Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\080910_caecumcontent_pellet_triplicate
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 233 **Hits:** 491
beginning to assemble proteins .... proteins assembled 0.076978 sec
proteins filtered by unique peptides 0.006861 sec
proteins filtered by score
calculated protein coverage maps 0.059515 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.006742 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 16 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	64	12	214.25	27	1.97e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	64	12	214.25	45	1.97e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (C(
2	2.1	24	7	114.98	19	1.08e+009	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp
2	2.1	24	7	114.98	30	1.08e+009	50621.3	PA_Bse_meta_comb:2073574943	PA_Bse_meta_comb:2073574943 BaSeMet_00185990 Endoglucanase [Bankia setacea microbiome (C(
3	3.1	19	6	91.91	15	6.83e+008	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
3	3.1	19	6	91.91	32	6.83e+008	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
4	4.1	16	5	76.21	5	5.42e+008	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
4	4.1	16	5	76.21	5	5.42e+008	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
5	5.1	14	4	75.94	11	2.18e+008	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
5	5.1	14	4	75.94	20	2.18e+008	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
6	6.1	12	4	61.17	13	5.48e+008	76692.5	PA_Bse_meta_comb:2073574946	PA_Bse_meta_comb:2073574946 BaSeMet_00186020 Endoglucanase [Bankia setacea microbiome (C(
6	6.1	12	4	61.17	16	5.48e+008	62702.1	PA_BS12:2189571771	PA_BS12:2189571771 or0871 Endoglucanase [B. setacea BS12] 571 bp
7	7.1	14	3	54.57	8	7.58e+008	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
7	7.1	14	3	54.57	8	7.58e+008	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome (
8	8.1	13	4	53.70	5	2.99e+008	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
8	8.1	13	4	53.70	5	2.99e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.2	6	3	34.48	15	1.12e+008	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
9	9.1	13	3	51.69	8	9.94e+008	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
9	9.1	13	3	51.69	8	9.94e+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) [
9	9.1	9	2	37.42	4	9.79e+008	90871.9	PA_Bse08:2503995091	PA_Bse08:2503995091 BS08DRAFT_00035590 Cellulose or protein binding domain./Cellulose binding (
10	10.1	7	3	43.57	7	8.11e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
11	11.1	12	2	36.04	19	8.42e+008	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
12	12.1	8	2	33.76	12	1.99e+009	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
12	12.1	8	2	33.76	13	1.99e+009	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
13	13.1	8	2	31.14	4	1.12e+008	40145.6	PA_Bse02:2503999765	PA_Bse02:2503999765 BS02DRAFT_00005000 Cellulose or protein binding domain. [B. setacea BS02
13	13.1	8	2	31.14	8	1.12e+008	23197.0	PA_Bse_meta_comb:2073559086	PA_Bse_meta_comb:2073559086 BaSeMet_00027420 hypothetical protein [Bankia setacea microbiome
14	14.1	5	2	23.41	7	7.37e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setace
15	15.1	2	2	20.45	21	2.03e+007	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
Totals:	451	118							

