Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\092012_OGL_TotalCaecum090712_Triplicate_FASP
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 336 **Hits:** 1110
beginning to assemble proteins .... proteins assembled 0.181136 sec
proteins filtered by unique peptides 0.014608 sec
proteins filtered by score
calculated protein coverage maps 0.056486 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.006867 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 17 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	145	11	197.88	32	5.18e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding
1	1.1	145	11	197.88	53	5.18e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (C
2	2.1	77	8	133.56	20	5.42e+011	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 b
2	2.1	77	8	133.56	34	5.42e+011	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
2	2.2	39	4	73.39	16	3.78e+010	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
2	2.2	36	3	57.02	4	3.62e+010	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
2	2.2	30	3	52.18	19	3.67e+010	23858.3	PA_Bse02:2504000230	PA_Bse02:2504000230 BS02DRAFT_00014530 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
2	2.2	27	2	35.81	3	3.51e+010	77060.3	PA_BS12:2189570194	PA_BS12:2189570194 or3425 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 730 b
2	2.2	27	2	35.81	4	3.51e+010	59632.4	PA_Bse_meta_comb:2073585294	PA_Bse_meta_comb:2073585294 BaSeMet_00289500 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
2	2.2	27	2	35.81	11	3.51e+010	23855.3	PA_Bse02:2503999190	PA_Bse02:2503999190 BS02DRAFT_00027250 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
2	2.3	27	2	34.35	15	3.26e+010	23418.9	PA_Bse_meta_comb:2073570681	PA_Bse_meta_comb:2073570681 BaSeMet_00143370 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
2	2.4	27	2	31.70	3	3.23e+010	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolas
2	2.4	27	2	31.70	3	3.23e+010	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
3	3.1	21	4	68.61	23	9.64e+009	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
3	3.1	21	4	68.61	24	9.64e+009	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
4	4.1	9	4	55.27	9	7.24e+009	72837.7	PA_BS12:2189569651	PA_BS12:2189569651 or2957 Glycosyl hydrolase family 53./Cellulose or protein binding domain. [B. set
4	4.1	9	4	55.27	14	7.24e+009	49401.7	PA_Bse_meta_comb:2073560554	PA_Bse_meta_comb:2073560554 BaSeMet_00042100 Arabinogalactan endo-1,4-beta-galactosidase [B
5	5.1	9	3	45.93	6	1.05e+010	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
5	5.1	9	3	45.93	6	1.05e+010	77103.2	PA_Bse_meta_comb:2073565540	PA_Bse_meta_comb:2073565540 BaSeMet_00091960 cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) [
5	5.1	6	2	33.86	3	1.03e+010	90871.9	PA_Bse08:2503995091	PA_Bse08:2503995091 BS08DRAFT_00035590 Cellulose or protein binding domain./Cellulose binding
5	5.2	5	2	32.25	4	1.25e+009	87140.5	PA_Bse02:2503999088	PA_Bse02:2503999088 BS02DRAFT_00000960 Cellulose or protein binding domain./Glycosyl hydrolas
6	6.1	7	3	44.72	12	1.59e+009	52143.8	PA_BS12:2189568458	PA_BS12:2189568458 or1762 Glycosyl hydrolase family 45./Cellulose or protein binding domain./Cellulo
6	6.1	7	3	44.72	12	1.59e+009	52143.8	PA_Bse_meta_comb:2073579483	PA_Bse_meta_comb:2073579483 BaSeMet_00231390 Glycosyl hydrolase family 45./Cellulose or protei
7	7.1	8	3	40.45	11	1.09e+009	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding dom
7	7.1	8	3	40.45	11	1.09e+009	42082.7	PA_Bse_meta_comb:2073581124	PA_Bse_meta_comb:2073581124 BaSeMet_00247800 Uncharacterized protein conserved in bacteria [B
7	7.2	12	2	31.59	6	3.88e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
7	7.2	12	2	31.59	6	3.88e+008	39870.6	PA_Bse_meta_comb:2073593369	PA_Bse_meta_comb:2073593369 BaSeMet_00370250 Uncharacterized protein conserved in bacteria [B
8	8.1	6	3	39.90	9	1.72e+009	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
8	8.1	6	3	39.90	9	1.72e+009	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome
9	9.1	13	2	38.12	8	4.28e+009	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 b
9	9.1	13	2	38.12	9	4.28e+009	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
10	10.1	3	2	25.38	7	1.60e+009	72721.8	PA_BS12:2189568163	PA_BS12:2189568163 or1494 Arabinogalactan endo-1,4-beta-galactosidase [B. setacea BS12] 679 bp
10	10.1	3	2	25.38	8	1.60e+009	69866.3	PA_Bse_meta_comb:2073566948	PA_Bse_meta_comb:2073566948 BaSeMet_00106040 Arabinogalactan endo-1,4-beta-galactosidase [B
11	11.1	3	2	22.78	6	7.90e+008	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding
12	12.1	2	2	22.39	3	1.57e+008	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp

12	12.1	2	2	22.39	8	1.57e+008	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
Totals:	905	122							

