Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\011011_OGLgill1_frations
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 336 **Hits:** 911
Data Directory: msdataSM\011311OGLGill1_fractions
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 44 **Hits:** 165
beginning to assemble proteins .... proteins assembled 0.154078 sec
proteins filtered by unique peptides 0.018967 sec
proteins filtered by score
calculated protein coverage maps 0.08766 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.039966 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 58 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	159.63	24	3.06e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	44	9	159.63	41	3.06e+010	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	49	7	129.92	19	5.19e+009	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
2	2.1	49	7	129.92	33	5.19e+009	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
3	3.1	6	4	66.47	20	1.82e+008	34007.6	PA_BS12:2189567864	PA_BS12:2189567864 or1190 Transaldolase [B. setacea BS12] 311 bp
3	3.1	6	4	66.47	20	1.82e+008	33949.6	PA_Bse_meta_comb:2073584304	PA_Bse_meta_comb:2073584304 BaSeMet_00279600 transaldolase (EC 2.2.1.2) [Bankia setacea micro
3	3.1	5	3	51.60	14	1.52e+008	33845.5	PA_Bse08:2503994737	PA_Bse08:2503994737 BS08DRAFT_00032510 transaldolase [B. setacea BS08 (Isolate from shipworm
3	3.1	3	2	33.45	31	7.00e+007	10806.4	PA_Bse_meta_comb:2073579380	PA_Bse_meta_comb:2073579380 BaSeMet_00230360 transaldolase (EC 2.2.1.2) [Bankia setacea micro
3	3.2	7	4	53.34	20	1.75e+008	33705.4	PA_BSC2:2534576639	PA_BSC2:2534576639 Bsc2_04328 transaldolase (EC 2.2.1.2) [Alteromonadacea bacterium Bsc2]
3	3.2	7	4	53.34	20	1.75e+008	33675.4	PA_Bse_meta_comb:2073570868	PA_Bse_meta_comb:2073570868 BaSeMet_00145240 transaldolase (EC 2.2.1.2) [Bankia setacea micro
4	4.1	9	4	65.68	51	6.42e+008	12099.0	PA_Bse02:2503998071	PA_Bse02:2503998071 BS02DRAFT_00012490 Nitrogen regulatory protein P-II. [B. setacea BS02 (Isola
4	4.1	9	4	65.68	51	6.42e+008	12099.0	PA_Bse_meta_comb:2073590737	PA_Bse_meta_comb:2073590737 BaSeMet_00343930 nitrogen regulatory protein P-II [Bankia setacea
4	4.1	6	2	29.53	25	2.23e+008	12165.0	PA_Bse08:2503996512	PA_Bse08:2503996512 BS08DRAFT_00003980 Nitrogen regulatory protein P-II. [B. setacea BS08 (Isola
4	4.2	9	4	65.25	51	6.75e+008	12111.0	PA_BS12:2189569075	PA_BS12:2189569075 or2390 Nitrogen regulatory protein PII [B. setacea BS12] 112 bp
4	4.2	9	4	65.25	51	6.75e+008	12111.0	PA_Bse_meta_comb:2073596293	PA_Bse_meta_comb:2073596293 BaSeMet_00399490 nitrogen regulatory protein P-II [Bankia setacea
4	4.3	9	4	64.12	51	7.04e+008	12099.0	PA_BSC2:2534574907	PA_BSC2:2534574907 Bsc2_02594 nitrogen regulatory protein P-II family [Alteromonadacea bacterium
4	4.3	9	4	64.12	51	7.04e+008	12099.0	PA_Bse_meta_comb:2073591701	PA_Bse_meta_comb:2073591701 BaSeMet_00353570 nitrogen regulatory protein P-II [Bankia setacea
4	4.3	9	4	64.12	53	7.04e+008	11726.4	PA_Bse_meta_comb:2073579200	PA_Bse_meta_comb:2073579200 BaSeMet_00228560 nitrogen regulatory protein P-II [Bankia setacea
5	5.1	8	4	64.34	41	2.03e+008	12471.3	PA_Bse02:2503998471	PA_Bse02:2503998471 BS02DRAFT_00025200 ribosomal protein L7/L12 [B. setacea BS02 (Isolate fror
5	5.1	8	4	64.34	41	2.03e+008	12471.3	PA_Bse_meta_comb:2073556360	PA_Bse_meta_comb:2073556360 BaSeMet_00000160 LSU ribosomal protein L12P [Bankia setacea mi
5	5.2	9	3	48.45	30	2.58e+008	12772.7	PA_Bse08:2503995486	PA_Bse08:2503995486 BS08DRAFT_00039490 ribosomal protein L7/L12 [B. setacea BS08 (Isolate fror
6	6.1	6	4	62.66	34	1.60e+008	20313.3	PA_Bse_meta_comb:2073575697	PA_Bse_meta_comb:2073575697 BaSeMet_00193530 Protein of unknown function VcgC/VcgE (DUF27
6	6.1	5	3	46.65	30	1.50e+008	18453.2	PA_Bse02:2503999825	PA_Bse02:2503999825 Protein of unknown function VcgC/VcgE (DUF2780). [B. setacea BS02 (Isolate f
7	7.1	10	5	60.80	16	5.13e+008	44282.5	PA_BSC2:2534573496	PA_BSC2:2534573496 Bsc2_01181 translation elongation factor 1A (EF-1A/EF-Tu) [Alteromonadacea b
7	7.1	10	5	60.80	16	5.13e+008	44282.5	PA_Bse_meta_comb:2073587015	PA_Bse_meta_comb:2073587015 BaSeMet_00306710 translation elongation factor 1A (EF-1A/EF-Tu) [
7	7.1	6	3	32.77	9	5.01e+008	44395.5	PA_BS12:2189570755	PA_BS12:2189570755 or4000 GTPases - translation elongation factors [B. setacea BS12] 407 bp
7	7.1	6	3	32.77	9	5.01e+008	44335.5	PA_Bse_meta_comb:2073563152	PA_Bse_meta_comb:2073563152 BaSeMet_00068080 translation elongation factor 1A (EF-1A/EF-Tu) [
7	7.1	4	2	27.12	28	1.03e+007	9849.9	PA_Bse_meta_comb:2073591525	PA_Bse_meta_comb:2073591525 BaSeMet_00351810 translation elongation factor 1A (EF-1A/EF-Tu) [
7	7.2	9	4	52.90	13	5.73e+008	44298.7	PA_Bse02:2503998465	PA_Bse02:2503998465 BS02DRAFT_00025140 translation elongation factor TU [B. setacea BS02 (Isola
7	7.2	9	4	52.90	13	5.73e+008	44266.6	PA_Bse_meta_comb:2073556354	PA_Bse_meta_comb:2073556354 BaSeMet_00000100 translation elongation factor 1A (EF-1A/EF-Tu) [
8	8.1	15	4	57.22	17	3.14e+008	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.1	9	2	30.15	3	1.97e+008	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)

