

## FIGURE LEGENDS

1

2 **Figure S1: Production and purification of PspA-His derivatives in *E. coli*.** His-tagged PspA

3 derivatives were produced in *E. coli* BL21/pLysS and purified as described in Materials and

4 Methods. Aliquots from various fractions were then incubated with SDS-loading dye and

5 resolved by SDS-PAGE on 12% gels. Gels were stained with Coomassie brilliant blue. L,

6 protein ladder; TCL, total cell lysate; FT, flow-throw; W1, wash 1; W2, wash 2; E1, elute 1; E2,

7 elute 2; E3, elute 3; E4, elute 4; E5, elute 5. PspA<sub>Mtb</sub>, PspA from *M. tuberculosis*; PspA<sub>Mtb</sub>ΔH1,

8 PspA from *M. tuberculosis* missing residues 1-22; PspA<sub>Rho</sub>, PspA from *Rhococcous jostii* RHA1;

9 PspA<sub>Eco</sub>, PspA from *Escherichia coli* BL21.

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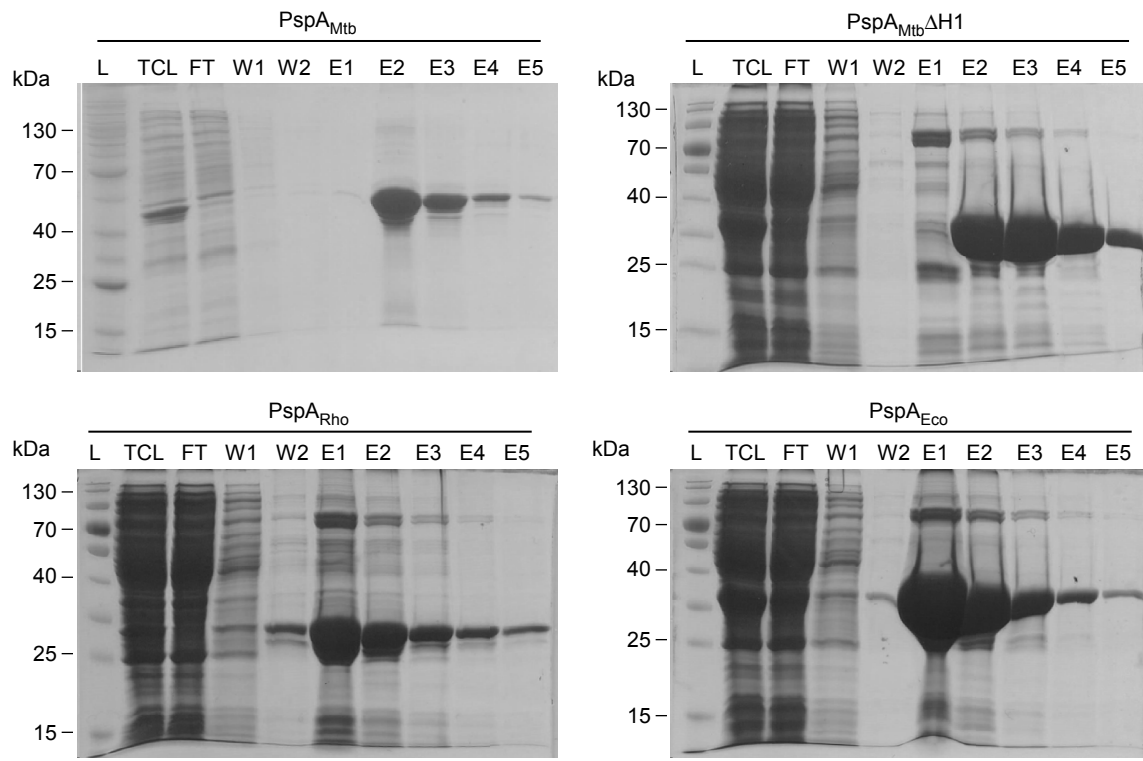


Figure S1

Table S1. Oligonucleotides used in this study

Primer name	Sequence <sup>a</sup> (5' to 3')	Purpose
2744c_H1FWDNheI	GCTAGCCATGCCGACCCCAAGGTGCAGA	<i>pspA<sub>Mtb</sub></i> ΔH1 forward primer for insertion into pET24b expression vector
Rv2744cRev4-NotI	GCGGCCGCCTGACCGTAGGGCTGCTC	<i>pspA<sub>Mtb</sub></i> ΔH1 reverse primer for insertion into pET24b expression vector
2744cFpSE100PstI	CTGCAGATGGCCAATCCGTTTCGTTAAAGCC	<i>pspA<sub>Mtb</sub></i> ΔH1 forward primer for insertion into pSE100
2744cRpSE100EcoRV	GATATCCATCTGACCGTAGGGCTGCTC	<i>pspA<sub>Mtb</sub></i> ΔH1 reverse primer for insertion into pSE100
GFPmut3_no_fusion_F	GGATCCCAGTAAACCACAACAACCTTTTCACTGG	Forward primer for cloning <i>gfpmut3</i> alone
GFPmut3_both_R	AAGCTTTTTGTATAGTTCATGCATGCC	Reverse primer for cloning <i>gfpmut3</i> alone or with fusion to H1 domain
GFPmut3_fusion_F	GGATCCAGTAAAGGCGAAGAACCTTTTCACTGG	<i>gfpmut3</i> forward cloning primer for fusion to H1 domain
H1_truncation_F	GGATCCCATGGCCAATCCGTTTCGTTAAAGCC	Forward primer to generate 1xH1- <i>gfpmut3</i> fusion
MSMEG_4703_HelixF	GATCCGGAGATGCTCGACGAGCTCTCGACCGGGTGGAGCCGTTTCTCGGTGGACCTCATCG	Sense oligonucleotide for cloning MSMEG_4703 amphipathic helix in front of <i>gfpmut3</i>
MSMEG_4703_HelixR	GATCCGATGAGGTCCACCGAGAAACGGCTCCACCCGGTTCGAGAGCTCGTTCGAGCACTCCG	Anti-sense oligonucleotide for MSMEG_4703

F_Eco_pspA_pET24	CCCGGATCCGATGGGTATTTTTCTCGCTTTGCCG	amphipathic helix in front of <i>gfpmut3</i> <i>pspA<sub>Eco</sub></i> common forward primer
R_Eco_pspA_pSE100	CCCAAGCTTTTATTGATTGATTGTCTTGCTTCAAAAAGGC	<i>pspA<sub>Eco</sub></i> reverse primer for insertion into pSE100-derived vectors
F_Rho_pspA_BamHI	CCCGGATCCGATGGCTAATCCTTTCGTCAAGGG	<i>pspA<sub>Rho</sub></i> common forward primer
R_Rho_pspA_HindIII	CCCAAGCTTCTACTGCGCGGCCGGTCTGGCC	<i>pspA<sub>Rho</sub></i> reverse primer for insertion into pSE100-derived vectors
Eco_R_pET24real	CCCCCTCGAGCGCTTGATTGTCTTGCTTCATTTTGGC	<i>pspA<sub>Eco</sub></i> reverse primer for insertion into pET24b expression vector
Rho_R_pET24real	TTTAAGCTTCGCTGCGCGGCCGGTCTGGCC	<i>pspA<sub>Rho</sub></i> reverse primer for insertion into pET24b expression vector
Rv2744cFWD-NheI	GCTAGCGCCAATCCGTTTCGTTAAAGCC	<i>pspA<sub>Mtb</sub></i> forward primer for future mutagenesis reactions
Rv2744c_Rev_BglII	AGATCTGCCTGACCGTAGGGCTGCTCGGC	<i>pspA<sub>Mtb</sub></i> reverse primer for future mutagenesis reactions
Amp_Rev	[Phos]GTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGG	Mutagenesis reverse primer (provided with Change-IT kit)
Rv2744c_F5A_single	[Phos]GCTAGCGCCAATCCG <u>GCC</u> GTTAAAGCCTGGAAG	<i>pspA<sub>Mtb</sub></i> F5A mutagenesis primer
Rv2744c_W9A_mut	[Phos]AATCCGTTTCGTTAAAGCC <u>GCC</u> AAGTACCTCATGGCGCTG	<i>pspA<sub>Mtb</sub></i> W9A mutagenesis primer
Rv2744c_F5A/W9A_double	[Phos]GCTAGCGCCAATCCG <u>GCC</u> GTTAAAGCC <u>GCC</u> AAG	<i>pspA<sub>Mtb</sub></i> F5A/W9A mutagenesis primer
Rv2744c_F16A_mut	[Phos]AAGTACCTCATGGCGCTG <u>GCC</u> AGCTCGAAGATCGACGAG	<i>pspA<sub>Mtb</sub></i> F16A mutagenesis primer

