Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\030411_OGL_Gill2_pass1/030411_OGL_GILL2-PASS1
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 140 **Hits:** 354
Data Directory: msdataSM\030511_OGL_Gill2_pass23
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 298 **Hits:** 758
beginning to assemble proteins .... proteins assembled 0.172291 sec
proteins filtered by unique peptides 0.015863 sec
proteins filtered by score
calculated protein coverage maps 0.066972 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.023253 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 32 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	69	10	162.63	33	1.51e+010	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]
1	1.1	31	4	67.64	13	8.77e+009	57219.5	PA_Bse08:2503995261	PA_Bse08:2503995261 BS08DRAFT_00037250 chaperonin GroL [B. setacea BS08 (Isolate from shipw
1	1.1	18	2	32.05	6	3.95e+009	57147.5	PA_Bse02:2503998519	PA_Bse02:2503998519 BS02DRAFT_00025680 chaperonin GroL [B. setacea BS02 (Isolate from shipw
1	1.1	18	2	32.05	6	3.95e+009	55514.7	PA_Bse_meta_comb:2073565377	PA_Bse_meta_comb:2073565377 BaSeMet_00090330 chaperonin GroL [Bankia setacea microbiome (
1	1.1	5	2	25.67	6	2.12e+007	57360.8	PA_Bse_meta_comb:2073567036	PA_Bse_meta_comb:2073567036 BaSeMet_00106920 chaperonin GroL [Bankia setacea microbiome (
1	1.1	5	2	25.67	6	2.12e+007	57128.5	PA_BS12:2189568147	PA_BS12:2189568147 or1478 Chaperonin GroEL (HSP60 family) [B. setacea BS12] 549 bp
2	2.1	29	9	109.20	32	7.18e+009	52481.4	PA_BSC2:2534576897	PA_BSC2:2534576897 Bsc2_04586 pyruvate kinase (EC 2.7.1.40) [Alteromonadacea bacterium Bsc2]
2	2.1	29	9	109.20	32	7.18e+009	52481.4	PA_Bse_meta_comb:2073595609	PA_Bse_meta_comb:2073595609 BaSeMet_00392650 pyruvate kinase (EC 2.7.1.40) [Bankia setacea n
2	2.1	15	4	50.87	14	3.90e+009	51344.1	PA_Bse08:2503997695	PA_Bse08:2503997695 pyruvate kinase [B. setacea BS08 (Isolate from shipworm gill tissue)]
2	2.1	8	3	34.16	12	2.47e+009	52516.3	PA_Bse_meta_comb:2073595711	PA_Bse_meta_comb:2073595711 BaSeMet_00393670 pyruvate kinase (EC 2.7.1.40) [Bankia setacea n
2	2.1	8	3	34.16	12	2.47e+009	52055.7	PA_BS12:2189571918	PA_BS12:2189571918 or1025 Pyruvate kinase [B. setacea BS12] 482 bp
3	3.1	37	4	68.21	15	1.52e+010	44282.5	PA_BSC2:2534573496	PA_BSC2:2534573496 Bsc2_01181 translation elongation factor 1A (EF-1A/EF-Tu) [Alteromonadacea b
3	3.1	37	4	68.21	15	1.52e+010	44282.5	PA_Bse_meta_comb:2073587015	PA_Bse_meta_comb:2073587015 BaSeMet_00306710 translation elongation factor 1A (EF-1A/EF-Tu) [
4	4.1	15	5	63.66	24	5.16e+009	45984.9	PA_Bse_meta_comb:2073595342	PA_Bse_meta_comb:2073595342 BaSeMet_00389980 Capsid protein (F protein). [Bankia setacea micr
5	5.1	12	4	61.60	38	3.75e+009	12099.0	PA_BSC2:2534574907	PA_BSC2:2534574907 Bsc2_02594 nitrogen regulatory protein P-II family [Alteromonadacea bacterium
5	5.1	12	4	61.60	38	3.75e+009	12099.0	PA_Bse_meta_comb:2073591701	PA_Bse_meta_comb:2073591701 BaSeMet_00353570 nitrogen regulatory protein P-II [Bankia setacea
5	5.1	12	4	61.60	39	3.75e+009	11726.4	PA_Bse_meta_comb:2073579200	PA_Bse_meta_comb:2073579200 BaSeMet_00228560 nitrogen regulatory protein P-II [Bankia setacea
5	5.1	9	3	45.51	28	2.73e+009	12111.0	PA_BS12:2189569075	PA_BS12:2189569075 or2390 Nitrogen regulatory protein PII [B. setacea BS12] 112 bp
5	5.1	9	3	45.51	28	2.73e+009	12111.0	PA_Bse_meta_comb:2073596293	PA_Bse_meta_comb:2073596293 BaSeMet_00399490 nitrogen regulatory protein P-II [Bankia setacea
5	5.1	9	3	45.51	28	2.73e+009	12099.0	PA_Bse02:2503998071	PA_Bse02:2503998071 BS02DRAFT_00012490 Nitrogen regulatory protein P-II. [B. setacea BS02 (Isol
5	5.1	9	3	45.51	28	2.73e+009	12099.0	PA_Bse_meta_comb:2073590737	PA_Bse_meta_comb:2073590737 BaSeMet_00343930 nitrogen regulatory protein P-II [Bankia setacea
6	6.1	6	4	59.77	47	2.09e+009	22353.9	PA_Bse_meta_comb:2073589276	PA_Bse_meta_comb:2073589276 BaSeMet_00329320 FKBP-type peptidyl-prolyl cis-trans isomerases 1
6	6.1	5	3	46.34	33	1.96e+009	22339.9	PA_BSC2:2534573752	PA_BSC2:2534573752 Bsc2_01438 FKBP-type peptidyl-prolyl cis-trans isomerases 1 [Alteromonadacea
7	7.1	17	4	57.02	22	2.38e+009	38663.6	PA_BSC2:2534576404	PA_BSC2:2534576404 Bsc2_04093 3-isopropylmalate dehydrogenase (EC 1.1.1.85) [Alteromonadacea
7	7.1	17	4	57.02	22	2.38e+009	38663.6	PA_Bse_meta_comb:2073570441	PA_Bse_meta_comb:2073570441 BaSeMet_00140970 3-isopropylmalate dehydrogenase (EC 1.1.1.85)
7	7.1	11	3	40.75	60	9.77e+008	10618.1	PA_BSC2:2534576487	PA_BSC2:2534576487 Bsc2_04176 Isocitrate/isopropylmalate dehydrogenase [Alteromonadacea bacte
8	8.1	15	4	56.30	20	3.36e+009	33705.4	PA_BSC2:2534576639	PA_BSC2:2534576639 Bsc2_04328 transaldolase (EC 2.2.1.2) [Alteromonadacea bacterium Bsc2]
8	8.1	15	4	56.30	20	3.36e+009	33675.4	PA_Bse_meta_comb:2073570868	PA_Bse_meta_comb:2073570868 BaSeMet_00145240 transaldolase (EC 2.2.1.2) [Bankia setacea micr
8	8.1	8	2	30.84	9	2.04e+009	34007.6	PA_BS12:2189567864	PA_BS12:2189567864 or1190 Transaldolase [B. setacea BS12] 311 bp
8	8.1	8	2	30.84	9	2.04e+009	33949.6	PA_Bse_meta_comb:2073584304	PA_Bse_meta_comb:2073584304 BaSeMet_00279600 transaldolase (EC 2.2.1.2) [Bankia setacea micr
8	8.1	8	2	30.84	9	2.04e+009	33845.5	PA_Bse08:2503994737	PA_Bse08:2503994737 BS08DRAFT_00032510 transaldolase [B. setacea BS08 (Isolate from shipworm
9	9.1	32	3	55.85	29	2.38e+010	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom

