Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\041511_OGL_Caecum2_fractions
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 213 **Hits:** 392
beginning to assemble proteins .... proteins assembled 0.063426 sec
proteins filtered by unique peptides 0.005061 sec
proteins filtered by score
calculated protein coverage maps 0.016008 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.002151 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 10 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	98	10	174.18	28	4.54e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding d
1	1.1	98	10	174.18	48	4.54e+010	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	13	3	46.56	9	1.64e+008	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
2	2.1	13	3	46.56	21	1.64e+008	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
3	3.1	20	3	45.96	43	1.63e+009	9122.7	PA_Bse_meta_comb:2073586100	PA_Bse_meta_comb:2073586100 BaSeMet_00297560 hypothetical protein [Bankia setacea microbiome
4	4.1	9	3	42.67	29	1.92e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiome
5	5.1	8	2	37.59	5	1.71e+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	8	2	37.59	9	1.71e+008	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [I
6	6.1	16	2	36.64	6	1.56e+008	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
6	6.1	16	2	36.64	6	1.56e+008	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome ((
7	7.1	25	2	35.30	12	6.89e+008	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
7	7.1	25	2	35.30	13	6.89e+008	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia seta
8	8.1	17	2	33.54	41	3.41e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Combi
9	9.1	5	2	23.06	10	9.61e+007	40145.6	PA_Bse02:2503999765	PA_Bse02:2503999765 BS02DRAFT_00005000 Cellulose or protein binding domain. [B. setacea BS02 (I
9	9.1	5	2	23.06	18	9.61e+007	23197.0	PA_Bse_meta_comb:2073559086	PA_Bse_meta_comb:2073559086 BaSeMet_00027420 hypothetical protein [Bankia setacea microbiome
10	10.1	2	2	22.25	34	1.87e+007	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome
Totals:	378	52							

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	98	10	174.18	28	4.54e+010	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	097-3601.6193.6304.3	3	20.87	11.14	98.3	4.12e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
2	097-3602.6520.6562.3	3	20.41	10.66	98.9	2.05e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
3	097-1701.7545.7545.2	2	20.22	20.22	96.7	1.27e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
4	097-1701.6277.6388.3	3	19.83	11.36	97.8	6.69e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
5	097-1701.6171.6254.0	3	19.61	10.08	95.2	7.10e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
6	097-1701.6177.6232.0	3	19.38	11.49	98.4	4.33e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
7	097-1701.6394.6452.0	3	19.25	10.12	96.4	6.12e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
8	097-3601.6309.6374.3	3	19.07	11.01	93.3	3.01e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
9	097-3602.6291.6359.0	3	19.05	8.12	94.0	3.44e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562

