Table S1: Summary of MetSV specific spacers with one until six mismatches in *M. mazei* draft genomes

Number of mis-matches	Spacer length	Spacer name	Spacer position	consensus repeat sequence	# of repeats	# of spacers	Accession number	Strain	Start position (MetSV genome)	End position (MetSV genome)
1	37	contig_16302_CRISPR2_S16	1	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	114	113	NZ_CP009513.1	M. mazei LYC	407	443
2	36	contig_16302_CRISPR1_S30	1	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	37	36	NZ_CP009513.1	M. mazei LYC	4313	4348
4	35	contig_16302_CRISPR1_S31	35	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	37	36	NZ_CP009513.1	M. mazei LYC	1580	1613
4	36	contig_16302_CRISPR1_S26	33	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	37	36	NZ_CP009513.1	M. mazei LYC	9298	9333
4	36	contig_20787_CRISPR1_S2	1	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	87	86	NZ_JJPO01000025.1	M. mazei strain 3.H.A.2.1 scaffold8_1_size73144-refined	8146	8175
4	36	contig_8256_CRISPR1_S2	1	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	87	86	JJPO01000025.1	M. mazei strain 3.H.A.2.1 scaffold8_1_size73144-refined	8146	8175
4	37	contig_16302_CRISPR1_S32	1	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	37	36	NZ_CP009513.1	M. mazei LYC	2739	2775
4	38	contig_16300_CRISPR2_S5	8	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	140	139	NZ_CP009511.1	M. mazei SarPi	3116	3153
4	43	contig_188	43	GAGCAAGATCCACTAA	75	74	NZ_JJPE01000147	M. mazei strain	9445	9478

		64_CRISPR2_S34		AACAAGGATTGAAAC			.1	3.F.A.2.3 scaffold90_1_size12997-refined		
4	43	contig_6146_CRISPR2_S34	43	GAGCAAGATCCACTAAAACAAGGATTGAAAC	75	74	JJPE01000147.1	M. mazei strain 3.F.A.2.3 scaffold90_1_size12997-refined	9445	9478
5	35	contig_15639_CRISPR1_S24	1	ATTTCAATCCACACACCCGCGAAGGGTGCGAC	52	51	JJOV01000045.1	Methanosarcina sp. 2.H.A.1B.4 scaffold35_1_size39257-refined	6419	6452
5	35	contig_16303_CRISPR1_S4	1	ATTCGCGAGCAAGATCCATTAAAACAAGGATTGAAAC	76	75	NZ_CP009514.1	M. mazei C16	3583	3617
5	35	contig_17077_CRISPR1_S24	1	ATTTCAATCCACACACCCGCGAAGGGTGCGAC	52	51	NZ_JJOV01000045.1	Methanosarcina sp. 2.H.A.1B.4 scaffold35_1_size39257-refined	6419	6452
5	36	contig_10932_CRISPR1_S42	36	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	54	53	JJQD01000055.1	M. mazei strain 1.F.A.2.8 scaffold51_1_size22620-refined	6401	6436
5	36	contig_16301_CRISPR2_S61	36	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	73	72	NZ_CP009512.1	M. mazei S-6	6401	6436
5	36	contig_20865_CRISPR1_S31	36	ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAAC	73	72	NZ_JJPP01000017.1	M. mazei strain 3.H.A.2.4 scaffold36_1_size53364-refined	6401	6436
5	36	contig_514_CRISPR1_S42	36	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	54	53	NZ_JJQD01000055.1	M. mazei strain 1.F.A.2.8 scaffold51_1_size22620-refined	6401	6436

5	36	contig_8407_CRISPR1_S31	36	ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAAC	73	72	JJPP01000017.1	M. mazei strain 3.H.A.2.4 scaffold36_1_size53364-refined	6401	6436
6	32	contig_12674_CRISPR1_S54	2	GAGTTCCCCACAAGCGTGGGGATGAACCG	66	65	JJQL01000088.1	Methanosarcina sp. 1.H.A.2.2 scaffold26_1_size92283-refined	224	251
6	32	contig_2251_CRISPR1_S54	2	GAGTTCCCCACAAGCGTGGGGATGAACCG	66	65	NZ_JJQL01000088.1	Methanosarcina sp. 1.H.A.2.2 scaffold26_1_size92283-refined	224	251
6	34	contig_10948_CRISPR1_S45	2	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	48	47	JJQD01000187.1	M. mazei strain 1.F.A.2.8 scaffold47_1_size23004-refined	1352	1381
6	34	contig_18600_CRISPR1_S62	34	ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAAC	79	78	NZ_JJPC01000112.1	M. mazei strain 3.F.A.1B.1 scaffold26_1_size43992-refined	5418	5447
6	34	contig_20299_CRISPR1_S62	34	ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAAC	73	72	NZ_JJPM01000068.1	M. mazei strain 3.H.A.1A.1 scaffold225_1_size8925-refined	5418	5447
6	34	contig_437_CRISPR1_S45	2	GTTTCAATCCTTGTTTTAATGGATCTTGCTCGCGAAT	48	47	NZ_JJQD01000187.1	M. mazei strain 1.F.A.2.8 scaffold47_1_size23004-refined	1352	1381
6	34	contig_5784_CRISPR1_S62	34	ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAAC	79	78	JJPC01000112.1	M. mazei strain 3.F.A.1B.1 scaffold26_1_size43992-refined	5418	5447
6	34	contig_786	34	ATTCGAGAGCAAGATC	73	72	JJPM01000068.1	M. mazei strain	5418	5447

		6_CRISPR1_S62		CACTAAAACAAGGATTGAAAC				3.H.A.1A.1 scaffold225_1_size8925-refined		
6	35	contig_11385_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	106	105	JJQE01000092.1	M. mazei strain 1.F.M.0.5 scaffold84_1_size12949-refined	9479	9505
6	35	contig_12995_CRISPR1_S46	34	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	134	133	JJQN01000148.1	M. mazei strain 1.H.A.2.6 scaffold63_1_size20235-refined	5995	6029
6	35	contig_13199_CRISPR1_S5	31	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	104	103	JJOU01000103.1	M. mazei strain 2.F.T.2.6 scaffold12_1_size52753-refined	3995	4026
6	35	contig_14069_CRISPR1_S39	2	ATTCGCGAGCAAGATCCATTAAAACAAGGATTGAAAC	183	182	JJQQ01000060.1	M. mazei strain 1.H.M.0.1 scaffold31_1_size37607-refined	7735	7767
6	35	contig_16873_CRISPR1_S5	31	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	104	103	NZ_JJOU01000103.1	M. mazei strain 2.F.T.2.6 scaffold12_1_size52753-refined	3995	4026
6	35	contig_18427_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	107	106	NZ_JJPB01000021.1	M. mazei strain 3.F.A.1A.3 scaffold85_1_size13020-refined	9479	9505
6	35	contig_18761_CRISPR1_S39	1	ATTCGTGAGCAAGATCCATTAAAACAAGGATTGAAAC	54	53	NZ_JJPD01000191.1	M. mazei strain 3.F.A.2.12 scaffold130_1_size9136-refined	9479	9505
6	35	contig_19113_CRISPR	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATT	108	107	NZ_JJPF01000076.1	M. mazei strain 3.F.A.2.5	9479	9505

		1_S39		GAAAC				scaffold102_1_size13109-refined		
6	35	contig_19285_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	106	105	NZ_JJPG01000029.1	M. mazei strain 3.F.A.2.6 scaffold88_1_size12957-refined	9479	9505
6	35	contig_19514_CRISPR1_S38	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	105	104	NZ_JJPH01000059.1	M. mazei strain 3.F.A.2.7 scaffold83_1_size12932-refined	9479	9505
6	35	contig_20064_CRISPR1_S3	34	ATCGCAATCGGTTAGAAAACTCGTTAGAGATTGAAAC	64	63	NZ_JJPL01000042.1	M. mazei strain 3.F.T.2.1 scaffold49_1_size29560-refined	4739	4767
6	35	contig_2617_CRISPR1_S46	34	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	134	133	NZ_JJQN01000148.1	M. mazei strain 1.H.A.2.6 scaffold63_1_size20235-refined	5995	6029
6	35	contig_3427_CRISPR1_S39	2	ATTCGCGAGCAAGATCCATTAAAACAAGGATTGAAAC	183	182	NZ_JJQQ01000060.1	M. mazei strain 1.H.M.0.1 scaffold31_1_size37607-refined	7735	7767
6	35	contig_4402_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	107	106	JJPB01000021.1	M. mazei strain 3.F.A.1A.3 scaffold85_1_size13020-refined	9479	9505
6	35	contig_5964_CRISPR1_S39	1	ATTCGTGAGCAAGATCCATTAAAACAAGGATTGAAAC	54	53	JJPD01000191.1	M. mazei strain 3.F.A.2.12 scaffold130_1_size9136-refined	9479	9505
6	35	contig_600_CRISPR1_S	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATT	106	105	NZ_JJQE01000092.1	M. mazei strain 1.F.M.0.5	9479	9505

		39		GAAAC				scaffold84_1_size12949-refined		
6	35	contig_6277_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	108	107	JJPF01000076.1	M. mazei strain 3.F.A.2.5 scaffold102_1_size13109-refined	9479	9505
6	35	contig_6502_CRISPR1_S39	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	106	105	JJPG01000029.1	M. mazei strain 3.F.A.2.6 scaffold88_1_size12957-refined	9479	9505
6	35	contig_6683_CRISPR1_S38	1	ATTCGCGAGCAAGATCCACTAAAACAAGGATTGAAAC	105	104	JJPH01000059.1	M. mazei strain 3.F.A.2.7 scaffold83_1_size12932-refined	9479	9505
6	35	contig_7581_CRISPR1_S3	34	ATCGCAATCGGTTAGAAAACTCGTTAGAGATTGAAAC	63	62	JJPL01000042.1	M. mazei strain 3.F.T.2.1 scaffold49_1_size29560-refined	4739	4767
6	36	contig_12995_CRISPR1_S125	36	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	134	133	JJQN01000148.1	M. mazei strain 1.H.A.2.6 scaffold63_1_size20235-refined	10342	10376
6	36	contig_15689_CRISPR1_S8	4	ATTGCAATTGGTTTGAAAACTCGTTAGAGATTGAAAC	105	104	JJOV01000033.1	Methanosarcina sp. 2.H.A.1B.4 scaffold8_1_size95506-refined	4213	4248
6	36	contig_16301_CRISPR2_S34	36	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	73	72	NZ_CP009512.1	M. mazei S-6	10342	10376
6	36	contig_16302_CRISPR2_S24	3	ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC	114	113	NZ_CP009513.1	M. mazei LYC	4971	5005

6	*36*	*contig_17065_CRISPR1_S8*	*4*	*ATTGCAATTGGTTTGAAAACTCGTTAGAGATTGAAAC*	*105*	*104*	*NZ_JJOV01000033.1*	*Methanosarcina sp. 2.H.A.1B.4 scaffold8_1_size95506-refined*	*4213*	*4248*
6	*36*	*contig_2617_CRISPR1_S125*	*36*	*ATTCGTGAGCAAGATCCACTAAAACAAGGATTGAAAC*	*134*	*133*	*NZ_JJQN01000148.1*	*M. mazei strain 1.H.A.2.6 scaffold63_1_size20235-refined*	*10342*	*10376*
6	*37*	*contig_16303_CRISPR1_S50*	*33*	*ATTCGCGAGCAAGATCCATTAAAACAAGGATTGAAAC*	*76*	*75*	*NZ_CP009514.1*	*M. mazei C16*	*2473*	*2508*
6	*39*	*contig_15689_CRISPR1_S9*	*38*	*ATTGCAATTGGTTTGAAAACTCGTTAGAGATTGAAAC*	*105*	*104*	*JJOV01000033.1*	*Methanosarcina sp. 2.H.A.1B.4 scaffold8_1_size95506-refined*	*9382*	*9416*
6	*39*	*contig_17065_CRISPR1_S9*	*38*	*ATTGCAATTGGTTTGAAAACTCGTTAGAGATTGAAAC*	*105*	*104*	*NZ_JJOV01000033.1*	*Methanosarcina sp. 2.H.A.1B.4 scaffold8_1_size95506-refined*	*9382*	*9416*

Table S2: Primer used in this study

ORF or genome region	**Primer set**	**Sequence 5´=>3´**
Spacer 1-29 IB-locus	C1_for C1_rev2	TGCGTAGATTGCTGTTACCGG TCCCCTGTTTTCCAGATACCG
Spacer 1-9 IIIC-locus	CRISPR_IIIC_for CRISPR_IIICsp_r	GATTTCAAAACCCTTCCACAG AATGCTAAACTCACGGGAAAC
qRT-PCR primer		
MM1215	MM1215 for MM1215 rev	TCAAGAGCGAGGGCATGAATG GCACTACCGAGAACAATAGCC
MM1621	MM1621 for MM1621 rev	TAGGAGGTTTTCTCGGAAGCG AAGCGTATCTCCATCAAGCCC
MM2181	MM2181 for MM2181 rev	GCCTCCATGAGAAGAATGCTC CTTCAAGGTCTCCAACTCCTG
MM0002	MM_0002 qrt for MM_0002 qrt rev	TTTGACCCTCTTCTGGGATGG TCAGCTGTTAGCTTCTCTCCG
MM0276	MM_0276 qrt for MM_0276 qrt rev	GGCCCAGAAATGGATCTGAAG TTCTGCCCCCTTATCATCACC
MM0490	MM_0490 qrt for MM_0490 qrt rev	TCTTCTCCTGCTCCTGTTCTC AGAGAATTGACCGAAGGCTCC
MM0807	MM_0807 qrt for MM_0807 qrt rev	GTTCCTCCTCTTACAAAGCCG TCCAACTGCATTCAGCCTGTC
MM1009	MM_1009 qrt for MM_1009 qrt rev	AAGCGTTGGTCAGGCAATTCG GGGCAACATTGTCAGCAGTAC
MM1601	MM1601 qrt for MM1601 qrt rev	TCTCGCACAGAATGTATCGGC GCACTTTTAAGGTCATCCCCG
MM2021	MM_2021 qrt for MM_2021 qrt rev	TAAGGGAAGATCTGCAGGGGA ACCCAGCGGAGTAATCGAAGT
MM2833	MM_2833 qrt for MM_2833 qrt rev	AACGGGGTTGAATTTCGCGCT TTTGTTACGTCCCTGCCGTCT
MM3096	MM_3096 qrt for MM_3096 qrt rev	CTCTAGGGGCATCAAACGGAA ACTGCCCGGAAATTCCTGTGA
MM0565	MM565 for MM565 rev	CCTGTTATTATCTGTGTGACGC ATGACCTGGTTGCCTCTATC
MM0564	MM564 for MM564 rev	ATTTTTGATGTGTTGTATGG TTTGTTGAAGAAGGTTTTTG
MM0563	MM563 for MM563 rev	GGGGAAGGAAAAAGTCAGTC CATTAATTAGTGCTGCGGTG
MM0562	MM562 for MM562 rev	GACTGCTTGGTTTTTAGGG GGAGAAAGCACTTGAATACC
MM0561	MM561 for MM561 rev	TGTATGGCACATGACTTTGG ACGGGCATCTTTTACACTTC
MM0560	MM560 for MM560 rev	CGGATTAGACGAAGGTTCAA TAAAGCGAGCCAAGGAGTT
MM0559	MM559 for MM559 rev	AATGGCAGAAGCAGAAACC AAACCGTCCTGTCAATGTG
MM0558	MM558 for MM 558 rev	GGGCTTTACAGGGTTCAGA ATTATCTCGTCGCTGACAAG

MM0557	MM557 for MM557 rev	AGCAACAGCCTGGTCAAAG TCCGGTAACAGCAATCTACG
leader IB	leader IB for leader IB rev	AGGGTTTGATAATTTTCCAG AAAAGCGGTGTTAAGTCA
MM3353	qRTMM3353 for qRTMM3353 rev	ATGGTATGGTCCTTATATCGT CTGAATCGTAGATTTTCTGC
MM3354	qRTMM3354 for qRTMM3354 rev	CAGGCACTCATGAAAGATAC GGTCGTTTCTAAGAGTCTAATCC
MM3355	qRTMM3355 for qRTMM3355 rev	CTCAACAACGCTACCTATTC CATGATTTTTTCCCTTTAGTG
MM3356	qRTMM3356 for2 qRTMM3356 rev2	AGTTCTTGTGACAAACCATC TTCTCTTTATTTGTCCTCGG
MM3357	qRTMM3357 for qRTMM3357 rev	ACTGTCAGATAATTTCCGAG CAAAAGAGTAGCTGGGTAATG
MM3358	qRTMM3358 for qRTMM3358 rev	AGAGGAATAGGAGAATACGC GATAGCCACCAGTTATTTCC
MM3359	qRTMM3359 for qRTMM3359 rev	ATGAGTCCAGGGAATATTAAG TACTGCACAAGAGGGTAGC
MM3360	qRTMM3360 for qRTMM3360 rev	CCTGAGAGAGTTAAGGAAGC TCAATAGACCCTTCGGTAG
leader IIIC	qRTIIICcrRNA for qRTIIICcrRNA r2	TCCAAACCACTAAAAAAACC AAGGATCTCATACGTGAATTAG
RT-PCR primer (one step RT-PCR)		
MSV06	MSVORF6 rt for MSVORF6 rt rev	TTCAGGCGTCAACAGATGCAG GCTTCATCATCGCCTTCTATC
MSV07	MSVORF7 rt for MSVORF7 rt rev	ACGACTTATCCGGGTTACTGG CCTATTGCTTCGCCTAATGCC
MSV13	MSVORF13 rt for MSVORF13 rt rev	ATAGACGCCTACAGAATCCCC ATCTACCGAAGCCGGTCTTTG
MSV15	MSVORF15 rt for MSVORF15 rt rev	TTGGGATTCCTTCGCTATCGG TCCGCCGTCGATTATTGGAAC
MSV19	MSVORF19 rt for MSVORF19 rt rev	TGGACAATACGGCGACTAACC TAACATCAATACCGGCGGGTG
MSV22	MSVORF22 rt for MSVORF22 rt rev	TATGTGCCGGATGTGATAGG TGGCGTATCCGTTGGTAAAGG

Table S3: MSV ORF proteins identified via stacking gel SDS-PAGE – LC-MS analysis in Sample #1 (viral proteins extracted via filtration). PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF5			**10**	**49**	**4**	**4**	**92**	**10.7**	**High**
	19_TGISINVTLSDGSTGTLQR		2						
	7_ITNYSLSFFK		2						
	63_LVWGLYDMR		2						
	63_LVWGLYDMR	1xOxidation [M8]	2						
	42_FNVMQGK		2						
ORF6			**29**	**36**	**8**	**8**	**244**	**28.5**	**High**
	104_VMMPIVNVEQPQQIEEALPAAK	2xOxidation [M2; M3]	4						
	104_VMMPIVNVEQPQQIEEALPAAK	1xOxidation [M2]	1						
	104_VMMPIVNVEQPQQIEEALPAAK		2						
	211_MIESWLQNFFK		3						
	45_QQMQEALR		3						
	165_YDDDATDSEEIEGDDEAGGEK		3						
	6_ALSFNQK		7						
	22_ANPDKSYNQLEK		1						
	27_SYNQLEK		3						
	13_MDAFLK		2						
ORF7			**26**	**26**	**9**	**9**	**359**	**41.2**	**High**
	140_VTIAGNALALFR		2						
	67_YYVTFLDSMNDFK		1						

	317_AEGSCLELFVK	1xCarbamidomethyl [C5]	2						
	123_ALNIFFDVLR		5						
	328_YLLNSLYGK		2						
	161_VNVELDNK		4						
	215_KGEGLEVLLALLNNPR		4						
	256_LYFPTSK		4						
	207_YPNPQMLR		2						
ORF8			**6**	**41**	**3**	**3**	**79**	**9.2**	**High**
	41_IPVNFTEPASQSQLIR		2						
	32_LWGIEELTR		2						
	72_VNPTTWK		2						
ORF10			**24**	**46**	**4**	**4**	**117**	**13.5**	**High**
	4_TSDVIELLESGENDTAK		4						
	21_IKEQTGASESLITR		13						
	23_EQTGASESLITR		4						
	49_QEEAKEEEEEEPTDEEIDGIITK		3						
ORF13			**26**	**44**	**7**	**7**	**202**	**23.2**	**High**
	46_VLCLDPLNVIDGEIDAYR	1xCarbamidomethyl [C3]	5						
	151_NIGVVMSTQRPASVDTGVIGLTDYLVLFR	1xOxidation [M6]	2						
	108_CDWLFPALTFR	1xCarbamidomethyl [C1]	4						
	91_NVVVYFNEMLR	1xOxidation [M9]	2						
	21_TISIIGGK		8						
	46_VLCLDPLNVIDGEIDAYRIPIR	1xCarbamidomethyl [C3]	2						
	38_MLLDQSKR	1xOxidation [M1]	3						
ORF15			**63**	**52**	**6**	**6**	**102**	**10.3**	**High**

	8_KAVTFESGSLWDSFAIGAVK		29						
	50_GAAGVVIQSAIK		17						
	9_AVTFESGSLWDSFAIGAVK		12						
	33_AMIPVVGNGSLK		1						
	1_MVDLVPK	1xOxidation [M1]	3						
	50_GAAGVVIQSAIKGK		1						
ORF16			**263**	**82**	**12**	**12**	**146**	**15.7**	**High**
	105_GVTAIAANGWVTIGSYTVPAQEEIR		4						
	41_LAPIVPMSQATLREDDKILVEYK		13						
	41_LAPIVPMSQATLREDDK	1xOxidation [M7]	16						
	41_LAPIVPMSQATLREDDK		8						
	64_TGTASQITGTSCSAR	1xCarbamidomethyl [C12]	22						
	22_QVLYETGSEIAVLGGSDPR		23						
	11_IVKTDASETVR		10						
	88_TGNVAESFLR		29						
	41_LAPIVPMSQATLR		9						
	41_LAPIVPMSQATLR	1xOxidation [M7]	31						
	130_LGQSIAENSR		22						
	54_EDDKILVEYK		32						
	41_LAPIVPMSQATLREDDKILVEYK	1xOxidation [M7]	19						
	58_ILVEYK		15						
	98_SSDVFAR		10						
ORF17			**11**	**36**	**2**	**2**	**55**	**6.4**	**High**
	34_IAVCLESVSLTLK	1xCarbamidomethyl [C4]	2						
	47_DIKDDLK		9						
ORF18			**7**	**55**	**3**	**3**	**106**	**10.9**	**High**

