Supplementary Data for McKenzie J.L. et al 2011

Supplementary Fig. 1.

Trypsin digestion of the VapBC complex and subsequent purification of VapC by anion exchange chromatography. Shown is the chromatogram for the anion exchange purification, trypsin is eluted early, while VapC is eluted later at approx 20% elution buffer, corresponding to 200 mM NaCl. The molecular weight marker at the left side of the gel shows molecular masses in kilodaltons, and bands corresponding to peaks on the chromatogram are labelled (Trypsin and VapC).

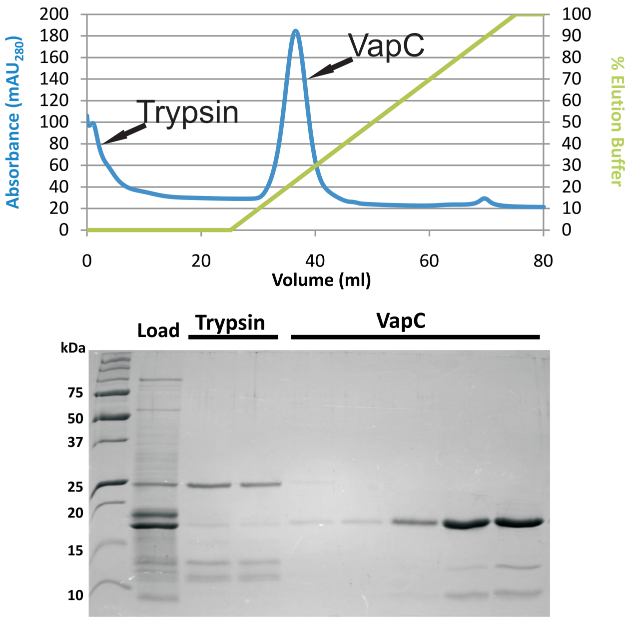
Supplementary Fig. 2.

Additional *in vitro* ribonuclease activity assays of VapC against Pentaprobe RNAs. Seven Pentaprobe RNAs were tested in total, six in the forward direction (922-927) and one reverse complement (932, the reverse complement to 926). VapC cleaved only a subset of pentaprobe RNAs across the time course (time indicated in min across top of gel) in the presence of 6 mM $MgCl_2$. Ribonuclease activity is inhibited by 12 mM EDTA and RNA only negative controls (-VapC) demonstrate no non-specific degradation of the substrates by contaminating ribonucleases. VapC activity is inhibited when in complex with VapB (VapBC). The molecular weight marker on the left of the gel shows molecular masses of single-stranded RNA (ssRNA) in bases.

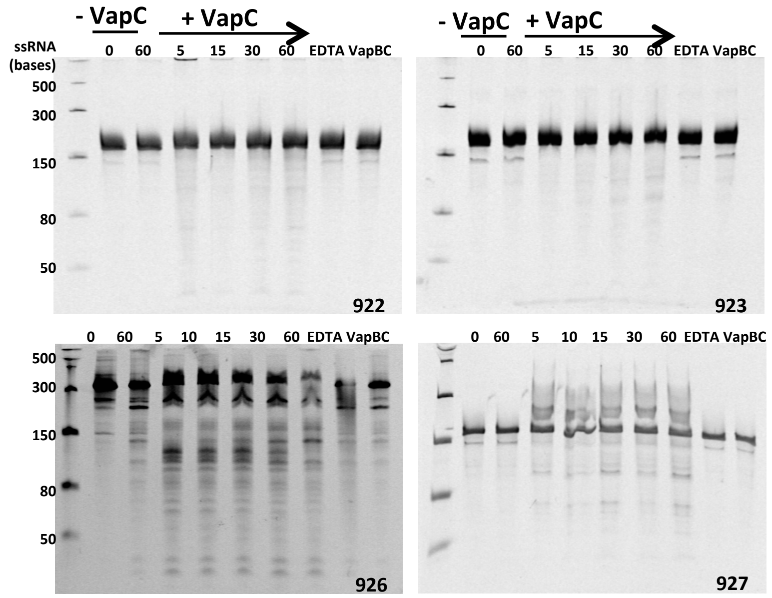
Supplementary Fig. 3.

VapC from *M. smegmatis* does not cleave *M. smegmatis* initiator tRNA *in vitro*.
VapC (61.35 pmoles) displays no ribonuclease activity against tRNA fMet (MSMEG_1965) in the presence of 6 mM $MgCl_2$ (time points in minutes indicated along the top of the gel). Negative controls show no non-specific degradation of RNA due to contaminating ribonucleases and include: RNA only controls (–VapC) and addition of 12 mM EDTA to the assay reaction. Double RNA bands are due to premature termination of the transcription reaction due to the high GC content of the RNA. A molecular weight marker at the left side of the gel shows molecular masses of ssRNA in bases.

Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3

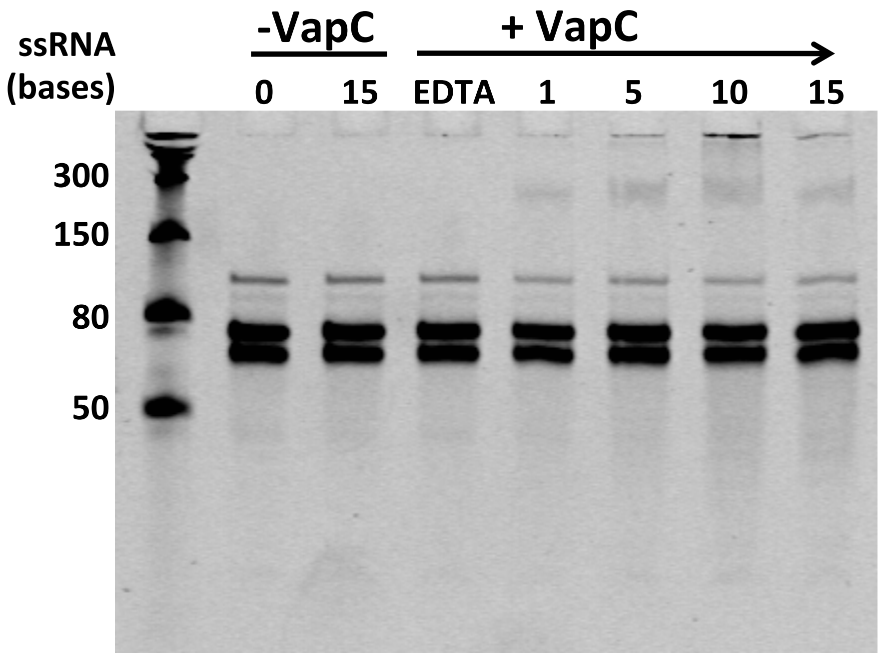


Table S1. Oligonucleotides used in this study

Oligo name	Sequence 5'-3'
MSMEG_0061M F	GACGACCTGGGTATCGACAT
MSMEG_0061M R	CAGGTATTCCTTGCGGTCAG
MSMEG_0515M F	CGCGATCGTCTACAACAAGA
MSMEG_0515M R	GAGTTGAACGCAGCCTTCTC
MSMEG_0539M F	GACAACCTGTCCGACCTCAT
MSMEG_0539M R	GTCGATCAGGATGCTCTTGC
MSMEG_0649M F	AGGAAGGTGTGGTCAAGTCG
MSMEG_0649M R	CCCTTGTCGATCATGGTCTT
MSMEG_1283M F	TGGCTCTAAGCATCAAACACC
MSMEG_1283M R	CAGGATCGATTCGGCTGT
MSMEG_1712M F	CGACGGCAAGTTCAATTACA
MSMEG_1712M R	GTACTGACGGTTCGGCAGAG
MSMEG_4182M F	GGCATCTTCACGTCCTTTGT
MSMEG_4182M R	ATCTTGTGTGTGGCAACGAG
MSMEG_4643M F	GCGAAAGGAACGAAGTGAAG
MSMEG_4643M R	GGTGTTGATGGACCAGTTGC
MSMEG_5571M F	GACTCGCTGAACCTCGACAT
MSMEG_5571M R	ACGGTCTTGGTGGGATACAG
MSMEG_5782M F	ACTCGACCTGAACTCGCTGT
MSMEG_5782M R	GGAAGTGAGCAAACGCTCTT
SigA F	GACTCTTCCTCGTCCCACAC
SigA R	GAAGACACCGACCTGGAACT
MSMEG_1546Q F	GATGGACGCCGTGATGTC
MSMEG_1546Q R	CGTACTGGGTCTCCAACTCC
MSMEG_2121Q F	GACGTGTTCTCCGACCAGTTACT
MSMEG_2121Q R	GAACATCACACTCAGCGGAATG
MSMEG_2122Q F	TCGAGGTCGGTATAGGCATC
MSMEG_2122Q R	TCGGCGTACATGACGTACAA
MSMEG_2123Q F	GGTCCCCGACCAGATGCT

MSMEG_2123Q R	GGCCATCTCGAAGTTCATCAC
MSMEG_2124Q F	CGGCCATCCAAGCCTTT
MSMEG_2124Q R	CTCCGAAAACGGTGAACACA
MSMEG_6239Q F	CGAAGGACCATGAGATCACC
MSMEG_6239Q R	GTATCGGTGACGATGCAGAA
MSMEG_6758Q F	CAGCACGGCGTTTCATGA
MSMEG_6758Q R	CAGCGGCCCGACAATG
MSMEG_6759Q F	ACACAACCCGGTCGAGATCT
MSMEG_6759Q R	GCTTGGCGGCGTTGAG
MSMEG_6761Q F	CGACGAGTTGCTCGAAATCA
MSMEG_6761Q R	GTAGTACGCCTCCACCTTGAGATAC
MSMEG_ 2124 RT R	CAGTTGGTCGCACTCGACATGG
MSMEG_2124 RT F	GTAGCCAGCCGTGTCCCG
932 50 Fwd	GTGCTGGAATTCTGCAGATCTCCA
932 150 Rev	ATCGGGTCATGTAGTGCTACGTTACGGCC
T7 932 50 Fwd	TAATACGACTCACTATAGGGGTGCTGGAATTCTGCAGATC
MSMEG_2124 77-98 RT F	ATGGTCCAGATCACATTCGACA
pCDNA3 PP F	AGAGAACCCACTGCTTACTGGCT
pCDNA3PP R	AGCGAGCTCTAGCATTTAGGTGACA
pUC/M13 F	CGCCAGGGTTTTCCCAGTCACGAC
pUC/M13 R	TCACACAGGAAACAGCTATGAC
MS_2124 T7 pGEM F	TAATACGACTCACTATAGGGAGACCTTCCGTCGGAACTTCAGC
MS_2124 T7 pGEM R	CTCAGTTGGTCGCACTCGAC
MSMEG_1965 RNA F	CGCGGGGTGGAGCAGCTCGGTA
MSMEG_1965 RNA R	TAGTAGCGGGGACAGGATTCGA
MSMEG_1965 RNA T7 F	GAGCTAATACGACTCACTATAGGGCGCGGGGTGGAGCA
MSMEG_2121 RNA F	ATGACGGTCGGCATCGTCGTCG
MSMEG_2121 RNA R	TCAGCCGAGCAGGTCACGCAC
MSMEG_2121 RNA T7 F	CCGCGTAATACGACTCACTATAGGGAGAATGACGGTCGGCATCGTCG
MSMEG_2122 RNA F	ATGGACCTGTCGACACTGACCGCCTG

MSMEG_2122 RNA R	TCATGAAGTGCTCCCCGCCGCG
MSMEG_2122 RNA T7 F	CACCCCTAATACGACTCACTATAGGGAGAATGGACCTGTCGACACTG
MSMEG_2123 RNA F	ATGAAAAAGCTCATCAACGATCCCG
MSMEG_2123 RNA R	TCAGCATCCCCTCCGCAGTG
MSMEG_2123 RNA T7 F	GTCGATAATACGACTCACTATAGGGAGAATGAAAAAGCTCATCAACG
MSMEG_2124 (-5’UTR) RNA F	GAGCCGTCATTGATCCAGAAAC
MSMEG_2124 (-5’UTR) RNA R	GAGCCGTCATTGATCCAGAAAC
MSMEG_2124 (-5’UTR) RNA T7F	TCGATAATACGACTCACTATAGGGATGGACGAGCCGTCATTGATC
T7 F (Sequencing)	TAATACGACTCACTATAGGG
T7 R	TAGTTATTGCTCAGCGGTGG
932 RNA Oligo 1 21-50	GGAAUUCUGCAGAUCUCCAACCUCACACCA
932 RNA Oligo 2 41-70	CCUCACACCACAUUACACUGGGGUGAUAUA
932 RNA Oligo 3 61-90	GGGGUGAUAUAAUAUGAUGCCGGGCGGGGGCCG
932 RNA Oligo 4 81-110	GGGCCGUAACGUAGCACUACAUGACCCGAUACGCUA
932 RNA Oligo 5 101-130	CCGAUACGCUAGGUGGGAUUAGGCAUCACAC
932 RNA Oligo 6 121-150	AGGCAUCACACUGGCGGCCGCUCGAGCAUGC
932 RNA Oligo 7 141-170	UAGAGGGCCCUAUUCUAUAGUGUCACCUAAA
932 RNA Oligo 8 161-190	CGAGCAUGCAUCUAGCUAAAUGCUAGAGCUCG
932 RNA Oligo 9	CACACUGGCGGCCGCUUAACGGCCGCCAGUGUG

Table S2 Summary dataset of expression ratios in response to VapC

Locus	GeneN	GeneS	Gene mean	Adj p value
MSMEG_0001	DNA polymerase III, beta subunit	dnaN	0.946	1.77E-01
MSMEG_0002	6-phosphogluconate dehydrogenase, decarboxylating	NA	1.016	7.38E-01
MSMEG_0003	DNA replication and repair protein RecF	NA	1.088	3.68E-01
MSMEG_0004	hypothetical protein	NA	0.992	5.18E-01
MSMEG_0005	DNA gyrase, B subunit	gyrB	0.784	2.58E-03
MSMEG_0006	DNA gyrase, A subunit	gyrA	0.854	4.44E-02
MSMEG_0007	conserved hypothetical protein	NA	1.020	6.97E-01
MSMEG_0009	hypothetical protein	NA	1.640	3.35E-01
MSMEG_0011	FAD-binding 9, siderophore-interacting	NA	1.435	7.44E-02
MSMEG_0012	ferric enterobactin transport system permease protein FepD	NA	1.419	1.63E-01
MSMEG_0013	ferric enterobactin transport system permease protein FepG; this gene contains a fran	NA	1.070	6.51E-01
MSMEG_0014	Formyl transferase	NA	0.957	4.90E-01
MSMEG_0015	ferric enterobactin transport ATP-binding protein FepC	NA	0.988	9.01E-01
MSMEG_0016	conserved domain protein	NA	1.253	1.27E-01
MSMEG_0017	ABC transporter, permease/ATP-binding protein	NA	1.000	1.00E+00
MSMEG_0018	ABC transporter, permease/ATP-binding protein	NA	1.218	4.48E-01
MSMEG_0019	amino acid adenylation	NA	0.930	2.50E-01
MSMEG_0020	Periplasmic binding protein	NA	0.914	6.96E-02
MSMEG_0021	aspartate 1-decarboxylase	panD	0.809	8.01E-03
MSMEG_0022	L-ornithine 5-monooxygenase	NA	0.772	2.89E-02
MSMEG_0023	conserved hypothetical protein	NA	0.774	1.23E-02
MSMEG_0024	peptidyl-prolyl cis-trans isomerase B	NA	0.881	6.16E-02
MSMEG_0025	conserved hypothetical protein	NA	1.000	9.99E-01
MSMEG_0026	putative membrane protein	NA	0.922	7.24E-02
MSMEG_0027	conserved hypothetical protein	NA	0.995	9.37E-01
MSMEG_0028	serine-threonine protein kinase	NA	0.886	1.41E-02
MSMEG_0029	anthranilate synthase component 2	NA	1.072	2.20E-01

MSMEG_0030	serine/threonine protein kinase PknA	pknA	0.827	8.69E-04
MSMEG_0031	Penicillin binding protein transpeptidase domain protein	NA	0.892	1.24E-01
MSMEG_0032	cell cycle protein, FtsW/RodA/SpoVE family protein	NA	0.988	8.06E-01
MSMEG_0033	protein phosphatase 2C	NA	0.875	6.72E-02
MSMEG_0034	FHA domain protein	NA	0.940	2.44E-01
MSMEG_0035	FHA domain protein	NA	1.051	7.00E-01
MSMEG_0036	hypothetical protein	NA	1.342	1.05E-01
MSMEG_0038	putative glucose-methanol-choline oxidoreductase; this region contains one or more p	NA	1.092	3.86E-01
MSMEG_0039	small membrane hydrophobic protein	NA	1.097	3.18E-01
MSMEG_0040	conserved hypothetical protein	NA	1.056	2.66E-01
MSMEG_0041	conserved hypothetical protein	NA	0.968	5.52E-01
MSMEG_0042	TetR-family protein transcriptional regulator	NA	1.105	5.45E-02
MSMEG_0043	extradiol ring-cleavage dioxygenase, class III enzyme, subunit B	NA	1.180	7.48E-02
MSMEG_0044	hypothetical protein	NA	0.947	3.67E-01
MSMEG_0045	hypothetical protein	NA	0.936	4.20E-01
MSMEG_0046	conserved hypothetical protein	NA	1.003	9.81E-01
MSMEG_0047	hypothetical protein	NA	0.787	5.01E-02
MSMEG_0048	pyridoxamine 5'-phosphate oxidase family protein	NA	0.687	8.50E-03
MSMEG_0049	pirin domain protein	NA	1.103	2.18E-01
MSMEG_0050	conserved hypothetical protein	NA	0.897	1.14E-01
MSMEG_0051	transcription factor WhiB family protein	NA	0.939	4.13E-01
MSMEG_0052	conserved hypothetical protein	NA	1.155	1.62E-01
MSMEG_0053	conserved hypothetical protein	NA	0.996	9.16E-01
MSMEG_0053	conserved hypothetical protein	NA	1.115	2.64E-02
MSMEG_0055	hypothetical protein	NA	0.946	1.23E-01
MSMEG_0056	hypothetical protein	NA	0.880	1.30E-01
MSMEG_0057	conserved hypothetical protein	NA	0.866	1.15E-02
MSMEG_0058	conserved hypothetical protein	NA	0.838	4.49E-02
MSMEG_0059	ATPase, AAA family protein	NA	0.870	3.04E-02
MSMEG_0060	conserved hypothetical protein	NA	0.741	4.40E-03
MSMEG_0061	ftsk/spoiiie family protein	NA	0.676	2.15E-03

MSMEG_0062	ftsk/spoiiie family protein	NA	0.651	7.71E-03
MSMEG_0063	PE family protein	NA	0.847	6.04E-02
MSMEG_0064	ppe family protein	NA	0.827	1.53E-03
MSMEG_0065	conserved hypothetical protein	NA	0.828	5.86E-03
MSMEG_0066	early secretory antigenic target, 6 kDa	NA	0.759	2.68E-02
MSMEG_0067	conserved hypothetical protein	NA	0.807	5.32E-02
MSMEG_0068	probable conserved transmembrane protein	NA	0.718	1.94E-03
MSMEG_0069	translation initiation factor IF-2 protein	NA	0.789	1.26E-01
MSMEG_0070	hypothetical protein	NA	0.725	5.97E-04
MSMEG_0071	conserved hypothetical protein	NA	0.607	1.22E-02
MSMEG_0071	conserved hypothetical protein	NA	0.689	3.01E-02
MSMEG_0076	antigen MTB48	NA	0.934	4.05E-01
MSMEG_0077	hypothetical protein	NA	0.836	1.05E-01
MSMEG_0078	hypothetical protein	NA	0.856	5.94E-02
MSMEG_0079	hypothetical protein	NA	0.826	1.14E-02
MSMEG_0080	conserved hypothetical protein	NA	0.914	1.50E-01
MSMEG_0081	conserved hypothetical protein	NA	0.807	2.93E-02
MSMEG_0082	conserved hypothetical protein	NA	0.976	6.66E-01
MSMEG_0083	membrane-anchored mycosin mycp1	NA	0.962	1.49E-01
MSMEG_0084	phosphocarrier protein hpr	NA	0.779	4.98E-02
MSMEG_0085	PTS system, Fru family protein, IIABC components	NA	0.730	2.74E-02
MSMEG_0086	1-phosphofructokinase	NA	0.807	1.35E-01
MSMEG_0087	glucitol operon repressor	NA	0.938	3.38E-01
MSMEG_0088	phosphoenolpyruvate-protein phosphotransferase	ptsI	0.554	2.11E-03
MSMEG_0089	chromosome condensation protein	NA	0.838	2.87E-01
MSMEG_0090	conserved hypothetical protein	NA	1.121	4.17E-01
MSMEG_0091	putative transcriptional regulator	NA	1.352	1.02E-01
MSMEG_0092	probable transcriptional regulatory protein	NA	0.851	1.49E-01
MSMEG_0093	methyltransferase	NA	1.017	7.11E-01
MSMEG_0094	hypothetical protein	NA	1.196	9.72E-03
MSMEG_0095	methyltransferase	NA	0.983	6.40E-01

MSMEG_0096	peroxisomal hydratase-dehydrogenase-epimerase	NA	0.880	1.06E-01
MSMEG_0097	oxidoreductase, zinc-binding dehydrogenase family protein	NA	1.011	9.02E-01
MSMEG_0098	methyltransferase	NA	0.929	4.90E-02
MSMEG_0099	conserved hypothetical protein	NA	1.142	3.31E-01
MSMEG_0100	phosphotyrosine protein phosphatase ptpb	NA	1.012	9.04E-01
MSMEG_0101	conserved hypothetical protein	NA	1.160	1.66E-01
MSMEG_0102	putative acyl-CoA dehydrogenase	NA	0.900	6.90E-02
MSMEG_0103	major facilitator family protein transporter	NA	1.224	9.77E-02
MSMEG_0104	transcriptional regulator, LysR family protein	NA	0.914	6.66E-01
MSMEG_0105	DNA-binding response regulator, LuxR family protein	NA	1.412	1.24E-01
MSMEG_0106	sensory histidine kinase	NA	1.049	1.54E-01
MSMEG_0107	cell envelope-related function transcriptional attenuator common domain	NA	1.042	6.36E-02
MSMEG_0108	acyl-CoA dehydrogenase	NA	0.868	7.65E-02
MSMEG_0109	NAD(P) transhydrogenase, beta subunit	pntB	0.885	1.54E-01
MSMEG_0110	NAD(P) transhydrogenase, alpha subunit	pntA	0.918	1.72E-01
MSMEG_0111	putative magnesium transport protein	NA	0.995	9.34E-01
MSMEG_0112	hypothetical protein	NA	1.138	3.72E-01
MSMEG_0113	taurine transport system permease protein TauC	NA	1.057	2.43E-01
MSMEG_0114	extracellular solute-binding protein, family protein 3	NA	0.866	5.81E-02
MSMEG_0115	haloacid dehalogenase, type II	dehII	1.096	4.55E-01
MSMEG_0116	taurine import ATP-binding protein TauB	NA	1.079	6.23E-01
MSMEG_0117	hydrolase	NA	1.096	7.30E-01
MSMEG_0118	conserved hypothetical protein	NA	0.952	6.28E-01
MSMEG_0119	conserved hypothetical protein	NA	0.994	9.78E-01
MSMEG_0120	probable transcriptional regulatory protein	NA	1.004	9.36E-01
MSMEG_0121	rhamnolipids biosynthesis 3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.081	1.02E-01
MSMEG_0122	putative periplasmic solute-binding protein	NA	1.026	5.50E-01
MSMEG_0123	hypothetical protein	NA	0.755	2.55E-02
MSMEG_0124	transcriptional regulator, GntR family protein	NA	1.203	3.50E-01
MSMEG_0125	integral membrane protein	NA	1.125	6.60E-01
MSMEG_0126	mandelate racemase/muconate lactonizing enzyme	NA	2.527	4.14E-01

MSMEG_0127	oxidoreductase, zinc-binding dehydrogenase family protein	NA	0.792	1.17E-02
MSMEG_0128	thioesterase superfamily protein	NA	0.957	2.63E-02
MSMEG_0129	cyclase/dehydrase family protein	NA	1.014	9.12E-01
MSMEG_0130	transcriptional regulator, GntR family protein	NA	0.851	1.91E-01
MSMEG_0131	AMP-binding enzyme, putative	NA	0.625	5.96E-03
MSMEG_0132	conserved hypothetical protein	NA	0.820	9.28E-02
MSMEG_0133	ABC-transporter integral membrane protein	NA	0.764	1.21E-02
MSMEG_0134	virulence factor Mce family protein	NA	0.746	1.06E-02
MSMEG_0135	virulence factor Mce family protein	NA	0.781	1.07E-02
MSMEG_0136	virulence factor Mce family protein, putative	NA	0.729	4.46E-02
MSMEG_0137	virulence factor mce family protein	NA	0.616	3.61E-03
MSMEG_0138	virulence factor Mce family protein	NA	0.616	4.76E-04
MSMEG_0139	mce-family protein mce1f	NA	0.607	3.67E-03
MSMEG_0140	probable conserved mce associated membrane protein	NA	0.809	4.71E-03
MSMEG_0141	probable conserved mce associated transmembrane protein	NA	0.912	2.10E-01
MSMEG_0142	conserved hypothetical protein	NA	0.688	2.92E-04
MSMEG_0143	probable conserved mce associated membrane protein	NA	0.761	5.28E-03
MSMEG_0144	HNH endonuclease	NA	1.077	3.63E-01
MSMEG_0145	conserved hypothetical protein	NA	0.712	1.37E-02
MSMEG_0146	mosc domain protein	NA	1.040	5.82E-01
MSMEG_0147	C-5 sterol desaturase	NA	0.757	1.11E-01
MSMEG_0148	transcriptional regulator, TetR family protein	NA	0.841	2.87E-02
MSMEG_0149	ThiC family protein	NA	0.992	9.80E-01
MSMEG_0150	NAD(P) transhydrogenase beta subunit	NA	1.264	1.68E-01
MSMEG_0151	PntAB protein	NA	1.019	8.75E-01
MSMEG_0152	Alanine dehydrogenase/pyridine nucleotide transhydrogenase	NA	1.265	2.15E-01
MSMEG_0153	2-dehydropantoate 2-reductase	panE	1.239	1.37E-01
MSMEG_0154	pyruvate kinase	pyk	1.704	1.27E-01
MSMEG_0155	transcriptional regulator	NA	1.194	1.68E-01
MSMEG_0156	transcriptional regulator, LysR family protein	NA	1.149	1.60E-01
MSMEG_0157	oxalyl-CoA decarboxylase	NA	1.311	2.27E-01

MSMEG_0158	formyl-coenzyme A transferase	NA	1.109	1.76E-01
MSMEG_0159	formate dehydrogenase, gamma subunit	NA	1.133	2.40E-01
MSMEG_0160	formate dehydrogenase, beta subunit	NA	1.434	3.53E-01
MSMEG_0161	formate dehydrogenase, alpha subunit	NA	1.301	4.13E-01
MSMEG_0162	NAD-dependent formate dehydrogenase delta subunit	NA	0.969	8.14E-01
MSMEG_0163	conserved hypothetical protein	NA	0.974	6.73E-01
MSMEG_0164	transmembrane transport protein	NA	0.931	3.84E-01
MSMEG_0165	formate dehydrogenase family protein accessory protein FdhD	fdhD	1.439	4.85E-02
MSMEG_0166	GntR-family protein transcriptional regulator	NA	1.115	1.46E-01
MSMEG_0167	transmembrane transport protein	NA	0.767	2.03E-02
MSMEG_0168	formyl-coenzyme A transferase	NA	0.999	9.94E-01
MSMEG_0169	hypothetical protein	NA	1.740	1.74E-02
MSMEG_0170	transmembrane transport protein	NA	1.059	5.31E-01
MSMEG_0171	histone deacetylase superfamily protein	NA	1.321	2.29E-01
MSMEG_0172	probable conserved transmembrane protein, putative	NA	2.100	3.85E-03
MSMEG_0173	hypothetical protein	NA	2.035	1.05E-01
MSMEG_0174	putative inner membrane protein	NA	1.487	1.15E-02
MSMEG_0175	FAD dependent oxidoreductase, putative	NA	1.021	9.12E-01
MSMEG_0176	glutamine ABC transporter periplasmic-binding protein	NA	0.907	4.14E-01
MSMEG_0177	ABC polar amino acid family protein transporter, inner membrane subunit	NA	0.971	7.86E-01
MSMEG_0178	ATP-binding protein	NA	1.042	7.89E-01
MSMEG_0179	transcriptional regulator, GntR family protein	NA	0.988	8.49E-01
MSMEG_0180	putative HTH-type transcriptional regulator	NA	1.089	3.67E-01
MSMEG_0181	alpha-ketoglutarate-dependent taurine dioxygenase	NA	0.975	8.26E-01
MSMEG_0182	epoxide hydrolase 1	NA	0.869	4.10E-02
MSMEG_0183	conserved hypothetical protein	NA	1.130	4.28E-01
MSMEG_0184	transferase	NA	1.139	7.05E-01
MSMEG_0185	MmpL6 protein	NA	1.023	9.02E-01
MSMEG_0186	MmpS2 protein	NA	1.513	1.40E-03
MSMEG_0187	acetyltransferase	NA	1.039	5.22E-01
MSMEG_0188	MarR-family protein transcriptional regulator	NA	1.238	1.27E-01

MSMEG_0189	conserved hypothetical protein	NA	1.057	2.55E-01
MSMEG_0190	integral membrane transport protein	NA	1.141	9.83E-02
MSMEG_0191	BadF/BadG/BcrA/BcrD ATPase family protein	NA	1.296	5.74E-02
MSMEG_0192	transcriptional regulator, RpiR family protein	NA	1.374	1.01E-01
MSMEG_0193	putative glucokinase regulator	NA	1.275	1.05E-01
MSMEG_0194	serine esterase, cutinase family protein	NA	0.898	8.45E-02
MSMEG_0195	steroid monooxygenase	NA	1.130	7.94E-01
MSMEG_0196	putative dehydrogenase	NA	0.982	9.05E-01
MSMEG_0197	nudix hydrolase	NA	0.921	7.76E-01
MSMEG_0198	acyl-CoA dehydrogenase, C- domain protein	NA	1.074	6.73E-01
MSMEG_0199	aminoglycoside phosphotransferase; this gene contains a frame shift which is not the	NA	0.920	6.52E-01
MSMEG_0200	hypothetical protein	NA	0.962	7.01E-01
MSMEG_0201	hypothetical protein	NA	0.978	6.28E-01
MSMEG_0204	hypothetical protein	NA	0.853	1.58E-01
MSMEG_0205	tetracenomycin polyketide synthesis hydroxylase TcmH	NA	0.929	5.17E-02
MSMEG_0206	acyltransferase 3	NA	1.331	4.79E-01
MSMEG_0207	MarR-family protein transcriptional regulator	NA	1.284	2.01E-02
MSMEG_0208	ribonuclease	NA	1.005	8.43E-01
MSMEG_0209	ribonuclease inhibitor	NA	1.225	1.77E-01
MSMEG_0210	LprO protein	NA	0.979	7.16E-01
MSMEG_0211	ABC transporter, ATP-binding protein	NA	1.159	2.71E-01
MSMEG_0212	lyase	NA	1.045	6.45E-01
MSMEG_0213	transcriptional regulator	NA	1.015	7.43E-01
MSMEG_0214	L-sorbosone dehydrogenase	NA	0.959	7.54E-01
MSMEG_0215	YhhW family protein	NA	0.864	1.41E-02
MSMEG_0216	3-hydroxyacyl-CoA dehydrogenase	NA	0.872	1.99E-01
MSMEG_0217	alcohol dehydrogenase B	NA	2.757	2.98E-01
MSMEG_0218	3-demethylubiquinone-9 3-methyltransferase	NA	0.974	7.64E-01
MSMEG_0219	RNA polymerase sigma-70 factor, family protein	NA	0.744	3.16E-03
MSMEG_0220	monoglyceride lipase	NA	1.001	9.94E-01
MSMEG_0221	secreted protein	NA	0.844	3.99E-02

MSMEG_0222	conserved hypothetical protein	NA	0.869	5.56E-02
MSMEG_0223	conserved hypothetical protein	NA	0.989	9.21E-01
MSMEG_0224	O-methyltransferase MdmC	NA	0.979	6.38E-01
MSMEG_0225	MmpL4 protein	NA	1.100	6.00E-02
MSMEG_0226	MmpS5 protein	NA	0.928	5.38E-02
MSMEG_0227	transcriptional regulator, TetR family protein	NA	1.001	9.81E-01
MSMEG_0228	adenylate and Guanylate cyclase catalytic domain protein	NA	1.791	3.06E-01
MSMEG_0229	dihydroxy-acid dehydratase	ilvD	1.096	3.37E-01
MSMEG_0230	conserved hypothetical protein	NA	1.453	8.82E-02
MSMEG_0231	conserved hypothetical protein	NA	1.043	7.19E-01
MSMEG_0232	sugar transporter family protein	NA	1.583	1.63E-01
MSMEG_0233	lipoprotein Lpps	NA	0.867	6.02E-02
MSMEG_0234	metallopeptidase	NA	0.853	1.96E-02
MSMEG_0235	probable conserved membrane protein	NA	1.069	4.03E-01
MSMEG_0236	putative conserved transmembrane protein	NA	0.937	2.34E-01
MSMEG_0238	O-acetylhomoserine/O-acetylserine sulfhydrylase	NA	0.898	1.06E-01
MSMEG_0239	O-acetylhomoserine/O-acetylserine sulfhydrylase	NA	0.827	1.92E-02
MSMEG_0240	conserved hypothetical protein	NA	0.826	9.05E-02
MSMEG_0241	MmpL11 protein	NA	0.878	5.05E-02
MSMEG_0242	conserved hypothetical protein	NA	1.273	1.28E-02
MSMEG_0243	conserved hypothetical protein	NA	0.966	6.57E-01
MSMEG_0244	two component response transcriptional regulatory protein prra	NA	1.242	2.48E-01
MSMEG_0245	probable conserved transmembrane protein	NA	1.051	4.47E-01
MSMEG_0246	sensor-type histidine kinase PrrB	NA	1.093	3.76E-01
MSMEG_0247	secreted peptidase	NA	0.994	8.31E-01
MSMEG_0248	conserved hypothetical protein	NA	0.884	3.67E-01
MSMEG_0249	integral membrane protein	NA	1.156	1.70E-01
MSMEG_0250	membrane protein, MmpL family protein	NA	0.992	7.63E-01
MSMEG_0251	conserved hypothetical protein	NA	1.008	8.53E-01
MSMEG_0252	tRNA (guanine-N(7)-)-methyltransferase	trmB	1.000	9.77E-01
MSMEG_0253	conserved hypothetical protein	NA	1.185	2.16E-01

MSMEG_0254	conserved hypothetical protein	NA	1.075	6.73E-01
MSMEG_0255	phosphoenolpyruvate carboxykinase	NA	0.863	1.05E-01
MSMEG_0256	conserved hypothetical protein	NA	0.979	8.09E-01
MSMEG_0257	acyl-CoA synthase	NA	0.915	6.87E-01
MSMEG_0258	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.069	7.11E-01
MSMEG_0259	enoyl-CoA hydratase/isomerase	NA	0.877	2.87E-01
MSMEG_0260	DNA-binding protein	NA	0.922	2.19E-01
MSMEG_0261	p40 protein	NA	1.137	4.10E-01
MSMEG_0262	conserved hypothetical protein	NA	1.113	2.87E-01
MSMEG_0263	amidohydrolase 3	NA	0.901	3.96E-01
MSMEG_0264	transmembrane transport protein	NA	0.937	7.10E-01
MSMEG_0265	uracil DNA glycosylase superfamily protein	NA	1.014	9.14E-01
MSMEG_0266	arginine decarboxylase	NA	1.387	4.62E-01
MSMEG_0267	esterase	NA	1.479	3.81E-01
MSMEG_0268	transcriptional regulator, GntR family protein	NA	1.051	4.16E-01
MSMEG_0269	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.793	1.60E-02
MSMEG_0270	aminoglycoside phosphotransferase	NA	1.021	9.19E-01
MSMEG_0271	conserved hypothetical protein	NA	1.938	3.73E-01
MSMEG_0272	propanediol utilization protein PduA	NA	0.904	2.44E-01
MSMEG_0273	ethanolamine utilization protein EutN	NA	1.584	3.73E-01
MSMEG_0274	hypothetical protein	NA	1.081	7.19E-01
MSMEG_0275	bacterial microcompartments protein family protein	NA	1.257	3.66E-01
MSMEG_0276	aldehyde-alcohol dehydrogenase	NA	1.028	8.11E-01
MSMEG_0277	putative aminotransferase	NA	1.073	5.80E-01
MSMEG_0278	hypothetical protein	NA	0.982	7.73E-01
MSMEG_0279	amino acid permease	NA	1.035	6.75E-01
MSMEG_0280	alpha/beta hydrolase fold	NA	0.807	3.17E-02
MSMEG_0281	choline dehydrogenase	NA	0.866	7.50E-02
MSMEG_0282	conserved hypothetical protein	NA	0.899	4.17E-02
MSMEG_0283	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.180	2.36E-01
MSMEG_0284	ribosyldihydronicotinamide dehydrogenase (quinone)	NA	1.076	2.89E-01

MSMEG_0285	transcriptional regulator TetR family protein	NA	1.843	2.64E-01
MSMEG_0286	GntR-family protein transcriptional regulator	NA	0.893	5.47E-01
MSMEG_0287	conserved hypothetical protein	NA	1.206	1.36E-01
MSMEG_0288	FAD dependent oxidoreductase, putative	NA	1.378	1.69E-01
MSMEG_0289	alpha/beta hydrolase fold family protein	NA	0.823	2.53E-02
MSMEG_0290	acyltransferase, ws/dgat/mgat subfamily protein	NA	0.787	3.02E-03
MSMEG_0291	dioxygenase, TauD/TfdA family protein	NA	0.822	1.88E-01
MSMEG_0292	conserved hypothetical protein	NA	1.806	3.60E-01
MSMEG_0293	Rieske [2Fe-2S] domain protein	NA	0.980	4.46E-01
MSMEG_0294	3-oxoacyl-(acyl-carrier-protein) reductase	fabG	2.948	4.10E-01
MSMEG_0295	oxidoreductase, FAD-binding	NA	17.440	3.92E-01
MSMEG_0296	transcriptional regulator, MarR family protein	NA	1.121	6.03E-01
MSMEG_0297	amidohydrolase	NA	0.999	9.95E-01
MSMEG_0298	conserved hypothetical protein	NA	2.045	4.11E-01
MSMEG_0299	Rieske [2Fe-2S] domain protein	NA	0.914	3.70E-01
MSMEG_0300	amidohydrolase family protein	NA	1.051	8.29E-01
MSMEG_0301	oxidoreductase, FAD-binding	NA	0.955	6.78E-01
MSMEG_0302	peptidase, S9A/B/C families	NA	2.187	3.24E-01
MSMEG_0303	alcohol dehydrogenase, zinc-containing	NA	1.308	8.95E-02
MSMEG_0304	acyl-CoA synthase	NA	1.137	5.16E-03
MSMEG_0305	acyltransferase domain protein	NA	0.968	7.04E-01
MSMEG_0306	arylamine N-acetyltransferase	NA	1.511	3.89E-01
MSMEG_0307	transcriptional regulator, AraC family protein	NA	1.649	7.06E-03
MSMEG_0308	dihydrofolate reductase	NA	1.314	2.38E-02
MSMEG_0309	aldehyde dehydrogenase family protein	NA	0.899	1.71E-02
MSMEG_0310	SAM-dependent methyltransferase; this gene contains a frame shift which is not the r	NA	1.010	8.87E-01
MSMEG_0311	glycosyltransferase	NA	1.172	4.43E-02
MSMEG_0312	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	eda	1.277	1.27E-01
MSMEG_0313	phosphogluconate dehydratase	edd	1.070	5.84E-01
MSMEG_0314	glucose-6-phosphate 1-dehydrogenase	zwf	1.069	4.24E-01
MSMEG_0315	probable conserved transmembrane protein	NA	1.004	9.47E-01

MSMEG_0316	putative NagC regulator	NA	1.146	8.07E-03
MSMEG_0317	conserved hypothetical protein	NA	0.832	1.00E-02
MSMEG_0318	AMP-dependent synthetase and ligase	NA	1.063	4.88E-01
MSMEG_0319	acyltransferase	NA	1.190	2.21E-01
MSMEG_0320	putative phosphotriesterase	NA	1.354	2.19E-01
MSMEG_0321	transcriptional regulator	NA	0.993	9.16E-01
MSMEG_0322	glyoxylase family protein; this gene contains a frame shift which is not the result of se	NA	2.997	4.26E-01
MSMEG_0323	acyl-CoA dehydrogenase, short-chain specific, putative	NA	1.943	3.26E-01
MSMEG_0324	conserved hypothetical protein	NA	0.792	2.15E-02
MSMEG_0325	conserved hypothetical protein	NA	0.934	7.90E-01
MSMEG_0326	AMP-dependent synthetase and ligase	NA	1.075	5.19E-01
MSMEG_0327	aldehyde dehydrogenase	NA	1.338	4.39E-01
MSMEG_0328	hypothetical protein	NA	1.007	9.61E-01
MSMEG_0329	FMN oxidoreductase	NA	1.351	6.55E-02
MSMEG_0330	transcriptional regulator, LuxR family protein	NA	0.670	1.04E-01
MSMEG_0331	transcriptional regulator, LuxR family protein	NA	0.665	7.78E-02
MSMEG_0332	2-nitropropane dioxygenase, NPD	NA	1.104	4.96E-01
MSMEG_0333	Carboxyl transferase domain protein	NA	1.049	5.01E-01
MSMEG_0334	acetyl-/propionyl-coenzyme A carboxylase alpha chain	NA	1.143	3.86E-01
MSMEG_0335	enoyl-CoA hydratase/isomerase	NA	1.119	4.09E-01
MSMEG_0336	conserved hypothetical protein	NA	1.104	6.60E-01
MSMEG_0337	conserved hypothetical protein	NA	1.097	7.44E-01
MSMEG_0338	acyl-CoA dehydrogenase fadE12	NA	0.948	5.72E-01
MSMEG_0339	FMN-dependent monooxygenase	NA	1.493	4.46E-01
MSMEG_0340	enoyl-CoA hydratase/isomerase family protein	NA	1.112	5.45E-01
MSMEG_0341	conserved hypothetical protein	NA	1.128	2.35E-02
MSMEG_0342	hypothetical protein	NA	1.012	8.39E-01
MSMEG_0343	TetR-family protein transcriptional regulator	NA	0.904	2.80E-01
MSMEG_0344	conserved hypothetical protein	NA	1.233	1.57E-01
MSMEG_0345	conserved hypothetical protein	NA	3.096	4.16E-01
MSMEG_0346	virulence factor	NA	1.253	3.18E-01

MSMEG_0347	virulence factor Mce family protein	NA	0.931	5.48E-01
MSMEG_0348	mce-family protein mce3c	NA	1.092	3.81E-01
MSMEG_0349	virulence factor mce family protein	NA	0.961	2.10E-01
MSMEG_0350	virulence factor Mce family protein	NA	0.677	1.24E-02
MSMEG_0351	virulence factor mce family protein	NA	0.978	8.80E-01
MSMEG_0352	conserved hypothetical protein	NA	0.750	6.35E-03
MSMEG_0353	conserved hypothetical protein	NA	0.843	1.57E-01
MSMEG_0354	conserved hypothetical protein	NA	0.951	8.32E-01
MSMEG_0355	conserved hypothetical protein	NA	0.843	1.86E-02
MSMEG_0356	acetyltransferase	NA	0.841	9.30E-02
MSMEG_0357	transmembrane transport protein	NA	1.831	4.25E-01
MSMEG_0358	ribonucleoside-diphosphate reductase, beta subunit	NA	0.797	1.93E-01
MSMEG_0359	conserved hypothetical protein	NA	1.056	5.00E-01
MSMEG_0360	conserved hypothetical protein	NA	1.129	5.10E-01
MSMEG_0361	Glycosyl hydrolase family protein 3	NA	1.093	6.55E-01
MSMEG_0362	amidohydrolase 2	NA	1.035	6.66E-01
MSMEG_0363	TetR-family protein regulatory protein	NA	1.151	4.20E-01
MSMEG_0364	hypothetical protein	NA	1.034	4.47E-01
MSMEG_0365	conserved hypothetical protein	NA	0.729	1.38E-04
MSMEG_0366	hypothetical protein	NA	0.785	2.25E-03
MSMEG_0367	O-demethylpuromycin-O-methyltransferase	NA	1.059	7.91E-01
MSMEG_0368	hypothetical protein	NA	1.163	3.14E-03
MSMEG_0369	hypothetical protein	NA	1.053	4.11E-01
MSMEG_0370	conserved hypothetical protein	NA	1.191	7.84E-02
MSMEG_0371	MaoC like domain protein	NA	1.038	7.41E-01
MSMEG_0372	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.171	1.89E-01
MSMEG_0373	3-ketoacyl-CoA thiolase	NA	1.017	8.16E-01
MSMEG_0374	glycolate oxidase subunit	NA	1.165	6.30E-01
MSMEG_0375	phospholipase D family protein	NA	0.923	4.72E-01
MSMEG_0376	transcriptional regulator, AraC family protein	NA	0.728	8.90E-04
MSMEG_0377	nitrile hydratase	NA	1.339	2.30E-03

MSMEG_0378	nitrile hydratase, alpha subunit	nthA	1.304	5.49E-02
MSMEG_0379	nitrile hydratase activator P14k	NA	1.247	3.98E-01
MSMEG_0380	MmpS4 protein	NA	0.774	9.23E-04
MSMEG_0381	Mmp14a protein	NA	0.725	4.27E-03
MSMEG_0382	putative transport protein	NA	0.692	2.18E-02
MSMEG_0383	conserved hypothetical protein	NA	1.105	3.36E-01
MSMEG_0384	glucose-1-phosphate thymidylyltransferase	rfbA	0.833	1.30E-02
MSMEG_0385	hypothetical glycosyl transferase	NA	1.192	3.21E-01
MSMEG_0386	NAD dependent epimerase/dehydratase family protein	NA	0.953	4.24E-02
MSMEG_0387	Rmt2 protein	NA	0.884	1.85E-01
MSMEG_0388	Macrocin-O-methyltransferase	tylF	0.778	1.37E-03
MSMEG_0389	hypothetical glycosyl transferase	NA	0.770	7.55E-03
MSMEG_0390	putative acyltransferase	NA	0.796	4.96E-02
MSMEG_0391	Rmt3 protein	NA	0.999	9.74E-01
MSMEG_0392	hypothetical glycosyl transferase	NA	1.032	3.91E-01
MSMEG_0393	Fmt protein	NA	1.039	7.39E-01
MSMEG_0394	hypothetical protein	NA	1.108	6.88E-01
MSMEG_0395	hypothetical protein	NA	1.085	6.51E-01
MSMEG_0396	hypothetical protein	NA	1.100	1.41E-01
MSMEG_0399	conserved domain protein	NA	0.979	7.94E-01
MSMEG_0400	peptide synthetase	NA	0.989	7.63E-01
MSMEG_0401	putative non-ribosomal peptide synthase	NA	0.836	4.70E-01
MSMEG_0402	linear gramicidin synthetase subunit D	NA	0.618	6.36E-04
MSMEG_0403	integral membrane protein	NA	0.683	2.88E-03
MSMEG_0404	sigma associated protein	NA	0.826	4.56E-02
MSMEG_0405	extra cytoplasmic sigma factor	NA	0.935	1.04E-02
MSMEG_0406	acyl-coA-dehydrogenase	NA	0.719	4.00E-02
MSMEG_0407	conserved hypothetical protein	NA	0.894	4.45E-01
MSMEG_0408	type I modular polyketide synthase	NA	0.695	2.45E-03
MSMEG_0409	Condensation domain protein	NA	0.723	2.98E-03
MSMEG_0410	MmpL protein	NA	0.599	2.76E-03

MSMEG_0411	acyl-CoA synthase	NA	0.683	3.11E-03
MSMEG_0412	conserved hypothetical protein	NA	0.677	3.11E-04
MSMEG_0413	conserved hypothetical protein	NA	1.142	2.30E-01
MSMEG_0414	oxidoreductase, 2OG-Fe(II) oxygenase family protein	NA	0.935	4.45E-01
MSMEG_0415	NADH-fmn oxidoreductase	NA	1.050	4.61E-01
MSMEG_0416	hypothetical protein	NA	0.933	5.14E-01
MSMEG_0417	succinate dehydrogenase	NA	0.878	4.40E-01
MSMEG_0418	succinate dehydrogenase flavoprotein subunit	NA	0.665	1.13E-03
MSMEG_0419	integral membrane protein	NA	0.891	6.94E-01
MSMEG_0420	conserved hypothetical protein	NA	0.784	3.93E-01
MSMEG_0421	hypothetical protein	NA	1.592	3.58E-01
MSMEG_0422	transferase	NA	1.318	6.50E-02
MSMEG_0423	conserved hypothetical protein	NA	1.353	2.18E-01
MSMEG_0424	Hsp20/alpha crystallin family protein	NA	1.156	9.81E-02
MSMEG_0425	putative membrane protein DcsA	NA	1.668	3.13E-01
MSMEG_0426	transcriptional regulator, GntR family protein	NA	2.241	2.77E-01
MSMEG_0427	nitrite reductase [NAD(P)H], large subunit	nirB	0.880	7.79E-02
MSMEG_0428	nitrite reductase [NAD(P)H] small subunit	NA	1.473	4.36E-01
MSMEG_0429	putative ferric uptake regulator	NA	1.333	2.37E-01
MSMEG_0431	secreted protein	NA	1.302	9.58E-02
MSMEG_0432	uroporphyrinogen-III synthetase	NA	1.241	1.72E-01
MSMEG_0433	nitrite extrusion protein	NA	1.146	3.89E-01
MSMEG_0434	aminoglycoside 2'-N-acetyltransferase (AAC(2')-Id)	NA	1.100	2.96E-01
MSMEG_0435	allophanate hydrolase subunit 2	NA	0.895	4.86E-01
MSMEG_0436	allophanate hydrolase subunit 1	NA	0.974	8.72E-01
MSMEG_0437	conserved hypothetical integral membrane protein	NA	1.111	1.03E-01
MSMEG_0438	Periplasmic binding protein	NA	0.750	5.37E-03
MSMEG_0439	conserved hypothetical protein	NA	1.492	1.46E-01
MSMEG_0440	hypothetical protein	NA	0.929	1.72E-01
MSMEG_0441	conserved hypothetical protein, putative	NA	0.785	8.53E-03
MSMEG_0442	tetracyclin repressor, C- all-alpha domain protein	NA	1.121	3.94E-01

MSMEG_0443	hydrolase, carbon-nitrogen family protein	NA	0.763	6.77E-02
MSMEG_0444	agmatine deiminase	NA	0.747	5.15E-02
MSMEG_0445	amidohydrolase family protein	NA	0.972	2.95E-01
MSMEG_0446	putrescine importer	NA	1.047	5.26E-01
MSMEG_0447	conserved hypothetical protein	NA	1.605	7.29E-02
MSMEG_0448	transcriptional regulator, MarR family protein	NA	1.165	1.13E-01
MSMEG_0449	transporter, major facilitator family protein, putative	NA	4.530	1.52E-01
MSMEG_0450	hypothetical protein	NA	1.590	3.83E-01
MSMEG_0451	oxidoreductase, FAD-linked	NA	1.352	4.79E-01
MSMEG_0452	inner membrane permease YgbN	NA	0.627	1.99E-02
MSMEG_0453	shikimate kinase	aroK	0.737	9.31E-02
MSMEG_0454	GntR-family protein transcriptional regulator	NA	1.300	1.19E-01
MSMEG_0455	aldehyde dehydrogenase	NA	0.975	6.99E-01
MSMEG_0456	DNA gyrase subunit A	NA	1.341	8.08E-02
MSMEG_0457	DNA topoisomerase IV subunit B	NA	1.360	7.05E-03
MSMEG_0458	two-component system sensor kinase	NA	1.065	4.87E-01
MSMEG_0459	two-component system response regulator	NA	0.903	1.82E-01
MSMEG_0460	alpha/beta hydrolase fold	NA	1.520	3.69E-01
MSMEG_0461	CinZ protein	NA	1.225	3.80E-01
MSMEG_0462	MmpS4 protein	NA	1.349	3.86E-01
MSMEG_0463	MmpL4 protein	NA	1.724	1.21E-01
MSMEG_0464	phosphomethylpyrimidine kinase	NA	1.024	4.82E-01
MSMEG_0465	transcriptional regulator, TetR family protein	NA	0.963	3.36E-01
MSMEG_0466	hypothetical protein	NA	1.009	8.99E-01
MSMEG_0467	membrane transport protein	NA	0.351	2.23E-04
MSMEG_0468	integral membrane protein	NA	1.001	9.92E-01
MSMEG_0469	transcriptional regulatory protein PadR-	NA	1.211	5.20E-01
MSMEG_0470	para-nitrobenzyl esterase	NA	0.870	5.64E-01
MSMEG_0471	transcriptional regulator LysR family protein	NA	1.021	7.27E-01
MSMEG_0472	putative lipoprotein	NA	0.914	9.00E-02
MSMEG_0473	transcriptional regulator, LuxR family protein	NA	1.767	3.21E-02

MSMEG_0474	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	NA	1.425	3.18E-01
MSMEG_0475	nucleotide-sugar dehydrogenase	NA	1.204	1.82E-01
MSMEG_0476	chitin synthase	NA	1.629	1.22E-01
MSMEG_0477	hypothetical protein	NA	1.629	2.42E-01
MSMEG_0478	secreted protein, putative	NA	1.328	2.32E-01
MSMEG_0479	hypothetical protein	NA	1.033	8.46E-01
MSMEG_0480	transcriptional regulator, GntR family protein	NA	1.157	2.12E-01
MSMEG_0481	FAD dependent oxidoreductase	NA	1.015	9.29E-01
MSMEG_0482	dihydroxy-acid dehydratase	NA	1.544	9.24E-02
MSMEG_0483	shikimate transporter	NA	1.337	1.53E-01
MSMEG_0484	formamidase	NA	0.930	2.93E-01
MSMEG_0485	amidase	NA	1.288	4.94E-01
MSMEG_0486	putative ABC transporter, periplasmic protein	NA	2.718	3.99E-01
MSMEG_0487	ABC transporter permease	NA	1.478	3.94E-01
MSMEG_0488	ABC transporter ATP-binding protein	NA	1.091	5.91E-01
MSMEG_0489	racemase	NA	1.940	5.78E-02
MSMEG_0490	enoyl-CoA hydratase	NA	1.243	1.37E-01
MSMEG_0491	transcriptional regulator, LacI family protein	NA	1.218	2.13E-02
MSMEG_0492	conserved hypothetical protein	NA	1.164	1.90E-02
MSMEG_0493	hypothetical protein	NA	1.701	3.49E-03
MSMEG_0494	hypothetical protein	NA	1.723	2.68E-03
MSMEG_0495	glycerol dehydratase reactivase chain A, putative; this gene contains a frame shift whi	NA	1.092	4.98E-01
MSMEG_0496	coenzyme B12-dependent glycerol dehydrogenase small subunit	NA	0.939	6.19E-01
MSMEG_0497	glycerol dehydratase large subunit	NA	0.959	6.89E-01
MSMEG_0498	hypothetical protein	NA	1.074	1.79E-01
MSMEG_0499	amino acid permease-associated region	NA	2.101	4.60E-01
MSMEG_0500	regulator of polyketide synthase expression, putative	NA	1.198	6.68E-02
MSMEG_0501	glucosamine-6-phosphate deaminase 1	NA	0.758	1.78E-01
MSMEG_0502	glucosidase	NA	0.920	6.21E-01
MSMEG_0503	DeoR-family protein transcriptional regulator	NA	0.897	2.33E-01
MSMEG_0504	carbohydrate kinase	NA	1.284	2.21E-01

MSMEG_0505	probable sugar ABC transporter, substrate-binding protein, putative	NA	0.794	1.93E-02
MSMEG_0506	ABC transporter, permease protein	NA	0.749	7.78E-02
MSMEG_0507	probable sugar ABC transporter, permease protein	NA	1.002	9.93E-01
MSMEG_0508	glycerol-phosphate porter	NA	0.855	5.31E-01
MSMEG_0509	transcriptional regulatory protein	NA	1.087	3.39E-01
MSMEG_0510	D-tagatose-bisphosphate aldolase, class II, non-catalytic subunit	NA	1.666	5.19E-03
MSMEG_0511	putative sugar isomerase, AgaS family protein	NA	0.907	1.98E-01
MSMEG_0512	BadF/BadG/BcrA/BcrD ATPase family protein	NA	0.945	2.64E-01
MSMEG_0513	integral membrane protein	NA	0.986	8.67E-01
MSMEG_0514	alpha-galactosidase	NA	0.820	1.32E-01
MSMEG_0515	probable sugar transporter sugar binding lipoprotein	NA	1.753	1.14E-01
MSMEG_0516	sugar transport system	NA	1.214	3.51E-01
MSMEG_0517	sugar binding-protein dependent transporter system permease	NA	0.984	7.60E-01
MSMEG_0518	ABC transporter, nucleotide binding/ATPase protein, sn-Glycerol-3-phosphate	NA	1.164	5.52E-01
MSMEG_0519	conserved hypothetical protein	NA	0.856	1.34E-01
MSMEG_0520	porin	NA	0.916	8.10E-03
MSMEG_0521	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.022	8.85E-01
MSMEG_0521	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.266	7.38E-03
MSMEG_0522	pp24 protein	NA	1.125	7.04E-01
MSMEG_0523	DNA-binding protein	NA	1.079	5.36E-01
MSMEG_0524	short chain dehydrogenase	NA	1.272	5.36E-01
MSMEG_0525	hypothetical protein	NA	1.064	3.33E-01
MSMEG_0526	oxidoreductase, GMC family protein	NA	1.099	4.65E-01
MSMEG_0527	2-hydroxycyclohexnecarboxyl-CoA dehydrogenase	NA	1.509	3.89E-01
MSMEG_0528	conserved hypothetical protein	NA	1.100	5.95E-01
MSMEG_0529	probable serine/threonine-protein kinase PknK	NA	1.169	3.17E-01
MSMEG_0530	short chain dehydrogenase	NA	1.039	7.59E-01
MSMEG_0531	putative acyl-CoA dehydrogenase	NA	0.831	6.45E-02
MSMEG_0532	transcriptional regulator, TetR family protein	NA	0.781	9.46E-03
MSMEG_0533	gp236 protein	NA	1.216	6.77E-02
MSMEG_0534	permease, major facilitator family protein	NA	1.303	6.89E-02

MSMEG_0535	GntR-family protein transcriptional regulator	NA	1.238	2.75E-01
MSMEG_0536	intracellular protease, PfpI family protein	NA	1.179	3.48E-01
MSMEG_0537	conserved hypothetical protein	NA	0.964	6.91E-01
MSMEG_0537	conserved hypothetical protein	NA	1.052	6.13E-01
MSMEG_0538	regulatory protein, MarR	NA	1.123	2.82E-01
MSMEG_0539	transcriptional regulator, Crp/Fnr family protein	NA	0.676	2.16E-02
MSMEG_0540	transcriptional regulator, putative	NA	1.079	3.05E-01
MSMEG_0541	hypothetical protein	NA	0.984	6.18E-01
MSMEG_0542	antar domain protein	NA	1.142	3.40E-02
MSMEG_0543	conserved hypothetical protein	NA	1.047	4.71E-01
MSMEG_0544	transcriptional regulator	NA	1.218	1.27E-01
MSMEG_0545	transcriptional regulator, LuxR family protein	NA	1.319	1.77E-01
MSMEG_0546	conserved hypothetical protein	NA	1.357	5.32E-02
MSMEG_0547	ISMsm5, transposase	NA	0.941	2.36E-01
MSMEG_0548	chromosome replication initiation inhibitor protein	NA	1.358	2.38E-03
MSMEG_0549	ABC transporter, permease protein	NA	1.106	4.79E-01
MSMEG_0550	sulfonate binding protein	NA	1.020	8.35E-01
MSMEG_0551	ABC nitrate/sulfonate/bicarbonate transporter, ATPase subunit	NA	1.064	4.76E-01
MSMEG_0552	conserved hypothetical protein	NA	1.370	2.08E-02
MSMEG_0553	probable sugar ABC transporter, substrate-binding protein, putative	NA	1.106	5.51E-01
MSMEG_0554	ABC transporter permease protein, putative	NA	1.200	7.51E-02
MSMEG_0555	ABC transporter permease protein	NA	1.270	3.05E-01
MSMEG_0556	ABC transporter, nucleotide binding/ATPase protein	NA	1.089	6.29E-01
MSMEG_0557	hypothetical protein	NA	1.060	4.43E-01
MSMEG_0558	conserved hypothetical protein	NA	1.102	3.00E-01
MSMEG_0559	conserved domain protein	NA	1.169	6.18E-01
MSMEG_0560	dihydrodipicolinate reductase, N-terminus domain protein	dapB	0.753	2.84E-01
MSMEG_0561	putative TetR family protein receptor protein	NA	1.187	1.15E-01
MSMEG_0562	conserved hypothetical protein	NA	1.184	9.79E-02
MSMEG_0563	hypothetical protein	NA	0.936	4.75E-01
MSMEG_0564	xanthine/uracil permease	NA	1.350	1.65E-01

MSMEG_0565	putative glycosyl transferases group 1	NA	0.860	3.91E-01
MSMEG_0566	aliphatic amidase	NA	0.889	5.44E-01
MSMEG_0567	selenophosphate synthetase	NA	1.070	7.52E-01
MSMEG_0568	radical SAM domain protein	NA	1.197	3.96E-01
MSMEG_0569	flavoprotein involved in K+ transport	NA	0.976	8.91E-01
MSMEG_0570	conserved hypothetical protein	NA	1.196	6.89E-02
MSMEG_0571	hydrolase, carbon-nitrogen family protein	NA	1.440	4.58E-01
MSMEG_0572	conserved hypothetical protein	NA	1.641	3.10E-01
MSMEG_0573	putative ECF sigma factor RpoE1	NA	1.172	6.52E-02
MSMEG_0574	putative ECF sigma factor RpoE1	NA	3.949	3.88E-01
MSMEG_0575	MmpS1 protein	NA	1.281	2.21E-01
MSMEG_0576	MmpL4 protein	NA	1.997	3.83E-02
MSMEG_0577	major facilitator superfamily protein, putative	NA	1.085	6.27E-01
MSMEG_0578	acyl-CoA dehydrogenase, middle domain protein	NA	1.187	4.93E-01
MSMEG_0579	helix-turn-helix, Fis-type	NA	1.537	5.02E-02
MSMEG_0580	conserved hypothetical protein	NA	1.137	1.90E-02
MSMEG_0581	4-aminobutyrate transaminase	gabT	1.040	7.87E-01
MSMEG_0582	succinic semialdehyde dehydrogenase	NA	1.112	6.63E-01
MSMEG_0583	probable membrane protein	NA	0.979	8.16E-01
MSMEG_0584	hypothetical protein	NA	0.935	7.59E-01
MSMEG_0585	L-carnitine dehydratase/bile acid-inducible protein F	NA	0.948	7.02E-01
MSMEG_0586	stas domain, putative	NA	0.882	3.57E-01
MSMEG_0587	L-rhamnose 1-epimerase	rhaU	1.013	9.28E-01
MSMEG_0588	putative rhamnose tranport protein, MFS family protein	NA	1.120	5.06E-01
MSMEG_0589	L-rhamnose isomerase	rhaI	0.855	2.42E-01
MSMEG_0590	rhamnulose-1-phosphate aldolase/alcohol dehydrogenase	rhaD	1.279	2.83E-01
MSMEG_0591	rhamnulokinase	rhaB	1.030	6.90E-01
MSMEG_0592	putative rhamnose catabolism operon transcriptional regulator	NA	1.276	2.04E-01
MSMEG_0593	conserved hypothetical protein	NA	1.137	5.29E-01
MSMEG_0594	iron-sulfur cluster binding protein	NA	0.937	4.76E-01
MSMEG_0595	glycolate oxidase	NA	0.817	2.11E-02

MSMEG_0596	bacterial regulatory protein, GntR family protein	NA	1.091	3.32E-01
MSMEG_0597	conserved hypothetical protein	NA	1.061	6.24E-01
MSMEG_0598	hypothetical protein	NA	1.373	3.17E-01
MSMEG_0599	acyl-CoA synthase	NA	0.782	1.21E-03
MSMEG_0600	dehydrogenase	NA	1.582	2.99E-02
MSMEG_0601	conserved hypothetical protein	NA	1.096	1.23E-01
MSMEG_0602	hypothetical protein	NA	1.170	3.51E-01
MSMEG_0603	putative acyl-CoA dehydrogenase	NA	0.501	5.83E-03
MSMEG_0604	glyoxylate reductase	NA	0.681	4.94E-03
MSMEG_0605	conserved hypothetical protein	NA	0.650	5.63E-03
MSMEG_0606	transcriptional regulator, TetR family protein	NA	0.892	1.75E-01
MSMEG_0607	methyltransferase, putative, family protein	NA	1.081	3.76E-01
MSMEG_0608	glyoxalase family protein	NA	0.905	1.01E-01
MSMEG_0609	helix-turn-helix domain protein	NA	0.899	6.77E-01
MSMEG_0610	beta-lactamase	NA	1.475	2.65E-01
MSMEG_0611	para-nitrobenzyl esterase	NA	1.213	3.91E-01
MSMEG_0612	transcriptional regulator, TetR family protein	NA	1.083	6.65E-01
MSMEG_0613	conserved hypothetical protein	NA	0.942	5.94E-01
MSMEG_0614	methyltransferase	NA	1.031	7.82E-01
MSMEG_0615	ATPase, AAA family protein	NA	0.860	2.59E-02
MSMEG_0616	conserved hypothetical protein	NA	0.998	8.65E-01
MSMEG_0617	ftsk/spoiiie family protein	NA	1.068	8.33E-01
MSMEG_0618	pe family protein	NA	1.227	3.79E-01
MSMEG_0619	ppe family protein	NA	1.041	8.33E-01
MSMEG_0620	pe family protein	NA	0.913	8.08E-01
MSMEG_0621	low molecular weight protein antigen 7	NA	0.959	8.75E-01
MSMEG_0622	putative DNA-binding protein	NA	0.798	9.25E-02
MSMEG_0623	secretion protein Snm4	snm	0.899	4.87E-01
MSMEG_0624	subtilase family protein	NA	1.031	7.98E-01
MSMEG_0625	conserved hypothetical protein	NA	1.285	5.99E-02
MSMEG_0626	conserved hypothetical protein	NA	0.914	7.31E-01

MSMEG_0627	glycosyl transferase, family protein 39	NA	0.985	9.17E-01
MSMEG_0628	amidohydrolase family protein	NA	0.897	6.31E-02
MSMEG_0629	trans-aconitate 2-methyltransferase	NA	1.069	5.99E-01
MSMEG_0630	conserved hypothetical protein	NA	1.918	1.01E-01
MSMEG_0631	sulfatase family protein, authentic frameshift; this gene contains a frame shift which is	NA	0.913	1.09E-01
MSMEG_0632	conserved hypothetical protein	NA	0.811	6.55E-02
MSMEG_0633	PAP2 superfamily protein	NA	1.216	2.71E-01
MSMEG_0634	PAP2 superfamily protein	NA	1.066	8.19E-01
MSMEG_0635	putative conserved exported protein	NA	0.620	4.30E-03
MSMEG_0636	conserved hypothetical protein	NA	0.953	1.95E-01
MSMEG_0637	iron-sulfur binding oxidoreductase	NA	1.468	3.73E-01
MSMEG_0638	conserved hypothetical proline and threonine rich protein	NA	1.005	9.60E-01
MSMEG_0639	oligopeptide transport ATP-binding protein AppF	NA	0.921	8.12E-02
MSMEG_0640	oligopeptide transport ATP-binding protein OppD	NA	0.942	2.63E-01
MSMEG_0641	binding-protein-dependent transport systems inner membrane component	NA	0.892	1.49E-01
MSMEG_0642	hypothetical ABC transporter permease protein YliD	NA	0.857	4.35E-02
MSMEG_0643	extracellular solute-binding protein, family protein 5, putative	NA	1.049	5.74E-02
MSMEG_0644	cupin domain protein	NA	0.950	5.00E-01
MSMEG_0645	putative beta-1,3-glucanase	NA	0.905	1.97E-01
MSMEG_0646	putative transporter	NA	0.977	4.22E-01
MSMEG_0647	phosphonate ABC transporter, ATP-binding protein	phnC	1.095	2.82E-01
MSMEG_0648	hypothetical protein	NA	0.976	7.21E-01
MSMEG_0649	phosphonate-binding periplasmic protein	NA	1.683	1.14E-02
MSMEG_0650	GntR-family protein transcriptional regulator	NA	1.043	3.07E-01
MSMEG_0651	putative conserved exported protein	NA	1.048	8.64E-01
MSMEG_0652	hypothetical protein	NA	1.009	8.66E-01
MSMEG_0653	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	1.085	1.51E-01
MSMEG_0654	conserved hypothetical protein	NA	1.249	5.75E-01
MSMEG_0655	glucose 1-dehydrogenase, putative	NA	1.184	5.52E-01
MSMEG_0656	transcriptional regulator, TetR family protein	NA	1.289	1.01E-01
MSMEG_0657	Rieske 2Fe-2S domain protein	NA	1.036	8.28E-01

MSMEG_0658	polyamine ABC-transporter, inner membrane subunit	NA	0.987	8.78E-01
MSMEG_0659	polyamine ABC transporter permease protein	NA	0.965	6.88E-01
MSMEG_0660	Bacterial extracellular solute-binding protein	NA	1.205	3.15E-01
MSMEG_0661	glutamate-1-semialdehyde 2,1-aminomutase	NA	0.876	2.76E-01
MSMEG_0662	putrescine transport ATP-binding protein PotG	NA	0.981	8.98E-01
MSMEG_0663	TetR-family protein transcriptional regulator	NA	1.140	3.22E-02
MSMEG_0664	FAD dependent oxidoreductase	NA	1.215	3.57E-01
MSMEG_0665	sarcosine oxidase subunit beta, putative	NA	0.962	8.42E-01
MSMEG_0666	acetyl-CoA synthetase, putative	NA	1.148	5.77E-01
MSMEG_0667	butyryl-CoA dehydrogenase	NA	0.989	8.64E-01
MSMEG_0668	integral membrane protein	NA	1.052	6.39E-01
MSMEG_0669	hypothetical protein	NA	0.912	2.20E-01
MSMEG_0670	FAD dependent oxidoreductase	NA	0.984	9.43E-01
MSMEG_0671	S-(hydroxymethyl)glutathione dehydrogenase	NA	0.973	9.30E-01
MSMEG_0672	conserved hypothetical protein	NA	1.233	5.81E-01
MSMEG_0673	hypothetical protein	NA	0.892	8.28E-03
MSMEG_0674	ErfK/YbiS/YcfS/YnhG family protein	NA	1.013	8.27E-01
MSMEG_0675	putative cytochrome P450 144	NA	0.990	8.37E-01
MSMEG_0676	putative transcriptional regulatory protein	NA	1.449	4.18E-02
MSMEG_0678	deoxycytidine triphosphate deaminase	dcd	1.250	6.85E-02
MSMEG_0679	conserved hypothetical protein	NA	1.200	2.29E-03
MSMEG_0680	UDP-glucose 6-dehydrogenase	NA	1.554	1.98E-01
MSMEG_0681	P450 heme-thiolate protein	NA	0.979	5.54E-01
MSMEG_0682	conserved hypothetical protein, putative	NA	0.937	2.19E-01
MSMEG_0683	conserved hypothetical protein	NA	0.874	6.80E-02
MSMEG_0684	aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding	NA	1.237	2.43E-01
MSMEG_0685	oxidoreductase, molybdopterin-binding subunit	NA	1.536	5.66E-01
MSMEG_0686	oxidoreductase	NA	1.104	2.99E-01
MSMEG_0687	conserved hypothetical protein	NA	1.371	1.06E-01
MSMEG_0688	aspartate aminotransferase	NA	1.590	4.45E-03
MSMEG_0689	hypothetical protein	NA	1.169	4.32E-01

MSMEG_0690	iron-sulfur cluster-binding protein	NA	1.022	4.63E-01
MSMEG_0691	putative transcriptional regulatory protein	NA	0.922	3.78E-01
MSMEG_0692	conserved hypothetical protein	NA	0.965	5.41E-01
MSMEG_0693	conserved hypothetical protein	NA	1.039	5.18E-01
MSMEG_0694	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.846	7.98E-02
MSMEG_0695	isoniazid inductible protein IniA	NA	0.925	3.62E-01
MSMEG_0696	alanine-rich protein	NA	1.258	4.76E-01
MSMEG_0697	integral membrane protein	NA	1.419	3.69E-01
MSMEG_0698	isoniazid inductible protein IniC	NA	1.735	2.89E-01
MSMEG_0699	conserved hypothetical proline rich protein	NA	15.080	3.79E-01
MSMEG_0700	hypothetical protein	NA	1.200	5.85E-02
MSMEG_0701	hypothetical protein	NA	1.730	2.63E-01
MSMEG_0702	monooxygenase	NA	1.240	1.17E-01
MSMEG_0703	conserved hypothetical protein	NA	0.868	5.12E-03
MSMEG_0704	LpqJ protein	NA	0.948	7.03E-01
MSMEG_0705	putative permease of the major facilitator superfamily protein	NA	1.015	7.06E-01
MSMEG_0706	4-carboxy-4-hydroxy-2-oxoadipate aldolase	NA	1.020	7.61E-01
MSMEG_0707	conserved hypothetical protein	NA	1.368	2.60E-01
MSMEG_0708	transcriptional regulator, LysR family protein	NA	1.174	4.16E-02
MSMEG_0709	chaperone protein DnaK	dnaK	1.033	6.81E-01
MSMEG_0710	co-chaperone GrpE	grpE	1.000	1.00E+00
MSMEG_0711	chaperone protein DnaJ	dnaJ	1.227	7.28E-02
MSMEG_0712	transcriptional regulator, TetR family protein	NA	1.179	2.56E-01
MSMEG_0713	transcriptional regulator, MerR family protein	NA	1.230	1.17E-01
MSMEG_0714	acyl-CoA dehydrogenase	NA	0.915	6.38E-01
MSMEG_0715	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.152	4.50E-01
MSMEG_0716	major facilitator superfamily protein	NA	1.089	5.67E-01
MSMEG_0717	aldose 1-epimerase subfamily protein	NA	1.164	6.51E-02
MSMEG_0718	acetyl-CoA synthetase	NA	1.640	3.83E-01
MSMEG_0719	flavohemoprotein	NA	1.112	1.08E-01
MSMEG_0720	integral membrane protein	NA	1.086	3.89E-01

MSMEG_0721	RemQ protein; this gene contains a frame shift which is not the result of sequencing e	NA	1.193	3.06E-01
MSMEG_0721	RemQ protein; this gene contains a frame shift which is not the result of sequencing e	NA	1.350	1.19E-01
MSMEG_0722	conserved hypothetical protein	NA	1.165	1.42E-01
MSMEG_0723	conserved hypothetical protein	NA	1.324	3.35E-01
MSMEG_0725	IS1137, transposase orfB	NA	1.065	3.33E-01
MSMEG_0726	hypothetical protein	NA	0.939	5.30E-01
MSMEG_0727	hypothetical protein	NA	1.008	9.54E-01
MSMEG_0728	hypothetical protein	NA	0.822	1.79E-02
MSMEG_0729	conserved hypothetical protein	NA	0.997	9.75E-01
MSMEG_0730	oleandomycin glycosyltransferase	NA	1.050	7.00E-01
MSMEG_0731	conserved hypothetical protein	NA	0.927	4.81E-01
MSMEG_0732	chaperone ClpB	NA	1.264	2.20E-01
MSMEG_0733	dihydrodipicolinate reductase, N-terminus domain protein	dapB	0.717	9.72E-03
MSMEG_0734	Rieske [2Fe-2S] domain protein	NA	0.922	6.37E-01
MSMEG_0735	putative transcriptional regulator	NA	1.511	1.24E-01
MSMEG_0736	conserved hypothetical protein	NA	0.932	4.15E-02
MSMEG_0737	dehydrogenase	NA	1.259	2.48E-02
MSMEG_0738	conserved hypothetical protein	NA	1.178	1.03E-01
MSMEG_0739	spou rRNA methylase family protein	NA	1.188	6.81E-02
MSMEG_0740	glycosyl hydrolase family protein 76	NA	1.044	2.30E-01
MSMEG_0741	conserved hypothetical protein	NA	1.017	8.79E-01
MSMEG_0742	probable transcriptional regulatory protein	NA	0.980	9.00E-01
MSMEG_0743	xanthine dehydrogenase	NA	1.090	1.16E-01
MSMEG_0744	carbon monoxide dehydrogenase medium chain	NA	1.080	3.54E-01
MSMEG_0745	[2Fe-2S] binding domain protein	NA	1.008	9.71E-01
MSMEG_0746	carbon-monoxide dehydrogenase, large subunit	NA	0.968	5.23E-01
MSMEG_0747	carbon monoxide dehydrogenase F protein	NA	2.250	4.22E-01
MSMEG_0748	ATPase associated with various cellular activities, AAA_5	NA	1.565	4.65E-01
MSMEG_0749	carbon monoxide dehydrogenase subunit G (CoxG) family protein	NA	0.972	7.59E-01
MSMEG_0750	membrane protein	NA	0.965	3.45E-01
MSMEG_0751	conserved hypothetical protein	NA	1.275	4.89E-01