10	10.1	8	3	51.81	13	7.46e+008	38937.1	PA_BSC2:2534573407	PA_BSC2:2534573407 Bsc2_01092 fructose-bisphosphate aldolase (EC 4.1.2.13) [Alteromonadacea ba
10	10.1	8	3	51.81	13	7.46e+008	38921.1	PA_Bse_meta_comb:2073595811	PA_Bse_meta_comb:2073595811 BaSeMet_00394670 fructose-bisphosphate aldolase (EC 4.1.2.13) [B
11	11.1	7	3	49.46	16	1.20e+009	35299.3	PA_BSC2:2534572582	PA_BSC2:2534572582 Bsc2_00266 malate dehydrogenase [Alteromonadacea bacterium Bsc2]
11	11.1	7	3	49.46	16	1.20e+009	35299.3	PA_Bse_meta_comb:2073561056	PA_Bse_meta_comb:2073561056 BaSeMet_00047120 malate dehydrogenase (NAD) (EC 1.1.1.37) [Ba
11	11.1	6	2	38.28	11	1.06e+009	35386.5	PA_BS12:2189571789	PA_BS12:2189571789 or0889 Malate/lactate dehydrogenases [B. setacea BS12] 327 bp
11	11.1	6	2	38.28	11	1.06e+009	35354.4	PA_Bse_meta_comb:2073574964	PA_Bse_meta_comb:2073574964 BaSeMet_00186200 malate dehydrogenase (NAD) (EC 1.1.1.37) [Ba
12	12.1	5	3	46.50	6	8.18e+007	78518.0	PA_Bse02:2503998694	PA_Bse02:2503998694 BS02DRAFT_00016310 type IV pilus secretin (or competence protein) PilQ [B. s
12	12.1	5	3	46.50	6	8.18e+007	78518.0	PA_Bse_meta_comb:2073578282	PA_Bse_meta_comb:2073578282 BaSeMet_00219380 type IV pilus secretin (or competence protein) Pi
12	12.1	3	2	28.54	28	4.39e+007	14422.5	PA_Bse_meta_comb:2073571049	PA_Bse_meta_comb:2073571049 BaSeMet_00147050 Type II secretory pathway, component HofQ [Ba
13	13.1	7	3	44.40	50	6.57e+009	9105.4	PA_BSC2:2534572633	PA_BSC2:2534572633 Bsc2_00317 Bacterial nucleoid DNA-binding protein [Alteromonadacea bacteriur
13	13.1	7	3	44.40	50	6.57e+009	9105.4	PA_Bse_meta_comb:2073595431	PA_Bse_meta_comb:2073595431 BaSeMet_00390870 bacterial nucleoid protein HU beta subunit [Bank
13	13.1	4	2	25.62	34	2.32e+009	9164.5	PA_Bse08:2503994572	PA_Bse08:2503994572 BS08DRAFT_00030860 Bacterial DNA-binding protein. [B. setacea BS08 (Isolat
13	13.1	4	2	25.62	34	2.32e+009	9107.5	PA_BS12:2189570079	PA_BS12:2189570079 or3306 Bacterial nucleoid DNA-binding protein [B. setacea BS12] 90 bp
13	13.1	4	2	25.62	34	2.32e+009	9075.4	PA_Bse_meta_comb:2073588110	PA_Bse_meta_comb:2073588110 BaSeMet_00317660 bacterial nucleoid protein HU beta subunit [Bank
14	14.1	8	4	43.79	14	4.76e+008	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
14	14.1	8	4	43.79	25	4.76e+008	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
15	15.1	62	2	39.48	19	2.88e+010	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
16	16.1	9	3	37.08	13	2.71e+009	51876.6	PA_BSC2:2534574029	PA_BSC2:2534574029 Bsc2_01715 glutamine synthetase, type I [Alteromonadacea bacterium Bsc2]
16	16.1	9	3	37.08	14	2.71e+009	48220.4	PA_Bse_meta_comb:2073598029	PA_Bse_meta_comb:2073598029 BaSeMet_00416850 L-glutamine synthetase (EC 6.3.1.2) [Bankia set
16	16.1	3	2	22.98	8	4.75e+008	51644.4	PA_BS12:2189570461	PA_BS12:2189570461 or3700 Glutamine synthetase [B. setacea BS12] 468 bp
16	16.1	3	2	22.98	8	4.75e+008	51644.4	PA_Bse_meta_comb:2073593800	PA_Bse_meta_comb:2073593800 BaSeMet_00374560 L-glutamine synthetase (EC 6.3.1.2) [Bankia set
17	17.1	9	3	36.91	21	5.46e+008	17704.7	PA_BSC2:2534573498	PA_BSC2:2534573498 Bsc2_01183 SSU ribosomal protein S7P [Alteromonadacea bacterium Bsc2]
17	17.1	9	3	36.91	21	5.46e+008	17704.7	PA_Bse_meta_comb:2073587017	PA_Bse_meta_comb:2073587017 BaSeMet_00306730 SSU ribosomal protein S7P [Bankia setacea mic
17	17.1	8	2	26.06	19	4.99e+008	17585.6	PA_BS12:2189570753	PA_BS12:2189570753 or3998 Ribosomal protein S7 [B. setacea BS12] 156 bp
17	17.1	8	2	26.06	19	4.99e+008	17585.6	PA_Bse_meta_comb:2073563150	PA_Bse_meta_comb:2073563150 BaSeMet_00068060 SSU ribosomal protein S7P [Bankia setacea mic
18	18.1	11	2	34.85	41	4.47e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
19	19.1	6	2	34.39	16	6.48e+008	16139.8	PA_BSC2:2534574197	PA_BSC2:2534574197 Bsc2_01883 cyanate hydratase [Alteromonadacea bacterium Bsc2]
19	19.1	6	2	34.39	16	6.48e+008	16139.8	PA_Bse_meta_comb:2073567349	PA_Bse_meta_comb:2073567349 BaSeMet_00110050 cyanate hydratase [Bankia setacea microbiome
20	20.1	4	3	33.54	11	6.22e+008	49992.5	PA_Bse_meta_comb:2073595049	PA_Bse_meta_comb:2073595049 BaSeMet_00387050 D-glucuronate isomerase (EC 5.3.1.12) [Bankia
20	20.1	3	2	20.15	7	4.90e+008	53697.7	PA_BSC2:2534573486	PA_BSC2:2534573486 Bsc2_01171 D-glucuronate isomerase (EC 5.3.1.12) [Alteromonadacea bacteriu
21	21.1	6	2	29.82	8	1.07e+009	37181.7	PA_BSC2:2534573415	PA_BSC2:2534573415 Bsc2_01100 UDP-glucose pyrophosphorylase (EC 2.7.7.9) [Alteromonadacea ba
21	21.1	6	2	29.82	9	1.07e+009	30163.7	PA_Bse_meta_comb:2073567499	PA_Bse_meta_comb:2073567499 BaSeMet_00111550 UDP-glucose pyrophosphorylase (EC 2.7.7.9) [E
22	22.1	2	2	28.99	9	2.72e+008	38327.9	PA_Bse_meta_comb:2073590044	PA_Bse_meta_comb:2073590044 BaSeMet_00337000 phosphate ABC transporter substrate-binding pr
22	22.1	2	2	28.99	9	2.72e+008	37743.4	PA_BSC2:2534574320	PA_BSC2:2534574320 Bsc2_02006 phosphate ABC transporter substrate-binding protein, PhoT family (
23	23.1	3	2	28.11	2	4.60e+008	118803.8	PA_BSC2:2534573281	PA_BSC2:2534573281 Bsc2_00965 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]
23	23.1	3	2	28.11	2	4.60e+008	118803.8	PA_Bse_meta_comb:2073587930	PA_Bse_meta_comb:2073587930 BaSeMet_00315860 TonB-dependent receptor [Bankia setacea micro
24	24.1	12	2	26.89	30	5.59e+009	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome
25	25.1	5	2	26.15	4	4.63e+008	43102.8	PA_Bse_meta_comb:2073591868	PA_Bse_meta_comb:2073591868 BaSeMet_00355240 2-oxoglutarate dehydrogenase E2 component (E
25	25.1	5	2	26.15	4	4.63e+008	42998.6	PA_BSC2:2534576536	PA_BSC2:2534576536 Bsc2_04225 2-oxoglutarate dehydrogenase E2 component (EC 2.3.1.61) [Altero
26	26.1	14	2	25.24	8	1.46e+009	36105.1	PA_BS12:2189567940	PA_BS12:2189567940 or1263 Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate deh
26	26.1	14	2	25.24	8	1.46e+009	36105.1	PA_Bse_meta_comb:2073595898	PA_Bse_meta_comb:2073595898 BaSeMet_00395540 glyceraldehyde-3-phosphate dehydrogenase, typ
27	27.1	4	2	24.52	7	1.39e+008	41997.7	PA_BSC2:2534576868	PA_BSC2:2534576868 Bsc2_04557 Phosphoglycerate dehydrogenase and related dehydrogenases [Alt
27	27.1	4	2	24.52	7	1.39e+008	41997.7	PA_Bse_meta_comb:2073556947	PA_Bse_meta_comb:2073556947 BaSeMet_00006030 D-3-phosphoglycerate dehydrogenase (EC 1.1.1
28	28.1	2	2	22.35	27	2.06e+008	19039.9	PA_BSC2:2534573441	PA_BSC2:2534573441 Bsc2_01126 LSU ribosomal protein L6P [Alteromonadacea bacterium Bsc2]
28	28.1	2	2	22.35	27	2.06e+008	19039.9	PA_Bse_meta_comb:2073591310	PA_Bse_meta_comb:2073591310 BaSeMet_00349660 LSU ribosomal protein L6P [Bankia setacea mic
29	29.1	3	2	22.07	8	7.21e+007	36669.8	PA_BSC2:2534573291	PA_BSC2:2534573291 Bsc2_00976 ketol-acid reductoisomerase (EC 1.1.1.86) [Alteromonadacea bacte
29	29.1	3	2	22.07	8	7.21e+007	36669.8	PA_Bse_meta_comb:2073590205	PA_Bse_meta_comb:2073590205 BaSeMet_00338610 ketol-acid reductoisomerase (EC 1.1.1.86) [Bank
30	30.1	14	1	21.50	10	1.30e+009	12588.4	PA_BSC2:2534573502	PA_BSC2:2534573502 Bsc2_01187 LSU ribosomal protein L12P [Alteromonadacea bacterium Bsc2]

30	30.1	14	1	21.50	10	1.30e+009	12588.4	PA_Bse_meta_comb:2073587021	PA_Bse_meta_comb:2073587021 BaSeMet_00306770 LSU ribosomal protein L12P [Bankia setacea mi
31	31.1	2	2	20.22	5	4.75e+008	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 b
31	31.1	2	2	20.22	9	4.75e+008	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
32	32.1	3	2	20.01	10	5.36e+008	27993.3	PA_BSC2:2534573471	PA_BSC2:2534573471 Bsc2_01156 Dehydrogenases with different specificities (related to short-chain a
Totals:	910	241							

