Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\080410_caecum_content
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 58 **Hits:** 161
Data Directory: msdataSM\080510_caecum_contents_duplicate
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 116 **Hits:** 305
beginning to assemble proteins .... proteins assembled 0.06811 sec
proteins filtered by unique peptides 0.007659 sec
proteins filtered by score
calculated protein coverage maps 0.060192 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.007478 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 15 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	44	9	162.08	20	7.27e+009	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	42	8	152.37	33	7.26e+009	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	15	6	86.12	12	5.03e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
2	2.1	6	2	30.91	2	2.08e+008	78391.5	PA_Bse02:2503998382	PA_Bse02:2503998382 BS02DRAFT_00024320 Cellulose or protein binding domain./Cellulose binding (
2	2.1	6	2	30.91	4	2.08e+008	50267.5	PA_Bse_meta_comb:2073595739	PA_Bse_meta_comb:2073595739 BaSeMet_00393950 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	6	2	30.91	14	2.08e+008	15283.0	PA_Bse_meta_comb:2073592399	PA_Bse_meta_comb:2073592399 BaSeMet_00360550 Cellulase (glycosyl hydrolase family 5). [Bankia s
2	2.1	5	2	26.67	38	1.47e+008	10516.5	PA_Bse_meta_comb:2073579941	PA_Bse_meta_comb:2073579941 BaSeMet_00235970 Cellulase (glycosyl hydrolase family 5). [Bankia s
3	3.1	15	5	84.20	14	3.32e+008	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
3	3.1	15	5	84.20	14	3.32e+008	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome (
4	4.1	15	5	80.31	9	3.22e+008	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
4	4.1	15	5	80.31	20	3.22e+008	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
5	5.1	14	5	66.99	20	9.96e+008	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
5	5.1	14	5	66.99	21	9.96e+008	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
5	5.1	5	2	26.92	5	1.80e+008	38283.0	PA_Bse08:2503995336	PA_Bse08:2503995336 BS08DRAFT_00038010 Cellulose or protein binding domain. [B. setacea BS08
5	5.1	5	2	26.92	7	1.80e+008	26461.7	PA_Bse_meta_comb:2073585634	PA_Bse_meta_comb:2073585634 BaSeMet_00292900 Cellulose or protein binding domain. [Bankia set
5	5.1	5	2	26.92	12	1.80e+008	15995.4	PA_Bse_meta_comb:2073569070	PA_Bse_meta_comb:2073569070 BaSeMet_00127260 hypothetical protein [Bankia setacea microbiome
5	5.1	5	2	26.92	13	1.80e+008	14432.7	PA_Bse_meta_comb:2073578186	PA_Bse_meta_comb:2073578186 BaSeMet_00218420 hypothetical protein [Bankia setacea microbiome
5	5.1	5	2	26.92	15	1.80e+008	12333.4	PA_Bse_meta_comb:2073567328	PA_Bse_meta_comb:2073567328 BaSeMet_00109840 hypothetical protein [Bankia setacea microbiome
5	5.2	7	3	37.76	9	1.91e+008	40145.6	PA_Bse02:2503999765	PA_Bse02:2503999765 BS02DRAFT_00005000 Cellulose or protein binding domain. [B. setacea BS02
5	5.2	7	3	37.76	11	1.91e+008	32736.4	PA_Bse08:2503997065	PA_Bse08:2503997065 BS08DRAFT_00007680 Cellulose or protein binding domain. [B. setacea BS08
5	5.2	7	3	37.76	16	1.91e+008	23197.0	PA_Bse_meta_comb:2073559086	PA_Bse_meta_comb:2073559086 BaSeMet_00027420 hypothetical protein [Bankia setacea microbiome
6	6.1	10	5	66.49	9	4.36e+008	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
6	6.1	10	5	66.49	10	4.36e+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) [
6	6.1	7	4	53.40	7	2.24e+008	90871.9	PA_Bse08:2503995091	PA_Bse08:2503995091 BS08DRAFT_00035590 Cellulose or protein binding domain./Cellulose binding (
7	7.1	14	4	62.37	12	3.70e+008	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 b
7	7.1	14	4	62.37	13	3.70e+008	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
7	7.1	4	2	23.62	4	1.32e+008	57718.9	PA_Bse08:2503996244	PA_Bse08:2503996244 BS08DRAFT_00001320 Cellulose or protein binding domain./Cellulose binding (
8	8.1	11	5	59.02	5	2.28e+008	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolas
8	8.1	11	5	59.02	5	2.28e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
9	9.1	10	3	48.78	29	1.08e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
10	10.1	7	3	42.42	7	1.42e+008	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp
10	10.1	7	3	42.42	11	1.42e+008	50621.3	PA_Bse_meta_comb:2073574943	PA_Bse_meta_comb:2073574943 BaSeMet_00185990 Endoglucanase [Bankia setacea microbiome (Co

