Supplementary data

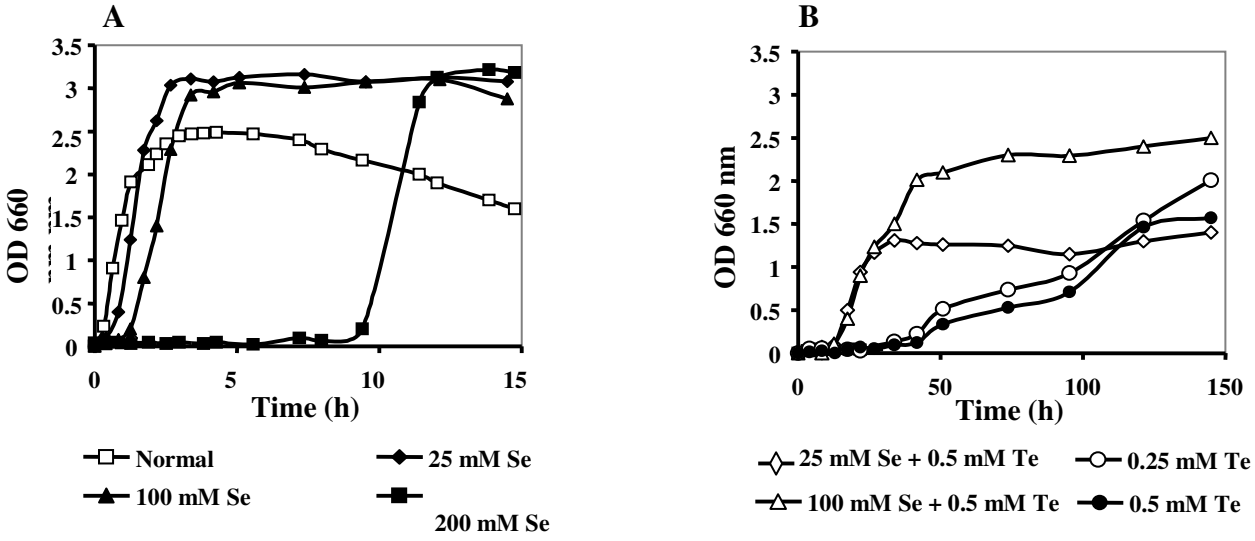
Supplementary Fig. 1. Growth curve of *Halomonas* sp. strain MAM in NB (8% NaCl) amended with different amounts of Se (25, 100, 200 mM), Te (0.25, 0.5 mM) oxyanions, 25 mM Se + 0.5 mM Te, 100 mM Se + 0.5 mM Te and control cultures without any added oxyanions. Sterile oxyanions were added at time zero.

Supplementary Fig. 2. Effect of salinity on (A) Te and (B) Se resistance (expressed as MIC) in *Halomonas* sp. strain MAM. (A): MIC of Te in Te amended NA (black column) and in Te + 25 mM Se amended NA (white column); (B): MIC of Se in Se amended NA. The histogram shows the average percent volume and standard deviation of three biological replicates.

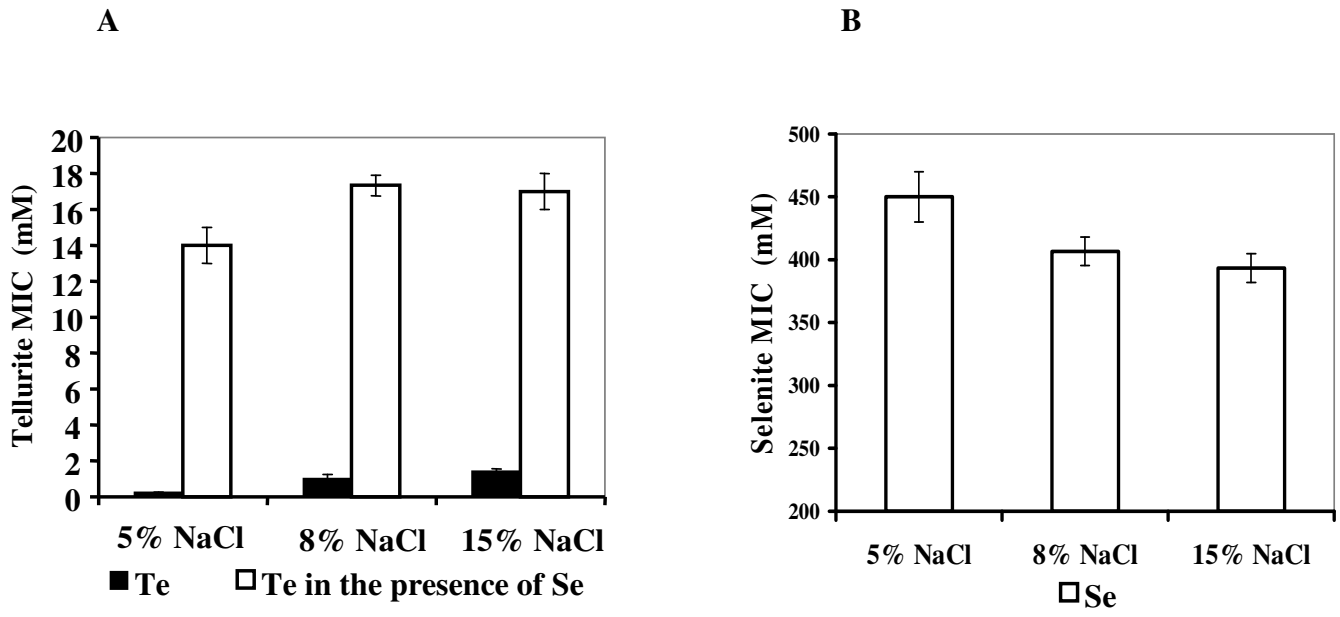
Supplementary Fig. 3. A representative normal 2-DE image of proteins extracted from *Halomonas* sp. strain MAM using TRI® Reagent. Numbered spots correspond to responsive proteins. Arrows indicate proteins identified by MS.

Supplementary Fig. 4. A representative 2-DE image of proteins extracted from *Halomonas* sp. strain MAM after Te treatment. Numbered spots correspond to responsive up-regulated proteins. Arrows indicate proteins identified by MS.

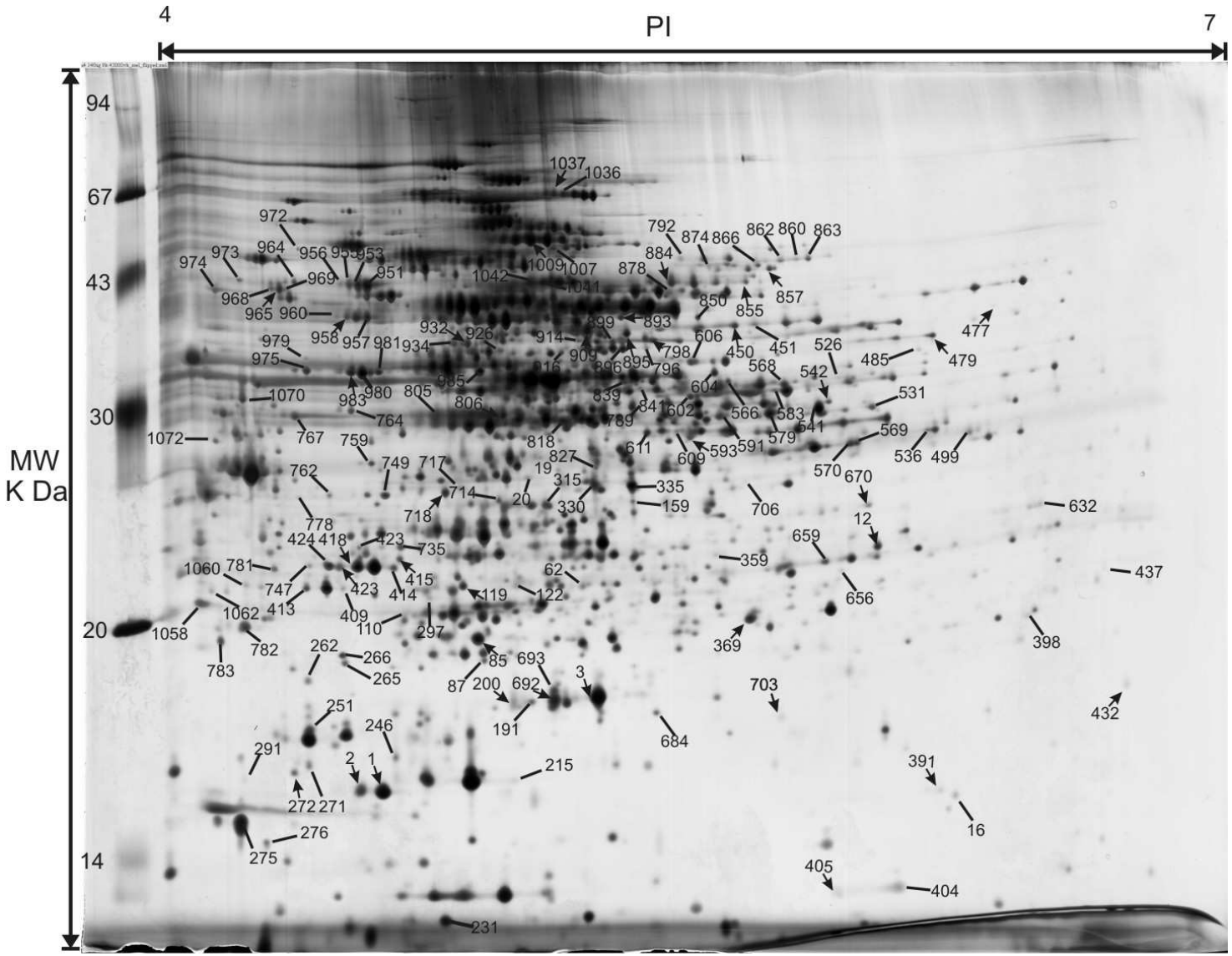
Supplementary Fig. 5. Expression pattern of four representative proteins under control (Normal), Te, Se and Te+Se stress.



