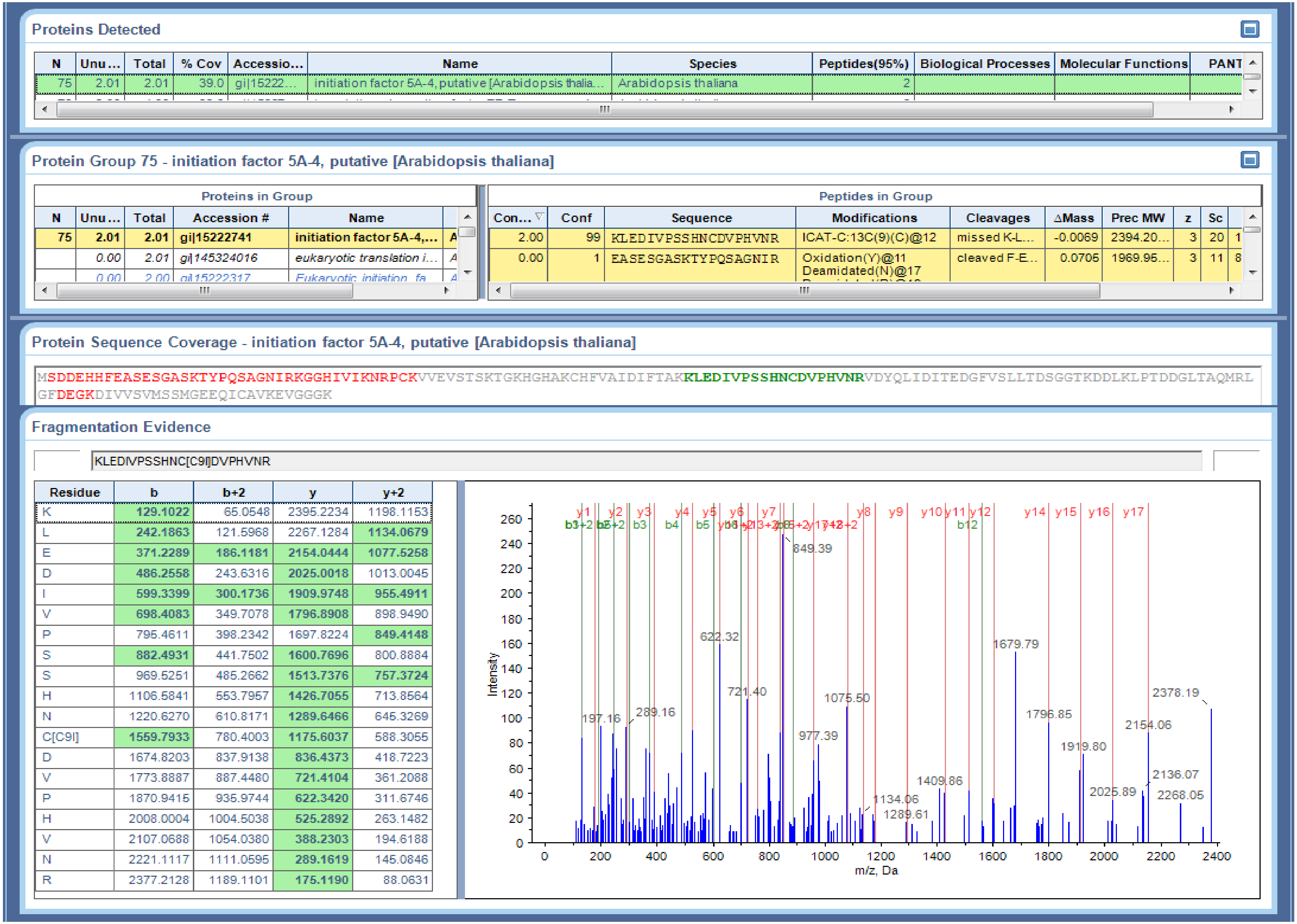
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	HCGISHTGSFK	ICAT-C:13C(9)(C)@2		-0.0203	1408.67…	2	18	9
0.20	38	VKHCGISHTGSFK	No ICAT(C)@4	cleaved W-…	-0.0390	1399.66…	2	14	9
0.14	**27**	**NRSNAVNPFSAK**	**Deamidated(N)@1**	**missed R-S…**	**0.0912**	**1304.73…**	**3**	**11**	**7**
0.02	**5**	**ADFGAVMDVLK**	**Oxidation(D)@8**		**-0.0736**	**1180.50…**	**2**	**10**	**8**
0.02	**4**	**KLRNQGVIAPTDR**	**Oxidation(R)@3** **Oxidation(N)@4**	**cleaved F-…**	**-0.0627**	**1498.75…**	**2**	**12**	**8**
0.00	**< 1**	**TGVALTALFK**	**Thr->Pro@1**	**cleaved H-…**	**-0.0173**	**1015.58…**	**2**	**11**	**7**
0.00	**< 1**	**DEARRNR**	**Deamidated(R)@5**	**missed R-R…**	**0.0483**	**916.4958**	**2**	**5**	**1**
0.00	**< 1**	**DEARRNR**	**Deamidated(R)@5** **Deamidated(N)@6** **Deamidated(R)@7**	**missed R-R…**	**0.0595**	**918.4751**	**2**	**6**	**7**
0.00	**< 1**	**DFKPMTASTTFASAIQI**		**cleaved I-G…**	**-0.0244**	**1827.88…**	**2**	**9**	**7**
0.00	**< 1**	**DLGMTVLVSQVNRLRK**	**Oxidation(D)@1**	**missed R-L…**	**-0.1048**	**1861.88…**	**3**	**9**	**2**

Protein Sequence Coverage - threonine synthase [Arabidopsis thaliana]

```
MASSCLFNASVSSLNPKQDPIRRHRSTSLLRHRPVVISCTADGNNIKAPIETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHDMEALKRFDGAYW
RDLFDSRVGKSTWPYGSGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMKRPVVGVGCASTGDTSAALSAYCASAGIPSIVFLPA
NKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPIYLANSLNSLRLEGQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKDF
KPMTASTTFASAIQIGDPVSIDRAVYALKKCNGIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVM
DVLKSYLGSNTLTS
```

gi|15222741 Initiation factor 5A-4, putative



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
75	2.01	2.01	39.0	gi|15222…	initiation factor 5A-4, putative [Arabidopsis thalia…	Arabidopsis thaliana	2			

Protein Group 75 - initiation factor 5A-4, putative [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	A
75	**2.01**	**2.01**	**gi|15222741**	**initiation factor 5A-4,…**	**A**
	0.00	*2.01*	*gi|145324016*	*eukaryotic translation i…*	*A*
	0.00	*2.00*	*gi|15222317*	*Eukaryotic initiation fa*	*A*

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	KLEDIVPSSHNCDVPHVNR	ICAT-C:13C(9)(C)@12	missed K-L…	-0.0069	2394.20…	3	20	1
0.00	1	EASESGASKTYPQSAGNIR	Oxidation(Y)@11 Deamidated(N)@17	cleaved F-E…	0.0705	1969.95…	3	11	8

Protein Sequence Coverage - initiation factor 5A-4, putative [Arabidopsis thaliana]

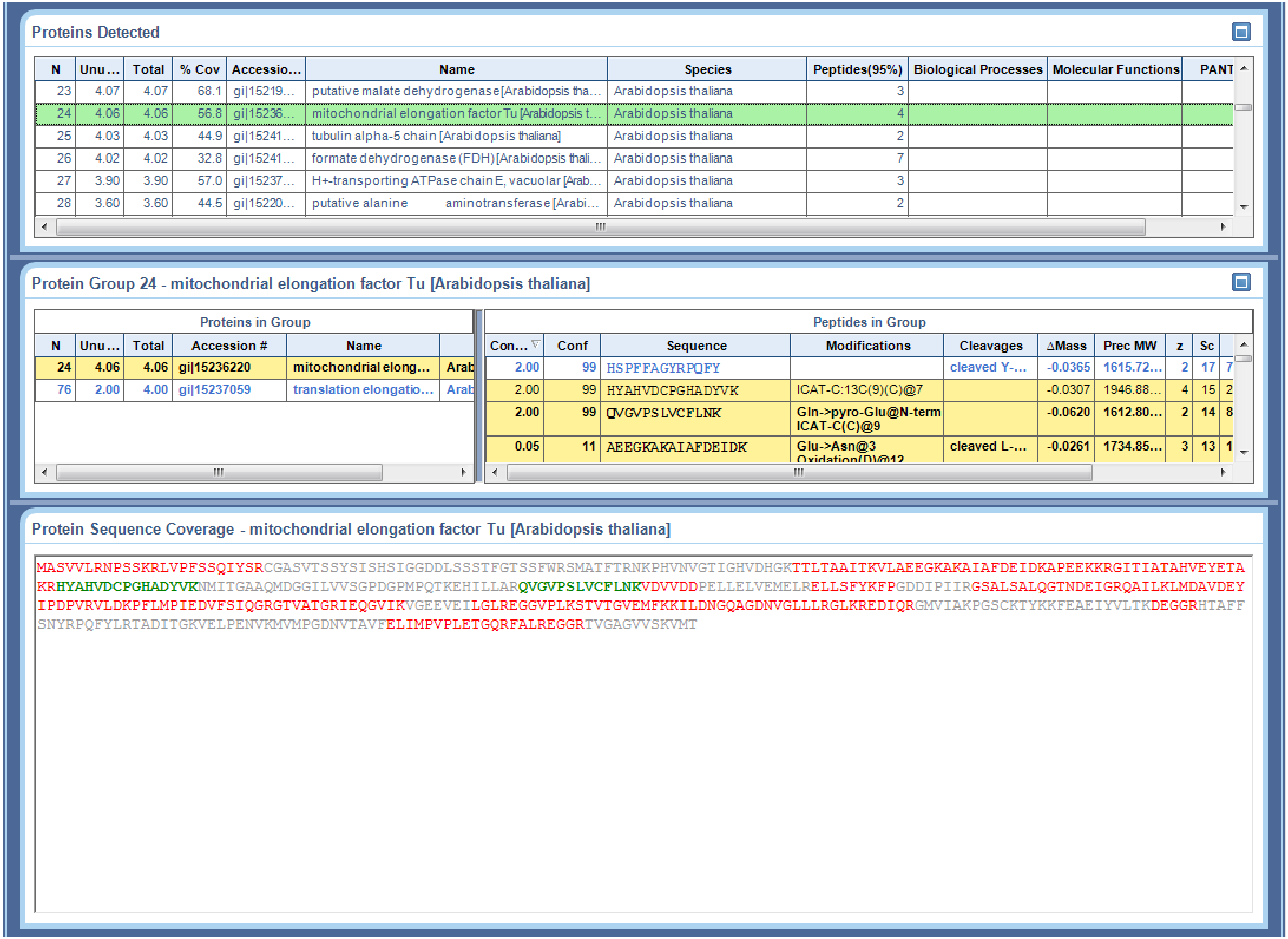
MSDDEHHFEASESGASKTYPQSAGNIRKGGHIVIKNRPCKVVEVSTSKTGKHGHAKCHFVAIDIFTAK**KLEDIVPSSHNCDVPHVNR**VDYQLIDITEDGFVSLLTDSGGTKDDLKLPTDDGLTAQMRL
GFDEGKDIVVSVMSSMGEEQICAVKEVGGGK

Fragmentation Evidence

KLEDIVPSSHNC[C9I]DVPHVNR

Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2395.2234	1198.1153
L	**242.1863**	121.5968	2267.1284	**1134.0679**
E	**371.2289**	**186.1181**	**2154.0444**	**1077.5258**
D	**486.2558**	243.6316	**2025.0018**	1013.0045
I	**599.3399**	**300.1736**	**1909.9748**	**955.4911**
V	**698.4083**	349.7078	**1796.8908**	898.9490
P	795.4611	398.2342	1697.8224	**849.4148**
S	**882.4931**	441.7502	**1600.7696**	800.8884
S	969.5251	485.2662	**1513.7376**	**757.3724**
H	1106.5841	553.7957	**1426.7055**	713.8564
N	1220.6270	610.8171	**1289.6466**	645.3269
C[C9I]	**1559.7933**	780.4003	**1175.6037**	588.3055
D	1674.8203	837.9138	**836.4373**	418.7223
V	1773.8887	887.4480	**721.4104**	361.2088
P	1870.9415	935.9744	**622.3420**	311.6746
H	2008.0004	1004.5038	**525.2892**	263.1482
V	2107.0688	1054.0380	**388.2303**	194.6188
N	2221.1117	1111.0595	**289.1619**	145.0846
R	2377.2128	1189.1101	**175.1190**	88.0631

gi|15236220 Mitochondrial elongation factor Tu



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
23	4.07	4.07	68.1	gi|15219…	putative malate dehydrogenase [Arabidopsis tha…	Arabidopsis thaliana	3			
24	4.06	4.06	56.8	gi|15236…	mitochondrial elongation factor Tu [Arabidopsis t…	Arabidopsis thaliana	4			
25	4.03	4.03	44.9	gi|15241…	tubulin alpha-5 chain [Arabidopsis thaliana]	Arabidopsis thaliana	2			
26	4.02	4.02	32.8	gi|15241…	formate dehydrogenase (FDH) [Arabidopsis thali…	Arabidopsis thaliana	7			
27	3.90	3.90	57.0	gi|15237…	H+-transporting ATPase chain E, vacuolar [Arab…	Arabidopsis thaliana	3			
28	3.60	3.60	44.5	gi|15220…	putative alanine aminotransferase [Arabi…	Arabidopsis thaliana	2			

Protein Group 24 - mitochondrial elongation factor Tu [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
24	4.06	4.06	gi|15236220	mitochondrial elong…	Arab
76	2.00	4.00	gi|15237059	translation elongatio…	Arab

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	HSPFFAGYRPQFY		cleaved Y-…	-0.0365	1615.72…	2	17	7
2.00	99	HYAHVDCPGHADYVK	ICAT-C:13C(9)(C)@7		-0.0307	1946.88…	4	15	2
2.00	99	QVGVPSLVCFLNK	Gln->pyro-Glu@N-term ICAT-C(C)@9		-0.0620	1612.80…	2	14	8
0.05	11	AEEGKAKAIAFDEIDK	Glu->Asn@3 Oxidation(D)@12	cleaved L-…	-0.0261	1734.85…	3	13	1

Protein Sequence Coverage - mitochondrial elongation factor Tu [Arabidopsis thaliana]

```
MASVVLRNPSSKRLVPFSSQIYSRCGASVTSSYSISHSIGGDDLSSSTFGTSSFWRSMATFTRNKPHVNVGTIGHVDHGKTTLTAAITKVLAEEGKAKAIAFDEIDKAPEEKKRGITIATAHVEYETA
KRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSGPDGPMPQTKEHILLARQVGVPSLVCFLNKVDVVDDPELLELVEMELRELLSFYKFPGDDIPIIRGSALSALQGTNDEIGRQAILKLMDAVDEY
IPDPVRVLDKPFLMPIEDVFSIQGRGTVATGRIEQGVIKVGEEVEILGLREGGVPLKSTVTGVEMFKKILDNGQAGDNVGLLLRGLKREDIQRGMVIAKPGSCKTYKKFEAEIYVLTKDEGGRHTAFF
SNYRPQFYLRTADITGKVELPENVKMVMPGDNVTAVFELIMPVPLETGQRFALREGGRTVGAGVVSKVMT
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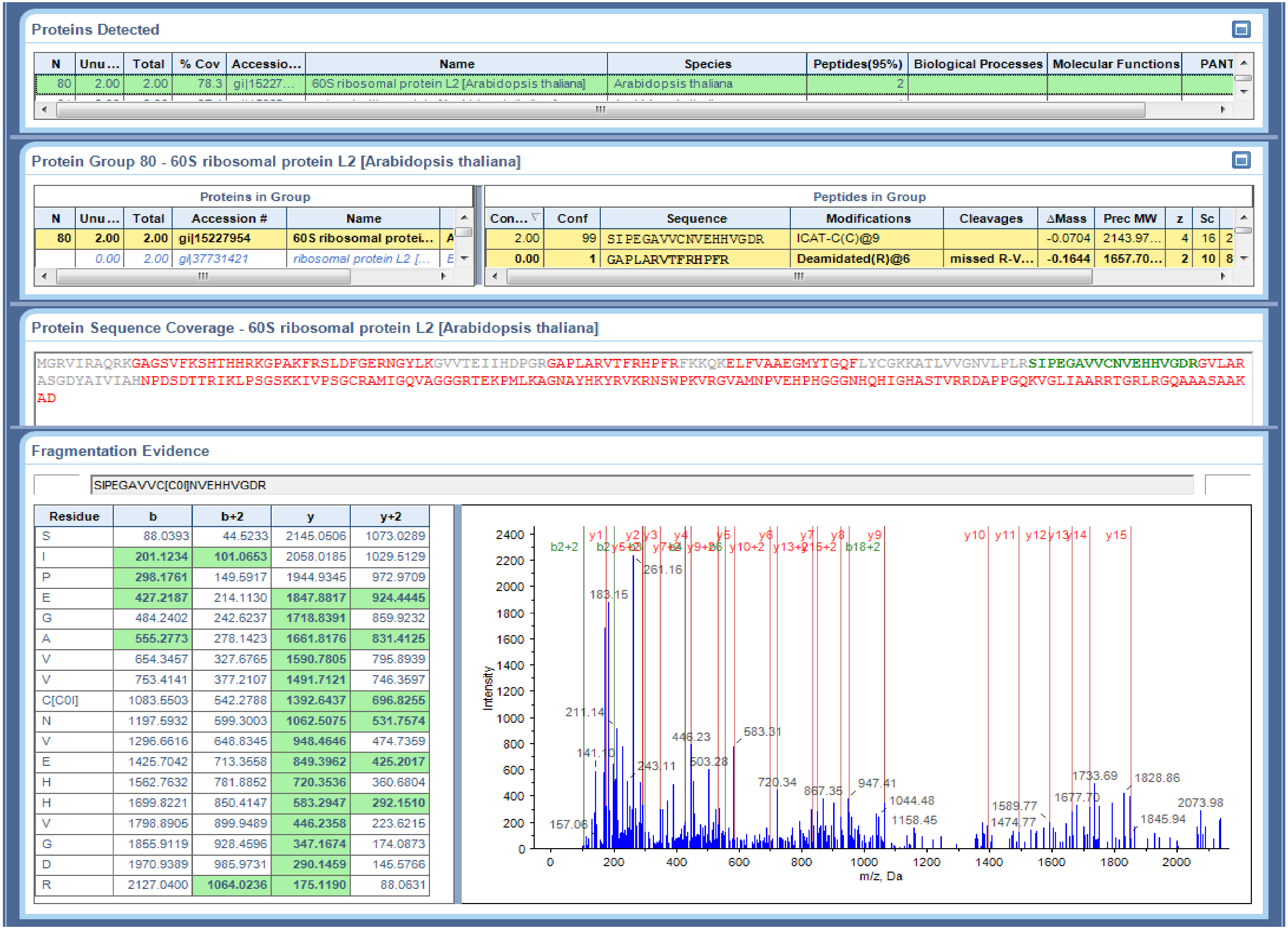
gi|15227954 60S ribosomal protein L2



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
80	2.00	2.00	78.3	gi|15227…	60S ribosomal protein L2 [Arabidopsis thaliana]	Arabidopsis thaliana	2			

Protein Group 80 - 60S ribosomal protein L2 [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
80	2.00	2.00	gi|15227954	60S ribosomal protei…	A
	0.00	2.00	gi|37731421	ribosomal protein L2 […	E

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	SIPEGAVVCNVEHHVGDR	ICAT-C(C)@9		-0.0704	2143.97…	4	16	2
0.00	1	GAPLARVTFRHPFR	Deamidated(R)@6	missed R-V…	-0.1644	1657.70…	2	10	8

Protein Sequence Coverage - 60S ribosomal protein L2 [Arabidopsis thaliana]

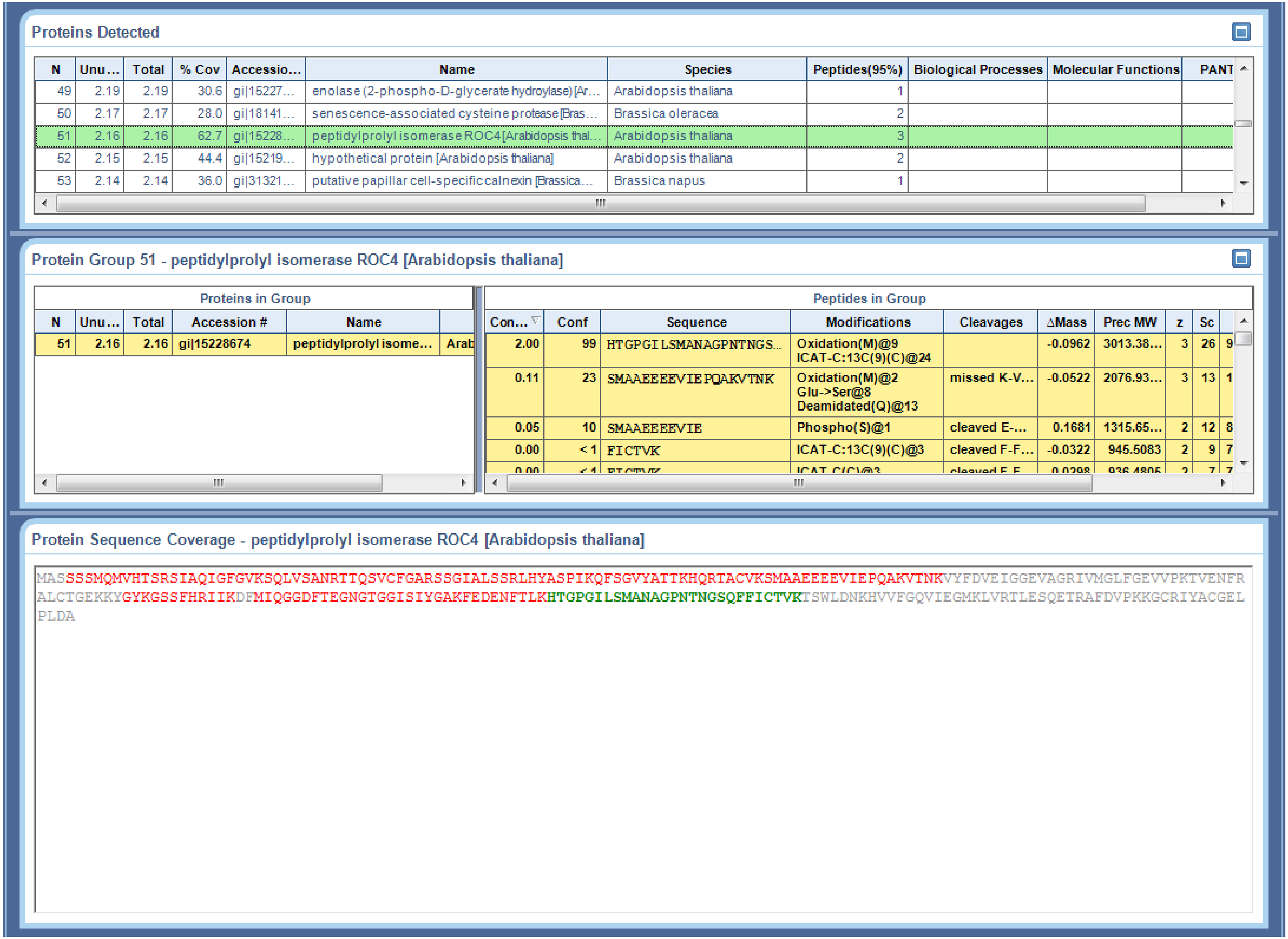
MGRVIRAQRKGAGSVFKSHTHHRKGPAKFRSLDFGERNGYLKGVVTEIIHDPGRGAPLARVTFRHPFRFKKQKELFVAAEGMYTGQFLYCGKKATLVVGNVLPLRSIPEGAVVCNVEHHVGDRGVLAR
ASGDYAIVIAHNPDSDTTRIKLPSGSKKIVPSGCRAMIGQVAGGGRTEKPMLKAGNAYHKYRVKRNSWPKVRGVAMNPVEHPHGGGNHQHIGHASTVRRDAPPGQKVGLIAARRTGRLRGQAAASAAK
AD

Fragmentation Evidence

SIPEGAVVC[C0I]NVEHHVGDR

Residue	b	b+2	y	y+2
S	88.0393	44.5233	2145.0506	1073.0289
I	**201.1234**	**101.0653**	2058.0185	1029.5129
P	**298.1761**	149.5917	1944.9345	972.9709
E	**427.2187**	214.1130	**1847.8817**	**924.4445**
G	484.2402	242.6237	**1718.8391**	859.9232
A	**555.2773**	278.1423	**1661.8176**	**831.4125**
V	654.3457	327.6765	**1590.7805**	795.8939
V	753.4141	377.2107	**1491.7121**	746.3597
C[C0I]	1083.5503	542.2788	**1392.6437**	**696.8255**
N	1197.5932	599.3003	**1062.5075**	**531.7574**
V	1296.6616	648.8345	**948.4646**	474.7359
E	1425.7042	713.3558	**849.3962**	**425.2017**
H	1562.7632	781.8852	**720.3536**	360.6804
H	1699.8221	850.4147	**583.2947**	**292.1510**
V	1798.8905	899.9489	**446.2358**	223.6215
G	1855.9119	928.4596	**347.1674**	174.0873
D	1970.9389	985.9731	**290.1459**	145.5766
R	2127.0400	**1064.0236**	**175.1190**	88.0631

gi|15228674 Peptidylprolyl isomerase ROC4



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
49	2.19	2.19	30.6	gi|15227…	enolase (2-phospho-D-glycerate hydroylase) [Ar…	Arabidopsis thaliana	1			
50	2.17	2.17	28.0	gi|18141…	senescence-associated cysteine protease [Bras…	Brassica oleracea	2			
51	2.16	2.16	62.7	gi|15228…	peptidylprolyl isomerase ROC4 [Arabidopsis thal…	Arabidopsis thaliana	3			
52	2.15	2.15	44.4	gi|15219…	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	2			
53	2.14	2.14	36.0	gi|31321…	putative papillar cell-specific calnexin [Brassica…	Brassica napus	1			

Protein Group 51 - peptidylprolyl isomerase ROC4 [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
51	2.16	2.16	gi|15228674	peptidylprolyl isome…	Arab

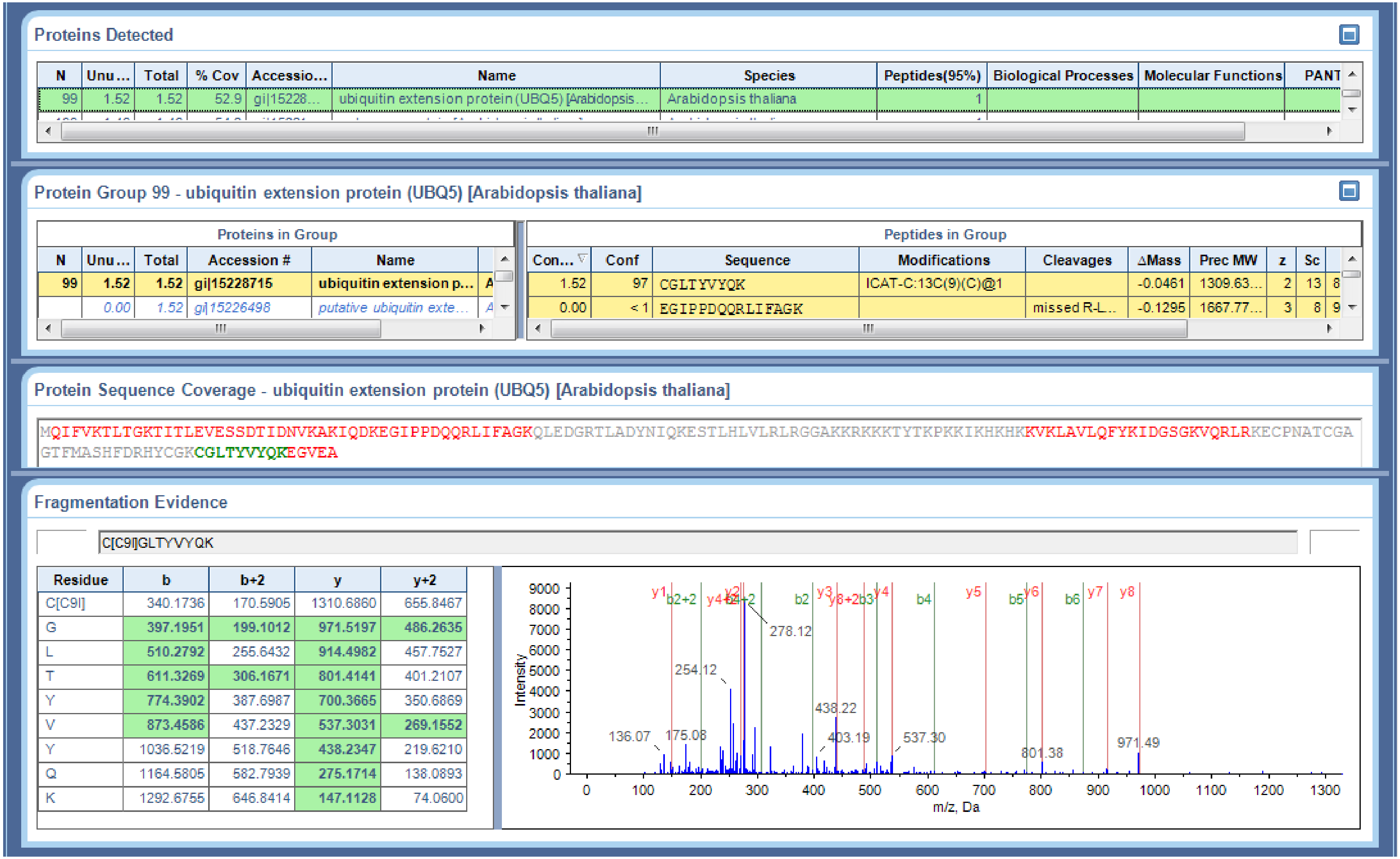
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
2.00	99	HTGPGILSMANAGPNTNGS…	Oxidation(M)@9 ICAT-C:13C(9)(C)@24		-0.0962	3013.38…	3	26	9
0.11	23	SMAAEEEEVIEPQAKVTNK	Oxidation(M)@2 Glu->Ser@8 Deamidated(Q)@13	missed K-V…	-0.0522	2076.93…	3	13	1
0.05	10	SMAAEEEEVIE	Phospho(S)@1	cleaved E-…	0.1681	1315.65…	2	12	8
0.00	< 1	FICTVK	ICAT-C:13C(9)(C)@3	cleaved F-F…	-0.0322	945.5083	2	9	7
0.00	< 1	FICTVK	ICAT-C(C)@3	cleaved F-F	0.0298	936.4805	2	7	7

Protein Sequence Coverage - peptidylprolyl isomerase ROC4 [Arabidopsis thaliana]

MASSSSMQMVHTSRSIAQIGFGVKSQLVSANRTTQSVCFGARSSGIALSSRLHYASPIKQFSGVYATTKHQRTACVKSMAAEEEEVIEPQAKVTNKVYFDVEIGGEVAGRIVMGLFGEVVPKTVENFR
ALCTGEKKYGYKGSSFHRIIKDFMIQGGDFTEGNGTGGISIYGAKFEDENFTLKHTGPGILSMANAGPNTNGSQFFICTVKTSWLDNKHVVFGQVIEGMKLVRTLESQETRAFDVPKKGCRIYACGEL
PLDA

gi|15228715 Ubiquitin extension protein (UBQ5)



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
99	1.52	1.52	52.9	gi|15228…	ubiquitin extension protein (UBQ5) [Arabidopsis…	Arabidopsis thaliana	1			

Protein Group 99 - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
99	**1.52**	**1.52**	**gi|15228715**	**ubiquitin extension p…**	**A**
	0.00	*1.52*	*gi|15226498*	*putative ubiquitin exte…*	*A*

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	
1.52	97	CGLTYVYQK	ICAT-C:13C(9)(C)@1		-0.0461	1309.63…	2	13	8
0.00	< 1	EGIPPDQQRLIFAGK		missed R-L…	-0.1295	1667.77…	3	8	9

Protein Sequence Coverage - ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

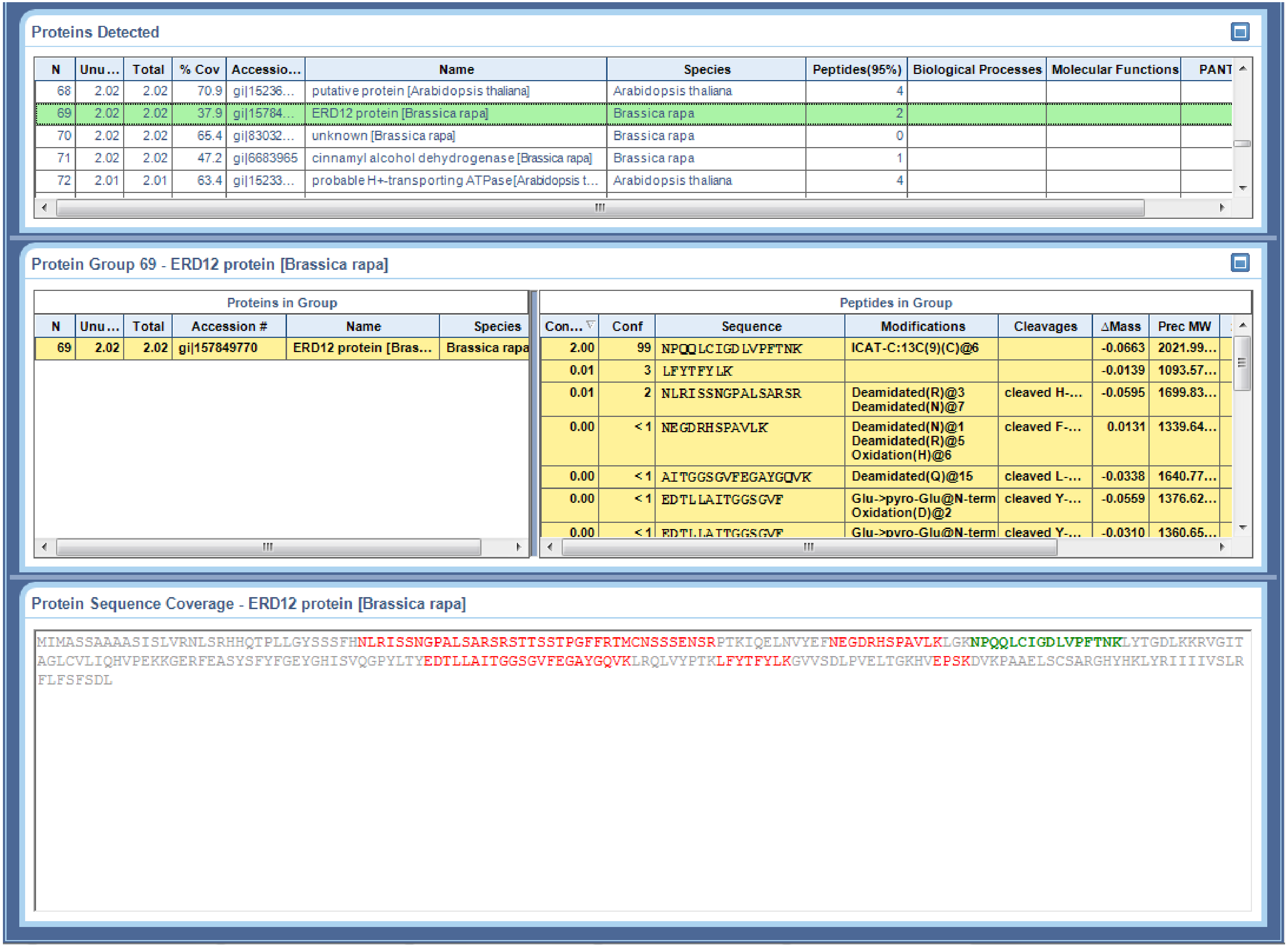
MQIFVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLADYNIQKESTLHLVLRLRGGAKKRKKKTYTKPKKIKHKHKKVKLAVLQFYKIDGSGKVQRLRKECPNATCGA
GTFMASHFDRHYCGKCGLTYVYQKEGVEA

Fragmentation Evidence

C[C9I]GLTYVYQK

Residue	b	b+2	y	y+2
C[C9I]	340.1736	170.5905	1310.6860	655.8467
G	397.1951	199.1012	971.5197	486.2635
L	510.2792	255.6432	914.4982	457.7527
T	611.3269	306.1671	801.4141	401.2107
Y	774.3902	387.6987	700.3665	350.6869
V	873.4586	437.2329	537.3031	269.1552
Y	1036.5219	518.7646	438.2347	219.6210
Q	1164.5805	582.7939	275.1714	138.0893
K	1292.6755	646.8414	147.1128	74.0600

gi|157849770 Early response to dehydration protein (ERD12)



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
68	2.02	2.02	70.9	gi|15236…	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	4			
69	2.02	2.02	37.9	gi|15784…	ERD12 protein [Brassica rapa]	Brassica rapa	2			
70	2.02	2.02	65.4	gi|83032…	unknown [Brassica rapa]	Brassica rapa	0			
71	2.02	2.02	47.2	gi|6683965	cinnamyl alcohol dehydrogenase [Brassica rapa]	Brassica rapa	1			
72	2.01	2.01	63.4	gi|15233…	probable H+-transporting ATPase [Arabidopsis t…	Arabidopsis thaliana	4			

Protein Group 69 - ERD12 protein [Brassica rapa]

Proteins in Group

N	Unu…	Total	Accession #	Name	Species
69	2.02	2.02	gi|157849770	ERD12 protein [Bras…	Brassica rapa

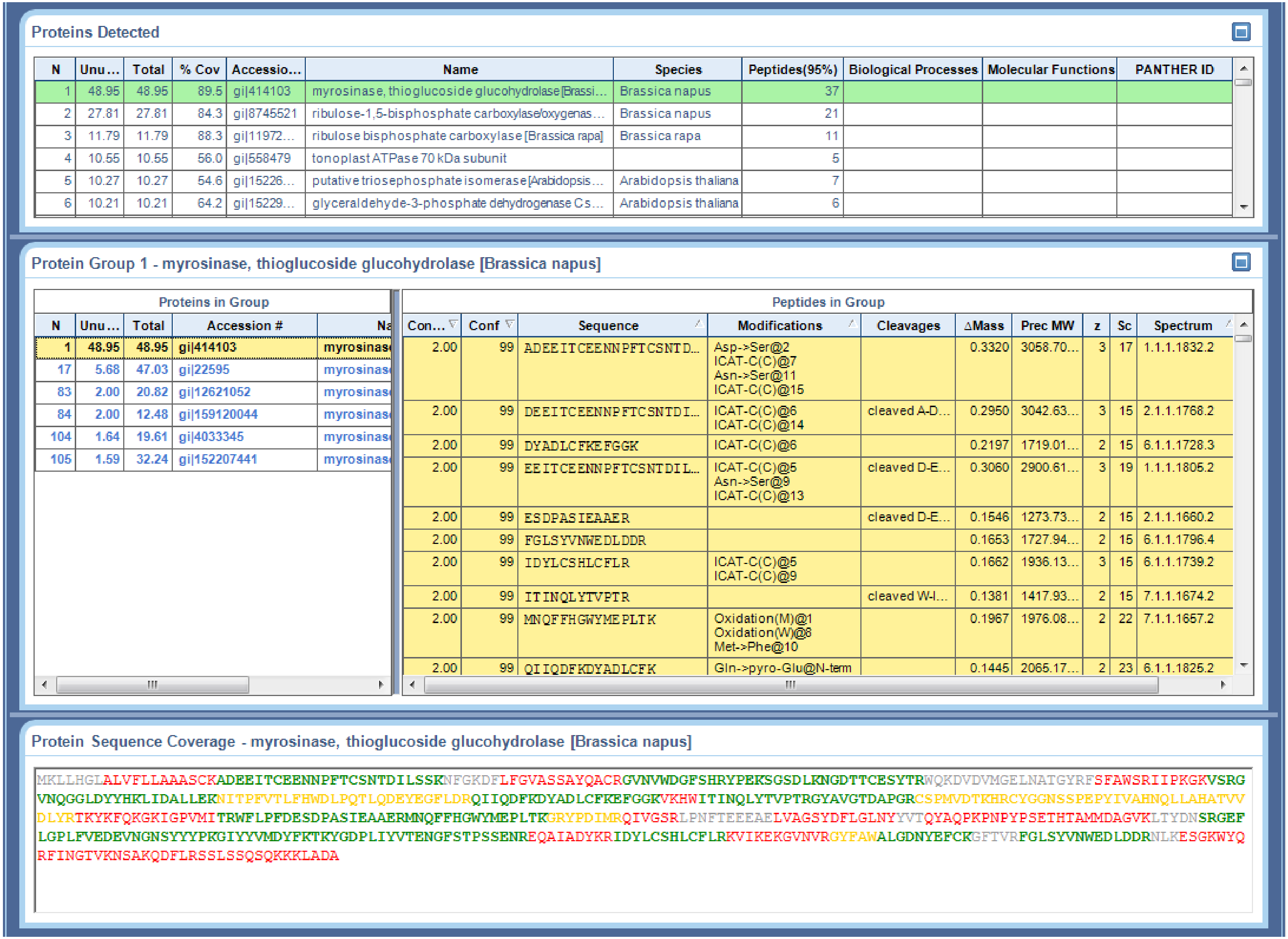
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	NPQQLCIGDLVPFTNK	ICAT-C:13C(9)(C)@6		-0.0663	2021.99…
0.01	3	LFYTFYLK			-0.0139	1093.57…
0.01	2	NLRISSNGPALSARSR	Deamidated(R)@3 Deamidated(N)@7	cleaved H-…	-0.0595	1699.83…
0.00	< 1	NEGDRHSPAVLK	Deamidated(N)@1 Deamidated(R)@5 Oxidation(H)@6	cleaved F-…	0.0131	1339.64…
0.00	< 1	AITGGSGVFEGAYGQVK	Deamidated(Q)@15	cleaved L-…	-0.0338	1640.77…
0.00	< 1	EDTLLAITGGSGVF	Glu->pyro-Glu@N-term Oxidation(D)@2	cleaved Y-…	-0.0559	1376.62…
0.00	< 1	EDTLLAITGGSGVF	Glu->pyro-Glu@N-term	cleaved Y-…	-0.0310	1360.65…

Protein Sequence Coverage - ERD12 protein [Brassica rapa]

MIMASSAAAASISLVRNLSRHHQTPLLGYSSSFHNLRISSNGPALSARSRSTTSSTPGFFRTMCNSSSENSRPTKIQELNVYEFNEGDRHSPAVLKLGKNPQQLCIGDLVPFTNKLYTGDLKKRVGIT
AGLCVLIQHVPEKKGERFEASYSFYFGEYGHISVQGPYLTYEDTLLAITGGSGVFEGAYGQVKLRQLVYPTKLFYTFYLKGVVSDLPVELTGKHVEPSKDVKPAAELSCSARGHYHKLYRIIIIVSLR
FLFSFSDL

gi|414103 Myrosinase, thioglucoside glucohydrolase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
1	48.95	48.95	89.5	gi|414103	myrosinase, thioglucoside glucohydrolase [Brassi…	Brassica napus	37			
2	27.81	27.81	84.3	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas…	Brassica napus	21			
3	11.79	11.79	88.3	gi|11972…	ribulose bisphosphate carboxylase [Brassica rapa]	Brassica rapa	11			
4	10.55	10.55	56.0	gi|558479	tonoplast ATPase 70 kDa subunit		5			
5	10.27	10.27	54.6	gi|15226…	putative triosephosphate isomerase [Arabidopsis…	Arabidopsis thaliana	7			
6	10.21	10.21	64.2	gi|15229…	glyceraldehyde-3-phosphate dehydrogenase C s…	Arabidopsis thaliana	6			

Protein Group 1 - myrosinase, thioglucoside glucohydrolase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accession #	Na
1	48.95	48.95	gi|414103	myrosinase
17	5.68	47.03	gi|22595	myrosinase
83	2.00	20.82	gi|12621052	myrosinase
84	2.00	12.48	gi|159120044	myrosinase
104	1.64	19.61	gi|4033345	myrosinase
105	1.59	32.24	gi|152207441	myrosinase

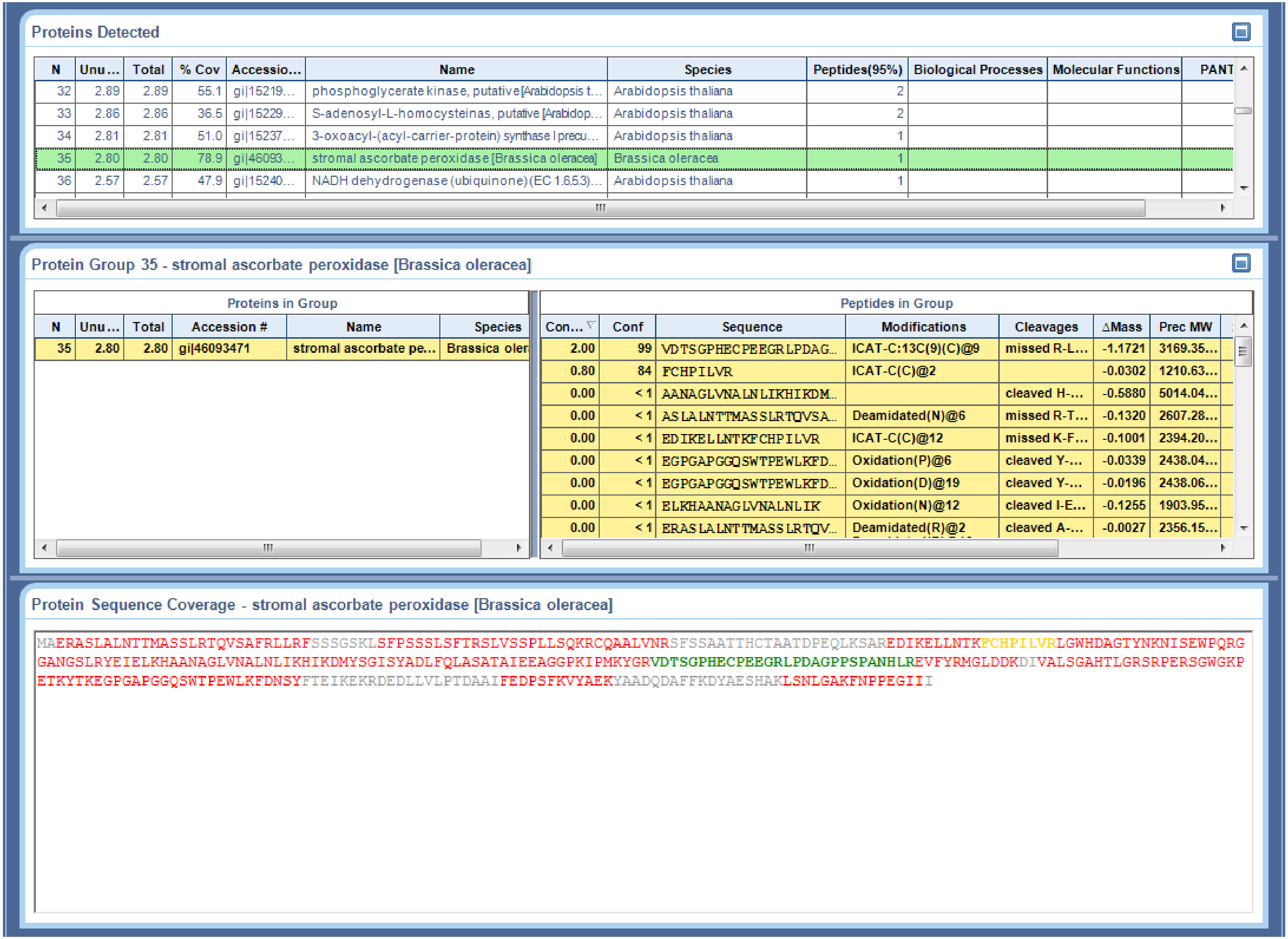
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	ADEEITCEENNPFTCSNTD…	Asp->Ser@2 ICAT-C(C)@7 Asn->Ser@11 ICAT-C(C)@15		0.3320	3058.70…	3	17	1.1.1.1832.2
2.00	99	DEEITCEENNPFTCSNTDI…	ICAT-C(C)@6 ICAT-C(C)@14	cleaved A-D…	0.2950	3042.63…	3	15	2.1.1.1768.2
2.00	99	DYADLCFKEFGGK	ICAT-C(C)@6		0.2197	1719.01…	2	15	6.1.1.1728.3
2.00	99	EEITCEENNPFTCSNTDIL…	ICAT-C(C)@5 Asn->Ser@9 ICAT-C(C)@13	cleaved D-E…	0.3060	2900.61…	3	19	1.1.1.1805.2
2.00	99	ESDPASIEAAER		cleaved D-E…	0.1546	1273.73…	2	15	2.1.1.1660.2
2.00	99	FGLSYVNWEDLDDR			0.1653	1727.94…	2	15	6.1.1.1796.4
2.00	99	IDYLCSHLCFLR	ICAT-C(C)@5 ICAT-C(C)@9		0.1662	1936.13…	3	15	6.1.1.1739.2
2.00	99	ITINQLYTVPTR		cleaved W-I…	0.1381	1417.93…	2	15	7.1.1.1674.2
2.00	99	MNQFFHGWYMEPLTK	Oxidation(M)@1 Oxidation(W)@8 Met->Phe@10		0.1967	1976.08…	2	22	7.1.1.1657.2
2.00	99	QIIQDFKDYADLCFK	Gln->pyro-Glu@N-term		0.1445	2065.17…	2	23	6.1.1.1825.2

Protein Sequence Coverage - myrosinase, thioglucoside glucohydrolase [Brassica napus]

```
MKLLHGLALVFLLAAASCKADEEITCEENNPFTCSNTDILSSKNFGKDFLFGVASSAYQACRGVNVWDGFSHRYPEKSGSDLKNGDTTCESYTRWQKDVDVMGELNATGYRFSFAWSRIIPKGKVSRG
VNQGGLDYYHKLIDALLEKNITPFVTLFHWDLPQTLQDEYEGFLDRQIIQDFKDYADLCFKEFGGKVKHWITINQLYTVPTRGYAVGTDAPGRCSPMVDTKHRCYGGNSSPEPYIVAHNQLLAHATVV
DLYRTKYKFQKGKIGPVMITRWFLPFDESDPASIEAAERMNQFFHGWYMEPLTKGRYPDIMRQIVGSRLPNFTEEEAELVAGSYDFLGLNYYVTQYAQPKPNPYPSETHTAMMDAGVKLTYDNSRGEF
LGPLFVEDEVNGNSYYYPKGIYYVMDYFKTKYGDPLIYVTENGFSTPSSENREQAIADYKRIDYLCSHLCFLRKVIKEKGVNVRGYFAWALGDNYEFCKGFTVRFGLSYVNWEDLDDRNLKESGKWYQ
RFINGTVKNSAKQDFLRSSLSSQSQKKKLADA
```

gi|46093471 Stromal ascorbate peroxidase



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
32	2.89	2.89	55.1	gi|15219...	phosphoglycerate kinase, putative[Arabidopsis t...	Arabidopsis thaliana	2			
33	2.86	2.86	36.5	gi|15229...	S-adenosyl-L-homocysteinas, putative [Arabidop...	Arabidopsis thaliana	2			
34	2.81	2.81	51.0	gi|15237...	3-oxoacyl-(acyl-carrier-protein) synthase I precu...	Arabidopsis thaliana	1			
35	2.80	2.80	78.9	gi|46093...	stromal ascorbate peroxidase [Brassica oleracea]	Brassica oleracea	1			
36	2.57	2.57	47.9	gi|15240...	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3)...	Arabidopsis thaliana	1			

Protein Group 35 - stromal ascorbate peroxidase [Brassica oleracea]

Proteins in Group

N	Unu...	Total	Accession #	Name	Species
35	2.80	2.80	gi|46093471	stromal ascorbate pe...	Brassica oler

Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	VDTSGPHECPEEGRLPDAG...	ICAT-C:13C(9)(C)@9	missed R-L...	-1.1721	3169.35...
0.80	84	FCHPILVR	ICAT-C(C)@2		-0.0302	1210.63...
0.00	< 1	AANAGLVNALNLIKHIKDM...		cleaved H-...	-0.5880	5014.04...
0.00	< 1	ASLALNTTMASSLRTQVSA...	Deamidated(N)@6	missed R-T...	-0.1320	2607.28...
0.00	< 1	EDIKELLNTKFCHPILVR	ICAT-C(C)@12	missed K-F...	-0.1001	2394.20...
0.00	< 1	EGPGAPGGQSWTPEWLKFD...	Oxidation(P)@6	cleaved Y-...	-0.0339	2438.04...
0.00	< 1	EGPGAPGGQSWTPEWLKFD...	Oxidation(D)@19	cleaved Y-...	-0.0196	2438.06...
0.00	< 1	ELKHAANAGLVNALNLIK	Oxidation(N)@12	cleaved I-E...	-0.1255	1903.95...
0.00	< 1	ERASLALNTTMASSLRTQV...	Deamidated(R)@2	cleaved A-...	-0.0027	2356.15...

Protein Sequence Coverage - stromal ascorbate peroxidase [Brassica oleracea]

```
MAERASLALNTTMASSLRTQVSAFRLLRFSSSGSKLSFPSSSLSFTRSLVSSPLLSQKRCQAALVNRSFSSAATTHCTAATDPEQLKSAREDIKELLNTKFCHPILVRLGWHDAGTYNKNISEWPQRG
GANGSLRYEIELKHAANAGLVNALNLIKHIKDMYSGISYADLFQLASATAIEEAGGPKIPMKYGRVDTSGPHECPEEGRLPDAGPPSPANHLREVFYRMGLDDKDIVALSGAHTLGRSRPERSGWGKP
ETKYTKEGPGAPGGQSWTPEWLKFDNSYFTEIKEKRDEDLLVLPTDAAIFEDPSFKVYAEKYAADQDAFFKDYAESHAKLSNLGAKFNPPEGIII
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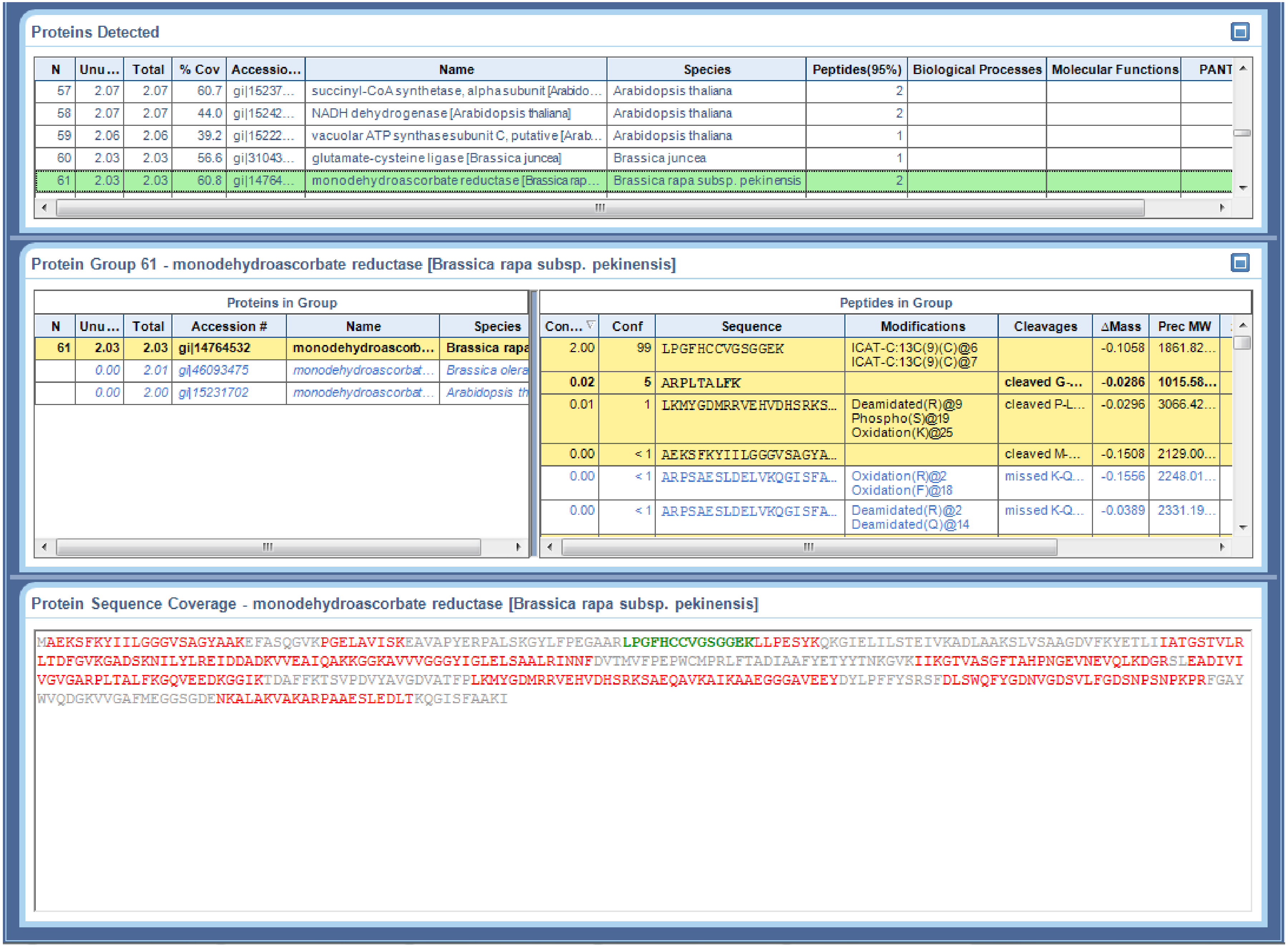
gi|14764532 Monodehydroascorbate reductase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
57	2.07	2.07	60.7	gi|15237…	succinyl-CoA synthetase, alpha subunit [Arabido…	Arabidopsis thaliana	2			
58	2.07	2.07	44.0	gi|15242…	NADH dehydrogenase [Arabidopsis thaliana]	Arabidopsis thaliana	2			
59	2.06	2.06	39.2	gi|15222…	vacuolar ATP synthase subunit C, putative [Arab…	Arabidopsis thaliana	1			
60	2.03	2.03	56.6	gi|31043…	glutamate-cysteine ligase [Brassica juncea]	Brassica juncea	1			
61	2.03	2.03	60.8	gi|14764…	monodehydroascorbate reductase [Brassica rap…	Brassica rapa subsp. pekinensis	2			

Protein Group 61 - monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]

Proteins in Group

N	Unu…	Total	Accession #	Name	Species
61	**2.03**	**2.03**	**gi|14764532**	**monodehydroascorb…**	**Brassica rapa**
	0.00	*2.01*	*gi|46093475*	*monodehydroascorbat…*	*Brassica olera*
	0.00	*2.00*	*gi|15231702*	*monodehydroascorbat…*	*Arabidopsis th*

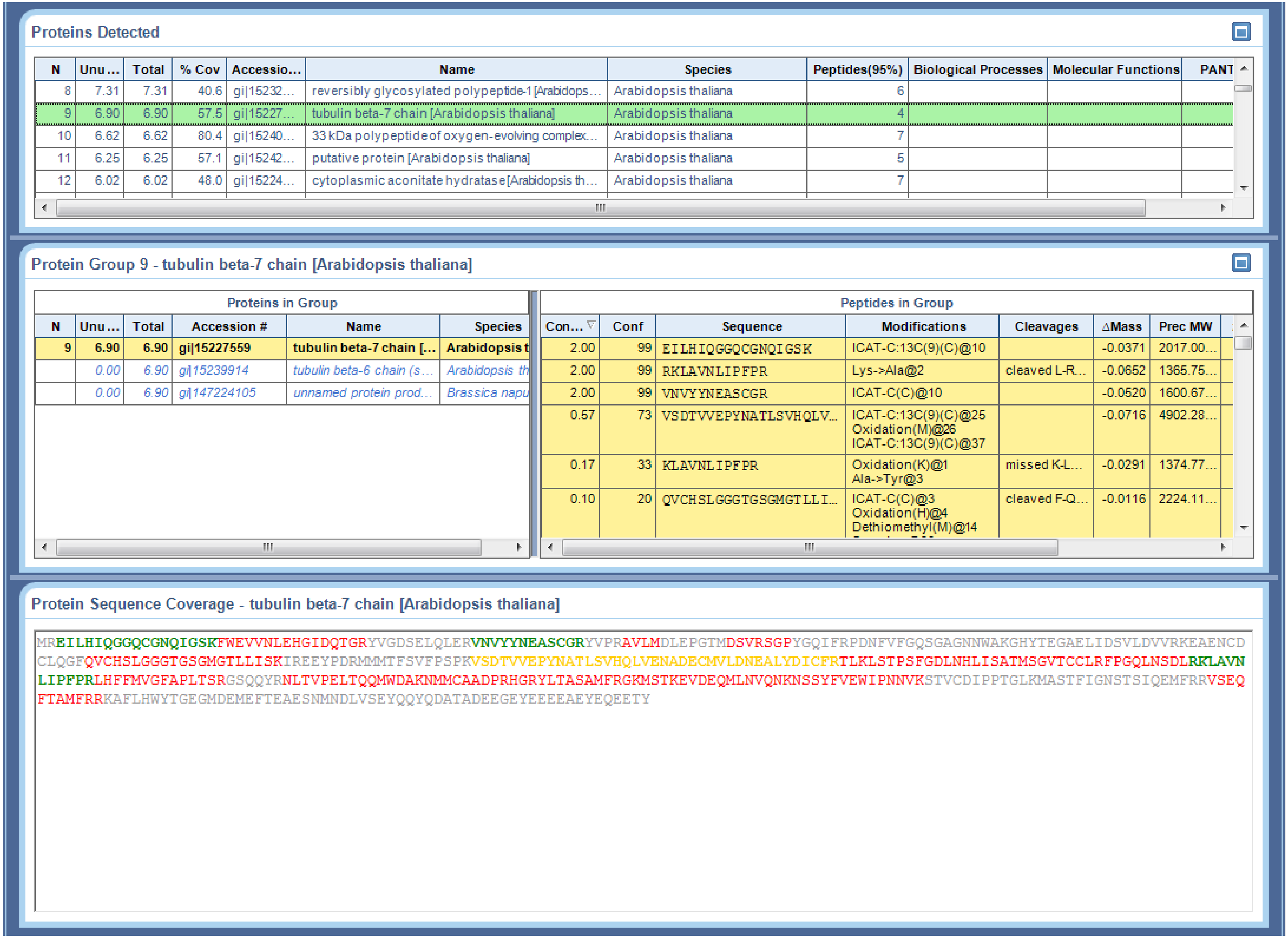
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	LPGFHCCVGSGGEK	ICAT-C:13C(9)(C)@6 ICAT-C:13C(9)(C)@7		-0.1058	1861.82…
0.02	**5**	**ARPLTALFK**		**cleaved G-…**	**-0.0286**	**1015.58…**
0.01	1	LKMYGDMRRVEHVDHSRKS…	Deamidated(R)@9 Phospho(S)@19 Oxidation(K)@25	cleaved P-L…	-0.0296	3066.42…
0.00	< 1	AEKSFKYIIILGGGVSAGYA…		cleaved M-…	-0.1508	2129.00…
0.00	< 1	ARPSAESLDELVKQGISFA…	Oxidation(R)@2 Oxidation(F)@18	missed K-Q…	-0.1556	2248.01…
0.00	< 1	ARPSAESLDELVKQGISFA…	Deamidated(R)@2 Deamidated(Q)@14	missed K-Q…	-0.0389	2331.19…

Protein Sequence Coverage - monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]

MAEKSFKYIIILGGGVSAGYAAKEFASQGVKPGELAVISKEAVAPYERPALSKGYLFPEGAARLPGFHCCVGSGGEKLLPESYKQKGIELILSTEIVKADLAAKSLVSAAGDVFKYETLIIATGSTVLR
LTDFGVKGADSKNILYLREIDDADKVVEAIQAKKGGKAVVVGGGYIGLELSAALRINNFDVTMVFPEPWCMPRLFTADIAAFYETYYTNKGVKIIKGTVASGFTAHPNGEVNEVQLKDGRSLEADIVI
VGVGARPLTALFKGQVEEDKGGIKTDAFFKTSVPDVYAVGDVATFPLKMYGDMRRVEHVDHSRKSAEQAVKAIKAAEGGGAVEEYDYLPFFYSRSFDLSWQFYGDNVGDSVLFGDSNPSNPKPRFGAY
WVQDGKVVGAFMEGGSGDENKALAKVAKARPAAESLEDLTKQGISFAAKI

gi|15227559 Tubulin beta-7 chain



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
8	7.31	7.31	40.6	gi|15232...	reversibly glycosylated polypeptide-1 [Arabidops...	Arabidopsis thaliana	6			
9	6.90	6.90	57.5	gi|15227...	tubulin beta-7 chain [Arabidopsis thaliana]	Arabidopsis thaliana	4			
10	6.62	6.62	80.4	gi|15240...	33 kDa polypeptide of oxygen-evolving complex...	Arabidopsis thaliana	7			
11	6.25	6.25	57.1	gi|15242...	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	5			
12	6.02	6.02	48.0	gi|15224...	cytoplasmic aconitate hydratase [Arabidopsis th...	Arabidopsis thaliana	7			

Protein Group 9 - tubulin beta-7 chain [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name	Species
9	**6.90**	**6.90**	**gi|15227559**	**tubulin beta-7 chain [...**	**Arabidopsis t**
	0.00	*6.90*	*gi|15239914*	*tubulin beta-6 chain (s...*	*Arabidopsis th*
	0.00	*6.90*	*gi|147224105*	*unnamed protein prod...*	*Brassica napu*

Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	EILHIQGGQCGNQIGSK	ICAT-C:13C(9)(C)@10		-0.0371	2017.00...
2.00	99	RKLAVNLIPFPR	Lys->Ala@2	cleaved L-R...	-0.0652	1365.75...
2.00	99	VNVYYNEASCGR	ICAT-C(C)@10		-0.0520	1600.67...
0.57	73	VSDTVVEPYNATLSVHQLV...	ICAT-C:13C(9)(C)@25 Oxidation(M)@26 ICAT-C:13C(9)(C)@37		-0.0716	4902.28...
0.17	33	KLAVNLIPFPR	Oxidation(K)@1 Ala->Tyr@3	missed K-L...	-0.0291	1374.77...
0.10	20	QVCHSLGGGTGSGMGTLLI...	ICAT-C(C)@3 Oxidation(H)@4 Dethiomethyl(M)@14	cleaved F-Q...	-0.0116	2224.11...

Protein Sequence Coverage - tubulin beta-7 chain [Arabidopsis thaliana]

```
MREILHIQGGQCGNQIGSKFWEVVNLEHGIDQTGRYVGDSELQLERVNVYYNEASCGRYVPRAVLMDLEPGTMDSVRSGPYGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELIDSVLDVVRKEAENCD
CLQGFQVCHSLGGGTGSGMGTLLISKIREEYPDRMMMTFSVFPSPKVSDTVVEPYNATLSVHQLVENADECMVLDNEALYDICFRTLKLSTPSFGDLNHLISATMSGVTCCLRFPGQLNSDLRKLAVN
LIPFPRLHFFMVGFAPLTSRGSQQYRNLTVPELTQQMWDAKNMMCAADPRHGRYLTASAMFRGKMSTKEVDEQMLNVQNKNSSYFVEWIPNNVKSTVCDIPPTGLKMASTFIGNSTSIQEMFRRVSEQ
FTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQDATADEEGEYEEEEAEYEQEETY
```

gi|15235668 Extensin-like protein

Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
81	2.00	2.00	27.4	gi|15235…	extensin-like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			

Protein Group 81 - extensin-like protein [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	Speci
81	**2.00**	**2.00**	**gi|15235668**	**extensin-like protein…**	**Arabidops**
	0.00	*2.00*	*gi|15230120*	*disease resistance pro…*	*Arabidopsi*

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	IPASICQLPK	ICAT-C:13C(9)(C)@6		-0.0564	1304.70…
0.00	**1**	**MKKTIQILLF**	**Dethiomethyl(M)@1**	**cleaved F-F…**	**-0.1528**	**1202.57…**

Protein Sequence Coverage - extensin-like protein [Arabidopsis thaliana]

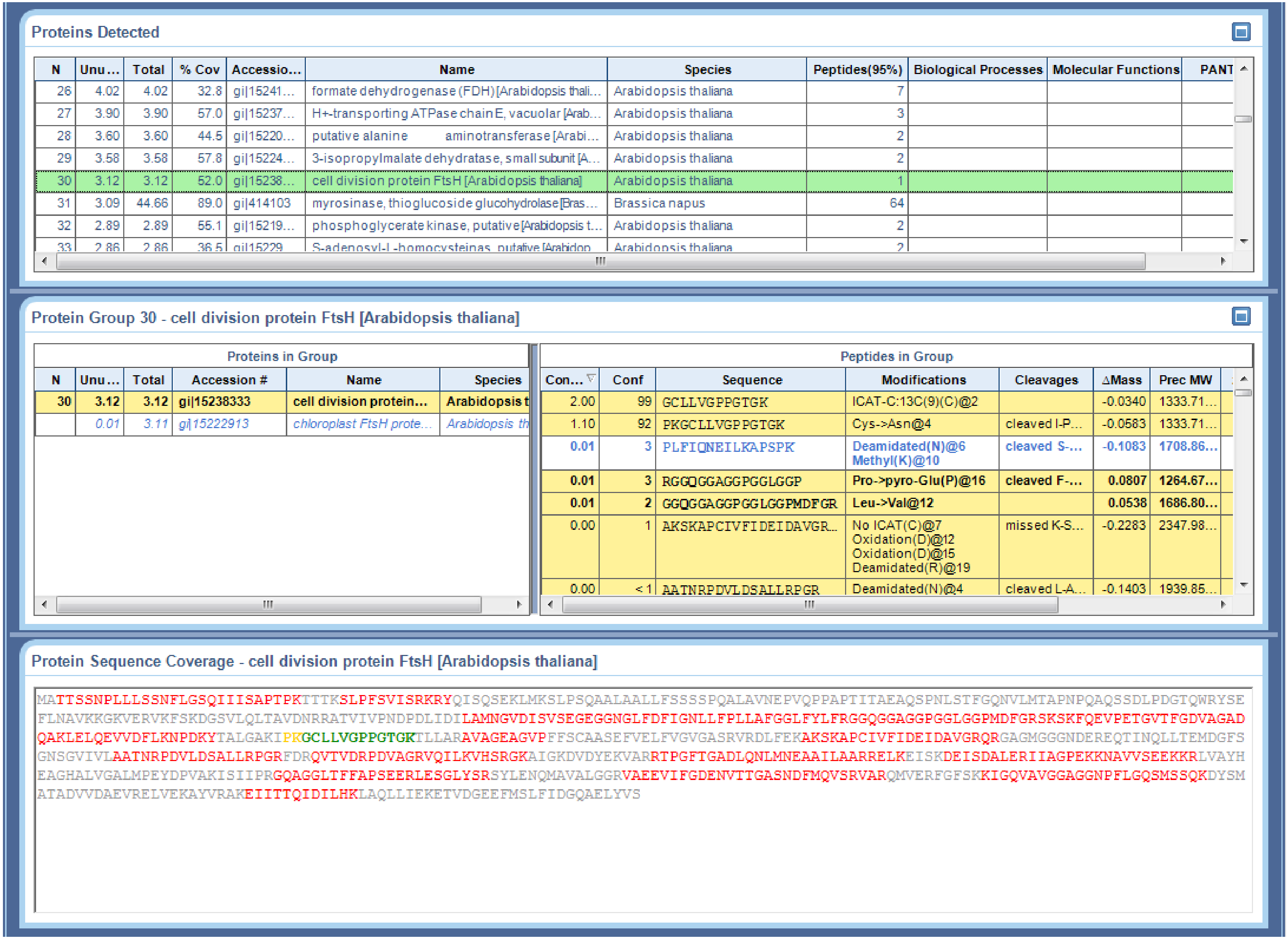
```
MKKTIQILLFFFFLINLTNALSISSDGGVLSDNEVRHIQRRQLLEFAERSVKITVDPSLNFENPRLRNAYIALQAWKQAILSDPNNFTSNWIGSNVCNYTGVFCSPALDNRKIRTVAGIDLNHADIAG
YLPEELGLLSDLALFHVNSNRFCGTVPHRFNRLKLLFELDLSNNRFAGKFPTVVLQLPSLKFLDLRFNEFEGTVPKELFSKDLDAIFINHNRFRFELPENFGDSPVSVIVLANNRFHGCVPSSLVEMK
NLNEIIFMNNGLNSCLPSDIGRLKNVTVFDVSFNELVGPLPESVGEMVSVEQLNVAHNMLSGKIPASICQLPKLENFTYSYNFFTGEAPVCLRLPEFDDRRNCLPGRPAQRSPGQCKAFLSRPPVNCG
SFSCGRSVSPRPPVVTPLPPPSLPSPPPPAPIFSTPPTLTSPPPPSPPPPVYSPPPPPPPPPPVYSPPPPPPPPPPPPVYSPPPPPPPPPPPPPVYSPPPPSPPPPPPPVYSPPPPPPPPPPPPVYSP
PPPPVYSSPPPPPSPAPTPVYCTRPPPPPPHSPPPPQFSPPPPEPYYYSSPPPPHSSPPPHSPPPPHSPPPPIYPYLSPPPPPTPVSSPPPTPVYSPPPPPPCIEPPPPPPCIEYSPPPPPPVVHYSS
PPPPPVYYSSPPPPPVYYSSPPPPPPVHYSSPPPPEVHYHSPPPPSPVHYSSPPPPSAPCEESPPPAPVVHHSPPPPMVHHSPPPPVIHQSPPPPSPEYEGPLPPVIGVSYASPPPPPFY
```

Fragmentation Evidence

IPASIC[C9I]QLPK

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1305.7646	**653.3859**
P	**211.1441**	106.0757	**1192.6805**	596.8439
A	**282.1812**	141.5942	**1095.6278**	**548.3175**
S	**369.2132**	185.1103	**1024.5907**	512.7990
I	**482.2973**	241.6523	**937.5586**	469.2830
C[C9I]	821.4637	**411.2355**	824.4746	412.7409
Q	**949.5223**	475.2648	**485.3082**	243.1577
L	**1062.6063**	531.8068	**357.2496**	**179.1285**
P	1159.6591	580.3332	**244.1656**	122.5864
K	**1287.7540**	644.3807	**147.1128**	74.0600

gi|15238333 Cell division protein FtsH



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
26	4.02	4.02	32.8	gi|15241…	formate dehydrogenase (FDH) [Arabidopsis thali…	Arabidopsis thaliana	7			
27	3.90	3.90	57.0	gi|15237…	H+-transporting ATPase chain E, vacuolar [Arab…	Arabidopsis thaliana	3			
28	3.60	3.60	44.5	gi|15220…	putative alanine aminotransferase [Arabi…	Arabidopsis thaliana	2			
29	3.58	3.58	57.8	gi|15224…	3-isopropylmalate dehydratase, small subunit [A…	Arabidopsis thaliana	2			
30	3.12	3.12	52.0	gi|15238…	cell division protein FtsH [Arabidopsis thaliana]	Arabidopsis thaliana	1			
31	3.09	44.66	89.0	gi|414103	myrosinase, thioglucoside glucohydrolase [Bras…	Brassica napus	64			
32	2.89	2.89	55.1	gi|15219…	phosphoglycerate kinase, putative [Arabidopsis t…	Arabidopsis thaliana	2			
33	2.86	2.86	36.5	gi|15229	S-adenosyl-L-homocysteinas, putative [Arabidop	Arabidopsis thaliana	2			

Protein Group 30 - cell division protein FtsH [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	Species
30	3.12	3.12	gi|15238333	cell division protein…	Arabidopsis t
	0.01	*3.11*	*gi|15222913*	*chloroplast FtsH prote…*	*Arabidopsis th*

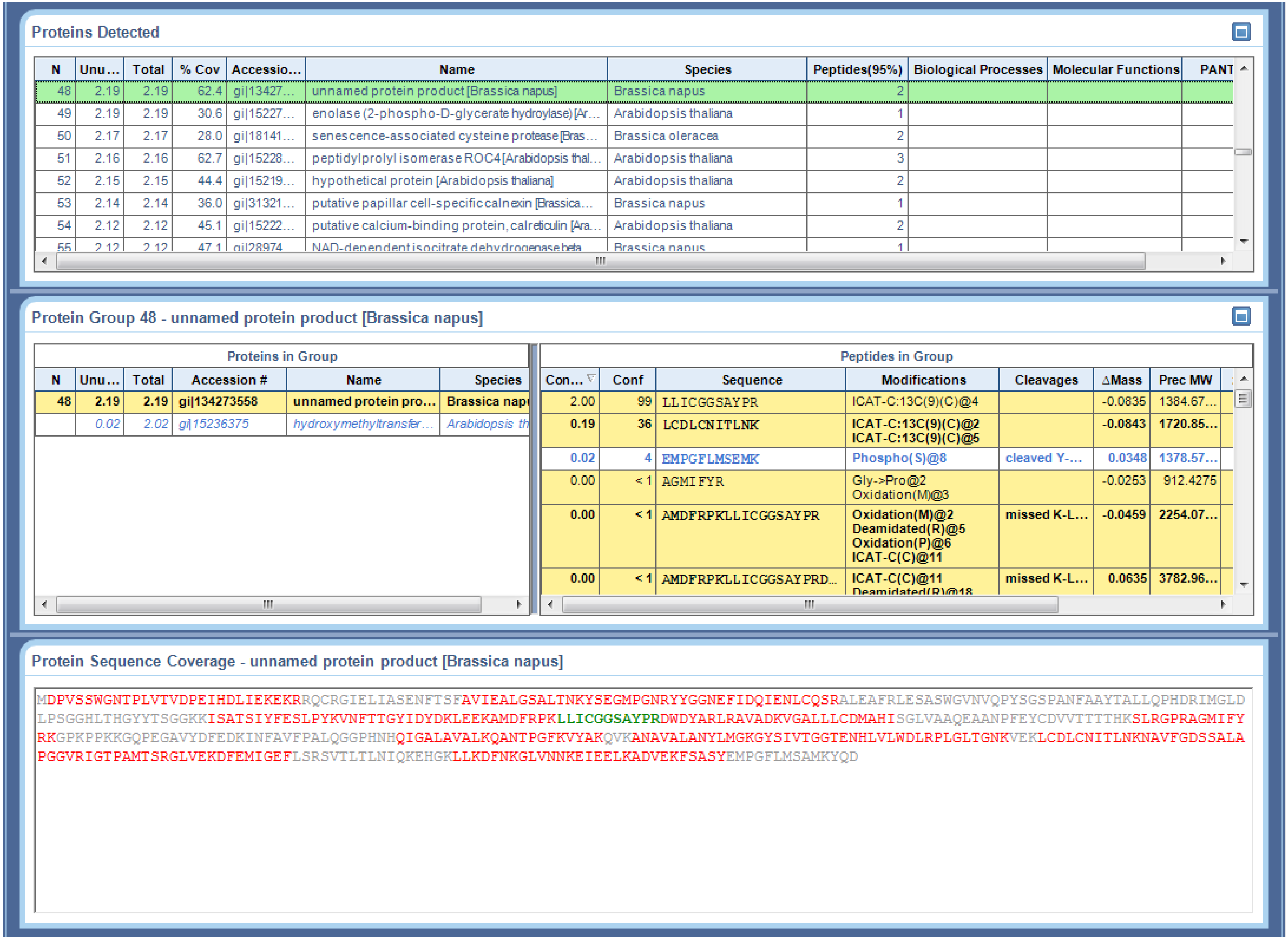
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	GCLLVGPPGTGK	ICAT-C:13C(9)(C)@2		-0.0340	1333.71…
1.10	92	PKGCLLVGPPGTGK	Cys->Asn@4	cleaved I-P…	-0.0583	1333.71…
0.01	3	PLFIQNEILKAPSPK	Deamidated(N)@6 Methyl(K)@10	cleaved S-…	-0.1083	1708.86…
0.01	3	RGGQGGAGGPGGLGGP	Pro->pyro-Glu(P)@16	cleaved F-…	0.0807	1264.67…
0.01	2	GGQGGAGGPGGLGGPMDFGR	Leu->Val@12		0.0538	1686.80…
0.00	1	AKSKAPCIVFIDEIDAVGR…	No ICAT(C)@7 Oxidation(D)@12 Oxidation(D)@15 Deamidated(R)@19	missed K-S…	-0.2283	2347.98…
0.00	< 1	AATNRPDVLDSALLRPGR	Deamidated(N)@4	cleaved L-A…	-0.1403	1939.85…

Protein Sequence Coverage - cell division protein FtsH [Arabidopsis thaliana]

MATTSSNPLLLSSNFLGSQIIISAPTPKTTTKSLPFSVISRKRYQISQSEKLMKSLPSQAALAALLFSSSSPQALAVNEPVQPPAPTITAEAQSPNLSTFGQNVLMTAPNPQAQSSDLPDGTQWRYSE
FLNAVKKGKVERVKFSKDGSVLQLTAVDNRRATVIVPNDPDLIDILAMNGVDISVSEGEGGNGLFDFIGNLLFPLLAFGGLFYLFRGGQGGAGGPGGLGGPMDFGRSKSKFQEVPETGVTFGDVAGAD
QAKLELQEVVDFLKNPDKYTALGAKIPKGCLLVGPPGTGKTLLARAVAGEAGVPFFSCAASEFVELFVGVGASRVRDLFEKAKSKAPCIVFIDEIDAVGRQRGAGMGGGNDEREQTINQLLTEMDGFS
GNSGVIVLAATNRPDVLDSALLRPGRFDRQVTVDRPDVAGRVQILKVHSRGKAIGKDVDYEKVARRTPGFTGADLQNLMNEAAILAARRELKEISKDEISDALERIIAGPEKKNAVVSEEKKRLVAYH
EAGHALVGALMPEYDPVAKISIIPRGQAGGLTFFAPSEERLESGLYSRSYLENQMAVALGGRVAEEVIFGDENVTTGASNDFMQVSRVARQMVERFGFSKKIGQVAVGGAGGNPFLGQSMSSQKDYSM
ATADVVDAEVRELVEKAYVRAKEIITTQIDILHKLAQLLIEKETVDGEEFMSLFIDGQAELYVS

gi|134273558 Unnamed protein product



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
48	2.19	2.19	62.4	gi|13427…	unnamed protein product [Brassica napus]	Brassica napus	2			
49	2.19	2.19	30.6	gi|15227…	enolase (2-phospho-D-glycerate hydroylase) [Ar…	Arabidopsis thaliana	1			
50	2.17	2.17	28.0	gi|18141…	senescence-associated cysteine protease [Bras…	Brassica oleracea	2			
51	2.16	2.16	62.7	gi|15228…	peptidylprolyl isomerase ROC4 [Arabidopsis thal…	Arabidopsis thaliana	3			
52	2.15	2.15	44.4	gi|15219…	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	2			
53	2.14	2.14	36.0	gi|31321…	putative papillar cell-specific calnexin [Brassica…	Brassica napus	1			
54	2.12	2.12	45.1	gi|15222…	putative calcium-binding protein, calreticulin [Ara…	Arabidopsis thaliana	2			
55	2.12	2.12	47.1	gi|28974…	NAD-dependent isocitrate dehydrogenase beta	Brassica napus	1			

Protein Group 48 - unnamed protein product [Brassica napus]

Proteins in Group

N	Unu…	Total	Accession #	Name	Species
48	**2.19**	**2.19**	**gi|134273558**	**unnamed protein pro…**	**Brassica nap**
	0.02	*2.02*	*gi|15236375*	*hydroxymethyltransfer…*	*Arabidopsis th*

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	LLICGGSAYPR	ICAT-C:13C(9)(C)@4		-0.0835	1384.67…
0.19	**36**	**LCDLCNITLNK**	**ICAT-C:13C(9)(C)@2 ICAT-C:13C(9)(C)@5**		**-0.0843**	**1720.85…**
0.02	4	EMPGFLMSEMK	Phospho(S)@8	cleaved Y-…	0.0348	1378.57…
0.00	< 1	AGMIFYR	Gly->Pro@2 Oxidation(M)@3		-0.0253	912.4275
0.00	**< 1**	**AMDFRPKLLICGGSAYPR**	**Oxidation(M)@2 Deamidated(R)@5 Oxidation(P)@6 ICAT-C(C)@11**	**missed K-L…**	**-0.0459**	**2254.07…**
0.00	**< 1**	**AMDFRPKLLICGGSAYPRD…**	**ICAT-C(C)@11 Deamidated(R)@18**	**missed K-L…**	**0.0635**	**3782.96…**

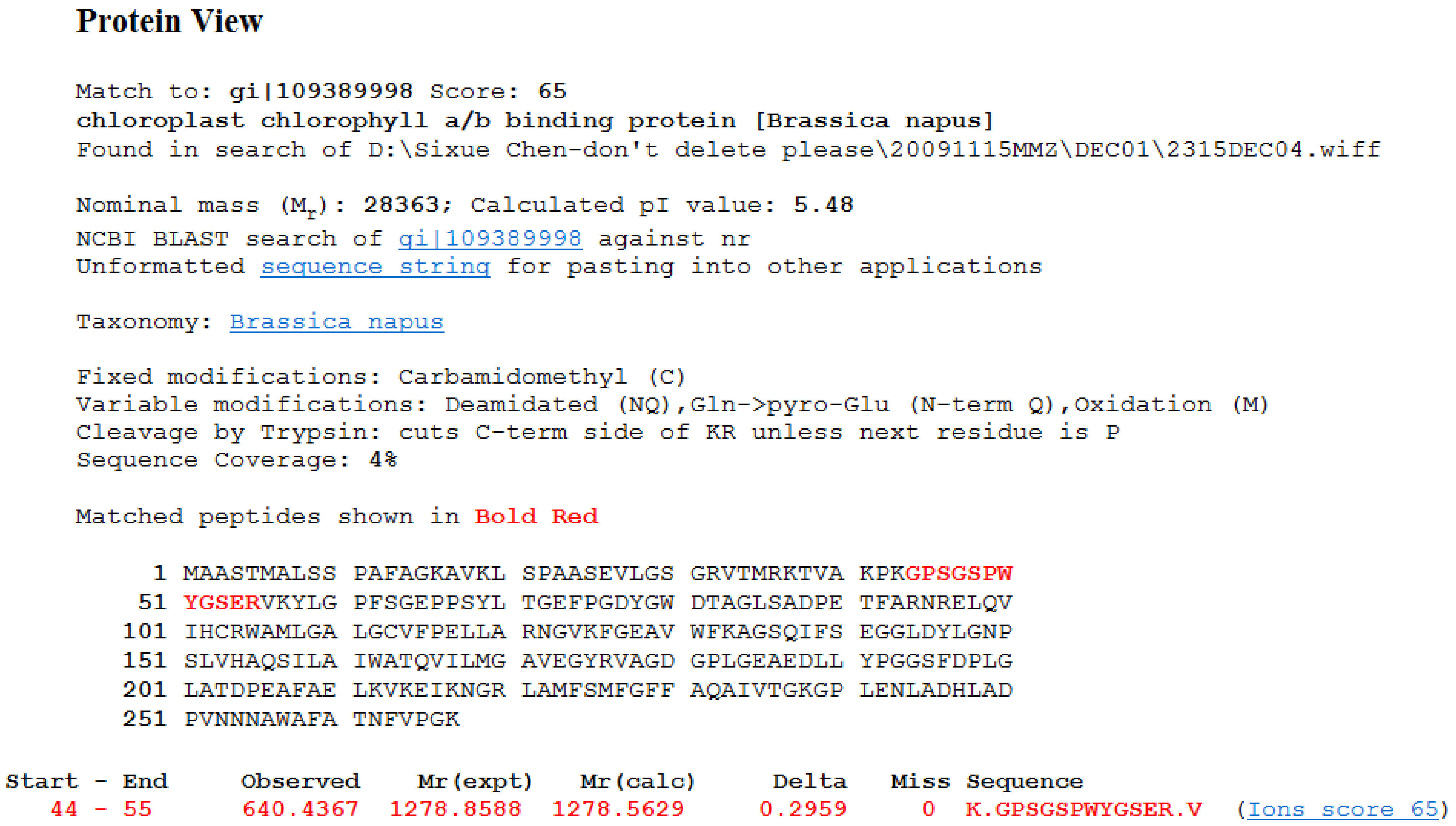
Protein Sequence Coverage - unnamed protein product [Brassica napus]

```
MDPVSSWGNTPLVTVDPEIHDLIEKEKRRQCRGIELIASENFTSFAVIEALGSALTNKYSEGMPGNRYYGGNEFIDQIENLCQSRALEAFRLESASWGVNVQPYSGSPANFAAYTALLQPHDRIMGLD
LPSGGHLTHGYYTSGGKKISATSIYFESLPYKVNFTTGYIDYDKLEEKAMDFRPKLLICGGSAYPRDWDYARLRAVADKVGALLLCDMAHISGLVAAQEAANPFEYCDVVTTTTHKSLRGPRAGMIFY
RKGPKPPKKGQPEGAVYDFEDKINFAVFPALQGGPHNHQIGALAVALKQANTPGFKVYAKQVKANAVALANYLMGKGYSIVTGGTENHLVLWDLRPLGLTGNKVEKLCDLCNITLNKNAVFGDSSALA
PGGVRIGTPAMTSRGLVEKDFEMIGEFLSRSVTLTLNIQKEHGKLLKDFNKGLVNNKEIEELKADVEKFSASYEMPGFLMSAMKYQD
```

Figure S6

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to MeJA treatment in guard cells by redox DIGE.

gi|109389998 Chlorophyll a/b binding protein



Protein View

```
Match to: gi|109389998 Score: 65
chloroplast chlorophyll a/b binding protein [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2315DEC04.wiff

Nominal mass (Mr): 28363; Calculated pI value: 5.48
NCBI BLAST search of gi|109389998 against nr
Unformatted sequence string for pasting into other applications

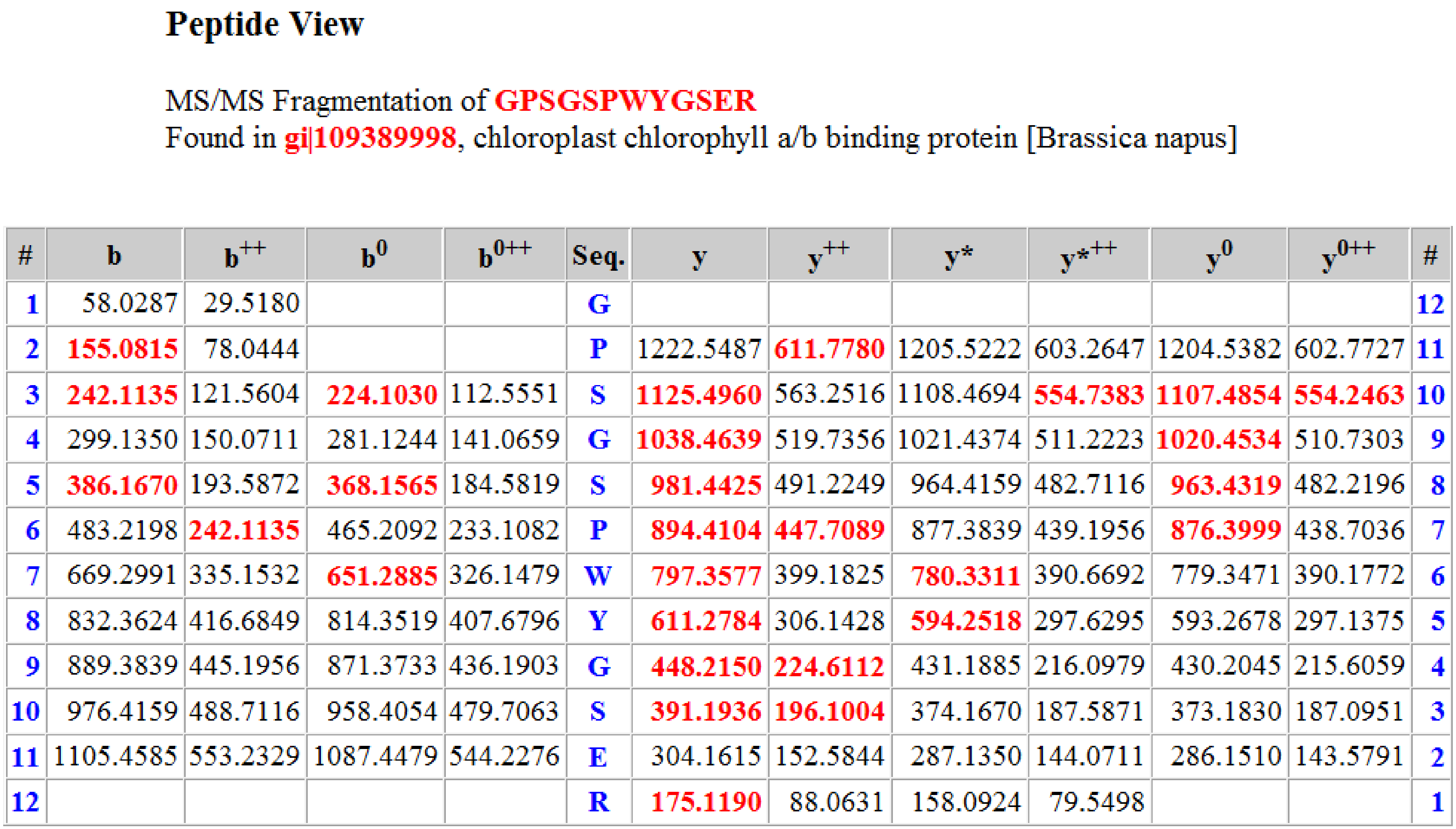
Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%

Matched peptides shown in Bold Red

      1 MAASTMALSS PAFAGKAVKL SPAASEVLGS GRVTMRKTVA KPKGPSGSPW
     51 YGSERVKYLG PFSGEPPSYL TGEFPGDYGW DTAGLSADPE TFARNRELQV
    101 IHCRWAMLGA LGCVFPELLA RNGVKFGEAV WFKAGSQIFS EGGLDYLGNP
    151 SLVHAQSILA IWATQVILMG AVEGYRVAGD GPLGEAEDLL YPGGSFDPLG
    201 LATDPEAFAE LKVKEIKNGR LAMFSMFGFF AQAIVTGKGP LENLADHLAD
    251 PVNNNAWAFA TNFVPGK

Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
  44 - 55     640.4367  1278.8588  1278.5629    0.2959     0  K.GPSGSPWYGSER.V   (Ions score 65)
```

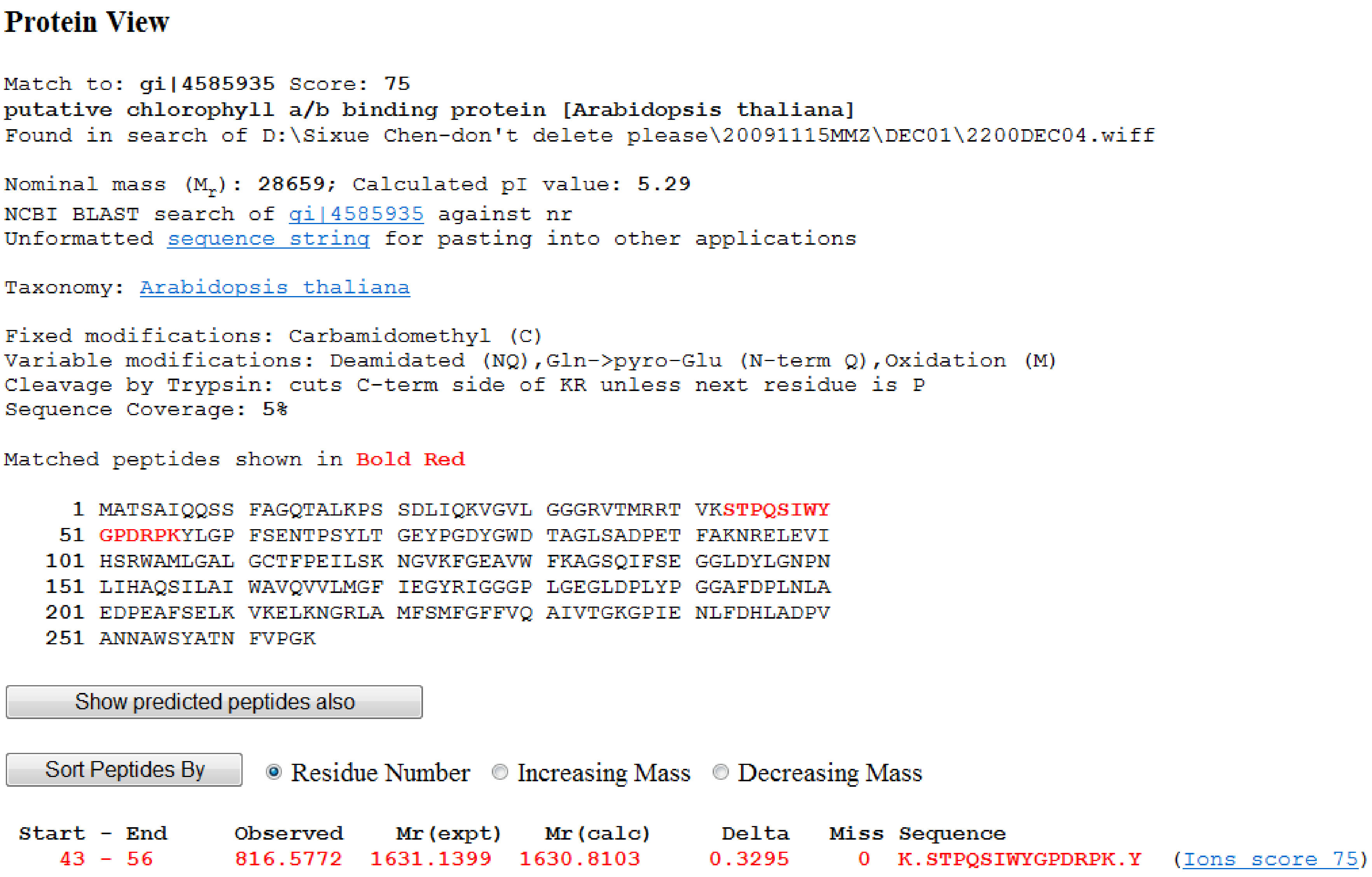


Peptide View

MS/MS Fragmentation of **GPSGSPWYGSER**
Found in **gi|109389998**, chloroplast chlorophyll a/b binding protein [Brassica napus]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	58.0287	29.5180			**G**							**12**
2	**155.0815**	78.0444			**P**	1222.5487	**611.7780**	1205.5222	603.2647	1204.5382	602.7727	**11**
3	**242.1135**	121.5604	**224.1030**	112.5551	**S**	**1125.4960**	563.2516	1108.4694	**554.7383**	**1107.4854**	**554.2463**	**10**
4	299.1350	150.0711	281.1244	141.0659	**G**	**1038.4639**	519.7356	1021.4374	511.2223	**1020.4534**	510.7303	**9**
5	**386.1670**	193.5872	**368.1565**	184.5819	**S**	**981.4425**	491.2249	964.4159	482.7116	**963.4319**	482.2196	**8**
6	483.2198	**242.1135**	465.2092	233.1082	**P**	**894.4104**	**447.7089**	877.3839	439.1956	**876.3999**	438.7036	**7**
7	669.2991	335.1532	**651.2885**	326.1479	**W**	**797.3577**	399.1825	**780.3311**	390.6692	779.3471	390.1772	**6**
8	832.3624	416.6849	814.3519	407.6796	**Y**	**611.2784**	306.1428	**594.2518**	297.6295	593.2678	297.1375	**5**
9	889.3839	445.1956	871.3733	436.1903	**G**	**448.2150**	**224.6112**	431.1885	216.0979	430.2045	215.6059	**4**
10	976.4159	488.7116	958.4054	479.7063	**S**	**391.1936**	**196.1004**	374.1670	187.5871	373.1830	187.0951	**3**
11	1105.4585	553.2329	1087.4479	544.2276	**E**	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
12					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

gi|4585935 Light harvesting chlorophyll A/B binding protein



Protein View

Match to: **gi|4585935** Score: **75**
putative chlorophyll a/b binding protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2200DEC04.wiff

Nominal mass (M_r): **28659**; Calculated pI value: **5.29**
NCBI BLAST search of gi|4585935 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in **Bold Red**

```
  1 MATSAIQQSS FAGQTALKPS SDLIQKVGVL GGGRVTMRRT VKSTPQSIWY
 51 GPDRPKYLGP FSENTPSYLT GEYPGDYGWD TAGLSADPET FAKNRELEVI
101 HSRWAMLGAL GCTFPEILSK NGVKFGEAVW FKAGSQIFSE GGLDYLGNPN
151 LIHAQSILAI WAVQVVLMGF IEGYRIGGGP LGEGLDPLYP GGAFDPLNLA
201 EDPEAFSELK VKELKNGRLA MFSMFGFFVQ AIVTGKGPIE NLFDHLADPV
251 ANNAWSYATN FVPGK
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

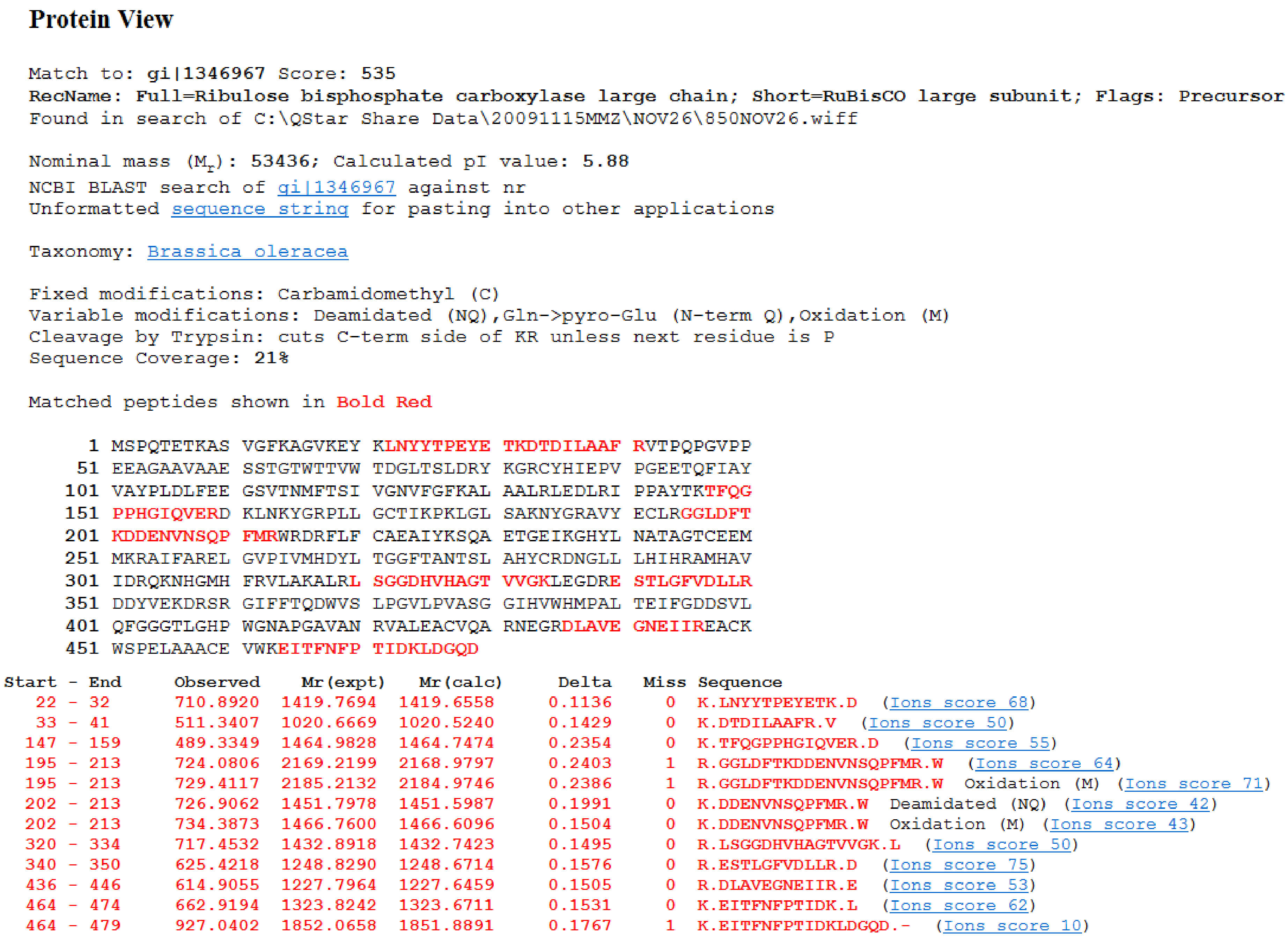
```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   43 - 56     816.5772  1631.1399  1630.8103   0.3295     0  K.STPQSIWYGPDRPK.Y   (Ions score 75)
```

Peptide View

MS/MS Fragmentation of **STPQSIWYGPDRPK**
Found in **gi|4585935**, putative chlorophyll a/b binding protein [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	189.0870	95.0471			171.0764	86.0418	T	1544.7856	772.8964	1527.7591	764.3832	1526.7750	763.8912	13
3	286.1397	143.5735			268.1292	134.5682	P	**1443.7379**	**722.3726**	1426.7114	713.8593	1425.7274	713.3673	12
4	414.1983	207.6028	397.1718	199.0895	396.1878	**198.5975**	Q	**1346.6852**	673.8462	1329.6586	665.3329	1328.6746	664.8409	11
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	S	**1218.6266**	609.8169	1201.6000	601.3037	1200.6160	600.8116	10
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	I	**1131.5946**	566.3009	1114.5680	557.7876	1113.5840	557.2956	9
7	800.3937	**400.7005**	783.3672	392.1872	782.3832	391.6952	W	**1018.5105**	509.7589	1001.4839	501.2456	**1000.4999**	500.7536	8
8	963.4571	482.2322	946.4305	473.7189	945.4465	473.2269	Y	**832.4312**	416.7192	815.4046	408.2060	814.4206	407.7139	7
9	1020.4785	510.7429	1003.4520	502.2296	1002.4680	501.7376	G	**669.3679**	335.1876	652.3413	326.6743	651.3573	326.1823	6
10	1117.5313	559.2693	1100.5047	550.7560	1099.5207	550.2640	P	**612.3464**	306.6768	595.3198	298.1636	594.3358	297.6715	5
11	1232.5582	616.7828	1215.5317	608.2695	1214.5477	607.7775	D	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	4
12	1388.6593	694.8333	1371.6328	686.3200	1370.6488	685.8280	R	**400.2667**	200.6370	383.2401	192.1237			3
13	1485.7121	743.3597	1468.6856	734.8464	1467.7015	734.3544	P	244.1656	122.5864	227.1390	114.0731			2
14							K	147.1128	74.0600	130.0863	65.5468			1

gi|1346967 Ribulose bisphosphate carboxylase large chain



Protein View

```
Match to: gi|1346967 Score: 535
RecName: Full=Ribulose bisphosphate carboxylase large chain; Short=RuBisCO large subunit; Flags: Precursor
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\850NOV26.wiff

Nominal mass (Mr): 53436; Calculated pI value: 5.88
NCBI BLAST search of gi|1346967 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica oleracea

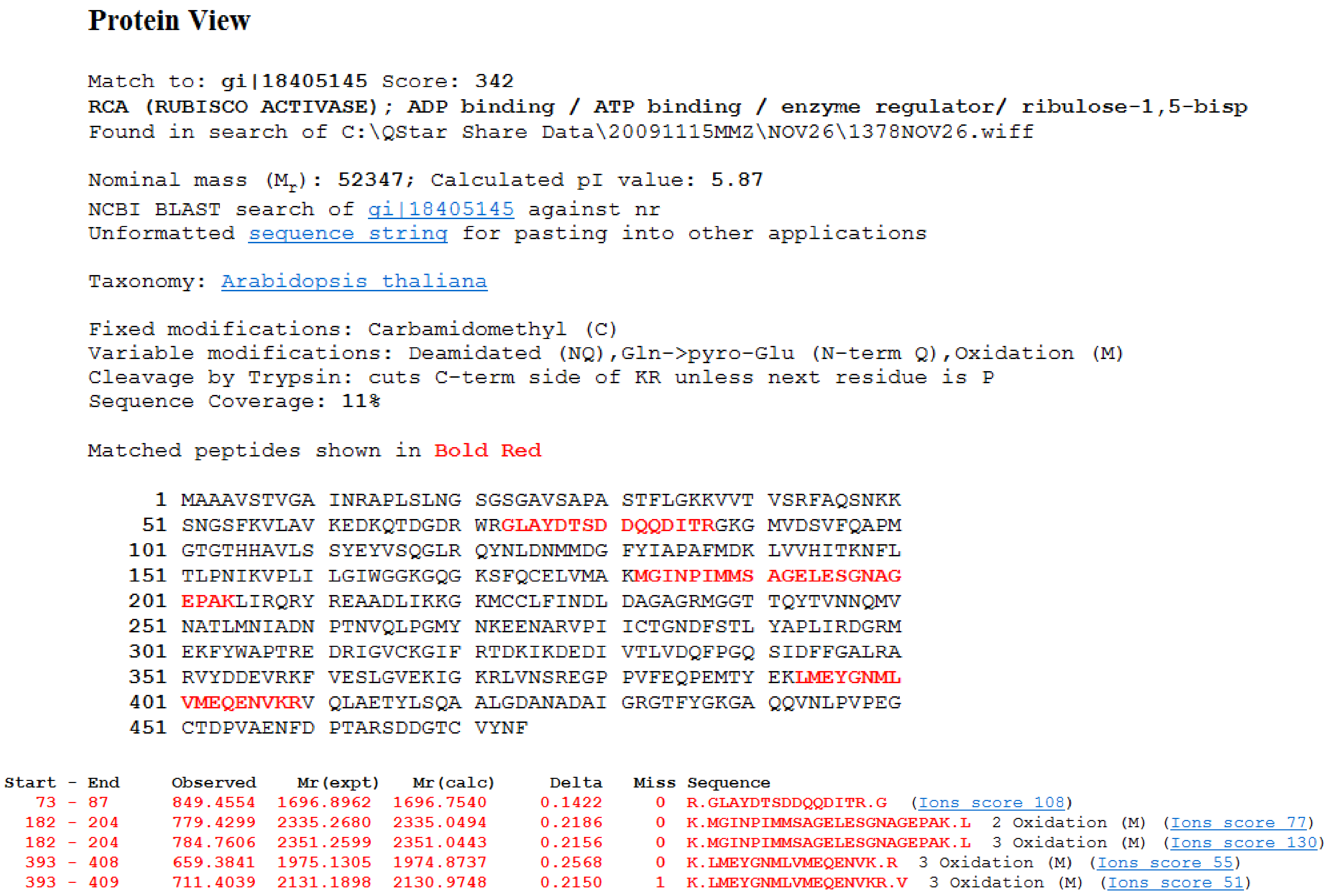
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 21%

Matched peptides shown in Bold Red

       1 MSPQTETKAS VGFKAGVKEY KLNYYTPEYE TKDTDILAAF RVTPQPGVPP
      51 EEAGAAVAAE SSTGTWTTVW TDGLTSLDRY KGRCYHIEPV PGEETQFIAY
     101 VAYPLDLFEE GSVTNMFTSI VGNVFGFKAL AALRLEDLRI PPAYTKTFQG
     151 PPHGIQVERD KLNKYGRPLL GCTIKPKLGL SAKNYGRAVY ECLRGGLDFT
     201 KDDENVNSQP FMRWRDRFLF CAEAIYKSQA ETGEIKGHYL NATAGTCEEM
     251 MKRAIFAREL GVPIVMHDYL TGGFTANTSL AHYCRDNGLL LHIHRAMHAV
     301 IDRQKNHGMH FRVLAKALRL SGGDHVHAGT VVGKLEGDRE STLGFVDLLR
     351 DDYVEKDRSR GIFFTQDWVS LPGVLPVASG GIHVWHMPAL TEIFGDDSVL
     401 QFGGGTLGHP WGNAPGAVAN RVALEACVQA RNEGRDLAVE GNEIIREACK
     451 WSPELAAACE VWKEITFNFP TIDKLDGQD

Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  22 - 32       710.8920  1419.7694  1419.6558    0.1136     0   K.LNYYTPEYETK.D  (Ions score 68)
  33 - 41       511.3407  1020.6669  1020.5240    0.1429     0   K.DTDILAAFR.V  (Ions score 50)
 147 - 159      489.3349  1464.9828  1464.7474    0.2354     0   K.TFQGPPHGIQVER.D  (Ions score 55)
 195 - 213      724.0806  2169.2199  2168.9797    0.2403     1   R.GGLDFTKDDENVNSQPFMR.W  (Ions score 64)
 195 - 213      729.4117  2185.2132  2184.9746    0.2386     1   R.GGLDFTKDDENVNSQPFMR.W  Oxidation (M)  (Ions score 71)
 202 - 213      726.9062  1451.7978  1451.5987    0.1991     0   K.DDENVNSQPFMR.W  Deamidated (NQ)  (Ions score 42)
 202 - 213      734.3873  1466.7600  1466.6096    0.1504     0   K.DDENVNSQPFMR.W  Oxidation (M)  (Ions score 43)
 320 - 334      717.4532  1432.8918  1432.7423    0.1495     0   R.LSGGDHVHAGTVVGK.L  (Ions score 50)
 340 - 350      625.4218  1248.8290  1248.6714    0.1576     0   R.ESTLGFVDLLR.D  (Ions score 75)
 436 - 446      614.9055  1227.7964  1227.6459    0.1505     0   R.DLAVEGNEIIR.E  (Ions score 53)
 464 - 474      662.9194  1323.8242  1323.6711    0.1531     0   K.EITFNFPTIDK.L  (Ions score 62)
 464 - 479      927.0402  1852.0658  1851.8891    0.1767     1   K.EITFNFPTIDKLDGQD.-  (Ions score 10)
```

gi|18405145 Rubisco activase (RCA)



Protein View

```
Match to: gi|18405145 Score: 342
RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisp
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (Mr): 52347; Calculated pI value: 5.87
NCBI BLAST search of gi|18405145 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

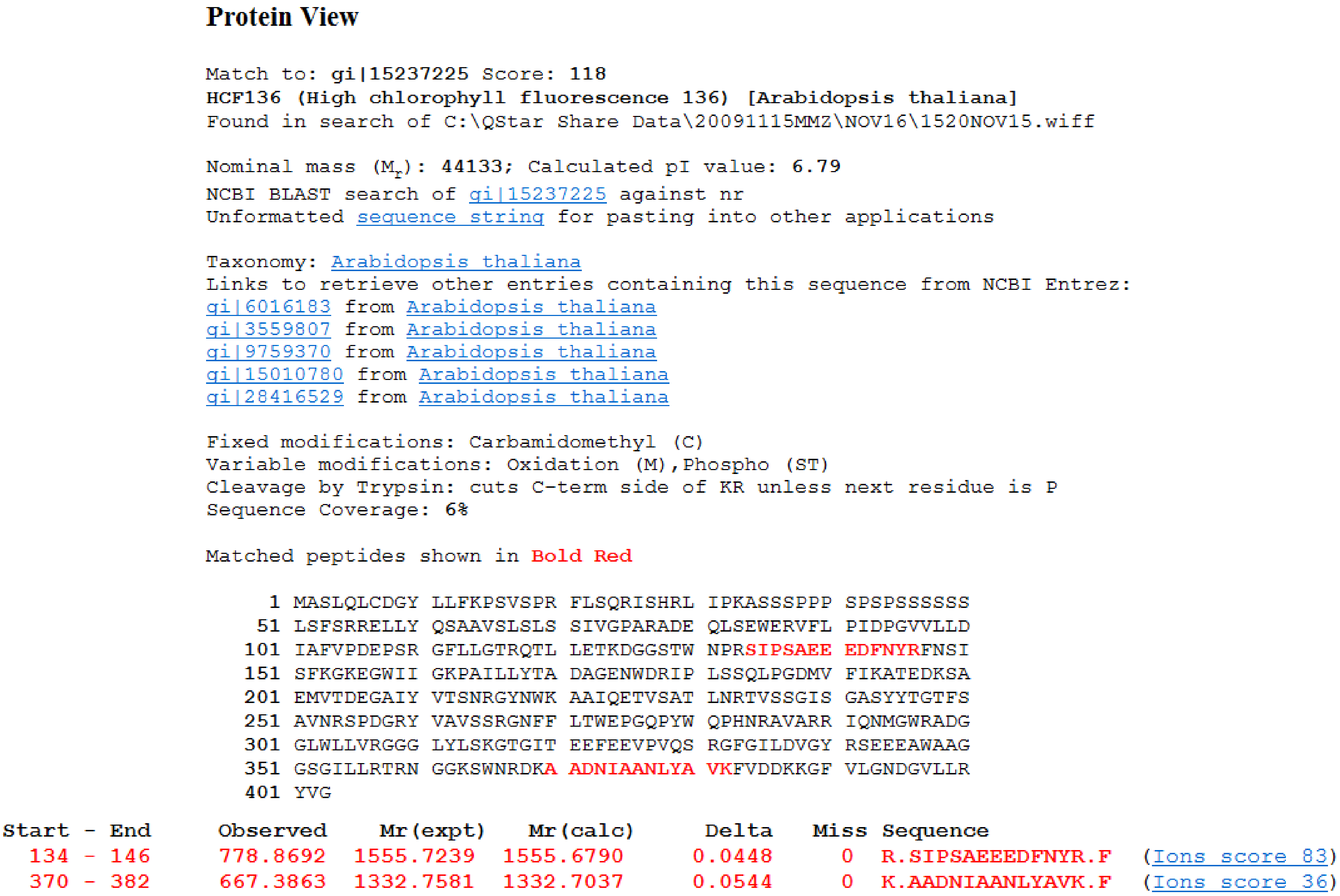
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%

Matched peptides shown in Bold Red

      1 MAAAVSTVGA INRAPLSLNG SGSGAVSAPA STFLGKKVVT VSRFAQSNKK
     51 SNGSFKVLAV KEDKQTDGDR WRGLAYDTSD DQQDITRGKG MVDSVFQAPM
    101 GTGTHHAVLS SYEYVSQGLR QYNLDNMMDG FYIAPAFMDK LVVHITKNFL
    151 TLPNIKVPLI LGIWGGKGQG KSFQCELVMA KMGINPIMMS AGELESGNAG
    201 EPAKLIRQRY REAADLIKKG KMCCLFINDL DAGAGRMGGT TQYTVNNQMV
    251 NATLMNIADN PTNVQLPGMY NKEENARVPI ICTGNDFSTL YAPLIRDGRM
    301 EKFYWAPTRE DRIGVCKGIF RTDKIKDEDI VTLVDQFPGQ SIDFFGALRA
    351 RVYDDEVRKF VESLGVEKIG KRLVNSREGP PVFEQPEMTY EKLMEYGNML
    401 VMEQENVKRV QLAETYLSQA ALGDANADAI GRGTFYGKGA QQVNLPVPEG
    451 CTDPVAENFD PTARSDDGTC VYNF

Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   73 - 87      849.4554  1696.8962  1696.7540    0.1422     0  R.GLAYDTSDDQQDITR.G   (Ions score 108)
  182 - 204     779.4299  2335.2680  2335.0494    0.2186     0  K.MGINPIMMSAGELESGNAGEPAK.L  2 Oxidation (M)  (Ions score 77)
  182 - 204     784.7606  2351.2599  2351.0443    0.2156     0  K.MGINPIMMSAGELESGNAGEPAK.L  3 Oxidation (M)  (Ions score 130)
  393 - 408     659.3841  1975.1305  1974.8737    0.2568     0  K.LMEYGNMLVMEQENVK.R  3 Oxidation (M)  (Ions score 55)
  393 - 409     711.4039  2131.1898  2130.9748    0.2150     1  K.LMEYGNMLVMEQENVKR.V  3 Oxidation (M)  (Ions score 51)
```

gi|15237225 High chlorophyll fluorescence 136 (HCF136)



Protein View

Match to: **gi|15237225** Score: **118**
HCF136 (High chlorophyll fluorescence 136) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1520NOV15.wiff

Nominal mass (M_r): **44133**; Calculated pI value: **6.79**
NCBI BLAST search of gi|15237225 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|6016183 from Arabidopsis thaliana
gi|3559807 from Arabidopsis thaliana
gi|9759370 from Arabidopsis thaliana
gi|15010780 from Arabidopsis thaliana
gi|28416529 from Arabidopsis thaliana

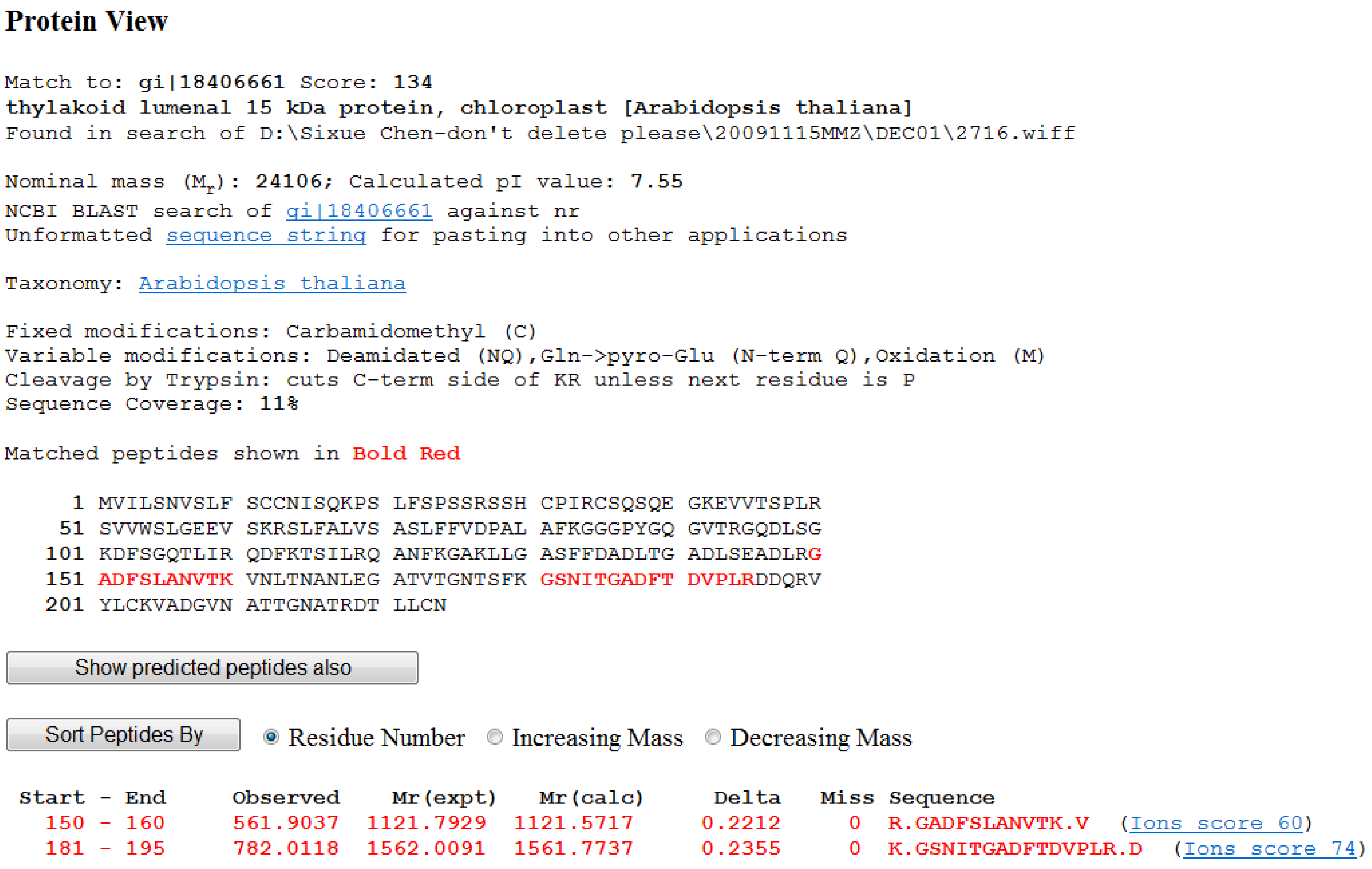
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

```
  1 MASLQLCDGY LLFKPSVSPR FLSQRISHRL IPKASSSPPP SPSPSSSSSS
 51 LSFSRRELLY QSAAVSLSLS SIVGPARADE QLSEWERVFL PIDPGVVLLD
101 IAFVPDEPSR GFLLGTRQTL LETKDGGSTW NPRSIPSAEE EDFNYRFNSI
151 SFKGKEGWII GKPAILLYTA DAGENWDRIP LSSQLPGDMV FIKATEDKSA
201 EMVTDEGAIY VTSNRGYNWK AAIQETVSAT LNRTVSSGIS GASYYTGTFS
251 AVNRSPDGRY VAVSSRGNFF LTWEPGQPYW QPHNRAVARR IQNMGWRADG
301 GLWLLVRGGG LYLSKGTGIT EEFEEVPVQS RGFGILDVGY RSEEEAWAAG
351 GSGILLRTRN GGKSWNRDKA ADNIAANLYA VKFVDDKKGF VLGNDGVLLR
401 YVG
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
134 - 146	778.8692	1555.7239	1555.6790	0.0448	0	**R.SIPSAEEEDFNYR.F**	(Ions score 83)
370 - 382	667.3863	1332.7581	1332.7037	0.0544	0	**K.AADNIAANLYAVK.F**	(Ions score 36)

gi|18406661 Thylakoid lumenal 15 kDa protein, chloroplast



Protein View

Match to: **gi|18406661** Score: **134**
thylakoid lumenal 15 kDa protein, chloroplast [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2716.wiff

Nominal mass (M_r): **24106**; Calculated pI value: **7.55**
NCBI BLAST search of gi|18406661 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

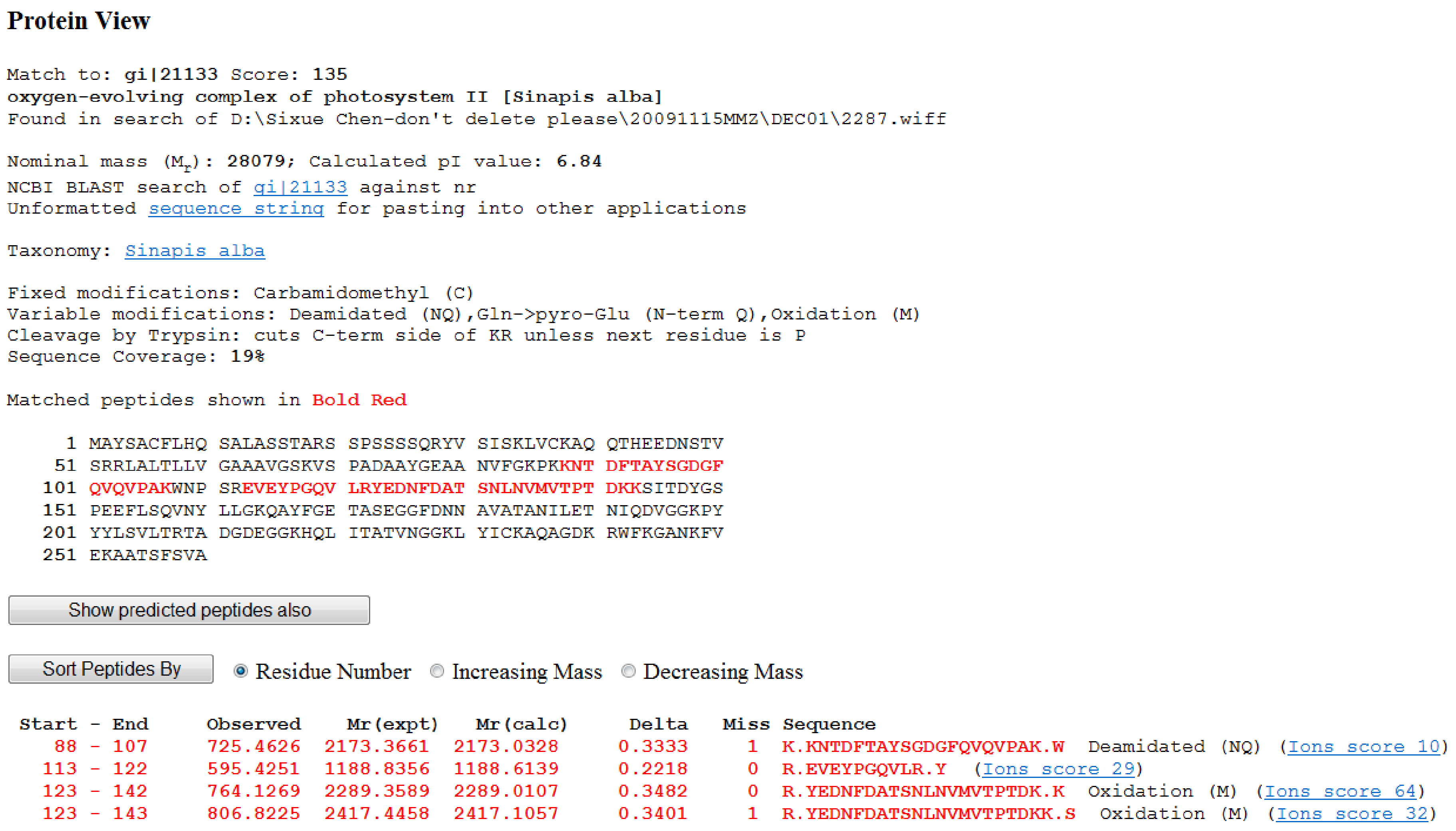
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
      1 MVILSNVSLF SCCNISQKPS LFSPSSRSSH CPIRCSQSQE GKEVVTSPLR
     51 SVVWSLGEEV SKRSLFALVS ASLFFVDPAL AFKGGGPYGQ GVTRGQDLSG
    101 KDFSGQTLIR QDFKTSILRQ ANFKGAKLLG ASFFDADLTG ADLSEADLRG
    151 ADFSLANVTK VNLTNANLEG ATVTGNTSFK GSNITGADFT DVPLRDDQRV
    201 YLCKVADGVN ATTGNATRDT LLCN
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss  Sequence
  150 - 160      561.9037  1121.7929  1121.5717    0.2212     0  R.GADFSLANVTK.V   (Ions score 60)
  181 - 195      782.0118  1562.0091  1561.7737    0.2355     0  K.GSNITGADFTDVPLR.D  (Ions score 74)
```

gi|21133 Oxygen-evolving complex of photosystem II



Protein View

Match to: **gi|21133** Score: **135**
oxygen-evolving complex of photosystem II [Sinapis alba]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2287.wiff

Nominal mass (M_r): **28079**; Calculated pI value: **6.84**
NCBI BLAST search of gi|21133 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Sinapis alba

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

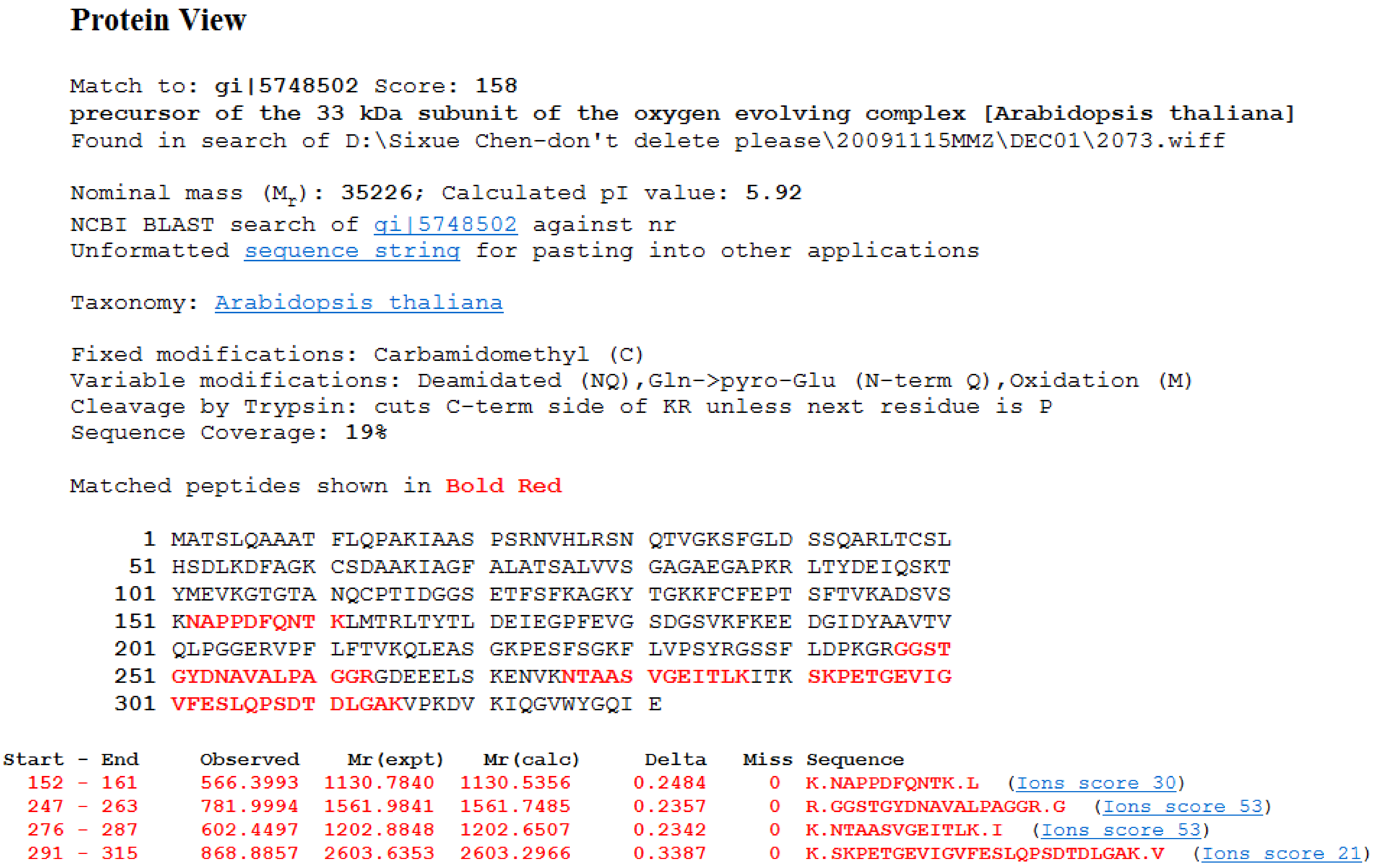
Matched peptides shown in **Bold Red**

```
  1 MAYSACFLHQ SALASSTARS SPSSSSQRYV SISKLVCKAQ QTHEEDNSTV
 51 SRRLALTLLV GAAAVGSKVS PADAAYGEAA NVFGKPKKNT DFTAYSGDGF
101 QVQVPAKWNP SREVEYPGQV LRYEDNFDAT SNLNVMVTPT DKKSITDYGS
151 PEEFLSQVNY LLGKQAYFGE TASEGGFDNN AVATANILET NIQDVGGKPY
201 YYLSVLTRTA DGDEGGKHQL ITATVNGGKL YICKAQAGDK RWFKGANKFV
251 EKAATSFSVA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   88 - 107     725.4626  2173.3661  2173.0328    0.3333     1 K.KNTDFTAYSGDGFQVQVPAK.W  Deamidated (NQ)  (Ions score 10)
  113 - 122     595.4251  1188.8356  1188.6139    0.2218     0 R.EVEYPGQVLR.Y   (Ions score 29)
  123 - 142     764.1269  2289.3589  2289.0107    0.3482     0 R.YEDNFDATSNLNVMVTPTDK.K  Oxidation (M)  (Ions score 64)
  123 - 143     806.8225  2417.4458  2417.1057    0.3401     1 R.YEDNFDATSNLNVMVTPTDKK.S  Oxidation (M)  (Ions score 32)
```

gi|5748502 Precursor of the 33 kDa subunit of the oxygen evolving complex



Protein View

Match to: **gi|5748502** Score: **158**
precursor of the 33 kDa subunit of the oxygen evolving complex [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2073.wiff

Nominal mass (M_r): **35226**; Calculated pI value: **5.92**
NCBI BLAST search of gi|5748502 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

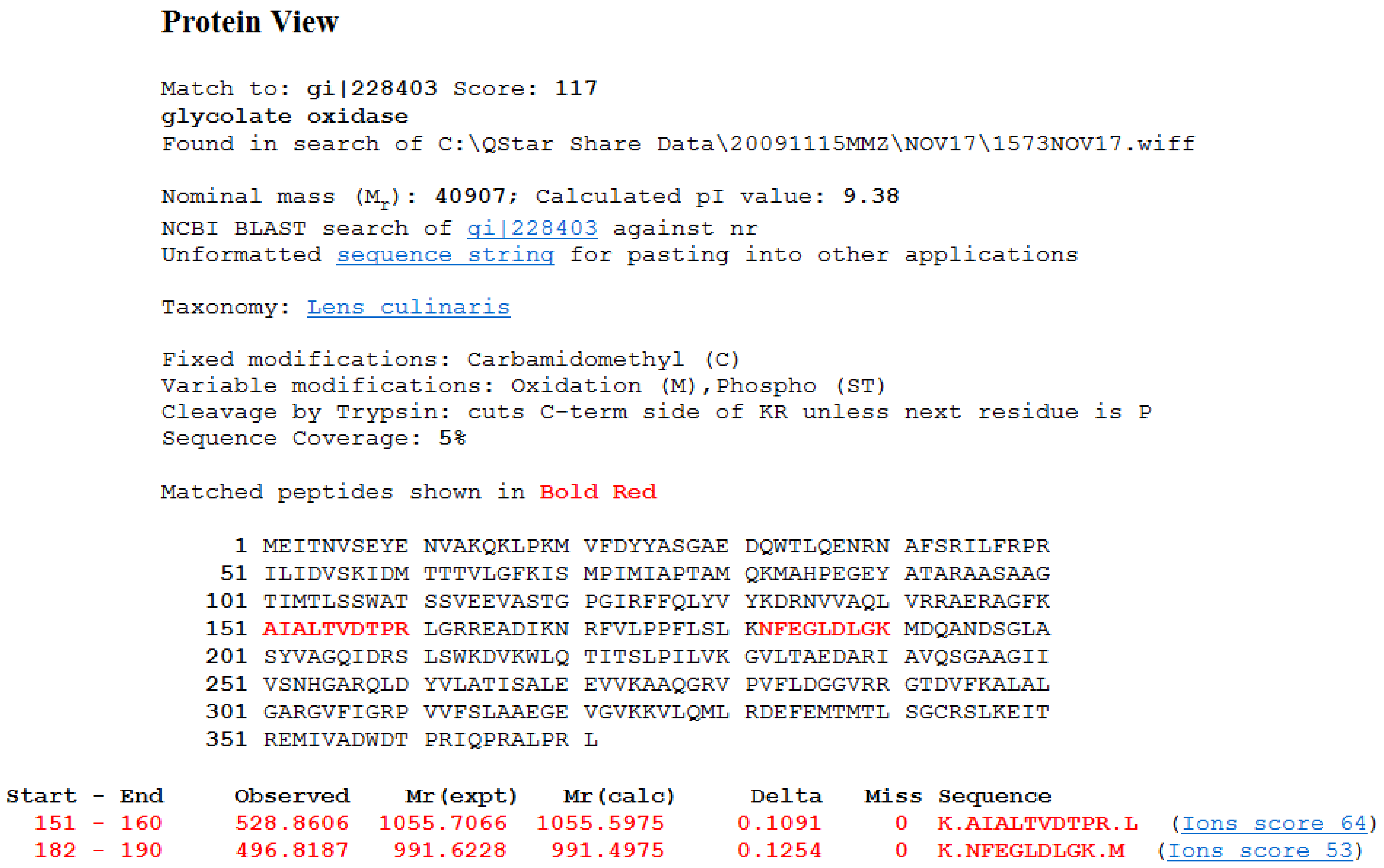
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
  1 MATSLQAAAT FLQPAKIAAS PSRNVHLRSN QTVGKSFGLD SSQARLTCSL
 51 HSDLKDFAGK CSDAAKIAGF ALATSALVVS GAGAEGAPKR LTYDEIQSKT
101 YMEVKGTGTA NQCPTIDGGS ETFSFKAGKY TGKKFCFEPT SFTVKADSVS
151 KNAPPDFQNT KLMTRLTYTL DEIEGPFEVG SDGSVKFKEE DGIDYAAVTV
201 QLPGGERVPF LFTVKQLEAS GKPESFSGKF LVPSYRGSSF LDPKGRGGST
251 GYDNAVALPA GGRGDEEELS KENVKNTAAS VGEITLKITK SKPETGEVIG
301 VFESLQPSDT DLGAKVPKDV KIQGVWYGQI E
```

```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
  152 - 161     566.3993   1130.7840   1130.5356    0.2484     0  K.NAPPDFQNTK.L  (Ions score 30)
  247 - 263     781.9994   1561.9841   1561.7485    0.2357     0  R.GGSTGYDNAVALPAGGR.G  (Ions score 53)
  276 - 287     602.4497   1202.8848   1202.6507    0.2342     0  K.NTAASVGEITLK.I  (Ions score 53)
  291 - 315     868.8857   2603.6353   2603.2966    0.3387     0  K.SKPETGEVIGVFESLQPSDTDLGAK.V  (Ions score 21)
```

gi|228403 Glycolate oxidase



Protein View

Match to: **gi|228403** Score: **117**
glycolate oxidase
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r): **40907**; Calculated pI value: **9.38**
NCBI BLAST search of gi|228403 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Lens culinaris

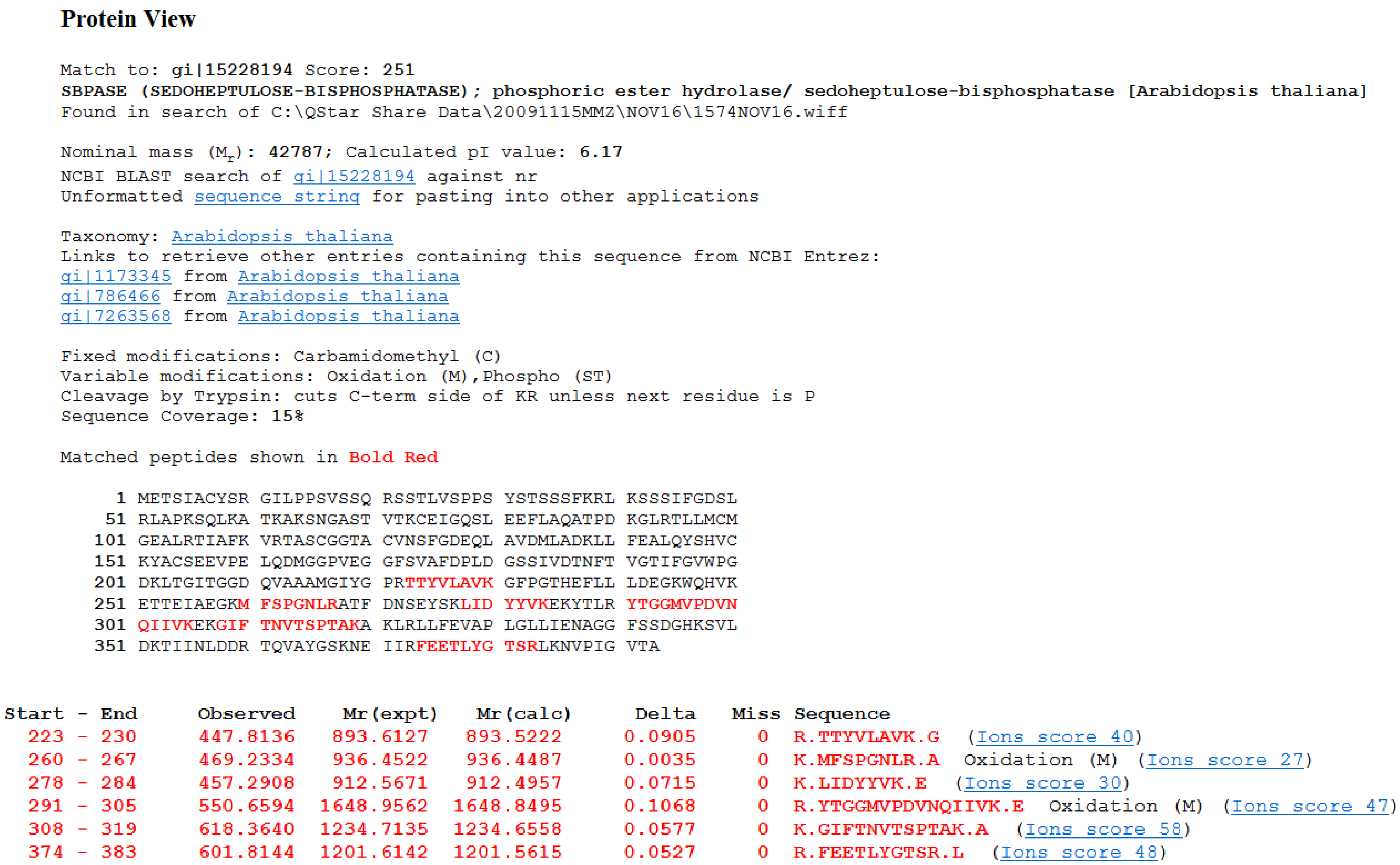
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```
  1 MEITNVSEYE NVAKQKLPKM VFDYYASGAE DQWTLQENRN AFSRILFRPR
 51 ILIDVSKIDM TTTVLGFKIS MPIMIAPTAM QKMAHPEGEY ATARAASAAG
101 TIMTLSSWAT SSVEEVASTG PGIRFFQLYV YKDRNVVAQL VRRAERAGFK
151 AIALTVDTPR LGRREADIKN RFVLPPFLSL KNFEGLDLGK MDQANDSGLA
201 SYVAGQIDRS LSWKDVKWLQ TITSLPILVK GVLTAEDARI AVQSGAAGII
251 VSNHGARQLD YVLATISALE EVVKAAQGRV PVFLDGGVRR GTDVFKALAL
301 GARGVFIGRP VVFSLAAEGE VGVKKVLQML RDEFEMTMTL SGCRSLKEIT
351 REMIVADWDT PRIQPRALPR L
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
 151 - 160      528.8606  1055.7066  1055.5975    0.1091     0  K.AIALTVDTPR.L   (Ions score 64)
 182 - 190      496.8187   991.6228   991.4975    0.1254     0  K.NFEGLDLGK.M   (Ions score 53)
```

gi|15228194 Sedoheptulose-bisphosphatase (SBPASE)



Protein View

```
Match to: gi|15228194 Score: 251
SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1574NOV16.wiff

Nominal mass (Mr): 42787; Calculated pI value: 6.17
NCBI BLAST search of gi|15228194 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1173345 from Arabidopsis thaliana
gi|786466 from Arabidopsis thaliana
gi|7263568 from Arabidopsis thaliana

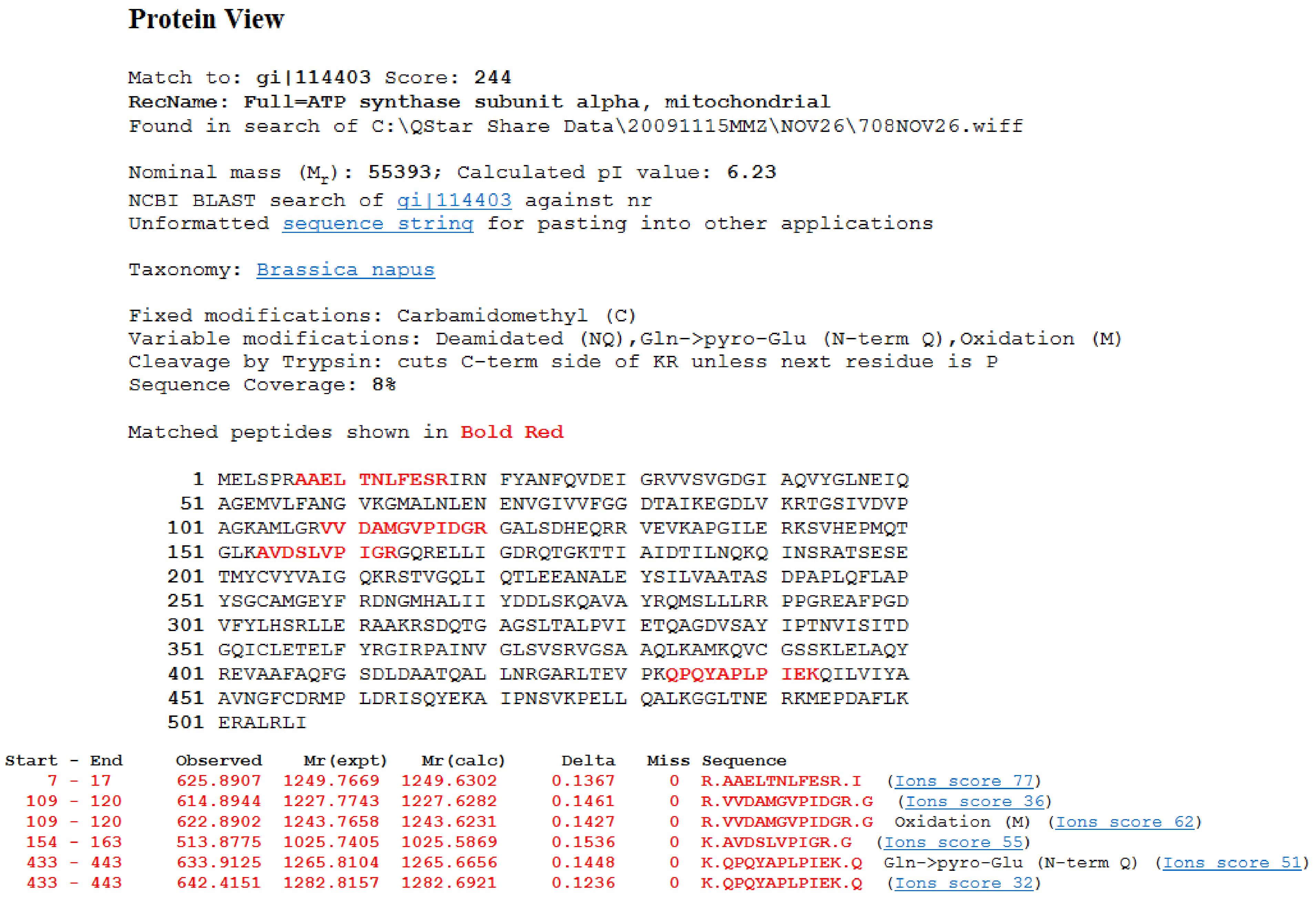
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in Bold Red

     1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
    51 RLAPKSQLKA TKAKSNGAST VTKCEIGQSL EEFLAQATPD KGLRTLLMCM
   101 GEALRTIAFK VRTASCGGTA CVNSFGDEQL AVDMLADKLL FEALQYSHVC
   151 KYACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
   201 DKLTGITGGD QVAAAMGIYG PRTTYVLAVK GFPGTHEFLL LDEGKWQHVK
   251 ETTEIAEGKM FSPGNLRATF DNSEYSKLID YYVKEKYTLR YTGGMVPDVN
   301 QIIVKEKGIF TNVTSPTAKA KLRLLFEVAP LGLLIENAGG FSSDGHKSVL
   351 DKTIINLDDR TQVAYGSKNE IIRFEETLYG TSRLKNVPIG VTA
```

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
  223 - 230    447.8136   893.6127   893.5222   0.0905     0  R.TTYVLAVK.G  (Ions score 40)
  260 - 267    469.2334   936.4522   936.4487   0.0035     0  K.MFSPGNLR.A  Oxidation (M)  (Ions score 27)
  278 - 284    457.2908   912.5671   912.4957   0.0715     0  K.LIDYYVK.E  (Ions score 30)
  291 - 305    550.6594  1648.9562  1648.8495   0.1068     0  R.YTGGMVPDVNQIIVK.E  Oxidation (M)  (Ions score 47)
  308 - 319    618.3640  1234.7135  1234.6558   0.0577     0  K.GIFTNVTSPTAK.A  (Ions score 58)
  374 - 383    601.8144  1201.6142  1201.5615   0.0527     0  R.FEETLYGTSR.L  (Ions score 48)
```

gi|114403 ATP synthase subunit alpha, mitochondrial



Protein View

Match to: gi|114403 Score: 244
RecName: Full=ATP synthase subunit alpha, mitochondrial
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\708NOV26.wiff

Nominal mass (M_r): 55393; Calculated pI value: 6.23
NCBI BLAST search of gi|114403 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

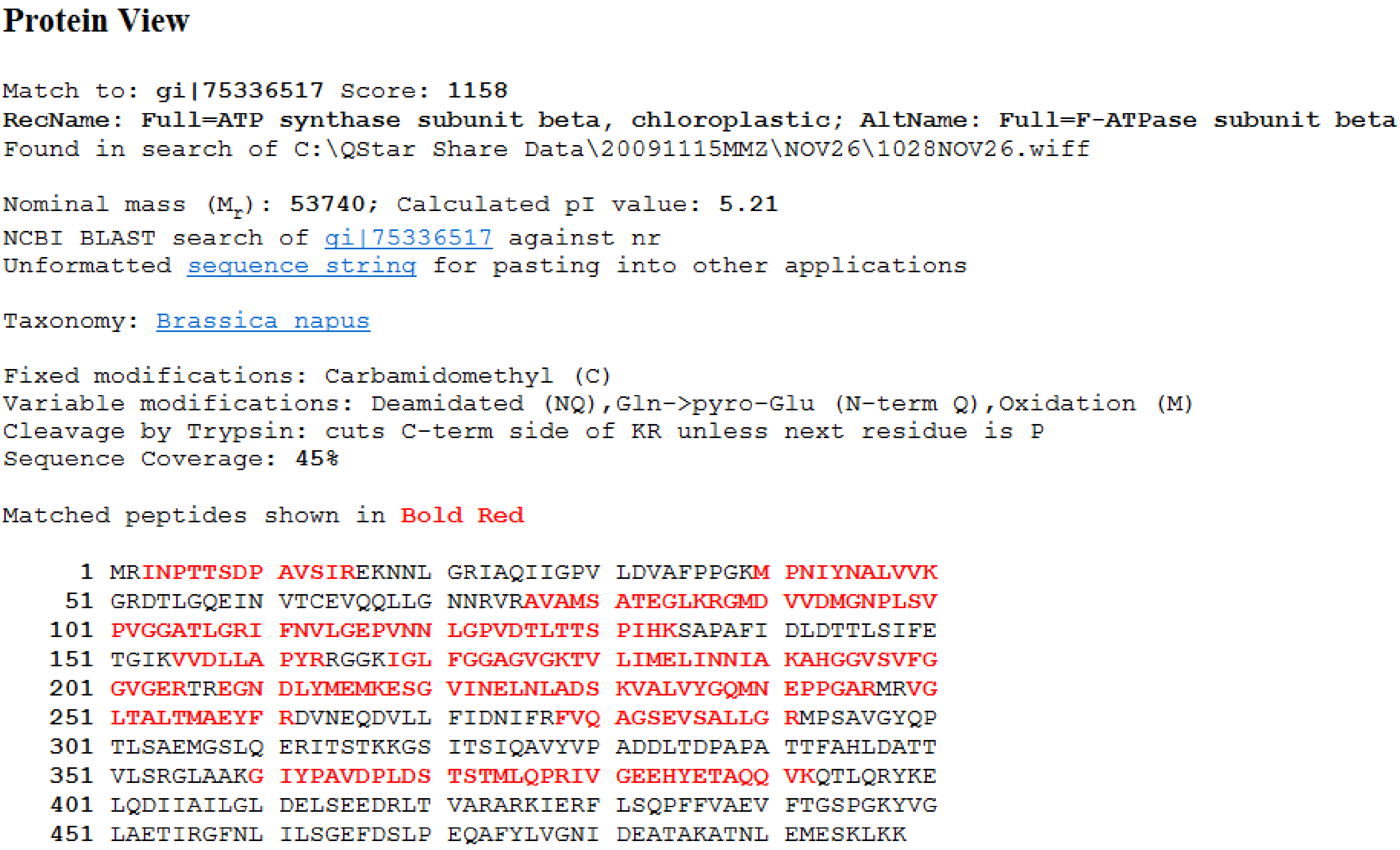
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```
  1 MELSPRAAEL TNLFESRIRN FYANFQVDEI GRVVSVGDGI AQVYGLNEIQ
 51 AGEMVLFANG VKGMALNLEN ENVGIVVFGG DTAIKEGDLV KRTGSIVDVP
101 AGKAMLGRVV DAMGVPIDGR GALSDHEQRR VEVKAPGILE RKSVHEPMQT
151 GLKAVDSLVP IGRGQRELLI GDRQTGKTTI AIDTILNQKQ INSRATSESE
201 TMYCVYVAIG QKRSTVGQLI QTLEEANALE YSILVAATAS DPAPLQFLAP
251 YSGCAMGEYF RDNGMHALII YDDLSKQAVA YRQMSLLLRR PPGREAFPGD
301 VFYLHSRLLE RAAKRSDQTG AGSLTALPVI ETQAGDVSAY IPTNVISITD
351 GQICLETELF YRGIRPAINV GLSVSRVGSA AQLKAMKQVC GSSKLELAQY
401 REVAAFAQFG SDLDAATQAL LNRGARLTEV PKQPQYAPLP IEKQILVIYA
451 AVNGFCDRMP LDRISQYEKA IPNSVKPELL QALKGGLTNE RKMEPDAFLK
501 ERALRLI
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   7 - 17       625.8907  1249.7669  1249.6302    0.1367     0  R.AAELTNLFESR.I   (Ions score 77)
 109 - 120      614.8944  1227.7743  1227.6282    0.1461     0  R.VVDAMGVPIDGR.G   (Ions score 36)
 109 - 120      622.8902  1243.7658  1243.6231    0.1427     0  R.VVDAMGVPIDGR.G  Oxidation (M)  (Ions score 62)
 154 - 163      513.8775  1025.7405  1025.5869    0.1536     0  K.AVDSLVPIGR.G  (Ions score 55)
 433 - 443      633.9125  1265.8104  1265.6656    0.1448     0  K.QPQYAPLPIEK.Q  Gln->pyro-Glu (N-term Q)  (Ions score 51)
 433 - 443      642.4151  1282.8157  1282.6921    0.1236     0  K.QPQYAPLPIEK.Q  (Ions score 32)
```

gi|75336517 ATP synthase subunit beta, chloroplastic



Protein View

Match to: **gi|75336517** Score: **1158**
RecName: Full=ATP synthase subunit beta, chloroplastic; AltName: Full=F-ATPase subunit beta
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1028NOV26.wiff

Nominal mass (M_r): **53740**; Calculated pI value: **5.21**
NCBI BLAST search of gi|75336517 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

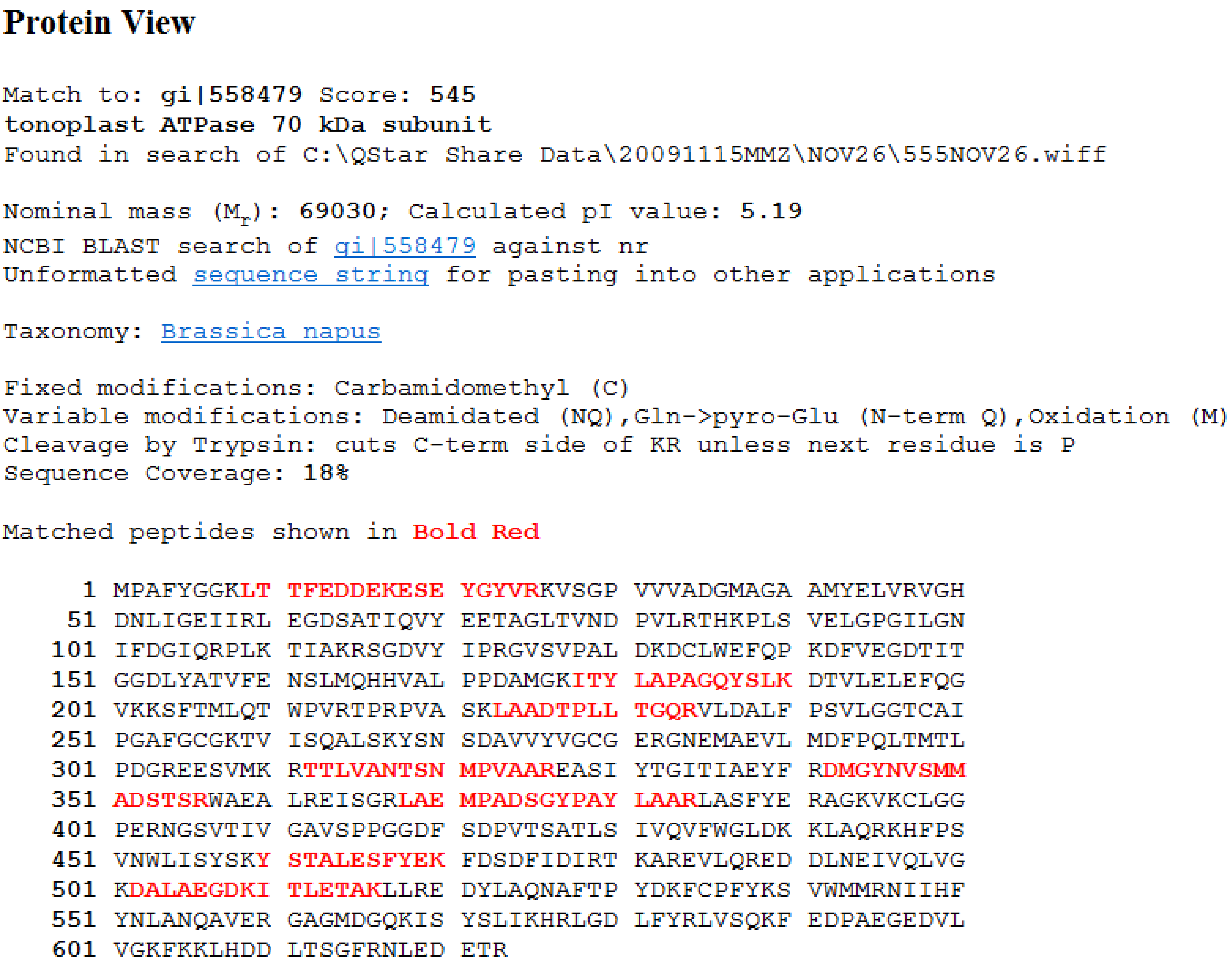
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

1 MR**INPTTSDP AVSIR**EKNNL GRIAQIIGPV LDVAFPPGK**M PNIYNALVVK**
51 GRDTLGQEIN VTCEVQQLLG NNRVR**AVAMS ATEGLKRGMD VVDMGNPLSV**
101 **PVGGATLGRI FNVLGEPVNN LGPVDTLTTS PIHK**SAPAFI DLDTTLSIFE
151 TGIK**VVDLLA PYR**RGGK**IGL FGGAGVGKTV LIMELINNIA KAHGGVSVFG**
201 **GVGER**T**REGN DLYMEMKESG VINELNLADS KVALVYGQMN EPPGAR**MRV**G**
251 **LTALTMAEYF R**DVNEQDVLL FIDNIFR**FVQ AGSEVSALLG R**MPSAVGYQP
301 TLSAEMGSLQ ERITSTKKGS ITSIQAVYVP ADDLTDPAPA TTFAHLDATT
351 VLSRGLAAK**G IYPAVDPLDS TSTMLQPRIV GEEHYETAQQ VK**QTLQRYKE
401 LQDIIAILGL DELSEEDRLT VARARKIERF LSQPFFVAEV FTGSPGKYVG
451 LAETIRGFNL ILSGEFDSLP EQAFYLVGNI DEATAKATNL EMESKLKK

```
Start - End     Observed   Mr(expt)   Mr(calc)      Delta   Miss Sequence
   3 - 15     685.9302  1369.8459  1369.7201     0.1258     0  R.INPTTSDPAVSIR.E   (Ions score 60)
  40 - 50     631.4198  1260.8251  1260.6900     0.1351     0  K.MPNIYNALVVK.G  (Ions score 54)
  40 - 50     639.4316  1276.8487  1276.6849     0.1638     0  K.MPNIYNALVVK.G  Oxidation (M)  (Ions score 70)
  76 - 86     539.3524  1076.6903  1076.5536     0.1367     0  R.AVAMSATEGLK.R  (Ions score 83)
  76 - 86     547.3542  1092.6938  1092.5485     0.1453     0  R.AVAMSATEGLK.R  Oxidation (M)  (Ions score 38)
  76 - 86     547.3542  1092.6938  1092.5485     0.1453     0  R.AVAMSATEGLK.R  Oxidation (M)  (Ions score 61)
  76 - 86     547.3542  1092.6938  1092.5485     0.1453     0  R.AVAMSATEGLK.R  Oxidation (M)  (Ions score 46)
  76 - 86     547.3542  1092.6938  1092.5485     0.1453     0  R.AVAMSATEGLK.R  Oxidation (M)  (Ions score 64)
  87 - 109    777.4621  2329.3644  2329.1519     0.2125     1  K.RGMDVVDMGNPLSVPVGGATLGR.I  2 Oxidation (M)  (Ions score 63)
  88 - 109    720.0981  2157.2725  2157.0559     0.2166     0  R.GMDVVDMGNPLSVPVGGATLGR.I  Oxidation (M)  (Ions score 51)
  88 - 109    725.4145  2173.2218  2173.0508     0.1710     0  R.GMDVVDMGNPLSVPVGGATLGR.I  2 Oxidation (M)  (Ions score 61)
 110 - 134    892.8789  2675.6150  2675.4170     0.1979     0  R.IFNVLGEPVNNLGPVDTLTTSPIHK.S  Deamidated (NQ)  (Ions score 82)
 155 - 163    523.3724  1044.7303  1044.5968     0.1336     0  K.VVDLLAPYR.R  (Ions score 44)
 168 - 178    488.3479   974.6813   974.5549     0.1263     0  K.IGLFGGAGVGK.T  (Ions score 56)
 179 - 191    744.9739  1487.9332  1487.8269     0.1063     0  K.TVLIMELINNIAK.A  Deamidated (NQ); Oxidation (M)  (Ions score 39)
 192 - 205    664.9092  1327.8039  1327.6633     0.1406     0  K.AHGGVSVFGGVGER.T  (Ions score 65)
 208 - 217    615.3373  1228.6600  1228.5104     0.1496     0  R.EGNDLYMEMK.E  (Ions score 50)
 208 - 217    623.3247  1244.6349  1244.5053     0.1296     0  R.EGNDLYMEMK.E  Oxidation (M)  (Ions score 44)
 208 - 217    631.3301  1260.6456  1260.5002     0.1454     0  R.EGNDLYMEMK.E  2 Oxidation (M)  (Ions score 27)
 218 - 231    744.9251  1487.8357  1487.7467     0.0890     0  K.ESGVINELNLADSK.V  (Ions score 73)
 232 - 246    801.4679  1600.9213  1600.8031     0.1182     0  K.VALVYGQMNEPPGAR.M  (Ions score 104)
 232 - 246    809.4494  1616.8842  1616.7981     0.0862     0  K.VALVYGQMNEPPGAR.M  Oxidation (M)  (Ions score 84)
 249 - 261    744.4500  1486.8855  1486.7490     0.1365     0  R.VGLTALTMAEYFR.D  Oxidation (M)  (Ions score 80)
 278 - 291    717.4532  1432.8918  1432.7674     0.1244     0  R.FVQAGSEVSALLGR.M  (Ions score 68)
 360 - 378    687.7553  2060.2440  2060.0248     0.2192     0  K.GIYPAVDPLDSTSTMLQPR.I  (Ions score 98)
 360 - 378    693.0804  2076.2195  2076.0198     0.1997     0  K.GIYPAVDPLDSTSTMLQPR.I  Oxidation (M)  (Ions score 88)
 379 - 392    815.9650  1629.9155  1629.7998     0.1157     0  R.IVGEEHYETAQQVK.Q  (Ions score 67)
 379 - 392    544.3609  1630.0609  1629.7998     0.2611     0  R.IVGEEHYETAQQVK.Q  (Ions score 48)
```

gi|558479 Tonoplast ATPase 70 kDa subunit



Protein View

Match to: **gi|558479** Score: **545**
tonoplast ATPase 70 kDa subunit
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\555NOV26.wiff

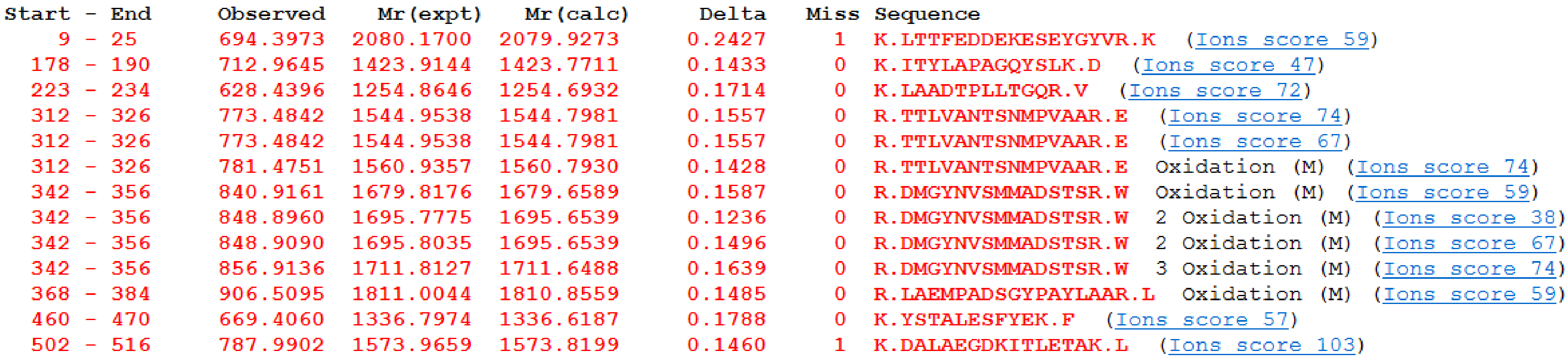
Nominal mass (M_r): **69030**; Calculated pI value: **5.19**
NCBI BLAST search of gi|558479 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

1 MPAFYGGK**LT TFEDDEKESE YGYVR**KVSGP VVVADGMAGA AMYELVRVGH
51 DNLIGEIIRL EGDSATIQVY EETAGLTVND PVLRTHKPLS VELGPGILGN
101 IFDGIQRPLK TIAKRSGDVY IPRGVSVPAL DKDCLWEFQP KDFVEGDTIT
151 GGDLYATVFE NSLMQHHVAL PPDAMGK**ITY LAPAGQYSLK** DTVLELEFQG
201 VKKSFTMLQT WPVRTPRPVA SK**LAADTPLL TGQR**VLDALF PSVLGGTCAI
251 PGAFGCGKTV ISQALSKYSN SDAVVYVGCG ERGNEMAEVL MDFPQLTMTL
301 PDGREESVMK R**TTLVANTSN MPVAAR**EASI YTGITIAEYF R**DMGYNVSMM**
351 **ADSTSR**WAEA LREISGR**LAE MPADSGYPAY LAAR**LASFYE RAGKVKCLGG
401 PERNGSVTIV GAVSPPGGDF SDPVTSATLS IVQVFWGLDK KLAQRKHFPS
451 VNWLISYSK**Y STALESFYEK** FDSDFIDIRT KAREVLQRED DLNEIVQLVG
501 K**DALAEGDKI TLETAK**LLRE DYLAQNAFTP YDKFCPFYKS VWMMRNIIHF
551 YNLANQAVER GAGMDGQKIS YSLIKHRLGD LFYRLVSQKF EDPAEGEDVL
601 VGKFKKLHDD LTSGFRNLED ETR



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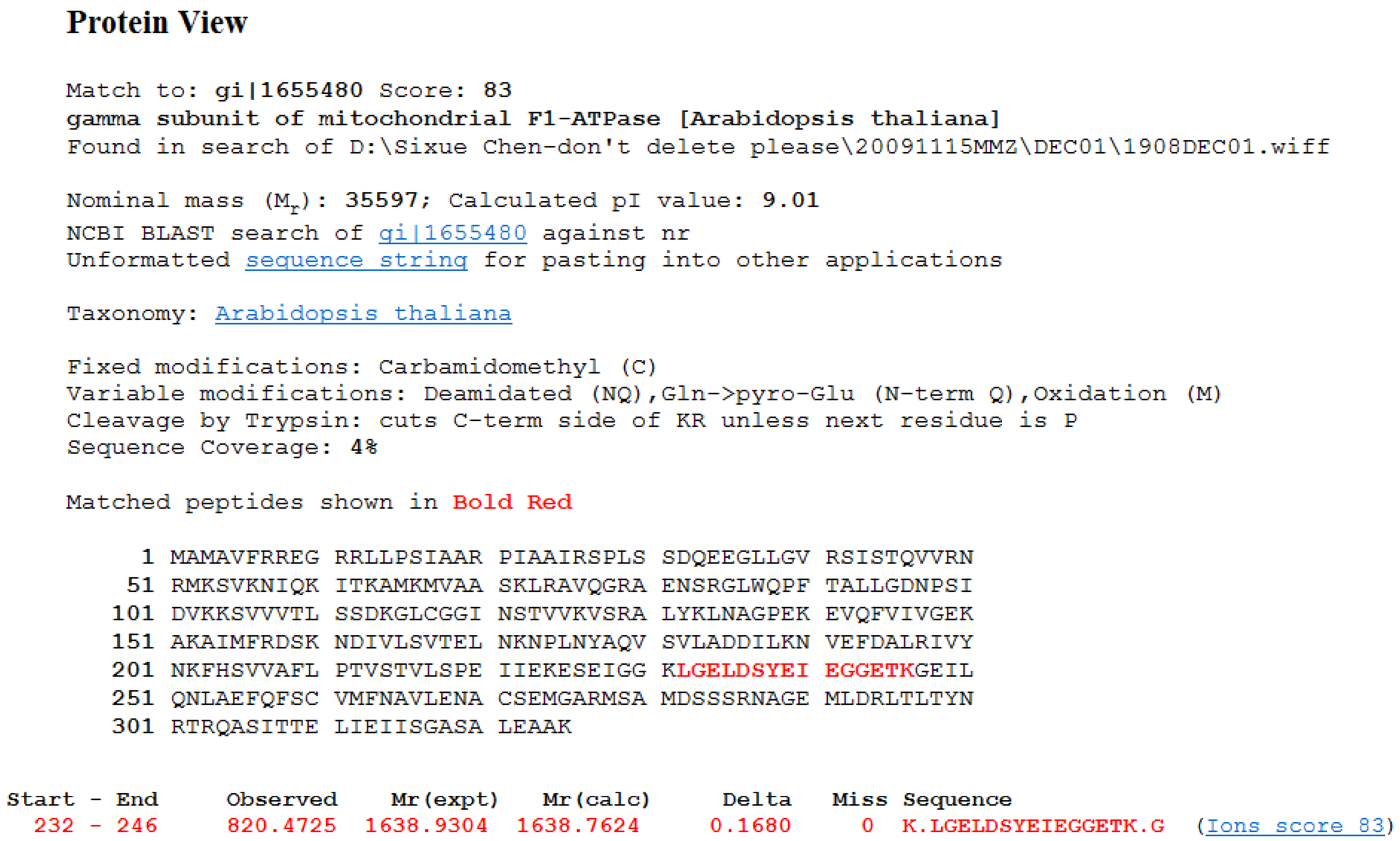
Start - End      Observed    Mr(expt)   Mr(calc)      Delta    Miss Sequence
   9 - 25        694.3973  2080.1700  2079.9273     0.2427     1  K.LTTFEDDEKESEYGYVR.K   (Ions score 59)
 178 - 190       712.9645  1423.9144  1423.7711     0.1433     0  K.ITYLAPAGQYSLK.D   (Ions score 47)
 223 - 234       628.4396  1254.8646  1254.6932     0.1714     0  K.LAADTPLLTGQR.V   (Ions score 72)
 312 - 326       773.4842  1544.9538  1544.7981     0.1557     0  R.TTLVANTSNMPVAAR.E   (Ions score 74)
 312 - 326       773.4842  1544.9538  1544.7981     0.1557     0  R.TTLVANTSNMPVAAR.E   (Ions score 67)
 312 - 326       781.4751  1560.9357  1560.7930     0.1428     0  R.TTLVANTSNMPVAAR.E  Oxidation (M)  (Ions score 74)
 342 - 356       840.9161  1679.8176  1679.6589     0.1587     0  R.DMGYNVSMMADSTSR.W  Oxidation (M)  (Ions score 59)
 342 - 356       848.8960  1695.7775  1695.6539     0.1236     0  R.DMGYNVSMMADSTSR.W  2 Oxidation (M)  (Ions score 38)
 342 - 356       848.9090  1695.8035  1695.6539     0.1496     0  R.DMGYNVSMMADSTSR.W  2 Oxidation (M)  (Ions score 67)
 342 - 356       856.9136  1711.8127  1711.6488     0.1639     0  R.DMGYNVSMMADSTSR.W  3 Oxidation (M)  (Ions score 74)
 368 - 384       906.5095  1811.0044  1810.8559     0.1485     0  R.LAEMPADSGYPAYLAAR.L  Oxidation (M)  (Ions score 59)
 460 - 470       669.4060  1336.7974  1336.6187     0.1788     0  K.YSTALESFYEK.F   (Ions score 57)
 502 - 516       787.9902  1573.9659  1573.8199     0.1460     1  K.DALAEGDKITLETAK.L   (Ions score 103)
```

gi|1655480 Gamma subunit of mitochondrial F1-ATPase



Protein View

Match to: **gi|1655480** Score: **83**
gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1908DEC01.wiff

Nominal mass (M_r): **35597**; Calculated pI value: **9.01**
NCBI BLAST search of gi|1655480 against nr
Unformatted sequence string for pasting into other applications

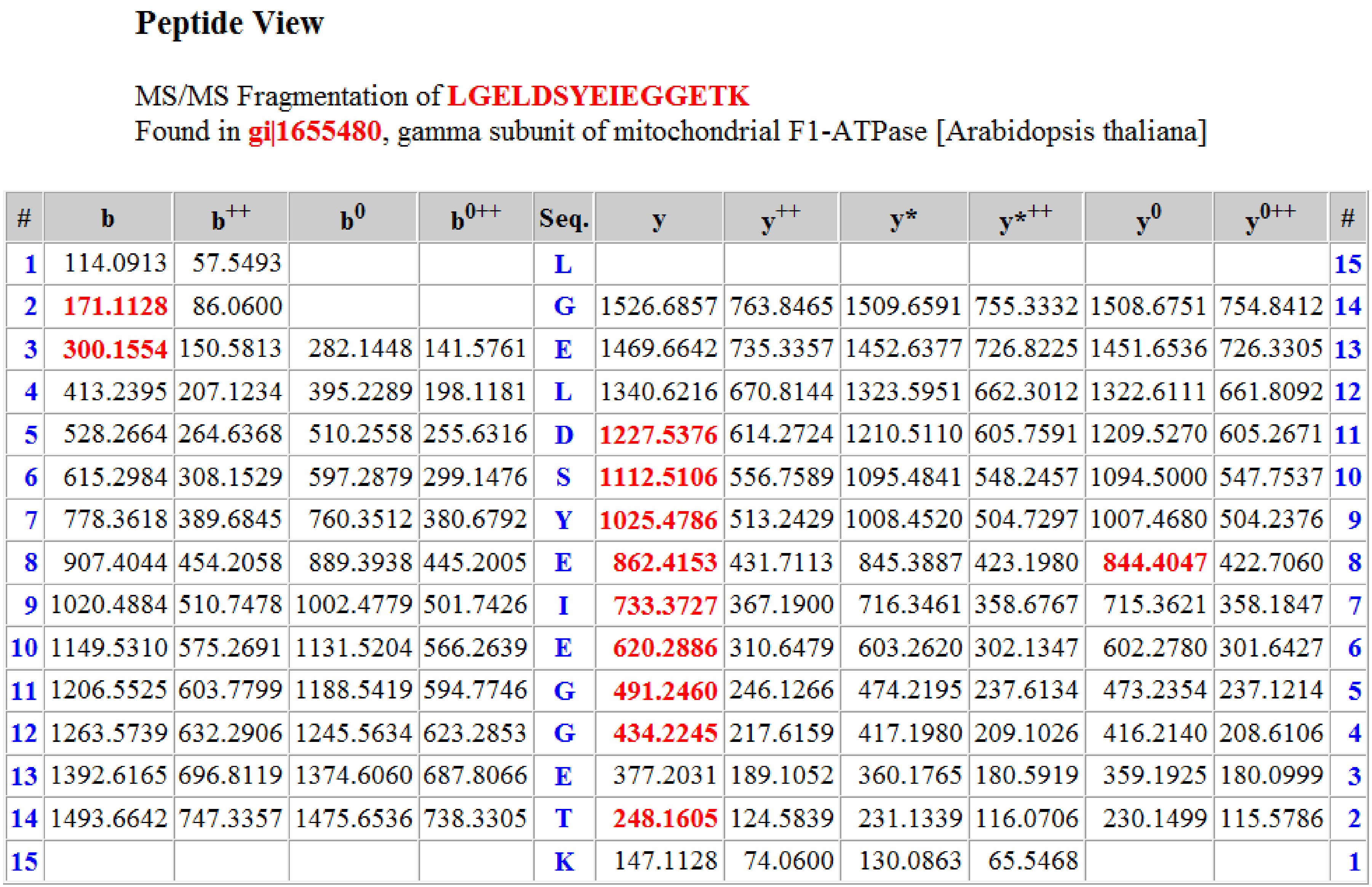
Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**

```
  1 MAMAVFRREG RRLLPSIAAR PIAAIRSPLS SDQEEGLLGV RSISTQVVRN
 51 RMKSVKNIQK ITKAMKMVAA SKLRAVQGRA ENSRGLWQPF TALLGDNPSI
101 DVKKSVVVTL SSDKGLCGGI NSTVVKVSRA LYKLNAGPEK EVQFVIVGEK
151 AKAIMFRDSK NDIVLSVTEL NKNPLNYAQV SVLADDILKN VEFDALRIVY
201 NKFHSVVAFL PTVSTVLSPE IIEKESEIGG KLGELDSYEI EGGETKGEIL
251 QNLAEFQFSC VMFNAVLENA CSEMGARMSA MDSSSRNAGE MLDRLTLTYN
301 RTRQASITTE LIEIISGASA LEAAK
```

```
Start - End     Observed     Mr(expt)   Mr(calc)      Delta   Miss  Sequence
  232 - 246     820.4725    1638.9304  1638.7624     0.1680     0  K.LGELDSYEIEGGETK.G   (Ions score 83)
```

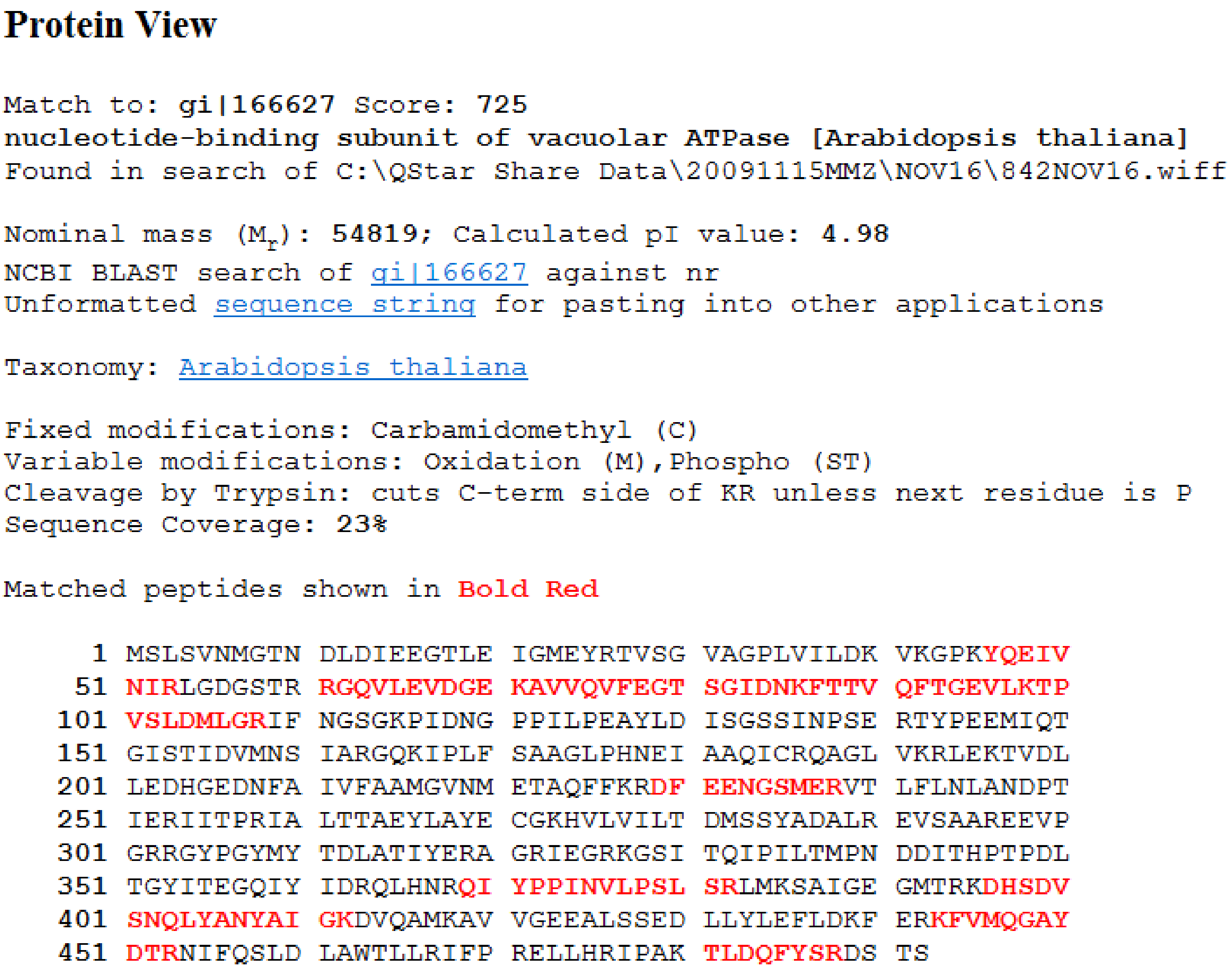


Peptide View

MS/MS Fragmentation of **LGELDSYEIEGGETK**
Found in **gi|1655480**, gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493			L							15
2	**171.1128**	86.0600			G	1526.6857	763.8465	1509.6591	755.3332	1508.6751	754.8412	14
3	**300.1554**	150.5813	282.1448	141.5761	E	1469.6642	735.3357	1452.6377	726.8225	1451.6536	726.3305	13
4	413.2395	207.1234	395.2289	198.1181	L	1340.6216	670.8144	1323.5951	662.3012	1322.6111	661.8092	12
5	528.2664	264.6368	510.2558	255.6316	D	**1227.5376**	614.2724	1210.5110	605.7591	1209.5270	605.2671	11
6	615.2984	308.1529	597.2879	299.1476	S	**1112.5106**	556.7589	1095.4841	548.2457	1094.5000	547.7537	10
7	778.3618	389.6845	760.3512	380.6792	Y	**1025.4786**	513.2429	1008.4520	504.7297	1007.4680	504.2376	9
8	907.4044	454.2058	889.3938	445.2005	E	**862.4153**	431.7113	845.3887	423.1980	**844.4047**	422.7060	8
9	1020.4884	510.7478	1002.4779	501.7426	I	**733.3727**	367.1900	716.3461	358.6767	715.3621	358.1847	7
10	1149.5310	575.2691	1131.5204	566.2639	E	**620.2886**	310.6479	603.2620	302.1347	602.2780	301.6427	6
11	1206.5525	603.7799	1188.5419	594.7746	G	**491.2460**	246.1266	474.2195	237.6134	473.2354	237.1214	5
12	1263.5739	632.2906	1245.5634	623.2853	G	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	4
13	1392.6165	696.8119	1374.6060	687.8066	E	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
14	1493.6642	747.3357	1475.6536	738.3305	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
15					K	147.1128	74.0600	130.0863	65.5468			1

gi|166627 Nucleotide-binding subunit of vacuolar ATPase



Protein View

Match to: gi|166627 Score: 725
nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\842NOV16.wiff

Nominal mass (M_r): **54819**; Calculated pI value: **4.98**
NCBI BLAST search of gi|166627 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

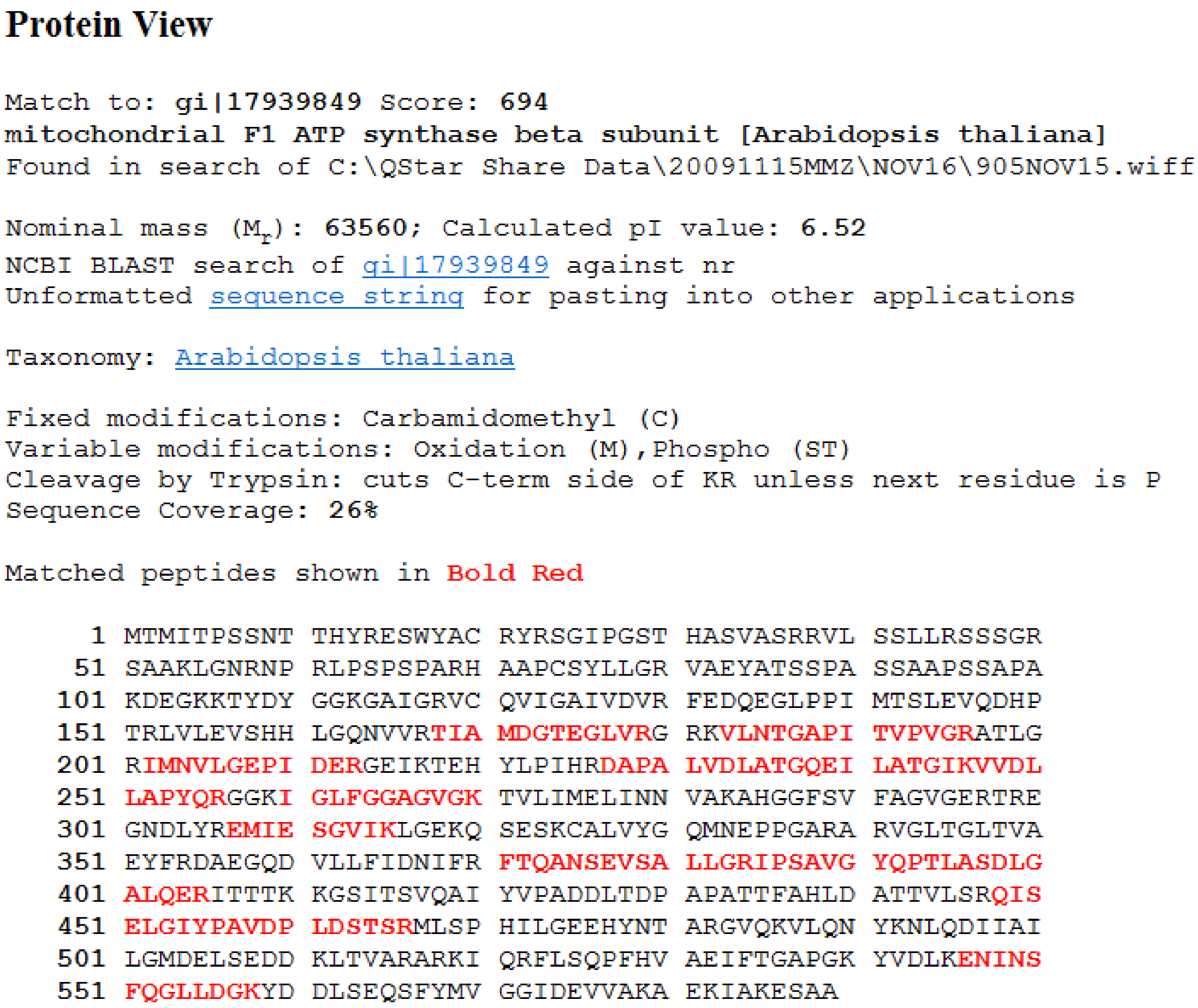
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

1 MSLSVNMGTN DLDIEEGTLE IGMEYRTVSG VAGPLVILDK VKGPK**YQEIV**
51 **NIR**LGDGSTR **RGQVLEVDGE** **KAVVQVFEGT** **SGIDNKFTTV** **QFTGEVLKTP**
101 **VSLDMLGR**IF NGSGKPIDNG PPILPEAYLD ISGSSINPSE RTYPEEMIQT
151 GISTIDVMNS IARGQKIPLF SAAGLPHNEI AAQICRQAGL VKRLEKTVDL
201 LEDHGEDNFA IVFAAMGVNM ETAQFFKR**DF** **EENGSMER**VT LFLNLANDPT
251 IERIITPRIA LTTAEYLAYE CGKHVLVILT DMSSYADALR EVSAAREEVP
301 GRRGYPGYMY TDLATIYERA GRIEGRKGSI TQIPILTMPN DDITHPTPDL
351 TGYITEGQIY IDRQLHNR**QI** **YPPINVLPSL** **SR**LMKSAIGE GMTRK**DHSDV**
401 **SNQLYANYAI** **GK**DVQAMKAV VGEEALSSED LLYLEFLDKF ER**KFVMQGAY**
451 **DTR**NIFQSLD LAWTLLRIFP RELLHRIPAK **TLDQFYSR**DS TS

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   46 - 53      517.8113  1033.6081  1033.5556    0.0525    0   K.YQEIVNIR.L   (Ions score 42)
   61 - 71      615.3594  1228.7043  1228.6412    0.0631    1   R.RGQVLEVDGEK.A   (Ions score 79)
   62 - 71      537.3120  1072.6095  1072.5401    0.0694    0   R.GQVLEVDGEK.A   (Ions score 65)
   72 - 86      521.9743  1562.9010  1562.7941    0.1070    0   K.AVVQVFEGTSGIDNK.F   (Ions score 59)
   87 - 98      685.3925  1368.7705  1368.7289    0.0416    0   K.FTTVQFTGEVLK.T   (Ions score 63)
   99 - 108     544.8297  1087.6449  1087.5696    0.0753    0   K.TPVSLDMLGR.I   (Ions score 79)
  229 - 238     607.2803  1212.5460  1212.4717    0.0743    0   R.DFEENGSMER.V   (Ions score 65)
  369 - 382     798.9929  1595.9712  1595.9035    0.0677    0   R.QIYPPINVLPSLSR.L   (Ions score 48)
  396 - 412     632.3287  1893.9643  1893.8857    0.0786    0   K.DHSDVSNQLYANYAIGK.D   (Ions score 61)
  443 - 453     444.5888  1330.7445  1330.6340    0.1105    1   R.KFVMQGAYDTR.N  Oxidation (M)  (Ions score 59)
  444 - 453     602.3073  1202.6000  1202.5390    0.0609    0   K.FVMQGAYDTR.N  Oxidation (M)  (Ions score 55)
  481 - 488     515.2851  1028.5556  1028.4927    0.0629    0   K.TLDQFYSR.D   (Ions score 52)
```

gi|17939849 Mitochondrial F1 ATP synthase beta subunit



Protein View

Match to: **gi|17939849** Score: **694**
mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\905NOV15.wiff

Nominal mass (M_r): **63560**; Calculated pI value: **6.52**
NCBI BLAST search of gi|17939849 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

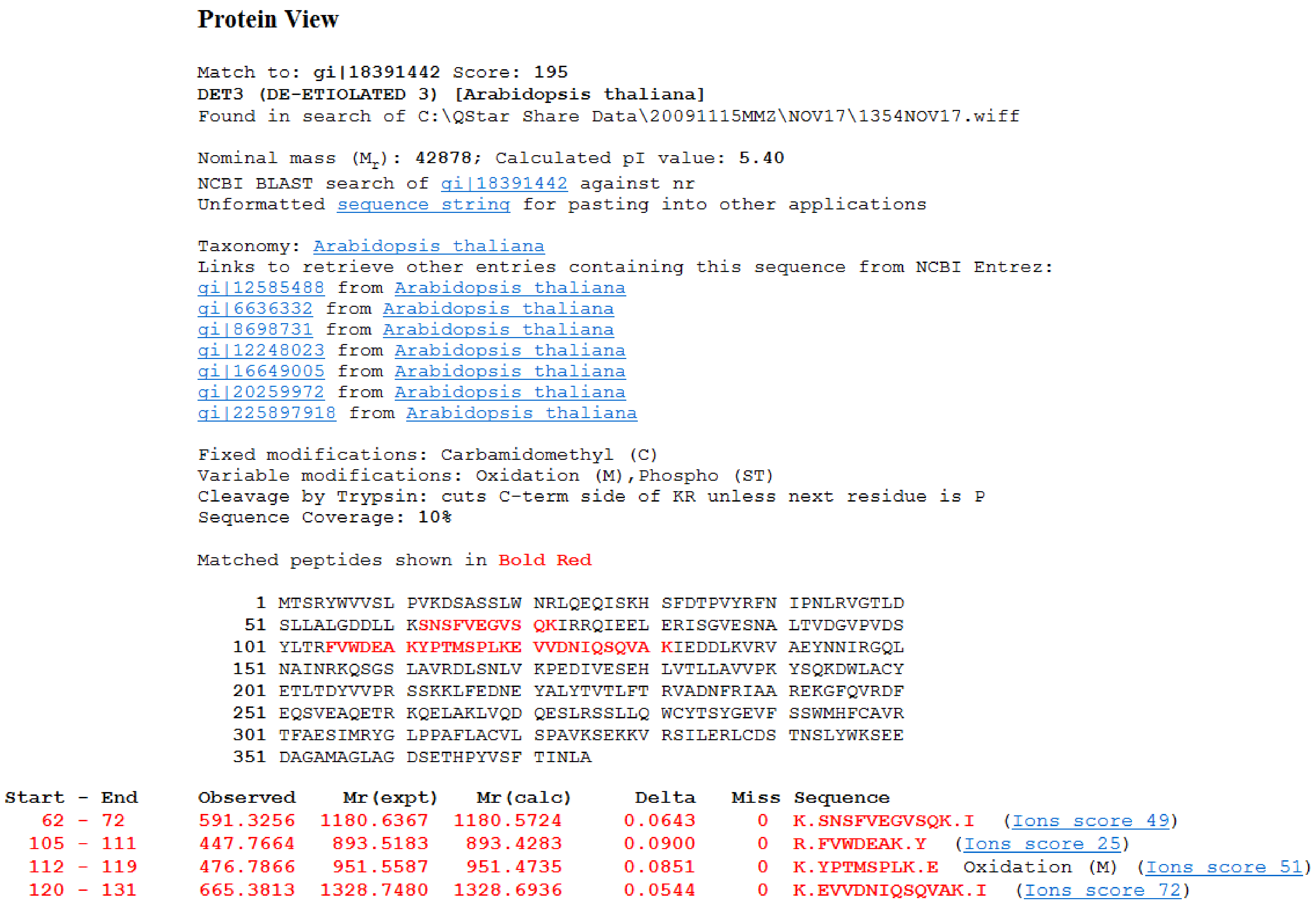
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 26%

Matched peptides shown in **Bold Red**

1 MTMITPSSNT THYRESWYAC RYRSGIPGST HASVASRRVL SSLLRSSSGR
51 SAAKLGNRNP RLPSPSPARH AAPCSYLLGR VAEYATSSPA SSAAPSSAPA
101 KDEGKKTYDY GGKGAIGRVC QVIGAIVDVR FEDQEGLPPI MTSLEVQDHP
151 TRLVLEVSHH LGQNVVR**TIA** **MDGTEGLVR**G RK**VLNTGAPI** **TVPVGR**ATLG
201 R**IMNVLGEPI** **DER**GEIKTEH YLPIHR**DAPA** **LVDLATGQEI** **LATGIKVVDL**
251 **LAPYQR**GGK**I** **GLFGGAGVGK** TVLIMELINN VAKAHGGFSV FAGVGERTRE
301 GNDLYR**EMIE** **SGVIK**LGEKQ SESKCALVYG QMNEPPGARA RVGLTGLTVA
351 EYFRDAEGQD VLLFIDNIFR **FTQANSEVSA** **LLGRIPSAVG** **YQPTLASDLG**
401 **ALQER**ITTTK KGSITSVQAI YVPADDLTDP APATTFAHLD ATTVLSR**QIS**
451 **ELGIYPAVDP** **LDSTSR**MLSP HILGEEHYNT ARGVQKVLQN YKNLQDIIAI
501 LGMDELSEDD KLTVARARKI QRFLSQPFHV AEIFTGAPGK YVDLK**ENINS**
551 **FQGLLDGK**YD DLSEQSFYMV GGIDEVVAKA EKIAKESAA

```
Start - End     Observed   Mr(expt)   Mr(calc)      Delta  Miss Sequence
  168 - 179     631.8573  1261.7001  1261.6336     0.0665     0 R.TIAMDGTEGLVR.G  (Ions score 51)
  168 - 179     639.8494  1277.6842  1277.6286     0.0556     0 R.TIAMDGTEGLVR.G Oxidation (M) (Ions score 73)
  183 - 196     697.4355  1392.8565  1392.8089     0.0475     0 K.VLNTGAPITVPVGR.A  (Ions score 69)
  202 - 213     693.3860  1384.7575  1384.7020     0.0555     0 R.IMNVLGEPIDER.G  (Ions score 46)
  202 - 213     701.3786  1400.7426  1400.6969     0.0456     0 R.IMNVLGEPIDER.G Oxidation (M) (Ions score 63)
  227 - 246     666.0608  1995.1606  1995.0888     0.0718     0 R.DAPALVDLATGQEILATGIK.V  (Ions score 73)
  247 - 256     587.3593  1172.7041  1172.6553     0.0488     0 K.VVDLLAPYQR.G  (Ions score 53)
  260 - 270     488.3183   974.6221   974.5549     0.0671     0 K.IGLFGGAGVGK.T  (Ions score 48)
  307 - 315     503.3072  1004.5998  1004.5212     0.0786     0 R.EMIESGVIK.L  (Ions score 32)
  307 - 315     511.3004  1020.5862  1020.5161     0.0700     0 R.EMIESGVIK.L Oxidation (M) (Ions score 37)
  371 - 384     498.3023  1491.8851  1491.7681     0.1170     0 R.FTQANSEVSALLGR.I  (Ions score 86)
  385 - 405     729.4237  2185.2494  2185.1379     0.1115     0 R.IPSAVGYQPTLASDLGALQER.I  (Ions score 85)
  448 - 466     687.7084  2060.1035  2060.0426     0.0609     0 R.QISELGIYPAVDPLDSTSR.M  (Ions score 56)
  546 - 558     717.8957  1433.7768  1433.7150     0.0618     0 K.ENINSFQGLLDGK.Y  (Ions score 50)
```

gi|18391442 De-etiolated 3 (DET3)



Protein View

Match to: **gi|18391442** Score: **195**
DET3 (DE-ETIOLATED 3) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff

Nominal mass (M_r): **42878**; Calculated pI value: **5.40**
NCBI BLAST search of gi|18391442 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12585488 from Arabidopsis thaliana
gi|6636332 from Arabidopsis thaliana
gi|8698731 from Arabidopsis thaliana
gi|12248023 from Arabidopsis thaliana
gi|16649005 from Arabidopsis thaliana
gi|20259972 from Arabidopsis thaliana
gi|225897918 from Arabidopsis thaliana

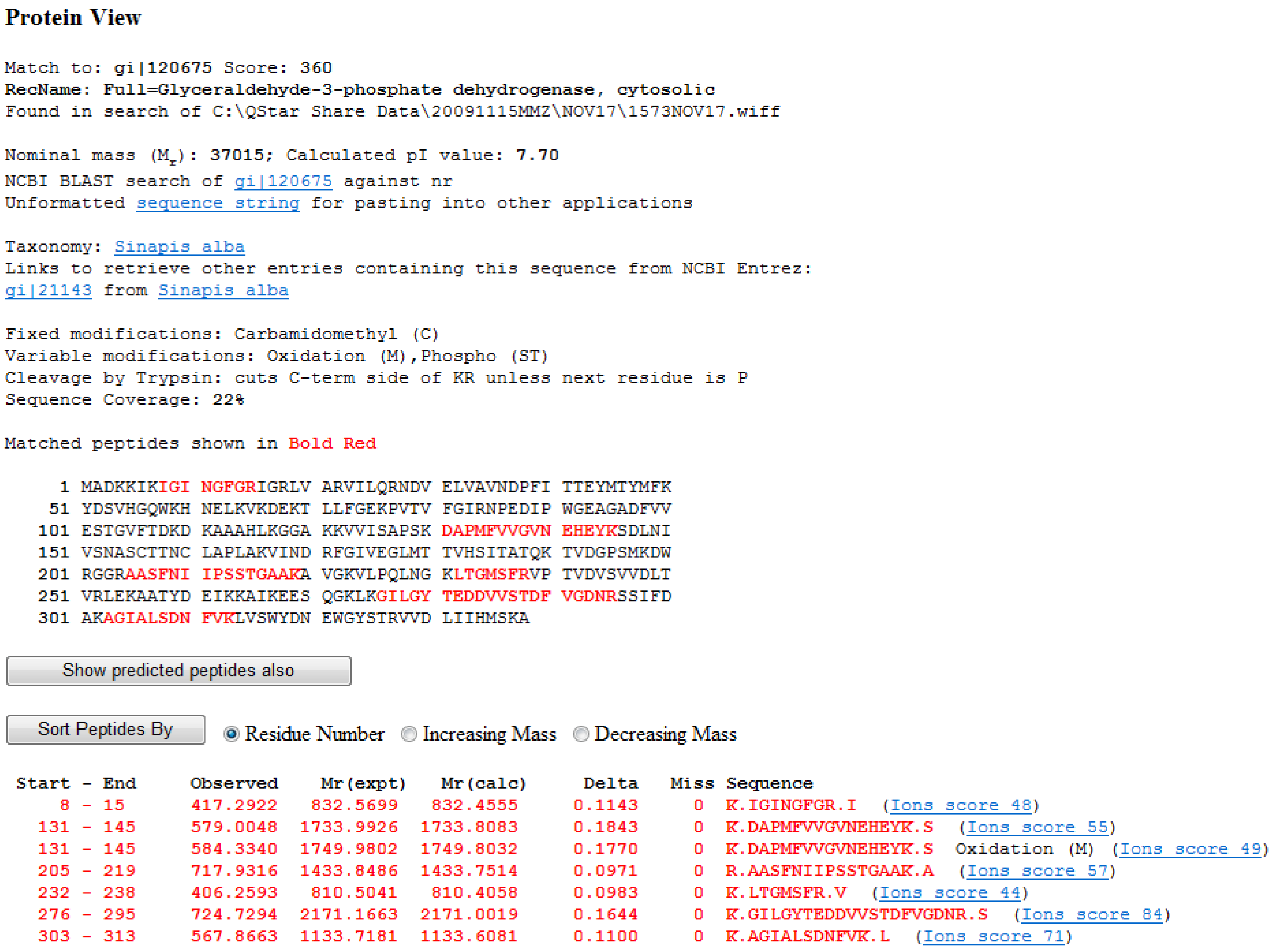
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
  1 MTSRYWVVSL PVKDSASSLW NRLQEQISKH SFDTPVYRFN IPNLRVGTLD
 51 SLLALGDDLL KSNSFVEGVS QKIRRQIEEL ERISGVESNA LTVDGVPVDS
101 YLTRFVWDEA KYPTMSPLKE VVDNIQSQVA KIEDDLKVRV AEYNNIRGQL
151 NAINRKQSGS LAVRDLSNLV KPEDIVESEH LVTLLAVVPK YSQKDWLACY
201 ETLTDYVVPR SSKKLFEDNE YALYTVTLFT RVADNFRIAA REKGFQVRDF
251 EQSVEAQETR KQELAKLVQD QESLRSSLLQ WCYTSYGEVF SSWMHFCAVR
301 TFAESIMRYG LPPAFLACVL SPAVKSEKKV RSILERLCDS TNSLYWKSEE
351 DAGAMAGLAG DSETHPYVSF TINLA
```

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   62 - 72      591.3256  1180.6367  1180.5724   0.0643     0 K.SNSFVEGVSQK.I  (Ions score 49)
  105 - 111     447.7664   893.5183   893.4283   0.0900     0 R.FVWDEAK.Y  (Ions score 25)
  112 - 119     476.7866   951.5587   951.4735   0.0851     0 K.YPTMSPLK.E  Oxidation (M)  (Ions score 51)
  120 - 131     665.3813  1328.7480  1328.6936   0.0544     0 K.EVVDNIQSQVAK.I  (Ions score 72)
```

gi|120675 Glyceraldehyde-3-phosphate dehydrogenase, cytosolic



Protein View

```
Match to: gi|120675 Score: 360
RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (Mr): 37015; Calculated pI value: 7.70
NCBI BLAST search of gi|120675 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Sinapis alba
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|21143 from Sinapis alba

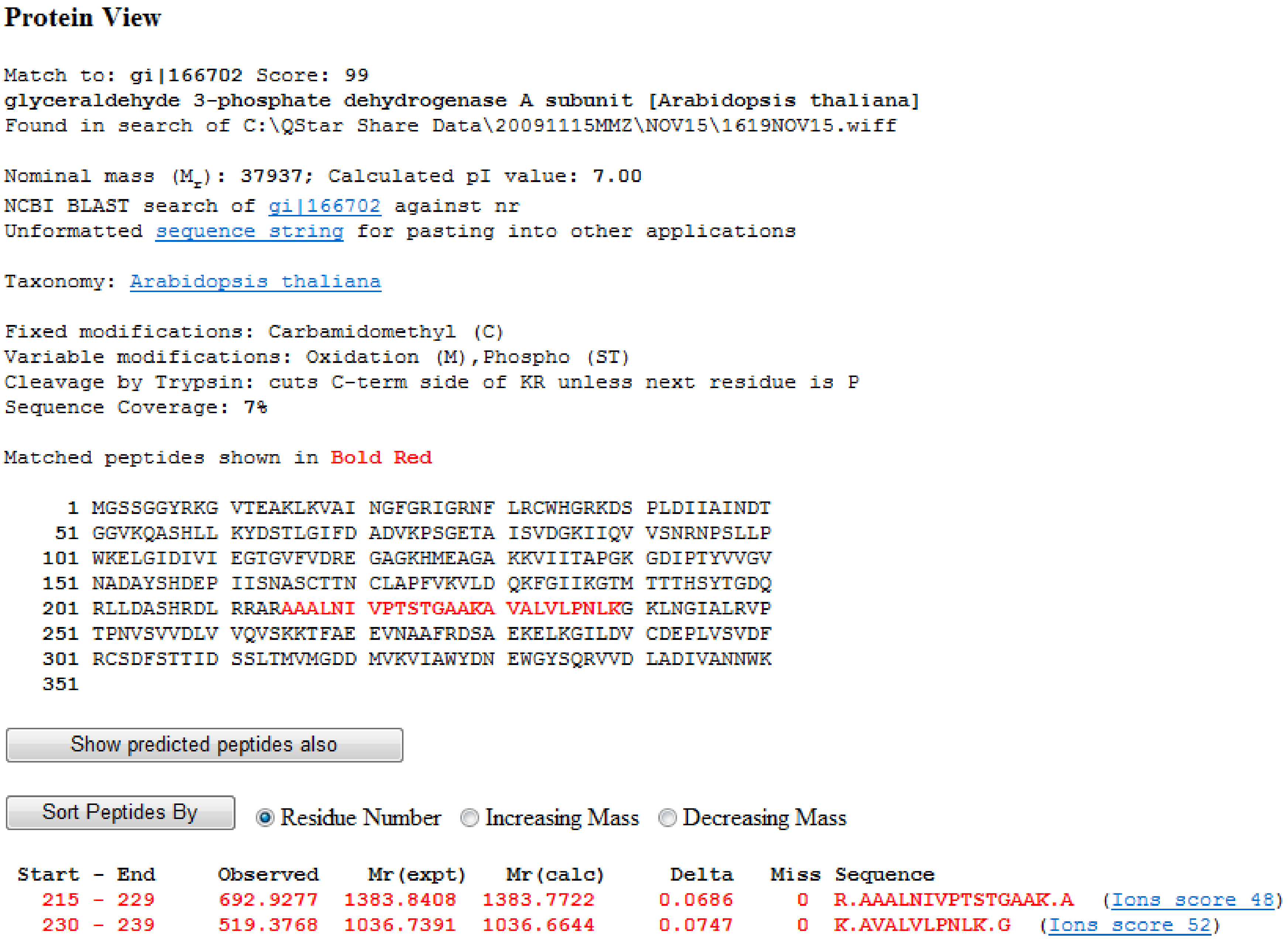
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 22%

Matched peptides shown in Bold Red

    1 MADKKIKIGI NGFGRIGRLV ARVILQRNDV ELVAVNDPFI TTEYMTYMFK
   51 YDSVHGQWKH NELKVKDEKT LLFGEKPVTV FGIRNPEDIP WGEAGADFVV
  101 ESTGVFTDKD KAAAHLKGGA KKVVISAPSK DAPMFVVGVN EHEYKSDLNI
  151 VSNASCTTNC LAPLAKVIND RFGIVEGLMT TVHSITATQK TVDGPSMKDW
  201 RGGRAASFNI IPSSTGAAKA VGKVLPQLNG KLTGMSFRVP TVDVSVVDLT
  251 VRLEKAATYD EIKKAIKEES QGKLKGILGY TEDDVVSTDF VGDNRSSIFD
  301 AKAGIALSDN FVKLVSWYDN EWGYSTRVVD LIIHMSKA
```

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
    8 - 15     417.2922    832.5699    832.4555    0.1143     0   K.IGINGFGR.I   (Ions score 48)
  131 - 145    579.0048   1733.9926   1733.8083    0.1843     0   K.DAPMFVVGVNEHEYK.S   (Ions score 55)
  131 - 145    584.3340   1749.9802   1749.8032    0.1770     0   K.DAPMFVVGVNEHEYK.S  Oxidation (M)  (Ions score 49)
  205 - 219    717.9316   1433.8486   1433.7514    0.0971     0   R.AASFNIIPSSTGAAK.A   (Ions score 57)
  232 - 238    406.2593    810.5041    810.4058    0.0983     0   K.LTGMSFR.V   (Ions score 44)
  276 - 295    724.7294   2171.1663   2171.0019    0.1644     0   K.GILGYTEDDVVSTDFVGDNR.S   (Ions score 84)
  303 - 313    567.8663   1133.7181   1133.6081    0.1100     0   K.AGIALSDNFVK.L   (Ions score 71)
```

gi|166702 Glyceraldehyde 3-phosphate dehydrogenase A subunit



Protein View

Match to: gi|166702 Score: 99
glyceraldehyde 3-phosphate dehydrogenase A subunit [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1619NOV15.wiff

Nominal mass (M_r): 37937; Calculated pI value: 7.00
NCBI BLAST search of gi|166702 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

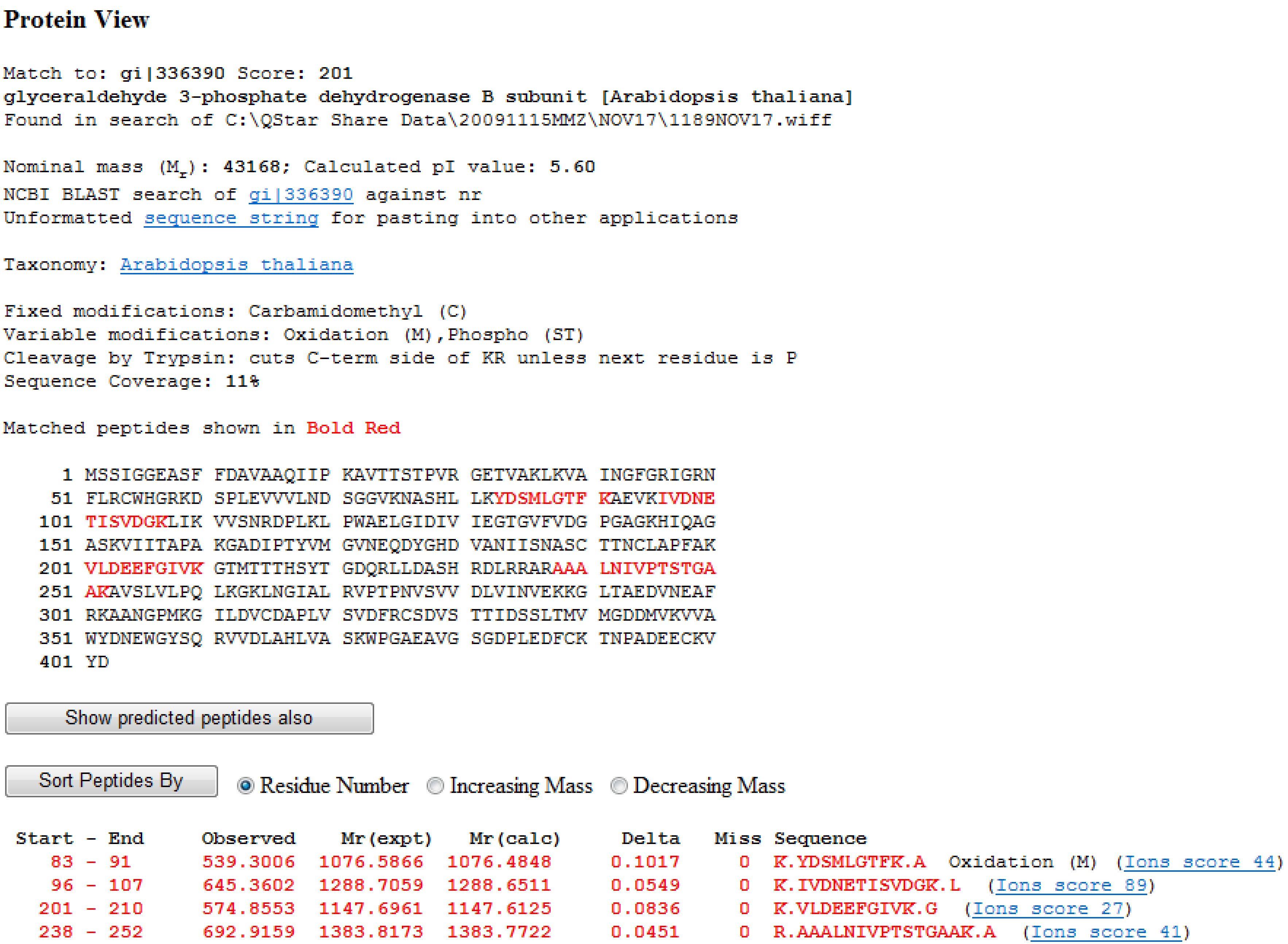
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

```
      1 MGSSGGYRKG VTEAKLKVAI NGFGRIGRNF LRCWHGRKDS PLDIIAINDT
     51 GGVKQASHLL KYDSTLGIFD ADVKPSGETA ISVDGKIIQV VSNRNPSLLP
    101 WKELGIDIVI EGTGVFVDRE GAGKHMEAGA KKVIITAPGK GDIPTYVVGV
    151 NADAYSHDEP IISNASCTTN CLAPFVKVLD QKFGIIKGTM TTTHSYTGDQ
    201 RLLDASHRDL RRARAAALNI VPTSTGAAKA VALVLPNLKG KLNGIALRVP
    251 TPNVSVVDLV VQVSKKTFAE EVNAAFRDSA EKELKGILDV CDEPLVSVDF
    301 RCSDFSTTID SSLTMVMGDD MVKVIAWYDN EWGYSQRVVD LADIVANNWK
    351
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
  215 - 229      692.9277  1383.8408  1383.7722   0.0686     0  R.AAALNIVPTSTGAAK.A  (Ions score 48)
  230 - 239      519.3768  1036.7391  1036.6644   0.0747     0  K.AVALVLPNLK.G  (Ions score 52)
```

gi|336390 Glyceraldehyde 3-phosphate dehydrogenase B subunit



Protein View

Match to: gi|336390 Score: 201
glyceraldehyde 3-phosphate dehydrogenase B subunit [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (M_r): **43168**; Calculated pI value: **5.60**
NCBI BLAST search of gi|336390 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

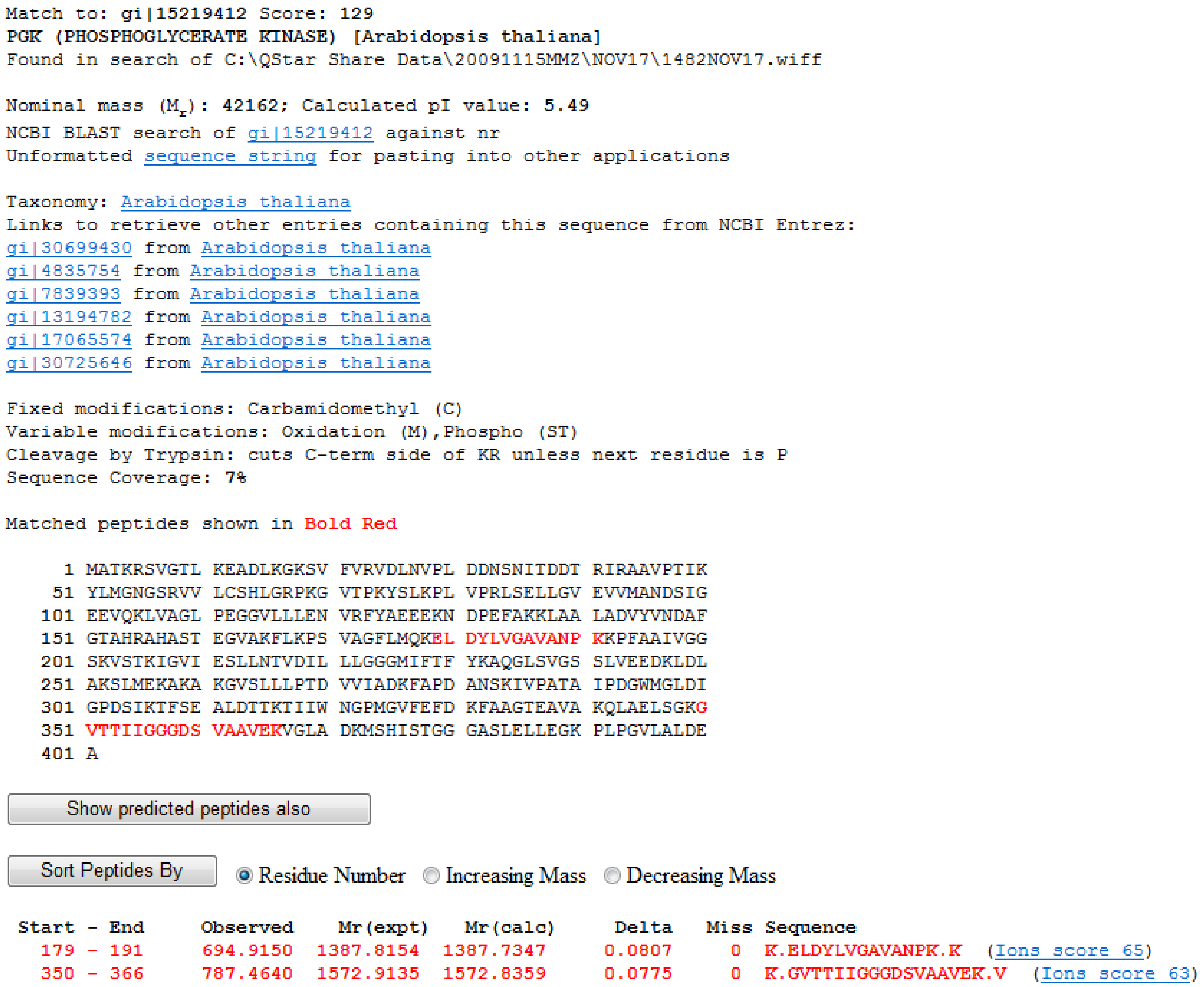
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
  1 MSSIGGEASF FDAVAAQIIP KAVTTSTPVR GETVAKLKVA INGFGRIGRN
 51 FLRCWHGRKD SPLEVVVLND SGGVKNASHL LKYDSMLGTF KAEVKIVDNE
101 TISVDGKLIK VVSNRDPLKL PWAELGIDIV IEGTGVFVDG PGAGKHIQAG
151 ASKVIITAPA KGADIPTYVM GVNEQDYGHD VANIISNASC TTNCLAPFAK
201 VLDEEFGIVK GTMTTTHSYT GDQRLLDASH RDLRRARAAA LNIVPTSTGA
251 AKAVSLVLPQ LKGKLNGIAL RVPTPNVSVV DLVINVEKKG LTAEDVNEAF
301 RKAANGPMKG ILDVCDAPLV SVDFRCSDVS TTIDSSLTMV MGDDMVKVVA
351 WYDNEWGYSQ RVVDLAHLVA SKWPGAEAVG SGDPLEDFCK TNPADEECKV
401 YD
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   83 - 91       539.3006  1076.5866  1076.4848    0.1017     0  K.YDSMLGTFK.A  Oxidation (M)  (Ions score 44)
   96 - 107      645.3602  1288.7059  1288.6511    0.0549     0  K.IVDNETISVDGK.L  (Ions score 89)
  201 - 210      574.8553  1147.6961  1147.6125    0.0836     0  K.VLDEEFGIVK.G  (Ions score 27)
  238 - 252      692.9159  1383.8173  1383.7722    0.0451     0  R.AAALNIVPTSTGAAK.A  (Ions score 41)
```

gi|15219412 Phosphoglycerate kinase (PGK)



Match to: gi|15219412 Score: 129
PGK (PHOSPHOGLYCERATE KINASE) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1482NOV17.wiff

Nominal mass (M_r): **42162**; Calculated pI value: **5.49**
NCBI BLAST search of gi|15219412 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|30699430 from Arabidopsis thaliana
gi|4835754 from Arabidopsis thaliana
gi|7839393 from Arabidopsis thaliana
gi|13194782 from Arabidopsis thaliana
gi|17065574 from Arabidopsis thaliana
gi|30725646 from Arabidopsis thaliana

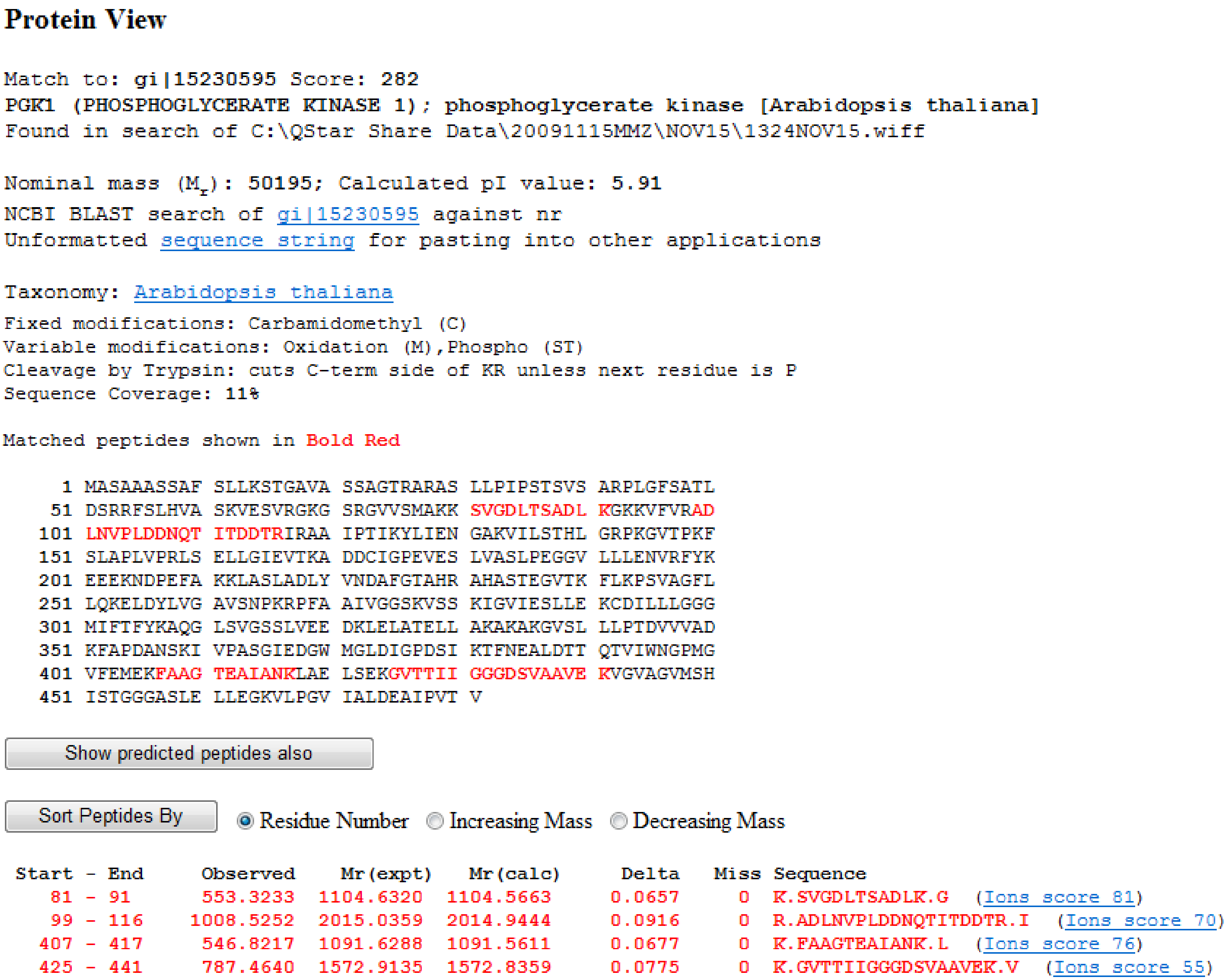
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

Matched peptides shown in **Bold Red**

```
  1 MATKRSVGTL KEADLKGKSV FVRVDLNVPL DDNSNITDDT RIRAAVPTIK
 51 YLMGNGSRVV LCSHLGRPKG VTPKYSLKPL VPRLSELLGV EVVMANDSIG
101 EEVQKLVAGL PEGGVLLLEN VRFYAEEEKN DPEFAKKLAA LADVYVNDAF
151 GTAHRAHAST EGVAKFLKPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
201 SKVSTKIGVI ESLLNTVDIL LLGGGMIFTF YKAQGLSVGS SLVEEDKLDL
251 AKSLMEKAKA KGVSLLLPTD VVIADKFAPD ANSKIVPATA IPDGWMGLDI
301 GPDSIKTFSE ALDTTKTIIW NGPMGVFEFD KFAAGTEAVA KQLAELSGKG
351 VTTIIGGGDS VAAVEKVGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
401 A
```

```
Start - End    Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
 179 - 191     694.9150  1387.8154  1387.7347   0.0807     0  K.ELDYLVGAVANPK.K   (Ions score 65)
 350 - 366     787.4640  1572.9135  1572.8359   0.0775     0  K.GVTTIIGGGDSVAAVEK.V   (Ions score 63)
```

gi|15230595 Phosphoglycerate kinase 1 (PGK1)



Protein View

Match to: gi|15230595 Score: 282
PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1324NOV15.wiff

Nominal mass (M_r): 50195; Calculated pI value: 5.91
NCBI BLAST search of gi|15230595 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

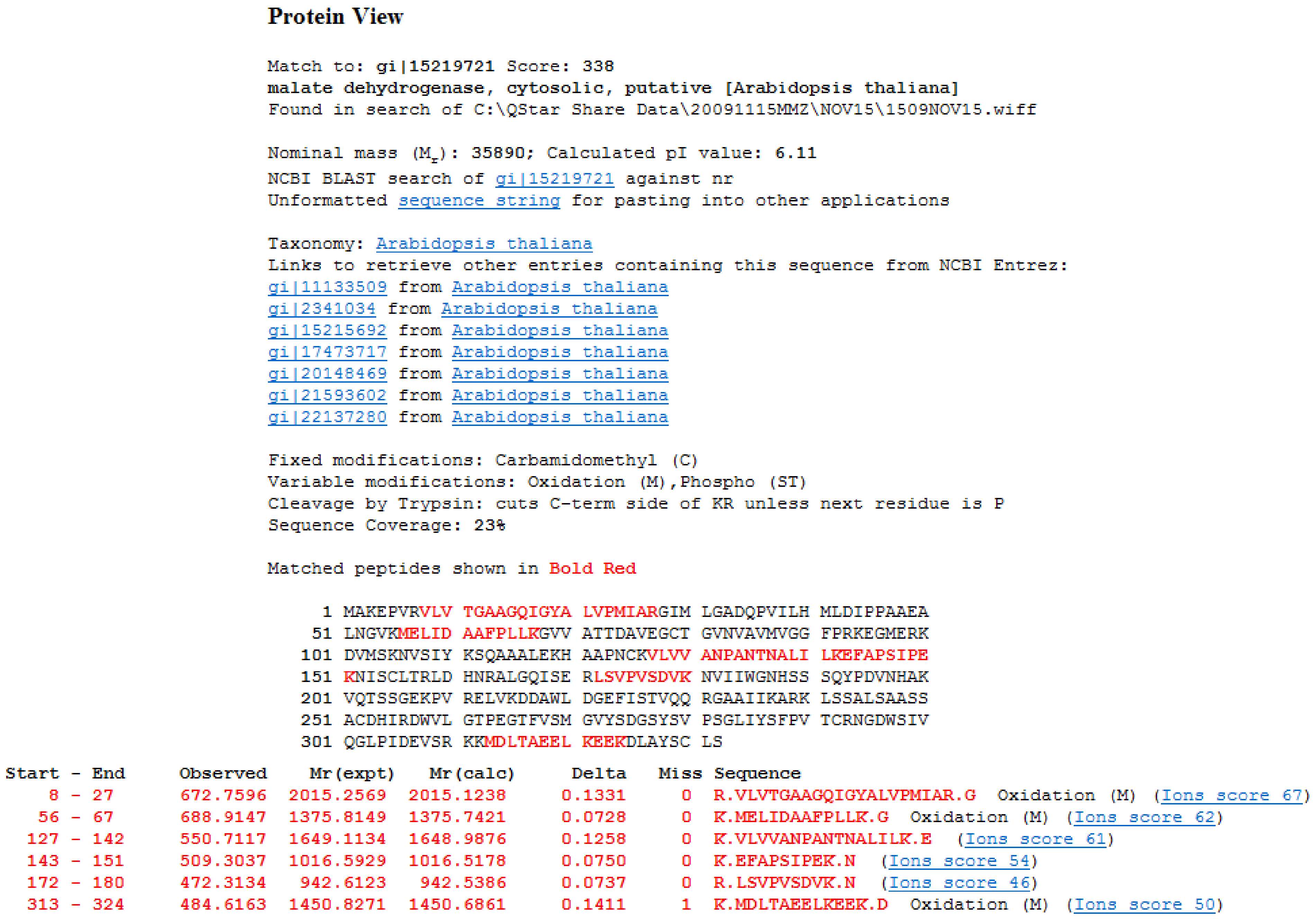
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

```
  1 MASAAASSAF SLLKSTGAVA SSAGTRARAS LLPIPSTSVS ARPLGFSATL
 51 DSRRFSLHVA SKVESVRGKG SRGVVSMAKK SVGDLTSADL KGKKVFVRAD
101 LNVPLDDNQT ITDDTRIRAA IPTIKYLIEN GAKVILSTHL GRPKGVTPKF
151 SLAPLVPRLS ELLGIEVTKA DDCIGPEVES LVASLPEGGV LLLENVRFYK
201 EEEKNDPEFA KKLASLADLY VNDAFGTAHR AHASTEGVTK FLKPSVAGFL
251 LQKELDYLVG AVSNPKRPFA AIVGGSKVSS KIGVIESLLE KCDILLLGGG
301 MIFTFYKAQG LSVGSSLVEE DKLELATELL AKAKAKGVSL LLPTDVVVAD
351 KFAPDANSKI VPASGIEDGW MGLDIGPDSI KTFNEALDTT QTVIWNGPMG
401 VFEMEKFAAG TEAIANKLAE LSEKGVTTII GGGDSVAAVE KVGVAGVMSH
451 ISTGGGASLE LLEGKVLPGV IALDEAIPVT V
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   81 - 91      553.3233  1104.6320  1104.5663    0.0657     0  K.SVGDLTSADLK.G   (Ions score 81)
   99 - 116    1008.5252  2015.0359  2014.9444    0.0916     0  R.ADLNVPLDDNQTITDDTR.I   (Ions score 70)
  407 - 417     546.8217  1091.6288  1091.5611    0.0677     0  K.FAAGTEAIANK.L   (Ions score 76)
  425 - 441     787.4640  1572.9135  1572.8359    0.0775     0  K.GVTTIIGGGDSVAAVEK.V   (Ions score 55)
```

gi|15219721 Malate dehydrogenase, cytosolic, putative



Protein View

```
Match to: gi|15219721 Score: 338
malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff

Nominal mass (Mr): 35890; Calculated pI value: 6.11
NCBI BLAST search of gi|15219721 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|11133509 from Arabidopsis thaliana
gi|2341034 from Arabidopsis thaliana
gi|15215692 from Arabidopsis thaliana
gi|17473717 from Arabidopsis thaliana
gi|20148469 from Arabidopsis thaliana
gi|21593602 from Arabidopsis thaliana
gi|22137280 from Arabidopsis thaliana

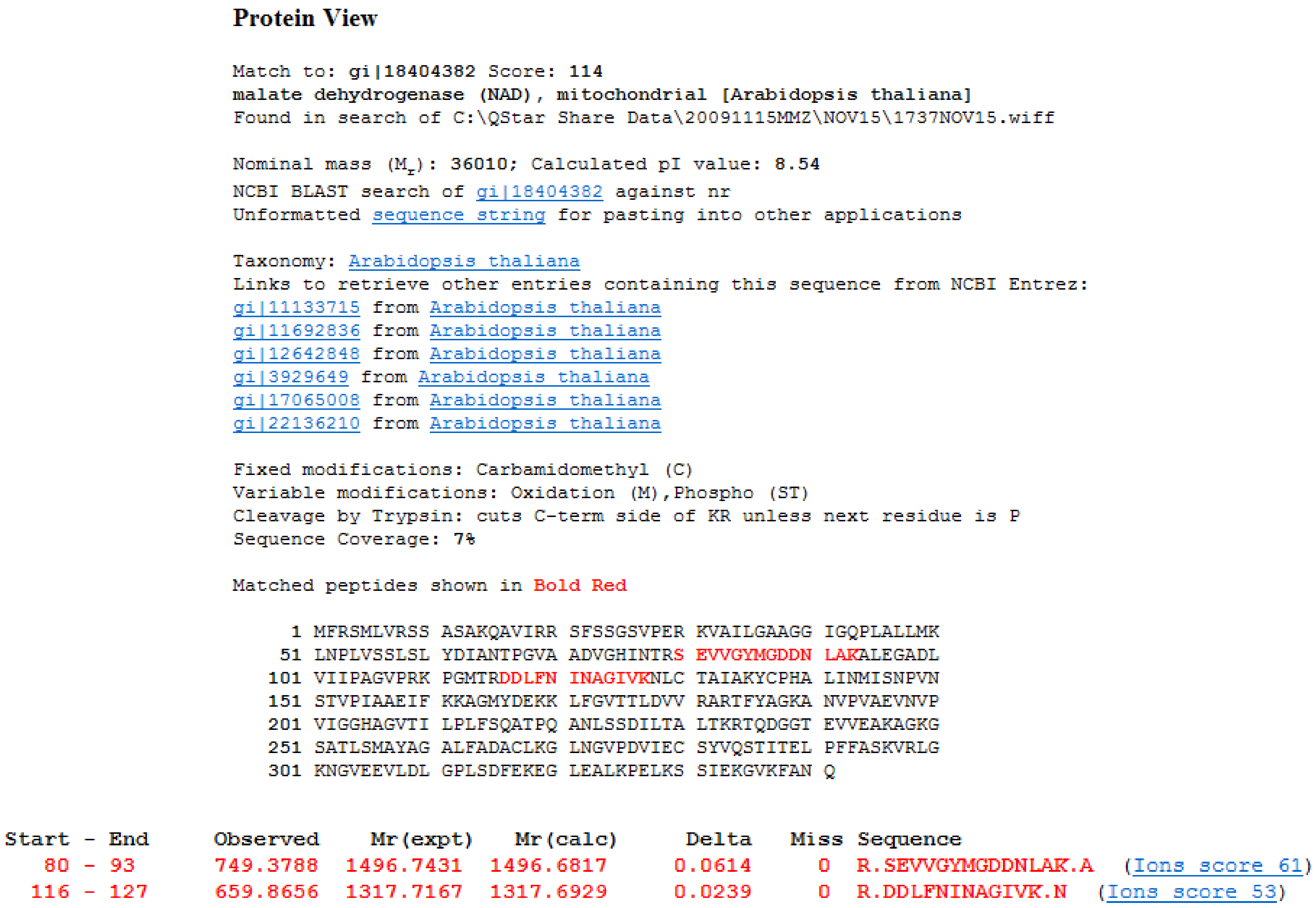
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 23%

