Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\081910_GC_pellet_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 82 **Hits:** 187
Data Directory: msdataSM\081910_GC_tissue
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 45 **Hits:** 98
Data Directory: msdataSM\081910_GS_pellet_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 32 **Hits:** 85
Data Directory: msdataSM\081910_GS_tissue
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 72 **Hits:** 157
beginning to assemble proteins .... proteins assembled 0.070078 sec
proteins filtered by unique peptides 0.008497 sec
proteins filtered by score
calculated protein coverage maps 0.084826 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.029255 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 43 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	23	10	151.55	36	3.24e+009	59772.4	PA_Bse08:2503995076	PA_Bse08:2503995076 BS08DRAFT_00035440 nitrogenase molybdenum-iron protein beta chain [B. se
2	2.1	7	6	83.57	16	2.18e+008	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
2	2.1	7	6	83.57	27	2.18e+008	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
3	3.1	10	6	79.05	36	9.05e+008	28933.2	PA_BS12:2189568903	PA_BS12:2189568903 or2222 Putative salt-induced outer membrane protein [B. setacea BS12] 260 bp
3	3.1	9	5	63.45	30	8.84e+008	28217.6	PA_Bse_meta_comb:2073562517	PA_Bse_meta_comb:2073562517 BaSeMet_00061730 Putative salt-induced outer membrane protein [B
4	4.1	6	6	77.90	11	1.54e+009	108814.9	PA_BS12:2189569860	PA_BS12:2189569860 or3165 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12
4	4.1	6	6	77.90	11	1.54e+009	108814.9	PA_Bse_meta_comb:2073560924	PA_Bse_meta_comb:2073560924 BaSeMet_00045800 TonB-dependent receptor [Bankia setacea microc
4	4.2	2	2	20.50	2	1.67e+008	109417.8	PA_Bse02:2504000752	PA_Bse02:2504000752 BS02DRAFT_00023490 TonB-dependent receptor [B. setacea BS02 (Isolate fro
4	4.2	2	2	20.50	2	1.67e+008	109417.8	PA_Bse_meta_comb:2073563726	PA_Bse_meta_comb:2073563726 BaSeMet_00073820 TonB-dependent receptor [Bankia setacea microc
5	5.1	12	6	75.15	18	1.13e+009	57219.5	PA_Bse08:2503995261	PA_Bse08:2503995261 BS08DRAFT_00037250 chaperonin GroL [B. setacea BS08 (Isolate from shipwo
5	5.1	3	2	24.55	4	1.90e+008	57360.8	PA_Bse_meta_comb:2073567036	PA_Bse_meta_comb:2073567036 BaSeMet_00106920 chaperonin GroL [Bankia setacea microbiome (C
5	5.1	3	2	24.55	4	1.90e+008	57128.5	PA_BS12:2189568147	PA_BS12:2189568147 or1478 Chaperonin GroEL (HSP60 family) [B. setacea BS12] 549 bp
5	5.2	10	5	67.93	16	9.55e+008	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]
5	5.3	9	5	65.52	17	6.40e+008	57147.5	PA_Bse02:2503998519	PA_Bse02:2503998519 BS02DRAFT_00025680 chaperonin GroL [B. setacea BS02 (Isolate from shipwo
5	5.3	9	5	65.52	18	6.40e+008	55514.7	PA_Bse_meta_comb:2073565377	PA_Bse_meta_comb:2073565377 BaSeMet_00090330 chaperonin GroL [Bankia setacea microbiome (C
6	6.1	7	5	73.81	8	7.21e+008	106594.3	PA_Bse_meta_comb:2073586734	PA_Bse_meta_comb:2073586734 BaSeMet_00303900 TonB-dependent receptor [Bankia setacea microc
7	7.1	11	5	71.48	36	1.10e+009	29434.1	PA_Bse_meta_comb:2073593916	PA_Bse_meta_comb:2073593916 BaSeMet_00375720 Outer membrane protein (porin) [Bankia setacea
7	7.1	9	3	46.58	15	9.79e+008	32809.2	PA_Bse02:2504001059	PA_Bse02:2504001059 BS02DRAFT_00030400 Gram-negative porin. [B. setacea BS02 (Isolate from sh
7	7.1	6	2	29.13	44	6.31e+008	11606.9	PA_Bse_meta_comb:2073587998	PA_Bse_meta_comb:2073587998 BaSeMet_00316540 Outer membrane protein (porin) [Bankia setacea
8	8.1	7	5	69.52	6	1.25e+009	126855.7	PA_Bse02:2504001037	PA_Bse02:2504001037 BS02DRAFT_00030180 TonB-dependent receptor [B. setacea BS02 (Isolate fro
8	8.1	6	4	52.20	8	1.24e+009	79685.5	PA_Bse_meta_comb:2073583788	PA_Bse_meta_comb:2073583788 BaSeMet_00274440 TonB-dependent Receptor Plug Domain. [Bankia
8	8.1	4	2	34.13	35	4.43e+008	10762.9	PA_Bse_meta_comb:2073595596	PA_Bse_meta_comb:2073595596 BaSeMet_00392520 TonB-dependent Receptor Plug Domain. [Bankia
9	9.1	13	4	67.62	7	4.22e+008	100788.0	PA_Bse_meta_comb:2073596195	PA_Bse_meta_comb:2073596195 BaSeMet_00398510 TonB-dependent receptor [Bankia setacea microc
9	9.2	10	4	65.45	31	4.06e+008	19640.4	PA_Bse_meta_comb:2073597966	PA_Bse_meta_comb:2073597966 BaSeMet_00416220 Outer membrane receptor for ferrienterochelin a
10	10.1	7	4	58.77	35	4.26e+008	27641.5	PA_Bse02:2504001159	PA_Bse02:2504001159 BS02DRAFT_00031400 FKBP-type peptidyl-prolyl cis-trans isomerase./Domain
10	10.1	7	4	58.77	35	4.26e+008	27641.5	PA_Bse_meta_comb:2073579700	PA_Bse_meta_comb:2073579700 BaSeMet_00233560 FKBP-type peptidyl-prolyl cis-trans isomerases 1
11	11.1	7	4	58.49	9	1.11e+009	56014.8	PA_Bse08:2503995077	PA_Bse08:2503995077 BS08DRAFT_00035450 nitrogenase molybdenum-iron protein alpha chain [B. s
12	12.1	6	4	57.70	21	6.91e+008	33845.5	PA_Bse08:2503994737	PA_Bse08:2503994737 BS08DRAFT_00032510 transaldolase [B. setacea BS08 (Isolate from shipworm

