Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\051111_OGL_BS21_10fracs
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 481 **Hits:** 977
beginning to assemble proteins .... proteins assembled 0.155937 sec
proteins filtered by unique peptides 0.018474 sec
proteins filtered by score
calculated protein coverage maps 0.104152 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.017317 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 28 Proteins listed

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
1	1.1	168	16	281.49	34	2.93e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	165	14	257.91	53	2.93e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	65	9	162.87	24	8.78e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
2	2.1	65	9	162.87	41	8.78e+010	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
3	3.1	47	10	160.39	22	6.95e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
3	3.1	47	10	160.39	49	6.95e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
3	3.2	12	6	97.14	13	1.68e+009	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia seta
3	3.2	12	6	97.14	13	1.68e+009	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02 (
4	4.1	35	8	146.03	11	5.21e+010	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp
4	4.2	5	2	29.53	4	4.10e+009	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase
5	5.1	18	10	132.34	15	1.81e+009	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.1	15	9	112.46	14	1.30e+009	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
5	5.2	20	8	138.41	38	4.30e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.2	9	4	75.50	39	1.03e+009	23858.3	PA_Bse02:2504000230	PA_Bse02:2504000230 BS02DRAFT_00014530 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.2	6	3	48.77	5	7.45e+008	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.2	5	2	34.57	15	7.35e+008	23855.3	PA_Bse02:2503999190	PA_Bse02:2503999190 BS02DRAFT_00027250 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.2	7	2	29.21	7	5.35e+008	38604.4	PA_Bse02:2503998988	PA_Bse02:2503998988 BS02DRAFT_00026880 Cellulose or protein binding domain./Cellulose binding (
6	6.1	9	6	90.95	17	7.87e+008	74714.6	PA_Bse08:2503995453	PA_Bse08:2503995453 BS08DRAFT_00039170 Cellulose or protein binding domain./Cellulose binding (
7	7.1	11	6	78.64	16	1.26e+009	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
8	8.1	4	3	48.52	10	6.20e+008	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (
9	9.1	10	4	45.81	2	1.22e+009	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
9	9.1	10	4	45.81	2	1.22e+009	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
10	10.1	15	3	43.06	47	8.04e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
11	11.1	5	2	33.62	6	7.22e+008	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding dom
11	11.1	5	2	33.62	6	7.22e+008	42082.7	PA_Bse_meta_comb:2073581124	PA_Bse_meta_comb:2073581124 BaSeMet_00247800 Uncharacterized protein conserved in bacteria [B
11	11.2	6	2	28.96	6	9.42e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
12	12.1	6	2	32.34	4	1.06e+008	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolase
12	12.1	6	2	32.34	4	1.06e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase
13	13.1	5	3	31.68	5	3.06e+008	73439.4	PA_Bse08:2503994248	PA_Bse08:2503994248 BS08DRAFT_00028400 Cellulose or protein binding domain./Chitin binding dom
14	14.1	4	2	31.00	9	9.87e+008	40574.0	PA_Bse_meta_comb:2073563645	PA_Bse_meta_comb:2073563645 BaSeMet_00073010 Lysophospholipase L1 and related esterases [Ba
14	14.1	4	2	31.00	9	9.87e+008	40138.6	PA_BS12:2189567930	PA_BS12:2189567930 or1254 Lysophospholipase L1 and related esterases [B. setacea BS12] 387 bp
15	15.1	3	2	30.61	3	1.07e+008	90871.9	PA_Bse08:2503995091	PA_Bse08:2503995091 BS08DRAFT_00035590 Cellulose or protein binding domain./Cellulose binding (
15	15.1	3	2	30.61	3	1.07e+008	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
15	15.1	3	2	30.61	4	1.07e+008	77103.2	PA_Bse_meta_comb:2073565540	PA_Bse_meta_comb:2073565540 BaSeMet_00091960 cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) [
16	16.1	5	2	29.85	8	2.99e+008	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding (

17	17.1	2	2	29.00	4	1.94e+007	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp
17	17.1	2	2	29.00	6	1.94e+007	50621.3	PA_Bse_meta_comb:2073574943	PA_Bse_meta_comb:2073574943 BaSeMet_00185990 Endoglucanase [Bankia setacea microbiome (C
18	18.1	3	2	28.45	7	2.10e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
18	18.1	3	2	28.45	7	2.10e+008	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome
19	19.1	5	2	28.39	7	6.94e+008	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setace
20	20.1	3	2	28.23	9	3.88e+008	43875.0	PA_Bse08:2503995778	PA_Bse08:2503995778 Cellulose or protein binding domain./Cellulase (glycosyl hydrolase family 5). [B.