MSMEG_0752	fructose-bisphosphate aldolase, class II	fbaA	0.962	6.13E-01
MSMEG_0753	conserved hypothetical protein	NA	0.845	2.59E-02
MSMEG_0754	conserved hypothetical protein	NA	1.039	4.94E-01
MSMEG_0755	cobalt-zinc-cadmium resistance protein	NA	1.321	4.52E-03
MSMEG_0756	peptidase, M50B family protein	NA	1.083	5.34E-01
MSMEG_0757	hypothetical protein	NA	4.891	1.57E-02
MSMEG_0758	conserved hypothetical protein	NA	1.101	1.98E-01
MSMEG_0759	adenylosuccinate synthetase	purA	0.931	1.95E-01
MSMEG_0760	thioesterase family protein	NA	0.983	5.85E-01
MSMEG_0761	conserved domain protein	NA	1.153	2.84E-01
MSMEG_0762	cytochrome P450 FAS1	NA	0.902	1.60E-02
MSMEG_0763	antibiotic transporter	NA	0.946	3.77E-01
MSMEG_0764	Na+/H+ antiporter	NA	1.088	4.49E-01
MSMEG_0765	zinc finger, UBP-type	NA	1.013	8.91E-01
MSMEG_0766	phosphoribosylglycinamide formyltransferase 2	purT	0.887	1.01E-01
MSMEG_0767	hypothetical protein	NA	0.864	9.52E-02
MSMEG_0768	conserved hypothetical protein	NA	1.126	5.44E-02
MSMEG_0769	O-succinylhomoserine sulfhydrylase	metZ	1.233	1.15E-01
MSMEG_0770	hypothetical protein	NA	1.255	2.84E-02
MSMEG_0771	hypothetical oxidoreductase YqjQ	NA	0.911	3.59E-01
MSMEG_0772	phytase	NA	1.061	7.19E-01
MSMEG_0773	acetyltransferase	NA	1.002	9.91E-01
MSMEG_0774	flavin-dependent oxidoreductase; this gene contains a frame shift which is not the res	NA	2.148	1.36E-02
MSMEG_0775	metallo-beta-lactamase superfamily protein	NA	0.973	4.44E-01
MSMEG_0776	conserved hypothetical protein	NA	1.351	1.13E-01
MSMEG_0777	F420-dependent glucose-6-phosphate dehydrogenase	NA	0.832	3.81E-02
MSMEG_0778	putative transcriptional regulator	NA	1.086	2.29E-01
MSMEG_0779	short-chain dehydrogenase/reductase SDR	NA	1.375	2.15E-01
MSMEG_0780	phosphotransferase enzyme family protein	NA	1.649	3.64E-01
MSMEG_0781	amino acid permease	NA	1.546	3.22E-03
MSMEG_0782	aminotransferase class-III	NA	1.379	2.54E-02

MSMEG_0783	phosphate acetyltransferase	pta	1.155	1.50E-02
MSMEG_0784	acetate kinase	ackA	0.948	4.26E-01
MSMEG_0785	conserved hypothetical protein	NA	1.217	3.59E-01
MSMEG_0786	serine/threonine protein kinase	NA	0.823	3.55E-01
MSMEG_0787	Bacterial extracellular solute-binding protein, family protein 3	NA	1.039	8.37E-01
MSMEG_0788	putative conserved membrane protein	NA	0.790	2.15E-02
MSMEG_0789	thiamine-phosphate pyrophosphorylase	thiE	0.889	1.67E-01
MSMEG_0790	hydrolase, NUDIX family protein	NA	1.026	5.64E-01
MSMEG_0791	glycine oxidase ThiO	thiO	0.868	9.62E-02
MSMEG_0792	thiamine biosynthesis protein ThiS	thiS	0.819	3.59E-03
MSMEG_0793	thiazole biosynthesis protein ThiG	thiG	0.847	8.64E-02
MSMEG_0794	conserved hypothetical protein	NA	0.895	2.12E-01
MSMEG_0795	ABC transporter ATP-binding protein	NA	0.829	2.49E-01
MSMEG_0796	ABC transporter integral membrane subunit	NA	0.860	1.67E-02
MSMEG_0797	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.742	3.01E-02
MSMEG_0797	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.075	6.83E-01
MSMEG_0798	hypothetical protein	NA	0.692	9.52E-02
MSMEG_0799	hypothetical protein	NA	0.866	4.65E-02
MSMEG_0800	hypothetical protein	NA	0.856	2.54E-01
MSMEG_0803	hypothetical protein	NA	1.036	7.18E-01
MSMEG_0803	hypothetical protein	NA	1.339	1.43E-01
MSMEG_0804	hypothetical protein	NA	0.973	7.93E-01
MSMEG_0805	conserved hypothetical protein	NA	1.191	8.44E-03
MSMEG_0806	hydrolase	NA	0.889	1.57E-01
MSMEG_0807	leupeptin-inactivating enzyme 1	NA	0.982	8.91E-01
MSMEG_0808	possible chalcone synthase Pks10	NA	1.192	3.89E-01
MSMEG_0809	isoprenylcysteine carboxyl methyltransferase	NA	1.175	4.94E-01
MSMEG_0810	putative pyrimidine permease RutG	NA	1.047	4.63E-01
MSMEG_0811	oxidoreductase	NA	1.140	6.82E-01
MSMEG_0812	amino acid transporter	NA	1.326	8.35E-02
MSMEG_0813	conserved hypothetical protein	NA	1.130	1.28E-01

MSMEG_0814	membrane protein	NA	0.917	1.69E-01
MSMEG_0815	transcriptional regulator, TetR family protein	NA	0.985	7.53E-01
MSMEG_0816	flavin-binding monooxygenase	NA	0.785	9.75E-03
MSMEG_0817	LysR-family protein transcriptional regulator	NA	2.545	3.57E-01
MSMEG_0818	transporter, major facilitator family protein	NA	2.019	2.25E-01
MSMEG_0819	N-carbamoyl-L-amino acid amidohydrolase	NA	1.541	7.49E-02
MSMEG_0820	conserved hypothetical protein	NA	1.873	4.08E-01
MSMEG_0821	glutamyl-tRNA(Gln) amidotransferase subunit A	NA	1.791	6.75E-02
MSMEG_0822	cytochrome P450	NA	1.024	9.11E-01
MSMEG_0823	conserved hypothetical protein	NA	1.051	8.52E-01
MSMEG_0824	conserved hypothetical protein	NA	0.703	5.46E-03
MSMEG_0825	phosphomethylpyrimidine kinase	thiD	0.731	8.84E-04
MSMEG_0826	thiamine biosynthesis protein ThiC	thiC	0.710	7.45E-04
MSMEG_0827	major facilitator superfamily protein MFS_1	NA	1.586	2.12E-01
MSMEG_0828	immunogenic protein MPT63	NA	1.255	1.51E-01
MSMEG_0829	exodeoxyribonuclease III	xth	1.083	4.17E-01
MSMEG_0830	acetyltransferase, gnat family protein	NA	1.299	9.71E-02
MSMEG_0831	short chain dehydrogenase	NA	1.275	1.12E-01
MSMEG_0832	peptide deformylase	def	1.116	7.80E-02
MSMEG_0833	conserved hypothetical protein	NA	0.989	9.36E-01
MSMEG_0834	tuberculin related peptide	NA	0.861	5.19E-04
MSMEG_0835	copper/zinc superoxide dismutase	sodC	1.035	7.05E-01
MSMEG_0836	carboxylate-amine ligase	NA	1.045	4.37E-01
MSMEG_0837	hypothetical protein	NA	0.800	3.91E-02
MSMEG_0838	AsnC-family protein transcriptional regulator	NA	1.381	2.30E-01
MSMEG_0839	ATP-dependent protease La (LON) domain subfamily protein	NA	1.138	1.48E-02
MSMEG_0840	hypothetical protein	NA	0.746	9.02E-04
MSMEG_0841	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	0.830	1.02E-01
MSMEG_0842	hypothetical protein	NA	0.950	4.41E-01
MSMEG_0843	multisubunit Na+/H+ antiporter, G subunit	NA	1.146	6.52E-02
MSMEG_0844	multiple resistance and pH regulation protein F	NA	1.213	2.05E-02

MSMEG_0845	multisubunit Na+/H+ antiporter	NA	1.205	7.78E-02
MSMEG_0846	NADH-ubiquinone oxidoreductase/multisubunit na+/h+ antiporter, d subunit	NA	1.269	9.02E-02
MSMEG_0847	NADH-ubiquinone/plastoquinone oxidoreductase chain 4l family protein	NA	1.309	3.60E-02
MSMEG_0848	NADH ubiquinone oxidoreductase subunit 5	NA	1.174	4.13E-02
MSMEG_0849	oxygenase	NA	1.781	6.41E-03
MSMEG_0850	conserved hypothetical protein	NA	1.007	9.65E-01
MSMEG_0851	Citrate transporter	NA	0.984	8.71E-01
MSMEG_0852	CBS domain protein	NA	0.831	7.84E-02
MSMEG_0853	conserved hypothetical protein	NA	0.805	6.00E-02
MSMEG_0854	two-component system sensor kinase	NA	0.921	4.60E-01
MSMEG_0855	conserved hypothetical protein	NA	1.149	2.84E-01
MSMEG_0856	DNA-binding response regulator, LuxR family protein	NA	1.081	6.30E-01
MSMEG_0857	conserved hypothetical protein	NA	1.133	4.69E-02
MSMEG_0858	cell division control protein Cdc48	NA	0.874	2.37E-01
MSMEG_0859	transcriptional regulator, TetR family protein	NA	0.900	1.84E-01
MSMEG_0860	CDP-diacylglycerol--serine O-phosphatidyltransferase	NA	0.965	4.69E-01
MSMEG_0861	phosphatidylserine decarboxylase	psd	0.926	2.65E-01
MSMEG_0862	molybdopterin biosynthesis protein MoeA	NA	0.987	8.52E-01
MSMEG_0863	short chain dehydrogenase	NA	1.024	4.99E-01
MSMEG_0864	bacterial membrane flanked domain family protein	NA	1.114	1.91E-01
MSMEG_0865	bacterial membrane flanked domain family protein	NA	1.183	3.14E-01
MSMEG_0866	DNA or RNA helicase of superfamily protein II	NA	1.100	6.25E-01
MSMEG_0867	hydrolase	NA	1.132	2.80E-02
MSMEG_0868	hypothetical protein	NA	0.954	6.67E-01
MSMEG_0869	hypothetical protein	NA	0.972	7.16E-01
MSMEG_0870	oxidoreductase	NA	2.176	3.72E-01
MSMEG_0871	putative aldehyde or xanthine dehydrogenase, molybdopterin binding subunit protein	NA	0.921	5.48E-01
MSMEG_0872	twin-arginine translocation pathway signal	NA	1.271	3.95E-01
MSMEG_0873	hypothetical protein	NA	1.229	3.97E-01
MSMEG_0874	transcriptional regulator, GntR family protein	NA	0.971	4.40E-01
MSMEG_0875	putative sialic acid transporter	NA	0.844	3.99E-02

MSMEG_0876	short chain dehydrogenase	NA	0.974	3.87E-01
MSMEG_0877	dihydrodipicolinate synthase	NA	0.940	4.66E-01
MSMEG_0878	transcriptional regulator	NA	0.883	1.36E-01
MSMEG_0879	hypothetical protein	NA	0.899	3.70E-02
MSMEG_0880	chaperonin GroL	groL	0.557	5.74E-04
MSMEG_0881	conserved hypothetical protein	NA	1.384	2.77E-02
MSMEG_0882	conserved hypothetical protein	NA	1.020	8.75E-01
MSMEG_0883	amidohydrolase family protein	NA	1.055	3.64E-01
MSMEG_0884	glyoxalase family protein	NA	0.994	9.36E-01
MSMEG_0885	conserved hypothetical protein	NA	0.835	4.57E-01
MSMEG_0886	serine/threonine-protein kinase PknD	NA	0.985	8.70E-01
MSMEG_0887	conserved hypothetical protein	NA	0.999	9.84E-01
MSMEG_0888	conserved hypothetical protein	NA	1.347	4.61E-01
MSMEG_0889	succinic semialdehyde dehydrogenase	NA	0.716	1.98E-03
MSMEG_0890	HD domain protein	NA	0.941	3.28E-01
MSMEG_0891	polyphosphate kinase 2	NA	1.292	3.14E-01
MSMEG_0892	conserved hypothetical protein	NA	0.871	2.13E-01
MSMEG_0893	hypothetical protein	NA	1.018	8.86E-01
MSMEG_0894	dihydrodipicolinate reductase	NA	0.775	2.59E-02
MSMEG_0895	bacterial regulatory protein, GntR family protein	NA	0.954	3.02E-01
MSMEG_0896	integral membrane transport protein	NA	1.053	7.48E-01
MSMEG_0897	conserved hypothetical protein	NA	1.373	9.01E-02
MSMEG_0898	tagatose-1,6-bisphosphate aldolase GatY	NA	1.269	1.77E-02
MSMEG_0899	prolyl oligopeptidase family protein	NA	1.655	3.60E-01
MSMEG_0900	eptc-inducible aldehyde dehydrogenase	NA	0.748	4.77E-02
MSMEG_0901	conserved hypothetical protein	NA	0.894	3.64E-02
MSMEG_0902	cyclopropane-fatty-acyl-phospholipid synthase 1	NA	1.218	3.77E-01
MSMEG_0903	dihydrolipoamide dehydrogenase	lpdA	0.841	5.78E-02
MSMEG_0904	probable conserved membrane protein	NA	1.064	4.89E-01
MSMEG_0905	4-carboxymuconolactone decarboxylase domain protein	pcaC	1.064	2.45E-01
MSMEG_0906	DNA-binding protein	NA	1.155	2.04E-01

MSMEG_0907	conserved hypothetical protein	NA	1.062	8.08E-01
MSMEG_0908	hypothetical protein	NA	0.859	1.90E-01
MSMEG_0909	acyl-ACP thioesterase superfamily protein	NA	0.978	7.18E-01
MSMEG_0910	hypothetical protein	NA	1.067	7.94E-01
MSMEG_0911	isocitrate lyase	aceA	1.037	6.25E-01
MSMEG_0912	3-hydroxybutyryl-CoA dehydrogenase	NA	1.066	4.38E-01
MSMEG_0913	methoxy mycolic acid synthase 1	NA	0.700	1.17E-03
MSMEG_0914	conserved hypothetical protein	NA	1.010	8.52E-01
MSMEG_0915	polyphosphate kinase 2 superfamily protein	NA	0.986	5.34E-01
MSMEG_0916	transcriptional regulator, TetR family protein	NA	0.999	9.92E-01
MSMEG_0917	conserved hypothetical protein	NA	0.997	9.33E-01
MSMEG_0918	transcriptional regulator, XRE family protein	NA	0.956	1.47E-01
MSMEG_0919	heparin-binding hemagglutinin	NA	0.962	1.85E-01
MSMEG_0920	conserved hypothetical protein	NA	1.005	6.71E-01
MSMEG_0921	conserved hypothetical protein	NA	0.975	5.72E-01
MSMEG_0922	deoxyribose-phosphate aldolase	deoC	1.085	5.33E-01
MSMEG_0923	conserved hypothetical protein	NA	1.181	9.22E-02
MSMEG_0924	hydrolase, carbon-nitrogen family protein	NA	0.853	6.07E-02
MSMEG_0925	conserved hypothetical protein	NA	1.542	4.05E-01
MSMEG_0926	conserved hypothetical protein	NA	0.980	6.98E-01
MSMEG_0927	conserved hypothetical protein	NA	1.118	1.73E-01
MSMEG_0928	UDP-N-acetylenolpyruvoylglucosamine reductase	murB	0.942	5.86E-01
MSMEG_0929	ErfK/YbiS/YcfS/YnhG family protein	NA	1.158	6.75E-02
MSMEG_0930	serine 3-dehydrogenase	NA	0.895	5.25E-02
MSMEG_0931	hypothetical protein	NA	1.370	2.32E-01
MSMEG_0932	ROK family protein	NA	0.906	2.03E-01
MSMEG_0933	conserved hypothetical protein	NA	0.986	7.44E-01
MSMEG_0934	conserved hypothetical protein	NA	1.107	4.49E-01
MSMEG_0935	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	NA	1.045	2.57E-01
MSMEG_0936	sensor histidine kinase SenX3	senX3	1.194	4.64E-02
MSMEG_0937	DNA-binding response regulator RegX3	regX3	1.008	8.80E-01

MSMEG_0938	conserved hypothetical protein	NA	0.956	3.45E-01
MSMEG_0939	Ppx/GppA phosphatase family protein	NA	0.862	1.48E-01
MSMEG_0940	conserved hypothetical protein	NA	0.941	2.13E-01
MSMEG_0941	AP endonuclease, family protein 2	NA	0.915	2.33E-01
MSMEG_0942	conserved hypothetical protein	NA	0.889	6.63E-02
MSMEG_0943	pyrroline-5-carboxylate reductase	proC	1.065	2.93E-01
MSMEG_0944	DNA binding domain, excisionase family protein	NA	1.027	7.41E-01
MSMEG_0945	conserved domain protein	NA	1.035	7.82E-01
MSMEG_0946	NAD dependent epimerase/dehydratase family protein	NA	1.067	3.82E-01
MSMEG_0947	acyltransferase	NA	1.105	2.63E-01
MSMEG_0948	conserved hypothetical protein	NA	1.164	3.77E-01
MSMEG_0949	HAD-superfamily protein subfamily protein IB hydrolase, TIGR01490	NA	1.101	3.63E-01
MSMEG_0950	hypothetical protein	NA	1.113	4.99E-01
MSMEG_0951	glutaredoxin 2	NA	1.073	1.23E-01
MSMEG_0952	glutamyl-tRNA reductase	hemA	0.971	6.09E-01
MSMEG_0953	porphobilinogen deaminase	hemC	0.958	3.12E-01
MSMEG_0954	uroporphyrinogen-III synthase	hemD	1.112	8.74E-02
MSMEG_0955	hypothetical protein	NA	1.786	3.05E-01
MSMEG_0956	delta-aminolevulinic acid dehydratase	hemB	1.118	2.61E-01
MSMEG_0957	hypothetical protein	NA	1.118	1.66E-01
MSMEG_0958	hypothetical protein	NA	1.040	5.57E-01
MSMEG_0959	putative conserved transmembrane protein	NA	0.955	3.14E-01
MSMEG_0960	putative transmembrane protein	NA	1.035	6.69E-01
MSMEG_0961	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.956	6.04E-01
MSMEG_0962	TetR-family protein transcriptional regulator	NA	1.054	4.32E-01
MSMEG_0963	hypothetical protein	NA	1.481	3.75E-02
MSMEG_0964	pyridoxamine 5'-phosphate oxidase family protein	NA	1.114	2.34E-01
MSMEG_0965	porin	NA	0.827	1.95E-02
MSMEG_0966	conserved hypothetical protein	NA	1.487	1.22E-01
MSMEG_0967	conserved hypothetical protein	NA	1.236	5.68E-01
MSMEG_0968	cytochrome P450	NA	2.410	2.83E-01

MSMEG_0969	glutamate-1-semialdehyde-2,1-aminomutase	hemL	1.391	1.05E-04
MSMEG_0970	phosphoglycerate mutase family protein	NA	1.087	3.04E-01
MSMEG_0971	conserved hypothetical protein	NA	1.062	4.53E-01
MSMEG_0972	cytochrome C biogenesis protein transmembrane region	NA	0.733	9.00E-04
MSMEG_0973	conserved membrane protein	NA	0.880	2.46E-02
MSMEG_0974	cytochrome c-type biogenesis protein CcsB	ccsB	1.003	9.65E-01
MSMEG_0975	conserved hypothetical protein	NA	0.946	5.94E-01
MSMEG_0976	conserved hypothetical protein	NA	1.107	5.09E-01
MSMEG_0977	conserved hypothetical protein	NA	1.322	4.55E-02
MSMEG_0978	aminotransferase, class V superfamily protein	NA	1.183	1.05E-01
MSMEG_0979	keratin associated protein	NA	1.105	2.17E-01
MSMEG_0980	signal transduction histidine kinase	NA	1.620	4.46E-01
MSMEG_0981	two-component system regulator	NA	1.347	1.00E-01
MSMEG_0982	immunogenic protein	NA	1.489	1.81E-01
MSMEG_0983	two-component system response regulator	NA	1.223	3.08E-02
MSMEG_0984	trap transporter, 4tm/12tm fusion protein	NA	0.974	8.62E-01
MSMEG_0985	sugar transporter family protein	NA	1.097	2.84E-02
MSMEG_0986	RemM protein	NA	1.145	8.44E-02
MSMEG_0987	hypothetical protein	NA	0.984	5.50E-01
MSMEG_0988	1,4-dihydroxy-2-naphthoate octaprenyltransferase	menA	1.145	2.38E-01
MSMEG_0989	conserved hypothetical protein	NA	1.048	4.41E-01
MSMEG_0990	methylthioadenosine phosphorylase	mtaP	1.039	5.40E-01
MSMEG_0991	NAD-dependent epimerase/dehydratase	NA	1.065	4.24E-01
MSMEG_0992	2-nitropropane dioxygenase, NPD	NA	0.809	1.24E-01
MSMEG_0993	histidine kinase	NA	1.107	3.59E-01
MSMEG_0994	DNA-binding response regulator ResD	resD	1.096	5.36E-01
MSMEG_0995	glycosyl transferase, family protein 2	NA	0.951	8.74E-01
MSMEG_0996	conserved hypothetical protein	NA	1.042	6.78E-01
MSMEG_0997	conserved hypothetical protein	NA	1.214	4.69E-01
MSMEG_0998	oxidoreductase, molybdopterin binding	NA	1.091	6.64E-01
MSMEG_0999	integral membrane protein	NA	1.396	1.20E-03

MSMEG_1000	hypothetical protein	NA	0.931	6.19E-01
MSMEG_1001	acetyltransferase, gnat family protein, putative	NA	1.188	1.80E-01
MSMEG_1004	This is the transposed copy of the gene fragment that was disrupted by an IS1096 elen	NA	1.108	4.57E-01
MSMEG_1060	putative Lsr2 protein	NA	1.168	1.92E-01
MSMEG_1061	phosphohydrolase	NA	1.228	6.16E-02
MSMEG_1062	O-succinylbenzoic acid--CoA ligase	NA	0.931	5.89E-01
MSMEG_1063	conserved hypothetical protein	NA	1.054	2.80E-01
MSMEG_1064	phosphate/sulphate permease	NA	1.673	1.20E-03
MSMEG_1065	conserved hypothetical protein	NA	1.567	4.75E-03
MSMEG_1066	conserved hypothetical protein	NA	1.493	3.54E-03
MSMEG_1067	conserved hypothetical protein	NA	1.391	9.81E-02
MSMEG_1068	regulatory protein	NA	1.214	1.21E-01
MSMEG_1069	amino acid permease-associated region	NA	0.958	7.75E-01
MSMEG_1070	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.020	8.22E-01
MSMEG_1071	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.842	1.82E-01
MSMEG_1072	agmatinase	speB	0.937	5.40E-01
MSMEG_1073	oxidoreductase, short-chain dehydrogenase/reductase family protein	NA	1.152	1.06E-01
MSMEG_1074	polysaccharide deacetylase	NA	0.855	1.40E-01
MSMEG_1075	naphthoate synthase	menB	0.936	2.70E-01
MSMEG_1076	conserved hypothetical protein	NA	1.052	8.70E-01
MSMEG_1077	conserved hypothetical protein	NA	0.987	8.99E-01
MSMEG_1078	hydrolase	NA	1.018	8.06E-01
MSMEG_1079	hypothetical protein	NA	1.577	3.44E-01
MSMEG_1080	large subunit of N,N-dimethylformamidase	NA	1.630	4.87E-01
MSMEG_1081	hypothetical protein	NA	1.124	3.47E-01
MSMEG_1082	putative response regulator	NA	0.930	2.75E-01
MSMEG_1083	hypothetical protein	NA	0.995	9.88E-01
MSMEG_1084	peptide/opine/nickel uptake family protein ABC transporter, periplasmic substrate-bin	NA	0.967	7.96E-01
MSMEG_1085	dipeptide transport system permease protein DppB	NA	1.135	2.13E-01
MSMEG_1086	ABC transporter permease protein	NA	1.237	5.90E-01
MSMEG_1087	oligopeptide ABC transporter ATP-binding protein; this gene contains a frame shift wh	NA	0.956	6.24E-02

MSMEG_1087	oligopeptide ABC transporter ATP-binding protein; this gene contains a frame shift wh	NA	1.043	3.31E-01
MSMEG_1088	glutamyl-tRNA(Gln)/aspartyl-tRNA(Asn) amidotransferase, A subunit	gatA	0.956	7.36E-01
MSMEG_1089	hypothetical protein	NA	0.944	4.80E-01
MSMEG_1090	amidase	NA	1.162	2.37E-01
MSMEG_1091	urease accessory protein UreE 1	NA	1.980	4.70E-01
MSMEG_1092	urease accessory protein UreF	NA	0.843	4.07E-01
MSMEG_1093	urease gamma/beta subunit	NA	0.915	6.42E-01
MSMEG_1094	urease, alpha subunit	ureC	0.968	9.25E-01
MSMEG_1095	urease accessory protein UreG	ureG	6.695	3.95E-01
MSMEG_1096	urease accessory protein UreD, putative	NA	0.917	3.19E-01
MSMEG_1097	glycosyl transferase, group 2 family protein	NA	1.437	4.68E-01
MSMEG_1098	acyl-CoA synthase	NA	0.998	9.91E-01
MSMEG_1099	hypothetical protein	NA	1.169	2.16E-01
MSMEG_1100	dgpf protein	NA	1.080	4.67E-01
MSMEG_1101	hypothetical protein	NA	0.945	8.13E-01
MSMEG_1102	twin-arginine translocation pathway signal	NA	1.344	1.79E-01
MSMEG_1103	O-succinylbenzoate synthase	NA	1.070	4.43E-01
MSMEG_1104	hypothetical protein	NA	1.279	5.11E-02
MSMEG_1105	phthiodiolone ketoreductase; this gene contains a frame shift which is not the result o	NA	0.882	5.07E-01
MSMEG_1105	phthiodiolone ketoreductase; this gene contains a frame shift which is not the result o	NA	1.486	4.20E-02
MSMEG_1106	transcriptional regulator, AraC family protein	NA	0.983	6.30E-01
MSMEG_1107	isonitrile hydratase, putative	NA	0.983	9.53E-01
MSMEG_1108	hydrolase, alpha/beta fold family protein	NA	1.027	6.97E-01
MSMEG_1109	2-oxoglutarate decarboxylase	NA	1.331	1.09E-01
MSMEG_1110	probable conserved transmembrane protein	NA	1.208	1.21E-01
MSMEG_1111	conserved hypothetical protein	NA	1.077	2.19E-01
MSMEG_1112	aconitate hydratase, putative	NA	1.197	5.86E-01
MSMEG_1113	glycosyl transferase	NA	0.974	8.60E-01
MSMEG_1114	short chain dehydrogenase	NA	2.463	3.35E-02
MSMEG_1115	menaquinone biosynthesis methyltransferase UbiE	NA	1.025	7.48E-01
MSMEG_1116	gamma-glutamylisopropylamide synthetase	NA	0.740	6.06E-02

MSMEG_1117	transcriptional regulator	NA	0.775	8.28E-02
MSMEG_1118	amino acid permease	NA	0.734	8.76E-02
MSMEG_1119	glutamine amidotransferase, class I	NA	1.150	4.64E-01
MSMEG_1120	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	NA	0.681	1.74E-01
MSMEG_1121	conserved hypothetical protein	NA	1.540	5.62E-01
MSMEG_1122	hypothetical protein	NA	0.724	4.61E-02
MSMEG_1123	cobalamin synthesis protein	NA	1.108	4.16E-01
MSMEG_1124	putative ferredoxin FdxA	NA	1.091	1.29E-01
MSMEG_1125	regulatory protein, ArsR	NA	1.209	1.21E-01
MSMEG_1126	hypothetical protein	NA	0.959	6.82E-01
MSMEG_1127	probable conserved transmembrane protein	NA	1.006	8.78E-01
MSMEG_1128	conserved hypothetical protein	NA	1.229	3.28E-01
MSMEG_1129	D-amino-acid dehydrogenase	NA	1.082	8.72E-01
MSMEG_1130	hypothetical protein	NA	1.171	5.09E-01
MSMEG_1131	tryptophan-rich sensory protein	NA	1.643	1.45E-01
MSMEG_1132	FAD binding domain, putative	NA	1.328	2.43E-02
MSMEG_1133	bifunctional short chain isoprenyl diphosphate synthase	NA	1.030	1.65E-01
MSMEG_1134	putative protease HtpX	NA	0.983	7.69E-01
MSMEG_1135	hypothetical protein	NA	2.379	3.34E-01
MSMEG_1136	conserved hypothetical protein	NA	0.847	2.10E-02
MSMEG_1137	amino acid permease-associated region	NA	0.931	5.67E-01
MSMEG_1138	alcohol dehydrogenase 1	NA	1.198	4.45E-01
MSMEG_1139	transcription regulator	NA	1.022	8.40E-01
MSMEG_1140	glycerol-3-phosphate dehydrogenase 2 [NAD(P)+] (NAD(P)H-dependent glycerol-3-phc	NA	1.316	3.74E-02
MSMEG_1141	ABC-transporter integral membrane protein	NA	0.905	3.55E-01
MSMEG_1142	ABC-transporter integral membrane protein	NA	1.527	5.16E-01
MSMEG_1143	mce related protein	NA	0.815	4.93E-01
MSMEG_1144	virulence factor Mce family protein	NA	0.560	6.11E-03
MSMEG_1145	virulence factor Mce family protein	NA	0.839	4.49E-01
MSMEG_1146	virulence factor Mce family protein	NA	0.814	3.49E-01
MSMEG_1147	mce related protein	NA	0.746	6.52E-02

MSMEG_1148	mce related protein	NA	0.904	7.20E-01
MSMEG_1149	conserved hypothetical protein	NA	0.802	5.60E-02
MSMEG_1150	conserved hypothetical protein	NA	0.967	9.22E-01
MSMEG_1151	DNA-binding protein	NA	0.845	1.01E-03
MSMEG_1152	citrate-proton symporter	NA	1.037	3.64E-01
MSMEG_1153	FAD dependent oxidoreductase	NA	0.888	2.18E-01
MSMEG_1154	formyl-coenzyme A transferase	NA	0.851	5.04E-02
MSMEG_1155	carnitinyl-CoA dehydratase	NA	0.974	9.18E-01
MSMEG_1156	dihydrodipicolinate synthetase	NA	0.851	3.15E-01
MSMEG_1157	short chain dehydrogenase	NA	1.077	7.03E-01
MSMEG_1158	5-oxovalerate dehydrogenase	NA	0.875	3.49E-01
MSMEG_1159	ABC transporter component A	NA	1.033	9.05E-01
MSMEG_1160	ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component	NA	1.210	5.20E-01
MSMEG_1161	taurine transport system permease protein TauC	NA	1.058	4.59E-01
MSMEG_1162	nitrilotriacetate monooxygenase component A	NA	0.988	8.91E-01
MSMEG_1163	hypothetical protein	NA	1.026	5.55E-01
MSMEG_1164	putative transporter; this region contains one or more premature stops and/or frames	NA	1.027	6.27E-01
MSMEG_1164	putative transporter; this region contains one or more premature stops and/or frames	NA	1.198	1.87E-01
MSMEG_1164	putative transporter; this region contains one or more premature stops and/or frames	NA	4.318	2.20E-01
MSMEG_1165	conserved hypothetical protein	NA	0.893	2.41E-01
MSMEG_1167	cytochrome P450	NA	0.885	3.41E-01
MSMEG_1168	putative transcriptional regulator	NA	1.422	1.89E-01
MSMEG_1169	integral membrane transport protein	NA	1.282	5.58E-02
MSMEG_1170	conserved domain protein	NA	1.547	5.51E-02
MSMEG_1171	Low molecular weight phosphotyrosine protein phosphatase	NA	1.076	7.55E-01
MSMEG_1172	arsenical-resistance protein	arsB	1.169	1.25E-01
MSMEG_1173	transcriptional regulator, ArsR family protein	NA	1.238	1.15E-01
MSMEG_1174	cadmium inducible protein cadi	NA	0.960	6.80E-01
MSMEG_1175	putative transcriptional regulatory protein	NA	1.318	2.85E-02
MSMEG_1176	hypothetical protein	NA	0.875	4.63E-03
MSMEG_1177	cytosine/purines/uracil/thiamine/allantoin permease family protein	NA	1.261	4.62E-01

MSMEG_1178	transcriptional regulator	NA	0.872	5.37E-02
MSMEG_1179	urocanate hydratase	hutU	1.187	5.69E-01
MSMEG_1180	N-carbamoyl-L-amino acid hydrolase	NA	1.339	1.71E-01
MSMEG_1181	formiminoglutamate deiminase	hutF	0.854	2.23E-01
MSMEG_1182	imidazolonepropionase	hutI	1.041	8.35E-01
MSMEG_1183	histidine ammonia-lyase	hutH	2.325	4.44E-01
MSMEG_1184	serine esterase, cutinase family protein	NA	1.034	8.12E-01
MSMEG_1185	transcriptional regulator, AsnC family protein	NA	1.165	5.94E-01
MSMEG_1186	putative permease	NA	1.117	5.23E-01
MSMEG_1187	N-acyl-D-aspartate deacylase	NA	1.068	2.33E-01
MSMEG_1188	conserved hypothetical protein	NA	1.176	8.18E-02
MSMEG_1189	conserved hypothetical protein	NA	0.989	8.28E-01
MSMEG_1190	serine/threonine-protein kinase PknD	NA	1.428	9.87E-02
MSMEG_1191	hypothetical protein	NA	1.034	7.34E-01
MSMEG_1192	M23 peptidase domain protein	NA	1.110	7.53E-01
MSMEG_1193	TROVE domain protein	NA	1.649	5.25E-02
MSMEG_1194	hypothetical protein	NA	0.936	2.96E-01
MSMEG_1195	conserved hypothetical protein	NA	1.034	5.75E-01
MSMEG_1196	SNF2 domain protein	NA	1.323	3.56E-02
MSMEG_1197	transcriptional regulator, LuxR family protein	NA	0.797	4.56E-02
MSMEG_1198	hypothetical protein	NA	1.467	4.80E-03
MSMEG_1199	conserved hypothetical protein	NA	1.114	2.36E-01
MSMEG_1200	serine/threonine-protein kinase PknD	NA	0.867	7.88E-02
MSMEG_1201	hypothetical protein	NA	1.176	2.33E-01
MSMEG_1202	hypothetical protein	NA	0.370	1.31E-03
MSMEG_1203	methoxy mycolic acid synthase 1	NA	0.761	3.86E-02
MSMEG_1204	3-oxoacyl-[acyl-carrier-protein] synthase 2	NA	1.113	4.09E-01
MSMEG_1205	cyclopropane-fatty-acyl-phospholipid synthase 1	NA	0.955	6.33E-01
MSMEG_1206	hypothetical protein	NA	1.120	2.52E-02
MSMEG_1207	glycosyltransferase, group I	NA	0.958	6.47E-01
MSMEG_1208	glycosyltransferase, group I	NA	0.941	4.41E-01

MSMEG_1209	glycosidase	NA	0.998	9.85E-01
MSMEG_1210	conserved hypothetical protein	NA	1.248	6.86E-02
MSMEG_1211	Fatty acid desaturase	NA	0.766	6.20E-03
MSMEG_1212	hypothetical protein	NA	0.820	1.61E-01
MSMEG_1213	cytochrome P450 monooxygenase	NA	1.084	2.33E-01
MSMEG_1214	oxidoreductase	NA	1.728	3.06E-01
MSMEG_1215	serine/threonine-protein kinase PknE, putative	NA	1.138	1.30E-02
MSMEG_1216	ABC-type transport system periplasmic substrate-binding protein	NA	1.008	9.70E-01
MSMEG_1217	ABC-type transport system ATP-binding protein I	NA	1.252	1.31E-01
MSMEG_1218	ABC-type transport system ATP-binding protein II	NA	0.874	3.48E-01
MSMEG_1219	ABC-type transport system permease protein II	NA	1.050	6.90E-02
MSMEG_1220	ABC-type transport system permease protein I	NA	0.940	1.57E-01
MSMEG_1221	rifampin ADP-ribosyl transferase	NA	1.080	3.27E-01
MSMEG_1222	ISMsm6, transposase	NA	1.289	4.04E-01
MSMEG_1223	hypothetical protein	NA	1.153	2.15E-01
MSMEG_1224	rifampin ADP-ribosyl transferase	NA	1.042	7.81E-01
MSMEG_1225	conserved hypothetical protein	NA	0.706	6.64E-02
MSMEG_1226	sulfatase-modifying factor 1	NA	1.076	6.70E-01
MSMEG_1227	transcriptional regulator, GntR family protein	NA	0.890	1.25E-02
MSMEG_1228	sulfatase	NA	0.902	5.45E-01
MSMEG_1229	DNA gyrase, B subunit	gyrB	1.357	4.52E-01
MSMEG_1230	hypothetical protein	NA	1.216	4.02E-01
MSMEG_1231	inner membrane protein YidH	NA	0.822	4.50E-02
MSMEG_1232	ABC transporter substrate-binding protein	NA	0.977	6.92E-01
MSMEG_1233	ABC transporter permease protein; this gene contains a frame shift which is not the re	NA	0.927	4.73E-01
MSMEG_1234	taurine import ATP-binding protein TauB	NA	1.137	2.08E-01
MSMEG_1235	sulfate permease	NA	1.344	9.25E-02
MSMEG_1236	Mpr protein	NA	0.840	2.04E-01
MSMEG_1237	hypothetical protein	NA	0.894	3.55E-01
MSMEG_1238	type III restriction enzyme, res subunit	NA	0.849	1.42E-02
MSMEG_1240	conserved hypothetical protein	NA	0.798	4.03E-01

MSMEG_1241	conserved hypothetical protein	NA	0.740	4.33E-02
MSMEG_1242	cysteine desulfurase IscS	iscS	0.970	5.04E-01
MSMEG_1243	conserved hypothetical protein	NA	0.973	3.14E-01
MSMEG_1244	conserved hypothetical protein	NA	0.896	5.45E-02
MSMEG_1245	phosphoadenosine phosphosulfate reductase	NA	0.657	1.06E-03
MSMEG_1246	conserved hypothetical protein	NA	0.705	7.94E-03
MSMEG_1247	conserved hypothetical protein	NA	0.911	1.09E-02
MSMEG_1248	hypothetical protein	NA	0.839	2.39E-01
MSMEG_1249	ISMsm7, transposase orfB	NA	1.027	8.24E-01
MSMEG_1250	ISMsm7, transposase orfA	NA	1.044	6.14E-01
MSMEG_1251	conserved hypothetical protein	NA	0.930	5.67E-01
MSMEG_1252	conserved hypothetical protein	NA	0.829	1.13E-02
MSMEG_1253	conserved hypothetical protein	NA	0.925	3.94E-01
MSMEG_1254	DEAD/DEAH box helicase	NA	0.793	2.28E-03
MSMEG_1255	UvrD/Rep helicase	NA	0.737	6.48E-03
MSMEG_1256	hypothetical protein	NA	0.741	5.35E-03
MSMEG_1259	hypothetical protein	NA	1.132	1.95E-02
MSMEG_1260	hypothetical protein	NA	1.019	8.07E-01
MSMEG_1261	hypothetical protein	NA	1.029	6.05E-01
MSMEG_1262	conserved hypothetical protein	NA	0.941	9.99E-02
MSMEG_1263	conserved hypothetical protein	NA	0.612	1.87E-02
MSMEG_1264	prophage Lp1 protein 5	NA	0.871	3.63E-01
MSMEG_1265	conserved hypothetical protein	NA	0.763	7.12E-03
MSMEG_1266	ankyrin-repeat containing protein	NA	1.105	5.39E-01
MSMEG_1267	putative ribosylglycohydrolase; this gene contains a frame shift which is not the result	NA	1.411	2.30E-01
MSMEG_1268	nudix hydrolase	NA	1.039	7.25E-01
MSMEG_1269	Ser/Thr protein phosphatase family protein	NA	1.132	2.54E-01
MSMEG_1270	hypothetical protein	NA	1.170	9.20E-02
MSMEG_1271	hypothetical protein	NA	1.274	4.32E-01
MSMEG_1272	putative ribosylglycohydrolase	NA	1.198	5.60E-02
MSMEG_1273	conserved hypothetical protein	NA	1.218	4.38E-02

MSMEG_1274	gluconolactonase	NA	1.833	3.65E-01
MSMEG_1275	HNH nuclease, putative	NA	1.045	5.94E-01
MSMEG_1276	hypothetical protein	NA	1.001	9.92E-01
MSMEG_1277	hypothetical protein	NA	1.395	3.17E-02
MSMEG_1278	death-on-curing protein	NA	1.214	8.25E-02
MSMEG_1279	conserved hypothetical protein	NA	1.174	6.75E-02
MSMEG_1280	hypothetical cytosolic protein	NA	1.021	7.43E-01
MSMEG_1281	conserved hypothetical protein	NA	1.110	4.20E-01
MSMEG_1282	hypothetical cytosolic protein	NA	1.206	2.28E-01
MSMEG_1283	probable ribbon-helix-helix transcription factor, family protein	NA	0.005	2.15E-08
MSMEG_1284	PIN domain protein	NA	1.845	2.08E-01
MSMEG_1285	tetratricopeptide repeat family protein	NA	0.983	7.32E-01
MSMEG_1286	sulfatase family protein	NA	1.040	4.39E-01
MSMEG_1287	cyclase/dehydrase superfamily protein	NA	0.868	2.55E-01
MSMEG_1288	conserved hypothetical protein	NA	0.958	6.41E-01
MSMEG_1289	conserved hypothetical protein	NA	1.129	5.01E-02
MSMEG_1290	dihydroxy-acid dehydratase	ilvD	2.103	1.02E-01
MSMEG_1291	putative oxidoreductase	NA	1.099	5.80E-01
MSMEG_1292	FAD binding domain in molybdopterin dehydrogenase protein	NA	0.888	4.76E-01
MSMEG_1293	xanthine/uracil permeases family protein	NA	0.784	2.68E-01
MSMEG_1294	allantoicase	NA	8.067	3.38E-01
MSMEG_1295	transthyretin	NA	0.995	9.66E-01
MSMEG_1296	uricase	NA	0.953	7.65E-01
MSMEG_1297	hydroxydechloroatrazine ethylaminohydrolase	NA	1.806	2.75E-01
MSMEG_1298	guanine deaminase	NA	1.044	8.50E-02
MSMEG_1299	oxidoreductase, 2OG-Fe(II) oxygenase family protein	NA	1.278	3.48E-01
MSMEG_1300	hypothetical protein	NA	0.972	8.27E-01
MSMEG_1301	NanT3	NA	1.686	2.48E-01
MSMEG_1302	alkylphosphonate uptake protein	NA	0.977	9.11E-01
MSMEG_1303	putative transcriptional regulator	NA	2.186	2.73E-01
MSMEG_1304	rhizopine catabolism protein	NA	1.583	2.98E-01

MSMEG_1305	TetR family protein regulatory protein	NA	1.194	3.15E-01
MSMEG_1306	aldehyde dehydrogenase (NAD) family protein	NA	0.926	5.41E-01
MSMEG_1307	EthD protein	NA	1.256	2.07E-01
MSMEG_1308	peptidase S15	NA	1.124	1.20E-01
MSMEG_1309	conserved hypothetical protein	NA	0.883	1.89E-01
MSMEG_1311	oligopeptide transporter, OPT family protein	NA	1.025	6.07E-01
MSMEG_1312	hypothetical protein	NA	0.822	1.71E-01
MSMEG_1313	secreted protein	NA	1.208	9.17E-03
MSMEG_1314	hypothetical protein	NA	1.142	1.21E-02
MSMEG_1315	transporter, small conductance mechanosensitive ion channel (MscS) family protein	NA	1.189	5.12E-01
MSMEG_1316	peptide chain release factor 3	prfC	1.158	1.36E-01
MSMEG_1317	transcriptional regulator	NA	1.116	4.06E-01
MSMEG_1318	polysaccharide deacetylase family protein	NA	1.062	4.96E-01
MSMEG_1319	Asp/Glu racemase	NA	1.076	7.50E-01
MSMEG_1320	major facilitator superfamily protein MFS_1	NA	1.073	1.99E-01
MSMEG_1321	5-carboxymethyl-2-hydroxymuconate delta-isomerase	NA	0.935	7.77E-01
MSMEG_1322	ErfK/YbiS/YcfS/YnhG family protein	NA	1.014	3.54E-01
MSMEG_1323	hypothetical protein	NA	1.154	2.32E-01
MSMEG_1324	hypothetical protein	NA	1.497	1.47E-01
MSMEG_1325	exodeoxyribonuclease V, alpha subunit	recD	1.055	7.38E-01
MSMEG_1326	hypothetical protein	NA	1.283	4.42E-01
MSMEG_1327	exodeoxyribonuclease V, beta subunit	recB	0.819	4.36E-02
MSMEG_1328	exodeoxyribonuclease V, gamma subunit	recC	0.866	3.73E-02
MSMEG_1329	major facilitator superfamily protein MFS_1, putative	NA	1.160	3.33E-01
MSMEG_1330	MarR-family protein transcriptional regulator	NA	1.162	3.64E-02
MSMEG_1331	enoyl-CoA hydratase	NA	1.047	6.31E-01
MSMEG_1332	conserved hypothetical protein	NA	0.939	3.75E-01
MSMEG_1333	conserved hypothetical protein	NA	1.783	9.94E-03
MSMEG_1334	metallo-beta-lactamase family protein	NA	1.196	3.88E-03
MSMEG_1335	transcriptional regulator, BadM/Rrf2 family protein	NA	1.705	1.70E-01
MSMEG_1336	flavohemoprotein, putative	NA	1.359	1.97E-02

MSMEG_1339	ribosomal protein L33	rpmG	0.944	6.92E-01
MSMEG_1340	conserved hypothetical protein	NA	0.927	2.80E-01
MSMEG_1341	MaoC family protein	NA	1.297	7.90E-03
MSMEG_1342	conserved hypothetical protein	NA	1.375	1.34E-02
MSMEG_1344	translocase	NA	1.068	4.06E-01
MSMEG_1345	transcription antitermination protein NusG	NA	1.164	3.67E-02
MSMEG_1346	ribosomal protein L11	rplK	1.105	5.09E-01
MSMEG_1347	ribosomal protein L1	rplA	1.174	2.92E-02
MSMEG_1348	RNA polymerase ECF-subfamily protein sigma factor	NA	0.975	9.29E-01
MSMEG_1349	dgpf domain family protein	NA	1.037	3.14E-01
MSMEG_1350	cyclopropane-fatty-acyl-phospholipid synthase 1	NA	0.876	4.29E-02
MSMEG_1351	cyclopropane-fatty-acyl-phospholipid synthase 1	NA	0.775	1.02E-03
MSMEG_1352	hydrolase, alpha/beta fold family protein	NA	1.064	2.92E-01
MSMEG_1353	ABC1 family protein	NA	1.102	3.22E-02
MSMEG_1354	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.817	4.65E-02
MSMEG_1355	transcriptional regulator, TetR family protein	NA	1.310	1.13E-01
MSMEG_1356	conserved hypothetical protein	NA	1.174	2.82E-02
MSMEG_1357	conserved hypothetical protein	NA	0.999	9.80E-01
MSMEG_1358	conserved hypothetical protein	NA	1.286	2.83E-01
MSMEG_1359	DeoR-family protein transcriptional regulator	NA	1.171	5.99E-01
MSMEG_1360	endonuclease/exonuclease/phosphatase	NA	1.181	2.05E-01
MSMEG_1361	alpha-mannosidase	NA	1.018	7.33E-01
MSMEG_1362	conserved hypothetical protein	NA	1.016	8.25E-01
MSMEG_1363	glucokinase	NA	0.856	4.43E-02
MSMEG_1364	50S ribosomal protein L10	NA	0.943	2.23E-01
MSMEG_1365	ribosomal protein L7/L12	rplL	1.070	1.31E-01
MSMEG_1366	ABC transporter, ATP-binding protein	NA	0.670	1.26E-03
MSMEG_1367	DNA-directed RNA polymerase, beta subunit	rpoB	1.377	4.74E-02
MSMEG_1368	DNA-directed RNA polymerase, beta' subunit	rpoC	1.151	1.58E-01
MSMEG_1369	LacI-family protein transcriptional regulator	NA	2.036	1.54E-03
MSMEG_1370	2-deoxy-scyllo-inosamine dehydrogenase	NA	1.262	1.61E-01

MSMEG_1371	conserved hypothetical protein	NA	1.076	1.89E-01
MSMEG_1372	ABC transporter ATP-binding protein	NA	0.916	4.37E-01
MSMEG_1373	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease compone	NA	0.930	8.27E-01
MSMEG_1374	ribose ABC transporter, periplasmic binding protein	NA	0.710	1.37E-01
MSMEG_1375	tagatose-1,6-bisphosphate aldolase GatY	NA	1.236	1.83E-02
MSMEG_1376	putative xylulose kinase	NA	0.990	8.79E-01
MSMEG_1377	DeoR-family protein transcriptional regulator	NA	1.150	2.54E-01
MSMEG_1378	1-phosphofructokinase	NA	1.335	3.35E-01
MSMEG_1379	conserved hypothetical protein	NA	1.076	3.53E-01
MSMEG_1380	transcriptional regulator	NA	1.097	2.98E-01
MSMEG_1381	MmpS5 protein	NA	1.628	7.60E-03
MSMEG_1382	MmpL5 protein	NA	1.423	6.44E-03
MSMEG_1383	endonuclease IV	NA	0.973	6.70E-01
MSMEG_1384	conserved hypothetical protein	NA	1.075	8.28E-01
MSMEG_1385	PAP2 superfamily protein	NA	0.935	3.63E-01
MSMEG_1386	hypothetical protein	NA	1.278	4.64E-01
MSMEG_1387	putative acyl-CoA dehydrogenase	NA	0.887	5.41E-03
MSMEG_1388	enoyl-CoA hydratase	NA	0.884	1.92E-01
MSMEG_1389	conserved hypothetical protein	NA	0.961	7.67E-01
MSMEG_1390	enoyl-CoA hydratase	NA	1.046	7.24E-01
MSMEG_1391	transcriptional regulator, LysR family protein	NA	1.445	1.76E-01
MSMEG_1392	alcohol dehydrogenase, class IV	NA	0.840	3.82E-01
MSMEG_1393	conserved hypothetical protein	NA	0.957	4.85E-01
MSMEG_1394	probable conserved transmembrane protein	NA	0.877	2.22E-01
MSMEG_1395	lipoprotein, putative	NA	1.062	5.31E-01
MSMEG_1396	LprB protein	NA	0.960	6.22E-01
MSMEG_1397	transcriptional regulator, TetR family protein	NA	1.148	3.75E-02
MSMEG_1398	ribosomal protein S12	rpsL	1.052	5.35E-01
MSMEG_1399	ribosomal protein S7	rpsG	1.031	4.51E-01
MSMEG_1400	elongation factor G; this gene contains a frame shift which is not the result of sequenc	NA	0.989	9.67E-01
MSMEG_1400	elongation factor G; this gene contains a frame shift which is not the result of sequenc	NA	1.475	2.04E-01

MSMEG_1401	translation elongation factor Tu	tuf	1.122	6.95E-01
MSMEG_1402	hypothetical protein	NA	1.083	3.68E-01
MSMEG_1403	cutinase superfamily protein	NA	1.429	3.85E-02
MSMEG_1406	conserved hypothetical protein	NA	0.940	4.83E-01
MSMEG_1407	Na(+)/H(+) antiporter; this gene contains a frame shift which is not the result of seque	NA	1.141	1.62E-01
MSMEG_1407	Na(+)/H(+) antiporter; this gene contains a frame shift which is not the result of seque	NA	1.510	2.60E-02
MSMEG_1408	arginine/ornithine antiporter; this region contains one or more premature stops and/c	NA	0.949	4.12E-01
MSMEG_1408	arginine/ornithine antiporter; this region contains one or more premature stops and/c	NA	1.021	7.53E-01
MSMEG_1408	arginine/ornithine antiporter; this region contains one or more premature stops and/c	NA	1.232	1.32E-01
MSMEG_1409	arginine deiminase	arcA	1.224	4.20E-01
MSMEG_1410	carveol dehydrogenase	NA	1.046	4.87E-01
MSMEG_1411	universal stress protein family protein	NA	1.327	3.29E-02
MSMEG_1412	amino acid permease	NA	1.007	9.73E-01
MSMEG_1413	ornithine--oxo-acid transaminase	rocD	0.801	6.65E-02
MSMEG_1414	Amidinotransferase	NA	0.800	8.32E-02
MSMEG_1415	AsnC-family protein transcriptional regulator	NA	1.112	2.81E-01
MSMEG_1416	Pyridine nucleotide-disulphide oxidoreductase	NA	1.110	6.28E-02
MSMEG_1417	glyoxalase family protein	NA	0.868	2.80E-01
MSMEG_1418	RNA polymerase ECF-type sigma factor	NA	0.843	2.46E-01
MSMEG_1419	conserved hypothetical protein	NA	1.543	3.23E-02
MSMEG_1420	probable transcriptional regulatory protein	NA	1.481	2.78E-01
MSMEG_1421	hypothetical protein	NA	0.879	2.90E-01
MSMEG_1422	conserved hypothetical protein	NA	0.895	1.97E-01
MSMEG_1423	radical SAM domain protein	NA	0.969	6.60E-01
MSMEG_1424	FMN-dependent dehydrogenase	NA	0.932	2.12E-01
MSMEG_1425	creatininase subfamily protein	NA	1.061	1.35E-01
MSMEG_1426	probable membrane sugar transferase	NA	0.988	8.97E-01
MSMEG_1427	transmembrane efflux protein	NA	0.843	3.75E-01
MSMEG_1428	glucose-methanol-choline oxidoreductase	NA	0.855	8.63E-03
MSMEG_1429	cytochrome P450-terp	NA	1.161	5.69E-01
MSMEG_1430	transcriptional regulator, TetR family protein	NA	1.076	7.01E-01

MSMEG_1431	cytochrome P450-terp	NA	1.432	4.21E-01
MSMEG_1432	acetylcholinesterase	NA	1.208	8.58E-02
MSMEG_1433	thioesterase	NA	1.040	7.27E-01
MSMEG_1434	conserved hypothetical protein	NA	1.178	4.06E-02
MSMEG_1435	ribosomal protein S10	rpsJ	1.006	9.52E-01
MSMEG_1436	ribosomal protein L3	rplC	0.866	1.24E-01
MSMEG_1437	ribosomal protein L4/L1 family protein	rplD	1.035	4.44E-01
MSMEG_1438	ribosomal protein L23	rplW	0.967	4.67E-01
MSMEG_1439	ribosomal protein L2	rplB	1.071	6.33E-01
MSMEG_1440	ribosomal protein S19	rpsS	1.124	5.68E-02
MSMEG_1441	50S ribosomal protein L22	NA	1.136	1.01E-01
MSMEG_1442	ribosomal protein S3	rpsC	1.105	1.80E-01
MSMEG_1443	ribosomal protein L16	rplP	1.068	5.12E-01
MSMEG_1444	ribosomal protein L29	rpmC	1.035	5.10E-01
MSMEG_1445	30S ribosomal protein S17	NA	1.401	8.45E-03
MSMEG_1446	NTP pyrophosphohydrolase	NA	1.588	3.91E-03
MSMEG_1447	transcriptional regulator, MerR family protein	NA	1.492	2.27E-02
MSMEG_1448	integral membrane transporter	NA	1.509	3.57E-02
MSMEG_1449	fasciclin domain protein; this gene contains a frame shift which is not the result of seq	NA	0.915	8.03E-01
MSMEG_1450	hypothetical protein	NA	1.048	6.21E-01
MSMEG_1451	arylsulfatase	NA	0.892	2.57E-01
MSMEG_1452	sulfatase-modifying factor 1	NA	1.151	1.99E-01
MSMEG_1453	Citrate transporter	NA	1.273	3.33E-01
MSMEG_1454	hypothetical protein	NA	1.124	7.30E-01
MSMEG_1455	putative multidrug resistance protein	NA	1.058	8.10E-01
MSMEG_1456	hypothetical protein	NA	1.424	9.36E-02
MSMEG_1457	conserved hypothetical protein	NA	0.898	4.36E-01
MSMEG_1458	tena/thi-4 family protein	NA	0.987	9.44E-01
MSMEG_1459	Rieske [2Fe-2S] domain protein	NA	1.134	5.02E-01
MSMEG_1460	Pyridine nucleotide-disulphide oxidoreductase	NA	1.117	6.46E-01
MSMEG_1461	5-oxovalerate dehydrogenase	NA	1.019	3.09E-01

MSMEG_1462	ferredoxin	NA	0.840	1.40E-01
MSMEG_1463	gamma-glutamyltranspeptidase	NA	1.022	9.33E-01
MSMEG_1464	translation initiation inhibitor	NA	1.030	8.03E-01
MSMEG_1465	ribosomal protein L14	rplN	1.244	1.43E-03
MSMEG_1466	ribosomal protein L24	rplX	1.183	9.87E-03
MSMEG_1467	50S ribosomal protein L5	NA	1.295	1.29E-01
MSMEG_1468	ribosomal protein S14p/S29e	rpsN	1.248	3.35E-02
MSMEG_1469	ribosomal protein S8	rpsH	1.092	3.04E-01
MSMEG_1470	50S ribosomal protein L6	NA	1.125	5.57E-01
MSMEG_1471	ribosomal protein L18	rplR	1.199	5.72E-02
MSMEG_1472	ribosomal protein S5	rpsE	1.007	8.35E-01
MSMEG_1473	ribosomal protein L30	rpmD	1.193	1.87E-03
MSMEG_1474	ribosomal protein L15	rplO	1.064	4.56E-01
MSMEG_1475	conserved hypothetical protein	NA	1.201	7.57E-02
MSMEG_1476	signal peptide peptidase SppA, 67K type	sppA	0.985	8.13E-01
MSMEG_1477	major facilitator superfamily protein	NA	0.853	2.31E-02
MSMEG_1478	transporter, LysE family protein	NA	0.938	1.39E-01
MSMEG_1479	methyltransferase, putative, family protein	NA	1.020	6.70E-01
MSMEG_1480	methyltransferase	NA	1.109	6.21E-01
MSMEG_1481	methyltransferase	NA	1.100	5.06E-01
MSMEG_1482	methyltransferase	NA	0.998	9.81E-01
MSMEG_1483	preprotein translocase, SecY subunit	NA	0.942	6.34E-02
MSMEG_1484	adenylate kinase	NA	0.938	2.97E-01
MSMEG_1485	methionine aminopeptidase, type I	map	0.911	3.83E-02
MSMEG_1486	RNA polymerase sigma-70 factor	NA	0.947	5.17E-01
MSMEG_1487	conserved hypothetical protein	NA	0.957	3.74E-01
MSMEG_1488	acetolactate synthase	NA	0.944	7.33E-01
MSMEG_1489	conserved hypothetical protein	NA	1.444	6.05E-01
MSMEG_1490	3-oxoacyl-ACP synthase III	NA	1.094	6.03E-01
MSMEG_1491	histidinol-phosphate aminotransferase 2	NA	1.167	2.70E-01
MSMEG_1492	transcriptional regulator, MarR family protein	NA	1.168	2.32E-01

MSMEG_1493	sensor histidine kinase	NA	1.129	3.90E-01
MSMEG_1493	sensor histidine kinase	NA	1.688	9.13E-02
MSMEG_1494	transcriptional regulatory protein DegU	NA	1.235	1.38E-01
MSMEG_1495	HAD-superfamily protein hydrolase subfamily protein IA, variant 3, putative	NA	0.915	5.70E-01
MSMEG_1496	3-hydroxyisobutyrate dehydrogenase	mmsB	1.288	4.14E-01
MSMEG_1497	acyl-CoA dehydrogenase family protein member 8	NA	0.836	9.99E-02
MSMEG_1498	methylmalonate-semialdehyde dehydrogenase	mmsA	0.871	4.09E-01
MSMEG_1499	oxygenase	NA	1.044	7.02E-01
MSMEG_1500	TetR family protein transcriptional regulatory protein	NA	0.899	4.08E-01
MSMEG_1501	methyltransferase, putative, family protein	NA	1.068	8.40E-01
MSMEG_1502	ABC transporter, ATP-binding protein	NA	0.978	4.79E-01
MSMEG_1503	probable antibiotic-transport integral membrane leucine and valine rich protein abc tr	NA	0.864	9.89E-02
MSMEG_1504	probable antibiotic-transport integral membrane leucine and alanine and valine rich p	NA	1.165	4.62E-01
MSMEG_1505	integral membrane protein	NA	1.516	4.52E-01
MSMEG_1506	transcriptional regulator, TetR family protein	NA	1.109	4.40E-01
MSMEG_1507	D-aminopeptidase	NA	1.010	7.93E-01
MSMEG_1508	amino acid permease-associated region	NA	0.945	4.06E-01
MSMEG_1509	TetR-family protein transcriptional regulator	NA	1.286	1.63E-01
MSMEG_1510	dTDP-4-dehydrorhamnose 3,5-epimerase	NA	1.227	2.21E-02
MSMEG_1511	putative oxidoreductase	NA	1.359	1.59E-02
MSMEG_1512	dTDP-glucose 4,6-dehydratase	rfbB	1.090	2.33E-01
MSMEG_1513	conserved hypothetical protein	NA	0.853	3.00E-02
MSMEG_1514	conserved hypothetical protein	NA	1.240	1.01E-01
MSMEG_1515	two-component sensor histidine kinase	NA	0.955	5.75E-01
MSMEG_1516	thioredoxin reductase	NA	1.338	7.18E-02
MSMEG_1517	spfh domain/band 7 family protein, putative	NA	0.874	8.22E-02
MSMEG_1518	hypothetical protein	NA	1.034	6.42E-01
MSMEG_1519	translation initiation factor IF-1	infA	1.138	6.68E-01
MSMEG_1520	ribosomal protein L36	rpmJ	1.008	9.31E-01
MSMEG_1521	ribosomal protein S13p/S18e	rpsM	0.984	8.59E-01
MSMEG_1522	ribosomal protein S11	rpsK	0.990	5.59E-01

MSMEG_1523	ribosomal protein S4	rpsD	1.033	5.73E-01
MSMEG_1524	DNA-directed RNA polymerase, alpha subunit	rpoA	1.052	2.98E-01
MSMEG_1525	50S ribosomal protein L17	NA	0.871	2.07E-02
MSMEG_1526	probable cutinase	NA	1.166	3.85E-02
MSMEG_1527	tRNA pseudouridine synthase A	truA	1.406	3.83E-02
MSMEG_1528	cutinase	NA	1.245	1.15E-01
MSMEG_1529	serine esterase, cutinase family protein	NA	1.549	1.71E-03
MSMEG_1530	integral membrane protein	NA	2.842	4.23E-03
MSMEG_1531	conserved hypothetical protein	NA	1.311	4.12E-02
MSMEG_1532	antibiotic biosynthesis monooxygenase	NA	1.441	3.48E-01
MSMEG_1533	subtilase family protein	NA	1.140	5.15E-01
MSMEG_1534	probable conserved membrane protein	NA	1.291	2.17E-01
MSMEG_1535	conserved hypothetical protein	NA	1.280	1.58E-01
MSMEG_1536	ftsk/spoiiie family protein	NA	0.860	8.24E-02
MSMEG_1537	conserved hypothetical protein	NA	1.234	6.10E-01
MSMEG_1538	conserved hypothetical protein	NA	1.015	8.54E-01
MSMEG_1539	conserved hypothetical protein	NA	0.488	2.17E-02
MSMEG_1540	ATP-dependent RNA helicase	NA	1.683	4.24E-02
MSMEG_1541	hypothetical protein	NA	1.212	4.25E-01
MSMEG_1542	transcriptional regulator	NA	0.812	2.65E-02
MSMEG_1543	eptc-inducible aldehyde dehydrogenase	NA	0.459	4.69E-03
MSMEG_1544	PduO protein	NA	0.742	2.08E-01
MSMEG_1545	conserved hypothetical protein	NA	0.894	1.53E-01
MSMEG_1546	coenzyme B12-dependent glycerol dehydrogenase small subunit	NA	0.506	1.31E-03
MSMEG_1547	glycerol dehydratase large subunit	NA	0.494	2.14E-03
MSMEG_1548	propanediol utilization: dehydratase, medium subunit	NA	0.508	1.01E-02
MSMEG_1549	glycerol dehydratase reactivation factor large subunit; this gene contains a frame shift	NA	0.597	1.57E-02
MSMEG_1550	PduH protein	NA	0.661	2.13E-01
MSMEG_1551	hypothetical protein	NA	1.105	5.65E-01
MSMEG_1552	ethanolamine permease	eat	0.840	6.46E-05
MSMEG_1553	ethanolamine ammonia-lyase, large subunit	eutB	0.867	2.70E-01

MSMEG_1554	ethanolamine ammonia-lyase, light chain	eutC	0.720	5.76E-02
MSMEG_1555	conserved hypothetical protein, authentic frameshift; this gene contains a frame shift	NA	1.235	9.14E-02
MSMEG_1556	ribosomal protein L13	rplM	1.032	7.32E-01
MSMEG_1557	ribosomal protein S9	rpsI	1.025	2.04E-01
MSMEG_1558	conserved hypothetical protein	NA	0.967	7.56E-01
MSMEG_1559	phosphoglucosamine mutase	glmM	1.111	1.35E-01
MSMEG_1560	conserved hypothetical protein	NA	1.791	1.45E-02
MSMEG_1561	LysR-family protein trancsriptional regulator	NA	1.019	7.34E-01
MSMEG_1562	conserved hypothetical alanine and proline rich protein; this gene contains a frame shi	NA	1.042	6.53E-01
MSMEG_1562	conserved hypothetical alanine and proline rich protein; this gene contains a frame shi	NA	1.625	9.13E-03
MSMEG_1563	short-chain dehydrogenase/reductase SDR	NA	1.008	8.69E-01
MSMEG_1564	lignostilbene-alpha,beta-dioxygenase	NA	1.164	2.97E-01
MSMEG_1565	transcriptional regulator, TetR family protein	NA	0.953	2.14E-01
MSMEG_1566	oxidoreductase	NA	0.997	9.74E-01
MSMEG_1567	conserved hypothetical protein	NA	1.252	1.09E-01
MSMEG_1568	glucosamine--fructose-6-phosphate aminotransferase, isomerizing	glmS	1.000	9.98E-01
MSMEG_1569	hypothetical protein	NA	1.042	4.53E-01
MSMEG_1570	carboxylesterase	NA	1.111	6.41E-01
MSMEG_1571	integral membrane protein	NA	1.968	4.05E-01
MSMEG_1572	transcriptional regulator, GntR family protein	NA	1.947	3.25E-01
MSMEG_1573	carbohydrate kinase family protein	NA	0.881	6.11E-02
MSMEG_1574	glutamate decarboxylase	NA	0.903	2.61E-01
MSMEG_1575	alanine racemase	alr	1.237	1.55E-01
MSMEG_1576	alpha/beta hydrolase fold	NA	1.096	3.22E-01
MSMEG_1577	conserved hypothetical protein	NA	0.962	3.78E-01
MSMEG_1578	peptidase M22, glycoprotease	NA	1.059	3.37E-01
MSMEG_1579	ribosomal-protein-alanine acetyltransferase	rimI	0.943	2.98E-01
MSMEG_1580	O-sialoglycoprotein endopeptidase	NA	1.036	7.62E-01
MSMEG_1581	conserved hypothetical protein	NA	0.941	1.50E-01
MSMEG_1582	chaperonin GroS	groS	0.677	8.91E-04
MSMEG_1583	chaperonin GroL	groL	0.669	1.44E-05

MSMEG_1584	hypothetical protein	NA	1.015	8.55E-01
MSMEG_1585	cupin domain protein	NA	1.001	9.92E-01
MSMEG_1586	beta-lactamase	NA	0.944	2.22E-01
MSMEG_1587	alpha/beta hydrolase fold	NA	1.262	2.49E-01
MSMEG_1588	conserved hypothetical protein	NA	1.718	3.80E-01
MSMEG_1589	hypothetical protein	NA	1.014	8.68E-01
MSMEG_1590	hypothetical protein	NA	1.168	6.49E-01
MSMEG_1591	TnpC protein	NA	0.902	5.13E-01
MSMEG_1591	TnpC protein	NA	1.757	2.01E-01
MSMEG_1592	hypothetical protein	NA	0.854	1.00E-02
MSMEG_1593	hypothetical protein	NA	1.121	7.02E-01
MSMEG_1594	enoyl-CoA hydratase	NA	0.997	9.57E-01
MSMEG_1595	putative oxidoreductase	NA	1.733	2.61E-01
MSMEG_1596	transcriptional regulator	NA	1.263	3.08E-02
MSMEG_1597	Transcription factor WhiB	NA	1.017	9.00E-01
MSMEG_1598	conserved hypothetical protein	NA	0.951	3.68E-01
MSMEG_1599	RNA polymerase sigma-70 factor	NA	1.203	1.10E-02
MSMEG_1600	conserved hypothetical protein	NA	1.215	1.68E-02
MSMEG_1601	conserved hypothetical protein	NA	0.883	7.64E-02
MSMEG_1602	inosine-5'-monophosphate dehydrogenase	guaB	1.118	1.81E-01
MSMEG_1603	IMP dehydrogenase family protein	NA	1.159	2.95E-01
MSMEG_1604	FAD dependent oxidoreductase	NA	1.135	1.51E-02
MSMEG_1605	phosphate transport system regulatory protein PhoU	phoU	1.467	2.10E-01
MSMEG_1606	benzoylformate decarboxylase	NA	0.958	6.93E-01
MSMEG_1607	putative tautomerase	NA	1.109	1.57E-01
MSMEG_1608	glycosyl transferase	NA	0.982	8.92E-01
MSMEG_1609	beta-phosphoglucomutase hydrolase; this gene contains a frame shift which is not the	NA	0.791	2.04E-01
MSMEG_1610	glutamine-hydrolyzing GMP synthase	NA	0.998	9.81E-01
MSMEG_1611	transcriptional regulator, TetR family protein, putative	NA	1.056	4.90E-01
MSMEG_1612	extracellular solute-binding protein, family protein 3	NA	1.083	4.03E-01
MSMEG_1613	ABC polar amino acid transporter, inner membrane subunit	NA	0.787	1.91E-02

MSMEG_1614	glutamine transport ATP-binding protein GlnQ	NA	1.014	8.06E-01
MSMEG_1615	gamma-glutamyltranspeptidase	ggt	0.941	6.97E-01
MSMEG_1616	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	0.944	5.16E-01
MSMEG_1617	kumamolisin	NA	1.139	1.01E-01
MSMEG_1618	hypothetical protein	NA	1.139	3.28E-02
MSMEG_1619	hypothetical protein	NA	1.226	5.44E-01
MSMEG_1620	conserved hypothetical protein	NA	1.381	3.28E-01
MSMEG_1621	pyrimidine-specific ribonucleoside hydrolase RihA	NA	0.951	2.67E-01
MSMEG_1622	putative DNA repair polymerase	NA	1.062	7.56E-01
MSMEG_1623	short chain dehydrogenase	NA	1.031	8.44E-01
MSMEG_1624	universal stress protein family protein	NA	1.512	2.84E-01
MSMEG_1625	amino acid transporter, putative	NA	0.872	3.06E-01
MSMEG_1626	putative DNA-binding protein	NA	1.073	3.64E-01
MSMEG_1627	hypothetical protein	NA	0.770	3.23E-02
MSMEG_1628	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.054	4.38E-01
MSMEG_1629	hypothetical protein	NA	0.801	6.20E-03
MSMEG_1630	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	NA	1.065	7.34E-01
MSMEG_1631	DNA-binding protein	NA	1.152	4.76E-01
MSMEG_1632	hypothetical protein	NA	0.838	1.83E-02
MSMEG_1633	DNA polymerase III, alpha subunit, putative	NA	1.164	9.54E-02
MSMEG_1634	probable forkhead-associated protein	NA	0.706	1.27E-03
MSMEG_1635	nitroreductase family protein	NA	0.867	3.02E-02
MSMEG_1636	RNA methyltransferase, TrmH family protein, group 2	NA	1.066	6.20E-01
MSMEG_1637	periplasmic sensor signal transduction histidine kinase	NA	0.919	8.32E-02
MSMEG_1638	Roadblock/LC7 domain protein	NA	1.073	7.06E-02
MSMEG_1639	conserved hypothetical protein	NA	1.020	7.65E-01
MSMEG_1640	ATP/GTP-binding protein	NA	1.016	7.99E-01
MSMEG_1641	conserved hypothetical protein	NA	1.090	1.44E-01
MSMEG_1642	ABC transporter, ATP-binding protein	NA	1.133	1.22E-01
MSMEG_1643	hypothetical protein	NA	0.990	8.97E-01
MSMEG_1644	hypothetical protein	NA	1.144	1.30E-01

MSMEG_1645	NADH:flavin oxidoreductase/nadh oxidase	NA	1.166	1.51E-01
MSMEG_1646	ribosomal RNA adenine dimethylase family protein	NA	1.764	5.74E-02
MSMEG_1647	tetrahydrofolate dehydrogenase/cyclohydrolase FolD	NA	1.062	1.79E-01
MSMEG_1648	putative transcriptional regulator	NA	1.158	3.28E-01
MSMEG_1649	FAD dependent oxidoreductase	NA	0.976	7.88E-01
MSMEG_1650	methyltransferase type 11	NA	0.796	2.99E-02
MSMEG_1651	homoserine O-acetyltransferase	metX	0.827	5.44E-02
MSMEG_1652	O-acetylhomoserine sulfhydrylase	NA	0.899	1.66E-01
MSMEG_1653	hypothetical protein	NA	1.273	4.79E-01
MSMEG_1654	isocitrate dehydrogenase, NADP-dependent	NA	0.930	3.52E-01
MSMEG_1655	hydrolase, alpha/beta fold family protein, putative	NA	0.777	5.83E-03
MSMEG_1656	exodeoxyribonuclease III	xth	0.952	2.92E-01
MSMEG_1657	tryptophanyl-tRNA synthetase	trpS	0.937	1.37E-01
MSMEG_1658	ribonuclease, putative	NA	1.087	9.31E-02
MSMEG_1659	multidrug resistance protein, SMR family protein	NA	1.334	9.34E-02
MSMEG_1660	oxidoreductase, 2-nitropropane dioxygenase family protein	NA	1.151	1.33E-02
MSMEG_1661	D-alanyl-D-alanine carboxypeptidase	NA	0.851	3.72E-03
MSMEG_1662	taurine-pyruvate aminotransferase	NA	0.796	1.50E-02
MSMEG_1663	transcriptional regulator, AsnC family protein	NA	0.747	4.06E-04
MSMEG_1664	hypothetical protein	NA	0.808	4.67E-02
MSMEG_1665	aldehyde dehydrogenase (NAD) family protein	NA	0.993	8.14E-01
MSMEG_1666	RNA polymerase sigma-70 factor	NA	1.034	6.79E-01
MSMEG_1667	IS110 family transposase, truncation; identified by similarity to OMNI:MT3430	NA	1.493	1.64E-01
MSMEG_1668	pyridoxamine 5'-phosphate oxidase family protein	NA	1.044	3.23E-01
MSMEG_1669	succinate dehydrogenase, iron-sulfur protein	sdhB	0.931	3.14E-01
MSMEG_1670	succinate dehydrogenase, flavoprotein subunit	sdhA	0.739	7.20E-03
MSMEG_1671	succinate dehydrogenase hydrophobic membrane anchor protein SdhD	NA	0.929	1.27E-02
MSMEG_1672	succinate dehydrogenase, cytochrome b556 subunit	sdhC	0.788	4.62E-02
MSMEG_1673	cytidine deaminase	cdd	1.064	4.33E-01
MSMEG_1674	hypothetical protein	NA	0.820	2.61E-01
MSMEG_1675	pyrimidine-nucleoside phosphorylase	NA	1.035	6.15E-01