12	12.1	4	3	41.83	14	4.78e+008	34007.6	PA_BS12:2189567864	PA_BS12:2189567864 or1190 Transaldolase [B. setacea BS12] 311 bp
12	12.1	4	3	41.83	14	4.78e+008	33949.6	PA_Bse_meta_comb:2073584304	PA_Bse_meta_comb:2073584304 BaSeMet_00279600 transaldolase (EC 2.2.1.2) [Bankia setacea micr
12	12.1	3	2	29.95	9	3.63e+008	33705.4	PA_BSC2:2534576639	PA_BSC2:2534576639 Bsc2_04328 transaldolase (EC 2.2.1.2) [Alteromonadacea bacterium Bsc2]
12	12.1	3	2	29.95	9	3.63e+008	33675.4	PA_Bse_meta_comb:2073570868	PA_Bse_meta_comb:2073570868 BaSeMet_00145240 transaldolase (EC 2.2.1.2) [Bankia setacea micr
12	12.1	2	2	22.18	32	2.67e+008	10806.4	PA_Bse_meta_comb:2073579380	PA_Bse_meta_comb:2073579380 BaSeMet_00230360 transaldolase (EC 2.2.1.2) [Bankia setacea micr
13	13.1	5	4	53.93	4	2.26e+008	115295.3	PA_BS12:2189568198	PA_BS12:2189568198 or1530 Outer membrane receptor for ferrienterochelin and colicins [B. setacea BS
14	14.1	8	3	49.56	10	1.21e+009	44282.5	PA_BSC2:2534573496	PA_BSC2:2534573496 Bsc2_01181 translation elongation factor 1A (EF-1A/EF-Tu) [Alteromonadacea b
14	14.1	8	3	49.56	10	1.21e+009	44282.5	PA_Bse_meta_comb:2073587015	PA_Bse_meta_comb:2073587015 BaSeMet_00306710 translation elongation factor 1A (EF-1A/EF-Tu) [
14	14.1	3	2	30.37	28	7.54e+007	9849.9	PA_Bse_meta_comb:2073591525	PA_Bse_meta_comb:2073591525 BaSeMet_00351810 translation elongation factor 1A (EF-1A/EF-Tu) [
14	14.1	6	2	29.69	6	1.17e+009	44395.5	PA_BS12:2189570755	PA_BS12:2189570755 or4000 GTPases - translation elongation factors [B. setacea BS12] 407 bp
14	14.1	6	2	29.69	6	1.17e+009	44335.5	PA_Bse_meta_comb:2073563152	PA_Bse_meta_comb:2073563152 BaSeMet_00068080 translation elongation factor 1A (EF-1A/EF-Tu) [
14	14.2	7	3	38.18	9	1.28e+009	44298.7	PA_Bse02:2503998465	PA_Bse02:2503998465 BS02DRAFT_00025140 translation elongation factor TU [B. setacea BS02 (Isola
14	14.2	7	3	38.18	9	1.28e+009	44266.6	PA_Bse_meta_comb:2073556354	PA_Bse_meta_comb:2073556354 BaSeMet_00000100 translation elongation factor 1A (EF-1A/EF-Tu) [
14	14.3	2	2	25.14	6	6.69e+007	44255.6	PA_Bse08:2503995480	PA_Bse08:2503995480 BS08DRAFT_00039430 translation elongation factor TU [B. setacea BS08 (Isola
15	15.1	7	3	48.66	29	6.12e+009	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
16	16.1	7	4	47.92	6	1.12e+009	102017.5	PA_Bse08:2503996049	PA_Bse08:2503996049 BS08DRAFT_00012470 TonB-dependent receptor [B. setacea BS08 (Isolate fro
17	17.1	7	3	47.24	21	4.61e+008	12471.3	PA_Bse02:2503998471	PA_Bse02:2503998471 BS02DRAFT_00025200 ribosomal protein L7/L12 [B. setacea BS02 (Isolate fror
17	17.1	7	3	47.24	21	4.61e+008	12471.3	PA_Bse_meta_comb:2073556360	PA_Bse_meta_comb:2073556360 BaSeMet_00000160 LSU ribosomal protein L12P [Bankia setacea mi
17	17.1	6	2	30.13	10	1.65e+008	12772.7	PA_Bse08:2503995486	PA_Bse08:2503995486 BS08DRAFT_00039490 ribosomal protein L7/L12 [B. setacea BS08 (Isolate fror
18	18.1	5	4	47.01	17	9.23e+008	42092.0	PA_BSC2:2534574460	PA_BSC2:2534574460 Bsc2_02147 hypothetical protein [Alteromonadacea bacterium Bsc2]
18	18.1	5	4	47.01	17	9.23e+008	42043.9	PA_Bse_meta_comb:2073562800	PA_Bse_meta_comb:2073562800 BaSeMet_00064560 hypothetical protein [Bankia setacea microbiome
19	19.1	8	3	41.86	11	8.97e+008	36127.2	PA_Bse08:2503993973	PA_Bse08:2503993973 BS08DRAFT_00026510 glyceraldehyde-3-phosphate dehydrogenase, type I [B.
20	20.1	7	3	41.04	15	1.83e+008	35386.5	PA_BS12:2189571789	PA_BS12:2189571789 or0889 Malate/lactate dehydrogenases [B. setacea BS12] 327 bp
20	20.1	7	3	41.04	15	1.83e+008	35354.4	PA_Bse_meta_comb:2073574964	PA_Bse_meta_comb:2073574964 BaSeMet_00186200 malate dehydrogenase (NAD) (EC 1.1.1.37) [Ba
20	20.1	7	3	41.04	15	1.83e+008	35299.3	PA_BSC2:2534572582	PA_BSC2:2534572582 Bsc2_00266 malate dehydrogenase [Alteromonadacea bacterium Bsc2]
20	20.1	7	3	41.04	15	1.83e+008	35299.3	PA_Bse_meta_comb:2073561056	PA_Bse_meta_comb:2073561056 BaSeMet_00047120 malate dehydrogenase (NAD) (EC 1.1.1.37) [Ba
20	20.2	3	3	34.62	18	1.40e+008	35600.6	PA_Bse08:2503994614	PA_Bse08:2503994614 BS08DRAFT_00031280 malate dehydrogenase [B. setacea BS08 (Isolate from
21	21.1	14	2	39.81	19	5.91e+009	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
22	22.1	2	2	37.84	5	1.37e+008	115945.6	PA_Bse08:2503996008	PA_Bse08:2503996008 BS08DRAFT_00012060 TonB-dependent receptor [B. setacea BS08 (Isolate fro
23	23.1	2	2	33.77	14	1.14e+008	17663.6	PA_Bse02:2503998467	PA_Bse02:2503998467 BS02DRAFT_00025160 ribosomal protein S7, bacterial/organelle [B. setacea BS
23	23.1	2	2	33.77	14	1.14e+008	17663.6	PA_Bse_meta_comb:2073556356	PA_Bse_meta_comb:2073556356 BaSeMet_00000120 SSU ribosomal protein S7P [Bankia setacea mic
24	24.1	3	2	33.40	10	4.07e+007	52481.4	PA_BSC2:2534576897	PA_BSC2:2534576897 Bsc2_04586 pyruvate kinase (EC 2.7.1.40) [Alteromonadacea bacterium Bsc2]
24	24.1	3	2	33.40	10	4.07e+007	52481.4	PA_Bse_meta_comb:2073595609	PA_Bse_meta_comb:2073595609 BaSeMet_00392650 pyruvate kinase (EC 2.7.1.40) [Bankia setacea n
25	25.1	3	2	27.44	16	3.05e+007	19750.3	PA_Bse08:2503995045	PA_Bse08:2503995045 BS08DRAFT_00035130 flavodoxin, long chain [B. setacea BS08 (Isolate from s
26	26.1	4	2	26.89	33	1.44e+007	12111.0	PA_BS12:2189569075	PA_BS12:2189569075 or2390 Nitrogen regulatory protein PII [B. setacea BS12] 112 bp
26	26.1	4	2	26.89	33	1.44e+007	12111.0	PA_Bse_meta_comb:2073596293	PA_Bse_meta_comb:2073596293 BaSeMet_00399490 nitrogen regulatory protein P-II [Bankia setacea
26	26.1	4	2	26.89	33	1.44e+007	12099.0	PA_BSC2:2534574907	PA_BSC2:2534574907 Bsc2_02594 nitrogen regulatory protein P-II family [Alteromonadacea bacterium
26	26.1	4	2	26.89	33	1.44e+007	12099.0	PA_Bse02:2503998071	PA_Bse02:2503998071 BS02DRAFT_00012490 Nitrogen regulatory protein P-II. [B. setacea BS02 (Isola
26	26.1	4	2	26.89	33	1.44e+007	12099.0	PA_Bse_meta_comb:2073590737	PA_Bse_meta_comb:2073590737 BaSeMet_00343930 nitrogen regulatory protein P-II [Bankia setacea
26	26.1	4	2	26.89	33	1.44e+007	12099.0	PA_Bse_meta_comb:2073591701	PA_Bse_meta_comb:2073591701 BaSeMet_00353570 nitrogen regulatory protein P-II [Bankia setacea
26	26.1	4	2	26.89	34	1.44e+007	11726.4	PA_Bse_meta_comb:2073579200	PA_Bse_meta_comb:2073579200 BaSeMet_00228560 nitrogen regulatory protein P-II [Bankia setacea
27	27.1	3	2	25.42	33	2.53e+008	9164.5	PA_Bse08:2503994572	PA_Bse08:2503994572 BS08DRAFT_00030860 Bacterial DNA-binding protein. [B. setacea BS08 (Isolat
27	27.2	3	2	23.94	34	9.84e+007	9107.5	PA_Bse02:2503999877	PA_Bse02:2503999877 BS02DRAFT_00006580 Bacterial DNA-binding protein. [B. setacea BS02 (Isolat
27	27.2	3	2	23.94	34	9.84e+007	9075.4	PA_Bse_meta_comb:2073579833	PA_Bse_meta_comb:2073579833 BaSeMet_00234890 bacterial nucleoid protein HU beta subunit [Bank
28	28.1	2	2	25.29	10	3.02e+008	28847.5	PA_BS12:2189569790	PA_BS12:2189569790 or3098 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [B. setacea BS12] 265 b
28	28.1	2	2	25.29	10	3.02e+008	28847.5	PA_Bse_meta_comb:2073568597	PA_Bse_meta_comb:2073568597 BaSeMet_00122530 FKBP-type peptidyl-prolyl cis-trans isomerases 1
29	29.1	2	2	24.37	3	1.67e+008	105318.6	PA_BS12:2189568779	PA_BS12:2189568779 or2098 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12
30	30.1	2	2	23.39	2	2.01e+008	118803.8	PA_BSC2:2534573281	PA_BSC2:2534573281 Bsc2_00965 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]