	69_SEASAIPTIETGGGMDLSQLIPVALIIGGAVIIK	1xOxidation [M15]	1						
	42_SYSIQYPTYQVQIDSPLASQTTK		4						
	42_SYSIQYPTYQVQIDSPLASQTTKK		2						
ORF19			**37**	**83**	**7**	**7**	**90**	**10.2**	**High**
	71_GEFYAYTTAPAGIDVR		4						
	19_AYLAIQNMDNTATNLLFILPEQSEPETFIK		1						
	55_GYGLFELQDCK	1xCarbamidomethyl [C10]	2						
	19_AYLAIQNMDNTATNLLFILPEQSEPETFIK	1xOxidation [M8]	2						
	1_MKIPVNTVIK	1xOxidation [M1]	12						
	3_IPVNTVIK		3						
	1_MKIPVNTVIK		5						
	69_QKGEFYAYTTAPAGIDVR		2						
	49_SGFCIR	1xCarbamidomethyl [C4]	6						
ORF20			**35**	**55**	**10**	**10**	**247**	**26.3**	**High**
	81_FLTLTSGTLAGSSATR		3						
	22_GGEEGTAGLYACK	1xCarbamidomethyl [C12]	4						
	129_IACFGFAPAFNSLPISNR	1xCarbamidomethyl [C3]	3						
	152_SGNVWYCAYASQAVAVSSLPLGR	1xCarbamidomethyl [C7]	3						
	189_QEGSSNIDIVR		6						
	175_NLQSGDICTVR	1xCarbamidomethyl [C8]	3						
	186_LDRQEGSSNIDIVR		6						

	54_YLDGADNPDVWFPIPGGGGGTVVYDNR		1						
	35_TILNEHR		2						
	47_EYHLVGK		4						
ORF21			**84**	**75**	**16**	**16**	**277**	**28.3**	**High**
	174_LPTGASTSTQYTLPSNVGDLLK		6						
	72_MINDPVISGSNEVIK	1xOxidation [M1]	11						
	109_ETDGSLSSSLAQVFGTESQK		7						
	213_IGAYTPVSDPLQALK		4						
	87_TNPEIPIDTTTKK		9						
	151_SIGETVIGFLTDSYKESK		4						
	151_SIGETVIGFLTDSYK		13						
	234_SSSGSSNSLTTPK		4						
	72_MINDPVISGSNEVIK		5						
	213_IGAYTPVSDPLQALKDSGIVK		2						
	87_TNPEIPIDTTTK		5						
	100_SALTSSTPK		4						
	202_ASMQEAINQTK		2						
	99_KSALTSSTPK		4						
	26_TEDVGSGGNFGGLGGGGTLEGFEGVTDSGTPYNISFPAVDPSPIIK		1						
	7_AIIGVGVIAAAYLYMSGSK		2						
	201_KASMQEAINQTK		1						
ORF22			**62**	**52**	**15**	**15**	**334**	**37.9**	**High**
	244_LYIDGTSGDTFK		4						
	58_LDAWLEGCEGWIQSTR	1xCarbamidomethyl [C8]	3						
	121_TISFLGSAVPGSYNIR		4						
	57_RLDAWLEGCEGWIQSTR	1xCarbamidometh	4						

		yl [C9]							
	4_NLPSIYYVYANK		4						
	47_IESYDIGDLR		4						
	105_LLNFTANAFK		2						
	305_FTMDSVEHPYPAKPSPEPK	1xOxidation [M3]	7						
	144_GSVPANASATDNR		4						
	305_FTMDSVEHPYPAKPSPEPK		5						
	75_NEFNELETNLFDLDK		2						
	227_MVINCPDRPFVR	1xCarbamidomethyl [C5]; 1xOxidation [M1]	7						
	98_LSTDSLK		5						
	16_TYEEEIK		4						
	23_AYLIENFSAVGQLNISNSSGCGFK	1xCarbamidomethyl [C21]	1						
	47_IESYDIGDLRR		2						

Table S4: MSV ORF proteins identified via stacking gel SDS-PAGE – LC-MS analysis in Sample #2 (viral proteins extracted via filtration and washed). PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF5			**21**	**61**	**6**	**6**	**92**	**10.7**	**High**
	7_ITNYSLSFFK		2						
	7_ITNYSLSFFKDR		4						
	19_TGISINVTLSDGSTGTLQR		4						
	63_LVWGLYDMR	1xOxidation [M8]	5						
	63_LVWGLYDMR		1						
	42_FNVMQGK		2						
	54_MGYTHPDFK		3						
ORF6			**68**	**46**	**10**	**10**	**244**	**28.5**	**High**
	211_MIESWLQNFFK		3						
	211_MIESWLQNFFK	1xOxidation [M1]	3						
	165_YDDDATDSEEIEGDDEAGGEK		6						
	104_VMMPIVNVEQPQQIEEALPAAK		2						
	104_VMMPIVNVEQPQQIEEALPAAK	1xOxidation [M]	10						
	104_VMMPIVNVEQPQQIEEALPAAK	2xOxidation [M2; M3]	6						
	22_ANPDKSYNQLEK		4						
	45_QQMQEALR		9						
	27_SYNQLEK		3						
	6_ALSFNQK		6						
	13_MDAFLK		9						

	44_RQQMQEALR		2							
	186_IFSGLINSNQYLDFMFPKPEDLANK		1							
	13_MDAFLK	1xOxidation [M1]	4							
ORF7			**72**	**40**	**13**	**13**	**359**	**41.2**	**High**
	40_ILYSGSNLISLSK		3							
	215_KGEGLEVLLALLNNPR		11							
	80_TSLEALGEAIGLKK		3							
	328_YLLNSLYGK		6							
	140_VTIAGNALALFR		3							
	263_TGTMEGYYNFPELR	1xOxidation [M4]	3							
	67_YYVTFLDSMNDFK	1xOxidation [M9]	3							
	317_AEGSCLELFVK	1xCarbamidomethyl [C5]	1							
	123_ALNIFFDVLR		8							
	161_VNVELDNK		7							
	67_YYVTFLDSMNDFK		2							
	207_YPNPQMLR		8							
	256_LYFPTSK		6							
	207_YPNPQMLR	1xOxidation [M6]	4							
	169_FHLSYYGGR		4							
ORF8			**15**	**42**	**4**	**4**	**79**	**9.2**	**High**
	41_IPVNFTEPASQSQLIR		5							
	32_LWGIEELTR		3							
	72_VNPTTWK		6							
	31_KLWGIEELTR		1							
ORF10			**61**	**59**	**5**	**5**	**117**	**13.5**	**High**
	21_IKEQTGASESLITR		24							
	4_TSDVIELLESGENDTAK		6							
	49_QEEAKEEEEEEPTDEEIDGIITK		24							
	23_EQTGASESLITR		6							

	103_ASEMPVFCPGCGAEF	2xCarbamidomethyl [C8; C11]	1						
ORF13			**57**	**45**	**9**	**9**	**202**	**23.2**	**High**
	46_VLCLDPLNVIDGEIDAYR	1xCarbamidomethyl [C3]	12						
	46_VLCLDPLNVIDGEIDAYRIPIR	1xCarbamidomethyl [C3]	5						
	151_NIGVVMSTQRPASVDTGVIGLTDYLVLFR		3						
	151_NIGVVMSTQRPASVDTGVIGLTDYLVLFR	1xOxidation [M6]	7						
	108_CDWLFPALTFR	1xCarbamidomethyl [C1]	3						
	91_NVVVYFNEMLR		1						
	91_NVVVYFNEMLR	1xOxidation [M9]	3						
	21_TISIIGGK		10						
	38_MLLDQSK		3						
	38_MLLDQSK	1xOxidation [M1]	5						
	38_MLLDQSKR	1xOxidation [M1]	3						
	38_MLLDQSKR		1						
	46_VLCLDPLNVIDGEIDAYRIPIRK	1xCarbamidomethyl [C3]	1						
ORF15			**113**	**87**	**7**	**7**	**102**	**10.3**	**High**
	8_KAVTFESGSLWDSFAIGAVK		39						
	9_AVTFESGSLWDSFAIGAVK		19						
	50_GAAGVVIQSAIKGK		7						
	50_GAAGVVIQSAIK		34						
	67_IIGSAFAIDAVEDAVQALIVPIIDGGSDTGGNIDNW		4						
	1_MVDLVPK	1xOxidation [M1]	6						
	33_AMIPVVGNGSLK	1xOxidation [M2]	4						
ORF16			**378**	**82**	**12**	**12**	**146**	**15.7**	**High**
	11_IVKTDASETVR		11						
	105_GVTAIAANGWVTIGSYTVPAQEEIR		7						
	130_LGQSIAENSR		25						
	41_LAPIVPMSQATLREDDKILVEYK	1xOxidation [M7]	34						
	41_LAPIVPMSQATLREDDKILVEYK		27						

	41_LAPIVPMSQATLREDDK	1xOxidation [M7]	22							
	41_LAPIVPMSQATLREDDK		14							
	41_LAPIVPMSQATLR	1xOxidation [M7]	43							
	41_LAPIVPMSQATLR		14							
	22_QVLYETGSEIAVLGGSDPR		23							
	88_TGNVAESFLR		51							
	64_TGTASQITGTSCSAR	1xCarbamidomethyl [C12]	30							
	54_EDDKILVEYK		45							
	58_ILVEYK		17							
	98_SSDVFAR		15							
ORF17			**14**	**36**	**2**	**2**	**55**	**6.4**	**High**	
	34_IAVCLESVSLTLK	1xCarbamidomethyl [C4]	4							
	47_DIKDDLK		10							
ORF18			**6**	**23**	**2**	**2**	**106**	**10.9**	**High**	
	42_SYSIQYPTYQVQIDSPLASQTTK		4							
	42_SYSIQYPTYQVQIDSPLASQTTKK		2							
ORF19			**85**	**83**	**7**	**7**	**90**	**10.2**	**High**	
	55_GYGLFELQDCK	1xCarbamidomethyl [C10]	4							
	69_QKGEFYAYTTAPAGIDVR		9							
	71_GEFYAYTTAPAGIDVR		11							
	19_AYLAIQNMDNTATNLLFILPEQSEPETFIK	1xOxidation [M8]	3							
	1_MKIPVNTVIK		8							
	49_SGFCIR	1xCarbamidomethyl [C4]	11							
	3_IPVNTVIK		5							
ORF20			**72**	**55**	**10**	**10**	**247**	**26.3**	**High**	
	129_IACFGFAPAFNSLPISNR	1xCarbamidomethyl [C3]	10							
	186_LDRQEGSSNIDIVR		11							
	54_YLDGADNPDVWFPIPGGGGGTVVYDNR		1							
	152_SGNVWYCAYASQAVAVSSLPLGR	1xCarbamidomethyl [C7]	4							

	175_NLQSGDICTVR	1xCarbamidomethyl [C8]	8						
	189_QEGSSNIDIVR		12						
	81_FLTLTSGTLAGSSATR		6						
	22_GGEEGTAGLYACK	1xCarbamidomethyl [C12]	9						
	35_TILNEHR		5						
	47_EYHLVGK		6						
ORF21			**110**	**58**	**14**	**14**	**277**	**28.3**	**High**
	174_LPTGASTSTQYTLPSNVGDLLK		11						
	72_MINDPVISGSNEVIK		6						
	72_MINDPVISGSNEVIK	1xOxidation [M1]	18						
	213_IGAYTPVSDPLQALK		5						
	87_TNPEIPIDTTTK		8						
	87_TNPEIPIDTTTKK		13						
	151_SIGETVIGFLTDSYKESK		4						
	151_SIGETVIGFLTDSYK		16						
	234_SSSGSSNSLTTPK		5						
	109_ETDGSLSSSLAQVFGTESQK		8						
	213_IGAYTPVSDPLQALKDSGIVK		2						
	100_SALTSSTPK		6						
	202_ASMQEAINQTK		3						
	129_TNDRGDYYATSAGGGAGAIK		1						
	99_KSALTSSTPK		4						
ORF22			**139**	**52**	**16**	**16**	**334**	**37.9**	**High**
	105_LLNFTANAFK		5						
	227_MVINCPDRPFVR	1xCarbamidomethyl [C5]	9						
	227_MVINCPDRPFVR	1xCarbamidomethyl [C5]; 1xOxidation [M1]	14						
	75_NEFNELETNLFDLDK		2						
	244_LYIDGTSGDTFK		11						

	47_IESYDIGDLRR		6						
	47_IESYDIGDLR		9						
	58_LDAWLEGCEGWIQSTR	1xCarbamidomethyl [C8]	4						
	57_RLDAWLEGCEGWIQSTR	1xCarbamidomethyl [C9]	8						
	74_RNEFNELETNLFDLDK		5						
	4_NLPSIYYVYANK		7						
	121_TISFLGSAVPGSYNIR		9						
	305_FTMDSVEHPYPAKPSPEPK	1xOxidation [M3]	13						
	305_FTMDSVEHPYPAKPSPEPK		9						
	144_GSVPANASATDNR		6						
	16_TYEEEIK		9						
	98_LSTDSLK		12						
	23_AYLIENFSAVGQLNISNSSGCGFK	1xCarbamidomethyl [C21]	1						

Table S5A: MetSV ORF proteins identified in protein band 71 via tryptic digestion. PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF1			**7**	**40**	**3**	**3**	**55**	**6.5**	**High**
	28_KDPETEAALLLMSR	1xOxidation [M12]	1						
	1_MIHITGDK	1xOxidation [M1]	4						
	1_MIHITGDK		1						
	29_DPETEAALLLMSR	1xOxidation [M11]	1						
ORF2			**3**	**76**	**3**	**3**	**41**	**5**	**High**
	16_FNTFLNTPLWEDDLTK		1						
	1_MFNSITNK	1xOxidation [M1]	1						
	9_IYSLMTR	1xOxidation [M5]	1						
ORF5			**9**	**49**	**4**	**4**	**92**	**10.7**	**High**
	54_MGYTHPDFK	1xOxidation [M1]	3						
	19_TGISINVTLSDGSTGTLQR		1						
	54_MGYTHPDFK		1						
	7_ITNYSLSFFK		3						
	42_FNVMQGK	1xOxidation [M4]	1						
ORF8			**5**	**42**	**4**	**4**	**79**	**9.2**	**High**
	41_IPVNFTEPASQSQLIR		1						
	32_LWGIEELTR		1						
	31_KLWGIEELTR		1						
	72_VNPTTWK		2						

ORF9			**7**	**53**	**4**	**4**	**62**	**7.7**	**High**
	45_LLELVFDYR		2						
	4_QDIENLIK		2						
	34_EQEYIQEEK		1						
	12_LKEEYIK		2						
ORF10			**2**	**12**	**2**	**2**	**117**	**13.5**	**High**
	23_EQTGASESLITR		1						
	21_IKEQTGASESLITR		1						
ORF11			**2**	**36**	**2**	**2**	**47**	**5.8**	**High**
	19_TALIFNEK		1						
	30_TYHFDQTIR		1						
ORF13			**2**	**7**	**2**	**2**	**202**	**23.2**	**High**
	21_TISIIGGK		1						
	38_MLLDQSK	1xOxidation [M1]	1						
ORF15			**266**	**100**	**14**	**14**	**102**	**10.3**	**High**
	50_GAAGVVIQSAIKGKTGK		1						
	50_GAAGVVIQSAIKGK		1						
	8_KAVTFESGSLWDSFAIGAVKAIEER		1						
	8_KAVTFESGSLWDSFAIGAVK		4						
	50_GAAGVVIQSAIK		138						
	45_SAVAKGAAGVVIQSAIKGK		3						
	45_SAVAKGAAGVVIQSAIK		2						
	9_AVTFESGSLWDSFAIGAVKAIEER		1						
	9_AVTFESGSLWDSFAIGAVK		79						
	33_AMIPVVGNGSLKSAVAKGAAGVVIQSAIK		2						
	33_AMIPVVGNGSLKSAVAKGAAGVVIQSAIK	1xOxidation [M2]	1						
	33_AMIPVVGNGSLKSAVAK	1xOxidation [M2]	3						
	33_AMIPVVGNGSLKSAVAK		1						
	33_AMIPVVGNGSLK	1xOxidation [M2]	5						

	1_MVDLVPK	1xOxidation [M1]	11						
	33_AMIPVVGNGSLK		6						
	67_IIGSAFAIDAVEDAVQALIVPIIDGGSDTGGNIDNW		2						
	1_MVDLVPK		5						
ORF16			**32**	**75**	**9**	**9**	**146**	**15.7**	**High**
	130_LGQSIAENSR		4						
	105_GVTAIAANGWVTIGSYTVPAQEEIR		4						
	41_LAPIVPMSQATLR		3						
	64_TGTASQITGTSCSAR	1xCarbamidomethyl [C12]	3						
	88_TGNVAESFLR		5						
	22_QVLYETGSEIAVLGGSDPR		3						
	54_EDDKILVEYK		2						
	58_ILVEYK		4						
	41_LAPIVPMSQATLR	1xOxidation [M7]	3						
	98_SSDVFAR		1						
ORF17			**4**	**36**	**2**	**2**	**55**	**6.4**	**High**
	34_IAVCLESVSLTLK	1xCarbamidomethyl [C4]	1						
	47_DIKDDLK		3						
ORF19			**73**	**86**	**7**	**7**	**90**	**10.2**	**High**
	1_MKIPVNTVIK	1xOxidation [M1]	7						
	55_GYGLFELQDCK	1xCarbamidomethyl [C10]	4						
	71_GEFYAYTTAPAGIDVR		6						
	69_QKGEFYAYTTAPAGIDVR		3						
	19_AYLAIQNMDNTATNLLFILPEQSEPETFIK		6						
	19_AYLAIQNMDNTATNLLFILPEQSEPETFIK	1xOxidation [M8]	3						
	3_IPVNTVIK		36						
	1_MKIPVNTVIK		3						
	11_LVRPNIDR		5						
ORF20			**5**	**28**	**5**	**5**	**247**	**26.3**	**High**

	22_GGEEGTAGLYACK	1xCarbamidomethyl [C12]	1						
	54_YLDGADNPDVWFPIPGGGGGTVVYDNR		1						
	189_QEGSSNIDIVR		1						
	175_NLQSGDICTVR	1xCarbamidomethyl [C8]	1						
	47_EYHLVGK		1						
ORF21			**3**	**17**	**3**	**3**	**277**	**28.3**	**High**
	213_IGAYTPVSDPLQALK		1						
	7_AIIGVGVIAAAYLYMSGSK		1						
	87_TNPEIPIDTTTK		1						
ORF22			**6**	**16**	**5**	**5**	**334**	**37.9**	**High**
	75_NEFNELETNLFDLDK		1						
	4_NLPSIYYVYANK		1						
	74_RNEFNELETNLFDLDK		2						
	305_FTMDSVEHPYPAKPSPEPK	1xOxidation [M3]	1						
	16_TYEEEIK		1						

Table S5B: MetSV ORF proteins identified in protein band 73 via GluC digestion. PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF1			**3**	**25**	**1**	**1**	**55**	**6.5**	**High**
	34_AALLLMSRCRLKHE	1xCarbamidomethyl [C9]; 1xOxidation [M6]	2						
	34_AALLLMSRCRLKHE	1xCarbamidomethyl [C9]	1						
ORF4			**2**	**73**	**2**	**2**	**41**	**4.8**	**High**
	33_RTLSSFGRC	1xCarbamidomethyl [C9]	1						
	9_VNRGKSSHLLFKCPNCMTKKE	2xCarbamidomethyl [C13; C16]; 1xOxidation [M17]	1						
ORF9			**2**	**13**	**2**	**2**	**62**	**7.7**	**High**
	8_NLIKLKE		1						
	8_NLIKLKEE		1						
ORF13			**3**	**10**	**2**	**2**	**202**	**23.2**	**High**
	130_FTPHFTGSKE		2						
	192_LLKYRIADKE		1						
ORF15			**191**	**100**	**13**	**13**	**102**	**10.3**	**High**
	4_LVPKKAVTFE		21						
	1_MVDLVPKKAVTFE	1xOxidation [M1]	13						
	1_MVDLVPKKAVTFE		8						
	20_SFAIGAVKAIE		1						
	20_SFAIGAVKAIEE		120						
	14_SGSLWDSFAIGAVKAIE		1						
	14_SGSLWDSFAIGAVKAIEE		16						

	80_AVQALIVPIIDGGSD		2						
	80_AVQALIVPIIDGGSDTGGNID		1						
	79_DAVQALIVPIID		2						
	91_GGSDTGGNIDNW		1						
	80_AVQALIVPIID		2						
	32_RAMIPVVGNGSLKSAVAKGAAGVVIQSAIKGKTGKIIGSAFAIDAVED	1xOxidation [M3]	2						
	32_RAMIPVVGNGSLKSAVAKGAAGVVIQSAIKGKTGKIIGSAFAIDAVE		1						
ORF16			**16**	**31**	**5**	**5**	**146**	**15.7**	**High**
	39_PRLAPIVPMSQATLRE		1						
	39_PRLAPIVPMSQATLRE	1xOxidation [M9]	4						
	6_AGDIRIVKTDASE		2						
	31_IAVLGGSDPRLAPIVPMSQATLRE	1xOxidation [M17]	6						
	31_IAVLGGSDPRLAPIVPMSQATLRED		1						
	31_IAVLGGSDPRLAPIVPMSQATLRE		1						
	94_SFLRSSD		1						
ORF19			**19**	**70**	**5**	**5**	**90**	**10.2**	**High**
	1_MKIPVNTVIKLVRPNID	1xOxidation [M1]	3						
	1_MKIPVNTVIKLVRPNID		1						
	45_TFIKSGFCIRGYGLFE	1xCarbamidomethyl [C8]	2						
	73_FYAYTTAPAGIDVRVLE		8						
	73_FYAYTTAPAGIDVRVLEL		3						
	28_NTATNLLFILPE		2						
ORF20			**2**	**10**	**2**	**2**	**247**	**26.3**	**High**
	15_VLALINRGGEE		1						
	26_GTAGLYACKTILNE	1xCarbamidomethyl [C8]	1						

Table S6A: MetSV ORF proteins identified in protein band 70 via tryptic digestion. PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF10			**4**	**30**	**3**	**3**	**117**	**13.5**	**High**
	49_QEEAKEEEEEEPTDEEIDGIITK		2						
	54_EEEEEEPTDEEIDGIITK		1						
	23_EQTGASESLITR		1						
ORF13			**2**	**9**	**2**	**2**	**202**	**23.2**	**High**
	108_CDWLFPALTFR	1xCarbamidomethyl [C1]	1						
	21_TISIIGGK		1						
ORF15			**3**	**24**	**2**	**2**	**102**	**10.3**	**High**
	50_GAAGVVIQSAIK		2						
	33_AMIPVVGNGSLK	1xOxidation [M2]	1						
ORF16			**739**	**94**	**21**	**21**	**146**	**15.7**	**High**
	1_MAATDAGDIR		1						
	22_QVLYETGSEIAVLGGSDPR		99						
	58_ILVEYKTGTASQITGTSCSAR	1xCarbamidomethyl [C18]	1						
	130_LGQSIAENSR		63						
	11_IVKTDASETVRQVLYETGSEIAVLGGSDPR		1						
	11_IVKTDASETVR		3						
	98_SSDVFAR		5						
	98_SSDVFARGVTAIAANGWVTIGSYTVPAQEEIR		2						
	64_TGTASQITGTSCSAR	1xCarbamidomethyl [C12]	78						

	88_TGNVAESFLRSSDVFAR		1							
	88_TGNVAESFLR		139							
	14_TDASETVRQVLYETGSEIAVLGGSDPR		3							
	14_TDASETVR		3							
	58_ILVEYK		123							
	54_EDDKILVEYKTGTASQITGTSCSAR	1xCarbamidomethyl [C22]	2							
	54_EDDKILVEYK		11							
	105_GVTAIAANGWVTIGSYTVPAQEEIR		10							
	41_LAPIVPMSQATLREDDKILVEYK	1xOxidation [M7]	1							
	41_LAPIVPMSQATLREDDK		1							
	41_LAPIVPMSQATLR	1xOxidation [M7]	119							
	41_LAPIVPMSQATLR		72							
	130_LGQSIAENSRLYFNLVE		1							
ORF20			**3**	**15**	**3**	**3**	**247**	**26.3**	**High**
	22_GGEEGTAGLYACK	1xCarbamidomethyl [C12]	1							
	81_FLTLTSGTLAGSSATR		1							
	47_EYHLVGK		1							
ORF21			**5**	**22**	**4**	**4**	**277**	**28.3**	**High**
	87_TNPEIPIDTTTK		1							
	151_SIGETVIGFLTDSYK		2							
	109_ETDGSLSSSLAQVFGTESQK		1							
	213_IGAYTPVSDPLQALK		1							

Table S6 B: MetSV ORF proteins identified in protein band 72 via GluC digestion. PSMs, peptide spectral matches; AAs, amino acid residues in ORF protein; MW, molecular weight; Protein FDR, protein level false discovery rate (high, FDR <1%).