MSMEG_1676	adenosine deaminase	add	0.925	2.59E-01
MSMEG_1677	aspartate ammonia-lyase	aspA	0.643	8.45E-04
MSMEG_1678	transcriptional regulator, LysR family protein	NA	0.917	2.25E-01
MSMEG_1679	AmiB	NA	0.586	3.49E-04
MSMEG_1680	conserved hypothetical protein	NA	0.608	9.37E-04
MSMEG_1681	endoribonuclease L-PSP superfamily protein	NA	0.566	6.89E-04
MSMEG_1682	flavin-containing monooxygenase FMO	NA	0.694	1.08E-02
MSMEG_1683	cytosine/purine/uracil/thiamine/allantoin permease family protein	NA	0.711	7.40E-03
MSMEG_1684	conserved hypothetical protein	NA	0.839	2.10E-02
MSMEG_1685	hypothetical protein	NA	1.126	4.83E-01
MSMEG_1686	NPL/P60-family protein secreted protein	NA	0.943	6.88E-01
MSMEG_1687	hypothetical protein	NA	1.107	5.04E-01
MSMEG_1688	cupin domain protein	NA	1.065	6.01E-01
MSMEG_1689	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.020	3.60E-01
MSMEG_1690	putative ECF sigma factor RpoE1	NA	1.276	5.65E-01
MSMEG_1691	transcriptional regulatory protein	NA	0.919	5.13E-01
MSMEG_1692	ECF-family protein RNA polymerase sigma factor	NA	1.032	7.82E-01
MSMEG_1693	succinate dehydrogenase [ubiquinone] flavoprotein subunit	NA	0.946	7.19E-01
MSMEG_1694	uracil phosphoribosyltransferase	upp	1.005	8.99E-01
MSMEG_1695	phosphoglucomutase/phosphomannomutase	NA	1.153	3.45E-01
MSMEG_1696	regulatory protein, MarR	NA	1.233	1.21E-01
MSMEG_1697	hypothetical protein	NA	1.398	4.65E-01
MSMEG_1698	putative ammonia monooxygenase superfamily protein	NA	2.174	2.22E-01
MSMEG_1699	pentachlorophenol 4-monooxygenase	NA	0.980	9.32E-01
MSMEG_1700	TetR-family protein transcriptional regulator	NA	1.184	1.71E-01
MSMEG_1701	purine nucleotide phosphorylase	NA	0.997	9.74E-01
MSMEG_1702	amidohydrolase	NA	1.198	3.98E-02
MSMEG_1703	amidohydrolase	NA	1.224	2.13E-01
MSMEG_1704	ABC transporter	NA	0.615	2.66E-02
MSMEG_1705	D-xylose transport ATP-binding protein XylG	NA	0.679	2.53E-02
MSMEG_1706	xylose transport system permease protein XylH	NA	0.707	1.76E-02

MSMEG_1707	phosphatase YfbT	NA	1.241	7.30E-02
MSMEG_1708	ribose operon repressor, putative	NA	1.028	7.59E-01
MSMEG_1709	inner membrane ABC transporter permease protein YjfF	NA	0.939	7.50E-01
MSMEG_1710	ribose transport system permease protein RbsC	NA	0.786	6.67E-02
MSMEG_1711	ATP binding protein of ABC transporter	NA	0.539	3.03E-02
MSMEG_1712	ABC transporter periplasmic-binding protein YtfQ	NA	0.305	8.23E-04
MSMEG_1713	L-ribulokinase	araB	0.722	3.19E-01
MSMEG_1714	L-ribulose-5-phosphate 4-epimerase UlaF	NA	0.778	1.84E-01
MSMEG_1715	L-arabinose isomerase	araA	0.674	1.80E-01
MSMEG_1716	IS3 family protein element, transposase orfA	NA	0.855	2.27E-01
MSMEG_1717	ISMsm8, transposase	NA	1.074	5.68E-01
MSMEG_1718	This gene is disrupted by an IS element.; IS3 family element, transposase orfB, interru	NA	1.080	2.00E-02
MSMEG_1719	This gene is disrupted by an IS element.; IS3 family element, transposase orfB, interru	NA	1.089	1.52E-01
MSMEG_1721	IS1137, transposase orfB	NA	1.113	5.91E-01
MSMEG_1722	hypothetical protein	NA	0.883	2.95E-02
MSMEG_1723	hypothetical protein	NA	1.172	7.73E-02
MSMEG_1724	conserved hypothetical protein	NA	1.032	4.31E-01
MSMEG_1729	This gene is disrupted by an ISMsm1 element.; ISMsm5, transposase, interruption-N; i	NA	0.936	3.09E-01
MSMEG_1731	IS6120, transposase	NA	0.959	4.51E-01
MSMEG_1731	IS6120, transposase	NA	1.052	1.25E-01
MSMEG_1731	IS6120, transposase	NA	1.225	3.11E-02
MSMEG_1732	Transposase IS116/IS110/IS902 family protein	NA	1.052	7.74E-01
MSMEG_1733	conserved hypothetical protein	NA	1.041	5.19E-01
MSMEG_1734	conserved hypothetical protein	NA	1.058	9.64E-02
MSMEG_1735	dihydrolipoamide dehydrogenase	NA	1.104	3.44E-01
MSMEG_1736	glycerol-3-phosphate dehydrogenase 2	NA	1.074	7.95E-02
MSMEG_1737	RNA pseudouridine synthase family protein	NA	1.036	5.43E-01
MSMEG_1738	probable conserved transmembrane protein	NA	1.388	2.47E-02
MSMEG_1739	enoyl-CoA hydratase/isomerase family protein	NA	0.991	9.54E-01
MSMEG_1740	dehydrogenase/reductase SDR family protein member 4	NA	0.788	1.91E-02
MSMEG_1741	TetR-family protein transcriptional regulator	NA	1.104	3.75E-01

MSMEG_1742	oxidoreductase	NA	1.192	3.05E-01
MSMEG_1743	Fatty acid desaturase	NA	1.437	2.12E-03
MSMEG_1744	hypothetical protein	NA	1.052	4.01E-01
MSMEG_1745	transcriptional regulator	NA	1.021	7.58E-01
MSMEG_1746	6-hydroxy-D-nicotine oxidase	NA	1.110	4.94E-01
MSMEG_1747	RNA polymerase sigma-70 factor	NA	0.850	3.82E-01
MSMEG_1749	putative monooxygenase	NA	2.117	2.24E-02
MSMEG_1750	hypothetical protein	NA	1.234	2.30E-01
MSMEG_1750	hypothetical protein	NA	2.246	1.64E-01
MSMEG_1751	norsolorinic acid reductase	NA	1.049	5.05E-01
MSMEG_1752	hypothetical protein	NA	1.063	4.83E-01
MSMEG_1753	MTA/SAH nucleosidase	mtnN	0.883	3.18E-01
MSMEG_1754	conserved hypothetical protein	NA	1.109	4.82E-01
MSMEG_1755	anti-sigm factor, ChrR	NA	1.472	6.95E-02
MSMEG_1756	endonuclease VIII and dna n-glycosylase with an ap lyase activity	NA	1.130	5.28E-01
MSMEG_1757	DEAD/DEAH box helicase	NA	0.997	9.91E-01
MSMEG_1758	hypothetical protein	NA	1.036	8.91E-01
MSMEG_1759	hypothetical protein	NA	0.902	6.16E-01
MSMEG_1760	short-chain dehydrogenase/reductase SDR	NA	1.124	1.49E-01
MSMEG_1761	integral membrane protein	NA	0.919	4.58E-01
MSMEG_1762	piperideine-6-carboxylic acid dehydrogenase	NA	1.337	4.24E-01
MSMEG_1763	leucine-responsive regulatory protein	NA	1.177	1.67E-01
MSMEG_1764	L-lysine-epsilon aminotransferase	NA	1.318	1.74E-01
MSMEG_1765	restriction endonuclease family protein	NA	1.274	4.22E-01
MSMEG_1766	conserved hypothetical protein	NA	1.173	5.70E-01
MSMEG_1767	conserved hypothetical protein	NA	1.140	6.60E-01
MSMEG_1768	conserved hypothetical protein	NA	1.400	4.68E-01
MSMEG_1769	UsfY protein	NA	1.038	8.39E-01
MSMEG_1770	conserved hypothetical protein	NA	1.443	4.91E-01
MSMEG_1771	methylase, putative	NA	1.294	4.99E-01
MSMEG_1772	conserved hypothetical protein	NA	1.199	4.24E-01

MSMEG_1773	conserved hypothetical protein	NA	1.130	6.42E-01
MSMEG_1774	conserved hypothetical protein	NA	1.543	3.40E-01
MSMEG_1775	cytochrome P450 monooxygenase	NA	1.736	2.89E-01
MSMEG_1776	ribonuclease Z	NA	1.457	1.99E-01
MSMEG_1777	UsfY protein	NA	1.132	6.85E-01
MSMEG_1778	conserved hypothetical protein	NA	1.064	1.56E-01
MSMEG_1779	hypothetical protein	NA	1.611	1.84E-01
MSMEG_1780	hypothetical protein	NA	1.037	3.90E-01
MSMEG_1781	hypothetical protein	NA	1.076	7.30E-01
MSMEG_1782	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.129	7.47E-01
MSMEG_1783	hypothetical protein	NA	2.040	2.96E-01
MSMEG_1784	type I topoisomerase	NA	1.139	3.54E-01
MSMEG_1785	hypothetical protein	NA	1.187	2.59E-01
MSMEG_1786	stas domain, putative	NA	0.715	5.41E-02
MSMEG_1787	RsbW protein	NA	1.215	6.51E-01
MSMEG_1788	conserved hypothetical protein	NA	1.118	6.85E-01
MSMEG_1789	conserved hypothetical protein	NA	1.086	6.69E-01
MSMEG_1790	conserved hypothetical protein	NA	1.108	7.53E-01
MSMEG_1791	UsfY protein	NA	1.162	2.71E-01
MSMEG_1792	conserved hypothetical protein	NA	1.046	9.00E-01
MSMEG_1793	membrane protein	NA	0.905	4.36E-02
MSMEG_1794	dehydrogenase	NA	1.577	3.34E-01
MSMEG_1795	2-deoxy-scyllo-inosamine dehydrogenase	NA	0.899	5.04E-01
MSMEG_1796	membrane protein	NA	1.087	7.53E-01
MSMEG_1797	salicylate esterase	NA	3.847	3.65E-01
MSMEG_1798	major facilitator superfamily protein	NA	0.991	9.70E-01
MSMEG_1799	transcriptional regulator	NA	0.890	1.51E-01
MSMEG_1800	hypothetical protein	NA	1.097	4.24E-01
MSMEG_1801	hypothetical protein	NA	1.354	5.78E-01
MSMEG_1802	ChaB protein	NA	1.164	5.73E-01
MSMEG_1803	RsbW protein	NA	0.870	1.62E-02

MSMEG_1804	RNA polymerase sigma-F factor	NA	0.922	5.34E-02
MSMEG_1805	conserved hypothetical protein	NA	1.252	2.20E-01
MSMEG_1806	conserved hypothetical protein	NA	1.084	4.41E-01
MSMEG_1807	acetyl-/propionyl-coenzyme A carboxylase alpha chain	NA	0.915	1.53E-01
MSMEG_1808	Fe-S metabolism associated SufE	NA	0.922	1.41E-01
MSMEG_1809	putative thiosulfate sulfurtransferase	NA	0.907	6.09E-02
MSMEG_1810	hypothetical protein	NA	1.547	5.40E-02
MSMEG_1811	septum formation protein Maf	maf	1.154	2.83E-01
MSMEG_1812	conserved hypothetical protein	NA	1.076	5.13E-01
MSMEG_1813	propionyl-CoA carboxylase beta chain	NA	0.909	3.25E-01
MSMEG_1814	hypothetical protein	NA	1.062	7.19E-01
MSMEG_1815	hypothetical protein	NA	1.042	5.61E-01
MSMEG_1816	hypothetical protein; this region contains one or more premature stops and/or frames	NA	0.912	4.90E-01
MSMEG_1816	hypothetical protein; this region contains one or more premature stops and/or frames	NA	2.671	2.81E-01
MSMEG_1817	probable conserved transmembrane protein	NA	1.282	1.12E-01
MSMEG_1818	Bacterial membrane flanked domain protein	NA	1.066	6.20E-01
MSMEG_1819	phosphoribosylaminoimidazole carboxylase, ATPase subunit	purK	1.017	5.92E-01
MSMEG_1820	phosphoribosylaminoimidazole carboxylase, catalytic subunit	purE	1.081	1.29E-01
MSMEG_1821	acyl-CoA dehydrogenase	NA	1.001	9.78E-01
MSMEG_1822	biotin-[acetyl-CoA-carboxylase] ligase	NA	1.337	8.34E-02
MSMEG_1823	conserved hypothetical protein	NA	1.025	5.66E-01
MSMEG_1824	transcriptional regulator, LytR family protein	NA	0.891	2.20E-01
MSMEG_1825	dTDP-4-dehydrorhamnose reductase	rfbD	1.151	1.21E-01
MSMEG_1826	dTDP-RhA:a-D-GlcNAc-diphosphoryl polyprenol, a-3-L-rhamnosyl transferase	NA	1.332	1.75E-02
MSMEG_1827	hydrolase, nudix family protein, putative	NA	0.974	8.93E-01
MSMEG_1828	Nucleotidyl transferase; this gene contains a frame shift which is not the result of seq	NA	1.222	2.89E-02
MSMEG_1829	F420-0:gamma-glutamyl ligase	NA	0.987	8.65E-01
MSMEG_1830	lppg:fo 2-phospho-l-lactate transferase	cofD	0.947	4.40E-01
MSMEG_1831	Transcription factor WhiB	NA	0.996	9.69E-01
MSMEG_1832	conserved hypothetical protein	NA	1.163	5.19E-01
MSMEG_1833	conserved hypothetical protein	NA	0.977	8.45E-01

MSMEG_1834	phosphomannomutase/phosphoglucomutase	NA	1.061	3.96E-02
MSMEG_1835	TobH protein	NA	1.024	5.35E-01
MSMEG_1836	mannose-6-phosphate isomerase, class I	manA	0.986	5.58E-01
MSMEG_1837	secreted protein	NA	0.906	1.52E-01
MSMEG_1838	cationic amino acid transporter	NA	0.930	2.57E-01
MSMEG_1839	alkane 1-monooxygenase	NA	0.749	6.17E-02
MSMEG_1840	rubredoxin	NA	0.920	3.47E-01
MSMEG_1841	rubredoxin	NA	1.406	2.84E-01
MSMEG_1842	transcriptional regulator, TetR family protein	NA	0.966	5.54E-01
MSMEG_1843	adenosylhomocysteinase; this gene contains a frame shift which is not the result of se	ahcY	0.908	2.62E-01
MSMEG_1843	adenosylhomocysteinase; this gene contains a frame shift which is not the result of se	ahcY	0.988	8.10E-01
MSMEG_1844	conserved hypothetical protein	NA	1.013	9.09E-01
MSMEG_1845	YghA protein	NA	1.264	4.03E-01
MSMEG_1846	polysulphide reductase, NrfD	NA	1.252	3.24E-01
MSMEG_1847	4Fe-4S ferredoxin, iron-sulfur binding protein	NA	1.004	9.53E-01
MSMEG_1848	formate dehydrogenase-O, major subunit; this gene contains a frame shift which is no	NA	0.870	3.27E-01
MSMEG_1848	formate dehydrogenase-O, major subunit; this gene contains a frame shift which is no	NA	1.415	1.64E-01
MSMEG_1849	selenocysteine-specific translation elongation factor	selB	1.042	8.87E-01
MSMEG_1850	L-seryl-tRNA selenium transferase	selA	0.996	9.68E-01
MSMEG_1852	selenide, water dikinase	selD	1.040	7.95E-01
MSMEG_1853	Na+/H+ antiporter NhaA; this gene contains a frame shift which is not the result of sec	NA	0.944	5.60E-01
MSMEG_1853	Na+/H+ antiporter NhaA; this gene contains a frame shift which is not the result of sec	NA	1.157	2.64E-01
MSMEG_1854	valosin containing protein-1	NA	0.974	5.86E-01
MSMEG_1855	tetratricopeptide repeat protein, putative	NA	1.197	2.02E-01
MSMEG_1856	hypothetical protein	NA	1.203	1.23E-01
MSMEG_1859	hypothetical protein	NA	2.142	4.52E-01
MSMEG_1860	hypothetical protein	NA	0.911	5.38E-01
MSMEG_1861	hypothetical protein	NA	0.829	7.28E-02
MSMEG_1862	transposase	NA	0.767	1.03E-03
MSMEG_1862	transposase	NA	0.829	5.94E-04
MSMEG_1863	putative transposase	NA	0.844	5.39E-02

MSMEG_1863	putative transposase	NA	0.880	1.03E-01
MSMEG_1864	transposase	NA	0.759	6.02E-02
MSMEG_1866	transposase B	NA	0.767	2.93E-02
MSMEG_1867	transposase	NA	0.835	6.73E-02
MSMEG_1868	hypothetical protein	NA	0.718	4.35E-03
MSMEG_1869	hypothetical protein	NA	0.716	1.14E-02
MSMEG_1870	conserved hypothetical protein	NA	1.839	5.02E-01
MSMEG_1871	conserved hypothetical protein	NA	1.019	6.59E-01
MSMEG_1872	conserved hypothetical protein	NA	1.017	8.37E-01
MSMEG_1873	thymidylate kinase	NA	0.877	2.17E-02
MSMEG_1874	DNA-binding response regulator MtrA	mtrA	0.873	1.97E-02
MSMEG_1875	sensor histidine kinase MtrB	NA	1.622	5.52E-01
MSMEG_1876	LpqB protein	NA	1.000	9.99E-01
MSMEG_1877	conserved hypothetical protein	NA	0.959	7.27E-01
MSMEG_1878	S30AE family protein	NA	0.675	1.63E-03
MSMEG_1879	hypothetical protein	NA	1.129	4.15E-01
MSMEG_1880	hypothetical alanine arginine proline rich protein	NA	1.097	4.47E-01
MSMEG_1881	preprotein translocase, SecA subunit	secA	1.049	7.21E-01
MSMEG_1882	acyltransferase, ws/dgat/mgat subfamily protein	NA	1.089	3.32E-01
MSMEG_1883	glycine betaine transporter OpuD	NA	1.162	9.98E-02
MSMEG_1884	conserved hypothetical protein	NA	1.139	6.62E-02
MSMEG_1885	2Fe-2S iron-sulfur cluster binding domain protein	NA	1.113	3.00E-01
MSMEG_1886	Fatty acid desaturase	NA	1.160	3.55E-01
MSMEG_1887	hypothetical protein	NA	1.359	1.02E-01
MSMEG_1888	methyltransferase	NA	0.949	3.16E-01
MSMEG_1889	putative ribosome small subunit-dependent GTPase RsgA	NA	1.026	7.42E-01
MSMEG_1890	3-phosphoshikimate 1-carboxyvinyltransferase	aroA	1.149	1.86E-01
MSMEG_1891	conserved hypothetical protein	NA	1.062	4.18E-01
MSMEG_1892	transferase	NA	1.069	2.69E-02
MSMEG_1893	UbiE/COQ5 methyltransferase	NA	0.874	6.13E-02
MSMEG_1894	short chain dehydrogenase	NA	0.938	2.60E-01

MSMEG_1895	HTH-type transcriptional regulator AlsR	NA	1.775	1.99E-01
MSMEG_1896	beta-ketothiolase	NA	0.905	1.00E-01
MSMEG_1897	3-oxoadipate enol-lactonase	pcaD	0.966	8.29E-01
MSMEG_1898	succinyl-CoA:3-ketoacid-coenzyme A transferase 1, precursor	NA	1.027	8.27E-01
MSMEG_1899	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B	NA	1.038	7.54E-01
MSMEG_1900	D-alanyl-D-alanine carboxypeptidase family protein	NA	1.004	9.32E-01
MSMEG_1900	D-alanyl-D-alanine carboxypeptidase family protein	NA	1.135	7.99E-02
MSMEG_1901	DNA-binding HTH domain containing protein, putative	NA	1.191	4.15E-01
MSMEG_1902	transcriptional regulator	NA	1.189	1.79E-01
MSMEG_1903	caib/baif family protein	NA	1.337	1.04E-01
MSMEG_1904	acyl-CoA dehydrogenase	NA	1.161	1.28E-01
MSMEG_1905	acyl-CoA dehydrogenase protein	NA	1.200	1.33E-01
MSMEG_1906	toluate 1,2-dioxygenase electron transfer component	NA	1.216	5.95E-01
MSMEG_1907	toluate 1,2-dioxygenase beta subunit	NA	1.133	3.36E-01
MSMEG_1908	benzoate 1,2-dioxygenase alpha subunit	NA	1.061	7.19E-01
MSMEG_1909	putative HTH-type transcriptional regulator YnfL	NA	0.844	5.04E-01
MSMEG_1910	muconate cycloisomerase	NA	0.944	7.32E-01
MSMEG_1911	catechol 1,2-dioxygenase	catA	0.698	3.93E-02
MSMEG_1912	muconolactone delta-isomerase 1	NA	0.849	8.55E-02
MSMEG_1913	YbaK/ebsC protein	ybaK	1.190	1.05E-01
MSMEG_1914	RNA polymerase sigma-70 factor, family protein	NA	0.965	8.11E-01
MSMEG_1915	anti-sigma factor, family protein	NA	1.062	5.20E-01
MSMEG_1916	hypothetical protein	NA	1.294	1.24E-01
MSMEG_1917	conserved domain protein	NA	0.954	3.60E-01
MSMEG_1918	sensor histidine kinase	NA	1.082	2.37E-01
MSMEG_1919	Transcription factor WhiB	NA	1.540	2.90E-01
MSMEG_1920	diacylglycerol kinase, catalytic region	NA	1.246	3.23E-02
MSMEG_1921	SEC-C motif domain protein	NA	1.246	2.39E-02
MSMEG_1922	3-dehydroquinate dehydratase, type II	aroQ	1.108	3.75E-02
MSMEG_1923	membrane protein	NA	1.312	1.42E-01
MSMEG_1924	N-acetyltransferase Ats1	NA	0.940	7.05E-01

MSMEG_1925	isochorismate synthase DhbC	NA	1.000	9.99E-01
MSMEG_1926	phosphoglycerate mutase family protein	NA	1.114	2.75E-01
MSMEG_1927	cobyrinic Acid a,c-diamide synthase	NA	0.909	1.62E-01
MSMEG_1928	regulatory protein	NA	1.235	4.33E-01
MSMEG_1929	conserved hypothetical protein	NA	1.017	9.05E-01
MSMEG_1930	DEAD/DEAH box helicase	NA	0.831	2.36E-02
MSMEG_1931	conserved hypothetical protein	NA	0.931	2.05E-02
MSMEG_1932	MmpS3 protein	NA	0.745	3.95E-03
MSMEG_1933	hypothetical protein	NA	1.004	9.36E-01
MSMEG_1934	ATP-binding protein	NA	1.046	8.24E-01
MSMEG_1935	TetR-family protein transcriptional regulator	NA	0.953	5.64E-01
MSMEG_1936	conserved hypothetical protein	NA	0.981	4.86E-01
MSMEG_1937	molybdopterin biosynthesis protein MoeB	NA	0.999	9.79E-01
MSMEG_1938	conserved hypothetical protein	NA	1.016	6.68E-01
MSMEG_1939	6-O-methylguanine DNA methyltransferase, DNA binding domain subfamily protein	NA	1.275	1.59E-02
MSMEG_1940	hydrolase, alpha/beta fold family protein	NA	1.283	4.55E-01
MSMEG_1941	helicase, UvrD/Rep family protein	NA	1.059	5.25E-01
MSMEG_1942	integral membrane protein	NA	0.999	9.75E-01
MSMEG_1943	ATP-dependent DNA helicase	NA	0.831	2.50E-02
MSMEG_1944	membrane protein	NA	0.970	2.14E-01
MSMEG_1945	ion channel membrane protein	NA	0.928	8.62E-02
MSMEG_1946	NADH pyrophosphatase	NA	1.110	1.91E-01
MSMEG_1947	conserved hypothetical protein	NA	1.257	2.03E-01
MSMEG_1948	hypothetical protein	NA	1.421	4.72E-01
MSMEG_1949	hypothetical protein	NA	1.747	2.33E-01
MSMEG_1950	conserved hypothetical protein	NA	1.358	4.11E-01
MSMEG_1951	conserved domain protein	NA	1.221	4.44E-01
MSMEG_1952	ATP-dependent DNA helicase	NA	1.257	8.63E-02
MSMEG_1953	transcription factor WhiB	NA	1.611	2.23E-02
MSMEG_1954	ABC1 family protein	NA	1.009	8.85E-01
MSMEG_1955	conserved hypothetical protein	NA	0.947	1.26E-01

MSMEG_1956	hypothetical protein	NA	1.214	2.97E-01
MSMEG_1957	conserved hypothetical protein	NA	0.919	1.51E-01
MSMEG_1958	PDZ domain family protein	NA	0.848	2.01E-02
MSMEG_1959	putative membrane protein	NA	0.871	1.67E-02
MSMEG_1960	hypothetical protein	NA	1.135	4.93E-02
MSMEG_1961	conserved hypothetical protein	NA	0.971	6.33E-01
MSMEG_1962	hypothetical protein	NA	0.973	6.50E-01
MSMEG_1963	putative transcriptional regulatory protein	NA	1.245	4.00E-01
MSMEG_1964	mitomycin radical oxidase	NA	1.165	5.61E-01
MSMEG_1966	hypothetical protein	NA	1.172	5.41E-01
MSMEG_1967	TetR-family protein transcriptional regulator	NA	1.204	3.14E-02
MSMEG_1968	putative oxidoreductase	NA	1.115	1.49E-01
MSMEG_1969	MerR-family protein transcriptional regulator	NA	1.455	9.44E-02
MSMEG_1970	sigma factor	NA	1.198	5.14E-01
MSMEG_1971	propane monooxygenase hydroxylase large subunit	NA	1.040	7.90E-01
MSMEG_1972	methane monooxygenase component C	NA	0.974	9.10E-01
MSMEG_1973	propane monooxygenase hydroxylase small subunit; this gene contains a frame shift w	NA	0.807	3.73E-01
MSMEG_1973	propane monooxygenase hydroxylase small subunit; this gene contains a frame shift w	NA	1.125	3.07E-01
MSMEG_1974	propane monooxygenase coupling protein	NA	1.285	2.25E-01
MSMEG_1975	amidohydrolase 2	NA	0.892	1.23E-01
MSMEG_1976	conserved hypothetical protein	NA	1.167	3.76E-01
MSMEG_1977	alcohol dehydrogenase	NA	0.960	7.50E-01
MSMEG_1978	chaperonin GroL	groL	0.897	2.50E-01
MSMEG_1979	antibiotic biosynthesis monooxygenase	NA	0.933	7.58E-02
MSMEG_1980	monooxygenase	NA	1.161	6.75E-02
MSMEG_1981	conserved hypothetical protein	NA	0.991	8.78E-01
MSMEG_1982	acyl-CoA synthase	NA	0.875	6.39E-02
MSMEG_1983	major facilitator family protein transporter	NA	1.005	8.75E-01
MSMEG_1984	haloacetate dehalogenase H-1	NA	0.990	8.41E-01
MSMEG_1985	transcriptional regulator, LysR family protein	NA	1.114	4.75E-01
MSMEG_1986	tartrate dehydrogenase	NA	0.940	7.37E-01

MSMEG_1987	conserved hypothetical protein	NA	1.487	2.82E-01
MSMEG_1988	conserved hypothetical protein	NA	0.953	8.03E-01
MSMEG_1989	phenoxybenzoate dioxygenase beta subunit	NA	1.307	1.59E-01
MSMEG_1990	conserved hypothetical protein	NA	1.033	2.78E-01
MSMEG_1991	isovaleryl-CoA dehydrogenase	NA	1.014	8.95E-01
MSMEG_1992	L-carnitine dehydratase/bile acid-inducible protein F	NA	1.185	4.18E-01
MSMEG_1993	MaoC like domain protein	NA	0.891	3.98E-01
MSMEG_1994	HpcH/HpaI aldolase	NA	1.147	4.51E-01
MSMEG_1995	transcriptional regulator MdcY family protein	NA	1.206	1.02E-01
MSMEG_1996	N5,N10- methylenetetrahydromethanopterin reductase-related protein	NA	1.253	6.06E-03
MSMEG_1997	N-acyl-D-glutamate amidohydrolase	NA	0.982	5.68E-01
MSMEG_1998	hydrolase, alpha/beta fold family protein	NA	1.013	9.03E-01
MSMEG_1999	hypothetical protein	NA	1.254	5.42E-01
MSMEG_2000	conserved hypothetical protein	NA	1.214	7.12E-02
MSMEG_2001	sugar transporter	NA	1.213	7.06E-01
MSMEG_2004	arabinose-proton symporter	NA	1.618	5.74E-02
MSMEG_2005	sugar phosphate isomerase/epimerase	NA	1.266	1.61E-01
MSMEG_2006	2,3-dihydroxybiphenyl 1,2-dioxygenase	NA	1.470	6.05E-02
MSMEG_2007	putative HpcE protein	NA	1.549	3.63E-03
MSMEG_2008	hypothetical protein	NA	0.928	4.52E-01
MSMEG_2009	regulatory protein GntR, HTH:GntR, C-	NA	1.333	5.94E-03
MSMEG_2010	stress responsive A/B Barrel Domain superfamily protein	NA	1.082	1.33E-01
MSMEG_2011	transcriptional regulator, LacI family protein	NA	1.426	3.70E-01
MSMEG_2012	histidinol dehydrogenase	hisD	1.296	3.97E-01
MSMEG_2013	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.389	4.04E-01
MSMEG_2014	molybdenum import ATP-binding protein ModC	NA	1.224	2.25E-01
MSMEG_2015	molybdate ABC transporter, permease protein	modB	1.088	4.08E-01
MSMEG_2016	molybdate ABC transporter, periplasmic molybdate-binding protein	modA	1.197	1.58E-01
MSMEG_2017	transcriptional regulator, MerR family protein	NA	1.121	1.29E-01
MSMEG_2018	cytochrome P450 107B1; this gene contains a frame shift which is not the result of seq	NA	1.392	2.48E-01
MSMEG_2019	short-chain dehydrogenase/reductase SDR	NA	1.138	1.50E-01

MSMEG_2020	hyi family protein, authentic frameshift; this gene contains a frame shift which is not tl	NA	1.137	3.59E-01
MSMEG_2021	lipopolysaccharide biosynthesis acyltransferase, M	NA	1.113	1.68E-01
MSMEG_2022	GntT protein, putative	NA	1.069	7.95E-01
MSMEG_2023	CAIB/BAIF family protein	NA	0.968	8.95E-01
MSMEG_2024	hydroxymethylglutaryl-CoA lyase	NA	1.418	5.09E-01
MSMEG_2025	putative IclR family protein transcriptional regulator	NA	0.979	3.36E-01
MSMEG_2026	short chain dehydrogenase	NA	1.164	1.01E-01
MSMEG_2027	conserved hypothetical protein TIGR00026	NA	1.866	4.95E-02
MSMEG_2028	chloramphenicol resistance protein	NA	1.057	3.13E-01
MSMEG_2029	3-ketoacyl-ACP/CoA redutase	NA	1.015	8.81E-01
MSMEG_2030	transcriptional regulator, TetR family protein	NA	1.094	3.51E-01
MSMEG_2031	hypothetical protein	NA	1.347	1.05E-01
MSMEG_2032	conserved hypothetical protein	NA	0.911	3.12E-01
MSMEG_2033	oxidoreductase, zinc-binding dehydrogenase family protein	NA	0.871	7.61E-02
MSMEG_2034	aryl-alcohol dehydrogenase	NA	1.459	4.97E-01
MSMEG_2035	amine oxidase [flavin-containing] B	NA	1.131	1.82E-01
MSMEG_2036	hydrolase, alpha/beta fold family protein	NA	2.626	2.28E-01
MSMEG_2037	conserved hypothetical protein	NA	0.892	3.37E-01
MSMEG_2038	monooxygenase, flavin-binding family protein	NA	0.882	1.84E-02
MSMEG_2039	putative transcriptional regulator	NA	1.033	6.49E-01
MSMEG_2040	hypothetical protein	NA	2.939	2.75E-01
MSMEG_2041	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.734	3.18E-02
MSMEG_2042	phosphotransferase enzyme family protein	NA	0.889	1.79E-01
MSMEG_2043	transcriptional regulator, TetR family protein	NA	1.282	3.60E-01
MSMEG_2044	integral membrane transport protein	NA	0.856	9.15E-02
MSMEG_2045	monoxygenase	NA	1.001	9.92E-01
MSMEG_2046	GlcNAc-PI de-N-acetylase family protein	NA	0.857	4.27E-02
MSMEG_2047	probable enoyl-CoA hydratase	NA	0.984	7.81E-01
MSMEG_2048	alcohol dehydrogenase	NA	1.119	3.38E-01
MSMEG_2049	putative transcriptional regulator, TetR family protein	NA	0.959	8.51E-01
MSMEG_2050	NADH-quinone oxidoreductase, N subunit	nuoN	1.108	4.61E-01

MSMEG_2051	NADH-quinone oxidoreductase, M subunit	nuoM	1.108	1.50E-01
MSMEG_2052	NADH-quinone oxidoreductase, L subunit	nuoL	0.844	4.54E-01
MSMEG_2053	NADH-quinone oxidoreductase, k subunit	nuoK	1.101	6.51E-01
MSMEG_2054	NADH dehydrogenase subunit j	NA	0.974	7.16E-01
MSMEG_2055	NADH-quinone oxidoreductase, I subunit	nuoI	1.018	8.12E-01
MSMEG_2056	NADH-quinone oxidoreductase, H subunit	nuoH	1.718	5.05E-01
MSMEG_2057	NADH-quinone oxidoreductase, G subunit	nuoG	0.946	5.43E-01
MSMEG_2058	NADH-quinone oxidoreductase, F subunit	nuoF	0.972	3.21E-01
MSMEG_2059	NADH-quinone oxidoreductase chain e	NA	1.049	7.52E-01
MSMEG_2060	NADH-quinone oxidoreducatase, D subunit	nuoD	1.038	8.19E-01
MSMEG_2061	NADH-quinone oxidoreductase chain c	NA	1.226	3.68E-01
MSMEG_2062	NADH-quinone oxidoreductase, B subunit	nuoB	1.022	8.40E-01
MSMEG_2063	NADH-quinone oxidoreductase, a subunit	nuoA	1.189	6.51E-02
MSMEG_2064	two-component system response regulator	NA	1.111	3.83E-01
MSMEG_2065	YceI like family protein	NA	1.031	9.08E-01
MSMEG_2066	conserved hypothetical protein	NA	0.931	6.80E-01
MSMEG_2067	methyltransferase type 12	NA	1.089	2.83E-01
MSMEG_2068	hypothetical protein	NA	0.832	1.22E-01
MSMEG_2069	phosphotransferase enzyme family protein	NA	0.992	9.76E-01
MSMEG_2070	acyl-CoA dehydrogenase family protein	NA	0.732	3.72E-02
MSMEG_2071	transcriptional regulator, TetR family protein	NA	1.303	3.98E-01
MSMEG_2072	3-hydroxy-3-methylglutaryl-CoA lyase	NA	0.771	9.21E-02
MSMEG_2073	CAIB/BAIF family protein	NA	0.918	4.72E-01
MSMEG_2074	conserved hypothetical protein	NA	0.736	8.25E-03
MSMEG_2075	homogentisate 1,2-dioxygenase	hmgA	0.746	9.13E-05
MSMEG_2076	conserved hypothetical protein	NA	1.043	7.22E-01
MSMEG_2077	acyl-CoA dehydrogenase, C- domain protein	NA	1.266	3.46E-01
MSMEG_2078	antigen 85-C	NA	1.045	4.40E-01
MSMEG_2079	alcohol dehydrogenase	NA	0.914	2.29E-01
MSMEG_2080	putative acyl-CoA dehydrogenase	NA	0.986	7.05E-01
MSMEG_2081	putative acyl-CoA dehydrogenase	NA	0.768	8.86E-03

MSMEG_2082	hypothetical protein	NA	0.912	4.73E-01
MSMEG_2083	inositol monophosphatase	hisN	0.974	7.51E-01
MSMEG_2084	conserved hypothetical protein	NA	0.981	6.01E-01
MSMEG_2085	NADPH-ferredoxin reductase fpra; this gene contains a frame shift which is not the res	NA	0.894	2.28E-02
MSMEG_2086	peptide chain release factor 2	prfB	1.157	1.41E-02
MSMEG_2087	transporter, small conductance mechanosensitive ion channel (MscS) family protein	NA	1.161	1.83E-01
MSMEG_2088	hypothetical proline-rich protein	NA	1.067	1.47E-01
MSMEG_2089	cell division ATP-binding protein FtsE	ftsE	1.245	2.41E-02
MSMEG_2090	putative cell division protein FtsX	NA	0.921	2.22E-01
MSMEG_2091	SsrA-binding protein	smpB	1.042	1.12E-01
MSMEG_2092	D-aminopeptidase	NA	1.161	2.83E-01
MSMEG_2094	56kDa selenium binding protein	NA	1.077	7.11E-01
MSMEG_2095	serine esterase, cutinase family protein	NA	1.003	9.52E-01
MSMEG_2096	integral membrane protein	NA	1.295	4.15E-02
MSMEG_2097	Acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	NA	0.922	3.29E-01
MSMEG_2098	fumarylacetoacetate hydrolase family protein	NA	0.963	8.08E-01
MSMEG_2099	ABC transporter, substrate binding protein [nitrate/sulfonate], putative	NA	1.121	5.70E-01
MSMEG_2100	peptidase family protein M20/M25/M40	NA	1.036	8.09E-01
MSMEG_2101	taurine ABC transporter, permease protein; this gene contains a frame shift which is n	NA	1.532	3.70E-01
MSMEG_2102	nitrate transport ATP-binding protein NrtD	NA	1.249	1.33E-01
MSMEG_2103	5,10-methylenetetrahydromethanopterin reductase	NA	1.046	8.26E-01
MSMEG_2104	GntR-family protein transcriptional regulator	NA	0.840	8.77E-02
MSMEG_2105	ATP dependent DNA ligase	NA	1.093	6.21E-01
MSMEG_2106	putative transcriptional regulator	NA	1.347	1.89E-02
MSMEG_2107	conserved hypothetical protein	NA	1.002	9.76E-01
MSMEG_2108	conserved hypothetical protein	NA	0.995	9.49E-01
MSMEG_2109	conserved hypothetical protein	NA	1.226	4.33E-01
MSMEG_2110	conserved hypothetical protein	NA	1.047	1.82E-01
MSMEG_2111	chorismate mutase	NA	1.086	3.54E-01
MSMEG_2112	secreted protein	NA	1.052	7.40E-01
MSMEG_2113	hypothetical protein	NA	1.165	3.34E-01

MSMEG_2114	glucose-6-phosphate isomerase, putative	NA	0.800	1.57E-02
MSMEG_2115	conserved hypothetical protein	NA	1.111	6.32E-01
MSMEG_2116	PTS system, glucose-specific IIBC component	NA	0.753	1.21E-02
MSMEG_2117	beta-glucoside-specific EII permease	NA	0.758	2.54E-02
MSMEG_2118	glucosamine-6-phosphate isomerase	nagB	0.731	3.29E-02
MSMEG_2119	N-acetylglucosamine-6-phosphate deacetylase	nagA	0.726	1.07E-02
MSMEG_2120	tetratricopeptide repeat family protein	NA	1.166	3.51E-01
MSMEG_2121	multiphosphoryl transfer protein (MTP)	NA	0.469	3.74E-04
MSMEG_2122	dihydroxyacetone kinase, L subunit	NA	0.511	2.04E-03
MSMEG_2123	dihydroxyacetone kinase, DhaK subunit	dhaK	0.452	6.61E-05
MSMEG_2124	glycerol uptake facilitator, MIP channel	NA	0.366	6.19E-04
MSMEG_2125	glycerol operon regulatory protein	NA	0.976	5.76E-01
MSMEG_2126	hypothetical protein	NA	1.318	2.94E-01
MSMEG_2127	conserved hypothetical protein	NA	1.171	2.86E-01
MSMEG_2128	malonyl CoA decarboxylase	NA	0.967	7.90E-01
MSMEG_2129	hypothetical protein	NA	1.051	3.95E-01
MSMEG_2130	putative acyl-CoA dehydrogenase	NA	1.058	8.26E-01
MSMEG_2131	acyl-CoA synthase	NA	0.897	4.34E-01
MSMEG_2132	acyl carrier protein Acp	NA	0.959	7.09E-01
MSMEG_2133	conserved hypothetical protein, putative	NA	0.931	5.88E-01
MSMEG_2134	CrcB protein	crcB	1.104	4.36E-01
MSMEG_2135	putative CrcB protein	NA	1.451	3.11E-03
MSMEG_2136	phosphoglucomutase, alpha-D-glucose phosphate-specific	pgm	0.888	3.50E-01
MSMEG_2137	permease of the major facilitator superfamily protein	NA	1.230	2.92E-01
MSMEG_2139	hypothetical protein	NA	1.065	6.24E-01
MSMEG_2140	Fic protein family protein	NA	1.404	1.07E-01
MSMEG_2141	gp35 protein	NA	1.392	3.35E-01
MSMEG_2142	gp36 protein	NA	0.956	1.95E-01
MSMEG_2143	hypothetical protein	NA	1.177	7.72E-03
MSMEG_2144	conserved hypothetical protein	NA	1.108	2.23E-01
MSMEG_2145	conserved domain protein	NA	1.044	7.55E-01

MSMEG_2146	gp15 protein	NA	1.223	3.07E-01
MSMEG_2147	gp16 protein; this gene contains a frame shift which is not the result of sequencing err	NA	1.036	4.32E-01
MSMEG_2148	HNH endonuclease domain protein	NA	1.113	6.16E-01
MSMEG_2149	hypothetical protein	NA	1.072	3.62E-01
MSMEG_2150	putative transposition helper protein	NA	0.901	4.37E-01
MSMEG_2150	putative transposition helper protein	NA	1.293	2.32E-01
MSMEG_2151	transposase IstA protein, putative	NA	0.923	6.00E-01
MSMEG_2151	transposase IstA protein, putative	NA	1.924	2.99E-01
MSMEG_2152	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	1.107	2.06E-01
MSMEG_2153	transcriptional regulator, TetR family protein	NA	1.169	2.03E-01
MSMEG_2154	conserved hypothetical protein	NA	1.377	1.98E-01
MSMEG_2155	trans-2-enoyl-CoA reductase	NA	1.638	4.57E-01
MSMEG_2156	conserved hypothetical protein	NA	0.912	2.56E-01
MSMEG_2157	hypothetical protein	NA	0.866	4.27E-01
MSMEG_2158	hypothetical protein	NA	1.267	2.54E-01
MSMEG_2159	conserved hypothetical protein	NA	0.879	5.96E-01
MSMEG_2160	hypothetical protein	NA	1.088	7.01E-01
MSMEG_2161	FadD9 protein; this region contains one or more premature stops and/or frameshifts v	NA	0.901	1.98E-01
MSMEG_2161	FadD9 protein; this region contains one or more premature stops and/or frameshifts v	NA	1.075	4.41E-01
MSMEG_2161	FadD9 protein; this region contains one or more premature stops and/or frameshifts v	NA	1.412	1.28E-01
MSMEG_2162	MmcJ protein	NA	0.927	1.73E-01
MSMEG_2163	aldehyde dehydrogenase	NA	0.886	1.27E-01
MSMEG_2164	transcriptional regulator, putative	NA	1.039	7.48E-01
MSMEG_2165	transketolase, N- subunit	NA	1.669	4.88E-01
MSMEG_2166	transketoloase, C half	NA	0.825	7.55E-02
MSMEG_2167	aminopeptidase, putative	NA	0.760	1.14E-01
MSMEG_2168	hypothetical protein	NA	1.215	5.77E-01
MSMEG_2169	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	accD	1.297	1.15E-01
MSMEG_2170	3-hydroxyisobutyrate dehydrogenase family protein	NA	0.969	5.90E-01
MSMEG_2171	L-carnitine dehydratase/bile acid-inducible protein F	NA	1.224	3.74E-01
MSMEG_2172	dicarboxylate-carrier protein	NA	0.840	2.57E-01

MSMEG_2173	GntR-family protein transcriptional regulator	NA	1.053	1.25E-01
MSMEG_2174	superfamily protein I DNA or RNA helicase	NA	0.897	8.54E-02
MSMEG_2175	nitrilotriacetate monooxygenase component A	NA	1.823	3.38E-02
MSMEG_2176	conserved hypothetical protein	NA	0.991	6.46E-01
MSMEG_2177	fmnh2-utilizing oxygenase	NA	1.645	2.08E-01
MSMEG_2178	integral membrane protein	NA	1.173	5.12E-01
MSMEG_2179	transcriptional regulatory protein	NA	1.000	9.87E-01
MSMEG_2180	RemK protein	NA	9.594	3.39E-01
MSMEG_2181	cell filamentation protein	NA	22.577	3.83E-01
MSMEG_2182	transcriptional regulator	NA	1.101	2.72E-01
MSMEG_2183	conserved hypothetical protein	NA	0.977	8.02E-01
MSMEG_2184	amino acid permease	NA	1.080	3.55E-01
MSMEG_2185	conserved hypothetical protein	NA	2.276	4.23E-01
MSMEG_2186	conserved hypothetical protein	NA	0.900	2.12E-01
MSMEG_2187	urea amidolyase	NA	1.168	1.03E-01
MSMEG_2188	integral membrane protein	NA	1.361	1.34E-01
MSMEG_2189	allophanate hydrolase	atzF	1.261	2.98E-02
MSMEG_2190	acyl-CoA dehydrogenase domain protein	NA	2.258	2.70E-01
MSMEG_2191	acyl-CoA dehydrogenase family protein	NA	1.141	9.69E-02
MSMEG_2192	conserved hypothetical protein	NA	1.023	8.36E-01
MSMEG_2193	transcriptional regulator, TetR family protein	NA	1.011	7.48E-01
MSMEG_2194	MerR-family protein transcriptional regulator	NA	0.925	4.28E-01
MSMEG_2195	transcriptional regulator, TetR family protein	NA	0.959	4.15E-01
MSMEG_2196	sensory box/response regulator	NA	0.942	2.78E-03
MSMEG_2197	hypothetical protein	NA	1.159	1.33E-01
MSMEG_2198	ThiF family protein	NA	0.964	3.05E-01
MSMEG_2199	conserved hypothetical protein	NA	0.976	6.64E-01
MSMEG_2200	formyltetrahydrofolate deformylase	purU	0.987	8.39E-01
MSMEG_2201	ZbpA protein	NA	0.790	1.82E-02
MSMEG_2202	dimethylaniline monooxygenase [N-oxide-forming] 5	NA	0.834	9.11E-03
MSMEG_2203	alpha/beta hydrolase	NA	0.801	1.28E-01

MSMEG_2204	carveol dehydrogenase ((+)-trans-carveol dehydrogenase)	NA	1.218	9.70E-02
MSMEG_2205	putative acyl-CoA dehydrogenase	NA	1.117	2.27E-02
MSMEG_2206	3-oxoacyl-(acyl-carrier-protein) reductase	fabG	1.189	7.06E-02
MSMEG_2207	beta-ketothiolase	NA	1.101	3.33E-01
MSMEG_2208	acyl-CoA dehydrogenase	NA	1.041	6.36E-01
MSMEG_2209	transcriptional regulator, GntR family protein	NA	1.016	8.47E-01
MSMEG_2210	CaiB/BaiF family protein; this gene contains a frame shift which is not the result of seq	NA	1.075	5.37E-01
MSMEG_2210	CaiB/BaiF family protein; this gene contains a frame shift which is not the result of seq	NA	1.430	2.10E-01
MSMEG_2211	DNA-binding protein	NA	0.942	6.84E-01
MSMEG_2212	short chain dehydrogenase	NA	1.224	2.43E-01
MSMEG_2213	O-methyltransferase	NA	0.993	9.80E-01
MSMEG_2214	alcohol dehydrogenase B; this region contains one or more premature stops and/or fra	NA	1.282	3.63E-01
MSMEG_2215	AMP-binding enzyme	NA	1.050	7.54E-01
MSMEG_2216	AMP-binding enzyme	NA	1.141	7.00E-01
MSMEG_2217	AMP-dependent synthetase and ligase	NA	1.013	8.47E-01
MSMEG_2218	enoyl-CoA hydratase/isomerase family protein	NA	1.067	5.10E-01
MSMEG_2219	enoyl-CoA hydratase/isomerase family protein	NA	2.104	1.64E-01
MSMEG_2220	enoyl-CoA hydratase/isomerase	NA	0.938	6.98E-01
MSMEG_2222	hypothetical protein	NA	0.711	6.35E-02
MSMEG_2222	hypothetical protein	NA	2.019	3.24E-01
MSMEG_2223	enoyl-CoA hydratase/isomerase family protein	NA	1.157	4.38E-01
MSMEG_2224	acetyl-CoA C-acyltransferase	NA	1.210	1.31E-01
MSMEG_2225	transcriptional regulator, TetR family protein	NA	0.946	4.03E-01
MSMEG_2226	hypothetical protein	NA	1.017	8.81E-01
MSMEG_2227	carnitinyl-CoA dehydratase	NA	1.003	9.74E-01
MSMEG_2228	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.941	5.45E-01
MSMEG_2229	enoyl-CoA hydratase	NA	1.027	3.74E-01
MSMEG_2230	amidohydrolase family protein	NA	0.981	8.76E-01
MSMEG_2231	AMP-binding enzyme	NA	0.991	8.33E-01
MSMEG_2232	amidohydrolase family protein	NA	1.602	3.49E-01
MSMEG_2233	acyl-CoA dehydrogenase, C- domain protein	NA	1.090	4.94E-01

MSMEG_2234	acyl-CoA dehydrogenase, middle domain protein	NA	0.949	7.72E-01
MSMEG_2235	amidohydrolase family protein	NA	1.397	2.96E-01
MSMEG_2236	putative thiolase	NA	1.252	5.19E-01
MSMEG_2237	anaerobic dehydrogenase, typically	NA	1.698	1.60E-01
MSMEG_2238	aldehyde dehydrogenase (NAD) family protein	NA	0.991	9.20E-01
MSMEG_2239	transcriptional regulator, TetR family protein	NA	1.103	4.68E-01
MSMEG_2240	cytochrome P450	NA	1.114	3.66E-01
MSMEG_2241	medium chain acyl-CoA synthetase	NA	1.504	2.96E-01
MSMEG_2242	coniferyl aldehyde dehydrogenase	NA	1.123	3.82E-01
MSMEG_2243	isochorismatase family protein	NA	1.056	8.31E-01
MSMEG_2244	Rieske [2Fe-2S] domain protein	NA	0.973	7.33E-01
MSMEG_2245	bile-acid 7-alpha dehydratase	NA	1.045	5.88E-01
MSMEG_2246	conserved hypothetical protein	NA	1.340	6.36E-02
MSMEG_2247	dihydrokaempferol 4-reductase	NA	1.067	8.02E-01
MSMEG_2248	two-component system sensor kinase	NA	1.249	1.18E-01
MSMEG_2249	conserved hypothetical protein	NA	1.017	8.52E-01
MSMEG_2250	hypothetical protein	NA	1.065	7.56E-01
MSMEG_2251	nitrate/nitrite response regulator protein	NA	1.071	5.16E-01
MSMEG_2252	flavin-type hydroxylase	NA	0.994	9.33E-01
MSMEG_2253	hypothetical protein	NA	1.046	8.40E-01
MSMEG_2254	oxalate decarboxylase OxdC, putative	NA	1.543	2.45E-01
MSMEG_2255	Carboxyl transferase domain protein	NA	0.927	2.05E-01
MSMEG_2256	conserved hypothetical protein	NA	0.953	4.91E-01
MSMEG_2257	cytochrome P450-terp	NA	1.125	5.65E-01
MSMEG_2258	conserved hypothetical protein	NA	0.633	9.97E-04
MSMEG_2259	carbon starvation protein A	NA	0.646	5.28E-03
MSMEG_2260	putative transcriptional regulator	NA	1.031	5.30E-01
MSMEG_2261	hypothetical protein	NA	1.041	2.41E-01
MSMEG_2262	hydrogenase-2, small subunit	hybA	0.887	3.48E-01
MSMEG_2263	hydrogenase-2, large subunit	hybC	1.103	5.84E-01
MSMEG_2264	peptidase M52, hydrogen uptake protein	NA	0.905	2.43E-01

MSMEG_2265	hypothetical protein	NA	1.152	3.32E-01
MSMEG_2266	hypothetical protein	NA	0.837	1.58E-02
MSMEG_2267	tetratricopeptide repeat domain protein	NA	0.902	6.20E-01
MSMEG_2268	conserved hypothetical protein	NA	0.970	8.66E-01
MSMEG_2269	NHL repeat protein	NA	1.058	5.39E-01
MSMEG_2270	hypothetical protein	NA	0.860	2.52E-01
MSMEG_2271	hydrogenase accessory protein HypB	hypB	0.708	4.19E-03
MSMEG_2271	hydrogenase accessory protein HypB	hypB	0.763	5.46E-03
MSMEG_2272	hydrogenase nickel insertion protein HypA	hypA	0.814	1.47E-01
MSMEG_2273	[NiFe] hydrogenase maturation protein HypF	hypF	0.646	2.19E-02
MSMEG_2274	hydrogenase assembly chaperone HypC/HupF	hypC	0.631	6.38E-03
MSMEG_2275	hydrogenase expression/formation protein HypD	hypD	0.568	5.18E-03
MSMEG_2276	hydrogenase expression/formation protein HypE	hypE	0.982	8.39E-01
MSMEG_2277	DNA ligase I, ATP-dependent	dnl1	1.947	3.35E-01
MSMEG_2278	membrane-bound oxidoreductase	NA	0.799	8.83E-02
MSMEG_2279	3-hydroxyacyl-CoA dehydrogenase type-2	NA	1.258	1.12E-01
MSMEG_2280	pyruvate dehydrogenase	NA	0.932	8.27E-02
MSMEG_2281	This gene is disrupted by an IS1096 element.; conserved hypothetical protein, interrup	NA	1.099	3.91E-01
MSMEG_2284	This gene is disrupted by an IS1096 element.; conserved hypothetical protein, interrup	NA	1.187	3.11E-02
MSMEG_2285	methyltransferase type 11	NA	1.023	9.39E-01
MSMEG_2286	aminoglycoside phosphotransferase	NA	0.908	3.21E-01
MSMEG_2286	aminoglycoside phosphotransferase	NA	1.161	3.90E-01
MSMEG_2287	transport protein	NA	1.010	9.22E-01
MSMEG_2287	transport protein	NA	1.080	4.18E-01
MSMEG_2288	conserved hypothetical protein	NA	1.030	8.38E-01
MSMEG_2288	conserved hypothetical protein	NA	1.072	6.34E-01
MSMEG_2289	cytochrome p450	NA	0.600	5.36E-03
MSMEG_2289	cytochrome p450	NA	0.751	2.10E-02
MSMEG_2290	transcriptional regulator, TetR family protein	NA	1.050	2.74E-01
MSMEG_2290	transcriptional regulator, TetR family protein	NA	1.104	1.33E-01
MSMEG_2291	short chain dehydrogenase	NA	1.018	7.77E-01

MSMEG_2291	short chain dehydrogenase	NA	1.098	2.37E-01
MSMEG_2292	alkaline phosphatase	NA	1.354	8.76E-02
MSMEG_2292	alkaline phosphatase	NA	1.588	5.77E-02
MSMEG_2293	conserved hypothetical protein	NA	1.065	4.14E-01
MSMEG_2293	conserved hypothetical protein	NA	1.336	1.37E-01
MSMEG_2294	DNA polymerase IV	dinB	0.802	6.79E-02
MSMEG_2294	DNA polymerase IV	dinB	1.074	4.50E-01
MSMEG_2295	transcriptional regulator, TetR family protein	NA	0.877	3.34E-02
MSMEG_2295	transcriptional regulator, TetR family protein	NA	1.046	4.43E-01
MSMEG_2296	secreted protein	NA	2.592	2.43E-02
MSMEG_2297	glutaredoxin	NA	0.839	6.37E-03
MSMEG_2297	glutaredoxin	NA	0.871	5.17E-03
MSMEG_2298	protein NrdI; this gene contains a frame shift which is not the result of sequencing err	NA	0.752	2.58E-03
MSMEG_2298	protein NrdI; this gene contains a frame shift which is not the result of sequencing err	NA	0.803	1.36E-02
MSMEG_2299	ribonucleoside-diphosphate reductase, alpha subunit	NA	0.756	5.43E-03
MSMEG_2299	ribonucleoside-diphosphate reductase, alpha subunit	NA	0.852	2.22E-04
MSMEG_2300	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.924	3.84E-01
MSMEG_2300	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.065	4.60E-01
MSMEG_2300	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.987	2.56E-01
MSMEG_2301	glyoxalase/bleomycin resistance protein/dioxygenase	NA	1.028	7.33E-01
MSMEG_2301	glyoxalase/bleomycin resistance protein/dioxygenase	NA	1.191	5.10E-02
MSMEG_2302	conserved hypothetical protein	NA	1.678	3.06E-01
MSMEG_2303	integral membrane transporter	NA	0.850	1.80E-01
MSMEG_2303	integral membrane transporter	NA	0.938	4.53E-01
MSMEG_2304	hypothetical protein	NA	0.875	1.83E-01
MSMEG_2305	TetR-family protein transcriptional regulator	NA	1.008	8.32E-01
MSMEG_2306	putative acetyltransferase	NA	1.341	1.08E-01
MSMEG_2307	conserved hypothetical protein	NA	1.102	4.20E-01
MSMEG_2307	conserved hypothetical protein	NA	1.268	8.75E-02
MSMEG_2308	geranylgeranyl reductase	NA	0.914	1.15E-01
MSMEG_2309	probable transcriptional regulatory protein	NA	0.940	3.49E-01

MSMEG_2309	probable transcriptional regulatory protein	NA	0.974	7.01E-01
MSMEG_2310	monooxygenase	NA	1.065	6.44E-02
MSMEG_2310	monooxygenase	NA	1.182	3.27E-03
MSMEG_2311	conserved hypothetical protein	NA	1.395	5.45E-04
MSMEG_2311	conserved hypothetical protein	NA	1.458	1.70E-03
MSMEG_2312	hypothetical protein	NA	0.947	5.60E-01
MSMEG_2313	ribonucleoside-diphosphate reductase, beta subunit	NA	0.809	4.17E-04
MSMEG_2313	ribonucleoside-diphosphate reductase, beta subunit	NA	0.866	2.16E-03
MSMEG_2314	putative esterase family protein	NA	0.998	9.81E-01
MSMEG_2314	putative esterase family protein	NA	1.139	2.43E-01
MSMEG_2315	conserved hypothetical protein	NA	0.877	4.92E-02
MSMEG_2315	conserved hypothetical protein	NA	1.026	5.44E-01
MSMEG_2316	monooxygenase, NtaA/SnaA/SoxA family; this gene contains a frame shift which is not	NA	1.167	3.48E-01
MSMEG_2316	monooxygenase, NtaA/SnaA/SoxA family; this gene contains a frame shift which is not	NA	1.326	9.53E-02
MSMEG_2316	monooxygenase, NtaA/SnaA/SoxA family; this gene contains a frame shift which is not	NA	2.490	2.83E-01
MSMEG_2317	alcohol dehydrogenase, zinc-containing	NA	1.246	4.64E-02
MSMEG_2317	alcohol dehydrogenase, zinc-containing	NA	1.322	4.47E-02
MSMEG_2318	GTP cyclohydrolase II	NA	1.027	5.55E-01
MSMEG_2318	GTP cyclohydrolase II	NA	1.109	1.79E-02
MSMEG_2319	Periplasmic binding protein	NA	1.030	5.88E-01
MSMEG_2319	Periplasmic binding protein	NA	1.111	9.33E-02
MSMEG_2320	cytochrome c oxidase, subunit I; this gene contains a frame shift which is not the resul	ctaD	0.858	6.33E-02
MSMEG_2320	cytochrome c oxidase, subunit I; this gene contains a frame shift which is not the resul	ctaD	0.985	7.84E-01
MSMEG_2321	phosphoserine phosphatase	serB	1.019	8.09E-01
MSMEG_2321	phosphoserine phosphatase	serB	1.060	5.13E-01
MSMEG_2322	hypothetical protein	NA	1.055	5.17E-01
MSMEG_2322	hypothetical protein	NA	1.112	3.07E-01
MSMEG_2323	GntR-family protein transcriptional regulator	NA	1.184	8.46E-02
MSMEG_2324	hypothetical protein	NA	0.936	3.39E-01
MSMEG_2325	integral membrane protein	NA	0.901	3.00E-01
MSMEG_2325	integral membrane protein	NA	1.047	3.48E-01

MSMEG_2326	ABC-type molybdenum transport system, ATPase component	NA	1.054	5.09E-01
MSMEG_2326	ABC-type molybdenum transport system, ATPase component	NA	1.122	2.65E-01
MSMEG_2327	nudix hydrolase	NA	0.921	8.70E-02
MSMEG_2327	nudix hydrolase	NA	0.965	4.66E-01
MSMEG_2328	probable enoyl-CoA hydratase	NA	0.930	4.13E-02
MSMEG_2328	probable enoyl-CoA hydratase	NA	0.965	2.61E-01
MSMEG_2329	methyltransferase, UbiE/COQ5 family protein	NA	0.955	2.88E-01
MSMEG_2329	methyltransferase, UbiE/COQ5 family protein	NA	1.053	3.62E-01
MSMEG_2330	SAM-dependent methyltransferase	NA	1.074	3.03E-01
MSMEG_2330	SAM-dependent methyltransferase	NA	1.241	7.25E-03
MSMEG_2331	immunogenic protein MPB64/MPT64	NA	1.121	3.44E-02
MSMEG_2331	immunogenic protein MPB64/MPT64	NA	1.212	6.86E-03
MSMEG_2332	amino acid carrier protein	NA	1.137	8.05E-02
MSMEG_2332	amino acid carrier protein	NA	1.255	2.88E-02
MSMEG_2333	conserved hypothetical protein	NA	0.977	7.26E-01
MSMEG_2334	hypothetical protein	NA	1.391	2.90E-01
MSMEG_2335	hexapeptide transferase family protein	NA	1.140	1.53E-01
MSMEG_2336	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.975	8.65E-01
MSMEG_2336	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.106	4.44E-01
MSMEG_2337	isopentenyl-diphosphate delta-isomerase, type 2	fni	1.110	5.58E-01
MSMEG_2337	isopentenyl-diphosphate delta-isomerase, type 2	fni	1.173	3.90E-01
MSMEG_2340	hypothetical protein	NA	1.085	7.53E-01
MSMEG_2341	conserved hypothetical protein	NA	0.986	8.86E-01
MSMEG_2342	putative glycosyltransferase	NA	1.099	5.84E-01
MSMEG_2343	methylesterase	NA	1.019	7.38E-01
MSMEG_2344	dehydrogenase	NA	1.304	4.14E-01
MSMEG_2345	lycopene cyclase; this gene contains a frame shift which is not the result of sequencin	NA	1.160	6.63E-01
MSMEG_2346	phytoene synthase	NA	1.157	2.36E-01
MSMEG_2347	phytoene dehydrogenase	NA	1.059	8.64E-01
MSMEG_2348	glycosyl transferase, group 1 family protein; this gene contains a frame shift which is n	NA	0.783	1.40E-02
MSMEG_2348	glycosyl transferase, group 1 family protein; this gene contains a frame shift which is n	NA	0.865	7.88E-02

MSMEG_2349	glycosyl hydrolase, family protein 57	NA	0.984	8.12E-01
MSMEG_2350	conserved hypothetical protein	NA	0.861	6.23E-02
MSMEG_2351	electron transfer flavoprotein, beta subunit	etfB	0.714	5.94E-04
MSMEG_2352	electron transfer flavoprotein, alpha subunit	etfA	0.906	2.49E-01
MSMEG_2353	secreted protein	NA	1.495	2.05E-01
MSMEG_2354	oxidoreductase	NA	1.711	2.15E-01
MSMEG_2355	conserved hypothetical protein	NA	1.491	2.52E-01
MSMEG_2356	acyltransferase	NA	1.971	3.50E-01
MSMEG_2357	cysteine desulfurase	NA	1.082	3.53E-01
MSMEG_2358	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	trmU	1.066	1.76E-01
MSMEG_2359	methionine synthase, vitamin-B12 independent	NA	0.923	2.07E-01
MSMEG_2360	4-coumarate:CoA ligase	NA	0.991	8.13E-01
MSMEG_2361	phosphoribosylglycinamide formyltransferase	NA	0.997	9.57E-01
MSMEG_2362	DNA ligase, NAD-dependent	ligA	1.205	3.21E-01
MSMEG_2363	amino acid-binding ACT	NA	1.004	9.55E-01
MSMEG_2364	glutamyl-tRNA(Gln) amidotransferase, C subunit	gatC	0.905	3.71E-02
MSMEG_2365	glutamyl-tRNA(Gln) amidotransferase subunit A	NA	0.896	2.47E-01
MSMEG_2366	6-phosphofructokinase 1; this gene contains a frame shift which is not the result of se	NA	0.978	7.84E-01
MSMEG_2367	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	NA	1.258	7.42E-02
MSMEG_2368	transcriptional regulator, TetR family protein domain protein, putative	NA	1.057	5.85E-01
MSMEG_2369	LppZ protein	NA	1.105	3.68E-02
MSMEG_2370	DoxX subfamily protein, putative	NA	0.955	2.49E-01
MSMEG_2371	Low molecular weight protein antigen 6	NA	1.166	1.56E-02
MSMEG_2372	acetolactate synthase, large subunit, biosynthetic type	ilvB	1.175	1.30E-01
MSMEG_2373	acetolactate synthase, small subunit	ilvN	1.124	1.02E-01
MSMEG_2374	ketol-acid reductoisomerase	ilvC	1.294	5.55E-03
MSMEG_2375	NAD(P)H:quinone oxidoreductase, type IV	wrbA	1.248	4.12E-02
MSMEG_2376	conserved hypothetical protein	NA	1.675	2.09E-01
MSMEG_2377	P49 protein	NA	1.246	2.16E-01
MSMEG_2378	D-3-phosphoglycerate dehydrogenase	serA	1.015	8.81E-01
MSMEG_2379	3-isopropylmalate dehydrogenase	leuB	0.990	8.74E-01

MSMEG_2380	sugar transporter family protein	NA	1.448	3.63E-02
MSMEG_2381	conserved hypothetical protein	NA	1.388	4.34E-02
MSMEG_2382	5-carboxymethyl-2-hydroxymuconate delta-isomerase	NA	1.033	5.30E-01
MSMEG_2383	glutamyl-tRNA synthetase	gltX	0.998	9.60E-01
MSMEG_2386	transcriptional regulator, IclR family protein	NA	1.134	2.30E-01
MSMEG_2387	3-isopropylmalate dehydratase, large subunit	leuC	0.873	2.97E-02
MSMEG_2388	3-isopropylmalate dehydratase, small subunit	leuD	0.888	4.55E-03
MSMEG_2389	DNA-binding protein HU	hup	0.928	4.40E-01
MSMEG_2390	hydrolase, NUDIX family protein	NA	1.054	3.48E-01
MSMEG_2391	polyphosphate kinase	ppk	0.980	7.44E-01
MSMEG_2392	conserved hypothetical protein	NA	0.973	2.17E-01
MSMEG_2393	NAD-dependent glycerol-3-phosphate dehydrogenase	gpsA	1.121	2.81E-02
MSMEG_2394	putative cystathionine gamma-synthase	NA	1.129	2.88E-01
MSMEG_2395	D-alanine--D-alanine ligase	NA	1.335	1.26E-02
MSMEG_2396	conserved hypothetical protein	NA	1.164	3.34E-01
MSMEG_2397	transcriptional regulatory protein, AsnC family protein	NA	1.145	4.61E-02
MSMEG_2398	thiamine-monophosphate kinase	thiL	1.132	2.41E-01
MSMEG_2399	uracil-DNA glycosylase	ung	1.138	2.48E-01
MSMEG_2400	ribosomal protein L28	rpmB	1.275	1.53E-01
MSMEG_2401	hypothetical protein	NA	1.093	6.52E-01
MSMEG_2402	dihydroxyacetone kinase	NA	0.869	2.28E-02
MSMEG_2403	ATP-dependent DNA helicase RecG	recG	1.056	4.40E-01
MSMEG_2404	extracellular deoxyribonuclease	NA	0.835	1.14E-01
MSMEG_2405	MarR-family protein transcriptional regulator	NA	2.532	2.02E-01
MSMEG_2406	transcriptional regulator, TetR family protein, putative	NA	1.086	7.63E-01
MSMEG_2407	morphine 6-dehydrogenase	NA	1.194	1.49E-01
MSMEG_2408	2,5-diketo-D-gluconic acid reductase A	NA	1.163	7.98E-02
MSMEG_2409	alpha/beta hydrolase fold family protein	NA	0.967	7.37E-01
MSMEG_2410	putative serine-threonine protein kinase	NA	1.003	9.35E-01
MSMEG_2411	conserved integral membrane protein	NA	1.171	1.50E-01
MSMEG_2412	pyruvate carboxylase	pyc	1.087	3.59E-01

MSMEG_2413	putative methyltransferase	NA	1.308	1.04E-01
MSMEG_2414	pantetheine-phosphate adenylyltransferase	coaD	1.241	2.20E-02
MSMEG_2415	hemerythrin HHE cation binding region	NA	1.218	3.57E-01
MSMEG_2416	conserved hypothetical protein	NA	0.856	5.69E-02
MSMEG_2417	conserved hypothetical protein	NA	1.039	3.43E-01
MSMEG_2418	ribonuclease III	rnc	0.983	7.13E-01
MSMEG_2419	formamidopyrimidine-DNA glycosylase	mutM	1.359	3.71E-02
MSMEG_2420	hypothetical protein	NA	0.950	1.32E-01
MSMEG_2421	conserved hypothetical protein	NA	1.171	1.04E-01
MSMEG_2422	acylphosphatase	NA	1.030	5.29E-01
MSMEG_2423	chromosome segregation protein SMC	smc	0.936	2.31E-01
MSMEG_2424	signal recognition particle-docking protein FtsY	ftsY	1.135	3.58E-02
MSMEG_2425	ammonium transporter	amt	0.862	1.14E-01
MSMEG_2426	nitrogen regulatory protein P-II	NA	0.872	3.32E-01
MSMEG_2427	protein-P-II uridylyltransferase	glnD	1.127	1.68E-01
MSMEG_2428	DNA-binding protein	NA	0.865	3.70E-01
MSMEG_2429	aldo/keto reductase	NA	1.004	9.85E-01
MSMEG_2430	signal recognition particle protein	ffh	1.049	4.19E-01
MSMEG_2431	amidohydrolase 3	NA	1.014	8.58E-01
MSMEG_2432	D-alanyl-D-alanine carboxypeptidase	NA	0.982	8.91E-01
MSMEG_2433	D-alanyl-D-alanine carboxypeptidase	NA	0.907	1.68E-01
MSMEG_2434	conserved hypothetical protein	NA	0.977	5.97E-01
MSMEG_2435	30S ribosomal protein S16	NA	0.937	4.46E-01
MSMEG_2436	conserved hypothetical protein	NA	0.928	1.23E-01
MSMEG_2437	16S rRNA processing protein RimM	rimM	0.976	7.87E-01
MSMEG_2438	tRNA (guanine-N1)-methyltransferase	trmD	0.904	2.10E-01
MSMEG_2439	LppW protein	NA	1.025	7.99E-01
MSMEG_2440	ribosomal protein L19	rplS	1.038	8.04E-01
MSMEG_2441	signal peptidase I	lepB	1.010	8.48E-01
MSMEG_2442	ribonuclease HII	NA	1.007	9.34E-01
MSMEG_2443	conserved hypothetical protein	NA	0.956	6.15E-01

MSMEG_2444	dienelactone hydrolase family protein	NA	1.018	8.31E-02
MSMEG_2445	conserved hypothetical protein	NA	0.945	6.10E-01
MSMEG_2446	conserved hypothetical protein	NA	1.124	2.14E-01
MSMEG_2447	regulatory protein	NA	1.310	7.34E-02
MSMEG_2448	hypothetical protein	NA	1.570	6.03E-03
MSMEG_2449	methylmalonate-semialdehyde dehydrogenase	mmsA	1.213	1.80E-01
MSMEG_2450	adenosylmethionine--8-amino-7-oxononanoate transaminase	NA	1.189	1.42E-01
MSMEG_2451	HAD-superfamily protein hydrolase, subfamily protein IIA	NA	2.742	3.22E-01
MSMEG_2452	hypothetical protein	NA	1.137	2.06E-01
MSMEG_2453	transcriptional regulator, GntR family protein	NA	1.161	7.50E-02
MSMEG_2454	translation initiation inhibitor	NA	1.189	1.21E-02
MSMEG_2455	carbon monoxide dehydrogenase subunit G (CoxG) superfamily protein	NA	0.974	9.05E-01
MSMEG_2456	5,10-methylenetetrahydromethanopterin reductase	NA	0.964	5.32E-01
MSMEG_2457	hypothetical protein	NA	1.043	7.51E-01
MSMEG_2458	hypothetical protein	NA	0.894	6.57E-02
MSMEG_2459	transporter ATPase	NA	0.785	3.56E-02
MSMEG_2460	transporter permease 1	NA	0.797	1.83E-01
MSMEG_2461	transporter permease 2, putative	NA	0.802	1.20E-01
MSMEG_2462	carbon-monoxide dehydrogenase	NA	0.885	4.53E-01
MSMEG_2463	nicotine dehydrogenase chain A	NA	0.924	4.34E-01
MSMEG_2464	[2Fe-2S] binding domain protein	NA	1.131	6.77E-01
MSMEG_2465	adenine deaminase	NA	0.750	1.91E-01
MSMEG_2466	glutaryl-CoA dehydrogenase	NA	0.922	5.03E-02
MSMEG_2467	transketolase, central region	NA	1.023	9.07E-01
MSMEG_2468	L-carnitine dehydratase/bile acid-inducible protein F	NA	0.842	5.07E-02
MSMEG_2469	AMP-dependent synthetase and ligase	NA	0.951	3.47E-02
MSMEG_2470	acyl-CoA thioesterase	NA	1.127	3.89E-01
MSMEG_2471	pyruvate dehydrogenase alpha subunit	NA	1.265	4.36E-01
MSMEG_2472	AsnC-family protein transcriptional regulator	NA	1.366	1.41E-01
MSMEG_2473	sugar transporter; this gene contains a frame shift which is not the result of sequencin	NA	1.060	6.65E-01
MSMEG_2473	sugar transporter; this gene contains a frame shift which is not the result of sequencin	NA	1.238	6.39E-02

MSMEG_2474	probable cutinase Cut3	NA	0.982	4.55E-01
MSMEG_2475	putative oxidoreductase YdbC	NA	1.043	3.07E-01
MSMEG_2476	MarR family protein transcriptional regulatory protein	NA	0.951	7.50E-02
MSMEG_2477	cyclopentanol dehydrogenase	NA	1.163	5.80E-02
MSMEG_2478	fumarylacetoacetate hydrolase family protein	NA	1.023	8.32E-01
MSMEG_2479	hypothetical protein	NA	1.154	4.67E-01
MSMEG_2480	transcriptional regulator, GntR family protein, putative	NA	1.698	1.13E-01
MSMEG_2481	conserved hypothetical protein	NA	1.591	2.68E-01
MSMEG_2482	hypothetical protein	NA	1.493	3.02E-01
MSMEG_2483	transcriptional regulator, IclR family protein	NA	1.245	2.63E-01
MSMEG_2484	conserved hypothetical protein	NA	0.976	5.32E-01
MSMEG_2485	monooxygenase, FAD-binding	NA	1.015	8.24E-01
MSMEG_2486	major facilitator superfamily protein	NA	1.018	7.99E-01
MSMEG_2487	4-aminobutyrate aminotransferase	NA	1.229	4.76E-01
MSMEG_2488	[NADP+] succinate-semialdehyde dehydrogenase	NA	1.367	1.24E-01
MSMEG_2489	transcriptional regulator, GntR family protein, putative	NA	1.148	1.17E-01
MSMEG_2490	decarboxylase	NA	1.096	2.61E-01
MSMEG_2491	acetylornithine deacetylase	NA	1.154	6.29E-01
MSMEG_2492	D-lactate dehydrogenase	NA	1.290	1.39E-01
MSMEG_2493	aminotransferase, class I and II family protein	NA	1.237	1.04E-01
MSMEG_2494	Xaa-Pro aminopeptidase	NA	0.985	7.83E-01
MSMEG_2495	decarboxylase	NA	1.076	5.58E-01
MSMEG_2496	NAD-binding protein	NA	1.090	1.15E-01
MSMEG_2497	amidase family protein	NA	0.950	7.04E-01
MSMEG_2498	conserved hypothetical protein	NA	0.817	9.69E-02
MSMEG_2499	ABC transporter, membrane spanning protein, putative	NA	1.259	4.24E-01
MSMEG_2500	conserved hypothetical protein	NA	0.963	7.14E-01
MSMEG_2501	ABC nitrate/sulfonate/bicarbonate family protein transporter, inner membrane subun	NA	0.716	7.07E-04
MSMEG_2502	transporter ATPase	NA	1.135	7.58E-01
MSMEG_2503	hypothetical protein	NA	0.721	2.48E-02
MSMEG_2504	3-isopropylmalate dehydratase small subunit	NA	1.402	6.05E-01