30	30.1	2	2	23.39	2	2.01e+008	118803.8	PA_Bse_meta_comb:2073587930	PA_Bse_meta_comb:2073587930 BaSeMet_00315860 TonB-dependent receptor [Bankia setacea micro
31	31.1	2	2	22.92	11	2.88e+008	29305.8	PA_Bse02:2503998171	PA_Bse02:2503998171 BS02DRAFT_00013480 Protein of unknown function (DUF3450). [B. setacea BS
31	31.1	2	2	22.92	11	2.88e+008	29305.8	PA_Bse_meta_comb:2073584294	PA_Bse_meta_comb:2073584294 BaSeMet_00279500 Protein of unknown function (DUF3450). [Bankia
32	32.1	6	1	20.76	18	2.01e+010	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
33	33.1	2	1	20.65	2	3.67e+007	68581.6	PA_Bse08:2503997242	PA_Bse08:2503997242 BS08DRAFT_00017410 chaperone protein DnaK [B. setacea BS08 (Isolate fron
34	34.1	2	2	20.32	6	9.27e+007	98379.6	PA_BSC2:2534573844	PA_BSC2:2534573844 Bsc2_01530 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]
35	35.1	1	1	20.06	9	3.78e+007	12421.2	PA_BS12:2189570749	PA_BS12:2189570749 or3994 Ribosomal protein L7/L12 [B. setacea BS12] 123 bp
35	35.1	1	1	20.06	9	3.78e+007	12421.2	PA_Bse_meta_comb:2073563146	PA_Bse_meta_comb:2073563146 BaSeMet_00068020 LSU ribosomal protein L12P [Bankia setacea mi
Totals:	461	255							

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	23	10	151.55	36	3.24e+009	59772.4	PA_Bse08:2503995076	PA_Bse08:2503995076 BS08DRAFT_00035440 nitrogenase molybdenum-iron protein beta chain [B. setacea BS08

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.7340.7346.3	3	19.20	11.01	93.6	1.69e+008	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
2	043-0801.6971.6982.2	2	18.59	13.84	94.9	2.32e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
3	044-1001.8012.8016.2	2	17.59	12.79	94.9	2.16e+008	(K)FSLWGDPDFVMGLTK(F)	1712.836
4	044-1001.4496.4503.0	2	16.85	8.20	93.8	1.85e+008	(R)ENFEETPSQENIDEVFK(W)	2054.920
5	045-1201.11685.11685.0	3	15.95	15.95	83.2	6.89e+007	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
6	044-1001.7329.7339.2	2	15.42	15.42	90.8	1.77e+008	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
7	043-0801.5220.5244.2	2	14.62	7.07	94.2	1.33e+007	(R)IGFPIFDR(H)	964.526
8	045-1201.11544.11544.0	3	14.34	6.65	74.1	1.98e+007	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
9	044-1001.6781.6799.0	2	13.92	6.10	83.2	3.43e+008	(K)INLVPGFETYLGNYR(V)	1755.907
10	044-1001.6805.6838.3	3	13.67	6.45	87.0	9.94e+007	(K)INLVPGFETYLGNYR(V)	1755.907
11	043-0801.4111.4113.2	2	13.05	13.05	77.2	5.81e+007	(R)LMQETDYNYDLIR(-)	1673.785
12	044-1001.4999.5005.0	3	12.85	6.23	81.4	5.08e+008	(R)SLVFTNKPDFMIGNSYGK(F)	2018.006
13	044-1001.5406.5426.2	2	12.63	5.92	94.7	1.87e+008	(R)IGFPIFDR(H)	964.526
14	044-1001.4053.4053.2	2	12.32	12.32	75.3	2.94e+008	(R)LMQETDYNYDLIR(-)	1673.785
15	044-1001.7353.7363.0	3	12.18	4.55	81.2	1.63e+008	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
16	046-1401.8070.8070.0	3	12.18	8.75	86.5	4.97e+006	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
17	043-0801.4895.4909.0	3	12.14	12.14	71.8	4.33e+007	(R)SLVFTNKPDFMIGNSYGK(F)	2018.006
18	046-1401.9526.9526.0	3	12.06	12.06	73.0	8.45e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
19	046-1401.8056.8056.0	3	11.93	5.88	74.9	4.81e+006	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
20	043-0801.6058.6063.2	2	10.08	3.91	68.8	2.10e+007	(K)INLVPGFETYLGNYR(V)	1755.907
21	044-1001.6787.6787.2	2	9.62	3.97	72.2	3.26e+008	(K)INLVPGFETYLGNYR(V)	1755.907
22	044-1001.5038.5038.2	2	8.91	4.99	65.7	1.44e+008	(R)SLVFTNKPDFMIGNSYGK(F)	2018.006
23	044-1001.8072.8072.2	2	8.70	8.70	60.2	1.59e+008	(K)FSLWGDPDFVMGLTK(F)	1712.836

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	7	6	83.57	16	2.18e+008	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding domain./Cel

MH^+

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	Matched (Da)
1	043-0801.5197.5211.0	3	19.46	13.04	91.5	2.95e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	043-0801.3829.3829.0	3	16.25	8.00	85.0	4.85e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
3	043-0801.5679.5702.0	3	15.88	10.23	87.4	3.36e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
4	043-0801.5591.5605.2	2	12.54	5.88	86.0	2.42e+007	(R)EWQDALVDYMVEK(D)	1625.752
5	043-0801.4426.4472.0	3	11.29	3.69	81.7	4.00e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
6	043-0801.5386.5386.0	3	8.15	4.43	79.7	2.12e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
7	043-0801.5600.5600.2	2	6.40	2.15	65.2	2.13e+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
3	3.1	10	6	79.05	36	9.05e+008	28933.2	PA_BS12:2189568903	PA_BS12:2189568903 or2222 Putative salt-induced outer membrane protein [B. setacea BS12] 260 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	043-0801.3615.3639.2	2	17.78	17.78	91.6	4.22e+007	(K)FSGYDYQGTLAAGYSNR(L)	1869.841
2	043-0801.5283.5297.2	2	15.60	15.60	88.4	2.12e+007	(K)AGFSIYNNSVVLDNIEK(T)	1882.955
3	045-1201.3630.3630.0	2	14.47	14.47	82.4	8.97e+007	(K)FSGYDYQGTLAAGYSNR(L)	1869.841
4	043-0801.4011.4014.2	2	13.20	9.94	77.6	6.46e+007	(K)FTQTLSSDIAFDSAK(N)	1630.796
5	045-1201.3643.3643.0	2	12.94	12.94	82.0	8.13e+007	(K)FSGYDYQGTLAAGYSNR(L)	1869.841
6	043-0801.5673.5720.2	2	11.37	5.69	80.8	7.20e+007	(K)WLNNYVIEGFYK(E)	1545.774
7	043-0801.4762.4781.2	2	11.02	11.02	71.6	3.68e+007	(K)SISAEAELGALTTSGNTQSNAFK(G)	2297.126
8	045-1201.5913.5927.2	2	10.78	10.78	77.5	2.29e+008	(K)WLNNYVIEGFYK(E)	1545.774
9	045-1201.4741.4765.2	2	10.23	10.23	70.5	2.50e+008	(K)SISAEAELGALTTSGNTQSNAFK(G)	2297.126
10	045-1201.2684.2720.0	2	10.08	5.67	81.4	1.82e+007	(K)YFMSAQSDYK(L)	1239.536

