

Supplementary Table 1

	Protein name	SSP	Peptide sequences	Mascot score	Protein coverage (%)	Approximate Experimental pI/MW(KDa)	Sub-cellular localization ^a	Trans-membrane spans ^b
1 2 3 4	elongation factor Tu	4403 5401 5403 6301	ADLVDDAELLELVEMEVR AIDQPFLMPIEDVFSISGR GITINTAHVEYNSN EHILLSR QVGVPYIVVFLNK DLLSTYDFPGDDTPHIGSAR MALEGKDDNEMGTTAVK KLVETLDAYIPEPVR LVETLDAYIPEPVR VQDPLEIVGLR FTAENVYVLSK FTAENVYVLSKEEGGR TIAMEDGLR QVGVPYIVVFLNK ADLVDDAELLELVEMEVR DLLSTYDFPGDDTPHIGSAR KLVETLDAYIPEPVR LVETLDAYIPEPVR VQDPLEIVGLR FTAENVYVLSK TIAMEDGLR TVGAGVVAK MALEGKDDNEMGTTAVK KLVETLDAYIPEPVR VQDPLEIVGLR FTAENVYVLSK	70 33 63 29 54 67 33 65 43 49 41 27 57 49 94 97 46 14 49 45 46 35 25 16 62 56	9 33 26 13	5.4/45 5.6/50 5.5/50 5.8/45	C 0.272	0
5 6 7	outer membrane porin OprE3 (OprD-family)	5501 5502 6501	LLPESFTGTLITSK VFVEYPISIF LLPESFTGTLITSK FTQEAR SINVFGGSYK FTDNFTASLYTADNEDVMKK LAYVVGDNINTR NNANPQGFGEGKER VFVEYPISIF ISNTVLK LLPESFTGTLITSK SINVFGGSYK FTDNFTASLYTADNEDVMKK LAYVVGDNINTR	56 49 27 15 42 23 58 17 38 43 71 43 22 33	5 19 24	5.7/55 5.5/50 5.8/50	OM 0.941 PS 0.342	0

			YVVQDGPak VFVEYPISIF	34 38				
8 9	outer membrane porin OprE (OprD- family)	7501 7503	LLPQTFEGGTIQSK YGGLDYK LTPDLTLQYYYSNLEDFYK QHFLGATHVFK IADDQSFk ASVAYLR FIVNYTYsFL LLPQTFEGGTIQSK YGGLDYK LTPDLTLQYYYSNLEDFYK IADDQSFk ASVAYLR FIVNYTYsFL	57 29 74 13 37 37 36 59 26 40 48 25 20	17 15	6.1/50 6.3/50	OM 0.935 PS 0.282	0
10 11 12	outer membrane porin (OprD-family)	7601 8501 8601	GTSEQDEAKGFIDGQSLSGSTR MGLANVK VSNTTLTVGR QSVDTPMIAYIGNR SLQISYVLNMAPYGVPLK FNLYNAR AQADGSLDEFr MGLANVK VSNTTLTVGR AQADGSLDEFr GTSEQDEAKGFIDGQSLSGSTR MGLANVK VSNTTLTVGR QSVDTPMIAYIGNR TEQSLSK SLQISYVLNMAPYGVPLK FNLYNAR GWGIDGTHYR ATYTAHR AQADGSLDEFr	29 34 56 85 25 34 64 25 53 70 26 23 52 54 40 31 40 50 27 86	19 6 24	6.2/60 6.5/50 6.4/60	OM 0.928 PS 0.195	0
13	outer membrane protein (OprD- family)	1401	VGDQFTALPVFATDDSR LIVEYPLSIL	56 46	6	4.7/45	OM 0.930 PS 0.221	0
14	outer membrane lipoprotein OprI	0003	LTATEDAAAR KADDAMAAAQK ADDAMAAAQKAQQTADeANER AQQTADeANER	52 40 12 40	38	4.2/<10	OM 0.790 IM 0.700	0
15	OprF	0211	NFKNDGTNPGVR NDGTNPGVR	33 30	3	4.5/35	OM 0.666 PS 0.154	0
16	peptidoglycan- associated	3101	GGDNAGEGAVDPNAGYGANTGAVDG- -SLSEEAALR	46 32	30	5.2/15	PS 0.353 OM 0.198	0