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	69	10	162.63	33	1.51e+010	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	006-0901.4232.4280.2	2	21.50	15.53	100.0	1.58e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
2	006-0902.4212.4237.2	2	20.41	20.41	98.7	1.24e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
3	005-0801.4335.4373.2	2	20.28	17.16	97.1	4.21e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
4	005-0802.4346.4427.2	2	20.25	20.25	96.5	5.37e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
5	005-0802.4946.4974.0	2	19.63	12.85	97.9	3.27e+008	(K)MLAGVNVLADAVK(I)	1300.730
6	006-0902.4788.4793.0	2	19.57	12.05	96.6	6.13e+007	(K)MLAGVNVLADAVK(I)	1300.730
7	005-0801.4920.4957.0	2	19.52	13.39	95.9	4.63e+008	(K)MLAGVNVLADAVK(I)	1300.730
8	006-0901.5110.5154.0	2	19.05	12.30	96.4	1.75e+008	(K)MLAGVNVLADAVK(I)	1300.730
9	005-0801.2747.2788.0	2	18.31	11.98	96.2	2.78e+008	(R)QIVTNAGDEASVIAEK(V)	1644.844
10	005-0801.2757.2769.0	2	18.27	11.71	95.3	5.59e+007	(R)QIVTNAGDEASVIAEK(V)	1644.844
11	005-0802.2774.2774.3	3	17.88	17.88	89.5	7.31e+006	(R)QIVTNAGDEASVIAEK(V)	1644.844
12	005-0802.3490.3511.0	2	17.31	13.08	91.0	1.38e+008	(K)EISVIVDGAGSAEDIK(A)	1602.823
13	006-0901.6560.6560.0	2	17.08	10.63	90.8	7.26e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
14	006-0901.4757.4809.2	2	16.97	10.00	87.1	1.44e+008	(K)MLAGVNVLADAVK(I)	1300.730
15	006-0901.2793.2810.0	2	16.54	9.65	90.7	3.31e+007	(R)QIVTNAGDEASVIAEK(V)	1644.844
16	005-0802.6764.6764.0	2	16.18	10.09	84.3	1.13e+008	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
17	005-0802.2758.2806.0	2	16.11	10.23	93.3	1.02e+008	(R)QIVTNAGDEASVIAEK(V)	1644.844
18	005-0801.5018.5055.2	2	16.05	8.30	87.6	1.37e+009	(K)MLAGVNVLADAVK(I)	1300.730
19	006-0901.2785.2827.0	2	15.92	9.49	89.1	1.18e+008	(R)QIVTNAGDEASVIAEK(V)	1644.844
20	005-0802.6736.6802.0	3	15.81	10.37	82.4	4.88e+008	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
21	005-0801.5760.5803.0	2	15.62	7.19	91.6	3.40e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
22	006-0902.2797.2802.0	2	15.36	7.32	86.0	2.80e+007	(R)QIVTNAGDEASVIAEK(V)	1644.844
23	005-0802.3526.3526.2	2	15.19	10.73	89.0	1.36e+008	(K)EISVIVDGAGSAEDIK(A)	1602.823
24	005-0801.4475.4475.2	2	15.16	10.15	86.3	9.32e+008	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
25	005-0801.1697.1726.0	2	14.97	14.97	90.1	7.80e+006	(K)VGAATEVEMK(E)	1034.519
26	005-0802.5726.5780.0	2	14.94	8.17	87.8	4.06e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
27	006-0901.6432.6502.0	3	14.32	8.46	82.4	1.81e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
28	005-0802.3985.4028.2	2	14.09	6.92	92.3	3.64e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
29	005-0802.6782.6782.0	2	13.92	8.37	81.8	1.05e+008	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
30	006-0901.3573.3609.0	2	13.86	8.96	85.2	1.80e+008	(K)EISVIVDGAGSAEDIK(A)	1602.823
31	006-0901.6538.6546.0	3	13.84	7.45	77.0	1.42e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
32	005-0801.5997.6022.0	3	13.58	7.57	77.7	9.98e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
33	006-0902.5397.5397.0	2	13.46	5.91	85.3	2.02e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
34	006-0901.3495.3503.2	2	13.43	9.49	85.4	4.83e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823

35	005-0801.7096.7170.0	3	13.42	13.42	80.3	1.12e+009	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
36	006-0901.5322.5353.2	2	12.86	3.31	90.3	1.68e+008	(R)ELLPVLETVAK(A)	1211.725
37	005-0801.6007.6007.2	2	12.73	7.06	85.1	4.50e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
38	006-0901.6069.6069.0	3	12.68	7.31	75.5	6.33e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
39	007-1001.4910.4938.0	2	12.58	2.23	89.9	1.64e+007	(R)ELLPVLETVAK(A)	1211.725
40	005-0801.5752.5752.0	3	12.56	12.56	76.9	5.67e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
41	006-0902.4926.4998.2	2	12.37	2.77	90.6	8.05e+007	(R)ELLPVLETVAK(A)	1211.725
42	005-0801.3466.3466.0	2	12.30	8.13	80.9	8.26e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823
43	006-0901.5446.5446.0	2	12.28	3.26	87.7	1.10e+008	(R)ELLPVLETVAK(A)	1211.725
44	006-0901.4985.5060.2	2	12.24	2.73	87.8	6.77e+007	(R)ELLPVLETVAK(A)	1211.725
45	009-1202.4193.4193.0	3	12.06	6.79	74.5	1.47e+007	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
46	005-0801.3992.3992.0	3	11.94	5.98	83.0	9.15e+007	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
47	007-1001.4764.4764.2	2	11.92	5.95	80.1	6.89e+006	(K)MLAGVNVLADAVK(I)	1300.730
48	005-0801.1694.1700.2	2	11.55	11.55	78.1	2.50e+006	(K)VGAATEVEMK(E)	1034.519
49	007-1002.4754.4754.2	2	11.27	5.84	85.3	1.23e+007	(K)MLAGVNVLADAVK(I)	1300.730
50	005-0802.1680.1702.0	2	11.22	7.30	85.6	1.69e+006	(K)VGAATEVEMK(E)	1034.519
51	005-0801.3945.4015.2	2	11.00	4.59	88.7	4.90e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
52	006-0901.4118.4134.2	2	10.96	4.51	79.8	5.85e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
53	001-0402.5874.5874.0	3	10.70	10.70	70.9	7.05e+006	(K)EGVITVEEGNSLENELDVVEGMQFDR(G)	2908.352
54	007-1002.4898.4954.0	2	10.56	2.48	79.8	2.83e+007	(R)ELLPVLETVAK(A)	1211.725
55	006-0901.3926.3954.2	2	10.53	4.41	73.2	2.06e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
56	005-0801.4005.4048.2	2	10.44	2.12	86.2	8.94e+008	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
57	005-0802.5736.5736.0	3	10.27	6.90	70.2	5.99e+008	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
58	007-1001.4789.4789.0	2	10.23	5.44	76.1	6.79e+006	(K)MLAGVNVLADAVK(I)	1300.730
59	006-0902.6026.6026.0	3	10.22	4.38	71.1	5.53e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
60	006-0901.3651.3651.0	2	10.19	10.19	71.9	9.76e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823
61	006-0901.3468.3468.0	2	10.08	10.08	72.1	6.18e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823
62	006-0902.3494.3494.2	2	9.82	4.59	74.5	3.96e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823
63	007-1001.3495.3495.0	2	9.77	4.86	77.0	1.37e+007	(K)EISVIVDGAGSAEDIK(A)	1602.823
64	007-1002.2817.2817.0	2	9.04	4.13	79.2	6.77e+006	(R)QIVTNAGDEASVIAEK(V)	1644.844
65	008-1101.5156.5156.0	3	8.39	8.39	76.8	1.71e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
66	008-1101.4606.4606.0	2	8.18	3.92	67.4	1.36e+007	(K)MLAGVNVLADAVK(I)	1300.730
67	005-0801.1818.1818.0	2	7.45	7.45	90.6	2.12e+006	(K)VGAATEVEMK(E)	1034.519
68	009-1201.3960.3960.0	2	7.11	1.36	93.5	6.29e+006	(R)AAVEEGVVPGGGVSLIR(A)	1609.891
69	006-0902.6071.6071.0	2	6.94	3.54	84.8	2.19e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195

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	29	9	109.20	32	7.18e+009	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	005-0802.9258.9304.0	3	17.37	17.37	79.3	3.14e+008	(R)AETVADDQILDDIILASDAVMVAR(G)	2544.287
2	006-0902.4141.4170.2	2	16.31	7.64	89.3	6.92e+007	(R)FAEGPIQLEIGDK(F)	1416.738
3	005-0801.3801.3816.0	2	15.64	7.29	90.1	6.95e+008	(K)IVSTLGPATDEPGILEK(L)	1739.943
4	006-0901.4401.4424.2	2	15.63	7.44	86.6	1.67e+008	(R)FAEGPIQLEIGDK(F)	1416.738