Protein	**Peptide Sequence** (prefix = location in protein)	**Modifications**	**# PSMs**	**Coverage [%]**	**# Peptides**	**# Unique Peptides**	**# AAs**	**MW [kDa]**	**Protein FDR**
ORF15			**3**	**18**	**2**	**2**	**102**	**10.3**	**High**
	20_SFAIGAVKAIEE		2						
	14_SGSLWDSFAIGAVKAIEE		1						
ORF16			**818**	**97**	**24**	**24**	**146**	**15.7**	**High**
	137_NSRLYFNLVE		97						
	39_PRLAPIVPMSQATLRE		53						
	39_PRLAPIVPMSQATLRE	1xOxidation [M9]	94						
	39_PRLAPIVPMSQATLRED		1						
	39_PRLAPIVPMSQATLREDD		1						
	39_PRLAPIVPMSQATLREDD	1xOxidation [M9]	2						
	39_PRLAPIVPMSQATLRED	1xOxidation [M9]	1						
	94_SFLRSSD		5						
	94_SFLRSSDVFARGVTAIAANGWVTIGSYTVPAQE		4						
	62_YKTGTASQITGTSCSARIPIRRKNVRTGNVAE	1xCarbamidomethyl [C14]	41						
	94_SFLRSSDVFARGVTAIAANGWVTIGSYTVPAQEE		11						
	27_TGSEIAVLGGSD		1						
	27_TGSEIAVLGGSDPRLAPIVPMSQATLRE		1						
	19_TVRQVLYE		130						
	19_TVRQVLYETGSE		1						
	101_VFARGVTAIAANGWVTIGSYTVPAQE		1						
	101_VFARGVTAIAANGWVTIGSYTVPAQEE		7						

	9_IRIVKTDASE		6							
	127_EIRLGQSIAE		8							
	127_EIRLGQSIAENSRLYFNLVE		1							
	6_AGDIRIVKTDASE		6							
	16_ASETVRQVLYE		1							
	31_IAVLGGSDPRLAPIVPMSQATLRED	1xOxidation [M17]	9							
	128_IRLGQSIAE		103							
	31_IAVLGGSDPRLAPIVPMSQATLRED		3							
	31_IAVLGGSDPRLAPIVPMSQATLRE	1xOxidation [M17]	119							
	31_IAVLGGSDPRLAPIVPMSQATLRE		106							
	128_IRLGQSIAENSRLYFNLVE		1							
	55_DDKILVE		4							
ORF21			**2**	**12**	**2**	**2**	**277**	**28.3**	**High**
	155_TVIGFLTDSYKE		1							
	207_AINQTKIGAYTPVSDPLQALKD		1							

Table S7: Transcriptome analysis of aggregated *M. mazei* cells past infection with MetSV vs. uninfected cells using microarrays.

#ORF	Gene product/protein	fold regulation	standard derivation
1	Dipeptide ABC transporter. binding protein	1.08	0.6
2	Dipeptide ABC transporter. binding protein	0.13	0.08
3	Hypothetical protein	0.35	0.17
4	Dipeptide ABC transporter. permease protein	0.3	0.28
5	Dipeptide ABC transporter. permease protein	0.26	0.08
6	Metal-dependent hydrolase	0.37	0.26
7	Dipeptide ABC transporter. ATP-binding protein	0.34	0.32
8	Conserved protein	1.7	0.59
10	Hypothetical protein	0.7	0.26
11	Conserved protein	0.96	0.65
17	Ubiquinone/menaquinone biosynthesis methyltransferase	1.63	0.77
19	Conserved protein	2.36	0.2
23	Conserved protein	1.07	0.33
24	Hypothetical protein	2.07	0.79
25	Hypothetical protein	1.65	0.35
28	Superfamily I DNA and RNA helicase	1.57	0.35
31	Hypothetical protein	1.27	0.17
32	Conserved protein	1.25	0.28
35	Conserved protein	0.76	0.48
36	Hypothetical protein	1.15	0.5
37	Argininosuccinate synthase	0.66	0.2
38	Carbamoyl-phosphate synthase large chain	0.43	0.06
39	Carbamoyl-phosphate synthase small chain	0.38	0.07

41	Glycine betaine transporter. permease protein (OtaB)	1.54	0.42
42	Glycine betaine transporter. substrate-binding protein (OtaC)	2.02	0.64
44	Hypothetical protein	2.58	0.33
45	Hypothetical protein	2.07	0.54
46	Hypothetical protein	1.26	0.44
47	Acetylornithine aminotransferase	0.82	0.54
48	Aldehyde dehydrogenase	0.98	0.48
49	Conserved protein	1.72	0.11
50	Glutamyl-tRNA (Gln) amidotransferase	1.16	0.42
52	Transposase	1.29	0.24
55	Universal stress protein	2.02	0.45
56	Heterodisulfate reductase. subunit HdrA	2.04	1.03
57	Tungsten formylmethanofuran dehydrogenase. subunit F	0.86	0.42
58	Tungsten formylmethanofuran dehydrogenase. subunit G	0.93	0.82
59	Tungsten formylmethanofuran dehydrogenase subunit B	1.2	1.05
60	Tungsten formylmethanofuran dehydrogenase subunit D	1.56	0.23
61	Conserved protein	1.49	0.37
62	Putative methyltransferase	1.48	0.09
63	Cell surface glycoprotein (s-layer protein)	0.95	0.14
64	Cell surface glycoprotein (s-layer protein)	0.96	0.82
66	Conserved protein	0.7	0.18
67	Hypothetical protein	1.89	0.19
68	N-methylhydantoinase	1.6	1.2
69	Sodium-dependent transporter	2.35	0.18
70	Putative ribosomal RNA methyltransferase	0.42	0.24
71	Conserved protein	0.51	0.06

72	Thermosome beta-subunit	0.65	0.49
73	Ribose 5-phosphate isomerase	0.43	0.04
74	Aspartyl-tRNA synthetase	0.31	0.12
77	Hypothetical protein	0.21	0.18
78	Xanthine-guanine phosphoribosyltransferase	1.39	0.98
79	Conserved protein	1.01	0.24
80	Hypothetical protein	58.19	61.55
81	Hypothetical protein	0.5	0.03
82	Phosphoserine phosphatase	0.44	0.03
86	Hypothetical protein	0.56	0.11
87	Pyrimidine-nucleoside phosphorylase	0.96	0.55
89	Hypothetical protein	0.83	0.47
90	Conserved protein	2.43	1.85
91	ABC transporter. permease protein	2.88	1.12
92	Conserved protein	3.25	0.88
93	Cobyric acid synthase CbiP	2.45	1.18
95	Conserved protein	1.2	0.55
97	Ornithine cyclodeaminase	1.85	0.09
98	Conserved protein	1.02	0.52
99	Tetratrico peptide repeat protein	3.34	0.83
100	Conserved protein	2.79	0.86
102	Serine/threonine protein phosphatase	1.96	1.05
103	O-linked N-acetylglucosamine transferase	1.56	0.55
105	Hypothetical protein	1.46	0.54
108	Hypothetical protein	0.44	0.2
109	Cysteine desulfhydrase	2.12	1.03
110	NifU protein	2.61	2.03

112	Hypothetical protein	1.1	0.29
113	Conserved protein	1.13	0.12
114	Conserved protein	0.7	0
115	Putative transmembrane efflux protein	1.91	0.43
116	Transcriptional regulator. MarR family	2.92	1.48
117	Hypothetical protein	0.32	0.2
118	CTP synthase	0.44	0.22
119	Hypothetical protein	0.78	0.36
120	Conserved protein	0.53	0.05
121	Carbon monoxide dehydrogenase	3.47	2.08
122	Iron-sulfur-binding protein	4.08	2.27
123	Universal stress protein	0.88	0.4
125	Universal stress protein	0.83	0.57
126	PmbA protein	0.82	0.66
127	Zinc metalloprotease	0.82	0.39
128	ATP-dependent protease La	0.65	0.51
129	Conserved protein	1.26	0.27
131	Conserved protein	0.99	0.24
133	Threonine synthase	1.55	1.71
134	Sulfopyruvate decarboxylase alpha chain	1.66	0.83
135	Ferredoxin oxidoreductase	0.93	0.09
137	Conserved protein	0.93	0.35
138	Conserved protein	18.24	2.1
139	Cytochrome c-type biogenesis protein	1.89	1.01
141	Conserved protein	0.45	0.17
142	Orotate phosphoribosyltransferase	0.44	0.08
144	Phosphoribosylamine--glycine ligase	0.47	0.36

145	Ornithine carbamoyltransferase	1.01	0.18
147	Iron-sulfur flavoprotein	1.24	0.49
148	Conserved protein	1.1	0.37
149	Hypothetical protein	1.4	0.14
152	DNA integration/recombination/invertion protein	0.86	0.63
153	Conserved protein	0.72	0.21
154	Conserved protein	1.15	0.27
155	Conserved protein	0.35	0.16
156	Type III restriction enzyme	0.93	0.46
157	ATP-dependent DNA helicase	1.15	0.04
158	ATP-dependent DNA helicase	1.09	0.11
159	Hypothetical protein	2.23	0.76
161	Hypothetical protein	1.26	0.29
162	Conserved protein	1.39	0.09
163	DNA repair protein	0.8	0.21
164	ATP-dependent protease La	1.23	0.54
166	Homospermidine synthase	1.03	0.02
167	Cobalt-zinc-cadmium resistance protein	0.65	0.13
169	Hypothetical sensory transduction histidine kinase	0.36	0.19
171	Transposase	0.72	0.28
173	AdoCbi amidohydrolase CbiZ	0.9	0.59
174	Methanol corrinoid protein MtaC3	12.09	7.76
175	Methanol:corrinoid methyltransferase MtaB3	5.2	3.33
176	Methylcobalamin:coenzyme M methyltransferase MtaA2	8.12	4.93
178	Conserved protein	1.43	0.11
181	Conserved protein	1.27	0.03

182	Thiamine biosynthesis protein	0.38	0.05
183	DNA topoisomerase III	1.28	0.19
184	SSU ribosomal protein S3AE	0.28	0.18
185	Short chain dehydrogenase/reductase	1.37	0.37
187	Nucleotidyltransferase	2.41	1.05
188	Putative nucleotidyltransferase	2.27	0.27
201	Conserved protein	1.09	0
204	Hypothetical protein	1.66	0.01
205	Conserved protein	0.82	0.05
208	Hypothetical protein	1.69	0.67
209	Hypothetical protein	1.45	0.3
210	Conserved protein	0.92	0.47
212	Conserved protein	0.45	0.2
213	Putative single-stranded-DNA-specific exonuclease	0.84	0.32
216	Conserved protein	0.49	0.02
218	Hypothetical protein	0.96	0.24
219	Conserved protein	2.12	0.56
221	Fe-S oxidoreductase	0.7	0.16
222	Thiazole biosynthetic enzyme	0.36	0.02
223	Hypothetical protein	1.18	0.1
225	Conserved protein	6.66	10
227	Conserved protein	2.29	1.89
230	Sodium-calcium exchanger	0.37	0.14
233	Alanyl-tRNA synthetase	0.59	0.18
235	Conserved protein	1.15	0.12
236	Putative mechanosensitive ion channel	2.57	0.53
237	Conserved protein	1.31	0.83

239	Conserved protein	5.44	3.58
241	Potential ferredoxin oxidoreductase	0.42	0.28
242	Glycerol-3-phosphate cytidylyltransferase	0.47	0.19
243	Aspartate aminotransferase	0.53	0.39
244	Riboflavin synthase. subunit beta	0.48	0.39
245	Riboflavin synthase. subunit alpha	0.44	0.37
247	Putative inosine monophosphate dehydrogenase	0.43	0.21
250	Transposase	0.7	0.11
251	Transposase	0.42	0.1
253	Replication factor c subunit	1.03	0.28
254	N5-METHYL-H4MPT:COENZYME M METHYLTRANSFERASE. SUBUNIT X	0.53	0.18
255	N5-methyl-H4MPT:coenzyme M methyltransferase. subunit A homolog	0.86	0.45
256	N5-methyl-H4MPT:coenzyme M methyltransferase. subunit H homolog	0.73	0.09
257	Hypothetical protein	2.04	1.42
259	Dihydroxy-acid dehydratase	0.6	0.31
261	Uncharacterized flavoprotein	2.73	1.03
262	Conserved protein	1.33	0.81
263	Conserved protein	1.85	1.19
267	Conserved protein	0.67	0.07
268	Conserved protein	1.52	0.56
269	Hypothetical protein	1.43	0.04
270	Conserved protein	1.32	0.2
271	Conserved protein	1.26	0.47
272	Hypothetical protein	1.04	0.05
276	Superfamily II DNA and RNA helicase	9.11	12.02

277	T/G-SPECIFIC DNA GLYCOSYLASE	0.7	0.03
278	DNA-cytosine methyltransferase	0.46	0.36
279	Membrane alanine aminopeptidase	1.05	0.41
281	Hypothetical protein	1.18	0.17
282	Threonine synthase	0.6	0.23
283	Leucyl-tRNA synthetase	0.6	0.2
284	Amidohydrolase (putative)	0.6	0.41
285	Conserved protein	0.46	0.33
286	Hypothetical protein	0.33	0.23
287	Deoxyhypusine synthase	0.45	0.38
288	Transcriptional regulator. ArsR family	0.67	0.48
289	Transcriptional regulator	0.67	0.44
290	Hypothetical protein	1.23	0.02
291	Hypothetical protein	1.68	0.03
292	Conserved protein	2.49	0.47
293	Conserved protein	3.5	1.66
294	Na+/H+ antiporter	2.46	1.62
297	Glycine betaine transporter. ATP-binding protein	0.96	0.29
298	Glycine betaine-binding protein	1.11	0.54
299	Glucose-1-phosphate thymidylyltransferase	0.99	0.63
300	Glucosamine-fructose-6-phosphate aminotransferase [isomerizing]	0.69	0.52
301	Phosphoglucomutase/phosphomannomutase	0.96	0.68
302	Glucose-1-phosphate thymidylyltransferase	0.58	0.37
303	Hypothetical protein	2.09	0.59
305	Conserved protein	0.71	0.35
306	Metal-dependent hydrolases	0.43	0.06

307	Uroporphyrin-III C-methyltransferase	0.79	0.21
308	Uroporphyrinogen-III synthase	1.11	0
309	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family	0.75	0.18
312	Hypothetical protein	0.88	0
314	Valyl-tRNA synthetase	0.39	0.2
316	Flagella related protein FlaJ	0.94	0.23
323	Flagellin B1 precursor	0.94	0.18
325	Chemotaxis protein methyltransferase CheR	0.95	0.22
326	Chemotaxis protein CheD	0.97	0.19
327	Chemotaxis protein CheC	1.11	0.07
329	Protein-glutamate methylesterase CheB	2.71	2.82
330	Chemotaxis protein CheY	1.4	0.5
333	Methyl-accepting chemotaxis protein	1	0.26
334	Hypothetical protein	0.71	0.54
335	3-Hydroxy-3-methylglutaryl-coenzyme A reductase	0.98	0.12
337	Tryptophan synthase. beta chain	0.49	0.04
338	hydroxymethylpyrimidine kinase	1.25	0.29
339	small nuclear ribonucleoprotein	0.31	0.28
340	LSU ribosomal protein L37E	0.33	0.31
341	Amidophosphoribosyltransferase	0.35	0.32
342	Hypothetical protein	1.04	0
344	Probable cation efflux pump	0.77	0.03
345	Transcriptional regulator	0.73	0.15
346	Transcriptional regulator. MarR family	0.77	0
347	Hypothetical protein	1.88	1.92
348	Putative cation efflux pump	1.34	0.09

350	Putative molybdopterin biosynthesis protein	1.51	0.02
351	Conserved protein	28.65	44.48
352	Hypothetical protein	72.67	96.7
356	Conserved protein	0.93	0.17
357	Glutamate dehydrogenase	1.19	0.27
358	Acetyl-CoA synthetase. alpha subunit	2.55	1.31
359	Hypothetical protein	2.12	1.08
360	Sulfite reductase. assimilatory-type	1.27	0.67
362	Sulfite reductase. assimilatory-type	2.13	2.68
363	Hypothetical protein	2.56	2.58
364	Hypothetical protein	3.37	1.74
365	Hypothetical protein	2.43	0.61
366	Ferredoxin	2.68	0.98
368	Hypothetical protein	1.72	1.35
369	Hypothetical protein	2.63	0.02
370	Chorismate mutase / prephenate dehydratase	0.49	0.02
371	Conserved protein	0.91	0.29
372	MoxR-like ATPase	0.77	0.24
373	Hypothetical protein	0.87	0.13
374	Conserved protein	0.77	0.09
375	Conserved protein	1.15	0.1
376	Conserved protein	3.4	1.79
377	Integral membrane protein	1.2	0.42
378	Sugar-phosphate nucleotidyltransferase	1.06	0.14
379	Conserved protein	1.26	0.21
380	Peptidyl-prolyl cis-trans isomerase	0.49	0.02
381	Peptidyl-prolyl cis-trans isomerase	0.72	0.16

382	Peptidyl-prolyl cis-trans isomerase	0.46	0.26
383	Hypothetical protein	0.9	0.43
384	Conserved protein	1.56	0.22
385	Hypothetical protein	0.21	0.07
386	Hypothetical protein	1.29	0.23
387	Heterodisulfate reductase. subunit HdrA	0.67	0.38
388	Heterodisulfate reductase. subunit HdrC	0.79	0.51
389	Heterodisulfate reductase. subunit HdrB	0.76	0.57
390	Surface layer protein (putative)	1.44	0.2
391	Hypothetical protein	1.37	0.84
395	Surface layer protein (putative)	0.98	0.25
401	Conserved protein	1.24	0.19
403	Hypothetical protein similar to C-terminal domain of HdrB	1.1	0.48
404	Hypothetical protein	0.92	0.37
405	Surface layer protein (putative)	2.28	2.4
407	Hypothetical protein similar to C-terminal domain of HdrB	1.8	0.79
408	Hypothetical protein	2.48	0.96
409	3-Isopropylmalate dehydratase	0.35	0.18
410	Hypothetical protein	1.52	1.11
419	Pyruvate synthase. subunit beta	2.53	0.78
420	Pyruvate synthase. subunit alpha	3.54	3.23
423	Conserved protein	0.55	0.25
424	Histidinol dehydrogenase	0.5	0.14
426	RNase L inhibitor	0.68	0.32
427	Hypothetical protein	0.43	0.18

428	Conserved protein	0.64	0.27
429	Type I restriction-modification system methylation subunit	1.11	0.14
431	Type I restriction-modification system restriction subunit	1.96	0.8
435	Conserved protein	1.15	0.11
436	Thioredoxin	0.78	0.4
437	Hypothetical protein	0.62	0.02
438	Methylenetetrahydrofolate reductase	1.55	1.42
439	Zinc finger protein	1.9	0.93
440	Dihydropteroate synthase	2.53	0.75
441	Methylenetetrahydrofolate dehydrogenase (NADP+)/ methylenetetrahydrofolate cyclohydrolase	0.33	0.1
442	Serine hydroxymethyltransferase	0.31	0.11
443	Phosphoribosylglycinamide formyltransferase	0.31	0.24
444	HTH DNA-binding protein	1.21	0.7
445	Hypothetical protein	0.54	0.06
446	NAD+ synthetase	0.49	0.1
447	Cell division control protein (AAA family ATPase)	2.19	1.77
448	Hypothetical protein	2.2	0.58
449	SAM-dependent methyltransferases	1.31	0.21
451	Hypothetical protein	5.4	6.45
453	Conserved protein	29.38	51.32
455	Hypothetical protein	1.18	0.06
456	Hydrolase (HAD superfamily)	1.76	0.49
457	Recombination/repair protein RadA	0.67	0.5
458	Cytidylyltransferase	0.55	0.05
459	Conserved protein	0.62	0.15

460	Probable endonuclease IV	0.86	0
461	5-Methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	3.82	3.98
462	Cobalt transport ATP-binding protein CbiO	1.49	0.46
463	Cobalt ABC transporter. permease protein CbiQ	1.67	0.29
464	Cobalt transport protein CbiN	20.76	21.85
465	Cobalamin biosynthesis protein CbiM	22.62	25.25
466	CbiM protein	0.41	0.22
467	Conserved protein	8.14	7.11
468	Conserved protein	0.38	0.33
469	Hypothetical protein	0.77	0.42
471	tRNA nucleotidyltransferase	1.67	0.17
472	ADP-specific phosphofructokinase	2.28	0.03
473	ADP-specific phosphofructokinase	2.48	0.25
474	Glutamate N-acetyltransferase /amino-acid acetyltransferase	0.99	0.85
475	Putative inosine-5'-monophosphate dehydrogenase	1.22	0.62
476	N-acetyl-gamma-glutamyl-phosphate reductase	0.63	0.49
477	Hypothetical protein	2.97	0.51
478	Hypothetical protein	1.91	0.4
479	Conserved protein	0.32	0.17
481	Acetyltransferase	0.7	0.31
483	Small heat shock protein	3.11	2.71
484	Hypothetical protein	0.66	0.11
485	Phosphoglycerate kinase	0.48	0.25
488	Ferredoxin	0.86	0.31
489	Ferredoxin	0.8	0.28