10	097-3601.6073.6173.3	3	18.89	11.50	86.7	2.90e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
11	097-3602.6401.6513.3	3	18.73	7.49	96.5	3.65e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
12	097-3602.7966.8020.0	3	18.64	11.55	95.8	7.69e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
13	097-3601.6106.6185.0	3	18.54	14.41	92.4	1.01e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
14	097-3602.6221.6319.3	3	18.49	12.48	88.4	2.29e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
15	098-3701.6599.6625.0	3	18.49	9.05	92.9	6.37e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
16	097-3602.7460.7535.2	2	18.14	18.14	95.3	2.71e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
17	097-1701.7402.7459.2	2	18.07	18.07	95.1	6.07e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
18	098-1801.6600.6632.0	3	17.65	14.24	85.4	3.86e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
19	097-1701.7926.7995.0	3	17.62	10.58	95.2	1.20e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
20	097-3601.7785.7841.0	3	17.60	9.57	94.8	6.84e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
21	097-1701.7396.7449.3	3	17.24	10.56	88.2	4.26e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
22	099-3802.6989.6996.0	3	17.03	17.03	82.1	3.27e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
23	097-3601.7170.7223.2	2	16.94	12.18	93.8	2.31e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
24	098-3702.6482.6560.0	3	16.92	8.36	90.8	3.76e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
25	097-3601.7331.7403.0	2	16.78	11.32	79.7	1.77e+008	(R)EWQDALVDYMVEK(D)	1625.752
26	097-3602.7942.7948.2	2	16.19	16.19	77.6	4.33e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
27	097-3602.7511.7571.3	3	16.07	9.36	85.1	1.01e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
28	097-1701.3542.3602.3	3	16.05	9.52	88.6	4.06e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
29	097-3602.3788.3805.2	2	16.05	16.05	90.9	1.25e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
30	097-3602.7156.7197.0	2	15.95	15.95	80.5	2.75e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
31	097-1701.7523.7543.0	3	15.94	7.16	87.0	1.39e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
32	098-1801.6729.6760.0	3	15.83	8.86	88.8	5.69e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
33	099-3801.9141.9159.0	3	15.83	15.83	79.8	8.67e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
34	097-3601.3554.3558.2	2	15.54	15.54	91.6	2.00e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
35	097-3601.7441.7457.2	2	15.34	8.85	70.3	6.53e+007	(R)EWQDALVDYMVEK(D)	1625.752
36	097-3602.6339.6437.3	3	15.23	9.06	83.5	1.63e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
37	097-3602.7583.7661.2	2	15.23	10.19	76.8	1.94e+008	(R)EWQDALVDYMVEK(D)	1625.752
38	098-3702.6618.6686.0	3	15.22	7.72	87.2	6.22e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
39	097-3602.7324.7360.3	3	15.21	11.25	71.7	2.28e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
40	097-3601.7272.7272.2	2	15.15	10.70	90.2	2.06e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
41	097-3601.6439.6439.0	3	15.13	8.61	85.4	1.17e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
42	097-1701.7111.7173.0	2	15.01	15.01	78.9	3.84e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
43	097-1701.3585.3604.2	2	14.96	14.96	91.5	8.68e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
44	097-3602.7586.7586.2	2	14.94	14.94	88.7	1.55e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
45	097-3601.4703.4713.0	3	14.87	6.04	87.9	9.77e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
46	097-1701.3786.3832.2	2	14.76	14.76	81.9	6.63e+007	(R)AGWDEHFGYLR(D)	1350.623
47	098-3702.9128.9146.0	3	14.55	14.55	70.3	7.12e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
48	100-3902.8058.8065.0	3	14.49	7.58	90.7	1.18e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
49	098-3702.9139.9139.0	3	14.41	14.41	72.5	5.45e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
50	097-1701.7284.7356.2	2	14.40	14.40	82.4	2.12e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
51	098-1801.6545.6584.2	2	14.18	7.49	90.1	1.68e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
52	097-1701.7907.7946.2	2	13.93	13.93	73.9	5.48e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
53	097-3602.6222.6317.2	2	13.83	7.70	84.6	3.28e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
54	097-3602.4906.4918.0	3	13.73	6.11	84.4	8.94e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
55	097-3602.7323.7401.2	2	13.64	8.84	85.1	1.11e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
56	097-3601.3631.3631.0	3	13.59	7.58	78.6	2.32e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
57	098-3701.6516.6581.0	3	13.53	7.84	83.5	4.78e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562