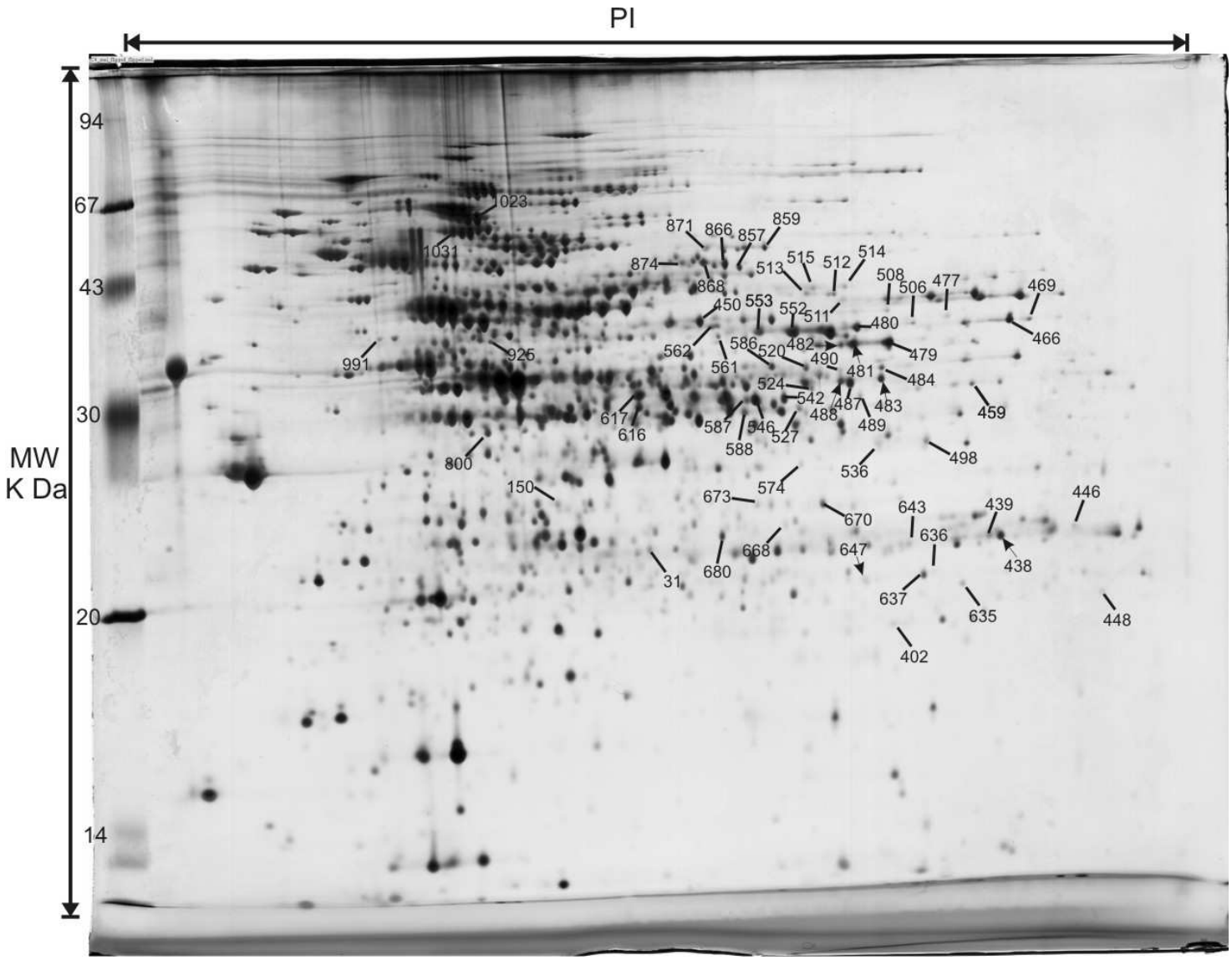
Supplementary Fig. 1



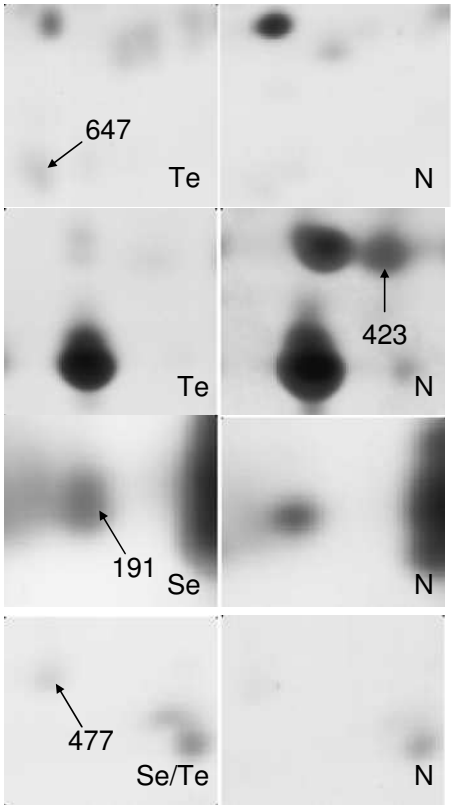
Supplementary Fig. 2



Supplementary Fig. 3



Supplementary Fig. 4



Supplementary Fig. 5

Supplementary Table 1. Useful features for differentiating *Halomonas* sp. strain MAM from other related species of the genus *Halomonas*. Data were obtained from Mata et al. (2002), and this study (Mata et al. 2002).

Characteristics	**Strain MAM**	***H. elongata***	***H. euryhalina***
Morphology	Short rod	Rod	Rod
Facultative anaerobe	+	+	-
Motility	+	+	-
Temperature range for growth (ºC)	10-50	4-45	4-45
NaCl concentration for growth range(% w/v)	0.5-32	0-20	0.5-25
NaCl optimum	5	3-8	7.5
pH range for growth	5-10	5-10	5-10
Nitrate reduction	+	+	+
Nitrite reduction	+	-	-
Hydrolysis of:			
Tween 80	-	-	+
Tween 20	+	-	+
Susceptibility to:			
amoxicillin	-	-	-
polymyxin B	+	-	+

Supplementary Table 2. Induction factors (the average percent volumes of protein spots in Te, Se, and Te+Se treatment/the average percent volumes of protein spots in normal condition) of responsive spots. Spots shown in gray are significant (*P*<5%).