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	145	11	197.88	32	5.18e+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	067-0702.4400.4485.3	3	21.64	13.27	89.8	6.92e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
2	067-0301.4420.4440.3	3	21.40	9.05	96.7	3.79e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
3	067-0701.4409.4488.0	3	21.20	11.57	90.8	4.58e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
4	067-0301.4560.4669.2	2	20.40	12.92	98.0	1.83e+010	(R)EWQDALVDYMVEK(D)	1625.752
5	067-0301.4689.4780.2	2	19.91	12.24	98.2	1.06e+010	(R)EWQDALVDYMVEK(D)	1625.752
6	067-0701.4790.4887.2	2	19.73	16.38	96.6	2.01e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.059
7	067-0701.4268.4383.0	3	19.56	8.10	86.7	9.10e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
8	067-0702.4782.4867.2	2	19.27	19.27	97.2	1.84e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.059
9	067-0301.4378.4437.3	3	19.09	12.78	91.4	2.22e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
10	067-0702.4249.4365.3	3	18.65	12.10	92.9	2.11e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
11	067-0301.4792.4882.2	2	18.62	15.15	95.1	1.51e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.059
12	067-0702.9062.9062.0	3	18.51	12.36	89.3	5.73e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
13	067-0701.3047.3117.2	2	18.40	18.40	94.0	7.23e+008	(R)AGWDEHFGYLR(D)	1350.623
14	067-0701.6291.6354.3	3	18.06	18.06	88.5	1.75e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
15	067-0702.4409.4511.2	2	17.88	11.31	96.7	5.14e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
16	067-0301.4259.4372.3	3	17.84	9.98	86.0	2.34e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
17	067-0701.4256.4372.2	2	17.81	9.99	94.5	7.98e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
18	067-0701.9075.9114.0	3	17.69	10.81	89.8	5.86e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
19	067-0701.4254.4375.3	3	17.43	10.25	88.3	2.47e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
20	067-0702.4692.4698.0	2	17.29	8.89	81.1	9.14e+009	(R)EWQDALVDYMVEK(D)	1625.752
21	067-0301.4815.4883.3	3	17.05	11.06	87.2	6.74e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.059
22	067-0701.2921.2921.3	3	17.03	7.77	88.5	5.93e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
23	067-0301.2907.2964.3	3	16.99	9.95	90.2	9.49e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
24	067-0702.4283.4402.2	2	16.64	9.81	89.5	9.12e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
25	067-0301.4395.4435.2	2	16.58	10.31	88.8	4.08e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
26	067-0301.7063.7161.0	2	16.50	10.68	89.6	3.73e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
27	067-0702.4371.4407.3	3	16.41	9.49	79.9	1.70e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
28	067-0301.4281.4394.0	3	16.38	7.88	81.5	8.03e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
29	067-0701.4788.4888.3	3	16.36	10.84	84.7	8.46e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.059
30	067-0702.5402.5428.0	2	16.32	12.06	89.8	5.96e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
31	067-0702.8911.8976.0	3	16.32	9.99	84.6	1.20e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
32	067-0301.4270.4386.2	2	16.23	10.05	91.8	7.03e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
33	067-0701.4378.4411.2	2	16.23	10.40	91.8	5.46e+009	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
34	067-0702.8790.8905.0	3	16.07	10.04	84.9	1.73e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
35	067-0702.4274.4392.0	3	15.97	5.74	83.5	1.07e+010	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
36	067-0301.3039.3072.2	2	15.94	15.94	90.4	8.76e+008	(R)AGWDEHFGYLR(D)	1350.623
37	067-0702.6304.6422.3	3	15.87	15.87	84.5	3.59e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210

38	067-0301.6242.6349.2	2	15.82	11.14	76.9	3.65e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
39	067-0701.6850.6869.2	2	15.62	15.62	90.8	9.14e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
40	067-0301.3038.3071.0	3	15.39	6.27	83.0	6.79e+008	(R)AGWDEHFGYLR(D)	1350.623
41	067-0701.3143.3149.0	3	15.39	6.74	84.0	1.70e+008	(R)AGWDEHFGYLR(D)	1350.623
42	067-0701.4839.4839.0	3	15.38	7.08	81.0	1.21e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
43	067-0301.4617.4637.3	3	15.28	4.03	94.1	4.25e+008	(R)EWQDALVDYMVEK(D)	1625.752
44	067-0301.6364.6482.2	2	15.09	8.71	63.0	4.95e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
45	067-0701.6249.6358.2	2	15.01	10.37	73.6	3.87e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
46	067-0702.8915.8915.0	3	14.94	8.12	84.8	1.09e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
47	067-0301.6812.6832.0	3	14.92	9.87	82.8	1.07e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
48	067-0702.7030.7074.2	2	14.85	14.85	86.0	2.55e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
49	067-0701.2923.2930.2	2	14.72	9.84	89.4	1.92e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
50	067-0702.4791.4868.3	3	14.58	9.19	80.1	7.08e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.059
51	067-0702.2922.2997.2	2	14.43	10.43	89.6	2.77e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
52	067-0301.2905.2909.2	2	14.23	10.66	87.2	2.51e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
53	067-0301.5601.5672.0	2	13.90	13.90	85.2	6.32e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
54	067-0702.3053.3058.2	2	13.81	13.81	87.4	5.71e+008	(R)AGWDEHFGYLR(D)	1350.623
55	067-0701.6517.6562.2	2	13.71	9.63	65.4	2.38e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
56	067-0701.6808.6848.0	2	13.59	8.60	79.5	9.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
57	067-0301.6296.6388.3	3	13.56	13.56	79.0	2.49e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
58	067-0701.6110.6138.0	2	13.44	9.97	86.2	6.20e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
59	067-0301.6851.6963.2	2	13.40	13.40	86.6	1.10e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
60	067-0301.9025.9119.0	3	13.38	7.20	73.7	9.95e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
61	067-0701.4638.4642.0	3	13.37	4.22	82.4	1.72e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
62	067-0301.2773.2821.2	2	13.32	7.62	79.7	2.47e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
63	067-0702.2936.2942.3	3	13.23	4.93	82.0	5.90e+008	(R)AAEQEMWSHITPGVDR(E)	1826.849
64	067-0301.9507.9507.0	3	13.20	6.00	73.0	9.31e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
65	067-0301.11267.11290.2	2	13.13	13.13	82.9	2.24e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
66	067-0701.8863.8973.0	3	13.12	6.87	79.4	1.23e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
67	067-0702.6394.6512.3	3	13.11	8.12	76.6	3.12e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
68	067-0701.6414.6532.3	3	13.01	13.01	78.1	3.34e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
69	067-0702.6502.6502.2	2	12.92	12.92	70.7	2.12e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
70	067-0701.4394.4467.3	3	12.91	3.51	78.2	6.58e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
71	067-0301.2766.2796.3	3	12.85	12.85	81.0	4.29e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
72	067-0701.5488.5594.0	2	12.84	12.84	78.1	8.77e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
73	067-0301.7881.7881.0	2	12.75	12.75	83.6	4.58e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
74	067-0702.4605.4704.0	3	12.67	4.72	78.9	2.12e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
75	067-0701.4243.4358.2	2	12.66	7.46	75.2	1.92e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
76	067-0701.7079.7152.0	2	12.66	12.66	80.3	3.16e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
77	067-0301.4408.4434.0	3	12.57	5.42	77.8	4.57e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
78	067-0701.4504.4541.0	2	12.55	5.79	76.1	6.63e+008	(R)EEYSCGGGAANDDPYNESIWLDNLR(E)	2845.201
79	067-0702.6796.6803.0	2	12.38	7.73	70.2	8.88e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
80	067-0702.6179.6179.0	2	12.37	12.37	73.0	1.18e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
81	067-0702.9042.9042.0	3	12.36	4.47	71.6	5.93e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
82	067-0701.6269.6386.2	2	12.23	12.23	66.9	4.19e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
83	067-0301.7109.7168.2	2	12.14	12.14	81.5	2.74e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
84	067-0701.11128.11128.0	2	12.09	8.83	77.1	4.91e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
85	067-0301.8908.9019.0	3	12.07	7.26	72.4	1.46e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843