11	11.1	5	3	42.07	8	2.63e+008	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
11	11.1	5	3	42.07	14	2.63e+008	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
12	12.1	6	3	36.77	16	4.65e+008	40574.0	PA_Bse_meta_comb:2073563645	PA_Bse_meta_comb:2073563645 BaSeMet_00073010 Lysophospholipase L1 and related esterases [Ba
12	12.1	6	3	36.77	17	4.65e+008	40138.6	PA_BS12:2189567930	PA_BS12:2189567930 or1254 Lysophospholipase L1 and related esterases [B. setacea BS12] 387 bp
13	13.1	4	2	28.83	1	1.21e+008	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
13	13.1	4	2	28.83	1	1.21e+008	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
14	14.1	2	2	20.93	4	4.16e+006	109063.9	PA_Bse02:2503998993	PA_Bse02:2503998993 BS02DRAFT_00000010 TonB-dependent receptor [B. setacea BS02 (Isolate fro
14	14.1	2	2	20.93	4	4.16e+006	109063.9	PA_Bse_meta_comb:2073560314	PA_Bse_meta_comb:2073560314 BaSeMet_00039700 TonB-dependent receptor [Bankia setacea micro
Totals:	397	143							

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	44	9	162.08	20	7.27e+009	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	091-0901.3842.3931.0	3	22.92	17.18	98.4	2.15e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	091-0801.3849.3938.0	3	21.65	17.83	92.9	1.51e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
3	091-0901.4194.4200.2	2	20.42	12.96	98.4	9.41e+007	(R)EWQDALVDYMVEK(D)	1625.752
4	091-0901.1768.1781.0	3	20.21	11.28	93.2	2.02e+007	(R)LDANPPYADADR(E)	1317.608
5	091-2301.1758.1788.0	3	20.21	11.24	93.0	7.58e+006	(R)LDANPPYADADR(E)	1317.608
6	091-0901.3444.3460.0	3	20.20	11.93	97.9	9.29e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
7	091-2301.3841.3921.0	3	20.08	20.08	91.1	1.12e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
8	091-2301.4271.4299.2	2	19.88	16.46	98.4	7.52e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
9	091-0801.1753.1815.0	3	19.71	12.45	93.5	2.24e+007	(R)LDANPPYADADR(E)	1317.608
10	091-2301.4160.4223.2	2	19.40	11.89	98.0	2.00e+008	(R)EWQDALVDYMVEK(D)	1625.752
11	091-0901.4283.4287.2	2	18.20	14.32	95.6	4.37e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
12	091-2301.3428.3444.0	3	18.17	10.92	96.9	1.82e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
13	091-2301.2968.2988.2	2	17.95	11.78	95.5	1.47e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
14	091-0901.3240.3323.2	2	17.39	17.39	93.0	9.85e+007	(R)AGWDEHFGYLR(D)	1350.623
15	091-0801.2990.3025.3	3	17.11	9.68	90.2	5.74e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
16	091-0901.3226.3231.0	3	17.01	9.94	93.7	8.15e+007	(R)AGWDEHFGYLR(D)	1350.623
17	091-2301.4181.4216.3	3	16.77	6.10	94.4	2.69e+007	(R)EWQDALVDYMVEK(D)	1625.752
18	091-2301.3193.3200.2	2	16.36	16.36	88.2	8.05e+007	(R)AGWDEHFGYLR(D)	1350.623
19	091-0801.4193.4209.3	3	16.27	5.04	94.1	9.84e+006	(R)EWQDALVDYMVEK(D)	1625.752
20	091-0801.3449.3454.0	3	16.03	9.06	92.0	6.66e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
21	091-2301.3181.3186.0	3	15.93	8.65	91.6	9.92e+007	(R)AGWDEHFGYLR(D)	1350.623
22	091-0801.3854.3896.0	3	15.91	9.35	73.3	1.49e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
23	091-0801.1769.1797.0	2	15.78	8.14	91.4	7.55e+008	(R)LDANPPYADADR(E)	1317.608
24	091-0901.1776.1804.0	2	15.78	8.15	91.3	6.78e+008	(R)LDANPPYADADR(E)	1317.608
25	091-0901.1686.1773.0	2	15.76	7.17	91.2	6.98e+008	(R)LDANPPYADADR(E)	1317.608
26	091-0801.3230.3232.0	3	15.42	8.34	91.4	7.12e+007	(R)AGWDEHFGYLR(D)	1350.623
27	091-0901.4203.4232.3	3	15.28	4.59	94.9	1.37e+007	(R)EWQDALVDYMVEK(D)	1625.752
28	091-0801.1679.1765.0	2	15.23	6.66	90.0	7.52e+008	(R)LDANPPYADADR(E)	1317.608
29	091-0801.3229.3246.0	2	14.98	11.42	84.2	5.69e+007	(R)AGWDEHFGYLR(D)	1350.623
30	091-2301.1668.1755.0	2	14.77	8.21	91.2	2.39e+008	(R)LDANPPYADADR(E)	1317.608