5	006-0901.4180.4189.0	2	13.29	7.16	83.5	7.05e+007	(R)FAEGPIQLEIGDK(F)	1416.738
6	005-0802.3745.3809.0	2	13.23	7.71	79.7	4.17e+008	(K)IVSTLGPATDEPGILEK(L)	1739.943
7	005-0801.4289.4330.0	2	13.12	7.45	79.1	8.11e+008	(R)FAEGPIQLEIGDK(F)	1416.738
8	005-0802.4249.4271.0	2	12.58	6.50	80.5	2.40e+008	(R)FAEGPIQLEIGDK(F)	1416.738
9	005-0802.5058.5058.2	2	12.26	4.94	74.9	2.03e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
10	005-0801.5052.5052.2	2	11.69	5.91	78.7	2.45e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
11	005-0802.5070.5070.2	2	11.66	11.66	67.0	2.00e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
12	006-0901.4503.4510.2	2	10.92	10.92	73.1	2.77e+008	(K)EGLEDGDLVLITK(G)	1401.748
13	006-0901.3723.3723.0	2	10.78	4.07	72.5	1.73e+008	(K)IVSTLGPATDEPGILEK(L)	1739.943
14	004-0701.3768.3768.0	2	10.60	4.01	71.8	3.48e+008	(K)IVSTLGPATDEPGILEK(L)	1739.943
15	005-0801.8968.8968.0	3	10.51	10.51	71.8	2.71e+008	(R)AEVFDVANAVLDGTDAVMLSAETAAGK(Y)	2665.303
16	008-1102.3712.3712.0	2	10.42	5.08	74.0	2.13e+007	(K)IVSTLGPATDEPGILEK(L)	1739.943
17	004-0701.5681.5681.2	2	9.77	4.15	68.0	1.79e+008	(R)GVQPVLFQSGEIPYIETNAR(A)	2218.151
18	005-0802.5047.5076.2	2	9.65	4.38	72.8	2.36e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
19	005-0801.4241.4285.0	2	9.55	4.71	74.5	3.45e+008	(R)FAEGPIQLEIGDK(F)	1416.738
20	006-0901.3758.3758.0	2	9.22	5.37	69.5	1.83e+008	(K)IVSTLGPATDEPGILEK(L)	1739.943
21	007-1001.4199.4199.0	2	8.90	8.90	69.0	2.01e+007	(K)EGLEDGDLVLITK(G)	1401.748
22	005-0801.5029.5029.2	2	8.83	3.53	62.8	2.32e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
23	005-0801.9929.9929.0	2	8.68	4.81	66.5	2.76e+008	(R)AETVADDQILDDIILASDAVMVAR(G)	2544.287
24	006-0901.3694.3694.0	2	8.41	2.92	85.7	7.47e+007	(K)YPVQTVEAMVR(V)	1292.667
25	005-0802.5016.5016.2	2	8.06	2.15	64.1	1.86e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
26	005-0801.4829.4829.0	2	8.01	4.19	73.8	3.57e+008	(R)GDLGVEIGDAQLIGVQK(H)	1711.923
27	005-0802.5033.5033.2	2	7.67	2.70	69.1	1.94e+008	(R)DVNPEDMLLLDDGR(V)	1601.748
28	007-1002.4101.4101.0	2	7.19	4.04	64.2	1.74e+007	(R)FAEGPIQLEIGDK(F)	1416.738
29	005-0802.4351.4368.0	2	6.82	6.82	60.3	3.61e+008	(K)EGLEDGDLVLITK(G)	1401.748

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	37	4	68.21	15	1.52e+010	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	005-0801.2751.2758.0	3	19.93	19.93	96.1	3.39e+007	(R)GITIATSHVEYDSPER(H)	1774.861
2	005-0802.2722.2734.0	3	19.55	13.66	93.9	3.27e+007	(R)GITIATSHVEYDSPER(H)	1774.861
3	004-0702.2725.2760.0	3	18.79	18.79	93.6	2.45e+007	(R)GITIATSHVEYDSPER(H)	1774.861
4	005-0801.6520.6619.2	2	18.24	13.13	91.5	6.71e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
5	005-0801.2724.2743.0	3	18.05	18.05	93.9	6.83e+007	(R)GITIATSHVEYDSPER(H)	1774.861
6	005-0802.2742.2771.0	2	17.74	7.01	93.5	1.84e+007	(R)GITIATSHVEYDSPER(H)	1774.861
7	005-0801.2755.2755.2	2	16.96	8.37	92.7	1.27e+007	(R)GITIATSHVEYDSPER(H)	1774.861
8	006-0902.2773.2791.0	3	16.73	11.10	81.6	1.01e+007	(R)GITIATSHVEYDSPER(H)	1774.861
9	006-0901.2773.2795.0	3	16.62	16.62	84.9	3.50e+007	(R)GITIATSHVEYDSPER(H)	1774.861
10	005-0801.6790.6839.2	2	16.18	11.11	89.9	1.18e+009	(R)GIINVGEEMEIIGIK(D)	1614.878
11	005-0802.6527.6558.0	2	16.06	9.97	84.9	4.56e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
12	004-0701.9034.9111.2	2	15.23	7.84	89.0	1.21e+009	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
13	004-0702.2743.2743.0	3	15.23	10.84	83.6	2.26e+007	(R)GITIATSHVEYDSPER(H)	1774.861
14	005-0802.4358.4410.0	2	14.81	7.04	92.9	1.05e+009	(K)LVEALDSYIPQPER(A)	1629.849

15	004-0702.8535.8598.2	2	14.71	6.42	88.7	3.83e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
16	005-0801.4473.4537.2	2	14.71	7.95	88.7	2.02e+009	(K)LVEALDSYIPQPER(A)	1629.849
17	005-0801.6801.6801.0	2	13.89	8.25	82.4	9.34e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
18	005-0801.8479.8514.2	2	13.62	5.85	85.3	5.13e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
19	005-0801.8974.9033.0	2	13.61	4.09	85.0	1.38e+009	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
20	004-0701.8592.8592.0	3	13.49	6.87	81.2	1.69e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
21	005-0801.4409.4409.2	2	13.48	7.19	88.8	7.63e+008	(K)LVEALDSYIPQPER(A)	1629.849
22	005-0802.6487.6487.0	2	13.42	7.23	77.9	3.07e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
23	005-0801.9027.9027.0	2	13.09	2.64	83.0	2.22e+009	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
24	006-0901.2769.2769.0	3	12.94	12.94	78.2	8.23e+006	(R)GITIATSHVEYDSPER(H)	1774.861
25	006-0901.7545.7545.2	2	12.29	7.86	72.3	8.94e+007	(R)GIINVGEEMEIIGIK(D)	1614.878
26	004-0701.8576.8590.2	2	12.10	4.25	84.1	3.11e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
27	006-0901.7583.7583.0	2	11.96	6.63	69.9	8.84e+007	(R)GIINVGEEMEIIGIK(D)	1614.878
28	003-0601.8704.8704.0	3	11.87	6.69	70.8	7.59e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
29	003-0601.8693.8693.2	2	10.26	3.64	75.6	1.27e+008	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
30	005-0801.2759.2759.0	2	10.11	4.79	88.9	1.59e+007	(R)GITIATSHVEYDSPER(H)	1774.861
31	008-1102.2800.2800.0	3	9.68	9.68	85.4	3.68e+006	(R)GITIATSHVEYDSPER(H)	1774.861
32	003-0601.4494.4494.0	2	9.56	3.01	72.4	9.80e+007	(K)LVEALDSYIPQPER(A)	1629.849
33	006-0901.4274.4274.2	2	9.41	3.85	65.7	2.30e+008	(K)LVEALDSYIPQPER(A)	1629.849
34	005-0802.6584.6584.0	2	9.06	9.06	63.0	3.12e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
35	003-0602.8137.8137.0	2	8.70	2.39	73.5	7.49e+007	(R)AIDQPFLMPIEDVFSISGR(G)	2135.085
36	006-0901.8356.8356.0	2	8.33	8.33	61.0	2.24e+008	(R)GIINVGEEMEIIGIK(D)	1614.878
37	002-0502.5683.5683.0	2	7.82	3.93	76.3	1.30e+007	(R)GIINVGEEMEIIGIK(D)	1614.878

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.1	15	5	63.66	24	5.16e+009	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	004-0701.8008.8100.0	3	15.26	6.56	83.1	9.94e+008	(R)AYNLIFNTFFNDDQIQEPVNIDEDWSK(S)	3275.517
2	004-0701.8477.8477.0	3	14.13	14.13	83.7	1.10e+009	(R)AYNLIFNTFFNDDQIQEPVNIDEDWSK(S)	3275.517
3	004-0701.7242.7279.2	2	13.90	13.90	73.0	5.06e+008	(R)LLPMNDTMSQEADTLGEVGGYMLGTK(R)	2771.294
4	003-0602.2922.2922.0	2	12.50	5.62	80.2	5.70e+007	(R)LQMEADIYGEK(D)	1296.615
5	003-0601.7029.7137.0	3	12.02	4.76	70.6	9.49e+008	(R)LLPMNDTMSQEADTLGEVGGYMLGTK(R)	2771.294
6	003-0601.2900.2911.0	2	11.69	5.58	86.8	8.12e+007	(R)LQMEADIYGEK(D)	1296.615
7	004-0702.4380.4380.0	2	11.05	2.51	77.5	2.61e+008	(K)QYETTMLVDPLSDK(K)	1639.789
8	003-0602.4564.4598.0	2	10.95	6.56	73.5	1.31e+008	(K)TTYTSAEDGILHINEADFR(D)	2153.015
9	004-0701.4564.4564.0	2	10.77	6.99	79.3	1.47e+008	(K)TTYTSAEDGILHINEADFR(D)	2153.015
10	003-0601.2939.2959.2	2	10.21	4.40	80.2	1.30e+008	(R)LQMEADIYGEK(D)	1296.615
11	003-0601.4805.4805.2	2	9.63	9.63	72.5	1.91e+008	(K)TTYTSAEDGILHINEADFR(D)	2153.015
12	004-0702.2885.2894.0	2	9.46	4.94	60.3	6.27e+007	(R)LQMEADIYGEK(D)	1296.615
13	004-0701.2825.2854.0	2	9.45	3.14	69.1	2.42e+008	(R)LQMEADIYGEK(D)	1296.615
14	003-0601.4820.4820.2	2	9.37	5.53	70.5	1.97e+008	(K)TTYTSAEDGILHINEADFR(D)	2153.015
15	004-0701.2871.2923.0	2	8.63	3.44	62.7	1.04e+008	(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
5	5.1	12	4	61.60	38	3.75e+009	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	003-0602.6312.6378.0	2	24.00	19.45	100.0	4.54e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
2	003-0601.6676.6722.2	2	21.92	21.92	98.7	5.77e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
3	003-0601.6669.6748.0	2	21.79	17.41	96.7	6.43e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
4	003-0601.6329.6410.0	2	20.83	20.83	97.2	3.35e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
5	003-0602.6343.6351.3	3	20.02	14.59	89.6	1.30e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
6	003-0601.6713.6736.3	3	18.52	11.13	90.0	2.29e+008	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
7	003-0601.4754.4801.0	2	16.09	11.68	85.9	3.09e+008	(K)IFVSTLEQVVR(I)	1290.742
8	003-0601.6372.6372.3	3	15.31	9.61	83.3	9.60e+007	(K)LEVAVADDQLDSVVEAISK(A)	2001.039
9	003-0602.4755.4773.2	2	14.75	10.68	82.1	2.28e+008	(K)IFVSTLEQVVR(I)	1290.742
10	003-0601.4983.5042.0	2	14.69	11.39	86.9	4.85e+008	(K)IFVSTLEQVVR(I)	1290.742
11	003-0601.5045.5045.0	2	10.95	3.86	73.6	8.71e+007	(R)GAEYVVDFLPK(T)	1237.647
12	003-0601.6419.6419.0	3	10.56	5.75	71.9	1.80e+008	(K)TKLEVAVADDQLDSVVEAISK(A)	2230.182

