Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\082010_OGL_1
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 55 **Hits:** 106
Data Directory: msdataSM\082010_OGL_7
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 83 **Hits:** 131
Data Directory: msdataSM\082010_OGL_2
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 59 **Hits:** 92
Data Directory: msdataSM\082010_OGL_3
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 75 **Hits:** 126
Data Directory: msdataSM\082010_OGL_4
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 96 **Hits:** 120
Data Directory: msdataSM\082010_OGL_6
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 51 **Hits:** 72
beginning to assemble proteins .... proteins assembled 0.101641 sec
proteins filtered by unique peptides 0.00848 sec
proteins filtered by score
calculated protein coverage maps 0.033628 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.007377 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 20 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	59	12	160.77	43	1.74e+009	59772.4	PA_Bse08:2503995076	PA_Bse08:2503995076 BS08DRAFT_00035440 nitrogenase molybdenum-iron protein beta chain [B. se
2	2.1	61	8	122.59	25	8.38e+008	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
2	2.1	61	8	122.59	44	8.38e+008	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
3	3.1	30	9	121.89	30	6.97e+008	56014.8	PA_Bse08:2503995077	PA_Bse08:2503995077 BS08DRAFT_00035450 nitrogenase molybdenum-iron protein alpha chain [B. s
4	4.1	50	7	109.26	20	1.34e+009	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
4	4.1	50	7	109.26	33	1.34e+009	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
5	5.1	14	5	65.10	9	5.60e+008	108814.9	PA_BS12:2189569860	PA_BS12:2189569860 or3165 Outer membrane receptor proteins, mostly Fe transport [B. setacea BS12
5	5.1	14	5	65.10	9	5.60e+008	108814.9	PA_Bse_meta_comb:2073560924	PA_Bse_meta_comb:2073560924 BaSeMet_00045800 TonB-dependent receptor [Bankia setacea micro
6	6.1	9	4	56.72	23	2.08e+008	32101.1	PA_Bse08:2503995078	PA_Bse08:2503995078 BS08DRAFT_00035460 nitrogenase iron protein [B. setacea BS08 (Isolate from
7	7.1	42	3	55.10	29	4.87e+009	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
8	8.1	12	3	40.59	28	2.55e+008	19750.3	PA_Bse08:2503995045	PA_Bse08:2503995045 BS08DRAFT_00035130 flavodoxin, long chain [B. setacea BS08 (Isolate from s
9	9.1	66	2	38.88	19	7.37e+009	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
10	10.1	24	2	36.10	41	2.43e+010	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Com
11	11.1	3	2	30.36	45	1.14e+008	11693.1	PA_Bse_meta_comb:2073580990	PA_Bse_meta_comb:2073580990 BaSeMet_00246460 ATP:guanido phosphotransferase, C-terminal ca
12	12.1	9	2	28.04	8	8.59e+007	44255.6	PA_Bse08:2503995480	PA_Bse08:2503995480 BS08DRAFT_00039430 translation elongation factor TU [B. setacea BS08 (Isola
13	13.1	7	2	28.02	8	1.70e+008	36127.2	PA_Bse08:2503993973	PA_Bse08:2503993973 BS08DRAFT_00026510 glyceraldehyde-3-phosphate dehydrogenase, type I [B.
14	14.1	5	2	27.69	16	9.19e+007	27641.5	PA_Bse02:2504001159	PA_Bse02:2504001159 BS02DRAFT_00031400 FKBP-type peptidyl-prolyl cis-trans isomerase./Domain
14	14.1	5	2	27.69	16	9.19e+007	27641.5	PA_Bse_meta_comb:2073579700	PA_Bse_meta_comb:2073579700 BaSeMet_00233560 FKBP-type peptidyl-prolyl cis-trans isomerases 1
15	15.1	8	2	26.69	8	1.40e+008	44282.5	PA_BSC2:2534573496	PA_BSC2:2534573496 Bsc2_01181 translation elongation factor 1A (EF-1A/EF-Tu) [Alteromonadacea b
15	15.1	8	2	26.69	8	1.40e+008	44282.5	PA_Bse_meta_comb:2073587015	PA_Bse_meta_comb:2073587015 BaSeMet_00306710 translation elongation factor 1A (EF-1A/EF-Tu) [
16	16.1	7	2	26.02	2	3.35e+007	126855.7	PA_Bse02:2504001037	PA_Bse02:2504001037 BS02DRAFT_00030180 TonB-dependent receptor [B. setacea BS02 (Isolate fro
17	17.1	2	2	26.00	11	1.94e+007	28847.5	PA_BS12:2189569790	PA_BS12:2189569790 or3098 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [B. setacea BS12] 265 b
17	17.1	2	2	26.00	11	1.94e+007	28847.5	PA_Bse_meta_comb:2073568597	PA_Bse_meta_comb:2073568597 BaSeMet_00122530 FKBP-type peptidyl-prolyl cis-trans isomerases 1
18	18.1	7	1	20.32	8	6.40e+007	35600.6	PA_Bse08:2503994614	PA_Bse08:2503994614 BS08DRAFT_00031280 malate dehydrogenase [B. setacea BS08 (Isolate from

19	19.1	2	2	20.31	10	1.04e+007	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
20	20.1	2	1	20.24	43	2.07e+007	8413.8	PA_Bse_meta_comb:2073579231	PA_Bse_meta_comb:2073579231 BaSeMet_00228870 Histones H3 and H4 [Bankia setacea microbiom
Totals:	559	99							