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	64	12	214.25	27	1.97e+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	072-1901.5310.5399.3	3	21.33	21.33	96.7	1.93e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	072-1801.5979.5982.2	2	20.90	17.16	98.6	7.05e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
3	072-1801.5335.5408.3	3	20.81	20.81	96.3	1.69e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
4	072-1701.5360.5458.0	3	20.79	20.79	95.9	1.29e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
5	072-1701.5226.5357.3	3	20.58	15.83	91.6	1.71e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
6	072-1801.5776.5793.2	2	19.91	12.45	98.3	1.02e+008	(R)EWQDALVDYMVEK(D)	1625.752
7	072-1701.5774.5784.2	2	19.44	10.99	98.9	7.24e+007	(R)EWQDALVDYMVEK(D)	1625.752
8	072-1801.3641.3665.0	3	18.87	9.89	94.4	1.10e+008	(R)LDANPPYADADREGYEFTR(E)	2199.995
9	072-1901.5768.5808.2	2	18.86	11.23	97.0	1.36e+008	(R)EWQDALVDYMVEK(D)	1625.752
10	072-1701.5877.5984.2	2	18.63	11.57	94.6	1.51e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
11	072-1801.5213.5327.3	3	18.61	12.73	92.0	1.83e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
12	072-1801.5874.5966.2	2	18.50	15.33	95.2	1.50e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
13	072-1801.5794.5811.3	3	18.39	7.67	97.2	1.55e+007	(R)EWQDALVDYMVEK(D)	1625.752
14	072-1701.5480.5593.0	3	18.18	10.83	94.3	1.11e+010	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
15	072-1801.4572.4584.0	3	18.15	10.42	96.1	1.55e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
16	072-1801.5492.5598.0	3	18.12	10.78	93.3	1.19e+010	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
17	072-1901.5489.5595.0	3	18.09	10.92	92.9	9.85e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
18	072-1801.7011.7038.2	2	17.79	17.79	94.5	8.27e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
19	072-1901.5879.5978.2	2	17.65	13.34	95.2	1.62e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
20	072-1701.4556.4616.0	3	17.57	10.60	93.8	1.55e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
21	072-1701.5993.5993.2	2	17.55	14.24	94.7	6.73e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
22	072-1901.5805.5809.3	3	17.35	6.70	96.2	1.64e+007	(R)EWQDALVDYMVEK(D)	1625.752
23	072-1801.5863.5951.3	3	17.15	11.40	87.3	6.08e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
24	072-1801.5345.5409.4	4	17.08	10.96	90.7	1.72e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
25	072-1701.5351.5398.4	4	17.06	12.40	90.4	1.38e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
26	072-1801.5957.5981.3	3	16.67	12.62	87.7	5.58e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
27	072-1701.5983.5992.3	3	16.54	11.62	85.3	3.78e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
28	072-1901.4154.4201.0	3	16.52	9.08	93.5	4.74e+007	(R)AGWDEHFGYLR(D)	1350.623
29	072-1901.5194.5307.3	3	16.52	16.52	80.4	2.02e+010	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
30	072-1801.2397.2422.0	2	16.32	8.97	92.3	5.87e+006	(R)LDANPPYADADR(E)	1317.608
31	072-1901.5869.5976.3	3	16.10	11.53	86.2	6.41e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
32	072-1701.5868.5976.3	3	16.05	8.96	85.6	6.26e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
33	072-1701.5793.5820.3	3	15.77	5.82	94.4	1.78e+007	(R)EWQDALVDYMVEK(D)	1625.752
34	072-1701.3956.3982.2	2	15.71	12.06	92.6	5.72e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
35	072-1901.7032.7032.2	2	15.61	15.61	76.4	6.19e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
36	072-1901.4556.4558.0	3	15.57	7.78	92.2	1.11e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
37	072-1801.6734.6774.0	3	15.55	15.55	82.0	2.45e+007	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
38	072-1801.4166.4168.0	3	15.52	7.72	93.6	5.02e+007	(R)AGWDEHFGYLR(D)	1350.623
39	072-1701.3943.3948.0	3	15.38	9.20	86.6	3.56e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
40	072-1901.6736.6773.0	3	15.25	15.25	80.2	2.45e+007	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
41	072-1701.2387.2409.0	2	15.23	7.14	89.4	6.57e+006	(R)LDANPPYADADR(E)	1317.608
42	072-1801.3943.3948.0	3	15.14	8.37	82.3	3.39e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
43	072-1801.6292.6300.0	3	15.02	15.02	84.1	1.33e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
44	072-1701.4153.4159.0	3	14.95	6.17	92.8	4.09e+007	(R)AGWDEHFGYLR(D)	1350.623