Rc2744c_Y11A_mut	[Phos]TTCGTTAAAGCCTGGAAGGCCCTCATGGCGCTGTTTCAGC	<i>pspA<sub>Mtb</sub></i> Y11A mutagenesis primer
Rv2744c_K7A_mut	[Phos]GCCAATCCGTTTCGTTGCCGCCTTGAAGTACCTC	<i>pspA<sub>Mtb</sub></i> K7A mutagenesis primer
H1GFP_F_W9E	[Phos]AATCCGTTTCGTTAAAGCCGAAAAGTACCTCATGGCGCTG	<i>pspA<sub>Mtb</sub></i> W9E mutagenesis primer
pSE100R2	ATAACGTTCTCGGCTCGATGATCCC	Sequencing primer for pSE100-based vectors
pSE100F2	CGAGCGGGAGAACTCCCTATCAGT	Sequencing primer for pSE100-based vectors
M13_Reverse	CAGGAAACAGCTATGAC	Sequencing primer for pCR2.1-TOPO
M13_Forward_(-20)	GTAAAACGACGGCCAG	Sequencing primer for pCR2.1-TOPO
T7 Promoter	TAATACGACTCACTATAGGG	Sequencing primer for pSTBlue-1
SP6 Promoter	GATTTAGGTGACACTATAG	Sequencing primer for pSTBlue-1

<sup>a</sup> [Phos], primer contains 5' phosphorylation modification for use with Quick Change mutagenesis kit. Line indicates mutated residues.

Table S2. *M. smegmatis* proteins possessing a PspA<sub>Mtb</sub> H1-like amphipathic helix.

Uniprot #	Unique proteins	Gene	Protein	Amphipathic helix properties					
				Helix position	Helix sequence	H	μH	z	# Large Hydrophobic face residues (LIFMWY)
A0QT14	1	add	Adenosine deaminase	319-336	RLVEAFGYGWSDLERFTI	0.537	0.468	-1	5
P0CH36	2	adhC1	NADP-dependent alcohol dehydrogenase C 1	231-248	TFDKLAGSFDLILNTVSA	0.535	0.483	-1	5
P0CH37	3	adhC2	NADP-dependent alcohol dehydrogenase C 2	231-248	TFDKLAGSFDLILNTVSA	0.535	0.483	-1	5
A0QRE7	4	amiD	Amidase	351-368	RLRTLQAAWNEMFTGID	0.509	0.474	0	6
A0QVJ3	5	asnB	Asparagine synthase (Glutamine-hydrolyzing)	108-126	YHHWGD R FVEHLKGMFAFA	0.544	0.499	0	6
A0R203	6	atpFH	ATP synthase subunit b-delta	198-215	GLTNLADELASVAKLLLS	0.529	0.479	-1	5
A0QR36	7	ccdA	Cytochrome C biogenesis protein transmembrane region	234-255	GAALVTGLWNEFVS YVRDAFVS	0.598	0.384	-1	6
A0R3Q0	8	cheR	CheR methyltransferase, SAM binding domain protein	51-69	LDVLQASSDEFSALFN TIL	0.587	0.507	-3	7
A0R574	9	clpC1	ATP-dependent Clp protease ATP-binding subunit ClpC1	725-743	DEIIQMVDLMIGRVS NQLK	0.444	0.496	-1	5
A0QS49	10	cmaA1	Cyclopropane-fatty-acyl-phospholipid synthase 1	10-27	ELQSIYDISNEFYELFLG	0.589	0.474	-4	7
A0R063	11	cobU	Cobinamide kinase / cobinamide phosphate guanyltransferase	78-96	HVATLVDDIGGWLTATMDR	0.491	0.46	-2	5
A0QXA8	12	cydA	Cytochrome D ubiquinol oxidase subunit 1	75-93	QFGMNWSEYSRFVGDIFGA	0.517	0.458	-1	5
A0QXA8	12	cydA	Cytochrome D ubiquinol oxidase subunit 1	42-59	TGNDTWYRLTRFFGKLFL	0.56	0.485	2	6
A0R6P3	13	cyp123	Cytochrome P450	236-256	NAGTETVGR LFGWLGKLLGEH	0.425	0.477	0	6
A0R0W6	14	cysT	Sulfate ABC transporter, permease protein CysT	50-67	LWQAAGGGWDAFWRAVTS	0.607	0.541	0	5
A0R310	15	dctA	Aerobic C4-dicarboxylate transport protein	43-60	EVGKSVGVLGTMFVNLIK	0.561	0.492	1	5
A0QNP4	16	dehII	Haloacid dehalogenase, type II	56-73	DFFTLGQQVLRMLADIHG	0.603	0.478	-1	7
A0QXD9	17	eltP	Erythritol/L-threitol-binding protein	440-457	FFDTTKDWAVALQDIYGG	0.507	0.501	-2	6
A0R614	18	embB	Probable arabinosyltransferase A	1010-1027	DTWQDGINGLLGITDLL	0.558	0.511	-3	6
A0QNS5	19	erg3	C-5 sterol desaturase	215-232	LDKNYGGILIFDRMFGS	0.577	0.472	0	7
A0QW55	20	erg3	C-5 sterol desaturase	206-223	IDKNYGGVFIVWDR LFGT	0.592	0.488	0	6

A0R6J9	21	est	Beta-lactamase	28-45	RAIEQIWDSVRYWYQSGL	0.517	0.519	0	6
A0R666	22	ethR	HTH-type transcriptional regulator EthR	130-147	EFKEFWSGLMQKWIAATA	0.582	0.5	0	6
A0QTW7	23	fadE3	Acyl-CoA dehydrogenase FadE3	68-85	VQVAEELARGWMSLAGAM	0.513	0.474	-1	5
A0QNU6	24	frc	Formyl-CoA:oxalate CoA-transferase	99-117	KQIFTDLVSRVDILVENFG	0.498	0.477	-1	5
A0QWW2	25	gapA	Glyceraldehyde-3-phosphate dehydrogenase	167-185	LAKVLNDEFQIVKGLMTTI	0.579	0.549	0	5
A0QYF7	26	gcvP	Glycine dehydrogenase (decarboxylating)	535-552	RKLIADLQSWLTAITGYD	0.514	0.472	0	7
A0R1C2	27	gdh	NAD-specific glutamate dehydrogenase	892-910	ATFSDIANEVAKSYGFWLG	0.506	0.454	-1	5
A0QT70	28	glpD2	Glycerol-3-phosphate dehydrogenase	443-462	VRHLLDRYGSLIGEVLALAD	0.511	0.513	-1	7
A0QXA1	29	gltB	Ferredoxin-dependent glutamate synthase 1	1162-1179	FVENFFTFIAEDIRRYLA	0.603	0.529	-1	6
A0QR00	30	gpmA	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	175-192	VLIAAHGNSLRALVKYLD	0.536	0.471	1	6
A0QSV0	31	guaA	GMP synthase [glutamine-hydrolyzing]	181-199	QQVLSRFLHDFAGIDATWT	0.552	0.472	-1	5
A0R401	32	hisD	Histidinol dehydrogenase	341-359	YFLKRLRNYGSLFLGRWST	0.532	0.444	4	7
A0QUN9	33	hypD	Hydrogenase expression/formation protein HypD	41-58	IIRNGIDQLLEGSVEFVH	0.513	0.476	-2	6
A0QVM7	34	infB	Translation initiation factor IF-2	491-508	SVIYQAIDEIEAALKGML	0.547	0.518	-2	6
A0R397	35	kdpC	Potassium-transporting ATPase KdpC subunit	3-20	FTNIVRQHTAALRALLAL	0.592	0.486	2	6
A0R2B1	36	kgd	Multifunctional 2-oxoglutarate metabolism enzyme	972-989	LWEAQFGDFVNGAQSIIID	0.539	0.52	-3	5
A0QR49	37	kgtP	Dicarboxylic acid transport integral membrane protein KgtP	22-39	IWNTIRGSSGNLVEWYDV	0.542	0.495	-1	6
A0R4Z6	38	kstR2	HTH-type transcriptional repressor KstR2	64-82	RDFLDWLFGRYQQILDAT	0.513	0.459	-1	7
A0R0Y9	39	lepA	Elongation factor 4	224-241	FDSVYDIYRGVVTYVRVV	0.581	0.49	0	5
A0QT91	40	lhr	ATP-dependent DNA helicase	1193-1210	ILETLGHGGAYFFRQLTD	0.542	0.492	-1	6
A0R5U1	41	lys1	Saccharopine dehydrogenase	256-275	YGLGSEFIDVLKTLHKLGLD	0.523	0.424	-1	9
A0QYV1	42	lysX	Lysylphosphatidylglycerol biosynthesis bifunctional protein LysX	680-697	LFAQLRDWSGEVQLLLLDN	0.544	0.488	-2	6
A0R0U9	43	mbtB	Phenyloxazoline synthase mbtB	1063-1080	SLERALAAILGELLSVAD	0.534	0.5	-2	5
A0QNR4	44	mce1C	MCE-family protein MCE1c	278-296	QDLADILTVAGKFITSLAE	0.512	0.505	-2	6
A0R4F8	45	mce-2	MCE-family protein MCE1a	138-156	ATGVTTEFNTLFETIMRIT	0.543	0.478	-1	6
A0QNR3	46	mce2B	MCE-family protein MCE1b	161-179	SLITIFQQGGGTINDILDQ	0.53	0.484	-2	7