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	6	6	77.90	11	1.54e+009	108814.9	PA_BS12:2189569860	PA_BS12:2189569860 or3165 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12] 1002 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.7009.7028.0	3	20.34	20.34	94.3	4.82e+008	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
2	045-1201.2817.2838.2	2	17.52	13.40	94.9	3.34e+007	(K)TSAFAQANFAK(D)	1155.580
3	045-1201.4460.4460.0	2	12.49	12.49	84.5	1.71e+008	(K)LATSLAVSYGDSTLLNNQGR(L)	2080.068
4	045-1201.5466.5497.0	3	12.08	4.96	84.2	5.38e+008	(K)ETDPELSALLSWNHDDK(L)	1969.914
5	045-1201.9458.9461.0	3	9.28	3.73	72.9	1.82e+008	(K)EVLGTLNGEYFLLPASVTSNGLDFTDVPSSMVSGLNVSK(S)	4058.032
6	045-1201.4118.4118.2	2	6.19	6.19	62.8	1.37e+008	(R)LPDVTIADSLQR(I)	1327.722

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.2	2	2	20.50	2	1.67e+008	109417.8	PA_Bse02:2504000752	

PA_Bse02:2504000752 BS02DRAFT_00023490 TonB-dependent receptor [B. setacea BS02 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	045-1201.2961.2961.0	2	14.31	14.31	87.6	3.01e+007	(R)SLNMDEGFSGSAR(L)	1370.601
2	045-1201.4118.4118.2	2	6.19	6.19	62.8	1.37e+008	(K)LPDVTIADSLQR(I)	1327.722

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	12	6	75.15	18	1.13e+009	57219.5	PA_Bse08:2503995261	PA_Bse08:2503995261 BS08DRAFT_00037250 chaperonin GroL [B. setacea BS08 (Isolate from shipworm gill tissu

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	045-1201.1874.1880.0	2	16.79	16.79	91.3	5.64e+006	(K)VGAATEVEMK(E)	1034.519
2	044-1001.4815.4815.2	2	15.59	15.59	86.1	1.32e+008	(R)AVSAIADLTGDNEDQDAGIGIAR(R)	2272.106
3	044-1001.6338.6338.0	3	15.12	11.70	86.1	2.18e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
4	044-1001.6344.6344.0	3	14.96	11.55	81.4	2.14e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
5	044-1001.1875.1885.0	2	14.46	14.46	86.6	2.41e+006	(K)VGAATEVEMK(E)	1034.519
6	044-1001.6340.6351.0	2	14.45	7.97	86.8	8.12e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
7	043-0801.5697.5697.0	3	11.70	11.70	70.3	2.72e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
8	044-1001.2468.2468.0	2	10.16	3.38	70.4	5.57e+006	(R)QIVTNSGDEASVVAEK(V)	1646.824
9	043-0801.4315.4315.0	2	9.73	3.80	80.0	1.78e+007	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
10	044-1001.4241.4254.2	2	8.62	2.91	75.8	2.43e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
11	044-1001.5994.6013.0	2	7.76	7.76	61.3	1.82e+008	(K)MLAGVNILADAVK(I)	1314.746
12	044-1001.2462.2462.0	2	7.05	7.05	65.6	5.50e+006	(R)QIVTNSGDEASVVAEK(V)	1646.824

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	10	5	67.93	16	9.55e+008	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	045-1201.1874.1880.0	2	16.79	16.79	91.3	5.64e+006	(K)VGAATEVEMK(E)	1034.519
2	044-1001.4815.4815.2	2	15.59	15.59	86.1	1.32e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
3	044-1001.6338.6338.0	3	15.12	11.70	86.1	2.18e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
4	044-1001.6344.6344.0	3	14.96	11.55	81.4	2.14e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
5	044-1001.1875.1885.0	2	14.46	14.46	86.6	2.41e+006	(K)VGAATEVEMK(E)	1034.519
6	044-1001.6340.6351.0	2	14.45	7.97	86.8	8.12e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
7	043-0801.5697.5697.0	3	11.70	11.70	70.3	2.72e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
8	043-0801.3088.3094.0	2	10.70	10.70	71.5	1.39e+007	(R)QIVTNAGDEASVIAEK(V)	1644.844
9	043-0801.4315.4315.0	2	9.73	3.80	80.0	1.78e+007	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
10	044-1001.4241.4254.2	2	8.62	2.91	75.8	2.43e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891

Group	Subgroup	Spectra	Distinct Peptides	Distinct Summed MS/MS	% AA	Total Protein	Protein MW	Database	Protein Name

(#)	(#)	(#)	(#)	Search Score	Coverage	Spectral Intensity	(Da)	Accession #	
5	5.3	9	5	65.52	17	6.40e+008	57147.5	PA_Bse02:2503998519	PA_Bse02:2503998519 BS02DRAFT_00025680 chaperonin GroL [B. setacea BS02 (Isolate from shipworm gill tissu

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.1874.1880.0	2	16.79	16.79	91.3	5.64e+006	(K)VGAATEVEMK(E)	1034.519
2	045-1201.11177.11177.0	3	15.46	9.38	89.6	1.60e+007	(K)AMLQDIAILTGGTVISEEIGLDLESATLEHLGQAK(R)	3636.905
3	044-1001.6338.6338.0	3	15.12	11.70	86.1	2.18e+008	(R)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
4	044-1001.6344.6344.0	3	14.96	11.55	81.4	2.14e+008	(R)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
5	044-1001.1875.1885.0	2	14.46	14.46	86.6	2.41e+006	(K)VGAATEVEMK(E)	1034.519
6	044-1001.6340.6351.0	2	14.45	7.97	86.8	8.12e+007	(R)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
7	043-0801.5697.5697.0	3	11.70	11.70	70.3	2.72e+007	(R)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
8	045-1201.2419.2426.0	2	10.03	10.03	72.2	5.53e+006	(R)QIVENAGEEGSVVADK(V)	1644.808
9	045-1201.3997.3997.0	2	8.12	8.12	77.3	6.98e+007	(K)AVIAAVEYIK(S)	1076.636

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	5	73.81	8	7.21e+008	106594.3	PA_Bse_meta_comb:2073586734	PA_Bse_meta_comb:2073586734 BaSeMet_00303900 TonB-dependent receptor [Bankia setacea micro

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.3698.3708.2	2	17.64	10.03	96.9	1.15e+008	(R)MGVTGISGTVNLK(T)	1276.694
2	046-1401.6256.6281.0	3	15.92	8.34	82.8	1.74e+007	(R)SYTTTLPSLNINYALADDINLR(F)	2468.267
3	045-1201.7417.7417.0	3	15.55	6.79	76.5	5.44e+008	(R)ASATIIDAISAEDIGKLPDVTISDSLQR(I)	2899.526
4	045-1201.2216.2243.2	2	13.13	7.18	85.4	3.12e+006	(R)SAGEGAAINIR(G)	1058.559
5	045-1201.2153.2208.0	2	11.57	4.46	82.4	6.79e+006	(R)ASIETSINAK(R)	1033.553
6	046-1401.6279.6279.0	3	11.54	8.20	72.1	1.31e+007	(R)ASATIIDAISAEDIGKLPDVTISDSLQR(I)	2899.526
7	045-1201.2038.2118.0	2	11.51	3.66	82.4	2.06e+007	(R)ASIETSINAK(R)	1033.553