45	072-1901.3955.3999.2	2	14.89	11.40	88.7	5.38e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
46	072-1801.3952.3995.2	2	14.47	9.00	88.7	6.07e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
47	072-1901.6300.6328.0	3	14.26	10.00	78.3	1.58e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
48	072-1701.2405.2405.0	2	14.22	6.87	88.3	5.39e+006	(R)LDANPPYADADR(E)	1317.608
49	072-1901.2390.2394.2	2	14.18	8.54	87.8	4.13e+006	(R)LDANPPYADADR(E)	1317.608
50	072-1901.2429.2429.0	2	14.14	5.04	87.0	4.68e+006	(R)LDANPPYADADR(E)	1317.608
51	072-1901.3944.3950.0	3	13.84	6.47	75.3	2.47e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
52	072-1901.5493.5520.0	3	13.79	6.86	87.0	8.09e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
53	072-1801.5262.5399.2	2	13.53	10.52	72.1	1.05e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
54	072-1801.3687.3697.2	2	12.77	5.14	76.5	1.44e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
55	072-1701.5601.5601.0	3	12.54	6.63	83.0	1.06e+010	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
56	072-1801.2404.2404.0	2	12.23	4.79	90.0	5.46e+006	(R)LDANPPYADADR(E)	1317.608
57	072-1801.5861.5861.0	2	12.06	7.14	85.3	6.48e+007	(R)EWQDALVDYMVEK(D)	1625.752
58	072-1701.3687.3699.2	2	11.76	6.20	76.7	1.50e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
59	072-1901.6342.6342.0	3	10.75	10.75	73.8	1.06e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
60	072-1901.2419.2419.0	2	9.56	4.24	81.1	4.61e+006	(R)LDANPPYADADR(E)	1317.608
61	072-1701.4636.4636.0	3	9.48	4.16	74.6	6.90e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
62	072-1901.6403.6403.0	3	8.98	8.98	71.1	8.61e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
63	072-1701.2381.2381.0	2	7.94	3.76	97.6	4.48e+006	(R)LDANPPYADADR(E)	1317.608
64	072-1701.7039.7039.2	2	7.34	3.81	81.2	3.00e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

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	24	7	114.98	19	1.08e+009	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1801.5733.5739.0	3	20.20	20.20	95.9	2.16e+007	(R)HEPSDDETNPSGAPMELYVGNTFWADDNSR(T)	3351.414
2	072-1901.4510.4510.0	3	19.64	10.37	95.5	1.28e+008	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
3	072-1901.4505.4517.0	3	19.18	10.70	95.2	1.41e+008	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
4	072-1701.5731.5737.0	3	18.74	18.74	96.8	1.71e+007	(R)HEPSDDETNPSGAPMELYVGNTFWADDNSR(T)	3351.414
5	072-1801.4530.4536.0	3	17.98	9.34	92.8	1.25e+008	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
6	072-1701.4499.4503.0	3	17.38	7.90	90.9	1.05e+008	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
7	072-1801.5712.5752.0	3	16.92	16.92	89.2	2.75e+007	(R)HEPSDDETNPSGAPMELYVGNTFWADDNSR(T)	3351.414
8	072-1701.6445.6445.0	3	15.96	15.96	83.0	2.92e+007	(K)IDVPHGEEFSNPNWGENLFEAGDNPIDIPK(E)	3350.561
9	072-1801.6399.6405.0	3	15.74	15.74	90.0	3.56e+007	(K)IDVPHGEEFSNPNWGENLFEAGDNPIDIPK(E)	3350.561
10	072-1701.2730.2774.0	3	15.73	5.55	89.0	1.17e+007	(R)LDARPPYVDADR(D)	1387.697
11	072-1901.4706.4746.0	2	15.51	10.49	88.5	2.92e+007	(R)DNESGWGEWGGFDER(K)	1740.689
12	072-1901.4026.4085.0	2	15.37	9.36	86.9	8.67e+007	(R)TIQQTMDEITAR(G)	1406.695
13	072-1701.4726.4743.2	2	15.01	10.93	87.6	2.20e+007	(R)DNESGWGEWGGFDER(K)	1740.689
14	072-1801.2737.2770.0	3	14.99	6.25	89.9	1.09e+007	(R)LDARPPYVDADR(D)	1387.697
15	072-1901.2725.2766.0	3	14.91	6.21	87.2	7.78e+006	(R)LDARPPYVDADR(D)	1387.697
16	072-1701.5721.5721.0	3	13.85	13.85	82.3	1.47e+007	(R)HEPSDDETNPSGAPMELYVGNTFWADDNSR(T)	3351.414
17	072-1701.4032.4038.0	2	13.35	7.36	83.3	7.29e+007	(R)TIQQTMDEITAR(G)	1406.695
18	072-1901.4524.4531.2	2	12.75	7.36	87.9	3.25e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
19	072-1701.5045.5045.0	3	12.57	5.87	87.8	2.39e+007	(K)EQLVFSPHTYGPSVFVQR(M)	2091.066