20	20.2	4	2	27.32	6	3.39e+008	60457.4	PA_BS12:2189569899	PA_BS12:2189569899 or3204 Cellulase (glycosyl hydrolase family 5)./Cellulose or protein binding doma
20	20.2	4	2	27.32	10	3.39e+008	39020.2	PA_Bse_meta_comb:2073558688	PA_Bse_meta_comb:2073558688 BaSeMet_00023440 Cellulase (glycosyl hydrolase family 5). [Bankia
21	21.1	3	2	24.52	7	7.77e+007	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 b
21	21.1	3	2	24.52	8	7.77e+007	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
22	22.1	24	1	20.75	4	1.71e+009	43475.8	PA_BS12:2189567935	PA_BS12:2189567935 or1258 Lysophospholipase L1 and related esterases [B. setacea BS12] 419 bp
22	22.1	24	1	20.75	4	1.71e+009	42177.2	PA_Bse_meta_comb:2073563649	PA_Bse_meta_comb:2073563649 BaSeMet_00073050 Predicted solute binding protein [Bankia setacea
23	23.1	3	2	20.48	10	6.24e+007	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
23	23.1	3	2	20.48	11	6.24e+007	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
Totals:	901	205							

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
1	1.1	168	16	281.49	34	2.93e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.6495.6540.0	3	22.88	15.43	98.1	2.03e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	079-1501.6920.6937.0	3	21.39	15.35	98.4	1.66e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
3	078-1101.6920.6995.0	3	20.94	11.78	99.1	4.33e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
4	079-1501.7330.7437.0	3	20.82	15.68	96.6	1.59e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
5	079-1501.6808.6884.0	3	20.29	20.29	96.3	6.21e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
6	079-1501.9113.9183.5	5	20.12	20.12	90.8	1.70e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
7	079-1501.7628.7678.2	2	19.97	11.43	99.4	1.49e+010	(R)EWQDALVDYMVEK(D)	1625.752
8	079-1501.7474.7616.0	2	19.92	11.39	98.4	2.43e+010	(R)EWQDALVDYMVEK(D)	1625.752
9	080-1601.5233.5317.0	3	19.90	10.13	98.5	3.87e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
10	080-1601.4248.4368.2	2	19.74	19.74	96.2	7.72e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
11	080-1601.8734.8809.0	3	19.72	19.72	94.6	1.20e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
12	078-1101.8007.8100.0	3	19.66	19.66	94.5	1.06e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
13	079-1501.8096.8212.3	3	19.65	12.07	96.3	9.57e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
14	072-0501.5019.5084.0	3	19.31	19.31	88.7	2.81e+006	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
15	080-1601.6722.6804.0	3	19.31	9.57	97.3	1.92e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
16	080-1601.8350.8386.0	3	19.30	14.59	95.8	1.21e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
17	079-1501.7619.7649.2	2	19.23	19.23	96.8	2.39e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
18	079-1501.7861.7988.2	2	19.01	15.88	95.3	1.74e+010	(R)AGWDEHFGYLR(D)	1350.623
19	080-1601.5718.5753.3	3	19.00	10.59	96.2	5.37e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
20	080-1601.9183.9190.0	3	18.90	14.76	86.9	2.52e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
21	078-1101.7915.8040.2	2	18.84	18.84	97.3	1.55e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
22	079-1501.8103.8229.0	2	18.82	18.82	97.0	1.02e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
23	080-1601.7589.7604.2	2	18.68	18.68	96.1	4.60e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
24	078-1101.7663.7777.0	2	18.58	18.58	97.2	5.04e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981

25	078-1101.8049.8172.2	2	18.30	18.30	96.6	1.69e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
26	078-1101.8178.8228.2	2	18.30	18.30	96.7	9.34e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
27	078-1101.7783.7909.2	2	18.24	18.24	95.8	1.18e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
28	078-1101.7294.7325.2	2	18.20	13.19	95.2	8.34e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
29	080-1601.10872.10937.2	2	18.20	14.25	95.9	1.54e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
30	080-1601.8435.8532.0	3	18.16	13.65	92.4	4.35e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
31	080-1601.5615.5734.2	2	18.10	14.85	95.2	4.42e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
32	079-1501.7471.7602.2	2	18.04	14.16	94.2	2.43e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
33	079-1501.9104.9106.0	3	17.89	17.89	78.9	6.68e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
34	080-1601.3876.3885.2	2	17.63	14.55	92.9	3.51e+008	(R)AGWDEHFGYLR(D)	1350.623
35	079-1501.8227.8323.3	3	17.62	10.07	95.1	1.03e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
36	078-1101.8009.8020.0	3	17.61	12.22	90.5	8.31e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
37	079-1501.7338.7438.0	2	17.55	11.73	85.5	9.92e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
38	080-1601.7923.8020.0	3	17.48	12.13	89.4	3.43e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
39	079-1501.7487.7487.2	2	17.40	11.82	89.6	6.25e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
40	079-1501.7735.7852.2	2	17.40	14.31	93.2	9.57e+009	(R)AGWDEHFGYLR(D)	1350.623
41	079-1501.7992.8090.2	2	17.39	17.39	93.2	1.29e+010	(R)AGWDEHFGYLR(D)	1350.623
42	071-0401.5766.5822.2	2	17.34	12.90	90.8	9.74e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
43	071-0401.6536.6573.2	2	17.32	14.26	80.6	1.65e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
44	080-1601.5594.5713.3	3	17.27	7.57	87.6	7.58e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