Matched peptides shown in Bold Red

    1 MAKEPVRVLV TGAAGQIGYA LVPMIARGIM LGADQPVILH MLDIPPAAEA
   51 LNGVKMELID AAFPLLKGVV ATTDAVEGCT GVNVAVMVGG FPRKEGMERK
  101 DVMSKNVSIY KSQAAALEKH AAPNCKVLVV ANPANTNALI LKEFAPSIPE
  151 KNISCLTRLD HNRALGQISE RLSVPVSDVK NVIIWGNHSS SQYPDVNHAK
  201 VQTSSGEKPV RELVKDDAWL DGEFISTVQQ RGAAIIKARK LSSALSAASS
  251 ACDHIRDWVL GTPEGTFVSM GVYSDGSYSV PSGLIYSFPV TCRNGDWSIV
  301 QGLPIDEVSR KKMDLTAEEL KEEKDLAYSC LS

Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   8 - 27      672.7596  2015.2569  2015.1238     0.1331     0  R.VLVTGAAGQIGYALVPMIAR.G  Oxidation (M) (Ions score 67)
  56 - 67      688.9147  1375.8149  1375.7421     0.0728     0  K.MELIDAAFPLLK.G  Oxidation (M) (Ions score 62)
 127 - 142     550.7117  1649.1134  1648.9876     0.1258     0  K.VLVVANPANTNALILK.E  (Ions score 61)
 143 - 151     509.3037  1016.5929  1016.5178     0.0750     0  K.EFAPSIPEK.N  (Ions score 54)
 172 - 180     472.3134   942.6123   942.5386     0.0737     0  R.LSVPVSDVK.N  (Ions score 46)
 313 - 324     484.6163  1450.8271  1450.6861     0.1411     1  K.MDLTAEELKEEK.D  Oxidation (M) (Ions score 50)
```

gi|18404382 Malate dehydrogenase (NAD), mitochondrial



Protein View

Match to: **gi|18404382** Score: **114**
malate dehydrogenase (NAD), mitochondrial [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1737NOV15.wiff

Nominal mass (M_r): **36010**; Calculated pI value: **8.54**
NCBI BLAST search of gi|18404382 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|11133715 from Arabidopsis thaliana
gi|11692836 from Arabidopsis thaliana
gi|12642848 from Arabidopsis thaliana
gi|3929649 from Arabidopsis thaliana
gi|17065008 from Arabidopsis thaliana
gi|22136210 from Arabidopsis thaliana

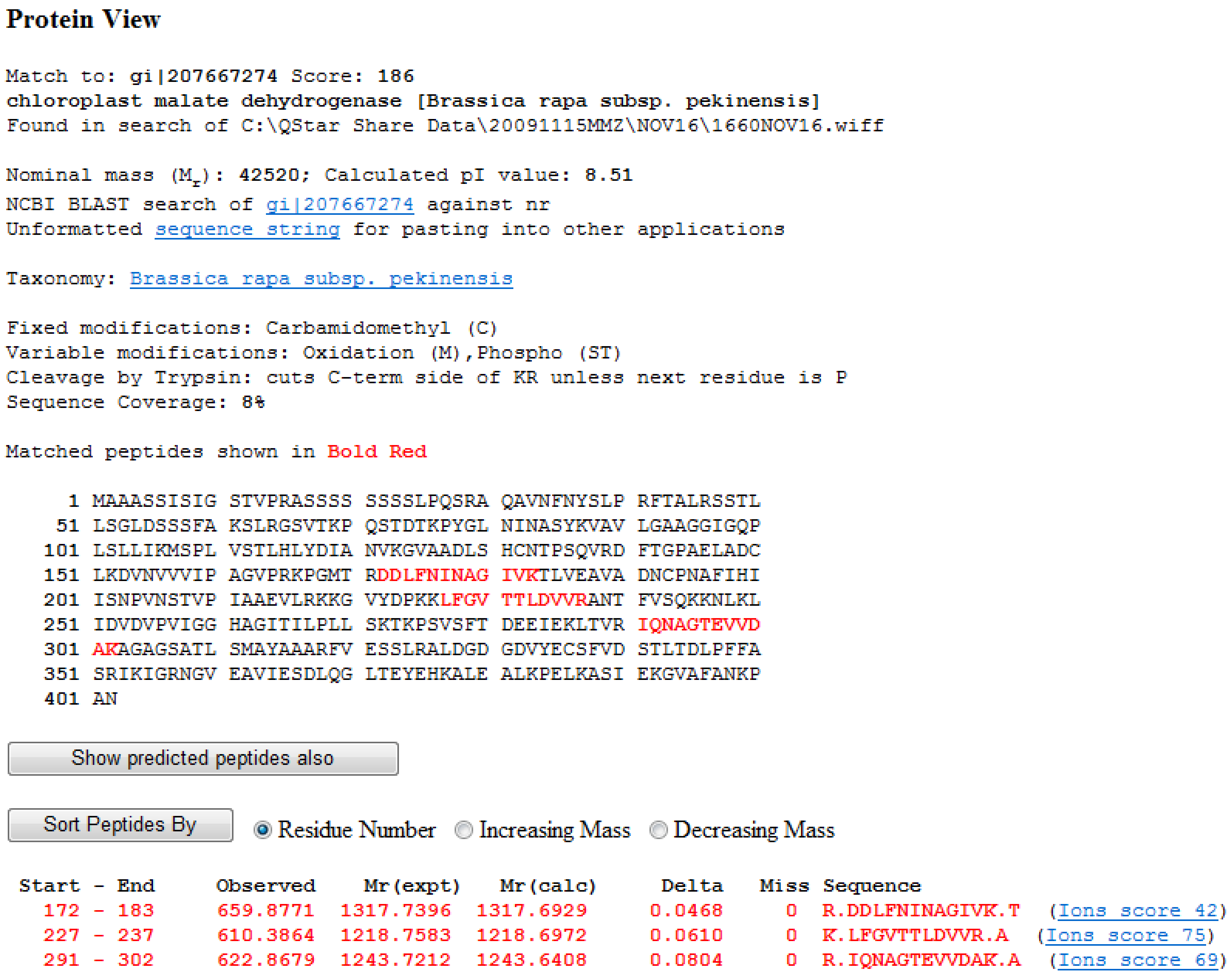
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

Matched peptides shown in **Bold Red**

```
  1 MFRSMLVRSS ASAKQAVIRR SFSSGSVPER KVAILGAAGG IGQPLALLMK
 51 LNPLVSSLSL YDIANTPGVA ADVGHINTRS EVVGYMGDDN LAKALEGADL
101 VIIPAGVPRK PGMTRDDLFN INAGIVKNLC TAIAKYCPHA LINMISNPVN
151 STVPIAAEIF KKAGMYDEKK LFGVTTLDVV RARTFYAGKA NVPVAEVNVP
201 VIGGHAGVTI LPLFSQATPQ ANLSSDILTA LTKRTQDGGT EVVEAKAGKG
251 SATLSMAYAG ALFADACLKG LNGVPDVIEC SYVQSTITEL PFFASKVRLG
301 KNGVEEVLDL GPLSDFEKEG LEALKPELKS SIEKGVKFAN Q
```

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   80 - 93      749.3788  1496.7431  1496.6817    0.0614     0  R.SEVVGYMGDDNLAK.A    (Ions score 61)
  116 - 127     659.8656  1317.7167  1317.6929    0.0239     0  R.DDLFNINAGIVK.N     (Ions score 53)
```

gi|207667274 Chloroplast malate dehydrogenase



Protein View

```
Match to: gi|207667274 Score: 186
chloroplast malate dehydrogenase [Brassica rapa subsp. pekinensis]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1660NOV16.wiff

Nominal mass (Mr): 42520; Calculated pI value: 8.51
NCBI BLAST search of gi|207667274 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

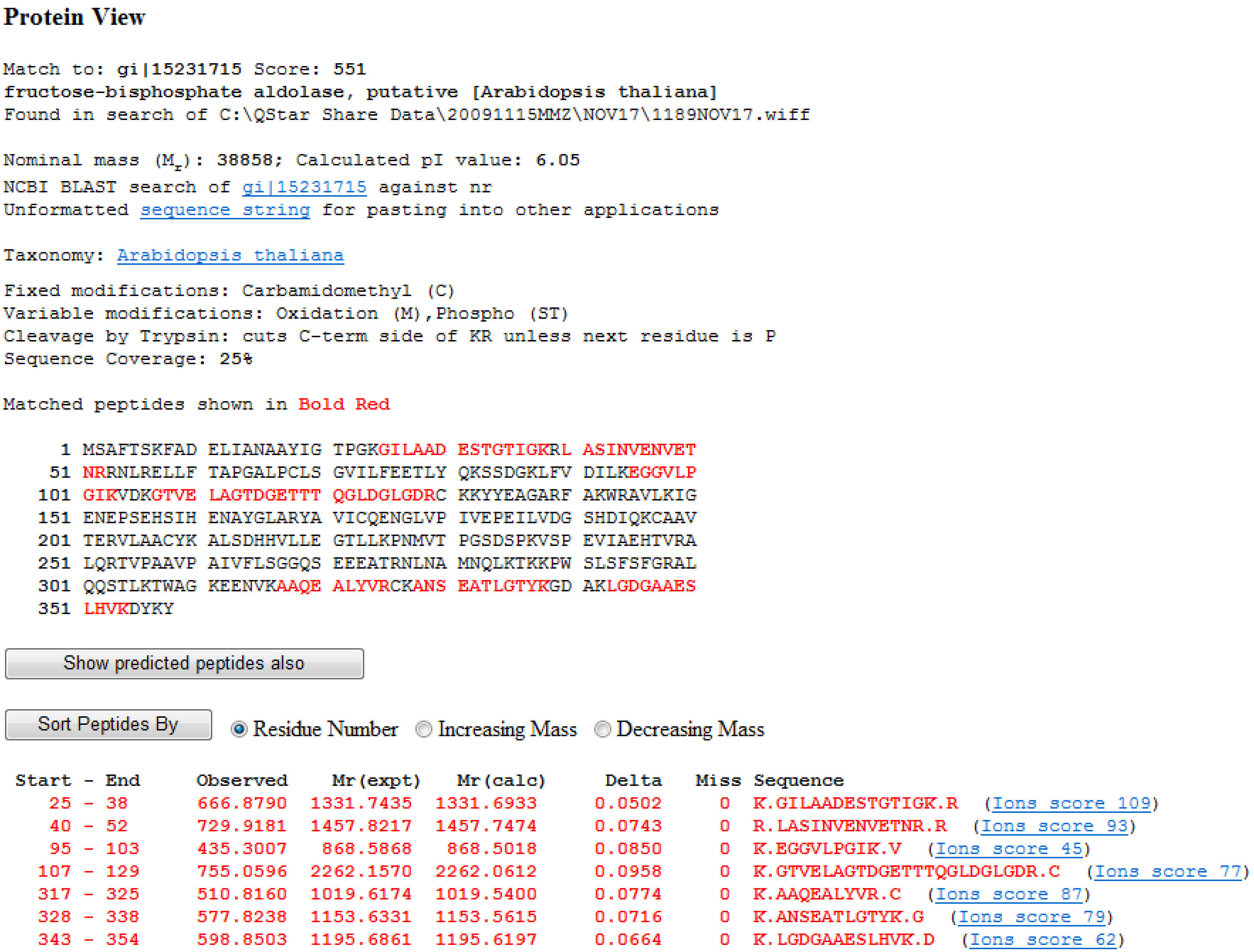
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in Bold Red

      1 MAAASSISIG STVPRASSSS SSSSLPQSRA QAVNFNYSLP RFTALRSSTL
     51 LSGLDSSSFA KSLRGSVTKP QSTDTKPYGL NINASYKVAV LGAAGGIGQP
    101 LSLLIKMSPL VSTLHLYDIA NVKGVAADLS HCNTPSQVRD FTGPAELADC
    151 LKDVNVVVIP AGVPRKPGMT RDDLFNINAG IVKTLVEAVA DNCPNAFIHI
    201 ISNPVNSTVP IAAEVLRKKG VYDPKKLFGV TTLDVVRANT FVSQKKNLKL
    251 IDVDVPVIGG HAGITILPLL SKTKPSVSFT DEEIEKLTVR IQNAGTEVVD
    301 AKAGAGSATL SMAYAAARFV ESSLRALDGD GDVYECSFVD STLTDLPFFA
    351 SRIKIGRNGV EAVIESDLQG LTEYEHKALE ALKPELKASI EKGVAFANKP
    401 AN
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   172 - 183     659.8771  1317.7396  1317.6929    0.0468     0 R.DDLFNINAGIVK.T   (Ions score 42)
   227 - 237     610.3864  1218.7583  1218.6972    0.0610     0 K.LFGVTTLDVVR.A    (Ions score 75)
   291 - 302     622.8679  1243.7212  1243.6408    0.0804     0 R.IQNAGTEVVDAK.A   (Ions score 69)
```

gi|15231715 Fructose-bisphosphate aldolase, putative



Protein View

```
Match to: gi|15231715 Score: 551
fructose-bisphosphate aldolase, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (Mr): 38858; Calculated pI value: 6.05
NCBI BLAST search of gi|15231715 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 25%

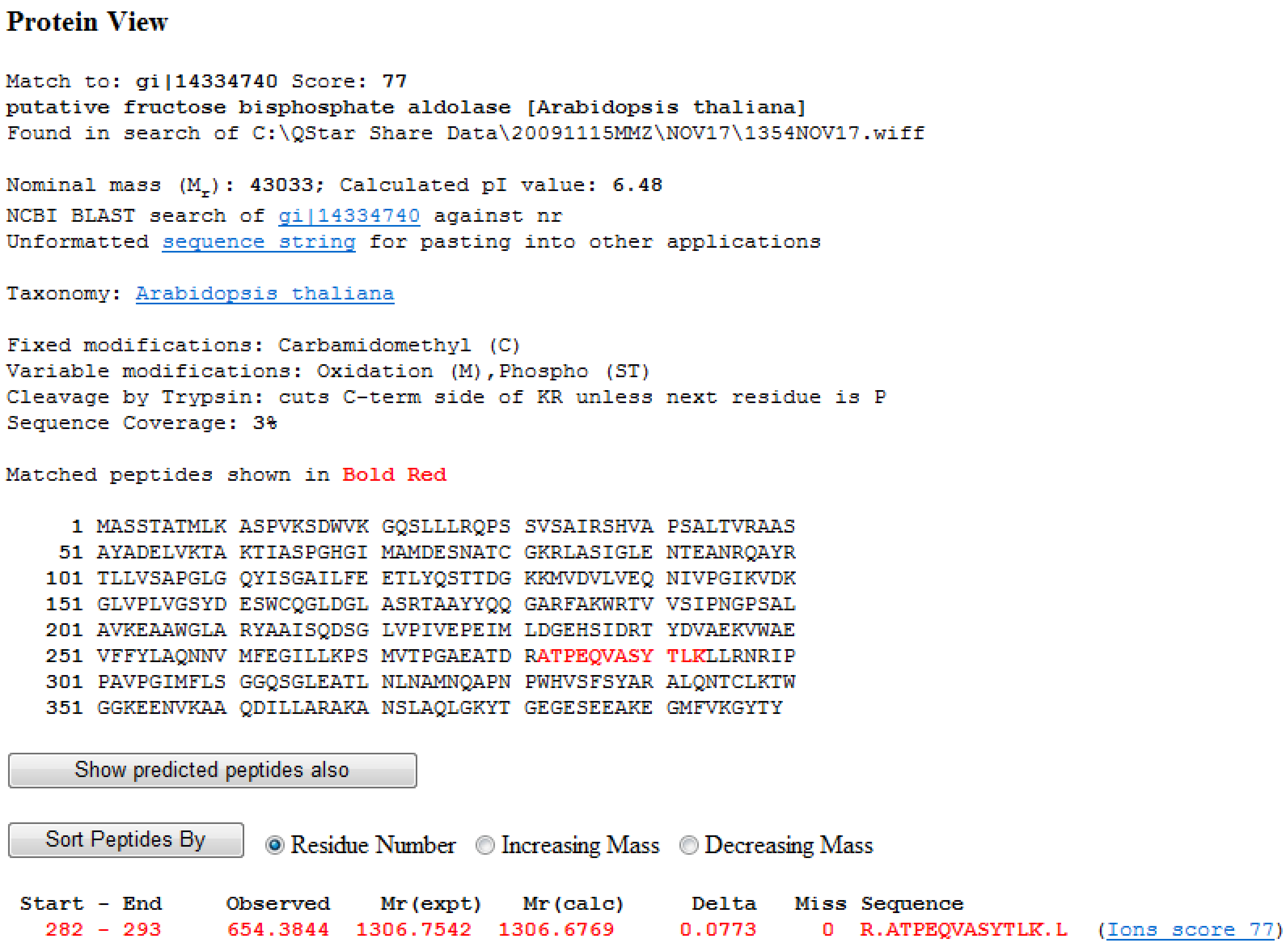
Matched peptides shown in Bold Red

     1 MSAFTSKFAD ELIANAAYIG TPGKGILAAD ESTGTIGKRL ASINVENVET
    51 NRRNLRELLF TAPGALPCLS GVILFEETLY QKSSDGKLFV DILKEGGVLP
   101 GIKVDKGTVE LAGTDGETTT QGLDGLGDRC KKYYEAGARF AKWRAVLKIG
   151 ENEPSEHSIH ENAYGLARYA VICQENGLVP IVEPEILVDG SHDIQKCAAV
   201 TERVLAACYK ALSDHHVLLE GTLLKPNMVT PGSDSPKVSP EVIAEHTVRA
   251 LQRTVPAAVP AIVFLSGGQS EEEATRNLNA MNQLKTKKPW SLSFSFGRAL
   301 QQSTLKTWAG KEENVKAAQE ALYVRCKANS EATLGTYKGD AKLGDGAAES
   351 LHVKDYKY
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   25 - 38     666.8790  1331.7435  1331.6933    0.0502     0  K.GILAADESTGTIGK.R   (Ions score 109)
   40 - 52     729.9181  1457.8217  1457.7474    0.0743     0  R.LASINVENVETNR.R   (Ions score 93)
   95 - 103    435.3007   868.5868   868.5018    0.0850     0  K.EGGVLPGIK.V   (Ions score 45)
  107 - 129    755.0596  2262.1570  2262.0612    0.0958     0  K.GTVELAGTDGETTTQGLDGLGDR.C   (Ions score 77)
  317 - 325    510.8160  1019.6174  1019.5400    0.0774     0  K.AAQEALYVR.C   (Ions score 87)
  328 - 338    577.8238  1153.6331  1153.5615    0.0716     0  K.ANSEATLGTYK.G   (Ions score 79)
  343 - 354    598.8503  1195.6861  1195.6197    0.0664     0  K.LGDGAAESLHVK.D   (Ions score 62)
```

gi|14334740 Putative fructose bisphosphate aldolase



Protein View

Match to: gi|14334740 Score: 77
putative fructose bisphosphate aldolase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff

Nominal mass (M_r): 43033; Calculated pI value: 6.48
NCBI BLAST search of gi|14334740 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in **Bold Red**

```
    1 MASSTATMLK ASPVKSDWVK GQSLLLRQPS SVSAIRSHVA PSALTVRAAS
   51 AYADELVKTA KTIASPGHGI MAMDESNATC GKRLASIGLE NTEANRQAYR
  101 TLLVSAPGLG QYISGAILFE ETLYQSTTDG KKMVDVLVEQ NIVPGIKVDK
  151 GLVPLVGSYD ESWCQGLDGL ASRTAAYYQQ GARFAKWRTV VSIPNGPSAL
  201 AVKEAAWGLA RYAAISQDSG LVPIVEPEIM LDGEHSIDRT YDVAEKVWAE
  251 VFFYLAQNNV MFEGILLKPS MVTPGAEATD RATPEQVASY TLKLLRNRIP
  301 PAVPGIMFLS GGQSGLEATL NLNAMNQAPN PWHVSFSYAR ALQNTCLKTW
  351 GGKEENVKAA QDILLARAKA NSLAQLGKYT GEGESEEAKE GMFVKGYTY
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

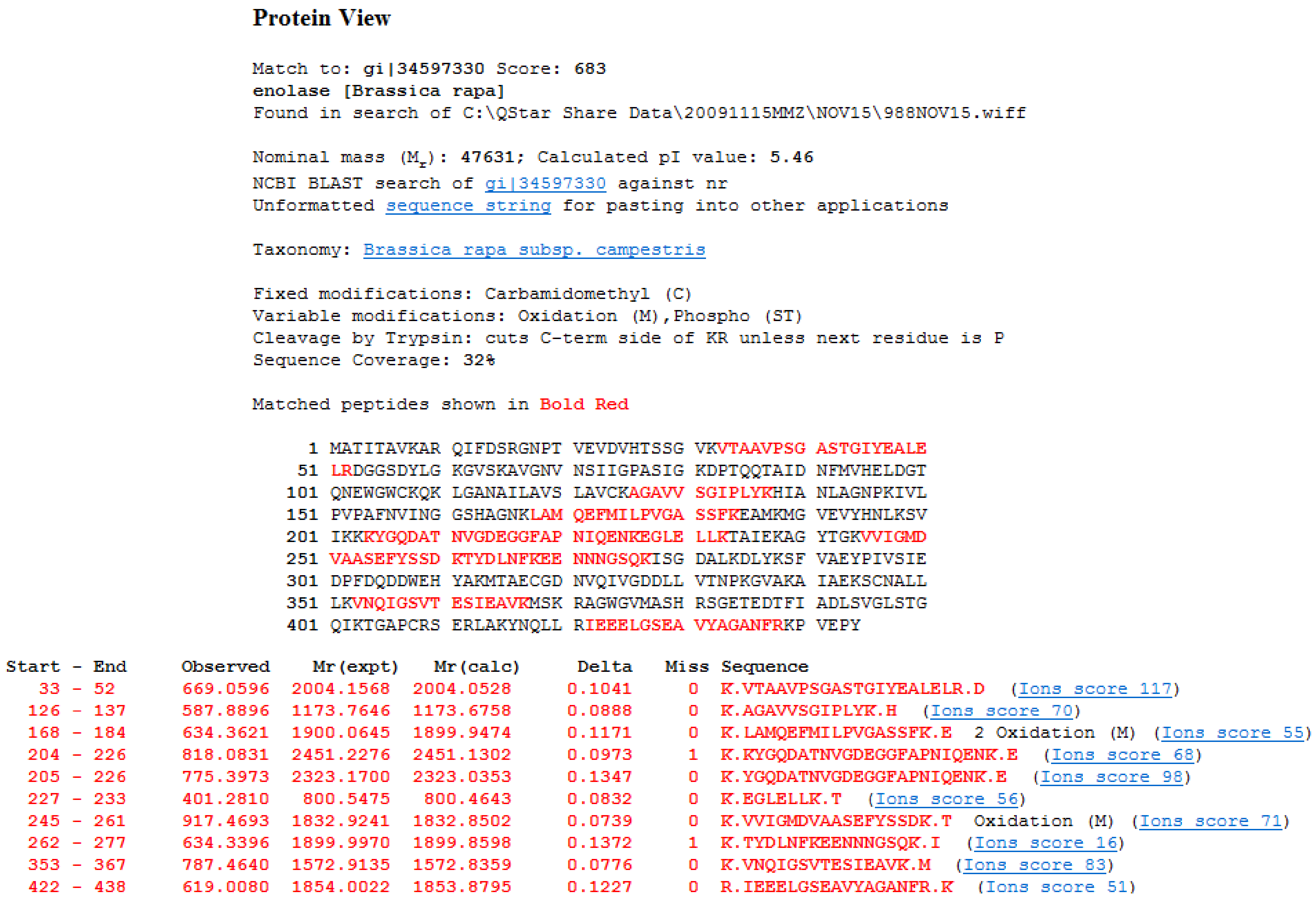
```
 Start - End     Observed     Mr(expt)    Mr(calc)      Delta   Miss  Sequence
   282 - 293     654.3844    1306.7542   1306.6769     0.0773      0  R.ATPEQVASYTLK.L    (Ions score 77)
```

Peptide View

MS/MS Fragmentation of **ATPEQVASYTLK**
Found in **gi|14334740**, putative fructose bisphosphate aldolase [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	173.0921	87.0497			155.0815	78.0444	T	1236.6470	618.8272	1219.6205	610.3139	1218.6365	609.8219	11
3	270.1448	135.5761			252.1343	126.5708	P	**1135.5994**	**568.3033**	1118.5728	**559.7900**	1117.5888	559.2980	10
4	399.1874	200.0974			381.1769	191.0921	E	**1038.5466**	519.7769	1021.5201	511.2637	**1020.5360**	510.7717	9
5	**527.2460**	264.1266	510.2195	255.6134	509.2354	255.1214	Q	**909.5040**	455.2556	**892.4775**	446.7424	891.4934	446.2504	8
6	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	V	**781.4454**	391.2264	**764.4189**	382.7131	763.4349	382.2211	7
7	697.3515	349.1794	680.3250	340.6661	679.3410	340.1741	A	**682.3770**	341.6921	665.3505	333.1789	664.3665	332.6869	6
8	784.3836	392.6954	767.3570	384.1821	766.3730	383.6901	S	**611.3399**	306.1736	594.3134	297.6603	593.3293	297.1683	5
9	947.4469	474.2271	930.4203	465.7138	929.4363	465.2218	Y	**524.3079**	262.6576	507.2813	**254.1443**	506.2973	253.6523	4
10	1048.4946	524.7509	1031.4680	516.2376	1030.4840	515.7456	T	**361.2445**	181.1259	344.2180	172.6126	343.2340	172.1206	3
11	1161.5786	581.2930	1144.5521	572.7797	1143.5681	572.2877	L	**260.1969**	130.6021	243.1703	122.0888			2
12							K	**147.1128**	74.0600	130.0863	65.5468			1

gi|34597330 Enolase



Protein View

```
Match to: gi|34597330 Score: 683
enolase [Brassica rapa]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\988NOV15.wiff

Nominal mass (Mr): 47631; Calculated pI value: 5.46
NCBI BLAST search of gi|34597330 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. campestris

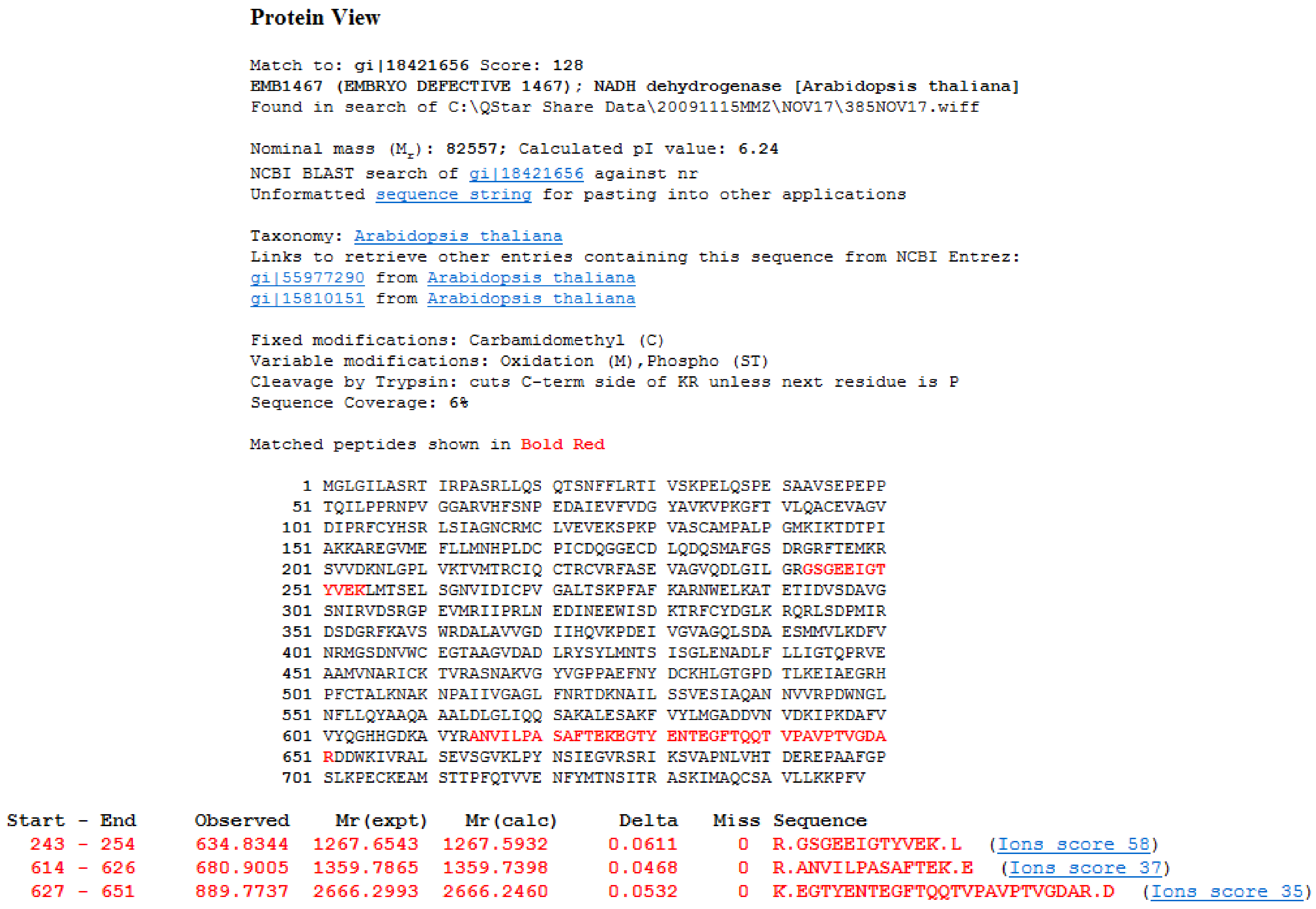
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 32%

Matched peptides shown in Bold Red

     1 MATITAVKAR QIFDSRGNPT VEVDVHTSSG VKVTAAVPSG ASTGIYEALE
    51 LRDGGSDYLG KGVSKAVGNV NSIIGPASIG KDPTQQTAID NFMVHELDGT
   101 QNEWGWCKQK LGANAILAVS LAVCKAGAVV SGIPLYKHIA NLAGNPKIVL
   151 PVPAFNVING GSHAGNKLAM QEFMILPVGA SSFKEAMKMG VEVYHNLKSV
   201 IKKKYGQDAT NVGDEGGFAP NIQENKEGLE LLKTAIEKAG YTGKVVIGMD
   251 VAASEFYSSD KTYDLNFKEE NNNGSQKISG DALKDLYKSF VAEYPIVSIE
   301 DPFDQDDWEH YAKMTAECGD NVQIVGDDLL VTNPKGVAKA IAEKSCNALL
   351 LKVNQIGSVT ESIEAVKMSK RAGWGVMASH RSGETEDTFI ADLSVGLSTG
   401 QIKTGAPCRS ERLAKYNQLL RIEEELGSEA VYAGANFRKP VEPY

Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  33 - 52       669.0596  2004.1568  2004.0528    0.1041     0  K.VTAAVPSGASTGIYEALELR.D   (Ions score 117)
 126 - 137      587.8896  1173.7646  1173.6758    0.0888     0  K.AGAVVSGIPLYK.H   (Ions score 70)
 168 - 184      634.3621  1900.0645  1899.9474    0.1171     0  K.LAMQEFMILPVGASSFK.E   2 Oxidation (M)  (Ions score 55)
 204 - 226      818.0831  2451.2276  2451.1302    0.0973     1  K.KYGQDATNVGDEGGFAPNIQENK.E   (Ions score 68)
 205 - 226      775.3973  2323.1700  2323.0353    0.1347     0  K.YGQDATNVGDEGGFAPNIQENK.E   (Ions score 98)
 227 - 233      401.2810   800.5475   800.4643    0.0832     0  K.EGLELLK.T   (Ions score 56)
 245 - 261      917.4693  1832.9241  1832.8502    0.0739     0  K.VVIGMDVAASEFYSSDK.T   Oxidation (M)  (Ions score 71)
 262 - 277      634.3396  1899.9970  1899.8598    0.1372     1  K.TYDLNFKEENNNGSQK.I   (Ions score 16)
 353 - 367      787.4640  1572.9135  1572.8359    0.0776     0  K.VNQIGSVTESIEAVK.M   (Ions score 83)
 422 - 438      619.0080  1854.0022  1853.8795    0.1227     0  R.IEEELGSEAVYAGANFR.K   (Ions score 51)
```

gi|18421656 EMB1467 (embryo defective 1467); NADH dehydrogenase



Protein View

Match to: gi|18421656 Score: 128
EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\385NOV17.wiff

Nominal mass (M_r): 82557; Calculated pI value: 6.24
NCBI BLAST search of gi|18421656 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|55977290 from Arabidopsis thaliana
gi|15810151 from Arabidopsis thaliana

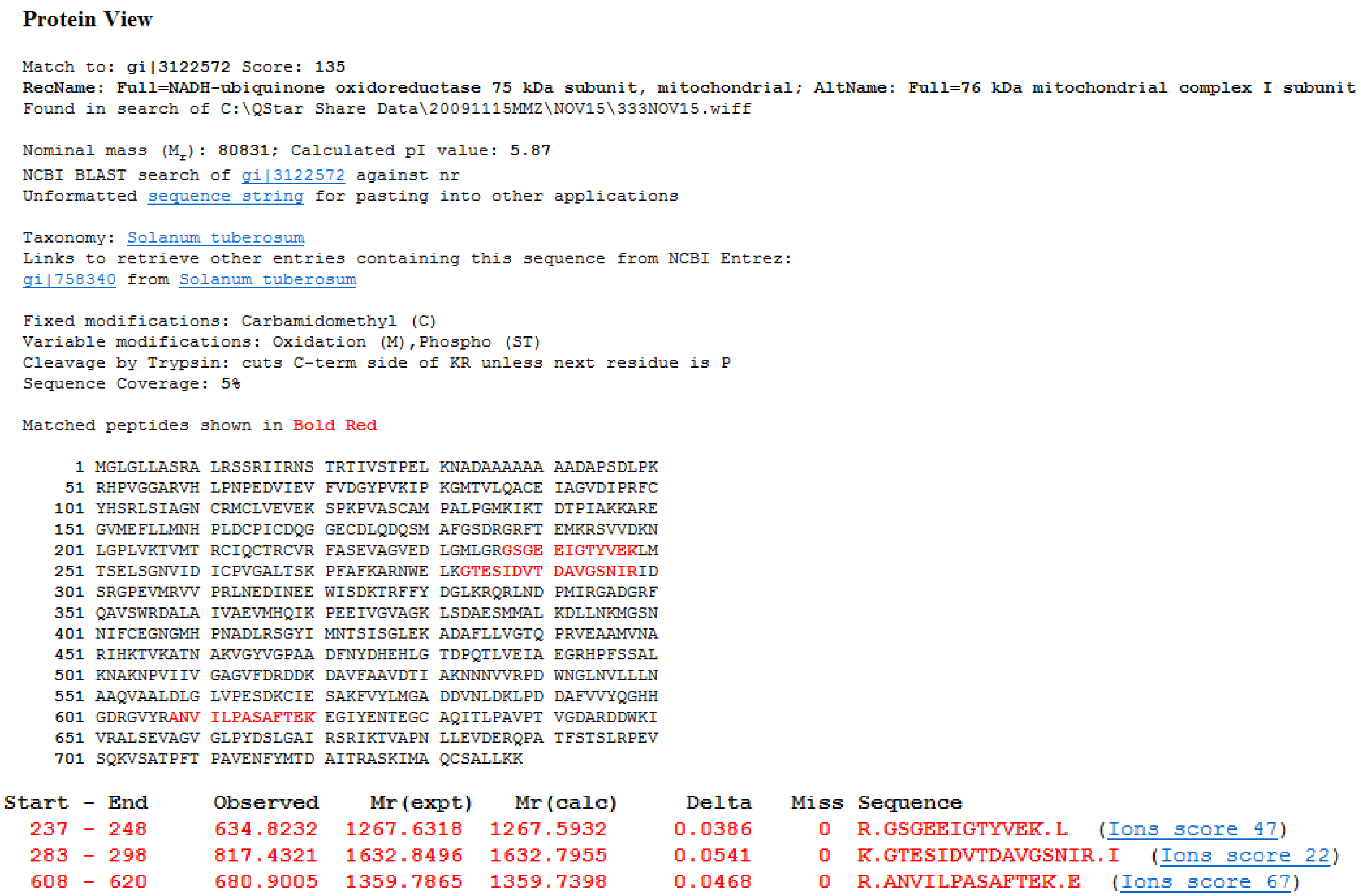
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

```
   1 MGLGILASRT IRPASRLLQS QTSNFFLRTI VSKPELQSPE SAAVSEPEPP
  51 TQILPPRNPV GGARVHFSNP EDAIEVFVDG YAVKVPKGFT VLQACEVAGV
 101 DIPRFCYHSR LSIAGNCRMC LVEVEKSPKP VASCAMPALP GMKIKTDTPI
 151 AKKAREGVME FLLMNHPLDC PICDQGGECD LQDQSMAFGS DRGRFTEMKR
 201 SVVDKNLGPL VKTVMTRCIQ CTRCVRFASE VAGVQDLGIL GRGSGEEIGT
 251 YVEKLMTSEL SGNVIDICPV GALTSKPFAF KARNWELKAT ETIDVSDAVG
 301 SNIRVDSRGP EVMRIIPRLN EDINEEWISD KTRFCYDGLK RQRLSDPMIR
 351 DSDGRFKAVS WRDALAVVGD IIHQVKPDEI VGVAGQLSDA ESMMVLKDFV
 401 NRMGSDNVWC EGTAAGVDAD LRYSYLMNTS ISGLENADLF LLIGTQPRVE
 451 AAMVNARICK TVRASNAKVG YVGPPAEFNY DCKHLGTGPD TLKEIAEGRH
 501 PFCTALKNAK NPAIIVGAGL FNRTDKNAIL SSVESIAQAN NVVRPDWNGL
 551 NFLLQYAAQA AALDLGLIQQ SAKALESAKF VYLMGADDVN VDKIPKDAFV
 601 VYQGHHGDKA VYRANVILPA SAFTEKEGTY ENTEGFTQQT VPAVPTVGDA
 651 RDDWKIVRAL SEVSGVKLPY NSIEGVRSRI KSVAPNLVHT DEREPAAFGP
 701 SLKPECKEAM STTPFQTVVE NFYMTNSITR ASKIMAQCSA VLLKKPFV
```

```
Start - End     Observed    Mr(expt)    Mr(calc)      Delta   Miss  Sequence
  243 - 254     634.8344   1267.6543   1267.5932     0.0611      0  R.GSGEEIGTYVEK.L   (Ions score 58)
  614 - 626     680.9005   1359.7865   1359.7398     0.0468      0  R.ANVILPASAFTEK.E   (Ions score 37)
  627 - 651     889.7737   2666.2993   2666.2460     0.0532      0  K.EGTYENTEGFTQQTVPAVPTVGDAR.D   (Ions score 35)
```

gi|3122572 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial



Protein View

Match to: gi|3122572 Score: 135
RecName: Full=NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial; AltName: Full=76 kDa mitochondrial complex I subunit
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\333NOV15.wiff

Nominal mass (M_r): 80831; Calculated pI value: 5.87
NCBI BLAST search of gi|3122572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Solanum tuberosum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|758340 from Solanum tuberosum

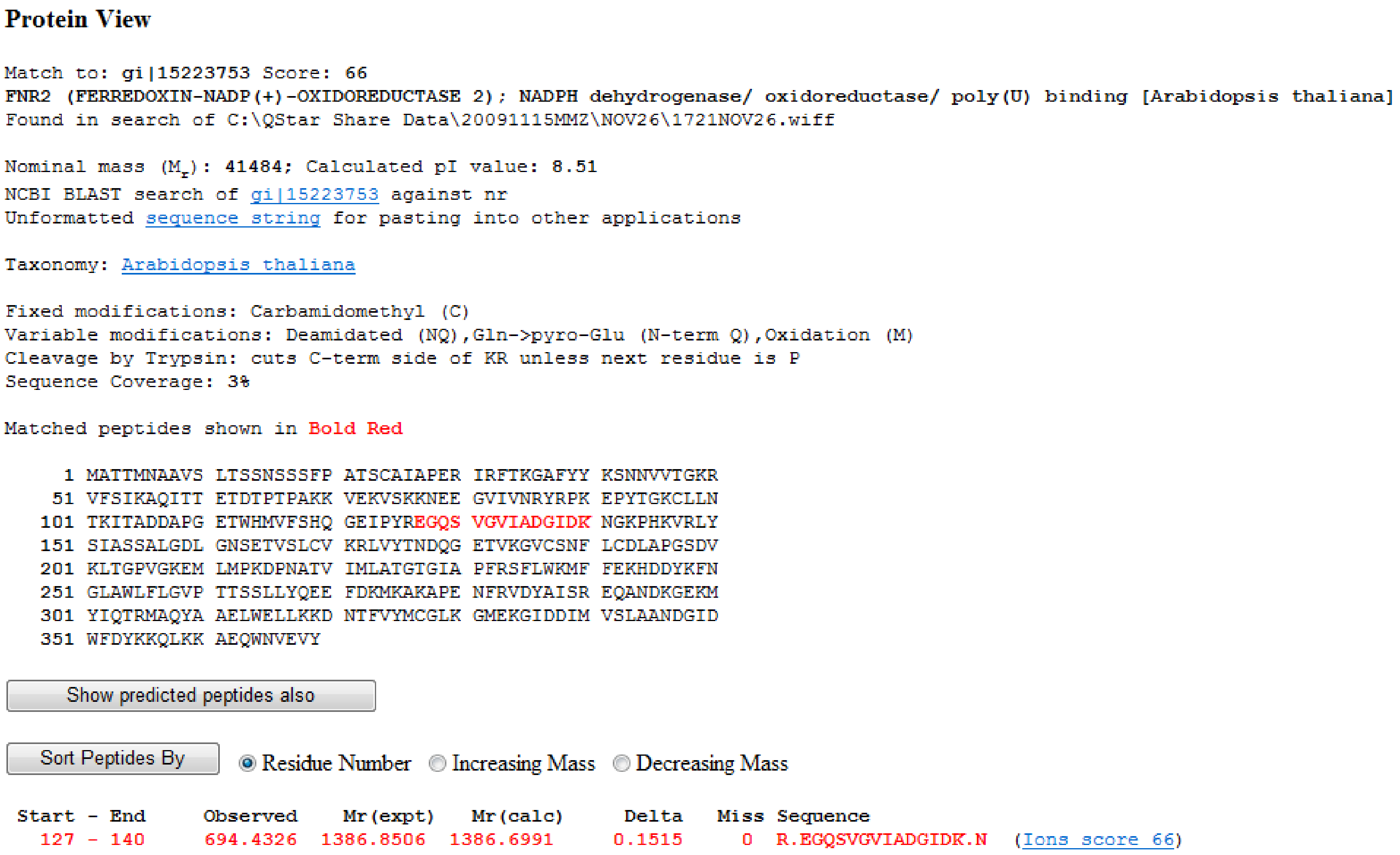
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in **Bold Red**

```
  1 MGLGLLASRA LRSSRIIRNS TRTIVSTPEL KNADAAAAAA AADAPSDLPK
 51 RHPVGGARVH LPNPEDVIEV FVDGYPVKIP KGMTVLQACE IAGVDIPRFC
101 YHSRLSIAGN CRMCLVEVEK SPKPVASCAM PALPGMKIKT DTPIAKKARE
151 GVMEFLLMNH PLDCPICDQG GECDLQDQSM AFGSDRGRFT EMKRSVVDKN
201 LGPLVKTVMT RCIQCTRCVR FASEVAGVED LGMLGRGSGE EIGTYVEKLM
251 TSELSGNVID ICPVGALTSK PFAFKARNWE LKGTESIDVT DAVGSNIRID
301 SRGPEVMRVV PRLNEDINEE WISDKTRFFY DGLKRQRLND PMIRGADGRF
351 QAVSWRDALA IVAEVMHQIK PEEIVGVAGK LSDAESMMAL KDLLNKMGSN
401 NIFCEGNGMH PNADLRSGYI MNTSISGLEK ADAFLLVGTQ PRVEAAMVNA
451 RIHKTVKATN AKVGYVGPAA DFNYDHEHLG TDPQTLVEIA EGRHPFSSAL
501 KNAKNPVIIV GAGVFDRDDK DAVFAAVDTI AKNNNVVRPD WNGLNVLLLN
551 AAQVAALDLG LVPESDKCIE SAKFVYLMGA DDVNLDKLPD DAFVVYQGHH
601 GDRGVYRANV ILPASAFTEK EGIYENTEGC AQITLPAVPT VGDARDDWKI
651 VRALSEVAGV GLPYDSLGAI RSRIKTVAPN LLEVDERQPA TFSTSLRPEV
701 SQKVSATPFT PAVENFYMTD AITRASKIMA QCSALLKK
```

```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
  237 - 248     634.8232   1267.6318   1267.5932    0.0386     0   R.GSGEEIGTYVEK.L   (Ions score 47)
  283 - 298     817.4321   1632.8496   1632.7955    0.0541     0   K.GTESIDVTDAVGSNIR.I   (Ions score 22)
  608 - 620     680.9005   1359.7865   1359.7398    0.0468     0   R.ANVILPASAFTEK.E   (Ions score 67)
```

gi|15223753 Ferredoxin-NADP(+)-oxidoreductase 2 (FNR2)



Protein View

Match to: **gi|15223753** Score: **66**
FNR2 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 2); NADPH dehydrogenase/ oxidoreductase/ poly(U) binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1721NOV26.wiff

Nominal mass (M_r): **41484**; Calculated pI value: **8.51**
NCBI BLAST search of gi|15223753 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

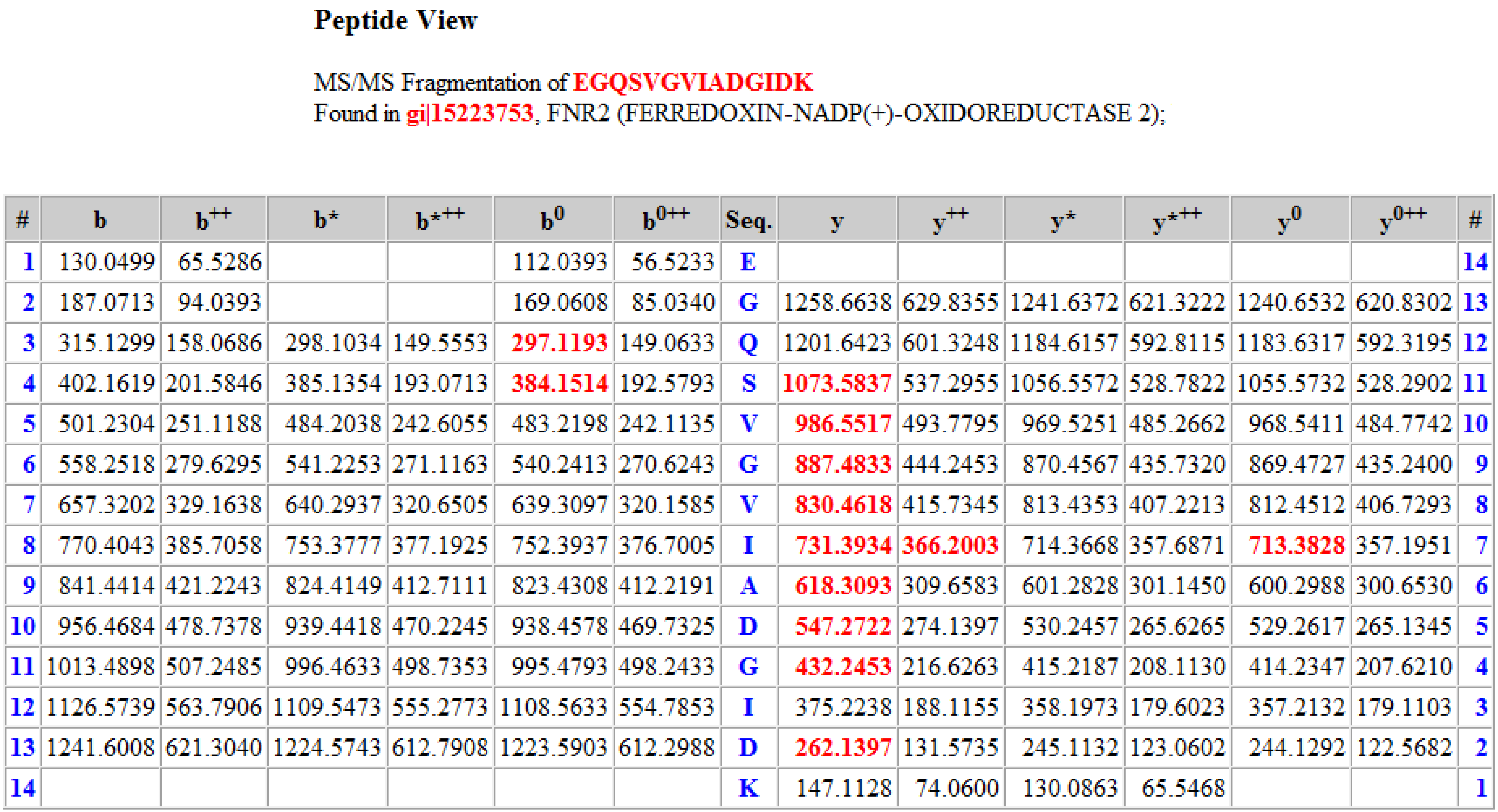
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **3%**

Matched peptides shown in **Bold Red**

```
  1 MATTMNAAVS LTSSNSSSFP ATSCAIAPER IRFTKGAFYY KSNNVVTGKR
 51 VFSIKAQITT ETDTPTPAKK VEKVSKKNEE GVIVNRYRPK EPYTGKCLLN
101 TKITADDAPG ETWHMVFSHQ GEIPYREGQS VGVIADGIDK NGKPHKVRLY
151 SIASSALGDL GNSETVSLCV KRLVYTNDQG ETVKGVCSNF LCDLAPGSDV
201 KLTGPVGKEM LMPKDPNATV IMLATGTGIA PFRSFLWKMF FEKHDDYKFN
251 GLAWLFLGVP TTSSLLYQEE FDKMKAKAPE NFRVDYAISR EQANDKGEKM
301 YIQTRMAQYA AELWELLKKD NTFVYMCGLK GMEKGIDDIM VSLAANDGID
351 WFDYKKQLKK AEQWNVEVY
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
   127 - 140    694.4326   1386.8506   1386.6991    0.1515      0  R.EGQSVGVIADGIDK.N   (Ions score 66)
```

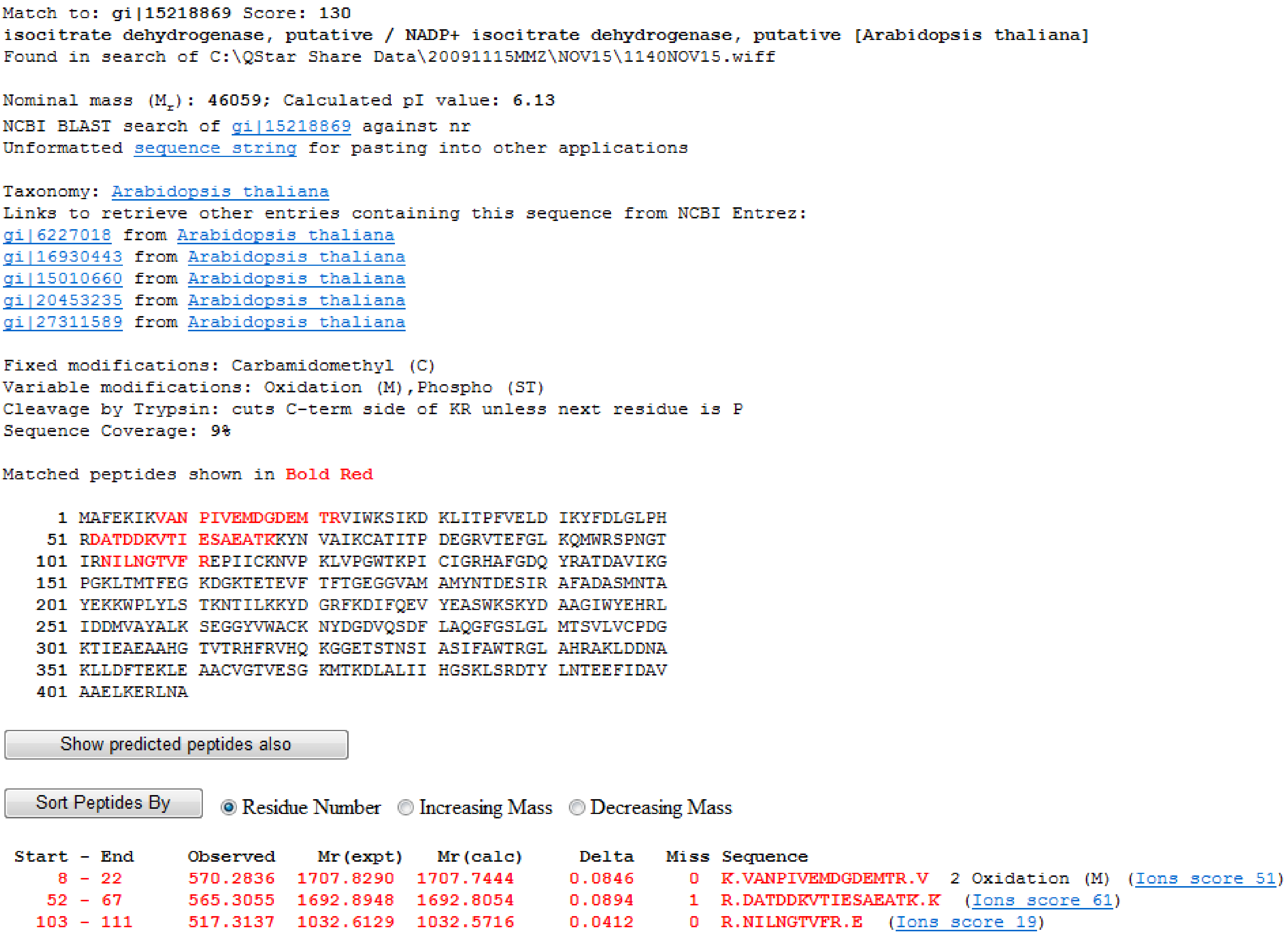


Peptide View

MS/MS Fragmentation of **EGQSVGVIADGIDK**
Found in **gi|15223753**, FNR2 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 2);

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	187.0713	94.0393			169.0608	85.0340	G	1258.6638	629.8355	1241.6372	621.3222	1240.6532	620.8302	13
3	315.1299	158.0686	298.1034	149.5553	**297.1193**	149.0633	Q	1201.6423	601.3248	1184.6157	592.8115	1183.6317	592.3195	12
4	402.1619	201.5846	385.1354	193.0713	**384.1514**	192.5793	S	**1073.5837**	537.2955	1056.5572	528.7822	1055.5732	528.2902	11
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	V	**986.5517**	493.7795	969.5251	485.2662	968.5411	484.7742	10
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	G	**887.4833**	444.2453	870.4567	435.7320	869.4727	435.2400	9
7	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	V	**830.4618**	415.7345	813.4353	407.2213	812.4512	406.7293	8
8	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	I	**731.3934**	**366.2003**	714.3668	357.6871	**713.3828**	357.1951	7
9	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	A	**618.3093**	309.6583	601.2828	301.1450	600.2988	300.6530	6
10	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	D	**547.2722**	274.1397	530.2457	265.6265	529.2617	265.1345	5
11	1013.4898	507.2485	996.4633	498.7353	995.4793	498.2433	G	**432.2453**	216.6263	415.2187	208.1130	414.2347	207.6210	4
12	1126.5739	563.7906	1109.5473	555.2773	1108.5633	554.7853	I	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1241.6008	621.3040	1224.5743	612.7908	1223.5903	612.2988	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
14							K	147.1128	74.0600	130.0863	65.5468			1

gi|15218869 NADP+ isocitrate dehydrogenase, putative



```
Match to: gi|15218869 Score: 130
isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (Mr): 46059; Calculated pI value: 6.13
NCBI BLAST search of gi|15218869 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|6227018 from Arabidopsis thaliana
gi|16930443 from Arabidopsis thaliana
gi|15010660 from Arabidopsis thaliana
gi|20453235 from Arabidopsis thaliana
gi|27311589 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

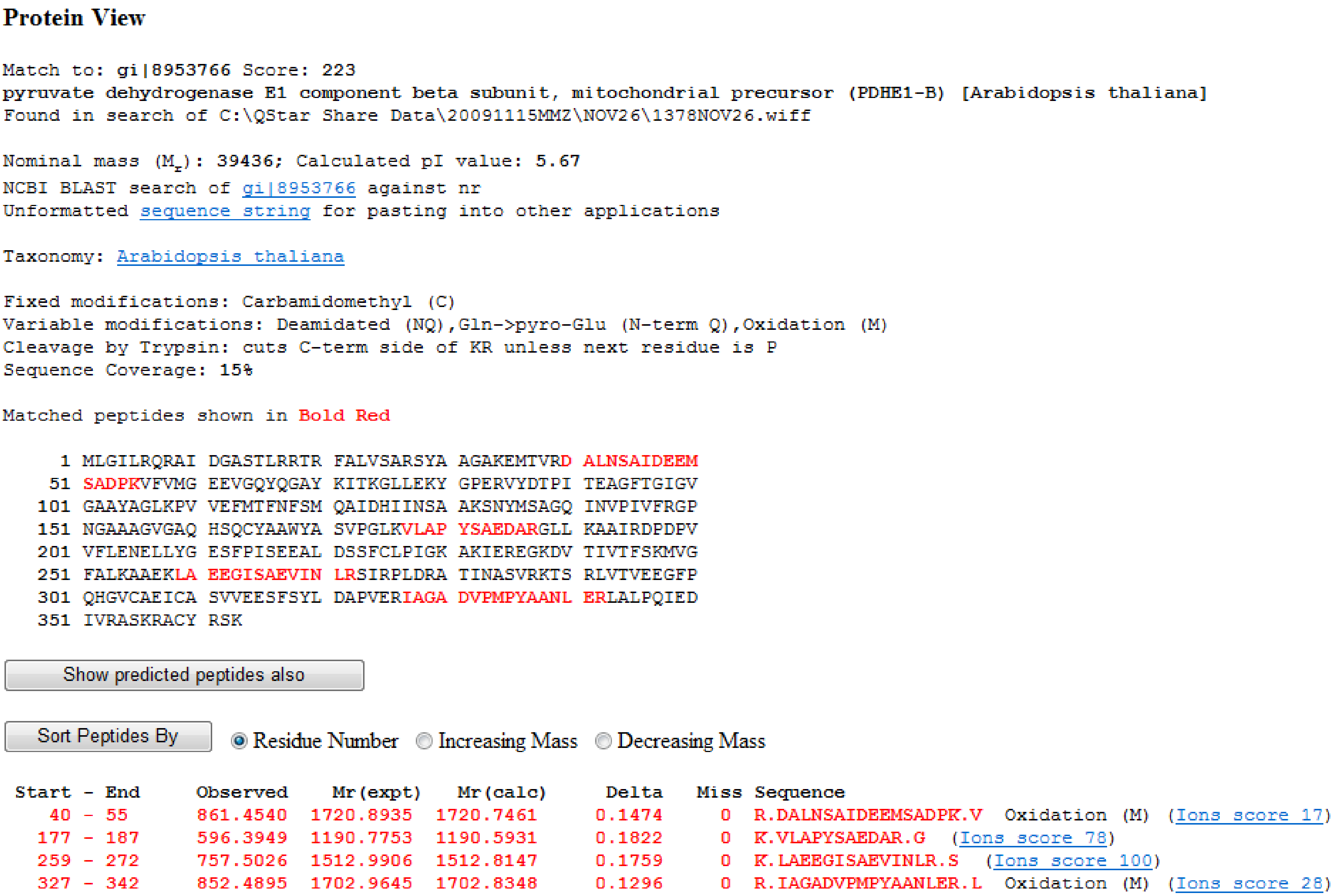
Matched peptides shown in Bold Red

     1 MAFEKIKVAN PIVEMDGDEM TRVIWKSIKD KLITPFVELD IKYFDLGLPH
    51 RDATDDKVTI ESAEATKKYN VAIKCATITP DEGRVTEFGL KQMWRSPNGT
   101 IRNILNGTVF REPIICKNVP KLVPGWTKPI CIGRHAFGDQ YRATDAVIKG
   151 PGKLTMTFEG KDGKTETEVF TFTGEGGVAM AMYNTDESIR AFADASMNTA
   201 YEKKWPLYLS TKNTILKKYD GRFKDIFQEV YEASWKSKYD AAGIWYEHRL
   251 IDDMVAYALK SEGGYVWACK NYDGDVQSDF LAQGFGSLGL MTSVLVCPDG
   301 KTIEAEAAHG TVTRHFRVHQ KGGETSTNSI ASIFAWTRGL AHRAKLDDNA
   351 KLLDFTEKLE AACVGTVESG KMTKDLALII HGSKLSRDTY LNTEEFIDAV
   401 AAELKERLNA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta    Miss  Sequence
    8 - 22       570.2836   1707.8290  1707.7444    0.0846     0   K.VANPIVEMDGDEMTR.V  2 Oxidation (M)  (Ions score 51)
   52 - 67       565.3055   1692.8948  1692.8054    0.0894     1   R.DATDDKVTIESAEATK.K  (Ions score 61)
  103 - 111      517.3137   1032.6129  1032.5716    0.0412     0   R.NILNGTVFR.E  (Ions score 19)
```

gi|520478 Pyruvate dehydrogenase E1 beta subunit



Protein View

```
Match to: gi|8953766 Score: 223
pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (PDHE1-B) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (Mr): 39436; Calculated pI value: 5.67
NCBI BLAST search of gi|8953766 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

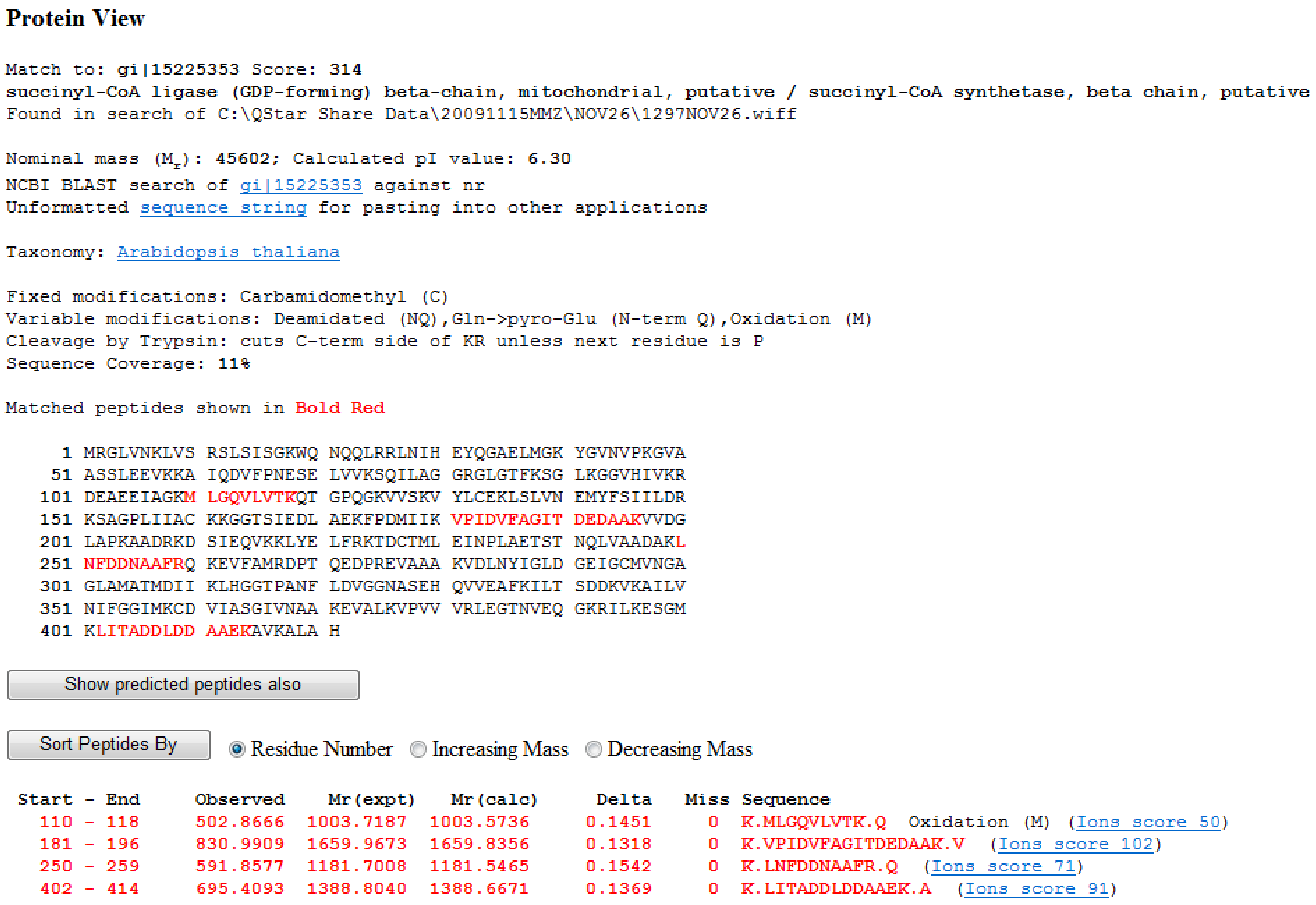
Matched peptides shown in Bold Red

     1 MLGILRQRAI DGASTLRRTR FALVSARSYA AGAKEMTVRD ALNSAIDEEM
    51 SADPKVFVMG EEVGQYQGAY KITKGLLEKY GPERVYDTPI TEAGFTGIGV
   101 GAAYAGLKPV VEFMTFNFSM QAIDHIINSA AKSNYMSAGQ INVPIVFRGP
   151 NGAAAGVGAQ HSQCYAAWYA SVPGLKVLAP YSAEDARGLL KAAIRDPDPV
   201 VFLENELLYG ESFPISEEAL DSSFCLPIGK AKIEREGKDV TIVTFSKMVG
   251 FALKAAEKLA EEGISAEVIN LRSIRPLDRA TINASVRKTS RLVTVEEGFP
   301 QHGVCAEICA SVVEESFSYL DAPVERIAGA DVPMPYAANL ERLALPQIED
   351 IVRASKRACY RSK
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   40 - 55      861.4540  1720.8935  1720.7461    0.1474     0  R.DALNSAIDEEMSADPK.V  Oxidation (M)  (Ions score 17)
  177 - 187     596.3949  1190.7753  1190.5931    0.1822     0  K.VLAPYSAEDAR.G  (Ions score 78)
  259 - 272     757.5026  1512.9906  1512.8147    0.1759     0  K.LAEEGISAEVINLR.S  (Ions score 100)
  327 - 342     852.4895  1702.9645  1702.8348    0.1296     0  R.IAGADVPMPYAANLER.L  Oxidation (M)  (Ions score 28)
```

gi|15225353 Succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial



Protein View

Match to: gi|15225353 Score: 314
succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1297NOV26.wiff

Nominal mass (M_r): **45602**; Calculated pI value: **6.30**
NCBI BLAST search of gi|15225353 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

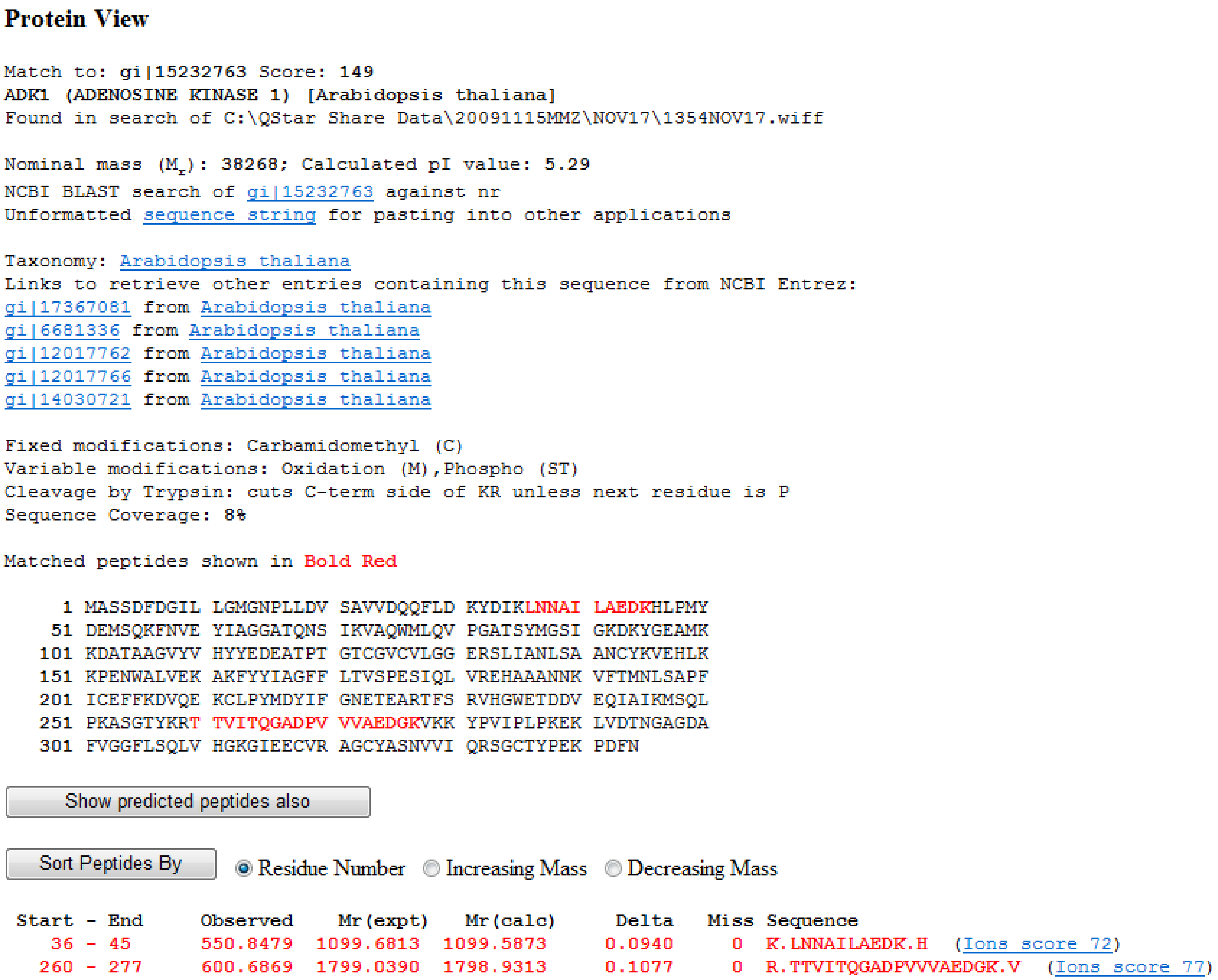
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
  1 MRGLVNKLVS RSLSISGKWQ NQQLRRLNIH EYQGAELMGK YGVNVPKGVA
 51 ASSLEEVKKA IQDVFPNESE LVVKSQILAG GRGLGTFKSG LKGGVHIVKR
101 DEAEEIAGKM LGQVLVTKQT GPQGKVVSKV YLCEKLSLVN EMYFSIILDR
151 KSAGPLIIAC KKGGTSIEDL AEKFPDMIIK VPIDVFAGIT DEDAAKVVDG
201 LAPKAADRKD SIEQVKKLYE LFRKTDCTML EINPLAETST NQLVAADAKL
251 NFDDNAAFRQ KEVFAMRDPT QEDPREVAAA KVDLNYIGLD GEIGCMVNGA
301 GLAMATMDII KLHGGTPANF LDVGGNASEH QVVEAFKILT SDDKVKAILV
351 NIFGGIMKCD VIASGIVNAA KEVALKVPVV VRLEGTNVEQ GKRILKESGM
401 KLITADDLDD AAEKAVKALA H
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   110 - 118     502.8666  1003.7187  1003.5736    0.1451     0 K.MLGQVLVTK.Q  Oxidation (M)  (Ions score 50)
   181 - 196     830.9909  1659.9673  1659.8356    0.1318     0 K.VPIDVFAGITDEDAAK.V  (Ions score 102)
   250 - 259     591.8577  1181.7008  1181.5465    0.1542     0 K.LNFDDNAAFR.Q  (Ions score 71)
   402 - 414     695.4093  1388.8040  1388.6671    0.1369     0 K.LITADDLDDAAEK.A  (Ions score 91)
```

gi|15232763 Adenosine kinase 1 (ADK1)



Protein View

Match to: gi|15232763 Score: 149
ADK1 (ADENOSINE KINASE 1) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1354NOV17.wiff

Nominal mass (M_r): 38268; Calculated pI value: 5.29
NCBI BLAST search of gi|15232763 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|17367081 from Arabidopsis thaliana
gi|6681336 from Arabidopsis thaliana
gi|12017762 from Arabidopsis thaliana
gi|12017766 from Arabidopsis thaliana
gi|14030721 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

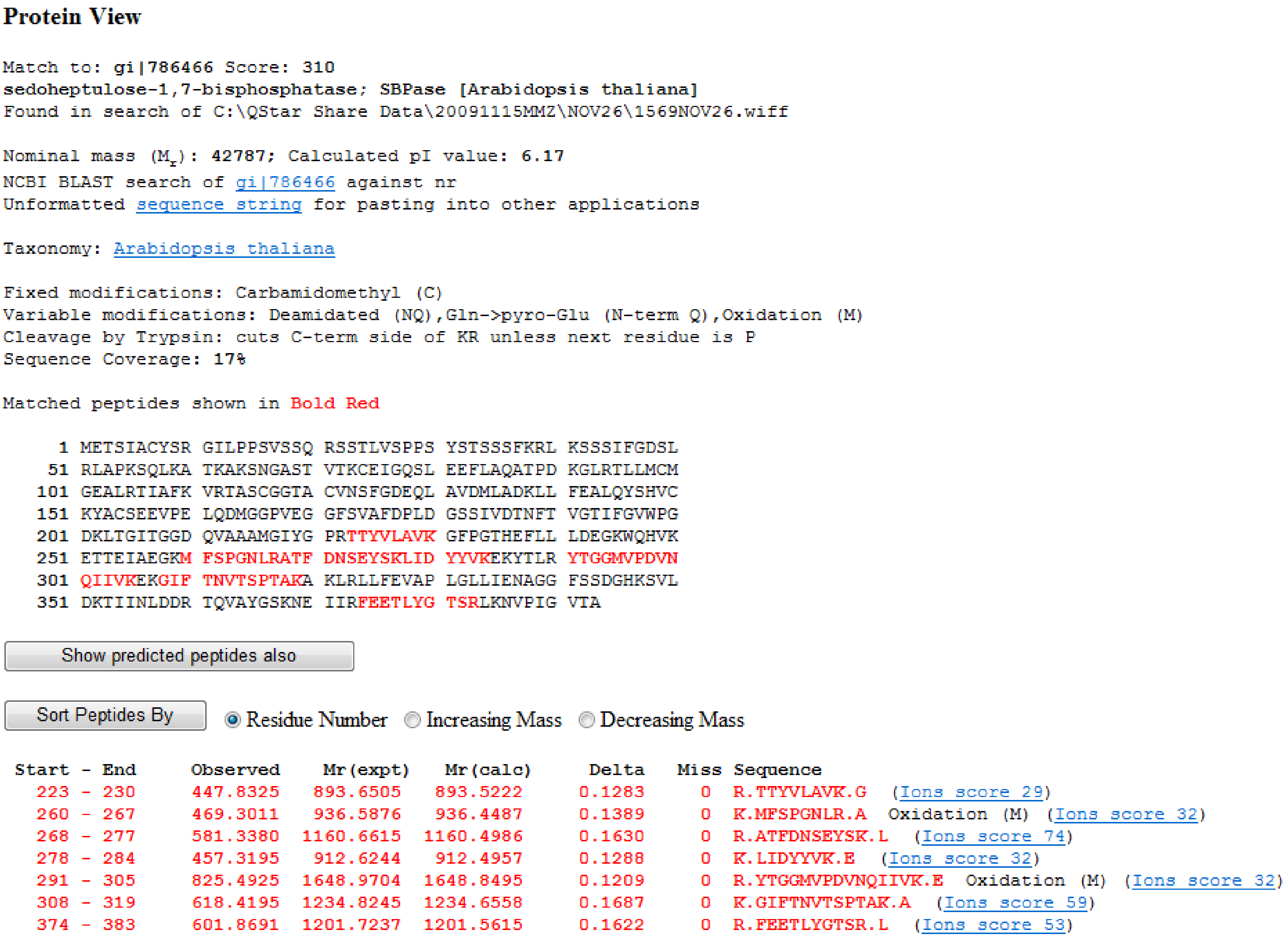
Matched peptides shown in **Bold Red**

```
  1 MASSDFDGIL LGMGNPLLDV SAVVDQQFLD KYDIKLNNAI LAEDKHLPMY
 51 DEMSQKFNVE YIAGGATQNS IKVAQWMLQV PGATSYMGSI GKDKYGEAMK
101 KDATAAGVYV HYYEDEATPT GTCGVCVLGG ERSLIANLSA ANCYKVEHLK
151 KPENWALVEK AKFYYIAGFF LTVSPESIQL VREHAAANNK VFTMNLSAPF
201 ICEFFKDVQE KCLPYMDYIF GNETEARTFS RVHGWETDDV EQIAIKMSQL
251 PKASGTYKRT TVITQGADPV VVAEDGKVKK YPVIPLPKEK LVDTNGAGDA
301 FVGGFLSQLV HGKGIEECVR AGCYASNVVI QRSGCTYPEK PDFN
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   36 - 45       550.8479  1099.6813  1099.5873    0.0940     0  K.LNNAILAEDK.H  (Ions score 72)
  260 - 277      600.6869  1799.0390  1798.9313    0.1077     0  R.TTVITQGADPVVVAEDGK.V  (Ions score 77)
```

gi|1173347 Sedoheptulose-1,7-bisphosphatase



Protein View

```
Match to: gi|786466 Score: 310
sedoheptulose-1,7-bisphosphatase; SBPase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1569NOV26.wiff

Nominal mass (Mr): 42787; Calculated pI value: 6.17
NCBI BLAST search of gi|786466 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

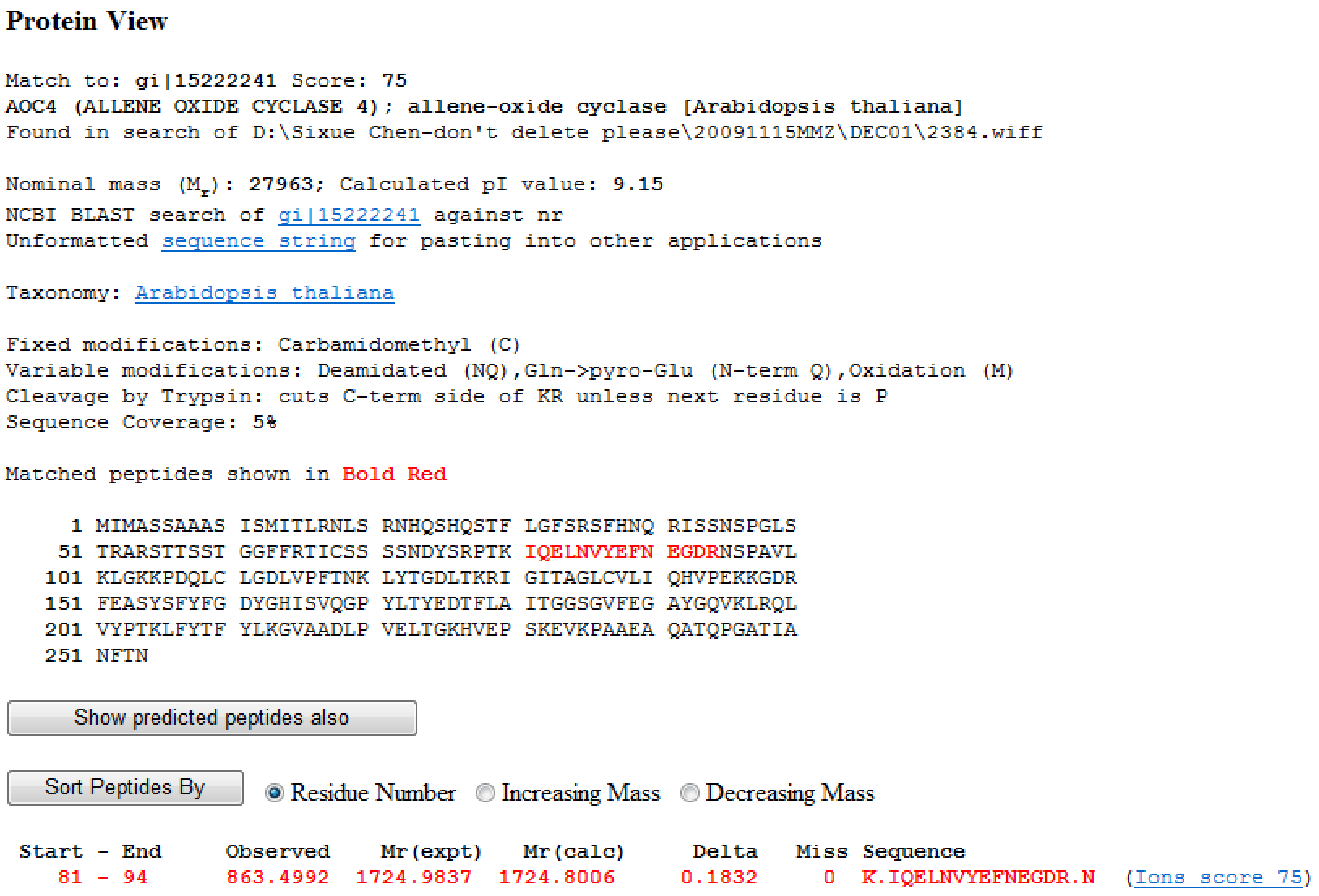
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 17%

Matched peptides shown in Bold Red

    1 METSIACYSR GILPPSVSSQ RSSTLVSPPS YSTSSSFKRL KSSSIFGDSL
   51 RLAPKSQLKA TKAKSNGAST VTKCEIGQSL EEFLAQATPD KGLRTLLMCM
  101 GEALRTIAFK VRTASCGGTA CVNSFGDEQL AVDMLADKLL FEALQYSHVC
  151 KYACSEEVPE LQDMGGPVEG GFSVAFDPLD GSSIVDTNFT VGTIFGVWPG
  201 DKLTGITGGD QVAAAMGIYG PRTTYVLAVK GFPGTHEFLL LDEGKWQHVK
  251 ETTEIAEGKM FSPGNLRATF DNSEYSKLID YYVKEKYTLR YTGGMVPDVN
  301 QIIVKEKGIF TNVTSPTAKA KLRLLFEVAP LGLLIENAGG FSSDGHKSVL
  351 DKTIINLDDR TQVAYGSKNE IIRFEETLYG TSRLKNVPIG VTA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   223 - 230     447.8325   893.6505   893.5222    0.1283     0  R.TTYVLAVK.G   (Ions score 29)
   260 - 267     469.3011   936.5876   936.4487    0.1389     0  K.MFSPGNLR.A  Oxidation (M)  (Ions score 32)
   268 - 277     581.3380  1160.6615  1160.4986    0.1630     0  R.ATFDNSEYSK.L   (Ions score 74)
   278 - 284     457.3195   912.6244   912.4957    0.1288     0  K.LIDYYVK.E   (Ions score 32)
   291 - 305     825.4925  1648.9704  1648.8495    0.1209     0  R.YTGGMVPDVNQIIVK.E   Oxidation (M)  (Ions score 32)
   308 - 319     618.4195  1234.8245  1234.6558    0.1687     0  K.GIFTNVTSPTAK.A   (Ions score 59)
   374 - 383     601.8691  1201.7237  1201.5615    0.1622     0  R.FEETLYGTSR.L   (Ions score 53)
```

gi|15222241 Allene oxide cyclase 4 (AOC4)



Protein View

Match to: gi|15222241 Score: 75
AOC4 (ALLENE OXIDE CYCLASE 4); allene-oxide cyclase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2384.wiff

Nominal mass (M_r): 27963; Calculated pI value: 9.15
NCBI BLAST search of gi|15222241 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

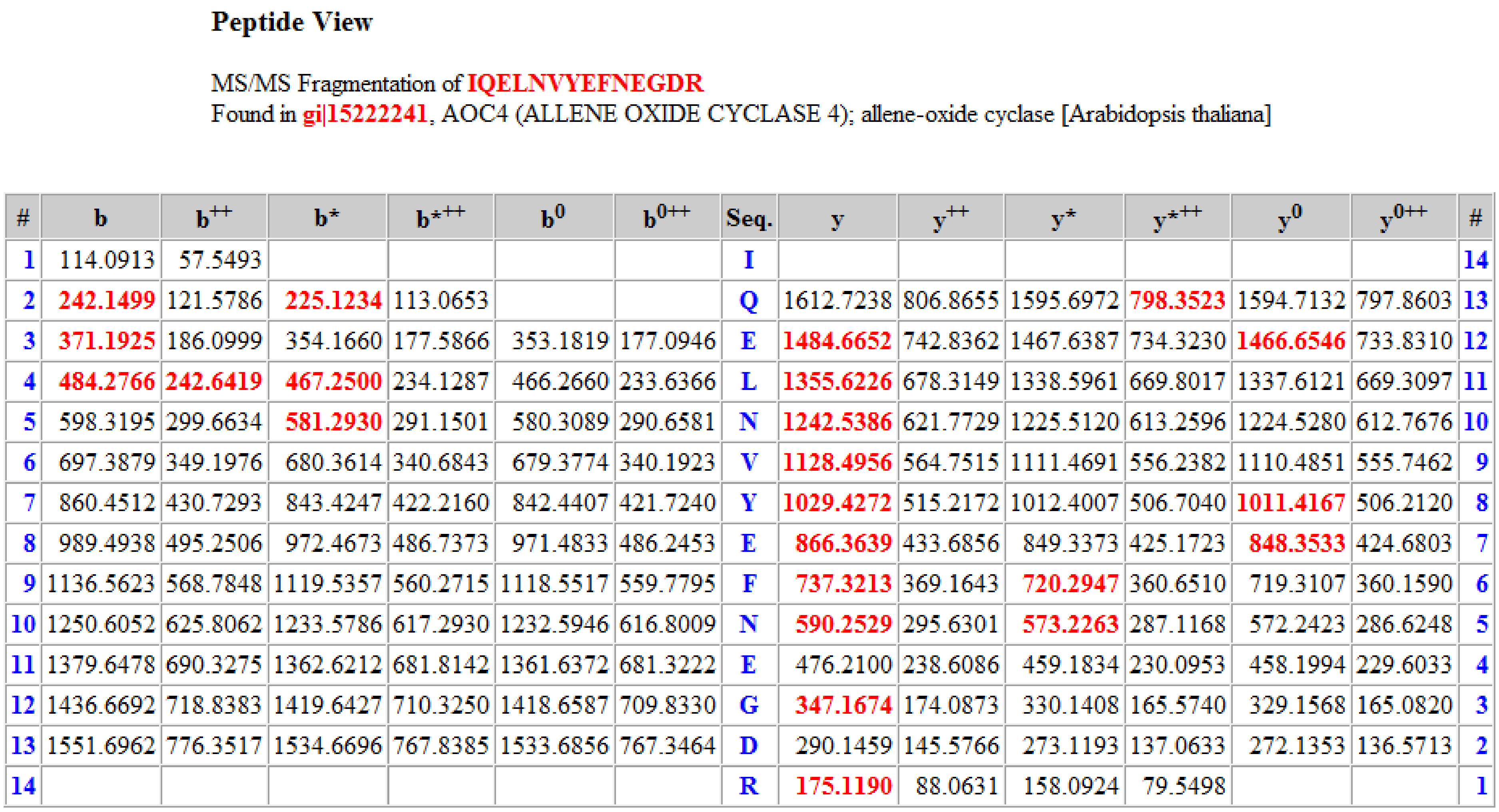
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in **Bold Red**

```
  1 MIMASSAAAS ISMITLRNLS RNHQSHQSTF LGFSRSFHNQ RISSNSPGLS
 51 TRARSTTSST GGFFRTICSS SSNDYSRPTK IQELNVYEFN EGDRNSPAVL
101 KLGKKPDQLC LGDLVPFTNK LYTGDLTKRI GITAGLCVLI QHVPEKKGDR
151 FEASYSFYFG DYGHISVQGP YLTYEDTFLA ITGGSGVFEG AYGQVKLRQL
201 VYPTKLFYTF YLKGVAADLP VELTGKHVEP SKEVKPAAEA QATQPGATIA
251 NFTN
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
    81 - 94     863.4992  1724.9837  1724.8006    0.1832     0  K.IQELNVYEFNEGDR.N   (Ions score 75)
```

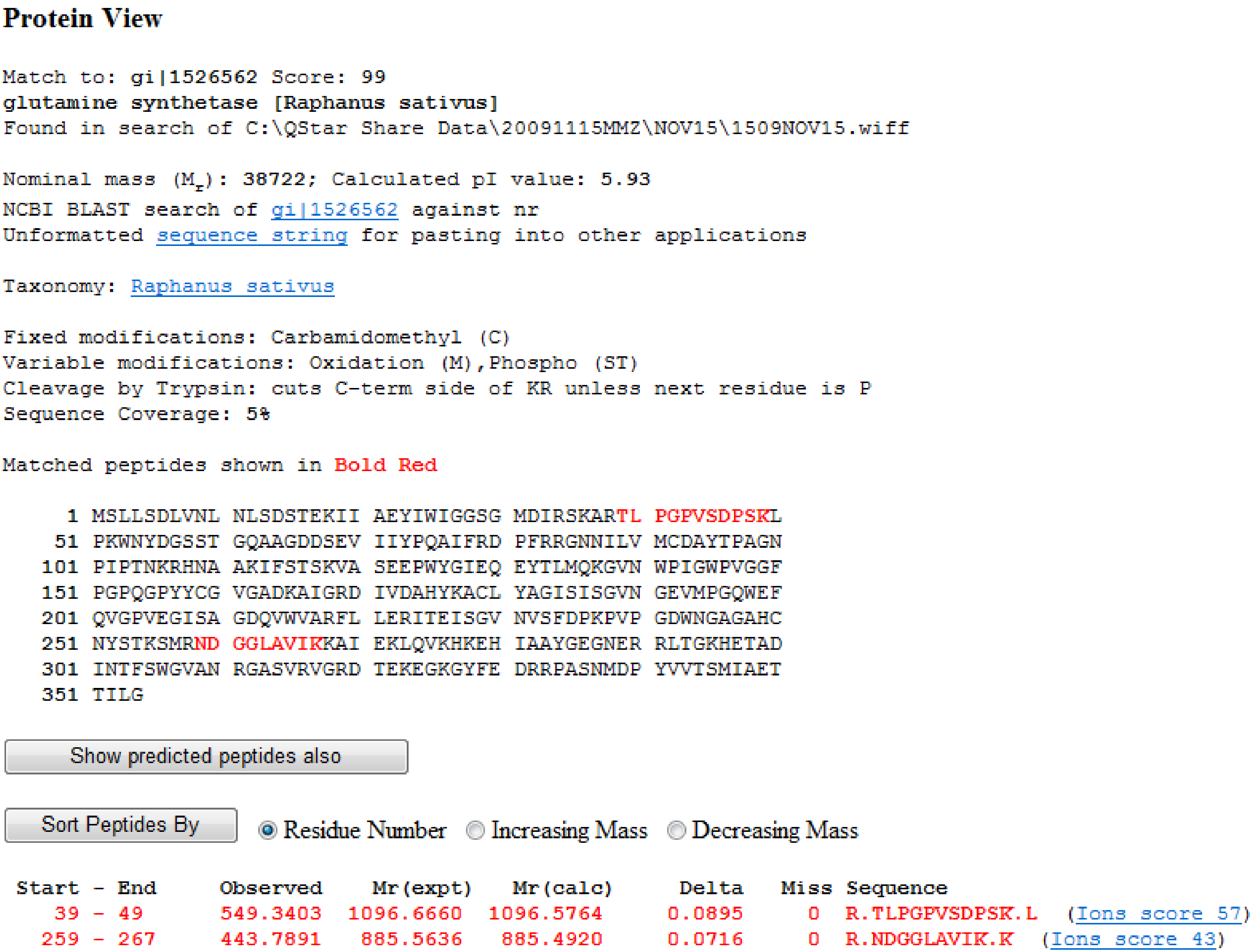


Peptide View

MS/MS Fragmentation of **IQELNVYEFNEGDR**
Found in **gi|15222241**, AOC4 (ALLENE OXIDE CYCLASE 4); allene-oxide cyclase [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**I**							**14**
2	**242.1499**	121.5786	**225.1234**	113.0653			**Q**	1612.7238	806.8655	1595.6972	**798.3523**	1594.7132	797.8603	**13**
3	**371.1925**	186.0999	354.1660	177.5866	353.1819	177.0946	**E**	**1484.6652**	742.8362	1467.6387	734.3230	**1466.6546**	733.8310	**12**
4	**484.2766**	**242.6419**	**467.2500**	234.1287	466.2660	233.6366	**L**	**1355.6226**	678.3149	1338.5961	669.8017	1337.6121	669.3097	**11**
5	598.3195	299.6634	**581.2930**	291.1501	580.3089	290.6581	**N**	**1242.5386**	621.7729	1225.5120	613.2596	1224.5280	612.7676	**10**
6	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	**V**	**1128.4956**	564.7515	1111.4691	556.2382	1110.4851	555.7462	**9**
7	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	**Y**	**1029.4272**	515.2172	1012.4007	506.7040	**1011.4167**	506.2120	**8**
8	989.4938	495.2506	972.4673	486.7373	971.4833	486.2453	**E**	**866.3639**	433.6856	849.3373	425.1723	**848.3533**	424.6803	**7**
9	1136.5623	568.7848	1119.5357	560.2715	1118.5517	559.7795	**F**	**737.3213**	369.1643	**720.2947**	360.6510	719.3107	360.1590	**6**
10	1250.6052	625.8062	1233.5786	617.2930	1232.5946	616.8009	**N**	**590.2529**	295.6301	**573.2263**	287.1168	572.2423	286.6248	**5**
11	1379.6478	690.3275	1362.6212	681.8142	1361.6372	681.3222	**E**	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	**4**
12	1436.6692	718.8383	1419.6427	710.3250	1418.6587	709.8330	**G**	**347.1674**	174.0873	330.1408	165.5740	329.1568	165.0820	**3**
13	1551.6962	776.3517	1534.6696	767.8385	1533.6856	767.3464	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
14							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

gi|1526562 Glutamine synthetase



Protein View

```
Match to: gi|1526562 Score: 99
glutamine synthetase [Raphanus sativus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff

Nominal mass (Mr): 38722; Calculated pI value: 5.93
NCBI BLAST search of gi|1526562 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Raphanus sativus

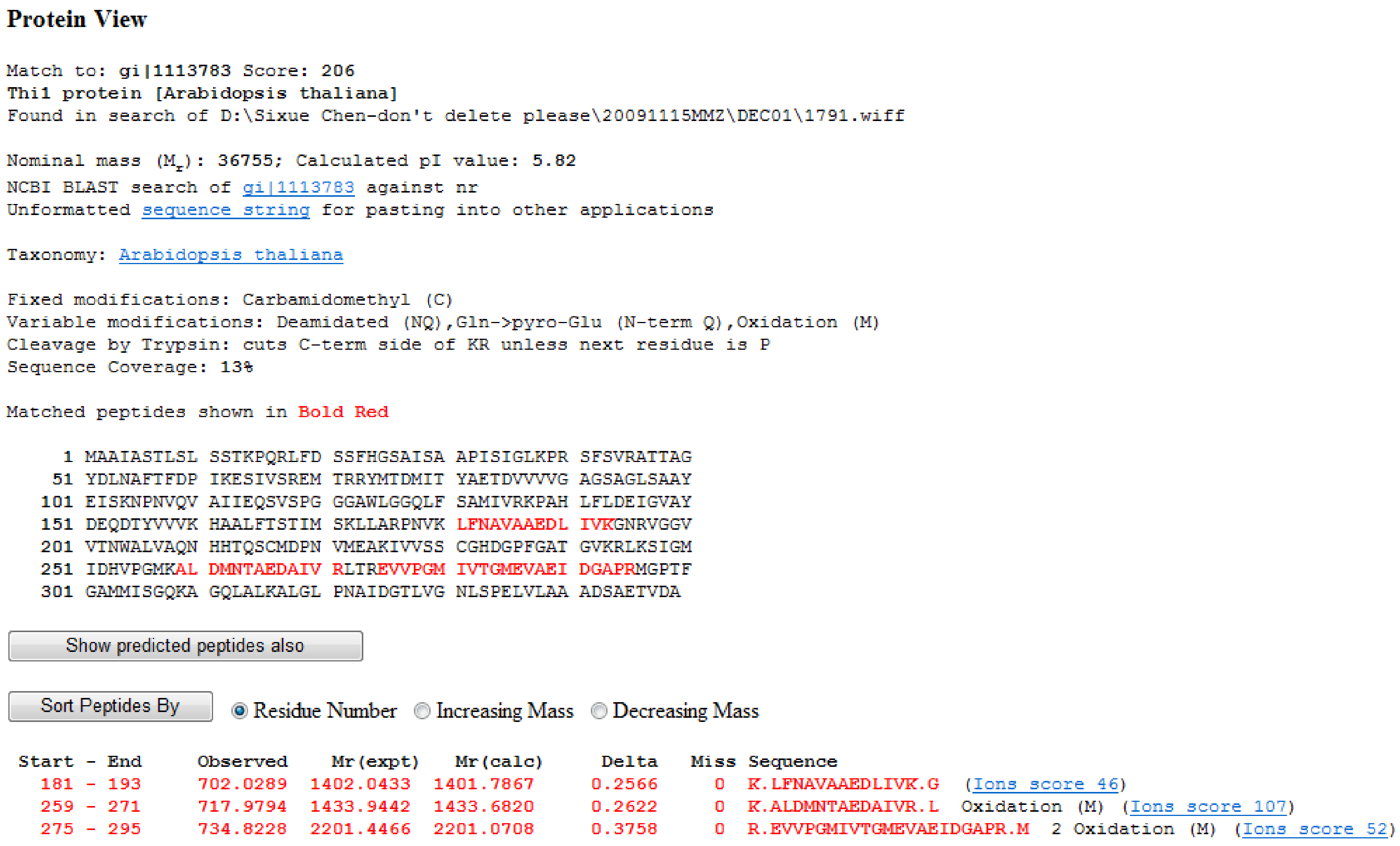
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

      1 MSLLSDLVNL NLSDSTEKII AEYIWIGGSG MDIRSKARTL PGPVSDPSKL
     51 PKWNYDGSST GQAAGDDSEV IIYPQAIFRD PFRRGNNILV MCDAYTPAGN
    101 PIPTNKRHNA AKIFSTSKVA SEEPWYGIEQ EYTLMQKGVN WPIGWPVGGF
    151 PGPQGPYYCG VGADKAIGRD IVDAHYKACL YAGISISGVN GEVMPGQWEF
    201 QVGPVEGISA GDQVWVARFL LERITEISGV NVSFDPKPVP GDWNGAGAHC
    251 NYSTKSMRND GGLAVIKKAI EKLQVKHKEH IAAYGEGNER RLTGKHETAD
    301 INTFSWGVAN RGASVRVGRD TEKEGKGYFE DRRPASNMDP YVVTSMIAET
    351 TILG
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
   39 - 49     549.3403  1096.6660  1096.5764    0.0895     0  R.TLPGPVSDPSK.L   (Ions score 57)
  259 - 267    443.7891   885.5636   885.4920    0.0716     0  R.NDGGLAVIK.K     (Ions score 43)
```

gi|1113783 Thi1 protein



Protein View

```
Match to: gi|1113783 Score: 206
Thi1 protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (Mr): 36755; Calculated pI value: 5.82
NCBI BLAST search of gi|1113783 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

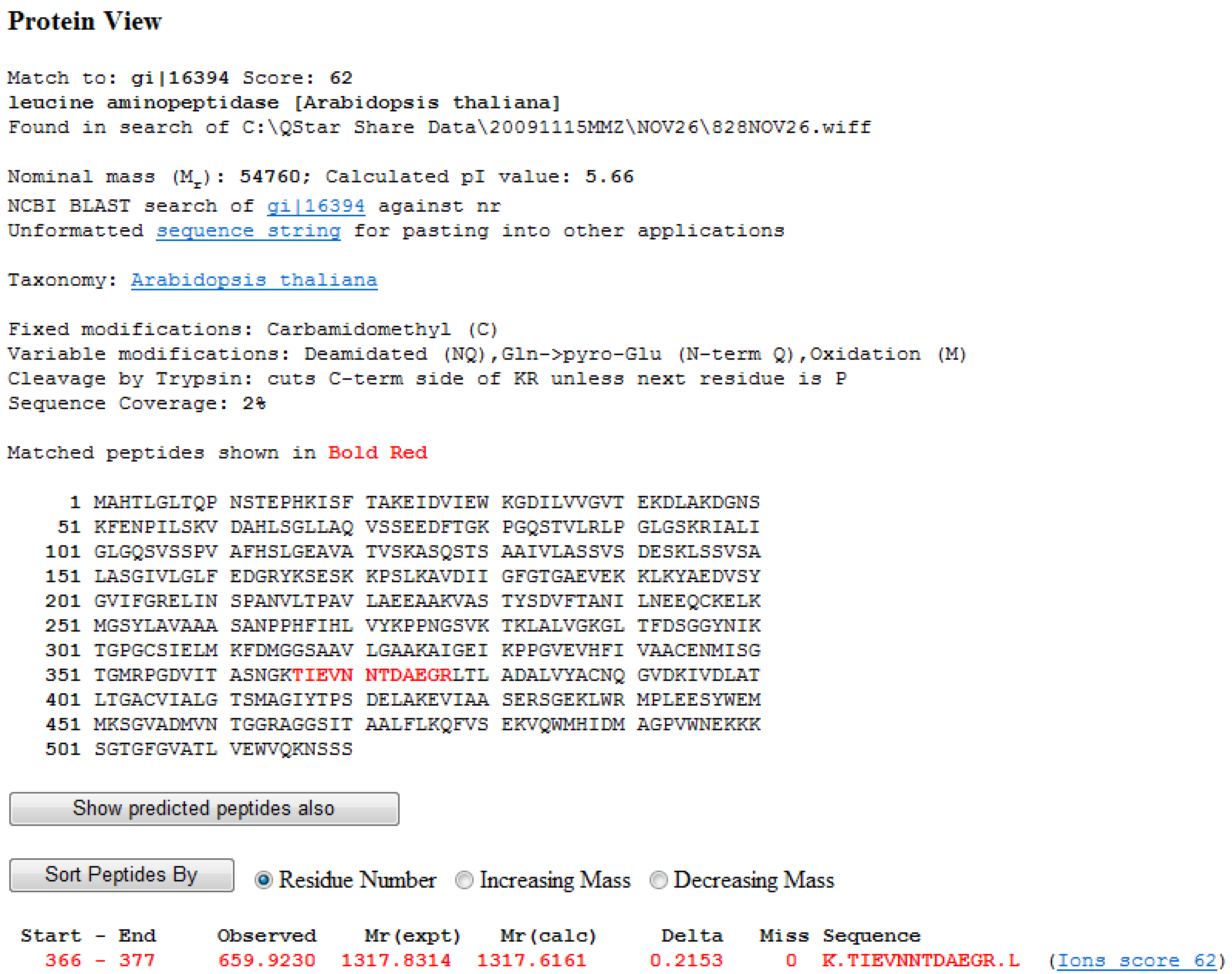
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%

Matched peptides shown in Bold Red

     1 MAAIASTLSL SSTKPQRLFD SSFHGSAISA APISIGLKPR SFSVRATTAG
    51 YDLNAFTFDP IKESIVSREM TRRYMTDMIT YAETDVVVVG AGSAGLSAAY
   101 EISKNPNVQV AIIEQSVSPG GGAWLGGQLF SAMIVRKPAH LFLDEIGVAY
   151 DEQDTYVVVK HAALFTSTIM SKLLARPNVK LFNAVAAEDL IVKGNRVGGV
   201 VTNWALVAQN HHTQSCMDPN VMEAKIVVSS CGHDGPFGAT GVKRLKSIGM
   251 IDHVPGMKAL DMNTAEDAIV RLTREVVPGM IVTGMEVAEI DGAPRMGPTF
   301 GAMMISGQKA GQLALKALGL PNAIDGTLVG NLSPELVLAA ADSAETVDA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   181 - 193     702.0289  1402.0433  1401.7867    0.2566     0  K.LFNAVAAEDLIVK.G   (Ions score 46)
   259 - 271     717.9794  1433.9442  1433.6820    0.2622     0  K.ALDMNTAEDAIVR.L  Oxidation (M)  (Ions score 107)
   275 - 295     734.8228  2201.4466  2201.0708    0.3758     0  R.EVVPGMIVTGMEVAEIDGAPR.M  2 Oxidation (M)  (Ions score 52)
```

gi|16394 Leucine aminopeptidase



Protein View

```
Match to: gi|16394 Score: 62
leucine aminopeptidase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\828NOV26.wiff

Nominal mass (Mr): 54760; Calculated pI value: 5.66
NCBI BLAST search of gi|16394 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%

Matched peptides shown in Bold Red

    1 MAHTLGLTQP NSTEPHKISF TAKEIDVIEW KGDILVVGVT EKDLAKDGNS
   51 KFENPILSKV DAHLSGLLAQ VSSEEDFTGK PGQSTVLRLP GLGSKRIALI
  101 GLGQSVSSPV AFHSLGEAVA TVSKASQSTS AAIVLASSVS DESKLSSVSA
  151 LASGIVLGLF EDGRYKSESK KPSLKAVDII GFGTGAEVEK KLKYAEDVSY
  201 GVIFGRELIN SPANVLTPAV LAEEAAKVAS TYSDVFTANI LNEEQCKELK
  251 MGSYLAVAAA SANPPHFIHL VYKPPNGSVK TKLALVGKGL TFDSGGYNIK
  301 TGPGCSIELM KFDMGGSAAV LGAAKAIGEI KPPGVEVHFI VAACENMISG
  351 TGMRPGDVIT ASNGKTIEVN NTDAEGRLTL ADALVYACNQ GVDKIVDLAT
  401 LTGACVIALG TSMAGIYTPS DELAKEVIAA SERSGEKLWR MPLEESYWEM
  451 MKSGVADMVN TGGRAGGSIT AALFLKQFVS EKVQWMHIDM AGPVWNEKKK
  501 SGTGFGVATL VEWVQKNSSS
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

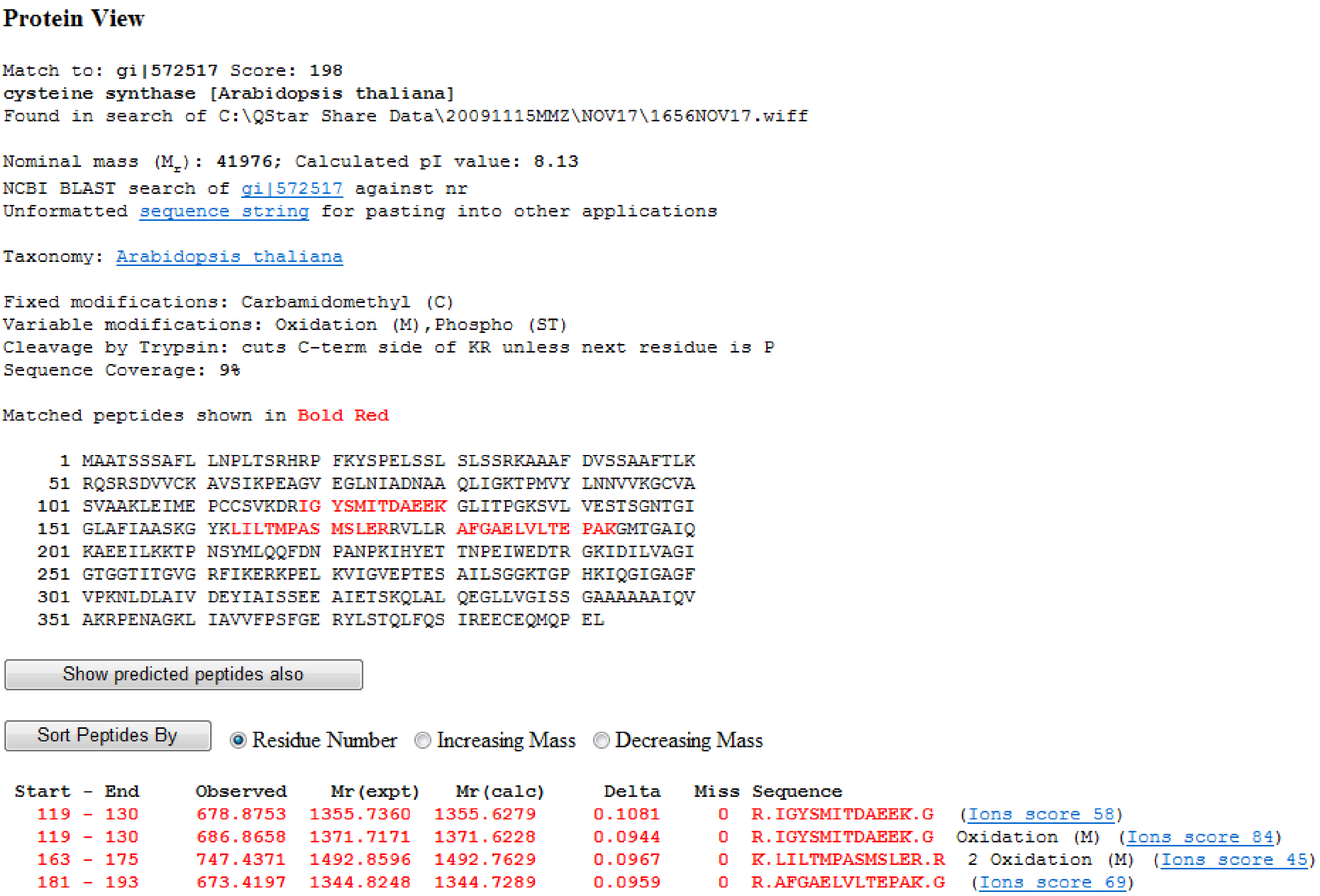
```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  366 - 377     659.9230  1317.8314  1317.6161    0.2153     0  K.TIEVNNTDAEGR.L   (Ions score 62)
```

Peptide View

MS/MS Fragmentation of **TIEVNNTDAEGR**
Found in **gi|16394**, leucine aminopeptidase [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	**215.1390**	108.0731			197.1285	99.0679	I	1217.5757	609.2915	1200.5491	600.7782	1199.5651	600.2862	11
3	**344.1816**	172.5944			326.1710	163.5892	E	**1104.4916**	552.7494	1087.4651	544.2362	1086.4810	543.7442	10
4	443.2500	222.1287			425.2395	213.1234	V	**975.4490**	488.2281	958.4225	479.7149	957.4384	479.2229	9
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	N	**876.3806**	438.6939	**859.3540**	430.1807	858.3700	429.6887	8
6	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	N	**762.3377**	381.6725	745.3111	373.1592	744.3271	372.6672	7
7	772.3836	386.6954	755.3570	378.1821	754.3730	377.6901	T	**648.2947**	324.6510	631.2682	316.1377	630.2842	315.6457	6
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	D	**547.2471**	274.1272	530.2205	265.6139	**529.2365**	265.1219	5
9	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	A	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	4
10	1087.4902	544.2487	1070.4637	535.7355	1069.4796	535.2435	E	361.1830	181.0951	**344.1565**	172.5819	343.1724	172.0899	3
11	1144.5117	572.7595	1127.4851	564.2462	1126.5011	563.7542	G	**232.1404**	116.5738	**215.1139**	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1

gi|572517 Cysteine synthase



Protein View

Match to: gi|572517 Score: 198
cysteine synthase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1656NOV17.wiff

Nominal mass (M_r): **41976**; Calculated pI value: **8.13**
NCBI BLAST search of gi|572517 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

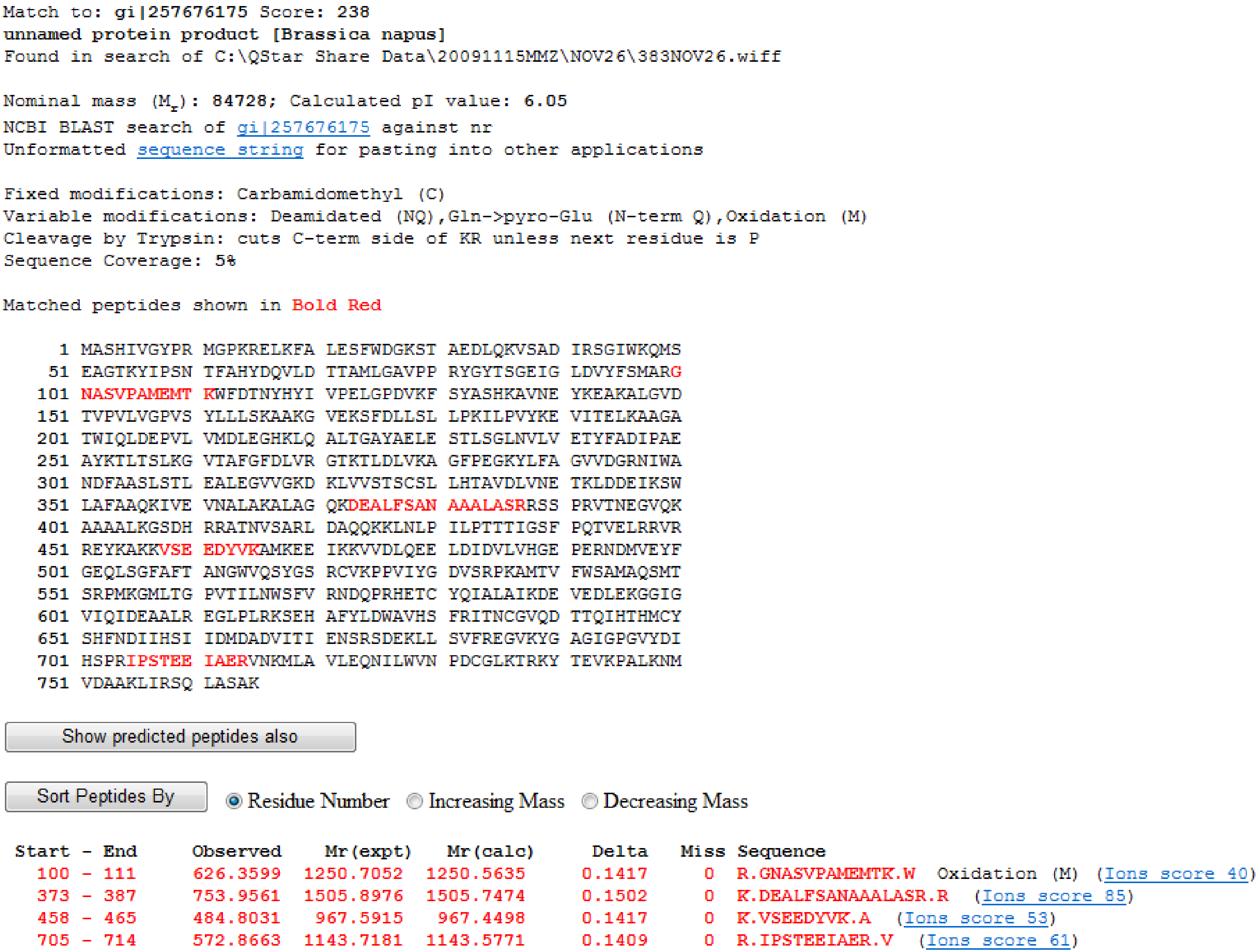
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

