

**Supplemental TABLE I.**

**Summary of decreased and increased protein spots in *R. capsulatus* DsbA-null mutant and revertant compared to the wild-type strain MT1131**

Micromass Protein-Lynx Global Server (Version 2.0, Waters/Micromass) search parameters for peptide mass fingerprint (PMF): database, *R. capsulatus* (Integrated Genomics Inc., Chicago, USA); enzyme, trypsin; miss cleavage sites, 1; no fixed or variable modification was applied; mass accuracy, 40 ppm; instrument type, MALDI-TOF-MS. SEQUEST (Version 3.1) search parameters for available MS/MS data: same database and enzyme with the PMF data analysis; the number of maximal internal (missed) cleavage sites, 2; mass tolerance for precursor ion, 2.5; mass tolerance for fragment ion, 1.0; no modification was considered. Matching peptides were filtered according to correlation scores ( $X_{\text{corr}}$  at least 1.5, 2.0 and 3.0 for 1+, 2+ and 3+ charged peptides, respectively) to give high confidence of protein identification; instrument type, nLC-ESI-MS/MS. Experimental Mr and the pI's were calculated using PDQuest 2D-gel analysis software (Version 7.2-Bio-Rad)

ORF #	Protein Name	SSP# <sup>a</sup>	Gene Name	Cys <sup>b</sup>	PDQuest								[Score	Cov%	NMP] <sup>d</sup>	z	$\Delta M$	$X_{\text{corr}}$ <sup>e</sup>	Peptide MS sequence
					Theoretical		Experimental		MD20 <sup>c</sup>		MD20R3 <sup>c</sup>								
					Mr	pI	Mr	pI	MT1131	MT1131	MT1131	MT1131							
<b>DECREASED PROTEINS</b>																			
RRC00091	Spermidine/Putrescine-Binding Periplasmic Protein	1402	<i>potD</i>	2	38.43	4.60	40.26	4.41	0.18	0.17	8.2	42.6	13						
														2	0.4	4.85	(K) YGDAPTYSFYGDDDEAYQK		
														2	0.4	3.91	(R) ALLDNIGYGHSSLK		
														2	0.2	3.86	(R) DAGLIEPWPAK		
														3	-1.0	3.67	(K) APILPQVPNDPQQR		
														2	0.2	3.46	(K) APILPQVPNDPQQR		
														1	0.2	2.94	(R) DAGLIEPWPAK		
														3	-1.1	2.88	(R) ALLDNIGYGHSSLK		
														2	0.0	2.80	(R) NENYPVAFQR		
														2	0.1	2.29	(K) YLDSPIFK		
														1	0.0	2.26	(K) YLDSPIFK		
														2	-1.0	2.26	(K) YLDSPIFKDDK		
RRC00677	Sorbitol-Binding Periplasmic Protein	2502		3	47.76	4.85	46.74	4.55	0.13	0.14				2	0.3	4.98	(K) VEWVTLEENVLR		
														2	0.4	3.63	(R) TSLYENPEYQK		
														2	0.5	2.87	(K) DYTALVASK		
														1	-0.5	2.84	(K) VEWVTLEENVLR		
														1	-1.0	2.80	(K) PQFDGEAWK		
														1	-0.5	2.57	(R) TSLYENPEYQK		
														1	-0.3	2.16	(K) FVEWATSK		
RRC00677	Sorbitol-Binding Periplasmic Protein	2503		3	47.76	4.85	46.74	4.56	0.12	0.13				2	-0.6	3.56	(K) AGLTMPAEPTWDDVK		
														2	0.7	3.38	(R) TSLYENPEYQK		