45	079-1501.7188.7293.3	3	17.17	9.59	91.8	4.53e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
46	072-0501.6523.6535.0	3	17.10	17.10	89.3	2.82e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
47	080-1601.7884.7943.0	2	17.06	11.73	93.6	1.23e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
48	080-1601.8164.8270.3	3	17.02	17.02	88.2	6.55e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
49	080-1601.5744.5754.2	2	16.95	13.81	93.2	1.80e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
50	080-1601.6537.6565.0	3	16.95	10.38	90.3	4.91e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
51	078-1101.8941.8945.0	3	16.82	16.82	79.1	4.36e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
52	079-1501.6871.6871.2	2	16.75	11.83	93.7	4.35e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
53	071-0401.6518.6570.3	3	16.73	16.73	88.9	1.94e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
54	079-1501.8234.8322.2	2	16.67	16.67	94.3	1.02e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
55	080-1601.3707.3744.2	2	16.67	16.67	93.0	8.50e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
56	079-1501.7435.7457.3	3	16.63	9.02	90.6	4.73e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
57	079-1501.7299.7400.3	3	16.62	7.94	90.3	8.37e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
58	079-1501.8190.8276.3	3	16.61	16.61	89.6	2.96e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
59	071-0401.4266.4284.0	3	16.60	8.57	94.4	1.00e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
60	071-0401.5488.5506.0	3	16.53	16.53	86.4	3.78e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
61	079-1501.9847.9876.5	5	16.43	16.43	75.6	2.93e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
62	078-1101.8072.8074.0	2	16.25	13.03	79.0	2.90e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
63	079-1501.7450.7458.2	2	16.14	16.14	92.2	3.05e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
64	078-1101.7434.7438.2	2	16.13	7.89	93.6	7.46e+007	(R)EWQDALVDYMVEK(D)	1625.752
65	080-1601.8273.8343.3	3	15.99	15.99	88.4	7.00e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
66	080-1601.5960.6022.2	2	15.88	12.47	83.9	2.29e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
67	080-1601.7367.7465.3	3	15.87	8.46	87.5	1.91e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
68	078-1101.7106.7192.3	3	15.83	7.97	85.2	1.20e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
69	079-1501.6921.6929.0	3	15.78	11.17	87.3	5.74e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
70	072-0501.6289.6330.0	3	15.69	10.46	82.8	2.99e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
71	080-1601.11332.11344.0	3	15.68	15.68	85.1	7.16e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
72	078-1101.7446.7451.0	3	15.66	10.30	86.7	2.21e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060

73	079-1501.7325.7436.2	2	15.66	15.66	90.7	5.47e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
74	079-1501.9095.9179.4	4	15.66	6.90	88.1	1.80e+009	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
75	072-0501.9918.9918.3	3	15.61	15.61	83.9	1.58e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
76	077-1001.7673.7702.0	3	15.52	7.66	92.2	1.57e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
77	080-1601.8044.8153.0	3	15.52	10.15	89.6	3.31e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
78	079-1501.8002.8002.0	3	15.43	5.39	83.0	2.06e+008	(R)AGWDEHFGYLR(D)	1350.623
79	079-1501.7601.7648.3	3	15.33	7.44	84.2	3.75e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
80	079-1501.8181.8261.0	2	15.31	9.39	65.4	9.48e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
81	072-0501.6623.6659.0	3	15.10	15.10	85.3	2.15e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
82	079-1501.7207.7319.2	2	15.08	11.56	91.9	3.26e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
83	078-1101.7441.7445.2	2	14.97	14.97	86.6	2.35e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
84	071-0401.3713.3743.0	3	14.91	7.39	86.7	7.73e+005	(R)AAEQEMWSHITPGVDR(E)	1826.850
85	078-1101.7063.7085.0	3	14.78	4.53	90.8	2.44e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
86	072-0501.6713.6713.0	3	14.75	14.75	80.4	5.84e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
87	080-1601.7474.7531.2	2	14.72	14.72	72.4	7.00e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
88	080-1601.7586.7592.0	3	14.68	9.31	84.3	8.40e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
89	078-1101.7157.7203.2	2	14.51	14.51	91.4	4.42e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
90	078-1101.7576.7630.2	2	14.50	11.25	80.8	1.53e+009	(R)AGWDEHFGYLR(D)	1350.623
91	071-0401.5212.5212.0	3	14.40	10.00	90.2	5.27e+006	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
92	080-1601.6000.6085.3	3	14.37	8.13	71.1	2.67e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
93	080-1601.3687.3752.3	3	14.31	8.35	82.8	3.41e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
94	080-1601.7271.7276.2	2	14.27	14.27	82.0	4.56e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
95	080-1601.7473.7530.3	3	14.22	8.31	84.6	1.64e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
96	071-0401.6628.6628.0	3	14.14	14.14	71.7	2.67e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
97	079-1501.7029.7029.0	3	14.07	4.21	83.2	1.71e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
98	078-1101.7289.7369.3	3	14.05	8.67	82.0	1.29e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