8	8.2	9	4	48.06	6	1.31e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.2	7	3	35.71	4	7.98e+007	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
9	9.1	11	3	55.90	50	6.92e+008	9107.5	PA_BS12:2189570079	PA_BS12:2189570079 or3306 Bacterial nucleoid DNA-binding protein [B. setacea BS12] 90 bp
9	9.1	11	3	55.90	50	6.92e+008	9075.4	PA_Bse_meta_comb:2073588110	PA_Bse_meta_comb:2073588110 BaSeMet_00317660 bacterial nucleoid protein HU beta subunit [Bank
9	9.2	11	3	53.12	50	6.35e+008	9164.5	PA_Bse08:2503994572	PA_Bse08:2503994572 BS08DRAFT_00030860 Bacterial DNA-binding protein. [B. setacea BS08 (Isolat
9	9.3	11	3	52.84	50	1.01e+009	9105.4	PA_BSC2:2534572633	PA_BSC2:2534572633 Bsc2_00317 Bacterial nucleoid DNA-binding protein [Alteromonadacea bacteriur
9	9.3	11	3	52.84	50	1.01e+009	9105.4	PA_Bse_meta_comb:2073595431	PA_Bse_meta_comb:2073595431 BaSeMet_00390870 bacterial nucleoid protein HU beta subunit [Bank
9	9.4	6	2	39.82	33	4.51e+008	9107.5	PA_Bse02:2503999877	PA_Bse02:2503999877 BS02DRAFT_00006580 Bacterial DNA-binding protein. [B. setacea BS02 (Isolat
9	9.4	6	2	39.82	33	4.51e+008	9075.4	PA_Bse_meta_comb:2073579833	PA_Bse_meta_comb:2073579833 BaSeMet_00234890 bacterial nucleoid protein HU beta subunit [Bank
10	10.1	13	3	55.27	29	3.78e+009	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
11	11.1	7	4	53.35	10	2.42e+009	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding
12	12.1	6	3	43.45	10	2.58e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
12	12.1	6	3	43.45	10	2.58e+008	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome
12	12.2	3	2	29.94	3	1.60e+008	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase
13	13.1	6	3	42.62	12	1.71e+008	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]
14	14.1	3	3	41.73	9	1.01e+008	61419.7	PA_BS12:2189569223	PA_BS12:2189569223 or2536 Ribosomal protein S1 [B. setacea BS12] 559 bp
14	14.1	3	3	41.73	9	1.01e+008	61419.7	PA_Bse_meta_comb:2073580582	PA_Bse_meta_comb:2073580582 BaSeMet_00242380 SSU ribosomal protein S1P [Bankia setacea mic
14	14.1	2	2	32.78	6	6.72e+007	61781.1	PA_Bse08:2503994885	PA_Bse08:2503994885 BS08DRAFT_00033540 ribosomal protein S1 [B. setacea BS08 (Isolate from sh
14	14.1	2	2	32.78	6	6.72e+007	61632.0	PA_BSC2:2534572871	PA_BSC2:2534572871 Bsc2_00555 SSU ribosomal protein S1P [Alteromonadacea bacterium Bsc2]
14	14.1	2	2	32.78	6	6.72e+007	61632.0	PA_Bse_meta_comb:2073599440	PA_Bse_meta_comb:2073599440 BaSeMet_00430960 SSU ribosomal protein S1P [Bankia setacea mic
14	14.1	2	2	24.35	5	8.27e+007	61873.4	PA_Bse02:2504000428	PA_Bse02:2504000428 BS02DRAFT_00020240 ribosomal protein S1 [B. setacea BS02 (Isolate from sh
14	14.1	2	2	24.35	5	8.27e+007	61873.4	PA_Bse_meta_comb:2073589355	PA_Bse_meta_comb:2073589355 BaSeMet_00330110 SSU ribosomal protein S1P [Bankia setacea mic
15	15.1	8	3	41.56	24	4.86e+007	27641.5	PA_Bse02:2504001159	PA_Bse02:2504001159 BS02DRAFT_00031400 FKBP-type peptidyl-prolyl cis-trans isomerase./Domain
15	15.1	8	3	41.56	24	4.86e+007	27641.5	PA_Bse_meta_comb:2073579700	PA_Bse_meta_comb:2073579700 BaSeMet_00233560 FKBP-type peptidyl-prolyl cis-trans isomerases 1
16	16.1	12	2	38.50	19	1.42e+009	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
17	17.1	9	3	38.08	47	6.83e+008	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
18	18.1	7	3	37.82	18	2.71e+007	28847.5	PA_BS12:2189569790	PA_BS12:2189569790 or3098 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [B. setacea BS12] 265 b
18	18.1	7	3	37.82	18	2.71e+007	28847.5	PA_Bse_meta_comb:2073568597	PA_Bse_meta_comb:2073568597 BaSeMet_00122530 FKBP-type peptidyl-prolyl cis-trans isomerases 1
19	19.1	4	3	37.48	8	8.44e+007	52481.4	PA_BSC2:2534576897	PA_BSC2:2534576897 Bsc2_04586 pyruvate kinase (EC 2.7.1.40) [Alteromonadacea bacterium Bsc2]
19	19.1	4	3	37.48	8	8.44e+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
20	20.1	12	3	36.91	4	1.22e+008	108814.9	PA_BS12:2189569860	PA_BS12:2189569860 or3165 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12
20	20.1	12	3	36.91	4	1.22e+008	108814.9	PA_Bse_meta_comb:2073560924	PA_Bse_meta_comb:2073560924 BaSeMet_00045800 TonB-dependent receptor [Bankia setacea micro
21	21.1	15	3	36.18	18	2.93e+008	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
21	21.1	15	3	36.18	19	2.93e+008	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
22	22.1	8	2	36.18	30	2.87e+008	12588.4	PA_BSC2:2534573502	PA_BSC2:2534573502 Bsc2_01187 LSU ribosomal protein L12P [Alteromonadacea bacterium Bsc2]
22	22.1	8	2	36.18	30	2.87e+008	12588.4	PA_Bse_meta_comb:2073587021	PA_Bse_meta_comb:2073587021 BaSeMet_00306770 LSU ribosomal protein L12P [Bankia setacea mi
23	23.1	7	3	35.88	32	1.71e+008	13597.6	PA_Bse02:2503999073	PA_Bse02:2503999073 BS02DRAFT_00000810 ribosomal protein L19, bacterial type [B. setacea BS02
23	23.1	7	3	35.88	32	1.71e+008	13597.6	PA_Bse_meta_comb:2073588915	PA_Bse_meta_comb:2073588915 BaSeMet_00325710 LSU ribosomal protein L19P [Bankia setacea mi
23	23.1	6	2	27.23	23	1.65e+008	13444.4	PA_Bse08:2503995028	PA_Bse08:2503995028 BS08DRAFT_00034960 ribosomal protein L19, bacterial type [B. setacea BS08
23	23.1	6	2	27.23	24	1.65e+008	12831.7	PA_Bse_meta_comb:2073565100	PA_Bse_meta_comb:2073565100 BaSeMet_00087560 LSU ribosomal protein L19P [Bankia setacea mi
23	23.2	7	3	35.37	34	1.93e+008	13449.5	PA_BSC2:2534573050	PA_BSC2:2534573050 Bsc2_00734 LSU ribosomal protein L19P [Alteromonadacea bacterium Bsc2]
23	23.2	7	3	35.37	34	1.93e+008	13449.5	PA_Bse_meta_comb:2073589786	PA_Bse_meta_comb:2073589786 BaSeMet_00334420 LSU ribosomal protein L19P [Bankia setacea mi
24	24.1	3	3	35.38	13	9.46e+006	30592.3	PA_BS12:2189569048	PA_BS12:2189569048 or2361 hypothetical protein [B. setacea BS12] 276 bp
24	24.1	3	3	35.38	14	9.46e+006	28929.3	PA_Bse_meta_comb:2073579603	PA_Bse_meta_comb:2073579603 BaSeMet_00232590 hypothetical protein [Bankia setacea microbiome
25	25.1	4	2	35.17	32	1.58e+008	12186.2	PA_BSC2:2534574917	PA_BSC2:2534574917 Bsc2_02604 nitrogen regulatory protein P-II family [Alteromonadacea bacterium
25	25.1	4	2	35.17	32	1.58e+008	12186.2	PA_Bse_meta_comb:2073573632	PA_Bse_meta_comb:2073573632 BaSeMet_00172880 nitrogen regulatory protein P-II [Bankia setacea
26	26.1	9	2	34.22	30	2.14e+008	12421.2	PA_BS12:2189570749	PA_BS12:2189570749 or3994 Ribosomal protein L7/L12 [B. setacea BS12] 123 bp
26	26.1	9	2	34.22	30	2.14e+008	12421.2	PA_Bse_meta_comb:2073563146	PA_Bse_meta_comb:2073563146 BaSeMet_00068020 LSU ribosomal protein L12P [Bankia setacea mi

27	27.1	6	2	31.58	4	6.74e+007	78518.0	PA_Bse02:2503998694	PA_Bse02:2503998694 BS02DRAFT_00016310 type IV pilus secretin (or competence protein) PilQ [B. s
27	27.1	6	2	31.58	4	6.74e+007	78518.0	PA_Bse_meta_comb:2073578282	PA_Bse_meta_comb:2073578282 BaSeMet_00219380 type IV pilus secretin (or competence protein) Pi
28	28.1	9	2	31.57	28	1.20e+008	13501.0	PA_BSC2:2534573446	PA_BSC2:2534573446 Bsc2_01131 LSU ribosomal protein L14P [Alteromonadacea bacterium Bsc2]
28	28.1	9	2	31.57	28	1.20e+008	13501.0	PA_Bse_meta_comb:2073591305	PA_Bse_meta_comb:2073591305 BaSeMet_00349610 LSU ribosomal protein L14P [Bankia setacea mi
28	28.2	6	2	29.03	28	1.14e+008	13487.0	PA_BS12:2189570790	PA_BS12:2189570790 or4034 Ribosomal protein L14 [B. setacea BS12] 122 bp
28	28.2	6	2	29.03	28	1.14e+008	13487.0	PA_Bse_meta_comb:2073590551	PA_Bse_meta_comb:2073590551 BaSeMet_00342070 LSU ribosomal protein L14P [Bankia setacea mi
29	29.1	2	2	30.95	28	2.57e+007	9318.7	PA_BS12:2189569390	PA_BS12:2189569390 or2703 Ribosomal protein S16 [B. setacea BS12] 82 bp
30	30.1	3	2	30.36	6	7.70e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
30	30.2	2	2	25.89	6	2.26e+008	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding dom
30	30.2	2	2	25.89	6	2.26e+008	42082.7	PA_Bse_meta_comb:2073581124	PA_Bse_meta_comb:2073581124 BaSeMet_00247800 Uncharacterized protein conserved in bacteria [E
31	31.1	4	2	30.24	6	4.91e+007	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
31	31.1	4	2	30.24	6	4.91e+007	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome
32	32.1	2	2	28.76	21	4.12e+007	13381.5	PA_BS12:2189569387	PA_BS12:2189569387 or2700 Ribosomal protein L19 [B. setacea BS12] 118 bp
32	32.1	2	2	28.76	21	4.12e+007	13381.5	PA_Bse_meta_comb:2073578698	PA_Bse_meta_comb:2073578698 BaSeMet_00223540 LSU ribosomal protein L19P [Bankia setacea mi
33	33.1	9	2	28.05	19	2.45e+008	17704.7	PA_BSC2:2534573498	PA_BSC2:2534573498 Bsc2_01183 SSU ribosomal protein S7P [Alteromonadacea bacterium Bsc2]
33	33.1	9	2	28.05	19	2.45e+008	17704.7	PA_Bse_meta_comb:2073587017	PA_Bse_meta_comb:2073587017 BaSeMet_00306730 SSU ribosomal protein S7P [Bankia setacea mic
33	33.1	9	2	28.05	19	2.45e+008	17585.6	PA_BS12:2189570753	PA_BS12:2189570753 or3998 Ribosomal protein S7 [B. setacea BS12] 156 bp
33	33.1	9	2	28.05	19	2.45e+008	17585.6	PA_Bse_meta_comb:2073563150	PA_Bse_meta_comb:2073563150 BaSeMet_00068060 SSU ribosomal protein S7P [Bankia setacea mic
34	34.1	3	2	26.34	6	7.11e+007	49567.7	PA_Bse08:2503996612	PA_Bse08:2503996612 BS08DRAFT_00014510 xylose isomerase [B. setacea BS08 (Isolate from shipw
35	35.1	2	2	26.24	10	8.04e+007	47257.4	PA_Bse02:2504001097	PA_Bse02:2504001097 BS02DRAFT_00030780 transcription termination factor Rho [B. setacea BS02 (
35	35.1	2	2	26.24	10	8.04e+007	47257.4	PA_Bse_meta_comb:2073590662	PA_Bse_meta_comb:2073590662 BaSeMet_00343180 transcription termination factor Rho [Bankia seta
35	35.1	2	2	26.24	10	8.04e+007	47249.7	PA_Bse08:2503996520	PA_Bse08:2503996520 BS08DRAFT_00004060 transcription termination factor Rho [B. setacea BS08 (
35	35.1	2	2	26.24	10	8.04e+007	47154.6	PA_BS12:2189568577	PA_BS12:2189568577 or1880 Transcription termination factor [B. setacea BS12] 419 bp
35	35.1	2	2	26.24	10	8.04e+007	47154.6	PA_Bse_meta_comb:2073581679	PA_Bse_meta_comb:2073581679 BaSeMet_00253350 transcription termination factor Rho [Bankia seta
36	36.1	4	2	24.97	8	5.73e+007	38937.1	PA_BSC2:2534573407	PA_BSC2:2534573407 Bsc2_01092 fructose-bisphosphate aldolase (EC 4.1.2.13) [Alteromonadacea ba
36	36.1	4	2	24.97	8	5.73e+007	38921.1	PA_Bse_meta_comb:2073595811	PA_Bse_meta_comb:2073595811 BaSeMet_00394670 fructose-bisphosphate aldolase (EC 4.1.2.13) [B
37	37.1	2	2	23.73	19	1.31e+008	18210.9	PA_Bse02:2504000647	PA_Bse02:2504000647 BS02DRAFT_00022430 bacterioferritin [B. setacea BS02 (Isolate from shipworn
37	37.1	2	2	23.73	19	1.31e+008	18210.9	PA_Bse_meta_comb:2073593298	PA_Bse_meta_comb:2073593298 BaSeMet_00369540 bacterioferritin [Bankia setacea microbiome (Cor
38	38.1	2	2	23.26	6	6.70e+007	49480.7	PA_BSC2:2534574372	PA_BSC2:2534574372 Bsc2_02058 D-xylose isomerase (EC 5.3.1.5) [Alteromonadacea bacterium Bsc2
38	38.1	2	2	23.26	6	6.70e+007	49480.7	PA_Bse_meta_comb:2073588584	PA_Bse_meta_comb:2073588584 BaSeMet_00322400 D-xylose isomerase (EC 5.3.1.5) [Bankia setace
39	39.1	3	2	22.94	9	2.17e+008	45984.9	PA_Bse_meta_comb:2073595342	PA_Bse_meta_comb:2073595342 BaSeMet_00389980 Capsid protein (F protein). [Bankia setacea micr
40	40.1	2	2	22.92	20	1.87e+007	22353.9	PA_Bse_meta_comb:2073589276	PA_Bse_meta_comb:2073589276 BaSeMet_00329320 FKBP-type peptidyl-prolyl cis-trans isomerases 1
40	40.1	2	2	22.92	20	1.87e+007	22339.9	PA_BSC2:2534573752	PA_BSC2:2534573752 Bsc2_01438 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [Alteromonadacea
41	41.1	2	2	22.62	5	8.63e+006	49486.1	PA_Bse02:2503998172	PA_Bse02:2503998172 BS02DRAFT_00013490 MotA/TolQ/ExbB proton channel family. [B. setacea BS
41	41.1	2	2	22.62	5	8.63e+006	49486.1	PA_Bse_meta_comb:2073584293	PA_Bse_meta_comb:2073584293 BaSeMet_00279490 outer membrane transport energization protein E
42	42.1	5	2	22.15	50	2.38e+008	12370.2	PA_Bse_meta_comb:2073564350	PA_Bse_meta_comb:2073564350 BaSeMet_00080060 ATP-dependent protease Clp, ATPase subunit [I
43	43.1	2	1	21.50	25	2.89e+007	7243.1	PA_Bse02:2503998197	PA_Bse02:2503998197 BS02DRAFT_00013740 "Cold-shock" DNA-binding domain. [B. setacea BS02 (
44	44.1	2	2	21.13	11	6.95e+007	36312.3	PA_Bse02:2504001165	PA_Bse02:2504001165 BS02DRAFT_00031460 general secretion pathway protein C [B. setacea BS02
44	44.1	2	2	21.13	11	6.95e+007	36280.2	PA_Bse_meta_comb:2073579706	PA_Bse_meta_comb:2073579706 BaSeMet_00233620 general secretion pathway protein C [Bankia set
45	45.1	4	2	21.06	17	1.19e+008	22697.8	PA_BS12:2189570780	PA_BS12:2189570780 or4024 Ribosomal protein L3 [B. setacea BS12] 214 bp
45	45.1	4	2	21.06	17	1.19e+008	22697.8	PA_Bse_meta_comb:2073578947	PA_Bse_meta_comb:2073578947 BaSeMet_00226030 LSU ribosomal protein L3P [Bankia setacea mic
Totals:	902	343							