86	067-0701.4624.4624.0	3	11.97	2.09	75.0	1.61e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
87	067-0301.9154.9154.0	3	11.77	8.08	71.8	5.50e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
88	067-0301.5487.5590.0	2	11.71	6.75	75.9	9.69e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
89	067-0702.2771.2793.2	2	11.69	6.20	79.3	2.16e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
90	067-0702.4246.4366.2	2	11.60	6.28	74.1	1.84e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
91	067-0701.5600.5655.0	2	11.52	7.91	80.4	6.55e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
92	067-0702.2775.2792.3	3	11.50	11.50	77.9	4.85e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
93	067-0702.5619.5634.0	2	11.29	11.29	76.3	5.23e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
94	067-0301.11954.11954.0	3	11.26	8.00	79.6	6.18e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
95	067-0301.5757.5847.2	2	11.14	5.68	64.1	7.06e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
96	067-0701.11068.11140.0	2	11.09	7.62	79.7	9.68e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
97	067-0301.6745.6745.0	3	11.07	5.02	71.1	7.69e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
98	067-0701.2776.2798.3	3	11.00	11.00	77.9	4.29e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
99	067-0701.2782.2786.2	2	10.94	10.94	74.9	2.12e+008	(R)CGSWFGLEGQHEPK(D)	1631.727
100	067-0702.6123.6123.0	2	10.93	10.93	71.7	6.00e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
101	067-0301.11238.11238.0	2	10.55	10.55	70.8	4.25e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
102	067-0702.3161.3161.0	2	10.54	7.46	77.8	2.14e+008	(R)AGWDEHFGYLR(D)	1350.623
103	067-0701.4855.4855.0	3	10.46	3.61	79.1	1.18e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
104	067-0701.4823.4823.0	3	10.41	10.41	71.7	1.08e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
105	067-0301.7927.7927.0	2	10.35	10.35	73.3	3.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
106	067-0702.6183.6183.0	2	10.14	6.80	60.8	1.36e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
107	067-0702.9070.9070.0	3	10.11	6.90	73.6	5.43e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
108	067-0301.4622.4622.0	3	10.09	2.89	80.6	1.69e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3623.605
109	067-0301.11102.11102.0	2	9.94	9.94	71.4	7.08e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
110	067-0702.4915.4915.0	2	9.51	9.51	62.0	4.65e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.059
111	067-0701.6199.6199.0	2	9.43	9.43	68.7	4.88e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
112	067-0702.6822.6822.0	2	9.41	3.17	68.1	7.43e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
113	067-0301.7116.7116.0	2	9.40	2.62	63.2	1.95e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
114	067-0702.11199.11199.0	2	9.36	9.36	71.3	2.39e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
115	067-0702.8955.8955.0	2	9.34	9.34	77.0	2.98e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
116	067-0702.7060.7060.2	2	9.14	9.14	63.9	1.37e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
117	067-0701.7877.7883.0	2	9.04	9.04	63.9	4.00e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
118	067-0702.5803.5803.2	2	8.96	8.96	61.5	4.74e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
119	067-0301.7861.7861.0	2	8.92	8.92	67.3	5.22e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
120	067-0702.7726.7816.0	2	8.89	8.89	62.8	5.92e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
121	067-0301.6160.6160.2	2	8.86	8.86	69.4	5.11e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
122	067-0701.7845.7845.0	2	8.85	8.85	62.5	4.51e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
123	067-0702.11125.11125.0	2	8.75	8.75	66.3	5.78e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
124	067-0702.5659.5659.0	2	8.62	8.62	68.8	4.60e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
125	067-0702.7241.7241.0	2	8.61	3.11	64.3	1.56e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
126	067-0701.11145.11145.0	2	8.48	8.48	66.4	3.75e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
127	067-0702.11185.11205.0	2	8.48	3.96	65.6	4.27e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
128	067-0702.11223.11223.0	2	8.45	8.45	78.0	1.61e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
129	067-0301.11087.11087.0	2	8.43	8.43	68.6	7.04e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
130	067-0702.11252.11252.0	2	8.31	3.67	64.8	1.57e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
131	067-0301.11278.11278.0	2	8.27	8.27	72.2	1.80e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
132	067-0301.3179.3179.0	2	8.09	8.09	63.7	1.81e+008	(R)AGWDEHFGYLR(D)	1350.623
133	067-0702.7247.7247.0	2	8.03	8.03	65.8	1.55e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210

134	067-0301.6571.6571.0	2	7.90	7.90	76.2	5.17e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
135	067-0702.11257.11257.0	2	7.84	7.84	62.5	1.38e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
136	067-0701.11024.11024.0	2	7.60	7.60	64.2	1.41e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
137	067-0702.11005.11005.0	2	7.51	7.51	68.5	6.78e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
138	067-0301.7343.7343.0	2	7.34	7.34	65.9	1.52e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
139	067-0701.5850.5868.0	2	7.28	7.28	60.5	5.49e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
140	067-0702.7970.7970.0	2	7.19	7.19	65.7	9.68e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
141	067-0701.6555.6555.0	2	7.15	7.15	65.3	5.36e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.049
142	067-0702.7019.7019.0	2	6.89	6.89	63.9	1.95e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
143	067-0301.11800.11800.0	2	6.62	6.62	60.4	3.55e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
144	067-0702.11234.11234.0	2	6.29	3.25	66.2	1.63e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210
145	067-0702.11026.11026.0	2	6.08	6.08	62.6	6.73e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.210

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	77	8	133.56	20	5.42e+011	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	067-0702.6339.6457.2	2	21.50	13.86	100.0	4.31e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
2	067-0701.6428.6545.0	3	20.09	12.26	91.4	1.89e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
3	067-0301.6319.6438.3	3	19.62	13.81	92.7	2.36e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
4	067-0701.6393.6509.2	2	19.46	11.78	98.4	4.70e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
5	067-0701.6515.6560.2	2	19.45	11.76	98.1	1.56e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
6	067-0702.6205.6324.2	2	19.41	11.73	96.7	3.24e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
7	067-0702.1978.2001.2	2	19.35	9.91	96.8	1.55e+008	(R)DCAALASNGELR(I)	1276.595
8	067-0702.2593.2609.2	2	19.22	19.22	96.0	8.91e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.912
9	067-0301.6384.6506.2	2	18.95	10.76	98.3	5.27e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
10	067-0301.6512.6565.2	2	18.94	11.28	97.7	2.09e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
11	067-0701.6270.6388.2	2	18.94	10.76	97.7	3.74e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
12	067-0702.6236.6357.0	3	18.81	11.22	86.4	1.77e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
13	067-0701.2070.2106.2	2	18.76	8.89	95.6	1.60e+008	(R)DCAALASNGELR(I)	1276.595
14	067-0702.2076.2107.2	2	18.74	9.49	95.4	1.64e+008	(R)DCAALASNGELR(I)	1276.595
15	067-0301.2066.2096.2	2	18.71	9.46	94.8	1.33e+008	(R)DCAALASNGELR(I)	1276.595
16	067-0301.6265.6381.2	2	18.43	9.77	97.5	3.55e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
17	067-0702.6466.6564.2	2	18.43	11.84	97.7	1.51e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
18	067-0301.6441.6558.3	3	18.32	11.60	86.5	2.22e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
19	067-0702.1631.1720.2	2	18.20	9.74	93.6	3.54e+009	(R)DCAALASNGELR(I)	1276.595
20	067-0702.1722.1825.2	2	17.68	8.72	93.3	4.43e+009	(R)DCAALASNGELR(I)	1276.595
21	067-0701.1767.1837.2	2	17.67	8.69	93.0	3.22e+009	(R)DCAALASNGELR(I)	1276.595
22	067-0702.1836.1911.2	2	17.67	9.69	92.6	1.21e+009	(R)DCAALASNGELR(I)	1276.595
23	067-0701.7589.7625.0	2	17.52	11.16	93.4	2.88e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
24	067-0301.3220.3294.3	3	17.42	11.56	90.1	1.92e+008	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.967
25	067-0301.7897.7915.2	2	17.22	11.03	73.5	6.28e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.985
26	067-0301.1974.1979.0	2	17.21	9.38	93.4	1.29e+008	(R)DCAALASNGELR(I)	1276.595
27	067-0702.6368.6477.3	3	17.16	13.62	84.1	1.61e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262