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
6	6.1	6	4	59.77	47	2.09e+009	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	005-0801.6356.6403.2	2	19.34	14.47	95.4	2.34e+008	(K)GVVDALEGNTPEVSDADLNAAFAEIR(G)	2673.301
2	005-0802.6347.6354.2	2	17.62	11.79	90.5	1.57e+008	(K)GVVDALEGNTPEVSDADLNAAFAEIR(G)	2673.301
3	005-0802.9244.9256.0	3	14.79	6.60	86.0	3.76e+008	(R)GEPAEFPVNGVIAGWTEALQLMPVGAK(W)	2781.429
4	005-0802.4279.4279.0	3	13.43	6.43	74.2	1.26e+008	(K)KPGITVTESGLQYEILASGDGEKPTASSTVR(T)	3191.644
5	005-0801.3551.3586.0	2	12.21	8.43	81.6	3.66e+008	(K)QLSENTFEGMNYNAVAK(G)	1915.886
6	005-0801.9898.9898.0	3	11.78	5.08	76.7	8.30e+008	(R)GEPAEFPVNGVIAGWTEALQLMPVGAK(W)	2781.429

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	17	4	57.02	22	2.38e+009	38663.6	PA_BSC2:2534576404	PA_BSC2:2534576404 Bsc2_04093 3-isopropylmalate dehydrogenase (EC 1.1.1.85) [Alteromonadacea bacterium B

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	006-0901.7691.7794.2	2	16.27	5.93	94.3	2.57e+008	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095
2	006-0901.8445.8535.2	2	15.97	3.51	93.2	6.09e+008	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095
3	006-0901.5256.5256.2	2	14.57	14.57	83.7	1.09e+008	(K)VSTDEMGDAVVAALAH(-)	1585.753
4	006-0902.4829.4880.2	2	14.20	14.20	83.1	7.39e+007	(K)VSTDEMGDAVVAALAH(-)	1585.753
5	006-0902.7656.7656.0	3	13.96	4.90	76.8	6.23e+007	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095

6	006-0901.10045.10063.0	3	13.67	8.24	78.5	1.68e+008	(R)SGLYEPVHGSAPDIAGQGIANPLATILSAAMLLR(Y)	3403.805
7	006-0901.8653.8653.0	2	13.66	4.38	85.8	2.78e+008	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095
8	006-0901.5268.5268.2	2	13.28	13.28	75.4	1.14e+008	(K)VSTDEMGDAVVAALAH(-)	1585.753
9	006-0901.3362.3381.0	2	12.51	8.94	73.2	9.84e+007	(R)SDAADAIEAAVGK(V)	1217.601
10	006-0901.4916.4916.2	2	12.27	12.27	75.6	5.12e+007	(K)VSTDEMGDAVVAALAH(-)	1585.753
11	006-0901.5286.5286.2	2	11.66	7.90	76.1	1.06e+008	(K)VSTDEMGDAVVAALAH(-)	1585.753
12	006-0901.8569.8569.0	3	11.08	2.34	70.9	1.02e+008	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095
13	006-0902.3303.3303.0	2	11.03	11.03	70.9	2.29e+007	(R)SDAADAIEAAVGK(V)	1217.601
14	006-0901.5211.5211.0	2	10.53	10.53	67.6	1.03e+008	(K)VSTDEMGDAVVAALAH(-)	1585.753
15	006-0901.5298.5298.0	2	10.40	3.73	72.5	1.02e+008	(K)VSTDEMGDAVVAALAH(-)	1585.753
16	006-0901.7811.7811.2	2	9.46	3.05	67.7	9.63e+007	(K)IVLLPGDGIGPEIVAEAVK(V)	1890.095
17	006-0901.3303.3303.0	2	7.88	7.88	61.8	2.84e+007	(R)SDAADAIEAAVGK(V)	1217.601

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	56.30	20	3.36e+009	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	006-0901.4027.4040.2	2	16.24	8.89	86.4	1.93e+008	(R)YQPLDATTNPSLLYK(A)	1723.891
2	006-0901.4069.4069.0	2	15.60	6.91	91.6	7.09e+007	(K)QFSDVVADTGDIEAIK(R)	1707.844
3	005-0801.4158.4165.0	2	15.08	9.26	91.8	1.25e+008	(K)QFSDVVADTGDIEAIK(R)	1707.844
4	005-0802.6685.6685.2	2	14.60	11.15	83.7	1.82e+008	(R)GFVADQINLENFLK(A)	1607.843
5	005-0801.4233.4246.0	2	14.36	8.43	92.7	3.66e+008	(K)QFSDVVADTGDIEAIK(R)	1707.844
6	006-0901.4299.4299.0	2	12.99	6.51	84.2	1.72e+008	(K)QFSDVVADTGDIEAIK(R)	1707.844
7	005-0801.7008.7008.2	2	11.57	5.37	73.6	4.84e+008	(R)GFVADQINLENFLK(A)	1607.843
8	006-0902.7611.7611.2	2	10.04	10.04	66.8	9.00e+007	(R)GFVADQINLENFLK(A)	1607.843
9	005-0802.6018.6018.0	2	9.86	6.15	74.9	2.95e+008	(R)LTISPQLLGELEADTGK(L)	1784.965
10	005-0801.6712.6712.0	2	9.79	9.79	70.5	2.16e+008	(R)GFVADQINLENFLK(A)	1607.843
11	005-0801.7011.7011.0	2	9.17	5.77	68.1	4.19e+008	(R)GFVADQINLENFLK(A)	1607.843
12	008-1102.3978.3978.0	2	8.60	8.60	64.7	1.86e+007	(K)QFSDVVADTGDIEAIK(R)	1707.844
13	005-0801.6673.6673.0	2	8.12	2.41	66.4	2.24e+008	(R)GFVADQINLENFLK(A)	1607.843
14	006-0901.8493.8493.0	2	7.94	4.81	60.7	2.33e+008	(R)GFVADQINLENFLK(A)	1607.843
15	005-0802.6022.6022.0	2	7.63	7.63	73.5	2.72e+008	(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
9	9.1	32	3	55.85	29	2.38e+010	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	004-0701.5255.5285.2	2	21.00	11.43	100.0	6.17e+009	(K)TVTAMDVVYALK(R)	1310.703
2	004-0702.5198.5204.2	2	19.96	10.31	99.1	1.57e+009	(K)TVTAMDVVYALK(R)	1310.703
3	004-0701.5165.5167.2	2	18.35	9.64	95.9	1.30e+009	(K)TVTAMDVVYALK(R)	1310.703