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	59	12	160.77	43	1.74e+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	064-1701.8227.8281.0	3	21.21	12.45	96.2	3.73e+007	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
2	064-1801.8220.8226.0	3	20.70	10.30	95.4	2.35e+007	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
3	064-1601.8240.8288.0	3	19.40	12.45	91.9	6.52e+007	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
4	064-1801.6785.6794.2	2	17.54	12.79	93.5	5.44e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
5	064-1701.6817.6823.2	2	17.53	12.87	93.6	5.92e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
6	067-2801.6898.6904.2	2	17.53	12.86	93.3	7.69e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
7	064-1601.6804.6822.2	2	16.53	11.63	92.6	5.16e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
8	067-2901.6918.6918.2	2	16.52	13.32	92.8	7.76e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
9	063-1201.9917.9917.0	3	15.61	8.14	82.8	1.76e+007	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
10	064-1601.9991.9991.0	3	15.42	9.05	82.3	5.73e+007	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
11	063-1201.8217.8217.0	3	14.99	10.72	77.8	7.83e+006	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
12	064-1801.8208.8208.0	3	14.63	9.72	80.3	2.03e+007	(K)TWMHEIPTLNIPMGLEWTDEFLMK(V)	2932.409
13	064-1601.9986.9994.2	2	14.17	14.17	87.4	9.01e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
14	064-1801.9935.9935.2	2	13.68	10.30	82.9	5.27e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
15	067-2801.9923.9923.0	3	13.60	7.32	78.5	5.85e+006	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
16	064-1701.9974.9979.2	2	13.54	13.54	86.5	9.82e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
17	067-2901.6772.6772.2	2	13.48	13.48	84.9	1.85e+007	(K)DMSVESTLLCDPEEILDTPADGEYR(I)	2798.239
18	063-1201.6764.6781.2	2	13.32	9.40	86.0	2.14e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
19	067-2801.10041.10041.0	2	12.93	9.38	84.7	3.83e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
20	067-2801.10046.10046.0	3	12.76	7.93	79.8	7.07e+006	(R)QTTLGYEGAMQILTTLVNSVLER(L)	2537.329
21	064-1601.4116.4121.0	2	12.68	7.13	86.3	2.25e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
22	064-1701.4135.4135.0	3	12.63	7.28	75.9	2.41e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
23	067-2901.6352.6352.2	2	12.33	12.33	81.8	3.67e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
24	062-0901.4221.4228.0	2	12.17	5.22	85.5	6.51e+006	(R)ENFEETPSQENIDEVFK(W)	2054.920
25	064-1801.4141.4150.2	2	12.17	5.83	86.1	2.02e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
26	067-2801.9929.9929.0	3	12.02	5.27	80.4	5.73e+006	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
27	064-1601.9727.9727.0	3	11.71	4.66	77.0	1.12e+007	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
28	064-1701.6223.6251.0	2	11.69	6.61	80.6	6.23e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
29	064-1601.9709.9709.0	3	11.67	6.48	83.0	1.20e+007	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
30	064-1801.5801.5801.0	3	11.67	11.67	81.6	1.43e+007	(K)INLVPGFETYLGNYR(V)	1755.907
31	064-1801.4134.4134.0	3	11.41	3.59	79.0	1.83e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
32	064-1701.4136.4136.0	2	11.17	4.61	85.7	2.84e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
33	064-1701.4790.4790.0	2	11.17	5.04	88.0	4.85e+007	(R)IGFPIFDR(H)	964.526
34	067-3001.4854.4868.2	2	11.03	3.62	81.6	2.85e+007	(R)IGFPIFDR(H)	964.526
35	063-1201.4147.4147.0	2	10.79	3.18	74.6	1.32e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
36	067-3001.6269.6294.2	2	10.77	10.77	70.6	3.01e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082

37	064-1601.5795.5821.0	2	10.74	3.23	76.0	5.70e+007	(K)INLVPGFETYLGNYR(V)	1755.907
38	064-1801.5803.5838.2	2	10.74	4.98	74.7	4.36e+007	(K)INLVPGFETYLGNYR(V)	1755.907
39	064-1701.5794.5818.0	2	10.71	3.11	73.7	4.86e+007	(K)INLVPGFETYLGNYR(V)	1755.907
40	064-1801.1718.1749.0	2	10.68	5.68	97.7	1.75e+006	(R)IYAGGTSQEEIK(D)	1295.648
41	067-2901.5932.5953.0	2	10.67	3.61	71.2	4.47e+007	(K)INLVPGFETYLGNYR(V)	1755.907
42	064-1601.6216.6252.2	2	10.56	10.56	73.6	8.28e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
43	062-0901.4215.4215.0	2	10.55	5.02	80.8	6.84e+006	(R)ENFEETPSQENIDEVFK(W)	2054.920
44	067-2901.4874.4874.0	2	10.50	4.28	82.2	1.73e+007	(R)IGFPIFDR(H)	964.526
45	064-1801.6238.6244.0	2	10.48	10.48	72.0	6.61e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
46	064-1601.9721.9721.0	3	10.46	4.40	73.4	1.17e+007	(K)DGLQNCNAIYKPDMIAVSTTCMAEVIGDDLNAFITNSK(V)	4075.912
47	067-2801.3739.3743.0	2	10.41	10.41	74.1	5.59e+007	(R)LMQETDYNYDLIR(-)	1673.785
48	067-2801.4583.4594.0	3	10.39	6.50	74.1	6.38e+007	(R)SLVFTNKPDFMIGNSYGK(F)	2018.006
49	062-0901.4642.4642.0	3	10.35	4.40	71.6	2.25e+007	(R)SLVFTNKPDFMIGNSYGK(F)	2018.006
50	064-1801.4844.4844.0	2	10.21	3.90	87.5	3.28e+007	(R)IGFPIFDR(H)	964.526
51	063-1301.6787.6787.0	2	10.11	3.76	80.9	1.88e+007	(K)FSLWGDPDFVMGLTK(F)	1712.836
52	067-2801.6354.6354.2	2	9.53	9.53	68.1	4.65e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
53	067-2901.3740.3764.2	2	9.14	9.14	67.1	4.25e+007	(R)LMQETDYNYDLIR(-)	1673.785
54	064-1601.1720.1724.0	2	9.10	4.66	94.5	1.49e+006	(R)IYAGGTSQEEIK(D)	1295.648
55	062-0801.4220.4220.0	2	8.84	5.28	92.7	6.47e+006	(R)ENFEETPSQENIDEVFK(W)	2054.920
56	064-1701.4129.4129.0	3	8.52	8.52	70.4	2.48e+007	(R)ENFEETPSQENIDEVFK(W)	2054.920
57	067-3001.6313.6313.0	2	7.98	7.98	64.9	1.98e+007	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
58	062-1001.6140.6140.0	2	7.69	2.60	85.2	8.88e+006	(K)DAPNALNTFLVQPWQLNK(T)	2069.082
59	064-1801.1716.1716.0	2	6.25	2.64	100.0	1.42e+006	(R)IYAGGTSQEEIK(D)	1295.648

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	61	8	122.59	25	8.38e+008	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	066-2601.2985.3004.0	3	19.64	8.89	96.6	5.61e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
2	066-2601.7992.7999.0	3	19.22	13.68	94.5	9.24e+006	(R)WFPEAFQTLVENAYPAL(-)	1995.986
3	062-0901.5292.5292.0	3	18.58	13.85	87.1	8.14e+006	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
4	063-1301.2988.2995.0	3	18.53	5.68	93.7	2.01e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
5	062-1001.3094.3105.0	3	18.48	7.02	93.1	1.19e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
6	061-0401.3078.3100.0	3	17.91	10.90	92.3	1.07e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
7	061-0501.5279.5286.0	3	17.68	17.68	88.4	1.16e+007	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
8	061-0601.5944.5969.2	2	17.23	10.88	88.7	9.68e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
9	061-0501.3095.3119.0	3	16.50	7.55	87.4	9.37e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
10	061-0401.5928.5958.3	3	16.28	12.24	91.1	8.89e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
11	061-0501.5940.5977.2	2	16.17	9.15	86.4	1.20e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
12	061-0401.5935.5966.2	2	15.74	9.73	88.8	9.04e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
13	061-0501.5922.5965.3	3	15.42	9.37	87.6	1.35e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
14	061-0601.5937.5943.0	3	15.12	11.03	89.2	8.88e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
15	062-0801.5955.5971.0	3	15.07	9.91	90.1	6.87e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
16	061-0601.5279.5300.0	3	15.00	15.00	78.2	1.09e+007	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959