A0QRK0	47	mce2B	MCE-family protein Mce6B	236-253	LVESMGSIKVVRLSTI	0.527	0.491	1	5
A0QPC2	48	mce3B	MCE-family protein MCE3b	196-213	IGEVIGNLDVLLGSLGEQ	0.552	0.511	-3	6
A0R4N8	49	mce4A	Virulence factor Mce family protein	136-155	DVQLEVNTLFQTLSDLLDKI	0.501	0.532	-3	6
A0R4N7	50	mce4B	MCE-family protein MCE4b	191-210	DQLISDVIANLNTVLGTVDE	0.439	0.476	-4	5
A0R6Q4	51	mdcC	Malonate decarboxylase acyl carrier protein	48-65	TSVDGFDTVWQDTLARFF	0.515	0.472	-2	5
A0R6Q9	52	metE	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	195-212	RLGELVSVYQGQLELLAD	0.588	0.511	-2	6
A0QNF0	53	MSMEG_0018	ABC transporter, permease/ATP-binding protein	419-436	IADLRRWVATITQEVHVF	0.59	0.48	0	5
A0QNF1	54	MSMEG_0019	Amino acid adenylation	1056-1073	DVRTLAGMWTDLLTAIAS	0.596	0.518	-1	5
A0QNF1	54	MSMEG_0019	Amino acid adenylation	5135-5156	SVAELGELWVAALRELGLATG	0.531	0.44	-2	7
A0QNF1	54	MSMEG_0019	Amino acid adenylation	1230-1247	DDLHTMIETVHHIVADGW	0.527	0.487	-4	5
A0QNI3	55	MSMEG_0054	ISMsm2, transposase	287-305	TSSSWLNLVERWFAELTTK	0.511	0.482	0	5
A0QNJ7	56	MSMEG_0067	Conserved hypothetical proline and alanine rich protein	348-365	GLFQKATRGVLTSTISGLV	0.537	0.487	2	5
A0QNP5	57	MSMEG_0117	Alpha/beta hydrolase fold protein	73-91	FDYTFDALADLTEGLLTHL	0.612	0.541	-4	7
A0QNU5	58	MSMEG_0167	Transmembrane transport protein	301-319	SLKAIINGTGRGVIGWISD	0.499	0.456	1	5
A0QNV3	59	MSMEG_0175	FAD dependent oxidoreductase, putative	154-171	LLTTLTAAIAEAGGRFVR	0.515	0.476	1	6
A0QNW1	60	MSMEG_0184	Transferase	149-166	EQLSAVLATMARHFTAHW	0.556	0.48	0	6
A0QNY4	61	MSMEG_0206	Acyltransferase	579-598	GFVSYDQAWLDGLTRLVTVL	0.602	0.528	-1	7
A0QNY8	62	MSMEG_0211	ABC transporter, ATP-binding protein	377-394	MIRHLGSALTDVTVVFDE	0.519	0.511	-2	5
A0QP24	63	MSMEG_0247	Secreted peptidase	283-301	NHIVQDIGDGVYAFYAHLQ	0.513	0.452	-2	5
A0QP36	64	MSMEG_0258	Oxidoreductase, short chain dehydrogenase/reductase family protein	95-112	LVDEWDAMIDVNVRRLLN	0.511	0.493	-3	5
A0QP37	65	MSMEG_0260	DNA-binding protein	188-205	AVLTELDRSAEFTELWS	0.523	0.478	-3	5
A0QP54	66	MSMEG_0277	Aminotransferase class-III	321-339	SMVHYIADIFDTGLRRIQA	0.499	0.492	0	6
A0QP81	67	MSMEG_0304	Acyl-CoA synthase	332-349	DVVIAFMDFRGDVIYNNY	0.543	0.471	-2	7
A0QPE3	68	MSMEG_0368	Conserved hypothetical alanine and proline rich protein	195-212	MEQIISDIGQYGAMLNRI	0.507	0.511	-1	6
A0QPF2	69	MSMEG_0377	Nitrile hydratase	85-103	KFRYYEKWLGGISQFFVVK	0.453	0.446	2	5
A0QPF4	70	MSMEG_0379	Nitrile hydratase activator P14k	39-56	WSEFQQSLIDAIGAWDAS	0.542	0.517	-3	5



A0QPG0	71	MSMEG_0385	Putative glycosyl transferase	83-100	EALGVTISQWEDIGKTLV	0.512	0.501	-2	5
A0QPG1	72	MSMEG_0386	NAD dependent epimerase/dehydratase family protein	240-259	GQSLTNSYTGIVALFARLAR	0.47	0.478	2	6
A0QPR4	73	MSMEG_0489	Putative recemase	246-263	YLTLNLALEKLAELFED	0.528	0.497	-3	8
A0QPR7	74	MSMEG_0492	Conserved hypothetical integral membrane protein	123-140	RISREFGGAWGWLAAVLS	0.606	0.507	1	5
A0QPX1	75	MSMEG_0547	ISMsm5, transposase	304-329	RGSFNKSVKELIAAISAFIEGWNQRAH	0.373	0.469	1	7
A0QPX2	76	MSMEG_0549	ABC transporter, permease protein	44-61	GDLWTHLQTSVSRVFAGY	0.54	0.493	0	5
A0QPZ0	77	MSMEG_0567	Selenophosphate synthetase	268-285	RAVLDRIGGIAAASSAW	0.524	0.481	1	5
A0QQ29	78	MSMEG_0606	Putative transcriptional regulatory protein TetR	114-131	VSQLAMVSDDFAQYWAEI	0.578	0.484	-3	5
A0QQ75	79	MSMEG_0654	Uncharacterized protein	195-212	AALRRAARYASGWWSFLT	0.519	0.474	3	6
A0QQ85	80	MSMEG_0664	FAD dependent oxidoreductase	174-197	RAVADITRLLTMSIADLLDDWFE S	0.522	0.495	-3	7
A0QQA1	81	MSMEG_0681	p450 heme-thiolate protein	255-273	GFETTVNLLGNGIRMLLDH	0.519	0.494	-1	5
A0QQD4	82	MSMEG_0715	3-oxoacyl-[acyl-carrier-protein] reductase	74-92	AVDMVVDTWGRLDAVILNA	0.57	0.462	-2	5
A0QQD6	83	MSMEG_0718	Acetyl-CoA synthetase	85-109	RVAGLLTRQVESWITALAAWRS GLV	0.582	0.467	2	7
A0QQE7	84	MSMEG_0729	Uncharacterized protein	55-72	ALTALFIEVSNLFGRLDK	0.568	0.499	0	6
A0QQF3	85	MSMEG_0735	Putative transcriptional regulator	97-114	LRQRVAGIIDMLYDGLTA	0.512	0.475	0	5
A0QQG1	86	MSMEG_0743	Xanthine dehydrogenase	1-18	MLGGVRDVLGTL SAVWES	0.573	0.546	-1	5
A0QQQ4	87	MSMEG_0838	AsnC-family protein transcriptional regulator	278-297	WDVLTEVITRTGEDLITVLD	0.552	0.56	-4	5
A0QQY2	88	MSMEG_0917	Uncharacterized protein	378-395	TEYGVEITAITETIERW	0.523	0.48	-3	6
A0QQZ9	89	MSMEG_0934	Uncharacterized protein	114-132	VLGQVLEAVDSDFNLTLEL	0.571	0.519	-4	5
A0QRA2	90	MSMEG_1043	GntR-family protein transcriptional regulator	451-471	QLAEAVELLARAWHSITGTIG	0.548	0.532	-1	5
A0QRC4	91	MSMEG_1066	Uncharacterized protein	1-18	MTETTTTFMDNVLGWLHK	0.531	0.474	-1	6
A0QRE2	92	MSMEG_1084	ABC transporter, solute-binding protein	409-427	QEWISYLGWWARGMQDGVG	0.528	0.503	-1	6
A0QRH4	93	MSMEG_1118	Amino acid permease	92-109	ISRGLGRIVGLGSGLLTT	0.558	0.486	2	6
A0QRH6	94	MSMEG_1120	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	203-220	LTKDISRFIALEGRVWSV	0.531	0.485	1	5
A0QRI9	95	MSMEG_1133	Bifunctional short chain isoprenyl diphosphate synthase	204-221	RLGGIVGTAFQIADDIID	0.514	0.499	-2	6
A0QRK1	96	MSMEG_1145	MCE-family protein Mce6C	241-258	STIGSLMNQSNLLAEFV	0.527	0.477	-1	6