28	067-0701.1659.1764.2	2	17.15	8.70	92.6	4.44e+009	(R)DCAALASNGELR(I)	1276.595
29	067-0702.7826.7832.2	2	17.07	11.51	77.3	5.25e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.985
30	067-0702.2184.2252.0	2	16.83	9.42	81.2	2.10e+008	(R)DCAALASNGELR(I)	1276.595
31	067-0701.6301.6422.3	3	16.79	11.41	84.5	2.06e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
32	067-0301.1651.1757.2	2	16.63	7.63	92.0	4.75e+009	(R)DCAALASNGELR(I)	1276.595
33	067-0301.1759.1823.2	2	16.63	8.16	92.0	3.64e+009	(R)DCAALASNGELR(I)	1276.595
34	067-0701.3222.3323.3	3	16.54	10.41	92.5	2.00e+008	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.967
35	067-0701.2424.2456.2	2	16.31	8.11	88.3	3.40e+007	(R)DCAALASNGELR(I)	1276.595
36	067-0702.6497.6553.3	3	16.27	10.09	78.5	4.27e+009	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
37	067-0701.7876.7912.2	2	16.24	9.40	72.8	5.76e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.985
38	067-0301.6284.6402.0	3	15.60	10.15	79.9	1.98e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
39	067-0301.2163.2243.2	2	15.37	8.92	81.9	2.00e+008	(R)DCAALASNGELR(I)	1276.595
40	067-0301.5387.5492.0	2	15.15	6.70	85.5	7.75e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.021
41	067-0702.2306.2375.0	2	14.95	8.37	82.8	7.88e+007	(R)DCAALASNGELR(I)	1276.595
42	067-0701.2185.2253.2	2	14.69	8.00	79.2	2.21e+008	(R)DCAALASNGELR(I)	1276.595
43	067-0701.5389.5498.0	2	14.61	8.66	64.6	7.39e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.021
44	067-0301.2558.2561.2	2	14.52	14.52	85.9	1.29e+008	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.912
45	067-0701.7760.7848.3	3	14.50	8.78	71.8	1.38e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.985
46	067-0301.7714.7761.0	2	14.43	9.86	85.6	2.50e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
47	067-0301.2256.2335.0	2	14.42	7.35	83.2	1.75e+008	(R)DCAALASNGELR(I)	1276.595
48	067-0702.7474.7546.0	2	14.25	8.05	88.9	1.09e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
49	067-0701.2338.2364.0	2	14.06	7.80	78.2	4.92e+007	(R)DCAALASNGELR(I)	1276.595
50	067-0701.7415.7415.0	2	13.78	8.63	81.3	6.47e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
51	067-0701.6321.6443.3	3	13.70	9.40	77.5	2.24e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
52	067-0702.3258.3258.3	3	13.50	6.95	81.8	8.44e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.967
53	067-0301.2457.2457.2	2	13.32	8.41	82.4	6.68e+007	(R)DCAALASNGELR(I)	1276.595
54	067-0301.1889.1905.2	2	13.30	7.73	67.4	4.21e+008	(R)DCAALASNGELR(I)	1276.595
55	067-0702.7722.7803.3	3	13.28	8.44	73.8	1.06e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.985
56	067-0301.7515.7521.0	2	13.02	9.10	85.3	9.14e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
57	067-0702.11270.11270.0	2	12.58	12.58	71.1	1.29e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
58	067-0701.3315.3414.2	2	12.53	12.53	79.9	1.00e+009	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.967
59	067-0702.5386.5456.0	2	12.21	3.81	85.8	7.16e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.021
60	067-0702.2641.2659.3	3	12.14	12.14	70.7	1.79e+008	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.912
61	067-0702.11284.11284.0	2	12.12	12.12	63.6	2.07e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
62	067-0702.8177.8177.0	2	12.08	12.08	76.8	1.06e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
63	067-0702.7342.7342.0	2	10.90	6.63	78.7	1.03e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
64	067-0702.7647.7647.0	2	10.70	5.91	72.6	2.38e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
65	067-0301.1669.1675.1	1	10.69	3.62	86.7	1.65e+009	(R)DCAALASNGELR(I)	1276.595
66	067-0301.8242.8242.0	2	10.47	6.81	71.0	9.03e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
67	067-0702.6384.6501.3	3	10.26	4.88	73.0	1.51e+010	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
68	067-0702.7862.7862.0	2	10.07	5.69	67.2	1.98e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
69	067-0701.7733.7733.0	2	9.85	9.85	68.6	1.39e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
70	067-0301.7719.7719.0	2	8.84	8.84	67.2	1.57e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
71	067-0702.10991.10991.0	2	8.80	8.80	63.7	7.28e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
72	067-0702.7337.7337.0	2	8.72	8.72	67.2	9.03e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
73	067-0702.11024.11024.0	2	8.37	8.37	60.2	7.46e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162
74	067-0701.1676.1680.1	1	8.27	2.51	86.6	1.54e+009	(R)DCAALASNGELR(I)	1276.595
75	067-0702.10972.10972.0	2	8.08	8.08	60.3	7.53e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.162

76	067-0702.1678.1678.1	1	7.16	3.07	82.8	1.24e+009	(R)DCAALASNGELR(I)	1276.595
77	067-0702.0934.0942.0	2	6.18	1.50	96.9	2.13e+005	(R)IADGGFQR(Y)	863.437