17	061-0601.5320.5320.0	3	14.43	14.43	84.8	1.05e+007	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
18	066-2401.7999.7999.0	3	14.15	14.15	83.8	5.95e+006	(R)WFPEAFQTLVENAYPAL(-)	1995.986
19	063-1301.6892.6892.0	3	14.14	14.14	73.8	2.92e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
20	062-0901.5943.5943.0	2	14.07	8.32	82.9	8.03e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
21	062-0801.5953.5953.0	2	14.01	8.20	80.9	6.63e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
22	062-1001.5296.5296.0	3	13.81	13.81	88.8	7.55e+006	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
23	061-0501.3102.3102.0	3	13.66	13.66	75.6	8.59e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
24	062-1001.5299.5299.0	3	12.71	12.71	75.0	8.28e+006	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
25	062-0901.5949.5975.0	3	12.61	12.61	81.6	1.01e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
26	061-0401.5274.5274.0	3	12.27	8.80	78.3	7.65e+006	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
27	067-3001.7984.7984.2	2	12.24	7.97	78.3	7.23e+006	(R)WFPEAFQTLVENAYPAL(-)	1995.986
28	066-2601.7008.7008.0	3	12.21	12.21	72.2	5.32e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
29	067-2901.8022.8022.0	2	12.11	8.55	77.8	1.05e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
30	067-2801.8075.8075.2	2	11.90	11.90	75.0	1.12e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
31	062-0801.3327.3363.0	2	11.47	7.20	67.7	1.34e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
32	061-0601.3549.3549.0	3	11.46	11.46	83.6	6.26e+006	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
33	067-2801.7025.7025.0	2	11.38	4.40	76.1	2.00e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
34	062-0901.5304.5304.0	3	11.36	5.61	90.4	8.18e+006	(K)GTNNGVNSISGFASNSANYTPVTEPYLSNPDLQVGGGQIK(S)	4067.959
35	062-0801.5944.5944.0	3	11.34	11.34	73.5	5.40e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
36	066-2401.7951.7951.0	2	10.99	5.15	71.4	1.63e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
37	061-0601.5925.5925.0	2	10.92	4.67	74.9	5.55e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
38	062-1001.5961.5974.0	2	10.90	3.46	76.4	6.92e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
39	061-0401.3851.3851.0	3	10.85	6.68	73.6	6.43e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
40	063-1401.3229.3229.0	2	10.84	7.12	77.8	2.97e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
41	066-2401.6117.6117.0	3	10.84	10.84	75.2	1.91e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
42	061-0601.3337.3366.0	2	10.83	5.04	70.7	1.16e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
43	061-0401.3347.3352.2	2	10.58	5.32	70.7	8.98e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
44	061-0501.6722.6722.0	3	10.41	10.41	72.9	5.69e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
45	066-2401.6104.6104.0	2	10.36	4.91	73.1	2.59e+007	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
46	067-2801.8066.8066.2	2	10.00	10.00	66.7	1.24e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
47	062-0801.5965.5965.0	2	9.87	4.70	70.4	6.29e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
48	066-2401.3209.3209.0	2	9.82	4.20	76.2	3.09e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
49	066-2601.3205.3211.0	2	9.73	6.20	73.1	2.86e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
50	061-0501.3342.3351.2	2	9.58	5.98	67.5	1.03e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
51	063-1201.7865.7865.2	2	9.52	4.49	62.2	1.05e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
52	062-0901.3321.3346.0	2	9.50	4.30	63.7	1.56e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
53	061-0601.5974.5974.0	2	9.34	3.06	74.3	6.82e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
54	067-3001.3244.3244.0	2	9.09	4.48	74.0	2.11e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
55	066-2501.3216.3216.2	2	8.80	4.85	68.9	2.79e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
56	061-0601.6736.6736.0	3	8.17	2.36	77.1	5.81e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
57	063-1301.7860.7860.2	2	7.86	3.46	70.0	1.19e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
58	061-0401.5986.5986.0	2	7.51	2.57	67.4	4.93e+006	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
59	062-1001.3324.3340.0	2	7.51	2.06	62.7	1.12e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
60	066-2401.3241.3241.0	2	6.60	6.60	60.9	3.20e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
61	063-1301.7875.7875.0	2	6.57	6.57	80.1	1.04e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986