```
  1 MAATSSSAFL LNPLTSRHRP FKYSPELSSL SLSSRKAAAF DVSSAAFTLK
 51 RQSRSDVVCK AVSIKPEAGV EGLNIADNAA QLIGKTPMVY LNNVVKGCVA
101 SVAAKLEIME PCCSVKDRIG YSMITDAEEK GLITPGKSVL VESTSGNTGI
151 GLAFIAASKG YKLILTMPAS MSLERRVLLR AFGAELVLTE PAKGMTGAIQ
201 KAEEILKKTP NSYMLQQFDN PANPKIHYET TNPEIWEDTR GKIDILVAGI
251 GTGGTITGVG RFIKERKPEL KVIGVEPTES AILSGGKTGP HKIQGIGAGF
301 VPKNLDLAIV DEYIAISSEE AIETSKQLAL QEGLLVGISS GAAAAAAIQV
351 AKRPENAGKL IAVVFPSFGE RYLSTQLFQS IREECEQMQP EL
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
  119 - 130     678.8753  1355.7360  1355.6279    0.1081    0  R.IGYSMITDAEEK.G   (Ions score 58)
  119 - 130     686.8658  1371.7171  1371.6228    0.0944    0  R.IGYSMITDAEEK.G  Oxidation (M)  (Ions score 84)
  163 - 175     747.4371  1492.8596  1492.7629    0.0967    0  K.LILTMPASMSLER.R  2 Oxidation (M)  (Ions score 45)
  181 - 193     673.4197  1344.8248  1344.7289    0.0959    0  R.AFGAELVLTEPAK.G   (Ions score 69)
```

gi|257676175 Unnamed protein product, containing CIMS (cobalamine independent methonine synthase) domain



Match to: gi|257676175 Score: 238
unnamed protein product [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\383NOV26.wiff

Nominal mass (M_r): 84728; Calculated pI value: 6.05
NCBI BLAST search of gi|257676175 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

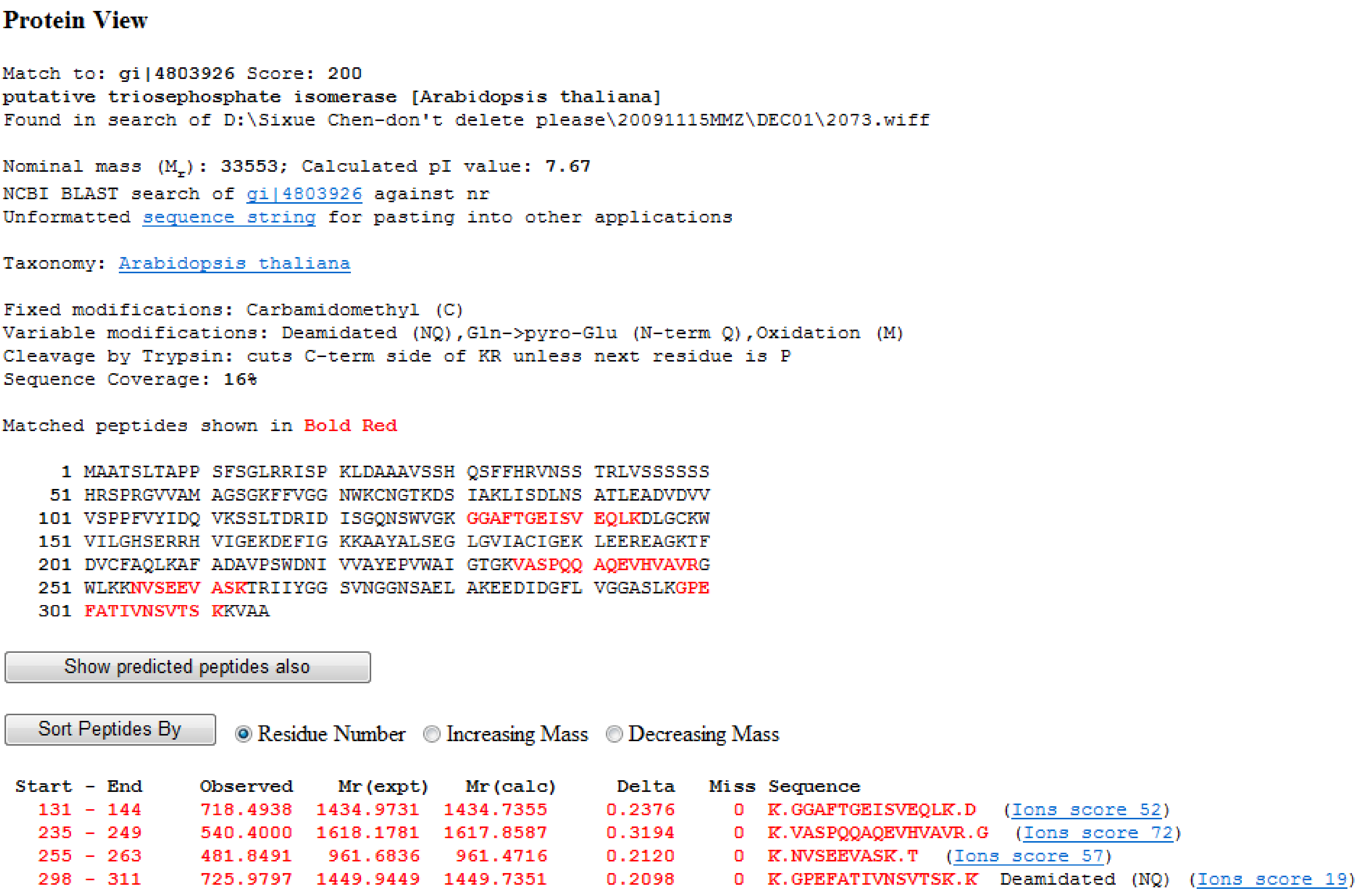
Matched peptides shown in **Bold Red**

```
  1 MASHIVGYPR MGPKRELKFA LESFWDGKST AEDLQKVSAD IRSGIWKQMS
 51 EAGTKYIPSN TFAHYDQVLD TTAMLGAVPP RYGYTSGEIG LDVYFSMARG
101 NASVPAMEMT KWFDTNYHYI VPELGPDVKF SYASHKAVNE YKEAKALGVD
151 TVPVLVGPVS YLLLSKAAKG VEKSFDLLSL LPKILPVYKE VITELKAAGA
201 TWIQLDEPVL VMDLEGHKLQ ALTGAYAELE STLSGLNVLV ETYFADIPAE
251 AYKTLTSLKG VTAFGFDLVR GTKTLDLVKA GFPEGKYLFA GVVDGRNIWA
301 NDFAASLSTL EALEGVVGKD KLVVSTSCSL LHTAVDLVNE TKLDDEIKSW
351 LAFAAQKIVE VNALAKALAG QKDEALFSAN AAALASRRSS PRVTNEGVQK
401 AAAALKGSDH RRATNVSARL DAQQKKLNLP ILPTTTIGSF PQTVELRRVR
451 REYKAKKVSE EDYVKAMKEE IKKVVDLQEE LDIDVLVHGE PERNDMVEYF
501 GEQLSGFAFT ANGWVQSYGS RCVKPPVIYG DVSRPKAMTV FWSAMAQSMT
551 SRPMKGMLTG PVTILNWSFV RNDQPRHETC YQIALAIKDE VEDLEKGGIG
601 VIQIDEAALR EGLPLRKSEH AFYLDWAVHS FRITNCGVQD TTQIHTHMCY
651 SHFNDIIHSI IDMDADVITI ENSRSDEKLL SVFREGVKYG AGIGPGVYDI
701 HSPRIPSTEE IAERVNKMLA VLEQNILWVN PDCGLKTRKY TEVKPALKNM
751 VDAAKLIRSQ LASAK
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  100 - 111      626.3599  1250.7052  1250.5635    0.1417     0  R.GNASVPAMEMTK.W  Oxidation (M)  (Ions score 40)
  373 - 387      753.9561  1505.8976  1505.7474    0.1502     0  K.DEALFSANAAALASR.R   (Ions score 85)
  458 - 465      484.8031   967.5915   967.4498    0.1417     0  K.VSEEDYVK.A   (Ions score 53)
  705 - 714      572.8663  1143.7181  1143.5771    0.1409     0  R.IPSTEEIAER.V   (Ions score 61)
```

gi|4803926 Putative triosephosphate isomerase



Protein View

```
Match to: gi|4803926 Score: 200
putative triosephosphate isomerase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2073.wiff

Nominal mass (Mr): 33553; Calculated pI value: 7.67
NCBI BLAST search of gi|4803926 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

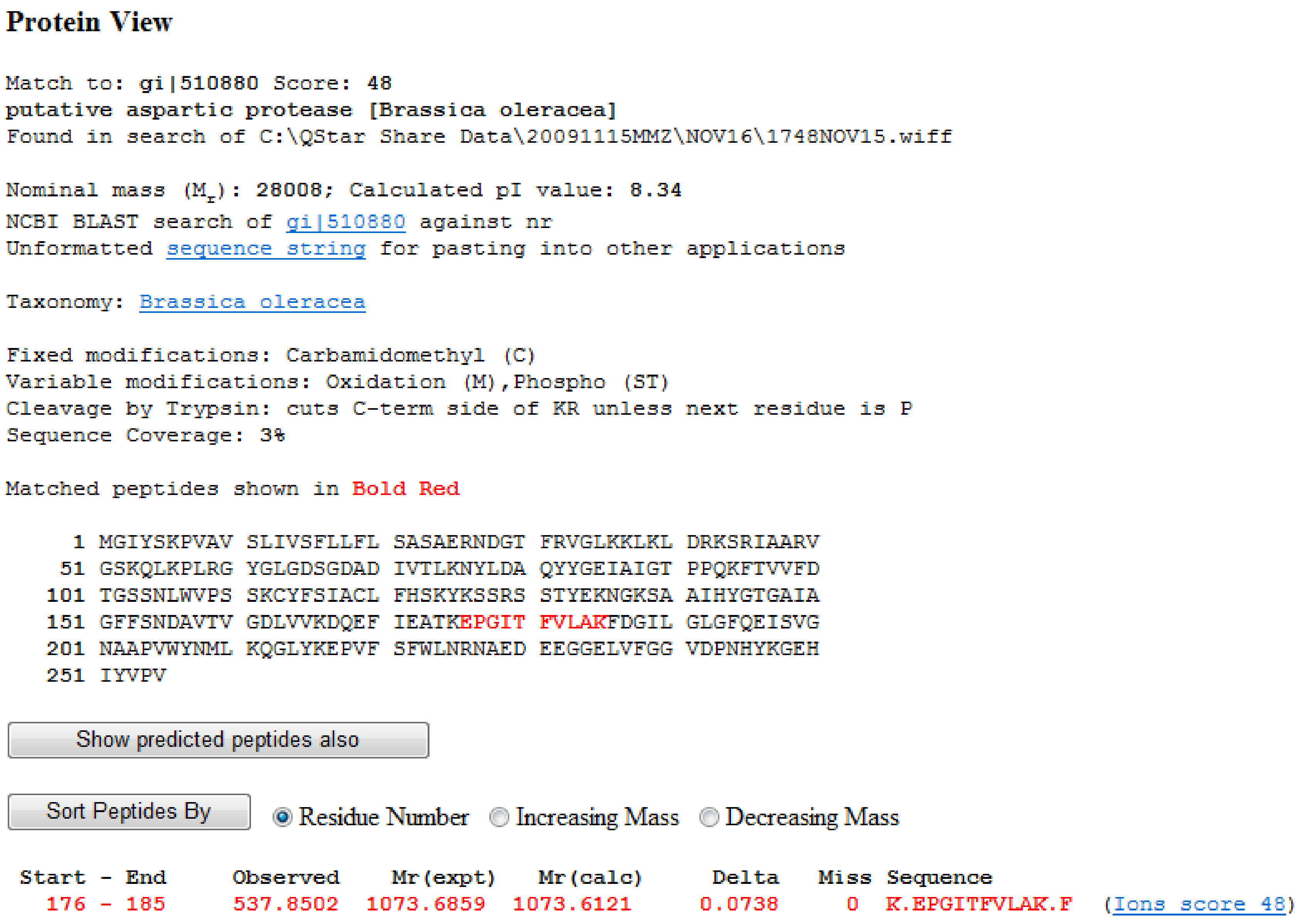
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%

Matched peptides shown in Bold Red

    1 MAATSLTAPP SFSGLRRISP KLDAAAVSSH QSFFHRVNSS TRLVSSSSSS
   51 HRSPRGVVAM AGSGKFFVGG NWKCNGTKDS IAKLISDLNS ATLEADVDVV
  101 VSPPFVYIDQ VKSSLTDRID ISGQNSWVGK GGAFTGEISV EQLKDLGCKW
  151 VILGHSERRH VIGEKDEFIG KKAAYALSEG LGVIACIGEK LEEREAGKTF
  201 DVCFAQLKAF ADAVPSWDNI VVAYEPVWAI GTGKVASPQQ AQEVHVAVRG
  251 WLKKNVSEEV ASKTRIIYGG SVNGGNSAEL AKEEDIDGFL VGGASLKGPE
  301 FATIVNSVTS KKVAA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   131 - 144     718.4938  1434.9731  1434.7355   0.2376     0 K.GGAFTGEISVEQLK.D  (Ions score 52)
   235 - 249     540.4000  1618.1781  1617.8587   0.3194     0 K.VASPQQAQEVHVAVR.G  (Ions score 72)
   255 - 263     481.8491   961.6836   961.4716   0.2120     0 K.NVSEEVASK.T  (Ions score 57)
   298 - 311     725.9797  1449.9449  1449.7351   0.2098     0 K.GPEFATIVNSVTSK.K Deamidated (NQ) (Ions score 19)
```

gi|510880 Putative aspartic protease



Protein View

Match to: gi|510880 Score: 48
putative aspartic protease [Brassica oleracea]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1748NOV15.wiff

Nominal mass (M_r): **28008**; Calculated pI value: **8.34**
NCBI BLAST search of gi|510880 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica oleracea

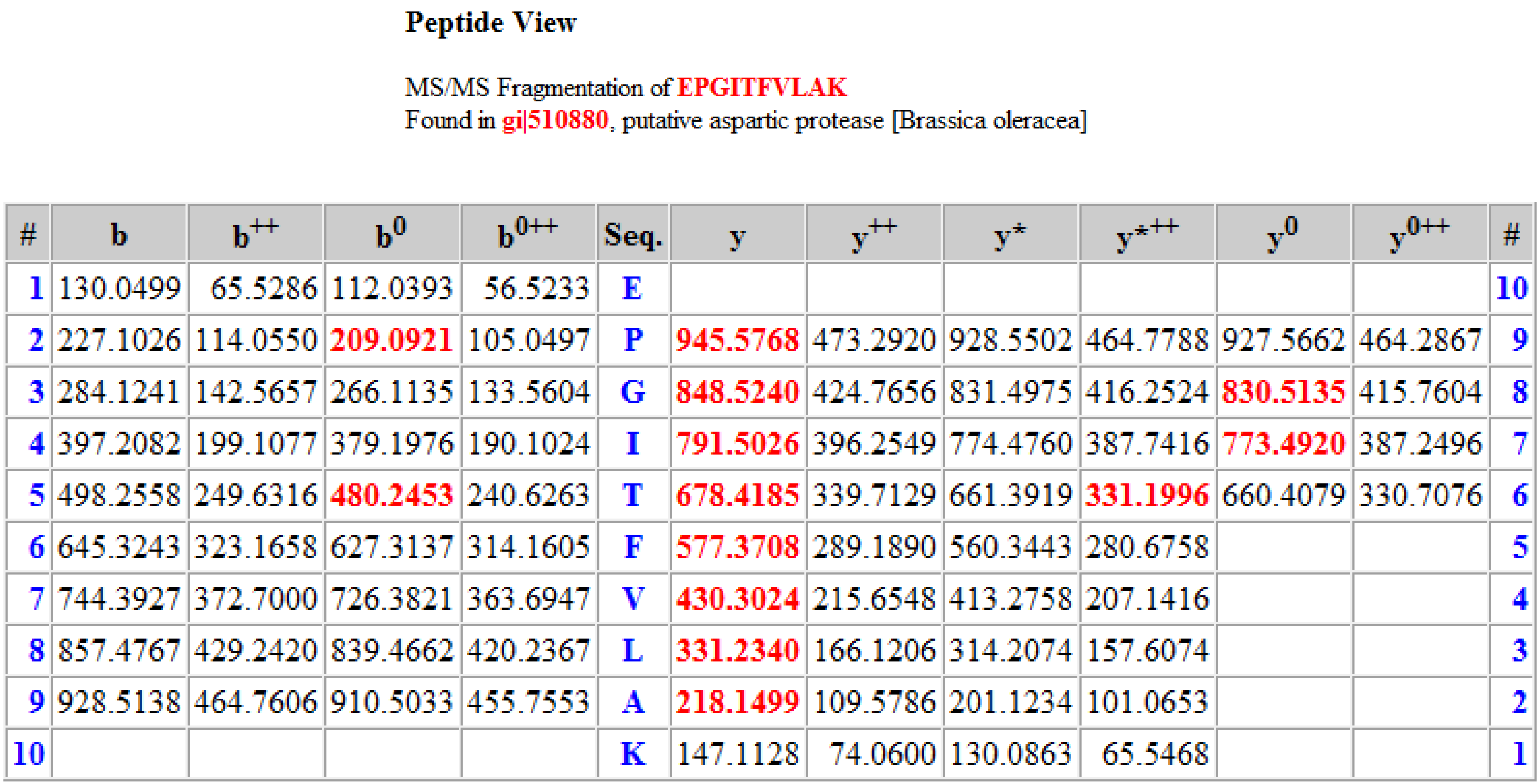
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **3%**

Matched peptides shown in **Bold Red**

```
     1 MGIYSKPVAV SLIVSFLLFL SASAERNDGT FRVGLKKLKL DRKSRIAARV
    51 GSKQLKPLRG YGLGDSGDAD IVTLKNYLDA QYYGEIAIGT PPQKFTVVFD
   101 TGSSNLWVPS SKCYFSIACL FHSKYKSSRS STYEKNGKSA AIHYGTGAIA
   151 GFFSNDAVTV GDLVVKDQEF IEATKEPGIT FVLAKFDGIL GLGFQEISVG
   201 NAAPVWYNML KQGLYKEPVF SFWLNRNAED EEGGELVFGG VDPNHYKGEH
   251 IYVPV
```

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   176 - 185     537.8502  1073.6859  1073.6121    0.0738     0  K.EPGITFVLAK.F   (Ions score 48)
```

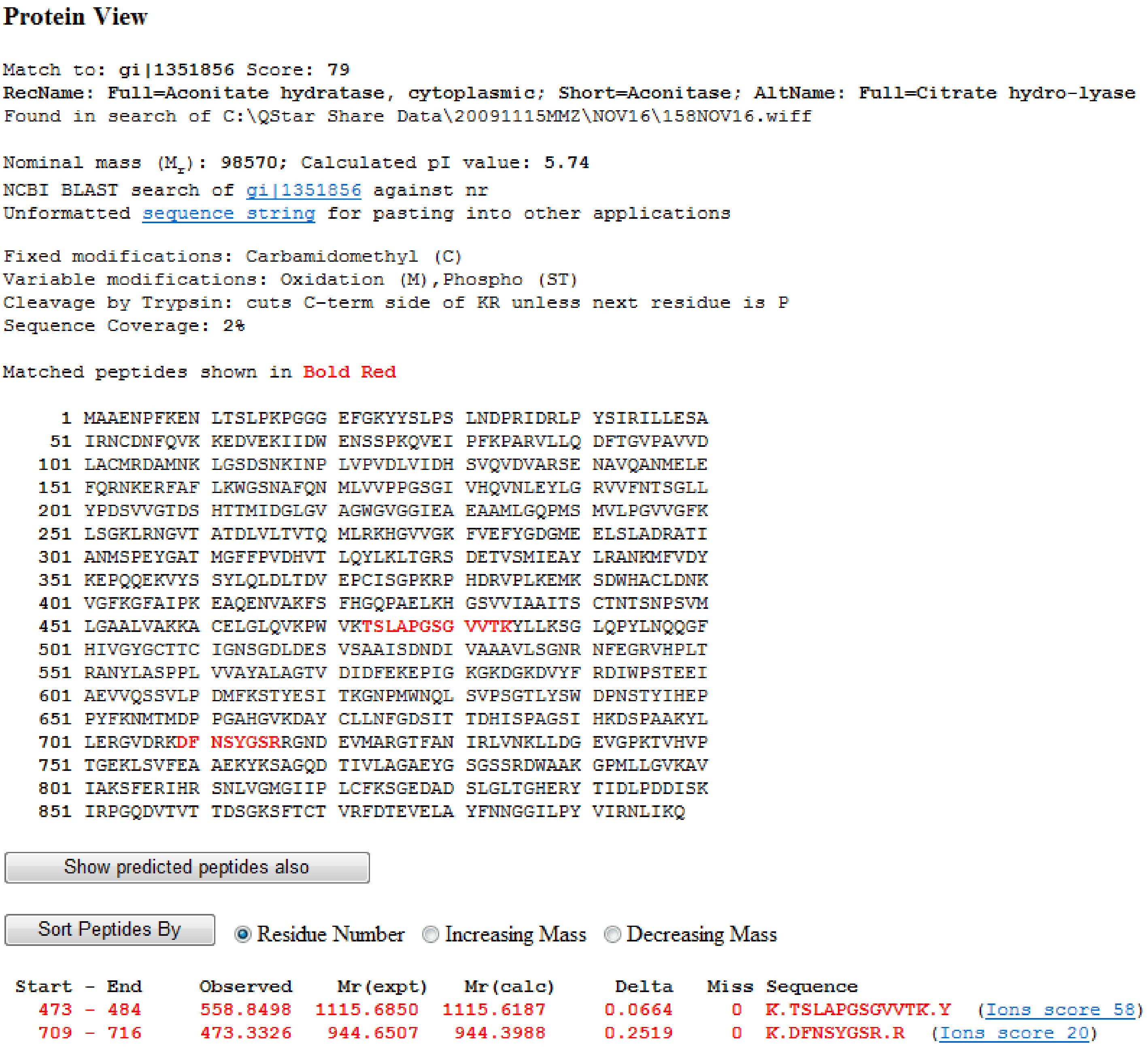


Peptide View

MS/MS Fragmentation of **EPGITFVLAK**
Found in **gi|510880**, putative aspartic protease [Brassica oleracea]

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	227.1026	114.0550	209.0921	105.0497	P	945.5768	473.2920	928.5502	464.7788	927.5662	464.2867	9
3	284.1241	142.5657	266.1135	133.5604	G	848.5240	424.7656	831.4975	416.2524	830.5135	415.7604	8
4	397.2082	199.1077	379.1976	190.1024	I	791.5026	396.2549	774.4760	387.7416	773.4920	387.2496	7
5	498.2558	249.6316	480.2453	240.6263	T	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
6	645.3243	323.1658	627.3137	314.1605	F	577.3708	289.1890	560.3443	280.6758			5
7	744.3927	372.7000	726.3821	363.6947	V	430.3024	215.6548	413.2758	207.1416			4
8	857.4767	429.2420	839.4662	420.2367	L	331.2340	166.1206	314.2074	157.6074			3
9	928.5138	464.7606	910.5033	455.7553	A	218.1499	109.5786	201.1234	101.0653			2
10					K	147.1128	74.0600	130.0863	65.5468			1

gi|1351856 Aconitate hydratase, cytoplasmic



Protein View

Match to: gi|1351856 Score: 79
RecName: Full=Aconitate hydratase, cytoplasmic; Short=Aconitase; AltName: Full=Citrate hydro-lyase
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\158NOV16.wiff

Nominal mass (M_r): **98570**; Calculated pI value: **5.74**
NCBI BLAST search of gi|1351856 against nr
Unformatted sequence string for pasting into other applications

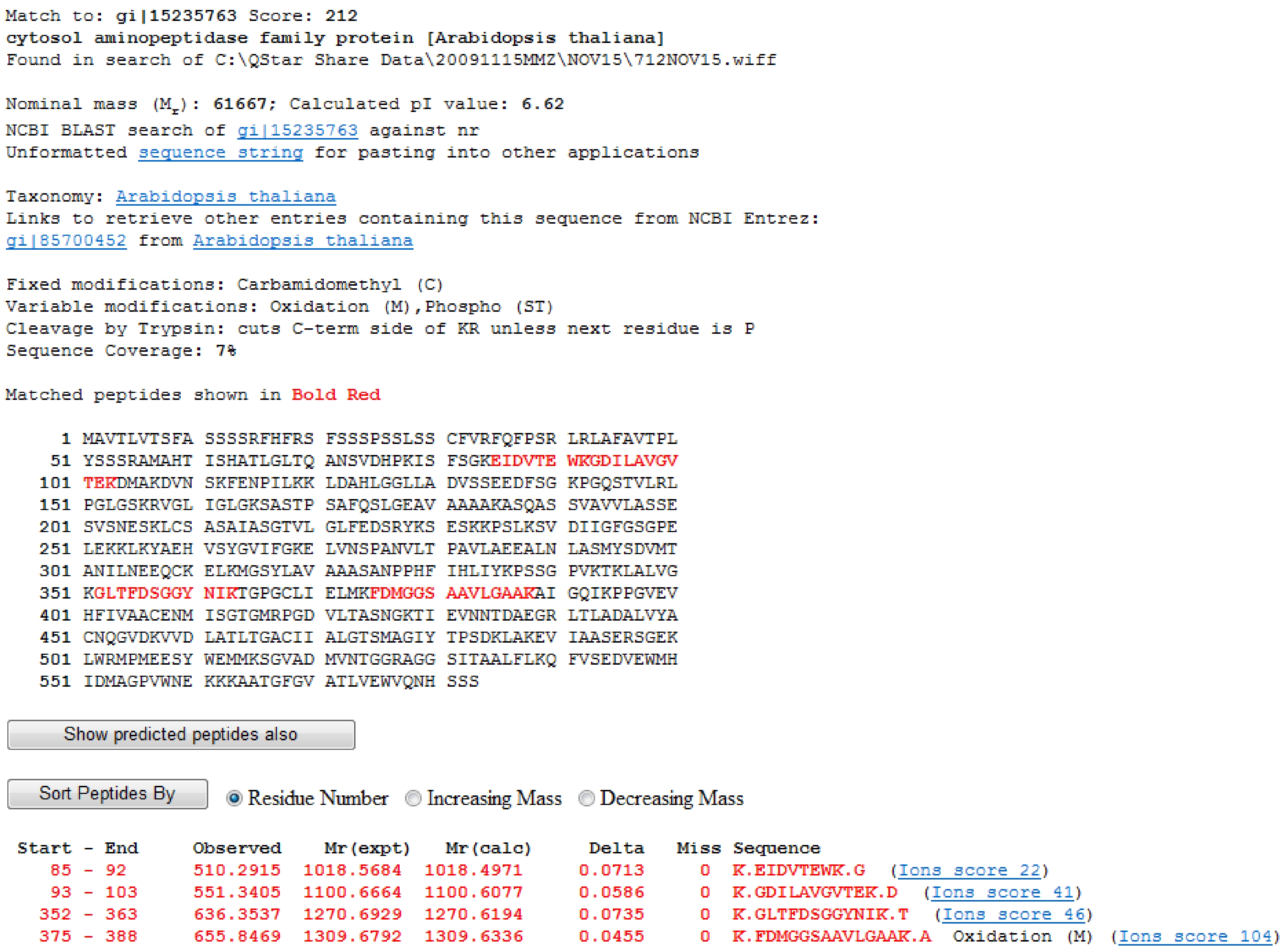
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

```
  1 MAAENPFKEN LTSLPKPGGG EFGKYYSLPS LNDPRIDRLP YSIRILLESA
 51 IRNCDNFQVK KEDVEKIIDW ENSSPKQVEI PFKPARVLLQ DFTGVPAVVD
101 LACMRDAMNK LGSDSNKINP LVPVDLVIDH SVQVDVARSE NAVQANMELE
151 FQRNKERFAF LKWGSNAFQN MLVVPPGSGI VHQVNLEYLG RVVFNTSGLL
201 YPDSVVGTDS HTTMIDGLGV AGWGVGGIEA EAAMLGQPMS MVLPGVVGFK
251 LSGKLRNGVT ATDLVLTVTQ MLRKHGVVGK FVEFYGDGME ELSLADRATI
301 ANMSPEYGAT MGFFPVDHVT LQYLKLTGRS DETVSMIEAY LRANKMFVDY
351 KEPQQEKVYS SYLQLDLTDV EPCISGPKRP HDRVPLKEMK SDWHACLDNK
401 VGFKGFAIPK EAQENVAKFS FHGQPAELKH GSVVIAAITS CTNTSNPSVM
451 LGAALVAKKA CELGLQVKPW VKTSLAPGSG VVTKYLLKSG LQPYLNQQGF
501 HIVGYGCTTC IGNSGDLDES VSAAISDNDI VAAAVLSGNR NFEGRVHPLT
551 RANYLASPPL VVAYALAGTV DIDFEKEPIG KGKDGKDVYF RDIWPSTEEI
601 AEVVQSSVLP DMFKSTYESI TKGNPMWNQL SVPSGTLYSW DPNSTYIHEP
651 PYFKNMTMDP PGAHGVKDAY CLLNFGDSIT TDHISPAGSI HKDSPAAKYL
701 LERGVDRKDF NSYGSRRGND EVMARGTFAN IRLVNKLLDG EVGPKTVHVP
751 TGEKLSVFEA AEKYKSAGQD TIVLAGAEYG SGSSRDWAAK GPMLLGVKAV
801 IAKSFERIHR SNLVGMGIIP LCFKSGEDAD SLGLTGHERY TIDLPDDISK
851 IRPGQDVTVT TDSGKSFTCT VRFDTEVELA YFNNGGILPY VIRNLIKQ
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
473 - 484	558.8498	1115.6850	1115.6187	0.0664	0	K.TSLAPGSGVVTK.Y	(Ions score 58)
709 - 716	473.3326	944.6507	944.3988	0.2519	0	K.DFNSYGSR.R	(Ions score 20)

gi|15235763 Cytosol aminopeptidase family protein



Match to: **gi|15235763** Score: **212**
cytosol aminopeptidase family protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\712NOV15.wiff

Nominal mass (M_r): **61667**; Calculated pI value: **6.62**
NCBI BLAST search of gi|15235763 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|85700452 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

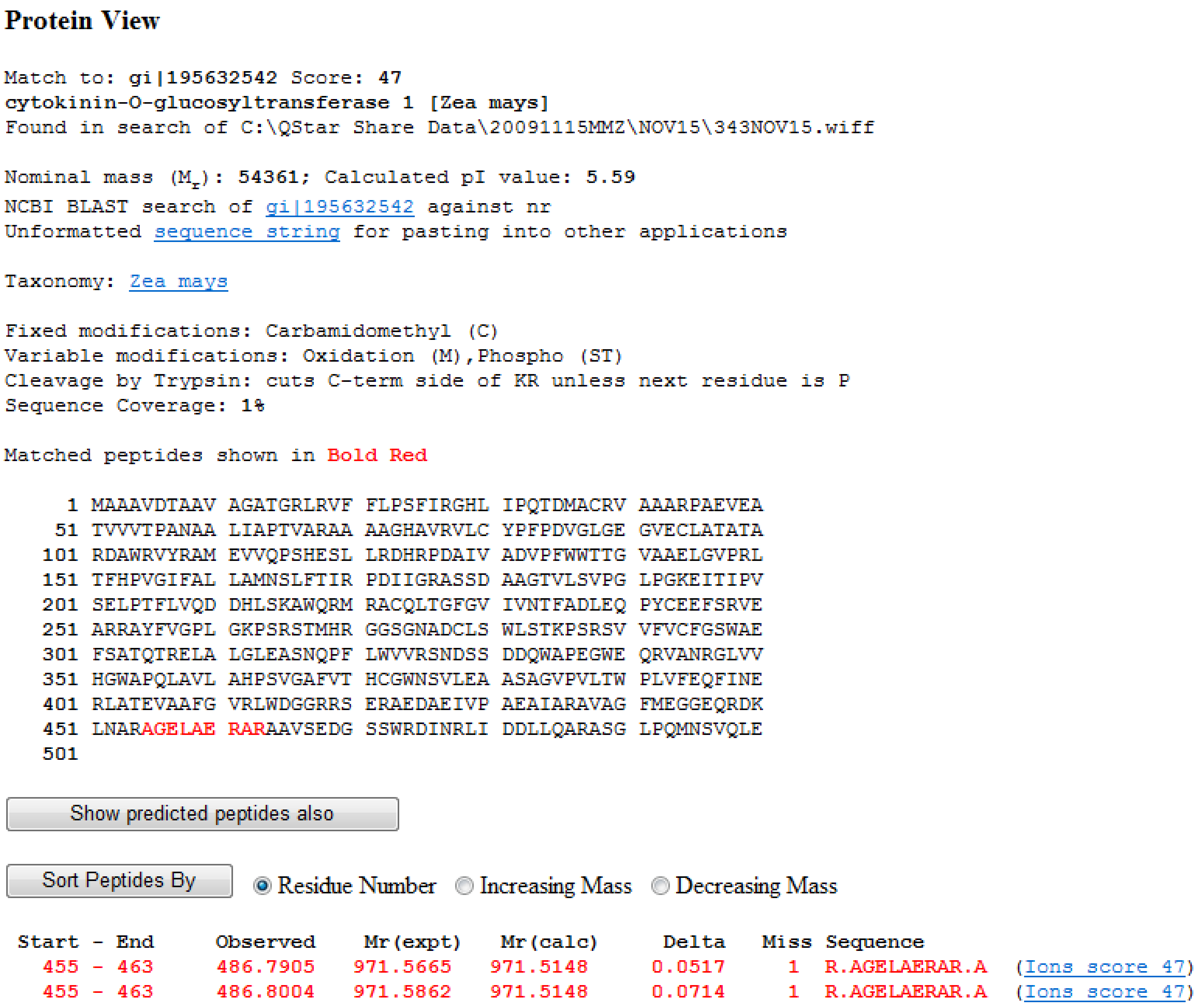
Matched peptides shown in **Bold Red**

```
  1 MAVTLVTSFA SSSSRFHFRS FSSSPSSLSS CFVRFQFPSR LRLAFAVTPL
 51 YSSSRAMAHT ISHATLGLTQ ANSVDHPKIS FSGKEIDVTE WKGDILAVGV
101 TEKDMAKDVN SKFENPILKK LDAHLGGLLA DVSSEEDFSG KPGQSTVLRL
151 PGLGSKRVGL IGLGKSASTP SAFQSLGEAV AAAAKASQAS SVAVVLASSE
201 SVSNESKLCS ASAIASGTVL GLFEDSRYKS ESKKPSLKSV DIIGFGSGPE
251 LEKKLKYAEH VSYGVIFGKE LVNSPANVLT PAVLAEEALN LASMYSDVMT
301 ANILNEEQCK ELKMGSYLAV AAASANPPHF IHLIYKPSSG PVKTKLALVG
351 KGLTFDSGGY NIKTGPGCLI ELMKFDMGGS AAVLGAAKAI GQIKPPGVEV
401 HFIVAACENM ISGTGMRPGD VLTASNGKTI EVNNTDAEGR LTLADALVYA
451 CNQGVDKVVD LATLTGACII ALGTSMAGIY TPSDKLAKEV IAASERSGEK
501 LWRMPMEESY WEMMKSGVAD MVNTGGRAGG SITAALFLKQ FVSEDVEWMH
551 IDMAGPVWNE KKKAATGFGV ATLVEWVQNH SSS
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
    85 - 92      510.2915  1018.5684  1018.4971    0.0713     0  K.EIDVTEWK.G   (Ions score 22)
    93 - 103     551.3405  1100.6664  1100.6077    0.0586     0  K.GDILAVGVTEK.D   (Ions score 41)
   352 - 363     636.3537  1270.6929  1270.6194    0.0735     0  K.GLTFDSGGYNIK.T   (Ions score 46)
   375 - 388     655.8469  1309.6792  1309.6336    0.0455     0  K.FDMGGSAAVLGAAK.A  Oxidation (M)  (Ions score 104)
```

gi|195632542 Cytokinin-O-glucosyltransferase 1



Protein View

```
Match to: gi|195632542 Score: 47
cytokinin-O-glucosyltransferase 1 [Zea mays]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\343NOV15.wiff

Nominal mass (Mr): 54361; Calculated pI value: 5.59
NCBI BLAST search of gi|195632542 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

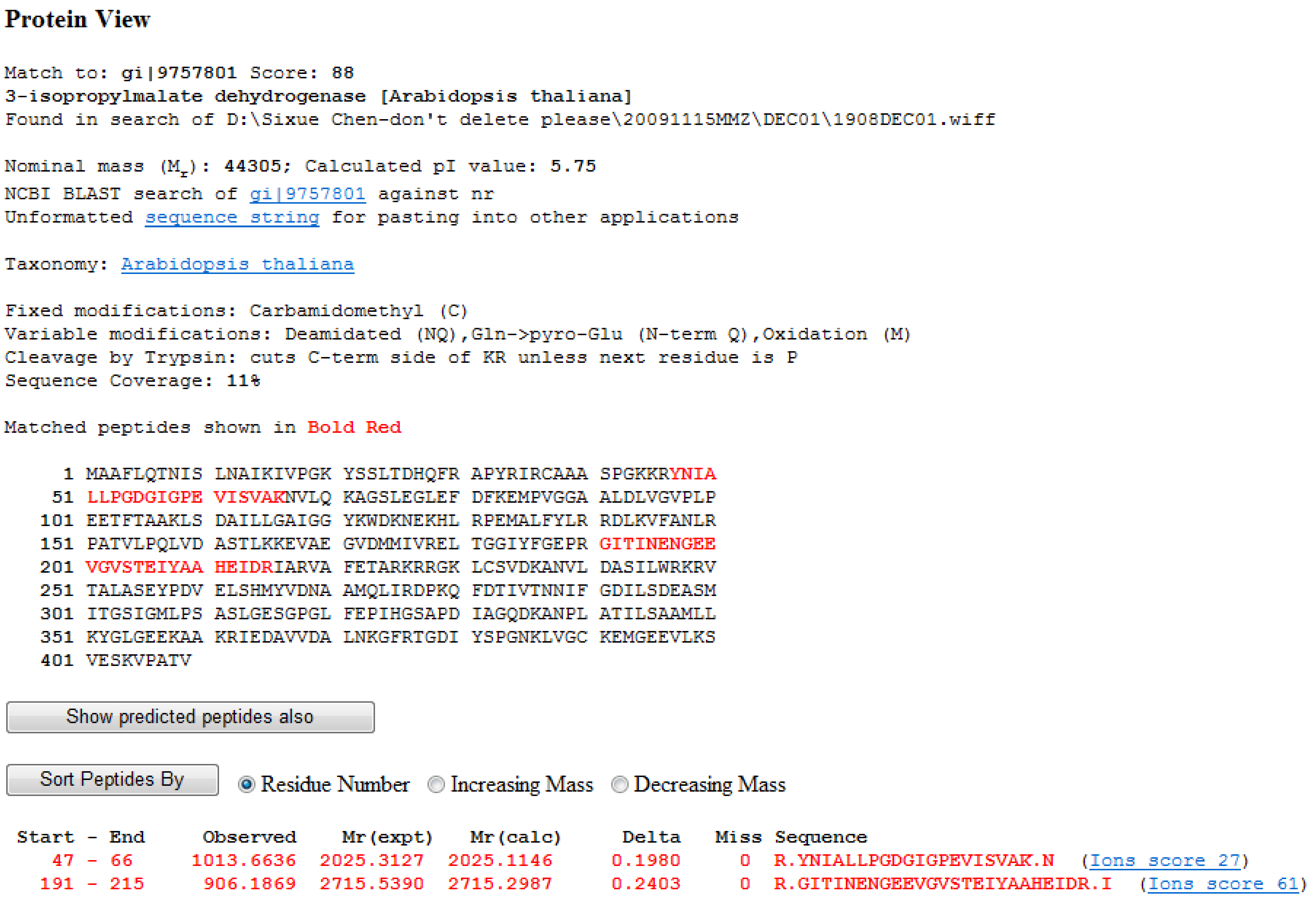
Matched peptides shown in Bold Red

    1 MAAAVDTAAV AGATGRLRVF FLPSFIRGHL IPQTDMACRV AAARPAEVEA
   51 TVVVTPANAA LIAPTVARAA AAGHAVRVLC YPFPDVGLGE GVECLATATA
  101 RDAWRVYRAM EVVQPSHESL LRDHRPDAIV ADVPFWWTTG VAAELGVPRL
  151 TFHPVGIFAL LAMNSLFTIR PDIIGRASSD AAGTVLSVPG LPGKEITIPV
  201 SELPTFLVQD DHLSKAWQRM RACQLTGFGV IVNTFADLEQ PYCEEFSRVE
  251 ARRAYFVGPL GKPSRSTMHR GGSGNADCLS WLSTKPSRSV VFVCFGSWAE
  301 FSATQTRELA LGLEASNQPF LWVVRSNDSS DDQWAPEGWE QRVANRGLVV
  351 HGWAPQLAVL AHPSVGAFVT HCGWNSVLEA ASAGVPVLTW PLVFEQFINE
  401 RLATEVAAFG VRLWDGGRRS ERAEDAEIVP AEAIARAVAG FMEGGEQRDK
  451 LNARAGELAE RARAAVSEDG SSWRDINRLI DDLLQARASG LPQMNSVQLE
  501
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   455 - 463     486.7905   971.5665   971.5148    0.0517     1  R.AGELAERAR.A   (Ions score 47)
   455 - 463     486.8004   971.5862   971.5148    0.0714     1  R.AGELAERAR.A   (Ions score 47)
```

gi|9757801 3-isopropylmalate dehydrogenase



Protein View

```
Match to: gi|9757801 Score: 88
3-isopropylmalate dehydrogenase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1908DEC01.wiff

Nominal mass (Mr): 44305; Calculated pI value: 5.75
NCBI BLAST search of gi|9757801 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

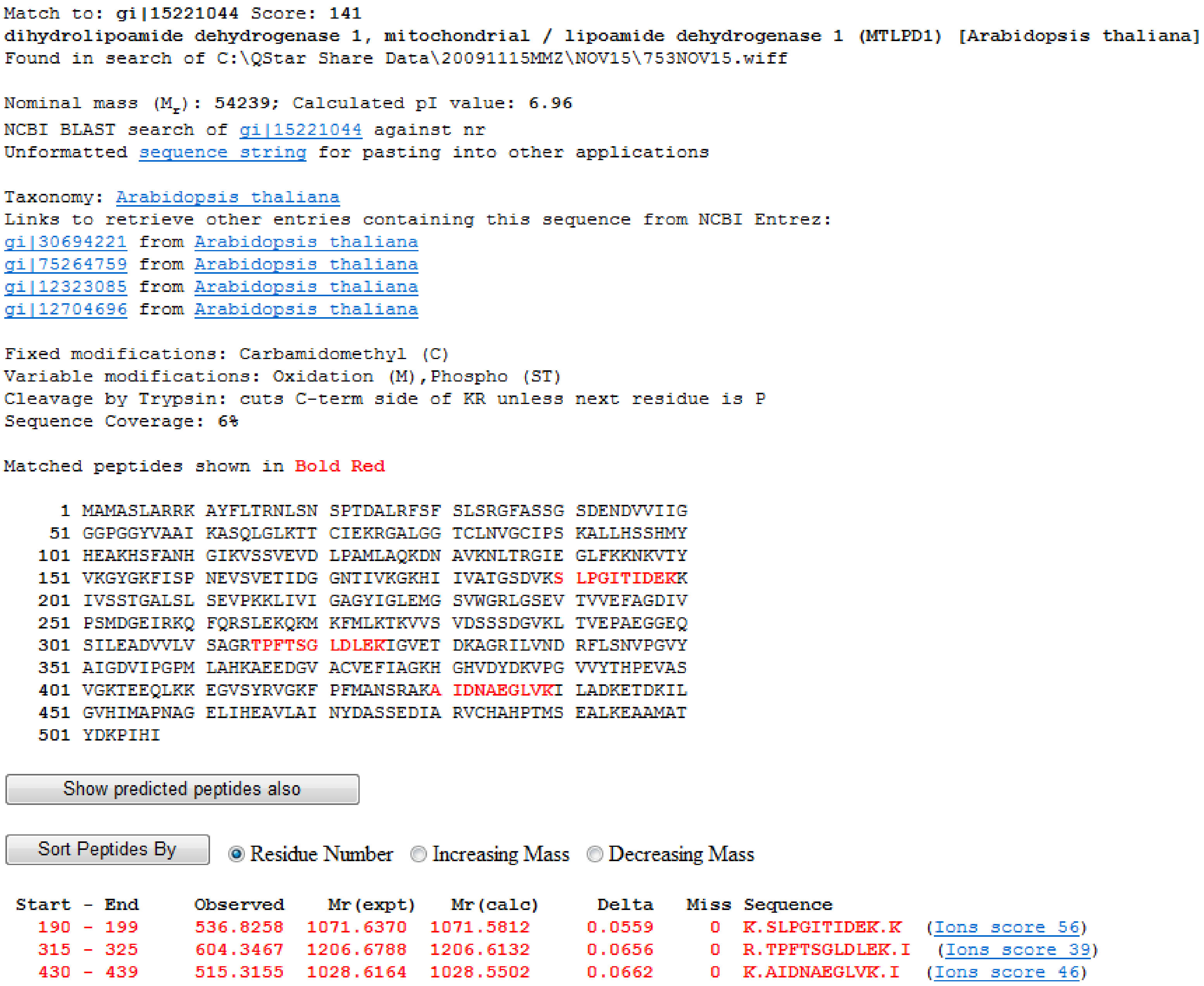
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 11%

Matched peptides shown in Bold Red

     1 MAAFLQTNIS LNAIKIVPGK YSSLTDHQFR APYRIRCAAA SPGKKRYNIA
    51 LLPGDGIGPE VISVAKNVLQ KAGSLEGLEF DFKEMPVGGA ALDLVGVPLP
   101 EETFTAAKLS DAILLGAIGG YKWDKNEKHL RPEMALFYLR RDLKVFANLR
   151 PATVLPQLVD ASTLKKEVAE GVDMMIVREL TGGIYFGEPR GITINENGEE
   201 VGVSTEIYAA HEIDRIARVA FETARKRRGK LCSVDKANVL DASILWRKRV
   251 TALASEYPDV ELSHMYVDNA AMQLIRDPKQ FDTIVTNNIF GDILSDEASM
   301 ITGSIGMLPS ASLGESGPGL FEPIHGSAPD IAGQDKANPL ATILSAAMLL
   351 KYGLGEEKAA KRIEDAVVDA LNKGFRTGDI YSPGNKLVGC KEMGEEVLKS
   401 VESKVPATV
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
    47 - 66     1013.6636  2025.3127  2025.1146    0.1980     0  R.YNIALLPGDGIGPEVISVAK.N  (Ions score 27)
   191 - 215     906.1869  2715.5390  2715.2987    0.2403     0  R.GITINENGEEVGVSTEIYAAHEIDR.I  (Ions score 61)
```

gi|15221044 Dihydrolipoamide dehydrogenase 1, mitochondrial



Match to: gi|15221044 Score: 141
dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\753NOV15.wiff

Nominal mass (M_r): 54239; Calculated pI value: 6.96
NCBI BLAST search of gi|15221044 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|30694221 from Arabidopsis thaliana
gi|75264759 from Arabidopsis thaliana
gi|12323085 from Arabidopsis thaliana
gi|12704696 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

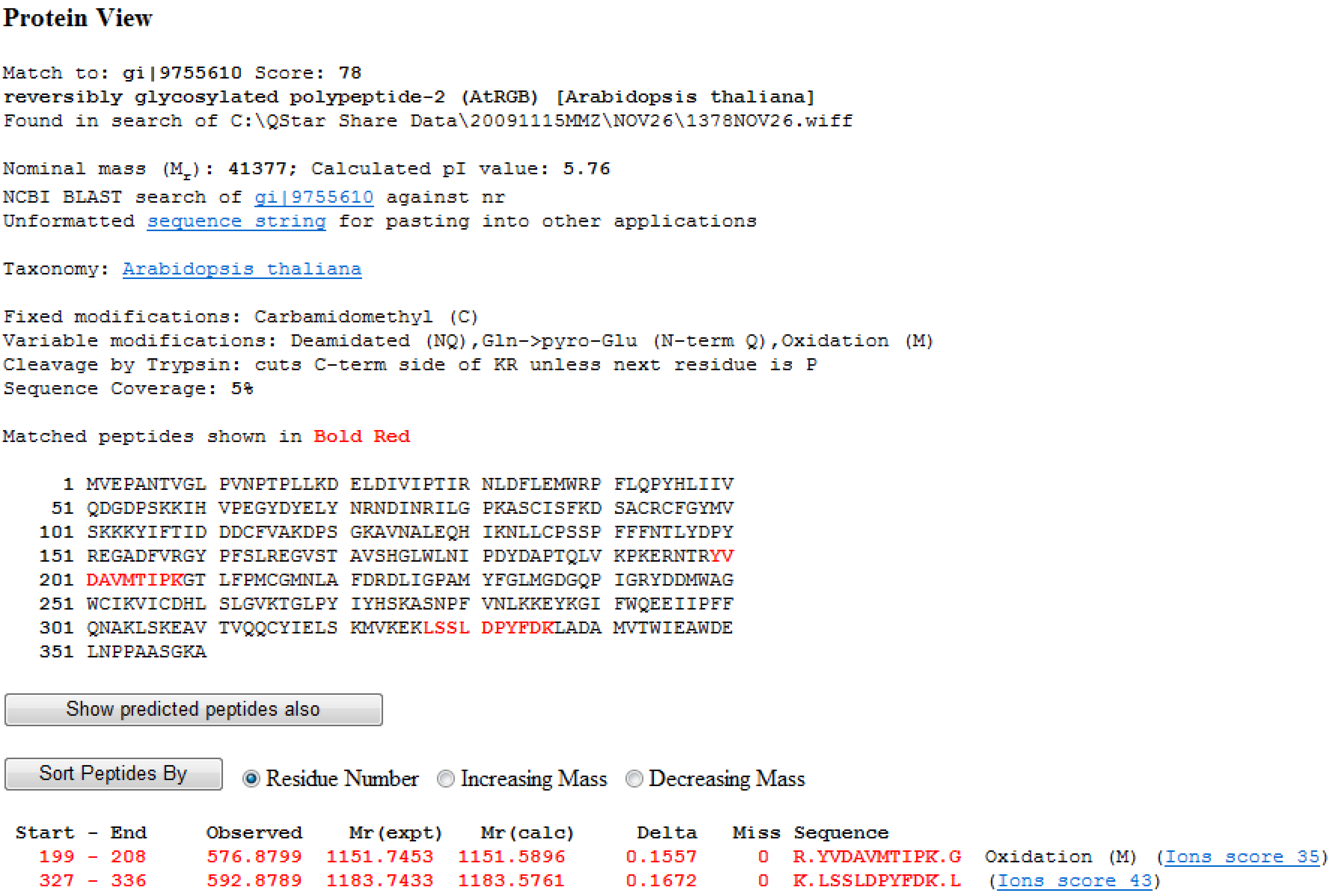
Matched peptides shown in **Bold Red**

```
  1 MAMASLARRK AYFLTRNLSN SPTDALRFSF SLSRGFASSG SDENDVVIIG
 51 GGPGGYVAAI KASQLGLKTT CIEKRGALGG TCLNVGCIPS KALLHSSHMY
101 HEAKHSFANH GIKVSSVEVD LPAMLAQKDN AVKNLTRGIE GLFKKNKVTY
151 VKGYGKFISP NEVSVETIDG GNTIVKGKHI IVATGSDVKS LPGITIDEKK
201 IVSSTGALSL SEVPKKLIVI GAGYIGLEMG SVWGRLGSEV TVVEFAGDIV
251 PSMDGEIRKQ FQRSLEKQKM KFMLKTKVVS VDSSSDGVKL TVEPAEGGEQ
301 SILEADVVLV SAGRTPFTSG LDLEKIGVET DKAGRILVND RFLSNVPGVY
351 AIGDVIPGPM LAHKAEEDGV ACVEFIAGKH GHVDYDKVPG VVYTHPEVAS
401 VGKTEEQLKK EGVSYRVGKF PFMANSRAKA IDNAEGLVKI LADKETDKIL
451 GVHIMAPNAG ELIHEAVLAI NYDASSEDIA RVCHAHPTMS EALKEAAMAT
501 YDKPIHI
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   190 - 199     536.8258  1071.6370  1071.5812    0.0559     0  K.SLPGITIDEK.K   (Ions score 56)
   315 - 325     604.3467  1206.6788  1206.6132    0.0656     0  R.TPFTSGLDLEK.I   (Ions score 39)
   430 - 439     515.3155  1028.6164  1028.5502    0.0662     0  K.AIDNAEGLVK.I   (Ions score 46)
```

gi|9755610 Reversibly glycosylated polypeptide-2 (AtRGB)



Protein View

Match to: **gi|9755610** Score: **78**

reversibly glycosylated polypeptide-2 (AtRGB) [Arabidopsis thaliana]

Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1378NOV26.wiff

Nominal mass (M_r): **41377**; Calculated pI value: **5.76**

NCBI BLAST search of gi|9755610 against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 5%

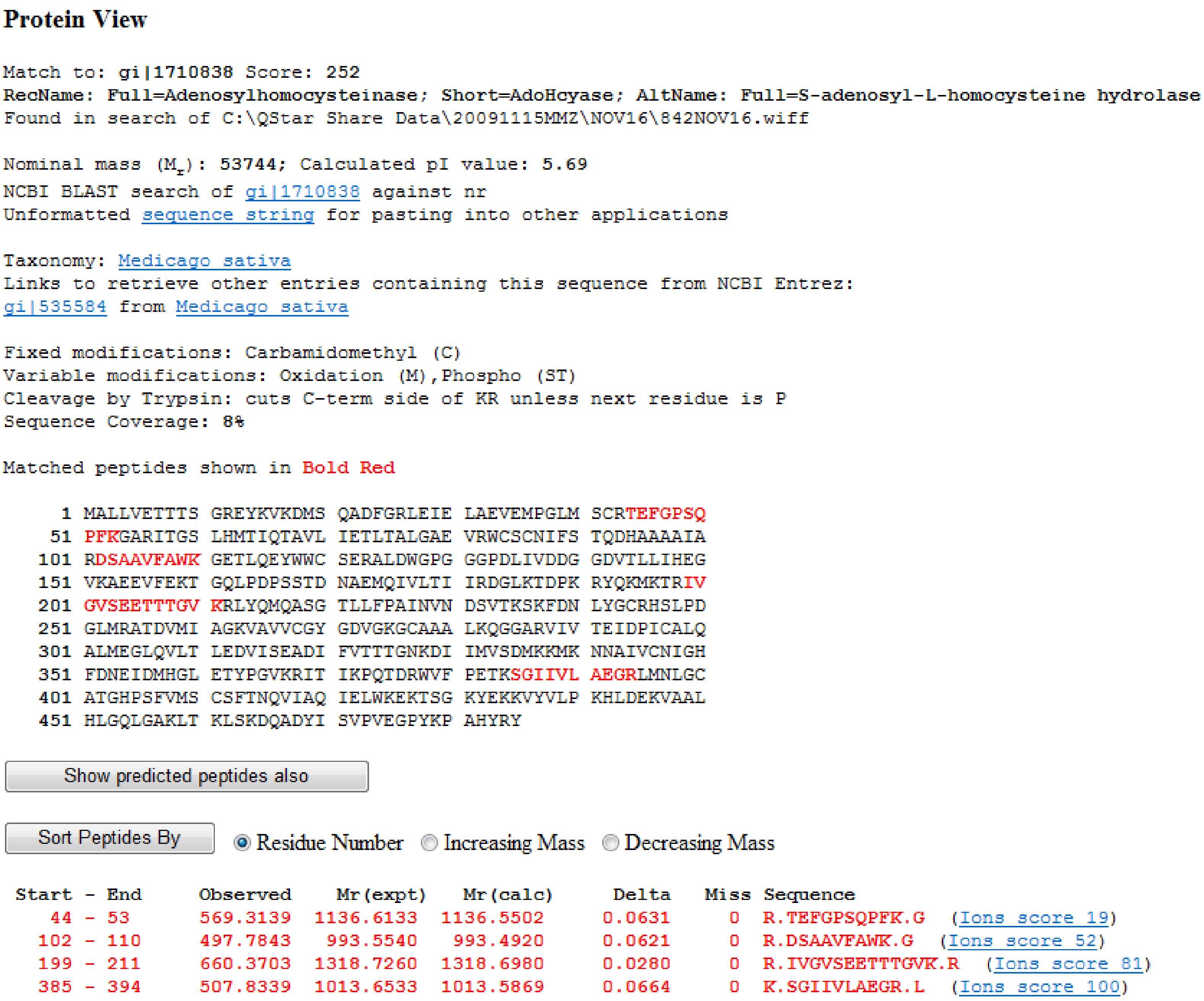
Matched peptides shown in **Bold Red**

```
  1 MVEPANTVGL PVNPTPLLKD ELDIVIPTIR NLDFLEMWRP FLQPYHLIIV
 51 QDGDPSKKIH VPEGYDYELY NRNDINRILG PKASCISFKD SACRCFGYMV
101 SKKKYIFTID DDCFVAKDPS GKAVNALEQH IKNLLCPSSP FFFNTLYDPY
151 REGADFVRGY PFSLREGVST AVSHGLWLNI PDYDAPTQLV KPKERNTRYV
201 DAVMTIPKGT LFPMCGMNLA FDRDLIGPAM YFGLMGDGQP IGRYDDMWAG
251 WCIKVICDHL SLGVKTGLPY IYHSKASNPF VNLKKEYKGI FWQEEIIPFF
301 QNAKLSKEAV TVQQCYIELS KMVKEKLSSL DPYFDKLADA MVTWIEAWDE
351 LNPPAASGKA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   199 - 208     576.8799  1151.7453  1151.5896    0.1557      0  R.YVDAVMTIPK.G  Oxidation (M)  (Ions score 35)
   327 - 336     592.8789  1183.7433  1183.5761    0.1672      0  K.LSSLDPYFDK.L  (Ions score 43)
```

gi|1710838 S-adenosyl-L-homocysteine hydrolase



Protein View

```
Match to: gi|1710838 Score: 252
RecName: Full=Adenosylhomocysteinase; Short=AdoHcyase; AltName: Full=S-adenosyl-L-homocysteine hydrolase
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\842NOV16.wiff

Nominal mass (Mr): 53744; Calculated pI value: 5.69
NCBI BLAST search of gi|1710838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Medicago sativa
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|535584 from Medicago sativa

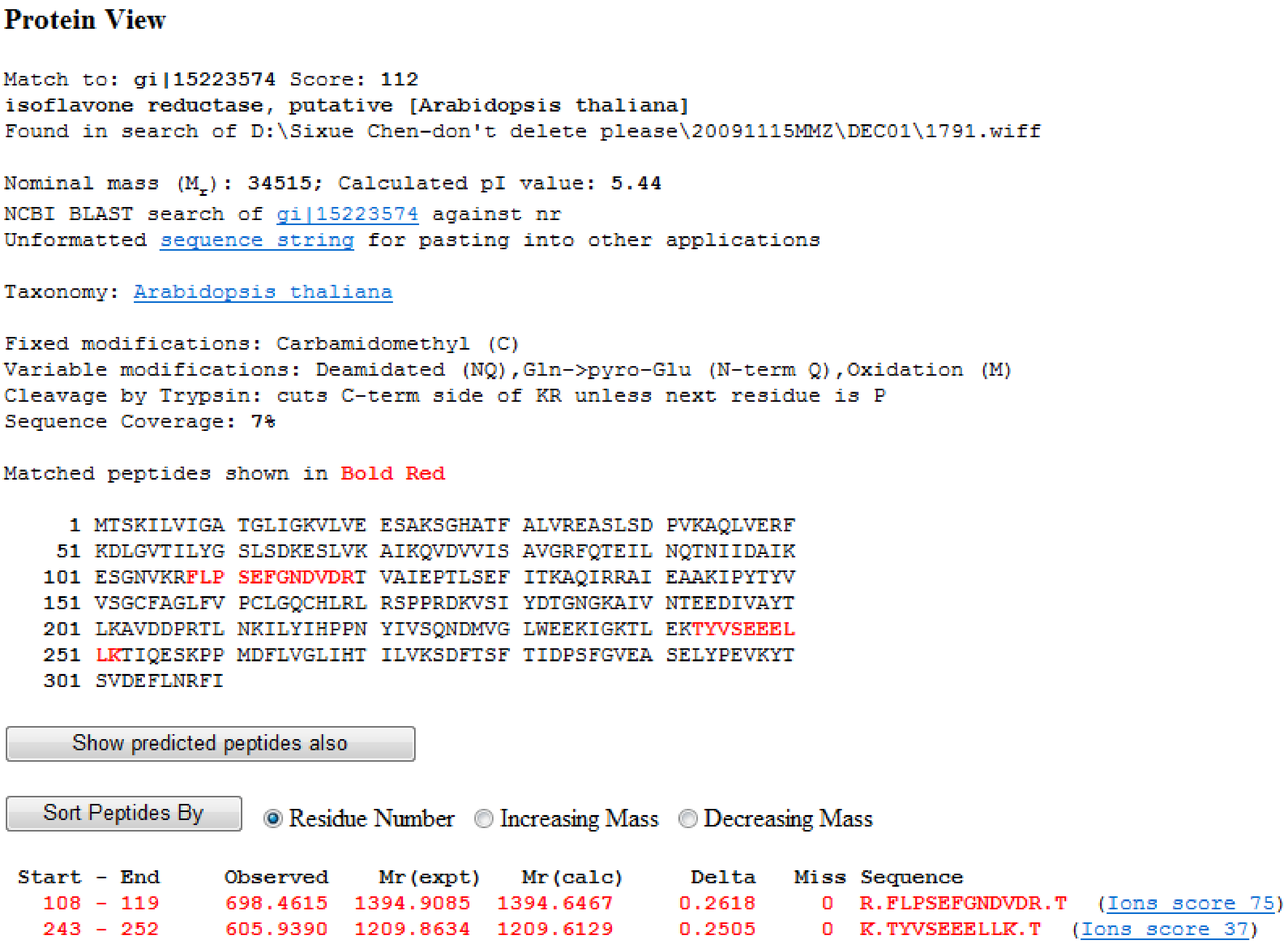
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in Bold Red

     1 MALLVETTTS GREYKVKDMS QADFGRLEIE LAEVEMPGLM SCRTEFGPSQ
    51 PFKGARITGS LHMTIQTAVL IETLTALGAE VRWCSCNIFS TQDHAAAAIA
   101 RDSAAVFAWK GETLQEYWWC SERALDWGPG GGPDLIVDDG GDVTLLIHEG
   151 VKAEEVFEKT GQLPDPSSTD NAEMQIVLTI IRDGLKTDPK RYQKMKTRIV
   201 GVSEETTTGV KRLYQMQASG TLLFPAINVN DSVTKSKFDN LYGCRHSLPD
   251 GLMRATDVMI AGKVAVVCGY GDVGKGCAAA LKQGGARVIV TEIDPICALQ
   301 ALMEGLQVLT LEDVISEADI FVTTTGNKDI IMVSDMKKMK NNAIVCNIGH
   351 FDNEIDMHGL ETYPGVKRIT IKPQTDRWVF PETKSGIIVL AEGRLMNLGC
   401 ATGHPSFVMS CSFTNQVIAQ IELWKEKTSG KYEKKVYVLP KHLDEKVAAL
   451 HLGQLGAKLT KLSKDQADYI SVPVEGPYKP AHYRY
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   44 - 53      569.3139  1136.6133  1136.5502    0.0631     0  R.TEFGPSQPFK.G  (Ions score 19)
  102 - 110     497.7843   993.5540   993.4920    0.0621     0  R.DSAAVFAWK.G  (Ions score 52)
  199 - 211     660.3703  1318.7260  1318.6980    0.0280     0  R.IVGVSEETTTGVK.R  (Ions score 81)
  385 - 394     507.8339  1013.6533  1013.5869    0.0664     0  K.SGIIVLAEGR.L  (Ions score 100)
```

gi|15223574 Isoflavone reductase, putative



Protein View

Match to: gi|15223574 Score: 112
isoflavone reductase, putative [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (M_r): 34515; Calculated pI value: 5.44
NCBI BLAST search of gi|15223574 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

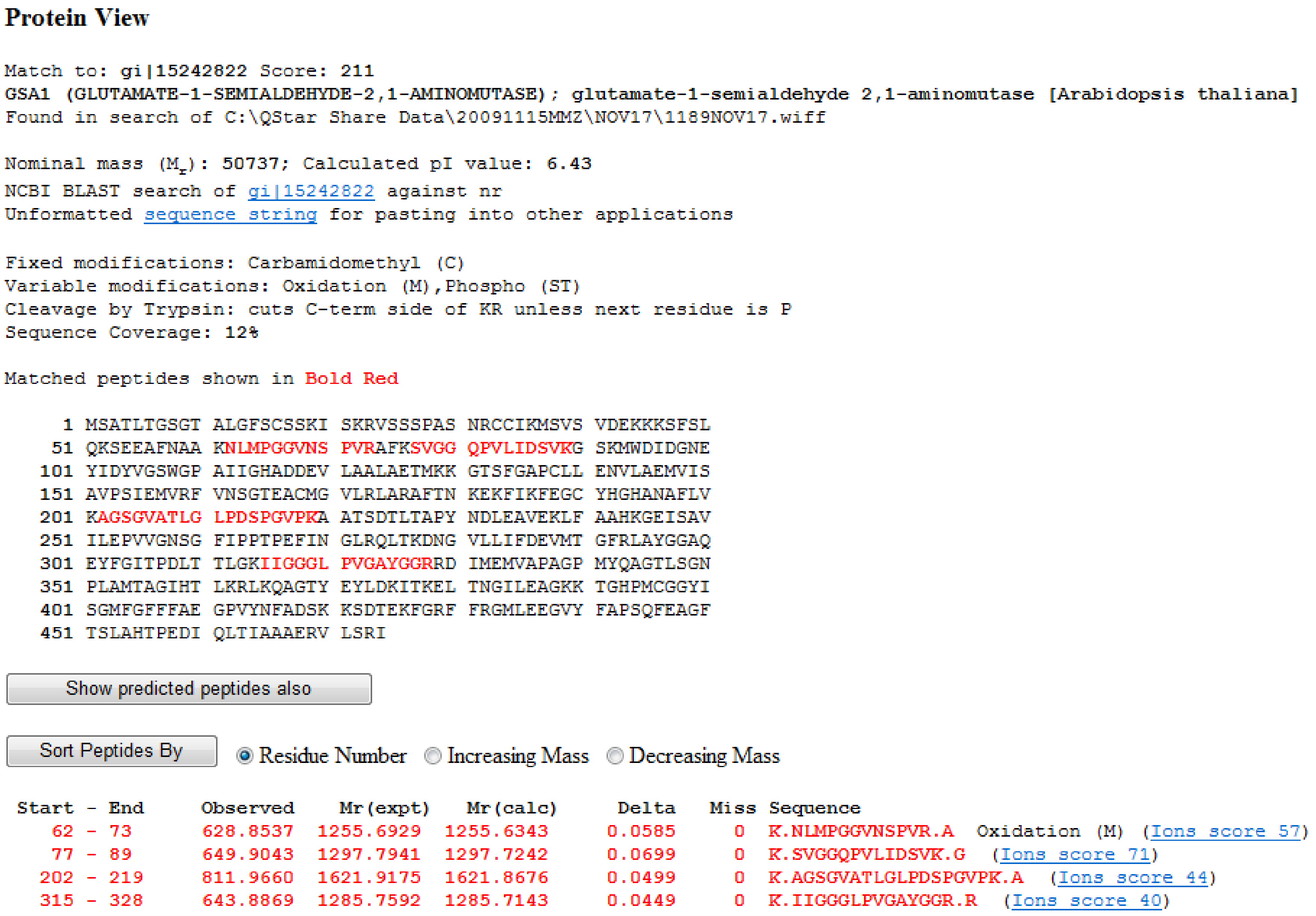
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

```
  1 MTSKILVIGA TGLIGKVLVE ESAKSGHATF ALVREASLSD PVKAQLVERF
 51 KDLGVTILYG SLSDKESLVK AIKQVDVVIS AVGRFQTEIL NQTNIIDAIK
101 ESGNVKRFLP SEFGNDVDRT VAIEPTLSEF ITKAQIRRAI EAAKIPYTYV
151 VSGCFAGLFV PCLGQCHLRL RSPPRDKVSI YDTGNGKAIV NTEEDIVAYT
201 LKAVDDPRTL NKILYIHPPN YIVSQNDMVG LWEEKIGKTL EKTYVSEEEL
251 LKTIQESKPP MDFLVGLIHT ILVKSDFTSF TIDPSFGVEA SELYPEVKYT
301 SVDEFLNRFI
```

```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
  108 - 119     698.4615   1394.9085   1394.6467    0.2618     0   R.FLPSEFGNDVDR.T   (Ions score 75)
  243 - 252     605.9390   1209.8634   1209.6129    0.2505     0   K.TYVSEEELLK.T   (Ions score 37)
```

gi|15242822 Glutamate-1-semialdehyde-2,1-aminomutase (GSA1)



Protein View

```
Match to: gi|15242822 Score: 211
GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (Mr): 50737; Calculated pI value: 6.43
NCBI BLAST search of gi|15242822 against nr
Unformatted sequence string for pasting into other applications

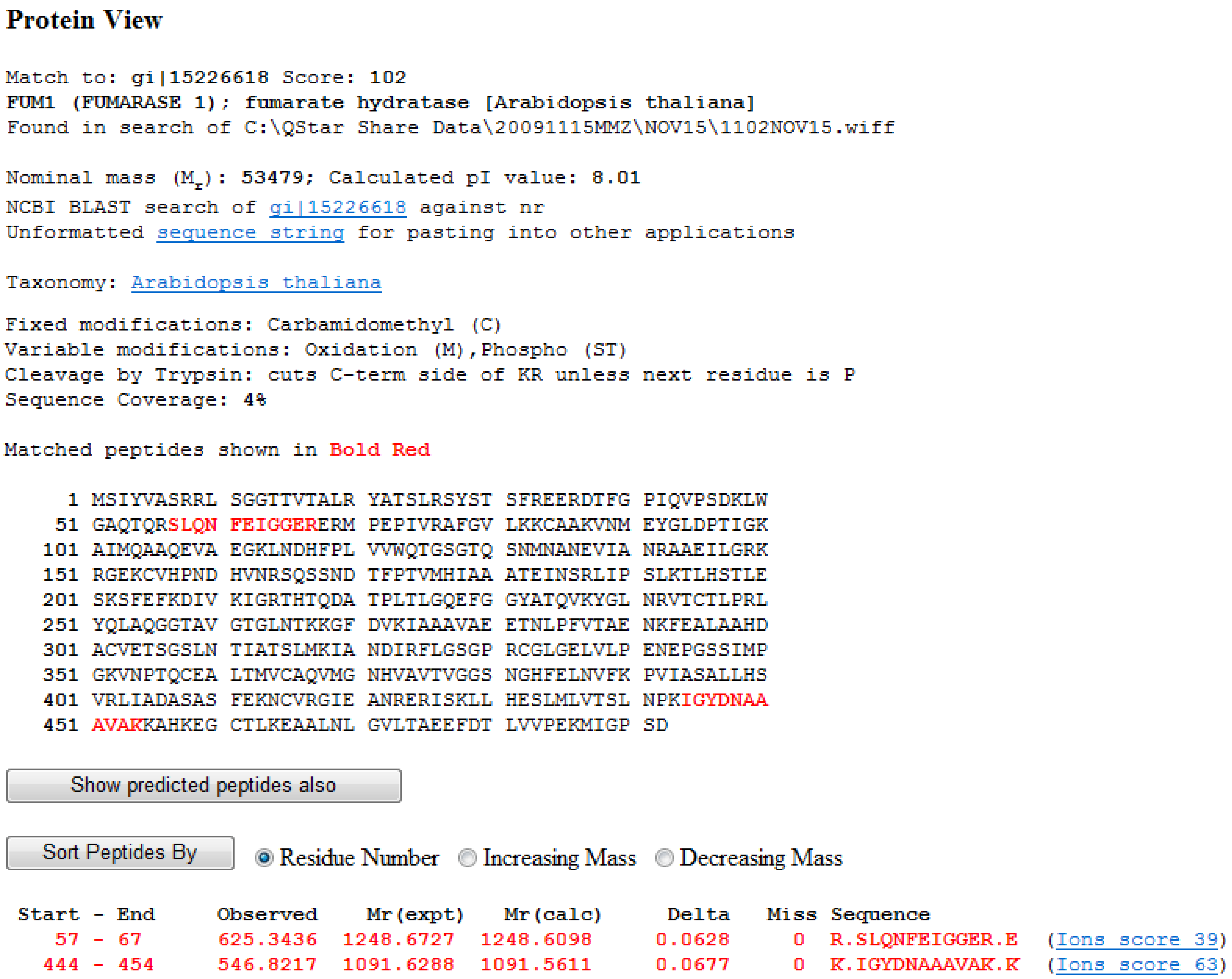
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%

Matched peptides shown in Bold Red

     1 MSATLTGSGT ALGFSCSSKI SKRVSSSPAS NRCCIKMSVS VDEKKKSFSL
    51 QKSEEAFNAA KNLMPGGVNS PVRAFKSVGG QPVLIDSVKG SKMWDIDGNE
   101 YIDYVGSWGP AIIGHADDEV LAALAETMKK GTSFGAPCLL ENVLAEMVIS
   151 AVPSIEMVRF VNSGTEACMG VLRLARAFTN KEKFIKFEGC YHGHANAFLV
   201 KAGSGVATLG LPDSPGVPKA ATSDTLTAPY NDLEAVEKLF AAHKGEISAV
   251 ILEPVVGNSG FIPPTPEFIN GLRQLTKDNG VLLIFDEVMT GFRLAYGGAQ
   301 EYFGITPDLT TLGKIIGGGL PVGAYGGRRD IMEMVAPAGP MYQAGTLSGN
   351 PLAMTAGIHT LKRLKQAGTY EYLDKITKEL TNGILEAGKK TGHPMCGGYI
   401 SGMFGFFFAE GPVYNFADSK KSDTEKFGRF FRGMLEEGVY FAPSQFEAGF
   451 TSLAHTPEDI QLTIAAAERV LSRI
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   62 - 73      628.8537  1255.6929  1255.6343    0.0585     0  K.NLMPGGVNSPVR.A  Oxidation (M)  (Ions score 57)
   77 - 89      649.9043  1297.7941  1297.7242    0.0699     0  K.SVGGQPVLIDSVK.G  (Ions score 71)
  202 - 219     811.9660  1621.9175  1621.8676    0.0499     0  K.AGSGVATLGLPDSPGVPK.A  (Ions score 44)
  315 - 328     643.8869  1285.7592  1285.7143    0.0449     0  K.IIGGGLPVGAYGGR.R  (Ions score 40)
```

gi|15226618 Fumarate hydratase (FUM1)



Match to: gi|15226618 Score: 102
FUM1 (FUMARASE 1); fumarate hydratase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (M_r): 53479; Calculated pI value: 8.01
NCBI BLAST search of gi|15226618 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%

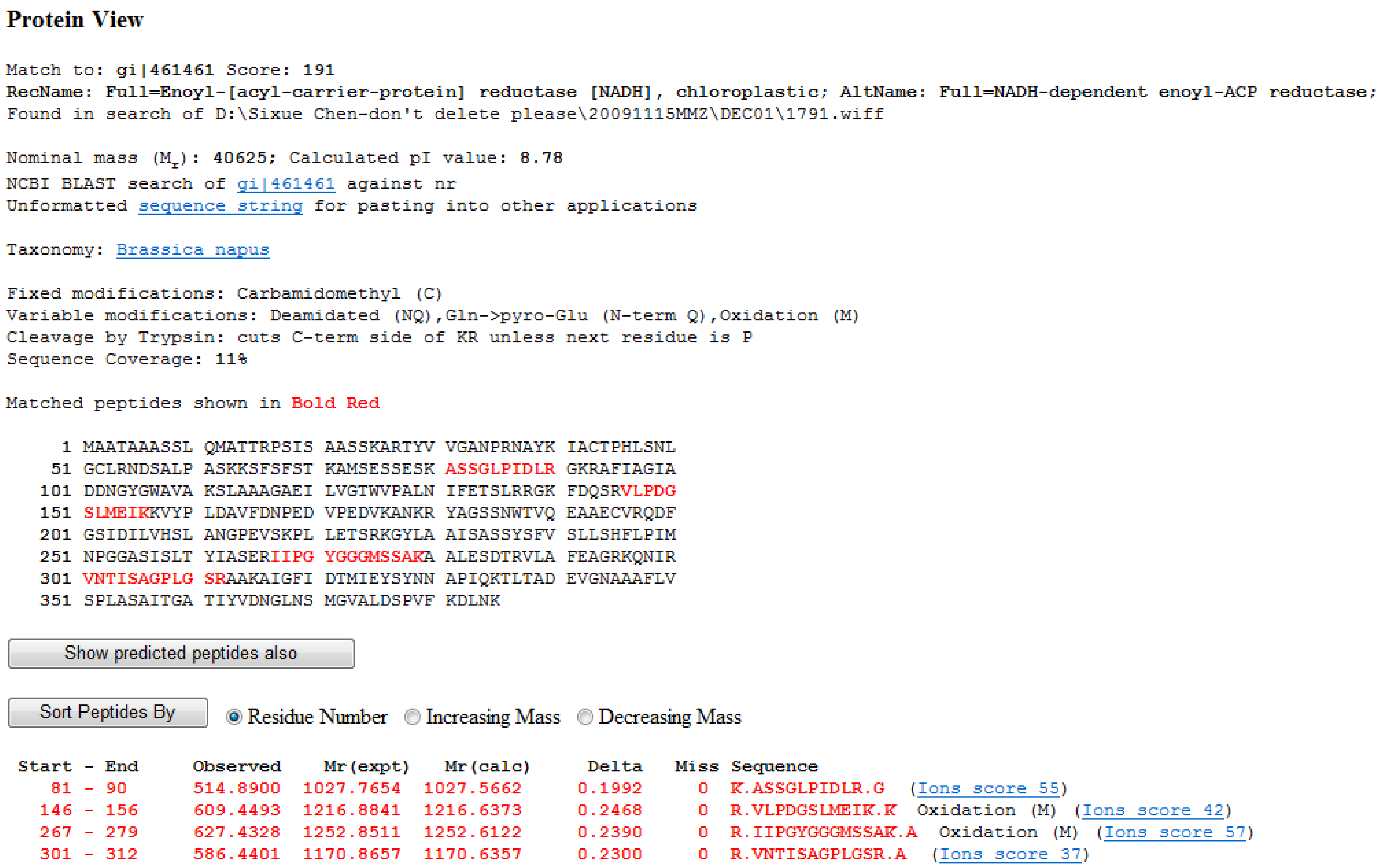
Matched peptides shown in **Bold Red**

```
  1 MSIYVASRRL SGGTTVTALR YATSLRSYST SFREERDTFG PIQVPSDKLW
 51 GAQTQRSLQN FEIGGERERM PEPIVRAFGV LKKCAAKVNM EYGLDPTIGK
101 AIMQAAQEVA EGKLNDHFPL VVWQTGSGTQ SNMNANEVIA NRAAEILGRK
151 RGEKCVHPND HVNRSQSSND TFPTVMHIAA ATEINSRLIP SLKTLHSTLE
201 SKSFEFKDIV KIGRTHTQDA TPLTLGQEFG GYATQVKYGL NRVTCTLPRL
251 YQLAQGGTAV GTGLNTKKGF DVKIAAAVAE ETNLPFVTAE NKFEALAAHD
301 ACVETSGSLN TIATSLMKIA NDIRFLGSGP RCGLGELVLP ENEPGSSIMP
351 GKVNPTQCEA LTMVCAQVMG NHVAVTVGGS NGHFELNVFK PVIASALLHS
401 VRLIADASAS FEKNCVRGIE ANRERISKLL HESLMLVTSL NPKIGYDNAA
451 AVAKKAHKEG CTLKEAALNL GVLTAEEFDT LVVPEKMIGP SD
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   57 - 67       625.3436  1248.6727  1248.6098    0.0628     0  R.SLQNFEIGGER.E   (Ions score 39)
  444 - 454      546.8217  1091.6288  1091.5611    0.0677     0  K.IGYDNAAAVAK.K   (Ions score 63)
```

gi|461461 Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic



Protein View

Match to: **gi|461461** Score: **191**
RecName: Full=Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic; AltName: Full=NADH-dependent enoyl-ACP reductase;
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1791.wiff

Nominal mass (M_r): **40625**; Calculated pI value: **8.78**
NCBI BLAST search of gi|461461 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

1 MAATAAASSL QMATTRPSIS AASSKARTYV VGANPRNAYK IACTPHLSNL
51 GCLRNDSALP ASKKSFSFST KAMSESSESK **ASSGLPIDLR** GKRAFIAGIA
101 DDNGYGWAVA KSLAAAGAEI LVGTWVPALN IFETSLRRGK FDQSR**VLPDG**
151 **SLMEIK**KVYP LDAVFDNPED VPEDVKANKR YAGSSNWTVQ EAAECVRQDF
201 GSIDILVHSL ANGPEVSKPL LETSRKGYLA AISASSYSFV SLLSHFLPIM
251 NPGGASISLT YIASER**IIPG YGGGMSSAK**A ALESDTRVLA FEAGRKQNIR
301 **VNTISAGPLG SR**AAKAIGFI DTMIEYSYNN APIQKTLTAD EVGNAAAFLV
351 SPLASAITGA TIYVDNGLNS MGVALDSPVF KDLNK

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
81 - 90	514.8900	1027.7654	1027.5662	0.1992	0	K.ASSGLPIDLR.G (Ions score 55)
146 - 156	609.4493	1216.8841	1216.6373	0.2468	0	R.VLPDGSLMEIK.K Oxidation (M) (Ions score 42)
267 - 279	627.4328	1252.8511	1252.6122	0.2390	0	R.IIPGYGGGMSSAK.A Oxidation (M) (Ions score 57)
301 - 312	586.4401	1170.8657	1170.6357	0.2300	0	R.VNTISAGPLGSR.A (Ions score 37)

gi|5881963 Dihydrolipoamide S-acetyltransferase

Protein View

Match to: gi|5881963 Score: 64
dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1001NOV26.wiff

Nominal mass (M_r): 50106; Calculated pI value: 8.33
NCBI BLAST search of gi|5881963 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

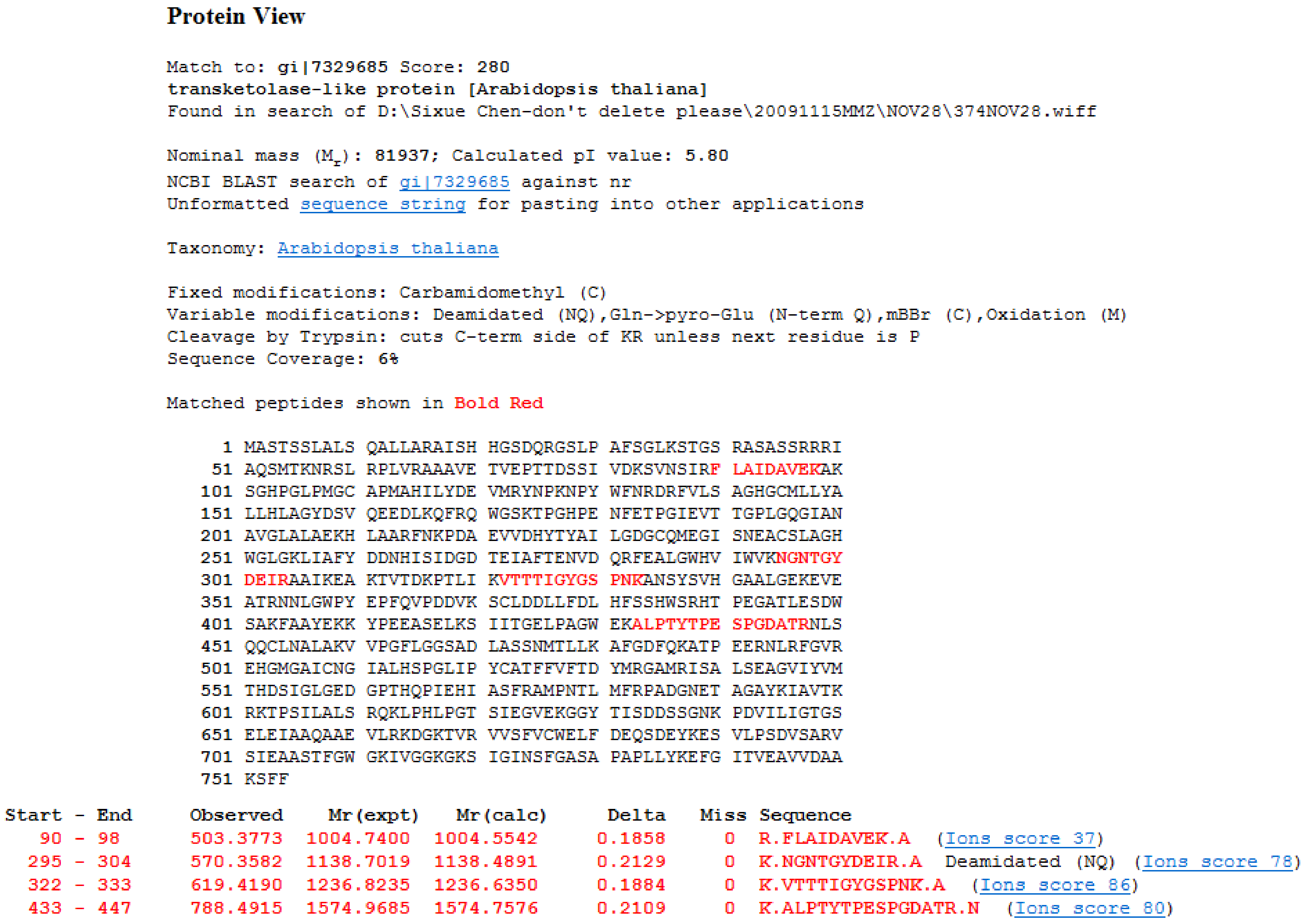
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

```
  1 MAVSSSSFLS TASLTNSKSN ISFASSVSPS LRSVVFRSTT PATSHRRSMT
 51 VRSKIREIFM PALSSTMTEG KIVSWIKTEG EKLAKGESVV VVESDKADMD
101 VETFYDGYLA AIVVGEGETA PVGAAIGLLA ETEAEIEEAK SKAASKSSSS
151 VAEAVVPSPP PVTSSPAPAI AQPAPVTAVS DGPRKTVATP YAKKLAKQHK
201 VDIESVAGTG PFGRITASDV ETAAGIAPSK SSIAPPPPPP PPVTAKATTT
251 NLPPLLPDSS IVPFTAMQSA VSKNMIESLS VPTFRVGYPV NTDALDALYE
301 KVKPKGVTMT ALLAKAAGMA LAQHPVVNAS CKDGKSFSYN SSINIAVAVA
351 INGGLITPVL QDADKLDLYL LSQKWKELVG KARSKQLQPH EYNSGTFTLS
401 NLGMFGVDRF DAILPPGQGA IMAVGASKPT VVADKDGFFS VKNTMLVNVT
451 ADHRIVYGAD LAAFLQTFAK IIENPDSLTL
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
   57 - 71       837.4634  1672.9122  1672.7688   0.1434     0  R.EIFMPALSSTMTEGK.I  2 Oxidation (M) (Ions score 21)
  286 - 301      884.5085  1767.0025  1766.8727   0.1298     0  R.VGYPVNTDALDALYEK.V  (Ions score 43)
```

gi|7329685 Transketolase-like protein



Protein View

```
Match to: gi|7329685 Score: 280
transketolase-like protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\NOV28\374NOV28.wiff

Nominal mass (Mr): 81937; Calculated pI value: 5.80
NCBI BLAST search of gi|7329685 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

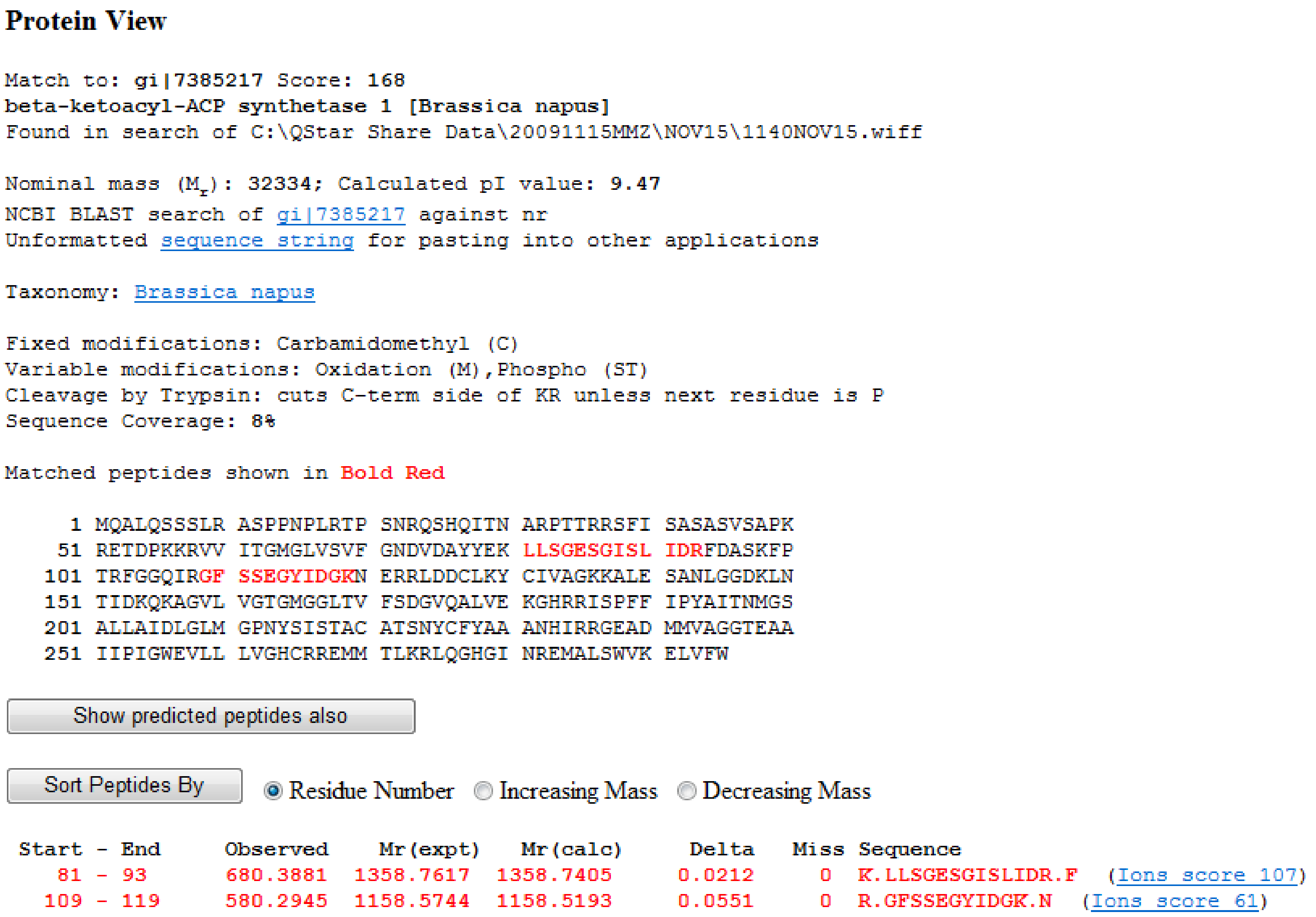
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),mBBr (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in Bold Red

     1 MASTSSLALS QALLARAISH HGSDQRGSLP AFSGLKSTGS RASASSRRRI
    51 AQSMTKNRSL RPLVRAAAVE TVEPTTDSSI VDKSVNSIRF LAIDAVEKAK
   101 SGHPGLPMGC APMAHILYDE VMRYNPKNPY WFNRDRFVLS AGHGCMLLYA
   151 LLHLAGYDSV QEEDLKQFRQ WGSKTPGHPE NFETPGIEVT TGPLGQGIAN
   201 AVGLALAEKH LAARFNKPDA EVVDHYTYAI LGDGCQMEGI SNEACSLAGH
   251 WGLGKLIAFY DDNHISIDGD TEIAFTENVD QRFEALGWHV IWVKNGNTGY
   301 DEIRAAIKEA KTVTDKPTLI KVTTTIGYGS PNKANSYSVH GAALGEKEVE
   351 ATRNNLGWPY EPFQVPDDVK SCLDDLLFDL HFSSHWSRHT PEGATLESDW
   401 SAKFAAYEKK YPEEASELKS IITGELPAGW EKALPTYTPE SPGDATRNLS
   451 QQCLNALAKV VPGFLGGSAD LASSNMTLLK AFGDFQKATP EERNLRFGVR
   501 EHGMGAICNG IALHSPGLIP YCATFFVFTD YMRGAMRISA LSEAGVIYVM
   551 THDSIGLGED GPTHQPIEHI ASFRAMPNTL MFRPADGNET AGAYKIAVTK
   601 RKTPSILALS RQKLPHLPGT SIEGVEKGGY TISDDSSGNK PDVILIGTGS
   651 ELEIAAQAAE VLRKDGKTVR VVSFVCWELF DEQSDEYKES VLPSDVSARV
   701 SIEAASTFGW GKIVGGKGKS IGINSFGASA PAPLLYKEFG ITVEAVVDAA
   751 KSFF

Start - End     Observed    Mr(expt)   Mr(calc)      Delta   Miss  Sequence
   90 -  98    503.3773   1004.7400  1004.5542     0.1858     0  R.FLAIDAVEK.A  (Ions score 37)
  295 - 304    570.3582   1138.7019  1138.4891     0.2129     0  K.NGNTGYDEIR.A  Deamidated (NQ)  (Ions score 78)
  322 - 333    619.4190   1236.8235  1236.6350     0.1884     0  K.VTTTIGYGSPNK.A  (Ions score 86)
  433 - 447    788.4915   1574.9685  1574.7576     0.2109     0  K.ALPTYTPESPGDATR.N  (Ions score 80)
```

gi|7385217 Beta-ketoacyl-ACP synthetase 1



Protein View

```
Match to: gi|7385217 Score: 168
beta-ketoacyl-ACP synthetase 1 [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (Mr): 32334; Calculated pI value: 9.47
NCBI BLAST search of gi|7385217 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

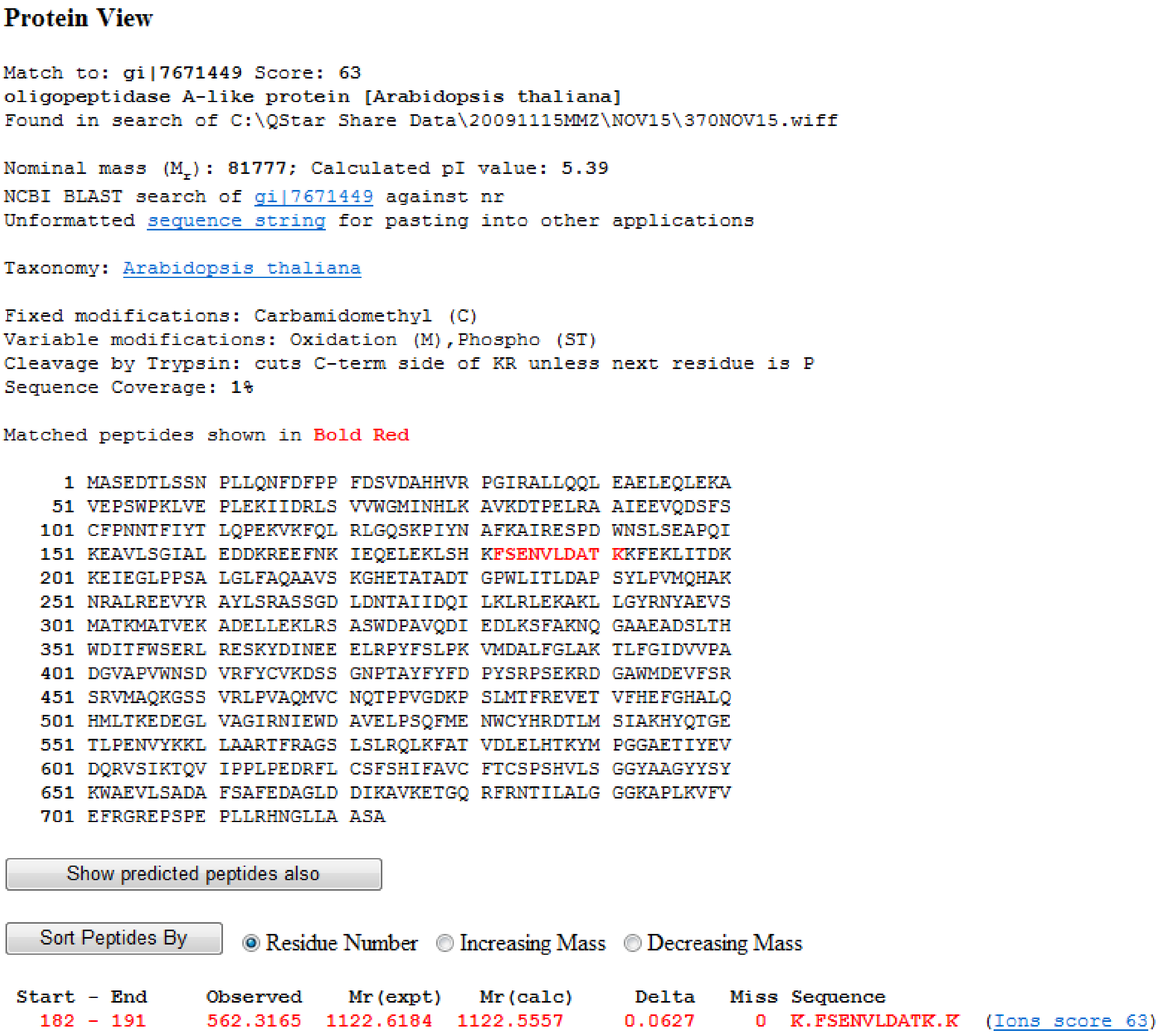
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in Bold Red

     1 MQALQSSSLR ASPPNPLRTP SNRQSHQITN ARPTTRRSFI SASASVSAPK
    51 RETDPKKRVV ITGMGLVSVF GNDVDAYYEK LLSGESGISL IDRFDASKFP
   101 TRFGGQIRGF SSEGYIDGKN ERRLDDCLKY CIVAGKKALE SANLGGDKLN
   151 TIDKQKAGVL VGTGMGGLTV FSDGVQALVE KGHRRISPFF IPYAITNMGS
   201 ALLAIDLGLM GPNYSISTAC ATSNYCFYAA ANHIRRGEAD MMVAGGTEAA
   251 IIPIGWEVLL LVGHCRREMM TLKRLQGHGI NREMALSWVK ELVFW
```

```
 Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
   81 - 93      680.3881   1358.7617   1358.7405    0.0212     0  K.LLSGESGISLIDR.F  (Ions score 107)
  109 - 119     580.2945   1158.5744   1158.5193    0.0551     0  R.GFSSEGYIDGK.N  (Ions score 61)
```

gi|7671449 Oligopeptidase A-like protein



Protein View

```
Match to: gi|7671449 Score: 63
oligopeptidase A-like protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\370NOV15.wiff

Nominal mass (Mr): 81777; Calculated pI value: 5.39
NCBI BLAST search of gi|7671449 against nr
Unformatted sequence string for pasting into other applications

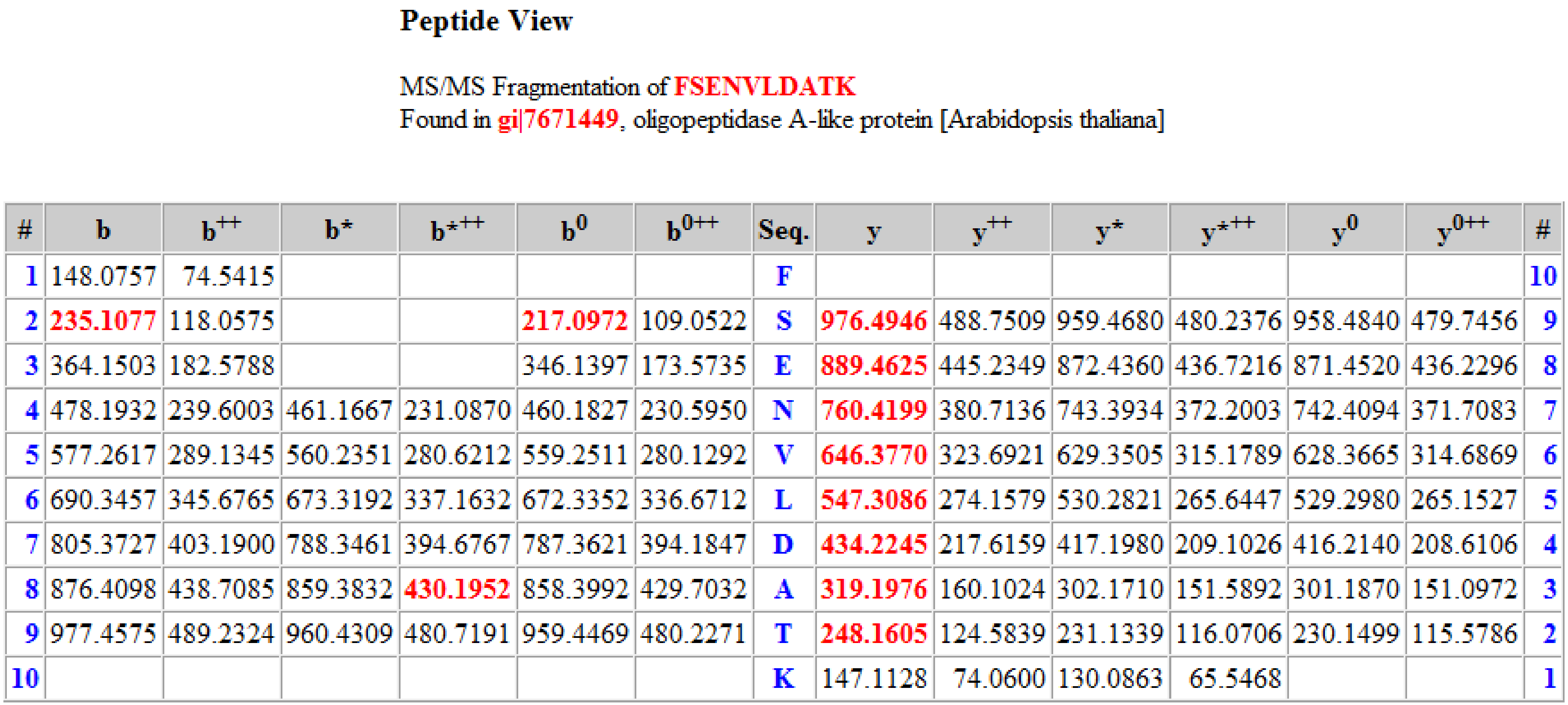
Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

Matched peptides shown in Bold Red

     1 MASEDTLSSN PLLQNFDFPP FDSVDAHHVR PGIRALLQQL EAELEQLEKA
    51 VEPSWPKLVE PLEKIIDRLS VVWGMINHLK AVKDTPELRA AIEEVQDSFS
   101 CFPNNTFIYT LQPEKVKFQL RLGQSKPIYN AFKAIRESPD WNSLSEAPQI
   151 KEAVLSGIAL EDDKREEFNK IEQELEKLSH KFSENVLDAT KKFEKLITDK
   201 KEIEGLPPSA LGLFAQAAVS KGHETATADT GPWLITLDAP SYLPVMQHAK
   251 NRALREEVYR AYLSRASSGD LDNTAIIDQI LKLRLEKAKL LGYRNYAEVS
   301 MATKMATVEK ADELLEKLRS ASWDPAVQDI EDLKSFAKNQ GAAEADSLTH
   351 WDITFWSERL RESKYDINEE ELRPYFSLPK VMDALFGLAK TLFGIDVVPA
   401 DGVAPVWNSD VRFYCVKDSS GNPTAYFYFD PYSRPSEKRD GAWMDEVFSR
   451 SRVMAQKGSS VRLPVAQMVC NQTPPVGDKP SLMTFREVET VFHEFGHALQ
   501 HMLTKEDEGL VAGIRNIEWD AVELPSQFME NWCYHRDTLM SIAKHYQTGE
   551 TLPENVYKKL LAARTFRAGS LSLRQLKFAT VDLELHTKYM PGGAETIYEV
   601 DQRVSIKTQV IPPLPEDRFL CSFSHIFAVC FTCSPSHVLS GGYAAGYYSY
   651 KWAEVLSADA FSAFEDAGLD DIKAVKETGQ RFRNTILALG GGKAPLKVFV
   701 EFRGREPSPE PLLRHNGLLA ASA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   182 - 191     562.3165  1122.6184  1122.5557    0.0627     0  K.FSENVLDATK.K    (Ions score 63)
```

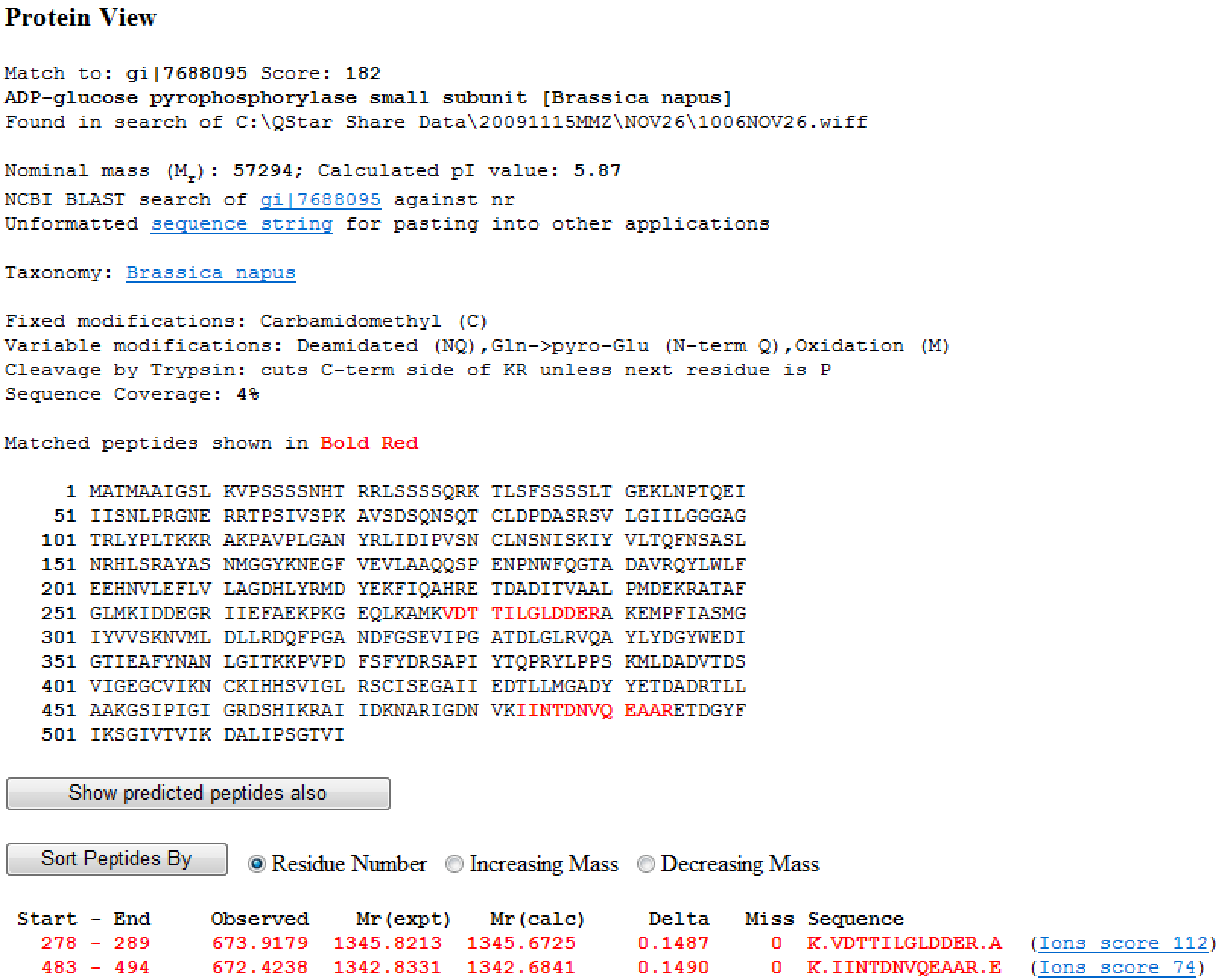


Peptide View

MS/MS Fragmentation of **FSENVLDATK**
Found in **gi|7671449**, oligopeptidase A-like protein [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					**F**							**10**
2	**235.1077**	118.0575			**217.0972**	109.0522	**S**	**976.4946**	488.7509	959.4680	480.2376	958.4840	479.7456	**9**
3	364.1503	182.5788			346.1397	173.5735	**E**	**889.4625**	445.2349	872.4360	436.7216	871.4520	436.2296	**8**
4	478.1932	239.6003	461.1667	231.0870	460.1827	230.5950	**N**	**760.4199**	380.7136	743.3934	372.2003	742.4094	371.7083	**7**
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	**V**	**646.3770**	323.6921	629.3505	315.1789	628.3665	314.6869	**6**
6	690.3457	345.6765	673.3192	337.1632	672.3352	336.6712	**L**	**547.3086**	274.1579	530.2821	265.6447	529.2980	265.1527	**5**
7	805.3727	403.1900	788.3461	394.6767	787.3621	394.1847	**D**	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	**4**
8	876.4098	438.7085	859.3832	**430.1952**	858.3992	429.7032	**A**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
9	977.4575	489.2324	960.4309	480.7191	959.4469	480.2271	**T**	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
10							**K**	147.1128	74.0600	130.0863	65.5468			**1**

gi|7688095 ADP-glucose pyrophosphorylase small subunit



Protein View

Match to: gi|7688095 Score: 182
ADP-glucose pyrophosphorylase small subunit [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1006NOV26.wiff

Nominal mass (M_r): 57294; Calculated pI value: 5.87
NCBI BLAST search of gi|7688095 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

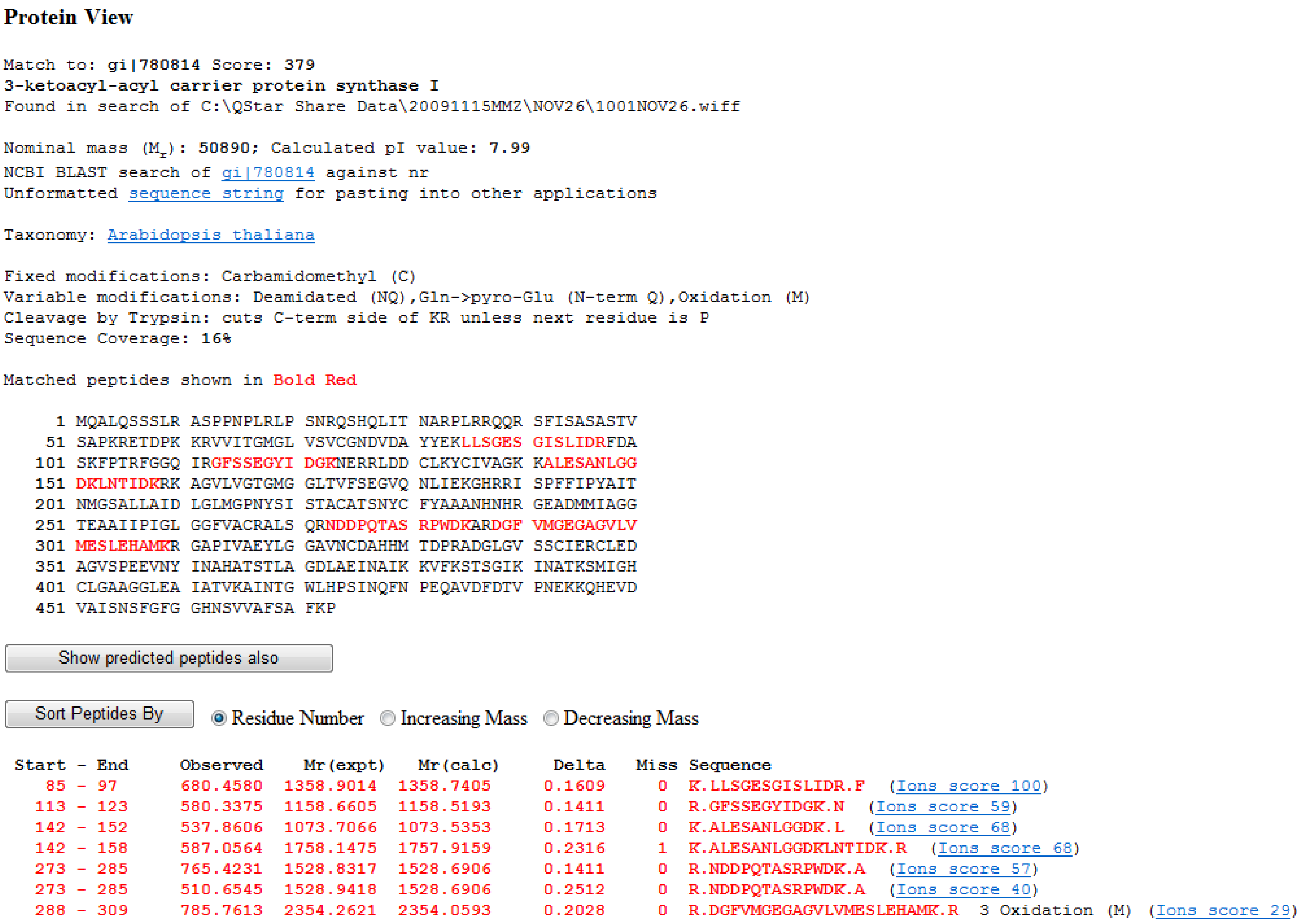
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%

Matched peptides shown in **Bold Red**

```
  1 MATMAAIGSL KVPSSSSNHT RRLSSSSQRK TLSFSSSSLT GEKLNPTQEI
 51 IISNLPRGNE RRTPSIVSPK AVSDSQNSQT CLDPDASRSV LGIILGGGAG
101 TRLYPLTKKR AKPAVPLGAN YRLIDIPVSN CLNSNISKIY VLTQFNSASL
151 NRHLSRAYAS NMGGYKNEGF VEVLAAQQSP ENPNWFQGTA DAVRQYLWLF
201 EEHNVLEFLV LAGDHLYRMD YEKFIQAHRE TDADITVAAL PMDEKRATAF
251 GLMKIDDEGR IIEFAEKPKG EQLKAMKVDT TILGLDDERA KEMPFIASMG
301 IYVVSKNVML DLLRDQFPGA NDFGSEVIPG ATDLGLRVQA YLYDGYWEDI
351 GTIEAFYNAN LGITKKPVPD FSFYDRSAPI YTQPRYLPPS KMLDADVTDS
401 VIGEGCVIKN CKIHHSVIGL RSCISEGAII EDTLLMGADY YETDADRTLL
451 AAKGSIPIGI GRDSHIKRAI IDKNARIGDN VKIINTDNVQ EAARETDGYF
501 IKSGIVTVIK DALIPSGTVI
```

```
 Start - End      Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   278 - 289      673.9179   1345.8213  1345.6725    0.1487     0  K.VDTTILGLDDER.A   (Ions score 112)
   483 - 494      672.4238   1342.8331  1342.6841    0.1490     0  K.IINTDNVQEAAR.E   (Ions score 74)
```

gi|780814 3-ketoacyl-acyl carrier protein synthase I



Protein View

Match to: gi|780814 Score: 379
3-ketoacyl-acyl carrier protein synthase I
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1001NOV26.wiff

Nominal mass (M_r): 50890; Calculated pI value: 7.99
NCBI BLAST search of gi|780814 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%

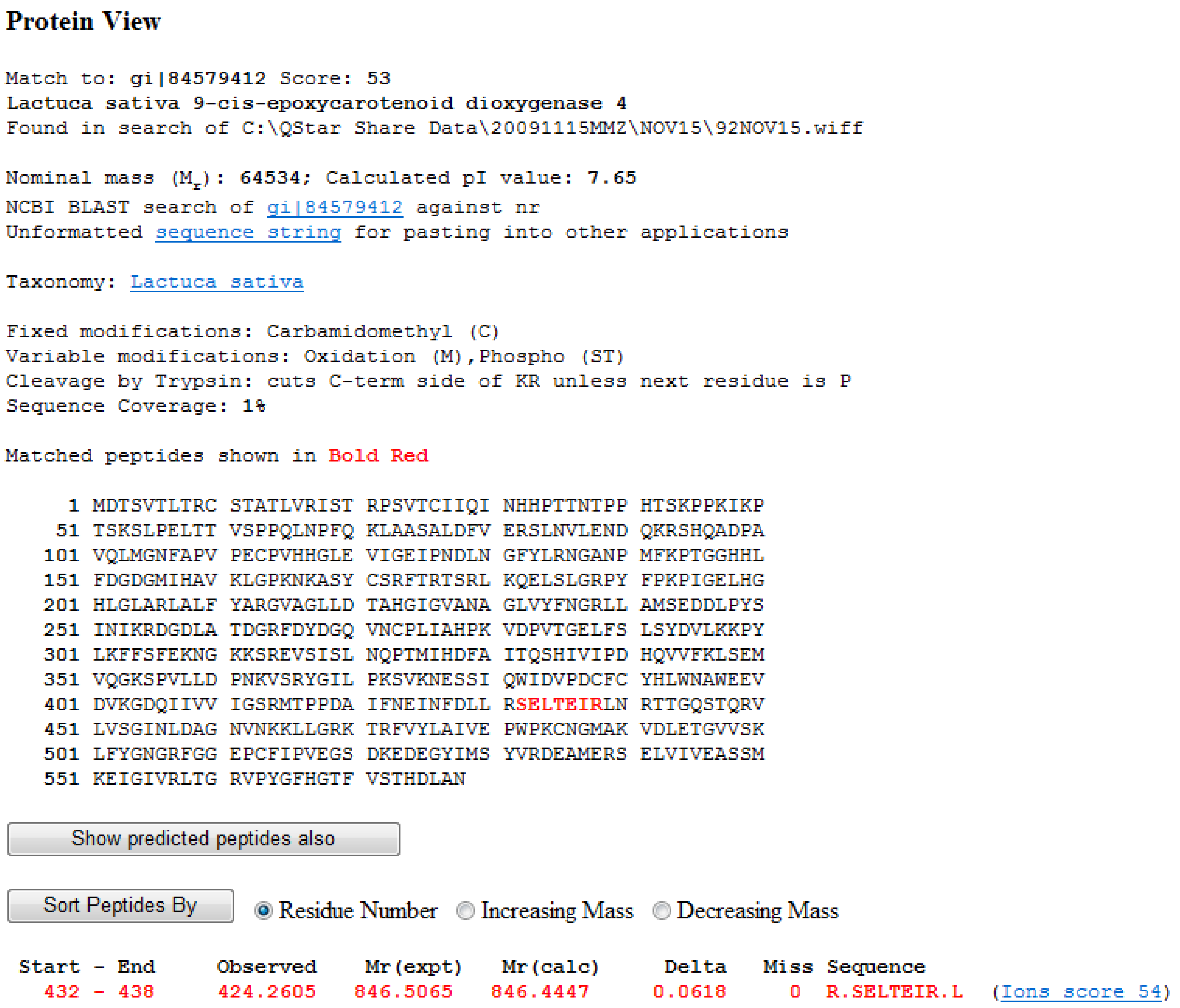
Matched peptides shown in **Bold Red**

```
  1 MQALQSSSLR ASPPNPLRLP SNRQSHQLIT NARPLRRQQR SFISASASTV
 51 SAPKRETDPK KRVVITGMGL VSVCGNDVDA YYEKLLSGES GISLIDRFDA
101 SKFPTRFGGQ IRGFSSEGYI DGKNERRLDD CLKYCIVAGK KALESANLGG
151 DKLNTIDKRK AGVLVGTGMG GLTVFSEGVQ NLIEKGHRRI SPFFIPYAIT
201 NMGSALLAID LGLMGPNYSI STACATSNYC FYAAANHNHR GEADMMIAGG
251 TEAAIIPIGL GGFVACRALS QRNDDPQTAS RPWDKARDGF VMGEGAGVLV
301 MESLEHAMKR GAPIVAEYLG GAVNCDAHHM TDPRADGLGV SSCIERCLED
351 AGVSPEEVNY INAHATSTLA GDLAEINAIK KVFKSTSGIK INATKSMIGH
401 CLGAAGGLEA IATVKAINTG WLHPSINQFN PEQAVDFDTV PNEKKQHEVD
451 VAISNSFGFG GHNSVVAFSA FKP
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  85 - 97       680.4580  1358.9014  1358.7405    0.1609     0  K.LLSGESGISLIDR.F  (Ions score 100)
 113 - 123      580.3375  1158.6605  1158.5193    0.1411     0  R.GFSSEGYIDGK.N  (Ions score 59)
 142 - 152      537.8606  1073.7066  1073.5353    0.1713     0  K.ALESANLGGDK.L  (Ions score 68)
 142 - 158      587.0564  1758.1475  1757.9159    0.2316     1  K.ALESANLGGDKLNTIDK.R  (Ions score 68)
 273 - 285      765.4231  1528.8317  1528.6906    0.1411     0  R.NDDPQTASRPWDK.A  (Ions score 57)
 273 - 285      510.6545  1528.9418  1528.6906    0.2512     0  R.NDDPQTASRPWDK.A  (Ions score 40)
 288 - 309      785.7613  2354.2621  2354.0593    0.2028     0  R.DGFVMGEGAGVLVMESLEHAMK.R  3 Oxidation (M)  (Ions score 29)
```

gi|84579412 9-cis-epoxycarotenoid dioxygenase 4



Protein View

Match to: gi|84579412 Score: 53
Lactuca sativa 9-cis-epoxycarotenoid dioxygenase 4
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\92NOV15.wiff

Nominal mass (M_r): 64534; Calculated pI value: 7.65
NCBI BLAST search of gi|84579412 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Lactuca sativa

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

Matched peptides shown in **Bold Red**