spot #	Te/ N	Se/ N	Te+Se/ N	spot #	Te/ N	Se/ N	Te+Se/ N	spot #	Te/ N	Se/ N	Te+Se/ N
2	0.2	1.11	0.85	**481**	3.12	1.25	1.61	**762**	0.34	0.76	0.47
1	0.45	1.22	0.93	**482**	2.95	1.87	2.75	**764**	0.24	1.08	0.79
3	0.52	1.32	1.33	**483**	2.09	0.95	1.21	**767**	0.39	0.33	0.42
12	0.54	1.22	1.3	**484**	1.92	1.27	1.77	**781**	0.49	1.24	0.94
16	0.86	1.34	1.5	**485**	absent	1.79	1.88	**782**	0.27	0.19	0.09
19	0.92	0.68	0.72	**487**	1.71	1.03	0.92	**783**	0.27	1.67	0.69
20	0.61	0.3	0.71	**488**	1.58	0.72	1.09	**789**	1.68	1.66	2.45
29	1.6	1.28	2.12	**489**	1.65	1.32	1.22	**792**	0.82	0.61	1.01
31	1.69	1.04	1.02	**490**	1.91	1.22	1.75	**796**	0.65	0.54	0.81
62	1.03	0.52	0.39	**498**	2.93	2.22	2.45	**805**	0.65	0.52	0.38
82	0.52	0.79	0.56	**499**	absent	absent	absent	**806**	0.73	0.61	0.55
85	0.69	1.38	1.2	**506**	present			**818**	1.15	0.87	0.59
87	1.11	1.48	1.7	**508**	present			**827**	0.59	0.49	0.53
110	1.87	2.23	2.55	**511**	2.51	1.42	1.44	**839**	1.13	1.57	1.62
119	0.54	1.09	1.09	**512**	1.95	0.85	1.42	**841**	1.35	0.73	0.6
122	0.48	0.82	0.84	**513**	2.4	0.98	1.52	**850**	0.81	0.64	0.74
150	3.25	2.1	1.89	**514**	present			**857**	1.75	1.27	1.44
152	absent	1.52	1.7	**515**	present			**859**	2.59	1.03	1.36
159	0.82	0.52	0.65	**520**	1.84	1.01	1.79	**860**	absent	0.28	0.43
191	0.73	1.46	1.22	**524**	1.89	1.4	1.99	**862**	absent	absent	absent
200	0.58	1.49	1.5	**526**	1.84	1.45	2.95	**866**	2.83	1.33	1.64
215	0.62	absent	absent	**527**	1.78	1.03	1.35	**868**	2.74	1.19	1.56
231	0.34	1.2	0.83	**531**	0.88	0.58	0.77	**871**	2.35	1.5	1.76
235	0.7	1.21	1.82	**536**	4.39	2.01	2.31	**874**	1.93	0.88	1.55
251	1.39	1.62	1.1	**541**	0.67	0.73	0.63	**878**	1.14	1.49	1.72
262	0.52	1.31	1.21	**542**	2.44	0.99	1.44	**884**	0.92	0.62	0.79
265	0.5	0.56	0.64	**546**	6.09	2.41	2.33	**893**	0.59	1.88	1.76
266	1.06	1.85	1.86	**552**	2.16	0.97	1.65	**895**	0.69	0.69	0.66
271	0.47	1.4	1.26	**553**	2.96	1	0.8	**896**	0.52	0.74	0.68
272	absent	1.08	0.8	**561**	2.4	1.2	2.05	**899**	0.74	0.33	0.86
275	0.43	0.7	0.51	**562**	2.02	1	1.42	**909**	0.51	0.92	1.07
276	1.66	1.55	1.11	**566**	2.29	2.43	2.53	**914**	1.89	1.78	1.81
291	1.09	absent	absent	**568**	0.64	0.62	0.55	**916**	0.58	0.73	0.88
297	0.79	absent	absent	**569**	2.36	4.76	3.78	**925**	1.52	0.98	0.98
315	0.44	1.05	0.85	**574**	present			**926**	0.71	0.52	0.5
330	0.76	0.54	0.64	**579**	0.95	0.7	0.68	**932**	1.52	0.79	0.63
335	1.16	0.62	0.75	**583**	1.21	1.55	1.69	**934**	1.24	0.73	0.48
345	0.33	1.65	1.61	**586**	2.58	0.87	1.59	**951**	0.31	0.76	0.94
359	1.23	1.34	1.48	**587**	present			**953**	0.24	0.76	1.07
361	1.14	1.07	1.78	**588**	present			**955**	0.31	0.61	0.81
369	0.64	1.61	1.44	**591**	1.12	0.57	0.56	**956**	0.13	0.8	1.06
391	2.03	1.15	2.26	**602**	1.07	0.59	0.67	**957**	0.6	0.48	0.84
398	1.09	0.48	0.68	**604**	1.03	0.67	0.8	**958**	0.32	0.57	1.3
401	0.96	1.8	1.59	**606**	0.86	0.48	0.74	**960**	absent	0.7	1.45
402	1.59	1.31	1.52	**609**	0.75	0.57	0.83	**964**	0.37	0.88	0.78

404	1.21	1.82	1.25
405	1.9	3.28	1.74
409	0.55	1.23	1.27
413	0.88	1.69	1.52
414	0.36	1.51	1.2
415	0.27	0.79	1.04
418	0.65	1.48	1.43
421	0.51	1.99	1.92
423	0.37	1.47	1.25
424	0.38	1.13	0.86
432	1.04	1.34	1.55
437	1.15	0.89	1.75
438	2.05	0.82	1.73
439	1.85	1.09	1.97
446	1.68	1.16	1.67
448	1.52	0.87	1.08
450	2.1	0.98	1.54
451	0.99	0.66	0.83
459	1.89	1.01	1.25
465	0.85	1.62	1.63
466	3.81	1.67	2.14
469	present		
477	3.01	1.84	2.28
479	3.26	1.66	1.67
480	1.67	0.93	1.1

611	0.33	0.42	0.37
616	1.63	1.08	1.11
617	1.96	1.44	1.69
632	1.19	1.38	1.75
635	2.77	1.57	2.24
636	1.62	1.51	2.12
637	2.2	1.16	2.01
643	1.72	1	1.21
647	2.22	0.79	2.01
656	0.7	absent	0.47
659	1.84	1.3	1.63
668	present		present
670	2.6	0.85	1.51
673	1.78	0.95	1.42
680	1.7	1.36	1.54
684	0.59	1.27	1.06
692	0.52	1.48	1.62
693	0.36	1.85	1.86
703	0.91	1.19	1.52
714	0.43	1.38	1.35
718	0.69	0.71	0.53
735	0.56	0.84	0.81
747	0.49	1.36	0.93
749	0.29	1.18	0.87
759	0.36	0.81	0.7

965	0.34	0.83	0.71
968	0.42	1.03	0.99
969	absent	0.75	0.69
972	0.5	0.73	0.7
973	0.76	1.49	1.6
974	0.8	1.45	1.73
975	0.41	0.88	0.7
979	absent	0.54	0.64
980	0.6	1.31	1.06
981	0.41	0.75	0.56
983	0.48	0.95	0.78
991	present	present	present
1007	1.33	1.69	1.59
1023	1.51	1.36	1.38
1031	2.15	1.78	1.95
1036	0.52	1	0.99
1037	0.57	1.01	0.88
1041	1.5	1.55	1.14
1042	0.77	0.75	0.68
1058	0.36	2.22	1.26
1060	absent	absent	absent
1062	0.29	1.21	1
1072	0.4	1.07	1.13

Supplementary Table 3A. Proteins identified by MALDI TOF/TOF.

	Expression level									
Sopt #	**Te/N**	**Se/N**	**Te+Se/ N**	**Protien Homologouges**	**Accesion #**	**Score/ %Sequence Coverage**	**Exp/ Theo pI**	**Exp/ Theo MW**	**PMF/ MS-MS**	**Species**
1	0.45**	1.23	0.93	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	ZP_00419975	132/18%	4.6/5.2	16/20.9	3/1	[Azotobacter vinelandii AvOP]
2	0.2**	1.11	0.85**	alkyl hydroperoxide reductase, C22 subunit	ZP_01195816	133/15%	4.6/5.1	16/20.5	3/1	[Xanthobacter autotropicus PY2]
3	0.52**	1.32**	1.33	Aspartate/glutamate/uridylate kinase	ZP_00472949	167/36%	5.2/6.3	18/27.4	4/1	[Chromohalobacter salexigens DSM 3043]
12	0.54**	1.22	1.3	Aspartate/glutamate/uridylate kinase	ZP_00472949	323/37%	6.0/6.3	23/27.4	11/3	[Chromohalobacter salexigens DSM 3043]
85	0.69*	1.38**	1.2	Peroxidase	ABE57543	112/12%	4.9/4.7	20/23.6	2/1	[Chromohalobacter salexigens DSM 3043]
119	0.53*	1.08	1.09	COG0489: ATPases involved in chromosome partitioning	ZP_00242546	127/15%	4.9/5.9	22/38.4	3/1	[Rubrivivax gelatinosus PM1]
191	0.73	1.46*	1.22	protein of unknown function DUF47	ABE58072	119/9%	5.0/4.9	18/25.7	4/4	[Chromohalobacter salexigens DSM 3043]
200	0.57*	1.49	1.5	adenine phosphoribosyltransferase	ABE59449	134/28%	5.0/5.2	18/19.8	5/3	[Chromohalobacter salexigens DSM 3043]
272	absent	1.08	0.79	toluene tolerance	ABE59568.	133/7%	4.4/4.4	16/25.0	3/2	[Chromohalobacter salexigens DSM 3043]
369	0.63	1.6	1.44**	electron transfer flavoprotein beta-subunit	ABE58966	129/16%	5.7/5.6	20/26.9	7/4	[Chromohalobacter salexigens DSM 3043]
391	2.03	1.15	2.26*	transcription antitermination protein NusG	ABE57771	203/31%	6.2/5.6	16/20.4	4/2	[Chromohalobacter salexigens DSM 3043]
405	1.9	3.28**	1.74	ribosomal protein L10	gil91795635	178/13%	5.9/5.6	13/18.0	2/2	[Chromohalobacter salexigens DSM 3043]
415	0.54*	0.79	1.04	TRAP dicarboxylate transporter, DctP subunit	ABE57634	146/18%	4.7/4.7	23/37.4	5/2	[Chromohalobacter salexigens DSM 3043]
418	0.65*	1.48**	1.43*	electron transfer flavoprotein alpha subunit precursor	AAQ84564	201/31%	4.5/8.2	22/33.2	6/2	[Sus scrofa]
423	0.37*	1.47	1.25	Electron transfer flavoprotein, alpha subunit	ZP_01100992	98/5%	4.5/4.5	22/32	2/1	[Colwellia psychrerythraea 34H]
438	2.05*	0.82	1.73	5,10-methylene-tetrahydrofolate dehydrogenase/cyclohydrolase	AAN67878	113/26%	6.5/6.0	24/30.9	5/1	[Pseudomonas putida KT2440]
450	2.1**	0.98	1.54**	Adenylosuccinate synthetase	ABE58637	256/23%	5.6/5.4	38/47.4	11/2	[Chromohalobacter salexigens DSM 3043]