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

(#)	(#)	(#)	Peptides (#)	MS/MS Search Score	Coverage	Spectral Intensity	MW (Da)	Accession #	Protein Name
3	3.1	30	9	121.89	30	6.97e+008	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	064-1801.7104.7104.0	3	19.23	13.18	93.0	1.27e+007	(R)EEAEALIQEVLEIYPEK(A)	2003.023
2	064-1801.7448.7495.2	2	16.81	10.55	84.3	2.82e+007	(R)YNIPWMEFNFFGPTR(T)	1918.895
3	064-1701.7488.7518.2	2	16.67	11.12	81.6	4.23e+007	(R)YNIPWMEFNFFGPTR(T)	1918.895
4	064-1601.7130.7143.0	3	16.63	10.61	90.5	1.57e+007	(R)EEAEALIQEVLEIYPEK(A)	2003.023
5	064-1801.6927.6927.0	3	16.62	7.28	91.7	2.29e+007	(K)GISINSECPIGLIGDDIEAVAK(Q)	2214.133
6	064-1601.7480.7529.2	2	15.47	8.44	77.9	4.92e+007	(R)YNIPWMEFNFFGPTR(T)	1918.895
7	064-1701.2759.2769.0	2	15.24	15.24	87.1	9.30e+006	(K)IAEQFDETIQAK(T)	1392.701
8	067-2901.2772.2790.0	2	14.98	14.98	83.0	1.45e+007	(K)IAEQFDETIQAK(T)	1392.701
9	064-1601.6942.6942.0	3	14.26	2.93	76.7	2.18e+007	(K)GISINSECPIGLIGDDIEAVAK(Q)	2214.133
10	064-1601.2750.2757.0	2	14.13	9.68	84.3	8.39e+006	(K)IAEQFDETIQAK(T)	1392.701
11	064-1801.6915.6915.0	3	13.87	2.14	77.7	2.13e+007	(K)GISINSECPIGLIGDDIEAVAK(Q)	2214.133
12	067-3001.7574.7574.0	2	13.68	9.65	82.0	8.57e+006	(R)YNIPWMEFNFFGPTR(T)	1918.895
13	067-2801.2795.2795.2	2	12.81	12.81	74.9	1.03e+007	(K)IAEQFDETIQAK(T)	1392.701
14	064-1801.2759.2764.0	2	12.79	12.79	78.2	8.68e+006	(K)IAEQFDETIQAK(T)	1392.701
15	064-1801.7466.7466.0	2	12.38	7.09	86.8	7.21e+006	(K)EMGNSTLIFDDLTGYEFEEFVR(K)	2612.187
16	062-0901.6880.6880.0	3	12.00	7.74	100.0	1.76e+006	(R)EEAEALIQEVLEIYPEK(A)	2003.023
17	067-2901.5957.6004.0	2	11.84	11.84	72.2	5.94e+007	(K)LVDEIETLFPLNK(G)	1530.842
18	064-1801.6937.6937.0	2	11.64	11.64	75.9	3.03e+007	(K)GISINSECPIGLIGDDIEAVAK(Q)	2214.133
19	067-3001.2768.2772.0	2	11.50	11.50	69.3	9.65e+006	(K)IAEQFDETIQAK(T)	1392.701
20	064-1801.3552.3552.2	2	10.76	10.76	73.9	2.31e+007	(K)DMDMTVNNPCWK(N)	1453.591
21	064-1601.4391.4391.0	2	9.88	9.88	69.7	1.84e+007	(R)VVAQWSGDGTISEMELTPK(V)	2048.001
22	064-1601.5838.5902.2	2	9.54	5.87	71.6	6.46e+007	(K)LVDEIETLFPLNK(G)	1530.842
23	064-1801.7502.7502.0	2	9.50	9.50	100.0	6.45e+006	(K)EMGNSTLIFDDLTGYEFEEFVR(K)	2612.187
24	062-0901.5841.5841.0	2	9.48	4.34	74.3	4.73e+006	(K)LVDEIETLFPLNK(G)	1530.842
25	067-3001.5906.5985.2	2	9.47	6.04	73.5	4.85e+007	(K)LVDEIETLFPLNK(G)	1530.842
26	064-1601.3516.3516.2	2	9.14	9.14	62.4	2.33e+007	(K)DMDMTVNNPCWK(N)	1453.591
27	062-0801.1922.1922.0	3	9.13	9.13	77.7	3.12e+006	(R)GVSQSLGHHIANDSVR(D)	1676.847
28	067-2801.5959.5990.2	2	8.71	4.76	69.6	5.73e+007	(K)LVDEIETLFPLNK(G)	1530.842
29	064-1801.5863.5894.2	2	8.49	5.16	73.1	4.60e+007	(K)LVDEIETLFPLNK(G)	1530.842
30	067-2801.7240.7240.0	2	6.54	6.54	61.0	1.89e+007	(R)EEAEALIQEVLEIYPEK(A)	2003.023

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	50	7	109.26	20	1.34e+009	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	061-0601.4954.4988.0	3	22.91	17.80	98.6	4.79e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	061-0401.4967.4979.0	3	20.72	14.75	95.4	4.78e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
3	062-1001.4959.4998.0	3	20.19	20.19	94.4	3.31e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410

4	066-2401.5035.5041.0	3	19.72	19.72	89.7	6.63e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
5	062-0901.4945.4978.0	3	19.63	15.52	94.4	3.03e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
6	062-0801.4963.5001.0	3	19.55	19.55	93.1	2.74e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
7	063-1301.4961.4992.0	3	18.73	12.46	88.5	5.91e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
8	061-0501.4954.4960.0	3	18.54	14.50	92.3	3.19e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
9	067-3001.5017.5017.0	3	18.10	18.10	87.5	3.76e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
10	061-0601.3635.3660.0	3	17.47	5.89	87.8	8.06e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
11	062-0801.5133.5187.0	3	17.41	8.55	90.2	2.84e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
12	061-0601.4950.4950.0	3	17.38	17.38	84.9	2.94e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
13	063-1301.3482.3494.0	3	17.35	9.69	87.2	2.85e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
14	061-0501.3635.3641.0	3	17.09	9.42	90.2	8.65e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
15	066-2601.5560.5560.3	3	16.84	11.56	85.9	4.34e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
16	061-0501.5428.5467.3	3	16.58	16.58	89.6	2.33e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
17	061-0401.4220.4225.0	3	16.56	8.30	92.3	8.48e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
18	067-3001.5517.5517.0	3	16.44	11.36	87.7	2.60e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
19	061-0401.5438.5438.2	2	16.31	16.31	91.6	7.83e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
20	062-0901.5437.5437.0	3	16.26	9.10	89.5	1.42e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
21	061-0401.5420.5459.3	3	15.88	11.35	88.2	2.39e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
22	066-2601.5034.5038.0	3	15.36	9.82	73.4	6.01e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
23	063-1201.4960.4972.0	3	15.33	15.33	81.6	4.89e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
24	062-0801.5449.5449.0	3	15.32	15.32	85.3	1.03e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
25	061-0401.3641.3646.0	3	15.22	7.94	83.4	7.29e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
26	066-2501.5026.5032.0	3	14.89	14.89	81.0	8.44e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
27	063-1301.3463.3487.0	3	14.86	8.73	80.5	2.55e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
28	061-0601.5432.5438.0	3	14.74	9.04	82.8	2.37e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
29	066-2601.3441.3456.0	3	14.72	3.54	83.2	2.63e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
30	061-0401.5123.5129.0	3	14.71	7.22	87.8	3.50e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
31	063-1401.3480.3480.0	3	13.86	6.22	79.7	1.70e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
32	062-0901.5484.5484.0	3	13.78	13.78	77.3	1.26e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
33	067-2901.5021.5047.0	3	13.61	13.61	75.3	6.18e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
34	062-0901.3627.3627.0	3	13.56	5.89	78.6	6.50e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
35	062-1001.5444.5461.0	3	13.55	9.46	81.9	2.10e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
36	063-1201.3471.3499.0	3	13.36	6.86	76.4	2.41e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
37	061-0601.4229.4232.0	3	12.98	3.77	88.3	1.11e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
38	067-2901.3452.3452.0	3	12.84	5.89	77.4	1.86e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
39	062-1001.5137.5143.0	3	12.61	3.60	82.5	2.52e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
40	062-0801.5005.5005.0	3	12.54	4.10	74.6	1.92e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
41	062-0901.5129.5129.0	3	11.98	7.10	71.7	3.04e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
42	061-0501.5122.5122.0	3	11.92	4.91	82.0	3.30e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
43	062-0901.3623.3623.0	3	11.58	6.60	72.5	6.75e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
44	062-0901.4213.4213.0	3	11.35	5.37	79.0	8.17e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
45	061-0501.4248.4248.0	3	11.34	3.97	83.1	7.28e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
46	061-0401.5015.5015.0	3	11.17	11.17	71.9	3.89e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
47	066-2501.5539.5539.0	3	10.43	7.28	80.4	2.92e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
48	061-0601.6495.6495.0	3	10.17	10.17	90.8	2.40e+006	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
49	062-0801.4224.4224.0	3	10.10	2.08	75.1	8.50e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
50	061-0401.5310.5310.0	2	7.90	3.97	74.1	6.21e+006	(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
5	5.1	14	5	65.10	9	5.60e+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	063-1301.6073.6116.0	3	21.87	15.02	90.0	9.44e+007	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
2	063-1401.6078.6078.0	3	21.01	16.63	96.1	6.37e+007	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
3	063-1201.6062.6098.0	3	20.02	16.08	92.4	8.33e+007	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
4	063-1401.6067.6085.0	3	18.81	15.61	88.7	6.58e+007	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
5	063-1201.6043.6043.0	3	14.87	14.87	79.2	6.12e+007	(R)NATNIVDAVSAEDIGRLPDVTIADSLQR(I)	2953.523
6	063-1201.7705.7705.0	3	13.06	5.81	79.1	2.95e+007	(K)EVLGTLNGEYFLLPASVTSNGLDFTDVPSSMVSGLNVSK(S)	4058.032
7	063-1301.5112.5112.0	3	12.06	5.72	80.5	4.38e+007	(K)ETDPELSALLSWNHDDK(L)	1969.914
8	063-1301.2596.2596.2	2	11.99	11.99	79.2	7.14e+006	(K)TSAFAQANFAK(D)	1155.580
9	063-1401.7721.7733.0	3	11.31	3.15	82.2	1.94e+007	(K)EVLGTLNGEYFLLPASVTSNGLDFTDVPSSMVSGLNVSK(S)	4058.032
10	063-1201.2596.2596.0	2	10.66	10.66	71.6	8.95e+006	(K)TSAFAQANFAK(D)	1155.580
11	063-1301.7712.7735.0	3	10.59	2.61	77.7	2.59e+007	(K)EVLGTLNGEYFLLPASVTSNGLDFTDVPSSMVSGLNVSK(S)	4058.032
12	063-1301.2583.2583.2	2	7.50	7.50	66.5	8.37e+006	(K)TSAFAQANFAK(D)	1155.580
13	063-1401.2598.2598.0	2	6.56	6.56	61.1	8.23e+006	(K)TSAFAQANFAK(D)	1155.580
14	063-1201.3794.3826.0	2	6.12	2.93	60.4	3.98e+007	(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
6	6.1	9	4	56.72	23	2.08e+008	32101.1	PA_Bse08:2503995078	PA_Bse08:2503995078 BS08DRAFT_00035460 nitrogenase iron protein [B. setacea BS08 (Isolate from shipworm g