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	159.63	24	3.06e+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	059-1401.5595.5595.2	2	19.88	12.81	98.6	8.36e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
2	059-1401.5916.5950.2	2	19.80	15.91	96.9	5.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
3	059-1401.5311.5355.3	3	19.35	6.15	96.6	6.13e+007	(R)EWQDALVDYMVEK(D)	1625.752
4	064-1601.4864.4871.0	3	19.22	13.42	88.4	9.02e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
5	060-1501.5157.5205.2	2	18.82	11.43	96.6	7.12e+007	(R)EWQDALVDYMVEK(D)	1625.752
6	059-1401.5296.5351.2	2	18.33	10.97	97.0	5.10e+008	(R)EWQDALVDYMVEK(D)	1625.752
7	065-1701.5178.5217.2	2	18.30	9.81	96.0	1.45e+007	(R)EWQDALVDYMVEK(D)	1625.752
8	059-1401.5439.5546.2	2	18.14	10.72	95.4	2.70e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
9	059-1401.5124.5236.0	3	18.04	8.09	92.2	5.61e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
10	064-1601.5272.5278.2	2	17.94	11.22	93.1	6.96e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
11	060-1501.4975.5006.0	3	17.90	9.27	90.4	5.40e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
12	059-1401.5241.5259.0	3	17.86	8.20	91.0	3.95e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
13	059-1401.3539.3545.2	2	17.77	13.28	92.8	1.06e+008	(R)AGWDEHFGYLR(D)	1350.623
14	060-1501.5644.5663.0	2	17.66	12.72	95.2	1.80e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
15	060-1501.5618.5629.0	3	16.84	12.29	88.9	4.80e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
16	064-1601.4961.4965.0	3	16.76	9.16	92.6	4.48e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
17	065-1701.4971.4974.0	3	15.89	7.97	91.1	3.93e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
18	060-1501.5280.5329.2	2	15.81	8.21	92.0	1.52e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
19	064-1601.5581.5642.0	3	15.72	8.53	86.8	3.74e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
20	059-1401.3369.3408.2	2	15.66	7.41	92.9	1.65e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
21	064-1601.3501.3520.2	2	15.46	15.46	91.5	8.07e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
22	060-1501.5178.5189.3	3	15.39	6.11	83.1	1.11e+007	(R)EWQDALVDYMVEK(D)	1625.752
23	059-1401.3355.3407.3	3	15.36	8.02	84.5	1.31e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
24	064-1601.6340.6391.0	3	15.20	15.20	81.8	1.63e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
25	060-1501.3453.3515.0	3	15.15	7.19	80.3	6.86e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
26	060-1501.6419.6469.2	2	14.74	5.70	69.0	2.05e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
27	059-1401.3988.4003.2	2	14.71	14.71	87.8	5.72e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
28	059-1401.6127.6127.2	2	14.28	10.79	84.0	3.51e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
29	059-1401.5431.5542.3	3	14.17	6.48	81.2	5.18e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
30	059-1401.5544.5619.3	3	13.82	5.56	76.8	3.88e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
31	060-1501.3475.3499.2	2	13.78	9.40	89.1	1.02e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
32	064-1601.4767.4829.3	3	13.67	6.18	80.3	1.09e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
33	064-1601.3472.3512.0	3	13.51	5.19	77.9	5.70e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
34	065-1701.5543.5565.0	3	12.93	8.77	72.7	1.02e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
35	059-1401.5921.5968.0	3	12.72	12.72	74.8	1.50e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
36	065-1701.5281.5319.0	3	12.59	5.41	73.0	2.83e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
37	059-1401.6719.6765.3	3	12.22	12.22	74.2	1.27e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
38	064-1601.3668.3688.2	2	11.86	8.27	73.4	1.43e+007	(R)AGWDEHFGYLR(D)	1350.623
39	059-1401.5422.5422.0	3	11.40	5.02	70.2	8.75e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
40	059-1401.6164.6164.2	2	9.20	5.91	71.5	2.91e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
41	059-1401.10388.10388.0	2	8.85	5.54	76.0	2.68e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
42	059-1401.4038.4038.2	2	8.37	8.37	60.6	3.62e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
43	065-1701.5556.5556.0	2	7.97	4.35	85.6	4.15e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
44	059-1401.10393.10393.0	2	7.47	7.47	67.4	2.19e+006	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

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	49	7	129.92	19	5.19e+009	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	058-1301.2911.2962.2	2	21.39	17.32	98.4	9.94e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
2	059-1401.2944.2995.2	2	20.93	17.35	98.9	6.68e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
3	060-1501.2975.3020.2	2	20.93	17.28	98.9	3.53e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
4	060-1501.6682.6700.2	2	20.42	11.86	97.7	2.35e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
5	065-1701.3003.3017.0	3	20.02	9.27	94.4	7.78e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
6	064-1601.2967.3008.2	2	19.83	19.83	97.6	5.77e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
7	065-1701.7122.7168.2	2	19.76	19.76	96.3	4.34e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
8	065-1701.6546.6604.0	3	19.70	9.45	85.1	3.06e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
9	060-1501.7240.7244.2	2	18.67	14.43	95.6	6.27e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
10	064-1601.6616.6624.2	2	18.35	10.90	95.5	1.69e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
11	064-1601.3225.3264.2	2	17.84	10.53	96.0	1.38e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
12	064-1601.7174.7252.2	2	17.70	11.81	94.7	5.57e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
13	058-1301.5781.5822.2	2	17.28	10.69	90.9	3.64e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
14	058-1301.7763.7767.2	2	17.25	8.81	92.7	4.29e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
15	059-1401.6080.6131.2	2	17.23	11.13	89.6	2.54e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
16	060-1501.7533.7585.3	3	17.00	10.54	79.9	1.35e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
17	065-1701.7406.7477.2	2	16.98	9.88	92.6	3.81e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
18	060-1501.7531.7609.2	2	16.73	10.34	92.4	1.94e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
19	065-1701.5772.5811.2	2	16.72	10.56	88.6	9.93e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
20	065-1701.3276.3281.2	2	16.65	8.59	91.5	1.13e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
21	065-1701.3028.3030.2	2	16.15	16.15	93.2	5.66e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
22	060-1501.6641.6711.0	3	16.07	6.81	80.7	1.29e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
23	060-1501.3681.3691.2	2	15.98	10.47	88.9	2.12e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
24	064-1601.3701.3740.2	2	15.98	9.23	88.9	2.51e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
25	058-1301.3136.3141.0	2	15.97	6.63	93.4	8.05e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
26	060-1501.5807.5827.0	2	15.66	7.62	86.2	5.10e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
27	064-1601.7459.7471.2	2	15.66	9.52	90.1	1.92e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
28	060-1501.7232.7285.3	3	15.62	8.75	84.3	2.62e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
29	059-1401.3165.3220.0	2	15.44	8.18	92.6	2.09e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
30	064-1601.5778.5820.2	2	15.22	7.13	88.7	6.52e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
31	058-1301.3541.3547.2	2	14.93	7.57	87.7	8.11e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
32	059-1401.3611.3635.2	2	14.90	7.62	87.0	9.44e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
33	064-1601.7167.7213.3	3	14.82	9.91	71.8	2.38e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
34	058-1301.6708.6774.0	3	14.64	4.36	74.6	5.11e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
35	060-1501.5815.5877.3	3	14.37	8.83	86.9	4.25e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
36	065-1701.5769.5830.3	3	13.90	8.13	81.9	1.22e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
37	065-1701.3763.3835.2	2	13.84	6.52	85.8	7.39e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
38	058-1301.5805.5851.3	3	13.83	5.86	86.9	2.09e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
39	064-1601.6591.6638.0	3	13.53	2.80	73.9	1.21e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
40	064-1601.5763.5838.3	3	13.04	7.97	81.6	5.95e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022