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	2.2	39	4	73.39	16	3.78e+010	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	067-0702.2640.2655.3	3	21.21	16.43	96.0	1.67e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
2	067-0702.2634.2685.3	3	20.38	20.38	95.9	1.75e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
3	067-0702.1978.2001.2	2	19.35	9.91	96.8	1.55e+008	(R)DCAALASNGELR(I)	1276.595
4	067-0701.2070.2106.2	2	18.76	8.89	95.6	1.60e+008	(R)DCAALASNGELR(I)	1276.595
5	067-0702.2076.2107.2	2	18.74	9.49	95.4	1.64e+008	(R)DCAALASNGELR(I)	1276.595
6	067-0301.2066.2096.2	2	18.71	9.46	94.8	1.33e+008	(R)DCAALASNGELR(I)	1276.595
7	067-0702.1631.1720.2	2	18.20	9.74	93.6	3.54e+009	(R)DCAALASNGELR(I)	1276.595
8	067-0702.1722.1825.2	2	17.68	8.72	93.3	4.43e+009	(R)DCAALASNGELR(I)	1276.595
9	067-0701.1767.1837.2	2	17.67	8.69	93.0	3.22e+009	(R)DCAALASNGELR(I)	1276.595
10	067-0702.1836.1911.2	2	17.67	9.69	92.6	1.21e+009	(R)DCAALASNGELR(I)	1276.595
11	067-0301.1974.1979.0	2	17.21	9.38	93.4	1.29e+008	(R)DCAALASNGELR(I)	1276.595
12	067-0701.1659.1764.2	2	17.15	8.70	92.6	4.44e+009	(R)DCAALASNGELR(I)	1276.595
13	067-0702.2184.2252.0	2	16.83	9.42	81.2	2.10e+008	(R)DCAALASNGELR(I)	1276.595
14	067-0301.1651.1757.2	2	16.63	7.63	92.0	4.75e+009	(R)DCAALASNGELR(I)	1276.595
15	067-0301.1759.1823.2	2	16.63	8.16	92.0	3.64e+009	(R)DCAALASNGELR(I)	1276.595
16	067-0301.4833.4915.2	2	16.46	13.37	89.4	1.08e+009	(K)GFPSTLGMLIDTGR(N)	1464.752
17	067-0301.5138.5189.0	2	16.37	10.62	88.8	4.79e+008	(R)YQNEYIAGITEIIGDSK(Y)	1913.949
18	067-0701.2424.2456.2	2	16.31	8.11	88.3	3.40e+007	(R)DCAALASNGELR(I)	1276.595
19	067-0301.2625.2672.0	3	16.02	11.10	84.0	1.47e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
20	067-0701.4827.4891.2	2	16.00	11.81	90.1	1.18e+009	(K)GFPSTLGMLIDTGR(N)	1464.752
21	067-0702.4829.4870.2	2	15.96	12.36	89.7	9.49e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
22	067-0701.2634.2660.0	3	15.74	12.11	76.7	1.52e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
23	067-0301.2163.2243.2	2	15.37	8.92	81.9	2.00e+008	(R)DCAALASNGELR(I)	1276.595
24	067-0702.5108.5169.2	2	15.34	12.27	87.9	6.46e+008	(R)YQNEYIAGITEIIGDSK(Y)	1913.949
25	067-0702.2306.2375.0	2	14.95	8.37	82.8	7.88e+007	(R)DCAALASNGELR(I)	1276.595
26	067-0701.2185.2253.2	2	14.69	8.00	79.2	2.21e+008	(R)DCAALASNGELR(I)	1276.595
27	067-0301.2256.2335.0	2	14.42	7.35	83.2	1.75e+008	(R)DCAALASNGELR(I)	1276.595
28	067-0701.2338.2364.0	2	14.06	7.80	78.2	4.92e+007	(R)DCAALASNGELR(I)	1276.595
29	067-0701.5120.5189.0	2	13.99	7.08	81.4	4.95e+008	(R)YQNEYIAGITEIIGDSK(Y)	1913.949
30	067-0301.2457.2457.2	2	13.32	8.41	82.4	6.68e+007	(R)DCAALASNGELR(I)	1276.595
31	067-0301.1889.1905.2	2	13.30	7.73	67.4	4.21e+008	(R)DCAALASNGELR(I)	1276.595
32	067-0701.2817.2822.0	3	12.67	12.67	75.2	1.95e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
33	067-0701.2652.2657.2	2	12.58	6.30	87.6	1.77e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
34	067-0702.2645.2662.2	2	11.07	4.80	87.2	2.17e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
35	067-0301.1669.1675.1	1	10.69	3.62	86.7	1.65e+009	(R)DCAALASNGELR(I)	1276.595
36	067-0301.2640.2656.2	2	9.45	2.56	83.3	1.82e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
37	067-0301.2808.2814.0	3	9.33	5.95	70.1	2.04e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209

38	067-0701.1676.1680.1	1	8.27	2.51	86.6	1.54e+009	(R)DCAALASNGELR(I)	1276.595
39	067-0702.1678.1678.1	1	7.16	3.07	82.8	1.24e+009	(R)DCAALASNGELR(I)	1276.595

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	2.3	27	2	34.35	15	3.26e+010	23418.9	PA_Bse_meta_comb:2073570681	PA_Bse_meta_comb:2073570681 BaSeMet_00143370 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [I