4	004-0702.2840.2854.2	2	17.89	11.21	96.7	2.36e+008	(R)ISGLIYEETR(G)	1180.621
5	004-0701.2799.2870.2	2	17.38	9.82	96.6	9.80e+008	(R)ISGLIYEETR(G)	1180.621
6	003-0601.4134.4138.0	2	16.96	6.51	98.3	4.33e+008	(K)VFLENVIR(D)	989.578
7	004-0701.2842.2927.2	2	16.88	10.09	96.2	3.51e+008	(R)ISGLIYEETR(G)	1180.621
8	003-0601.2861.2881.2	2	16.86	10.18	96.0	3.59e+008	(R)ISGLIYEETR(G)	1180.621
9	003-0601.3959.3986.0	2	16.47	5.96	98.7	4.10e+008	(K)VFLENVIR(D)	989.578
10	008-1101.3931.3937.0	2	16.44	7.07	97.4	1.26e+007	(K)VFLENVIR(D)	989.578
11	005-0801.3942.3951.0	2	16.06	5.99	92.3	2.25e+008	(K)VFLENVIR(D)	989.578
12	003-0602.3964.3979.0	2	15.96	5.96	98.2	4.78e+008	(K)VFLENVIR(D)	989.578
13	004-0701.3824.3831.0	2	15.71	4.96	98.3	2.35e+009	(K)VFLENVIR(D)	989.578
14	004-0702.4001.4001.0	2	15.46	5.56	98.5	7.91e+008	(K)VFLENVIR(D)	989.578
15	004-0701.5406.5406.0	2	15.39	7.60	96.9	3.42e+009	(K)TVTAMDVVYALK(R)	1310.703
16	004-0702.3883.3977.0	2	15.23	5.51	99.0	1.68e+009	(K)VFLENVIR(D)	989.578
17	003-0602.2862.2927.2	2	15.11	9.59	89.1	1.22e+008	(R)ISGLIYEETR(G)	1180.621
18	007-1001.4142.4221.0	2	15.08	6.26	93.1	3.55e+007	(K)VFLENVIR(D)	989.578
19	004-0701.3872.3876.0	2	14.72	4.76	98.8	8.08e+008	(K)VFLENVIR(D)	989.578
20	007-1001.4244.4244.2	2	14.70	6.57	88.9	1.49e+007	(K)VFLENVIR(D)	989.578
21	008-1101.3942.3942.0	2	14.15	5.71	95.7	1.83e+007	(K)VFLENVIR(D)	989.578
22	003-0601.5514.5514.2	2	14.03	6.00	88.4	2.40e+008	(K)TVTAMDVVYALK(R)	1310.703
23	004-0702.2933.2933.2	2	13.56	9.35	82.3	1.71e+008	(R)ISGLIYEETR(G)	1180.621
24	003-0601.2875.2923.0	2	13.21	5.46	80.2	1.07e+008	(R)ISGLIYEETR(G)	1180.621
25	005-0801.2880.2884.0	2	12.89	6.85	83.0	3.99e+007	(R)ISGLIYEETR(G)	1180.621
26	004-0701.5159.5159.0	2	10.05	10.05	69.1	9.44e+008	(K)TVTAMDVVYALK(R)	1310.703
27	004-0701.2908.2908.2	2	9.02	5.25	72.3	2.60e+008	(R)ISGLIYEETR(G)	1180.621
28	003-0601.2851.2851.0	2	8.99	3.65	74.2	1.83e+008	(R)ISGLIYEETR(G)	1180.621
29	008-1101.2908.2974.0	2	8.79	4.52	67.3	3.59e+007	(R)ISGLIYEETR(G)	1180.621
30	005-0801.2892.2892.2	2	8.63	8.63	64.2	3.82e+007	(R)ISGLIYEETR(G)	1180.621
31	006-0901.2909.2909.2	2	8.45	5.38	68.6	1.11e+007	(R)ISGLIYEETR(G)	1180.621
32	005-0802.2876.2876.2	2	8.34	4.90	65.5	2.43e+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
10	10.1	8	3	51.81	13	7.46e+008	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	007-1001.3029.3064.2	2	19.80	11.13	96.9	3.14e+007	(K)AEGQQAQILGAVSGAK(H)	1527.813
2	008-1101.3032.3058.0	2	17.93	12.00	92.4	1.97e+007	(K)AEGQQAQILGAVSGAK(H)	1527.813
3	009-1201.3332.3351.0	3	16.02	6.80	91.7	6.40e+006	(K)ILDAVKPGVLTGDDVQK(V)	1767.986
4	006-0901.7242.7304.2	2	15.99	9.52	82.6	4.28e+008	(R)LEQAFADLNAIDVL(-)	1531.801
5	008-1101.3036.3036.2	2	13.74	7.03	83.1	1.63e+007	(K)AEGQQAQILGAVSGAK(H)	1527.813
6	006-0901.6611.6694.2	2	12.55	9.21	64.7	1.91e+008	(R)LEQAFADLNAIDVL(-)	1531.801
7	008-1102.6391.6400.2	2	12.40	7.94	68.2	4.45e+007	(R)LEQAFADLNAIDVL(-)	1531.801
8	009-1202.3339.3356.0	3	11.69	3.62	81.0	8.69e+006	(K)ILDAVKPGVLTGDDVQK(V)	1767.986

Distinct Total

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
11	11.1	7	3	49.46	16	1.20e+009	35299.3	PA_BSC2:2534572582	PA_BSC2:2534572582 Bsc2_00266 malate dehydrogenase [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0801.9266.9330.0	3	22.12	11.33	96.9	1.94e+008	(K)DQPVILQMLEITPALEALK(G)	2122.183
2	005-0802.9181.9248.0	3	19.50	10.20	94.3	1.93e+008	(K)DQPVILQMLEITPALEALK(G)	2122.183
3	005-0802.3859.3859.2	2	16.16	16.16	88.0	1.23e+008	(K)VLVVGNPANTNALIAQR(N)	1749.997
4	005-0801.9265.9336.2	2	15.89	10.28	93.2	2.61e+008	(K)DQPVILQMLEITPALEALK(G)	2122.183
5	005-0802.9204.9209.2	2	14.93	8.13	88.8	1.90e+008	(K)DQPVILQMLEITPALEALK(G)	2122.183
6	005-0801.4185.4185.0	2	11.18	4.19	86.4	1.34e+008	(K)VEQDWYESDYIPTVQQR(G)	2155.994
7	005-0801.9248.9248.2	2	8.06	8.06	61.8	1.01e+008	(K)DQPVILQMLEITPALEALK(G)	2122.183

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
12	12.1	5	3	46.50	6	8.18e+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	001-0402.4760.4838.2	2	17.96	10.19	98.8	2.02e+007	(R)ELLIFVTPR(I)	1087.652
2	001-0401.4770.4819.2	2	17.48	9.86	99.5	1.77e+007	(R)ELLIFVTPR(I)	1087.652
3	002-0502.3085.3093.0	3	15.10	7.86	81.5	1.93e+007	(K)QQATIESGSEVPYQEESASGGTTTAFK(D)	2803.291
4	002-0501.2775.2779.2	2	13.44	8.13	85.5	1.32e+007	(R)LDVTPQITPDNR(I)	1368.712
5	002-0502.2788.2788.2	2	11.13	6.51	78.0	1.14e+007	(R)LDVTPQITPDNR(I)	1368.712

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
13	13.1	7	3	44.40	50	6.57e+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	004-0701.5355.5446.0	2	18.78	10.10	96.4	1.04e+009	(R)ALDAVTESIASALK(E)	1388.764
2	004-0701.5469.5587.0	2	18.73	11.16	95.3	2.43e+009	(R)ALDAVTESIASALK(E)	1388.764
3	004-0702.5349.5390.0	2	18.15	9.51	94.6	7.85e+008	(R)ALDAVTESIASALK(E)	1388.764
4	004-0701.4872.4872.0	2	14.13	14.13	82.0	6.47e+008	(K)SELVEAIAASADISK(A)	1503.791
5	004-0702.6732.6768.2	2	11.49	7.79	77.7	4.45e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
6	004-0701.7028.7028.0	2	10.42	4.35	79.8	9.86e+008	(K)EGDQVALVGFGTFLVK(E)	1679.901
7	004-0701.4780.4780.0	2	8.44	8.44	64.1	2.38e+008	(K)SELVEAIAASADISK(A)	1503.791

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

				Score					
14	14.1	8	4	43.79	14	4.76e+008	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	006-0902.4909.4909.0	3	13.01	13.01	75.1	6.24e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	006-0901.4940.4940.0	3	11.59	5.82	76.6	6.22e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
3	006-0901.5948.5948.0	3	11.27	6.76	77.4	8.59e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
4	006-0901.6992.6992.0	3	11.09	7.68	71.1	8.73e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
5	006-0902.5612.5612.0	3	9.50	3.44	100.0	3.11e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
6	006-0901.6061.6061.0	3	9.03	5.49	70.4	6.77e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
7	006-0902.5615.5615.0	3	8.85	2.37	73.8	2.54e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
8	005-0802.9784.9784.0	3	8.42	8.42	78.1	5.42e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843

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	62	2	39.48	19	2.88e+010	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	005-0801.4260.4280.0	2	21.91	14.96	98.6	1.44e+009	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
2	005-0802.4173.4234.0	2	21.37	15.24	98.1	5.40e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
3	005-0801.4187.4253.0	2	19.72	15.01	95.9	7.26e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
4	006-0901.4154.4169.0	2	19.09	11.60	93.8	5.89e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
5	006-0902.4629.4661.2	2	17.57	8.21	92.4	2.76e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
6	007-1001.4561.4587.2	2	17.11	10.37	92.6	1.74e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
7	006-0902.5133.5202.2	2	17.05	7.45	91.7	6.40e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
8	005-0801.5129.5162.0	2	17.04	8.00	91.1	2.77e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
9	006-0901.5174.5213.2	2	17.04	8.21	91.6	4.96e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
10	006-0902.5259.5297.0	2	16.97	7.93	89.6	5.15e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
11	005-0801.4827.4925.2	2	16.57	7.61	91.9	2.39e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
12	005-0801.4994.5096.0	2	16.53	9.34	91.3	4.11e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
13	006-0901.5008.5052.0	2	16.53	7.09	91.5	3.05e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
14	006-0901.5454.5454.2	2	16.44	7.44	90.0	3.59e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
15	009-1201.5587.5666.0	2	16.44	10.54	90.4	5.09e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
16	006-0901.4693.4723.3	3	16.32	8.64	87.9	2.36e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
17	005-0801.5006.5091.3	3	16.21	6.56	86.9	1.82e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
18	006-0901.5340.5424.2	2	16.08	7.04	91.9	3.59e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
19	005-0802.4830.4937.3	3	16.07	7.36	85.4	1.13e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
20	006-0901.4675.4747.2	2	16.03	5.96	91.0	5.14e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
21	007-1002.4562.4605.2	2	15.99	9.62	90.2	2.17e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
22	008-1101.4488.4494.2	2	15.99	6.98	90.7	3.62e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
23	007-1001.5459.5553.2	2	15.94	10.29	89.4	2.50e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
24	007-1001.5585.5690.0	2	15.81	9.16	87.5	5.21e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
25	005-0802.4822.4920.2	2	15.52	7.06	91.1	2.05e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
26	006-0902.4739.4739.0	2	15.52	7.13	91.1	1.67e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055