```
  1 MDTSVTLTRC STATLVRIST RPSVTCIIQI NHHPTTNTPP HTSKPPKIKP
 51 TSKSLPELTT VSPPQLNPFQ KLAASALDFV ERSLNVLEND QKRSHQADPA
101 VQLMGNFAPV PECPVHHGLE VIGEIPNDLN GFYLRNGANP MFKPTGGHHL
151 FDGDGMIHAV KLGPKNKASY CSRFTRTSRL KQELSLGRPY FPKPIGELHG
201 HLGLARLALF YARGVAGLLD TAHGIGVANA GLVYFNGRLL AMSEDDLPYS
251 INIKRDGDLA TDGRFDYDGQ VNCPLIAHPK VDPVTGELFS LSYDVLKKPY
301 LKFFSFEKNG KKSREVSISL NQPTMIHDFA ITQSHIVIPD HQVVFKLSEM
351 VQGKSPVLLD PNKVSRYGIL PKSVKNESSI QWIDVPDCFC YHLWNAWEEV
401 DVKGDQIIVV IGSRMTPPDA IFNEINFDLL RSELTEIRLN RTTGQSTQRV
451 LVSGINLDAG NVNKKLLGRK TRFVYLAIVE PWPKCNGMAK VDLETGVVSK
501 LFYGNGRFGG EPCFIPVEGS DKEDEGYIMS YVRDEAMERS ELVIVEASSM
551 KEIGIVRLTG RVPYGFHGTF VSTHDLAN
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

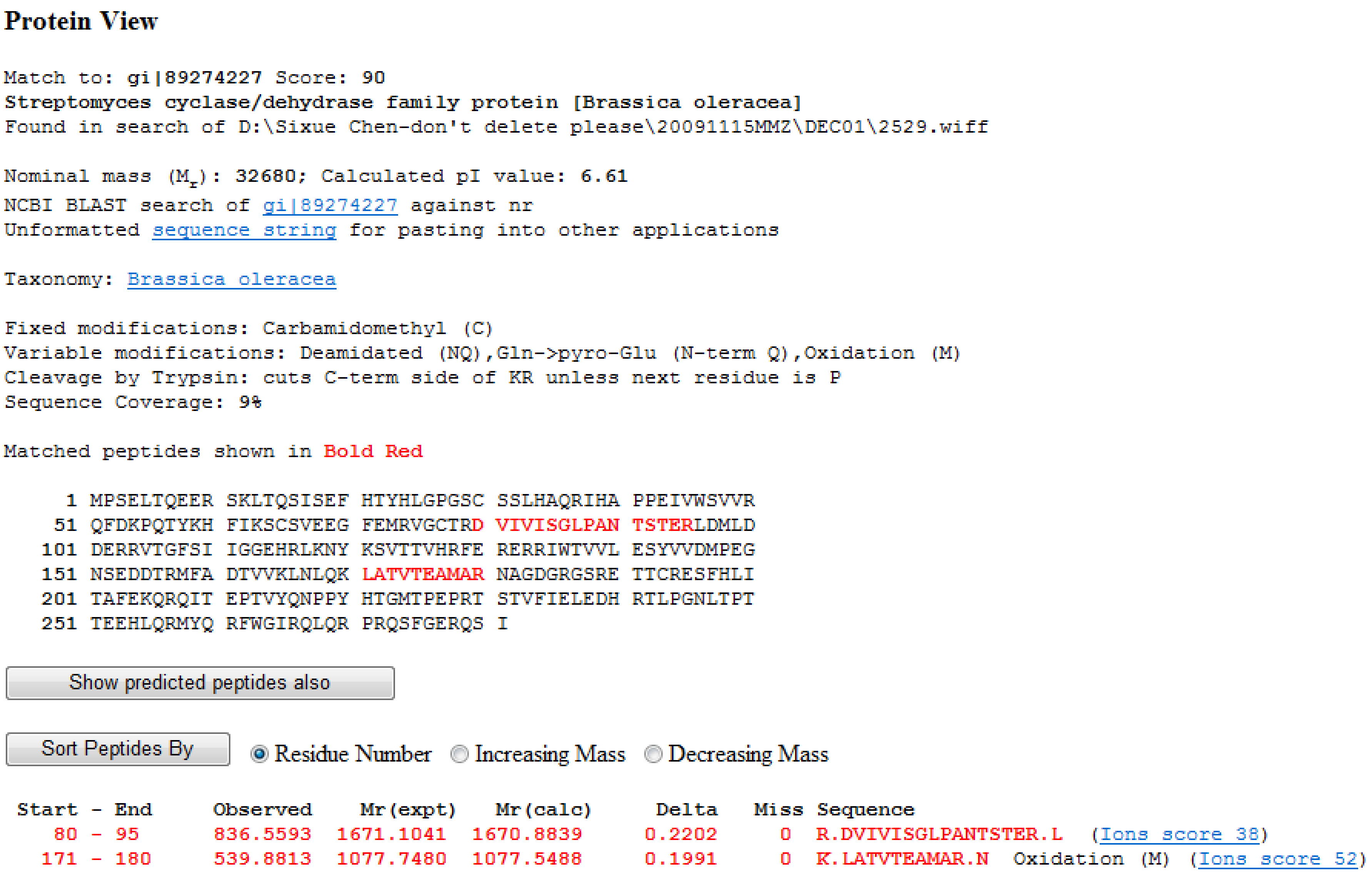
```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  432 - 438      424.2605   846.5065   846.4447    0.0618     0 R.SELTEIR.L   (Ions score 54)
```

Peptide View

MS/MS Fragmentation of **SELTEIR**
Found in **gi|84579412**, Lactuca sativa 9-cis-epoxycarotenoid dioxygenase 4

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233	70.0287	35.5180	**S**							**7**
2	**217.0819**	109.0446	199.0713	100.0393	**E**	**760.4199**	380.7136	743.3934	372.2003	**742.4094**	371.7083	**6**
3	330.1660	165.5866	312.1554	156.5813	**L**	**631.3774**	316.1923	614.3508	307.6790	**613.3668**	307.1870	**5**
4	431.2136	216.1105	413.2031	207.1052	**T**	**518.2933**	259.6503	501.2667	251.1370	**500.2827**	250.6450	**4**
5	560.2562	280.6318	542.2457	271.6265	**E**	**417.2456**	209.1264	400.2191	200.6132	**399.2350**	200.1212	**3**
6	673.3403	337.1738	655.3297	328.1685	**I**	**288.2030**	144.6051	271.1765	136.0919			**2**
7					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

gi|89274227 Streptomyces cyclase/dehydrase family protein



Protein View

Match to: gi|89274227 Score: 90
Streptomyces cyclase/dehydrase family protein [Brassica oleracea]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2529.wiff

Nominal mass (M_r): 32680; Calculated pI value: 6.61
NCBI BLAST search of gi|89274227 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica oleracea

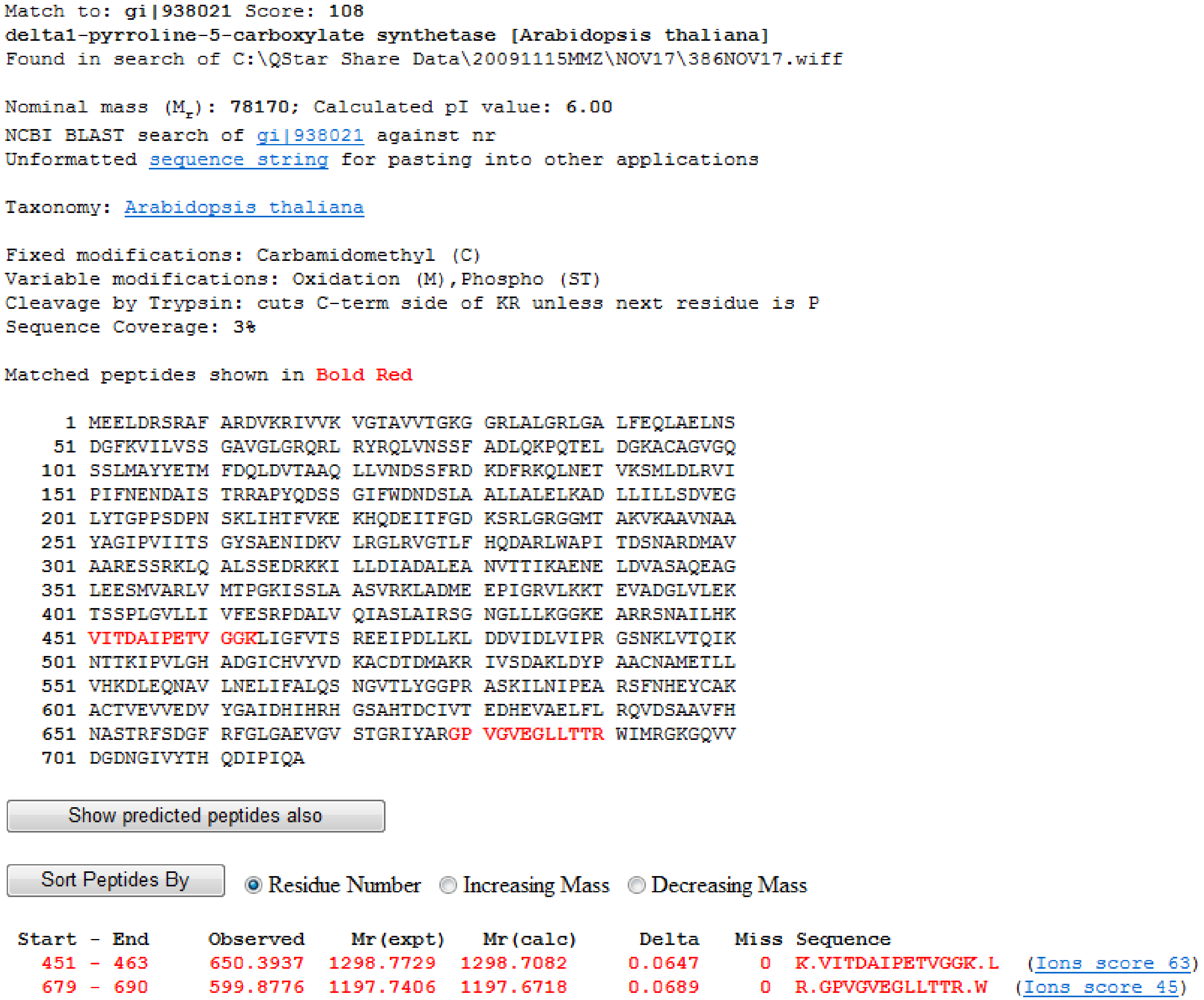
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

Matched peptides shown in **Bold Red**

```
  1 MPSELTQEER SKLTQSISEF HTYHLGPGSC SSLHAQRIHA PPEIVWSVVR
 51 QFDKPQTYKH FIKSCSVEEG FEMRVGCTRD VIVISGLPAN TSTERLDMLD
101 DERRVTGFSI IGGEHRLKNY KSVTTVHRFE RERRIWTVVL ESYVVDMPEG
151 NSEDDTRMFA DTVVKLNLQK LATVTEAMAR NAGDGRGSRE TTCRESFHLI
201 TAFEKQRQIT EPTVYQNPPY HTGMTPEPRT STVFIELEDH RTLPGNLTPT
251 TEEHLQRMYQ RFWGIRQLQR PRQSFGERQS I
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   80 - 95      836.5593  1671.1041  1670.8839   0.2202     0  R.DVIVISGLPANTSTER.L   (Ions score 38)
  171 - 180     539.8813  1077.7480  1077.5488   0.1991     0  K.LATVTEAMAR.N  Oxidation (M)  (Ions score 52)
```

gi|938021 Delta1-pyrroline-5-carboxylate synthetase



```
Match to: gi|938021 Score: 108
delta1-pyrroline-5-carboxylate synthetase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\386NOV17.wiff

Nominal mass (Mr): 78170; Calculated pI value: 6.00
NCBI BLAST search of gi|938021 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

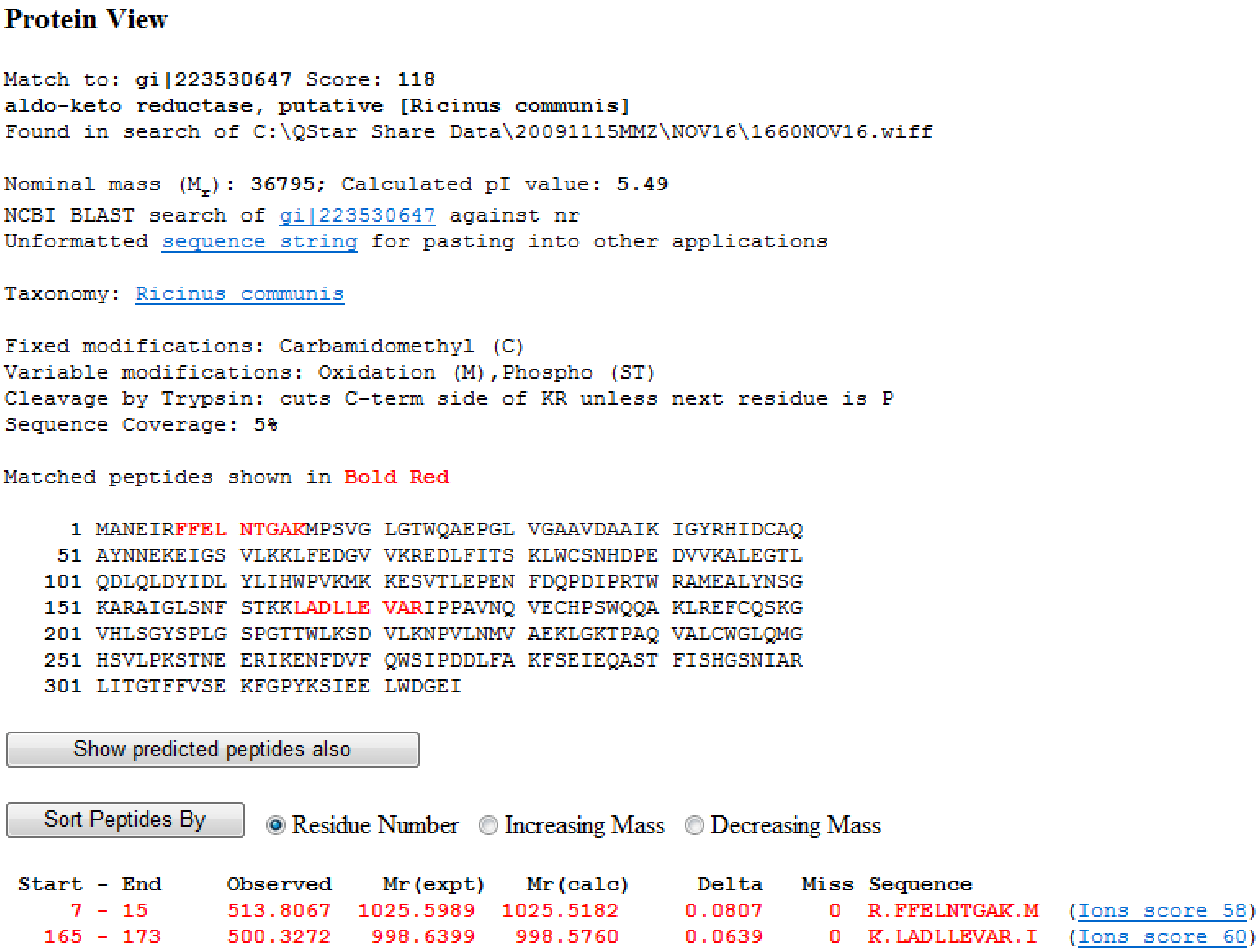
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in Bold Red

     1 MEELDRSRAF ARDVKRIVVK VGTAVVTGKG GRLALGRLGA LFEQLAELNS
    51 DGFKVILVSS GAVGLGRQRL RYRQLVNSSF ADLQKPQTEL DGKACAGVGQ
   101 SSLMAYYETM FDQLDVTAAQ LLVNDSSFRD KDFRKQLNET VKSMLDLRVI
   151 PIFNENDAIS TRRAPYQDSS GIFWDNDSLA ALLALELKAD LLILLSDVEG
   201 LYTGPPSDPN SKLIHTFVKE KHQDEITFGD KSRLGRGGMT AKVKAAVNAA
   251 YAGIPVIITS GYSAENIDKV LRGLRVGTLF HQDARLWAPI TDSNARDMAV
   301 AARESSRKLQ ALSSEDRKKI LLDIADALEA NVTTIKAENE LDVASAQEAG
   351 LEESMVARLV MTPGKISSLA ASVRKLADME EPIGRVLKKT EVADGLVLEK
   401 TSSPLGVLLI VFESRPDALV QIASLAIRSG NGLLLKGGKE ARRSNAILHK
   451 VITDAIPETV GGKLIGFVTS REEIPDLLKL DDVIDLVIPR GSNKLVTQIK
   501 NTTKIPVLGH ADGICHVYVD KACDTDMAKR IVSDAKLDYP AACNAMETLL
   551 VHKDLEQNAV LNELIFALQS NGVTLYGGPR ASKILNIPEA RSFNHEYCAK
   601 ACTVEVVEDV YGAIDHIHRH GSAHTDCIVT EDHEVAELFL RQVDSAAVFH
   651 NASTRFSDGF RFGLGAEVGV STGRIYARGP VGVEGLLTTR WIMRGKGQVV
   701 DGDNGIVYTH QDIPIQA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   451 - 463     650.3937  1298.7729  1298.7082    0.0647     0  K.VITDAIPETVGGK.L  (Ions score 63)
   679 - 690     599.8776  1197.7406  1197.6718    0.0689     0  R.GPVGVEGLLTTR.W  (Ions score 45)
```

gi|223530647 Aldo-keto reductase, putative



Protein View

Match to: gi|223530647 Score: 118
aldo-keto reductase, putative [Ricinus communis]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1660NOV16.wiff

Nominal mass (M_r): 36795; Calculated pI value: 5.49
NCBI BLAST search of gi|223530647 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Ricinus communis

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

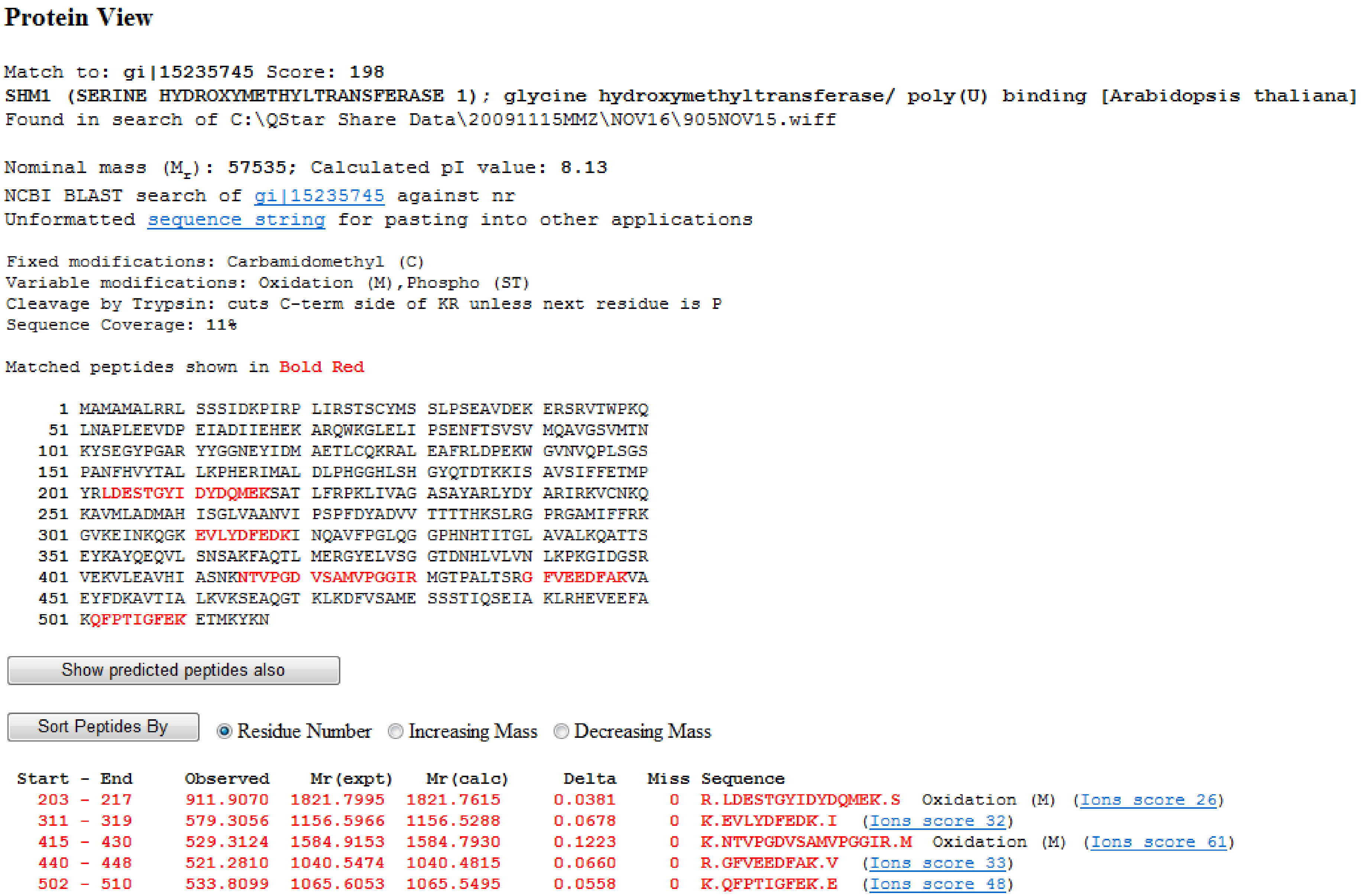
Matched peptides shown in **Bold Red**

```
  1 MANEIRFFEL NTGAKMPSVG LGTWQAEPGL VGAAVDAAIK IGYRHIDCAQ
 51 AYNNEKEIGS VLKKLFEDGV VKREDLFITS KLWCSNHDPE DVVKALEGTL
101 QDLQLDYIDL YLIHWPVKMK KESVTLEPEN FDQPDIPRTW RAMEALYNSG
151 KARAIGLSNF STKKLADLLE VARIPPAVNQ VECHPSWQQA KLREFCQSKG
201 VHLSGYSPLG SPGTTWLKSD VLKNPVLNMV AEKLGKTPAQ VALCWGLQMG
251 HSVLPKSTNE ERIKENFDVF QWSIPDDLFA KFSEIEQAST FISHGSNIAR
301 LITGTFFVSE KFGPYKSIEE LWDGEI
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)  Mr(calc)     Delta  Miss Sequence
    7 - 15     513.8067 1025.5989 1025.5182    0.0807    0  R.FFELNTGAK.M   (Ions score 58)
  165 - 173    500.3272  998.6399  998.5760    0.0639    0  K.LADLLEVAR.I   (Ions score 60)
```

gi|15235745 Serine hydroxymethytransferase 1 (SHM1)



Protein View

Match to: gi|15235745 Score: 198

SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase/ poly(U) binding [Arabidopsis thaliana]

Found in search of C:\QStar Share Data\20091115MMZ\NOV16\905NOV15.wiff

Nominal mass (M_r): 57535; Calculated pI value: 8.13

NCBI BLAST search of gi|15235745 against nr

Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M),Phospho (ST)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

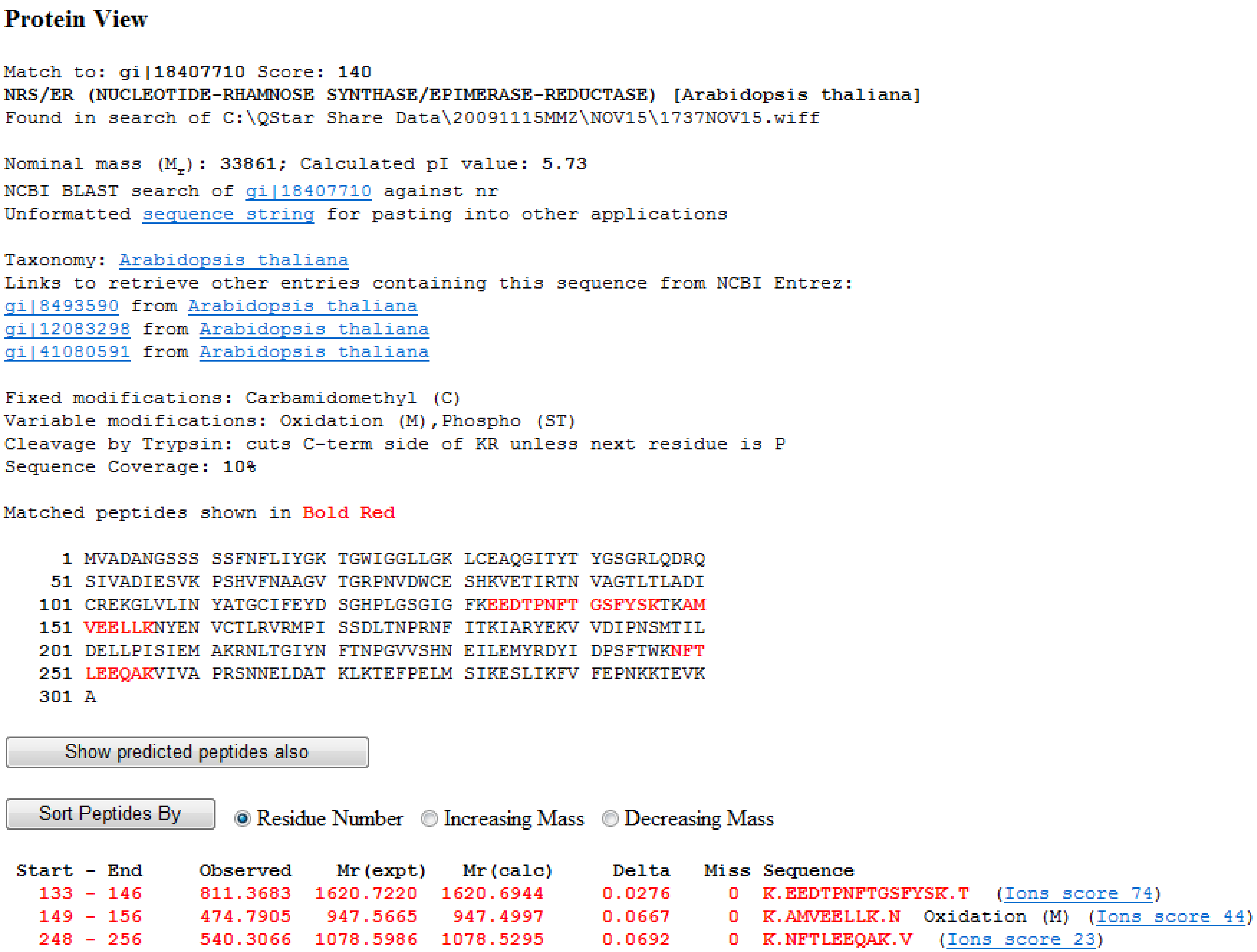
```
  1 MAMAMALRRL SSSIDKPIRP LIRSTSCYMS SLPSEAVDEK ERSRVTWPKQ
 51 LNAPLEEVDP EIADIIEHEK ARQWKGLELI PSENFTSVSV MQAVGSVMTN
101 KYSEGYPGAR YYGGNEYIDM AETLCQKRAL EAFRLDPEKW GVNVQPLSGS
151 PANFHVYTAL LKPHERIMAL DLPHGGHLSH GYQTDTKKIS AVSIFFETMP
201 YRLDESTGYI DYDQMEKSAT LFRPKLIVAG ASAYARLYDY ARIRKVCNKQ
251 KAVMLADMAH ISGLVAANVI PSPFDYADVV TTTTHKSLRG PRGAMIFFRK
301 GVKEINKQGK EVLYDFEDKI NQAVFPGLQG GPHNHTITGL AVALKQATTS
351 EYKAYQEQVL SNSAKFAQTL MERGYELVSG GTDNHLVLVN LKPKGIDGSR
401 VEKVLEAVHI ASNKNTVPGD VSAMVPGGIR MGTPALTSRG FVEEDFAKVA
451 EYFDKAVTIA LKVKSEAQGT KLKDFVSAME SSSTIQSEIA KLRHEVEEFA
501 KQFPTIGFEK ETMKYKN
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  203 - 217     911.9070  1821.7995  1821.7615    0.0381     0   R.LDESTGYIDYDQMEK.S  Oxidation (M) (Ions score 26)
  311 - 319     579.3056  1156.5966  1156.5288    0.0678     0   K.EVLYDFEDK.I  (Ions score 32)
  415 - 430     529.3124  1584.9153  1584.7930    0.1223     0   K.NTVPGDVSAMVPGGIR.M  Oxidation (M) (Ions score 61)
  440 - 448     521.2810  1040.5474  1040.4815    0.0660     0   R.GFVEEDFAK.V  (Ions score 33)
  502 - 510     533.8099  1065.6053  1065.5495    0.0558     0   K.QFPTIGFEK.E  (Ions score 48)
```

gi|18407710 Nucleotide-rhamnose synthase/epimerase-reductase (NRS/ER)



Protein View

Match to: gi|18407710 Score: 140
NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/EPIMERASE-REDUCTASE) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1737NOV15.wiff

Nominal mass (M_r): 33861; Calculated pI value: 5.73
NCBI BLAST search of gi|18407710 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|8493590 from Arabidopsis thaliana
gi|12083298 from Arabidopsis thaliana
gi|41080591 from Arabidopsis thaliana

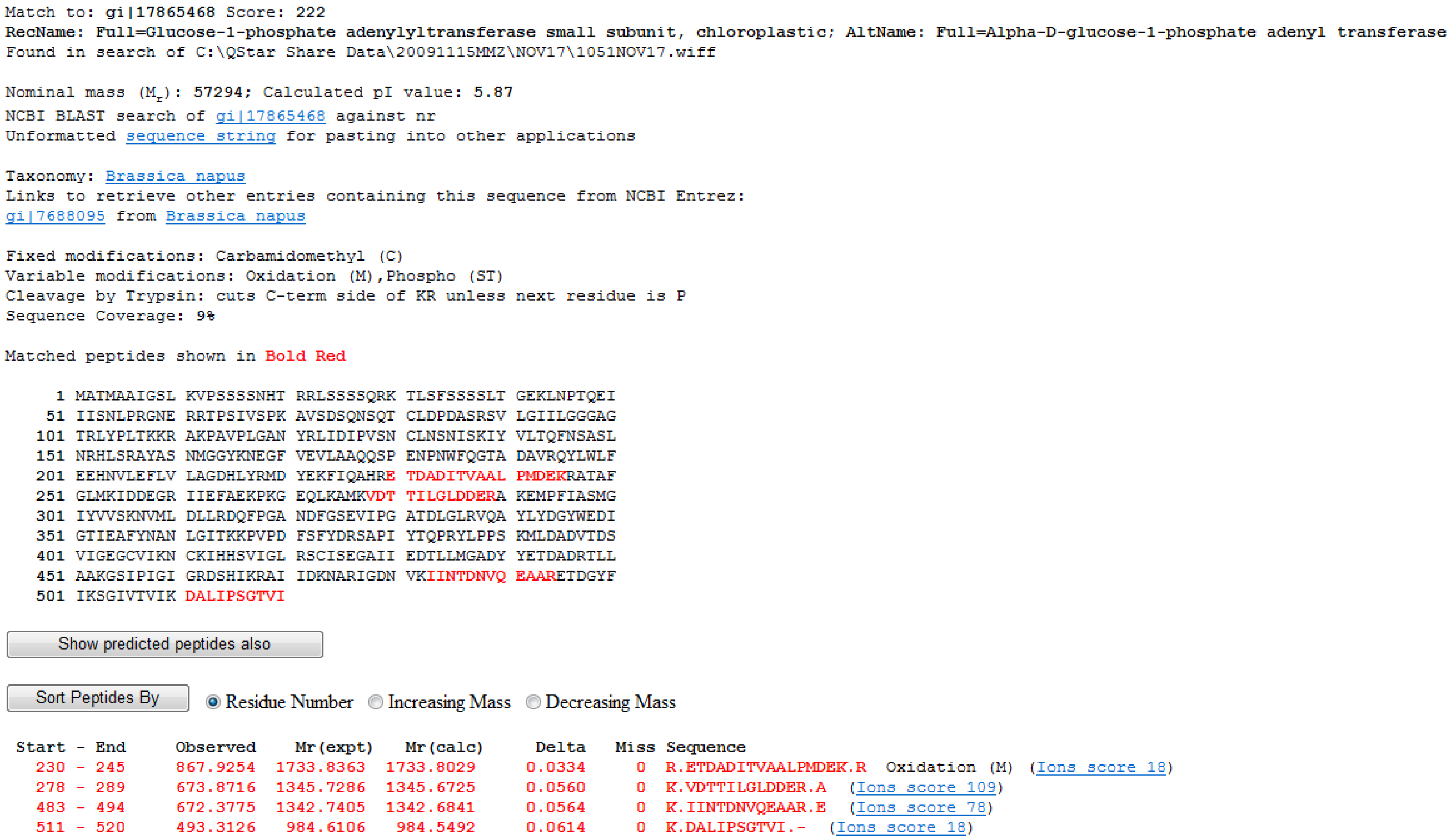
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%

Matched peptides shown in **Bold Red**

```
  1 MVADANGSSS SSFNFLIYGK TGWIGGLLGK LCEAQGITYT YGSGRLQDRQ
 51 SIVADIESVK PSHVFNAAGV TGRPNVDWCE SHKVETIRTN VAGTLTLADI
101 CREKGLVLIN YATGCIFEYD SGHPLGSGIG FKEEDTPNFT GSFYSKTKAM
151 VEELLKNYEN VCTLRVRMPI SSDLTNPRNF ITKIARYEKV VDIPNSMTIL
201 DELLPISIEM AKRNLTGIYN FTNPGVVSHN EILEMYRDYI DPSFTWKNFT
251 LEEQAKVIVA PRSNNELDAT KLKTEFPELM SIKESLIKFV FEPNKKTEVK
301 A
```

```
 Start - End     Observed    Mr(expt)   Mr(calc)      Delta   Miss  Sequence
  133 - 146      811.3683   1620.7220  1620.6944     0.0276    0   K.EEDTPNFTGSFYSK.T   (Ions score 74)
  149 - 156      474.7905    947.5665   947.4997     0.0667    0   K.AMVEELLK.N  Oxidation (M)  (Ions score 44)
  248 - 256      540.3066   1078.5986  1078.5295     0.0692    0   K.NFTLEEQAK.V   (Ions score 23)
```

gi|17865468 Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic



Match to: gi|17865468 Score: 222
RecName: Full=Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic; AltName: Full=Alpha-D-glucose-1-phosphate adenyl transferase
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1051NOV17.wiff

Nominal mass (M_r): 57294; Calculated pI value: 5.87
NCBI BLAST search of gi|17865468 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|7688095 from Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

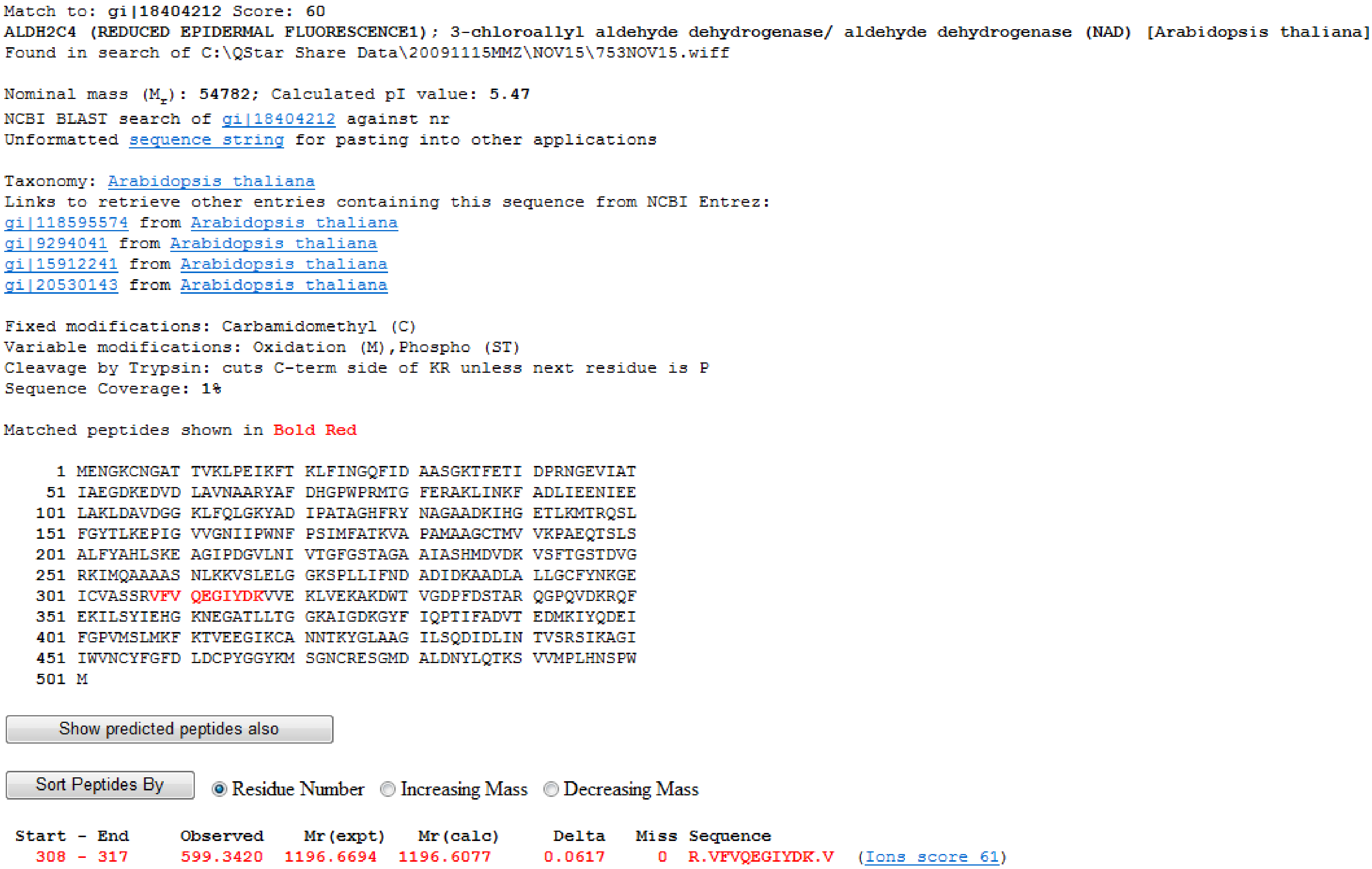
Matched peptides shown in **Bold Red**

```
  1 MATMAAIGSL KVPSSSSNHT RRLSSSSQRK TLSFSSSSLT GEKLNPTQEI
 51 IISNLPRGNE RRTPSIVSPK AVSDSQNSQT CLDPDASRSV LGIILGGGAG
101 TRLYPLTKKR AKPAVPLGAN YRLIDIPVSN CLNSNISKIY VLTQFNSASL
151 NRHLSRAYAS NMGGYKNEGF VEVLAAQQSP ENPNWFQGTA DAVRQYLWLF
201 EEHNVLEFLV LAGDHLYRMD YEKFIQAHRE TDADITVAAL PMDEKRATAF
251 GLMKIDDEGR IIEFAEKPKG EQLKAMKVDT TILGLDDERA KEMPFIASMG
301 IYVVSKNVML DLLRDQFPGA NDFGSEVIPG ATDLGLRVQA YLYDGYWEDI
351 GTIEAFYNAN LGITKKPVPD FSFYDRSAPI YTQPRYLPPS KMLDADVTDS
401 VIGEGCVIKN CKIHHSVIGL RSCISEGAII EDTLLMGADY YETDADRTLL
451 AAKGSIPIGI GRDSHIKRAI IDKNARIGDN VKIINTDNVQ EAARETDGYF
501 IKSGIVTVIK DALIPSGTVI
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End    Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
  230 - 245    867.9254  1733.8363  1733.8029   0.0334     0 R.ETDADITVAALPMDEK.R  Oxidation (M)  (Ions score 18)
  278 - 289    673.8716  1345.7286  1345.6725   0.0560     0 K.VDTTILGLDDER.A  (Ions score 109)
  483 - 494    672.3775  1342.7405  1342.6841   0.0564     0 K.IINTDNVQEAAR.E  (Ions score 78)
  511 - 520    493.3126   984.6106   984.5492   0.0614     0 K.DALIPSGTVI.-  (Ions score 18)
```

gi|18404212 3-chloroallyl aldehyde dehydrogenase



Match to: gi|18404212 Score: 60
ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\753NOV15.wiff

Nominal mass (M_r): 54782; Calculated pI value: 5.47
NCBI BLAST search of gi|18404212 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|118595574 from Arabidopsis thaliana
gi|9294041 from Arabidopsis thaliana
gi|15912241 from Arabidopsis thaliana
gi|20530143 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

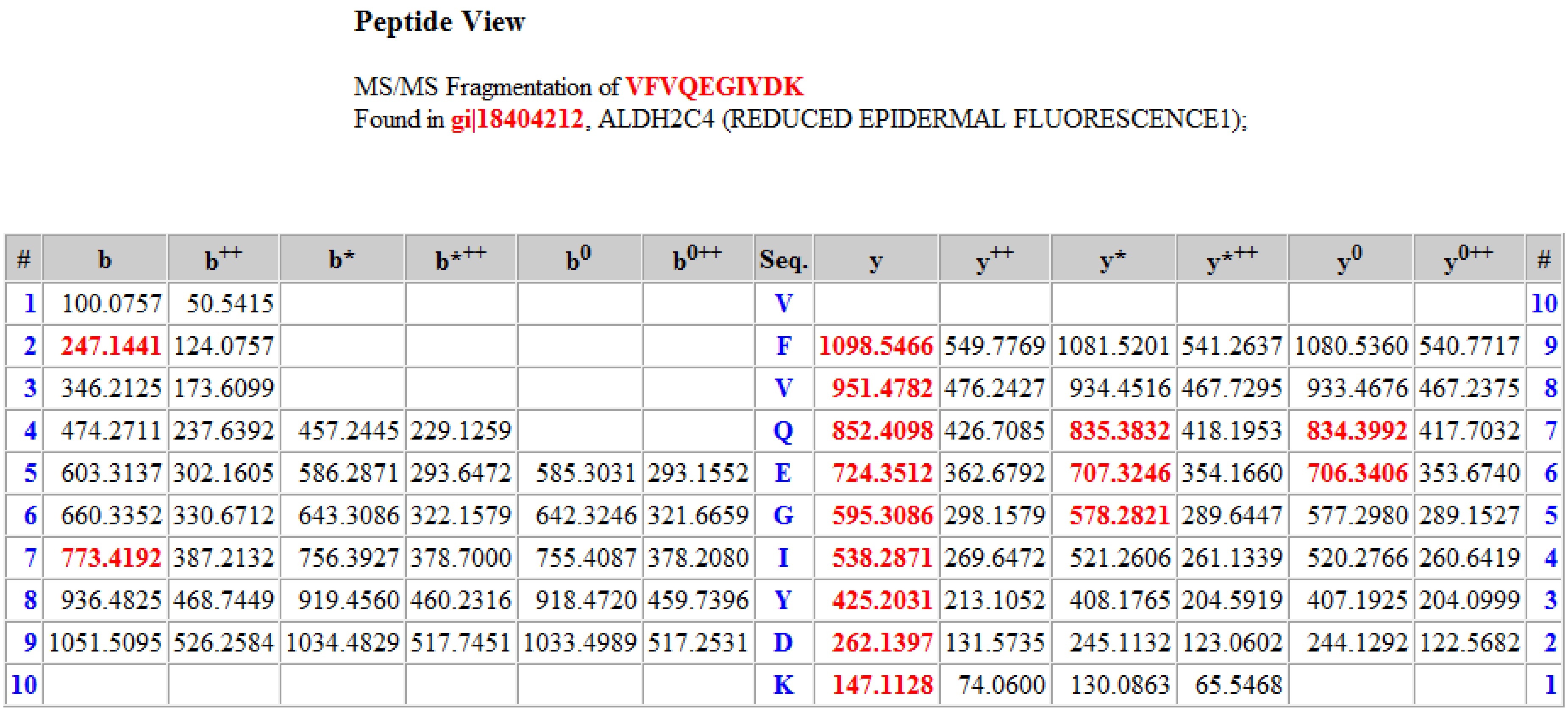
Matched peptides shown in **Bold Red**

```
  1 MENGKCNGAT TVKLPEIKFT KLFINGQFID AASGKTFETI DPRNGEVIAT
 51 IAEGDKEDVD LAVNAARYAF DHGPWPRMTG FERAKLINKF ADLIEENIEE
101 LAKLDAVDGG KLFQLGKYAD IPATAGHFRY NAGAADKIHG ETLKMTRQSL
151 FGYTLKEPIG VVGNIIPWNF PSIMFATKVA PAMAAGCTMV VKPAEQTSLS
201 ALFYAHLSKE AGIPDGVLNI VTGFGSTAGA AIASHMDVDK VSFTGSTDVG
251 RKIMQAAAAS NLKKVSLELG GKSPLLIFND ADIDKAADLA LLGCFYNKGE
301 ICVASSRVFV QEGIYDKVVE KLVEKAKDWT VGDPFDSTAR QGPQVDKRQF
351 EKILSYIEHG KNEGATLLTG GKAIGDKGYF IQPTIFADVT EDMKIYQDEI
401 FGPVMSLMKF KTVEEGIKCA NNTKYGLAAG ILSQDIDLIN TVSRSIKAGI
451 IWVNCYFGFD LDCPYGGYKM SGNCRESGMD ALDNYLQTKS VVMPLHNSPW
501 M
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   308 - 317     599.3420  1196.6694  1196.6077    0.0617     0 R.VFVQEGIYDK.V   (Ions score 61)
```

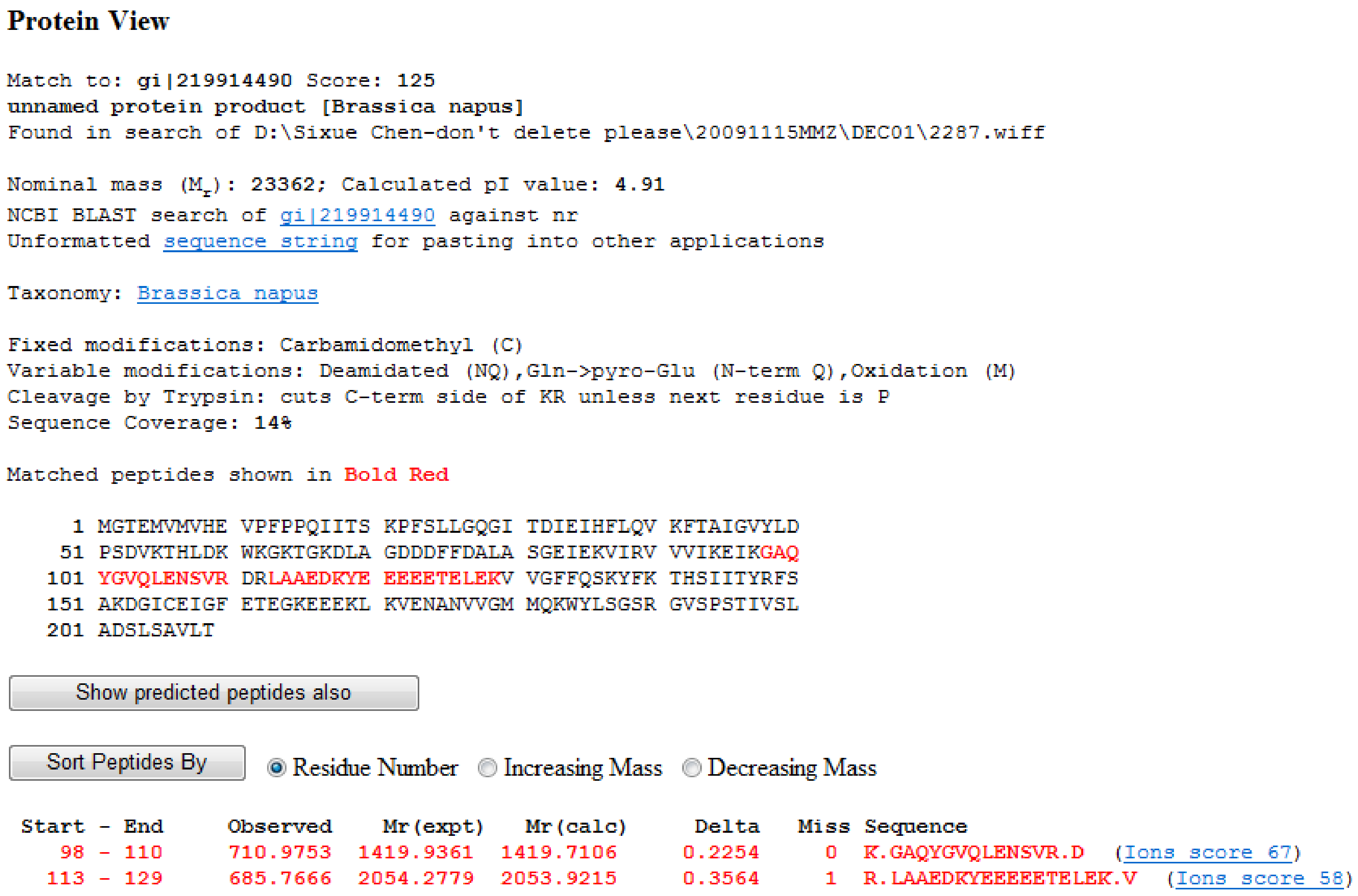


Peptide View

MS/MS Fragmentation of **VFVQEGIYDK**
Found in **gi|18404212**, ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1);

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							10
2	**247.1441**	124.0757					F	**1098.5466**	549.7769	1081.5201	541.2637	1080.5360	540.7717	9
3	346.2125	173.6099					V	**951.4782**	476.2427	934.4516	467.7295	933.4676	467.2375	8
4	474.2711	237.6392	457.2445	229.1259			Q	**852.4098**	426.7085	**835.3832**	418.1953	**834.3992**	417.7032	7
5	603.3137	302.1605	586.2871	293.6472	585.3031	293.1552	E	**724.3512**	362.6792	**707.3246**	354.1660	**706.3406**	353.6740	6
6	660.3352	330.6712	643.3086	322.1579	642.3246	321.6659	G	**595.3086**	298.1579	**578.2821**	289.6447	577.2980	289.1527	5
7	**773.4192**	387.2132	756.3927	378.7000	755.4087	378.2080	I	**538.2871**	269.6472	521.2606	261.1339	520.2766	260.6419	4
8	936.4825	468.7449	919.4560	460.2316	918.4720	459.7396	Y	**425.2031**	213.1052	408.1765	204.5919	407.1925	204.0999	3
9	1051.5095	526.2584	1034.4829	517.7451	1033.4989	517.2531	D	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	**147.1128**	74.0600	130.0863	65.5468			1

gi|219914490 Unnamed protein product, containing chalcone-flavanone isomerase domain



Protein View

```
Match to: gi|219914490 Score: 125
unnamed protein product [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2287.wiff

Nominal mass (Mr): 23362; Calculated pI value: 4.91
NCBI BLAST search of gi|219914490 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 14%

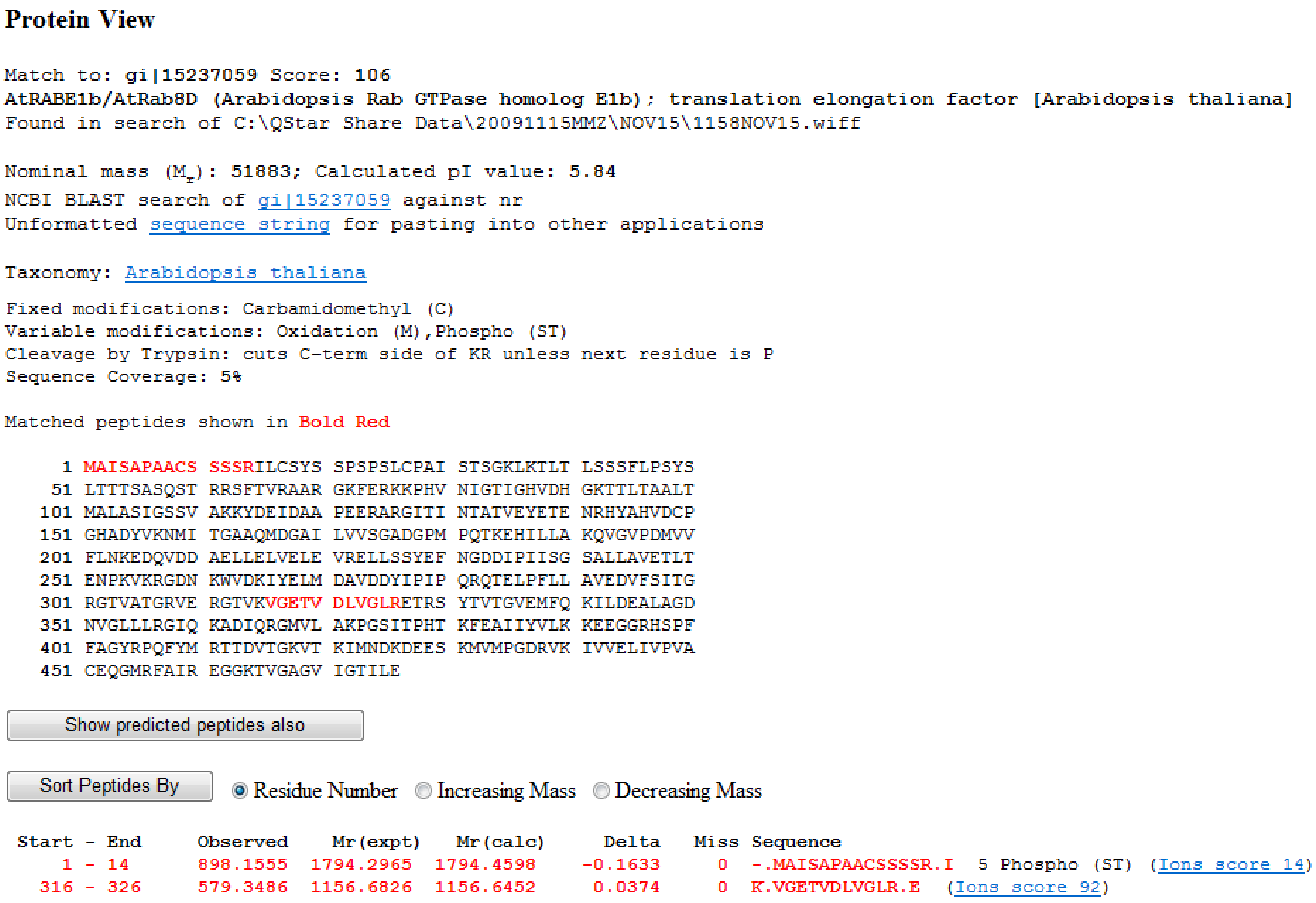
Matched peptides shown in Bold Red

      1 MGTEMVMVHE VPFPPQIITS KPFSLLGQGI TDIEIHFLQV KFTAIGVYLD
     51 PSDVKTHLDK WKGKTGKDLA GDDDFFDALA SGEIEKVIRV VVIKEIKGAQ
    101 YGVQLENSVR DRLAAEDKYE EEEETELEKV VGFFQSKYFK THSIITYRFS
    151 AKDGICEIGF ETEGKEEEKL KVENANVVGM MQKWYLSGSR GVSPSTIVSL
    201 ADSLSAVLT
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)      Delta   Miss Sequence
    98 - 110     710.9753  1419.9361  1419.7106     0.2254     0  K.GAQYGVQLENSVR.D   (Ions score 67)
   113 - 129     685.7666  2054.2779  2053.9215     0.3564     1  R.LAAEDKYEEEEETELEK.V   (Ions score 58)
```

gi|15237059 Arabidopsis Rab GTPase homolog E1b (AtRABE1b/AtRab8D)



Protein View

```
Match to: gi|15237059 Score: 106
AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1158NOV15.wiff

Nominal mass (Mr): 51883; Calculated pI value: 5.84
NCBI BLAST search of gi|15237059 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

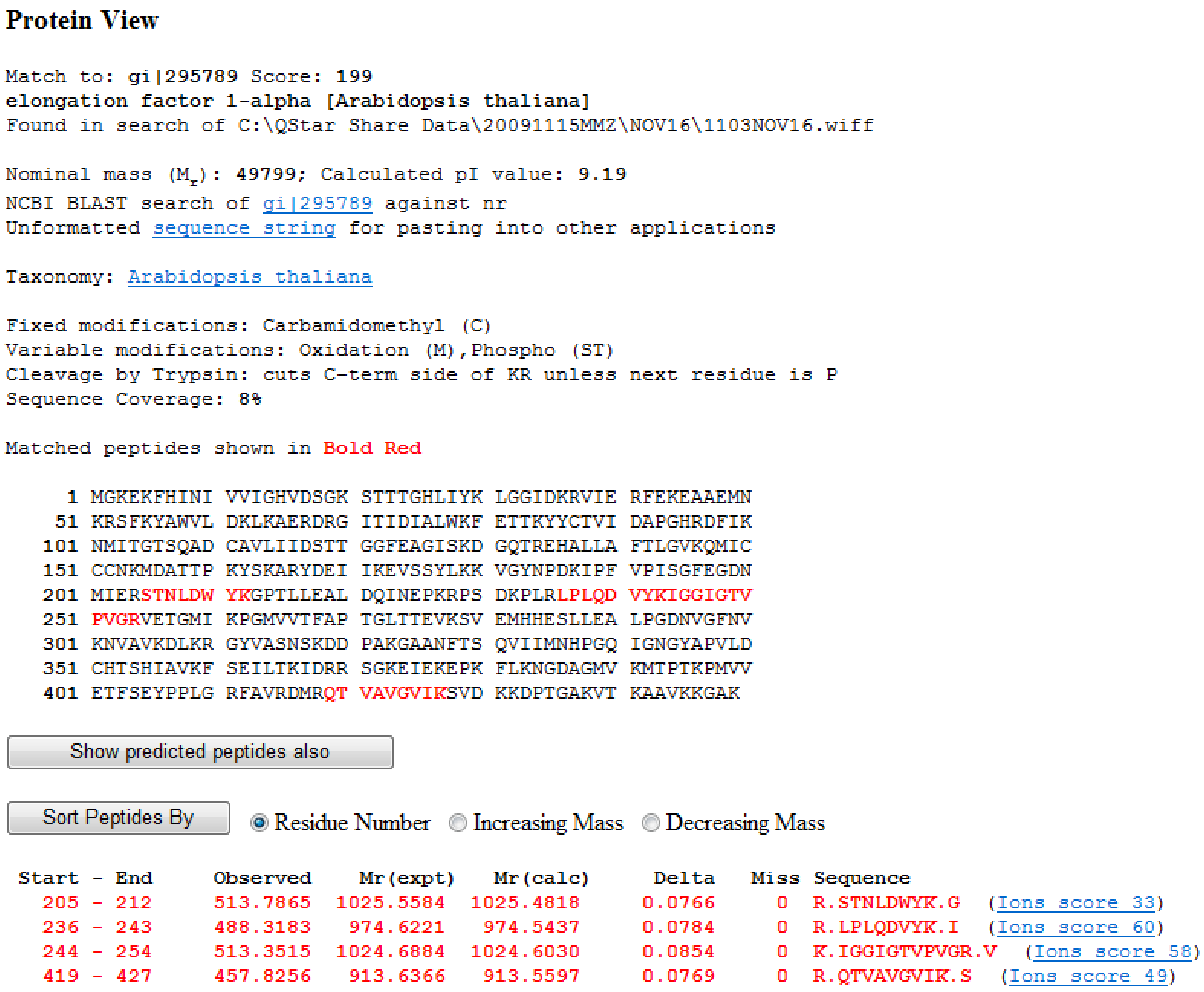
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 5%

Matched peptides shown in Bold Red

      1 MAISAPAACS SSSRILCSYS SPSPSLCPAI STSGKLKTLT LSSSFLPSYS
     51 LTTTSASQST RRSFTVRAAR GKFERKKPHV NIGTIGHVDH GKTTLTAALT
    101 MALASIGSSV AKKYDEIDAA PEERARGITI NTATVEYETE NRHYAHVDCP
    151 GHADYVKNMI TGAAQMDGAI LVVSGADGPM PQTKEHILLA KQVGVPDMVV
    201 FLNKEDQVDD AELLELVELE VRELLSSYEF NGDDIPIISG SALLAVETLT
    251 ENPKVKRGDN KWVDKIYELM DAVDDYIPIP QRQTELPFLL AVEDVFSITG
    301 RGTVATGRVE RGTVKVGETV DLVGLRETRS YTVTGVEMFQ KILDEALAGD
    351 NVGLLLRGIQ KADIQRGMVL AKPGSITPHT KFEAIIYVLK KEEGGRHSPF
    401 FAGYRPQFYM RTTDVTGKVT KIMNDKDEES KMVMPGDRVK IVVELIVPVA
    451 CEQGMRFAIR EGGKTVGAGV IGTILE
```

```
  Start - End      Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
     1 - 14      898.1555  1794.2965  1794.4598   -0.1633     0  -.MAISAPAACSSSSR.I  5 Phospho (ST)  (Ions score 14)
   316 - 326     579.3486  1156.6826  1156.6452    0.0374     0  K.VGETVDLVGLR.E   (Ions score 92)
```

gi|295789 Elongation factor 1-alpha



Protein View

Match to: gi|295789 Score: 199
elongation factor 1-alpha [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1103NOV16.wiff

Nominal mass (M_r): 49799; Calculated pI value: 9.19
NCBI BLAST search of gi|295789 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

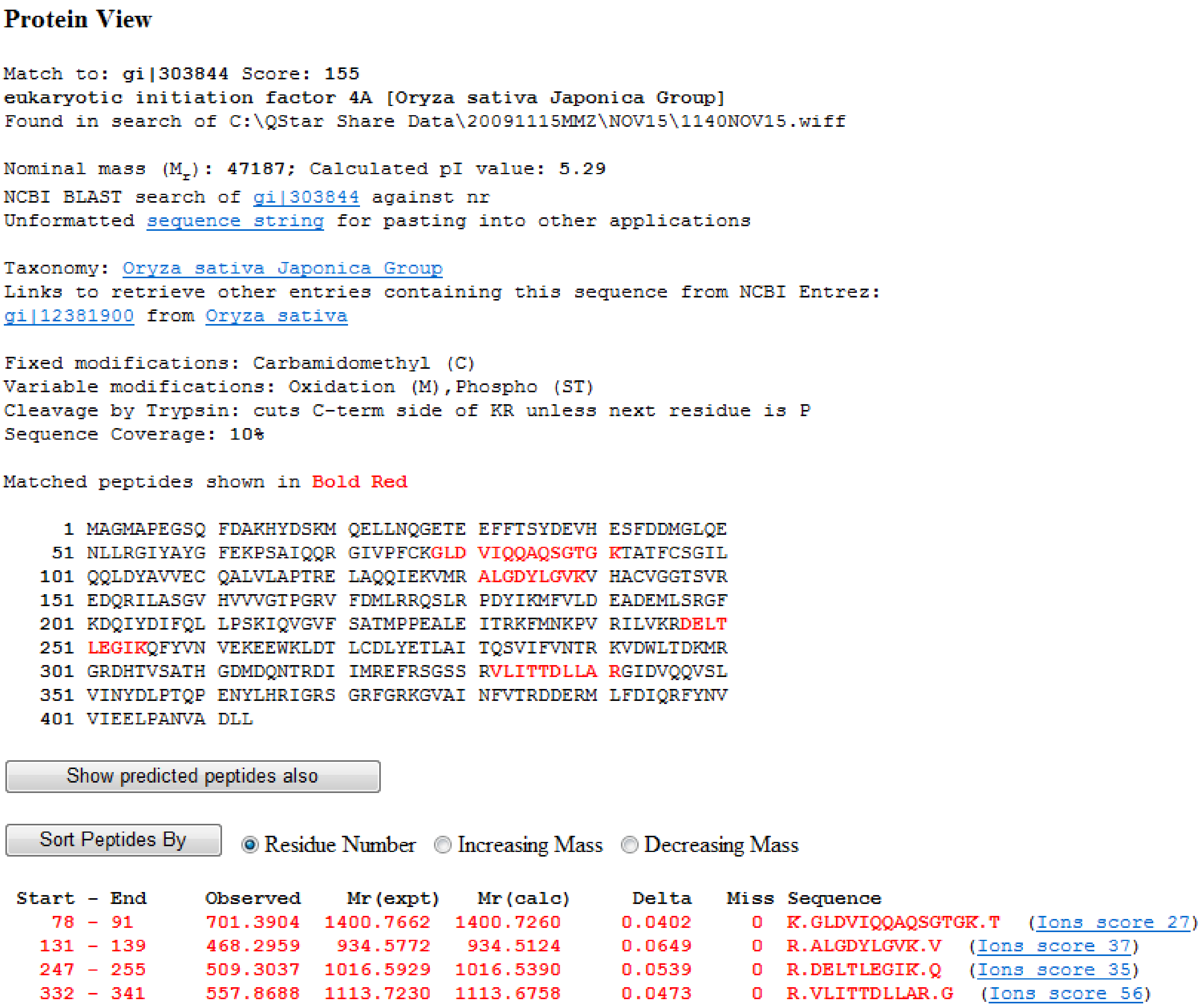
Matched peptides shown in **Bold Red**

```
  1 MGKEKFHINI VVIGHVDSGK STTTGHLIYK LGGIDKRVIE RFEKEAAEMN
 51 KRSFKYAWVL DKLKAERDRG ITIDIALWKF ETTKYYCTVI DAPGHRDFIK
101 NMITGTSQAD CAVLIIDSTT GGFEAGISKD GQTREHALLA FTLGVKQMIC
151 CCNKMDATTP KYSKARYDEI IKEVSSYLKK VGYNPDKIPF VPISGFEGDN
201 MIERSTNLDW YKGPTLLEAL DQINEPKRPS DKPLRLPLQD VYKIGGIGTV
251 PVGRVETGMI KPGMVVTFAP TGLTTEVKSV EMHHESLLEA LPGDNVGFNV
301 KNVAVKDLKR GYVASNSKDD PAKGAANFTS QVIIMNHPGQ IGNGYAPVLD
351 CHTSHIAVKF SEILTKIDRR SGKEIEKEPK FLKNGDAGMV KMTPTKPMVV
401 ETFSEYPPLG RFAVRDMRQT VAVGVIKSVD KKDPTGAKVT KAAVKKGAK
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
  205 - 212     513.7865  1025.5584  1025.4818    0.0766    0  R.STNLDWYK.G   (Ions score 33)
  236 - 243     488.3183   974.6221   974.5437    0.0784    0  R.LPLQDVYK.I   (Ions score 60)
  244 - 254     513.3515  1024.6884  1024.6030    0.0854    0  K.IGGIGTVPVGR.V   (Ions score 58)
  419 - 427     457.8256   913.6366   913.5597    0.0769    0  R.QTVAVGVIK.S   (Ions score 49)
```

gi|303844 Eukaryotic initiation factor 4A



Protein View

Match to: gi|303844 Score: 155
eukaryotic initiation factor 4A [Oryza sativa Japonica Group]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r): 47187; Calculated pI value: 5.29
NCBI BLAST search of gi|303844 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12381900 from Oryza sativa

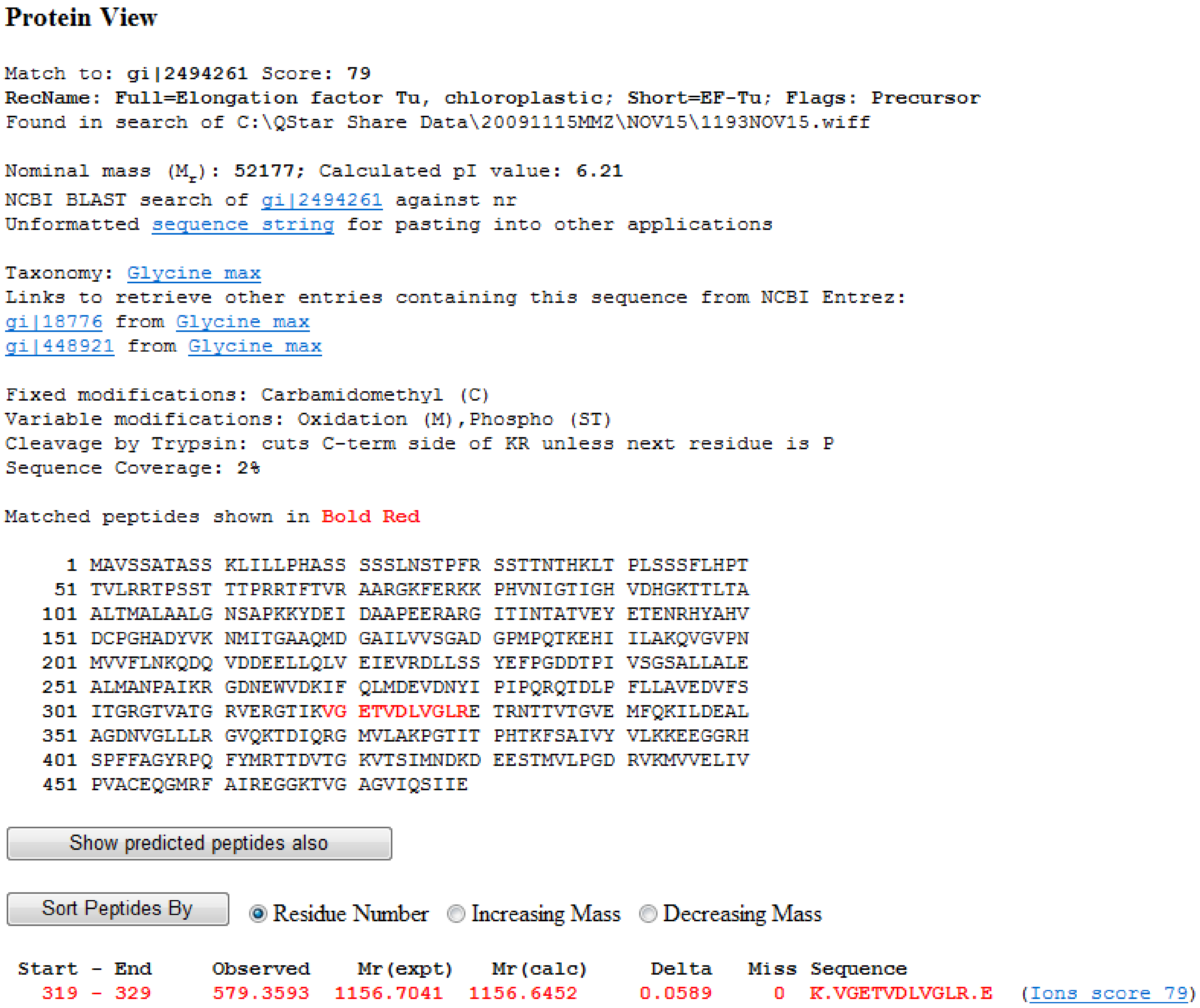
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%

Matched peptides shown in **Bold Red**

```
  1 MAGMAPEGSQ FDAKHYDSKM QELLNQGETE EFFTSYDEVH ESFDDMGLQE
 51 NLLRGIYAYG FEKPSAIQQR GIVPFCKGLD VIQQAQSGTG KTATFCSGIL
101 QQLDYAVVEC QALVLAPTRE LAQQIEKVMR ALGDYLGVKV HACVGGTSVR
151 EDQRILASGV HVVVGTPGRV FDMLRRQSLR PDYIKMFVLD EADEMLSRGF
201 KDQIYDIFQL LPSKIQVGVF SATMPPEALE ITRKFMNKPV RILVKRDELT
251 LEGIKQFYVN VEKEEWKLDT LCDLYETLAI TQSVIFVNTR KVDWLTDKMR
301 GRDHTVSATH GDMDQNTRDI IMREFRSGSS RVLITTDLLA RGIDVQQVSL
351 VINYDLPTQP ENYLHRIGRS GRFGRKGVAI NFVTRDDERM LFDIQRFYNV
401 VIEELPANVA DLL
```

```
 Start - End    Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   78 - 91      701.3904  1400.7662  1400.7260   0.0402    0   K.GLDVIQQAQSGTGK.T  (Ions score 27)
  131 - 139     468.2959   934.5772   934.5124   0.0649    0   R.ALGDYLGVK.V  (Ions score 37)
  247 - 255     509.3037  1016.5929  1016.5390   0.0539    0   R.DELTLEGIK.Q  (Ions score 35)
  332 - 341     557.8688  1113.7230  1113.6758   0.0473    0   R.VLITTDLLAR.G  (Ions score 56)
```

gi|2494261 Elongation factor Tu, chloroplastic



Protein View

Match to: gi|2494261 Score: 79
RecName: Full=Elongation factor Tu, chloroplastic; Short=EF-Tu; Flags: Precursor
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1193NOV15.wiff

Nominal mass (M_r): 52177; Calculated pI value: 6.21
NCBI BLAST search of gi|2494261 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Glycine max
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|18776 from Glycine max
gi|448921 from Glycine max

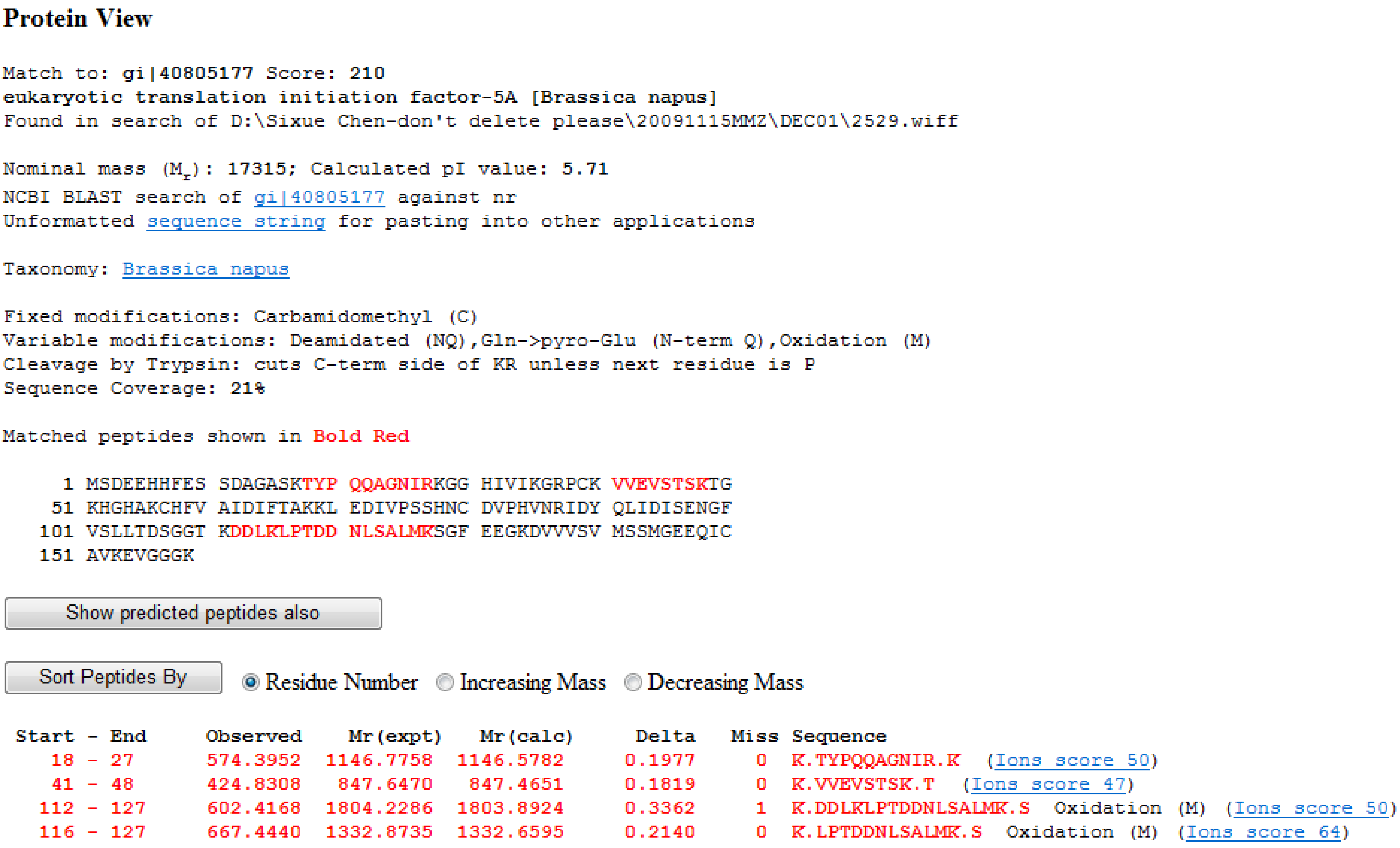
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%

Matched peptides shown in **Bold Red**

```
    1 MAVSSATASS KLILLPHASS SSSLNSTPFR SSTTNTHKLT PLSSSFLHPT
   51 TVLRRTPSST TTPRRTFTVR AARGKFERKK PHVNIGTIGH VDHGKTTLTA
  101 ALTMALAALG NSAPKKYDEI DAAPEERARG ITINTATVEY ETENRHYAHV
  151 DCPGHADYVK NMITGAAQMD GAILVVSGAD GPMPQTKEHI ILAKQVGVPN
  201 MVVFLNKQDQ VDDEELLQLV EIEVRDLLSS YEFPGDDTPI VSGSALLALE
  251 ALMANPAIKR GDNEWVDKIF QLMDEVDNYI PIPQRQTDLP FLLAVEDVFS
  301 ITGRGTVATG RVERGTIKVG ETVDLVGLRE TRNTTVTGVE MFQKILDEAL
  351 AGDNVGLLLR GVQKTDIQRG MVLAKPGTIT PHTKFSAIVY VLKKEEGGRH
  401 SPFFAGYRPQ FYMRTTDVTG KVTSIMNDKD EESTMVLPGD RVKMVVELIV
  451 PVACEQGMRF AIREGGKTVG AGVIQSIIE
```

```
 Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
   319 - 329     579.3593   1156.7041   1156.6452    0.0589     0  K.VGETVDLVGLR.E   (Ions score 79)
```

gi|40805177 Eukaryotic translation initiation factor-5A



Protein View

Match to: gi|40805177 Score: 210
eukaryotic translation initiation factor-5A [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2529.wiff

Nominal mass (M_r): **17315**; Calculated pI value: **5.71**
NCBI BLAST search of gi|40805177 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

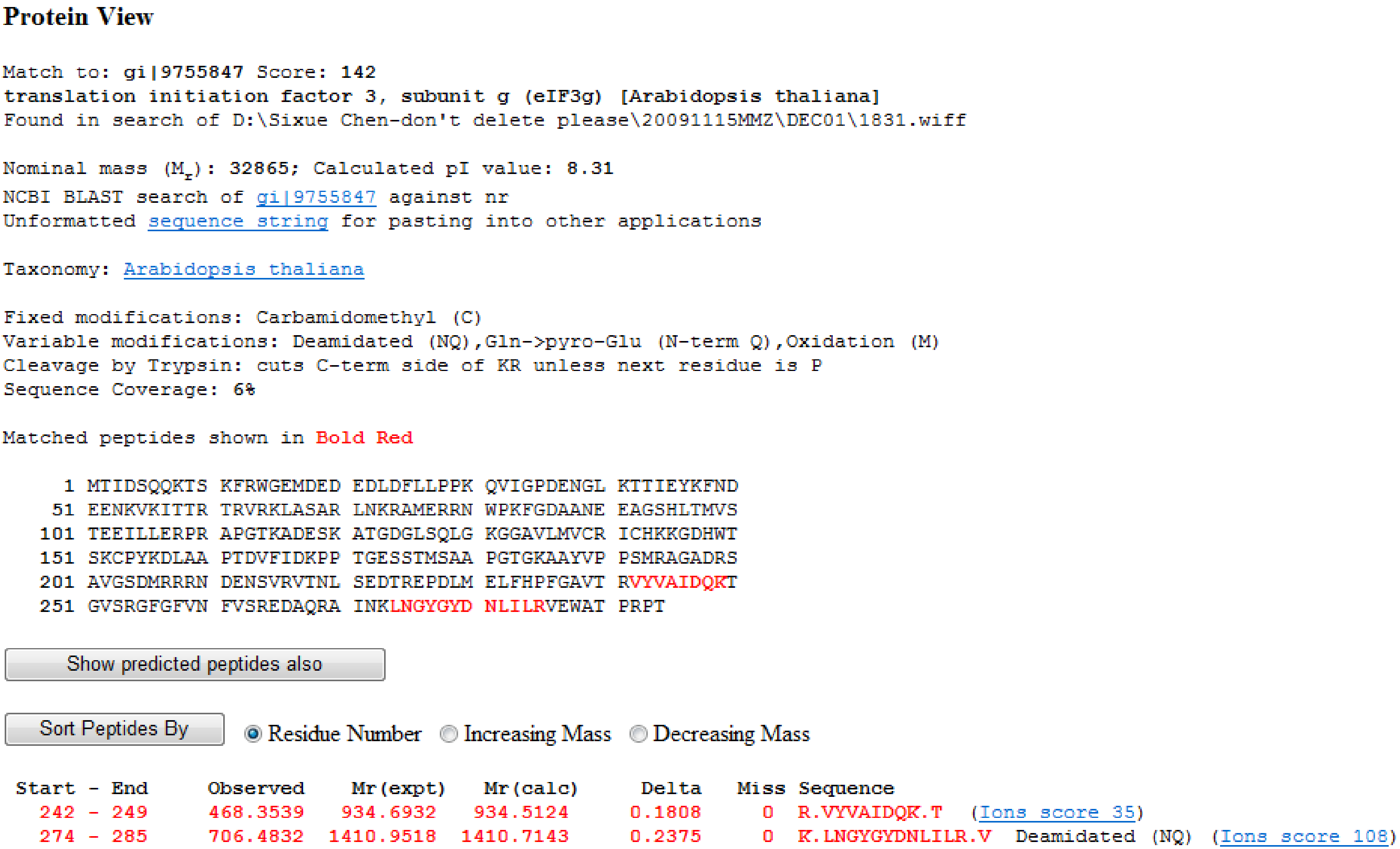
```
  1 MSDEEHHFES SDAGASKTYP QQAGNIRKGG HIVIKGRPCK VVEVSTSKTG
 51 KHGHAKCHFV AIDIFTAKKL EDIVPSSHNC DVPHVNRIDY QLIDISENGF
101 VSLLTDSGGT KDDLKLPTDD NLSALMKSGF EEGKDVVVSV MSSMGEEQIC
151 AVKEVGGGK
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   18 - 27      574.3952   1146.7758  1146.5782    0.1977     0  K.TYPQQAGNIR.K   (Ions score 50)
   41 - 48      424.8308    847.6470   847.4651    0.1819     0  K.VVEVSTSK.T   (Ions score 47)
  112 - 127     602.4168   1804.2286  1803.8924    0.3362     1  K.DDLKLPTDDNLSALMK.S   Oxidation (M)  (Ions score 50)
  116 - 127     667.4440   1332.8735  1332.6595    0.2140     0  K.LPTDDNLSALMK.S   Oxidation (M)  (Ions score 64)
```

gi|9755847 Translation initiation factor 3, subunit g (eIF3g)



Protein View

Match to: gi|9755847 Score: 142
translation initiation factor 3, subunit g (eIF3g) [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1831.wiff

Nominal mass (M_r): 32865; Calculated pI value: 8.31
NCBI BLAST search of gi|9755847 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

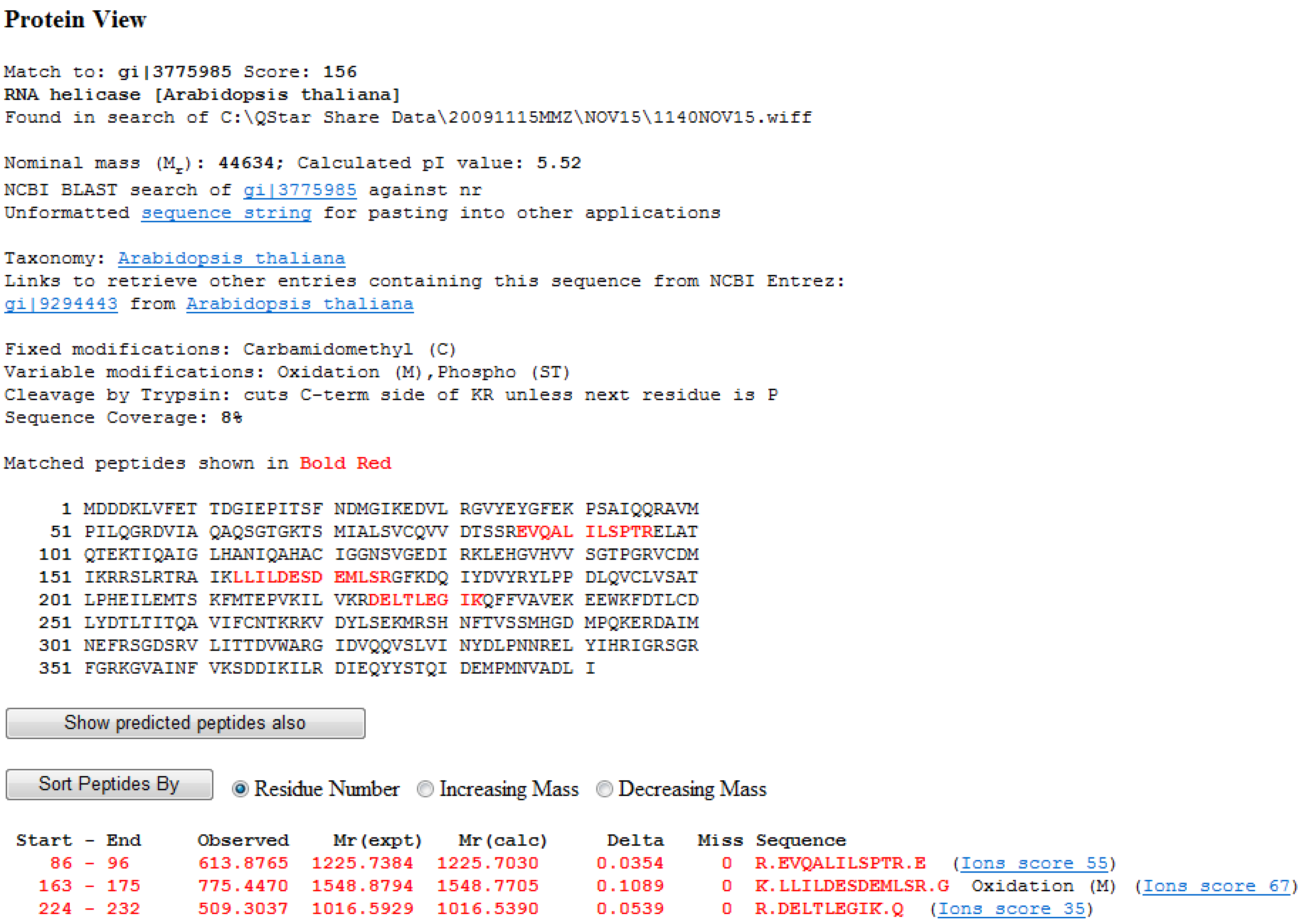
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

```
  1 MTIDSQQKTS KFRWGEMDED EDLDFLLPPK QVIGPDENGL KTTIEYKFND
 51 EENKVKITTR TRVRKLASAR LNKRAMERRN WPKFGDAANE EAGSHLTMVS
101 TEEILLERPR APGTKADESK ATGDGLSQLG KGGAVLMVCR ICHKKGDHWT
151 SKCPYKDLAA PTDVFIDKPP TGESSTMSAA PGTGKAAYVP PSMRAGADRS
201 AVGSDMRRRN DENSVRVTNL SEDTREPDLM ELFHPFGAVT RVYVAIDQKT
251 GVSRGFGFVN FVSREDAQRA INKLNGYGYD NLILRVEWAT PRPT
```

```
Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
  242 - 249     468.3539   934.6932   934.5124   0.1808      0  R.VYVAIDQK.T   (Ions score 35)
  274 - 285     706.4832  1410.9518  1410.7143   0.2375      0  K.LNGYGYDNLILR.V   Deamidated (NQ)  (Ions score 108)
```

gi|3775985 RNA helicase



Protein View

Match to: gi|3775985 Score: 156
RNA helicase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1140NOV15.wiff

Nominal mass (M_r): 44634; Calculated pI value: 5.52
NCBI BLAST search of gi|3775985 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|9294443 from Arabidopsis thaliana

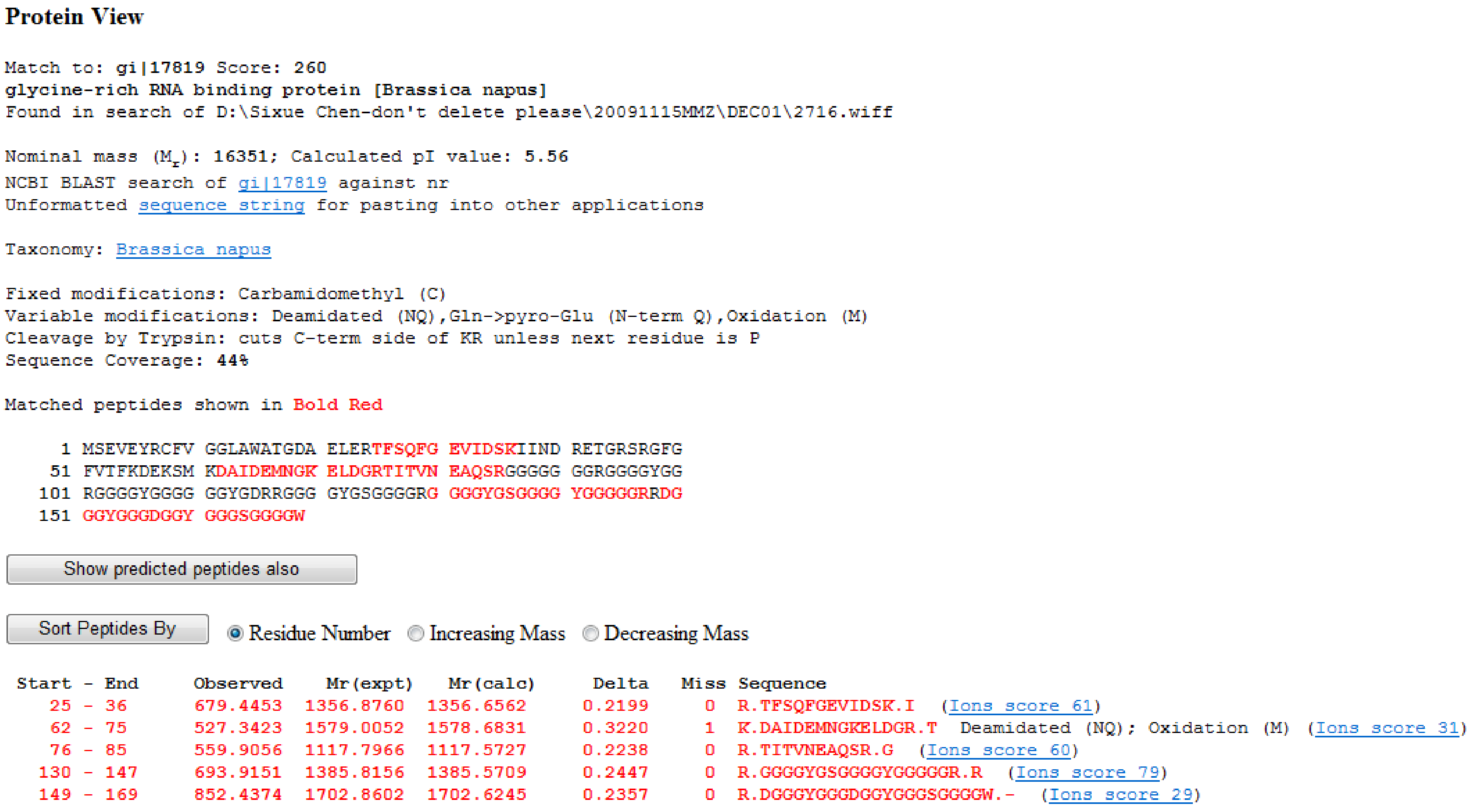
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```
  1 MDDDKLVFET TDGIEPITSF NDMGIKEDVL RGVYEYGFEK PSAIQQRAVM
 51 PILQGRDVIA QAQSGTGKTS MIALSVCQVV DTSSREVQAL ILSPTRELAT
101 QTEKTIQAIG LHANIQAHAC IGGNSVGEDI RKLEHGVHVV SGTPGRVCDM
151 IKRRSLRTRA IKLLILDESD EMLSRGFKDQ IYDVYRYLPP DLQVCLVSAT
201 LPHEILEMTS KFMTEPVKIL VKRDELTLEG IKQFFVAVEK EEWKFDTLCD
251 LYDTLTITQA VIFCNTKRKV DYLSEKMRSH NFTVSSMHGD MPQKERDAIM
301 NEFRSGDSRV LITTDVWARG IDVQQVSLVI NYDLPNNREL YIHRIGRSGR
351 FGRKGVAINF VKSDDIKILR DIEQYYSTQI DEMPMNVADL I
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   86 - 96      613.8765  1225.7384  1225.7030   0.0354    0  R.EVQALILSPTR.E   (Ions score 55)
  163 - 175     775.4470  1548.8794  1548.7705   0.1089    0  K.LLILDESDEMLSR.G  Oxidation (M)  (Ions score 67)
  224 - 232     509.3037  1016.5929  1016.5390   0.0539    0  R.DELTLEGIK.Q   (Ions score 35)
```

gi|17819 Glycine-rich RNA binding protein



Protein View

```
Match to: gi|17819 Score: 260
glycine-rich RNA binding protein [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2716.wiff

Nominal mass (Mr): 16351; Calculated pI value: 5.56
NCBI BLAST search of gi|17819 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

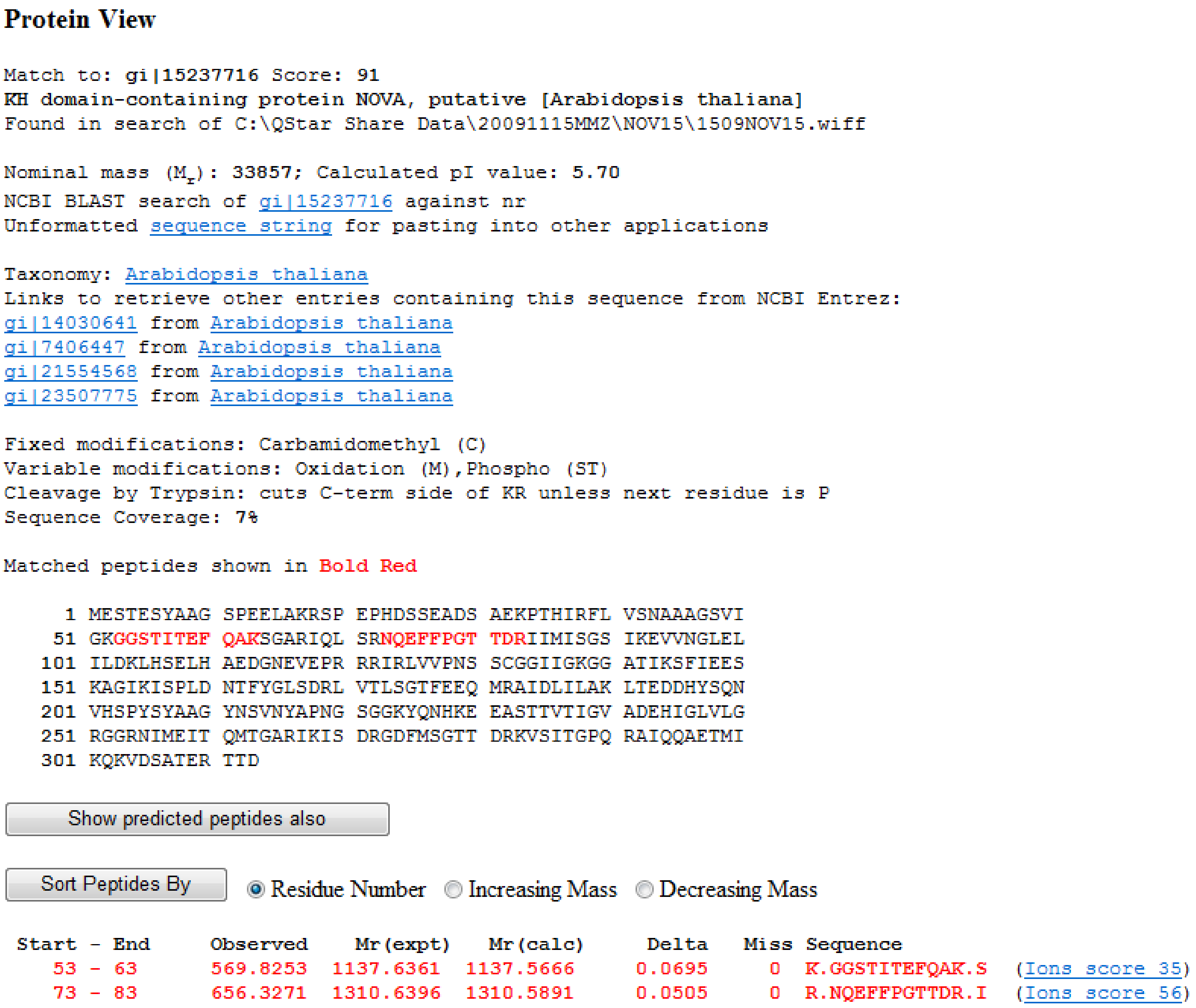
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 44%

Matched peptides shown in Bold Red

     1 MSEVEYRCFV GGLAWATGDA ELERTFSQFG EVIDSKIIND RETGRSRGFG
    51 FVTFKDEKSM KDAIDEMNGK ELDGRTITVN EAQSRGGGGG GGRGGGGYGG
   101 RGGGGYGGGG GGYGDRRGGG GYGSGGGGRG GGGYGSGGGG YGGGGGRRDG
   151 GGYGGGDGGY GGGSGGGGW
```

```
 Start - End      Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
    25 - 36       679.4453   1356.8760   1356.6562    0.2199     0  R.TFSQFGEVIDSK.I   (Ions score 61)
    62 - 75       527.3423   1579.0052   1578.6831    0.3220     1  K.DAIDEMNGKELDGR.T  Deamidated (NQ); Oxidation (M)  (Ions score 31)
    76 - 85       559.9056   1117.7966   1117.5727    0.2238     0  R.TITVNEAQSR.G  (Ions score 60)
   130 - 147      693.9151   1385.8156   1385.5709    0.2447     0  R.GGGGYGSGGGGYGGGGGR.R  (Ions score 79)
   149 - 169      852.4374   1702.8602   1702.6245    0.2357     0  R.DGGGYGGGDGGYGGGSGGGGW.-  (Ions score 29)
```

gi|15237716 KH domain-containing protein NOVA, putative



Protein View

Match to: gi|15237716 Score: 91
KH domain-containing protein NOVA, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1509NOV15.wiff

Nominal mass (M_r): 33857; Calculated pI value: 5.70
NCBI BLAST search of gi|15237716 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|14030641 from Arabidopsis thaliana
gi|7406447 from Arabidopsis thaliana
gi|21554568 from Arabidopsis thaliana
gi|23507775 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

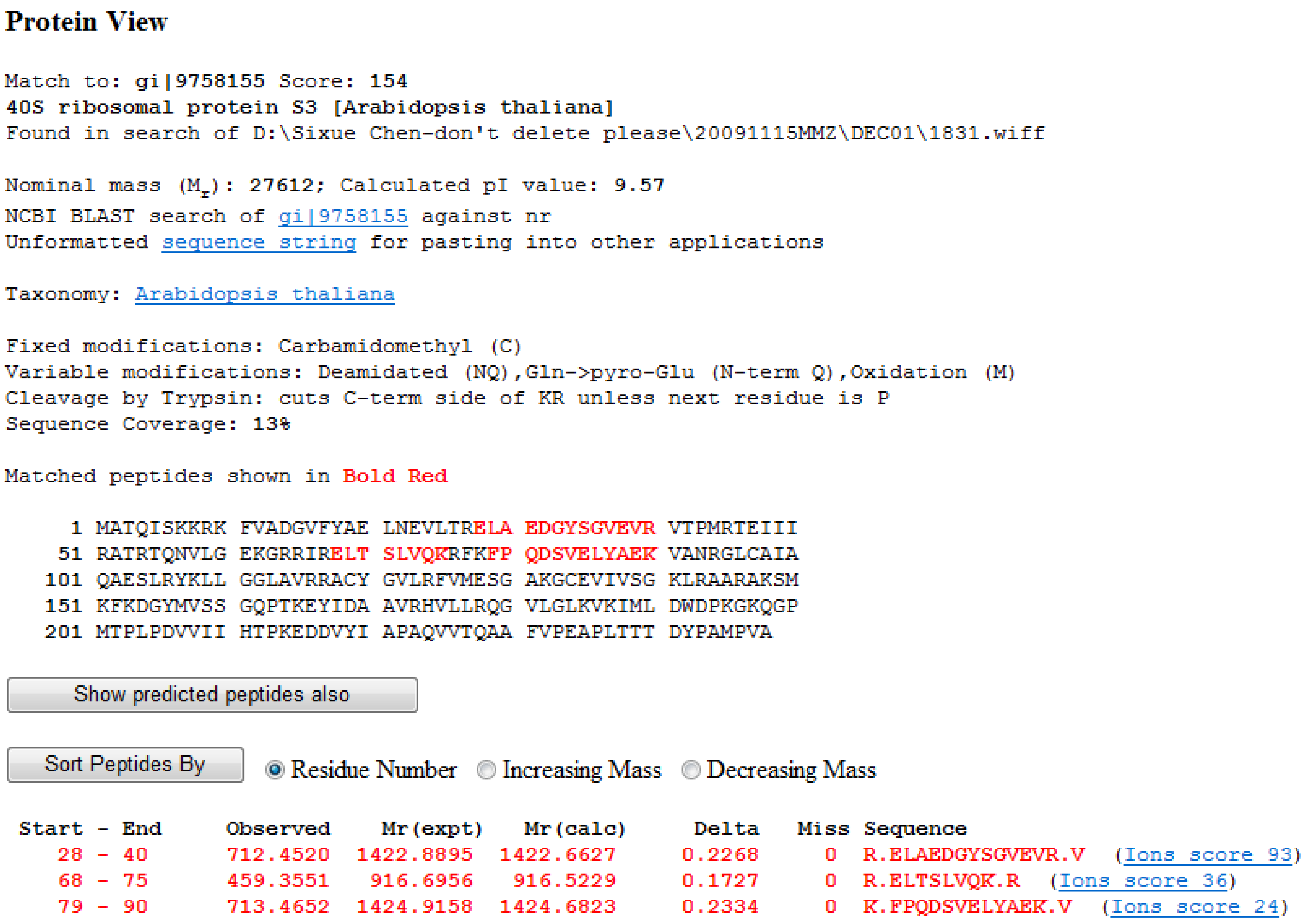
Matched peptides shown in **Bold Red**

```
     1 MESTESYAAG SPEELAKRSP EPHDSSEADS AEKPTHIRFL VSNAAAGSVI
    51 GKGGSTITEF QAKSGARIQL SRNQEFFPGT TDRIIMISGS IKEVVNGLEL
   101 ILDKLHSELH AEDGNEVEPR RRIRLVVPNS SCGGIIGKGG ATIKSFIEES
   151 KAGIKISPLD NTFYGLSDRL VTLSGTFEEQ MRAIDLILAK LTEDDHYSQN
   201 VHSPYSYAAG YNSVNYAPNG SGGKYQNHKE EASTTVTIGV ADEHIGLVLG
   251 RGGRNIMEIT QMTGARIKIS DRGDFMSGTT DRKVSITGPQ RAIQQAETMI
   301 KQKVDSATER TTD
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   53 - 63       569.8253   1137.6361  1137.5666    0.0695     0   K.GGSTITEFQAK.S    (Ions score 35)
   73 - 83       656.3271   1310.6396  1310.5891    0.0505     0   R.NQEFFPGTTDR.I    (Ions score 56)
```

gi|9758155 40S ribosomal protein S3



Protein View

```
Match to: gi|9758155 Score: 154
40S ribosomal protein S3 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1831.wiff

Nominal mass (Mr): 27612; Calculated pI value: 9.57
NCBI BLAST search of gi|9758155 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%

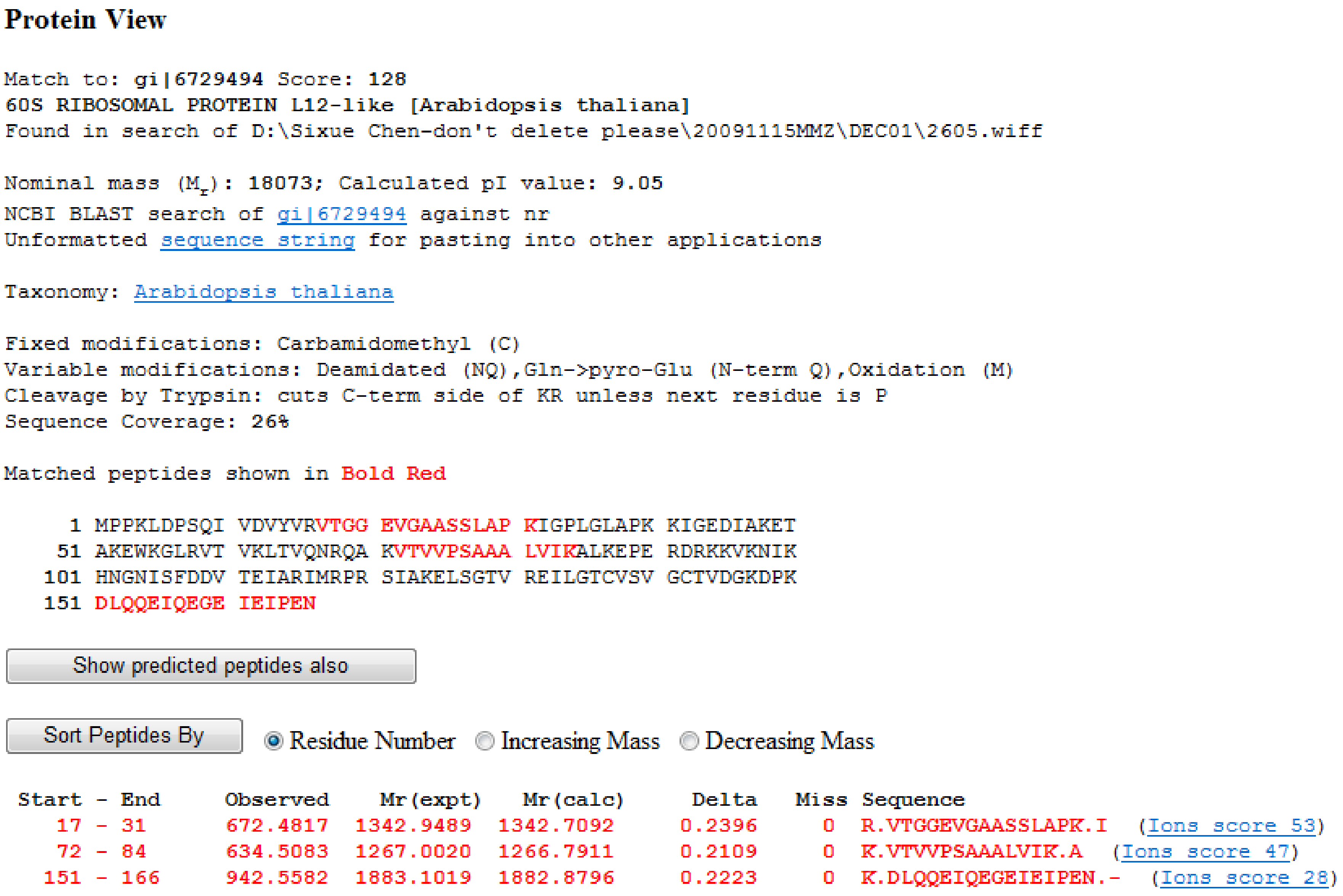
Matched peptides shown in Bold Red

     1 MATQISKKRK FVADGVFYAE LNEVLTRELA EDGYSGVEVR VTPMRTEIII
    51 RATRTQNVLG EKGRRIRELT SLVQKRFKFP QDSVELYAEK VANRGLCAIA
   101 QAESLRYKLL GGLAVRRACY GVLRFVMESG AKGCEVIVSG KLRAARAKSM
   151 KFKDGYMVSS GQPTKEYIDA AVRHVLLRQG VLGLKVKIML DWDPKGKQGP
   201 MTPLPDVVII HTPKEDDVYI APAQVVTQAA FVPEAPLTTT DYPAMPVA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   28 - 40       712.4520   1422.8895  1422.6627    0.2268     0  R.ELAEDGYSGVEVR.V   (Ions score 93)
   68 - 75       459.3551    916.6956   916.5229    0.1727     0  R.ELTSLVQK.R   (Ions score 36)
   79 - 90       713.4652   1424.9158  1424.6823    0.2334     0  K.FPQDSVELYAEK.V   (Ions score 24)
```

gi|6729494 60S ribosomal protein L12-like



Protein View

```
Match to: gi|6729494 Score: 128
60S RIBOSOMAL PROTEIN L12-like [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2605.wiff

Nominal mass (Mr): 18073; Calculated pI value: 9.05
NCBI BLAST search of gi|6729494 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 26%

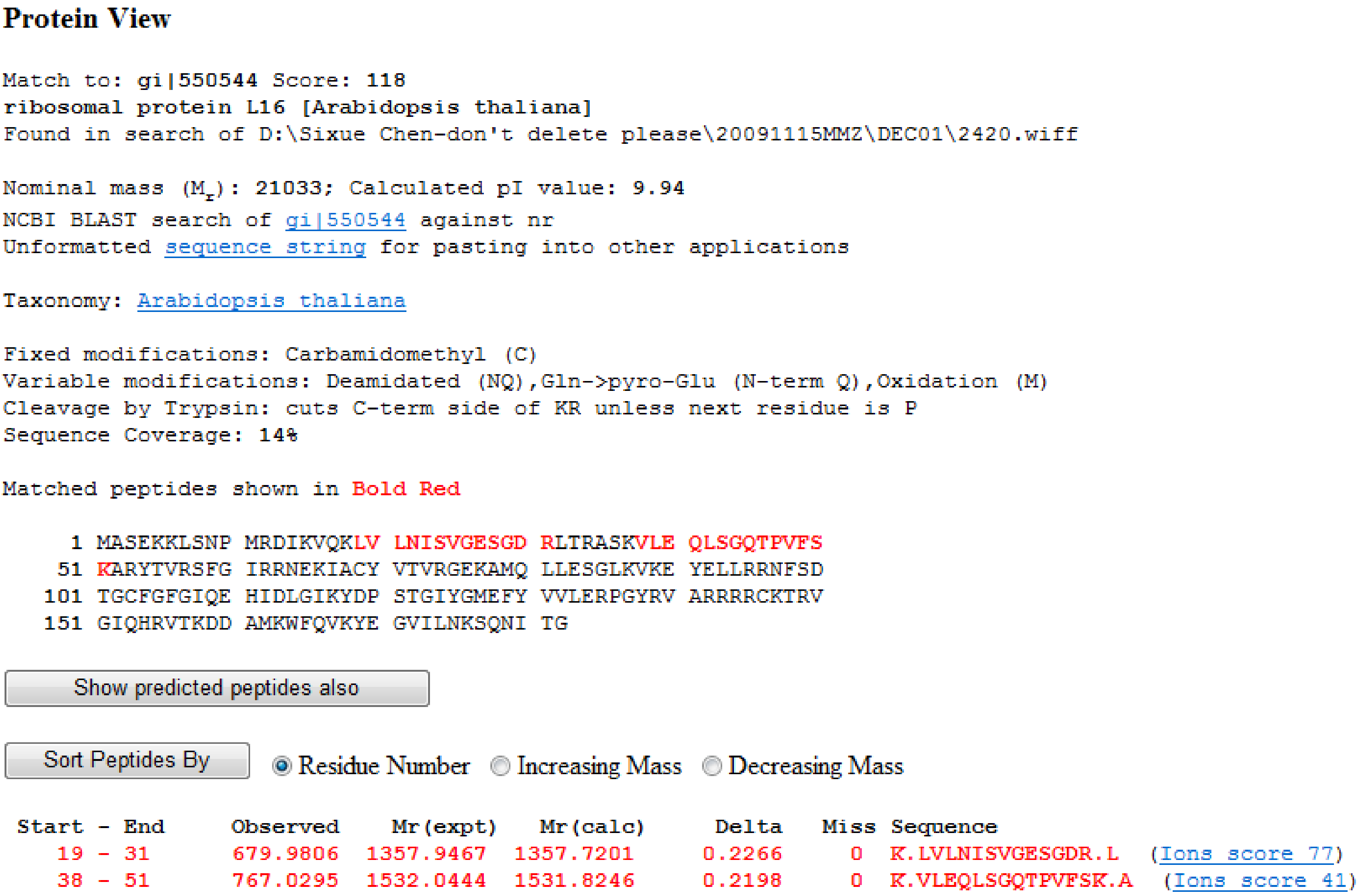
Matched peptides shown in Bold Red

     1 MPPKLDPSQI VDVYVRVTGG EVGAASSLAP KIGPLGLAPK KIGEDIAKET
    51 AKEWKGLRVT VKLTVQNRQA KVTVVPSAAA LVIKALKEPE RDRKKVKNIK
   101 HNGNISFDDV TEIARIMRPR SIAKELSGTV REILGTCVSV GCTVDGKDPK
   151 DLQQEIQEGE IEIPEN
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss  Sequence
   17 - 31     672.4817  1342.9489  1342.7092    0.2396     0  R.VTGGEVGAASSLAPK.I   (Ions score 53)
   72 - 84     634.5083  1267.0020  1266.7911    0.2109     0  K.VTVVPSAAALVIK.A   (Ions score 47)
  151 - 166    942.5582  1883.1019  1882.8796    0.2223     0  K.DLQQEIQEGEIEIPEN.-   (Ions score 28)
```

gi|550544 RIbosomal protein L16



Protein View

Match to: gi|550544 Score: 118
ribosomal protein L16 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2420.wiff

Nominal mass (M_r): 21033; Calculated pI value: 9.94
NCBI BLAST search of gi|550544 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 14%

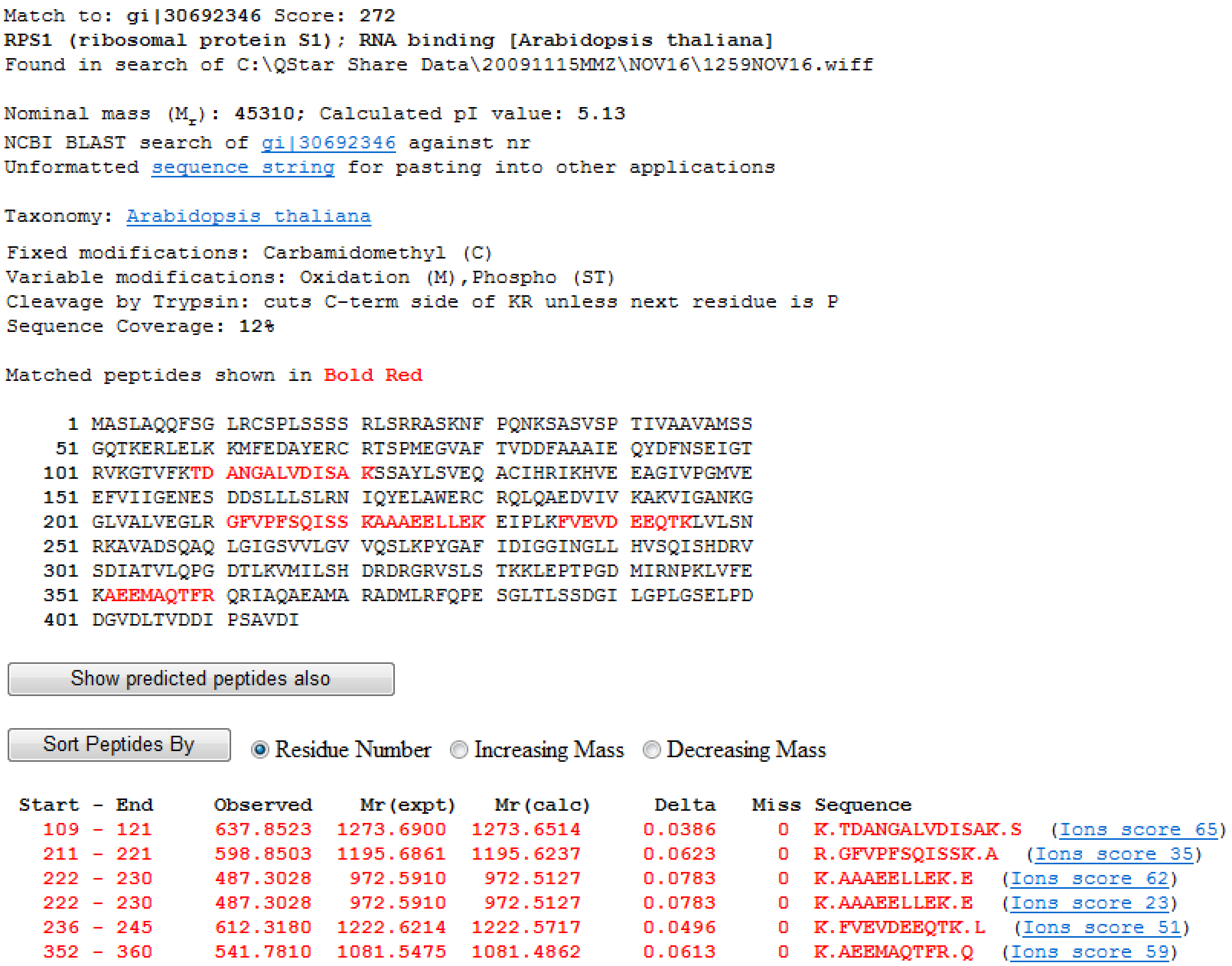
Matched peptides shown in **Bold Red**

```
  1 MASEKKLSNP MRDIKVQKLV LNISVGESGD RLTRASKVLE QLSGQTPVFS
 51 KARYTVRSFG IRRNEKIACY VTVRGEKAMQ LLESGLKVKE YELLRRNFSD
101 TGCFGFGIQE HIDLGIKYDP STGIYGMEFY VVLERPGYRV ARRRRCKTRV
151 GIQHRVTKDD AMKWFQVKYE GVILNKSQNI TG
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   19 - 31       679.9806  1357.9467  1357.7201    0.2266     0  K.LVLNISVGESGDR.L   (Ions score 77)
   38 - 51       767.0295  1532.0444  1531.8246    0.2198     0  K.VLEQLSGQTPVFSK.A   (Ions score 41)
```

gi|30692346 Ribosomal protein S1; RNA binding



```
Match to: gi|30692346 Score: 272
RPS1 (ribosomal protein S1); RNA binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\1259NOV16.wiff

Nominal mass (Mr): 45310; Calculated pI value: 5.13
NCBI BLAST search of gi|30692346 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