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0702.1978.2001.2	2	19.35	9.91	96.8	1.55e+008	(R)DCAALASNGELR(I)	1276.595
2	067-0701.2070.2106.2	2	18.76	8.89	95.6	1.60e+008	(R)DCAALASNGELR(I)	1276.595
3	067-0702.2076.2107.2	2	18.74	9.49	95.4	1.64e+008	(R)DCAALASNGELR(I)	1276.595
4	067-0301.2066.2096.2	2	18.71	9.46	94.8	1.33e+008	(R)DCAALASNGELR(I)	1276.595
5	067-0702.1631.1720.2	2	18.20	9.74	93.6	3.54e+009	(R)DCAALASNGELR(I)	1276.595
6	067-0702.1722.1825.2	2	17.68	8.72	93.3	4.43e+009	(R)DCAALASNGELR(I)	1276.595
7	067-0701.1767.1837.2	2	17.67	8.69	93.0	3.22e+009	(R)DCAALASNGELR(I)	1276.595
8	067-0702.1836.1911.2	2	17.67	9.69	92.6	1.21e+009	(R)DCAALASNGELR(I)	1276.595
9	067-0301.1974.1979.0	2	17.21	9.38	93.4	1.29e+008	(R)DCAALASNGELR(I)	1276.595
10	067-0701.1659.1764.2	2	17.15	8.70	92.6	4.44e+009	(R)DCAALASNGELR(I)	1276.595
11	067-0702.2184.2252.0	2	16.83	9.42	81.2	2.10e+008	(R)DCAALASNGELR(I)	1276.595
12	067-0301.1651.1757.2	2	16.63	7.63	92.0	4.75e+009	(R)DCAALASNGELR(I)	1276.595
13	067-0301.1759.1823.2	2	16.63	8.16	92.0	3.64e+009	(R)DCAALASNGELR(I)	1276.595
14	067-0701.2424.2456.2	2	16.31	8.11	88.3	3.40e+007	(R)DCAALASNGELR(I)	1276.595
15	067-0301.2163.2243.2	2	15.37	8.92	81.9	2.00e+008	(R)DCAALASNGELR(I)	1276.595
16	067-0701.5882.5902.0	2	15.00	7.31	84.5	2.46e+008	(R)YQDEYIAGITEIIGDPAYSGIR(I)	2444.198
17	067-0702.2306.2375.0	2	14.95	8.37	82.8	7.88e+007	(R)DCAALASNGELR(I)	1276.595
18	067-0701.2185.2253.2	2	14.69	8.00	79.2	2.21e+008	(R)DCAALASNGELR(I)	1276.595
19	067-0301.2256.2335.0	2	14.42	7.35	83.2	1.75e+008	(R)DCAALASNGELR(I)	1276.595
20	067-0701.2338.2364.0	2	14.06	7.80	78.2	4.92e+007	(R)DCAALASNGELR(I)	1276.595
21	067-0301.2457.2457.2	2	13.32	8.41	82.4	6.68e+007	(R)DCAALASNGELR(I)	1276.595
22	067-0301.1889.1905.2	2	13.30	7.73	67.4	4.21e+008	(R)DCAALASNGELR(I)	1276.595
23	067-0702.5807.5807.0	2	12.49	6.58	72.9	3.26e+008	(R)YQDEYIAGITEIIGDPAYSGIR(I)	2444.198
24	067-0301.1669.1675.1	1	10.69	3.62	86.7	1.65e+009	(R)DCAALASNGELR(I)	1276.595
25	067-0301.5868.5868.0	2	9.89	5.21	65.4	2.10e+008	(R)YQDEYIAGITEIIGDPAYSGIR(I)	2444.198
26	067-0701.1676.1680.1	1	8.27	2.51	86.6	1.54e+009	(R)DCAALASNGELR(I)	1276.595
27	067-0702.1678.1678.1	1	7.16	3.07	82.8	1.24e+009	(R)DCAALASNGELR(I)	1276.595

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	2.4	27	2	31.70	3	3.23e+010	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolases family 6.

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0702.1978.2001.2	2	19.35	9.91	96.8	1.55e+008	(R)DCAALASNGELR(I)	1276.595

2	067-0701.2070.2106.2	2	18.76	8.89	95.6	1.60e+008	(R)DCAALASNGELR(I)	1276.595
3	067-0702.2076.2107.2	2	18.74	9.49	95.4	1.64e+008	(R)DCAALASNGELR(I)	1276.595
4	067-0301.2066.2096.2	2	18.71	9.46	94.8	1.33e+008	(R)DCAALASNGELR(I)	1276.595
5	067-0702.1631.1720.2	2	18.20	9.74	93.6	3.54e+009	(R)DCAALASNGELR(I)	1276.595
6	067-0702.1722.1825.2	2	17.68	8.72	93.3	4.43e+009	(R)DCAALASNGELR(I)	1276.595
7	067-0701.1767.1837.2	2	17.67	8.69	93.0	3.22e+009	(R)DCAALASNGELR(I)	1276.595
8	067-0702.1836.1911.2	2	17.67	9.69	92.6	1.21e+009	(R)DCAALASNGELR(I)	1276.595
9	067-0301.1974.1979.0	2	17.21	9.38	93.4	1.29e+008	(R)DCAALASNGELR(I)	1276.595
10	067-0701.1659.1764.2	2	17.15	8.70	92.6	4.44e+009	(R)DCAALASNGELR(I)	1276.595
11	067-0702.2184.2252.0	2	16.83	9.42	81.2	2.10e+008	(R)DCAALASNGELR(I)	1276.595
12	067-0301.1651.1757.2	2	16.63	7.63	92.0	4.75e+009	(R)DCAALASNGELR(I)	1276.595
13	067-0301.1759.1823.2	2	16.63	8.16	92.0	3.64e+009	(R)DCAALASNGELR(I)	1276.595
14	067-0701.2424.2456.2	2	16.31	8.11	88.3	3.40e+007	(R)DCAALASNGELR(I)	1276.595
15	067-0301.2163.2243.2	2	15.37	8.92	81.9	2.00e+008	(R)DCAALASNGELR(I)	1276.595
16	067-0702.2306.2375.0	2	14.95	8.37	82.8	7.88e+007	(R)DCAALASNGELR(I)	1276.595
17	067-0701.2185.2253.2	2	14.69	8.00	79.2	2.21e+008	(R)DCAALASNGELR(I)	1276.595
18	067-0301.2256.2335.0	2	14.42	7.35	83.2	1.75e+008	(R)DCAALASNGELR(I)	1276.595
19	067-0701.2338.2364.0	2	14.06	7.80	78.2	4.92e+007	(R)DCAALASNGELR(I)	1276.595
20	067-0301.2457.2457.2	2	13.32	8.41	82.4	6.68e+007	(R)DCAALASNGELR(I)	1276.595
21	067-0301.1889.1905.2	2	13.30	7.73	67.4	4.21e+008	(R)DCAALASNGELR(I)	1276.595
22	067-0702.7396.7396.0	2	12.35	6.89	84.0	1.55e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.303
23	067-0701.7411.7445.0	2	11.62	6.94	77.4	1.63e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.303
24	067-0301.1669.1675.1	1	10.69	3.62	86.7	1.65e+009	(R)DCAALASNGELR(I)	1276.595
25	067-0301.7409.7426.0	2	8.48	3.06	64.6	1.60e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.303
26	067-0701.1676.1680.1	1	8.27	2.51	86.6	1.54e+009	(R)DCAALASNGELR(I)	1276.595
27	067-0702.1678.1678.1	1	7.16	3.07	82.8	1.24e+009	(R)DCAALASNGELR(I)	1276.595

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	21	4	68.61	23	9.64e+009	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0702.2193.2251.2	2	19.71	11.54	99.0	1.23e+009	(K)SLDVQVYNECR(S)	1382.637
2	067-0301.2185.2242.2	2	19.21	10.13	98.9	1.36e+009	(K)SLDVQVYNECR(S)	1382.637
3	067-0701.2195.2252.2	2	19.21	11.00	98.9	1.21e+009	(K)SLDVQVYNECR(S)	1382.637
4	067-0301.2775.2779.0	3	18.53	8.23	91.8	2.36e+008	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
5	067-0301.2280.2354.2	2	16.47	10.34	84.3	5.60e+008	(K)SLDVQVYNECR(S)	1382.637
6	067-0301.2967.2967.0	2	16.30	16.30	89.1	1.62e+008	(K)AGYDWTYQQLSGHECDDVR(F)	2299.967
7	067-0701.2971.2978.2	2	16.11	16.11	85.8	1.58e+008	(K)AGYDWTYQQLSGHECDDVR(F)	2299.967
8	067-0702.2980.3013.2	2	15.94	15.94	91.0	1.96e+008	(K)AGYDWTYQQLSGHECDDVR(F)	2299.967
9	067-0701.2787.2854.3	3	15.63	6.25	82.7	3.17e+008	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
10	067-0702.2801.2807.2	2	15.54	15.54	89.9	6.23e+007	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
11	067-0701.2290.2365.0	2	14.83	8.76	81.1	4.66e+008	(K)SLDVQVYNECR(S)	1382.637
12	067-0702.2789.2794.0	3	14.55	6.40	83.7	2.19e+008	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
13	067-0301.2962.2962.0	2	14.44	14.44	66.8	1.67e+008	(K)AGYDWTYQQLSGHECDDVR(F)	2299.967