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	062-1001.4456.4456.0	3	16.88	8.31	87.4	3.79e+007	(R)NTDREDDLIIALAEK(L)	1715.882
2	062-0801.3029.3057.2	2	16.18	16.18	94.0	1.18e+007	(R)MTVIEYDPTAK(Q)	1267.624
3	062-0901.4709.4732.3	3	15.52	9.37	81.2	2.43e+007	(K)STTTQNLVAALAEAGQK(V)	1702.898
4	062-0901.4460.4487.0	3	15.28	5.24	78.7	3.15e+007	(R)NTDREDDLIIALAEK(L)	1715.882
5	062-0801.4467.4520.0	3	15.09	6.27	75.4	3.64e+007	(R)NTDREDDLIIALAEK(L)	1715.882
6	062-1001.3049.3049.2	2	15.03	15.03	91.0	9.12e+006	(R)MTVIEYDPTAK(Q)	1267.624
7	062-1001.4452.4490.0	3	14.06	4.39	74.6	4.22e+007	(R)NTDREDDLIIALAEK(L)	1715.882
8	062-0901.3021.3056.2	2	12.89	12.89	89.0	1.29e+007	(R)MTVIEYDPTAK(Q)	1267.624
9	062-0901.7515.7515.0	3	8.14	8.14	79.7	2.13e+006	(K)AQNTIMEMAAEAGTVEDLELEDVLR(T)	2748.307