31	091-0801.4286.4292.2	2	14.65	14.65	89.0	2.37e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
32	091-2301.4259.4263.0	3	14.30	14.30	79.4	4.92e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
33	091-2301.1760.1772.0	2	14.27	6.66	91.1	2.32e+008	(R)LDANPPYADADR(E)	1317.608
34	091-0901.4274.4280.0	3	14.25	9.57	81.3	3.10e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
35	091-2301.3465.3465.2	2	14.13	14.13	87.2	9.34e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
36	091-2301.4043.4049.0	3	13.40	6.62	82.5	1.02e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
37	091-0901.3334.3334.2	2	13.35	9.17	85.0	2.82e+007	(R)AGWDEHFGYLR(D)	1350.623
38	091-0801.4269.4269.0	3	12.52	12.52	78.0	1.62e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
39	091-0901.3535.3535.0	3	11.48	4.10	77.0	7.14e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
40	091-0801.4262.4262.0	3	11.18	11.18	74.8	1.18e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
41	091-0801.4270.4270.0	2	9.75	4.35	95.1	2.06e+007	(R)EWQDALVDYMVEK(D)	1625.752
42	091-2301.2058.2058.0	2	9.71	4.64	79.9	5.28e+006	(K)NGSVFPVR(C)	875.474
43	091-0801.2067.2067.0	2	9.34	4.50	83.6	6.96e+006	(K)NGSVFPVR(C)	875.474
44	091-0901.4183.4183.0	2	8.50	5.20	66.2	6.14e+007	(R)EWQDALVDYMVEK(D)	1625.752

