Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\080210_OGL_gill2_zip_duplicate
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 0 **Hits:** 0
Data Directory: msdataSM\080210_OGL_gill3_zip_duplicate
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 6 **Hits:** 15
Data Directory: msdataSM\080310_OGL_gill2_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 5 **Hits:** 5
Data Directory: msdataSM\080310_OGL_gill3_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 12 **Hits:** 23
Data Directory: msdataSM\080410_gill2_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 14 **Hits:** 29
Data Directory: msdataSM\080410_gill3_zip
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 16 **Hits:** 25
beginning to assemble proteins .... proteins assembled 0.013293 sec
proteins filtered by unique peptides 0.001489 sec
proteins filtered by score
calculated protein coverage maps 0.017153 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.001564 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 8 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	15	6	87.50	20	3.14e+008	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]
1	1.1	6	3	42.76	10	1.51e+008	57219.5	PA_Bse08:2503995261	PA_Bse08:2503995261 BS08DRAFT_00037250 chaperonin GroL [B. setacea BS08 (Isolate from shipw
1	1.1	5	2	29.63	6	1.18e+008	57147.5	PA_Bse02:2503998519	PA_Bse02:2503998519 BS02DRAFT_00025680 chaperonin GroL [B. setacea BS02 (Isolate from shipw
1	1.1	5	2	29.63	6	1.18e+008	55514.7	PA_Bse_meta_comb:2073565377	PA_Bse_meta_comb:2073565377 BaSeMet_00090330 chaperonin GroL [Bankia setacea microbiome (C
2	2.1	14	4	61.97	40	3.88e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
3	3.1	12	4	47.82	10	8.20e+007	109063.9	PA_Bse02:2503998993	PA_Bse02:2503998993 BS02DRAFT_00000010 TonB-dependent receptor [B. setacea BS02 (Isolate fro
3	3.1	12	4	47.82	10	8.20e+007	109063.9	PA_Bse_meta_comb:2073560314	PA_Bse_meta_comb:2073560314 BaSeMet_00039700 TonB-dependent receptor [Bankia setacea micro
4	4.1	5	2	30.59	18	5.99e+007	27641.5	PA_Bse02:2504001159	PA_Bse02:2504001159 BS02DRAFT_00031400 FKBP-type peptidyl-prolyl cis-trans isomerase./Domain
4	4.1	5	2	30.59	18	5.99e+007	27641.5	PA_Bse_meta_comb:2073579700	PA_Bse_meta_comb:2073579700 BaSeMet_00233560 FKBP-type peptidyl-prolyl cis-trans isomerases 1
5	5.1	2	2	28.06	4	3.13e+007	109777.4	PA_Bse02:2503999606	PA_Bse02:2503999606 BS02DRAFT_00003500 TonB-dependent receptor [B. setacea BS02 (Isolate fro
5	5.1	2	2	28.06	5	3.13e+007	92261.9	PA_Bse_meta_comb:2073556678	PA_Bse_meta_comb:2073556678 BaSeMet_00003340 TonB-dependent receptor [Bankia setacea micro
6	6.1	2	2	27.41	9	6.77e+007	38937.1	PA_BSC2:2534573407	PA_BSC2:2534573407 Bsc2_01092 fructose-bisphosphate aldolase (EC 4.1.2.13) [Alteromonadacea ba
6	6.1	2	2	27.41	9	6.77e+007	38921.1	PA_Bse_meta_comb:2073595811	PA_Bse_meta_comb:2073595811 BaSeMet_00394670 fructose-bisphosphate aldolase (EC 4.1.2.13) [B
7	7.1	2	2	26.33	12	4.26e+007	35965.2	PA_Bse02:2503999320	PA_Bse02:2503999320 BS02DRAFT_00011490 glyceraldehyde-3-phosphate dehydrogenase, type I [B.
7	7.1	2	2	26.33	12	4.26e+007	35965.2	PA_Bse_meta_comb:2073585080	PA_Bse_meta_comb:2073585080 BaSeMet_00287360 glyceraldehyde-3-phosphate dehydrogenase, typ
8	8.1	1	1	20.15	18	2.59e+007	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
Totals:	92	42							

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	15	6	87.50	20	3.14e+008	56981.3	PA_BSC2:2534576049	PA_BSC2:2534576049 Bsc2_03736 chaperonin GroL [Alteromonadacea bacterium Bsc2]