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	42	3	55.10	29	4.87e+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	066-2601.5008.5092.2	2	21.00	10.20	100.0	2.68e+008	(K)TVTAMDVVYALK(R)	1310.703
2	067-2901.5007.5096.2	2	21.00	10.16	100.0	3.70e+008	(K)TVTAMDVVYALK(R)	1310.703
3	067-3001.5000.5044.2	2	19.46	10.95	99.0	2.59e+008	(K)TVTAMDVVYALK(R)	1310.703
4	063-1201.4975.5009.2	2	17.87	7.51	96.1	1.01e+008	(K)TVTAMDVVYALK(R)	1310.703
5	064-1801.4983.5007.2	2	17.86	10.70	96.2	8.91e+007	(K)TVTAMDVVYALK(R)	1310.703
6	063-1301.5000.5042.0	2	17.84	9.13	95.6	8.88e+007	(K)TVTAMDVVYALK(R)	1310.703
7	066-2401.4994.4999.2	2	17.80	10.10	94.2	1.55e+008	(K)TVTAMDVVYALK(R)	1310.703
8	063-1201.2873.2898.0	2	17.41	10.14	97.4	2.00e+007	(R)ISGLIYEETR(G)	1180.621
9	063-1401.2887.2903.2	2	17.39	10.58	96.5	1.74e+007	(R)ISGLIYEETR(G)	1180.621
10	067-2801.5019.5091.0	2	17.39	7.63	97.1	3.29e+008	(K)TVTAMDVVYALK(R)	1310.703
11	063-1301.2887.2929.2	2	17.33	11.12	95.0	2.03e+007	(R)ISGLIYEETR(G)	1180.621
12	064-1601.4970.4982.2	2	17.31	9.10	94.6	7.39e+007	(K)TVTAMDVVYALK(R)	1310.703
13	064-1801.2885.2901.2	2	16.84	10.64	95.2	1.85e+007	(R)ISGLIYEETR(G)	1180.621
14	064-1701.4970.5000.2	2	16.81	10.25	95.0	7.70e+007	(K)TVTAMDVVYALK(R)	1310.703
15	066-2501.4995.5086.2	2	16.76	10.27	93.7	3.53e+008	(K)TVTAMDVVYALK(R)	1310.703
16	067-2901.3810.3874.0	2	16.69	7.31	97.4	2.88e+008	(K)VFLENVIR(D)	989.578
17	066-2401.3798.3864.0	2	16.42	7.56	96.6	2.42e+008	(K)VFLENVIR(D)	989.578
18	064-1801.3835.3865.0	2	16.16	6.99	96.0	7.31e+007	(K)VFLENVIR(D)	989.578
19	067-3001.3809.3827.0	2	16.13	6.98	95.0	2.29e+008	(K)VFLENVIR(D)	989.578
20	063-1401.3839.3857.0	2	15.92	5.75	96.4	8.33e+007	(K)VFLENVIR(D)	989.578
21	066-2601.3817.3855.0	2	15.87	6.53	95.0	1.49e+008	(K)VFLENVIR(D)	989.578
22	063-1401.4961.4995.0	2	15.70	8.08	91.8	8.18e+007	(K)TVTAMDVVYALK(R)	1310.703
23	064-1601.3795.3840.0	2	15.13	5.98	94.9	1.01e+008	(K)VFLENVIR(D)	989.578
24	067-2801.3793.3861.0	2	15.13	5.48	95.3	2.25e+008	(K)VFLENVIR(D)	989.578
25	063-1201.3846.3891.0	2	15.12	5.97	94.3	1.05e+008	(K)VFLENVIR(D)	989.578
26	064-1701.3829.3868.0	2	15.08	5.92	93.1	7.23e+007	(K)VFLENVIR(D)	989.578
27	066-2601.2859.2943.0	2	15.01	9.57	86.7	4.11e+007	(R)ISGLIYEETR(G)	1180.621
28	066-2501.5040.5040.0	3	14.88	7.67	86.7	1.70e+007	(K)TVTAMDVVYALK(R)	1310.703
29	064-1601.2866.2888.2	2	14.79	9.07	93.8	1.92e+007	(R)ISGLIYEETR(G)	1180.621
30	067-2801.2864.2896.0	2	14.69	7.45	90.7	6.27e+007	(R)ISGLIYEETR(G)	1180.621
31	067-2901.2872.2903.0	2	14.64	9.00	89.2	4.59e+007	(R)ISGLIYEETR(G)	1180.621
32	066-2501.3804.3831.0	2	14.62	6.27	94.8	2.63e+008	(K)VFLENVIR(D)	989.578
33	063-1301.3848.3854.0	2	14.57	6.01	92.9	9.15e+007	(K)VFLENVIR(D)	989.578
34	067-2801.5040.5040.0	3	14.31	8.14	85.4	1.19e+007	(K)TVTAMDVVYALK(R)	1310.703
35	067-2801.2950.2969.2	2	14.26	8.42	92.7	3.70e+007	(R)ISGLIYEETR(G)	1180.621
36	064-1701.2885.2889.2	2	14.24	8.49	91.9	1.19e+007	(R)ISGLIYEETR(G)	1180.621
37	066-2501.5094.5094.0	2	13.99	6.57	88.2	2.14e+008	(K)TVTAMDVVYALK(R)	1310.703
38	066-2501.2877.2938.0	2	13.63	7.95	89.1	4.36e+007	(R)ISGLIYEETR(G)	1180.621
39	067-3001.2874.2926.0	2	13.09	7.42	88.1	5.38e+007	(R)ISGLIYEETR(G)	1180.621
40	066-2401.2853.2905.0	2	12.36	6.37	82.5	3.60e+007	(R)ISGLIYEETR(G)	1180.621
41	066-2401.2947.2947.2	2	11.73	6.49	83.4	1.57e+007	(R)ISGLIYEETR(G)	1180.621
42	064-1801.2941.2941.0	2	9.47	5.17	65.6	1.27e+007	(R)ISGLIYEETR(G)	1180.621

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	12	3	40.59	28	2.55e+008	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	067-2901.8449.8511.2	2	16.22	13.02	95.5	1.94e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
2	067-3001.8373.8454.2	2	15.75	7.98	95.9	1.70e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
3	067-2801.8476.8509.0	2	14.71	7.78	94.9	2.39e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
4	064-1701.6004.6004.0	2	14.46	10.86	89.3	3.49e+007	(K)YLILGTPTLGEGELPGLSADCEK(E)	2376.201
5	063-1401.8284.8323.0	2	13.74	13.74	87.3	1.44e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
6	064-1701.8323.8397.2	2	13.28	13.28	88.9	2.75e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
7	064-1801.8316.8323.0	2	12.85	6.75	89.8	1.53e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
8	063-1201.6004.6004.2	2	12.46	8.82	81.7	2.19e+007	(K)YLILGTPTLGEGELPGLSADCEK(E)	2376.201
9	063-1301.8287.8317.0	2	12.11	12.11	79.0	1.40e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
10	064-1601.8350.8385.2	2	11.19	11.19	83.9	2.99e+007	(R)LNTWLAQIAPEFGLPI(-)	1782.979
11	067-2801.6153.6153.0	2	10.73	6.48	81.3	1.70e+007	(K)YLILGTPTLGEGELPGLSADCEK(E)	2376.201
12	064-1601.3817.3817.0	2	9.91	9.91	64.1	1.99e+007	(K)IGIFFGSNTGNTR(K)	1383.702

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	66	2	38.88	19	7.37e+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	063-1301.4190.4233.0	2	21.55	17.07	93.6	4.53e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
2	064-1801.4171.4176.0	2	21.23	17.97	96.2	3.74e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
3	063-1201.4186.4225.0	2	20.23	15.53	88.8	5.07e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
4	064-1601.4167.4189.0	2	20.09	14.25	93.7	4.92e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
5	064-1701.4173.4196.0	2	19.00	12.76	92.4	5.53e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
6	063-1401.4191.4221.0	2	18.29	14.24	89.0	5.42e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
7	067-2801.4201.4232.0	2	17.71	14.02	88.3	9.65e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
8	061-0401.4748.4769.3	3	17.33	9.79	88.8	4.61e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
9	062-0901.4742.4806.3	3	16.65	7.94	85.6	6.63e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
10	062-1001.4748.4807.3	3	16.55	7.98	84.6	6.12e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
11	066-2501.4805.4810.0	3	16.13	7.05	85.1	8.41e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
12	064-1701.4716.4727.0	2	15.99	15.99	91.4	6.78e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
13	063-1201.4750.4757.0	2	15.91	15.91	89.8	5.21e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
14	061-0501.4758.4762.2	2	15.37	15.37	88.7	2.13e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
15	063-1401.4718.4747.2	2	15.37	15.37	88.7	6.46e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
16	066-2501.4168.4198.0	3	15.30	8.41	84.1	5.04e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
17	062-1001.4754.4767.2	2	14.94	14.94	89.9	3.55e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
18	062-0801.4761.4767.2	2	14.81	14.81	88.5	3.52e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
19	067-3001.4213.4230.0	2	14.76	14.76	82.5	7.81e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
20	061-0401.4766.4805.2	2	14.72	14.72	86.3	2.81e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
21	064-1601.4704.4725.0	2	14.60	14.60	85.0	6.11e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
22	061-0501.4293.4293.2	2	14.59	14.59	83.7	5.84e+006	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
23	066-2501.4210.4228.2	2	14.54	14.54	79.8	9.62e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
24	064-1701.4147.4202.0	3	14.53	8.84	80.8	3.24e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150