A0QRK6	97	MSMEG_1150	Conserved secreted protein	89-106	YLSTLVGNWMKAGQKMVA	0.531	0.494	2	6
A0QRK8	98	MSMEG_1152	Citrate-proton symporter	226-243	EQNAGTWGGVLKHWIGLL	0.604	0.519	0	6
A0QRL3	99	MSMEG_1157	Short chain dehydrogenase	104-121	IDTIGDLLLLKTHVRLVKA	.515.	483	1	6
A0QRL6	100	MSMEG_1160	ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component	177-194	SLQDELLRIWQATGKTIL	0.533	0.526	0	5
A0QRL7	101	MSMEG_1161	Taurine transport system permease protein	68-86	GQLWEHVSASLSRALAGFA	0.513	0.483	0	5
A0QRP3	102	MSMEG_1189	Uncharacterized protein	268-285	WLMGIGRIDIDAFHGIAEN	0.518	0.483	-2	5
A0QRU1	103	MSMEG_1238	Type III restriction enzyme	421-439	LAIISAIEGLVQKHSRVIV	0.635	0.423	1	5
A0QRV5	104	MSMEG_1252	Uncharacterized protein	1374-1391	GMSVRALMDNFGELITQI	0.542	0.509	-1	6
A0QRY8	105	MSMEG_1286	Sulfatase	330-349	GELLGAHGGLHQKWFNLYDE	0.425	0.473	-2	7
A0QS05	106	MSMEG_1303	Putative transcriptional regulator	197-214	LIGELTSAHNEFARLWAA	0.536	0.545	-1	6
A0QSC6	107	MSMEG_1431	Cytochrome P450-terp	211-228	SAEELNAVILDFFNLYFTE	0.539	0.493	-4	6
A0QSC7	108	MSMEG_1432	Carboxylic ester hydrolase	459-476	QALADQMIGYWSQFVRTG	0.591	0.47	0	6
A0QSN0	109	MSMEG_1536	Cell division FtsK/SpoIIIE	835-852	WSTLRTEFESLESTITTL	0.511	0.475	-2	6
A0QSN1	110	MSMEG_1537	Conserved hypothetical alanine and valine rich protein	43-61	IVDDHFVTVEDLWTRVLGT	0.583	0.465	-3	5
A0QSW1	111	MSMEG_1621	Pyrimidine-specific ribonucleoside hydrolase RihA	329-347	TVFFDRFISRVGAFQAQLT	0.536	0.466	2	6
A0QSW5	112	MSMEG_1626	Putative DNA-binding protein	200-218	TALVDELSAASTDFGDWWA	0.507	0.472	-4	5
A0QSX6	113	MSMEG_1637	Histidine kinase	476-498	VGSAAGDLIHLLAELLDNALRYS	0.508	0.475	-2	8
A0QTA9	114	MSMEG_1775	Cytochrome P450	168-185	ADEFMTAWWRLVRRRLTLG	0.586	0.487	1	6
A0QTE5	115	MSMEG_1811	Maf-like protein MSMEG_1811/MSMEI_1767	191-208	LRALFERLEVSVADLWSA	0.559	0.503	-1	6
A0QTH0	116	MSMEG_1838	Cationic amino acid transporter	124-141	VAKGWSSYLGTVFNFGGG	0.546	0.468	1	5
A0QTL4	117	MSMEG_1886	Fatty acid desaturase	339-356	TGSFLVQYGKTRWRTIAKL	0.514	0.489	3	6
A0QTT5	118	MSMEG_1957	Uncharacterized protein	48-65	MGDLGQIFTKLGEMFSGA	0.508	0.538	-1	7
A0QTU1	119	MSMEG_1963	Putative transcriptional regulatory protein	891-908	VLRAQLRWMEAVLATWRG	0.587	0.521	2	6
A0QTV3	120	MSMEG_1977	Alcohol dehydrogenase	280-297	ISTEINFIGNLVGSYNDL	0.541	0.479	-2	7
A0QTW2	121	MSMEG_1986	Tartrate dehydrogenase	88-105	SLWGSLIQFRRHFDQYVN	0.524	0.482	1	6
A0QTZ6	122	MSMEG_2022	Gluconate permease	77-99	AILQQTGAIQRLVETLLRWFGAK	0.557	0.431	2	5

A0QTZ9	123	MSMEG_2025	Putative IclR family protein transcriptional regulator	239-256	WVDLVVGYAEQITRSLGG	0.553	0.532	-1	5
A0QU11	124	MSMEG_2037	Uncharacterized protein	112-129	LIGALRAIFDAWQTGERL	0.571	0.481	0	5
A0QU67	125	MSMEG_2096	Probable membrane transporter protein	176-193	NAIKNLLGMVANTTAGVF	0.518	0.476	1	5
A0QU92	126	MSMEG_2122	Dihydroxyacetone kinase, L subunit	1-18	MDLSTLTAWLREYARLID	0.552	0.483	-1	5
A0QUD9	127	MSMEG_2173	GntR-family protein transcriptional regulator	158-177	AHSSLLAKLMHEIAGLIRET	0.486	0.486	0	7
A0QUE5	128	MSMEG_2179	Transcriptional regulator, TetR family	133-151	ETLAAGYREWMALLEASFE	0.485	0.484	-3	7
A0QUE5	128	MSMEG_2179	Transcriptional regulator, TetR family	192-209	LSDTFRFMVNYLRLFATD	0.584	0.476	0	6
A0QUF0	129	MSMEG_2184	Amino acid permease	101-118	YQWSRRMGGEVIGWFGGW	0.602	0.484	1	7
A0QUF7	130	MSMEG_2191	Acyl-CoA dehydrogenase	319-337	SSMLKVLSTELSQILTELS	0.557	0.469	-1	7
A0QUL3	131	MSMEG_2248	Two-component system sensor kinase	567-584	MSHVVDGLAGLYADLQEL	0.541	0.522	-3	6
A0QUM5	132	MSMEG_2261	Uncharacterized protein	97-114	LAGLANSLATLSGGLVKA	0.531	0.479	1	5
A0QUU7	133	MSMEG_2340	Uncharacterized protein	129-146	IDSAAAVADWLQGFIDEL	0.572	0.509	-4	6
A0QV46	134	MSMEG_2444	Dienelactone hydrolase	211-228	AATTDAWTRVFAFFDEHL	0.528	0.481	-2	5
A0QV73	135	MSMEG_2471	Pyruvate dehydrogenase E1 component	504-521	ETNLVGLLGELGATWSRW	0.579	0.527	-1	6
A0QVA0	136	MSMEG_2500	Uncharacterized protein	377-395	RLIAQRFAQIAQRFAHVLD	0.458	0.498	2	5
A0QVG3	137	MSMEG_2564	Alcohol dehydrogenase, zinc-binding protein	89-106	DHVVGWASGFDGLMEQVI	0.579	0.501	-3	5
A0QVG6	138	MSMEG_2567	Cyclohexanone monooxygenase	426-443	EVMAQFIADIDRWMQGTV	0.544	0.54	-2	6
A0QVT8	139	MSMEG_2691	Acetyltransferase, gnat family protein	25-42	LEKNLVTLYESVQEFWVA	0.587	0.499	-2	6
A0QVU2	140	MSMEG_2695	35 kDa protein	5-23	FVKAWKYLMAFSSKVDEY	0.578	0.539	1	6
A0QVW5	141	MSMEG_2719	Hydrogen:quinone oxidoreductase	217-234	ATIQLMTDYMTRLMRYVE	0.526	0.493	0	8
A0QW15	142	MSMEG_2772	Amino acid permease	475-494	ALFVLMKLIHRHYDTVAREL	0.587	0.503	1	6
A0QW38	143	MSMEG_2795	Transmembrane transport protein	180-197	QDVLGGWREALGSWTVLA	0.569	0.476	-1	5
A0QW49	144	MSMEG_2805	ISMsm5, transposase	304-323	RGSFN SVKELIAAISAFIEG	0.442	0.496	0	6
A0QW69	145	MSMEG_2837	Nitrate reductase NarB	318-336	GELIGTAERLLSTVLQGFY	0.571	0.487	-1	6
A0QW73	146	MSMEG_2841	Putative monooxygenase	172-189	QWAE EYEVVYKLWEGSW	0.532	0.468	-3	6
A0QW87	147	MSMEG_2855	Virulence factor Mce family protein	132-152	DHVTVEINTIFEKLVLSKI	0.498	0.518	-1	6
A0QWF9	148	MSMEG_2928	Uncharacterized protein	309-327	FLNALVDFATEGFGALANM	0.622	0.513	-2	7