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	15	6	86.12	12	5.03e+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	091-0801.3855.3901.0	3	17.77	11.04	87.7	1.68e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
2	091-0801.1657.1662.0	3	16.84	8.05	91.1	3.26e+007	(R)LDAKPPYADAER(E)	1345.675
3	091-2301.1635.1650.0	3	16.77	7.98	90.4	4.25e+007	(R)LDAKPPYADAER(E)	1345.675
4	091-0901.1655.1730.0	3	16.09	6.48	91.9	5.78e+007	(R)LDAKPPYADAER(E)	1345.675
5	091-0901.3854.3897.0	3	15.22	9.70	81.0	2.32e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
6	091-0801.2443.2450.2	2	14.32	7.16	92.5	1.67e+007	(K)ALGINVVR(F)	841.526
7	091-0901.2439.2472.2	2	14.30	7.71	92.0	1.89e+007	(K)ALGINVVR(F)	841.526
8	091-0901.2512.2519.0	2	14.07	6.21	94.4	3.27e+007	(R)QAMEDFIK(L)	981.471
9	091-2301.2428.2434.2	2	13.71	6.43	88.4	1.70e+007	(K)ALGINVVR(F)	841.526
10	091-0901.2402.2453.2	2	13.29	7.30	85.1	6.83e+007	(R)TIQQTMDEIK(A)	1206.604
11	091-2301.2480.2487.0	2	12.80	4.93	93.7	3.44e+007	(R)QAMEDFIK(L)	981.471
12	091-2301.2357.2362.0	2	12.20	5.03	81.5	6.24e+007	(R)TIQQTMDEIK(A)	1206.604
13	091-0801.2402.2407.0	2	11.90	3.93	79.1	6.61e+007	(R)TIQQTMDEIK(A)	1206.604
14	091-2301.2191.2191.0	3	9.83	9.83	71.1	5.82e+006	(R)EGYSCSASGNPDSVTTVHAYDESK(W)	2504.052
15	091-0801.1691.1727.2	2	9.11	2.89	83.5	8.03e+006	(R)LDAKPPYADAER(E)	1345.675

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	15	5	84.20	14	3.32e+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	091-2301.3492.3516.2	2	20.39	20.39	97.9	1.96e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814

2	091-2301.3642.3665.0	3	18.37	18.37	88.7	5.15e+007	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
3	091-0901.3683.3686.0	2	16.74	9.95	93.0	2.88e+007	(R)DAFGNDWIIK(S)	1178.585
4	091-0801.3527.3527.2	2	16.54	12.89	89.9	6.60e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
5	091-2301.3668.3689.3	3	15.82	9.05	86.0	2.25e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
6	091-0901.3524.3532.2	2	15.57	10.78	90.8	7.90e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
7	091-0901.3697.3704.0	3	15.21	8.71	85.1	9.14e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
8	091-2301.3671.3690.2	2	14.91	9.72	87.8	1.38e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
9	091-0801.3705.3711.2	2	14.65	9.17	92.1	4.24e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
10	091-0801.3697.3703.0	3	13.33	8.94	81.9	8.80e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
11	091-0801.3683.3683.0	3	13.10	13.10	91.4	1.05e+007	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
12	091-0901.3694.3717.2	2	13.01	7.89	90.2	5.41e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
13	091-0801.3239.3244.2	2	12.88	12.88	73.9	5.28e+007	(K)AEEIEEWIR(D)	1174.574
14	091-0901.3239.3244.0	2	12.81	12.81	72.8	4.75e+007	(K)AEEIEEWIR(D)	1174.574
15	091-2301.3201.3205.2	2	11.28	11.28	62.6	4.32e+007	(K)AEEIEEWIR(D)	1174.574

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	15	5	80.31	9	3.22e+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	091-2301.3606.3659.0	3	19.47	13.07	89.7	3.44e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
2	091-0901.3617.3637.0	3	19.00	12.14	90.4	2.63e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
3	091-0801.2557.2611.0	3	16.54	6.62	94.3	4.52e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
4	091-0801.3622.3689.0	3	15.70	8.56	83.9	2.91e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
5	091-2301.2822.2840.0	3	15.19	8.02	81.4	4.77e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
6	091-0901.2544.2550.0	3	14.74	14.74	92.8	2.44e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
7	091-2301.2769.2795.2	2	14.64	14.64	89.0	1.76e+007	(K)GAIVVGAFDER(I)	1133.595
8	091-0801.2861.2867.0	3	14.53	6.80	76.7	4.47e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
9	091-2301.4689.4718.0	2	14.47	7.15	94.7	3.81e+006	(R)WIPWNTPILQ(-)	1267.684
10	091-0901.2794.2816.2	2	14.03	14.03	86.5	2.13e+007	(K)GAIVVGAFDER(I)	1133.595
11	091-0901.4688.4724.0	2	13.75	7.01	90.4	1.91e+006	(R)WIPWNTPILQ(-)	1267.684
12	091-0801.2816.2846.2	2	13.39	13.39	89.6	2.00e+007	(K)GAIVVGAFDER(I)	1133.595
13	091-0801.4694.4724.0	2	12.34	7.30	87.1	1.64e+006	(R)WIPWNTPILQ(-)	1267.684
14	091-2301.4698.4698.0	2	8.25	8.25	100.0	3.06e+006	(R)WIPWNTPILQ(-)	1267.684
15	091-0801.4692.4692.0	2	7.23	3.24	81.2	1.20e+006	(R)WIPWNTPILQ(-)	1267.684