													1	-0.8	2.69	(K)	VEWVTLLEENVLR
													1	-0.3	2.65	(R)	TSLYENPEYQK
													2	0.7	2.41	(K)	EGWANVPPGTR
													1	0.0	2.18	(K)	FVEWATSK
													2	0.3	2.14	(K)	FVEWATSK
RRC00724	D-Xylose Binding Periplasmic Protein	1301	<i>xyfF</i>	2	35.03	4.29	36.88	4.38	0.61	0.51	8.2	29.2	8				
													2	0.2	4.58	(K)	SVAGATEWTSPAGTK
													2	-0.5	3.95	(K)	IVGEAYTDGWLPAQAQR
													3	-1.4	3.61	(R)	GGQQEVLQAAIDAGDIK
													2	-1.9	3.26	(R)	VALGTQTVSVWK
													2	0.0	3.25	(R)	GGQQEVLQAAIDAGDIK
													1	0.2	3.24	(K)	SVAGATEWTSPAGTK
RRC00775	Lysine-Arginine-Ornithine-Binding Protein	101	<i>argT</i>	2	25.18	5.10	27.63	4.26	0.27	0.23			2	0.6	5.25	(R)	KQTIDFSDNYNPPAASAYVATK
													2	-0.4	4.04	(K)	GVVAAQVGTIQADYVAK
													2	-0.7	2.76	(K)	NGEADAVFADK
													2	-0.2	2.68	(K)	ADGSLNAMIK
													1	0.7	2.46	(K)	KWFGDDAPVF
													1	-0.6	2.27	(K)	NGEADAVFADK
													2	0.2	2.18	(K)	WFGDDAPVF
													1	-0.6	1.83	(K)	WFGDDAPVF
RRC00804	Acriflavin Resistance Protein E	9202	<i>acrA</i>	1	36.36	8.55	36.60	5.94	0.61	0.01			2	0.3	3.83	(R)	GVAPLATLEAAAAK
													2	0.2	3.30	(R)	EAVIDVPDDLRL
													2	-0.1	3.10	(R)	PAEAVPVTLGQR
													2	0.2	1.90	(R)	SVTPGQQLGPR
RRC00984	ABC Transporter Substrate-Binding Protein	2401		2	35.20	4.70	41.75	4.55	0.23	0.21	8.1	57.5	13				
													2	0.2	5.50	(K)	APEGAYTLEITNEALK
													2	0.3	5.10	(R)	TVATLMGGGSDPVITK
													2	0.3	4.86	(K)	LTAGSNGALDVADYER
													3	-1.0	3.92	(K)	APEGAYTLEITNEALK
													2	0.3	3.75	(K)	LGIPTTGGADGVEVLK
													2	0.2	3.56	(K)	QGFNVDPLLQK
													1	0.2	2.63	(K)	LVNIAQPFK
RRC01044	Iron(III)-Binding Periplasmic Protein	5302		2	35.50	5.24	38.00	5.35	0.20	0.23	8.1	38.0	9				
													2	0.0	4.60	(K)	LLEYLTSDAAQK
													3	-0.9	3.41	(K)	DGGTHVNISGAAIAK