MSMEG_2505	3-isopropylmalate dehydratase large subunit	NA	0.914	6.73E-01
MSMEG_2506	carboxyvinyl-carboxyphosphonate phosphorylmutase	NA	0.707	1.15E-02
MSMEG_2507	IclR-family protein transcriptional regulator	NA	0.837	3.20E-01
MSMEG_2508	conserved hypothetical protein	NA	0.891	1.75E-01
MSMEG_2509	Mg-chelatase subunits D/I family protein, ComM subfamily protein	NA	1.070	6.76E-01
MSMEG_2510	smf family protein; this gene contains a frame shift which is not the result of sequenci	NA	0.875	2.67E-01
MSMEG_2510	smf family protein; this gene contains a frame shift which is not the result of sequenci	NA	1.175	3.69E-01
MSMEG_2511	siderophore utilization protein	NA	0.852	1.42E-01
MSMEG_2512	lactate 2-monooxygenase	NA	0.959	5.90E-01
MSMEG_2513	hypothetical protein	NA	0.971	7.44E-01
MSMEG_2514	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	0.773	1.77E-01
MSMEG_2514	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.161	4.63E-01
MSMEG_2515	tyrosine recombinase XerC	xerC	0.893	1.81E-01
MSMEG_2516	putative oxidoreductase	NA	0.924	1.04E-01
MSMEG_2517	hydrolase, alpha/beta fold family protein, putative	NA	0.967	7.32E-01
MSMEG_2518	peptidase M23B	NA	0.847	1.23E-01
MSMEG_2519	ribosomal protein S2	rpsB	1.126	1.24E-02
MSMEG_2520	translation elongation factor Ts	tsf	1.011	7.86E-01
MSMEG_2521	amidase	NA	1.340	3.96E-02
MSMEG_2522	efflux ABC transporter, permease protein	NA	1.061	7.27E-01
MSMEG_2523	efflux ABC transporter, permease protein, putative	NA	1.258	4.83E-01
MSMEG_2524	ABC transporter, ATP-binding protein	NA	1.439	3.33E-01
MSMEG_2525	amino acid permease superfamily protein	NA	0.881	2.24E-01
MSMEG_2526	copper methylamine oxidase	NA	1.102	6.23E-01
MSMEG_2527	hypothetical protein	NA	1.589	2.69E-02
MSMEG_2528	glycerate kinase	NA	0.876	3.18E-02
MSMEG_2529	glyoxylate reductase	NA	0.868	3.12E-02
MSMEG_2530	4-carboxymuconolactone decarboxylase domain protein	pcaC	0.988	7.25E-01
MSMEG_2531	GntR family protein transcriptional regulator	NA	0.907	4.82E-01
MSMEG_2532	dehydroquinase dehydratase, type II	aroQ	0.910	2.98E-01
MSMEG_2533	hypothetical protein	NA	0.629	5.35E-03

MSMEG_2534	putative carboxylesterase protein	NA	0.758	1.38E-01
MSMEG_2535	dehydrogenase/reductase SDR family protein member 10	NA	1.019	8.36E-01
MSMEG_2536	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.794	2.56E-01
MSMEG_2537	transporter protein	NA	0.665	4.74E-03
MSMEG_2538	MarR-family protein transcriptional regulator	NA	0.880	1.79E-01
MSMEG_2539	thiopurine S-methyltransferase (tpmt) superfamily protein	NA	0.851	2.36E-01
MSMEG_2540	uridylate kinase	pyrH	0.769	7.63E-04
MSMEG_2541	ribosome recycling factor	frr	0.835	2.69E-03
MSMEG_2542	integral membrane protein DUF6	NA	2.060	1.34E-02
MSMEG_2543	phosphatidate cytidylyltransferase	cdsA	0.980	8.55E-01
MSMEG_2544	transcriptional regulator, LysR family protein	NA	1.199	1.30E-01
MSMEG_2545	radical SAM enzyme, Cfr family protein	NA	1.088	2.57E-01
MSMEG_2546	transcriptional Regulator, GntR family protein	NA	1.009	9.40E-01
MSMEG_2547	transcriptional regulator	NA	1.081	1.03E-01
MSMEG_2548	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.957	6.72E-01
MSMEG_2549	major facilitator superfamily protein	NA	1.308	3.09E-01
MSMEG_2550	glyoxylate reductase	NA	1.351	4.71E-01
MSMEG_2551	hypothetical protein	NA	0.785	1.80E-01
MSMEG_2552	aldehyde dehydrogenase (NAD) family protein	NA	0.833	1.63E-01
MSMEG_2553	transcriptional regulator, TetR family protein	NA	0.871	3.30E-02
MSMEG_2554	phosphotransferase enzyme family protein	NA	1.132	3.22E-02
MSMEG_2555	hypothetical protein	NA	0.909	5.26E-01
MSMEG_2556	beta-glucosidase	NA	0.957	5.41E-01
MSMEG_2557	transcriptional regulator, TetR family protein	NA	1.111	3.37E-01
MSMEG_2558	NikQ protein	NA	1.317	2.07E-01
MSMEG_2559	conserved domain protein	NA	0.954	4.44E-01
MSMEG_2560	conserved hypothetical protein	NA	1.011	8.61E-01
MSMEG_2561	gluconolactonase	NA	1.043	7.06E-01
MSMEG_2562	conserved hypothetical protein	NA	1.528	1.56E-01
MSMEG_2563	cytochrome P450 superfamily protein	NA	1.264	3.24E-01
MSMEG_2564	oxidoreductase, zinc-binding dehydrogenase family protein	NA	1.089	7.75E-01

MSMEG_2565	4-hydroxy-2-oxovalerate aldolase	NA	0.934	7.02E-01
MSMEG_2566	3-alpha-(or 20-beta)-hydroxysteroid dehydrogenase	NA	0.837	1.77E-01
MSMEG_2567	probable monooxygenase	NA	1.096	6.25E-01
MSMEG_2568	LipW protein	NA	0.899	5.13E-01
MSMEG_2569	oxidoreductase, 2OG-Fe(II) oxygenase family protein	NA	0.824	4.44E-02
MSMEG_2570	xanthine/uracil permease	NA	1.083	3.23E-01
MSMEG_2571	cupin 2, conserved barrel	NA	0.837	2.96E-03
MSMEG_2572	conserved hypothetical protein	NA	0.857	7.99E-02
MSMEG_2573	conserved hypothetical protein	NA	0.939	4.67E-01
MSMEG_2574	conserved hypothetical protein	NA	1.014	8.78E-01
MSMEG_2575	conserved hypothetical protein	NA	0.997	9.56E-01
MSMEG_2576	deoxyribodipyrimidine photo-lyase	NA	1.048	5.72E-01
MSMEG_2577	hypothetical protein	NA	1.199	2.63E-01
MSMEG_2578	1-deoxy-D-xylulose 5-phosphate reductoisomerase	dxr	0.911	9.93E-02
MSMEG_2579	zinc metalloprotease	NA	0.862	6.19E-02
MSMEG_2580	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	ispG	1.000	9.89E-01
MSMEG_2581	acetyltransferase	NA	1.124	3.85E-01
MSMEG_2582	conserved hypothetical protein	NA	1.000	9.82E-01
MSMEG_2583	putative transcriptional regulator	NA	1.218	3.12E-02
MSMEG_2584	penicillin-binding protein, putative	NA	0.851	4.30E-03
MSMEG_2585	conserved hypothetical protein	NA	1.087	7.49E-02
MSMEG_2586	conserved hypothetical protein, putative	NA	1.434	6.81E-02
MSMEG_2587	methionine aminopeptidase, type I	map	1.206	3.98E-02
MSMEG_2588	cobyric acid synthase CobQ	cobQ	1.306	9.44E-03
MSMEG_2589	conserved hypothetical protein	NA	1.010	8.72E-01
MSMEG_2590	AraC-family protein transcriptional regulator	NA	1.260	2.16E-01
MSMEG_2591	hypothetical protein	NA	1.232	2.11E-01
MSMEG_2592	conserved hypothetical protein	NA	0.980	7.49E-01
MSMEG_2593	gnat-family protein acetyltransferase	NA	0.955	4.91E-01
MSMEG_2594	asparagine synthase (glutamine-hydrolyzing)	asnB	0.888	2.34E-01
MSMEG_2595	gamma-glutamylisopropylamide synthetase	NA	0.912	3.02E-01

MSMEG_2596	peptidase C26	NA	0.963	3.30E-01
MSMEG_2597	aldehyde dehydrogenase	NA	0.914	2.36E-01
MSMEG_2598	short chain dehydrogenase	NA	1.159	4.23E-01
MSMEG_2599	GntR-family protein transcriptional regulator	NA	1.006	9.39E-01
MSMEG_2600	regulatory protein	NA	0.929	2.87E-02
MSMEG_2601	protocatechuate 3,4-dioxygenase, beta subunit	pcaH	0.837	2.89E-01
MSMEG_2602	protocatechuate 3,4-dioxygenase, alpha subunit	pcaG	0.825	2.71E-01
MSMEG_2603	3-carboxy-cis,cis-muconate cycloisomerase	pcaB	0.662	2.98E-02
MSMEG_2604	4-carboxymuconolactone decarboxylase	pcaC	1.606	4.05E-01
MSMEG_2605	transcriptional regulator, GntR family protein	NA	1.142	1.50E-01
MSMEG_2606	ArsR-family protein transcriptional regulator	NA	1.146	3.43E-01
MSMEG_2607	cobalamin biosynthesis protein CbiM	cbiM	0.914	3.21E-02
MSMEG_2608	cobalt transport protein CbiM	NA	0.929	7.68E-02
MSMEG_2609	cobalt ABC transporter, permease protein CbiQ	cbiQ	1.059	2.26E-01
MSMEG_2610	cobalt transport protein ATP-binding subunit	NA	1.076	3.17E-01
MSMEG_2611	pyridine nucleotide-disulphide oxidoreductase family protein	NA	0.810	5.21E-02
MSMEG_2612	conserved hypothetical protein	NA	0.848	5.80E-03
MSMEG_2613	malate:quinone-oxidoreductase	mqo	1.218	1.15E-02
MSMEG_2614	ElaA protein	NA	1.288	2.84E-04
MSMEG_2615	chelatase	NA	1.016	5.48E-01
MSMEG_2616	cob(I)alamin adenosyltransferase	cobO	0.708	7.73E-03
MSMEG_2617	cobyrinic Acid a,c-diamide synthase	cobB	0.735	3.96E-03
MSMEG_2618	uroporphyrin-III C-methyltransferase	cobA	1.126	1.09E-01
MSMEG_2619	efflux protein	NA	1.186	2.04E-01
MSMEG_2620	hypothetical protein	NA	1.181	3.01E-01
MSMEG_2621	prolyl-tRNA synthetase	proS	1.128	2.58E-01
MSMEG_2622	conserved hypothetical alanine rich protein	NA	1.225	1.98E-01
MSMEG_2623	Tat (twin-arginine translocation) pathway signal sequence domain protein	NA	1.129	8.06E-02
MSMEG_2624	conserved hypothetical protein	NA	1.012	6.74E-01
MSMEG_2625	transcription termination factor NusA	nusA	1.040	4.33E-01
MSMEG_2626	conserved hypothetical protein	NA	0.895	1.00E-01

MSMEG_2627	hypothetical protein	NA	1.196	3.40E-01
MSMEG_2628	translation initiation factor IF-2	infB	1.047	7.74E-01
MSMEG_2629	ribosome-binding factor A	rbfA	1.287	8.73E-02
MSMEG_2630	DHH family protein	NA	1.262	1.28E-01
MSMEG_2631	MATE efflux family protein	NA	1.427	3.33E-01
MSMEG_2632	SAM-dependent methyltransferase	NA	0.913	7.66E-02
MSMEG_2633	ABC transporter ATP-binding protein	NA	1.368	3.91E-01
MSMEG_2634	conserved hypothetical protein	NA	0.657	1.62E-01
MSMEG_2635	ABC transporter permease protein	NA	1.386	2.00E-01
MSMEG_2636	regulatory protein, LacI	NA	1.260	4.76E-01
MSMEG_2637	oxidoreductase, Gfo/Idh/MocA family protein	NA	0.928	6.60E-01
MSMEG_2638	conserved hypothetical protein	NA	0.995	9.59E-01
MSMEG_2639	integral membrane protein	NA	1.456	7.68E-02
MSMEG_2640	3-dehydroshikimate dehydratase	NA	0.915	7.25E-01
MSMEG_2641	enoyl-CoA hydratase	NA	1.035	5.20E-01
MSMEG_2642	conserved hypothetical protein	NA	0.883	4.66E-02
MSMEG_2643	conserved hypothetical protein	NA	0.944	4.04E-01
MSMEG_2644	putative hydrolase	NA	0.938	3.96E-01
MSMEG_2645	conserved hypothetical protein	NA	0.904	2.54E-02
MSMEG_2647	metallophosphoesterase	NA	0.843	9.70E-02
MSMEG_2648	Sfp-type phosphopantetheinyl transferase	NA	0.917	2.10E-01
MSMEG_2649	tRNA pseudouridine synthase B	truB	0.970	6.91E-01
MSMEG_2650	acyl-CoA dehydrogenase	NA	1.106	6.49E-01
MSMEG_2651	alkanesulfonate monooxygenase family protein	NA	1.086	5.67E-01
MSMEG_2652	iron repressor protein	NA	1.228	4.47E-03
MSMEG_2653	riboflavin biosynthesis protein RibF	ribF	0.989	2.97E-01
MSMEG_2654	ribosomal protein S15	rpsO	1.218	3.65E-01
MSMEG_2655	LppU protein	NA	1.292	7.27E-03
MSMEG_2656	guanosine pentaphosphate synthetase I/polyribonucleotide nucleotidyltransferase	gpsI	1.161	2.24E-01
MSMEG_2657	peptidase, M16 family protein	NA	1.284	8.91E-02
MSMEG_2658	beta-lactamase	NA	1.154	2.50E-01

MSMEG_2659	alanine dehydrogenase	ald	1.012	9.33E-01
MSMEG_2660	transcriptional regulator, AsnC family protein	NA	1.184	4.69E-02
MSMEG_2661	domain of unknown function (306) family protein	NA	0.978	8.43E-01
MSMEG_2662	hypothetical protein	NA	1.167	5.17E-01
MSMEG_2663	conserved hypothetical protein	NA	0.833	5.19E-01
MSMEG_2664	dihydrodipicolinate reductase	dapB	1.037	4.42E-01
MSMEG_2665	conserved hypothetical protein	NA	1.058	5.22E-01
MSMEG_2666	multimeric flavodoxin WrbA	NA	0.992	8.71E-01
MSMEG_2667	HpcH/HpaI aldolase/citrate lyase family protein, putative	NA	1.051	4.36E-01
MSMEG_2668	conserved hypothetical protein	NA	1.038	6.52E-01
MSMEG_2669	hydrolase	NA	0.793	9.91E-05
MSMEG_2670	thymidylate synthase	thyA	0.918	2.32E-01
MSMEG_2671	dihydrofolate reductase	folA	1.002	9.62E-01
MSMEG_2672	acyl-CoA synthase	NA	1.299	2.55E-01
MSMEG_2673	similar at the nucleotide level to IS1137 in the IS Finder database. This gene is disrupte	NA	1.039	8.53E-01
MSMEG_2674	similar at the nucleotide level to IS1137 in the IS Finder database. This gene is disrupte	NA	1.295	2.68E-01
MSMEG_2675	ISMsm8, transposase	NA	0.954	7.45E-01
MSMEG_2676	IS1137, transposase orfA	NA	1.043	7.97E-01
MSMEG_2676	IS1137, transposase orfA	NA	1.182	3.40E-01
MSMEG_2677	conserved large membrane protein	NA	1.099	7.17E-01
MSMEG_2678	hypothetical protein	NA	1.438	4.59E-01
MSMEG_2679	conserved hypothetical protein	NA	0.974	7.81E-01
MSMEG_2680	amino acid transporter	NA	1.187	1.29E-01
MSMEG_2681	proline imino-peptidase	NA	1.183	6.84E-02
MSMEG_2682	transcriptional regulator	NA	1.125	2.61E-02
MSMEG_2683	thymidylate synthase, flavin-dependent	thyX	1.181	1.07E-01
MSMEG_2684	dihydrodipicolinate synthase	dapA	1.132	4.02E-03
MSMEG_2685	metallo-beta-lactamase superfamily protein	NA	1.139	2.16E-01
MSMEG_2686	conserved hypothetical protein	NA	1.041	7.10E-01
MSMEG_2687	carveol dehydrogenase	NA	0.962	6.43E-01
MSMEG_2688	antibiotic biosynthesis monooxygenase domain protein	NA	0.834	1.37E-02

MSMEG_2689	hypothetical protein	NA	1.014	9.11E-01
MSMEG_2690	DNA translocase FtsK	NA	1.499	6.61E-03
MSMEG_2691	acetyltransferase, gnat family protein	NA	1.381	5.85E-03
MSMEG_2692	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	pgsA	0.991	8.39E-01
MSMEG_2693	competence-damaged protein	NA	1.201	1.46E-01
MSMEG_2694	transcriptional regulator, XRE family protein	NA	0.885	2.42E-01
MSMEG_2695	35 kDa protein	NA	0.834	3.97E-02
MSMEG_2696	putative conserved membrane alanine rich protein	NA	0.972	3.17E-01
MSMEG_2697	conserved hypothetical protein	NA	0.975	6.15E-01
MSMEG_2698	conserved hypothetical protein	NA	0.974	7.11E-01
MSMEG_2699	conserved hypothetical protein	NA	0.994	8.98E-01
MSMEG_2700	conserved hypothetical protein	NA	1.029	8.48E-01
MSMEG_2701	hypothetical protein	NA	0.917	2.65E-01
MSMEG_2702	hydrogenase expression/formation protein HypD	hypD	0.987	9.25E-01
MSMEG_2703	hydrogenase assembly chaperone HypC/HupF	hypC	2.344	4.23E-01
MSMEG_2704	transposase; this gene contains a frame shift which is not the result of sequencing erro	NA	1.101	4.22E-02
MSMEG_2705	hydrogenase expression/formation protein HypE	hypE	1.098	3.37E-01
MSMEG_2706	phosphoheptose isomerase	gmhA	0.977	7.73E-01
MSMEG_2707	hypothetical protein	NA	1.024	3.41E-01
MSMEG_2708	hypothetical protein	NA	1.117	5.70E-01
MSMEG_2709	hypothetical protein	NA	0.967	7.98E-01
MSMEG_2710	hypothetical protein	NA	0.696	5.69E-02
MSMEG_2711	[NiFe] hydrogenase maturation protein HypF	hypF	1.000	9.97E-01
MSMEG_2712	hydrogenase assembly chaperone HypC/HupF	hypC	1.011	9.60E-01
MSMEG_2713	peptidase M52, hydrogen uptake protein	NA	1.341	5.08E-01
MSMEG_2714	hypothetical protein	NA	1.612	9.12E-02
MSMEG_2715	conserved hypothetical protein	NA	1.042	7.98E-01
MSMEG_2716	conserved hypothetical protein	NA	1.129	6.15E-01
MSMEG_2717	conserved hypothetical protein	NA	2.536	2.69E-01
MSMEG_2718	iron-sulfur cluster-binding protein, Rieske family protein, putative	NA	0.926	2.73E-01
MSMEG_2719	hydrogen:quinone oxidoreductase	NA	0.974	8.66E-01

MSMEG_2720	NADH ubiquinone oxidoreductase, 20 kda subunit	NA	0.728	1.47E-01
MSMEG_2721	hydrogenase accessory protein HypB	hypB	1.154	5.45E-01
MSMEG_2722	hydrogenase nickel insertion protein HypA	hypA	1.141	4.53E-01
MSMEG_2723	protein RecA	recA	0.847	4.03E-02
MSMEG_2724	regulatory protein RecX	NA	1.111	9.25E-03
MSMEG_2725	glutamate transporter permease protein GluD	NA	0.859	5.67E-02
MSMEG_2726	glutamate permease	NA	0.856	8.03E-02
MSMEG_2727	glutamate binding protein	NA	0.801	6.69E-03
MSMEG_2728	glutamate transport ATP-binding protein GluA	NA	1.125	6.20E-02
MSMEG_2729	tRNA-I(6)A37 thiotransferase enzyme MiaB	miaB	1.227	6.05E-03
MSMEG_2730	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.083	3.47E-01
MSMEG_2730	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.250	3.75E-02
MSMEG_2731	ATPase involved in DNA repair	NA	1.422	4.52E-02
MSMEG_2732	conserved hypothetical protein	NA	1.365	3.81E-01
MSMEG_2733	conserved hypothetical protein	NA	1.203	2.15E-01
MSMEG_2734	tRNA delta(2)-isopentenylpyrophosphate transferase	miaA	1.271	1.88E-01
MSMEG_2735	diaminopimelate epimerase	dapF	1.223	4.81E-02
MSMEG_2736	GTP-binding protein	NA	1.524	7.91E-02
MSMEG_2737	ppe family protein	NA	1.359	3.64E-01
MSMEG_2738	biotin sulfoxide reductase	NA	1.077	4.71E-01
MSMEG_2739	conserved hypothetical protein	NA	0.861	3.86E-02
MSMEG_2740	LexA repressor	lexA	1.045	3.79E-01
MSMEG_2741	hypothetical protein	NA	0.972	7.88E-01
MSMEG_2742	DNA-damage-inducible protein	NA	1.095	2.39E-01
MSMEG_2743	transcriptional regulator, NrdR family protein	nrdR	1.027	6.46E-01
MSMEG_2744	thymidylate synthase	NA	0.942	3.66E-01
MSMEG_2745	hydrolase; this gene contains a frame shift which is not the result of sequencing error;	NA	1.233	1.34E-01
MSMEG_2746	conserved hypothetical alanine and leucine rich protein	NA	1.461	2.32E-02
MSMEG_2747	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.029	7.33E-01
MSMEG_2747	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.323	2.16E-01
MSMEG_2748	soluble pyridine nucleotide transhydrogenase	sthA	0.967	7.31E-01

MSMEG_2749	conserved hypothetical protein	NA	1.013	9.37E-01
MSMEG_2750	iron-dependent repressor IdeR	NA	0.887	3.72E-02
MSMEG_2751	hypothetical protein	NA	0.910	1.11E-01
MSMEG_2752	sigma factor SigB	NA	0.814	2.58E-02
MSMEG_2753	conserved hypothetical protein	NA	0.923	7.48E-02
MSMEG_2754	conserved hypothetical protein	NA	1.049	8.06E-01
MSMEG_2755	conserved hypothetical protein	NA	0.985	6.25E-01
MSMEG_2756	conserved hypothetical protein	NA	1.166	1.79E-01
MSMEG_2757	glutathione S-transferase domain protein	NA	0.961	5.04E-01
MSMEG_2758	sigma factor MysA	NA	0.967	2.99E-01
MSMEG_2759	hypothetical protein	NA	1.367	5.89E-02
MSMEG_2760	polyphosphate glucokinase	NA	0.862	1.24E-02
MSMEG_2761	putative secreted alanine rich protein	NA	1.118	3.54E-02
MSMEG_2762	inositol-1-monophosphatase	NA	0.938	6.70E-01
MSMEG_2763	conserved hypothetical protein	NA	1.041	7.47E-01
MSMEG_2764	probable conserved alanine rich transmembrane protein	NA	1.076	2.15E-01
MSMEG_2765	deoxyuridine 5'-triphosphate nucleotidohydrolase	NA	1.194	9.67E-03
MSMEG_2766	conserved hypothetical protein	NA	1.148	8.17E-02
MSMEG_2767	conserved hypothetical protein	NA	0.912	3.54E-01
MSMEG_2768	OB-fold nucleic acid binding domain protein	NA	0.943	7.25E-01
MSMEG_2769	TrkB protein	NA	0.945	3.70E-01
MSMEG_2770	probable conserved integral membrane alanine and leucine rich protein	NA	0.967	6.10E-01
MSMEG_2771	TrkA protein	NA	0.965	5.30E-01
MSMEG_2772	amino acid permease	NA	1.060	3.62E-01
MSMEG_2773	hypothetical RNA methyltransferase	NA	1.283	1.65E-02
MSMEG_2774	diguanylate cyclase (ggdef) domain protein	NA	1.074	1.58E-01
MSMEG_2775	Na+/H+ antiporter NhaA	nhaA	0.968	6.03E-01
MSMEG_2776	1-deoxy-D-xylulose-5-phosphate synthase	dxs	1.132	1.50E-01
MSMEG_2777	alpha/beta hydrolase fold	NA	1.351	3.31E-02
MSMEG_2778	ribonuclease D	NA	0.864	3.70E-02
MSMEG_2778	ribonuclease D	NA	1.263	1.35E-01

MSMEG_2779	conserved hypothetical protein	NA	0.874	3.37E-03
MSMEG_2780	uroporphyrinogen decarboxylase	hemE	1.052	2.46E-01
MSMEG_2781	protoporphyrinogen oxidase	hemG	1.063	4.98E-01
MSMEG_2782	conserved hypothetical protein	NA	1.036	3.14E-01
MSMEG_2783	hypothetical protein	NA	1.111	7.44E-02
MSMEG_2784	methionine-R-sulfoxide reductase	msrB	1.093	9.58E-02
MSMEG_2785	putative conserved integral membrane protein	NA	1.101	1.08E-01
MSMEG_2786	hydrolase, alpha/beta fold family protein	NA	1.253	7.04E-02
MSMEG_2787	putative riboflavin biosynthesis protein RibD	NA	1.087	4.31E-01
MSMEG_2788	ATP/GTP-binding integral membrane protein	NA	1.419	1.01E-02
MSMEG_2789	acetyltransferase, GNAT family protein	NA	1.121	2.83E-01
MSMEG_2790	conserved hypothetical protein	NA	1.074	3.25E-01
MSMEG_2791	pyridoxamine 5'-phosphate oxidase family protein	NA	1.709	5.98E-03
MSMEG_2792	Clp amino terminal domain protein	NA	0.842	2.07E-01
MSMEG_2793	sensor-type histidine kinase PrrB	NA	1.199	2.76E-02
MSMEG_2794	transcriptional regulator, GntR family protein	NA	1.429	3.04E-02
MSMEG_2795	transmembrane transport protein	NA	1.996	1.73E-02
MSMEG_2796	integral membrane protein	NA	0.935	2.06E-01
MSMEG_2797	LysR-family protein transcriptional regulator	NA	0.781	1.99E-01
MSMEG_2798	hypothetical protein	NA	0.823	2.30E-01
MSMEG_2799	phospho-2-dehydro-3-deoxyheptonate aldolase	NA	1.116	1.52E-01
MSMEG_2800	NADPH-dependent fmn reductase	NA	0.819	2.19E-02
MSMEG_2801	hypothetical protein	NA	1.158	5.62E-01
MSMEG_2802	hypothetical protein	NA	0.965	5.99E-01
MSMEG_2802	hypothetical protein	NA	1.158	1.67E-01
MSMEG_2803	hypothetical protein	NA	1.103	2.69E-01
MSMEG_2804	two-component system sensor kinase	NA	0.871	4.15E-01
MSMEG_2805	ISMsm5, transposase	NA	0.876	9.93E-03
MSMEG_2805	ISMsm5, transposase	NA	0.970	7.08E-01
MSMEG_2805	ISMsm5, transposase	NA	1.070	4.89E-01
MSMEG_2806	two-component system response regulator	NA	0.893	5.49E-03

MSMEG_2807	two-component system response regulator	NA	1.004	9.59E-01
MSMEG_2808	short-chain dehydrogenase/reductase SDR	NA	0.887	5.40E-01
MSMEG_2809	conserved hypothetical protein	NA	0.890	5.88E-01
MSMEG_2810	major facilitator superfamily protein	NA	2.876	4.16E-01
MSMEG_2811	hydride transferase 1	NA	0.949	6.52E-01
MSMEG_2812	C-5 sterol desaturase	NA	1.352	5.30E-01
MSMEG_2813	sensor kinase	NA	2.172	2.04E-01
MSMEG_2814	two component system response regulator; this gene contains a frame shift which is n	NA	5.616	3.92E-01
MSMEG_2815	putative tape-measure protein; this region contains one or more premature stops and	NA	0.943	7.27E-01
MSMEG_2815	putative tape-measure protein; this region contains one or more premature stops and	NA	1.523	1.86E-01
MSMEG_2816	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.149	5.29E-01
MSMEG_2817	ABC efflux pump, fused inner membrane and ATPase subunits	NA	0.763	1.20E-02
MSMEG_2818	ISMsm1, transposase orfB	NA	0.882	2.51E-01
MSMEG_2818	ISMsm1, transposase orfB	NA	1.077	3.07E-01
MSMEG_2819	ISMsm1, transposase orfA	NA	0.898	2.80E-01
MSMEG_2819	ISMsm1, transposase orfA	NA	1.198	1.87E-01
MSMEG_2820	hypothetical protein	NA	0.671	3.00E-03
MSMEG_2822	transposase, truncation	NA	0.756	2.66E-03
MSMEG_2823	This gene is disrupted by an IS1549 element.; IS1549, transposase, interruption-N; ide	NA	0.880	4.52E-01
MSMEG_2823	This gene is disrupted by an IS1549 element.; IS1549, transposase, interruption-N; ide	NA	0.905	5.71E-01
MSMEG_2824	IS1549, transposase	NA	0.862	2.28E-01
MSMEG_2824	IS1549, transposase	NA	0.947	6.46E-01
MSMEG_2824	IS1549, transposase	NA	1.036	7.70E-01
MSMEG_2824	IS1549, transposase	NA	1.253	2.70E-01
MSMEG_2826	hypothetical protein	NA	0.719	1.75E-02
MSMEG_2827	hypothetical protein	NA	1.301	2.15E-01
MSMEG_2830	ISMsm4, transposase	NA	1.080	6.37E-01
MSMEG_2830	ISMsm4, transposase	NA	1.502	1.51E-01
MSMEG_2831	hypothetical protein	NA	0.850	1.06E-01
MSMEG_2832	hypothetical protein	NA	1.097	2.91E-01
MSMEG_2837	nitrate reductase NarB	NA	0.996	8.97E-01

MSMEG_2838	conserved hypothetical protein	NA	1.004	9.74E-01
MSMEG_2839	transcriptional accessory protein	NA	1.031	1.93E-01
MSMEG_2840	conserved hypothetical protein	NA	1.102	4.57E-01
MSMEG_2841	putative monooxygenase	NA	0.994	9.70E-01
MSMEG_2842	nitrilotriacetate monooxygenase component A	ssuD	0.984	8.03E-01
MSMEG_2843	nitrilotriacetate monooxygenase component A	ssuD	0.924	1.61E-01
MSMEG_2844	ABC transporter, ATP-binding protein	NA	1.236	2.97E-01
MSMEG_2845	ABC transporter permease protein	NA	1.139	4.59E-01
MSMEG_2846	ABC transporter permease protein	NA	1.560	1.95E-01
MSMEG_2847	bacterial extracellular solute-binding protein, family protein 5	NA	1.471	1.12E-01
MSMEG_2848	transmembrane efflux protein	NA	0.973	7.52E-01
MSMEG_2849	transcriptional regulatory protein	NA	0.813	3.03E-02
MSMEG_2850	mycobacterial family protein 11 protein	NA	1.243	1.18E-01
MSMEG_2851	conserved hypothetical protein	NA	2.746	3.43E-01
MSMEG_2852	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.117	5.43E-01
MSMEG_2853	conserved hypothetical protein	NA	1.054	8.27E-01
MSMEG_2854	conserved hypothetical protein	NA	2.448	3.58E-01
MSMEG_2855	virulence factor Mce family protein	NA	0.977	8.34E-01
MSMEG_2856	virulence factor Mce family protein	NA	1.047	7.56E-01
MSMEG_2857	virulence factor Mce family protein	NA	1.340	3.58E-01
MSMEG_2858	virulence factor mce family protein	NA	0.972	8.43E-01
MSMEG_2859	virulence factor Mce family protein	NA	1.089	6.12E-01
MSMEG_2860	virulence factor mce family protein	NA	0.891	2.92E-01
MSMEG_2861	conserved hypothetical protein	NA	0.991	9.11E-01
MSMEG_2862	conserved hypothetical protein	NA	0.914	1.47E-01
MSMEG_2863	conserved hypothetical protein	NA	0.997	9.65E-01
MSMEG_2864	conserved hypothetical protein	NA	1.435	3.72E-01
MSMEG_2865	conserved hypothetical protein	NA	1.244	3.41E-01
MSMEG_2866	thioesterase family protein	NA	2.008	2.23E-01
MSMEG_2867	3-ketosteroid dehydrogenase	NA	1.050	7.39E-01
MSMEG_2868	transcriptional regulator, PadR family protein	NA	1.035	7.61E-01

MSMEG_2869	3-ketosteroid-delta-1-dehydrogenase	NA	0.887	1.71E-01
MSMEG_2870	oxygenase KshA	NA	1.004	9.86E-01
MSMEG_2871	conserved hypothetical protein	NA	1.050	3.26E-01
MSMEG_2872	short-chain dehydrogenase/reductase SDR	NA	1.174	1.82E-01
MSMEG_2873	3-ketosteroid-delta4	NA	0.810	2.02E-01
MSMEG_2874	conserved hypothetical protein	NA	0.739	1.08E-01
MSMEG_2875	esterase	NA	1.149	1.70E-01
MSMEG_2876	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.174	5.02E-01
MSMEG_2877	conserved hypothetical protein	NA	1.188	5.64E-01
MSMEG_2878	putative acyl-CoA dehydrogenase	NA	1.090	4.44E-01
MSMEG_2879	acyl-CoA dehydrogenase	NA	0.974	4.62E-01
MSMEG_2880	enoyl-CoA hydratase	NA	0.899	1.31E-01
MSMEG_2881	aldehyde dehydrogenase	NA	1.058	5.72E-01
MSMEG_2882	5-exo-alcohol dehydrogenase	NA	0.949	6.40E-01
MSMEG_2883	feruloyl-CoA synthetase	NA	0.900	7.41E-02
MSMEG_2884	cyclohexanone monooxygenase	NA	1.271	4.10E-01
MSMEG_2885	short-chain dehydrogenase/reductase SDR	NA	1.166	2.11E-01
MSMEG_2886	stress responsive A/B Barrel Domain family protein	NA	2.066	3.94E-01
MSMEG_2887	conserved hypothetical protein	NA	1.606	2.77E-01
MSMEG_2888	lipase	NA	2.129	3.54E-01
MSMEG_2889	NADH:flavin oxidoreductase/nadh oxidase	NA	0.854	5.49E-01
MSMEG_2890	putative transcriptional regulator	NA	0.955	5.18E-01
MSMEG_2891	biphenyl-2,3-diol 1,2-dioxygenase 1	NA	1.056	3.78E-01
MSMEG_2892	pigment production hydroxylase	NA	1.210	3.18E-01
MSMEG_2893	oxidoreductase, NAD/FAD-binding	NA	1.136	6.65E-01
MSMEG_2894	steroid monooxygenase	NA	0.975	8.64E-01
MSMEG_2895	short chain oxidoreductase	NA	0.919	3.27E-01
MSMEG_2896	conserved hypothetical protein	NA	1.300	1.29E-01
MSMEG_2897	conserved hypothetical protein	NA	1.000	9.98E-01
MSMEG_2898	transcriptional regulator, TetR family protein	NA	1.137	2.81E-01
MSMEG_2899	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.197	2.09E-02

MSMEG_2900	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase	NA	0.789	7.44E-03
MSMEG_2901	conserved hypothetical protein	NA	1.196	1.98E-01
MSMEG_2902	hydrolase, putative	NA	1.020	8.05E-01
MSMEG_2903	transposase; this gene contains a frame shift which is not the result of sequencing errc	NA	0.916	1.72E-01
MSMEG_2903	transposase; this gene contains a frame shift which is not the result of sequencing errc	NA	1.042	4.96E-01
MSMEG_2903	transposase; this gene contains a frame shift which is not the result of sequencing errc	NA	1.118	6.54E-02
MSMEG_2904	MmcI protein	NA	0.988	9.02E-01
MSMEG_2905	transcriptional regulator	NA	1.240	2.97E-01
MSMEG_2906	conserved hypothetical protein	NA	2.132	1.00E-01
MSMEG_2907	hypothetical oxidoreductase YeiQ	NA	1.015	8.05E-01
MSMEG_2908	2-Keto-3-deoxy-gluconate kinase	NA	0.977	8.90E-01
MSMEG_2909	starvation-sensing protein RspA	NA	1.080	6.64E-01
MSMEG_2910	transcriptional regulator, GntR family protein	NA	1.129	7.64E-02
MSMEG_2911	integral membrane transport protein	NA	1.155	6.09E-01
MSMEG_2912	inner membrane metabolite transport protein YdfJ	NA	0.939	4.09E-01
MSMEG_2913	hydrolase	NA	1.891	4.13E-01
MSMEG_2914	L-idonate 5-dehydrogenase	NA	0.958	6.89E-01
MSMEG_2915	sensor histidine kinase	NA	1.011	8.95E-01
MSMEG_2916	DNA-binding response regulator, PhoP family protein	NA	1.067	7.04E-01
MSMEG_2917	hypothetical protein	NA	0.951	5.05E-01
MSMEG_2918	short-chain dehydrogenase/reductase SDR	NA	1.132	4.75E-01
MSMEG_2919	2-dehydropantoate 2-reductase	NA	1.014	8.92E-01
MSMEG_2920	aldo/keto reductase	NA	1.473	1.12E-01
MSMEG_2921	NADPH-flavin oxidoreductase	NA	3.621	3.62E-01
MSMEG_2922	conserved hypothetical protein	NA	1.097	7.71E-03
MSMEG_2923	dehydrogenase/reductase SDR family protein member 1	NA	1.079	4.74E-01
MSMEG_2924	permease binding-protein component	NA	0.769	2.16E-01
MSMEG_2925	permease membrane component	NA	1.565	4.73E-01
MSMEG_2926	glycine betaine/carnitine/choline transport ATP-binding protein opuCA	NA	1.110	7.31E-01
MSMEG_2927	ABC transporter, permease protein OpuCB	NA	1.204	6.13E-01
MSMEG_2928	conserved hypothetical protein	NA	1.294	3.46E-02

MSMEG_2929	thioesterase family protein	NA	1.032	4.24E-01
MSMEG_2930	conserved hypothetical protein TIGR02611	NA	0.964	3.70E-01
MSMEG_2931	threonyl-tRNA synthetase	thrS	1.060	2.73E-01
MSMEG_2932	HIT family protein hydrolase	NA	1.100	2.57E-01
MSMEG_2933	phosphatidylinositol synthase	NA	1.131	5.79E-02
MSMEG_2934	lipid A biosynthesis lauroyl acyltransferase	NA	1.077	1.99E-01
MSMEG_2935	phosphatidylinositol alpha-mannosyltransferase	NA	1.172	7.09E-02
MSMEG_2936	hydrolase, nudix family protein	NA	0.824	1.54E-02
MSMEG_2937	pyridoxine biosynthesis protein	NA	1.252	1.45E-02
MSMEG_2938	acyl-CoA thioesterase II	tesB	1.241	4.63E-02
MSMEG_2939	glutamine amidotransferase subunit PdxT	NA	1.167	2.33E-01
MSMEG_2940	conserved hypothetical protein	NA	0.978	6.43E-01
MSMEG_2941	NAD dependent epimerase/dehydratase family protein	NA	1.202	1.49E-01
MSMEG_2942	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	NA	1.053	3.60E-01
MSMEG_2943	crossover junction endodeoxyribonuclease RuvC	ruvC	0.875	2.07E-02
MSMEG_2944	holliday junction DNA helicase RuvA	ruvA	0.857	1.81E-02
MSMEG_2945	holliday junction DNA helicase RuvB	ruvB	0.913	1.38E-01
MSMEG_2946	transmembrane protein	NA	1.075	1.85E-01
MSMEG_2947	polyketide cyclase	NA	0.778	5.04E-03
MSMEG_2948	6-oxocamphor hydrolase	NA	0.843	2.24E-02
MSMEG_2949	carbon-monoxide dehydrogenase	NA	0.859	3.55E-01
MSMEG_2950	carbon monoxide dehydrogenase, medium chain	NA	1.844	2.46E-01
MSMEG_2951	[2Fe-2S] binding domain protein	NA	1.594	8.76E-02
MSMEG_2952	transport gene	NA	1.005	8.36E-01
MSMEG_2953	ethyl tert-butyl ether degradation EthD	NA	0.812	9.95E-03
MSMEG_2954	LacI-family protein transcriptional regulator	NA	0.941	2.54E-01
MSMEG_2955	conserved hypothetical protein	NA	1.029	7.52E-01
MSMEG_2956	NAD dependent epimerase/dehydratase family protein	NA	1.121	6.96E-01
MSMEG_2957	conserved hypothetical protein	NA	1.353	3.89E-03
MSMEG_2958	conserved hypothetical protein	NA	1.144	5.71E-01
MSMEG_2959	4-aminobutyrate transaminase	gabT	1.192	3.63E-01

MSMEG_2960	preprotein translocase, YajC subunit	yajC	0.898	5.79E-02
MSMEG_2961	protein-export membrane protein SecD	secD	0.832	1.68E-02
MSMEG_2962	protein-export membrane protein SecF	NA	0.880	2.97E-01
MSMEG_2963	bacterial extracellular solute-binding protein, family protein 5	NA	0.762	2.43E-02
MSMEG_2964	adenine phosphoribosyltransferase	NA	0.761	6.95E-03
MSMEG_2965	GTP pyrophosphokinase	relA	1.303	5.30E-02
MSMEG_2966	major facilitator family protein transporter	NA	1.087	2.22E-01
MSMEG_2967	conserved hypothetical protein	NA	0.998	9.77E-01
MSMEG_2968	conserved hypothetical protein	NA	0.951	5.89E-02
MSMEG_2969	NADH:flavin oxidoreductase/nadh oxidase	NA	0.986	9.59E-01
MSMEG_2970	polysaccharide deacetylase	NA	0.954	6.30E-01
MSMEG_2971	regulatory protein	NA	1.126	1.77E-01
MSMEG_2972	permease, cytosine/purines, uracil, thiamine, allantoin family protein	NA	0.932	3.88E-01
MSMEG_2972	permease, cytosine/purines, uracil, thiamine, allantoin family protein	NA	1.135	3.81E-01
MSMEG_2973	peptidyl-prolyl cis-trans isomerase	NA	1.082	6.17E-01
MSMEG_2974	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	NA	0.950	4.68E-01
MSMEG_2975	metallo-beta-lactamase family protein	NA	1.147	7.48E-02
MSMEG_2976	histidyl-tRNA synthetase	hisS	1.002	9.84E-01
MSMEG_2977	hypothetical protein	NA	1.197	3.86E-01
MSMEG_2978	ABC transporter ATP-binding protein	NA	0.866	3.26E-01
MSMEG_2979	ABC transporter ATP-binding protein	NA	0.832	3.29E-01
MSMEG_2980	putative membrane protein	NA	0.739	3.43E-02
MSMEG_2981	branched-chain amino acid ABC-type transport system, permease component	NA	0.649	8.13E-04
MSMEG_2982	putative periplasmic binding protein	NA	0.867	2.66E-01
MSMEG_2983	conserved hypothetical protein	NA	1.073	7.68E-01
MSMEG_2984	putative hydrolase	NA	1.352	3.20E-01
MSMEG_2985	fumarate hydratase class I, anaerobic	NA	2.200	3.76E-01
MSMEG_2986	amidohydrolase, AtzE family protein	NA	1.331	5.95E-01
MSMEG_2987	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	2.300	3.81E-01
MSMEG_2988	carbon-nitrogen hydrolase family protein	NA	3.875	4.19E-01
MSMEG_2989	LacI family protein transcriptional regulator	NA	0.792	9.40E-03

MSMEG_2990	Fe-S protein, radical SAM family protein	NA	1.093	7.35E-01
MSMEG_2991	permease of the major facilitator superfamily protein	NA	1.624	2.21E-02
MSMEG_2992	putative acyl-CoA dehydrogenase	NA	0.759	1.53E-01
MSMEG_2993	acyl-CoA dehydrogenase, C- domain protein	NA	1.205	2.30E-01
MSMEG_2994	amidohydrolase family protein	NA	1.014	7.07E-01
MSMEG_2995	transcriptional regulator, TetR family protein	NA	1.337	3.36E-01
MSMEG_2996	conserved hypothetical protein	NA	0.981	9.24E-01
MSMEG_2997	conserved hypothetical protein	NA	1.366	3.25E-01
MSMEG_2998	conserved hypothetical protein	NA	1.099	2.72E-01
MSMEG_2998	conserved hypothetical protein	NA	1.249	5.98E-02
MSMEG_2999	conserved protein	NA	1.033	7.01E-01
MSMEG_3000	metallopeptidase, zinc binding	NA	0.998	9.74E-01
MSMEG_3001	conserved hypothetical protein	NA	1.154	2.06E-01
MSMEG_3002	para-nitrobenzyl esterase	NA	1.003	9.86E-01
MSMEG_3003	aspartyl-tRNA synthetase	aspS	1.078	3.78E-01
MSMEG_3004	conserved hypothetical protein TIGR00026	NA	1.189	2.53E-01
MSMEG_3005	hydroxyacyl-CoA dehydrogenase	NA	1.195	5.73E-01
MSMEG_3006	Fe-dependent alcohol dehydrogenase	NA	1.649	2.42E-01
MSMEG_3007	succinate-semialdehyde dehydrogenase	NA	1.384	4.77E-01
MSMEG_3008	putative sigma 54 type regulator	NA	0.931	7.49E-01
MSMEG_3009	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	NA	1.076	7.05E-01
MSMEG_3010	acetyl-hydrolase	NA	0.914	4.81E-01
MSMEG_3011	steroid monooxygenase	NA	0.961	7.89E-01
MSMEG_3012	acetyl-CoA acetyltransferases	NA	1.747	1.28E-01
MSMEG_3013	putative transcriptional regulator family protein	NA	1.095	8.28E-02
MSMEG_3014	conserved hypothetical protein	NA	0.917	4.40E-01
MSMEG_3015	conserved hypothetical protein	NA	1.186	1.37E-01
MSMEG_3016	conserved hypothetical protein	NA	1.158	6.35E-01
MSMEG_3017	conserved hypothetical protein	NA	2.083	4.68E-01
MSMEG_3018	transglutaminase domain protein	NA	0.967	7.00E-01
MSMEG_3019	conserved hypothetical protein	NA	0.996	9.78E-01

MSMEG_3020	conserved hypothetical protein	NA	1.044	4.65E-01
MSMEG_3021	AAA ATPase, central region	NA	1.075	2.06E-01
MSMEG_3022	transglycosylase associated protein	NA	1.023	9.01E-01
MSMEG_3023	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.679	5.84E-02
MSMEG_3024	conserved hypothetical protein	NA	1.084	7.11E-01
MSMEG_3025	alanyl-tRNA synthetase	alaS	1.125	2.61E-02
MSMEG_3026	conserved hypothetical protein	NA	1.152	1.50E-01
MSMEG_3027	conserved hypothetical protein	NA	1.109	2.48E-01
MSMEG_3028	shikimate-5-dehydrogenase	aroE	1.064	4.40E-01
MSMEG_3029	peptidase, A24 (type IV prepilin peptidase) family protein	NA	1.159	1.14E-01
MSMEG_3030	chorismate synthase	aroC	1.060	2.64E-01
MSMEG_3031	shikimate kinase	NA	1.194	2.27E-02
MSMEG_3032	conserved hypothetical protein	NA	0.870	1.29E-02
MSMEG_3033	3-dehydroquinate synthase	aroB	1.046	6.52E-01
MSMEG_3034	metallopeptidase, M24 family protein	NA	0.880	1.73E-02
MSMEG_3035	translation elongation factor P	efp	0.962	3.61E-01
MSMEG_3036	transcription antitermination factor NusB	nusB	1.172	4.42E-02
MSMEG_3037	regulatory protein; this gene contains a frame shift which is not the result of sequenci	NA	1.186	1.02E-01
MSMEG_3038	hypothetical protein	NA	1.017	7.15E-01
MSMEG_3039	monooxygenase	NA	1.073	1.12E-01
MSMEG_3040	beta-lactamase	NA	0.999	9.93E-01
MSMEG_3041	thiopurine S-methyltransferase (tpmt) superfamily protein	NA	1.088	8.09E-02
MSMEG_3042	PyrR bifunctional protein	NA	1.103	1.08E-01
MSMEG_3043	aspartate carbamoyltransferase	pyrB	0.953	1.01E-01
MSMEG_3044	dihydroorotase	NA	0.938	1.58E-01
MSMEG_3045	integral membrane protein	NA	0.926	2.47E-01
MSMEG_3046	carbamoyl-phosphate synthase, small subunit	carA	0.813	1.38E-02
MSMEG_3047	carbamoyl-phosphate synthase, large subunit	carB	0.811	1.91E-02
MSMEG_3048	orotidine 5'-phosphate decarboxylase	pyrF	0.950	6.41E-01
MSMEG_3049	hypothetical protein	NA	1.017	9.29E-01
MSMEG_3050	integration host factor	NA	0.825	1.40E-01

MSMEG_3051	guanylate kinase	NA	0.833	2.87E-05
MSMEG_3052	hypothetical protein	NA	1.756	3.79E-01
MSMEG_3053	DNA-directed RNA polymerase, omega subunit	rpoZ	1.083	1.88E-02
MSMEG_3054	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	coaBC	0.841	2.54E-02
MSMEG_3055	S-adenosylmethionine synthetase	metK	0.823	3.27E-03
MSMEG_3056	ABC transporter ATP-binding protein	NA	1.001	9.81E-01
MSMEG_3057	ABC-type metal ion transport system, permease component	NA	0.873	3.75E-02
MSMEG_3058	lipoprotein, nlpa family protein	NA	0.802	3.08E-02
MSMEG_3058	lipoprotein, nlpa family protein	NA	0.820	3.00E-02
MSMEG_3059	esterase	NA	0.934	1.78E-01
MSMEG_3060	conserved hypothetical protein	NA	1.049	6.10E-01
MSMEG_3061	primosomal protein N'	priA	1.110	1.43E-01
MSMEG_3062	conserved hypothetical protein	NA	0.981	9.41E-01
MSMEG_3063	LemA protein	NA	0.938	1.66E-01
MSMEG_3064	methionyl-tRNA formyltransferase	fmt	1.014	8.39E-01
MSMEG_3065	ribosomal RNA small subunit methyltransferase B	sun	1.119	1.02E-01
MSMEG_3066	ribulose-phosphate 3-epimerase	rpe	1.180	1.51E-03
MSMEG_3067	riboflavin biosynthesis protein RibD	ribD	1.119	1.28E-02
MSMEG_3068	hypothetical protein	NA	1.249	2.58E-02
MSMEG_3069	aminoglycosides/tetracycline-transport integral membrane protein	NA	1.068	5.35E-01
MSMEG_3070	LprG protein	NA	1.140	2.38E-01
MSMEG_3071	riboflavin synthase, alpha subunit	ribE	0.974	6.21E-01
MSMEG_3072	riboflavin biosynthesis protein ribAB	NA	0.922	7.43E-02
MSMEG_3073	6,7-dimethyl-8-ribityllumazine synthase	ribE	1.038	5.76E-01
MSMEG_3074	conserved hypothetical protein	NA	1.013	6.96E-01
MSMEG_3075	acetyltransferase, GNAT family protein	NA	1.407	1.47E-01
MSMEG_3076	gamma-glutamyltransferase	ggt	0.852	5.54E-02
MSMEG_3077	hypothetical protein	NA	1.278	3.23E-01
MSMEG_3078	excinuclease ABC, C subunit	uvrC	1.238	7.60E-03
MSMEG_3079	conserved hypothetical protein	NA	0.965	3.95E-01
MSMEG_3080	conserved hypothetical protein	NA	1.163	8.52E-02

MSMEG_3081	conserved hypothetical protein	NA	1.133	9.98E-02
MSMEG_3082	soul heme-binding protein	NA	1.719	6.82E-03
MSMEG_3083	nucleoside-diphosphate sugar epimerase	NA	1.960	1.67E-01
MSMEG_3084	glyceraldehyde-3-phosphate dehydrogenase, type I	gap	0.973	5.92E-01
MSMEG_3085	phosphoglycerate kinase	pgk	0.912	3.56E-01
MSMEG_3086	triosephosphate isomerase	tpiA	1.036	7.12E-01
MSMEG_3087	preprotein translocase, SecG subunit	secG	1.219	8.09E-02
MSMEG_3088	O-methyltransferase; this gene contains a premature stop which is not the result of se	NA	1.272	1.88E-01
MSMEG_3088	O-methyltransferase; this gene contains a premature stop which is not the result of se	NA	1.399	3.46E-02
MSMEG_3089	deoxyribose-phosphate aldolase	deoC	0.945	6.82E-01
MSMEG_3090	ribose transport system permease protein RbsC	NA	0.570	1.54E-02
MSMEG_3091	ribose transport ATP-binding protein RbsA	NA	0.969	8.12E-01
MSMEG_3092	transcriptional regulator, sugar-binding family protein	NA	2.085	5.16E-01
MSMEG_3093	putative sugar kinase protein	NA	0.872	5.30E-01
MSMEG_3094	oxidoreductase, zinc-binding dehydrogenase family protein	NA	0.634	4.08E-02
MSMEG_3095	D-ribose-binding periplasmic protein	NA	0.554	2.39E-03
MSMEG_3096	hypothetical protein	NA	0.970	8.26E-01
MSMEG_3097	phosphoenolpyruvate carboxylase	ppc	0.986	7.00E-01
MSMEG_3098	conserved hypothetical protein	NA	1.313	1.61E-02
MSMEG_3099	6-phosphogluconolactonase	pgl	0.879	1.64E-01
MSMEG_3100	OpcA protein	opcA	0.933	6.20E-01
MSMEG_3101	glucose-6-phosphate 1-dehydrogenase	zwf	0.949	6.62E-01
MSMEG_3102	transaldolase	tal	0.892	3.02E-01
MSMEG_3103	transketolase	tkt	0.987	8.98E-01
MSMEG_3104	hypothetical protein	NA	1.138	3.67E-01
MSMEG_3105	protoheme IX farnesyltransferase	cyoE	1.044	4.35E-01
MSMEG_3106	quinone oxidoreductase	NA	0.954	5.90E-01
MSMEG_3107	conserved hypothetical protein	NA	1.239	1.93E-01
MSMEG_3108	ABC transporter, ATPase subunit	NA	0.866	4.92E-01
MSMEG_3109	binding-protein-dependent transport systems inner membrane component	NA	0.898	1.42E-01
MSMEG_3110	binding-protein-dependent transport systems inner membrane component	NA	1.096	5.30E-01

MSMEG_3111	extracellular solute-binding protein, family protein 1	NA	1.017	8.81E-01
MSMEG_3112	estradiol 17-beta-dehydrogenase 8	NA	0.925	2.09E-01
MSMEG_3113	carbohydrate kinase, fggy	NA	1.085	3.13E-01
MSMEG_3114	conserved hypothetical protein	NA	1.041	5.73E-01
MSMEG_3115	regulatory protein, DeoR	NA	1.221	3.34E-02
MSMEG_3116	inositol-1-monophosphatase	NA	0.911	3.29E-01
MSMEG_3117	cytochrome aa3 controlling protein	NA	1.517	3.21E-02
MSMEG_3118	ABC transporter efflux protein, DrrB family protein	NA	1.031	7.57E-01
MSMEG_3119	ABC transporter, ATP-binding subunit	NA	1.063	9.91E-02
MSMEG_3120	conserved hypothetical protein	NA	1.003	7.05E-01
MSMEG_3121	DNA-binding protein	NA	0.807	8.45E-03
MSMEG_3122	FeS assembly protein SufB	sufB	1.057	3.80E-01
MSMEG_3123	FeS assembly protein SufD	sufD	0.959	4.30E-01
MSMEG_3124	FeS assembly ATPase SufC	sufC	1.084	1.67E-02
MSMEG_3125	cysteine desulfurase	NA	0.994	9.38E-01
MSMEG_3126	SUF system FeS assembly protein, NifU family protein	NA	0.913	1.67E-01
MSMEG_3127	conserved protein, DUF59	NA	0.915	3.18E-02
MSMEG_3128	hypothetical protein	NA	0.940	5.04E-01
MSMEG_3129	putative HTH-type transcriptional regulator	NA	1.227	4.33E-02
MSMEG_3130	hypothetical protein	NA	1.074	2.90E-01
MSMEG_3131	AMP-binding protein	NA	0.954	6.47E-01
MSMEG_3132	DNA-binding protein	NA	1.027	5.43E-01
MSMEG_3133	hypothetical protein	NA	0.985	9.21E-01
MSMEG_3134	cytochrome P450 107B1	NA	0.967	7.67E-01
MSMEG_3135	hypothetical protein	NA	1.118	6.08E-01
MSMEG_3136	heme peroxidase superfamily protein	NA	0.896	2.96E-01
MSMEG_3137	oxidoreductase	NA	2.676	1.50E-02
MSMEG_3138	thioredoxin	trx	1.051	3.74E-01
MSMEG_3139	enoyl-CoA hydratase/isomerase	NA	1.298	3.75E-02
MSMEG_3140	ABC transporter ATP-binding protein, possibly in EF-3 subfamily protein	NA	1.574	2.61E-02
MSMEG_3141	conserved domain protein	NA	1.593	7.89E-02

MSMEG_3142	HTH-type transcriptional repressor AcnR	NA	1.058	8.21E-02
MSMEG_3143	aconitate hydratase 1	acnA	0.954	1.65E-01
MSMEG_3144	putative membrane protein	NA	1.081	1.07E-01
MSMEG_3145	secreted cell wall-associated hydrolase	NA	0.939	4.95E-01
MSMEG_3146	invasin 1	NA	0.926	8.89E-02
MSMEG_3147	ATPase, MoxR family protein	moxR	0.831	1.07E-01
MSMEG_3148	conserved hypothetical protein	NA	0.952	5.58E-01
MSMEG_3149	conserved hypothetical protein	NA	0.761	7.76E-03
MSMEG_3150	3-oxoacyl-(acyl-carrier-protein) reductase	fabG	0.817	2.60E-03
MSMEG_3151	[NADH] enoyl-[acyl-carrier-protein] reductase	NA	1.064	4.09E-01
MSMEG_3152	ferrochelatase	hemH	1.019	7.56E-01
MSMEG_3153	conserved hypothetical protein	NA	1.444	7.83E-03
MSMEG_3154	membrane protein implicated in regulation of membrane protease activity	NA	1.060	4.75E-01
MSMEG_3155	band 7 protein	NA	0.960	2.97E-01
MSMEG_3156	conserved hypothetical protein	NA	1.019	7.73E-01
MSMEG_3157	conserved hypothetical protein	NA	1.161	3.25E-03
MSMEG_3158	methylmalonyl-CoA mutase, small subunit	mutA	0.782	2.44E-03
MSMEG_3159	methylmalonyl-CoA mutase large subunit	NA	0.698	6.08E-03
MSMEG_3160	LAO/AO transport system ATPase	NA	0.642	2.90E-03
MSMEG_3161	conserved hypothetical protein	NA	0.634	4.39E-04
MSMEG_3162	beta-lactamase	NA	0.675	1.37E-02
MSMEG_3163	gp55 protein	NA	0.997	9.73E-01
MSMEG_3164	hypothetical protein	NA	0.856	6.95E-02
MSMEG_3168	phenolpthIocerol synthesis type-i polyketide synthase ppse	NA	0.964	5.18E-01
MSMEG_3169	isoleucyl-tRNA synthetase	ileS	0.834	1.83E-02
MSMEG_3170	conserved domain protein	NA	1.230	1.07E-01
MSMEG_3171	conserved hypothetical protein	NA	0.981	6.05E-01
MSMEG_3172	DNA polymerase IV 1	NA	1.048	6.59E-01
MSMEG_3173	L-asparaginase	NA	1.164	1.19E-02
MSMEG_3174	lipoprotein signal peptidase	NA	1.309	4.80E-02
MSMEG_3175	ribosomal large subunit pseudouridine synthase D	NA	1.068	3.59E-01

MSMEG_3176	RarD protein	rarD	1.035	6.63E-01
MSMEG_3177	probable transcriptional regulatory protein, putative	NA	1.136	6.51E-01
MSMEG_3178	DNA polymerase III alpha subunit	NA	0.812	1.23E-02
MSMEG_3179	pyridoxamine 5'-phosphate oxidase family protein	NA	1.241	4.20E-01
MSMEG_3180	transcriptional regulator, MerR family protein	NA	1.279	2.04E-01
MSMEG_3181	conserved hypothetical protein	NA	1.006	9.53E-01
MSMEG_3182	hypothetical protein	NA	1.298	1.29E-01
MSMEG_3183	threonine dehydratase	ilvA	1.697	1.08E-03
MSMEG_3184	malto-oligosyltrehalose trehalohydrolase	treZ	0.893	1.99E-01
MSMEG_3185	putative maltooligosyl trehalose synthase; this gene contains a frame shift which is no	NA	0.912	3.58E-01
MSMEG_3185	putative maltooligosyl trehalose synthase; this gene contains a frame shift which is no	NA	1.166	3.65E-01
MSMEG_3186	glycogen debranching enzyme GlgX	glgX	1.252	4.43E-01
MSMEG_3187	putative acyltransferase domain protein	NA	0.805	1.12E-03
MSMEG_3188	adenosylmethionine-8-amino-7-oxononanoate transaminase	bioA	1.123	3.98E-01
MSMEG_3189	8-amino-7-oxononanoate synthase	bioF	1.234	2.77E-01
MSMEG_3190	dethiobiotin synthase	bioD	1.002	9.85E-01
MSMEG_3191	conserved hypothetical protein	NA	1.069	2.95E-01
MSMEG_3192	conserved hypothetical protein, putative	NA	1.515	5.46E-02
MSMEG_3193	transcriptional regulator, TetR family protein	NA	1.213	7.59E-02
MSMEG_3194	biotin synthase	bioB	0.794	1.03E-02
MSMEG_3195	conserved hypothetical protein	NA	0.903	1.56E-01
MSMEG_3196	conserved hypothetical protein	NA	1.008	9.02E-01
MSMEG_3197	lipase	NA	1.155	2.35E-01
MSMEG_3198	hydrolase, NUDIX family protein	NA	1.117	1.93E-03
MSMEG_3199	quinolinate synthetase complex, A subunit	nadA	1.022	6.88E-01
MSMEG_3200	L-aspartate oxidase	nadB	0.885	3.32E-01
MSMEG_3201	nicotinate-nucleotide pyrophosphorylase	nadC	0.913	1.87E-01
MSMEG_3202	hypothetical protein	NA	0.971	8.83E-01
MSMEG_3203	transporter, LysE family protein	NA	1.289	8.07E-03
MSMEG_3204	conserved hypothetical protein	NA	0.930	2.11E-01
MSMEG_3205	histidinol dehydrogenase	hisD	1.081	1.21E-01

MSMEG_3206	histidinol-phosphate aminotransferase	hisC	1.316	5.41E-02
MSMEG_3207	imidazoleglycerol-phosphate dehydratase	hisB	1.375	5.50E-02
MSMEG_3208	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	hisH	1.164	9.19E-02
MSMEG_3209	bifunctional HisA/TrpF protein	NA	1.197	2.11E-01
MSMEG_3210	inositol monophosphate phosphatase	NA	1.133	2.04E-01
MSMEG_3211	imidazoleglycerol phosphate synthase, cyclase subunit	hisF	1.077	5.21E-01
MSMEG_3212	phosphoribosyl-AMP pyrophosphatase/phosphoribosyl-ATP cyclohydrolase	hisIE	1.306	1.11E-01
MSMEG_3213	conserved hypothetical protein	NA	1.217	6.26E-02
MSMEG_3214	hypothetical protein	NA	1.063	4.46E-01
MSMEG_3215	ABC-type molybdenum transport system, ATPase component/photorepair protein Phr	NA	0.989	6.53E-01
MSMEG_3216	peroxiredoxin Q	NA	1.034	5.77E-01
MSMEG_3217	anthranilate synthase component I	trpE	1.181	1.25E-01
MSMEG_3218	trp region conserved hypothetical membrane protein	NA	1.219	2.82E-02
MSMEG_3219	indole-3-glycerol phosphate synthase	trpC	0.982	7.16E-01
MSMEG_3220	tryptophan synthase, beta subunit	trpB	0.889	1.63E-01
MSMEG_3221	tryptophan synthase, alpha subunit	trpA	1.075	3.74E-01
MSMEG_3222	prolipoprotein diacylglyceryl transferase	NA	0.815	3.42E-02
MSMEG_3223	TM2 domain protein	NA	0.819	4.44E-02
MSMEG_3224	conserved hypothetical protein	NA	0.929	5.23E-01
MSMEG_3225	ferredoxin-dependent glutamate synthase 1	NA	0.984	8.05E-01
MSMEG_3226	glutamate synthase, NADH/nadph, small subunit	NA	1.039	8.18E-01
MSMEG_3227	pyruvate kinase	pyk	0.973	7.60E-01
MSMEG_3228	acyl-CoA thioesterase II	NA	1.050	4.47E-01
MSMEG_3229	conserved hypothetical protein	NA	1.096	2.23E-01
MSMEG_3230	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease/ATP-binding pr	NA	0.857	2.39E-01
MSMEG_3231	ABC transporter, CydDC cysteine exporter (CydDC-E) family protein, permease/ATP-bir	cydD	1.094	3.85E-01
MSMEG_3232	cytochrome D ubiquinol oxidase, subunit II	cydB	1.166	6.91E-02
MSMEG_3233	cytochrome D ubiquinol oxidase subunit 1	NA	1.440	3.10E-03
MSMEG_3234	integral membrane protein	NA	1.390	2.77E-02
MSMEG_3235	ABC-type amino acid transport system, secreted component	NA	1.298	1.83E-02
MSMEG_3236	ABC-type amino acid transport system, permease component	NA	1.197	1.12E-01

MSMEG_3237	ATP-binding protein	NA	1.152	1.26E-01
MSMEG_3238	3-mercaptopyruvate sulfurtransferase	NA	1.206	4.14E-02
MSMEG_3239	two-component system sensor kinase	NA	0.902	1.53E-01
MSMEG_3240	DNA-binding response regulator, LuxR family protein	NA	0.986	8.73E-01
MSMEG_3241	conserved hypothetical protein	NA	1.176	6.23E-01
MSMEG_3242	starvation-inducible DNA-binding protein or fine tangled pili major subunit	NA	1.040	7.98E-01
MSMEG_3243	adenylate cyclase; this gene contains a frame shift which is not the result of sequencin	NA	0.901	2.91E-01
MSMEG_3244	hypothetical protein	NA	1.265	2.27E-01
MSMEG_3246	response regulator	NA	0.886	2.85E-01
MSMEG_3247	branched-chain amino acid ABC transporter substrate-binding protein	NA	0.885	3.76E-02
MSMEG_3248	ABC transporter branched chain amino acid transport permease	NA	0.772	1.44E-02
MSMEG_3249	branched-chain amino acid ABC transporter, permease protein	NA	0.805	3.42E-02
MSMEG_3250	ABC transporter, ATP-binding protein	NA	0.843	1.21E-02
MSMEG_3251	branched-chain amino acid ABC transporter ATP-binding protein	NA	0.885	3.87E-02
MSMEG_3252	membrane protein	NA	0.990	7.43E-01
MSMEG_3253	conserved hypothetical protein	NA	0.690	4.62E-05
MSMEG_3254	RDD family protein, putative	NA	1.087	3.90E-01
MSMEG_3255	DoxX subfamily protein, putative	NA	1.325	2.89E-01
MSMEG_3256	mucin-associated surface protein	NA	0.873	2.44E-02
MSMEG_3257	xylulokinase	xylB	1.062	4.74E-01
MSMEG_3258	hypothetical protein	NA	0.932	1.96E-01
MSMEG_3259	acyl-CoA dehydrogenase	NA	0.959	5.87E-01
MSMEG_3260	LysR-family protein transcriptional regulator	NA	1.169	2.88E-01
MSMEG_3261	conserved hypothetical protein	NA	0.854	3.90E-02
MSMEG_3262	L-xylulose reductase	NA	0.925	6.28E-02
MSMEG_3263	xylulose kinase	NA	0.956	5.15E-01
MSMEG_3264	transcriptional regulator	NA	0.920	3.93E-01
MSMEG_3265	arabitol-phosphate dehydrogenase	NA	0.727	3.32E-03
MSMEG_3266	maltose/maltodextrin-binding protein	NA	0.706	1.77E-02
MSMEG_3267	transporter	NA	0.591	4.34E-02
MSMEG_3268	ABC transporter, permease protein	NA	0.842	5.50E-02

MSMEG_3269	putative sugar ABC transporter ATP-binding protein	NA	0.593	1.58E-02
MSMEG_3270	SN-glycerol-3-phosphate ABC transporter, ATP-binding protein	NA	0.793	2.10E-01
MSMEG_3271	dihydroxyacetone kinase	NA	0.802	2.90E-01
MSMEG_3272	ribose 5-phosphate isomerase	NA	0.943	7.80E-02
MSMEG_3273	glutamyl aminopeptidase, M42 family protein	NA	1.242	3.59E-01
MSMEG_3274	MerR-family protein transcriptional regulator	NA	1.186	4.38E-01
MSMEG_3275	RNA polymerase sigma factor, sigma-70 family protein	NA	0.927	2.26E-01
MSMEG_3276	integral membrane protein	NA	1.337	1.24E-01
MSMEG_3277	polyamine ABC transporter integral membrane protein	NA	0.881	1.08E-02
MSMEG_3278	conserved hypothetical protein	NA	1.270	7.99E-02
MSMEG_3279	polyamine ABC transporter permease protein	NA	0.861	1.65E-01
MSMEG_3280	polyamine-binding lipoprotein	NA	0.825	5.34E-02
MSMEG_3281	spermidine/putrescine ABC transporter ATP-binding subunit	NA	0.925	1.88E-01
MSMEG_3282	hypothetical protein	NA	0.916	5.21E-01
MSMEG_3283	membrane transport protein	NA	1.189	1.02E-01
MSMEG_3284	transcriptional regulator, MarR family protein	NA	0.945	1.10E-01
MSMEG_3285	3-isopropylmalate dehydrogenase	NA	0.928	2.38E-01
MSMEG_3286	methyltransferase	NA	0.871	6.51E-03
MSMEG_3287	hydrolase, alpha/beta fold family protein	NA	0.796	7.17E-03
MSMEG_3288	LysM domain protein	NA	1.457	4.02E-01
MSMEG_3289	gp61 protein	NA	1.052	7.86E-01
MSMEG_3290	regulatory protein	NA	0.849	3.34E-01
MSMEG_3291	hypothetical protein	NA	0.938	5.91E-01
MSMEG_3292	DNA-binding protein	NA	1.193	5.42E-01
MSMEG_3293	hypothetical protein	NA	1.164	3.22E-01
MSMEG_3294	hypothetical protein	NA	2.612	3.98E-01
MSMEG_3295	hypothetical protein	NA	1.079	4.18E-01
MSMEG_3296	ECF-family protein sigma factor H	NA	1.197	6.60E-01
MSMEG_3297	transcriptional regulator, CadC	NA	0.581	1.49E-02
MSMEG_3298	response regulator receiver domain protein	NA	0.611	1.76E-02
MSMEG_3299	putative oxidoreductase; this gene contains a frame shift which is not the result of seq	NA	0.621	3.25E-02

MSMEG_3300	oxidoreductase, Gfo/Idh/MocA family protein	NA	0.778	2.44E-01
MSMEG_3301	conserved hypothetical protein	NA	1.262	6.13E-01
MSMEG_3302	short-chain dehydrogenase/reductase SDR	NA	0.577	5.29E-03
MSMEG_3303	carboxylic ester hydrolase	NA	0.781	4.26E-03
MSMEG_3304	succinate semialdehyde dehydrogenase	NA	1.209	4.61E-01
MSMEG_3305	integral membrane protein DUF6	NA	1.277	2.47E-01
MSMEG_3306	zinc-binding alcohol dehydrogenase	NA	1.030	7.03E-01
MSMEG_3307	methyltransferase FkbM; this gene contains a frame shift which is not the result of sec	NA	0.987	9.20E-01
MSMEG_3307	methyltransferase FkbM; this gene contains a frame shift which is not the result of sec	NA	1.687	1.99E-01
MSMEG_3308	universal stress protein family protein, putative	NA	1.114	1.97E-01
MSMEG_3309	conserved hypothetical protein	NA	1.087	1.75E-01
MSMEG_3310	integral membrane protein	NA	1.335	2.91E-01
MSMEG_3311	acyl carrier protein	NA	0.984	9.35E-01
MSMEG_3312	hemerythrin HHE cation binding domain subfamily protein, putative	NA	1.115	7.98E-01
MSMEG_3313	xylose repressor, putative	NA	1.092	1.14E-01
MSMEG_3314	transport protein	NA	1.672	8.27E-02
MSMEG_3315	hypothetical protein	NA	0.947	2.29E-01
MSMEG_3316	transporter, major facilitator family protein	NA	1.042	7.08E-01
MSMEG_3317	dihydrodipicolinate reductase, N-terminus domain protein	dapB	1.077	7.73E-01
MSMEG_3318	oxidoreductase	NA	0.952	6.75E-01
MSMEG_3319	repressor protein	NA	1.533	1.60E-01
MSMEG_3320	LysR-family transcriptional regulator; this gene contains a frame shift which is not the	NA	1.065	6.79E-01
MSMEG_3321	ATP/GTP-binding protein	NA	0.876	5.23E-01
MSMEG_3322	hypothetical protein	NA	1.117	3.37E-01
MSMEG_3323	conserved hypothetical protein	NA	1.080	1.45E-01
MSMEG_3324	hypothetical protein	NA	1.139	6.71E-01
MSMEG_3325	conserved hypothetical protein	NA	1.076	7.25E-01
MSMEG_3326	carboxylate-amine ligase	NA	0.843	5.17E-03
MSMEG_3327	hypothetical protein	NA	0.849	5.81E-02
MSMEG_3328	hypothetical protein	NA	0.905	1.06E-01
MSMEG_3329	hypothetical protein	NA	0.817	6.89E-02

MSMEG_3330	conserved domain protein	NA	0.745	5.47E-03
MSMEG_3331	hypothetical protein	NA	0.921	3.63E-01
MSMEG_3332	transcriptional regulator, TetR family protein	NA	0.910	4.06E-01
MSMEG_3333	putative fatty acid desaturase, authentic frameshift; this gene contains a frame shift w	NA	0.845	3.76E-02
MSMEG_3334	hypothetical protein	NA	0.969	2.37E-01
MSMEG_3335	transcriptional regulator, IclR family protein, putative	NA	0.964	7.82E-01
MSMEG_3336	hydrolase	NA	0.903	2.37E-01
MSMEG_3337	hypothetical protein	NA	0.887	1.77E-01
MSMEG_3338	oxidoreductase, FAD/FMN-binding	NA	0.954	7.45E-01
MSMEG_3339	hypothetical protein	NA	1.045	7.68E-01
MSMEG_3340	hypothetical protein	NA	0.980	8.31E-01
MSMEG_3341	Transposase IS116/IS110/IS902 family protein	NA	0.777	1.11E-01
MSMEG_3342	hypothetical protein	NA	1.139	4.07E-01
MSMEG_3343	hypothetical protein	NA	1.178	6.74E-02
MSMEG_3344	hypothetical protein	NA	0.870	5.50E-02
MSMEG_3345	transcriptional regulator, GntR family protein	NA	1.037	5.47E-01
MSMEG_3346	putative hydroxyacid aldolase	NA	0.867	4.13E-01
MSMEG_3347	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	NA	0.806	7.12E-02
MSMEG_3348	bacterial extracellular solute-binding protein, family protein 7	NA	1.315	4.78E-01
MSMEG_3349	trap dicarboxylate transporter, dctq subunit, putative	NA	0.991	9.24E-01
MSMEG_3350	TRAP transporter, DctM-like membrane protein	NA	1.140	5.82E-01
MSMEG_3351	hypothetical protein	NA	1.825	3.79E-01
MSMEG_3352	hypothetical protein	NA	0.823	1.30E-01
MSMEG_3353	hypothetical protein	NA	0.914	1.60E-01
MSMEG_3354	TetR family protein transcriptional regulatory protein	NA	1.180	2.40E-01
MSMEG_3355	conserved hypothetical protein	NA	0.952	5.25E-01
MSMEG_3356	conserved hypothetical protein TIGR00026	NA	0.894	1.92E-01
MSMEG_3357	metal-dependent phosphohydrolase, HD subdomain	NA	1.010	9.19E-01
MSMEG_3358	YaeQ protein	NA	1.193	1.28E-01
MSMEG_3359	cis-3-chloroacrylic acid dehalogenase, putative	NA	1.029	7.19E-01
MSMEG_3360	transcriptional regulator, putative	NA	1.390	6.33E-04