477	3.01**	1.84	2.28**	TRAP dicarboxylate transporter, DctP subunit	ABE57634	141/21%	6.3/4.7	39/37.4	7/2	[Chromohalobacter salexigens DSM 3043]
479	3.26**	1.66*	1.67	Acetyl-CoA carboxylase, biotin carboxylase	ZP_01143780	146/21%	6.2/6.3	36/49.2	8/3	[Geobacter uraniumreducens Rf4]
481	3.12**	1.25	1.61**	acetyl-CoA carboxylase, biotin carboxylase	ABE59635	267/19%	6.1/5.7	36/49.0	10/4	[Chromohalobacter salexigens DSM 3043]
482	2.95**	1.87	2.75**	aminotransferase class-III	ABE60071	161/26%	6.0/5.8	36/50.8	11/2	[Chromohalobacter salexigens DSM 3043]
483	2.09**	0.95	1.21	phosphofructokinase	ABE58887	127/12%	6.1/6.3	33/46	7/2	[Chromohalobacter salexigens DSM 3043]]
542	2.44**	0.99	1.44	chorismate mutase	ABE59517	211/27%	5.9/5.7	31/41.8	8/3	[Chromohalobacter salexigens DSM 3043]
593	0.57*	0.57	0.73	enoly-coenzyme A hydratase/isomerase family protein	AAN69092	79/11%	5.5/5.1	28/39.6	3/1	[Pseudomonas putida KT2440]
647	2.22**	0.79	2.01	ABC transporter	ZP_00629207	87/31%	6.1/6.7	21/29.1	5/1	[Paracoccus denitrificans PD1222]
670	2.6**	0.85	1.51	Ribose-phosphate pyrophosphokinase	EAM24191	171/27%	5.7/5.6	20/34.0	10/1	[Chromohalobacter salexigens DSM 3043]
703	0.9	1.19	1.52*	ATP-dependent Clp protease proteolytic subunit	Q6LNW0	75/18%	5.7/5.3	17/22.0	5/2	[Photobacterium]
718	0.69	0.7	0.52**	carbamate kinase	ZP_01206088	103/12%	4.8/5.3	26/33.3	2/1	[Mycobacterium vanbaalenii PYR-1]
806	0.73	0.61**	0.55**	succinyl-CoA synthetase, beta subunit [	ABE58575	142/20%	5/4.8.0	30/44.0	6/2	[Chromohalobacter salexigens DSM 3043]
857	1.75**	1.28**	1.44**	aldehyde dehydrogenase	ABE60151	177/11%	5.7/5.4	44/52.2	5/3	[Chromohalobacter salexigens DSM 3043]
884	0.92	0.62**	0.79	Succinate dehydrogenase or fumarate reductase, flavoprotein	ABE58570	332/33%	5.4/5.3	42/64.7	16/4	[Chromohalobacter salexigens DSM 3043]
893	0.59*	1.88*	1.76*	methylmalonate-semialdehyde dehydrogenase	ABE58482	224/16%	5.3/5.3	38/53.7	7/3	[Chromohalobacter salexigens DSM 3043]
895	0.69*	0.69*	0.66**	3-isopropylmalate dehydratase large subunit	ABE59800	404/15%	5.3/5.0	37/52.7	5/3	[Chromohalobacter salexigens DSM 3043]
909	0.51**	0.92	1.07	Protein of unknown function DUF1338	ABE58025	106/16%	5.2/5.1	37/50.9	9/1	[Chromohalobacter salexigens DSM 3043]
932	1.52	0.79	0.63*	ATP synthase beta chain	CAG77407	149/23%	4.9/4.8	36/50	7/2	[Chromohalobacter salexigens DSM 3043]
1037	0.57**	1	0.88	translation elongation factor G	ABE57780	149/16%	5.1/4.9	67/78.2	8/5	[Chromohalobacter salexigens DSM 3043]

Supplemantary Table 3B- Expression level of identified proteins which showed significant change in response to treatments.

		Average %volume				Standard deviation			
Sopt #	Accession #	Normal	Te	Se	Te+Se	Noraml	Te	Se	Te+Se
895	ABE59800	0.10	0.07	0.07	0.07	0.004	0.019	0.016	0.003
1	ZP_00419975	0.49	0.22	0.60	0.45	0.025	0.097	0.042	0.013
2	ZP_01195816	0.24	0.05	0.27	0.20	0.057	0.037	0.094	0.098
85	ABE57543	0.30	0.21	0.41	0.36	0.026	0.063	0.050	0.067
423	ZP_01100992	0.07	0.03	0.11	0.09	0.019	0.010	0.047	0.029
415	ABE57634	0.05	0.02	0.04	0.05	0.006	0.005	0.019	0.029
983	AAO75405	0.13	0.06	0.12	0.10	0.009	0.022	0.010	0.021
119	ZP_00242546	0.10	0.05	0.11	0.11	0.003	0.025	0.012	0.014
958	ABB49496	0.08	0.03	0.04	0.10	0.028	0.007	0.003	0.022
1037	ABE57780	0.06	0.04	0.06	0.05	0.008	0.008	0.010	0.016
965	ABC82684	0.07	0.03	0.06	0.05	0.019	0.015	0.011	0.009
200	ABE59449	0.09	0.05	0.13	0.13	0.014	0.007	0.060	0.033
3	ZP_00472949	0.65	0.34	0.86	0.87	0.042	0.142	0.075	0.190
12	ZP_00472949	0.12	0.06	0.14	0.15	0.010	0.011	0.062	0.028
593	AAN69092	0.06	0.04	0.04	0.05	0.014	0.014	0.003	0.017
909	ABE58025	0.21	0.10	0.19	0.22	0.025	0.005	0.085	0.051
272	ABE59568.	0.06		0.06	0.05	0.023		0.027	0.026
418	AAQ84564	0.25	0.16	0.36	0.35	0.054	0.044	0.035	0.050
893	ABE58482	0.06	0.03	0.11	0.10	0.006	0.009	0.032	0.024
884	ABE58570	0.14	0.13	0.08	0.11	0.015	0.041	0.016	0.031
806	ABE58575	0.12	0.09	0.08	0.07	0.012	0.041	0.022	0.018
718	ZP_01206088	0.10	0.07	0.07	0.05	0.013	0.029	0.023	0.016
932	CAG77407	0.06	0.10	0.05	0.04	0.010	0.025	0.005	0.005
369	ABE58966	0.16	0.10	0.26	0.23	0.024	0.058	0.093	0.029
703	Q6LNW0	0.03	0.03	0.03	0.04	0.006	0.013	0.011	0.005
391	ABE57771	0.04	0.09	0.05	0.10	0.028	0.038	0.020	0.013
405	gi|91795635	0.03	0.06	0.10	0.05	0.021	0.041	0.032	0.023
191	ABE58072	0.07	0.05	0.10	0.08	0.009	0.013	0.014	0.010
647	ZP_00629207	0.02	0.05	0.02	0.04	0.008	0.007	0.006	0.018
670	EAM24191	0.04	0.10	0.03	0.06	0.004	0.020	0.013	0.037
542	ABE59517	0.04	0.10	0.04	0.06	0.003	0.025	0.013	0.015
483	AAU92465	0.04	0.10	0.04	0.06	0.011	0.023	0.011	0.016
438	AAN67878	0.06	0.12	0.05	0.10	0.029	0.029	0.007	0.016
477	ABE57634	0.01	0.02	0.01	0.02	0.003	0.004	0.007	0.003
450	ABE58637	0.08	0.17	0.08	0.12	0.015	0.021	0.029	0.017
482	ABE60071	0.02	0.05	0.03	0.04	0.003	0.013	0.015	0.008
432	EAO23070	0.03	0.03	0.04	0.05	0.007	0.007	0.015	0.002
481	ABE59635	0.05	0.15	0.06	0.08	0.013	0.038	0.018	0.007
479	ZP_01143780	0.06	0.19	0.09	0.09	0.012	0.037	0.018	0.029
857	ABE60151	0.04	0.08	0.06	0.06	0.004	0.013	0.006	0.009

Supplementary table 3C. Proteins identified by MALDI TOF/TOF.