58	097-3602.7475.7517.0	2	13.49	9.31	68.9	1.09e+008	(R)EWQDALVDYMVEK(D)	1625.752
59	097-1701.7647.7647.2	2	13.40	8.36	79.4	9.99e+007	(R)EWQDALVDYMVEK(D)	1625.752
60	097-3601.3550.3622.3	3	13.09	6.55	77.4	8.13e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
61	096-3202.6628.6628.0	3	13.07	6.56	82.6	1.13e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
62	098-1801.9096.9127.0	3	13.07	13.07	74.8	1.56e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
63	097-3601.7241.7289.3	3	12.96	7.88	77.3	1.63e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
64	097-3602.3772.3834.3	3	12.86	6.97	75.7	1.96e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
65	097-3602.6483.6554.4	4	12.80	6.58	75.6	5.27e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
66	097-1701.10628.10644.0	2	12.68	8.53	74.4	1.60e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
67	097-3602.6284.6284.0	3	12.68	12.68	74.4	7.11e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
68	097-3601.7236.7301.0	2	12.38	6.76	75.5	6.75e+007	(R)EWQDALVDYMVEK(D)	1625.752
69	097-3601.7800.7860.2	2	12.19	12.19	77.2	5.54e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
70	097-3601.7362.7362.0	2	12.18	12.18	72.8	4.57e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
71	097-1701.6475.6507.2	2	11.84	3.43	80.1	6.76e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
72	097-3602.10602.10602.0	2	11.81	11.81	75.8	8.91e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
73	097-3602.7673.7680.0	2	11.67	6.24	80.7	4.03e+007	(R)EWQDALVDYMVEK(D)	1625.752
74	097-1701.6152.6152.2	2	11.54	5.53	87.5	3.24e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
75	097-1701.6295.6412.4	4	11.50	4.29	77.0	1.28e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
76	097-3602.7150.7203.2	2	11.22	11.22	66.2	2.71e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
77	097-3601.6341.6341.2	2	11.17	5.16	91.8	6.94e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
78	097-3602.6616.6616.2	2	10.98	4.62	87.9	5.93e+006	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
79	097-3601.6331.6371.4	4	10.77	4.40	73.7	4.74e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
80	097-1701.7135.7135.0	2	10.61	10.61	69.3	1.58e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
81	097-3601.6212.6326.4	4	10.56	2.19	71.6	8.52e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
82	097-3602.10626.10626.0	2	10.40	10.40	71.2	1.23e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
83	098-1801.9082.9082.0	3	10.39	10.39	72.5	9.58e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
84	098-3701.6504.6524.2	2	10.39	5.91	80.9	8.40e+006	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
85	097-3602.7939.8021.2	2	9.98	9.98	68.4	6.19e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
86	097-3601.6996.7050.0	2	9.91	9.91	63.8	4.60e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
87	097-3601.7146.7146.0	2	9.87	9.87	61.4	7.60e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
88	097-3602.6374.6478.4	4	9.76	3.90	71.2	5.39e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
89	097-3602.8033.8033.0	2	9.63	9.63	60.3	3.34e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
90	097-1701.7105.7105.0	2	9.54	9.54	63.5	1.33e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
91	097-1701.7938.8018.2	2	9.34	9.34	60.9	7.77e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
92	097-3602.7239.7281.2	2	9.18	9.18	62.0	6.27e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
93	096-3201.6809.6809.0	3	8.98	4.00	76.2	1.02e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
94	097-3602.10608.10608.0	2	8.57	8.57	61.7	8.87e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
95	098-3702.6697.6697.0	3	8.34	3.56	85.8	1.52e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
96	097-3601.3756.3762.0	2	8.28	8.28	65.6	2.40e+007	(R)AGWDEHFGYLR(D)	1350.623
97	089-2402.5537.5537.0	3	8.12	8.12	74.6	1.78e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
98	097-3602.6640.6640.2	2	7.18	4.01	87.4	5.91e+006	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562