MSMEG_3361	conserved hypothetical protein	NA	1.322	2.50E-01
MSMEG_3362	enoyl-CoA hydratase	NA	2.374	3.83E-01
MSMEG_3363	regulatory protein, TetR	NA	0.638	3.87E-03
MSMEG_3364	RhtB family protein transporter	NA	0.686	1.79E-03
MSMEG_3365	transcriptional regulator, AraC family protein	NA	0.728	8.95E-03
MSMEG_3366	isonitrile hydratase, putative	NA	0.627	8.52E-03
MSMEG_3367	short-chain dehydrogenase/reductase SDR	NA	0.877	4.42E-02
MSMEG_3368	hypothetical protein	NA	0.874	2.68E-01
MSMEG_3369	putative transport protein	NA	1.162	6.24E-01
MSMEG_3370	hypothetical protein	NA	1.020	8.99E-01
MSMEG_3371	short-chain dehydrogenase/reductase SDR; this region contains one or more prematu	NA	1.050	6.03E-01
MSMEG_3372	transcriptional regulator, ArsR family protein	NA	1.355	4.81E-02
MSMEG_3373	major facilitator superfamily protein MFS_1	NA	1.637	2.19E-02
MSMEG_3374	conserved hypothetical protein	NA	1.089	2.47E-01
MSMEG_3375	alcohol dehydrogenase	NA	0.726	1.56E-02
MSMEG_3376	beta-lactamase	NA	0.788	1.38E-02
MSMEG_3377	hypothetical protein	NA	1.196	7.29E-02
MSMEG_3378	beta-lactamase	NA	0.974	7.82E-01
MSMEG_3379	2-deoxy-D-gluconate 3-dehydrogenase	NA	1.155	1.19E-01
MSMEG_3380	pyridoxamine 5'-phosphate oxidase-related, FMN-binding	NA	0.842	7.03E-02
MSMEG_3381	acyl carrier protein phosphodiesterase	NA	0.960	5.03E-01
MSMEG_3382	transcriptional regulator, ArsR family protein	NA	1.163	1.88E-01
MSMEG_3383	hypothetical protein	NA	1.009	9.11E-01
MSMEG_3384	isoflavone reductase	NA	1.228	3.04E-02
MSMEG_3385	hypothetical protein	NA	3.328	2.97E-01
MSMEG_3386	shikimate transporter	NA	1.014	7.05E-01
MSMEG_3387	aldehyde dehydrogenase (NAD) family protein	NA	0.881	5.55E-01
MSMEG_3388	S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase	NA	1.418	4.05E-01
MSMEG_3389	putative acetolactate synthase	NA	0.896	7.14E-01
MSMEG_3390	enoyl-CoA hydratase	NA	1.139	8.54E-01
MSMEG_3391	L-carnitine dehydratase/bile acid-inducible protein F	NA	0.829	3.59E-02

MSMEG_3392	acyl-CoA dehydrogenase domain protein	NA	0.960	8.09E-01
MSMEG_3393	putative acyl-CoA dehydrogenase	NA	0.665	3.22E-03
MSMEG_3394	cupin domain protein	NA	0.924	1.53E-01
MSMEG_3395	short chain dehydrogenase	NA	0.965	6.66E-01
MSMEG_3396	transcriptional regulator, IclR family protein	NA	1.067	1.93E-01
MSMEG_3397	acetylornithine deacetylase	NA	1.265	2.81E-01
MSMEG_3398	integral membrane transport protein	NA	0.960	4.89E-01
MSMEG_3399	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.076	1.35E-01
MSMEG_3399	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.594	1.38E-02
MSMEG_3400	glutamyl-tRNA(Gln) amidotransferase subunit A	NA	1.146	5.76E-01
MSMEG_3401	LamB/YcsF family protein	NA	1.218	2.22E-01
MSMEG_3402	cytosine permease, putative	NA	0.941	7.64E-01
MSMEG_3403	formamidase	NA	0.946	2.41E-01
MSMEG_3404	HNH endonuclease domain protein	NA	1.086	3.67E-01
MSMEG_3405	methylenomycin A resistance protein	NA	1.719	2.70E-01
MSMEG_3406	putative transcriptional regulator, TetR family protein	NA	1.417	1.03E-02
MSMEG_3407	epoxide hydrolase	NA	0.935	3.73E-01
MSMEG_3408	conserved hypothetical protein	NA	1.379	5.40E-02
MSMEG_3409	oxidoreductase	NA	1.700	9.67E-02
MSMEG_3410	transcriptional regulator, TetR family protein	NA	1.624	1.01E-01
MSMEG_3411	MOSC domain protein	NA	1.073	4.20E-01
MSMEG_3412	polysaccharide deacetylase family protein	NA	0.996	9.18E-01
MSMEG_3413	MerR-family transcriptional regulator; this gene contains a frame shift which is not the	NA	0.899	4.17E-01
MSMEG_3413	MerR-family transcriptional regulator; this gene contains a frame shift which is not the	NA	1.148	3.23E-01
MSMEG_3414	conserved hypothetical protein	NA	1.377	8.20E-02
MSMEG_3415	MarR-family protein regulatory protein	NA	1.816	1.21E-01
MSMEG_3416	protein of unknown function DUF6, transmembrane, putative	NA	1.120	3.04E-01
MSMEG_3417	conserved hypothetical protein	NA	0.952	5.92E-01
MSMEG_3418	conserved hypothetical protein	NA	1.083	6.85E-01
MSMEG_3419	hypothetical protein	NA	1.196	5.61E-01
MSMEG_3420	gluconate 5-dehydrogenase	NA	1.540	3.65E-01

MSMEG_3421	inner membrane metabolite transport protein YdfJ	NA	0.946	8.42E-01
MSMEG_3422	D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding	NA	0.998	9.69E-01
MSMEG_3423	probable IclR family protein regulator	NA	0.958	7.02E-01
MSMEG_3424	transcriptional regulator, MerR family protein	NA	1.008	9.64E-01
MSMEG_3425	TetR-family protein transcriptional regulator	NA	1.261	8.12E-02
MSMEG_3426	short chain dehydrogenase	NA	1.469	6.69E-02
MSMEG_3427	metal dependent hydrolase	NA	2.274	3.69E-01
MSMEG_3428	conserved hypothetical protein	NA	1.118	4.01E-01
MSMEG_3429	O-acyl transferase	NA	0.996	9.66E-01
MSMEG_3430	SAM-dependent methyltransferase	NA	0.894	5.61E-02
MSMEG_3431	choline dehydrogenase	NA	1.223	3.69E-01
MSMEG_3432	choline dehydrogenase	NA	1.100	3.64E-01
MSMEG_3434	peptidyl-prolyl cis-trans isomerase, fkbp-type domain protein	NA	1.213	3.04E-02
MSMEG_3435	conserved hypothetical protein	NA	1.095	1.76E-01
MSMEG_3436	conserved hypothetical protein	NA	1.040	6.83E-01
MSMEG_3437	putative esterase family protein	NA	0.987	9.40E-01
MSMEG_3438	hypothetical protein	NA	1.012	7.56E-01
MSMEG_3439	hypothetical protein	NA	1.385	4.76E-01
MSMEG_3440	L-serine ammonia-lyase	sdaA	0.972	7.14E-01
MSMEG_3441	hypothetical protein	NA	1.102	4.53E-01
MSMEG_3442	cyclohexadienyl dehydratase	NA	1.081	7.76E-01
MSMEG_3443	hypothetical protein	NA	1.120	6.50E-01
MSMEG_3444	choline dehydrogenase	NA	1.320	3.73E-01
MSMEG_3445	5,10-methylenetetrahydromethanopterin reductase	NA	1.273	7.84E-02
MSMEG_3446	hypothetical protein	NA	1.028	9.18E-01
MSMEG_3447	two-component system response regulator	NA	1.069	6.08E-01
MSMEG_3448	two-component system sensor kinase	NA	0.865	1.23E-02
MSMEG_3449	DNA-binding protein	NA	1.154	4.84E-02
MSMEG_3450	haloacid dehalogenase, type II	dehII	0.925	5.27E-01
MSMEG_3451	short-chain dehydrogenase/reductase	NA	1.127	1.90E-01
MSMEG_3452	TetR family protein transcriptional regulator	NA	1.053	7.04E-01

MSMEG_3453	hypothetical protein	NA	0.969	8.48E-01
MSMEG_3454	hypothetical protein	NA	0.877	1.16E-01
MSMEG_3455	heat shock protein 15	hslR	1.037	3.08E-01
MSMEG_3456	hydroxylaminobenzene mutase	NA	1.979	3.54E-01
MSMEG_3457	DoxD family protein/pyridine nucleotide-disulfide oxidoreductase	NA	0.765	4.29E-03
MSMEG_3458	conserved hypothetical protein	NA	1.284	3.25E-01
MSMEG_3459	conserved hypothetical protein	NA	0.831	3.62E-03
MSMEG_3460	ferric uptake regulation protein	NA	0.880	3.14E-02
MSMEG_3461	catalase/peroxidase HPI	katG	0.886	5.04E-01
MSMEG_3462	oxidoreductase	NA	0.964	7.77E-01
MSMEG_3463	putative esterase	NA	1.164	2.77E-01
MSMEG_3464	alcohol dehydrogenase	NA	1.030	7.93E-01
MSMEG_3465	acyl-CoA synthase	NA	1.057	4.26E-01
MSMEG_3466	hypothetical protein	NA	1.699	3.01E-01
MSMEG_3467	conserved hypothetical protein	NA	1.298	4.44E-02
MSMEG_3468	AMP-binding enzyme	NA	1.017	8.23E-01
MSMEG_3469	TetR family protein transcriptional regulator	NA	1.097	1.83E-01
MSMEG_3470	NAD-dependent epimerase/dehydratase	NA	1.574	6.16E-02
MSMEG_3471	GTP cyclohydrolase	NA	0.920	3.72E-01
MSMEG_3472	conserved hypothetical protein	NA	0.815	2.57E-01
MSMEG_3473	uracil phosphoribosyltransferase	upp	0.944	5.34E-01
MSMEG_3474	probable conserved integral membrane protein	NA	1.083	1.79E-01
MSMEG_3475	conserved hypothetical protein	NA	1.195	5.96E-02
MSMEG_3476	peptidase, M48 family protein	NA	1.097	4.41E-01
MSMEG_3477	possible inv protein	NA	0.960	6.14E-01
MSMEG_3478	tena/thi-4 family protein	NA	0.910	4.17E-02
MSMEG_3479	thiol peroxidase	NA	0.677	1.62E-04
MSMEG_3480	streptomycin 6-kinase (Streptidine kinase) (Streptomycin6-phosphotransferase) (APH(	NA	0.846	9.32E-02
MSMEG_3481	O-succinylbenzoate synthase	NA	1.225	1.19E-01
MSMEG_3482	hypothetical protein	NA	0.918	4.59E-01
MSMEG_3483	mosc domain protein	NA	1.112	3.14E-01

MSMEG_3484	cupin domain protein	NA	1.469	4.80E-01
MSMEG_3485	putative ECF sigma factor RpoE1	NA	3.493	4.09E-01
MSMEG_3486	catalase KatA	katA	0.975	9.06E-01
MSMEG_3487	metal-dependent phosphohydrolase	NA	1.181	2.60E-01
MSMEG_3488	transcriptional regulator, AraC family protein	NA	1.074	6.31E-01
MSMEG_3489	conserved hypothetical protein, putative	NA	1.089	2.45E-01
MSMEG_3490	putative membrane acyltransferase	NA	0.999	9.83E-01
MSMEG_3491	conserved hypothetical protein	NA	1.106	1.97E-01
MSMEG_3492	phosphodiesterase	NA	1.176	3.31E-01
MSMEG_3493	putative secreted protein	NA	0.956	4.85E-01
MSMEG_3494	putative secreted protein	NA	0.886	1.71E-01
MSMEG_3495	MmpS5 protein	NA	0.985	6.37E-01
MSMEG_3496	MmpL4 protein	NA	1.117	1.29E-01
MSMEG_3497	transcriptional regulator, ArsR family protein	NA	1.072	1.39E-01
MSMEG_3498	hypothetical protein	NA	1.397	3.42E-01
MSMEG_3499	conserved hypothetical protein	NA	1.188	2.99E-02
MSMEG_3500	conserved hypothetical protein	NA	1.309	5.02E-02
MSMEG_3501	hypothetical protein	NA	0.985	6.33E-01
MSMEG_3502	hypothetical protein	NA	1.410	1.97E-02
MSMEG_3503	conserved hypothetical protein	NA	0.929	1.40E-01
MSMEG_3504	probable membrane protein	NA	0.858	3.41E-02
MSMEG_3505	6-aminohexanoate-cyclic-dimer hydrolase	NA	0.956	6.15E-01
MSMEG_3506	putative amino acid decarboxylase, Pyridoxal-dependent protein	NA	1.055	6.52E-01
MSMEG_3507	fructose-bisphosphate aldolase class-I	NA	0.897	5.42E-03
MSMEG_3508	hydrolase, alpha/beta hydrolase fold family protein	NA	0.880	1.76E-01
MSMEG_3509	conserved hypothetical protein	NA	0.932	1.24E-01
MSMEG_3511	hydroxylase	NA	1.086	9.51E-02
MSMEG_3512	competence damage-inducible protein A	NA	0.985	6.16E-01
MSMEG_3513	enhanced intracellular survival protein	NA	1.349	5.66E-02
MSMEG_3514	hypothetical protein	NA	0.809	5.02E-03
MSMEG_3515	3-alpha-(or 20-beta)-hydroxysteroid dehydrogenase	NA	1.171	2.42E-01

MSMEG_3516	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.917	3.99E-01
MSMEG_3517	HAD-superfamily protein subfamily protein IB hydrolase	NA	1.007	9.35E-01
MSMEG_3518	conserved hypothetical protein	NA	1.869	1.56E-01
MSMEG_3519	oxidoreductase, 2-nitropropane dioxygenase family protein	NA	1.004	9.74E-01
MSMEG_3520	TetR-family protein transcriptional regulator	NA	0.855	4.38E-02
MSMEG_3521	molybdopterin oxidoreductase	NA	0.899	3.73E-01
MSMEG_3522	dopamine receptor D4	NA	0.971	8.13E-01
MSMEG_3523	probable membrane protein	NA	1.094	1.41E-01
MSMEG_3524	linalool 8-monooxygenase	NA	1.040	7.58E-01
MSMEG_3525	transcriptional regulator, XRE family protein	NA	0.819	1.17E-01
MSMEG_3526	conserved hypothetical protein	NA	0.867	3.51E-01
MSMEG_3527	putative HTH-type transcriptional regulator	NA	1.236	3.24E-03
MSMEG_3528	ErfK/YbiS/YcfS/YnhG family protein	NA	1.130	1.23E-01
MSMEG_3529	fatty acid hydroxylase	NA	1.091	4.20E-01
MSMEG_3530	conserved hypothetical protein	NA	1.064	7.46E-01
MSMEG_3531	conserved hypothetical protein	NA	0.879	1.76E-02
MSMEG_3532	serine/threonine dehydratase family protein	NA	0.939	4.05E-01
MSMEG_3533	Di-/tripeptide transporter	NA	1.086	3.51E-01
MSMEG_3534	4-hydroxybenzoyl-CoA thioesterase	NA	1.007	8.85E-01
MSMEG_3535	agmatinase	speB	0.959	7.90E-01
MSMEG_3536	sugar transport protein	NA	1.510	3.48E-01
MSMEG_3537	hypothetical protein	NA	1.555	3.55E-01
MSMEG_3538	cyclopropane-fatty-acyl-phospholipid synthase 1	NA	0.818	8.23E-03
MSMEG_3539	hypothetical protein	NA	0.823	1.79E-01
MSMEG_3540	conserved hypothetical protein	NA	0.914	2.07E-01
MSMEG_3541	cytochrome C biogenesis protein transmembrane region	NA	1.522	1.48E-01
MSMEG_3542	conserved hypothetical protein	NA	0.940	3.17E-01
MSMEG_3543	soluble secreted antigen MPT53	NA	1.147	3.16E-01
MSMEG_3544	conserved hypothetical protein	NA	1.095	9.12E-02
MSMEG_3545	hypothetical protein	NA	0.998	9.49E-01
MSMEG_3546	conserved hypothetical protein	NA	1.019	8.55E-01

MSMEG_3547	ectoine/hydroxyectoine ABC transporter solute-binding protein	ehuB	1.061	6.28E-01
MSMEG_3548	ectoine/hydroxyectoine ABC transporter, permease protein EhuC	ehuC	0.867	3.85E-01
MSMEG_3549	ectoine/hydroxyectoine ABC transporter, permease protein EhuD	ehuD	1.007	8.67E-01
MSMEG_3550	ectoine/hydroxyectoine ABC transporter, ATP-binding protein	ehuA	0.943	3.95E-01
MSMEG_3551	linalool 8-monooxygenase	NA	0.755	9.50E-02
MSMEG_3552	conserved hypothetical protein	NA	1.333	1.06E-02
MSMEG_3553	dihydropyrimidinase	hydA	0.889	3.26E-01
MSMEG_3554	N5,N10-methylene- tetrahydromethanopterin reductase	NA	0.737	1.06E-01
MSMEG_3555	hydrolase	NA	1.217	6.13E-01
MSMEG_3556	integral membrane transporter	NA	0.785	2.33E-02
MSMEG_3557	amino acid permease-associated region	NA	1.108	3.39E-01
MSMEG_3558	carboxymethylenebutenolidase	NA	1.014	9.65E-01
MSMEG_3559	short chain dehydrogenase	NA	1.082	6.51E-01
MSMEG_3560	conserved hypothetical protein	NA	1.069	5.25E-01
MSMEG_3561	glutamine synthetase, catalytic domain	glnA	0.984	8.74E-01
MSMEG_3562	4-carboxymuconolactone decarboxylase domain protein	pcaC	1.064	2.35E-01
MSMEG_3563	drug transporter	NA	1.095	4.67E-01
MSMEG_3564	bacterioferritin	bfr	0.825	3.73E-02
MSMEG_3565	hypothetical protein	NA	1.488	2.35E-01
MSMEG_3566	FadD16 protein	NA	0.985	8.94E-01
MSMEG_3567	enoyl-CoA hydratase	NA	1.063	1.35E-01
MSMEG_3568	conserved hypothetical protein	NA	2.608	1.83E-01
MSMEG_3569	conserved hypothetical protein	NA	0.910	6.20E-03
MSMEG_3570	conserved hypothetical protein	NA	1.262	2.02E-01
MSMEG_3571	thioesterase family protein	NA	1.163	4.69E-02
MSMEG_3572	transcriptional regulator, TetR family protein	NA	1.387	2.22E-01
MSMEG_3573	integral membrane protein, putative	NA	1.722	7.83E-02
MSMEG_3574	TPR domain protein	NA	0.947	6.14E-01
MSMEG_3575	cytidine/deoxycytidylate deaminase, zinc-binding region	NA	0.956	2.17E-01
MSMEG_3576	alpha-amylase 3	NA	0.905	1.28E-01
MSMEG_3577	calpastatin	NA	1.345	8.84E-03

MSMEG_3578	putative cyclase	NA	1.003	9.71E-01
MSMEG_3579	probable conserved transmembrane protein	NA	0.823	2.08E-01
MSMEG_3580	antigen 85-C	NA	0.754	1.10E-02
MSMEG_3581	FabG protein	NA	1.899	2.53E-01
MSMEG_3582	ATP-dependent protease La	lon	2.130	1.96E-01
MSMEG_3583	monooxygenase	NA	1.575	1.04E-01
MSMEG_3584	membrane protein, MmpL family protein	NA	1.065	5.66E-01
MSMEG_3585	MmpS2 protein	NA	1.183	1.50E-01
MSMEG_3586	major facilitator family protein transporter	NA	0.833	5.77E-01
MSMEG_3587	D-serine/D-alanine/glycine transporter	NA	1.097	3.77E-01
MSMEG_3588	hypothetical protein	NA	0.994	9.63E-01
MSMEG_3589	conserved hypothetical protein	NA	1.228	4.02E-01
MSMEG_3590	conserved hypothetical protein	NA	0.957	7.93E-01
MSMEG_3591	conserved hypothetical protein	NA	1.059	7.77E-01
MSMEG_3592	hypothetical protein	NA	0.960	4.10E-01
MSMEG_3593	conserved hypothetical protein	NA	1.036	6.48E-01
MSMEG_3594	anthranilate dioxygenase reductase	NA	1.580	4.53E-01
MSMEG_3595	conserved hypothetical protein	NA	0.870	2.88E-01
MSMEG_3596	ATPase	NA	0.887	1.31E-01
MSMEG_3596	ATPase	NA	1.098	1.72E-01
MSMEG_3598	periplasmic sugar-binding proteins	NA	0.784	4.65E-03
MSMEG_3599	sugar-binding transcriptional regulator, LacI family protein	NA	0.702	1.01E-02
MSMEG_3600	hypothetical protein	NA	1.021	7.80E-01
MSMEG_3601	ribose/xylose/arabinose/galactoside ABC-type transport systems, permease compone	NA	0.656	6.94E-03
MSMEG_3602	ribose transport ATP-binding protein RbsA	NA	0.822	2.29E-01
MSMEG_3603	oxidoreductase, zinc-binding dehydrogenase family protein	NA	0.942	8.88E-01
MSMEG_3604	sorbitol utilization protein SOU2	NA	0.759	2.40E-01
MSMEG_3605	sorbitol dehydrogenase	NA	0.846	6.63E-02
MSMEG_3606	transcriptional regulator	NA	0.896	3.17E-01
MSMEG_3607	short chain dehydrogenase	NA	0.889	1.52E-01
MSMEG_3608	acetyl-CoA acetyltransferase	NA	0.918	2.04E-01

MSMEG_3609	hydride transferase 1	NA	1.092	3.52E-01
MSMEG_3610	conserved hypothetical protein	NA	1.161	3.85E-01
MSMEG_3611	D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase	xfp	0.861	3.68E-01
MSMEG_3612	probable conserved integral membrane protein	NA	0.954	6.26E-01
MSMEG_3613	conserved hypothetical protein	NA	1.105	4.15E-01
MSMEG_3614	hypothetical protein	NA	1.384	3.40E-02
MSMEG_3615	zinc-binding alcohol dehydrogenase family protein	NA	0.988	9.00E-01
MSMEG_3616	integral membrane protein	NA	0.839	2.77E-04
MSMEG_3617	hypothetical protein	NA	1.017	8.99E-01
MSMEG_3618	alanine and proline-rich secreted protein apa	NA	0.896	4.38E-02
MSMEG_3619	short chain dehydrogenase	NA	0.995	9.40E-01
MSMEG_3620	conserved hypothetical protein	NA	0.855	7.78E-02
MSMEG_3621	NADH dehydrogenase	ndh	1.152	2.69E-01
MSMEG_3622	conserved hypothetical protein	NA	1.106	6.98E-01
MSMEG_3623	urease accessory protein UreG	ureG	0.714	1.93E-02
MSMEG_3624	urease accessory protein uref	NA	1.056	7.87E-01
MSMEG_3625	urease, alpha subunit	ureC	0.807	1.93E-01
MSMEG_3626	urease, beta subunit	ureB	0.987	9.04E-01
MSMEG_3627	urease, gamma subunit	ureA	0.904	7.04E-03
MSMEG_3628	ComA operon protein 2	NA	0.966	6.29E-01
MSMEG_3629	conserved hypothetical protein	NA	1.562	3.37E-01
MSMEG_3630	transcriptional repressor, CopY family protein	NA	1.222	3.08E-01
MSMEG_3631	integral membrane protein	NA	1.197	5.02E-02
MSMEG_3632	6-phosphogluconate dehydrogenase, decarboxylating	gnd	0.933	2.14E-01
MSMEG_3633	ferric cations import ATP-binding protein FbpC	NA	1.190	5.88E-01
MSMEG_3634	IMP dehydrogenase family protein	NA	0.969	7.21E-01
MSMEG_3635	iron(III)-transport system permease protein SfuB	NA	0.946	5.01E-01
MSMEG_3636	ferric iron-binding periplasmic protein of ABC transporter	NA	0.966	5.10E-01
MSMEG_3637	CBS domain protein	NA	1.141	2.44E-01
MSMEG_3638	CBS domain protein	NA	1.219	5.28E-02
MSMEG_3639	conserved hypothetical protein	NA	0.931	4.06E-01

MSMEG_3640	malate synthase G	glcB	0.953	4.12E-02
MSMEG_3641	conserved hypothetical protein	NA	1.014	8.87E-01
MSMEG_3642	glycine dehydrogenase	gcvP	1.417	1.70E-01
MSMEG_3643	hypothetical protein	NA	1.474	2.35E-01
MSMEG_3644	transcriptional regulator, MerR family protein	NA	0.865	9.49E-02
MSMEG_3645	conserved hypothetical protein	NA	1.089	8.68E-02
MSMEG_3646	transcriptional regulator, MerR family protein	NA	1.104	2.67E-01
MSMEG_3647	forkhead-associated protein	NA	1.117	2.65E-01
MSMEG_3648	glycine cleavage system H protein	gcvH	0.911	2.14E-01
MSMEG_3649	conserved hypothetical protein	NA	1.025	7.58E-01
MSMEG_3650	integral membrane protein	NA	1.073	3.29E-01
MSMEG_3651	membrane associated protein	NA	1.048	3.27E-01
MSMEG_3652	CDP-diacylglycerol-glycerol-3-phosphate	NA	0.930	1.88E-01
MSMEG_3653	hypothetical protein	NA	1.170	4.15E-01
MSMEG_3654	ATPase SecA2	NA	1.088	2.87E-01
MSMEG_3655	ABC transporter, permease/ATP-binding protein	NA	0.947	3.06E-01
MSMEG_3656	ABC transporter, permease/ATP-binding protein	NA	1.117	2.74E-01
MSMEG_3657	succinate dehydrogenase	NA	0.827	3.51E-03
MSMEG_3658	conserved hypothetical protein	NA	0.952	3.56E-01
MSMEG_3659	TetR-family protein transcriptional regulator	NA	1.425	9.92E-03
MSMEG_3660	conserved hypothetical protein TIGR00026	NA	1.219	1.96E-01
MSMEG_3661	conserved hypothetical protein	NA	1.081	4.60E-01
MSMEG_3662	mannose-binding lectin	NA	0.863	6.94E-02
MSMEG_3663	oxidoreductase	NA	1.098	3.94E-01
MSMEG_3664	transporter, monovalent cation:proton antiporter-2 (CPA2) family protein	NA	1.078	8.09E-01
MSMEG_3665	TrkA domain protein	NA	1.012	8.68E-01
MSMEG_3666	C-5 sterol desaturase	NA	0.837	3.24E-02
MSMEG_3667	para-nitrobenzyl esterase	NA	0.779	1.60E-03
MSMEG_3668	acyl-CoA dehydrogenase	NA	1.255	3.77E-01
MSMEG_3669	conserved hypothetical protein	NA	1.020	5.46E-01
MSMEG_3670	transporter, small multidrug resistance (SMR) family protein	NA	1.256	2.38E-01

MSMEG_3671	integral membrane protein	NA	1.051	4.76E-01
MSMEG_3672	transporter, small multidrug resistance (SMR) family protein	NA	1.260	1.60E-01
MSMEG_3673	4-alpha-glucanotransferase	malQ	1.079	7.14E-01
MSMEG_3674	hypothetical protein	NA	0.919	7.97E-02
MSMEG_3675	metal-dependent hydrolase	NA	1.074	1.43E-02
MSMEG_3676	phenoxybenzoate dioxygenase beta subunit	NA	1.283	2.94E-01
MSMEG_3677	serine/threonine protein kinase	NA	0.941	1.38E-01
MSMEG_3678	hypothetical protein	NA	1.240	1.41E-01
MSMEG_3679	phosphohydrolase	NA	1.210	3.47E-01
MSMEG_3680	hypothetical protein	NA	3.220	3.76E-03
MSMEG_3681	conserved hypothetical protein	NA	1.075	3.70E-01
MSMEG_3682	conserved hypothetical protein	NA	1.549	2.56E-01
MSMEG_3683	conserved hypothetical protein	NA	1.149	7.16E-02
MSMEG_3684	nuclear transport factor 2 (NTF2) domain family protein	NA	1.223	3.54E-02
MSMEG_3685	conserved hypothetical protein	NA	0.885	2.09E-01
MSMEG_3686	conserved hypothetical protein	NA	1.141	4.71E-02
MSMEG_3687	medium chain acyl-CoA synthetase	NA	1.091	1.63E-02
MSMEG_3688	conserved hypothetical protein	NA	0.869	3.53E-02
MSMEG_3689	sodium:solute symporter	NA	1.025	7.16E-01
MSMEG_3690	transcriptional regulatory protein; this gene contains a frame shift which is not the res	NA	1.050	4.92E-01
MSMEG_3691	galactose-1-phosphate uridylyltransferase	galT	1.120	3.50E-01
MSMEG_3692	galactokinase	galK	1.280	4.84E-02
MSMEG_3693	cytochrome P450 monooxygenase	NA	1.176	4.95E-01
MSMEG_3694	feruloyl-CoA synthetase	NA	1.020	8.70E-01
MSMEG_3695	conserved hypothetical protein	NA	1.153	2.61E-01
MSMEG_3698	hypothetical protein	NA	1.052	5.87E-01
MSMEG_3699	conserved hypothetical protein	NA	1.532	3.53E-02
MSMEG_3700	peroxidase	NA	1.069	6.06E-01
MSMEG_3701	conserved hypothetical protein	NA	0.989	9.44E-01
MSMEG_3703	hypothetical protein	NA	0.766	5.52E-02
MSMEG_3703	hypothetical protein	NA	1.789	1.86E-01

MSMEG_3704	3-alpha-hydroxysteroid dehydrogenase	NA	0.917	1.20E-02
MSMEG_3705	major facilitator superfamily protein MFS_1	NA	0.794	3.46E-02
MSMEG_3706	isocitrate lyase	aceA	1.238	6.10E-01
MSMEG_3707	conserved hypothetical protein	NA	0.962	8.82E-01
MSMEG_3708	catalase	NA	0.977	8.26E-01
MSMEG_3709	conserved hypothetical protein	NA	1.053	6.62E-01
MSMEG_3710	cytochrome b561 family protein	NA	1.064	5.13E-01
MSMEG_3711	hypothetical protein	NA	1.244	4.41E-01
MSMEG_3712	hypothetical protein	NA	1.988	3.24E-01
MSMEG_3713	hypothetical protein	NA	1.372	1.04E-01
MSMEG_3714	conserved hypothetical protein	NA	1.023	6.64E-01
MSMEG_3715	linear gramicidin synthetase subunit C	NA	1.057	3.17E-01
MSMEG_3716	hypothetical protein	NA	1.116	7.62E-01
MSMEG_3717	short-chain dehydrogenase/reductase SDR; this gene contains a frame shift which is n	NA	0.952	3.11E-01
MSMEG_3717	short-chain dehydrogenase/reductase SDR; this gene contains a frame shift which is n	NA	1.859	2.95E-01
MSMEG_3718	conserved hypothetical protein	NA	1.070	5.21E-01
MSMEG_3719	sodium/calcium exchanger protein	NA	0.932	5.13E-01
MSMEG_3720	recombination activating protein 1	NA	0.730	2.60E-02
MSMEG_3721	coenzyme PQQ biosynthesis protein E	pqqE	1.002	9.47E-01
MSMEG_3722	bifunctional coenzyme PQQ synthesis protein C/D	NA	1.030	6.07E-01
MSMEG_3723	coenzyme PQQ biosynthesis protein C	pqqC	0.939	8.31E-01
MSMEG_3724	coenzyme PQQ biosynthesis protein B	pqqB	1.443	1.85E-01
MSMEG_3725	coenzyme PQQ biosynthesis protein A	pqqA	0.852	6.53E-02
MSMEG_3726	alcohol dehydrogenase	NA	0.935	5.42E-01
MSMEG_3727	hypothetical protein	NA	0.715	9.01E-03
MSMEG_3728	hypothetical protein	NA	1.004	9.83E-01
MSMEG_3729	catalase/peroxidase HPI	katG	0.997	9.33E-01
MSMEG_3730	helix-turn-helix, Fis-type, putative	NA	1.248	4.65E-01
MSMEG_3731	dipeptidase 2	NA	1.154	4.50E-01
MSMEG_3732	hypothetical protein	NA	0.998	9.76E-01
MSMEG_3733	conserved hypothetical protein	NA	0.876	2.59E-02

MSMEG_3735	YtnM protein	NA	1.312	4.81E-02
MSMEG_3736	hypothetical protein	NA	1.696	6.35E-02
MSMEG_3737	integral membrane protein	NA	1.327	5.97E-02
MSMEG_3738	GTP-binding protein EngA	NA	1.141	8.28E-02
MSMEG_3739	cytidylate kinase	cmk	1.111	2.77E-01
MSMEG_3740	ribosomal large subunit pseudouridine synthase B	rluB	1.142	1.86E-02
MSMEG_3741	transcriptional regulator	NA	1.005	8.26E-01
MSMEG_3742	segregation and condensation protein A	scpA	1.094	1.80E-01
MSMEG_3743	SpoOJ regulator protein	soj	2.384	3.68E-01
MSMEG_3744	tyrosine recombinase XerD	xerD	1.305	3.84E-01
MSMEG_3745	MutT/nudix family protein	NA	1.060	1.20E-01
MSMEG_3746	CTP synthase	pyrG	1.048	1.88E-01
MSMEG_3747	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.024	7.64E-01
MSMEG_3748	thiamin pyrophosphokinase, catalytic domain protein	NA	1.029	8.04E-01
MSMEG_3749	DNA repair protein RecN; this gene contains a frame shift which is not the result of sec	NA	0.922	4.02E-01
MSMEG_3749	DNA repair protein RecN; this gene contains a frame shift which is not the result of sec	NA	1.120	5.20E-02
MSMEG_3750	inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATP NADkinase)	NA	0.927	5.77E-02
MSMEG_3751	hemolysin A	NA	1.078	3.88E-01
MSMEG_3752	conserved hypothetical protein	NA	1.156	9.14E-02
MSMEG_3753	hydrolase	NA	1.124	3.05E-01
MSMEG_3754	TPR-repeat-containing protein	NA	1.449	1.47E-01
MSMEG_3758	tyrosyl-tRNA synthetase	tyrS	0.969	2.88E-01
MSMEG_3759	3-methyladenine DNA glycosylase	NA	1.077	6.24E-01
MSMEG_3760	conserved hypothetical protein	NA	1.025	5.63E-01
MSMEG_3761	putative Clp protease subunit	NA	1.007	9.36E-01
MSMEG_3762	ABC transporter ATP-binding protein	NA	1.031	7.35E-01
MSMEG_3763	ABC transporter efflux protein, DrrB family protein	NA	0.965	8.85E-01
MSMEG_3764	conserved hypothetical protein	NA	1.044	1.68E-01
MSMEG_3765	transcriptional regulator	NA	1.183	2.51E-02
MSMEG_3766	hypothetical protein	NA	1.059	8.67E-02
MSMEG_3767	acyl-CoA synthase	NA	1.135	4.20E-01

MSMEG_3768	macrolide-transport ATP-binding protein abc transporter	NA	0.970	5.85E-01
MSMEG_3769	argininosuccinate lyase	argH	1.154	1.71E-01
MSMEG_3770	argininosuccinate synthase	argG	0.965	6.48E-01
MSMEG_3771	arginine repressor	argR	1.096	3.45E-01
MSMEG_3772	ornithine carbamoyltransferase	argF	1.064	5.86E-01
MSMEG_3773	acetylornithine aminotransferase	argD	1.184	1.55E-01
MSMEG_3774	acetylglutamate kinase	argB	1.091	3.62E-01
MSMEG_3775	arginine biosynthesis bifunctional protein ArgJ	argJ	1.144	1.10E-01
MSMEG_3776	N-acetyl-gamma-glutamyl-phosphate reductase	argC	1.159	1.17E-01
MSMEG_3777	phenylalanyl-tRNA synthetase, beta subunit	pheT	1.144	1.54E-01
MSMEG_3778	phenylalanyl-tRNA synthetase, alpha subunit	pheS	1.106	3.74E-01
MSMEG_3779	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.230	1.17E-01
MSMEG_3780	adenylate and Guanylate cyclase catalytic domain protein	NA	1.030	7.12E-01
MSMEG_3781	conserved hypothetical protein	NA	0.991	7.71E-01
MSMEG_3782	endoribonuclease L-PSP, putative	NA	0.967	5.97E-01
MSMEG_3783	acyl-CoA dehydrogenase	NA	1.153	3.12E-01
MSMEG_3784	transcriptional regulator, IclR family protein	NA	1.123	6.52E-01
MSMEG_3785	PfkB-family protein carbohydrate kinase	NA	1.441	5.01E-01
MSMEG_3786	D-amino acid deaminase	NA	0.842	4.01E-01
MSMEG_3787	D-aminoacylase	NA	0.951	6.80E-01
MSMEG_3788	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	eda	1.078	4.03E-01
MSMEG_3789	inner membrane permease YgbN	NA	1.153	4.07E-01
MSMEG_3790	RNA methyltransferase, TrmH family protein	NA	1.285	9.53E-02
MSMEG_3791	ribosomal protein L20	rplT	1.208	8.79E-03
MSMEG_3792	ribosomal protein L35	rpmI	1.092	4.00E-01
MSMEG_3793	translation initiation factor IF-3	infC	0.944	5.26E-01
MSMEG_3794	hypothetical protein	NA	0.908	4.19E-01
MSMEG_3795	conserved hypothetical protein	NA	1.143	4.43E-01
MSMEG_3796	lysyl-tRNA synthetase	NA	0.981	8.70E-01
MSMEG_3797	putative esterase family protein	NA	1.155	2.40E-01
MSMEG_3798	conserved hypothetical protein	NA	1.101	2.81E-01

MSMEG_3799	conserved hypothetical protein	NA	1.218	1.35E-01
MSMEG_3800	conserved hypothetical protein	NA	1.358	3.02E-01
MSMEG_3801	conserved hypothetical protein	NA	1.249	4.27E-01
MSMEG_3802	tetratricopeptide repeat family protein	NA	1.097	2.01E-01
MSMEG_3803	lipoprotein LpqH	NA	1.067	2.52E-01
MSMEG_3804	conserved hypothetical protein	NA	0.984	7.19E-01
MSMEG_3805	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.125	3.37E-01
MSMEG_3806	conserved hypothetical protein	NA	1.020	5.97E-01
MSMEG_3807	TetR-type regulator	NA	1.049	3.38E-01
MSMEG_3808	excinuclease ABC, A subunit	uvrA	1.266	5.96E-02
MSMEG_3809	conserved hypothetical protein	NA	1.018	6.09E-01
MSMEG_3810	hydrolase	NA	1.134	5.20E-01
MSMEG_3811	universal stress protein family protein, putative	NA	1.273	4.32E-03
MSMEG_3812	acyl-CoA thioesterase	NA	1.208	2.89E-02
MSMEG_3813	NAD-dependent epimerase/dehydratase	NA	1.066	2.79E-01
MSMEG_3815	possible drug efflux membrane protein	NA	1.021	8.03E-01
MSMEG_3816	excinuclease ABC, B subunit	uvrB	0.958	2.84E-01
MSMEG_3817	conserved hypothetical protein	NA	0.939	6.78E-01
MSMEG_3818	thermolabile glutaminase	NA	1.122	2.61E-01
MSMEG_3819	conserved hypothetical protein	NA	1.007	7.67E-01
MSMEG_3820	hypothetical protein	NA	0.938	3.55E-01
MSMEG_3821	amino acid permease	NA	0.823	3.70E-01
MSMEG_3822	regulatory protein GntR, HTH	NA	1.074	2.17E-01
MSMEG_3823	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.156	9.88E-02
MSMEG_3824	conserved hypothetical protein	NA	1.055	7.94E-01
MSMEG_3825	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.307	2.76E-01
MSMEG_3826	hypothetical protein	NA	1.441	2.91E-01
MSMEG_3827	glutamine synthetase	NA	2.295	4.02E-01
MSMEG_3828	glutamine synthetase	NA	2.838	4.23E-01
MSMEG_3829	esterase	NA	0.740	4.07E-02
MSMEG_3830	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.936	3.31E-01

MSMEG_3831	dephospho-CoA kinase; this gene contains a frame shift which is not the result of sequ	NA	1.143	2.83E-01
MSMEG_3832	4-hydroxyacetophenone monooxygenase	NA	1.019	5.49E-01
MSMEG_3833	30S ribosomal protein S1	NA	0.793	4.74E-02
MSMEG_3834	putative TetR-family protein transcriptional regulator	NA	1.193	1.60E-02
MSMEG_3835	YesF protein	NA	1.501	1.76E-02
MSMEG_3836	conserved hypothetical protein	NA	1.338	6.11E-02
MSMEG_3837	conserved hypothetical protein	NA	1.045	6.82E-01
MSMEG_3838	integral membrane protein	NA	0.909	6.14E-03
MSMEG_3839	DNA polymerase I	NA	1.045	4.37E-01
MSMEG_3840	LysR-family protein transcriptional regulator	NA	1.568	1.17E-02
MSMEG_3841	monooxygenase, FAD-binding	NA	1.096	4.06E-01
MSMEG_3842	putative esterase	NA	1.102	2.10E-01
MSMEG_3843	conserved hypothetical protein	NA	0.999	9.94E-01
MSMEG_3844	lipid-transfer protein	NA	1.152	8.11E-02
MSMEG_3845	conserved domain protein	NA	1.397	2.45E-01
MSMEG_3846	phosphotransferase enzyme family protein	NA	0.795	2.49E-01
MSMEG_3847	copper methylamine oxidase	NA	0.851	7.97E-02
MSMEG_3848	para-nitrobenzyl esterase	NA	0.964	4.81E-01
MSMEG_3849	hypothetical protein	NA	1.059	5.28E-01
MSMEG_3850	alkanesulfonate monooxygenase family protein	NA	1.020	8.86E-01
MSMEG_3851	LppI protein	NA	0.865	5.50E-02
MSMEG_3852	aliphatic sulfonate binding protein	NA	1.060	6.79E-01
MSMEG_3853	putative aliphatic sulfonates transport ATP-binding protein SsuB	NA	1.155	3.56E-01
MSMEG_3854	putative aliphatic sulfonates transport permease protein SsuC	NA	1.051	4.90E-01
MSMEG_3855	hypothetical protein	NA	0.708	6.42E-02
MSMEG_3856	transcriptional regulator, CadC	NA	1.073	3.56E-01
MSMEG_3857	conserved hypothetical protein	NA	1.012	5.74E-01
MSMEG_3858	conserved hypothetical protein	NA	0.965	8.39E-01
MSMEG_3859	glycosyl transferase, group 2 family protein	NA	1.083	1.25E-01
MSMEG_3860	polyprenol-monophosphomannose synthase Ppm1	NA	1.038	7.04E-01
MSMEG_3861	amidohydrolase 3	NA	0.969	7.61E-01

MSMEG_3862	FxsA cytoplasmic membrane protein	NA	0.788	2.30E-04
MSMEG_3863	pyridoxamine 5'-phosphate oxidase family protein	NA	0.881	1.42E-02
MSMEG_3864	cobaltochelatase, CobN subunit	cobN	1.001	9.83E-01
MSMEG_3865	hypothetical protein	NA	1.068	7.89E-01
MSMEG_3866	conserved hypothetical protein	NA	1.016	9.10E-01
MSMEG_3867	ATPase family protein associated with various cellular activities (AAA)	NA	0.989	8.77E-01
MSMEG_3868	conserved hypothetical protein	NA	0.977	7.85E-01
MSMEG_3869	conserved hypothetical protein	NA	1.066	3.01E-01
MSMEG_3870	alpha-ketoglutarate-dependent taurine dioxygenase	NA	1.129	5.29E-01
MSMEG_3871	precorrin-3B synthase	cobG	1.152	2.19E-01
MSMEG_3872	precorrin-8X methylmutase	NA	1.121	3.12E-01
MSMEG_3873	cobalamin biosynthesis protein cobIJ	NA	1.143	1.34E-01
MSMEG_3874	transcriptional regulator, TetR family protein	NA	1.291	2.04E-01
MSMEG_3875	precorrin-6x reductase	cobK	1.006	9.64E-01
MSMEG_3876	phosphotransferase enzyme family protein, putative	NA	0.990	9.48E-01
MSMEG_3877	precorrin-4 C11-methyltransferase	cobM	0.923	2.49E-01
MSMEG_3878	precorrin-6Y C5,15-methyltransferase (decarboxylating)	cobL	1.063	3.12E-01
MSMEG_3879	short chain dehydrogenase	NA	1.168	7.58E-03
MSMEG_3880	nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	NA	1.008	9.13E-01
MSMEG_3881	proline dipeptidase	NA	0.918	4.84E-02
MSMEG_3882	glyoxalase family protein	NA	1.235	6.46E-02
MSMEG_3883	5'-3' exonuclease	NA	0.902	4.22E-02
MSMEG_3884	conserved hypothetical protein	NA	0.843	1.58E-02
MSMEG_3885	DEAD/DEAH box helicase	NA	0.963	2.48E-01
MSMEG_3886	twin arginine-targeting protein translocase TatC	tatC	1.077	2.35E-03
MSMEG_3887	twin arginine-targeting protein translocase, TatA/E family protein	tatA	1.072	5.50E-01
MSMEG_3888	conserved hypothetical protein	NA	1.088	6.99E-01
MSMEG_3889	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.866	3.99E-04
MSMEG_3889	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.035	6.27E-01
MSMEG_3890	proteasome component	NA	0.827	3.45E-03
MSMEG_3891	hydrolase	NA	0.892	4.70E-01

MSMEG_3892	hypothetical protein	NA	1.007	9.58E-01
MSMEG_3893	hypothetical protein	NA	0.847	2.09E-01
MSMEG_3894	proteasome alpha subunit	NA	0.878	5.57E-02
MSMEG_3895	proteasome beta subunit	NA	0.887	1.89E-01
MSMEG_3896	conserved hypothetical protein	NA	0.913	3.48E-01
MSMEG_3897	proteasome component	NA	0.952	2.14E-01
MSMEG_3898	ectoine hydroxylase	thpD	1.033	6.57E-01
MSMEG_3899	ectoine synthase	ectC	0.949	5.21E-01
MSMEG_3900	diaminobutyrate--2-oxoglutarate aminotransferase	ectB	1.017	8.69E-01
MSMEG_3901	L-2,4-diaminobutyric acid acetyltransferase	ectA	0.995	9.58E-01
MSMEG_3902	ATPase, AAA family protein	NA	1.039	7.25E-01
MSMEG_3903	Low molecular weight antigen MTB12	NA	1.130	2.98E-01
MSMEG_3904	LppK protein	NA	1.450	2.78E-02
MSMEG_3905	conserved hypothetical protein	NA	1.346	3.90E-02
MSMEG_3906	tRNA (adenine-N(1)-)-methyltransferase	NA	1.342	6.62E-02
MSMEG_3907	RecB family protein exonuclease	NA	0.921	3.67E-01
MSMEG_3908	conserved hypothetical protein	NA	0.945	5.00E-01
MSMEG_3909	conserved hypothetical protein	NA	1.019	8.71E-01
MSMEG_3910	conserved hypothetical protein	NA	1.231	2.21E-02
MSMEG_3911	oxidoreductase	NA	1.164	3.75E-01
MSMEG_3912	acetoacetyl-CoA reductase	NA	0.972	7.63E-01
MSMEG_3913	short chain dehydrogenase; this gene contains a frame shift which is not the result of	NA	1.435	5.50E-02
MSMEG_3914	beta-lactamase	NA	1.704	1.31E-01
MSMEG_3915	NAD-dependent alcohol dehydrogenase	NA	1.000	9.99E-01
MSMEG_3916	hypothetical protein	NA	1.138	1.14E-01
MSMEG_3917	hypothetical protein	NA	1.033	7.27E-01
MSMEG_3918	hypothetical protein	NA	1.072	1.49E-01
MSMEG_3919	hypothetical protein	NA	0.795	9.95E-03
MSMEG_3920	hypothetical protein	NA	0.809	2.12E-02
MSMEG_3921	hypothetical protein	NA	1.026	7.37E-01
MSMEG_3922	hypothetical protein	NA	0.831	3.81E-02

MSMEG_3923	conserved hypothetical protein	NA	1.215	2.00E-02
MSMEG_3924	peptide synthetase ScpsB, putative	NA	0.931	7.38E-01
MSMEG_3925	AttM/AiiB family protein	NA	1.529	4.40E-01
MSMEG_3926	cation-transporting ATPase Pma1	NA	2.110	4.29E-01
MSMEG_3927	peptidase M52, hydrogen uptake protein	NA	0.997	9.83E-01
MSMEG_3928	[NiFe] hydrogenase, alpha subunit, putative	NA	1.027	5.85E-01
MSMEG_3929	[NiFe] hydrogenase, delta subunit, putative	NA	1.334	1.58E-02
MSMEG_3930	[NiFe] hydrogenase, gamma subunit, putative	NA	0.993	9.64E-01
MSMEG_3931	[NiFe] hydrogenase, beta subunit, putative	NA	0.931	3.55E-01
MSMEG_3932	14 kDa antigen	NA	1.144	4.59E-01
MSMEG_3933	conserved hypothetical protein	NA	0.950	7.39E-01
MSMEG_3934	phosphoenolpyruvate synthase	NA	1.095	5.91E-01
MSMEG_3935	conserved hypothetical protein	NA	1.371	4.40E-01
MSMEG_3936	universal stress protein family protein	NA	1.230	1.65E-01
MSMEG_3937	conserved hypothetical protein	NA	1.072	7.37E-01
MSMEG_3938	hypothetical protein	NA	1.371	4.05E-01
MSMEG_3939	universal stress protein family protein	NA	1.298	3.40E-01
MSMEG_3940	universal stress protein family protein	NA	1.226	3.79E-01
MSMEG_3941	GAF family protein	NA	1.687	1.87E-01
MSMEG_3942	conserved hypothetical protein	NA	1.058	3.30E-01
MSMEG_3943	conserved hypothetical protein	NA	1.012	8.23E-01
MSMEG_3944	two component transcriptional regulatory protein devr	NA	0.836	2.59E-01
MSMEG_3945	universal stress protein family protein	NA	0.932	7.07E-01
MSMEG_3946	probable conserved transmembrane protein	NA	0.846	4.01E-01
MSMEG_3947	6-phosphofructokinase isozyme 2	NA	0.984	7.69E-01
MSMEG_3948	acyltransferase, ws/dgat/mgat subfamily protein	NA	0.958	7.27E-01
MSMEG_3948	acyltransferase, ws/dgat/mgat subfamily protein	NA	1.240	7.40E-02
MSMEG_3949	hypothetical protein	NA	1.575	4.43E-01
MSMEG_3950	universal stress protein family protein	NA	0.956	8.22E-01
MSMEG_3951	conserved hypothetical protein	NA	1.208	1.61E-01
MSMEG_3952	conserved hypothetical protein	NA	0.906	1.54E-01

MSMEG_3953	conserved hypothetical protein	NA	1.292	3.53E-01
MSMEG_3954	trehalose 6-phosphate phosphorylase	NA	1.017	8.67E-01
MSMEG_3955	conserved hypothetical protein	NA	1.029	6.85E-01
MSMEG_3956	alkylhydroperoxidase AhpD	NA	0.960	2.26E-01
MSMEG_3957	conserved 13e12 repeat family protein	NA	4.119	3.16E-01
MSMEG_3958	glyoxalase/bleomycin resistance protein/dioxygenase	NA	0.847	1.12E-02
MSMEG_3959	transcriptional regulator	NA	0.904	4.97E-01
MSMEG_3960	transcriptional regulator	NA	1.091	4.18E-01
MSMEG_3961	transcriptional regulator	NA	1.140	3.30E-01
MSMEG_3962	lactate 2-monooxygenase	NA	0.733	2.05E-02
MSMEG_3963	hypothetical protein	NA	1.123	5.58E-01
MSMEG_3964	pyruvate dehydrogenase	NA	0.908	3.34E-02
MSMEG_3965	hypothetical protein	NA	0.801	1.77E-02
MSMEG_3966	hypothetical protein	NA	0.779	5.80E-04
MSMEG_3967	TonB-dependent receptor	NA	1.028	8.89E-01
MSMEG_3968	hypothetical protein	NA	1.229	2.93E-01
MSMEG_3969	hypothetical protein	NA	0.811	2.39E-01
MSMEG_3970	glutamyl-tRNA(Gln) amidotransferase subunit A	NA	0.975	9.05E-01
MSMEG_3971	hypothetical protein	NA	1.057	4.95E-01
MSMEG_3972	transcriptional regulator, LysR family protein	NA	1.189	2.91E-01
MSMEG_3973	N-methylhydantoinase	NA	1.039	3.18E-01
MSMEG_3974	hydantoin utilization protein A; this gene contains a frame shift which is not the result	NA	0.947	7.41E-01
MSMEG_3975	regulatory protein, putative	NA	1.152	2.84E-01
MSMEG_3976	DNA-binding protein	NA	0.777	1.89E-01
MSMEG_3977	conserved hypothetical protein	NA	1.422	5.24E-02
MSMEG_3978	beta-lactamase	NA	1.125	3.05E-02
MSMEG_3979	alpha/beta hydrolase; this gene contains a frame shift which is not the result of seque	NA	1.107	2.66E-01
MSMEG_3980	transcriptional regulator, GntR family protein	NA	1.031	6.03E-01
MSMEG_3981	L-carnitine dehydratase/bile acid-inducible protein F	NA	0.864	3.91E-01
MSMEG_3982	acyl-CoA dehydrogenase	NA	1.021	8.95E-01
MSMEG_3983	L-carnitine dehydratase/bile acid-inducible protein F; this gene contains a frame shift	NA	0.899	1.66E-01

MSMEG_3983	L-carnitine dehydratase/bile acid-inducible protein F; this gene contains a frame shift	NA	1.089	2.97E-01
MSMEG_3984	Transposase IS116/IS110/IS902 family protein	NA	0.884	2.25E-01
MSMEG_3984	Transposase IS116/IS110/IS902 family protein	NA	1.086	5.13E-01
MSMEG_3985	integral membrane transport protein	NA	0.836	1.77E-01
MSMEG_3986	acetyl-coenzyme A synthetase	NA	0.950	6.09E-01
MSMEG_3987	FAD dependent oxidoreductase	NA	0.943	3.61E-01
MSMEG_3988	transcriptional regulator, AsnC family protein	NA	1.171	2.49E-01
MSMEG_3989	peptidase M20D, amidohydrolase	NA	1.717	8.98E-02
MSMEG_3990	putative transporter	NA	1.037	8.51E-01
MSMEG_3991	cyclase	NA	1.039	5.02E-01
MSMEG_3992	integral membrane transport protein	NA	0.919	3.78E-01
MSMEG_3993	Asp/Glu racemase	NA	0.972	6.87E-01
MSMEG_3994	short chain dehydrogenase	NA	0.865	6.15E-02
MSMEG_3995	N-carbamoyl-L-amino acid amidohydrolase	NA	1.036	3.81E-01
MSMEG_3996	dihydropyrimidinase	hydA	0.932	7.55E-01
MSMEG_3997	regulatory protein	NA	1.105	3.63E-01
MSMEG_3998	MmsAB operon regulatory protein	NA	1.209	4.92E-01
MSMEG_3999	ABC transporter periplasmic-binding protein YphF	NA	0.855	1.96E-02
MSMEG_4000	hypothetical ABC transporter ATP-binding protein YphE	NA	1.049	8.05E-01
MSMEG_4001	ribose transport system permease protein RbsC	NA	0.793	7.98E-02
MSMEG_4002	oxidoreductase, zinc-binding dehydrogenase family protein	NA	0.838	5.73E-02
MSMEG_4003	conserved hypothetical protein	NA	0.828	1.32E-02
MSMEG_4004	3-oxoacyl-[acyl-carrier-protein] reductase	NA	0.739	1.34E-01
MSMEG_4005	calcium-binding protein	NA	1.081	8.32E-01
MSMEG_4006	transcriptional regulator, CdaR, putative	NA	0.964	8.05E-01
MSMEG_4007	oxidoreductase, 2OG-Fe(II) oxygenase family protein	NA	1.020	6.48E-01
MSMEG_4008	oxidoreductase, 2OG-Fe(II) oxygenase family protein	NA	1.002	9.85E-01
MSMEG_4009	vanillate O-demethylase oxidoreductase	NA	0.997	9.55E-01
MSMEG_4010	glyoxalase family protein	NA	0.984	7.11E-01
MSMEG_4011	putative pyrimidine permease RutG	NA	1.209	4.28E-01
MSMEG_4012	dihydropyrimidinase	hydA	1.528	4.36E-01

MSMEG_4013	oxidoreductase	NA	1.089	6.52E-01
MSMEG_4014	N-carbamoyl-L-amino acid amidohydrolase	NA	0.900	4.08E-01
MSMEG_4015	hypothetical protein	NA	1.381	2.81E-01
MSMEG_4016	conserved hypothetical protein	NA	0.956	5.86E-01
MSMEG_4017	BmyD protein	NA	1.474	2.53E-01
MSMEG_4018	nucleotidyltransferase domain protein	NA	1.119	5.07E-01
MSMEG_4019	AMP-dependent synthetase and ligase	NA	1.933	3.95E-01
MSMEG_4020	enoyl-CoA hydratase/isomerase family protein	NA	1.611	5.17E-01
MSMEG_4021	hypothetical protein	NA	0.996	9.87E-01
MSMEG_4022	TetR-family protein transcriptional regulator	NA	1.272	1.14E-02
MSMEG_4023	oxidoreductase	NA	1.235	1.11E-01
MSMEG_4024	transcriptional regulator, TetR family protein	NA	1.234	5.64E-03
MSMEG_4025	transcriptional regulator, LysR family protein	NA	1.467	2.79E-01
MSMEG_4026	hypothetical protein	NA	0.903	3.86E-01
MSMEG_4027	zinc-containing alcohol dehydrogenase superfamily protein	NA	1.085	6.94E-01
MSMEG_4028	hypothetical protein	NA	1.278	7.91E-03
MSMEG_4029	conserved hypothetical protein	NA	1.049	5.65E-01
MSMEG_4030	conserved hypothetical protein	NA	0.839	1.63E-01
MSMEG_4031	hypothetical protein	NA	1.037	8.58E-01
MSMEG_4032	zinc-binding alcohol dehydrogenase	NA	1.226	3.01E-01
MSMEG_4033	TetR-family protein transcriptional regulator	NA	1.028	8.44E-01
MSMEG_4034	NAD dependent epimerase/dehydratase family protein	NA	0.754	8.33E-02
MSMEG_4035	citrate synthase	NA	0.806	2.17E-01
MSMEG_4036	crotonobetaine/carnitine-CoA ligase	NA	0.974	5.63E-01
MSMEG_4037	hypothetical protein	NA	0.951	4.58E-01
MSMEG_4038	vanillin dehydrogenase	NA	0.915	5.63E-01
MSMEG_4039	aryl-alcohol dehydrogenase	NA	1.055	8.88E-01
MSMEG_4040	nitroreductase	NA	0.861	3.83E-01
MSMEG_4041	hydroxyquinol 1,2-dioxygenase	NA	0.940	6.36E-01
MSMEG_4042	transcriptional regulator, GntR family protein	NA	0.794	3.59E-02
MSMEG_4043	amidohydrolase 2	NA	0.858	3.94E-03

MSMEG_4044	GAF domain protein	NA	0.764	4.79E-02
MSMEG_4045	muconolactone delta-isomerase	NA	1.055	1.39E-01
MSMEG_4046	L-carnitine dehydratase/bile acid-inducible protein F	NA	1.340	4.44E-01
MSMEG_4047	dihydropteroate synthase	NA	0.991	9.49E-01
MSMEG_4048	cyclase	NA	0.622	5.19E-02
MSMEG_4049	sugar transporter, permease protein	NA	0.927	4.87E-01
MSMEG_4050	hypothetical protein	NA	1.931	1.82E-01
MSMEG_4051	hypothetical protein	NA	1.550	1.66E-01
MSMEG_4052	hypothetical protein	NA	1.083	5.34E-01
MSMEG_4053	transcriptional regulatory protein	NA	1.379	4.46E-01
MSMEG_4054	hypothetical protein	NA	0.948	6.97E-01
MSMEG_4055	short-chain dehydrogenase/reductase SDR	NA	1.013	6.39E-01
MSMEG_4056	conserved secreted protein	NA	1.059	7.64E-01
MSMEG_4057	transcriptional regulator, GntR family protein	NA	0.887	4.59E-01
MSMEG_4058	major facilitator superfamily protein	NA	1.031	5.99E-01
MSMEG_4059	haloacid dehalogenase, type II	NA	0.728	2.15E-02
MSMEG_4060	aspartate aminotransferase; this gene contains a frame shift which is not the result of	NA	0.726	1.72E-03
MSMEG_4060	aspartate aminotransferase; this gene contains a frame shift which is not the result of	NA	0.899	3.17E-01
MSMEG_4061	translation initiation inhibitor	NA	1.039	5.11E-01
MSMEG_4062	glutamyl-tRNA(Gln) amidotransferase subunit A	NA	1.061	7.73E-01
MSMEG_4063	amidohydrolase family protein	NA	1.349	5.62E-02
MSMEG_4064	zinc-binding alcohol dehydrogenase	NA	1.120	1.64E-01
MSMEG_4065	feruloyl-CoA synthetase	NA	2.887	4.56E-01
MSMEG_4066	conserved hypothetical protein	NA	0.988	8.74E-01
MSMEG_4067	zinc-containing alcohol dehydrogenase superfamily protein	NA	0.858	7.03E-02
MSMEG_4068	hypothetical protein	NA	1.034	4.12E-01
MSMEG_4069	hypothetical protein	NA	0.982	9.41E-01
MSMEG_4070	transcriptional regulator, TetR family protein, putative	NA	1.076	2.40E-01
MSMEG_4071	conserved hypothetical protein; this region contains one or more premature stops anc	NA	1.537	7.81E-02
MSMEG_4072	ISMsm5, transposase	NA	0.987	5.77E-01
MSMEG_4073	DNA-binding protein; this gene contains a frame shift which is not the result of sequen	NA	1.081	2.08E-01

MSMEG_4074	peroxisomal trans-2-enoyl-CoA reductase	NA	1.273	2.88E-01
MSMEG_4075	CoA-binding protein	NA	0.960	6.41E-01
MSMEG_4076	butyryl-CoA dehydrogenase	NA	1.092	7.79E-01
MSMEG_4077	enoyl-CoA hydratase	NA	0.950	5.02E-01
MSMEG_4078	hypothetical metabolite transport protein YaaU	NA	0.850	3.73E-01
MSMEG_4079	putative hydrolase	NA	0.969	6.76E-01
MSMEG_4080	fmnh2-utilizing oxygenase; this gene contains a frame shift which is not the result of se	NA	1.210	3.68E-01
MSMEG_4082	monoxygenase	NA	0.641	1.80E-03
MSMEG_4083	putative monooxygenase	NA	0.704	2.39E-04
MSMEG_4084	putative acyl-CoA dehydrogenase	NA	0.808	3.66E-03
MSMEG_4085	nitrilotriacetate monooxygenase component A	NA	0.836	1.27E-02
MSMEG_4086	nitrilotriacetate monooxygenase component A	ssuD	0.808	2.25E-02
MSMEG_4087	major facilitator superfamily protein	NA	0.890	4.73E-02
MSMEG_4090	putative IclR family protein transcriptional regulator	NA	0.711	3.88E-03
MSMEG_4091	nitrilotriacetate monooxygenase component A	ssuD	0.818	7.20E-02
MSMEG_4092	alkanal monooxygenase	NA	0.816	2.09E-01
MSMEG_4093	oxidoreductase, aldo/keto reductase family protein	NA	0.940	4.66E-01
MSMEG_4094	acyl-CoA dehydrogenase	NA	1.039	6.62E-01
MSMEG_4095	putative monooxygenase	NA	0.950	6.60E-01
MSMEG_4096	nitrilotriacetate monooxygenase component A	ssuD	1.522	3.21E-01
MSMEG_4097	acyl-CoA dehydrogenase domain protein	NA	2.066	2.48E-01
MSMEG_4098	ABC transporter ATP-binding protein	NA	1.056	2.32E-01
MSMEG_4099	ABC transporter permease protein	NA	1.742	4.14E-01
MSMEG_4100	ABC transporter permease protein	NA	1.772	1.20E-01
MSMEG_4101	ABC-type transporter, substrate binding protein	NA	1.040	5.70E-01
MSMEG_4102	conserved hypothetical protein	NA	0.938	7.35E-01
MSMEG_4103	alkanesulfonate monooxygenase	NA	1.113	6.04E-01
MSMEG_4104	transporter, major facilitator family protein	NA	1.024	8.18E-01
MSMEG_4105	transposase subunit	NA	0.899	2.55E-01
MSMEG_4105	transposase subunit	NA	0.993	9.54E-01
MSMEG_4106	transposase	NA	1.070	5.52E-01

MSMEG_4106	transposase	NA	1.235	2.48E-02
MSMEG_4107	phosphoglycerate mutase, putative	NA	0.961	5.43E-01
MSMEG_4108	NAD(P) transhydrogenase, beta subunit	pntB	0.906	3.37E-01
MSMEG_4109	NAD(P) transhydrogenase, alpha subunit	pntA	0.887	2.18E-01
MSMEG_4110	3-hydroxyacyl-CoA dehydrogenase	NA	0.715	1.29E-01
MSMEG_4111	alpha-methylacyl-CoA racemase	NA	0.758	4.90E-02
MSMEG_4112	cyclohexanecarboxylate-CoA ligase	NA	0.692	1.09E-02
MSMEG_4113	acyl-CoA dehydrogenase	NA	0.743	2.38E-02
MSMEG_4114	naphthoate synthase	menB	0.859	1.03E-01
MSMEG_4115	3-hydroxybutyryl-CoA dehydrogenase	NA	0.878	2.64E-01
MSMEG_4116	3-hydroxybutyryl-CoA dehydrogenase	NA	0.832	1.21E-01
MSMEG_4117	2-deoxy-D-gluconate 3-dehydrogenase	NA	0.838	4.18E-02
MSMEG_4118	acyl-CoA dehydrogenase	NA	0.962	6.58E-01
MSMEG_4119	3-hydroxybutyryl-CoA dehydratase	NA	0.933	5.23E-02
MSMEG_4120	CAIB/BAIF family protein	NA	0.947	1.53E-01
MSMEG_4121	GntR-family protein transcriptional regulator	NA	1.254	1.51E-02
MSMEG_4122	major facilitator family protein transporter	NA	1.004	9.61E-01
MSMEG_4123	3-hydroxyisobutyrate dehydrogenase	NA	1.293	1.87E-01
MSMEG_4124	conserved hypothetical protein	NA	1.068	5.70E-01
MSMEG_4125	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.906	6.48E-02
MSMEG_4126	hydrolase, isochorismatase family protein	NA	1.093	1.81E-01
MSMEG_4127	TnpC protein	NA	0.907	1.87E-01
MSMEG_4128	conserved hypothetical protein	NA	0.900	1.66E-01
MSMEG_4129	hypothetical protein	NA	1.074	2.16E-01
MSMEG_4130	polysaccharide deacetylase family protein	NA	3.274	2.51E-01
MSMEG_4131	hypothetical protein	NA	1.188	1.39E-01
MSMEG_4133	transposase	NA	0.807	2.18E-04
MSMEG_4134	TnpC protein; this gene contains a frame shift which is not the result of sequencing err	NA	0.668	2.17E-02
MSMEG_4134	TnpC protein; this gene contains a frame shift which is not the result of sequencing err	NA	1.028	7.31E-01
MSMEG_4135	possible lysine decarboxylase superfamily protein	NA	1.034	8.68E-01
MSMEG_4136	dTDP-glucose 4,6-dehydratase	NA	0.944	6.73E-01

MSMEG_4137	hypothetical protein	NA	1.238	3.17E-01
MSMEG_4138	aliphatic nitrilase	NA	2.926	3.79E-01
MSMEG_4139	major facilitator superfamily MFS_1; this gene contains a frame shift which is not the r	NA	1.027	6.71E-01
MSMEG_4140	GntR-family protein transcriptional regulator	NA	1.234	5.46E-01
MSMEG_4141	conserved hypothetical protein	NA	1.757	1.63E-02
MSMEG_4142	transcriptional repressor, TetR family protein, putative	NA	1.023	4.92E-01
MSMEG_4143	conserved hypothetical protein	NA	0.803	7.14E-02
MSMEG_4144	transcriptional regulator, LysR family protein	NA	0.831	5.78E-02
MSMEG_4145	cupin 2 protein	NA	1.007	7.28E-01
MSMEG_4146	quinone oxidoreductase	NA	1.179	4.84E-01
MSMEG_4147	major facilitator superfamily protein MFS_1, putative	NA	1.401	1.06E-01
MSMEG_4148	lipase	NA	0.751	2.69E-02
MSMEG_4149	acetaldehyde dehydrogenase	NA	0.972	5.19E-01
MSMEG_4150	4-hydroxy-2-oxovalerate aldolase	NA	0.965	7.01E-01
MSMEG_4151	conserved domain protein	NA	1.132	5.42E-01
MSMEG_4152	phenoxybenzoate dioxygenase beta subunit	NA	1.071	1.10E-01
MSMEG_4153	cytochrome P450	NA	1.213	2.94E-01
MSMEG_4154	transposase, Mutator family protein	NA	1.205	3.62E-01
MSMEG_4155	transposase A	NA	0.973	6.72E-01
MSMEG_4156	putative transposase	NA	3.062	4.05E-01
MSMEG_4157	putative transposase	NA	1.025	7.28E-01
MSMEG_4158	putative transposase	NA	0.892	2.14E-03
MSMEG_4160	hypothetical protein	NA	1.275	2.35E-01
MSMEG_4161	hypothetical protein	NA	0.949	4.57E-01
MSMEG_4162	conserved hypothetical protein	NA	0.995	9.82E-01
MSMEG_4163	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.099	1.28E-02
MSMEG_4164	3-hydroxybutyryl-CoA dehydratase	NA	1.030	8.84E-01
MSMEG_4165	[NAD+] benzaldehyde dehydrogenase	NA	1.158	7.37E-01
MSMEG_4166	acyl-CoA dehydrogenase	NA	0.684	6.79E-02
MSMEG_4167	alcohol dehydrogenase B	NA	0.737	2.09E-02
MSMEG_4168	propionate CoA-transferase	NA	0.848	2.66E-01

MSMEG_4169	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.116	4.61E-01
MSMEG_4170	ribose transport ATP-binding protein RbsA	NA	1.077	5.15E-01
MSMEG_4171	ribose transport system permease protein RbsC	NA	0.829	2.61E-01
MSMEG_4172	D-ribose-binding periplasmic protein RbsB	NA	0.684	3.36E-02
MSMEG_4173	MaoC family protein	NA	1.134	1.63E-01
MSMEG_4174	transcriptional regulator, IclR family protein	NA	1.001	9.95E-01
MSMEG_4175	transcriptional regulator, ArsR family protein	NA	1.288	3.19E-02
MSMEG_4176	conserved hypothetical protein	NA	1.237	2.12E-02
MSMEG_4177	mercuric reductase; this gene contains a frame shift which is not the result of sequenc	NA	0.910	3.64E-01
MSMEG_4178	flavodoxin/nitric oxide synthase	NA	1.404	7.51E-03
MSMEG_4179	probable conserved integral membrane protein	NA	1.114	1.40E-01
MSMEG_4180	ATP phosphoribosyltransferase	hisG	1.003	9.51E-01
MSMEG_4181	phosphoribosyl-ATP pyrophosphohydrolase	NA	1.131	2.49E-01
MSMEG_4182	arabinose-proton symporter	NA	1.236	1.26E-01
MSMEG_4183	phosphoglycolate phosphatase, chromosomal	NA	1.379	4.20E-03
MSMEG_4184	dtdp-glucose-46-dehydratase	NA	1.059	6.29E-01
MSMEG_4185	methionine synthase	metH	0.829	1.55E-02
MSMEG_4186	conserved hypothetical protein	NA	1.034	5.12E-01
MSMEG_4187	conserved hypothetical protein	NA	0.730	4.72E-03
MSMEG_4188	short chain dehydrogenase	NA	0.908	2.41E-01
MSMEG_4189	cysteinyl-tRNA synthetase	cysS	1.052	6.16E-01
MSMEG_4190	inositol monophosphatase family protein	NA	1.059	3.37E-01
MSMEG_4191	conserved hypothetical protein	NA	1.085	3.93E-02
MSMEG_4192	conserved hypothetical protein	NA	1.015	7.40E-01
MSMEG_4193	phosphoglycerate mutase family protein	NA	0.801	1.02E-02
MSMEG_4194	undecaprenol kinase, putative	NA	0.908	1.85E-02
MSMEG_4195	conserved hypothetical protein	NA	1.224	4.33E-01
MSMEG_4196	LppL protein	NA	1.091	9.36E-02
MSMEG_4197	conserved hypothetical protein	NA	1.029	4.63E-01
MSMEG_4198	dihydroorotate oxidase	pyrD	0.935	2.38E-01
MSMEG_4199	conserved hypothetical protein	NA	0.851	8.35E-02

MSMEG_4200	peptidase M20	NA	1.035	6.42E-01
MSMEG_4202	conserved hypothetical protein	NA	1.255	4.12E-01
MSMEG_4203	peptidase S8 and S53, subtilisin, kexin, sedolisin	NA	0.885	2.33E-01
MSMEG_4204	catalase	NA	1.072	2.53E-01
MSMEG_4205	putative transcriptional regulator	NA	1.408	1.68E-01
MSMEG_4206	Molybdopterin oxidoreductase; this gene contains a frame shift which is not the result	NA	0.947	6.28E-01
MSMEG_4206	Molybdopterin oxidoreductase; this gene contains a frame shift which is not the result	NA	1.062	5.39E-01
MSMEG_4207	universal stress protein family protein	NA	0.839	4.55E-01
MSMEG_4208	integral membrane protein	NA	1.088	7.33E-01
MSMEG_4209	integral membrane protein	NA	1.808	4.08E-01
MSMEG_4210	secreted protein	NA	1.014	9.23E-01
MSMEG_4211	two component system histidine kinase	NA	1.215	5.51E-01
MSMEG_4212	transcriptional regulatory protein CitT	NA	1.136	1.64E-01
MSMEG_4213	cytochrome P450 hydroxylase	NA	1.487	3.02E-01
MSMEG_4214	glutamine amidotransferase	NA	1.470	9.03E-03
MSMEG_4215	phosphoribosyltransferase	NA	1.860	3.11E-03
MSMEG_4216	conserved hypothetical protein	NA	1.087	3.35E-01
MSMEG_4217	DivIVA protein	NA	1.049	5.60E-01
MSMEG_4218	possible conserved transmembrane protein	NA	1.037	5.96E-01
MSMEG_4219	conserved hypothetical protein	NA	0.930	6.33E-01
MSMEG_4220	conserved hypothetical protein	NA	0.980	5.50E-01
MSMEG_4221	conserved hypothetical protein	NA	1.135	2.59E-01
MSMEG_4222	cell division protein FtsZ	ftsZ	1.047	4.04E-01
MSMEG_4223	hypothetical protein	NA	0.999	9.91E-01
MSMEG_4224	hypothetical protein	NA	1.018	7.49E-01
MSMEG_4225	putative Cell division protein FtsQ	NA	0.919	2.94E-01
MSMEG_4226	UDP-N-acetylmuramate--alanine ligase	murC	1.036	3.33E-01
MSMEG_4227	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferas	murG	1.140	2.15E-01
MSMEG_4228	cell division protein FtsW	ftsW	1.067	8.61E-02
MSMEG_4229	UDP-N-acetylmuramoylalanine--D-glutamate ligase	murD	1.034	5.16E-01
MSMEG_4230	phospho-N-acetylmuramoyl-pentapeptide- transferase	mraY	1.158	2.06E-01

MSMEG_4231	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	NA	0.924	2.12E-01
MSMEG_4232	UDP-N-acetylmuramoylalanyl-D-glutamate-2, 6-diaminopimelate ligase	NA	1.079	3.84E-01
MSMEG_4233	Penicillin binding protein transpeptidase domain protein	NA	0.828	5.84E-02
MSMEG_4234	conserved hypothetical protein	NA	0.806	4.03E-03
MSMEG_4235	S-adenosyl-methyltransferase MraW	mraW	0.828	1.26E-02
MSMEG_4236	MraZ protein	mraZ	0.976	3.80E-01
MSMEG_4237	probable conserved transmembrane protein	NA	1.149	1.15E-01
MSMEG_4238	conserved hypothetical protein	NA	1.195	3.51E-02
MSMEG_4239	LppM protein	NA	1.127	1.03E-01
MSMEG_4240	polyprenyl synthetase	NA	0.896	9.99E-02
MSMEG_4241	possible conserved integral membrane protein	NA	0.960	6.26E-01
MSMEG_4242	transcriptional regulatory protein	NA	1.294	3.51E-02
MSMEG_4243	serine/threonine-protein kinase PK-1	NA	1.348	1.06E-02
MSMEG_4244	3-deoxy-7-phosphoheptulonate synthase	NA	0.954	3.64E-01
MSMEG_4245	conserved hypothetical protein	NA	1.035	8.90E-02
MSMEG_4246	probable conserved integral membrane protein	NA	1.022	5.81E-01
MSMEG_4247	probable conserved integral membrane protein	NA	0.982	7.06E-01
MSMEG_4248	1-acylglycerol-3-phosphate O-acyltransferase	NA	0.866	5.20E-02
MSMEG_4249	conserved hypothetical protein	NA	0.967	6.62E-01
MSMEG_4250	putative membrane transport ATPase	NA	1.084	4.19E-01
MSMEG_4251	cyclase/dehydrase	NA	0.873	8.45E-02
MSMEG_4252	conserved hypothetical protein	NA	0.853	1.69E-02
MSMEG_4253	glycosyl transferase, group 1 family protein	NA	1.018	8.98E-01
MSMEG_4254	AMP-binding enzyme	NA	0.763	7.21E-03
MSMEG_4255	conserved hypothetical protein	NA	1.245	2.25E-03
MSMEG_4256	NLP/P60 family protein	NA	1.107	4.12E-01
MSMEG_4257	conserved hypothetical protein	NA	0.832	1.92E-01
MSMEG_4258	anthranilate phosphoribosyltransferase	trpD	1.139	4.51E-02
MSMEG_4259	DNA polymerase III, epsilon subunit	NA	1.143	5.54E-01
MSMEG_4260	cytochrome c oxidase subunit 3	NA	0.850	3.61E-02
MSMEG_4261	ubiquinol-cytochrome c reductase cytochrome c subunit	NA	0.973	6.41E-01