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	072-3701.4727.4746.0	3	17.77	17.77	89.5	1.72e+007	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
2	072-0701.3774.3787.0	2	15.83	11.74	87.0	2.70e+007	(K)MLAGVNVLADAVK(I)	1300.730
3	072-0701.2604.2604.2	2	15.39	15.39	83.8	3.07e+007	(K)SVAAGMNPMDLK(R)	1233.597
4	072-3701.4180.4180.0	3	14.24	14.24	79.4	2.26e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
5	072-3601.4723.4723.0	3	13.28	13.28	75.5	1.05e+007	(K)SIAQVGTISANSDTQVGDIIAEAMGK(V)	2576.288
6	072-0701.3402.3402.0	3	13.13	13.13	74.7	3.22e+007	(R)AVASIADLTGDNEDQDAGIGIAR(R)	2272.106
7	086-1501.3809.3816.2	2	12.91	8.42	80.7	1.26e+007	(K)MLAGVNVLADAVK(I)	1300.730
8	072-0701.4201.4211.0	3	12.28	6.50	77.0	2.18e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
9	072-3601.4175.4175.0	3	12.05	5.39	74.9	2.22e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
10	072-3601.4163.4163.0	3	11.59	8.41	74.9	2.10e+007	(K)ASDDAGDGTTTATVLAQSIVNEGLK(S)	2434.195
11	086-1501.3802.3802.0	2	11.34	7.00	73.2	1.15e+007	(K)MLAGVNVLADAVK(I)	1300.730
12	072-0701.3925.3943.2	2	11.14	5.51	80.1	2.09e+007	(R)ELLPVLETVAK(A)	1211.725
13	072-0701.3792.3792.0	2	10.85	10.85	68.6	2.72e+007	(K)MLAGVNVLADAVK(I)	1300.730
14	086-1501.3932.3978.0	2	10.60	4.68	66.9	1.69e+007	(R)ELLPVLETVAK(A)	1211.725
15	072-3601.3756.3756.0	2	7.49	7.49	61.8	1.97e+007	(K)MLAGVNVLADAVK(I)	1300.730

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	14	4	61.97	40	3.88e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiome

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	071-0601.3849.3872.2	2	16.82	7.94	94.9	4.06e+006	(K)TVTAMDVVYALK(R)	1310.703
2	086-1501.2406.2436.2	2	16.30	11.14	94.2	5.91e+007	(R)ISGLIYEETR(G)	1180.621
3	085-1401.3891.3915.2	2	16.28	8.39	93.6	2.58e+006	(K)TVTAMDVVYALK(R)	1310.703
4	086-1501.3952.3970.0	2	15.73	8.21	93.0	7.79e+007	(K)TVTAMDVVYALK(R)	1310.703
5	086-1501.3212.3224.0	2	15.65	6.52	95.7	6.29e+007	(K)VFLENVIR(D)	989.578
6	072-0701.3153.3159.0	2	14.91	5.67	96.0	6.76e+007	(K)VFLENVIR(D)	989.578
7	072-0701.2325.2343.2	2	14.35	8.80	88.8	5.40e+007	(R)ISGLIYEETR(G)	1180.621
8	086-1501.2013.2029.0	3	13.20	4.04	90.2	2.27e+007	(R)DNIQGITKPAIR(R)	1325.754
9	071-0601.3161.3166.0	2	13.04	4.70	90.6	4.29e+006	(K)VFLENVIR(D)	989.578
10	071-0601.1966.1972.2	2	12.94	8.32	78.3	5.87e+006	(R)DNIQGITKPAIR(R)	1325.754
11	071-0601.1960.1976.0	3	12.69	3.76	89.6	2.98e+006	(R)DNIQGITKPAIR(R)	1325.754
12	071-0601.1955.1955.0	2	9.54	9.54	66.3	5.99e+006	(R)DNIQGITKPAIR(R)	1325.754
13	085-1401.2019.2019.0	3	8.56	2.37	83.0	3.70e+006	(R)DNIQGITKPAIR(R)	1325.754
14	072-0701.1965.1965.0	2	6.66	6.66	81.6	1.42e+007	(R)DNIQGITKPAIR(R)	1325.754

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	12	4	47.82	10	8.20e+007	109063.9	PA_Bse02:2503998993	PA_Bse02:2503998993 BS02DRAFT_00000010 TonB-dependent receptor [B. setacea BS02 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev	SPI	Spectrum	Sequence	MH+