Spot 1

gi|67159414 Mass: 20867 Score: 132 Expect: 2.2e-007 Peptides matched: 4

Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Azotobacter vinelandii AvO]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1410.71	1409.70	1409.80	-0.10	131	143	0	118	IQIIELNAGNIGR
1410.71	1409.70	1409.80	-0.10	131	143	0		IQIIELNAGNIGR
1422.71	1421.71	1421.76	-0.05	1	12	0		MSLINTEVKPFK + Oxidation (M)
2439.09	2438.09	2438.33	-0.24	121	143	1		GTFVVDPQGKIQIIELNAGNIGR

Spot 2

gi|89357994 Mass: 20467 Score: 133 Expect: 1.8e-007 Peptides matched: 4

alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides [Xanthobacter autotrop]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1230.5	1229.50	1229.57	-0.07	81	91	0		AWHDSSETIGK
1933.84	1932.83	1932.96	-0.12	64	80	0		LGVEIYSVSTDTHFTHK
1933.84	1932.83	1932.96	-0.12	64	80	0	119	LGVEIYSVSTDTHFTHK
2061.93	2060.93	2061.05	-0.13	63	80	1		KLGVEIYSVSTDTHFTHK

Spot 3

gi|67676198 Mass: 27382 Score: 167 Expect: 7e-011 Peptides matched: 5

Aspartate/glutamate/uridylate kinase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1460.7	1459.70	1459.79	-0.09	208	220	0		LGVMDLTAICLVR
2279.03	2278.02	2278.26	-0.23	23	43	1		ILLKLSGEALIGEHEFGIDPK
2967.13	2966.12	2966.41	-0.29	136	163	0	150	YLTSGDVVIFSAGTGNPFFTTDSAACLR
2967.13	2966.12	2966.41	-0.29	136	163	0		YLTSGDVVIFSAGTGNPFFTTDSAACLR
3085.07	3084.07	3084.45	-0.39	74	103	1		GAALHAAGMERVTGDHMGMLATVMNGLAMR + Oxidation (M)

Spot 12

gi|67676198 Mass: 27382 Score: 323 Expect: 1.8e-026 Peptides matched: 14

Aspartate/glutamate/uridylate kinase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.38	884.37	884.38	-0.01	221	227	0		DHDMPVR + Oxidation (M)
1099.49	1098.48	1098.52	-0.04	74	84	0		GAALHAAGMER + Oxidation (M)
1460.69	1459.69	1459.79	-0.10	208	220	0		LGVMDLTAICLVR
1460.69	1459.69	1459.79	-0.10	208	220	0	99	LGVMDLTAICLVR
1476.68	1475.67	1475.78	-0.11	208	220	0		LGVMDLTAICLVR + Oxidation (M)

1476.68	1475.67	1475.78	-0.11	208	220	0	48	LGVMDLTAICLVR + Oxidation (M)
1790.72	1789.72	1789.85	-0.13	115	130	0		VMSAIPMSGVVEHYDR
1822.71	1821.70	1821.84	-0.14	115	130	0		VMSAIPMSGVVEHYDR + 2 Oxidation (M)
1962.8	1961.79	1961.95	-0.15	115	131	1		VMSAIPMSGVVEHYDRR + Oxidation (M)
1978.79	1977.79	1977.94	-0.15	115	131	1		VMSAIPMSGVVEHYDRR + 2 Oxidation (M)
2004.96	2003.95	2003.94	0.01	85	103	0		VTGDHMGMLATVMNGLAMR
2021.03	2020.02	2019.94	0.08	85	103	0		VTGDHMGMLATVMNGLAMR + Oxidation (M)
2967.17	2966.16	2966.41	-0.25	136	163	0	189	YLTSGDVVIFSAGTGNPFFTTDSAACLR

Spot 85

gil91795404 Mass: 23566 Score: 112 Expect: 1.1e-05 Peptides matched: 3

Peroxidase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1710.81	1709.8	1709.79	0.01	40	54	0	105	DFTPVCTTELGEVSR
1710.81	1709.8	1709.79	0.01	40	54	0		DFTPVCTTELGEVSR
1179.66	1178.65	1178.63	0.02	135	145	0		LTLTYPASTGR

Spot 119

gil47572503 Mass: 38379 Score: 127 Expect: 3.6e-07 Matched peptides:4

COG0489: ATPases involved in chromosome partitioning [Rubrivivax gelatinosus PM1]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1477.78	1476.77	1476.71	0.07	189	201	0		GPMATQALEQMLR 2 Oxidation (M)
2163.18	2162.17	2162.23	-0.06	230	250	0	118	VPLTGAVIVTTPQDIALLDAR
2163.18	2162.17	2162.23	-0.06	230	250	0		VPLTGAVIVTTPQDIALLDAR
2374.14	2373.14	2373.14	-0.01	313	335	0		EQADAGRPTVVSDPDGDIAGIYK

Spot 191

gil91795933 Mass:25660 Score: 119 Expect: 2.3e-06 Peptides matched:8

protein of unknown function DUF47 [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1501.86	1500.85	1500.81	0.04	71	83	0	55	LNLPNTMFLPVSR
1501.86	1500.85	1500.81	0.04	71	83	0		LNLPNTMFLPVSR
1517.85	1516.84	1516.81	0.03	71	83	0	27	LNLPNTMFLPVSR Oxidation (M)
1517.85	1516.84	1516.81	0.03	71	83	0		LNLPNTMFLPVSR Oxidation (M)
975.57	974.56	974.52	0.04	102	110	0	58	DITGIMLGR
975.57	974.56	974.52	0.04	102	110	0		DITGIMLGR
991.55	990.55	990.52	0.03	102	110	0	34	DITGIMLGR Oxidation (M)
991.55	990.55	990.52	0.03	102	110	0		DITGIMLGR Oxidation (M)

Spot 200

gil91797310 Mass: 19813 Score: 134 Expect: 7.1e-08 Peptides matched: 8

adenine phosphoribosyltransferase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
958.52	957.51	957.48	0.03	2	9	0		SIYGDYIK
1512.79	1511.78	1511.75	0.03	14	26	0	20	TVPDWPQPGVNFR
1512.79	1511.78	1511.75	0.03	14	26	0		TVPDWPQPGVNFR
1114.67	1113.67	1113.63	0.04	40	48	1	41	KLIDSFVHR
1114.67	1113.67	1113.63	0.04	40	48	1		KLIDSFVHR
986.58	985.57	985.53	0.04	41	48	0	46	LIDSFVHR
986.58	985.57	985.53	0.04	41	48	0		LIDSFVHR
2183.15	2182.14	2182.15	0.04	142	163	0		SGGQVVETATIIDLPELGGAQK

Spot 272

gil91797429 Mass:25205 Score: 133 Expect: 9e-08 Peptides matched:5

toluene tolerance [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
953.52	952.51	952.48	0.03	80	88	0	82	YIGASVMGR
953.52	952.51	952.48	0.03	80	88	0		YIGASVMGR
969.51	968.5	968.47	0.03	80	88	0		YIGASVMGR Oxidation (M)
970.53	969.53	969.49	0.03	116	123	0	45	GLVTFDYR
970.53	969.53	969.49	0.03	116	123	0		GLVTFDYR

Spot 369

gil87118367 Mass: 26808 Score: 200 Expect: 3.5e-014 Peptides matched: 5

electron transfer flavoprotein beta-subunit [Marinomonas sp. MED121]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1068.52	1067.51	1067.60	-0.09	217	226	0		VISVTPPAER
2282.08	2281.07	2281.25	-0.18	158	179	0	180	EIDGGLQTLAISLPAVVTTDLR
2282.08	2281.07	2281.25	-0.18	158	179	0		EIDGGLQTLAISLPAVVTTDLR
2704.93	2703.93	2704.36	-0.43	25	48	1		AVELANVKMSINPFCEIAVEEAVR + Oxidation (M)
2891.33	2890.33	2890.58	-0.25	158	184	1		EIDGGLQTLAISLPAVVTTDLRLNEPR

Spot 391

gil67676686 Mass: 20379 Score: 203 Expect: 1.8e-014 Peptides matched: 7

transcription antitermination protein NusG [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1131.59	1130.59	1130.68	-0.10	154	163	0		LQVSVLIFGR
1131.59	1130.59	1130.68	-0.10	154	163	0	91	LQVSVLIFGR

1476.62	1475.62	1475.75	-0.13	164	176	0		STPVELEFAQVEK
1485.59	1484.58	1484.71	-0.13	5	16	0		WYVVHAYSGFEK
1485.59	1484.58	1484.71	-0.13	5	16	0	98	WYVVHAYSGFEK
2226.88	2225.87	2226.05	-0.17	132	151	0		VVDGPFADFNGVVEEVNYEK
2226.88	2225.87	2226.05	-0.17	132	151	0		VVDGPFADFNGVVEEVNYEK

Spot 405

gil91795635 Mass: 18207 Score: 178 Expect: 2.8e-12 Peptides matched: 4

ribosomal protein L10 [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2328.27	2327.27	2327.23	0.03	9	31	1	79	KAIVAEVSEAAQDALSVVVADSR
2328.27	2327.27	2327.23	0.03	9	31	1		
2200.18	2199.17	2199.14	0.04	10	31	0	89	AIVAEVSEAAQDALSVVVADSR
2200.18	2199.17	2199.14	0.04	10	31	0		