20	072-1901.5024.5034.0	3	12.38	7.49	86.3	2.20e+007	(K)EQLVFSPHTYGPSVFVQR(M)	2091.066
21	072-1801.4538.4573.2	2	11.98	5.59	87.7	3.19e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
22	072-1801.6387.6387.0	3	11.88	11.88	76.7	2.60e+007	(K)IDVPHGEEFSNPNWGENLFEAGDNPIDIPK(E)	3350.561
23	072-1701.4512.4548.2	2	11.48	5.51	87.4	2.93e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
24	072-1801.4726.4738.0	2	10.69	5.93	79.6	2.77e+007	(R)DNESGWGEWGGFDER(K)	1740.689

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	19	6	91.91	15	6.83e+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	072-1901.4810.4838.0	3	18.42	11.72	88.1	5.63e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
2	072-1901.3752.3759.0	3	16.17	9.08	81.0	8.22e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
3	072-1701.4792.4807.0	3	16.09	8.22	81.4	6.50e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
4	072-1801.3351.3368.0	3	15.53	6.13	86.9	4.25e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
5	072-1801.4994.4994.0	2	15.05	7.21	78.9	1.97e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
6	072-1901.4971.4979.2	2	14.64	6.72	81.6	2.42e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
7	072-1801.4976.4981.0	3	14.16	5.96	86.7	1.89e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
8	072-1901.3681.3700.2	2	13.81	13.81	87.9	3.45e+007	(K)GAIVVGAFDER(I)	1133.595
9	072-1701.4953.4981.0	3	13.37	5.50	85.5	2.29e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
10	072-1901.4960.4989.0	3	13.07	5.76	84.6	2.36e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
11	072-1801.6219.6219.0	3	12.93	12.93	85.5	1.32e+007	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
12	072-1701.3676.3680.2	2	12.91	12.91	83.5	2.88e+007	(K)GAIVVGAFDER(I)	1133.595
13	072-1701.4959.4966.0	2	12.69	5.26	83.7	1.95e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
14	072-1701.3745.3751.0	3	12.42	5.11	75.9	9.06e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
15	072-1801.3749.3756.0	3	12.18	3.83	70.3	7.51e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
16	072-1901.6221.6221.0	3	12.00	12.00	71.9	1.54e+007	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
17	072-1801.3690.3695.2	2	11.76	11.76	80.5	2.54e+007	(K)GAIVVGAFDER(I)	1133.595
18	072-1901.6212.6212.0	3	11.31	11.31	80.4	1.55e+007	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
19	072-1701.6248.6248.0	3	9.01	9.01	71.5	9.93e+006	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672