A0QWP7	149	MSMEG_3017	Uncharacterized protein	861-878	ELADLLDAIHIGLRDLAT	0.526	0.497	-3	6
A0QWP8	150	MSMEG_3018	Transglutaminase domain protein	153-170	LIEVLRDLTSRIYTDFTY	0.565	0.505	-1	7
A0QWV7	151	MSMEG_3079	Nucleotide-binding protein MSMEG_3079/MSMEI_3001	222-240	GALEFLDITYHRLLDVVIDG	0.554	0.486	-3	7
A0QWZ8	152	MSMEG_3121	DNA-binding protein	219-238	EAFAEILGTHVQRLATIVNG	0.485	0.466	-1	5
A0QX09	153	MSMEG_3132	DNA-binding protein	166-183	NWEGLTAWAVRWLRDFTG	0.571	0.543	0	5
A0QX63	154	MSMEG_3187	Putative acyltransferase domain protein	219-236	DQATAYYNSFARAWELLL	0.516	0.481	-1	6
A0QXC2	155	MSMEG_3249	Branched chain amino acid transport permease	170-188	TLGFGEIIRLMADNLSGIT	0.554	0.461	-2	6
A0QXC4	156	MSMEG_3251	Branched-chain amino acid ABC transporter ATP-binding protein	182-200	VISQIFRIIADINSQGTTV	0.587	0.482	0	5
A0QXD2	157	MSMEG_3259	Acyl-CoA dehydrogenase	87-104	LAHILRVHFSVVEELQRA	0.537	0.508	0	5
A0QXD5	158	MSMEG_3263	Xylulose kinase	343-360	LFRAAYEGISFGIRQILE	0.578	0.478	0	7
A0QXE6	159	MSMEG_3273	Aminopeptidase	38-56	YVDGLWTDAAAGNLVGLLRG	0.536	0.443	-1	5
A0QXE7	160	MSMEG_3274	MerR-family protein transcriptional regulator	138-156	SQIGAWFAASVDTLQRALS	0.506	0.455	0	5
A0QXF8	161	MSMEG_3285	3-isopropylmalate dehydrogenase	238-257	NMFGDILSDLTGQLSGSLGM	0.532	0.466	-2	6
A0QXG5	162	MSMEG_3292	DNA-binding protein	195-212	ELITELLHTSTRFRNLWS	0.532	0.495	0	6
A0QXI4	163	MSMEG_3313	ROK-family transcriptional regulator	306-323	LAEVATSLGRGIGGLVNL	0.535	0.534	0	5
A0QXL9	164	MSMEG_3350	TRAP dicarboxylate transporter, DctM subunit	285-302	WIREIGESLREAIGLTAM	0.51	0.477	-1	6
A0QXM9	165	MSMEG_3360	Transcriptional regulator, TetR family	120-137	LTAVISRGFRDVIIVLSA	0.598	498	1	5
A0QXQ3	166	MSMEG_3385	Uncharacterized protein	78-95	IWDRTLTKLVALDNTIID	0.564	0.51	-1	7
A0QXT9	167	MSMEG_3423	IclR family transcriptional regulator	78-95	LGS AFLSGFNQIREFYRV	0.528	0.469	1	6
A0QXW8	168	MSMEG_3452	TetR family protein transcriptional regulator	121-138	FADSLTMLTEAVGTLLEA	0.576	0.508	-3	6
A0QXZ0	169	MSMEG_3474	Probable conserved integral membrane protein	138-156	WGALEQRWGRIVAALVSTV	0.612	0.575	1	5
A0QXZ4	170	MSMEG_3478	Aminopyrimidine aminohydrolase	24-43	LTF SARLWQQIETVYEEILA	0.633	0.464	-2	8
A0QXZ6	171	MSMEG_3480	Aminoglycoside/hydroxyurea antibiotic resistance kinase	21-38	WVDGLAKLVRTQIGDWEL	0.556	0.509	-1	5
A0QY08	172	MSMEG_3492	Phosphodiesterase	219-239	TAWLMQLRQVDRLVESIVETL	0.572	0.513	-1	5
A0QY46	173	MSMEG_3531	Uncharacterized protein	154-171	SRAIGSVRGLVGWLERLL	0.547	0.514	2	6
A0QY67	174	MSMEG_3552	Uncharacterized protein	99-121	EKLTAAIHRDFSVLWAAFRELAE	0.441	0.512	-1	7
A0QY87	175	MSMEG_3572	Transcriptional regulator, TetR family	146-163	TRFLVGGFVEVLRSWMED	0.571	0.501	-1	5