99	080-1601.7368.7466.2	2	14.03	14.03	71.5	7.70e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
100	080-1601.7695.7766.0	2	14.01	11.00	79.4	1.26e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
101	078-1101.7344.7363.2	2	14.00	14.00	66.6	2.84e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
102	080-1601.6870.6896.0	3	13.93	13.93	81.6	2.31e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
103	079-1501.11324.11324.0	3	13.88	13.88	80.6	8.31e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
104	080-1601.8681.8777.0	3	13.87	13.87	78.5	1.80e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
105	079-1501.5642.5666.0	2	13.86	7.39	94.4	1.13e+006	(R)LDANPPYADADR(E)	1317.608
106	075-0801.7694.7710.0	3	13.75	13.75	76.3	2.19e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
107	079-1501.7025.7071.0	3	13.20	6.07	81.9	1.37e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
108	073-0601.9844.9872.3	3	13.11	7.84	79.4	2.18e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
109	072-0501.9640.9719.3	3	13.03	13.03	80.0	7.92e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
110	080-1601.10990.10990.0	2	13.03	9.99	85.6	1.07e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
111	079-1501.8500.8523.0	3	12.85	12.85	72.7	1.17e+008	(K)ERLVLSPHTYGPSVFVQR(Q)	2085.124
112	071-0401.10123.10123.0	2	12.81	7.92	74.0	3.08e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
113	073-0601.7043.7043.0	3	12.78	12.78	80.0	8.18e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
114	072-0501.5556.5556.0	3	12.74	5.09	82.2	1.37e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
115	079-1501.10819.10819.2	2	12.48	12.48	79.4	2.61e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
116	073-0601.10007.10007.0	3	12.42	8.04	81.7	9.68e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
117	071-0401.6622.6622.0	3	12.32	9.04	73.3	3.52e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
118	072-0501.6725.6725.0	3	12.29	12.29	96.3	5.62e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
119	080-1601.10920.10920.0	3	12.16	8.13	86.6	4.50e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
120	072-0501.6665.6665.0	3	12.12	12.12	71.7	9.00e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

121	079-1501.4672.4695.0	2	12.03	5.39	81.4	4.69e+005	(R)VDSQGNITK(N)	961.495
122	079-1501.6616.6631.2	2	11.55	4.61	87.6	8.55e+006	(K)NGSVFPVR(C)	875.474
123	080-1601.4081.4081.0	2	11.48	11.48	80.0	8.36e+006	(R)AGWDEHFGYLR(D)	1350.623
124	079-1501.10834.10854.2	2	11.33	5.87	82.3	1.93e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
125	072-0501.6507.6507.0	3	11.31	7.19	86.4	4.35e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
126	079-1501.11035.11035.0	2	11.16	7.45	77.6	9.28e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
127	072-0501.9990.9990.0	3	11.06	4.25	74.4	1.57e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
128	071-0401.10032.10105.2	2	11.03	11.03	64.2	5.83e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
129	080-1601.10843.10843.0	2	10.93	10.93	77.0	9.53e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
130	073-0601.9803.9803.2	2	10.73	10.73	73.3	2.30e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
131	071-0401.8615.8615.0	3	10.56	6.41	74.0	5.60e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
132	080-1601.10760.10760.0	2	10.55	10.55	75.0	8.15e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
133	076-0901.7551.7551.0	2	10.51	10.51	63.0	2.25e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
134	078-1101.8375.8380.0	3	10.44	10.44	75.8	1.71e+009	(K)ERLVLSPHTYGPSVFVQR(Q)	2085.124
135	072-0501.5062.5062.0	3	10.42	10.42	86.6	2.61e+006	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
136	073-0601.10150.10150.2	2	10.27	10.27	67.9	5.06e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
137	080-1601.5229.5229.0	3	10.16	10.16	71.0	2.89e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
138	073-0601.9921.9958.2	2	10.08	10.08	65.3	3.83e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
139	072-0501.6582.6582.2	2	10.05	10.05	82.6	2.34e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
140	073-0601.10206.10206.0	2	10.05	3.94	73.4	1.85e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
141	080-1601.3887.3891.1	1	9.99	4.04	85.2	1.87e+008	(R)AGWDEHFGYLR(D)	1350.623
142	078-1101.7050.7065.2	2	9.94	9.94	80.9	6.53e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
143	079-1501.10916.10916.2	2	9.82	9.82	87.8	1.05e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
144	077-1001.7679.7679.0	2	9.80	9.80	63.9	1.51e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
145	079-1501.8286.8286.0	3	9.78	9.78	94.5	1.48e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
146	080-1601.6846.6900.2	2	9.72	9.72	80.2	2.53e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
147	079-1501.11041.11041.2	2	9.61	6.17	70.6	8.88e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
148	071-0401.10099.10099.0	2	9.56	9.56	69.7	3.27e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
149	072-0501.9942.9948.0	2	9.43	9.43	61.3	5.02e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
150	072-0501.8366.8366.0	3	9.39	3.20	72.9	4.68e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
151	080-1601.8070.8070.2	2	9.33	5.25	86.9	8.66e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
152	080-1601.5966.5966.2	2	9.32	9.32	74.5	1.25e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