				Score	(%)	Intensity		Matched (Da)
1	085-1401.5008.5081.0	3	17.59	17.59	90.4	1.14e+007	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
2	085-1401.4996.5075.0	3	16.44	16.44	88.3	1.22e+007	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
3	085-1401.4497.4545.0	3	15.58	15.58	84.9	5.55e+006	(R)FGVLAAFTSSQADLANYYEGK(Q)	2252.088
4	086-1501.5112.5112.0	3	14.76	14.76	79.8	4.70e+006	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
5	085-1401.4991.5056.0	3	13.69	13.69	85.4	1.10e+007	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
6	086-1501.4620.4620.0	3	12.82	8.05	80.4	4.18e+006	(R)FGVLAAFTSSQADLANYYEGK(Q)	2252.088
7	085-1401.5068.5068.0	3	12.58	12.58	78.5	6.04e+006	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
8	086-1501.4617.4617.0	3	10.57	5.04	75.0	4.33e+006	(R)FGVLAAFTSSQADLANYYEGK(Q)	2252.088
9	086-1501.5106.5106.0	3	9.24	9.24	81.1	4.84e+006	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
10	086-1501.5251.5251.0	3	8.51	4.95	82.2	9.29e+006	(R)GLPQVSTQLNGESYLGANSITDFQPNFGDIPSQLFK(G)	3882.919
11	086-1501.5115.5115.0	2	7.76	2.85	72.5	2.99e+006	(R)NFQDVLPALNVAWDVSDDVK(I)	2245.114
12	085-1401.5960.5960.0	2	6.14	2.40	64.6	5.42e+006	(R)SSTIEATAEWYLAPGSMLTAGIFR(I)	2572.276

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	5	2	30.59	18	5.99e+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	086-1501.5909.5915.0	3	15.66	15.66	81.7	1.80e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
2	085-1401.5788.5830.0	3	15.13	15.13	81.9	2.09e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405
3	085-1401.5080.5080.0	3	14.93	6.51	80.7	3.93e+006	(K)AIEISSLDDQVSYMLGFNMAR(Q)	2360.127
4	086-1501.5184.5184.0	3	14.14	5.71	79.7	3.52e+006	(K)AIEISSLDDQVSYMLGFNMAR(Q)	2360.127
5	086-1501.5879.5879.0	3	12.05	12.05	70.9	1.35e+007	(K)QFDFAINPELIALAVTEVNAGTEQR(Y)	2746.405

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	2	2	28.06	4	3.13e+007	109777.4	PA_Bse02:2503999606	PA_Bse02:2503999606 BS02DRAFT_00003500 TonB-dependent receptor [B. setacea BS02 (Isolate from shipwor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	085-1401.5465.5465.0	3	14.44	4.09	83.0	2.20e+006	(R)AFDFANLASEVIGGVDVYK(T)	2015.013
2	085-1401.5560.5560.0	3	13.62	7.91	76.3	2.91e+007	(R)EITEEVTSAYVELNQAFDLGDMPGNVVAGLR(Y)	3337.626

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	2	2	27.41	9	6.77e+007	38937.1	PA_BSC2:2534573407	PA_BSC2:2534573407 Bsc2_01092 fructose-bisphosphate aldolase (EC 4.1.2.13) [Alteromonadacea bacterium Bsc2

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	072-0701.2421.2421.0	2	14.51	14.51	79.3	2.05e+007	(K)AEGQQAQILGAVSGAK(H)	1527.813

2	072-0701.2697.2703.0	3	12.90	5.32	72.2	4.72e+007	(K)ILDAVKPGVLTGDDVQK(V)	1767.986

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.1	2	2	26.33	12	4.26e+007	35965.2	PA_Bse02:2503999320	PA_Bse02:2503999320 BS02DRAFT_00011490 glyceraldehyde-3-phosphate dehydrogenase, type I [B. setacea BS

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	085-1401.6056.6090.0	3	19.49	19.49	92.7	3.86e+007	(R)DNVEVVGINDLLDVDYIAYMLK(Y)	2511.269
2	085-1401.9868.9868.0	2	6.84	6.84	79.6	4.01e+006	(K)WGEIGADFVAEATGIFLTK(E)	2025.033

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	1	1	20.15	18	2.59e+007	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	072-0701.5285.5303.3	3	20.15	9.95	93.7	2.59e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391