													2	0.3	3.37	(K) DGGTHVNISGAAIAK
													1	-0.3	2.48	(K) LYAEANFEYPPVK
RRC01044	Iron(III)-Binding Periplasmic Protein	6302	2	35.50	5.24	37.85	5.43	0.18	0.22	8.2	23.3	6				
													1	-0.5	3.72	(K) DGGTHVNISGAAIAK
													2	0.3	3.36	(K) LYAEANFEYPPVK
													1	0.4	3.06	(K) LLEYLTSDAQK
RRC01089	5'-Nucleotidase Precursor (EC 3.1.3.5)	3602	<i>yunD</i>	4	54.37	4.59	54.5	4.61	0.67	0.57			2	0.4	5.68	(K) SAGGEPILLDASVTPDAAVAAR
													2	0.3	2.98	(K) VQFPLVSGNLDLSR
													2	0.1	2.56	(R) FPQVAGLR
													2	1.4	2.32	(K) ADVQALTDQGVTK
													1	0.0	2.03	(R) FPQVAGLR
RRC01127	D-Ribose Binding Periplasmic Protein	102	<i>rbsB</i>	1	32.94	4.38	32.38	4.32	0.00	0.00	8.2	57.5	14			
													2	0.6	4.76	(K) AILDNAGADATVAAVQK
													2	0.5	4.10	(R) SQGYHDIIDQYPDLK
													2	0.4	4.07	(K) QSELFDSAIAAGVK
													2	0.5	4.07	(R) TDVVVVGFDGSNDVR
													3	-1.3	3.24	(R) SQGYHDIIDQYPDLK
													2	0.5	3.09	(K) ATVLQPAYAQAQMAVEQADK
													2	0.2	2.90	(K) GDYAELLGK
													1	-0.4	2.27	(K) GDYAELLGK
RRC01127	D-Ribose Binding Periplasmic Protein	1102		1	32.94	4.38	30.45	4.36	0.38	0.28	8.2	54.0	11			
													2	0.3	5.32	(R) SQGYHDIIDQYPDLK
													2	0.4	4.30	(R) TDVVVVGFDGSNDVR
													2	-0.7	2.60	(K) GDYAELLGK
													1	-0.2	2.16	(K) GDYAELLGK
RRC01245	Spermidine/Putrescine-Binding Periplasmic Protein	1302		2	37.56	4.49	38.31	4.48	0.01	0.01	8.1	31.0	9			
													2	0.3	4.83	(K) VTITDFDSNDTALAK
													2	0.2	3.43	(R) LGNPDVAYGYPK
													2	-1.9	3.29	(R) YANGIAGSEAFLEPMK
													2	0.2	3.11	(K) WLSMDYSTVEK
													3	-0.8	2.80	(K) ALDYQNAIWTELQK
													2	-1.2	2.52	(K) TAPELTPPAEFADK
RRC01245	Spermidine/Putrescine-Binding Periplasmic Protein	2301		2	37.56	4.49	38.33	4.52	0.24	0.26	8.2	23.7	9			
													2	-0.7	3.61	(K) ALDYQNAIWTELQK

													2	-1.7	1.79	(K)	VTITDFDSNDTALAK	
													1	-2.4	2.57	(R)	LGNPDVAYGYPK	
													1	0.1	1.82	(K)	VRDTLLAAKPK	
RRC01333	Periplasmic Oligopeptide-Binding Protein (OppA)	2702	<i>oppA</i>	2	57.80	4.50	57.11	4.55	0.37	0.01			2	0.1	3.20	(R)	HGYTEANPLK	
													2	0.0	3.09	(K)	APWSELEIR	
													2	-1.3	2.50	(R)	VNFYPTEDATAAVR	
													1	0.0	2.23	(R)	AAWFADYK	
													1	0.0	1.91	(K)	APWSELEIR	
													1	-0.9	1.79	(K)	IGPTLATYYYGFK	
													1	0.1	1.57	(R)	AVDATTLEVTLK	
RRC02708	ABC Transporter Substrate-Binding Protein	1504	<i>motA</i>	2	41.97	4.84	46.71	4.51	0.00	0.00			2	0.4	5.15	(K)	SPIWTDPTFWADHDTLNEK	
													2	0.6	3.92	(K)	SSNALVGLYQDGK	
													2	0.2	3.66	(R)	FFAAEVAEGK	
													2	0.3	2.97	(K)	FLAFSTDTQR	
													1	1.0	2.80	(K)	SSNALVGLYQDGK	
													1	0.2	2.76	(R)	FFAAEVAEGK	
RRC02708	ABC Transporter Substrate-Binding Protein	1502		2	41.97	4.84	46.72	4.40	0.44	0.52			2	0.4	4.37	(K)	SPIWTDPTFWADHDTLNEK	
													2	-0.8	3.87	(R)	KSSNALVGLYQDGK	
													2	0.1	3.63	(R)	FFAAEVAEGK	
													2	0.2	3.39	(K)	FLAFSTDTQR	
													1	0.2	3.02	(R)	FFAAEVAEGK	
RRC02708	ABC Transporter Substrate-Binding Protein	1603		2	41.97	4.84	46.78	4.41	0.69	0.64			2	0.1	4.48	(K)	INSIDADNPATPLK	
													1	0.1	2.54	(R)	FFAAEVAEGK	
													2	-0.1	2.02	(K)	SSNALVGLYQDGK	
													2	-0.4	1.94	(K)	FLAFSTDTQR	
RRC02807	Oligopeptide-Binding Protein OppA	3802	<i>appA</i>	8	61.57	4.53	61.31	4.56	0.34	0.27	8.2	33.7	19					
														2	0.4	3.88	(K)	LLDEAGWTDTDGDGIR
														2	0.2	3.83	(K)	TNDVAVFEANPHYR
														3	-1.0	3.31	(K)	TNDVAVFEANPHYR
														2	0.0	3.16	(K)	QIDPSVFFGGDAGSPDTFQK
														2	0.3	2.92	(K)	IEAVDPLTVK
														2	0.3	2.13	(R)	QALSMADR
														2	-0.7	2.05	(K)	EMLTTADAGAR
														3	-0.8	2.05	(K)	APKPEDQWQGENIPR
														2	-0.8	1.71	(R)	LAAEIPTLENGGVSADGK