490	Phycocyanin alpha-subunit phycocyanobilin lyase	113.01	96.7
491	Conserved protein	169.9	124.24
492	Hypothetical protein	119.32	150.9
495	Acetate kinase	5.14	2.99
496	Phosphate acetyltransferase	6.38	2.6
497	Iron-sulfur flavoprotein (Isf)	0.74	0.46
498	Putative chloride channel protein	0.7	0.04
500	Hypothetical protein	1.4	0.04
501	3-Demethylubiquinone-9 3-methyltransferase	1.85	0.76
502	Translation initiation inhibitor	1.54	0.91
505	Methylcobalamin:coenzyme M methyltransferase MtbA	1.16	0.19
506	Conserved protein	0.86	0.02
510	GTP-binding protein	1.1	0.31
511	Conserved protein	0.83	0.21
512	tRNA-intron endonuclease	1.07	0.77
513	Cobyrinic acid a.c-diamide synthase	1.81	0.91
514	Nitrogenase iron protein	0.8	0.48
515	Conserved protein	1.13	1.04
516	Hypothetical protein	1.18	1.23
517	Conserved protein	1.21	1.35
518	Hypothetical sensory transduction histidine kinase	1.17	0.54
519	Hypothetical protein	0.62	0.02
520	Hypothetical protein	0.66	0.03
523	Hypothetical protein	2.44	0.54
524	Hypothetical protein	2.27	0.61
526	Hypothetical protein	1.78	0.25
529	Hydrolase	0.43	0.08

530	Amino acid permease	0.74	0.02
533	Conserved protein	1.51	0.11
537	Hypothetical protein	1.34	0.79
541	Conserved protein	0.87	0.32
542	Hypothetical protein	0.69	0.24
544	Exoribonuclease II	1.13	0.5
550	Hypothetical protein	1	0.32
552	Hypothetical protein	0.5	0.05
559	Hypothetical protein	1.27	0.06
562	Hypothetical protein	2.37	1.01
566	Hypothetical protein	1.55	0.73
567	Acetyltransferase	1.26	0.58
570	ABC transporter. ATP-binding protein	0.53	0.16
572	Alkaline phosphatase	0.67	0.02
577	Phosphate transport ATP-binding protein	0.75	0.06
578	Phosphate-binding protein	0.27	0.03
582	Glycosyltransferase	1.27	0.18
583	Conserved protein	3.98	2.26
584	Conserved protein	0.85	0.45
586	Sulfate adenylyltransferase	2.73	1.14
587	Conserved protein	0.7	0.32
588	Conserved protein	0.65	0.37
589	Conserved protein	0.48	0.36
590	Glycerol-1-phosphate dehydrogenase (putative)	0.88	0.5
591	Conserved membrane protein	0.8	0.33
592	Integral membrane protein	0.77	0.35
593	Conserved protein	0.47	0.21

594	Protein translation initiation factor 2 subunit gamma (IF-2g)	0.46	0.22
595	Conserved protein	0.31	0.24
596	DNA-directed RNA polymerase subunit E'	0.39	0.26
597	DNA-directed RNA polymerase subunit E"	0.57	0.23
598	Hypothetical protein	0.36	0.1
599	SSU ribosomal protein S24E	0.47	0.05
600	30S ribosomal protein S27ae	0.41	0.14
602	O-sialoglycoprotein endopeptidase	0.36	0.08
603	Nucleoside-triphosphatase	0.26	0.14
604	Conserved protein	1.38	0.58
607	Ferredoxin	1.28	0.75
608	Probable radical-forming protein	0.55	0.3
609	Conserved protein	0.6	0.08
610	Acetyltransferases	4.33	4.27
612	NH3-dependent NAD(+) synthetase	2.23	1.39
613	Conserved protein	3.11	1.42
614	Long-chain-fatty-acid--CoA ligase	2.29	1.22
615	Conserved protein	2.16	1.44
616	Conserved protein	1.74	0.04
617	Conserved protein	0.21	0.08
618	Undecaprenyl pyrophosphate synthetase	1.26	0.11
620	Conserved protein	1.81	0.8
621	Hypothetical protein	1.03	0.36
626	Nicotinamide-nucleotide adenylyltransferase	0.3	0.13
627	F420H2 dehydrogenase. subunit FpoF	0.21	0.18
628	Coenzyme F420-dependent N5.N10-methylene	0.25	0.29

	tetrahydromethanopterin reductase		
629	Zinc finger protein	1.29	0.78
630	Zinc finger protein	1.04	0.68
631	Hypothetical protein similar to COX locus protein	1.45	1.25
632	Desulfoferrodoxin	1.37	1.11
633	Cytochrome c	1.73	1.09
634	Iron-sulfur flavoprotein	3.78	1.84
635	Flavoprotein	1.66	1.4
636	Conserved protein	2.37	1.29
637	Putative flavodoxin	3.97	1.34
638	Putative flavodoxin	3.41	1.16
642	Isocitrate dehydrogenase [NADP]	0.6	0.21
643	Conserved protein	0.72	0.05
644	Conserved protein	1.03	0.26
645	3-Isopropylmalate dehydratase	0.65	0.02
647	Oligosaccharyl transferase	1.58	0.66
648	Glycosyl transferase	1.01	0.23
649	Glycosyl transferase	1.2	0.01
651	Glycosyltransferase involved in cell wall biogenesis	1.11	0.09
652	Glycosyltransferase involved in cell wall biogenesis	0.94	0.55
654	Mannosyltransferase	0.86	0.5
656	Polysaccharide ABC transporter. ATP-binding protein	0.91	0.29
657	Polysaccharide ABC transporter. permease protein	0.96	0.19
658	GDP-fucose synthetase	1.36	0.2
660	Mannose-6-phosphate isomerase/mannose-1-phosphate guanylyl transferase	1.33	0.2
663	Probable dihydroorotate dehydrogenase electron transfer	0.46	0.15

	subunit		
666	Putative nickel-responsive regulator NikR	3.91	2.45
667	Nitroreductase family protein	2.07	1.34
668	Ketol-acid reductoisomerase	0.83	0.36
669	Acetolactate synthase small subunit	0.44	0.36
670	Acetolactate synthase large subunit	0.46	0.36
671	2-Isopropylmalate synthase	0.52	0.51
673	Conserved protein	1.35	0.2
674	Prefoldin beta subunit	0.43	0.25
675	Conserved protein	0.59	0.37
676	Coenzyme F390 synthetase/phenylacetyl-CoA ligase	0.34	0.14
677	Acetolactate synthase small subunit	0.57	0.44
678	Conserved protein	0.53	0.16
679	Conserved protein	0.67	0.04
680	Conserved protein	1.85	0.72
681	Conserved protein	1.66	0.51
682	Integral membrane protein	1.56	0.39
684	CO dehydrogenase/acetyl-CoA synthase. alpha subunit	16.85	0.69
685	CO dehydrogenase/acetyl-CoA synthase. epsilon subunit	12.59	0.43
686	CO dehydrogenase/acetyl-CoA synthase. beta subunit	5.65	1.33
687	Nickel-insertion protein CooH	4.78	0.58
688	CO dehydrogenase/acetyl-CoA synthase. delta subunit	4.28	2.66
689	CO dehydrogenase/acetyl-CoA synthase. gamma subunit	3.09	2.63
690	Conserved protein	0.49	0.43
691	Hypothetical protein	0.53	0.21
692	Transcription initiation factor IIE. alpha subunit	0.42	0.29
693	Conserved protein	0.38	0.19

694	Proteasome. beta subunit	0.83	0.66
695	Cleavage and polyadenylation specificity factor. 100 kD subunit	1.06	0.67
696	Beta-phosphoglucomutase	0.45	0.36
697	Cell division protein	1.09	0.75
698	Dihydropteroate synthase	1.35	0.15
699	Conserved protein	1.48	0.58
700	Vacuolar-type H+-pyrophosphatase	0.47	0.1
702	Hypothetical permease	0.9	0.17
703	Hypothetical permease	0.9	0.04
704	Conserved protein	0.44	0.27
705	Conserved protein	0.85	0.6
706	ZPR1-related zinc finger protein	0.85	0.68
707	Prolyl-tRNA synthetase	0.54	0.26
708	Conserved protein	0.65	0.57
709	Conserved protein	1.56	0.47
710	Hypothetical protein	2.07	0.91
713	Conserved protein	0.92	0.21
714	Fructose-bisphosphate aldolase	0.97	0.47
715	Pyruvate kinase	0.78	0.31
716	Hypothetical protein	0.81	0.55
717	Hypothetical protein	1.32	0.4
722	Nitrogenase molybdenum-iron protein alpha chain	0.49	0.05
725	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	0.76	0.23
727	Molybdenum transporter. permease protein	1.09	0.57
730	SAM-dependent methyltransferases	1.84	0.85

737	Conserved protein	0.96	0.18
738	Conserved protein	0.77	0.05
741	Universal stress protein	1.34	0.36
742	Arsenical-resistance protein	2.29	0.92
743	Conserved protein	0.71	0.16
744	Conserved protein	0.52	0.27
745	Conserved protein	5.34	8.62
747	ATP-dependent RNA helicase	0.36	0.2
748	Conserved protein	0.9	0.09
750	Dihydropyrimidinase	2.26	0.74
751	Putative serine/threonine protein phosphatase	0.92	0.06
752	Conserved protein	2.01	1.29
753	Conserved protein	0.53	0.29
754	Conserved protein	0.55	0.01
755	Conserved protein	0.37	0.02
757	NifB protein	0.74	0.49
758	Conserved protein	1.37	0.13
759	NifB protein	5.92	8.44
760	Ferredoxin	0.24	0.13
761	Thiamin-monophosphate kinase	0.51	0.23
762	Conserved protein	0.79	0.54
763	Conserved protein	0.55	0.33
764	Conserved protein	0.54	0.36
765	Conserved protein	1.1	0.39
767	Conserved protein	0.55	0.24
768	Glycosyl transferase	0.52	0.37
769	Phosphohydrolase	0.37	0.1

770	Conserved protein	0.27	0.19
772	Conserved protein	0.64	0.11
774	Conserved protein	0.66	0.69
775	Conserved protein	0.93	0.47
776	Conserved protein	0.87	0.4
777	Hydrogenase maturation protein	1.23	0.73
778	A1AO H+ ATPASE. SUBUNIT D	0.88	0.91
779	A1AO H+ ATPASE. SUBUNIT B	0.85	0.71
780	A1AO H+ ATPASE. SUBUNIT A	0.66	0.6
781	A1AO H+ ATPASE. SUBUNIT F	0.66	0.52
782	A1AO H+ ATPASE. SUBUNIT C	0.6	0.61
783	A1AO H+ ATPASE. SUBUNIT E	0.5	0.38
784	A1AO H+ ATPASE. SUBUNIT K	0.55	0.46
785	A1AO H+ ATPASE. SUBUNIT I	0.71	0.75
786	A1AO H+ ATPASE. SUBUNIT H	0.77	0.7
788	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family	0.53	0.21
789	Geranyltranstransferase/Farnesyltranstransferase/ Hexaprenyl diphosphate synthase	0.74	0.26
790	Hypothetical protein	0.97	0.22
792	Hypothetical protein	3.78	2.03
794	ADP-ribosylglycohydrolase	1.12	0.64
796	Hypothetical protein	0.73	0.4
797	Hypothetical protein	3.53	1.01
798	26S Proteasome regulatory subunit RPT2/S4	1.06	0.29
799	Hypothetical protein	0.62	0.1
800	Hypothetical protein	0.69	0.61

801	Adenylosuccinate synthetase	0.29	0.08
802	SSU ribosomal protein S19E	0.24	0.21
803	Double-stranded DNA-binding protein	0.24	0.18
804	Conserved hypothetical protein	0.23	0.23
805	LSU ribosomal protein L39E	0.22	0.16
806	LSU ribosomal protein L31E	0.27	0.23
807	Protein translation initiation factor 6 (IF-6)	0.24	0.25
808	50S ribosomal protein LX	0.29	0.25
809	Prefoldin. alpha subunit	0.4	0.21
810	Signal recognition particle. subunit Ffh/SRP54	0.52	0.46
811	Stress-responsive transcriptional regulator	0.81	0.47
813	Conserved protein	2.79	1.06
814	Probable peroxiredoxin	2.07	0.01
817	Pyrroline-5-carboxylate reductase	0.63	0.19
818	Glutamate 5-kinase	0.44	0.05
819	Gamma-glutamyl phosphate reductase	0.78	0.19
820	Conserved protein	0.61	0.27
821	Conserved protein	0.7	0.26
823	Conserved protein	0.38	0.21
824	Universal stress protein	0.57	0.41
825	Conserved protein	0.67	0.48
826	Conserved protein	0.78	0.19
827	Conserved protein	0.38	0.22
828	Conserved protein	0.59	0.41
829	Conserved protein	0.47	0.19
830	Molybdopterin biosynthesis MoeA protein	1.3	0.18
831	Molybdopterin converting factor. small subunit	0.79	0.42

833	Conserved protein	0.83	0.61
835	Cation-transporting ATPase	3.45	1.06
836	Conserved protein	1.2	0.2
837	Conserved protein	1.84	0.6
838	Succinate-semialdehyde dehydrogenase [NADP+]	0.93	0.16
840	Glycosyltransferases involved in cell wall biogenesis (putative)	0.79	0.13
841	Transcriptional regulator. ArsR family	0.99	0.29
842	Conserved protein	0.57	0.33
843	Coenzyme F390 synthetase/phenylacetyl-CoA ligase	0.92	0.27
844	Hypothetical protein	2.28	0.15
845	Conserved protein	1.77	0.09
846	Conserved protein	7.97	9.62
849	Bacterioferritin comigratory protein	1.33	0.08
850	Conserved protein	1.51	0.19
853	Conserved protein	0.93	0.05
854	Cell division cycle protein 48 homolog	0.54	0.21
855	Phosphoribosylamidoimidazole-succinocarboxamide synthase	0.32	0.12
856	Conserved protein	1.14	0.13
857	Conserved protein	0.8	0.51
858	Protein translation initiation factor 1 (IF-1)	0.79	0.49
859	Conserved protein	3.37	3.08
860	Phosphoribosylformylglycinamidine synthase	0.37	0.14
861	Alpha-amylase	2.76	2.18
862	Alpha-amylase	1.15	0.42
863	Conserved protein	1.46	0.53

864	Glucoamylase	2.79	1.93
865	Seryl-tRNA synthetase	0.87	0.54
866	Periplasmic serine protease	1.63	0.53
867	Methionyl-tRNA synthetase	0.57	0.3
868	Adenylate cyclase	0.93	0.54
869	Conserved protein	0.63	0.62
870	Beta-ketoacyl synthase/ thiolase	0.52	0.18
871	Hydroxymethylglutaryl-CoA synthase	0.95	0.5
872	Putative transcriptional regulator	1.25	0.88
873	Conserved protein	1.56	0.71
876	Hypothetical protein	1.2	0.06
882	Conserved protein	0.69	0.18
883	Conserved protein	0.28	0.09
884	Conserved protein	7.62	8.07
886	DNA polymerase IV	1.41	0.34
887	Cobalt transport ATP-binding protein CbiO	0.66	0.13
888	Cobalt ABC transporter. permease protein CbiQ	0.82	0.41
889	Hypothetical protein	5.89	6.09
892	Hypothetical protein	2.78	2.54
893	Cobalamin biosynthesis protein CbiM	1.72	2.19
894	Hypothetical protein	1.68	1.75
895	Endonuclease III	1.65	0.6
898	Bifunctional purine biosynthesis protein PurH	0.49	0.33
899	Conserved protein	0.89	0.71
901	Cation-transporting ATPase	3	1.16
902	Putative methyltransferase	1.89	0.66
903	Transcriptional regulator	5.12	1.68

904	Phosphoglycerate mutase	0.4	0.19
905	Conserved protein	0.89	0.16
906	Flap endonuclease-1 (RAD27/FEN1 family)	1.61	0.22
907	Hypothetical protein	0.94	0.24
908	Conserved protein	1.17	0.04
909	Conserved protein	1.14	0.62
910	Potassium/copper-transporting ATPase	1.19	0.06
912	Conserved protein	0.77	0.65
913	Conserved protein	1.69	0.05
914	Conserved protein	1.39	0.82
915	Conserved protein	1.4	0.87
916	Conserved protein	0.96	0.74
917	Conserved protein	1.37	0.24
918	4-Carboxymuconolactone decarboxylase	0.71	0.48
919	Conserved protein	0.93	0.43
920	MutT related protein	1.39	1.22
921	Aldehyde ferredoxin oxidoreductase	0.95	0.19
922	Protein iranslation initiation factor 5A (IF-5A)	0.28	0.17
923	Agmatinase	0.48	0.24
924	Conserved protein	0.31	0.24
925	Conserved protein	0.23	0.16
928	Conserved protein	1.11	0.67
931	Hypothetical protein	1.67	0.29
933	Glutathione-regulated potassium-efflux system protein	2.15	0.68
939	Putative flagella-related protein FlaH	1.37	0.09
940	Putative flavodoxin	4.88	2.87
941	Adenylosuccinate lyase	0.34	0.03

943	Geranylgeranylglyceryl diphosphate synthase	0.4	0.05
945	Iron-sulfur flavoprotein	1.42	0.25
946	PUTATIVE NADPH-FLAVIN OXIDOREDUCTASE	4.11	1.89
947	Conserved protein	1.91	0.14
948	Sensory transduction histidine kinases	1.26	0.17
949	Hypothetical protein	0.7	0.25
950	ABC transporter. ATP-binding protein	0.53	0.08
951	ABC transporter. permease protein	4.63	4.67
952	Hypothetical protein	2.56	1.86
953	ABC transporter. ATP-binding protein	1.95	1.5
962	Conserved protein	1.59	0.65
964	Glutamine synthetase	0.92	0.01
966	Glutamate synthase. large chain	0.24	0.16
967	Glutamate synthase. large chain	0.4	0.17
968	Glutamate synthase. large chain	0.34	0.18
969	F420 hydrogenase/dehydrogenase. beta subunit	0.34	0.14
971	Hypothetical protein	1.75	0.23
977	F420-dependent NADP reductase	0.46	0.28
978	Hypothetical protein	0.67	0.06
979	Heterodisulfate reductase. subunit HdrB	0.81	0.06
980	Heterodisulfate reductase. subunit HdrB	1.04	0.26
983	Conserved protein	0.9	0.26
984	Conserved protein	1.29	0.12
985	Conserved protein	0.81	0.68
986	hypothetical protein	1.02	0.49
987	Conserved protein	0.6	0.37
988	Conserved protein	0.43	0.39

989	Conserved protein	0.26	0.05
990	Nucleotide-binding protein	0.38	0.06
991	Thiol-disulfide isomerase/thioredoxin	0.47	0.31
992	Cytochrome c-type biogenesis protein	0.73	0.09
994	Precorrin-8X methylmutase	2.01	0.23
995	Precorrin-3B C17-methyltransferase	1.52	0.8
996	Cobalamin biosynthesis protein CbiG	0.93	0.75
997	Cobalamin biosynthesis protein CbiG	1.12	1.28
998	Precorrin-4 C11-methyltransferase	0.81	0.65
999	Precorrin-2 C20-methyltransferase	1.26	0.2
1000	Precorrin-6Y C5_15-methyltransferase [decarboxylating]	1.49	0.19
1002	2-Isopropylmalate synthase	0.84	0.22
1003	Isocitrate dehydrogenase [NADP]	0.47	0.16
1004	Putative molybdenum cofactor biosynthesis protein	0.81	0.45
1005	HTH DNA-binding protein	0.54	0.07
1006	26S Proteasome regulatory subunit RPT2/S5	0.78	0.68
1008	Cell division protein	0.58	0.49
1009	Protein translocase. subunit SecE	0.06	0.04
1010	Putative transcription antitermination protein nusG	0.26	0.28
1011	LSU ribosomal protein L11P	0.49	0.5
1012	LSU ribosomal protein L1P	0.32	0.28
1013	LSU ribosomal protein L10P	0.29	0.24
1014	LSU ribosomal protein L12AE	0.45	0.41
1015	Molybdenum cofactor biosynthesis enzyme (Fe-S oxidoreductase family)	1.46	0.22
1019	Iron-sulfur cluster-binding protein	1.91	0.27

1020	O6-methylguanine-DNA methyltransferase	2.81	0.57
1022	Conserved protein	6.4	3.92
1023	Conserved protein	3.97	1.8
1024	Conserved protein	1.82	1.32
1025	Thiamine biosynthesis protein	0.15	0.11
1026	Dolichol-phosphate mannosyltransferase	0.9	0.5
1027	Transcription initiation factor TFIIB	3.45	5.88
1028	Transcription initiation factor TFIIB	0.55	0.14
1029	Hypothetical protein	1.35	0.21
1030	Conserved protein	1.33	1.04
1031	Chromosome partition protein	1.87	0.67
1032	Conserved protein	1.94	0.22
1033	Ferrous iron transport protein B	0.93	0.16
1034	Transcriptional repressor	0.79	0.04
1035	Amino-acid acetyltransferase	0.45	0.26
1036	BioY protein	0.51	0.26
1037	Cobalt transport ATP-binding protein CbiO	0.63	0.3
1038	Cobalt transport ATP-binding protein CbiO	0.64	0.37
1039	Cobalt ABC transporter. permease protein CbiQ	0.7	0.56
1040	Predicted transcriptional regulator	2.51	1.17
1041	Transporter	2.55	0.76
1042	Transcriptional regulator	2.29	0.02
1044	Transposase	0.89	0.5
1045	Branched-chain amino acid aminotransferase	0.49	0.39
1046	Molybdopterin biosynthesis protein	1.07	0.32
1047	GTP-binding protein	0.33	0.07
1048	D-alanine-D-alanine ligase related protein	1.55	0.08

1049	Arsenite permease	0.83	0.5
1050	Conserved protein	0.86	0.4
1051	Chromosomal protein MC1	1.57	1.29
1053	Putative Sensory protein	2.79	1.52
1055	Trimethylamine corrionid protein	9.98	5.8
1056	Putative ATP-dependent Na+ efflux pump	1.68	0.39
1057	ABC transporter. ATP-binding protein	1.77	0.7
1058	Diaminohydroxyphosphoribosylaminopyrimidine reductase	2.02	0.57
1059	Formate hydrogenlyase subunit 3	0.76	0.02
1060	Formate hydrogenlyase subunit 4	0.43	0.01
1061	Hydrogenase-4 component E	0.43	0.1
1062	Hydrogenase-4 component F	0.67	0.1
1063	Formate hydrogenlyase subunit 5 precursor	0.62	0.03
1064	Formate hydrogenlyase subunit 7	0.53	0.14
1068	Two-component response regulator	1.06	0.43
1070	Methylcobalamin:coenzyme M methyltransferase MtaA1	0.43	0.38
1071	Conserved protein	0.89	0.9
1072	Conserved protein	1.03	0.78
1073	Methanol corrinoid protein MtaC2	8.01	3.6
1074	Methanol:corrinoid methyltransferase MtaB2	13.48	1.21
1075	Putative regulatory protein	13.69	2.22
1076	Cation efflux protein	14.67	6.29
1077	Conserved protein	1.91	0.92
1078	Conserved protein	1.22	0.8
1079	Conserved protein	0.88	0.08