	lipoprotein OprL		ALDVHAK VVLEGNTDER	48				
17 18	carbohydrate- selective porin OprB	3401 4507	LAITER YFDGALDVK LGYYYSTAK ATNVVDNYQQVGLVYK GAFDARPK IHVNDDEVK SPGGVDEVNALVAGLK YSDQFALGAHLDLQK YFDGALDVK LGYYYSTAK GLSLFANFTVHDK ATNVVDNYQQVGLVYK GAFDARPK IHVNDDEVK SPGGVDEVNALVAGLK	39 36 41 93 32 24 93 27 26 23 38 78 22 28 59	16 21	5.1/50 5.2/50	OM 0.944 PS 0.379	1*
19	efflux transporter, RND family, MFP subunit	7301	LQAEASLK VLAPISGR AGVNANAILAPQQGVTR VSDATNVK	35 43 36 41	10	6.1/45	OM 0.790 IM 0.700	0
20	CzcB family cobalt/zinc/cadmium efflux membrane transporter	3601	AAGVALEAAAPR DLGTVVSFPGEIR VPGVVEAVQANLGETVK GQVLAVIASQQISDLR ISAEQDYLQAR VGAIGASVNSVGGNR APFDAVVVEK VSSPDMNVEVEGK VGYYVGSLLGEQNR TPDGFDTRPVK	53 53 62 90 33 56 59 67 61 14	31	5.3/60	PS 0.897 OM 0.339	1
21	TonB-dependent hemoglobin/transferrin in/lactoferrin family receptor	6901	ISNGNVVLER GYDGQGEAGVTQPANLDR	57 58	3	5.7/90	IM 0.217	1*
22	hypothetical protein PputGB1_4051, similar to an Outer membrane receptor for siderophore	6902	VGIFYSEINPQVDAGVR NGVVSLFTDSDFGNGFTGSR TDYSNLPNSDADVDTLQVDLEAK	60 48 33	14	6.0/90	OM 0.428 PS 0.223	1°
23 24	TonB-dependent receptor	3701 3703	QLAAPSTVLEGDNLLQQQHGSGLGETL- -NK IPDSPIEGIHGAGELR YDSNYGSVAESGVR DLDGPFSSVK AISADLALR	26 46 61 14 53	22 17	5.1/80 5.2/80	OM 0.935 PS 0.277	0

			NYIGLIGTGNLR FYGIEAQDR YGSFALELSGDYTR NLDSGEPLPR FDIGQSQWLAFFVR GENLTDQTVR SVEVGLR VPYLQSEAFR MLFGMGSLSLGELAGER LTGPSLSSLVAK LGIANLNPDTADHEF	54 29 57 34 53 60 38 35 63 37 29				
25	TonB-dependent siderophore receptor	1903	YTAPLVDTPR DTNALTLQDALR GFDAQGDYLDGVR EIFAIESVEVAK GAAGGTINLVSK LSLAAALFR TALLTTSVHF	45 61 63 76 39 66 41	10	4.8/85	IM 0.147	1°
26 27	TonB-dependent siderophore receptor	1904 2901	AEQASTDYKVEK YTAPLVDTPR SVTVIPQQVIK DTNALTLQDALR GFDAQGDYLDGVR EIFAIESVEVAK GPNSAIGGR GAAGGTINLVSK LNLMTHEENVAGR YDHFDQYR AFSTHFANQAAGR TALLTTSVHF AEQASTDYKVEK YTAPLVDTPR SVTVIPQQVIK DTNALTLQDALR GFDAQGDYLDGVR EIFAIESVEVAK GPNSAIGGR GAAGGTINLVSK YTFDGNVQFSDTVAGR LNLMTHEENVAGR DKVNYDR HGNSMQDYILTQPDDSK VQVDTTTYENVGETR VQGIELSASGK LTVGGGAFYVDDVYGSVANTTMVDS- -YVR	61 72 45 58 71 66 31 38 42 20 55 62 53 53 41 71 78 58 38 31 81 53 23 38 27 25 32	17 33	4.9/85 4.9/85	IM 0.198	1°