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	16	5	76.21	5	5.42e+008	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1901.6592.6592.0	3	18.91	12.87	88.2	5.57e+006	(R)VDTNGTVSLIEDSMNNPNGIALSPNEDVLYVGGDSYR(V)	3925.840
2	072-1901.2554.2560.0	3	16.08	8.46	92.2	1.98e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
3	072-1901.4486.4534.0	2	14.87	7.31	92.5	7.00e+007	(R)ALPENLDQVYLK(A)	1402.758
4	072-1701.4488.4560.2	2	14.31	6.72	89.0	7.21e+007	(R)ALPENLDQVYLK(A)	1402.758
5	072-1801.2540.2545.0	3	13.94	6.36	85.9	1.37e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
6	072-1701.4773.4790.0	3	13.92	7.74	85.9	5.04e+007	(R)ASDGTLYFTDPDYQQGTTDGQSITGVYR(V)	3056.376

7	072-1801.4502.4518.0	2	13.83	7.00	89.2	6.65e+007	(R)ALPENLDQVYLK(A)	1402.758
8	072-1701.2546.2582.0	3	12.45	3.24	86.3	2.62e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
9	072-1701.4745.4745.0	2	12.43	8.14	77.8	1.34e+007	(R)TAVASTYNGSVFNSPNDLIR(A)	2126.052
10	072-1901.4728.4728.0	2	12.19	8.80	82.4	2.04e+007	(R)TAVASTYNGSVFNSPNDLIR(A)	2126.052
11	072-1901.4778.4778.0	3	12.10	4.34	76.4	5.09e+007	(R)ASDGTLYFTDPDYQQGTTDGQSITGVYR(V)	3056.376
12	072-1901.4774.4774.0	3	11.65	11.65	74.8	4.98e+007	(R)ASDGTLYFTDPDYQQGTTDGQSITGVYR(V)	3056.376
13	072-1901.4732.4732.0	3	11.22	11.22	73.9	2.91e+007	(R)TAVASTYNGSVFNSPNDLIR(A)	2126.052
14	072-1901.4768.4768.0	3	8.84	8.84	71.3	2.82e+007	(R)TAVASTYNGSVFNSPNDLIR(A)	2126.052
15	072-1901.6610.6610.0	3	8.81	8.81	88.2	5.45e+006	(R)VDTNGTVSLIEDSMNNPNGIALSPNEDVLYVGGDSYR(V)	3925.840
16	072-1901.4739.4739.0	2	8.36	8.36	61.2	2.01e+007	(R)TAVASTYNGSVFNSPNDLIR(A)	2126.052

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	14	4	75.94	11	2.18e+008	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	072-1701.3846.3861.0	3	21.77	21.77	97.8	1.61e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
2	072-1701.7218.7246.0	3	21.07	21.07	92.0	1.31e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
3	072-1901.3851.3867.0	3	20.53	20.53	95.0	1.91e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
4	072-1801.7225.7259.0	3	20.50	16.34	89.5	1.39e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
5	072-1801.3656.3685.2	2	19.06	9.75	95.5	2.65e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
6	072-1901.3666.3693.2	2	17.30	10.54	95.2	2.88e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
7	072-1901.3862.3862.0	3	16.53	16.53	84.2	1.91e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
8	072-1701.3662.3668.2	2	16.37	11.09	91.2	2.85e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
9	072-1701.7222.7222.0	3	14.97	14.97	88.2	9.26e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
10	072-1701.3873.3873.0	3	14.47	14.47	81.5	1.56e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
11	072-1901.6453.6453.0	3	14.04	14.04	80.5	6.43e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
12	072-1901.7221.7221.0	3	12.74	12.74	82.7	9.55e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
13	072-1801.6459.6459.0	3	10.53	10.53	77.5	5.89e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
14	072-1801.6438.6438.0	3	8.24	3.50	80.0	6.32e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022