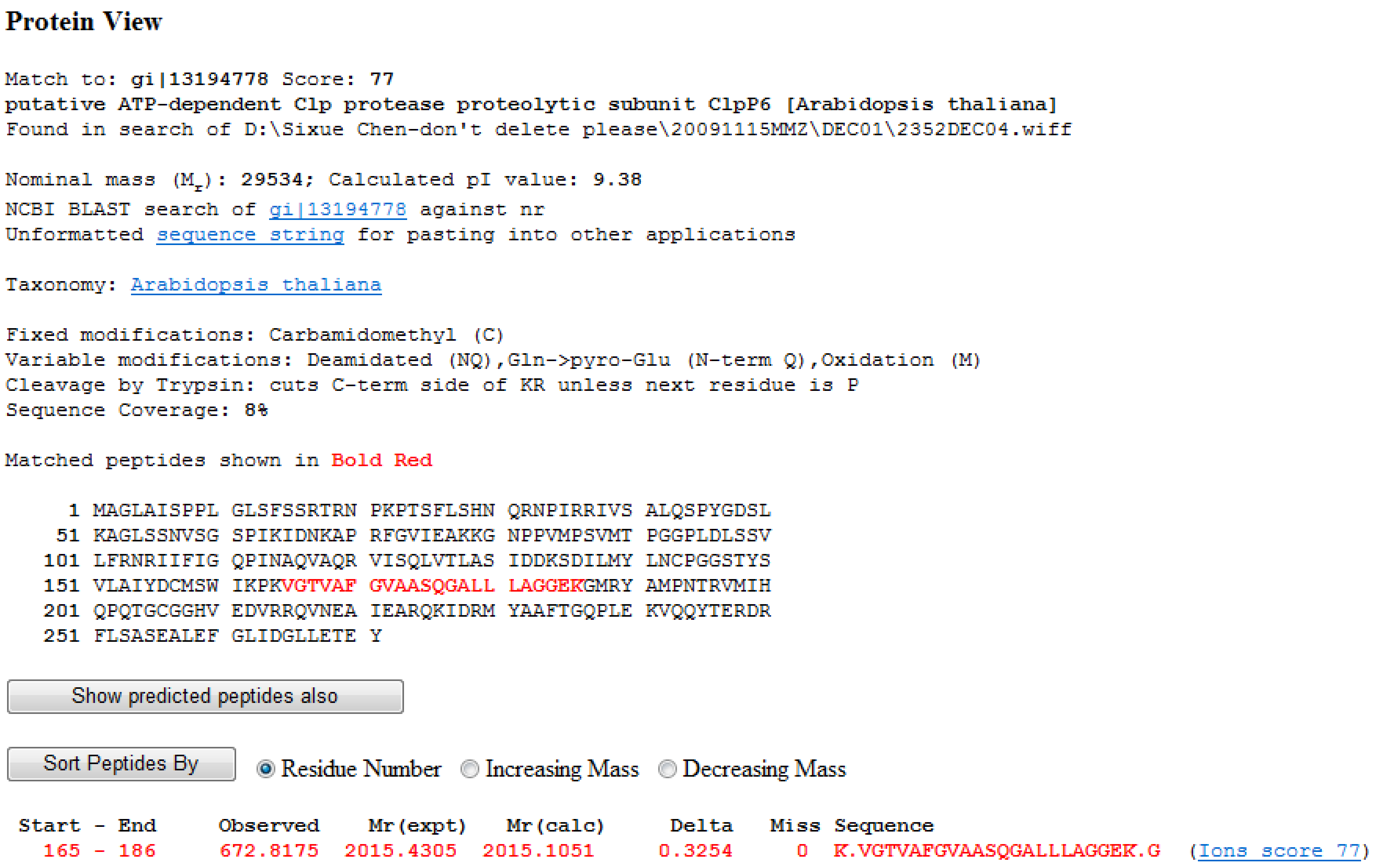
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 12%

Matched peptides shown in Bold Red

     1 MASLAQQFSG LRCSPLSSSS RLSRRASKNF PQNKSASVSP TIVAAVAMSS
    51 GQTKERLELK KMFEDAYERC RTSPMEGVAF TVDDFAAAIE QYDFNSEIGT
   101 RVKGTVFKTD ANGALVDISA KSSAYLSVEQ ACIHRIKHVE EAGIVPGMVE
   151 EFVIIGENES DDSLLLSLRN IQYELAWERC RQLQAEDVIV KAKVIGANKG
   201 GLVALVEGLR GFVPFSQISS KAAAEELLEK EIPLKFVEVD EEQTKLVLSN
   251 RKAVADSQAQ LGIGSVVLGV VQSLKPYGAF IDIGGINGLL HVSQISHDRV
   301 SDIATVLQPG DTLKVMILSH DRDRGRVSLS TKKLEPTPGD MIRNPKLVFE
   351 KAEEMAQTFR QRIAQAEAMA RADMLRFQPE SGLTLSSDGI LGPLGSELPD
   401 DGVDLTVDDI PSAVDI
```

```
 Start - End     Observed    Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   109 - 121     637.8523   1273.6900  1273.6514    0.0386     0  K.TDANGALVDISAK.S   (Ions score 65)
   211 - 221     598.8503   1195.6861  1195.6237    0.0623     0  R.GFVPFSQISSK.A   (Ions score 35)
   222 - 230     487.3028    972.5910   972.5127    0.0783     0  K.AAAEELLEK.E   (Ions score 62)
   222 - 230     487.3028    972.5910   972.5127    0.0783     0  K.AAAEELLEK.E   (Ions score 23)
   236 - 245     612.3180   1222.6214  1222.5717    0.0496     0  K.FVEVDEEQTK.L   (Ions score 51)
   352 - 360     541.7810   1081.5475  1081.4862    0.0613     0  K.AEEMAQTFR.Q   (Ions score 59)
```

gi|13194778 Putative ATP-dependent Clp protease proteolytic subunit ClpP6



Protein View

Match to: gi|13194778 Score: 77
putative ATP-dependent Clp protease proteolytic subunit ClpP6 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2352DEC04.wiff

Nominal mass (M_r): 29534; Calculated pI value: 9.38
NCBI BLAST search of gi|13194778 against nr
Unformatted sequence string for pasting into other applications

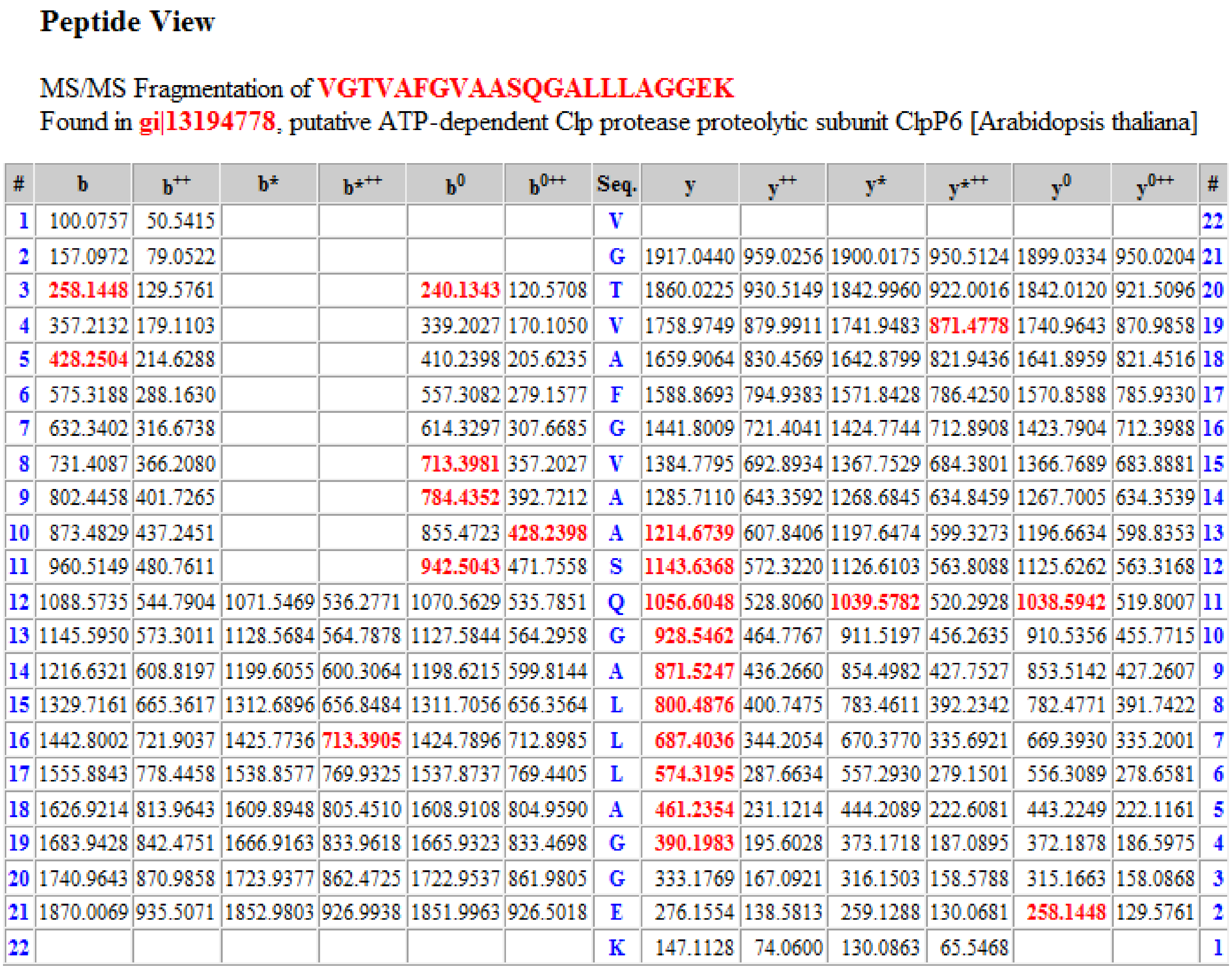
Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

1 MAGLAISPPL GLSFSSRTRN PKPTSFLSHN QRNPIRRIVS ALQSPYGDSL
51 KAGLSSNVSG SPIKIDNKAP RFGVIEAKKG NPPVMPSVMT PGGPLDLSSV
101 LFRNRIIFIG QPINAQVAQR VISQLVTLAS IDDKSDILMY LNCPGGSTYS
151 VLAIYDCMSW IKPK**VGTVAF GVAASQGALL LAGGEK**GMRY AMPNTRVMIH
201 QPQTGCGGHV EDVRRQVNEA IEARQKIDRM YAAFTGQPLE KVQQYTERDR
251 FLSASEALEF GLIDGLLETE Y

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
165 - 186	672.8175	2015.4305	2015.1051	0.3254	0	K.VGTVAFGVAASQGALLLAGGEK.G	(Ions score 77)

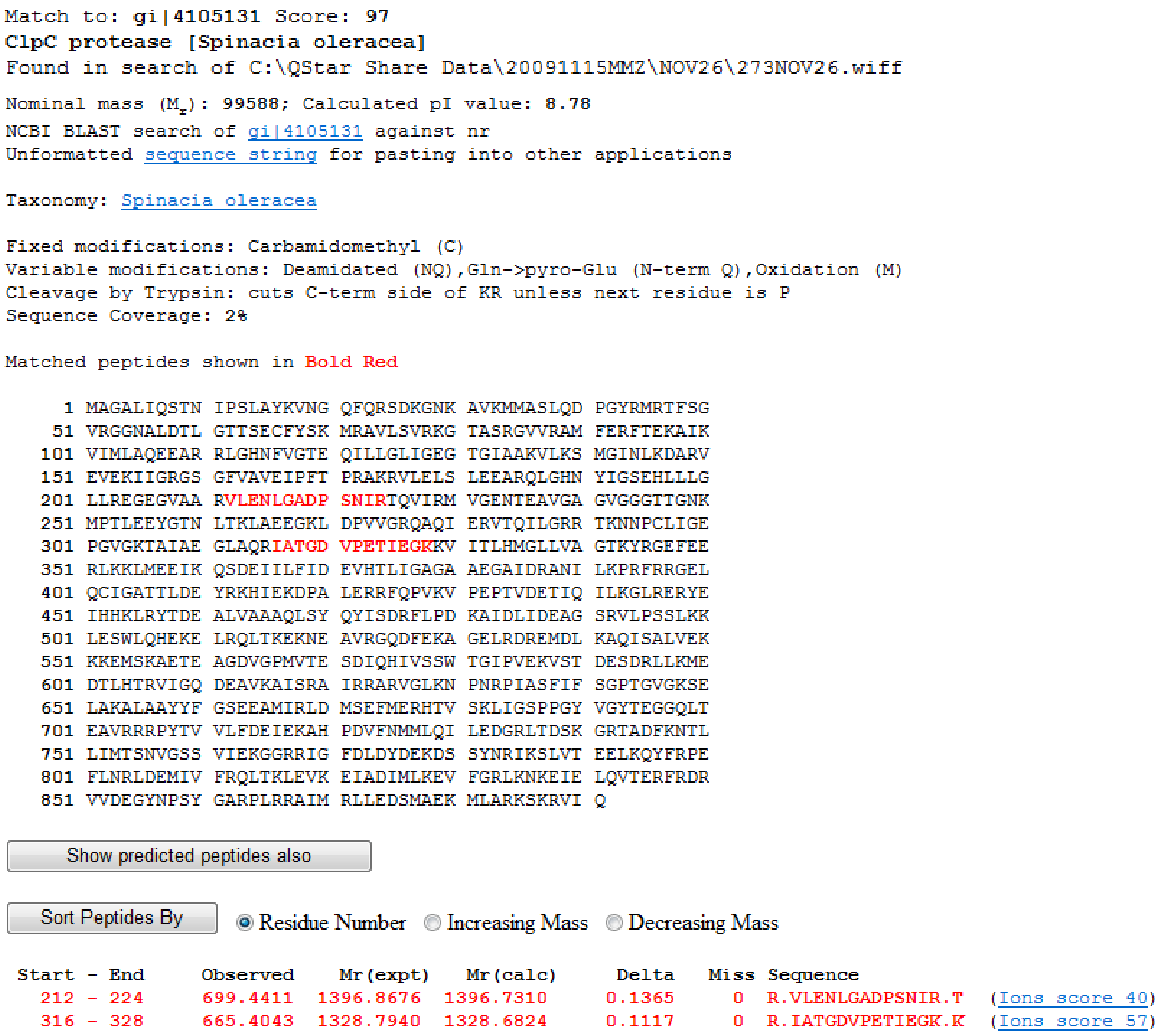


Peptide View

MS/MS Fragmentation of **VGTVAFGVAASQGALLLAGGEK**
Found in **gi|13194778**, putative ATP-dependent Clp protease proteolytic subunit ClpP6 [Arabidopsis thaliana]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							22
2	157.0972	79.0522					G	1917.0440	959.0256	1900.0175	950.5124	1899.0334	950.0204	21
3	**258.1448**	129.5761			**240.1343**	120.5708	T	1860.0225	930.5149	1842.9960	922.0016	1842.0120	921.5096	20
4	357.2132	179.1103			339.2027	170.1050	V	1758.9749	879.9911	1741.9483	**871.4778**	1740.9643	870.9858	19
5	**428.2504**	214.6288			410.2398	205.6235	A	1659.9064	830.4569	1642.8799	821.9436	1641.8959	821.4516	18
6	575.3188	288.1630			557.3082	279.1577	F	1588.8693	794.9383	1571.8428	786.4250	1570.8588	785.9330	17
7	632.3402	316.6738			614.3297	307.6685	G	1441.8009	721.4041	1424.7744	712.8908	1423.7904	712.3988	16
8	731.4087	366.2080			**713.3981**	357.2027	V	1384.7795	692.8934	1367.7529	684.3801	1366.7689	683.8881	15
9	802.4458	401.7265			**784.4352**	392.7212	A	1285.7110	643.3592	1268.6845	634.8459	1267.7005	634.3539	14
10	873.4829	437.2451			855.4723	**428.2398**	A	**1214.6739**	607.8406	1197.6474	599.3273	1196.6634	598.8353	13
11	960.5149	480.7611			**942.5043**	471.7558	S	**1143.6368**	572.3220	1126.6103	563.8088	1125.6262	563.3168	12
12	1088.5735	544.7904	1071.5469	536.2771	1070.5629	535.7851	Q	**1056.6048**	528.8060	**1039.5782**	520.2928	**1038.5942**	519.8007	11
13	1145.5950	573.3011	1128.5684	564.7878	1127.5844	564.2958	G	**928.5462**	464.7767	911.5197	456.2635	910.5356	455.7715	10
14	1216.6321	608.8197	1199.6055	600.3064	1198.6215	599.8144	A	**871.5247**	436.2660	854.4982	427.7527	853.5142	427.2607	9
15	1329.7161	665.3617	1312.6896	656.8484	1311.7056	656.3564	L	**800.4876**	400.7475	783.4611	392.2342	782.4771	391.7422	8
16	1442.8002	721.9037	1425.7736	**713.3905**	1424.7896	712.8985	L	**687.4036**	344.2054	670.3770	335.6921	669.3930	335.2001	7
17	1555.8843	778.4458	1538.8577	769.9325	1537.8737	769.4405	L	**574.3195**	287.6634	557.2930	279.1501	556.3089	278.6581	6
18	1626.9214	813.9643	1609.8948	805.4510	1608.9108	804.9590	A	**461.2354**	231.1214	444.2089	222.6081	443.2249	222.1161	5
19	1683.9428	842.4751	1666.9163	833.9618	1665.9323	833.4698	G	**390.1983**	195.6028	373.1718	187.0895	372.1878	186.5975	4
20	1740.9643	870.9858	1723.9377	862.4725	1722.9537	861.9805	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
21	1870.0069	935.5071	1852.9803	926.9938	1851.9963	926.5018	E	276.1554	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
22							K	147.1128	74.0600	130.0863	65.5468			1

gi|4105131 ClpC protease



Match to: gi|4105131 Score: 97
ClpC protease [Spinacia oleracea]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\273NOV26.wiff

Nominal mass (M_r): 99588; Calculated pI value: 8.78
NCBI BLAST search of gi|4105131 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Spinacia oleracea

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%

Matched peptides shown in **Bold Red**

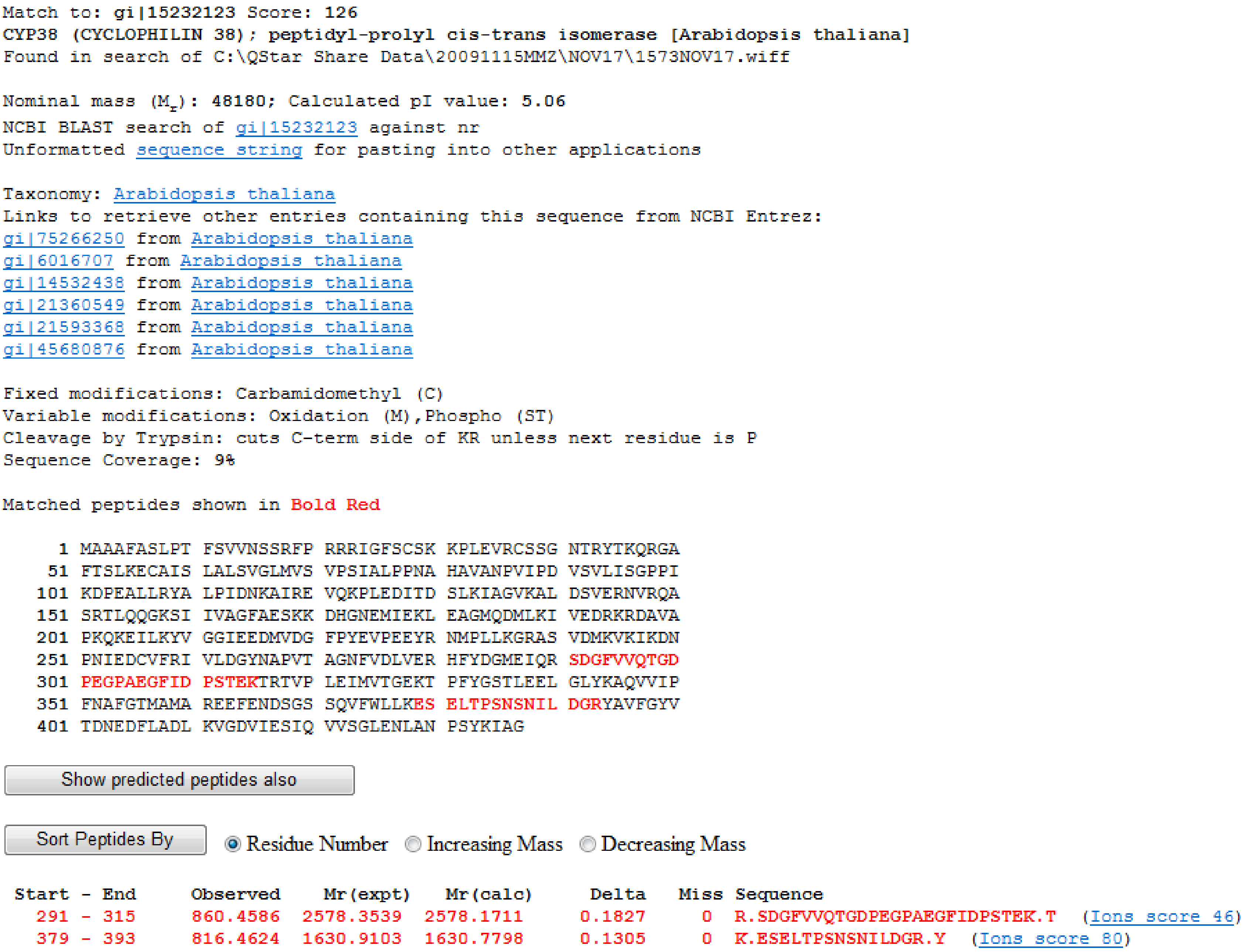
```
  1 MAGALIQSTN IPSLAYKVNG QFQRSDKGNK AVKMMASLQD PGYRMRTFSG
 51 VRGGNALDTL GTTSECFYSK MRAVLSVRKG TASRGVVRAM FERFTEKAIK
101 VIMLAQEEAR RLGHNFVGTE QILLGLIGEG TGIAAKVLKS MGINLKDARV
151 EVEKIIGRGS GFVAVEIPFT PRAKRVLELS LEEARQLGHN YIGSEHLLLG
201 LLREGEGVAA RVLENLGADP SNIRTQVIRM VGENTEAVGA GVGGGTTGNK
251 MPTLEEYGTN LTKLAEEGKL DPVVGRQAQI ERVTQILGRR TKNNPCLIGE
301 PGVGKTAIAE GLAQRIATGD VPETIEGKKV ITLHMGLLVA GTKYRGEFEE
351 RLKKLMEEIK QSDEIILFID EVHTLIGAGA AEGAIDRANI LKPRFRRGEL
401 QCIGATTLDE YRKHIEKDPA LERRFQPVKV PEPTVDETIQ ILKGLRERYE
451 IHHKLRYTDE ALVAAAQLSY QYISDRFLPD KAIDLIDEAG SRVLPSSLKK
501 LESWLQHEKE LRQLTKEKNE AVRGQDFEKA GELRDREMDL KAQISALVEK
551 KKEMSKAETE AGDVGPMVTE SDIQHIVSSW TGIPVEKVST DESDRLLKME
601 DTLHTRVIGQ DEAVKAISRA IRRARVGLKN PNRPIASFIF SGPTGVGKSE
651 LAKALAAYYF GSEEAMIRLD MSEFMERHTV SKLIGSPPGY VGYTEGGQLT
701 EAVRRRPYTV VLFDEIEKAH PDVFNMMLQI LEDGRLTDSK GRTADFKNTL
751 LIMTSNVGSS VIEKGGRRIG FDLDYDEKDS SYNRIKSLVT EELKQYFRPE
801 FLNRLDEMIV FRQLTKLEVK EIADIMLKEV FGRLKNKEIE LQVTERFRDR
851 VVDEGYNPSY GARPLRRAIM RLLEDSMAEK MLARKSKRVI Q
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End    Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
 212 - 224     699.4411  1396.8676  1396.7310   0.1365     0 R.VLENLGADPSNIR.T   (Ions score 40)
 316 - 328     665.4043  1328.7940  1328.6824   0.1117     0 R.IATGDVPETIEGK.K   (Ions score 57)
```

gi|15232123 Cyclophilin 38 (CYP38); peptidyl-prolyl cis-trans isomerase



Match to: gi|15232123 Score: 126
CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r): 48180; Calculated pI value: 5.06
NCBI BLAST search of gi|15232123 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|75266250 from Arabidopsis thaliana
gi|6016707 from Arabidopsis thaliana
gi|14532438 from Arabidopsis thaliana
gi|21360549 from Arabidopsis thaliana
gi|21593368 from Arabidopsis thaliana
gi|45680876 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

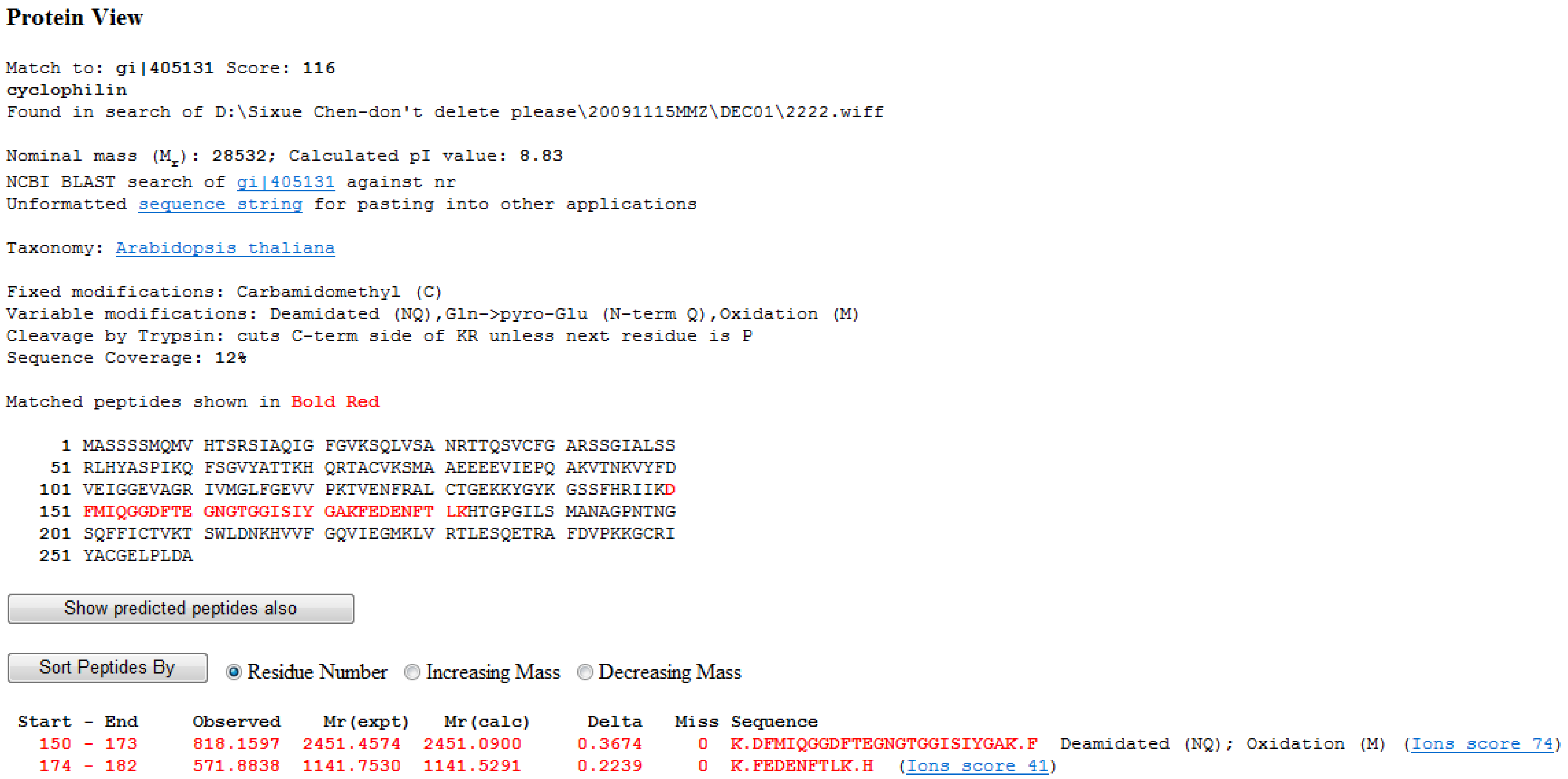
Matched peptides shown in **Bold Red**

```
  1 MAAAFASLPT FSVVNSSRFP RRRIGFSCSK KPLEVRCSSG NTRYTKQRGA
 51 FTSLKECAIS LALSVGLMVS VPSIALPPNA HAVANPVIPD VSVLISGPPI
101 KDPEALLRYA LPIDNKAIRE VQKPLEDITD SLKIAGVKAL DSVERNVRQA
151 SRTLQQGKSI IVAGFAESKK DHGNEMIEKL EAGMQDMLKI VEDRKRDAVA
201 PKQKEILKYV GGIEEDMVDG FPYEVPEEYR NMPLLKGRAS VDMKVKIKDN
251 PNIEDCVFRI VLDGYNAPVT AGNFVDLVER HFYDGMEIQR SDGFVVQTGD
301 PEGPAEGFID PSTEKTRTVP LEIMVTGEKT PFYGSTLEEL GLYKAQVVIP
351 FNAFGTMAMA REEFENDSGS SQVFWLLKES ELTPSNSNIL DGRYAVFGYV
401 TDNEDFLADL KVGDVIESIQ VVSGLENLAN PSYKIAG
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)      Delta   Miss  Sequence
  291 - 315     860.4586  2578.3539  2578.1711     0.1827      0  R.SDGFVVQTGDPEGPAEGFIDPSTEK.T   (Ions score 46)
  379 - 393     816.4624  1630.9103  1630.7798     0.1305      0  K.ESELTPSNSNILDGR.Y   (Ions score 80)
```

gi|405131 Cyclophilin



Protein View

Match to: **gi|405131** Score: **116**
cyclophilin
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2222.wiff

Nominal mass (M_r): **28532**; Calculated pI value: **8.83**
NCBI BLAST search of gi|405131 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

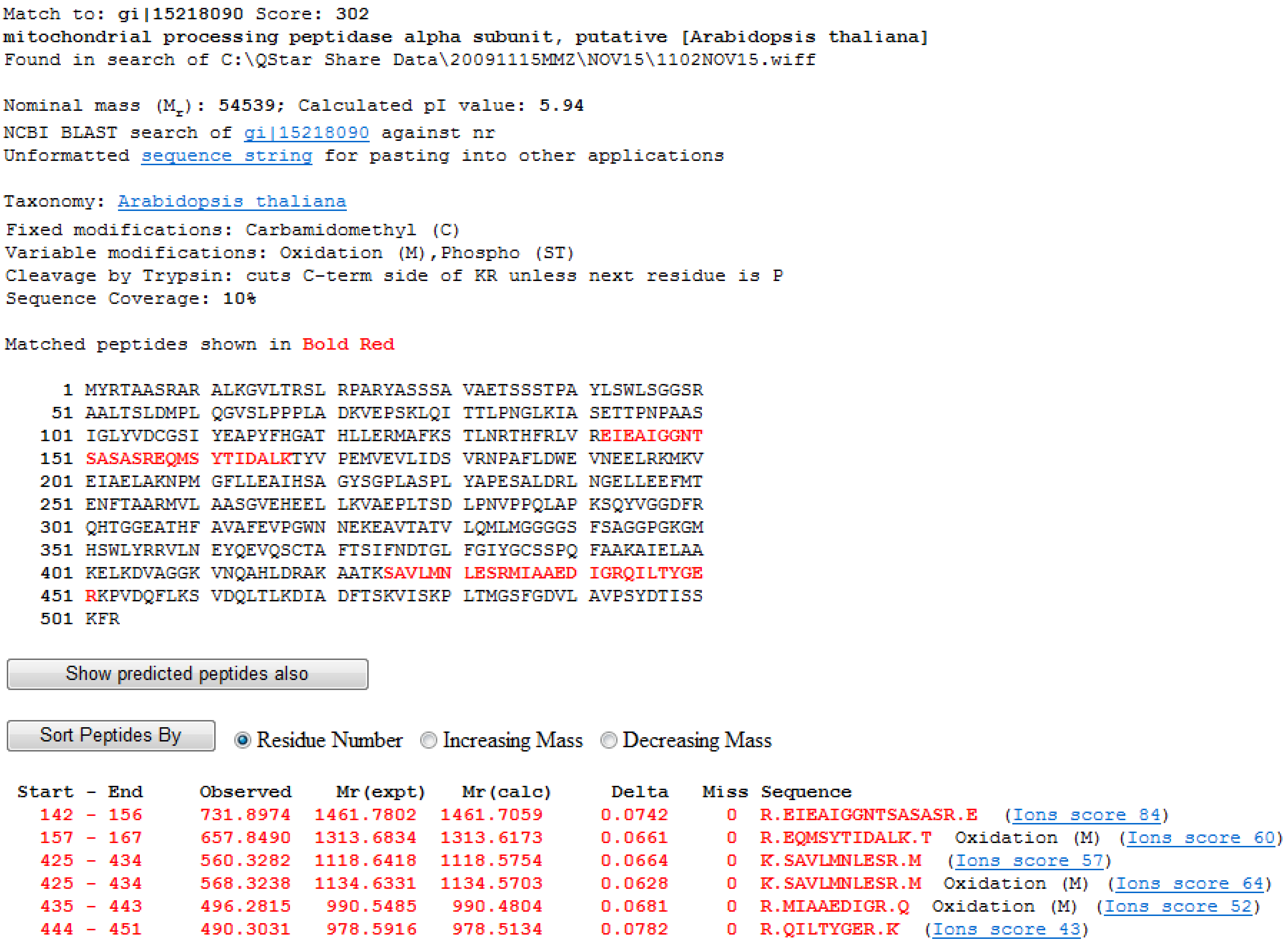
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
     1 MASSSSMQMV HTSRSIAQIG FGVKSQLVSA NRTTQSVCFG ARSSGIALSS
    51 RLHYASPIKQ FSGVYATTKH QRTACVKSMA AEEEEVIEPQ AKVTNKVYFD
   101 VEIGGEVAGR IVMGLFGEVV PKTVENFRAL CTGEKKYGYK GSSFHRIIKD
   151 FMIQGGDFTE GNGTGGISIY GAKFEDENFT LKHTGPGILS MANAGPNTNG
   201 SQFFICTVKT SWLDNKHVVF GQVIEGMKLV RTLESQETRA FDVPKKGCRI
   251 YACGELPLDA
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   150 - 173     818.1597  2451.4574  2451.0900    0.3674     0 K.DFMIQGGDFTEGNGTGGISIYGAK.F  Deamidated (NQ); Oxidation (M) (Ions score 74)
   174 - 182     571.8838  1141.7530  1141.5291    0.2239     0 K.FEDENFTLK.H  (Ions score 41)
```

gi|15218090 Mitochondrial processing peptidase alpha subunit, putative



Match to: gi|15218090 Score: 302
mitochondrial processing peptidase alpha subunit, putative [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (M_r): 54539; Calculated pI value: 5.94
NCBI BLAST search of gi|15218090 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 10%

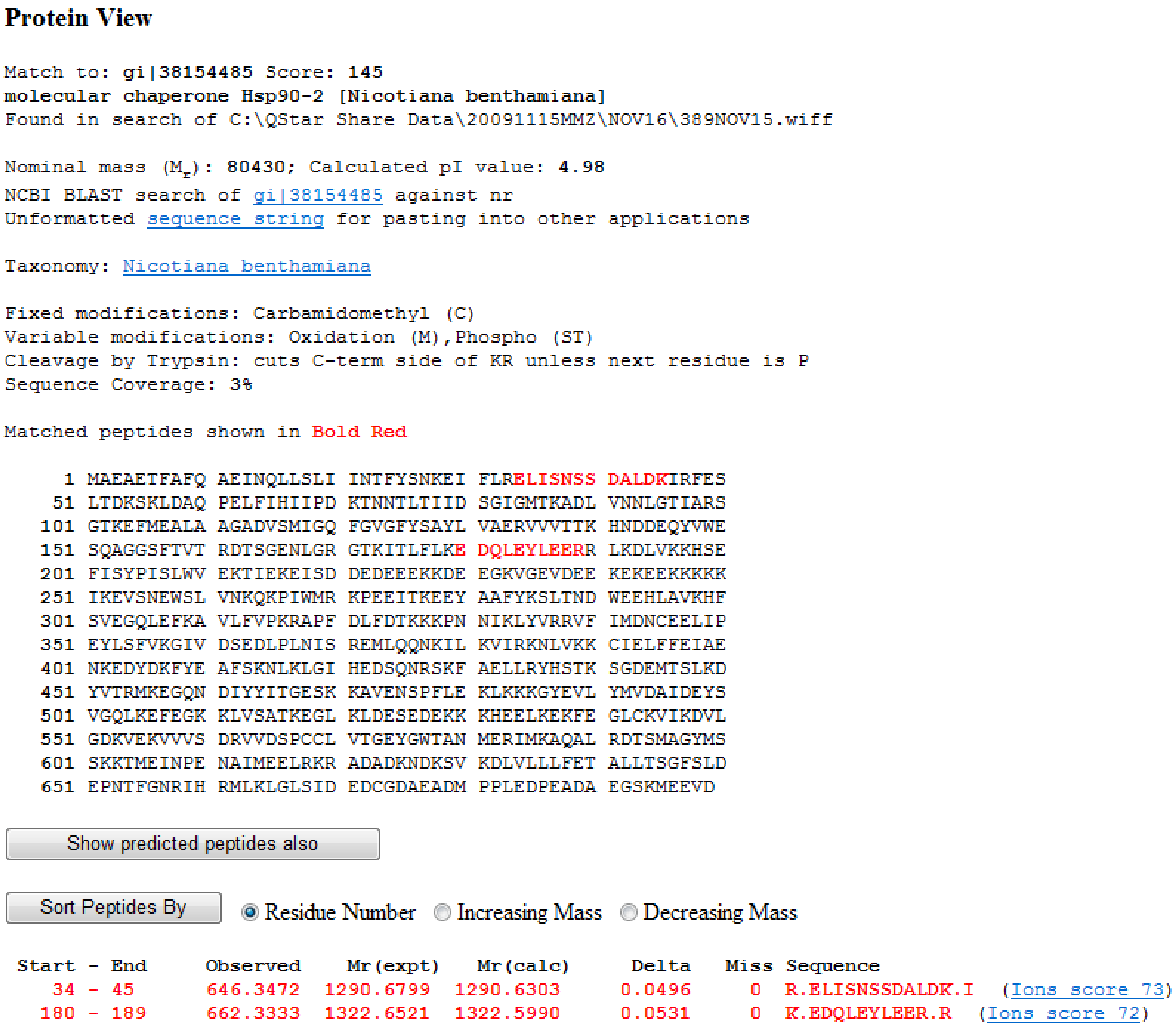
Matched peptides shown in **Bold Red**

1 MYRTAASRAR ALKGVLTRSL RPARYASSSA VAETSSSTPA YLSWLSGGSR
51 AALTSLDMPL QGVSLPPPLA DKVEPSKLQI TTLPNGLKIA SETTPNPAAS
101 IGLYVDCGSI YEAPYFHGAT HLLERMAFKS TLNRTHFRLV R**EIEAIGGNT**
151 **SASASREQMS YTIDALK**TYV PEMVEVLIDS VRNPAFLDWE VNEELRKMKV
201 EIAELAKNPM GFLLEAIHSA GYSGPLASPL YAPESALDRL NGELLEEFMT
251 ENFTAARMVL AASGVEHEEL LKVAEPLTSD LPNVPPQLAP KSQYVGGDFR
301 QHTGGEATHF AVAFEVPGWN NEKEAVTATV LQMLMGGGGS FSAGGPGKGM
351 HSWLYRRVLN EYQEVQSCTA FTSIFNDTGL FGIYGCSSPQ FAAKAIELAA
401 KELKDVAGGK VNQAHLDRAK AATK**SAVLMN LESRMIAAED IGRQILTYGE**
451 **R**KPVDQFLKS VDQLTLKDIA DFTSKVISKP LTMGSFGDVL AVPSYDTISS
501 KFR

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  142 - 156     731.8974  1461.7802  1461.7059    0.0742     0  R.EIEAIGGNTSASASR.E   (Ions score 84)
  157 - 167     657.8490  1313.6834  1313.6173    0.0661     0  R.EQMSYTIDALK.T  Oxidation (M)  (Ions score 60)
  425 - 434     560.3282  1118.6418  1118.5754    0.0664     0  K.SAVLMNLESR.M  (Ions score 57)
  425 - 434     568.3238  1134.6331  1134.5703    0.0628     0  K.SAVLMNLESR.M  Oxidation (M)  (Ions score 64)
  435 - 443     496.2815   990.5485   990.4804    0.0681     0  R.MIAAEDIGR.Q  Oxidation (M)  (Ions score 52)
  444 - 451     490.3031   978.5916   978.5134    0.0782     0  R.QILTYGER.K  (Ions score 43)
```

gi|38154485 Molecular chaperone Hsp90-2



Protein View

```
Match to: gi|38154485 Score: 145
molecular chaperone Hsp90-2 [Nicotiana benthamiana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\389NOV15.wiff

Nominal mass (Mr): 80430; Calculated pI value: 4.98
NCBI BLAST search of gi|38154485 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Nicotiana benthamiana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

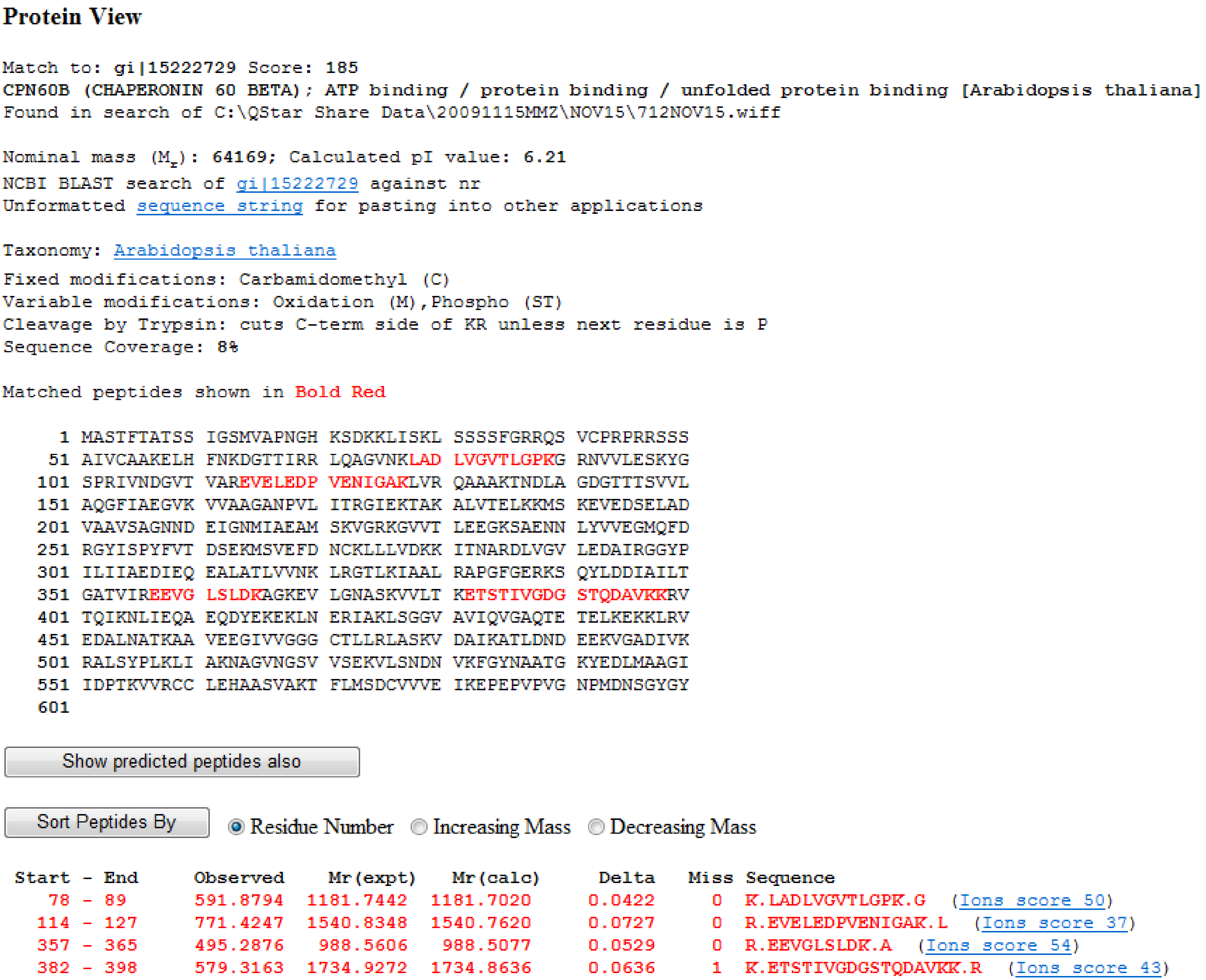
Matched peptides shown in Bold Red

     1 MAEAETFAFQ AEINQLLSLI INTFYSNKEI FLRELISNSS DALDKIRFES
    51 LTDKSKLDAQ PELFIHIIPD KTNNTLTIID SGIGMTKADL VNNLGTIARS
   101 GTKEFMEALA AGADVSMIGQ FGVGFYSAYL VAERVVVTTK HNDDEQYVWE
   151 SQAGGSFTVT RDTSGENLGR GTKITLFLKE DQLEYLEERR LKDLVKKHSE
   201 FISYPISLWV EKTIEKEISD DEDEEEKKDE EGKVGEVDEE KEKEEKKKKK
   251 IKEVSNEWSL VNKQKPIWMR KPEEITKEEY AAFYKSLTND WEEHLAVKHF
   301 SVEGQLEFKA VLFVPKRAPF DLFDTKKKPN NIKLYVRRVF IMDNCEELIP
   351 EYLSFVKGIV DSEDLPLNIS REMLQQNKIL KVIRKNLVKK CIELFFEIAE
   401 NKEDYDKFYE AFSKNLKLGI HEDSQNRSKF AELLRYHSTK SGDEMTSLKD
   451 YVTRMKEGQN DIYYITGESK KAVENSPFLE KLKKKGYEVL YMVDAIDEYS
   501 VGQLKEFEGK KLVSATKEGL KLDESEDEKK KHEELKEKFE GLCKVIKDVL
   551 GDKVEKVVVS DRVVDSPCCL VTGEYGWTAN MERIMKAQAL RDTSMAGYMS
   601 SKKTMEINPE NAIMEELRKR ADADKNDKSV KDLVLLLFET ALLTSGFSLD
   651 EPNTFGNRIH RMLKLGLSID EDCGDAEADM PPLEDPEADA EGSKMEEVD
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
    34 - 45      646.3472  1290.6799  1290.6303    0.0496     0   R.ELISNSSDALDK.I   (Ions score 73)
   180 - 189     662.3333  1322.6521  1322.5990    0.0531     0   K.EDQLEYLEER.R   (Ions score 72)
```

gi|15222729 Chaperonin 60 beta (CPN60B)



Protein View

Match to: gi|15222729 Score: 185
CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\712NOV15.wiff

Nominal mass (M_r): 64169; Calculated pI value: 6.21
NCBI BLAST search of gi|15222729 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

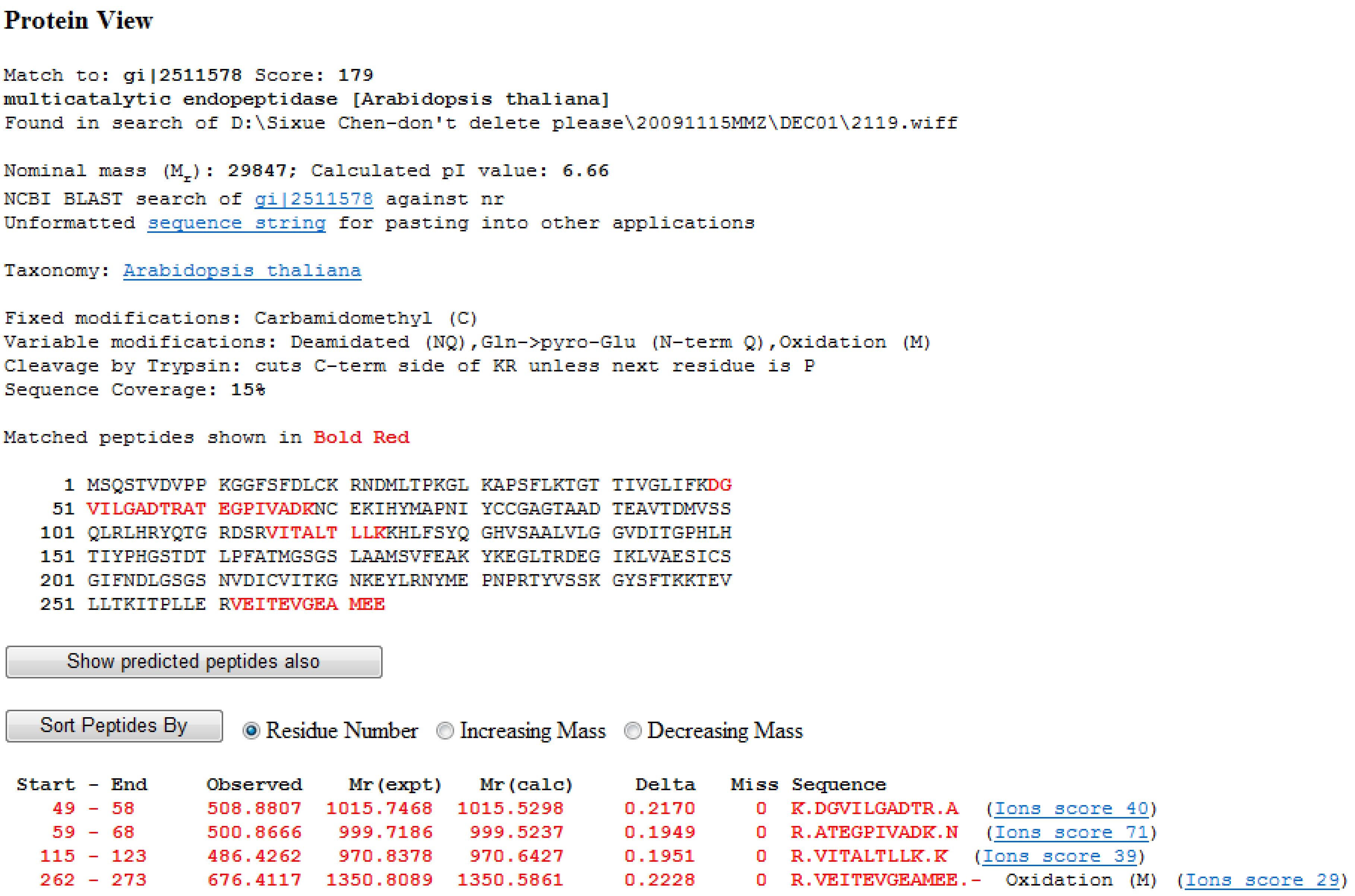
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

Matched peptides shown in **Bold Red**

```
  1 MASTFTATSS IGSMVAPNGH KSDKKLISKL SSSSFGRRQS VCPRPRRSSS
 51 AIVCAAKELH FNKDGTTIRR LQAGVNKLAD LVGVTLGPKG RNVVLESKYG
101 SPRIVNDGVT VAREVELEDP VENIGAKLVR QAAAKTNDLA GDGTTTSVVL
151 AQGFIAEGVK VVAAGANPVL ITRGIEKTAK ALVTELKKMS KEVEDSELAD
201 VAAVSAGNND EIGNMIAEAM SKVGRKGVVT LEEGKSAENN LYVVEGMQFD
251 RGYISPYFVT DSEKMSVEFD NCKLLLVDKK ITNARDLVGV LEDAIRGGYP
301 ILIIAEDIEQ EALATLVVNK LRGTLKIAAL RAPGFGERKS QYLDDIAILT
351 GATVIREEVG LSLDKAGKEV LGNASKVVLT KETSTIVGDG STQDAVKKRV
401 TQIKNLIEQA EQDYEKEKLN ERIAKLSGGV AVIQVGAQTE TELKEKKLRV
451 EDALNATKAA VEEGIVVGGG CTLLRLASKV DAIKATLDND EEKVGADIVK
501 RALSYPLKLI AKNAGVNGSV VSEKVLSNDN VKFGYNAATG KYEDLMAAGI
551 IDPTKVVRCC LEHAASVAKT FLMSDCVVVE IKEPEPVPVG NPMDNSGYGY
601
```

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
78 - 89	591.8794	1181.7442	1181.7020	0.0422	0	K.LADLVGVTLGPK.G (Ions score 50)
114 - 127	771.4247	1540.8348	1540.7620	0.0727	0	R.EVELEDPVENIGAK.L (Ions score 37)
357 - 365	495.2876	988.5606	988.5077	0.0529	0	R.EEVGLSLDK.A (Ions score 54)
382 - 398	579.3163	1734.9272	1734.8636	0.0636	1	K.ETSTIVGDGSTQDAVKK.R (Ions score 43)

gi|2511578 20S proteasome beta subunit; multicatalytic endopeptidase



Protein View

Match to: gi|2511578 Score: 179
multicatalytic endopeptidase [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2119.wiff

Nominal mass (M_r): 29847; Calculated pI value: 6.66
NCBI BLAST search of gi|2511578 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

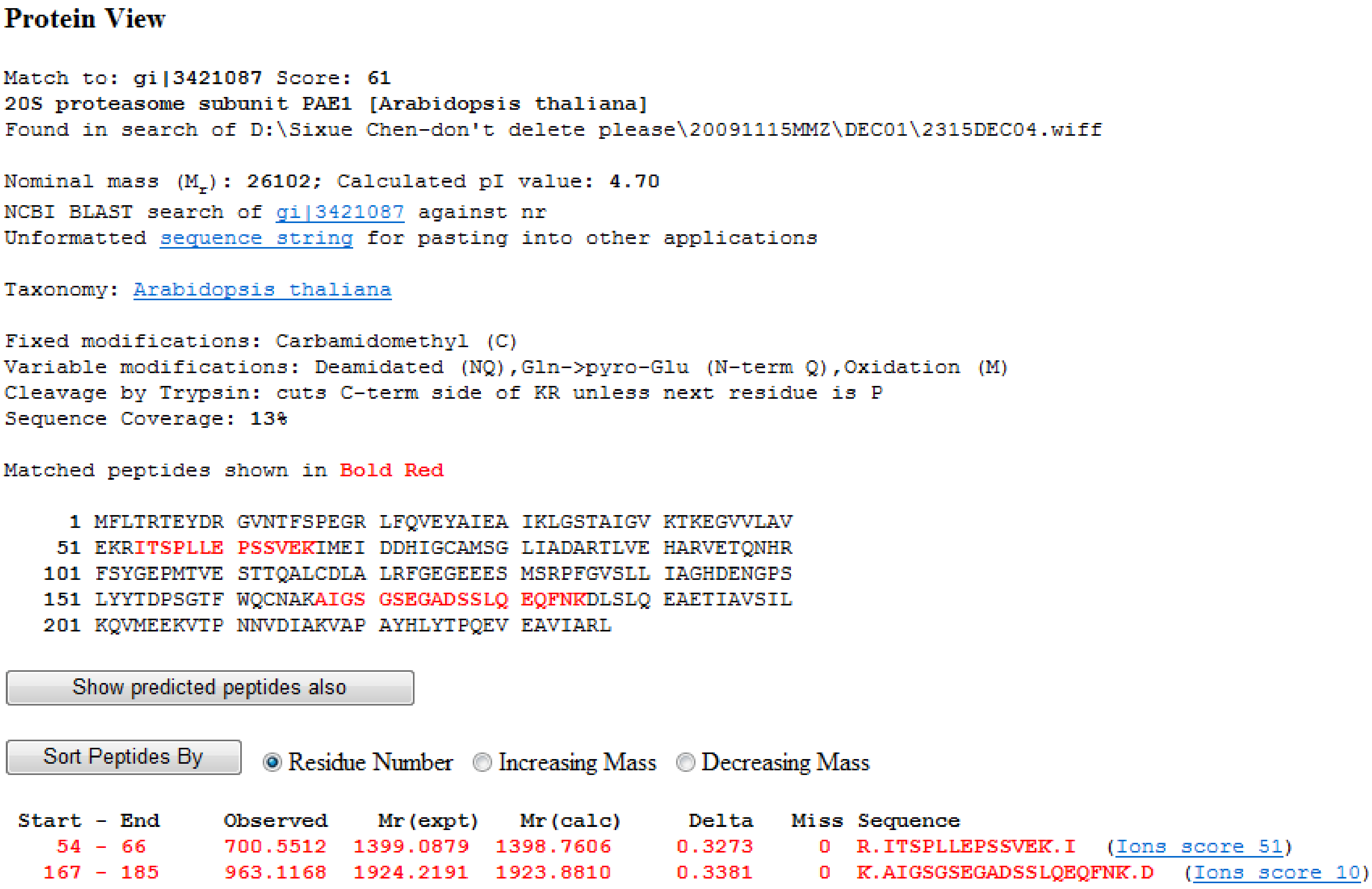
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in **Bold Red**

```
  1 MSQSTVDVPP KGGFSFDLCK RNDMLTPKGL KAPSFLKTGT TIVGLIFKDG
 51 VILGADTRAT EGPIVADKNC EKIHYMAPNI YCCGAGTAAD TEAVTDMVSS
101 QLRLHRYQTG RDSRVITALT LLKKHLFSYQ GHVSAALVLG GVDITGPHLH
151 TIYPHGSTDT LPFATMGSGS LAAMSVFEAK YKEGLTRDEG IKLVAESICS
201 GIFNDLGSGS NVDICVITKG NKEYLRNYME PNPRTYVSSK GYSFTKKTEV
251 LLTKITPLLE RVEITEVGEA MEE
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   49 - 58      508.8807  1015.7468  1015.5298    0.2170     0  K.DGVILGADTR.A   (Ions score 40)
   59 - 68      500.8666   999.7186   999.5237    0.1949     0  R.ATEGPIVADK.N   (Ions score 71)
  115 - 123     486.4262   970.8378   970.6427    0.1951     0  R.VITALTLLK.K   (Ions score 39)
  262 - 273     676.4117  1350.8089  1350.5861    0.2228     0  R.VEITEVGEAMEE.-  Oxidation (M)  (Ions score 29)
```

gi|3421087 20S proteasome subunit PAE1



Protein View

Match to: gi|3421087 Score: 61
20S proteasome subunit PAE1 [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2315DEC04.wiff

Nominal mass (M_r): 26102; Calculated pI value: 4.70
NCBI BLAST search of gi|3421087 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

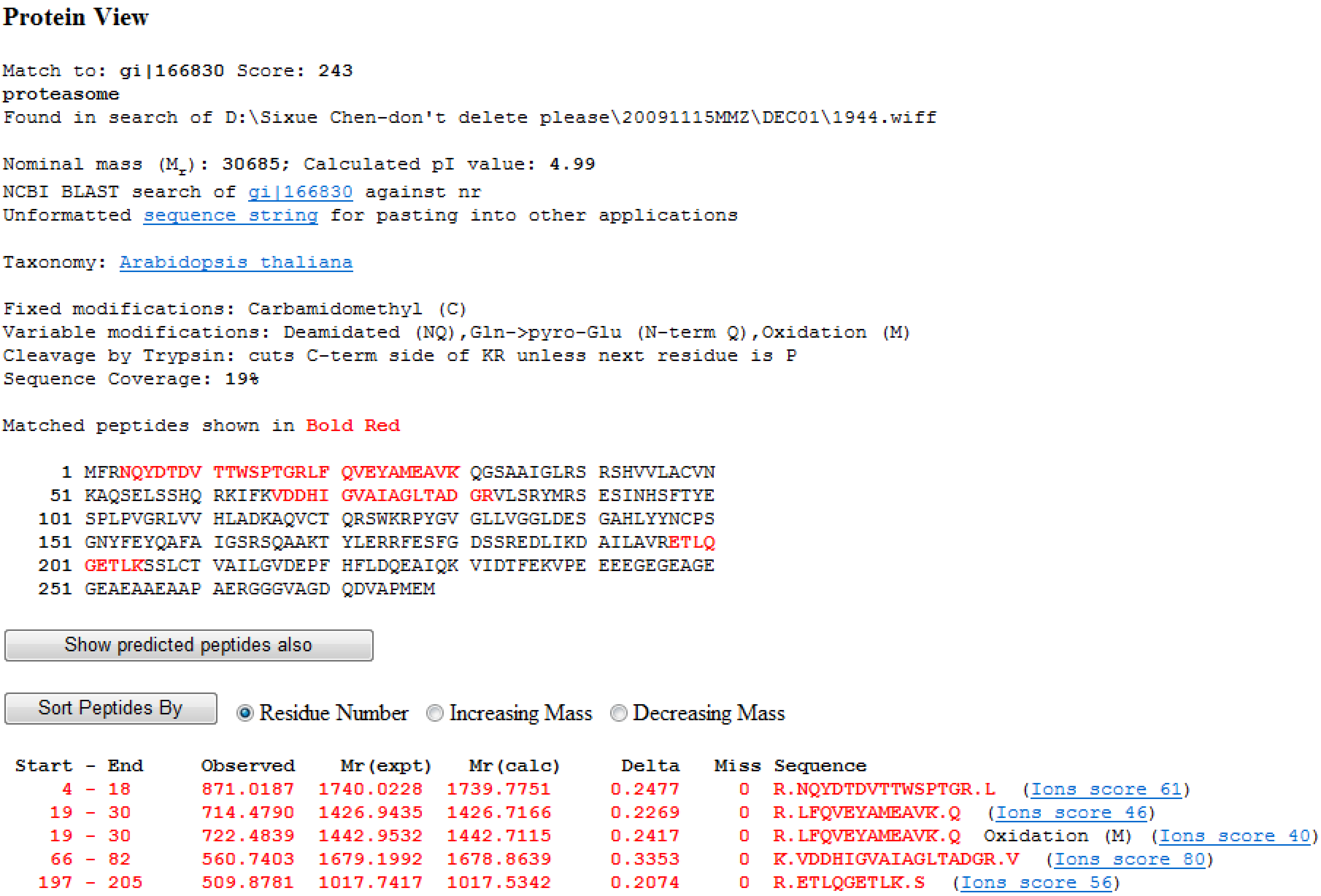
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 13%

Matched peptides shown in **Bold Red**

```
      1 MFLTRTEYDR GVNTFSPEGR LFQVEYAIEA IKLGSTAIGV KTKEGVVLAV
     51 EKRITSPLLE PSSVEKIMEI DDHIGCAMSG LIADARTLVE HARVETQNHR
    101 FSYGEPMTVE STTQALCDLA LRFGEGEEES MSRPFGVSLL IAGHDENGPS
    151 LYYTDPSGTF WQCNAKAIGS GSEGADSSLQ EQFNKDLSLQ EAETIAVSIL
    201 KQVMEEKVTP NNVDIAKVAP AYHLYTPQEV EAVIARL
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   54 - 66      700.5512  1399.0879  1398.7606   0.3273     0  R.ITSPLLEPSSVEK.I     (Ions score 51)
  167 - 185     963.1168  1924.2191  1923.8810   0.3381     0  K.AIGSGSEGADSSLQEQFNK.D   (Ions score 10)
```

gi|166830 Proteasome



Protein View

```
Match to: gi|166830 Score: 243
proteasome
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1944.wiff

Nominal mass (Mr): 30685; Calculated pI value: 4.99
NCBI BLAST search of gi|166830 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 19%

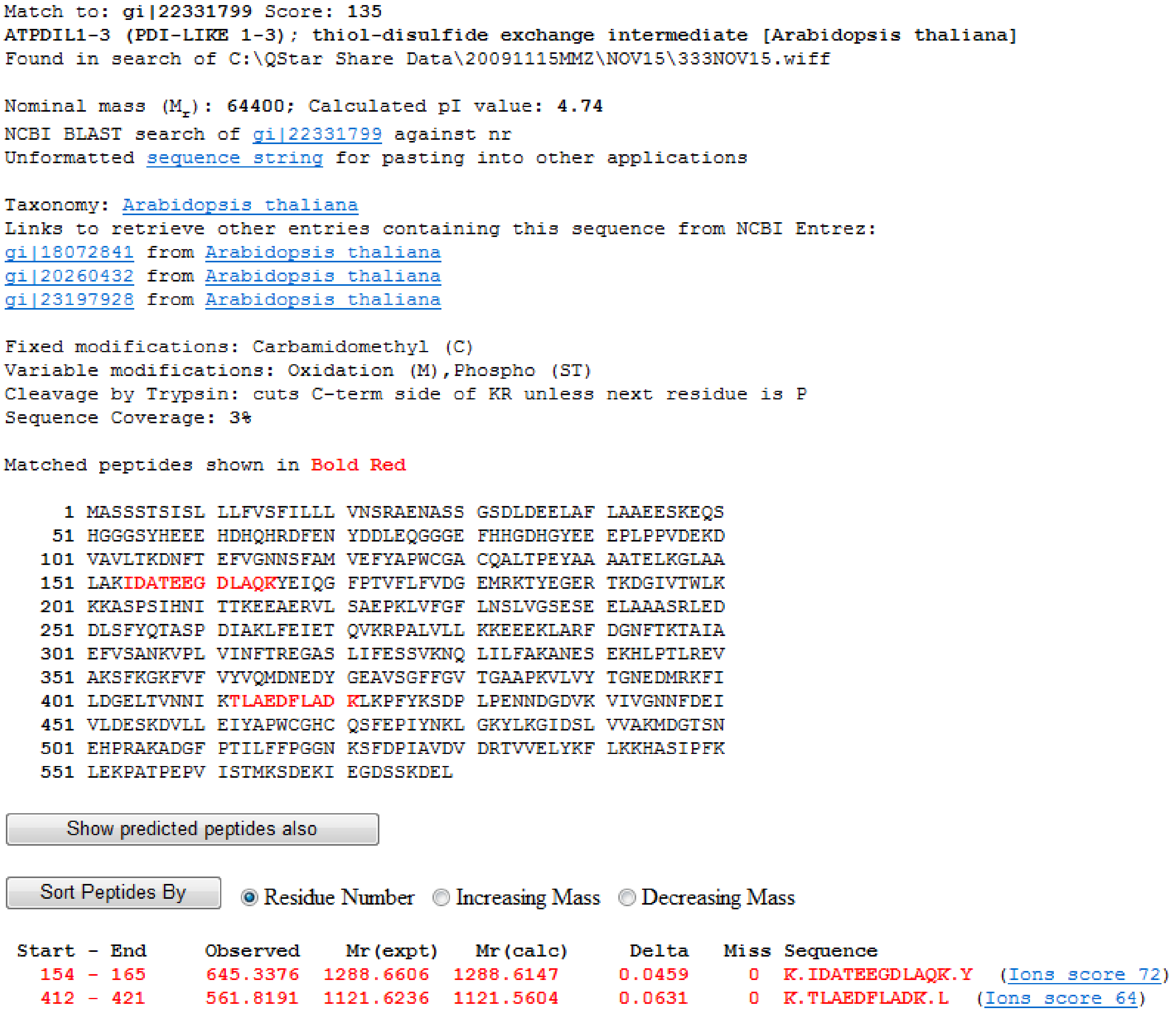
Matched peptides shown in Bold Red

     1 MFRNQYDTDV TTWSPTGRLF QVEYAMEAVK QGSAAIGLRS RSHVVLACVN
    51 KAQSELSSHQ RKIFKVDDHI GVAIAGLTAD GRVLSRYMRS ESINHSFTYE
   101 SPLPVGRLVV HLADKAQVCT QRSWKRPYGV GLLVGGLDES GAHLYYNCPS
   151 GNYFEYQAFA IGSRSQAAKT YLERRFESFG DSSREDLIKD AILAVRETLQ
   201 GETLKSSLCT VAILGVDEPF HFLDQEAIQK VIDTFEKVPE EEEGEGEAGE
   251 GEAEAAEAAP AERGGGVAGD QDVAPMEM
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
    4 - 18     871.0187  1740.0228  1739.7751    0.2477     0  R.NQYDTDVTTWSPTGR.L  (Ions score 61)
   19 - 30     714.4790  1426.9435  1426.7166    0.2269     0  R.LFQVEYAMEAVK.Q  (Ions score 46)
   19 - 30     722.4839  1442.9532  1442.7115    0.2417     0  R.LFQVEYAMEAVK.Q  Oxidation (M)  (Ions score 40)
   66 - 82     560.7403  1679.1992  1678.8639    0.3353     0  K.VDDHIGVAIAGLTADGR.V  (Ions score 80)
  197 - 205    509.8781  1017.7417  1017.5342    0.2074     0  R.ETLQGETLK.S  (Ions score 56)
```

gi|22331799 ATPDIL1-3 (PDI-LIKE 1-3); thiol-disulfide exchange intermediate



```
Match to: gi|22331799 Score: 135
ATPDIL1-3 (PDI-LIKE 1-3); thiol-disulfide exchange intermediate [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\333NOV15.wiff

Nominal mass (Mr): 64400; Calculated pI value: 4.74
NCBI BLAST search of gi|22331799 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|18072841 from Arabidopsis thaliana
gi|20260432 from Arabidopsis thaliana
gi|23197928 from Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

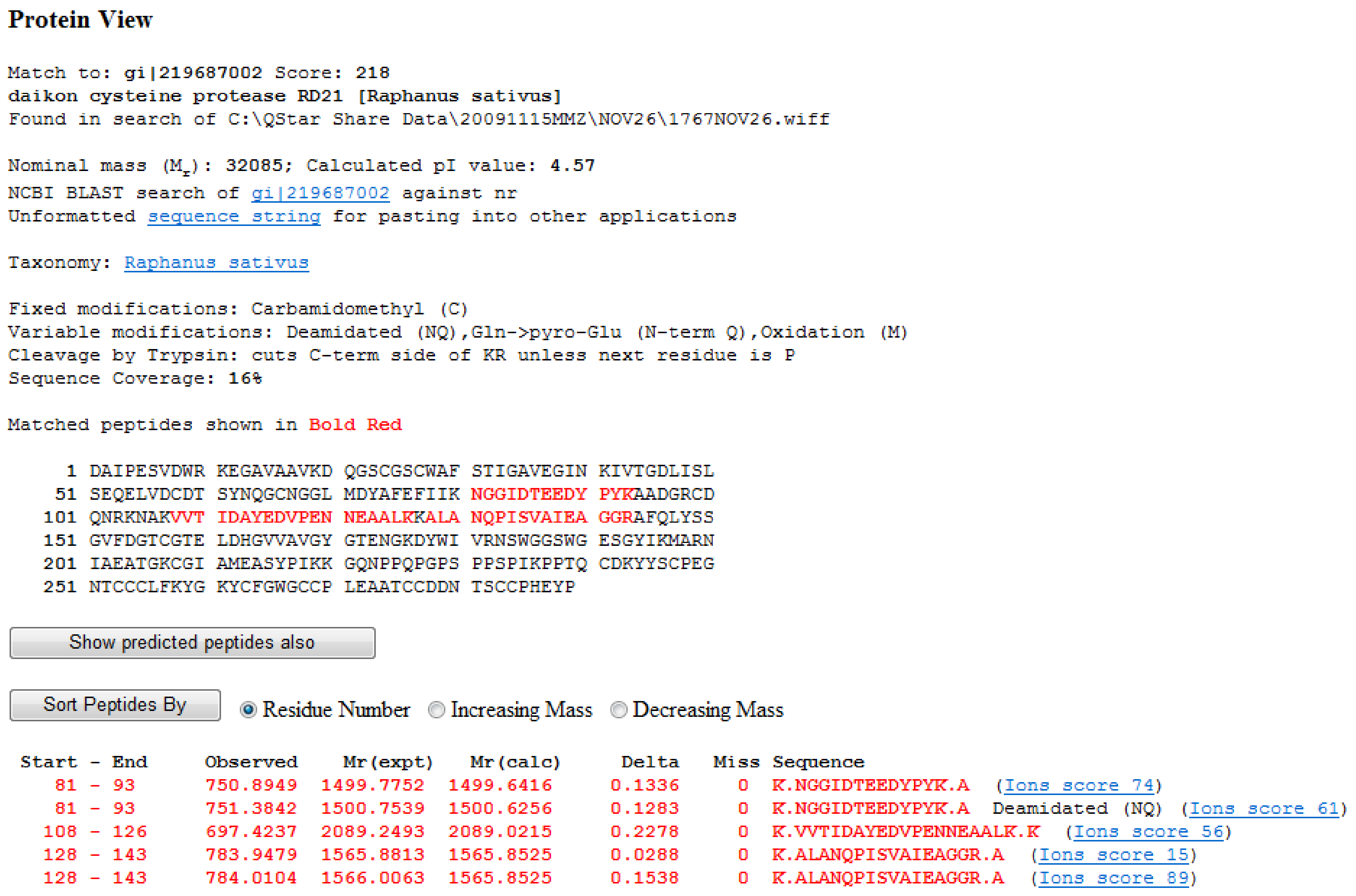
Matched peptides shown in Bold Red

    1 MASSSTSISL LLFVSFILLL VNSRAENASS GSDLDEELAF LAAEESKEQS
   51 HGGGSYHEEE HDHQHRDFEN YDDLEQGGGE FHHGDHGYEE EPLPPVDEKD
  101 VAVLTKDNFT EFVGNNSFAM VEFYAPWCGA CQALTPEYAA AATELKGLAA
  151 LAKIDATEEG DLAQKYEIQG FPTVFLFVDG EMRKTYEGER TKDGIVTWLK
  201 KKASPSIHNI TTKEEAERVL SAEPKLVFGF LNSLVGSESE ELAAASRLED
  251 DLSFYQTASP DIAKLFEIET QVKRPALVLL KKEEEKLARF DGNFTKTAIA
  301 EFVSANKVPL VINFTREGAS LIFESSVKNQ LILFAKANES EKHLPTLREV
  351 AKSFKGKFVF VYVQMDNEDY GEAVSGFFGV TGAAPKVLVY TGNEDMRKFI
  401 LDGELTVNNI KTLAEDFLAD KLKPFYKSDP LPENNDGDVK VIVGNNFDEI
  451 VLDESKDVLL EIYAPWCGHC QSFEPIYNKL GKYLKGIDSL VVAKMDGTSN
  501 EHPRAKADGF PTILFFPGGN KSFDPIAVDV DRTVVELYKF LKKHASIPFK
  551 LEKPATPEPV ISTMKSDEKI EGDSSKDEL
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)  Mr(calc)     Delta  Miss Sequence
   154 - 165    645.3376  1288.6606 1288.6147    0.0459     0  K.IDATEEGDLAQK.Y  (Ions score 72)
   412 - 421    561.8191  1121.6236 1121.5604    0.0631     0  K.TLAEDFLADK.L  (Ions score 64)
```

gi|219687002 Daikon cysteine protease RD21



Protein View

Match to: gi|219687002 Score: 218
daikon cysteine protease RD21 [Raphanus sativus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1767NOV26.wiff

Nominal mass (M_r): 32085; Calculated pI value: 4.57
NCBI BLAST search of gi|219687002 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Raphanus sativus

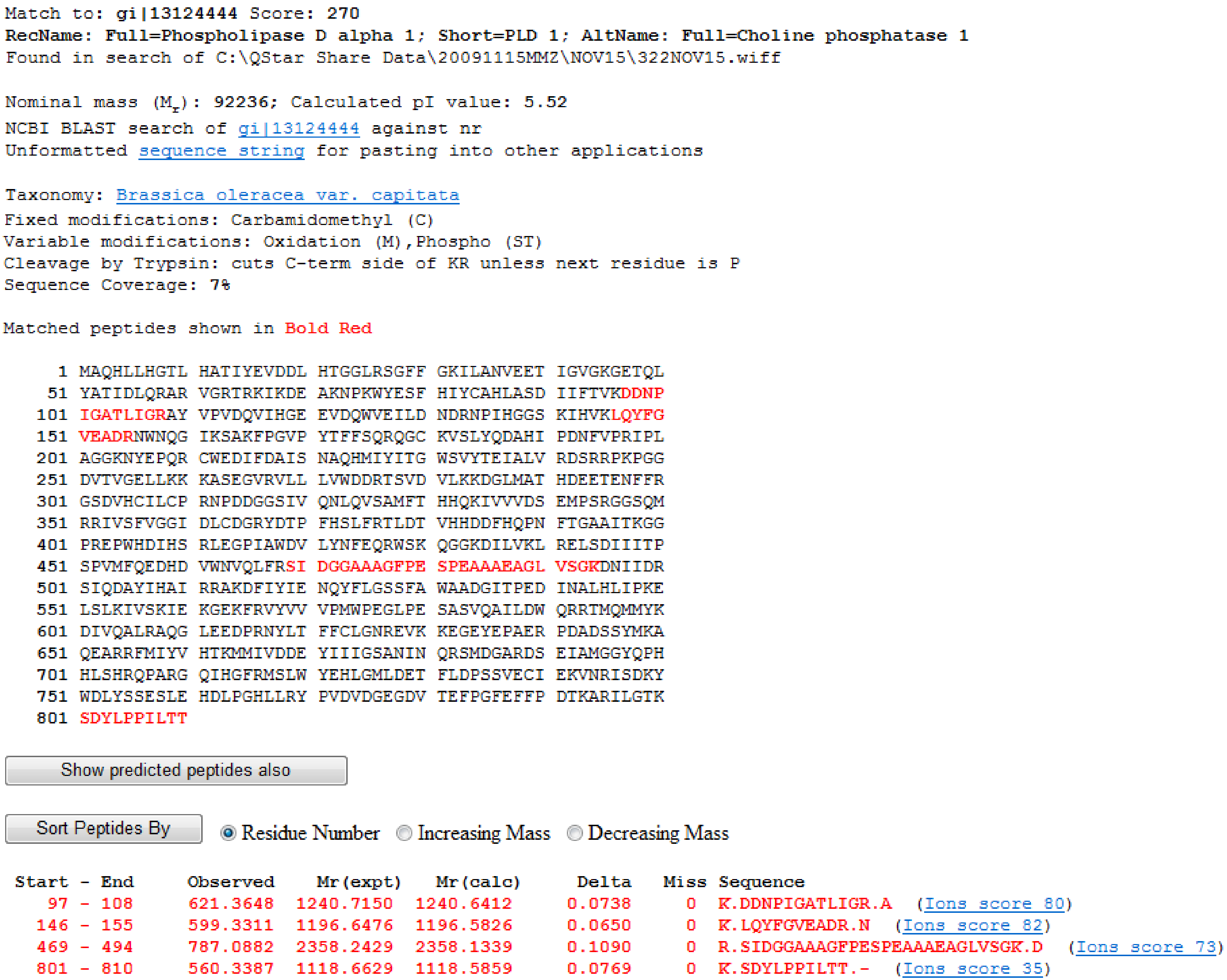
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 16%

Matched peptides shown in **Bold Red**

```
  1 DAIPESVDWR KEGAVAAVKD QGSCGSCWAF STIGAVEGIN KIVTGDLISL
 51 SEQELVDCDT SYNQGCNGGL MDYAFEFIIK NGGIDTEEDY PYKAADGRCD
101 QNRKNAKVVT IDAYEDVPEN NEAALKKALA NQPISVAIEA GGRAFQLYSS
151 GVFDGTCGTE LDHGVVAVGY GTENGKDYWI VRNSWGGSWG ESGYIKMARN
201 IAEATGKCGI AMEASYPIKK GQNPPQPGPS PPSPIKPPTQ CDKYYSCPEG
251 NTCCCLFKYG KYCFGWGCCP LEAATCCDDN TSCCPHEYP
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   81 - 93      750.8949  1499.7752  1499.6416    0.1336     0  K.NGGIDTEEDYPYK.A  (Ions score 74)
   81 - 93      751.3842  1500.7539  1500.6256    0.1283     0  K.NGGIDTEEDYPYK.A  Deamidated (NQ)  (Ions score 61)
  108 - 126     697.4237  2089.2493  2089.0215    0.2278     0  K.VVTIDAYEDVPENNEAALK.K  (Ions score 56)
  128 - 143     783.9479  1565.8813  1565.8525    0.0288     0  K.ALANQPISVAIEAGGR.A  (Ions score 15)
  128 - 143     784.0104  1566.0063  1565.8525    0.1538     0  K.ALANQPISVAIEAGGR.A  (Ions score 89)
```

gi|13124444 Phospholipase D alpha 1 (PLD1)



Match to: gi|13124444 Score: 270
RecName: Full=Phospholipase D alpha 1; Short=PLD 1; AltName: Full=Choline phosphatase 1
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\322NOV15.wiff

Nominal mass (M_r): **92236**; Calculated pI value: **5.52**
NCBI BLAST search of gi|13124444 against nr
Unformatted sequence string for pasting into other applications

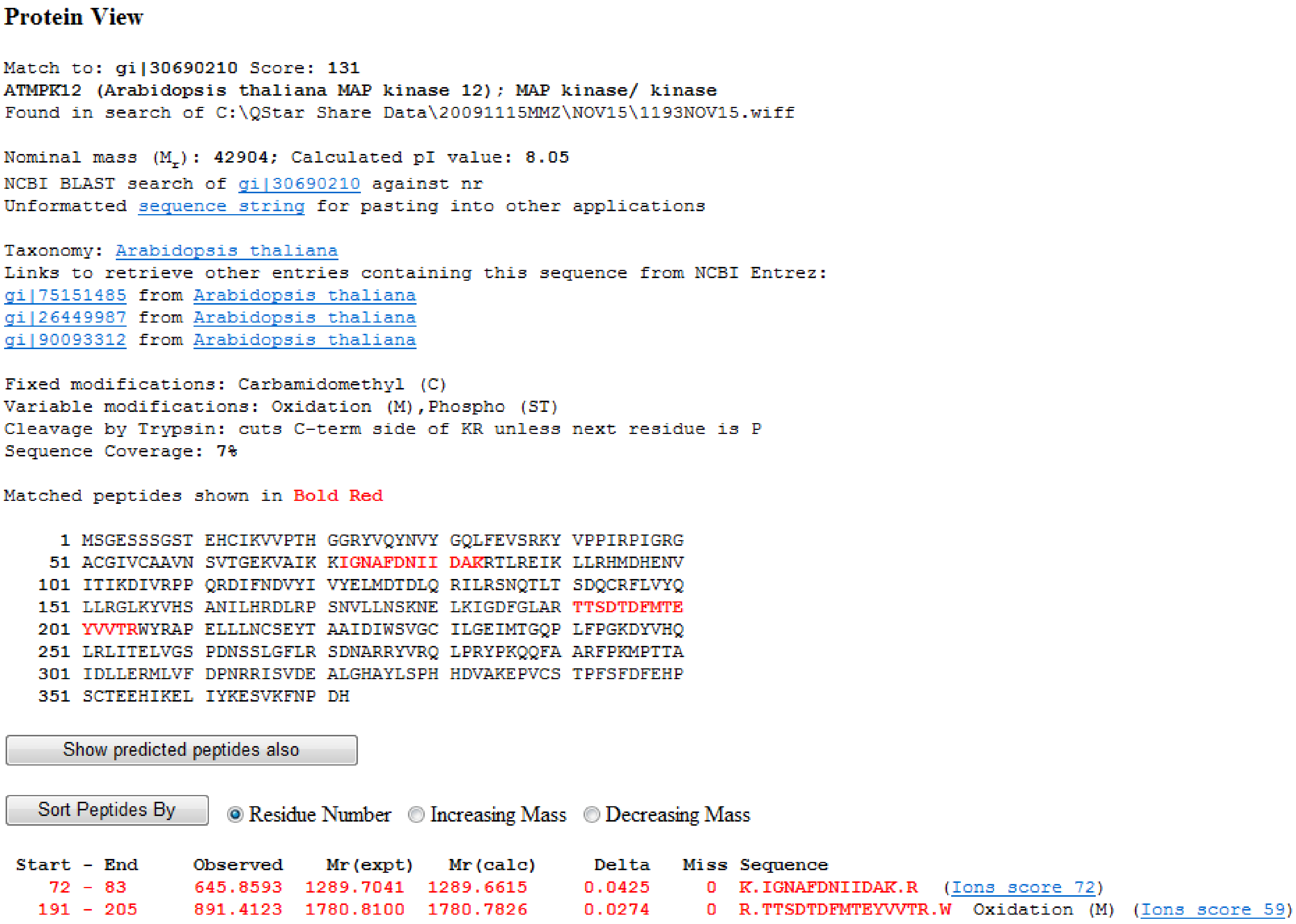
Taxonomy: Brassica oleracea var. capitata
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

Matched peptides shown in **Bold Red**

```
  1 MAQHLLHGTL HATIYEVDDL HTGGLRSGFF GKILANVEET IGVGKGETQL
 51 YATIDLQRAR VGRTRKIKDE AKNPKWYESF HIYCAHLASD IIFTVKDDNP
101 IGATLIGRAY VPVDQVIHGE EVDQWVEILD NDRNPIHGGS KIHVKLQYFG
151 VEADRNWNQG IKSAKFPGVP YTFFSQRQGC KVSLYQDAHI PDNFVPRIPL
201 AGGKNYEPQR CWEDIFDAIS NAQHMIYITG WSVYTEIALV RDSRRPKPGG
251 DVTVGELLKK KASEGVRVLL LVWDDRTSVD VLKKDGLMAT HDEETENFFR
301 GSDVHCILCP RNPDDGGSIV QNLQVSAMFT HHQKIVVVDS EMPSRGGSQM
351 RRIVSFVGGI DLCDGRYDTP FHSLFRTLDT VHHDDFHQPN FTGAAITKGG
401 PREPWHDIHS RLEGPIAWDV LYNFEQRWSK QGGKDILVKL RELSDIIITP
451 SPVMFQEDHD VWNVQLFRSI DGGAAAGFPE SPEAAAEAGL VSGKDNIIDR
501 SIQDAYIHAI RRAKDFIYIE NQYFLGSSFA WAADGITPED INALHLIPKE
551 LSLKIVSKIE KGEKFRVYVV VPMWPEGLPE SASVQAILDW QRRTMQMMYK
601 DIVQALRAQG LEEDPRNYLT FFCLGNREVK KEGEYEPAER PDADSSYMKA
651 QEARRFMIYV HTKMMIVDDE YIIIGSANIN QRSMDGARDS EIAMGGYQPH
701 HLSHRQPARG QIHGFRMSLW YEHLGMLDET FLDPSSVECI EKVNRISDKY
751 WDLYSSESLE HDLPGHLLRY PVDVDGEGDV TEFPGFEFFP DTKARILGTK
801 SDYLPPILTT
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   97 - 108     621.3648  1240.7150  1240.6412    0.0738      0  K.DDNPIGATLIGR.A  (Ions score 80)
  146 - 155     599.3311  1196.6476  1196.5826    0.0650      0  K.LQYFGVEADR.N  (Ions score 82)
  469 - 494     787.0882  2358.2429  2358.1339    0.1090      0  R.SIDGGAAAGFPESPEAAAEAGLVSGK.D  (Ions score 73)
  801 - 810     560.3387  1118.6629  1118.5859    0.0769      0  K.SDYLPPILTT.-  (Ions score 35)
```

gi|30690210 Arabidopsis thaliana MAP kinase 12 (ATMPK12); MAP kinase



Protein View

Match to: gi|30690210 Score: 131
ATMPK12 (Arabidopsis thaliana MAP kinase 12); MAP kinase/ kinase
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1193NOV15.wiff

Nominal mass (M_r): 42904; Calculated pI value: 8.05
NCBI BLAST search of gi|30690210 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|75151485 from Arabidopsis thaliana
gi|26449987 from Arabidopsis thaliana
gi|90093312 from Arabidopsis thaliana

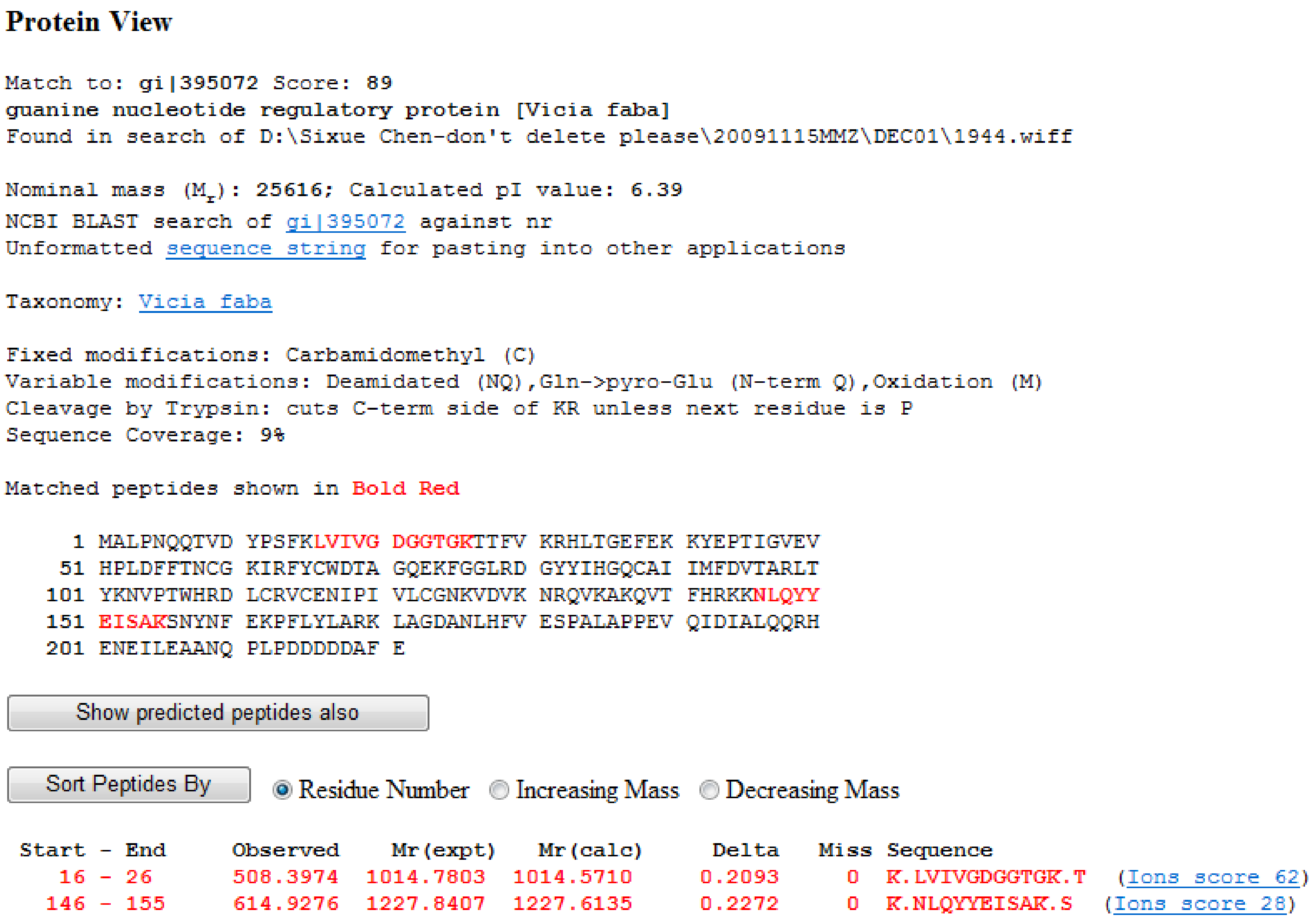
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 7%

Matched peptides shown in **Bold Red**

1 MSGESSSGST EHCIKVVPTH GGRYVQYNVY GQLFEVSRKY VPPIRPIGRG
51 ACGIVCAAVN SVTGEKVAIK K**IGNAFDNII DAK**RTLREIK LLRHMDHENV
101 ITIKDIVRPP QRDIFNDVYI VYELMDTDLQ RILRSNQTLT SDQCRFLVYQ
151 LLRGLKYVHS ANILHRDLRP SNVLLNSKNE LKIGDFGLAR **TTSDTDFMTE**
201 **YVVTR**WYRAP ELLLNCSEYT AAIDIWSVGC ILGEIMTGQP LFPGKDYVHQ
251 LRLITELVGS PDNSSLGFLR SDNARRYVRQ LPRYPKQQFA ARFPKMPTTA
301 IDLLERMLVF DPNRRISVDE ALGHAYLSPH HDVAKEPVCS TPFSFDFEHP
351 SCTEEHIKEL IYKESVKFNP DH

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
    72 - 83      645.8593  1289.7041  1289.6615    0.0425     0 K.IGNAFDNIIDAK.R  (Ions score 72)
   191 - 205     891.4123  1780.8100  1780.7826    0.0274     0 R.TTSDTDFMTEYVVTR.W  Oxidation (M)  (Ions score 59)
```

gi|395072 Guanine nucleotide regulatory protein (Ran2)



Protein View

Match to: gi|395072 Score: 89
guanine nucleotide regulatory protein [Vicia faba]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1944.wiff

Nominal mass (M_r): 25616; Calculated pI value: 6.39
NCBI BLAST search of gi|395072 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Vicia faba

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 9%

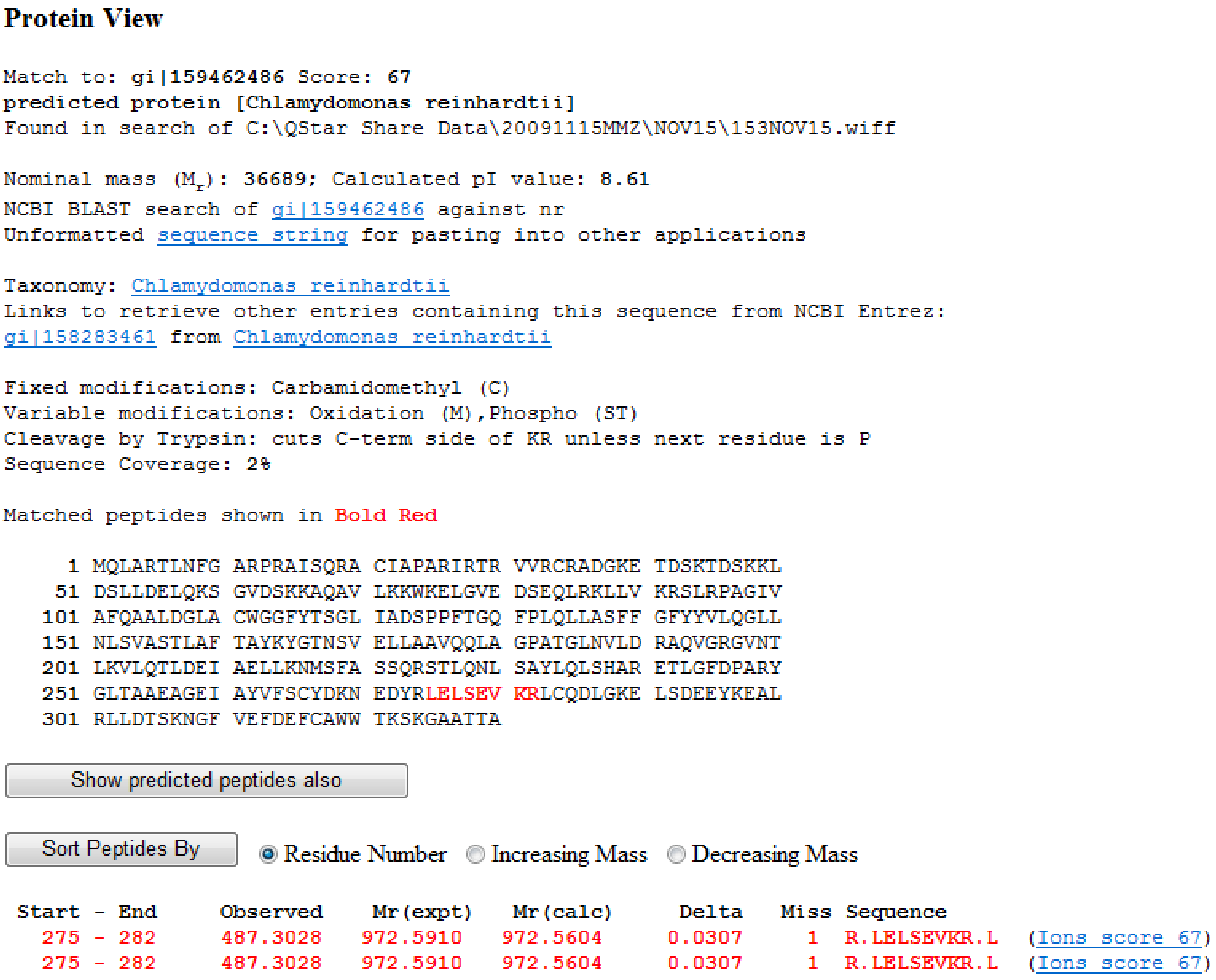
Matched peptides shown in Bold Red

```
  1 MALPNQQTVD YPSFKLVIVG DGGTGKTTFV KRHLTGEFEK KYEPTIGVEV
 51 HPLDFFTNCG KIRFYCWDTA GQEKFGGLRD GYYIHGQCAI IMFDVTARLT
101 YKNVPTWHRD LCRVCENIPI VLCGNKVDVK NRQVKAKQVT FHRKKNLQYY
151 EISAKSNYNF EKPFLYLARK LAGDANLHFV ESPALAPPEV QIDIALQQRH
201 ENEILEAANQ PLPDDDDDAF E
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
16 - 26	508.3974	1014.7803	1014.5710	0.2093	0	K.LVIVGDGGTGK.T	(Ions score 62)
146 - 155	614.9276	1227.8407	1227.6135	0.2272	0	K.NLQYYEISAK.S	(Ions score 28)

gi|159462486 Predicted protein, containing calcium binding motif



Protein View

Match to: gi|159462486 Score: 67
predicted protein [Chlamydomonas reinhardtii]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\153NOV15.wiff

Nominal mass (M_r): 36689; Calculated pI value: 8.61
NCBI BLAST search of gi|159462486 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Chlamydomonas reinhardtii
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|158283461 from Chlamydomonas reinhardtii

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%

Matched peptides shown in **Bold Red**

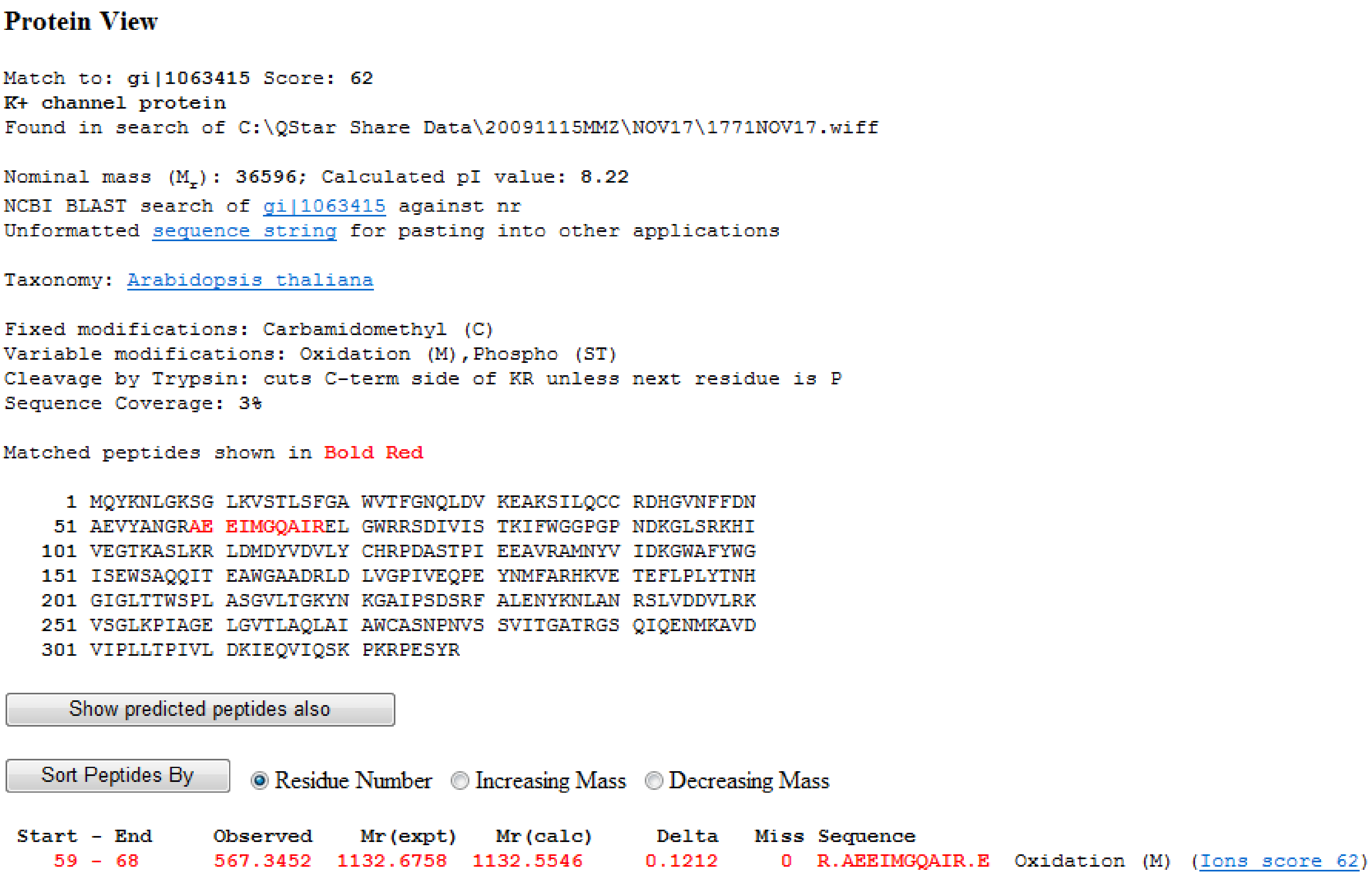
```
  1 MQLARTLNFG ARPRAISQRA CIAPARIRTR VVRCRADGKE TDSKTDSKKL
 51 DSLLDELQKS GVDSKKAQAV LKKWKELGVE DSEQLRKLLV KRSLRPAGIV
101 AFQAALDGLA CWGGFYTSGL IADSPPFTGQ FPLQLLASFF GFYYVLQGLL
151 NLSVASTLAF TAYKYGTNSV ELLAAVQQLA GPATGLNVLD RAQVGRGVNT
201 LKVLQTLDEI AELLKNMSFA SSQRSTLQNL SAYLQLSHAR ETLGFDPARY
251 GLTAAEAGEI AYVFSCYDKN EDYRLELSEV KRLCQDLGKE LSDEEYKEAL
301 RLLDTSKNGF VEFDEFCAWW TKSKGAATTA
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
   275 - 282     487.3028    972.5910    972.5604    0.0307     1   R.LELSEVKR.L   (Ions score 67)
   275 - 282     487.3028    972.5910    972.5604    0.0307     1   R.LELSEVKR.L   (Ions score 67)
```

gi|1063415 Potassium channel protein



Protein View

```
Match to: gi|1063415 Score: 62
K+ channel protein
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1771NOV17.wiff

Nominal mass (Mr): 36596; Calculated pI value: 8.22
NCBI BLAST search of gi|1063415 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 3%

Matched peptides shown in Bold Red

     1 MQYKNLGKSG LKVSTLSFGA WVTFGNQLDV KEAKSILQCC RDHGVNFFDN
    51 AEVYANGRAE EIMGQAIREL GWRRSDIVIS TKIFWGGPGP NDKGLSRKHI
   101 VEGTKASLKR LDMDYVDVLY CHRPDASTPI EEAVRAMNYV IDKGWAFYWG
   151 ISEWSAQQIT EAWGAADRLD LVGPIVEQPE YNMFARHKVE TEFLPLYTNH
   201 GIGLTTWSPL ASGVLTGKYN KGAIPSDSRF ALENYKNLAN RSLVDDVLRK
   251 VSGLKPIAGE LGVTLAQLAI AWCASNPNVS SVITGATRGS QIQENMKAVD
   301 VIPLLTPIVL DKIEQVIQSK PKRPESYR
```

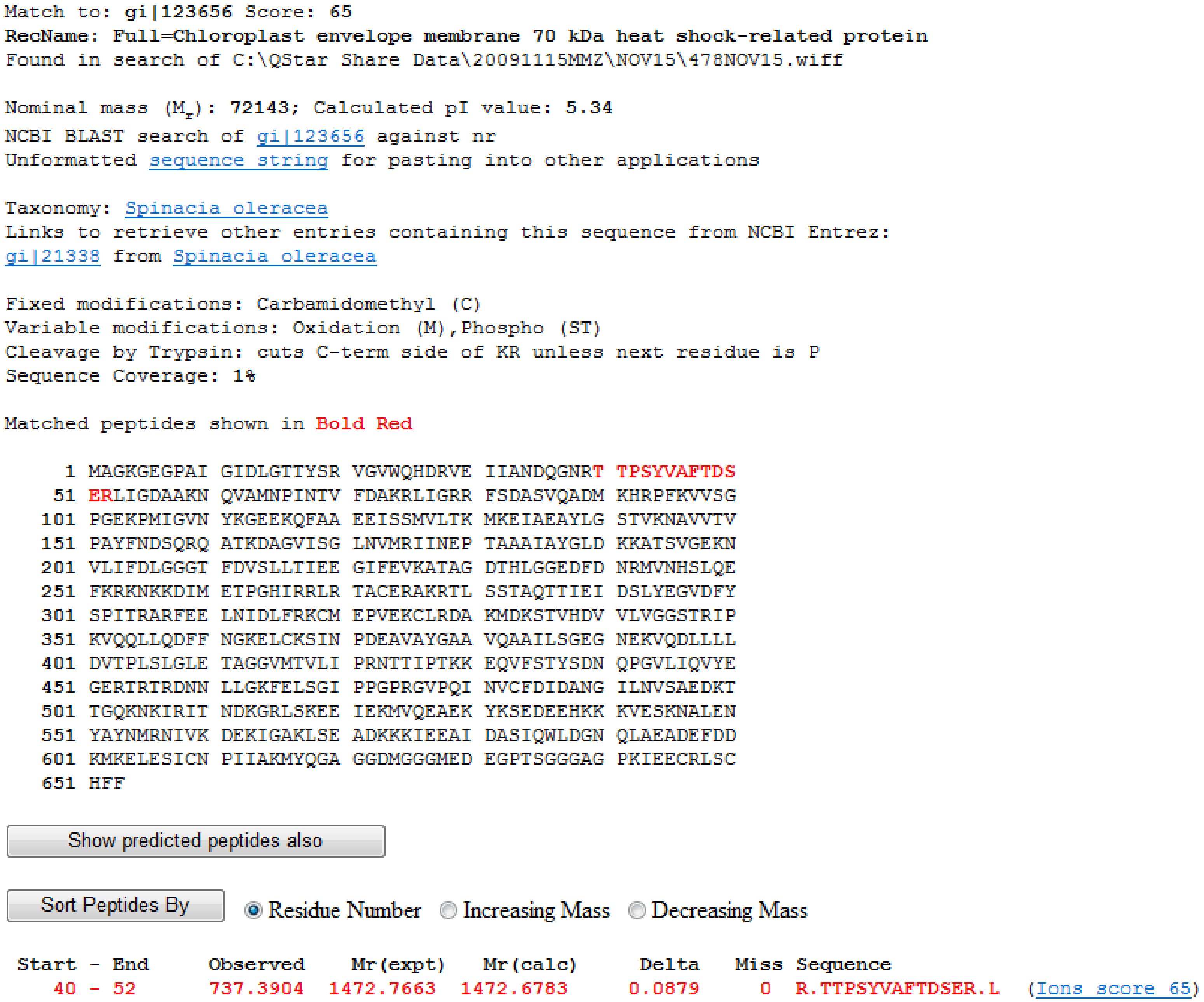
```
 Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss Sequence
    59 - 68      567.3452   1132.6758   1132.5546     0.1212     0  R.AEEIMGQAIR.E  Oxidation (M)  (Ions score 62)
```

Peptide View

MS/MS Fragmentation of **AEEIMGQAIR**
Found in **gi|1063415**, K+ channel protein

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**10**
2	**201.0870**	101.0471			183.0764	92.0418	**E**	**998.5265**	499.7669	981.5000	491.2536	980.5160	490.7616	**9**
3	**330.1296**	165.5684			312.1190	156.5631	**E**	**869.4839**	435.2456	852.4574	426.7323	**851.4734**	**426.2403**	**8**
4	443.2136	222.1105			425.2031	213.1052	**I**	**740.4414**	370.7243	723.4148	362.2110			**7**
5	**526.2508**	263.6290			**508.2402**	254.6237	**M**	**627.3573**	314.1823	610.3307	305.6690			**6**
6	583.2722	292.1397			565.2617	283.1345	**G**	**544.3202**	272.6637	527.2936	264.1504			**5**
7	711.3308	356.1690	694.3043	347.6558	693.3202	347.1638	**Q**	**487.2987**	244.1530	470.2722	235.6397			**4**
8	782.3679	391.6876	765.3414	383.1743	764.3573	382.6823	**A**	**359.2401**	180.1237	342.2136	171.6104			**3**
9	895.4520	448.2296	878.4254	439.7164	877.4414	439.2243	**I**	288.2030	144.6051	271.1765	136.0919			**2**
10							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

gi|123656 Chloroplast envelope membrane 70 kDa heat shock-related protein



```
Match to: gi|123656 Score: 65
RecName: Full=Chloroplast envelope membrane 70 kDa heat shock-related protein
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\478NOV15.wiff

Nominal mass (Mr): 72143; Calculated pI value: 5.34
NCBI BLAST search of gi|123656 against nr
Unformatted sequence string for pasting into other applications

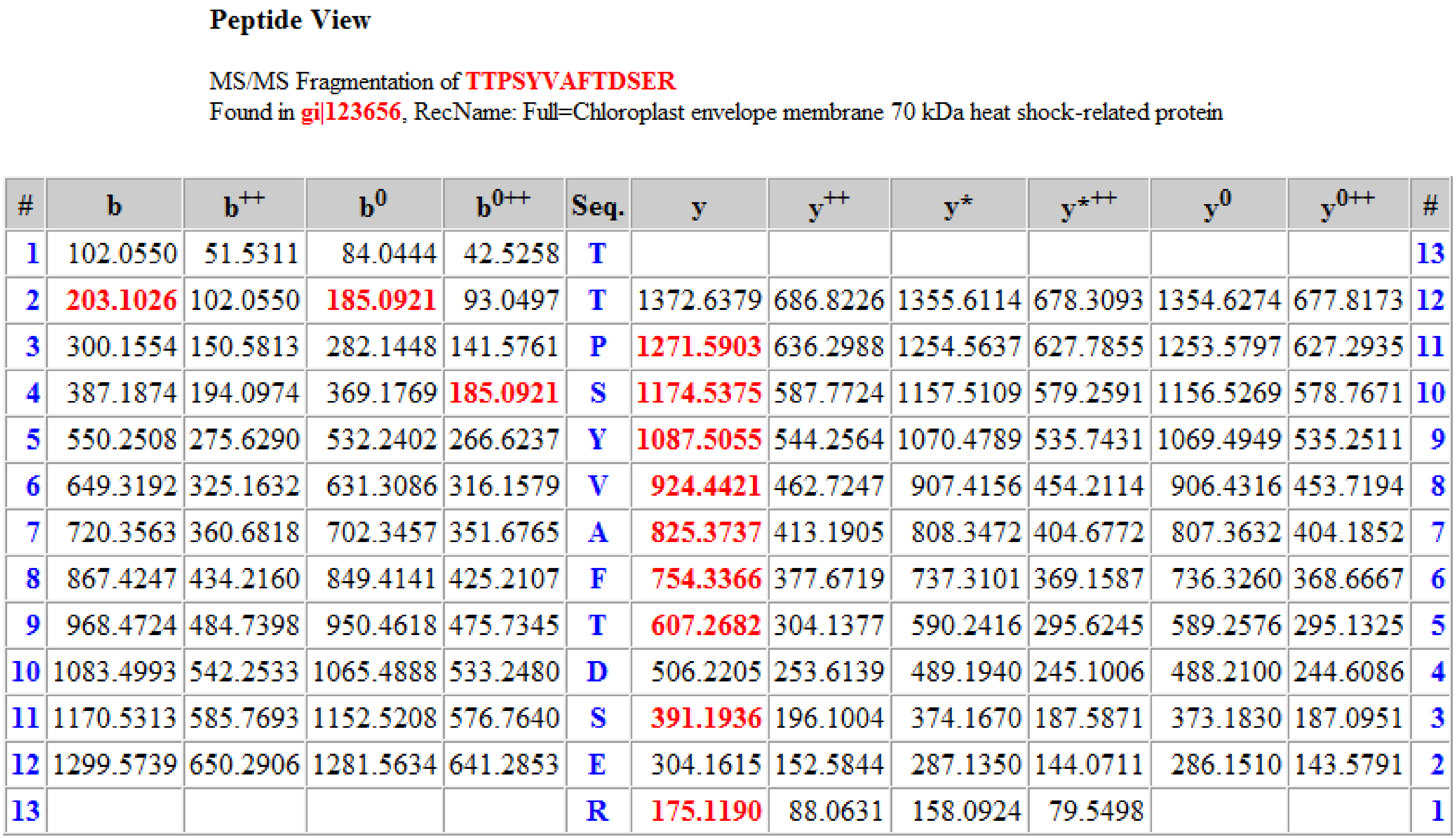
Taxonomy: Spinacia oleracea
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|21338 from Spinacia oleracea

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

Matched peptides shown in Bold Red

     1 MAGKGEGPAI GIDLGTTYSR VGVWQHDRVE IIANDQGNRT TPSYVAFTDS
    51 ERLIGDAAKN QVAMNPINTV FDAKRLIGRR FSDASVQADM KHRPFKVVSG
   101 PGEKPMIGVN YKGEEKQFAA EEISSMVLTK MKEIAEAYLG STVKNAVVTV
   151 PAYFNDSQRQ ATKDAGVISG LNVMRIINEP TAAAIAYGLD KKATSVGEKN
   201 VLIFDLGGGT FDVSLLTIEE GIFEVKATAG DTHLGGEDFD NRMVNHSLQE
   251 FKRKNKKDIM ETPGHIRRLR TACERAKRTL SSTAQTTIEI DSLYEGVDFY
   301 SPITRARFEE LNIDLFRKCM EPVEKCLRDA KMDKSTVHDV VLVGGSTRIP
   351 KVQQLLQDFF NGKELCKSIN PDEAVAYGAA VQAAILSGEG NEKVQDLLLL
   401 DVTPLSLGLE TAGGVMTVLI PRNTTIPTKK EQVFSTYSDN QPGVLIQVYE
   451 GERTRTRDNN LLGKFELSGI PPGPRGVPQI NVCFDIDANG ILNVSAEDKT
   501 TGQKNKIRIT NDKGRLSKEE IEKMVQEAEK YKSEDEEHKK KVESKNALEN
   551 YAYNMRNIVK DEKIGAKLSE ADKKKIEEAI DASIQWLDGN QLAEADEFDD
   601 KMKELESICN PIIAKMYQGA GGDMGGGMED EGPTSGGGAG PKIEECRLSC
   651 HFF
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss  Sequence
   40 - 52       737.3904  1472.7663  1472.6783    0.0879     0  R.TTPSYVAFTDSER.L   (Ions score 65)
```

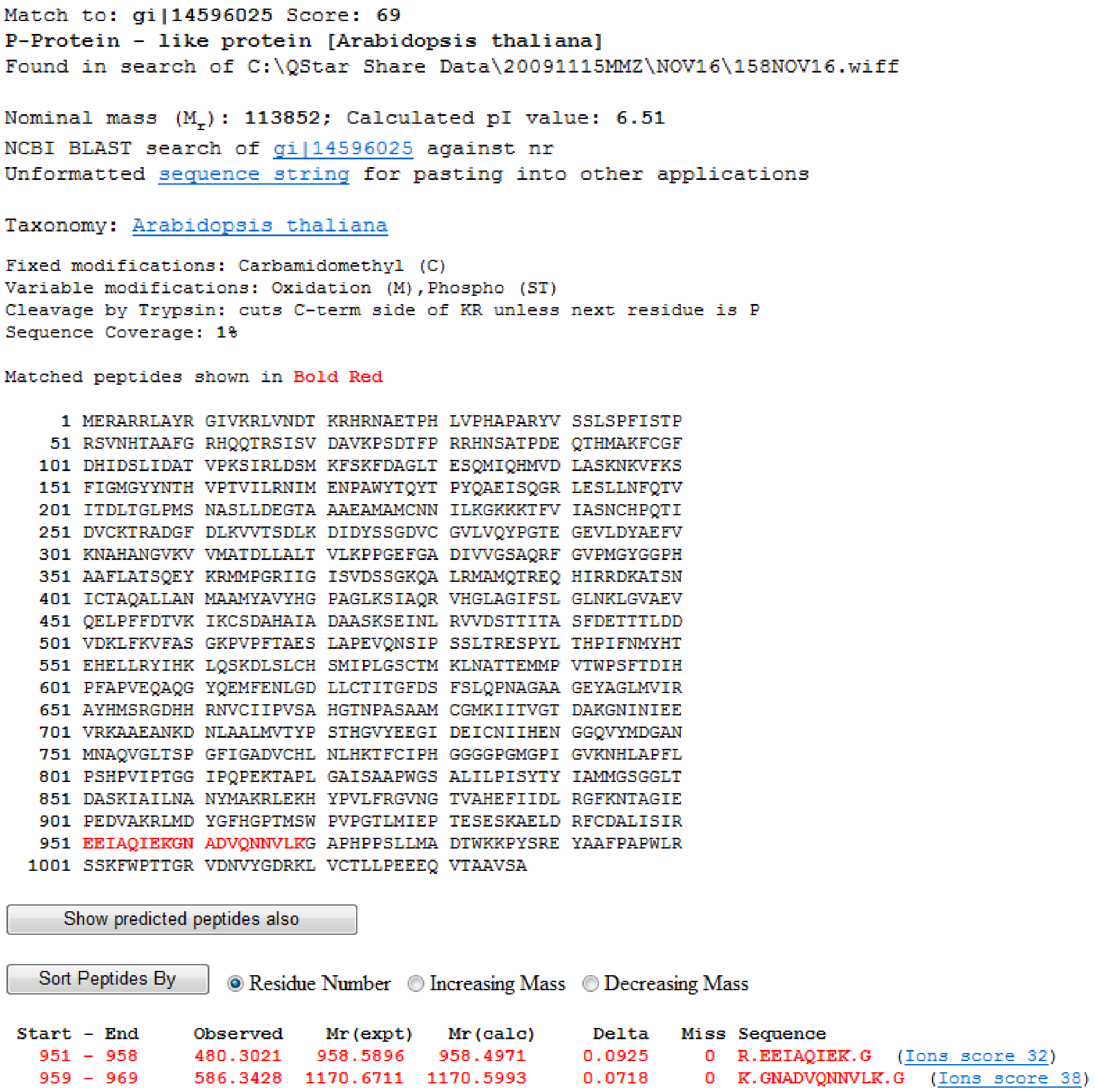


Peptide View

MS/MS Fragmentation of **TTPSYVAFTDSER**
Found in **gi|123656**, RecName: Full=Chloroplast envelope membrane 70 kDa heat shock-related protein

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							13
2	203.1026	102.0550	185.0921	93.0497	T	1372.6379	686.8226	1355.6114	678.3093	1354.6274	677.8173	12
3	300.1554	150.5813	282.1448	141.5761	P	1271.5903	636.2988	1254.5637	627.7855	1253.5797	627.2935	11
4	387.1874	194.0974	369.1769	185.0921	S	1174.5375	587.7724	1157.5109	579.2591	1156.5269	578.7671	10
5	550.2508	275.6290	532.2402	266.6237	Y	1087.5055	544.2564	1070.4789	535.7431	1069.4949	535.2511	9
6	649.3192	325.1632	631.3086	316.1579	V	924.4421	462.7247	907.4156	454.2114	906.4316	453.7194	8
7	720.3563	360.6818	702.3457	351.6765	A	825.3737	413.1905	808.3472	404.6772	807.3632	404.1852	7
8	867.4247	434.2160	849.4141	425.2107	F	754.3366	377.6719	737.3101	369.1587	736.3260	368.6667	6
9	968.4724	484.7398	950.4618	475.7345	T	607.2682	304.1377	590.2416	295.6245	589.2576	295.1325	5
10	1083.4993	542.2533	1065.4888	533.2480	D	506.2205	253.6139	489.1940	245.1006	488.2100	244.6086	4
11	1170.5313	585.7693	1152.5208	576.7640	S	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
12	1299.5739	650.2906	1281.5634	641.2853	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13					R	175.1190	88.0631	158.0924	79.5498			1

gi|14596025 P-Protein - like protein



Match to: gi|14596025 Score: 69
P-Protein - like protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV16\158NOV16.wiff

Nominal mass (M_r): 113852; Calculated pI value: 6.51
NCBI BLAST search of gi|14596025 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 1%

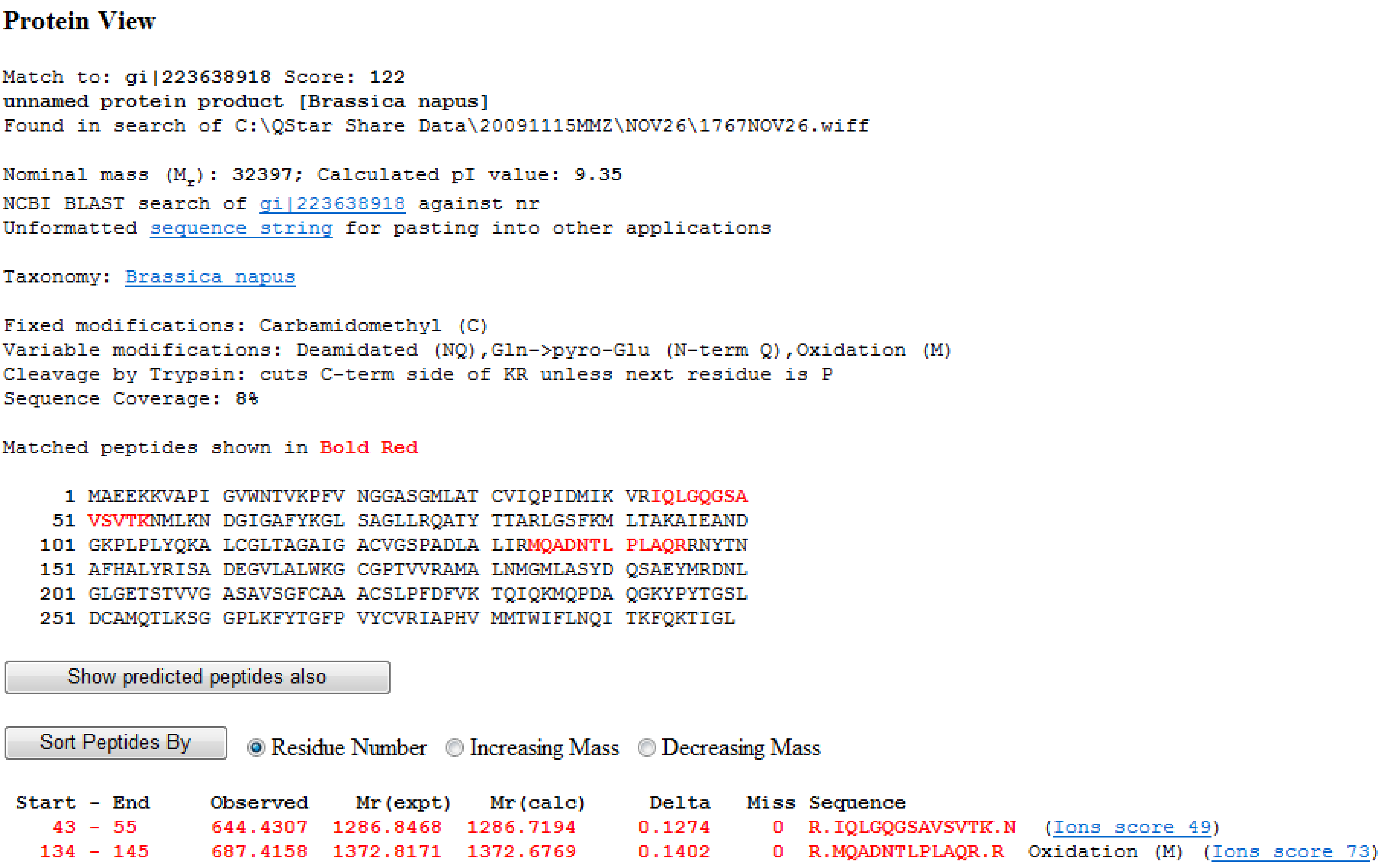
Matched peptides shown in **Bold Red**