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	5	66.99	20	9.96e+008	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	091-0801.2627.2627.2	2	19.10	11.51	96.9	3.34e+007	(K)SLDVQVYNECR(S)	1325.616

2	091-0901.2628.2632.2	2	17.52	10.84	95.0	4.27e+007	(K)SLDVQVYNECR(S)	1325.616
3	091-2301.2588.2603.2	2	15.46	10.64	93.2	2.77e+007	(K)SLDVQVYNECR(S)	1325.616
4	091-0901.2418.2496.2	2	14.09	9.43	86.3	1.64e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
5	091-0801.3163.3163.0	3	13.82	13.82	86.0	1.06e+007	(K)AGYDWTYQQLSGHECDDVR(F)	2242.946
6	091-2301.2481.2488.2	2	13.58	8.22	84.9	7.70e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
7	091-0901.2579.2637.2	2	13.56	7.14	90.0	5.46e+007	(K)SLDVQVYNECR(S)	1325.616
8	091-2301.2393.2397.2	2	13.54	9.61	84.6	1.02e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
9	091-0801.2520.2520.2	2	13.13	8.06	87.1	7.55e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
10	091-0801.2431.2514.2	2	13.07	6.72	84.8	1.63e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
11	091-2301.2781.2798.0	3	12.16	5.07	83.1	8.09e+007	(R)SQFGNNWFGGHR(N)	1406.635
12	091-0901.2840.2882.2	2	12.11	12.11	76.5	7.01e+007	(R)SQFGNNWFGGHR(N)	1406.635
13	091-2301.2796.2874.2	2	12.05	8.05	80.9	7.34e+007	(R)SQFGNNWFGGHR(N)	1406.635
14	091-2301.2051.2115.0	2	7.82	4.12	62.3	2.17e+007	(K)QNWGMMR(Q)	922.403

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	7	3	37.76	9	1.91e+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	091-0801.2627.2627.2	2	19.10	11.51	96.9	3.34e+007	(R)SLDVQVYNECR(S)	1325.616
2	091-0901.2628.2632.2	2	17.52	10.84	95.0	4.27e+007	(R)SLDVQVYNECR(S)	1325.616
3	091-2301.2588.2603.2	2	15.46	10.64	93.2	2.77e+007	(R)SLDVQVYNECR(S)	1325.616
4	091-0901.2579.2637.2	2	13.56	7.14	90.0	5.46e+007	(R)SLDVQVYNECR(S)	1325.616
5	091-0801.2480.2480.0	2	10.84	4.05	75.6	5.13e+006	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
6	091-0901.2391.2391.0	2	8.94	4.12	79.5	5.72e+006	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
7	091-2301.2051.2115.0	2	7.82	4.12	62.3	2.17e+007	(K)QNWGMMR(Q)	922.403

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	10	5	66.49	9	4.36e+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	091-2301.3600.3600.0	3	17.17	17.17	75.8	3.51e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
2	091-0801.3608.3644.0	3	16.28	16.28	81.3	2.14e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
3	091-0801.3181.3263.0	2	13.88	5.46	90.4	5.18e+007	(K)YVVNGGISVWK(L)	1221.663
4	091-0901.3181.3214.2	2	13.87	8.25	90.8	3.51e+007	(K)YVVNGGISVWK(L)	1221.663
5	091-2301.2171.2236.0	2	13.09	8.23	88.4	6.33e+007	(K)ASSNTAQTWELR(Q)	1363.661
6	091-2301.4358.4358.0	3	12.25	7.95	93.5	2.27e+006	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
7	091-0901.2210.2216.0	2	12.02	7.10	85.9	6.46e+007	(K)ASSNTAQTWELR(Q)	1363.661
8	091-0801.2207.2278.0	2	10.27	5.19	82.5	8.40e+007	(K)ASSNTAQTWELR(Q)	1363.661
9	091-0801.2152.2157.0	2	10.10	2.40	92.1	2.78e+007	(K)LLNMYER(A)	938.477
10	091-2301.3172.3255.0	2	9.57	9.57	68.1	5.02e+007	(K)YVVNGGISVWK(L)	1221.663