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	13	3	46.56	9	1.64e+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	095-3102.6669.6699.0	2	18.08	18.08	93.4	1.15e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
2	095-1201.6414.6481.2	2	15.99	15.99	91.1	1.73e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
3	095-1201.6493.6506.0	2	15.27	15.27	89.2	1.28e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
4	095-3101.6984.7011.0	2	14.78	6.19	87.9	1.29e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
5	095-3101.6582.6582.0	2	14.57	9.20	85.2	5.87e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
6	095-3101.6957.6962.0	3	13.70	13.70	76.5	2.34e+007	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
7	095-3102.6955.7030.0	2	12.73	3.13	85.0	1.43e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
8	095-3102.7038.7038.0	2	12.14	4.35	81.3	6.27e+006	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
9	095-3101.6574.6574.0	2	10.72	10.72	75.8	4.91e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
10	095-3101.6882.6953.0	2	10.32	2.36	77.8	1.41e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
11	095-1201.6513.6513.0	2	9.83	5.32	74.5	9.40e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
12	095-1201.6693.6771.2	2	8.95	3.05	72.1	2.65e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
13	095-3102.6641.6641.0	2	7.68	7.68	81.4	4.94e+006	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.1	20	3	45.96	43	1.63e+009	9122.7	PA_Bse_meta_comb:2073586100	PA_Bse_meta_comb:2073586100 BaSeMet_00297560 hypothetical protein [Bankia setacea microbiome (

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	095-1201.8007.8065.2	2	19.52	14.28	94.8	5.56e+008	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
2	095-3101.8055.8111.2	2	19.29	13.98	95.0	1.54e+008	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
3	093-1001.5548.5644.2	2	18.04	13.40	89.4	2.80e+008	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
4	093-2902.5614.5688.2	2	18.03	10.97	88.6	7.66e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
5	095-1201.4091.4119.0	2	16.76	7.82	94.6	8.11e+005	(R)GSVEVEMK(H)	878.429
6	094-3001.8174.8219.2	2	16.33	12.79	74.7	6.57e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
7	095-3101.4429.4471.2	2	15.72	8.74	93.6	4.27e+005	(R)GSVEVEMK(H)	878.429
8	095-1201.4004.4062.0	2	15.42	7.74	91.7	4.86e+005	(R)GSVEVEMK(H)	878.429
9	095-3101.8044.8122.3	3	15.19	8.81	83.1	1.35e+008	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
10	094-3002.8259.8289.2	2	14.72	11.54	74.0	5.30e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
11	095-3102.8057.8126.3	3	12.79	6.58	76.1	1.57e+008	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
12	094-3002.8265.8279.0	3	11.91	5.31	73.7	3.37e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
13	095-1201.10355.10355.2	2	11.40	11.40	71.8	1.45e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
14	095-1201.7146.7194.0	2	9.68	4.90	80.3	4.47e+007	(K)HVVSGVQVR(G)	980.564
15	095-1201.10147.10147.0	2	9.29	4.80	66.5	1.57e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
16	100-2001.8093.8093.0	2	8.95	3.28	66.7	1.52e+007	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
17	095-3101.7274.7274.0	2	8.84	3.82	83.5	1.95e+007	(K)HVVSGVQVR(G)	980.564
18	095-3101.10421.10421.0	2	8.47	8.47	62.7	9.60e+006	(R)GQAHIDLPLTISISTDLEK(S)	2051.103
19	095-1201.1745.1745.0	2	7.25	3.15	93.4	1.50e+005	(R)GSVEVEMK(H)	878.429
20	095-3101.4315.4315.0	2	6.67	2.35	91.3	1.48e+005	(R)GSVEVEMK(H)	878.429