41	059-1401.6973.7053.0	3	12.42	3.51	70.3	2.17e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
42	058-1301.7527.7527.0	2	12.39	12.39	77.8	4.78e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
43	065-1701.3771.3771.2	2	12.23	5.35	81.8	3.77e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
44	064-1601.5862.5895.0	2	11.53	5.14	82.6	4.27e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
45	060-1501.3765.3775.0	2	11.47	3.30	79.1	1.40e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
46	058-1301.5895.5895.0	2	11.37	5.51	78.2	1.79e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
47	059-1401.2948.3007.4	4	11.18	7.17	71.7	3.32e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
48	065-1701.3085.3085.0	3	10.99	10.99	82.4	2.69e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
49	059-1401.6223.6240.2	2	10.24	3.86	73.9	6.49e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.1	6	4	66.47	20	1.82e+008	34007.6	PA_BS12:2189567864	PA_BS12:2189567864 or1190 Transaldolase [B. setacea BS12] 311 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	059-1401.6340.6340.2	2	18.15	6.81	92.5	6.18e+007	(R)GFVADQINLENFLK(S)	1607.843
2	059-1401.3537.3552.2	2	17.49	8.20	90.8	2.12e+007	(K)QYSDVVADTGDIEAIK(R)	1723.839
3	059-1401.3809.3851.2	2	15.96	10.91	89.8	4.02e+007	(R)YQPLDATTNPSLLYK(A)	1723.891
4	059-1401.6264.6264.0	2	14.87	8.14	86.6	3.02e+007	(R)LTISPQLLGELEADNGVLER(A)	2167.161
5	060-1501.6035.6035.0	2	13.63	6.88	84.1	2.04e+007	(R)GFVADQINLENFLK(S)	1607.843
6	064-1601.3886.3886.2	2	11.71	8.27	84.3	8.58e+006	(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
3	3.2	7	4	53.34	20	1.75e+008	33705.4	PA_BSC2:2534576639	PA_BSC2:2534576639 Bsc2_04328 transaldolase (EC 2.2.1.2) [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	059-1401.6340.6340.2	2	18.15	6.81	92.5	6.18e+007	(R)GFVADQINLENFLK(A)	1607.843
2	059-1401.3809.3851.2	2	15.96	10.91	89.8	4.02e+007	(R)YQPLDATTNPSLLYK(A)	1723.891
3	060-1501.6035.6035.0	2	13.63	6.88	84.1	2.04e+007	(R)GFVADQINLENFLK(A)	1607.843
4	059-1401.4068.4068.0	2	11.75	6.35	85.7	1.55e+007	(K)QFSDVVADTGDIEAIK(R)	1707.844
5	064-1601.3886.3886.2	2	11.71	8.27	84.3	8.58e+006	(R)YQPLDATTNPSLLYK(A)	1723.891
6	064-1601.5496.5496.0	2	7.48	7.48	62.4	1.20e+007	(R)LTISPQLLGELEADTGK(L)	1784.965
7	060-1501.5505.5505.0	2	7.46	7.46	60.4	1.67e+007	(R)LTISPQLLGELEADTGK(L)	1784.965

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.1	9	4	65.68	51	6.42e+008	12099.0	PA_Bse02:2503998071	PA_Bse02:2503998071 BS02DRAFT_00012490 Nitrogen regulatory protein P-II. [B. setacea BS02 (Isolate from shi

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

1	056-0801.5884.5935.2	2	18.19	18.19	87.7	3.02e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
2	056-0801.4707.4743.0	2	17.96	7.61	96.2	4.60e+007	(K)IFVSSLEQVIR(I)	1290.742
3	057-0901.5944.5944.2	2	16.69	16.69	79.3	7.12e+007	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
4	055-0701.4292.4312.3	3	16.34	16.34	85.0	2.50e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
5	055-0701.4290.4306.2	2	15.47	11.46	90.6	4.17e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
6	056-0801.4570.4636.0	2	13.19	4.16	88.8	4.89e+007	(R)GAEYVVDFLPK(T)	1237.647
7	055-0701.9742.9742.0	2	12.00	12.00	79.3	1.21e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
8	056-0801.4223.4223.0	2	7.70	4.08	63.5	9.18e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
9	055-0701.9941.9941.0	2	6.18	6.18	82.9	3.03e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965

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	9	4	65.25	51	6.75e+008	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	056-0801.5884.5935.2	2	18.19	18.19	87.7	3.02e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
2	057-0901.5360.5396.2	2	17.53	8.94	92.0	7.89e+007	(K)IFVSVLEQVVR(I)	1288.763
3	057-0901.5944.5944.2	2	16.69	16.69	79.3	7.12e+007	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
4	055-0701.4292.4312.3	3	16.34	16.34	85.0	2.50e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
5	055-0701.4290.4306.2	2	15.47	11.46	90.6	4.17e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
6	056-0801.4570.4636.0	2	13.19	4.16	88.8	4.89e+007	(R)GAEYVVDFLPK(T)	1237.647
7	055-0701.9742.9742.0	2	12.00	12.00	79.3	1.21e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
8	056-0801.4223.4223.0	2	7.70	4.08	63.5	9.18e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
9	055-0701.9941.9941.0	2	6.18	6.18	82.9	3.03e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965

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	4.3	9	4	64.12	51	7.04e+008	12099.0	PA_BSC2:2534574907	PA_BSC2:2534574907 Bsc2_02594 nitrogen regulatory protein P-II family [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	056-0801.5884.5935.2	2	18.19	18.19	87.7	3.02e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
2	057-0901.5944.5944.2	2	16.69	16.69	79.3	7.12e+007	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
3	056-0801.4364.4414.0	2	16.40	10.46	88.7	1.08e+008	(K)IFVSTLEQVVR(I)	1290.742
4	055-0701.4292.4312.3	3	16.34	16.34	85.0	2.50e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
5	055-0701.4290.4306.2	2	15.47	11.46	90.6	4.17e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
6	056-0801.4570.4636.0	2	13.19	4.16	88.8	4.89e+007	(R)GAEYVVDFLPK(T)	1237.647
7	055-0701.9742.9742.0	2	12.00	12.00	79.3	1.21e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
8	056-0801.4223.4223.0	2	7.70	4.08	63.5	9.18e+007	(R)EALSEIGVQGITVTEVK(G)	1772.965
9	055-0701.9941.9941.0	2	6.18	6.18	82.9	3.03e+006	(R)EALSEIGVQGITVTEVK(G)	1772.965

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

			(#)	Search Score		Intensity	(Da)		
5	5.1	8	4	64.34	41	2.03e+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	059-1401.4224.4235.2	2	18.18	12.38	94.4	6.62e+007	(K)TDFDVVLTSVGEK(K)	1409.716
2	059-1401.2203.2226.0	3	17.61	11.20	95.4	3.17e+006	(K)KQLEEAGASVELK(-)	1401.759
3	056-0801.2194.2200.0	3	15.95	9.14	87.4	6.19e+005	(K)KQLEEAGASVELK(-)	1401.759
4	056-0801.2455.2533.2	2	14.81	9.95	86.7	9.10e+006	(K)QLEEAGASVELK(-)	1273.664
5	059-1401.2495.2562.2	2	13.94	8.70	87.2	2.12e+007	(K)QLEEAGASVELK(-)	1273.664
6	060-1501.9537.9541.2	2	13.74	13.74	75.5	4.17e+007	(K)EDIINAIAEMSVTDVVELISAMEEK(F)	2749.353
7	064-1601.9473.9480.2	2	12.18	12.18	65.7	5.90e+007	(K)EDIINAIAEMSVTDVVELISAMEEK(F)	2749.353
8	064-1601.2502.2502.0	2	6.50	2.92	100.0	1.62e+006	(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
5	5.2	9	3	48.45	30	2.58e+008	12772.7	PA_Bse08:2503995486	PA_Bse08:2503995486 BS08DRAFT_00039490 ribosomal protein L7/L12 [B. setacea BS08 (Isolate from shipworm

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	059-1401.2203.2226.0	3	17.61	11.20	95.4	3.17e+006	(K)KQLEEAGASVELK(-)	1401.759
2	058-1301.9922.9922.2	2	16.03	9.69	81.8	2.59e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
3	056-0801.2194.2200.0	3	15.95	9.14	87.4	6.19e+005	(K)KQLEEAGASVELK(-)	1401.759
4	065-1701.9412.9412.2	2	15.11	15.11	77.2	1.41e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
5	056-0801.2455.2533.2	2	14.81	9.95	86.7	9.10e+006	(K)QLEEAGASVELK(-)	1273.664
6	058-1301.9919.9927.3	3	14.18	14.18	70.7	4.40e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
7	059-1401.2495.2562.2	2	13.94	8.70	87.2	2.12e+007	(K)QLEEAGASVELK(-)	1273.664
8	059-1401.10055.10055.0	2	10.51	10.51	64.6	1.38e+008	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
9	064-1601.2502.2502.0	2	6.50	2.92	100.0	1.62e+006	(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
6	6.1	6	4	62.66	34	1.60e+008	20313.3	PA_Bse_meta_comb:2073575697	PA_Bse_meta_comb:2073575697 BaSeMet_00193530 Protein of unknown function VcgC/VcgE (DUF278

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	055-0701.2715.2723.0	2	19.17	15.73	98.7	5.89e+006	(K)EVTEEVADQAATMEK(Q)	1650.753
2	058-1301.3262.3262.0	2	16.01	8.18	88.6	1.09e+007	(K)FADTASSFLDQSGK(G)	1473.686
3	058-1301.6556.6607.2	2	13.95	6.75	76.5	1.02e+008	(K)SLLSAIPGASTLMSAAPALK(K)	1899.063
4	058-1301.5761.5761.2	2	13.53	7.23	83.2	3.13e+007	(K)AASQLTSQFESLGLGADMIPK(F)	2164.096
5	055-0701.2711.2711.2	2	13.26	13.26	89.3	5.36e+006	(K)EVTEEVADQAATMEK(Q)	1650.753
6	055-0701.2737.2737.0	2	10.47	5.96	68.8	5.38e+006	(K)EVTEEVADQAATMEK(Q)	1650.753

Distinct

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.1	10	5	60.80	16	5.13e+008	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	058-1301.2805.2809.0	3	17.69	17.69	91.6	2.73e+006	(R)GITIATSHVEYDSPER(H)	1774.861
2	058-1301.7644.7679.2	2	14.09	4.16	83.8	9.13e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
3	055-0701.7475.7531.2	2	13.62	2.12	85.1	9.59e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
4	064-1601.2808.2808.0	3	12.41	12.41	85.9	2.40e+006	(R)GITIATSHVEYDSPER(H)	1774.861
5	056-0801.7898.7933.2	2	12.03	3.13	81.8	2.84e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
6	064-1601.2795.2795.0	3	11.16	11.16	86.0	2.63e+006	(R)GITIATSHVEYDSPER(H)	1774.861
7	053-0502.5858.5858.0	2	10.34	4.88	64.0	4.59e+006	(R)GIINVGEEMEIIGIK(D)	1614.878
8	058-1301.2700.2700.2	2	9.43	4.75	79.0	2.51e+006	(K)TTLTAALTR(V)	947.553
9	053-0501.3501.3520.0	2	9.25	4.82	72.3	1.35e+007	(K)FEAEVYVLSK(D)	1184.620
10	053-0502.3506.3506.2	2	8.97	4.22	72.0	1.34e+007	(K)FEAEVYVLSK(D)	1184.620