Spot 415

gil91795495 Mass: 37450 Score: 146 Expect: 4.5e-09 Peptides matched:7

TRAP dicarboxylate transporter, DctP subunit [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2032.08	2031.07	2031.01	0.06	1	17	1		VLAFFGGGK
895.52	894.51	894.5	0.01	152	160	0		MTQNWIDPNASRRPFAK
1051.63	1050.62	1050.6	0.02	152	161	1	30	VLAFFGGGKR
1051.63	1050.62	1050.6	0.02	152	161	1		VLAFFGGGKR
2057.07	2056.06	2056.05	0.01	231	248	0	99	FHEVAPHIGLSEHDITVR
2057.07	2056.06	2056.05	0.01	231	248	0		FHEVAPHIGLSEHDITVR
1666.81	1665.8	1665.81	-0.02	266	281	1		EAVMAAAQEAASYARK

Spot 418

gil35384836 Mass: 33206 Score: 201 Expect: 2.8e-014 Peptides matched: 8

electron transfer flavoprotein alpha subunit precursor [Sus scrofa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1668.74	1667.73	1667.94	-0.20	51	66	1		VAGVAKVLVAQHDAYK
1920.71	1919.71	1919.90	-0.20	231	249	0		AAVDAGFVPNDMQVGQTGK + Oxidation (M)
1920.71	1919.71	1919.90	-0.20	231	249	0	99	AAVDAGFVPNDMQVGQTGK + Oxidation (M)
2016.87	2015.87	2016.05	-0.19	169	187	1		ASSASPVGISEWLDQKLTK
2351.08	2350.08	2350.31	-0.23	250	272	0		IVAPELYIAVGISGAIQHLAGMK
2365.02	2364.01	2364.18	-0.17	83	103	1		QFNYTHICAGASAFGKNLLPR
2367.08	2366.07	2366.30	-0.23	250	272	0	80	IVAPELYIAVGISGAIQHLAGMK + Oxidation (M)
2367.08	2366.07	2366.30	-0.23	250	272	0		IVAPELYIAVGISGAIQHLAGMK + Oxidation (M)

Spot 423

gil71146182 Mass: 32070 Score: 98 Expect: 0.00032 Peptides matched: 3

electron transfer flavoprotein, alpha subunit [Colwellia psychrerythraea 34H]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1640.92	1639.91	1639.93	-0.01	211	227	1	92	LLDGIADKLGAAIGASR
1640.92	1639.91	1639.93	-0.01	211	227	1		LLDGIADKLGAAIGASR
815.47	814.47	814.47	0	219	227	0		LGAAIGASR

Spot 438

gil26988989 Mass: 30889 Score: 113 Expect: 1.8e-005 Peptides matched: 6

5,10-methylene-tetrahydrofolate dehydrogenase/cyclohydrolase [Pseudomonas putida KT2440]

Obsreved	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1194.61	1193.60	1193.70	-0.10	135	144	0		IPLLRPCTPK
1389.54	1388.53	1388.65	-0.11	119	130	0	90	DVDGFHPYNIGR
1389.54	1388.53	1388.65	-0.11	119	130	0		DVDGFHPYNIGR
1662.69	1661.68	1661.98	-0.30	131	144	1		LAQRIPLLRPCTPK
2035.88	2034.88	2035.18	-0.31	203	222	1		ADLVVVAAGKPGLVKGEWVK
3313.03	3312.03	3311.55	0.48	57	85	0		DCEEVGFISQAFDLPSETTQQALTELIDR

Spot 450

gil67676547 Mass: 47411 Score: 256 Expect: 8.9e-020 Peptides matched: 13

Adenylosuccinate synthetase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
857.35	856.34	856.42	-0.08	149	155	0		LGDMLHR + Oxidation (M)
1032.4	1031.39	1031.48	-0.09	295	304	0		GHEFGATTGR
1194.46	1193.46	1193.57	-0.11	308	317	0		CGWFDAVALR
1194.46	1193.46	1193.57	-0.11	308	317	0	102	CGWFDAVALR
1256.57	1255.56	1255.68	-0.11	333	343	0		LDVLDGLENIR
1350.55	1349.54	1349.67	-0.13	307	317	1		RCGWFDAVALR
1501.62	1500.62	1500.76	-0.14	4	17	0		NVVVLGTQWGDEGK
1626.7	1625.70	1625.86	-0.16	318	332	0		HAVQINSVSGLCLTK
1635.75	1634.75	1634.90	-0.15	100	113	0	96	LSPACPLILPYHVR
1635.75	1634.75	1634.90	-0.15	100	113	0		LSPACPLILPYHVR
1686.71	1685.71	1685.87	-0.17	4	19	1		NVVVLGTQWGDEGKGK
1779.71	1778.70	1778.87	-0.17	34	50	0		FQGGHNAGHTLVIDGEK
2864.28	2863.27	2863.52	-0.25	318	343	1		HAVQINSVSGLCLTKLDVLDGLENIR

Spot 477

gil91795495 Mass: 37450 Score: 141 Expect: 1.4e-08 Peptides matched: 9

TRAP dicarboxylate transporter, DctP subunit [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
895.5	894.49	894.5	0	152	160	0		VLAFFGGGK
1051.61	1050.6	1050.6	0.01	152	161	1	23	VLAFFGGGKR
1051.61	1050.6	1050.6	0.01	152	161	1		VLAFFGGGKR
2611.28	2610.27	2610.34	-0.07	206	228	0		EIYTGLQLGAIDGLLNEAEWIHR
2057.02	2056.01	2056.05	-0.04	231	248	0	96	FHEVAPHIGLSEHDITVR
2057.02	2056.01	2056.05	-0.04	231	248	0		FHEVAPHIGLSEHDITVR
2237.11	2236.11	2236.05	0.05	260	280	1		LDDAQREAVMAAAQEAASYAR
1666.78	1665.77	1665.81	-0.04	266	281	1		EAVMAAAQEAASYARK
1682.88	1681.87	1681.81	0.06	266	281	1		EAVMAAAQEAASYARK Oxidation (M)

Spot 479

gil88938314 Mass: 49257 Score: 146 Expect: 4.5e-09 Peptides matched: 11

Acetyl-CoA carboxylase, biotin carboxylase [Geobacter uraniumreducens Rf4]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1324.81	1323.8	1323.8	0	5	16	1	4	VLIANRGEIALR
1324.81	1323.8	1323.8	0	5	16	1		VLIANRGEIALR
1026.64	1025.64	1025.63	0	11	19	1		GEIALRVIR
1745.91	1744.9	1744.83	0.07	265	280	0		AVGYNSVGTMEFLVDK Oxidation (M)
2008.06	2007.05	2007.05	0	293	310	0	118	VQVEHPVTEMVTGVDIVR
2008.06	2007.05	2007.05	0	293	310	0		VQVEHPVTEMVTGVDIVR
2024.06	2023.05	2023.04	0.01	293	310	0	63	VQVEHPVTEMVTGVDIVR Oxidation (M)
2024.06	2023.05	2023.04	0.01	293	310	0		VQVEHPVTEMVTGVDIVR Oxidation (M)
1656.84	1655.83	1655.8	0.02	325	338	1		QSDIKINGHSIECR
1480.77	1479.76	1479.8	-0.04	388	400	1		LIVHAETRDDAIK
2311.15	2310.14	2310.17	-0.03	423	442	2		RIMANKDFIEGNIDTGFLEK

Spot 481

gil91797496 Mass:49049 Score: 267 Expect: 3.6e-21 peptides matched:14

acetyl-CoA carboxylase, biotin carboxylase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1172.7	1171.69	1171.67	0.01	1	10	1		MLDKVLIANR
1188.7	1187.69	1187.67	0.02	1	10	1		MLDKVLIANR Oxidation (M)
1324.83	1323.82	1323.8	0.03	5	16	1	19	VLIANRGEIALR
1324.83	1323.82	1323.8	0.03	5	16	1		VLIANRGEIALR
1126.62	1125.61	1125.57	0.04	35	43	1		ADRELMHVR

1058.7	1057.7	1057.66	0.03	152	160	1	44	RIGYPVIIK
1058.7	1057.7	1057.66	0.03	152	160	1		RIGYPVIIK
902.59	901.58	901.56	0.02	153	160	0		IGYPVIIK
2234.17	2233.16	2233.12	0.03	210	229	0	93	HVEVQVLADGQGNAIHLYDR
2234.17	2233.16	2233.12	0.03	210	229	0		HVEVQVLADGQGNAIHLYDR
2380.2	2379.2	2379.12	0.08	368	388	0		MDSHIYTGYSVPPHYDSLLGK
2396.21	2395.2	2395.12	0.08	368	388	0		MDSHIYTGYSVPPHYDSLLGK Oxidation (M)
1313.75	1312.74	1312.72	0.02	405	416	0	82	NALDELLVEGIK
1313.75	1312.74	1312.72	0.02	405	416	0		NALDELLVEGIK