14	067-0701.2402.2413.2	2	14.21	7.34	76.7	2.27e+007	(K)SLDVQVYNECR(S)	1382.637
15	067-0701.4662.4662.0	2	14.07	9.63	86.1	5.62e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
16	067-0702.2287.2311.2	2	13.08	9.24	76.2	5.80e+008	(K)SLDVQVYNECR(S)	1382.637
17	067-0301.2947.3028.3	3	12.91	8.40	83.6	1.06e+009	(K)AGYDWTYQQLSGHECDDVR(F)	2299.967
18	067-0301.2800.2822.2	2	12.86	12.86	78.3	7.97e+007	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
19	067-0701.2808.2812.2	2	10.61	10.61	64.0	6.04e+007	(R)QCHSAWSGYGSGDYDVSAAMNSNK(S)	2592.051
20	067-0301.4679.4679.2	2	8.76	8.76	69.1	4.67e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
21	067-0301.4685.4685.2	2	8.74	8.74	67.7	4.63e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072

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	9	4	55.27	9	7.24e+009	72837.7	PA_BS12:2189569651	PA_BS12:2189569651 or2957 Glycosyl hydrolase family 53./Cellulose or protein binding domain. [B. setacea BS12] 6

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0701.3899.3975.0	2	18.29	10.40	96.4	1.26e+009	(K)DVMVVEVGTPWNDGEAR(E)	1873.875
2	067-0301.3888.3969.2	2	17.16	11.74	84.3	1.35e+009	(K)DVMVVEVGTPWNDGEAR(E)	1873.875
3	067-0702.3886.3959.0	2	16.04	10.60	83.1	1.08e+009	(K)DVMVVEVGTPWNDGEAR(E)	1873.875
4	067-0702.4541.4573.0	2	13.69	13.69	74.1	6.21e+008	(R)VWVNPNGGWYSSIDDVVQK(A)	2163.050
5	067-0301.4757.4791.2	2	11.65	7.55	83.3	7.27e+008	(R)DNGANFDIIGASSYPTTSDMAWR(T)	2489.104
6	067-0701.2668.2668.0	2	11.64	4.55	89.6	1.90e+007	(R)EIIADVISK(V)	987.572
7	067-0301.2667.2667.0	2	11.01	2.87	91.3	2.15e+007	(R)EIIADVISK(V)	987.572
8	067-0701.4748.4808.2	2	10.35	5.05	76.4	1.05e+009	(R)DNGANFDIIGASSYPTTSDMAWR(T)	2489.104
9	067-0702.4728.4802.2	2	7.26	7.26	64.4	1.11e+009	(R)DNGANFDIIGASSYPTTSDMAWR(T)	2489.104

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	9	3	45.93	6	1.05e+010	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-terminal ig-like do

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0301.3143.3178.0	2	18.04	10.85	94.6	2.81e+008	(K)YVVNGGISVWK(L)	1221.663
2	067-0301.5107.5172.2	2	15.82	6.27	90.9	2.88e+009	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.152
3	067-0702.3151.3190.0	2	14.74	6.56	87.1	1.80e+008	(K)YVVNGGISVWK(L)	1221.663
4	067-0702.5071.5140.2	2	12.28	4.88	88.2	3.13e+009	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.152
5	067-0701.2149.2175.0	2	12.07	12.07	76.2	7.59e+007	(K)ASSNTAQTWELR(Q)	1363.660
6	067-0701.5111.5205.2	2	11.76	3.78	76.9	2.03e+009	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.152
7	067-0701.5211.5241.2	2	10.97	3.00	77.5	1.79e+009	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.152
8	067-0301.2140.2158.0	2	9.55	9.55	65.8	8.15e+007	(K)ASSNTAQTWELR(Q)	1363.660
9	067-0702.2151.2159.0	2	9.36	4.33	74.3	3.43e+007	(K)ASSNTAQTWELR(Q)	1363.660

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name

				Score					
5	5.2	5	2	32.25	4	1.25e+009	87140.5	PA_Bse02:2503999088	PA_Bse02:2503999088 BS02DRAFT_00000960 Cellulose or protein binding domain./Glycosyl hydrolase family 9./N

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0301.3143.3178.0	2	18.04	10.85	94.6	2.81e+008	(K)YVVNGGISVWK(L)	1221.663
2	067-0702.3151.3190.0	2	14.74	6.56	87.1	1.80e+008	(K)YVVNGGISVWK(L)	1221.663
3	067-0301.5558.5597.0	2	14.21	6.43	86.9	2.99e+008	(K)GIIIDDGALNIPESNNNVSDLLDEAR(W)	2767.374
4	067-0701.5569.5576.0	2	13.73	5.94	88.0	2.27e+008	(K)GIIIDDGALNIPESNNNVSDLLDEAR(W)	2767.374
5	067-0702.5523.5530.0	2	11.02	3.88	79.7	2.67e+008	(K)GIIIDDGALNIPESNNNVSDLLDEAR(W)	2767.374

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
6	6.1	7	3	44.72	12	1.59e+009	52143.8	PA_BS12:2189568458	PA_BS12:2189568458 or1762 Glycosyl hydrolase family 45./Cellulose or protein binding domain./Cellulose binding d

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0702.2505.2531.2	2	17.81	17.81	89.3	1.12e+008	(K)DELGYNASLSQYK(S)	1487.701
2	067-0701.6640.6681.2	2	14.35	14.35	77.0	3.24e+008	(R)GLTDLQQGCQWYVDWFEAADNPSLK(Y)	2941.346
3	067-0301.6645.6650.0	2	14.26	14.26	78.2	2.68e+008	(R)GLTDLQQGCQWYVDWFEAADNPSLK(Y)	2941.346
4	067-0702.6582.6588.0	2	12.74	12.74	70.6	2.77e+008	(R)GLTDLQQGCQWYVDWFEAADNPSLK(Y)	2941.346
5	067-0701.3130.3171.0	3	12.56	5.73	76.8	2.94e+008	(R)CFEIQFTGSSHNGGNDPGSAALSGK(R)	2538.131
6	067-0701.2497.2512.2	2	8.98	8.98	60.6	1.17e+008	(K)DELGYNASLSQYK(S)	1487.701
7	067-0301.2497.2503.0	2	8.05	8.05	63.1	1.93e+008	(K)DELGYNASLSQYK(S)	1487.701