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

			(#)	Search Score		Intensity	(Da)		
4	4.1	9	3	42.67	29	1.92e+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	095-3102.7283.7283.2	2	15.73	7.39	99.2	1.53e+007	(K)VFLENVIR(D)	989.578
2	095-3101.5658.5718.0	2	15.30	8.97	93.8	8.33e+006	(R)ISGLIYEETR(G)	1180.621
3	095-3102.5670.5744.0	2	14.27	8.47	92.8	6.12e+006	(R)ISGLIYEETR(G)	1180.621
4	095-3101.7273.7273.0	2	13.01	4.18	90.5	1.47e+007	(K)VFLENVIR(D)	989.578
5	095-1201.5437.5509.2	2	12.99	6.31	85.7	4.59e+007	(R)ISGLIYEETR(G)	1180.621
6	095-1201.5342.5399.0	2	12.14	4.87	89.0	1.43e+007	(R)ISGLIYEETR(G)	1180.621
7	095-1201.7364.7371.0	2	11.64	8.09	78.7	2.88e+007	(K)TVTAMDVVYALK(R)	1310.703
8	095-3102.7432.7488.2	2	8.81	5.80	72.2	3.19e+007	(K)TVTAMDVVYALK(R)	1310.703
9	095-3101.7479.7479.0	2	8.58	4.77	77.8	2.70e+007	(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
5	5.1	8	2	37.59	5	1.71e+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	093-2901.7514.7572.0	2	20.40	12.20	97.2	3.34e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
2	093-2901.3009.3029.0	3	17.19	7.38	81.3	2.22e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
3	093-2901.7544.7547.0	3	16.99	9.48	87.5	7.64e+006	(R)WFPEAFQTLVENAYPAL(-)	1995.986
4	093-2902.7690.7765.2	2	16.68	9.15	91.0	2.76e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
5	093-1001.7882.7951.2	2	15.52	10.18	87.2	3.89e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
6	093-2901.7520.7520.2	2	13.77	6.48	80.9	2.16e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
7	093-2902.7728.7728.0	3	13.76	13.76	79.4	7.23e+006	(R)WFPEAFQTLVENAYPAL(-)	1995.986
8	093-2901.7602.7602.2	2	9.22	5.29	79.4	1.27e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986

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	16	2	36.64	6	1.56e+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	096-3202.6142.6220.0	2	20.42	16.77	98.3	6.91e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
2	096-1301.6228.6300.0	2	18.73	15.11	94.5	9.68e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
3	096-3202.6255.6268.0	2	17.01	17.01	89.9	3.66e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
4	096-3201.6320.6361.0	2	16.66	12.51	92.8	5.05e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
5	096-3202.6605.6676.2	2	16.22	10.39	94.1	1.94e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
6	097-3601.4466.4466.0	2	16.06	12.82	90.3	4.98e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
7	096-1301.6684.6734.0	2	15.08	8.57	91.1	1.76e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
8	096-1301.6307.6352.2	2	14.50	9.86	89.5	8.34e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814