Spot 482

gil91797932 Mass: 50773 Score: 161 Expect: 1.4e-10 Peptides matched: 13

aminotransferase class-III [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1296.68	1295.67	1295.71	-0.04	13	23	1		KVTFHASTHLR
1168.61	1167.61	1167.61	-0.01	14	23	0		VTFHASTHLR
2050.95	2049.94	2049.96	-0.02	50	67	0		EFIDGFAGLYCVNIGYGR
1131.59	1130.58	1130.6	-0.02	102	112	0		ILELAGPGMSK Oxidation (M)
1778.78	1777.77	1777.78	-0.01	113	128	0		VYYGMSGSDANETQLK Oxidation (M)
1351.7	1350.69	1350.7	-0.01	132	142	0	32	YYNNVLGRPQK
1351.7	1350.69	1350.7	-0.01	132	142	0		YYNNVLGRPQK
1479.78	1478.78	1478.8	-0.02	132	143	1		YYNNVLGRPQKK
1504.75	1503.74	1503.77	-0.03	151	166	0		GYHGSGIASGSLTGLK
1825.9	1824.89	1824.91	-0.02	254	269	0	81	YDVLLIADEVVCGFGR
1825.9	1824.89	1824.91	-0.02	254	269	0		YDVLLIADEVVCGFGR
1064.57	1063.56	1063.58	-0.02	396	404	1		RAFFDPALK
1741.88	1740.88	1740.93	-0.05	405	421	1		VGPRVSAAAMSENLIAR

Spot 483

gil91796748 Mass: 46103 Score: 127 Expect: 3.6e-07 Matched peptides: 9

phosphofructokinase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1326.76	1325.76	1325.72	0.04	130	141	0		MGYPLTAIHVPK
1342.77	1341.76	1341.71	0.05	130	141	0		MGYPLTAIHVPK Oxidation (M)
1049.63	1048.62	1048.57	0.05	184	192	0	25	VFVLEVMGR
1049.63	1048.62	1048.57	0.05	184	192	0		VFVLEVMGR
1065.62	1064.61	1064.57	0.04	184	192	0		VFVLEVMGR Oxidation (M)
1355.81	1354.8	1354.76	0.04	270	283	0		QLGGVAPTLAGMIK

2126.13	2125.12	2125.04	0.08	284	300	1		QDLGYKYHWAVADYLQR
1421.75	1420.75	1420.69	0.06	290	300	0	88	YHWAVADYLQR
1421.75	1420.75	1420.69	0.06	290	300	0		YHWAVADYLQR

Spot 542

gil91797378 Mass:41799 Score: 211 Expect: 1.4e-15 Peptides matched: 11

chorismate mutase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
871.5	870.49	870.5	-0.02	65	71	1		EAQVLRR
1793.98	1792.97	1792.94	0.04	105	121	0	65	VAYLGPEGTFTQQAALK
1793.98	1792.97	1792.94	0.04	105	121	0		VAYLGPEGTFTQQAALK
945.55	944.55	944.51	0.03	176	183	0	25	ICGEVVLR
945.55	944.55	944.51	0.03	176	183	0		ICGEVVLR
1815.97	1814.96	1814.92	0.04	199	213	1		ISRIYSHPQSLAQCR
1899.03	1898.02	1897.97	0.05	237	254	1		LIKSEWHSAAIAGDMAAK
1629.87	1628.86	1628.81	0.05	261	274	1		VAEKIEDRPDNSTR
1743.93	1742.92	1742.89	0.04	299	313	0	87	NQPGALHDLLEPFHR
1743.93	1742.92	1742.89	0.04	299	313	0		NQPGALHDLLEPFHR
882.52	881.51	881.51	0	314	320	1		HKIDLTR

Spot 593

gil26990203 Mass:39585 Score: 79 Expect: 0.024 Peptides matched:4

enoly-coenzyme A hydratase/isomerase family protein [Pseudomonas putida KT2440]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1398.68	1397.68	1397.74	-0.06	225	237	0		LGTQVLDDAPLEK
2163.06	2162.05	2161.99	0.06	295	312	1		GRELGIDDCFAMELHLDR Oxidation (M)
1296.77	1295.76	1295.76	0	326	336	2	71	ALIIDKDKQPR
1296.77	1295.76	1295.76	0	326	336	2		ALIIDKDKQPR

Spot 649

gil69934071 Mass: 29139 Score: 87 Expect: 0.0038 Peptides matched:6

ABC transporter [Paracoccus denitrificans PD1222]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
999.59	998.58	998.58	0	34	44	0		LALIGPSGSGK
1905.13	1904.13	1904.04	0.09	45	61	1		TTILRILMTLEDISGGR Oxidation (M)
2311.22	2310.21	2310.18	0.03	89	106	2		MRRHIGMVFQHFNLFPHK Oxidation (M)
1681.87	1680.86	1680.79	0.07	144	158	1	72	ADYMPSQLSGGQKQR Oxidation (M)
1681.87	1680.86	1680.79	0.07	144	158	1		ADYMPSQLSGGQKQR Oxidation (M)
2438.27	2437.27	2437.27	0	227	248	2		GRIVEQGPPAQIFTAPQEDRTK

Spot 670

gi|67675711 Mass: 34033 Score: 171 Expect: 2.6e-011 Peptides matched: 11

Ribose-phosphate pyrophosphokinase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
903.44	902.44	902.45	-0.01	19	26	0		VAESLDNR
1340.76	1339.76	1339.78	-0.03	288	300	0		QLSVAGLIAEAIR
1369.76	1368.75	1368.77	-0.02	183	194	1		QLNADLAIIDKR
1492.65	1491.64	1491.68	-0.04	301	313	1		RVSNEESVSAMFH
1496.86	1495.85	1495.88	-0.03	288	301	1		QLSVAGLIAEAIRR
1508.65	1507.64	1507.67	-0.03	301	313	1		RVSNEESVSAMFH + Oxidation (M)
1609.93	1608.93	1608.97	-0.04	286	300	1		IRQLSVAGLIAEAIR
1899.90	1898.90	1898.84	0.05	214	230	0		TCVVVDDMVDTAGTLCK + Oxidation (M)
1930.94	1929.93	1929.98	-0.05	159	176	0		QNYDDLVVVSPDVGGVVR
1930.94	1929.93	1929.98	-0.05	159	176	0	104	QNYDDLVVVSPDVGGVVR
2158.19	2157.18	2157.12	0.06	159	178	1		QNYDDLVVVSPDVGGVVRAR

Spot 703

gi|60389653 Mass:22053 Score: 75 Expect: 0.054 Peptides matched:7

ATP-dependent Clp protease proteolytic subunit (Endopeptidase Clp)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
3200.62	3199.61	3199.56	0.05	1	28	2		MSPITDALVPMVVEQTSRGERSYDIYSR
2185.08	2184.07	2184.12	-0.05	2	21	1		SPITDALVPMVVEQTSRGER
903.46	902.45	902.41	0.04	22	28	0		SYDIYSR
903.46	902.45	902.41	0.04	22	28	0	32	SYDIYSR
1065.57	1064.56	1064.52	0.04	117	124	1		RYCLPNSR
909.46	908.46	908.42	0.04	118	124	0	16	YCLPNSR
909.46	908.46	908.42	0.04	118	124	0		YCLPNSR

Spot 718

gi|90203442 Mass: 33304 Score: 103 Expect: 9e-05 Peptides matched: 3

carbamate kinase [Mycobacterium vanbaalenii PYR-1]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1209.82	1208.81	1208.76	0.05	3	14	0	96	IVIALGGNAILR
1209.82	1208.81	1208.76	0.05	3	14	0		IVIALGGNAILR
3136.61	3135.61	3135.49	0.11	246	273	2		ITPDELETMHFAAGSMGPKVEAACRFVR Oxidation (M)

Spot 806

gi|91796436 Mass: 44038 Score: 142 Expect: 1.1e-08 Peptides matched: 8

succinyl-CoA synthetase, beta subunit [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1337.74	1336.73	1336.7	0.03	31	42	0		QLFADYGLPVSK
2225.05	2224.05	2224.12	-0.07	92	110	1		AFAEQWLGKNLVTFQTDEK
1982.14	1981.14	1981.1	0.04	165	182	1		ILKAEIDPLVGAQPYQAR
1627.89	1626.88	1626.84	0.04	168	182	0	52	AEIDPLVGAQPYQAR
1627.89	1626.88	1626.84	0.04	168	182	0		AEIDPLVGAQPYQAR
1257.81	1256.8	1256.76	0.04	334	345	0	69	AVLVNIFGGIVR
1257.81	1256.8	1256.76	0.04	334	345	0		AVLVNIFGGIVR
2271.31	2270.31	2270.25	0.06	382	404	0		LASSGLNIIAATSLTDAAQQVVK

Spot 857

gil91798012 Mass: 52257 Score: 177 Expect: 3.6e-12 Peptides matched: 8

aldehyde dehydrogenase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1549.98	1548.98	1548.92	0.05	243	257	0		ILALELGGNNPLVVK
2663.38	2662.37	2662.3	0.08	391	415	1		DWDEAIALANDTRYGLSAGLIGGER
1192.68	1191.68	1191.62	0.05	404	415	0	53	YGLSAGLIGGER
1192.68	1191.68	1191.62	0.05	404	415	0		YGLSAGLIGGER
1150.6	1149.6	1149.55	0.05	416	424	0	78	ADWDDFLLR
1150.6	1149.6	1149.55	0.05	416	424	0		ADWDDFLLR
929.54	928.53	928.49	0.04	427	434	0	33	AGIVNWNR
929.54	928.53	928.49	0.04	427	434	0		AGIVNWNR