			YDAMAAYKL NVDLQLNVQNLNEVYYDK AFSTHFANQAAGR TALLTTSVHF	42 17 26 56				
28	TonB-dependent siderophore receptor	4901	YMPGIVSASFGSDTR GFEPTQFLDGLPLPR QINFASGK DDTGATSQFRPIQGTK FLNQGDATNTQR SEVQDGIYK SVVASASYK	71 71 36 33 63 17 25	10	5.3/85	OM 0.947 PS 0.409	1*
29	3-ketoacyl-(acyl- carrier-protein) reductase	6202	QGATVIGTATSASGAER LGQADEIAK	48 39	10	5.8/25	IM 0.111	1°
30	PpiC-type peptidyl- prolyl cis-trans isomerase	4701	RQLMQQLGK TGIAGSSFVTDQQVDAFAR ANPAAVKVSDDEVK SAFFDQVK LAKGEDFAK DLKTPLVEQR VHTSAPFGR EGGEGITANR AGQQDFAAYR	26 36 22 22 46 20 22 31 54	17	5.3/75	IM 0.109	1°*
31	peptidylprolyl isomerase FKBP- type	1202	ASYGIGLNMGK SLAQEGMEDLDSK AVALGIEDAVGK KPGVVTTASGLQYEVVKK VFDSSVER	50 68 45 22 48	24	4.8/28	IM 0.828 OM 0.700	1°
32	ATP-dependent protease peptidase subunit - HslV	7102	VVMGGDGQVSLGNTVMK LEAMLAVANK	45 29	15	6.2/18	C 0.233	0
33	HflK protein	6503	TGITVTQVNVQSAAAPR EVQEAFFDDVIR	98 48	6	5.7/50	IM 0.355	1°*
34	metalloprotease - outer membrane protein	0601	VPYLQSEAFR VDVKDITPEK MLFGMGSLSLGELAGER NVYLGEYTR LTGPSLSSLVAK ADPAADATLK LGIANLNPDTADHEF	55 51 85 33 41 41 46	18	4.6/60	OM 0.790 IM 0.700	0
35	organic solvent tolerance protein OstA	2902	DESPTYINAK RGENAIIR GLLMEGEFR SGSAMFHYQPEDNPNK GLGGVVGNK	29 32 39 27 53	5	5.1/100	OM 0.676 PS 0.249	1*

36	flagellar hook protein FlgE	0401	SFNIGLSGLYAANK QLDVTGNNIANVNTTGFK AEFADVYAGANR LSMNSTTSYNTETAR TISTESTIMQTHQMT	59 43 70 89 52	16	4.5/45	C 0.147	0
37	flagellar basal body L-ring protein FlgH	4202	VGDIITITLNER NAGSQIQK IAGLIRADDIATDNTVPSTR ADDIATDNTVPSTR	53 29 18 34	17	5.3/25	OM 0.790 IM 0.700	1*
38	L-sorbose dehydrogenase	7502	QSLVLPNGDILVAEGR LYVANQDALVR YLYVGIGSNSNITER	61 53 54	9	6.2/50	OM 0.790 IM 0.700	0
39 40 41 42	hypothetical protein PputGB1_4051	2401 2402 2403 9903	ANGSINQAQYNELQGD LAKETK MSSFEQK VGIFYSEINPQVDAGVR VATGSSADAR STNQSLDNYFEK DNVDGDGVQFK HDAQLYAAQLGTK NGVVSLFTDSDFGNGFTGSR VGYEIDK VGYEIDKNFALGAAYMMAK TDYSLNLPNSDADVDTLQVDLEAK ANGSINQAQYNELQGD LAKETK MSSFEQK VATGSSADAR STNQSLDNYFEK DNVDGDGVQFK HDAQLYAAQLGTK NGVVSLFTDSDFGNGFTGSR NFALGAAYMMAK MSSFEQK VGIFYSEINPQVDAGVR VATGSSADAR STNQSLDNYFEK DNVDGDGVQFK HDAQLYAAQLGTK NGVVSLFTDSDFGNGFTGSR NFALGAAYMMAK VGIFYSEINPQVDAGVR NGVVSLFTDSDFGNGFTGSR VGYEIDKNFALGAAYMMAK	55 17 77 56 55 35 59 97 42 33 40 19 23 49 16 53 47 55 41 20 52 49 63 65 74 80 46 42 45 38	37 26 24 13	4.9/45 5.0/50 5.1/45 6.8/>100	OM 0.428 PS 0.223	1*
43	hypothetical protein PputW619_1163	0210	DRDGEGLLVLSR SDGQAVDAESEQEVDK SDGQAVDAESEQEVDKVV LK	53 58 25	13	4.1/35	IM 0.790 OM 0.700	0