1080	Conserved protein	0.86	0.52
1082	GTP-binding protein	0.95	0.45
1083	Undecaprenyl pyrophosphate synthetase	1.01	0.34
1084	Hypothetical protein	0.81	0.41
1086	Metal-dependent hydrolase	0.94	0.28
1087	ABC transporter. ATP-binding protein	1.89	1.04
1088	ABC transporter. ATP-binding protein	1.61	0.77
1089	Putative DNA integration/recombination/invertion protein	1	0.49
1092	Thiol-disulfide isomerase/thioredoxin related protein	0.83	0.13
1095	Iron-sulfur-binding protein	1.72	2.04
1096	Thermosome. gamma subunit	0.53	0.49
1098	Conserved protein	1.27	0
1101	Archaeosine tRNA-ribosyltransferase	0.33	0.25
1102	Hypothetical protein	0.41	0.07
1103	Hypothetical protein	0.52	0.12
1104	Oxidoreductase (flavoprotein)	0.43	0.07
1105	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family	0.82	0.04
1106	Putative phosphoserine phosphatase	0.36	0.19
1107	Putative phosphoserine phosphatase	0.35	0.26
1108	F420-dependent methylenetetrahydromethanopterin dehydrogenase	0.28	0.34
1110	Conserved protein	1.51	0.53
1112	Conserved protein	0.59	0.07
1113	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	0.91	0.4
1114	Conserved protein	0.58	0.13

1115	Conserved protein	0.63	0.27
1116	Hypothetical protein	10.63	7.68
1118	Conserved protein	0.93	0.09
1119	Conserved protein	0.79	0.17
1120	Conserved protein	1.26	0.44
1121	Glycosyl transferase	3.68	2.4
1122	Oxidoreductase (hypothetical)	1.18	0.11
1123	Hypothetical protein	1.92	0.34
1124	O-antigen translocase	0.4	0.15
1125	Conserved protein	0.45	0.23
1126	Glycosyl transferase	1.56	0.26
1128	Conserved protein	1.98	0.94
1129	Conserved protein	1.43	0.14
1130	Hypothetical protein	0.72	0.05
1131	Hypothetical protein	1.04	0.33
1132	UDP-glucose 6-dehydrogenase	0.88	0.97
1133	UTP--glucose-1-phosphate uridylyltransferase	0.69	0.38
1134	UDP-glucose 4-epimerase	0.85	0.4
1138	Glycosyl transferase	0.29	0.13
1139	Dolichyl-phosphate mannose synthase related protein	0.63	0.11
1140	Dolichyl-phosphate mannose synthase related protein	0.73	0.02
1141	Glycosyl transferase	0.61	0.34
1142	Glycosyl transferase	0.7	0.41
1143	Glycosyl transferase	1.06	0.58
1144	Disaggregase	1.09	0.64
1146	Conserved protein	1.23	1.09
1147	Dolichol-phosphate mannosyltransferase	0.78	0.82

1148	Conserved protein	0.41	0.28
1149	Conserved protein	0.61	0.31
1150	Conserved protein	0.5	0.2
1151	Acetyltransferase	0.91	0.17
1152	Aspartate aminotransferase	0.88	0.21
1153	Myo-inositol 2-dehydrogenase	0.7	0.21
1154	NDP-N-acetyl-D-galactosaminuronic acid dehydrogenase	0.8	0.48
1155	Conserved protein	0.79	0.27
1156	O-antigen translocase	0.56	0.25
1157	Conserved protein	0.71	0.33
1158	Conserved protein	0.65	0.47
1159	Hypothetical protein	0.56	0.07
1162	UDP-N-acetylglucosamine 4-epimerase	0.94	0.56
1163	Nucleotidyltransferase	1.33	0.09
1164	Putative nucleotidyltransferase	1.28	0.07
1166	dTDP-4-dehydrorhamnose 3.5-epimerase	0.57	0.1
1169	Glucose-1-phosphate thymidylyltransferase	1.31	0.14
1170	UDP-N-acetylglucosamine 2-epimerase	1.42	0.22
1172	UDP-N-acetyl-D-mannosamine 6-dehydrogenase	1.66	0.54
1173	Conserved protein	0.56	0.08
1176	Conserved transmembrane protein	1.32	0
1179	Glycosyl transferase	1.72	0.54
1180	Oxidoreductase (hypothetical)	1.29	0.47
1181	Conserved protein	0.73	0.02
1183	Dolichyl-phosphate mannose synthase related protein	0.67	0.25
1184	Dolichyl-phosphate mannose synthase related protein	1.88	0.6

1185	Conserved protein	0.96	0.06
1189	Conserved protein	1	0.1
1190	Conserved protein	2.22	2.25
1192	Transposase	0.57	0.27
1193	dTDP-glucose 4.6-dehydratase	0.45	0.21
1194	Conserved protein	1.38	0.41
1196	Conserved protein	1.44	0.51
1199	Conserved protein	0.38	0.28
1200	SSU ribosomal protein S17E	0.4	0.08
1201	Dihydrodipicolinate synthase	0.23	0.17
1202	Dihydrodipicolinate reductase	0.3	0.13
1204	Conserved protein	3.56	2.87
1206	Conserved protein	2.2	0.6
1210	Conserved protein	1.81	0.24
1211	Conserved protein	1.4	0.51
1212	Aspartate carbamoyltransferase. regulatory subunit	0.71	0.33
1213	Aspartate carbamoyltransferase. catalytic subunit	0.83	0.51
1215	Hexulose-6-phosphate synthase	1.2	0.14
1218	GMP synthase [glutamine-hydrolyzing]	0.27	0.11
1219	Fe-S oxidoreductase	0.42	0.16
1220	Acetylglutamate kinase	0.82	0.16
1221	Chromosomal protein MC1	0.66	0.67
1222	Conserved protein	0.37	0.35
1223	Conserved protein	0.92	0.2
1224	Conserved protein	1.4	0.09
1225	F420 hydrogenase/dehydrogenase. beta subunit	0.4	0.26
1226	Glutamyl-tRNA (Gln) amidotransferase. subunit C	0.6	0.22

1228	Glutamyl-tRNA (Gln) amidotransferase. subunit B	0.78	0.31
1231	SAM-dependent methyltransferases	1.14	0.07
1234	Conserved protein	0.75	0.06
1235	5-Methylcytosine-specific restriction enzyme	1.11	0.46
1236	Protease HTPX	0.77	0.33
1237	Thymidylate synthase	0.86	0.01
1238	3-Phosphoshikimate 1-carboxyvinyltransferase	0.95	0.12
1240	Methyl-coenzyme M reductase. alpha subunit	0.53	0.29
1241	Methyl-coenzyme M reductase. gamma subunit	0.38	0.35
1242	Methyl-coenzyme M reductase. operon protein C	0.31	0.28
1243	Methyl-coenzyme M reductase. operon protein D	0.31	0.3
1244	Methyl-coenzyme M reductase. beta subunit	0.42	0.35
1245	Conserved protein	0.68	0.23
1246	DNA polymerase II large subunit	1.28	0.54
1247	Conserved protein	0.72	0.06
1248	SUA5 protein	0.85	0.22
1249	Ribulose bisphosphate carboxylase large chain	1.06	0.07
1252	Conserved protein	0.75	0.18
1253	Cation transporter	1.26	1.14
1254	Putative heat shock protein	1.2	0.1
1255	Putative heat shock protein	1.49	0
1256	CdcH protein	1.46	0.81
1257	Transcriptional regulator. ArsR family	1.62	0.77
1261	Conserved protein	0.72	0.35
1262	Xanthine-guanine phosphoribosyltransferase	0.62	0.18
1264	Hypothetical protein	1.71	0.31
1265	Hypothetical protein	1.45	0.09

1266	Conserved protein	2.37	1.71
1267	Signal recognition particle. subunit FFH/SRP54	1.14	0.04
1268	Hypothetical protein	1.25	0.19
1270	GMP synthase [glutamine-hydrolyzing]	0.35	0.08
1271	2-Dehydro-3-desoxyphosphoheptanote aldolase	0.34	0.17
1272	3-Dehydroquinate synthase	0.42	0.21
1273	3-Dehydroquinate dehydratase	0.38	0.33
1274	Shikimate 5-dehydrogenase	0.36	0.19
1275	Prephenate dehydrogenase	0.41	0.18
1276	Hypothetical protein	0.73	0.54
1277	Methyltransferase	3.32	2.61
1278	Triosephosphate isomerase	0.48	0.27
1279	Orotidine 5'-phosphate decarboxylase family protein	0.39	0.14
1281	Conserved protein	6.67	0.89
1282	Conserved protein	3.56	2.87
1284	2-Isopropylmalate synthase	0.28	0.13
1285	Sec-independent transport protein TatD	0.29	0.14
1286	hypothetical protein	0.3	0.04
1287	Fe-S oxidoreductase	0.53	0.26
1288	Conserved protein	0.9	0.2
1289	Conserved protein	1	0.24
1290	Fe-S oxidoreductase	0.45	0.01
1291	(S)-2-Hydroxy-acid dehydrogenase	0.56	0.26
1292	Archaeosine tRNA-ribosyltransferase	0.29	0.04
1293	Ribosomal protein S18 alanine acetyltransferase	0.44	0.07
1294	Conserved protein	1.79	2.72
1295	DNA primase	0.58	0.4

1296	NADH oxidase	0.8	0.4
1297	RNA 3'-terminal phosphate cyclase	0.74	0.29
1299	Replication factor-A protein	0.53	0.07
1301	Conserved protein	1.15	0.68
1302	Conserved protein	1.63	1
1303	Conserved protein	0.84	0.88
1304	Conserved protein	0.48	0.4
1305	Conserved protein	0.78	0.64
1306	HTH DNA-binding protein	0.49	0.33
1307	Conserved protein	1.69	0.67
1309	Protein translation elongation factor 1A (EF-1A)	0.39	0.17
1310	Hypothetical protein	0.4	0.3
1311	Conserved protein	0.56	0.42
1312	Conserved protein	0.47	0.06
1313	UMP/CMP kinase related protein	0.39	0.18
1314	Origin recognition complex subunit	0.53	0.18
1317	Glutamate decarboxylase	0.61	0.09
1318	Conserved protein	2.07	0.69
1319	Pheromone shutdown protein	0.67	0.08
1320	Conserved protein	1.82	0.62
1321	Formylmethanofuran--tetrahydromethanopterin formyltransferase	0.49	0.39
1324	Chemotaxis protein methyltransferase CheR	0.78	0.38
1326	Chemotaxis receptor methylesterase. CheB	1.26	0.33
1327	Chemotaxis protein CheY	1.29	0.17
1328	Two-component response regulator	4.07	1.03
1329	Methyl-accepting chemotaxis protein	2.54	1.47

1332	Iron-dependent repressor	7.13	7.07
1333	Zinc ABC transporter. zinc-binding protein	8.22	6.73
1334	Zinc ABC transporter. ATP-binding protein	3.3	1.73
1335	Zinc ABC transporter. permease protein	2.4	1.72
1336	Hypothetical protein	0.52	0.09
1337	Hypothetical protein	1.09	0.22
1339	Pyruvate:ferredoxin oxidoreductase. beta subunit	0.26	0.11
1340	Pyruvate:ferredoxin oxidoreductase. alpha subunit	0.25	0.18
1341	Pyruvate:ferredoxin oxidoreductase. delta subunit	0.24	0.15
1342	Pyruvate:ferredoxin oxidoreductase. gamma subunit	0.26	0.17
1344	Signal sequence peptidase	0.88	0.28
1345	DNA polymerase II small subunit	0.87	0.33
1346	Fe-S oxidoreductase	0.39	0.16
1347	Peptide chain release factor	0.38	0.1
1348	Arginyl-tRNA synthetase	0.4	0.13
1349	Conserved protein	0.66	0.03
1352	5-Methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	1.47	0.19
1353	Conserved protein	0.63	0.32
1354	Hypothetical protein	0.98	0.16
1355	Conserved protein	0.37	0.36
1356	Tram domain protein	0.37	0.33
1357	Tram domain protein	0.35	0.32
1358	Putative methyltransferase	0.37	0.35
1359	Hypothetical protein	0.36	0.22
1360	ABC transporter. ATP-binding protein	0.6	0.36
1361	ABC transporter. permease protein	1.57	0.16

1362	ABC transporter. periplasmic binding protein	0.84	0.84
1364	S-layer protein	0.81	0.42
1365	Thiamin-monophosphate kinase	0.6	0.4
1366	Ribonucleoside-triphosphate reductase activating enzyme	0.87	0.69
1367	Anaerobic ribonucleoside-triphosphate reductase	1.74	0.43
1368	Glutaredoxin-like protein	0.59	0.45
1370	Myo-inositol-1-phosphate synthase	0.57	0.33
1371	Archaeal protein Translation Initiation Factor 2B subunit 1 (aIF-2B1)	0.39	0.06
1372	Hypothetical protein	0.42	0.29
1373	Hydrolase of the alpha/beta superfamily	0.53	0.33
1374	DNA mismatch repair protein	3.28	3.85
1375	Polyphosphate kinase	1.14	0.43
1376	Exopolyphosphatase	0.62	0.03
1377	Hypothetical protein	0.98	0.2
1378	Origin recognition complex subunit	1.85	0.14
1379	Thermosome_ alpha subunit	0.62	0.55
1380	Chaperone protein	1.64	1.27
1381	Chaperone protein	1.94	1.05
1382	Conserved protein	0.39	0.13
1383	Phenylalanyl-tRNA synthetase. alpha chain	0.38	0.03
1384	Superfamily I DNA and RNA helicase	0.84	0.31
1385	Conserved protein	0.51	0.05
1386	Hypothetical protein	0.51	0
1387	ATP-dependent RNA helicase	1.1	0.61
1388	Glycyl-tRNA synthetase	0.47	0.15

1389	Conserved protein	0.85	0.36
1390	Probable transcriptional regulator	0.35	0.15
1391	Survival protein	0.48	0.21
1392	Hypothetical protein	0.65	0.29
1393	Molybdenum cofactor biosynthesis protein A	0.62	0.39
1394	Cobyrinic acid a.c-diamide synthase	0.54	0.19
1395	Consered protein	1.65	0.22
1396	Conserved protein	0.51	0.44
1397	DNA polymerase sliding clamp	0.32	0.27
1398	DNA-directed RNA polymerase subunit M	0.2	0.07
1399	MutT-like protein	0.25	0.07
1401	Hypothetical protein	0.52	0.27
1403	CDP-diacylglycerol--serine O-phosphatidyltransferase	0.5	0.51
1404	Conserved protein	0.74	0.06
1405	Histidinol-phosphate aminotransferase	0.8	0.19
1406	Acetylornithine aminotransferase	0.88	0.06
1407	Conserved protein	0.79	0.05
1408	Archaeosine tRNA-ribosyltransferase	0.26	0.05
1409	Hypothetical protein	0.32	0.16
1410	Hypothetical protein	0.47	0.18
1411	Hypothetical protein	1.35	0.06
1412	Hypothetical protein	1.34	0.3
1414	Conserved protein	1.06	0.35
1415	Conserved protein	1.08	0.27
1416	Phosphoribosylformylglycinamidine cyclo-ligase	0.31	0.1
1417	Aspartate kinase	0.29	0.16
1418	3-Phosphonopyruvate decarboxylase	0.47	0.02

1419	Small heat shock protein	2.27	1.38
1420	Hypothetical protein	1.59	0.74
1421	Conserved protein	0.47	0
1422	Hypothetical protein	0.43	0.11
1423	dCMP deaminase	0.48	0.11
1424	Protein translocase. subunit SecF	0.57	0.42
1425	Protein translocase. subunit SecD	0.77	0.06
1426	REPLICATION FACTOR C SUBUNIT	0.74	0.22
1427	Conserved protein	0.81	0.41
1430	Transposase	0.82	0.34
1433	Hypothetical protein	1.01	0.14
1434	Monomethylamine permease MtmP (C-terminal domain)	1.2	0.12
1435	Monomethylamine permease MtmP	1.38	1.1
1437	Monomethylamine:corrinoid methyltransferase MtmB1	13.89	9.56
1438	Monomethylamine corrinoid protein MtmC1	12.35	7.98
1439	Methylcobalamin:coenzyme M methyltransferase MtbA2	0.69	0.41
1440	Conserved protein	2.28	0.85
1441	Inorganic pyrophosphatase	0.22	0.08
1443	PylC (Pyrrolysine synthesis)	4.21	0.27
1445	Lysly-tRNA synthetase (PylS)	2.28	0.65
1447	Hypothetical protein	0.24	0.1
1448	Hypothetical protein	1.02	0.14
1449	Conserved protein	0.8	0.06
1450	Fe-S oxidoreductase	0.92	0.27
1451	Universal stress protein	2	0.53
1452	Universal stress protein	2.5	1.84

1454	Universal stress protein	2.12	0.66
1455	Universal stress protein	1.45	1.06
1456	Universal stress protein	2.38	1.32
1457	Conserved protein	0.52	0.01
1458	Conserved protein	0.73	0.22
1459	Hypothetical protein	1.43	0.33
1461	Cation-transporting ATPase	2.23	1.17
1462	Hypothetical protein	2.3	0.17
1469	Conserved protein	1.27	0.03
1470	Phenylalanyl-tRNA synthetase. alpha chain	0.44	0.04
1471	Tryptophanyl-tRNA synthetase	0.29	0.06
1472	Putative nucleotidytransferase	0.84	0.03
1473	Conserved protein	0.78	0.08
1474	Metallo cofactor biosynthesis protein (moaA/ nifB /pqqE family	1.21	0.17
1475	Probable translation initiation factor 2 beta subunit	0.26	0.2
1476	LSU ribosomal protein L10E	0.24	0.18
1477	Pyruvate formate-lyase activating enzyme	1.07	0.25
1478	Molybdenum cofactor biosynthesis protein B	0.76	0
1479	SWF/SNF FAMILY HELICASE	1.03	0.13
1480	Conserved protein	0.95	0.49
1484	Conserved protein	1.69	0.07
1485	Conserved protein	0.41	0
1486	Alanyl-tRNA synthetase	0.67	0.3
1487	Methyltransferase	0.41	0.08
1489	3-Isopropylmalate dehydrogenase	0.32	0.12
1490	3-Isopropylmalate dehydratase	0.24	0.13

1491	Putative nucleotidytransferase	0.98	0.85
1492	Conserved protein	4.76	0.31
1493	Conserved protein	0.48	0.14
1494	Hypothetical transcriptional regulatory protein	0.87	0.07
1495	tRNA pseudouridine synthase A	0.7	0.2
1496	Putative methyltransferase	0.82	0.42
1497	Conserved protein	0.53	0.41
1498	Hypothetical protein	1	0.28
1499	Methionine aminopeptidase	1.24	0.19
1500	Xaa-Pro aminopeptidase	0.97	0.39
1502	S-adenosylmethionine synthetase	0.57	0.24
1503	ATP phosphoribosyltransferase	0.54	0.3
1504	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	0.9	0.17
1505	Imidazoleglycerol-phosphate dehydratase	0.55	0.16
1506	FdhD protein	1.22	0.49
1508	Hypothetical protein	0.61	0.05
1509	Hypothetical protein	1.22	0.77
1511	Hypothetical protein	0.84	0.63
1513	Hypothetical protein	11.44	15.53
1515	Transporter	1.04	0.52
1517	Cysteine desulfurase	0.72	0
1518	Conserved protein	0.36	0.21
1519	Amino-acid acetyltransferase	1.02	0.33
1520	Conserved protein	1.13	0.48
1521	Phosphoglucomutase/phosphomannomutase	1.03	0.63
1522	Putative FeS oxidoreductase	0.65	0.39

1523	Zinc metalloprotease	0.92	0.16
1524	Conserved protein	0.85	0.05
1525	Conserved protein	0.55	0.25
1526	4-Hydroxybenzoate decarboxylase	0.82	0.02
1527	Citrate (si) synthase	0.59	0.53
1528	Aconitate hydratase	0.6	0.21
1529	Hypothetical protein	0.89	0.38
1530	Hypothetical protein	0.85	0.15
1531	Putative regulartory protein	1.05	0.19
1533	Molybdopterin biosynthesis MoeB protein/ThiF protein	1.28	0.03
1535	L-fuculose phosphate aldolase	0.6	0.33
1536	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	0.64	0.35
1537	Conserved protein	0.62	0.4
1538	Replication factor c subunit	0.62	0.13
1539	Hypothetical protein	1.25	0.8
1540	Tetrahydromethanopterin S-methyltransferase. subunit H	0.35	0.23
1541	Tetrahydromethanopterin S-methyltransferase. subunit G	0.3	0.15
1542	Tetrahydromethanopterin S-methyltransferase. subunit F	0.27	0.25
1543	Tetrahydromethanopterin S-methyltransferase. subunit A	0.32	0.28
1544	Tetrahydromethanopterin S-methyltransferase. subunit B	0.27	0.19
1545	Tetrahydromethanopterin S-methyltransferase. subunit C	0.32	0.21
1546	Tetrahydromethanopterin S-methyltransferase. subunit D	0.32	0.28
1547	Tetrahydromethanopterin S-methyltransferase. subunit E	0.4	0.19
1548	Protoglobin-like protein	0.32	0.21
1549	Sodium/proline symporter	0.28	0.08
1550	putative molybdenum transport protein ModA	0.51	0.26

1551	Hypothetical protein	0.5	0.08
1552	Hypothetical protein	0.32	0.21
1553	TRANSPORTER. RND superfamily	0.58	0.13
1554	Transcriptional regulator	0.46	0.04
1555	Putative metal dependent hydrolase	0.64	0.02
1556	Conserved protein	0.38	0.05
1557	Signal recognition particle SEC65 subunit	0.8	0.21
1558	Hypothetical protein	1.69	0.34
1559	Hypothetical protein	0.74	0.59
1561	ABC transporter. tungsten-binding protein	1.22	0.51
1562	TUNGSTEN TRANSPORTER. PERMEASE PROTEIN	4.71	4.2
1563	TUNGSTEN TRANSPORTER. ATP BINDING PROTEIN	0.86	0.38
1564	Molybdenum formylmethanofuran dehydrogenase. subunit	0.44	0.34
1565	Molybdenum formylmethanofuran dehydrogenase. subunit	0.41	0.31
1566	Molybdenum formylmethanofuran dehydrogenase. subunit	0.48	0.21
1567	Molybdenum formylmethanofuran dehydrogenase. subunit	0.41	0.27
1568	Molybdenum formylmethanofuran dehydrogenase. subunit	0.52	0.28
1569	Molybdenum formylmethanofuran dehydrogenase. subunit	0.62	0.35
1570	Conserved protein	2.27	0.5
1571	Conserved protein	2.38	0.5
1572	Conserved protein	0.86	0.4
1574	Conserved protein	2.21	1.54