A0QY93	176	MSMEG_3578	Putative cyclase	169-187	SGWSAANALFNGFFREIVT	0.558	0.447	0	6
A0QYA9	177	MSMEG_3594	Anthranilate dioxygenase reductase	182-199	LLGALGAEVAEVFAQLHR	0.549	0.505	-1	5
A0QYF9	178	MSMEG_3644	Transcriptional regulator, MerR family protein	82-100	LVLKIVKRLLDTGISLHNI	0.649	0.429	2	6
A0QYG0	179	MSMEG_3645	Uncharacterized protein	56-73	LTHDLIRDLIAALGHSLK	0.537	0.5	0	7
A0QYH1	180	MSMEG_3656	ABC transporter, permease/ATP-binding protein	37-57	TLIARFTTWGRQFWRVTGGYF	0.65	0.504	3	8
A0QYL5	181	MSMEG_3701	Uncharacterized protein	315-335	FTTLFGGTDSLKRLWHNLATM	0.568	0.434	1	6
A0QYM8	182	MSMEG_3715	Linear gramicidin synthetase subunit C	653-670	FADVVDVLQDLLDHHAAL	0.563	0.54	-4	5
A0QYQ8	183	MSMEG_3748	Conserved membrane protein	142-160	GLVAHLEAFAGNTIEFIRS	0.536	0.448	-1	6
A0QYR7	184	MSMEG_3761	Clp, N terminal	34-51	LVGVLQSAGRDLGALLAG	0.546	0.467	0	5
A0QYV0	185	MSMEG_3795	Uncharacterized protein	61-78	RRLITALAGLVTASAEYL	0.547	0.483	1	6
A0QYV7	186	MSMEG_3802	Tetratricopeptide TPR_4	323-341	SWLSIFRGAFDEATQLVAE	0.531	0.491	-2	6
A0QYZ1	187	MSMEG_3837	Uncharacterized protein	222-239	DVISGTSRLIAGFVQIAQ	0.551	0.472	0	5
A0QZ66	188	MSMEG_3915	NAD-dependent alcohol dehydrogenase	299-316	SYFGSFWGNYNLDEVLA	0.569	0.51	-2	7
A0QZ82	189	MSMEG_3931	[NiFe] hydrogenase, beta subunit, putative	5-22	AGIHRLVATLIDRGYRVI	0.523	0.529	2	6
A0QZF6	190	MSMEG_4008	2OG-Fe(II) oxygenase	146-163	AAWTTYFHAMNDLARKLM	0.521	0.512	1	7
A0QZF6	190	MSMEG_4008	2OG-Fe(II) oxygenase	245-262	DALVVNIGDLMAQWTNDL	0.554	0.526	-3	6
A0QZF8	191	MSMEG_4010	Glyoxalase family protein	9-28	SVFASDIEKLSTFYADLLGL	0.597	0.425	-2	6
A0QZG1	192	MSMEG_4013	Methylenetetrahydromethanopterin reductase	156-173	KVLDLIGRHADGFILQLA	0.578	0.47	0	5
A0QZH2	193	MSMEG_4024	Transcriptional regulator, TetR family protein	135-153	FAEGYWRWITLLEDGFHRM	0.637	0.567	-1	7
A0QZH2	193	MSMEG_4024	Transcriptional regulator, TetR family protein	365-384	YDRWLALFYDGMTAMVRQHD	0.475	0.494	-1	7
A0QZH2	193	MSMEG_4024	Transcriptional regulator, TetR family protein	192-209	LVDATQFLVNYIRMFADK	0.552	0.474	0	5
A0QZI4	194	MSMEG_4036	Crotonobetaine/carnitine-CoA ligase	226-246	SSFWSVDVAKYGATVFNAIGAM	0.537	0.459	0	6
A0QZL8	195	MSMEG_4072	ISMsm5, transposase	299-324	RGSFNSVKELIAAISAFIEGWNQRAH	0.373	0.469	1	7
A0QZR4	196	MSMEG_4120	CAIB/BAIF family protein	86-103	DVLLRLIDSADAFLQSMN	0.513	0.503	-2	6
A0QZU0	197	MSMEG_4148	Lipase	81-99	WAHGGQWVRTTVDLLDTFF	0.651	0.49	-1	6
A0QZU7	198	MSMEG_4155	Transposase A	21-39	NTIKAYAHDLKDWFTFLGG	0.481	0.517	0	6
A0QZV4	199	MSMEG_4162	Uncharacterized protein	210-227	MATVIDIIGTHVDRVRGI	0.527	0.473	0	5

A0R000	200	MSMEG_4211	Two component system histidine kinase	444-461	LATDVITLLGNLVDNAVE	0.557	0.471	-3	5
A0R091	201	MSMEG_4302	Adenylate cyclase, putative	221-238	TDALHRAIAEHLDELLVW	0.538	0.476	-3	6
A0R0G4	202	MSMEG_4377	Amino acid permease family protein, putative	81-101	GSIQWTKRLAGNVAGWFAGW	0.598	0.551	2	7
A0R0H1	203	MSMEG_4384	Penicillin binding protein transpeptidase domain protein	95-112	LQGTNLGLIGYLRGIDDV	0.526	0.545	-1	6
A0R0H5	204	MSMEG_4388	ABC transporter	461-478	TIQAQVLDLLTDLQEQLG	0.516	0.48	-3	5
A0R0K9	205	MSMEG_4422	Oxidoreductase	196-214	EFSTILAGLGSEVTHLVRG	0.512	0.471	-1	5
A0R0L7	206	MSMEG_4430	ATP-dependent transcriptional regulator, MalT-like, LuxR family	328-349	LDMSRHWYRYHHLFGELLRAEL	0.512	0.416	0	8
A0R0N1	207	MSMEG_4443	Uncharacterized protein	44-62	SQLYGLLDRVRDLGLELVS	0.479	0.446	-1	5
A0R0Q5	208	MSMEG_4470	ABC transporter	140-158	MFDTLTANIDGLAAVFARV	0.582	0.546	-1	6
A0R0S3	209	MSMEG_4489	Uncharacterized protein	6-24	DLLQRLSTVLAEVMSVAEE	0.451	0.501	-3	5
A0R0S6	210	MSMEG_4492	Amidase	282-300	EILAAALQTIADHLGELGHT	0.518	0.463	-3	6
A0R0U5	211	MSMEG_4511	Linear gramicidin synthetase subunit B	746-763	IADKFHATFDSLLHNFYG	0.528	0.529	-1	6
A0R0Y4	212	MSMEG_4551	Monooxygenase	161-178	MAQEFVEVTKLWEGSWE	0.521	0.477	-3	6
A0R0Z4	213	MSMEG_4561	ABC Fe <sup>3+</sup> -siderophores transporter, periplasmic binding protein	168-185	LTFDTLFDEINQLARMFD	0.531	0.518	-3	6
A0R113	214	MSMEG_4582	VWA containing CoxE-like protein	140-157	LATLIAQIVEAYGRYTSS	0.536	0.487	0	6
A0R117	215	MSMEG_4586	ABC nitrate/sulfonate/bicarbonate family protein transporter, periplasmic ligand binding protein	250-267	LQDFFGRLSGFWDWYKAN	0.563	0.495	0	7
A0R133	216	MSMEG_4601	Transcriptional regulator AraC family	174-191	WWANALHVSERTVARLFR	0.508	0.501	2	5
A0R190	217	MSMEG_4665	IolE protein	26-43	YTRFLDEVASAGYRWIEL	0.508	0.528	-1	6
A0R1A9	218	MSMEG_4685	Oxidoreductase	142-160	AMRKLSDLLALFAHALGL	0.579	0.449	0	8
A0R1C6	219	MSMEG_4703	Glycerol-3-phosphate acyltransferase	212-229	EMLDELSTGWSRFSVDLI	0.539	0.545	-3	7
A0R1E0	220	MSMEG_4718	Transcriptional regulator, TetR family protein	61-78	LVELLVGISTRLLDGARE	0.511	0.492	-1	6
A0R1J5	221	MSMEG_4776	Glyoxalase/bleomycin resistance protein/dioxygenase	15-32	VVADLDDAISRWLQMGVVG	0.521	0.49	-2	5
A0R1J8	222	MSMEG_4779	Probable regulatory protein	50-67	VHYYFRTMDDLFLAVFRR	0.583	0.468	1	6
A0R1K6	223	MSMEG_4787	Virulence factor Mce family protein	194-212	SGNIVDIKLNLTFTVTLR	0.507	0.489	1	6
A0R1L1	224	MSMEG_4793	Virulence factor Mce family protein	161-180	SSLIQIFQGGDTLSSLMSK	0.468	0.443	0	5
A0R1M3	225	MSMEG_4805	Acyl-CoA dehydrogenase	352-370	HYFASWFERYARSFGGTIA	0.522	0.5	1	7