MSMEG_4262	ubiquinol-cytochrome c reductase iron-sulfur subunit	NA	0.963	5.21E-01
MSMEG_4263	ubiquinol-cytochrome c reductase cytochrome b subunit	NA	0.902	3.75E-01
MSMEG_4264	conserved hypothetical protein	NA	0.997	9.54E-01
MSMEG_4265	MmpS3 protein	NA	1.109	3.31E-02
MSMEG_4266	hypothetical protein	NA	1.163	2.14E-01
MSMEG_4267	probable cytochrome c oxidase polypeptide 4	NA	0.997	9.39E-01
MSMEG_4268	cytochrome c oxidase subunit 2	NA	1.196	7.47E-03
MSMEG_4269	asparagine synthase (glutamine-hydrolyzing)	asnB	1.022	5.38E-01
MSMEG_4270	adenosine kinase	NA	0.991	6.97E-01
MSMEG_4271	conserved hypothetical protein	NA	1.013	8.79E-01
MSMEG_4272	HesB/YadR/YfhF family protein	NA	1.035	6.39E-01
MSMEG_4273	integral membrane protein	NA	1.025	6.25E-01
MSMEG_4274	Cobinamide kinase	cobU	1.353	1.90E-01
MSMEG_4275	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	NA	1.076	5.20E-01
MSMEG_4276	branched-chain amino acid aminotransferase	ilvE	1.175	1.34E-01
MSMEG_4277	cobalamin 5'-phosphate synthase	cobS	0.962	8.36E-01
MSMEG_4278	glycine cleavage system T protein	gcvT	0.939	1.17E-01
MSMEG_4279	adenylate and Guanylate cyclase catalytic domain protein	NA	1.026	4.72E-01
MSMEG_4280	short chain dehydrogenase	NA	0.970	9.01E-01
MSMEG_4281	cytosol aminopeptidase	NA	0.982	8.75E-01
MSMEG_4282	conserved hypothetical protein	NA	1.005	9.10E-01
MSMEG_4283	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase	sucB	0.999	9.90E-01
MSMEG_4284	conserved hypothetical protein	NA	1.197	6.42E-02
MSMEG_4285	lipoyltransferase	lipB	0.936	5.52E-01
MSMEG_4286	lipoic acid synthetase	lipA	0.854	1.09E-02
MSMEG_4287	integral membrane protein	NA	0.949	3.90E-01
MSMEG_4288	integral membrane protein	NA	0.880	3.89E-02
MSMEG_4289	amidohydrolase	NA	1.263	3.61E-01
MSMEG_4290	glutamine synthetase, type I	glnA	1.055	2.20E-01
MSMEG_4291	D-tyrosyl-tRNA(Tyr) deacylase	dtd	1.388	1.62E-02
MSMEG_4292	integral membrane protein	NA	1.086	3.24E-01

MSMEG_4293	glutamate-ammonia-ligase adenylyltransferase	NA	1.232	1.33E-02
MSMEG_4294	glutamine synthetase, type I	glnA	1.132	2.12E-02
MSMEG_4295	hydrolase, alpha/beta fold family protein	NA	0.969	5.97E-01
MSMEG_4296	protease	NA	0.996	9.40E-01
MSMEG_4297	acyltransferase, ws/dgat/mgat subfamily protein	NA	0.944	4.93E-01
MSMEG_4298	3-methyl-2-oxobutanoate hydroxymethyltransferase	panB	0.990	9.27E-01
MSMEG_4299	enoyl-CoA hydratase/isomerase	NA	1.028	7.99E-01
MSMEG_4300	transcription regulator AmtR	NA	1.730	2.56E-02
MSMEG_4301	acyl-CoA synthase	NA	1.222	1.99E-01
MSMEG_4302	adenylate cyclase, putative	NA	1.216	8.15E-02
MSMEG_4303	methyltransferase	NA	1.936	3.01E-02
MSMEG_4304	regulatory protein	NA	1.044	6.15E-01
MSMEG_4305	phosphoglycerate mutase	NA	0.939	3.37E-01
MSMEG_4306	conserved hypothetical protein	NA	0.928	8.59E-02
MSMEG_4307	conserved hypothetical protein	NA	1.012	8.96E-01
MSMEG_4308	5'-nucleotidase	NA	1.388	4.39E-02
MSMEG_4309	Low molecular weight protein-tyrosine-phosphatase	NA	1.321	7.68E-02
MSMEG_4310	cobalamin biosynthesis protein CobD	cobD	1.134	2.55E-01
MSMEG_4311	conserved hypothetical protein	NA	1.173	1.13E-01
MSMEG_4312	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.765	4.27E-02
MSMEG_4313	glyoxalase/bleomycin resistance protein/dioxygenase	NA	0.840	1.68E-01
MSMEG_4314	hypothetical protein	NA	1.010	8.04E-01
MSMEG_4315	RNA polymerase sigma factor, sigma-70 family protein	NA	0.803	2.66E-01
MSMEG_4316	methylated-DNA--protein-cysteine methyltransferase	NA	1.327	5.94E-01
MSMEG_4317	conserved hypothetical protein	NA	0.918	4.13E-01
MSMEG_4318	hypothetical protein	NA	1.178	6.87E-01
MSMEG_4320	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	NA	1.246	7.99E-02
MSMEG_4321	conserved hypothetical protein	NA	0.880	2.08E-02
MSMEG_4322	conserved hypothetical protein	NA	1.053	2.03E-01
MSMEG_4323	pyruvate dehydrogenase E1 component	NA	0.904	1.11E-01
MSMEG_4324	conserved hypothetical protein	NA	1.114	4.82E-01

MSMEG_4325	malonyl CoA-acyl carrier protein transacylase	NA	0.744	6.48E-03
MSMEG_4326	acyl carrier protein	acpP	0.919	3.02E-01
MSMEG_4327	3-oxoacyl-[acyl-carrier-protein] synthase 1	NA	0.801	7.78E-02
MSMEG_4328	3-oxoacyl-[acyl-carrier-protein] synthase 2	NA	0.830	4.54E-02
MSMEG_4329	propionyl-CoA carboxylase beta chain	NA	0.631	3.63E-03
MSMEG_4330	short chain dehydrogenase	NA	1.103	2.48E-01
MSMEG_4331	putative transcriptional regulator	NA	1.113	5.58E-01
MSMEG_4332	glycerol-3-phosphate dehydrogenase 1	NA	0.930	6.30E-01
MSMEG_4333	transcriptional regulator, TetR family protein	NA	1.295	3.21E-02
MSMEG_4334	flavoprotein	NA	1.385	2.41E-01
MSMEG_4335	conserved hypothetical protein	NA	1.050	6.62E-01
MSMEG_4336	conserved hypothetical protein	NA	1.052	7.62E-01
MSMEG_4337	beta-lactamase	NA	1.034	6.77E-01
MSMEG_4338	possible transcriptional regulatory protein	NA	1.037	6.53E-01
MSMEG_4339	tetratricopeptide repeat family protein	NA	1.011	7.58E-01
MSMEG_4340	NAD/mycothiol-dependent formaldehyde dehydrogenase	NA	0.830	6.20E-02
MSMEG_4341	hypothetical protein	NA	1.489	4.52E-01
MSMEG_4342	metallo-beta-lactamase family protein	NA	0.839	6.69E-02
MSMEG_4343	hypothetical protein	NA	1.254	1.71E-01
MSMEG_4344	putative monooxygenase	NA	1.046	7.86E-01
MSMEG_4345	conserved hypothetical protein	NA	1.438	3.62E-01
MSMEG_4346	conserved hypothetical protein	NA	1.056	3.04E-01
MSMEG_4347	conserved hypothetical protein	NA	1.114	2.33E-02
MSMEG_4348	acetolactate synthase large subunit	NA	0.773	1.42E-01
MSMEG_4349	conserved hypothetical proline rich protein	NA	0.910	3.41E-01
MSMEG_4350	dihydrodipicolinate reductase	dapB	1.201	4.51E-01
MSMEG_4351	hypothetical oxidoreductase YjgI	NA	2.049	1.91E-03
MSMEG_4352	putative secreted protein	NA	0.933	3.51E-01
MSMEG_4353	conserved hypothetical protein	NA	0.884	3.90E-02
MSMEG_4354	dipeptide-binding protein of ABC transport system	NA	0.681	5.76E-03
MSMEG_4355	peptide ABC transporter, permease protein	NA	1.086	1.85E-01

MSMEG_4356	inner membrane ABC transporter permease protein YddQ	NA	0.860	1.74E-01
MSMEG_4357	ABC transporter, ATP-binding protein	NA	0.960	8.06E-01
MSMEG_4358	D-beta-hydroxybutyrate dehydrogenase	NA	1.103	7.34E-02
MSMEG_4359	hypothetical protein	NA	2.026	3.25E-01
MSMEG_4360	conserved hypothetical protein	NA	1.010	9.44E-01
MSMEG_4361	conserved hypothetical protein	NA	1.009	8.82E-01
MSMEG_4362	universal stress protein family protein	NA	1.094	1.11E-01
MSMEG_4363	conserved hypothetical protein	NA	1.007	9.31E-01
MSMEG_4364	hypothetical protein	NA	1.218	1.70E-01
MSMEG_4365	conserved hypothetical protein	NA	1.114	5.56E-02
MSMEG_4366	serine/threonine-protein kinase PknD	NA	1.483	2.28E-01
MSMEG_4367	formamidase	NA	0.950	5.76E-01
MSMEG_4368	putative regulatory protein, FmdB family protein	NA	0.738	3.46E-03
MSMEG_4369	hypothetical protein	NA	1.032	7.55E-01
MSMEG_4370	regulatory protein	NA	1.258	1.64E-01
MSMEG_4371	vanillate O-demethylase oxidoreductase	NA	1.005	8.89E-01
MSMEG_4372	capreomycidine hydroxylase	NA	1.259	2.94E-01
MSMEG_4373	polysaccharide deacetylase, putative	NA	2.452	3.61E-01
MSMEG_4374	agmatinase	speB	1.299	6.96E-02
MSMEG_4375	3-oxoacyl-[acyl carrier protein] reductase	NA	1.633	2.29E-01
MSMEG_4376	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.036	2.71E-01
MSMEG_4377	amino acid permease family protein, putative	NA	1.225	1.12E-01
MSMEG_4378	two-component system response regulator	NA	1.144	5.72E-01
MSMEG_4379	isochorismatase hydrolase	NA	0.912	5.35E-02
MSMEG_4380	ABC transporter, permease/ATP-binding protein	NA	1.631	3.84E-01
MSMEG_4381	amidase	NA	0.771	1.30E-01
MSMEG_4382	dehydrogenase/reductase SDR family protein member 10	NA	0.976	9.23E-01
MSMEG_4383	MmpL5 protein	NA	1.083	4.45E-01
MSMEG_4384	Penicillin binding protein transpeptidase domain protein	NA	1.302	1.61E-01
MSMEG_4385	ABC transporter oligopeptide binding protein	NA	1.330	4.80E-01
MSMEG_4386	ABC transporter permease protein	NA	1.047	5.21E-01

MSMEG_4387	ABC transporter permease protein	NA	1.004	9.70E-01
MSMEG_4388	ABC transporter ATP-binding protein	NA	0.872	2.49E-01
MSMEG_4389	monooxygenase, NtaA/SnaA/SoxA family protein	NA	1.129	5.19E-01
MSMEG_4390	hypothetical protein	NA	0.965	6.93E-01
MSMEG_4391	acyl-CoA dehydrogenase-family protein	NA	1.203	4.11E-01
MSMEG_4392	organophopsphate acid anhydrase	NA	1.424	4.00E-02
MSMEG_4393	carboxyvinyl-carboxyphosphonate phosphorylmutase	NA	1.116	5.17E-01
MSMEG_4394	LysR family protein transcriptional regulatory protein	NA	0.897	1.43E-01
MSMEG_4395	excalibur domain family protein	NA	1.073	5.13E-01
MSMEG_4396	isochorismatase hydrolase	NA	0.626	1.97E-03
MSMEG_4397	transcriptional regulator, MerR family protein	NA	1.053	3.73E-01
MSMEG_4398	conserved hypothetical protein	NA	1.215	2.41E-01
MSMEG_4399	conserved hypothetical protein	NA	0.883	2.84E-02
MSMEG_4400	alcohol dehydrogenase, zinc-containing	NA	1.171	2.13E-01
MSMEG_4401	phosphonoacetaldehyde hydrolase	NA	1.181	2.84E-01
MSMEG_4404	hypothetical protein	NA	1.002	9.81E-01
MSMEG_4405	putative ECF sigma factor RpoE1	NA	1.182	5.20E-01
MSMEG_4406	UsfY protein	NA	1.055	7.28E-01
MSMEG_4407	conserved hypothetical protein	NA	0.910	6.64E-01
MSMEG_4408	integral membrane protein	NA	1.050	7.36E-01
MSMEG_4409	hypothetical protein	NA	1.283	3.10E-01
MSMEG_4410	hypothetical protein	NA	1.173	6.46E-01
MSMEG_4411	oxidoreductase FAD-binding region	NA	1.185	7.26E-02
MSMEG_4412	oxidoreductase, molybdopterin binding	NA	2.279	2.99E-01
MSMEG_4413	hypothetical protein	NA	1.074	5.03E-01
MSMEG_4414	conserved hypothetical protein	NA	0.975	8.12E-01
MSMEG_4415	transaldolase	tal	1.066	6.23E-01
MSMEG_4416	hypothetical protein	NA	1.111	3.25E-01
MSMEG_4417	methionine-S-sulfoxide reductase	msrA	1.001	9.96E-01
MSMEG_4418	methionine-R-sulfoxide reductase	msrB	0.944	6.31E-01
MSMEG_4419	glucose-1-dehydrogenase	NA	1.058	7.10E-01

MSMEG_4420	cupin 2, conserved barrel	NA	1.148	3.04E-01
MSMEG_4421	conserved hypothetical protein	NA	1.218	3.04E-01
MSMEG_4422	oxidoreductase	NA	1.062	7.91E-01
MSMEG_4423	oxidoreductase	NA	1.107	7.91E-01
MSMEG_4424	endoribonuclease L-PSP	NA	1.655	2.18E-01
MSMEG_4425	putative oxidoreductase	NA	1.053	7.27E-01
MSMEG_4426	secreted protein	NA	0.972	9.08E-01
MSMEG_4427	transmembrane efflux pump	NA	1.157	5.06E-01
MSMEG_4428	conserved hypothetical protein	NA	1.190	4.13E-01
MSMEG_4429	hypothetical protein	NA	0.971	4.81E-01
MSMEG_4430	transcriptional regulator	NA	0.919	2.74E-01
MSMEG_4431	putative regulatory protein	NA	1.093	7.11E-01
MSMEG_4432	hypothetical protein	NA	1.165	3.78E-01
MSMEG_4433	dehydrogenase	NA	0.993	9.22E-01
MSMEG_4434	Cof protein	NA	1.064	6.45E-01
MSMEG_4435	dimethylmenaquinone methyltransferase	NA	1.511	1.56E-01
MSMEG_4436	transketolase	NA	1.490	3.58E-01
MSMEG_4437	cytochrome c oxidase, subunit I	ctaD	2.588	4.36E-01
MSMEG_4438	hypothetical protein	NA	0.948	8.27E-01
MSMEG_4439	acetyltransferase	NA	1.202	3.16E-02
MSMEG_4440	glucose-1-dehydrogenase	NA	1.014	9.37E-01
MSMEG_4441	cupin domain protein	NA	1.042	5.73E-01
MSMEG_4442	zinc-binding oxidoreductase	NA	1.342	5.59E-01
MSMEG_4443	hypothetical protein	NA	1.014	8.71E-01
MSMEG_4444	hypothetical protein	NA	1.134	5.68E-01
MSMEG_4445	hypothetical protein	NA	1.252	2.41E-01
MSMEG_4446	dihydrolipoamide dehydrogenase; this gene contains a premature stop which is not th	lpdA	1.011	8.68E-01
MSMEG_4447	conserved hypothetical protein	NA	0.948	7.38E-01
MSMEG_4448	transcriptional modulator of MazE	NA	0.953	4.88E-01
MSMEG_4449	putative transcriptional regulator	NA	1.001	9.83E-01
MSMEG_4450	alpha/beta hydrolase	NA	1.227	2.93E-01

MSMEG_4451	probable monooxygenase	NA	0.856	3.49E-01
MSMEG_4453	conserved hypothetical protein	NA	1.239	1.15E-01
MSMEG_4454	L-threonine aldolase, low-specificity	ltaE	1.279	1.47E-01
MSMEG_4455	beta-lactamase	NA	0.841	1.77E-01
MSMEG_4456	conserved hypothetical protein	NA	0.834	6.53E-03
MSMEG_4457	regulatory protein, AsnC/Lrp	NA	1.370	5.10E-01
MSMEG_4458	transmembrane transport protein	NA	1.252	2.71E-01
MSMEG_4459	agmatinase	speB	1.042	7.57E-01
MSMEG_4460	acetolactate synthase	NA	0.919	3.13E-01
MSMEG_4460	acetolactate synthase	NA	1.130	3.03E-01
MSMEG_4461	conserved hypothetical integral membrane protein	NA	1.170	3.89E-01
MSMEG_4462	sodium:solute symporter	NA	1.441	1.73E-01
MSMEG_4463	CalR5 protein	NA	1.146	6.72E-01
MSMEG_4464	modulator of DNA gyrase	NA	1.051	8.31E-01
MSMEG_4465	cutinase	NA	2.061	1.18E-02
MSMEG_4466	ABC transporter, permease protein UspA	NA	1.165	6.80E-01
MSMEG_4467	ABC transporter, permease protein UspE	NA	0.975	6.45E-01
MSMEG_4468	Bacterial extracellular solute-binding protein UspC	NA	1.065	6.75E-01
MSMEG_4469	cobalt transport protein	NA	1.239	9.56E-02
MSMEG_4470	ABC transporter	NA	1.244	5.01E-02
MSMEG_4471	MarR-family protein transcriptional regulator	NA	1.012	7.50E-01
MSMEG_4472	multidrug-efflux transporter protein	NA	1.096	1.97E-01
MSMEG_4473	Integral membrane protein	NA	1.151	8.71E-02
MSMEG_4474	acyl-CoA oxidase	NA	0.992	8.75E-01
MSMEG_4475	LppP protein	NA	1.008	8.72E-01
MSMEG_4476	hypothetical protein	NA	0.805	5.70E-02
MSMEG_4477	hydrolase, alpha/beta hydrolase fold family protein	NA	1.503	1.73E-02
MSMEG_4479	conserved hypothetical protein	NA	1.260	2.22E-02
MSMEG_4480	conserved hypothetical protein	NA	0.976	5.69E-01
MSMEG_4481	hypothetical protein	NA	1.405	1.26E-04
MSMEG_4482	DNA primase	NA	0.984	8.32E-01

MSMEG_4483	deoxyguanosinetriphosphate triphosphohydrolase	NA	1.096	2.25E-01
MSMEG_4484	putative conserved transmembrane protein	NA	1.660	4.88E-01
MSMEG_4485	glycyl-tRNA synthetase	glyS	0.997	9.44E-01
MSMEG_4486	transcriptional regulator, ArsR family protein	NA	0.975	6.14E-01
MSMEG_4487	ferric uptake regulation protein	NA	1.039	5.76E-01
MSMEG_4488	hydrolase, nudix family protein	NA	1.007	9.48E-01
MSMEG_4489	conserved hypothetical protein	NA	1.043	3.66E-01
MSMEG_4490	undecaprenyl diphosphate synthase	uppS	0.947	5.77E-02
MSMEG_4491	DNA repair protein RecO	recO	0.968	4.72E-01
MSMEG_4492	amidase	NA	1.000	9.94E-01
MSMEG_4493	GTP-binding protein Era	era	1.360	4.76E-02
MSMEG_4494	conserved hypothetical protein	NA	1.102	3.89E-01
MSMEG_4495	CBS domain protein	NA	1.081	4.51E-01
MSMEG_4496	conserved hypothetical protein	NA	1.020	7.59E-01
MSMEG_4497	PhoH family protein	NA	1.026	5.15E-01
MSMEG_4498	hypothetical protein	NA	1.487	2.31E-01
MSMEG_4499	hypothetical protein	NA	2.582	8.64E-03
MSMEG_4500	hypothetical protein	NA	1.222	5.82E-01
MSMEG_4501	sodium:dicarboxylate symporter	NA	1.144	3.16E-01
MSMEG_4502	conserved hypothetical protein	NA	1.185	1.32E-01
MSMEG_4503	hypothetical protein	NA	1.310	4.71E-01
MSMEG_4504	chaperone protein DnaJ	dnaJ	1.067	4.96E-01
MSMEG_4505	heat-inducible transcription repressor HrcA	hrcA	1.111	5.52E-02
MSMEG_4506	hypothetical protein	NA	1.085	6.37E-01
MSMEG_4507	conserved hypothetical protein	NA	1.025	7.48E-01
MSMEG_4508	conserved domain protein	NA	1.040	3.40E-01
MSMEG_4509	MbtG protein	NA	1.354	2.83E-01
MSMEG_4510	peptide synthetase mbtf	NA	1.114	3.39E-01
MSMEG_4511	linear gramicidin synthetase subunit B	NA	1.166	4.79E-01
MSMEG_4512	polyketide synthetase mbtd	NA	0.872	2.28E-01
MSMEG_4513	polyketide synthase	NA	1.131	6.93E-01

MSMEG_4514	Thioesterase domain protein	NA	1.053	3.11E-01
MSMEG_4515	putative non-ribosomal peptide synthetase	NA	1.919	3.32E-01
MSMEG_4516	2,3-dihydroxybenzoate-AMP ligase	NA	1.215	2.45E-01
MSMEG_4517	TetR-type transcriptional regulator of sulfur metabolism	NA	1.071	7.00E-01
MSMEG_4518	conserved hypothetical protein	NA	0.978	9.37E-01
MSMEG_4519	NrtC protein	NA	1.029	8.88E-01
MSMEG_4520	sulfate/thiosulfate import ATP-binding protein CysA	NA	1.294	1.62E-01
MSMEG_4521	Tat (twin-arginine translocation) pathway signal sequence	NA	0.951	1.01E-01
MSMEG_4522	ISMsm2, transposase	NA	0.957	2.50E-01
MSMEG_4522	ISMsm2, transposase	NA	1.018	6.00E-01
MSMEG_4523	binding-protein-dependent transport systems inner membrane component	NA	1.060	4.53E-01
MSMEG_4524	anthranilate synthase component I	NA	1.410	5.35E-01
MSMEG_4525	putative oxygen-independent coproporphyrinogen III oxidase	NA	1.379	2.79E-02
MSMEG_4526	hypothetical protein	NA	1.149	3.69E-01
MSMEG_4527	ferredoxin sulfite reductase	NA	1.473	8.93E-02
MSMEG_4528	phosphoadenosine phosphosulfate reductase	NA	1.490	5.03E-02
MSMEG_4529	secreted protein	NA	1.482	5.84E-02
MSMEG_4530	sulfate ABC transporter, ATP-binding protein	cysA	1.154	5.16E-01
MSMEG_4531	sulfate ABC transporter, permease protein CysW	cysW	0.997	9.67E-01
MSMEG_4532	sulfate ABC transporter, permease protein CysT	cysT	0.961	7.77E-01
MSMEG_4533	sulfate-binding protein	NA	0.918	2.28E-01
MSMEG_4534	putative conserved membrane protein	NA	1.059	4.15E-01
MSMEG_4535	glycoside hydrolase	NA	1.324	1.71E-02
MSMEG_4536	conserved hypothetical protein	NA	1.278	5.99E-03
MSMEG_4537	major membrane protein I	NA	0.796	3.34E-02
MSMEG_4538	cysteine desulphurase, SufS	NA	1.037	7.80E-01
MSMEG_4539	alkanesulfonate monooxygenase	NA	1.465	1.43E-01
MSMEG_4540	acetyltransferase, gnat family protein	NA	1.417	1.14E-02
MSMEG_4541	ABC transporter, ATP-binding protein	NA	1.109	3.66E-01
MSMEG_4542	oligopeptide transport integral membrane protein	NA	0.956	7.47E-01
MSMEG_4543	ABC transporter system integral membrane protein	NA	1.234	3.67E-01

MSMEG_4544	methyltransferase small domain superfamily protein	NA	1.300	6.76E-02
MSMEG_4545	bacterial extracellular solute-binding protein, family protein 5	NA	0.949	7.26E-01
MSMEG_4546	oxidoreductase; this gene contains a frame shift which is not the result of sequencing	NA	1.610	5.19E-02
MSMEG_4547	acyl-CoA dehydrogenase family protein	NA	1.185	4.64E-01
MSMEG_4548	acetyltransferase, gnat family protein	NA	0.969	7.86E-01
MSMEG_4549	amino acid permease-associated region, putative	NA	0.958	7.35E-01
MSMEG_4551	monoxygenase	NA	1.047	8.57E-01
MSMEG_4552	nitrilotriacetate monooxygenase component A	ssuD	1.694	2.12E-01
MSMEG_4553	GAF domain, putative	NA	0.942	2.00E-01
MSMEG_4554	probable serine/threonine-protein kinase PknH, putative	NA	1.686	6.64E-02
MSMEG_4555	LppR protein	NA	1.171	2.57E-01
MSMEG_4556	GTP-binding protein LepA	lepA	1.114	2.09E-02
MSMEG_4557	ABC transporter, ATP-binding protein	NA	0.835	1.76E-01
MSMEG_4558	conserved hypothetical protein	NA	1.123	2.53E-01
MSMEG_4559	ABC transporter, membrane spanning protein	NA	0.906	5.52E-01
MSMEG_4560	periplasmic binding protein	NA	1.006	9.68E-01
MSMEG_4561	ABC Fe3+-siderophores transporter, periplasmic binding protein	NA	0.984	9.15E-01
MSMEG_4562	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.284	1.62E-01
MSMEG_4563	puromycin N-acetyltransferase	NA	0.893	1.86E-02
MSMEG_4564	CBS domain protein	NA	1.014	8.23E-01
MSMEG_4565	oxidoreductase	NA	1.162	6.60E-01
MSMEG_4566	conserved 13e12 repeat family protein; this gene contains a frame shift which is not th	NA	0.769	1.08E-01
MSMEG_4566	conserved 13e12 repeat family protein; this gene contains a frame shift which is not th	NA	1.117	1.23E-01
MSMEG_4567	conserved hypothetical protein	NA	1.049	3.14E-01
MSMEG_4568	ribonuclease Z	NA	1.189	5.92E-01
MSMEG_4569	conserved hypothetical protein	NA	1.151	1.00E-01
MSMEG_4570	conserved hypothetical protein	NA	1.091	5.46E-01
MSMEG_4571	ribosomal protein S20	rpsT	1.011	9.21E-01
MSMEG_4572	DNA polymerase III, delta subunit	NA	3.983	1.93E-01
MSMEG_4573	competence protein	NA	1.311	3.03E-01
MSMEG_4574	DNA-binding protein	NA	1.253	3.92E-01

MSMEG_4575	hypothetical protein	NA	0.969	7.80E-01
MSMEG_4576	SpfH domain protein	NA	0.991	9.11E-01
MSMEG_4577	DegV family protein	NA	0.963	7.49E-01
MSMEG_4578	conserved hypothetical protein	NA	1.056	6.61E-01
MSMEG_4579	phosphoglycerate mutase family protein	NA	0.977	3.00E-01
MSMEG_4580	conserved domain protein	NA	0.913	1.98E-03
MSMEG_4581	nicotinate (nicotinamide) nucleotide adenylyltransferase	nadD	0.929	1.06E-01
MSMEG_4582	conserved hypothetical protein	NA	0.642	9.63E-02
MSMEG_4582	conserved hypothetical protein	NA	1.097	2.20E-01
MSMEG_4583	ATPase associated with various cellular activities	NA	0.854	1.86E-02
MSMEG_4584	gamma-glutamyl phosphate reductase	proA	0.939	5.81E-01
MSMEG_4585	ribokinase	rbsK	1.148	2.45E-01
MSMEG_4586	ABC nitrate/sulfonate/bicarbonate family protein transporter, periplasmic ligand bindi	NA	0.781	9.22E-02
MSMEG_4587	putative aliphatic sulfonates transport ATP-binding protein SsuB	NA	1.090	5.41E-01
MSMEG_4588	ABC nitrate/sulfonate/bicarbonate family protein transporter, inner membrane subun	NA	0.894	4.95E-01
MSMEG_4589	rhodanese domain protein/cystathionine beta-lyase	NA	0.893	5.50E-01
MSMEG_4590	nitrilotriacetate monooxygenase component A	ssuD	0.914	6.69E-01
MSMEG_4591	hypothetical protein	NA	1.205	1.68E-01
MSMEG_4592	acyl-CoA dehydrogenase family protein	NA	1.241	1.43E-01
MSMEG_4593	acyl-CoA dehydrogenase	NA	0.951	6.18E-01
MSMEG_4594	hypothetical protein	NA	1.085	3.31E-02
MSMEG_4595	probable serine/threonine-protein kinase PknH, putative	NA	0.784	2.60E-03
MSMEG_4596	hypothetical protein	NA	0.678	2.01E-02
MSMEG_4597	putative conserved lipoprotein lpph	lppH	0.977	6.72E-01
MSMEG_4598	putative conserved lipoprotein lpph	lppH	0.935	3.79E-02
MSMEG_4599	hypothetical protein	NA	0.980	7.90E-01
MSMEG_4600	hypothetical protein	NA	0.863	1.10E-01
MSMEG_4601	transcriptional regulator, AraC family protein	NA	1.100	4.57E-02
MSMEG_4602	hypothetical protein	NA	0.732	2.24E-02
MSMEG_4603	integral membrane protein; this gene contains a frame shift which is not the result of	NA	1.488	1.35E-01
MSMEG_4604	hypothetical protein	NA	1.077	3.66E-01

MSMEG_4605	ankyrin; this gene contains a premature stop which is not the result of sequencing erro	NA	0.938	6.34E-01
MSMEG_4605	ankyrin; this gene contains a premature stop which is not the result of sequencing erro	NA	0.964	8.01E-01
MSMEG_4606	hypothetical protein	NA	0.954	5.38E-01
MSMEG_4606	hypothetical protein	NA	1.536	3.14E-01
MSMEG_4607	hypothetical protein	NA	0.925	7.56E-01
MSMEG_4609	transcriptional regulator LysR family protein	NA	1.383	4.08E-02
MSMEG_4610	IgiC, putative	NA	1.227	2.55E-01
MSMEG_4611	carrier protein	NA	1.076	3.27E-01
MSMEG_4612	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	0.851	1.09E-01
MSMEG_4612	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	0.993	9.51E-01
MSMEG_4613	hypothetical protein	NA	0.940	4.89E-01
MSMEG_4614	GAF family protein	NA	1.002	9.83E-01
MSMEG_4615	replicative DNA helicase; this region contains one or more premature stops and/or fra	NA	1.051	8.97E-02
MSMEG_4615	replicative DNA helicase; this region contains one or more premature stops and/or fra	NA	1.209	2.81E-02
MSMEG_4616	acyl-CoA dehydrogenase family protein; this gene contains a frame shift which is not t	NA	1.124	2.32E-01
MSMEG_4617	glutamine-dependent NAD+ synthetase	nadE	1.254	1.30E-01
MSMEG_4618	isochorismatase family protein	NA	1.220	5.54E-01
MSMEG_4619	putative cytochrome P450 126	NA	1.049	5.95E-01
MSMEG_4620	NAD-dependent deacetylase 1	NA	1.008	9.07E-01
MSMEG_4621	glutamate 5-kinase	proB	1.549	3.54E-02
MSMEG_4622	transcriptional regulator, TetR family protein	NA	0.993	9.65E-01
MSMEG_4623	GTP-binding protein Obg/CgtA	NA	1.471	7.86E-02
MSMEG_4624	ribosomal protein L27	rpmA	1.133	7.67E-02
MSMEG_4625	ribosomal protein L21	rplU	1.149	4.40E-01
MSMEG_4626	ribonuclease, Rne/Rng family protein	NA	0.937	2.58E-01
MSMEG_4627	nucleoside diphosphate kinase	NA	0.904	1.87E-01
MSMEG_4628	conserved hypothetical protein	NA	1.138	1.18E-01
MSMEG_4629	FolC bifunctional protein; this gene contains a frame shift which is not the result of sec	folC	1.062	1.50E-01
MSMEG_4630	valyl-tRNA synthetase	valS	1.299	2.35E-02
MSMEG_4631	conserved hypothetical protein	NA	0.899	2.55E-01
MSMEG_4632	saccharopine dehydrogenase	NA	1.145	2.57E-02

MSMEG_4633	peptidase S9, prolyl oligopeptidase	NA	1.173	1.54E-01
MSMEG_4634	hypothetical protein	NA	1.109	4.58E-01
MSMEG_4635	ammonium transporter family protein	NA	1.036	8.83E-01
MSMEG_4636	hypothetical protein	NA	1.064	6.78E-01
MSMEG_4637	conserved hypothetical protein	NA	1.074	3.85E-01
MSMEG_4638	vanillate O-demethylase oxidoreductase	NA	1.520	3.92E-01
MSMEG_4639	conserved hypothetical protein	NA	1.119	7.19E-01
MSMEG_4640	secreted protein	NA	1.347	1.51E-01
MSMEG_4641	salicylate hydroxylase	NA	1.111	3.03E-01
MSMEG_4642	hypothetical protein	NA	1.044	6.14E-01
MSMEG_4643	resuscitation-promoting factor	NA	2.468	5.53E-02
MSMEG_4644	molybdopterin-guanine dinucleotide biosynthesis protein A	NA	1.167	2.04E-01
MSMEG_4645	alpha oxoglutarate ferredoxin oxidoreductase, beta subunit	orB	1.077	4.03E-01
MSMEG_4646	pyruvate synthase	NA	1.172	7.58E-03
MSMEG_4647	carbohydrate kinase, PfkB, putative	NA	1.236	8.95E-03
MSMEG_4648	DNA-binding protein	NA	1.050	7.93E-01
MSMEG_4649	phytanoyl-CoA dioxygenase	NA	1.109	7.24E-01
MSMEG_4650	hypothetical oxidoreductase YisS	NA	0.897	6.02E-01
MSMEG_4651	AP endonuclease, family protein 2	NA	0.862	1.65E-01
MSMEG_4652	D-oliose 4-ketoreductase	NA	0.936	5.25E-04
MSMEG_4653	AP endonuclease, family protein 2 superfamily protein	NA	1.045	5.37E-01
MSMEG_4654	aldo/keto reductase	NA	1.025	8.16E-01
MSMEG_4655	transcriptional regulator, AraC family protein	NA	1.190	1.89E-01
MSMEG_4656	sugar ABC transporter ATP-binding protein	NA	0.728	9.08E-03
MSMEG_4657	ABC transporter membrane protein	NA	0.706	1.60E-02
MSMEG_4658	sugar ABC transporter substrate-binding protein	NA	0.672	4.33E-04
MSMEG_4659	GntR-family protein transcriptional regulator	NA	1.027	6.78E-01
MSMEG_4660	hypothetical protein	NA	0.874	3.38E-01
MSMEG_4661	sugar kinase, ribokinase family protein	NA	0.682	1.02E-02
MSMEG_4662	deoxyribose-phosphate aldolase superfamily protein	NA	0.787	1.67E-01
MSMEG_4663	protein IolB	NA	0.562	1.88E-03

MSMEG_4664	IolD protein	NA	0.655	4.17E-02
MSMEG_4665	IolE protein	NA	0.767	4.81E-03
MSMEG_4666	myo-inositol 2-dehydrogenase	NA	0.947	8.33E-01
MSMEG_4667	transcriptional regulator, LysR family protein	NA	0.995	9.34E-01
MSMEG_4668	oxidoreductase alpha (molybdopterin) subunit	NA	1.043	5.54E-01
MSMEG_4669	formate dehydrogenase family protein accessory protein FdhD	fdhD	1.019	9.23E-01
MSMEG_4670	N-glycosylation	NA	0.610	6.76E-02
MSMEG_4671	ATP-dependent Clp protease, ATP-binding subunit ClpX	clpX	1.042	3.77E-01
MSMEG_4672	Clp protease	clpP	1.059	4.35E-01
MSMEG_4673	Clp protease	clpP	0.956	5.60E-02
MSMEG_4674	trigger factor	tig	1.025	1.75E-01
MSMEG_4677	hypothetical protein	NA	1.360	2.10E-01
MSMEG_4678	hypothetical protein	NA	0.782	3.52E-03
MSMEG_4679	hypothetical protein	NA	1.008	8.33E-01
MSMEG_4680	carboxylesterase, putative	lipP	1.153	2.93E-01
MSMEG_4681	conserved hypothetical protein	NA	1.266	6.15E-03
MSMEG_4682	Na+/H+ antiporter	NA	1.066	4.02E-01
MSMEG_4683	putative formamidopyrimidine-DNA glycosylase	NA	0.920	3.89E-01
MSMEG_4684	ribose 5-phosphate isomerase	NA	0.820	4.82E-03
MSMEG_4685	oxidoreductase	NA	0.979	8.15E-01
MSMEG_4686	putative oxidoreductase YdbC	NA	1.098	2.94E-01
MSMEG_4687	cytosine deaminase	NA	1.071	1.35E-01
MSMEG_4688	conserved hypothetical protein, putative	NA	1.101	2.81E-01
MSMEG_4689	conserved hypothetical protein	NA	0.845	8.30E-02
MSMEG_4690	aminopeptidase N	pepN	0.991	9.52E-01
MSMEG_4691	HNH nuclease	NA	1.307	2.44E-02
MSMEG_4692	conserved hypothetical protein	NA	1.217	2.89E-01
MSMEG_4693	conserved hypothetical protein	NA	1.150	9.43E-02
MSMEG_4694	HNH endonuclease family protein	NA	1.382	6.36E-02
MSMEG_4695	protozoan/cyanobacterial globin family protein	NA	1.070	1.52E-01
MSMEG_4696	alpha-amylase family protein	NA	0.736	6.03E-03

MSMEG_4697	conserved hypothetical protein	NA	1.190	1.73E-01
MSMEG_4698	conserved hypothetical protein	NA	1.014	6.37E-01
MSMEG_4699	NAD-glutamate dehydrogenase	NA	1.026	6.73E-01
MSMEG_4700	ABC-transporter protein, ATP binding component	NA	1.152	6.02E-02
MSMEG_4701	single-strand binding protein	NA	1.700	1.11E-02
MSMEG_4702	ABC-type transporter, permease components	NA	1.414	5.07E-03
MSMEG_4703	glycerol-3-phosphate acyltransferase	NA	0.745	1.30E-01
MSMEG_4704	acyltransferase family protein	NA	1.017	8.46E-01
MSMEG_4705	acyltransferase, ws/dgat/mgat subfamily protein	NA	1.076	5.03E-01
MSMEG_4707	non-heme bromoperoxidase BPO-A2	NA	1.678	2.98E-01
MSMEG_4708	putative methyltransferase	NA	0.814	1.23E-01
MSMEG_4709	enoyl-CoA hydratase	NA	1.071	2.04E-01
MSMEG_4710	dihydrolipoamide acetyltransferase	NA	0.933	4.71E-01
MSMEG_4711	pyruvate dehydrogenase E1 component subunit beta	NA	0.985	9.34E-01
MSMEG_4712	pyruvate dehydrogenase E1 component, alpha subunit	NA	0.824	2.99E-02
MSMEG_4713	HpcH/HpaI aldolase/citrate lyase family protein	NA	0.734	1.38E-02
MSMEG_4714	MoaC domain protein	NA	0.750	1.43E-02
MSMEG_4715	acyl-CoA dehydrogenase	NA	0.764	2.48E-02
MSMEG_4716	acetyl-/propionyl-coenzyme A carboxylase alpha chain	NA	0.864	9.20E-02
MSMEG_4717	Carboxyl transferase domain protein	NA	0.924	2.97E-01
MSMEG_4718	transcriptional regulator, TetR family protein	NA	1.103	1.56E-01
MSMEG_4719	peptidase S9, prolyl oligopeptidase	NA	1.083	2.93E-01
MSMEG_4720	conserved hypothetical protein	NA	1.130	4.07E-02
MSMEG_4721	permease of the major facilitator superfamily protein	NA	1.179	1.69E-01
MSMEG_4722	short-chain dehydrogenase	NA	1.216	5.57E-02
MSMEG_4723	conserved hypothetical protein	NA	0.876	1.48E-01
MSMEG_4724	oligoribonuclease	NA	1.087	2.92E-01
MSMEG_4726	carbamoyl-phosphate synthase small chain	NA	1.078	6.99E-01
MSMEG_4727	mycocerosic acid synthase	NA	1.561	1.78E-01
MSMEG_4728	condensation domain protein	NA	0.856	2.37E-03
MSMEG_4729	conserved hypothetical protein	NA	1.168	1.90E-01

MSMEG_4730	conserved hypothetical protein	NA	0.840	1.30E-01
MSMEG_4730	conserved hypothetical protein	NA	1.044	6.31E-01
MSMEG_4731	acyl-CoA synthase	NA	1.120	3.79E-01
MSMEG_4732	glycosyl transferase, group 2 family protein, putative	NA	1.040	6.71E-01
MSMEG_4733	putative membrane protein	NA	1.057	4.77E-01
MSMEG_4734	hypothetical protein	NA	1.212	2.07E-01
MSMEG_4735	conserved hypothetical protein	NA	1.258	5.92E-02
MSMEG_4736	conserved hypothetical protein	NA	1.415	5.52E-02
MSMEG_4737	conserved hypothetical protein	NA	1.127	2.17E-02
MSMEG_4738	hypothetical protein	NA	1.652	8.44E-04
MSMEG_4739	conserved hypothetical protein	NA	1.195	1.64E-01
MSMEG_4740	Glycosyltransferase family protein 28	NA	1.118	5.14E-02
MSMEG_4741	MmpL protein	NA	1.194	5.92E-02
MSMEG_4742	clavaldehyde dehydrogenase	NA	0.800	6.71E-03
MSMEG_4743	conserved hypothetical protein	NA	1.009	9.45E-01
MSMEG_4744	conserved hypothetical protein	NA	0.951	6.78E-01
MSMEG_4745	ErfK/YbiS/YcfS/YnhG family protein	NA	1.146	6.32E-03
MSMEG_4747	hypothetical protein	NA	1.175	6.45E-01
MSMEG_4748	hypothetical protein	NA	1.045	8.64E-01
MSMEG_4749	hypothetical protein	NA	2.301	6.61E-02
MSMEG_4750	ornithine carbamoyltransferase	NA	1.728	1.71E-02
MSMEG_4751	hypothetical protein	NA	1.095	3.86E-01
MSMEG_4752	conserved hypothetical protein	NA	1.235	3.79E-01
MSMEG_4753	antioxidant, AhpC/TSA family protein	NA	0.822	9.82E-02
MSMEG_4754	K+-dependent Na+/Ca+ exchanger related-protein	NA	1.289	1.31E-01
MSMEG_4755	peptidase M20	NA	1.274	7.16E-02
MSMEG_4756	holo-(acyl-carrier-protein) synthase	acpS	1.157	2.13E-01
MSMEG_4757	fatty acid synthase	NA	1.093	5.96E-01
MSMEG_4759	hypothetical protein	NA	0.913	4.33E-01
MSMEG_4759	hypothetical protein	NA	1.029	8.38E-01
MSMEG_4760	conserved hypothetical protein; this region contains one or more premature stops anc	NA	3.092	3.89E-01

MSMEG_4761	ABC transporter ATP-binding protein	NA	1.064	2.54E-01
MSMEG_4762	ABC transporter binding protein	NA	1.027	8.83E-01
MSMEG_4763	ABC transporter permease protein	NA	1.032	8.54E-01
MSMEG_4764	ABC transporter permease protein	NA	0.906	5.30E-01
MSMEG_4765	transcriptional regulator, MerR family protein	NA	1.409	4.42E-02
MSMEG_4766	low temperature requirement protein LtrA	ltrA	1.256	1.98E-01
MSMEG_4767	major facilitator superfamily protein permease	NA	1.642	4.30E-04
MSMEG_4768	transcriptional regulator	NA	0.995	9.68E-01
MSMEG_4769	conserved hypothetical protein	NA	1.085	6.30E-01
MSMEG_4770	conserved hypothetical protein	NA	0.958	4.55E-02
MSMEG_4771	conserved hypothetical protein	NA	0.918	1.10E-02
MSMEG_4772	acyl-CoA synthase	NA	1.017	8.81E-01
MSMEG_4773	amidohydrolase family protein	NA	0.817	1.55E-01
MSMEG_4774	AMP-dependent synthetase and ligase	NA	1.122	7.16E-01
MSMEG_4775	enoyl-CoA hydratase/isomerase family protein	NA	1.356	2.58E-01
MSMEG_4776	glyoxalase/bleomycin resistance protein/dioxygenase	NA	2.098	3.79E-01
MSMEG_4777	conserved hypothetical protein	NA	1.079	1.47E-01
MSMEG_4778	putative thiolase	NA	1.634	5.27E-01
MSMEG_4779	probable regulatory protein	NA	1.010	8.81E-01
MSMEG_4780	cytochrome p450	NA	1.131	6.04E-01
MSMEG_4781	conserved hypothetical protein	NA	0.800	3.07E-01
MSMEG_4781	conserved hypothetical protein	NA	1.034	8.08E-01
MSMEG_4782	conserved hypothetical protein	NA	0.968	8.16E-01
MSMEG_4783	conserved hypothetical protein	NA	0.931	6.09E-01
MSMEG_4784	conserved hypothetical protein	NA	0.940	4.77E-01
MSMEG_4785	mce-family protein mce1f	NA	0.939	4.11E-01
MSMEG_4786	virulence factor mce family protein	NA	1.053	6.94E-01
MSMEG_4787	virulence factor mce family protein	NA	1.056	5.89E-01
MSMEG_4788	virulence factor mce family protein; this region contains one or more premature stops	NA	1.110	7.58E-03
MSMEG_4789	hypothetical protein	NA	1.382	4.83E-01
MSMEG_4791	IS1096, tnpR protein	NA	0.915	2.59E-01

MSMEG_4791	IS1096, tnpR protein	NA	1.304	3.27E-01
MSMEG_4792	virulence factor mce family protein	NA	1.396	3.58E-01
MSMEG_4793	virulence factor Mce family protein	NA	1.135	1.29E-01
MSMEG_4794	virulence factor	NA	1.177	2.19E-01
MSMEG_4795	ABC-transporter integral membrane protein	NA	0.932	4.82E-03
MSMEG_4796	conserved hypothetical protein	NA	0.923	4.48E-01
MSMEG_4797	hypothetical protein	NA	1.106	1.95E-01
MSMEG_4798	L-carnitine dehydratase/bile acid-inducible protein F	NA	1.016	7.32E-01
MSMEG_4799	aldehyde dehydrogenase (NAD) family protein	NA	1.027	7.65E-01
MSMEG_4800	3-oxoacyl-(acyl-carrier-protein) reductase, putative	NA	0.946	5.81E-01
MSMEG_4801	carveol dehydrogenase	NA	0.975	9.28E-01
MSMEG_4802	conserved domain protein	NA	0.860	3.13E-01
MSMEG_4803	cytochrome P450 superfamily protein	NA	1.307	3.08E-02
MSMEG_4804	conserved hypothetical protein	NA	1.111	3.94E-01
MSMEG_4805	acyl-CoA dehydrogenase	NA	1.513	4.45E-01
MSMEG_4806	putative acyl-CoA dehydrogenase	NA	0.968	7.45E-01
MSMEG_4807	amidohydrolase family protein	NA	7.030	3.92E-01
MSMEG_4808	amidohydrolase family protein	NA	1.063	5.29E-01
MSMEG_4809	Rieske [2Fe-2S] domain, putative	NA	1.184	3.45E-01
MSMEG_4810	conserved hypothetical protein	NA	1.049	7.17E-01
MSMEG_4811	conserved hypothetical protein	NA	1.094	4.77E-01
MSMEG_4812	respiratory-chain NADH dehydrogenase domain, 51 kda subunit	NA	0.929	6.77E-01
MSMEG_4813	conserved domain protein	NA	0.953	8.11E-01
MSMEG_4814	conserved hypothetical protein	NA	7.318	3.56E-01
MSMEG_4815	conserved hypothetical protein	NA	1.082	2.37E-01
MSMEG_4816	6-phosphogluconate dehydrogenase, NAD-binding	NA	0.866	9.69E-02
MSMEG_4817	6-phosphogluconate dehydrogenase, NAD-binding	NA	2.615	3.92E-01
MSMEG_4818	putative cytochrome P450 123	NA	1.173	5.09E-01
MSMEG_4819	conserved domain protein	NA	1.125	2.11E-01
MSMEG_4820	conserved hypothetical protein	NA	1.016	8.32E-01
MSMEG_4821	conserved hypothetical protein	NA	1.160	5.29E-01

MSMEG_4822	conserved domain protein	NA	1.071	8.29E-01
MSMEG_4823	cytochrome p450	NA	0.806	3.49E-01
MSMEG_4824	hypothetical protein	NA	1.034	7.42E-01
MSMEG_4825	transcriptional repressor, TetR family protein, putative	NA	0.798	6.26E-02
MSMEG_4826	putative acyl-CoA dehydrogenase	NA	0.888	5.24E-01
MSMEG_4827	aminoglycoside phosphotransferase	NA	0.707	4.57E-02
MSMEG_4828	alcohol dehydrogenase, zinc-binding	NA	0.992	9.16E-01
MSMEG_4829	cytochrome P450	NA	0.869	9.20E-03
MSMEG_4830	conserved hypothetical protein	NA	0.836	3.44E-01
MSMEG_4831	transcriptional regulator, TetR family protein	NA	0.749	1.98E-01
MSMEG_4832	acyl-CoA dehydrogenase	NA	0.895	2.64E-02
MSMEG_4833	putative acyl-CoA dehydrogenase	NA	0.943	6.79E-01
MSMEG_4834	L-carnitine dehydratase/bile acid-inducible protein F	NA	0.914	1.33E-01
MSMEG_4835	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.026	9.19E-01
MSMEG_4836	FadE12_1	NA	2.046	2.25E-01
MSMEG_4837	amidohydrolase 2	NA	1.784	3.84E-01
MSMEG_4838	hypothetical protein	NA	0.964	8.12E-01
MSMEG_4839	carboxymuconolactone decarboxylase	NA	1.050	5.19E-01
MSMEG_4840	Rieske [2Fe-2S] domain protein	NA	0.898	5.12E-01
MSMEG_4841	conserved hypothetical protein	NA	1.117	3.07E-01
MSMEG_4842	amidohydrolase	NA	4.794	3.89E-01
MSMEG_4843	conserved hypothetical protein	NA	1.012	9.29E-01
MSMEG_4844	acyl-CoA dehydrogenase	NA	0.840	1.65E-01
MSMEG_4845	putative acyl-CoA dehydrogenase	NA	1.050	5.36E-01
MSMEG_4846	probable enoyl-CoA hydratase	NA	0.987	5.38E-01
MSMEG_4847	transcriptional regulator, TetR family protein	NA	1.164	3.00E-02
MSMEG_4848	hypothetical protein	NA	1.395	4.79E-02
MSMEG_4849	carveol dehydrogenase	NA	1.299	1.29E-03
MSMEG_4850	short-chain dehydrogenase/reductase SDR	NA	1.059	6.46E-01
MSMEG_4851	caib/baif family protein	NA	1.119	3.00E-01
MSMEG_4852	enoyl-CoA hydratase, putative	NA	0.793	4.10E-01

MSMEG_4853	peptidase, M24 family protein	NA	0.706	1.53E-02
MSMEG_4854	peptidase, M24 family protein	NA	1.138	6.08E-01
MSMEG_4855	amidohydrolase family protein	NA	0.998	9.95E-01
MSMEG_4856	cytochrome P450	NA	1.045	7.94E-01
MSMEG_4857	conserved domain protein	NA	0.897	7.28E-01
MSMEG_4858	transcriptional regulator, TetR family protein	NA	0.975	8.22E-01
MSMEG_4859	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.039	3.84E-01
MSMEG_4860	hydrolase, alpha/beta fold family protein, putative	NA	0.999	9.95E-01
MSMEG_4861	cyclase	NA	1.014	8.94E-01
MSMEG_4862	3-alpha-hydroxysteroid dehydrogenase	NA	1.281	3.14E-01
MSMEG_4863	conserved hypothetical protein	NA	0.944	7.41E-01
MSMEG_4864	3-ketosteroid dehydrogenase	NA	3.027	3.64E-01
MSMEG_4865	metapyrocatechase 1	NA	0.960	7.14E-01
MSMEG_4866	3-(3-hydroxy-phenyl)propionate hydroxylase	NA	1.038	7.81E-01
MSMEG_4867	2-hydroxy-6-ketonona-2,4-dienedoic acid hydrolase	NA	1.023	9.11E-01
MSMEG_4868	transcriptional regulator, IclR family protein, C- domain protein	NA	1.072	5.40E-01
MSMEG_4869	LAO/AO transport system ATPase	NA	0.953	6.75E-01
MSMEG_4870	FAD binding domain, putative	NA	0.939	6.23E-01
MSMEG_4871	3-hydroxyacyl-CoA dehydrogenase type-2	NA	1.016	7.46E-01
MSMEG_4872	short chain dehydrogenase	NA	0.852	3.78E-01
MSMEG_4873	enoyl-CoA hydratase/isomerase	NA	1.318	2.11E-01
MSMEG_4874	putative acyl-CoA dehydrogenase	NA	0.905	2.42E-01
MSMEG_4875	putative acyl-CoA dehydrogenase	NA	1.377	2.49E-01
MSMEG_4876	acyl-CoA synthase	NA	0.976	8.91E-01
MSMEG_4877	CaiB/BaiF family protein	NA	1.411	1.63E-01
MSMEG_4878	2Fe-2S iron-sulfur cluster binding domain protein	NA	1.752	2.02E-01
MSMEG_4879	conserved hypothetical protein	NA	1.065	7.07E-01
MSMEG_4880	methylmalonyl-CoA mutase C-terminal domain protein	NA	2.165	1.71E-01
MSMEG_4881	methylmalonyl-CoA mutase, N-terminus of large subunit	NA	1.034	7.62E-01
MSMEG_4882	short chain dehydrogenase	NA	2.105	4.09E-01
MSMEG_4883	AMP-dependent synthetase and ligase	NA	1.099	1.41E-01

MSMEG_4884	conserved hypothetical protein	NA	1.028	7.45E-01
MSMEG_4885	conserved hypothetical protein	NA	1.039	4.40E-01
MSMEG_4886	major facilitator family protein transporter	NA	0.964	6.77E-01
MSMEG_4887	cytochrome P450	NA	0.882	2.02E-01
MSMEG_4888	periplasmic binding proteins and sugar binding domain of the LacI family protein, puta	NA	0.997	9.86E-01
MSMEG_4889	integral membrane transport protein	NA	1.381	4.91E-01
MSMEG_4890	alkylhydroperoxidase, AhpD family protein	ahpD	0.847	1.91E-01
MSMEG_4891	alkylhydroperoxide reductase	NA	1.000	9.93E-01
MSMEG_4892	conserved hypothetical protein	NA	1.170	5.63E-01
MSMEG_4893	Putative neutral zinc metallopeptidase	NA	1.136	2.86E-02
MSMEG_4894	conserved hypothetical protein	NA	0.925	2.78E-02
MSMEG_4895	hypothetical protein	NA	1.988	3.83E-01
MSMEG_4896	non-ribosomal peptide synthetase	NA	1.057	2.48E-01
MSMEG_4898	conserved hypothetical protein	NA	1.170	1.46E-01
MSMEG_4899	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family protein	rdgB	1.237	1.11E-01
MSMEG_4900	Pks14 protein	NA	1.033	4.50E-01
MSMEG_4901	ribonuclease PH	rph	1.387	4.04E-02
MSMEG_4902	metal-dependent hydrolase of the beta-lactamase superfamily protein III	NA	1.189	9.59E-02
MSMEG_4903	glutamate racemase	murI	1.043	6.63E-01
MSMEG_4904	rhomboid family protein	NA	0.946	3.59E-01
MSMEG_4905	cysteine synthase B	cysM	0.990	8.40E-01
MSMEG_4906	ThiS family protein	NA	0.847	2.33E-02
MSMEG_4907	Mov34/MPN/PAD-1 family protein	NA	0.926	1.99E-02
MSMEG_4908	endo-type 6-aminohexanoate oligomer hydrolase	NA	0.857	2.46E-02
MSMEG_4909	conserved hypothetical protein	NA	0.932	3.94E-01
MSMEG_4910	ATP-dependent Clp protease adaptor protein ClpS	NA	0.982	8.87E-01
MSMEG_4911	putative nicotinate phosphoribosyltransferase	pncB	0.841	9.29E-03
MSMEG_4912	putative helicase	NA	1.147	5.06E-01
MSMEG_4913	LpqM protein	NA	0.966	2.83E-01
MSMEG_4914	virginiamycin B hydrolase	NA	0.988	8.91E-01
MSMEG_4915	alpha-glucan phosphorylase family protein	NA	0.949	4.05E-01

MSMEG_4916	alpha-amylase family protein	NA	0.821	3.24E-01
MSMEG_4917	tetratricopeptide repeat domain protein	NA	1.200	3.37E-02
MSMEG_4918	1,4-alpha-glucan branching enzyme	glgB	0.827	1.22E-01
MSMEG_4919	conserved hypothetical protein	NA	1.180	1.25E-02
MSMEG_4920	acetyl-CoA acetyltransferase	NA	0.974	5.43E-01
MSMEG_4921	methylmalonyl-CoA epimerase	mce	0.883	9.15E-02
MSMEG_4922	conserved hypothetical protein	NA	1.035	4.69E-01
MSMEG_4923	conserved hypothetical protein	NA	1.019	8.33E-01
MSMEG_4924	adenylate cyclase, family protein 3	NA	0.991	9.17E-01
MSMEG_4925	transcriptional regulator, Ada family protein/DNA-3-methyladenine glycosylase II	NA	1.193	4.01E-02
MSMEG_4926	IS1096, tnpA protein	NA	1.043	8.63E-01
MSMEG_4926	IS1096, tnpA protein	NA	1.263	4.75E-01
MSMEG_4927	IS1096, tnpR protein	NA	0.916	5.30E-02
MSMEG_4928	methylated-DNA--protein-cysteine methyltransferase	NA	1.021	8.70E-01
MSMEG_4932	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA	1.084	1.35E-01
MSMEG_4933	conserved hypothetical protein	NA	0.898	5.10E-02
MSMEG_4934	ATP:cob(I)alamin adenosyltransferase	NA	0.962	2.84E-01
MSMEG_4935	ATP synthase F1, epsilon subunit	atpC	0.858	2.30E-02
MSMEG_4936	ATP synthase F1, beta subunit	atpD	0.875	2.15E-01
MSMEG_4937	ATP synthase F1, gamma subunit	atpG	0.793	1.60E-02
MSMEG_4938	ATP synthase F1, alpha subunit	atpA	0.756	6.08E-03
MSMEG_4939	ATP synthase delta chain	NA	0.751	1.31E-02
MSMEG_4940	bacteriophage lysis protein	NA	0.948	4.16E-02
MSMEG_4941	ATP synthase F0, C subunit	atpE	0.865	2.19E-02
MSMEG_4942	ATP synthase F0, A subunit	atpB	0.767	3.41E-04
MSMEG_4943	conserved hypothetical protein	NA	0.897	4.98E-03
MSMEG_4944	hypothetical protein	NA	0.901	1.49E-01
MSMEG_4947	glycosyl trasferase	NA	1.014	8.35E-01
MSMEG_4948	Sua5/YciO/YrdC/YwlC family protein	NA	1.167	1.04E-02
MSMEG_4949	modification methylase, HemK family protein	NA	0.968	7.62E-01
MSMEG_4950	peptide chain release factor 1	prfA	0.923	1.97E-01

MSMEG_4951	ribosomal protein L31	rpmE	1.035	8.88E-01
MSMEG_4952	acyl-CoA synthase	NA	1.197	2.46E-01
MSMEG_4953	putative transcriptional regulator	NA	1.099	2.74E-01
MSMEG_4954	transcription termination factor Rho	rho	1.272	1.47E-03
MSMEG_4955	homoserine kinase	thrB	1.132	2.96E-01
MSMEG_4956	threonine synthase	thrC	0.983	7.15E-01
MSMEG_4957	homoserine dehydrogenase	NA	1.009	9.15E-01
MSMEG_4958	diaminopimelate decarboxylase	lysA	1.197	2.44E-02
MSMEG_4959	arginyl-tRNA synthetase	argS	1.137	2.43E-01
MSMEG_4961	hypothetical protein	NA	3.030	7.90E-03
MSMEG_4962	RemO protein	NA	1.236	1.66E-01
MSMEG_4963	peptide synthetase ScpsB, putative	NA	1.032	8.16E-01
MSMEG_4964	transcriptional regulator, TetR family protein	NA	1.377	2.03E-01
MSMEG_4965	hypothetical protein	NA	1.117	3.67E-01
MSMEG_4966	CalU12 protein	NA	1.061	3.30E-01
MSMEG_4967	conserved hypothetical protein	NA	1.101	2.03E-01
MSMEG_4968	two-component system sensor kinase	NA	1.773	1.27E-02
MSMEG_4969	two-component system response regulator	NA	1.400	7.19E-02
MSMEG_4970	hypothetical protein	NA	1.300	5.19E-02
MSMEG_4971	oxidoreductase	NA	1.223	1.99E-01
MSMEG_4972	acetyltransferase	NA	1.461	4.36E-02
MSMEG_4973	glyoxalase/bleomycin resistance protein/dioxygenase	NA	0.973	5.16E-01
MSMEG_4974	rrf2 family protein (putative transcriptional regulator)	NA	1.112	1.13E-01
MSMEG_4975	flavin-nucleotide-binding protein	NA	0.928	3.20E-01
MSMEG_4976	isochorismatase hydrolase	NA	0.891	1.44E-01
MSMEG_4977	3'(2'),5'-bisphosphate nucleotidase, putative	NA	0.929	3.56E-01
MSMEG_4978	sulfate adenylytransferase, large subunit/adenylylsulfate kinase	cysNC	0.412	7.54E-05
MSMEG_4979	sulfate adenylyltransferase, small subunit	cysD	0.493	7.88E-04
MSMEG_4980	major facilitator superfamily protein MFS_1	NA	1.556	3.32E-01
MSMEG_4981	phosphotransferase enzyme family protein, putative	NA	0.935	5.70E-01
MSMEG_4982	conserved hypothetical protein	NA	1.112	3.11E-01

MSMEG_4983	transcriptional regulator, TetR family protein	NA	1.114	4.21E-01
MSMEG_4984	conserved hypothetical protein, putative	NA	1.440	2.49E-01
MSMEG_4985	carbonic anhydrase	NA	0.808	2.17E-02
MSMEG_4986	glycosyl transferase, family protein 39	NA	0.985	8.78E-01
MSMEG_4987	glycosyl transferase	NA	1.358	4.03E-01
MSMEG_4988	integral membrane protein	NA	2.238	4.11E-01
MSMEG_4989	sensor histidine kinase	NA	1.111	4.09E-01
MSMEG_4990	DNA-binding response regulator	NA	1.081	7.09E-01
MSMEG_4991	hypothetical protein	NA	0.809	8.20E-02
MSMEG_4992	hypothetical protein	NA	0.976	8.97E-01
MSMEG_4993	hypothetical protein	NA	1.057	7.82E-01
MSMEG_4994	flagella membrane glycoprotein 1B, putative	NA	1.214	6.06E-01
MSMEG_4995	oligopeptide transport system permease protein AppB	NA	1.098	4.47E-01
MSMEG_4996	ABC transporter, permease protein OppC	oppC	0.913	2.95E-01
MSMEG_4997	ABC transporter, ATP-binding protein OppD	oppD	0.809	2.34E-01
MSMEG_4998	hydrolase, alpha/beta fold family protein	NA	1.250	1.55E-01
MSMEG_4999	bacterial extracellular solute-binding protein, family protein 5	NA	0.990	8.39E-01
MSMEG_5000	transcriptional regulator, LysR family protein	NA	1.315	1.15E-01
MSMEG_5001	pesticide degrading monooxygenase	NA	1.012	7.14E-01
MSMEG_5002	conserved hypothetical protein	NA	1.116	2.77E-01
MSMEG_5003	O-methyltransferase, family protein 3	NA	1.093	3.37E-01
MSMEG_5004	DNA repair exonuclease	NA	0.980	8.49E-01
MSMEG_5005	LprC protein	NA	0.952	2.04E-01
MSMEG_5006	phosphohistidine phosphatase	NA	0.972	5.71E-01
MSMEG_5007	LprB protein	NA	0.975	6.93E-01
MSMEG_5008	ABC transporter, ATP-binding protein	NA	1.019	8.77E-01
MSMEG_5009	ABC transporter	NA	1.455	4.00E-01
MSMEG_5010	conserved hypothetical protein	NA	0.917	1.59E-01
MSMEG_5011	hypothetical protein	NA	0.291	5.88E-04
MSMEG_5012	trans-sialidase, putative	NA	0.997	9.80E-01
MSMEG_5013	conserved hypothetical protein	NA	1.060	5.41E-01

MSMEG_5014	copper-translocating P-type ATPase	NA	1.549	4.10E-01
MSMEG_5015	secreted protein	NA	0.954	4.68E-01
MSMEG_5016	conserved domain protein	NA	0.965	5.61E-01
MSMEG_5017	lipoprotein	NA	0.790	1.92E-02
MSMEG_5018	Adenylate and Guanylate cyclase catalytic domain protein	NA	1.064	7.59E-01
MSMEG_5019	regulatory protein	NA	0.782	1.95E-01
MSMEG_5020	acetoin(diacetyl) reductase	NA	0.789	6.74E-02
MSMEG_5021	alcohol dehydrogenase, zinc-containing	NA	1.147	5.59E-01
MSMEG_5022	flavin-containing monooxygenase FMO	NA	0.907	9.13E-02
MSMEG_5023	chitooligosaccharide deacetylase	NA	1.476	2.37E-01
MSMEG_5024	T/U mismatch-specific DNA glycosylase	NA	1.010	5.05E-01
MSMEG_5025	putative transcriptional regulator	NA	1.037	6.26E-01
MSMEG_5026	conserved hypothetical protein	NA	0.928	7.13E-01
MSMEG_5027	glyoxalase family protein	NA	0.959	7.02E-01
MSMEG_5028	HIT family protein	NA	0.868	1.24E-02
MSMEG_5029	alkanal monooxygenase alpha chain	NA	1.196	1.89E-01
MSMEG_5030	conserved hypothetical protein TIGR00026	NA	1.002	9.68E-01
MSMEG_5031	uracil-DNA glycosylase superfamily protein	NA	1.934	4.49E-01
MSMEG_5032	putative transcriptional regulator	NA	1.139	8.01E-02
MSMEG_5033	Tap protein; this gene contains a frame shift which is not the result of sequencing erro	NA	0.906	4.74E-01
MSMEG_5033	Tap protein; this gene contains a frame shift which is not the result of sequencing erro	NA	1.192	2.12E-01
MSMEG_5034	hypothetical protein	NA	0.954	4.71E-01
MSMEG_5035	conserved hypothetical protein	NA	0.900	3.81E-01
MSMEG_5036	rhomboid family protein	NA	1.065	4.71E-01
MSMEG_5037	oxidoreductase, FAD-binding	NA	1.066	4.65E-01
MSMEG_5038	putative cytochrome P450 123	NA	1.080	5.21E-01
MSMEG_5039	Siderophore-interacting protein	NA	1.018	6.96E-01
MSMEG_5040	transcriptional regulator, TetR family protein	NA	1.245	3.21E-01
MSMEG_5041	probable acyltransferase	NA	1.158	2.60E-01
MSMEG_5042	ATP-dependent rna helicase, dead/deah box family protein	NA	1.050	1.26E-01
MSMEG_5043	LprE protein	NA	0.905	2.77E-02

MSMEG_5044	ATPase	NA	0.895	3.71E-01
MSMEG_5045	D-2-hydroxyglutarate dehydrogenase	NA	0.981	9.27E-01
MSMEG_5046	drug transporter	NA	1.406	3.14E-02
MSMEG_5047	drug resistance transporter Bcr/CflA subfamily protein	NA	1.801	1.11E-02
MSMEG_5048	conserved hypothetical protein	NA	1.099	2.45E-01
MSMEG_5049	2-oxoglutarate dehydrogenase, E1 component	sucA	0.909	1.83E-01
MSMEG_5050	methionine aminopeptidase, type I	map	1.295	1.83E-01
MSMEG_5051	major facilitator superfamily protein	NA	1.359	1.74E-02
MSMEG_5052	DNA-binding protein	NA	1.154	2.28E-02
MSMEG_5053	short chain alcohol dehydrogenase	NA	1.077	1.01E-01
MSMEG_5054	ABC transporter, quaternary amine uptake transporter (QAT) family protein, substrate	NA	0.994	9.24E-01
MSMEG_5055	NAD-dependent malic enzyme	NA	0.989	8.50E-01
MSMEG_5056	magnesium and cobalt transport protein CorA	corA	1.119	1.21E-01
MSMEG_5057	conserved hypothetical protein	NA	0.735	1.46E-03
MSMEG_5058	ABC transporter, ATP-binding protein SugC	NA	0.657	4.32E-04
MSMEG_5059	ABC transporter, permease protein SugB	NA	0.685	8.71E-05
MSMEG_5060	ABC transporter, permease protein SugA	NA	0.731	1.24E-04
MSMEG_5061	Bacterial extracellular solute-binding protein	NA	0.766	2.96E-04
MSMEG_5062	conserved hypothetical protein	NA	0.900	1.62E-02
MSMEG_5063	integral membrane protein	NA	1.025	8.36E-01
MSMEG_5064	malyl-CoA lyase	NA	0.939	2.23E-01
MSMEG_5065	Mg/Co/Ni transporter MgtE	NA	1.140	2.21E-01
MSMEG_5066	integral membrane protein	NA	1.080	5.07E-02
MSMEG_5067	secreted protein	NA	0.837	6.93E-02
MSMEG_5068	Mrp protein	NA	1.033	1.43E-01
MSMEG_5069	sec-independent translocase	NA	0.862	1.96E-03
MSMEG_5070	Trypsin	NA	0.938	3.11E-01
MSMEG_5071	conserved hypothetical protein	NA	0.942	3.86E-01
MSMEG_5072	extracytoplasmic function alternative sigma factor	NA	0.911	3.11E-01
MSMEG_5073	O-methyltransferase, family protein 3	NA	1.042	4.30E-01
MSMEG_5074	probable transcriptional regulatory protein	NA	0.951	5.97E-01

MSMEG_5075	ABC transporter ATP-binding protein	NA	0.704	2.41E-02
MSMEG_5076	ABC transporter membrane-spanning protein	NA	0.803	7.52E-02
MSMEG_5077	probable conserved integral membrane protein	NA	0.979	9.27E-01
MSMEG_5078	glucose-1-phosphate adenylyltransferase	glgC	1.094	6.28E-01
MSMEG_5079	conserved hypothetical protein	NA	1.029	7.04E-01
MSMEG_5080	glycogen synthase	NA	1.063	5.96E-01
MSMEG_5081	conserved hypothetical protein	NA	0.927	5.82E-01
MSMEG_5082	DNA-3-methyladenine glycosylase I	tag	1.062	6.14E-02
MSMEG_5083	conserved hypothetical protein	NA	1.046	3.68E-02
MSMEG_5084	glycosyl transferase, group 2 family protein	NA	1.087	3.87E-01
MSMEG_5085	dihydropteroate synthase	folP	1.213	1.42E-01
MSMEG_5086	very-long-chain acyl-CoA synthetase	NA	1.128	2.51E-02
MSMEG_5087	conserved hypothetical protein	NA	1.456	2.65E-02
MSMEG_5088	tetratricopeptide repeat family protein	NA	1.684	3.35E-01
MSMEG_5089	conserved hypothetical protein	NA	0.723	1.60E-02
MSMEG_5090	conserved hypothetical protein	NA	0.830	1.90E-02
MSMEG_5091	hypothetical protein	NA	0.828	2.93E-03
MSMEG_5092	hypothetical protein	NA	1.167	4.60E-01
MSMEG_5095	This gene is disrupted by an IS1096 element.; ISMsm1, transposase orfB, truncation; ic	NA	1.227	2.44E-01
MSMEG_5097	hypothetical protein	NA	1.186	1.70E-01
MSMEG_5098	hypothetical protein	NA	2.462	3.86E-01
MSMEG_5099	conserved hypothetical protein	NA	1.115	3.75E-01
MSMEG_5100	pyruvate ferredoxin/flavodoxin oxidoreductase family protein	NA	1.168	7.38E-02
MSMEG_5100	pyruvate ferredoxin/flavodoxin oxidoreductase family protein	NA	1.206	2.82E-02
MSMEG_5101	hypothetical protein	NA	1.237	9.13E-02
MSMEG_5102	ABC transporter ATP-binding protein	NA	1.359	3.27E-02
MSMEG_5103	succinyl-diaminopimelate desuccinylase	dapE	1.216	8.60E-02
MSMEG_5104	tetrahydropicolinate succinylase	NA	1.195	3.52E-02
MSMEG_5105	hypothetical protein	NA	1.171	1.76E-01
MSMEG_5106	HNH endonuclease	NA	1.019	9.00E-01
MSMEG_5107	secreted protein	NA	1.096	1.28E-01

MSMEG_5108	conserved hypothetical protein	NA	1.139	4.93E-01
MSMEG_5109	conserved hypothetical protein	NA	1.031	8.16E-01
MSMEG_5110	sulfatase; this region contains one or more premature stops and/or frameshifts which	NA	0.874	5.65E-01
MSMEG_5111	conserved hypothetical protein	NA	1.003	8.71E-01
MSMEG_5112	hypothetical protein	NA	1.144	8.92E-02
MSMEG_5113	conserved hypothetical protein; this region contains one or more premature stops anc	NA	0.988	6.91E-01
MSMEG_5114	acyl-CoA synthase	NA	1.079	5.16E-02
MSMEG_5115	hypothetical protein	NA	0.743	2.27E-01
MSMEG_5116	conserved hypothetical protein	NA	1.637	4.58E-01
MSMEG_5117	proline dehydrogenase	NA	1.127	3.16E-01
MSMEG_5118	nudix hydrolase	NA	1.023	3.72E-01
MSMEG_5119	1-pyrroline-5-carboxylate dehydrogenase	pruA	1.105	5.21E-01
MSMEG_5120	conserved hypothetical protein	NA	0.946	4.13E-01
MSMEG_5121	aminotransferase, classes I and II	NA	1.080	1.51E-01
MSMEG_5122	ferredoxin	NA	1.065	2.94E-01
MSMEG_5123	acyl-CoA dehydrogenase, C- domain protein; this gene contains a frame shift which is	NA	1.818	2.93E-01
MSMEG_5124	2,4-dienoyl-coA reductase	NA	1.001	9.76E-01
MSMEG_5125	YceI like family protein	NA	1.271	3.34E-01
MSMEG_5126	FO synthase	NA	0.973	6.08E-01
MSMEG_5127	hypothetical protein	NA	1.405	1.90E-02
MSMEG_5128	conserved hypothetical protein	NA	1.151	6.65E-01
MSMEG_5129	N-Acetyl-1-D-myo-Inosityl-2-Amino-2-Deoxy-alpha- D-Glucopyranoside Deacetylase M	NA	0.916	2.91E-01
MSMEG_5130	bacterial extracellular solute-binding protein, family protein 5	NA	1.190	1.02E-02
MSMEG_5131	hypothetical protein	NA	0.997	9.52E-01
MSMEG_5132	GTP-binding protein TypA/BipA	typA	1.384	2.31E-02
MSMEG_5133	hypothetical protein	NA	1.155	4.09E-01
MSMEG_5134	hypothetical protein	NA	1.001	9.97E-01
MSMEG_5135	hypothetical protein	NA	0.969	7.12E-01
MSMEG_5136	helix-turn-helix motif	NA	1.089	7.70E-01
MSMEG_5137	respiratory nitrate reductase, gamma subunit	narI	1.065	5.48E-01
MSMEG_5138	nitrate reductase molybdenum cofactor assembly chaperone	narJ	1.637	2.33E-01