1575	Conserved protein	1.76	0.71
1576	Conserved protein	0.66	0.46
1577	Nicotinate-nucleotide pyrophosphorylase	0.48	0.08
1578	Molybdate ABC transporter. ATP-binding protein	0.45	0.08
1579	Molybdate ABC transporter. permease protein	0.5	0.25
1581	Putative NAD(P)H oxidoreductase	1.79	0.76
1582	Iron-sulfur flavoprotein	2.11	1.3
1583	Conserved protein	1.88	1.57
1584	NADPH-flavin oxidoreductase	1.8	0.37
1585	Iron-sulfur flavoprotein	2.33	0.57
1586	Transcriptional regulator. MarR family	0.77	0.07
1587	DNA repair helicase	0.95	0.28
1588	Surface layer protein (putative)	1.1	0.81
1589	Surface layer protein (putative)	1.77	0.66
1590	Conserved protein	1.32	1.01
1591	Conserved protein	3.07	1.99
1592	Conserved protein	0.58	0.21
1593	Probable RNA processing protein	0.43	0.05
1594	Fibrillarin	0.39	0.17
1595	Conserved protein	15.06	15.88
1596	Conserved protein	79.98	91.13
1597	Integral membrane protein	32.61	25.37
1598	Conserved protein	24.92	23.98
1601	Cobalamin biosynthesis protein CobN	49.82	57.2
1603	Conserved protein	0.44	0.29
1604	Tungsten formylmethanofuran dehydrogenase subunit E	0.41	0.3
1605	Conserved protein	0.69	0.14

1606	Archaeal protein Translation Initiation Factor 2B subunit 2aIF-2B2	1.28	0.1
1607	Acetyltransferase	1.43	0.02
1608	ABC transporter. ATP-binding protein	1.46	0.25
1610	Hypothetical protein	1.17	0.2
1611	Uridylate kinase	0.4	0.22
1612	Conserved protein	5.47	6.14
1614	Transcriptional regulator. TetR family	0.75	0.16
1615	Oxidoreductase. aldo/keto family	0.9	0.03
1616	Phosphoribosylaminoimidazole carboxylase	0.56	0.29
1617	Conserved protein	0.72	0.23
1618	Aspartate-semialdehyde dehydrogenase	0.39	0.27
1619	Ferredoxin	0.48	0.5
1620	Conserved protein	0.94	0.21
1621	Cobalamin biosynthesis protein CobW	0.43	0.31
1625	Conserved protein	0.94	0.1
1626	Conserved protein	0.56	0.12
1627	Fructose-bisphosphate aldolase	0.31	0.09
1631	IRON-SULFUR FLAVOPROTEIN	2.18	0.06
1632	Iron-sulfur flavoprotein	1.06	0.06
1633	ABC transporter. ATP-binding protein	1.16	0.01
1634	Transcriptional regulator	1.08	0.12
1635	Beta-phosphoglucomutase /glucose-1-phosphate phosphodismutase	1.33	0.01
1636	Glycosyltransferase	1.56	0.65
1645	Hypothetical protein	0.65	0.13
1647	Methanol:corrinoid methyltransferase MtaB1	0.9	0.91

1648	Methanol corrinoid protein MtaC1	1.11	1.25
1649	Conserved protein	0.48	0.33
1650	Conserved protein	0.35	0.22
1651	Conserved protein	0.57	0.24
1652	Ferredoxin	0.74	0.16
1655	Conserved protein	1.26	0.5
1660	Mg2+ transporter MgtE	1.79	0.95
1661	Type I restriction-modification system restriction subunit	3.12	2.9
1663	Conserved protein	1.19	0.37
1664	Conserved protein	0.77	0.17
1665	Conserved protein	0.82	0.18
1667	Type I restriction-modification system specificity subunit	0.91	0.33
1669	Type I restriction-modification system methylation subunit	0.79	0.4
1671	Hypothetical sensory transduction histidine kinase	2.42	0.79
1674	Hypothetical protein	0.39	0.05
1675	Conserved protein	0.37	0.14
1676	Conserved protein	0.91	0.46
1678	Conserved protein	1.67	0.57
1680	Precorrin-6Y C5.15-methyltransferase [decarboxylating]	0.67	0.17
1681	CbiD protein	0.6	0.02
1682	DNA mismatch repair protein	0.77	0.07
1683	DNA mismatch repair protein	0.71	0
1685	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1.34	0.45
1687	Dimethylamine corrinoid protein MtbC1	21.76	26.54
1688	Trimethylamine:corrinoid methyltransferase MttB1	28.17	31.85

1689	Trimethylamine:corrinoid methyltransferase MttB1 (C-terminal domain)	36.26	28.53
1690	Trimethylamine corrionid protein MttC1	54.46	11.25
1691	Trimethylamine permease	52.95	17.19
1692	Conserved protein	29.81	15.44
1695	Conserved protein	1.94	0.4
1696	Lysyl-tRNA synthetase. class I	0.71	0.1
1697	LysM	0.78	0.17
1698	Conserved protein	1.57	0.28
1699	Conserved protein	0.31	0.16
1701	Putative nucleoside-diphosphate-sugar epimerase	0.79	0.08
1702	Conserved protein	3.3	2.74
1703	Conserved protein	0.46	0.11
1704	Histidine biosynthesis protein	0.56	0.1
1705	Conserved protein	1.55	0.53
1706	Protein-L-isoaspartate O-methyltransferase	1.24	0.31
1707	Conserved protein	0.76	0.01
1709	Conserved protein	0.58	0.24
1710	3.4 Dihydroxy-2-butanone 4-phosphate synthase	0.65	0
1712	Chorismate synthase	0.75	0.07
1713	Conserved protein	2.43	1.15
1717	Conserved protein	0.86	0.49
1718	Conserved protein	0.84	0.61
1726	Heme biosynthesis protein	0.51	0.04
1728	Heme biosynthesis protein	0.36	0.07
1729	Transposase	0.59	0.23
1736	Transposase	9.66	12.58

1740	S-layer protein	0.55	0.24
1741	Glutamyl-tRNA reductase	0.89	0.03
1742	Delta-aminolevulinic acid dehydratase	0.82	0.02
1743	Glutamate-1-semialdehyde 2.1-aminomutase	0.87	0.08
1744	Porphobilinogen deaminase	0.79	0.12
1745	Dihydroorotate dehydrogenase	0.9	0.2
1747	2-Hydroxy-2.4-diene-1.7-dioate isomerase	1.22	0.37
1748	Conserved protein	1.13	0.04
1749	Glutamyl-tRNA synthetase	0.73	0.24
1750	Conserved protein	0.65	0.26
1752	Conserved protein	0.61	0.04
1753	D-3-phosphoglycerate dehydrogenase	0.63	0.22
1754	Conserved protein	0.96	0.25
1755	LSU ribosomal protein L18E	0.26	0.23
1756	LSU ribosomal protein L13P	0.27	0.25
1757	SSU ribosomal protein S9P	0.27	0.24
1758	DNA-directed RNA polymerase subunit N	0.26	0.2
1759	DNA-directed RNA polymerase subunit K	0.31	0.24
1760	SSU ribosomal protein S2P	0.44	0.25
1761	Conserved protein	0.38	0.25
1762	Mevalonate kinase	0.57	0.11
1763	Archaeal kinase	0.9	0.06
1764	Isopentenyl-diphosphate delta-isomerase	0.97	0.17
1766	Zn-dependent hydrolase	0.56	0.26
1767	Geranyltranstransferase	0.56	0.33
1768	Hypothetical protein	2.26	0.68
1770	Pyruvate. phosphate dikinase	0.3	0.17

1771	Hypothetical protein	0.45	0.39
1772	Transcription initiation factor IIB	0.65	0.5
1773	Conserved protein	1.62	0.44
1774	Hypothetical protein	1.05	0.62
1775	Methyltransferase	0.34	0.18
1776	Thiol-specific antioxidant protein	1.11	0.55
1778	Cobalt-zinc-cadmium resistance protein	1.08	0.18
1779	Hypothetical protein	1.18	0.31
1780	Hypothetical protein	1.83	0.55
1782	Sodium/glutamate symport carrier protein	1.67	1.21
1788	HTH DNA-binding protein	0.64	0.1
1789	Hypothetical protein	2.16	0.88
1790	Conserved protein	2.39	0.17
1791	Conserved protein	1.73	0.37
1792	Hypothetical protein	1.16	0.16
1793	Hypothetical protein	3.08	1.16
1794	Hypothetical protein	1.63	0.99
1795	Iron-sulfur cluster-binding protein	1.06	0.15
1796	Conserved protein	1.31	0.72
1797	10 kDa chaperonin	1.78	0.37
1798	GroEL protein	1.32	0.79
1802	Aspartate aminotransferase	0.54	0.36
1803	Hypothetical protein	4.48	1.19
1804	Rubrerythrin	0.65	0.34
1805	Conserved protein	0.47	0.29
1806	DNA primase	0.51	0.2
1807	Protein translation initiation factor 2 subunit alpha IF-2a	0.37	0.14

1808	SSU ribosomal protein S27E	0.31	0.27
1809	LSU ribosomal protein L44E	0.33	0.27
1810	Conserved protein	0.81	0.31
1811	DNA primase small subunit	1.81	0.88
1813	Conserved protein	0.53	0
1814	Hypothetical protein	1.06	0.05
1816	Conserved protein	1.34	1.43
1818	Conserved protein	1.09	0.77
1821	Replication factor c subunit	0.65	0.28
1823	Putative small multi-drug export protein	0.95	0.64
1824	Ferredoxin	0.61	0.48
1825	DNA binding protein	0.86	0.38
1826	Methyltransferase	0.6	0.28
1827	Pyruvate carboxylase (biotin-containing) subunit B	0.49	0.13
1828	Pyruvate carboxylase. subunit A	0.5	0.18
1829	Biotin-[acetyl-CoA-carboxylase] synthetase/biotin operon repressor	0.44	0.27
1830	Conserved protein	1.28	0.47
1833	Phosphoserine phosphatase	0.7	0.44
1834	Conserved protein	1.01	0.41
1835	Conserved protein	1.17	0.12
1836	Cell division control protein (MCM family)	0.66	0.6
1837	RNA methylase	0.69	0.36
1838	Ferredoxin	0.47	0.02
1842	Sulfite reductase. assimilatory-type	5.99	6.94
1843	Heterodisulfide reductase. subunit HdrE	0.45	0.35
1844	Heterodisulfide reductase. subunit HdrD	0.64	0.51

1845	Conserved protein	0.83	0.79
1846	Conserved protein	0.99	0.45
1847	Hypothetical protein	0.71	0.02
1849	Geranylgeranyl reductase	1.6	0.82
1850	RNase P	5.25	7.42
1851	Hypothetical protein	0.66	0.48
1852	Conserved protein	1.08	0.46
1853	Conserved protein	0.7	0.54
1854	Archaeal flavoprotein	1.04	0.12
1855	Dipeptide/oligopeptide ABC transporter. ATP-binding protein	3.27	2.51
1856	Dipeptide/ oligopeptide ABC transporter. ATP-binding protein	4.16	2.3
1858	Dipeptide/ oligopeptide ABC transporter. permease	5.2	3.04
1859	Dipeptide/ oligopeptide binding protein	3.79	0.45
1861	Conserved protein	0.11	0.05
1862	Transporter	0.57	0.29
1863	Transcriptional regulator. MarR family	0.46	0.14
1864	Conserved protein	1.73	1.19
1865	Conserved protein	1.85	0.58
1869	Conserved protein	0.62	0.42
1870	Conserved protein	1.18	0.18
1871	Vanillate decarboxylase protein	1.95	0.06
1872	Conserved protein	1.86	0.73
1873	Phosphohydrolase	1.55	0.4
1874	Methyltransferase	0.68	0.11
1875	Conserved protein	0.69	0.74

1876	Purine phosphoribosyltransferase	0.53	0.23
1877	Diphthamide synthase subunit	0.68	0.17
1878	Methyltransferase	0.54	0.12
1879	putative RNA-binding protein	0.66	0.28
1880	DNA-directed RNA polymerase subunit L	0.46	0.17
1881	Conserved protein	0.63	0.02
1883	Conserved protein	0.5	0.28
1885	Diaminopimelate decarboxylase	0.51	0.3
1890	Conserved protein	7.36	9.54
1896	Phenylacetic acid degradation protein	0.64	0.22
1897	Hypothetical protein	0.46	0.25
1899	Hypothetical protein	0.48	0.22
1902	Hypothetical protein	1.19	0.41
1903	Transcriptional regulator. MarR family	11.03	14.37
1904	Hypothetical membrane spanning protein	0.74	0.14
1908	Hypothetical protein	0.88	0.35
1909	Glutathione-regulated potassium-efflux system protein	0.15	0.05
1911	Cysteinyl-tRNA synthetase	1.39	0.38
1913	ATP-dependent protease La	2.89	2.16
1914	Hypothetical protein	0.93	0.22
1915	Hypothetical sensory transduction histidine kinase	2.97	0.87
1916	Lysyl-tRNA synthetase. class II	0.41	0.09
1917	ATP-dependent RNA helicase	2.54	1.33
1921	Hypothetical protein	2.07	0.44
1922	Hypothetical protein	1.59	0.29
1923	Hypothetical protein	1.24	0.16
1924	Hypothetical protein	4.04	4.18

1925	hypothetical protein	1.4	0.38
1928	Phosphinothricin acetyltransferase	1.45	0.22
1929	Hypothetical protein	1.12	0.89
1931	Sensory Transduction protein Kinase	3.43	0.33
1932	Methylcobalamin:coenzyme M methyltransferase MtbA3	1.13	0.35
1933	Integral membrane protein	0.56	0.31
1934	Hypothetical protein	0.92	0.29
1935	Acetyltransferase	1.57	0.77
1936	Conserved protein	1.03	0.39
1937	Hypothetical protein	0.67	0.17
1938	Hypothetical protein	0.2	0.12
1939	Glutamine-binding protein	0.88	0.21
1940	Glutamine transporter. permease protein	0.91	0.63
1941	Glutamine transporter. ATP-binding protein	1.11	0.42
1943	Conserved protein	1.81	0.18
1948	Oxidoreductase. aldo/keto family	0.7	0.14
1949	Methyltransferase	1.12	0.11
1951	Hypothetical protein	23.82	29.47
1952	Cobalt-zinc-cadmium resistance protein	2.3	1.45
1954	NifU protein	1.72	1.47
1955	Cysteine desulfurase NifS	1.92	1.14
1956	Hypothetical protein	2.18	0.92
1957	Hypothetical transcriptional regulatory protein	1.53	0.52
1958	Hit-like protein. involved in cell-cycle regulation	1.28	0.34
1961	Hypothetical protein	1.09	0.35
1962	Conserved protein	1.18	0.03

1963	Tyrosyl-tRNA synthetase	0.46	0.13
1964	hypothetical protein	0.56	0.33
1965	Hypothetical protein	0.84	0.35
1966	Malate dehydrogenase	0.29	0.07
1967	Hypothetical protein	0.54	0.01
1968	Cupin-type phosphoglucose isomerases	0.77	0.67
1969	Hypothetical protein	0.98	0.17
1970	Single-stranded-DNA-specific exonuclease RecJ	0.82	0.06
1971	Conserved protein	0.74	0.05
1973	Conserved protein	3.27	4.49
1974	Histone acetyltransferase (ELP3 faminly)	0.66	0.23
1975	Conserved protein	0.89	0.49
1976	Conserved protein	0.28	0.1
1977	Conserved protein	1.07	0.35
1978	Tungsten formylmethanofuran dehydrogenase subunit C	0.76	0.42
1979	Tungsten formylmethanofuran dehydrogenase subunit A	1.33	0.84
1980	Tungsten formylmethanofuran dehydrogenase subunit B	1.85	0.78
1981	Tungsten formylmethanofuran dehydrogenase subunit D	1.15	0.37
1984	Hypothetical protein	0.75	0.11
1985	Hypothetical protein	1.49	1
1986	Regulatory protein (putative)	0.67	0.39
1989	Hypothetical protein	1.15	0.4
1990	Hypothetical protein	1.39	0.12
1992	Hypothetical protein	2.68	1.52
1993	ABC transporter. ATP-binding protein	3.12	0.14
1994	Cobalt transport ATP-binding protein CbiO	2.42	0.06
1995	Cobalt ABC transporter. permease protein CbiQ	5.9	3.46

1996	Cobalt transport ATP-binding protein CbiO	6.34	4.9
1997	Cobalt transport permease CbiM analog	6.46	1.45
1998	Cobalamin biosynthesis protein CobN	13.17	14.46
1999	Hypothetical protein	7.83	5.37
2000	Hypothetical protein	12.52	9.58
2001	Hypothetical protein	29.25	10.97
2002	Conserved protein	6.88	5.03
2003	Magnesium-chelatase subunit	6.1	7.53
2005	Phosphate-binding protein	0.34	0.01
2007	Phosphate transporter. permease protein	0.49	0.03
2008	Phosphate transporter. permease protein	0.43	0.03
2009	Phosphate transporter. ATP-binding protein	0.41	0.03
2010	Phosphate transport system protein	0.98	0.28
2011	Dihydroorotase	1.27	1.14
2012	Putative RNA-binding protein	0.4	0.31
2013	Serine/threonine protein kinase	0.57	0.57
2014	Translation initiation factor 1A (EIF-1A)	0.64	0.47
2015	Hypothetical protein	0.8	0.09
2016	HesB protein	0.34	0.23
2017	Conserved protein	0.48	0.17
2018	Conserved protein	2.67	0.8
2019	Phosphoribosyl-AMP cyclohydrolase	0.47	0.06
2020	TWITCHING MOBILITY (PilT) related protein	0.48	0.15
2021	Conserved protein	12.07	15.59
2022	TRANSPORTER. LysE family	1.12	0.92
2026	Hypothetical protein	2.78	0.87
2027	Hypothetical protein	0.84	0.39

2028	Hypothetical protein	2.57	0.47
2029	Conserved protein	1.93	0.52
2030	Amidotransferase hisH	0.62	0.1
2031	Hydrogenase expression/formation protein	1.41	1.11
2032	Nodulation protein	1.51	0
2033	Stomatin-like protein	0.86	0.46
2034	Conserved protein	0.56	0.34
2035	Orotate phosphoribosyltransferase	0.74	0.34
2036	Conserved protein	0.43	0.16
2037	Conserved protein	0.8	0.06
2038	Conserved protein	1.26	0.54
2039	SSU ribosomal protein S8E	0.24	0.14
2040	TRANSCRIPTIONAL REGULATORY PROTEIN. ASNC FAMILY	0.37	0.18
2041	Aspartate aminotransferase	0.84	0.01
2042	Archaeal transcriptional regulator	0.88	0.24
2043	Hypothetical protein	0.4	0.19
2045	Conserved protein	1.1	0.13
2046	Trimethylamine Permease MttP2	2.26	1.49
2047	Trimethylamine corrionid protein MttC2	2.72	2.3
2049	Trimethylamine:corrinoid methyltransferase MttB2	3.86	1.86
2050	Dimethylamine:corrinoid methyltransferase MtbB2 (C-terminal domain)	1.6	0.21
2051	Dimethylamine:corrinoid methyltransferase MtbB2	1.83	1.03
2052	Dimethylamine corrinoid protein MtbC2	2.84	2.19
2053	Conserved protein	0.65	0.13
2054	ABC transporter. ATP-binding protein	0.64	0.26

2055	ABC transporter. ATP-binding protein	0.88	0.05
2056	AdoCbi-P nucleotidyltransferase CobY	1.28	0.19
2057	Cobalamin [5'-phosphate] synthase CobS	1.26	0.2
2058	Hypothetical protein	1.73	1.16
2059	Cobalamin biosynthesis protein CbiB	1.02	1
2060	Histidinol-phosphate aminotransferase	0.54	0.58
2061	Histidyl-tRNA synthetase	0.34	0.07
2066	SSU ribosomal protein S15P	0.43	0.14
2067	Ferric enterobactin ABC transporter. ATP-binding protein (FepC)	1.4	1.03
2068	Ferric enterobactin ABC transporter. permease protein (FepG)	0.94	0.87
2069	Ferric enterobactin ABC transporter. solute binding protein (FepB)	2.23	1.33
2070	Nicotinate-nucleotide pyrophosphorylase	0.8	0.18
2071	Conserved protein	1.17	0.04
2072	Putative dinucleotide-utilizing enzyme	0.42	0.26
2073	Quinolinate synthetase A	0.35	0.12
2074	Conserved protein	0.7	0.38
2076	S-adenosylmethionine synthetase	1.4	0.68
2077	Conserved protein	1.7	0.75
2078	Conserved protein	6.43	3.35
2079	Thioredoxin	3.17	1.52
2083	Orotidine 5'-phosphate decarboxylase	0.47	0.18
2084	CO dehydrogenase/acetyl-CoA synthase. gamma subunit	2.87	2.01
2087	CO dehydrogenase/acetyl-CoA synthase. beta subunit	5.34	3.74
2088		1.18	0.66
2089	CO dehydrogenase/acetyl-CoA synthase. alpha subunit	2.15	1.52

2090	HTH DNA-binding protein	1.15	0.32
2091	Probable transport channel protein	1.24	0.32
2092	CODH nickel-insertion accessory protein (iron-sulfur protein)	2.18	0.86
2093	Indolepyruvate oxidoreductase. subunit	0.61	0.06
2095	Hypothetical protein	0.85	0.75
2096	UDP-N-acetylglucosamine-1-phosphate transferase	1.1	0.57
2098	Conserved protein	0.9	0.3
2102	Glycosyl transferase	0.98	0.52
2103	Putative Methyltransferase	0.98	0.08
2105	Putative glycosyltransferase	1.13	0.1
2108	Conserved protein	0.9	0.42
2109	Glycosyl transferase	0.95	0.14
2111	Galactoside O-acetyltransferase	1.17	0.47
2112	Hypothetical protein	3.24	3.14
2113	Hypothetical protein	0.75	0.15
2115	Protease HTPX homolog	0.84	0.51
2117	Hypothetical protein	2.26	0.48
2118	Hypothetical protein	1.42	1.24
2119	Hypothetical protein	64.89	47.55
2122	Putative serine/threonine protein kinase	0.86	0.54
2124	LSU ribosomal protein L3P	0.33	0.21
2125	LSU ribosomal protein L4	0.26	0.16
2126	LSU ribosomal protein L23P	0.29	0.23
2127	LSU ribosomal protein L2P	0.3	0.23
2128	SSU ribosomal protein S19P	0.32	0.19
2129	LSU ribosomal protein L22P	0.29	0.25