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	11	5	71.48	36	1.10e+009	29434.1	PA_Bse_meta_comb:2073593916	PA_Bse_meta_comb:2073593916 BaSeMet_00375720 Outer membrane protein (porin) [Bankia setacea r

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.4631.4637.2	2	18.83	18.83	97.1	3.35e+008	(K)VNVSWQSADEGEYNELELR(N)	2238.032
2	046-1401.4499.4499.0	3	17.30	13.56	82.5	3.85e+006	(K)VNVSWQSADEGEYNELELR(N)	2238.032
3	045-1201.4627.4634.0	3	16.23	16.23	80.7	2.76e+008	(K)VNVSWQSADEGEYNELELR(N)	2238.032
4	045-1201.7475.7475.2	2	15.77	15.77	88.9	1.57e+008	(K)VDLFNDMEGDIATTLTTNDVR(A)	2340.103
5	045-1201.3856.3876.2	2	14.60	10.33	86.5	1.11e+008	(R)ATNSVAYTTPSSSPVAVNVQVVNK(E)	2433.262
6	045-1201.2124.2135.2	2	11.98	5.49	90.6	2.89e+006	(K)SLSVGADYK(L)	939.479
7	045-1201.7535.7535.0	2	11.65	11.65	65.6	1.67e+008	(K)VDLFNDMEGDIATTLTTNDVR(A)	2340.103
8	046-1401.6296.6296.0	3	11.28	11.28	75.4	3.24e+007	(K)VDLFNDMEGDIATTLTTNDVR(A)	2340.103
9	046-1401.6371.6371.0	3	10.30	10.30	72.0	1.11e+007	(K)GTEDLGNGLTAIYQLETGVNFDDNGNFSK(R)	3089.434

10	046-1401.4494.4494.0	3	10.17	10.17	79.1	3.87e+006	(K)VNVSWQSADEGEYNELELR(N)	2238.032
11	046-1401.4511.4511.2	2	6.08	6.08	79.7	1.61e+006	(K)VNVSWQSADEGEYNELELR(N)	2238.032

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	7	5	69.52	6	1.25e+009	126855.7	PA_Bse02:2504001037	PA_Bse02:2504001037 BS02DRAFT_00030180 TonB-dependent receptor [B. setacea BS02 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.2320.2326.0	3	17.50	11.15	92.8	2.45e+007	(K)NDPDHFSAEGSGAVVR(G)	1657.757
2	045-1201.2556.2588.2	2	17.32	13.12	94.6	1.59e+007	(K)TEMQISEDGYTQGR(S)	1614.707
3	045-1201.5875.5875.0	2	16.63	10.60	87.9	2.07e+008	(R)EADTFVDAISASDIGALPDR(S)	2062.993
4	045-1201.5878.5878.0	2	14.78	7.36	86.6	2.07e+008	(R)EADTFVDAISASDIGALPDR(S)	2062.993
5	045-1201.2338.2359.2	2	14.47	14.47	88.7	5.30e+006	(K)NDPDHFSAEGSGAVVR(G)	1657.757
6	045-1201.6464.6481.0	2	9.84	3.87	72.3	5.09e+008	(R)GLSFQDVAPELMSSVK(L)	1707.863
7	045-1201.4974.4974.0	2	8.23	8.23	64.9	2.87e+008	(R)FFEDGFVTSLK(G)	1289.642

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	4	67.62	7	4.22e+008	100788.0	PA_Bse_meta_comb:2073596195	PA_Bse_meta_comb:2073596195 BaSeMet_00398510 TonB-dependent receptor [Bankia setacea micro

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	046-1401.7775.7817.0	3	23.00	23.00	100.0	8.34e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
2	045-1201.9713.9726.0	3	19.04	19.04	92.4	7.46e+007	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
3	045-1201.3916.3922.2	2	15.88	15.88	88.9	1.83e+008	(K)ADIATGGLGGTINIK(T)	1400.775
4	045-1201.3042.3066.2	2	14.94	8.58	92.4	3.54e+007	(R)NMPTVTIDGTAGDK(G)	1419.679
5	046-1401.7163.7163.0	3	13.80	13.80	83.5	3.30e+006	(R)FITEEATSVFAQFAGSFK(I)	1979.976
6	045-1201.9714.9722.2	2	13.79	13.79	78.6	9.27e+007	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
7	046-1401.7788.7788.2	2	12.31	12.31	89.1	4.71e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
8	046-1401.7805.7805.2	2	11.42	11.42	81.0	4.70e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
9	046-1401.7140.7140.0	3	11.06	11.06	74.7	3.49e+006	(R)FITEEATSVFAQFAGSFK(I)	1979.976
10	046-1401.7152.7152.0	3	10.11	10.11	92.6	3.29e+006	(R)FITEEATSVFAQFAGSFK(I)	1979.976
11	046-1401.7800.7800.2	2	9.98	6.80	91.4	5.10e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
12	046-1401.7161.7161.0	3	9.55	9.55	82.7	3.22e+006	(R)FITEEATSVFAQFAGSFK(I)	1979.976
13	046-1401.3884.3884.0	2	7.65	7.65	87.8	7.20e+005	(K)ADIATGGLGGTINIK(T)	1400.775

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	9.2	10	4	65.45	31	4.06e+008	19640.4	PA_Bse_meta_comb:2073597966	PA_Bse_meta_comb:2073597966 BaSeMet_00416220 Outer membrane receptor for ferrienterochelin an

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

1	046-1401.7775.7817.0	3	23.00	23.00	100.0	8.34e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
2	045-1201.9713.9726.0	3	19.04	19.04	92.4	7.46e+007	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
3	045-1201.3916.3922.2	2	15.88	15.88	88.9	1.83e+008	(K)ADIATGGLGGTINIK(T)	1400.775
4	045-1201.3092.3097.0	2	14.51	7.51	91.6	2.31e+007	(R)NMPTVTIDGTAGEDK(G)	1548.722
5	045-1201.9714.9722.2	2	13.79	13.79	78.6	9.27e+007	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
6	046-1401.7788.7788.2	2	12.31	12.31	89.1	4.71e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
7	045-1201.2340.2370.0	2	12.06	6.68	82.7	8.84e+006	(R)ASMAQSIDVK(R)	1049.530
8	046-1401.7805.7805.2	2	11.42	11.42	81.0	4.70e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
9	046-1401.7800.7800.2	2	9.98	6.80	91.4	5.10e+006	(R)AFDFANIASEVIYGVDVYK(T)	2121.054
10	046-1401.3884.3884.0	2	7.65	7.65	87.8	7.20e+005	(K)ADIATGGLGGTINIK(T)	1400.775

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	4	58.77	35	4.26e+008	27641.5	PA_Bse02:2504001159	PA_Bse02:2504001159 BS02DRAFT_00031400 FKBP-type peptidyl-prolyl cis-trans isomerase./Domain amino term

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	046-1401.5475.5481.0	3	18.12	9.77	84.9	8.13e+006	(K)EGVIQTESGLQYEIITAGDGAIPTAK(D)	2661.362
2	046-1401.7956.8020.0	3	15.16	15.16	81.7	1.52e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
3	045-1201.10532.10537.0	3	14.69	8.07	85.6	3.75e+008	(R)GEPAEFPVGSLIPGWVEALQLMPVGSK(W)	2808.465
4	046-1401.7967.7967.0	3	12.84	12.84	72.2	1.16e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
5	046-1401.7960.7960.0	3	11.26	11.26	70.8	1.04e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
6	045-1201.2267.2267.0	2	10.80	6.07	88.1	2.94e+006	(R)YSDEEMQATMR(A)	1360.551
7	045-1201.2272.2272.0	2	8.97	5.20	90.0	2.94e+006	(R)YSDEEMQATMR(A)	1360.551