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	4	62.37	12	3.70e+008	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	091-2301.2034.2038.2	2	19.97	14.10	99.0	2.46e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
2	091-0901.2060.2068.2	2	19.44	13.57	98.4	2.51e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
3	091-0901.2059.2065.3	3	19.30	9.75	94.5	3.11e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
4	091-0801.2066.2071.2	2	18.88	13.62	96.5	2.42e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
5	091-0801.2060.2065.3	3	18.81	11.44	94.6	2.76e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
6	091-2301.3218.3222.0	3	18.78	18.78	86.5	3.50e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
7	091-2301.2029.2033.3	3	18.16	9.70	91.1	2.93e+007	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
8	091-2301.2284.2319.2	2	16.98	10.30	91.6	4.09e+007	(K)NDWNATIVR(A)	1088.549
9	091-0901.2305.2316.2	2	16.53	9.86	92.5	4.13e+007	(K)NDWNATIVR(A)	1088.549
10	091-0901.3251.3255.0	3	16.25	16.25	81.3	1.91e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
11	091-0801.3253.3253.0	3	15.35	15.35	84.0	1.53e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
12	091-2301.3232.3232.2	2	14.52	14.52	88.5	6.30e+006	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
13	091-0801.2307.2311.2	2	13.09	7.55	85.5	3.70e+007	(K)NDWNATIVR(A)	1088.549
14	091-0801.2720.2731.2	2	6.64	6.64	64.9	1.32e+007	(R)QNNISHLNWAVSDK(A)	1625.804

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	11	5	59.02	5	2.28e+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	091-0901.3974.3996.0	2	15.10	9.76	90.0	1.14e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
2	091-0801.3991.4009.0	2	14.64	9.20	90.4	8.94e+006	(R)GLPSNIGMLIDTGR(N)	1443.763
3	091-0901.3003.3028.2	2	13.97	10.31	86.9	4.75e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
4	091-2301.3971.3978.0	2	13.42	7.13	86.4	1.79e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
5	091-2301.2993.2998.2	2	12.12	7.95	84.8	5.01e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
6	091-0901.3399.3399.0	2	11.47	4.69	99.1	9.28e+006	(R)VLVENAYPPL(-)	1114.615
7	091-0801.3008.3044.0	2	10.59	4.67	83.1	4.32e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
8	091-0901.2200.2200.0	2	10.19	3.26	70.4	7.28e+006	(R)VVLSNGDQWTR(N)	1274.649
9	091-2301.3405.3405.0	2	9.90	2.10	96.3	1.03e+007	(R)VLVENAYPPL(-)	1114.615
10	091-0801.3432.3475.0	2	8.29	2.65	77.7	1.24e+007	(R)WFPEAFR(V)	952.468
11	091-0901.3418.3418.2	2	7.92	3.13	97.1	9.43e+006	(R)VLVENAYPPL(-)	1114.615

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	10	3	48.78	29	1.08e+008	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	091-0801.4046.4088.2	2	18.93	11.21	98.1	5.70e+006	(K)TVTAMDVVYALK(R)	1310.703
2	091-2301.4041.4068.2	2	17.87	7.02	96.4	9.09e+006	(K)TVTAMDVVYALK(R)	1310.703
3	091-0801.3342.3350.0	2	16.65	7.53	95.5	1.31e+007	(K)VFLENVIR(D)	989.578
4	091-2301.3324.3336.0	2	16.14	7.03	95.4	1.51e+007	(K)VFLENVIR(D)	989.578
5	091-0901.3351.3370.0	2	15.59	6.56	93.4	1.68e+007	(K)VFLENVIR(D)	989.578
6	091-0901.4063.4068.0	2	15.25	6.62	93.1	5.65e+006	(K)TVTAMDVVYALK(R)	1310.703
7	091-0801.3326.3352.0	2	14.58	5.51	92.7	1.36e+007	(K)VFLENVIR(D)	989.578
8	091-2301.2477.2484.2	2	13.20	8.06	91.3	1.11e+007	(R)ISGLIYEETR(G)	1180.621
9	091-0801.2527.2527.2	2	11.95	7.26	90.9	1.28e+007	(R)ISGLIYEETR(G)	1180.621
10	091-0901.4040.4040.0	2	7.58	3.64	84.9	5.03e+006	(K)TVTAMDVVYALK(R)	1310.703