A0R1M3	225	MSMEG_4805	Acyl-CoA dehydrogenase	251-268	MMWLGAFADRIDNMLADFN	0.601	0.49	-2	7
A0R1N3	226	MSMEG_4815	Thioesterase	226-243	ENVWEAGTDALAAIGAMF	0.508	0.468	-3	5
A0R1S0	227	MSMEG_4852	Enoyl-CoA hydratase, putative	258-277	EYMGSLLSAFFESMGNGVAN	0.482	0.431	-2	7
A0R1S4	228	MSMEG_4856	Cytochrome P450	279-298	KVIANAVEELMRYLSIIQTG	0.508	0.476	0	5
A0R1T9	229	MSMEG_4871	3-hydroxyacyl-CoA dehydrogenase type-2	103-120	LDGFKKTIEFYLTAVFNV	0.601	0.471	0	6
A0R1U8	230	MSMEG_4880	Methylmalonyl-CoA mutase C-terminal domain protein	31-48	FEVIYTGIRQRIEDIVSI	0.562	0.495	-1	6
A0R1U9	231	MSMEG_4881	Methylmalonyl-CoA mutase, N-terminus of large subunit	323-340	LASVLGGVQSMFTAAWDE	0.588	0.476	-2	5
A0R1W1	232	MSMEG_4893	Putative neutral zinc metalloproteinase	300-317	ITEDLLTDVMDSLGQIFA	0.587	0.5	-4	7
A0R1Z7	233	MSMEG_4934	ATP:cob(I)alamin adenosyltransferase	160-177	KYLNRLSDLLFILSRVAN	0.529	0.49	2	6
A0R231	234	MSMEG_4968	Two-component system sensor kinase	89-106	TRFWKGVAAHHLRMIYDL	0.592	0.544	2	7
A0R262	235	MSMEG_4998	Hydrolase, alpha/beta fold family protein	213-237	LDRQLDLLLDGHTLLWRTLGRV	0.514	0.501	1	8
A0R2B5	236	MSMEG_5053	Short chain alcohol dehydrogenase	247-264	KILDVIVRITGSGYQRLF	0.567	0.494	2	7
A0R2D8	237	MSMEG_5076	ABC transporter membrane-spanning protein	202-220	LIRGVGDVIDNSGSILSWF	0.632	0.532	-2	6
A0R2E9	238	MSMEG_5087	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	125-142	TLEEFFEAWTAGYLGMDH	0.556	0.484	-4	6
A0R2H7	239	MSMEG_5117	L-proline dehydrogenase	155-173	SIVRDLRTEFDWLGTVLQA	0.513	0.464	-1	5
A0R2H9	240	MSMEG_5120	Transcriptional regulator, CdaR	464-481	VLAETLRVYLDSEFGDVAA	0.526	0.482	-2	5
A0R2J8	241	MSMEG_5140	Nitrate reductase, alpha subunit	202-219	AGSRFVELIGGVMTSFYD	0.543	0.502	-1	6
A0R2Q5	242	MSMEG_5197	Acyl-CoA dehydrogenase	357-376	GRIQTIFGGTTEIMKEIIGR	0.415	0.494	1	7
A0R2U4	243	MSMEG_5237	Conserved membrane protein	50-68	QRLLRRFNSGIAVTLTVLA	0.531	0.468	3	6
A0R2U9	244	MSMEG_5241	GAF family protein	423-440	VDDLQAVISEIRTAIFDL	0.538	0.521	-3	5
A0R2Z6	245	MSMEG_5288	Putative serine/threonine protein kinase	374-391	DAIGFWQRLHHTFAAVLR	0.594	0.535	1	6
A0R342	246	MSMEG_5335	Formamidase	276-293	MGGFIDMHVDLIKGGMET	0.512	0.472	-2	7
A0R347	247	MSMEG_5341	Alpha/beta superfamily hydrolase	378-397	LGAVHRAHQVFDWLDEIVG	0.58	0.492	-2	5
A0R352	248	MSMEG_5346	TetR-family protein transcriptional regulator	182-201	QTLDEINELATNVVDLLITG	0.485	0.444	-4	5
A0R377	249	MSMEG_5372	Sensor protein KdpD	287-304	RVLRLDAAASLGATLHTVI	0.544	0.509	1	5
A0R377	249	MSMEG_5372	Sensor protein KdpD	111-128	WQDVEELLNAGITVISTV	0.602	0.482	-3	5

A0R379	250	MSMEG_5374	Glutamate--ammonia ligase	202-220	GDEIDHILSILRDHIVALG	0.531	0.483	-3	6
A0R398	251	MSMEG_5395	Sensor protein KdpD	653-674	AELLATIEESVDALTALVGNLL	0.585	0.518	-4	7
A0R398	251	MSMEG_5395	Sensor protein KdpD	114-131	WQDVDELLNAGITVISTV	0.594	0.482	-3	5
A0R3F9	252	MSMEG_5458	Acetyltransferase Pat	124-141	MFDRLVRIARQRLAAFIT	0.511	0.47	3	5
A0R3K1	253	MSMEG_5501	Uncharacterized protein	485-503	NDITYAIAAALTQIVEGIR	0.505	0.476	-1	5
A0R3M9	254	MSMEG_5530	Putative aliphatic sulfonates transport permease protein SsuC	268-285	SYSLVRLLELLLLSWRNG	0.569	0.479	2	6
A0R3M9	254	MSMEG_5530	Putative aliphatic sulfonates transport permease protein SsuC	111-134	VVLAVLAGLTRTGEDLLDWTMQL	0.714	0.447	-2	9
A0R3R4	255	MSMEG_5567	Transcriptional regulator, TetR family	81-98	GSYQEDLLHFLNQTFKLL	0.553	0.499	-1	5
A0R3S6	256	MSMEG_5579	MarR-family protein transcriptional regulator	13-33	NRTWAHFLESTTLILDELNRQ	0.397	0.473	-1	6
A0R3U2	257	MSMEG_5595	MarR family transcriptional regulator	12-29	YEMWRGYLDSTRLLLLRAL	0.555	0.539	1	9
A0R3X9	258	MSMEG_5633	AMP-dependent synthetase and ligase	269-287	VDSLKKAALAYGQIFVQLY	0.566	0.509	1	7
A0R403	259	MSMEG_5658	Epoxide hydrolase	145-162	GIGRIAQAWDTLMTRLGY	0.532	0.505	1	6
A0R404	260	MSMEG_5659	ABC transporter, ATP-binding protein	157-175	VEAIQDMLETGFDSLITAV	0.554	0.505	-4	5
A0R441	261	MSMEG_5696	'Cold-shock' DNA-binding domain protein	102-119	ELHGMVEDMITLLESADVQ	0.531	0.489	-4	6
A0R4F5	262	MSMEG_5815	Betaine aldehyde dehydrogenase	75-93	MLVGLADVVEHLDELAGL	0.603	0.5	-4	6
A0R4I7	263	MSMEG_5849	RelA/SpoT domain protein	154-171	SFEQLRSELLRLMELIAG	0.522	0.492	-1	6
A0R4I9	264	MSMEG_5850	Transcriptional regulator, TetR family protein	49-68	TYYFSSLDLIAKAVEYIGM	0.588	0.398	-2	7
A0R4J3	265	MSMEG_5854	Transcriptional regulator, TetR family protein	68-85	VHAASGFLDRLAAHLSGI	0.531	0.467	0	5
A0R4M2	266	MSMEG_5884	3-hydroxyisobutyrate dehydrogenase family protein	181-198	IASVIESLGEAMALVGKA	0.531	0.473	-1	5
A0R4N0	267	MSMEG_5891	ISMsm5, transposase	304-329	RGSFNVSVELIAAISAFIEGWNQRAH	0.373	0.469	1	7
A0R4N2	268	MSMEG_5894	Uncharacterized protein	151-168	LEKIDEIAKNASVLISVW	0.522	0.491	-1	6
A0R4N5	269	MSMEG_5897	MCE-family protein MCE4d	279-296	FTQILTDHSEDIEQLLHV	0.511	0.5	-4	6
A0R4P0	270	MSMEG_5902	Conserved hypothetical integral membrane protein Yrbe4a	10-28	RAVGGFVEMSLDTFAKIFR	0.472	0.547	1	5
A0R4P7	271	MSMEG_5909	NAD-dependent epimerase/dehydratase	239-256	VLVSFNEWIDILEQGVGR	0.599	0.513	-2	6
A0R4V2	272	MSMEG_5964	Glycosyl transferase, group 1, putative	388-405	AAAIDSYEDWIVGLAESI	0.548	0.494	-4	6
A0R4V7	273	MSMEG_5969	Uncharacterized protein	158-178	GNLLNILKNFDHIFVSVRDAV	0.524	0.507	0	6
A0R4Y6	274	MSMEG_5998	Uncharacterized protein	18-35	AKSTGTLIKWMSRFQTFLL	0.559	0.494	3	6