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	7	4	58.49	9	1.11e+009	56014.8	PA_Bse08:2503995077	PA_Bse08:2503995077 BS08DRAFT_00035450 nitrogenase molybdenum-iron protein alpha chain [B. setacea BS0

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.2983.3020.0	2	17.26	12.02	88.8	1.70e+008	(K)IAEQFDETIQAK(T)	1392.701
2	044-1001.2883.2902.0	3	16.09	5.55	86.7	1.79e+007	(R)KIAEQFDETIQAK(T)	1520.796
3	043-0801.2991.3007.0	2	14.32	14.32	79.7	3.48e+007	(K)IAEQFDETIQAK(T)	1392.701
4	044-1001.6908.6976.0	2	13.16	8.03	86.5	4.72e+008	(K)LVDEIETLFPLNK(G)	1530.842
5	043-0801.6143.6185.2	2	11.99	6.75	82.3	4.18e+007	(K)LVDEIETLFPLNK(G)	1530.842
6	044-1001.4891.4891.2	2	11.98	11.98	80.8	1.90e+008	(R)VVAQWSGDGTISEMELTPK(V)	2048.001
7	044-1001.4897.4897.0	2	9.86	9.86	73.3	1.86e+008	(R)VVAQWSGDGTISEMELTPK(V)	2048.001

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	4	57.70	21	6.91e+008	33845.5	PA_Bse08:2503994737	PA_Bse08:2503994737 BS08DRAFT_00032510 transaldolase [B. setacea BS08 (Isolate from shipworm gill tissue)]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	043-0801.6426.6443.2	2	19.65	15.36	98.0	2.70e+007	(R)GFVADQINLENFLK(A)	1607.843
2	044-1001.7328.7333.0	2	19.35	15.76	97.2	1.84e+008	(R)GFVADQINLENFLK(A)	1607.843
3	044-1001.7478.7529.0	3	15.87	6.81	93.6	1.95e+008	(R)LTISPDLLGALEADTGKLER(A)	2112.155
4	043-0801.6564.6568.0	3	12.75	5.09	89.7	1.77e+007	(R)LTISPDLLGALEADTGKLER(A)	2112.155
5	044-1001.3501.3501.0	3	11.88	5.59	76.7	1.15e+008	(K)QYSDVVADTGDIEAIKR(Y)	1879.940
6	044-1001.4199.4199.2	2	10.30	5.46	72.8	1.53e+008	(R)YQPLDATTNPSLLYK(A)	1723.891

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	5	4	53.93	4	2.26e+008	115295.3	PA_BS12:2189568198	PA_BS12:2189568198 or1530 Outer membrane receptor for ferrienterochelin and colicins [B. setacea BS12] 1069 b

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	045-1201.3469.3473.2	2	17.78	13.58	96.6	9.69e+007	(R)ASLEAAMDIK(R)	1048.535
2	045-1201.3231.3246.2	2	17.67	17.67	92.7	9.60e+007	(K)ASIATGGIGATVNVK(T)	1358.764
3	045-1201.2045.2045.0	2	10.91	5.88	97.6	1.47e+006	(R)VNGEGAEITVR(G)	1144.596
4	045-1201.3194.3202.0	2	7.57	7.57	70.1	3.01e+007	(K)LDGSFEFDNGR(F)	1256.555
5	045-1201.2034.2034.0	2	6.62	2.76	91.3	1.48e+006	(R)VNGEGAEITVR(G)	1144.596

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	8	3	49.56	10	1.21e+009	44282.5	PA_BSC2:2534573496	PA_BSC2:2534573496 Bsc2_01181 translation elongation factor 1A (EF-1A/EF-Tu) [Alteromonadacea bacterium Bs

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	043-0801.3038.3061.0	3	19.87	19.87	95.9	2.19e+007	(R)GITIATSHVEYDSPER(H)	1774.861
2	045-1201.9451.9527.3	3	19.19	19.19	89.5	3.96e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
3	043-0801.7896.7906.3	3	18.73	18.73	90.6	2.74e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
4	045-1201.9444.9450.2	2	12.63	6.41	85.0	4.91e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
5	043-0801.7889.7895.2	2	12.47	6.83	78.9	2.23e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
6	045-1201.9539.9539.0	3	11.99	11.99	74.0	2.02e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
7	043-0801.3067.3067.0	3	11.56	11.56	77.5	2.04e+007	(R)GITIATSHVEYDSPER(H)	1774.861
8	045-1201.2930.2959.0	2	10.50	4.73	76.4	3.31e+007	(K)TTLTAALTR(V)	947.553

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	14.2	7	3	38.18	9	1.28e+009	44298.7	PA_Bse02:2503998465	PA_Bse02:2503998465 BS02DRAFT_00025140 translation elongation factor TU [B. setacea BS02 (Isolate from ship

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

1	045-1201.9451.9527.3	3	19.19	19.19	89.5	3.96e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
2	043-0801.7896.7906.3	3	18.73	18.73	90.6	2.74e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
3	045-1201.9444.9450.2	2	12.63	6.41	85.0	4.91e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
4	043-0801.7889.7895.2	2	12.47	6.83	78.9	2.23e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
5	045-1201.9539.9539.0	3	11.99	11.99	74.0	2.02e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
6	045-1201.2930.2959.0	2	10.50	4.73	76.4	3.31e+007	(K)TTLTAALTR(V)	947.553
7	045-1201.4027.4027.0	2	8.49	3.01	70.2	1.06e+008	(K)VGEEISIVGIK(D)	1143.662

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	14.3	2	2	25.14	6	6.69e+007	44255.6	PA_Bse08:2503995480	PA_Bse08:2503995480 BS08DRAFT_00039430 translation elongation factor TU [B. setacea BS08 (Isolate from shi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.11056.11056.2	2	14.64	9.09	86.0	3.39e+007	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
2	045-1201.2930.2959.0	2	10.50	4.73	76.4	3.31e+007	(K)TTLTAALTR(V)	947.553

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	7	3	48.66	29	6.12e+009	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	044-1001.5591.5645.2	2	18.43	10.76	98.2	4.69e+009	(K)TVTAMDVVYALK(R)	1310.703
2	043-0801.5307.5325.2	2	17.91	8.09	97.5	2.65e+008	(K)TVTAMDVVYALK(R)	1310.703
3	044-1001.5643.5643.0	3	16.00	8.70	84.2	1.14e+008	(K)TVTAMDVVYALK(R)	1310.703
4	043-0801.3193.3211.2	2	15.80	10.03	94.0	5.89e+007	(R)ISGLIYEETR(G)	1180.621
5	044-1001.3171.3175.2	2	15.31	7.48	94.4	6.28e+008	(R)ISGLIYEETR(G)	1180.621
6	043-0801.4262.4272.0	2	14.43	4.44	87.7	2.35e+008	(K)VFLENVIR(D)	989.578
7	044-1001.4195.4200.0	2	14.07	5.50	92.5	1.24e+008	(K)VFLENVIR(D)	989.578

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
16	16.1	7	4	47.92	6	1.12e+009	102017.5	PA_Bse08:2503996049	PA_Bse08:2503996049 BS08DRAFT_00012470 TonB-dependent receptor [B. setacea BS08 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.7472.7491.2	2	16.42	8.84	87.2	1.85e+008	(R)ILPSFSAVYDVVNNVK(V)	1764.954
2	045-1201.7406.7412.2	2	13.96	13.96	72.5	2.59e+008	(R)ILPSFSAVYDVVNNVK(V)	1764.954
3	044-1001.7522.7543.0	2	13.66	9.00	88.8	1.33e+008	(R)QVDLNMFPTELFK(S)	1581.799
4	044-1001.7516.7516.0	3	12.27	3.12	81.6	6.88e+007	(R)ILPSFSAVYDVVNNVK(V)	1764.954
5	044-1001.4762.4762.0	2	10.88	5.54	80.7	9.75e+007	(R)ANPADMFPNSEWDGSGIDK(I)	2050.882
6	045-1201.7411.7411.0	2	8.16	5.15	75.7	2.52e+008	(R)QVDLNMFPTELFK(S)	1581.799