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	42.42	7	1.42e+008	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	091-2301.3343.3349.0	3	17.54	9.10	90.6	2.52e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
2	091-0901.3371.3375.0	3	17.00	11.11	87.4	1.53e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
3	091-0801.3343.3382.0	3	15.89	11.05	80.6	1.55e+007	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083
4	091-0801.3048.3054.0	2	12.82	5.63	83.6	3.44e+007	(R)TIQQTMDEITAR(G)	1406.695
5	091-2301.3795.3795.0	3	12.06	6.41	79.4	9.14e+006	(K)EQLVFSPHTYGPSVFVQR(M)	2091.066
6	091-0901.3058.3064.0	2	11.59	5.30	78.4	3.42e+007	(R)TIQQTMDEITAR(G)	1406.695
7	091-2301.3361.3361.2	2	9.71	5.12	84.3	7.92e+006	(R)FPIAPQTLDPNDPQGSGDALK(N)	2181.083

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	5	3	42.07	8	2.63e+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	091-0901.2744.2750.2	2	16.94	8.99	91.8	7.62e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
2	091-2301.3110.3142.0	3	15.47	11.80	87.3	2.16e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
3	091-0801.2739.2741.0	2	15.29	9.00	88.1	6.27e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
4	091-2301.2711.2768.0	2	15.12	7.70	90.2	8.61e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
5	091-0901.2580.2580.0	3	9.66	9.66	70.5	1.69e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913

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	6	3	36.77	16	4.65e+008	40574.0	PA_Bse_meta_comb:2073563645	PA_Bse_meta_comb:2073563645 BaSeMet_00073010 Lysophospholipase L1 and related esterases [Bar

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	091-2301.3780.3780.2	2	14.20	8.51	83.8	7.45e+006	(K)IMPLGDSITGSPGCWR(A)	1689.809
2	091-0901.2975.3054.2	2	13.54	8.83	80.5	1.47e+008	(R)VTNLNNSIPSWASGK(S)	1587.813
3	091-2301.2952.2996.0	2	12.50	6.66	79.2	1.68e+008	(R)VTNLNNSIPSWASGK(S)	1587.813
4	091-0801.2989.3027.0	2	11.98	4.73	78.5	1.34e+008	(R)VTNLNNSIPSWASGK(S)	1587.813
5	091-0901.3727.3727.0	3	9.03	9.03	71.4	4.74e+006	(K)STSQSPITVVDQWNGFSANSDTSDGVHPNDSGNQK(I)	3676.639
6	091-0801.3794.3794.0	2	8.80	4.15	75.9	2.89e+006	(K)IMPLGDSITGSPGCWR(A)	1689.809

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
13	13.1	4	2	28.83	1	1.21e+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	091-0901.2055.2136.0	3	15.03	8.04	90.3	2.34e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
2	091-0801.3364.3370.0	2	13.80	5.40	89.2	4.34e+007	(R)ALPENLDQVYLK(A)	1402.758
3	091-0801.2101.2132.0	3	13.50	5.23	88.2	1.68e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
4	091-0901.3357.3363.0	2	12.71	3.91	85.4	3.74e+007	(R)ALPENLDQVYLK(A)	1402.758

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	2	2	20.93	4	4.16e+006	109063.9	PA_Bse02:2503998993	PA_Bse02:2503998993 BS02DRAFT_00000010 TonB-dependent receptor [B. setacea BS02 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	091-0801.4708.4708.0	3	10.51	10.51	92.8	1.17e+006	(R)FGVLAAFTSSQADLANYYEGK(Q)	2252.088
2	091-0901.9876.9876.0	3	10.42	10.42	70.1	2.99e+006	(R)NGANVSFQLDLGEGFELVADYFYTK(Q)	2797.336