25	061-0501.4746.4751.0	3	14.44	4.90	82.0	3.08e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
26	062-0801.4252.4327.0	3	14.42	7.93	80.4	7.94e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
27	062-0901.4248.4305.0	3	14.33	8.15	78.6	9.54e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
28	062-0901.4747.4764.2	2	14.31	14.31	88.2	4.34e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
29	061-0601.4746.4770.2	2	14.26	14.26	87.3	1.88e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
30	066-2401.4814.4820.3	3	14.22	6.77	77.5	8.71e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
31	067-2901.4186.4215.3	3	13.92	7.28	78.6	4.42e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
32	061-0501.4266.4326.0	3	13.90	6.94	79.9	8.19e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
33	061-0401.4267.4273.0	3	13.88	5.98	77.6	5.46e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
34	061-0601.4271.4274.0	3	13.72	6.99	80.1	6.25e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
35	067-3001.4183.4254.0	3	13.69	7.12	73.4	4.47e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
36	063-1301.4757.4786.3	3	13.68	6.25	78.4	6.62e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
37	063-1301.4743.4778.2	2	13.60	13.60	85.6	6.77e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
38	063-1401.4739.4745.3	3	13.60	5.07	79.2	5.83e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
39	062-1001.4254.4264.0	3	13.57	7.66	82.2	6.69e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
40	062-0801.4737.4789.3	3	13.54	5.80	74.8	5.84e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
41	063-1301.4166.4242.3	3	13.48	6.80	79.4	4.02e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
42	064-1701.4251.4265.0	3	13.39	5.78	80.2	9.74e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
43	067-2901.4790.4824.2	2	13.38	13.38	81.6	9.47e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
44	062-1001.4753.4753.0	3	13.32	7.55	76.3	4.48e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
45	064-1701.4714.4732.0	3	13.20	4.97	79.1	7.98e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
46	066-2401.4192.4223.0	2	12.96	12.96	77.8	7.44e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
47	064-1801.4152.4231.0	3	12.91	6.85	76.8	3.54e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
48	067-3001.4791.4842.2	2	12.68	12.68	78.7	1.06e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
49	066-2401.4178.4263.3	3	12.67	4.92	75.1	4.89e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
50	067-3001.4802.4816.3	3	12.59	5.23	72.1	8.85e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
51	064-1801.4725.4730.0	2	12.48	12.48	83.5	7.00e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
52	061-0601.4742.4755.0	3	12.45	4.61	71.5	2.90e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
53	063-1401.4155.4201.0	3	12.21	5.51	75.4	4.38e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
54	067-2901.4813.4825.3	3	12.16	5.85	77.4	8.68e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
55	067-2801.4824.4867.2	2	12.07	12.07	78.3	1.43e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
56	063-1201.4156.4239.3	3	11.97	3.50	77.9	3.69e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
57	066-2501.4799.4814.2	2	11.91	11.91	75.6	8.49e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
58	064-1601.4720.4738.3	3	11.87	5.24	74.9	7.31e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
59	066-2401.4798.4833.2	2	11.85	11.85	75.9	1.06e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
60	062-0901.4273.4273.0	2	11.67	7.03	78.7	7.15e+006	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
61	066-2601.4815.4875.2	2	11.37	11.37	75.6	1.10e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
62	067-2901.4200.4243.2	2	11.37	11.37	71.5	8.75e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
63	061-0401.4319.4319.2	2	7.43	7.43	77.8	3.32e+006	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
64	062-1001.4730.4730.0	2	6.87	6.87	65.0	2.26e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
65	066-2601.4892.4892.0	2	6.81	6.81	68.0	5.15e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
66	066-2601.4254.4254.2	2	6.45	6.45	60.5	7.30e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150

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	24	2	36.10	41	2.43e+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	067-2801.7242.7334.3	3	21.26	12.48	95.8	3.87e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
2	067-2801.7358.7361.3	3	20.72	15.05	95.5	2.75e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
3	063-1301.7113.7163.3	3	20.26	12.53	95.9	1.45e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
4	066-2501.7229.7305.3	3	20.26	11.09	96.1	1.89e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
5	063-1201.7110.7114.0	3	20.17	12.41	95.3	9.38e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
6	067-3001.7192.7273.3	3	19.67	11.63	94.4	3.21e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
7	063-1401.7126.7198.0	3	19.62	11.61	93.4	1.45e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
8	066-2601.7230.7295.3	3	19.18	10.50	94.7	1.68e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
9	066-2401.7338.7338.0	3	19.14	19.14	95.1	1.87e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
10	066-2401.7208.7285.3	3	17.70	11.89	86.2	2.06e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
11	066-2401.10135.10135.2	2	14.84	14.84	81.2	4.91e+006	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
12	067-3001.7186.7274.2	2	14.11	7.23	89.2	1.56e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
13	067-3001.7335.7335.2	2	13.98	8.01	85.5	1.06e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
14	066-2401.7202.7283.2	2	13.66	7.98	89.8	8.87e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
15	067-2801.7238.7335.2	2	13.65	6.45	89.6	1.67e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
16	066-2501.7242.7306.2	2	13.60	6.26	88.2	6.71e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
17	067-2901.7264.7336.2	2	13.06	5.11	87.4	7.08e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
18	063-1301.7122.7145.2	2	12.57	6.51	86.2	8.23e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
19	066-2501.10174.10174.2	2	11.69	11.69	76.1	8.49e+006	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
20	066-2601.7226.7296.2	2	11.46	3.50	84.5	6.25e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
21	063-1201.7201.7201.2	2	10.92	4.71	74.9	2.63e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
22	063-1401.7142.7207.2	2	10.85	3.95	81.0	3.92e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
23	067-2801.7257.7362.2	2	10.45	2.31	84.3	1.87e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
24	063-1201.7132.7156.2	2	8.61	2.76	72.1	4.29e+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
11	11.1	3	2	30.36	45	1.14e+008	11693.1	PA_Bse_meta_comb:2073580990	PA_Bse_meta_comb:2073580990 BaSeMet_00246460 ATP:guanido phosphotransferase, C-terminal cat

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	064-1601.5776.5776.0	3	17.93	12.53	89.2	3.59e+007	(K)DLFNLVIQDYHAGDPSGCVK(H)	2191.049
2	064-1801.5762.5769.0	3	16.71	16.71	87.6	2.76e+007	(K)DLFNLVIQDYHAGDPSGCVK(H)	2191.049
3	064-1601.5591.5600.0	3	12.43	6.84	73.6	5.08e+007	(K)HPEPSFGTDAEIDSLGDLDPTGQFVVSTR(V)	3087.455