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	12	4	61.17	13	5.48e+008	76692.5	PA_Bse_meta_comb:2073574946	PA_Bse_meta_comb:2073574946 BaSeMet_00186020 Endoglucanase [Bankia setacea microbiome (Cor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1801.4932.4972.0	3	17.09	10.37	89.5	6.27e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119
2	072-1701.4918.4984.0	3	16.86	11.21	88.0	7.19e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119
3	072-1701.4407.4415.2	2	16.01	16.01	89.1	4.63e+007	(R)DIQQTMDEITER(G)	1478.680
4	072-1801.4426.4452.2	2	15.96	15.96	88.1	4.78e+007	(R)DIQQTMDEITER(G)	1478.680
5	072-1901.6073.6079.0	3	15.21	6.50	82.6	6.78e+007	(K)TPVPHGDEFSNPNWGENLFEAGDNIPDVPK(S)	3292.519
6	072-1801.6064.6073.0	3	13.04	9.78	74.0	7.69e+007	(K)TPVPHGDEFSNPNWGENLFEAGDNIPDVPK(S)	3292.519

7	072-1801.5089.5089.0	3	12.86	12.86	74.4	9.36e+006	(R)HEPNDDDTNPGGAPMELYVGNMSWADDHSR(D)	3327.371
8	072-1701.4928.4936.2	2	12.85	6.98	87.0	1.47e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119
9	072-1901.4949.4954.2	2	12.82	6.49	86.7	1.73e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119
10	072-1901.4923.4992.0	3	12.70	7.94	78.5	7.08e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119
11	072-1901.4415.4433.2	2	12.58	12.58	84.5	4.46e+007	(R)DIQQTMDEITER(G)	1478.680
12	072-1801.4967.4967.2	2	11.74	4.47	84.2	1.76e+007	(R)FPVVPQTLDPSDSQGTGSVLK(N)	2172.119

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	14	3	54.57	8	7.58e+008	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	072-1901.4752.4761.2	2	20.35	20.35	97.0	2.54e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
2	072-1701.4747.4767.2	2	19.84	19.84	96.9	2.78e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
3	072-1901.4977.5013.3	3	18.00	13.23	91.6	1.03e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909
4	072-1801.4759.4765.2	2	17.63	17.63	92.9	2.88e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
5	072-1701.4759.4759.0	3	17.54	13.36	90.6	1.76e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
6	072-1701.4977.5020.3	3	16.51	10.28	90.3	1.32e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909
7	072-1901.4756.4756.0	3	16.45	7.35	88.3	1.57e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
8	072-1701.4957.4991.2	2	16.22	9.39	93.2	2.71e+007	(R)DAFGNDWIIK(S)	1178.585
9	072-1901.4953.4986.2	2	16.18	8.52	92.3	1.93e+007	(R)DAFGNDWIIK(S)	1178.585
10	072-1801.4985.5049.2	2	16.13	11.65	92.8	7.92e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
11	072-1901.4982.4988.2	2	15.60	11.16	92.2	6.91e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
12	072-1701.4989.5022.2	2	15.57	9.93	91.4	8.79e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
13	072-1801.4974.4997.2	2	15.19	7.68	91.8	2.13e+007	(R)DAFGNDWIIK(S)	1178.585
14	072-1801.4990.4996.0	3	14.78	8.15	85.9	1.05e+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
8	8.1	13	4	53.70	5	2.99e+008	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	072-1701.7842.7913.0	3	17.42	8.45	83.2	1.01e+007	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
2	072-1801.7846.7852.0	3	17.14	9.10	85.6	8.86e+006	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
3	072-1901.7840.7920.0	3	16.58	8.18	86.3	1.08e+007	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
4	072-1801.5433.5438.0	2	15.67	11.16	92.2	3.70e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
5	072-1701.5430.5435.0	2	14.58	10.26	89.9	5.35e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
6	072-1901.5429.5455.0	2	14.58	9.97	90.1	5.12e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
7	072-1901.7852.7852.0	3	14.51	6.94	84.0	6.56e+006	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
8	072-1701.4007.4040.2	2	12.70	9.62	86.9	2.84e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
9	072-1901.4008.4029.2	2	12.19	8.56	86.2	2.54e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
10	072-1801.4022.4031.2	2	12.06	8.95	82.8	2.42e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781