													1	-0.6	1.58	(K) IEAVDPLTVK	
RRC02807	Oligopeptide-Binding Protein OppA	2703	8	61.57	4.53	60.46	4.55	0.37	0.33	8.2	15.2	9	2	0.3	3.85	(K) TNPYSAFVFGALAPILQK	
													2	0.2	3.58	(K) TNDVAVFEANPHYR	
													1	0.0	1.77	(K) IEAVDPLTVK	
RRC02811	Glutathione Peroxidase (EC 1.11.1.9)	5002	2	19.41	5.90	19.56	5.36	0.05	0.00	8.0	30.1	5				PMF SPECTRUM*	
													2	0.6	3.51	(K) GLIVLAVPSDDFK*	
													1	1.2	2.09	(R) AAFEPLLPGA*	
RRC02879	Periplasmic Component of Efflux System	5404	1	34.68	5.04	39.90	5.36	0.00	0.00	8.2	35.3	9	2	-0.4	5.79	(K) LLAAEAAVLQAEAAK	
													2	-0.6	5.78	(R) AQVQNATALIAAAEASR	
													3	-0.8	4.46	(K) LLAAEAAVLQAEAAK	
													2	-1.5	3.64	(R) LVLDPVPQYVVPAR	
													2	-1.1	3.24	(R) VSFVAPQAQFTPK	
													2	-0.4	2.81	(R) ATPDTPWPADLAVK	
													1	0.1	2.26	(K) IALEDLVIR	
RRC03149	Thiol:Disulfide interchange protein DsbA	8003	<i>dsbA</i>	4	23.38	6.00	19.27	5.64	0.00	0.00	8.0	30.5	7	2	0.4	4.94	(K) NASADAIEGTPTLVINGEK
													2	-0.2	2.94	(K) SWIGDGTPEPVIAENLR	
													1	0.1	2.85	(R) FHETVFGALK	
													2	0.1	2.66	(R) FHETVFGALK	
													1	0.0	1.87	(K) HDNMGYAELK	
RRC03395	Phosphate-Binding Periplasmic Protein	2404	<i>pstS</i>	5	37.01	4.70	40.90	4.56	0.57	0.31	8.1	59.0	16	2	-0.7	6.36	(K) ATGAYDLYMATAEGADEDK
													2	0.2	4.56	(R) IGYDGFVFSADIK	
													2	0.3	4.14	(K) LPAQDILTFIPGTK	
													2	0.3	3.81	(K) ANGVDEIMEVR	
													3	-0.9	3.43	(K) ATGAYDLYMATAEGADEDK	
													3	1.2	3.04	(K) LPAQDILTFIPGTK	
													1	0.2	2.62	(R) IGYDGFVFSADIK	
													2	-0.7	2.52	(R) VATINGIVPSTETIAK	
													2	0.1	2.49	(K) AHLGVIPGLK	
													1	0.1	1.70	(R) PLYFYVK	