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	9	2	28.04	8	8.59e+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	064-1801.9174.9191.2	2	16.14	9.34	86.6	8.38e+006	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110

2	064-1601.9197.9243.3	3	13.53	8.49	71.6	1.19e+007	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
3	064-1601.9200.9200.2	2	13.31	8.10	85.0	1.40e+007	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
4	064-1701.9194.9216.2	2	13.18	7.26	88.2	1.08e+007	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
5	064-1601.9195.9195.0	2	12.51	6.71	83.2	1.37e+007	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
6	064-1601.2730.2730.0	3	11.90	11.90	71.5	4.43e+006	(R)GITIATSHVEYDSPSR(H)	1732.851
7	064-1601.9212.9212.0	3	11.32	11.32	75.9	9.57e+006	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
8	064-1701.9221.9227.0	3	11.10	11.10	75.3	7.63e+006	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110
9	064-1801.9172.9172.0	3	10.64	6.27	76.0	5.53e+006	(R)AIDLPFLMPIEDVFSISGR(G)	2120.110

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	7	2	28.02	8	1.70e+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	064-1801.2130.2135.0	3	15.54	15.54	82.9	7.39e+006	(K)YDSTHGQFNGDVEVK(D)	1695.762
2	064-1601.2129.2156.0	3	15.29	15.29	81.3	1.32e+007	(K)YDSTHGQFNGDVEVK(D)	1695.762
3	064-1701.2148.2154.0	3	13.97	13.97	78.7	1.08e+007	(K)YDSTHGQFNGDVEVK(D)	1695.762
4	064-1601.4453.4467.2	2	12.48	9.04	78.3	4.02e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
5	064-1701.4466.4488.0	2	11.34	11.34	71.9	4.29e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
6	064-1701.4483.4483.0	2	11.01	11.01	71.1	2.80e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
7	064-1801.4479.4479.2	2	6.86	6.86	63.5	2.78e+007	(R)VPTPDVSVVDLTVR(L)	1496.832

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
14	14.1	5	2	27.69	16	9.19e+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	063-1401.8671.8713.0	3	16.27	8.91	85.3	2.24e+007	(R)GEPAEFPVGSLIPGWVEALQLMPVGSK(W)	2808.465
2	063-1301.8673.8734.0	3	16.21	8.31	84.7	2.53e+007	(R)GEPAEFPVGSLIPGWVEALQLMPVGSK(W)	2808.465
3	063-1201.8669.8710.0	3	14.74	5.63	84.0	3.41e+007	(R)GEPAEFPVGSLIPGWVEALQLMPVGSK(W)	2808.465
4	063-1301.2805.2805.0	2	11.42	11.42	74.3	5.01e+006	(R)GANLAGDEFDSSYER(G)	1630.699
5	063-1401.8716.8716.0	2	6.37	2.05	92.2	5.10e+006	(R)GEPAEFPVGSLIPGWVEALQLMPVGSK(W)	2808.465

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	2	26.69	8	1.40e+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	067-3001.7840.7843.0	3	18.17	18.17	88.1	1.06e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
2	067-2901.7903.7920.0	3	17.18	17.18	87.8	1.60e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085

3	067-2901.7890.7950.2	2	15.74	10.70	89.3	2.41e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
4	067-2801.7934.7976.2	2	15.70	9.83	88.2	2.55e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
5	067-3001.7851.7887.2	2	14.67	9.62	87.2	1.95e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
6	067-2801.7922.7966.0	3	13.94	13.94	76.7	2.04e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
7	067-2901.7959.7959.2	2	10.12	5.80	76.1	1.52e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
8	067-3001.2827.2827.0	3	8.52	8.52	76.4	8.94e+006	(R)GITIATSHVEYDSPER(H)	1774.861

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	2	26.02	2	3.35e+007	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	063-1401.2127.2156.0	3	15.76	10.74	89.4	4.23e+006	(K)NDPDHFSAEGSGAVVR(G)	1657.757
2	063-1301.2148.2155.0	3	15.02	8.89	87.3	3.79e+006	(K)NDPDHFSAEGSGAVVR(G)	1657.757
3	063-1201.2136.2136.0	3	10.94	10.94	81.0	4.37e+006	(K)NDPDHFSAEGSGAVVR(G)	1657.757
4	063-1301.2364.2364.0	2	10.26	5.27	81.1	5.45e+006	(K)TEMQISEDGYTQGR(S)	1614.707
5	063-1201.2369.2369.2	2	9.75	9.75	67.6	5.61e+006	(K)TEMQISEDGYTQGR(S)	1614.707
6	063-1301.2355.2355.2	2	7.93	7.93	73.3	4.99e+006	(K)TEMQISEDGYTQGR(S)	1614.707
7	063-1301.2346.2346.0	2	7.50	7.50	63.5	5.02e+006	(K)TEMQISEDGYTQGR(S)	1614.707

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	2	2	26.00	11	1.94e+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	063-1201.2763.2767.2	2	17.53	17.53	90.3	6.45e+006	(K)EGVVVAESGSGLQYK(I)	1522.775
2	063-1401.2742.2742.0	2	8.47	8.47	73.1	1.29e+007	(R)GTTLDGEEFDSSYSR(G)	1663.709

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	1	20.32	8	6.40e+007	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	067-2901.8978.9000.0	3	20.32	10.09	96.0	9.96e+006	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
2	067-3001.8920.8920.0	3	15.61	8.00	83.5	6.42e+006	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
3	067-2801.9008.9008.0	3	14.77	7.67	85.3	1.56e+007	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
4	067-2801.9003.9003.0	3	14.46	9.33	89.5	1.35e+007	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
5	067-3001.8959.8959.0	3	12.55	7.17	77.2	5.64e+006	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
6	067-3001.8926.8926.0	3	10.60	3.78	89.5	6.76e+006	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595
7	067-2901.8967.8967.0	3	9.26	4.89	83.4	6.09e+006	(R)IAGGEMLGQDQPIILQMLEISPALEALK(G)	2978.595

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	2	2	20.31	10	1.04e+007	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	061-0501.3207.3207.0	3	11.76	11.76	75.4	5.07e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
2	061-0401.3686.3686.0	2	8.55	8.55	76.2	5.32e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
20	20.1	2	1	20.24	43	2.07e+007	8413.8	PA_Bse_meta_comb:2073579231	PA_Bse_meta_comb:2073579231 BaSeMet_00228870 Histones H3 and H4 [Bankia setacea microbiome

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	066-2401.9615.9623.5	5	20.24	5.36	91.5	2.45e+006	(R)FQSSAVLALQEASEAYLVGLFEDTNLCAIHAK(R)	3438.726
2	066-2501.10157.10157.0	3	14.27	14.27	74.1	1.82e+007	(R)FQSSAVLALQEASEAYLVGLFEDTNLCAIHAK(R)	3438.726