153	079-1501.10825.10825.2	2	9.23	9.23	68.0	2.11e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
154	079-1501.10955.10955.2	2	9.06	9.06	71.0	7.64e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
155	080-1601.4046.4046.0	2	9.06	9.06	75.1	1.48e+007	(R)AGWDEHFGYLR(D)	1350.623
156	080-1601.10946.10946.0	2	9.04	9.04	68.3	8.77e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
157	071-0401.10197.10197.0	2	8.94	8.94	69.0	2.43e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
158	080-1601.11014.11014.0	2	8.91	8.91	68.8	9.81e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
159	072-0501.9760.9820.2	2	8.39	8.39	64.9	7.24e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
160	072-0501.6695.6695.0	3	8.21	8.21	80.0	6.43e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
161	080-1601.11347.11347.0	2	8.11	8.11	68.5	3.61e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
162	079-1501.4574.4647.0	2	7.81	2.68	95.4	6.05e+005	(R)VDSQGNITK(N)	961.495
163	071-0401.9896.9896.0	2	7.67	7.67	77.2	3.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
164	073-0601.9938.9938.2	2	7.57	2.81	69.8	2.48e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
165	073-0601.10231.10231.0	2	7.31	4.22	73.4	1.84e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
166	072-0501.6557.6557.2	2	7.19	7.19	72.2	2.21e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
167	080-1601.10855.10855.0	2	6.24	6.24	62.9	1.14e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
168	074-0701.10835.10835.0	2	6.02	2.50	66.7	1.98e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
2	2.1	65	9	162.87	24	8.78e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.9058.9160.3	3	22.80	17.01	97.8	2.14e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
2	080-1601.8700.8744.2	2	21.47	14.29	99.1	3.85e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
3	079-1501.6948.6951.0	3	21.33	11.19	97.3	1.82e+008	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
4	080-1601.3159.3192.0	3	21.18	9.57	98.1	4.94e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
5	078-1101.8850.8856.0	3	20.42	15.20	92.2	2.49e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
6	080-1601.8696.8748.0	3	20.35	20.35	92.5	2.05e+009	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
7	080-1601.9065.9148.2	2	20.27	20.27	96.3	1.09e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
8	080-1601.3883.3905.3	3	19.92	14.37	98.7	4.77e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
9	074-0701.8782.8799.2	2	19.67	19.67	95.5	2.41e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
10	078-1101.8730.8845.0	2	19.40	10.96	76.4	1.69e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
11	079-1501.8541.8545.2	2	19.38	13.13	96.5	1.55e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
12	073-0601.7794.7847.0	3	19.26	9.01	89.7	1.93e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
13	078-1101.7003.7032.2	2	19.00	19.00	83.4	5.73e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
14	079-1501.8908.8968.3	3	18.84	14.27	87.7	9.97e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
15	079-1501.8818.8928.2	2	18.37	10.42	75.0	1.10e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
16	080-1601.9130.9149.2	2	18.30	9.26	93.4	2.49e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
17	078-1101.8859.8864.2	2	17.61	17.61	93.7	1.61e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
18	080-1601.9019.9121.2	2	17.32	9.55	75.4	4.88e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
19	077-1001.8478.8519.2	2	17.18	10.33	69.4	9.97e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
20	079-1501.6626.6636.2	2	16.82	8.89	95.7	3.07e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
21	079-1501.8204.8210.3	3	16.82	12.16	91.3	1.47e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
22	078-1101.7054.7060.0	3	16.56	16.56	85.1	2.77e+008	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
23	079-1501.6649.6673.3	3	16.39	11.86	93.0	9.44e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
24	080-1601.8759.8759.4	4	16.31	12.92	97.7	2.43e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
25	078-1101.7943.7996.2	2	16.29	10.59	90.5	7.98e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
26	078-1101.7902.8005.3	3	16.21	10.08	93.0	6.76e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
27	073-0601.7326.7326.0	3	15.93	15.93	75.4	5.14e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
28	078-1101.6661.6680.2	2	15.90	7.61	92.0	3.64e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
29	072-0501.7373.7375.3	3	15.81	9.16	83.8	1.27e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
30	079-1501.8189.8231.2	2	15.75	10.13	89.4	3.05e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
31	079-1501.8914.8944.2	2	15.74	15.74	88.4	7.16e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
32	073-0601.7799.7799.0	3	15.66	8.59	88.5	1.06e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
33	076-0901.8757.8764.2	2	15.40	15.40	90.5	1.49e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
34	080-1601.3762.3777.0	3	15.34	8.53	80.1	1.58e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
35	078-1101.8854.8854.0	2	15.28	9.38	71.8	1.13e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
36	080-1601.6201.6294.2	2	15.26	9.80	89.4	3.75e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
37	079-1501.8065.8191.3	3	15.25	8.95	90.2	2.57e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
38	080-1601.8091.8152.0	3	15.21	9.24	89.9	2.04e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