7	045-1201.4484.4484.0	2	6.96	6.96	61.3	1.19e+008	(R)DSVGFSDEVFSDDMGK(M)	1734.717

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
17	17.1	7	3	47.24	21	4.61e+008	12471.3	PA_Bse02:2503998471	PA_Bse02:2503998471 BS02DRAFT_00025200 ribosomal protein L7/L12 [B. setacea BS02 (Isolate from shipworm

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.4661.4666.2	2	17.11	12.17	89.3	2.96e+008	(K)TDFDVVLTSVGEK(K)	1409.716
2	045-1201.2393.2423.0	3	16.49	9.96	92.1	1.13e+007	(K)KQLEEAGASVELK(-)	1401.759
3	044-1001.2415.2427.0	3	16.27	7.81	89.3	3.99e+006	(K)KQLEEAGASVELK(-)	1401.759
4	045-1201.2714.2780.0	2	13.64	6.49	84.0	7.46e+007	(K)QLEEAGASVELK(-)	1273.664
5	045-1201.2404.2404.2	2	13.28	8.34	85.3	5.29e+006	(K)KQLEEAGASVELK(-)	1401.759
6	045-1201.2800.2852.0	2	12.97	8.16	85.9	3.48e+007	(K)QLEEAGASVELK(-)	1273.664
7	044-1001.2709.2714.0	2	12.81	6.87	85.5	3.49e+007	(K)QLEEAGASVELK(-)	1273.664

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
18	18.1	5	4	47.01	17	9.23e+008	42092.0	PA_BSC2:2534574460	PA_BSC2:2534574460 Bsc2_02147 hypothetical protein [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.3706.3713.0	2	13.84	13.84	75.3	2.08e+008	(K)SLSLGGEYTLANR(E)	1380.712
2	045-1201.3790.3797.0	3	13.23	4.12	82.4	8.49e+007	(R)FNLGTTTTIGEHTLK(T)	1632.860
3	044-1001.3699.3699.0	2	12.69	12.69	70.8	2.05e+008	(K)SLSLGGEYTLANR(E)	1380.712
4	044-1001.4586.4602.2	2	11.68	11.68	79.6	2.96e+008	(R)IVTDQNPLPDFVGR(Y)	1570.823
5	045-1201.5614.5614.0	2	8.26	8.26	62.4	1.29e+008	(R)YTTGNFQFAVENPETTVTPFEGGGR(I)	2719.264

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
19	19.1	8	3	41.86	11	8.97e+008	36127.2	PA_Bse08:2503993973	PA_Bse08:2503993973 BS08DRAFT_00026510 glyceraldehyde-3-phosphate dehydrogenase, type I [B. setacea BS

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.4971.5004.2	2	15.92	11.20	83.6	3.55e+008	(R)VPTPDVSVVDLTVR(L)	1496.832
2	043-0801.2324.2327.0	3	15.31	15.31	84.7	4.21e+006	(K)YDSTHGQFNGDVEVK(D)	1695.762
3	043-0801.4811.4833.0	2	11.34	8.02	76.1	2.34e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
4	044-1001.4571.4571.0	2	10.63	10.63	74.1	2.01e+008	(K)VVELMEYMDSK(A)	1343.623
5	044-1001.2354.2354.2	2	10.41	7.27	69.3	4.54e+006	(K)YDSTHGQFNGDVEVK(D)	1695.762
6	044-1001.2347.2347.0	2	9.51	3.95	68.4	4.39e+006	(K)YDSTHGQFNGDVEVK(D)	1695.762
7	044-1001.2336.2336.2	2	9.44	9.44	68.2	4.21e+006	(K)YDSTHGQFNGDVEVK(D)	1695.762
8	044-1001.4608.4608.0	2	8.41	8.41	72.6	3.00e+008	(K)VVELMEYMDSK(A)	1343.623

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
20	20.1	7	3	41.04	15	1.83e+008	35386.5	PA_BS12:2189571789	PA_BS12:2189571789 or0889 Malate/lactate dehydrogenases [B. setacea BS12] 327 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	043-0801.8498.8541.0	3	22.10	15.36	96.1	8.73e+006	(K)DQPVILQMLEITPALEALK(G)	2122.183
2	044-1001.9752.9809.0	3	19.63	11.11	91.1	2.56e+007	(K)DQPVILQMLEITPALEALK(G)	2122.183
3	044-1001.9754.9792.2	2	16.14	13.01	93.4	1.16e+007	(K)DQPVILQMLEITPALEALK(G)	2122.183
4	044-1001.9772.9772.2	2	13.45	9.67	88.8	1.08e+007	(K)DQPVILQMLEITPALEALK(G)	2122.183
5	044-1001.4104.4104.2	2	10.82	10.82	67.7	1.15e+008	(K)VLVVGNPANTNALIAQR(N)	1749.997
6	043-0801.5251.5251.0	2	8.12	8.12	66.7	7.24e+006	(K)DLLEANAAIFSVQGK(A)	1575.838
7	043-0801.8514.8514.0	2	8.08	4.61	89.3	3.99e+006	(K)DQPVILQMLEITPALEALK(G)	2122.183

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
20	20.2	3	3	34.62	18	1.40e+008	35600.6	PA_Bse08:2503994614	PA_Bse08:2503994614 BS08DRAFT_00031280 malate dehydrogenase [B. setacea BS08 (Isolate from shipworm gi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.10202.10207.0	3	15.68	7.25	87.9	1.80e+007	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
2	044-1001.4104.4104.2	2	10.82	10.82	67.7	1.15e+008	(K)VLVVGNPANTNALIAQR(N)	1749.997
3	043-0801.5251.5251.0	2	8.12	8.12	66.7	7.24e+006	(K)DLLEANAAIFSVQGK(A)	1575.838

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
21	21.1	14	2	39.81	19	5.91e+009	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	043-0801.4522.4528.0	2	22.90	18.19	98.3	1.91e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
2	044-1001.4529.4575.0	2	21.73	18.04	95.6	3.64e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
3	045-1201.4405.4428.0	2	17.84	13.18	89.7	4.69e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
4	045-1201.5196.5224.0	2	16.91	16.91	90.0	5.02e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
5	046-1401.4835.4884.3	3	16.63	8.88	85.0	1.28e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
6	043-0801.5027.5032.3	3	16.59	9.12	85.9	3.39e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
7	045-1201.4392.4486.3	3	13.43	6.35	77.4	2.52e+009	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
8	044-1001.5372.5372.0	2	12.11	5.51	75.7	3.43e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
9	043-0801.5002.5033.2	2	11.34	11.34	73.7	3.41e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
10	043-0801.4501.4513.0	3	11.27	4.64	75.0	1.45e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
11	044-1001.4502.4508.0	3	10.55	3.83	71.2	1.44e+009	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
12	046-1401.4383.4387.0	3	10.43	4.69	70.1	1.73e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
13	046-1401.4839.4843.2	2	9.39	9.39	86.2	3.57e+006	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055

14	044-1001.11380.11380.0	2	6.82	6.82	61.6	9.10e+006	(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
22	22.1	2	2	37.84	5	1.37e+008	115945.6	PA_Bse08:2503996008	PA_Bse08:2503996008 BS08DRAFT_00012060 TonB-dependent receptor [B. setacea BS08 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.7727.7751.0	3	22.90	22.90	98.1	8.39e+007	(R)DNVNVVDSIVAEDIGKLPDTTITDSLQR(V)	3027.549
2	044-1001.8660.8690.0	3	14.94	10.79	90.0	5.34e+007	(R)HENSSQEILPSFNLNLFPTDDLVLR(F)	2898.464

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
23	23.1	2	2	33.77	14	1.14e+008	17663.6	PA_Bse02:2503998467	PA_Bse02:2503998467 BS02DRAFT_00025160 ribosomal protein S7, bacterial/organelle [B. setacea BS02 (Isolate