RRC03417	Flagellin	404	<i>fliC</i>	0	40.01	4.20	40.01	4.20	0.00	0.00	8.1	40.2	9	2	-0.7	4.04	(K) ISGAQFNGVNLISSSGNETILGSLDR
														2	0.1	3.31	(K) DNSAVWAISK
														2	0.0	2.43	(R) SGNTVSTNTINIAR
RRC03489	Peptidyl-Prolyl Cis-Trans Isomerase	1002	<i>ppiB</i>	0	20.32	4.60	19.30	4.43	0.25	0.31	8.2	37.3	5	3	-2.0	4.08	(R) ITQLANEHAYDDVVFHR
														2	-0.5	3.90	(K) GAPELNGLVEDPDYIVK
														2	0.5	3.60	(K) YGDLPAEFSNR
														2	0.5	2.64	(K) VVIDLLPDVAPGHVER
RRC03762	Molybdate-Binding Periplasmic Protein	4001	<i>modA</i>	3	30.76	5.19	26.06	4.94	0.01	0.01				1	-0.2	3.36	(K) SAPYGAAAEIVMQK
														2	0.4	3.34	(K) LGVYETLEPK
														2	-0.3	3.11	(K) TPEALEIIR
														2	0.4	2.94	(K) LVLWSADPAR
														2	0.2	2.68	(K) TDLEHVAIADPK
														1	0.0	2.30	(K) LVLWSADPAR
														1	0.0	1.89	(K) AYLDFLK
														1	-0.5	1.78	(K) TPEALEIIR
														1	0.4	1.78	(K) LGVYETLEPK
														1	-2.0	1.60	(K) EIGALFTEK
														1	0.0	1.51	(K) YGYVTE
RRC03799	Glutamate/Gln/Aspartate/Asparagine-Binding Protein	2201	<i>yhdW</i>	5	35.53	4.49	34.79	4.54	0.47	0.46	8.2	50.3	13	2	0.2	5.37	(K) ANLEEVAASTQNPEIR
														2	0.2	4.61	(R) GLNAQWTQGGLMYAPPFR
														2	0.3	4.59	(R) ATLPNAADIVLPEIISK
														3	-0.4	4.31	(K) ANLEEVAASTQNPEIR
														2	0.1	4.06	(K) AVAAAVLGDPMK
														2	0.0	3.78	(R) HGDNNWGDIVR
														2	0.2	3.35	(R) LLGLEDMGK
														2	0.3	2.87	(K) IGLDNDFAK
														2	0.0	2.42	(R) NSTWTFSR
														1	0.0	2.15	(K) IGLDNDFAK
RRC04018	Glutamin Binding Periplasmic Protein Precursor	1001	<i>glnH</i>	1	27.63	4.50	25.99	4.37	0.44	0.33				2	0.2	4.18	(K) LGAEDFGFIFPK
														2	-1.0	3.73	(R) GGDVDLVLTSTAGEGYAR
														2	-0.3	2.93	(K) TAVDFSDPYMR
														2	0.5	2.65	(K) MFETFGAGVEALR