2130	SSU ribosomal protein S3P	0.29	0.2
2131	LSU ribosomal protein L29P	0.29	0.19
2132	RNaseP subunitP29	0.31	0.19
2133	SSU ribosomal protein S17P	0.22	0.14
2134	LSU ribosomal protein L14P	0.26	0.2
2135	LSU ribosomal protein L24P	0.24	0.12
2136	SSU ribosomal protein S4E	0.39	0.19
2137	LSU ribosomal protein L5P	0.25	0.2
2138	SSU ribosomal protein S14P	0.22	0.18
2139	SSU ribosomal protein S8P	0.2	0.14
2140	LSU ribosomal protein L6P	0.18	0.13
2141	LSU ribosomal protein L32E	0.2	0.14
2142	LSU ribosomal protein L19E	0.21	0.13
2143	LSU ribosomal protein L18P	0.28	0.19
2144	SSU ribosomal protein S5P	0.33	0.21
2145	LSU ribosomal protein L30P	0.48	0.18
2146	LSU ribosomal protein L15P	0.28	0.2
2147	Protein translocase. subunit SecY	0.44	0.27
2148	Adenylate kinase	0.56	0.32
2150	Conserved protein	0.95	0.36
2152	Hypothetical protein	0.58	0
2153	Cytidylate kinase	0.43	0.3
2154	tRNA pseudouridine synthase	0.39	0.19
2155	SSU ribosomal protein S13P	0.35	0.34
2156	SSU ribosomal protein S4P	0.35	0.3
2157	SSU ribosomal protein S11P	0.38	0.34
2158	DNA-directed RNA polymerase. subunit D	0.55	0.24

2159	Hypothetical protein	0.83	0.08
2161	Hypothetical protein	0.95	0.39
2163	Hydrogenase expression/formation protein	0.61	0.27
2164	Hydrogenase expression/formation protein	0.4	0.05
2169	F420-nonreducing hydrogenase II. small subunit (VhtG)	0.31	0.13
2170	F420-nonreducing hydrogenase II. large subunit (VhtA)	1.07	0.3
2171	F420-nonreducing hydrogenase II. cytochrome b subunit (VhtC)	1.54	0.89
2172	Hydrogenase expression/formation protein	1.47	0.93
2173	Conserved protein	2.01	0.61
2174	Conserved protein	1.94	1.01
2178	Two component system histidine kinase	2.81	0.92
2179	Conserved protein	0.31	0.08
2180	GMP synthase [glutamine-hydrolyzing]	0.3	0.09
2181	Fructose-1.6-bisphosphatase	0.53	0.09
2182	Hypothetical protein	0.7	0.88
2184	TATA-box binding protein	1.02	0.21
2185	Hypothetical protein	1.77	0.81
2189	Rubrerythrin	1.04	0.4
2193	DNA repair protein (MRE11/RAD32 family)	0.94	0.23
2194	DNA repair protein RAD50	0.98	0.16
2196	Conserved protein	0.98	0.25
2198	Type I restriction-modification system methylation subunit	1.18	0.16
2199	Type I restriction-modification system specificity subunit	1.33	0.11
2202	Hypothetical protein	1.13	0
2203	Hypothetical protein	1.11	0.21

2204	Hypothetical protein	1.44	0.14
2205	Ribose-phosphate pyrophosphokinase	0.56	0.12
2206	Molybdenum cofactor biosynthesis protein C	0.82	0.06
2208	Putative sugar kinase	1.91	0.96
2209	Conserved protein	1.86	0.79
2210	Oligosaccharyl transferase	0.43	0.3
2211	Hypothetical protein	2.19	0.36
2212	Conserved protein	0.87	0.38
2213	Putative glycosyltransferase	1.04	0.43
2214	Polysaccharide ABC transporter. ATP-binding protein	0.78	0.56
2215	Polysaccharide ABC transporter. permease protein	0.64	0.39
2217	Conserved protein	1.39	0.09
2221	Glycosyltransferase	1.1	0.06
2222	Galactoside O-acetyltransferase	0.69	0.02
2223	Dolichyl-phosphate glucose synthetase	0.82	0.26
2224	Trp repressor binding protein	1.94	0.55
2225	Glucoamylase	1.43	0.09
2226	Glucoamylase	1.3	0.1
2227	Acetyltransferase	1.61	0.7
2228	Amidohydrolase (putative)	1.76	0.56
2233	Conserved protein	2.19	1.35
2234	Conserved protein	3.67	1.74
2235	Conserved protein	9.07	8.21
2236	Conserved protein	2.25	0.56
2237	Transcriptional regulator. ArsR family	1.07	0.44
2242	Transcriptional regulator. ArsR family	1.85	0.85
2243	Putative methyltransferase	1.69	0.54

2246	Transcriptional regulator. ArsR family	1.4	0.05
2250	Conserved protein	1.14	0.03
2251	Tetrahydromethanopterin S-methyltransferase. subunit A	0.81	0.04
2252	Conserved protein	0.44	0.21
2256	Conserved protein	1.05	0
2257	Conserved protein	1.45	0.08
2258	Conserved protein	0.9	0.32
2260	Hypothetical protein	1	0.44
2261	Conserved protein	1.3	0.16
2262	Conserved protein	2.1	0.88
2263	SSU ribosomal protein S10P	0.43	0.46
2264	Protein translation elongation factor 1A (EF-1A)	0.33	0.28
2265	Protein translation elongation factor 2	0.38	0.33
2266	SSU ribosomal protein S7P	0.28	0.21
2267	SSU ribosomal protein S12P	0.25	0.19
2268	NusA protein homolog	0.36	0.22
2269	LSU ribosomal protein L30E	0.29	0.25
2270	DNA-directed RNA polymerase. subunit A"	0.82	0.3
2271	DNA-directed RNA polymerase. subunit A'	0.72	0.4
2272	DNA-directed RNA polymerase. subunit B"	0.75	0.33
2273	DNA-directed RNA polymerase. subunit B'	0.45	0.19
2274	DNA-directed RNA polymerase. subunit H	0.54	0.07
2275	Hypothetical sensory transduction histidine kinase	4.15	0.98
2276	Hypothetical sensory transduction histidine kinase	1.7	0.4
2278	Adenosylhomocysteinase	0.91	0.17
2279	Chlorohydrolase family protein	1.07	0.1
2280	Conserved protein	0.65	0.02

2281	Hypothetical protein	0.4	0.25
2282	Conserved protein	0.36	0.07
2283	DNA/pantothenate metabolism flavoprotein	0.57	0.11
2285	Conserved protein	0.4	0.11
2286	Conserved protein	1.02	0.69
2287	Hypothetical protein	0.43	0.21
2288	Methyltranferase involved in cell division	0.46	0.16
2289	Hypothetical protein	0.54	0.05
2290	Cell surface protein	0.65	0.02
2292	Type I restriction-modification system restriction subunit	0.92	0
2293	Type I restriction-modification system specificity subunit	1.18	0.38
2294	Type I restriction-modification system methylation subunit	0.79	0.07
2295	Surface layer protein (putative)	1.46	0.42
2297	Conserved protein	1.45	0.31
2300	Metal-dependent hydrolase	0.4	0.09
2301	Carbon monoxide dehydrogenase	2.51	1.86
2302	Conserved protein	0.34	0.07
2303	Transcriptional regulator	0.29	0.05
2305	Sodium/proline symporter	1.36	1.28
2306	L-asparaginase	1.14	0.36
2307	Argininosuccinate lyase	0.5	0.16
2309	Hypothetical protein	1.89	0.82
2310	Ubiquinone biosynthesis protein	3.51	2.09
2312	F420-nonreducing hydrogenase I. cytochrome b subunit (VhoC)	0.41	0.09
2314	F420-nonreducing hydrogenase I. small subunit (VhoG)	1.79	1.04

2315	Hydrogenase expression/formation protein	2.01	0.53
2316	Hydrogenase expression/formation protein	1.01	0.61
2317	Hydrogenase expression/formation protein	1.05	0.53
2319	Hydrogenase expression/formation protein	1.54	0.02
2320	Ech Hydrogenase. Subunit A	0.54	0.38
2321	Ech Hydrogenase. Subunit B	0.51	0.42
2322	Ech Hydrogenase. Subunit C	0.64	0.59
2323	Ech Hydrogenase. Subunit D	0.78	0.43
2324	Ech Hydrogenase. Subunit E	0.92	0.56
2325	Ech Hydrogenase. Subunit F	0.71	0.35
2326	COP associated protein	2.17	1.02
2327	COP associated protein	1.42	0.72
2328	Copper-exporting ATPase	2.58	1.85
2329	Conserved protein	1.2	0.13
2330	Hypothetical protein	0.72	0.11
2331	Uncharacterized permease	2.34	1.34
2333	Multidrug efflux pump	1.97	0.92
2334	Conserved protein	1.28	0.47
2335	Conserved protein	0.66	0.16
2336	Translation initiation factor 1A (EIF-1A)	1.21	0.17
2337	Conserved protein	1.76	0.8
2338	Conserved protein in Methanosarcina spec.	0.44	0.68
2340	Acetolactate synthase	1.33	0.09
2341	Succinate-semialdehyde dehydrogenase [NADP+]	1.3	0.35
2343	Copper-binding protein	1.33	0.2
2346	Methyltransferase	1.55	1.52
2348	O-linked N-acetyglucosamine transferase	0.83	0.14

2350	O-linked N-acetyglucosamine transferase	4.43	2.7
2351	Transcriptional regulator	2.43	0.33
2353	Thioredoxin reductase	1.98	0.75
2354	Thioredoxin	1.43	0.97
2355	Diphthine synthase	0.49	0.18
2357	Hypothetical protein	0.4	0.09
2358	6-Phosphofructokinase (ADP)	0.48	0.08
2359	Conserved protein	0.5	0.04
2360	Phosphoribosylaminoimidazole carboxylase. catalytic subunit	0.7	0.14
2362	Shikimate kinase	1.06	0.28
2363	Conserved protein	0.54	0.09
2364	GTP-binding protein	0.59	0.29
2365	Conserved protein	0.68	0.32
2366	Conserved protein	0.62	0.38
2367	Hexulose-6-phosphate isomerase	0.35	0.32
2368	Aspartate aminotransferase	0.55	0.05
2369	Cytochrome c-type biogenesis protein	1.32	0.77
2370	GTP-binding protein	0.45	0.05
2371	Conserved protein	0.55	0.16
2373	3-Isopropylmalate dehydratase	0.5	0.14
2375	Conserved protein	0.91	0.05
2376	Conserved protein	1.62	0.04
2378	Conserved transmembrane protein	0.84	0.27
2379	5'-Methylthioadenosine phosphorylase	0.83	0.05
2380	ATP-dependent DNA helicase	0.61	0.23
2381	Conserved protein	1.44	0.36

2382	Hypothetical protein	0.44	0.36
2383	Small nuclear riboprotein (snRNA) homolog	0.42	0.33
2384	Conserved protein	0.66	0.4
2385	Conserved protein	2.46	1.19
2386	Hypothetical protein	0.19	0.21
2387	Cobalt transport ATP-binding protein CbiO	0.16	0.12
2388	Cobalt ABC transporter. permease protein CbiQ	0.16	0.17
2392	Long-chain-fatty-acid--CoA ligase	0.35	0.18
2393	Conserved protein	0.49	0.22
2394	Transcriptional regulator. MerR family	0.4	0.3
2395	NADH:flavin oxidoreductases	3.56	2.83
2397	Heme exporter. protein B	4.29	5.11
2398	ABC transporter. ATP-binding protein	1.53	0.33
2399	Peptide methionine sulfoxide reductase	3.87	1.01
2400	Hypothetical protein	3.96	0.8
2401	Conserved protein	4.33	3.16
2402	Hypothetical protein	2.69	1.54
2403	Potassium channel protein	0.88	0.2
2404	Cation transporter	0.74	0.19
2405	Cation transporter	0.77	0.37
2406	Conserved protein	1.11	0.28
2407	Conserved protein	1.45	0.54
2409	Conserved protein	1.54	0.22
2413	Conserved protein	0.97	0.14
2414	Hypothetical protein	0.64	0.12
2415	Hypothetical protein	1.1	0.01
2417	Type II DNA topoisomerase VI. subunit B	0.72	0.32

2419	DNA gyrase. subunit B	1.4	1.04
2420	DNA gyrase. subunit A	1.92	0.49
2422	Conserved protein	1.08	0.46
2423	Superoxide dismutase	4.46	2.59
2424	Conserved protein	1.14	0.18
2426	Dienelactone hydrolase	1.56	0.65
2427	Methylthiol:coenzyme M methyltransferase MtsA	2.42	0.96
2428	Methylthiol:coenzyme M methyltransferase MtsB	4.19	3.06
2432	Putative pyridoxine biosynthesis protein	0.49	0.15
2433	Imidazoleglycerol-phosphate synthase	0.48	0.02
2437	Transposase	0.44	0.17
2443	Conserved protein	1.42	0.33
2446	Transcriptional regulator. ArsR family	1.44	1.09
2448	Transposase	1.01	0
2452	Conserved protein	0.72	0.29
2454	ABC transporter. permease protein	2.8	0.83
2455	ABC transporter. ATP-binding protein	2.91	0.55
2456	Dipeptide/oligopeptide transporter. ATP-binding protein	1.56	1.64
2457	Dipeptide/oligopeptide transporter. permease protein	1.89	1.67
2458	Dipeptide/oligopeptide transporter. permease protein	1.48	1.56
2459	Methyltransferase	1.14	1.09
2460	Dipeptide/oligopeptide-binding protein	1.24	1.26
2462	SSU ribosomal protein S6E	0.34	0.16
2463	Protein translation initiation factor IF2	0.31	0.18
2464	Nucleoside diphosphate kinase	0.27	0.25
2465	LSU ribosomal protein L24E	0.29	0.25
2466	SSU ribosomal protein S28E	0.21	0.2

2467	LSU ribosomal protein L7AE	0.22	0.22
2470	Surface layer protein (putative)	1.99	0.57
2471	Hypothetical protein	0.91	0.28
2472	Nucleotidyltransferase	1.18	0.23
2473	Hypothetical protein	1.13	0.17
2478	Chloride channel (putative)	1.6	0.07
2479	F420H2 dehydrogenase. subunitO	0.4	0.49
2480	F420H2 dehydrogenase. subunitN	0.33	0.39
2481	F420H2 dehydrogenase. subunitM	0.39	0.41
2482	F420H2 dehydrogenase. subunitL	0.34	0.37
2483	F420H2 dehydrogenase. subunitK	0.25	0.32
2484	F420H2 dehydrogenase. subunitJ2	0.38	0.34
2485	F420H2 dehydrogenase. subunitJ1	0.33	0.34
2486	F420H2 dehydrogenase. subunitI	0.33	0.28
2487	F420H2 dehydrogenase. subunitH	0.24	0.26
2489	F420H2 dehydrogenase. subunitC	0.37	0.18
2490	F420H2 dehydrogenase. subunitB	0.21	0.23
2491	F420H2 dehydrogenase. subunitA	0.18	0.12
2492	Putative Ferredoxin	0.51	0.4
2493	Oxidoreductase (hypothetical)	0.7	0.23
2494	FO synthase. subunit CofG	0.83	0.38
2495	F420 biosynthesis protein FbiC	0.61	0.53
2496	FO synthase. subunit CofH	0.47	0.22
2497	4-Methyl-5(B-hydroxyethyl)-thiazole monophosphate synthase	0.73	0.5
2498	Conserved protein	0.59	0.06
2499	Geranylgeranyl reductase	0.58	0.12

2500	Trk system potassium uptake protein	1.09	0.42
2501	Trk system potassium uptake protein	1.63	1.06
2502	Trk system potassium uptake protein	0.76	0.5
2503	Trk system potassium uptake protein TrkA	0.6	0.21
2504	Chaperone protein DnaJ	1	0.82
2505	Chaperone protein	0.91	0.51
2506	GrpE protein	0.63	0.67
2508	Heat shock protein	0.59	0.38
2510	Hypothetical protein	0.34	0.19
2511	Hypothetical protein	0.52	0.18
2512	1-Pyrroline-5-carboxylate synthetase	0.38	0.21
2513	Hypothetical protein	0.33	0.08
2514	Archaeal protein Translation Elongation Factor 1. subunit beta	0.37	0.06
2516	Probable transcriptional regulator	1.48	0.19
2517	Thiamine biosynthesis protein	0.63	0.04
2519	GTP-binding protein homolog	0.56	0.34
2520	Conserved protein	1.56	0.03
2522	Universal stress protein	1.7	0.9
2523	Hypothetical protein	1.83	0.04
2524	Phage shock protein A	1.82	0.06
2525	Hypothetical protein	0.68	0.38
2526	Conserved protein	0.57	0.2
2527	Hypothetical protein	0.73	0.48
2528	N2.N2-dimethylguanosine tRNA methyltransferase	0.6	0.03
2529	Hypothetical protein	1.14	0.01
2531	Hypothetical protein	2.34	0.29

2534	Conserved hypothetical protein	0.54	0
2535	Conserved hypothetical protein	0.46	0.09
2536	LSU ribosomal protein L21E	0.41	0.19
2537	Hypothetical protein	0.57	0.11
2538	Conserved hypothetical protein	0.78	0.35
2539	Dimethyladenosine transferase	1.11	0.05
2541	Cation-transporting ATPase	0.52	0
2542	Phosphohydrolase (MUTT/NUDIX family protein)	0.96	0.2
2545	Hypothetical protein	0.68	0.1
2546	Transcriptional regulator (TetR family)	1.73	0.77
2547	Putative ferredoxin	1.45	0.46
2550	Hypothetical protein	1.44	1.21
2552	Hypothetical protein	0.8	0.3
2553	Putative hydrolase	2.33	0.92
2554	Acetyltransferase	1.13	0.17
2555	Hypothetical protein	1.17	0.49
2556	ATP-dependent RNA helicase	1.45	0.7
2557	Catalase	4.76	2.7
2558	Hypothetical protein	0.94	0.66
2559	Hypothetical protein	2.03	0.22
2561	Conserved hypothetical protein	1.21	0.13
2562	Hypothetical protein	0.82	0.39
2563	Ferredoxin	1.65	0.37
2564	Hypothetical protein	0.56	0.15
2565	Pyruvate formate-lyase activating enzyme	8.42	11.57
2566	CODH nickel-insertion accessory protein CooC	1.48	0.89
2567	ABC transporter. periplasmic binding protein	5.87	2.36

2568	ABC transporter. permease protein	3.16	3.65
2569	ABC transporter. permease protein	8.2	2.44
2570	ABC transporter. ATP-binding protein	2.55	2.81
2571	ABC transporter. ATP-binding protein	4.17	2.3
2572	Methyltransferase	3.72	2.21
2573	Iron dependent transcriptional repressor	1.21	0.05
2575	Hypothetical protein	0.28	0.15
2577	Ferrous iron transport protein A	0.22	0.12
2578	Ferrous iron transport protein A	0.34	0.14
2582	Hypothetical protein	0.8	0.08
2583	Sec-independent protein translocase. protein	0.85	0.05
2584	Sec-independent protein translocase protein TatA	0.54	0.23
2585	Sec-independent protein translocase. protein	0.51	0.24
2586	Sec-independent protein translocase. protein	1.32	0.28
2592	Hypothetical protein	2.5	0.49
2593	Hypothetical protein	0.52	0.38
2594	Hypothetical protein	3.99	3.44
2595	Hypothetical protein	0.93	0.33
2596	Hypothetical protein	1.84	0.5
2597	Hypothetical protein	2.83	0.47
2598	Hypothetical protein	2.66	1
2599	Hypothetical protein	1.51	0.44
2602	Hypothetical protein	3.07	0.38
2603	Hypothetical protein	3.26	2.15
2604	Conserved protein	0.97	0.2
2605	Conserved protein	1.18	0.15
2606	Hypothetical protein	1.26	0.01

2607	Nucleotidyltransferase	1.44	0.33
2608	Nucleotidyltransferase	1.37	0.13
2609	Nucleotidyltransferase	1.57	0.51
2612	Probable ATP-dependent helicase	1.12	0.2
2613	LemA protein	1.92	0.71
2614	Hypothetical protein	1.48	1.35
2615	Hypothetical protein	1.29	0
2616	LSU ribosomal protein L15E	0.41	0.2
2617	Hypothetical protein	0.59	0.1
2618	Hypothetical protein	0.42	0.13
2619	Hypothetical protein	0.7	0.35
2620	Proteasome. subunit-alpha	0.46	0.35
2621	Hypothetical protein	0.62	0.52
2622	Hypothetical protein	0.54	0.53
2623	Ribonuclease	0.45	0.36
2624	Ribonuclease	0.46	0.29
2625	LSU ribosomal protein L37AE	0.34	0.21
2626	Putative nucleotidyltransferase	0.55	0.36
2627	Conserved protein	0.71	0.46
2628	Conserved protein	0.46	0.35
2629	Hypothetical sensory transduction histidine kinase	3.85	2.75
2631	Hypothetical protein	1.38	0.11
2632	NAD-dependent malic enzyme	1.28	0.11
2634	2-Keto acid:ferredoxin oxidoreductase subunit alpha	0.84	0.04
2635	Putative pyruvate:ferredoxin oxidoreductase	0.74	0.12
2636	Coenzyme F390 synthetase/phenylacetyl-CoA ligase	2.77	3.36
2639	Conserved protein	3.29	1.08

2640	Magnesium and cobalt transport protein CorA	1.9	0.79
2642	Hypothetical protein	1.59	0.17
2643	Hypothetical protein	0.6	0.11
2644	Putative molybdopterin converting factor	1.17	0.07
2645	Aldehyde ferredoxin oxidoreductase. tungsten-containing	1.46	0.1
2649	Aspartate aminotransferase	0.42	0.22
2650	Hydrolase	1.28	0.14
2652	Hypothetical protein	1.65	0.66
2653	N5.N10-methenyltetrahydromethanopterin cyclohydrolase	0.49	0.46
2654	Hypothetical protein	0.56	0.16
2656	Peptidyl-prolyl cis-trans isomerase	0.33	0.18
2657	transcriptional regulator	2.31	0.81
2658	Acetyltransferase	1.59	0.38
2659	Acetyltransferase	0.89	0.32
2663	Conserved protein	5.15	3.66
2664	Conserved protein	2.13	1.91
2666	Conserved protein	1.55	0.13
2667	Conserved protein	1.88	0.24
2668	Hypothetical protein	1.43	0.49
2669	Conserved protein	1.87	0.08
2672	Conserved protein	1.51	0.27
2674	Conserved protein	4	3.45
2676	Conserved protein	0.92	0.07
2677	Conserved protein	1.82	0.41
2679	Conserved protein	1.01	0.32