MSMEG_5139	nitrate reductase, beta subunit	narH	1.484	3.90E-01
MSMEG_5140	nitrate reductase, alpha subunit	NA	1.182	4.40E-01
MSMEG_5141	nitrate/nitrite transporter protein	NA	1.277	3.39E-01
MSMEG_5142	beta-glucosidase A	NA	1.120	3.98E-01
MSMEG_5143	HTH-type transcriptional regulator DegA	NA	1.191	3.61E-01
MSMEG_5144	xylosidase/arabinosidase	NA	1.010	8.59E-01
MSMEG_5145	extracellular solute-binding protein, family protein 1	NA	0.835	1.18E-02
MSMEG_5146	binding protein dependent transport protein	NA	0.862	3.41E-01
MSMEG_5147	sugar ABC-transporter integral membrane protein	NA	0.998	9.88E-01
MSMEG_5148	CTP pyrophosphohydrolase	NA	0.883	1.63E-01
MSMEG_5149	conserved transmembrane protein	NA	0.912	3.42E-01
MSMEG_5150	putative pterin-4-alpha-carbinolamine dehydratase	NA	0.887	1.85E-01
MSMEG_5152	hypothetical protein	NA	0.706	1.63E-02
MSMEG_5152	hypothetical protein	NA	0.802	7.18E-02
MSMEG_5153	conserved hypothetical protein	NA	0.866	1.48E-01
MSMEG_5154	conserved hypothetical protein	NA	0.830	5.30E-01
MSMEG_5155	nitroreductase	NA	0.855	3.00E-01
MSMEG_5156	base excision DNA repair protein, HhH-GPD family protein	NA	0.863	6.73E-02
MSMEG_5157	hypothetical protein	NA	0.860	9.78E-02
MSMEG_5158	sensor histidine kinase	NA	1.014	8.94E-01
MSMEG_5159	DNA-binding response regulator, putative	NA	1.088	1.91E-01
MSMEG_5160	putative integral membrane protein	NA	1.058	6.40E-01
MSMEG_5161	transmembrane transport protein	NA	1.103	3.68E-01
MSMEG_5162	cinnamoyl ester hydrolase	NA	1.086	6.09E-01
MSMEG_5163	ABC proline/glycine betaine family protein transporter, periplasmic ligand binding pro	NA	0.997	9.63E-01
MSMEG_5164	zinc-binding alcohol dehydrogenase family protein	NA	1.128	6.55E-01
MSMEG_5165	integral membrane protein	NA	0.856	3.10E-01
MSMEG_5166	Na+/solute symporter	NA	1.354	3.67E-01
MSMEG_5167	major facilitator superfamily protein MFS_1	NA	0.918	7.48E-01
MSMEG_5168	conserved hypothetical protein	NA	1.039	7.90E-01
MSMEG_5169	conserved hypothetical protein	NA	0.948	6.36E-01

MSMEG_5170	pyridoxamine 5'-phosphate oxidase family protein	NA	0.869	8.67E-02
MSMEG_5171	conserved hypothetical protein	NA	1.059	3.15E-01
MSMEG_5172	conserved hypothetical protein	NA	1.132	1.51E-01
MSMEG_5173	O-methyltransferase, putative	NA	1.023	6.76E-01
MSMEG_5174	regulatory protein GntR, HTH	NA	1.028	8.41E-01
MSMEG_5175	NAD-dependent deacetylase	NA	0.950	4.55E-01
MSMEG_5176	methyltransferase type 11	NA	0.849	1.58E-01
MSMEG_5177	regulatory protein, TetR	NA	0.895	4.14E-01
MSMEG_5178	integral membrane protein	NA	0.792	2.97E-01
MSMEG_5179	DoxX subfamily protein, putative	NA	2.065	6.97E-02
MSMEG_5180	conserved hypothetical protein	NA	0.972	8.49E-01
MSMEG_5182	2-Nitropropane dioxygenase	NA	0.995	9.41E-01
MSMEG_5183	3-Hydroxyacyl-CoA dehydrogenase	NA	1.102	3.89E-01
MSMEG_5184	alpha-methylacyl-CoA racemase, putative	NA	1.119	4.88E-01
MSMEG_5185	enoyl-CoA hydratase PaaB	NA	1.315	3.44E-02
MSMEG_5186	HicB family protein	NA	1.525	3.51E-01
MSMEG_5187	tetracycline-resistance determinant TetV	NA	1.569	7.38E-02
MSMEG_5188	caax amino protease family protein	NA	1.272	8.00E-03
MSMEG_5189	oxidoreductase	NA	1.252	3.61E-01
MSMEG_5190	TetR-family protein transcriptional regulator	NA	2.607	3.54E-01
MSMEG_5191	siderophore binding protein	NA	1.065	3.63E-01
MSMEG_5192	aldo/keto reductase	NA	1.568	5.72E-02
MSMEG_5193	transcriptional regulator, AraC family protein	NA	1.322	1.52E-01
MSMEG_5194	integral membrane protein	NA	1.102	2.47E-01
MSMEG_5195	hypothetical protein	NA	1.176	5.04E-01
MSMEG_5196	fasciclin domain protein	NA	0.767	8.91E-02
MSMEG_5197	long-chain specific acyl-CoA dehydrogenase	NA	0.938	2.42E-01
MSMEG_5198	carnitinyl-CoA dehydratase	NA	0.898	2.33E-01
MSMEG_5199	putative acyl-CoA dehydrogenase	NA	0.952	3.70E-01
MSMEG_5200	hypothetical protein	NA	1.309	6.03E-01
MSMEG_5201	regulatory protein GntR, HTH	NA	1.215	2.34E-02

MSMEG_5202	conserved membrane protein	NA	1.175	4.44E-01
MSMEG_5203	DoxX subfamily protein, putative	NA	0.945	1.55E-01
MSMEG_5204	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	2.009	1.22E-01
MSMEG_5205	conserved hypothetical protein	NA	1.090	6.26E-01
MSMEG_5206	regulatory protein	NA	1.401	4.32E-02
MSMEG_5207	conserved hypothetical protein	NA	1.046	7.11E-01
MSMEG_5208	conserved hypothetical protein	NA	1.022	4.40E-01
MSMEG_5209	hydrolase, alpha/beta fold family protein	NA	0.809	3.59E-03
MSMEG_5210	hydrolase	NA	0.955	5.47E-01
MSMEG_5211	aminotransferase class-III	NA	0.986	9.18E-01
MSMEG_5212	conserved hypothetical protein	NA	1.083	6.45E-01
MSMEG_5213	conserved hypothetical protein	NA	0.900	4.31E-01
MSMEG_5214	RNA polymerase sigma-70 factor	NA	2.146	3.88E-01
MSMEG_5215	conserved hypothetical protein	NA	0.969	7.13E-01
MSMEG_5216	glyoxalase family protein	NA	0.914	6.65E-01
MSMEG_5217	hypothetical protein	NA	0.961	3.32E-01
MSMEG_5218	conserved hypothetical protein	NA	0.943	2.73E-01
MSMEG_5219	riboflavin biosynthesis protein RibD C- domain protein	NA	0.949	4.76E-01
MSMEG_5220	esterase/lipase/thioesterase	NA	1.086	5.63E-01
MSMEG_5221	GCN5-related N-acetyltransferase	NA	0.956	2.83E-01
MSMEG_5222	GTP-binding protein YchF	ychF	0.954	5.33E-01
MSMEG_5223	conserved hypothetical protein	NA	1.057	4.93E-02
MSMEG_5224	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	ispH	1.087	2.41E-01
MSMEG_5225	conserved hypothetical protein	NA	0.969	4.32E-01
MSMEG_5226	exodeoxyribonuclease VII, large subunit	xseA	1.122	9.27E-02
MSMEG_5227	exodeoxyribonuclease VII, small subunit	xseB	1.091	5.85E-01
MSMEG_5228	3-beta hydroxysteroid dehydrogenase/isomerase family protein	NA	0.877	5.31E-02
MSMEG_5228	3-beta hydroxysteroid dehydrogenase/isomerase family protein	NA	0.974	5.46E-01
MSMEG_5229	hypothetical protein	NA	1.143	1.47E-01
MSMEG_5230	conserved hypothetical protein	NA	1.228	7.80E-02
MSMEG_5231	hypothetical protein	NA	1.113	3.89E-01

MSMEG_5232	hypothetical protein	NA	0.915	5.39E-01
MSMEG_5233	RmlD substrate binding domain superfamily protein	NA	0.847	1.85E-01
MSMEG_5234	short-chain dehydrogenase/reductase SDR	NA	0.812	9.31E-02
MSMEG_5235	short chain dehydrogenase family protein	NA	0.917	6.09E-01
MSMEG_5236	dienelactone hydrolase family protein	NA	1.131	1.55E-01
MSMEG_5237	conserved hypothetical protein	NA	0.934	6.51E-01
MSMEG_5238	conserved hypothetical protein	NA	1.127	7.50E-03
MSMEG_5239	fructose-1,6-bisphosphatase, class II	glpX	0.844	8.88E-02
MSMEG_5240	fumarate hydratase class II	NA	0.968	7.26E-01
MSMEG_5241	GAF family protein	NA	1.062	3.76E-01
MSMEG_5242	acyltransferase, ws/dgat/mgat subfamily protein	NA	1.406	1.78E-01
MSMEG_5243	helix-turn-helix motif	NA	1.677	1.12E-01
MSMEG_5244	two component transcriptional regulatory protein devr	NA	1.251	8.19E-02
MSMEG_5245	universal stress protein family protein	NA	1.141	4.05E-01
MSMEG_5246	conserved hypothetical protein	NA	3.107	4.02E-01
MSMEG_5247	PhoH family protein	NA	1.182	1.04E-01
MSMEG_5248	acyl-[ACP] desaturase	NA	1.241	6.42E-03
MSMEG_5249	serine hydroxymethyltransferase	glyA	1.068	1.92E-01
MSMEG_5250	CalR9 protein	NA	1.042	2.99E-01
MSMEG_5251	hypothetical protein	NA	1.010	7.98E-01
MSMEG_5252	pantothenate kinase	coaA	1.091	9.86E-02
MSMEG_5253	conserved hypothetical protein	NA	1.059	4.36E-01
MSMEG_5254	conserved hypothetical protein	NA	1.101	5.22E-01
MSMEG_5255	conserved hypothetical protein	NA	1.028	7.70E-01
MSMEG_5256	undecaprenyl diphosphate synthase	uppS	1.028	7.22E-01
MSMEG_5257	channel protein, hemolysin III family protein	NA	1.342	6.80E-03
MSMEG_5258	steroid delta-isomerase	NA	1.016	8.90E-01
MSMEG_5259	conserved hypothetical protein	NA	1.043	8.01E-01
MSMEG_5260	conserved hypothetical protein	NA	0.981	4.26E-01
MSMEG_5261	mycothiol conjugate amidase Mca	NA	0.950	2.71E-02
MSMEG_5262	conserved hypothetical protein	NA	1.073	6.50E-01

MSMEG_5263	transcription elongation factor GreA	NA	1.280	1.23E-02
MSMEG_5264	conserved hypothetical protein	NA	1.212	8.99E-02
MSMEG_5264	conserved hypothetical protein	NA	1.537	5.69E-02
MSMEG_5265	putative cystathionine gamma-synthase	NA	1.143	7.75E-02
MSMEG_5266	RDD family protein	NA	1.094	3.31E-02
MSMEG_5267	glutaryl-CoA dehydrogenase	NA	0.968	5.67E-01
MSMEG_5268	conserved hypothetical protein	NA	0.758	3.35E-03
MSMEG_5269	hypothetical protein	NA	0.966	5.11E-01
MSMEG_5270	cystathionine beta-synthase	NA	1.268	5.29E-02
MSMEG_5271	esterase	NA	0.891	3.49E-01
MSMEG_5272	conserved exported protein	NA	1.120	2.28E-01
MSMEG_5273	beta-ketoadipyl CoA thiolase	NA	0.935	2.33E-01
MSMEG_5274	phosphoribosylglycinamide formyltransferase 2	purT	1.126	1.41E-02
MSMEG_5275	permease of the major facilitator superfamily protein	NA	0.966	6.60E-01
MSMEG_5276	enoyl-CoA hydratase	NA	0.880	3.09E-02
MSMEG_5277	probable enoyl-CoA hydratase	NA	1.100	2.38E-02
MSMEG_5278	conserved membrane-spanning protein	NA	1.109	5.08E-01
MSMEG_5279	conserved hypothetical protein	NA	1.290	1.18E-01
MSMEG_5280	cysteine dioxygenase type I superfamily protein	NA	1.091	4.80E-01
MSMEG_5281	LpqV protein	NA	1.027	4.04E-01
MSMEG_5282	transcriptional regulator	NA	2.771	3.61E-01
MSMEG_5283	hydrolase, CocE/NonD family protein	NA	1.498	2.07E-02
MSMEG_5284	patatin	NA	1.602	2.06E-03
MSMEG_5285	phospholipase, patatin family protein	NA	1.068	1.65E-01
MSMEG_5286	dihydrodipicolinate reductase, N-terminus domain protein	dapB	0.790	6.15E-02
MSMEG_5287	dehydrogenase	NA	1.087	6.51E-01
MSMEG_5288	putative serine/threonine protein kinase	NA	1.401	1.92E-01
MSMEG_5289	hypothetical protein	NA	0.944	4.79E-01
MSMEG_5290	hypothetical protein	NA	1.097	3.12E-01
MSMEG_5291	acyl-CoA synthase	NA	1.169	3.17E-01
MSMEG_5292	hypothetical protein	NA	1.291	4.67E-02

MSMEG_5293	hypothetical protein	NA	1.310	5.33E-03
MSMEG_5294	hypothetical protein	NA	1.377	3.59E-02
MSMEG_5295	peroxisomal-coenzyme A synthetase	NA	1.077	5.58E-01
MSMEG_5296	hypothetical protein	NA	1.546	5.32E-01
MSMEG_5297	oxalyl-CoA decarboxylase	NA	0.932	3.74E-01
MSMEG_5298	hypothetical protein	NA	1.414	4.85E-02
MSMEG_5299	hypothetical protein	NA	1.777	3.37E-01
MSMEG_5300	short-chain type dehydrogenase/reductase	NA	1.114	6.19E-02
MSMEG_5301	transcriptional regulator	NA	1.545	1.37E-01
MSMEG_5302	aerobic C4-dicarboxylate transport protein	NA	0.578	2.61E-02
MSMEG_5303	sodium/proline symporter	putP	0.927	4.53E-01
MSMEG_5304	two-component sensor kinase	NA	0.901	2.37E-01
MSMEG_5305	choline dehydrogenase	NA	0.983	9.11E-01
MSMEG_5306	two-component system response regulator	NA	1.031	8.47E-01
MSMEG_5307	TetR-family protein transcriptional regulator	NA	1.038	8.91E-01
MSMEG_5308	conserved hypothetical protein	NA	1.164	3.51E-01
MSMEG_5309	conserved hypothetical protein	NA	1.637	1.25E-01
MSMEG_5310	SAM-dependent methyltransferase	NA	1.325	4.37E-01
MSMEG_5311	conserved hypothetical protein	NA	0.841	2.07E-01
MSMEG_5312	ABC-type multidrug transport system ATPase component	NA	1.195	4.91E-02
MSMEG_5313	hypothetical protein	NA	1.014	9.34E-01
MSMEG_5314	conserved hypothetical protein	NA	1.837	4.38E-01
MSMEG_5315	gp35 protein	NA	1.000	9.99E-01
MSMEG_5316	glutamine ABC transporter, ATP-binding protein	NA	0.883	1.12E-01
MSMEG_5317	conserved hypothetical protein	NA	0.996	9.83E-01
MSMEG_5318	glutamine ABC transporter, permease/substrate-binding protein	NA	0.822	4.15E-02
MSMEG_5319	alkylhydroperoxidase AhpD core	NA	1.453	6.63E-02
MSMEG_5320	hypothetical protein	NA	0.942	5.15E-01
MSMEG_5321	hypothetical protein	NA	0.846	6.32E-02
MSMEG_5322	hypothetical protein	NA	1.096	3.90E-01
MSMEG_5323	conserved hypothetical protein	NA	0.958	5.66E-01

MSMEG_5324	conserved hypothetical protein	NA	1.074	7.73E-01
MSMEG_5325	hypothetical protein	NA	1.041	6.94E-01
MSMEG_5326	hypothetical protein	NA	1.098	3.78E-01
MSMEG_5327	hypothetical protein	NA	0.955	7.81E-01
MSMEG_5328	conserved hypothetical protein	NA	1.354	1.84E-01
MSMEG_5329	conserved hypothetical protein	NA	1.530	1.29E-02
MSMEG_5330	SIS domain protein	NA	1.081	2.23E-01
MSMEG_5331	UDP-glucoronosyl and UDP-glucosyl transferase family; this gene contains a frame shif	NA	1.025	7.47E-01
MSMEG_5331	UDP-glucoronosyl and UDP-glucosyl transferase family; this gene contains a frame shif	NA	1.183	3.28E-02
MSMEG_5332	transcriptional regulator, TetR family protein	NA	1.193	4.50E-01
MSMEG_5333	hypothetical protein	NA	0.808	8.95E-03
MSMEG_5334	conserved hypothetical protein	NA	1.163	3.06E-01
MSMEG_5335	formamidase	NA	1.269	2.95E-01
MSMEG_5336	amidate substrates transporter protein	NA	0.980	8.10E-01
MSMEG_5337	putative regulatory protein, FmdB family; this gene contains a frame shift which is not	NA	0.903	5.36E-01
MSMEG_5338	regulatory protein, MarR	NA	1.021	5.35E-02
MSMEG_5339	nitrile hydratase regulator1	NA	1.388	2.13E-01
MSMEG_5340	TetR-family protein transcriptional regulator	NA	1.289	1.04E-02
MSMEG_5341	dipeptidyl aminopeptidase/acylaminoacyl peptidase	NA	0.848	3.94E-01
MSMEG_5342	conserved hypothetical protein	NA	0.923	5.63E-01
MSMEG_5343	conserved hypothetical protein	NA	0.954	8.13E-01
MSMEG_5344	hypothetical protein	NA	1.012	9.55E-01
MSMEG_5345	glycosyl hydrolases family protein 16	NA	0.980	8.78E-01
MSMEG_5346	TetR-family protein transcriptional regulator	NA	1.232	5.52E-01
MSMEG_5347	transporter, major facilitator family protein	NA	0.861	7.03E-01
MSMEG_5348	medium-chain fatty acid-CoA ligase	NA	0.822	3.63E-01
MSMEG_5349	conserved hypothetical protein, putative	NA	0.932	5.08E-01
MSMEG_5350	PPE family protein, putative	NA	1.065	1.52E-01
MSMEG_5351	hypothetical protein	NA	1.215	2.29E-01
MSMEG_5352	conserved hypothetical protein	NA	0.888	3.67E-01
MSMEG_5353	putative methyltransferase	NA	1.122	5.42E-01

MSMEG_5354	O-methyltransferase, family protein 2	NA	1.241	3.58E-02
MSMEG_5355	hypothetical protein	NA	0.944	3.70E-01
MSMEG_5356	hypothetical protein	NA	1.409	4.64E-02
MSMEG_5357	conserved hypothetical protein	NA	0.952	4.29E-01
MSMEG_5358	acetamidase/Formamidase family protein	NA	0.950	6.50E-01
MSMEG_5359	cyanate hydratase	cynS	1.083	1.81E-01
MSMEG_5360	formate/nitrate transporter	NA	1.088	7.22E-01
MSMEG_5361	hypothetical protein	NA	1.007	9.76E-01
MSMEG_5362	hypothetical protein	NA	1.141	2.25E-01
MSMEG_5363	hypothetical protein	NA	1.274	1.64E-01
MSMEG_5364	amidohydrolase 2	NA	1.113	5.74E-02
MSMEG_5365	RNA polymerase sigma-70 factor	NA	1.055	2.87E-01
MSMEG_5366	conserved hypothetical protein	NA	0.764	1.72E-01
MSMEG_5367	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.990	3.25E-01
MSMEG_5368	ectoine/hydroxyectoine ABC transporter solute-binding protein	ehuB	0.725	9.59E-03
MSMEG_5369	ectoine/hydroxyectoine ABC transporter, permease protein EhuC	ehuC	0.699	1.01E-02
MSMEG_5370	ectoine/hydroxyectoine ABC transporter, permease protein EhuD	ehuD	0.642	1.66E-04
MSMEG_5371	ectoine/hydroxyectoine ABC transporter, ATP-binding protein	ehuA	0.639	6.28E-04
MSMEG_5372	sensor protein KdpD	NA	1.045	8.70E-01
MSMEG_5373	nitrilase 2	NA	1.281	3.57E-01
MSMEG_5374	glutamate--ammonia ligase	NA	1.217	5.97E-01
MSMEG_5375	GntR-family protein transcriptional regulator	NA	1.197	1.13E-01
MSMEG_5376	conserved hypothetical protein	NA	1.163	4.47E-01
MSMEG_5377	hypothetical protein	NA	1.517	5.19E-01
MSMEG_5381	hypothetical protein	NA	1.026	7.27E-01
MSMEG_5382	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	1.014	9.35E-01
MSMEG_5383	dehydrogenase/reductase SDR family protein member 4	NA	1.574	8.78E-02
MSMEG_5384	hypothetical protein	NA	1.659	2.89E-01
MSMEG_5385	metallo-beta-lactamase family protein	NA	2.325	1.12E-01
MSMEG_5386	rhodanese-like domain protein	NA	1.284	3.05E-01
MSMEG_5387	conserved hypothetical protein	NA	1.222	4.94E-01

MSMEG_5388	conserved hypothetical protein	NA	0.910	4.76E-01
MSMEG_5389	LysA protein	NA	1.270	2.65E-01
MSMEG_5390	conserved hypothetical protein	NA	0.989	9.11E-01
MSMEG_5391	hypothetical protein	NA	0.982	8.56E-01
MSMEG_5392	K+-transporting ATPase, A subunit	kdpA	0.910	4.72E-01
MSMEG_5393	K+-transporting ATPase, B subunit	kdpB	1.193	2.54E-01
MSMEG_5394	potassium-transporting ATPase C chain	NA	1.126	1.97E-01
MSMEG_5395	sensor protein KdpD	NA	0.899	1.36E-01
MSMEG_5396	KDP operon transcriptional regulatory protein KdpE	NA	1.223	1.57E-02
MSMEG_5397	ATP-dependent DNA helicase RecQ	recQ	1.195	1.98E-01
MSMEG_5399	ATP-dependent DNA helicase RecQ	NA	1.212	2.29E-01
MSMEG_5400	dehydrogenase	NA	1.176	3.16E-01
MSMEG_5401	conserved hypothetical protein	NA	1.057	2.37E-01
MSMEG_5402	dehydrogenase DhgA	NA	1.417	3.24E-01
MSMEG_5403	cadmium-translocating P-type ATPase	cadA	0.916	2.21E-01
MSMEG_5404	propionate--CoA ligase	NA	0.870	2.65E-01
MSMEG_5405	transcriptional regulator, ArsR family protein	NA	1.252	2.93E-02
MSMEG_5406	hypothetical protein	NA	1.311	6.34E-01
MSMEG_5407	integral membrane protein	NA	1.065	4.43E-01
MSMEG_5408	prolipoprotein diacylglyceryl transferase	lgt	0.831	3.77E-02
MSMEG_5409	conserved hypothetical protein	NA	1.287	5.12E-01
MSMEG_5410	radical SAM domain protein	NA	1.084	2.49E-01
MSMEG_5411	conserved hypothetical protein	NA	1.075	6.52E-01
MSMEG_5412	immunogenic protein MPT63	NA	0.893	1.70E-01
MSMEG_5413	exopolyphosphatase	NA	1.171	1.41E-01
MSMEG_5414	septum formation initiator subfamily protein, putative	NA	0.900	2.69E-01
MSMEG_5415	enolase	eno	0.867	2.75E-02
MSMEG_5416	LpqU protein	NA	0.979	7.41E-01
MSMEG_5417	hypothetical protein	NA	0.964	7.53E-01
MSMEG_5418	iron permease FTR1	NA	0.943	5.44E-01
MSMEG_5419	lipoprotein; this gene contains a frame shift which is not the result of sequencing erro	NA	0.764	5.35E-02

MSMEG_5420	Tat-translocated enzyme	NA	0.613	4.22E-03
MSMEG_5421	hypothetical protein	NA	0.585	1.10E-02
MSMEG_5422	transcriptional regulator, MazG family protein	NA	1.344	6.96E-03
MSMEG_5423	transcription-repair coupling factor	mfd	1.387	3.34E-04
MSMEG_5424	transcriptional regulator, TetR family protein	NA	1.187	8.69E-02
MSMEG_5426	UDP-N-acetylglucosamine pyrophosphorylase	glmU	1.052	3.94E-01
MSMEG_5427	ribose-phosphate pyrophosphokinase	NA	1.104	2.99E-02
MSMEG_5428	arsenate reductase	arsC	1.088	1.53E-02
MSMEG_5429	LpqT protein	NA	0.919	3.53E-02
MSMEG_5429	LpqT protein	NA	0.993	7.56E-01
MSMEG_5430	retinol dehydrogenase 13	NA	1.087	3.52E-02
MSMEG_5431	ribosomal protein L25, Ctc-form	NA	1.153	2.98E-02
MSMEG_5432	peptidyl-tRNA hydrolase	pth	1.218	4.05E-02
MSMEG_5433	4Fe-4S binding domain protein	NA	3.125	3.55E-01
MSMEG_5434	hypothetical protein	NA	0.887	5.25E-01
MSMEG_5435	acyl-CoA synthase	NA	0.954	7.22E-01
MSMEG_5436	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	ispE	1.139	3.19E-01
MSMEG_5437	probable serine/threonine-protein kinase PknB	NA	0.781	2.57E-01
MSMEG_5438	dimethyladenosine transferase	ksgA	1.145	4.92E-02
MSMEG_5439	resuscitation-promoting factor RpfB	NA	1.070	4.54E-01
MSMEG_5440	deoxyribonuclease	NA	1.023	5.49E-01
MSMEG_5441	methionyl-tRNA synthetase	metG	0.968	6.45E-01
MSMEG_5442	glutamate dehydrogenase	NA	1.040	6.83E-01
MSMEG_5443	dehydrogenase	NA	1.018	8.41E-01
MSMEG_5444	RNA polymerase sigma-70 factor, TIGR02957 family protein	NA	1.049	7.18E-01
MSMEG_5445	conserved hypothetical protein	NA	1.048	5.15E-01
MSMEG_5446	para-aminobenzoate synthase, component I	pabB	1.213	4.10E-01
MSMEG_5447	dolichyl-phosphate-mannose-protein mannosyltransferase	NA	1.235	3.90E-02
MSMEG_5448	arginine deiminase	arcA	1.001	9.87E-01
MSMEG_5449	conserved hypothetical protein	NA	1.281	4.95E-01
MSMEG_5450	redox-sensitive transcriptional activator SoxR	soxR	1.254	3.30E-02

MSMEG_5451	alkylated DNA repair protein	NA	1.311	5.13E-02
MSMEG_5452	conserved hypothetical protein	NA	1.016	8.83E-01
MSMEG_5453	conserved hypothetical protein	NA	1.196	5.75E-01
MSMEG_5454	choloylglycine hydrolase, putative	NA	1.054	6.47E-01
MSMEG_5455	pe family protein	NA	1.062	1.95E-01
MSMEG_5456	MK35 lipoprotein	NA	0.654	4.33E-02
MSMEG_5457	shikimate 5-dehydrogenase	NA	0.846	3.17E-01
MSMEG_5458	cyclic nucleotide-binding protein	NA	0.974	8.92E-01
MSMEG_5459	hypothetical protein	NA	1.071	6.66E-01
MSMEG_5460	conserved hypothetical protein	NA	1.213	2.41E-01
MSMEG_5461	hypothetical protein	NA	1.117	4.64E-01
MSMEG_5462	RarD protein	rarD	1.021	7.96E-01
MSMEG_5463	6-phosphogluconate dehydrogenase, NAD-binding	NA	1.048	3.72E-01
MSMEG_5464	integral membrane transport protein	NA	1.422	3.40E-01
MSMEG_5465	transcriptional regulator, AraC family protein	NA	1.013	9.09E-01
MSMEG_5466	oxidoreductase	NA	1.051	4.80E-01
MSMEG_5468	conserved hypothetical protein	NA	0.854	7.29E-02
MSMEG_5469	acetyltransferase, GNAT family protein	NA	1.091	2.89E-02
MSMEG_5470	molybdopterin biosynthesis protein MoeA 1	NA	1.025	7.52E-01
MSMEG_5471	UTP-glucose-1-phosphate uridylyltransferase	galU	0.924	5.55E-02
MSMEG_5472	5,10-methenyltetrahydrofolate synthetase	NA	0.866	3.14E-01
MSMEG_5473	transporter	NA	0.724	2.24E-01
MSMEG_5474	universal stress protein family protein	NA	1.067	3.25E-01
MSMEG_5475	acetate operon repressor	NA	1.082	4.98E-01
MSMEG_5476	glyoxylate carboligase	gcl	1.051	4.28E-01
MSMEG_5477	2-hydroxy-3-oxopropionate reductase	NA	1.180	2.37E-01
MSMEG_5478	hydroxypyruvate isomerase, putative	NA	0.995	9.58E-01
MSMEG_5479	type I antifreeze protein	NA	1.033	6.68E-01
MSMEG_5480	hypothetical protein	NA	1.123	1.14E-01
MSMEG_5481	conserved hypothetical protein	NA	1.637	3.83E-01
MSMEG_5482	large conductance mechanosensitive channel protein	mscL	0.988	8.92E-01

MSMEG_5483	porin	NA	0.779	4.24E-03
MSMEG_5484	conserved hypothetical protein	NA	1.196	3.06E-01
MSMEG_5485	molybdopterin biosynthesis protein	NA	0.974	1.20E-01
MSMEG_5486	peptidase S1 and S6, chymotrypsin/Hap	NA	0.871	5.41E-03
MSMEG_5487	sensor histidine kinase	NA	0.970	5.33E-01
MSMEG_5488	DNA-binding response regulator	NA	0.998	9.49E-01
MSMEG_5489	ribosomal protein L32	rpmF	1.622	3.87E-01
MSMEG_5490	conserved hypothetical protein	NA	0.875	4.10E-01
MSMEG_5491	putative acyl-CoA dehydrogenase	NA	0.773	5.88E-02
MSMEG_5492	acetyl-CoA carboxylase carboxyltransferase	NA	0.693	4.81E-02
MSMEG_5493	acetyl-/propionyl-coenzyme A carboxylase alpha chain	NA	0.829	3.42E-01
MSMEG_5494	acyl-CoA dehydrogenase fadE12	NA	1.107	7.88E-01
MSMEG_5495	enoyl-CoA hydratase	NA	1.125	6.03E-01
MSMEG_5496	MscS Mechanosensitive ion channel	NA	0.830	2.86E-01
MSMEG_5497	conserved hypothetical protein	NA	1.563	4.52E-01
MSMEG_5498	conserved hypothetical protein	NA	1.058	3.92E-01
MSMEG_5499	conserved hypothetical protein	NA	1.711	3.98E-01
MSMEG_5500	hypothetical protein	NA	0.892	3.14E-01
MSMEG_5501	hypothetical protein	NA	0.937	6.00E-01
MSMEG_5502	hypothetical protein	NA	0.687	4.22E-03
MSMEG_5503	hypothetical protein	NA	1.159	5.32E-01
MSMEG_5504	conserved secreted protein	NA	1.149	6.90E-01
MSMEG_5505	conserved hypothetical protein	NA	1.142	5.64E-02
MSMEG_5506	hypothetical protein	NA	1.848	1.39E-01
MSMEG_5507	hypothetical protein	NA	2.336	1.10E-02
MSMEG_5508	alkaline phosphatase	NA	0.960	7.52E-01
MSMEG_5509	conserved hypothetical protein	NA	0.912	4.65E-01
MSMEG_5510	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.838	3.88E-01
MSMEG_5511	von Willebrand factor, type A	NA	0.841	8.45E-02
MSMEG_5512	magnesium chelatase	NA	0.935	4.10E-01
MSMEG_5513	serine/threonine-protein kinase PknE	NA	1.220	2.52E-02

MSMEG_5514	hypothetical protein	NA	0.971	6.97E-01
MSMEG_5515	bifunctional purine biosynthesis protein PurH	purH	0.859	1.06E-01
MSMEG_5516	phosphoribosylglycinamide formyltransferase	purN	0.970	6.46E-01
MSMEG_5517	conserved hypothetical protein	NA	1.236	2.20E-01
MSMEG_5518	antigen 34 kDa	NA	0.950	5.92E-01
MSMEG_5519	monooxygenase	NA	0.944	1.98E-01
MSMEG_5520	conserved hypothetical protein	NA	0.900	3.58E-01
MSMEG_5521	acetyl-CoA acetyltransferase	NA	1.283	1.39E-01
MSMEG_5522	transcriptional Regulator, TetR family protein	NA	0.943	4.47E-01
MSMEG_5523	peptidase	NA	2.286	4.77E-01
MSMEG_5524	succinyl-CoA synthetase, alpha subunit	sucD	0.835	8.37E-03
MSMEG_5525	succinyl-CoA synthetase, beta subunit	sucC	0.803	1.81E-02
MSMEG_5526	peptidoglycan-binding LysM	NA	0.938	2.97E-01
MSMEG_5527	conserved hypothetical protein	NA	1.124	6.06E-02
MSMEG_5528	hypothetical protein	NA	1.385	5.01E-01
MSMEG_5529	hypothetical protein	NA	1.182	5.66E-01
MSMEG_5530	putative aliphatic sulfonates transport permease protein SsuC	NA	1.020	8.73E-01
MSMEG_5531	ABC transporter ATP-binding protein	NA	1.073	7.78E-01
MSMEG_5532	FAD dependent oxidoreductase	NA	1.007	9.29E-01
MSMEG_5533	4Fe-4S ferredoxin, iron-sulfur binding	NA	1.171	5.11E-01
MSMEG_5534	ATP-dependent DNA helicase PcrA	pcrA	1.112	9.84E-02
MSMEG_5535	hypothetical protein	NA	1.096	6.36E-01
MSMEG_5536	chorismate mutase	NA	1.129	2.94E-01
MSMEG_5537	conserved integral membrane protein	NA	1.043	7.02E-01
MSMEG_5538	[NADP+] succinate-semialdehyde dehydrogenase	NA	0.972	4.40E-01
MSMEG_5539	hypothetical protein	NA	1.179	2.37E-01
MSMEG_5540	conserved hypothetical protein	NA	1.076	6.30E-01
MSMEG_5541	glucose-6-phosphate isomerase	pgi	0.840	3.56E-02
MSMEG_5542	transcriptional regulator, HTH_3 family protein	NA	1.093	6.78E-01
MSMEG_5543	hypothetical protein	NA	1.217	4.98E-01
MSMEG_5544	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.003	9.53E-01

MSMEG_5545	formamidopyrimidine-DNA glycosylase	NA	1.074	2.90E-01
MSMEG_5546	membrane spanning protein	NA	0.818	9.48E-03
MSMEG_5547	conserved hypothetical protein	NA	1.223	2.10E-01
MSMEG_5548	precorrin-6A synthase (deacetylating)	cobF	0.959	4.31E-01
MSMEG_5549	conserved hypothetical protein	NA	0.848	1.68E-01
MSMEG_5550	protein-glutamate methylesterase; this gene contains a frame shift which is not the re	NA	0.982	9.21E-01
MSMEG_5550	protein-glutamate methylesterase; this gene contains a frame shift which is not the re	NA	3.267	3.38E-01
MSMEG_5551	stas domain protein	NA	1.172	4.42E-01
MSMEG_5552	conserved hypothetical protein	NA	0.951	5.97E-01
MSMEG_5553	CheR methyltransferase, SAM binding domain protein	cheR	0.932	1.58E-04
MSMEG_5554	antar domain protein	NA	0.995	8.07E-01
MSMEG_5555	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.001	9.92E-01
MSMEG_5556	MFS permease	NA	1.296	1.67E-02
MSMEG_5557	conserved hypothetical protein	NA	0.963	7.12E-01
MSMEG_5558	hypothetical protein	NA	1.486	1.97E-03
MSMEG_5559	metabolite/sugar transport protein	NA	1.794	4.27E-01
MSMEG_5560	hypothetical protein	NA	1.245	4.23E-01
MSMEG_5561	HPP family protein	NA	1.482	2.35E-02
MSMEG_5562	RNase H	rnhA	0.798	1.19E-02
MSMEG_5563	AraC-family protein transcriptional regulator	NA	1.308	3.39E-03
MSMEG_5564	NAD(P)H dehydrogenase, quinone family protein	NA	0.996	9.62E-01
MSMEG_5565	conserved hypothetical protein	NA	0.854	1.66E-01
MSMEG_5566	transcriptional regulator	NA	2.310	3.09E-01
MSMEG_5567	transcriptional regulator, TetR family protein	NA	1.324	4.58E-03
MSMEG_5568	clavaldehyde dehydrogenase	NA	1.434	1.57E-02
MSMEG_5569	clavaldehyde dehydrogenase	NA	1.351	2.83E-02
MSMEG_5570	DNA ligase	NA	4.280	3.65E-01
MSMEG_5571	ABC transporter ATP-binding protein	NA	0.554	3.06E-03
MSMEG_5572	sugar ABC transporter permease protein	NA	0.567	1.37E-02
MSMEG_5573	sugar ABC transporter permease protein	NA	0.502	2.01E-02
MSMEG_5574	substrate binding protein	NA	0.520	1.20E-03

MSMEG_5575	repressor	NA	0.595	2.30E-03
MSMEG_5576	D-mannonate oxidoreductase	NA	0.805	5.91E-02
MSMEG_5577	fructokinase	NA	0.841	4.60E-01
MSMEG_5578	hypothetical protein	NA	0.951	5.30E-01
MSMEG_5579	MarR-family protein transcriptional regulator	NA	0.973	5.61E-01
MSMEG_5580	Ku protein	NA	1.060	3.36E-01
MSMEG_5581	conserved hypothetical integral membrane protein	NA	1.049	4.61E-01
MSMEG_5582	hypothetical protein	NA	0.800	1.24E-01
MSMEG_5583	HNH endonuclease	NA	1.456	3.88E-01
MSMEG_5584	short chain dehydrogenase	NA	0.825	1.51E-01
MSMEG_5585	hypothetical protein	NA	0.943	5.73E-01
MSMEG_5586	conserved hypothetical protein	NA	0.638	3.92E-02
MSMEG_5587	hypothetical protein	NA	0.850	2.55E-02
MSMEG_5588	hypothetical protein	NA	0.937	4.85E-01
MSMEG_5589	manganese transport protein MntH	NA	1.183	1.42E-01
MSMEG_5590	carboxylate-amine ligase Nfa27300	NA	1.131	6.08E-01
MSMEG_5591	conserved hypothetical protein	NA	0.955	4.11E-01
MSMEG_5592	conserved hypothetical protein	NA	0.946	6.88E-01
MSMEG_5593	pyruvate dehydrogenase	NA	0.909	3.14E-01
MSMEG_5594	ferredoxin-dependent glutamate synthase	NA	0.933	1.44E-01
MSMEG_5595	MarR-family protein transcriptional regulator	NA	1.085	3.73E-01
MSMEG_5596	oxidoreductase	NA	1.484	3.49E-01
MSMEG_5597	transcriptional regulator, TetR family protein	NA	1.441	1.56E-01
MSMEG_5599	hypothetical protein	NA	2.482	3.40E-01
MSMEG_5600	conserved hypothetical protein	NA	1.128	2.82E-01
MSMEG_5601	hypothetical protein	NA	1.179	1.32E-02
MSMEG_5602	conserved hypothetical protein	NA	1.118	7.09E-02
MSMEG_5603	transcriptional regulator, ArsR family protein	NA	1.306	5.14E-01
MSMEG_5604	integral membrane protein	NA	0.982	9.29E-01
MSMEG_5605	cytochrome bd ubiquinol oxidase, subunit I	NA	1.495	4.11E-01
MSMEG_5606	cytochrome bd-I oxidase subunit II	NA	1.890	3.60E-01

MSMEG_5607	hypothetical protein	NA	1.211	3.85E-01
MSMEG_5608	acetyl-CoA acetyltransferase	NA	0.755	7.32E-03
MSMEG_5609	carotenoid oxygenase	NA	1.237	1.58E-01
MSMEG_5610	putative transcriptional regulator family protein	NA	1.303	2.55E-01
MSMEG_5611	spore protein	NA	1.529	2.45E-02
MSMEG_5612	amino-acid acetyltransferase	NA	1.485	1.80E-02
MSMEG_5613	probable conserved transmembrane protein	NA	1.345	1.06E-02
MSMEG_5614	conserved hypothetical protein	NA	13.013	3.82E-01
MSMEG_5615	conserved hypothetical protein	NA	1.293	3.38E-02
MSMEG_5616	glyoxalase/bleomycin resistance protein/dioxygenase	NA	1.306	3.67E-01
MSMEG_5617	immunogenic protein MPT63	NA	1.203	5.44E-01
MSMEG_5618	acyl-CoA dehydrogenase	NA	1.171	3.69E-01
MSMEG_5619	acyl-CoA dehydrogenase domain protein	NA	1.110	4.36E-01
MSMEG_5620	enoyl-CoA hydratase	NA	0.985	9.05E-01
MSMEG_5621	putative acyl-CoA dehydrogenase	NA	0.874	1.79E-01
MSMEG_5622	putative acyl-CoA dehydrogenase	NA	0.934	4.85E-01
MSMEG_5623	L-carnitine dehydratase/bile acid-inducible protein F	NA	1.066	5.57E-01
MSMEG_5624	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.949	6.97E-01
MSMEG_5625	cyclododecanone monooxygenase	NA	1.172	6.17E-01
MSMEG_5626	luciferase	NA	1.058	2.08E-01
MSMEG_5627	Rieske [2Fe-2S] domain protein	NA	0.912	3.27E-01
MSMEG_5628	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.145	4.79E-01
MSMEG_5629	conserved hypothetical protein	NA	0.790	2.09E-02
MSMEG_5630	transcriptional regulator, GntR family protein	NA	1.016	6.79E-01
MSMEG_5631	AMP-dependent synthetase and ligase	NA	1.014	9.32E-01
MSMEG_5632	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.823	3.09E-01
MSMEG_5633	feruloyl-CoA synthetase	NA	0.940	6.19E-01
MSMEG_5634	conserved hypothetical protein	NA	0.826	5.67E-02
MSMEG_5635	conserved hypothetical protein	NA	0.933	6.11E-01
MSMEG_5636	P-type ATPase - metal cation transport	NA	1.107	2.27E-01
MSMEG_5637	penicillin-binding protein 4	NA	1.108	6.56E-02

MSMEG_5638	metallo-beta-lactamase family protein	NA	0.876	2.18E-01
MSMEG_5639	enoyl-CoA hydratase	NA	0.968	7.33E-01
MSMEG_5640	amylo-alpha-1,6-glucosidase	NA	1.225	1.92E-01
MSMEG_5641	glycosyl transferase, group 1 family protein	NA	0.868	2.70E-02
MSMEG_5642	acetyl-coenzyme a carboxylase carboxyl transferase	NA	1.132	2.41E-01
MSMEG_5643	conserved hypothetical protein	NA	1.697	3.74E-01
MSMEG_5644	membrane protein	NA	1.082	4.78E-01
MSMEG_5645	conserved hypothetical protein	NA	1.112	3.61E-01
MSMEG_5646	conserved hypothetical protein	NA	1.571	4.47E-02
MSMEG_5647	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.298	1.45E-01
MSMEG_5648	hypothetical protein	NA	1.004	9.74E-01
MSMEG_5649	acyl-CoA synthase	NA	0.736	9.25E-02
MSMEG_5650	AMP-dependent synthetase and ligase	NA	2.212	4.20E-01
MSMEG_5651	transcriptional regulator, LuxR family protein	NA	0.662	1.62E-02
MSMEG_5652	alpha/beta hydrolase fold	NA	1.329	4.56E-01
MSMEG_5653	cytosine/purine/uracil/thiamine/allantoin permease family protein	NA	1.404	3.34E-01
MSMEG_5654	transcriptional regulator, LysR family protein	NA	1.099	1.68E-01
MSMEG_5655	hydrolase, carbon-nitrogen family protein	NA	1.443	2.21E-01
MSMEG_5656	histidinol dehydrogenase	hisD	0.956	3.02E-01
MSMEG_5657	transcriptional regulator, LysR family protein	NA	1.159	6.86E-02
MSMEG_5658	epoxide hydrolase	NA	1.013	7.85E-01
MSMEG_5659	ABC transporter, ATP-binding protein	NA	1.566	2.22E-02
MSMEG_5660	ABC transporter ATP-binding protein	NA	1.495	1.51E-02
MSMEG_5661	ABC transporter ATP-binding protein	NA	1.111	4.21E-01
MSMEG_5662	DNA-binding response regulator PrrA	prrA	1.195	8.58E-02
MSMEG_5663	sensor-type histidine kinase PrrB	NA	1.084	5.89E-01
MSMEG_5664	binding protein	NA	0.912	1.36E-01
MSMEG_5665	hypothetical protein	NA	1.041	7.57E-01
MSMEG_5666	conserved hypothetical protein	NA	1.063	4.12E-01
MSMEG_5667	phytoene dehydrogenase	NA	1.285	7.07E-02
MSMEG_5668	putative transcriptional regulator	NA	6.087	3.67E-01

MSMEG_5670	efflux membrane protein	NA	1.660	7.90E-02
MSMEG_5671	YbaK/prolyl-tRNA synthetase associated region	NA	1.781	7.08E-02
MSMEG_5672	citrate synthase I	gltA	1.198	1.49E-01
MSMEG_5673	transcriptional regulator	NA	1.215	4.13E-01
MSMEG_5674	membrane transport protein	NA	0.942	6.42E-01
MSMEG_5675	pyridoxamine 5'-phosphate oxidase	pdxH	0.842	8.59E-02
MSMEG_5676	citrate synthase	NA	1.021	4.32E-01
MSMEG_5677	conserved hypothetical protein	NA	1.057	5.67E-01
MSMEG_5678	glyoxalase/bleomycin resistance protein/dioxygenase	NA	0.832	3.89E-03
MSMEG_5679	putative DNA-binding protein	NA	0.926	5.26E-01
MSMEG_5680	glyoxalase family protein	NA	0.901	2.05E-01
MSMEG_5681	probable ferredoxin/ferredoxin--NADP reductase	NA	0.821	6.29E-02
MSMEG_5682	conserved hypothetical protein	NA	0.741	1.83E-02
MSMEG_5683	methionine aminopeptidase, type I	map	0.896	4.75E-01
MSMEG_5684	phosphoserine aminotransferase, putative	NA	1.097	1.77E-01
MSMEG_5685	DNA-binding protein	NA	1.115	1.91E-01
MSMEG_5686	conserved hypothetical protein	NA	1.269	1.99E-02
MSMEG_5687	23s ribosomal RNA methyltransferase	NA	1.315	5.00E-02
MSMEG_5688	regulatory protein, MarR	NA	1.833	2.05E-04
MSMEG_5689	conserved hypothetical protein	NA	1.190	5.98E-02
MSMEG_5690	conserved hypothetical protein	NA	1.105	1.70E-01
MSMEG_5691	conserved hypothetical protein	NA	1.109	3.23E-01
MSMEG_5692	conserved hypothetical protein	NA	1.167	2.56E-01
MSMEG_5693	transporter, major facilitator family protein	NA	1.225	4.15E-02
MSMEG_5694	conserved hypothetical protein	NA	1.015	6.46E-01
MSMEG_5695	glutathione S-transferase	NA	1.496	2.49E-02
MSMEG_5696	'Cold-shock' DNA-binding domain protein	NA	1.211	4.03E-02
MSMEG_5697	integral membrane protein	NA	0.860	1.26E-02
MSMEG_5698	molybdenum cofactor biosynthesis protein A	moaA	0.905	7.06E-02
MSMEG_5699	ThiS family protein	NA	0.977	7.68E-01
MSMEG_5700	secreted protein	NA	0.834	1.49E-02

MSMEG_5701	molybdopterin converting factor, subunit 2	moaE	1.090	4.26E-01
MSMEG_5702	molybdenum cofactor synthesis domain protein	NA	0.844	2.04E-02
MSMEG_5703	molybdenum cofactor biosynthesis protein C	moaC	0.828	4.69E-03
MSMEG_5704	conserved hypothetical protein	NA	0.706	2.70E-03
MSMEG_5705	conserved hypothetical protein	NA	1.319	1.21E-01
MSMEG_5706	DNA or RNA helicase of superfamily protein II	NA	1.041	1.51E-01
MSMEG_5707	cupin domain protein	NA	1.105	6.86E-03
MSMEG_5708	hypothetical protein	NA	0.941	2.53E-01
MSMEG_5709	conserved hypothetical protein	NA	0.928	2.76E-01
MSMEG_5710	hypothetical protein	NA	0.917	4.04E-01
MSMEG_5711	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.852	4.36E-01
MSMEG_5712	LysR-family protein transcriptional regulator	NA	1.039	6.97E-01
MSMEG_5713	major facilitator family protein transporter	NA	1.108	9.44E-02
MSMEG_5714	short-chain dehydrogenase/reductase SDR	NA	0.941	5.19E-01
MSMEG_5715	conserved hypothetical protein	NA	0.939	4.37E-01
MSMEG_5716	hypothetical protein	NA	0.991	9.66E-01
MSMEG_5717	pyridoxamine 5'-phosphate oxidase family protein	NA	0.843	1.53E-02
MSMEG_5718	transcriptional regulator, TetR family protein	NA	1.047	5.94E-01
MSMEG_5719	oxidoreductase	NA	1.398	3.29E-01
MSMEG_5720	putative 3-hydroxyacyl-CoA dehydrogenase	NA	0.832	3.41E-02
MSMEG_5721	acetyl-CoA acetyltransferase	NA	0.752	2.38E-03
MSMEG_5722	conserved hypothetical protein	NA	1.544	3.20E-01
MSMEG_5723	endoribonuclease L-psp family protein	NA	1.218	4.61E-02
MSMEG_5724	bacterial regulatory protein, MarR family protein	NA	1.013	8.99E-01
MSMEG_5725	PLP-dependent aminotransferases	NA	1.141	1.61E-01
MSMEG_5726	conserved hypothetical protein	NA	1.018	8.70E-01
MSMEG_5727	allantoicase	alc	0.993	9.40E-01
MSMEG_5728	polysaccharide deacetylase family protein	NA	1.096	3.31E-01
MSMEG_5729	hydantoin racemase	NA	1.114	8.27E-02
MSMEG_5730	permease for cytosine/purines, uracil, thiamine, allantoin transporter	NA	1.145	4.64E-01
MSMEG_5731	transcriptional regulator, GntR family protein	NA	2.162	2.03E-03

MSMEG_5732	monooxygenase	NA	2.148	1.61E-02
MSMEG_5733	universal stress protein family protein	NA	1.225	1.80E-01
MSMEG_5734	alpha-methylacyl-CoA racemase	NA	1.075	4.97E-01
MSMEG_5735	indole-3-pyruvate decarboxylase	NA	1.138	4.19E-01
MSMEG_5736	cyclase/dehydrase	NA	1.028	7.32E-01
MSMEG_5737	hypothetical protein	NA	1.057	7.98E-01
MSMEG_5738	conserved hypothetical protein	NA	1.165	2.30E-01
MSMEG_5739	putative long-chain fatty-acid--CoA ligase	NA	3.212	1.86E-01
MSMEG_5740	hypothetical protein	NA	1.174	8.11E-02
MSMEG_5741	conserved hypothetical protein	NA	1.294	8.97E-02
MSMEG_5742	acyltransferase domain protein	NA	1.084	7.05E-01
MSMEG_5743	patatin	NA	1.186	9.62E-02
MSMEG_5744	gas vesicle protein K	gvpK	1.346	2.89E-01
MSMEG_5745	gas vesicle synthesis protein	NA	0.989	9.01E-01
MSMEG_5746	gas vesicle protein	NA	0.931	2.63E-01
MSMEG_5747	hypothetical protein	NA	1.012	8.66E-01
MSMEG_5748	hypothetical protein	NA	0.955	2.44E-01
MSMEG_5749	hypothetical protein	NA	0.856	4.19E-02
MSMEG_5750	hypothetical protein	NA	1.063	3.32E-02
MSMEG_5751	putative adhesin/hemolysin	NA	1.023	7.33E-01
MSMEG_5752	conserved hypothetical protein	NA	1.321	5.97E-01
MSMEG_5753	serine/threonine specific protein phosphatase	NA	1.730	5.80E-03
MSMEG_5754	gp41 protein	NA	1.133	4.02E-01
MSMEG_5759	pe family protein	NA	1.038	7.82E-01
MSMEG_5760	GntR-family protein regulator	NA	2.393	3.88E-01
MSMEG_5761	cupin domain protein	NA	1.190	3.09E-01
MSMEG_5762	zinc-binding oxidoreductase	NA	1.369	3.41E-01
MSMEG_5763	conserved hypothetical protein	NA	1.297	3.36E-01
MSMEG_5764	putative cyanamide hydratase	NA	0.974	5.07E-01
MSMEG_5765	globin	NA	1.129	5.60E-01
MSMEG_5766	conserved hypothetical protein	NA	0.933	3.44E-01

MSMEG_5767	conserved hypothetical protein	NA	1.095	1.32E-01
MSMEG_5768	conserved hypothetical protein	NA	1.041	5.13E-01
MSMEG_5769	hypothetical protein	NA	1.317	2.28E-03
MSMEG_5770	hypothetical protein	NA	1.226	4.52E-02
MSMEG_5771	hypothetical protein	NA	1.198	1.16E-02
MSMEG_5772	cytospin-A, putative	NA	1.513	2.05E-02
MSMEG_5773	fatty acid desaturase	NA	1.281	1.11E-01
MSMEG_5774	tRNA-dihydrouridine synthase, putative	NA	1.195	1.21E-01
MSMEG_5775	LytR/CpsA/Psr family protein	NA	1.164	9.24E-03
MSMEG_5776	phosphate transport system regulatory protein PhoU	phoU	1.147	7.09E-02
MSMEG_5777	transcription regulator	NA	1.275	1.12E-01
MSMEG_5778	alcohol dehydrogenase, zinc-binding	NA	1.513	7.39E-02
MSMEG_5779	phosphate ABC transporter, ATP-binding protein	pstB	1.329	2.87E-02
MSMEG_5780	phosphate ABC transporter, permease protein PstA	pstA	1.413	5.49E-02
MSMEG_5781	phosphate ABC transporter, permease protein PstC	pstC	1.714	1.11E-03
MSMEG_5782	phosphate ABC transporter, phosphate-binding protein PstS	pstS	1.850	8.41E-04
MSMEG_5783	acetyltransferase, GNAT family; this gene contains a frame shift which is not the result	NA	0.995	9.08E-01
MSMEG_5784	transcriptional regulatory protein	NA	0.902	7.42E-04
MSMEG_5785	probable exported protein	NA	1.029	6.26E-01
MSMEG_5786	thiredoxin	NA	1.195	3.71E-02
MSMEG_5787	hypothetical protein	NA	2.469	3.39E-01
MSMEG_5788	integral membrane protein	NA	0.978	7.90E-01
MSMEG_5789	putative thiosulfate sulfurtransferase	NA	1.016	8.34E-01
MSMEG_5790	SseC protein	NA	1.349	1.47E-01
MSMEG_5791	conserved hypothetical protein	NA	1.073	3.86E-01
MSMEG_5792	conserved hypothetical protein	NA	1.061	4.69E-01
MSMEG_5793	hypothetical protein	NA	0.910	2.37E-01
MSMEG_5794	hypothetical protein	NA	0.718	6.62E-02
MSMEG_5795	4-amino-4-deoxychorismate lyase	NA	1.052	3.30E-01
MSMEG_5796	Glycine cleavage T-protein (aminomethyl transferase)	NA	1.233	4.02E-02
MSMEG_5797	conserved hypothetical protein	NA	1.593	1.16E-01

MSMEG_5798	phosphoribosylformylglycinamidine cyclo-ligase	purM	1.004	8.96E-01
MSMEG_5799	nucleoside-diphosphate-sugar epimerase	NA	1.136	5.70E-01
MSMEG_5800	amidophosphoribosyltransferase	purF	0.999	9.78E-01
MSMEG_5801	hydroxylase	NA	0.942	5.57E-01
MSMEG_5802	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	1.134	2.62E-01
MSMEG_5803	hypothetical protein	NA	1.078	3.12E-01
MSMEG_5804	conserved hypothetical protein	NA	0.954	5.38E-01
MSMEG_5805	hypothetical protein	NA	0.942	3.69E-01
MSMEG_5806	hypothetical protein	NA	1.015	9.29E-01
MSMEG_5807	D-methionine transport ATP-binding protein MetN	NA	1.372	1.55E-01
MSMEG_5808	binding-protein-dependent transport systems inner membrane component	NA	1.127	3.31E-01
MSMEG_5809	lipoprotein YaeC, putative	NA	0.988	9.35E-01
MSMEG_5810	putative monooxygenase	NA	1.033	7.90E-01
MSMEG_5811	transcriptional regulator, TetR family protein	NA	1.056	3.75E-01
MSMEG_5812	carveol dehydrogenase	NA	1.250	2.66E-01
MSMEG_5813	carveol dehydrogenase	NA	0.981	9.59E-01
MSMEG_5814	4-carboxymuconolactone decarboxylase domain protein	pcaC	0.713	1.32E-01
MSMEG_5815	betaine aldehyde dehydrogenase	NA	2.110	4.29E-01
MSMEG_5816	conserved hypothetical protein	NA	1.344	1.90E-02
MSMEG_5817	conserved hypothetical protein	NA	1.081	3.17E-01
MSMEG_5818	virulence factor Mce family protein	NA	1.366	2.56E-01
MSMEG_5819	pyridoxamine 5'-phosphate oxidase family protein	NA	0.953	4.88E-01
MSMEG_5820	hypothetical protein	NA	1.182	1.75E-01
MSMEG_5821	caax amino protease family protein	NA	1.673	2.51E-01
MSMEG_5822	conserved hypothetical protein	NA	0.851	2.00E-01
MSMEG_5823	conserved membrane-spanning protein	NA	1.130	3.77E-01
MSMEG_5824	phosphoribosylformylglycinamidine synthase II	purL	1.027	5.32E-01
MSMEG_5825	Na+/H+ antiporter	NA	1.284	1.93E-01
MSMEG_5826	pyruvate decarboxylase	NA	0.897	3.61E-01
MSMEG_5827	glyoxalase family protein	NA	1.035	6.28E-01
MSMEG_5828	aspartyl aminopeptidase	NA	1.106	2.80E-01

MSMEG_5829	Dyp-type peroxidase	NA	0.920	2.49E-02
MSMEG_5830	29 kda antigen Cfp29	NA	0.843	3.57E-02
MSMEG_5831	phosphoribosylformylglycinamidine synthase I	purQ	0.947	4.78E-01
MSMEG_5832	phosphoribosylformylglycinamidine synthase, PurS protein	purS	1.009	8.43E-01
MSMEG_5833	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	1.503	5.84E-02
MSMEG_5834	metallo-beta-lactamase superfamily protein	NA	1.006	8.61E-01
MSMEG_5835	fumarate reductase/succinate dehydrogenase flavoprotein	NA	1.039	7.40E-01
MSMEG_5836	conserved hypothetical protein	NA	1.312	1.13E-01
MSMEG_5837	glutathione peroxidase family protein	NA	0.890	6.49E-03
MSMEG_5838	TetR-family protein transcriptional regulator	NA	1.045	2.97E-01
MSMEG_5839	protease 2	NA	0.989	8.16E-01
MSMEG_5840	conserved hypothetical protein	NA	0.998	9.67E-01
MSMEG_5841	phosphoribosylaminoimidazole-succinocarboxamide synthase	purC	1.032	7.01E-01
MSMEG_5842	conserved hypothetical protein	NA	0.858	2.51E-01
MSMEG_5843	conserved hypothetical protein	NA	1.032	3.72E-01
MSMEG_5844	conserved hypothetical protein	NA	1.058	8.40E-01
MSMEG_5845	putative C4-dicarboxylate transporter	NA	1.050	7.11E-01
MSMEG_5846	NikQ protein	NA	1.232	2.01E-01
MSMEG_5847	adenylosuccinate lyase	purB	1.127	2.67E-01
MSMEG_5848	amino acid permease-associated region	NA	1.001	9.81E-01
MSMEG_5849	conserved hypothetical protein	NA	1.111	8.42E-02
MSMEG_5850	transcriptional regulator, TetR family protein	NA	0.997	9.79E-01
MSMEG_5851	putative esterase superfamily protein	NA	1.444	3.55E-01
MSMEG_5852	phosphoribosylamine--glycine ligase	purD	1.012	8.67E-01
MSMEG_5853	cytochrome P450	NA	0.905	5.41E-01
MSMEG_5854	transcriptional regulator, TetR family protein	NA	0.950	1.19E-01
MSMEG_5855	conserved hypothetical protein	NA	1.249	4.21E-01
MSMEG_5856	4-carboxymuconolactone decarboxylase domain protein	pcaC	0.670	1.09E-03
MSMEG_5857	hypothetical oxidoreductase	NA	0.794	9.12E-02
MSMEG_5858	3-oxoacyl-[acyl-carrier-protein] reductase	NA	1.000	9.99E-01
MSMEG_5859	aldehyde dehydrogenase (NAD) family protein	NA	0.840	3.48E-01

MSMEG_5860	transcriptional regulator, TetR family protein	NA	1.013	8.43E-01
MSMEG_5861	cytochrome P450 109	NA	0.903	5.28E-01
MSMEG_5862	short chain dehydrogenase	NA	0.926	4.01E-01
MSMEG_5863	cytochrome P450 51	NA	0.849	4.62E-02
MSMEG_5864	cytochrome P450 51	NA	0.804	6.17E-02
MSMEG_5865	conserved hypothetical protein	NA	1.008	9.27E-01
MSMEG_5866	alcohol dehydrogenase B	NA	0.634	4.29E-02
MSMEG_5867	nuclear transport factor 2 (NTF2) domain superfamily protein	NA	0.937	3.32E-01
MSMEG_5868	hypothetical protein	NA	1.134	2.68E-01
MSMEG_5869	putative short chain dehydrogenase	NA	0.896	5.95E-01
MSMEG_5870	sensor histidine kinase PhoR	NA	1.160	4.84E-01
MSMEG_5871	HIT family protein	NA	1.053	1.27E-01
MSMEG_5872	DNA-binding response regulator PhoP	phoP	0.872	2.32E-01
MSMEG_5873	conserved hypothetical protein	NA	1.172	6.89E-02
MSMEG_5875	hypothetical protein	NA	0.951	3.61E-01
MSMEG_5876	H-N-H endonuclease F-TflIV	NA	1.168	1.16E-01
MSMEG_5877	conserved hypothetical protein	NA	0.953	6.43E-01
MSMEG_5878	serine esterase, cutinase family protein	NA	0.861	2.37E-01
MSMEG_5879	D-alanyl-D-alanine dipeptidase	NA	0.892	1.34E-01
MSMEG_5880	nicotine dehydrogenase	NA	1.226	3.98E-01
MSMEG_5881	putative carbon monoxide dehydrogenase subunit G	NA	0.788	1.57E-01
MSMEG_5882	carbon monoxide dehydrogenase medium chain	NA	0.970	7.50E-01
MSMEG_5883	[2Fe-2S] binding domain protein	NA	1.171	6.25E-01
MSMEG_5884	3-hydroxyisobutyrate dehydrogenase family protein	NA	1.987	3.55E-01
MSMEG_5885	short chain dehydrogenase	NA	0.876	8.42E-03
MSMEG_5886	enoyl-CoA hydratase	NA	0.889	2.48E-01
MSMEG_5887	intersectin-EH binding protein Ibp1	NA	1.007	9.44E-01
MSMEG_5888	conserved hypothetical protein	NA	1.141	2.83E-01
MSMEG_5889	conserved hypothetical protein	NA	0.927	1.75E-03
MSMEG_5890	conserved hypothetical protein	NA	0.993	9.20E-01
MSMEG_5892	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	NA	1.141	2.70E-01

MSMEG_5893	conserved hypothetical protein	NA	0.818	1.52E-02
MSMEG_5894	conserved hypothetical protein	NA	0.734	2.52E-04
MSMEG_5895	virulence factor mce family protein	NA	0.703	8.92E-04
MSMEG_5896	virulence factor Mce family protein	NA	0.817	2.39E-03
MSMEG_5897	virulence factor mce family protein	NA	0.751	6.80E-03
MSMEG_5898	virulence factor Mce family protein	NA	0.927	1.96E-03
MSMEG_5899	virulence factor Mce family protein	NA	0.875	7.08E-02
MSMEG_5900	virulence factor Mce family protein	NA	0.800	2.36E-03
MSMEG_5901	TrnB2 protein	NA	0.883	4.51E-02
MSMEG_5902	conserved hypothetical protein	NA	0.892	6.52E-02
MSMEG_5903	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.936	2.94E-01
MSMEG_5904	conserved domain protein	NA	0.827	1.58E-01
MSMEG_5905	hypothetical protein	NA	1.005	9.83E-01
MSMEG_5906	putative acyl-CoA dehydrogenase	NA	1.091	6.02E-01
MSMEG_5907	acyl-CoA dehydrogenase	NA	1.093	4.96E-01
MSMEG_5908	acyl-CoA synthase	NA	1.199	3.57E-01
MSMEG_5909	oxidoreductase	NA	0.771	2.30E-01
MSMEG_5910	quinone binding protein	NA	1.014	8.29E-01
MSMEG_5911	AraC family protein transcriptional regulator	NA	1.087	4.87E-01
MSMEG_5912	succinic semialdehyde dehydrogenase	NA	0.791	5.92E-02
MSMEG_5913	dioxygenase	NA	1.276	3.86E-01
MSMEG_5914	acyl-CoA synthase	NA	1.118	6.34E-01
MSMEG_5915	enoyl-CoA hydratase	NA	1.071	3.86E-01
MSMEG_5916	hypothetical protein	NA	1.014	9.24E-01
MSMEG_5917	conserved hypothetical protein	NA	0.812	2.26E-01
MSMEG_5918	P450 heme-thiolate protein	NA	1.487	3.64E-01
MSMEG_5919	conserved hypothetical protein	NA	1.295	4.09E-01
MSMEG_5920	FMN-dependent monooxygenase	NA	0.921	4.62E-02
MSMEG_5921	conserved hypothetical protein	NA	1.007	9.70E-01
MSMEG_5922	lipid-transfer protein	NA	0.954	8.08E-01
MSMEG_5923	acetyl-CoA acetyltransferase	NA	1.054	6.54E-01

MSMEG_5924	conserved hypothetical protein	NA	0.860	1.05E-01
MSMEG_5925	Rieske [2Fe-2S] domain protein	NA	0.930	3.51E-01
MSMEG_5926	putative secreted protein	NA	1.398	1.30E-01
MSMEG_5927	conserved hypothetical protein	NA	1.141	2.87E-01
MSMEG_5928	conserved hypothetical protein	NA	1.530	4.74E-02
MSMEG_5929	conserved hypothetical protein	NA	1.206	6.75E-02
MSMEG_5930	conserved hypothetical protein	NA	0.906	2.18E-01
MSMEG_5931	short chain dehydrogenase	NA	0.989	9.37E-01
MSMEG_5932	conserved hypothetical protein	NA	1.000	1.00E+00
MSMEG_5933	conserved hypothetical protein	NA	1.319	1.35E-02
MSMEG_5934	conserved hypothetical protein	NA	1.261	5.19E-01
MSMEG_5935	ATP-dependent DNA helicase	NA	1.165	3.36E-01
MSMEG_5936	conserved hypothetical protein	NA	1.035	4.38E-01
MSMEG_5937	4-hydroxy-2-oxovalerate aldolase	NA	0.840	3.03E-02
MSMEG_5938	hypothetical protein	NA	1.005	8.40E-01
MSMEG_5939	acetaldehyde dehydrogenase	NA	0.805	4.38E-03
MSMEG_5940	2-keto-4-pentenoate hydratase	NA	0.890	9.01E-02
MSMEG_5941	3-ketosteroid dehydrogenase	NA	1.132	4.69E-02
MSMEG_5942	AMP-dependent synthetase and ligase	NA	0.968	7.72E-01
MSMEG_5943	putative peroxisomal multifunctional enzyme type 2	NA	1.036	5.82E-01
MSMEG_5944	glucose-methanol-choline oxidoreductase	NA	1.533	1.96E-01
MSMEG_5945	conserved hypothetical protein	NA	1.185	6.13E-01
MSMEG_5946	hypothetical protein	NA	0.978	9.28E-01
MSMEG_5947	serine O-acetyltransferase	cysE	0.914	2.32E-01
MSMEG_5948	glycosyl transferase	NA	1.008	9.56E-01
MSMEG_5949	conserved hypothetical protein	NA	0.938	5.09E-01
MSMEG_5950	putative colanic acid biosynthesis acetyltransferase WcaF	NA	0.995	9.80E-01
MSMEG_5951	glycosyl transferase, group 1, putative	NA	1.045	6.09E-01
MSMEG_5952	conserved hypothetical protein, putative	NA	0.832	1.42E-01
MSMEG_5953	hypothetical protein	NA	1.344	3.87E-01
MSMEG_5954	cell surface polysaccharide biosynthesis, putative	NA	1.053	3.14E-01

MSMEG_5955	protein-tyrosine kinase, putative	NA	1.033	7.48E-01
MSMEG_5956	NAD dependent epimerase/dehydratase family protein	NA	1.032	8.66E-01
MSMEG_5957	GDP-mannose 6-dehydrogenase AlgD	algD	1.018	5.49E-01
MSMEG_5958	hypothetical protein	NA	1.000	9.97E-01
MSMEG_5959	conserved hypothetical protein	NA	0.748	8.51E-02
MSMEG_5960	O-antigen polymerase, putative	NA	1.078	5.55E-01
MSMEG_5961	glycosyl transferase, group 2 family protein, putative	NA	0.959	7.89E-01
MSMEG_5962	glycosyl transferase, family protein 2	NA	0.935	5.39E-01
MSMEG_5963	glycosyl transferase, family protein 2	NA	0.904	3.40E-01
MSMEG_5964	glycosyl transferase, group 1, putative	NA	1.184	4.66E-01
MSMEG_5965	hypothetical protein	NA	0.808	1.40E-01
MSMEG_5966	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.890	7.27E-02
MSMEG_5967	glucose-methanol-choline oxidoreductase	NA	0.994	9.34E-01
MSMEG_5968	polysaccharide biosynthesis protein	NA	0.836	6.12E-02
MSMEG_5969	conserved hypothetical protein	NA	1.106	2.93E-01
MSMEG_5970	probable glutamate-1-semialdehyde 2,1-aminomutase	NA	1.034	8.51E-01
MSMEG_5971	conserved hypothetical protein	NA	2.817	3.59E-01
MSMEG_5972	hypothetical protein	NA	1.019	8.27E-01
MSMEG_5973	hypothetical protein	NA	0.934	5.77E-01
MSMEG_5974	hypothetical protein	NA	1.759	3.52E-01
MSMEG_5975	methyltransferase type 12, putative	NA	0.773	1.41E-01
MSMEG_5976	epimerase/dehydratase	NA	0.933	4.21E-01
MSMEG_5977	dTDP-4-dehydrorhamnose 3,5-epimerase	rfbC	1.402	3.72E-01
MSMEG_5978	GlcNAc-PI de-N-acetylase family protein	NA	0.673	5.04E-03
MSMEG_5979	transferase	NA	0.717	7.19E-03
MSMEG_5980	methyltransferase	NA	1.032	7.58E-01
MSMEG_5981	glycosyl transferase, putative	NA	1.304	4.44E-01
MSMEG_5982	UDP-glucose 6-dehydrogenase	NA	1.200	7.41E-02
MSMEG_5983	glucose-1-phosphate thymidylyltransferase	rfbA	1.165	2.44E-01
MSMEG_5984	undecaprenyl-phosphate galactosephosphotransferase	NA	1.260	2.27E-01
MSMEG_5985	NAD dependent epimerase/dehydratase family protein	NA	0.900	4.80E-01

MSMEG_5986	glucosamine--fructose-6-phosphate aminotransferase, isomerizing	glmS	1.539	1.23E-01
MSMEG_5987	two-component regulator	NA	1.007	8.90E-01
MSMEG_5988	hypothetical protein	NA	0.989	6.14E-01
MSMEG_5989	hypothetical protein	NA	1.087	1.01E-01
MSMEG_5990	lipid-transfer protein	NA	2.880	3.73E-01
MSMEG_5991	MaoC like domain, putative	NA	1.391	4.98E-01
MSMEG_5992	conserved hypothetical protein	NA	1.942	3.94E-01
MSMEG_5993	putative acyl-CoA dehydrogenase	NA	0.825	3.14E-01
MSMEG_5994	putative acyl-CoA dehydrogenase	NA	0.909	4.57E-01
MSMEG_5995	P450 heme-thiolate protein	NA	1.057	7.15E-01
MSMEG_5996	acetyl-CoA acetyltransferase	NA	1.081	7.35E-02
MSMEG_5997	conserved hypothetical protein	NA	1.216	4.88E-01
MSMEG_5998	conserved hypothetical protein	NA	1.049	6.03E-01
MSMEG_5999	short chain dehydrogenase	NA	0.934	4.75E-01
MSMEG_6000	short chain dehydrogenase	NA	1.243	2.28E-01
MSMEG_6001	enoyl-CoA hydratase	NA	0.895	1.93E-01
MSMEG_6002	coenzyme A transferase, subunit A	NA	1.032	7.45E-01
MSMEG_6003	coenzyme A transferase, subunit B	NA	0.995	9.59E-01
MSMEG_6004	oxidoreductase, 2-nitropropane dioxygenase family protein	NA	0.962	7.25E-01
MSMEG_6005	conserved hypothetical protein	NA	1.364	2.71E-01
MSMEG_6006	conserved hypothetical protein	NA	1.127	3.20E-02
MSMEG_6007	cation diffusion facilitator family transporter; this gene contains a frame shift which is	NA	0.871	3.82E-01
MSMEG_6007	cation diffusion facilitator family transporter; this gene contains a frame shift which is	NA	1.308	1.96E-01
MSMEG_6008	acetyl-CoA acetyltransferase	NA	0.960	3.19E-01
MSMEG_6009	transcriptional regulator, TetR family protein	NA	1.052	4.31E-01
MSMEG_6010	hypothetical protein	NA	1.703	2.27E-01
MSMEG_6011	short chain dehydrogenase	NA	1.328	5.12E-02
MSMEG_6012	putative acyl-CoA dehydrogenase	NA	1.220	1.29E-01
MSMEG_6013	probable fatty-acid-coa ligase fadd3 (fatty-acid-coa synthetase); this gene contains a fr	fadD	1.116	6.33E-01
MSMEG_6013	probable fatty-acid-coa ligase fadd3 (fatty-acid-coa synthetase); this gene contains a fr	fadD	1.368	1.76E-01
MSMEG_6014	putative acyl-CoA dehydrogenase	NA	1.066	7.49E-01

MSMEG_6015	putative acyl-CoA dehydrogenase	NA	0.946	6.25E-01
MSMEG_6016	putative acyl-CoA dehydrogenase	NA	0.915	3.89E-01
MSMEG_6017	aminotransferase, class I	NA	0.965	7.64E-01
MSMEG_6018	xylose transport system permease protein XylH	NA	0.627	2.39E-02
MSMEG_6019	ABC-type sugar transport system ATPase component	NA	1.202	7.50E-01
MSMEG_6020	D-xylose-binding periplasmic protein	NA	0.905	5.15E-01
MSMEG_6021	xylose isomerase	xylA	0.608	2.57E-02
MSMEG_6022	xylose repressor, ROK-family protein transcriptional regulator	NA	1.084	3.13E-01
MSMEG_6023	transposase	NA	1.147	2.44E-01
MSMEG_6024	acetoacetyl-CoA synthase	NA	1.002	9.56E-01
MSMEG_6025	conserved hypothetical protein	NA	1.216	3.81E-01
MSMEG_6026	3-hydroxybutyrate dehydrogenase	NA	0.715	1.64E-02
MSMEG_6027	major facilitator superfamily protein MFS_1	NA	0.607	4.43E-02
MSMEG_6028	transcriptional regulator, LysR family protein	NA	1.050	5.72E-01
MSMEG_6029	conserved hypothetical protein	NA	0.769	2.97E-02
MSMEG_6030	cytochrome p450	NA	1.539	8.37E-03
MSMEG_6031	carveol dehydrogenase	NA	1.628	1.26E-01
MSMEG_6032	transcriptional regulator, TetR family protein	NA	1.070	1.95E-01
MSMEG_6033	hypothetical protein	NA	0.954	4.97E-01
MSMEG_6034	hypothetical protein	NA	0.985	7.64E-01
MSMEG_6035	nitrilotriacetate monooxygenase component B	NA	0.956	8.19E-01
MSMEG_6036	biphenyl-2,3-diol 1,2-dioxygenase	NA	0.979	8.91E-01
MSMEG_6037	2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase	NA	0.857	3.52E-02
MSMEG_6038	pigment production hydroxylase	NA	0.891	1.27E-01
MSMEG_6039	oxidoreductase, electron transfer component	NA	1.214	1.06E-01
MSMEG_6040	conserved hypothetical protein	NA	1.039	5.86E-01
MSMEG_6041	putative acyl-CoA dehydrogenase	NA	1.180	2.97E-01
MSMEG_6042	transcriptional regulator, TetR family protein	NA	1.383	4.09E-03
MSMEG_6043	trehalose-phosphatase	otsB	1.155	2.26E-01
MSMEG_6044	periplasmic binding proteins and sugar binding domain of the LacI family protein, puta	NA	1.196	2.13E-01
MSMEG_6045	ABC heavy metal transporter, inner membrane subunit	NA	1.110	1.30E-01