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.1	8	3	40.45	11	1.09e+009	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding domain. [B. seta

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0701.4754.4761.0	2	14.61	9.86	83.7	2.28e+008	(R)VLTWADFEDQPFCDR(Q)	1898.838
2	067-0702.4752.4771.0	2	13.62	13.62	78.6	1.99e+008	(R)VLTWADFEDQPFCDR(Q)	1898.838
3	067-0701.2029.2088.2	2	13.25	8.64	89.7	9.17e+007	(R)HVIYGEWGR(D)	1116.559
4	067-0702.2028.2108.2	2	13.25	8.64	89.4	1.11e+008	(R)HVIYGEWGR(D)	1116.559
5	067-0301.3746.3746.0	2	12.59	12.59	76.9	1.22e+008	(R)QVGSISMNEGAGLLSATCNVPSR(S)	2348.133
6	067-0702.3774.3774.0	2	12.42	12.42	70.9	1.22e+008	(R)QVGSISMNEGAGLLSATCNVPSR(S)	2348.133
7	067-0301.2010.2083.2	2	11.99	6.36	88.8	8.85e+007	(R)HVIYGEWGR(D)	1116.559
8	067-0701.3747.3747.0	2	8.82	8.82	64.5	1.30e+008	(R)QVGSISMNEGAGLLSATCNVPSR(S)	2348.133

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.2	12	2	31.59	6	3.88e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0301.1359.1365.3	3	18.34	9.11	95.0	4.83e+006	(K)NEGSGTLSANCNVPSR(S)	1662.750
2	067-0702.1361.1379.3	3	17.40	8.51	96.7	4.56e+006	(K)NEGSGTLSANCNVPSR(S)	1662.750
3	067-0701.1356.1389.3	3	16.82	7.59	94.3	5.23e+006	(K)NEGSGTLSANCNVPSR(S)	1662.750
4	067-0701.2029.2088.2	2	13.25	8.64	89.7	9.17e+007	(R)HVIYGEWGR(D)	1116.559
5	067-0702.2028.2108.2	2	13.25	8.64	89.4	1.11e+008	(R)HVIYGEWGR(D)	1116.559
6	067-0701.1347.1425.2	2	12.68	5.50	83.0	2.78e+007	(K)NEGSGTLSANCNVPSR(S)	1662.750
7	067-0301.2010.2083.2	2	11.99	6.36	88.8	8.85e+007	(R)HVIYGEWGR(D)	1116.559
8	067-0702.1351.1360.0	2	11.44	7.20	80.0	1.69e+007	(K)NEGSGTLSANCNVPSR(S)	1662.750
9	067-0301.1345.1345.0	2	10.43	5.24	76.0	1.43e+007	(K)NEGSGTLSANCNVPSR(S)	1662.750
10	067-0301.1350.1350.0	2	10.28	3.48	78.5	1.61e+007	(K)NEGSGTLSANCNVPSR(S)	1662.750
11	067-0702.1533.1533.0	2	9.08	9.08	73.9	4.02e+006	(K)NEGSGTLSANCNVPSR(S)	1662.750
12	067-0301.1605.1605.0	2	6.54	2.23	82.4	2.67e+006	(K)NEGSGTLSANCNVPSR(S)	1662.750

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
8	8.1	6	3	39.90	9	1.72e+009	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0701.3251.3274.2	2	14.03	10.98	77.5	2.00e+008	(K)AEEIEEWIR(D)	1174.574
2	067-0301.3859.3864.0	3	13.81	10.58	78.7	6.69e+008	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.198
3	067-0301.3244.3273.2	2	13.57	13.57	80.8	1.83e+008	(K)AEEIEEWIR(D)	1174.574
4	067-0301.3982.4001.2	2	12.06	7.85	74.8	3.33e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909
5	067-0702.3267.3273.0	2	11.07	11.07	67.4	1.48e+008	(K)AEEIEEWIR(D)	1174.574
6	067-0701.4005.4005.2	2	10.65	5.55	75.2	1.83e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
9	9.1	13	2	38.12	8	4.28e+009	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0701.2270.2304.2	2	20.96	15.58	98.8	5.34e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
2	067-0702.2050.2105.3	3	20.33	13.89	96.2	2.81e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
3	067-0701.2051.2104.3	3	19.85	12.10	96.4	3.03e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
4	067-0301.2050.2094.3	3	19.80	12.37	94.9	2.40e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
5	067-0301.2260.2274.2	2	19.45	13.48	98.3	5.11e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
6	067-0301.2040.2093.2	2	19.42	14.15	97.5	5.27e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
7	067-0702.2049.2104.2	2	18.94	13.19	98.2	6.89e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
8	067-0701.2045.2103.2	2	18.41	12.40	97.3	6.78e+008	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911

9	067-0702.2275.2300.2	2	18.36	13.08	95.5	5.17e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
10	067-0702.3446.3492.2	2	17.16	12.42	92.1	4.86e+008	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
11	067-0301.3488.3488.2	2	17.12	13.76	90.4	5.67e+008	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
12	067-0701.3443.3443.2	2	14.68	14.68	82.0	3.13e+008	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
13	067-0702.2355.2378.0	2	9.49	9.49	63.1	3.65e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
10	10.1	3	2	25.38	7	1.60e+009	72721.8	PA_BS12:2189568163	PA_BS12:2189568163 or1494 Arabinogalactan endo-1,4-beta-galactosidase [B. setacea BS12] 679 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0301.8108.8155.0	2	14.19	14.19	92.0	3.56e+008	(K)QGQYDFLYDLTNAVENLNGFK(G)	2449.167
2	067-0701.8104.8140.0	2	12.05	12.05	86.8	2.94e+008	(K)QGQYDFLYDLTNAVENLNGFK(G)	2449.167
3	067-0301.6313.6313.0	3	11.19	3.08	78.6	9.46e+008	(R)DTLTSMQNAGVLPDMVQVGNEVNPGMCWDLGR(I)	3504.602

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
11	11.1	3	2	22.78	6	7.90e+008	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	067-0701.5926.5962.0	2	12.03	4.46	81.9	3.23e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.121
2	067-0301.5911.5976.2	2	10.97	6.25	80.7	3.02e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.121
3	067-0702.3816.3816.2	2	10.75	10.75	62.7	1.65e+008	(R)AAMYTEEEGYIFDAGVANK(V)	2078.938

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
12	12.1	2	2	22.39	3	1.57e+008	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	067-0702.3901.3901.0	2	13.09	4.05	78.4	1.16e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.955
2	067-0301.2740.2751.2	2	9.30	9.30	61.5	4.11e+007	(K)GAIVVGAFDER(I)	1133.595