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.2	9	4	52.90	13	5.73e+008	44298.7	PA_Bse02:2503998465	PA_Bse02:2503998465 BS02DRAFT_00025140 translation elongation factor TU [B. setacea BS02 (Isolate from shi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.3316.3344.0	3	18.93	10.51	91.7	2.37e+007	(R)GITIATSHVEYDSPIR(H)	1758.903
2	059-1401.3356.3356.0	3	15.55	9.70	88.6	2.67e+007	(R)GITIATSHVEYDSPIR(H)	1758.903
3	058-1301.7644.7679.2	2	14.09	4.16	83.8	9.13e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
4	055-0701.7475.7531.2	2	13.62	2.12	85.1	9.59e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
5	058-1301.3332.3332.0	2	12.28	6.94	83.8	1.16e+007	(R)GITIATSHVEYDSPIR(H)	1758.903
6	056-0801.7898.7933.2	2	12.03	3.13	81.8	2.84e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
7	060-1501.3441.3441.0	3	11.63	11.63	71.4	7.12e+006	(R)GITIATSHVEYDSPIR(H)	1758.903
8	059-1401.3620.3620.0	2	10.45	4.59	74.5	3.04e+007	(K)VGEEISIVGIK(D)	1143.662
9	058-1301.2700.2700.2	2	9.43	4.75	79.0	2.51e+006	(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
8	8.1	15	4	57.22	17	3.14e+008	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [I

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	060-1501.5422.5463.2	2	15.89	15.89	88.9	2.80e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
2	059-1401.5646.5680.2	2	14.84	11.78	87.1	3.70e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
3	064-1601.5386.5462.0	2	14.81	8.25	86.6	4.48e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
4	064-1601.5425.5438.2	2	14.35	14.35	87.0	2.61e+007	(K)GFPSTLGMLIDTGR(N)	1464.752

5	060-1501.3092.3097.0	3	14.26	6.59	72.4	8.88e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
6	064-1601.7966.7985.0	2	13.78	4.34	90.7	3.46e+007	(R)WFPEAFQTLLENAYPPL(-)	2036.017
7	059-1401.3491.3523.2	2	13.29	8.49	88.3	2.84e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
8	065-1701.3637.3653.0	2	12.79	7.26	87.1	5.29e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
9	058-1301.3029.3035.0	3	12.78	7.78	73.2	1.16e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
10	065-1701.5453.5484.2	2	12.70	9.31	70.4	1.10e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
11	064-1601.3578.3609.2	2	12.68	7.44	85.7	1.30e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
12	064-1601.8002.8002.0	2	10.40	2.88	78.5	3.07e+007	(R)WFPEAFQTLLENAYPPL(-)	2036.017
13	065-1701.3626.3626.0	2	9.64	4.73	87.5	4.88e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
14	064-1601.3085.3085.0	3	9.27	9.27	72.2	8.76e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
15	060-1501.5373.5373.2	2	7.58	7.58	62.5	2.08e+007	(K)GFPSTLGMLIDTGR(N)	1464.752

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
8	8.2	9	4	48.06	6	1.31e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	059-1401.3491.3523.2	2	13.29	8.49	88.3	2.84e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
2	064-1601.7293.7305.0	3	12.81	4.71	74.5	1.10e+007	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
3	065-1701.3637.3653.0	2	12.79	7.26	87.1	5.29e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
4	064-1601.3578.3609.2	2	12.68	7.44	85.7	1.30e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
5	059-1401.6996.7032.2	2	12.35	12.35	74.6	4.10e+007	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
6	064-1601.6618.6618.2	2	10.79	6.24	69.7	1.04e+007	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
7	065-1701.3626.3626.0	2	9.64	4.73	87.5	4.88e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
8	060-1501.4885.4885.2	2	9.61	9.61	70.1	1.37e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
9	065-1701.4916.4916.2	2	7.71	7.71	63.1	3.45e+006	(R)GLPSNIGMLIDTGR(N)	1443.763

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	11	3	55.90	50	6.92e+008	9107.5	PA_BS12:2189570079	PA_BS12:2189570079 or3306 Bacterial nucleoid DNA-binding protein [B. setacea BS12] 90 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.5258.5312.2	2	20.73	12.03	95.5	1.19e+008	(R)ALDAVTESIAAALK(E)	1372.769
2	058-1301.4429.4435.2	2	18.35	13.91	91.8	6.08e+007	(K)SELVEAIAASADISK(A)	1503.791
3	058-1301.6012.6074.2	2	16.82	7.46	95.2	1.54e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
4	058-1301.6082.6096.3	3	16.40	8.95	89.6	3.44e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
5	058-1301.4303.4387.2	2	12.98	7.78	71.8	1.37e+008	(K)SELVEAIAASADISK(A)	1503.791
6	059-1401.4568.4568.2	2	12.17	7.06	71.4	2.37e+007	(K)SELVEAIAASADISK(A)	1503.791
7	059-1401.6355.6360.2	2	11.93	4.81	86.2	4.07e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
8	057-0901.6124.6155.0	2	10.98	2.87	81.1	7.57e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
9	058-1301.10128.10128.2	2	9.34	5.10	67.9	4.70e+006	(K)SELVEAIAASADISK(A)	1503.791
10	058-1301.10031.10031.0	2	6.75	2.59	77.7	1.89e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901

11	059-1401.4545.4545.2	2	6.56	6.56	61.2	2.23e+007	(K)SELVEAIAASADISK(A)	1503.791

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	11	3	53.12	50	6.35e+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	058-1301.4429.4435.2	2	18.35	13.91	91.8	6.08e+007	(K)SELVEAIAASADISK(A)	1503.791
2	058-1301.5103.5129.2	2	17.95	17.95	92.0	6.25e+007	(R)ALDAVTESIANALK(E)	1415.775
3	058-1301.6012.6074.2	2	16.82	7.46	95.2	1.54e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
4	058-1301.6082.6096.3	3	16.40	8.95	89.6	3.44e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
5	058-1301.4303.4387.2	2	12.98	7.78	71.8	1.37e+008	(K)SELVEAIAASADISK(A)	1503.791
6	059-1401.4568.4568.2	2	12.17	7.06	71.4	2.37e+007	(K)SELVEAIAASADISK(A)	1503.791
7	059-1401.6355.6360.2	2	11.93	4.81	86.2	4.07e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
8	057-0901.6124.6155.0	2	10.98	2.87	81.1	7.57e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
9	058-1301.10128.10128.2	2	9.34	5.10	67.9	4.70e+006	(K)SELVEAIAASADISK(A)	1503.791
10	058-1301.10031.10031.0	2	6.75	2.59	77.7	1.89e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
11	059-1401.4545.4545.2	2	6.56	6.56	61.2	2.23e+007	(K)SELVEAIAASADISK(A)	1503.791

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	9.3	11	3	52.84	50	1.01e+009	9105.4	PA_BSC2:2534572633	PA_BSC2:2534572633 Bsc2_00317 Bacterial nucleoid DNA-binding protein [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.4429.4435.2	2	18.35	13.91	91.8	6.08e+007	(K)SELVEAIAASADISK(A)	1503.791
2	058-1301.4866.4913.0	2	17.67	9.39	95.0	4.42e+008	(R)ALDAVTESIASALK(E)	1388.764
3	058-1301.6012.6074.2	2	16.82	7.46	95.2	1.54e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
4	058-1301.6082.6096.3	3	16.40	8.95	89.6	3.44e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
5	058-1301.4303.4387.2	2	12.98	7.78	71.8	1.37e+008	(K)SELVEAIAASADISK(A)	1503.791
6	059-1401.4568.4568.2	2	12.17	7.06	71.4	2.37e+007	(K)SELVEAIAASADISK(A)	1503.791
7	059-1401.6355.6360.2	2	11.93	4.81	86.2	4.07e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
8	057-0901.6124.6155.0	2	10.98	2.87	81.1	7.57e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
9	058-1301.10128.10128.2	2	9.34	5.10	67.9	4.70e+006	(K)SELVEAIAASADISK(A)	1503.791
10	058-1301.10031.10031.0	2	6.75	2.59	77.7	1.89e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
11	059-1401.4545.4545.2	2	6.56	6.56	61.2	2.23e+007	(K)SELVEAIAASADISK(A)	1503.791

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	9.4	6	2	39.82	33	4.51e+008	9107.5	PA_Bse02:2503999877	PA_Bse02:2503999877 BS02DRAFT_00006580 Bacterial DNA-binding protein. [B. setacea BS02 (Isolate from shipv

				Fwd-Rev	SPI	Spectrum		MH^+

#	Filename	z	Score	Score	(%)	Intensity	Sequence	Matched (Da)
1	057-0901.4319.4390.0	2	23.00	14.42	100.0	1.27e+008	(R)ALDAVTDSIAGALK(E)	1344.738
2	058-1301.6012.6074.2	2	16.82	7.46	95.2	1.54e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
3	058-1301.6082.6096.3	3	16.40	8.95	89.6	3.44e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
4	059-1401.6355.6360.2	2	11.93	4.81	86.2	4.07e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
5	057-0901.6124.6155.0	2	10.98	2.87	81.1	7.57e+007	(K)EGDQVALVGFGTFLVK(E)	1679.901
6	058-1301.10031.10031.0	2	6.75	2.59	77.7	1.89e+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
10	10.1	13	3	55.27	29	3.78e+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	057-0901.4644.4719.2	2	20.43	9.60	98.2	3.38e+009	(K)TVTAMDVVYALK(R)	1310.703
2	057-0901.2887.2921.2	2	17.89	11.56	96.7	1.97e+008	(R)ISGLIYEETR(G)	1180.621
3	057-0901.3689.3718.0	2	16.95	5.95	97.9	5.25e+007	(K)VFLENVIR(D)	989.578
4	065-1701.2949.2979.2	2	16.81	10.72	94.7	3.94e+006	(R)ISGLIYEETR(G)	1180.621
5	052-0401.4935.4986.0	2	15.66	8.74	91.6	5.28e+006	(K)TVTAMDVVYALK(R)	1310.703
6	065-1701.3998.4019.0	2	14.65	5.44	95.9	5.06e+006	(K)VFLENVIR(D)	989.578
7	065-1701.4952.4990.0	2	14.44	7.40	84.6	5.75e+006	(K)TVTAMDVVYALK(R)	1310.703
8	058-1301.2909.2909.0	2	14.33	8.95	87.9	1.04e+007	(R)ISGLIYEETR(G)	1180.621
9	065-1701.4959.4959.0	2	13.06	8.27	69.5	4.20e+006	(K)TVTAMDVVYALK(R)	1310.703
10	065-1701.2955.2955.0	2	12.81	7.49	88.6	3.11e+006	(R)ISGLIYEETR(G)	1180.621
11	064-1601.3944.3944.0	2	12.58	4.19	92.8	1.10e+007	(K)VFLENVIR(D)	989.578
12	058-1301.4735.4758.2	2	12.50	7.42	67.9	5.55e+007	(K)TVTAMDVVYALK(R)	1310.703
13	057-0901.4921.4921.0	2	9.10	3.46	67.6	3.71e+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
11	11.1	7	4	53.35	10	2.42e+009	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	059-1401.6305.6350.0	3	15.14	10.73	80.6	5.33e+008	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
2	059-1401.4804.4888.3	3	14.71	4.89	72.5	1.70e+009	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
3	064-1601.5984.6007.0	3	14.67	9.70	78.4	2.04e+007	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
4	064-1601.4768.4775.0	3	13.78	9.24	79.1	4.55e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
5	059-1401.4067.4082.0	3	12.98	2.69	84.2	4.13e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
6	060-1501.4766.4793.0	3	12.75	8.68	74.5	7.95e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
7	065-1701.2867.2867.0	2	10.52	3.63	79.7	2.55e+006	(R)TIQQTMDEIK(A)	1206.604