9	097-1701.6094.6094.0	2	14.32	8.94	86.5	2.93e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
10	096-3201.6775.6792.2	2	14.14	8.09	92.5	1.04e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
11	096-3202.6642.6642.0	3	11.26	11.26	71.3	3.34e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
12	096-3202.6707.6707.0	2	10.57	3.41	87.4	6.41e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
13	096-3201.6751.6751.2	2	9.57	4.75	76.9	6.31e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
14	097-3601.4825.4825.0	2	9.56	5.19	73.4	3.32e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
15	097-3601.4830.4830.0	2	8.89	3.53	66.0	3.28e+006	(R)SDFTQYWDQITPENEGK(W)	2057.909
16	097-3601.6004.6004.0	2	6.62	3.23	62.3	1.79e+007	(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
7	7.1	25	2	35.30	12	6.89e+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	094-3002.6698.6764.2	2	18.71	15.30	95.7	1.72e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
2	094-3001.6617.6645.2	2	18.14	13.94	94.5	1.62e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
3	093-2901.2891.2944.2	2	16.59	11.98	86.6	2.15e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
4	094-1101.6600.6600.2	2	16.36	11.87	90.9	2.26e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
5	093-2901.3075.3088.0	2	15.69	9.47	89.5	1.13e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
6	093-2901.2985.2999.0	2	15.09	7.75	86.2	5.71e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
7	093-1001.3025.3071.0	2	14.96	8.27	83.0	6.96e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
8	094-3002.6781.6788.0	2	14.71	8.44	88.2	1.06e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
9	093-2902.3099.3145.0	2	14.49	9.14	84.5	1.42e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
10	093-1001.10443.10443.0	2	14.42	8.41	86.1	9.70e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
11	097-1701.3138.3168.0	2	14.11	4.60	86.0	9.02e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
12	093-1001.5303.5303.2	2	14.07	14.07	80.5	4.57e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
13	094-3001.6714.6714.2	2	13.87	13.87	82.9	9.12e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
14	094-3001.6740.6740.2	2	13.84	13.84	81.2	6.66e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
15	093-2902.3234.3270.2	2	13.08	8.47	85.5	1.44e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
16	094-1101.6865.6865.2	2	11.57	11.57	71.7	2.20e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
17	093-2902.3105.3105.0	2	11.20	6.43	75.0	1.14e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
18	094-3002.6949.6949.2	2	10.85	10.85	74.7	6.11e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
19	097-3601.3112.3112.0	2	10.85	5.81	71.2	1.56e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
20	094-1101.6611.6611.0	2	8.54	8.54	62.4	2.72e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
21	094-1101.6605.6605.2	2	7.76	7.76	62.2	2.49e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
22	093-1001.10456.10456.0	2	7.73	7.73	72.9	8.39e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
23	093-2901.10005.10005.0	2	7.33	7.33	65.5	6.77e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
24	094-3002.7030.7030.0	2	6.39	6.39	73.2	6.84e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
25	093-1001.10509.10509.0	2	6.16	6.16	60.8	7.43e+006	(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
8	8.1	17	2	33.54	41	3.41e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Combi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	093-1001.7221.7221.0	3	18.11	18.11	88.1	4.93e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
2	095-3102.9899.9901.2	2	15.43	15.43	77.3	2.60e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
3	093-1001.7120.7189.3	3	15.32	7.06	73.5	1.08e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
4	095-1201.9897.9930.2	2	14.83	14.83	77.3	3.84e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
5	095-1201.8243.8290.3	3	14.56	8.78	72.6	1.49e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
6	093-2901.6864.6915.2	2	13.60	6.72	87.8	1.61e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
7	096-3202.9549.9549.2	2	13.16	13.16	78.9	1.01e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
8	093-1001.7211.7265.2	2	13.10	5.15	87.8	1.41e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
9	095-1201.8204.8275.0	2	13.04	6.21	85.7	5.00e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
10	095-3102.8283.8338.0	2	12.90	6.03	83.1	2.78e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
11	093-2902.6966.7004.0	2	12.55	4.76	87.1	4.40e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
12	093-2901.6920.6920.0	3	12.38	5.93	76.5	1.38e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
13	096-3201.9670.9683.2	2	11.89	11.89	66.2	1.70e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
14	093-2901.6783.6852.2	2	10.28	3.04	80.5	1.89e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
15	095-3101.8262.8318.0	2	10.22	4.46	78.7	2.13e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
16	095-1201.8317.8335.0	2	9.73	3.32	77.8	3.16e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
17	095-3101.9859.9876.2	2	9.72	9.72	60.7	3.32e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562

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	5	2	23.06	10	9.61e+007	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	093-2902.3159.3192.0	2	14.67	7.35	88.5	2.60e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
2	093-2902.3174.3174.0	2	12.67	6.44	88.0	2.34e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
3	093-2901.2965.2979.0	2	12.59	4.23	85.5	3.14e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
4	093-2902.3147.3147.2	2	9.44	5.99	68.9	1.11e+007	(R)NGSSGLSNPNTTDINNFK(R)	1879.879
5	094-3002.6659.6659.0	2	8.39	8.39	78.9	4.21e+006	(R)FLASAMMETEVMDTNYTYGDGK(S)	2474.057

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	2	2	22.25	34	1.87e+007	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome (

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	096-3202.5881.5881.0	2	11.45	5.86	87.5	1.35e+006	(R)EGQGFISGAELR(H)	1263.633
2	096-3201.7776.7776.0	2	10.80	10.80	69.0	1.74e+007	(K)DTGTFADFMEAFK(T)	1479.647