39	080-1601.8135.8180.2	2	15.20	9.66	87.7	1.46e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
40	073-0601.7873.7873.2	2	14.94	14.94	84.9	6.15e+006	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163

41	078-1101.8761.8761.3	3	14.93	14.93	79.0	2.95e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
42	072-0501.7344.7344.2	2	14.85	14.85	83.1	3.54e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
43	080-1601.6295.6300.3	3	14.45	11.10	88.9	1.82e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
44	079-1501.8061.8177.2	2	14.22	8.99	88.2	3.97e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
45	071-0401.7332.7380.3	3	14.15	9.39	75.8	3.28e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
46	080-1601.9028.9102.3	3	14.08	14.08	74.3	1.28e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
47	080-1601.3889.3895.0	2	13.94	7.23	87.3	5.37e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
48	077-1001.8473.8534.2	2	13.83	7.56	68.5	1.01e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
49	080-1601.3962.4041.2	2	13.80	10.75	84.6	4.89e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
50	080-1601.6200.6289.3	3	13.71	7.01	79.9	2.14e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
51	076-0901.8750.8750.0	3	13.69	6.84	78.2	2.48e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
52	071-0401.7426.7426.0	3	13.19	9.23	78.5	4.33e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
53	080-1601.6299.6360.2	2	13.13	8.26	85.6	2.99e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
54	072-0501.7349.7349.2	2	13.07	13.07	83.5	4.03e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
55	071-0401.7333.7376.2	2	12.56	12.56	76.2	1.25e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
56	078-1101.8447.8462.2	2	12.52	8.73	75.4	1.21e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
57	074-0701.8786.8786.0	3	11.62	11.62	71.9	3.86e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
58	080-1601.3178.3178.2	2	11.00	11.00	100.0	4.76e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
59	080-1601.3183.3183.2	2	10.82	10.82	73.8	4.12e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
60	080-1601.9016.9016.0	2	10.76	10.76	67.6	1.64e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
61	080-1601.3423.3423.0	2	8.75	2.93	92.6	8.40e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
62	080-1601.3579.3579.0	3	8.06	8.06	76.3	2.01e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
63	078-1101.7088.7088.2	2	7.75	4.74	74.4	8.81e+006	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
64	079-1501.6065.6065.0	2	7.75	1.97	100.0	2.70e+005	(R)IADGGFQR(Y)	863.438
65	078-1101.7105.7105.2	2	6.78	6.78	85.7	8.74e+006	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.1	47	10	160.39	22	6.95e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	079-1501.8315.8332.2	2	20.17	20.17	95.5	4.65e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
2	079-1501.6869.6896.2	2	19.79	19.79	96.5	1.19e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
3	079-1501.7143.7215.3	3	19.05	10.97	92.6	6.18e+008	(R)MIDVLQQTSGHNLDASR(I)	1884.924
4	078-1101.6999.7019.2	2	18.85	10.02	91.9	1.26e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
5	080-1601.4638.4705.2	2	18.77	18.77	96.3	2.66e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
6	080-1601.4751.4810.2	2	18.53	7.75	89.3	1.36e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
7	078-1101.8236.8236.0	3	18.01	10.05	88.6	1.03e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
8	080-1601.4619.4622.2	2	17.71	17.71	89.7	1.89e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
9	080-1601.6365.6435.2	2	17.67	17.67	94.5	4.06e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
10	079-1501.8299.8326.3	3	17.59	10.87	89.7	5.36e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
11	079-1501.7153.7231.2	2	17.48	17.48	87.3	3.24e+008	(R)MIDVLQQTSGHNLDASR(I)	1884.924
12	080-1601.6395.6444.0	3	17.43	12.80	91.3	1.44e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
13	080-1601.6515.6566.2	2	17.37	9.80	92.5	2.44e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
14	079-1501.7034.7038.0	3	16.78	5.70	86.6	2.15e+008	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952

15	078-1101.7148.7148.3	3	16.67	4.40	82.1	2.77e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
16	080-1601.4594.4661.3	3	16.47	9.90	87.7	9.91e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
17	079-1501.6967.6973.2	2	16.28	8.59	88.8	3.82e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
18	080-1601.3469.3493.2	2	15.56	10.39	94.2	1.92e+007	(K)GAIVVGAFDER(I)	1133.595
19	078-1101.6797.6803.2	2	15.54	8.09	93.7	2.35e+007	(K)GAIVVGAFDER(I)	1133.595
20	080-1601.6522.6522.0	3	15.37	15.37	83.0	1.36e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
21	080-1601.6531.6531.2	2	15.33	7.27	90.2	1.53e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
22	079-1501.6762.6768.0	2	15.06	6.05	94.0	4.24e+007	(K)GAIVVGAFDER(I)	1133.595
23	080-1601.6315.6373.0	2	14.91	8.68	94.4	1.69e+008	(R)WIPWNTPILQ(-)	1267.684
24	079-1501.7242.7361.0	2	14.90	9.88	94.4	1.27e+009	(R)WIPWNTPILQ(-)	1267.684
25	071-0401.5754.5754.0	3	14.79	10.22	83.2	5.47e+006	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
26	078-1101.7278.7283.0	2	14.70	10.03	91.6	1.52e+008	(R)WIPWNTPILQ(-)	1267.684
27	079-1501.7369.7404.0	2	14.41	8.11	94.2	9.16e+008	(R)WIPWNTPILQ(-)	1267.684
28	078-1101.6998.7057.3	3	14.18	4.80	87.6	9.91e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