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

(#)	(#)	(#)	Peptides (#)	MS/MS Search Score	Coverage	Spectral Intensity	MW (Da)	Accession #	Protein Name
12	12.1	6	3	43.45	10	2.58e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate from shipw

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.4298.4298.0	3	15.19	8.75	79.5	2.61e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
2	058-1301.5590.5603.0	3	14.98	10.39	87.3	2.95e+007	(K)RPAMDWLMNYLGR(-)	1622.794
3	058-1301.4317.4328.2	2	14.58	5.24	90.4	3.06e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
4	058-1301.6197.6234.2	2	13.28	9.56	80.9	8.84e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
5	058-1301.4309.4309.0	3	11.84	8.47	81.6	2.70e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
6	058-1301.6207.6207.0	2	9.82	4.51	62.7	5.62e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888

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	12.2	3	2	29.94	3	1.60e+008	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase family 10./

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.4406.4411.2	2	16.66	10.31	92.9	1.49e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
2	058-1301.6197.6234.2	2	13.28	9.56	80.9	8.84e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
3	058-1301.6207.6207.0	2	9.82	4.51	62.7	5.62e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888

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	6	3	42.62	12	1.71e+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	059-1401.4706.4717.0	2	17.90	7.82	93.8	9.40e+007	(K)MLAGVNVLADAVK(I)	1300.730
2	059-1401.2848.2864.0	2	14.89	9.24	81.4	3.90e+006	(R)QIVTNAGDEASVIAEK(V)	1644.844
3	060-1501.4700.4700.0	2	14.36	9.10	82.5	1.37e+007	(K)MLAGVNVLADAVK(I)	1300.730
4	064-1601.2832.2832.0	2	10.73	7.14	94.2	2.34e+006	(R)QIVTNAGDEASVIAEK(V)	1644.844
5	059-1401.8065.8065.0	3	9.83	2.18	73.2	5.57e+007	(R)KAMLQDIAILTGATVISEEVGLDLEGATLEHLGQAKR(F)	3891.090
6	065-1701.2874.2874.0	2	6.26	2.45	93.2	1.08e+006	(R)QIVTNAGDEASVIAEK(V)	1644.844

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	3	3	41.73	9	1.01e+008	61419.7	PA_BS12:2189569223	PA_BS12:2189569223 or2536 Ribosomal protein S1 [B. setacea BS12] 559 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0701.7712.7727.0	3	17.38	8.99	83.5	1.78e+007	(K)VVNLGDEVEVMILDIDEER(R)	2187.086

2	057-0901.5015.5033.0	3	15.40	9.07	91.2	4.94e+007	(K)KGDELETVVLAIDPER(E)	1783.944
3	057-0901.4485.4485.2	2	8.95	8.95	62.2	3.34e+007	(K)QLDEDPFTIYVGTNDK(G)	1854.876

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	8	3	41.56	24	4.86e+007	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	064-1601.2771.2782.0	2	17.16	17.16	93.0	4.07e+006	(R)GANLAGDEFDSSYER(G)	1630.699
2	060-1501.2793.2798.2	2	15.65	15.65	92.0	4.69e+006	(R)GANLAGDEFDSSYER(G)	1630.699
3	065-1701.7874.7874.0	3	12.55	6.87	74.3	6.17e+006	(R)QTGEYDIEPNAVLVFDLELLEIK(S)	2648.371
4	065-1701.7687.7717.0	3	11.85	11.85	74.8	1.86e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
5	064-1601.2794.2794.0	2	11.28	8.02	84.3	4.34e+006	(R)GANLAGDEFDSSYER(G)	1630.699
6	064-1601.2776.2776.0	2	10.58	5.21	77.5	3.83e+006	(R)GANLAGDEFDSSYER(G)	1630.699
7	060-1501.2776.2776.0	2	8.39	5.12	82.3	3.52e+006	(R)GANLAGDEFDSSYER(G)	1630.699
8	064-1601.2762.2762.0	2	7.45	7.45	83.1	3.38e+006	(R)GANLAGDEFDSSYER(G)	1630.699

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	12	2	38.50	19	1.42e+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	059-1401.4086.4124.0	2	22.38	14.46	98.1	4.55e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
2	060-1501.4131.4131.2	2	18.63	12.79	94.0	1.04e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
3	065-1701.4623.4670.3	3	16.12	8.19	84.3	1.82e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
4	059-1401.4633.4725.2	2	15.47	7.21	90.3	3.46e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
5	064-1601.4600.4648.2	2	14.16	5.12	77.9	3.63e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
6	064-1601.4608.4638.3	3	13.77	5.88	78.7	2.69e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
7	060-1501.4596.4618.2	2	13.74	5.88	78.8	4.73e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
8	065-1701.4176.4229.0	3	13.56	8.45	73.0	2.34e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
9	059-1401.4064.4122.3	3	13.12	6.47	76.1	4.39e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
10	059-1401.4645.4751.3	3	12.99	4.02	72.3	4.01e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
11	065-1701.4635.4641.2	2	12.56	6.54	83.1	9.69e+006	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
12	058-1301.4581.4599.2	2	9.60	6.01	65.2	1.95e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
17	17.1	9	3	38.08	47	6.83e+008	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	064-1601.9579.9583.2	2	15.78	15.78	82.6	6.27e+007	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
2	058-1301.9981.10007.2	2	14.53	14.53	84.7	2.56e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
3	065-1701.9498.9498.2	2	13.20	8.54	64.8	1.69e+007	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
4	058-1301.7024.7024.2	2	13.08	3.07	87.3	5.83e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
5	057-0901.7196.7250.2	2	13.06	3.82	87.3	1.88e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
6	058-1301.7002.7032.2	2	10.66	2.82	77.9	5.80e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
7	059-1401.7284.7284.2	2	10.55	3.85	76.6	2.11e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
8	058-1301.2474.2506.0	2	9.22	2.04	74.7	2.18e+006	(R)HLQLAIR(N)	850.526
9	059-1401.7271.7271.2	2	8.55	3.07	66.7	1.92e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391

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	7	3	37.82	18	2.71e+007	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	064-1601.4209.4217.0	2	14.81	8.32	90.5	7.01e+006	(R)AGTGAIPTAADTVLVNYR(G)	1789.945
2	064-1601.2755.2755.0	2	13.66	7.16	95.2	2.65e+006	(K)EGVVVAESGSGLQYK(I)	1522.775
3	064-1601.2760.2760.0	2	9.69	9.69	85.5	2.30e+006	(K)EGVVVAESGSGLQYK(I)	1522.775
4	064-1601.2729.2729.0	2	9.35	5.52	97.4	4.66e+006	(R)GTTLDGEEFDSSYSR(G)	1663.709
5	060-1501.2757.2757.2	2	8.22	8.22	62.3	2.40e+006	(R)GTTLDGEEFDSSYSR(G)	1663.709
6	064-1601.2724.2724.0	2	7.66	7.66	93.3	4.69e+006	(R)GTTLDGEEFDSSYSR(G)	1663.709
7	057-0901.2742.2742.0	2	7.00	3.03	100.0	3.37e+006	(K)EGVVVAESGSGLQYK(I)	1522.775

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
19	19.1	4	3	37.48	8	8.44e+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	059-1401.3833.3833.2	2	14.32	6.47	91.9	1.44e+007	(K)LIIAGVNVVR(M)	1053.678
2	059-1401.3725.3737.0	2	13.21	6.13	79.9	2.52e+007	(K)IVSTLGPATDEPGILEK(L)	1739.943
3	059-1401.4207.4225.0	2	9.95	9.95	70.3	3.91e+007	(K)EGLEDGDLVLITK(G)	1401.748
4	064-1601.3807.3807.0	2	9.42	5.56	74.3	5.71e+006	(K)IVSTLGPATDEPGILEK(L)	1739.943

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	12	3	36.91	4	1.22e+008	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	055-0701.2578.2588.2	2	15.17	15.17	89.9	3.07e+006	(K)TSAFAQANFAK(D)	1155.580
2	056-0801.4832.4848.3	3	11.49	2.18	82.7	6.48e+007	(K)ETDPELSALLSWNHDDK(L)	1969.914

3	055-0701.2572.2572.0	2	11.24	11.24	76.4	8.79e+006	(K)TSAFAQANFAK(D)	1155.580
4	055-0502.2560.2560.2	2	10.58	10.58	70.8	2.02e+006	(K)TSAFAQANFAK(D)	1155.580
5	055-0502.3628.3647.2	2	10.25	4.78	72.0	1.65e+007	(K)DLTDTISLTGNAGVR(Y)	1532.792
6	055-0501.2552.2552.0	2	8.57	5.42	70.3	1.83e+006	(K)TSAFAQANFAK(D)	1155.580
7	055-0501.2573.2573.0	2	8.28	4.02	82.6	2.21e+006	(K)TSAFAQANFAK(D)	1155.580
8	055-0502.2549.2549.0	2	8.16	4.15	76.4	2.05e+006	(K)TSAFAQANFAK(D)	1155.580
9	055-0701.3675.3681.2	2	7.43	7.43	62.5	1.32e+007	(K)DLTDTISLTGNAGVR(Y)	1532.792
10	055-0501.2548.2548.0	2	6.79	6.79	72.2	1.84e+006	(K)TSAFAQANFAK(D)	1155.580
11	056-0801.2562.2562.0	2	6.43	6.43	85.8	3.25e+006	(K)TSAFAQANFAK(D)	1155.580
12	055-0502.2554.2554.0	2	6.05	2.89	87.2	2.02e+006	(K)TSAFAQANFAK(D)	1155.580