```
   1 MERARRLAYR GIVKRLVNDT KRHRNAETPH LVPHAPARYV SSLSPFISTP
  51 RSVNHTAAFG RHQQTRSISV DAVKPSDTFP RRHNSATPDE QTHMAKFCGF
 101 DHIDSLIDAT VPKSIRLDSM KFSKFDAGLT ESQMIQHMVD LASKNKVFKS
 151 FIGMGYYNTH VPTVILRNIM ENPAWYTQYT PYQAEISQGR LESLLNFQTV
 201 ITDLTGLPMS NASLLDEGTA AAEAMAMCNN ILKGKKKTFV IASNCHPQTI
 251 DVCKTRADGF DLKVVTSDLK DIDYSSGDVC GVLVQYPGTE GEVLDYAEFV
 301 KNAHANGVKV VMATDLLALT VLKPPGEFGA DIVVGSAQRF GVPMGYGGPH
 351 AAFLATSQEY KRMMPGRIIG ISVDSSGKQA LRMAMQTREQ HIRRDKATSN
 401 ICTAQALLAN MAAMYAVYHG PAGLKSIAQR VHGLAGIFSL GLNKLGVAEV
 451 QELPFFDTVK IKCSDAHAIA DAASKSEINL RVVDSTTITA SFDETTTLDD
 501 VDKLFKVFAS GKPVPFTAES LAPEVQNSIP SSLTRESPYL THPIFNMYHT
 551 EHELLRYIHK LQSKDLSLCH SMIPLGSCTM KLNATTEMMP VTWPSFTDIH
 601 PFAPVEQAQG YQEMFENLGD LLCTITGFDS FSLQPNAGAA GEYAGLMVIR
 651 AYHMSRGDHH RNVCIIPVSA HGTNPASAAM CGMKIITVGT DAKGNINIEE
 701 VRKAAEANKD NLAALMVTYP STHGVYEEGI DEICNIIHEN GGQVYMDGAN
 751 MNAQVGLTSP GFIGADVCHL NLHKTFCIPH GGGGPGMGPI GVKNHLAPFL
 801 PSHPVIPTGG IPQPEKTAPL GAISAAPWGS ALILPISYTY IAMMGSGGLT
 851 DASKIAILNA NYMAKRLEKH YPVLFRGVNG TVAHEFIIDL RGFKNTAGIE
 901 PEDVAKRLMD YGFHGPTMSW PVPGTLMIEP TESESKAELD RFCDALISIR
 951 EEIAQIEKGN ADVQNNVLKG APHPPSLLMA DTWKKPYSRE YAAFPAPWLR
1001 SSKFWPTTGR VDNVYGDRKL VCTLLPEEEQ VTAAVSA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End     Observed    Mr(expt)    Mr(calc)     Delta   Miss  Sequence
  951 - 958     480.3021    958.5896    958.4971    0.0925     0   R.EEIAQIEK.G   (Ions score 32)
  959 - 969     586.3428   1170.6711   1170.5993    0.0718     0   K.GNADVQNNVLK.G   (Ions score 38)
```

gi|223638918 Unnamed protein product, containing pfam00153 domain



Protein View

```
Match to: gi|223638918 Score: 122
unnamed protein product [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1767NOV26.wiff

Nominal mass (Mr): 32397; Calculated pI value: 9.35
NCBI BLAST search of gi|223638918 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 8%

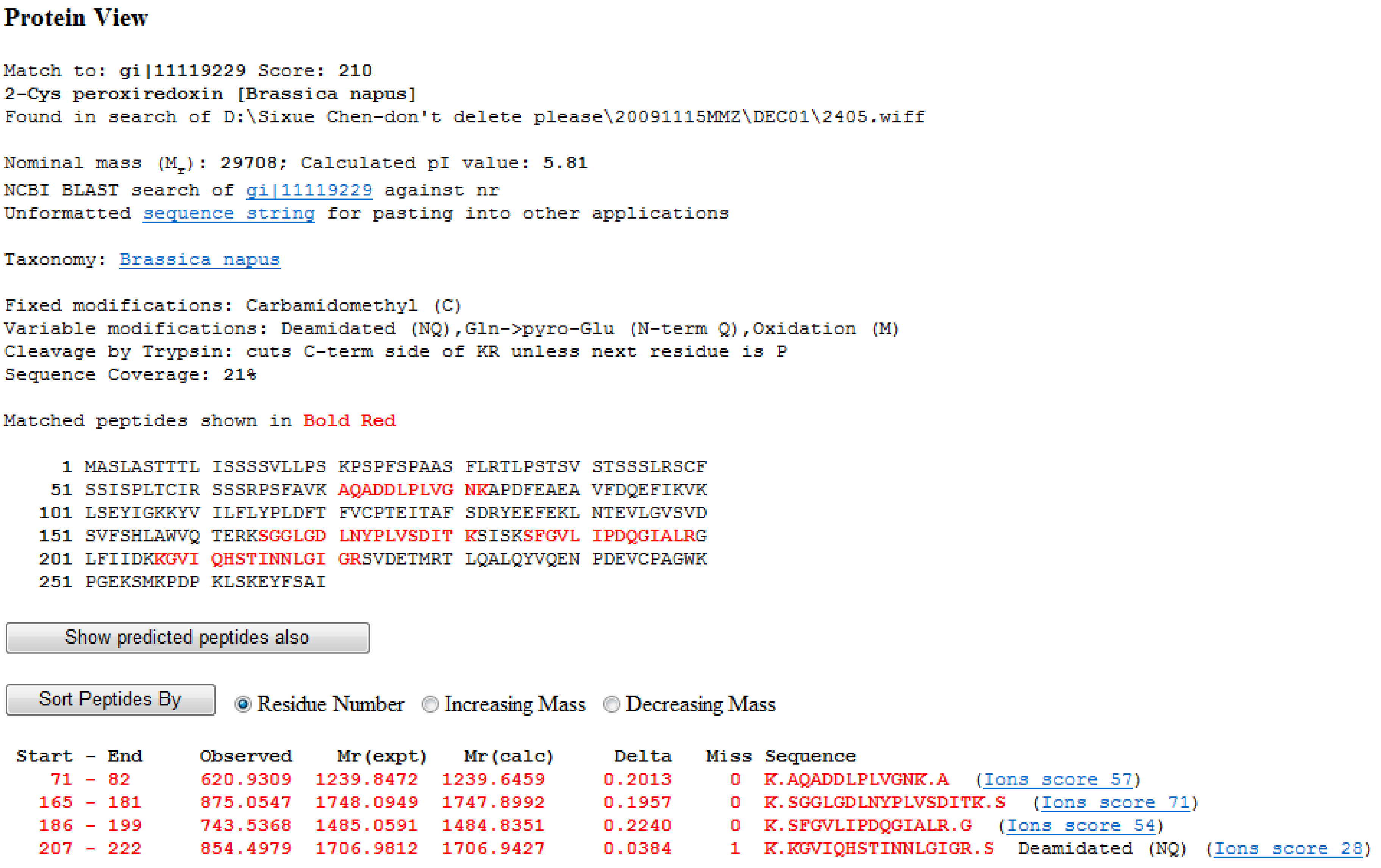
Matched peptides shown in Bold Red

     1 MAEEKKVAPI GVWNTVKPFV NGGASGMLAT CVIQPIDMIK VRIQLGQGSA
    51 VSVTKNMLKN DGIGAFYKGL SAGLLRQATY TTARLGSFKM LTAKAIEAND
   101 GKPLPLYQKA LCGLTAGAIG ACVGSPADLA LIRMQADNTL PLAQRRNYTN
   151 AFHALYRISA DEGVLALWKG CGPTVVRAMA LNMGMLASYD QSAEYMRDNL
   201 GLGETSTVVG ASAVSGFCAA ACSLPFDFVK TQIQKMQPDA QGKYPYTGSL
   251 DCAMQTLKSG GPLKFYTGFP VYCVRIAPHV MMTWIFLNQI TKFQKTIGL
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   43 - 55      644.4307  1286.8468  1286.7194    0.1274     0  R.IQLGQGSAVSVTK.N   (Ions score 49)
  134 - 145     687.4158  1372.8171  1372.6769    0.1402     0  R.MQADNTLPLAQR.R  Oxidation (M)  (Ions score 73)
```

gi|11119229 2-Cys peroxiredoxin



Protein View

Match to: **gi|11119229** Score: **210**

2-Cys peroxiredoxin [Brassica napus]

Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2405.wiff

Nominal mass (M_r): **29708**; Calculated pI value: **5.81**

NCBI BLAST search of gi|11119229 against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

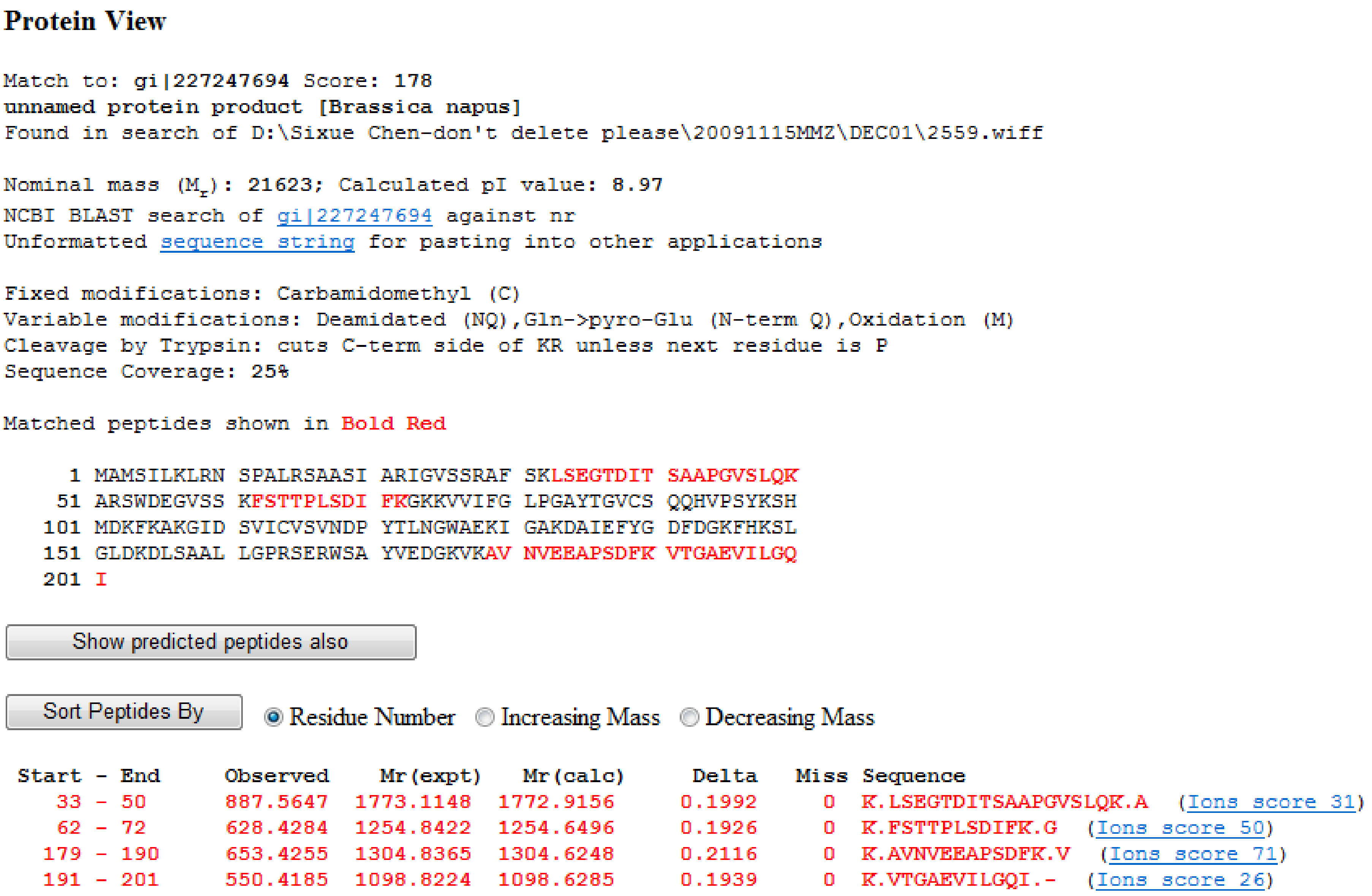
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
     1 MASLASTTTL ISSSSVLLPS KPSPFSPAAS FLRTLPSTSV STSSSLRSCF
    51 SSISPLTCIR SSSRPSFAVK AQADDLPLVG NKAPDFEAEA VFDQEFIKVK
   101 LSEYIGKKYV ILFLYPLDFT FVCPTEITAF SDRYEEFEKL NTEVLGVSVD
   151 SVFSHLAWVQ TERKSGGLGD LNYPLVSDIT KSISKSFGVL IPDQGIALRG
   201 LFIIDKKGVI QHSTINNLGI GRSVDETMRT LQALQYVQEN PDEVCPAGWK
   251 PGEKSMKPDP KLSKEYFSAI
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   71 - 82       620.9309  1239.8472  1239.6459    0.2013     0  K.AQADDLPLVGNK.A   (Ions score 57)
  165 - 181      875.0547  1748.0949  1747.8992    0.1957     0  K.SGGLGDLNYPLVSDITK.S   (Ions score 71)
  186 - 199      743.5368  1485.0591  1484.8351    0.2240     0  K.SFGVLIPDQGIALR.G   (Ions score 54)
  207 - 222      854.4979  1706.9812  1706.9427    0.0384     1  K.KGVIQHSTINNLGIGR.S   Deamidated (NQ)  (Ions score 28)
```

gi|227247694 Unnamed protein product, containing cd03013 domain



Protein View

```
Match to: gi|227247694 Score: 178
unnamed protein product [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2559.wiff

Nominal mass (Mr): 21623; Calculated pI value: 8.97
NCBI BLAST search of gi|227247694 against nr
Unformatted sequence string for pasting into other applications

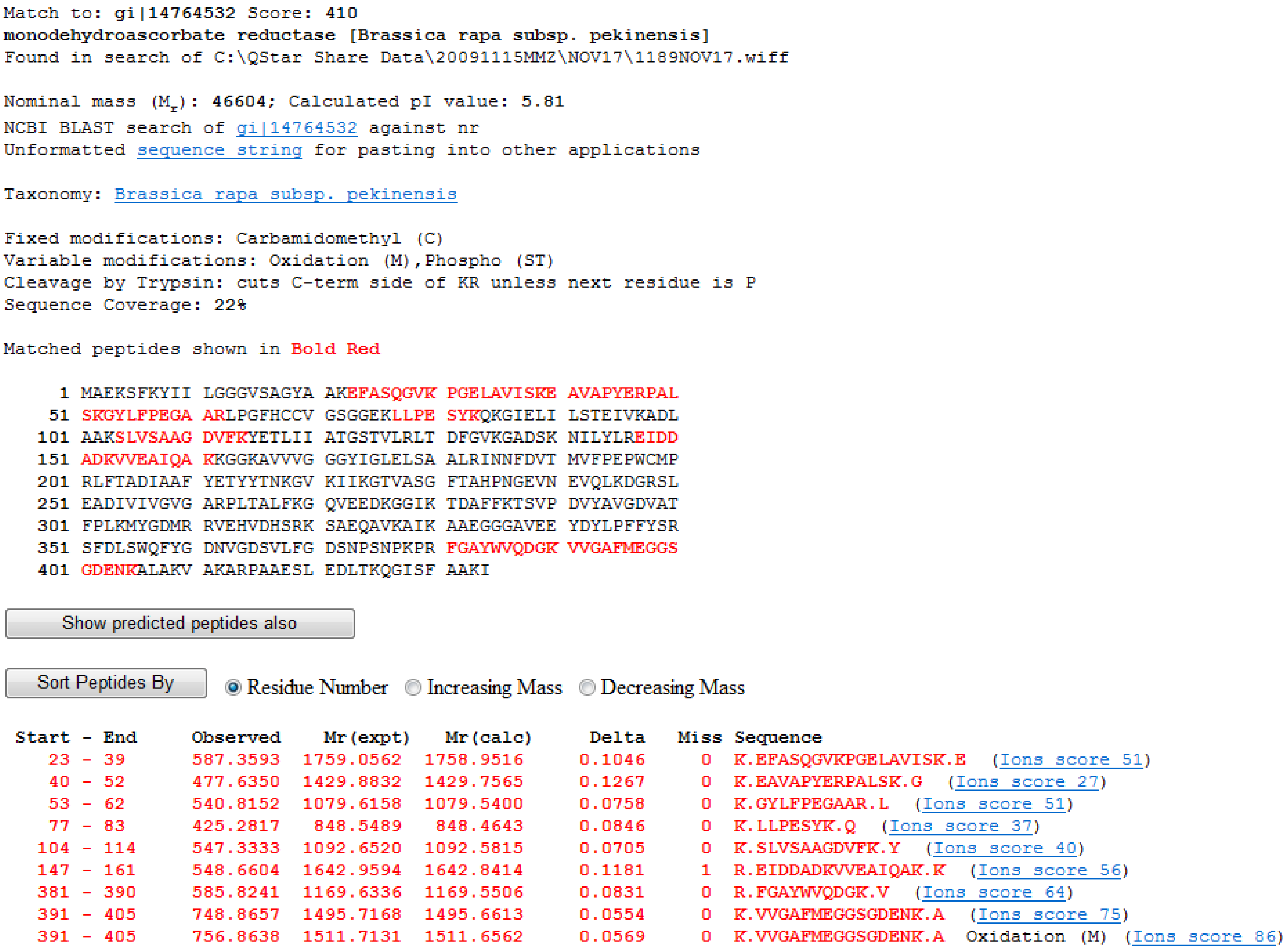
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 25%

Matched peptides shown in Bold Red

     1 MAMSILKLRN SPALRSAASI ARIGVSSRAF SKLSEGTDIT SAAPGVSLQK
    51 ARSWDEGVSS KFSTTPLSDI FKGKKVVIFG LPGAYTGVCS QQHVPSYKSH
   101 MDKFKAKGID SVICVSVNDP YTLNGWAEKI GAKDAIEFYG DFDGKFHKSL
   151 GLDKDLSAAL LGPRSERWSA YVEDGKVKAV NVEEAPSDFK VTGAEVILGQ
   201 I
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   33 - 50       887.5647  1773.1148  1772.9156    0.1992     0  K.LSEGTDITSAAPGVSLQK.A   (Ions score 31)
   62 - 72       628.4284  1254.8422  1254.6496    0.1926     0  K.FSTTPLSDIFK.G  (Ions score 50)
  179 - 190      653.4255  1304.8365  1304.6248    0.2116     0  K.AVNVEEAPSDFK.V  (Ions score 71)
  191 - 201      550.4185  1098.8224  1098.6285    0.1939     0  K.VTGAEVILGQI.-  (Ions score 26)
```

gi|14764532 Monodehydroascorbate reductase



Match to: gi|14764532 Score: 410
monodehydroascorbate reductase [Brassica rapa subsp. pekinensis]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1189NOV17.wiff

Nominal mass (M_r): 46604; Calculated pI value: 5.81
NCBI BLAST search of gi|14764532 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica rapa subsp. pekinensis

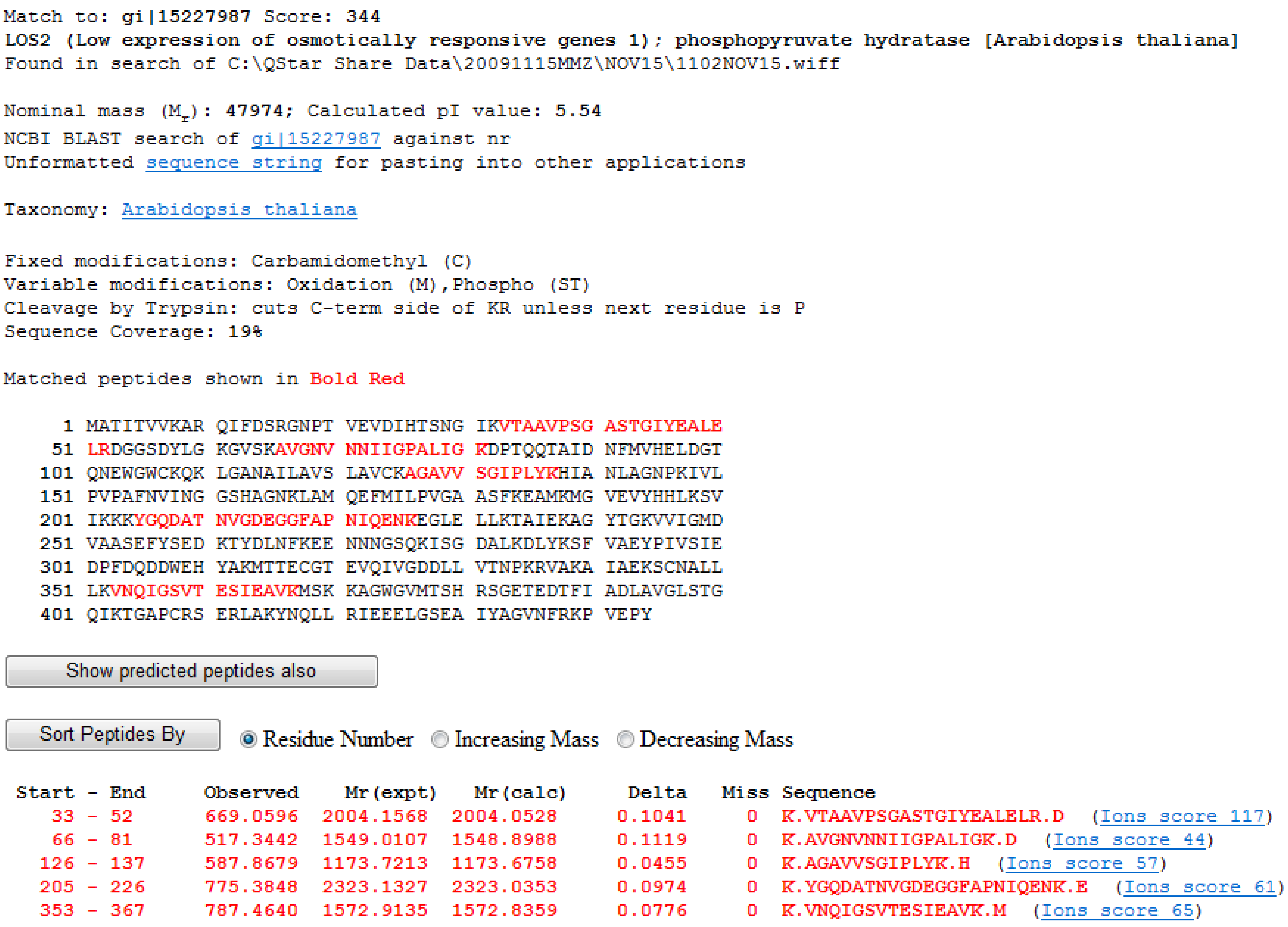
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 22%

Matched peptides shown in **Bold Red**

```
  1 MAEKSFKYII LGGGVSAGYA AKEFASQGVK PGELAVISKE AVAPYERPAL
 51 SKGYLFPEGA ARLPGFHCCV GSGGEKLLPE SYKQKGIELI LSTEIVKADL
101 AAKSLVSAAG DVFKYETLII ATGSTVLRLT DFGVKGADSK NILYLREIDD
151 ADKVVEAIQA KKGGKAVVVG GGYIGLELSA ALRINNFDVT MVFPEPWCMP
201 RLFTADIAAF YETYYTNKGV KIIKGTVASG FTAHPNGEVN EVQLKDGRSL
251 EADIVIVGVG ARPLTALFKG QVEEDKGGIK TDAFFKTSVP DVYAVGDVAT
301 FPLKMYGDMR RVEHVDHSRK SAEQAVKAIK AAEGGGAVEE YDLYPFFYSR
351 SFDLSWQFYG DNVGDSVLFG DSNPSNPKPR FGAYWVQDGK VVGAFMEGGS
401 GDENKALAKV AKARPAAESL EDLTKQGISF AAKI
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   23 - 39       587.3593  1759.0562  1758.9516    0.1046     0  K.EFASQGVKPGELAVISK.E   (Ions score 51)
   40 - 52       477.6350  1429.8832  1429.7565    0.1267     0  K.EAVAPYERPALSK.G   (Ions score 27)
   53 - 62       540.8152  1079.6158  1079.5400    0.0758     0  K.GYLFPEGAAR.L   (Ions score 51)
   77 - 83       425.2817   848.5489   848.4643    0.0846     0  K.LLPESYK.Q   (Ions score 37)
  104 - 114      547.3333  1092.6520  1092.5815    0.0705     0  K.SLVSAAGDVFK.Y   (Ions score 40)
  147 - 161      548.6604  1642.9594  1642.8414    0.1181     1  R.EIDDADKVVEAIQAK.K   (Ions score 56)
  381 - 390      585.8241  1169.6336  1169.5506    0.0831     0  R.FGAYWVQDGK.V   (Ions score 64)
  391 - 405      748.8657  1495.7168  1495.6613    0.0554     0  K.VVGAFMEGGSGDENK.A   (Ions score 75)
  391 - 405      756.8638  1511.7131  1511.6562    0.0569     0  K.VVGAFMEGGSGDENK.A  Oxidation (M)  (Ions score 86)
```

gi|15227987 Low expression of osmotically responsive genes 1 (LOS2)



```
Match to: gi|15227987 Score: 344
LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\1102NOV15.wiff

Nominal mass (Mr): 47974; Calculated pI value: 5.54
NCBI BLAST search of gi|15227987 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 19%

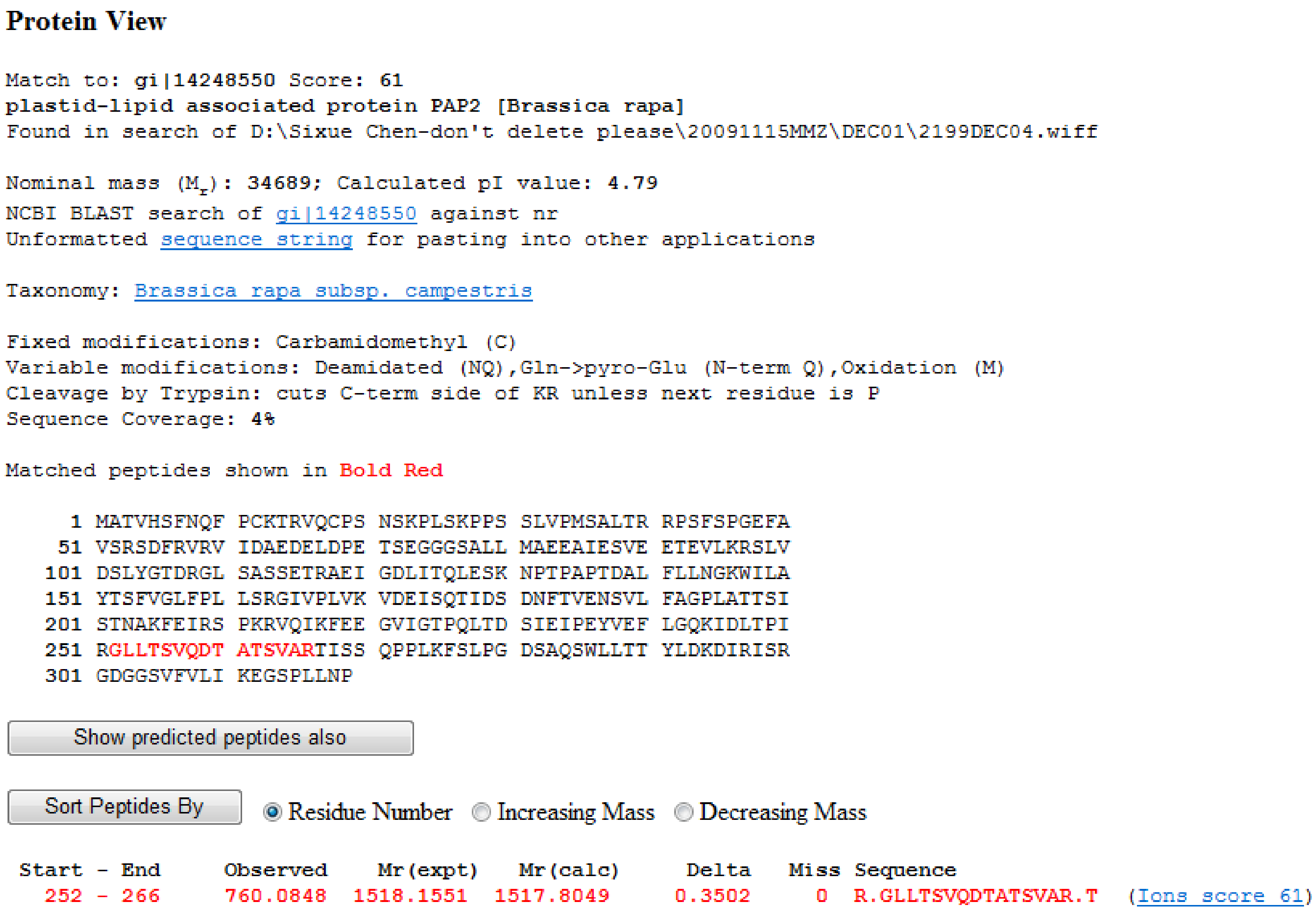
Matched peptides shown in Bold Red

     1 MATITVVKAR QIFDSRGNPT VEVDIHTSNG IKVTAAVPSG ASTGIYEALE
    51 LRDGGSDYLG KGVSKAVGNV NNIIGPALIG KDPTQQTAID NFMVHELDGT
   101 QNEWGWCKQK LGANAILAVS LAVCKAGAVV SGIPLYKHIA NLAGNPKIVL
   151 PVPAFNVING GSHAGNKLAM QEFMILPVGA ASFKEAMKMG VEVYHHLKSV
   201 IKKKYGQDAT NVGDEGGFAP NIQENKEGLE LLKTAIEKAG YTGKVVIGMD
   251 VAASEFYSED KTYDLNFKEE NNNGSQKISG DALKDLYKSF VAEYPIVSIE
   301 DPFDQDDWEH YAKMTTECGT EVQIVGDDLL VTNPKRVAKA IAEKSCNALL
   351 LKVNQIGSVT ESIEAVKMSK KAGWGVMTSH RSGETEDTFI ADLAVGLSTG
   401 QIKTGAPCRS ERLAKYNQLL RIEEELGSEA IYAGVNFRKP VEPY
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End      Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   33 - 52       669.0596  2004.1568  2004.0528    0.1041     0  K.VTAAVPSGASTGIYEALELR.D  (Ions score 117)
   66 - 81       517.3442  1549.0107  1548.8988    0.1119     0  K.AVGNVNNIIGPALIGK.D  (Ions score 44)
  126 - 137      587.8679  1173.7213  1173.6758    0.0455     0  K.AGAVVSGIPLYK.H  (Ions score 57)
  205 - 226      775.3848  2323.1327  2323.0353    0.0974     0  K.YGQDATNVGDEGGFAPNIQENK.E  (Ions score 61)
  353 - 367      787.4640  1572.9135  1572.8359    0.0776     0  K.VNQIGSVTESIEAVK.M  (Ions score 65)
```

gi|14248550 Plastid-lipid associated protein PAP2



Protein View

Match to: gi|14248550 Score: 61
plastid-lipid associated protein PAP2 [Brassica rapa]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2199DEC04.wiff

Nominal mass (M_r): 34689; Calculated pI value: 4.79
NCBI BLAST search of gi|14248550 against nr
Unformatted sequence string for pasting into other applications

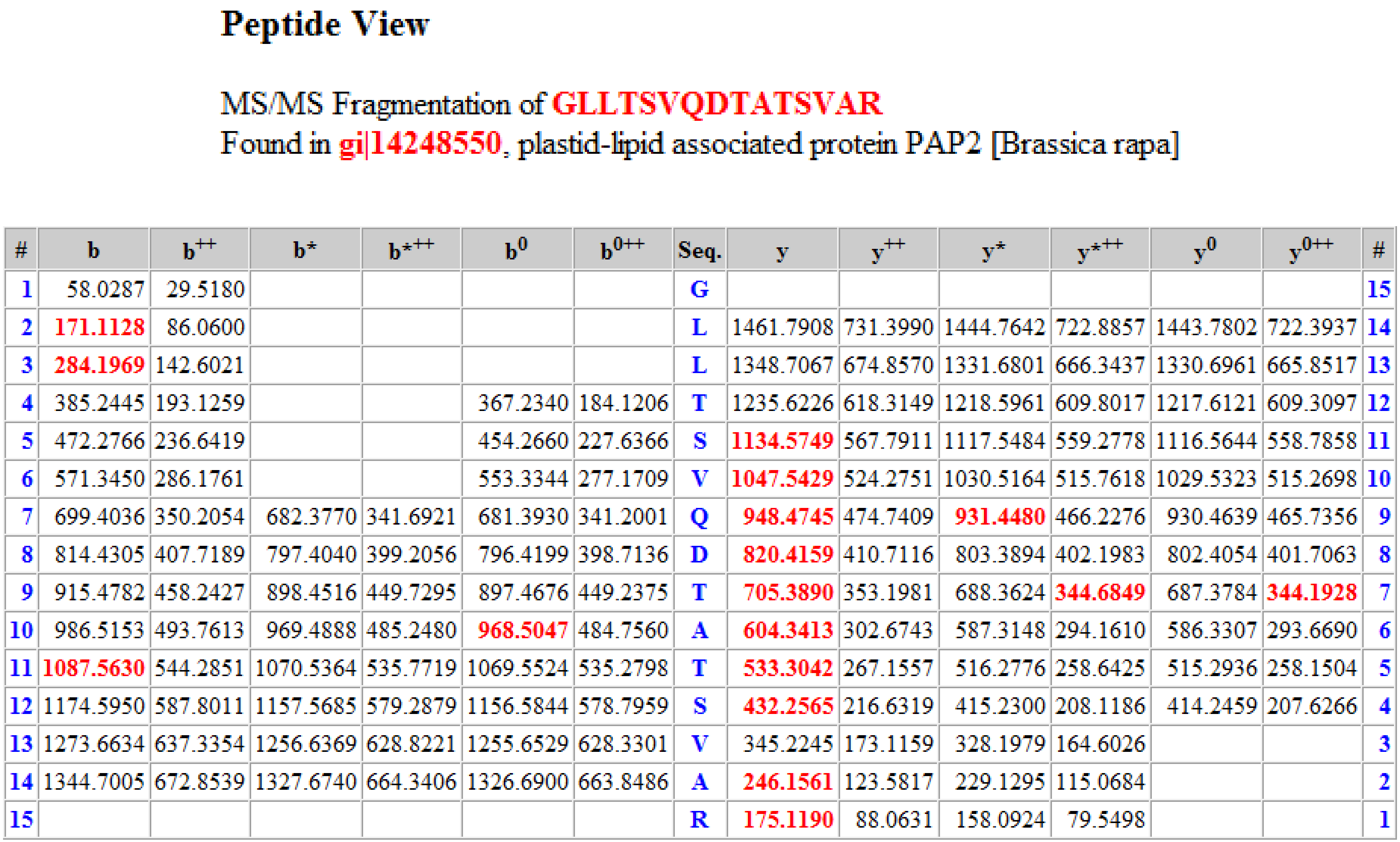
Taxonomy: Brassica rapa subsp. campestris

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 4%

Matched peptides shown in **Bold Red**

```
  1 MATVHSFNQF PCKTRVQCPS NSKPLSKPPS SLVPMSALTR RPSFSPGEFA
 51 VSRSDFRVRV IDAEDELDPE TSEGGGSALL MAEEAIESVE ETEVLKRSLV
101 DSLYGTDRGL SASSETRAEI GDLITQLESK NPTPAPTDAL FLLNGKWILA
151 YTSFVGLFPL LSRGIVPLVK VDEISQTIDS DNFTVENSVL FAGPLATTSI
201 STNAKFEIRS PKRVQIKFEE GVIGTPQLTD SIEIPEYVEF LGQKIDLTPI
251 RGLLTSVQDT ATSVARTISS QPPLKFSLPG DSAQSWLLTT YLDKDIRISR
301 GDGGSVFVLI KEGSPLLNP
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
  252 - 266      760.0848  1518.1551  1517.8049    0.3502     0  R.GLLTSVQDTATSVAR.T   (Ions score 61)
```

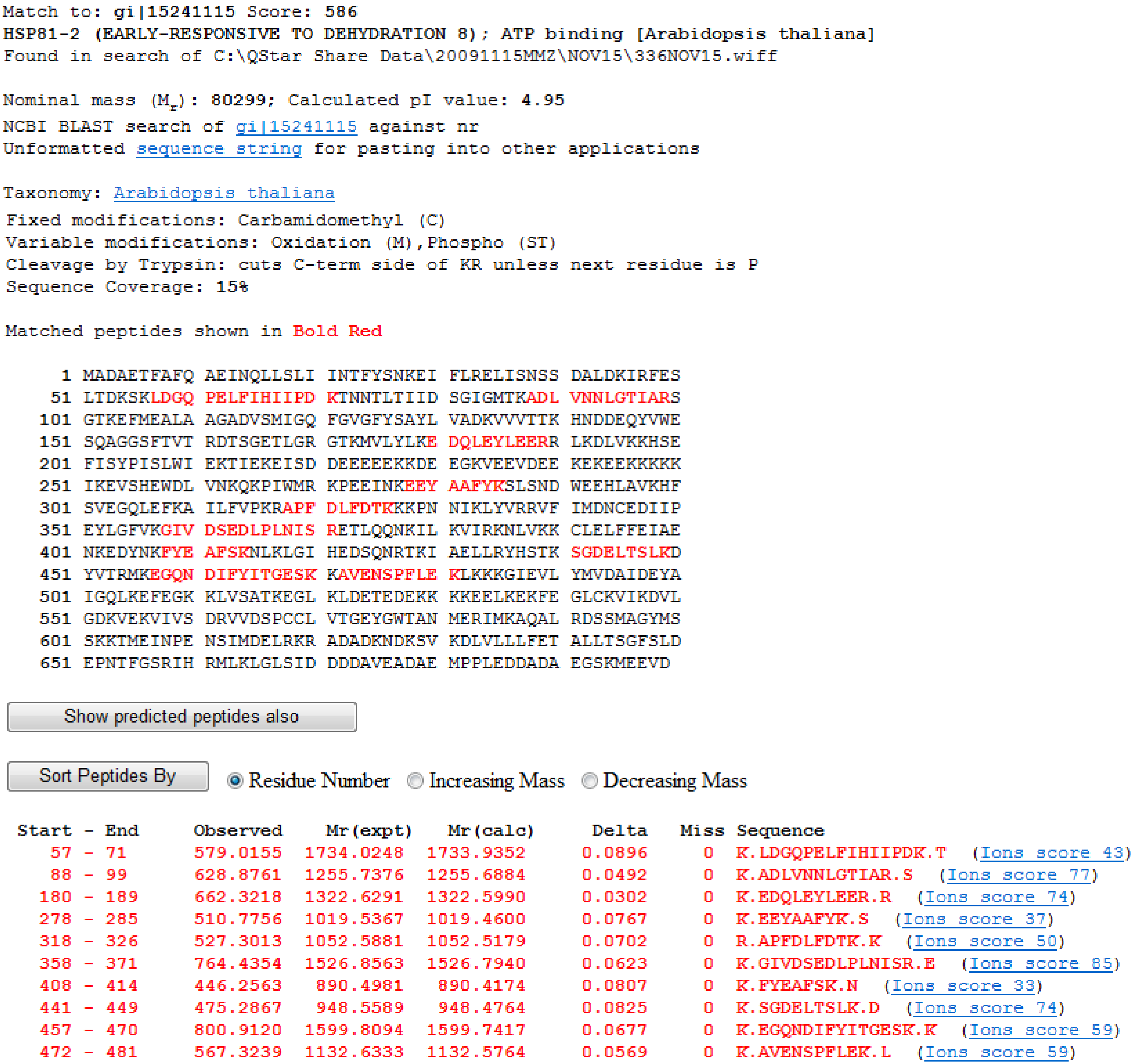


Peptide View

MS/MS Fragmentation of **GLLTSVQDTATSVAR**
Found in **gi|14248550**, plastid-lipid associated protein PAP2 [Brassica rapa]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**171.1128**	86.0600					L	1461.7908	731.3990	1444.7642	722.8857	1443.7802	722.3937	14
3	**284.1969**	142.6021					L	1348.7067	674.8570	1331.6801	666.3437	1330.6961	665.8517	13
4	385.2445	193.1259			367.2340	184.1206	T	1235.6226	618.3149	1218.5961	609.8017	1217.6121	609.3097	12
5	472.2766	236.6419			454.2660	227.6366	S	**1134.5749**	567.7911	1117.5484	559.2778	1116.5644	558.7858	11
6	571.3450	286.1761			553.3344	277.1709	V	**1047.5429**	524.2751	1030.5164	515.7618	1029.5323	515.2698	10
7	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	Q	**948.4745**	474.7409	**931.4480**	466.2276	930.4639	465.7356	9
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	D	**820.4159**	410.7116	803.3894	402.1983	802.4054	401.7063	8
9	915.4782	458.2427	898.4516	449.7295	897.4676	449.2375	T	**705.3890**	353.1981	688.3624	**344.6849**	687.3784	**344.1928**	7
10	986.5153	493.7613	969.4888	485.2480	**968.5047**	484.7560	A	**604.3413**	302.6743	587.3148	294.1610	586.3307	293.6690	6
11	**1087.5630**	544.2851	1070.5364	535.7719	1069.5524	535.2798	T	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	5
12	1174.5950	587.8011	1157.5685	579.2879	1156.5844	578.7959	S	**432.2565**	216.6319	415.2300	208.1186	414.2459	207.6266	4
13	1273.6634	637.3354	1256.6369	628.8221	1255.6529	628.3301	V	345.2245	173.1159	328.1979	164.6026			3
14	1344.7005	672.8539	1327.6740	664.3406	1326.6900	663.8486	A	**246.1561**	123.5817	229.1295	115.0684			2
15							R	**175.1190**	88.0631	158.0924	79.5498			1

gi|15241115 Early-responsive to dehydration 8 (HSP81-2)



```
Match to: gi|15241115 Score: 586
HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\336NOV15.wiff

Nominal mass (Mr): 80299; Calculated pI value: 4.95
NCBI BLAST search of gi|15241115 against nr
Unformatted sequence string for pasting into other applications

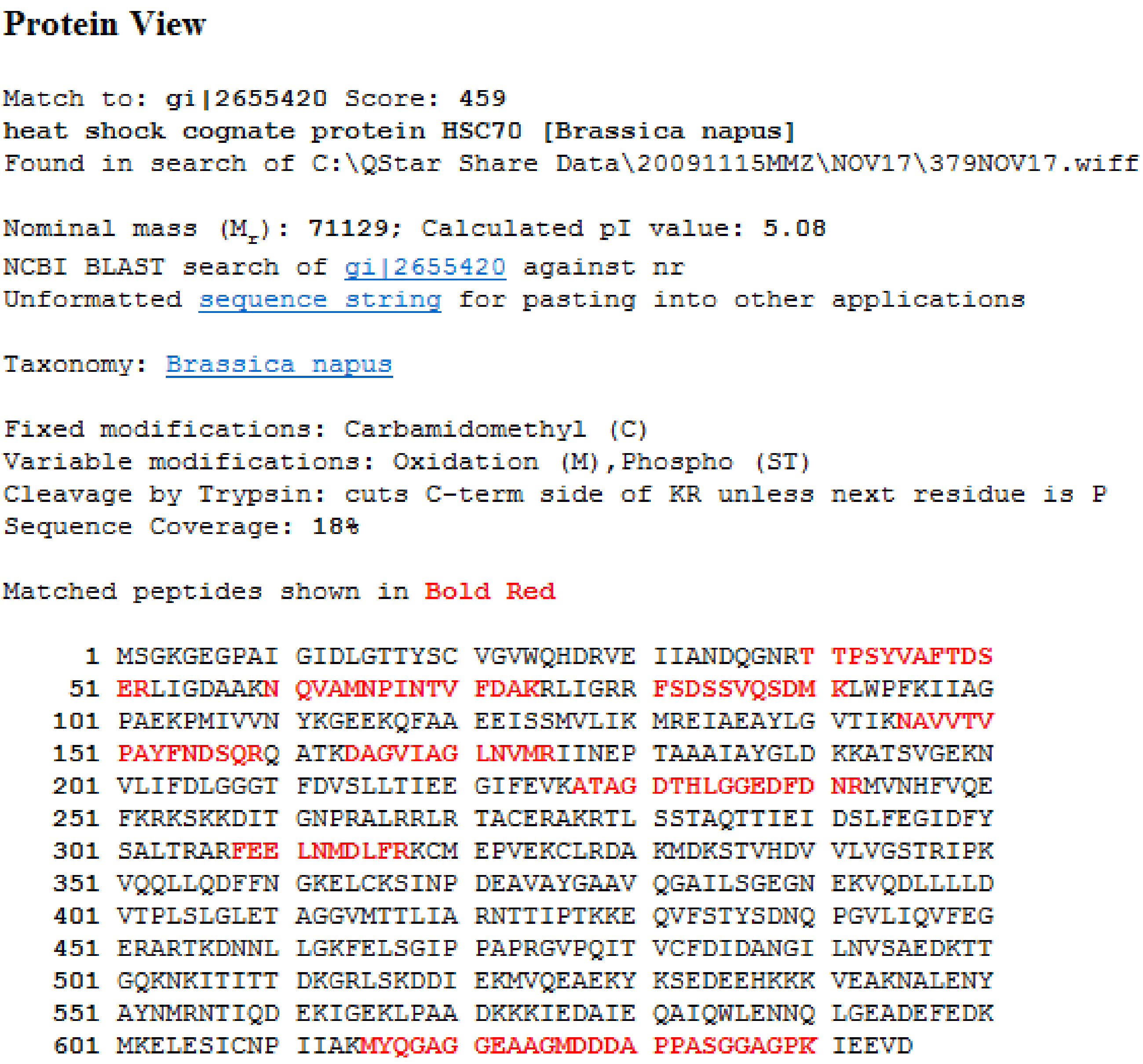
Taxonomy: Arabidopsis thaliana
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in Bold Red

     1 MADAETFAFQ AEINQLLSLI INTFYSNKEI FLRELISNSS DALDKIRFES
    51 LTDKSKLDGQ PELFIHIIPD KTNNTLTIID SGIGMTKADL VNNLGTIARS
   101 GTKEFMEALA AGADVSMIGQ FGVGFYSAYL VADKVVVTTK HNDDEQYVWE
   151 SQAGGSFTVT RDTSGETLGR GTKMVLYLKE DQLEYLEERR LKDLVKKHSE
   201 FISYPISLWI EKTIEKEISD DEEEEEKKDE EGKVEEVDEE KEKEEKKKKK
   251 IKEVSHEWDL VNKQKPIWMR KPEEINKEEY AAFYKSLSND WEEHLAVKHF
   301 SVEGQLEFKA ILFVPKRAPF DLFDTKKKPN NIKLYVRRVF IMDNCEDIIP
   351 EYLGFVKGIV DSEDLPLNIS RETLQQNKIL KVIRKNLVKK CLELFFEIAE
   401 NKEDYNKFYE AFSKNLKLGI HEDSQNRTKI AELLRYHSTK SGDELTSLKD
   451 YVTRMKEGQN DIFYITGESK KAVENSPFLE KLKKKGIEVL YMVDAIDEYA
   501 IGQLKEFEGK KLVSATKEGL KLDETEDEKK KKEELKEKFE GLCKVIKDVL
   551 GDKVEKVIVS DRVVDSPCCL VTGEYGWTAN MERIMKAQAL RDSSMAGYMS
   601 SKKTMEINPE NSIMDELRKR ADADKNDKSV KDLVLLLFET ALLTSGFSLD
   651 EPNTFGSRIH RMLKLGLSID DDDAVEADAE MPPLEDDADA EGSKMEEVD
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
    57 - 71     579.0155  1734.0248  1733.9352   0.0896     0  K.LDGQPELFIHIIPDK.T   (Ions score 43)
    88 - 99     628.8761  1255.7376  1255.6884   0.0492     0  K.ADLVNNLGTIAR.S   (Ions score 77)
   180 - 189    662.3218  1322.6291  1322.5990   0.0302     0  K.EDQLEYLEER.R   (Ions score 74)
   278 - 285    510.7756  1019.5367  1019.4600   0.0767     0  K.EEYAAFYK.S   (Ions score 37)
   318 - 326    527.3013  1052.5881  1052.5179   0.0702     0  R.APFDLFDTK.K   (Ions score 50)
   358 - 371    764.4354  1526.8563  1526.7940   0.0623     0  K.GIVDSEDLPLNISR.E   (Ions score 85)
   408 - 414    446.2563   890.4981   890.4174   0.0807     0  K.FYEAFSK.N   (Ions score 33)
   441 - 449    475.2867   948.5589   948.4764   0.0825     0  K.SGDELTSLK.D   (Ions score 74)
   457 - 470    800.9120  1599.8094  1599.7417   0.0677     0  K.EGQNDIFYITGESK.K   (Ions score 59)
   472 - 481    567.3239  1132.6333  1132.5764   0.0569     0  K.AVENSPFLEK.L   (Ions score 59)
```

gi|2655420 Heat shock cognate protein HSC70



Protein View

Match to: gi|2655420 Score: 459
heat shock cognate protein HSC70 [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\379NOV17.wiff

Nominal mass (M_r): 71129; Calculated pI value: 5.08
NCBI BLAST search of gi|2655420 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

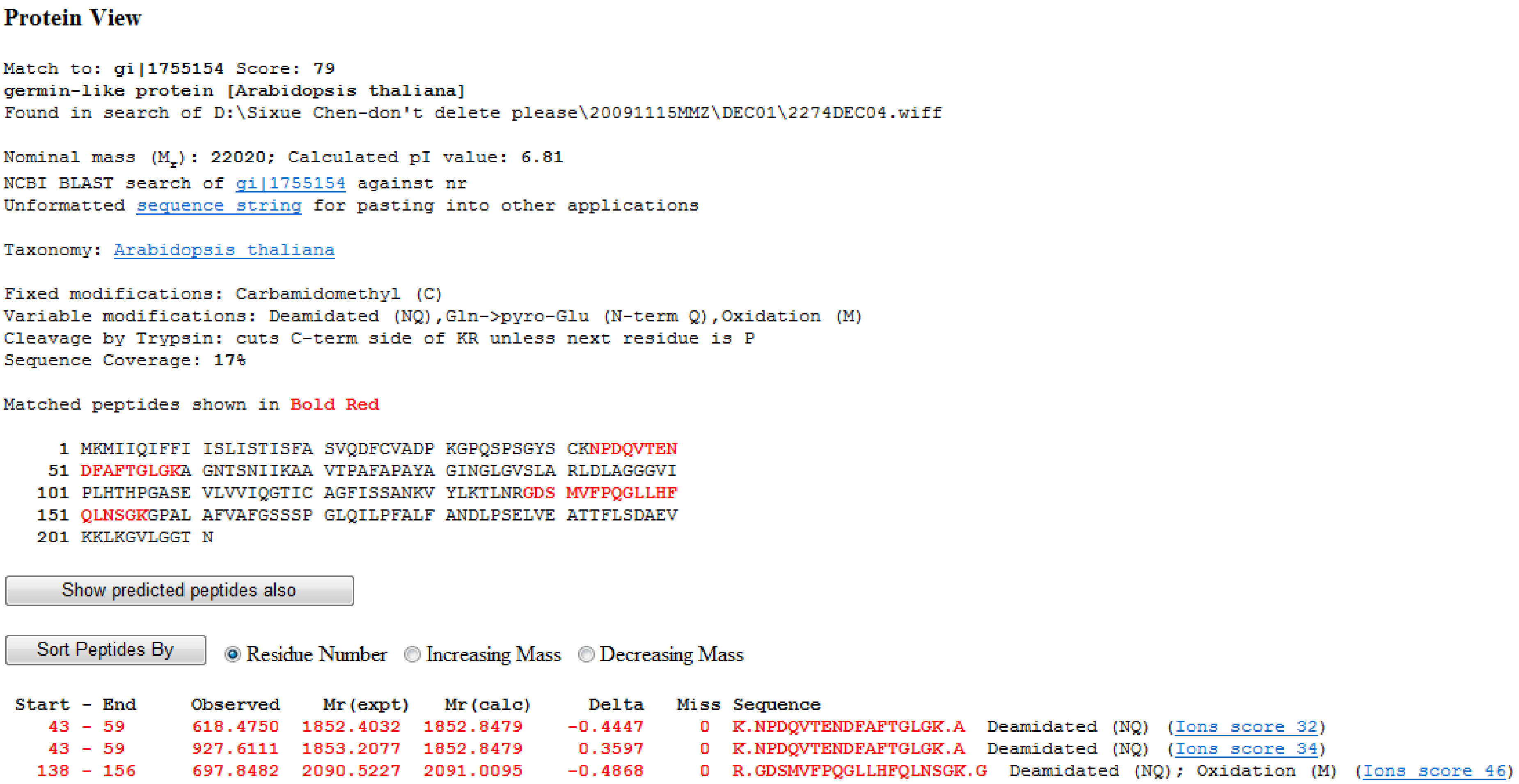
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 18%

Matched peptides shown in **Bold Red**

1 MSGKGEGPAI GIDLGTTYSC VGVWQHDRVE IIANDQGNR**T TPSYVAFTDS**
51 **ERLIGDAAKN QVAMNPINTV FDAK**RLIGRR **FSDSSVQSDM K**LWPFKIIAG
101 PAEKPMIVVN YKGEEKQFAA EEISSMVLIK MREIAEAYLG VTIK**NAVVTV**
151 **PAYFNDSQR**Q ATK**DAGVIAG LNVMR**IINEP TAAAIAYGLD KKATSVGEKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVK**ATAG DTHLGGEDFD NR**MVNHFVQE
251 FKRKSKKDIT GNPRALRRLR TACERAKRTL SSTAQTTIEI DSLFEGIDFY
301 SALTRAR**FEE LNMDLFR**KCM EPVEKCLRDA KMDKSTVHDV VLVGSTRIPK
351 VQQLLQDFFN GKELCKSINP DEAVAYGAAV QGAILSGEGN EKVQDLLLLD
401 VTPLSLGLET AGGVMTTLIA RNTTIPTKKE QVFSTYSDNQ PGVLIQVFEG
451 ERARTKDNNL LGKFELSGIP PAPRGVPQIT VCFDIDANGI LNVSAEDKTT
501 GQKNKITITT DKGRLSKDDI EKMVQEAEKY KSEDEEHKKK VEAKNALENY
551 AYNMRNTIQD EKIGEKLPAA DKKKIEDAIE QAIQWLENNQ LGEADEFEDK
601 MKELESICNP IIAK**MYQGAG GEAAGMDDDA PPASGGAGPK** IEEVD

```
Start - End     Observed    Mr(expt)   Mr(calc)     Delta    Miss Sequence
   40 - 52      737.3662  1472.7178  1472.6783     0.0395     0  R.TTPSYVAFTDSER.L   (Ions score 82)
   60 - 74      831.4414  1660.8682  1660.8243     0.0439     0  K.NQVAMNPINTVFDAK.R   (Ions score 39)
   81 - 91      615.8024  1229.5903  1229.5234     0.0669     0  R.FSDSSVQSDMK.L   (Ions score 39)
  145 - 159     560.9835  1679.9286  1679.8267     0.1019     0  K.NAVVTVPAYFNDSQR.Q   (Ions score 49)
  164 - 175     608.3919  1214.7692  1214.6441     0.1250     0  K.DAGVIAGLNVMR.I   (Ions score 57)
  164 - 175     616.3564  1230.6983  1230.6391     0.0593     0  K.DAGVIAGLNVMR.I  Oxidation (M)  (Ions score 49)
  227 - 242     559.2825  1674.8258  1674.7234     0.1024     0  K.ATAGDTHLGGEDFDNR.M   (Ions score 56)
  308 - 317     665.3352  1328.6559  1328.6071     0.0488     0  R.FEELNMDLFR.K  Oxidation (M)  (Ions score 72)
  615 - 640     804.0228  2409.0464  2408.9849     0.0615     0  K.MYQGAGGEAAGMDDDAPPASGGAGPK.I  2 Oxidation (M)  (Ions score 69)
```

gi|1755154 Germin-like protein



Protein View

Match to: gi|1755154 Score: 79
germin-like protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2274DEC04.wiff

Nominal mass (M_r): 22020; Calculated pI value: 6.81
NCBI BLAST search of gi|1755154 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

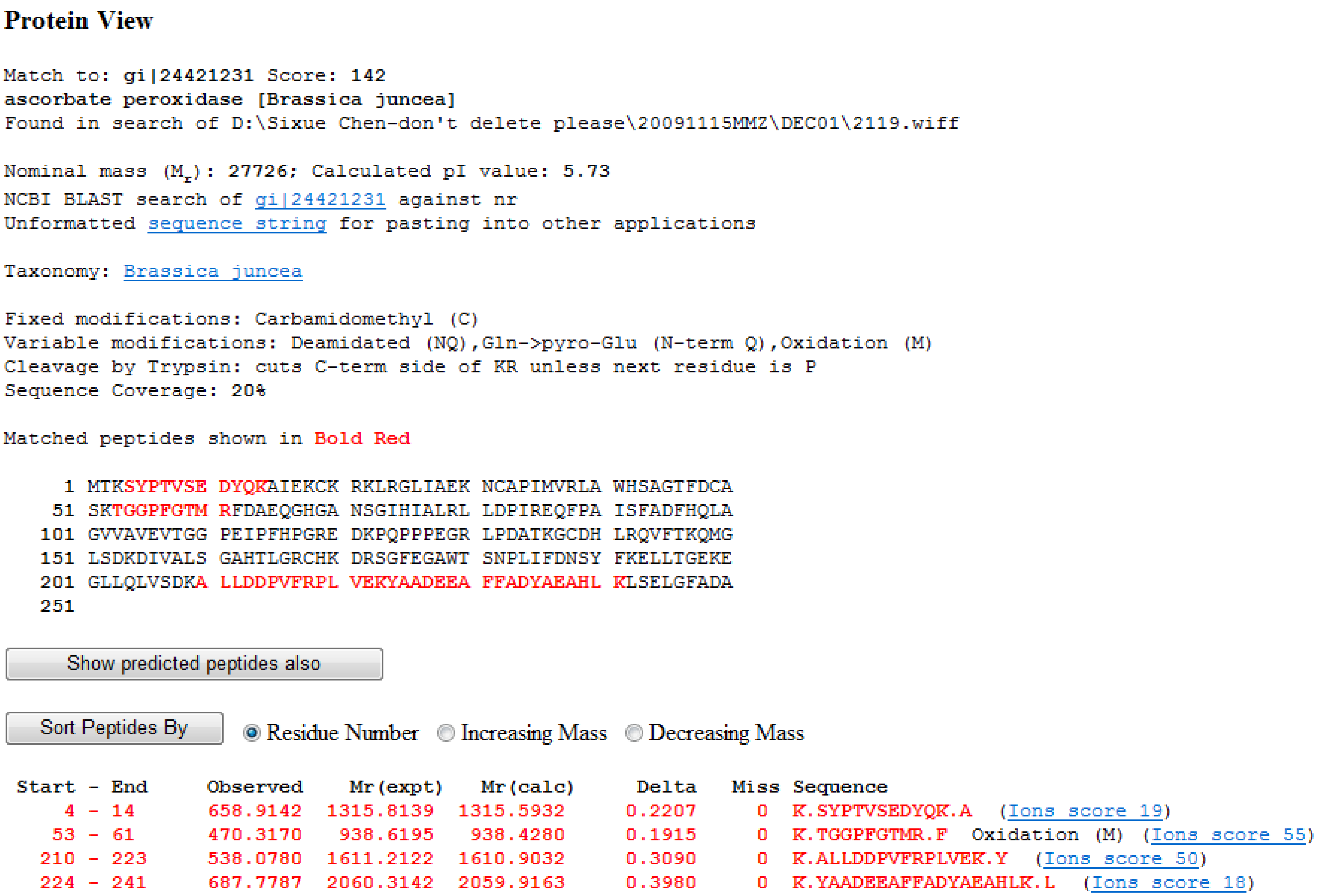
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 17%

Matched peptides shown in **Bold Red**

```
     1 MKMIIQIFFI ISLISTISFA SVQDFCVADP KGPQSPSGYS CKNPDQVTEN
    51 DFAFTGLGKA GNTSNIIKAA VTPAFAPAYA GINGLGVSLA RLDLAGGGVI
   101 PLHTHPGASE VLVVIQGTIC AGFISSANKV YLKTLNRGDS MVFPQGLLHF
   151 QLNSGKGPAL AFVAFGSSSP GLQILPFALF ANDLPSELVE ATTFLSDAEV
   201 KKLKGVLGGT N
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   43 - 59       618.4750  1852.4032  1852.8479   -0.4447    0  K.NPDQVTENDFAFTGLGK.A  Deamidated (NQ) (Ions score 32)
   43 - 59       927.6111  1853.2077  1852.8479    0.3597    0  K.NPDQVTENDFAFTGLGK.A  Deamidated (NQ) (Ions score 34)
  138 - 156      697.8482  2090.5227  2091.0095   -0.4868    0  R.GDSMVFPQGLLHFQLNSGK.G  Deamidated (NQ); Oxidation (M) (Ions score 46)
```

gi|24421231 Ascorbate peroxidase



Protein View

Match to: gi|24421231 Score: 142
ascorbate peroxidase [Brassica juncea]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2119.wiff

Nominal mass (M_r): 27726; Calculated pI value: 5.73
NCBI BLAST search of gi|24421231 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica juncea

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 20%

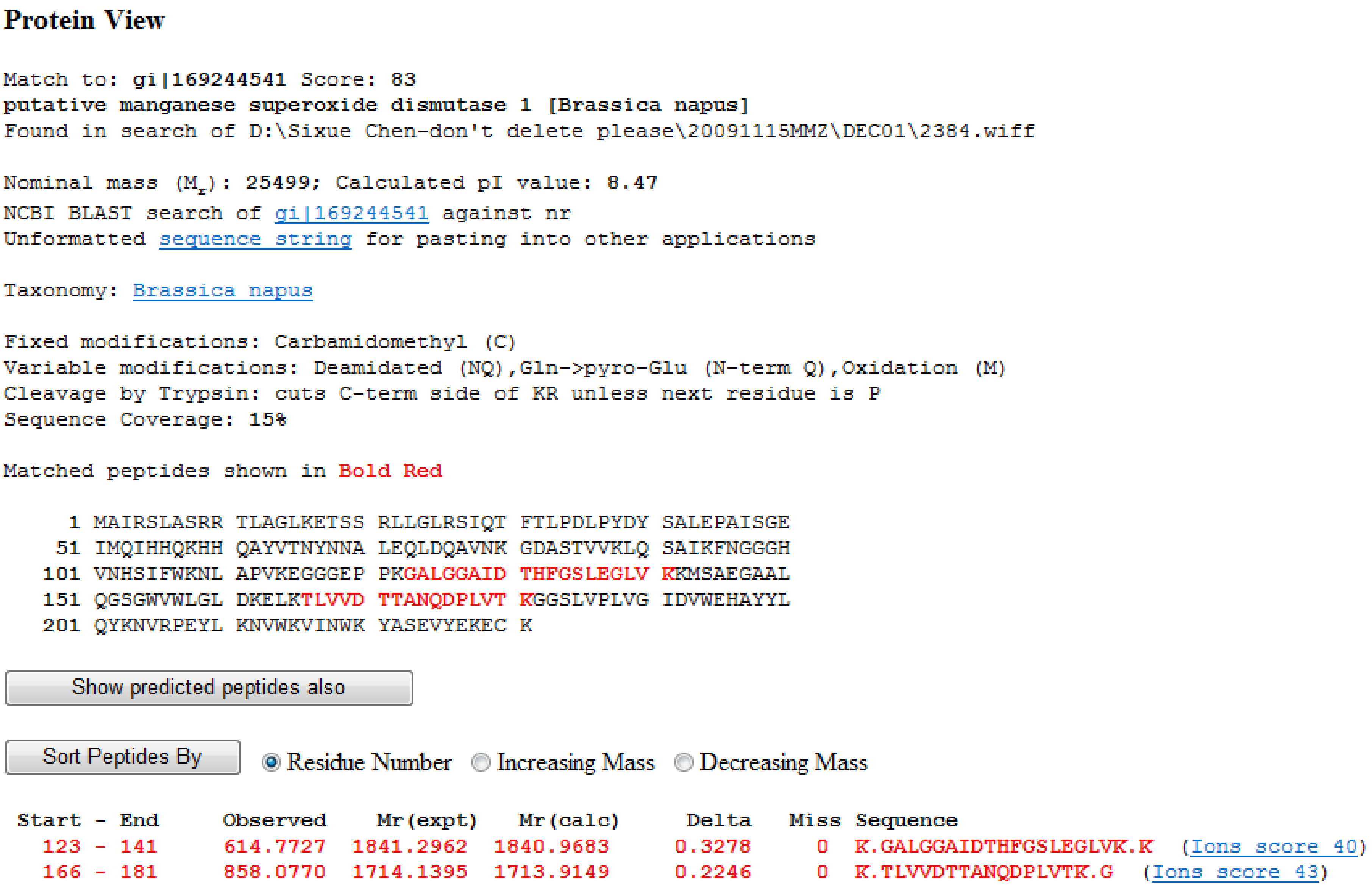
Matched peptides shown in **Bold Red**

```
     1 MTKSYPTVSE DYQKAIEKCK RKLRGLIAEK NCAPIMVRLA WHSAGTFDCA
    51 SKTGGPFGTM RFDAEQGHGA NSGIHIALRL LDPIREQFPA ISFADFHQLA
   101 GVVAVEVTGG PEIPFHPGRE DKPQPPPEGR LPDATKGCDH LRQVFTKQMG
   151 LSDKDIVALS GAHTLGRCHK DRSGFEGAWT SNPLIFDNSY FKELLTGEKE
   201 GLLQLVSDKA LLDDPVFRPL VEKYAADEEA FFADYAEAHL KLSELGFADA
   251
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
     4 - 14      658.9142  1315.8139  1315.5932    0.2207     0  K.SYPTVSEDYQK.A   (Ions score 19)
    53 - 61      470.3170   938.6195   938.4280    0.1915     0  K.TGGPFGTMR.F  Oxidation (M)  (Ions score 55)
   210 - 223     538.0780  1611.2122  1610.9032    0.3090     0  K.ALLDDPVFRPLVEK.Y   (Ions score 50)
   224 - 241     687.7787  2060.3142  2059.9163    0.3980     0  K.YAADEEAFFADYAEAHLK.L   (Ions score 18)
```

gi|169244541 Putative manganese superoxide dismutase 1



Protein View

Match to: gi|169244541 Score: 83
putative manganese superoxide dismutase 1 [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2384.wiff

Nominal mass (M_r): 25499; Calculated pI value: 8.47
NCBI BLAST search of gi|169244541 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

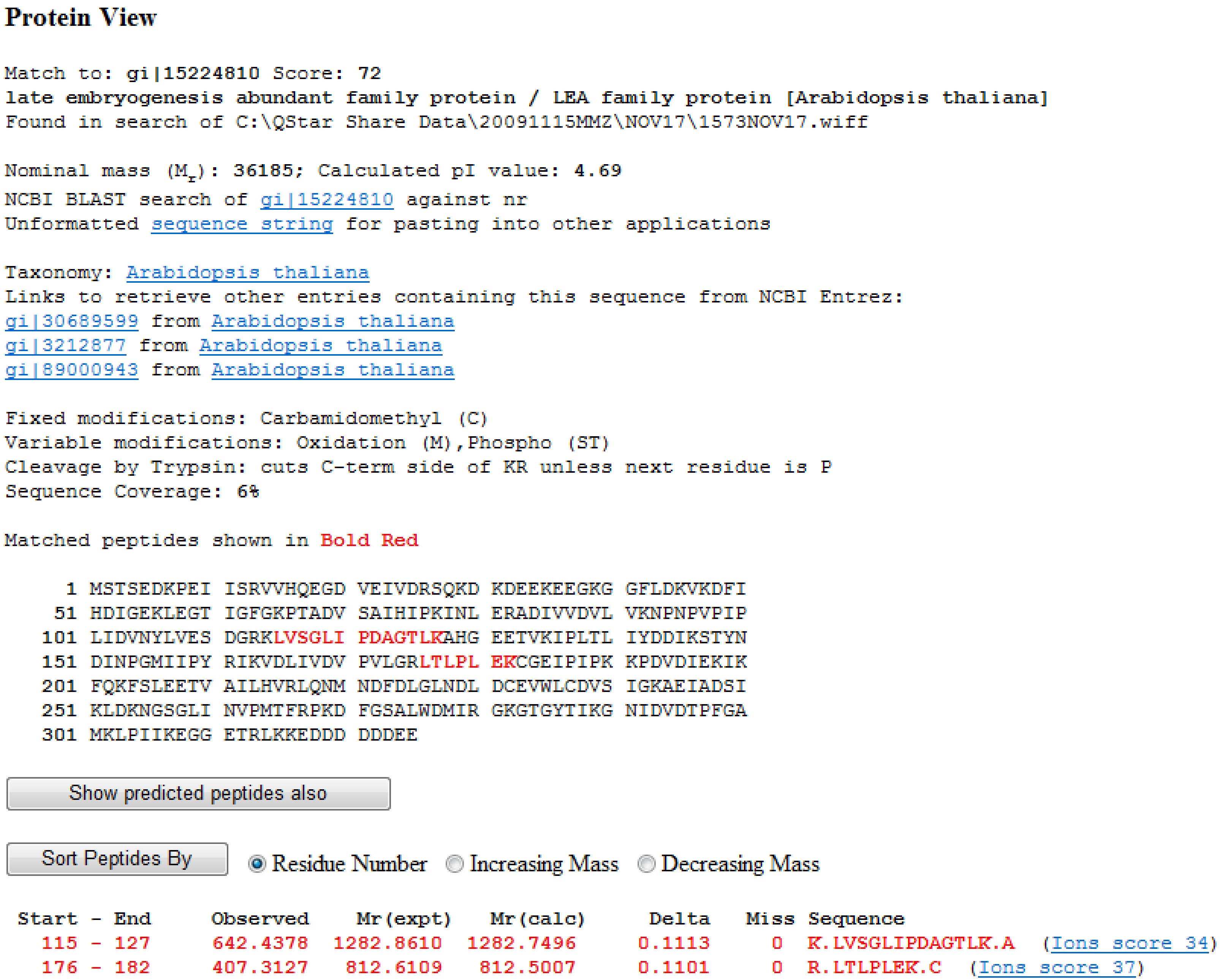
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in **Bold Red**

```
     1 MAIRSLASRR TLAGLKETSS RLLGLRSIQT FTLPDLPYDY SALEPAISGE
    51 IMQIHHQKHH QAYVTNYNNA LEQLDQAVNK GDASTVVKLQ SAIKFNGGGH
   101 VNHSIFWKNL APVKEGGGEP PKGALGGAID THFGSLEGLV KKMSAEGAAL
   151 QGSGWVWLGL DKELKTLVVD TTANQDPLVT KGGSLVPLVG IDVWEHAYYL
   201 QYKNVRPEYL KNVWKVINWK YASEVYEKEC K
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta  Miss Sequence
   123 - 141     614.7727  1841.2962  1840.9683    0.3278     0  K.GALGGAIDTHFGSLEGLVK.K  (Ions score 40)
   166 - 181     858.0770  1714.1395  1713.9149    0.2246     0  K.TLVVDTTANQDPLVTK.G  (Ions score 43)
```

gi|15224810 Late embryogenesis abundant (LEA) family protein



Protein View

Match to: gi|15224810 Score: 72
late embryogenesis abundant family protein / LEA family protein [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\1573NOV17.wiff

Nominal mass (M_r): 36185; Calculated pI value: 4.69
NCBI BLAST search of gi|15224810 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|30689599 from Arabidopsis thaliana
gi|3212877 from Arabidopsis thaliana
gi|89000943 from Arabidopsis thaliana

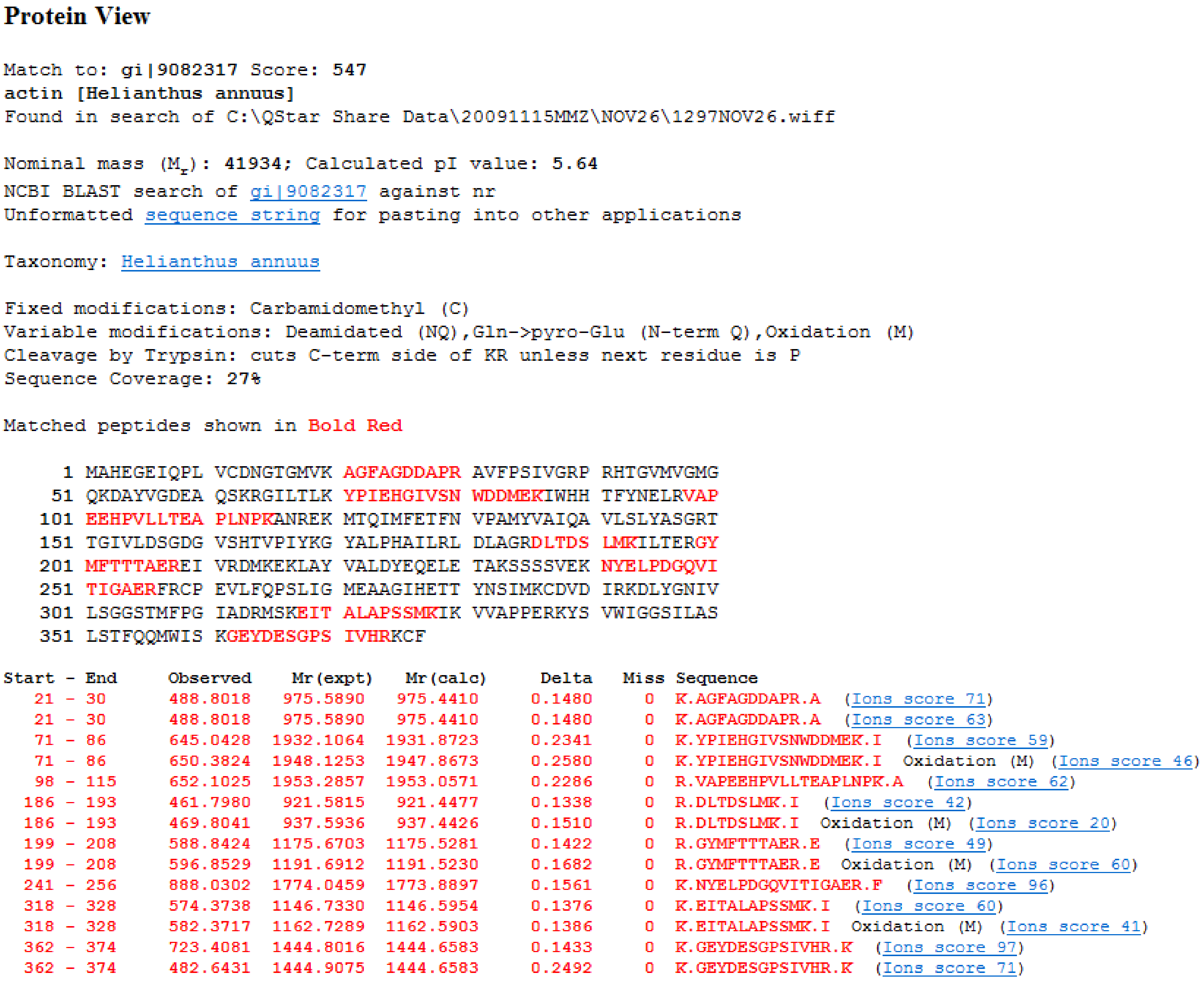
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 6%

Matched peptides shown in **Bold Red**

```
  1 MSTSEDKPEI ISRVVHQEGD VEIVDRSQKD KDEEKEEGKG GFLDKVKDFI
 51 HDIGEKLEGT IGFGKPTADV SAIHIPKINL ERADIVVDVL VKNPNPVPIP
101 LIDVNYLVES DGRKLVSGLI PDAGTLKAHG EETVKIPLTL IYDDIKSTYN
151 DINPGMIIPY RIKVDLIVDV PVLGRLTLPL EKCGEIPIPK KPDVDIEKIK
201 FQKFSLEETV AILHVRLQNM NDFDLGLNDL DCEVWLCDVS IGKAEIADSI
251 KLDKNGSGLI NVPMTFRPKD FGSALWDMIR GKGTGYTIKG NIDVDTPFGA
301 MKLPIIKEGG ETRLKKEDDD DDDEE
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   115 - 127     642.4378  1282.8610  1282.7496    0.1113     0  K.LVSGLIPDAGTLK.A  (Ions score 34)
   176 - 182     407.3127   812.6109   812.5007    0.1101     0  R.LTLPLEK.C  (Ions score 37)
```

gi|9082317 Actin



Protein View

```
Match to: gi|9082317 Score: 547
actin [Helianthus annuus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV26\1297NOV26.wiff

Nominal mass (Mr): 41934; Calculated pI value: 5.64
NCBI BLAST search of gi|9082317 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Helianthus annuus

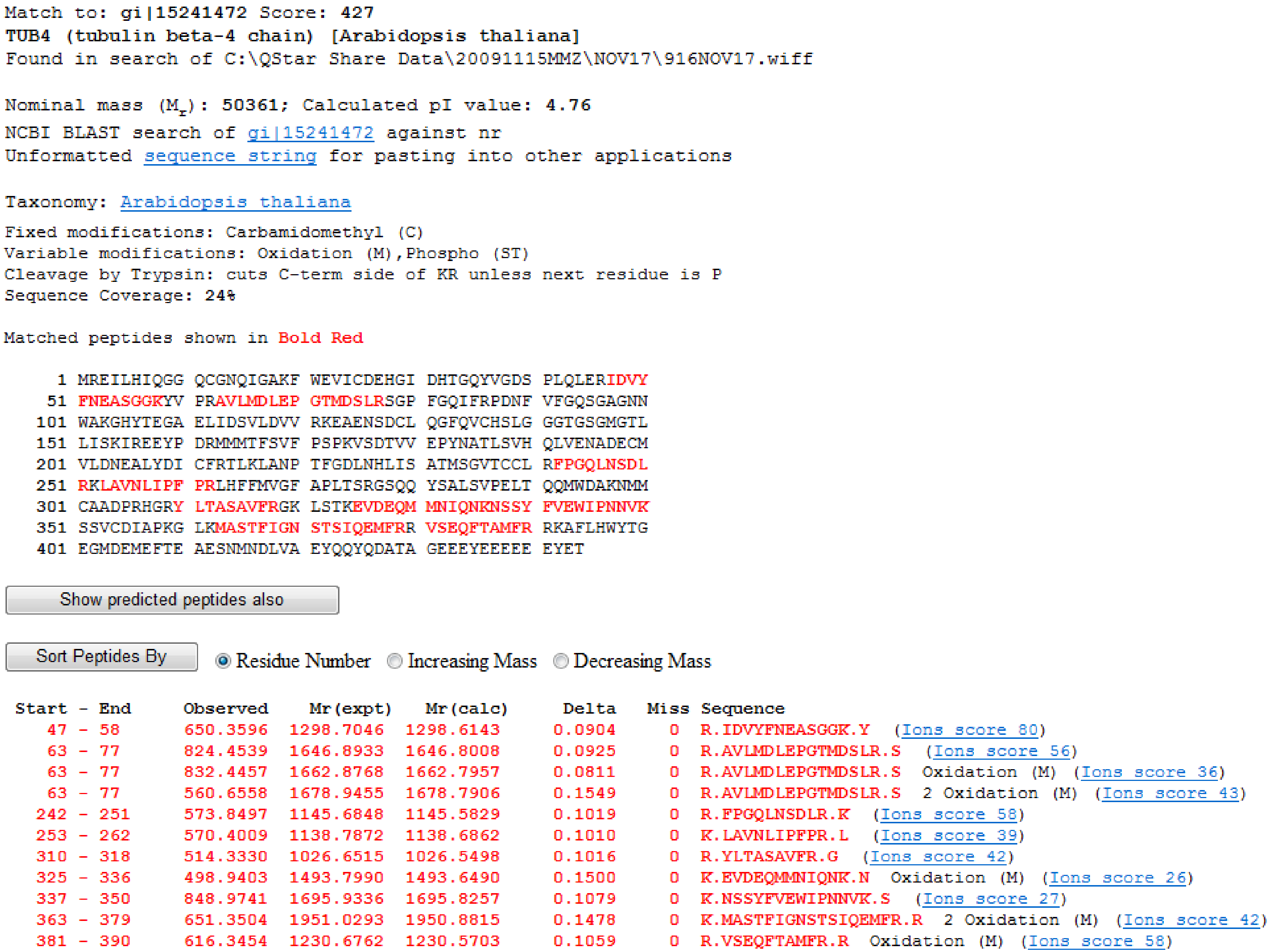
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 27%

Matched peptides shown in Bold Red

     1 MAHEGEIQPL VCDNGTGMVK AGFAGDDAPR AVFPSIVGRP RHTGVMVGMG
    51 QKDAYVGDEA QSKRGILTLK YPIEHGIVSN WDDMEKIWHH TFYNELRVAP
   101 EEHPVLLTEA PLNPKANREK MTQIMFETFN VPAMYVAIQA VLSLYASGRT
   151 TGIVLDSGDG VSHTVPIYKG YALPHAILRL DLAGRDLTDS LMKILTERGY
   201 MFTTTAEREI VRDMKEKLAY VALDYEQELE TAKSSSSVEK NYELPDGQVI
   251 TIGAERFRCP EVLFQPSLIG MEAAGIHETT YNSIMKCDVD IRKDLYGNIV
   301 LSGGSTMFPG IADRMSKEIT ALAPSSMKIK VVAPPERKYS VWIGGSILAS
   351 LSTFQQMWIS KGEYDESGPS IVHRKCF

Start - End     Observed   Mr(expt)   Mr(calc)    Delta   Miss Sequence
   21 - 30      488.8018   975.5890   975.4410   0.1480     0  K.AGFAGDDAPR.A   (Ions score 71)
   21 - 30      488.8018   975.5890   975.4410   0.1480     0  K.AGFAGDDAPR.A   (Ions score 63)
   71 - 86      645.0428  1932.1064  1931.8723   0.2341     0  K.YPIEHGIVSNWDDMEK.I   (Ions score 59)
   71 - 86      650.3824  1948.1253  1947.8673   0.2580     0  K.YPIEHGIVSNWDDMEK.I  Oxidation (M)  (Ions score 46)
   98 - 115     652.1025  1953.2857  1953.0571   0.2286     0  R.VAPEEHPVLLTEAPLNPK.A   (Ions score 62)
  186 - 193     461.7980   921.5815   921.4477   0.1338     0  R.DLTDSLMK.I   (Ions score 42)
  186 - 193     469.8041   937.5936   937.4426   0.1510     0  R.DLTDSLMK.I  Oxidation (M)  (Ions score 20)
  199 - 208     588.8424  1175.6703  1175.5281   0.1422     0  R.GYMFTTTAER.E   (Ions score 49)
  199 - 208     596.8529  1191.6912  1191.5230   0.1682     0  R.GYMFTTTAER.E  Oxidation (M)  (Ions score 60)
  241 - 256     888.0302  1774.0459  1773.8897   0.1561     0  K.NYELPDGQVITIGAER.F   (Ions score 96)
  318 - 328     574.3738  1146.7330  1146.5954   0.1376     0  K.EITALAPSSMK.I   (Ions score 60)
  318 - 328     582.3717  1162.7289  1162.5903   0.1386     0  K.EITALAPSSMK.I  Oxidation (M)  (Ions score 41)
  362 - 374     723.4081  1444.8016  1444.6583   0.1433     0  K.GEYDESGPSIVHR.K   (Ions score 97)
  362 - 374     482.6431  1444.9075  1444.6583   0.2492     0  K.GEYDESGPSIVHR.K   (Ions score 71)
```

gi|15241472 TUB4 (tubulin beta-4 chain)



```
Match to: gi|15241472 Score: 427
TUB4 (tubulin beta-4 chain) [Arabidopsis thaliana]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\916NOV17.wiff

Nominal mass (Mr): 50361; Calculated pI value: 4.76
NCBI BLAST search of gi|15241472 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 24%

Matched peptides shown in Bold Red

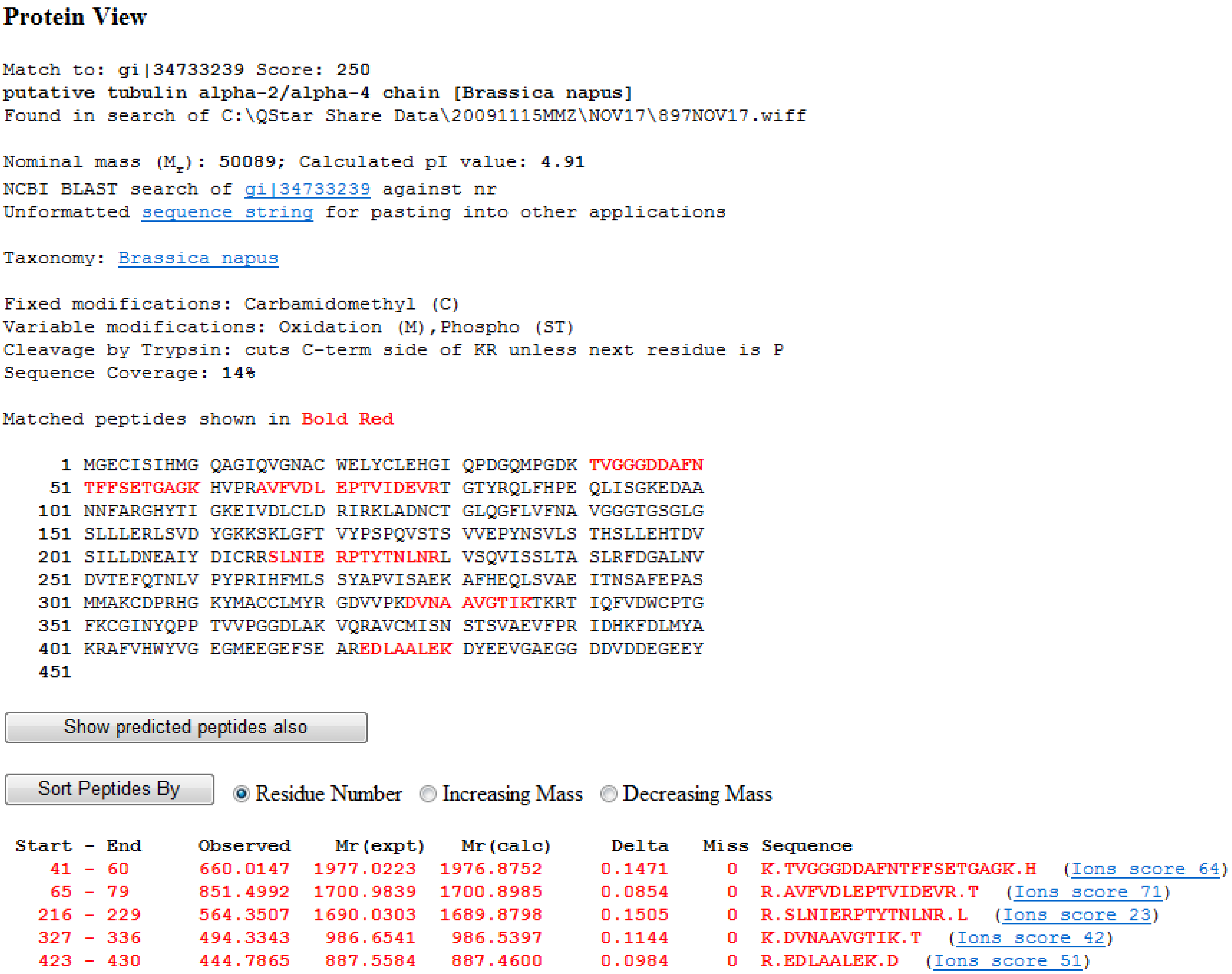
     1 MREILHIQGG QCGNQIGAKF WEVICDEHGI DHTGQYVGDS PLQLERIDVY
    51 FNEASGGKYV PRAVLMDLEP GTMDSLRSGP FGQIFRPDNF VFGQSGAGNN
   101 WAKGHYTEGA ELIDSVLDVV RKEAENSDCL QGFQVCHSLG GGTGSGMGTL
   151 LISKIREEYP DRMMMTFSVF PSPKVSDTVV EPYNATLSVH QLVENADECM
   201 VLDNEALYDI CFRTLKLANP TFGDLNHLIS ATMSGVTCCL RFPGQLNSDL
   251 RKLAVNLIPF PRLHFFMVGF APLTSRGSQQ YSALSVPELT QQMWDAKNMM
   301 CAADPRHGRY LTASAVFRGK LSTKEVDEQM MNIQNKNSSY FVEWIPNNVK
   351 SSVCDIAPKG LKMASTFIGN STSIQEMFRR VSEQFTAMFR RKAFLHWYTG
   401 EGMDEMEFTE AESNMNDLVA EYQQYQDATA GEEEYEEEEE EYET
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   47 - 58      650.3596  1298.7046  1298.6143    0.0904     0  R.IDVYFNEASGGK.Y  (Ions score 80)
   63 - 77      824.4539  1646.8933  1646.8008    0.0925     0  R.AVLMDLEPGTMDSLR.S  (Ions score 56)
   63 - 77      832.4457  1662.8768  1662.7957    0.0811     0  R.AVLMDLEPGTMDSLR.S  Oxidation (M)  (Ions score 36)
   63 - 77      560.6558  1678.9455  1678.7906    0.1549     0  R.AVLMDLEPGTMDSLR.S  2 Oxidation (M)  (Ions score 43)
  242 - 251     573.8497  1145.6848  1145.5829    0.1019     0  R.FPGQLNSDLR.K  (Ions score 58)
  253 - 262     570.4009  1138.7872  1138.6862    0.1010     0  K.LAVNLIPFPR.L  (Ions score 39)
  310 - 318     514.3330  1026.6515  1026.5498    0.1016     0  R.YLTASAVFR.G  (Ions score 42)
  325 - 336     498.9403  1493.7990  1493.6490    0.1500     0  K.EVDEQMMNIQNK.N  Oxidation (M)  (Ions score 26)
  337 - 350     848.9741  1695.9336  1695.8257    0.1079     0  K.NSSYFVEWIPNNVK.S  (Ions score 27)
  363 - 379     651.3504  1951.0293  1950.8815    0.1478     0  K.MASTFIGNSTSIQEMFR.R  2 Oxidation (M)  (Ions score 42)
  381 - 390     616.3454  1230.6762  1230.5703    0.1059     0  R.VSEQFTAMFR.R  Oxidation (M)  (Ions score 58)
```

gi|34733239 Putative tubulin alpha-2/alpha-4 chain



Protein View

Match to: gi|34733239 Score: 250
putative tubulin alpha-2/alpha-4 chain [Brassica napus]
Found in search of C:\QStar Share Data\20091115MMZ\NOV17\897NOV17.wiff

Nominal mass (M_r): **50089**; Calculated pI value: **4.91**
NCBI BLAST search of gi|34733239 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

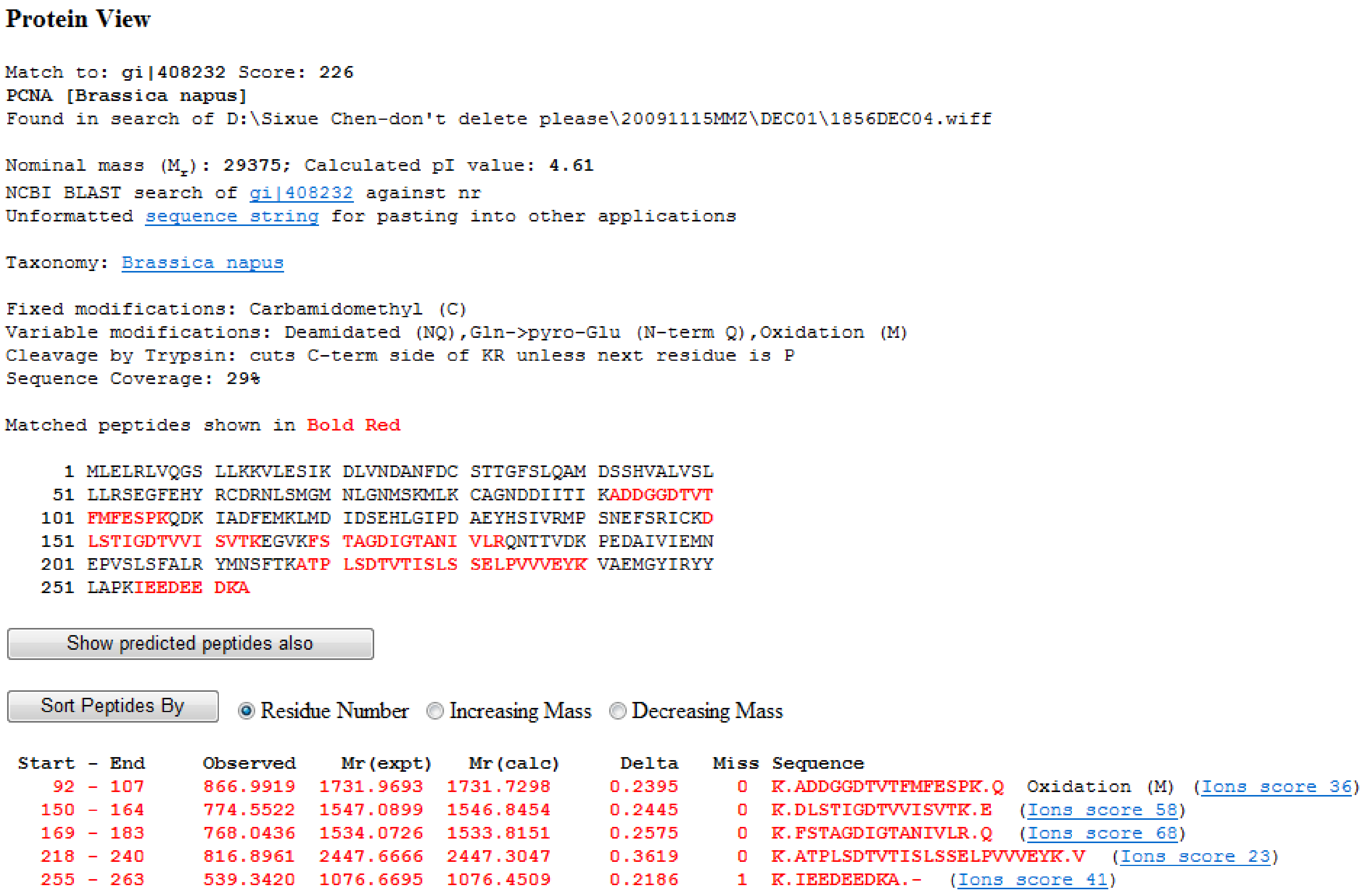
```
  1 MGECISIHMG QAGIQVGNAC WELYCLEHGI QPDGQMPGDK TVGGGDDAFN
 51 TFFSETGAGK HVPRAVFVDL EPTVIDEVRT GTYRQLFHPE QLISGKEDAA
101 NNFARGHYTI GKEIVDLCLD RIRKLADNCT GLQGFLVFNA VGGGTGSGLG
151 SLLLERLSVD YGKKSKLGFT VYPSPQVSTS VVEPYNSVLS THSLLEHTDV
201 SILLDNEAIY DICRRSLNIE RPTYTNLNRL VSQVISSLTA SLRFDGALNV
251 DVTEFQTNLV PYPRIHFMLS SYAPVISAEK AFHEQLSVAE ITNSAFEPAS
301 MMAKCDPRHG KYMACCLMYR GDVVPKDVNA AVGTIKTKRT IQFVDWCPTG
351 FKCGINYQPP TVVPGGDLAK VQRAVCMISN STSVAEVFPR IDHKFDLMYA
401 KRAFVHWYVG EGMEEGEFSE AREDLAALEK DYEEVGAEGG DDVDDEGEEY
451
```

Show predicted peptides also

Sort Peptides By ● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
Start - End    Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
  41 - 60      660.0147  1977.0223  1976.8752    0.1471      0  K.TVGGGDDAFNTFFSETGAGK.H  (Ions score 64)
  65 - 79      851.4992  1700.9839  1700.8985    0.0854      0  R.AVFVDLEPTVIDEVR.T  (Ions score 71)
 216 - 229     564.3507  1690.0303  1689.8798    0.1505      0  R.SLNIERPTYTNLNR.L  (Ions score 23)
 327 - 336     494.3343   986.6541   986.5397    0.1144      0  K.DVNAAVGTIK.T  (Ions score 42)
 423 - 430     444.7865   887.5584   887.4600    0.0984      0  R.EDLAALEK.D  (Ions score 51)
```

gi|408232 Proliferating cell nuclear antigen



Protein View

```
Match to: gi|408232 Score: 226
PCNA [Brassica napus]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\1856DEC04.wiff

Nominal mass (Mr): 29375; Calculated pI value: 4.61
NCBI BLAST search of gi|408232 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Brassica napus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 29%

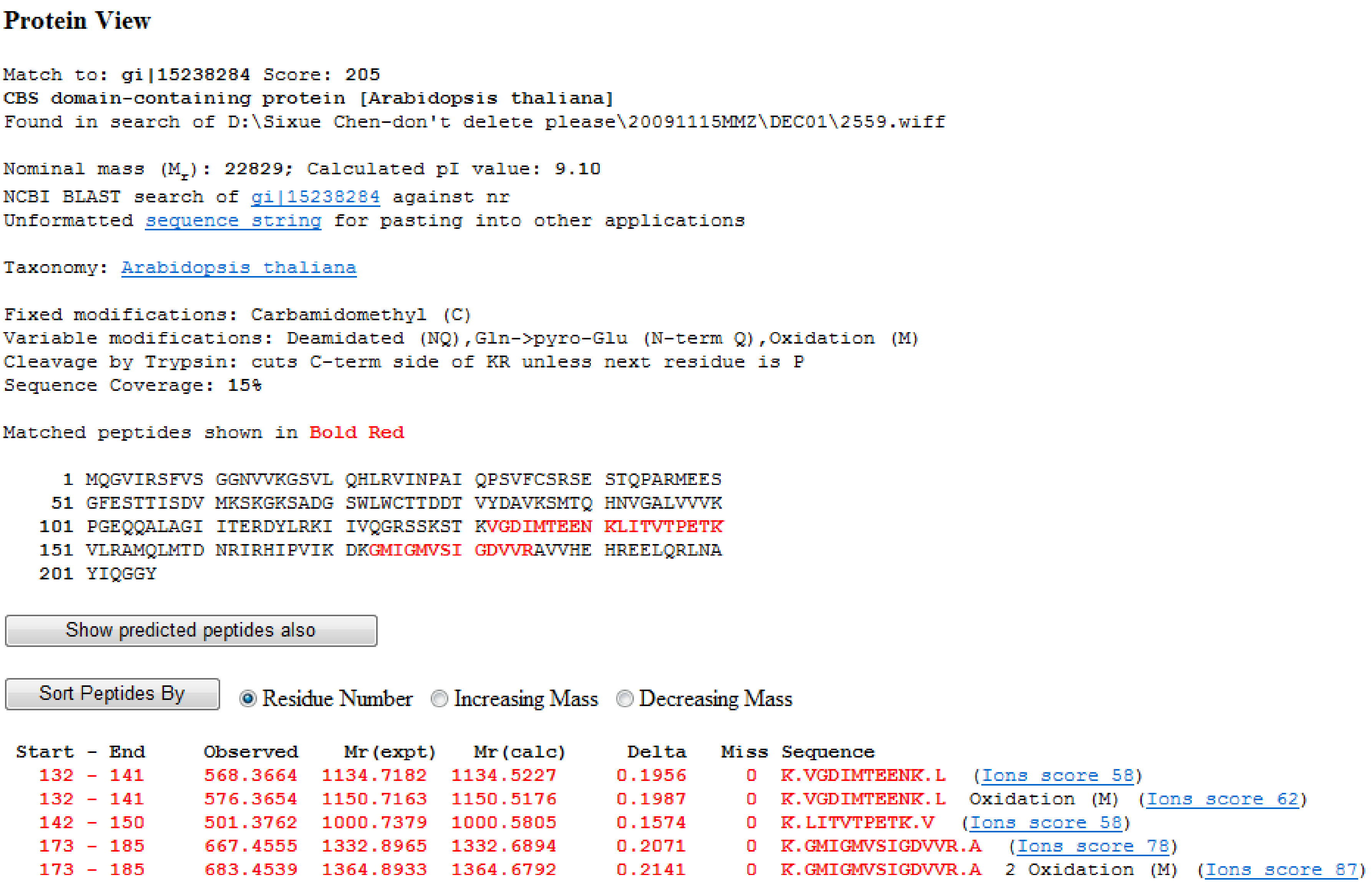
Matched peptides shown in Bold Red

      1 MLELRLVQGS LLKKVLESIK DLVNDANFDC STTGFSLQAM DSSHVALVSL
     51 LLRSEGFEHY RCDRNLSMGM NLGNMSKMLK CAGNDDIITI KADDGGDTVT
    101 FMFESPKQDK IADFEMKLMD IDSEHLGIPD AEYHSIVRMP SNEFSRICKD
    151 LSTIGDTVVI SVTKEGVKFS TAGDIGTANI VLRQNTTVDK PEDAIVIEMN
    201 EPVSLSFALR YMNSFTKATP LSDTVTISLS SELPVVVEYK VAEMGYIRYY
    251 LAPKIEEDEE DKA
```

● Residue Number ○ Increasing Mass ○ Decreasing Mass

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss  Sequence
   92 - 107     866.9919  1731.9693  1731.7298    0.2395     0   K.ADDGGDTVTFMFESPK.Q  Oxidation (M)  (Ions score 36)
  150 - 164     774.5522  1547.0899  1546.8454    0.2445     0   K.DLSTIGDTVVISVTK.E  (Ions score 58)
  169 - 183     768.0436  1534.0726  1533.8151    0.2575     0   K.FSTAGDIGTANIVLR.Q  (Ions score 68)
  218 - 240     816.8961  2447.6666  2447.3047    0.3619     0   K.ATPLSDTVTISLSSELPVVVEYK.V  (Ions score 23)
  255 - 263     539.3420  1076.6695  1076.4509    0.2186     1   K.IEEDEEDKA.-  (Ions score 41)
```

gi|15238284 CBS domain-containing protein



Protein View

Match to: gi|15238284 Score: 205
CBS domain-containing protein [Arabidopsis thaliana]
Found in search of D:\Sixue Chen-don't delete please\20091115MMZ\DEC01\2559.wiff

Nominal mass (M_r): 22829; Calculated pI value: 9.10
NCBI BLAST search of gi|15238284 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

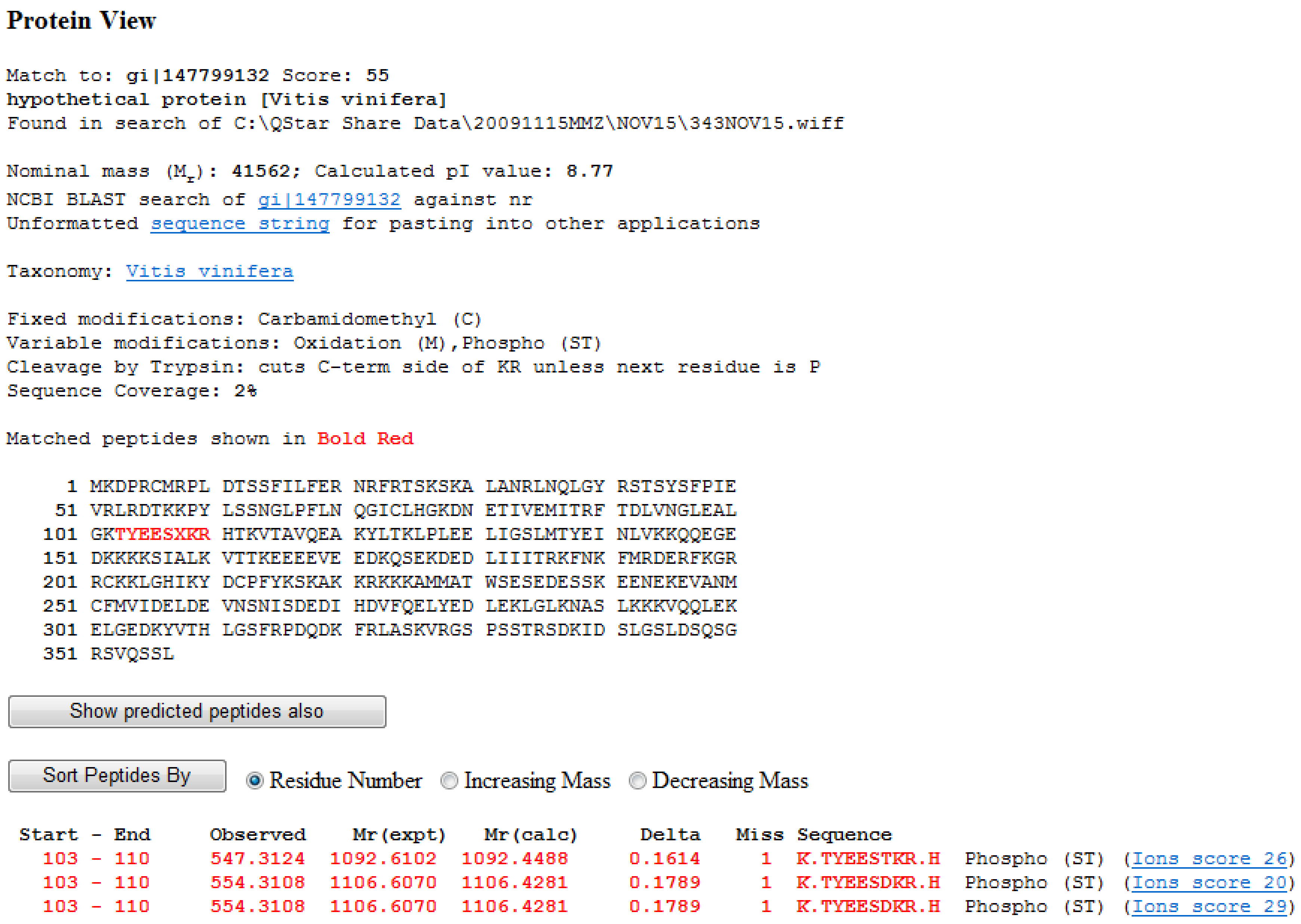
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Deamidated (NQ),Gln->pyro-Glu (N-term Q),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 15%

Matched peptides shown in **Bold Red**

```
     1 MQGVIRSFVS GGNVVKGSVL QHLRVINPAI QPSVFCSRSE STQPARMEES
    51 GFESTTISDV MKSKGKSADG SWLWCTTDDT VYDAVKSMTQ HNVGALVVVK
   101 PGEQQALAGI ITERDYLRKI IVQGRSSKST KVGDIMTEEN KLITVTPETK
   151 VLRAMQLMTD NRIRHIPVIK DKGMIGMVSI GDVVRAVVHE HREELQRLNA
   201 YIQGGY
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)    Delta  Miss Sequence
   132 - 141     568.3664  1134.7182  1134.5227   0.1956     0 K.VGDIMTEENK.L   (Ions score 58)
   132 - 141     576.3654  1150.7163  1150.5176   0.1987     0 K.VGDIMTEENK.L  Oxidation (M)  (Ions score 62)
   142 - 150     501.3762  1000.7379  1000.5805   0.1574     0 K.LITVTPETK.V   (Ions score 58)
   173 - 185     667.4555  1332.8965  1332.6894   0.2071     0 K.GMIGMVSIGDVVR.A   (Ions score 78)
   173 - 185     683.4539  1364.8933  1364.6792   0.2141     0 K.GMIGMVSIGDVVR.A  2 Oxidation (M)  (Ions score 87)
```

gi|147799132 Hypothetical protein



Protein View

```
Match to: gi|147799132 Score: 55
hypothetical protein [Vitis vinifera]
Found in search of C:\QStar Share Data\20091115MMZ\NOV15\343NOV15.wiff

Nominal mass (Mr): 41562; Calculated pI value: 8.77
NCBI BLAST search of gi|147799132 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Vitis vinifera

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M),Phospho (ST)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 2%

Matched peptides shown in Bold Red

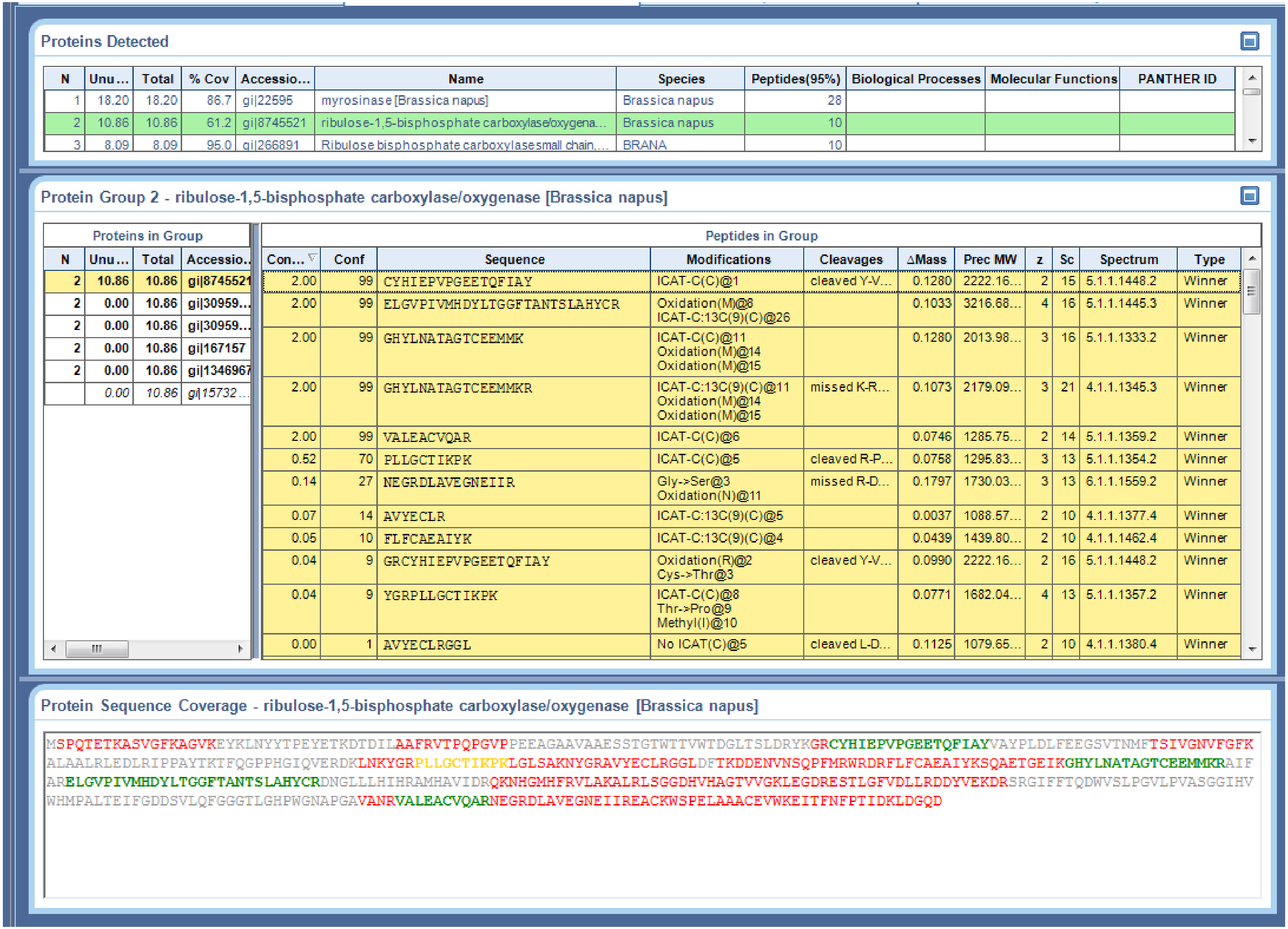
      1 MKDPRCMRPL DTSSFILFER NRFRTSKSKA LANRLNQLGY RSTSYSFPIE
     51 VRLRDTKKPY LSSNGLPFLN QGICLHGKDN ETIVEMITRF TDLVNGLEAL
    101 GKTYEESXKR HTKVTAVQEA KYLTKLPLEE LIGSLMTYEI NLVKKQQEGE
    151 DKKKKSIALK VTTKEEEEVE EDKQSEKDED LIIITRKFNK FMRDERFKGR
    201 RCKKLGHIKY DCPFYKSKAK KRKKKAMMAT WSESEDESSK EENEKEVANM
    251 CFMVIDELDE VNSNISDEDI HDVFQELYED LEKLGLKNAS LKKKVQQLEK
    301 ELGEDKYVTH LGSFRPDQDK FRLASKVRGS PSSTRSDKID SLGSLDSQSG
    351 RSVQSSL
```

```
 Start - End     Observed   Mr(expt)   Mr(calc)     Delta   Miss Sequence
   103 - 110     547.3124  1092.6102  1092.4488    0.1614      1 K.TYEESTKR.H   Phospho (ST) (Ions score 26)
   103 - 110     554.3108  1106.6070  1106.4281    0.1789      1 K.TYEESDKR.H   Phospho (ST) (Ions score 20)
   103 - 110     554.3108  1106.6070  1106.4281    0.1789      1 K.TYEESDKR.H   Phospho (ST) (Ions score 29)
```

Figure S7

This set of supplemental data contains the information of the coverage, peptides and MS/MS spectrum (if only one peptide identified for the protein) of each protein identified to be redox sensitive to MeJA treatment in guard cells by ICAT.

gi|8745521 Ribulose-1,5-bisphosphate carboxylase / oxygenase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
1	18.20	18.20	86.7	gi|22595	myrosinase [Brassica napus]	Brassica napus	28			
2	10.86	10.86	61.2	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygena…	Brassica napus	10			
3	8.09	8.09	95.0	gi|266891	Ribulose bisphosphate carboxylase small chain,…	BRANA	10			

Protein Group 2 - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accessio…
2	**10.86**	**10.86**	**gi|8745521**
2	0.00	10.86	gi|30959…
2	0.00	10.86	gi|30959…
2	0.00	10.86	gi|167157
2	0.00	10.86	gi|1346967
	0.00	*10.86*	*gi|15732…*