11	072-1901.7847.7847.0	3	10.78	7.68	79.1	6.14e+006	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
12	072-1701.4613.4613.2	2	7.91	4.59	68.1	1.50e+007	(R)VLVENAYPPL(-)	1114.615
13	072-1801.4002.4002.0	2	7.11	7.11	69.5	2.24e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781

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	8.2	6	3	34.48	15	1.12e+008	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	072-1701.6249.6249.2	2	12.82	12.82	77.1	4.75e+006	(R)YQNEYIAGITEIIGDSK(Y)	1913.950
2	072-1701.4007.4040.2	2	12.70	9.62	86.9	2.84e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
3	072-1901.4008.4029.2	2	12.19	8.56	86.2	2.54e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
4	072-1801.4022.4031.2	2	12.06	8.95	82.8	2.42e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
5	072-1901.6653.6653.0	3	8.96	8.96	72.9	7.08e+006	(R)NGWGGANRPSGASSSTDLNTYVDESRIDR(R)	3082.421
6	072-1801.4002.4002.0	2	7.11	7.11	69.5	2.24e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781

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	3	51.69	8	9.94e+008	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	072-1901.4440.4456.0	3	22.38	19.28	97.2	6.99e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
2	072-1801.4458.4476.0	3	20.81	17.55	95.7	8.02e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
3	072-1701.4425.4449.0	3	19.73	19.73	94.2	7.57e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
4	072-1901.6038.6044.0	3	15.04	9.04	89.5	1.41e+008	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
5	072-1801.6033.6040.0	3	14.43	8.37	86.7	1.55e+008	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
6	072-1701.6956.6956.0	3	14.27	9.28	75.4	2.96e+006	(K)MALIALAYDFTGNDSYAK(A)	1963.948
7	072-1701.6042.6059.3	3	13.44	6.03	86.1	2.19e+008	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
8	072-1801.6947.6947.0	3	13.22	7.28	80.6	3.92e+006	(K)MALIALAYDFTGNDSYAK(A)	1963.948
9	072-1801.6937.6937.0	3	12.99	7.50	75.2	4.16e+006	(K)MALIALAYDFTGNDSYAK(A)	1963.948
10	072-1801.6933.6933.0	3	12.20	5.04	73.3	4.36e+006	(K)MALIALAYDFTGNDSYAK(A)	1963.948
11	072-1701.6062.6082.2	2	12.15	4.11	83.0	6.80e+007	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
12	072-1801.6051.6105.2	2	12.09	4.56	81.3	9.51e+007	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
13	072-1901.6060.6095.2	2	11.83	6.47	80.9	7.44e+007	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153

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	7	3	43.57	7	8.11e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)

1	072-1801.5264.5264.0	3	15.59	15.59	80.9	3.12e+008	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
2	072-1801.3200.3239.2	2	14.93	6.46	87.5	4.69e+007	(R)TIQQTMDEIK(A)	1206.604
3	072-1901.3201.3253.2	2	14.43	6.37	86.3	6.00e+007	(R)TIQQTMDEIK(A)	1206.604
4	072-1701.3195.3206.2	2	14.35	6.93	86.1	4.25e+007	(R)TIQQTMDEIK(A)	1206.604
5	072-1901.6665.6665.0	3	13.05	13.05	76.4	6.68e+006	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
6	072-1801.6658.6658.0	3	12.15	12.15	71.3	5.99e+006	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
7	072-1701.5260.5260.0	3	11.38	11.38	71.6	3.37e+008	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368

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	12	2	36.04	19	8.42e+008	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea microb