MSMEG_6046	cation ABC transporter, ATP-binding protein, putative	NA	1.134	5.06E-01
MSMEG_6047	cation ABC transporter, periplasmic cation-binding protein, putative	NA	1.101	1.16E-01
MSMEG_6048	cobalamin synthesis protein/P47K	NA	1.779	4.56E-01
MSMEG_6049	secreted protein	NA	0.891	9.78E-02
MSMEG_6050	solute-binding lipoprotein	NA	1.138	1.14E-01
MSMEG_6051	ABC transporter protein, integral membrane subunit; this gene contains a frame shift	NA	0.980	6.71E-01
MSMEG_6051	ABC transporter protein, integral membrane subunit; this gene contains a frame shift	NA	1.347	5.02E-03
MSMEG_6052	ABC transport protein, ATP-binding subunit	NA	1.199	3.05E-01
MSMEG_6053	cob(II)yrinic acid a,c-diamide reductase	bluB	0.929	4.49E-01
MSMEG_6054	LamB/YcsF	NA	0.950	2.01E-01
MSMEG_6055	hypothetical protein	NA	0.992	9.70E-01
MSMEG_6056	transposase; this gene contains a frame shift which is not the result of sequencing err	NA	0.993	8.79E-01
MSMEG_6056	transposase; this gene contains a frame shift which is not the result of sequencing err	NA	1.139	1.07E-01
MSMEG_6057	MspD protein	NA	0.689	2.96E-02
MSMEG_6058	cadmium transporting P-type ATPase	NA	0.937	1.80E-01
MSMEG_6059	conserved hypothetical protein	NA	1.087	3.94E-01
MSMEG_6060	permease	NA	1.065	3.75E-01
MSMEG_6061	conserved hypothetical protein	NA	0.992	8.64E-01
MSMEG_6062	Fe uptake system permease	NA	1.031	7.80E-01
MSMEG_6063	Fe uptake system integral membrane protein	NA	1.198	1.55E-01
MSMEG_6064	lipoprotein	NA	0.946	3.60E-01
MSMEG_6065	ribosomal protein S18	rpsR	1.149	1.15E-01
MSMEG_6066	30S ribosomal protein S14	NA	1.674	3.21E-01
MSMEG_6067	ribosomal protein L33	rpmG	1.717	2.43E-01
MSMEG_6068	ribosomal protein L28	rpmB	1.244	1.40E-01
MSMEG_6069	CobW/P47K C- domain protein	NA	1.548	1.72E-01
MSMEG_6070	ribosomal protein L31	rpmE	1.238	2.89E-01
MSMEG_6071	metallo-beta-lactamase superfamily protein	NA	1.029	6.25E-01
MSMEG_6072	Citrate transporter	NA	0.941	7.05E-01
MSMEG_6073	RNA methyltransferase, TrmH family protein, group 3	NA	1.153	8.81E-02
MSMEG_6074	cysteinyl-tRNA synthetase	cysS	1.051	3.96E-01

MSMEG_6075	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	ispF	0.844	6.60E-03
MSMEG_6076	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	ispD	0.798	1.99E-02
MSMEG_6077	transcriptional regulator, CarD family protein	NA	0.923	2.97E-01
MSMEG_6078	LpqE protein	NA	0.901	2.69E-02
MSMEG_6079	DNA repair protein RadA	radA	1.784	1.95E-01
MSMEG_6080	conserved hypothetical protein	NA	1.055	4.48E-01
MSMEG_6081	conserved hypothetical protein	NA	0.908	8.42E-02
MSMEG_6082	carbonic anhydrase	NA	0.916	9.15E-02
MSMEG_6083	base excision DNA repair protein, HhH-GPD family protein	NA	1.098	7.49E-01
MSMEG_6084	AraC-family transcriptional regulator; this gene contains a frame shift which is not the	NA	1.007	9.33E-01
MSMEG_6085	hydrolase, alpha/beta hydrolase fold family protein	NA	1.052	7.52E-01
MSMEG_6086	antibiotic biosynthesis monooxygenase domain protein	NA	0.950	1.70E-01
MSMEG_6087	beta-lactamase	NA	0.918	2.75E-03
MSMEG_6088	phosphoglycerate mutase	NA	1.242	1.88E-01
MSMEG_6089	conserved hypothetical protein	NA	1.054	6.56E-01
MSMEG_6090	conserved hypothetical protein	NA	0.909	1.39E-01
MSMEG_6091	negative regulator of genetic competence ClpC/mecB	NA	1.060	2.64E-01
MSMEG_6092	Lsr2 protein	NA	1.205	3.25E-01
MSMEG_6093	hypothetical protein	NA	2.118	3.57E-01
MSMEG_6094	lysyl-tRNA synthetase	lysS	1.137	4.34E-02
MSMEG_6095	D-amino acid deaminase	NA	1.527	3.70E-01
MSMEG_6096	Bvg accessory factor family protein	NA	1.016	7.96E-01
MSMEG_6097	pantoate--beta-alanine ligase	panC	0.996	9.31E-01
MSMEG_6098	chalcone/stilbene synthase family protein	NA	1.072	3.40E-01
MSMEG_6099	probable conserved transmembrane protein rich in alanine	NA	0.872	2.70E-03
MSMEG_6100	conserved hypothetical protein	NA	0.926	5.62E-01
MSMEG_6101	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	folK	0.939	3.84E-01
MSMEG_6102	dihydroneopterin aldolase	folB	1.011	8.86E-01
MSMEG_6103	dihydropteroate synthase	folP	1.046	6.19E-01
MSMEG_6104	GTP cyclohydrolase I	folE	0.986	4.68E-01
MSMEG_6105	cell division protein	NA	0.982	9.23E-01

MSMEG_6106	epoxide hydrolase	NA	0.657	5.49E-03
MSMEG_6107	limonene 1,2-monooxygenase	NA	0.678	2.70E-03
MSMEG_6108	zinc-binding dehydrogenase	NA	0.951	5.37E-01
MSMEG_6109	LpqG protein	NA	1.054	4.37E-01
MSMEG_6110	hypoxanthine phosphoribosyltransferase	hpt	1.137	2.18E-01
MSMEG_6111	tRNA(Ile)-lysidine synthetase	tilS	0.949	4.27E-01
MSMEG_6112	conserved hypothetical protein	NA	1.003	9.41E-01
MSMEG_6113	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase	dacB	1.007	8.92E-01
MSMEG_6114	inorganic pyrophosphatase	ppa	0.802	1.32E-02
MSMEG_6115	phosphoglycerate dehydrogenase	NA	1.309	4.30E-01
MSMEG_6116	conserved hypothetical protein	NA	1.111	1.76E-01
MSMEG_6117	glucarate dehydratase	NA	1.095	3.28E-01
MSMEG_6118	IclR-family protein transcriptional regulator	NA	0.859	1.02E-01
MSMEG_6119	conserved hypothetical protein	NA	0.961	6.15E-01
MSMEG_6120	peptide transport system ATP-binding protein	NA	1.301	4.53E-01
MSMEG_6121	dipeptide transport ATP-binding protein DppD	NA	0.986	9.36E-01
MSMEG_6122	ABC transporter, membrane spanning protein	NA	1.157	2.15E-01
MSMEG_6123	ABC transporter, membrane spanning protein	NA	0.958	4.07E-01
MSMEG_6124	putative ABC transporter periplasmic oligopeptide-binding protein	NA	1.061	5.77E-01
MSMEG_6125	transcriptional regulatory protein	NA	1.166	1.04E-01
MSMEG_6126	D-isomer specific 2-hydroxyacid dehydrogenase	NA	1.244	1.11E-01
MSMEG_6127	anti-anti-sigma factor	NA	0.940	4.02E-01
MSMEG_6128	two-component system response regulator	NA	0.853	1.91E-01
MSMEG_6129	conserved hypothetical protein	NA	0.800	1.01E-02
MSMEG_6130	two-component sensor protein	NA	0.811	8.04E-02
MSMEG_6131	magnesium or manganese-dependent protein phosphatase	NA	1.031	6.52E-01
MSMEG_6132	glucarate dehydratase	NA	0.904	6.65E-01
MSMEG_6133	5-dehydro-4-deoxyglucarate dehydratase	NA	1.157	7.72E-01
MSMEG_6134	NADP-dependent fatty aldehyde dehydrogenase	NA	1.038	8.19E-01
MSMEG_6135	hypothetical protein	NA	1.337	1.88E-01
MSMEG_6136	membrane protein, TerC family protein	NA	0.965	3.08E-01

MSMEG_6137	non-ribosomal peptide synthetase	NA	1.037	7.88E-01
MSMEG_6138	metallopeptidase	NA	0.869	9.59E-02
MSMEG_6139	putative HTH-type transcriptional regulator	NA	1.068	5.25E-01
MSMEG_6140	membrane protein	NA	1.295	4.88E-01
MSMEG_6141	N-acyl-D-glutamate amidohydrolase	NA	1.168	9.43E-02
MSMEG_6142	nucleoside-diphosphate-sugar epimerase	NA	1.110	1.87E-01
MSMEG_6143	conserved hypothetical protein	NA	1.275	5.88E-02
MSMEG_6144	pe family protein	NA	1.039	6.01E-01
MSMEG_6145	hypothetical protein	NA	0.938	6.18E-01
MSMEG_6146	ISMsm3, transposase	NA	0.883	4.23E-01
MSMEG_6146	ISMsm3, transposase	NA	1.389	1.93E-01
MSMEG_6147	conserved hypothetical protein	NA	1.782	4.02E-01
MSMEG_6150	4-carboxymuconolactone decarboxylase	NA	0.943	3.13E-01
MSMEG_6151	alpha/beta hydrolase fold-1	NA	1.041	7.86E-01
MSMEG_6153	DNA polymerase III subunit delta	NA	1.011	9.29E-01
MSMEG_6154	adenylate cyclase, family protein 3	NA	1.119	1.81E-01
MSMEG_6157	DNA topoisomerase I	topA	0.956	4.66E-01
MSMEG_6158	conserved hypothetical protein	NA	0.966	3.74E-01
MSMEG_6159	conserved domain protein	NA	0.840	3.86E-01
MSMEG_6160	ATP-dependent rna helicase, dead/deah box family protein	NA	1.131	2.98E-01
MSMEG_6163	conserved hypothetical protein	NA	1.115	2.57E-01
MSMEG_6164	conserved hypothetical protein	NA	0.893	1.46E-02
MSMEG_6165	conserved hypothetical protein	NA	1.479	6.31E-03
MSMEG_6166	hypothetical protein	NA	1.043	5.78E-01
MSMEG_6167	bacterial type II secretion system protein F domain	NA	0.998	9.89E-01
MSMEG_6168	bacterial type II secretion system protein F domain	NA	0.831	6.47E-02
MSMEG_6169	type II/IV secretion system protein	NA	1.069	9.69E-02
MSMEG_6170	hypothetical protein	NA	1.725	1.81E-01
MSMEG_6171	conserved hypothetical protein	NA	1.627	3.72E-01
MSMEG_6172	hypothetical protein	NA	1.710	3.41E-01
MSMEG_6173	morphological differentiation-associated protein	NA	1.195	7.67E-02

MSMEG_6174	transcriptional regulator, IclR family protein	NA	1.498	6.36E-02
MSMEG_6175	2-keto-3-deoxy-galactonokinase	NA	1.230	3.87E-02
MSMEG_6176	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	NA	1.118	6.57E-01
MSMEG_6177	galactonate dehydratase	NA	0.909	3.84E-01
MSMEG_6178	D-galactonate transporter	NA	1.060	7.13E-01
MSMEG_6179	acetyl-coenzyme A synthetase	NA	0.619	7.46E-03
MSMEG_6180	secreted protein	NA	1.129	4.24E-05
MSMEG_6181	conserved hypothetical protein	NA	1.063	5.17E-01
MSMEG_6182	conserved hypothetical protein	NA	0.846	1.55E-02
MSMEG_6183	serine protease	NA	1.008	8.82E-01
MSMEG_6184	hydrolase, alpha/beta fold family protein	NA	1.075	1.49E-01
MSMEG_6185	NTP pyrophosphohydrolase	NA	0.924	3.75E-01
MSMEG_6186	conserved hypothetical protein	NA	0.882	1.19E-01
MSMEG_6187	endonuclease III	nth	0.936	5.72E-02
MSMEG_6188	conserved hypothetical protein	NA	0.981	7.61E-01
MSMEG_6189	transcriptional regulator, Crp/Fnr family protein	NA	0.988	8.23E-01
MSMEG_6190	metallo-beta-lactamase family protein	NA	1.358	4.12E-01
MSMEG_6191	translation initiation inhibitor	NA	0.992	9.12E-01
MSMEG_6192	conserved hypothetical protein	NA	0.982	6.33E-01
MSMEG_6193	anion-transporting ATPase	NA	0.938	1.51E-01
MSMEG_6194	beta-lactamase related protein	NA	0.975	8.35E-01
MSMEG_6195	ion-transporting ATPase	NA	0.958	4.21E-01
MSMEG_6196	gaba permease	NA	1.002	9.87E-01
MSMEG_6197	diaminopimelate decarboxylase	NA	0.816	1.38E-02
MSMEG_6198	DNA-binding protein, putative	NA	1.151	5.38E-01
MSMEG_6199	Transcription factor WhiB	NA	0.687	4.19E-02
MSMEG_6200	hypothetical protein	NA	1.032	8.65E-01
MSMEG_6201	Transglycosylase	NA	1.065	4.49E-01
MSMEG_6202	secreted protein	NA	1.172	6.78E-02
MSMEG_6203	cysteine synthase/cystathionine beta-synthase family protein	NA	1.400	1.24E-03
MSMEG_6205	hypothetical protein	NA	1.093	1.50E-01

MSMEG_6206	serine/threonine protein kinase PksC	NA	1.059	6.27E-01
MSMEG_6207	conserved hypothetical protein	NA	1.255	1.83E-01
MSMEG_6208	palmitoyl-CoA hydrolase	NA	1.206	1.66E-01
MSMEG_6209	conserved hypothetical protein	NA	0.860	8.12E-02
MSMEG_6210	conserved hypothetical protein	NA	1.025	8.15E-01
MSMEG_6211	hypothetical protein	NA	1.129	7.28E-01
MSMEG_6212	hemerythrin HHE cation binding domain subfamily protein, putative	NA	1.334	5.61E-01
MSMEG_6213	Manganese containing catalase	NA	1.018	9.52E-01
MSMEG_6214	GatB/Yqey domain protein	NA	0.883	8.33E-02
MSMEG_6215	conserved hypothetical protein	NA	0.928	1.15E-01
MSMEG_6216	integral membrane protein	NA	0.940	5.87E-01
MSMEG_6217	integral membrane protein	NA	0.818	1.65E-02
MSMEG_6218	secreted protein	NA	0.846	2.76E-01
MSMEG_6219	ATPase family protein associated with various cellular activities (AAA)	NA	0.761	1.24E-02
MSMEG_6220	lipoprotein	NA	0.898	3.80E-01
MSMEG_6221	integral membrane protein	NA	1.086	7.84E-03
MSMEG_6222	integral membrane protein	NA	1.098	1.64E-01
MSMEG_6223	TetR family protein transcriptional repressor LfrR	NA	1.060	1.60E-01
MSMEG_6224	Retinal pigment epithelial membrane protein	NA	0.579	1.29E-02
MSMEG_6225	proton antiporter efflux pump	NA	1.531	1.53E-02
MSMEG_6226	transcriptional regulator, PadR family protein domain protein	NA	0.911	2.63E-01
MSMEG_6227	transcriptional regulator, PadR family protein	NA	0.909	1.51E-02
MSMEG_6228	hypothetical protein	NA	1.129	6.21E-01
MSMEG_6229	glycerol kinase	glpK	0.888	7.92E-02
MSMEG_6230	probable acyltransferase	NA	1.154	4.15E-01
MSMEG_6231	conserved hypothetical protein	NA	1.465	3.05E-01
MSMEG_6232	catalase KatA	katA	1.735	4.34E-01
MSMEG_6233	conserved hypothetical protein	NA	2.066	3.99E-01
MSMEG_6234	CBS domain pair protein	NA	0.964	5.66E-01
MSMEG_6235	thiopurine S-methyltransferase (tpmt) superfamily protein	NA	0.916	2.17E-01
MSMEG_6236	two-component system, regulatory protein	NA	0.698	1.18E-01

MSMEG_6237	conserved hypothetical protein	NA	0.796	1.74E-01
MSMEG_6238	putative two-component system sensor kinase	NA	0.589	3.49E-02
MSMEG_6239	1,3-propanediol dehydrogenase	NA	0.565	1.44E-02
MSMEG_6240	conserved hypothetical protein	NA	0.695	1.84E-01
MSMEG_6241	ATPase associated with various cellular activities, AAA-5	NA	0.578	1.15E-01
MSMEG_6242	alcohol dehydrogenase, iron-containing	NA	0.496	3.94E-02
MSMEG_6243	response regulator receiver domain protein	NA	0.788	4.33E-02
MSMEG_6244	TetR-family protein transcriptional regulator	NA	1.306	8.64E-02
MSMEG_6245	chloramphenicol resistance protein	NA	1.311	2.32E-01
MSMEG_6246	pyridoxal-phosphate-dependent transferase	NA	1.144	3.15E-01
MSMEG_6247	conserved hypothetical protein	NA	1.173	1.03E-01
MSMEG_6248	conserved hypothetical protein	NA	1.437	4.34E-02
MSMEG_6249	conserved hypothetical protein	NA	1.367	1.41E-02
MSMEG_6250	glutamate--cysteine ligase	NA	1.197	2.18E-02
MSMEG_6251	conserved hypothetical protein	NA	1.138	6.64E-02
MSMEG_6252	conserved hypothetical protein	NA	1.154	7.58E-02
MSMEG_6253	fur family protein transcriptional regulator	NA	1.215	1.22E-01
MSMEG_6254	hypothetical protein	NA	6.409	2.74E-01
MSMEG_6255	conserved hypothetical protein	NA	2.230	1.37E-02
MSMEG_6256	aspartate-semialdehyde dehydrogenase	asd	1.386	5.50E-02
MSMEG_6257	asparate kinase, monofunctional class	NA	1.544	1.52E-02
MSMEG_6258	nitroreductase family protein	NA	0.911	2.57E-01
MSMEG_6259	ammonium transporter	amt	1.005	9.68E-01
MSMEG_6260	glutamine synthetase, type III	glnT	3.351	4.36E-01
MSMEG_6261	glutamine amidotransferase, class II	NA	1.099	5.44E-01
MSMEG_6262	FwdC/FmdC family protein	NA	0.801	3.25E-02
MSMEG_6263	glutamate synthase family protein	NA	1.247	3.67E-01
MSMEG_6264	putative oxidoreductase	NA	0.803	1.46E-01
MSMEG_6265	transcriptional regulator	NA	0.931	4.82E-01
MSMEG_6266	thiocyanate hydrolase beta subunit	NA	0.872	1.43E-01
MSMEG_6267	thiocyanate hydrolase gamma subunit	NA	0.760	3.16E-03

MSMEG_6268	putative ScnB protein	NA	0.843	2.81E-01
MSMEG_6269	magnesium transporter	mgtE	0.926	3.38E-01
MSMEG_6270	hypothetical protein	NA	1.897	2.26E-01
MSMEG_6271	2-isopropylmalate synthase	leuA	1.146	4.03E-02
MSMEG_6272	NAD-glutamate dehydrogenase	NA	1.375	2.25E-02
MSMEG_6273	integral membrane protein	NA	1.648	3.11E-03
MSMEG_6274	conserved hypothetical protein	NA	1.150	3.23E-01
MSMEG_6275	DNA polymerase III subunit epsilon	NA	0.916	2.86E-01
MSMEG_6276	mur ligase family protein	NA	1.292	3.24E-02
MSMEG_6277	cobyric acid synthase	NA	1.181	4.89E-02
MSMEG_6278	metallo-beta-lactamase superfamily protein, putative	NA	0.966	6.83E-01
MSMEG_6279	recombination protein RecR	recR	0.893	2.37E-01
MSMEG_6280	conserved hypothetical protein	NA	0.906	4.99E-02
MSMEG_6281	N-acetylmuramoyl-L-alanine amidase	NA	1.071	5.46E-01
MSMEG_6282	KanY protein	NA	0.960	6.99E-02
MSMEG_6283	FAD binding domain protein	NA	0.950	2.10E-01
MSMEG_6284	cyclopropane-fatty-acyl-phospholipid synthase	NA	0.995	8.50E-01
MSMEG_6285	DNA polymerase III gamma/tau subunit	NA	1.201	2.70E-02
MSMEG_6286	aspartate transaminase	NA	1.183	1.68E-02
MSMEG_6288	conserved hypothetical protein	NA	0.961	5.05E-01
MSMEG_6289	Trypsin	NA	1.167	2.36E-01
MSMEG_6290	putative DNA-binding protein	NA	1.064	2.87E-02
MSMEG_6291	D-amino-acid dehydrogenase	NA	0.780	9.93E-02
MSMEG_6292	transcription elongation factor GreA	NA	0.675	1.78E-02
MSMEG_6293	transcriptional regulatory protein	NA	0.834	1.04E-01
MSMEG_6294	caib/baif family protein	NA	0.879	6.67E-01
MSMEG_6295	shikimate transporter	NA	0.691	1.59E-02
MSMEG_6296	5-exo-alcohol dehydrogenase	NA	0.712	5.85E-03
MSMEG_6297	aldehyde dehydrogenase	NA	1.192	2.16E-01
MSMEG_6298	malyl-CoA lyase	NA	1.713	3.96E-01
MSMEG_6299	glyoxylate reductase	NA	0.889	2.85E-01

MSMEG_6300	transcriptional regulator, GntR family protein	NA	0.926	2.50E-01
MSMEG_6301	DNA polymerase LigD, polymerase domain	ligD	0.899	1.55E-01
MSMEG_6302	DNA ligase	NA	0.905	2.53E-01
MSMEG_6303	para-nitrobenzyl esterase	NA	0.950	7.54E-01
MSMEG_6304	DNA ligase	NA	1.236	5.38E-01
MSMEG_6305	conserved hypothetical protein	NA	1.013	9.67E-01
MSMEG_6306	glutamyl-tRNA synthetase	gltX	0.992	9.53E-01
MSMEG_6307	glutamine-binding periplasmic protein/glutamine transport system permease protein	NA	0.808	4.51E-03
MSMEG_6308	hypothetical protein	NA	1.146	5.19E-02
MSMEG_6309	ABC transporter, ATP-binding protein	NA	0.790	2.49E-02
MSMEG_6310	4-hydroxybutyrate coenzyme A transferase	NA	1.085	4.00E-01
MSMEG_6311	saccharopine dehydrogenase	lys1	1.207	2.14E-02
MSMEG_6312	cytochrome P450 107B1	NA	0.921	4.12E-01
MSMEG_6313	queuine tRNA-ribosyltransferase	tgt	1.107	3.04E-01
MSMEG_6314	haloalkane dehalogenase 1	NA	1.149	4.40E-01
MSMEG_6315	lipoprotein LpqH	NA	1.154	8.87E-02
MSMEG_6316	lipoprotein LpqH	NA	1.361	1.12E-02
MSMEG_6317	lipolytic enzyme, G-D-S-L	NA	0.834	3.30E-01
MSMEG_6318	putative diol dehydratase reactivation protein	NA	1.415	1.51E-01
MSMEG_6319	penicillin-binding protein, transpeptidase	NA	0.876	3.31E-01
MSMEG_6320	diol dehydrase gamma subunit	NA	1.238	1.93E-02
MSMEG_6321	glycerol dehydratase large subunit	NA	1.230	4.99E-02
MSMEG_6322	bifunctional wax ester synthase/acyl-CoA diacylglycerol acyltransferase	NA	1.039	8.79E-01
MSMEG_6323	hypothetical protein	NA	0.989	9.57E-01
MSMEG_6324	peroxidase	NA	1.327	1.62E-01
MSMEG_6325	conserved hypothetical protein	NA	1.356	4.83E-01
MSMEG_6327	cytidine and deoxycytidylate deaminase family protein	NA	1.014	8.46E-01
MSMEG_6328	conserved hypothetical protein	NA	1.156	4.11E-01
MSMEG_6329	conserved hypothetical protein	NA	1.137	1.20E-01
MSMEG_6330	prephenate dehydrogenase	NA	1.286	1.40E-01
MSMEG_6331	ABC transporter, permease protein ProZ	NA	2.422	3.89E-01

MSMEG_6332	amino acid ABC transporter, permease protein	NA	1.039	7.24E-01
MSMEG_6333	amino acid ABC transporter, ATP-binding protein	NA	1.161	2.46E-01
MSMEG_6334	ABC transporter, quaternary amine uptake transporter (QAT) family protein, substrate	NA	1.466	9.86E-02
MSMEG_6335	hypothetical protein	NA	1.199	1.35E-01
MSMEG_6336	conserved hypothetical protein	NA	0.803	4.72E-03
MSMEG_6337	Phosphotransferase enzyme family protein	NA	1.079	4.14E-01
MSMEG_6338	phosphoglycerate mutase family protein, putative	NA	1.302	1.09E-01
MSMEG_6339	metallo-beta-lactamase family protein	NA	1.095	3.19E-01
MSMEG_6340	short-chain dehydrogenase/reductase SDR	NA	0.926	1.52E-01
MSMEG_6341	6-phosphogluconate dehydrogenase, NAD-binding	NA	0.827	3.10E-01
MSMEG_6342	oxidoreductase	NA	0.718	3.90E-02
MSMEG_6343	conserved hypothetical protein	NA	0.899	6.41E-02
MSMEG_6344	transcriptional regulator	NA	1.205	2.35E-01
MSMEG_6345	conserved hypothetical protein	NA	1.116	3.80E-01
MSMEG_6346	hypothetical protein	NA	1.181	6.78E-02
MSMEG_6347	hypothetical protein	NA	1.114	1.84E-01
MSMEG_6348	hypothetical protein	NA	0.987	9.22E-01
MSMEG_6351	histidinol-phosphate aminotransferase	hisC	0.918	7.03E-02
MSMEG_6352	conserved hypothetical protein	NA	0.868	6.04E-04
MSMEG_6353	delta3,5-delta2,4-dienoyl-CoA isomerase	NA	0.978	7.60E-01
MSMEG_6354	serine esterase, cutinase family protein	NA	1.080	6.50E-01
MSMEG_6355	hypothetical protein	NA	1.048	8.64E-01
MSMEG_6356	probable transcriptional regulator, AraC family protein, putative	NA	0.902	2.37E-01
MSMEG_6357	hypothetical protein	NA	1.137	4.61E-01
MSMEG_6358	mesocentin	NA	0.967	5.18E-01
MSMEG_6359	trypsin domain protein	NA	1.006	9.54E-01
MSMEG_6361	transcriptional regulator, MarR family protein	NA	1.317	1.66E-01
MSMEG_6362	quinone oxidoreductase	NA	1.247	2.72E-03
MSMEG_6363	cysteine desulfurase family protein	NA	1.368	4.16E-02
MSMEG_6364	conserved hypothetical protein; this gene contains a frame shift which is not the resul	NA	0.916	2.65E-01
MSMEG_6365	conserved hypothetical protein	NA	0.852	1.02E-02

MSMEG_6366	O-antigen export system, ATP-binding protein	NA	0.925	1.39E-01
MSMEG_6367	glycosyl transferase, group 2 family protein	NA	0.952	4.97E-01
MSMEG_6368	DNA-binding protein	NA	1.087	4.88E-01
MSMEG_6368	DNA-binding protein	NA	1.522	1.69E-01
MSMEG_6369	O-antigen export system, permease protein	NA	0.870	3.70E-02
MSMEG_6370	4-carboxymuconolactone decarboxylase	pcaC	1.252	1.67E-01
MSMEG_6371	GntR-family protein regulator	NA	1.734	3.25E-01
MSMEG_6372	membrane protein	NA	1.139	5.26E-02
MSMEG_6373	conserved hypothetical protein	NA	1.273	2.24E-01
MSMEG_6374	2-dehydropantoate 2-reductase	panE	1.289	2.02E-01
MSMEG_6375	transporter, major facilitator family protein	NA	1.336	2.64E-01
MSMEG_6376	transcriptional regulator LacI family protein	NA	1.344	2.93E-01
MSMEG_6377	hypothetical protein	NA	1.063	5.52E-01
MSMEG_6378	senescence marker protein-30	NA	0.950	6.45E-01
MSMEG_6379	transporter, major facilitator family protein	NA	0.964	7.05E-01
MSMEG_6380	hypothetical protein	NA	0.816	5.45E-02
MSMEG_6381	conserved hypothetical protein	NA	0.831	3.00E-01
MSMEG_6382	oxidoreductase, FAD-binding	NA	0.872	1.33E-03
MSMEG_6383	transcription regulator FurA	NA	0.781	1.47E-01
MSMEG_6384	catalase/peroxidase HPI	katG	0.623	9.87E-05
MSMEG_6385	hypothetical oxidoreductase in MprA 5'region	NA	0.976	6.72E-01
MSMEG_6386	membrane protein	NA	0.883	6.97E-03
MSMEG_6387	probable arabinosyltransferase A	NA	0.981	6.90E-01
MSMEG_6388	probable arabinosyltransferase B	NA	1.024	7.87E-01
MSMEG_6389	probable arabinosyltransferase A	NA	0.931	4.02E-01
MSMEG_6390	transporter, major facilitator family protein	NA	1.266	6.49E-03
MSMEG_6391	propionyl-CoA carboxylase beta chain	NA	0.802	1.21E-02
MSMEG_6392	polyketide synthase	NA	0.803	2.17E-02
MSMEG_6393	acyl-CoA synthase	NA	1.018	7.09E-01
MSMEG_6394	conserved hypothetical protein	NA	1.027	6.18E-01
MSMEG_6395	conserved hypothetical protein	NA	1.172	1.15E-01

MSMEG_6396	antigen 85-C	NA	1.216	6.94E-02
MSMEG_6397	hypothetical protein	NA	1.595	7.79E-02
MSMEG_6398	antigen 85-A	NA	1.121	2.81E-01
MSMEG_6399	antigen 85-C	NA	1.216	3.36E-02
MSMEG_6400	probable conserved transmembrane protein	NA	0.853	9.77E-03
MSMEG_6401	prenyltransferase, UbiA family protein	NA	0.927	2.33E-01
MSMEG_6402	PAP2 superfamily protein	NA	0.951	8.16E-02
MSMEG_6403	bifunctional udp-galactofuranosyl transferase glft	NA	0.915	7.49E-02
MSMEG_6404	UDP-galactopyranose mutase	glf	0.677	2.63E-03
MSMEG_6405	Erp protein	NA	0.819	4.08E-02
MSMEG_6406	N-acetylmuramoyl-L-alanine amidase	NA	0.889	2.17E-01
MSMEG_6407	Cof-like hydrolase	NA	0.988	8.64E-01
MSMEG_6408	acyltransferase family protein	NA	1.004	9.43E-01
MSMEG_6409	acyltransferase family protein	NA	0.962	4.71E-01
MSMEG_6410	Rieske 2Fe-2S family protein	NA	1.040	3.43E-01
MSMEG_6411	conserved hypothetical protein	NA	1.271	3.45E-02
MSMEG_6412	conserved hypothetical protein	NA	0.992	8.70E-01
MSMEG_6413	seryl-tRNA synthetase	serS	1.189	1.07E-01
MSMEG_6414	conserved hypothetical protein	NA	1.107	1.13E-02
MSMEG_6415	conserved hypothetical protein	NA	1.331	2.67E-02
MSMEG_6416	phosphoglycerate mutase family protein	NA	0.934	5.52E-01
MSMEG_6417	conserved hypothetical protein	NA	1.126	8.63E-02
MSMEG_6418	prephenate dehydratase	NA	0.925	2.08E-01
MSMEG_6419	conserved hypothetical protein	NA	1.729	1.40E-01
MSMEG_6420	abortive infection protein	NA	1.030	7.67E-01
MSMEG_6421	transcriptional regulator	NA	1.173	2.04E-01
MSMEG_6422	ferritin family protein	NA	1.122	1.91E-02
MSMEG_6423	Glycerophosphoryl diester phosphodiesterase family protein	NA	0.988	7.77E-01
MSMEG_6424	probable conserved transmembrane protein	NA	0.901	2.17E-01
MSMEG_6425	rhodanese-like domain protein	NA	1.027	7.58E-01
MSMEG_6426	conserved hypothetical protein	NA	0.547	1.57E-03

MSMEG_6427	[Mn] superoxide dismutase	NA	0.679	1.53E-03
MSMEG_6428	conserved hypothetical protein	NA	1.048	7.66E-01
MSMEG_6429	hypothetical protein	NA	0.951	7.28E-01
MSMEG_6430	hypothetical protein	NA	1.073	5.61E-01
MSMEG_6431	conserved hypothetical protein	NA	1.042	6.08E-01
MSMEG_6432	conserved hypothetical protein	NA	0.965	3.93E-01
MSMEG_6433	hypothetical protein	NA	0.936	4.80E-01
MSMEG_6434	conserved hypothetical protein	NA	0.972	6.42E-01
MSMEG_6435	hypothetical protein	NA	0.906	7.49E-02
MSMEG_6436	copper resistance protein CopC	NA	0.859	1.10E-01
MSMEG_6437	copper resistance protein D	NA	0.947	7.22E-01
MSMEG_6438	hypothetical protein	NA	1.100	9.21E-02
MSMEG_6439	regulator of ribonuclease activity A	NA	1.061	2.37E-01
MSMEG_6440	monooxygenase, flavin-binding family protein	NA	1.109	2.02E-01
MSMEG_6441	transcriptional regulator, TetR family protein	NA	1.132	2.42E-02
MSMEG_6442	integral membrane protein	NA	0.999	9.92E-01
MSMEG_6443	DNA polymerase IV	dinP	1.073	4.96E-01
MSMEG_6444	YiaAB two helix domain protein	NA	1.030	8.51E-01
MSMEG_6445	PHP domain protein	NA	1.368	3.28E-01
MSMEG_6446	hypothetical protein	NA	0.998	9.83E-01
MSMEG_6447	hypothetical protein	NA	0.926	3.94E-01
MSMEG_6448	hypothetical protein	NA	1.894	1.28E-01
MSMEG_6449	conserved hypothetical protein	NA	0.944	5.61E-01
MSMEG_6450	hypothetical protein	NA	0.942	2.98E-01
MSMEG_6451	transcriptional regulator, ArsR family protein	NA	1.456	1.21E-01
MSMEG_6452	[NADP+] succinate-semialdehyde dehydrogenase	NA	1.046	6.84E-01
MSMEG_6453	sulfate permease	NA	1.550	2.79E-01
MSMEG_6454	conserved hypothetical protein	NA	1.458	5.46E-02
MSMEG_6455	conserved hypothetical protein	NA	1.155	3.17E-01
MSMEG_6456	conserved hypothetical protein	NA	1.117	4.32E-01
MSMEG_6457	oxidoreductase molybdopterin binding domain, putative	NA	1.027	8.75E-01

MSMEG_6458	glutamate synthase, small subunit	NA	0.844	1.53E-02
MSMEG_6459	ferredoxin-dependent glutamate synthase 1	NA	0.778	2.01E-02
MSMEG_6460	hypothetical protein	NA	1.106	5.29E-01
MSMEG_6461	hypothetical protein	NA	3.147	4.03E-01
MSMEG_6464	conserved hypothetical protein	NA	1.174	1.53E-01
MSMEG_6465	chloride channel	NA	1.074	5.74E-01
MSMEG_6466	aquaporin Z	NA	1.042	1.70E-01
MSMEG_6467	starvation-induced DNA protecting protein	NA	1.095	7.91E-01
MSMEG_6468	conserved hypothetical protein	NA	1.337	3.86E-01
MSMEG_6469	conserved hypothetical protein	NA	1.072	2.94E-01
MSMEG_6470	hypothetical protein	NA	1.906	1.50E-01
MSMEG_6471	glycine/D-amino acid oxidase	NA	1.047	4.40E-01
MSMEG_6472	hypothetical protein	NA	1.729	8.87E-02
MSMEG_6473	tetracenomycin polyketide synthesis O-methyltransferase TcmP	NA	0.958	7.95E-01
MSMEG_6474	nucleoside-diphosphate-sugar epimerase	NA	1.275	9.15E-02
MSMEG_6475	conserved hypothetical protein	NA	0.872	3.98E-02
MSMEG_6476	conserved hypothetical protein	NA	0.980	7.63E-01
MSMEG_6477	methionine-S-sulfoxide reductase	msrA	0.943	2.85E-01
MSMEG_6478	putative cytochrome P450 135B1	NA	1.048	6.10E-01
MSMEG_6479	putative transcriptional regulator	NA	1.071	6.54E-01
MSMEG_6480	putative transcriptional regulatory protein	NA	1.038	2.59E-01
MSMEG_6481	conserved hypothetical protein	NA	1.139	1.06E-01
MSMEG_6482	secreted protein	NA	1.105	3.13E-01
MSMEG_6483	methyltransferase type 11	NA	0.908	2.15E-01
MSMEG_6484	glycosyl transferase	NA	1.013	6.94E-01
MSMEG_6485	ATP binding protein	NA	1.035	8.30E-01
MSMEG_6486	oxidoreductase, FAD/FMN-binding	NA	0.859	1.70E-01
MSMEG_6487	2-hydroxy-3-carboxy-6-oxo-7-methylocta-2, 4-dienoate decarboxylase	NA	0.984	9.20E-01
MSMEG_6488	conserved hypothetical protein	NA	0.811	4.54E-02
MSMEG_6489	2,6-dihydroxypyridine hydroxylase	NA	1.028	1.28E-01
MSMEG_6490	major facilitator superfamily protein	NA	1.250	4.84E-01

MSMEG_6491	aldehyde dehydrogenase	NA	1.103	4.95E-01
MSMEG_6492	GAF domain protein, putative	NA	1.430	1.25E-01
MSMEG_6493	hypothetical protein	NA	3.467	2.53E-01
MSMEG_6494	ABC nitrate/sulfonate/bicarbonate family protein transporter, inner membrane subun	NA	1.070	1.88E-01
MSMEG_6495	ABC nitrate/sulfonate/bicarbonate family protein transporter, inner membrane subun	NA	0.913	2.46E-01
MSMEG_6496	nitrate/sulfonate/bicarbonate ABC transporter ATPase subunit	NA	0.863	1.79E-01
MSMEG_6497	hypothetical protein	NA	1.851	8.31E-02
MSMEG_6498	hypothetical protein	NA	1.850	4.88E-02
MSMEG_6499	conserved hypothetical protein	NA	1.006	9.16E-01
MSMEG_6500	conserved hypothetical protein	NA	1.154	4.33E-01
MSMEG_6501	hypothetical protein	NA	0.904	4.73E-01
MSMEG_6502	conserved hypothetical protein	NA	0.792	1.21E-02
MSMEG_6503	transcriptional regulator, TetR family protein	NA	0.989	9.16E-01
MSMEG_6504	conserved hypothetical protein	NA	1.498	4.50E-01
MSMEG_6505	NfnB protein	NA	1.785	2.42E-01
MSMEG_6506	nicotinamidase/pyrazinamidase	NA	1.090	1.15E-01
MSMEG_6507	glycogen debranching enzyme GlgX	glgX	0.934	3.54E-01
MSMEG_6508	MarR-family protein transcriptional regulator	NA	1.111	1.42E-01
MSMEG_6509	ABC-type drug export system, ATP-binding protein	NA	2.519	3.64E-01
MSMEG_6510	ABC-type drug export system, membrane protein	NA	1.248	3.80E-01
MSMEG_6511	acyl-CoA dehydrogenase domain protein	NA	0.849	1.96E-01
MSMEG_6512	acyl-CoA dehydrogenase domain protein	NA	0.860	1.44E-01
MSMEG_6513	membrane transport protein	NA	0.862	3.28E-02
MSMEG_6514	trehalose synthase-fused probable maltokinase	NA	0.784	1.83E-02
MSMEG_6515	trehalose synthase	treS	0.769	8.25E-03
MSMEG_6516	hypothetical protein	NA	1.098	5.29E-01
MSMEG_6517	hypothetical protein	NA	1.057	6.96E-01
MSMEG_6518	conserved hypothetical protein	NA	0.874	9.54E-02
MSMEG_6519	pyridoxamine 5'-phosphate oxidase family protein	NA	1.017	8.52E-01
MSMEG_6520	orotate phosphoribosyltransferase	NA	0.937	4.13E-01
MSMEG_6521	sulfate/thiosulfate import ATP-binding protein CysA 2	NA	0.895	2.06E-01

MSMEG_6522	ABC transporter, inner membrane subunit	NA	0.934	7.56E-01
MSMEG_6523	ABC transporter, membrane spanning protein	NA	0.810	2.10E-02
MSMEG_6524	ABC Polyamine/Opine/Phosphonate transporter, periplasmic ligand binding protein	NA	0.859	2.58E-02
MSMEG_6525	hypothetical protein	NA	1.160	3.24E-01
MSMEG_6526	pyridoxamine 5'-phosphate oxidase family protein	NA	1.185	5.53E-01
MSMEG_6527	transcriptional regulator, TetR family protein	NA	1.028	8.47E-01
MSMEG_6528	conserved hypothetical protein	NA	0.826	2.67E-01
MSMEG_6529	conserved hypothetical protein	NA	1.075	4.00E-01
MSMEG_6530	cytochrome c oxidase subunit III family protein	NA	0.773	8.56E-02
MSMEG_6531	conserved hypothetical protein	NA	1.166	2.68E-01
MSMEG_6532	transcriptional regulatory protein	NA	0.795	1.63E-01
MSMEG_6533	conserved hypothetical protein	NA	1.854	2.26E-01
MSMEG_6534	hypothetical protein	NA	1.097	5.77E-01
MSMEG_6535	translation elongation factor EF-G	NA	1.415	4.83E-01
MSMEG_6536	carboxymuconolactone decarboxylase	NA	1.176	9.52E-02
MSMEG_6537	transcriptional regulator, TetR family protein	NA	1.548	2.90E-01
MSMEG_6538	3-oxoacyl-(acyl-carrier-protein) reductase, putative	NA	1.165	2.16E-01
MSMEG_6539	conserved hypothetical protein	NA	0.953	6.61E-01
MSMEG_6540	virulence factor Mce family protein	NA	0.820	3.10E-02
MSMEG_6541	anti-sigma factor antagonist	NA	0.964	6.09E-01
MSMEG_6542	B12 binding domain protein	NA	0.797	7.96E-02
MSMEG_6543	GAF domain protein; this gene contains a frame shift which is not the result of sequen	NA	0.837	9.39E-03
MSMEG_6543	GAF domain protein; this gene contains a frame shift which is not the result of sequen	NA	0.877	1.40E-02
MSMEG_6544	transport-associated, putative	NA	0.834	6.48E-02
MSMEG_6545	phosphoglycerate mutase family protein	NA	1.154	5.06E-01
MSMEG_6546	transcriptional regulatory protein	NA	0.847	1.14E-01
MSMEG_6547	amidohydrolase 2	NA	0.992	9.08E-01
MSMEG_6548	Rieske iron-sulfur protein	NA	0.929	7.18E-01
MSMEG_6549	conserved hypothetical protein	NA	0.699	7.63E-03
MSMEG_6550	hypothetical protein	NA	0.481	4.34E-03
MSMEG_6550	hypothetical protein	NA	0.620	2.58E-03

MSMEG_6551	hypothetical protein	NA	0.625	4.67E-02
MSMEG_6552	conserved hypothetical protein	NA	1.233	1.49E-01
MSMEG_6553	ABC transporter ATP-binding protein	NA	0.886	5.96E-01
MSMEG_6554	hypothetical ABC transporter ATP-binding protein	NA	1.023	6.66E-01
MSMEG_6555	transcriptional regulator, TetR family protein, putative	NA	0.858	2.05E-01
MSMEG_6556	putative transcriptional regulator	NA	0.733	8.81E-04
MSMEG_6557	dehydrogenase	NA	1.160	6.08E-02
MSMEG_6558	putative enoyl-CoA hydratase	NA	0.763	9.19E-04
MSMEG_6559	hypothetical protein	NA	1.151	2.33E-01
MSMEG_6560	acyl dehydratase	NA	0.995	9.24E-01
MSMEG_6561	nonspecific lipid-transfer protein	NA	1.060	5.81E-01
MSMEG_6562	putative acyl-CoA dehydrogenase	NA	1.262	9.91E-02
MSMEG_6563	dihydrokaempferol 4-reductase	NA	1.116	5.19E-02
MSMEG_6564	transcriptional regulator, TetR family protein	NA	2.212	3.11E-01
MSMEG_6565	conserved hypothetical protein	NA	1.151	1.97E-01
MSMEG_6566	hypothetical protein	NA	1.488	4.35E-02
MSMEG_6567	iron-dependent peroxidase	NA	0.904	3.67E-01
MSMEG_6568	regulatory protein, LuxR, putative	NA	1.118	7.58E-01
MSMEG_6569	conserved hypothetical protein	NA	0.894	1.00E-01
MSMEG_6570	integral membrane protein	NA	0.962	6.29E-01
MSMEG_6571	conserved hypothetical protein	NA	0.925	4.13E-02
MSMEG_6572	methyltransferase	NA	1.164	4.71E-01
MSMEG_6573	conserved hypothetical protein	NA	0.951	5.48E-01
MSMEG_6574	conserved hypothetical protein	NA	0.911	1.03E-01
MSMEG_6575	beta-lactamase	NA	1.000	9.99E-01
MSMEG_6576	pyridoxamine 5'-phosphate oxidase family protein	NA	0.985	9.50E-01
MSMEG_6577	methylmalonyl-CoA carboxyltransferase 12S subunit	NA	1.018	7.98E-01
MSMEG_6578	hypothetical protein	NA	1.088	2.68E-02
MSMEG_6579	conserved hypothetical protein	NA	1.043	8.83E-01
MSMEG_6580	transcriptional regulator family protein	NA	0.975	6.91E-01
MSMEG_6581	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	0.921	3.96E-01

MSMEG_6582	pyridine nucleotide-disulphide oxidoreductase domain protein	NA	1.267	4.47E-01
MSMEG_6583	antigen 85-C	NA	0.887	1.87E-01
MSMEG_6584	acyl-CoA dehydrogenase	NA	0.895	6.77E-01
MSMEG_6585	acyl-CoA dehydrogenase	NA	0.667	1.42E-02
MSMEG_6586	alpha/beta hydrolase, putative	NA	0.845	2.41E-01
MSMEG_6587	ATP-dependent helicase HrpA	hrpA	1.388	6.98E-02
MSMEG_6588	fumarylacetoacetate	NA	0.719	3.30E-02
MSMEG_6590	conserved hypothetical protein	NA	0.844	9.52E-02
MSMEG_6591	aminotransferase, class V family protein	NA	1.139	3.29E-01
MSMEG_6592	short-chain dehydrogenase/reductase SDR	NA	0.791	1.08E-01
MSMEG_6593	ATP-binding protein	NA	0.966	8.27E-01
MSMEG_6594	amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine	NA	1.112	3.88E-01
MSMEG_6595	secreted protein	NA	0.988	8.45E-01
MSMEG_6596	conserved hypothetical protein	NA	0.984	7.23E-01
MSMEG_6597	hydrolase of the alpha/beta superfamily protein	NA	1.132	1.55E-01
MSMEG_6598	6,7-dimethyl-8-ribityllumazine synthase	NA	0.981	7.00E-01
MSMEG_6599	regulatory protein, LuxR; this gene contains a frame shift which is not the result of seq	NA	0.830	2.24E-01
MSMEG_6599	regulatory protein, LuxR; this gene contains a frame shift which is not the result of seq	NA	1.998	3.80E-01
MSMEG_6600	transposase	NA	1.053	8.41E-01
MSMEG_6601	hypothetical protein	NA	0.946	3.16E-01
MSMEG_6602	oxidoreductase	NA	0.744	3.50E-02
MSMEG_6603	NADH:flavin oxidoreductase/nadh oxidase	NA	0.808	2.92E-01
MSMEG_6604	transcriptional regulator, TetR family protein	NA	1.021	8.06E-01
MSMEG_6605	transcriptional regulatory protein	NA	1.031	8.56E-01
MSMEG_6606	hypothetical protein	NA	0.998	9.91E-01
MSMEG_6607	hypothetical protein	NA	1.231	3.51E-01
MSMEG_6608	hypothetical protein	NA	1.663	2.10E-01
MSMEG_6609	hypothetical protein	NA	1.739	5.54E-02
MSMEG_6610	protein of unknown function DUF58, putative	NA	1.517	3.54E-01
MSMEG_6611	hypothetical protein	NA	2.226	3.39E-01
MSMEG_6612	ATPase, MoxR family protein	moxR	1.467	5.21E-01

MSMEG_6613	conserved hypothetical protein	NA	0.984	9.35E-01
MSMEG_6614	integral membrane protein	NA	0.947	6.61E-01
MSMEG_6615	hypothetical protein	NA	1.016	9.69E-01
MSMEG_6616	S-(hydroxymethyl)glutathione dehydrogenase	NA	1.179	6.31E-01
MSMEG_6617	nudix hydrolase	NA	0.968	5.98E-01
MSMEG_6618	DEAD/DEAH box helicase; this gene contains a frame shift which is not the result of se	NA	1.252	5.25E-01
MSMEG_6619	conserved hypothetical protein; this gene contains a frame shift which is not the result	NA	1.089	2.34E-01
MSMEG_6620	conserved hypothetical protein	NA	1.170	1.08E-01
MSMEG_6621	bacterial luciferase family protein	NA	1.043	8.73E-01
MSMEG_6622	cytochrome P450 monooxygenase	NA	1.196	3.99E-01
MSMEG_6623	dehydrogenase	NA	1.236	1.62E-01
MSMEG_6624	conserved hypothetical protein	NA	1.149	5.60E-01
MSMEG_6625	glyoxalase family protein	NA	1.027	8.63E-01
MSMEG_6626	short-chain dehydrogenase/reductase SDR	NA	1.034	8.10E-01
MSMEG_6627	nitroreductase family protein	NA	0.687	7.28E-03
MSMEG_6628	transcriptional regulator, TetR family protein	NA	0.867	7.09E-02
MSMEG_6629	malonate decarboxylase, epsilon subunit	mdcH	0.934	4.36E-01
MSMEG_6630	glyoxalase family protein	NA	0.883	1.79E-01
MSMEG_6631	phosphoribosyl-dephospho-CoA transferase MdcG	mdcG	0.937	7.90E-01
MSMEG_6632	beta subunit of malonate decarboxylase	NA	0.949	1.03E-01
MSMEG_6633	malonate decarboxylase acyl carrier protein	mdcC	1.028	8.11E-01
MSMEG_6634	triphosphoribosyl-dephospho-CoA synthase MdcB	mdcB	0.798	3.01E-02
MSMEG_6635	alpha subunit of malonate decarboxylase	NA	1.122	2.35E-01
MSMEG_6636	[Mn] superoxide dismutase	NA	0.926	5.14E-01
MSMEG_6637	hypothetical protein	NA	1.226	1.86E-01
MSMEG_6638	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	metE	0.976	7.22E-01
MSMEG_6639	transcriptional regulator, GntR family protein, putative	NA	1.029	5.47E-01
MSMEG_6640	hypothetical protein	NA	1.336	5.71E-01
MSMEG_6641	nitrilotriacetate monooxygenase component A	NA	1.694	2.86E-02
MSMEG_6642	caib/baif family protein	NA	1.179	5.09E-01
MSMEG_6643	DNA-binding protein	NA	0.989	6.21E-01

MSMEG_6644	malyl-CoA lyase	NA	1.067	5.68E-01
MSMEG_6645	2-methylcitrate dehydratase 2	NA	0.913	5.76E-01
MSMEG_6646	methylisocitrate lyase	prpB	1.856	2.22E-01
MSMEG_6647	citrate synthase 2	NA	2.366	2.54E-01
MSMEG_6648	pyruvate carboxylase	pyc	1.024	8.95E-01
MSMEG_6649	conserved hypothetical protein	NA	0.882	5.52E-01
MSMEG_6650	hypothetical protein	NA	1.046	4.58E-01
MSMEG_6651	hypothetical protein	NA	1.083	5.36E-01
MSMEG_6652	hypothetical protein	NA	1.025	9.16E-01
MSMEG_6653	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	0.882	4.85E-01
MSMEG_6653	hypothetical protein; this gene contains a frame shift which is not the result of sequen	NA	1.067	4.94E-01
MSMEG_6654	TnpC protein	NA	0.891	5.17E-01
MSMEG_6655	conserved hypothetical protein	NA	0.882	4.07E-01
MSMEG_6656	conserved hypothetical protein	NA	0.635	9.45E-03
MSMEG_6657	alpha subunit of malonate decarboxylase	NA	1.287	4.21E-01
MSMEG_6658	alpha/beta hydrolase fold	NA	0.939	6.69E-01
MSMEG_6659	hypothetical protein	NA	0.891	4.66E-01
MSMEG_6660	permease, cytosine/purines, uracil, thiamine, allantoin family protein	NA	0.942	9.65E-02
MSMEG_6661	O-methyltransferase, putative	NA	0.870	3.19E-02
MSMEG_6662	short chain dehydrogenase	NA	0.875	4.08E-01
MSMEG_6663	C5-O-methyltransferase	NA	1.006	9.74E-01
MSMEG_6664	methylenetetrahydrofolate reductase family protein, putative	NA	0.877	4.89E-01
MSMEG_6665	integral membrane protein	NA	1.161	4.88E-01
MSMEG_6666	conserved hypothetical protein	NA	0.966	6.74E-01
MSMEG_6667	conserved hypothetical protein	NA	0.815	2.69E-01
MSMEG_6668	ABC transporter, periplasmic substrate-binding protein, putative	NA	1.459	1.81E-01
MSMEG_6669	ABC transporter, permease protein	NA	1.368	3.88E-01
MSMEG_6670	ABC transporter, permease protein, putative	NA	0.967	8.01E-01
MSMEG_6671	sulfate/thiosulfate import ATP-binding protein CysA	NA	1.127	3.35E-01
MSMEG_6672	type I phosphodiesterase	NA	1.196	6.48E-02
MSMEG_6673	6-aminohexanoate-cyclic-dimer hydrolase	NA	1.693	3.59E-01

MSMEG_6674	transcriptional regulator, LysR family protein	NA	1.205	5.40E-02
MSMEG_6675	hypothetical protein	NA	2.469	2.01E-01
MSMEG_6676	probable conserved transmembrane protein	NA	1.216	9.54E-02
MSMEG_6677	transcriptional regulator, LysR family protein	NA	1.367	1.51E-01
MSMEG_6678	conserved hypothetical protein	NA	1.037	6.86E-01
MSMEG_6679	metallo-beta-lactamase family protein	NA	1.034	7.84E-01
MSMEG_6680	integral membrane protein	NA	1.128	1.67E-01
MSMEG_6681	hypothetical protein	NA	0.794	1.99E-02
MSMEG_6682	RNA polymerase sigma-70 factor, putative	NA	1.164	4.17E-01
MSMEG_6683	probable peroxiredoxin, putative	NA	0.914	4.18E-01
MSMEG_6684	agarase	NA	1.527	2.70E-01
MSMEG_6685	4-aminobutyrate transaminase	gabT	0.662	5.96E-03
MSMEG_6686	glutaryl-CoA dehydrogenase	NA	0.708	4.89E-02
MSMEG_6687	aldehyde dehydrogenase, thermostable	NA	0.916	6.58E-01
MSMEG_6688	regulatory protein	NA	1.271	4.39E-01
MSMEG_6689	CAIB/BAIF family protein	NA	0.880	3.65E-01
MSMEG_6690	glutamine amidotransferase class-I	NA	1.270	4.90E-02
MSMEG_6691	glutamine amidotransferase	NA	1.257	4.44E-01
MSMEG_6692	putative glutamine-binding periplasmic protein	NA	1.144	6.25E-01
MSMEG_6693	glutamine synthetase III	NA	1.344	6.72E-01
MSMEG_6694	conserved domain protein	NA	0.819	1.46E-02
MSMEG_6695	cytochrome P450	NA	1.047	7.94E-01
MSMEG_6696	hypothetical protein	NA	1.226	2.41E-01
MSMEG_6699	conserved hypothetical protein	NA	0.959	6.84E-01
MSMEG_6700	regulatory protein	NA	1.015	8.09E-01
MSMEG_6701	amino acid permease	NA	1.119	4.57E-01
MSMEG_6702	[NADP+] succinate-semialdehyde dehydrogenase	NA	1.196	3.56E-01
MSMEG_6703	N5,N10- methylenetetrahydromethanopterin reductase-related protein	NA	1.223	3.30E-01
MSMEG_6704	shikimate 5-dehydrogenase	NA	1.001	9.97E-01
MSMEG_6705	regulatory protein	NA	0.882	1.28E-01
MSMEG_6706	hypothetical protein	NA	1.201	4.27E-01

MSMEG_6707	hypothetical protein	NA	2.910	4.15E-01
MSMEG_6708	epoxide hydrolase	NA	1.005	9.86E-01
MSMEG_6709	cyclopentanol dehydrogenase	NA	1.129	6.13E-01
MSMEG_6710	hydrolase, alpha/beta fold family protein	NA	0.816	3.10E-01
MSMEG_6711	4-hydroxybenzoate transporter	NA	1.207	5.15E-01
MSMEG_6712	maleylacetate reductase	NA	0.962	5.32E-01
MSMEG_6713	hydroxyquinol 1,2-dioxygenase	NA	1.253	1.88E-01
MSMEG_6714	conserved hypothetical protein	NA	0.959	7.51E-01
MSMEG_6715	AP endonuclease, family protein 2	NA	0.842	1.65E-01
MSMEG_6716	AP endonuclease, family protein 2	NA	1.139	6.50E-01
MSMEG_6717	oxidoreductase, Gfo/Idh/MocA family protein	NA	1.815	4.72E-01
MSMEG_6718	transporter, major facilitator family protein	NA	1.117	5.59E-01
MSMEG_6719	epoxide hydrolase	NA	0.975	8.79E-01
MSMEG_6720	epoxide hydrolase	NA	0.686	1.30E-02
MSMEG_6721	hypothetical protein	NA	1.008	9.69E-01
MSMEG_6722	conserved hypothetical protein	NA	0.881	1.66E-01
MSMEG_6723	conserved hypothetical protein	NA	1.187	1.35E-01
MSMEG_6724	ABC-type cobalt transport system	NA	1.000	9.96E-01
MSMEG_6725	ABC transporter, ATP-binding protein	NA	1.021	7.75E-01
MSMEG_6726	ABC transporter, permease protein	NA	1.127	1.92E-01
MSMEG_6727	amino acid permease-associated region	NA	1.192	6.99E-01
MSMEG_6728	conserved hypothetical protein	NA	1.152	5.92E-01
MSMEG_6729	DNA-binding protein	NA	0.970	7.01E-01
MSMEG_6730	putative oxidoreductase YdbC	NA	1.123	3.29E-01
MSMEG_6731	transcriptional regulatory protein	NA	0.902	2.26E-01
MSMEG_6732	integral membrane protein	NA	1.104	4.36E-01
MSMEG_6733	hydrolase, carbon-nitrogen family protein	NA	1.090	4.54E-01
MSMEG_6734	dibenzothiophene desulfurization enzyme A	NA	0.994	8.59E-01
MSMEG_6735	amino acid permease, putative	NA	1.294	3.42E-01
MSMEG_6736	LacI-family protein transcriptional regulator	NA	0.949	7.74E-01
MSMEG_6737	putative membrane protein	NA	1.014	5.21E-01

MSMEG_6738	probable transcriptional regulator YdhC	NA	1.090	4.73E-03
MSMEG_6739	hypothetical protein	NA	0.962	6.58E-01
MSMEG_6740	1-aminocyclopropane-1-carboxylate deaminase	NA	1.050	3.49E-01
MSMEG_6741	antar domain protein	NA	1.171	2.15E-01
MSMEG_6742	conserved hypothetical protein	NA	1.493	3.65E-01
MSMEG_6743	lactoylglutathione lyase	NA	1.401	3.87E-01
MSMEG_6744	oxidoreductase FAD/NAD	NA	1.088	6.58E-01
MSMEG_6745	transcriptional regulator, GntR family protein	NA	1.115	1.70E-01
MSMEG_6746	oxidoreductase, aldo/keto reductase family protein	NA	0.859	5.35E-02
MSMEG_6747	oxidoreductase	NA	1.585	1.58E-01
MSMEG_6748	ATPase component of ABC transporters with duplicated ATPase domains	NA	1.080	1.90E-01
MSMEG_6749	conserved hypothetical protein	NA	1.020	7.70E-01
MSMEG_6750	hypothetical protein	NA	1.062	2.06E-01
MSMEG_6751	hypothetical protein	NA	1.423	4.10E-01
MSMEG_6752	endoglucanase A	NA	0.956	4.06E-01
MSMEG_6753	oxidoreductase, short chain dehydrogenase/reductase family protein	NA	3.936	1.18E-01
MSMEG_6754	MaoC like domain protein	NA	0.998	9.58E-01
MSMEG_6755	isoflavone reductase	NA	1.767	1.34E-02
MSMEG_6756	glycerol kinase	glpK	0.843	1.88E-02
MSMEG_6757	glycerol operon regulatory protein	NA	0.682	5.86E-04
MSMEG_6758	transport integral membrane protein	NA	0.585	2.11E-04
MSMEG_6759	glycerol kinase	glpK	0.476	8.11E-04
MSMEG_6760	conserved hypothetical protein	NA	0.998	9.59E-01
MSMEG_6761	glycerol-3-phosphate dehydrogenase 2	NA	0.475	7.42E-04
MSMEG_6762	transcriptional regulator	NA	1.128	3.27E-01
MSMEG_6763	oxidoreductase	NA	0.946	6.56E-01
MSMEG_6764	transcriptional regulator, TetR family protein	NA	1.016	8.06E-01
MSMEG_6765	ABC-2 type transporter superfamily protein	NA	1.369	2.11E-01
MSMEG_6766	ABC transporter, ATP-binding protein, NodI family protein	NA	0.962	7.85E-01
MSMEG_6767	mycocerosic acid synthase	NA	0.993	9.63E-01
MSMEG_6768	halogenase	NA	1.271	5.28E-01

MSMEG_6769	transporter, monovalent cation:proton antiporter-2 (CPA2) family protein	NA	1.191	5.39E-02
MSMEG_6770	conserved hypothetical protein	NA	1.019	9.09E-01
MSMEG_6771	conserved hypothetical protein	NA	0.891	2.40E-02
MSMEG_6772	homoserine O-acetyltransferase	NA	1.154	5.06E-01
MSMEG_6773	CaiB/BaiF family protein	NA	1.061	3.45E-01
MSMEG_6774	enoyl-CoA hydratase	NA	1.167	1.50E-01
MSMEG_6775	major facilitator superfamily protein transporter	NA	1.400	1.25E-01
MSMEG_6776	transcriptional regulator, LysR family protein	NA	1.040	4.63E-01
MSMEG_6777	probable enoyl-CoA hydratase	NA	1.072	8.16E-01
MSMEG_6778	hypothetical protein	NA	1.240	2.53E-02
MSMEG_6779	conserved hypothetical protein, putative	NA	0.923	3.99E-01
MSMEG_6780	phenazine biosynthesis protein PhzF	NA	0.989	9.29E-01
MSMEG_6781	hypothetical protein	NA	1.187	2.92E-01
MSMEG_6782	hypothetical protein	NA	1.114	4.28E-01
MSMEG_6783	integral membrane protein	NA	0.769	7.36E-04
MSMEG_6784	beta-lactamase	NA	0.925	5.33E-02
MSMEG_6785	triosephosphate isomerase	tpiA	1.197	4.04E-01
MSMEG_6786	conserved hypothetical protein	NA	0.703	8.17E-02
MSMEG_6787	ribose 5-phosphate isomerase	NA	0.966	7.22E-01
MSMEG_6788	dihydroxyacetone kinase	NA	0.847	2.00E-01
MSMEG_6789	transcriptional regulator, GntR family protein	NA	1.062	1.54E-01
MSMEG_6790	AP endonuclease, family protein 2	NA	0.747	2.19E-01
MSMEG_6791	3-hydroxybutyryl-CoA dehydrogenase	NA	0.760	2.75E-02
MSMEG_6792	inner membrane permease YgbN	NA	0.966	6.86E-01
MSMEG_6793	hypothetical protein	NA	0.891	2.66E-01
MSMEG_6794	DNA-binding protein	NA	1.333	4.14E-01
MSMEG_6795	enoyl-CoA hydratase/isomerase family protein	NA	0.944	7.78E-01
MSMEG_6796	hypothetical protein	NA	0.974	7.95E-01
MSMEG_6797	carboxymuconolactone decarboxylase	NA	1.077	3.20E-01
MSMEG_6798	ribose operon repressor	rbsR	1.003	9.63E-01
MSMEG_6799	aldo/keto reductase; this gene contains a frame shift which is not the result of sequen	NA	1.065	3.78E-01

MSMEG_6800	phosphoribulokinase/uridine kinase	NA	0.927	4.68E-03
MSMEG_6801	kinase, pfkB family protein	NA	0.941	6.66E-01
MSMEG_6802	ABC transporter ATP-binding protein	NA	1.178	7.28E-01
MSMEG_6803	ribose transport system permease protein RbsC	NA	0.710	4.11E-02
MSMEG_6804	sugar ABC transporter substrate-binding protein	NA	0.688	5.03E-03
MSMEG_6805	beta-lactamase	NA	1.189	2.09E-01
MSMEG_6806	excinuclease ABC, A subunit	uvrA	1.423	2.39E-01
MSMEG_6807	transcriptional regulator, TetR family protein	NA	1.464	1.93E-01
MSMEG_6808	hypothetical protein	NA	1.006	9.69E-01
MSMEG_6809	CbbQ protein	cbbQ	1.600	3.79E-01
MSMEG_6810	nitric oxide reductase activase protein; this gene contains a frame shift which is not th	NA	1.066	8.19E-01
MSMEG_6811	conserved hypothetical protein	NA	1.291	1.30E-02
MSMEG_6812	major facilitator superfamily; this gene contains a frame shift which is not the result of	NA	1.263	5.01E-02
MSMEG_6813	amidohydrolase 2	NA	1.083	4.17E-01
MSMEG_6814	helix-turn-helix, Fis-type	NA	1.619	3.45E-01
MSMEG_6815	secreted protein	NA	1.078	3.71E-01
MSMEG_6816	molybdopterin oxidoreductase	NA	1.288	2.76E-01
MSMEG_6817	RNA polymerase sigma factor, sigma-70 family protein	NA	7.587	4.02E-01
MSMEG_6818	dehydrogenase	NA	1.035	8.35E-01
MSMEG_6819	conserved domain protein; this gene contains a frame shift which is not the result of s	NA	1.401	4.52E-01
MSMEG_6819	conserved domain protein; this gene contains a frame shift which is not the result of s	NA	2.453	2.42E-01
MSMEG_6820	acid phosphatase SurE	surE	1.096	5.95E-01
MSMEG_6821	NLP/P60 family protein	NA	0.962	7.55E-01
MSMEG_6822	beta-lactamase	NA	0.883	9.63E-02
MSMEG_6823	short-chain dehydrogenase/reductase SDR	NA	0.924	3.89E-02
MSMEG_6824	MarR-family protein regulatory protein	NA	1.071	3.70E-01
MSMEG_6825	caax amino protease family protein, putative	NA	1.947	1.54E-01
MSMEG_6826	L-lactate permease	NA	1.144	7.43E-01
MSMEG_6827	hypothetical protein	NA	1.835	4.28E-01
MSMEG_6828	transcriptional regulator	NA	1.695	2.55E-01
MSMEG_6829	transcriptional regulatory protein	NA	1.224	8.74E-02

MSMEG_6830	conserved hypothetical protein	NA	1.215	8.72E-02
MSMEG_6831	hydrolase, alpha/beta hydrolase fold family protein	NA	1.544	2.32E-01
MSMEG_6832	conserved hypothetical protein	NA	0.990	8.89E-01
MSMEG_6833	alcohol dehydrogenase	NA	5.442	3.91E-01
MSMEG_6834	alcohol dehydrogenase	NA	1.092	5.42E-01
MSMEG_6835	Fatty acid desaturase	NA	0.983	8.43E-01
MSMEG_6836	putative oxidoreductase	NA	1.137	6.36E-01
MSMEG_6837	haloalkane dehalogenase	NA	1.112	4.39E-01
MSMEG_6838	putative esterase	NA	0.935	5.25E-01
MSMEG_6839	transcriptional regulator, AraC family protein	NA	1.088	3.52E-01
MSMEG_6840	LysR-family protein transcriptional regulator	NA	1.556	3.31E-01
MSMEG_6841	hypothetical protein	NA	1.253	4.92E-01
MSMEG_6842	2,2-dialkylglycine decarboxylase	NA	1.312	1.07E-01
MSMEG_6843	NAD-dependent epimerase/dehydratase	NA	0.868	3.13E-01
MSMEG_6844	trap-t family protein transporter, dctp	NA	1.093	3.62E-01
MSMEG_6845	trap dicarboxylate transporter, dctm subunit	NA	0.897	3.41E-01
MSMEG_6846	putative C4 decarboxylate transport protein	NA	1.198	3.34E-01
MSMEG_6847	conserved hypothetical protein	NA	1.638	1.40E-01
MSMEG_6848	putative oxidoreductase	NA	3.825	2.31E-01
MSMEG_6849	LysR-family protein transcriptional regulator	NA	1.243	1.14E-01
MSMEG_6850	alpha/beta hydrolase	NA	1.791	4.23E-01
MSMEG_6851	phosphatidylethanolamine-binding protein	NA	0.929	6.52E-01
MSMEG_6852	putative carboxylesterase/lipase	NA	1.048	8.07E-01
MSMEG_6853	3-isopropylmalate dehydratase small subunit	NA	1.317	8.03E-02
MSMEG_6854	3-isopropylmalate dehydratase large subunit	NA	0.954	3.92E-01
MSMEG_6855	carboxyvinyl-carboxyphosphonate phosphorylmutase	NA	0.987	9.12E-01
MSMEG_6856	MmgE/PrpD family protein	NA	1.080	5.82E-01
MSMEG_6857	putative transcription regulator	NA	0.946	5.81E-01
MSMEG_6858	epoxide hydrolase 1	NA	1.391	1.93E-01
MSMEG_6859	oxidoreductase	NA	2.870	4.88E-02
MSMEG_6860	conserved hypothetical protein	NA	0.998	9.72E-01

MSMEG_6861	cupin domain protein	NA	1.205	3.38E-01
MSMEG_6862	putative transcription regulator	NA	1.134	4.38E-01
MSMEG_6863	class II aldolase/adducin domain protein	NA	0.934	2.33E-01
MSMEG_6864	putative transcription regulator	NA	1.200	1.06E-01
MSMEG_6865	ABC transporter solute binding lipoprotein	NA	1.314	1.75E-01
MSMEG_6866	dipeptide transport system permease protein DppB	NA	7.136	3.86E-01
MSMEG_6867	oligopeptide ABC transporter integral membrane protein	NA	1.398	1.81E-01
MSMEG_6868	oligopeptide ABC transporter ATP-binding protein; this gene contains a frame shift wh	NA	0.777	1.51E-01
MSMEG_6868	oligopeptide ABC transporter ATP-binding protein; this gene contains a frame shift wh	NA	2.544	4.01E-01
MSMEG_6869	regulatory protein	NA	1.021	7.41E-01
MSMEG_6870	creatinine amidohydrolase	NA	1.149	4.92E-01
MSMEG_6871	isomerase	NA	0.970	8.08E-01
MSMEG_6872	beta-lactamase	NA	0.843	5.12E-01
MSMEG_6873	enoyl-CoA hydratase/isomerase; this gene contains a frame shift which is not the resul	NA	0.944	7.07E-01
MSMEG_6873	enoyl-CoA hydratase/isomerase; this gene contains a frame shift which is not the resul	NA	1.227	2.86E-01
MSMEG_6874	aldehyde dehydrogenase	NA	0.830	3.15E-01
MSMEG_6875	endoribonuclease L-PSP family protein	NA	0.752	4.89E-02
MSMEG_6876	branched chain amino acid transport ATP-binding protein	NA	1.033	8.32E-01
MSMEG_6877	branched-chain amino acid transport system ATP-binding protein	NA	0.919	6.02E-01
MSMEG_6878	inner-membrane translocator	NA	1.078	7.16E-01
MSMEG_6879	integral membrane protein of the ABC-type Nat permease for neutral amino acids Nat	NA	0.735	8.62E-02
MSMEG_6880	hydrophobic amino acid ABC transporter, putative	NA	0.924	3.94E-01
MSMEG_6881	transcriptional regulator, GntR family protein	NA	1.034	7.75E-01
MSMEG_6882	LysR-family protein transcriptional regulator	NA	1.252	2.50E-01
MSMEG_6883	hypothetical protein; this region contains one or more premature stops and/or frames	NA	0.921	4.02E-01
MSMEG_6884	NADP oxidoreductase, coenzyme f420-dependent:6-phosphogluconate dehydrogenas	NA	2.371	3.19E-01
MSMEG_6885	MmcI protein	NA	0.927	3.38E-01
MSMEG_6886	transcriptional regulator	NA	1.129	2.36E-01
MSMEG_6887	amidohydrolase family protein	NA	1.078	7.96E-01
MSMEG_6888	transposase subunit	NA	2.005	3.35E-01
MSMEG_6889	transposase	NA	1.092	4.10E-01

MSMEG_6890	antibiotic biosynthesis monooxygenase domain protein	NA	0.873	2.95E-01
MSMEG_6891	ribonuclease H; this region contains one or more premature stops and/or frameshifts	NA	0.972	7.80E-01
MSMEG_6892	replicative DNA helicase	NA	0.913	7.46E-02
MSMEG_6893	hypothetical protein	NA	0.956	7.40E-01
MSMEG_6894	ribosomal protein L9	rplI	1.232	5.16E-02
MSMEG_6895	ribosomal protein S18	rpsR	0.863	1.21E-01
MSMEG_6896	single-stranded DNA-binding protein	NA	0.877	5.81E-02
MSMEG_6897	ribosomal protein S6	rpsF	1.026	9.09E-01
MSMEG_6898	hypothetical protein	NA	1.028	6.29E-01
MSMEG_6899	conserved hypothetical protein	NA	0.859	6.85E-03
MSMEG_6900	penicillin-binding protein 1	NA	0.943	2.45E-01
MSMEG_6901	conserved hypothetical protein	NA	0.974	8.11E-01
MSMEG_6902	putative membrane protein	NA	1.004	9.46E-01
MSMEG_6903	transcriptional regulator, PadR family protein	NA	0.839	3.02E-02
MSMEG_6904	myo-inositol-1-phosphate synthase	NA	0.769	1.45E-02
MSMEG_6906	putative hydrolase	NA	0.906	1.74E-02
MSMEG_6907	MmcI protein	NA	0.867	3.74E-02
MSMEG_6908	putative HTH-type transcriptional regulator	NA	1.082	1.70E-01
MSMEG_6909	amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine fa	NA	0.923	4.28E-01
MSMEG_6911	ABC transporter, ATP-binding protein GluA	NA	1.032	7.96E-01
MSMEG_6913	putative transcriptional regulatory protein	NA	0.987	8.70E-01
MSMEG_6914	conserved hypothetical protein	NA	1.295	5.87E-02
MSMEG_6916	short chain dehydrogenase	NA	1.099	5.78E-02
MSMEG_6917	leucyl-tRNA synthetase	leuS	1.323	3.74E-02
MSMEG_6919	proline-rich 28 kDa antigen	NA	1.056	9.74E-02
MSMEG_6920	hypothetical protein	NA	1.082	2.51E-01
MSMEG_6921	conserved hypothetical protein	NA	0.996	9.70E-01
MSMEG_6922	transporter, major facilitator family protein	NA	1.796	2.81E-02
MSMEG_6923	conserved hypothetical protein	NA	1.080	3.05E-01
MSMEG_6925	conserved hypothetical protein	NA	1.540	2.56E-01
MSMEG_6926	tRNA adenylyltransferase	NA	1.097	6.37E-02

MSMEG_6927	MutT/nudix family protein	NA	0.988	6.07E-01
MSMEG_6928	conserved hypothetical protein	NA	1.303	1.32E-02
MSMEG_6929	integral membrane protein MviN, putative	NA	1.193	3.36E-01
MSMEG_6930	hypothetical protein	NA	1.740	3.86E-01
MSMEG_6931	RNA polymerase sigma-70 factor	NA	1.322	8.87E-02
MSMEG_6932	conserved hypothetical protein	NA	0.921	1.08E-01
MSMEG_6933	thioredoxin-disulfide reductase	trxB	0.981	8.08E-01
MSMEG_6934	thioredoxin	trx	1.019	6.42E-01
MSMEG_6935	N-acetylmuramoyl-L-alanine amidase	NA	1.281	4.04E-03
MSMEG_6936	conserved hypothetical protein	NA	1.102	3.15E-01
MSMEG_6938	ParB-like partition proteins	NA	0.872	1.58E-01
MSMEG_6939	Soj family protein	NA	0.960	4.38E-01
MSMEG_6940	methyltransferase GidB	gidB	1.048	4.75E-01
MSMEG_6941	R3H domain-containing protein	NA	1.110	4.20E-01
MSMEG_6942	membrane protein OxaA	NA	1.148	9.48E-03
MSMEG_6944	conserved hypothetical protein, putative	NA	1.009	7.36E-01
MSMEG_6945	ribonuclease P protein component	rnpA	0.966	7.98E-02
MSMEG_6946	ribosomal protein L34	rpmH	1.079	6.94E-01
MSMEG_6947	chromosomal replication initiator protein DnaA	dnaA	0.957	1.43E-01

Results are based on four biological repeats (adjusted P values are shown), which included two dye swaps.