27	006-0901.5556.5556.0	2	15.49	7.18	89.9	2.56e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
28	008-1102.4472.4501.2	2	15.49	6.49	90.5	4.85e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
29	006-0901.5472.5472.3	3	15.48	6.61	81.4	3.02e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
30	008-1101.5321.5400.0	2	15.40	9.01	89.7	1.34e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
31	006-0902.5144.5180.0	3	15.39	7.44	83.5	5.36e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
32	007-1002.5326.5403.0	2	15.33	7.96	87.5	7.37e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
33	007-1001.5722.5722.2	2	14.99	6.84	89.7	3.54e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
34	005-0801.5262.5304.2	2	14.87	6.72	89.4	5.81e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
35	007-1002.4568.4585.0	3	14.76	6.85	80.5	1.76e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
36	008-1102.4496.4519.3	3	14.57	4.67	76.6	4.23e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
37	005-0801.4853.4900.3	3	14.42	5.43	81.8	1.06e+009	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
38	007-1001.5334.5420.2	2	14.33	8.21	88.1	9.66e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
39	006-0901.5169.5233.0	3	14.32	7.00	79.1	7.66e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
40	006-0901.5058.5124.3	3	14.21	6.66	79.2	2.71e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
41	006-0902.4662.4715.3	3	13.74	5.75	79.4	2.15e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
42	008-1101.4484.4544.3	3	13.74	7.36	79.0	5.53e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
43	008-1101.5338.5381.3	3	13.55	5.94	77.7	1.07e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
44	007-1002.5415.5422.0	2	13.34	5.22	86.1	5.83e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
45	006-0901.4126.4134.0	3	13.10	7.98	82.7	2.35e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
46	005-0802.4289.4289.2	2	12.98	8.53	90.4	2.34e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
47	005-0802.5072.5072.2	2	12.91	6.65	82.5	1.37e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
48	003-0602.4857.4857.0	2	12.74	6.80	84.8	7.85e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
49	006-0901.6304.6406.0	3	12.49	4.51	73.6	4.94e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
50	005-0801.12861.12926.2	2	12.47	5.35	81.0	6.74e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
51	006-0901.4793.4793.0	3	12.14	5.96	74.1	1.19e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
52	008-1101.5445.5445.0	2	11.00	5.24	81.0	6.88e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
53	005-0801.12060.12060.0	2	10.98	6.68	76.7	2.04e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
54	006-0901.4426.4426.2	2	10.90	3.44	73.5	8.47e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
55	005-0801.5191.5191.2	2	10.89	10.89	77.2	1.64e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
56	006-0901.6418.6455.0	3	9.93	5.62	71.7	2.38e+008	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
57	005-0801.12988.12988.0	2	9.77	9.77	65.5	3.50e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
58	005-0802.11939.11939.0	2	8.84	2.36	81.6	2.35e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
59	005-0802.11881.11881.0	2	8.16	3.76	68.0	2.02e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
60	005-0801.4810.4810.0	2	8.10	4.97	65.7	4.49e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
61	005-0801.12716.12716.0	2	6.71	3.09	62.7	5.02e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
62	005-0801.11884.11884.2	2	6.03	2.69	64.4	1.75e+008	(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
16	16.1	9	3	37.08	13	2.71e+009	51876.6	PA_BSC2:2534574029	PA_BSC2:2534574029 Bsc2_01715 glutamine synthetase, type I [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	004-0701.8329.8367.0	2	14.10	7.29	83.4	3.37e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192
2	004-0702.8292.8298.0	2	13.26	7.11	80.9	2.33e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192
3	003-0601.8404.8480.0	2	12.71	6.31	79.3	1.62e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192

4	003-0601.8421.8451.0	2	12.69	4.64	78.1	1.50e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192
5	005-0801.11356.11356.0	2	12.48	3.53	73.8	5.14e+007	(R)FPDPIANPYLAFAAMLMAGLDGVK(N)	2522.283
6	004-0701.8766.8791.0	2	12.02	5.26	80.2	9.95e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192
7	005-0801.12282.12282.0	2	10.68	3.73	72.1	1.77e+008	(R)FPDPIANPYLAFAAMLMAGLDGVK(N)	2522.283
8	004-0702.8263.8291.0	3	10.50	2.25	70.7	3.60e+008	(K)STGLGDTAFFGPEPEFFVFDDIK(W)	2536.192
9	005-0801.5007.5007.0	3	10.50	5.18	89.6	2.47e+008	(K)GGYFPVPPVDSLHDIR(A)	1768.902

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	36.91	21	5.46e+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	003-0601.9410.9462.0	3	17.16	8.38	86.6	8.66e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
2	003-0601.9471.9474.2	2	16.90	11.71	89.1	5.49e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
3	003-0602.9393.9396.0	3	16.20	6.81	87.3	4.68e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
4	003-0601.10099.10117.0	3	16.19	6.89	87.6	7.59e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
5	003-0602.9452.9468.2	2	16.01	11.95	90.9	6.86e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
6	003-0601.9992.9992.0	3	10.85	4.98	75.0	4.67e+007	(K)MNKDPLEIFGEALENIAPLVEVK(S)	2569.359
7	003-0601.9528.9528.0	2	9.87	5.59	68.4	3.84e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
8	003-0601.10118.10118.2	2	9.79	6.40	69.1	6.56e+007	(K)DPLEIFGEALENIAPLVEVK(S)	2196.180
9	003-0602.4377.4377.0	2	8.90	3.38	67.7	6.22e+007	(R)IVYGALELVR(E)	1132.673

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	11	2	34.85	41	4.47e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Combi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0802.7728.7808.0	3	17.75	8.67	88.3	3.89e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
2	004-0702.11662.11668.2	2	17.10	17.10	87.4	2.31e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
3	004-0701.12725.12749.2	2	15.33	11.60	90.1	4.33e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
4	005-0801.11754.11763.2	2	14.85	14.85	83.3	1.68e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
5	005-0802.11573.11579.2	2	13.80	13.80	75.3	1.28e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
6	005-0801.12692.12705.2	2	13.77	9.89	82.1	3.47e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
7	006-0901.12018.12018.2	2	13.75	13.75	84.2	4.51e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
8	004-0701.7815.7860.2	2	13.57	3.21	87.0	4.48e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
9	004-0701.8206.8262.0	2	13.05	4.48	85.9	1.07e+009	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
10	004-0702.7781.7829.2	2	13.02	3.22	85.6	3.88e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
11	005-0801.8253.8253.2	2	8.62	3.28	87.0	4.17e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391

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

				Score					
19	19.1	6	2	34.39	16	6.48e+008	16139.8	PA_BSC2:2534574197	PA_BSC2:2534574197 Bsc2_01883 cyanate hydratase [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	006-0902.4603.4635.0	2	17.24	9.63	90.9	3.48e+007	(K)LDVTEAIILAK(K)	1185.709
2	006-0902.3991.4037.2	2	17.15	11.62	91.9	1.15e+008	(R)LYEVVGVYGDTLK(E)	1455.774
3	006-0901.4198.4260.2	2	17.05	13.21	89.7	3.10e+008	(R)LYEVVGVYGDTLK(E)	1455.774
4	006-0901.4671.4671.0	2	15.57	15.57	85.3	2.75e+007	(K)LDVTEAIILAK(K)	1185.709
5	006-0901.4879.4970.0	2	14.13	10.60	83.3	1.54e+008	(K)LDVTEAIILAK(K)	1185.709
6	007-1001.4498.4498.0	2	13.76	6.86	81.3	6.23e+006	(K)LDVTEAIILAK(K)	1185.709

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
20	20.1	4	3	33.54	11	6.22e+008	49992.5	PA_Bse_meta_comb:2073595049	PA_Bse_meta_comb:2073595049 BaSeMet_00387050 D-glucuronate isomerase (EC 5.3.1.12) [Bankia s

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0801.3369.3369.2	2	13.39	13.39	74.1	1.32e+008	(R)AMAVEDATEYNNYIDR(L)	1874.823
2	005-0802.8995.8995.2	2	12.28	12.28	74.8	1.58e+008	(R)LGEVADVTISSFDDLITALR(V)	2135.124
3	005-0802.8986.8986.0	2	9.06	3.34	66.3	1.44e+008	(R)LGEVADVTISSFDDLITALR(V)	2135.124
4	005-0801.5354.5354.0	2	7.87	7.87	64.3	1.88e+008	(R)QIEALSQLGLLSR(F)	1427.822

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	6	2	29.82	8	1.07e+009	37181.7	PA_BSC2:2534573415	PA_BSC2:2534573415 Bsc2_01100 UDP-glucose pyrophosphorylase (EC 2.7.7.9) [Alteromonadacea bacterium Bsc

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0802.3841.3841.2	2	16.68	16.68	89.8	1.07e+008	(K)NNEVQLTDALMTQAK(N)	1675.833
2	005-0801.7736.7782.0	2	13.14	5.48	88.8	2.68e+008	(R)YILTPDIFEIIK(N)	1464.835
3	005-0801.3837.3837.0	2	12.97	12.97	80.2	1.29e+008	(K)NNEVQLTDALMTQAK(N)	1675.833
4	005-0802.7710.7756.0	2	12.85	4.95	81.8	3.13e+008	(R)YILTPDIFEIIK(N)	1464.835
5	005-0802.3858.3858.0	2	12.10	12.10	72.5	1.17e+008	(K)NNEVQLTDALMTQAK(N)	1675.833
6	005-0801.3821.3821.2	2	10.91	10.91	72.3	1.37e+008	(K)NNEVQLTDALMTQAK(N)	1675.833

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
22	22.1	2	2	28.99	9	2.72e+008	38327.9	PA_Bse_meta_comb:2073590044	PA_Bse_meta_comb:2073590044 BaSeMet_00337000 phosphate ABC transporter substrate-binding pro

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	003-0601.4920.4948.2	2	16.79	8.68	93.8	1.68e+008	(K)VQASFVDGTEPTFETIADGR(Y)	2140.020

2	003-0601.2775.2802.2	2	12.20	5.76	83.3	1.04e+008	(K)IEVLGPPPTSGTR(D)	1323.727

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	3	2	28.11	2	4.60e+008	118803.8	PA_BSC2:2534573281	PA_BSC2:2534573281 Bsc2_00965 TonB-dependent receptor [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	004-0702.3921.3921.2	2	19.18	15.04	94.4	1.71e+008	(R)EAVGVVDAISAEDIGK(M)	1572.812
2	004-0701.3890.3933.2	2	17.06	13.32	92.5	1.88e+008	(R)EAVGVVDAISAEDIGK(M)	1572.812
3	004-0701.3145.3145.0	2	8.93	8.93	66.8	1.02e+008	(K)MPDANLAESLQR(I)	1344.658