44	hypothetical protein PputW619_2767	0501	ERYEAQQNALMVLEQR FSVETGLTYTHYDTR YNVDQR FLDESENWPDVATLR	28 26 41 49	12	4.5/50	OM 0.899 PS 0.241	0
45 46	outer membrane porin, OprD	8503 7506	TGLSVAGATADSNK IADDQSFKTDLR LLPQTFEGGTIQSK TGLSVAGATADSNKFR YGGLDYK TGLSVAGATADSNK IADDQSFKTDLR TGLSVAGATADSNKFR	37 26 31 66 32 66 27 52	9 7	6.3/55 6.2/55	OM 0.937 PS 0.305	1*
47	outer membrane porin, OprH	8202	LFGGGSLSGMTK LTSSAQTYLAATYKF	43 32	12	6.1/18	OM 0.937 PS 0.295	0
48	3-ketoacyl-(acyl- carrier-protein) reductase, FadB2x	9305	GAIASLTLPAAAR ASLAAGVPFPFR ASLAAGVPFPFR ASLAAGVPFPFR LGRPQEYAALAR LGRPQEYAALAR VMLVDLNAQAVEAK VMLVDLNAQAVEAK	39 31 46 52 45 59 29 88	19	6.8/25	PS 0.885 OM 0.109	0
49	extracellular ligand- binding receptor	8407	IGIAGPK AIVDAIK SFDADPENK TPTGTLSYDEK TGPVTQYGDMQFIGAK TIGLDSAQGPAAAGNYIADHVKPK	35 48 38 39 67 39	19	6.3/50	PS 0.937 OM 0.299	0
50 51	anti-oxidant AhpCTSA-family protein, similar to AhpC	5203 6301	SQIVNDLPLGR AYDVESEGGVAFR IPDFQAR SQIVNDLPLGR AYDVESEGGVAFR AYDVESEGGVAFR AYDVESEGGVAFR	64 94 19 51 45 87 94	12 15	5.2/23 5.5/23	C 0.085	0
52 53	alkyl hydroperoxide reductase, AhpC	5208 5902	IVELNDGGVGR GTFVINPEGQIK GEFVQVSEADLK LGVEIYGVSTDTHFTHK GTFVINPEGQIK NFDVLIEEAGLADR	46 40 56 39 44 79	27 13	5.3/23 5.2/80	C 0.301	0
54	thiol peroxidase	4203	SLKDFAGK AVVVLDENDK FCGAEGLENVK	30 39 43	17	5.0/18	IM 0.104	1°
55	gamma-	5207	VELVIGTPGGSR	24	5	5.4/20	PS 0.942	0