2681	Hypothetical protein	1.02	0.55
2691	Hypothetical protein	0.66	0.17
2697	Hypothetical protein	1.52	0.36
2702	Hypothetical protein	0.86	0.27
2703	Type I restriction-modification system specificity subunit	2.04	0.8
2704	Type I restriction-modification system methylation subunit	1.58	0.57
2705	Type I restriction-modification system restriction subunit	4.38	2.89
2706	Conserved protein	9.32	13.58
2708	Conserved protein	1.65	0.02
2709	Conserved protein	2.01	0.18
2710	Conserved protein	1.42	0.2
2711	Conserved protein	1.29	0.59
2712	Conserved protein	0.78	0.11
2713	Homoserine dehydrogenase	0.71	0.04
2714	ATP-dependent DNA ligase	1.15	0.15
2715	Hypothetical protein	0.93	0.15
2717	Conserved protein	1.12	0.04
2718	Hypothetical protein	0.67	0.16
2719	Conserved protein	0.75	0.15
2721	Conserved protein	3.47	1.58
2722	Hypothetical protein	4.71	1.53
2723	Phosphoenolpyruvate synthase	4.85	3.31
2724	Hypothetical protein	3.04	1.63
2725	Transposase	1.39	0.25
2726	Hypothetical protein	1.18	0.05

2727	Conserved protein	1.46	0
2728	Hypothetical protein	1.88	1.68
2730	Conserved protein	1.11	0.38
2732	Conserved protein	1.28	0.35
2737	Conserved protein	0.84	0.1
2740	Type I restriction-modification system methylation subunit	0.84	0.2
2742	Hypothetical protein	0.68	0.25
2743	Hypothetical protein	1.78	0.89
2745	Conserved protein	1.24	0.45
2748	Hypothetical sensory transduction histidine kinase	1.63	0.81
2749	Aminoacyl-histidine dipeptidase	1.98	1
2751	Conserved protein	1.77	0.06
2754	Conserved protein	0.51	0.36
2756	Hypothetical protein	0.96	0.43
2758	Hypothetical protein	0.93	0.45
2760	Hypothetical protein	1.13	0.14
2763	Putative DNA recombinase	0.73	0.23
2764	Hypothetical protein	3.33	1.52
2765	Hypothetical protein	12.21	12.89
2766	Hypothetical protein	2.18	1.28
2768	Conserved protein	8	9.64
2769	Iron-containing alcohol dehydrogenase	1.72	0.25
2772	Conserved protein	0.79	0.48
2773	Two component system histidine kinase	1.99	1.33
2774	Conserved protein	1.7	0.72
2779	Putative phosphoglycerate mutase	1.49	0.31

2781	Conserved protein	2	1.3
2782	Glyceraldehyde 3-phosphate dehydrogenase	0.88	0.71
2783	Suppressor protein SuhB homolog	0.83	0.46
2784	Hypothetical protein	1.12	0.06
2785	2-Isopropylmalate synthase	0.92	0.23
2786	Conserved protein	1.55	0.17
2787	Conserved protein	4.08	2.47
2788	Indolepyruvate oxidoreductase. alpha subunit	40.47	56.57
2789	Hypothetical protein	0.58	0.07
2790	Iron-sulfur flavoprotein	1.06	0.02
2792	Molybdopterin converting factor. subunit 2	0.77	0.06
2793	Molybdopterin-guanine dinucleotide biosynthesis protein	0.73	0.03
2794	Hypothetical protein	0.61	0.16
2795	Conserved protein	0.6	0.32
2796	Conserved protein	0.46	0.13
2800	Conserved protein	1.97	1.44
2802	Hypothetical protein	1.41	0.3
2803	Carbon monoxide dehydrogenase accessory protein	1.78	1.12
2805	Asparagine synthetase [glutamine-hydrolyzing]	0.44	0.02
2806	Hypothetical protein	0.39	0.11
2807	Phosphoribosylformylglycinamidine synthase	0.59	0.25
2808	Conserved protein	1.11	0.3
2809	Conserved protein	1.4	0.22
2810	Conserved protein	1.16	0.11
2811	Conserved protein	0.51	0.09
2812	Phenylalanyl-tRNA synthetase. beta chain	0.76	0.1

2813	Hypothetical protein	1.34	0.02
2816	Conserved protein	2.78	1.31
2817	Anthranilate synthase. component II	0.06	0.03
2818	Anthranilate synthase. component I	0.08	0.04
2819	N-5'-phosphoribosyl)anthranilate isomerase	0.09	0.1
2820	Anthranilate phosphoribosyltransferase	0.89	1.34
2821	Tryptophan synthase. alpha chain	0.41	0.53
2822	Tryptophan synthase. beta chain	0.14	0.09
2823	Indole-3-glycerol phosphate synthase	0.19	0.18
2824	Coenzyme F420-dependent glucose-6-phosphate dehydrogenase	2.03	1.36
2827	Hypothetical protein	1.08	0.03
2829	Peptidyl-prolyl cis-trans isomerase	1.15	0.1
2831	ABC transporter. permease protein	1.97	0.51
2832	ABC transporter. permease protein	0.49	0.41
2833	ABC transporter. ATP-binding protein	74.98	61.67
2834	Hypothetical protein	1.34	0.55
2835	Hypothetical protein	0.39	0.13
2836	Enolase	0.57	0.44
2839	MoxR-like ATPase	1.66	0.23
2840	Hypothetical protein	1.78	0.13
2842	5-Nitroimidazole antibiotic resistance protein	1.16	0.02
2844	Hypothetical protein	1.41	0.98
2845	Hypothetical protein	1.24	0.39
2848	Conserved protein	0.59	0.15
2849	Hypothetical permease	5.26	6.69
2850	ABC transporter. permease protein	1.85	0.61

2851	Transcriptional regulator. MarR family	0.18	0.01
2853	Hypothetical protein	3.03	3.51
2855	ABC transporter. permease protein	0.78	0.52
2857	Hypothetical protein	2.23	0.7
2859	Hypothetical protein	1.28	0.04
2860	Conserved protein	1.76	1.97
2861	Transcriptional regulator. ArsR family	0.9	0.06
2862	Hypothetical protein	1.12	0.72
2867	Coenzyme F390 synthetase/phenylacetyl-CoA ligase	1.72	0.62
2869	Hypothetical protein	2.08	0.25
2870	Hypothetical protein	1.91	0.69
2871	Hypothetical protein	2.28	0.32
2872	Methyltransferase	1.24	0.49
2873	L-sorbosone dehydrogenase	1.64	1.29
2874	Conserved protein	1.52	0.95
2876	DNA polymerase IV	1.99	0.22
2879	Tetratrico peptide repeat protein	1.94	0.54
2882	Conserved protein	1.89	0.63
2885	Metalloendopeptidases (putative)	1.3	0.63
2886	Hypothetical sensory transduction histidine kinase	1.07	0.64
2887	Conserved protein	0.98	0.33
2889	Hypothetical protein	1.57	1.09
2890	Hypothetical protein	1.09	0.75
2891	ABC transporter. permease protein	1.12	0.63
2892	ABC transporter. permease protein	1.61	0.16
2893	Hypothetical protein	1.12	0.5
2894	Hypothetical protein	0.85	0.1

2895	Transcriptional regulator	0.96	0.56
2899	Conserved protein	3.39	1.42
2900	Conserved protein	2.18	0.61
2909	Conserved protein	1.53	0.22
2910	Adenine deaminase	1.1	0.11
2911	Phosphoserine aminotransferase	2.06	1.14
2912	5-Oxoprolinase	0.53	0.03
2915	Hypothetical protein	1.64	1.06
2916	Flavoprotein	1.48	0.21
2917	Oxidoreductase. aldo/keto family	0.67	0.09
2919	Hypothetical protein	2.02	0.54
2920	Ribosomal-protein-alanine acetyltransferase	1.78	0.26
2923	Hypothetical protein	1.45	1.16
2928	Hypothetical protein	1.45	0.71
2929	Hypothetical protein	1.29	0.84
2930	Hypothetical protein	0.47	0.19
2931	Hydrolase	5.24	3.98
2932	Conserved protein	1.29	0.67
2933	Conserved protein	2.54	0.46
2937	Conserved protein	3.24	1.96
2938	Conserved protein	2.37	1.51
2939	Serine O-acetyltransferase	0.78	0.36
2940	Conserved protein	1.25	0.68
2941	Hypothetical protein	2.08	0.1
2942	Conserved protein	1.11	0.21
2943	Lipopolysaccharide N-acetylglucosaminyltransferase	0.9	0.4
2948	Conserved protein	0.62	0.12

2949	Hypothetical protein	0.73	0.67
2950	Conserved protein	0.81	0.41
2951	Hypothetical protein	0.61	0.41
2952	Conserved protein	2.13	0.92
2953	Transcriptional regulator	0.52	0.16
2954	Transcriptional regulator	1.29	0.54
2955	Hypothetical sensory transduction histidine kinase	1.78	0.24
2956	Conserved protein	0.85	0.65
2957	Transposase	0.39	0.23
2958	Conserved protein	1.67	0.2
2959	Hypothetical protein	2.31	1.39
2960	Hypothetical protein	0.81	0.41
2962	Dimethylamine:corrinoid methyltransferase MtbB3	34.93	36.99
2963	Dimethylamine:corrinoid methyltransferase MtbB3 (C-terminal domain)	35.14	23.65
2965	Hypothetical sensory transduction histidine kinase	1.78	0.16
2966	Conserved protein	2.14	0.31
2967	Isoleucyl-tRNA synthetase	0.82	0.54
2968	Conserved protein	0.66	0.1
2972	Hypothetical protein	3.01	0.15
2973	Hypothetical protein	0.77	0.23
2976	Type I restriction-modification system restriction subunit	1.44	0.1
2977	Hypothetical protein	1.25	0.08
2978	Type I restriction-modification system specificity subunit	0.94	0.04
2979	Hypothetical protein	1.28	0.01
2980	Hypothetical protein	1.1	0.18

2981	Type I restriction-modification system methylation subunit	1.23	0.1
2982	Antibiotic resistence protein	1.38	1.3
2987	Hypothetical protein	1.35	0.26
2988	Conserved protein	2.27	0.76
2989	Pyruvate formate-lyase activating enzyme	2.16	0.81
2993	Phosphoglycerate mutase	3.77	4.02
2994	Conserved protein	0.85	0.28
2995	Hypothetical protein	0.65	0.37
2996	Hypothetical protein	0.67	0.41
2997	Hypothetical protein	1.15	0.68
2998	Transposase	1.28	0.77
3000	DNA repair helicase (RAD25/XPB family)	1.63	0.17
3004	Conserved protein	1.64	0.41
3005	Acetyltransferase	0.52	0.16
3006	Probable resolvase/ recombinase	1.74	0.57
3007	Probable transcriptional regulator	1.45	0.04
3009	Membrane metalloprotease	0.62	0.06
3010	Periplasmic divalent cation tolerance protein	10.68	16.16
3011	Hypothetical protein	1.63	1.24
3012	Hypothetical protein	3.41	1.15
3013	ABC transporter. permease protein	3.64	3.92
3014	Conserved protein	6.68	4.14
3017	ABC transporter. permease protein	3.69	2.47
3018	Conserved protein	10.2	11.14
3019	Conserved protein	6.17	2.28
3020	Conserved protein	7.67	4.93

3021	ABC transporter. ATP-binding protein	3.88	1.51
3022	Conserved protein	10.11	8.37
3023	Conserved protein	9.66	6.65
3024	Conserved protein	3.2	4.74
3025	Hypothetical protein	1.66	1.47
3030	Conserved protein	1.77	0.19
3032	Conserved protein	1.49	0.7
3036	Hypothetical protein	1.27	0.19
3042	Coenzyme F420 hydrogenase. beta subunit	0.62	0.23
3043	Coenzyme F420 hydrogenase. gamma subunit	0.5	0.4
3044	Coenzyme F420 hydrogenase. delta subunit	0.58	0.45
3045	Coenzyme F420 hydrogenase. alpha subunit	0.74	0.42
3056	Competence-like protein	1.18	0.16
3058	Iron-sulfur flavoprotein	1.52	0.04
3059	Conserved protein	1.71	0.76
3063	Calcium dependent protease	3.39	2.94
3068	Conserved protein	1.83	0.93
3076	DNA topoisomerase I	0.62	0.34
3077	Probable transcriptional regulator	0.61	0.07
3078	mRNA 3'-end processing factor	1.97	0.64
3079	Hypothetical protein	2.15	1.97
3080	Hypothetical protein	1.89	0.29
3085	Cystathionine gamma-synthase	4.37	2.78
3086	Nicotinate phosphoribosyltransferase	1.72	0.13
3089	Hypothetical protein	1.2	0.68
3090	Hypothetical protein	1.01	0.24
3091	Phycocyanin alpha-subunit phycocyanobilin lyase	88.11	63.03

	related protein. CpcE/NblB family		
3092	Hypothetical protein	34.82	27.53
3093	Hypothetical protein	9.4	4.13
3094	Hypothetical protein	3.94	2.78
3095	ABC transporter. ATP-binding protein	25.17	22.38
3096	Hypothetical protein	18.49	23.65
3097	Hypothetical protein	17.35	21.08
3098	ABC transporter. permease protein	11.9	13.87
3099	Two component system histidine kinase	2.49	0.71
3100	Hypothetical protein	2.95	1.31
3101	Two component system histidine kinase	4.67	0.82
3103	Hypothetical protein	1.14	1.21
3104	Hypothetical protein	1.74	1.94
3105	Probable cytosine deaminase	1.23	0.3
3107	Hypothetical protein	0.96	0.05
3108	Hypothetical protein	0.83	0.3
3109	Glycogen phosphorylase	2.3	0.11
3110	Hypothetical protein	0.81	0.43
3111	Hypothetical protein	1	0.24
3112	Conserved protein	1.07	0.24
3113	Oligoendopeptidase F	1.27	0.09
3115	Hypothetical protein	0.97	0.1
3116	Hypothetical protein	1.73	1.36
3117	Transcriptional regulator. MarR family	1.21	0.05
3118	ATP-dependent protease La	3.64	1.71
3119	Iron-sulfur flavoprotein	2.31	0.12
3120	Hypothetical protein	0.79	0.06

3121	Hypothetical protein	0.34	0.08
3122	Putative hydrolase	1.17	0.11
3123	Hypothetical protein	0.63	0.05
3126	Hypothetical protein	1.13	0.34
3127	Hypothetical protein	0.45	0.18
3130	Hypothetical protein	0.33	0.18
3131	Fructokinase	0.76	0.12
3132	Hypothetical protein	0.89	0.61
3133	Hypothetical protein	1.39	0.63
3134	Protease HTPX	1.3	0.71
3135	ABC transporter. ATP-binding protein	1.01	0.62
3137	TRANSPORTER. LysE family	21.04	28.93
3139	Large-conductance mechanosensitive channel	1.24	0.19
3141	Type I restriction-modification system restriction subunit	3.14	0.06
3142	Type I restriction-modification system specificity subunit	0.98	0.21
3143	Hypothetical protein	0.95	0.16
3146	Hypothetical protein	1.79	0.85
3147	Type I restriction-modification system methylation subunit	0.52	0.06
3148	Exodeoxyribonuclease III	1.05	0.46
3149	Hypothetical protein	3.4	0.4
3151	Hypothetical protein	1.66	0.32
3152	Hypothetical protein	1.66	0.18
3155	Hypothetical protein	1.21	0.52
3166	Hypothetical protein	0.71	0.08
3169	Hypothetical protein	2.72	0.27

3171	Hypothetical protein	1.08	0.36
3173	Transcriptional regulator. ArsR family	1.38	0.24
3175	Hypothetical protein	1.51	0.4
3177	Hypothetical protein	1.21	0.24
3178	Hypothetical protein	3.79	4.11
3179	Transcriptional regulator	0.33	0.06
3180	Putative acetyl-CoA synthetase	0.39	0.16
3181	Ketoisovalerate oxidoreductase subunit	0.37	0.21
3182	Ketoisovalerate oxidoreductase subunit	0.52	0.16
3183	Ketoisovalerate oxidoreductase subunit	0.55	0.4
3184	Conserved protein	1.38	1.32
3185	Ornithine decarboxylase	2.58	3.82
3187	Flavodoxin	4.38	0.88
3188	Glutamine synthetase	0.35	0.2
3189	Potassium channel protein	1.95	0.24
3190	Hypothetical protein	0.64	0.01
3191	Hypothetical protein	0.58	0.33
3192	Hypothetical membrane spanning protein	0.76	0.45
3193	Hypothetical membrane associated protein	0.66	0.4
3194	Uncharacterized membrane protein	0.51	0.26
3195	Transcriptional regulator. MarR family	0.42	0.17
3198	Hypothetical protein	1.48	0.16
3199	Transporter	0.53	0.28
3202	Conserved protein	2.17	1.05
3207	Protease (putative)	0.74	0.26
3209	Transporter	0.54	0.3
3212	Hypothetical protein	0.11	0.03

3213	Prismane protein	0.64	0.4
3216	Conserved protein	1.01	0.36
3219	Conserved protein	1.96	0.25
3220	Transporter	3.25	0.69
3223	ABC transporter. ATP-binding protein	3.82	3.46
3226	Conserved protein	1.36	0.43
3230	Phosphate permease	0.2	0.05
3231	Conserved protein	0.63	0.26
3234	Hydroxyethylthiazole kinase	0.37	0.12
3235	Thiamin-phosphate pyrophosphorylase	0.57	0.32
3239	Hypothetical protein	1.58	0.67
3240	Probable transcriptional regulator	0.9	0.4
3243	Hypothetical protein	0.56	0.12
3244	Hypothetical protein	0.71	0.26
3255	Hypothetical protein	4.06	3.41
3257	Conserved protein	1.36	0.23
3262	Branched-chain amino acid transport protein	0.3	0.23
3263	Branched-chain amino acid transport protein	0.37	0.23
3267	Conserved protein	2.24	0.46
3268	NADPH-flavin oxidoreductase	1.15	0.06
3269	Serine O-acetyltransferase	2.01	0.65
3270	Ferredoxin-thioredoxin reductase. catalytic chain	0.87	0.08
3271	Glutaredoxin	1.31	0.18
3274	Hypothetical protein	0.53	0.31
3275	Conserved protein	1.8	0.92
3276	Hypothetical protein	2.84	0.97
3277	Protease I	2.33	0.79

3278	Hypothetical Membrane Spanning protein	0.98	0.17
3279	Dihydrolipoamide dehydrogenase	2.4	1.73
3282	Probable ATP-dependent helicase	0.56	0.12
3284	Transcriptional regulator	0.9	0.46
3286	Hypothetical protein	1.33	0.26
3287	Hypothetical protein	2.25	0.52
3288	Conserved protein	6.56	7.49
3289	Excinuclease ABC. subunit B	1.44	0.35
3291	Excinuclease ABC. subunit A	1.1	0.72
3293	Iron-sulfur cluster-binding protein	1.22	0.25
3295	Hypothetical sensory transduction histidine kinase	0.7	0.13
3298	Glutamate dehydrogenase	1.13	0.06
3299	Hypothetical protein	1.12	0.48
3300	Phosphoadenosine phosphosulfate reductase	0.47	0.1
3304	Threonyl-tRNA synthetase	0.43	0.2
3305	Putative DNA or RNA helicase of superfamily II	1.98	0.04
3307	Conserved protein	1.4	0.2
3308	Conserved protein	0.61	0.06
3309	Ferredoxin	0.87	0.59
3310	Transcriptional regulator. AraC family	2.08	0.91
3311	Acetyltransferase	1.63	0.73
3313	Hypothetical protein	0.91	0.31
3314	N-5'-phosphoribosyl)anthranilate isomerase	0.48	0.12
3315	Hypothetical protein	0.7	0.08
3320	Oligopeptide transporter. permease protein	3.27	1.58
3321	Oligopeptide transporter. permease protein	2.93	0.77
3322	Oligopeptide-binding protein OppA	3.19	1.55

3323	Oligopeptide transporter. ATP-binding protein	2.69	0.24
3324	Oligopeptide transporter. ATP-binding protein	3.94	3.28
3325	Permease. Na+/H+-dicarboxylate symporter	1.8	0.71
3326	Aldehyde ferredoxin oxidoreductase	3.06	0.2
3327	Ferredoxin	2.83	0.57
3330	O-linked N-acetylglucosamine transferase	1.11	0.32
3332	Putative ferredoxin	1.88	0.52
3334	Monomethylamine corrinoid protein MtmC2	11.46	7.24
3335	Monomethylamine:corrinoid methyltransferase MtmB2	10.91	11.2
3336	Monomethylamine:corrinoid methyltransferase MtmB2 (C-terminal domain)	12.59	8.49
3338	Hypothetical protein	3.23	1.83
3339	Hypothetical protein	2.84	1.66
3340	Hypothetical protein	2.52	0.81
3342	Conserved protein	0.32	0.13
3345	Hypothetical protein	0.17	0.11
3346	Hypothetical protein	2.78	0.39
3350	Hypothetical protein	2.47	1.08
3351	Hypothetical protein	3.07	0.47
3352	Hypothetical protein	1.4	0.09
3370	Hypothetical protein	2.02	0.45
3371	Conserved protein	1.11	0.52
3372	new orf	0.73	0.28
3373	new orf	0.6	0.29
3376	new orf	1.03	0.69
3377	new orf	1.61	1.69
3380	new orf	1.53	2.5

3385	new orf	0.57	0.78
3387	new orf	0.61	0.04
3389	new orf	2.69	2.99
3390	new orf	15.56	19.8
3393	new orf	2.69	0.22
3395	new orf	1.35	0.87
3396	new orf	1.29	0.18
3404	new orf	1.1	0.84
3405	new orf	2.51	2.13
3407	new orf	1.84	1.18
3410	new orf	1.55	0.2
3413	new orf	0.33	0.09
3414	new orf	0.83	0.29

Table S8: Fold regulation of genes involved in cell appendix formation in cells forming aggregates after virus stress vs. unstressed cells determined by microarray analyses.

ORF #	annotation	predicted function	fold regulation
MM316	FlaJ		1
MM317	FlaI		n. d.
MM318	FlaH		n. d.
MM322	Flagellin B1 precursor		n. d.
MM323	Flagellin B1 precursur		1
MM412	FlaJ		1
MM413	FlaI		n. d.
MM414	FlaH		n. d.
MM418	Flagellin B1		n. d.
MM937	FlaJ		n. d.
MM938	FlaI		n. d.
MM939	FlaH		~1
MM2020	twiching mobility		0,5 +/- 0,1
MM477	hypothetical protein	Pili_N Domain	2,9 +/- 0,5
MM527	hypothetical protein	n. d.	n. d.
MM1118	hypothetical protein	Disaggr. Domain	1
MM1120	hypothetical protein	Disaggr. Domain	1

MM1510	hypothetical protein	Pilin_N Domain	
MM1511	hypothetical protein	Pilin_N Domain	1
MM1570	hypothetical protein	n. d.	n. d.
MM2543	hypothetical protein	n. d.	n. d.
MM2828	hypothetical protein	n. d.	n. d.