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.11191.11241.0	3	17.96	12.27	83.9	4.09e+007	(R)DPLEVFSEALENIAPLVEVK(S)	2212.175
2	045-1201.10659.10682.0	3	15.81	10.11	93.3	7.36e+007	(K)TNRDPLEVFSEALENIAPLVEVK(S)	2583.367

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
24	24.1	3	2	33.40	10	4.07e+007	52481.4	PA_BSC2:2534576897	PA_BSC2:2534576897 Bsc2_04586 pyruvate kinase (EC 2.7.1.40) [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.9808.9808.0	3	16.97	16.97	87.8	9.99e+006	(R)AETVADDQILDDIILASDAVMVAR(G)	2544.287
2	044-1001.9814.9814.0	3	16.94	10.14	88.8	1.02e+007	(R)AETVADDQILDDIILASDAVMVAR(G)	2544.287
3	044-1001.9501.9519.0	3	16.43	16.43	77.8	2.05e+007	(R)AEVFDVANAVLDGTDAVMLSAETAAGK(Y)	2665.303

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
25	25.1	3	2	27.44	16	3.05e+007	19750.3	PA_Bse08:2503995045	PA_Bse08:2503995045 BS08DRAFT_00035130 flavodoxin, long chain [B. setacea BS08 (Isolate from shipworm gill

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	043-0801.8440.8450.2	2	16.85	8.63	97.2	5.49e+006	(R)LNTWLAQIAPEFGLPI(-)	1782.979
2	043-0801.4316.4316.0	2	10.59	7.01	72.0	1.97e+007	(K)IGIFFGSNTGNTR(K)	1383.702
3	043-0801.8484.8484.0	2	7.84	4.37	96.1	5.31e+006	(R)LNTWLAQIAPEFGLPI(-)	1782.979

Distinct Total

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
26	26.1	4	2	26.89	33	1.44e+007	12111.0	PA_BS12:2189569075	PA_BS12:2189569075 or2390 Nitrogen regulatory protein PII [B. setacea BS12] 112 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	046-1401.4621.4627.0	2	17.13	13.53	94.3	2.54e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965
2	046-1401.4614.4614.0	3	16.72	16.72	87.8	2.77e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965
3	046-1401.4632.4632.2	2	10.96	10.96	74.8	3.06e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965
4	046-1401.5824.5824.0	3	9.76	4.32	72.0	5.97e+006	(K)TKLEVAVADDQLDSVVEAISK(A)	2230.182

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
27	27.1	3	2	25.42	33	2.53e+008	9164.5	PA_Bse08:2503994572	PA_Bse08:2503994572 BS08DRAFT_00030860 Bacterial DNA-binding protein. [B. setacea BS08 (Isolate from shipv

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	046-1401.6252.6274.2	2	13.71	7.89	91.9	9.99e+006	(K)EGDQVALVGFGTFLVK(E)	1679.901
2	044-1001.6156.6156.0	2	11.71	11.71	73.9	1.58e+008	(R)ALDAVTESIANALK(E)	1415.775
3	044-1001.7394.7394.0	2	9.08	9.08	72.5	8.56e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
27	27.2	3	2	23.94	34	9.84e+007	9107.5	PA_Bse02:2503999877	PA_Bse02:2503999877 BS02DRAFT_00006580 Bacterial DNA-binding protein. [B. setacea BS02 (Isolate from shipv

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	046-1401.6252.6274.2	2	13.71	7.89	91.9	9.99e+006	(K)EGDQVALVGFGTFLVK(E)	1679.901
2	046-1401.5209.5209.2	2	10.23	10.23	95.4	2.80e+006	(K)SELIEAIAASADISK(A)	1517.806
3	044-1001.7394.7394.0	2	9.08	9.08	72.5	8.56e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
28	28.1	2	2	25.29	10	3.02e+008	28847.5	PA_BS12:2189569790	PA_BS12:2189569790 or3098 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [B. setacea BS12] 265 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.3028.3034.2	2	17.30	17.30	90.4	3.17e+007	(K)EGVVVAESGSGLQYK(I)	1522.775
2	045-1201.6227.6227.2	2	7.99	7.99	60.8	2.70e+008	(K)GWVEALQLMPVGSK(W)	1514.804

Group	Subgroup	Spectra	Distinct	Distinct Summed	% AA	Total Protein	Protein	Database

(#)	(#)	(#)	Peptides (#)	MS/MS Search Score	Coverage	Spectral Intensity	MW (Da)	Accession #	Protein Name
29	29.1	2	2	24.37	3	1.67e+008	105318.6	PA_BS12:2189568779	PA_BS12:2189568779 or2098 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12] 968 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.9534.9540.0	2	13.22	13.22	75.0	7.67e+007	(K)LLPSFSAVLDVVEDVK(L)	1730.958
2	045-1201.9596.9621.2	2	11.15	7.54	72.1	9.05e+007	(R)QVDLDLFPTELFGSLAVDK(T)	2107.096

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
30	30.1	2	2	23.39	2	2.01e+008	118803.8	PA_BSC2:2534573281	PA_BSC2:2534573281 Bsc2_00965 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.3018.3037.0	2	16.92	11.86	90.3	3.44e+007	(R)ASLEAAMDVK(R)	1034.519
2	045-1201.4189.4189.0	2	6.47	6.47	64.6	1.67e+008	(R)EAVGVVDAISAEDIGK(M)	1572.812

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
31	31.1	2	2	22.92	11	2.88e+008	29305.8	PA_Bse02:2503998171	PA_Bse02:2503998171 BS02DRAFT_00013480 Protein of unknown function (DUF3450). [B. setacea BS02 (Isolate

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.3954.3973.2	2	13.98	13.98	83.1	1.99e+008	(R)AWVELDAGEYR(A)	1308.622
2	045-1201.8552.8552.0	2	8.94	3.40	72.5	8.87e+007	(R)MLEGLEQFVSLDLPFHTEER(Q)	2390.170

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
32	32.1	6	1	20.76	18	2.01e+010	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	044-1001.8520.8520.3	3	20.76	11.21	95.7	5.34e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
2	043-0801.7258.7329.3	3	20.73	12.91	95.2	1.70e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
3	044-1001.8400.8509.3	3	19.66	10.78	94.0	8.57e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
4	044-1001.8405.8510.2	2	13.56	6.83	87.2	2.82e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
5	043-0801.7273.7330.2	2	12.98	6.47	84.8	2.29e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
6	044-1001.8521.8521.2	2	11.96	3.91	83.8	1.50e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391

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

			(#)	Search Score		Intensity	(Da)		
33	33.1	2	1	20.65	2	3.67e+007	68581.6	PA_Bse08:2503997242	PA_Bse08:2503997242 BS08DRAFT_00017410 chaperone protein DnaK [B. setacea BS08 (Isolate from shipworm

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	044-1001.2623.2673.0	2	20.65	16.57	94.8	1.93e+007	(K)MVLDAEANAEADR(K)	1404.643
2	044-1001.2648.2659.0	2	18.66	14.72	95.3	1.74e+007	(K)MVLDAEANAEADR(K)	1404.643

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
34	34.1	2	2	20.32	6	9.27e+007	98379.6	PA_BSC2:2534573844	PA_BSC2:2534573844 Bsc2_01530 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.10575.10581.0	3	11.78	11.78	74.6	6.98e+007	(R)GQYGTSDFDQVIGDLSYVFTDTLR(L)	2697.268
2	045-1201.10618.10618.0	3	8.54	5.14	82.4	2.28e+007	(R)WVETTVGGGASPIEESYSNLLPAINAIYEPMDDVLFR(A)	4053.980

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
35	35.1	1	1	20.06	9	3.78e+007	12421.2	PA_BS12:2189570749	PA_BS12:2189570749 or3994 Ribosomal protein L7/L12 [B. setacea BS12] 123 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	045-1201.3102.3122.2	2	20.06	14.03	96.1	3.78e+007	(K)DLEEAGASVELK(-)	1260.632