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	12	2	26.89	30	5.59e+009	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome (

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	004-0701.7110.7127.0	2	15.17	9.81	85.5	8.74e+008	(K)DTGTFADFMEAFK(T)	1479.647
2	005-0802.6713.6718.0	2	12.80	7.78	78.5	3.65e+008	(K)DTGTFADFMEAFK(T)	1479.647
3	004-0701.7093.7163.0	2	12.02	5.40	82.9	1.03e+009	(K)DTGTFADFMEAFK(T)	1479.647
4	005-0801.6730.6828.0	2	11.76	5.70	78.4	5.55e+008	(K)DTGTFADFMEAFK(T)	1479.647
5	005-0802.4866.4947.2	2	11.72	6.39	86.8	4.50e+008	(K)FEEFIPLYK(E)	1185.620
6	006-0901.5026.5097.2	2	11.60	6.16	83.6	1.38e+008	(K)FEEFIPLYK(E)	1185.620
7	004-0702.6779.6818.0	2	11.49	7.31	80.1	3.36e+008	(K)DTGTFADFMEAFK(T)	1479.647
8	006-0902.4743.4748.0	2	10.68	3.23	84.7	3.91e+007	(K)FEEFIPLYK(E)	1185.620
9	004-0701.4861.4917.2	2	10.52	5.30	77.6	4.01e+008	(K)FEEFIPLYK(E)	1185.620
10	004-0701.6811.6851.0	2	8.86	4.13	69.5	4.40e+008	(K)DTGTFADFMEAFK(T)	1479.647
11	004-0701.4938.4991.0	2	8.51	2.97	72.1	7.51e+008	(K)FEEFIPLYK(E)	1185.620
12	004-0702.6857.6857.0	2	7.69	7.69	69.1	2.11e+008	(K)DTGTFADFMEAFK(T)	1479.647

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
25	25.1	5	2	26.15	4	4.63e+008	43102.8	PA_Bse_meta_comb:2073591868	PA_Bse_meta_comb:2073591868 BaSeMet_00355240 2-oxoglutarate dehydrogenase E2 component (E(

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	006-0901.4096.4129.2	2	18.65	11.37	93.2	1.06e+008	(R)NVENMSIAEIENGVR(D)	1674.812
2	006-0902.4073.4108.2	2	15.35	8.51	86.5	7.98e+007	(R)NVENMSIAEIENGVR(D)	1674.812
3	006-0901.4827.4861.1	1	7.50	2.40	81.1	1.91e+008	(R)ILLEL(-)	600.397
4	006-0902.4791.4806.1	1	7.49	2.79	80.8	7.76e+007	(R)ILLEL(-)	600.397
5	007-1001.4701.4701.1	1	6.38	3.11	83.8	8.56e+006	(R)ILLEL(-)	600.397

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	14	2	25.24	8	1.46e+009	36105.1	PA_BS12:2189567940	PA_BS12:2189567940 or1263 Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0801.4578.4617.2	2	16.49	13.18	91.5	3.93e+008	(R)VPTPDVSVVDLTVR(L)	1496.832
2	008-1101.4336.4350.2	2	16.48	13.16	91.8	2.24e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
3	005-0802.4595.4608.2	2	15.69	10.83	87.4	2.19e+008	(R)VPTPDVSVVDLTVR(L)	1496.832
4	007-1001.4397.4465.2	2	14.87	14.87	85.2	3.50e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
5	006-0901.4468.4498.0	2	14.85	11.13	83.2	8.92e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
6	007-1002.4377.4381.2	2	13.10	13.10	84.8	2.03e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
7	009-1202.4366.4394.0	2	12.16	7.84	74.8	1.45e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
8	004-0701.4583.4635.0	2	12.04	8.21	80.0	3.06e+008	(R)VPTPDVSVVDLTVR(L)	1496.832
9	006-0902.4484.4512.0	2	10.74	5.79	67.8	5.16e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
10	007-1002.4348.4425.0	2	9.72	9.72	67.2	3.66e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
11	004-0702.4634.4634.0	2	9.61	5.71	73.4	1.77e+008	(R)VPTPDVSVVDLTVR(L)	1496.832
12	008-1101.4536.4587.2	2	8.75	2.69	73.3	4.71e+007	(K)DDTPMFVMGVNNTK(Y)	1568.709
13	008-1101.4310.4310.0	2	7.96	4.92	64.5	1.94e+007	(R)VPTPDVSVVDLTVR(L)	1496.832
14	008-1102.4527.4551.2	2	7.13	2.76	71.7	3.23e+007	(K)DDTPMFVMGVNNTK(Y)	1568.709

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
27	27.1	4	2	24.52	7	1.39e+008	41997.7	PA_BSC2:2534576868	PA_BSC2:2534576868 Bsc2_04557 Phosphoglycerate dehydrogenase and related dehydrogenases [Alteromonadac

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	007-1001.4148.4187.0	2	13.93	6.93	83.3	2.64e+007	(K)YSVGEEAAAPEAVLLR(S)	1674.870
2	007-1002.4132.4206.2	2	13.91	9.61	83.2	3.08e+007	(K)YSVGEEAAAPEAVLLR(S)	1674.870
3	006-0902.4205.4217.2	2	12.37	6.74	82.1	6.07e+007	(K)YSVGEEAAAPEAVLLR(S)	1674.870
4	006-0902.5299.5299.0	2	10.59	10.59	74.0	2.15e+007	(K)ELVLTGMLLSSR(G)	1318.740

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
28	28.1	2	2	22.35	27	2.06e+008	19039.9	PA_BSC2:2534573441	PA_BSC2:2534573441 Bsc2_01126 LSU ribosomal protein L6P [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	003-0601.6549.6579.0	3	14.58	8.05	83.3	1.24e+008	(K)TLNLTLGFSHPIDYDLPEGVSAETPSQTEIVLK(S)	3584.838
2	003-0601.4387.4387.0	2	7.77	7.77	66.3	8.18e+007	(R)ALVNNMVTGVSDGFEK(K)	1680.827

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

(#)	(#)	(#)	Peptides (#)	MS/MS Search Score	Coverage	Spectral Intensity	MW (Da)	Accession #	Protein Name
29	29.1	3	2	22.07	8	7.21e+007	36669.8	PA_BSC2:2534573291	PA_BSC2:2534573291 Bsc2_00976 ketol-acid reductoisomerase (EC 1.1.1.86) [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	006-0901.5938.5938.0	2	11.22	5.85	80.1	3.14e+007	(K)QFILEGQSNYPSMTAWR(R)	2027.965
2	006-0902.2838.2838.2	2	10.85	10.85	70.8	1.55e+007	(K)DSGVDVTVGLR(A)	1117.585
3	006-0901.4981.4981.0	2	8.94	2.49	80.9	2.51e+007	(K)QFILEGQSNYPSMTAWR(R)	2027.965

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
30	30.1	14	1	21.50	10	1.30e+009	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	006-0901.2692.2768.2	2	21.50	21.50	100.0	1.55e+008	(K)TQLEEAGASVELK(-)	1374.712
2	006-0901.2713.2719.2	2	20.32	16.44	97.0	2.04e+008	(K)TQLEEAGASVELK(-)	1374.712
3	006-0902.2694.2739.2	2	19.83	16.59	97.2	1.39e+008	(K)TQLEEAGASVELK(-)	1374.712
4	006-0901.2780.2808.2	2	19.73	16.30	95.7	8.60e+007	(K)TQLEEAGASVELK(-)	1374.712
5	003-0601.2689.2730.0	2	18.38	11.49	90.9	2.80e+008	(K)TQLEEAGASVELK(-)	1374.712
6	003-0602.2678.2695.0	2	18.38	14.18	90.2	1.15e+008	(K)TQLEEAGASVELK(-)	1374.712
7	003-0601.2681.2734.0	2	15.84	15.84	84.3	5.66e+007	(K)TQLEEAGASVELK(-)	1374.712
8	006-0902.2784.2784.2	2	14.24	14.24	88.5	4.57e+007	(K)TQLEEAGASVELK(-)	1374.712
9	002-0502.2731.2759.2	2	14.05	14.05	78.8	2.05e+007	(K)TQLEEAGASVELK(-)	1374.712
10	002-0501.2749.2749.2	2	12.70	8.86	77.1	3.92e+007	(K)TQLEEAGASVELK(-)	1374.712
11	002-0501.2748.2767.2	2	11.91	11.91	77.3	2.16e+007	(K)TQLEEAGASVELK(-)	1374.712
12	002-0501.2754.2754.2	2	10.98	6.73	69.5	1.98e+007	(K)TQLEEAGASVELK(-)	1374.712
13	004-0701.2687.2687.2	2	10.13	10.13	73.4	9.75e+007	(K)TQLEEAGASVELK(-)	1374.712
14	007-1001.2733.2738.0	2	9.97	6.78	60.1	1.59e+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
31	31.1	2	2	20.22	5	4.75e+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	005-0801.3175.3222.2	2	12.09	5.81	81.2	4.67e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
2	001-0401.6402.6402.0	3	8.13	8.13	71.4	7.06e+006	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262

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	3	2	20.01	10	5.36e+008	27993.3	PA_BSC2:2534573471	PA_BSC2:2534573471 Bsc2_01156 Dehydrogenases with different specificities (related to short-chain alcohol dehyd

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	005-0801.9132.9132.2	2	10.50	5.62	74.3	1.76e+008	(R)VPLLEMPLEEWELVIK(T)	1938.066
2	005-0802.5216.5216.2	2	9.51	9.51	65.0	1.85e+008	(R)VEGNPFNDFIINR(T)	1534.765
3	005-0802.9020.9020.2	2	9.06	3.06	70.5	1.75e+008	(R)VPLLEMPLEEWELVIK(T)	1938.066