29	080-1601.3383.3433.2	2	14.02	7.46	92.5	1.70e+007	(K)GAIVVGAFDER(I)	1133.595
30	079-1501.7047.7053.0	2	13.93	13.93	83.0	7.77e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
31	079-1501.6868.6930.3	3	13.18	13.18	75.8	2.63e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
32	071-0401.4573.4602.3	3	13.15	13.15	75.2	6.88e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
33	080-1601.4742.4742.0	2	12.25	3.67	85.6	9.96e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
34	072-0501.4631.4631.0	3	11.98	11.98	70.6	2.91e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
35	080-1601.6419.6419.0	2	11.75	8.16	88.8	2.02e+007	(R)WIPWNTPILQ(-)	1267.684
36	080-1601.3319.3325.0	3	11.60	2.48	83.2	4.68e+006	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
37	080-1601.6519.6519.0	2	11.20	2.59	82.6	1.42e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
38	078-1101.7332.7332.2	2	10.89	10.89	67.1	1.95e+007	(R)NGKGAIVVGAFDER(I)	1432.755
39	072-0501.5759.5759.0	3	10.59	3.70	83.0	2.84e+006	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
40	080-1601.3160.3160.2	2	10.00	10.00	100.0	1.08e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
41	072-0501.5765.5765.0	3	9.78	6.44	95.6	3.04e+006	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
42	080-1601.6330.6332.0	3	9.73	9.73	72.1	5.35e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
43	078-1101.7049.7049.0	3	9.38	5.01	71.4	8.96e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
44	071-0401.5369.5369.0	3	8.95	8.95	79.4	6.65e+006	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
45	080-1601.3155.3155.2	2	7.92	7.92	82.2	1.08e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
46	080-1601.3665.3665.2	2	7.64	7.64	69.7	2.49e+006	(K)GAIVVGAFDER(I)	1133.595
47	071-0401.4590.4590.2	2	6.01	6.01	73.9	2.33e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.2	12	6	97.14	13	1.68e+009	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia set

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	079-1501.8315.8332.2	2	20.17	20.17	95.5	4.65e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
2	080-1601.7775.7839.0	3	19.88	19.88	82.2	6.49e+007	(R)DGGSDPVALMSMVNYVQSNYNVDANR(I)	2816.262
3	078-1101.7427.7450.0	3	19.04	10.95	88.9	1.89e+008	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
4	078-1101.8236.8236.0	3	18.01	10.05	88.6	1.03e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
5	080-1601.4619.4622.2	2	17.71	17.71	89.7	1.89e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
6	079-1501.8299.8326.3	3	17.59	10.87	89.7	5.36e+008	(K)LPVDNHELLGMVAPR(G)	1660.884

7	080-1601.4893.4908.0	3	17.42	10.37	84.0	6.33e+007	(R)IQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
8	080-1601.4594.4661.3	3	16.47	9.90	87.7	9.91e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
9	080-1601.5066.5110.0	3	14.33	8.04	73.3	1.06e+008	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
10	080-1601.7588.7602.0	3	13.04	13.04	72.2	2.57e+007	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
11	080-1601.3674.3674.0	3	11.68	6.95	82.5	4.87e+006	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271
12	071-0401.5369.5369.0	3	8.95	8.95	79.4	6.65e+006	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.1	35	8	146.03	11	5.21e+010	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	079-1501.6513.6538.2	2	21.94	15.33	98.9	5.57e+006	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
2	080-1601.8489.8574.3	3	21.80	15.23	97.4	1.22e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
3	079-1501.8427.8481.2	2	21.14	12.44	95.1	7.20e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
4	079-1501.7108.7113.0	2	20.72	20.72	96.1	4.78e+008	(R)SDFGQYWDQITLENK(G)	1843.850
5	078-1101.7199.7231.2	2	20.40	20.40	98.7	3.17e+008	(R)SDFGQYWDQITLENK(G)	1843.850
6	080-1601.5988.6055.3	3	20.14	11.73	95.1	1.16e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
7	080-1601.6671.6727.2	2	20.12	12.40	94.4	1.17e+010	(R)IAALGLPIYISEYDIEK(T)	1908.037
8	079-1501.7217.7217.2	2	19.40	19.40	92.4	7.91e+008	(R)SDFGQYWDQITLENK(G)	1843.850
9	078-1101.8314.8341.2	2	19.10	11.43	93.6	7.93e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
10	080-1601.6556.6666.2	2	19.10	11.39	93.7	1.45e+010	(R)IAALGLPIYISEYDIEK(T)	1908.037
11	080-1601.8446.8499.2	2	19.08	10.43	93.2	2.04e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
12	080-1601.5195.5234.3	3	18.27	18.27	90.1	6.76e+007	(R)SDFGQYWDQITLENK(G)	1843.850
13	080-1601.5176.5182.0	2	18.00	18.00	92.4	4.17e+008	(R)SDFGQYWDQITLENK(G)	1843.850
14	079-1501.7481.7510.0	3	17.20	8.64	88.4	4.26e+008	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
15	078-1101.8324.8324.3	3	16.63	7.85	89.9	1.38e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
16	079-1501.7134.7210.3	3	16.43	16.43	85.8	3.05e+008	(R)SDFGQYWDQITLENK(G)	1843.850
17	079-1501.8420.8483.3	3	15.93	6.16	82.0	1.20e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
18	079-1501.8507.8509.2	2	15.43	15.43	90.7	9.93e+007	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
19	080-1601.6728.6728.3	3	15.32	5.44	88.4	6.71e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
20	080-1601.8518.8536.2	2	14.93	14.93	89.8	1.11e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
21	080-1601.4052.4061.0	2	14.90	6.81	91.8	9.18e+006	(K)AAEIEEWIR(D)	1116.569
22	079-1501.8494.8497.0	3	14.84	7.76	83.0	4.44e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