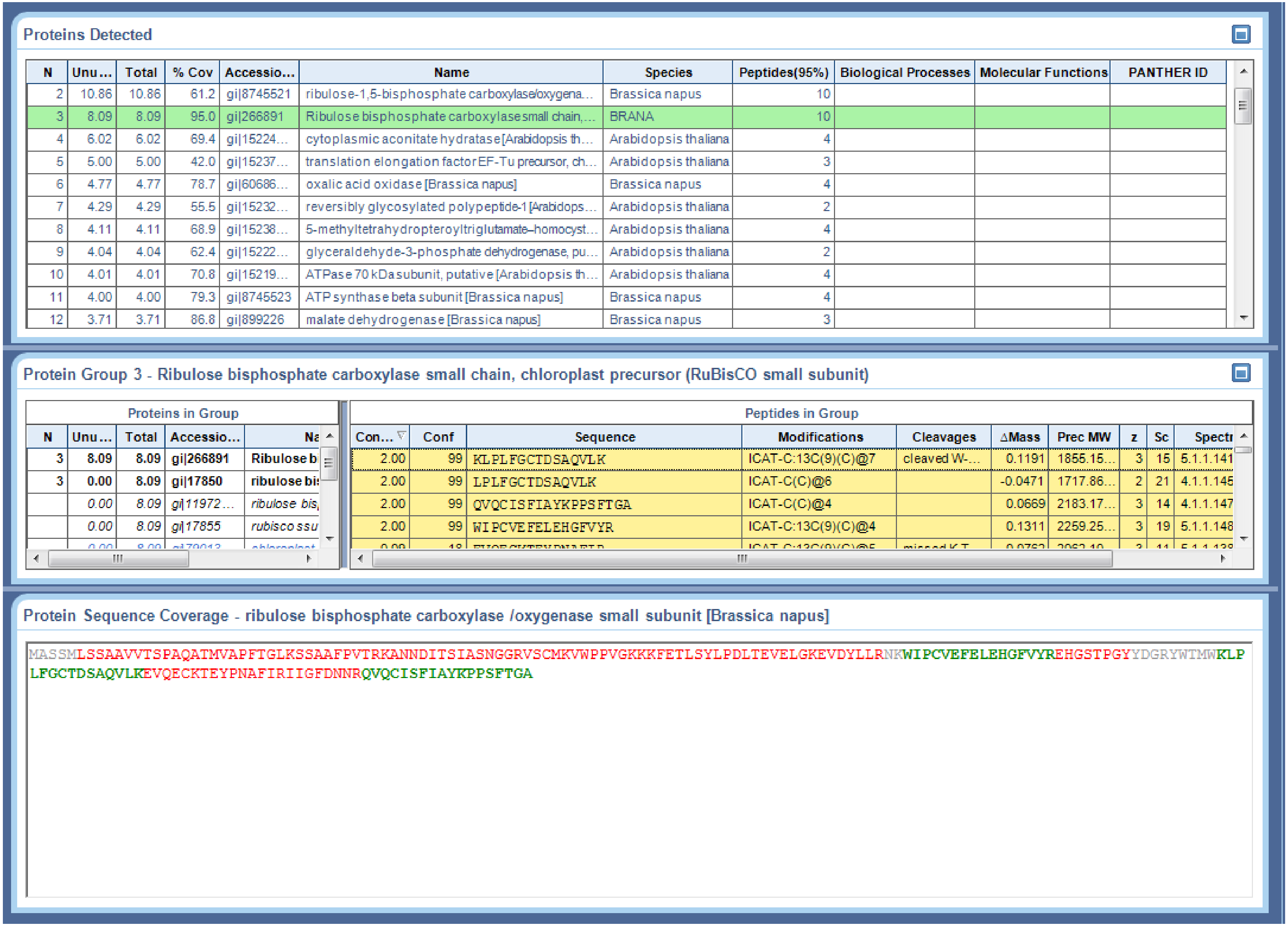
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum	Type
2.00	99	CYHIEPVPGEETQFIAY	ICAT-C(C)@1	cleaved Y-V…	0.1280	2222.16…	2	15	5.1.1.1448.2	Winner
2.00	99	ELGVPIVMHDYLTGGFTANTSLAHYCR	Oxidation(M)@8 ICAT-C:13C(9)(C)@26		0.1033	3216.68…	4	16	5.1.1.1445.3	Winner
2.00	99	GHYLNATAGTCEEMMK	ICAT-C(C)@11 Oxidation(M)@14 Oxidation(M)@15		0.1280	2013.98…	3	16	5.1.1.1333.2	Winner
2.00	99	GHYLNATAGTCEEMMKR	ICAT-C:13C(9)(C)@11 Oxidation(M)@14 Oxidation(M)@15	missed K-R…	0.1073	2179.09…	3	21	4.1.1.1345.3	Winner
2.00	99	VALEACVQAR	ICAT-C(C)@6		0.0746	1285.75…	2	14	5.1.1.1359.2	Winner
0.52	70	PLLGCTIKPK	ICAT-C(C)@5	cleaved R-P…	0.0758	1295.83…	3	13	5.1.1.1354.2	Winner
0.14	27	NEGRDLAVEGNEIIR	Gly->Ser@3 Oxidation(N)@11	missed R-D…	0.1797	1730.03…	3	13	6.1.1.1559.2	Winner
0.07	14	AVYECLR	ICAT-C:13C(9)(C)@5		0.0037	1088.57…	2	10	4.1.1.1377.4	Winner
0.05	10	FLFCAEAIYK	ICAT-C:13C(9)(C)@4		0.0439	1439.80…	2	10	4.1.1.1462.4	Winner
0.04	9	GRCYHIEPVPGEETQFIAY	Oxidation(R)@2 Cys->Thr@3	cleaved Y-V…	0.0990	2222.16…	2	16	5.1.1.1448.2	Winner
0.04	9	YGRPLLGCTIKPK	ICAT-C(C)@8 Thr->Pro@9 Methyl(I)@10		0.0771	1682.04…	4	13	5.1.1.1357.2	Winner
0.00	1	AVYECLRGGL	No ICAT(C)@5	cleaved L-D…	0.1125	1079.65…	2	10	4.1.1.1380.4	Winner

Protein Sequence Coverage - ribulose-1,5-bisphosphate carboxylase/oxygenase [Brassica napus]

```
MSPQTETKASVGFKAGVKEYKLNYYTPEYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYHIEPVPGEETQFIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFK
ALAALRLEDLRIPPAYTKTFQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEAIYKSQAETGEIKGHYLNATAGTCEEMMKRAIF
ARELGVPIVMHDYLTGGFTANTSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHVHAGTVVGKLEGDRESTLGFVDLLRDDYVEKDRSRGIFFTQDWVSLPGVLPVASGGIHV
WHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAVEGNEIIREACKWSPELAAACEVWKEITFNFPTIDKLDGQD
```

gi|17852 Ribulose bisphosphate carboxylase small chain, chloroplast precursor



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
2	10.86	10.86	61.2	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygena…	Brassica napus	10			
3	8.09	8.09	95.0	gi|266891	Ribulose bisphosphate carboxylase small chain,…	BRANA	10			
4	6.02	6.02	69.4	gi|15224…	cytoplasmic aconitate hydratase [Arabidopsis th…	Arabidopsis thaliana	4			
5	5.00	5.00	42.0	gi|15237…	translation elongation factor EF-Tu precursor, ch…	Arabidopsis thaliana	3			
6	4.77	4.77	78.7	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	4			
7	4.29	4.29	55.5	gi|15232…	reversibly glycosylated polypeptide-1 [Arabidops…	Arabidopsis thaliana	2			
8	4.11	4.11	68.9	gi|15238…	5-methyltetrahydropteroyltriglutamate–homocyst…	Arabidopsis thaliana	4			
9	4.04	4.04	62.4	gi|15222…	glyceraldehyde-3-phosphate dehydrogenase, pu…	Arabidopsis thaliana	2			
10	4.01	4.01	70.8	gi|15219…	ATPase 70 kDa subunit, putative [Arabidopsis th…	Arabidopsis thaliana	4			
11	4.00	4.00	79.3	gi|8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	4			
12	3.71	3.71	86.8	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	3			

Protein Group 3 - Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit)

Proteins in Group

N	Unu…	Total	Accessio…	Na
3	**8.09**	**8.09**	**gi|266891**	**Ribulose b**
3	**0.00**	**8.09**	**gi|17850**	**ribulose bi**
	0.00	*8.09*	*gi|11972…*	*ribulose bis*
	0.00	*8.09*	*gi|17855*	*rubisco ssu*

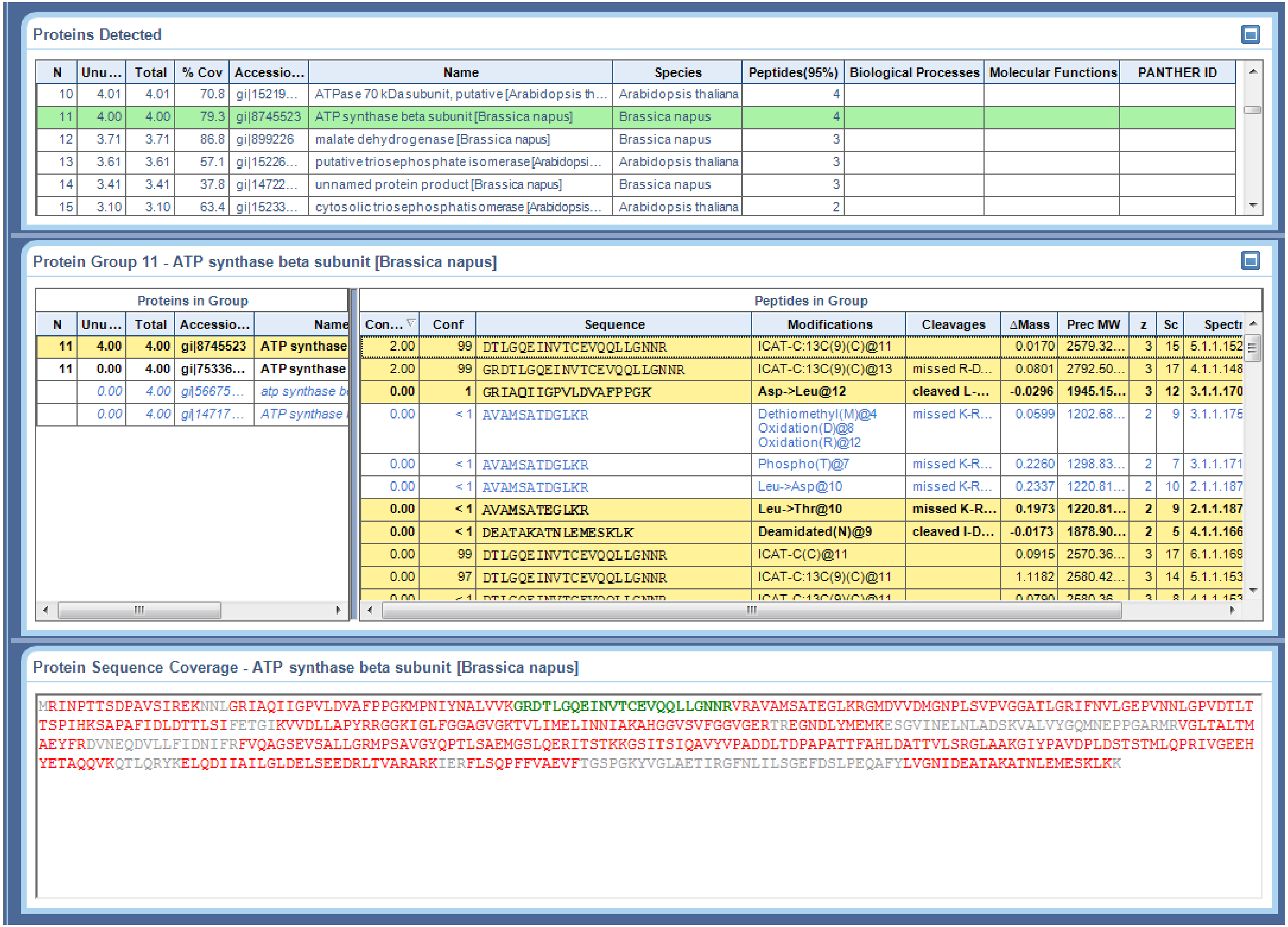
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectr
2.00	99	KLPLFGCTDSAQVLK	ICAT-C:13C(9)(C)@7	cleaved W-…	0.1191	1855.15…	3	15	5.1.1.141
2.00	99	LPLFGCTDSAQVLK	ICAT-C(C)@6		-0.0471	1717.86…	2	21	4.1.1.145
2.00	99	QVQCISFIAYKPPSFTGA	ICAT-C(C)@4		0.0669	2183.17…	3	14	4.1.1.147
2.00	99	WIPCVEFELEHGFVYR	ICAT-C:13C(9)(C)@4		0.1311	2259.25…	3	19	5.1.1.148

Protein Sequence Coverage - ribulose bisphosphate carboxylase /oxygenase small subunit [Brassica napus]

MASSMLSSAAVVTSPAQATMVAPFTGLKSSAAFPVTRKANNDITSIASNGGRVSCMKVWPPVGKKKFETLSYLPDLTEVELGKEVDYLLRNKWIPCVEFELEHGFVYREHGSTPGYYDGRYWTMWKLP
LFGCTDSAQVLKEVQECKTEYPNAFIRIIGFDNNRQVQCISFIAYKPPSFTGA

gi|8745523 ATP synthase beta subunit



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
10	4.01	4.01	70.8	gi|15219…	ATPase 70 kDa subunit, putative [Arabidopsis th…	Arabidopsis thaliana	4			
11	4.00	4.00	79.3	gi|8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	4			
12	3.71	3.71	86.8	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	3			
13	3.61	3.61	57.1	gi|15226…	putative triosephosphate isomerase [Arabidopsi…	Arabidopsis thaliana	3			
14	3.41	3.41	37.8	gi|14722…	unnamed protein product [Brassica napus]	Brassica napus	3			
15	3.10	3.10	63.4	gi|15233…	cytosolic triosephosphatisomerase [Arabidopsis…	Arabidopsis thaliana	2			

Protein Group 11 - ATP synthase beta subunit [Brassica napus]

Proteins in Group

N	Unu…	Total	Accessio…	Name
11	**4.00**	**4.00**	**gi|8745523**	**ATP synthase**
11	**0.00**	**4.00**	**gi|75336…**	**ATP synthase**
	0.00	*4.00*	*gi|56675…*	*atp synthase b*
	0.00	*4.00*	*gi|14717…*	*ATP synthase*

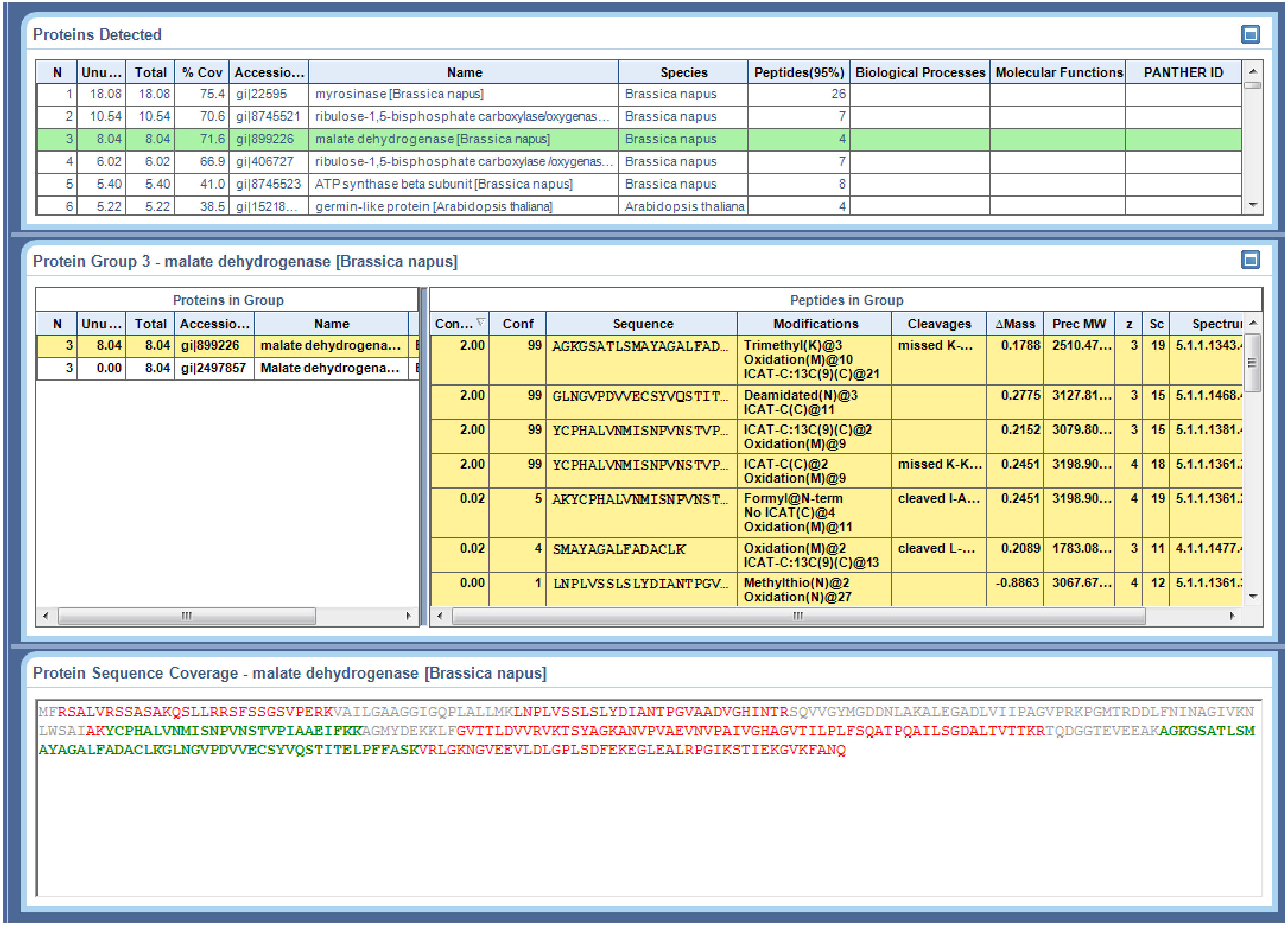
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectr
2.00	99	DTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@11		0.0170	2579.32…	3	15	5.1.1.152
2.00	99	GRDTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@13	missed R-D…	0.0801	2792.50…	3	17	4.1.1.148
0.00	**1**	**GRIAQIIGPVLDVAFPPGK**	**Asp->Leu@12**	**cleaved L-…**	**-0.0296**	**1945.15…**	**3**	**12**	**3.1.1.170**
0.00	< 1	AVAMSATDGLKR	Dethiomethyl(M)@4 Oxidation(D)@8 Oxidation(R)@12	missed K-R…	0.0599	1202.68…	2	9	3.1.1.175
0.00	< 1	AVAMSATDGLKR	Phospho(T)@7	missed K-R…	0.2260	1298.83…	2	7	3.1.1.171
0.00	< 1	AVAMSATDGLKR	Leu->Asp@10	missed K-R…	0.2337	1220.81…	2	10	2.1.1.187
0.00	**< 1**	**AVAMSATEGLKR**	**Leu->Thr@10**	**missed K-R…**	**0.1973**	**1220.81…**	**2**	**9**	**2.1.1.187**
0.00	**< 1**	**DEATAKATNLEMESKLK**	**Deamidated(N)@9**	**cleaved I-D…**	**-0.0173**	**1878.90…**	**2**	**5**	**4.1.1.166**
0.00	99	DTLGQEINVTCEVQQLLGNNR	ICAT-C(C)@11		0.0915	2570.36…	3	17	6.1.1.169
0.00	97	DTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@11		1.1182	2580.42…	3	14	5.1.1.153
0.00	< 1	DTLGQEINVTCEVQQLLGNNR	ICAT-C:13C(9)(C)@11		0.0790	2580.36	3	8	4.1.1.153

Protein Sequence Coverage - ATP synthase beta subunit [Brassica napus]

MRINPTTSDPAVSIREKNNLGRIAQIIGPVLDVAFPPGKMPNIYNALVVKGRDTLGQEINVTCEVQQLLGNNRVRAVAMSATEGLKRGMDVVDMGNPLSVPVGGATLGRIFNVLGEPVNNLGPVDTLT
TSPIHKSAPAFIDLDTTLSIFETGIKVVDLLAPYRRGGKIGLFGGAGVGKTVLIMELINNIAKAHGGVSVFGGVGERTREGNDLYMEMKESGVINELNLADSKVALVYGQMNEPPGARMRVGLTALTM
AEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPTLSAEMGSLQERITSTKKGSITSIQAVYVPADDLTDPAPATTFAHLDATTVLSRGLAAKGIYPAVDPLDSTSTMLQPRIVGEEH
YETAQQVKQTLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFFVAEVFTGSPGKYVGLAETIRGFNLILSGEFDSLPEQAFYLVGNIDEATAKATNLEMESKLKK

gi|899226 Malate dehydrogenase, mitochondrial precursor



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
1	18.08	18.08	75.4	gi|22595	myrosinase [Brassica napus]	Brassica napus	26			
2	10.54	10.54	70.6	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygenas…	Brassica napus	7			
3	8.04	8.04	71.6	gi|899226	malate dehydrogenase [Brassica napus]	Brassica napus	4			
4	6.02	6.02	66.9	gi|406727	ribulose-1,5-bisphosphate carboxylase /oxygenas…	Brassica napus	7			
5	5.40	5.40	41.0	gi|8745523	ATP synthase beta subunit [Brassica napus]	Brassica napus	8			
6	5.22	5.22	38.5	gi|15218…	germin-like protein [Arabidopsis thaliana]	Arabidopsis thaliana	4			

Protein Group 3 - malate dehydrogenase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accessio…	Name
3	8.04	8.04	gi|899226	malate dehydrogena…
3	0.00	8.04	gi|2497857	Malate dehydrogena…

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrur
2.00	99	AGKGSATLSMAYAGALFAD…	Trimethyl(K)@3 Oxidation(M)@10 ICAT-C:13C(9)(C)@21	missed K-…	0.1788	2510.47…	3	19	5.1.1.1343.
2.00	99	GLNGVPDVVECSYVQSTIT…	Deamidated(N)@3 ICAT-C(C)@11		0.2775	3127.81…	3	15	5.1.1.1468.
2.00	99	YCPHALVNMISNPVNSTVP…	ICAT-C:13C(9)(C)@2 Oxidation(M)@9		0.2152	3079.80…	3	15	5.1.1.1381.
2.00	99	YCPHALVNMISNPVNSTVP…	ICAT-C(C)@2 Oxidation(M)@9	missed K-K…	0.2451	3198.90…	4	18	5.1.1.1361.
0.02	5	AKYCPHALVNMISNPVNST…	Formyl@N-term No ICAT(C)@4 Oxidation(M)@11	cleaved I-A…	0.2451	3198.90…	4	19	5.1.1.1361.
0.02	4	SMAYAGALFADACLK	Oxidation(M)@2 ICAT-C:13C(9)(C)@13	cleaved L-…	0.2089	1783.08…	3	11	4.1.1.1477.
0.00	1	LNPLVSSLSLYDIANTPGV…	Methylthio(N)@2 Oxidation(N)@27		-0.8863	3067.67…	4	12	5.1.1.1361.

Protein Sequence Coverage - malate dehydrogenase [Brassica napus]

```
MFRSALVRSSASAKQSLLRRSFSSGSVPERKVAILGAAGGIGQPLALLMKLNPLVSSLSLYDIANTPGVAADVGHINTRSQVVGYMGDDNLAKALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKN
LWSAIAKYCPHALVNMISNPVNSTVPIAAEIFKKAGMYDEKKLFGVTTLDVVRVKTSYAGKANVPVAEVNVPAIVGHAGVTILPLFSQATPQAILSGDALTVTTKRTQDGGTEVEEAKAGKGSATLSM
AYAGALFADACLKGLNGVPDVVECSYVQSTITELPFFASKVRLGKNGVEEVLDLGPLSDFEKEGLEALRPGIKSTIEKGVKFANQ
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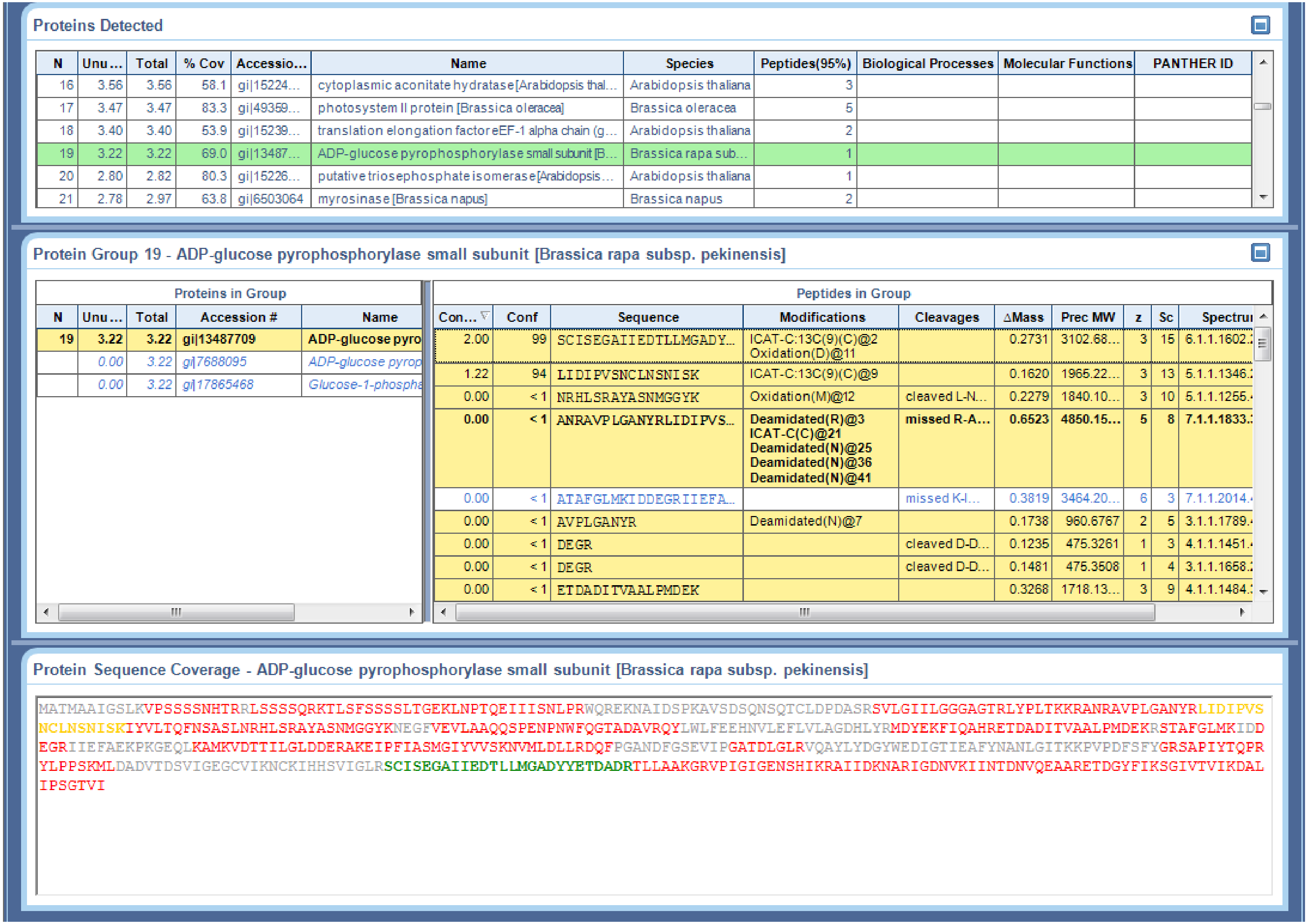
gi|13487709 ADP-glucose pyrophosphorylase small subunit



Proteins Detected

N	Unu...	Total	% Cov	Accessio...	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
16	3.56	3.56	58.1	gi|15224...	cytoplasmic aconitate hydratase [Arabidopsis thal...	Arabidopsis thaliana	3			
17	3.47	3.47	83.3	gi|49359...	photosystem II protein [Brassica oleracea]	Brassica oleracea	5			
18	3.40	3.40	53.9	gi|15239...	translation elongation factor eEF-1 alpha chain (g...	Arabidopsis thaliana	2			
19	3.22	3.22	69.0	gi|13487...	ADP-glucose pyrophosphorylase small subunit [B...	Brassica rapa sub...	1			
20	2.80	2.82	80.3	gi|15226...	putative triosephosphate isomerase [Arabidopsis...	Arabidopsis thaliana	1			
21	2.78	2.97	63.8	gi|6503064	myrosinase [Brassica napus]	Brassica napus	2			

Protein Group 19 - ADP-glucose pyrophosphorylase small subunit [Brassica rapa subsp. pekinensis]

Proteins in Group

N	Unu...	Total	Accession #	Name
19	**3.22**	**3.22**	**gi|13487709**	**ADP-glucose pyro**
	0.00	*3.22*	*gi|7688095*	*ADP-glucose pyrop*
	0.00	*3.22*	*gi|17865468*	*Glucose-1-phospha*

Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrui
2.00	99	SCISEGAIIEDTLLMGADY...	ICAT-C:13C(9)(C)@2 Oxidation(D)@11		0.2731	3102.68...	3	15	6.1.1.1602.
1.22	94	LIDIPVSNCLNSNISK	ICAT-C:13C(9)(C)@9		0.1620	1965.22...	3	13	5.1.1.1346.
0.00	< 1	NRHLSRAYASNMGGYK	Oxidation(M)@12	cleaved L-N...	0.2279	1840.10...	3	10	5.1.1.1255.
0.00	**< 1**	**ANRAVPLGANYRLIDIPVS...**	**Deamidated(R)@3 ICAT-C(C)@21 Deamidated(N)@25 Deamidated(N)@36 Deamidated(N)@41**	**missed R-A...**	**0.6523**	**4850.15...**	**5**	**8**	**7.1.1.1833.**
0.00	< 1	ATAFGLMKIDDEGRIIEFA...		missed K-I...	0.3819	3464.20...	6	3	7.1.1.2014.
0.00	< 1	AVPLGANYR	Deamidated(N)@7		0.1738	960.6767	2	5	3.1.1.1789.
0.00	< 1	DEGR		cleaved D-D...	0.1235	475.3261	1	3	4.1.1.1451.
0.00	< 1	DEGR		cleaved D-D...	0.1481	475.3508	1	4	3.1.1.1658.
0.00	< 1	ETDADITVAALPMDEK			0.3268	1718.13...	3	9	4.1.1.1484.

Protein Sequence Coverage - ADP-glucose pyrophosphorylase small subunit [Brassica rapa subsp. pekinensis]

```
MATMAAIGSLKVPSSSSNHTRRLSSSSQRKTLSFSSSSLTGEKLNPTQEIIISNLPRWQREKNAIDSPKAVSDSQNSQTCLDPDASRSVLGIILGGGAGTRLYPLTKKRANRAVPLGANYRLIDIPVS
NCLNSNISKIYVLTQFNSASLNRHLSRAYASNMGGYKNEGFVEVLAAQQSPENPNWFQGTADAVRQYLWLFEEHNVLEFLVLAGDHLYRMDYEKFIQAHRETDADITVAALPMDEKRSTAFGLMKIDD
EGRIIEFAEKPKGEQLKAMKVDTTILGLDDERAKEIPFIASMGIYVVSKNVMLDLLRDQFPGANDFGSEVIPGATDLGLRVQAYLYDGYWEDIGTIEAFYNANLGITKKPVPDFSFYGRSAPIYTQPR
YLPPSKMLDADVTDSVIGEGCVIKNCKIHHSVIGLRSCISEGAIIEDTLLMGADYYETDADRTLLAAKGRVPIGIGENSHIKRAIIDKNARIGDNVKIINTDNVQEAARETDGYFIKSGIVTVIKDAL
IPSGTVI
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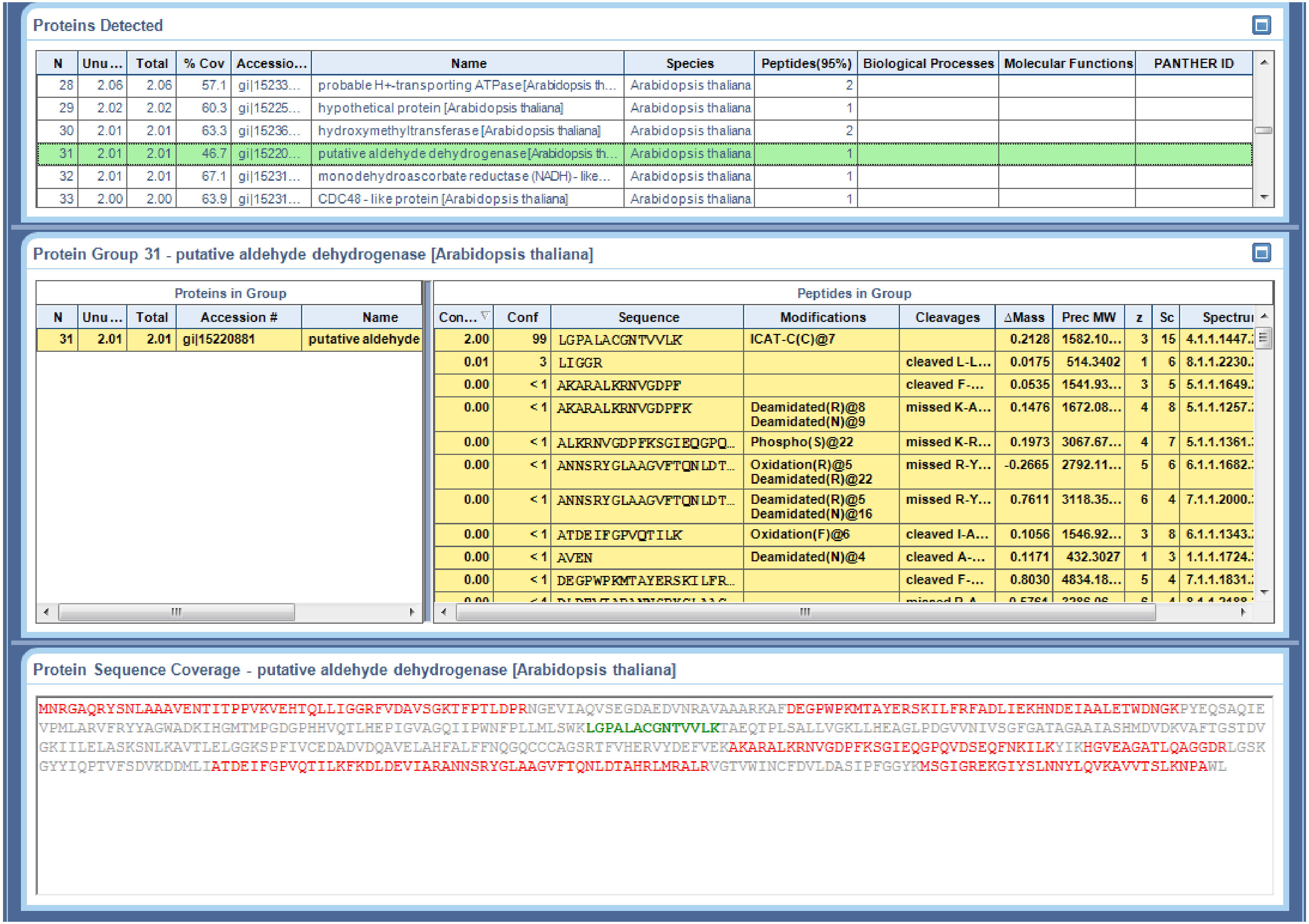
gi|15220881 Putative aldehyde dehydrogenase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
28	2.06	2.06	57.1	gi|15233…	probable H+-transporting ATPase [Arabidopsis th…	Arabidopsis thaliana	2			
29	2.02	2.02	60.3	gi|15225…	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
30	2.01	2.01	63.3	gi|15236…	hydroxymethyltransferase [Arabidopsis thaliana]	Arabidopsis thaliana	2			
31	2.01	2.01	46.7	gi|15220…	putative aldehyde dehydrogenase [Arabidopsis th…	Arabidopsis thaliana	1			
32	2.01	2.01	67.1	gi|15231…	monodehydroascorbate reductase (NADH) - like…	Arabidopsis thaliana	1			
33	2.00	2.00	63.9	gi|15231…	CDC48 - like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			

Protein Group 31 - putative aldehyde dehydrogenase [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
31	2.01	2.01	gi|15220881	putative aldehyde

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	LGPALACGNTVVLK	ICAT-C(C)@7		0.2128	1582.10…	3	15	4.1.1.1447.
0.01	3	LIGGR		cleaved L-L…	0.0175	514.3402	1	6	8.1.1.2230.
0.00	< 1	AKARALKRNVGDPF		cleaved F-…	0.0535	1541.93…	3	5	5.1.1.1649.
0.00	< 1	AKARALKRNVGDPFK	Deamidated(R)@8 Deamidated(N)@9	missed K-A…	0.1476	1672.08…	4	8	5.1.1.1257.
0.00	< 1	ALKRNVGDPFKSGIEQGPQ…	Phospho(S)@22	missed K-R…	0.1973	3067.67…	4	7	5.1.1.1361.
0.00	< 1	ANNSRYGLAAGVFTQNLDT…	Oxidation(R)@5 Deamidated(R)@22	missed R-Y…	-0.2665	2792.11…	5	6	6.1.1.1682.
0.00	< 1	ANNSRYGLAAGVFTQNLDT…	Deamidated(R)@5 Deamidated(N)@16	missed R-Y…	0.7611	3118.35…	6	4	7.1.1.2000.
0.00	< 1	ATDEIFGPVQTILK	Oxidation(F)@6	cleaved I-A…	0.1056	1546.92…	3	8	6.1.1.1343.
0.00	< 1	AVEN	Deamidated(N)@4	cleaved A-…	0.1171	432.3027	1	3	1.1.1.1724.
0.00	< 1	DEGPWPKMTAYERSKILFR…		cleaved F-…	0.8030	4834.18…	5	4	7.1.1.1831.

Protein Sequence Coverage - putative aldehyde dehydrogenase [Arabidopsis thaliana]

```
MNRGAQRYSNLAAAVENTITPPVKVEHTQLLIGGRFVDAVSGKTFPTLDPRNGEVIAQVSEGDAEDVNRAVAAARKAFDEGPWPKMTAYERSKILFRFADLIEKHNDEIAALETWDNGKPYEQSAQIE
VPMLARVFRYYAGWADKIHGMTMPGDGPHHVQTLHEPIGVAGQIIPWNFPLLMLSWKLGPALACGNTVVLKTAEQTPLSALLVGKLLHEAGLPDGVVNIVSGFGATAGAAIASHMDVDKVAFTGSTDV
GKIILELASKSNLKAVTLELGGKSPFIVCEDADVDQAVELAHFALFFNQGQCCCAGSRTFVHERVYDEFVEKAKARALKRNVGDPFKSGIEQGPQVDSEQFNKILKYIKHGVEAGATLQAGGDRLGSK
GYYIQPTVFSDVKDDMLIATDEIFGPVQTILKFKDLDEVIARANNSRYGLAAGVFTQNLDTAHRLMRALRVGTVWINCFDVLDASIPFGGYKMSGIGREKGIYSLNNYLQVKAVVTSLKNPAWL
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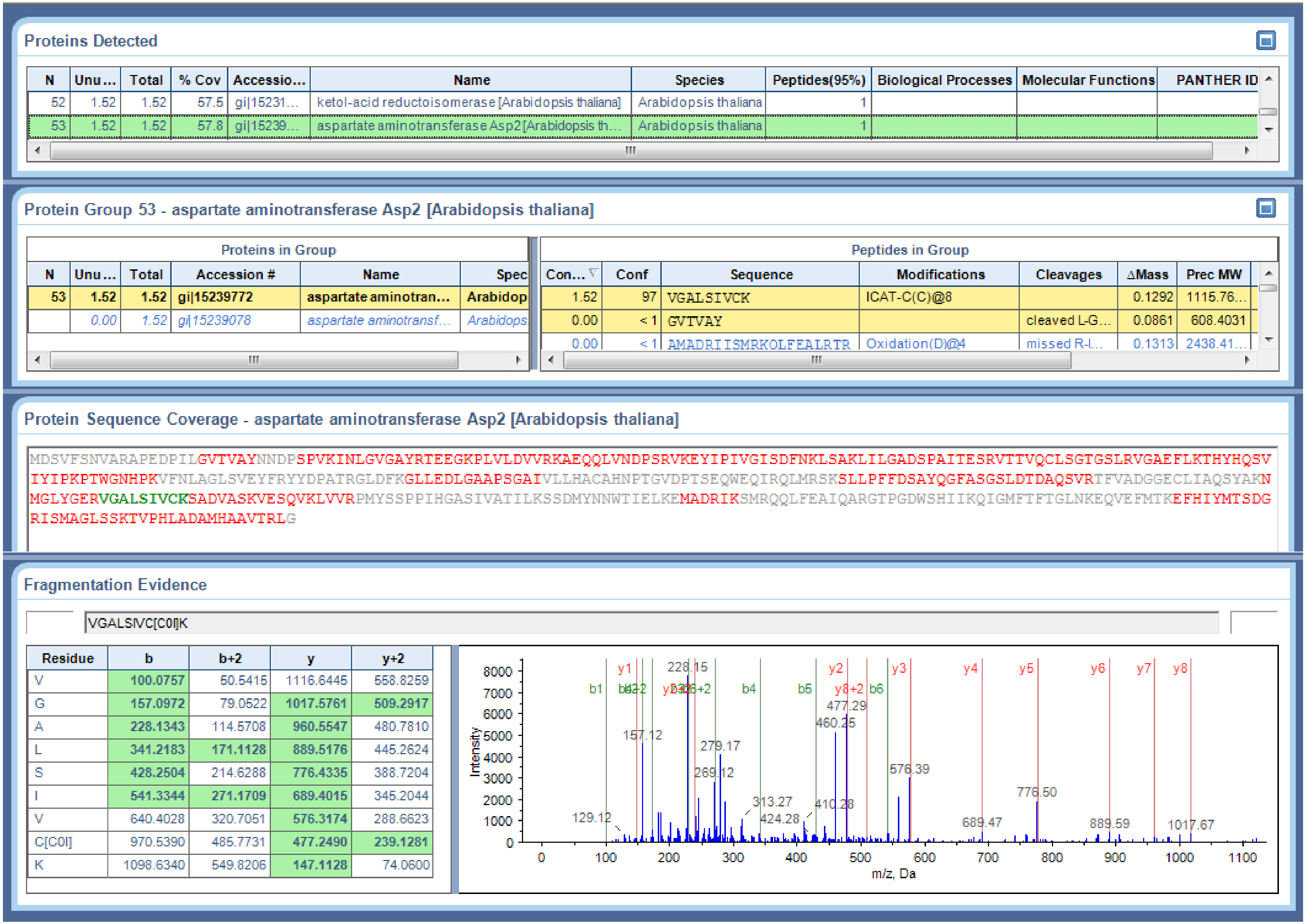
gi|15239772 Aspartate aminotransferase Asp2



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
52	1.52	1.52	57.5	gi|15231…	ketol-acid reductoisomerase [Arabidopsis thaliana]	Arabidopsis thaliana	1			
53	1.52	1.52	57.8	gi|15239…	aspartate aminotransferase Asp2 [Arabidopsis th…	Arabidopsis thaliana	1			

Protein Group 53 - aspartate aminotransferase Asp2 [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	Spec
53	1.52	1.52	gi|15239772	aspartate aminotran…	Arabidop
	0.00	1.52	gi|15239078	aspartate aminotransf…	Arabidops

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
1.52	97	VGALSIVCK	ICAT-C(C)@8		0.1292	1115.76…
0.00	< 1	GVTVAY		cleaved L-G…	0.0861	608.4031
0.00	< 1	AMADRIISMRKQLFEALRTR	Oxidation(D)@4	missed R-I…	0.1313	2438.41…

Protein Sequence Coverage - aspartate aminotransferase Asp2 [Arabidopsis thaliana]

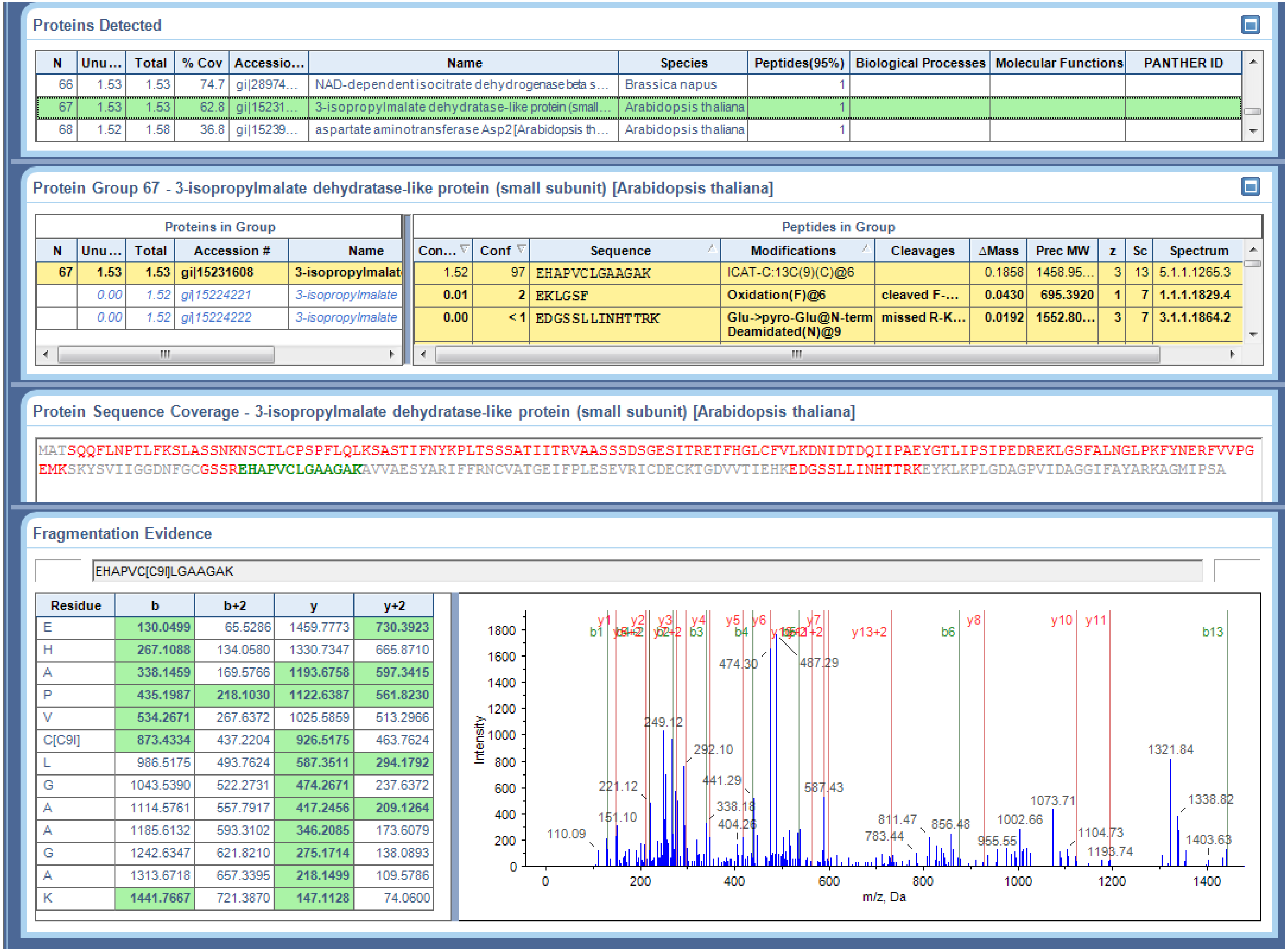
```
MDSVFSNVARAPEDPILGVTVAYNNDPSPVKINLGVGAYRTEEGKPLVLDVVRKAEQQLVNDPSRVKEYIPIVGISDFNKLSAKLILGADSPAITESRVTTVQCLSGTGSLRVGAEFLKTHYHQSV
IYIPKPTWGNHPKVFNLAGLSVEYFRYYDPATRGLDFKGLLEDLGAAPSGAIVLLHACAHNPTGVDPTSEQWEQIRQLMRSKSLLPFFDSAYQGFASGSLDTDAQSVRTFVADGGECLIAQSYAKN
MGLYGERVGALSIVCKSADVASKVESQVKLVVRPMYSSPPIHGASIVATILKSSDMYNNWTIELKEMADRIKSMRQQLFEAIQARGTPGDWSHIIKQIGMFTFTGLNKEQVEFMTKEFHIYMTSDG
RISMAGLSSKTVPHLADAMHAAVTRLG
```

Fragmentation Evidence

VGALSIVC[C0I]K

Residue	b	b+2	y	y+2
V	100.0757	50.5415	1116.6445	558.8259
G	157.0972	79.0522	1017.5761	509.2917
A	228.1343	114.5708	960.5547	480.7810
L	341.2183	171.1128	889.5176	445.2624
S	428.2504	214.6288	776.4335	388.7204
I	541.3344	271.1709	689.4015	345.2044
V	640.4028	320.7051	576.3174	288.6623
C[C0I]	970.5390	485.7731	477.2490	239.1281
K	1098.6340	549.8206	147.1128	74.0600

gi|15231608 3-isopropylmalate dehydratase-like protein (small subunit)



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
66	1.53	1.53	74.7	gi|28974…	NAD-dependent isocitrate dehydrogenase beta s…	Brassica napus	1			
67	1.53	1.53	62.8	gi|15231…	3-isopropylmalate dehydratase-like protein (small…	Arabidopsis thaliana	1			
68	1.52	1.58	36.8	gi|15239…	aspartate aminotransferase Asp2 [Arabidopsis th…	Arabidopsis thaliana	1			

Protein Group 67 - 3-isopropylmalate dehydratase-like protein (small subunit) [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
67	1.53	1.53	gi|15231608	3-isopropylmalat
	0.00	1.52	gi|15224221	3-isopropylmalate
	0.00	1.52	gi|15224222	3-isopropylmalate

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
1.52	97	EHAPVCLGAAGAK	ICAT-C:13C(9)(C)@6		0.1858	1458.95…	3	13	5.1.1.1265.3
0.01	2	EKLGSF	Oxidation(F)@6	cleaved F-…	0.0430	695.3920	1	7	1.1.1.1829.4
0.00	< 1	EDGSSLLINHTTRK	Glu->pyro-Glu@N-term Deamidated(N)@9	missed R-K…	0.0192	1552.80…	3	7	3.1.1.1864.2

Protein Sequence Coverage - 3-isopropylmalate dehydratase-like protein (small subunit) [Arabidopsis thaliana]

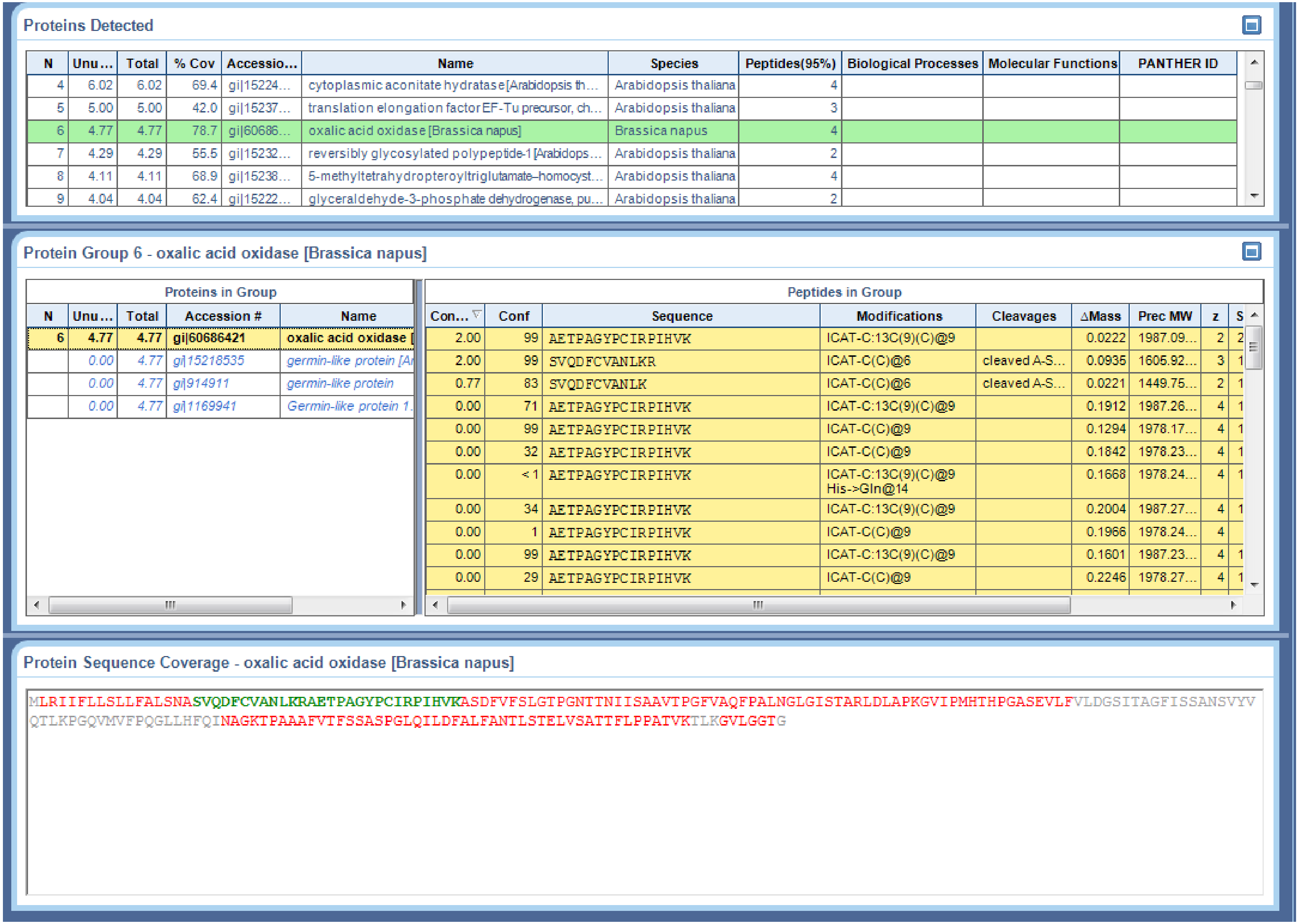
MATSQQFLNPTLFKSLASSNKNSCTLCPSPFLQLKSASTIFNYKPLTSSSATIITRVAASSSDSGESITRETFHGLCFVLKDNIDTDQIIPAEYGTLIPSIPEDREKLGSFALNGLPKFYNERFVVPG
EMKSKYSVIIGGDNFGCGSSREHAPVCLGAAGAKAVVAESYARIFFRNCVATGEIFPLESEVRICDECKTGDVVTIEHKEDGSSLLINHTTRKEYKLKPLGDAGPVIDAGGIFAYARKAGMIPSA

Fragmentation Evidence

EHAPVC[C9I]LGAAGAK

Residue	b	b+2	y	y+2
E	130.0499	65.5286	1459.7773	730.3923
H	267.1088	134.0580	1330.7347	665.8710
A	338.1459	169.5766	1193.6758	597.3415
P	435.1987	218.1030	1122.6387	561.8230
V	534.2671	267.6372	1025.5859	513.2966
C[C9I]	873.4334	437.2204	926.5175	463.7624
L	986.5175	493.7624	587.3511	294.1792
G	1043.5390	522.2731	474.2671	237.6372
A	1114.5761	557.7917	417.2456	209.1264
A	1185.6132	593.3102	346.2085	173.6079
G	1242.6347	621.8210	275.1714	138.0893
A	1313.6718	657.3395	218.1499	109.5786
K	1441.7667	721.3870	147.1128	74.0600

gi|60686421 Oxalic acid oxidase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
4	6.02	6.02	69.4	gi|15224…	cytoplasmic aconitate hydratase [Arabidopsis th…	Arabidopsis thaliana	4			
5	5.00	5.00	42.0	gi|15237…	translation elongation factor EF-Tu precursor, ch…	Arabidopsis thaliana	3			
6	4.77	4.77	78.7	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	4			
7	4.29	4.29	55.5	gi|15232…	reversibly glycosylated polypeptide-1 [Arabidops…	Arabidopsis thaliana	2			
8	4.11	4.11	68.9	gi|15238…	5-methyltetrahydropteroyltriglutamate–homocyst…	Arabidopsis thaliana	4			
9	4.04	4.04	62.4	gi|15222…	glyceraldehyde-3-phosphate dehydrogenase, pu…	Arabidopsis thaliana	2			

Protein Group 6 - oxalic acid oxidase [Brassica napus]

Proteins in Group

N	Unu…	Total	Accession #	Name
6	4.77	4.77	gi|60686421	oxalic acid oxidase [
	0.00	4.77	gi|15218535	germin-like protein [Ar
	0.00	4.77	gi|914911	germin-like protein
	0.00	4.77	gi|1169941	Germin-like protein 1.

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	S
2.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.0222	1987.09…	2	2
2.00	99	SVQDFCVANLKR	ICAT-C(C)@6	cleaved A-S…	0.0935	1605.92…	3	1
0.77	83	SVQDFCVANLK	ICAT-C(C)@6	cleaved A-S…	0.0221	1449.75…	2	1
0.00	71	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.1912	1987.26…	4	1
0.00	99	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1294	1978.17…	4	1
0.00	32	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1842	1978.23…	4	1
0.00	< 1	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9 His->Gln@14		0.1668	1978.24…	4	1
0.00	34	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.2004	1987.27…	4	1
0.00	1	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.1966	1978.24…	4	
0.00	99	AETPAGYPCIRPIHVK	ICAT-C:13C(9)(C)@9		0.1601	1987.23…	4	1
0.00	29	AETPAGYPCIRPIHVK	ICAT-C(C)@9		0.2246	1978.27…	4	1

Protein Sequence Coverage - oxalic acid oxidase [Brassica napus]

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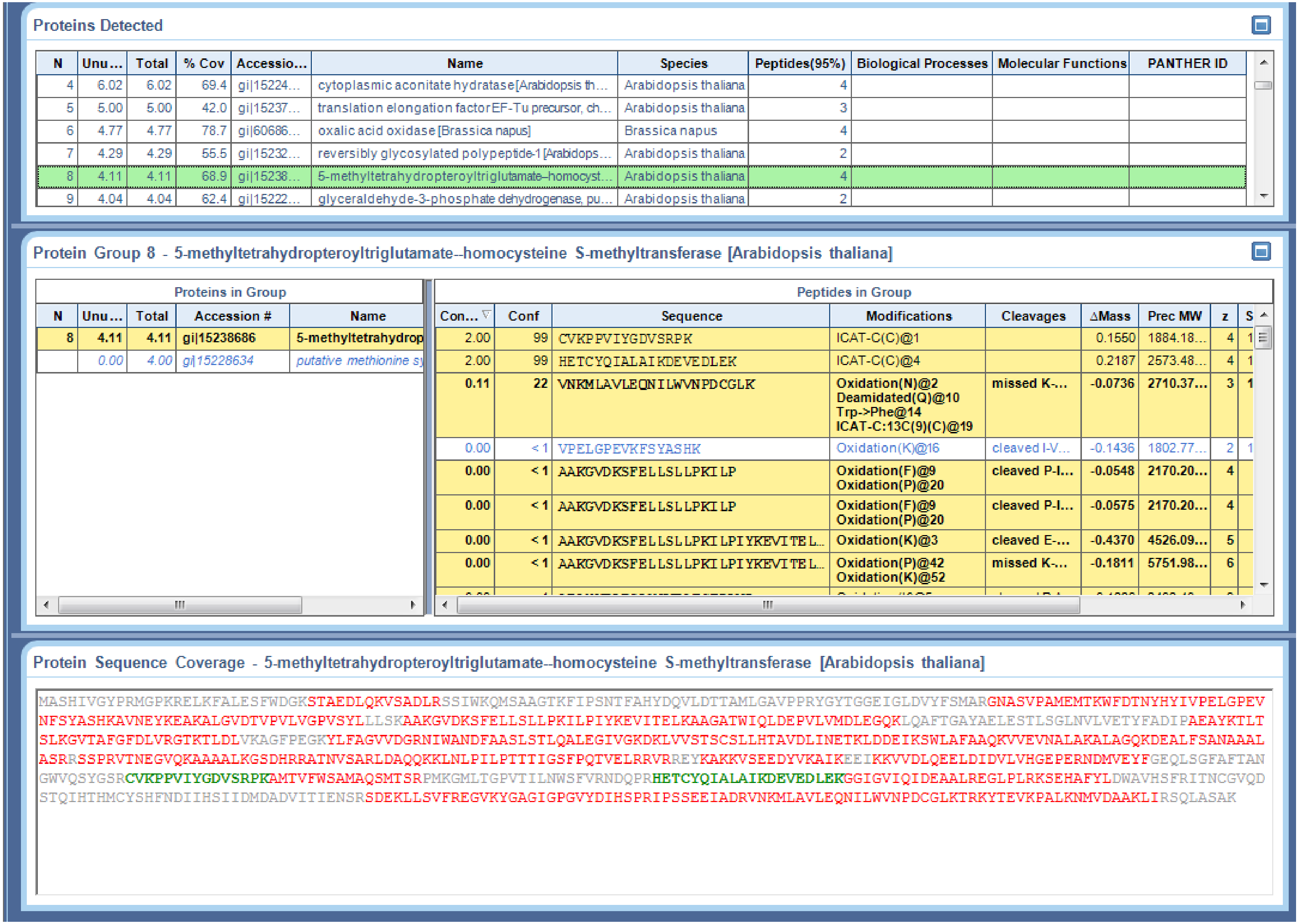
MLRIIFLLSLLFALSNASVQDFCVANLKRAETPAGYPCIRPIHVKASDFVFSLGTPGNTTNIISAAVTPGFVAQFPALNGLGISTARLDLAPKGVIPMHTHPGASEVLFVLDGSITAGFISSANSVYV
QTLKPGQVMVFPQGLLHFQINAGKTPAAAFVTFSSASPGLQILDFALFANTLSTELVSATTFLPPATVKTLKGVLGGTG
```

gi|15238686 Homocysteine S-methyltransferase



Proteins Detected

N	Unu…	Total	% Cov	Accessio…	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
4	6.02	6.02	69.4	gi|15224…	cytoplasmic aconitate hydratase [Arabidopsis th…	Arabidopsis thaliana	4			
5	5.00	5.00	42.0	gi|15237…	translation elongation factor EF-Tu precursor, ch…	Arabidopsis thaliana	3			
6	4.77	4.77	78.7	gi|60686…	oxalic acid oxidase [Brassica napus]	Brassica napus	4			
7	4.29	4.29	55.5	gi|15232…	reversibly glycosylated polypeptide-1 [Arabidops…	Arabidopsis thaliana	2			
8	4.11	4.11	68.9	gi|15238…	5-methyltetrahydropteroyltriglutamate--homocyst…	Arabidopsis thaliana	4			
9	4.04	4.04	62.4	gi|15222…	glyceraldehyde-3-phosphate dehydrogenase, pu…	Arabidopsis thaliana	2			

Protein Group 8 - 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
8	4.11	4.11	gi|15238686	5-methyltetrahydrop
	0.00	4.00	gi|15228634	putative methionine sy

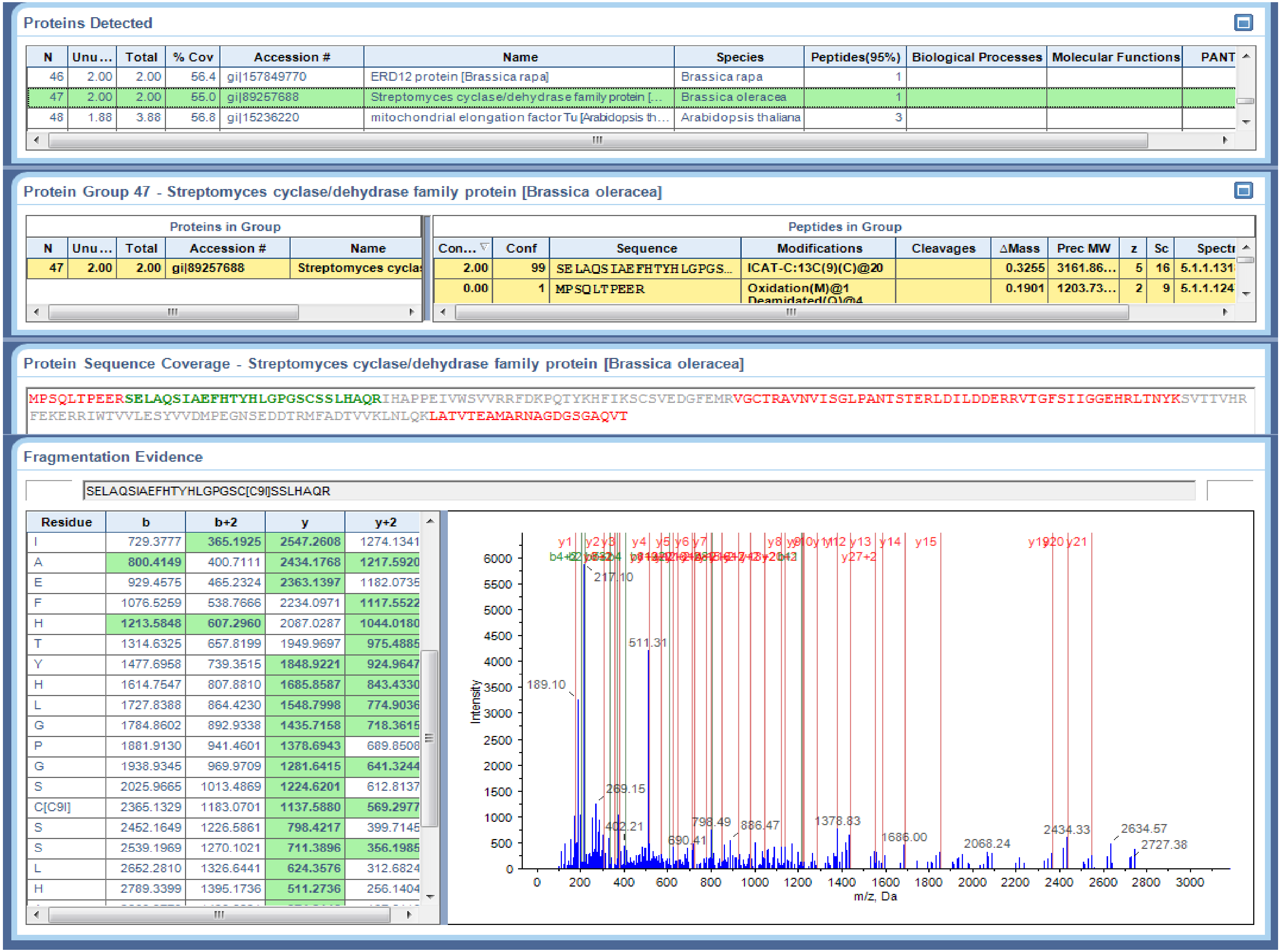
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	S
2.00	99	CVKPPVIYGDVSRPK	ICAT-C(C)@1		0.1550	1884.18…	4	1
2.00	99	HETCYQIALAIKDEVEDLEK	ICAT-C(C)@4		0.2187	2573.48…	4	1
0.11	22	VNKMLAVLEQNILWVNPDCGLK	Oxidation(N)@2 Deamidated(Q)@10 Trp->Phe@14 ICAT-C:13C(9)(C)@19	missed K-…	-0.0736	2710.37…	3	1
0.00	< 1	VPELGPEVKFSYASHK	Oxidation(K)@16	cleaved I-V…	-0.1436	1802.77…	2	1
0.00	< 1	AAKGVDKSFELLSLLPKILP	Oxidation(F)@9 Oxidation(P)@20	cleaved P-I…	-0.0548	2170.20…	4	
0.00	< 1	AAKGVDKSFELLSLLPKILP	Oxidation(F)@9 Oxidation(P)@20	cleaved P-I…	-0.0575	2170.20…	4	
0.00	< 1	AAKGVDKSFELLSLLPKILPIYKEVITEL…	Oxidation(K)@3	cleaved E-…	-0.4370	4526.09…	5	
0.00	< 1	AAKGVDKSFELLSLLPKILPIYKEVITEL…	Oxidation(P)@42 Oxidation(K)@52	missed K-…	-0.1811	5751.98…	6	

Protein Sequence Coverage - 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Arabidopsis thaliana]

```
MASHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIWKQMSAAGTKFIPSNTFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASVPAMEMTKWFDTNYHYIVPELGPEV
NFSYASHKAVNEYKEAKALGVDTVPVLVGPVSYLLLSKAAKGVDKSFELLSLLPKILPIYKEVITELKAAGATWIQLDEPVLVMDLEGQKLQAFTGAYAELESTLSGLNVLVETYFADIPAEAYKTLT
SLKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLFAGVVDGRNIWANDFAASLSTLQALEGIVGKDKLVVSTSCSLLHTAVDLINETKLDDEIKSWLAFAAQKVVEVNALAKALAGQKDEALFSANAAAL
ASRRSSPRVTNEGVQKAAAALKGSDHRRATNVSARLDAQQKKLNLPILPTTTIGSFPQTVELRRVRREYKAKKVSEEDYVKAIKEEIKKVVDLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTAN
GWVQSYGSRCVKPPVIYGDVSRPKAMTVFWSAMAQSMTSRPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDLEKGGIGVIQIDEAALREGLPLRKSEHAFYLDWAVHSFRITNCGVQD
STQIHTHMCYSHFNDIIHSIIDMDADVITIENSRSDEKLLSVFREGVKYGAGIGPGVYDIHSPRIPSSEEIADRVNKMLAVLEQNILWVNPDCGLKTRKYTEVKPALKNMVDAAKLIRSQLASAK
```

gi|89257688 Streptomyces cyclase / dehydrase family protein



Proteins Detected

N	Unu…	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
46	2.00	2.00	56.4	gi|157849770	ERD12 protein [Brassica rapa]	Brassica rapa	1			
47	2.00	2.00	55.0	gi|89257688	Streptomyces cyclase/dehydrase family protein […	Brassica oleracea	1			
48	1.88	3.88	56.8	gi|15236220	mitochondrial elongation factor Tu [Arabidopsis th…	Arabidopsis thaliana	3			

Protein Group 47 - Streptomyces cyclase/dehydrase family protein [Brassica oleracea]

Proteins in Group

N	Unu…	Total	Accession #	Name
47	2.00	2.00	gi|89257688	Streptomyces cyclas

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectr
2.00	99	SELAQSIAEFHTYHLGPGS…	ICAT-C:13C(9)(C)@20		0.3255	3161.86…	5	16	5.1.1.131
0.00	1	MPSQLTPEER	Oxidation(M)@1 Deamidated(Q)@4		0.1901	1203.73…	2	9	5.1.1.124

Protein Sequence Coverage - Streptomyces cyclase/dehydrase family protein [Brassica oleracea]

MPSQLTPEERSELAQSIAEFHTYHLGPGSCSSLHAQRIHAPPEIVWSVVRRFDKPQTYKHFIKSCSVEDGFEMRVGCTRAVNVISGLPANTSTERLDILDDERRVTGFSIIGGEHRLTNYKSVTTVHR
FEKERRIWTVVLESYVVDMPEGNSEDDTRMFADTVVKLNLQKLATVTEAMARNAGDGSAQVT

Fragmentation Evidence

SELAQSIAEFHTYHLGPGSC[C9I]SSLHAQR

Residue	b	b+2	y	y+2
I	729.3777	365.1925	2547.2608	1274.1341
A	800.4149	400.7111	2434.1768	1217.5920
E	929.4575	465.2324	2363.1397	1182.0735
F	1076.5259	538.7666	2234.0971	1117.5522
H	1213.5848	607.2960	2087.0287	1044.0180
T	1314.6325	657.8199	1949.9697	975.4885
Y	1477.6958	739.3515	1848.9221	924.9647
H	1614.7547	807.8810	1685.8587	843.4330
L	1727.8388	864.4230	1548.7998	774.9036
G	1784.8602	892.9338	1435.7158	718.3615
P	1881.9130	941.4601	1378.6943	689.8508
G	1938.9345	969.9709	1281.6415	641.3244
S	2025.9665	1013.4869	1224.6201	612.8137
C[C9I]	2365.1329	1183.0701	1137.5880	569.2977
S	2452.1649	1226.5861	798.4217	399.7145
S	2539.1969	1270.1021	711.3896	356.1985
L	2652.2810	1326.6441	624.3576	312.6824
H	2789.3399	1395.1736	511.2736	256.1404

gi|15235668 Extensin-like protein

Proteins Detected

N	Unu…	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
38	2.00	2.00	40.5	gi|15235668	extensin-like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
39	2.00	2.00	62.0	gi|15224339	unknown protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			

Protein Group 38 - extensin-like protein [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name
38	2.00	2.00	gi|15235668	extensin-like protei
	0.00	2.00	gi|15230120	disease resistance p

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spe
2.00	99	IPASICQLPK	ICAT-C:13C(9)(C)@6		0.1267	1304.88…	2	14	4.1.1.1
0.00	< 1	ADIGRLKNVTVF	Deamidated(R)@5	cleaved P-A…	0.1618	1349.88…	2	10	3.1.1.1

Protein Sequence Coverage - extensin-like protein [Arabidopsis thaliana]

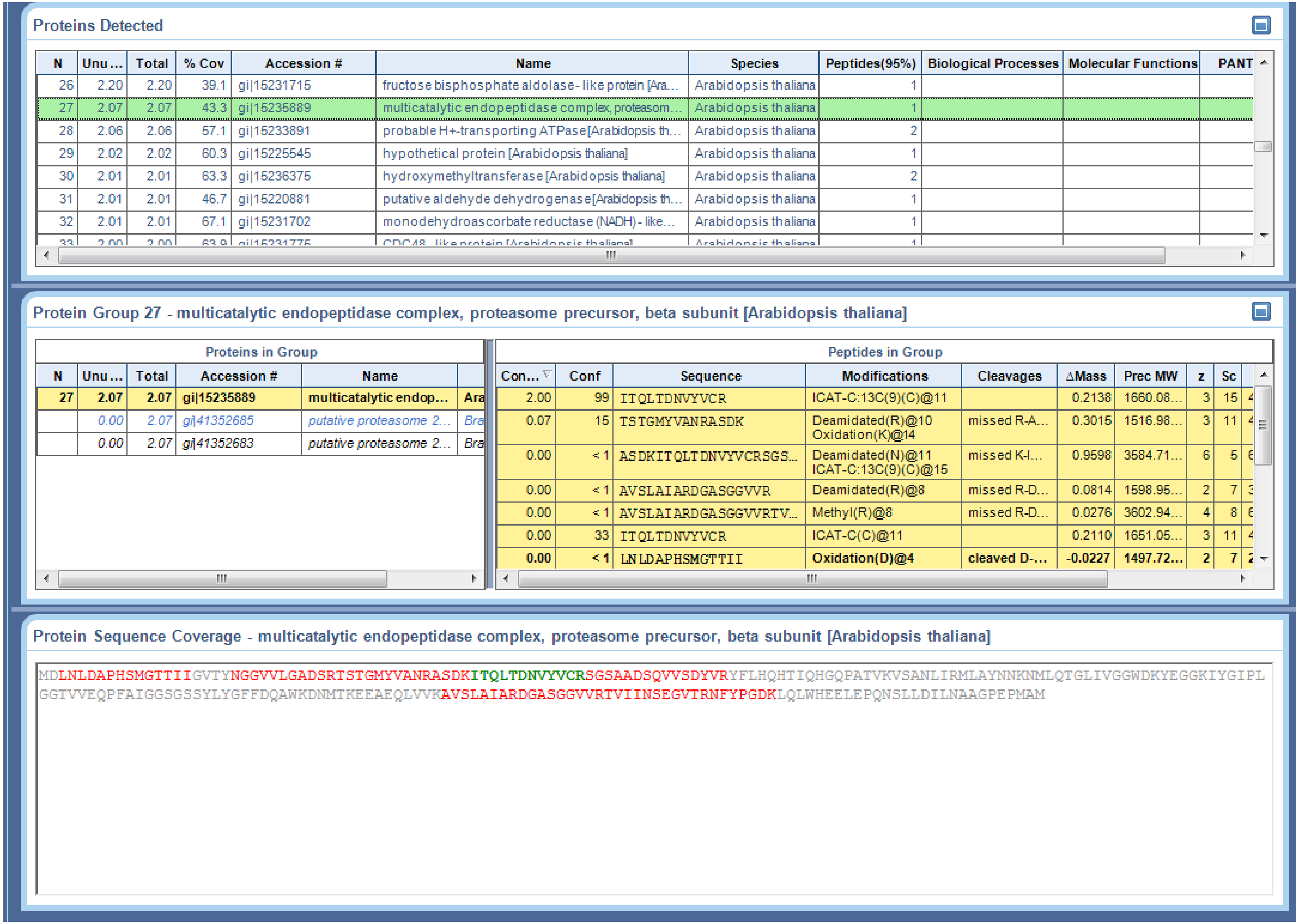
```
MKKTIQILLFFFFLINLTNALSISSDGGVLSDNEVRHIQRRQLLEFAERSVKITVDPSLNFENPRLRNAYIALQAWKQAILSDPNNFTSNWIGSNVCNYTGVFCSPALDNRKIRTVAGIDLNHADIAG
YLPEELGLLSDLALFHVNSNRFCGTVPHRFNRLKLLFELDLSNNRFAGKFPTVVLQLPSLKFLDLRFNEFEGTVPKELFSKDLDAIFINHNRFRFELPENFGDSPVSVIVLANNRFHGCVPSSLVEMK
NLNEIIFMNNGLNSCLPSDIGRLKNVTVFDVSFNELVGPLPESVGEMVSVEQLNVAHNMLSGKIPASICQLPKLENFTYSYNFFTGEAPVCLRLPEFDDRRNCLPGRPAQRSPGQCKAFLSRPPVNCG
SFSCGRSVSPRPPVVTPLPPPSLPSPPPPAPIFSTPPTLTSPPPPSPPPPVYSPPPPPPPPPPVYSPPPPPPPPPPVYSPPPPPPPPPPPPVYSPPPPSPPPPPPPPPVYSPPPPPPPPPPPPVYSP
PPPPVYSSPPPPPSPAPTPVYCTRPPPPPPHSPPPPQFSPPPPEPYYYSSPPPPHSSPPPHSPPPPHSPPPPIYPYLSPPPPPTPVSSPPPTPVYSPPPPPPCIEPPPPPPCIEYSPPPPPPVVHYSS
PPPPPVYYSSPPPPPVYYSSPPPPPPVHYSSPPPPEVHYHSPPPSPVHYSSPPPPPSAPCEESPPPAPVVHHSPPPPMVHHSPPPPVIHQSPPPPSPEYEGPLPPVIGVSYASPPPPPFY
```

Fragmentation Evidence

IPASIC[C9I]QLPK

Residue	b	b+2	y	y+2
I	114.0913	57.5493	1305.7646	653.3859
P	211.1441	106.0757	1192.6805	596.8439
A	282.1812	141.5942	1095.6278	548.3175
S	369.2132	185.1103	1024.5907	512.7990
I	482.2973	241.6523	937.5586	469.2830
C[C9I]	821.4637	411.2355	824.4746	412.7409
Q	949.5223	475.2648	485.3082	243.1577
L	1062.6063	531.8068	357.2496	179.1285
P	1159.6591	580.3332	244.1656	122.5864
K	1287.7540	644.3807	147.1128	74.0600

gi|15235889 Multicatalytic endopeptidase complex, beta subunit



Proteins Detected

N	Unu...	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANT
26	2.20	2.20	39.1	gi|15231715	fructose bisphosphate aldolase- like protein [Ara...	Arabidopsis thaliana	1			
27	2.07	2.07	43.3	gi|15235889	multicatalytic endopeptidase complex, proteasom...	Arabidopsis thaliana	1			
28	2.06	2.06	57.1	gi|15233891	probable H+-transporting ATPase[Arabidopsis th...	Arabidopsis thaliana	2			
29	2.02	2.02	60.3	gi|15225545	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
30	2.01	2.01	63.3	gi|15236375	hydroxymethyltransferase [Arabidopsis thaliana]	Arabidopsis thaliana	2			
31	2.01	2.01	46.7	gi|15220881	putative aldehyde dehydrogenase[Arabidopsis th...	Arabidopsis thaliana	1			
32	2.01	2.01	67.1	gi|15231702	monodehydroascorbate reductase (NADH)- like...	Arabidopsis thaliana	1			
33	2.00	2.00	63.9	gi|15231775	CDC48 - like protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			

Protein Group 27 - multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name	
27	2.07	2.07	gi|15235889	multicatalytic endop...	Ara
	0.00	2.07	gi|41352685	putative proteasome 2...	Bra
	0.00	2.07	gi|41352683	putative proteasome 2...	Bra

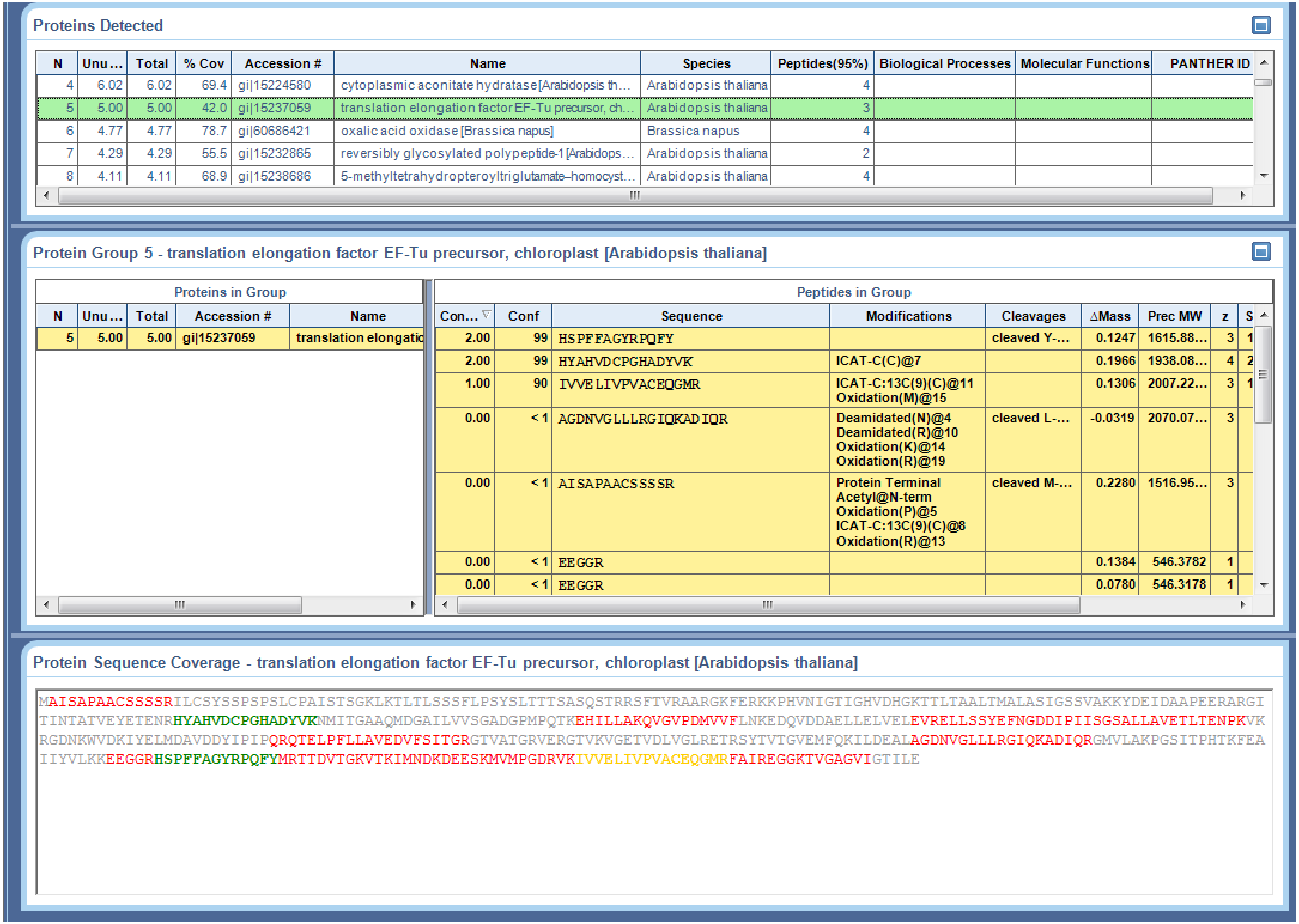
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc
2.00	99	ITQLTDNVYVCR	ICAT-C:13C(9)(C)@11		0.2138	1660.08...	3	15
0.07	15	TSTGMYVANRASDK	Deamidated(R)@10 Oxidation(K)@14	missed R-A...	0.3015	1516.98...	3	11
0.00	< 1	ASDKITQLTDNVYVCRSGS...	Deamidated(N)@11 ICAT-C:13C(9)(C)@15	missed K-I...	0.9598	3584.71...	6	5
0.00	< 1	AVSLAIARDGASGGVVR	Deamidated(R)@8	missed R-D...	0.0814	1598.95...	2	7
0.00	< 1	AVSLAIARDGASGGVVRTV...	Methyl(R)@8	missed R-D...	0.0276	3602.94...	4	8
0.00	33	ITQLTDNVYVCR	ICAT-C(C)@11		0.2110	1651.05...	3	11
0.00	**< 1**	**LNLDAPHSMGTTII**	**Oxidation(D)@4**	**cleaved D-...**	**-0.0227**	**1497.72...**	**2**	**7**

Protein Sequence Coverage - multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana]

MDLNLDAPHSMGTTIIGVTYNGGVVLGADSRTSTGMYVANRASDKITQLTDNVYVCRSGSAADSQVVSDYVRYFLHQHTIQHGQPATVKVSANLIRMLAYNNKNMLQTGLIVGGWDKYEGGKIYGIPL
GGTVVEQPFAIGGSGSSYLYGFFDQAWKDNMTKEEAEQLVVKAVSLAIARDGASGGVVRTVIINSEGVTRNFYPGDKLQLWHEELEPQNSLLDILNAAGPEPMAM

gi|15237059 Translation elongation factor EF-Tu precursor, chloroplast



Proteins Detected

N	Unu...	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
4	6.02	6.02	69.4	gi|15224580	cytoplasmic aconitate hydratase [Arabidopsis th...	Arabidopsis thaliana	4			
5	5.00	5.00	42.0	gi|15237059	translation elongation factor EF-Tu precursor, ch...	Arabidopsis thaliana	3			
6	4.77	4.77	78.7	gi|60686421	oxalic acid oxidase [Brassica napus]	Brassica napus	4			
7	4.29	4.29	55.5	gi|15232865	reversibly glycosylated polypeptide-1 [Arabidops...	Arabidopsis thaliana	2			
8	4.11	4.11	68.9	gi|15238686	5-methyltetrahydropteroyltriglutamate–homocyst...	Arabidopsis thaliana	4			

Protein Group 5 - translation elongation factor EF-Tu precursor, chloroplast [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name
5	5.00	5.00	gi|15237059	translation elongatio

Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	S
2.00	99	HSPFFAGYRPQFY		cleaved Y-...	0.1247	1615.88...	3	1
2.00	99	HYAHVDCPGHADYVK	ICAT-C(C)@7		0.1966	1938.08...	4	2
1.00	90	IVVELIVPVACEQGMR	ICAT-C:13C(9)(C)@11 Oxidation(M)@15		0.1306	2007.22...	3	1
0.00	< 1	AGDNVGLLLRGIQKADIQR	Deamidated(N)@4 Deamidated(R)@10 Oxidation(K)@14 Oxidation(R)@19	cleaved L-...	-0.0319	2070.07...	3	
0.00	< 1	AISAPAACSSSSR	Protein Terminal Acetyl@N-term Oxidation(P)@5 ICAT-C:13C(9)(C)@8 Oxidation(R)@13	cleaved M-...	0.2280	1516.95...	3	
0.00	< 1	EEGGR			0.1384	546.3782	1	
0.00	< 1	EEGGR			0.0780	546.3178	1	

Protein Sequence Coverage - translation elongation factor EF-Tu precursor, chloroplast [Arabidopsis thaliana]

```
MAISAPAACSSSSRILCSYSSPSPSLCPAISTSGKLKTLTLSSSFLPSYSLTTTSASQSTRRSFTVRAARGKFERKKPHVNIGTIGHVDHGKTTLTAALTMALASIGSSVAKKYDEIDAAPEERARGI
TINTATVEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSGADGPMPQTKEHILLAKQVGVPDMVVFLNKEDQVDDAELLELVELEVRELLSSYEFNGDDIPIISGSALLAVETLTENPKVK
RGDNKWVDKIYELMDAVDDYIPIPQRQTELPFLLAVEDVFSITGRGTVATGRVERGTVKVGETVDLVGLRETRSYTVTGVEMFQKILDEALAGDNVGLLLRGIQKADIQRGMVLAKPGSITPHTKFEA
IIYVLKKEEGGRHSPFFAGYRPQFYMRTTDVTGKVTKIMNDKDEESKMVMPGDRVKIVVELIVPVACEQGMRFAIREGGKTVGAGVIGTILE
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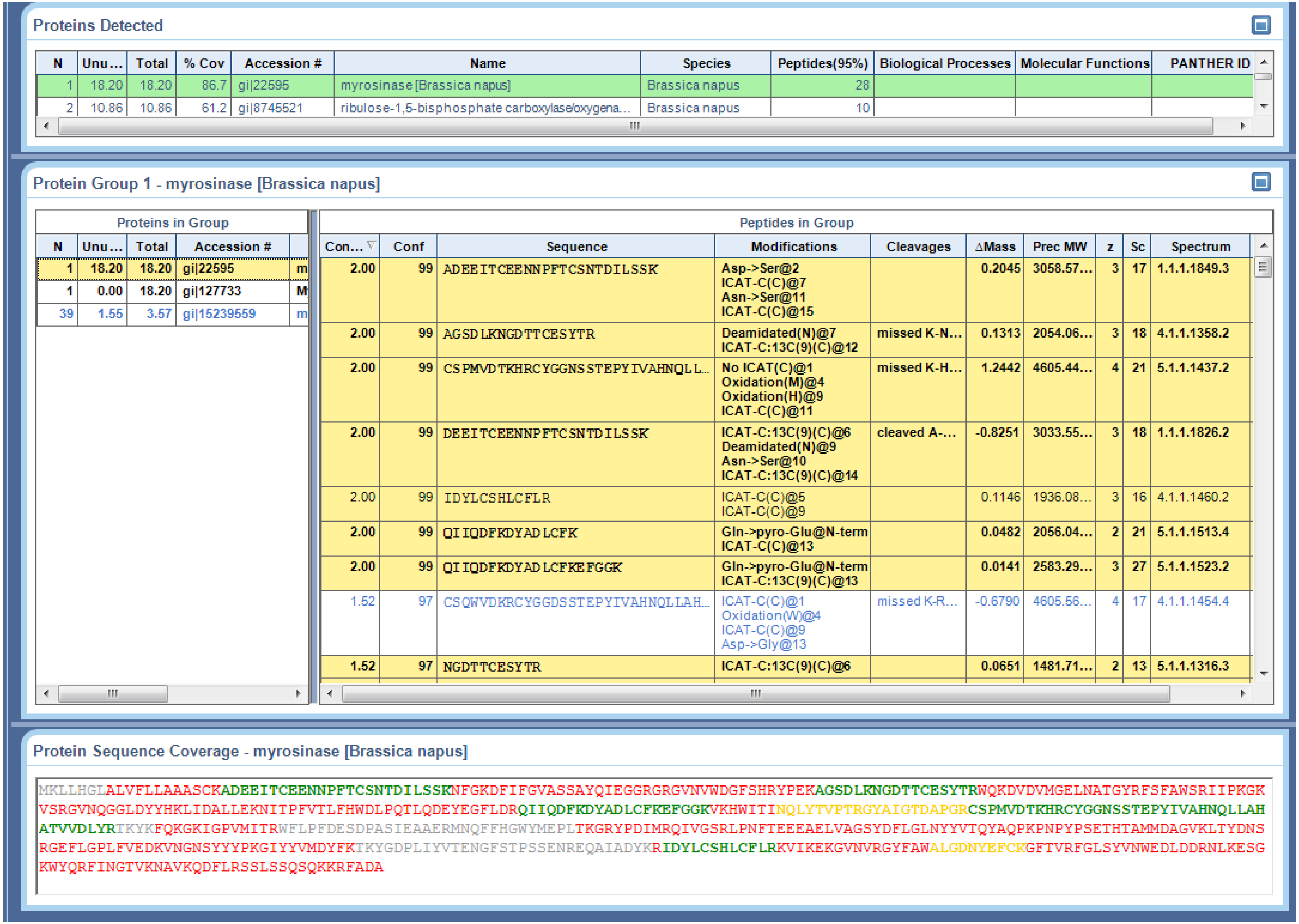
gi|414103 Myrosinase



Proteins Detected

N	Unu...	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
1	18.20	18.20	86.7	gi|22595	myrosinase [Brassica napus]	Brassica napus	28			
2	10.86	10.86	61.2	gi|8745521	ribulose-1,5-bisphosphate carboxylase/oxygena...	Brassica napus	10			

Protein Group 1 - myrosinase [Brassica napus]

Proteins in Group

N	Unu...	Total	Accession #	
1	18.20	18.20	gi|22595	m
1	0.00	18.20	gi|127733	M
39	1.55	3.57	gi|15239559	m

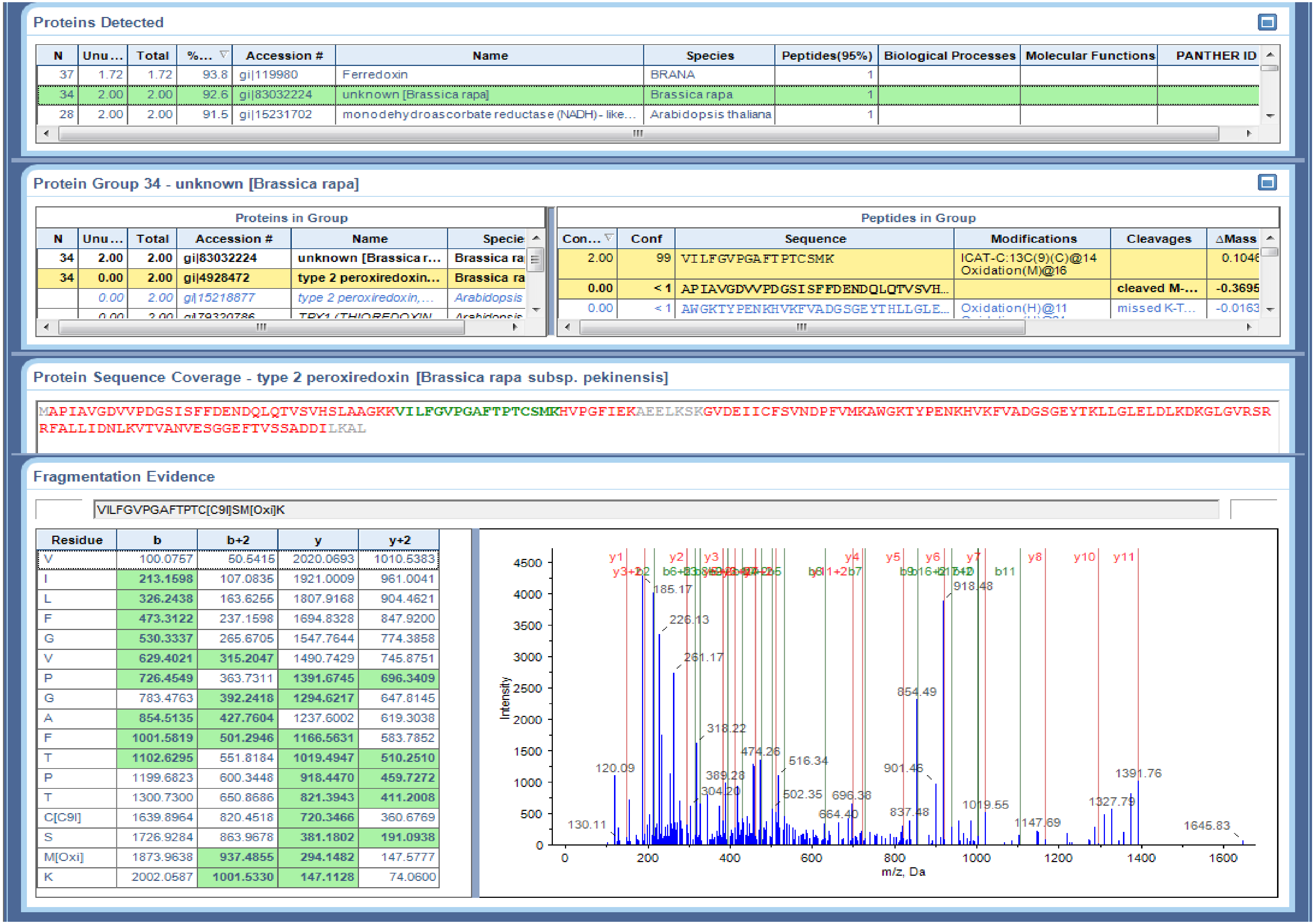
Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW	z	Sc	Spectrum
2.00	99	ADEEITCEENNPFTCSNTDILSSK	Asp->Ser@2 ICAT-C(C)@7 Asn->Ser@11 ICAT-C(C)@15		0.2045	3058.57...	3	17	1.1.1.1849.3
2.00	99	AGSDLKNGDTTCESYTR	Deamidated(N)@7 ICAT-C:13C(9)(C)@12	missed K-N...	0.1313	2054.06...	3	18	4.1.1.1358.2
2.00	99	CSPMVDTKHRCYGGNSSTEPYIVAHNQLL...	No ICAT(C)@1 Oxidation(M)@4 Oxidation(H)@9 ICAT-C(C)@11	missed K-H...	1.2442	4605.44...	4	21	5.1.1.1437.2
2.00	99	DEEITCEENNPFTCSNTDILSSK	ICAT-C:13C(9)(C)@6 Deamidated(N)@9 Asn->Ser@10 ICAT-C:13C(9)(C)@14	cleaved A-...	-0.8251	3033.55...	3	18	1.1.1.1826.2
2.00	99	IDYLCSHLCFLR	ICAT-C(C)@5 ICAT-C(C)@9		0.1146	1936.08...	3	16	4.1.1.1460.2
2.00	99	QIIQDFKDYADLCFK	Gln->pyro-Glu@N-term ICAT-C(C)@13		0.0482	2056.04...	2	21	5.1.1.1513.4
2.00	99	QIIQDFKDYADLCFKEFGGK	Gln->pyro-Glu@N-term ICAT-C:13C(9)(C)@13		0.0141	2583.29...	3	27	5.1.1.1523.2
1.52	97	CSQWVDKRCYGGDSSTEPYIVAHNQLLAH...	ICAT-C(C)@1 Oxidation(W)@4 ICAT-C(C)@9 Asp->Gly@13	missed K-R...	-0.6790	4605.56...	4	17	4.1.1.1454.4
1.52	97	NGDTTCESYTR	ICAT-C:13C(9)(C)@6		0.0651	1481.71...	2	13	5.1.1.1316.3

Protein Sequence Coverage - myrosinase [Brassica napus]

```
MKLLHGLALVFLLAAASCKADEEITCEENNPFTCSNTDILSSKNFGKDFIFGVASSAYQIEGGRGRGVNVWDGFSHRYPEKAGSDLKNGDTTCESYTRWQKDVDVMGELNATGYRFSFAWSRIIPKGK
VSRGVNQGGLDYYHKLIDALLEKNITPFVTLFHWDLPQTLQDEYEGFLDRQIIQDFKDYADLCFKEFGGKVKHWITINQLYTVPTRGYAIGTDAPGRCSPMVDTKHRCYGGNSSTEPYIVAHNQLLAH
ATVVDLYRTKYKFQKGKIGPVMITRWFLPFDESDPASIEAAERMNQFFHGWYMEPLTKGRYPDIMRQIVGSRLPNFTEEEAELVAGSYDFLGLNYYVTQYAQPKPNPYPSETHTAMMDAGVKLTYDNS
RGEFLGPLFVEDKVNGNSYYYPKGIYYVMDYFKTKYGDPLIYVTENGFSTPSSENREQAIADYKRIDYLCSHLCFLRKVIKEKGVNVRGYFAWALGDNYEFCKGFTVRFGLSYVNWEDLDDRNLKESG
KWYQRFINGTVKNAVKQDFLRSSLSSQSQKKRFADA
```

gi|4928472 Type 2 peroxiredoxin



Proteins Detected

N	Unu…	Total	%…	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
37	1.72	1.72	93.8	gi|119980	Ferredoxin	BRANA	1			
34	2.00	2.00	92.6	gi|83032224	unknown [Brassica rapa]	Brassica rapa	1			
28	2.00	2.00	91.5	gi|15231702	monodehydroascorbate reductase (NADH)- like…	Arabidopsis thaliana	1			

Protein Group 34 - unknown [Brassica rapa]

Proteins in Group

N	Unu…	Total	Accession #	Name	Specie
34	2.00	2.00	gi|83032224	unknown [Brassica r…	Brassica ra
34	0.00	2.00	gi|4928472	type 2 peroxiredoxin…	Brassica ra
	0.00	2.00	gi|15218877	type 2 peroxiredoxin,…	Arabidopsis

Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass
2.00	99	VILFGVPGAFTPTCSMK	ICAT-C:13C(9)(C)@14 Oxidation(M)@16		0.1046
0.00	< 1	APIAVGDVVPDGSISFFDENDQLQTVSVH…		cleaved M-…	-0.3695
0.00	< 1	AWGKTYPENKHVKFVADGSGEYTHLLGLE…	Oxidation(H)@11	missed K-T…	-0.0163

Protein Sequence Coverage - type 2 peroxiredoxin [Brassica rapa subsp. pekinensis]

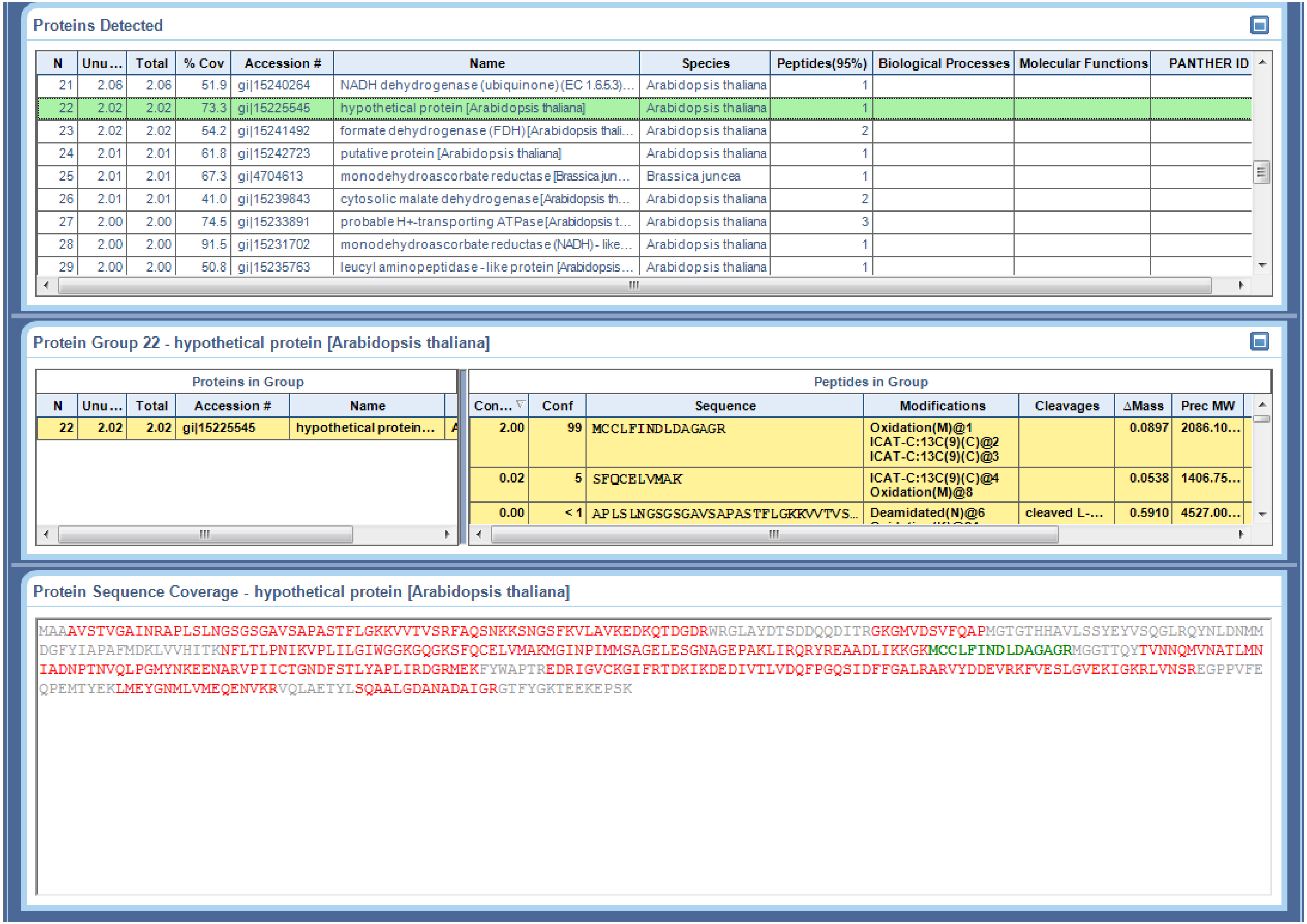
MAPIAVGDVVPDGSISFFDENDQLQTVSVHSLAAGKKVILFGVPGAFTPTCSMKHVPGFIEKAEELKSKGVDEIICFSVNDPFVMKAWGKTYPENKHVKFVADGSGEYTKLLGLELDLKDKGLGVRSR
RFALLIDNLKVTVANVESGGEFTVSSADDILKAL

Fragmentation Evidence

VILFGVPGAFTPTC[C9I]SM[Oxi]K

Residue	b	b+2	y	y+2
V	100.0757	50.5415	2020.0693	1010.5383
I	213.1598	107.0835	1921.0009	961.0041
L	326.2438	163.6255	1807.9168	904.4621
F	473.3122	237.1598	1694.8328	847.9200
G	530.3337	265.6705	1547.7644	774.3858
V	629.4021	315.2047	1490.7429	745.8751
P	726.4549	363.7311	1391.6745	696.3409
G	783.4763	392.2418	1294.6217	647.8145
A	854.5135	427.7604	1237.6002	619.3038
F	1001.5819	501.2946	1166.5631	583.7852
T	1102.6295	551.8184	1019.4947	510.2510
P	1199.6823	600.3448	918.4470	459.7272
T	1300.7300	650.8686	821.3943	411.2008
C[C9I]	1639.8964	820.4518	720.3466	360.6769
S	1726.9284	863.9678	381.1802	191.0938
M[Oxi]	1873.9638	937.4855	294.1482	147.5777
K	2002.0587	1001.5330	147.1128	74.0600

gi|15225545 Hypothetical protein



Proteins Detected

N	Unu…	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
21	2.06	2.06	51.9	gi|15240264	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3)…	Arabidopsis thaliana	1			
22	2.02	2.02	73.3	gi|15225545	hypothetical protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
23	2.02	2.02	54.2	gi|15241492	formate dehydrogenase (FDH) [Arabidopsis thali…	Arabidopsis thaliana	2			
24	2.01	2.01	61.8	gi|15242723	putative protein [Arabidopsis thaliana]	Arabidopsis thaliana	1			
25	2.01	2.01	67.3	gi|4704613	monodehydroascorbate reductase [Brassica jun…	Brassica juncea	1			
26	2.01	2.01	41.0	gi|15239843	cytosolic malate dehydrogenase [Arabidopsis th…	Arabidopsis thaliana	2			
27	2.00	2.00	74.5	gi|15233891	probable H+-transporting ATPase [Arabidopsis t…	Arabidopsis thaliana	3			
28	2.00	2.00	91.5	gi|15231702	monodehydroascorbate reductase (NADH) - like…	Arabidopsis thaliana	1			
29	2.00	2.00	50.8	gi|15235763	leucyl aminopeptidase - like protein [Arabidopsis…	Arabidopsis thaliana	1			

Protein Group 22 - hypothetical protein [Arabidopsis thaliana]

Proteins in Group

N	Unu…	Total	Accession #	Name	
22	2.02	2.02	gi|15225545	hypothetical protein…	A

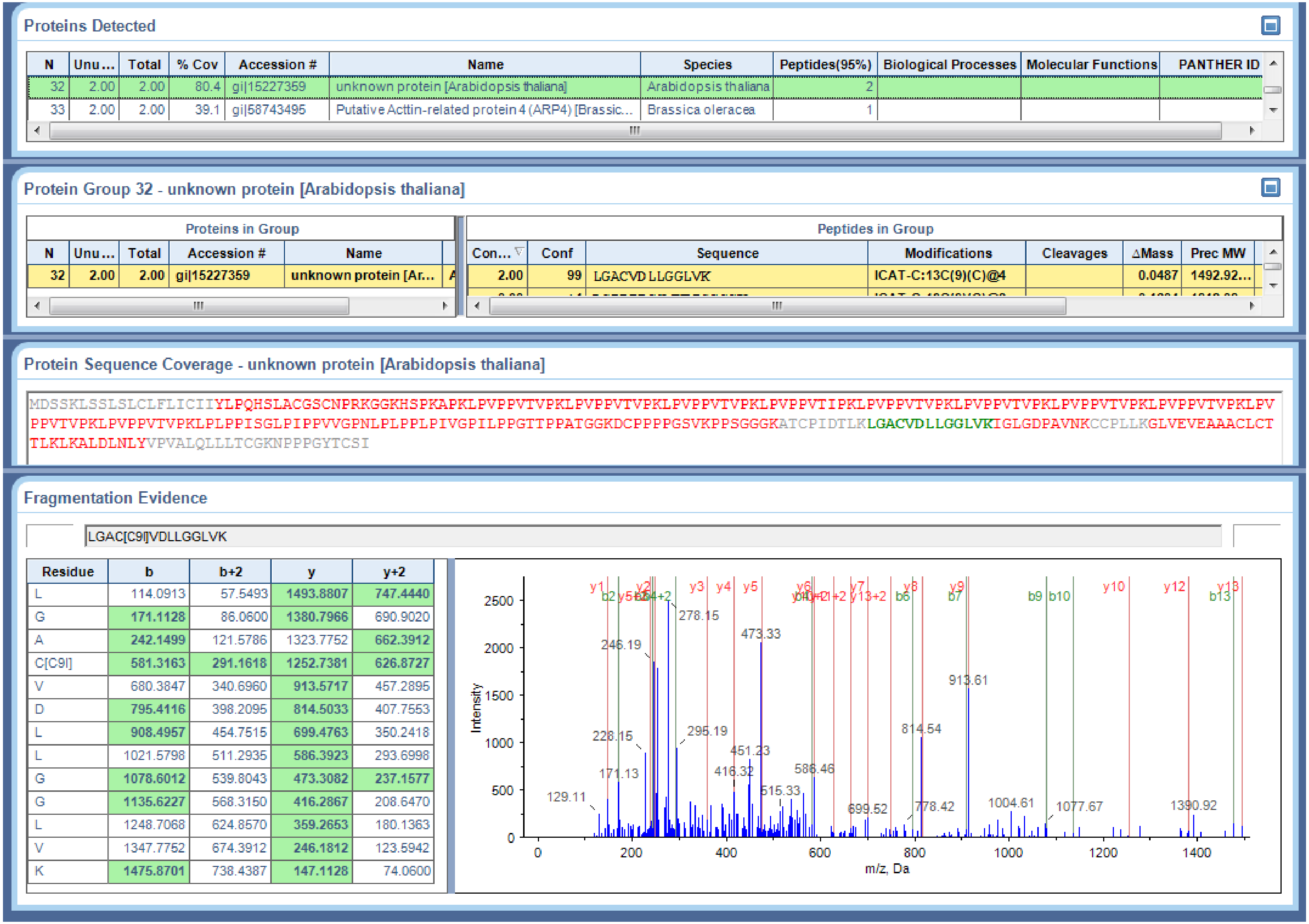
Peptides in Group

Con…	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	MCCLFINDLDAGAGR	Oxidation(M)@1 ICAT-C:13C(9)(C)@2 ICAT-C:13C(9)(C)@3		0.0897	2086.10…
0.02	5	SFQCELVMAK	ICAT-C:13C(9)(C)@4 Oxidation(M)@8		0.0538	1406.75…
0.00	< 1	APLSLNGSGSGAVSAPASTFLGKKVVTVS…	Deamidated(N)@6	cleaved L-…	0.5910	4527.00…

Protein Sequence Coverage - hypothetical protein [Arabidopsis thaliana]

```
MAAAVSTVGAINRAPLSLNGSGSGAVSAPASTFLGKKVVTVSRFAQSNKKSNGSFKVLAVKEDKQTDGDRWRGLAYDTSDDQQDITRGKGMVDSVFQAPMGTGTHHAVLSSYEYVSQGLRQYNLDNMM
DGFYIAPAFMDKLVVHITKNFLTLPNIKVPLILGIWGGKGQGKSFQCELVMAKMGINPIMMSAGELESGNAGEPAKLIRQRYREAADLIKKGKMCCLFINDLDAGAGRMGGTTQYTVNNQMVNATLMN
IADNPTNVQLPGMYNKEENARVPIICTGNDFSTLYAPLIRDGRMEKFYWAPTREDRIGVCKGIFRTDKIKDEDIVTLVDQFPGQSIDFFGALRARVYDDEVRKFVESLGVEKIGKRLVNSREGPPVFE
QPEMTYEKLMEYGNMLVMEQENVKRVQLAETYLSQAALGDANADAIGRGTFYGKTEEKEPSK
```

gi|15227359 Unknown protein



Proteins Detected

N	Unu...	Total	% Cov	Accession #	Name	Species	Peptides(95%)	Biological Processes	Molecular Functions	PANTHER ID
32	2.00	2.00	80.4	gi|15227359	unknown protein [Arabidopsis thaliana]	Arabidopsis thaliana	2			
33	2.00	2.00	39.1	gi|58743495	Putative Actin-related protein 4 (ARP4) [Brassic...	Brassica oleracea	1			

Protein Group 32 - unknown protein [Arabidopsis thaliana]

Proteins in Group

N	Unu...	Total	Accession #	Name
32	**2.00**	**2.00**	**gi|15227359**	**unknown protein [Ar...**

Peptides in Group

Con...	Conf	Sequence	Modifications	Cleavages	ΔMass	Prec MW
2.00	99	LGACVDLLGGLVK	ICAT-C:13C(9)(C)@4		0.0487	1492.92...

Protein Sequence Coverage - unknown protein [Arabidopsis thaliana]

MDSSKLSSLSLCLFLICIIYLPQHSLACGSCNPRKGGKHSPKAPKLPVPPVTVPKLPVPPVTVPKLPVPPVTVPKLPVPPVTIPKLPVPPVTVPKLPVPPVTVPKLPVPPVTVPKLPVPPVTVPKLPV
PPVTVPKLPVPPVTVPKLPLPPISGLPIPPVVGPNLPLPPLPIVGPILPPGTTPPATGGKDCPPPPGSVKPPSGGGKATCPIDTLKLGACVDLLGGLVKIGLGDPAVNKCCPLLKGLVEVEAAACLCT
TLKLKALDLNLYVPVALQLLLTCGKNPPPGYTCSI

Fragmentation Evidence

LGAC[C9I]VDLLGGLVK

Residue	b	b+2	y	y+2
L	114.0913	57.5493	**1493.8807**	**747.4440**
G	**171.1128**	86.0600	**1380.7966**	690.9020
A	**242.1499**	121.5786	1323.7752	**662.3912**
C[C9I]	**581.3163**	**291.1618**	**1252.7381**	**626.8727**
V	680.3847	340.6960	**913.5717**	457.2895
D	**795.4116**	398.2095	**814.5033**	407.7553
L	**908.4957**	454.7515	**699.4763**	350.2418
L	1021.5798	511.2935	**586.3923**	293.6998
G	**1078.6012**	539.8043	**473.3082**	**237.1577**
G	**1135.6227**	568.3150	**416.2867**	208.6470
L	1248.7068	624.8570	**359.2653**	180.1363
V	1347.7752	674.3912	**246.1812**	123.5942
K	**1475.8701**	738.4387	**147.1128**	74.0600

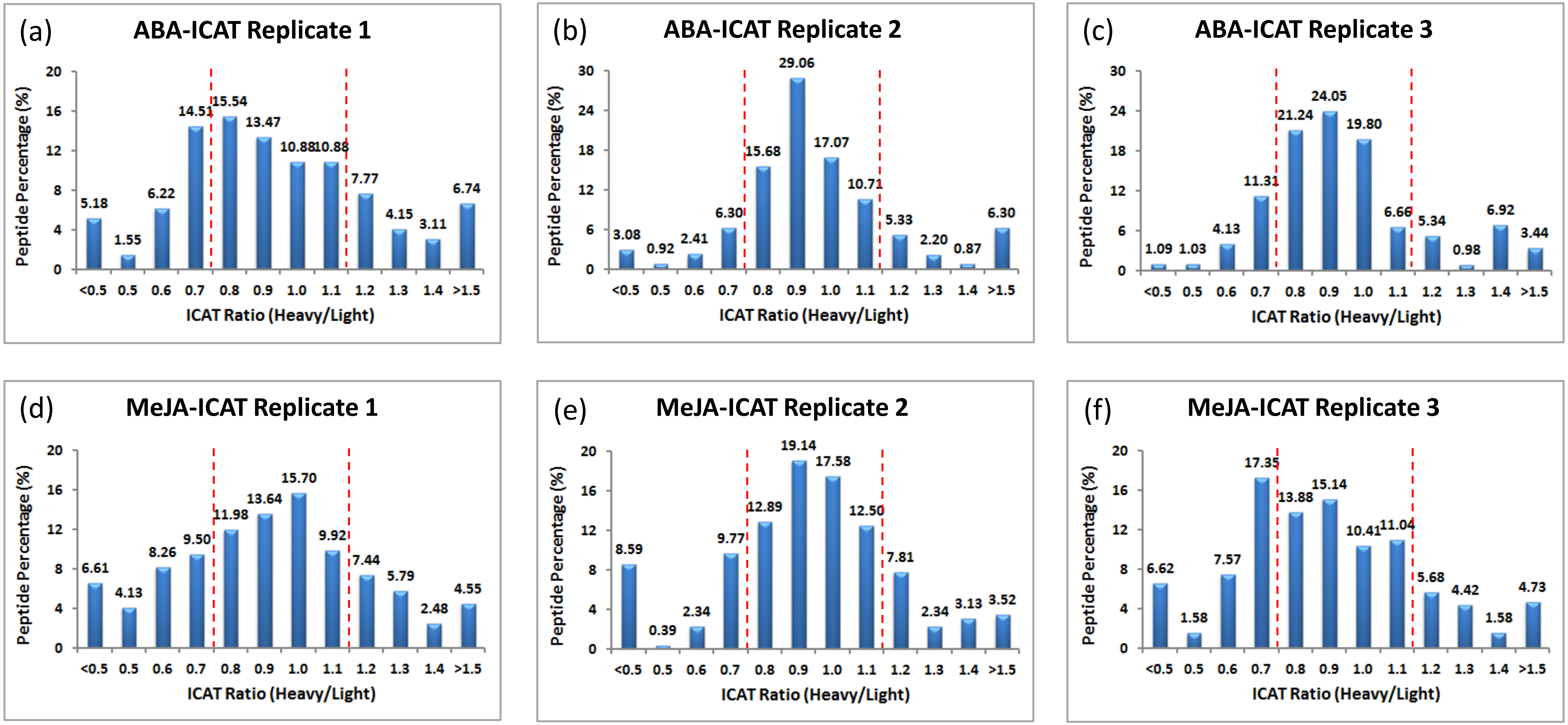


Figure S8. Histogram of measured ICAT ratio distribution of each experiment. (a)-(c) ICAT replicates 1, 2 and 3 of ABA treated guard cells. The overall average of the ABA-ICAT ratio is 1.023 and 71.27% of the peptides fall into the range of 0.8-1.2. (d)-(e) ICAT replicates 1, 2, and 3 of MeJA treated guard cells. The overall average of the MeJA-ICAT ratio is 1.031 and 69.54% of the peptides fall into the range of 0.8-1.2. In all six experiments, the average ICAT ratio is 1.024. Nearly 70% of the ICAT labeled peptides have the ratio within the range of 0.8-1.2. Therefore, a cut-off value of 20% change of the ICAT ion intensity (red dash in figure) was chosen to reflect the genuine quantitative differences.