RRC04050	Periplasmic Leucine-Binding Proteins	4605	3	37.59	6.40	48.41	5.11	0.39	0.49	8.2	29.6	14					
													2	0.3	4.49	(R) DGFETLNLTEAR	
													2	0.3	4.22	(K) AAGAGDQLGTVLYSR	
													2	-0.1	2.80	(K) ITLVYHNSAYGK	
													1	-0.1	1.91	(K) SQWLQIR	
RRC04139	Acyl-CoA Thioesterase I Precursor (EC 3.1.2-)	1004	<i>tesA</i>	1	24.16	5.30	22.70	4.51	0.14	0.01	8.1	57.0	11			PMF SPECTRUM*	
													2	0.3	5.54	(R) GAEVTVINAGVSGDTTSGGR*	
													2	0.7	2.37	(R) DLPVALVGLK*	
RRC04244	Nucleoside Binding Protein	4302		1	38.59	5.10	38.48	4.87	0.35	0.22				2	0.2	4.75	(K) IGDITEAVPAEVK
													2	0.5	4.09	(K) VVTSFIENVPEGPDAER	
													1	0.0	2.59	(K) IGDITEAVPAEVK	
RRC04244	Nucleoside Binding Protein	4303		1	38.59	5.10	38.59	5.08	0.62	0.47	8.2	53.9	16				
													2	0.4	4.17	(K) VVWAYTWFDPAK	
													2	0.2	3.91	(R) AENLATYDAR	
													2	0.2	3.87	(K) IGDITEAVPAEVK	
													2	-0.4	3.30	(K) ISDGSYHPFTGPLK	
													1	0.2	3.16	(K) IGDITEAVPAEVK	
													2	0.0	3.10	(K) KQDGSDWLAEGK	
													2	-0.5	2.51	(K) VVTSFIENVPEGPDAER	
													2	-0.4	2.04	(R) VASTIDNWPYYIK	
<b>INCREASED PROTEINS</b>																	
RRC00485	Outer-Membrane Lipoproteins Carrier Protein	7003	<i>lola</i>	0	21.97	5.96	24.05	5.53	4	4	8.0	21.7	7				
													2	0.3	3.50	(K) SNQIAEQYPLK*	
													2	0.2	3.44	(R) TPLNLILADR*	
RRC00485	Outer-Membrane Lipoproteins Carrier Protein	7005		0	21.97	5.96	22.84	5.53	2	2				2	0.3	3.64	(K) SNQIAEQYPLK
													2	0.5	3.40	(R) TPLNLILADR	
													2	-1.0	2.62	(K) SNQIAEQYPLKR	
RRC00951	Outer Membrane Protein	7002	<i>yiaD</i>	2	23.35	5.96	24.05	5.53	4	4				3	-1.1	4.70	(R) YPDTTVDVVGHGTSDGDAAYNQR
													2	-0.1	3.74	(R) GEEQPVASNLSAAGK	
													2	0.1	3.26	(R) DLYTLGSLNR	
													2	0.1	3.00	(R) ILIGAGVPSYR	
													2	-0.9	2.30	(R) DLDTNGVSVVR	

RRC01191	Mannitol-Binding Periplasmic Protein	4404	3	39.82	5.43	39.59	5.30	>10	>10	8.2	44.1	12							
													2	0.3	4.83	(K)	SLDTIYGGAEVLSK		
													2	0.1	4.38	(R)	KEINTVADLSGLK		
													2	0.3	3.75	(K)	GTLDATEWVGPYDDEK		
													2	0.2	3.39	(K)	IYDSMVAFR		
													2	0.0	3.29	(K)	EINTVADLSGLK		
													1	-0.3	2.89	(K)	SLDTIYGGAEVLSK		
													1	0.2	2.41	(R)	KEINTVADLSGLK		
													1	0.1	2.36	(K)	EINTVADLSGLK		
													1	0.1	1.94	(K)	IYDSMAFR		
RRC01208	DegP (EC 3.4.21.-)	2602	<i>degP</i>	0	51.57	4.84	51.42	4.66	>10	1.6	8.1	34.5	12						PMF SPECTRUM*
														2	0.2	4.27	(R)	AGDVIVEAGQPVTSLDDLK	
														2	0.4	3.37	(K)	VVGQLQEFGATR	
														1	0.0	1.76	(R)	FVAVPLQ	
RRC01208	DegP (EC 3.4.21.-)	2705		0	51.57	4.84	51.91	4.58	>10	1.7				2	0.3	6.34	(R)	AGDVIVEAGQPVTSLDDLK	
														2	0.2	4.63	(R)	AGKPVTLQVTLGQR	
														2	0.3	4.34	(K)	SGDVIIISFAGAPVK	
														2	0.2	3.79	(K)	VVGQLQEFGATR	
														3	-1.3	3.23	(R)	AGKPVTLQVTLGQR	
														1	0.6	3.22	(K)	SGDVIIISFAGAPVK	
														3	-0.5	3.14	(R)	AGDVIVEAGQPVTSLDDLK	
														2	-1.9	2.94	(K)	GEDGNTVADEISIEFANGK	
														1	0.0	2.90	(R)	AGKPVTLQVTLGQR	
														2	0.1	2.86	(R)	KSVLLLIR	
														2	0.1	2.53	(R)	RGWLGVK	
														1	-1.0	2.41	(K)	VVGQLQEFGATR	
														1	0.3	2.24	(R)	FVAVPLQ	
														1	-0.9	2.04	(K)	TDIALLK	
														1	0.0	1.90	(R)	KSVLLLIR	
														1	-1.1	1.58	(K)	SVLLLIR	
														1	0.0	1.52	(R)	RGWLGVK	
RRC01208	DegP (EC 3.4.21.-)	2706		0	51.54	4.84	52.40	4.56	>10	1.7				2	-0.7	2.97	(K)	VVGQLQEFGATR	
														1	1.1	2.40	(K)	SGDVIIISFAGAPVK	
														1	-0.9	2.11	(K)	VVGQLQEFGATR	
														1	0.3	1.66	(R)	AGKPVTLQVTLGQR	