	glutamyltransferase		VDGAKLETASDPR DGKVELVIGTPGGS	45 40			OM 0.356	
56	30S ribosomal protein S1	5903	GGFTVDVNGIR SVLEAENSAER NVLKEGEEIEAK RSVLEAENSAER SESFAELFEESLK SESFAELFEESLK EALLETQLQEGQQVK NAPEAAADTTMAALLR VGDEVHVALDAVEDGFGETK VGDEVHVALDAVEDGFGETK SEGVIPLEQFYNEAGELTIK	46 82 49 21 48 52 63 86 74 19 75	21	5.2/70	C 0.079	0
57	50S ribosomal protein L4	8204	VLITVSAVK LVVVQDFAVEAPK DVQGSDPVSLIAYEK	23 26 54	18	6.3/23	C 0.209	0
58	50S ribosomal protein L9	4101	VANLGNLGDK VANLGNLGDKVK ATVANAANLAAFEER ATVANAANLAAFEERR	26 31 89 34	18	5.0/15	C 0.099	0
59	trigger factor	7404	GTLVLGSGR ALLENENR LNPAGAPAVEPK SVVLEEQVVDTVLQK	26 27 20 23	10	6.1/50	C 0.222	0
60	flagellar cap protein FliD	6502	SLLGDVRK SALTAFQDAMK SVQSFVDAYNTLQK DYKITVASGATLQSVR	36 62 61 81	10	5.5/58	C 0.141	0
61	hypothetical protein PputW619_4292	7302	YNQVSLR YNQVSLR NSYPVYDSK MGGMDFSAPATR	36 36 18 40	12	5.9/30	PS 0.935 OM 0.281	0
62	ATP-dependent Clp protease, proteolytic subunit ClpP	7202	AYDIYSR AAEYGLIDSVYDKR	37 36	9	6.1/23	IM 0.123	1°
63	F ₀ F ₁ ATP synthase, β -subunit	5502	DTIAGFSGILK TVNMMELIR VALTGLTMAEK DVVPSVYNALK YTLAGTEVSALLGR YTLAGTEVSALLGR GLDVVDTGAAISVPVGK VALVYGQMNEPPGNR VQGAETTLEVQQQLGDEVVR GIHQPAPSFADQAGGNDLLETGIK	64 28 62 25 34 69 57 48 102 44	28	5.2/58	IM 0.035	0

64	F ₀ F ₁ ATP synthase, δ-subunit	8201	AGDLVIDGSVR AELTTLARPYAK	49 60	12	6.1/23	C 0.210	0
65	- Aspartate/ornithine carbamoyltransferase	6504	AILVSTLADL NNMGNSLLLIGAK GFKQEIVEELAK	18 15 42	10	6.0/50	C 0.396	0

Sup. Tab. 1: For each protein spot identified as modulated by Cd treatment, sequence of identified peptides, protein coverage (in %) and approximate pI/MW experimental value are presented. Moreover, the subcellular localization estimated by *in silico* analysis and the number of predicted transmembrane domains are also listed. SPP: standard spot protein. For spots corresponding to the same protein, blue/red colours have been used to distinguish identified peptides (and associated Mascot scores) and protein coverage values that are characteristic of each spot.

a: Subcellular localization was predicted *in silico* by means of the PSort algorithm, publicly available at <http://psort.hgc.jp/form.html>. Different cell compartments are indicated with bold letters, C: bacterial cytoplasm, OM: Outer Membrane, IM: Inner Membrane, PS: periplasmic space. The number indicates the score associated to each probable localization compartment.

b: Transmembrane spans were identified *in silico* by means of algorithms available at <http://psort.hgc.jp/form.html> (°) and <http://www.cbs.dtu.dk/services/TMHMM/> (*).

Supplementary Tab 2

Primer name	Primer sequence (5' → 3')	Protein Spot
30S-F	ACGTTGTTGCGCTTCTGGTC	56
30S-R	GGCGACTGGGTACCGTAC	
50S-F	CGCTAACCTGGGCAACCTG	58
50S-R	CACGCGTACGGTGGCTTCA	
Clp-F	TGGCCCGGTAGAGGACTAC	62
Clp-R	TTGATGGTCTCGAGGTCCTG	
CzcB-F	TGGCTGGCGATTACCGCGA	20
CzcB-R	GATTTGGCAGCCTTGCCTG	
FadB2-F	ATCTGGCCGTCATAGGCGG	48
FadB2-R	AGATGCTGGTCGAGGCTGG	
HflK-F	ATCACCGTTACCCAGGTCAA	33
HflK-R	TGCCCTCGACCATCTTGTC	
OprF-F	GAGTGGGGCCCGACCGT	15
OprF-R	CTTGCTTGACAGCGTTGGCA	
OprI-F	ATGAACAACGTTCTGAAATTCTC	14
OprI-R	TACTTGCGGCTGGCTTTGTC	
Asp/OrnTran-F	GTGAGCACAGCGACAAGCC	65
Asp/OrnTran-R	TGTGGAATGCCGGCAGGCA	
TonB-Rec-F	ACCAACAACGAGGGCGGTG	28
TonB-Rec-R	CGTTGACCGCTACCGATGC	

Sup. Tab. 2: Sequences of primers utilized for the amplification of DNA probes to test the RNA abundance of selected genes.