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	15	3	36.18	18	2.93e+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	060-1501.2885.2907.2	2	15.68	6.42	88.5	9.05e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
2	055-0701.2806.2812.2	2	15.55	7.49	85.3	2.39e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
3	064-1601.2869.2884.2	2	15.07	8.77	86.1	8.91e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
4	064-1601.3025.3057.2	2	14.16	8.75	87.5	2.40e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
5	055-0502.2936.2944.0	2	14.15	7.36	87.6	2.73e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
6	057-0901.2983.2989.2	2	14.13	7.81	86.4	1.21e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
7	059-1401.2884.2889.2	2	13.91	6.54	80.7	4.20e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
8	055-0701.2931.2954.2	2	13.65	7.77	87.8	3.09e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
9	056-0801.2951.2957.2	2	12.52	5.42	83.8	2.41e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
10	058-1301.2984.3022.2	2	12.46	6.75	82.0	2.86e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
11	055-0501.2895.2925.2	2	11.93	6.21	80.4	1.52e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
12	060-1501.3036.3050.2	2	11.46	4.80	80.1	1.89e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
13	055-0502.4933.4933.0	3	10.48	4.48	74.2	1.51e+007	(K)QSYQNAGADRRFLASAMMETEVMDTNYTYGDAK(S)	3734.653
14	055-0701.6632.6638.2	2	10.02	4.34	92.4	3.98e+007	(R)FWVEIPAI(-)	974.535
15	055-0501.6375.6375.2	2	9.04	3.85	93.1	1.10e+007	(R)FWVEIPAI(-)	974.535

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	8	2	36.18	30	2.87e+008	12588.4	PA_BSC2:2534573502	PA_BSC2:2534573502 Bsc2_01187 LSU ribosomal protein L12P [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	059-1401.2760.2817.2	2	20.15	13.15	94.8	2.52e+007	(K)TQLEEAGASVELK(-)	1374.712
2	056-0801.2715.2727.2	2	18.62	14.61	94.1	2.40e+007	(K)TQLEEAGASVELK(-)	1374.712
3	058-1301.9922.9922.2	2	16.03	9.69	81.8	2.59e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
4	065-1701.9412.9412.2	2	15.11	15.11	77.2	1.41e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
5	058-1301.9919.9927.3	3	14.18	14.18	70.7	4.40e+007	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340

6	059-1401.2785.2785.0	3	13.58	13.58	82.4	3.14e+006	(K)TQLEEAGASVELK(-)	1374.712
7	059-1401.10055.10055.0	2	10.51	10.51	64.6	1.38e+008	(K)EDILNAIAEMSVMDVVELVEAMEEK(F)	2807.340
8	059-1401.2821.2821.0	2	10.32	7.24	85.5	1.26e+007	(K)TQLEEAGASVELK(-)	1374.712

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	7	3	35.88	32	1.71e+008	13597.6	PA_Bse02:2503999073	PA_Bse02:2503999073 BS02DRAFT_00000810 ribosomal protein L19, bacterial type [B. setacea BS02 (Isolate fron

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	054-0601.4342.4356.2	2	14.20	9.73	74.6	2.63e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
2	054-0601.4260.4314.0	2	13.43	5.43	70.6	4.78e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
3	054-0602.2978.3009.2	2	13.03	7.64	75.8	9.34e+006	(R)LQAYEGVVIGK(R)	1176.663
4	054-0601.4280.4280.0	3	11.66	4.27	78.2	2.52e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
5	054-0602.4257.4315.2	2	10.28	5.24	60.1	5.04e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
6	054-0601.2982.2986.2	2	9.39	3.58	70.5	5.56e+006	(R)LQAYEGVVIGK(R)	1176.663
7	054-0601.2886.2886.2	2	8.65	4.22	68.9	6.36e+006	(K)IIQELENEQLK(Q)	1356.738

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	23.2	7	3	35.37	34	1.93e+008	13449.5	PA_BSC2:2534573050	PA_BSC2:2534573050 Bsc2_00734 LSU ribosomal protein L19P [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	054-0601.4342.4356.2	2	14.20	9.73	74.6	2.63e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
2	054-0601.4260.4314.0	2	13.43	5.43	70.6	4.78e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
3	054-0602.2978.3009.2	2	13.03	7.64	75.8	9.34e+006	(R)LQAYEGVVIGK(R)	1176.663
4	054-0601.4280.4280.0	3	11.66	4.27	78.2	2.52e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
5	054-0602.4257.4315.2	2	10.28	5.24	60.1	5.04e+007	(K)QELPEFSPGDTVVVQVK(V)	1871.976
6	054-0601.2982.2986.2	2	9.39	3.58	70.5	5.56e+006	(R)LQAYEGVVIGK(R)	1176.663
7	054-0601.4822.4822.2	2	8.14	8.14	65.5	2.88e+007	(K)NNIIQELENEQLK(Q)	1584.823

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	3	35.38	13	9.46e+006	30592.3	PA_BS12:2189569048	PA_BS12:2189569048 or2361 hypothetical protein [B. setacea BS12] 276 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	065-1701.4953.4965.2	2	13.76	10.51	88.7	3.83e+006	(R)AILIQTFNPSDLR(T)	1487.822
2	065-1701.3768.3779.2	2	12.69	3.85	85.6	2.79e+006	(K)SQDMPVDELMER(S)	1449.635
3	065-1701.3174.3174.0	2	8.93	4.63	83.6	2.83e+006	(R)SGVNAQIVQIPEK(V)	1382.764

Distinct

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
25	25.1	4	2	35.17	32	1.58e+008	12186.2	PA_BSC2:2534574917	PA_BSC2:2534574917 Bsc2_02604 nitrogen regulatory protein P-II family [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.8691.8708.3	3	19.82	8.23	82.5	3.68e+007	(K)LELVLGDDLIEQAVEAITK(A)	2069.138
2	057-0901.8904.8909.0	3	19.51	7.29	89.8	2.98e+007	(K)LELVLGDDLIEQAVEAITK(A)	2069.138
3	058-1301.8690.8711.2	2	15.70	10.80	84.1	6.64e+007	(K)LELVLGDDLIEQAVEAITK(A)	2069.138
4	054-0601.4278.4313.2	2	15.35	8.50	89.3	2.55e+007	(R)NALSEIGVQGMTVTEVK(G)	1775.921

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
26	26.1	9	2	34.22	30	2.14e+008	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	055-0501.2768.2791.0	2	22.25	14.41	100.0	1.17e+007	(K)DLEEAGASVELK(-)	1260.632
2	055-0701.2764.2775.2	2	22.25	14.63	100.0	1.67e+007	(K)DLEEAGASVELK(-)	1260.632
3	055-0701.2793.2835.2	2	21.75	14.54	100.0	1.61e+007	(K)DLEEAGASVELK(-)	1260.632
4	055-0502.2782.2793.2	2	21.25	13.24	100.0	1.14e+007	(K)DLEEAGASVELK(-)	1260.632
5	058-1301.2804.2820.2	2	19.64	13.50	97.7	6.77e+006	(K)DLEEAGASVELK(-)	1260.632
6	064-1601.2821.2821.0	2	15.15	8.64	81.7	2.75e+006	(K)DLEEAGASVELK(-)	1260.632
7	065-1701.9406.9410.2	2	11.97	11.97	70.4	3.35e+007	(K)EDIINAIADMSVTDVVELITAMEEK(F)	2749.353
8	059-1401.10054.10054.0	2	11.78	6.96	77.0	1.11e+008	(K)EDIINAIADMSVTDVVELITAMEEK(F)	2749.353
9	059-1401.2824.2824.0	2	10.17	5.78	84.4	3.87e+006	(K)DLEEAGASVELK(-)	1260.632

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	6	2	31.58	4	6.74e+007	78518.0	PA_Bse02:2503998694	PA_Bse02:2503998694 BS02DRAFT_00016310 type IV pilus secretin (or competence protein) PilQ [B. setacea BS0

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	053-0501.4635.4653.2	2	17.68	10.11	98.1	1.32e+007	(R)ELLIFVTPR(I)	1087.652
2	054-0601.4750.4777.2	2	17.17	9.75	97.5	1.86e+007	(R)ELLIFVTPR(I)	1087.652
3	053-0502.4634.4634.2	2	17.12	9.79	96.1	1.08e+007	(R)ELLIFVTPR(I)	1087.652
4	054-0602.4723.4723.2	2	16.35	6.75	95.9	1.25e+007	(R)ELLIFVTPR(I)	1087.652
5	064-1601.3148.3148.0	3	13.90	3.92	81.4	5.52e+006	(K)QQATIESGSEVPYQEESASGGTTTAFK(D)	2803.291
6	055-0701.3083.3083.2	2	11.72	3.71	85.8	6.82e+006	(K)QQATIESGSEVPYQEESASGGTTTAFK(D)	2803.291

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

				Score					
28	28.1	9	2	31.57	28	1.20e+008	13501.0	PA_BSC2:2534573446	PA_BSC2:2534573446 Bsc2_01131 LSU ribosomal protein L14P [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0501.3357.3357.0	2	16.52	12.02	93.0	1.28e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
2	055-0502.3359.3359.0	2	16.00	11.59	93.5	9.29e+006	(-)MIQTESYLDVADNSGAR(R)	1869.865
3	055-0701.3359.3359.2	2	15.39	15.39	92.4	1.30e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
4	055-0501.3661.3661.2	2	15.05	9.26	88.5	1.08e+007	(R)FDDNAAVLLNQQEAPVGTR(I)	2058.026
5	055-0701.3713.3713.2	2	13.95	9.64	86.5	9.68e+006	(R)FDDNAAVLLNQQEAPVGTR(I)	2058.026
6	055-0502.3653.3653.0	2	13.87	8.31	88.9	1.22e+007	(R)FDDNAAVLLNQQEAPVGTR(I)	2058.026
7	055-0501.3347.3355.0	3	10.07	10.07	71.3	1.98e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
8	055-0701.3381.3381.0	3	9.67	9.67	71.9	2.20e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
9	055-0502.3671.3671.2	2	8.26	4.33	70.9	1.07e+007	(R)FDDNAAVLLNQQEAPVGTR(I)	2058.026

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	28.2	6	2	29.03	28	1.14e+008	13487.0	PA_BS12:2189570790	PA_BS12:2189570790 or4034 Ribosomal protein L14 [B. setacea BS12] 122 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0501.3357.3357.0	2	16.52	12.02	93.0	1.28e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
2	055-0502.3359.3359.0	2	16.00	11.59	93.5	9.29e+006	(-)MIQTESYLDVADNSGAR(R)	1869.865
3	055-0701.3359.3359.2	2	15.39	15.39	92.4	1.30e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
4	055-0501.3743.3749.0	3	12.51	3.81	74.8	3.71e+007	(R)FDDNAAVLLTQQNAPVGTR(I)	2030.031
5	055-0501.3347.3355.0	3	10.07	10.07	71.3	1.98e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865
6	055-0701.3381.3381.0	3	9.67	9.67	71.9	2.20e+007	(-)MIQTESYLDVADNSGAR(R)	1869.865

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
29	29.1	2	2	30.95	28	2.57e+007	9318.7	PA_BS12:2189569390	PA_BS12:2189569390 or2703 Ribosomal protein S16 [B. setacea BS12] 82 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0701.3054.3084.2	2	17.65	11.57	92.3	1.34e+007	(R)LDYWAGQGAQISDR(V)	1579.751
2	055-0701.3949.3966.0	2	13.30	4.49	86.1	1.22e+007	(R)VGFFNPIAR(G)	1020.563