23	080-1601.6588.6710.3	3	14.63	5.43	81.6	2.65e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
24	080-1601.4654.4660.0	3	14.57	14.57	71.8	3.66e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
25	080-1601.8465.8501.3	3	14.57	5.22	87.0	4.10e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
26	078-1101.7406.7439.2	2	14.41	8.87	89.8	4.12e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
27	078-1101.8910.8931.0	3	14.26	7.93	81.3	6.51e+008	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352
28	079-1501.6266.6285.0	2	14.07	4.77	91.8	1.80e+006	(K)WAQVEPQR(D)	1013.517
29	080-1601.6966.6985.0	2	13.89	13.89	77.4	2.29e+007	(R)SDFGQYWDQITLENK(G)	1843.850
30	080-1601.6002.6056.2	2	13.75	9.04	85.7	1.68e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
31	079-1501.8967.9083.0	3	13.37	4.82	73.3	2.86e+009	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352
32	079-1501.6161.6194.2	2	13.21	5.93	90.4	1.24e+006	(K)WAQVEPQR(D)	1013.517
33	078-1101.7381.7469.0	3	12.45	12.45	76.2	7.71e+008	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
34	080-1601.9063.9084.0	3	11.28	6.88	70.6	3.26e+008	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352

35	079-1501.9008.9008.2	2	7.93	4.01	75.2	1.60e+008	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.2	5	2	29.53	4	4.10e+009	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase family 10./

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.6554.6576.2	2	15.27	11.77	92.7	1.09e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888
2	078-1101.8910.8931.0	3	14.26	7.93	81.3	6.51e+008	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352
3	079-1501.8967.9083.0	3	13.37	4.82	73.3	2.86e+009	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352
4	080-1601.9063.9084.0	3	11.28	6.88	70.6	3.26e+008	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352
5	079-1501.9008.9008.2	2	7.93	4.01	75.2	1.60e+008	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
5	5.1	18	10	132.34	15	1.81e+009	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.8754.8819.2	2	19.88	19.88	97.6	2.06e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
2	080-1601.8765.8788.3	3	19.21	9.76	94.3	1.05e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
3	079-1501.8567.8599.2	2	18.21	14.91	93.9	2.03e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
4	080-1601.5478.5478.0	3	18.21	14.02	88.4	8.54e+007	(R)GQEDYVIINIANEPVGNNQPSSMWINDHR(S)	3310.555
5	079-1501.7414.7459.0	2	15.64	10.56	92.0	4.44e+008	(R)GLPSNIGMLIDTGR(N)	1443.763
6	080-1601.4641.4656.0	3	15.19	15.19	85.0	7.74e+007	(R)NGWGGPGRPTAVSTSTDLETYINESR(L)	2765.313
7	080-1601.5153.5187.0	2	14.52	10.35	89.1	6.07e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
8	080-1601.3778.3789.2	2	13.33	9.44	88.7	8.23e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
9	079-1501.6774.6780.2	2	12.79	8.87	88.2	1.98e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
10	079-1501.9205.9213.0	2	12.46	6.69	78.2	7.36e+007	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
11	078-1101.7328.7349.0	2	12.15	7.22	80.9	3.91e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
12	080-1601.2775.2802.2	2	11.49	11.49	73.2	4.20e+006	(R)HSLIELGR(L)	924.527
13	071-0401.7526.7526.0	3	11.38	11.38	74.4	7.31e+006	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
14	080-1601.7235.7235.0	3	10.12	10.12	71.2	3.06e+007	(R)NGWGGPGRPTAVSTSTDLETYINESR(L)	2765.313
15	079-1501.7516.7542.0	2	10.06	10.06	66.5	4.06e+008	(R)HSLIELGR(L)	924.527
16	080-1601.7244.7244.0	2	9.31	3.60	67.8	7.06e+006	(R)GLPSNIGMLIDTGR(N)	1443.763
17	078-1101.7361.7366.0	2	7.76	2.76	77.6	3.08e+007	(R)WFPEAFR(V)	952.468
18	080-1601.2694.2694.2	2	7.00	3.01	100.0	1.12e+006	(R)VVLSNGDQWTR(N)	1274.649

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
5	5.2	20	8	138.41	38	4.30e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [I

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.5977.6015.2	2	21.37	21.37	97.7	1.35e+008	(R)YQNEYIAGITEIIGDSK(Y)	1913.950
2	080-1601.6812.6864.0	3	19.56	19.56	88.2	2.06e+007	(K)GANSIAGFASNSANYTPVTEPYLQDPNLQVGGNPIR(S)	3732.826
3	079-1501.9309.9368.0	2	19.50	10.44	100.0	2.14e+009	(R)WFPEAFQTLLENAYPPL(-)	2036.017
4	080-1601.5831.5897.2	2	17.99	17.99	95.1	3.06e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
5	079-1501.8279.8310.2	2	17.06	17.06	91.4	3.77e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
6	071-0401.7785.7785.2	2	16.58	16.58	89.3	6.75e+006	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
7	080-1601.7286.7363.2	2	15.88	15.88	86.7	1.13e+008	(K)IAYESTFVWMDR(I)	1517.710
8	080-1601.9425.9442.2	2	15.42	15.42	84.6	4.25e+007	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
9	080-1601.7381.7477.2	2	15.35	15.35	86.1	2.01e+008	(K)IAYESTFVWMDR(I)	1517.710
10	080-1601.5119.5122.2	2	15.34	15.34	85.9	6.83e+007	(K)IAYESTFVWMDR(I)	1517.710
11	080-1601.3409.3409.0	3	14.20	8.65	80.3	9.33e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
12	080-1601.3778.3789.2	2	13.33	9.44	88.7	8.23e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
13	080-1601.6839.6839.0	3	13.33	13.33	74.2	1.45e+007	(K)GANSIAGFASNSANYTPVTEPYLQDPNLQVGGNPIR(S)	3732.826
14	080-1601.7624.7631.2	2	13.10	13.10	82.7	2.84e+007	(K)IAYESTFVWMDR(I)	1517.710
15	079-1501.6774.6780.2	2	12.79	8.87	88.2	1.98e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
16	078-1101.9204.9209.0	2	11.97	6.00	62.2	5.50e+008	(R)WFPEAFQTLLENAYPPL(-)	2036.017
17	077-1001.8905.8905.0	3	11.74	7.21	78.0	2.93e+007	(R)WFPEAFQTLLENAYPPL(-)	2036.017
18								