A0R511	275	MSMEG_6024	Acetoacetyl-CoA synthase	115-132	WKELLGRTAAFADALVSL	0.562	0.508	0	6
A0R5A5	276	MSMEG_6122	ABC transporter, membrane spanning protein	125-143	SVIGMWAGYHRGWRETAM	0.551	0.456	1	6
A0R5G0	277	MSMEG_6178	D-galactonate transporter	372-389	KRLGLTGGMFNFIGNLS	0.579	0.521	2	8
A0R5H9	278	MSMEG_6197	Diaminopimelate decarboxylase	282-299	LFDGTYTVVTEFGRALTA	0.534	0.472	-1	5
A0R5J7	279	MSMEG_6216	Integral membrane protein	144-162	VTIGQAWERLRGRLALIG	0.572	0.445	2	6
A0R5R4	280	MSMEG_6283	FAD binding domain protein	185-202	FHSITDLVAAMDRIIETG	0.521	0.498	-2	6
A0R5Y9	281	MSMEG_6363	Cysteine desulfurase family protein	297-314	GVYLSRLFDYLQTSLSL	0.587	0.517	1	8
A0R5Z4	282	MSMEG_6368	DNA-binding protein	79-96	WSVIVRGTAELLQTAEDI	0.528	0.5	-2	5
A0R684	283	MSMEG_6459	Ferredoxin-dependent glutamate synthase 1	1181-1199	VENFFMFIAEEVRELMAQL	0.616	0.534	-3	6
A0R690	284	MSMEG_6465	Chloride channel	154-172	HISAGFGSLLTRWLNLSDE	0.537	0.501	-1	7
A0R6B7	285	MSMEG_6492	GAF domain protein, putative	20-37	LSHVLAIEAETARSLGFG	0.587	0.495	-1	6
A0R6D3	286	MSMEG_6508	MarR family transcriptional regulator	133-150	IEHLAKGLDVLAELTRLL	0.566	0.52	-1	7
A0R6F7	287	MSMEG_6532	Transcriptional regulator, TetR family	95-113	EFDQTLRSILAVVVDLHHD	0.472	0.476	-3	5
A0R6H0	288	MSMEG_6546	Transcriptional regulatory protein	133-150	ISDGGFFQTLANLVAEALD	0.547	0.474	-3	6
A0R6H8	289	MSMEG_6554	Hypothetical ABC transporter ATP-binding protein	492-509	ASSFRRRLDEYIGFLVAW	0.517	0.496	1	6
A0R6L1	290	MSMEG_6588	Fumarylacetoacetate	283-300	GDTLTLILDDIGRIEHTI	0.514	0.497	-3	5
A0R6L6	291	MSMEG_6591	Aminotransferase class V	287-304	VDALQDMLESLGATIVSA	0.516	0.494	-3	5
A0R6M6	292	MSMEG_6603	NADH:flavin oxidoreductase/nadh oxidase	38-56	KAITAAILRGVLRVFTDFR	0.509	0.448	3	5
A0R6P2	293	MSMEG_6621	Bacterial luciferase family protein	265-282	HTATLEFIDHYAEMLGKL	0.513	0.478	-2	7
A0R6R3	294	MSMEG_6642	Caib/baif family protein	106-123	WNMSYETLRRINDQIVML	0.514	0.472	0	5
A0R6S7	295	MSMEG_6657	Alpha subunit of malonate decarboxylase	121-138	GAIHTYVELYARMFTDLA	0.584	0.49	-1	7
A0R6V9	296	MSMEG_6688	Purine catabolism PurC domain protein	425-442	LLAGGDELIDALTAFLRH	0.568	0.534	-2	7
A0R6Z2	297	MSMEG_6722	Uncharacterized protein	158-176	TWAQFTQYWEQQLDELSVA	0.528	0.468	-3	5
A0R730	298	MSMEG_6761	Glycerol-3-phosphate dehydrogenase	435-452	VAHLLGRYGTLDLELLEI	0.577	0.486	-2	7
A0R732	299	MSMEG_6762	Transcriptional regulator	79-96	VATVRSVSQMLAELEQIW	0.578	0.471	-1	5
A0R738	300	MSMEG_6768	Halogenase	453-471	GLIALSNRMQSFFREWAAV	0.571	0.487	1	6
A0R738	300	MSMEG_6768	Halogenase	383-408	AQISDTLYRSLTDMWLRVYQDQ YTLM	0.517	0.384	-1	9

A0R743	301	MSMEG_6773	CaiB/BaiF family protein	133-150	GVDGIMQAVTGLMSTLGE	0.514	0.5	-2	5
A0R749	302	MSMEG_6779	Uncharacterized protein	53-70	VSDFLDGFVRGFLVSGIRH	0.528	0.528	0	6
A0R751	303	MSMEG_6781	Uncharacterized protein	154-171	VNDLIFGTFREIERLMGL	0.573	0.497	-1	6
A0R776	304	MSMEG_6807	Transcriptional regulator, TetR family	60-77	LFLAVSDRYWRRYFDNFA	0.532	0.471	1	7
A0R7C4	305	MSMEG_6858	Epoxide hydrolase	150-167	ITRIARAWDTLMVSLGYQ	0.597	0.47	1	6
A0R7C5	306	MSMEG_6859	Oxidoreductase	106-123	LADWHRTIDVNIGGVLNV	0.548	0.491	-1	5
A0R7E9	307	MSMEG_6886	Transcriptional regulator	11-28	SYTEEVFGLLGKRWGLI	0.573	0.479	0	5
A0R714	308	MSMEG_6928	Uncharacterized protein	554-571	DDIIGGIAGVTGRLWGLT	0.586	0.492	-1	6
A0R715	309	MSMEG_6929	Integral membrane protein MviN	1026-1043	VMATILSRIFGDVGGGIN	0.595	0.473	0	6
A0R143	310	nadE	Glutamine-dependent NAD(+) synthetase	612-634	SYSLKEIRHWLQVFAQRFYSFSQ	0.519	0.418	2	7
A0QU33	311	nuoD	NADH-quinone oxidoreductase subunit D	346-363	IAKIMGRSMEGLIHFKL	0.553	0.488	2	6
A0R260	312	oppD	ABC transporter, ATP-binding protein OppD	537-554	SIQAGIINLLLDLQDRFG	0.593	0.481	-1	6
A0R712	313	pcnB	Poly(A) polymerase PcnA	72-90	QKFLRGWSDALWDTGIEFG	0.495	0.452	-1	5
A0QQ68	314	phnE	Phosphate-import permease protein PhnE	50-67	TALIDGSDNIVALLQRFMI	0.579	0.513	-1	7
A0QNL6	315	ptsI	Phosphoenolpyruvate-protein phosphotransferase	95-114	SEAVDQFIDMFTKMGLMAE	0.44	0.506	-3	7
A0QS46	316	rplA	50S ribosomal protein L1	94-117	IVGSDDLIEKIQQGFLDFDAAIAT	0.484	0.381	-4	7
A0QSD8	317	rplP	50S ribosomal protein L16	52-69	IAINRHIKRGKWWINIF	0.528	0.53	4	5
A0QS66	318	rpoC	DNA-directed RNA polymerase subunit beta'	835-852	IKSSFREGLTVLEYFINT	0.518	0.482	0	6
A0QW02	319	rpoD	RNA polymerase sigma factor SigA	390-407	SFTLLQDQLQSVLETSE	0.511	0.499	-3	5
A0R5B0	320	rsfB	Anti-sigma factor antagonist	99-116	GIADVVDLFDLDEALSS	0.516	0.472	-4	5
A0QY50	321	speB	Agmatinase	223-240	MTWHTMQEIWDRGFKAVM	0.574	0.481	0	5
A0R118	322	ssuB	Aliphatic sulfonates import ATP-binding protein SsuB	53-70	LLRILAGLEDATSGHLRI	0.536	0.472	0	6
A0QW75	323	ssuD	Nitrilotriacetate monooxygenase	370-388	QIVGTAETAADIITQWIDE	0.48	0.473	-4	5
A0QQ53	324	stf0	Trehalose 2-sulfotransferase	184-201	VITMLRAQEEGWRAWFTE	0.512	0.468	-1	5
A0R3M4	325	sucC	Succinate--CoA ligase [ADP-forming] subunit beta	166-183	LDAAAVTIQKLWEVFKVE	0.547	0.497	-1	5
A0R2C2	326	sugA	ABC sugar transporter, permease component	260-277	DNLFKAFNVGLGSAISVL	0.583	0.471	0	6
A0QWG2	327	thrS	Threonine--tRNA ligase	544-566	HRALFGSIERFFGVLTEHYAGAF	0.55	0.492	0	8

A0QYW4	328	uvrA	UvrABC system protein A	872-889	GLHFEDIRKLLKVINGLV	0.542	0.537	1	6
A0QYW4	328	uvrA	UvrABC system protein A	813-833	ISSIHRYLKTLVDVGLGYVRL	0.596	0.479	2	6
A0QUX9	329	wrbA	Flavodoxin/nitric oxide synthase	93-110	AAQFRAFIDSLGGLWAQG	0.556	0.49	0	6
A0QYC6	330	xfp	Probable phosphoketolase	486-503	YEAHVHIVDSMLNQHVKW	0.594	0.509	-1	6