													2	-0.7	1.50	(R) AGKPVTLQVTLGQR
													1	0.0	1.43	(R) KSVLLLIR
													1	-0.3	1.38	(R) GWLGVK
													1	-0.1	1.33	(K) SVLLLIR
RRC01208	DegP (EC 3.4.21.-)	3609	0	51.54	4.84	52.85	4.61	>10	1.7				2	0.4	6.88	(R) AGDVIVEAGQPVTSLDDLK
													2	0.3	4.74	(K) SGDVIIIFAGAPVK
													2	0.2	4.23	(R) AGKPVTLQVTLGQR
													2	0.3	3.98	(R) VADAPVGQAVDVVVMR
													3	-0.8	3.65	(R) AGKPVTLQVTLGQR
													2	-1.1	3.48	(R) GNSGGPLFSMDGK
													2	0.9	3.29	(K) EFGMPNMPQGGPQR
													3	-0.7	3.27	(K) VVGQLQEFGATR
													2	0.2	3.11	(K) VVGQLQEFGATR
													2	0.1	3.05	(R) KSVLLLIR
													1	0.0	2.86	(K) VVGQLQEFGATR
													1	0.1	2.59	(R) GNSGGPLFSMDGK
													1	-0.1	2.49	(R) FVAVPLQ
													2	-1.0	2.27	(K) EPLPFVSGDSDTMR
RRC01299	Taurine-Binding Periplasmic Protein	208	2	34.91	4.60	35.20	4.37	>10	>10	8.1	26.0	8				PMF SPECTRUM*
RRC01654	Hypothetical Exported Protein	2704	2	56.26	4.50	58.83	4.56	>10	>10	8.2	30.2	12				
													2	0.2	4.52	(R) LDSAAGSLALDR
													2	-0.6	3.67	(R) TVSEGVFAAEQAR
													2	0.2	3.50	(R) GVALVLSTAR
													2	0.1	2.51	(K) QALDALQNPK
													1	0.1	1.54	(R) GVALVLSTAR
RRC02959	CDP-Diacylglycerol-Glycerol-3-Phosphate 3-Phosphatidyltransferase (EC 2.7.8.5)	2107	<i>pgsA</i>	0	23.02	10.02	29.23	4.55	6	5			2	1.5	2.43	(R) EFIGADAGKLVTK*
													2	1.2	2.40	(R) EFIGADAGKLVTK
RRC03107	Zinc Protease (EC 3.4.99.-)	2601	<i>ymfH</i>	0	49.75	4.70	49.56	4.56	>10	>10	8.2	48.3	19			
													2	0.2	5.74	(R) ASQIYEQDDTEALQR
													2	0.2	5.35	(R) YYAPNDAVLVVAGDVTPDQVK
													2	0.2	4.19	(R) AAQFLNSPYGTPVIGWR
													2	0.3	3.99	(K) GTDTLAAGELSK
													2	-0.1	3.86	(R) APVVVQMVWYR
													2	0.2	2.78	(K) DVDLPSAEAAALDK