Spot 884

gil67677580 Mass: 64733 Score: 332 Expect: 2.2e-027 Peptides matched: 20

Succinate dehydrogenase or fumarate reductase, flavoprotein subunit:Succinate dehydrogenase, flavop

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1095.42	1094.41	1094.49	-0.08	69	76	0		WHMYDTVK + Oxidation (M)
1111.62	1110.62	1110.68	-0.06	328	337	1		RLPGIVELSK
1164.5	1163.49	1163.57	-0.08	295	304	0		AMVMEILEGR + Oxidation (M)
1180.5	1179.49	1179.56	-0.07	295	304	0		AMVMEILEGR + 2 Oxidation (M)
1280.59	1279.58	1279.67	-0.09	116	126	0		IYQRPFGGQSK
1280.59	1279.58	1279.67	-0.09	116	126	0	61	IYQRPFGGQSK
1407.61	1406.60	1406.68	-0.08	262	274	1		GEGGYLINKDGER
1459.74	1458.73	1458.82	-0.09	402	415	0	139	LGGNSLLDLVVFGR
1459.74	1458.73	1458.82	-0.09	402	415	0		LGGNSLLDLVVFGR
1632.72	1631.71	1631.81	-0.11	97	110	0		AVFELEHMGLPFSR

1648.71	1647.70	1647.81	-0.11	97	110	0		AVFELEHMGLPFSR + Oxidation (M)
1648.71	1647.70	1647.81	-0.11	97	110	0	20	AVFELEHMGLPFSR + Oxidation (M)
1670.64	1669.64	1669.74	-0.10	545	557	1	41	YDYPDRDDANWLK
1670.64	1669.64	1669.74	-0.10	545	557	1		YDYPDRDDANWLK
1722.82	1721.81	1721.92	-0.11	144	158	0		TGHALLHTLYQNNLK
2122.17	2121.16	2121.10	0.06	2	22	1		SNMRSLTFDAIIIGGGGSGLR
2167.96	2166.96	2167.09	-0.14	211	231	0		IYASTTNALINTGDGIGMALR + Oxidation (M)
2221.76	2220.76	2221.07	-0.32	97	115	1		AVFELEHMGLPFSRFDNGR
2236.76	2235.75	2235.89	-0.14	77	96	0		GGDYITDQEAAEYMCSEGPK + Oxidation (M)
2529.02	2528.01	2528.13	-0.12	45	68	0		SHTVSAQGGITCAIASADPNDDWR

Spot 893

gil91796343 Mass: 53745 Score: 224 Expect: 7.1e-17 Peptides matched:10

methylmalonate-semialdehyde dehydrogenase [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
801.42	800.41	800.39	0.03	67	72	0		VMFNFK Oxidation (M)
1399.76	1398.75	1398.71	0.04	73	84	0		QLLEQNADEIAR
2066.12	2065.11	2065.12	-0.01	217	235	1	122	VKAVSFVGSTPIAETIYQR
2066.12	2065.11	2065.12	-0.01	217	235	1		VKAVSFVGSTPIAETIYQR
2451.31	2450.3	2450.26	0.04	372	392	0		VTPDMTCYLEEIFGPVLLVVR
2467.33	2466.32	2466.25	0.07	372	392	0		VTPDMTCYLEEIFGPVLLVVR Oxidation (M)
1707.88	1706.87	1706.87	0	454	469	1		RSLFGDLAAYGPDAVR
1551.81	1550.8	1550.77	0.03	455	469	0	65	SLFGDLAAYGPDAVR
1551.81	1550.8	1550.77	0.03	455	469	0		SLFGDLAAYGPDAVR
772.45	771.44	771.4	0.04	481	487	0	15	WPSAGVR

Spot 895

gil67675604 Mass: 52748 Score: 404 Expect: 1.4e-034 Peptides matched: 8

3-isopropylmalate dehydratase large subunit [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1811.82	1810.81	1810.92	-0.11	197	215	0		IGTAGGTGYAIEFAGSAIR
1811.82	1810.81	1810.92	-0.11	197	215	0	143	IGTAGGTGYAIEFAGSAIR
1833.85	1832.85	1832.95	-0.11	31	46	0		HLLHEVTSPQAFEGLR
1833.85	1832.85	1832.95	-0.11	31	46	0	114	HLLHEVTSPQAFEGLR
1992.94	1991.94	1991.89	0.05	425	442	1		LGTGEHCASTSNRNFEGR
2205.02	2204.02	2204.15	-0.14	449	470	0		THLVSPAMAAAAAIAGHFVDVR
2205.02	2204.02	2204.15	-0.14	449	470	0	137	THLVSPAMAAAAAIAGHFVDVR
2221.01	2220.01	2220.15	-0.14	449	470	0		THLVSPAMAAAAAIAGHFVDVR + Oxidation

(M)

Spot 909

gil67676895 Mass: 50936 Score: 106 Expect: 8.9e-005 Peptides matched: 10

Protein of unknown function DUF1338 [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
835.47	834.47	834.50	-0.03	126	132	0		VFTSLLR
878.40	877.39	877.43	-0.04	288	294	0		FGEIEQR
1088.50	1087.50	1087.53	-0.03	238	247	1		RMPAAGMNPK + Oxidation (M)
1092.53	1091.52	1091.58	-0.06	210	218	0		LIADVVCFR
1130.50	1129.49	1129.56	-0.06	346	354	0	87	QGLAFFEYR
1130.50	1129.49	1129.56	-0.06	346	354	0		QGLAFFEYR
1141.56	1140.55	1140.62	-0.07	219	228	0		GPHINHLTPR
2855.15	2854.14	2854.39	-0.24	17	41	0		AMSAMYQAEVPQYETLLELVAEVNR
2871.15	2870.14	2870.38	-0.24	17	41	0		AMSAMYQAEVPQYETLLELVAEVNR + Oxidation (M)
2887.16	2886.15	2886.38	-0.23	17	41	0		AMSAMYQAEVPQYETLLELVAEVNR + 2 Oxidation (M)

Spot 932

gil91798489 Mass: 49695 Score: 149 Expect: 2.3e-09 Peptides matched:9

ATP synthase F1, beta subunit [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1669.04	1668.03	1667.96	0.07	5	19	0		IVQIIGAVIDVEFPR
1893.98	1892.98	1892.9	0.07	163	180	0		NIATEHSGYSVFAGVGER
1384.81	1383.81	1383.84	-0.04	215	227	1		LRVALTGLTIAEK
1366.8	1365.8	1365.73	0.07	234	244	0		DVLLFVDNIYR
1366.8	1365.8	1365.73	0.07	234	244	0	53	DVLLFVDNIYR
1450.86	1449.85	1449.78	0.07	245	258	0		YTLAGTEVSALLGR
1450.86	1449.85	1449.78	0.07	245	258	0	73	YTLAGTEVSALLGR
2018.12	2017.11	2017.04	0.08	322	340	0		SIAELGIYPAIDPLDSTSR
2163.15	2162.14	2162.07	0.07	367	385	1		ELKDIIAILGMDELSDEDK Oxidation (M)

Spot 1037

gil91795641 Mass: 78230 Score: 149 Expect: 2.3e-09 Matched peptides: 13

translation elongation factor G [Chromohalobacter salexigens DSM 3043]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2068.11	2067.1	2067.06	0.04	84	101	0	60	INIIDTPGHVDFTIEVER
2068.11	2067.1	2067.06	0.04	84	101	0		INIIDTPGHVDFTIEVER

2557.37	2556.36	2556.3	0.06	15	128	0		VLDGAVVVLCGSSGVQPQTETVWR	
1550.89	1549.88	1549.85	0.03	324	337	0	54	IATDPFVGTLTFIR	
1550.89	1549.88	1549.85	0.03	324	337	0		IATDPFVGTLTFIR	
1479.74	1478.73	1478.74	-0.01	376	389	0		EVYAGDIAACIGLK	
1720.85	1719.84	1719.86	-0.02	431	446	1		MGTALGKLAQEDPSFR	
1835.01	1834	1833.97	0.03	476	491	1	17	EFKVDANIGKPQVAYR	
1835.01	1834	1833.97	0.03	476	491	1		EFKVDANIGKPQVAYR	
1754.92	1753.91	1753.87	0.04	659	674	0	7	ATVPLAEMFGYATDLR	
1754.92	1753.91	1753.87	0.04	659	674	0		ATVPLAEMFGYATDLR	
1770.92	1769.91	1769.87	0.04	659	674	0	0	ATVPLAEMFGYATDLR	Oxidation (M)
1770.92	1769.91	1769.87	0.04	659	674	0		ATVPLAEMFGYATDLR	Oxidation (M)