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1901.4638.4656.0	2	20.57	20.57	93.6	2.45e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
2	072-1701.4643.4657.0	2	18.01	18.01	93.0	2.12e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
3	072-1801.4658.4668.2	2	17.11	17.11	86.1	2.24e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
4	072-1701.5103.5122.0	3	15.47	8.60	84.9	3.13e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
5	072-1901.5099.5135.0	3	15.27	7.13	85.1	3.35e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
6	072-1801.5112.5123.0	3	14.74	5.62	84.5	3.83e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
7	072-1901.4618.4636.0	3	14.41	9.06	77.2	2.24e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
8	072-1901.5132.5132.0	2	13.37	13.37	80.0	1.75e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
9	072-1801.4628.4633.0	3	12.15	6.47	74.8	2.01e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
10	072-1701.5112.5112.0	2	11.80	5.37	83.9	1.40e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
11	072-1701.4614.4628.0	3	10.40	4.66	71.3	2.02e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
12	072-1901.5108.5108.0	2	6.04	6.04	71.4	1.27e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055

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	8	2	33.76	12	1.99e+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	072-1801.5735.5735.0	3	17.09	17.09	87.1	3.02e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
2	072-1701.3237.3322.2	2	16.67	10.91	88.8	5.16e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
3	072-1901.3241.3325.2	2	16.11	11.21	87.4	5.59e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
4	072-1801.3240.3322.2	2	15.64	10.96	87.7	5.13e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
5	072-1801.3335.3350.2	2	15.13	9.10	86.8	9.71e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
6	072-1901.3334.3352.2	2	14.05	8.86	85.1	1.45e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
7	072-1701.3327.3327.2	2	13.52	8.27	83.6	1.05e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
8	072-1801.5730.5730.0	3	10.95	10.95	70.3	2.55e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072

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

			(#)	Search Score		Intensity	(Da)		
13	13.1	8	2	31.14	4	1.12e+008	40145.6	PA_Bse02:2503999765	PA_Bse02:2503999765 BS02DRAFT_00005000 Cellulose or protein binding domain. [B. setacea BS02 (Isolate from

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1701.3192.3196.2	2	16.72	11.50	90.5	1.31e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
2	072-1801.3187.3193.2	2	16.19	10.97	89.9	1.21e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
3	072-1901.3187.3212.0	2	14.66	8.50	88.1	1.55e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
4	072-1901.2885.2896.0	3	14.42	8.83	88.5	1.44e+007	(R)NGSSGLSNPNTTDINNFKR(G)	2035.980
5	072-1801.2882.2926.0	3	13.08	7.52	90.8	1.39e+007	(R)NGSSGLSNPNTTDINNFKR(G)	2035.980
6	072-1701.2883.2899.0	3	12.42	6.72	88.5	1.59e+007	(R)NGSSGLSNPNTTDINNFKR(G)	2035.980
7	072-1901.3337.3337.2	2	12.02	7.82	83.0	1.31e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
8	072-1701.3216.3216.0	2	6.96	2.80	72.5	1.43e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
14	14.1	5	2	23.41	7	7.37e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setacea BS12] 541

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1901.3117.3122.0	3	12.40	12.40	73.5	9.74e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
2	072-1701.3093.3093.0	3	12.23	12.23	71.4	8.78e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
3	072-1801.4359.4370.0	3	11.01	11.01	77.3	1.93e+007	(R)QLGMNPGDNHETLIALR(G)	1878.950
4	072-1901.4339.4359.0	3	10.97	7.07	79.8	2.44e+007	(R)QLGMNPGDNHETLIALR(G)	1878.950
5	072-1801.3110.3127.0	3	9.35	9.35	72.1	1.16e+007	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
15	15.1	2	2	20.45	21	2.03e+007	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiome

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-1701.2771.2771.0	3	12.58	4.80	88.2	5.17e+006	(R)DNIQGITKPAIR(R)	1325.754
2	072-1901.3312.3312.0	2	7.87	4.64	77.9	1.51e+007	(R)ISGLIYEETR(G)	1180.621