													1	-0.2	1.88	(R) LELVMK
RRC03108	Zinc Protease	2501	0	46.69	4.54	46.43	4.55	10	14	8.1	42.5	18				PMF SPECTRUM*
													2	0.1	2.72	(K) TYLTGAYPLR*
													3	-0.1	2.35	(R) GALTDPHFQASVDR*
RRC03108	Zinc Protease	1506	0	46.69	4.54	46.70	4.55	>10	>10	8.1	40.4	16				PMF SPECTRUM*
RRC03327	Protease (Transglutaminase-Like Protein)	601	10	67.05	8.11	51.41	9.50	4	5				2	-0.1	4.63	(K) QYSAYGFTVTPGAVAR
													2	-0.2	3.32	(R) TNSQMSYGALSYTMSSK
													2	0.4	2.54	(K) GDSLMPEGADAAELGDAIAK
RRC03455	Outer Membrane Protein/DsbA-like thioredoxin domain	2106	2	26.79	4.57	27.03	4.54	5	7				2	0.3	4.73	(K) AVLAQMNSEEVTSVLR
													2	0.2	4.35	(K) EFPILSDQSVLAAR
													2	0.3	3.67	(K) AYEVVDEVLKK
													2	-0.6	3.62	(K) KAYEVVDEVLKK
													2	0.2	3.20	(K) AYEVVDEVLKK
													3	-1.2	2.64	(K) AYEVVDEVLKK
													1	0.1	2.30	(K) AYEVVDEVLKK
													2	0.8	2.20	(K) AYLMENPEVLVEAINK
													1	0.1	2.14	(K) AYEVVDEVLKK
RRC03455	Outer Membrane Protein/DsbA-like thioredoxin domain	2102	2	26.79	4.57	28.35	4.55	3	3				2	-1.0	3.18	(K) EFPILSDQSVLAAR
													1	-0.9	2.59	(K) AYEVVDEVLKK
													1	0.0	2.38	(K) AYEVVDEVLKK
RRC04027	Periplasmic Glucans Biosynthesis Protein MdoG	4806	<i>mdoG</i>	1	62.62	5.38	58.48	5.27	5	7			2	0.2	3.44	(R) LASSYFSETAPK
													2	0.2	2.43	(K) DFDDYRPK
													1	-0.1	1.46	(K) VHSDSGLGIVR
RRC04580	Peptidyl-Prolyl Cis-Trans Isomerase (EC 5.2.1.8)	3207	0	30.84	5.00	31.08	4.77	5	8				2	0.3	4.86	(K) AEIDGGADFATVAK
													2	0.5	3.91	(R) LGAAPTLEEATEELSGDLR
													2	0.1	3.72	(R) RDEIALEVER
													2	0.3	2.74	(R) VEGIDPAVLK
													3	-1.5	2.54	(R) RDEIALEVER

<sup>a</sup> SSP# corresponds to the spot numbers given by the image analysis program PDQuest. <sup>b</sup> Cys indicates the number of cysteine residues found.

<sup>c</sup> MD20/MT1131 and MD20R3/MT1131 indicate the ratio of a given spot between these strains. Note that all proteins listed except PgaA which is an integral membrane protein, have a putative signal sequence recognized by the program Signal

<sup>d</sup> Protein identification by MALDI-TOF-MS / peptide mass fingerprint (PMF) and the corresponding score, cov% (percentage of coverage) and NMP (number of matched peptides) are indicated.

<sup>e</sup> Protein identification by nLC-MS/MS and the corresponding z (charge), ΔM (mass difference) and X<sub>corr</sub> (scores) values are indicated.

\* Spectra are provided in Supplemental Figure 1 and 2.