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	3	2	30.36	6	7.70e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp

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

1	056-0801.5898.5988.0	3	19.30	15.00	97.0	5.05e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
2	056-0801.2453.2499.0	2	11.06	6.09	91.4	1.15e+007	(R)HVIYGEWGR(D)	1116.559
3	056-0801.5923.5968.2	2	10.21	10.21	70.9	2.53e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039

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	30.2	2	2	25.89	6	2.26e+008	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding domain. [B. seta

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	056-0801.5887.5892.2	2	14.83	8.63	93.1	2.15e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
2	056-0801.2453.2499.0	2	11.06	6.09	91.4	1.15e+007	(R)HVIYGEWGR(D)	1116.559

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	4	2	30.24	6	4.91e+007	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	058-1301.4406.4411.2	2	16.66	10.31	92.9	1.49e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
2	064-1601.4247.4247.2	2	13.58	13.58	76.9	8.23e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
3	058-1301.4134.4134.2	2	10.78	10.78	71.9	1.80e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
4	064-1601.4259.4259.0	2	7.50	3.14	70.8	7.94e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814

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	2	2	28.76	21	4.12e+007	13381.5	PA_BS12:2189569387	PA_BS12:2189569387 or2700 Ribosomal protein L19 [B. setacea BS12] 118 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0701.4777.4787.0	2	16.63	11.32	92.3	1.73e+007	(K)NTIIQELENEQLK(Q)	1571.828
2	055-0701.3093.3107.2	2	12.13	5.58	81.8	2.39e+007	(K)FSPGDTVVVQVK(V)	1275.695

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
33	33.1	9	2	28.05	19	2.45e+008	17704.7	PA_BSC2:2534573498	PA_BSC2:2534573498 Bsc2_01183 SSU ribosomal protein S7P [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	056-0801.9430.9460.0	3	17.72	8.24	88.9	3.92e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
2	055-0701.9093.9099.0	3	15.00	7.15	82.4	7.69e+006	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180

3	057-0901.9347.9368.0	3	14.43	5.82	78.3	4.57e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
4	057-0901.9387.9387.0	2	14.41	8.21	79.1	4.03e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
5	055-0701.9106.9106.0	3	12.93	5.39	79.2	7.80e+006	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
6	057-0901.3980.3980.0	2	10.33	3.46	66.0	1.97e+007	(R)IVYGALELVR(E)	1132.673
7	057-0901.9392.9392.2	2	10.20	4.85	69.0	3.85e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
8	056-0801.9443.9443.2	2	9.18	3.81	63.0	2.40e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
9	056-0801.9439.9439.2	2	6.76	6.76	68.0	2.21e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180

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	3	2	26.34	6	7.11e+007	49567.7	PA_Bse08:2503996612	PA_Bse08:2503996612 BS08DRAFT_00014510 xylose isomerase [B. setacea BS08 (Isolate from shipworm gill tissu

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	058-1301.4404.4422.0	2	14.61	7.53	78.8	3.06e+007	(K)GADFETGSLSLEQLAK(I)	1665.834
2	058-1301.4006.4006.0	2	11.73	6.94	71.5	2.02e+007	(K)IAYEGPDSDNPFAFK(Y)	1670.770
3	058-1301.4013.4013.0	2	10.71	7.35	74.6	2.03e+007	(K)IAYEGPDSDNPFAFK(Y)	1670.770

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	2	2	26.24	10	8.04e+007	47257.4	PA_Bse02:2504001097	PA_Bse02:2504001097 BS02DRAFT_00030780 transcription termination factor Rho [B. setacea BS02 (Isolate from

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	057-0901.9060.9094.0	2	18.60	11.23	94.9	6.25e+007	(R)SGEDIYGDGVLEILQDGFGFLR(S)	2400.172
2	057-0901.4133.4133.0	2	7.64	7.64	69.1	1.79e+007	(R)SAGASYLAGPDDIYVSPSQIR(R)	2167.067

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
36	36.1	4	2	24.97	8	5.73e+007	38937.1	PA_BSC2:2534573407	PA_BSC2:2534573407 Bsc2_01092 fructose-bisphosphate aldolase (EC 4.1.2.13) [Alteromonadacea bacterium Bsc2

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	064-1601.6186.6186.2	2	17.63	11.11	91.6	1.40e+007	(R)LEQAFADLNAIDVL(-)	1531.801
2	060-1501.6221.6229.2	2	17.60	10.68	92.2	2.37e+007	(R)LEQAFADLNAIDVL(-)	1531.801
3	064-1601.6153.6153.2	2	11.44	5.79	66.7	1.28e+007	(R)LEQAFADLNAIDVL(-)	1531.801
4	060-1501.3028.3028.0	2	7.34	4.27	88.8	6.86e+006	(K)AEGQQAQILGAVSGAK(H)	1527.813

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
37	37.1	2	2	23.73	19	1.31e+008	18210.9	PA_Bse02:2504000647	

PA_Bse02:2504000647 BS02DRAFT_00022430 bacterioferritin [B. setacea BS02 (Isolate from shipworm gill tissue)]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	059-1401.7065.7083.2	2	13.51	2.94	90.6	8.86e+007	(R)ILFLEGLPNLQDLGK(L)	1669.953
2	059-1401.2936.2981.0	3	10.22	10.22	73.3	4.20e+007	(K)ELAEHEYEESIDEMK(H)	1851.796

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
38	38.1	2	2	23.26	6	6.70e+007	49480.7	PA_BSC2:2534574372	PA_BSC2:2534574372 Bsc2_02058 D-xylose isomerase (EC 5.3.1.5) [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	058-1301.4728.4745.2	2	13.80	7.94	78.8	3.66e+007	(R)ALIVADDLIQNSPIEK(M)	1738.959
2	058-1301.3664.3668.0	2	9.46	2.27	66.5	3.04e+007	(K)IAYEGPESDNPLAFK(Y)	1650.802

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
39	39.1	3	2	22.94	9	2.17e+008	45984.9	PA_Bse_meta_comb:2073595342	PA_Bse_meta_comb:2073595342 BaSeMet_00389980 Capsid protein (F protein). [Bankia setacea microl

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	057-0901.6319.6319.2	2	14.32	14.32	82.9	2.65e+007	(R)LLPMNDTMSQEADTLGEVGGYMLGTK(R)	2771.294
2	057-0901.6298.6321.0	3	10.45	4.51	72.6	1.74e+008	(R)LLPMNDTMSQEADTLGEVGGYMLGTK(R)	2771.294
3	057-0901.2927.2954.0	2	8.62	3.81	69.9	1.64e+007	(R)LQMEADIYGEK(D)	1296.615

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
40	40.1	2	2	22.92	20	1.87e+007	22353.9	PA_Bse_meta_comb:2073589276	PA_Bse_meta_comb:2073589276 BaSeMet_00329320 FKBP-type peptidyl-prolyl cis-trans isomerases 1

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	058-1301.8405.8405.2	2	12.11	6.11	75.6	7.78e+006	(R)GEPAEFPVNGVIAGWTEALQLMPVGAK(W)	2781.429
2	058-1301.3448.3448.0	2	10.81	6.71	78.4	1.10e+007	(K)QLSENTFEGMNYNAVAK(G)	1915.886

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
41	41.1	2	2	22.62	5	8.63e+006	49486.1	PA_Bse02:2503998172	PA_Bse02:2503998172 BS02DRAFT_00013490 MotA/TolQ/ExbB proton channel family. [B. setacea BS02 (Isolate f

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

1	065-1701.5586.5634.0	3	14.94	2.97	86.2	6.64e+006	(K)GIVHLLEEESAGLIAEK(S)	1807.981
2	065-1701.3812.3812.2	2	7.68	7.68	71.1	1.99e+006	(K)AASLDELLK(M)	959.541

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
42	42.1	5	2	22.15	50	2.38e+008	12370.2	PA_Bse_meta_comb:2073564350	PA_Bse_meta_comb:2073564350 BaSeMet_00080060 ATP-dependent protease Clp, ATPase subunit [B

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	059-1401.4708.4748.0	3	12.90	5.23	77.0	1.50e+008	(K)DLEPEDLVRYGLIPEFVGRLPVIATLDELDK(D)	3524.889
2	060-1501.4648.4683.0	3	10.95	4.43	77.8	3.62e+007	(K)DLEPEDLVRYGLIPEFVGRLPVIATLDELDK(D)	3524.889
3	060-1501.4071.4075.0	3	9.25	2.01	70.9	1.30e+007	(K)QYAKLFEMEGVEVDFRDDALDAVAEK(A)	2988.430
4	065-1701.4673.4673.0	3	8.78	2.86	85.3	6.32e+006	(K)DLEPEDLVRYGLIPEFVGRLPVIATLDELDK(D)	3524.889
5	060-1501.4652.4652.0	3	8.51	5.41	72.5	3.31e+007	(K)DLEPEDLVRYGLIPEFVGRLPVIATLDELDK(D)	3524.889

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
43	43.1	2	1	21.50	25	2.89e+007	7243.1	PA_Bse02:2503998197	PA_Bse02:2503998197 BS02DRAFT_00013740 "Cold-shock" DNA-binding domain. [B. setacea BS02 (Isolate from

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	054-0601.2935.2940.0	2	21.50	16.73	100.0	1.39e+007	(K)TLAEGQQVEFSVSQGAK(G)	1778.892
2	054-0601.2933.2951.3	3	20.21	15.53	96.3	1.51e+007	(K)TLAEGQQVEFSVSQGAK(G)	1778.892

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
44	44.1	2	2	21.13	11	6.95e+007	36312.3	PA_Bse02:2504001165	PA_Bse02:2504001165 BS02DRAFT_00031460 general secretion pathway protein C [B. setacea BS02 (Isolate from

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0502.5519.5554.3	3	10.85	2.71	74.3	5.17e+007	(K)LFEEVGLQSGDIVTSVNGR(E)	2020.035
2	055-0502.8301.8357.2	2	10.28	3.06	80.2	1.78e+007	(R)AIIADGNDQQLYRIGEEIAK(A)	2217.151

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
45	45.1	4	2	21.06	17	1.19e+008	22697.8	PA_BS12:2189570780	PA_BS12:2189570780 or4024 Ribosomal protein L3 [B. setacea BS12] 214 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	055-0502.5068.5068.0	2	13.33	5.43	81.6	2.17e+007	(R)IFTDDGLSVPVTVVEVDPNR(I)	2172.119
2	055-0701.5102.5119.0	2	11.83	2.15	82.8	5.69e+007	(R)IFTDDGLSVPVTVVEVDPNR(I)	2172.119

3	055-0501.5047.5067.0	2	11.78	3.63	80.0	3.57e+007	(R)IFTDDGLSVPVTVVEVDPNR(I)	2172.119
4	055-0502.3086.3086.0	2	7.73	7.73	75.5	4.26e+006	(K)NAETDGYEAVQVTVGSR(R)	1795.846